## Distribution of AbrB and Abh on the *Bacillus subtilis* genome and its implication on their function

枯草菌ゲノム上の AbrB と Abh の分布と、その機能の解釈

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# 題目 Distribution of AbrB and Abh on the *Bacillus subtilis* genome and its implication on their function

AbrB is a global transcriptional regulator of *Bacillus subtilis* that represses the expression of many post-exponential genes during exponential growth. Although, AbrB has been extensively studied both genetically and biochemically and many of its DNA-binding sites are known, it is still unclear how this protein selects the correct set of binding sites to achieve its proper function, since its binding region so far determined possesses no apparent consensus sequence. AbrB paralog Abh has high structural similarity to AbrB in its DNA-binding domain, suggesting a common structural basis for their DNA binding. However, they possess a subtle structural difference which may play an important role in DNA target specificity. Abh has been shown to bind and regulate some of the same promoter with AbrB, but its regulatory role has not been studied systematically.

Here, for the first time, we report the *in vivo* distribution of AbrB and Abh on the *B*. *subtilis* genome during exponential growth using a modified ChIP-chip method, ChAP (Chromatin affinity precipitation)-chip method. We demonstrated that AbrB and Abh bind to 643 and 411 sites, respectively throughout the genome both in protein coding (58%) and intergenic (42%) regions and that almost all Abh-binding sites overlapped with those of AbrB in wild type cells. We showed that AbrB and Abh form complexes *in vivo* and that hetero-complex were dominant to homo-complexes. ChAP- chip analysis of *abrB* and *abh* mutants indicated that AbrB/Abh binding regions contain various types of sequences with

different specificities and affinities for AbrB/Abh homomers and heteromers. We identified 3 major types of sequences composing of two TGGNA motifs connected by A/T-rich sequences, differing in orientation and spacing, which contribute significantly to effective binding of different composition of AbrB and Abh complexes to genome. We assessed the direct involvement of such complexes in control of gene expression using transcriptome analysis. Our data confirmed that AbrB usually acts as a repressor, although it also activates a number of transcriptional units (TUs). In contrast, the ability of Abh to act as a transcriptional regulator was limited under our experimental conditions. We found that changes in AbrB/Abh levels affect their binding at several promoters and consequently transcriptional regulation. Interestingly, among of AbrB- and Abh-binding sites, only 103 AbrB- and 7 Abh-binding sites were suggested to directly affect transcription while most of their binding events had no impact on transcription level. This result suggests an interesting possibility that AbrB/Abh binding is analogous to nucleoid-associated protein binding in Escherichia coli. Thus, our results reveal novel, important properties of AbrB and Abh, and our work contributes to a deeper understanding of the cellular roles played by AbrB and Abh as transcriptional regulators, and possibly as nucleoid architectural proteins.

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#### **INTRODUCTION**

*Bacillus subtilis* is a Gram positive, spore-forming bacterium which has been used as a model bacterium in biochemical, genetic and molecular biological studies. The availability of complete genome sequence data of this bacterium has accelerated *B. subtilis* research in systematic genome-wide analyses of gene functions, which will enable discovery of functional networks of gene products that support dynamic microbial life.

B. subtilis is well known for its ability to differentiate from vegetative growing cells into metabolically inactive spore, accompanied by the preceeding production of various extra-cellular enzymes and antibiotics valuable for industrial application, contributing this organism to become interesting model bacterium. These physiological changes are induced, once cells sense suboptimal environmental conditions and then undergo transition phase from the exponential growth to the stationary phase. This process requires re-direction of the expression of various genes involved in the adaptive response and survival. Such genes are normally silenced by a group of proteins called "transition-state regulators" which primarily function to prevent inappropriate expression of the genes during exponential growth. Well characterized members of this class of regulatory protein are AbrB, Hpr, SinR and CodY (Phillips & Strauch, 2002; Strauch & Hoch, 1993). All are DNA-binding global transcriptional regulators and there are many overlaps between their individual regulon. AbrB is a key transition state regulator which interconnects most of these regulators (Figure 1). During the transition phase, AbrB has been known to play an essential role in the reorganization of expression of more than 100 post-exponential-phase genes with different biological functions including biofilm formation, antibiotic production, motility, development of competence for DNA uptake, synthesis of extracellular enzymes, and sporulation. Although the protein function has been extensively studied both genetically and biochemically, its molecular

mechanism how this protein selects the correct set of binding sites remains mysterious since its binding sequence so far determined share no apparent consensus sequence.





### **1.** Regulation of the *abrB* expression

The *abrB* (<u>Antibiotic resistance protein B</u>) gene was first isolated as a gene whose inactivation suppresses a mutation of a master regulator for entry to the sporulation process, Spo0A. The *spo0A* null mutant shows impairments both in sporulation and in a wide variety of cellular processes induced in the transition stage, such as antibiotic production, motility, and genetic competence. In the suppressor mutant, most of the pleiotropic effects during the transition state are restored, but sporulation was not. Thus, *abrB* was discovered as a "transition-state regulator".

AbrB is a 94 amino acids protein with a molecular weight of 10.4 kDa. The *abrB* gene is transcribed as a single transcriptional unit (TU) from two promoters, P1 and the downstream P2, which are differentially regulated by Spo0A and AbrB itself (Perego et al, 1988). Spo0A repressed *abrB* expression only from P2 promoter, whereas AbrB negatively regulate its own expression from both P1 and P2 promoters. Negative regulation from P2 promoter occurs at only high concentration of AbrB and Spo0A. Expression of AbrB is growth-phase-dependent; it is synthesized at high levels from lag to the exponential phase, but its expression level decreases when the cell enters stationary phase. Rapidly reduction of AbrB expression at entry into the stationary phase is mediated by the phosphorelated form of the Spo0A (O'Reilly & Devine, 1997; Strauch et al, 1990). However, it was reported that a low level of AbrB is still expressed during stationary phase from P1 promoter which is not repressed by Spo0A (Strauch et al, 1989b). Recently, it has been reported that Spo0A activates expression of AbrB, antirepressor of AbrB, which forms a complex with AbrB and prevents the latter protein from binding to DNA (Banse et al, 2008). This mechanism might work to inactivate remaining AbrB in the stationary phase.

## 2. Mode of transcription regulation by AbrB

AbrB was known to regulate expression of numerous genes with distinct biological functions in 3 different ways. (1) AbrB mainly acts as a transcriptional repressor, and genes under this mode of control are constitutively expressed in *abrB* mutant. (2) AbrB acts as "preventor"; *abrB* mutation restores expression of some genes under its control during the transition-state in *spo0A* mutant cells, but does not cause their constitutively expression during vegetative growth in the wild type background, indicating that AbrB acts in concert with other regulators in the regulatory network of transition state regulators shown in Figure 1. Expression of *spoVG*, *aprE* and *dpp* genes is controlled by AbrB in this manner (Ferrari et al, 1988; Slack et al, 1991; Zuber & Losick, 1987). (3) AbrB acts as an activator of some genes, such as *rbs*, *citB*, and *hut* (Fisher et al, 1994; Kim et al, 2003; Strauch, 1995a). However, no direct interaction of AbrB with RNA polymerase has yet been demonstrated.

AbrB has been demonstrated to have specific *in vitro* DNA-binding activity towards promoter sequences of genes which were genetically demonstrated to be under the control of AbrB (Strauch, 1995b; Strauch, 1995c; Strauch et al, 1989b). Although AbrB-binding sites have been extensively studied *in vitro*, it is still unclear how AbrB selects binding sites. *In vitro* selection of optimal AbrB-binding sites identified a relevant TGGNA motif (Xu & Strauch, 1996); however, this motif did not resemble known AbrB binding sites in the *B. subtilis* genome, for which the consensus sequence WAWWTTTWCAAAAAAW had been suggested (Strauch, 1995b). To date, examination of more than 40 chromosomal AbrB binding sites has failed to identify a consensus sequence that adequately explains AbrB site selection and recognition, and it has been hypothesized that AbrB binding instead requires a specific three-dimensional conformation of the DNA helix (Bobay et al, 2004; Bobay et al, 2006; Phillips & Strauch, 2002).

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## 3. Structure of the AbrB protein

Purified full length AbrB exists as tetrameric form in solution (Benson et al, 2002; Bobay et al, 2004; Cavanagh et al, 2002). AbrB contains two functional domains, DNA binding and multimerization domains. The N-terminal domain (1-53 residues) functions as DNA binding domain and also has ability to dimerize, while the C-terminal domain (54-92 residues) has solely an ability to dimerize (Furbass & Marahiel, 1991; Xu et al, 1996). N-terminal domains of two AbrB molecules form a single DNA-binding domain with extensive interactions making a domain swap fold so called a swapped-hairpin barrel (Figure 2B) (Bobay et al, 2005; Coles et al, 2005), and two AbrB dimers further multimerize to a tetramer via C-terminal interactions, yielding a protein with a stable DNA-binding activity (Figure 2C) (Benson et al, 2002; Bobay et al, 2004; Vaughn et al, 2001; Xu & Strauch, 2001; Yao & Strauch, 2005).

The secondary structure of the AbrB N-terminal domain monomer contains four  $\beta$ -strands, one  $\alpha$ -helix, and 3 loop regions as illustrated in Figure 2A. AbrB has a considerable amount of positive charge resulting from arginine and lysine residues, and mutagenic analysis identified residues R8, R15, R23, and R24 as critical for DNA binding of AbrB (Bobay et al, 2005; Sullivan et al, 2008; Vaughn et al, 2000). The NMR studies of the DNA-binding domains of AbrB and paralogs thereof, together with re-evaluation of previous experimental results, allowed a structural model of the complex between the N-terminal domain of AbrB and the target DNA sequence to be constructed. The model indicates that structural flexibility in the loop regions LP1, which connect  $\beta$ 1 and  $\beta$ 2, and LP2, which connect  $\alpha$ 1 and  $\beta$ 3, of the DNA-binding domain of the AbrB monomer allows AbrB to appropriately reorient during complex formation with target DNA sequences, enabling the arginine residues (R8, R15, R23, and R24) to make suitable contact with various DNA targets (Sullivan et al, 2008). The positioning of AbrB tetramer in complexes with DNA target is illustrated in Figure 2C.



Figure 2. Secondary and quaternary structure of AbrB. (A) Schematical diagram showing the positions of the  $\alpha$ -helical and  $\beta$ -strand secondary structure, as well as loop regions of AbrB N-terminal DNA binding domain. (B) The a swapped-hairpin barrel formed by of two molecules of AbrB N-terminal domain. (C) Positioning of AbrB tetramer in complexes formation with DNA. From (Sullivan et al, 2008)

## 4. Characteristics of AbrB as a nucleoid associated protein

Several proteins participating in organization of genomic DNA into nucleoids, nucleoidassociated proteins, also act as transcriptional regulators in *E. coli*, and the proteins include HU, H-NS, StpA, Fis, Lrp and IHF (Ali Azam et al, 1999). However, homologs of these proteins are absent from *B. subtilis*, with the exception of HU. AbrB was once considered to be a nucleoidassociated protein because, although the proteins are not related in amino acid sequence, the growth cycle-dependent expression of *abrB* is similar to that of *fis* in *E. coli* and *Salmonella typhimurium* (O'Reilly & Devine, 1997). AbrB possesses the general characteristics of nucleoid proteins identified in *E. coli*. Such proteins are small in size and abundant, with a high proportion of positively charged amino acids. The proteins participate in transcriptional regulation of various genes with diverse functions. Furthermore, the proteins bind to degenerate consensus sequences biased toward a preponderance of A and T residues, and such a binding event generates a bend in DNA (Strauch & Ayazifar, 1995). However, the role of AbrB in organization of the *B. subtilis* nucleoid structure has not been determined.

#### 5. Conservation of AbrB protein in bacteria

AbrB orthologs and paralogs have been found in genomic sequences of all *Bacillus*, *Clostridium*, and *Listeria* species. AbrB has been shown to be involved in induction of virulence factors in *Bacillus cereus* and *Bacillus anthracis* (Lucking et al, 2009; Saile & Koehler, 2002). In addition, AbrB sequences are found sporadically in various bacterial species such as *Geobacillus*, *Oceanobacillus*, *Pyrococcus*, *Pasteria*, *Staphylococcus*, *Streptococcus*, *Thermoanaerobacter*, *Heliobacterium etc.* and also in archaea, (MBGD, <u>http://mbgd.genome.ad.jp/</u>), although the functions of the encoded proteins have not yet been determined. Furthermore, AbrB-like proteins, with DNA-binding motifs similar to those of AbrB have been widely identified in cyanobacteria (Coles et al, 2005; Ishii & Hihara, 2008), and regulate several physiological and metabolic processes, including carbon and hydrogen metabolism, nitrogen fixation, and toxin production (Agervald et al, 2010; Ishii & Hihara, 2008; Lieman-Hurwitz et al, 2009; Oliveira & Lindblad, 2008; Shalev-Malul et al, 2008).

*B. subtilis* expresses two AbrB paralog, Abh and SpoVT, with N-terminal DNA-binding domains highly homologous to that of AbrB but diverge substantially in sequence and size of the C-terminal domain. The three-dimensional structures of the DNA-binding domains of these proteins are similar, suggesting a common structural basis for DNA binding. However, subtle structural differences between the proteins have also been identified and these may play important

roles in the specificity of DNA targeting (Bobay et al, 2006; Sullivan et al, 2008). SpoVT is a regulator of forespore-specific genes that are expressed at later stages of sporulation depending on sigma-G activity, and SpoVT is not a transition-state regulator (Bagyan et al, 1996).

Abh is encoded by *abh* gene. It composed of 92 amino acids with molecular weight of 10.1 kDa. Abh show 58% overall identity to AbrB (Figure 3) and its N-terminal domain has 74% identity to the DNA binding domain of AbrB. It is highly expressed during exponential phase as is AbrB. Transcription of *abh* gene is under the control of three ECF sigma factors, largely by SigX and a smaller contribution from SigM, and SigW (Luo & Helmann, 2009; Murray et al, 2009). Mutation of *abrB* resulted in an approximately twofold increase in *abh* transcription (Strauch et al, 2007) suggesting that AbrB regulate abh expression. Strain with a mutation in abh showed alteration in the production of antimicrobial compounds directed against some other Bacillus species and Gram-positive microbes and alteration in biofilm architecture during biofilm formation (Lopez et al, 2009; Luo & Helmann, 2009; Murray et al, 2009; Strauch et al, 2007). Abh has been shown to regulate some of the same operons with AbrB. Genes which are identified to be regulated by Abh include five well-characterized antimicrobial operons, sunA, sboA-alb, yqxM-sipW-tasA, sdpABC and skfABCDEFGH, sigW encoding an alternate RNA polymerase sigma factor directing the transcription of an antibiosis regulon, *slr* encoding a transcriptional activator of competence development and sporulation genes, and eps operon encoding exopolysaccharide for biofilm formation. Four of these are negatively controlled, *sboA-alb*, *yqxM*sipW-tasA, sdpABC and skfABCDEFGH, while the other four are positively controlled, sunA, sigW, slr and eps operon. Clear binding of Abh were mapped in the promoter region of sunA and sboA suggesting the direct regulation. Its binding sites in these two promoter regions were overlapped with AbrB binding sites, but different slightly in the appearance of regions protected as determined by in vitro DNaseI footprinting (Strauch et al, 2007). The studies suggested that the

role of Abh at *sunA* operon is to counteract repression mediated by AbrB (Luo & Helmann, 2009). However the molecular mechanism of action is still unclear. Neither the regulatory role of Abh nor the molecular mechanism of Abh action has been systematically studied.

	(1)	1		1	0			20	)			30				40				50	)	
AbrB 168	(1)	<mark>MKS</mark> T	g <mark>i</mark> vi	RKV	DEI	GR <mark>N</mark>	7 <mark>V</mark> I	PIH	LRF	TL.	G <mark>IA</mark>	EKI	AL	EI	(VD	d <mark>ek</mark>	II	LK	KYB	K PI	NMT	<mark>C</mark> Q
Abh 168	(1)	MKS I	G <mark>V</mark> VI	RKV	DEI	GR <mark>1</mark>	. <mark>V</mark> M	PIE	ELRF	AL I	D <mark>IA</mark>	IKI	SI	EF	VD	G <mark>D</mark> K	II	LK	KYI	K P I	HGV	<mark>C</mark> L
Consensus	(1)	MKS	GIVI	RKV	DEI	GRI	IVI	PIE	ELRF	L	IA	KI	AII	ΞŦ	FVD	DK	ΙI	LΚ	KYI	KΡ		С
	(1)		60			70	)			80					94							
AbrB 168	(1) (1)	V <mark>TGE</mark>	60 <mark>VS</mark> D	<mark>DN</mark> I	.KL <mark>Z</mark>	70 <mark>A</mark> G <mark>GF</mark>	) <mark><l< mark="">V</l<></mark>	<mark>LS</mark> I	K <mark>eg</mark> a	80 EQ	IIS	S <mark>EΙÇ</mark>	2NQ	LQ1	94 NLK							
AbrB 168 Abh 168	(1) (1) (1)	VTGE MTGE	60 VSD ITS	<mark>DN</mark> I ENK	KL <mark>X</mark>	70 AG <mark>GI</mark> N <mark>GI</mark>	) <lv <it< th=""><th>LS LS</th><th>K<mark>EG</mark> P<mark>EG</mark></th><th>80 EQ QL</th><th>IIS LLE</th><th>S<mark>EIÇ</mark> C<mark>EIÇ</mark></th><th>0NQ DAA</th><th>LQI LKI</th><th>94 NLK E</th><th></th><th></th><th></th><th></th><th></th><th></th><th></th></it<></lv 	LS LS	K <mark>EG</mark> P <mark>EG</mark>	80 EQ QL	IIS LLE	S <mark>EIÇ</mark> C <mark>EIÇ</mark>	0NQ DAA	LQI LKI	94 NLK E							

**Figure 3. Alignment of AbrB and Abh**. Identical residues are shown in yellow, similar residues are shown in green and dissimilar residues are show in white.

Here, for the first time, we determined the *in vivo* distribution of AbrB binding on the *B*. *subtilis* genome during exponential growth when AbrB principally functions, using a modified ChIP-chip method, ChAP (Chromatin affinity precipitation)-chip method (Ishikawa et al, 2007). In parallel, we studied binding of Abh, whose regulatory roles have not been systematically evaluated to date. Furthermore, we analyzed changes of AbrB/Abh binding profiles and transcriptome profiles in *abrB*- and *abh*-deleted cells, to investigate detailed molecular actions of AbrB/Abh.

## **METERIALS and METHODS**

## 1. Bacterial strains, and growth conditions

The *B. subtilis* strains used in the present study, the wild-type 168 strain and derivatives thereof, are listed in Table 1. The methods to construct mutant strains are described below. Luria-Bertani (LB) medium, supplemented with appropriate antibiotics [10  $\mu$ g/ml kanamycin (Km), 150  $\mu$ g/ml spectinomycin (Spec), 0.5  $\mu$ g/ml erythromycin (Erm), and/or 5  $\mu$ g/ml chloramphenicol, (Cm)], was used for cell growth. Cells growing exponentially at 37°C in LB medium supplemented with appropriate antibiotic(s) were inoculated into larger volumes of culture medium, without any antibiotic, at a commencement OD<sub>600</sub> value of 0.01.

Strains	Genotype <sup><i>a</i></sup>	Source or reference <sup>b</sup>	
168	trpC2	Pasteur stock	
OC001	168 abrB -2HC -spec	This study	
OC002	168 abh-2HC-cm	This study	
OC003	168 abrB ::spec	This study	
OC004	168 abh ::km	This study	
OC005	168 abrB::spec_abh::km	$OC003 \rightarrow OC004$	
OC006	168 abrB-2HC-spec abh ::km	$OC004 \rightarrow OC001$	
OC007	168 abh -2HC -cm abrB ::spec	$OC003 \rightarrow OC002$	
OC008	168 rsiX :: erm		
OC009	168 pO- <i>abh</i>		

 Table 1. B. subtilis strains used in this study

<sup>*a*</sup> Antibiotic resistance genes are expressed as follows: *spec*, spectinomycin; *cm*, chloramphenicol; *km*, kanamycin; *erm*, erythromycin.

<sup>b</sup> Arrows indicate construction of new strains by transformation with genome DNA

## 2. Primers

## Primers used in this study are listed in Table 2.

Table	2	Duimon	maad	÷	this	atuda
Table	<i>z</i> .	Primers	usea	m	tnis	study

Name	sociones <sup>a</sup> b	Position on B. su	btilis genome or	- Reference	
Ituite	sequence	start	end	strand	Reference
2H	TCAATAGTAAACAAAATGATTGACG	45,235	45,259	-	
abrB-FR-2HC	ggtgatgcgatcctctcatTTTAAGGTTTTGAAGCTGGTTTTG	44,849	44,872	+	
abrB-BF	cggaaggatactacatcctggCCTTAAATAATCATTTCTTGTAC	44,833	44,855	-	
abrB-BR	AGAAAAGAAGAAGGAGCTTGAAGCC	44,377	44,401	+	
abh-FF	TATCTTGTAATTCTTATAGAAAGCG	1,517,050	1,517,074	+	
abh-FR-2HC	ggtgatgcgatcctctcatTTCTTTTAAAGCGGCTTGAATTTC	1,517,424	1,517,447	-	
abh-BF	cggaaggatactacatcctggCGCTTTAAAAGAATAAAATTATGC	1,517,435	1,517,458	+	
abh-BR	TTTTCTTAACCAGCTGCTGTTTC	1,517,813	1,517,835	-	
abh2HC_CF	GGTGTGCGTCGGTAAAGAAATGTTTTTG	1,516,964	1,516,991	+	
abh2HC_CR	GCATTCGTTTGAAATACGATTTCCTGC	1,517,900	1,517,926	-	
abrB2HC_CF	AAAGGATTTTTAGTAGGATAATAGC	45,337	45,361	-	
abrB2HC_CR	GCATTAACAGCTCTTATTGCTTCAGG	44,300	44,325	+	
abrB-metS-F	AGGACGAGAGCGGCGATAAG	45,569	45,588	-	
abrB-metS-R	gctcttctggtggagtctatccCATTCTCCTCCCAAGAGATAC	45,134	45,154	+	
abrB-yabC-F	cggaaggatactacatcctggAAACTTGCAGGCGGTAAATTG	44,915	44,935	-	
abrB-yabC-R	GAGATCGGGAAATTGCTGTAACAC	44,487	44,510	+	
U-abh-F	CTGATGGTGTGCAAACGACTACGTTCGG	1,516,567	1,516,594	+	
U-abh-R	gctcttctggtggagtctatccGGATGTACCTCAATATATCG	1,517,104	1,517,123	-	
D-abh-F2	cggaaggatactacatcctgGCTGCTTCTCGAAGAAATTCAAGCC	1,517,411	1,517,435	+	
D-abh-R	AACCCGGTTATAGATGCCCACGCTTGG	1,517,951	1,517,977	-	
abh-gwF	aaaaagcaggctcgCATCCTTAAAACATTACATGAG	1,517,119	1,517,140	+	
abh-gw-r	agaaagctgggtcGCATAATTTTATTCTTTTAAAGCGG	1,517,434	1,517,458	+	
abrB-B1-F	aaaaagcaggctcgATTTAAACAAATAAGTATCTCTTGG	45,144	45,168	-	
abrB-B1-R	AACTACACGTCCTAATTCATCAAC	45.080	45,103	+	
abrB-B2-F	CGTAAAGTTGATGAATTAGGAC	45.088	45,109	-	
pPAL7-abrB-F1	aagetttgAAATCTACTGGTATTGTACGTAAAGTTG	45.100	45,127	-	
pPAL7-abrB-R	aattettaTGATTATTTAAGGTTTTGAAGCTGG	44.843	44.867	+	
pPAL7-abh-F	aaggetttgAAATCAATAGGTGTTGTGAGAAAAG	1 517 175	1 517 199	+	
pPAL7-abh-R	aattettaGCATAATTTTATTCTTTTAAAGCGG	1.517.434	1.517.458	_	
DrsiX-F-f	AGAAGACCTTCTTCAAGAGGTTTATATCCG	2 414 287	2 414 316	-	
DrsiX-F-r	actettetagtggagtetatec CCTGAGGGGAACGATGGTCTTTAACTGCCG	2 413 801	2 413 830	+	
DrsiX-B-f		2 412 810	2 412 839	-	
DrsiX-B-r	GGATTGCCGATTCCAGCAAAGCAAGGATAGG	2 412 352	2 412 381	+	
sigX_u_F		2,112,392	2 414 423		
rsiX-d-r	AAGTCGTGATTTGACATCACCACATAGACG	2,412,234	2,412,263	+	
pPAL7-F		nPAL 7	2,112,205		Bio-Rad
pPAL7-R	ATTCCTCACCCCTCCCACCAC	pPAL7			Bio-Rad
DC-2HC-F	ATCAGAGGATCGCATCACC	pMUTin2HC			This study
DC-2HC-R	actictt ctagtagagt ctatecTCATCTATTTATTGAACCTCC	pMUTin2HC			This study
rPCR_CmF2	gettereggeggagetareeren en e	pDI T3			Morimoto T et al 2002
rPCR-CmP2	ggatagattetagtatatagtatagtetcatteggCCCCTACACCATCTCCCACC	pDL13			Morimoto T. et al. 2002
rPCR-KmF		pDG780			Guerout-Fleury AM et al 1995
rPCR-KmR		pDG780			Guerout-Fleury AM et al. 1995
rDCP SpacE		pDG700			Ishikawa S at al. 2006
rPCR-SpecR		pJL02 pH 62			Ishikawa S et al. 2000
rPCP ormP		pJL02			This study
rPCP ormE	ggatagattetaataataagageeeeeeeeeeeeeeeee	pMUTm2HC			This study This study
mM121EeDottD2		pMUTallo &	MITTOLIC		This study Johiltorno S at al 2006
A domton ottD1	ggggaccactitgtacaagaaagctgggtcGAGCTCTCATCTATTTAATGG	pivit Tilinis & j	pwiutilizhe		This study, Islikawa S et al, 2000
Adapter attD1	GGGGGGAGAGIIIGIACAAAAAGCAGGUUG	and Sile			Invitrogen
Adapter-attB2	GGGGAUUAUTTTGTAUAAGAAAGUTGGGTU	antB2 site	MUTEDIC		This study, Jabiltonia S at -1 2004
TorDEn-T		pNUTTHE & ]	MUTERAUC		This study, Islikawa S et al, 2006
TERSINALD		pNU ImHis & j	pivi O Tin2HC		mis study, Isnikawa S et al, 2006
PDONK-F	TUGUGTTAAUGUTAGUATUGATUTUG	pDONK201			Invitogen
PDONK-K	GTGTCTCAAAATCTCTGATGTTAC	pDUNK201			invitrogen
2HC-F	gcc <u>gtcgacgaattccccgggctcgag</u> ATGAGAGGATCGCATCACC	pO2HCGW			This study
2HC-R	gcc <u>gagctc</u> TCATCTATTTATTGATGCTGCGACAAGGCAGG	pO2HCGW			This study

<sup>a</sup> Lowercase letters indicate annealing sequences for recombinant PCR.
 <sup>b</sup> Underlined sequences indicate recognition sites of restriction enzymes.

## 3. Construction of *B. subtilis* strains expressing AbrB C-terminally tagged with 12 histidines and a chitin-binding domain (AbrB-2HC), and an analogous form of Abh (Abh-2HC)

To construct an integration vector permitting fusion of the 2HC (12 histidines plus a chitinbinding domain) coding sequence at the end of a target gene, pO2HCGW was first made by insertion of an rfA cassette (Gateway Vector Conversion System; Invitrogen) into the *Stu*I site of plasmid pO2HC (Ishikawa et al, 2006). The Gateway cassette fused with the 2HC-encoding sequence was amplified from the plasmid using 2HC-F and 2HC-R primers, and cloned between the *Sal*I and *Sac*I sites of plasmid pMUTinNC (Morimoto et al. 2002), to create plasmid pMUTin2HC.

To construct a DNA cassette containing *abrB-2HC*, the *abrB* gene without the termination codon was amplified from *B. subtilis* genomic DNA using primers *abrB*-FF and *abrB*-FR-2HC. The coding sequence of the 2HC tag was amplified from plasmid pMUTin2HC using primers DC-2HC-F and DC-2HC-R. A spectinomycin-resistance gene was amplified from plasmid pJL62 (Ishikawa et al, 2006) using primers rPCR-SpecF and rPCR-SpecR. The downstream region of the *abrB* gene was amplified from *B. subtilis* genomic DNA using primers abrB-BF and abrB-BR. Next, the four fragments were joined by recombinant PCR using primers abrB-FF and abrB-BR, and employed to transform wild-type *B. subtilis* cells followed by double cross-over recombination, with selection for spectinomycin resistance, to create the OC001 strain.

The Abh-2HC-expressing strain was similarly constructed. The *abh* gene without the termination codon was amplified from *B. subtilis* genomic DNA using primers abh-FF and abh-FR-2HC. The 2HC coding sequence was amplified as described above. A chloramphenicol-resistance gene was amplified from plasmid pDLT3 (Morimoto et al, 2002) using the primers rPCR-CmF2 and rPCR-CmR2. The downstream region of the *abh* gene was amplified from *B. subtilis* genomic DNA using primers abh-BF and abh-BR. Next, the *abh* and 2HC fragments were

joined using primers abh-FF and DC-2HC-R, and the chloramphenicol resistance gene and the downstream region of *abh* were connected using primers rPCR-CmF2 and abh-BR. Finally, the two fragments thus obtained were joined employing primers abh-FF and abh-BR, and next used to transform cells of strain 168, followed by selection for chloramphenicol resistance, to obtain the OC002 strain.

#### 4. Construction of $\triangle abrB$ , $\triangle abh$ , and double mutant strains

To obtain the *abrB* and *abh* deletion mutants (strains OC003 and OC004, respectively), an antibiotic-resistance cassette, encoding either spectinomycin- or kanamycin-resistance, and flanked by upstream and downstream regions of *abrB* or *abh*, was used.

Regions upstream and downstream of *abrB* were amplified from *B. subtilis* genomic DNA using the primer sets abrB-metS-F/abrB-metS-R and abrB-yabC-F/abrB-yabC-R, respectively. A spectinomycin-resistance gene with a promoter region was amplified from plasmid pJL62 (Ishikawa et al, 2006) using primers rPCR-SpecF and rPCR-SpecR. The resulting three fragments were joined by recombinant PCR using primers abrB-metS-F and abrB-yabC-R, and integrated into the *B. subtilis* genome by double crossover recombination with selection for spectinomycin-resistance.

The upstream and downstream regions of *abh* were amplified from *B. subtilis* genomic DNA using the primer sets U-*abh*-F/U-*abh*-R and D-*abh*-F2/D-*abh*-R, respectively. A kanamycin-resistance gene with a promoter was amplified from plasmid pDG780 (Guerout-Fleury et al, 1995) using the primers rPCR-KmF and rPCR-KmR. The resulting three fragments were joined by recombinant PCR employing primers U-*abh*-F and D-*abh*-R, and integrated into the *B. subtilis* genome with selection for kanamycin-resistance.

*abrB abh* double mutant strain was obtained by transformation of the OC004 strain with the genomic DNA of OC003 strain (OC005). The genomic DNAs of OC004 and OC003 strains were also employed to transform the OC001 and OC002 strains to obtain OC006 and OC007 strains, respectively, as indicated in Table 1.

#### 5. Antibody production and purification

Plasmids permitting overexpression of AbrB-12His or Abh-12His in E. coli cells were constructed using the recombinational Gateway cloning system (Invitrogen). To obtain an abrB-12xhis fragment, the 5' portion of abrB together with the SD sequence was amplified from B. subtilis genomic DNA using primers abrB-B1-F and abrB-B1-R. The 3' portion of abrB fused with 12xhis was amplified from the pMUTinHis $\Delta abrB$  plasmid (Ishikawa et al., unpublished), a derivative of pMUTinHis (Ishikawa et al., 2006) harboring 250 bp of the 3' portion of *abrB*, without the stop codon, using primers abrB-B2-F and pM12HisR-attB2. Next, the two fragments were fused by recombinant PCR using primers abrB-B1-F and pM12HisR-attB2. The abh-12xhis fragment was amplified from genomic DNA of the strain 168abhHis, in which the 12xhis sequence had been fused to the 3' end of the abh gene by a technique involving use of the pMUTinHis $\Delta abh$  plasmid (Ishikawa et al., unpublished), employing the primers abh-gwF and pM12HisR-attB2. Recombination sites susceptible to recombinase action were added to the amplified fragments, by PCR, using the adapter primers Adapter-attB1 and Adapter-attB2, and the fragments were cloned into the entry vector pDONR201 (Invitrogen), followed by transfer to the pOGW destination vector (Ishikawa et al. 2006), according to the Gateway technology instructions. The resulting plasmids pO-abrB12xhis and pO-abh12xhis were transformed into E. coli C600 and DH5a, respectively.

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*E. coli* C600 cells harboring pO-abrB12xhis and DH5 $\alpha$  cells with plasmid pO-*abh12xhis* were grown in 400 ml aliquots of LB medium supplemented with 5 µg/ml tetracycline, at 37°C with vigorous shaking. When cell cultures attained OD<sub>600</sub> values of 1.0, IPTG was added to a final concentration of 1 mM, and cells were cultured for 3 further hours. Next, cells were harvested by centrifugation and washed once with Tris-buffered saline (50 mM Tris-HCl [pH 7.5], with 150 mM NaCl). Cells were disrupted by sonication on ice using an Astrason Ultrasonic Processor XL (Misonix) for 10 minutes (4 sec "on" and 10 sec "off", at output level 5) in 12 ml UT buffer (100 mM HEPES [pH 7.5], 50 mM imidazole, 8 M urea, 500 mM NaCl, 0.3% [v/v] Triton X-100, and 1 mM DTT) containing 1 mM PMSF. After removal of cell debris by centrifugation, 900 µl amounts of MagneHis (Promega) were added to supernatants, followed by incubation at room temperature for 2 hours with gentle rotation. The MagneHis beads were next washed five times with 15 ml amounts of the same buffer, and bound proteins were eluted in 5 ml UT buffer containing 250 mM imidazole.

Anti-AbrB and -Abh antibodies were raised in rabbits by injection of purified AbrB-12xHis and Abh-12xHis proteins, respectively, at the facilities of the Medical & Biological Laboratories Co., Ltd, Japan. Crude antibodies against AbrB and Abh were subjected to purification by affinity chromatography, according to the protocol described in Molecular Cloning: A Laboratory Manual (Sambrook & Russell, 2001), to remove antibodies that crossreacted with AbrB and Abh or with other *B. subtilis*-encoded proteins. In brief, all proteins extracted from OC003 ( $\Delta abrB$ ) and OC004 ( $\Delta abh$ ) cells were bound to Affi-Gel 10 (Bio-Rad) prior to packing into columns, and anti-AbrB and -Abh antibodies were incubated with resin to which proteins from  $\Delta abrB$  and  $\Delta abh$  cells, respectively, were bound. Antibodies in the flowthrough fractions were collected, and used in Western blotting experiments.

#### 6. In vivo interaction of AbrB and Abh

Thirty-five milliliter amounts of exponentially growing cells cultured to an  $OD_{600}$  of 0.4 were harvested by centrifugation. Cell pellets were washed with 10 mL of 50 mM HEPES pH 8.0 and resuspended in 1.5 mL of the same buffer. Dithiobis(succinimidyl propionate) (DSP) (Pierce) was added to cell suspensions to a final concentration of 2 mM, and cells were incubated on ice for 5 min, 15 min, or 25 min, followed by quenching of the cross-linking reaction by addition of 1 M Tris-HCl (pH 7.5) to a final concentration of 20 mM, followed by incubation on ice for 15 min. Next, cells were washed once with 1.5 mL TBS buffer (50 mM Tris-HCl [pH 7.5] and 150 mM NaCl) and stored frozen at -80°C. The frozen cells were dissolved in 1.4 mL buffer containing 100 mM Tris-HCl, 250 mM NaCl, 20% (v/v) glycerol, 50 mM imidazole with 1 mM PMSF, and 1 x protease inhibitor cocktail (Roche) and disrupted by sonication on ice using an Astrason Ultrasonic Processor XL (Misonix) over 10 minutes (4 sec "on" and 10 sec "off", at output level 4.5). Genome DNA and RNA in cell lysates were digested by addition of DNase I to  $10 \,\mu g/mL$ and RNase A to 200 µg/mL, respectively, for 30 min at 37°C in the presence of 10 mM MgCl<sub>2</sub>. Cell debris was removed by centrifugation and each supernatant (80 µL) was mixed with 20 µL of 5 x SDS sample buffer (250 mM Tris [pH 6.8], 10% [w/v] SDS, and 50% [v/v] glycerol] in the absence of the (commonly included) reducing agent  $\beta$ -mercaptoethanol, followed by boiling for 10 min. After separation of 12.5 µL amounts of cell lysates on 10-20% (w/v) SDS-PAGE, proteins on the gels were electrotransferred to Immobilon-PSQ membranes (Millipore) using 100 volts for 2 hours. Next, the membranes were probed with primary antibodies, either an anti-AbrB or an anti-Abh antibody, followed by incubation with horseradish peroxidase-conjugated goat antirabbit IgG (Bio-Rad), and the SNAP ID Protein Detection System (Millipore) was employed to

develop protein bands. Finally, membranes were incubated with an ECL substrate (Amersham) and exposed to X-ray film.

## 7. Determination of the molecular numbers of AbrB and Abh molecules in B. subtilis cells

To eliminate the possibility that the antibodies might recognize tagged and untagged proteins with different efficiencies, we purified AbrB and Abh proteins lacking tag sequences using the Profinity eXact<sup>TM</sup> protein purification system (Bio-Rad), and employed these proteins as standards in quantitative analysis of cellular protein levels. To construct AbrB and Abh expression vectors, sequences encoding AbrB and Abh were amplified from *B. subtilis* genomic DNA using primer sets pPAL7-abrB-F1/pPAL7-abrB-R and pPAL7-abh-F/pPAL7-abh-R, respectively, and cloned into a T7 expression plasmid, RIC-Ready pPAL7 (Bio-Rad). Overexpression in *E. coli* cells and purification of AbrB and Abh proteins were performed according to the manufacturer's instructions. The concentrations of purified AbrB and Abh were determined by comparing protein band intensities with those of known concentrations of lysozyme, after SDS-PAGE separation and staining with Coomassie Brilliant Blue.

To determine the levels of AbrB and Abh in *B. subtilis* cells, the wild-type strain and derivatives thereof, the  $\Delta abrB$  and  $\Delta abh$  mutants, were cultured to OD<sub>600</sub> values of 0.4 in LB medium, and harvested. Cells were washed once with chilled killing buffer [20mMC Tris-HCl (pH. 7.5), 5mM MgCl<sub>2</sub>, 20mM NaN<sub>3</sub>] and store freezen at -80°C. Frozen cells were diluted in a buffer containing [100 mM Tris-HCl, 250 mM NaCl, 20% (v/v) glycerol, 50 mM imidazole] with 1 mM PMSF, and 1 x protease inhibitor cocktail (Roche) to a final OD600 of 0.0125 and disrupted by sonication on ice for 5 min using the conditions described above for antibody production and purification. Cell debris was removed by centrifugation. Various amounts of AbrB

and Abh standard protein preparations were mixed with cell lysates of  $\Delta abrB$  and  $\Delta abh$  cells, respectively. Wild-type,  $\Delta abrB$ , and  $\Delta abh$  lysates, and protein standards, were mixed with 5x SDS buffer (0.25M Tris-HCl [pH 6.8], 10% [w/v] SDS, 50% [v/v] glycerol, 25% [v/v]  $\beta$ mercaptoethanol, 0.01% [w/v] bromophenol blue]) and boiled for 10 minutes at 95°C. To detect AbrB, cell lysates from 0.05 OD<sub>600</sub> units of wild-type and  $\Delta abh$  cells, and AbrB standard protein at four different concentrations, were separated using 8-16% (w/v) SDS-PAGE. For Abh detection, cell lysates from 0.1 OD<sub>600</sub> units of wild-type and  $\Delta abrB$  cells, and Abh standard protein at four different concentrations, were employed. After electrophoresis, gels were directly probed with anti-AbrB or -Abh antibodies, and proteins reacting with these antibodies were detected using an in-gel chemiluminescence detection kit (Pierce). The signal intensities of protein bands on X-ray films were quantified using the NIH-Image program (http://rsb.info.nih.gov/nih-image/), and the levels of AbrB and Abh were determined by comparing protein band intensities with those of standard proteins (Figure 9).

The number of *Bacillus subtilis* 168 cells per 1  $OD_{600}$  unit at  $OD_{600}$  of 0.4 was determined by counting on bacteria counting chamber (Erma). The cells were cultured in the same manner as describe above. At  $OD_{600}$  of 0.4, about two  $OD_{600}$  unit of cells were harvested and washed once with 10 mM Tris-HCl pH7.5 followed by fixing in 70% ethanol for overnight at 4°C. Fixed cells were washed once with 10 mM Tris-HCl pH7.5 and resuspended in 400 µl of the same buffer. Then, the cell suspension was mildly sonicated to remove bacterial chain using an Bioruptor sonicator UCD-250 (Cosmo Bio) in a water bath at 4°C for 2 minutes (2 sec "on" and 8 sec "off", at L-amplitude). Cells were diluted for 10 times and 7 µl were applied to the counting chamber. Triplicate independent experiments were performed.

#### 8. Analysis of AbrB and Abh interaction in vitro by Native-PAGE

Tag-free AbrB and Abh used in this experiment were purified and determined the concentrations as described in determination of the molecular numbers of AbrB and Abh molecules in *B. subtilis* cells section. Two micrograms of AbrB and Abh only, mixture of equal amount (2µg) of them were mixed with 5x sample buffer (0.25M Tris-HCl [pH 6.8], 50% [v/v] glycerol, 0.01% [w/v] bromophenol blue]) on ice. Samples with mixture of AbrB and Abh were subjected to heat at 25°C or 42°C for 10 minute. Then the samples were separated using 5-20% Native-PAGE in native running buffer (25 mM Tris, 192 mM Glycine) using 6 mA at 4°C. Protein molecular weight markers for non-denaturing polyacrylamide gel electrophoresis (Sigma) were run in parallel. The proteins on gel were visualized by staining with Coomassie Brilliant Blue.

### 9. ChAP-chip analysis.

## 9.1 ChAP-chip procedure

ChAP-chip analysis of AbrB-2HC and Abh-2HC was performed as described previously (Ishikawa et al, 2007), with the following modifications. Cells collected from 400 mL culture were treated with RNaseA at a final concentration of 200  $\mu$ g/mL in 3 mL of buffer containing 0.1 M Tris-HCl (pH 7.5), 0.2 M NaCl, 1% (v/v) Triton X-100, 0.1% (w/v) Na-deoxycholate, 0.2% (w/v) Brij 58, and 20% (v/v) glycerol, for 30 min at 37°C with shaking (230 rpm), and next washed once with the same buffer without RNaseA, followed by sonication in modified UT buffer (the concentration of imidazole was reduced to 10 mM, and 10 mM  $\beta$ -mercaptoethanol was added instead of 1 mM DTT). Dynabead Talon (100  $\mu$ L amounts; Invitrogen) was used instead of MagneHis beads during the ChAP procedure. A newly designed

custom high-resolution Affymetrix tiling array of the *B. subtilis* genome was employed in the present study; details of the array design and probe information are available in the ArrayExpress database (http://www.ebi.ac.uk/microarray-as/ae/) under accession code A-AFFY-161.

## 9.2 Data normalization

All probes on the Affymetrix tiling array were mapped to the recently revised *B. subtilis* genome sequence (GenBank no. NC\_000964) using the In Silico Molecular Cloning program, Array Edition (In Silico Biolog), and 242,413 probes that had been uniquely mapped on the genome were selected for study. The signal intensities of perfectly matched probes (only) were used in the following calculations. Signals on ribosomal RNA genes were removed from analysis because of the high copy number of such genes in the genome. Raw data from eight experiments (a duplicate analysis of four strains) were pre-processed using the following steps. First, the signal intensities from DNA in the affinity-purified fraction (ChAP DNA) were divided by those from the DNA of the entire cell extract prior to affinity purification (control DNA), thus identifying enrichment factors in the ChAP fraction. Second, signals considered to be outliers of each dataset were identified and removed using t-testing (p-values  $\leq 0.001$ ), under the assumption that the mean of the signal intensities of six probes around any particular probe should be equal to that of the probe in question. Third, median signal intensity levels in each experiment were normalized to the means of the median values obtained from eight experiments, using the following equation (Figure 4A):

$$\hat{x}_{i,j} = x_{i,j} \times \frac{Q_{0.5}}{Q_{0.5}(x_{i,j})}$$

where  $\hat{x}_{i,j}$  is a normalized value,  $x_{i,j}$  is the relative intensity of the *i*th probe in experiment *j*,  $Q_{0.5}(x_{i,j})$  is the median intensity of all probes used in experiment *j*, and  $\overline{Q}_{0.5}$  is the mean of  $Q_{0.5}(x_{i,j})$  from *j*=1 to *j*=k.

Finally, the binding signal intensities of AbrB-2HC in wild-type (OC001) and  $\Delta abh$  (OC006) backgrounds, and those of Abh-2HC in the wild-type (OC002) and  $\Delta abrB$  (OC007) backgrounds, were obtained by averaging of data from two replicate experiments.

## 9.3 Detection and quantitative analysis of AbrB/Abh binding sites

First, we extracted possible protein binding sites in each strain, by searching for regions wherein at least four probes separated by intervals of less than 100 bp showed binding intensities above the chosen threshold value, which was 0.88 (the 95<sup>th</sup> percentile of all probe data; Figure 4B and 5). Next, overlapping protein binding regions extracted for each strain were merged and defined as possible binding regions (PBRs). Some peaks were divided by visual examination if several clearly defined peaks were evident. Finally, AbrB and Abh binding intensities to the 928 PBRs of the four strains were calculated as the sums of probe signal intensities within each PBR, after subtraction of background signals, which were defined as those equal to or less than 0.4 (the 40<sup>th</sup> percentile value; see Figure 4B).



**Figure 4. Normalization of ChAP-chip results.** (A) Box-and- whisker plot demonstrating the distribution of probe values of eight individual ChAP-chip results both before and after application of the normalization procedure described in the Methods section of the main text; descriptions of the individual samples are indicated below each box plot. Log<sub>2</sub> intensities of all probes in each array are plotted. The upper and lower limits of the boxes indicate the 75<sup>th</sup> and 25<sup>th</sup> percentiles, respectively, and the line across the boxes indicates median values. Outliers with values more than 1.5-fold of the interquartile range of the 75<sup>th</sup> percentile, or less than (continued)

1.5-fold the interquartile range of the 25<sup>th</sup> percentile, are shown as filled circles. (B) Cumulative plots of the percentiles of probes (y-axis) against increasing probe intensity values (x-axis), for the eight sets of ChAP-chip data, both before (A) and after (B) normalization, are shown. The 40<sup>th</sup> and 90<sup>th</sup> percentile values, corresponding to probe intensities of 0.4 and 0.88, used as background and peak threshold values, respectively, are indicated.



**Figure 5. Detection of AbrB/Abh binding sites.** Regions where at least four probes (indicated in red), with between-probe intervals of less than 100 bp, yielded signal intensities above the threshold value of 0.88 were computationally extracted for various strains (Peak regions). Next, regions overlapping in different strains were merged to define possible AbrB/Abh binding regions (PBRs), and the sum of AbrB or Abh binding signals of all probes in each PBR was calculated for each strain, after subtracting a background value of 0.4. Probe intensities less than the threshold value (indicated in green) for PBRs were also included in the calculation of the AbrB/Abh binding intensities of each PBR.

#### **10.** High-resolution transcriptome analysis

Cells from 40 mL aliquots of exponentially growing cultures (OD<sub>600</sub> values of 0.4) were harvested by centrifugation and washed once with 1 mL amounts of 10 mM Tris-HCl (pH 7.5). Cell pellets were immediately frozen in liquid nitrogen prior to storage at -80°C. RNA extraction, synthesis of complementary DNA (cDNA), terminal labeling, and hybridization with the oligonucleotide tiling chip used for ChAP-chip analysis, were all performed according to the Affymetrix instruction manual, as previously reported (Morimoto et al, 2008). Processing of hybridization signal data, background correction, data normalization, and calculation of expression levels of individual genes, were all performed as previously described (Rukmana et al, 2009). Finally, the transcriptional signal intensities were obtained by averaging of data from two replicate experiments.

## 11. Overexpression of Abh in wild type 168 strain

#### **11.1** Contruction of *ArsiX* strains

To obtain the *rsiX* deletion mutants, OC008, an antibiotic-resistance cassette, encoding erythromycin-resistance flanked by upstream and downstream regions of *rsiX*, was used. Regions upstream and downstream of *rsiX* were amplified from *B. subtilis* genomic DNA using the primer sets DrsiX-F-f/DrsiX-F-r and DrsiX-B-f/DrsiX-B-r, respectively. A erythromycin-resistance gene with a promoter region was amplified from plasmid pMutinHis (Ishikawa et al, 2006) using primers rPCR-ermF and rPCR-ermR. The resulting three fragments were joined by recombinant PCR using primers DrsiX-F-f and DrsiX-B-r, and integrated into the *B. subtilis* genome by double crossover recombination with selection for erythromycin resistance. The sequences around the

recombination sites were confirmed by sequencing using primer sigX-u-F and rsiX-d-r primers to avoid mutation.

## 11.2 Construction of plasmid for over-expression of Abh from the *spac* promoter.

Plasmids for overexpression of *abh* in wild-type 168 cells were constructed using the recombinational Gateway cloning system (Invitrogen). The coding sequences with stop codon of *abh* gene were amplified from the wild-type 168 genome by PCR using primer abh-gwF and abh-gw-r. The recombination sites were added and the fragment was cloned into entry vector pDONR201 followed by transfer to the pOGW destination vector as described for Antibody production and purification. The resulting plasmid pO-abh was transformed into wild-type 168 cells, generating the strain OC009.

## 11.3 Determination of Abh expression in overexpressing cells (OC009) compared to that of in $\Delta rsiX$ strain (OC008)

Semi-dry western blotting was employed to determine the amount of Abh in OC008 and in OC009 strain. The OC008 cells were cultured in LB medium at 37°C to OD<sub>600</sub> of 0.4. OC009 cells were cultured in the same manner in the medium supplemented with various concentration of IPTG. Fifty milliliters of cells were harvested, washed and sonicated in the same manner as describe for *in vivo* interaction of AbrB and Abh. Cell lysates of both strains were subjected to semi-dry western blotting analysis using Trans-Blot<sup>®</sup> SD Semi-Dry Elecltrophoretic Transfer Cell (Bio-Rad) according to the manufacturer's instructions. The IPTG concentration which induces Abh expression in OC009 cells to the comparable level to that of in OC008 strain was selected as a culture condition for further genome- wide transcriptome analysis.
#### RESULTS

#### 1. AbrB and Abh form homodimers and heterodimers in vivo

Previously, it has been shown that AbrB and Abh share overlapping binding sites *in vitro* (Strauch et al, 2007), suggesting that these proteins may perhaps bind as heteromers to DNA. To investigate this possibility, we treated exponentially growing *B. subtilis* cells with DSP [dithiobis(succinimidyl propionate)], a membrane-permeable chemical cross-linker, and analyzed cross-linked proteins in the cell lysates by Western blotting using specific antibodies against AbrB and Abh. The cross-reactivity of antibodies for both of AbrB and Abh was depleted as described in Materials and Methods and the specificity was confirmed by Western blotting as shown in Figure 6.

Because the molecular weights of AbrB and Abh (10.4 kDa and 10.1 kDa, respectively) are similar, the proteins are not adequately separated on SDS-PAGE. Thus, we constructed strains expressing C-terminal 2HC (12 histidines plus a chitin-binding domain)-tagged AbrB (AbrB-2HC) or Abh (Abh-2HC) [designated as strains OC001 and OC002, respectively (Table 1)]. Fusion of 2HC to AbrB generates a protein easily distinguishable from Abh on SDS-PAGE, and vice versa. We confirmed that tagging with 2HC did not affect growth rate or gene expression profile during exponential growth (Figure 7). We also successfully constructed a further two strains that expressed AbrB-2HC in a  $\Delta abh$  background (strain OC006) and Abh-2HC in a  $\Delta abrB$  background (strain OC007).



Figure 6. Western blot analysis of the cross-reactivity of AbrB and Abh antibody before and after purification. The same amount (0.1  $OD_{600}$  unit) of cell lysate of wild type *Bacillus subtilis* 168 (wt),  $\Delta abrB$ ,  $\Delta abh$  and  $\Delta abrB \Delta abh$  mutant strains were separated by SDS-PAGE in the order as indicated followed by Western blot analysis using un-purified (Un-P) and purified (P) AbrB and Abh antibody as labelled at the top of picture. The expose time are shown below the picture.



**Figure 7.** Growth rates and transcriptome profiles of OC001 (abrB-2HC) and OC002 (abh-2HC) cells. (A) Growth curves of abrB-2HC, abh-2HC, and wild-type cells in LB medium at 37°C. (B) A log-scale scatter plot of the transcriptional intensity of each gene in exponentially growing abrB-2HC (y-axis) and wild-type (x-axis) cells. (C) A log-scale scatter plot of transcriptional intensities in exponentially growing abh-2HC (y-axis) and wild-type (x-axis) cells. The averaged signal intensities from two independent experiments are plotted in B and C.

Using an anti-AbrB antibody, Western blotting of cell lysates from DSP-treated OC001 cells expressing AbrB-2HC revealed three clear bands (Figure 8A). The molecular weights of two of the bands corresponded to those of the AbrB-2HC monomer and dimer, and that of the remaining band was matched to an AbrB-2HC/Abh heterodimer. Indeed, the third band was not detected in a *Aabh* background (Figure 8A). In addition, only this band was detected using an anti-Abh antibody, confirming that the band contained the AbrB-2HC/Abh heterodimer (Figure 8B). These results indicate that a certain proportion of AbrB and Abh exist as a heterodimer complex in vivo. In addition, when the cross-linking time was extended, unresolved high-molecular weight bands were detected. The proportions of these bands increased in parallel with the disappearance of monomer bands when cells were treated with greater concentrations of DSP (data not shown), suggesting that complexes larger than dimers were also formed in vivo. Previous in vitro studies have demonstrated that, although full-length AbrB forms a tetramer through interactions of the Cterminal domains of individual proteins, an AbrBN53 mutant protein lacking the C-terminal domain can form a stable dimer with DNA-binding activity (Benson et al, 2002). Presently, the predominant molecular forms of AbrB/Abh in vivo are not known, and it is not clear whether the dimer forms detected in the present work were formed *via* interaction of N-terminal or C-terminal domains.

Notably, in the  $\Delta abh$  background, the level of the AbrB dimer was significantly increased compared with the amount seen in an  $abh^+$  background (Figure 8A). When the same experiments were performed using the Abh-2HC-expressing strains OC002 and OC007, Abh homodimer levels were low in the  $abrB^+$  background but a marked increase in Abh dimer formation was observed in  $\Delta abrB$  cells (Figure 8C). The number of Abh molecules per cell under our experimental conditions was 32,700 ±6,500 and 45,600 ± 6,900 in wild-type and  $\Delta abrB$  cells, respectively, whereas the figure for AbrB was 65,800  $\pm$  14,200 and 80,200  $\pm$  9,100 in wild-type and  $\Delta abh$  cells, respectively (Figure 9). Although relative quantities of various multimeric forms of AbrB/Abh in the cell cannot be estimated exactly in this method, these results may suggest that many of Abh molecules would be present in a complex with AbrB (an AbrB/Abh heteromer) in wild-type cells. Furthermore, increase in Abh dimer in  $\Delta abrB$  cells may indicate that Abh would be released from the complexes with AbrB to form Abh homomers when the cellular levels of AbrB decreased.



**Figure 8.** AbrB and Abh interaction *in vivo*. Western blot analysis of exponentially growing *B. subtilis* cells, either untreated or treated with 2 mM DSP for 5, 15, or 25 minutes. Lysates of cells expressing AbrB-2HC in the  $abh^+$  or  $\Delta abh$  background were probed using anti-AbrB antibody (A) or anti-Abh antibody (B). Cells expressing Abh-2HC in the  $abrB^+$  or  $\Delta abrB$  background were probed using anti-Abh antibody (C). Electrophoretic mobilities of AbrB/Abh monomers, dimers, and heteromers, as well as those of proteins in a pre-stained broad-range marker mix (Bio-Rad), are indicated.



Figure 9. Determination of AbrB and Abh concentrations in exponentially growing wildtype cells. (A) Coomassie Brilliant Blue staining of purified tag free-AbrB and -Abh proteins (5 and 10 µl amounts, respectively) separated by 10-20% (w/v) SDS-PAGE, together with various amounts (0.2-1.2 µg) of lysozyme. The concentrations of purified AbrB and Abh proteins were determined to be 94.2 and 64.3 ng/µl, respectively, using the standard curve shown below the gel image. (B) In-gel chemiluminescence detection of AbrB in wild-type (wt) and  $\Delta abh$  cells using anti-AbrB antibody. The levels of AbrB in wild-type and  $\Delta abh$  cell lysates were determined using the standard curves indicated below the gel images. Protein molecular numbers per cell were calculated assuming that 1 OD<sub>600</sub> unit contained 2.41 x 10<sup>8</sup> cells. Experiments (continued)

were performed in triplicate. (C) The numbers of molecules of Abh/cell were determined as described above in (B), using an anti-Abh antibody. The increase in Abh level seen after *abrB* inactivation is consistent with data of a previous report (Strauch et al, 2007).

#### 2. AbrB and Abh interaction in vitro

To further confirm the interaction between AbrB and Abh, subunit exchange among purified AbrB and Abh *in vitro* was analyzed using Native-PAGE. AbrB or Abh alone appears as single band on Native-PAGE with slight different migration distances (Figure 10, lane 5 and lane 8). Since the electrophoretic mobility of proteins depends on the charge of the proteins and therefore reflects pI values of proteins, AbrB and Abh migrate differently, reflecting their pI values, 6.77 and 5.74 respectively. This result was consistent with a report that AbrB tetramer with R23S mutation migrate faster than wild-type AbrB tetramer due to loss of charge for the R23 (Vaughn et al, 2000) When equal amount of AbrB and Abh were mixed and incubated at 25°C for 10 min, we observed three bands with almost similar intensity (lane 6). Two of them correspond to migrations of AbrB homomer and Abh homomer, and the other one migrates between them suggesting that the band was AbrB/Abh heteromer. When mixture of AbrB and Abh are incubated at 42°C, the heteromer form becomes major (lane 7). This result confirmed that AbrB and Abh form heteromer, through subunit exchange, although we do not know that this subunit exchange occurs among monomer or dimer population.



**Figure 10. Interaction of AbrB and Abh** *in vitro*. Native-PAGE analysis of AbrB and Abh; 1: BSA, 2: chicken egg albumin, 3 α-lactalbumin, 4: carbonic anhydrase, 5: AbrB, 6: AbrB and Abh mixture incubated at 25°C, 7: AbrB and Abh mixture incubated at 42°C, 8: Abh. Migration of AbrB homomer, AbrB/Abh heteromer and Abh homomer are indicated.

#### 3. Profiling of genome-wide AbrB and Abh binding sites

We identified all binding sites for AbrB and Abh in the *B. subtilis* genome using the ChAP-chip method in the four strains described above: OC001 (*abrB-2HC abh*<sup>+</sup>), OC002 (*abh-2HC abrB*<sup>+</sup>), OC006 (*abrB-2HC \Delta abh*), and OC007 (*abh-2HC \Delta abrB*), and assessed the contributions of AbrB and Abh complex to the DNA binding. Purification of protein–DNA complexes and mapping of co-purified DNA fragments using a custom Affymetrix tiling chip, and comparative quantitative analysis of protein-binding signals were performed as described in the Materials and Methods. We identified hundreds of AbrB(-2HC) and Abh(-2HC) overlapping binding sites distributed throughout the *B. subtilis* genome (Supplementary Figure S1). Typical examples of AbrB- and Abh-binding signals along the genome in wild-type cells are presented in

Figure 11A, and an overview of AbrB and Abh binding signal sites is shown in Figure 11B. In addition, we found that deletion of *abrB* significantly affected the Abh-binding profile, whereas *abh* deletion had little impact on AbrB binding (Figure 11A).

To quantitatively compare AbrB and Abh binding in the four strains, we normalized the distribution of protein binding signal intensities, as described in the Materials and Methods. We observed low contiguous signals without any peak at many regions, probably due to contamination of free DNA in ChAP fraction, and normalization of median signal intensities resulted in similar background levels for eight experiments (Figure 4). We next computationally extracted the AbrB/Abh-binding sites of the various strains in instances where at least four probes at intervals of less than 100 bp showed signal intensities above a particular threshold (0.8) as shown in Figure 5, and overlapping binding DNA stretches in different strains were merged, thus defining 928 possible binding regions (PBRs) ranging from 75 bp to 2,167 bp in size (Supplementary Table S1). Additionally, we detected eight broad regions with contiguous binding signals (Supplementary Figure S1, Supplementary Table S1). These stretches overlapped with the wide binding regions of Spo0J and/or Noc around *oriC*, which are involved in the organization of higher-order nucleoid structure (Ishikawa et al, 2007; Wu et al, 2009), suggesting that co-existence of AbrB/Abh and Noc and/or Spo0J at the relevant regions might cross-link these proteins and co-purify DNA of such wide binding regions. In addition, some highly transcribed regions tended to show increased levels of background signal. Such DNA stretches were removed prior to the following analysis. Then to quantitatively compare AbrB/Abh binding in the four strains, the sum of AbrB- or Abhbinding signals derived from probes in each PBR was calculated for each strain (a total of 3,712 signal intensity values were used in the assessment), and these sums (in arbitrary units) were ranked and grouped into four classes: Very Low (< 2.0, class VL), Low (2.0-6.2, class L), Middle (6.2–17.8, class M), and High (> 17.8, class H), which corresponded to the 25<sup>th</sup>, 50<sup>th</sup>, 75<sup>th</sup>, and

100<sup>th</sup> percentiles, respectively (Figure 12). We defined PBRs with binding intensities greater than 6.2 (classes M and H) as having AbrB/Abh-binding sites, and 753 PBRs satisfied this criterion for either or both AbrB and Abh. This cut-off level detected about 75% of AbrB- and Abh-binding sites previously determined by *in vitro* experiments (Table 5), including overlapping binding sites for AbrB and Abh at *sunA*, *sboA*, *sdpA*, *skfA*, and *sigW* promoters (Strauch et al, 2007). As for promoter regions where we failed to detect AbrB/Abh binding in Table 5, AbrB/Abh-binding affinities to these promoters may be too low to be detectable under our *in vivo* conditions.



Figure 11. AbrB and Abh binding signals on the *B. subtilis* genome. (A) Distributions of AbrB binding signals in the  $abh^+$  and  $\Delta abh$  backgrounds, and Abh binding signals in  $abrB^+$  and  $\Delta abrB$  backgrounds, in the 2,180,000 bp to 2,222,000 bp region of the genome, are shown. Protein-binding signals for each probe in the region are indicated alongside the genomic coordinates. The top and bottom lines in each column indicate signal intensities of 5 and 0, respectively. The middle line shows the threshold values used to define AbrB and Abh binding peaks (0.4). The gene organization is schematically shown at the bottom. Protein-binding sites located in intergenic regions and coding regions are indicated using triangles and asterisks, respectively. (B) Distributions of AbrB (outer) and Abh (inner) binding signals over the entire genome. Clockwise and counter-clockwise ORFs are schematically indicated.



**Figure 12. Quantitative evaluation of AbrB/Abh binding sites.** Cumulative plots of the percentiles of number of PBRs (y-axis) against increasing AbrB or Abh binding intensities in the four strains (x-axis). The 25<sup>th</sup>, 50<sup>th</sup>, and 75<sup>th</sup> percentile values, corresponding to binding intensities of 2.0, 6.2, and 17.8, respectively, used to classify binding intensities into the VL, L, M, and H classes, are indicated.

#### 4. Most Abh binding sites overlap with those of AbrB in wild-type cells

Using the criteria outlined above, we detected 643 AbrB- and 411 Abh-binding sites in exponentially growing wild-type cells (Figure 13A). We found that most Abh-binding sites (390) overlapped with those for AbrB. This result is consistent with the presence of the AbrB/Abh heteromer in such cells, although simultaneous bindings of both AbrB- and Abh-homomers are also possible. We detected 21 Abh-specific binding sites with middle-level signal intensities (class M), but low-level signal intensities (class L) of AbrB binding were also observed at these positions. This was also seen for AbrB-specific binding sites; 123 of 253 such sites were associated with low-level Abh-binding signals. Thus, it seems that 130 AbrB-binding sites were AbrB-specific, whereas Abh-specific binding sites were not detected in wild-type cells. The presence of AbrB-specific binding sites and the absence of Abh-specific binding sites in wild-type cells were also evident when the scatter plots of AbrB and Abh binding intensities were viewed (Figure 13B).

We next evaluated the positions of AbrB- and Abh-binding sites (centers of PBRs). We found that 58% of binding sites were located in protein-encoding regions, whereas 42% were in intergenic regions (Supplementary Table S1, Supplementary Figure S1). Although AbrB- and Abh-binding sites were concentrated in intergenic regions (forming 13% of genomic DNA), a significant number of sites were in coding regions, unlike observations in general transcriptional regulators, which usually bind to the promoter regions of target genes.

# 5. AbrB markedly influences Abh-binding profile, whereas Abh has a minor effect on AbrB binding

To examine the contribution of AbrB/Abh interactions to DNA binding, we compared AbrB binding in  $abh^+$  and  $\Delta abh$  cells and Abh binding in  $abrB^+$  and  $\Delta abrB$  cells. The scatter plots of AbrB binding intensities in the presence and absence of Abh indicated that, although some AbrB binding intensities decreased in the absence of Abh, most such intensities were unaffected (Figure 13C). In contrast, AbrB deletion resulted in a re-organization of Abh binding intensities (Figure 13D). These results indicate that AbrB has the ability to bind to most target loci independent of Abh, whereas many Abh-binding events are dependent on the presence of AbrB.

To gain further insight into the effects of AbrB/Abh interactions on DNA binding, we classified PBRs based on AbrB and Abh binding intensities in the four strains. We first performed a hierarchical clustering analysis of all 753 PBRs based on AbrB/Abh binding classes in the four strains using the R statistical environment software (R Development Core Team, 2004). The PBRs formed several clusters (Figure 14A). However, it was apparent that the cluster positioning of many sites was ambiguous, probably because adjacent binding sites with different AbrB/Abh-binding properties were merged into a single PBR.

Theoretically, AbrB and Abh binding abilities to particular sites can be classified into 15 patterns (P01–P15) as shown in Table 3. To select PBRs with unambiguous binding patterns, we searched for PBRs that could be clearly assigned to 1 of the 15 patterns. To this end, we considered signal intensities of less than 6.2 (classes VL and L) as protein-binding- negative and those with intensities of more than 17.8 (class H) as positive. PBRs with intermediate signal intensities were not included in further analysis. As a result of this exercise, 160 PBRs with unambiguous binding patterns were extracted, possibly reflecting a fundamental mode of AbrB and Abh binding to target sequences (Table 3). The results of Table 3 indicate that AbrB/Abh binding to DNA falls into four major patterns, P01–P04, and four minor patterns, P05–P08. These results are generally consistent with the results of the hierarchical clustering analysis of all PBRs shown in Figure 14A. Typical examples of AbrB- and Abh-binding signals assigned to each profile are shown in Figure 14B, and the expected molecular species with the ability to bind to



Figure 13. Comparison of AbrB and Abh binding signals in various strains. (A) A Venn diagram of overlapping binding sites for AbrB and Abh in a wild-type background. The numbers in parentheses indicate the levels of confidence associated with the identification of particular AbrB- and Abh-specific binding sites (please see main text). (B) A log-scale scatter plot of the binding intensities of AbrB (x-axis) and Abh (y-axis) in 664 PBRs in a wild-type background. (C) A log-scale scatter plot of AbrB binding intensities in *abh*<sup>+</sup> (x-axis) and *Aabh* (y-axis) cells. (D) A log-scale scatter plot of Abh binding intensities in *abrB*<sup>+</sup> (x-axis) and *AabrB* cells.

DNA within each pattern are listed in Table 3. Some of AbrB/Abh bindings are expected to occur in a particular genetic background (indicated in parentheses in Table 3).

The other 4 minor profiles, P05-P08 are detected less than 5% for each of them. In the case of P05 and P06, AbrB and Abh share overlapping binding site in wild-type cells but AbrB binding is absent in the absence of Abh for both profile suggesting that AbrB bind these regions only as heteromer form with Abh. For the profile P05, the binding sites are exclusively recognized by heteromer while P06 can be recognized also by Abh homomer.

In the case of P07, only AbrB-binding is detected in the wild-type cells thus the regions would be bound by AbrB homomer. However, AbrB binding to this region is not detected in *abh* deletion mutant suggesting that AbrB bound with assistance of Abh or some factor other than Abh. This binding profile was unexpected and the molecular mechanism is not yet clear.

Last minor profile is P08, which Abh binding is not detected only in the wild-type cells, suggesting this region would be recognized by AbrB and Abh homomers, although this profile is quite minor.

From this result, among the 160 PBRs, AbrB-binding sites observed in wild-type cells were mostly retained in the absence of Abh (136/148), whereas about 44% of Abh binding sites in wild-type cells disappeared in the absence of AbrB (51/115). AbrB-homomer-specific binding sites in wild-type cells formed one of the major patterns (P03). However, Abh-homomer-specific binding was evident only in the absence of AbrB (P04), probably due to an increased concentration of Abh homomer. These results indicate that AbrB/Abh-binding sites include various sequences that differ in specificities and affinities for homomers and heteromers of AbrB and Abh.



Figure 14. Classification of PBRs according to AbrB and Abh binding profiles. (A) A cluster diagram of 753 PBRs based on AbrB binding intensities (in various classes) in  $abh^+$  and  $\Delta abh$  backgrounds, and Abh binding classes in  $abrB^+$  and  $\Delta abrB$  backgrounds. The VL, L, M, and H classes of AbrB/Abh binding are indicated in white, yellow, orange, and red, respectively. Clusters containing PBRs belonging to the four major binding profiles of the selected unambiguous PBRs summarized in Table 3 are marked by bold lines at the right of the diagram. (B) Typical examples of AbrB and Abh binding signals in PBRs belonging to classes P01- P08. The binding signals are shown as in Figure 11A. Gene organizations around selected PBRs are indicated at the bottom of each panel.

	Possibl	e binding	profiles		Molecules	expected to	be bound <sup>a</sup>	Assig	ned	
profile ID	AbrB in wild	AbrB in ∆abh	Abh in wild	Abh in ⊿abrB	AbrB homomer	AbrB/Abh heteromer	Abh homomer	number	%	Binding motif
P01	•	•	•	•	•	•	•	60	37.3	TNCCAWWWWTGGNA
P02	•	•	•	-	•	•	-	46	28.6	WWWWWCCAWWWWTGG
P03	•	•	-	-	•	-	-	29	18	not clear
P04	-	-	-	•	-	-	● (∆abrB)	13	8.1	TGGNAWTNCCA
P05	•	-	•	-	-	•	-	5	3.1	
P06	•	-	•	•	-	•	•	4	2.5	
P07	•	-	-	-	• (wild)	-	-	3	1.9	
P08	•	•	-	•	•	-	$(\Delta a br B)$	1	0.6	
P09	•	-	-	•	• (wild)	-	$(\Delta a b r B)$	0	0	
P10	-	•	•	•	• $(\Delta abh)$	-	•	0	0	
P11	-	•	•	-	• $(\Delta abh)$		• (wild)	0	0	
P12	-	•	-	•	• $(\Delta abh)$	-	$(\Delta a br B)$	0	0	
P13	-	•	-	-	$(\Delta abh)$	-	-	0	0	
P14	-	-	•	•	-	-	•	0	0	
P15	-	-	•	-	-	-	• (wild)	0	0	

Table 3 Classification of 160 PBRs with clear binding profiles

<sup>*a*</sup> If AbrB/Abh binding is expected to occur in a particular genetic background, it is indicated in parentheses.

# 6. A TGGNA motif identified *in vitro* acts as a determinant not only for AbrB but also for Abh binding *in vivo*

No consensus sequence has been identified that adequately explains AbrB site selection and recognition. We also failed to find consensus sequences in the 160 unambiguous PBRs or in any of the major binding patterns, P01–P04, using the MEME program [http://meme.nbcr.net (Bailey & Elkan, 1994)]. We suspected that the selected PBRs still included multiple AbrB/Abhbinding sites of different binding types. Thus, to eliminate such a possibility, we further selected only sites at which binding signal peaks were clearly triangular in shape, reflecting a simple AbrB/Abh-binding profile, by visual inspection (Supplementary Table S2) and manually selected 100-bp regions around the peak positions. This allowed identification of motifs specific for P01, P02, and P04 (Table 3 and Figure 15).

The consensus motif for sequences of the P01 pattern was TNCCA-WWWW-TGGNA, which was present in 21 of the 37 selected PBRs. Interestingly, this is an inverted repeat, with a 4bp interval, of TGGNA, which was identified as the basic motif for AbrB binding using *in vitro* selection experiments (Xu & Strauch, 1996). Furthermore, inverted repeats of the TGGNA motif, with inversion of direction compared with the P01 sequence, which were separated by 1 bp, were also found in 100% (12 of 12 selected PBRs) of Abh-homomer-specific binding sequences (class P04). From sequences of the P02 pattern, a variant of the P01-type motif was extracted, which lacked the terminal A or T on one end but had an additional series of W bases at the other end, thus forming WWWW-CCA-WWWW-TGG. This sequence was present in 14 of 18 selected PBRs. The Abh homomer does not bind to this sequence motif, suggesting that Abh binding may require strict conservation of the TGGNA motif.



**Figure 15.** Consensus sequences for AbrB/Abh binding. Consensus sequences identified in selected PBRs belonging to classes P01 (A), P02 (B), P03 (C), and P04 (D) are presented, together with the position(s) and direction(s) of the TGGNA motif(s) in each sequence. Possible binding modes of AbrB/Abh homotetramers and heterotetramers to each sequence are schematically presented (please see Discussion). Red coloration of double-stranded DNA indicates the TGGNA motif. Light and dark blue boxes show the N-terminal domains of two AbrB molecules that interact to form a DNA binding domain, whereas the light- and dark-blue arm-like structures extending from the boxes depict C- terminal domains that form (continued)

tetramers. Loop regions, which have been predicted to contact DNA and contribute to DNA recognition, are shown using triangles. Similar structures in Abh are shown in green.

In sequences of pattern P03, the AbrB-homomer-specific binding sequences, neither the TGGNA motif nor any other consensus sequence was detected, but A- and G-rich sequences were evident (Table 3 and Figure 15C). This may indicate that, in addition to TGGNA motif-dependent binding, AbrB has an ability to bind to other sequences, possibly by recognizing a particular conformation of three-dimensional DNA, as previously proposed.

To further evaluate the contribution of the TGGNA motif to genome-wide AbrB/Abh binding, we searched for the presence of two TGGNA motifs, in palindromic or tandem orientation, separated by 0 to 6 bp of W (A or T) spacer, allowing a single base mismatch, and determined if such sites were enriched in the 100-bp regions around the centers of 753 PBRs.

We found that palindromic or tandem motif pairs connected by 4–5 W bases were enriched in PBR sequences as shown in Table 4 supporting the involvement of the TGGNA motif in AbrB/Abh-binding. This result is consistent with *in vitro* experiments which have shown that AbrB binds to tandem repeats with 5 bp spacing (Xu & Strauch, 1996). It is interesting to note that the context of W (A or T) instead of N (any base) in the spacer region discovery in this study makes the recognition more strict because the coincidence of the motif with this spacer is significantly increased compare to that of N spacer. However, the coincidence of the motif was detected in only 166 of 753 PBRs (22%). This may indicate that TGGNA-motif-dependent AbrB/Abh binding is relatively relaxed in specificity and that other constraints are required to restrict the targets to PBR regions because a search for possible binding sites allowing a two basepair mismatch resulted in loss of site enrichment in PBR regions.

Sequence ID	paired TGGNA mo	tifs <sup>a</sup>	No. on genome <sup>b</sup>	No. in PBR <sup>c</sup>	coincidence (%) <sup>e</sup>	Enrichment (fold) <sup>d</sup>
Palindrome-1						
Pa1W0	TNCCA	TGGNA	1291	61	4.7	1.3
Pa1W1	TNCCA W	TGGNA	965	40	4.1	1.2
Pa1W2	TNCCA WW	TGGNA	620	29	4.7	1.3
Pa1W3	TNCCA WWW	TGGNA	394	20	5.1	1.4
Pa1W4	TNCCA WWWW	TGGNA	203	58	28.6	8.0
Pa1W5	TNCCA WWWWW	TGGNA	50	17	34.0	9.5
Pa1W6	TNCCA WWWWWW	TGGNA	64	9	14.1	3.9
Palindrome-2						
Pa2W0	TGGNA	TNCCA	1294	73	5.6	1.6
Pa2W1	TGGNA W	TNCCA	816	67	8.2	2.3
Pa2W2	TGGNA WW	TNCCA	555	38	6.8	1.9
Pa2W3	TGGNA WWW	TNCCA	276	18	6.5	1.8
Pa2W4	TGGNA WWWW	TNCCA	143	27	18.9	5.3
Pa2W5	TGGNA WWWWW	TNCCA	32	13	40.6	11.4
Pa2W6	TGGNA WWWWWW	TNCCA	44	2	4.5	1.3
Direct repeat						
DrW0	TGGNA	TGGNA	3026	123	4.1	1.1
DrW1	TGGNA W	TGGNA	2187	112	5.1	1.4
DrW2	TGGNA WW	TGGNA	1186	73	6.2	1.7
DrW3	TGGNA WWW	TGGNA	695	39	5.6	1.6
DrW4	TGGNA WWWW	TGGNA	410	69	16.8	4.7
DrW5	TGGNA WWWWW	TGGNA	83	26	31.3	8.8
DrW6	TGGNA WWWWWW	TGGNA	113	15	13.3	3.7

Table 4. Coincidence of various paired TGGNA motifs with AbrB/Abh peaks on the B. subtilis genome

<sup>*a*</sup> Query sequences for searching paired TGGNA motifs.

<sup>b</sup> Total number of sequences matched to query allowing 1 base mismatch.

<sup>c</sup> Numbers of matched sequences located within 100 bp of centers of PBRs.

<sup>d</sup> Proposed relevant sequences located in PBRs.

<sup>e</sup> Enrichment of matched sequences in PBR relative to the whole genome

#### 7. AbrB plays a major role in control of gene expression whereas Abh has a minor effect

To understand the correlation between AbrB/Abh binding and transcriptional regulation, we analyzed genome-wide transcriptional profiles in wild-type (strain 168),  $\Delta abrB$  (OC003),  $\Delta abh$ (OC004), and  $\Delta abrB \Delta abh$  (OC005) cells during exponential growth, using the Affymetrix tiling chip employed for ChAP-chip experiments, and the results are summarized in Supplementary Table S1. Scatter plots of the transcriptional intensities of each gene in deletion mutant cells compared with wild-type cells (Figure 16A and 16B) indicated that, as expected, deletion of *abrB* affected the expression of many genes, whereas *abh* deletion had little impact on the gene expression profile. Furthermore, the effect of the *abrB/abh* double deletion on the transcriptome was similar to that of the *abrB* deletion alone (Figure 16C).



Figure 16. Transcriptome analysis in  $\Delta abrB$  and  $\Delta abh$  mutants. Log-scale scatter plots of transcriptional intensities of each gene in  $\Delta abrB$  (A, y-axis) and  $\Delta abh$  (B, y-axis) cells compared to those of wild-type cells (A and B, x-axis), and  $\Delta abrB\Delta abh$  cells (C, y-axis), in comparison with that of  $\Delta abrB$  cells (C, x-axis). The averaged signal intensities from two independent experiments using each strain are plotted.

Next, we searched for genes that were up- or down-regulated by more than 2.5-fold in mutant cells compared with wild-type cells, and investigated if AbrB/Abh-binding signals

overlapped with the transcription start sites (TSSs) identified in our transcriptome analysis. We found that among 250 genes which were down-regulated by more than 2.5-fold in *AabrB* mutant cells, 171 genes with various functions belonging to 90 transcriptional units (TUs), are associated with AbrB at their TSSs suggesting that these TUs were specifically repressed by AbrB probably via protein binding to promoter regions (Table 5A). Notably, and consistent with the observation that *abh* deletion did not affect (or only marginally affected) expression, Abh-binding signals in the promoter regions of the 90 TUs were generally low (classes VL or L) in an *abrB* deletion background and major of them belong to profile P02 and P03 (Table 5A and figure 17). However, significant levels of Abh binding (classes M or H, P01) were detected in 20 operons, indicating that Abh binding in these regions did not significantly affect transcription (Table 5A and figure 17).

The AbrB-regulated TUs identified included 11 operons/genes previously reported to be directly repressed by AbrB; these were *spoVG*, *spoOE*, *sboAX-albABCDEFG*, *yknWXYZ*, *yxzE*, *tasA-sipW-yqxM*, *sunA-bdbB*, *skf* (*ybcO-ybcE*), *sdp*(*yvaWXY*), *yxaAB* and *eps*(*yvfF-yvek*) (Table 6). Derepression of the five TUs shown in Table 6, *sigH*, *sinIR*, *sigW-ybbM*, *comK*, and *slr*, was also seen in the *abrB* mutant, although the enhancement values (1.4–2.4-fold) were below our inclusion criterion. It is probable that expression levels of such genes during the exponential growth phase is lower than that in stationary phase, which has been examined in previous reports. No data supporting the previously reported direct repression by AbrB of a further six operons were obtained in the present work, although our data indicate that the *pbpE- racX*, *lia*, and *yvlABCD* operons were indirectly affected by *abrB* deletion. The reasons for these inconsistencies are not presently clear.

On the other hand, AbrB has previously been reported to act as a transcriptional activator of the ribose uptake (*rbs*) operon (Strauch, 1995a), and our data support this conclusion (Table 5B). In addition, we found that four other operons involved in carbohydrate utilization, *glp*, *gnt*, *gmu*, and *amyE*, were activated. Expression of the *citB* and *hut* operons has also been reported to be activated by AbrB (Fisher et al, 1994; Kim et al, 2003). However, we found no effect of AbrB on *hutB* expression and indirect repression of *citB* expression by AbrB. Transcription of other additional 42 genes whose AbrB bindings were not detected in their promoter region were also affected (decrease transcription level) in  $\Delta abrB$  suggesting that AbrB might indirectly activation those genes.

We also identified possible promoters directly regulated by Abh, although the number of such promoters was limited, as expected based on the overall effect of *abh* deletion on the transcriptome profile. In the case of the *glp* operon described above, strong Abh binding in a wild-type background and a moderate reduction of expression in an *abh*-deletion background were evident, indicating that the Abh homomer may act as an activator of this operon. At the *sunA* promoter, Abh bound with the same profile as shown by AbrB but had a different effect; Abh acted as an activator, whereas AbrB was a repressor, as previously reported (Luo & Helmann, 2009; Strauch et al, 2007) (Table 5C). We also found that Abh repressed the expression of six operons/genes, *yflA*, *ylaE*, *ctaCDEFG*, *yojL*, *ycdA* and *ywoF*, in a manner additive to the effect of AbrB (Table 5D). Finally, *abh* deletion resulted in stronger derepression of the *srf* operon compared with that seen with *abrB* deletion (Table 5E). However, Abh binding to the *srf* promoter in the *abrB*-deletion background was weak whereas AbrB binding was retained in the *abh*-deletion strain. Thus, the molecular mechanism by which *srf* operon expression is regulated by AbrB/Abh remains unclear.

These results clearly indicate that AbrB regulates the expression of many operons, acting mainly as a repressor but also as an activator in a limited number of instances. In contrast, Abh binding affords transcriptional regulation of only a small number of operons, at least during exponential growth.

							Expression ratio <sup>c</sup>		Signal intensity of RNA			NA		
Operon	Gene/	Alternate Gene	Gene Function	Start	End	Strand/ Center	abrB	∆abrB ∆abh	∆abh				AabrB	
operon	PBR ID	Name		Suit		position <sup>b</sup>	Abr B I	ninding <sup>c</sup>	Abh Bi	inding <sup>c</sup>	Wild	∆abrB	∆abh	∆abh
						-	wild	∆abh	wild	∆abrB				
A: Repr	essed by Al	brB												
	25	-		55586	56001	55794	12.3	18.0	2.6	2.5				
1	snoVG		regulator required for spore	55864	56157		3.36	3 42	1 20		7085	22826	24250	0115
1	spove		cortex synthesis	55604	50157	÷	3.30	5.42	1.29		7085	23820	24239	9115
	54			155037	155452	155245	10.6	17.7	6.2	4.1				
2	ybaJ		putative methyltransferase	155155	155922	+	2.39	2.53	0.88		1873	4476	4735	1639
2	75	1.64		213445	214387	213916	56.7	72.2	27.9	6.1	070	2022	0007	070
3	ybcO	skfA	sporulation killing factor A	213926	214093	+	8.96	11.20	1.11		8/9	/8//	9837	972
	ybcP	skfB	factor A	214160	215392	+	8.55	10.25	0.98		456	3900	4677	448
	ybcS	skfC	biosynthesis and export	215389	215946	+	7.10	8.29	1.06		423	2999	3503	449
			cell killing factor production,											
	ybcT	skfD	probable membrane-bound	215943	216878	+	6.75	7.82	1.06		528	3560	4123	560
			metalloprotease sporulation killing factor											
	ybdA	skfE	biosynthesis and export	216897	217616	+	7.96	8.79	1.21		407	3240	3579	493
	vbdB	skfF	sporulation killing factor	217681	219027	+	4.23	4.65	1.11		435	1842	2021	482
	<i></i>	~···j=	biosynthesis and export											
	ybdD	skfG	biosvnthesis and export	219074	219487	+	5.45	6.02	1.13		518	2821	3116	584
			sibling killing effect; sporulation											
	ybdE	skfH	killing factor biosynthesis and	219593	220018	+	4.87	4.98	1.23		141	687	702	174
4	whdN		export	224063	224020		22.60	24.08	1.01		265	5000	6621	260
4	80		putative pliage protein	224003	224920	-	36.5	59.9	20.9	51	205	3990	0021	209
	80			224495	225420	224958	36.5	59.9	20.9	51				
5	vbdO		putative phage protein	225052	226236	+	7.64	7.29	1.16	0.1	388	2969	2833	451
	92		1 0 1	249706	250104	249905	12.2	18.9	5.9	2.0				
6	ybfO		putative exported hydrolase	249967	251307	+	16.08	18.13	0.77		527	8471	9549	408
	ybfP		putative transcriptional regulator	251415	252302	+	8.95	9.95	0.98		547	4897	5443	536
	104			291016	292315	291666	85.5	135.3	56.5	31.7				
7	lin		secreted alkalinhilic linase	291757	292395	+	11.40	13.19	1.83	5117	980	11178	12933	1791
	167			544945	545292	545119	16.1	15.8	4.5	0.7				
8	yddJ		putative lipoprotein	545156	545536	+	2.49	3.42	1.07		243	605	830	261
	178		* * *	555944	556155	556050	8.8	6.9	1.4	0.2				
9	yddT		putative phage protein	556306	556992	+	4.55	6.17	0.71		1440	6552	8888	1017
	186			566484	567596	567040	34.3	57.4	23.2	5.4				
10	ydeH		putative integral inner membrane	567206	567652	+	3.24	2.61	1.24		397	1287	1036	494
11	vde I		protein	568834	569493		3.45	3 31	0.78		673	2322	2227	522
	187		nutative lipoprotein	569442	569704	569573	12.3	67	0.70	-03	075	2522	2221	522
	215		pututi e apopiotem	670580	670859	670720	8.1	8.3	3.2	0.9				
12	pspA		phage shock protein A homolog	670793	671476	+	2.92	3.08	1.49		4246	12395	13066	6323
	vdiG		nutative phage replication protein	671542	672567	+	3.11	3 37	1.66		2648	8778	8974	4388
	yujo			071042	672507		0.11	0.07	1.00		2040	0220	0010	4500
	ydjH		conserved hypothetical protein	672567	6/3331	+	2.90	3.13	1.58		2557	7418	8012 5269	4034
	ydjl		putative phage protein	0/3362	0/4333	+	2.66	2.85	1.47		1885	5016	5368	2111
13	ydjL	bdhA	dehydrogenase	677459	678499	-	3.88	3.84	0.60		5422	21036	20846	3267
	217			678604	679070	678837	19.7	27.3	2.0	0.8				
	235			723994	724426	724210	30.2	26.7	5.3	5.1				
14	yerI		putative kinase	724326	725336	+	4.48	4.27	0.97		2600	11644	11104	2526
	249			750123	750351	750237	4.1	6.5	0.2	-0.3				
15	rapH		response regulator aspartate phosphatase	750293	751588	+	8.28	8.14	0.87		330	2730	2684	285
16	yfmI		putative efflux transporter	818648	819868	-	2.45	2.78	0.89		245	600	681	218
	265			819466	820408	819937	69.5	95.1	57.3	9.7				

								Expressi	on ratio	с	Si	gnal inter	nsity of F	RNA
Operon	Gene/	Alternate Gene	Gene Function	Start	End	Strand/ Center	abrB	∆abrB ∆abh	∆abh				∆abrB	
-	PBR ID	Name				position $^{b}$	AbrB   wild	binding <sup>c</sup> ⊿abh	Abh B wild	inding <sup>c</sup> ∆abrB	Wild	∆abrB	∆abh	∆abh
	265			819466	820408	819937	69.5	95.1	57.3	9.7				
17	vfmH		function unknown and unique	820066	820137	+	26.13	27.09	0.93		799	20880	21647	741
17	ymai ymG		conserved hypothetical protein	820000	821667		AA 97	27.0) 46.47	1.00		210	9855	10184	218
	272		conserved hypothetical protein	842700	8/13800	8/3205	53.3	25.0	71.5	110.2	219	9855	10104	218
18	212		function unknown and unique	842597	843730	043293	3.68	5.40	1.02	110.2	222	877	1226	227
10	yjiC v#P		aconserved hypothetical protein	043307 942721	043739 042001	+	3.00	7.41	1.02		152	612	1220	170
	272		conserved hypothetical protein	1044042	1044457	1044250	4.03	22.1	5.4	2.0	152	015	1127	179
10	s25		function unknown and unique	1044345	1044506	1044250	3.82	2.5.1	1.01	2.0	742	2835	2227	750
19	378		function unknown and unque	1061535	1062273	1061004	40.7	21.7	45.3	5.4	742	2835	2331	750
20	vhaQ		putative ABC-2 type transport	1061899	1062795	+	3.67	3.55	1.76	5.4	2146	7869	7611	3784
	y ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		system ATP-binding protein putative ABC-2 type transport	1062788	1064047	+	3 78	3.60	1.86		2342	8851	8442	4368
	240.2		system permease protein	11002700	11201.00	1120020	11.0	10.1	2.1	0.4	2012	0001	0112	1500
21	349.2	ntdP	transcriptional regulator of the	1128872	1129168	1129020	6.53	6.14	2.1	-0.4	172	1126	1058	222
21	ynjm vicM	man	ntd operon	1263014	1264243	-	3.04	2.97	1.35		3035	9227	9004	4202
22	380		conserved hypothetical protein	1263088	1264793	126/301	81.0	87.7	21.5	22	5055	/221	2004	4202
23	widB		nutative exported protein	1269045	1269392	1204571	35.41	32.81	0.90	2.2	30/	13050	1203/	355
25	382		putative exported protein	1269157	1269894	1269526	40.9	64.6	13.9	-04	574	13737	12754	555
24	vidG		nutative acetyltransferase	1275650	1276156	-	5.13	4 17	0.95	0.4	370	1896	1544	352
2.	384		parative acception in an or conservation	1275939	1276439	1276189	23.9	36.1	38	14	570	1070	1011	002
25	ctaO		protoheme IX farnesyltransferase (heme Osynthase)	1278825	1279814	-	6.03	11.96	1.21		210	1265	2511	255
	387			1279033	1280502	1279768	101.4	133.9	112.4	202.3				
	427			1/20772	1/30136	1/2005/	19.0	18.8	0.7	17				
26	spo0E		phosphatase acting on Spo()A-P	1/20002	1/302/0	1427754	3.04	2.74	0.80	1.7	765	2330	2008	681
	438		phosphatase acting on SpooA-1	1429992	1450249	1467014	44.6	56.2	22.3	0.5	705	2330	2098	081
	450		penicillin-binding protein for	1400079	1407547	140/014	-1.0	50.2	22.5	0.5				
27	ykuA	pbpH	formation of rod-shaped peptidoglycan cell wall	1467109	1469166	+	3.10	3.19	0.76		1706	5288	5434	1301
	446			1491193	1491829	1491511	54.8	63.4	14.7	0.8				
28	ykuU		putative 2-cys peroxiredoxin	1491568	1492110	+	10.81	12.82	1.17		896	9689	11489	1051
	ykuV		thiol-disulfide isomerase	1492182	1492643	+	9.91	11.75	1.22		659	6529	7741	802
	449			1502685	1503117	1502901	17.7	9.8	6.3	10.0				
29	yknW		SdpC toxin resistance	1502889	1503584	+	3.76	4.28	1.53		4027	15157	17250	6150
	yknX		SdpC toxin resistance	1503589	1504722	+	3.42	4.01	1.44		3888	13306	15596	5605
	yknY		SdpC toxin resistance, probable ABC transport system ATP-	1504723	1505415	+	4.31	5.21	1.64		3241	13975	16877	5310
	yknZ		SdpC toxin resistance, probable ABC transport system permease	1505412	1506605	+	3.70	4.52	1.42		3401	12593	15366	4815
30	nprE		extracellular neutral	1539343	1540908	-	2.93	3.90	1.43		587	1719	2292	840
	459		пыланортоцеазе	1540714	1541180	1540947	21.4	11.8	4.0	-0.3				
31	vlbA		conserved hypothetical protein	1564654	1565016	-	4.80	4.77	1.95		1995	9578	9512	3888
	467			1564837	1565235	1565036	30.4	18.5	7.6	-0.2				
	474			1604600	1605032	1604816	24.7	26.5	6.1	44.2				
32	sigG		sporulation-specific sigma factor	1604927	1605709	+	2.32	2.54	0.93		250	581	634	233
33	ylaB		conserved hypothetical protein	1670466	1670951	-	28.68	32.60	2.36		458	13128	14919	1081
22	486		,	1670747	1671315	1671031	44.1	54.9	33.2	36.8				
34	vm7R		conserved hypothetical protein	1859209	1859565		4 87	6.66	0.89		322	1566	2142	286
54	ymaF		putative hydrolase	185964/	1860347	-	6.65	8.91	1 33		158	1047	1403	210
	530		r	1860178	1860729	1860454	35.6	41.7	10.9	0.6	100	1.047	1 100	210
35	vncM		conserved hypothetical protein	1902720	1903472		4 32	4,57	0.86	0.0	1605	6931	7335	1374
55	546			1903188	1903841	1903515	27.3	15.0	7.2	0.0	1000	0701	, 335	10/4
36	vnzD		Spo()A-P phosphatase	1922050	1922223		4 71	3.05	0.99	0.0	155	731	473	154
	555		T T T T T T T T T T T T T T T T T T T	1922092	1922490	1922291	24.9	22.1	6.7	-1.3	100	, , , 1		107
				/	//	/								

								Expressi	on ratio	с	Si	gnal inter	nsity of R	NA
Operon	Gene/ PBR ID	Alternate Gene	Gene Function	Start	End	Strand/ Center	abrB	∆abrB ∆abh	∆abh		33/21.4	A abuD	∆abrB	Achh
	F BK ID	Name				position <sup>b</sup>	AbrB wild	binding <sup>c</sup> ⊿abh	Abh B wild	inding <sup>c</sup> ⊿abrB	Wild	Дabrb	∆abh	⊿abn
37	ynfF	xynC	endo-xylanase	1941923	1943191	-	3.65	3.62	0.82		331	1207	1196	271
	rvnD		endo-1,4-beta-xylanase (xylanase	1943322	1944863	_	3 22	3.06	0.84		196	630	599	164
	<i>xyn</i> 2		D)	1044540	1045504	10.450.25	5.22	5.00	0.04	2.2	170	050	577	104
	565		44	1944549	1945524	1945037	65.3	108.7	6.1	-3.3	200	200	20.4	200
38	ppsE		plipastatin synthetase	1959407	1963246	-	1.87	1.89	1.00		209	390 422	394 427	208
	ppsD		plipastatin synthetase	1963254	19/4065	-	2.27	2.25	1.02		190	432	427	180
	ppsC		plipastatin synthetase	1974090	1981/5/	-	2.80	3.45	1.05		159	590	585	173
	ррѕв		plipastatin synthetase	1981//4	1989450	-	3.89	4.05	1.09		138	506	642	1/3
	581		piipastatiii syntiietase	1969461	1997100	-	4.36	4./1	1.05	15	150	390	042	142
	598			2049524	2050312	2049918	73.0	82.6	55.0	-1.5				
39	yobB		putative transcriptional regulator	2049324	2050312	+	12.22	18.14	0.99	50.7	152	1858	2759	150
	602.2		nomouetenophage	2061084	2061584	2061334	30.4	19.2	9.8	-2.0				
40	rapK		response regulator aspartate phosphatase	2061361	2062476	+	6.54	8.53	1.31		154	1003	1310	201
	phrK		secreted regulator of	2062473	2062595	+	3.80	4.15	1.17		761	2891	3157	889
	600		phosphatase RapK	2075007	2075405	2075206	16.6	76	5.4	20				
	009		nutative phage-related pre-neck	2073007	2073403	2073200	10.0	7.0	5.4	2.0				
41	yobO		appendage protein	2075417	2077837	+	2.87	4.62	1.05		177	509	820	186
	616			2087264	2087543	2087404	7.8	15.8	0.1	0.1				
42	yocD		putative carboxypeptidase	2087468	2088445	+	2.51	1.87	0.83		549	1377	1028	455
43	phy 639		phytase	2149306 2150419	2150454 2150714	- 2150567	2.98 9.2	3.32 11.1	1.08 1.2	-0.6	136	405	451	146
44	yorD		hypothetical protein; phage Spbeta	2186181	2186495	-	7.55	6.80	1.11		1453	10966	9881	1613
	652			2186205	2186857	2186531	56.1	76.4	23.8	1.4				
	655			2194874	2195527	2195201	64.8	93.1	29.3	-1.4				
45	yoqM		putative membrane bound protein; phage Spbeta	2195182	2195460	+	14.32	16.13	0.86		164	2353	2651	142
	671			2247251	2247836	2247544	43.7	28.0	25.6	16.3				
46	yomJ		putative phage immunity protein; phage Spbeta	2247613	2248296	+	3.30	3.19	1.70		521	1720	1659	886
47	680		(D) ( )	22/12/2	22/1653	22/1463	14.5	21.0	0.5	-1.1	126	162	520	112
4/	yolC		SP beta phage protein	22/1352	22/168/	+	3.40	3.89	0.85		130	463	530	113
48	yolB		phage SPbeta exported protein of unknown	2271730	2272086	-	4.30	3.77	0.62		545	2347	2054	339
	yolA		function; phage SPbeta	2272092	2272559	-	4.14	3.86	0.58		2374	9817	9171	1374
	681			2272343	2273165	2272754	57.5	85.7	-1.1	2.2				
49	yokL		putative acetyltransferase; phage SPbeta	2273185	2273718	-	2.35	2.37	0.95		748	1754	1775	712
	yok K		conserved hypothetical protein; phage SPbeta	2273754	2274332	-	2.78	2.84	1.10		804	2234	2282	881
	yok <b>J</b>		phage SPbeta	2274396	2274893	-	3.30	3.51	1.10		1006	3324	3528	1108
	yokI		phage SPbeta	2274902	2276617	-	5.16	5.46	0.97		415	2142	2266	401
	684			2276593	2276804	2276699	6.3	6.5	-0.2	0.1				
50	qcrC		menaquinol:cytochrome c oxidoreductase (cytochrome cc subunit)	2362307	2363074	-	4.42	4.44	2.01		1976	8737	8785	3975
	qcrB		menaquinol:cytochrome c oxidoreductase (cytochrome b subunit)	2363109	2363783	-	4.00	3.94	1.86		2703	10810	10640	5037
	qcrA		menaquinol:cytochrome c oxidoreductase (iron-sulfur subunit)	2363785	2364288	-	4.18	3.99	1.79		3527	14753	14064	6325
	714			2363990	2364626	2364308	51.4	67.0	42.9	2.4				
51	yphF		putative lipoprotein	2387051	2387785	-	2.27	2.57	1.65		735	1669	1891	1217
	yphE		conserved hypothetical protein	2387807	2388010	-	2.65	2.27	1.55		585	1548	1325	907
	721			2387824	2388358	2388091	25.1	18.7	34.1	29.1				

								Expressi	on ratio	с	Si	gnal inter	nsity of R	NA
Operon	Gene/	Alternate Gene	Gene Function	Start	End	Strand/ Center	abrB	∆abrB ∆abh	∆abh				AabrB	
operon	PBR ID	Name		Suit		position <sup>b</sup>	AbrBl	vinding <sup>c</sup>	Abh R	indina <sup>c</sup>	Wild	∆abrB	<u>A</u> abh	∆abh
							wild	Aabh	wild	AahrB				
52	sigF		sporulation-specific sigma	2442618	2443385	-	3.17	3.38	1.30		283	897	956	369
	spoIIAB		anti-sigma factor (antagonist of sigma(F)) and serine kinase	2443397	2443837	-	4.74	5.18	1.53		266	1261	1377	407
	spoIIAA		anti-anti-sigma factor (antagonist of SpoIIAB)	2443834	2444187	-	4.47	4.68	1.46		518	2315	2426	759
	dacF		D-alanyl-D-alanine carboxypeptidase	2444283	2445452	-	2.10	2.65	1.05		175	369	466	185
	737		(pencilifoliang protein)	2445284	2445818	2445551	52.2	24.6	43.4	3.6				
53	tasA		major biofilm matrix component	2552313	2553098	-	17.64	18.54	0.60		809	14267	14997	483
	sipW		type I signal peptidase	2553162	2553734	-	12.58	13.65	0.88		344	4328	4695	304
	yqxM		lipoprotein for biofilm formation	2553718	2554479	-	10.50	10.72	0.87		107	1119	1142	93
	766			2554237	2555179	2554708	78.4	98.8	33.7	-3.4				
	766			2554237	2555179	2554708	78.4	98.8	33.7	-3.4				
54	yqzG		putative exported protein	2554751	2555077	+	2.36	2.94	0.82		139	327	408	113
55	cccA		cytochrome c550	2598756	2599118	-	2.68	2.55	1.17		1261	3385	3219	1471
	781			2598862	2599685	2599274	78.4	67.5	54.9	5.4				
	783			2601854	2602490	2602172	44.3	58.1	19.2	4.5				
56	antE		dnaGoverlapping gene of	2602212	2602508	+	2.91	2.56	0.77		358	1041	915	274
	801			2659178	2659729	2659454	55.3	68.4	32.0	17.6				
57	phrE		regulator of phosphatase RapE	2659557	2659691	+	4.13	4.21	0.94		2708	11182	11409	2549
	802			2660130	2660375	2660253	6.6	9.5	0.5	0.2				
58	yqcG		putative phage DNA manipulating enzyme; skin element	2660329	2661924	+	2.35	2.61	0.84		854	2007	2227	720
59	yqxJ		hypothetical protein; skin element	2662778	2663140	-	3.77	4.57	0.73		437	1649	2000	319
	yqxI		hypothetical protein; skin element	2663156	2663635	-	7.21	8.29	0.92		665	4796	5513	610
	804			2663326	2663996	2663661	69.7	83.6	36.8	-1.1				
	809			2690577	2691043	2690810	25.2	30.7	3.9	-1.7				
60	yqaP		conserved hypothetical protein; skin element	2690868	2691797	+	3.59	3.74	0.89	_	2458	8812	9186	2197
	822			2738500	2738779	2738640	15.2	13.6	0.2	-1.0				
61	yrpD		putative lipoprotein	2738712	2739419	+	4.60	4.75	0.86		4973	22864	23602	4301
62	csn		chitosanase	2747210	2748043	-	11.95	11.94	0.67		725	8664	8653	485
	826		concourted hypothetical protein	2/4/86/	2/48265	2/48066	16.9	19.3	3.1	0.3				
63	yrzI		induced by formaldehyde	2778150	2778299	-	4.76	3.97	1.20	10	279	1331	1109	335
	842			21/8332	2779001	2//800/	31.5	61.6	35.9	0.9				
61	897		nutativa linonrotain	2952577	2955004	2952721	42.1	2.52	40.5	21.8	116	1751	1570	657
	961		putative ipopiotein	3186072	3186776	3186424	38.0	64.0	6.4	0.5	440	1751	1570	057
65	yuaR		conserved hypothetical protein	3186542	3187087	+	15.95	17.25	0.4	0.5	1128	17987	19456	513
66	tlnA		methyl-accepting chemotaxis	3207319	3209307	-	7.55	7 31	1.04		178	1345	1303	185
00	967		, i b	3209005	3209794	3209400	63.1	92.9	11.5	10	170	10.0	1000	100
67	dhbF		dihydroxy-benzoyl-glycin biosynthesis	3279544	3286680	-	12.72	11.86	1.02	110	1022	13001	12124	1045
	dhbB		dihydroxy-benzoyl-glycin biosynthesis	3286700	3287638	-	9.62	9.36	1.12		1467	14108	13733	1647
	dhbE		dihydroxy-benzoyl-glycin biosynthesis	3287666	3289285	-	7.88	7.55	1.14		1939	15282	14633	2207
	dhbC		dihydroxy-benzoyl-glycin biosynthesis	3289314	3290510	-	8.09	7.92	1.19		2378	19242	18821	2822
	dhbA		dihydroxy-benzoyl-glycin biosynthesis	3290536	3291321	-	6.68	6.79	1.17		2153	14379	14620	2514
	yuiI		trilactone hydrolase	3291515	3292459	-	6.22	6.13	1.20		1858	11557	11393	2225
	987			3292237	3292737	3292487	35.7	41.9	8.2	1.5				
	993			3342710	3343346	3343028	33.4	30.5	18.7	31.0				
68	yurI	bsn	extracellular ribonuclease	3343140	3344006	+	2.67	3.17	1.68		394	1052	1247	662

								Expressi	on ratio	c	Si	gnal inter	nsity of R	NA
Operon	Gene/	Alternate Gene	Gene Function	Start	End	Strand/ Center	abrB	∆abrB ∆abh	∆abh				∆abrB	
	PBR ID	Name				position $^{b}$	AbrB l	oinding <sup>c</sup>	Abh B	inding <sup>c</sup>	Wild	∆abrB	∆abh	∆abh
							wild	Aabb	wild	AahrR				
							-type	duon	-type	Autorb				
69	yvqJ		putative efflux protein	3398118	3399386	-	3.83	4.66	1.16		263	1009	1226	305
	1005		putative APC transporter (ATD	3399133	3399752	3399443	39.1	31.2	11.0	1.3				
70	yvrN		binding protein)	3411158	3412408	-	3.56	3.64	1.13		1397	4977	5079	1575
	yvrO		putative ABC transporter (ATP- binding protein)	3412380	3413069	-	3.23	3.37	1.02		1638	5286	5521	1676
	yvrP		putative ABC transporter component	3413053	3414246	-	3.11	3.14	1.10		1718	5343	5394	1881
	1008			3414093	3414491	3414292	21.3	25.7	7.2	0.6				
	1011			3426384	3426867	3426626	35.0	45.7	25.1	5.1				
71	yvgO		conserved hypothetical protein	3426832	3427317	+	7.29	12.70	1.14		261	1900	3310	297
	1019			3462747	3463723	3463235	61.9	101.9	45.2	9.9				
72	yvaW	sdpA	export of SdpC killing factor	3463320	3463796	+	83.02	80.54	1.30		94	7811	7577	122
	yvaX	sdpB	export of SdpC killing factor	3463793	3464764	+	71.62	68.36	1.23		148	10565	10083	181
	yvaY	spbC	killing factor SdpC	3464807	3465418	+	65.94	60.61	1.27		360	23744	21826	456
73	<i>yvfF</i>	epsO	putative pyruvyl transferase	3513146	3514114	-	8.58	9.73	0.90		297	2551	2894	267
	yvfE	epsN	putative aminotransferase	3514093	3515259	-	7.60	8.27	0.96		476	3615	3937	455
	yvfD	epsM	putative O-acetyltransferase	3515264	3515914	-	4.79	5.37	1.06		400	1914	2144	425
	yvfC	epsL	putative phosphotransferase involved inextracellular matrix synthesis	3515911	3516519	-	4.76	5.55	1.06		449	2136	2490	477
	yvfB	epsK	putative extracellular matrix componentexporter	3516516	3517553	-	5.43	6.39	1.06		386	2097	2470	409
	yvfA	epsJ	putative glycosyl transferase	3517703	3518032	-	3.70	4.38	0.88		1132	4188	4958	995
	yveT	epsI	putative polysaccharide pyruvyl transferase	3518029	3519063	-	7.27	8.33	0.97		568	4133	4736	552
	yveS	epsH	putative glycosyltransferase involved in biofilmformation	3519060	3520136	-	6.09	7.11	0.97		466	2840	3311	453
	yveR	epsG	biofilm extracellular matrix formation enzyme	3520141	3521175	-	6.95	7.77	1.10		452	3143	3512	498
	yveQ	epsF	putative glycosyltransferase involved inextracellular matrix formation	3521200	3522303	-	5.35	6.06	0.94		558	2983	3382	526
	yveP	epsE	putative glycosyltransferase	3522300	3523454	-	6.42	7.33	1.05		345	2216	2532	361
	yveO	epsD	putative extracellular matrix biosynthesisenzyme	3523447	3524283	-	6.39	7.07	0.99		382	2443	2700	380
	yveN	epsC	putative UDP-sugar epimerase	3524280	3525425	-	6.72	7.51	0.92		584	3924	4381	535
	yveM	epsB	protein tyrosine kinase	3525437	3527233	-	4.68	5.33	0.99		434	2029	2311	431
	yveL	epsA	modulator of protein tyrosine kinase EpsB	3527492	3528175	-	8.93	8.71	0.94		325	2903	2830	304
	yveK	slrR	transcriptional regulator involved in biofilm formatiom	3528181	3528885	-	8.83	7.98	0.91		349	3084	2790	317
	1032			3528707	3529292	3529000	18.8	19.9	4.7	-0.6				
	1032.1			3529302	3530142	3529722	45.5	62.1	25.8	8.0				
74	pnbA		para-nitrobenzyl esterase (intracellular esterase B)	3529665	3531134	+	10.02	11.25	1.72		787	7891	8855	1351
	1049			3600906	3601134	3601020	3.8	8.0	0.8	0.3				
75	yvnA		putative transcriptional regulator	3601104	3601577	+	4.08	3.16	0.80		224	916	709	179
76	cypX		putative monooxygenase (cytochrome P450)	3601618	3602835	-	4.42	4.51	0.78		581	2568	2621	454
	yvmC		conserved hypothetical protein	3602851	3603597	-	5.00	4.79	0.81		594	2970	2844	481
	1050			3603609	3604075	3603842	14.3	33.1	1.5	-0.6				
77	ywqE	ptpZ	protein tyrosine-phosphatase	3730032	3730796	-	2.88	2.59	0.98		612	1765	1582	603
	ywqD	ptkA	protein tyrosine kinase, phosphorylating Ugd, TuaD and	3730849	3731562	-	3.15	2.92	0.85		1723	5430	5038	1458
	ywqC	tkmA	modulator of PtkA protein	3731552	3732298	-	4.33	3.60	0.97		607	2631	2186	591
	1100			3732163	3732595	3732379	15.5	25.2	10.5	01				

							Expression ratio <sup>c</sup>		c	Signal intensity of RNA				
Operon	Gene/	Alternate Gene	Gene Function	Start	End	Strand/ Center	abrB	∆abrB ∆abh	∆abh				AahrR	
- <b>F</b>	PBR ID	Name				position <sup>b</sup>	Abr B b	inding <sup>c</sup>	Abh B	inding <sup>c</sup>	Wild	∆abrB	∆abh	∆abh
							wild	∆abh	wild	∆abrB				
	1129			3834673	3835139	3834906	26.1	36.4	7.7	2.4				
78	shoA		subtilosin A	3835081	3835212	+	10.54	11.78	0.98		562	5925	6624	553
	shoX		putative bacteriocin-like product	3835169	3835321	+	4 66	5.13	1.05		107	499	549	112
	1129.1		F	3835149	3835666	3835408	32.4	46.3	18.6	1.5				
79	albA		putative antilisterial bacteriocin (subtilosin) production enzyme	3835346	3836692	+	5.54	5.59	1.32	10	1502	8319	8398	1987
	albB		putative membrane component involved in subtilosin production	3836705	3836866	+	3.58	3.89	1.10		1906	6829	7409	2097
	albC		putative transporter involved in subtilosin production	3836863	3837582	+	3.91	4.04	1.14		1034	4043	4177	1176
	albD		proteininvolved in subtilosin production and immunity	3837575	3838885	+	3.61	3.78	1.13		937	3377	3537	1058
	albE		putative hydrolase involved in subtilosin production	3838875	3840035	+	4.02	4.36	1.13		412	1659	1800	468
	albF		putative peptidase involved in subtilosin production	3840040	3841320	+	3.17	3.62	1.12		419	1327	1518	467
	albG		putative integral inner membrane protein involved in subtilosin production and immunity	3841317	3842018	+	2.03	2.38	1.12		352	717	839	394
80	rocA		delta-1-pyrroline-5 carboxylate dehydrogenase	3877988	3879535	-	8.71	10.10	1.01		870	7576	8784	880
	rocG		glutamate dehydrogenase	3879762	3881036	-	6.69	8.91	0.98		728	4868	6481	714
	yweA		member of the processed secretome	3881213	3881677	-	11.21	12.85	1.06		1387	15543	17826	1475
	1141			3881491	3882178	3881835	41.9	61.7	10.9	2.5				
	1161			3933103	3933586	3933345	33.0	21.1	26.1	1.7				
81	ywbF		putative sugar permease	3933380	3934579	+	2.69	2.63	1.32		850	2289	2238	1122
	1168			3981638	3982342	3981990	43.8	47.6	60.9	33.2				
82	yxzE		putative bacteriocin	3981992	3982192	+	3.27	3.29	1.42		1379	4516	4543	1954
	1198			4064734	4065251	4064993	17.7	29.0	3.7	1.3				
83	yxeD		conserved hypothetical protein	4065225	4065578	+	2.23	2.86	0.76		130	289	371	98
84	yxbD		putative acetyltransferase	4094376	4094855	-	6.01	6.66	0.94		591	3555	3935	555
	1205			4094416	4095375	4094896	52.2	88.6	18.1	5.0				
85	yxbC		conserved hypothetical protein	4094935	4095927	-	16.77	18.41	0.84		283	4746	5212	239
	1206			4095385	4096650	4096018	55.6	100.0	34.5	2.7				
	1206			4095385	4096650	4096018	55.6	100.0	34.5	2.7				
86	yxbB		putative S-adenosylmethionine- dependentmethyltransferase	4096436	4097170	+	3.79	4.80	0.91		435	1649	2088	398
	yxbA	aslA	D-aspartate ligase	4097170	4097439	+	4.45	6.10	0.87		172	766	1050	150
	yxnB		hypothetical protein	4097443	4097925	+	2.94	4.17	0.76		240	706	1000	182
87	yxaL		PcrA associating protein	4101449	4102681	-	7.87	7.85	0.68		1319	10381	10360	894
	1213.2			4102406	4102991	4102699	36.6	72.8	21.3	5.7				
88	yxaJ		putative integral inner membrane protein	4102782	4103210	-	4.85	4.84	0.81		1612	7825	7803	1301
	1213.3		-	4102899	4103858	4103379	54.3	86.8	46.2	9.7				
89	yxaB		putative exopolysaccharide pyruvyl transferase	4109973	4111004	-	2.89	3.84	0.77		1273	3676	4887	982
	yxaA	glxK	glycerate kinase	4111097	4112245	-	3.46	5.04	0.94		762	2635	3841	716
	1215	-		4112045	4112612	4112329	27.8	45.4	13.7	7.8				

								Expressi	on ratio '	;	Si	gnal inter	nsity of R	NA
Operon	Gene/	Alternate Gene	Gene Function	Start	End	Strand/ Center	abrB	∆abrB ∆abh	∆abh				∆abrB	
	PBRID	Name				position $^{b}$	AbrB b	inding <sup>c</sup>	Abh Bi	nding <sup>c</sup>	Wild	∆abrB	∆abh	∆abh
							wild	∆abh	wild	∆abrB				
				4122721	4127403	Broad	-type		-type					
			involved in the synthesis and	4122721	4127405	bioau								
90	yydJ		export of a modified YydF peptide, conserved membrane protein	4123244	4123966	-	7.45	8.17	1.60		896	6673	7320	1431
	yydI		involved in the synthesis and export of a modified YydF peptide, similar to ABC transporter (ATP-binding protein)	4123987	4124616	-	8.59	9.69	1.59		908	7800	8804	1441
	yydH		involved in the synthesis and export of a modified YydF peptide, membrane-embedded metalloprotease	4124766	4125524	-	9.55	11.09	1.33		583	5566	6462	777
	yydG		involved in the synthesis and export of a modified YydF peptide	4125505	4126464	-	33.20	35.57	1.08		178	5917	6338	192
	yydF		involved in the synthesis and export of a modified YydF peptide	4126522	4126671	-	31.96	32.06	1.94		616	19673	19736	1197
B: Activ	ated by Ab	rB												
	318			1001253	1002144	1001699	43.0	74.5	35.7	22.2				
1	glpF		glycerol permease	1001834	1002658	+	0.15	0.27	0.77		13070	1897	3495	10108
	glpK		glycerol kinase	1002677	1004167	+	0.23	0.37	0.75		17074	3991	6353	12887
	glpD		glycerol-3-phosphate oxidase	1004308	1005975	+	0.12	0.19	0.51		6746	837	1312	3449
	1215			4112045	4112612	4112329	27.8	45.4	13.7	7.8				
2	gntR		transcriptional repressor of the gluconate operon (GntR family)	4112441	4113172	+	0.33	0.47	0.91		4768	1579	2218	4323
	gntK		gluconate kinase	4113165	4114706	+	0.23	0.43	0.84		7072	1650	3047	5936
	gntP		gluconate permease	4114735	4116081	+	0.29	0.44	0.90		8712	2483	3854	7811
	gntZ		NAD+-6-phosphogluconate dehydrogenase	4116104	4117510	+	0.41	0.48	0.96		12059	4929	5849	11599
	111			326835	327233	327034	12.2	11.0	11.2	2.1				
3	amyE		alpha-amylase	327169	329151	+	0.30	0.67	1.17		3944	1178	2629	4614
	196			625678	626177	625928	17.8	39.6	4.7	-1.3				
4	ydhM	gmuB	PTS oligo-beta-mannoside- specific enzyme IIB component,	626169	626480	+	0.34	0.45	0.82		6660	2284	2991	5476
	ydhN	gmuA	PTS oligo-beta-mannoside-	626480	626812	+	0.29	0.43	0.96		3545	1036	1509	3399
	ydhO	gmuC	specific enzyme IIC component, glucomannan utilization	626831	628159	+	0.34	0.47	0.88		3493	1179	1630	3075
	ydhP	gmuD	phospho-beta-glucosidase, glucomannan utilization	628177	629574	+	0.32	0.47	0.94		3704	1197	1734	3493
	ydhQ	gmuR	transcriptional regulator of the gmu operon (GntR family)	629717	630430	+	0.42	0.54	0.94		3457	1464	1877	3267
	ydhR	gmuE	fructokinase, glucomannan utilization	630459	631358	+	0.42	0.54	1.04		1852	778	993	1929
	ydhS	gmuF	mannose-6-phosphate isomerase, glucomannan utilization	631355	632302	+	0.40	0.51	0.96		3438	1387	1745	3308
	ydhT	gmuG	mannan endo-1,4-beta- mannosidase, glucomannan utilization	632321	633409	+	0.39	0.53	0.92		2289	904	1212	2116

							Expression ratio <sup>c</sup>			Sig	gnal inter	nsity of R	NA	
Operon	Gene/ PBR ID	Alternate Gene	Gene Function	Start	End	Strand/ Center	abrB	∆abrB ∆abh	∆abh		Wild	∆abrB	∆abrB	∆abh
		Name				position "	AbrB b	inding <sup>c</sup>	Abh Bi	nding <sup>c</sup>			∆abh	
							wild	∆abh	wild	∆abrB				
	1089			3700050	3700414	3700232	13.0	17.0	5.8	3.9				
5	rbsR		transcriptional repressor of the ribose operon	3700438	3701418	+	0.31	0.52	1.08		19128	5873	9899	20596
	rbsK		ribokinase	3701420	3702301	+	0.33	0.54	1.04		20943	6849	11352	21813
	rbsD		ribose ABC transporter (membrane bound ribose binding)	3702298	3702693	+	0.17	0.45	0.99		18453	3136	8237	18222
	rbsA		ribose ABC transporter (ATP- binding protein)	3702709	3704190	+	0.29	0.53	1.00		24106	7008	12751	24152
	rbsC		nbose ABC transporter (permease)	3704192	3705160	+	0.30	0.55	1.03		19886	6056	10947	20447
	rbsB		ribose ABC transporter (ribose- binding lipoprotein)	3705172	3706089	+	0.44	0.62	1.07		25093	11068	15540	26837
C: Repre	essed by A	brB and a	ctivated by Abh											
1	bdbB		thiol-disulfideoxidoreductase, sublancin biosynthesis	2264421	2264867	-	7.29	3.69	0.37		433	3155	1596	162
	yolJ		essential for sublancin production	2264864	2266132	-	6.87	4.00	0.33		505	3470	2017	167
	bdbA		thiol-disulfideoxidoreductase,	2266132	2266545	-	5.90	3.02	0.28		495	2922	1493	136
	sunT		sublancin 168 lantibiotic	2266542	2268659	-	6.56	3.21	0.33		240	1577	773	79
	sunA		sublancin 168 lantibiotic antimicrobialprecursor peptide	2268717	2268887	-	4.51	3.47	0.25		4390	19776	15215	1104
	679			2268518	2269715	2269117	108.3	130.6	48.3	38.4				
D: Addit	ively repr	essed by A	brB and Abh											
	272.1			843810	844395	844103	33.5	26.0	34.5	40.8				
1	yflA		putative amino acid transporter	844106	845521	+	1.48	2.62	1.05		565	838	1477	595
2	ylaE		putative exported protein	1544243	1544854	-	1.55	5.91	1.49		134	207	793	200
	461			1544352	1545549	1544951	37.4	38.3	39.8	171.0				
	465		auto abromo ana? avidasa	1559142	1560032	1559587	71.5	51.3	64.8	17.7				
3	ctaC		(subunit II)	1559773	1560843	+	5.43	5.88	2.43		658	3574	3868	1601
	ctaD		(subunit I)	1560876	1562744	+	4.94	5.35	2.47		928	4582	4963	2293
	ctaE		(subunit III)	1562744	1563367	+	6.01	6.04	2.92		531	3190	3209	1553
	ctaF		(subunit IV)	1563370	1563702	+	4.53	4.81	2.36		994	4504	4783	2347
	ctaG		cytochrome aa(3) assembly factor	1563729	1564622	+	4.25	4.24	2.14		731	3105	3099	1563
4	yojL	cwlS	peptidoglycan hydrolase (cell wall-bindingd,l-endopeptidase), associated with cell separation	2114627	2115871	-	4.93	11.41	3.24		390	1923	4452	1265
	626			2115365	2116392	2115879	46.7	29.8	76.3	181.5				
5	ycdA		putative lipoprotein	298990	300054	-	2.68	7.60	2.20		422	1131	3205	926
	107			299771	300798	300285	73.6	76.7	92.9	196.3				
6	ywoF 1108		putative pectate lyase	3749790	3751196	- 3751275	3.72	3.63	3.02	82	779	2899	2824	2350
E Ronzo	ssed by A	bh		5751050	5151499	5151215	- 31.4	15.9		0.2				
та перте	117 1			375931	376635	376283	45.4	45.4	34.0	37				
1	srfAA		surfactin synthetase	376525	387291	+	1 61	1 69	3 24	5.1	1120	1803	1888	3628
1	srfAR		surfactin synthetase	387304	398067	+	1.83	1 91	3.46		1230	2254	2351	4254
	srfAC		surfactin synthetase	398104	401928	+	1.85	1.87	3.28		1163	2148	2173	3819
	srf4D		surfactin synthetase	401957	402685	+	1.05	1.07	3.46		814	1583	1600	2817

<sup>a</sup> Transcriptional signals and AbrB/Abh binding signals in Table S2 were extracted and merged for possible TUs directly regulated by AbrB/Abh

<sup>b</sup> Coding strand of genes or center position of PBRs are indicated.

<sup>c</sup> Relative transcriptional signal intensities in *AabrB*, *AabrB Aabh*, and *Aabh* cells compared to that of wild-type cells are indicated for various genes. AbrB binding



**Figure 17. AbrB/Abh binding profile in the promoter region of gene repressed by AbrB.** Examples of AbrB/Abh binding in the promoter region of genes regulated by AbrB. The AbrB/Abh binding profiles in four strains are depicted as in Figure 11A. The gene organization of selected regions is indicated in the middle and AbrB regulated genes are indicated in dark gray. Below the gene map, transcriptional signals (y-axis) of each probe in the selected regions are presented separately for Watson (+) and Crick (-) strands.

	Previous	reports	ChAP-chip	Expr	ession ra	atio
Operon	Regulatio	r Reference	Binding intensity in wild- type cells <i>a</i>	∆abrB/ wild	∆abh ∆abrB/ wild	<i>∆abh</i> ∕ wild
AbrB regulated operons						
spoVG	Negative	Furbass et al, 1991; Zuber & Losick, 1987	12.3	3.4	3.5	1.3
spo0E	Negative	Strauch, 1995c; Strauch et al, 1989b	19.0	3.1	2.8	0.9
sboAX-albABCDEFG	Negative	Strauch et al, 2007; Zheng et al, 1999	26.1	10.9	12.2	1.0
yknWXYZ	Negative	Qian et al, 2002	17.7	3.8	4.3	1.5
yxzE	Negative	Qian et al, 2002	43.8	3.3	3.3	1.4
tasA-sipW-yqxM	Negative	Strauch et al, 2007	78.4	10.4	10.6	0.9
sunA-bdbB	Negative	Strauch et al, 2007	108.3	4.5	3.5	0.3
skf(ybcO-ybcE)	Negative	Strauch et al, 2007	27.9	8.9	11.2	1.1
sdp (yvaWXY)	Negative	Strauch et al, 2007	45.2	82.9	80.4	1.3
<i>yxaAB</i>	Negative	Nagorska et al, 2008	27.8	3.5	5.0	0.9
eps (yvfF-yvek)	Negative	Murray et al, 2009	18.8	4.7	5.3	1.0
sigH	Negative	Strauch, 1995b; Weir et al, 1991	13.1	1.4	1.4	1.0
sinIR	Negative	Shafikhani et al, 2002; Strauch, 1995c	12.3	1.7	1.9	0.8
sigW-ybbM	Negative	Qian et al, 2002	16.7	1.4	1.5	1.0
comK	Negative	Hamoen et al, 2003	21.5	1.7	1.7	1.0
slr	Negative	Murray et al, 2009	18.8	2.4	2.3	1.0
aprE	Negative	Ferrari et al, 1988; Strauch et al, 1989b	18.0	1.1	1.2	1.0
abrB	Negative	Strauch et al, 1989a; Strauch et al, 1989b	4.7	-	-	1.0
pbpE-racX	Negative	Popham & Setlow, 1993; Strauch, 1995b	ND	3.0	3.3	1.0
lia (yvqIHGFEC)	Negative	Hamon et al, 2004; Jordan et al, 2007	ND	1.9	2.1	0.9
yvlABCD	Negative	Qian et al, 2002	ND	1.5	1.5	1.1
dppABCDE	Negative	Slack et al, 1991	ND	1.2	1.2	1.1
ftsAZ	Negative	Gonzy-Treboul et al, 1992; Strauch, 1995b	ND	0.9	1.0	1.0
kinB-kapB	Negative	Strauch, 1995b	ND	0.9	0.9	0.9
rbsRKDACB	Positive	Strauch, 1995a	13.0	0.3	0.5	1.1
citB	Positive	Kim et al, 2003	ND	4.4	3.1	1.0
hut	Positive	Fisher et al, 1994	ND	0.6	0.7	0.9
Abh-regulated operons						
skf(ybcO-ybcE)	Negative	Lopez et al, 2009; Strauch et al, 2007	27.9	8.9	11.2	1.1
sdp (yvaWXY)	Negative	Lopez et al, 2009; Strauch et al, 2007	45.2	82.9	80.4	1.3
sboAX-albABCDEFG	Negative	Strauch et al, 2007	7.7	10.9	12.2	1.0
sunA-bdbB	Positive	Strauch et al, 2007	48.3	4.5	3.5	0.3
sigW-ybbM	Positive	Strauch et al, 2007	15.6	1.4	1.5	1.0
aprE	Positive	Strauch et al, 2007	ND	1.1	1.2	1.0

Table 6. Comparison of the data of the present study with previously reported information on AbrB- and/or Abh-regulated operons

<sup>*a*</sup> Binding intensity of AbrB/Abh is indicated if the promoter region overlaps with the center of the AbrB/Abh binding peak.
## 8. Genome-wide correlation between AbrB/Abh binding and transcription levels

In the present study, we identified 643 AbrB- and 411 Abh-binding sites. However, only 103 AbrB- and 7 Abh-binding sites have been suggested to directly affect transcription. Our analysis may underestimate the number of TUs directly regulated by AbrB/Abh because AbrB/Abh sites involved in regulation of TUs specifically induced at the transition phase, including genes under the control of AbrB as preventor, would not have been detected in our system. Abh is under the control of the ECF sigma factors SigX, SigM, and SigW (Luo & Helmann, 2009; Murray et al, 2009); hence, cell wall stress may modulate AbrB/Abh regulation. Even when these possibilities are considered, our results indicate that many AbrB/Abh binding events have no impact on transcription. In support of this idea, some binding sites are located in actively transcribed regions, such as those of the secDF, gltT, tkt, yrrO, and tyrS genes (Figure 18A). Indeed, scatter plots of AbrB binding intensities to PBRs, and ratios of PBR transcription intensities in *abrB*-deleted cells compared with wild-type cells, showed that most AbrB binding events had no impact on transcriptional level, regardless of whether the binding occurred in intergenic or coding regions (Figure 18B-D). Thus, the cellular roles of many AbrB/Abh binding events await further examination.



Figure 18. AbrB/Abh binding to actively transcribed regions. (A) Examples of AbrB/Abh binding to coding regions of highly transcribed genes are shown. The AbrB/Abh binding profiles in four strains are depicted as in Figure 11A. The gene organization of selected regions is indicated in the middle. Below the gene map, transcriptional signals (y-axis) of each probe in the selected regions are presented separately for Watson (+) and Crick (-) strands. (B) A scatter plot of log<sub>2</sub> binding intensity values of AbrB to intergenic regions (x-axis) and log<sub>2</sub> expression ratios of downstream genes in  $\Delta abrB$  cells compared to those in wild-type cells (y-axis). If (continued)

AbrB bound to the intergenic region of divergently transcribed genes, we plotted the expression ratios of both genes. (C) Scatter plot of  $\log_2$  binding intensity values of AbrB to coding regions (x-axis) and  $\log_2$  expression ratios of AbrB-bound genes in  $\Delta abrB$  cells compared to those in wild-type cells (y-axis). (D) The results shown in (B) and (C) are merged.

# 9. Overexpression of Abh counteracts the repression effect mediated by AbrB at the sublancin operon

Previous study demonstrated that Abh counteracts the repression effect of AbrB on expression of the sublancin operon, composed of *sunA*, *sunT*, *ybdA*, *yolJ* and *ybdB*, and suggested that Abh would compete AbrB binding to the promoter region (Luo & Helmann, 2009). In this study, this region was observed as binding profile type 1 (Supplementary Figure S1). Toward understanding the molecular mechanism of Abh function, we further investigated whether or not this model can universally apply to other promoter activities possessing simultaneous binding of AbrB and Abh. As mention above, promoter activity of *abh* gene is mainly controlled by  $\sigma^{X}$ , and  $\sigma^{X}$  itself is inactivated by anti- $\sigma^{X}$  (encoded by *rsiX*) (Brutsche & Braun, 1997; Murray et al, 2009). Thus, we assumed that highest expression of Abh should be promised in the absence of the anti- $\sigma^{X}$ . In fact, we confirmed overexpression of Abh in  $\Delta rsiX$  strain by Western blotting (Figure 19). Since  $\Delta rsiX$  strain would have other effects, e.g. induction of  $\sigma^{X}$  and consequent modulation of expression of genes under its control, we overexpressed Abh from IPTG-inducible promoter from multicopy plasmid in a wild strain (168), to a comparable level to that in  $\Delta rsiX$  strain, and compared the genome-wide transcriptional profile with that in a wild strain.



Figure 19. Abh expression level in *abh*-overexpressing cells compared to that of in  $\Delta rsiX$  cells. Western blot analysis of Abh in; (1) *abh*-overexpressing strain (OC009) induce with 75  $\mu$ M and (2) 50  $\mu$ M IPTG, (3)  $\Delta rsiX$  strain (OC008) and (4) wild-type 168 strain using anti-Abh antibody.

As previously reported, we observed clear induction of transcription for all genes in the sublancin operon, except for a *sunA* gene (Figure 20). We also detect the upregulation at other 3 operon/genes; *yonK*, *yuaIGF* and *tetL*. However, all of them are not AbrB repressed genes although slightly derepression (1.5 fold) is observed for *yuaIGF* in *abrB* mutant. In addition, no Abh binding are detected in the promoter region of these genes. This result indicates that the antagonistic effect of Abh to AbrB repression is specific for the sublancin operon, at least in the condition we used.



**Figure 20.** Activation of sublancin operon in Abh overexpressing cell. The AbrB/Abh binding profiles in four strains are depicted as in Figure 11A. The gene organization of selected regions is indicated in the middle and the sublancin operon is indicated in dark grey. Below the gene map, transcriptional signals are presented as described in Figure 18.

#### DISCUSSION

AbrB is one of the global transcriptional regulators of *B. subtilis*, and has been extensively studied both genetically and biochemically. AbrB has been shown to repress the expression of many genes, which are de-repressed during the transition from the exponential to the stationary phase of cell growth coupling with decrease of AbrB amount. Here, for the first time, we report the *in vivo* AbrB distribution over the entire *B. subtilis* genome during exponential growth, which AbrB predominantly functions. In parallel, we studied the AbrB paralog Abh, which had not previously been systematically investigated. We identified novel important properties of both AbrB and Abh, thus contributing to a deeper understanding of the roles played by these proteins as transcriptional regulators and, possibly, as nucleoid architectural proteins.

We demonstrated that AbrB and Abh bound to hundreds of sites throughout the genome in wild-type *B. subtilis* cells, and that almost all Abh-binding sites overlapped with sites for AbrB. The results of *in vivo* cross-linking experiments suggested that many of Abh molecules may exist in complex with AbrB-in wild-type cells, and that Abh would be released from complexes with AbrB to form Abh homomers when the cellular levels of AbrB decreased. Consistent with this hypothesis, Abh-specific binding sites were detected only in the absence of AbrB. Thus, our results strongly suggest that the context of oligomeric forms of AbrB/Abh, and binding of these forms to the genome, are intimately related. Although previous *in vitro* experiments suggested that tetramers were the basic functional units of AbrB/Abh, the predominant molecular species in cells requires further examination. In addition, the molecular basis of AbrB/Abh heteromer formation, and whether C-terminal and/or N-terminal interaction(s) are involved, is an important issue requiring clarification.

Examination of AbrB binding in  $abh^+$  and  $\Delta abh$  and Abh binding in  $abrB^+$  and  $\Delta abrB$ shown that AbrB has the ability to bind to most target loci independent of Abh, whereas many Abh-binding events are dependent on the presence of AbrB. Quantitative comparison of AbrB/Abh binding intensities to relevant binding sites, defined here as PBRs, in these genetic backgrounds revealed that PBRs contain various types of sequences with different specificities and affinities for AbrB/Abh homomers and heteromers. We attempted to identify the basic patterns of AbrB/Abh binding to PBR sequences, and found four major (P01–P04) and four minor (P05–P08) patterns (Table 3). Binding sites in the classes P01, P02, and P03 were recognizable by AbrB homomers. In addition, P01 sites were recognized by both Abh homomers and AbrB/Abh heteromers, and sites in the P02 class bound AbrB/Abh heteromers. P03 sites were specific for AbrB homomers. Interestingly, P04 sites were specific for Abh homomers, and Abh binding to these sites was detected only in the absence of AbrB. These results demonstrate that, although AbrB and Abh are similar in primary and tertiary structure, subtle structural differences are reflected in variations in target sequences, as might be anticipated.

Furthermore, by carefully selecting PBRs with single protein-binding peaks, we were able to extract consensus binding sequences for the P01, P02, and P04 classes. A previous *in vitro* SELEX (Systematic Evolution of Ligands by EXponential enrichment) study (Xu & Strauch, 1996) suggested that the TGGNA motif was a determinant of AbrB binding. Interestingly, our consensus sequences for the P01, P02, and P04 sites each contain two TGGNA motifs, differing in arrangement and spacing: TNCCA-WWW-TGGNA for P01 sequences, WWWW-CCA-WWWW-TGG for P02 sequences, and TGGNAWTTCCA for P04 sequences. These results indicate that, *in vivo*, a pair of TGGNA sequences acts as a determinant of both AbrB and Abh binding, at least in part, although direct demonstration of AbrB/Abh binding to the sequences

identified in the present work requires further investigation. The finding that Abh does not bind as a homomer to P02 sequences may indicate that Abh has a strict requirement for the TGGNA motif, whereas AbrB recognizes more diverse DNA sequences. The rather non-specific AG-rich consensus sequence of the P03 class, the AbrB-homomer-specific binding site, might also support this idea.

Although our AbrB/Abh-binding motifs contained inverted repeats of the TGGNA sequence separated by 4 bp spacer, in vitro experiments have shown that AbrB also binds to tandem repeats separated by 4 or 5 bp (Xu & Strauch, 1996). We evaluate the contribution of the TGGNA motif to genome-wide AbrB/Abh binding by searching for the presence of two TGGNA motifs, in palindromic or tandem orientation, separated by 0 to 6 bp of W (A or T), allowing a single base mismatch on genome, and determine if the motif were enriched in the 100-bp regions around the centers of 753 PBRs. Supporting the involvement of the TGGNA motif in AbrB/Abhbinding, palindromic or tandem motif pairs connected by 4–5 W bases were found to be enriched in PBR sequences. However, the motifs were detected in only 166 of 753 PBRs (22%). This may indicate that TGGNA-motif-dependent AbrB/Abh binding is relatively relaxed in specificity and that other constraints are required to restrict the targets to PBR regions because a search for possible binding sites allowing a two base-pair mismatch resulted in loss of site enrichment in PBR regions. In addition to this, AbrB can also bind to different classes of DNA sequences as indicated in case of AbrB homomer, (P03), possibly though recognizing a specific substructure of the DNA helix.

According to a recent docking model between AbrB and DNA, smallest unit for DNA binding is a AbrB dimer, which makes base pair-specific interactions with guanines in a TGGNA motif, and two of such AbrB dimers bind to TGGNA motifs spaced by 5bp and form a tetramer via two interactions between their flexible C-terminal regions (Sullivan et al, 2008) (also shown as

a cartoon in Figure 15). In vitro footprinting experiment shows binding pattern as observed that DNA sequence is covered by AbrB for about 20bp long, and actually this kind of sequences were detected in the SELEX study of Xu and Strauch (1997). However, many in vitro footprinting experiments indicated that an AbrB and Abh often cover more than 40 bp of sequence (32), and it has been proposed that such observations indicate simultaneous binding of more than two AbrB tetramers (Strauch et al, 2007; Sullivan et al, 2008). Multiple TGGNA motifs, M-5bp-M-4bp-M-5bp-M sequence on 44 bp fragments, where M indicates any direction of the TGGNA motif, were also identified in the SELEX study. Since they found that M-5bp-M sequence was minimum AbrB binding sequence in differently selected DNA fragments, they explained that the four TGGNA motifs were composed of two M-5bp-M units spaced by 4bp. Although Xu and Strauch did not mentioned, it seems to be very important that the distance between the two units is mostly 4bp and that the TGGNA motifs positioned at both ends were often quite different from the consensus sequence. In addition, in a set of DNA fragments selected by a different selection method, they also found out other consensus sequence, CCANATNTGG, that is also covered for more than 40 bp long by AbrB, even though no TGGNA motif exists at the surrounding regions. Interestingly, this consensus sequence is actually consistent with the middle sequence of M-5bp-M-5bp-M (underlined) and core sequence of TNCCA-WWWW-TGGNA for P01 sequences and WWWWW-CCA-WWWW-TGG for P02 sequences. Thus, in addition to minimum M-5bp-M sequence recognized by AbrB, M-4bp-M should be very important to explain the reason why 4bpspaced sequence has always longer, nearly twice, footprint protection region compared to 5bpspaced sequence. To reconcile these seemingly discrepancy, we assumed that 5bp-spaced sequence (M-5bp-M) would be tetramer specific, on the other hand, 4bp-spaced sequence (m-5bp-M-4bp-M-5bp-m, where m indicates any AbrB/Abh binding sequence including unrecognizable sequences as the motif) would be octamer specific as illustrated in Figure 21.

To form an octamer at the 4bp-spaced sequence, two binding model can be expected. In the first model, first binding action for 4bp-spaced binding would be similar to that of 5bp-spaced binding, but 4bp-spaced sequence may have two free C-terminal regions from tetramer formation. Thus, each C-terminal region can recruit one more dimer to form an octamer, depending on the neighboring sequences where should retain enough affinity for binding probably with 5bp apart with proper TGGNA motif. In the second model, AbrB and Abh always exist as tetramers and can recognize if m-5bp-M sequence exist, although the binding is not stable because of its week recognition. However, the binding can be stabilized if two m-5bp-M motifs are arranged with 4bp distance by forming additional interaction via two free C-terminal regions. In any case, multiple arrangements of sequences containing two TGGNA motifs may, thus, control AbrB/Abh binding to the genome.

Although the exact contribution of the TGGNA motif to genome-wide AbrB/Abh binding requires further investigation, our results indicate that an AbrB/Abh complex has the ability to recognize various configurations of the two motifs, as shown schematically in Figure 15. The crystal structure of full-length SpoVT has been recently reported (Asen et al, 2009), in which two monomers dimerized by N-terminal domain interactions form swapped-hairpin  $\beta$ -barrels and then tetramerize through formation of mixed helix bundles between the C-terminal domains. Dimerized N-terminal DNA-binding domains and C-terminal domains are connected by flexible linker sequences, and such flexibility would also allow the two DNA-binding domains of AbrB/Abh tetramers to adopt various conformations.

(A) tetramer specific binding for M-5bp-M sequence



(B) octoamer specific binding for m-5bp-M-4bp-M-5bp-m sequence 1



(C) octoamer specific binding for m-5bp-M-4bp-M-5bp-m sequence 2



**Figure 21. Binding model of AbrB and Abh**. (A–C) Binding models for (A) tetramer specific binding for M-5bp-M sequence, (B) the first model of octamer specific binding for m-5bp-M-4bp-M-5bp-m sequence, and (C) the 2<sup>nd</sup> model of octamer specific binding for m-5bp-M-4bp-M-5bp-m sequence. Red coloration of double-stranded DNA indicates the TGGNA motif. Light and dark brown boxes show the N-terminal domains of two AbrB or Abh molecules that interact to form a DNA binding domain, whereas the light- and dark- brown arm-like structures extending from the boxes depict C-terminal domains that form tetramers. Loop regions, which have been predicted to contact DNA and contribute to DNA recognition, are shown using triangles.

We assessed the direct contributions of AbrB and Abh binding to control of gene expression by comparing AbrB/Abh binding in, and the transcriptome profiles of, *abrB* and/or *abh* deletion mutant cells. Our data indicate that expression of at least 90 TUs (171 genes) would be specifically repressed by AbrB in exponentially growing cells. Newly identified AbrB-repressed genes include genes involved in cell-wall biosynthesis (*pbpH*, *dacF*), membrane biogenesis (*cccA*), chemotaxis (tlpA), antibiotic production (ppsABCDE), metabolism of amino acids and related molecules (rocA, rocG), detoxification (ykuU, yocD), protein modification (tkmA, ptkA, ptpZ), phage-related functions, and genes of unknown function, etc (Table 5). Also, it has been suggested that AbrB is involved in the activation of five operons/genes, rbs, glp, gnt, gmu, and amyE, related to carbohydrate utilization. Although Abh-binding signals in these genetic regions were generally low (in the classes VL or L) in  $\Delta abrB$  cells, signals in the M and H classes, but without any apparent effect on transcription level, were also observed. However, Abh has been suggested to repress the expression of six operons/genes, yflA, ylaE, ctaCDEFG, yojL, ycdA and ywoF, in a manner additive to repression by AbrB. In addition, our data support the direct activation by Abh, and repression by AbrB, of the sun operon (Luo & Helmann, 2009; Strauch et al, 2007). The different effects of Abh binding on transcription may be explained by the levels of Abh bound to promoter regions. However, no clear correlation between Abh binding intensity and derepression of transcription was observed in  $\Delta abrB$  cells (Table 5). It is also possible that the relative location of Abh-binding sites with respect to promoters is important when the detailed effects on transcription are considered, although the limited resolution of our protein binding maps did not allow us to examine this possibility. The AbrB-binding profiles on promoters repressed and activated by the protein were also apparently indistinguishable. Thus, the molecular basis by

which AbrB/Abh binding promotes repression or activation of transcription requires further detailed analysis.

Molecular mechanism of transcriptional repression and activation by AbrB binding has been discussed in many reviews (Klein & Marahiel, 2002; Phillips & Strauch, 2002; Strauch & Hoch, 1993). In case of repression, *in vitro* footprinting experiments demonstrated that promoter regions of AbrB-repressive genes were directly bound by AbrB, thus, AbrB binding at precise site of the promoter, e.g. -10 region, is to hinder recruitment of RNA polymerase, resulting in repression of gene transcription. In case of activation, although AbrB act as an activator has been known, direct interaction of AbrB to RNA polymerase, that increases recruitment of RNAP and thus activates transcription as seen for many of transcriptional activator, has not been reported. However, previous study regarding to rps operon, which is known to be activated by AbrB, have suggested an interesting mechanism (Strauch, 1995a). In his report, cre (catabolite-responsive element) sequence which is recognized by a catabolite repressor protein, CcpA, to repress a transcription probably by load block of elongation of RNA polymerase (Fujita, 2009), exists at the transcriptional start site of *rps* operon and AbrB binding site is overlapped with this sequence. Thus, it was suggested that AbrB binding at the region would compete out CcpA binding, then derepress the gene expression (Strauch, 1995a). In our result, it seems to be clear that AbrB does't have load block activity for RNA polymerase elongation because AbrB can bind to many transcriptionally active regions without reducing transcription, thus, this model would be reasonable to explain activation mechanism by AbrB binding. To evaluate this model can be fit to other five AbrB-activated operons/genes identified in this study, we compared the CcpA binding mapped previously in our laboratory (Oda, et al unpublished data) with AbrB binding in front of the five genes, and found out that AbrB binding at four of these including rps operon are

overlapped with CcpA binding, suggesting that competition with repressor for binding might be one of the regulatory mechanisms used by AbrB for gene activation.

In addition, it has been demonstrated that Abh counteracts the repression mediated by AbrB as observed in *sun* operon (Luo & Helmann, 2009). In an attempt to investigate the biological role in other gene promoters, we performed transcriptome analysis in Abh-overexpressing cells. Our result confirmed that Abh can counteract AbrB repression at *sun* operon, *sunT-bdbA-yolJ-bdbB*, but not for *sunA*. Although, we also found moderate derepression in other 3 operon/gene; *yonK*, *yuaIGH and tetL*, binding of Abh on promoter region of those genes is not detected and most of them is not AbrB repressed gene. Thus, the counteraction of AbrB repression by Abh is occurred at only specific promoter and it is not general regulatory mechanism, at least in the condition we tried. However, it seems that overexpression condition used in this experiment produced only lower number of Abh molecules than AbrB molecules. If just low level of AbrB is required for the repression, we may not observe the derepression effect in this experiment. Thus, to conclude counteracting effect of Abh on AbrB, further analysis using cells expressing higher level of Abh than AbrB should be tested.

We found that most Abh molecules were in a complex with AbrB in cells growing exponentially in LB medium, and Abh-homomer-specific binding sites were detected only in the absence of AbrB. Although we did not observe any changes in transcriptional levels around binding sites in exponentially growing  $\Delta abrB$  cells, Abh-homomer-specific binding sites may appear in wild-type cells in the stationary phase, after AbrB expression is repressed, to regulate expression of growth phase-dependent gene transcription. Supporting this idea, an alteration in biofilm architecture was observed in *abh*-deleted cells compared with wild-type cells during biofilm formation (Lopez et al, 2009; Murray et al, 2009). Conversely, a decrease in Abh level will increase AbrB homomer level and enhance protein binding to AbrB-homomer-specific binding sites. Interestingly, we found that the *ydjL* and *yolA* genes might be under this form of control (Table 5). The expression of these genes is repressed specifically by the AbrB homomer, and this repression is further enhanced in a  $\Delta abh$  background. This may indicate that reduction in the level of the AbrB homomer is one of the biological functions of Abh during the exponential growth phase under normal conditions. These observations indicate that regulation of the relative levels of AbrB and Abh is one of the strategies used to modulate the global gene expression profile and cope with environmental changes, by reorganizing AbrB/Abh binding along the whole genome.

Finally, and importantly, we found that most AbrB and Abh binding events did not affect transcription. Only 16% (103 of 643) of AbrB- and 1.7% (7 of 411) of Abh-binding sites was suggested to directly affect transcription although we accept that our data may underestimate the number of genes directly regulated by AbrB and/or Abh; assignment of the specific binding site to the nearest target gene might exclude genes which are directly controlled by binding from far sites, or some genes might be redundantly controlled. We also found that about half of the binding sites for these proteins are located in ORFs, and some such ORFs are actively transcribed in the presence or absence of AbrB/Abh. The other half of the binding sites are located in intergenic regions. However, binding to many such sites had no effect on transcription, even though the binding intensities were high. Recently, it has been shown that *E. coli* RutR, regulator for pyrimidine catabolism, binds mainly to coding regions with little or no effect on transcript levels (Shimada et al, 2008), and that NsrR, regulator for adaptive responses to nitric oxide, also binds many sites in coding regions (Partridge et al, 2009). It is possible that AbrB/Abh are transcriptional regulators with similar binding site preferences, although numbers of the binding

sites of RutR and NsrR on the genome were 20 and 62 respectively, much smaller than those of AbrB and Abh.

On the other hand, AbrB/Abh share some properties with E. coli nucleoid-associated proteins, which are abundant proteins of low molecular weight with a low sequence specificity for DNA binding, and the numerous AbrB/Abh binding sites along the whole genome found in the present work further extend the similarity. Furthermore, the mutual dependence of AbrB/Abh for DNA binding is reminiscent of a property of the E. coli nucleoid protein H-NS and its paralog StpA; H-NS binding is apparently StpA-independent, whereas many of StpA binding is H-NSdependent (Uyar et al, 2009). These results imply another interesting possibility that, although sequence similarities are lacking, AbrB and Abh might be functional homologs of H-NS and StpA. E. coli nucleoid proteins participate in diverse DNA-dependent functions, including transcription, replication, recombination, and the creation of higher-order structures in genomic DNA. AbrB/Abh may thus have function(s) other than transcriptional regulation. However, there is not yet any experimental evidence to support this hypothesis because *abrB abh* double mutant cells show no relevant phenotypic characteristics, such as an altered nucleoid morphology and AbrB and Abh cannot complement the hns and stpA deletion mutant phenotype in E.coli cell (data not shown).

Another possible hypothesis is that binding sites that are not involved in direct transcriptional regulation might act as pools of AbrB and Abh and enable gradual changes of AbrB/Abh bindings to promoter regions when AbrB/Abh levels are changed. Thus, even abrupt change in their levels might be followed by a gradual alteration of transcriptome, providing a time toward an overall response required to adapt to new conditions.

In summary, our ChAP-chip analysis, together with transcriptome profiling, revealed that AbrB and Abh are not simple transcriptional regulators. We disclosed a close relationship between AbrB and Abh with respect to genome-wide binding and transcriptional regulation. Thus, regulation of the relative levels of AbrB and Abh would be one of the strategies used to modulate the global gene expression profile and cope with environmental changes. Furthermore, it is possible that these proteins play roles similar to those of *E. coli* nucleoid-associated proteins. This insight may further our understanding of the molecular mechanism of nucleoid structure formation in *B. subtilis*, which is poorly understood at present.

## ACKNOWLEDGEMENTS

I would like to express my sincere gratitude and appreciation to my supervisor, Prof. Naotake Ogasawara, for his valuable advice, supervision, and crucial contributions throughout this study, and for the many good opportunities that he provided. He is a great supervisor. I am greatly indebted to Dr. Shu Ishikawa, who has been most responsible for helping me in this research. I greatly appreciate his advice, continuous guidance, discussions, and encouragement. I learned a lot from him. This work could not have been completed without his help.

My great appreciation is also extended to my colleagues; Dr. Hiroki Takahashi and Prof. Shigehiko Kanaya for bioinformatic analysis, Dr. Taku Oshima for his helpful suggestions and discussions and Mr. Takahiro Hishimoto, the first student working on this project, for construction of some strains used in this work during his master degree study.

My special thanks go to all the members of my advisory committee, Prof. Hisaji Maki, Prof. Hirotada Mori and Prof. Hiroshi Takagi, for their comments and suggestions about my work.

I am thankful to Dr. Ian Smith for his kind advice on my English writing and presentation throughout my study.

I would also like to thank Dr. Kasuo Kobayashi for his suggestions and discussion. I am very grateful to Dr. Takuya Morimoto, Mr. Hajime Okumura, Ms. Yoko Kusuya, Ms. Ebru Uyar and Ms. Eunha Chou for helping and supporting me in various ways. Their warm friendship makes my life in Japan so comfortable and enjoyable. I also thank all past and present members

of the Functional Genomics Laboratory and all of my friends for all their help and for making this work enjoyable.

I am particularly grateful for a Grant-in-Aid for Scientific Research (KAKENHI) on Priority Areas, Systems Genomics, from the Ministry of Education, Culture, Sports, Science, and Technology of Japan, and for a Japanese Government Scholarship for Foreign Research Students for financial support for my study.

Finally, my deepest gratitude goes to my parents, sisters and brothers for their understanding, encouragement and support throughout my study.

Onuma Chumsakul

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# SUPPLEMENTARY DATA

Supplementary T	Table S1. Summar	y of transcriptome	and ChAP-chip	analyses.

	gene					Trans	criptom	e analysis						Ch	AP-chip a	nalysis		
				Sig	nal intens	ity of RN	A <sup>a</sup>	Expr	ession rat	tio <sup>b</sup>		OPE				Binding	intensity c	
nama	etart	and	and			4		Ah.nD/	$\Delta abh$	A -hh /	PBR	ORF	etart	and	center	AbrB	Abh	Profile
name	Suit	chu	str	wild	∆abrB	AahrB	$\Delta abh$	wild	∆abrB/	wild	ID	Intergenic	Start	end	center	wild Aabh	wild AahrB	ID
						Auorb		wild	wild	where						-type	-type	
dnaA	410	1750	+	7078	6317	5750	7267	0.90	0.81	1.03		*Broad	1	3629				
dnaN vaaA	1939	3075	+	5465	48/6	4416	5247	0.91	0.81	0.95								
yuuA recF	3437	4549	+	6082	5370	4993	5632	0.85	0.78	0.94								
vaaB	4567	4725	+	7356	6416	6140	7508	0.87	0.84	1.02		1						
gyrB	4866	6782	+	8302	7450	7208	8174	0.90	0.87	0.98	5	gyrB	5815	6094	5955	3.0 4.2	2.8 12.5	
gyrA	6993	9458	+	8940	7550	7254	8606	0.85	0.81	0.96								
yaaC	14845	15792	-	243	203	216	224	0.84	0.89	0.92	7	yaaC	15471	16005	15738	21.0 12.7	28.3 5.1	
guaB	15913	17379	+	14698	10393	11161	13743	0.71	0.76	0.93								
dacA	17532	18863	+	8863	5643	4972	8512	0.64	0.56	0.96								
yaaD waaE	19060	19944	+	10767	9844	9/30	10360	0.87	0.86	0.91								
serS	20878	20350	+	9838	7030	7365	9434	0.88	0.87	0.90								
trnSL-Ser	22290	22382	+	12543	12042	12708	9641	0.90	1.01	0.82								
dck	22494	23147	-	4990	3025	3191	4992	0.61	0.64	0.99	10	dck	22781	23230	23006	11.9 10.9	22.3 39.2	
dgk	23144	23767	-	3704	2330	2247	3949	0.63	0.61	1.06								
yaaH	23866	25149	-	201	166	181	190	0.83	0.90	0.95								
yaaI	25219	25764	-	498	321	420	340	0.64	0.84	0.68								
yaaJ	25850	26335	+	1077	882	869	1003	0.82	0.81	0.94								
scr dnaV	26377	26/30	+	12697	2016	1/939	160//	1.39	1.39	1.26								
vaaK	20812	28503	+	15500	14269	14413	14814	0.07	0.07	0.95								
recR	28865	29461	+	6945	6574	6140	7091	0.92	0.89	1.02	11	recR	28901	29486	29194	10.7 7.0	23.3 46.6	
yaaL	29479	29703	+	5722	4843	4655	5498	0.85	0.81	0.97								
bofA	29770	30033	+	2171	1586	1548	2000	0.73	0.72	0.92								
csfB	35529	35723	+	331	322	355	290	0.98	1.07	0.89								
xpaC	35843	36457	+	1482	1179	1388	1735	0.80	0.94	1.17								
yaaN	36476	37636	+	1504	1263	1547	1629	0.84	1.04	1.09								
yaaO tmk	3//18	39160	+	2261	2104	1831	2340	0.76	0.82	1.04								
vaaO	39869	40198	+	6081	4657	4866	6236	0.71	0.74	1.04								
yaaR	40211	40651	+	5811	3975	4444	6155	0.69	0.77	1.06	13	vaaR	40082	40616	40349	44.6 18.3	34.6 5.0	P02
holB	40663	41652	+	4563	3099	3532	4788	0.68	0.77	1.05		2						
yaaT	41655	42482	+	6586	4558	5157	6633	0.69	0.78	1.01								
yabA	42497	42856	+	2822	1824	2051	3213	0.65	0.73	1.13								
yabB	42915	43658	+	2536	1547	1763	2381	0.61	0.70	0.94	14	yabB	43482	43676	43579	5.1 6.1	1.7 0.6	
yazA wahC	43645	43944	+	1810	1406	835	1524	0.41	0.46	0.83								
abrB	43919	44797	+	15102	1400	1620	14793	0.55	0.05	0.92								
uorb	11010	10100		10102			1175	0.00	0.00	0.90	15	Inter	45199	45325	45262	4.7 2.3	0.7 2.0	
metG	45631	47625	+	7112	6847	6826	7269	0.96	0.96	1.02		*Broad	45743	49864				
yabD	47704	48471	+	2706	2618	2664	2566	0.97	0.98	0.95		I.						
yabE	48627	49940	+	793	3208	2051	733	4.06	2.61	0.93		I						
rnmV	50085	50645	+	1925	1575	1230	1786	0.82	0.64	0.93								
ksgA vabG	51678	52550	+	4065	3008	2028	3592	0.74	0.65	0.88								
yu00 veg	52761	53021	+	10421	11411	10553	9289	1.10	1.01	0.89								
sspF	53181	53366	+	986	1280	1513	890	1.31	1.54	0.91								
ipk	53514	54383	+	5113	4804	4585	4985	0.94	0.90	0.97								
purR	54439	55296	+	7135	6625	6171	7297	0.93	0.86	1.02	24	purR	54906	55287	55097	13.4 7.1	14.5 10.2	
yabJ	55293	55670	+	8923	9278	9407	9362	1.04	1.05	1.05	25	Terrer	55506	5 ( 00 1	55704	12.2 18.0	26 25	
snoVG	55864	56157	+	7085	23826	24250	9115	3 38	3 45	1 28	25	mer	33380	50001	33/94	12.3 18.0	2.0 2.5	
gcaD	56350	57720	+	12324	8958	8554	11829	0.73	0.69	0.96	26	gcaD	56929	57123	57026	1.9 3.2	2.1 6.9	
prs	57743	58696	+	11962	8465	8204	12139	0.71	0.69	1.01		8						
ctc	58781	59395	+	18581	14563	15467	16073	0.78	0.83	0.86								
spoVC	59502	60068	+	3976	2375	2718	3322	0.60	0.69	0.83								
yabK	60128	60358	+	5427	3351	3727	4756	0.62	0.69	0.88								
mfd VT	60428	63961	+	3947	2680	3029	3552	0.68	0.77	0.90	27	mfd	61332	61645	61489	12.3 18.4	2.7 0.9	
spov1 vabM	64097	66413	+	1740	1230	1302	1761	0.77	0.88	1.01	28	vabM	65055	65240	65152	54 25	0.6 0.0	
vabN	66403	67872	+	4762	4351	4614	4807	0.91	0.97	1.01	20	yuoni	05055	05247	05152	5.4 2.5	0.0 0.0	
yabO	67875	68135	+	4397	3774	4158	4342	0.86	0.95	0.99								
yabP	68214	68516	+	2867	2470	2425	3172	0.86	0.85	1.11								
yabQ	68513	69148	+	4872	4714	4756	5124	0.97	0.98	1.05								
divIC	69166	69543	+	6129	7178	6617	6492	1.17	1.08	1.06								
yabR	69624	70010	+	14817	14925	14188	14977	1.01	0.96	1.01	29	yabR	69391	69890	69641	20.8 25.4	27.8 4.7	P02
spone vabS	73104	73941	+	419	522	546 440	5/3	0.77	1.04	0.89								
vabT	73807	74823	+	533	496	521	492	0.93	0.98	0.90								
yacA	74927	76345	+	3602	3582	3604	4271	0.99	1.00	1.18								
hprT	76342	76884	+	6103	5116	5040	7175	0.84	0.82	1.17		*Broad	76463	79104				
ftsH	76982	78895	+	20524	20731	21287	20838	1.01	1.04	1.02		1						

Supplemen	ntary Tabl	le S1. Sur	nma	ry of trai	iscriptor	me and ( Trans	ChAP-ch	ip analyse a analysis	es (contin	ued).				C	hAP-chin	analveie				
-	gene			Sior	nalintens	ity of RN		E analysis Evo	ression rat	tio <sup>b</sup>				C	inai -ciup a	111119515	Binding	intensity	С	
		,	pu	Sigi	iai interis	ily OF KIN	A	LAP	$\Delta abh$		PBR	ORF		,		Ab	rB	A	bh	Profile
name	start	end	stra	wild	∆abrB	$\Delta abh$	$\Delta abh$	$\Delta abrB/$	$\Delta abrB/$	$\Delta abh /$	ID	0r Intorconio	start	end	center	wild	A	wild	4 - L - D	ID
						∆ abrB		Wild	wild	wiid		Intergenic				-type	⊿ abn	-type	∆ abrB	
yacB	79090	79791	+	7006	3967	4807	7821	0.56	0.68	1.11		1								
hslO	79877	80752	+	6953	4557	5186	7982	0.65	0.74	1.15										
yacD cvsK	80799	81692	+	4812	2393 9268	10822	2308	0.54	1.09	1.12										
vabB	82861	84273	+	2932	2115	2197	2722	0.73	0.75	0.93										
pabA	84287	84871	+	4249	3470	3657	4184	0.82	0.86	0.98										
pabC	84871	85752	+	3764	3082	3047	3711	0.82	0.81	0.99										
sul	85734	86591	+	5775	4692	4783	5596	0.81	0.83	0.97										
folB	86584	86946	+	7284	6246	6213	7242	0.86	0.85	0.99										
joik vazB	80943	87607	+	5955	4817	4891	5905 7306	0.81	0.82	1.06										
vacF	87631	88632	+	8106	7353	7139	7997	0.05	0.88	0.99										
lysS	88724	90223	+	10405	9315	9004	10242	0.90	0.87	0.98										
trnJ-Leu1	95646	95731	+	21683	24426	24548	20522	1.13	1.13	0.94										
ctsR	101446	101910	+	3501	3407	4086	4819	0.98	1.17	1.37										
mcsA	101924	102481	+	3548	3746	4334	5106	1.09	1.25	1.44										
mcsB clpC	102481	105572	+	8720	11082	12089	11232	1.07	1.23	1.34										
radA	105509	107469	+	3086	3873	4056	3965	1.28	1.40	1.28										
yacK	107473	108555	+	5467	5488	5879	6347	1.00	1.07	1.16										
yacL	108671	109771	+	4759	4197	4443	5170	0.88	0.93	1.09	36	yacL	108848	109059	108954	3.6	3.5	7.1	7.4	
ispD	109786	110484	+	6417	5825	6056	6542	0.91	0.95	1.02										
ispF	110477	110953	+	5588	5017	5047	6144	0.90	0.90	1.10										
gltX avrF	111044	112495	+	11/59	2170	2121	12311	0.8/	0.86	1.05										
cysE	112/9/	113430	+	5450	3819	4085	5500	0.08	0.07	1.01										
yazC	114851	115282	+	4082	2947	3122	4260	0.72	0.77	1.05										
yacO	115266	116015	+	4567	3867	3769	4866	0.85	0.83	1.07										
yacP	116022	116534	+	5558	4176	4240	5527	0.75	0.76	0.99						_				
	116507	117252		7070	10.126	0025	7204	1.40	1.25	1.00	38	Inter	116396	116760	116578	13.1	16.1	9.2	4.0	
sigH romG_1	117346	117495	+	5308	10436 6384	9935 6403	7394 5240	1.42	1.35	1.00										
secE	117529	117708	+	4998	5815	5610	4921	1.18	1.10	1.01										
nusG	117887	118420	+	4079	3640	3160	3646	0.90	0.77	0.88	39	nusG	117858	117950	117904	1.9	3.2	1.7	2.1	
rplK	118588	119013	+	25543	24280	23122	25609	0.95	0.91	1.00	40	rplK	118419	118953	118686	7.4	24.0	10.6	8.1	
rplA	119107	119805	+	24092	22151	20805	24225	0.92	0.86	1.01	40.1	rplA	118963	119293	119128	2.9	8.6	3.9	1.8	
rplJ	120057	120557	+	25238	23925	22116	25027	0.95	0.88	0.99										
rplL why P	120604	120975	+	18467	16829	15391	5251	0.91	0.83	0.95										
удлВ	121005	121070	Ŧ	5191	5850	4725	5251	1.07	0.82	0.87	41	Inter	121360	122081	121721	50.3	65.9	56.9	10.5	
rpoB	121916	125497	+	13848	13696	13480	13538	0.99	0.97	0.98	41.1	rpoB	122091	122385	122238	13.3	9.1	13.1	5.5	
rpoC	125559	129158	+	17243	17617	17268	16819	1.02	1.00	0.97	42	rpoC	125627	126263	125945	21.6	31.0	24.5	47.2	P01
ybxF	129339	129587	+	26440	25323	23367	25618	0.96	0.88	0.97		*Broad	129520	132009						
rpsL	129701	130117	+	28914	28704	27643	28294	0.99	0.96	0.98										
rpsG fusA	130159	130629	+	25900	26022	23227	20113	1.00	0.90	1.01										
tuf	132881	132701	+	30935	30643	30129	31441	0.90	0.93	1.02		I								
ybaC	134170	135126	+	1048	721	716	1071	0.69	0.68	1.03										
											45	Inter	135096	135477	135287	4.6	14.3	5.8	7.7	
rpsJ	135362	135670	+	30765	29417	29022	31131	0.96	0.94	1.01		10								
rplC	135710	136339	+	24011	23381	22382	24446	0.97	0.93	1.02	46	rpIC	135980	136140	136060	1.2	4.1	2.3	2.3	
rpiD rpIW	136990	130990	+	20101	20190	24790	29378	0.96	0.93	0.95										
rplB	137309	138142	+	29552	29483	28640	29696	1.00	0.92	1.01										
rpsS	138200	138478	+	23258	23484	21417	24263	1.02	0.92	1.04										
rplV	138495	138836	+	31673	31879	30921	31279	1.01	0.98	0.99										
rpsC	138840	139496	+	24323	24773	22036	23941	1.02	0.91	0.98		_								
rplP	139498	139932	+	26685	2/217	25722	26806	1.02	0.96	1.00	47	rpI₽	139789	139863	139826	0.6	2.3	0.9	0.6	
rpmC rpsQ	139922	140122	+	24524	24143	21858	24512	0.98	0.89	1.00										
rpsQ rnlN	140449	140403	+	29582	28775	27733	28749	0.95	0.94	0.97										
rplX	140855	141166	+	27565	26879	24697	27078	0.97	0.90	0.98										
rplE	141193	141732	+	27393	26937	25348	27757	0.98	0.93	1.01										
rpsN_1	141755	141940	+	20981	19048	16950	20964	0.91	0.81	1.00										
rpsH	141972	142370	+	30272	29073	27961	29120	0.96	0.92	0.96										
rplF	142400	142939	+	23487	22261	20462	23185	0.95	0.87	0.99										
rptR maE	142972	143334	+	30357	29577	28215	29090	0.97	0.93	0.96										
rpsE rnmD	145559	143859	++	23033	24202	22491	24379 15570	0.95	0.88	0.96										
rplO	144083	144523	+	27726	26172	24154	26772	0.94	0.87	0.97										
secY	144525	145820	+	25488	24200	22235	25083	0.95	0.87	0.98	49	secY	144616	144827	144722	2.2	5.3	3.1	2.3	
adk	145875	146528	+	25010	23616	22049	24592	0.94	0.88	0.98										
тар	146525	147271	$^+$	22151	21058	18964	21778	0.95	0.86	0.98										

Supplement	ntary Tabl	le S1. Sur	nma	ry of trai	scriptor	ne and (	ChAP-ch	ip analyse o opolycic	es (contin	ued).				C	AD ohin a	molycic				
	gene			Sim	alintanci	Trans		E analysis	roccion re	tio <sup>b</sup>				C	AF-chip a	anaiysis	Dinding	intoncity	с	
			pu	l	iai iniciis		A	CAP	$\Delta abh$		PBR	ORF				At	orB	A	bh	Profile
name	start	end	stra	wild	∆abrB	$\Delta abh$ $\Delta abrB$	∆abh	∆ abrB/ wild	∆ <i>abrB/</i> wild	∆abh / wild	ID	or Intergenic	start	end	center	wild -type	$\Delta abh$	wild -type	∆abrB	ID
infA	147583	147801	+	22580	19982	17975	22553	0.88	0.79	1.00										
rpmJ	147835	147948	+	26552	24351	23151	27226	0.92	0.88	1.03	51	rpmJ	147795	147989	147892	0.9	2.3	2.5	6.3	
rpsM	147971	148330	+	24288	22069	20841	24342	0.92	0.86	1.00										
rpoA	148929	149873	+	26897	24099	23405	25877	0.90	0.87	0.96	52	rpoA	148764	149332	149048	5.0	11.3	17.4	25.0	
rplQ	149951	150313	+	25532	23299	21787	24179	0.91	0.85	0.95										
cbiO_1	150441	151286	+	2613	2637	2057	2310	1.10	0.79	0.86	53	cbiO	151161	151287	151224	4.3	2.1	1.6	1.1	
cbiO_2 vhaF	151301	152131	+	2041	2105	2237	2717	1.17	0.81	0.88										
truA	152935	153678	+	7062	4775	3764	6141	0.68	0.53	0.87										
rplM	153841	154278	+	28410	29162	26354	29229	1.03	0.93	1.03										
rpsI	154299	154691	+	24450	23473	21321	24104	0.96	0.87	0.98	<i></i>		155027	155450	155245	10.0	17.7	( )	4.1	
ybaJ ybaK	155155	155922	+	18/3	4476	4/35	1639	2.40	2.55	0.87	54	ybaJ	155037	155452	155245	10.6	17.7	6.2	4.1	
cwlD	156611	157324	+	267	303	383	225	1.13	1.42	0.84										
ybaL	157420	158478	+	12338	11629	12735	13779	0.94	1.03	1.12										
gerD	158514	159071	-	228	230	252	188	1.03	1.14	0.82										
kbaA vbaN	159181	159777	+	1949	2688	3251	2049	1.38	1.68	1.05										
trnI-Thr	165829	165904	+	9320	12025	12469	10609	1.31	1.34	1.17										
ybaR	177082	178518	+	2330	1478	1497	2139	0.64	0.64	0.92										
ybaS	178733	179584	+	1581	1037	1070	1435	0.66	0.68	0.91										
ybbA fauC	179594	180163	-	946	2618	2376	1033	2.77	2.50	1.09										
feuC feuB	180108	181332	-	1288	3426	3155	1448	2.66	2.43	1.03										
feuA	182368	183321	-	3471	7508	7326	3581	2.16	2.12	1.03										
ybbB	183412	185001	-	1629	1869	2292	1673	1.15	1.40	1.02										
whhC	195102	196426		265	227	207	242	1.20	1 46	0.02	57	Inter	185004	185164	185084	2.2	3.7	0.8	0.9	
ybbC ybbD	185192	188378	-	203	341	394	245	1.28	1.40	0.92	58 59	vbbD	183888	188156	180002	5.5	8.5	5.3	16.7	
ybbE	188406	189731	-	387	457	527	335	1.18	1.36	0.87	60	ybbE	188353	188496	188425	0.6	0.9	1.4	3.9	
ybbF	189788	191155	-	379	443	518	376	1.17	1.37	0.99	61	ybbF	190631	190910	190771	0.2	1.3	2.2	12.7	
ybbH	191181	192032	-	953	1216	1435	849	1.28	1.51	0.89										
whb.I	192049	192903	-	1939 556	497	539	500	0.90	0.97	0.81										
ybbK	193566	194021	-	747	683	727	746	0.91	0.97	1.00										
trnSL-Glu	194197	194265	+	2207	4635	5205	3572	2.52	3.01	1.45										
aia W	10/020	105401		0001	14225	14401	0004	1.44	1.47	1.00	63	Inter	194439	194956	194698	16.7	16.4	15.6	9.0	
sig w vhhM	194838	195401	+	5449	8069	8194	5555	1.44	1.47	1.00	64	vbbM	195595	195737	195666	3.5	2.8	1.4	0.4	
ybbP	196202	197023	+	4007	3237	3429	4217	0.81	0.86	1.06	65	ybbP	196241	196656	196449	8.4	19.6	3.2	1.2	
ybbR	197016	198467	+	5896	4996	5404	6305	0.85	0.92	1.07										
ybbT almS	198486	199832	+	7074	6867 7527	7110	7498	0.97	1.01	1.06	66	olmS	201258	201671	201515	5.1	6.6	11.0	14.2	
ybbU	200203	202063	+	431	350	305	422	0.81	0.98	0.97	00	gins	201558	2010/1	201313	5.1	0.0	11.0	14.5	
alkA	202533	203444	-	447	336	349	396	0.75	0.78	0.89	67	alkA	202464	202674	202569	1.5	1.7	1.8	7.7	
adaA	203715	204350	+	286	199	227	267	0.70	0.80	0.93										
adaB	204337	204876	+	454	330	345	545	0.73	0.76	1.22	60	Inter	205166	205309	205238	3.0	5.2	0.3	0.1	
ndhF	205395	206912	+	580	477	574	568	0.82	1.00	0.97	70	ndhF	205455	2055649	205552	1.9	2.8	4.6	6.3	
											71	ndhF	206220	206516	206368	11.1	6.9	12.3	1.4	
ybcC	206927	207169	+	253	199	258	213	0.78	1.02	0.83										
ybcD ybcF	20/166	209430	++	335	262 295	399 523	295	0.77	1.20	0.89	72	vbcF	209773	210154	209964	11.8	10.9	42	22	
ybcH	210210	210500	+	510	345	629	393	0.72	1.31	0.82	12	<i>j</i> 001	207113	210154	207704	11.0	10.7	7.2	2.2	
ybcI	210558	210932	+	558	407	604	431	0.72	1.12	0.80										
ybcL	211845	213017	+	760	722	726	781	0.95	0.96	1.03	73	ybcL	212476	212755	212616	4.3	7.7	4.8	14.3	
ybcM	213141	213455	+	747	693	698	747	0.94	0.94	1.00	75	Inter	213445	214387	213016	56.7	72.2	27.0	61	P02
ybcO	213926	214093	+	879	7877	9837	972	8.94	11.18	1.10	15	inci	213443	21+30/	213710	- 30.7	12.2	-27.9	0.1	102
ybcP	214160	215392	+	456	3900	4677	448	8.57	10.28	0.98										
ybcS	215389	215946	+	423	2999	3503	449	7.06	8.24	1.06	76	ybcS	215400	215560	215480	2.3	4.5	0.7	0.1	
ybcT	215943	216878	+	528	3560	4123	560	6.74	7.80	1.06	78	ybcT' ybcT	216012	216512	216262	22.0	23.9	13.3	9.5	
vbdA	216897	217616	+	407	3240	3579	493	7.95	8.76	1.21	/ ð. l	yber	210522	210801	210002	8.0	14.9	2.8	4.1	
ybdB	217681	219027	+	435	1842	2021	482	4.25	4.65	1.11										
ybdD	219074	219487	+	518	2821	3116	584	5.45	6.02	1.13	79	ybdD	219140	219283	219212	2.4	0.9	3.4	1.6	
ybdE	219593	220018	+	141	687	702	174	4.87	4.96	1.23										
ybdG ybdI	220264	221154	++	565 593	802 790	865 822	530 530	1.42	1.53	0.94										
ybdS ybdK	221240	222900	+	699	934	932	692	1.33	1.38	0.99										
ybdL	222970	223164	+	6279	6309	6412	5821	1.00	1.02	0.92										
ybdM	223207	223977	-	593	568	590	525	0.96	0.99	0.89										

Supplem	gene	c 51.5u	1016	iy or trai	scriptor	Trans	criptome	analysis	.s (contin	iucu).				C	hAP-chip a	analysis		
	0.			Sig	nal intensi	ity of RN	A <sup>a</sup>	Exp	ression ra	tio <sup>b</sup>		0.00		-		Binding	intensity c	
name	start	end	strand	wild	∆abrB	$\Delta abh$ $\Delta abrB$	∆abh	$\Delta abrB/$	$\Delta abh$ $\Delta abrB/$	$\Delta abh /$	PBR ID	ORF or Intergenic	start	end	center	AbrB wild	Abh wild A abrB	Profile ID
vbdN	224063	22/020		265	5000	6621	260	22.51	wild 25.01	1.01		8				-type	-type	
your	224003	224920		205	5770	0021	20)	22.51	25.01	1.01	80	Inter	224495	225420	224958	36.5 59.9	20.9 5.1	P02
ybdO	225052	226236	+	388	2969	2833	451	7.70	7.32	1.15								
ybxG csaA	226554	227942	+	2810	1663	1812	2571	0.59	0.65	0.92								
ybxH	228034	228510	+	480	419	495	427	0.85	1.03	0.89								
ybxI	228537	229340	-	526	1135	1208	583	2.16	2.30	1.11	81 82	ybxI Inter	228643 229306	228939 229619	228791 229463	2.6 2.4 12.4 9.5	3.0 11.4 3.3 1.5	
cypC	229513	230766	+	731	561	714	542	0.77	0.98	0.74								
ybyB	230807	231067	-	6685	4686	7705	2697	0.70	1.15	0.42	83	Inter	230547	231863	231205	56.0 49.6	52.1 224.0	P01
ybeC	231336	232955	+	6871	8206	7538	4769	1.20	1.10	0.70	84	ybeC	231941	232084	232013	0.9 1.1	1.5 4.0	
glpQ	233002	233883	-	22513	4521	6528	18033	0.20	0.29	0.80	85	glpQ	233760	233869	233815	0.7 1.1	1.5 3.6	
gip1 vheF	235982	235861	+	21075	4030	884	880	0.19	0.20	0.80	86	vbeF	235477	235858	235668	6.4 13.1	2.6 1.2	
ybfA	235953	236870	+	1113	720	799	976	0.65	0.72	0.88		J						
ybfB	236867	238117	+	885	631	736	798	0.71	0.84	0.90								
ybfE	238152	238436	-	1773	998	1131	2013	0.56	0.64	1.13	07	1.05	220070	220277	220170	15.0 00.0	0 6 1 1	
ybfF vbfG	238632	239543	-	3131	14/6	2112	2003	0.47	0.56	0.96	87	YDIF	238979	239377	239178	15.8 29.9	-0.6 -1.1	
ybjG vbfH	239032	241830	-	942	815	857	988	0.30	0.00	1.05								
ybfI	242822	243649	-	540	435	468	561	0.81	0.87	1.04								
purT	243880	245034	+	5299	5437	6005	4610	1.03	1.13	0.87								
	245170	046110		500	0.45	000	401	1.02	1.00	0.04	89	Inter	244980	245225	245103	8.3 9.7	2.7 -0.4	
mpr vhfI	245178 246082	246119	+++	522 205	945 448	989 466	220	1.82	2.27	0.94								
9090	210002	210100	·	200	110	100	220	2.17	2.27	1.07	90	Inter	246374	246653	246514	12.6 3.3	4.3 -0.3	
ybfK	246646	247536	+	1411	2354	2112	1527	1.67	1.50	1.08								
neeA	247732	248265	+	3213	1260	3740	3473	1 33	1 17	1.09	91	Inter	247411	247724	247568	5.8 12.5	0.7 1.4	
vbfM	248256	248203	+	3126	3508	3365	3235	1.13	1.08	1.04								
psd	248737	249528	+	3561	4077	3925	3636	1.15	1.11	1.03								
ybfN	249583	249861	+	914	893	906	849	0.98	0.99	0.93		<b>.</b> .	<b>2</b> 40 <b>2</b> 0 4		<b>2</b> 4000 <b>5</b>	10.0 10.0		
vhfO	249967	251307	+	527	8471	9549	408	16 31	18 69	0.78	92	Inter	249706	250104	249905	12.2 18.9	5.9 2.0	
ybf0 ybfP	251415	252302	+	547	4897	5443	536	8.96	9.99	0.78								
5.5											93	Inter	252137	252603	252370	14.5 25.8	7.1 10.4	
ybfQ	252502	253470	+	8186	10412	11299	7840	1.27	1.38	0.96								
gltP gam P	253506	254750	-	4087	2605	1238	745	1.18	1.43	0.86								
gamA	256811	257560	-	5480	4328	5255	4019	0.79	0.92	0.73								
ybgA	257779	258486	+	1293	843	934	1142	0.66	0.73	0.89								
ybgB	258520	258795	+	2019	1636	1893	1864	0.81	0.93	0.92								
ybgE vbgE	259004	260074	+	599	451	479	583	0.75	0.80	0.97								
yDg1 mmuM	261644	262591	-	42J 811	679	720	745	0.83	0.91	0.90								
ybgH	262720	264111	-	576	490	535	622	0.85	0.93	1.08								
ybgJ	264181	265164	-	281	210	235	274	0.75	0.84	0.98								
ycbA	265536	266699	+	925	706	821	835	0.76	0.89	0.90								
ycbB ychC	266/10	267654	+	392	940 308	328	371	0.84	0.95	1.00								
ycbC ycbD	268837	270303	+	434	321	326	467	0.74	0.75	1.08								
ycbE	270387	271754	+	400	333	355	430	0.83	0.89	1.09								
ycbF	271791	273158	+	410	312	329	455	0.76	0.80	1.13								
ycbG ycbH	273228	273929	+	1668	1606	1455	1403	0.96	0.87	0.84								
ycb11 vcbJ	274020	276749	+	2220	11016	10665	1639	4.98	4.82	0.74	96	vchJ	276294	276454	276374	3.4 2.4	4.8 2.7	
yczA	277151	277312	+	603	984	848	600	1.66	1.42	1.02		J						
ycbK	277333	278271	+	1229	1475	1448	1075	1.20	1.18	0.87	97	ycbK	277246	277644	277445	1.5 1.8	3.9 26.9	P04
ycbL	278368	279048	+	443	369	381	391	0.83	0.86	0.88								
ycbM ychN	279050	279526	+	1289	670	635	679	0.87	0.86	0.86								
vcbO	280640	280321	+	977	905	948	981	0.93	0.97	1.00								
ycbP	281309	281695	-	1122	779	1096	698	0.70	0.97	0.63								
cwlJ	282009	282437	+	361	371	371	341	1.04	1.04	0.96								
ycbR	282543	283274	+	794	562	565	720	0.71	0.71	0.91	90	Inter	283106	282764	283480	25 1 9 2	35.2 14.6	
phoD	283553	285223	+	335	265	297	340	0.79	0.89	1.02	70	inci	203170	203704	205400	- 23.1 9.2	14.0	
tatAD	285318	285530	+	300	251	271	325	0.84	0.91	1.08								
tatCD	285591	286328	+	567	580	624	509	1.02	1.10	0.89								
pcp	286325	286972	-	665	1127	1197	571	1.71	1.80	0.86	101	Inter	286460	287580	287025	51.3 01.4	23.3 15.0	
vcbU	287051	288163	+	565	843	813	493	1.49	1.44	0.87	101	inter	280460	28/389	28/025	- 51.5 91.4	25.5 15.0	
2					0.0			>										

#### Supplementary Table S1. Summary of transcriptome and ChAP-chip analyses (continued).

Suppleme	gene	ie 51. 50	1111112	ry of tra	iscripto	Trans	crintom	analysis	es (contin	ueu).				С	hAP-chin a	malysis		
	gene			Sig	nglintane	ity of RN		Evn	ression ra	tio <sup>b</sup>					in cupt	Binding	r intensity c	
			pu	JB	nai incris	ity of Kiv	A	Ехр	A ahh	40	PBR	ORF				AbrB	Abh	Profile
name	start	end	stra	wild	∆abrB	$\Delta abh$	$\Delta abh$	$\Delta abrB/$	$\Delta abrB/$	$\Delta abh /$	ID	Or Intensonio	start	end	center	wild , , ,	wild , , p	ID
						∆abrB		wild	wild	wild		Intergenic				-type △abh	-type ⊿ abrB	
											876	ysxD	2878206	2878536	2878371	18.2 2.3	18.9 0.5	P05
lmrB	288205	289644	-	1561	1667	1576	1650	1.11	1.03	1.05	103	lmrB	288671	289527	289099	31.3 26.6	42.5 112.8	P01
lmrA	289684	290250	-	1065	903	817	945	0.88	0.79	0.89								
yccC	290467	291594	+	484	390	439	460	0.81	0.91	0.95	104	Intor	201016	202215	201666	85.5 125.2	56.5 21.7	<b>D</b> 01
lin	291757	292395	+	980	11178	12933	1791	11 41	13 20	1.83	104	mer	291010	292313	291000	63.3 133.3	30.3 31.7	P01
vczC	292433	292816	-	882	1242	1331	741	1.42	1.51	0.84	105	vczC	292512	293114	292813	23.6 23.3	15.5 3.5	
yccF	293051	294127	+	6074	5556	5577	5625	0.92	0.92	0.93		<b>J</b> • •						
yccG	294167	295123	-	1324	1207	1168	1219	0.91	0.88	0.92								
yccH	295136	295837	-	927	928	883	934	1.00	0.95	1.01								
								0.04		0.00	106	Inter	295827	295987	295907	4.7 6.0	0.2 -0.2	
natA matP	295981	296721	+	1202	1220	1120	1142	0.91	0.84	0.89								
nai b vecK	290722	297002	+	818	1220	1/07	850	1.02	1.84	1.05								
vcdA	298990	300054	-	422	1131	3205	926	2.68	7.50	2.19								
,										,	107	Inter	299771	300798	300285	73.6 76.7	92.9 196.3	P01
ycdB	300382	301800	+	560	927	931	641	1.67	1.67	1.13	108	ycdB	301080	301359	301220	5.6 2.7	8.5 8.1	
ycdC	301987	303348	+	772	542	528	668	0.71	0.69	0.86								
ycdD	303356	303859	-	371	443	438	443	1.19	1.18	1.19								
											109	Inter	303597	304198	303898	37.2 33.4	26.0 -0.5	P02
rapJ	303982	305103	+	1151	2436	2582	1697	2.14	2.27	1.47								
ycar wadC	305210	303980	+	820	805	020	848 627	0.62	0.82	0.07								
ycaG ycdH	307884	308843	+	1446	548	599	1033	0.85	0.42	0.70								
ycdI ycdI	308899	309594	+	1956	999	910	1531	0.52	0.47	0.78								
yceA	309552	310394	+	2546	1591	1439	2271	0.63	0.57	0.89								
yceB	310432	311373	-	680	629	737	860	0.94	1.10	1.27								
yceC	311711	312310	+	12296	14684	15677	14118	1.19	1.27	1.15								
yceD	312332	312913	+	12887	15308	16923	14918	1.19	1.31	1.16								
yceE	312948	313526	+	11650	13302	14335	13368	1.14	1.23	1.15								
yceF vceG	313577	314350	+	14128	15558	5353	15065	1.09	1.15	1.07								
vceH	316064	317155	+	5254	6787	7466	5842	1.29	1.42	1.11								
yceI	317277	318479	+	1958	1249	1317	1698	0.64	0.67	0.87								
yceJ	318732	319904	-	373	321	340	376	0.86	0.91	1.01								
yceK	319973	320275	-	1195	1378	1207	1008	1.26	1.03	0.90								
											110	Inter	320154	320552	320353	16.4 2.4	14.8 10.7	
opuAA	320565	321821	+	3448	3742	3115	3458	1.08	0.90	1.00	110	opuAA	320545	321130	320838	27.7 2.8	50.8 42.7	P06
opuAB	321823	3220/1	+	4550	5002 4045	4300	4807	1.10	0.95	1.07								
amhX	323571	324740	-	554	451	508	564	0.82	0.92	1.00								
vcgA	325133	326323	+	316	418	427	324	1.32	1.35	1.03								
ycgB	326439	327020	+	1155	632	762	1195	0.55	0.66	1.03								
											111	Inter	326835	327233	327034	12.2 11.0	11.2 2.1	
amyE	327169	329151	+	3944	1178	2629	4614	0.29	0.61	1.16	112	amyE	327668	328049	327859	21.6 25.9	17.5 3.0	
ldh Lup	329328	330293	+	15105	13890	15045	14145	0.92	0.99	0.93								
lCIP mdr	330325	331950	+	2250	2512	1622	2540	0.84	0.80	0.77								
vcgE	333651	334118	+	685	513	522	707	0.75	0.76	1.03								
ycgF	334192	334821	+	870	702	647	751	0.81	0.74	0.87								
ycgG	334891	335652	+	607	498	427	578	0.82	0.70	0.95								
ycgH	335684	336817	-	361	350	384	367	0.97	1.06	1.02								
ycgI	336984	337718	+	503	425	479	541	0.85	0.95	1.08								
nadE	55/848 328716	338666	+	10/72	9897	10227	10572	0.92	0.95	0.98								
unit aroK	330585	340145	-	390 1650	418	381 1067	570 1450	1.08	0.97	0.97								
vcgJ	340173	340859	-	468	550	641	473	1.19	1.37	1.01								
ycgK	341052	342026	+	512	458	442	528	0.90	0.86	1.03								
cah	342098	343054	+	1354	1214	1314	1141	0.90	0.97	0.84								
ycgL	343138	343920	+	1678	1457	1513	1372	0.88	0.91	0.82								
ycgM	344111	345022	+	284	247	257	254	0.87	0.91	0.89								
ycgN	345039	346586	+	470	419	415	453	0.89	0.88	0.96							10 05	
ycg0	546782	348131	+	2101	1989	1887	1999	0.95	0.90	0.95	115	ycgU Inter	54/422 348110	54/599 348262	34/511 348101	3.9 5.5	1.8 0.5	
vcgP	348284	349519	+	003	960	997	990	0.08	1.01	1.00	110	11001	540119	346202	240191	4.0 1.3	-0.1 -0.7	
ycgO	349556	350413	-	2450	1905	2002	2500	0.78	0.82	1.00								
ycgR	350418	351302	-	1567	1117	1208	1677	0.71	0.78	1.07								
ycgS	351402	352256	-	243	221	232	254	0.91	0.95	1.04								
ycgT	352418	353428	+	5223	6373	6837	5472	1.22	1.31	1.05								
nasF	353460	354911	-	1598	1247	1184	1391	0.78	0.74	0.87								
nasE	354972	355292	-	1426	1177	1022	1231	0.83	0.72	0.87								
nasD nasC	355324	357741	-	432	298	316	361	0.71	0.76	0.85								
nuse	55/803	222223	-	203	242	230	218	0.00	0.91	0.99								

#### Supplementary Table S1. Summary of transcriptome and ChAP-chip analyses (continued).

	gene					Trans	criptom	e analysis						Cl	וAP-chip מ	nalysis		
				Sign	al intens	ity of RN.	A <sup>a</sup>	Exp	ression ra	tio <sup>b</sup>		OPE				Bindin	g intensity c	
name	start	end	and			Aabh		A abrB/	$\Delta abh$	Aabh /	PBR	or	start	end	center	AbrB	Abh	Profile
indite	Surt	end	str	wild .	∆ abrB	AahrB	$\Delta abh$	wild	$\Delta abrB/$	wild	ID	Intergenic	Start	end	center	wild Aabh	wild AahrB	ID
						Auorb		wiki	wild	W IICI		8				-type	-type	
nasB	360002	362314	-	273	241	255	282	0.88	0.93	1.03								
nasA	362494	363759	+	594	454	468	623	0.76	0.79	1.05								
yciA	363815	364732	+	224	194	212	209	0.86	0.95	0.93								
yciB veiC	365622	303313	+	258	271	200	227	0.75	0.77	0.88								
yere vekA	366864	367544	-	3720	271	202	3583	0.82	0.80	0.96								
vckB	367554	368417	-	4852	2918	2547	4323	0.60	0.53	0.89								
yckC	368795	369250	+	1035	1033	982	919	1.00	0.95	0.89								
yckD	369332	369664	+	229	505	594	201	2.19	2.57	0.88								
yckE	369818	371251	+	449	332	380	426	0.74	0.85	0.95								
nin	371288	371686	-	2309	825	771	2543	0.36	0.33	1.10								
nucA	371713	372156	-	5438	1507	1651	5109	0.28	0.30	0.94								
tlpC	372330	374051	-	723	628	588	813	0.88	0.81	1.12								
hxlB	374162	374719	-	870	867	755	961	1.00	0.86	1.10								
hxlA hulD	3/4/25	3/535/	-	1240	1119	1043	1297	0.90	0.84	1.04	117	had	275120	275021	275690	10.0 41.4	77 20	
nxik	373389	575951	+	939	00/	987	961	0.97	1.08	1.04	117	Inter	275021	375921	375080	19.9 41.4	24.0 2.7	P02
srfAA	376525	387291	+	1120	1803	1888	3628	1.60	1 68	3 23	117	Inter	575751	370035	570285	40.4 40.4	34.0 3.7	F02
srfAB	387304	398067	+	1230	2254	2351	4254	1.83	1.00	3.45	121	srfAB	390976	391187	391082	08 06	16 53	
0.9112	501501	270007		1200	2201	2001	1201	1.05		5.10	122	srfAB	393339	393465	393402	3.6 0.3	0.2 -0.2	
srfAC	398104	401928	+	1163	2148	2173	3819	1.85	1.87	3.29								
srfAD	401957	402685	+	814	1583	1600	2817	1.96	1.97	3.48								
ycxA	402786	404015	+	386	432	462	446	1.12	1.20	1.16								
ycxB	404030	404587	-	458	688	629	360	1.50	1.37	0.79								
											124	Inter	404457	404804	404631	13.0 18.1	5.9 -0.1	
ycxC	404641	405579	-	448	418	408	460	0.93	0.91	1.03								
ycxD	405/03	407037	+	430	1250	390	442	0.85	0.91	1.03								
sjp vezE	407210	407707	-	2012	1/20	1276	1704	0.98	0.67	0.85								
vckI	408777	409520	-	4828	3180	3064	4414	0.74	0.65	0.03								
vckJ	409534	410238	-	3989	2486	2337	3598	0.63	0.59	0.92	126	vckJ	410016	410414	410215	26.8 11.4	18.1 1.0	
yckK	410225	411031	-	8790	5461	5418	8437	0.62	0.62	0.96		<b>J</b> • •						
yclA	411146	412018	-	940	654	747	908	0.71	0.81	0.96								
yclB	412108	412722	+	405	309	330	427	0.76	0.81	1.06								
yclC	412725	414146	+	355	293	298	371	0.83	0.84	1.05								
yclD	414163	414852	+	536	431	447	550	0.81	0.84	1.03								
											128	Inter	414708	415021	414865	1.1 0.9	1.0 10.1	
yclE	414918	415763	+	407	330	340	408	0.81	0.84	1.00								
ycir	415805	41/281	-	224	2285	2373	3723	0.08	0.71	1.11								
yciG vc7F	417301	419313	+	204	200	402	210	0.80	1.02	0.90								
gerKA	419678	421312	+	362	341	353	420	0.94	0.97	1.16	129	øerK A	420301	420478	420390	39 62	24 17	
gerKC	421302	422525	+	487	450	495	443	0.92	1.02	0.91	,	Bound	120501	120170	.20070	5.5 0.2	2 1	
gerKB	422550	423671	+	511	488	528	501	0.95	1.03	0.98								
yclH	423776	424456	-	200	170	171	202	0.85	0.86	1.01								
yclI	424472	425932	-	230	196	210	232	0.85	0.91	1.01								
yclJ	426145	426828	+	715	523	517	697	0.73	0.72	0.97								
yclK	426815	428236	+	2031	1594	1644	1860	0.79	0.81	0.92								
~	120200				1000			0.00			130	Inter	428326	428417	428372	2.6 1.2	0.0 0.1	
rapC	428399	429547	+	1756	1209	1268	2321	0.69	0.72	1.33								
phrC	429531	429653	+	4283	11400	10586	4088	2.68	2.48	0.96								
vcIN	430191	431333	-	6175	540 6447	5/30	6326	1.04	0.88	1.02								
vclO	432883	433830	+	6786	6633	5907	6739	0.98	0.87	0.99								
vclP	433824	434582	+	9338	9555	8826	9362	1.02	0.95	1.00								
vclO	434604	435557	+	12565	12389	11802	12406	0.99	0.94	0.99								
ycnB	435604	437022	-	974	1085	901	934	1.14	0.92	0.94								
ycnC	437042	437920	-	1010	1119	857	925	1.14	0.85	0.90								
ycnD	438084	438833	-	3944	5248	5588	4402	1.36	1.43	1.12								
ycnE	438850	439137	-	3402	4233	4590	3627	1.28	1.38	1.07								
yczG	439277	439591	+	701	1180	1006	732	1.68	1.44	1.05								
gabR	439593	441032	-	277	264	284	290	0.96	1.03	1.04		. –						
gabT	441139	442449	+	308	259	265	325	0.84	0.86	1.05	132	gabT	441789	442000	441895	3.6 1.4	8.1 7.6	
gabD	442518	443906	+	4398	5268	6633	5366	1.21	1.53	1.22								
gicU adh	444029	444892	+	486	567	594	259	1.17	1.22	1.03								
gun vcnI	444912	446356	- -	201	3505	333	∠38 3148	1.74	2.09 0.85	1.00								
yen1	446360	447994	-	3421	3228	2927	2797	0.92	0.85	0.78								
vcnK	448029	448601	-	3309	4173	3653	2612	1.26	1.10	0.79								
vcnI.	448766	449119	+	437	414	354	410	0.95	0.82	0.94								
mtlA	449292	451124	+	2026	1310	1571	2355	0.67	0.78	1.15								
mtlD	451177	452277	+	788	489	600	874	0.62	0.76	1.11								
ycsA	452385	453449	+	3536	2475	2799	3490	0.70	0.80	0.99								

Supplem	entary Tab gene	ie S1. Sui	nma	ry of trai	nscriptor	me and ( Trans	_nAP-ch criptom	up analyse e analysis	es (contin	wea).				C	1AP-chip a	nalysis				
	8111			Sig	nal intens	ity of RN	A <sup>a</sup>	Exp	ression ra	tio <sup>b</sup>		0.0.0			p -		Binding	intensity	с	
name	etart	and	and	~		4h.h.		A abaD/	∆abh	A abb /	PBR	ORF	etart	and	center	At	brB	A	bh	Profile
ikune	start	cnu	str	wild	∆abrB	∆ abrB	$\Delta abh$	wild	$\Delta abrB/$	wild	ID	Intergenic	start	cha	center	wild	∆abh	wild	∆abrB	ID
								·	wild		122	Intor	152217	452712	452480	-type	17.8	-type	0.6	
sipU	453584	454147	+	2507	1874	1999	2232	0.76	0.81	0.89	155	mei	455247	455715	455480	0.5	17.0	2.3	0.0	
yczH	454257	454814	-	970	1086	1086	817	1.13	1.13	0.85										
ycsD	454900	455292	+	2698	2899	2709	2335	1.07	1.00	0.87										
ycsE E	455622	456371	+	4151	3942	4041	3971	0.95	0.98	0.96										
ycsF vcsG	456576	457349	+	685	966	987	613	1.10	1.20	0.88										
ycs0 vcsI	458584	459375	+	534	609	712	482	1.13	1.30	0.89										
, kipI	459419	460141	+	657	764	909	532	1.16	1.38	0.79										
kipA	460144	461157	+	642	707	750	562	1.09	1.16	0.86										
kipR	461173	461913	+	902	972	1073	747	1.08	1.18	0.82	137	kipR	461237	461499	461368	1.8	1.1	2.8	11.5	
ycsK	461988	462629	+	614	/88	/90	546	1.28	1.28	0.88	138	Inter	462478	462995	462737	42.5	177	20.4	0.2	
vczI	462802	463047	+	4258	3997	3862	5615	0.94	0.90	1.32	150	inter	402470	402775	402757	42.5	17.7	20.4	0.2	
yczJ	463053	463340	-	1463	1698	1715	1130	1.16	1.17	0.77										
pbpC	463491	465497	+	7243	6907	6450	6721	0.95	0.89	0.93	139	pbpC	463855	464236	464046	19.9	5.1	12.9	1.6	
ycsN	465599	466501	+	6938	7968	8018	6723	1.15	1.16	0.97										
mtik vdaB	400087	408//1	+	1808	1045	1152	1858	0.50	1.89	0.99	141	vdaB	468683	469302	468993	34.7	45.6	6.6	16	
ydaC	470514	471059	-	266	166	195	220	0.63	0.73	0.82	141	Jun	+00005	407502	-00775		-0.0	0.0	1.0	
ydaD	471267	472127	+	953	576	883	585	0.61	0.91	0.64										
ydaE	472143	472646	+	751	545	841	577	0.73	1.10	0.79										
ydaF	472731	473282	+	572	1736	2058	547	3.02	3.57	0.96										
yaaG ydaH	473300	475097	+	1589	5500 1789	1794	2930	0.74	1.00	0.38										
vdzA	475141	475431	-	2740	1656	1675	2321	0.60	0.61	0.85										
lrpC	475616	476050	+	1265	987	842	1115	0.79	0.67	0.90										
topB	476115	478298	+	4338	3801	3556	3942	0.88	0.82	0.91										
ydaJ	478501	479589	+	1204	939	765	1077	0.81	0.66	0.90	144	1-17	470870	490120	480000	10.4	25	26	1.5	
уаак	479570	480421	+	/10	554	490	052	0.80	0.70	0.91	144	ydaK ydaK	479869	480130	480000	26.3	3.5	3.0	9.0	
ydaL	480432	482141	+	757	600	543	752	0.80	0.72	0.98	144	ydaL	480668	481236	480952	30.5	2.9	34.2	15.7	
ydaM	482134	483396	+	1107	835	755	992	0.76	0.69	0.89										
ydaN	483402	485513	+	906	650	548	805	0.74	0.62	0.88	146	ydaN	484561	486200	485381	48.2	22.5	86.3	247.7	P01
ydaO	485989	487812	+	2250	3664	1044	1094	1.62	0.46	0.49	146	ydaO	486210	486778	486494	11.6	4.1	13.6	19.7	
mui 1 vdaP	48/8/1	488520	+	1128	1140	1634	680	1.04	1 46	0.85										
yuur	400507	470111		1120	1140	1054	000	1.01	1.40	0.00	148	Inter	489916	490382	490149	22.9	11.4	5.7	1.0	
ydaQ	490288	490578	+	473	358	400	396	0.76	0.85	0.84										
mntH	490702	491979	-	5301	5553	6359	5543	1.05	1.20	1.05	1.40	1.0	102220	100156	102202	0.0	0.0	1.0	27	
ydaS ydaT	492209	492466	-	1005	808 459	618	/14	0.82	1.17	0.75	149	ydaS	492330	492456	492393	0.2	0.2	1.2	3.6	
vdbA	493114	493932	+	1478	930	946	1415	0.63	0.64	0.96										
gsiB	494061	494432	+	5243	4958	7470	2404	0.99	1.43	0.55										
ydbB	494564	494905	+	555	591	630	547	1.06	1.13	0.98										
ydbC	494899	495258	+	787	824	886	639	1.04	1.12	0.80										
ydbD dctB	495295	496116	-	1106	899 1011	1296	938 1375	0.81	1.17	0.85										
dctS	497329	498936	+	674	610	631	637	0.05	0.94	0.94										
dctR	498926	499606	+	810	607	696	764	0.75	0.86	0.94										
dctP	499727	500992	+	15297	3733	7227	14690	0.23	0.41	0.96										
ydbI ydbI	501140	502192	+	4444	3117	2780	4136	0.70	0.63	0.93										
yaDJ vdhK	503415	504155	+	4209	4149	4121	4228	0.98	0.97	0.91										
Juon	000110	201122		1702	1070	1120	.220	0.70	0.00	0.00	152	Inter	504043	504305	504174	6.5	6.3	8.3	3.8	
ydbL	504250	504585	+	4293	5319	5036	3721	1.24	1.17	0.86										
ydbM	504713	505858	+	1703	1738	1806	1719	1.02	1.06	1.00										
ydbN ydbO	505883	506062	-	6227	8349 5482	8475 5242	4783	1.35	1.37	0.76										
yabO vdbP	507314	507634	-	7153	6401	6470	7650	0.89	0.90	1.13										
ddl	507809	508873	+	10459	9980	10222	11050	0.95	0.98	1.06										
murF	508945	510318	+	6878	5700	5616	6745	0.83	0.82	0.98										
ydbR	510667	512202	+	12004	12393	10745	11824	1.03	0.90	0.99										
ydbS ydbT	512375	512854	+	7297	9855	10322	7346	1.35	1.41	1.01										
yaD1 vdcA	512844	515176	+	5031 707	761	749	5229 707	1.32	1.40	1.04										
acpS	515271	515636	+	1335	1659	1693	1313	1.00	1.28	0.97										
ydcC	515697	516818	+	933	1211	1109	937	1.31	1.20	1.01										
alr	516933	518102	+	5912	5678	5634	6168	0.97	0.96	1.04	154	alr	517762	518075	517919	8.8	5.8	9.0	2.2	
ydcD	518218	518499	+	21363	22970	22052	21310	1.08	1.03	1.00										
yuCE rshR	518969	510703	+++	13/36	4671	10108 5010	5100	1.10	1.03	1.04	155	rsbR	519088	519384	519236	5.5	11.1	2.5	0.6	
rsbS	519798	520163	+	4263	4185	4665	4510	0.98	1.07	1.09	155	1301	517000	517504	517250	5.5	11.1	2.0	0.0	

Suppleme	gene	ie 51. 5ii	шпа	ry of tra	iscripto	Trans	criptom	e analysis	es (conun	iueu).				C	hAP-chip a	analysis			
	gene			Sig	nal intens	ity of RN	A a	Exp	ression ra	tio <sup>b</sup>				0.	in cup	Binding	intensity <sup>c</sup>		
	-44		pun		ikii incerts				$\Delta abh$		PBR	ORF	-44			AbrB	Abh	Profile	
name	start	end	stra	wild	∆abrB	$\Delta abh$	$\Delta abh$	∆ abrB/	$\Delta abrB/$	∆abh /	ID	Of Intergenic	start	end	center	wild A abh	wild A abrP	ID	
						<i>A abr</i> b		wiid	wild	wiid		Intergenie				-type	-type		
rsbT	520167	520568	+	7451	7461	7829	6919	1.00	1.05	0.93									
rsbU	520580	521587	+	5290	5844	6194	5721	1.11	1.17	1.08									
rsbV	521649	521978	+	9592	8182	8899	7131	0.85	0.93	0.74									
rsbW	521975	522457	+	13929	10765	11789	9964	0.77	0.85	0.70	150	· D	500 400	5007/7	522602	150 02	<b>10</b> 0.5		
sigB mbY	522417	523211	+	6697	5838	6788	4471	0.89	1.05	0.66	156	sıgB	522438	522767	522603	15.9 9.3	6.2 0.5		
ISUA	323211	323810	+	1298	7430	8101	4421	1.07	1.10	0.01	157	Intor	522780	524212	522006	12.0 22.5	27 20.8		
vdcF	524053	524346	+	554	364	383	513	0.64	0.69	0.91	157	mei	525780	324212	525990	12.0 22.3	2.1 29.0		
ydcI ydcG	524000	524540	+	891	872	862	865	0.04	0.09	0.97									
ydcH	524767	525210	+	518	449	465	491	0.87	0.91	0.94									
ydcI	525304	527463	+	3597	3194	3465	3991	0.89	0.97	1.11									
ydcK	527690	528142	+	642	543	556	698	0.85	0.87	1.08	159	ydcK	527809	528036	527923	7.6 4.0	2.3 0.8		
trnS-Leu1	528735	528819	+	801	1111	1242	945	1.41	1.56	1.24									
trnS-Leu2	528897	528983	+	1358	1512	1423	1384	1.12	1.06	1.06									
ydcL	529066	530172	-	314	427	521	285	1.35	1.64	0.91									
ydcM	530185	530694	-	593	626	719	492	1.06	1.20	0.84									
ydcN	530691	531074	-	836	620	709	718	0.75	0.83	0.86									
sacV	531348	531542	+	444	385	462	389	0.87	1.03	0.87									
yacO vdaP	522482	522862	+	247 431	18/	205	230	0.70	0.84	0.94									
yacı vdcO	532403	534341	+	451	110	360 120	200 137	0.87	0.08	0.90									
vdcR	534334	535392	+	180	169	182	175	0.80	1.01	0.97	164	vdcR	534609	534888	534749	11.1 2.5	9.8 16.1		
vdcS	535657	535926	+	395	359	409	371	0.91	1.04	0.94	101	Juert	221007	221000	001110	2.0	,		
ydcT	535965	536231	+	351	332	330	309	0.94	0.94	0.88									
yddA	536248	536556	+	179	173	192	169	0.97	1.08	0.95									
yddB	536546	537610	+	167	125	149	144	0.75	0.89	0.86									
yddC	537622	537870	+	307	281	338	308	0.91	1.09	1.01									
yddD	537883	538407	+	188	170	203	174	0.90	1.08	0.91	165	yddD	537822	537947	537885	1.6 1.7	3.6 1.1		
yddE	538295	540790	+	169	153	163	162	0.90	0.97	0.96									
yddF	540809	541135	+	169	139	152	168	0.84	0.93	0.99					<i></i>				
yddG	541139	543586	+	189	182	192	184	0.96	1.02	0.97	166	yddG	542004	542283	542144	2.6 1.2	4.7 13.7		
yaan vddI	545565	545002	+	244	104	205	210	0.84	0.84	0.97									
yuui	544567	545075	т	244	194	203	210	0.79	0.04	0.80	167	Inter	544945	545292	545119	16.1 15.8	45 07		
vdd.I	545156	545536	+	243	605	830	261	2.49	3.41	1.07	167	vddJ	545302	545530	545416	7.5 6.0	0.4 1.0		
vddK	545727	546527	-	2615	2176	2361	4114	0.83	0.90	1.57		<i></i>							
-											169	Inter	546373	547179	546776	77.5 89.2	28.4 3.9	P02	
rapI	546867	548042	+	211	248	284	194	1.16	1.34	0.92	170	rapI	547308	547740	547524	17.4 16.6	2.0 7.5		
phrI	547999	548118	+	1879	3151	3167	2086	1.71	1.70	1.12									
yddM	548271	549212	+	395	373	399	404	0.94	1.01	1.01	171	yddM	548022	549151	548587	57.0 17.3	31.5 105.3		
yddN	549783	550802	-	219	185	199	224	0.85	0.91	1.02									
	551060	551470		1070	0.22	0.12	1042	0.70	0.70	0.07	172	Inter	550912	551106	551009	3.6 3.1	0.7 0.4		
lrpA	551062	551472	+	1072	833	843	1043	0.78	0.78	0.96	172	Teste a	551000	551694	551495	74 62	1.5 01.1		
lum P	551505	552044		207	199	102	228	0.01	0.03	1 16	1/3	Inter	551286	551684	551485	7.4 6.3	1.5 21.1		
vddO	552159	552701	+	908	424	445	985	0.91	0.93	1.10	174	vddO	552102	552534	552318	26.4 27.0	84 72		
vddR	553254	554018	+	577	324	316	548	0.57	0.55	0.95	17.	Jung	002102	002001	002010	20.1 27.0	0.1 7.2		
vddS	554212	555522	+	542	511	514	541	0.94	0.95	1.00	176	yddS	554159	554268	554214	1.7 1.1	2.1 2.6		
-											177	yddS	554635	555237	554936	20.0 14.7	6.0 10.5		
											177	yddS	555247	555730	555489	26.4 27.2	10.3 6.2		
											178	Inter	555944	556155	556050	8.8 6.9	1.4 0.2		
yddT	556306	556992	+	1440	6552	8888	1017	4.93	6.50	0.89									
											180	Inter	557032	557549	557291	24.3 22.8	6.7 3.0		
ydeA	557952	558545	+	368	258	265	346	0.70	0.72	0.95	181	ydeA	558154	558433	558294	11.3 4.6	4.5 3.1		
G	550000	550000		1075	5200	4101	2014	1.22	1.02	0.07	181	Inter	558443	558892	558668	31.3 29.3	14.5 8.4		
cspC	558808	559008	+	4075	5390	4181	3914	1.32	1.03	0.96	182	Intor	550106	550217	550212	50 20	05 04		
vdaB	550605	560156		835	1453	1702	1376	1.74	2 10	1.68	162	mer	559100	339317	339212	3.9 5.0	0.5 0.4		
уисы	557075	500150	-	055	1455	1772	1570	1.74	2.17	1.00	183	Inter	560092	560286	560189	47 08	35 50		
ydzE	560724	560960	-	846	714	84.5	742	0.84	1.00	0.88	100		2 30072	2 30200	2 5010)	0.0	2.0 0.0		
ydeC	561058	561933	-	359	288	318	331	0.81	0.89	0.93									
ydeD	562046	563005	+	334	306	317	311	0.91	0.95	0.93									
ydeE	563158	564030	-	416	355	372	387	0.85	0.89	0.93	184	ydeE	563645	563873	563759	8.7 8.7	3.2 0.5		
ydeF	564248	565645	+	514	421	418	494	0.82	0.81	0.96									
											185	Inter	565583	565913	565748	13.0 3.7	14.7 10.6		
ydeG	565755	567047	+	524	492	523	569	0.94	1.00	1.08	186	ydeG	566484	567596	567040	34.3 57.4	23.2 5.4	P02	
ydeH	567206	567652	+	397	1287	1036	494	3.20	2.59	1.26									
ydeI	567889	568482	+	584	611	628	582	1.05	1.07	1.00									
ydeJ	568834	569493	-	673	2322	2227	522	3.47	3.30	0.78	107	Testo ::	5/0/12	50070 -	560570	12.2 65	0.0 0.0		
vdeV	560015	570770		277	260	251	271	1 10	1 10	1 17	187	mer	569442	309/04	209573	12.3 6.7	0.9 -0.3		
уаек	202213	510118	-	525	505	550	510	1.12	1.10	1.1/	189	Inter	570734	570004	570865	94 12	39 00		
vdeL	570933	572324	+	285	284	308	283	0.90	1.08	0.90	100	mer	510154	510770	570805	7.4 1.2	5.7 0.0		
,	2,0/00	2,2027		200	204	500	205	0.77	1.00	0.77									
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	Supplem	entary Tab	le S1. Sun	nma	ry of tra	nscripto	me and	ChAP-ch	ip analyse	es (contin	ued).				Cł	A D ohin a	nolucio		
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net         net <th></th> <th>gene</th> <th></th> <th></th> <th>Sim</th> <th>nalintana</th> <th>Trans</th> <th></th> <th>Evo</th> <th>roccion ro</th> <th>tio <sup>b</sup></th> <th>· ·</th> <th></th> <th></th> <th>U</th> <th>ар-спра</th> <th>anaiysis Dinding</th> <th>intonsity C</th> <th></th>		gene			Sim	nalintana	Trans		Evo	roccion ro	tio <sup>b</sup>	· ·			U	ар-спра	anaiysis Dinding	intonsity C	
mame         bit         mat         mat <th></th> <th></th> <th></th> <th>pu</th> <th>SIE</th> <th>nai interis</th> <th>ity of Kiv</th> <th>A</th> <th>Exp</th> <th>A abh</th> <th>0</th> <th>PBR</th> <th>ORF</th> <th></th> <th></th> <th></th> <th>AbrB</th> <th>Abh</th> <th>Profile</th>				pu	SIE	nai interis	ity of Kiv	A	Exp	A abh	0	PBR	ORF				AbrB	Abh	Profile
Unit         Unit <th< th=""><th>name</th><th>start</th><th>end</th><th>stra</th><th>wild</th><th>∆abrB</th><th>∆ abh A shuP</th><th><math>\Delta abh</math></th><th>∆ abrB/</th><th><math>\Delta abrB/</math></th><th>∆abh /</th><th>ID</th><th>Of Intergenic</th><th>start</th><th>end</th><th>center</th><th>wild 4 shh</th><th>wild 4 shaP</th><th>ID</th></th<>	name	start	end	stra	wild	∆abrB	∆ abh A shuP	$\Delta abh$	∆ abrB/	$\Delta abrB/$	∆abh /	ID	Of Intergenic	start	end	center	wild 4 shh	wild 4 shaP	ID
mlst         genus							Aubrb		wiid	wild	wiid		Intergenie				-type	-type	
biology         constraint          mate         mat	ydeM	572518	572943	+	1164	1061	1053	1071	0.91	0.90	0.92								
matrix         stype         stype <t< td=""><td>ydeN ydzE</td><td>572996</td><td>573568</td><td>-</td><td>848</td><td>790</td><td>848</td><td>884</td><td>0.95</td><td>1.02</td><td>1.06</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>	ydeN ydzE	572996	573568	-	848	790	848	884	0.95	1.02	1.06								
mark         system         System <td>yuzr vdeO</td> <td>574234</td> <td>575106</td> <td>+</td> <td>2873</td> <td>3199</td> <td>3011</td> <td>2853</td> <td>1.12</td> <td>1.05</td> <td>0.99</td> <td>189</td> <td>vdeO</td> <td>574423</td> <td>574583</td> <td>574503</td> <td>4.5 2.3</td> <td>1.2 0.4</td> <td></td>	yuzr vdeO	574234	575106	+	2873	3199	3011	2853	1.12	1.05	0.99	189	vdeO	574423	574583	574503	4.5 2.3	1.2 0.4	
hg/hg         Strate         Strae         Strae         Strae	ydeP	575256	575642	-	902	408	468	875	0.45	0.52	0.97		<b>J</b>						
bit A         Strate         Strae         Strae         Strae	ydeQ	575753	576346	+	377	259	276	302	0.70	0.74	0.80								
mat         mat <td>ydeR</td> <td>576490</td> <td>577677</td> <td>-</td> <td>297</td> <td>295</td> <td>300</td> <td>313</td> <td>0.99</td> <td>1.01</td> <td>1.05</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	ydeR	576490	577677	-	297	295	300	313	0.99	1.01	1.05								
model         styles         styles<	ydeS vdeT	570085	570420	+	21/6	1/58	100/	2052	0.81	0.77	0.94								
matrix         statize         Statize <th< td=""><td>vdfA</td><td>579433</td><td>580740</td><td>+</td><td>1867</td><td>1311</td><td>1259</td><td>1709</td><td>0.79</td><td>0.72</td><td>0.97</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<>	vdfA	579433	580740	+	1867	1311	1259	1709	0.79	0.72	0.97								
mlc         Size of Si	ydfB	581238	582023	+	325	437	455	328	1.35	1.41	1.02								
bild         Sets         Sets <th< td=""><td>ydfC</td><td>582080</td><td>583000</td><td>-</td><td>428</td><td>423</td><td>466</td><td>405</td><td>0.98</td><td>1.09</td><td>0.94</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<>	ydfC	582080	583000	-	428	423	466	405	0.98	1.09	0.94								
00/02         03/02         03/02         03/02         03/01         04/01 <th< td=""><td>ydfD</td><td>583133</td><td>584581</td><td>+</td><td>268</td><td>242</td><td>252</td><td>262</td><td>0.91</td><td>0.94</td><td>0.98</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<>	ydfD	583133	584581	+	268	242	252	262	0.91	0.94	0.98								
marge         second         second </td <td>yajE vdfE</td> <td>585412</td> <td>586092</td> <td>-</td> <td>1225</td> <td>1521</td> <td>522 1514</td> <td>1016</td> <td>1.71</td> <td>1.04</td> <td>0.95</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	yajE vdfE	585412	586092	-	1225	1521	522 1514	1016	1.71	1.04	0.95								
nptH         587388         588141 +         666         630         631         631         631         631         631         631         631         641           nptJ         588261         591454         591454         591454         591454         59145         59146         591454         2131         2883         631         630         63         42         100        100 <th< td=""><td>ydfG</td><td>586172</td><td>586615</td><td>-</td><td>2123</td><td>2416</td><td>2497</td><td>2109</td><td>1.14</td><td>1.18</td><td>0.99</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<>	ydfG	586172	586615	-	2123	2416	2497	2109	1.14	1.18	0.99								
map       588814       588874       588874       588874       588870       30       0.0       6.0       4.5         map       591847       59248       -       2.03       2.32       2.83       1.23       2.03       0.3       0.05       6.05       0.5         map       591847       592440       -       2.03       2.32       2.84       0.30       0.55       0.05       0.55	ydfH	587288	588511	+	686	630	635	651	0.92	0.93	0.95								
null         solution         solution <th< td=""><td>ydfI</td><td>588504</td><td>589145</td><td>+</td><td>577</td><td>518</td><td>484</td><td>602</td><td>0.90</td><td>0.84</td><td>1.04</td><td>190</td><td>ydfI</td><td>588873</td><td>589067</td><td>588970</td><td>3.0 0.9</td><td>6.9 4.5</td><td></td></th<>	ydfI	588504	589145	+	577	518	484	602	0.90	0.84	1.04	190	ydfI	588873	589067	588970	3.0 0.9	6.9 4.5	
mmm         systs         s	ydfJ nan	589261	591435	+	276	244	254	259	0.88	0.92	0.94								
matrix         systep         systep<	nap vdfK	592951	593640	-	366	342	2885	344	0.95	0.95	0.95								
ydyd         59462         59642         2         308         424         0.82         0.72         1.04         1/2         1/1         1/2         1/3         4.4         0.3           ydy         59668         59564         4         23         30         375         41         0.85         0.88         1.04           ydy         59685         59875         69887         6         1.06         1.08         0.88         0.14         1.05         1.8         1.05         1.05         1.05         1.05         1.05         1.05         1.05         1.05         1.04         1.05         1.0	ydfL	593730	594542	-	516	479	486	516	0.93	0.95	1.00								
bit         Symple         Symple <td>ydfM</td> <td>594653</td> <td>595546</td> <td>-</td> <td>405</td> <td>327</td> <td>308</td> <td>424</td> <td>0.82</td> <td>0.77</td> <td>1.04</td> <td>192</td> <td>ydfM</td> <td>594976</td> <td>595306</td> <td>595141</td> <td>7.2 13.4</td> <td>4.4 0.3</td> <td></td>	ydfM	594653	595546	-	405	327	308	424	0.82	0.77	1.04	192	ydfM	594976	595306	595141	7.2 13.4	4.4 0.3	
3070         596868         9         4         4         300         35         411         0.85         0.97         1.01           3070         59867         4         70         66         63         0.94         0.87         1.01           3070         59867         5         76         76         65         0.94         0.87         1.01           3071         59867         0         184         180         100         1.23         1.04         0.07         0.01         0.07         0.01	ydfN	596022	596642	+	238	196	205	263	0.83	0.86	1.10								
m/n         spins         s	ydfO ydfP	596658	597596	+	423	360	3/5	441	0.85	0.89	1.04								
mbdf         59861         59887         -         9         7         90         82         0.80         0.94         0.87           gdf         5976         600253         601270         +         198         187         185         0.96         0.44         0.03           gdf         601726         61125         197         184         100         123         111         108         0.09           gdf         601726         61125         198         187         185         0.86         0.85         0.82         0.85         0.85         0.85           gdf         601844         0.444         180         0.85         2.18         2.26         0.05         0.99         0.96         0.99         0.97         0.91         0.97         0.91         0.99         0.97         0.91         0.99         0.98         0.95         0.96         0.91         0.93         0.95         0.95         0.96         0.91         0.93         0.95         0.95         0.96         0.93         0.95         0.96         0.91         0.91         0.91         0.91         0.91         0.91         0.91         0.91         0.91         0.91         0.91 <td>yaj r vdfO</td> <td>598273</td> <td>598611</td> <td>+</td> <td>176</td> <td>165</td> <td>169</td> <td>164</td> <td>0.94</td> <td>0.87</td> <td>0.93</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	yaj r vdfO	598273	598611	+	176	165	169	164	0.94	0.87	0.93								
yd/R         60073         60140         1.34         1.84         1.60         1.23         1.04           carl         60126         60171         -         1.29         1.81         185         0.60         0.44         0.93           carl         601265         60171         -         1.29         1.81         185         0.86         0.95         0.2           yd/G         60175         60171         1.92         1.92         1.81         1.80         0.97         1.01         0.78           yd/G         601343         601344         1.34         130         3.74         1.82         1.80         0.80         - <t< td=""><td>ydzH</td><td>598651</td><td>598887</td><td>-</td><td>95</td><td>76</td><td>90</td><td>82</td><td>0.80</td><td>0.94</td><td>0.87</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>	ydzH	598651	598887	-	95	76	90	82	0.80	0.94	0.87								
yd/S         600563         601200 +         198         187         185         0.96         0.94         0.93           ydg/B         601925         601716 -         199         144         129         114         108         0.99           ydg/B         601925         60237 -         199         180         150         0.86         0.55         0.82           ydg/C         601344         4428         722         780         374         1.82         1.80         0.85           ydg/C         601344         0.444         130         1.31         1.37         2.66         0.95         1.81         1.81         1.80         0.85           ydg/C         601344         601945         60233         60179         3.22         0.87         0.87         0.81         0.99           ydg/L         601343         613964         -         0.21         1.37         1.35         2.01           ydg/L         613345         1.38         1.21         1.72         0.78         0.84         1.04         1.04         1.04         1.04         1.04         1.04         1.04         1.04         1.04         1.04         1.04         1.04         <	ydfR	599773	600450	-	134	134	166	140	1.00	1.23	1.04								
coll         coll         coll         j	ydfS	600563	601270	+	198	189	187	185	0.96	0.94	0.93								
μαμ         θ01/2         601/2         601/2         101	cotP vdaA	601285	601716	-	129	144	140	129	1.11	1.08	0.99								
ydc gdD         603143 603140         64143         4428 134         9722 135         786 135         1.80 137         1.80 2.50         2.47 2.50         1.80 0.95           ydc gdF         603647 604120         604120 172         1.32 2.72         2.35 2.72         2.35 2.72         2.35 2.72         2.35 2.72         2.35 2.82         2.47 2.73         1.07 0.75         0.87 0.99         0.85 0.87         0.81 0.87         0.84 0.84         0.92 0.85           ydgf         610345         610345         610345         610445         610445         610445         610289         113         7.8         3.5         -0.1           ydgf         61286         613475         1432         845         453 0.59         0.58         0.58         0.84         1.18           yddf         616346         611341         61134         61134         61383         0.7         0.2         0.8         0.67         0.99           yddf         616467         615417         61691 +         3478         247         0.07         0.8         0.8 </td <td>vdgB</td> <td>601985</td> <td>602257</td> <td>-</td> <td>190</td> <td>186</td> <td>194</td> <td>150</td> <td>0.80</td> <td>1.01</td> <td>0.32</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	vdgB	601985	602257	-	190	186	194	150	0.80	1.01	0.32								
gldp         603140         604344         1         3154         1378         2.50         2.47         1.07           gdp         603649         604120         605233         5<02         366         300         497         0.73         0.76         0.99           gdp         606243         60710         -         322         232         262         210         0.87         0.81         0.96           gdp         606335         61139         -         612         52         0.92         0.82         0.87         0.84         0.92           gdp         61335         61395         -         614         1014 <t< td=""><td>ydgC</td><td>602556</td><td>603143</td><td>+</td><td>4428</td><td>7922</td><td>7860</td><td>3764</td><td>1.82</td><td>1.80</td><td>0.85</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>	ydgC	602556	603143	+	4428	7922	7860	3764	1.82	1.80	0.85								
ydgE         6013647         601420         9         915         2009         885         2.18         2.26         0.95           ydgF         6060343         607619         -         322         282         284         310         0.87         0.81         0.96           ydgF         606393         -         207         174         1906         0.88         0.84         0.92         194         ydgH         610141         61043         610249         11.3         7.8         3.5         -0.1           ydgF         61136         612365         1934         417         154         2070         0.70         0.82         1.08           ydgK         61136         612365         1333         1217         1722         0.78         0.84         1.18           ydgK         61318         61184         1332         845         435         650         0.58         0.84         0.49           ydhG         61363         61583         1737         476         370         209         430         0.70         0.99           ydhG         61363         621691         63163         621671         610613         61737         7.8	ydgD	603140	603484	+	1344	3195	3154	1378	2.50	2.47	1.07								
cap2       004280       00923 - 302       360       380       497       0.7       0.9         dmB       607791       608309 - 2071       1770       1731       1752       2242       310       087       0.94       092         ydgG       608375       611376       624       551       528       52       0.32       0.93       0.85       1.08         ydgI       61286       612355       1934       1477       1554       2070       0.79       0.82       1.08         ydgI       61288       61386       614394       1433       1217       1722       0.78       0.84       1.18         ydgK       613186       614394       1433       121       1772       0.78       0.84       1.18         ydgK       615187       616091       -378       453       650       0.59       0.98       -	ydgE	603647	604120	+	932	1951	2009	885	2.18	2.26	0.95								
hybrid       Guadra	expZ vdaE	604280	605923	-	3272	2832	380 2642	3140	0.73	0.76	0.99								
ydgf       608478       608936 +       62.4       551       55.8       552       0.93       0.89       0.85         ydgf       611736       612365 -       1941       1147       1554       2070       0.79       0.82       1.08       610143       610436       610289       11.3       7.8       3.5       -0.1         ydgf       61138       61235 -       1941       1477       1554       2070       0.79       0.82       1.18         ydgf       613186       613186       613184       613184       613184       613184       613184       613184       613184       613184       61318       7.7       0.90       0.82       0.84       0.90       0.85       0.84       0.90       0.85       0.84       0.90       0.85       0.84       0.90       0.85       0.84       0.90       0.84       0.84       0.90       0.84       0.84       0.90       0.84       0.84       0.90       0.84       0.85       0.84       0.85       0.85       0.85       0.85       0.85       0.85       0.85       0.85       0.85       0.85       0.85       0.85       0.85       0.84       0.84       0.84       0.84       0.99	dinB	607791	608309	-	2071	1770	1743	1906	0.86	0.84	0.92								
ydgH       608933       611590       +       114       1014       97       1091       0.89       0.87       0.94       194 ydgH       610141       610436       610289       113       7.8       3.5       0.1         ydgJ       612381       612875       -       1459       138       1217       1722       0.78       0.82       1.08         ydgK       613186       614394       +       1432       804       845       136       0.55       0.58       0.58       0.84       -	ydgG	608478	608936	+	624	551	528	532	0.93	0.89	0.85								
ydgl       611736       612365       -       194       1477       1534       2070       0.79       0.82       1.08         ydgl       613186       614394       +       1432       188       127       0.72       0.78       0.84       1.18         ydgl       613186       614394       +       1432       804       815       0.56       0.59       0.88       0.84       1.18         ydhC       61517       616091       +       3478       2475       2691       3443       0.71       0.77       0.99         ydhE       615867       619577       -       306       118       0.63       0.68       0.85       0.83       0.7       0.2       0.8       0.67         ydhG       619436       619577       -       206       161       170       200       0.88       0.83       0.91       0.4       0.4         ydhG       621393       621764       2118       1982       170       2102       0.94       0.84       1.04         ydhG       621393       621764       2118       1982       170       2102       0.94       0.84       1.05         ydhG       622169 </td <td>ydgH</td> <td>608933</td> <td>611590</td> <td>+</td> <td>1164</td> <td>1014</td> <td>997</td> <td>1091</td> <td>0.89</td> <td>0.87</td> <td>0.94</td> <td>194</td> <td>ydgH</td> <td>610141</td> <td>610436</td> <td>610289</td> <td>11.3 7.8</td> <td>3.5 -0.1</td> <td></td>	ydgH	608933	611590	+	1164	1014	997	1091	0.89	0.87	0.94	194	ydgH	610141	610436	610289	11.3 7.8	3.5 -0.1	
hgg       01231       01203 - 1       133       121       1121	ydgI ydgI	611736	612365	-	1934	1477	1554	2070	0.79	0.82	1.08								
ydlB       614389       615168       783       456       453       659       0.58       0.58       0.58       0.84         ydlC       615417       616091       +       3478       2475       2691       3443       0.71       0.77       0.99         ydlE       617683       618828       +       1812       1130       1223       1518       0.63       0.68       0.85         ydlF       618667       619577       -       206       161       170       200       0.78       0.83       0.97       195 ydlF       619269       619497       619383       0.7       0.2       0.8       10.6         ydlAG       621393       621764       +       2118       1982       1770       2192       0.94       0.84       1.04         ydlH       622387       -       568       552       558       1.09       1.04       1.05         ydlL       624202       623897       +       527       568       552       558       1.09       1.04       1.05         ydlA       624202       626480 +       6606       2284       291       5476       0.34       0.43       0.33       0.45	yagJ vdøK	613186	614394	+	1432	804	845	1396	0.78	0.59	0.98								
ydhC       616417       61601       +       3478       2475       2691       3443       0.71       0.77       0.99         ydhC       616783       618527       +       1812       1130       1223       1518       0.63       0.84       0.99         ydhF       61867       619577       -       206       161       170       200       0.78       0.83       0.97       195 ydhF       619269       619497       619383       0.7       0.2       0.8       106         phoB       619643       621031       -       328       268       316       0.82       0.92       0.94       0.84       1.04         ydhG       621393       621764       +       2118       1852       1770       2192       0.94       0.84       1.04       1.05         ydhH       622325       623837       +       527       578       0.74       0.42       0.55       98         ydhL       62402       625638       2       430       342       990       421       0.49       0.63       0.61         ydhN       626169       626480       62612       3545       63135       3138       119       0.	ydhB	614389	615168	-	783	456	453	659	0.58	0.58	0.84								
ydhz       616218       61753 + 4       476       390       400       474       0.82       0.84       0.99         ydhz       616218       618828       +       1812       1130       1223       1518       0.63       0.68       0.85         ydhz       618636       619577 -       206       161       170       200       0.78       0.83       0.97       195 ydhF       619269       619497       619383       0.7       0.2       0.8       10.6         ydhz       621393       621764       +       2118       1982       170       2192       0.94       0.84       1.04         ydhz       622355       622337 -       966       854       997       880       0.88       1.03       0.91         ydhZ       622402       623897 +       516       450       535       538       0.87       1.04       1.05         ydhZ       624672       62583 8       4369       3428       208       4275       0.78       0.66       0.98         ydhN       626469       626480 +       6660       2284       291       5476       0.33       0.45       0.88         ydhP       62177	ydhC	615417	616091	+	3478	2475	2691	3443	0.71	0.77	0.99								
ydhF       617883       618828       4       1812       1130       1223       1518       0.03       0.08       0.88       0.85         ydhF       618867       619277       -       328       268       268       316       0.82       0.82       0.96       195       ydhF       619269       619497       619383       0.7       0.2       0.8       10.6         ydhG       621393       621737       -       328       268       268       316       0.82       0.82       0.90       195       ydhF       619269       619497       619383       0.7       0.2       0.8       10.6         ydhH       621840       622337       -       516       450       758       552       558       109       1.04       1.05       916       106       928       916       107       625678       626177       625928       17.8       394       4.7       -1.3         ydhN       626469       626480       +       6600       228       291       5476       0.34       0.44       0.83       0.87       0.88       0.88       0.61       0.94       0.94       0.95       916       108       0.81       0.81	ydhD	616218	617537	+	476	390	400	474	0.82	0.84	0.99								
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	ydhE ydhF	618867	618828	+	1812	1130	1223	200	0.63	0.68	0.85	105	wdbF	610260	610/07	610383	07 02	0.8 10.6	
ydhG 621393 621764 + 2118 1982 1770 2192 0.94 0.84 1.04 ydhH 621840 622337 - 968 854 997 880 0.88 1.03 0.91 ydhI 622355 622837 - 516 450 535 538 0.87 1.04 1.05 ydhK 624039 624656 + 1521 734 934 941 0.49 0.63 0.61 ydhL 624672 625838 - 4369 3428 2908 4275 0.78 0.66 0.98 ydhM 626169 626480 + 6660 2284 2991 5476 0.34 0.44 0.83 ydhN 626480 626812 + 3545 1036 1509 3399 0.29 0.42 0.95 ydhO 626831 628159 + 3493 1179 1630 3075 0.33 0.45 0.88 ydhP 628177 629574 + 3704 1197 1734 3493 0.32 0.46 0.94 ydhQ 629717 630430 + 3457 1464 1877 3267 0.42 0.54 0.95 ydhR 630459 631358 + 1852 778 993 1929 0.42 0.54 1.04 ydhZ 633470 633925 - 138 128 1714 3308 0.40 0.50 0.96 ydhU 633470 633925 - 138 128 151 134 0.93 1.10 0.97 198 ydhU 633345 633692 633519 7.5 2.5 11.6 200 thiL 640209 641186 + 1200 907 831 1194 0.76 0.69 1.00 ydiB 641201 641677 + 1245 910 927 1293 0.73 0.73 1.04 ydiC 641658 642347 + 3328 2793 2714 3361 0.73 0.71 0.87 gcp 642805 643845 + 4787 3930 3790 4348 0.82 0.79 0.91 202 gcp 643295 643387 643341 0.8 1.1 0.7 2.8 ydiF 644056 464317 + 3027 2813 2714 3361 0.73 0.71 0.87 gcp 642805 643845 + 4787 3930 3790 4348 0.82 0.79 0.91 202 gcp 643295 643387 643341 0.8 1.1 0.7 2.8 ydiF 64405 646041 + 3027 2813 2736 3449 0.93 0.90 1.14 204 moaC 646270 646532 646401 5.4 112 2.1 2.3	phoB	619643	621031	-	328	268	268	316	0.82	0.82	0.96	175	yuu	017207	01)4)/	017585	0.7 0.2	0.0 10.0	
ydhl       621840       622337       -       968       854       997       880       0.88       1.03       0.91         ydhl       622355       622837       -       516       450       535       538       0.87       1.04       1.05         ydhl       622020       62387       +       516       450       532       558       1.09       1.04       1.05         ydhl       624672       625838       -       4369       3428       2908       4275       0.78       0.66       0.98         ydhN       626169       626480       -       6660       2284       291       5476       0.34       0.44       0.83         ydhN       626480       626197       62619       3493       1179       1630       3025       0.42       0.95         ydhQ       628177       629174       4       343       144       1877       3267       0.42       0.54       0.95         ydhR       630459       631358       4       1852       778       933       129       0.42       0.54       0.93         ydhR       633455       633305       633305       3338       0.40       0.50	ydhG	621393	621764	+	2118	1982	1770	2192	0.94	0.84	1.04								
ydhl622355622837-5164505355380.871.041.05ydhl622020623897+5275685525581.091.041.05ydhl624039624656+15217349349410.490.630.61ydhl626169626480+66022284290842750.780.660.98ydhN626169626480626812+63541036150933990.290.420.95ydhO626831628159+34931179163030750.330.450.88ydhQ629717630430+34571464187732670.420.540.95ydhX631355631355632302+34381387174533080.400.500.96ydhX632321633409+2289904121221160.400.540.93ydhU633470633325-1381281511340.931.100.97198ydhU63345633696335197.52.511.62010ydhW632476423776428179109271230.730.751.04ydhS631355633925-1381281511340.931.100.97198ydhU633345633696335197.52.5 </td <td>ydhH</td> <td>621840</td> <td>622337</td> <td>-</td> <td>968</td> <td>854</td> <td>997</td> <td>880</td> <td>0.88</td> <td>1.03</td> <td>0.91</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	ydhH	621840	622337	-	968	854	997	880	0.88	1.03	0.91								
ydhk       622920       623897       +       327       308       352       538       1.09       1.04       1.05         ydhk       624039       624656       +       1521       734       934       944       0.49       0.63       0.61         ydhk       626472       625838       -       4369       3428       2908       4275       0.78       0.66       0.98         ydhM       626169       626480       +       660       2284       2991       5476       0.34       0.44       0.83         ydhN       6266480       626812       +       3545       1036       1509       3399       0.29       0.42       0.95         ydhQO       626831       628177       629574       +       3704       1179       1734       3493       0.32       0.46       0.94         ydhR       630459       631355       632302       +       3457       1464       1877       3267       0.42       0.54       0.95         ydhR       630459       631355       632302       +       3481       1745       3008       0.40       0.50       0.96         ydhT       632216       633409	ydhI	622355	622837	-	516	450	535	538	0.87	1.04	1.05								
ydhL       624672       625838       -       121       131       131       131       131       0.66       0.08         ydhL       624672       625838       -       439       3428       2908       475       0.78       0.66       0.098         ydhM       626169       626480       +       6660       2284       2991       5476       0.34       0.44       0.83         ydhN       6266480       626812       +       3545       1036       1509       3399       0.29       0.42       0.95         ydhO       6268159       63155       4393       1179       1630       3075       0.33       0.45       0.88         ydhQ       629717       630430       +       3457       1464       1877       3267       0.42       0.54       0.95         ydhR       630459       631355       631355       631355       631355       633692       63359       7.5       2.5       11.6       2011         ydhR       630459       633409       +       2289       904       1212       2116       0.40       0.54       0.93         ydhU       633470       633409       +       2289 <td>yanj vdhK</td> <td>622920</td> <td>624656</td> <td>+</td> <td>1521</td> <td>508 734</td> <td>934</td> <td>941</td> <td>0.49</td> <td>0.63</td> <td>0.61</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	yanj vdhK	622920	624656	+	1521	508 734	934	941	0.49	0.63	0.61								
ydhM       626169       626480       +       6660       228       2991       5476       0.34       0.44       0.83         ydhM       626480       626812       +       3545       1036       1509       3399       0.29       0.42       0.95         ydhN       626480       626812       +       3493       1179       1630       3075       0.33       0.44       0.83         ydhP       628177       629574       +       3493       1179       1734       3493       0.32       0.46       0.94         ydhR       630459       631358       +       1852       778       993       1929       0.42       0.54       0.95         ydhX       630459       631358       +       1852       778       993       1929       0.42       0.54       0.95         ydhV       633255       631355       632302       +       348       1387       1745       3308       0.40       0.50       0.96         ydhV       633470       6333295       -       134       0.93       1.10       0.97       198       ydhU       633345       633692       633519       7.5       2.5       11.6	ydhL	624672	625838	-	4369	3428	2908	4275	0.78	0.66	0.98								
ydhM       626169       626480       +       6660       228       2991       5476       0.34       0.44       0.83         ydhN       626480       626812       +       3545       1036       1509       3399       0.29       0.42       0.95         ydhO       626831       628159       +       3493       1179       1630       3075       0.33       0.45       0.88         ydhQ       628177       629574       +       3493       1197       1734       3493       0.32       0.46       0.94         ydhQ       629177       630430       +       3457       1464       1877       3267       0.42       0.54       0.95         ydhX       630459       631355       631355       632302       +       3483       1377       1745       3308       0.40       0.50       0.96         ydhV       6333409       631355       632302       -       348       1387       1745       3308       0.40       0.50       0.96         ydhU       633470       633349       -       18       111       0.41       0.93       1.10       0.97       198       ydhU       633345       633692												196	Inter	625678	626177	625928	17.8 39.6	4.7 -1.3	
ydhN       626480       6264812       +       3545       1036       1509       3399       0.29       0.42       0.95         ydhO       6264831       628159       +       3493       1179       1630       3075       0.33       0.45       0.88         ydhP       628177       639574       +       3493       1197       1734       3493       0.32       0.46       0.94         ydhQ       629177       630430       +       3457       1464       1877       3267       0.42       0.54       0.95         ydhR       630459       631355       +       1852       778       993       1929       0.42       0.54       0.95         ydhX       631355       632302       +       348       1387       1745       3308       0.40       0.50       0.96         ydhU       633470       6333295       -       138       128       104       0.93       1.10       0.97       198       ydhU       633345       633692       633519       7.5       2.5       11.6       2010         ydiB       641201       641677       +       1245       910       927       1233       0.73	ydhM	626169	626480	+	6660	2284	2991	5476	0.34	0.44	0.83								
ydhp       620537       620537       4       3473       1179       1030       3073       0.33       0.43       0.38         ydhP       628177       629574       3704       1197       1734       3493       0.32       0.46       0.94         ydhQ       629171       630430       4       3457       1464       1877       3267       0.42       0.54       0.95         ydhR       630459       631358       +       1852       778       993       1929       0.42       0.54       0.95         ydhX       631355       632302       +       348       1387       1745       3308       0.40       0.50       0.96         ydhU       633470       633292       -       138       122       2116       0.40       0.54       0.93         ydhU       633470       633292       -       138       128       151       134       0.93       1.10       0.97       198 ydhU       633345       633692       633519       7.5       2.5       11.6       200         ydiE       641201       641677       1245       910       927       1293       0.73       0.75       1.04       93	ydhN ydhO	626480	626812	+	3545	1036	1509	3399	0.29	0.42	0.95								
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	yanO ydhP	628177	629574	+	3704	11/9	1734	3493	0.33	0.45	0.88								
ydhR       630459       631358       +       1852       778       993       1929       0.42       0.54       1.04         ydhS       631355       632302       +       3438       1387       1745       3308       0.40       0.50       0.96         ydhT       632321       633409       +       2289       904       1212       2116       0.40       0.54       0.93         ydhU       633470       633925       -       138       128       1194       0.76       0.69       1.00         ydiB       641020       641186 +       1200       907       831       194       0.76       0.69       1.00         ydiB       641201       641677 +       1245       910       927       123       0.73       0.75       1.04         ydiC       641658       642347 +       3917       295       292       3632       0.76       0.76       0.93         ydiD       642557       642847 +       3917       295       2992       3632       0.76       0.76       0.93         ydiD       642557       642845       643847       4787       3930       3790       438       0.82       0.78	ydhQ	629717	630430	+	3457	1464	1877	3267	0.42	0.54	0.95								
ydhS       631355       632302       +       3438       1387       1745       3308       0.40       0.50       0.96         ydhI       632321       633409       +       2289       904       1212       2116       0.40       0.50       0.93         ydhU       633370       633392       -       138       128       121       2116       0.40       0.50       0.97       198       ydhU       633345       633692       633519       7.5       2.5       11.6       200         thiL       640209       641186       1200       907       831       1194       0.76       0.69       1.00         ydiB       641201       641677       +       1245       910       927       1293       0.73       0.75       1.04         ydiC       641658       642347       +       3917       2953       2992       3632       0.76       0.76       0.93         ydiD       642357       642847       +       3917       2953       2992       3632       0.76       0.76       0.93         ydiF       644075       642805       643845       +       4787       3930       3790       4348	ydhR	630459	631358	+	1852	778	993	1929	0.42	0.54	1.04								
yahr       652521       653409       +       2289       904       1212       2116       0.40       0.93       0.93         yahr       633470       633925       -       138       128       121       134       0.93       1.10       0.97       198       ydhU       633345       633692       633519       7.5       2.5       11.6       200         thiL       640209       641186       +       1200       907       831       1194       0.76       0.69       1.00         ydiB       641201       641677       +       1245       910       927       1293       0.73       0.75       1.04         ydiC       641658       642347       +       3917       2953       2992       3632       0.76       0.76       0.93         ydiC       642658       642347       +       3917       2953       2992       3632       0.76       0.76       0.93         ydiF       642655       643845       +       4787       3930       2714       361       0.73       0.71       0.87         gcp       644075       646063       -       2596       2248       2382       207       0.87	ydhS	631355	632302	+	3438	1387	1745	3308	0.40	0.50	0.96								
ydir       640209       64186 +       1200       907       831       1194       0.73       0.75       1.00         ydir       640209       641186 +       1200       907       831       1194       0.76       0.69       1.00         ydir       641201       641677 +       1245       910       927       1293       0.75       1.04         ydir       642635       642347 +       3917       2953       2992       3632       0.76       0.76       0.93         ydir       642557       642812 +       3828       2793       2714       361       0.73       0.71       0.87         gcp       642805       643845 +       4787       3930       3790       4348       0.82       0.79       0.91       202 gcp       643295       643341       0.8       1.1       0.7       2.8         ydir       644075       646003 -       2596       2248       2807       0.87       0.92       1.08       mac       646129       646532       646401       5.4       11.2       2.1       2.3	ydhT ydhU	632321	633409	+	2289	904	1212	2116	0.40	0.54	0.93	109	vdbU	632215	632602	632510	75 25	11.6 20.0	
ydiB       641201       641677       +       1245       910       927       1293       0.73       0.75       1.04         ydiC       641658       642347       +       3917       2953       2992       3632       0.76       0.76       0.93         ydiD       642357       642812       +       3828       2793       2714       3361       0.73       0.71       0.87         gcp       642805       643845       +       4787       3930       3790       4348       0.82       0.79       0.91       202 gcp       643295       643387       643341       0.8       1.1       0.7       2.8         ydiF       644075       646003       -       2596       2248       2382       2807       0.87       0.92       1.08         moaC       646129       646541       +       3027       2813       2736       3449       0.93       0.90       1.14       204       macC       646570       646532       646401       5.4       11.2       2.1       2.3	yan0 thiL	640209	641186	+	138	128	831	134 1194	0.93	0.69	1.00	198	yunU	033343	033092	033319	1.3 2.3	- 11.0 - 20.0	
ydiC       641658       642347       +       3917       2953       2992       3632       0.76       0.76       0.93         ydiD       642357       642812       +       3828       2793       2714       3361       0.73       0.71       0.87         gcp       642805       643845       +       4787       3930       3790       4348       0.82       0.79       0.91       202 gcp       643295       643387       643341       0.8       1.1       0.7       2.8         ydiF       644075       646003       -       2596       2248       2807       0.87       0.92       1.08         moaC       646129       646641       +       3027       2813       2736       3449       0.93       0.90       1.14       204 macC       646570       646532       646401       5.4       11.2       2.1       2.3	ydiB	641201	641677	+	1245	910	927	1293	0.73	0.75	1.04								
ydiD       642357       642812       +       3828       2793       2714       3361       0.73       0.71       0.87         gcp       642805       643845       +       4787       3930       3790       4348       0.82       0.79       0.91       202 gcp       643295       643347       643341       0.8       1.1       0.7       2.8         ydiF       644075       646003       -       2596       2248       2382       2807       0.87       0.92       1.08         moaC       646129       646614       +       3027       2813       2736       3449       0.93       0.90       1.14       204 moaC       646520       646532       646401       5.4       11.2       2.1       2.3	ydiC	641658	642347	+	3917	2953	2992	3632	0.76	0.76	0.93								
gcp         042805         043845         +         4/8/         3930         3/90         4.348         0.82         0.79         0.91         202         gcp         643295         643341         0.8         1.1         0.7         2.8           ydiF         644075         646003         -         2596         2248         2382         2807         0.87         0.92         1.08           moaC         646129         646641         +         3027         2813         2736         3449         0.93         0.90         1.14         204         moaC         646270         646532         646401         5.4         11.2         2.1         2.3	ydiD	642357	642812	+	3828	2793	2714	3361	0.73	0.71	0.87			(10005	< 1000F	(100)	0.0 1 :	0.7	
moaC 646129 646641 + 3027 2813 2736 3449 0.93 0.90 1.14 204 moaC 646270 646532 646401 5.4 11.2 2.1 2.3	gcp vdiF	642805	643845 646002	+	4787	3930 2240	5790	4348	0.82	0.79	0.91	202	gcp	643295	643387	643341	0.8 1.1	0.7 2.8	
	moaC	646129	646641	+	3027	2813	2736	3449	0.93	0.92	1.14	204	moaC	646270	646532	646401	5.4 11.2	2.1 2.3	

Supplem	entary Tab	le S1. Sur	nma	ry of trai	nscripto	me and (	hAP-ch	ip analyse o opolycic	es (contin	ued).				C	AD abin a	nolucie				
	gene			Sim	nalintana	ity of PN		E analysis	rossion rot	hio b				U.	AF-clip a	marysis	Dinding	intoncity (	с	
			pu	Sigi	nai interis	ity of Kin	A	Exp	Aahh	шо	PBR	ORF				Ał	orB	Al	bh	Profile
name	start	end	stra	wild	∆abrB	$\Delta abh$	$\Delta abh$	$\Delta abrB/$	$\Delta abrB/$	$\Delta abh /$	ID	Or Interconic	start	end	center	wild		wild	<u> </u>	ID
						∆ abrB		Wild	wild	wiid		mergenic				-type	⊿abn	-type	⊿ abrB	
ydiH	646638	647285	+	6801	6496	7194	7202	0.96	1.06	1.06	205	ydiH	646577	647110	646844	8.8	3.2	18.0	37.8	
tatAY	647307	647480	+	5725	5945	6237	5639	1.04	1.09	0.99										
tatCY	647487	648251	+	6897	7820	8357	7279	1.13	1.21	1.06										
yai <b>k</b> vdil	648289	640211	-	348/ 2610	3200	2140	2762	0.91	0.89	0.96										
yaiL	048477	049211	-	2019	2308	2445	2705	0.98	0.95	1.00	206	Inter	649263	649592	649428	13.6	11.3	12.2	27	
groES	649450	649734	+	27885	30634	30491	29986	1.10	1.10	1.07	200	inter	017205	01/0/2	019120	15.0		12.2	2.7	
groEL	649781	651415	+	23636	28952	29268	26974	1.23	1.24	1.14										
ydiM	652979	653359	+	650	897	861	777	1.43	1.34	1.12										
											207	Inter	653326	653910	653618	41.6	26.0	13.3	-0.8	
											208	Inter	654090	654284	654187	4.4	5.5	2.0	0.2	
ydiN	654526	654741	+	806	1044	1029	900	1.35	1.32	1.07	208	ydiN	654294	654964	654629	53.6	52.0	22.3	10.2	
ydiO	654//1	656054	+	3/51	3074	3297	4237	0.82	0.88	1.13	209	yaiO	655654	655/46	655700	2.6	0.9	0.3	0.0	
yaır vdiO	657731	657919	+	4490	156	4109	173	0.87	1.03	1.05	210	yuir	030402	030834	030018	17.5	10.2	0.1	3.5	
yuiQ	057751	057717		157	150	101	175	0.77	1.05	1.10	211	Inter	658476	659197	658837	34.9	47.9	21.3	4.4	P02
ydiR	659171	660112	+	2878	3292	3211	2509	1.14	1.12	0.87	212	ydiR	659513	660268	659891	28.7	22.1	10.4	0.8	
ydiS	660144	661175	+	3579	3991	3903	3293	1.11	1.09	0.92	212	ydiS	660567	661152	660860	46.2	62.0	16.7	1.0	
ydjA	661178	662575	+	2015	2215	2129	1898	1.09	1.05	0.94										
ydjB	663149	663484	+	464	599	582	512	1.30	1.26	1.10						_	_	_		
ydjC	663867	664217	+	342	362	385	345	1.07	1.14	0.98	214	ydjC	663814	663957	663886	0.9	1.3	0.2	4.6	
gutR	664323	666812	-	1425	974	1047	1310	0.68	0.73	0.92										
gutB autP	668149	669540	+	920	370	411	951 465	0.62	0.71	1.03										
vdiE	669635	670597	+	2485	2248	2617	2135	0.90	1.05	0.86										
<i>)j=</i>											215	Inter	670580	670859	670720	8.1	8.3	3.2	0.9	
pspA	670793	671476	+	4246	12395	13066	6323	2.94	3.13	1.50	215	pspA	670869	671216	671043	14.9	14.2	20.3	12.5	
ydjG	671542	672567	$^+$	2648	8228	8924	4388	3.14	3.43	1.68										
ydjH	672567	673331	+	2557	7418	8012	4034	2.92	3.17	1.59										
ydjI	673362	674333	+	1885	5016	5368	2777	2.66	2.86	1.48										
ydjJ	674380	675405	-	321	292	314	290	0.91	0.98	0.90	216	Teres a	(75740	(75974	(75911	1.0	26	0.4	0.1	
vdiK	675000	677411	-	441	342	385	131	0.77	0.87	0 00	210	mer	0/3/48	0/38/4	0/3811	1.0	5.0	0.4	0.1	
ydjK vdiL	677459	678499	-	5422	21036	20846	3267	3.92	3.88	0.60										
Juji	077105	0/01//		0.22	21000	20010	5207	5.72	5.00	0.00	217	Inter	678604	679070	678837	19.7	27.3	2.0	0.8	P03
ydjM	678938	679309	+	2312	3067	2848	2065	1.32	1.23	0.89										
ydjN	679375	680421	$^+$	1260	1909	1801	1178	1.53	1.44	0.92										
											218	Inter	680423	680940	680682	22.7	26.9	25.4	3.7	P02
ydj0	680803	681012	-	14357	17468	16829	13087	1.22	1.17	0.91										
ydjP vagA	681095	681910	-	2538	3997	4583	2596	1.60	1.86	1.03	220	1200 A	682080	682240	682160	1.5	12	2.5	4.8	
cot A	683010	684551	-	212	2229	2307	203	0.95	0.96	0.96	220	yeaA	082089	082249	082109	1.5	1.5	2.5	4.0	
gabP	684703	686112	-	297	532	585	310	1.79	1.96	1.05										
yeaB	686510	687382	+	587	479	471	559	0.82	0.80	0.95										
											222	Inter	687393	687655	687524	19.7	23.6	7.3	2.9	
yeaC	687535	688497	+	1439	1295	1211	1451	0.90	0.84	1.01	222	yeaC	687665	687961	687813	9.4	11.9	9.2	1.8	
yeaD	688881	689693	+	1728	1595	1520	1816	0.92	0.88	1.05										
yebA	689890	691857	+	1855	1622	1537	1842	0.87	0.83	0.99										
guaA	692090	693631	+	13030	9156	8468	12062	0.70	0.65	0.93	224	Intor	602564	602775	602670	1.1	1.4	0.3	6.4	
nhuG	694011	695333	+	4793	2651	1963	4974	0.57	0.40	1.03	224	mer	093304	093775	093070	1.1	1.4	0.5	0.4	
PUNO	574011		11	-175	2001	1705	1744	0.57	0.40	1.05	225	Inter	695128	695628	695378	13.5	8.0	19.4	23.5	
yebC	695535	696338	+	2423	2346	2593	3317	0.97	1.07	1.37	226	yebC	695859	696597	696228	14.5	27.4	2.8	2.7	
yebD	696497	696790	+	250	360	364	136	1.41	1.44	0.55										
yebE	696880	697434	+	1532	808	857	1277	0.53	0.56	0.83										
yebG	697434	697631	+	2430	1315	1414	1766	0.54	0.58	0.71	227	yebG	697355	697855	697605	16.9	24.8	17.6	45.1	
purE	697954	698442	+	2348	1322	994	2531	0.63	0.45	1.06										
purK purP	698435	099574 700866	+	2424	1315	10/1	2058	0.61	0.48	1.08										
purb purC	700939	700800	+	2578	1630	1342	2687	0.72	0.52	0.99										
purS	701657	701911	+	1571	1057	863	1800	0.81	0.59	1.05										
purQ	701908	702591	+	1345	918	783	1474	0.78	0.63	1.03	229	purQ	702030	702377	702204	10.7	7.0	19.6	12.2	
purL	702575	704803	+	1526	1009	864	1585	0.77	0.63	0.99	230	purL	703288	703584	703436	10.6	2.9	4.9	6.2	
purF	704779	706209	+	1948	1345	1162	1868	0.78	0.64	0.95										
purM	706311	707351	+	1324	895	810	1295	0.75	0.65	0.97										
purN	707348	707935	+	1560	955	860	1501	0.65	0.58	0.95										
purH	707932	710754	+	1685	1084	942	1520	0.72	0.60	0.93										
purD ve7C	7109480	711214	+	1459 836	908 1038	908 907	1339	0.70	1 10	0.93										
vecA	711358	712749	+	381	325	345	397	0.85	0.91	1.04										
yerA	713003	714745	+	8192	2713	4524	6588	0.34	0.53	0.79										
yerB	714772	715767	+	7438	4014	4889	6247	0.54	0.65	0.83										
yerC	715770	716084	+	4962	2366	3031	4419	0.48	0.58	0.86										

Supplen	nentary Tab	le S1. Sur	nma	ry of trai	nscripto	me and ( Trans	ChAP-ch	iip analys e analysis	es (contin	ued).				C	AP-chin	nalveie				
	gene			Sim	nal intens	ity of RN		e anaiysis Evi	ression ra	tio <sup>b</sup>				u	Ar-cup a	marysis	Binding	intensity	с	
	atast	and	pure	- 19181	ki inclis		A		$\Delta abh$		PBR	ORF	atout	and	conton	At	orB	A	bh	Profile
name	start	enu	stra	wild	∆abrB	∆abh ∆abrB	$\Delta abh$	∆ abrB wild	∆abrB/	∆ abh / wild	ID	Intergenic	start	enu	center	wild	∆abh	wild	∆abrB	ID
verD	716119	717696	-	399	335	456	289	0.84	wild 1.15	0.72						-type		-type		
											234	Inter	717535	717881	717708	11.6	5.7	8.3	3.9	
pcrB	717961	718647	+	2782	2392	1980	2715	0.86	6 0.71	0.97										
pcrA ligA	720952	720928	++	5131	4243	4080	5134	0.84	0.81	1.00										
yerH	722974	724164	+	7047	6521	6139	6991	0.93	0.87	0.99										
	== ( -=										235	Inter	723994	724426	724210	30.2	26.7	5.3	5.1	P03
yer1 sapB	724326	725336	+	2600	476	500	2526 698	4.49	4.28 0.71	0.97	236	yeri sanB	724572	724868	725485	58.4	5.6 64.8	5.1	224.9	P01
opuE	726179	727657	-	600	546	512	461	0.94	0.87	0.77	237	opuE	726170	726551	726361	3.7	2.8	6.5	10.0	
gatC	728071	728361	+	15376	13485	13122	14467	0.88	0.85	0.94										
gatA	728377	729834	+	12364	11684	11285	12569	0.95	5 0.91	1.02										
yerO	729848	732162	-	452	369	344	395	0.98	2 0.76	0.87										
yerP	732255	735452	+	5697	10168	10084	4924	1.79	0 1.77	0.86										
yerQ	735775	736686	+	4536	4612	3871	4211	1.02	0.85	0.93										
yefA vefB	736942	738321	+	2902	2720	2301	2457	0.95	0.79	0.84										
yefC	739175	739552	+	632	545	473	572	0.92	2 0.77	0.87	241	yefC	739158	739369	739264	4.9	6.6	1.6	0.7	
yeeA	739627	742266	+	572	511	441	529	0.91	0.77	0.91	242	yeeA	739940	740694	740317	50.2	82.1	60.0	58.4	P01
											243	yeeA	740909	741205	741057	3.5	8.1	2.4	1.8	
veeB	742278	744074	+	1590	1340	1278	1434	0.84	0.80	0.89	244	yeeA veeB	741759	741885	741822	3.8	3.5	0.4	-0.4	
,											245	yeeB	742558	743262	742910	33.7	60.1	3.2	-0.2	P03
yeeC	744187	745335	+	1348	1132	1052	1207	0.83	0.77	0.88	246	yeeC	744054	744520	744287	18.0	33.7	2.2	-0.2	P03
yeeD	745597	745902	-	86	69 204	71	63	0.80	0.83	0.74										
yezA veeF	745969	748898	-	777	1478	1558	579	1.94	1.13	0.74										
yeeG	749034	750131	+	286	291	321	285	1.02	1.13	1.00										
											249	Inter	750123	750351	750237	4.1	6.5	0.2	-0.3	
rapH veeI	750293	751588	+	330 8765	2730	2684	285 8383	8.23	8 8.01 0 0 90	0.87										
yeeK	752602	753039	+	397	402	405	436	1.03	1.03	1.10										
yezE	753154	753738	+	3846	4353	4514	3334	1.13	3 1.17	0.87										
yesE E	753817	754260	+	741	695	737	706	0.95	5 1.00	0.94										
yesF cot.IA	755244	755492	++	628 352	324	344	270	0.93	5 1.10 8 0.98	0.76										
cotJB	755437	755739	+	141	113	129	140	0.81	0.92	1.00										
cotJC	755754	756323	+	414	340	387	396	0.83	0.94	0.96										
yesJ vesK	756448	756990	+	2623	1985	1907 674	2260	0.76	5 0.73 8 0.62	0.86										
yesk	757430	758059	+	1213	700	1014	1243	0.58	0.81 0.81	1.02										
yesM	758056	759789	+	701	358	597	725	0.51	0.83	1.03										
yesN	759789	760895	+	441	268	377	429	0.61	0.86	0.97										
yes0 vesP	761044	762282	++	396 372	2/1 292	310	412 390	0.68	s 0.73 8 0.83	1.05										
yesQ	763212	764102	+	477	383	453	460	0.80	0.95	0.96										
yesR	764118	765152	+	548	372	415	587	0.68	0.76	1.07										
yesS vesT	765175	767460	+	421	343	367	452	0.81	0.87	1.08										
yes1 yesU	768165	768827	+	281	203	243	317	0.79	0.86	1.14										
yesV	768824	769450	+	455	403	439	487	0.88	8 0.97	1.07										
1100117	760571	771422		241	200	200	270	0.02	0.00	1.1/	251	Inter	769265	769816	769541	26.5	33.0	13.2	1.4	
yesw vesX	771479	773317	++	241 323	200 254	208	279	0.83	0.86 0.83	1.16 1.20	252	yesw	//0166	//0496	1/0331	3.3	5.5	2.9	17.8	
yesY	773475	774128	+	326	263	274	321	0.81	0.84	0.99										
yesZ	774136	776127	+	359	296	312	405	0.82	0.87	1.14										
yetA InIA	776171	778744	+	361	283	302	377	0.78	5 0.84	1.05	251	blA	770100	770795	770107	77	0.6	4.0	1.0	
lplB	780429	781385	++	434 443	200	317	405	0.57	6 0.04 6 0.71	0.95	254	ф. bB	780810	781308	781059	22.3	10.1	<u>30.5</u>	47.2	
lplC	781399	782286	+	514	367	400	564	0.71	0.77	1.10	257	þЮ	781658	781784	781721	1.3	0.6	0.9	3.4	
lplD	782295	783635	+	460	315	355	491	0.68	8 0.77	1.07										
yetF vetG	784450 / 18	784413 784827	+	567 8496	351	393 12364	554 9814	0.62	2 0.69 3 1.46	0.98										
yetH	784880	785242	-	3794	2273	2586	3264	0.60	0.69	0.86										
yetI	785522	786607	+	1955	1189	1132	1908	0.61	0.58	0.97										
yezB	786613	786897	+	5380	2938	2774	5283	0.55	0.52	0.97										
yezD	/8/052	18/219	+	105	105	104	122	1.01	0.99	1.16	259	Inter	787064	787513	787289	23.2	11.1	11.6	-1.2	
yetJ	787329	787973	+	6396	8237	7800	8483	1.29	1.22	1.32										
yet K	787973	788965	+	2293	2739	2589	2567	1.19	1.13	1.12										
yetL watM	788989	789492	-	214	175	186	203	0.82	2 0.87	0.95										
yenwi	109000	/ 20/04	+	338	400	510	514	0.85	v 0.93	0.93										

Supplem	entary Tab	le S1. Su	mma	ry of trai	iscriptor	me and C	ChAP-ch	ip analyse	es (contin	ued).				C	AD -htm					
	gene			Sior	al intone	Trans		Evo	roccion ro	tio <sup>b</sup>	· ·			U	iAP-cnip a	anaiysis	Dinding	intoncita	, c	
			pu	୍ରାହା	iai intens	ity of Kin	A	Exp	A abh	uo	PBR	ORF				Ał	orB		y Abh	Profile
name	start	end	stra	wild	∆abrB	∆abh ∆abrB	$\Delta abh$	∆abrB/ wild	$\Delta abrB/$	∆abh / wild	ID	or Intergenic	start	end	center	wild	∆abh	wild	∆abrB	ID
yetN	790799	791869	-	1370	991	908	1270	0.73	0.67	0.93						-type		-type		
yetO	792019	795204	+	292	290	314	301	1.00	1.08	1.04										
yfnI	795651	797570	+	11995	11856	11780	12570	0.99	0.98	1.05										
yfnH yfnG	798640	798570	+	280	220	238	296	0.79	0.85	1.06										
yfnG vfnF	799569	800480	+	296	254	268	200	0.82	0.80	0.90										
yfnE	800509	801687	+	313	285	288	323	0.91	0.92	1.03										
yfnD	801688	802623	+	405	372	366	389	0.92	0.90	0.96										
yfnC	802654	803883	-	1185	1576	1565	868	1.33	1.32	0.73										
yfnB yfnA	803994	804701	-	736	1206	863	710	1.20	1.17	0.97										
yjn24 vfmT	806428	807885	+	3707	6483	6159	4021	1.76	1.67	1.08										
yfmS	807899	808759	+	3681	6489	6254	4010	1.79	1.72	1.09										
yfmR	808894	810783	+	3810	3761	3959	4009	0.99	1.04	1.05										
yfmQ	810906	811352	+	4178	3458	2913	2944	0.79	0.65	0.72	261	yfmQ	811136	811279	811208	3.5	3.7	1.4	4 0.3	
yfmP	811477	811899	+	845	868	719	712	1.01	0.84	0.83										
yfmO	811965	813155	+	584	394	411	568	0.67	0.70	0.97										
yjmin vfmM	813440	815277	+	3004	2153	1943	2763	0.85	0.82	0.92										
yfmL	815450	816580	+	3063	1952	1733	2679	0.64	0.57	0.88										
yfmK	816648	817094	+	757	1958	1926	617	2.62	2.55	0.81										
yfmJ	817147	818166	-	2538	4598	5513	2985	1.82	2.18	1.17										
vfmI	818648	819868		245	600	681	218	2.44	2.77	0.89	263	Inter	818259	818827	818543	34.4	24.7	8.3	0.5	
<i>,,,,,,</i>	010010	019000		2.0	000	001	210	2	2	0.07	265	Inter	819466	820408	819937	69.5	95.1	57.3	<mark>3</mark> 9.7	
yfmH	820066	820137	+	799	20880	21647	741	26.82	27.91	0.91										
yfmG	820204	821667	+	219	9855	10184	218	44.96	46.46	1.00										
yfmF vfmF	822240	823040	-	5004 2418	4008	3806	4670	0.80	0.76	0.93										
yjmL vfmD	823055	825052	-	2418	1675	1468	2173	0.80	0.74	0.97										
yfmC	825124	826071	-	11528	7933	7364	11136	0.68	0.64	0.96										
yfmB	826180	826548	-	85	97	106	83	1.16	1.25	0.99										
yfmA	826589	826756	+	201	244	211	229	1.23	1.05	1.15										
yflT	826792	827139	+	2352	1688	3180	1048	0.77	1.36	0.52	2/7	,	00//0/	020075	007041	10.0	01.5	11.0	2.2	
pel vf1S	827330	828592	+	1708	1908	2042	1488	1.12	1.20	0.87	267	pel	826606	828075	827341	48.0	91.5	11.9	3.3	
yjus	020717	050155	т	504	515	515	550	0.04	0.04	0.94	268	Inter	830244	830319	830282	1.1	0.7	2.0	) 2.5	
citS	830282	831910	+	668	769	734	645	1.15	1.10	0.96										
citT	831882	832562	+	693	742	794	660	1.07	1.14	0.95										
yflP	832745	833524	+	498	513	540	469	1.03	1.08	0.94										
citM fIN	833720	835021	+	678 544	499	522	653 524	0.74	0.77	0.96										
yjuv vfIM	836071	837081	+	1371	1480	1374	1113	1.08	1.00	0.98										
vflL	837072	837347	-	639	627	608	556	0.98	0.95	0.87										
yflK	837414	838079	+	1453	1597	1592	1001	1.10	1.09	0.69										
yflJ	838120	838257	-	1522	1263	1032	1264	0.83	0.68	0.84										
yflI	838414	838569	-	2222	1843	1633	2280	0.82	0.73	1.04										
yflH vflC	838676	838990	-	5461 6407	4206	4634	5351	0.77	0.85	0.98										
yjiG	039012	037621	-	0407	2020	5094	0400	0.88	0.89	1.00	271	Inter	839645	840060	839853	14.4	16.8	8.9	) 11.1	
nagP	839993	841351	+	5960	4488	5094	5622	0.75	0.85	0.94	2,1		22,70.10	2.5000	22,0000					
yflE	841384	843333	-	7684	7631	6819	6892	0.99	0.89	0.90	272	yflE	842790	843800	843295	53.3	25.0	71.	5 110.2	P01
yflD	843434	843571	+	115	87	79	97	0.80	0.71	0.87										
yflC	843587	843739	+	223	822	1226	227	3.65	5.50	1.02										
yflB	843721	843981	+	152	613	1127	1/9	4.03	7.70	1.19	272	Inter	843810	844395	844103	33.5	26.0	34	5 40.8	P01
yflA	844106	845521	+	565	838	1477	595	1.49	2.69	1.04	212		0 10010	544575	51-105		20.0		10.0	101
yfkT	845518	846594	-	246	262	290	237	1.06	1.18	0.96	273	yfkT	845765	846129	845947	16.4	4.5	16.6	<u> </u>	
yfkS	846618	846818	-	206	218	240	253	1.06	1.17	1.22										
yfkR	846834	847988	-	189	166	180	196	0.88	0.95	1.03										
yfkQ tmrP	847969	849510	-	198	195	211	204	0.99	1.06	1.03		*Dao - J	840/04	051214						
treP treA	849703 851186	852871	+++	22408	11862	149/3	16663	0.53	0.66	0.99		Broad	849624	851314						
treR	852892	853608	+	15214	11494	12429	14913	0.76	0.82	0.98		I								
yfkO	853748	854413	+	10238	5998	6450	8972	0.59	0.64	0.88										
yfkN	854450	858838	-	315	380	423	283	1.20	1.34	0.90										
yfkM	859081	859599	+	2043	1802	2564	1102	0.88	1.25	0.54										
yfkL	859639	860829	-	1108	768	765	1013	0.69	0.69	0.92										
yfkK	860922	861137	-	1304	1201	961	948	0.92	0.73	0.73										
yfKJ vfkI	861879	862149	+	2192	1646	2047	2181	0.75	0.93	0.69										
yfkH	862172	862999	+	2138	2096	2380	1804	0.92	1.03	0.78	279	vfkH	862816	863078	862947	9.9	7.0	10.6	5 1.1	
yfkF	863198	864373	-	689	1048	1019	587	1.52	1.48	0.85	,	· · ·			=> .1					
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Supplem	entary Tab	ie 51. Su	unar	y or trai	scriptor	ne and ( Trans	_nAP-ch criptory	up analyse e analysie	s (contin	wea).				C	AP-obin o	nalysic		
	gene					TTails		c analysis		e b				u	IAI -Cilip a	Diadia	1	
			р	Sig	nal intensi	ty of RN	A	Expi	A abh	tio	PBR	ORF				AbrP	intensity	Profile
name	start	end	strar	wild	AahrB	$\Delta abh$	Aabh	$\Delta abrB/$	$\Delta abr B/$	$\Delta abh$ /	ID	or	start	end	center	wild	wild	ID
				VV IICI	2 uorb	∆abrB	<u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u></u>	wild	wild	wild		Intergenic				$\Delta abh$	$\Delta abrB$	
vfkE	864541	865596	+	745	464	555	448	0.65	0.80	0.60						gpo	type	
yfkD	865667	866461	+	737	527	589	396	0.72	0.83	0.53								
yfkC	866500	867342	-	2649	1817	1690	2464	0.69	0.64	0.93								
yfkB	867343	867804	-	3478	2259	2252	3374	0.65	0.65	0.97								
yfkA	867999	868463	-	1601	1072	933	1634	0.68	0.58	1.03								
yfjT	868608	868793	+	1831	1712	1637	1803	0.94	0.89	0.99								
vfiS	868894	869685	+	242	243	239	275	1.00	0.99	1.13								
yfjR	869723	870508	-	1010	1717	2104	1073	1.73	2.13	1.06								
vfiQ	870682	871641	-	1654	1757	1590	1612	1.06	0.96	0.97								
yfjP	871760	872623	+	924	811	765	964	0.88	0.83	1.04								
yfj0	872737	874137	+	2289	1659	1671	2267	0.73	0.73	0.99								
											283	Inter	874104	874587	874346	44.1 61.3	14.6 0.3	
											283	Inter	874597	875352	874975	56.9 86.7	34.8 14.1	
											284	Inter	875430	875658	875544	8.2 2.9	3.5 -0.1	
yfjN	875761	876738	+	1725	2146	1931	1981	1.25	1.12	1.15	285	yfjN	875872	876066	875969	6.3 4.0	4.8 4.9	
уfjM	876934	877386	+	771	1269	1169	847	1.67	1.53	1.10								
yfjL	877416	878105	+	1437	1866	1895	1392	1.31	1.32	0.97								
acoA	878337	879338	+	196	160	165	194	0.82	0.84	0.99								
acoB	879342	880370	+	343	271	284	349	0.79	0.83	1.03								
acoC	880384	881580	+	355	313	325	380	0.88	0.91	1.07	287	acoC	880224	880656	880440	13.5 14.1	25.9 24.7	
acoL	881601	882977	+	412	329	342	419	0.80	0.83	1.01								
acoR	883093	884910	+	1122	408	641	1072	0.37	0.55	0.95								
sspH	884964	885143	+	2110	810	1550	1815	0.42	0.75	0.83								
yfjF	885179	885508	-	1155	1197	1147	1014	1.04	0.99	0.88								
yfjE	885558	886016	-	706	668	717	565	0.95	1.01	0.80								
yfjD	886110	886667	-	418	372	393	362	0.89	0.93	0.87								
yfjC	886699	887466	-	318	239	270	220	0.77	0.84	0.71								
yfjB	887478	888701	-	375	269	288	311	0.71	0.76	0.82								
yfjA	888707	889021	-	310	283	264	280	0.91	0.85	0.90		•		000445	000450	201 120	22.4	
	000257	800704		1074	007	1064	1204	0.70	0.94	1.07	291	Inter	888894	889445	889170	28.1 15.9	23.6 20.0	
maiA	889357	890700	+	12/4	887	1064	1384	0.70	0.84	1.07								
yJIA m alD	890771	891555	+	807	023 540	702	18/	0.78	0.95	0.98								
mair	891330	893133	+	1100	1202	1500	1202	0.58	1.20	1.26								
yjib vfiC	893239	894900	+	1748	2201	2437	2236	1.19	1.39	1.20								
vfiD	896923	897327	+	649	873	839	472	1.29	1.45	0.74								
yjiD vfiF	807345	808202	+	782	00/	035	600	1.50	1.27	0.74								
vfiF	898296	899240	+	232	219	219	221	0.95	0.95	0.76								
yj11 vfiG	899415	900863	+	485	338	389	468	0.70	0.95	0.90	292	vfiG	899434	899730	899582	52 30	10.7 6.6	
vfiH	900890	901831	+	469	273	309	474	0.58	0.66	1.00	272	yno	077454	077750	077502	5.2 5.0	10.7 0.0	
vfiI	901841	903022	+	489	314	365	499	0.64	0.75	1.00								
<i>))1</i>	201011	/02022		.05	511	505		0.01	0.75	1.02	293	Inter	902919	903147	903033	10.0 4.8	1.5 0.0	
vfi I	903146	904348	+	902	1467	1208	870	1.63	1 34	0.97	275	mer	/02/1/	,05111	,000000	10.0	1.5 0.0	
vfiK	904345	905007	+	1034	1522	1279	892	1.46	1.22	0.86								
vfiL	905151	906086	+	236	196	191	253	0.83	0.81	1.07								
vfiM	906099	907289	+	267	249	248	285	0.93	0.93	1.07	294	vfiM	906523	906785	906654	12.8 0.9	5.3 -0.6	
vfiN	907303	908460	+	339	298	307	351	0.88	0.91	1.04		5						
padR	908533	909081	-	1000	769	648	995	0.77	0.65	1.00								
lipB	909354	909986	+	2104	1259	1323	1614	0.60	0.63	0.77								
yfiQ	910175	911263	+	365	358	366	316	0.98	1.01	0.87	295	yfiQ	910909	911086	910998	4.2 2.2	-0.2 0.2	
yfiR	911299	911916	-	924	1018	1030	812	1.11	1.12	0.88								
yfiS	911882	913135	-	507	679	713	415	1.34	1.40	0.82								
yfiT	913259	913795	+	2167	2774	2762	1560	1.29	1.27	0.72								
yfiU	913792	915348	-	262	259	287	270	0.99	1.10	1.03								
yfiV	915459	915941	-	1097	1023	990	1129	0.95	0.92	1.04								
yfiW	916113	916889	+	2389	3140	2962	2148	1.31	1.24	0.90								
yfiX	916864	918684	+	2634	3497	3330	2257	1.33	1.27	0.86								
yfiY	918702	919679	-	12160	11267	11051	12434	0.93	0.91	1.02								
yfiZ	919810	920811	+	3076	3056	2727	3012	0.99	0.89	0.98								
yfhA	920808	921839	+	4827	4589	4297	5045	0.95	0.90	1.04								
yfhB	921954	922835	+	1573	3232	3294	1147	2.05	2.06	0.72								
yfhC	922923	923507	+	11445	13732	13625	11433	1.20	1.19	0.99								
yfhD	923546	923737	-	970	1357	1908	728	1.39	1.95	0.75	<i>a</i> -	4.5						
yfhE	923804	923914	-	902	897	1085	776	0.99	1.19	0.86	298	ythE	923744	924023	923884	9.4 2.8	1.6 12.3	
yfhF	923969	924880	-	861	649	721	763	0.76	0.84	0.89								
recX	924969	925763	+	3057	2431	2393	2887	0.79	0.78	0.94								
yfhH	925765	926079	+	2863	2363	2391	2610	0.83	0.84	0.91								
yfhl	926222	927415	+	870	592	599	800	0.70	0.70	0.91								
sspK	927448	927600	-	166	177	199	204	1.20	1.34	1.29								
yfnJ	927725	92/994	+	1406	1377	1529	1593	1.01	1.11	1.13	200	Tuto a	007040	028222	030002	11.0 4.2	26 12	
fly P	020120	028457		2721	2520	2020	1476	0.07	1.50	0.51	299	inter	92/943	928222	928083	11.8 4.2	3.6 1.0	
yjn <b>K</b>	928139	928657	+	2/51	2550	3939	14/6	0.96	1.52	0.51								
yfnL	928742	929074	+	1161	1651	1969	963	1.52	1.92	0.85								

Suppleme	ntary Tab	le S1. Su	nma	ry of trai	iscriptor	me and (	ChAP-ch	ip analyse	es (contir	wed).				C	AD ahin a	nolucia				
	gene			Sior	al intone	Trans		Evo	raccion ro	tio b				U	iAP-cnip a	inalysis	Dinding	intoncity	с	
			ри	Sigi	iai intens	ity of Kin	A	Exp	A abh	uo	PBR	ORF				Al	orB	A	bh	Profile
name	start	end	stra	wild	∆abrB	∆abh ∆abrB	$\Delta abh$	∆abrB/ wild	$\Delta abrB/$	⊿abh / wild	ID	or Intergenic	start	end	center	wild	∆abh	wild	∆ abrB	ID
vfhM	929061	929921	+	1087	1597	1818	990	1.54	wild 1.81	0.93						-type		-type		
csbB	930154	931143	+	4740	3532	3912	4670	0.75	0.83	0.99										
yfhO	931340	933799	+	4431	3302	3678	4390	0.75	0.84	1.00										
yfhP	933792	934775	-	1117	1120	1290	1259	1.00	1.16	1.13										
yfnQ yfhS	936108	936332	+	208	2672	2728	3005 190	0.85	1.28	0.95										
fabL	936414	937166	+	7671	7195	6966	8069	0.94	0.91	1.05										
sspE	937235	937489	+	9440	12319	13664	9008	1.31	1.45	0.95										
ygaB	937578	937922	+	315	476	512	319	1.51	1.63	1.00										
ygaC	938066	938596	+	2560	3264	3051	2965	1.29	1.21	1.15										
ygaD ygaE	940503	941564	-	2056	1132	974	1659	0.57	0.93	0.81										
gsaB	941784	943073	-	5752	4373	4424	5369	0.76	0.77	0.93	301	gsaB	942258	942349	942304	3.0	2.2	1.6	0.9	
ygaF	943226	943699	+	1084	976	945	1087	0.90	0.87	1.00										
perR	943822	944259	+	7481	6893	7396	6906	0.92	0.99	0.92										
ygzB	944294	944647	-	2199	4241	3891	1976	1.95	1.78	0.90	202	Intor	044654	044705	044725	6.8	12	1.0	1.9	
vexA	944855	945739	+	3145	4417	4590	3058	1.41	1.47	0.97	302	mei	744034	<del>744</del> 7 <del>3</del> 3	944723	0.0	4.5	1.0	1.0	
trnD-Ser	950996	951087	+	15185	16799	16346	13134	1.09	1.07	0.85										
trnD-Phe	951465	951540	+	1743	910	857	1045	0.52	0.49	0.60										
trnD-Trp	951731	951804	+	4353	14511	13900	7865	3.50	3.36	1.82										
trnD-His	951829	951904	+	10542	16060	15786	9965	1.52	1.49	1.01										
trnD-Cys	952547	952631	+	3792	5583	6777	3207	1.19	1.83	1.22										
spo0M	952707	953483	-	8506	13119	13720	9423	1.54	1.61	1.11										
											309	Inter	953466	953711	953589	11.1	4.9	1.3	-0.2	
ygzA	953625	953828	+	142	121	130	148	0.85	0.91	1.03										
ygaJ thiC	954225	954980	+	867	681	784	852	0.78	0.90	0.98	211	thiC	055625	055802	055714	5.0	11	1.0	1.1	
veaK	957041	958144	-	134	112	116	123	0.94	0.91	0.90	312	voaK	957581	957893	957737	18.9	0.9	1.9	1.1	
senS	958626	958844	+	131	89	92	124	0.68	0.70	0.94	512	JBarr	201001	101010	201101		0.7	12.0		
katA	958871	960322	-	2565	1722	2044	2322	0.67	0.80	0.90										
ssuB	960686	961498	+	142	113	130	167	0.80	0.92	1.19										
ssuA ssuC	961516	962514	+	192	191 256	183	209	0.99	0.95	1.09										
ssuC ssuD	963364	964494	+	282	230	208	262	0.91	0.93	1.10										
											314	Inter	964448	964642	964545	9.3	0.8	3.5	0.4	
ygaN	964598	965134	+	436	454	462	505	1.04	1.06	1.16										
rpsN_2	965246	965515	+	567	439	468	551	0.78	0.83	0.97										
ygaO yhzB	965566	960000	-	943 670	603	809 667	880 759	0.93	0.80	0.94										
yhbA	967125	968432	+	490	423	370	478	0.90	0.77	0.95										
yhbB	968499	969434	+	203	163	167	222	0.80	0.83	1.11										
cspR	969472	969954	+	5286	3611	3373	5559	0.68	0.64	1.05										
yhbD whhE	970004	970720	+	540	487	421	493	0.89	0.77	0.91	216	whete D	070291	071095	070722	45.6	10 5	50.2	50.5	D01
ynde vhbF	970711	972143	+	1323	966	960	1081	0.82	0.78	0.86	510	YIDE	970381	971085	970755	45.0	40.3	- 36.3	52.5	P01
prkA	972493	974388	+	255	223	230	269	0.87	0.90	1.05										
yhbH	974568	975746	+	273	242	248	298	0.89	0.91	1.09										
yhbI	975906	976370	+	1168	390	326	922	0.34	0.28	0.78										
yhbJ yhcA	976406	97/0/1	+	2395	/3/ 816	/10 764	1922	0.30	0.29	0.80										
yhcH yhcB	978733	979263	+	2799	1065	1030	2073	0.34	0.36	0.73										
yhcC	979276	979650	+	1765	651	607	1314	0.37	0.34	0.74										
yhcD	979650	979805	+	74	92	78	115	1.23	1.05	1.52										
yhcE	979810	980571	+	800	655	586	716	0.82	0.73	0.90										
yncF yhcG	980574	980939	+	2156	1072	900 1574	1159	0.00	0.59	0.71										
yhe G vhcH	981656	982573	+	3431	2365	2272	2472	0.69	0.66	0.72										
yhcI	982566	983507	+	3074	2165	2077	2304	0.70	0.67	0.75										
cspB	983599	983802	-	31113	29499	28822	29989	0.95	0.93	0.96										
yhcJ whoK	984238	985029	+	1459	2788	2216	1366	1.93	1.54	0.93										
yncK yhcI	986322	980149	-+	1321	1/0/ 031	1444 016	2083	0.80	0.64	0.94										
yhcL yhcM	987753	988208	-	751	1143	1640	492	1.53	2.20	0.66										
yhcN	988358	988927	+	183	818	1149	167	4.46	6.26	0.91										
yhcO	989107	989406	+	118	107	122	122	0.90	1.03	1.03										
yhcP	989397	990014	+	196	168	171	188	0.86	0.87	0.96										
yhcQ yhcP	989946 990682	990599	-	177 414	005	1569	166 774	6.29 2.42	8.69 2.54	0.94										
yhcS	994332	994928	+	407	841	845	420	2.08	2.06	1.00										
yhcT	994958	995866	-	443	391	359	442	0.90	0.82	1.00										
yhcU	995977	996372	+	469	398	394	453	0.85	0.84	0.96										

	gene					Trans	criptom	e analysis			_			C	hAP-chip a	nalysis			
				Sig	nal intens	ity of RN	A <sup>a</sup>	Exp	ression ra	tio <sup>b</sup>		ODE					Binding	intensity c	
name	start	end	and			Aabh		A abrB/	$\Delta abh$	A abh /	PBR	or	start	end	center	Ab	rB	Abh	Profile
india	Surr	end	str	wild	∆abrB	$\Delta abrB$	$\Delta abh$	wild	$\Delta abrB/$	wild	ID	Intergenic	Start	chù	center	wild	∆abh	wild ⊿abrE	ID
	006500	00/021		296	(04	907	420	1.01	wild	1.12		ũ				-type		-type	
yhcV wheW	996509	996931	+	380	2412	2021	430	1.81	2.11	1.12									
yhc w vhcX	997736	999277	+	6795	7307	8141	7384	1.07	1.19	1.09									
<i></i>											317	Inter	999536	999713	999625	5.0	3.4	1.8 0.4	
yhxA	999697	1001049	+	1903	3353	3867	2030	1.76	2.03	1.07									-
glpP	1001077	1001655	+	3035	4160	4535	2915	1.37	1.49	0.96									
	1001024	1002650		12070	1007	2405	10100	0.14	0.04	0.74	318	Inter	1001253	1002144	1001699	43.0	74.5	35.7 22.3	P01
glpF alpK	1001834	1002658	+	13070	1897	5495 6353	10108	0.14	0.24	0.74									
gipK glnD	1002077	1004107	+	6746	837	1312	3449	0.23	0.35	0.74									
yhxB	1006107	1007804	+	8984	10493	10719	9690	1.17	1.20	1.08									
yhcY	1007953	1009092	+	607	856	877	505	1.40	1.43	0.83									
yhcZ	1009089	1009733	+	990	1724	1723	675	1.75	1.73	0.68									
yhdA	1009730	1010254	+	660	1054	1098	517	1.60	1.67	0.77									
yhdB	1010269	1010511	-	176	225	267	172	1.28	1.52	0.97									
yhdC b#F	1010/12	1011035	+	209	289	289	3803	1.40	1.39	0.86									
vhdE	1012695	1012342	-	1120	2726	2348	1059	2.44	2.09	0.94									
vgxB	1012030	1014896	-	463	488	691	410	1.07	1.48	0.91									
spoVR	1014927	1016333	+	143	117	124	137	0.82	0.87	0.96	319	spoVR	1015924	1016407	1016166	25.5	26.9	19.3 27.	P01
phoA	1016363	1017748	-	321	446	475	313	1.38	1.47	0.96									
											320	Inter	1017794	1018447	1018121	27.8	42.6	4.0 5.6	P03
lytE	1018280	1019311	+	4210	4139	3609	5275	0.98	0.85	1.25									
citR	1019330	1020256	-	694	505	576	766	0.74	0.84	1.11									
citA vhdF	1020365	1021465	+	9/1	432 641	460	804 965	0.44	0.47	0.82									
ynar vhdG	1021559	1022408	+	334	320	349	392	0.54	1.05	1 18									
yhdH	1024173	1025528	+	2139	1637	1441	1890	0.77	0.67	0.88									
yhdI	1025563	1026972	-	579	556	557	504	0.96	0.96	0.87									
yhdJ	1027082	1027510	+	357	428	453	281	1.19	1.28	0.78									
yhdK	1027541	1027831	-	955	933	936	1218	0.98	0.98	1.27									
yhdL	1027819	1028895	-	3429	3213	3297	3898	0.94	0.96	1.14									
sigM	1028885	1029376	-	2020	2269	2140	2474	1.14	1.06	1.23	221	Intor	1020405	1020725	1020570	0.2	4.0	12.1 6.9	
vhdN	1029573	1030568	+	1484	852	1454	712	0.58	1.02	0.45	321	mei	1029405	1029735	1029370	9.2	4.7	15.1 0.6	
yhdO	1030703	1031302	+	5234	5566	4307	5107	1.04	0.81	0.98									
yhdP	1031371	1032705	-	4078	3224	3598	4272	0.79	0.88	1.05									
yhdQ	1032766	1033197	-	3168	2795	2952	3412	0.88	0.93	1.08									
yhdR	1033354	1034535	+	1817	1902	2099	1684	1.05	1.16	0.92									
yhdS whaT	1034675	1034785	-	217	261	249	1026	1.22	1.16	1.04									
yna1 ccrB	1034802	1036247	+	2067	2380	2441	1930	1.15	1.18	0.94									
vhdW	1036996	1037727	-	873	979	860	851	1.12	0.97	0.96									
yhdX	1037961	1038068	+	446	389	533	244	0.87	1.17	0.55									
yhdY	1038217	1039332	+	1648	1502	1470	1845	0.92	0.90	1.11									
yhdZ	1039402	1040145	+	675	798	838	709	1.21	1.26	1.06									
yheN	1040169	1041017	-	3160	4109	3502	2480	1.32	1.12	0.80									
dat	1041302	1042150	+	1737	4933	5303	1505	2.84	3.04	0.85	222	-h-C	1042107	1042556	1042222	2.1	2.2	1.4 21	D04
nnaC	1042195	1045554	-	1/03	867	1/25	2302	0.81	0.75	0.49	322	mac	1045107	1045550	1045552	5.1	2.2	1.4 51.0	P04
man	1045001	1044101		1475	007	1455	154	0.50	0.90	0.47	323	Inter	1044042	1044457	1044250	24.5	23.1	5.4 2.0	P03
yheJ	1044345	1044506	+	742	2835	2337	750	3.84	3.14	1.01								210	
yheI	1044626	1046383	+	433	947	1068	481	2.19	2.47	1.11									_
yheH	1046380	1048401	+	559	1270	1356	612	2.29	2.44	1.09	324	yheH	1047289	1047398	1047344	2.6	0.9	2.6 0.4	
yheG	1048450	1049070	-	3388	2625	2664	3533	0.77	0.78	1.04									
yheF ann P	1049109	1049234	-	133	176	196	143	1.31	1.48	1.05									
sspB vhaF	1049339	1049542	-	495	2081	2806	285	4.26	5.80	1.08									
yneL	1049731	1049909	-	347	556	540	265	0.97	1.00	0.82	325	Inter	1049992	1050152	1050072	5.0	17	2.2 -0.3	
yheD	1050119	1051480	-	249	239	253	246	0.96	1.02	0.99	525		10.7772	1000102	- 00 00 12	5.0		2.2 0.3	
yheC	1051470	1052561	-	153	146	149	148	0.95	0.97	0.97									
yheB	1052828	1053961	+	2976	2460	2548	3265	0.83	0.86	1.09									
											326	Inter	1053834	1054181	1054008	10.3	4.0	6.3 0.2	
yheA	1054054	1054407	+	6418	5663	5394	6621	0.88	0.84	1.03									
yhaZ whaY	1054451	1055524	-	640	944	983	503	1.48	1.53	0.79									
yna¥ yha¥	1055/17	1055968	-+	397 131	450	405 272	315	1.13	1.02	0.94									
hemZ	1056989	1058494	+	1579	966	814	1371	0.03	0.05	0.87									
yhaU	1058512	1059738	-	786	880	1054	941	1.13	1.36	1.19									
yhaT	1059735	1060232	-	515	539	692	758	1.07	1.42	1.46									
yhaS	1060296	1060634	-	1379	1657	2008	1485	1.21	1.49	1.07									
yhaR	1060799	1061566	+	714	2008	2234	853	2.82	3.16	1.17									
yhaQ	1061899	1062795	+	2146	7869	7611	3784	3.68	3.56	1.77	328	yhaQ	1061535	1062273	1061904	40.7	21.7	45.3 5.4	P02

	gene					1 rans	riptome	analysis						C	плг-спра	marysis				
			_	Sig	nal intensi	ity of RN.	A <sup>a</sup>	Exp	ression ra	utio <sup>b</sup>		ORE					Binding	intensity c		
name	start	end	rand			Aabh		A ahrB/	$\Delta abh$	A abh /	PBR	or	start	end	center	Ab	rB	Ab	h	Profile
			st	wild	∆abrB	∆abrB	∆abh	wild	$\Delta abrB/$	wild	ID	Intergenic				wild	$\Delta abh$	wild	∆abrB	ID
1 0	10/0700	10/10/7		22.12	0051	0.1.12	42.00	2.70	wild	1.07		-				-type		-type		
vhaP	1062788	1064047	+	2342	8851	8442	4368	3.78	3.61	1.87										
what O	1065285	1069276	+	1970	2266	1852	2033	0.92	0.94	1.05										
shaM	1069350	1060204	+	2748	2300	2595	2911	0.80	0.95	1.06	220	vboM	1060210	1060211	1060265	2.2	27	0.1	0.2	
shal	1060410	1069621	- T	445	270	3393	104	0.92	0.95	1.11	329	ynaivi	1009219	1009311	1009205	2.2	2.7	0.1	-0.5	
arsA	1069672	1070550	T	16781	17023	17600	16571	1.07	1.05	0.00	330	nrs A	1070103	1070382	1070243	8.5	15.8	33	0.1	
vhaK	1071350	1070550	-	1263	853	785	1091	0.70	0.63	0.55	550	pisa	10/0105	1070302	1070245	0.5	15.0	5.5	0.1	
ynun	1071550	10/1004	-	1205	055	105	1071	0.70	0.05	0.00	331	Inter	1071446	1071793	1071620	6.8	14.1	2.5	39	
vha.I	1071628	1071867	-	509	399	360	531	0.79	0.71	1.06	001	mer	10/1110	10/1//0	10/1020	0.0		2.0	5.7	
vhaI	1072075	1072416	+	546	646	606	595	1.16	1.10	1.08										
hpr	1072413	1073024	-	2707	3035	3094	2247	1.12	1.14	0.83										
yhaH	1073202	1073558	-	4498	5007	4780	4257	1.14	1.07	0.96										
vhaG	1073951	1074469	-	3398	3431	3612	2925	1.01	1.06	0.86										
serC	1074594	1075673	-	5726	5597	5874	4774	0.98	1.03	0.84										
hit	1075820	1076257	-	7332	8685	8927	7385	1.19	1.22	1.01										
ecsA	1076745	1077488	+	2241	2879	3012	2323	1.30	1.37	1.04										
ecsB	1077481	1078707	+	3626	4934	5465	3829	1.37	1.52	1.06										
ecsC	1078727	1079437	+	3381	4240	4522	3291	1.26	1.36	0.97	332	ecsC	1079011	1079307	1079159	8.8	7.4	4.3	0.7	
yhaA	1079455	1080645	-	356	549	733	373	1.56	2.09	1.04										
vhfA	1080718	1082109	-	276	312	304	276	1.13	1.10	1.00										
yhgB	1082175	1082489	-	290	393	387	253	1.38	1.36	0.85										
yhgC	1082534	1083034	-	4198	7146	7455	5015	1.72	1.79	1.20										
pbpF	1083156	1085300	+	976	800	748	948	0.83	0.77	0.96										
hemE	1085422	1086483	+	3665	3172	3010	3495	0.89	0.83	0.96										
hemH	1086555	1087487	+	8285	7148	7145	8278	0.88	0.88	1.00										
hemY	1087502	1088914	+	4478	3981	3922	4440	0.92	0.90	1.00										
yhgD	1089060	1089635	+	2120	2649	2645	1772	1.22	1.19	0.84										
vhgE	1089706	1092033	+	2666	2524	2577	2265	0.94	0.95	0.85										
abHB	1092075	1093052	-	746	1523	1084	860	1.96	1.41	1.11										
vhfC	1093178	1093954	+	326	746	715	373	2.28	2.19	1.14										
yhfD	1094045	1094248	-	222	219	228	208	0.99	1.03	0.94										
vhfE	1094367	1095407	+	2692	5064	5316	2998	1.92	2.01	1.11										
ynjF .hT	1095420	1095827	+	310/	2880	12104	3401	1.8/	1.93	1.07	224	-1/T	1005925	100/570	100/202	20.5	26.9	42.2	27.0	DO 1
git I	1095804	109/155	-	12605	12018	12104	12374	1.00	0.96	0.98	225	git I Intor	1095825	1090579	1096202	15.8	20.8	43.3	0.8	P01
hfH	1007424	1007564	_	4027	2754	2877	2130	0.74	0.75	0.51	555	Inter	109/10/	1097581	1097374	15.0	1.5	5.0	0.8	
vhfI	1097716	1098450	+	5352	7907	8040	6851	1 48	1.51	1.28										
vhf I	1098463	1099458	+	7471	10547	10918	9312	1.40	1.51	1.20										
vhfK	1099523	1100167	+	5475	8256	8311	6416	1.42	1.47	1.24										
vhfI.	1100284	1101825	+	741	593	617	789	0.80	0.84	1.17										
vhfM	1101864	1102259	-	212	311	372	222	1.46	1.74	1.04	336	vhfM	1101808	1101934	1101871	3.8	1.0	0.2	-0.8	
vhfN	1102408	1103688	+	405	379	391	409	0.94	0.96	1.01		J						0.12		
aprE	1103727	1104872	-	231	244	275	238	1.06	1.19	1.03	337	aprE	1103695	1103804	1103750	3.5	1.3	0.3	0.4	
											338	Inter	1104800	1105130	1104965	18.0	11.8	1.9	-0.3	
yhfO	1105307	1105756	+	1343	1238	1125	1234	0.92	0.83	0.92										
yhfP	1105828	1106820	+	3527	4107	4328	3568	1.17	1.23	1.02										
yhfQ	1106962	1108008	+	10445	9472	8967	9559	0.91	0.86	0.92										
yhfR	1108040	1108621	-	3022	3093	3007	3312	1.06	1.02	1.12										
yhfS	1108692	1109786	-	546	595	591	512	1.10	1.09	0.93										
yhfT	1109783	1111222	-	790	804	832	706	1.02	1.06	0.88										
yhfU	1111229	1111789	-	238	234	245	247	0.98	1.03	1.04									_	
hemAT	1111924	1113222	-	2372	3784	3513	1935	1.66	1.50	0.82	340	hemAT	1112654	1113103	1112879	15.8	23.9	-0.1	-0.8	
											340	Inter	1113113	1113409	1113261	7.8	11.4	-0.2	0.4	
yhfW	1113361	1114890	-	170	227	234	160	1.34	1.39	0.94										
yhxC	1115002	1115859	+	194	222	240	209	1.14	1.24	1.07										
yhzC	1115887	1116120	-	382	298	360	295	0.79	0.95	0.78						_		_		
											342	Inter	1116123	1116520	1116322	21.5	14.0	4.4	1.3	
comK	1116413	1116991	+	583	955	965	559	1.68	1.66	0.96										
yhxD	1117038	1117937	-	461	390	507	311	0.85	1.10	0.68						_		_		
	1110	1110.5		125-1	00	00	0.10-			0 =-	344	Inter	1117992	1118186	1118089	5.0	6.4	0.1	0.1	
yhjA	1118154	1118423	+	12987	20690	20589	9108	1.60	1.59	0.70										
yhjB	1118466	1119935	-	336	378	389	346	1.12	1.16	1.03										
ynjC	1119932	1120132	-	318	449	482	318	1.41	1.51	1.00										
yhjD	1120340	1120702	-	169	110	124	152	0.65	0.74	0.90										
yhjE 	1120855	1121478	+	1155	1486	1404	1359	1.30	1.23	1.17										
sıpv	1121480	1121986	+	2209	2494	2574	2311	1.13	1.17	1.07	245	Inter-	1101070	1100101	1100077	1.0	10	4.4	5.0	
1.0	1100165	1102555	,		701		105	1 20		0.02	345	inter	1121970	1122181	1122076	1.2	6.2	4.4	5.0	
ynjG	1122166	1123665	+	527	/91	844	495	1.50	1.60	0.93										
njH doD	1125742	1124269	+	825	1021	1098	/04	1.26	1.35	0.85	217	alaP	1124402	1124607	1124550	0.0	12.8	1.6	0.1	
şıcr	1124427	1123032	-	250	224	229	214	0.97	0.99	0.94	247	gior	1124402	112409/	1124024	<b>0.0</b>	57.1	1.0	0.1	DO2
											34/ 347	giur deP	1124/0/	1125700	1125034	94.1	11.2	1.0	-0.8	1.02
vhi I	1125704	1126754		221	777	205	207	1.25	1 20	0.02	240	git.r vbiT	1125200	1123/00	1122222	14.2	6.1	0.0	-1.0	
yn <b>j</b> J	1125704	1120/30	-	221	211	305	207	1.25	1.58	0.93	548	չպյ	1120390	1120080	1120338	14.2	0.1	-0.1	-1.4	

Supplem	entary Tab gene	le S1. Su	mma	ry of trai	nscripto	me and ( Trans	ChAP-ch criptom	iip analyse e analysis	es (contin	ued).				С	hAP-chin s	analysis				
	gene			Sig	nal intens	ity of RN	A <sup>a</sup>	Exp	ression ra	tio <sup>b</sup>				C	пла -стра	Bi	inding	intensity	с	
name	start	end	and	5181		Acht	-	A abrD /	$\Delta abh$	Aabb /	PBR	ORF	start	end	center	AbrE	3	A	bh	Profile
name	Surr	chd	str	wild	∆abrB	$\Delta abrB$	∆abh	wild	$\Delta abrB/$	wild	ID	Intergenic	Start	end	center	wild A	abh	wild	∆abrB	ID
vhiK	1126759	1127619	-	133	158	178	124	1 18	wild 1 33	0.93						-type		-type		
yhjR yhjL	1127591	1128916	-	148	168	208	124	1.14	1.40	0.87	349	yhjL	1127716	1128267	1127992	19.8	17.4	4.9	2.1	
											349	yhjL	1128277	1128862	1128570	33.6	55.5	16.2	-0.7	
yhjM	1129020	1130009	+	172	1126	1058	232	6.53	6.14	1.35	349	yhjM	1128872	1129168	1129020	11.6	12.1	2.1	-0.4	
yhjN vhiO	1130223	1131377	-	445	2691	1633	522	5.95	3.43	1.16										
ynj0 vhiP	1131484	1132089	+	570	506	501	208 580	0.89	0.88	1.02										
yhjQ	1134560	1134886	-	163	118	142	167	0.73	0.88	1.01										
yhjℝ	1135004	1135441	-	200	169	181	183	0.84	0.90	0.92										
addB	1135625	1139125	+	1834	1759	1981	2029	0.96	1.09	1.10										
addA	1139112	1142810	+	3061	3428	3667	3505	1.14	1.21	1.14										
sbcD	1142882	1144057	+	2027	2332	2535	2334	1.17	1.27	1.13										
yir I visB	1144054	1147762	+	2025	3388	3137	2786	1.54	1.55	1.11										
gerPF	1147799	1148026	-	192	201	216	178	1.05	1.14	0.94										
gerPE	1148049	1148450	-	152	167	184	156	1.10	1.21	1.03										
gerPD	1148450	1148626	-	442	515	538	398	1.17	1.22	0.90										
gerPC	1148623	1149240	-	390	380	422	384	0.97	1.08	0.98						- CO. 4. 4	10.0			Dod
gerPB	1149263	1149505	-	177	180	184	1/1	1.02	1.04	0.97	352	gerPB	1148864	1149823	1149344	69.1 1	18.8	99.7	70.5	P01
yisI	1149311	1150325	-	215	242	225	175	1.13	1.05	0.81										
yisI yisJ	1150471	1151394	-	215	203	210	223	0.95	0.98	1.05										
yisK	1151549	1152454	+	1786	5834	6013	2241	3.27	3.38	1.25										
yisL	1152570	1152926	+	3716	4864	4804	3759	1.32	1.31	1.02										
					10000	10.50					353	Inter	1152706	1153376	1153041	39.6	25.7	28.6	8.7	
wprA	1153094	1155778	+	14565	18998	19726	20250	1.30	1.35	1.39										
yısın asnO	1156542	1158386	+	101	167	165	203	0.97	0.95	1.18										
vizA	1158516	1158995	-	225	331	356	237	1.47	1.58	1.06										
yisP	1159227	1160051	+	798	698	680	653	0.88	0.87	0.81										
yisQ	1160081	1161448	-	254	222	224	226	0.88	0.88	0.89										
yisR	1161572	1162435	+	526	469	445	458	0.89	0.85	0.87										
degA	1162453	1163466	+	1321	1122	1112	1226	0.85	0.84	0.92	254	Intor	1162484	1162678	1162591	18	68	0.0	1.2	
visS	1163675	1164703	+	1101	1435	1608	811	1.31	1.48	0.73	554	men	1105464	1105078	1105581	4.0	0.0	0.9	1.2	
yisT	1164754	1165263	-	756	3404	3401	912	4.65	4.55	1.19										
yisU	1165313	1165975	-	251	231	245	264	0.92	0.98	1.07										
yisV	1166042	1167496	+	452	429	440	520	0.95	0.97	1.15										
yisX wieV	1167504	1168142	-	1160	1266	1182	1150	1.10	1.03	0.99										
yis1 vis7	1169182	1169781	+	213	207	207	236	0.91	0.92	1.13										
sat 1	1169778	1170947	-	190	169	175	205	0.89	0.92	1.08										
yitB	1171060	1171770	-	248	207	217	228	0.84	0.88	0.93										
yitC	1171955	1172641	+	191	179	184	201	0.94	0.96	1.06	355	yitC	1172138	1172450	1172294	0.5	0.7	1.1	19.2	P04
yitD	1172638	1173396	+	215	211	208	257	0.98	0.97	1.20										
yitE vitE	1173441	1174070	-	223	217	225	230	0.97	1.01	1.04										
yur vitG	1175290	1176558	-	270 500	435	468	295 468	0.94	0.93	0.93										
yitH	1176670	1177518	-	1948	1598	1646	1785	0.82	0.85	0.93										
yitI	1177523	1177987	-	1668	1372	1404	1535	0.83	0.84	0.92										
yitJ	1178062	1179900	-	221	181	208	247	0.82	0.94	1.12										
yit K	1180214	1180705	-	2000	2244	2692	2029	1.13	1.35	1.01	0	5. <b>T</b>	110050	110105	11000 #7	0000	0.0-0-			DC
yıtL vitM	1180804	1181700	+	3362	2025	1842	2962	0.60	0.55	0.88	357	yıtL	1180501	1181204	1180853	27.0	23.9	38.5	81.1	P01
yu wi vitN	1182334	1182702	-	508 168	559 195	410	187	0.92	5.55 2.52	1.09										
yit O	1182834	1183046	-	392	328	458	429	0.83	1.18	1.12										
yit P	1183247	1183783	-	198	190	298	188	0.96	1.51	0.95										
											360	Inter	1182711	1184877	1183794	96.1 1	15.7	170.6	5 258.3	P01
yitQ	1184155	1184892	+	905	1023	968	795	1.13	1.06	0.87										
yttR pprP	1184912	1185205	+	757	758	721	836	1.00	0.95	1.10	360	nnrB	1184997	1186050	1185460	50.0	52.0	70.2	527	<b>P</b> O 1
прів	1103341	1100937	+	201	210	230	202	1.07	1.1/	1.00	361	nprB	1186536	1186730	1186633	1.9	1.1	3.2	52	101
yitS	1187004	1187855	-	1235	1386	1252	1267	1.12	1.01	1.02	501	-1	1100550	1100/30	11000000			5.2	5.2	
yitT	1187993	1188835	+	2422	1679	1758	2131	0.70	0.72	0.88										
ipi	1188950	1189309	+	2499	1922	1930	2197	0.77	0.77	0.88										
yit U	1189794	1190606	-	1766	2236	2301	2060	1.30	1.33	1.17										
yit V	1190727	1191494	+	2899	2870	2797	2761	1.00	0.97	0.95										
yıt W	1191558	1191866	+	5758	6580	6807	5712	1.14	1.18	0.99										
yu 1 vitZ	1192102	1193592	++	1426	10/0	1599	1390	1.21	1.15	0.98	363	vitZ	1193846	1194159	1194003	10.2	8.9	15.6	79	
argC	1194338	1195378	+	228	214	221	235	0.94	0.97	1.03	505	للمعار			11, 1005		.,	-10.0	1.7	
argJ	1195398	1196618	+	242	196	197	249	0.81	0.81	1.02										
argB	1196633	1197409	+	158	145	138	179	0.92	0.88	1.14										

suppiem	gene	ac 51. 5U	mna	ry of trai	uscriptoi	me and Trans	criptom	up analyse e analysis	es (contin	ueu).				С	hAP-chip a	nalysis				
	gene			Sig	nal intens	ity of RN	A <sup>a</sup>	Exn	ression ra	tio <sup>b</sup>					in the compt		Binding	intensity	с	
name	etart	and	and	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		4hh		A abaD/	$\Delta abh$	A abb /	PBR	ORF	etart	end	center	A	brB	A	bh	Profile
name	start	chu	str	wild	∆abrB	$\Delta abn$ $\Delta abrB$	$\Delta abh$	wild	$\Delta abrB/$	wild	ID	Intergenic	start	cita	center	wild	∆abh	wild	∆abrB	ID
araD	1107406	1108562		100	180	170	220	0.00	wild	1.16		, in the second				-type		-type		
carA	1197400	1198505	+	243	221	238	230	0.90	0.90	1.10										
carB_1	1199688	1202780	+	226	205	212	238	0.91	0.94	1.05										
argF	1202768	1203727	+	284	259	263	297	0.91	0.93	1.04	365	argF	1202958	1203288	1203123	11.9	15.2	4.6	2.9	
yjzC wi-D	1203813	1203992	+	122	113	112	125	0.93	0.92	1.02										
yj2D	1204058	1204225	-	5400	5219	4087	5150	0.90	0.80	0.94	366	Inter	1204131	1204665	1204398	31.4	18.0	40.4	12.1	
yjaU	1204472	1205206	+	184	328	320	300	1.79	1.74	1.62										
yjaV	1205288	1205695	+	172	154	148	179	0.89	0.86	1.04										
med	1205937	1206890	+	2306	2564	2053	2223	1.11	0.89	0.96	368	med	1206018	1206484	1206251	17.6	16.1	27.7	38.4	
vizB	1200905	1207090	-	2885	201	2383	237	0.92	0.90	1.18										
fabHA	1207530	1208468	+	5872	7209	5553	6386	1.22	0.94	1.08										
fabF	1208491	1209732	+	10379	12116	10140	10787	1.17	0.97	1.04										
yjaZ	1209808	1210593	+	188	193	188	181	1.02	1.00	0.96	369	yjaZ Intor	1210047	1210428	1210238	19.0	7.6	16.4	5.8	
appD	1210785	1211771	+	175	259	353	193	1.48	2.01	1.10	309	mer	1210438	1210887	1210005	- 55.0	50.7	11.2	0.8	
appF	1211768	1212757	+	134	273	378	137	2.04	2.83	1.02										
appA	1212845	1214476	+	188	817	1092	211	4.29	5.69	1.12										
appB appC	1214552	1215505	+	246	466	619 510	258	1.89	2.48	1.06										
vibA	1215522	1210433	+	251	396	468	214	1.78	1.86	1.00										
trpS	1217426	1218418	-	4775	4364	4440	4491	0.91	0.93	0.94	370	trpS	1217595	1217772	1217684	7.3	2.4	3.1	-0.1	
											371	Inter	1218445	1218639	1218542	5.2	6.2	2.1	1.5	
oppA	1219162	1220799	+	3262	7083	7824	2704	2.17	2.40	0.83										
орры	1220907	1221842	+	989	1479	2149	734	2.19	2.51	0.85										
oppD	1222768	1223844	+	1479	2974	3311	1114	1.98	2.20	0.75										
oppF	1223846	1224763	+	1797	3634	4088	1354	2.00	2.22	0.75										
yjbB wihC	1224870	1226087	+	297	5162	719	304	2.49	2.42	1.02										
sprA	1220231	1220829	+	13941	14672	16078	14236	1.05	1.05	1.04										
yjbE	1227448	1228104	-	279	270	264	310	0.97	0.95	1.12										
											374	Inter	1228101	1228346	1228224	11.8	2.7	0.9	-0.2	
mecA	1228381	1229037	+	2892	3365	3817	3230	1.16	1.32	1.12										
yjDF vibG	1229228	1230349	+	5591	8914	9126	5876	1.60	1.64	1.00										
yjbH	1232926	1233753	-	2933	2857	3414	3545	0.98	1.17	1.21										
yjbI	1233822	1234220	-	1864	1968	2017	2165	1.06	1.09	1.16										
yjbJ vib <b>V</b>	1234475	1235020	-	1892	1682	1505	2079	0.91	0.80	1.11										
yjbK vjbL	1235224	1236289	+	8179	6073	6587	9055	0.39	0.80	1.11	375	vjbL	1236143	1236319	1236231	5.8	2.6	1.5	0.4	
yjbM	1236318	1236953	+	9881	7600	8683	10319	0.77	0.88	1.04										
ppnK_1	1236972	1237772	+	6940	6118	6850	8195	0.88	0.98	1.18										
yjbO wibP	1237835	1238686	+	6571	5973	6454	7427	0.91	0.98	1.13	276	wihD	1228624	1228002	1229764	5.6	2.4	10.1	15.7	
yjb1 vjbQ	1238099	1239433	+	200 959	780	806	1053	0.88	0.88	1.04	370	yjor	1238024	1238903	1238704	5.0	5.4	10.1	15.7	
tenA	1241761	1242471	+	296	244	239	284	0.83	0.81	0.95										
tenI	1242446	1243063	+	393	351	335	389	0.90	0.85	0.97										
goxB	1243047	1244156	+	587	520	511	579	0.89	0.87	0.98										
thiG	1244130	1244550	+	374	333	424	369	0.86	0.74	0.97										
thiF	1245120	1246130	+	519	450	423	500	0.87	0.81	0.96										
yjbV	1246149	1246964	+	433	369	358	405	0.86	0.82	0.93										
fabI	1247100	1247876	+	7240	10818	8217	8373	1.50	1.13	1.17										
yjux cotZ	1247977	1248000	+	138	121	131	127	0.80	0.82	0.93										
cotY	1249328	1249816	-	115	124	127	121	1.07	1.10	1.05										
cotX	1249968	1250486	-	120	126	125	110	1.04	1.04	0.91										
cotW	1250585	1250902	-	146	99	108	107	0.68	0.73	0.73										
vicA	1250943	1251329	-+	101 379	98 370	96 382	9/ 413	0.97	0.95	0.96										
yjcB	1252170	1252385	+	258	226	231	259	0.88	0.90	1.00										
yjcC	1252649	1252951	+	157	141	134	130	0.90	0.86	0.83										
yjcD	1253025	1255304	-	1611	758	677	1449	0.47	0.42	0.90										
yjcE vicE	1255385	1255687	-	301	311	303	260	1.04	1.01	0.86										
yjer vicG	1255/48	1256689	-	4288 5237	7711	9002	4979	1.50	1.72	0.95										
yjcH	1256726	1257448	-	2766	4381	4731	2778	1.59	1.71	1.01										
yjcI	1257804	1258925	+	539	542	706	487	1.01	1.31	0.90										
yjcJ vicK	1258918	1260090	+	418	432	538	419	1.03	1.29	1.01										
yjc <b>n</b> vicL	1260738	1261928	-	343	315	335	399	2.16	2.17	1.10										
20 -				2.0						/										

Supplem	entary Tal	de S1. Su	mma	ry of trai	iscriptor	me and (	hAP-ch	ip analyse analysis	es (contin	ued).				C	hAP-chine	nalveic				
	gene				-1.5.4	Trans		e analysis		. b				U	IAF-CIIIP a	marysis	Disting	· · · · · · · · · · · · · · · · · · ·	с	
			pu	্রাণ্ড	iai intens	ity of KIN	A	Exp	A abh	10	PBR	ORF				AF	Binding vrB		bb	Profile
name	start	end	stra	wild	∆abrB	$\Delta abh$	$\Delta abh$	$\Delta abrB/$	$\Delta abrB/$	$\Delta abh /$	ID	Or Internetio	start	end	center	wild		wild	<u> p</u>	ID
						∆abrB		wild	wild	wild		Intergenic				-type	∆abh	-type	∆abrB	
trnSL-Va	1262101	1262176	+	11431	14544	14748	10233	1.27	1.29	0.90										
											379	Inter	1262543	1262873	1262708	10.4	3.6	1.3	0.1	
yjcM	1263014	1264243	-	3035	9227	9004	4202	3.03	2.97	1.39	200		12/2000	1261702	10 < 1001	01.0	07.7		2.2	000
yjcN	1264369	1264689	+	2319	3537	3128	1765	1.53	1.35	0.76	380	yjcN	1263988	1264793	1264391	81.9	87.7	21.5	2.2	P02
yjcO viaP	1265026	1265660	+	618	846 1072	1210	45/	1.37	1.35	0.74	291	vioD	1265671	1266205	1265028	16.1	21.6	1.1	0.0	
yjcr vicO	1265920	1200429	+	281	1072	610	224	1.73	2.15	0.88	301	yjer	1203071	1200203	1203938	10.1	51.0	1.1	0.0	
$y_{j} \in Q$ $v_{i} \in R$	1266886	1267413	+	147	124	130	130	0.85	0.90	0.92										
vicS	1267587	1267904	+	2491	2400	2548	1971	0.97	1.02	0.79										
yidA	1268141	1268896	+	2281	2469	2684	2238	1.08	1.18	0.98										
yjdB	1269045	1269392	-	394	13959	12934	355	35.47	32.85	0.90										
											382	Inter	1269157	1269894	1269526	40.9	64.6	13.9	-0.4	
manR	1269943	1271889	+	3693	644	1400	4641	0.20	0.34	1.23										
manP	1272037	1273806	+	9398	3544	6372	12511	0.36	0.62	1.48										
manA	1274005	1274952	+	11786	5538	8692	15351	0.45	0.68	1.41	202	<b>T</b> .	1074052	1075164	1075050	60	(1)	0.6	0.2	
	1275122	1275604		16102	0720	12200	10780	0.52	0.75	1.20	383	Inter	12/4953	12/5164	12/5059	6.0	6.4	0.6	0.3	
yjar vidG	1275650	1275004	+	370	0200	12290	352	5.12	1 10	0.96										
yjuO	1275050	1270150	-	570	1070	1544	552	5.12	4.17	0.70	384	Inter	1275939	1276439	1276189	23.9	36.1	3.8	14	P03
yjdH	1276388	1276792	-	141	160	173	139	1.14	1.22	0.98	504			12,0437	-2,010)	- 2017		5.0	1.7	
											385	Inter	1276636	1277000	1276818	9.1	13.2	2.1	0.3	
yjdI	1276997	1277476	+	1220	1055	1054	1108	0.87	0.86	0.90										
yjdJ	1277876	1278205	-	351	756	733	345	2.17	2.07	1.01										
											386	Inter	1277911	1278615	1278263	30.5	59.5	5.9	3.3	P03
ctaO	1278825	1279814	-	210	1265	2511	255	5.83	11.62	1.20	387	ctaO	1279033	1280502	1279768	101.4	133.9	112.4	202.3	P01
cotT	1279937	1280260	-	533	513	535	612	0.96	1.00	1.15										
yjeA	1280439	1281842	+	3034	1699	1593	1942	0.56	0.52	0.64										
yjfA 	1281882	1282355	-	372	427	448	359	1.16	1.20	0.94										
yJJB wifC	1282480	1282047	-	2855	4080	4969	184	1.05	1.75	0.95										
viaA	1282/74	1283703	+	385	488	508	483	1.28	1.04	1.10										
vigR	1284180	1284755	-	158	132	140	165	0.83	0.89	1.23										
vigC	1284901	1287858	+	467	443	658	394	0.95	1.40	0.86										
yjgD	1287851	1288411	+	578	599	898	455	1.07	1.54	0.84										
											389	Inter	1288383	1288730	1288557	14.8	9.7	2.1	-0.3	
yjhA	1288608	1289249	+	1841	2128	2348	936	1.14	1.24	0.50	389	yjhA	1288740	1289172	1288956	16.5	25.1	5.9	-0.3	
yjhB	1289442	1289954	+	489	683	780	412	1.40	1.58	0.84										
yjiA	1289985	1290263	-	161	136	133	150	0.84	0.82	0.93			10000000			1.0		1.0		
yjiB	1290654	1291844	+	460	1114	1489	449	2.44	3.27	0.96	390	yjiB	1290763	1291110	1290937	1.9	2.3	1.9	15.1	
yjic hand l	1291807	1293045	+	2464	2081	2417	457	3.15	3.93	1.00	392	ујіС	1292599	1292725	1292662	3.5	0.7	4.0	2.9	
nemD_1	1293446	1294200	+	2404	42081	415	2281	0.85	0.98	0.92										
vikB	1295058	1295810	-	492	369	345	444	0.74	0.74	0.89										
vilA	1295930	1296904	-	1008	828	796	926	0.82	0.79	0.92										
yjlB	1297036	1297533	+	673	371	445	456	0.57	0.67	0.66	393	yjı₿	1297240	1297825	1297533	44.1	5.6	24.2	16.4	
yjlC	1297922	1298344	+	17325	14800	14187	16085	0.86	0.82	0.93		••								
yjlD	1298384	1299562	+	18582	16723	15771	17579	0.90	0.85	0.95										
uxaC	1299760	1301181	+	1157	298	367	990	0.26	0.31	0.86	394	uxaC	1299875	1300460	1300168	25.3	16.7	8.2	2.7	
yjmB	1301249	1302628	+	304	193	202	293	0.63	0.67	0.97										
yjmC	1302733	1303746	+	327	190	217	334	0.58	0.67	1.03	ar :		1001	100.177	1001/-		10.5			
yjmD	1303752	1304771	+	418	281	304	437	0.68	0.73	1.08	395	ујтD	1304193	1304795	1304494	19.6	12.3	32.9	40.9	
uxuA vim E	1304/90	13058/5	+	514 197	210	150	329 200	0.07	0.71	1.08										
yjm <b>r</b> exuT	1305872	1308024	+	361	302	325	209	0.85	0.05	0.97										
exµR	1308112	1309113	+	552	757	700	503	1 38	1 27	0.97										
uxaB	1309190	1310632	+	269	200	210	275	0.75	0.78	1.02	396	uxaB	1309208	1309623	1309416	20.4	25.8	8.5	3.4	
uxaA	1310629	1312122	+	231	181	183	267	0.79	0.79	1.16										
yjnA	1312161	1312925	-	223	210	227	238	0.95	1.02	1.07										
yjoA	1313150	1313614	-	11808	13733	13815	13108	1.17	1.18	1.12										
ујоB	1313763	1315034	+	2798	3307	3553	2700	1.18	1.27	0.96						_				
											397	Inter	1314971	1315301	1315136	11.2	17.9	4.1	0.4	
rapA	1315179	1316315	+	1182	1452	1612	1390	1.25	1.39	1.20										
phrA	1316305	1316439	+	688	826	919	797	1.22	1.34	1.15										
yjpA	1316470	1316712	-	407	1306	1189	325	3.26	2.93	0.80										
xlyB	1316849	1317802	+	2241	1276	1600	2079	0.58	0.71	0.93	200	nia A	1217012	1210105	1210000	0.2	0.5	0.1	5.0	
yjqA viaP	1318222	1318216	-	5474	3360	5439 624	5208 724	1.03	0.99	0.92	398	ујqА	151/912	1318106	1318009	0.2	0.5	0.1	5.2	
yjų D viaC	1310001	1310924	+	1112	862	787	065	0.70	0.71	0.85										
xkdA	1319881	1320477	-	229	217	215	245	0.77	0.70	1.07										
				22)	21/	215	245	5.75	0.75	1.07	399	Inter	1320360	1320808	1320584	22.9	32.0	7.9	0.1	
xre	1320640	1320981	-	660	1074	878	618	1.70	1.32	0.94										
xkdB	1321325	1322158	+	406	228	238	324	0.56	0.59	0.81										
xkdC	1322058	1322858	+	383	228	246	356	0.59	0.65	0.93										

μge         Superine (3 4 30.4)         Superine (3 40.4)         Superine (3 4.4)         Super	Supplem	entary Tab	le S1. Sur	nma	ry of trai	nscriptor	me and (	ChAP-ch	ip analyse	es (contin	ued).				CL	AD ahin a	molyceia		
mar         mar <th></th> <th>gene</th> <th></th> <th></th> <th>Cion</th> <th>a lintanci</th> <th>Trans</th> <th>criptom</th> <th>E analysis</th> <th></th> <th>tio b</th> <th></th> <th></th> <th></th> <th>u</th> <th>ар-спір а</th> <th>inalysis Diadia</th> <th>intensity C</th> <th></th>		gene			Cion	a lintanci	Trans	criptom	E analysis		tio b				u	ар-спір а	inalysis Diadia	intensity C	
mame         ait         obj         diabol				р	্রাণ্ডা	nai intens	ity of RIN	A	Exp	A abh	00	PBR	ORF				AbrB	Abb	Profile
Unit         Unit <th< th=""><th>name</th><th>start</th><th>end</th><th>stra</th><th>wild</th><th>∆abrB</th><th><math>\Delta abh</math></th><th><math>\Delta abh</math></th><th><math>\Delta abrB/</math></th><th><math>\Delta abrB/</math></th><th><math>\Delta abh /</math></th><th>ID</th><th>Or Intergonia</th><th>start</th><th>end</th><th>center</th><th>wild A th</th><th>wild to to P</th><th>ID</th></th<>	name	start	end	stra	wild	∆abrB	$\Delta abh$	$\Delta abh$	$\Delta abrB/$	$\Delta abrB/$	$\Delta abh /$	ID	Or Intergonia	start	end	center	wild A th	wild to to P	ID
Lad         Lad <thlad< th=""> <thlad< th=""> <thlad< th=""></thlad<></thlad<></thlad<>							∆abrb		wiid	wild	wiid		mergenic				-type	-type	
mm         Light         Li	xkdD	1323110	1323460	+	365	170	187	298	0.47	0.51	0.82								
math         control         control <thcontrol< th=""> <thcontrol< th=""> <thcont< td=""><td>xtrA xpf</td><td>1323457</td><td>1323663</td><td>+</td><td>1024</td><td>409 216</td><td>443</td><td>714</td><td>0.40</td><td>0.43</td><td>0.70</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></thcont<></thcontrol<></thcontrol<>	xtrA xpf	1323457	1323663	+	1024	409 216	443	714	0.40	0.43	0.70								
math         End         End <td>xtmA</td> <td>1324404</td> <td>1325201</td> <td>+</td> <td>3074</td> <td>1200</td> <td>1367</td> <td>2305</td> <td>0.37</td> <td>0.40</td> <td>0.75</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	xtmA	1324404	1325201	+	3074	1200	1367	2305	0.37	0.40	0.75								
bdd         12080         12790         0        0        0         0	xtmB	1325198	1326499	+	2591	1094	1186	2062	0.42	0.46	0.80								
Lat         13880         12881         1	xkdE	1326503	1327990	+	3081	1351	1587	2461	0.44	0.52	0.80								
above         bases         bases <th< td=""><td>xkdF</td><td>1328010</td><td>1328837</td><td>+</td><td>7010</td><td>4118</td><td>4725</td><td>6111</td><td>0.58</td><td>0.67</td><td>0.87</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<>	xkdF	1328010	1328837	+	7010	4118	4725	6111	0.58	0.67	0.87								
add       131000       0       000       000       000       000         state       131311       131310       0.78       0.80       0.00       <	xkaG xkdH	1328803	1329798	+	5303 4680	2637	3253	3895	0.62	0.72	0.83								
jdd       j31403       j31404       j31304       j 406       j31404       j3140       j 406       j 406       j 406       j 406       j 407       <	xkdI	1330555	1331040	+	6925	4004	4744	5708	0.50	0.68	0.83								
idd       i	xkdJ	1331053	1331493	+	3783	2146	2530	3409	0.56	0.67	0.90								
zizze         Liszis is         Juzze	xkdK	1331712	1333106	+	6850	4096	4822	6281	0.60	0.70	0.92								
add       1343079       134307       134307       134307       134307       134307       13407       1410       135       17       134       12       136       13407       13407       13407       13407       13407       13407       13407       13407       13407       13407 </td <td>xkdM xkdN</td> <td>1333113</td> <td>1333556</td> <td>+</td> <td>4927</td> <td>2585</td> <td>3113</td> <td>4530</td> <td>0.52</td> <td>0.63</td> <td>0.92</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	xkdM xkdN	1333113	1333556	+	4927	2585	3113	4530	0.52	0.63	0.92								
glade         138422         138424 </td <td>xkdO</td> <td>1333048</td> <td>1334274</td> <td>+</td> <td>2461</td> <td>1220</td> <td>1398</td> <td>1958</td> <td>0.45</td> <td>0.53</td> <td>0.79</td> <td>401</td> <td>xkdO</td> <td>1335915</td> <td>1336483</td> <td>1336199</td> <td>30.7 48.3</td> <td>19.0 0.5</td> <td>P02</td>	xkdO	1333048	1334274	+	2461	1220	1398	1958	0.45	0.53	0.79	401	xkdO	1335915	1336483	1336199	30.7 48.3	19.0 0.5	P02
shade       1339045       1339045       1339045       134905	xkdP	1338222	1338929	+	3316	1566	1864	2413	0.47	0.57	0.73								
shaff       134992       134984       1000       142       168       2440       0.40       0.50       0.81         shaff       134066       134170       1       165       176       210       0.52       0.80         shaff       134066       134707       4       206       159       0.81	xkdQ	1338945	1339922	+	2630	1331	1656	2051	0.50	0.63	0.78								
Alead         134000 </td <td>xkdR</td> <td>1339922</td> <td>1340188</td> <td>+</td> <td>3006</td> <td>1482</td> <td>1683</td> <td>2440</td> <td>0.49</td> <td>0.56</td> <td>0.81</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	xkdR	1339922	1340188	+	3006	1482	1683	2440	0.49	0.56	0.81								
shuffer         141/07         141/07         14460         14460         14460         125         101         13         130         103         0.45         0.70         103         134         140         134939         134320         134130         124         0.4         2.8         0.5         0.	xkaS xkdT	1340243	1340070	+	2667	1399	1655	2135	0.52	0.59	0.80								
shot       1342542       1344646       2       2       0.01       13       132       0.01       13       132       0.01       13       132       0.01       13       0.01       0.02       0.01       0.02       0.01       0.02       0.01       0.01       0.02       0.01       0.01       0.01       0.01       0.02       0.01       0.02       0.01       0.02       0.01       0.02       0.01       0.01       0.01       0.01       0.01       0.02       0.01       0.02       0.01       0.02       0.01       0.02       0.01       0.01       0.01       0.01       0.01       0.01       0.01       0.01       0.01       0.01       0.01       0.01       0.01       0.02       0.01 </td <td>xkdU</td> <td>1341693</td> <td>1342271</td> <td>+</td> <td>1756</td> <td>942</td> <td>1083</td> <td>1503</td> <td>0.54</td> <td>0.62</td> <td>0.86</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	xkdU	1341693	1342271	+	1756	942	1083	1503	0.54	0.62	0.86								
xdW       134407       134407       13407       134107	xkdV	1342542	1344605	+	2510	1113	1342	1968	0.44	0.54	0.79	402	xkdV	1343939	1344320	1344130	12.7 0.4	2.8 0.3	
xizd.       144494       144500 +       610       7.2       891       12.2       0.45       0.56       0.82         xild.       134601       134599 -       0.481       130       0.52       0.81       0.82       0.91         xild.       134604       1346194       -4       0.80       0.82       0.91       0.81       0.81       0.82       0.91         xild.       134604       134794       -4       120       0.83       0.86       0.81       1.03         gm/X1       134794       14790       -       1119       1119       1139       1039       103       0.86       0.81       1.03         ydd.       135056       1351477       135070       -       151       70       105       0.85       0.67       0.87         ydd.       135056       135341       135155       135143       135155       135143       1310       121       0.64         ydd.       135355       135341       135165       135147       13565       135147       13565       1314       0.00       0.64       0.74       135155       135147       13565       1314       0.01       0.64       0.74       136458	xkdW	1344617	1344946	+	2283	1061	1324	1764	0.46	0.58	0.77								
μημη         13	xkdX xanA	1344943	1345107	+	1610	1200	1528	1321	0.45	0.56	0.82								
shaft       134632       134584       900       100       040       0.8       0.8       0.8         sm/BA       134794       1       121       140       130       100       041       140       130       020         sm/BA       134794       138700       1121       141       121       140       132       140       131       141       131 <th1< td=""><td>xhlA</td><td>1345151</td><td>1345390</td><td>+</td><td>6540</td><td>4012</td><td>5356</td><td>5926</td><td>0.55</td><td>0.82</td><td>0.84</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th1<>	xhlA	1345151	1345390	+	6540	4012	5356	5926	0.55	0.82	0.84								
xhA       1346601       134794       4       412       8283       369       4.89       0.68       0.85       1.03         gwDXB       134792       1348700       -       112       149       1355       177       103       102       104       133       123       104       133       123       104       134       123       106       04       134       02       057       1057       104       104       104       104       104       104       104       104       104       104       104       1040       1051       114       040       040       047       107       1050       050       05       105       050       050       105       050       050       105       050       050       105       050       050       105       050       105       050       050       105       050       050       117       118       40       000       117       134       1357       1354707       1354707       1354707       1354707       1354707       1354707       1354707       1354707       1354707       1354707       1354707       1354707       1354707       1354707       1354717       1357077       1357	xhlB	1346325	1346588	+	5009	3009	4096	4650	0.60	0.82	0.93								
specifies         134779         13478         13479         13479         13479         134879         134979         134879         1349799         1349799         134979	xlyA	1346601	1347494	+	4216	2883	3569	4349	0.68	0.85	1.03								
synth         13472         13470         1377         171         133         117         134         1.2         100         144803         134996         134400         85         107         222         117         180         170         180 <td>spoIISB</td> <td>1347754</td> <td>1347924</td> <td>-</td> <td>751</td> <td>1057</td> <td>1010</td> <td>694</td> <td>1.40</td> <td>1.33</td> <td>0.92</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	spoIISB	1347754	1347924	-	751	1057	1010	694	1.40	1.33	0.92								
jfield       1340793       155100       101       720       6075       6744       0.80       0.67       107       107       107       101 <td>sponsa nit</td> <td>1347924</td> <td>1348070</td> <td>-</td> <td>14159</td> <td>12418</td> <td>11496</td> <td>13821</td> <td>0.88</td> <td>0.81</td> <td>0.98</td> <td>404</td> <td>pit</td> <td>1348903</td> <td>1349896</td> <td>1349400</td> <td>8.5 10.7</td> <td>20.2 31.6</td> <td></td>	sponsa nit	1347924	1348070	-	14159	12418	11496	13821	0.88	0.81	0.98	404	pit	1348903	1349896	1349400	8.5 10.7	20.2 31.6	
yhkk       133086       135202       .       740       702       702       702       0.31       0.40       0.87       0.40       ykk       135155       1351841       135155       1351841       135155       1351841       135155       1351841       135165       1351841       135165       1351841       135165       1351841       135165       1351841       135165       1351841       135165       1351841       135165       1351841       135165       1351841       135165       1351841       135165       1351841       135165       1351841       135165       1351871       13517       13517       135177       1354707       1351414       13131414       1313144<	ykaA	1349793	1350410	-	9101	7260	6075	9744	0.80	0.67	1.07		r						
bc4A       1532391       153347       149       92       107       134       849       0.85       1.05       1.05       1.15       1.353470       1354371       1354707       1354372       1.8       4.0       109         ykc7       1357541       1357572       1.362       2.03       2.03       1.04       0.78       0.87         hrrA       1337431       135892       1.16       121       0.03       0.89       0.02       0.87       0.87         dpp4       1350708       1360532       +       2.03       2.33       2.48       219       1.15       1.22       1.07       1.8       4.0       109         dpp6       13604549       1361475       +       141       4.5       158       1.12       0.95       -<	ykbA	1350686	1352002	-	1751	740	702	1531	0.43	0.40	0.87	404	ykbA	1349906	1351477	1350692	68.5 20.2	171.1 304.7	P01
$ \begin{array}{c} y_{0} (z) \\ y_{0} (z) $		1252201	1252241		1140	002	1067	1224	0.80	0.05	1 15	405	ykbA	1351555	1351834	1351695	0.9 0.0	5.4 7.1	
ykcC       135754       136725       1       171       129       137       157       0.74       0.78       0.87         htrA       135724       1368252       1       1362       262       2785       1699       199       208       1.26         grod       1358714       1368522       203       233       248       219       1.15       1.22       1.07         dppB       1360532       203       233       248       219       1.15       1.22       1.07         dppC       136448       1364443       217       277       234       240       1.00       1.03       1.13         dppC       1365448       1365454       365       375       367       38       471       109       9.06       1.49       9.27       1.01       1.08         ykfD       1366149       130729       235       234       626       0.91       1.01       1.08       2.27       2.27       2.27       2.27       2.27       2.26       2.27       2.28       2.23       2.28       2.21       2.27       2.22       2.27       2.28       2.27       2.28       2.27       2.28       2.27       2.27       2.	ykcA vkcB	1353592	13555742	+	222	186	1007	235	0.89	0.93	1.15	407	vkcB	1354377	1354707	1354542	1.7 1.8	4.0 10.9	
hrvk       1357243       138892       -       1362       2228       2788       1699       1.0       3.2       1.6       124       1.0       9.0	ykcC	1355754	1356725	+	177	129	137	157	0.74	0.78	0.87								
prof       1358761       139879       +       1310       1223       1166       1214       0.93       0.89       0.92         dppA       1350781       1360324       203       233       248       210       1.15       122       1.07         dppB       1360549       1361475       +       141       145       158       144       1.03       1.12       0.95         dppC       1361481       1362448       1365107       +       205       358       471       0.99       0.96       1.29         dppE       1363448       1365107       +       236       236       282       1.01       1.08         ydfA       1365448       1366129       1367249       +       263       240       266       286       0.97       1.01         ydfA       1368149       1369132       +       386       802       318       0.62       0.97       0.50         ydgA       1370189       +       453       250       286       411       0.75       0.63       1.01         mp       1370189       1371180       -       523       266       707       0.56       1.01         ydk	htrA	1357243	1358592	-	1362	2629	2785	1699	1.99	2.08	1.26								
appp       1359/08       100332       +       2.03       2.33       2.49       2.19       1.13       1.22       0.95         dppD       1360481       1362443       +       2.17       2.17       2.24       2.46       1.00       1.03       1.13         dppD       1363488       1365107       +       2.05       197       2.13       2.24       0.96       1.04       1.09         ykfB       1366152       +       3.68       3.83       3.82       1.01       1.05       1.04         ykfB       1366152       +       3.68       3.70       3.77       1.00       0.97       1.01       1.08         ykfB       1360180       1370229       -       7.873       10.06       0.447       1.28       1.33       1.08         ykgA       1370389       1371180       -       6.02       3.18       0.62       0.97       0.50         ykkA       1373420       1373326       +       7.55       2.53       2.66       0.91       1.01       1.08         ykkA       137342       1374473       +       316       2.44       0.50       0.37       0.95       1.27         ykkA	proG	1358761	1359579	+	1310	1223	1166	1214	0.93	0.89	0.92								
uppp C       1361481       1362481       217       217       224       246       1.00       1.13         dppD       1362481       1362455       +       375       367       358       471       0.99       0.96       1.29         ykfA       1365481       356152       +       364       388       385       382       1.01       1.05       1.04         ykfA       1366143       1366152       +       364       388       385       382       1.01       1.05       1.04         ykfC       1367246       1368149       1360132       +       395       423       456       447       1.17       1.15       1.12         ykgB       1361010       1371888       +       4653       250       2805       4641       0.57       0.63       1.01       1.08         ykgA       1371340       137188       +       4553       250       2805       4641       0.57       0.53       1.01       1.01       1.08       1.01       1.01       1.08       1.01       1.01       1.01       1.01       1.01       1.01       1.01       1.01       1.01       1.01       1.01       1.01       1.01	appA dnnB	1359708	1361475	+	203	255	248	134	1.15	1.22	0.95								
dppD       1362448       1363455       +       367       375       367       378       471       0.99       0.96       1.29         dppD       1363488       1365107       +       025       197       213       224       0.96       1.04       1.09         ykfA       1365448       1365129       +       0.68       382       0.10       1.05       1.04         ykfA       1365448       1367249       +       0.38       423       240       266       286       0.91       1.01       1.08         ykfA       1370180       1370229       -       7873       10060       1440       4874       1.28       1.33       1.08         ykkA       1371340       1371858       4633       2550       250       4641       0.57       0.63       1.01         ykkA       1373373       1373737       160       137       148       115       0.86       0.92       0.52         ykkA       1373374       13747374       316       284       270       316       0.90       0.86       1.09       0.47       0.47       0.48       0.43       0.43       0.44       0.43       0.49       0.49	dppC	1361481	1362443	+	217	217	224	246	1.00	1.03	1.13								
dppE       1363458       1365107       +       205       197       213       224       0.96       1.04       1.09         ykfA       1366149       1367246       1367246       1368136       +       368       353       352       1.01       1.05       1.04       1.05         ykfD       1366149       1367246       1368136       +       368       370       357       377       1.00       0.97       1.01         ykgB       1369180       137029       -       7873       1006       0440       8474       1.28       1.33       1.08         ykgA       1370389       137180       -       623       388       602       318       0.62       0.97       0.50         ykkA       1373373       1373297       -       160       137       148       115       0.86       0.92       0.72         ykkA       1373453       137592       +       195       622       503       215       2.33       2.91       1.09         ykkA       1374561       1376478       +       330       355       405       0.91       0.82       0.93         ykkC       1375821       137600	dppD	1362448	1363455	+	375	367	358	471	0.99	0.96	1.29								
ykfa       1365448       1366122       +       368       385       382       1.01       1.03       1.04         ykfa       1366149       1367246       1368136       +       368       370       357       377       1.00       0.97       1.01         ykfa       1368149       1369132       +       368       370       357       377       1.00       0.97       1.01         ykfa       1369132       +       368       370       357       377       1.00       0.97       1.01         ykga       1370389       1371180       -       623       388       602       318       0.62       0.97       0.50         ykka       1371340       1371858       +       463       2550       266       707       0.36       0.37       0.95         ykka       1373373       1373737       -       160       137       148       115       0.86       0.92       0.72         ykka       137502       137453       316       244       427       280       2.03       1.09         ykka       137562       137601       137474       433       396       355       455       0.1 <td>dppE</td> <td>1363458</td> <td>1365107</td> <td>+</td> <td>205</td> <td>197</td> <td>213</td> <td>224</td> <td>0.96</td> <td>1.04</td> <td>1.09</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	dppE	1363458	1365107	+	205	197	213	224	0.96	1.04	1.09								
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	ykfA vkfB	1365448	1366152	+	364 263	368 240	385 266	382 286	1.01	1.05	1.04								
ykp       1368149       136912 +       395       423       456       447       1.07       1.15       1.12         ykg       1370209 -       7873       1006       1044       8474       1.28       1.33       1.08         ykg       1370389       1371180       -       623       388       602       318       1.02       -<	ykfC	1367246	1368136	+	368	370	357	377	1.00	0.97	1.00								
ykgA       1369180       1370229       -       7873       10060       1040       8474       1.28       1.33       1.08         ykgA       1370389       1371180       -       623       388       602       218       0.62       0.97       0.50         ykhA       1371340       1371185       +       4653       2550       266       707       0.36       0.37       0.95         ykHA       1373373       1373597       -       160       137       148       115       0.86       0.92       0.72         ykKA       137455       1375092       +       195       622       563       215       3.23       2.91       1.09         ykKC       1375082       137604       +       433       396       355       405       0.97       0.93         ykKC       137654       1377692       137899       +       413       396       355       405       0.91       0.82       0.93         prod       137641       1377802       137899       +       144       855       0.71       0.60       0.93         prod       137891       1380781       -       1414       1439	ykfD	1368149	1369132	+	395	423	456	447	1.07	1.15	1.12								
ykgA       1370389       1371180       -       623       338       602       318       0.52       0.97       0.50         ykhA       1371340       1371858       +       4653       2550       206       707       0.63       1.01         yktH       1373373       1373597       -       160       137       148       115       0.86       0.92       0.72         ykkH       1373472       1374473       +       316       284       270       316       0.90       0.86       1.00         ykkA       137455       1375092       +       195       622       63       2.15       3.23       2.91       1.00         ykkC       137582       137600       +       219       445       427       280       2.03       1.95       1.27         ykkD       1376161       137647       +       433       396       355       405       0.91       0.82       0.93         purU       137624       137879       +       312       203       2152       2900       0.71       0.69       0.93         proA       1380124       1380129       137802       137802       137809       4	ykgB	1369180	1370229	-	7873	10060	10440	8474	1.28	1.33	1.08								
Jahm 137207 137329 + 752 253 266 707 0.36 0.37 0.95 ykzH 1373373 1373597 - 160 137 148 115 0.86 0.92 0.72 ykjA 1373742 1374473 + 316 284 270 316 0.90 0.86 1.00 ykkA 1375652 1375602 + 195 622 563 215 3.23 2.91 1.09 ykzB 137562 1375600 + 219 445 427 280 2.03 1.95 1.27 ykzC 1375823 1376161 + 830 714 644 805 0.86 0.78 0.97 ykzD 1376161 1376478 + 433 396 355 405 0.91 0.82 0.93 purU 1376549 1377451 + 3570 267 1 2504 3192 0.75 0.70 0.90 proB 1377802 1378899 + 3125 2203 2152 2900 0.71 0.69 0.93 proA 1378811 1380128 1380709 + 2144 1439 1559 185 0.67 0.72 0.86 ykaA 1380284 13802709 + 2144 1439 1559 185 0.67 0.72 0.86 ykaA 1380284 13802709 + 2144 1439 1559 185 0.67 0.72 0.86 ykaA 1380284 138029 1 381183 - 1422 1210 1337 1268 0.85 0.94 0.89 ykzA 138126 1317457 + 1772 1584 2478 957 0.89 1.40 0.54 411 ykzA 1381271 1381414 1381343 3.9 1.2 2.2 1.5 ykaA 1380284 1380284 1380289 1 38263 - 162 153 155 182 0.94 0.89 ykzA 138126 131736 + 1772 1584 2478 957 0.89 1.40 0.54 411 ykzA 1381271 1381414 1381343 3.9 1.2 2.2 1.5 ykaA 138264 138266 1384914 - 361 531 593 355 1.47 1.63 0.97 ispA 138528 1386667 138649 132668 1382689 1382618 4.6 5.2 0.1 -0.3 metE 1382626 1384914 - 361 531 593 355 1.47 1.63 0.97 ispA 138530 1386289 - 164 166 168 155 1.01 1.02 0.95 kt3 1386212 1387345 + 8025 1109 11385 8546 1.38 1.42 1.06 xu xu x	ykgA vkh4	1370389	1371180	-	623 4653	388	602 2805	318	0.62	0.97	0.50								
ykH13733731373597-1601371481150.860.920.72ykjA13737421374473+3162842703160.900.861.00ykkA13754521375402137540213754021375402137540213754021375402137540213754021375402137614ykkB13750821375002+1956225632153.232.911.091.27ykkD13761611376478+4333963554050.910.820.93proB13778021378899+312520202.710.690.93proB137780213780911380158+48123389337445510.700.700.95410proA137984313801221379938.59.11.30.6ykAA13802841380709+21441439155918350.670.720.86411ykaA1381211138141413813433.91.22.21.5ykaA13802841380709+214414391551820.940.54411ykaA1381271138141413813433.91.22.21.5ykaA13812831386283-1621531551820.940.961.3guaD1381830138628138282713865121387354.	hmp	1372097	1373296	+	755	2550	266	707	0.36	0.37	0.95								
ykjA       1373742       1374473       +       316       284       270       316       0.90       0.86       1.00         ykkA       1374565       1375092       +       195       622       563       215       3.23       2.91       1.09         ykkB       1375082       1375000       +       219       445       427       280       2.03       1.95       1.27         ykkC       1375823       1376161       136074       +       433       396       355       405       0.91       0.82       0.93         purU       1376549       1377451       +       3570       2671       2504       3192       0.75       0.70       0.90         proA       137802       137809       +       3125       2203       2152       2900       0.71       0.69       0.93         yknA       1380284       1380709       +       4412       389       3374       4551       0.70       0.92       410       proA       1379843       1380122       1379983       8.5       9.1       1.3       0.6         yknA       1380284       1380170       1381183       -       1421       141       ykzA	ykzH	1373373	1373597	-	160	137	148	115	0.86	0.92	0.72								
ykka 1374565 137502 + 195 622 563 215 3.23 2.91 1.09 ykkB 1375082 137560 + 219 445 427 280 2.03 1.95 1.27 ykkC 1375823 1376161 + 830 714 644 805 0.86 0.78 0.97 ykkD 1376161 1376478 + 433 396 355 405 0.91 0.82 0.93 purU 1376549 1377851 + 3570 2671 2504 3192 0.75 0.70 0.90 proB 1377802 1378899 + 3125 2203 2152 2900 0.71 0.69 0.93 proA 1378911 1380158 + 4812 3389 3374 4551 0.70 0.70 0.95 410 proA 1379843 1380122 1379983 8.5 9.1 1.3 0.6 yklA 1380284 1380709 + 2144 1439 1559 1835 0.67 0.72 0.86 ykmA 1380740 1381183 - 1422 1210 1337 1268 0.85 0.94 0.89 ykzA 1381326 1381736 + 1772 1584 2478 957 0.89 1.40 0.54 411 ykzA 1381271 1381414 1381343 3.9 1.2 2.2 1.5 guaD 1381983 1382453 - 162 153 155 182 0.94 0.96 1.13 metE 1382626 1384914 - 361 531 593 355 1.47 1.63 0.97 ispA 138530 1386289 - 164 166 168 155 1.01 1.02 0.95 transmete 1382636 1384914 - 361 531 593 355 1.47 1.63 0.97 ykoB 1385376 1388140 - 371 326 347 373 0.89 0.94 1.01 ykoD 1388287 1389759 - 203 170 1818 234 0.84 0.89 1.14 415 ykoD 1389227 1389591 1389409 2.4 1.1 3.0 26.1 P04	ykjA	1373742	1374473	+	316	284	270	316	0.90	0.86	1.00								
jkkD       137300       11       14       15       12       14       15       15       12       15       0.70       0.90       0.82       0.93       0.90	ykkA wkkP	1374565	1375092	+	195	622	563	215	3.23	2.91	1.09								
$ ykkD = 1376161 1376478 + 433 396 355 405 0.91 0.82 0.93 \\ purU = 1376549 1377451 + 3570 2671 2504 3192 0.75 0.70 0.90 \\ proB = 1377802 1378899 + 3125 2203 2152 2900 0.71 0.69 0.93 \\ proA = 1378911 1380158 + 4812 3389 3374 4551 0.70 0.70 0.95 410 proA 1379843 1380122 1379983 8.5 9.1 1.3 0.6 \\ yklA = 1380284 1380709 + 2144 1439 1559 1835 0.67 0.72 0.86 \\ ykmA = 1380284 1380709 + 2144 1439 1559 1835 0.67 0.72 0.86 \\ ykmA = 1380284 1380709 + 2142 1210 1337 1268 0.85 0.94 0.89 \\ ykzA = 138126 1381736 + 1772 1584 2478 957 0.89 1.40 0.54 411 ykzA = 1381271 1381414 1381343 3.9 1.2 2.2 1.5 \\ guaD = 1381983 1382453 - 162 153 155 182 0.94 0.96 1.13 \\ metE = 1382626 1384914 - 361 531 593 355 1.47 1.63 0.97 \\ ispA = 1385310 1386289 - 164 166 168 155 1.01 1.02 0.95 \\ r = 1138128 1386667 1386443 \frac{33.4}{33.4} \frac{3.4}{3.5} \frac{7.5}{0.5} -0.4 \\ ykoB = 1385736 1388140 - 371 326 347 373 0.89 0.94 1.01 \\ ykoD = 1388287 1389759 - 203 170 181 224 0.84 0.89 0.41 14 415 ykoD = 1389227 1389591 1389409 2.4 1.1 3.0 26.1 P04 \\ ykoE = 1389746 1390345 - 212 208 226 229 0.98 1.07 1.08 \\ 0.99 = 0.98 0.99 0.108 0.$	ykkC	1375823	1376161	+	830	714	427 644	805	0.86	0.78	0.97								
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	ykkD	1376161	1376478	+	433	396	355	405	0.91	0.82	0.93								
proB13778021378899+31252203215229000.710.690.93proA13789111380158+48123389337445510.700.700.95410proA1379843138012213799838.59.11.30.6yklA13802841380709+21441439155918350.670.720.860.890.890.890.890.890.890.890.890.890.890.818130.60.818130.60.818130.60.818130.60.818130.60.818130.60.818130.60.818130.60.818130.60.890.818130.828180.860.880.890.890.8181830.8181830.830.830.8	purU	1376549	1377451	+	3570	2671	2504	3192	0.75	0.70	0.90								
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	proB	1377802	1378899	+	3125	2203	2152	2900	0.71	0.69	0.93	/10	pro A	1370842	1380122	1370092	85 01	13 06	
$ykmA = 1380740 \ 1381183 = 1422 \ 1210 \ 1337 \ 1268 \ 0.94 \ 0.89 \ 1.40 \ 0.54 \ 411 \ ykzA = 1381271 \ 1381414 \ 1381343 \ 3.9 \ 1.2 \ 2.2 \ 1.5 \ guaD = 1381983 \ 1382453 = 162 \ 153 \ 155 \ 182 \ 0.94 \ 0.96 \ 1.13 \ 412 \ Inter = 1382546 \ 1382689 \ 1382618 \ 4.6 \ 5.2 \ 0.1 \ -0.3 \ end{pmatrix}$	vklA	1378911	1380709	++	2144	5589 1439	1559	4551	0.70	0.70	0.95	410	pioA	13/9843	1300122	1319983	<u> </u>	1.5 0.0	
ykzA       1381326       1381326       1381326       1381326       1381326       1381326       1381326       1381326       1381326       1381326       1381326       1381326       1381326       1381326       138123       3.9       1.2       2.2       1.5         guaD       1381983       1382453       -       162       153       155       182       0.94       0.96       1.13       -       1381241       1381343       3.9       1.2       2.2       1.5         metE       1382626       1384914       -       361       531       593       355       1.47       1.63       0.97       -       138126       13812618       1382689       1382618       4.6       5.2       0.1       -0.3       -       -       -       -       -       -       -       -       -       -       -       -       -       -	ykmA	1380740	1381183	-	1422	1210	1337	1268	0.85	0.94	0.89								
guaD       1381983       1382453       -       162       153       155       182       0.94       0.96       1.13         metE       1382626       1384914       -       361       531       593       355       1.47       1.63       0.97         ispA       1385330       1386289       -       164       166       168       155       1.01       1.02       0.95         ykoB       138512       1387345       +       8025       1109       11385       8546       1.38       1.42       1.06         ykoC       1387376       1388140       -       371       326       347       373       0.89       0.44       1.01       1.02       0.95         ykoD       1387376       1388140       -       371       326       347       373       0.89       0.44       1.01       1.02       0.95         ykoD       1387376       1388140       -       371       326       347       373       0.89       0.44       1.01       1.01       1.02       0.84       0.89       1.14       415       ykoD       1389247       1389591       1389409       2.4       1.1       3.0       26.1 <td< td=""><td>ykzA</td><td>1381326</td><td>1381736</td><td>+</td><td>1772</td><td>1584</td><td>2478</td><td>957</td><td>0.89</td><td>1.40</td><td>0.54</td><td>411</td><td>ykzA</td><td>1381271</td><td>1381414</td><td>1381343</td><td>3.9 1.2</td><td>2.2 1.5</td><td></td></td<>	ykzA	1381326	1381736	+	1772	1584	2478	957	0.89	1.40	0.54	411	ykzA	1381271	1381414	1381343	3.9 1.2	2.2 1.5	
metE       1382626       1384914       -       361       531       593       355       1.47       1.63       0.97         ispA       1385330       1386289       -       164       166       168       155       1.01       1.02       0.95         ykoB       1385512       1387345       +       8025       1109       11385       8546       1.38       1.42       1.06         ykoB       1386512       1387345       +       8025       1109       11385       8546       1.38       1.42       1.06         ykoD       1388287       1389759       2.03       170       181       234       0.89       0.94       1.01         ykoE       1389746       1390345       2       203       170       181       234       0.84       0.89       1.14       415       ykoD       1389297       1389591       1389409       2.4       1.1       3.0       26.1       P04	guaD	1381983	1382453	-	162	153	155	182	0.94	0.96	1.13		<b>T</b> .	120251	1000 505	1002	10 -	0.1	
	metF	1382626	1384914	-	361	531	503	355	1 47	1.63	0 97	412	Inter	1582546	1382689	1.582618	4.6 5.2	0.1 -0.3	
413       Inter       1386512       1386667       1386443       33.4       34.8       7.5       -0.4         ykoB       1386512       1387345       +       8025       11099       11385       8546       1.38       1.42       1.06         ykoD       1388287       1389759       -       203       170       181       234       0.89       0.94       1.01         ykoE       1389746       1390345       -       212       208       226       229       0.98       1.07       1.08	ispA	1385330	1386289	-	164	166	168	155	1.47	1.03	0.97								
ykoB       1386512       1387345       +       8025       1109       11385       8546       1.38       1.42       1.06         ykoC       1387376       1388140       -       371       326       347       373       0.89       0.94       1.01         ykoD       1388287       1389759       -       203       170       181       234       0.84       0.89       1.14       415       ykoD       1389227       1389591       1389409       2.4       1.1       3.0       26.1       P04         ykoE       1389746       1390345       -       212       208       226       229       0.98       1.07       1.08												413	Inter	1386218	1386667	1386443	33.4 34.8	7.5 -0.4	
ykoC       138/3/6       1388140       -       371       326       347       373       0.89       0.94       1.01         ykoD       1388287       1389759       -       203       170       181       234       0.84       0.89       1.14       415       ykoD       1389227       1389591       1389409       2.4       1.1       3.0       26.1       P04         ykoE       1389746       1390345       -       212       208       226       229       0.98       1.07       1.08	ykoB	1386512	1387345	+	8025	11099	11385	8546	1.38	1.42	1.06								
ykoE 1389746 1390345 - 212 208 226 229 0.98 1.07 1.08	ykoC ykoD	1387376	1388140	-	371	326	347	373	0.89	0.94	1.01	115	vkoD	1380227	1380501	1380/00	24 11	30 261	P04
	ykoE	1389746	1390345	-	203	208	226	229	0.94	1.07	1.08	415	JROD	1307227	1507571		2.7 1.1	5.0 20.1	1.04

Supplen	nentary Tab	de S1. Su	nma	ry of trai	nscriptor	me and ( Trans	ChAP-ch	ip analyse e analysic	es (contin	ued).				C	hAP-chin (	malveie				
	gene			Sim	nal intere	ity of RN	A <sup>a</sup>	e anaiysis Evr	ression ra	tio <sup>b</sup>				U	њы -стпра		Binding	intensity "	2	
	-44		pun	Jage	iai incris		A		∆ abh		PBR	ORF	-44			At	orB	Al	bh	Profile
name	start	ena	stra	wild	∆abrB	$\Delta abh$ $\Delta abrB$	$\Delta abh$	∆ abrB/ wild	$\Delta abrB/$	∆ abh / wild	ID	OF Intergenic	start	ena	center	wild	Aabh	wild	AahrB	ID
						2 abrb		wiki	wild	wiici		inteligente				-type	2 uon	-type	2 uorb	
ykoF	1390347	1390949	-	275	246	244	316	0.90	0.89	1.15	417	-l-C	1201046	1201507	1201222	47.0	22.6	40.2	2.4	002
ykoG ykoH	1391200	1391940	+	585 753	044 852	000 866	042 856	1.11	1.13	1.08	417	укос	1391046	1391397	1391322	47.0	23.0	40.5	2.4	P02
ykoI ykoI	1393311	1393991	+	466	542	550	531	1.20	1.21	1.12										
ykoJ	1394083	1394595	+	916	1100	1202	908	1.21	1.32	0.98										
ykzD	1394678	1394815	+	98	110	104	102	1.15	1.07	1.05										
ykoK	1395321	1396676	+	3834	4846	5799	4189	1.27	1.51	1.09										
INFA	1390/19	1397051	-	237	255	202	229	1.08	1.11	0.97	/18	Inter	1306006	1307275	1307136	82	13.8	15	-0.3	
vkzB	1397246	1397401	+	234	231	249	236	0.99	1.07	1.01	410	miler	1370770	1571215	157/150	0.2	15.0	1.5	-0.5	
ykoL	1397489	1397671	+	132	139	135	120	1.05	1.02	0.90										
ykoM	1397804	1398268	+	3570	5680	6940	4196	1.59	1.93	1.17										
ykoN	1398283	1399404	-	110	110	110	123	1.00	1.00	1.12										
ykoP vkoO	1399496	1400047	+	158	156	141	160	0.98	0.89	1.01										
ykoQ ykoS	1401080	1400887	+	192	199	212	206	1.04	1 11	1.02	419	vkoS	1401569	1401695	1401632	1.0	03	0.5	42	
ykoT	1402787	1403800	+	222	231	256	237	1.04	1.15	1.07	,	Juob	1101203	1101000	1101052	1.0	0.5	0.0		
ligD	1403826	1405661	-	241	260	268	259	1.08	1.11	1.07	420	ligD	1405360	1405656	1405508	13.3	1.3	7.6	1.3	
ykoV	1405665	1406600	-	217	202	219	213	0.93	1.01	0.97							20.0			
ykoW	1406637	1408886	-	421	280	266	490	0.68	0.64	1.14	421	ykoW	1407400	1407832	1407616	22.7	20.9	7.7	-0.3	
vkoX	1409220	1409885	+	2691	2678	2592	2712	1.00	0.97	1.00	422	YKO W	1407978	1406274	1408120	11.1	0.0	1.1	-0.5	
ykoY	1409962	1410936	+	583	592	559	552	1.02	0.96	0.95										
sigI	1411200	1411955	$^+$	1347	999	1000	1461	0.74	0.74	1.08										
ykrI	1411952	1413097	+	1752	1706	1849	1843	0.98	1.06	1.05										
sspD	1413108	1413302	-	449	828	1103	400	1.82	2.42	0.88										
ykrK vkrL	1413433	1414134	+	10561	10783	11441	11538	1.02	1.09	1.05										
ykrM	1415375	1416724	+	1547	1035	910	1338	0.67	0.59	0.87										
ykzE	1417027	1417203	+	226	371	493	209	1.57	2.08	0.89										
ykrP	1417246	1418268	-	198	200	224	204	1.01	1.13	1.03										
kinE	1418521	1420737	+	302	903	971	323	2.97	3.22	1.06										
mtnA	1420734	1421231	-	2859	6048	7073	2039	2.11	2.49	0.72										
mtnK	1422549	1423748	-	2801	5334	6337	1956	1.90	2.27	0.70	426	mtnK	1422768	1422945	1422857	5.7	1.6	4.7	0.6	
ykrU	1424075	1424854	-	510	545	703	459	1.07	1.38	0.90										
ykrV	1424949	1426145	+	628	643	769	533	1.02	1.23	0.85										
mtnW	1426342	142/586	+	418	418	462	375	1.00	1.11	0.90										
mtnA mtnB	1427383	1428230	+	1164	1493	1887	829	1.13	1.63	0.70										
ykrZ	1428892	1429428	+	744	987	1200	584	1.32	1.60	0.78										
ykvA	1429469	1429789	-	1924	2796	2722	1721	1.45	1.41	0.89										
										0.00	427	Inter	1429772	1430136	1429954	19.0	18.8	9.7	1.7	
spo0E	1429992	1430249	+	276	2330	2098	681 313	3.11	2.77	0.88	128	000	1430214	1/130578	1/13/03/06	1/1 0	27	11.8	26	
eug kinD	1430333	1432314	-	1172	1703	1565	980	1.92	1.33	0.84	420	eag	1430214	1450578	1450590	14.7	2.1	11.0	2.0	
ykvE	1432507	1432944	+	3935	4279	3482	2719	1.09	0.88	0.69										
motB	1432984	1433769	-	2224	3135	2799	2392	1.42	1.25	1.06										
motA	1433741	1434553	-	1770	2707	2249	2179	1.56	1.28	1.22										
clnF	1/13/1036	1/137035		1187	1315	1653	2466	1 30	1.62	1.92	429	Inter	1434566	1434828	1434697	13.0	8.0	1.1	0.6	
vkvI	1434930	1437033	+	229	246	227	2400	1.07	0.99	1.92										
ykvJ	1438756	1439415	+	1693	816	798	1291	0.51	0.49	0.76										
ykvK	1439408	1439857	+	2384	1097	1162	1770	0.48	0.50	0.75										
ykvL	1439850	1440581	+	1944	866	878	1479	0.46	0.46	0.77										
ykvM vkvN	1440599	1441096	+	528	1495	1527	2676	0.45	0.46	0.81	421	abaN	1441672	1442225	1441000	52.2	01.9	10.6	15	<b>D</b> 02
vkvO	1442180	1442926	+	225	188	207	223	0.74	0.84	0.85	431	vkvO	1441072	1442920	1441999	6.3	7.1	3.7	0.9	102
ykvP	1443407	1444606	+	136	122	123	116	0.90	0.90	0.85	433	ykvP	1444222	1444756	1444489	36.3	6.7	10.5	-1.0	
ykvQ	1444946	1445644	+	128	129	124	125	1.03	0.98	0.99	434	ykvQ	1444987	1445657	1445322	42.8	56.1	14.1	-0.5	
ykvR	1446559	1446849	+	295	228	240	278	0.78	0.82	0.94										
	1446070	1447401		1072	1252	1277	1216	1.27	1.20	1.12	435	Inter	1446772	1447118	1446945	12.0	17.6	7.1	-0.7	
укиз	14409/0	144/401	-	1072	1352	13//	1210	1.27	1.29	1.12	436	Inter	1447350	1447935	1447643	49.4	40.3	24.4	3.1	P02
ykvT	1447814	1448440	+	119	101	100	101	0.85	0.84	0.85	450		1.47550		1.17.045				5.1	102
ykvU	1448558	1449895	+	218	222	235	245	1.02	1.08	1.13										
ykvV	1449946	1450443	+	397	347	335	387	0.86	0.84	0.95										
ykv W	1450679	1452592	+	361	370	412	346	1.03	1.14	0.94										
ykvY vkv7	1452999	1454090	+	5483 3030	5491 2309	5572 2706	5/02 3287	1.00	1.02	1.04										
glcT	1455400	1456257	+	2443	1529	1684	2557	0.63	0.70	1.05										
ptsG	1456496	1458595	+	15823	10215	8484	16054	0.65	0.54	1.02										
ptsH	1458693	1458959	+	22005	18851	18540	21590	0.86	0.84	0.98										

Supplen	nentary Tab	de S1. Su	mma	ry of tra	nscripto	me and (	ChAP-ch	ip analyse	es (contin	ued).				CI	A D ohin (	nolveic			
	gene			Sim	nal intene	ity of PN		e analysis Evo	ression ra	tio b	·			- Cl	AI -Chip a	Bindi	na inten	city <sup>C</sup>	
		,	pu	JBI	nai incris	ity of Kiv	A	LAP	$\Delta abh$	uo	PBR	ORF				AbrB	ing interr	Abh	Profile
name	start	end	stra	wild	∆abrB	∆abh ∆abrB	∆abh	∆ <i>abrB/</i> wild	∆abrB/ wild	⊿ <i>abh /</i> wild	ID	or Intergenic	start	end	center	wild -type ∆abi	wi -ty	$d \Delta abrB$	ID
ptsI	1458959	1460671	+	23431	21910	21855	24855	0.94	0.93	1.06									
splA	1460762	1461001	+	1531	1240	1312	1367	0.81	0.85	0.89									
splB	1461079	1462107	+	989	756	820	901	0.75	0.82	0.90									
ykwB mcnC	1462280	1462801	-	112	125	142	120	1.11	1.26	1.07									
vkwC	1465037	1465903	+	7295	6075	6831	6428	0.84	0.94	0.88									
ykwD	1465942	1466715	-	576	568	682	515	0.98	1.18	0.88	438	Inter	1466679	1467349	1467014	44.6 56	2 2	0.5	P02
vkuA	1467109	1469166	+	1706	5288	5434	1301	3.14	3.24	0.77	450	mer	1400077	1407547	1407014	44.0 50.	-	0.5	102
kinA	1469330	1471150	+	447	1262	1315	501	2.87	3.00	1.10									
patA	1471161	1472339	- 1	4569	3475	3713	4501	0.76	0.81	0.99									
cheV	1472906	1473817	+	1246	1713	1455	1430	1.39	1.17	1.13									
ykyB vkuC	1473861	1474325	-	2154	2193	2021	1613	1.27	1.17	0.91									
ykuC ykuD	1475819	1476313	-	2134	338	2000	341	1.00	1 15	1.00									
vkuE	1476370	1477233	-	253	275	257	273	1.11	1.04	1.08									
ykuF	1477376	1478140	+	460	324	335	464	0.70	0.73	1.00									
ykuG	1478441	1480723	+	3074	1298	1527	2690	0.42	0.50	0.87	440	ykuG	1478291	1478671	1478481	13.8 7.2	2	5.2 13.6	
vkuH	1480853	1481401	+	1130	980	925	1184	0.86	0.81	1 04	441	ykuG	14/9395	14/9997	14/9696	<u>- 34.0</u> 13.4		0.0 81.6	
vkuI	1481554	1482777	+	1211	1389	1398	1189	1.15	1.16	0.98									
ykuJ	1483423	1483662	+	9007	7835	7281	9530	0.87	0.81	1.06									
ykuK	1483772	1484290	+	8507	7830	6971	8786	0.92	0.82	1.03									
ykzF	1484424	1484621	+	9120	9256	8188	8889	1.02	0.90	0.98									
ykuL	1484759	1485202	+	2935	1030	1674	2670	0.35	0.56	0.91									
ccpC wkuN	1485351	1486232	+	4333	2051	2963	4002 5205	0.47	0.68	0.92									
vkuO	1486810	1480820	+	4989	11487	12615	5117	2.51	2.40	1.16									
ykuP	1487719	1488255	+	4369	10930	11510	4462	2.53	2.66	1.03									
ykuQ	1488280	1488990	+	15452	14596	14824	15434	0.94	0.96	1.00	444	ykuQ	1488337	1489075	1488706	47.3 74.	4 4	<b>2.2</b> 6.9	
ykuR	1489060	1490184	+	3918	3502	3823	4183	0.90	0.98	1.07									
vkuS	1490246	1490491	+	3990	4249	4815	4118	1.07	1.21	1.03	445	Inter	1490105	1490333	1490219	8.2 5.:	)	1.2 0.2	
yku5 vkuT	1490528	1491331	-	860	498	532	549	0.61	0.66	0.65									
<i></i>											446	Inter	1491193	1491829	1491511	54.8 63.	4 14	4.7 0.8	
ykuU	1491568	1492110	+	896	9689	11489	1051	11.17	13.32	1.16									
ykuV	1492182	1492643	+	659	6529	7741	802	10.09	12.03	1.21	4.47	<b>T</b> .	1.4000000	1.402276	1 40 2000	71.0 (7		C 1 CO 4	DOI
rok	1402004	1402660		5211	4600	1617	4670	0.87	0.88	0.88	447	Inter	1492383	1493376	1492880	/1.3 67.	4 3	5.1 58.4	P01
vknT	1493710	1494675	-	120	4000 99	102	104	0.87	0.85	0.87									
mobA	1494812	1495411	+	3347	2565	2451	3311	0.76	0.73	0.99									
moeB	1495462	1496481	+	2437	2085	1922	2521	0.86	0.79	1.03									
moeA	1496499	1497791	+	3313	2982	3001	3451	0.90	0.91	1.04									
mobB	1497752	1498273	+	3453	2909	3058	3408	0.84	0.89	0.99									
moaD	1498273	1498/40	+	1/091	1315	0280	1644	0.90	0.89	1.09									
vknU	1499196	1500953	+	194	228	249	193	1.17	1.28	0.99	448	vknU	1499506	1500329	1499918	45.6 15.1	4	3.3 98.9	
yknV	1500965	1502779	+	212	220	235	219	1.04	1.11	1.04		5							
yknW	1502889	1503584	+	4027	15157	17250	6150	3.76	4.32	1.54	449	yknW	1502685	1503117	1502901	17.7 9.8	3	6.3 10.0	
yknX	1503589	1504722	+	3888	13306	15596	5605	3.42	4.02	1.44									
yknY vkn7	1504723	1505415	+	3241	13975	16877	5310	4.35	5.27	1.66									
ynn2 fruR	1506885	1507640	+	2558	12393	1675	2592	0.51	0.67	1.45									
fruK	1507637	1508548	+	1382	511	693	1450	0.37	0.50	1.05									
fruA	1508563	1510470	+	2079	855	1091	2182	0.41	0.52	1.05									
sipT	1510615	1511196	+	1143	1267	1162	1414	1.11	1.03	1.24									
ykoA	1511230	1511499	-	920	983	815	946	1.06	0.88	1.03									
ykpA vkpP	1511680	1513302	+	8509	/324	0548	8393	0.86	0.77	0.99									
укрв ampS	1515559	1514270	-	2479 4689	5112	6369	5810	1.10	1.37	1.24	452	ampS	1514976	1515390	1515183	7.2 30	) 1	2.7 16.2	
ykpC	1515646	1515780	- (	1141	1497	1863	1772	1.38	1.69	1.55	.52				2.22.05	5.		. 10.2	
mreBH	1515881	1516888	-	1317	1801	2302	2284	1.44	1.84	1.71	453	mreBH	1516013	1516513	1516263	15.0 10.9	2	.3.4 49.8	
abh	1517172	1517450	+	15057	16595	28	94	1.10	0.00	0.01									
kinC	1517640	1518926	+	2432	2614	7215	5040	1.08	2.95	2.08									
ykqA vkaP	1518942	1519775	+	3502	3917	9189 7095	6570	1.12	2.62	1.88									
укцВ adeC	1519858	1520503	++	3040	5420 1843	1674	4909 1874	1.08	0.55	1.58									
vkqC	1522425	1524092	-	9407	10251	9527	9827	1.09	1.01	1.05									
ykzG	1524098	1524307	-	6117	6883	5748	6037	1.12	0.93	0.98									
ykrA	1524693	1525466	+	4904	4281	4252	4943	0.88	0.87	1.01									
def_1	1525502	1526056	i -	3328	2970	2556	3385	0.90	0.77	1.02		<b>T</b> .	1 50 55 -	100	100	0000			
n len A	1526502	1527200		1242	2202	1774	1416	1.60	1.20	1.05	455	Inter	1526281	1526696	1526489	<b>28.9</b> 10.8	5 10	0.0 1.1	
ук уА	1520592	132/209	+	1345	2282	1//0	1410	1.69	1.52	1.05									

Supplen	nentary Tat	ne S1. Sur	nma	ry of trai	nscriptor	ne and C	.nAP-cf	up analyse	s (contir	wed).				C	h A D ohin (	nolucio		
	gene					Trans	criptom	e analysis		. h				t	nAP-cnip a	anaiysis	· · · · ·	
			p	Sig	nal intens	ity of RN	A "	Exp	ression ra	tio	DDD	ORF				Binding	intensity "	Profile
name	start	end	stran	wild	AahrB	$\Delta abh$	Aabh	$\Delta abrB/$	$\Delta abh$	$\Delta abh$ /	ID	or	start	end	center	AbrB	Abh	ID
			50	wiid	Aubrb	$\Delta abrB$	∆ubh	wild	∠1 uurb/ wild	wild	10	Intergenic				$\Delta abh$	↓ AabrB	ID.
ndhA	1527633	1528748	+	23262	18263	18192	23019	0.78	0.78	0.99						-type	-type	
pdhB	1528752	1529729	+	25046	20158	20288	25312	0.80	0.81	1.01								
pdhC	1529844	1531172	+	25310	22164	22463	25182	0.88	0.89	0.99								
, pdhD	1531177	1532589	+	22660	19521	19753	22690	0.86	0.87	1.00								
slp	1532634	1533008	-	125	146	136	127	1.17	1.08	1.02								
speA	1533586	1535058	-	2801	1236	982	2305	0.45	0.35	0.84	456	speA	1533421	1534380	1533901	35.8 4.9	74.2 202.8	P06
yktA	1535243	1535509	+	3142	2272	2187	2353	0.72	0.69	0.74								
yktB	1535542	1536180	-	5566	5848	6193	5870	1.05	1.12	1.05								
ykzI	1536420	1536608	+	1263	667	1088	485	0.52	0.84	0.37								
yktC	1536748	1537545	+	1447	1523	1781	1377	1.10	1.28	0.95								
ykzC	1529077	153/999	+	238/	2383	2008	2313	1.03	1.10	1.06	457	alaD	1520573	1529740	1520661	5.5 2.0	24 47	
укіD	1556077	1556991	-	170	219	502	104	1.57	1.09	1.00	458	Inter	1538844	1539412	1539128	24 7 17 8	65 18	
nnrE	1539343	1540908	-	587	1719	2292	840	2.99	3 91	145	450	mer	1550044	1557412	1557120	24.7 17.0	0.5 1.0	
·· <i>r</i> ·=											459	Inter	1540714	1541180	1540947	21.4 11.8	4.0 -0.3	
ylaA	1541193	1543133	+	270	267	263	287	1.00	0.98	1.07								
ylaB	1543123	1543392	+	401	418	354	365	1.05	0.88	0.93								
ylaC	1543392	1543913	+	348	368	335	396	1.08	0.98	1.13								
ylaD	1543910	1544203	+	358	386	386	417	1.08	1.08	1.15								
ylaE	1544243	1544854	-	134	207	793	200	1.55	5.91	1.48								
				10.50							461	Inter	1544352	1545549	1544951	37.4 38.3	39.8 171.0	P01
ylaF	1545127	1545315	-	4259	4181	4197	3475	0.98	0.98	0.82	1.00	1.0	1546075	1546525	1546455	0.0 0.0	0.6 11	
ylaG	1545428	154/266	+	5742	/826	0540	5265	0.68	0.57	0.93	462	ylaG	1546375	1546535	1546455	0.9 2.0	0.6 4.1	
ylan ylan	1547525	1547040	+	4052	4313	2424	3303	0.73	0.02	0.95								
yla I	1547988	1548617	-	4055	2920	260	146	1 44	1.60	0.91								
vlaK	1548772	1550100	+	190	172	175	215	0.91	0.92	1 13								
vlaL	1550104	1550589	-	6073	7958	8260	7007	1.32	1.37	1.16								
ylaM	1550692	1551621	+	240	207	211	244	0.86	0.88	1.01								
ylaN	1551719	1552000	+	4448	4857	4742	4019	1.10	1.07	0.91								
ftsW	1552206	1553417	+	2477	2183	2054	2412	0.88	0.83	0.97								
pycA	1553492	1556938	+	8483	7793	7773	8433	0.92	0.92	0.99	463	pycA	1554076	1554474	1554275	12.4 9.6	23.0 25.7	
ctaA	1557341	1558261	-	2936	2460	2080	2477	0.81	0.69	0.84						_		
_											464	Inter	1558309	1558588	1558449	8.5 2.5	3.2 1.1	
ctaB	1558616	1559533	+	6765	7577	6751	7178	1.11	0.99	1.07	165	Teste a	1550142	15(0022	1550507	715 510	CA 0 17.7	
at a C	1550772	1560942		650	2574	2060	1601	5 1 5	5.06	2.40	405	Inter	1559142	1560052	1559587	/1.5 51.5	04.8 17.7	
ctaD	1560876	1562744	+	928	4582	4963	2293	4 96	5.40	2.49								
ctaE	1562744	1563367	+	531	3190	3209	1553	6.13	6.21	2.99								
ctaF	1563370	1563702	+	994	4504	4783	2347	4.59	4.90	2.41								
ctaG	1563729	1564622	+	731	3105	3099	1563	4.26	4.26	2.10								
ylbA	1564654	1565016	-	1995	9578	9512	3888	4.89	4.82	1.96								
											467	Inter	1564837	1565235	1565036	30.4 18.5	7.6 -0.2	
ylbB	1565156	1565608	+	590	657	576	577	1.15	1.00	0.97								
ylbC	1565685	1566725	+	706	611	595	697	0.87	0.85	0.98								
ylbD	1566957	1567355	+	249	163	190	204	0.66	0.77	0.81								
ylbE	1567371	1567610	+	138	105	105	158	0.76	0.76	1.13								
ylbF wlbC	1567726	1568175	+	4649	5136	5062	4523	1.10	1.09	0.97								
ywG	1568825	1560210	+	3540	2820	2702	2699	0.95	0.76	1.00								
coaD	1569383	1569868	+	4283	3629	3592	4150	0.77	0.70	0.97								
vlbJ	1569879	1571105	-	197	189	204	197	0.96	1.04	1.00								
vlbK	1571286	1572068	+	1315	1580	1552	1257	1.22	1.21	0.94								
ylbL	1572070	1573122	+	1940	2263	2343	1885	1.18	1.23	0.97								
ylbM	1573111	1574358	-	584	405	435	522	0.70	0.74	0.89								
ylbN	1574568	1575086	+	17454	15801	13931	17470	0.90	0.80	1.00								
rpmF	1575108	1575287	+	29449	26679	26211	28718	0.91	0.89	0.98								
ylbO	1575433	1576014	+	462	353	330	456	0.76	0.71	0.98								
ylbP	1576071	1576553	-	842	2088	3253	874	2.52	3.98	1.03								
ylbQ	1576713	157/609	+	756	625	592	863	0.85	0.80	1.14	460	- 11 A	1570151	15702/0	1570207	28 20	0.0 0.1	
yllA	157/680	15/9299	+	4005	5549	3572	4323	0.85	0.90	1.08	468	ушА	15/9151	15/9260	15/9206	2.8 2.0	0.0 0.1	
yub wraW	1570026	15/9850	+	4380	7224	40/5	4057	1.20	1.07	1.00								
ftsI	1580001	1581254	+	12330	12060	12078	11795	1.25	0.08	0.90								
jisL phnR	1581251	1583401	+	5061	4180	3813	4800	0.83	0.98	0.90	469	pbpB	1581191	1581538	1581365	13.6 4.8	14.9 0.2	
spoVD	1583518	1585455	+	227	185	185	246	0.81	0.75	1.07	-07	r°PD		1201220	1201303	4.0	0.2	
murE	1585631	1587115	+	7788	6523	5792	7323	0.84	0.74	0.94								
mraY	1587228	1588202	+	7806	6207	5545	7469	0.79	0.71	0.96								
murD	1588203	1589558	+	8894	7462	6671	8241	0.84	0.75	0.93								
spoVE	1589619	1590719	+	4642	3602	3236	4116	0.77	0.69	0.88								
murG	1590842	1591933	+	5309	4732	4122	5257	0.89	0.77	0.99								
murB	1591960	1592871	+	7913	7488	7514	8167	0.95	0.95	1.03								
div IB	1593002	1593793	$^+$	4274	3565	3532	4400	0.83	0.83	1.03								

Suppleme	gene	ie S1. Sur	nma	ry of trai	iscripto	ne and ( Trare	_nAP-cl crintor	up analyse e analysic	s (contin	wea).				C	hAP-chin	malysis		
	gene			Sim	nal intere	ity of RN	A <i>a</i>	E analysis	ression ra	tio <sup>b</sup>				t	алат -сшр а	Rinding	intensity c	
	ate -t	ar 1	pun	Jac	au nucils		.1		∆ abh		PBR	ORF	att	ar 1	agent	AbrB	Abh	Profile
name	start	end	stra	wild	∆abrB	$\Delta abh$ $\Delta abrB$	$\Delta abh$	∆ abrB/ wild	∆abrB/	∆abh / wild	ID	or Intergenic	start	end	center	wild Aabb	wild A ahrB	ID
						2 ubrb		wiki	wild	with		inteligente				-type	-type	
ylx W	1593790	1594485	+	4925	4436	4359	4660	0.90	0.88	0.94	470		1504424	1504051	1504602	27.9 25.1	261 40	D02
yix A shn	1594508	1595215	+	4095	3208	3100	3915	0.92	0.93	0.98	470	yixa	1594454	1594951	1594095	37.8 33.1	20.1 4.9	P02
ftsA	1595772	1597094	+	8150	7728	7806	8501	0.95	0.96	1.04								
ftsZ	1597130	1598278	+	12294	13213	13552	12201	1.08	1.10	0.99								
											471	Inter	1598260	1598691	1598476	26.0 29.9	1.3 -0.6	P03
bpr mallCA	1598580	1602881	+	200	185	193	207	0.92	0.96	1.02	472	bpr	1600537	1600680	1600609	0.5 0.7	0.6 5.9	
sponGA sigE	1604068	1604003	+	166	229	216	150	1.24	1.25	0.97								
5182	1001000	1001/07		100	22)	210	102	1107	1.50	0.71	474	Inter	1604600	1605032	1604816	24.7 26.5	6.1 44.2	P08
sigG	1604927	1605709	+	250	581	634	233	2.28	2.50	0.93								
ylmA	1605857	1606651	+	209	231	266	195	1.10	1.27	0.92								
ylmB ylmC	1606853	1608133	+	228	149	202	201	0.91	0.97	1.08								
ylmC vlmD	1608210	1609460	+	528 6087	4050	3851	5857	0.87	0.92	0.88								
ylmE	1609473	1610165	+	10742	7832	7735	10440	0.73	0.72	0.97								
ylmF	1610168	1610617	+	12274	9853	9834	11369	0.81	0.80	0.93								
ylmG	1610624	1610896	+	8583	8485	8232	8926	0.99	0.96	1.05								
ylmH divIVA	1611824	1611730	+	4305	3937	3826	4456 6773	0.91	0.89	1.04								
ileS	1612660	1615425	+ +	9021	7217	6638	8159	0.90	0.88	0.90								
ylyA	1615503	1615946	+	149	127	135	143	0.85	0.91	0.96								
lspA	1616049	1616513	+	3401	2514	2323	3329	0.74	0.68	0.98								
ylyB	1616515	1617426	+	5085	4248	3865	5020	0.84	0.76	0.99								
pyrR	1617609	1618154	+	6427	6472	4261	6632	1.09	0.67	1.03								
pyr1 nvrB	1619776	1620690	+	1747	1452	705	2387	1.32	0.44	1.05								
pyrC	1620674	1621960	+	1962	1985	962	2772	1.36	0.42	1.17	481	pyrC	1621549	1621845	1621697	8.7 1.8	12.6 4.8	
pyrAA	1621957	1623051	+	2728	2593	1370	3715	1.11	0.43	1.17								
carB_2	1623036	1626251	+	2622	2028	1165	3008	0.78	0.40	1.06								
pyrK	1626248	1627018	+	1899	1642	1060	1880	0.60	0.36	0.96								
pyrD pyrF	1627018	1628641	+	3084	1421	1000	2569	0.37	0.30	0.83								
pyrE	1628620	1629270	+	2965	1231	863	2429	0.44	0.31	0.83								
cysH	1629682	1630383	+	690	667	742	532	0.93	1.03	0.75								
cysP	1630395	1631459	+	618	673	718	526	1.06	1.13	0.85	40.2		1 (22 120	1 < 2 2 5 5 5 5	1 (22 102	41 15	2.0	
sat_2 cvsC	1631508	1632656	+	455	645 582	653	357	1.40	1.45	0.78	483	sat	1632429	1632555	1632492	4.1 1.5	2.8 0.0	
vlnD	1633361	1634134	+	486	667	739	384	1.37	1.52	0.79								
ylnE	1634137	1634922	+	1317	1356	1481	1198	1.01	1.10	0.91								
ylnF	1634903	1635391	+	2155	2226	2493	2052	1.03	1.16	0.95								
yloA wlaB	1635431	1637149	-	2686	2328	2353	2709	0.88	0.88	1.01								
yюБ vloC	1640020	1640895	+	6962	7400	6680	7271	1.06	0.91	1.05								
ylzA	1640972	1641241	+	10702	10941	9816	11417	1.02	0.92	1.07								
gmk	1641249	1641863	+	6557	5909	5393	6980	0.90	0.82	1.06								
rpoZ	1641867	1642070	+	13902	11781	11533	12323	0.85	0.83	0.89								
yloI	1642151	1643371	+	2228	1980	1882	2039	0.89	0.84	0.91								
def 2	1645812	1646294	+	2152	2611	2293	2637	0.94	0.90	0.90								
fmt	1646299	1647252	+	4601	3998	3832	4269	0.87	0.83	0.93								
yloM	1647239	1648582	+	4574	4104	4013	4377	0.90	0.88	0.96								
yloN	1648586	1649677	+	6664	5882	5774	6249	0.88	0.87	0.94								
prpC prkC	1650442	1652389	+	4385	4171 4079	3997 4960	4250 5364	0.95	0.91	0.97 n as								
yloQ	1652403	1653299	+	5065	4507	4573	4656	0.88	0.88	0.93	485	yloQ	1652438	1652666	1652552	8.5 3.4	5.5 2.7	
rpe	1653304	1653957	+	3918	3482	3545	3672	0.89	0.90	0.94								
yloS	1654030	1654674	+	2476	1924	1907	2535	0.78	0.77	1.03								
spoVM	1654746	1654826	+	2645	1636	1745	1958	0.61	0.66	0.72								
rpmB vloU	1655364	1655726	-+	18004	10576	15013	10/82	0.90	0.84	0.90 0.80								
yloV	1655742	1657403	+	6515	5569	5412	6032	0.86	0.83	0.93								
sdaAB	1657542	1658204	+	2390	1800	1708	2166	0.75	0.71	0.91								
sdaAA	1658230	1659132	+	3988	3208	3106	3491	0.80	0.78	0.87								
recG	1659110	1661158	+	1769	1758	1654	1675	0.99	0.93	0.94								
yıpC plsX	1661847	1662849	+	4126	6339	4772	4658	1.54	1.15	1.12								
fabD	1662867	1663820	+	7257	8980	7289	7547	1.34	0.99	1.03								
fabG_1	1663813	1664553	+	8949	11525	9100	9170	1.28	1.00	1.01								
acpP	1664637	1664870	+	23223	18918	19587	23201	0.82	0.84	1.00								
mc	1665010	1665759	+	7921	6312	5559	7454	0.79	0.70	0.94								
smc ftsY	1669440	1670420	++	4039	2019 3015	2515	3035 4054	0.65	0.59	0.90 0.80								
,	100/110	1010427		-1.1.7	2012	2120	+0.0+	0.07	0.00	0.09								

### Su mentary Table S1. Sur ary of transcriptome and ChAP-chip analyses (continued)

Suppler	gene	ne 51. Sui	nma	ry of trai	iscriptor	ne and Trans	criptom	ap analyse	s (conun	uea).				C	hAP-chins	nalveie			
	gene					TTans		c analysis		b				C		marysis	D'a d'a c		
			р	Sig	nal intens	ity of RN	A	Expi	ession ra	tio	PBR	ORF				A he	Binding .D	intensity	Profile
name	start	end	strar	wild	AahrB	$\Delta abh$	Aabh	$\Delta abrB/$	$\Delta abr B /$	$\Delta abh$ /	ID	or	start	end	center	wild	D	wild	ID
				when	<u> a</u> uono	∆abrB	<u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u></u>	wild	wild	wild		Intergenic				-type	$\Delta abh$	$\Delta abrB$	
vlaB	1670466	1670951	-	458	13128	14919	1081	29.03	33.04	2.36						type		type	
2.1											486	Inter	1670747	1671315	1671031	44.1	54.9	33.2 36.8	P01
ylxM	1671128	1671460	+	13670	18353	14821	11984	1.36	1.06	0.86									
ffh	1671474	1672814	+	11097	14942	12118	9177	1.38	1.08	0.83	487	ffh	1672583	1672964	1672774	7.8	0.1	5.1 29.7	
rpsP	1672920	1673192	+	14938	13811	12521	15586	0.93	0.84	1.04									
ylqC	1673192	1673437	+	22295	20048	18750	20785	0.90	0.84	0.93									
ylqD	1673559	1673945	+	5585	4164	3300	4628	0.74	0.58	0.84									
rimM	1673950	1674474	+	5507	4147	3681	4216	0.75	0.66	0.77									
trmD	1674471	1675202	+	5258	4265	3863	3696	0.81	0.73	0.70									
rplS	16/5333	1675689	+	32528	32221	31484	32172	0.99	0.97	0.99									
rogA mbP	1676751	1677518	+	1274	1460	1245	1161	1.05	0.00	0.92									
vlaG	1677550	1679280	+	1112	1337	1176	1029	1.10	1.08	0.88									
ylq0 ylaH	1679277	1679558	+	1195	1292	1158	956	1.27	0.98	0.77									
sucC	1679731	1680888	+	15544	20985	21183	14522	1.35	1.36	0.93									
sucD	1680917	1681819	+	14559	20821	21381	13796	1.43	1.47	0.95									
smf	1681880	1682773	+	505	847	854	453	1.70	1.71	0.91	488	smf	1682358	1682586	1682472	2.0	0.4	3.7 7.0	
											489	Inter	1682800	1683027	1682914	5.2	8.3	-0.3 -0.2	
topA	1682961	1685036	+	6279	6012	6013	6646	0.96	0.96	1.06									
gid	1685112	1686419	+	4517	3933	3359	4301	0.89	0.75	0.94									
xerC	1686487	1687401	+	5586	5992	4924	6181	1.10	0.89	1.11									
clpQ	1687414	1687959	+	5529	5798	5222	5984	1.07	0.95	1.08									
hslU	1687976	1689379	+	7247	7291	6704	7289	1.02	0.93	1.00									
codY	1689419	1690198	+	7779	7703	6947	7864	0.99	0.89	1.01								100 01	
<i>(</i> ]. D	1600579	1000077		2717	2001	2722	2090	1.12	0.00	1.12	491	Inter	1690178	1690865	1690522	66.9	27.2	12.3 2.4	
JIGB flaC	16905/8	1690907	+	6224	5081	6248	3080	1.13	0.99	1.13									
figC fi;E	1601420	1601750	+	4081	2527	0248	1026	1.04	0.99	1.11									
fliF	1691796	1693406	+	5748	5590	53219	6209	0.80	0.79	1.11									
fliG	1693419	1694435	+	5624	5528	5160	6095	0.98	0.92	1.00									
fliH	1694553	1695179	+	5805	5919	5709	6122	1.02	0.98	1.05									
fliI	1695166	1696488	+	4693	4943	4671	5028	1.05	1.00	1.07									
fliJ	1696491	1696934	+	5255	4930	4461	5642	0.94	0.85	1.08									
ylxF	1696946	1697587	+	3859	3891	3496	4288	1.01	0.91	1.11									
fliK	1697748	1699037	+	3045	3218	2951	3664	1.06	0.97	1.21									
flgD	1699034	1699456	+	1866	1918	1832	2226	1.03	0.98	1.20									
flgG	1699478	1700272	+	6903	7714	7346	7719	1.12	1.06	1.12						_			
											493	Inter	1700328	1700589	1700459	16.8	2.6	7.4 -0.5	
fliL	1700524	1700946	+	3313	3283	3230	3669	0.99	0.98	1.10									
JUM GIV	1701068	1702104	+	5094	6522	6008	6353	1.11	1.06	1.11									
JUY	1702120	1703104	+	3985	2050	0237	2071	1.09	1.04	1.07	404	oboV	1702166	1702462	1702214	7.1	5.2	0.2 6.0	
fli7	1703130	170/166	+	4530	4902	1/00	/818	1.02	1.00	1.02	474	che i	1703100	1703402	1703314	/.1	5.2	9.2 0.9	
fliP	1704159	1704824	+	3340	3451	3054	3681	1.03	0.91	1.00									
fliO	1704839	1705108	+	3404	3671	3376	3733	1.08	1.00	1.09									
fliR	1705116	1705895	+	3951	4238	3835	4153	1.07	0.98	1.04									
flhB	1705895	1706977	+	3158	3337	3064	3248	1.06	0.97	1.02									
flhA	1707010	1709043	+	3132	3287	2949	3208	1.06	0.95	1.00									
flhF	1709043	1710143	+	2763	3005	2718	2924	1.10	1.00	1.04	496	flhF	1709728	1709922	1709825	6.9	7.9	1.6 0.1	
ylxH	1710134	1711030	+	2073	2439	2185	2250	1.22	1.09	1.07	497	ylxH	1710153	1710364	1710259	0.9	1.6	0.2 10.3	
cheB	1711032	1712105	+	2706	3143	2784	2897	1.19	1.06	1.05									
cheA	1712111	1714126	+	3033	3535	3264	3250	1.18	1.09	1.05									
cheW	1714148	1714618	+	3713	4011	3838	3663	1.09	1.05	0.95	400	ahaC	1714/02	1714070	1714700	0.2	0.1	0.0 6.0	
cneC cheD	1/14037	1/15266	+	5011 1019	3/1/	5487	2024	1.25	1.18	1.03	498	cneC	1/14692	1/14868	1/14/80	-0.2	0.1	0.0 6.0	
cneD siaD	1/15203	1716550	+	1918	2/24	21/8	2024	1.19	1.16	1.01									
sıgD vlrI	1716570	1717082	+ +	2020	31423	3004	2072	1.13	1.09	1.02									
rnsR	1717226	1717966	+	21918	20240	17993	21331	0.02	0.82	0.97									
tsf	1718068	1718949	+	22369	20176	18813	21087	0.90	0.84	0.94	500	tsf	1718279	1718609	1718444	13.0	15.8	11.8 0.6	
pyrH	1719095	1719817	+	15844	13225	12196	14821	0.83	0.77	0.94	200							0.0	
frr	1719819	1720376	+	13013	10648	9843	11857	0.82	0.76	0.91									
											501	Inter	1720150	1720819	1720485	27.3	31.1	7.0 -0.4	
uppS	1720507	1721289	+	5406	4326	3840	4505	0.80	0.71	0.83									
cdsA	1721293	1722102	+	4808	3869	3450	3898	0.80	0.72	0.81							_		
dxr	1722164	1723330	+	8255	6652	6455	7617	0.81	0.78	0.92	502	dxr	1722393	1722536	1722465	4.2	1.8	1.9 0.7	
yluC	1723321	1724589	+	9890	8630	8365	9000	0.87	0.85	0.91									
proS	1724622	1726316	+	8306	7543	7483	8226	0.91	0.90	0.99									
polC	1726425	1730738	+	3574	2897	2700	3237	0.81	0.75	0.90									
ylxS	1731068	1731538	+	7784	8165	6805	7193	1.05	0.87	0.92									
nusA where	1/315/3	1/52688	+	10982	10/79	9668	105/6	0.98	0.88	0.94									
yıx K vlx O	1722070	1732391/	+	14222	1400/	12890	13083	1.02	0.91	0.90									
infR	1733301	1735/51	+	12171	113/5	10887	11049	0.02	0.91	0.95	502	infR	1734056	1735284	1735121	17.4	07	20.2 _0.2	
	1,55501	1100401	C	141/1	11040	10002	11040	0.75	0.09	0.71	205		1154750	1100400	.100141	17.7	0.7	-0.5	

Supplem	entary Tab	le S1. Su	nma	ry of trai	iscriptor	me and (	ChAP-ch	ip analys	es (contir	wed).					hAD alie -	nobrat				
	gene			Sior	nol intone	Trans		e analysis	ression re	tio b				t	лаг-спра	inalysis	Dinding	intonsity	c	
			р	Sigi	iai intens	ity of KIN	A	Exp	ression ra	do	PBR	ORF		_		A	brB	Intensity	Abh	Profile
name	start	end	stra	wild	∆abrB	∆abh ∆abrB	$\Delta abh$	∆abrB/ wild	∆ abrB/ wild	⊿abh / wild	ID	or Intergenic	start	end	center	wild -type	$\Delta abh$	wild -type	∆ abrB	ID
ylxP	1735448	1735726	+	17403	16288	15693	15371	0.93	0.90	0.88										
rbfA	1735743	1736096	+	6616	5904	5610	5437	0.90	0.85	0.82										
truB	1736178	1737107	+	3255	2392	2261	2690	0.73	0.69	0.83										
ribC rnsO	1738233	1738502	+	27126	27194	26529	27518	1.00	0.90	1.03										
pnpA	1738675	1740792	+	11032	10570	9575	10513	0.96	0.87	0.95										
ylx Y	1740910	1741869	+	2523	1766	1533	2072	0.72	0.61	0.80	504	ylxY	1740991	1741218	3 1741105	8.3	3.8	1.3	-0.2	
mlpA	1741909	1743138	+	2399	1795	1534	2049	0.76	0.64	0.84										
ymxH	1743216	1743473	+	291	205	208	293	0.71	0.72	1.00										
spov FA spoVFB	1743039	1744552	+	120	102	108	127	0.85	0.89	0.93										
asd	1745283	1746323	+	10094	8532	8463	9371	0.85	0.84	0.93										
dapG	1746415	1747629	+	9269	7568	7362	8617	0.82	0.79	0.93										
dapA	1747660	1748532	+	9557	8441	8232	9973	0.88	0.86	1.04										
ymfA	1748830	1750377	+	7186	6838	6141	6974	0.95	0.85	0.97	506	ymfA	1749219	1749600	1749410	19.6	7.1	5.7	1.4	
tepA spoIIIE	1751569	1751230	+	1540	228 1419	1300	1523	1.13	0.84	0.93										
sponing	1/01007	1100702		1010	,	1500	1020	0.72	0.01	0.70	507	Inter	1753860	1754054	1753957	0.7	0.9	2.3	6.1	
ymfC	1754075	1754800	+	1798	2211	1890	1853	1.23	1.06	1.03										
ymfD	1754939	1755313	+	355	419	443	359	1.18	1.24	0.99							_			
ymfE (E	1755565	1756149	+	416	542	487	416	1.30	1.16	0.98	508	ymfE	1755492	1756009	1755751	11.4	3.1	11.8	52.1	
ymjr vmfG	1756821	1757543	+	6684	9343	9002	7682	1.40	1.45	1.07										
ymfU ymfH	1757626	1758873	+	5451	7862	7969	6506	1.46	1.48	1.19										
fabG_2	1758928	1759656	+	2695	2463	2392	2567	0.96	0.91	0.94										
ymfJ	1759737	1759994	+	1135	2079	2149	1583	1.90	1.91	1.45	509	ymfJ	1759640	1760157	1759899	25.5	23.6	9.5	6.0	
ymfK	1760138	1760638	+	2388	2267	2329	2303	0.95	0.98	0.96										
ymfL vmfM	1760526	1761620	+	4127	3843	6280 3887	3740	0.99	0.94	0.92										
pgsA	1761895	1762476	+	2712	2172	2217	2905	0.80	0.82	1.07	511	pgsA	1762326	1762571	1762449	9.6	10.1	3.5	4.6	
cinA	1762494	1763744	+	4942	4243	4264	4447	0.86	0.86	0.90										
recA	1763917	1764960	+	8500	7073	7087	8421	0.83	0.83	0.99										
рврХ	1765128	1766303	+	6497	6408	6812	6230	0.99	1.05	0.96	512	pbpX nhnX	1765573	1765699	1765636	2.6	4.5	0.9	0.6	
vmdA	1766580	1768142	+	15959	18293	17791	16045	1.15	1.12	1.01	515	рорл	1/0011/	1700379	1700248	9.0	0.0	2.3	1.2	
ymdB	1768211	1769005	+	3010	2949	2737	2655	0.98	0.91	0.88										
spoVS	1769205	1769465	+	8047	13719	14313	8163	1.71	1.79	1.01										
tdh	1769731	1770774	+	1959	2295	2648	1988	1.17	1.36	1.02										
kbl vmcB	1772113	1773642	+	2773 7484	3017 7300	3661 7372	2830	1.09	1.32	0.98										
ymcA	1773644	1774075	+	4874	6031	6363	4750	1.25	1.31	0.97										
cotE	1774337	1774882	+	215	173	168	204	0.80	0.78	0.93										
mutS	1775015	1777591	+	1985	1689	1642	1947	0.85	0.83	0.98										
mutL	1777607	1779490	+	2682	2621	2614	2795	0.98	0.98	1.04	516	Inton	1770202	1700001	1770697	70.0	79.0	54.2	1225	D01
vm7D	1779888	1780343	-	438	696	681	393	1.62	1 54	0.93	510	mer	1779292	1780081	1//908/	79.0	/ / 8.0	54.3	5 155.5	PUI
ymcC	1780498	1781055	-	559	443	496	581	0.80	0.89	1.04										
pksA	1781176	1781793	+	511	572	521	510	1.13	1.01	0.97										
pksB	1781983	1782660	+	262	486	555	261	1.87	2.13	0.99		1.6	150207	100000	1002105					
pksC nksD	1784/02	1/83899	+	510 176	2168 1724	2378	452	4.30 0.81	4.66	0.88	518	pksC pksD	1/83066	1/83294	1784820	2.5	1.5	0.6	6.6	
pksE	1785290	1787593	+	164	1295	1296	169	7.85	7.84	1.02	519	PROD	1,04001	1,047//	1,04029	17.0	10.5	1.9	1.0	
acpK	1787654	1787902	+	137	1067	1201	128	7.91	8.90	0.94										
pksF	1787880	1789130	+	123	509	523	162	4.15	4.28	1.32										
pksG	1789131	1790393	+	208	922	921	235	4.43	4.41	1.13										
pksH nksI	1790381	1791100	+	103	3/3	362 340	114 128	3.03 3.13	3.53 3.00	1.11										
pksJ	1791994	1807131	+	165	545	518	120	3.27	3.09	1.09	521	pksJ	1791736	1792321	1792029	37.6	43.0	9.8	0.0	
-											522	pksJ	1794966	1795177	1795072	6.8	4.2	10.0	5.6	
pksL	1807115	1820731	+	228	463	474	235	1.99	2.03	1.02	524	pksL	1811065	1811854	1811460	4.2	0.8	5.9	136.1	P04
pksM	1820747	1833535	+	215	288	293	218	1.32	1.34	1.00	507	nkeN	1815017	1845077	1945010	27	4.0	1.0	2.2	
pksin pksR	1850084	1857715	+++	203	570 462	400 481	223	1.80	1.94	1.08	527	pksin pksR	1855537	1855680	1855609	2.7	4.0	-0.2	2.3	
pksS	1857854	1858984	-	2577	2739	2813	2700	1.05	1.09	1.04	221	r				- 0.1	0.0	0.2		
ymzB	1859209	1859565	-	322	1566	2142	286	4.86	6.65	0.88										
ymaE	1859644	1860342	-	158	1047	1403	210	6.65	8.87	1.31	_	_								
an aV	1020500	1041000		100	110	100	124	0.02	0.05	1.04	530	Inter	1860178	1860729	1860454	35.6	41.7	10.9	0.6	
aprx	1800280	1901908	-	128	119	122	154	0.92	0.95	1.04	531	apr <b>A</b> Inter	1862048	186288	1867468	7.3	3.1 27.3	4.7	1/./ 5 161.2	P01
ymaC	1862644	1863351	+	516	350	364	471	0.70	0.72	0.89	551		1002040	1002000	1002-100				101.2	. 01
ymaD	1863421	1863873	+	1634	1956	1953	1795	1.21	1.21	1.09										
ebrB	1863887	1864240	-	397	322	328	389	0.83	0.84	0.99										
ebrA	1864254	1864571	-	231	192	204	263	0.83	0.89	1.14										

Supplem	entary Tab gene	le S1. Su	mma	ry of trai	nscriptor	me and ( Trans	ChAP-ch	ip analyse e analysis	es (contin	ued).				Cł	AP-chin	analysis				
	guit			Sim	nal intens	ity of RN	A <sup>a</sup>	Fyn	ression ra	tio <sup>b</sup>					- 11 - Cinp a		Binding	intensity	с	
nama	ctort	and	pue	<u> </u>	IRCID	OI ININ			$\Delta abh$	4 . 1.1 /	PBR	ORF	ctort		contar	Ab	rB_	A	.bh	Profile
name	start	ena	strä	wild	∆abrB	∆abh ∆abrB	$\Delta abh$	∆ abrB/ wild	$\Delta abrB/$	∆abh / wild	ID	or Intergenic	start	end	center	wild	$\Delta abh$	wild	∆abrB	ID
vmaG	1864708	1865079	-	178	165	185	237	0.93	wild 1.05	1 34						-type		-type		
vmaF	1865072	1865485	+	115	99	96	119	0.95	0.84	1.03										
miaA	1865584	1866528	+	1314	1014	931	1237	0.77	0.71	0.94										
hfq	1866568	1866789	+	1936	6233	6323	2340	3.18	3.25	1.18										
ymzC	1866985	1867257	+	548	1757	1869	601	3.26	3.41	1.08										
ymzA	1867339	1867569	+	2417	3290	3345	2509	1.38	1.40	1.02										
nrdI_1 nrdF	186/812	1868204	+	2826	2035	2306	26/0 5317	0.95	0.82	0.95										
nrdF 1	1870284	1870200	+	4717	3544	3063	4325	0.75	0.64	0.92										
ymaB	1871323	1871943	+	3775	2692	2325	3136	0.72	0.61	0.82										
cwlC	1872007	1872774	-	121	116	109	128	0.96	0.90	1.05										
spoVK	1873398	1874366	+	202	135	137	173	0.67	0.68	0.84										
ynbA	1874587	1875591	+	2707	1905	1659	2316	0.70	0.61	0.86										
yndB alnR	1877155	1877562	+	2952 5436	4321	2101	2070 4632	0.70	0.73	0.91	533	olnR	1877076	1877253	1877165	3.9	40	15	16	
glnA	1877623	1878957	+	15330	13058	13623	14055	0.85	0.89	0.92	534	glnA	1877365	1877966	1877666	53.3	77.8	22.2	1.0	P02
8											535	Inter	1878691	1879854	1879273	84.5	86.4	15.6	2.8	
ynxB	1879285	1879575	+	294	594	635	300	2.02	2.20	1.02										
ynzF	1879821	1880165	+	296	732	790	312	2.48	2.67	1.07										
ynzG	1880296	1880547	+	74	127	141	69	1.71	1.90	0.92										
ynaB ynaC	1880807	1882039	+	/38 557	2003	1/89	807 537	2.62	2.39	1.11										
vnaD	1882374	1882886	+	83	124	129	98	1.49	1.59	1.16										
											537	Inter	1883179	1883474	1883327	11.9	4.7	0.8	-1.3	
ynaE	1883446	1884087	+	158	304	301	183	1.90	1.90	1.15										
ynaF	1884176	1884529	+	318	529	535	357	1.64	1.69	1.13									_	
C	1004572	1004040			(00	710	402	1.50	1.61	1.00	538	Inter	1884352	1884784	1884568	20.8	15.8	0.2	3.4	
ynaG ynaI	1885265	1885735	+	444	121	102	482	1.50	1.01	0.97	539	vnaI	1885253	1885923	1885588	39.1	44.6	11.1	12	
xvnP	1886560	1887951	+	529	402	442	524	0.76	0.83	0.99	557	yinni	1005255	1005725	1005500	57.1	44.0		1.2	
xynB	1887982	1889583	+	682	473	540	640	0.70	0.81	0.94	540	xynB	1889112	1889544	1889328	26.8	5.5	19.7	0.2	P05
xylR	1889720	1890772	-	613	572	510	681	0.96	0.84	1.13										
											542	Inter	1890863	1891125	1890994	5.5	4.3	3.3	5.9	
xylA	1891116	1892453	+	2451	3662	2901	2526	1.55	1.20	1.04										
vncB	1892004	1895221	-	1490	454	534	1026	0.36	0.42	0.81										
,											543	Inter	1895283	1895834	1895559	36.6	43.9	13.7	2.2	
yncC	1895632	1896891	+	237	176	191	280	0.75	0.81	1.19										
yncD	1897149	1898333	-	124	126	139	148	1.01	1.12	1.19										
yncE	1898797	1899258	+	1120	372	380	1007	0.33	0.34	0.90										
yncr	1899288	1899722	+	2303	1064	1155	2180	0.45	0.48	0.92	544	Inter	1899924	1900237	1900081	18.1	12.2	2.1	49	
vnzH	1900326	1900586	-	77	81	78	64	1.04	1.00	0.82	544	inter	10///24	1700257	1700001	10.1	12.2	2.1	4.2	
<i></i>											545	Inter	1900689	1900798	1900744	3.5	3.7	0.2	-0.3	
thyA_1	1901428	1902267	+	982	467	477	953	0.48	0.48	0.97										
yncM	1902720	1903472	-	1605	6931	7335	1374	4.38	4.57	0.85										
	1004204	1004560		1.40	105	104	111	0.74	0.72	0.70	546	Inter	1903188	1903841	1903515	27.3	15.0	7.2	0.0	
tatAC	1904204	1904560	-	1214	991	979	1000	0.74	0.73	0.79										
vndA	1905018	1905416	+	106	114	112	105	1.07	1.05	0.99	547	yndA	1905177	1905490	1905334	7.7	4.4	10.5	17.1	
yndB	1905481	1905915	-	3329	3602	3445	3084	1.08	1.03	0.93		-								
ynzB	1906222	1906410	+	184	120	115	129	0.65	0.62	0.70										
yndD	1906703	1908265	+	148	137	144	153	0.92	0.97	1.03										
yndE un dE	1908295	1909386	+	127	129	141	163	1.02	1.11	1.28										
упаг	1909370	1910390	+	147	150	150	145	0.88	0.92	0.90	548	Inter	1910482	1910930	1910706	29.2	27.3	-0.1	-0.9	P03
yndG	1910737	1911543	+	924	1479	1398	881	1.60	1.51	0.95										
yndH	1911548	1912165	+	684	1050	961	728	1.52	1.40	1.06	549	yndH	1912028	1912171	1912100	2.1	5.1	-0.2	-0.5	
yndJ	1912162	1913802	+	775	1234	1149	766	1.60	1.47	0.98										
117	1012020	1014204		10.12	1.640	1450	0.64	1.50	1.20	0.01	550	Inter	1913575	1914041	1913808	16.8	8.8	3.3	-1.5	
yndK	1913839	1914204	+	1043	1648	1456	964	1.59	1.38	0.91	551	rmdI	1014197	1014772	1014490	22.1	42.0	27	17	D02
ynaL vndM	1914450	1915754	+	211	236	274	226	1.12	1.30	1.07	551	ynur	171410/	1714//2	1714400	-32.1	43.7	5.7	1.7	105
yndN	1915872	1916306	+	2101	4463	5521	2360	2.16	2.70	1.13										
lexA	1916848	1917465	-	4224	4085	3466	4117	0.97	0.82	0.98										
yneA	1917615	1917932	+	325	245	239	317	0.76	0.74	0.98										
yneB	1917951	1918604	+	1092	597	637	946	0.55	0.58	0.86										
ynzC	1918668	1918901	+	2061	1313	1389	2076	0.64	0.67	1.01	660	tk t	1010977	1020200	1020072	24.0	20-5	2.4	0.1	<b>D</b> 02
IKI	1919070	19210/3	+	10350	10/14	10954	1/0/6	1.01	1.02	1.03	553 554	uki tkt	1919865	1920280	1920073	24.0 1.4	20.5	5.4	0.1	P03
yneE	1921226	1921672	+	343	233	262	337	0.68	0.77	0.94	554		1,20411	1,20003		1.4	5.0	1.5	5.4	
yneF	1921758	1921976	+	15432	10314	9866	14845	0.67	0.64	0.96										
ynzD	1922050	1922223	-	155	731	473	154	4.75	3.04	0.98										

Supplem	entary Tal gene	ne S1. Su	mma	ry of trai	nscripto	me and ( Trans	nAP-ch criptom	up analyse e analysis	es (contin	ued).				Cł	1AP-chin s	analysis				
	gene			Sig	nal intens	ity of RN	A <sup>a</sup>	Exp	ression ra	tio <sup>b</sup>		0.00		0.	in cup		Binding	intensity '	с	
nama	etart	and	and	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		4hh		A abaD/	$\Delta abh$	A abb /	PBR	ORF	etart	and	center	Abi	rB	A	bh	Profile
name	start	chù	str	wild	∆abrB	∆ abn A abrB	$\Delta abh$	∠ <i>aor</i> b/ wild	$\Delta abrB/$	⊿ <i>abn</i> / wild	ID	Intergenic	start	chù	center	wild	Aabh	wild	AabrB	ID
								·	wild		555	Intor	1022002	1022400	1022201	-type	22.1	-type	12	
ccdA	1922443	1923150	+	420	706	739	454	1.71	1.76	1.06	555	mer	1722072	1722470	1)222)1	24.7	22.1	0.7	-1.5	
yneI	1923239	1923601	+	1498	1935	1902	1479	1.28	1.26	0.97										
yneJ	1923680	1924171	+	2653	3261	3115	2877	1.23	1.18	1.09										
yneK	1924202	1924630	-	2514	2096	2052	1969	0.83	0.80	0.78										
cotM sepP	1924864	1925256	-	12	85 305	85 523	64 51	1.19	1.20	0.92										
ssp1	1925515	1925661	-	132	397	569	106	3.05	4.39	0.80										
citB	1925889	1928618	+	3981	17508	12863	4139	4.40	3.08	1.02	556	citB	1925832	1926349	1926091	40.0	18.9	36.9	13.1	
yneN	1928690	1929202	+	1077	6293	3908	1000	5.81	3.31	0.90										
sspN	1929473	1929619	+	144	584	953	152	4.04	6.60	1.05										
tlp vneP	1929656	1929907	+	138	580	555	1060	3.95	4.90	0.94	558	vnoP	1030065	1030208	1030137	23	4.5	0.0	-0.1	
vneO	1930424	1930723	+	1923	1057	1149	1755	0.55	0.60	0.91	550	ynei	1750005	1750200	1750157	2.5	4.5	0.9	-0.1	
yneR	1930754	1931041	-	4220	3811	3793	3926	0.90	0.90	0.93										
yneS	1931129	1931710	-	2828	2160	1690	2644	0.76	0.60	0.94										
yneT	1931880	1932287	+	2028	1943	2330	1895	0.96	1.15	0.93										
parE	1932686	1934653	+	4322	3110	3284	4224	0.72	0.76	0.98	550	nor C	1025226	1025512	1025424	5.5	0.2	4.2	12	
vnfC	1934037	1937685	+	4606	1067	1099	1464	0.78	0.80	0.90	559	parc	1955550	1955512	1955424	5.5	0.5	4.2	1.5	
alsT	1938134	1939531	+	4611	3542	2853	4087	0.05	0.62	0.89	561	alsT	1937970	1938334	1938152	23.6	3.7	12.6	1.2	
bglC	1939834	1941333	+	263	243	260	273	0.92	0.99	1.03						_				
ynfE	1941401	1941664	+	88	89	89	91	1.00	1.01	1.02	563	ynfE	1941285	1941750	1941518	20.4	2.6	12.7	41.0	
ynfF	1941923	1943191	-	331	1207	1196	271	3.66	3.59	0.81	563	ynfF	1941778	1942175	1941977	23.7	8.1	7.5	7.0	
xynD	1943322	1944863	-	196	630	599	164	3.22	3.02	0.82	564	xynD Intor	1943/33	1943859	1943/96	3.5	4.3	6.1	1.5	P02
vngA	1945458	1945904	+	94	84	88	117	0.89	0.94	1.25	505	mei	1744,047	1943324	1945057	05.5	100.7	0.1	-5.5	105
yngB	1945911	1946804	+	558	520	501	554	0.93	0.90	0.99										
yngC	1946877	1947473	+	2881	2852	2708	2936	0.99	0.94	1.02	567	yngC	1946929	1947106	1947018	2.1	1.2	1.0	4.8	
yngD	1947522	1948721	-	152	140	143	153	0.92	0.94	1.00										
yngE E	1948891	1950678	-	141	127	130	154	0.90	0.92	1.09										
yngF yngG	1950437	1951219	-	99 149	93 144	80 149	105	0.95	1.00	1.14										
vngH	1952390	1953724	-	138	116	112	152	0.84	0.81	1.10										
yngI	1953734	1955383	-	122	113	117	147	0.93	0.96	1.21										
yngJ	1955427	1956569	-	105	82	81	113	0.79	0.77	1.10										
ynzE	1956660	1956965	-	109	128	143	128	1.17	1.31	1.19	570	<b>T</b> .	105 (07.4	1057055	1057065	161	10.7	20.0	20.5	
VII aV	1057226	1058768		117	117	110	116	1.00	1.01	0.00	570	Inter	19568/4	1957255	195/065	16.1	12.7	28.8	29.6	
vngL	1957230	1958708	-	127	120	140	136	0.95	1.01	1.07										
ppsE	1959407	1963246	-	209	390	394	208	1.80	1.81	0.98										
ppsD	1963254	1974065	-	190	432	427	186	2.21	2.15	0.97	571	ppsD	1969250	1969342	1969296	1.2	1.2	1.7	2.5	
											572	ppsD	1969488	1969818	1969653	20.2	5.8	11.5	2.3	
C	1074000	1001757		160	500	507	172	2.41	2 20	1.01	573	ppsD	1970066	1970549	1970308	2.2	1.5	2.6	42.0	P04
ppsC ppsR	1974090	1981/3/	-	109	590 616	505 641	173	3.41	3.29	1.01	575	nnsB	1981762	1982075	1981919	15.4	28	12.9	24	
ppsb	1701774	1707450		150	010	041	175	5.05	5.91	1.00	576	ppsB	1982306	1982517	1982412	3.6	0.0	4.5	8.6	
											578	ppsB	1987270	1987430	1987350	4.6	0.7	2.7	0.6	
ppsA	1989481	1997166	-	136	596	642	142	4.32	4.63	1.04	580	ppsA	1992727	1993023	1992875	24.9	13.6	6.0	0.0	
	1007540	1000024		2.00	12/2	1462	150	2.05	4.17	1.00	581	Inter	1996943	1997460	1997202	19.6	16.7	1.0	-1.5	
dacC vor A	199/549	1999024	-	360	1303	1465	450	3.85	4.17	1.22										
voeA	2000169	2000055	-	646	4639	4696	683	7.30	7.35	1.04										
yoeB	2001846	2002391	+	7702	7094	6823	6933	0.96	0.92	0.90										
trnSL-Ar	g 2002484	2002559	-	705	3849	4041	677	4.88	5.13	0.96										
yoeC	2002869	2003156	-	556	440	446	472	0.80	0.82	0.85						12.0	-			504
voaD	2002472	2002702		204	221	271	211	1.08	0.88	1.00	582	Inter	2003046	2003733	2003390	43.0	78.7	38.2	21.4	P01
yoeD oot	2003472	2005/02	+	111	113	122	115	1.08	1 10	1.00										
yofA	2005751	2005650	-	218	471	457	273	2.18	2.09	1.03										
											583	Inter	2006616	2006759	2006688	4.9	1.4	3.0	-0.5	
yogA	2006736	2007725	+	186	253	279	176	1.35	1.47	0.93										
gltD	2007782	2009263	-	4197	714	1459	3202	0.17	0.35	0.76	504	alt A	2011/14	2011774	2011/04	2.2	1.2	4.0	5.1	
gIIA oltC	2009280	2015842	-+	5875 1427	517	1008	2865	0.13	0.26	0.74	584	gitA	2011614	2011/74	2011694	2.2	1.3	4.0	5.1	
proJ	2013989	2014091	-	723	672	715	681	0.48	1.01	0.91										
proH	2016055	2016948	-	745	718	702	722	0.99	0.99	0.95										
rtp	2017095	2017463	-	366	482	567	334	1.33	1.58	0.90										
fabG_3	2017763	2018479	-	12238	10877	11053	13089	0.89	0.91	1.07										
yoxC	2018630	2018935	+	766	369	600	296	0.48	0.78	0.38										
yoxB yoaA	2019006	2019776 2020317	+	158	113 340	133	110	0.73	0.86	0.70										
yoaB	2020433	2021677	-	201	181	193	231	0.90	0.96	1.15	589	yoaB	2021389	2021735	2021562	19.3	10.2	9.0	2.9	
e											/	- · · · ·								

suppien	ocinary 181 oene	лс э1. ЭШ	mar	y or tra	uscriptoi	me and ( Trans	criptom	up analyse e analysis	s (contir	ueu).				ՐԻ	AP-chin a	malvsis			
	gene			Sig	nal inters	ity of RN	A <sup>a</sup>	Fxm	ression ra	tio <sup>b</sup>						Rindi	ng intensi	tv <sup>c</sup>	
	atant	and	pur	515	nut incens	4 11			$\Delta abh$	4 11 /	PBR	ORF	atort	and	conton	AbrB	ing interior	Abh	Profile
name	start	end	stra	wild	∆abrB	$\Delta abh$ $\Lambda abrB$	$\Delta abh$	∆ abrB/ wild	∆abrB/	⊿ abh / wild	ID	Intergenic	start	ena	center	wild Aabi	wild	A abrB	ID
	2021551					10000			wild							-type	-type	e	
yoaC yoaD	2021771	2023234	-	221	122	137	210	0.77	0.87	0.98									
yoaD yoaE	2023232	2024280	-+	447	439	503	384	0.08	1.13	0.99									
yoaF	2026720	2027013	+	1380	1552	1474	1172	1.08	1.06	0.86									
yoaG	2027386	2027790	-	1604	1954	2136	1764	1.22	1.35	1.11									
yozQ	2028231	2028524	+	114	192	187	122	1.73	1.68	1.08									
yoaH	2028640	2030244	-	387	385	335	430	1.02	0.87	1.07									
yoal	2030972	2032099	+	84	1222	1250	/8	0.95	1.07	0.92									
voaK	2032130	2032034	-	354	473	516	414	1.34	1.30	1.16									
pelB	2033954	2034991	+	106	129	131	93	1.22	1.24	0.88									
yoaM	2035248	2035931	+	73	75	82	79	1.04	1.13	1.09									
yoaN	2036810	2037988	-	94	89	92	97	0.95	0.98	1.03									
yoaO yoaP	2038111	2038599	-	323	383	360	349	1.19	1.11	1.07									
yoar yoa0	2030819	2039374	-	98 140	102	115	104	0.94	1.10	0.89									
youQ yozF	2039002	2040230	-	93	97	142	68	1.05	1.32	0.74									
yoaR	2041138	2042049	-	133	131	139	149	0.98	1.04	1.12									
yoaS	2042396	2042878	+	394	314	325	387	0.80	0.82	0.98									
yozG	2042888	2043142	+	634	433	440	604	0.68	0.68	0.92	595	yozG	2042962	2043207 2	2043085	9.7 1.4	1 5.	.1 -0.8	
yoaT	2043248	2044042	+	702	587	631	683	0.85	0.91	0.95									
yoaU	2044100	2045058	-	274	234	250	2/1	0.85	0.94	0.97	506	Inter	201/010	2045179	045049	85 61	) 3	3 07	
voaV	2045139	2046017	+	186	168	163	191	0.90	0.87	1.02	570	mer	2044)1)	20451772	2043047	0.0	, .	.5 0.7	
yoaW	2046190	2046621	-	93	216	251	79	2.31	2.65	0.84									
yoaZ	2046885	2047517	-	114	128	126	118	1.11	1.09	1.01									
_											597	Inter	2047399	2047746 2	2047573	<b>18.2</b> 13.1	1.	.6 -0.6	
penP	2047743	2048663	+	2180	2044	2191	1886	0.95	1.01	0.86									
yobA yobB	2049100	2049322	-+	142	1858	2759	159	12.10	17.45	0.97	598	vobB	2049524	2050312	2049918	73.0 82	6 55	0 367	P01
pps	2050539	2053139	-	491	472	507	458	0.96	1.03	0.92	570	J002	2019921	2000012	2017710	15.0 02.	0 00	.0	
											599	Inter	2052992	2053594 2	2053293	46.0 64.	<mark>0</mark> 14.	.2 3.0	
xynA	2053809	2054450	-	4915	6872	6636	4578	1.39	1.35	0.93						_	_		
yobD	2055488	2055826	+	166	214	188	154	1.23	1.08	0.89	601	yobD	2055525	2055974 2	2055750	30.7 3.0	5 18	.4 -1.1	P05
yozH vozI	2055860	2056180	-	273	321	62 324	263	1.05	1.03	0.93									
vobE	2057012	2057671	+	481	282	373	523	0.60	0.79	1.09									
yobF	2057926	2058849	-	114	120	134	141	1.04	1.16	1.21									
yozJ	2059448	2059903	-	134	128	144	134	0.95	1.07	0.98							_		
											602	Inter	2059639	2060275 2	2059957	54.1 60.	4 17.	.7 0.6	201
											602 602	Inter	2060286	2061074 2	2060680	130.9 173.	4 113 2 0	<u>.3 64.6</u> 8 -2.0	P01
ranK	2061361	2062476	+	154	1003	1310	201	6.51	8.57	1.31	002	mer	2001004	2001504 2	2001554	50.4 17.	- ).	-2.0	
phrK	2062473	2062595	+	761	2891	3157	889	3.98	4.30	1.16									
yobH	2062721	2063332	-	165	156	187	215	0.94	1.13	1.29									
yozK	2063411	2063758	-	127	123	140	141	0.97	1.09	1.11									
yozL	2063751	2064044	-	46	39	35	40	0.85	0.77	0.85									
yozM vohI	2064255	2064588	+	806	755	740	763	0.93	0.91	0.90	604	vobI	2066218	2066463	2066341	77 71	0	9 -04	
<i>you</i> .	2001000	2000210		000	100	710	105	0.55	0.91	0.55	606	Inter	2068768	2069353 2	2069061	29.5 10.8	3 2.	.6 2.0	
yobJ	2069455	2070297	-	2009	2361	2471	2164	1.17	1.23	1.07	608	yobJ	2069805	2070371 2	2070088	40.3 28.	9 3.	.1 2.7	P03
yobK	2070497	2070955	-	809	1618	1668	779	1.99	2.07	0.95									
yobL	2070965	2072767	-	412	1052	1145	369	2.59	2.86	0.88									
yobM	2072869	2073357	-	538	2001	2137	466	3.74	4.00	0.86									
YODIN	2073650	2074990	+	102	92	97	99	0.90	0.95	0.97	609	Inter	2075007	2075405	2075206	16.6 7.0	5	4 20	
yobO	2075417	2077837	+	177	509	820	186	2.90	4.82	1.03	610	yobO	2076520	2076867 2	2076694	6.4 0.4	4 5.	4 25.6	
csaA	2078125	2078757		1151	1044	1000	096	0.01	0.05	0.62	011	inter	2077727	2078159 2	2077943	<b>18.1</b> 12.4	-0.	.4 -0.9	
vohO	2078423	2079547	-	631	554	620	542	0.89	1.00	0.85									
yobR	2079562	2080305	-	811	672	702	702	0.82	0.86	0.85									
yobS	2080383	2080958	-	382	296	301	343	0.77	0.78	0.88									
yobT	2080964	2081665	-	618	514	522	593	0.83	0.85	0.94									
yobU	2081742	2082224	-	130	142	146	119	1.09	1.12	0.91									
yobV	2082278	2083219	-	162	334	331	188	2.06	2.05	1.15									
youw vozA	2083425	2083970	+	1193	1173	149	1191	1.01	1.00	1.02									
yocA	2084514	2085191	+	3171	4960	4871	4078	1.58	1.55	1.28	613	yocA	2084918	2085197 2	2085058	10.4 3.9	3.	.1 -0.2	
yozB	2085281	2085817	-	2446	2898	2160	2454	1.20	0.88	1.02		-							
yocB	2085954	2086736	-	200	285	408	176	1.42	2.04	0.87	614	yocB	2086312	2086506 2	2086409	6.6 0.9	) 1.	.8 0.1	
	2005/007	2007.10.1			201	1.70	201	1.01	1.02	1.17	615	Inter	2086686	2086914 2	2086800	7.5 0.5	3.	.8 -0.8	
yocC	2086907	2087404	+	174	206	179	201	1.21	1.03	1.15	616	yocC	2087264	2087543 2	2087404	7.8 15.8	<b>5</b> 0.	.1 0.1	
yocD	208/468	2088445	+	549	13//	1028	455	2.59	1.90	0.83									

Supplen	cinary Tal	ле 51. Su	nmai	y or trai	iscriptoi	ne and ( Trare	crintor	up analyse e analysic	s (contir	wea).				C	hAP-chin	malysis				
	gene			Sim	nal intere	tv of PN		Even	ression re	tio <sup>b</sup>				<u> </u>	шэт -сшр 8		nding	intensity <sup>c</sup>		<u> </u>
			pu	ാള	KI HITEIIS	ny OF KIN	<b>1</b> 1	Expl	∆ ahh	uU	PBR	ORF		-		AhrR	nunna	Apl	1	Profile
name	start	end	stra	wild	∆abrB	$\Delta abh$	$\Delta abh$	$\Delta abrB/$	$\Delta abrB/$	$\Delta abh /$	ID	Or Intergonic	start	end	center	wild		wild	4 J D	ID
						∆abrB		Wild	wild	wild		mergenic				-type ⊿	abh	-type ∠	1 abrB	
des	2088607	2089665	+	1420	5580	4021	1224	3.94	2.84	0.87										
yocF	2089785	2090897	+	379	719	583	373	1.90	1.56	0.98										
yocG	2090916	2091515	+	881	1326	1165	802	1.51	1.33	0.90										
yocH	2092110	2092973	-	6180	5291	5781	6461	0.86	0.94	1.05										
yocl	2093221	2094996	-	983	676	666	917	0.68	0.68	0.92	(10	D	2005709	200/042	2005021	10.4	0.1	47	0.2	
acpD_1	2095501	2096187	-	5554 810	5491	3397	3032	0.65	0.64	1.05	018	acpD	2095798	2090043	2095921	10.4 -	0.1	4.7	0.2	
yock	2090558	2090907	-	314	406	331	276	1 31	1.05	0.34										
vocM	2097528	2098004	-	155	210	191	183	1.35	1.23	1.14	619	vocM	2097787	2098032	2097910	9.7	1.9	9.1	3.1	
yozN	2098071	2098334	+	93	95	100	96	1.02	1.08	1.03		-								
yocN	2098339	2098572	+	112	117	120	106	1.06	1.06	0.94										
yozO	2098658	2099002	-	1843	2604	2276	1743	1.43	1.26	0.93										
yozC	2099359	2099562	-	2597	1470	1607	1958	0.58	0.63	0.76										
dhaS	2099792	2101279	+	1277	4266	5006	1451	3.37	3.97	1.13	(21	10	2102000	2102452	2102270	20.2	0.0	17.1	5.0	
sqhC	2101380	2103278	+	121	129	131	133	1.06	1.08	1.09	621	sqnC	2102088	2102452	2102270	20.3	8.2	15.1	5.3	
soar vocR	2103208	2104113	+	155	128	520	182	0.82	0.85	1.17	623	vocP	2105250	2105512	2105381	83 1	0.6	2.0	17	
vocS	2104140	2105465	+	154	150	164	165	0.00	1.06	1.07	025	your	2105250	2105512	2105501	0.5 1	0.0	2.7	1.7	
odhB	2106717	2107970	-	22224	23224	23954	21940	1.05	1.08	0.99										
sucA	2107986	2110811	-	19663	20751	21475	20105	1.06	1.09	1.02										
yoj0	2111039	2113024	-	4971	4677	4909	5248	0.95	0.99	1.05										
yojN	2112966	2113880	-	3277	3034	3150	3658	0.94	0.97	1.12										
yojM	2113944	2114534	-	139	208	348	224	1.50	2.50	1.60										
yojL	2114627	2115871	-	390	1923	4452	1265	5.20	11.88	3.20										
	011/070	2117470		2.62		700	205	1.00	2.20	1.07	626	Inter	2115365	2116392	2115879	46.7	29.8	76.3	181.5	P01
yojK	2116253	211/4/0	-	363	107	/88	395	1.88	2.20	1.06										
yojj	2117/06	2118329	-	132	107	119	144	0.81	0.91	1.05	627	Inter	2118323	2118534	2118/20	2.0	1.0	0.8	5.4	
voil	2118594	2119952	+	651	672	600	573	1.06	0.92	0.88	628	voil	2118325	2110334	2110427	12.8	3.3	10.2	0.0	
yojH	2119968	2120816	+	1441	1386	1318	1191	0.97	0.91	0.83		J~J-								
yojG	2120842	2121270	-	5309	6075	5043	5952	1.15	0.95	1.12										
yojF	2121524	2121874	-	5338	6514	4812	5693	1.22	0.90	1.07										
yojE	2122225	2123121	-	1721	1087	959	1594	0.64	0.56	0.93										
yozR	2123220	2123693	+	109	116	122	134	1.07	1.13	1.22										
yojC	2123586	2123819	-	94	103	108	78	1.10	1.16	0.84										
yojB	2123/28	2123964	-	218	180	201	264	0.82	0.92	1.22										
yojA vodA	2124049	2125565	+	290	232	201 285	313	0.75	0.82	1.05										
your	2120710	2120107		270	20.	200	515	0.70	0.00	1.00	630	Inter	2126245	2126490	2126368	6.9	4.4	5.0	4.3	
yodB	2126544	2126882	-	536	620	566	474	1.15	1.04	0.86										
yodC	2127012	2127620	+	8524	10353	10748	8014	1.21	1.26	0.94										
yodD	2127663	2128265	-	205	147	167	308	0.71	0.82	1.42										
yodE	2128281	2129192	-	278	216	226	405	0.78	0.81	1.42								_		
IF.	0100574	0101066		244	211	252	272	1.16	1.21	1.00	632	Inter	2129305	2129533	2129419	8.5	1.8	6.9	1.8	
yodF	2129576	2131066	+	266	6246	352 6007	212	1.10	1.31	1.02	633	yodF	2130/6/	2130876	2130822	0.1	0.3	0.4	5.8	
vodH	2131101 2132654	2132301	+	154	170	172	153	1.11	1.07	0.99										
vodI	2132034	2133694	+	295	277	283	334	0.94	0.96	1.13										
yodJ	2133765	2134586	-	8530	7483	7203	8544	0.88	0.85	1.00										
deoD	2134669	2135370	-	12929	13090	13362	12798	1.01	1.03	0.99	634	deoD	2134626	2135024	2134825	25.6	18.4	14.2	0.4	
yodL	2135737	2136054	-	672	545	503	578	0.81	0.74	0.85										
yodM	2136112	2136723	-	958	855	762	904	0.92	0.80	0.93										
yozD	2136801	2136977	-	172	145	143	195	0.84	0.81	1.08										
yodN	2137236	2137916	-	139	120	120	133	0.87	0.87	0.95							1.0			
<b>.</b> E	2122067	2122201		022	072	044	076	0.06	1.02	0.05	635	Inter	2137924	2138101	2138013	4.6	1.9	5.6	4.7	
yoze kam A	2138007	2136291	-	922	0/3	944	102	0.90	1.05	1.02										
vodP	2130032	2140007	-	86	80	86	95	0.93	1.01	1.02										
vodO	2140901	2142211	-	125	109	118	137	0.88	0.95	1.11										
yodR	2142220	2142873	-	162	138	146	170	0.85	0.90	1.05										
yodS	2142858	2143547	-	144	114	120	179	0.79	0.84	1.24										
yodT	2143554	2144888	-	167	140	142	205	0.84	0.85	1.23	636	yodT	2143450	2143864	2143657	5.8	2.3	3.9	8.5	
cgeE	2145211	2145990	-	207	268	243	224	1.29	1.17	1.07										
cgeD	2146019	2147299	-	109	116	111	107	1.07	1.02	0.98	638	cgeD	2145948	2146261	2146105	11.6	4.6	0.2	3.6	
cgeC	2147364	2147669	-	91	84	96	82	0.92	1.05	0.90										
cgeA	214/8/4	21482/5	+	120	146	88	147	0.95	1.00	0.89										
суев	2148282	2149235	+	138	140	144	14/ 146	2.06	3 20	1.06										
pny	2147300	2150454	-	150	405	451	140	2.90	5.29	1.00	639	Inter	2150419	2150714	2150567	9.2 1	1.1	12	-0.6	
yodU	2150824	2151249	+	104	153	157	103	1.48	1.51	1.00	640	yodU	2151116	2151344	2151230	5.2	7.0	6.8	8.4	
yotN	2151284	2151460	-	86	74	84	86	0.87	0.98	1.00		-								
yotM	2151463	2152050	-	92	74	84	82	0.80	0.91	0.89										
yotL	2152125	2152367	+	38	66	59	39	1.78	1.55	1.05										

Supplem	gene	nc 51. 5U	an 118	ry or traf	scriptol	Trans	criptom	e analysis	la (condi	ucu).				С	hAP-chip	analysis				
	8			Sigr	nal intens	ity of RN	IA <sup>a</sup>	Exp	ression ra	tio b		ODE					Binding	intensity	c	
name	start	end	and			Aabh		A abrB/	$\Delta abh$	A abh /	PBR	or	start	end	center	A	brB	A	Abh	Profile
	Suit	ena	str	wild	∆abrB	$\Delta abrB$	$\Delta abh$	wild	$\Delta abrB/$	wild	ID	Intergenic	start	cild	contor	wild	$\Delta abh$	wild	∆abrB	ID
votK	2152360	2152554		07	63	78	106	0.66	wild 0.80	1.07						-type		-type		
votJ	2152638	2152850	_	39	37	35	38	0.00	0.92	0.99										
yotI	2152916	2153278	-	62	56	58	54	0.90	0.94	0.87										
yotH	2153275	2153448	-	156	125	127	134	0.80	0.81	0.86	641	yotH	2153241	2153605	2153423	19.4	2.4	2.3	-1.4	P07
yot $G$	2153464	2153781	-	80	76	77	80	0.94	0.96	1.00										
yotF	2153794	2153871	-	50	46	56	41	0.95	1.11	0.85										
yotE votD	2153903	2154049	-	279	82 180	235	227	0.70	0.78	0.88										
votC	2154085	2154447	_	68	52	55	76	0.04	0.80	1.10										
yotB	2154491	2155318	-	101	85	97	111	0.84	0.96	1.09										
sspC	2155437	2155655	+	74	162	178	73	2.15	2.36	0.99										
yosZ	2155846	2155911	-	927	603	730	733	0.65	0.78	0.77										
yosX	2155955	2156308	-	141	105	122	106	0.74	0.85	0.75	(12)		2156454	2156649	0156551	5.0	1.4	0.1	0.4	
yosW vosV	2156539	2156880	-	109 74	102	113	49	0.93	1.04	1.03	642 643	yos W vos V	2156454	2156648	2156551	13.3	1.4	-0.1	-0.4	
y03 v	2157027	2157517		/4	00	/1	47	0.01	0.95	0.05	643	Inter	2157321	2157274	2157546	32.2	8.6	6.2	5.5	
yosU	2157637	2157882	+	99	122	121	169	1.21	1.21	1.72										
yosT	2157922	2158371	-	261	323	367	185	1.24	1.41	0.70	643	yosT	2157781	2158144	2157963	26.2	4.9	2.4	0.3	P07
yosS	2158466	2158894	-	190	154	159	214	0.81	0.84	1.11										
yosR	2158940	2159182	-	134	120	142	134	0.90	1.06	1.00										
nrar_2	21591/9	21009/6	-	154	114	132	151	0.85	0.98	0.98	64/	Inter	2161214	2161323	2161269	1.0	11	-0.4	3.4	
vosN	2161306	2164812	-	96	86	93	96	0.89	0.97	0.99	044	21801	2101214	2101525	2101209	1.9	1.1	-0.4	5.4	
nrdI_2	2164775	2165164	-	74	57	61	72	0.77	0.82	0.96										
yosL	2165170	2165523	-	89	64	68	60	0.72	0.76	0.67										
yosK	2165611	2165811	-	88	57	65	74	0.65	0.73	0.83										
yosJ	2165856	2166050	-	139	124	152	106	0.89	1.10	0.76										
yosi vosH	2166237	2166707	-	150	130	02 144	160	0.98	0.91	1.12										
vosG	2166768	2167130	-	85	72	72	75	0.85	0.84	0.88										
yosF	2167173	2167298	-	105	81	85	84	0.78	0.82	0.81										
yosE	2167312	2167659	-	122	115	128	118	0.94	1.05	0.97										
yosD	2167674	2168069	-	123	85	83	88	0.69	0.67	0.71										
yosC	2168108	2168650	-	158	118	138	146	0.74	0.87	0.92										
yosB vosA	2168095	2168874	+	82 440	466	84 554	90 608	1.09	1.11	1.19										
vorZ	2169228	2169440	-	121	101	103	97	0.83	0.84	0.79										
yorY	2169507	2169689	-	81	67	76	85	0.83	0.94	1.05										
yorX	2169702	2169929	-	107	84	106	96	0.79	0.99	0.90										
yorW	2169969	2170334	-	106	98	107	95	0.93	1.01	0.90										
yorV	2170337	2170555	-	77	73	80	75	0.94	1.03	0.96										
mtbP vorT	2170599	21/1930	-	147	121	132	138	0.82	0.90	0.94										
vorS	2172130	2172648	-	61	61	63	61	1.00	1.04	0.99										
yorR	2172657	2173154	-	128	104	130	127	0.83	1.01	0.97										
yorQ	2173154	2173309	-	136	113	144	108	0.83	1.06	0.80										
yorP	2173302	2173517	-	132	145	143	121	1.09	1.09	0.91										
yorO	2173550	2173747	-	138	136	128	174	0.99	0.93	1.27										
yorn vorM	21/3/83	21/3952	-	1// 70	198	210	205	1.15	1.19	1.19	646	vorM	2173811	2174204	2174053	20.4	41.4	7.3	43	
,0114	21/4040	21/4/04	-	70	05	00	03	0.73	0.77	0.09	647	yorM	2174440	2174889	2174665	30.8	9.0	33.4	4 3.4	
yorL	2174792	2178709	-	98	81	91	86	0.83	0.93	0.88		J								
yorK	2178722	2180452	-	98	82	87	90	0.84	0.88	0.91										
yorJ	2180452	2181588	-	94	79	93	83	0.84	0.99	0.88										
yorI	2181604	2183118	-	77	68	73	73	0.88	0.95	0.94	CER	T North	0100001	2102644	0100010		00.0	10-1		DO 1
yorH vorG	2183133	2183603	-	114	93	101	81	0.81	0.88	0.71	050	yorn	2182991	2185644	2183318	-60.1	80.2	18.8	43.6	P01
yorF	2183040	2185614	-	103	149	136	78	1.20	1.03	0.76										
yorE	2185636	2186007	-	157	283	260	108	1.74	1.63	0.69										
yorD	2186181	2186495	-	1453	10966	9881	1613	7.56	6.87	1.10										
_											652	Inter	2186205	2186857	2186531	56.1	76.4	23.8	1.4	P02
yorC	2186572	2186952	-	1043	1388	1604	666	1.33	1.54	0.63										
yorB vorA	2187/015	218/311	-	1455	1822	1880	835	1.28	1.50	0.58										
voaZ	218/400	2189100	-	102	90 141	95 161	130	0.88	1.09	0.94										
yoqY	2190080	2190475	-	119	111	119	135	0.94	1.00	1.14										
voqX	2190530	2190751	-	112	81	87	143	0.75	0.78	1.24										
voqW	2190822	2191496	+	183	173	217	214	0.94	1.18	1.18										
ligB	2191566	2192378	+	61	60	64	63	1.00	1.06	1.06										
yoqU T	2192444	2192857	-	107	92	105	108	0.86	0.98	1.00										
yoqT	2193023	2193172	+	31	43	41	40	1.40	1.31	1.30										
yoqS voqR	2195249	2193596	-	260	183	19/	255	0.70	0.75	0.8/										
уочк	2193398	2193934	-	88	15	82	111	0.82	0.93	1.24										

Supplet	gene	ле 51. 5ш	11111111	y 01 ti ai	вспрю	Trans	criptom	analyse	s (conun	ucu).				0	hAP-chip a	analysis		
	gene			Sigr	nal intensi	ty of RN	A <sup>a</sup>	Exp	ression rat	tio <sup>b</sup>					in the second se	Binding	intensity c	
name	start	end	strand	wild	A ahrR	$\Delta abh$	Aabh	$\Delta abrB/$	$\Delta abh$ $\Delta abrB/$	$\Delta abh /$	PBR ID	ORF or	start	end	center	AbrB	Abh	Profile ID
D	2102014	2104255	.,	164	127	∆ abrB	179	wild	wild	wild		Intergenic				-type ∆abh	-type △ abrB	
yoqr	2193914	2194233	-	104	127	155	178	0.77	0.81	1.07	654	Inter	2194194	2194456	5 2194325	11.2 1.4	2.5 0.8	
yoq0	2194369	2194743	+	423	630	690	390	1.52	1.66	0.93								
yoqN voqM	2194/60	2194978	-	180	2353	2651	181	0.86	15 77	0.97	655	voaM	210/87/	2105527	2105201	64.8 03.1	29.3 -1.4	P02
yoqM voaL	2195182	2195400	-	133	102	111	142	0.76	0.83	0.80	656	voaL	2194874	2195527	3 2195201	11.4 3.0	8.2 -1.3	F02
yoqK	2196317	2196520	-	161	109	116	135	0.67	0.72	0.83		J~1						
yoqJ	2196540	2197055	-	178	125	166	171	0.70	0.93	0.95								
yoqI	2197266	2197460	-	60	56	68	79	0.96	1.13	1.27								
yoqH	2197509	2197961	-	122	121	126	115	0.99	1.03	0.94								
yoqG voqE	2198044	2198301	-	120	109	130	107	0.91	1.08	0.89								
yoqr voaE	2198558	2198349	2	124	100	110	102	0.85	0.88	0.87								
yoqD	2198776	2199531	-	163	125	143	140	0.77	0.87	0.86								
											657	Inter	2199481	2199624	2199553	4.5 2.0	0.3 -0.1	
yoqC	2199572	2199979	-	95	82	93	91	0.87	0.98	0.95								
yoqB	2199986	2200324	-	75	60	65	66	0.80	0.86	0.88								
yoqA	2200321	2200671	-	195	163	195	178	0.83	1.00	0.91								
yopZ vopY	2200684	2200887	-	218	187	201	200	0.86	0.88	0.73								
vonX	2200001	2201179	2	142	116	133	133	0.82	0.94	0.94								
yopW	2201577	2201912	-	92	79	77	82	0.85	0.83	0.87								
yopV	2202001	2202195	-	171	107	122	129	0.61	0.70	0.73								
yopU	2202307	2202504	-	536	312	322	429	0.58	0.60	0.80								
yopT	2202574	2202792	-	379	196	183	269	0.49	0.46	0.68	658	yopT	2202560	2202786	5 2202673	6.3 2.1	0.9 -1.3	
yopS	2202975	2203199	+	810	1052	757	689	1.28	0.92	0.84								
yopR	2203388	2204365	-	1677	1236	1210	1607	0.73	0.72	0.95								
yopQ yopP	2204389	2205771	-	216	223	237	201	1.02	0.73	0.99								
vonO	2205070	2200754	-	299	275	306	252	0.91	1.02	0.83								
yopN	2207204	2207521	-	741	662	641	750	0.87	0.85	0.98								
yopM	2207524	2207724	-	212	187	156	202	0.84	0.72	0.94								
yopL	2208051	2208176	-	4667	7257	7411	4559	1.56	1.59	0.98								
yopK	2208190	2209350	-	125	193	185	141	1.50	1.46	1.14						_		
	2200527	2200042		470	1200	1150	(20)	2.50	2.41	1.20	659	Inter	2209171	2209535	5 2209353	16.6 5.5	2.5 -0.4	
yopJ vopI	2209527	2209943	-	472	203	261	170	2.39	2.41	1.50								
vonH	2209943	2210478	2	143	233	201	170	1.55	1.53	1.08	660	vonH	2210752	2211099	2210926	13.7 4.0	5.8 -0.6	
yopG	2211080	2211211	-	371	836	753	409	2.27	2.00	1.05		J~P						
yopF	2211222	2211437	-	143	265	252	152	1.79	1.74	1.05								
yopE	2211441	2211692	-	424	711	698	477	1.71	1.67	1.11								
yopD	2212279	2212674	-	1107	2181	2097	1164	1.95	1.87	1.06								
yopC	2212732	2214060	-	403	925	797	470	2.24	1.94	1.16	661	yopC	2212792	2212884	2212838	2.9 1.5	1.9 1.5	
vonB	2214168	2214395		81	92	104	76	116	1 29	0.93	002	yopC	2213557	2214431	2213994	80.9 38.4	51.2 11.1	
vonA	2214100	2214373	2	244	382	391	287	1.10	1.61	1.15	662	vonA	2214441	2215298	3 2214870	67.0 68.5	27.0 3.4	P02
yonX	2216329	2216835	-	91	75	83	86	0.82	0.91	0.94		J~P						
yonV	2217163	2218395	-	65	61	67	62	0.93	1.03	0.96								
yonU	2218477	2218665	-	1538	1601	1556	1139	1.04	1.01	0.74								
yonT	2218980	2219156	-	370	312	290	294	0.82	0.78	0.78								
yonS	2219531	2220142	-	534	667	503	592	1.27	0.94	1.11	663	yonS	2219711	2219973	3 2219842	3.2 1.9	2.4 13.0	
yonk	2220257	2220585	-	221	292	212	255	1.51	0.95	1.12	664	Intor	2220206	2221452	2220870	587 025	20.0 64.1	<b>D</b> O 1
vonP	2221536	2221730	+	89	88	86	68	0.98	0.97	0.76	004	miler	2220300	2221432	2220077	50.7 72.5	57.7 04.1	101
vonO	2221770	2224289	+	77	73	79	70	0.95	1.03	0.91	665	vonO	2223111	2223288	3 2223200	3.9 1.8	0.7 0.7	
yonN	2224533	2224811	+	432	228	242	263	0.53	0.56	0.61		-						
											666	Inter	2224574	2225158	3 2224866	39.3 15.2	47.7 37.3	
yonK	2226493	2226684	+	115	72	85	55	0.63	0.74	0.49								
yonJ	2226701	2227918	+	207	153	179	155	0.74	0.87	0.75								
yoni yonH	222/952	2228362	-	1082	/58 70	/51	991 87	0.70	0.69	0.91								
yonG	2220301	2230104	+	93	75	90 82	84	0.72	0.87	0.91								
yonF	2230091	2231860	+	88	78	82	80	0.88	0.93	0.91								
yonE	2231878	2233398	+	126	100	110	105	0.79	0.87	0.83								
yonD	2233429	2234865	+	379	294	373	217	0.78	0.99	0.58								
yonC	2234890	2235426	+	214	186	215	172	0.87	1.00	0.80								
yonB	2235465	2236481	+	354	290	383	179	0.82	1.08	0.50								
yonA	2236517	2236987	+	471	358	444	306	0.78	0.96	0.67								
yomZ	2237002	223/397	+	330	261	320	199	0.80	0.98	0.61	667	vorrV	2227450	2227720	2727500	7.0 2.2	-07 08	
yom1 yomY	2231394	2237048	+	255	183	200	192	0.71	0.08	0.37	00/	youri	2231439	2231120	1 2231390	1.7 3.3	-0.7 -0.8	
yomW	2238279	2238785	+	259	198	2.60	162	0.77	1.01	0.63								
yomV	2238782	2239492	+	269	185	246	143	0.68	0.91	0.53								

Supplem	entary Tal	ole S1. Su	mma	ry of trai	nscripto	me and (	ChAP-ch	ip analyse	es (contin	ued).				Ch A D shin	onolygia		
	gene				11.1	Trans	criptom	e analysis		. b				ChAP-chip	anaiysis	· . ·. c	
			р	Sig	nal intens	ity of RN	Α."	Exp	ression rat	tio	PBR	ORF			AbrP	intensity	Profile
name	start	end	strar	wild	∆abrB	∆ abh	$\Delta abh$	∆ abrB/	$\Delta abrB/$	∆abh /	ID	Or	start	end center	wild Ashh	wild A shaP	ID
						∆ abrb		wiid	wild	wiid		Intergenie			-type	-type	
yomU	2239535	2240332	+	399	328	405	209	0.82	1.02	0.52							
yomT	2240961	2241188	+	184	146	180	149	0.79	0.96	0.79							
yomS vomR	2241252	2241008	+	159	128	152	144	0.92	1.09	1.04							
vomO	2241010	2242027	+	192	162	102	147	0.85	0.91	0.02							
vomP	2242030	2243100	+	127	102	120	68	0.82	0.94	0.54							
vomO	2243426	2243926	+	147	110	141	96	0.74	0.96	0.65	668	vomO	2243171	2243705 2243438	43.4 31.4	9.0 -1.8	
yomN	2243910	2244329	+	169	143	173	113	0.85	1.02	0.67	669	yomN	2243902	2244079 2243991	4.0 6.7	1.2 0.0	
yomM	2244343	2245344	$^+$	130	115	135	101	0.89	1.03	0.78							
yozP	2245347	2245676	-	111	137	167	90	1.23	1.51	0.82							
yomL	2245852	2246538	-	894	3428	4105	635	5.01	5.67	1.18		_					
	2247085	2247521		209	1502	1400	201	2 70	2 71	0.74	670	Inter	2246707	2246901 2246804	5.5 5.6	0.7 0.6	
yomk	2247085	2247331	+	398	1302	1462	501	3.78	5.71	0.74	671	Inter	2247251	2247836 224754	1 43.7 28.0	25.6 16.3	
vom.I	2247613	2248296	+	521	1720	1659	886	3.29	3.21	1.70	0/1	mer	2247231	2247030 224734-	43.7 20.0	23.0 10.3	
yomI	2248350	2255207	+	98	86	90	80	0.88	0.92	0.82	672	vomI	2251433	2251746 2251590	10.0 18.2	1.3 0.3	
2											673	yomI	2253065	2253565 2253315	5 <b>28.0</b> 7.9	44.6 71.3	
yomH	2255258	2256016	$^+$	59	51	50	52	0.87	0.85	0.89							
yomG	2256028	2258655	+	133	115	125	114	0.86	0.94	0.86	674	yomG	2257502	2257730 2257616	5 <u>8.1</u> 6.2	-0.1 -1.0	
											675	Inter	2258539	2258801 2258670	7.8 11.9	-0.4 -0.9	
yomF	2258671	2259492	+	109	99	116	97	0.90	1.06	0.89							
yomE	2259529	2261463	+	110	93	101	88	0.85	0.92	0.80							
yomD	2261633	2262457	+	/5	62 131	1/1	119	0.83	0.94	0.66							
bhlA	2262085	2203788	+	83	70	75	61	0.85	0.90	0.70							
bhlB	2263070	2264365	+	101	76	90	74	0.78	0.90	0.74							
bdbB	2264421	2264867	_	433	3155	1596	162	7.15	3.57	0.38 +	-						
yolJ	2264864	2266132	-	505	3470	2017	167	6.79	3.87	0.35 +	676	yolJ	2265118	2265346 2265232	2 7.7 6.3	1.8 4.9	
bdbA	2266132	2266545	-	495	2922	1493	136	5.60	2.78	0.27 +	677	bdbA	2266087	2266519 2266303	3 27.8 29.4	5.7 2.6	P03
sunT	2266542	2268659	-	240	1577	773	79	6.25	3.05	0.34 +	- 678	sunT	2266988	2267284 2267136	5 <u>9.3</u> 2.2	0.7 4.0	
sunA	2268717	2268887	-	4390	19776	15215	1104	4.47	3.45	0.25 +	-	_					
	22/0184	22(0501		5029	2091	2776	4550	0.62	0.76	•	679	Inter	2268518	2269715 2269117	108.3 130.6	48.3 38.4	P01
your	2209184	2209501	-	210	3081	3//0	4558	0.62	0.76	1.02							
volD	2209003	2270855	-	74	64	73	66	0.77	0.84	0.89							
volC	2271352	2271687	+	136	463	530	113	3.40	3.90	0.83	680	volC	2271272	2271653 2271463	3 14.5 21.0	0.5 -1.1	
yolB	2271730	2272086	-	545	2347	2054	339	4.26	3.77	0.61		5					
yolA	2272092	2272559	-	2374	9817	9171	1374	4.15	3.89	0.58							
											681	Inter	2272343	2273165 2272754	57.5 85.7	-1.1 2.2	P03
yokL	2273185	2273718	-	748	1754	1775	712	2.31	2.36	0.94		_					
	2272754	0074000		804	2224	2282	001	2.75	2.94	1.00	682	Inter	2273550	2273914 2273732	2 20.3 30.0	8.8 0.9	
yok L	2275754	2274552	-	1006	2234	3528	1108	2.73	2.04	1.08							
vokI	2274902	2276617	-	415	2142	2266	401	5.34	5.62	0.96							
<i></i>											684	Inter	2276593	2276804 2276699	6.3 6.5	-0.2 0.1	
yokH	2276717	2277274	-	984	2191	2207	883	2.17	2.24	0.91							
yokG	2277798	2278871	-	853	1940	1854	832	2.25	2.14	0.97							
											685	Inter	2278718	2279201 2278960	30.6 24.8	7.3 -1.8	
yokF	2279173	2280063	+	5973	6789	6213	3838	1.14	1.04	0.64							
yokE	2280077	2280559	+	1050	1020	1063	533	0.96	1.01	0.50	686	yokE	2280061	2280493 2280277	42.6 12.7	12.7 -0.3	D02
vokD	2280863	2281681	+	369	880	769	285	2 36	2.08	0.75	080	mer	2280303	2281003 2280733	24.6 23.1	-0.9 -0.5	P03
yokD vokC	2280303	2281001	-	146	149	152	159	1.00	1.03	1.08							
yoke vokB	2283054	2283764	-	168	338	345	248	1.98	2.02	1.46	687	vokB	2283087	2283519 2283303	10.2 5.3	1.4 10.7	
											687	Inter	2283529	2284131 2283830	66.7 55.3	15.3 3.8	
yokA	2283967	2285604	$^+$	407	477	453	403	1.15	1.09	0.98							
ypqP	2285626	2286249	+	451	542	498	424	1.22	1.10	0.96	688	Inter	2285501	2285814 2285658	8 8.1 13.8	13.7 18.5	
yppQ	2286293	2286724	-	2861	3867	4641	3829	1.34	1.61	1.34							
msrA	2286725	2287258	-	2193	2713	3252	2729	1.24	1.49	1.24							
ypoP	2287390	2287815	+	2398	2718	2514	2419	1.12	1.04	1.02							
ypnP ymmT	228/803	2289202	-	227	2082	2201	2120	0.70	1.02	0.92							
vnmS	2289274	2289408	-	2209	1763	1968	2077	0.94	0.86	0.93							
vpmR	2290054	2290821	-	1787	1790	1835	1739	1.00	1.03	0.97							
ypmQ	2290899	2291480	-	1028	1709	2023	1190	1.67	1.98	1.16							
ypmP	2291628	2291879	-	2088	3712	3338	1848	1.75	1.56	0.89							
ilvA	2291965	2293233	-	457	635	692	352	1.36	1.49	0.76							
yplP	2293482	2294477	+	810	1025	779	776	1.23	0.94	0.96	691	yplP	2294069	2294348 2294209	15.2 3.5	7.7 1.5	
yplQ	2294498	2295139	+	852	993	870	763	1.14	1.01	0.89							
ypkP	2295178	2295798	-	2482	2211	2171	2705	0.89	0.87	1.09							
dfrA thyA 2	2295799	2296305	-	2532	1958	1840	2506	0.77	0.72	0.98							
vniO	2290302	2297090	-	2402 5101	1943 4779	1049 5734	2009 51/19	0.79	1.01	0.90							
JPJ Q	22/1100		-	5171	-110	5454	5140	0.72	1.01	5.77							

Suppler	nentary Tal	de S1. Sur	nma	ry of trai	nscriptor	me and (	ChAP-ch	nip analyse o analyse	es (contin	ued).				C	hAP_chin	nalveic				
	gene			Sim	nal intens	ity of PN	A a	с anaiysis Eve	ression ro	tio <sup>b</sup>				u	алы -спір 8	matysis	Binding	intencity	с	
			pu	Sigi	ыа шиепя	ny OI KIN	A	Exp	$\Delta ahh$	uU	PBR	ORF				Ab	ынишg rB	A	bh	Profile
name	start	end	stra	wild	∆abrB	∆abh ∆abrB	∆abh	∆abrB/ wild	∆abrB/ wild	∆abh / wild	ID	or Intergenic	start	end	center	wild -type	∆abh	wild -type	∆abrB	ID
ypjP	2297731	2298342	-	2165	2136	2143	2248	0.99	0.99	1.04										
ypiP	2298602	2299120	-	1954	1667	1575	1814	0.87	0.81	0.91										
ypnP ilvD	2299417	2299851	-	431	351	6224 401	415	0.98	0.93	0.96										
ypgR	2301923	2303056	-	3725	4394	4712	4241	1.19	1.28	1.14										
ypgQ	2303116	2303733	-	1129	1647	2021	1287	1.46	1.79	1.13										
bsaA	2303749	2304231	-	698	941	1129	839	1.36	1.63	1.19										
metA	2304574	2305248	+	1092	1252	1245	1301	1.16	1.15	1.18	693	Inter	2305272	2305908	2305590	42.2	26.8	31.8	1.4	P02
ugtP cspD	2305/11	2306859	+	4888	3914	4080	4757	0.80	0.83	0.97										
degR	2307354	2307536	-	643	50540	468	614	0.79	0.72	0.95										
ypzA	2307692	2307961	+	179	496	434	166	2.68	2.33	0.94										
ypeQ	2307989	2308171	-	593	640	746	506	1.12	1.31	0.84										
ypeP	2308164	2308844	-	469	547	589	484	1.23	1.30	1.01								1.0		
wndP	2308027	2300616	+	527	412	380	503	0.77	0.74	1.12	694	Inter	2308740	2308951	2308846	6.2	2.2	1.8	-0.2	
ypa1 vpdO	2309527	2310014	+	1346	1075	1029	1351	0.80	0.74	1.00										
sspL	2310056	2310184	+	731	897	773	578	1.25	1.04	0.81										
ypcP	2310192	2311082	-	1036	893	804	1027	0.87	0.78	0.99										
ypbS	2311404	2311661	-	3451	3328	3232	3026	0.97	0.94	0.88										
ypbR	2311726	2315307	-	1640	1355	1450	1433	0.83	0.88	0.87										
ypbQ bcsA	2315043	2316149	-	142	124	109	130	1.10	1.19	1.05										
nbuX	2317324	2318640	-	1641	1470	1243	2126	1.04	0.84	1.05										
xpt	2318637	2319221	-	1393	1289	1111	1828	1.15	0.93	1.31										
ypwA	2319552	2321057	-	6190	10158	10339	7903	1.65	1.68	1.27										
kdgT	2321169	2322161	-	934	642	764	854	0.69	0.83	0.92										
kdgA	2322206	2322796	-	474	332	380	488	0.70	0.80	1.03										
кад <b>к</b> kdgR	2322798	2323772	-	991	803 906	943	890 856	0.81	0.95	0.90										
augre	2020010	202102)		207	,00	2.2	000	0.75	0.57	0.00	697	Inter	2324686	2325203	2324945	47.3	47.2	38.4	-0.7	P02
kduI	2325051	2325878	+	1205	1775	1994	1241	1.47	1.65	1.03										
kduD	2325880	2326644	+	511	721	786	544	1.40	1.53	1.06	698	kduD	2326012	2326342	2326177	17.9	13.9	9.5	8.2	
ypvA	2326685	2328610	-	3023	2002	1805	2631	0.66	0.60	0.87	700	ypvA	2327474	2327566	2327520	3.0	0.5	1.3	-0.1	
yptA vpsC	2328/12	2328903	-	3902	3438	3062	3525	0.88	0.68	0.81										
rnpB	2330517	2330917	-	33941	33967	34440	33440	1.00	1.01	0.99	702	mpB	2330330	2331034	2330682	37.4	88.9	44.9	7.5	
ypsB	2330976	2331272	-	9450	9136	9830	9711	0.97	1.04	1.03										
ypsA	2331350	2331892	-	2160	1747	1605	2032	0.83	0.75	0.94										
cotD	2331981	2332208	-	3739	4661	3816	3615	1.29	1.03	0.99	702	D		0000500	0000077	0.0	2.0	1.1	10.1	DO 4
yprB	2332521	2333762	-	1/1/	1510	1513	1425	0.88	0.88	0.83	/03	ургВ	2333220	2333533	2333377	2.3	2.0	1.1	19.4	P04
vpaE	2336130	2336636	-	7151	9960	10053	7167	1.41	1.42	1.00										
ypqA	2336774	2337193	+	108	91	93	100	0.84	0.87	0.94										
yppG	2337214	2337591	-	82	80	76	97	0.98	0.92	1.18										
yppF	2337779	2337967	+	2534	2104	2714	2148	0.83	1.07	0.85										
yppE	2338006	2338377	-	2171	2037	1975	1951	0.94	0.91	0.89										
sspD sspM	2338867	2338971	-+	120	211 106	128	139	1.75	1.84	0.80										
yppC	2338996	2339958	-	222	216	188	222	0.97	0.85	1.00										
recU	2339999	2340619	+	4808	5445	5094	5579	1.13	1.06	1.16										
ponA	2340641	2343385	+	6381	6337	6171	6591	0.99	0.97	1.03										
ypoC	2343461	2343955	-	3619	2570	2548	2942	0.71	0.70	0.81										
nth dnaD	2343952	2344611	-	4011 4736	2919	2870	3611 4120	0.73	0.72	0.90										
asnC	2345421	2346713	-	14228	11672	11577	13651	0.72	0.81	0.96										
aspB	2346857	2348038	-	15403	14804	15001	15108	0.96	0.97	0.98										
ypmB	2348061	2348546	-	9656	8755	8498	9516	0.91	0.88	0.99	706	ypmB	2348010	2348272	2348141	8.7	8.2	1.8	0.5	
ypmA	2348555	2348725	-	8640	7587	6644	8302	0.88	0.76	0.95	707	Inter-	2240/22	0240050	0240724	11.2	1.0		2.2	
dinC-	7310000	2351662		2955	3625	3157	3770	0.05	0.65	0.07	707	Inter	2348622	2348850	2548736	11.3	1.5	6.4	2.3	
panD	2340008	2352172	-	4961	4381	4375	4844	0.95	0.82	0.97										
panC	2352174	2353034	-	8235	7640	7558	8490	0.93	0.92	1.03										
panB	2353036	2353869	-	7225	6732	6538	7327	0.93	0.91	1.01										
birA	2354115	2355092	-	3282	3061	2954	3379	0.95	0.90	1.02										
cca	2355077	2356270	-	6570	6630	6657	6613	1.01	1.02	1.00										
ypjH vpiC	2356275	2358114	Ē	5952 5467	5856 5096	5954	6304 5669	0.99	1.00	1.06										
ypj0 mgsA	2357440	2358520	-	7913	7818	7958	8280	1.00	1.01	1.05										
dapB	2358536	2359339	-	6741	6716	6664	7251	0.99	0.99	1.08										
ypjD	2359351	2359686	-	5415	4801	4755	5257	0.89	0.88	0.97										
ypjC	2360051	2360698	+	1756	2315	2282	1634	1.32	1.30	0.92										

	gene					Trans	criptom	e analysis						C	hAP-chip a	nalysis				
			_	Sig	gnal intens	ity of RN	A <sup>a</sup>	Exp	ression rat	io <sup>b</sup>		ORF					Binding	intensity '	с	
name	start	end	rand			∆abh		∆abrB/	$\Delta abh$	∆abh /	PBR	or	start	end	center	Ab	orB	A	bh	Profile
			st	Wild	$\Delta abrB$	∆abrB	∆abh	wild	∆ abrB/	wild	ID	Intergenic				wild	$\Delta abh$	wild	∆abrB	ID
vniR	2360740	2361534		932	996	886	926	1.08	0.93	0.97	711	vniB	2360981	2361277	7 2361129	-type	2.5	-type	18.0	P04
vpiA	2361603	2362160	) -	659	808	715	686	1.00	1.07	1.03	/11	JPJD	2500501	2501277	2501127	2.7	2.5	1.5	10.0	104
qcrC	2362307	2363074	+ -	1976	5 8737	8785	3975	4.43	4.47	2.03										
											713	Inter	2363038	2363147	7 2363093	1.7	2.2	3.9	1.9	
qcrB	2363109	2363783	- 1	2703	3 10810	10640	5037	3.99	3.93	1.86										
qcrA	2363785	2364288	- 8	3527	14753	14064	6325	4.18	3.98	1.79										
	2264421	2264975	,	1704	: 2200	2121	2150	1.26	1.92	1.20	714	Inter	2363990	2364626	5 2364308	51.4	67.0	42.9	2.4	P02
ypır vniB	2364932	2365471	-	3349	3 2300 3 4265	5012	3753	1.50	1.82	1.28	/14	уриг	2304037	2303000	5 2304633	51.2	10.2	21.0	4.0	P02
vpiA	2365543	2366814	-	1623	3 1412	1430	1799	0.87	0.89	1.12										
aroE_1	2367150	2368436	<u>5</u> -	5385	5 4249	4591	4789	0.79	0.85	0.89										
tyrA	2368447	2369562	2 -	5025	5 3794	3985	4511	0.75	0.79	0.90	715	tyrA	2368886	2369165	5 2369026	8.6	8.9	3.0	0.9	
hisC	2369611	2370693	- 5	5438	4506	4549	5003	0.83	0.84	0.92										
trpA	2370704	2371507	-	911	1244	1132	904	1.34	1.24	0.96										
trpВ trpE	2371500	2372702		20	300 222	291	174	1.47	1.40	1.02										
trnC	2372085	2373330	, -	17:	183	165	150	1.30	1.25	1.12										
trpD	2374080	2375096	<u>.</u>	21	290	252	229	1.39	1.20	1.10										
trpE	2375068	2376615	; -	254	538	406	237	2.03	1.58	0.92										
aroH	2376831	2377214		7280	) 5690	6172	6263	0.78	0.85	0.86										
aroB	2377211	2378299	) -	5769	4899	5050	4887	0.86	0.88	0.85										
aroF	2378361	2379470	) -	4580	) 3846	4035	3933	0.84	0.88	0.86										
cheR ndk	2379545	2380315	- (	12102	11600 I	1029	1216	0.66	0.68	0.81										
nak henT	2380332	2382163	-	9204	5 11090	7170	9397	0.89	0.93	1.00										
ubiE	2382105	2382806	, 5 -	9119	7989	7743	9052	0.88	0.85	0.99	718	ubiE	2382010	2382408	3 2382209	24.4	20.8	8.9	2.5	
hepS	2382813	2383568	- 8	5102	4015	3930	5538	0.79	0.77	1.09										
mtrB	2383731	2383958	- 8	8413	6621	6612	8403	0.79	0.79	1.00										
folE	2383980	2384552		7127	5872	5678	7094	0.82	0.80	1.00	719	folE	2384152	2384397	7 2384275	11.6	9.6	13.8	5.9	
hbs	2384740	2385018	- 8	31656	5 31367	31673	32619	0.99	1.00	1.03	720	Inton	2205100	2285400	1 2285205	6.0	05	16	26	
spoIVA	2385392	2386870		130	5 135	155	173	0.99	1 13	1.26	720	mer	2363169	2383400	1 2363293	0.0	0.5	1.0	2.0	
vphF	2387051	2387785	, ; _	735	5 1669	1891	1217	2.27	2.60	1.65										
yphE	2387807	2388010	) -	585	5 1548	1325	907	2.57	2.23	1.51										
											721	Inter	2387824	2388358	3 2388091	25.1	18.7	34.1	29.1	P01
gpsA	2388348	2389385	5 -	5718	3 4433	4092	5397	0.78	0.72	0.95										
engA	2389403	2390713	5 -	7339	5553	5131	6527	0.76	0.70	0.89	722	Inton	2200527	2200074	2200752	20.4	20.7	0 5	0.0	
seaA	2391058	2391951	_	235	254	250	253	1.07	1.05	1.04	122	mer	2390327	2390970	3 2390732	50.4	20.7	0.3	-0.9	
yphA	2391948	2392547	-	323	326	330	317	1.01	1.02	0.98										
ypgA	2392799	2393857	- 1	2946	5 3789	3826	2744	1.29	1.31	0.93										
rpsA	2393861	2395009	) -	15193	3 17151	17970	15396	1.13	1.18	1.01										
cmk	2395242	2395916	<u>,</u> -	7258	3 5049	4421	6714	0.70	0.61	0.93										
ypfB	2395995	2396171	-	2352	2 1692	1694	2995	0.72	0.72	1.27										
ypjA vneB	2396210	2390805	, - 1 -	2500	1077	257	2515	1.84	2 21	0.95										
sleB	2398349	2399266	, j -	143	3 179	215	130	1.25	1.49	0.95	723	sleB	2398500	2398898	3 2398699	3.9	4.0	8.0	16.3	
ypdC	2399405	2400061	-	748	3 1325	1047	694	1.75	1.40	0.91	723	ypdC	2398908	2400105	5 2399507	65.1	76.9	94.4	201.0	P01
ypdA	2400181	2401155	; -	4390	4504	4584	4582	1.03	1.05	1.04										
gudB	2401264	2402544		17579	18052	17913	17876	1.03	1.02	1.02	724	gudB	2402257	2402689	9 2402473	14.9	22.8	13.9	6.2	
ypbH	2402700	2403284		5004	4634	5355	5233	0.92	1.07	1.05										
ypbG	2403443	2404222		1454	+ 1279 552	1432	576	0.88	1.00	1.18	725	unhE	2404246	2404016	5 2404581	52.4	197	20.2	0.1	<b>D</b> 02
vnhE	2404308	2405536	 5 -	2202	2 2102	1950	2089	0.96	0.88	0.95	125	ypor	2404240	2404710	2404581	52.4	40.7	20.2	-0.1	102
ypbD	2405487	2406056	<u>.</u> -	1070	983	950	1104	0.91	0.89	1.03										
recQ	2406116	2407606	<u>.</u> -	1575	5 1517	1581	1721	0.96	1.00	1.09										
ypbB	2407599	2408657	-	81	979	917	908	1.22	1.14	1.12										
fer	2408923	2409171	+	10667	8225	8320	9320	0.77	0.78	0.87										
ypaA	2409211	2409783	5 -	96: 270/	612 2311	2281	2547	0.63	0.66	1.03										
serA	2409889	2410053	, - , +	4982	2311	6161	4382	1.09	1.24	0.94	727	serA	2411131	2411376	5 2411254	13.2	2.6	9.6	2.5	
aroD	2411900	2412667	, <u> </u>	1700	5 1527	1463	1677	0.91	0.87	0.98	728	aroD	2412032	2412277	7 2412155	10.1	5.3	4.7	4.8	
rsiX	2412779	2413885	; -	4493	5071	5071	4413	1.14	1.14	0.99										
sigX	2413821	2414405	; -	2790	3167	2986	2823	1.14	1.09	1.02	729	sigX	2414242	2414487	7 2414365	8.5	1.3	6.7	1.8	
resE	2414609	2416378	- 8	7939	6211	6343	7150	0.78	0.80	0.90										
resD	2416375	2417097	-	7340	) 5660	5964	6514	0.76	0.81	0.89										
resC resP	2417178	2418236	) -	5842	4502	4516	5132	0.77	0.78	0.88										
resB resA	2418372	2420000	· -	5/90	5 4502 5 5872	4301 5732	3381 6600	0.77	0.75	0.93	730	resA	2420175	2420420	) 2420298	6.8	23	71	15	
rluB	2420674	2421363		5414	4793	4633	4996	0.89	0.85	0.90	750		2-120113	2-720420	, 2720270	0.0	2.5	7.1	1.5	
spmB	2421455	2421994	+ -	149	155	146	175	1.04	0.98	1.18										
spmA	2421999	2422589	) -	326	5 309	314	358	0.95	0.97	1.09										
dacB	2422577	2423725	:	225	2 215	210	234	0.01	0.87	0.96										

Supplem	entary Tal	de S1. Su	mma	ry of trar	iscriptor	me and C	hAP-ch	ip analyse	es (contin	ued).				CLAB 11	<u>.</u>		
	gene					Trans	criptom	e analysis		b				ChAP-chip a	analysis		
			pu	Sign	iai intens	ity of KIN	A	Exp	ression ra	uo	PBR	ORF			AbrB	Abh	Profile
name	start	end	stra	wild	∆abrB	∆abh ∆abrB	$\Delta abh$	∆ abrB/ wild	$\Delta abrB/$	∆abh / wild	ID	or Intergenic	start	end center	wild <i>Aabh</i>	wild <i>AabrB</i>	ID
ypuI	2423848	2424387	-	1847	1363	1137	1738	0.74	0.61	0.93					-type	-type	
уриН	2424442	2425035	-	4960	4137	3449	4725	0.83	0.69	0.95							
scpA	2425025	2425780	-	1776	1575	1228	1680	0.90	0.68	0.94	731	scpA	2425020	2425180 2425100	4.7 0.8	1.4 -0.5	
ypur rihT	2426001	2426585	+	3210	208 3969	254 3415	2960	1.24	1.06	0.97							
ribH	2427086	2427550	-	2864	3036	3007	2665	1.06	1.05	0.92							
ribA	2427583	2428779	-	3092	3215	3294	2737	1.04	1.06	0.88							
ribE wihD	2428794	2429441	-	1843	1917	1858	1598	1.04	1.01	0.87							
vduE	2429432 2430519	2430557	-	350	347	301	287	1.13	0.87	0.97							
ypuD	2430930	2431274	-	599	381	458	501	0.66	0.76	0.81							
sipS	2431509	2432063	-	3897	3881	3588	3914	1.00	0.93	1.01							
ypzC ypuC	2432330	2432566	+	140	139	151	396	0.99	1.08	0.82							
ypuC ypuB	2433336	2433539	-	237	199	228	326	0.98	0.96	1.37							
											732	Inter	2433452	2434173 2433813	63.5 74.4	38.2 16.1	
ypzD	2434205	2434417	+	60	59	67	55	0.99	1.11	0.91							
рріВ урнА	2434553	2434984	-+	13344	12/17 9625	12544	13176	0.95	0.94	0.99	733	VDUA	2435068	2435618 2435343	267 374	12.2 0.3	
lysA	2436139	2437458	-	2277	1627	1599	1856	0.71	0.70	0.81	,	J.P.a.r	2.55000	- 100010 2400040		0.5	
spoVAF	2437564	2439042	-	304	384	389	306	1.26	1.27	1.00	734	spoVAF	2437566	2437913 2437740	12.8 4.2	1.8 2.0	
spoVAE	2438993	2439964	-	206	245	266	205	1.18	1.28	0.99							
spoVAD spoVAC	2439966 2440995	2440982	-	131	1/2	180	149	1.31	1.37	1.13	735	snoVAC	2440507	2441619 2441063	104.6 130.8	531 78	
spoVAB	2441459	2441884	-	183	229	257	209	1.20	1.43	1.16	100	sponne	2110507	2111019 2111005	10110 12010		
spoVAA	2441894	2442496	-	64	85	101	66	1.32	1.57	1.03							
sigF	2442618	2443385	-	283	897	956	369	3.11	3.33	1.28							
SPOIIAB SDOIIAA	2443397 2443834	2443837	-	266 518	2315	2426	407	4.67	5.12	1.46							
dacF	2444283	2445452	-	175	369	466	185	2.09	2.64	1.05							
											737	Inter	2445284	2445818 2445551	52.2 24.6	43.4 3.6	P02
punA dama	2445607	2446422	-	10124	9924	10436	10702	0.98	1.03	1.06	720	duna	2447222	2447467 2447245	05 02	55 0.9	
arm xerD	2446435	2447619	-	2016	2142	10874	2062	1.06	0.98	1.01	/39	arm	2447222	2447467 2447345	9.5 9.2	5.5 0.8	
fur	2449029	2449478	-	3734	3184	3039	3684	0.86	0.82	0.99							
spoIIM	2449591	2450235	-	147	143	170	162	0.98	1.16	1.10							
yqkK	2450336	2450551	-	342	222	204	316	0.65	0.60	0.93							
mieA mleN	2450651	2451970	-	13928	8801	8813	12916	0.72	0.76	0.98	740	mleN	2452441	2452771 2452606	9.0 17.2	4.9 1.9	
aspA	2453535	2454962	-	15882	13887	13450	15295	0.87	0.85	0.96							
ansA	2455007	2455996	-	16460	14547	13656	15643	0.88	0.83	0.95							
ansR var K	2456178	2456528	+	1133	1509	990	958	1.35	0.89	0.87	741	vorV	2456013	2457250 2457086	157 84	0.8 2.5	
yqx <b>k</b> nudF	2450557	2458255	-	3842	3803	3966	3664	0.99	1.09	0.95	/41	уцхк	2430913	2437239 2437080	13.7 0.4	9.8 2.3	
yqkF	2458515	2459435	+	2469	3410	3622	2949	1.43	1.51	1.18							
yqkE	2459467	2459691	-	647	403	419	362	0.63	0.64	0.56							
yqkD vakC	2459853	2460770	+	286 3730	293	312	287	1.03	1.09	1.00							
yqkC yqkB	2461062	2461385	-	3602	3878	4009	3460	1.08	1.12	0.96							
yqkA	2461382	2462413	-	1106	1661	1833	791	1.49	1.65	0.71							
yqjZ	2462406	2462750	-	844	1260	1296	697 562	1.49	1.53	0.83							
yqj i vaiX	2462760	2463230	-	058 249	181	978	259	0.73	1.48	1.03							
yqjW	2463751	2464989	-	190	139	145	212	0.73	0.76	1.12							
yqzH	2465155	2465361	+	734	729	664	590	0.99	0.87	0.80							
yqjV	2465910	2467142	+	380	849	770	341	2.23	2.01	0.89							
yqjU vaiT	2467348	2467351	+	585 4261	3393	3449	476 3915	1.99	0.81	0.83							
coaA	2467738	2468697	-	3196	2398	2456	3076	0.75	0.77	0.96							
dsdA	2468769	2470115	-	1749	1426	1450	1692	0.82	0.83	0.96							
yqjQ	2470191	2470970	-	1586	1381	1273	1577	0.88	0.81	0.99							
yqjP proI	2470976	2471935	-+	41/ 861	363 607	558 516	426 741	0.87	0.82	0.87							
yqjN	2473217	2474860	-	688	809	921	746	1.17	1.33	1.07							
yqjM	2475032	2476048	+	1368	1583	1767	1563	1.17	1.29	1.14							
yqjL	2476158	2476919	+	4084	3887	4607	4701	0.95	1.13	1.15							
yqjK zwf	24778345	2479814	-+	1/52	10109	1047	1354	0.69	0.60	0.88	744	zwf	2478451	2478543 2478497	1.2 25	0.5 0.4	
yqjI	2479937	2481346	-	13937	12207	13522	14915	0.88	0.97	1.07	/ 44		2470431	2710345 2410491	1.2 2.3	0.0 0.4	
yqjH	2481456	2482700	-	520	462	438	574	0.89	0.84	1.09							
yqzJ	2482773	2483060	+	1976	2230	2071	2187	1.13	1.05	1.11							
yqjG vaiF	2483091	2483918	++	2185	2504	2322	2537	1.05	1.06	1.16							
JAJ 1		2.04020	- C	113	104	100	102	0.75	0.75	0.75							

Supplem	entary Tab	de S1. Su	nma	ry of trai	nscriptor	me and (	ChAP-ch	ip analyse	es (contir	wed).				C	h A D ahim a	nolucio				
	gene			Sim	al intene	ity of PN	Criptom	e analysis	ression re	tio <sup>b</sup>	·			t	пар-спір а	naiysis	Binding	intensity '	с	
		,	pu	Sigi	iai interis	ity of KIN	A	Exp	$\Delta abh$	.00	PBR	ORF		,		Al	brB	A	bh	Profile
name	start	end	stra	wild	∆abrB	∆abh ∆abrB	∆abh	∆ <i>abrB/</i> wild	∆ abrB/ wild	⊿ <i>abh /</i> wild	ID	or Intergenic	start	end	center	wild -type	∆abh	wild -type	∆abrB	ID
yqjE	2484867	2485982	-	7215	8007	8168	7377	1.11	1.13	1.02										
yqjD	2486000	2487520	-	5058	6071	5766	5455	1.20	1.14	1.08										
yąjC vaiB	248/51/	248/939	-	278	278	283	323	1.00	1.02	1.24	746	vaiB	2488345	2488488	2488417	3.5	1.2	4.4	0.6	
yqjA	2488723	2489691	-	1017	1005	844	934	1.00	0.82	0.91	747	yqjA	2489314	2489474	2489394	5.4	2.5	3.1	1.7	
yqiZ	2489762	2490484	-	931	642	570	841	0.71	0.62	0.89										
yqiY	2490477	2491136	-	700	519	465	663	0.77	0.69	0.95	740	voiV	2400046	2401549	2401247	50.7	21.4	10.0	0.2	D02
yqıx vaiW	2491217	2491984	-	7177	7082	7395	7293	0.32	1.03	1.01	/40	уціл	2490940	2491348	2491247	50.7	21.4	10.2	0.2	P02
bmrU	2492853	2493746	+	560	457	686	272	0.82	1.22	0.47										
bmr	2493847	2495016	+	731	844	833	685	1.16	1.15	0.94										
bmrR bkdB	2495089	2495925	+	428	351	408	397	0.83	0.95	0.92										
bkdAB	2493987	2497201	-	5663	5933	5814	5429	1.04	1.00	0.94										
bkdAA	2498281	2499273	-	5455	5858	5704	5323	1.08	1.04	0.97										
lpdV	2499347	2500720	-	4495	4906	4763	4478	1.09	1.06	0.99	749	lpdV	2499446	2499640	2499543	2.9	3.0	3.8	7.1	
buk bcd	2500741	2501832	-	3008	3814 3481	3680 3404	3/95	1.04	1.00	1.03										
ptb	2502957	2502945	-	2656	2691	2656	2741	1.03	1.02	1.03										
bkdR	2503981	2506059	-	2229	1857	2019	2259	0.84	0.91	1.01	752	bkdR	2503883	2504128	2504006	6.7	4.3	0.7	0.4	
yqzF	2506212	2506448	+	524	1276	1213	483	2.44	2.29	0.92										
yqiQ nrnD	2506490	2507395	-	305 184	285	291 178	317 197	0.93	0.96	1.05										
mmgD	2508846	2509964	-	201	189	192	225	0.94	0.95	1.12										
mmgC	2509998	2511134	-	146	133	136	154	0.91	0.94	1.06	753	mmgC	2510717	2510877	2510797	4.6	2.2	1.5	0.3	
mmgB	2511162	2511896	-	225	203	214	240	0.90	0.95	1.08	754	mmgB	2511312	2511642	2511477	2.6	0.8	2.1	26.2	P04
mmgA vaiK	2512046	2513227	-	205 457	450	1/6	258	0.78	0.86	1.28										
yqiI	2514163	2514783	-	172	151	136	208	0.88	0.79	1.21										
yqiH	2514798	2515091	-	190	172	182	195	0.90	0.95	1.01										
yqiG	2515623	2516741	+	3081	2166	2243	3821	0.73	0.75	1.24										
spo0A spoIVB	2518336	2518000	-	198	293	340	195	1.20	1.28	0.98	755	spoIVB	2518537	2519547	2519042	54.6	5 25.4	99.2	19.1	P01
recN	2519788	2521518	-	3825	3140	3111	3752	0.83	0.81	0.97		1								
ahrC	2521555	2522004	-	3947	3137	2846	3618	0.80	0.72	0.90		-				25.2		10.0		
yqxC dxs	2522139	2522948	-	6398	6669 4700	6487	6055	1.04	1.02	0.94	756	yqxC	2522022	2522556	2522289	35.3	1.2	2.6	3.3	
yqiD	2525093	2525911	-	2049	2058	1808	2063	1.07	0.91	1.01	151	uns	2525127	2525250	2525162	1.4	1.2	2.0	1.5	
yqiC	2525901	2526065	-	4043	3937	3690	3509	1.00	0.92	0.85										
xseA	2526151	2527497	-	2569	2508	2240	2403	1.01	0.90	0.93	750	( ID	2520125	2520226	2520221	0.1	1.0	( )	2.2	
folD nusB	2527635	2528486	2	8250	7076 8432	6758 7930	9273	0.86	0.82	0.96	/58	IOID	2528125	2528336	2528231	8.1	1.8	6.5	2.2	
yqhY	2529157	2529564	-	12036	12947	12344	12499	1.08	1.02	1.04										
accC	2529585	2530937	-	12163	12575	12308	12392	1.03	1.01	1.02										
accB	2530949	2531428	-	8994	9773	9179	9642	1.09	1.02	1.07										
spoIIIAII	2531384	2532240	-	125	106	110	110	0.79	0.82	0.93										
spoIIIAF	2532923	2533543	-	117	108	113	116	0.92	0.97	0.99										
spoIIIAE	2533540	2534757	-	196	182	195	220	0.93	0.99	1.12										
spoIIIAD spoIIIAC	2534776	2535177	-	182	185	178	183	1.02	0.98	1.01										
spoIIIAB	2535413	2535928	-	161	138	145	194	0.86	0.90	1.22	759	spoIIIAB	2535436	2535595	2535516	0.4	0.1	1.3	4.5	
spoIIIAA	2535922	2536845	-	151	135	131	179	0.89	0.86	1.18										
yqhV xfa	2536921	2537202	-	12002	12042	12054	12072	1.01	1.03	1.03										
ејр vahT	2537347	2537904	-	12993	12945	12954	14552	1.00	1.00	1.01										
yqhS	2538987	2539433	-	7868	8981	9093	8397	1.14	1.16	1.07										
yqhR	2539520	2540056	-	142	151	147	151	1.07	1.04	1.07	7.0	<b>T</b> .	2540000	0540007	2540140	10.0	5.0	0.7	0.5	
vahQ	2540283	2541239	+	1730	2001	1899	1449	1 14	1.09	0.83	760	Inter	2540008	2540287	2540148	10.9	5.2	0.7	-0.5	
yqhP	2541279	2541674	+	1437	1480	1416	1138	1.02	0.98	0.79	762	yqhP	2541266	2541460	2541363	3.1	1.6	3.1	8.5	
yqhO	2541671	2542546	-	195	177	187	214	0.91	0.96	1.09	_	_								
mntR wahM	2542672	2543100	-	3593	2658	2624	4109	0.74	0.73	1.15	763	mntR	2542813	2543194	2543004	18.2	5.1	11.3	33.0	
yqnM vqhL	2543200	2544607	+	4052	2707	5992 2267	3054	0.82	0.87	0.98										
gcvPB	2544642	2546108	-	828	1315	1371	726	1.58	1.65	0.87										
gcvPA	2546101	2547447	-	1481	2437	2661	1234	1.64	1.79	0.83										
gcvT vahH	2547477	2548565	- ⊥	1066	1807	1842	946 131	1.68	1.72	0.88 0.09										
yqhI yqhG	2549007	2551495	+ +	224	292	314	234	1.13	1.17	1.04										
											764	Inter	2551432	2551728	2551580	12.3	13.1	0.5	-0.6	
sinI	2551678	2551851	+	1095	1859	2040	905	1.71	1.87	0.81		· D		00000	0.5501.55	1.00				
SINK	2321885	20022220	+	2771	2946	2622	2458	1.07	0.95	0.89	/65	SINK	2551976	2552340	2002108	16.1	4 12	6.2	0.3	

	gene					Trans	criptom	e analysis						ChAP-ch	ip analysis			
				Sigr	nal intens	ity of RN	$A^{a}$	Expi	ession ra	tio <sup>b</sup>		OPE			Bin	ding ir	ntensity c	
name	start	end	and			A abh		A abrB/	$\Delta abh$	A abh /	PBR	or	start	end cente	AbrB		Abh	Profile
name	Suit	end	str	wild	∆abrB	AabrB	$\Delta abh$	wild	$\Delta abrB/$	wild	ID	Intergenic	Start	chu cenu	wild Aa	bh	wild AabrB	ID
	0550010	2552000		000	140/7	14007	402	17.00	wild	0.50					-type		-type	
tasA sinW	2552313	2553098	-	809	14267	14997	483	17.60	18.43	0.59								
sip w var M	2553718	2553734	-	344 107	4328	4095	304 93	12.60	10.63	0.88								
yqxin	2555710	2004477		107	1117	1142	15	10.42	10.05	0.07	766	Inter	2554237	2555179 25547	08 78.4 9	8.8	33.7 -3.4	P02
vazG	2554751	2555077	+	139	327	408	113	2.33	2.90	0.82								
yqzE	2555060	2555299	-	79	73	74	67	0.92	0.93	0.85								
comGG	2555370	2555744	-	182	171	188	176	0.94	1.03	0.96								
comGF	2555745	2556128	-	209	193	209	227	0.92	1.00	1.08								
comGE	2556154	2556501	-	83	68	77	95	0.82	0.94	1.17								
comGD	2556485	2556916	-	66	59	62	76	0.90	0.95	1.13								
comGC	2550900	2558187	-	119	90	199	111	1.02	0.85	0.93								
comGA	2558240	2559310	-	143	136	140	140	0.96	0.98	0.93								
vaxL	2559722	2560675	-	379	227	290	242	0.60	0.76	0.63								
yqhB	2560818	2562146	+	227	153	194	158	0.68	0.87	0.69								
vqhA	2562199	2563035	-	1002	399	426	347	0.44	0.51	0.32								
trnSL-Gh	2563122	2563195	+	2863	4528	4632	4454	1.65	1.70	1.45								
yqgZ	2563259	2563639	-	9055	5223	7294	3757	0.58	0.81	0.41								
											768	Inter	2563655	2563968 25638	12 14.9 9	9.4	3.9 1.4	
vqgY	2563871	2564116	+	2644	6590	7280	4589	2.49	2.75	1.74								
vqgX	2564156	2564791	-	8876	9545	10244	9518	1.08	1.16	1.07	760	Intor	2564704	2565027 25640	16 122 9	1	10 12	
vaaW	2564949	2565122	+	1235	2894	2963	1174	2 33	2 39	0.95	709	miei	2304794	2303037 23049	10 12.5 6		1.7 1.3	
vagV	2565183	2565467	-	2376	2472	2264	2279	1.06	0.96	0.96								
yqgU	2565470	2566531	-	2826	2943	2860	3050	1.05	1.02	1.08	770	yqgU	2565967	2566195 25660	81 2.8 0	).2	-0.7 9.9	
yqgT	2566593	2567723	-	599	830	827	756	1.42	1.40	1.26		. 10						
											771	Inter	2567514	2567979 25677	47 29.3 9	9.8	23.8 1.4	
vqgS	2567806	2569722	-	2653	3115	3300	2810	1.17	1.25	1.06								
glcK	2569838	2570803	-	2721	2510	2661	2836	0.92	0.98	1.04	773	glcK	2570540	2570835 25706	88 10.1 11	.6	3.1 0.6	
vqgQ	2570814	2571029	-	2137	1743	1919	2065	0.81	0.90	0.96								
yqgr vaaQ	2571159	2572002	-	3712	2640	2651	3370	0.88	0.80	0.02								
vagN	2572992	2573555	-	2906	2040	1978	2616	0.72	0.72	0.92								
rpmG_2	2573640	2573789	-	11475	9433	9089	11522	0.82	0.79	1.00								
yqgM	2573873	2574952	-	315	330	339	331	1.05	1.07	1.04								
vqgL	2574949	2575419	-	175	144	153	220	0.82	0.88	1.26								
yqzD	2575599	2575952	+	9355	8236	7666	9229	0.88	0.82	0.99								
yqzC	2575949	2576413	+	8898	8174	7587	8763	0.92	0.85	0.98								
pstBB	2576442	2577224	-	123	108	114	131	0.88	0.93	1.07								
psi DA nst A	2578065	2578044	-	120	106	122	143	1.11	1.02	1.20								
psiA pstC	2578949	2579878	-	254	290	266	271	1.14	1.05	1.02								
pstC	2579947	2580849	-	241	389	270	233	1.58	1.11	0.97								
obpA	2581003	2583153	-	7233	7143	6973	7458	0.99	0.96	1.03	775	pbpA	2581624	2581733 25816	79 3.8 0	0.8	1.3 2.0	
yqgE	2583267	2584559	-	181	182	209	185	1.01	1.16	1.02								
sodA	2584666	2585274	-	22088	25943	25792	23476	1.18	1.17	1.07	776	sodA	2584582	2584844 25847	13 7.0 7	.5	1.3 1.5	
vqgC	2585453	2585935	-	1572	2235	2253	1141	1.42	1.43	0.72								
vqgB	2586045	2586803	+	2058	1359	1325	2055	0.66	0.65	1.00		<b>T</b> .	2506060	2507250 25071			10 07	002
vaaA	2587220	7587657	_	1/224	16400	15624	11046	1 1 4	1.00	0.82	/// ררך	inter vog A	2585270	2587810 25871	10 - 22.5 - 2.05 - 14.4 - 10	2.0	3.5 4.9	P05
vafZ	2587934	2588233	+	187	148	13024	233	0.79	0.78	1.22	,,,,	J45A	2301310	2301017 23813	14.4		3.5 4.0	
spG	2588356	2589489	+	6568	5667	6010	6706	0.86	0.91	1.02								
vqfX	2589515	2589904	-	325	614	788	392	1.88	2.41	1.20								
vqfW	2590037	2590618	$^+$	1818	1411	1276	2084	0.77	0.70	1.16	779	yqfW	2590022	2590318 25901	70 <u>4.5</u> 1	.4	2.3 15.7	
zur	2590661	2591098	-	2470	2318	2525	2456	0.94	1.02	0.99								
vqfU	2591236	2592117	-	1107	1379	1512	1221	1.28	1.38	1.10								
vqfT	2592233	2592487	+	155	153	172	147	0.99	1.11	0.95								
vqfS	2592514	2593407	-	4900	3913	3803	4511	0.80	0.78	0.92								
vqjK vafO	2595417	2595645	+	140	4095	107	134	0.79	0.75	0.90	780	vafO	2595105	2595367 25952	36 11.2 7	4	59 32	
spH	2595768	2596712	+	3148	3003	2880	3153	0.03	0.93	1.01	, 30	74-2	2000100	2070001 20702			5.7 5.2	
vqfO	2596735	2597856	-	5909	5358	5427	5741	0.91	0.92	0.97								
vqfN	2597849	2598499	-	3738	3493	3280	3561	0.93	0.88	0.95								
cccA	2598756	2599118	-	1261	3385	3219	1471	2.87	2.69	1.18								
											781	Inter	2598862	2599685 25992	74 78.4 6	7.5	54.9 5.4	P02
sigA	2599447	2600562	-	9251	13118	12186	9245	1.43	1.33	1.00	782	sigA	2600375	2600654 26005	15 <u>12.1</u> 6	6.1	4.9 0.2	P0-
tnaG	2600761	2602572	-	4713	6686	6141	4904	1.42	1.30	1.04	783	dnaG	2601854	2602490 26021	12 44.3 5	8. <b>1</b>	19.2 4.5	P02
uttE warD	2602212	2602104	+	358 1214	1041	915 2727	2/4	2.93	2.57	0.77								
члD vafL	2603354	2604166	-	4311	4474	4470	4016	1.03	1.04	0.93								
vqzB	2604192	2604830	-	4229	4396	4468	3746	1.04	1.04	0.89								
şlyS	2604963	2607002	-	7098	5421	5275	6518	0.76	0.74	0.92								
elv0	2606995	2607882	-	3979	3291	2961	3817	0.83	0.74	0.96								

Suppens	gene	nc 51.5un		ly of trai	Benptoi	Trans	crintom	analysis	s (conun	ucu).				ChAP-chin :	analysis		
	gene			Sim	nalintene	ity of RN		Evo	ession rat	io <sup>b</sup>				Cillin Cillp	Binding	intensity c	
			Ы	Sigi		ILY OF KIN	A	Exp	A abh	10	PBR	ORF			AbrB	Abb	Profile
name	start	end	strai	wild	∆abrB	$\Delta abh$	∆abh	$\Delta abrB/$	A abrB/	$\Delta abh /$	ID	or	start	end center	wild	wild	ID
						∆abrB		wild	wild	wild		Intergenic			-type ∆abh	-type ∆ abrB	
recO	2608179	2608946	-	4165	4165	4310	4355	1.00	1.03	1.05					51		
era	2609274	2610179	-	6765	6878	7235	6906	1.01	1.07	1.02	785	cdd	2610031	2610310 2610171	4.6 3.0	8.6 9.5	
cdd	2610160	2610570	-	4641	4980	5402	4760	1.07	1.16	1.02	785	cdd	2610031	2610310 2610171	4.6 3.0	8.6 9.5	
											785	Inter	2610320	2611041 2610681	28.5 17.6	31.5 65.0	
dgkA	2610689	2611033	-	3418	3215	2884	3803	0.94	0.84	1.11							
yqfG	2611040	2611513	-	3279	3180	3238	3521	0.97	0.99	1.07							
yqfF	2611514	2613649	-	3369	3341	3413	3327	0.99	1.01	0.99							
pnoH wrfD	2013/28	2614087	-	9078	9391	98/1	8540	1.05	1.09	0.94							
yqfD vafC	2615800	2615880	-	339	322	307	292	0.95	1.08	0.80							
yqjC vafB	2616237	2616656	-	7744	9983	10667	6804	1 29	1.15	0.85							
vafA	2616681	2617676	-	6601	9042	9487	6376	1.37	1.44	0.97							
yqeZ	2617698	2619011	-	4665	6962	7054	4403	1.49	1.51	0.94	787	yqeZ	2617681	2617875 2617778	6.0 0.8	5.1 -0.2	
											788	yqeZ	2618429	2618657 2618543	3.7 3.2	7.2 4.1	
yqeY	2619142	2619588	-	22532	21445	21027	22921	0.96	0.93	1.02							
rpsU	2619603	2619776	-	24299	22007	21620	24168	0.91	0.89	1.00							
yqeW	2619940	2620872	+	241	235	254	254	0.97	1.05	1.05							
yqeV	2620909	2622264	-	6592	6247	5572	6630	0.96	0.85	1.00							
yqeU	2622264	2623034	-	3849	3149	2660	3593	0.83	0.70	0.93					_		
prmA	2623057	2623992	-	5349	4872	4299	5275	0.93	0.81	0.98	789	prmA	2623665	2623927 2623796	7.2 4.0	5.2 5.9	
dnaJ	2624017	2625135	-	9513	9307	8838	9315	0.99	0.93	0.98							
dnaK	2625335	262/170	-	17157	18934	18794	18720	1.11	1.10	1.09							
grpE hroA	2627194	2627757	-	18979	19429	19983	20357	1.03	1.05	1.07	700	hro A	2627762	2627005 2627824	25 20	10 00	
hamN	2628080	2620080	-	1919	1255	4/38	1744	0.70	0.79	1.10	790	IIICA	2027702	2027903 2027834	5.5 2.9	1.0 0.0	
lenA	2630133	2631971	-	4444	3559	3392	4253	0.70	0.03	0.95							
varA	2632105	2632443	-	115	131	150	103	1 14	1 30	0.89							
spoIIP	2632460	2633665	-	184	225	246	195	1.23	1.34	1.06							
gpr	2633728	2634834	-	155	201	221	178	1.30	1.43	1.15							
rpsT	2635038	2635304	+	20624	15428	16956	19656	0.76	0.82	0.95							
holA	2635319	2636362	-	1578	1367	1293	1557	0.87	0.82	0.99							
											791	Inter	2636364	2636711 2636538	23.6 12.2	12.9 -0.2	
comEC	2636766	2639096	-	258	292	282	291	1.13	1.09	1.13							
comEB	2639100	2639669	-	1506	907	814	1475	0.60	0.54	0.98							
comEA	2639736	2640353	-	164	124	134	174	0.76	0.82	1.05							
comER	2640437	2641258	+	241	239	263	267	0.99	1.09	1.11							
yqeM 	2641324	2642067	-	5497	5379	4286	5013	0.99	0.78	0.91							
yqeL K	2642064	2642420	-	/801	5167	0349	1039	0.92	0.81	0.90							
yqe <b>k</b> nadD	2042438	2042998	-	67/10	6184	5101	5920	0.91	0.78	0.80							
vael	2643569	2643859		6178	5571	4828	5461	0.92	0.77	0.88							
aroE 2	2643853	2644695	-	7552	6704	5767	6785	0.90	0.77	0.90							
vaeH	2644713	2645813	-	5476	4644	3977	5081	0.85	0.73	0.92	792	vaeH	2645068	2645483 2645276	20.6 14.2	4.5 0.0	
yqeG	2645817	2646335	-	3499	2933	2394	3271	0.85	0.69	0.92		21					
											793	Inter	2646122	2647047 2646585	50.7 73.7	21.2 6.4	
sda	2646679	2646837	+	491	1065	839	502	2.01	1.59	1.01							
yqeF	2647143	2647874	-	511	364	327	435	0.71	0.64	0.84	794	yqeF	2647244	2647625 2647435	20.8 7.7	17.7 2.6	
cwlH	2648126	2648878	-	142	140	138	153	0.99	0.97	1.07							
yqeD	2649065	2649691	+	822	770	707	904	0.95	0.87	1.10							
yqeC	2649710	2650603	-	244	214	227	281	0.87	0.93	1.13	704	<b>T</b> .	2650502	2651042 2650010	17.0 00.0	0.0 1.1	DOO
NaaD	7650055	7651500		511	2210	2240	410	207	670	0.02	/96	inter	2650593	2051042 2650818	17.9 22.0	-0.2 -1.1	P03
уцев пись	2030835	2031380	+	511	3512	3542	419	0.8/	0.79	0.85							
SDOWCP	2652210	2652680	+	141	154	100	113	0.95	1.57	0.03	707	SDOIVCR	2652270	2652759 2652560	11.2 21.5	19.6	
sporv CB	2652597	2654099	-	200	152	165	198	0.76	0.83	0.98	, , , ,	sported	2052570	2002107 2002009	11.2 21:3	-17.0 - 22.3	
arsC	2654548	2654967	-	1074	861	922	892	0.80	0.85	0.82							
arsB	2654979	2656019	-	755	617	678	695	0.81	0.89	0.92	798	arsB	2655353	2655683 2655518	14.7 1.7	3.3 0.7	
yqcK	2656042	2656482	-	132	102	109	117	0.75	0.82	0.87							
arsR	2656543	2656860	-	414	345	373	385	0.81	0.88	0.91							
yqcI	2657232	2657996	-	134	123	136	149	0.91	1.01	1.11	799	yqcI	2657512	2657672 2657592	0.8 0.6	0.1 5.2	
											800	Inter	2658124	2658641 2658383	23.6 18.2	2.9 9.2	
rapE	2658440	2659567	+	80	106	120	79	1.33	1.51	1.00	801	rapE	2659178	2659729 2659454	55.3 68.4	32.0 17.6	
phrE	2659557	2659691	+	2708	11182	11409	2549	4.13	4.21	0.94							
yqzI	2659801	2659959	+	52	85	90	63	1.65	1.78	1.21		-					
_		a							<i>.</i> .	c	802	Inter	2660130	2660375 2660253	6.6 9.5	0.5 0.2	
yqcG	2660329	2661924	+	854	2007	2227	720	2.38	2.63	0.85							
yqcF	2001939	2002517	+	633	966	1034	593	1.51	1.62	0.94	002	Into-	2642272	2662772 2662522	21 1 55	70 15	
var I	2662770	2663140		127	1640	2000	310	3 50	1 26	0.72	603	men	2002272	2002112 2002522	21.1 3.5	7.0 -1.3	
yqxJ vaxI	2663156	2663635	-	457	4796	5513	610	5.58 7.26	4.50 8.09	0.72							
1911	2000100	200000000		005		5515	510	7.20	5.07	5.74	804	Inter	2663326	2663996 2663661	69.7 83.6	36.8 -1.1	P02
cwlA	2663800	2664618	-	127	111	120	118	0.88	0.94	0.92	r		1000020	2000001			
yqxH	2664663	2665085	-	108	97	107	101	0.90	1.00	0.93							

Supplem	entary Tab	le S1. Sur	nma	ry of trai	iscriptor	me and (	hAP-ch	ip analyse	es (contin	ued).								
	gene				11.	Trans	criptom	e analysis		. b	·			ChAP-chip	analysis	. 1.	· . ·. c	
			ри	Sig	nal intens	ity of RN	A"	Exp	ression rat	tio	PBR	ORF			Abr	Sinding	Abb	Profile
name	start	end	straı	wild	∆abrB	∆abh ∆abrB	$\Delta abh$	∆abrB/ wild	$\Delta abrB/$	⊿ <i>abh /</i> wild	ID	or Intergenic	start	end center	wild	abh	wild <i>AabrB</i>	ID
yqxG	2665130	2666023	-	82	80	83	78	0.98	1.01	0.95					-type		-туре	
yqcE	2666111	2666275	-	184	175	181	159	0.95	0.98	0.87								
yqcD	2666272	2666607	-	76	76	77	85	0.99	1.01	1.12								
yqcC	2666617	2667717	-	119	109	113	133	0.92	0.95	1.12								
yqcB vacA	2667989	2668567	-	50 125	51 116	57	68 147	0.92	1.03	1.23								
yqcA vabT	2668551	2669597	-	220	200	210	249	0.91	0.95	1.13								
yqbS	2669590	2670015	-	130	118	129	137	0.90	0.99	1.05								
yqbR	2670028	2670291	-	171	152	163	148	0.90	0.98	0.88								
yqbQ	2670288	2671268	-	140	122	128	131	0.87	0.92	0.95								
yqbP	2671281	2671940	-	159	135	136	131	0.85	0.86	0.83	905	hO	2674172	2074552 2074202	5.5	1.0	( 1 20.5	
yqbO vahN	2676872	2677321	-	138	104	124	145	0.87	0.90	0.89	805	yqbO yqbN	2677011	2677205 2677108	5.5	1.8	0.4 <u>29.5</u> 7.2 1.7	
vadB	2677467	2677646	+	132	162	137	146	1.22	1.04	1.11	000	yquiv	2077011	2077205 2077108	5.1	2.0	1.2 1.7	
yqbM	2678369	2678812	-	221	177	175	223	0.80	0.79	1.01								
yqbL	2678815	2679219	-	153	151	165	129	0.99	1.08	0.85								
yqbK	2679297	2680214	-	182	160	154	209	0.88	0.84	1.14								
yqbJ	2680403	2680840	-	100	92	91	108	0.92	0.92	1.08								
yqb1 vahH	2680853	2681356	-	180	147	152	229	0.82	0.84	1.27								
yqb11 yqbG	2681712	2682107	-	204	104	204	220	0.97	1.00	1.14								
yqbF	2682111	2682422	-	78	87	81	67	1.13	1.00	0.87								
yqbE	2682433	2683368	-	110	115	119	111	1.05	1.08	1.00								
yqbD	2683387	2684355	-	132	130	128	124	0.99	0.97	0.94								
yqbC	2684388	2685041	-	231	434	376	239	1.88	1.63	1.04								
	0.00000	0.00000		100	101	00	107	0.04	0.00	1.00	807	Inter	2684916	2685246 2685081	14.3	11.0	2.3 -0.2	
yqbB yqbA	2685082	2685999	-	108	101	99 150	107	0.94	0.92	1.00								
yqDA vaaT	2687532	2688827	-	130	143	129	143	0.90	0.97	1.01								
vqaS	2688820	2689539	-	107	102	112	110	0.95	1.04	1.03								
yqaR	2689607	2690071	-	118	138	134	125	1.16	1.14	1.06								
											808	Inter	2689948	2690261 2690105	16.5	4.0	0.5 0.7	
yqaQ	2690215	2690670	-	200	198	199	204	0.99	1.00	1.02								
	2000000	2601707		2459	0010	0106	2107	2.00	2.76	0.00	809	Inter	2690577	2691043 2690810	25.2	30.7	3.9 -1.7	P03
yqaP yaaQ	2690808	2691/97	+	2458	8812	9180	2197	5.00	3.70	0.90								
yquO yaaN	2692159	2692587	-	201	174	127	197	0.87	0.94	0.99								
yqaM	2692823	2693764	-	111	98	108	94	0.89	0.98	0.85								
yqaL	2693646	2694347	-	115	100	111	116	0.87	0.97	1.01								
yqaK	2694399	2695253	-	129	111	115	115	0.86	0.89	0.89								
yqaJ	2695256	2696215	-	118	104	105	111	0.89	0.89	0.95								
yqal	2696321	2696515	-	85	74	76	87	0.87	0.89	1.02								
yqaH yaaG	2696645	2696902	-	80 140	135	85	/5	0.87	1.01	0.88								
yquO vadA	2697542	2697682	-	140	118	121	148	0.90	0.86	1.06								
yqaF	2697712	2697942	-	121	110	113	115	0.91	0.94	0.95								
yqaE	2698119	2698469	+	457	347	296	427	0.76	0.64	0.94								
yqaD	2698736	2698903	-	112	85	76	79	0.76	0.67	0.72								
-						10.5	4 50				810	Inter	2698907	2699373 2699140	35.6	7.0	16.1 7.3	
yqaC	2699259	2699795	-	138	164	185	158	1.19	1.34	1.14								
удав spoIIIC	2700064	2700382	+	217	153	175	259	0.71	0.82	1.18	811	spoIIIC	2700454	2700733 2700594	10.1	14.8	11.2 16.2	
vrkS	2701205	2701369	-	231	199	203	246	0.87	0.88	1.05	011	sponie	2700454	2100133 2100394	10.1	14.0	11.2 10.2	
<u>, , , , , , , , , , , , , , , , , , , </u>											812	Inter	2701355	2701872 2701614	27.4	44.0	19.0 5.9	P02
yrkR	2701914	2702333	-	291	243	268	308	0.86	0.94	1.07								
yrkQ	2702376	2703674	-	387	303	296	365	0.79	0.77	0.93								
yrkP	2703661	2704356	-	201	171	170	209	0.85	0.84	1.02								
yrkO wrk M	2/04624	2706010	+	344	253	265	323	0.74	0.78	0.92	017	velsN	2704912	2706080 2706001	4.0	24	0.5 0.1	
yrkiN vrkM	2706989	2700910	++	126	420	436	338 162	1.05	0.08	0.85	613	YIKIN	2700812	2/00969 2/00901	4.8	2.4	0.5 -0.1	
yrkL	2707401	2707925	-	2146	3007	3197	2228	1.05	1.50	1.04	814	yrkL	2707288	2707686 2707487	26.0	22.3	10.2 0.7	
				1.0	/						814	Inter	2707696	2708519 2708108	108.4	127.0	72.1 3.6	P02
yrkK	2708169	2708645	-	386	368	332	427	0.95	0.86	1.11								
yrkJ	2709228	2710013	-	105	93	97	111	0.89	0.93	1.07								
yrkI	2710074	2710301	-	93	67	85	90	0.73	0.92	0.97								
yrkH	2710335	2711222	-	247	194	198	263	0.79	0.80	1.06								
yrkG wrkE	2/11351	2/11461	-	205	168	185	181	0.82	0.90	0.88								
yrk F vrk F	2712546	2712300	-	204 163	207	221 160	250 182	0.79	0.84	1 1 1								
vrkD	2713175	2713366	-	830	763	726	777	0.90	0.85	0.93								
yrkC	2714159	2714719	-	619	962	871	649	1.55	1.40	1.06	815	yrkC	2714462	2714722 2714592	11.2	3.6	2.5 -0.4	
yrkB	2714945	2715091	-	278	196	214	225	0.68	0.77	0.82		-						
bltR	2715261	2716082	-	279	219	218	291	0.78	0.79	1.04								

suppien	gene	ne 51. Sur	umar	y oi trai	scriptor	ne and ( Trans	_nAP-ch criptore	up analyse e analysie	s (contir	wea).					hAP-chin o	malysis		
	gene			<b>C</b> 1	al inton-	Trails		c analysis	roccion c-	tio b				t	њат-сшра	Dinding	intoncity C	
			pu	Sigr	iai intensi	ty of KN	A	Exp	A abh	uΟ	PBR	ORF				AbrP 8	Approximation and a second sec	Profile
name	start	end	stra	wild	∆abrB	∆abh	$\Delta abh$	$\Delta abrB/$	$\Delta abrB/$	∆ abh /	ID	or	start	end	center	wild	wild	ID
						∆abr₿		wild	wild	wild		intergenic				-type ∆abh	-type	
blt	2716199	2717401	+	260	242	246	247	0.93	0.95	0.95								
bltD	2717570	2718028	+	351	317	323	312	0.90	0.92	0.89								
yrkA	2718185	2719489	-	2303	1923	2117	2446	0.83	0.92	1.06								
yrak vrdO	2719913	2721870	+	675	492	503	651	0.88	0.75	0.97	816	vrdO	2721109	2721286	2721198	58 05	54 -04	
trkA	2721004	2723030	-	156	149	148	152	0.95	0.94	0.96	010	yiuQ	2721107	2721200	2721190	5.6 0.5	5.4 -0.4	
czcD	2723118	2724053	-	203	201	228	175	1.00	1.10	0.87								
yrdN	2724340	2724729	-	228	248	243	234	1.09	1.07	1.03	817	yrdN	2724220	2724482	2724351	11.5 11.9	2.9 -0.4	
											817	Inter	2724492	2725145	2724819	83.3 118.0	73.4 16.8	
gltR	2725063	2725953	+	350	283	284	331	0.82	0.83	0.96								
yrdK hrmO	2726286	2726428	-	898	/05	628	862	0.86	0.81	1.00								
azlD	2720300	2728205	-	1172	859	887	1238	0.72	0.75	1.00								
azlC	2728202	2728966	-	1175	880	994	1182	0.75	0.84	1.00	818	azlC	2728521	2728749	2728635	0.6 0.2	-0.1 7.9	
azlB	2728979	2729452	-	861	546	612	776	0.63	0.71	0.90								
yrdF	2729786	2730061	-	106	89	84	96	0.84	0.79	0.90								
cypA	2730333	2731565	-	248	215	201	236	0.88	0.81	0.95								
yrdD	2731958	2732107	-	130	95	101	130	0.76	0.78	1.06	010	10	2722200	2722065	0722672	27.2 20.0	26 0.0	002
yraC yrdB	2732200	2733369	-	108	2076	114	123	1.04	1.06	0.92	819	yiuc	2152560	2732903	2752075	21.2 30.9	2.0 -0.9	P05
Jub	2/32//0	2100000		100			120	1.01	1.00	1.10	820	Inter	2733468	2734002	2733735	42.4 35.5	15.5 -1.6	
yrdA	2734179	2734682	-	980	1867	1787	952	1.96	1.81	0.99	821	yrdA	2734080	2734376	2734228	18.7 1.5	5.5 0.8	P07
aadK	2734908	2735762	-	519	583	612	537	1.13	1.18	1.04								
yrpB	2736141	2737184	+	451	790	924	415	1.76	2.05	0.92								
yrpC	2737534	2738331	+	218	182	184	230	0.83	0.85	1.06		<b>T</b> .	2720500	2720770	0720740	150 100	0.0 1.0	
um D	2728712	2720410		4072	22864	22602	4201	4.62	176	0.86	822	Inter	2738500	2/38//9	2738640	15.2 13.6	0.2 -1.0	
vrnE	2740583	2741338	-	177	135	150	185	4.02	0.85	1.05								
sigZ	2741470	2742000	-	264	236	247	283	0.90	0.94	1.06								
yrpG	2742165	2743115	+	329	317	334	362	0.96	1.01	1.08	823	yrpG	2742869	2743046	2742958	0.3 0.2	0.3 6.8	
yra0	2743389	2744705	-	495	353	410	495	0.71	0.83	1.00	824	yraO	2743651	2743964	2743808	1.0 0.4	0.6 21.7	P04
yraN	2744820	2745689	-	451	342	421	418	0.77	0.95	0.92	825	yraN	2745011	2745426	2745219	16.0 5.4	5.4 1.0	
M	2715921	2746027		200	106	105	220	0.08	0.07	1.10	825	yran	2745436	2/45851	2745644	<b>19.1</b> 14.2	1.5 -1.9	
csn	2743834	2748043	-	725	8664	8653	485	12.07	12.05	0.67								
con	27 17210	27 100 15		120	0001	0000	100	12.07	12.00	0.07	826	Inter	2747867	2748265	2748066	16.9 19.3	3.1 0.3	
											827	Inter	2748326	2748571	2748449	4.2 1.4	3.5 11.9	
yraL	2748486	2748749	+	1204	1265	1205	1385	1.05	1.01	1.15								
	2740004	27.40575		2.42	0.01	201	22.4	1.10	1.01	0.07	828	Inter	2748734	2748945	2748840	7.8 0.1	1.5 0.3	
yraK wra I	2750108	2/495/5	+	242	281	291	234	1.19	1.21	0.97								
yraJ vraI	2750517	2750951	-	876	1609	1716	893	1.83	1.80	1.18	829	vraI	2750604	2750764	2750684	4.3 2.7	1.5 0.6	
											829	Inter	2750774	2751206	2750990	26.6 14.8	6.6 0.3	
yraH	2751392	2751778	-	268	267	302	252	0.98	1.12	0.92								
yraG	2752027	2752272	+	148	188	230	131	1.26	1.54	0.89								
yraF	2752290	2752658	+	139	199	248	147	1.42	1.77	1.05	021		0750710	2752002	0750000	21.5 20.0	27 21	002
adhB	2/526//	2/53813	+	149	199	239	163	1.34	1.61	1.10	831	adhB	2752740	2/53093	2752903	21.5 20.0	3./ 3.1	P03
vraE	2753832	2754029	+	201	384	483	200	1 89	2 36	0.98	632	aund	2133149	2133613	2733612	2.1 0.9	1.0 3.7	
vraD	2754045	2754344	+	161	257	309	156	1.61	1.93	0.97								
yraB	2754607	2755029	-	360	219	222	350	0.61	0.62	0.96								
adhA	2755537	2756586	+	587	461	477	602	0.79	0.81	1.02	833	adhA	2755585	2756289	2755937	29.4 3.7	16.9 134.1	
yraA	2756717	2757226	+	7092	9162	10013	8803	1.33	1.44	1.25	834	yraA	2756656	2756799	2756728	3.5 1.0	0.1 0.5	
sacC	2757268	2759301	-	837	926	1188	582	1.15	1.49	0.68	835	sacC	2758237	2758312	2758275	2.3 0.6	0.0 0.0	
levG levF	2759458	2761115	-	1056	1150	1/101	517 745	1.22	1.58	0.66								
levF levE	2760300	2761620	-	879	1105	1402	597	1.10	1.42	0.09								
levD	2761620	2762060	-	1011	1160	1462	573	1.18	1.50	0.55								
levR	2762250	2765066	-	234	215	238	189	0.92	1.01	0.81								
aapA	2765783	2767162	+	921	561	528	878	0.62	0.58	0.96	836	aapA	2765870	2766200	2766035	8.0 15.3	3.1 2.8	
yrhP	2767269	2767901	-	1457	1123	1095	1412	0.77	0.75	0.97	837	yrhP	2767417	2768019	2767718	28.8 7.4	25.3 108.5	
yrhO	2768054	2768881	+	602	583	547	700	0.98	0.91	1.16	837	yrhO	2768029	2768359	2768194	11.1 6.8	1.9 6.1	
sigV	2769077	2769577	+	282	167	196	352	0.59	0.70	1.25								
yrhM vrhI	2/095/7	2772449	+	036 777	386 532	517	815	0.61	0.82	1.28								
yrnL vrhK	2772583	2772873	+	768	508	599 674	048 814	0.74	0.84	1.17								
yrhJ	2773117	2776281	-	2854	2476	3393	2981	0.87	1.18	1.04	839	yrhJ	2774098	2774309	2774204	3.9 3.7	2.1 11.3	
yrhI	2776297	2776881	-	1309	1097	1554	1426	0.84	1.18	1.09		<b>.</b> .						
											840	Inter	2776802	2777318	2777060	26.0 24.7	6.6 4.6	
yrhH	2777104	2777646	-	1526	882	1171	1883	0.58	0.77	1.23	840	yrhH	2777328	2777810	2777569	14.2 18.4	6.8 18.1	
yrzI	2778150	2778299	-	279	1331	1109	335	4.76	3.97	1.20	0.42	Tester	0770000	0770001	2778447	51 5 CA	55.0	
wrhC	7778680	2770480		3111	2177	1960	3012	0.67	0.60	1 20	842	inter	2118332	2779001	2778667	51.5 61.6	<u> </u>	
ymG	2110009	2119409	-	2111	21//	1000	5912	0.07	0.00	1.50								

Supplen	gene	ne 51. Sur	nma	ry of tra	nscriptor	ne and C Trans	_nap-cn	up analyse e analysis	s (conun	uea).				C	bAP-chin a	nalvsis			
	gene					TTails		c analysis		e b				<u> </u>		marysis Di			
			р	Sig	nal intens	ty of RN	A	Expi	ression ra	tio	PBR	ORF				AhaD	nding i	ALL	Profile
name	start	end	strar	wild	AahrB	$\Delta abh$	Aabh	$\Delta abrB/$	∆ abrB/	$\Delta abh$ /	ID	or	start	end	center	wild		wild	ID
			5,	W IICI	2 abrb	∆abrB	2 uon	wild	wild	wild		Intergenic				-type	abh	$\Delta abrB$	
vrhF	2779752	2780120	-	3904	1887	1810	3295	0.48	0.46	0.84						ijpo		Gpe	
yrhE	2780436	2783378	+	4586	3313	2658	5370	0.72	0.58	1.17	844	yrhE	2782581	2782809	2782695	7.8	1.8	4.3 10.0	
yrhD	2783397	2783879	+	3246	2086	1820	3516	0.64	0.56	1.09									
yrhC	2783915	2784145	-	377	529	524	459	1.41	1.40	1.22									
											845	Inter	2784026	2784356	5 2784191	18.9	9.3	4.1 -0.4	
yrhB	2784228	2785367	-	826	1186	1167	862	1.38	1.37	1.05									
yrhA	2785369	2786292	-	5047	932 5240	980	788	1.15	1.21	0.98									
min vrrT	2787073	2787714	-	3947	3349 775	784	0/5	0.90	0.93	1.08									
vr7A	27879073	2788110	+	3434	2454	2298	2844	0.72	0.67	0.83									
vrrS	2788147	2788848	-	4404	3890	3741	4599	0.89	0.85	1.05									
yrrR	2788913	2790667	-	549	461	456	555	0.86	0.84	1.00									
greA	2790721	2791194	-	10933	10844	10397	11200	0.99	0.95	1.02									
											848	Inter	2791302	2791479	2791391	8.7	1.6	2.6 -0.4	
udk	2791445	2792080	-	6351	4572	4020	6310	0.73	0.64	1.00							0.0	50 A	
yrrO	2792087	2793355	-	7451	5318	4943	7162	0.72	0.66	0.96	849	yrrO	2792645	2793162	2792904	35.2 1	0.8	58.1 60.2	
yrrn vrrM	2793374	2794505	-	1298	3258	4307	/100	0.00	0.39	0.98									
vrrL	2795114	2796196	-	3944	4582	4452	3676	1.17	1.14	0.93									
yrzB	2796327	2796608	-	15569	15048	14246	16498	0.96	0.91	1.06									
yrrK	2796626	2797042	-	10595	8045	8083	9965	0.76	0.76	0.94									
yrzL	2797050	2797316	-	8257	6247	5788	8160	0.76	0.70	0.99									
alaS	2797401	2800037	-	6973	5285	4883	6392	0.76	0.70	0.92	852	alaS	2799649	2799860	2799755	7.2	0.1	3.1 -0.5	
yrrI	2800368	2801429	-	306	322	341	330	1.05	1.12	1.08									
glnQ	2801585	2802313	+	120	106	108	129	0.88	0.90	1.08									
glnH	2802335	2803156	+	164	148	155	169	0.90	0.95	1.03									
ginM alnP	2803217	2803807	+	127	136	140	209	1.07	1.05	1.04									
vrrD	2804931	2805455	-	320	619	736	329	1.89	2.24	1.03	855	vrrD	2805021	2805198	2805110	7.2	7.3	1.4 -0.2	
vrrC	2805513	2807909	-	2837	2592	2328	2833	0.94	0.83	0.99	856	vrrC	2806908	2807170	2807039	5.0	2.7	8.2 1.7	
yrrB	2807934	2808554	-	3131	2888	2658	3216	0.94	0.86	1.02		5							
mnmA	2808640	2809764	-	7374	7208	6836	7622	0.98	0.93	1.03									
yrv0	2809786	2810925	-	5937	5921	5620	6155	1.00	0.95	1.04									
yrzC	2811027	2811362	-	2932	3037	3021	3043	1.04	1.04	1.04									
yrvN M	2811562	2812827	+	1049	783	801	1042	0.75	0.77	0.99									
yrvM arpS	2812809	2815035	-	2909	2039	7050	2411	0.70	0.65	0.85									
usp5 hisS	2815761	2817035	-	5046	4381	4307	4808	0.87	0.85	0.94									
vrzK	2817417	2817587	-	74	98	91	79	1.34	1.25	1.04	860	vrzK	2817092	2817896	5 2817494	47.8 3	38.5	74.0 46.2	P01
yrvJ	2817720	2819276	+	2153	2271	2100	2287	1.08	0.97	1.07		5							
yrv1	2819303	2819701	-	6111	5034	4673	5331	0.83	0.77	0.87									
relA	2819755	2821959	-	5223	4420	4118	4893	0.85	0.79	0.94	861	relA	2821358	2821535	2821447	3.3	5.0	1.8 0.7	
apt	2822127	2822639	-	7899	6667	6280	8003	0.84	0.80	1.01		_							
yrvE D	2822645	2825005	-	6203	5644	5171	6304	0.91	0.84	1.02	862	yrvE	2824928	2825003	2824966	0.1	0.1	0.2 2.6	
yrvD ymyC	2825072	2825395	-	4507	3/0/	3802	2407	0.80	0.90	0.90	862	umC	1815124	2825768	2825501	22.2 1	6.0	11.8 66	
yive	2023471	2823908	-	3039	5554	5402	5407	0.97	0.95	0.93	864	Inter	2825254	2825708	2825501	15.4 1	0.9	53 12	
secDF	2826126	2828339	-	9705	9229	9300	9570	0.95	0.96	0.99	865	secDF	2826798	2827213	2827006	22.9 2	23.1	35.9 31.8	P01
yrzD	2828378	2828674	-	5821	6010	5371	5716	1.03	0.92	0.98									
spoVB	2828790	2830346	+	186	184	187	216	0.99	1.00	1.16									
yrbG	2830350	2831006	-	163	177	195	159	1.08	1.20	0.98									
yrzE	2831141	2831593	+	334	317	343	333	0.96	1.03	1.00									
yajC	2831650	2831919	-	14264	14086	13770	14022	0.99	0.97	0.98									
tgt aucA	2831955	2833098	-	5550 8570	4591	4242 6324	7702	0.85	0.76	1.00									
циел	2655125	2034133	-	8575	0000	0324	1192	0.78	0.74	0.91	866	Inter	2834176	2834421	2834299	93	64	35 24	
ruvB	2834376	2835380	-	4354	3147	2903	4235	0.72	0.67	0.97	000	mer	203 1170	2031121	20012))	7.5	0	515 211	
ruvA	2835391	2835996	-	3101	1933	1783	2982	0.62	0.57	0.96									
bofC	2836135	2836647	-	727	374	532	461	0.52	0.77	0.63									
csbX	2836695	2838002	-	2299	930	1516	1721	0.40	0.66	0.75									
yrbE	2838073	2839098	-	3815	1339	2272	3705	0.36	0.58	0.97									
yrzF	2839336	2839728	+	1026	1170	1543	1244	1.14	1.51	1.21									
yrzG	2839761	2839982	+	1427	1678	2081	1860	1.17	1.44	1.30	927	Intor	2820071	2840405	2840120	14.4	12	22.1 44.2	
vr7H	2840304	2840525	+	581	400	331	526	0.71	0.58	0.80	60/	men	20398/1	2040405	2040138	14.4	4.2	23.1 44.3	
vrbD	2840836	2842290	+	276	236	247	299	0.86	0.90	1.08									
yrbC	2842331	2843053	-	1457	1538	1932	2060	1.08	1.35	1.41									
coxA	2843156	2843674	-	137	379	509	138	2.67	3.55	1.00									
safA	2843900	2845063	-	183	146	149	191	0.80	0.82	1.04	869	safA	2844002	2844162	2844082	5.5	4.8	1.8 1.1	
											869	safA	2844172	2844587	2844380	19.3	7.5	19.6 1.3	
nadA	2845180	2846286	-	248	186	196	221	0.75	0.79	0.89									
nadC	2846273	2847/142	-	234	176	189	289	0.75	0.81	1.22	070	nodD	201712-	284760	2847550	= 0	2.0	25 120	
паав	204/090	2048091	-	198	1/2	1/1	210	0.91	0.91	1.15	0/0	INNUD	204/430	204/081	204/009	3.8	3.7	5.5 15.9	

	gene					1 rans	criptome	: analysis						C	плг-спра	naiysis			
			_	Sigr	nal intens	ity of RN	A <sup>a</sup>	Exp	ression ra	tio <sup>b</sup>		ORE				]	Binding	intensity c	
name	start	end	strand	wild	∆abrB	∆abh	∆abh	∆abrB/	$\Delta abh$ $\Delta abrB/$	∆abh /	PBR ID	or	start	end	center	Abı wild	rB	Abh wild	Profile ID
						∆ abrB		Wild	wild	Wild		Intergenic				-type	⊿abn	-type	
nifS	2848794	2849981	+	127	124	128	135	0.98	1.01	1.06									
yrxA	2849941	2850477	+	1393	1784	1593	1391	1.34	1.17	1.02						_			
pheA	2850509	2851366	-	2179	2172	2051	1913	1.00	0.94	0.88	872	pheA	2850921	2851098	2851010	4.8	1.1	0.7 0.6	
pheB	2851383	2851826	-	3914	3932	3387	3508	1.00	0.86	0.89									
obgE	2851887	2853173	-	4652	5235	4462	4025	1.13	0.96	0.86									
spo0B	2853207	2853785	-	2516	3419	2481	2143	1.39	0.97	0.83									
rpmA	2854106	2854390	-	23818	22227	22325	23539	0.93	0.94	0.99									
ysxB	2854403	2854/41	-	2/512	26194	25103	27706	0.95	0.91	1.01									
rplU	2854/44	2855052	-	26127	25238	23995	26530	0.97	0.92	1.02									
SpoIVFB	2855199	2856065	-	403	396	412	400	0.98	1.02	0.99	072	on o IV/E A	2056522	2052070	2056705	14.1	20	20 04	
spoiv FA	2850058	2830832	-	12407	12074	12578	12116	0.80	0.85	0.90	8/3	SPOIVFA	2850552	28308/8	2856705	14.1	2.8	2.9 -0.4	
minD minC	2857811	2858/01	-	12497	12974	9776	12110	1.04	1.01	1.00									
mmeD	2858544	2850062		8210	7830	7/22	8725	0.96	0.98	1.00	875	mraD	2858860	2850122	2858001	43	3.1	10.4 9.7	
mrøC	2859059	2859931		13532	12894	12707	13244	0.95	0.91	0.98	015	med	2050000	2057122	2050771	4.5	5.1	10.4 9.7	
mreR	2859962	2860975	_	13169	13022	12366	13447	0.99	0.94	1.02									
radC	2861066	2861761	-	3753	4729	4301	4383	1.27	1 15	1.02									
maf	2861798	2862367	_	4650	5932	5369	4910	1.27	1.15	1.07									
snoIIR	2862520	2863518	-	180	155	160	184	0.86	0.89	1.07									
comC	2863652	2864398	-	382	394	404	395	1.03	1.06	1.02									
folC	2864538	2865830		4935	3470	3413	4492	0.71	0.70	0.91									
valS	2865890	2868532	-	9336	7179	6831	8648	0.77	0.73	0.93									
vsrE	2869029	2870054	-	202	197	187	198	0.97	0.93	0.97									
spoVID	2870087	2871814		185	160	161	194	0.86	0.87	1.04									
hemL.	2871945	2873237	_	5157	4704	4642	4912	0.00	0.90	0.95									
hemB	2873267	2874241	-	4752	4658	4170	4717	0.99	0.88	0.99									
hemD 2	2874238	2875026	-	2970	2732	2622	2793	0.93	0.89	0.94									
hemC	2875016	2875960	- (	2908	2583	2283	2809	0.88	0.78	0.95									
hemX	2875993	2876823	-	1748	1599	1412	1775	0.92	0.81	1.00									
hemA	2876831	2878198	-	4316	4150	4061	4304	0.96	0.94	1.00									
ysxD	2878362	2878925	+	877	571	532	664	0.65	0.61	0.76	876	ysxD	2878206	2878536	2878371	18.2	2.3	18.9 0.5	P05
engB	2878947	2879534	-	5669	5340	5319	5582	0.94	0.94	0.98		•							
lonA	2879531	2881855	-	4925	4718	4987	5204	0.96	1.01	1.06									
lonB	2882036	2883694	-	245	298	334	229	1.21	1.36	0.93									
											877	Inter	2883493	2883925	2883709	21.6	25.8	2.4 0.0	P03
clpX	2883846	2885108	-	11731	11461	12055	11929	0.98	1.03	1.02									
											878	Inter	2885108	2885285	2885197	2.8	4.1	4.3 5.4	
tig	2885381	2886655	-	23241	21750	21040	23007	0.94	0.91	0.99	879	tig	2885381	2885540	2885461	2.9	1.0	4.3 3.1	
ysoA	2886883	2887815	-	1154	1056	991	1173	0.91	0.86	1.01									
leuD	2888005	2888604	-	250	260	284	218	1.03	1.12	0.87									
leuC	2888617	2890035	-	295	336	399	301	1.13	1.32	1.02									
leuB	2890085	2891182	-	243	254	272	242	1.04	1.11	0.99									
leuA	2891203	2892759	-	236	270	341	214	1.13	1.42	0.91									
ilvC	2892746	2893774	-	359	411	476	351	1.14	1.32	0.97									
ilvH	2893791	2894315	-	214	301	336	216	1.40	1.55	1.01									
ilvB	2894312	2896036	-	238	308	343	241	1.28	1.41	1.00						_			
											881	Inter	2896532	2896912	2896722	14.4	11.0	1.4 -0.7	
ysnD	2896852	2897187	+	107	87	95	112	0.81	0.88	1.04									
ysnE	2897356	2897811	+	334	296	337	293	0.90	1.03	0.86									
ysnF	2897995	2898855	+	243	263	400	194	1.08	1.65	0.79									
trnSL-Arg	g 2898879	2898955	-	11441	16463	17220	11159	1.43	1.57	0.88									
ysnB	2899086	2899601	-	4612	4610	4782	4353	1.00	1.04	0.94							1.0	10 15	
ysnA	2899611	2900207	-	6075	5745	5795	5549	0.94	0.95	0.91	883	ysnA	2899983	2900160	2900072	5.5	1.9	1.2 1.7	
rph	2900220	2900957	-	5287	5087	4880	5019	0.96	0.92	0.95									
gerM	2901068	2902168	-	267	209	230	281	0.78	0.86	1.05									
racE	2902284	2903102	-	5388	4125	3647	5358	0.76	0.68	0.99									
ysmB	2903110	2903550	-	5021	4355	3666	4626	0.87	0.73	0.92	004	<b>.</b> .	2002/55	2002015	2002725	10	10	25 00	
	2002704	2004010		1744	1520	10/7	1074	0.07	1.00	1.07	884	Inter	2903655	2903815	2903735	4.2	4.6	3.5 0.8	
gerE	2903794	2904018	-	1/04	1528	1805	18/4	0.87	1.06	1.00									
ysmA JLD	2904134	2904577	-	19205	1500	1401	1/15	0.90	0.96	1.13									
sanD sdbA	2904040	2903401	-	10095	10400	17102	19330	0.88	0.96	1.05		*Droad	2004254	2004450					
sanzı sdbC	2903404	270/104	-	15220	11526	17102	15/31	0.03	0.91	1.05		Dioau	2700230	2900430					
velR	220/198	2907800	-	13529	0020	0207	10007	0.75	0.64	1.08									
ysid bsC	2908099	2908040	+	12041	9028	9392	10932	0.72	0.75	0.8/	804	beC	2009729	2000110	2008020	5.6	3.0	27 282	<b>D</b> 04
iyse	2000001	2709013	-	2014	918 1705	000	2/01	1.25	1.05	0.77	000	iyse	2708/38	2909119	2700929	5.0	5.0	2.1 28.3	r 04
usr uvrC	2709991 2010160	2710002	-	3644 1070	4/83	4000	1120	1.25	1.05	1.04									
uviC tryA	2012002	2711930	-	15/66	12002	940 17640	1120	0.65	1.15	1.04									
UAA XSA	2712092	2712400	-	10400	10000	1/008	13984	1.1/	1.15	1.03	807	¥69	2012124	2012260	2012247	4.0	5 2	80 72	
лзи etfA	2912129	2714210	-	2084	32/19	341	499 3700	0.82	1.00	0.05	00/	лъа	2713124	4713309	2713247	4.0	5.5	- 0.9 1.2	
otfR	2915446	2916210	-	2200 2004	35/11	1100 J	4220	0.01	0.74	0.93									
vsiB	2916234	2917010	-	2531	1872	7195	2381	0.72	0.80	0.00									
ysiD veiA	20170254	2017600	-	2531	25/2	2173	201	0.74	0.00	0.74	800	wiA	2017424	2017560	2017407	1.4	0.5	33 17	
y341	2717023	2717005	-	5540	2342	2019	5241	0.72	0.62	0.92	009	your	2717420	2711308	2711491	1.4	0.5	5.5 4.7	

Supplet	gene	ne 51. Sui	шпа	ry or tra	iscriptor	Trans	criptom	e analyse	s (conun	iueu).					ChAP-chip a	analysis				
	gene			Sig	nal intens	ity of RN	A <sup>a</sup>	Exp	ression ra	tio b		0.00			san cap	Binding	intensity c			
name	start	end	and	~ .0.		Aabh		A abrP/	$\Delta abh$	A abb /	PBR	ORF	start	end	center	AbrB	Abh	Profile		
IRTIC	start	chù	str	wild	∆abrB	∆ abrB	$\Delta abh$	vild	$\Delta abrB/$	wild	ID	Intergenic	start	chù	center	wild Aabh	wild AabrB	ID		
1-64	2017714	2010206		1596	1676	1040	1422	1.06	wild	0.00		-				-type	-type			
lCJA vshF	2917714	2919390	-	1380	1070	1909	3722	1.06	1.25	0.90										
mutSB	2920004	2922361	-	4066	4187	4147	3798	1.03	1.02	0.03										
yshC	2922382	2924094	-	3508	3567	3582	3434	1.02	1.02	0.98										
yshB	2924168	2924701	-	982	918	858	1122	0.93	0.89	1.14	891	yshB	2924174	2924555	5 2924365	24.6 11.1	6.6 0.5			
yshA	2924708	2924965	-	1262	1430	1236	1308	1.13	0.98	1.03	891	yshA	2924565	2925201	1 2924883	27.0 15.5	9.4 -0.5			
rnhC	2925099	2926040	+	1188	1435	1230	1342	1.21	1.04	1.14										
phe1	2926076	2928490	-	6821 5696	2028	53/5 1203	5283	0.83	0.79	0.92										
vsgA	2929895	2930641	-	1702	1273	1083	1514	0.74	0.63	0.89										
sspI	2930760	2930975	+	149	241	290	154	1.63	1.97	1.03										
ysfB	2931044	2932150	+	518	462	423	540	0.89	0.81	1.04										
ysfC	2932253	2933665	+	1517	12686	11100	1637	9.11	7.52	1.03										
ysfD	2933662	2934996	+	979	9202	8100	1101	10.09	8.33	1.05										
ysfE ast A	2935035	2935277	-	2/58	2000	2042	2/9/	0.60	0.73	1.01	803	oct A	2026220	2026522	2 2026126	52 20	4.4 0.5			
abfA	2937398	2938900	-	276	320	374	286	1.17	1.37	1.03	893	CSLA	2930329	293032.	5 2950420	5.5 2.0	4.4 0.5	1		
araQ	2938919	2939764	-	372	404	472	384	1.09	1.27	1.03										
araP	2939765	2940706	-	347	405	517	374	1.17	1.50	1.08										
araN	2940742	2942043	-	452	353	461	402	0.78	1.01	0.89										
araM	2942074	2943258	-	571	361	465	533	0.63	0.81	0.93										
araL araD	2943255	2944073	-	4/1	253	530	464	0.54	0.69	0.99										
araB	2944757	2946439	-	1183	510	740	1043	0.44	0.61	0.80										
araA	2946453	2947949	-	1335	567	789	1110	0.42	0.58	0.83	895	araA	2947277	2947488	8 2947383	1.4 1.0	3.4 8.2			
abnA	2948157	2949098	-	267	180	213	256	0.68	0.79	0.97										
ysdC	2949295	2950380	-	9020	10636	10836	9364	1.18	1.20	1.04										
ysdB	2950564	2950956	+	3595	3072	3661	3148	0.85	1.02	0.88										
ysdA mlT	2950972	2951241	-	3012	1842	1600	2130	0.64	0.54	0.72										
rpn rpmI	2951689	2951889	-	22339	21943	19747	21377	0.98	0.80	0.96										
infC	2951902	2952423	-	19589	18721	16293	19555	0.96	0.83	1.00										
yscA	2952595	2952819	+	43	39	40	35	0.90	0.92	0.82	897	yscA	2952377	2953064	4 2952721	42.1 60.6	40.5 21.8	P01		
yscB	2952869	2953501	+	446	1751	1570	657	3.98	3.52	1.47										
ysbB	2953533	2954228	-	3598	972	1269	3591	0.27	0.34	0.99										
ysbA hat	2954250	2954690	-	5320	1382	1/6/	5118	0.26	0.32	0.97										
lyl I lyt S	2954624	2955549	2	823	719	674	752	0.79	0.80	0.89										
vsaA	2957475	2958257	+	4250	3839	3599	3800	0.90	0.85	0.89										
thrS	2958298	2960229	-	11848	9166	8800	11123	0.77	0.74	0.94								_		
											898	Inter	2960044	2960510	0 2960277	12.6 4.6	23.9 41.3			
ytxC	2960626	2961471	-	2519	1903	1825	2391	0.75	0.72	0.95										
ytxB	2961550	2962191	-	3763	3152	2920	3617	0.84	0.77	0.96										
anai dnaB	2962225	2963100	-	2450	1888	1/03	2357	0.77	0.72	0.96										
nrdR	2964721	2965179	-	1336	1067	1126	1357	0.81	0.86	1.01										
speD	2965453	2965839	-	10226	6651	5817	9277	0.65	0.57	0.91										
											900	Inter	2965807	2965967	7 2965887	2.0 3.3	1.8 1.2			
gapB	2966072	2967094	-	1471	969	901	1209	0.65	0.60	0.81										
ytcD	2967300	2967680	-	657	485	482	657	0.75	0.74	1.01										
ytDD ythF	2969078	2969054	++	495 647	244	247	490 598	0.50	0.50	0.99	907	vtbF	2969020	2969419	8 2969219	79 10	74 277			
coaE	2969962	2970555	_	3626	3513	3525	3643	0.97	0.97	1.00	702	JUL	2757020	2707410	5 2767219	1.0	- 1.4 - 21.1			
ytaF	2970717	2971196	-	4867	5137	5342	5557	1.05	1.10	1.14										
mutM	2971368	2972204	-	3585	3725	3699	3825	1.04	1.03	1.07										
polA	2972221	2974863	-	3809	3527	3635	3898	0.93	0.96	1.02										
nh P	2075107	2076045		40.2 *	2002	2500	27/0	0.72	0.07	0.01	903	Inter	2974953	2975096	6 2975025	6.5 1.8	1.3 -0.3	I		
pnoK phoP	29/5107	29/0846	-	4024	2902	2003 2702	2/08	0.72	0.87	0.94										
pno <b>r</b> mdh	2977773	2978711	-	5244 16178	23143	23595	15166	1 43	0.80	0.90										
icd	2978755	2980026	-	17318	25070	25956	16650	1.45	1.50	0.96										
citZ	2980190	2981308	-	9485	17854	19155	9941	1.90	2.04	1.05										
ytwI	2981642	2982106	-	1361	651	642	1012	0.48	0.47	0.74										
ytvI	2982203	2983318	+	291	251	246	284	0.86	0.84	0.98	<i>c</i> -	<i>.</i> .					0.4			
fxsA	2983351	2983734	-	10795	7935	7950	10242	0.74	0.74	0.95	904	fxsA	2983623	2983749	9 2983686	2.1 3.3	0.6 0.2			
pyk pfk A	2983827	2985584	-	18563	14992	15215	18961	0.81	0.82	1.02	905	рук	2984762	2984871	1 2984817	0.5 0.7	0.7 3.7			
рјка ассА	2986770	2780380	-	14378 9866	9451	90203	14338 9472	0.70	0.71	1.00	906	accA	2986768	298738	7 2987078	56.4 76.9	45.4 26.0	P01		
aun	2700770	2701141	-	2000	7431	7028	7412	0.90	0.72	0.70	906	accA	2987397	298779	5 2987596	22.1 33.2	12.5 2.9	101		
accD	2987732	2988520	-	9163	9022	8579	8860	0.99	0.94	0.97										
											907	Inter	2988570	2989121	1 2988846	43.3 40.8	65.3 42.8	P01		
ytsJ	2988939	2990171	-	8082	6512	6764	8313	0.81	0.84	1.03	907	ytsJ	2989131	2989665	5 2989398	8.4 7.5	13.1 27.8			
											908	ytsJ	2989845	2989954	4 2989900	2.1 1.2	3.4 1.4			
Suppleme	gene	ie 51. 5ii	шпа	ry of tra	iscriptor	Trans	criptom	e analyse	s (conun	ueu).				0	hAP-chip a	nalvsis				
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	gene			Sim	nal intensi	ity of RN		Exp	ression ra	tio <sup>b</sup>					in tinpu	Bi	nding i	intensity <sup>c</sup>		
		,	pu		Ref HRCTES	ly of full			$\Delta abh$		PBR	ORF		,		AbrB	iding i	Abl	1	Profile
name	start	end	stra	wild	∆abrB	$\Delta abh$	$\Delta abh$	∆ abrB/	$\Delta abrB/$	∆abh /	ID	Of Intergenic	start	end	center	wild	abh	wild	1 abrP	ID
						Aubrb		wiid	wild	wiid		intergente				-type	uon	-type ∠	айны	
dnaE	2990308	2993655	-	2001	1573	1558	1984	0.79	0.78	0.99										
ytrI vtaI	2994133	2994636	+	146 3771	2828	3012	3870	0.80	0.84	0.85										
ytq1 ytp1	2996019	2996321	+	438	891	715	384	1.96	1.57	0.89										
ytoI	2996340	2997659	-	1226	1037	966	1124	0.85	0.78	0.92	909	ytoI	2997444	2997704	2997574	5.0	6.7	0.9	-0.6	
ytnM	2997835	2998737	-	266	236	261	303	0.89	0.98	1.14							_			
ytnL	2998756	3000006	-	177	157	160	170	0.89	0.91	0.96	910	ytnL	2998685	2998862	2 2998774	7.3	0.4	0.9	-0.6	D05
rihR	3000024	3000716	_	164	152	166	156	0.93	1.01	0.96	911	yuiL	2999407	2999802	2999000	22.4	1.5	32.5	2.0	P03
ytnJ	3000763	3002091	-	162	146	158	178	0.90	0.97	1.10										
ytnI	3002088	3002369	-	311	272	282	326	0.87	0.91	1.05										
ytmO	3002384	3003388	-	238	228	234	272	0.96	0.98	1.15										
ytmN	3003385	3004164	-	217	203	200	263	0.94	0.92	1.23										
ytmM vtmL	3004161	3004868	-	254	245 148	200	255	0.93	0.98	1.00	912	vtmI.	3005315	3005594	1 3005455	64	83	37	93	
ytmE ytmK	3005639	3006451	-	197	179	196	180	0.91	0.99	0.91	/12	Juins	5005515	500557	. 5005 155	0.1	0.5	5.7	7.5	
ytmJ	3006465	3007274	-	166	145	144	165	0.88	0.87	1.01										
ytmI	3007288	3007824	-	148	143	148	173	0.96	1.00	1.17										
ytlI wthI	3007977	3008903	+	185	171	176	178	0.92	0.95	0.96	913	ytlI	3007848	3008212	2 3008030	17.5 2	23.2	17.7	9.5	
$y_{IKL}$	3008954	3010467	-	3819	0405 4958	5424	5629 4874	1.27	1.41	1.11										
ytzD	3010594	3010830	-	196	176	181	193	0.90	0.95	1.00										
argH	3010790	3012175	-	588	484	478	556	0.83	0.81	0.95										
argG	3012172	3013383	-	585	433	445	488	0.75	0.77	0.85										
moaB	3013553	3014065	-	3082	2741	2333	2572	0.90	0.75	0.82										
ackA vtrK	3014150	3015337	-	8150	8608	8717	8738	1.11	0.96	0.94										
tDX	3015085	3017238	-	14907	17332	17985	16927	1.16	1.00	1.14										
ytfJ	3017348	3017803	-	224	555	716	195	2.45	3.15	0.86										
ytfI	3017817	3018497	-	251	266	268	273	1.06	1.07	1.09										
yteJ	3018572	3019066	-	7316	10176	10495	7779	1.39	1.43	1.06										
sppA	3019079	3020086	-	8807	11938	12686	8766	1.36	1.44	1.00	01/	Inter	3020080	3020435	3020262	15.2 1	63	83	0.0	
ppnK 2	3020272	3021075	+	4252	7263	8141	4762	1.72	1.92	1.12	714	mer	5020087	5020450	5020202	15.2 1	0.5	0.5	0.0	
ytcJ	3021107	3022696	-	4509	4040	4195	4842	0.90	0.93	1.07										
ytcI	3022716	3024311	-	5351	4613	4479	5569	0.86	0.84	1.04	916	ytcI	3023335	3023920	3023628	33.4	3.1	26.4	98.5	P06
sspA	3024484	3024693	-	4977	8174	9876	4595	1.64	1.99	0.92										
yiDJ nifZ	3024920	3023990	-	1684	1549	1452	1899	0.84	0.82	1.00										
braB	3027340	3028677	+	2056	1183	1064	1870	0.58	0.52	0.91										
ezrA	3028772	3030460	-	6273	6429	6170	5589	1.03	0.98	0.89										
hisJ	3030657	3031463	+	1103	789	789	1152	0.73	0.73	1.05										
yttP vtcP	3031460	3032083	-	198	234	204	173 5222	1.19	1.03	0.88										
yisr vtrP	3032738	3034477	+	1264	4393	1080	1210	0.85	0.78	0.99										
rpsD	3034772	3035374	+	19570	19015	17435	18827	0.97	0.89	0.96										
tyrS	3035645	3036913	-	7370	5803	5761	6956	0.79	0.78	0.95	918	tyrS	3035830	3036415	5 3036123	51.4 1	l 9.5	29.0	-0.2	P02
acsA	3037255	3038973	-	1810	2343	3059	1943	1.32	1.72	1.06										
acuA acuP	3039134	3039/66	+	2346	1092	1430	2016	0.47	0.60	0.86										
acuC	3040434	3041597	+	2298	1284	1631	2295	0.48	0.05	1.00										
ytxE	3041608	3042336	-	3534	1829	1674	3198	0.53	0.48	0.90	921	ytxE	3042205	3042348	3042277	4.3	5.4	1.3	1.4	
ytxD	3042326	3043144	-	2846	1572	1442	2610	0.56	0.51	0.91										
ccpA	3043207	3044211	-	5192	4568	4085	5071	0.88	0.79	0.98										
aroA vtx I	3044480	3045562	-	4134	9232 6434	6780	3361	0.92	0.99	0.97										
ytxH	3046148	3046606	-	6428	8257	8865	4596	1.29	1.39	0.71	923	ytxH	3046251	3046853	3046552	15.8 1	4.2	26.2	15.8	
ytxG	3046634	3047065	-	6936	8547	9428	4884	1.23	1.36	0.70										
murC	3047227	3048525	-	8834	8460	8059	9045	0.96	0.91	1.02										
ytpT	3048775	3050883	-	6904	5861	6010	7043	0.85	0.87	1.02										
yıps vtnR	3051792	3052397	-	12476	11729	11472	12147	0.82	0.81	0.99										
ytpQ	3052413	3053222	-	9026	9424	9352	9379	1.04	1.04	1.04										
ytpP	3053237	3053560	-	6268	6361	6045	6466	1.01	0.96	1.02										
ytoQ	3053795	3054241	+	5687	8532	8464	5919	1.52	1.49	1.04										
ytoP	3054296	3055369	-	4456	3213	3348	4333	0.72	0.75	0.97										
yızı malS	3055898	3057598	+	4388 3769	4060	4322	4250	1.72	2.04 1.15	0.99										
ytnP	3057680	3058450	-	4239	4840	4916	4153	1.14	1.16	0.98										
trmB	3058596	3059237	-	4504	2251	1837	3930	0.50	0.41	0.87										
ytzH	3059444	3059722	+	167	256	283	157	1.57	1.75	0.93										
ytmP amy¥	3059723	3062856	-	2067	2215	1955	2154 897	1.08	0.95	1.04										
	2000100	2002020		155	.100		071	1.2/	1.1)	5.75										

	gene					Transe	criptome	e analysis						C	hAP-chip a	nalysis				
			-	Sign	al intens	ity of RN.	A <sup>a</sup>	Exp	ression rat	tio <sup>b</sup>		ORF					Binding	intensity c		
name	start	end	rand			Aabh		A abrB/	$\Delta abh$	A abh /	PBR	or	start	end	center	Abi	rB	Ab	h	Profile
			st	wild .	∆abrB	∆abrB	∆abh	wild	$\Delta abrB/$	wild	ID	Intergenic				wild	$\Delta abh$	wild	∆ abrB	ID
. ID	20/2002	20/2011		2120	22/2	2070	2041	1.00	wild	0.05		-				-type		-type		
ytlR	3062882	3063811	-	2138	2263	2079	2041	1.06	0.97	0.95										
ytiQ vtIP	2064800	3065251	-	2350	2157	2102	2350	0.92	0.89	1.00										
ytti vtkP	3065500	3066435	+	3557	2447	2415	3579	0.85	0.84	1.00										
vtiP	3066469	3067860	-	3358	3907	3954	3488	1.16	1 18	1.00										
vtiP	3067957	3069255	+	1399	703	581	1314	0.55	0.44	0.93										
ythQ	3069294	3070451	-	2265	3131	3312	1988	1.38	1.46	0.88										
ythP	3070448	3071158	-	2272	3210	3542	1966	1.42	1.57	0.87										
ytzE	3071449	3071670	+	1459	1761	2959	1838	1.20	1.92	1.22										
ytzF	3071791	3072264	-	1501	1322	1293	1459	0.90	0.89	0.96										
ytzG	3072249	3072509	-	878	742	735	925	0.85	0.84	1.04										
ytgP	3072578	3074212	-	3032	2747	2588	3253	0.91	0.86	1.08										
ytfP	3074720	30/56/6	+	1392	1113	1103	1272	0.80	0.80	0.92										
opuD	3073803	3077622	+	2109	21//	2110	206	1.01	0.98	1.02										
yle v vteII	3077690	3078358	-	571	550	500	628	0.94	1.00	1.02	026	vteI	3077500	3077703	3077696	0.1	0.2	-0.2	5.8	
yte U vteT	3078380	3079666	-	312	258	286	333	0.98	0.92	1.10	120	yico	3011377	5011175	5077070	0.1	0.2	-0.2	5.0	
vteS	3079678	3080157	-	381	288	342	380	0.76	0.90	1.00										
yteR	3080178	3081299	-	319	226	247	353	0.71	0.77	1.11	927	yteR	3081135	3081414	3081275	6.0	6.2	4.5	2.6	
yteQ	3081307	3081798	-	225	182	207	286	0.81	0.92	1.28		•								
yteP	3081893	3082273	-	208	173	195	244	0.84	0.94	1.15										
											928	Inter	3082139	3082791	3082465	34.5	42.0	11.3	-0.8	
ytdP	3082489	3084807	+	220	348	419	216	1.58	1.90	0.98										
ytcQ	3084848	3086317	-	836	344	451	775	0.41	0.54	0.93										
ytcP	3086370	3087230	-	567	382	381	602	0.67	0.67	1.06										
yibQ hinI	2000275	2080462	-	308	2/3	280	302	0.89	0.93	1.00										
bioR	3089531	3009402	-	229	212	218	229	0.93	1.00	1.00	929	bioB	3089618	3090084	3089851	30.1	5.8	49.3	0.1	P05
bioD	3090541	3091236	-	178	174	190	197	0.92	1.00	1.11	930	bioD	3091029	3091257	3091143	8.1	0.8	0.7	-0.2	105
bioF	3091233	3092402	-	363	349	366	375	0.96	1.01	1.03									0.12	
bioA	3092392	3093738	-	258	243	256	262	0.94	0.99	1.02										
bioW	3093728	3094507	-	145	133	130	141	0.92	0.89	0.97										
ytaP	3094714	3095613	-	238	285	302	234	1.20	1.27	0.99	931	ytaP	3094616	3094827	3094722	6.6	1.9	1.1	0.0	
msmR	3095831	3096865	+	1057	225	356	937	0.25	0.33	0.89										
msmE	3096899	3098179	+	330	149	236	277	0.48	0.69	0.81										
amyD	3098172	3099083	+	209	161	204	194	0.78	0.96	0.92										
amyC	3099080	3099910	+	278	233	318	244	0.84	1.13	0.87										
melA sturF	3099930	3101226	+	400	207	2725	410	0.70	0.95	0.87										
yiwr IeuS	3101230	3104092	-	10072	8047	8104	10016	0.97	0.95	0.98										
vtvB	3104519	3104854	-	305	376	344	390	1.23	1.13	1.29										
,											933	Inter	3104850	3105112	3104981	9.3	9.5	1.9	1.3	
ytvA	3105259	3106044	+	1481	1226	1368	1580	0.84	0.94	1.07	934	ytvA	3105191	3105503	3105347	9.2	9.6	3.4	-0.4	
yttB	3106281	3107474	-	1111	862	800	973	0.81	0.73	0.88		•								
											935	Inter	3107451	3107849	3107650	11.7	23.0	0.5	1.9	
yttA	3107669	3108409	+	976	1315	1492	665	1.35	1.52	0.68										
ytsD	3108446	3110386	-	455	462	486	387	1.02	1.07	0.85										
ytsC	3110376	3111137	-	297	282	282	243	0.96	0.96	0.82										
ytsB	3111239	3112243	-	6/0	858	8/4	500	1.30	1.32	0.83										
yISA wtrE	3112230	211/228	-	2670	2542	2266	2000	1.23	1.22	0.89										
ytrF vtrE	3113028	3115023	2	1668	1674	1522	1320	0.95	0.84	0.78										
vtrD	3115038	3116015	-	1733	1569	1392	1364	0.88	0.79	0.78										
<i></i>											936	Inter	3115815	3116264	3116040	25.5	20.8	27.7	63.1	P01
ytrC	3116045	3117031	-	1539	1568	1299	1446	1.01	0.83	0.94	936	ytrC	3116274	3116655	3116465	25.6	30.2	13.3	15.2	
ytrB	3117025	3117903	-	1443	1415	1188	1219	0.97	0.82	0.84										
ytrA	3117896	3118288	-	1165	1078	870	919	0.91	0.74	0.78										
ytzC	3118614	3118886	-	520	539	651	406	1.01	1.22	0.78										
ytqA	3119048	3120016	+	1974	1771	1505	1958	0.90	0.76	0.99										
ytqB	3120013	3120597	+	3803	3343	3121	3419	0.89	0.82	0.90										
ytpB	3120587	3121690	-	4079	5192	5364	4771	1.30	1.34	1.18										
ytpA	3121711	3122490	-	5560	6942	6928	6024	1.26	1.27	1.08										
ytoA	3122539	3123054	+	569	137	741	649	1.30	1.30	1.15										
ytnA	3123299	3124690	-	/141	10050	0823	0476	0.92	0.96	0.91	0.20	acnD	3176007	3126224	3126155	2.2	57	1.1	0.6	
usnB matV	3124826	3120/24	-	11/95	10050	1019/	12102	0.85	0.86	1.03	938	asuB	3120083	5120226	3120133	3.2	5.7	1.1	0.6	
metK	51208/4	5128076	-	11383	9427	0234	11309	0.82	0.71	0.98	030	Inter	3128122	3128282	3128202	27	45	0.6	0.6	
nckA	3128579	3130162	+	3089	2689	2091	2681	0.88	0.66	0.87	159		5120123	5120203	5120203	2.1	4.5	0.0	0.0	
vtmB	3130201	3130443	-	3358	3059	3041	2667	0.00	0.91	0.79										
ytmA	3130495	3131268	-	992	861	860	994	0.87	0.87	0.99										
ytlA	3131419	3132108	+	236	216	231	274	0.91	0.98	1.17										
ytlB	3132105	3132422	+	116	116	135	104	1.01	1.17	0.90										
		2122217		161	137	146	179	0.86	0.91	1.12										

	gene					1 rans	criptom	e analysis		4				Chź	лг-спра	andiysis		
			_	Sig	nal intens	ity of RN	A <sup>a</sup>	Exp	ression ra	tio <sup>b</sup>		ORF				Binding	intensity c	
name	start	end	rand			∆abh		∆abrB/	$\Delta abh$	∆abh /	PBR	or	start	end	center	AbrB	Abh	Profile
			st	wild	∆abrB	∆abrB	∆abh	wild	$\Delta abrB/$	wild	ID	Intergenic				wild Aabh	wild ∆ abrB	ID
ID	2122102	2124004		277	204	292	20.9	1.00	wild	1.09						-type	-type	
ytiD thD	2124021	2124507	+	2//	294	283	298	1.00	1.03	1.08	041	r al - D	2122960	2124216 2	124042	12.2 20.5	50 07	
yikD wtkC	3134031	3134307	-	315	282	362	274	0.75	1.15	0.85	941	yukD	3133609	5154210 5	154045	12.2 20.3	3.9 -0.7	
dns	3135286	3135723	-	9957	10632	12829	8020	1.07	1.15	0.87								
- <i>r</i> -											943	Inter	3135586	3136052 3	3135819	25.7 8.3	9.6 0.7	
ytkA	3135986	3136423	-	4218	3861	4149	2842	0.92	0.99	0.67								
											944	Inter	3136351	3136562 3	3136457	3.9 9.0	0.8 -0.6	
luxS	3136543	3137016	-	4746	4416	4555	4683	0.93	0.96	0.99								
ytjA	3137145	3137372	+	656	565	522	595	0.86	0.79	0.91								
ytiB	3137369	3137932	-	4117	3105	3093	3719	0.76	0.75	0.90								
rpmE2	3138026	3138274	-	1089	661	920	542	0.61	0.85	0.49								
ythA	3138494	3139810	+	245	266	294	269	1.09	1.20	1.10								
ythB whC	3139854	3140894	+	394	4/5	518	3/5	1.20	1.31	0.95								
yinc mntD	3140945	3142012	+	1417	3606	3624	432	2.09	2.00	1.20								
mntC	3141123	3142012	-	1676	4721	4733	1780	2.51	2.51	1.01								
mntB	3143315	3144067	-	1651	4882	4778	1726	2.92	2.85	1.03								
mntA	3144086	3145006	-	1560	4038	4009	1590	2.54	2.52	1.01								
menC	3145286	3146401	-	1227	969	1002	1199	0.79	0.82	0.97								
menE	3146398	3147858	-	1866	1556	1640	1803	0.84	0.88	0.96								
menB	3147949	3148764	-	13381	13128	13031	13429	0.98	0.97	1.00								
ytxM	3148799	3149623	-	2776	1782	1712	2703	0.64	0.62	0.97								
menD	3149611	3151353	-	3577	2216	2164	3417	0.62	0.61	0.95								
menF	3151350	3152765	-	5259	3431	3680	5212	0.65	0.70	0.99								
											945	Inter	3152552	3153239 3	3152896	61.6 94.6	59.3 44.1	P01
yteA	3153054	3153773	+	184	251	272	206	1.38	1.50	1.13								
ytdA	3153/82	3154600	-	233	218	233	253	0.93	1.00	1.09								
yicA vtcB	3156055	31570058	+	162	1/2	147	161	0.91	0.99	1.13								
vtcC	3157008	3158231	+	110	101	104	94	0.00	0.91	0.85								
,nee	5157000	5150251		110	101	104	74	0.75	0.75	0.05	946	Inter	3158230	3158339 3	3158285	3.0 1.2	0.1 -0.4	
vtxO	3158305	3158736	-	123	97	101	102	0.79	0.82	0.83								
cotS	3158738	3159793	-	272	231	229	275	0.85	0.84	1.01								
cotSA	3159808	3160941	-	331	275	292	332	0.83	0.88	1.00								
ytaA	3161131	3162204	+	141	140	156	139	0.99	1.11	0.99	947	ytaA	3161103	3162096 3	3161600	57.7 81.0	83.7 185.0	P01
yta <b>B</b>	3162284	3162751	+	394	271	324	294	0.69	0.82	0.74								
glgP	3162782	3165178	-	252	266	281	256	1.06	1.11	1.01								
glgA	3165165	3166619	-	322	338	361	330	1.05	1.12	1.02	948	glgA	3165693	3165802 3	3165748	0.4 0.6	0.7 3.9	
glgD alaC	3166616	316/64/	-	345	359	386	363	1.04	1.12	1.05								
gigC alaP	316/0/1	3108813	-	240	180	200	254	1.03	1.10	1.00	040	alaP	2170215	2170241 2	170278	28 11	0.2 0.1	
gigD trnR_Sør?	3171023	3171113	-	17668	20703	19996	17420	1.00	1.00	0.98	747	gign	5170215	5170541 5	5170278	2.0 1.1	0.5 0.1	
trnB-Ile?	3171202	3171278	-	20103	27045	26053	18254	1.17	1.15	0.90								
trnB-His	3171378	3171453	-	5270	13564	11636	9571	2.52	2.22	1.71								
trnB-Ser1	3171741	3171832	-	12278	12685	13176	9760	0.98	1.06	0.85								
trnB-Met.	3171839	3171915	-	1906	1548	1270	1461	0.80	0.66	0.79								
trnB-Leul	3172451	3172537	-	23732	22619	23692	19678	0.96	1.01	0.86								
yuaJ	3178345	3178923	+	1300	1016	833	1107	0.79	0.63	0.85								
yuaI	3178965	3179486	-	906	1323	1577	838	1.46	1.74	0.92	957	yuaI	3178847	3179092 3	8178970	13.9 7.9	3.5 -0.3	
yuaG	3179504	3181033	-	620	1314	1319	554	2.06	2.13	0.89								
yuaF	3181054	3181578	-	391	878	765	410	2.20	1.95	1.07								
yuaE	3181746	3182234	+	2761	3285	3780	2922	1.19	1.38	1.05								
yuaD	3182240	3182818	-	1448	2418	2339	1301	1.68	1.62	0.90	059	Inton	2102722	2102004 2	107051	127 105	22 02	
ahsB	3182006	318/117		362	3/18	360	327	0.97	0 00	0.00	938	mer	5162725	3162964 3	162634	15.7 10.5	2.2 0.2	
gDSD ahsA	3184131	3185603	-	504	440	477	490	0.97	0.99	0.90								
yuaC	3185802	3186344	+	732	716	672	651	0.07	0.92	0.97								
Jude	5105002	5100511		152	/10	0.2	001	0.90	0.72	0.07	961	Inter	3186072	3186776 3	3186424	38.0 64.0	6.4 0.5	
yuaB	3186542	3187087	+	1128	17987	19456	513	16.49	17.66	0.46								
yuaA	3187453	3188121	+	527	574	615	500	1.07	1.17	0.96								
vubG	3188128	3189465	+	889	862	908	858	0.97	1.02	0.97								
yubF	3189501	3189764	-	11556	12520	12125	13309	1.08	1.05	1.15								
											962	Inter	3189608	3190091 3	8189850	44.7 19.1	26.1 10.0	
yubE	3189873	3190721	-	2225	2289	2170	2013	1.04	0.98	0.91	963	yubE	3190390	3190669 3	8190530	8.5 10.8	2.0 -0.7	
											963	Inter	3190680	3191060 3	3190870	<b>19.8</b> 10.9	14.5 -0.1	
yubD	3190882	3192417	-	553	383	400	562	0.71	0.73	1.01								
yubC	3192902	3193387	+	142	123	136	130	0.87	0.96	0.91								
trnSL-Ala	2102/74	3193566	-	9920	12185	11824	10268	1.23	1.19	1.04								
wpr	31930/4	3194304	-	5129	4383	5080	2910	1.49	1.00	0.93	96/	Inter	319/250	319/83/ 2	8194542	46.2 68.0	59.8 51.4	P01
wuhA	319/1507	3195762		2200	3675	3057	2454	1 59	1 72	1.07	904	111101	3174230	3174034 3	,174342	40.2 08.9		101
vulF	3195945	3196931	+	2299	2845	2771	2993	0.98	0.96	1.07								
vulE	3196972	3198246		544	386	511	505	0.71	0.94	0.93								
,	21/0/14	2120240		244	500	211	202	0.71	0.74	5.75								

Supplen	entary Tat	de S1. Sur	nmai	ry of tra	nscripto	me and C	hAP-ch	up analyse	s (contir	ued).				C	h A D ahim a	makaia				
	gene				11.1	Trans	criptom	e analysis		b				U	nAP-cnip a	inalysis		c		<u> </u>
			p	Sig	nal intens	ity of RN	Α	Expi	ession ra	tio	PBR	ORF				Aba	sinding:	intensity		Profile
name	start	end	strar	wild	∧ abrB	$\Delta abh$	Aabh	$\Delta abrB/$	A abrB/	$\Delta abh$ /	ID	or	start	end	center	wild	<u> </u>	wild		ID
					14010	∆abrB	Luon	wild	wild	wild		Intergenic				-tvpe △	labh	-type	1 abrB	
yulD	3198272	3198586	-	461	341	441	466	0.74	0.96	1.01						~ * *				
yulC	3198604	3200061	-	1062	714	874	955	0.67	0.83	0.90										
yulB	3200066	3200842	-	1502	859	1021	1403	0.57	0.68	0.93										
yuxG	3200899	3202968	-	1276	579	760	1243	0.46	0.58	0.98										
tlpB	3203106	3205094	-	773	612	561	854	0.81	0.73	1.09										
тсрА	3205208	320/193	-	2507	4507	4080	2044	1.78	1.00	1.05	965	Inter	3207135	3207380	3207258	5.6	07	1.1	0.6	
tlpA	3207319	3209307	-	178	1345	1303	185	7.56	7.35	1.05	966	tlpA	3208478	3208638	3208558	3.5	4.1	0.2	-0.3	
											967	Inter	3209005	3209794	3209400	63.1	92.9	11.5	1.0	
mcpB	3209484	3211472	-	1866	2454	2280	1933	1.33	1.23	1.03										
igi wuaU	3211030	3212307	+	1033	1564	1582	265	1.51	1.53	0.93										
yug0 vugT	3212072	3215520	-	335	289	283	348	0.87	0.85	1.03	968	VU9T	3214394	3214945	3214670	29.1	20.2	35.6	45.5	P01
yugS	3215201	3216505	-	358	309	337	359	0.87	0.94	1.00		1-8-								
yugP	3216533	3217210	-	1236	1116	1346	1573	0.91	1.10	1.28	969	yugP	3216128	3217053	3216591	46.1	27.2	76.9	127.7	P01
yugO	3217562	3218878	+	232	230	236	251	0.99	1.01	1.08	970	yugO	3217386	3217818	3217602	23.8	1.0	10.1	4.1	
yugN	3218875	3219279	-	2099	1791	2645	2204	0.85	1.25	1.05										
yugM	3219339	3219710	-	2038	1764	2415	2083	0.87	1.19	1.02										
pgi vuaK	3219709	3221124	-	15085	2023	2147	2511	0.74	0.79	1.05										
yugK vugJ	3222512	3223675	-	7745	10693	11063	8994	1.39	1.44	1.16										
yuzA	3223905	3224141	+	392	772	1089	337	1.99	2.80	0.87										
yugI	3224219	3224611	-	19585	16980	15293	18960	0.87	0.78	0.97										
alaT	3224813	3225973	-	7754	7073	7114	7056	0.91	0.92	0.91	972	alaT	3224815	3225043	3224929	1.4	1.0	1.4	8.3	
alaR	3225974	3226474	-	6348	5630	5666	6041	0.89	0.89	0.95										
yugF	3226622	3227443	+	264	270	284	244	1.02	1.07	0.92										
yugE patP	322/4/2	3227738	-	3271	2305	2328	2734	0.71	0.71	0.84										
kinB	3229108	3230397	+	337	3920	315	312	0.91	0.94	0.97										
kapB	3230443	3230829	+	2690	2749	2764	3028	1.03	1.03	1.13										
kapD	3230856	3231473	-	213	200	215	189	0.94	1.01	0.89										
yuxJ	3231684	3232862	+	217	232	237	225	1.08	1.10	1.05										
pbpD	3232955	3234829	+	3095	2833	2442	2525	0.92	0.79	0.81	973	pbpD	3233332	3233611	3233472	11.9	9.4	3.0	0.9	
yuxK	3234850	3235263	+	2447	2243	1991	1919	0.92	0.82	0.78										
yuj K vufI	3235400	3230080	-	2570	2303	1905	2548	0.92	0.74	1.07										
yujL vufM	3237795	3238502	+	2804	2231	2200	2784	0.80	0.79	0.99										
yufN	3239001	3240053	+	177	179	182	209	1.01	1.03	1.19										
yufO	3240129	3241661	+	197	159	176	202	0.80	0.89	1.02										
yufP	3241654	3242700	+	265	262	273	294	0.99	1.03	1.11										
yufQ	3242701	3243660	+	361	351	360	422	0.97	1.00	1.16										
maeN	3243814	3245160	+	5/55	1/81	1903	596/	0.31	0.34	1.04										
yuj S mrnA	3245190	3243411	+	3628	2627	2842	3443	0.91	0.78	0.98										
mrpB	3248040	3248471	+	3702	2775	2860	3617	0.75	0.77	0.98										
nrpC	3248471	3248812	+	3142	2452	2427	2946	0.78	0.77	0.94										
mrpD	3248805	3250286	+	3846	2990	3079	3625	0.78	0.80	0.94										
mrpE	3250292	3250768	+	2920	2104	2202	2925	0.72	0.76	1.00										
mrpF	3250768	3251052	+	2315	1644	1638	2226	0.71	0.71	0.96										
mrpG	3251036	3251410	+	1333	954 3520	3360	3048	0.72	0.77	0.87										
comA	3251848	3252492	-	3694	4191	4007	3768	1.14	1.09	1.03										
comP	3252573	3254882	-	2917	2498	2385	3443	0.86	0.82	1.18	977	comP	3253035	3253280	3253158	10.3	7.4	0.7	0.4	
											978	comP	3253324	3253518	3253421	2.8	4.7	1.2	0.4	
											979	comP	3253919	3254334	3254127	12.6	8.4	3.0	2.6	
comX	3254897	3255064	-	2441	1708	1658	3097	0.71	0.69	1.27								2.0	100	
comQ	3255052	3255951	-	2647	1880	1981	3214	0.71	0.75	1.22	980	comQ Intor	3255024	3255303	3255164	6.6 4.3	2.7	3.9	15.2	
deaO	3256136	3256276	-	201	138	155	163	0.69	0.77	0.82	981	mer	5250027	5250170	5230099	4.5	1.2	0.7	-0.4	
vuzC	3256737	3257105	+	658	490	492	701	0.75	0.75	1.08										
yuxH	3257081	3258310	-	3229	2482	2384	3224	0.77	0.74	0.99										
yueK	3258447	3259919	-	8069	7739	7902	8316	0.96	0.98	1.03										
yueJ	3259935	3260486	-	4830	4480	4638	5175	0.93	0.96	1.07										
yueI	3260583	3260981	-	3217	2554	2661	3362	0.80	0.84	1.05										
yueH	3261053	3261301	-	2815	2343	2351	2972	0.84	0.85	1.06										
yueG yueF	3261655	3267764	-	2005	2036 3277	2106	2439 3996	0.81	0.84	0.98										
vuzE	3262879	3263268	+	344	339	362	446	1.02	1.09	1.32										
yuzF	3263309	3263545	-	736	788	844	778	1.11	1.18	1.06										
yueE	3263722	3264252	-	1552	1090	1252	1471	0.72	0.82	0.94	982	yueE	3264119	3264347	3264233	1.9	-0.9	2.0	8.6	
yueD	3264450	3265181	-	3688	4544	4596	3882	1.26	1.26	1.06										
yueC	3265244	3265699	-	1770	2939	2794	1716	1.73	1.60	0.97		~	22.55	22/77-	20.575				0.5	
yueB	3265731	3268961	-	1947	2897	2863	1816	1.52	1.47	0.92	983	yueB	3266907	3267203	3267055	11.0	5.8	8.2	-0.2	

Supplet	gene	nc 51. 3U	u u U Ri	ry or trai	iscriptol	Trans	criptom	analysis	.s (conun	ucu).				ChAP-chip	analysis			
	0			Sig	nal intens	ity of RN	A <sup>a</sup>	Exp	ression rat	io <sup>b</sup>		OPE		•	Bindin	g intensity '		
name	start	end	rand			Λabh		A abrB/	$\Delta abh$	A abh /	PBR	or	start	end center	AbrB	A	bh	Profile
			st	wild	∆abrB	$\Delta abrB$	∆abh	wild	∆abrB/	wild	ID	Intergenic			wild ∆abh	wild	∆abrB	ID
vukA	3268958	3272581	-	1398	2121	2208	1360	1.57	1.60	0.96					-type	-type		
yukB	3272581	3273456	-	2099	2924	3182	2034	1.42	1.53	0.97								
yukC	3273484	3274839	-	1424	1750	2067	1389	1.25	1.47	0.97								
yukD	3274854	3275093	-	1724	2314	2835	1592	1.37	1.65	0.91								
уикс	5215251	5215419	-	17560	20177	27329	13749	1.51	1.57	0.91	984	Inter	3275288	3275975 3275632	56.7 64.5	19.7	4.5	P02
yukF	3275976	3277280	+	1022	839	840	960	0.83	0.83	0.94	985	yukF	3276019	3276179 3276099	2.7 2.5	3.1	4.3	
ald	3277348	3278484	+	7869	14999	14701	7606	1.91	1.87	0.97								
yuxI	3278597	3278920	+	1740	4527	5503	2259	2.60	3.16	1.30								
dhbF	3278838	3286680	-	1022	13001	12124	1075	12.72	11.77	1.28								
dhbB	3286700	3287638	-	1467	14108	13733	1647	9.62	9.33	1.12								
dhbE	3287666	3289285	-	1939	15282	14633	2207	7.88	7.55	1.14								
dhbC	3289314	3290510	-	2378	19242	18821	2822	8.09	7.92	1.19								
anbA vuil	3290530	3291321	-	2155	14579	14020	2514	6.08	6.79	1.17								
yuu	5271515	5272457		1050	11557	11575	2225	0.22	0.14	1.20	987	Inter	3292237	3292737 3292487	35.7 41.9	8.2	1.5	
yuiH	3292598	3293194	-	593	996	884	569	1.68	1.48	0.95								
yuiG	3293295	3293897	+	1054	914	878	1011	0.87	0.83	0.96								
yuur nenA	3293967 3295442	3295295	-	8/2	3254	304 3294	754 2766	0.66	0.65	0.84								
yuiD	3297102	3297578	+	704	703	726	783	1.00	1.03	1.11								
yuiC	3297609	3298265	-	803	978	1032	662	1.21	1.27	0.81								
yuiB	3298369	3298689	-	1067	1820	1642	919	1.70	1.53	0.86								
yuıA vumB	3298743	3298886	-	376 652	4/1	1332	437 640	1.27	2.06	1.18								
yumC	3300611	3301609	+	10904	10565	10473	11005	0.97	0.96	1.01								
yuzG	3301648	3301788	-	617	637	597	597	1.05	0.98	0.98								
guaC	3302067	3303047	+	1604	967	994	1599	0.68	0.68	1.00								
paiB naiA	3303121	3303744	-	765 405	923 592	1018 670	360	1.20	1.32	1.01								
yutM	3304624	3304986	-	9759	8769	9457	9432	0.90	0.97	0.97								
dapF	3305065	3305919	-	2986	1881	1830	2633	0.63	0.61	0.88								
yutK D	3306042	3307256	-	3159	528	560	2471	0.17	0.18	0.78								
yuzB vut I	3307393	3307629	-+	5773	540 5628	528 4797	676 4921	0.75	0.73	0.94								
yuzD	3308986	3309312	-	1950	1709	1768	1629	0.88	0.90	0.83								
yutI	3309412	3309747	+	8689	8951	8814	8891	1.03	1.01	1.02								
yuxL	3309789	3311762	-	566	1180	1184	618	2.08	2.08	1.08								
thrB thrC	3312796	3313854	-	2190	3272	3129	1425	1.49	1.44	0.85								
hom	3313854	3315155	-	1443	2045	1890	1286	1.40	1.28	0.88								
yutH	3315356	3316375	-	248	239	240	243	0.97	0.97	0.98								
yutG	3316528	3317028	+	166	149	163	146	0.89	0.98	0.88								
yutF vutE	3317854	3318288	-	6726	5512	5389	6717	0.85	0.80	1.00								
yutD	3318312	3318620	-	5044	3793	3854	5144	0.75	0.00	1.00								
yutC	3318702	3319334	+	323	313	341	338	0.98	1.08	1.05								
lipA	3319350	3320246	-	11561	10426	10222	11250	0.90	0.88	0.97	000		22204441	2220724 2220400	20.00	0.0	0.1	
yunA yunB	3320412	3321461	+	286	260 950	290 932	289	0.91	0.84	1.01	990	yunA	3320661	3320736 3320699	2.0 0.0	0.9	-0.1	
yunC	3322326	3322631	-	1311	1370	1438	1446	1.06	1.11	1.11								
yunD	3322696	3324084	-	3211	3146	3497	3326	0.98	1.09	1.04								
yunE	3324104	3324925	-	2303	2145	2317	2459	0.93	1.01	1.07								
yunF yunG	3325829	3326176	-	2056	2062	2266 1319	2179 1605	1.00	1.10	1.06								
pucH	3326273	3327613	-	362	266	279	342	0.73	0.77	0.94								
pucR	3327788	3329383	+	390	351	353	341	0.91	0.91	0.88								
pucJ	3329528	3330877	+	341	327	328	351	0.96	0.96	1.03								
pucK pucL	3332188	3333672	++	308 295	286 260	294 255	329 300	0.93	0.96	1.07								
pucM	3333651	3334016	+	461	418	431	439	0.91	0.93	0.95								
pucE	3334777	3335298	-	247	171	172	258	0.69	0.70	1.04								
pucD	3335289	3337526	-	281	241	242	296	0.86	0.86	1.05								
pucC pucR	3337527	3338360	-	253	211	222	286	0.84	0.88	1.14								
рис <b>ь</b> рисА	3338972	3339964	_	203	191	165	172	0.94	0.90	1.27								
yurG	3340193	3341443	-	569	628	634	618	1.10	1.12	1.09								
yurH	3341460	3342698	-	347	329	332	388	0.95	0.96	1.13	<i>c</i> -	<b>.</b> .						<b>n</b>
wer	33/21/0	33//004		204	1052	1247	667	760	2 17	1 60	993	Inter	3342710	5343346 3343028	33.4 30.5	18.7	31.0	P01
yur1 yurJ	3344040	3345143	-	903	791	777	917	2.08	0.86	1.08								
											994	Inter	3344852	3345539 3345196	5 21.7 17.4	16.6	66.8	

Supplem	entary Tal	de S1. Su	mma	ry of tra	nscripto	me and (	ChAP-ch	ip analys	es (contin	ued).				ChAP	ahin a	nolucio				
	gene			Sim	nal intens	ity of RN	Δ <sup><i>a</i></sup>	E analysis	ression rat	io <sup>b</sup>				UIAP	-спір а	naiysis	Binding	intensity <sup>c</sup>	2	
	atast	and	pur	- Bigi		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	A	LAP	∆ abh		PBR	ORF	atant			At	orB	At	bh	Profile
name	start	end	stra	wild	∆abrB	$\Delta abh$ $\Delta abrB$	$\Delta abh$	∆ abrB/ wild	$\Delta abrB/$	∆abh / wild	ID	or Intergenic	start	end ce	enter	wild	∆abh	wild	∆abrB	ID
V	22/5765	2246052		042	799	000	021	0.84	wild	1.00		, i				-type		-type		
yurK yurL	3346078	3346932	-	302	266	264	354	0.84	0.90	1.17										
yurM	3346946	3347848	-	266	228	242	273	0.86	0.91	1.03										
yurN	3347852	3348730	-	344	322	351	343	0.93	1.02	1.00										
yurO yurP	3348/88	3350056	-	182	259	253	185 264	0.88	0.92	1.02										
yurQ	3351339	3351713	-	4414	3312	3129	3770	0.75	0.32	0.86										
yurR	3351816	3352934	-	2614	2160	2096	2544	0.83	0.80	0.97										
sspG	3353093	3353239	+	359	269	236	276	0.75	0.66	0.77										
yur5 vurT	33535239	3353961	+	2596	2053	1948	2541	0.80	0.80	0.97										
yurU	3354620	3356017	-	16116	16223	16627	16314	1.01	1.03	1.01										
yurV	3356038	3356481	-	17816	17570	17660	17752	0.99	0.99	1.00										
csd vurY	3356471	3357691	-	11860	11944	12396	12077	1.01	1.05	1.02										
yurX yurY	3359022	3359807	-	14417	13312	13640	14431	0.92	0.95	1.00										
yurZ	3360332	3360709	-	205	278	331	184	1.35	1.56	0.89										
yusA	3360794	3361618	-	11468	7582	7501	10426	0.66	0.65	0.91										
yusB yusC	3362293	3363318	-	9359 6884	4864	4821	8752 6621	0.52	0.51	0.93										
yuse yusD	3363645	3363989	-	767	937	1101	757	1.29	1.53	0.99										
yusE	3364096	3364416	-	956	936	1122	1153	0.99	1.19	1.21										
yusF C	3364418	3364858	-	1938	1858	2066	1992	0.96	1.07	1.03										
yusG acvH	3365150	3365533	-	9555	10330	17292	9841 17348	1.09	1.06	1.05										
yusI	3365600	3365956	-	10570	8430	8956	10102	0.80	0.85	0.96										
yusJ	3366067	3367851	-	580	402	475	541	0.70	0.83	0.93										
yusK yusI	3367866	3369041	-	956 658	643 438	722	899 628	0.67	0.76	0.94										
yusL yusM	3371767	3372675	-	229	438	219	242	0.00	0.78	1.06										
yusN	3373028	3373360	+	175	341	441	127	1.97	2.56	0.73										
yus0	3373519	3373986	+	1921	1552	1251	1487	0.81	0.64	0.77	005	P	2274415	2274604 227		1.0	1.0	1.0	10.0	
yusP yusQ	3373983	3375608	+	3429	2804	2460	2870	0.81	0.71	0.84	995	yusP	3374415	33/4694 33/	4555	1.0	1.2	1.9	10.8	
yusQ yusR	3376046	3376435	-	352	307	311	377	0.82	0.85	1.07										
yusS	3376457	3376786	-	306	294	274	323	0.96	0.89	1.06										
yusT 	3376920	3377807	+	595	466	452	523	0.78	0.76	0.88										
yusU vusV	3378139	3378966	-	3378	5119	2002 5094	4351	1.40	1.59	1.09										
J											996	Inter	3379073	3379250 337	9162	6.3	4.9	3.0	2.6	
yusW	3379184	3379621	-	320	302	359	299	0.94	1.12	0.94										
yusX yusV	33/9/31	3381233	-	630 301	938	1245	658 423	1.49	1.99	1.03										
yus1 yusZ	3381660	3382502	+	628	562	629	585	0.90	1.00	0.94										
mrgA	3382592	3383053	+	5538	2659	2722	4573	0.48	0.50	0.83										
yvtA	3383097	3384473	-	1933	2456	2474	2158	1.28	1.28	1.12	999	yvtA	3382745	3384639 338	3692	81.4	102.5	175.0	282.4	P01
CSSK	3385425	3386780	+	1560	1405	1610	1734	0.94	1.03	1.11										
yuxN	3387140	3388015	+	1036	1246	1523	1339	1.20	1.48	1.30										
fumC	3388051	3389439	-	13668	18553	19246	14261	1.36	1.41	1.04										
gerAA gerAB	3389809	3391257	+	187	192 227	194 256	195 232	1.03	1.04	1.04	1002	gerAB	3391177	3391320 339	01249 02065	5.0	0.3	1.3	63.3	
gerAC	3392320	3393441	+	171	159	161	159	0.93	0.94	0.93	1003	gerAC	3392367	3393003 339	2685	33.9	51.9	15.2	8.2	
											1004	gerAC	3393200	3393547 339	3374	8.7	16.2	3.1	1.2	
yvqC	3393449	3394084	-	1435	1287	1188	1276	0.89	0.83	0.88										
yvqE vvaF	3394002	3395866	-	1301	1394	1472	1309	1.08	0.89	1.01										
yvqG	3395900	3396622	-	811	1101	890	802	1.37	1.10	1.00										
yvqH	3396872	3397549	-	1327	3002	2887	1218	2.25	2.17	0.92										
yvqI yvaI	3397576	3397956	-	1051	2029	2175	977 305	1.94	2.07	0.93										
y+45	5576110	2277200	-	203	1009	1220	505	5.64	4.00	1.10	1005	Inter	3399133	3399752 339	9443	<u>39.1</u>	31.2	11.0	1.3	
yvqK	3399563	3400144	-	1849	1213	1106	1685	0.66	0.60	0.91										
yvrA	3400167	3401495	-	3002	1923	1752	2522	0.64	0.58	0.84										
yvrB vvrC	3401495	3402556	-	2110 7748	1389	1305	1913 6906	0.66	0.62	0.91										
yvrD	3403861	3404652	+	2795	2309	2590	3003	0.85	0.96	1.09										
yvrE	3404690	3405568	-	2507	2151	2274	2346	0.86	0.91	0.94										
yvrG	3405640	3407361	-	3227	2959	2990	3171	0.92	0.93	0.98										
yvrH vvrI	340/3/9	3408488	-	255	445 271	415 278	518 262	0.84	0.78	0.96	1006	vvrI	3408534	3408813 340	8674	77	5.6	11.9	8.9	
oxdC	3409496	3410653	+	547	1424	1456	660	2.64	2.69	1.18	- 000		2.00004				0.0			
yvrL	3410714	3411124	+	406	673	678	484	1.70	1.68	1.20										

	gene					1 rans	criptom	e analysis		,			U	илг-спір а	matysis		
			_	Sig	nal intens	ity of RN	$\mathbf{A}^{a}$	Exp	ression ra	tio <sup>b</sup>	ORF				Binding	intensity c	
ame	start	end	and			Aabb		A abrP /	$\Delta abh$	A abh /	PBR	start	end	center	AbrB	Abh	Profile
unic	Start	cha	str	wild	$\Delta abrB$	A abrB	$\Delta abh$	zild	$\Delta abrB/$	wild	ID Intergenic	Start	cita	center	wild Aabb	wild A abrB	ID
						Aund		wiid	wild	wiki	intergente				-type	-type	
rN	3411158	3412408	-	1397	4977	5079	1575	3.56	3.63	1.13							
rO	3412380	3413069	-	1638	5286	5521	1676	3.23	3.38	1.03							
rP	3413053	3414246	-	1718	5343	5394	1881	3.13	3.15	1.10							
											1008 Inter	3414093	3414491	3414292	21.3 25.7	7.2 0.6	
шC	3414417	3415226	-	6261	7116	6566	5921	1.14	1.06	0.94							
шG	3415242	3416252	-	3674	3722	3511	3493	1.02	0.96	0.95							
uВ	3416252	3417406	-	3787	4036	3649	3634	1.07	0.97	0.96							
шD	3417504	3418451	+	10017	10307	10190	9618	1.04	1.03	0.96							
vsH	3418686	3420095	-	1347	759	628	1055	0.60	0.49	0.79	1009 vvsH	3419958	3420152	3420055	4.1 5.0	1.9 4.0	
ъJ	3420495	3420635	-	106	342	463	102	3.49	4.73	0.98							
, vsG	3420802	3421284	+	1186	755	661	938	0.64	0.56	0.79							
$\sqrt{g}J$	3421384	3423237	+	1153	951	933	1076	0.83	0.81	0.93							
eK .	3423265	3424191	-	2379	2168	1933	2298	0.91	0.81	0.97							
or.	3424302	3425084	+	2003	1420	1478	1841	0.70	0.74	0.92							
aM	3425188	3425748	+	1708	1394	1470	1597	0.70	0.74	0.92	1010 yveM	3425245	3425405	3425325	23 20	17 68	
aN	3425100	3426600		16196	20/15	20532	18873	1.26	1.27	1.16	1010 yvgin	5425245	5425405	5425525	2.5 2.0	1.7 0.0	
giv	3423113	3420009	-	10190	20415	20552	100/5	1.20	1.27	1.10	1011 Inter	2126281	2126867	2426626	25.0 45.7	25.1 5.1	P02
	2126022	2427217		261	1000	2210	207	7 77	12 75	1.12	1011 100	2426277	2427122	2427000	15 4 12 5	7.0 0.2	r 02
'gU wP	2427261	342/31/	+	201	1900	3310	297	1.27	12.75	1.13	1011 yvgO	34208//	342/122	3427000	13.4 13.5	7.0 9.2	
gr	2420/20	34293/3	-	1819	2109	1522	2303	1.18	1.28	1.26							
'sQ P	2421250	3431343	-	1448	13/3	1005	134/	0.95	1.06	0.93	1012 2	2421501	2421707	2421640	70 26	11.1	
gK	5431369	3433186	-	1327	1176	1291	1212	0.89	0.97	0.91	1012 yvgR	5431501	5431797	5451649	7.0 3.6	11.1 14.7	
gS	3433357	3435681	-	1319	1194	1253	1367	0.91	0.95	1.03							
gΤ	3435879	3436487	-	1957	883	800	1650	0.45	0.41	0.84							
lbC	3436674	3437090	-	5934	4414	4252	4928	0.74	0.72	0.83							
lbD	3437095	3437763	-	6459	4613	4517	5811	0.71	0.70	0.90							
yg₩	3437883	3439991	-	796	899	1029	924	1.15	1.29	1.14							
gX	3440151	3442562	-	1669	1275	1317	1515	0.77	0.79	0.90							
gY	3442643	3442852	-	1032	889	875	852	0.86	0.85	0.82							
gΖ	3442926	3443231	-	2019	1561	1589	1482	0.78	0.78	0.72							
aA	3443359	3444435	$^+$	9727	11846	14671	6956	1.22	1.51	0.72							
$pD_2$	3444472	3445107	-	1586	1412	1537	2008	0.90	0.97	1.25	1014 acpD	3444574	3445380	3444977	45.4 29.9	62.4 141.0	P01
aC	3445267	3447162	-	265	238	239	313	0.90	0.90	1.19	1014 yvaC	3445390	3445856	3445623	27.0 10.1	24.6 13.3	
vaD	3447325	3447726	-	1120	1146	1218	943	1.02	1.09	0.84	-						
чаE	3447723	3448082	-	1516	1540	1617	1300	1.02	1.07	0.86							
aF	3448079	3448651	-	734	721	747	678	0.98	1.02	0.92							
aG	3448762	3449556	-	1398	1543	1788	1114	1.10	1.28	0.79							
rA	3449742	3450101	-	32498	34536	35187	33154	1.06	1.08	1.02	1015 ssrA	3449674	3450361	3450018	32.5 44.7	39.1 54.3	P01
nnR	3450278	3450748	-	4144	4810	4570	4012	1 17	1 10	0.96							
nr	3450893	3453232	-	4736	4485	4638	4215	0.95	0.98	0.89	1016 mr	3452309	3453013	3452661	38.0 23.3	471 72	
	5150075	0100202				1050	.215	0.70	0.70	0.07	1016 mr	3453023	3453353	3453188	87 20	92 116	
vaK	3453251	3/153007	_	1026	1250	1200	4424	0.86	0.87	0.00	1010 111	0100020	0100000	5155100	0.7 2.0	7.2 11.0	
run vcG	3454123	345/353		16710	16382	15747	16506	0.00	0.07	0.90							
NAM	2454502	2455272	-	241	10502	13747	221	1.07	1.09	0.99							
vum v=C	2455212	2455545	Ŧ	241	470	202	231	0.02	0.08	1.06							
/2C	5455512	5455545	-	500	270	292	510	0.92	0.98	1.00	1017 Inter	2455520	2155602	2455611	22 25	1.9 0.7	
aN	2155507	2156104		1470	10.40	1040	1040	0.04	0.04	0.71	1017 Illel	5455559	5455082	5455011	5.2 2.3	1.0 0.7	
uiv	245(124	3430104	+	14/3	1248	1242	1049	0.84	0.84	0.71	1019 xm D	245/007	245//24	2456426	22.1 5.0	20.0 21-1	DOC
aO D	3430134	3430333	+	1584	1/14	1542	1401	1.08	0.97	0.88	1018 yvaP	3430237	3430034	245(12)	22.1 5.0	20.9 21.4	PUO
aP 0	3456396	345/106	+	871	741	723	895	0.85	0.83	1.03	1018 yvaP	3456237	5456634	5456436	22.1 5.0	20.9 21.4	P06
aQ DD	345/09/	3458/9/	+	//8	/95	702	/89	1.03	0.91	1.01							
D	5458837	3459517	-	232	234	227	234	1.01	0.98	1.01							
DUBC	3459534	3460454	-	291	339	327	297	1.16	1.12	1.02							
ouBB	3460466	3461119	-	334	387	386	346	1.16	1.15	1.04							
ouBA	3461136	3462281	-	244	264	256	260	1.08	1.05	1.07							
vaV	3462556	3463098	+	2799	3580	2814	1995	1.27	0.99	0.71							
											1019 Inter	3462747	3463723	3463235	61.9 101.9	45.2 9.9	
vaW	3463320	3463796	+	94	7811	7577	122	82.89	80.41	1.30							
vaX	3463793	3464764	+	148	10565	10083	181	71.16	68.06	1.24	1019 yvaX	3463733	3464250	3463992	19.4 14.1	6.2 6.5	
											1020 yvaX	3464481	3464980	3464731	28.4 21.0	7.0 5.8	
aY	3464807	3465418	+	360	23744	21826	456	65.74	60.61	1.25	1020 yvaY	3464991	3465372	3465182	23.6 11.6	6.5 7.1	
γaΖ	3465465	3466088	-	724	533	565	757	0.73	0.78	1.05	1021 yvaZ	3465468	3466001	3465735	14.1 7.8	3.3 2.0	
bΑ	3466085	3466357	-	478	420	435	547	0.87	0.91	1.14	-						
											1021 Inter	3466011	3466766	3466389	53.1 66.5	19.4 2.5	P02
DuCD	3466577	3467266	-	481	384	370	485	0.81	0.77	1.03							
mCC	3467284	3468195	-	424	378	310	410	0.78	0.76	1.00							
mCR	3468215	3468869	_	314	250	251	321	0.78	0.70	1.00							
MCA	2460001	2470022	-	221	209	201	240	0.03	0.00	1.03							
MCA	2470207	2470954	-	201	292	501	309	0.81	0.84	1.03							
or	54/0297	34/0854	+	581	467	501	557	0.80	0.86	0.96							
⊳bG	3470872	3471507	-	350	257	277	293	0.74	0.80	0.84							
bН	3471657	3472271	+	3143	2087	1970	2859	0.67	0.63	0.91							
											1022 Inter	3472165	3472478	3472322	12.9 9.7	0.1 -0.6	
ЪI	3472403	3473101	+	3222	1800	1607	2980	0.56	0.50	0.93							
ЪJ	3473137	3474954	-	4410	5097	4863	7113	1.16	1.10	1.62							
											1023 Inter	3474766	3475215	3474991	24.3 16.4	8.8 0.1	

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	gene					Trans	criptom	e analysis						(	ິ hAP-chip ຄ	nalysis				
				Sig	nal intens	ity of RN	A <sup>a</sup>	Exp	ression ra	tio <sup>b</sup>		ODE					Binding	intensity c		
name	etart	and	and			Anhl		A abaD/	$\Delta abh$	A abb /	PBR	ORF	etort	and	center	At	orB	Abł	h	Profile
name	start	enu	str	wild	∆abrB	∆ abn A ahrB	$\Delta abh$	⊿ abrb/ wild	$\Delta abrB/$	⊿ abn / wild	ID	Intergenic	start	enu	center	wild	Aabh	wild	1 <i>abr</i> B	ID
						Autorb		wiki	wild	W lici						-type	2 uon	-type	I UUID	
yvbK	3475074	3475541	+	1223	1631	1607	1654	1.35	1.31	1.36										
eno	3475586	3476878	-	18568	16553	17242	18027	0.89	0.93	0.97										
pgm trui A	3476908	3478443	-	22065	20155	21195	21827	0.91	0.96	0.99										
ipiA nak	2470228	2480412	-	10955	17608	10140	10524	0.91	0.95	1.01										
pgk aanA	3479228	3480412	-	22951	17106	17978	22756	0.92	0.93	0.99										
cggR	3481783	3482805	-	5272	4057	4380	5878	0.78	0.83	1.11										
araE	3483103	3484497	-	591	443	553	514	0.75	0.93	0.88										
araR	3484635	3485789	+	2444	1799	1799	2324	0.74	0.74	0.95										
yvbT	3485838	3486848	-	1290	1170	1075	1304	0.91	0.84	1.01										
yvbU	3487005	3487883	-	292	293	257	351	1.00	0.88	1.19										
yvbV	3487983	3488900	+	573	426	418	558	0.74	0.73	0.97										
yvbW	3488941	3490284	-	821	637	644	717	0.78	0.79	0.88	1024	yvbW	3489930	3490090	0 3490010	2.7	3.1	5.6	4.3	
yvbX	3490686	3491720	-	1811	1620	1652	1659	0.91	0.91	0.92										
yvbY	3491828	3492550	-	14692	11386	13049	14090	0.78	0.89	0.96										
yvfW	3492550	3493989	-	10466	8862 6001	10194	0048	0.74	0.85	0.98										
yvj v vvfI	3494010	3494732	-	10400	1042	1099	9948 708	1.17	1.24	0.93										
yvfC vvfT	3495526	3496512	-	664	1042	999	709	1.17	1.24	1.07										
vvfS	3496645	3497382	-	375	596	596	380	1.58	1.59	1.02										
yvfR	3497383	3498288	-	273	527	482	271	1.93	1.77	1.00										
											1025	Inter	3498243	3498590	0 3498417	16.0	14.8	13.7	8.9	
rsbQ	3498572	3499381	+	1650	1278	1165	1604	0.77	0.70	0.97										
rsbP	3499417	3500628	+	2442	1638	1517	2154	0.67	0.62	0.88										
yvfO	3500682	3501971	-	994	608	842	881	0.63	0.88	0.88										
lacA	3502051	3504114	-	1469	978	1535	1501	0.67	1.05	1.02										
yvfM	3504133	3504984	-	1218	683	1098	1252	0.56	0.91	1.03										
yvfL	3504988	3506244	-	1787	827	1318	1691	0.46	0.71	0.95	1020	<b>G</b> V	250(520	250722	C 250/002	(2)	27	10.0	00 E	
yvj <b>K</b> laoP	3500284	3507549	-	2449	781	14/0	2107	0.52	0.57	0.80	1026	yviĸ	3506539	3507220	0 3300883	0.3	2.7	10.0	82.5	
wyfI	3508862	3509389	-	1927	1734	1582	1659	0.70	0.72	0.94										
vvfH	3509811	3511502	+	3262	2607	3650	2644	0.90	1 10	0.80										
sigL	3511529	3512839	-	3172	2418	3019	2991	0.77	0.94	0.94										
vvfG	3512918	3513136	+	5014	3814	3831	4677	0.76	0.76	0.93										
yvfF	3513146	3514114	-	297	2551	2894	267	8.58	9.71	0.90										
yvfE	3514093	3515259	-	476	3615	3937	455	7.57	8.24	0.95										
yvfD	3515264	3515914	-	400	1914	2144	425	4.80	5.39	1.07										
yvfC	3515911	3516519	-	449	2136	2490	477	4.75	5.52	1.06	1028	yvfC	3515957	3516253	3 3516105	2.2	0.4	1.7	15.3	
yvfB	3516516	3517553	-	386	2097	2470	409	5.43	6.40	1.06										
yvfA T	3517703	3518032	-	1132	4188	4958	995	3.75	4.46	0.87										
yveT	3518029	3519063	-	568	4133	4736	552	7.29	8.36	0.97										
yves 	2520141	2521175	-	400	2840	2512	455	6.09	7.12	0.98										
yver wveQ	3520141	3522303	-	432	2083	3382	498 526	5.41	6.13	0.94										
yveQ vveP	3522300	3523454	-	345	2216	2532	361	6.44	7.38	1.06										
vveO	3523447	3524283	-	382	2443	2700	380	6.41	7.09	1.00										
yveN	3524280	3525425	-	584	3924	4381	535	6.75	7.55	0.92	1029	yveN	3524270	352444	7 3524359	3.9	1.7	4.8	1.1	
yveM	3525437	3527233	-	434	2029	2311	431	4.68	5.33	1.00										
yveL	3527492	3528175	-	325	2903	2830	304	8.99	8.80	0.94										
yveK	3528181	3528885	-	349	3084	2790	317	8.81	7.97	0.90										
											1032	Inter	3528707	3529292	2 3529000	18.8	19.9	4.7	-0.6	P03
slr	3529131	3529589	+	239	575	559	238	2.40	2.33	0.99										
pnbA	3529665	3531134	+	787	7891	8855	1351	10.08	11.32	1.71	1032	pnbA	3529302	3530142	2 3529722	45.5	62.1	25.8	8.0	
padC env eC	3531355	3531840	-	545	749	956	629	1.41	1.78	1.13										
yveG waF	3531863	3532150	-	275	494	5/1	427	1.81	2.07	1.55										
yver rac¥	35352220	35323120	-	544 1824	5104	182	49/	1.85	2.33	1.46										
nhnE	3533148	3534503	-	1624	4813	5055	1673	2.02	3.12	1.04										
sacB	3535042	3536463	+	197	137	154	146	0.70	0.79	0.75	1033	sacB	3534845	353541	2 3535129	23.8	5.9	8.9	-0.1	
yveB	3536537	3538087	+	246	209	221	241	0.85	0.90	0.98	- 555						5.7			
yveA	3538195	3539757	+	285	368	421	285	1.29	1.48	1.00										
yvdT	3539852	3540436	+	2597	1973	1936	2805	0.76	0.75	1.08										
yvdS	3540518	3540853	+	445	364	360	608	0.82	0.81	1.37										
yvdR	3540853	3541173	+	584	529	561	668	0.91	0.96	1.14										
yvdQ	3541209	3541721	-	361	581	671	387	1.65	1.91	1.10						_				
yvdP	3541973	3543316	-	245	227	233	246	0.93	0.95	1.00	1034	yvdP	3542494	354292	5 3542710	16.7	5.9	17.6	10.6	
yvd0	3543672	3544634	+	180	187	181	210	1.04	1.00	1.17										
trnQ-Arg	3544916	3544994	-	11605	12184	13213	8282	1.05	1.14	0.69										
clpP	3545264	3545857	+	14661	18917	19167	17609	1.30	1.31	1.20										
pgcM	3545903	3546583	-	884	671	707	817	0.76	0.80	0.92										
maiL	3546580	3550521	-	850	502	674	834	0.73	0.80	0.98	1025	wdv	3510200	351000	1 3540000	5 1	20	0.7	5.2	
yvan wdl	3550500	3551202	-	881 725	382	000	839 700	0.07	0.75	0.95	1035	yvun	5548082	334890	1 3348822	5.1	3.8	9.7	5.5	
yvas	2220209	3331393	-	125	493	55/	/00	0.08	0.77	0.96										

Supplen	entary Tal	ne SI. Sur	nmar	y of trai	iscriptor	ne and (	nAP-ch	up analyse e analyse	es (contir	wed).				C	hAP_chin a	malveic		
	gene			e:-	nol internet	Trans	a a	e analysis	modeler -	tio <sup>b</sup>				C	пл-спір а	maiysis Diadia	intoncit <sup>, c</sup>	
			р	Sigi	nal intensi	ny of RN	A	Exp	ression ra	UO	PBR	ORF				Abr D	Abb	Profile
name	start	end	straı	wild	∆abrB	$\Delta abh$	$\Delta abh$	$\Delta abrB/$	AabrB/	$\Delta abh /$	ID	or	start	end	center	wild	wild	ID
						∆abrB		wild	wild	wild		Intergenic				-type ∆abh	-type ∆ abrB	
yvdI	3551399	3552235	-	676	454	550	643	0.68	0.82	0.95						2.	21	
yvdH	3552236	3553543	-	535	385	448	554	0.72	0.84	1.04								
yvdG	3553583	3554836	-	584	379	437	568	0.65	0.75	0.97								
yvdF	3554932	3556701	-	403	374	444	398	0.93	1.10	0.99								
yvdE	3556814	3557764	-	273	267	310	280	0.98	1.14	1.03								
yvdD	3557970	3558545	-	4499	3293	3631	3953	0.73	0.81	0.88								
yvdC	3558662	3558982	+	2623	1826	1960	2048	0.69	0.74	0.78								
yvaB	3559009	2561212	-	226	520 250	252	211	0.80	0.91	0.99								
yvaA vvcT	3561596	3562573	-	6723	230	8247	7401	1.17	1.23	0.95	1037	MCT	3561025	3562280	3562107	80 19	12.0 25.9	
yve1 yveS	3562611	3564551	-	1650	1998	1994	1288	1.17	1.23	0.78	1057	yver	5501725	5502287	5502107	0.0 1.7	12.0 25.7	
vvcR	3564526	3565305	-	2621	3392	3302	2072	1.30	1.26	0.79								
yvcQ	3565388	3566458	-	2005	2588	2522	1519	1.29	1.25	0.76								
yvcP	3566452	3567165	-	1618	2184	1937	1306	1.35	1.20	0.80								
yvcN	3567557	3568321	-	5167	5798	5543	5480	1.12	1.07	1.06								
crh	3568322	3568579	-	3044	2999	2907	3232	0.99	0.96	1.06								
yvcL	3568603	3569553	-	4537	4629	4689	4562	1.02	1.03	1.00								
yvcK	3569576	3570529	-	5786	6436	6511	5802	1.11	1.13	1.00	1038	yvcK	3570170	3570262	3570216	3.1 1.6	0.8 0.0	
yvcJ	3570531	3571418	-	4867	4926	5140	4935	1.01	1.06	1.01								
yvcI	35/1443	35/1919	-	4106	4060	3/10	4193	0.99	0.90	1.02	1040	Inton	2571007	2572166	2572027	10.0 12.7	08 02	
try B	3577737	3573187		8200	7956	8251	0511	0.08	1.01	1.14	1040	Inter	35/188/	35/2100	5572027	10.9 15.7	0.8 0.2	
WVCF	3573393	3574814		12188	13696	12704	13202	1.12	1.01	1.14								
vvcD	3575195	3576649	-	3874	3522	3244	3388	0.91	0.84	0.88								
vvcC	3576775	3578544	-	2511	2639	2487	2236	1.05	0.99	0.89								
yvzA	3578709	3579068	-	555	1705	2381	556	3.08	4.09	0.99								
yvcB	3579083	3580993	-	644	1689	2331	647	2.61	3.45	1.00	1041	yvcB	3580217	3580445	3580331	11.0 0.8	7.6 0.5	
yvcA	3580995	3581720	-	311	495	674	322	1.57	2.11	1.03								
											1042	Inter	3581543	3582111	3581827	30.7 21.3	43.2 24.7	P01
hisI	3581966	3582595	-	546	410	417	564	0.75	0.76	1.03								
hisF	3582592	3583350	-	379	278	313	358	0.73	0.83	0.94								
hisA	3583347	3584084	-	401	283	329	418	0.71	0.82	1.04								
hisH hisD	3584081	3584/19	-	680	280	357	645	0.77	0.82	0.97								
nusD hisD	3585301	3586584	-	330	253	420	327	0.80	0.89	0.99								
hisG	3586581	3587222	-	260	197	223	282	0.76	0.84	1 10								
hisZ	3587215	3588390	-	432	378	389	475	0.88	0.90	1.10								
yvpB	3588641	3589393	+	693	342	321	659	0.49	0.46	0.95								
											1043	Inter	3588853	3590220	3589537	51.8 55.2	58.4 165.5	P01
yvpA	3589633	3590298	+	895	554	1349	904	0.62	1.51	1.01								
yvoF	3590318	3590836	-	3998	3384	3439	3989	0.85	0.86	1.00								
hprP	3590840	3591490	-	6690	5614	5724	6629	0.84	0.86	0.99	1045	hprP	3590759	3590951	3590855	1.1 1.2	2.0 4.9	
yvoD	3591487	3592425	-	6787	5709	5629	6686	0.84	0.83	0.99	1046	yvoD	3591284	3591852	3591568	21.3 25.6	35.6 45.6	P01
lgt hmuV	3592449	3593258	-	4928	3848	3980	4767	0.78	0.81	0.97								
nprĸ	3593272	3594204	-	2255	4201	4334	2046	0.79	0.82	0.96	1047	nogA	250/101	250/580	250/200	80 178	80 112	
nagA nagR	3595573	3596301	+	3649	3192	3278	3039	0.84	0.88	0.87	1047	nagA	3394191	3374387	3374370	0.0 17.0	0.0 11.2	
vvoA	3596319	3597050	+	2237	2255	2321	1969	1.01	1.04	0.88								
vvnB	3597070	3600939	-	423	513	510	389	1.21	1.20	0.92								
											1049	Inter	3600906	3601134	3601020	3.8 8.0	0.8 0.3	
yvnA	3601104	3601577	+	224	916	709	179	4.08	3.13	0.84								
cypX	3601618	3602835	-	581	2568	2621	454	4.40	4.50	0.78								
yvmC	3602851	3603597	-	594	2970	2844	481	4.98	4.75	0.81								
											1050	Inter	3603609	3604075	3603842	14.3 33.1	1.5 -0.6	
yvmB	3604023	3604532	+	859	593	694	746	0.69	0.81	0.86								
yvmA	3604553	3605764	+	520	457	486	535	0.89	0.94	1.04								
yvlD	3605792	3606151	-	5547	7092	12572	5549	1.27	1.37	0.99								
yviC	3000133	2607452	-	10451	7028	13572	6002	1.18	1.50	0.99								
yviB vvlA	3607477	3607803	-	2830	/928	8081 4278	2080	1.51	1.44	1.06								
yv kN	3608021	3608251	+	182	176	177	170	0.97	0.97	0.93								
vv7B	3608450	3608932	_	438	462	481	484	1.06	1.10	1.10								
uvrA	3609094	3611967	-	4284	4377	5393	4573	1.02	1.26	1.07	1051	uvrA	3609967	3610127	3610047	5.2 -0.4	3.2 1.4	
uv rB	3611975	3613960	-	3096	2741	3611	3261	0.89	1.17	1.05								
csbA	3614146	3614376	-	1665	1117	1122	1322	0.67	0.67	0.79								
											1052	Inter	3614523	3614768	3614646	4.4 6.2	0.7 -0.3	
yvkC	3614823	3617318	+	282	737	791	266	2.62	2.81	0.94								
yvkB	3617394	3617963	+	940	1151	1137	847	1.22	1.21	0.90								
yvkA	3617994	3619328	+	570	645	655	544	1.13	1.15	0.96								
minJ	3619376	3620569	-	2022	1983	1852	2106	0.98	0.92	1.04								
yvzD	3620648	3620986	-	700	862	660	900	1.24	0.96	1.30	1052	Inter	2621204	2621440	2621227	8.2 67	15 0 4	
	2621207	2622022		252	= (0	150	225	1.70	1.07	0.04	1053	inter	3021204	3021449	3021327	8.3 6.7	-1.5 -0.4	
yvjB	3621386	3622828	-	353	569	658	335	1.60	1.85	0.94								

Supplem	gene	ne 51. Su	шпа	ry of tra	iscripto	Trans	crintom	e analysis	es (contin	ueu).				C	hAP-chin a	nalysis				
	gene			Sim	nalintana	ity of DN		Evo	raccion ra	tio <sup>b</sup>				C.	n n -cmp a	14119 515	Dinding	intoncity c		
			р	Sig	nai mens	ity of KIN	A	Exp	A abh	0	PBR	ORF				Ab	vrB	A	h	Profile
name	start	end	stra	wild	AabrB	$\Delta abh$	Aabh	$\Delta abrB/$	A ahrB/	$\Delta abh /$	ID	or	start	end	center	wild	//D	wild	<i>/</i> 11	ID
				11 IICI	Labre	∆abrB	adon	wild	wild	wild		Intergenic				-type	$\Delta abh$	-type	∆abrB	
									Wild		1054	Inter	3622785	3622928	3622857	4.7	2.3	0.7	0.3	
ftsX	3622968	3623858	-	4539	4926	4479	4693	1.09	0.99	1.03										
ftsE	3623851	3624537	-	5513	5698	5200	5845	1.03	0.95	1.06	1055	ftsE	3623907	3624492	3624200	21.4	23.6	10.0	2.6	
2											1055	Inter	3624502	3624866	3624684	14.3	14.5	6.2	0.2	
cccB	3624771	3625109	-	7688	7797	7497	6929	1.02	0.98	0.90										
yvjA	3625158	3626003	-	1197	2494	2193	1408	2.08	1.79	1.17										
prfB	3626169	3627270	-	8022	8393	8043	7981	1.05	1.00	1.00										
secA	3627340	3629865	-	8874	9308	9230	9036	1.05	1.04	1.02										
yvyD	3630033	3630602	-	6741	9578	11654	5269	1.42	1.73	0.77	1056	yvyD	3630282	3630476	3630379	1.9	3.8	5.0	7.1	
fliT	3631180	3631521	-	4776	6890	6317	5300	1.46	1.33	1.12										
fliS	3631518	3631919	-	3491	5015	4841	3630	1.44	1.39	1.04										
fliD	3631941	3633437	-	4670	6700	6238	5267	1.44	1.34	1.13	1057	fliD	3632305	3632516	3632411	2.7	7.3	2.3	2.2	
yvyC	3633455	3633784	-	1514	1774	1725	1726	1.17	1.14	1.14										
hag	3634017	3634931	-	21033	26756	26939	24024	1.27	1.28	1.14										
csrA	3635076	3635300	-	3586	2537	2444	3265	0.71	0.68	0.91										
yviF	3635294	3635725	-	1489	1057	1048	1460	0.71	0.70	0.98										
yviE flat	2626269	2627264	-	998	954	4208	4254	0.96	0.85	1.02										
figL flaK	2627275	2629709	-	4105	4584	4398	4254	1.12	1.07	1.05										
JIGK VVVG	3638817	3639299		3845	4091	3737	4062	1.15	0.97	1.10										
fløM	3639315	3639581	-	4691	5758	5160	4721	1.07	1 10	1.00										
vvvF	3639662	3640081	-	1734	2207	1827	1816	1.28	1.04	1.00										
comFC	3640155	3640844	-	908	810	712	917	0.89	0.78	1.01										
comFB	3640841	3641137	-	1276	1042	1029	1210	0.82	0.81	0.95										
comFA	3641197	3642588	-	343	335	344	362	0.98	1.00	1.05										
yviA	3642694	3643539	-	2679	2109	1967	2574	0.79	0.73	0.96										
degU	3643637	3644326	-	5903	5674	5695	5274	0.96	0.96	0.89										
degS	3644409	3645566	-	3252	2777	2961	3147	0.85	0.91	0.97										
yvyE	3645783	3646436	$^+$	2649	2367	1939	2664	0.89	0.73	1.00										
yvhJ	3646436	3647611	+	4833	4467	3984	4673	0.92	0.82	0.97	1059	yvhJ	3647435	3647578	3647507	1.9	1.7	2.4	3.5	
tagO	3647684	3648760	-	3419	3300	2940	3753	0.97	0.86	1.10	1060	tagO	3647741	3647952	3647847	7.9	2.4	2.2	0.9	
tuaH	3648905	3650098	-	365	372	382	375	1.02	1.05	1.03									_	
tuaG	3650127	3650885	-	475	418	446	460	0.89	0.94	0.96	1061	tuaG	3650155	3650349	3650252	8.2	6.1	1.9	0.1	
tuaF	3650909	3651589	-	471	385	438	443	0.82	0.93	0.94		_								
tuaE	3651618	3653084	-	506	509	525	537	1.00	1.04	1.06	1062	tuaE	3651702	3652015	3651859	11.3	4.4	11.7	1.1	
tuaD	3653169	3654554	-	486	434	474	460	0.89	0.98	0.95										
tuaC	3054010	3055/85	-	264	238	239	282	0.90	0.91	1.07										
tua A	2657282	2657022	-	450	438	4//	454	1.02	1.00	0.90	1062	tuo A	2657788	2657000	2657804	2.6	62	0.0	0.1	
htC	3658140	3650630	-	2264	2520	2350	2014	1.05	1.00	1.20	1005	tuaA b#C	3658757	3658866	3658812	3.0	0.2	0.9	0.1	
iyiC	5050147	5057057		2204	252)	2337	2744	1.12	1.04	1.27	1065	Inter	3659539	3659767	3659653	7.3	2.1	1.8	0.0	
ht B	3659678	3661795	-	2745	2889	2533	3637	1.05	0.92	1 32	1065	htB	3660185	3660600	3660393	15.4	2.0	6.1	2.4	
.,											1067	lvtB	3660696	3660957	3660827	0.5	-0.8	0.1	13.8	
lytA	3661819	3662127	-	2907	2794	2549	3568	0.96	0.87	1.22										
2											1068	Inter	3662210	3662334	3662272	5.0	2.5	0.7	0.7	
lytR	3662311	3663231	+	6078	9151	9161	6360	1.51	1.51	1.05										
yvyH	3663271	3664413	-	3123	1798	1748	2803	0.58	0.56	0.90										
gtaB	3664659	3665537	$^+$	11831	10012	10701	10693	0.85	0.90	0.90	1069	gtaB	3665336	3665666	3665501	5.1	3.4	7.4	6.4	
											1070	Inter	3665948	3666210	3666079	6.6	9.4	1.4	2.0	
ggaB	3666239	3668941	-	605	740	751	1238	1.20	1.22	2.02	1071	ggaB	3666917	3667264	3667091	9.0	11.3	2.4	3.6	
											1072	ggaB	3667631	3667723	3667677	2.9	2.2	0.2	0.7	
ggaA	3669065	3670405	-	439	509	490	774	1.15	1.11	1.75	1074	ggaA	3669416	3670137	3669777	43.9	23.4	13.7	2.9	
											1074	ggaA	36/014/	3670528	3670338	10.2	3.5	3.5	4.3	
											1075	Inter	36/0659	36/1140	3670900	12.9	9.1	4.0	4.4	DO 1
											1075	Inter	2672206	30/1922	2672407	80.2	09.8	04.8	7.4	P01
taaH	3672504	3674177		6508	6042	6020	6818	0.92	0.01	1.03	1070	mei	3072300	3072087	3072497	0.0	2.0	0.0	7.4	
tagG	3674197	3675024	-	4002	4057	3638	4516	1.02	0.91	1.03										
tagE	3675189	3677429	-	4002	3813	3471	4260	0.89	0.91	0.99	1077	tagF	3675757	3676359	3676058	37.4	19.6	25.1	27	P02
	5075105	5077 (2)		.272	5015	5.71	.200	0.07	0.00	0.77	1078	tagF	3676692	3676903	3676798	5.9	2.5	1.7	0.0	102
											1079	tagF	3677151	3677668	3677410	16.8	15.2	0.7	-1.0	
tagE	3677429	3679450	-	3955	3445	3128	4013	0.87	0.79	1.01										
tagD	3679611	3680000	-	6262	6943	6064	6169	1.11	0.97	0.98										
-											1080	Inter	3679837	3680524	3680181	26.2	43.0	12.7	1.5	
tagA	3680400	3681170	+	3152	2710	2472	2959	0.86	0.78	0.94	1081	tagA	3680738	3681391	3681065	28.7	47.4	14.6	1.1	
tagB	3681203	3682348	+	1767	1363	1159	1716	0.78	0.66	0.98	1083	tagB	3682149	3682411	3682280	25.4	44.8	10.6	2.5	
tagC	3682468	3683796	+	452	308	331	338	0.68	0.73	0.75	1083	tagC	3682421	3682734	3682578	5.7	12.1	1.4	-0.1	
											1084	tagC	3683034	3683396	3683215	13.3	3.7	13.2	4.8	
lytD	3683856	3686498	-	2795	2019	1284	2514	0.74	0.46	0.90										
pmi	3686627	3687577	-	5255	3667	4089	5646	0.70	0.77	1.07										
gerBA	3687842	3689290	+	342	348	384	329	1.02	1.13	0.97										
gerBB	3689296	3690402	+	359	334	364	355	0.93	1.02	0.98										
gerBC	3690399	3691523	+	240	228	225	229	0.95	0.94	0.95										

	gene					Trans	criptom	e analysis						C	hAP-chip a	analysis				
				Sigr	nal intens	ity of RN	A <sup>a</sup>	Exp	ression ra	tio <sup>b</sup>		ORE					Binding	; intensity '	c	
name	start	end	and			Aabh		A abrB/	$\Delta abh$	A abh /	PBR	OKF	start	end	center	At	rΒ	A	bh	Profile
name	start	chù	str	wild	∆abrB	∆ abrB	$\Delta abh$	∠ <i>aurb</i> / wild	$\Delta abrB/$	⊿ aon / wild	ID	Intergenic	Start	CIRI	center	wild	Aabh	wild	AahrB	ID
						<u></u>		wiki	wild	W IICI		8				-type	1 uon	-type	2 uorb	
ywtG	3691560	3692933	-	1081	632	881	632	0.59	0.83	0.58		_								
	2002200	2604224		2100	2224	2220	2102	1.04	1.01	0.07	1085	Inter	3692961	3693307	3693134	10.9	15.9	0.4	-0.3	
ywtF	3693266	3694234	+	3198	3554	3238	5105	1.04	1.01	1.02										
ywi£ ywiD	3695284	3696525	т	1803	2128	2087	2253	1 10	1.16	1.03										
ywiD ywtC	3696666	3696833	-	238	163	155	263	0.68	0.65	1.11										
vwtB	3696848	3697990	-	367	202	228	396	0.55	0.62	1.09										
ywtA	3698009	3698458	-	751	425	553	732	0.57	0.74	0.98										
ywsC	3698473	3699654	-	369	198	235	327	0.54	0.64	0.89										
											1088	Inter	3699744	3699870	3699807	3.0	2.7	2.7	1.7	
											1089	Inter	3700050	3700414	3700232	13.0	17.0	5.8	3.9	
rbsR	3700438	3701418	+	19128	5873	9899	20596	0.30	0.48	1.07	1090	rbsR	3701291	3701501	3701396	2.6	5.8	4.3	5.2	
rbsK	3701420	3702301	+	20943	6849	11352	21813	0.31	0.50	1.04										
rbsD	3702298	3702693	+	18453	3130	8237	18222	0.16	0.42	0.98										
rhsC	370/102	3705160	+	10886	6056	100/7	24132	0.28	0.50	1.00										
rbsB	3705172	3706089	+	25093	11068	15540	26837	0.43	0.60	1.07	1091	rbsB	3705762	3706143	3705953	2.5	2.9	4.3	12.7	
ywsB	3706171	3706707	+	22332	10097	14431	23895	0.44	0.63	1.07	1091	ywsB	3706153	3706636	3706395	8.4	7.4	12.0	13.9	
ywsA	3706863	3707159	+	1415	485	673	1030	0.34	0.48	0.73		-								
ywrO	3707199	3707726	-	2975	6325	6068	3079	2.19	2.06	1.04										
alsD	3707826	3708593	-	779	328	339	622	0.42	0.43	0.80	1092	alsD	3708414	3708523	3708469	3.3	1.1	2.4	0.2	
alsS	3708655	3710370	-	397	239	254	406	0.61	0.64	1.02										
alsR	3710525	3711433	+	898	1249	1243	939	1.42	1.40	1.05										
ywrK	3711644	3712972	+	327	332	349	329	1.01	1.07	1.00										
ywrJ cotP	3/13029	3/13/06	-	237	218	244	230	0.92	1.03	0.97										
cotH	3715/00	3716124	-	241	211	220	219	0.83	0.94	0.92										
cotG	3716265	3716852	+	289	230	242	243	0.85	0.07	0.37	1093	cotG	3716387	3716530	3716459	0.7	3.0	1.6	43	
ywrF	3717026	3717643	+	1731	2216	2747	2084	1.29	1.60	1.20	1070	core	5710507	5710550	5/10.57	0.7	5.0	1.0	1.5	
2											1094	Inter	3717543	3717822	3717683	9.4	14.2	4.6	2.6	
ywrE	3717821	3718156	+	1152	1831	1677	1197	1.60	1.48	1.05										
ywrD	3718161	3719738	-	223	183	188	245	0.82	0.84	1.12										
ywrC	3719952	3720428	+	1142	729	717	1003	0.64	0.63	0.88										
ywrB	3720442	3721035	+	933	760	747	928	0.82	0.81	1.00										
ywrA	3721032	3721568	+	1145	957	972	1084	0.84	0.85	0.95	100 5					10.1				
ywqO	3721595	3721816	-	608	570	546	618	0.94	0.90	1.03	1095	ywqO	3721538	3722004	3721771	19.4	6.4	11.9	2.0	D01
ywqN mumM	3/21813	3/22358	-	372	333	352	384	0.89	0.94	1.03	1095	ywqN	3722014	3/22010	3722315	27.4	51.5		21.2	P01
ywqm wwaI	3722461	3724163	+	1927	3382	3613	1810	1.76	1.85	0.93										
ywqL ywaK	3724173	3724103	-	1927	3367	3286	1261	2 29	2.23	0.94										
vwa.I	3724627	3726435	-	878	2824	3405	603	3.21	3.76	0.68	1096	vwaJ	3724989	3725540	3725265	36.0	15.0	44.9	36.5	
ywqI	3726454	3726714	-	1686	4597	5677	894	2.77	3.28	0.52		J 4-								
ywqH	3726724	3727146	-	1449	3628	4632	784	2.48	3.10	0.52										
ywqG	3727538	3728323	-	892	2127	2196	886	2.41	2.46	0.99										
											1097	Inter	3728287	3728583	3728435	7.8	10.0	2.8	0.2	
ywqF	3728515	3729837	-	1368	2119	2068	1459	1.57	1.52	1.07										
ywqE	3730032	3730796	-	612	1765	1582	603	2.99	2.61	0.98										
ywqD	3730849	3731562	-	1723	5430	5038	1458	3.26	2.97	0.85										
ywqC	3/31352	3/32298	-	607	2031	2180	591	4.55	5.75	0.99	1100	Inton	2722162	2722505	2722270	15.5	25.2	10.5	0.1	
wwaR	3732879	3734489	+	1853	1481	1460	1652	0.81	0.79	0.89	1100	wwaB	3732103	3733904	3733807	6.2	49	10.5	1.6	
ywqB ywaA	3734476	3737244	+	2410	2220	2031	2116	0.94	0.85	0.89	1101	vwaA	3735206	3735366	3735286	0.2	1.6	1.0	5.7	
vwpJ	3737370	3738227	-	495	704	746	554	1.43	1.51	1.12		2 1								
glcR	3738233	3739009	-	583	773	780	600	1.33	1.34	1.03										
											1104	Inter	3738861	3739412	3739137	26.8	49.5	10.9	30.7	
ywpH	3739233	3739574	-	1198	2456	2709	1240	2.14	2.34	1.05										
ywpG	3739651	3740034	-	544	1237	1353	601	2.29	2.52	1.12										
											1105	Inter	3739796	3740347	3740072	31.9	50.6	13.6	1.0	
ywpF	3740209	3740619	+	3595	4138	4466	3351	1.15	1.24	0.93										
ywpE	3740758	3741066	-	366	306	279	290	0.84	0.76	0.79										
ywpD mscI	3741410	3742246	+	25/ 5109	252	242	249 1406	0.90	0.94	0.9/										
wwnR	3742784	3743182	-	4456	3507	3751	4400	0.70	0.73	0.00										
rapD	3743374	3744438	+	2673	3851	4110	2522	1 44	1 53	0.94										
flhP	3744461	3745267	1	4459	4196	3673	4863	0.96	0.83	1.09										
flhO	3745301	3746113	-	2194	1963	1617	2436	0.91	0.74	1.12										
											1107	Inter	3745644	3746688	3746166	24.3	19.5	36.2	135.6	P01
mbl	3746276	3747277	-	12237	12180	10292	11112	1.00	0.84	0.91										
spoIIID	3747443	3747724	-	359	274	281	242	0.76	0.78	0.68										
usd	3747739	3747849	-	52	59	66	54	1.14	1.32	1.02										
ywoH	3748074	3748487	+	413	321	284	351	0.77	0.68	0.84										
ywoG	3748509	3749699	+	938	822	816	909	0.88	0.87	0.97										
ywoF	5/49/90	3/51196	-	779	2899	2824	2350	3.75	3.64	3.05										

Supplen	entary Tab gene	ne SI. Su	mma	ry of trai	nscriptor	me and ( Trans	_nAP-ch criptom	ip analyse analysis	es (contin	ued).				ChAP-chin a	analysis		
	gene			Sig	nal intens	ity of RN	A <sup>a</sup>	Exp	ression rat	io <sup>b</sup>				Child - Chipt	Binding	intensity c	
name	etart	and	and	0.8	an interio	4h.h.			$\Delta abh$	1	PBR	ORF	etart	and canter	AbrB	Abh	Profile
name	Start	chu	str	wild	∆abrB	∆ abrB	$\Delta abh$	wild	$\Delta abrB/$	wild	ID	Intergenic	start	end center	wild ⊿abh	wild ∆ abrB	ID
									wild		1100	Inter	2751050	2751400 2751275	-type	-type	
vwoE	3751302	3752774	-	365	338	365	410	0.92	1.00	1.12	1108	mer	5751050	5751499 5751275	51.4 15.9	20.7 0.2	
ywoD	3752955	3754313	-	1292	1317	1316	1322	1.02	1.00	1.02							
ywoC	3754313	3754882	-	1935	2015	1994	2036	1.05	1.04	1.05							
ywoB	3755066	3755530	-	1488	1449	1391	1325	0.97	0.94	0.89							
nrgA	3755812	3757026	+	561	458	464	571	0.82	0.83	1.02	1109	nrgA	3755827	3755987 3755907	2.7 4.0	3.6 2.2	
nrgB vwoA	3757569	3758150	+	1422 4257	2042 4270	2992	1432 4948	1.42	2.08	1.04							
ywoA ywnJ	3758191	3758613	-	751	733	800	789	0.98	1.07	1.05							
spoIIQ	3758724	3759575	-	372	793	827	375	2.13	2.22	1.01							
ywnH	3759716	3760207	+	2863	2582	2535	2915	0.91	0.89	1.02							
ywnG	3760204	3760722	+	3762	3047	2966	3821	0.81	0.79	1.01							
ywnF	3761009	3/61443	-	937	/19	807	1028	0.77	0.86	1.10	1110	Intor	2761520	2761692 2761611	52 04	17 03	
vwnE	3761686	3763134	+	1466	1363	1381	1457	0.93	0.94	1.00	1110	inci	3701339	5701082 5701011	5.5 0.4	1.7 0.5	
mta	3763155	3763928	-	434	342	366	422	0.79	0.84	0.97							
											1111	Inter	3763834	3764266 3764050	29.7 4.2	10.9 -0.1	
ywnC	3764073	3764456	+	2410	2219	2076	3491	0.92	0.86	1.44							
ywnB	3764491	3765132	-	841	552	602	737	0.66	0.72	0.88							
ywnA wraC	3765200	3765601	-	3027	2100	2009	2621	0.69	0.66	0.87							
ureC ureB	3767442	3767816	-	229	221	239	260	0.94	1.01	1.03							
ureA	3767813	3768130	-	296	275	315	327	0.93	1.07	1.14							
csbD	3769127	3769315	-	4711	2520	3622	1405	0.54	0.77	0.31							
ywmF	3769388	3769867	-	542	418	478	471	0.77	0.88	0.87							
rapB	3770023	3771156	-	1045	2090	2103	1647	2.01	2.02	1.58	1110	<b>T</b> .	2770022	2771542 2771222	20.1 22.4	157 0.4	
moaA	3771348	3772373		5896	5013	5263	6307	0.85	0.89	1.07	1115	Inter	3770923	37/1542 37/1255	29.1 33.4	15./ 0.4	
fdhD	3772389	3773177	-	3189	2669	2578	3600	0.84	0.81	1.13							
ywmE	3773423	3773584	-	1625	1200	1565	918	0.73	0.96	0.57							
ywmD	3773678	3774352	-	514	806	779	559	1.56	1.52	1.10							
c	0004/00/	2775250		501	2.00	201	160	0.74	0.70	0.04	1115	Inter	3773949	3774857 3774403	42.1 65.0	33.8 10.6	
ywmC	3774676	3775359	-	501	369	391	468	0.74	0.78	0.94							
sponD murAA	3776972	3778282	-	13268	14294	13471	13918	1.09	1.02	1.05	1116	murAA	3777383	3777492 3777438	14 31	27 32	
ywmB	3778316	3779056	-	4019	5000	4317	4177	1.25	1.02	1.04	1110		5111505	5111152 5111150		2.7 5.2	
ywzB	3779185	3779415	-	3490	4997	3926	3391	1.45	1.11	0.97							
											1119	Inter	3779338	3779753 3779546	<b>19.0</b> 11.0	9.8 6.6	
ywmA	3779585	3780058	+	369	365	392	319	0.99	1.06	0.86							
atpC atpD	3780092	3781935	-	21947	21065	21014	21555	1.03	1.01	1.07							
atpG	3781961	3782824	-	21898	22243	21075	23176	1.02	1.00	1.07							
atpA	3782901	3784409	-	19872	20699	20221	21259	1.04	1.02	1.07							
atpH	3784426	3784971	-	19919	20487	19745	22996	1.03	0.99	1.15							
atpF	3784968	3785480	-	21676	21574	21366	24134	0.99	0.98	1.11							
atpE atp B	3785643	3785855	-	19703	19924	18861	20283	1.01	0.96	1.03							
аtрБ	3786643	3787026	-	8340	9238	7699	10502	1.10	0.93	1.15	1120	atnI	3786750	3787148 3786949	11.0 11.5	128 49	
	2700045	5.07020		0,40	200	1077	10002	1.10	0.75	1.20	1120	Inter	3787158	3787590 3787374	21.7 7.3	21.1 4.6	
ирр	3787449	3788078	-	9046	6739	6487	8355	0.75	0.72	0.92							
glyA	3788213	3789460	-	15077	12901	12585	14123	0.86	0.84	0.94							
ywlG	3789667	3790209	-	4192	3473	3614	4409	0.83	0.86	1.05							
ywiF ywlF	3790222	3791280	-	4556	5447 2082	3554 2104	4392	0.76	0.78	1.01							
ywlD	3791356	3791913	_	490	391	366	526	0.80	0.75	1.07							
ywlC	3791992	3793032	-	2252	1604	1505	2364	0.72	0.67	1.05							
ywlB	3793189	3793632	-	801	702	788	767	0.88	0.99	0.96							
spoIIR	3793699	3794373	-	613	546	573	581	0.89	0.94	0.94							
ywlA	3794514	3794876	+	853	817	800	945	0.95	0.93	1.10							
ywkF ywkF	3795240	3796106	-	2531	1/88	1/51	2048 2652	0.71 0.60	0.69	0.81							
prfA	3796108	3797178	-	11612	8511	8519	11328	0.73	0.07	0.97							
ywkD	3797304	3797690	+	1150	1066	1069	1080	0.93	0.93	0.94							
racA	3797812	3798366	+	1975	1978	2038	1763	1.00	1.03	0.89							
ywkB	3798400	3799359	-	766	542	550	809	0.70	0.72	1.05							
ywkA	3799441	3801189	-	657	307	337	746	0.46	0.51	1.12							
íak rom F	3802104	3802015	-	1589	24280	908 23084	1545	0.80	0.60	0.84							
rho	3802423	3803706	-	6470	7797	6467	6280	1.21	1.00	0.92							
glpX	3804113	3805078	-	10263	10739	10934	9937	1.05	1.07	0.97	1123	glpX	3804005	3804233 3804119	6.4 4.4	5.3 0.1	
murAB	3805109	3806398	-	8466	9073	8852	8868	1.07	1.05	1.05							
ywjH	3806777	3807415	-	20700	20564	21072	21572	0.99	1.02	1.04			20	20080			
fbaA	3807535	3808392	-	24503	24181	24081	24834	0.99	0.98	1.01	1124	tbaA	3807728	3807973 3807851	4.3 7.4	2.1 1.4	

Supplen	gene	le S1. Sur	nmai	y of trai	iscriptor	me and Trans	_nAP-cr crintom	up analyse e analysis	s (contir	ued).				C	hAP-chin a	malysis		
	gene			Sim	ol intene	ity of PN		Evo	receion re	tio <sup>b</sup>				C	плі-спра	Bindin	a intensity c	
			pu	JBI	iai interis.	ity of Kiv	A	Exp	Aahh	u0	PBR	ORF				AbrB	Abh	Profile
name	start	end	stra	wild	∆abrB	$\Delta abh$	$\Delta abh$	$\Delta abrB/$	$\Delta abrB/$	$\Delta abh /$	ID	Or Intergonic	start	end	center	wild A	wild	, ID
						∆abrB		Wild	wild	Wild		mergenic				-type ⊿ abh	-type ⊿ abr	В
spo0F	3808573	3808947	-	1211	2139	1888	1299	1.81	1.57	1.08								
ywjG	3809113	3809634	+	1822	1677	1700	1702	0.92	0.93	0.93								
pyrG	3809716	3811323	-	15619	11223	10212	15316	0.72	0.65	0.98								
rpoE	3811565	3812086	-	9789	7793	1511	9204	0.80	0.77	0.94	1125		2012002	2012207	2012240	24 24	5.5 14	2
acdA	3812269	3813408	-	698	437	496	/18	0.63	0.72	1.02	1125	acdA	3813083	3813396	3813240	3.4 3.4	5.5 14.	2
ywj1 vwiF	3815677	3816873	+	359	357	378	377	1.00	1.05	1.05								
uvsE	3816886	3817848	+	245	245	275	225	1.00	1.12	0.92								
ywjC	3817929	3818201	+	4773	1871	3263	2014	0.40	0.69	0.44								
ywjB	3818243	3818767	-	4188	5496	5438	3189	1.31	1.30	0.76								
ywjA	3818777	3820504	-	3927	4649	4749	3025	1.18	1.21	0.77								_
ywiE	3820593	3822095	-	1364	828	1132	651	0.61	0.85	0.46	1127	ywiE	3821753	3822015	3821884	6.9 8.8	10.0 -0.	5
narI	3822581	3823252	-	492	415	469	486	0.84	0.95	0.99								
narJ	3823249	3823803	-	427	338	330	474	0.79	0.77	1.11								
narH	3823829	3823292	-	225	208	270	307	0.78	0.80	1.05								
arfM	3829164	3829640	-	336	318	340	316	0.75	1.01	0.98								
vwiC	3829784	3830503	+	1077	1041	1092	962	0.97	1.01	0.89								
fnr	3830535	3831251	-	869	742	723	760	0.83	0.81	0.88								
, narK	3831350	3832537	-	524	446	476	510	0.85	0.91	0.97								
argS	3832673	3834343	-	6974	5153	4989	6628	0.74	0.72	0.95								
ywiB	3834340	3834768	-	3657	2575	2176	3618	0.70	0.59	0.99								
											1129	Inter	3834673	3835139	3834906	26.1 36.4	7.7 2.	4
sboA	3835081	3835212	+	562	5925	6624	553	10.92	12.18	0.99								
sboX	3835169	3835321	+	107	499 8210	549 8208	1027	4.27	4.77	1.12	1120	olla A	2925140	2025666	2025100	22.4 46.2		5 002
albA	3835340	3836092	+	1502	6820	8398	1987	3.52	2.28	1.52	1129	abA	3835149	3833000	3835408	32.4 40.3	18.0 I.	5 P02
alhC	3836863	3837582	+	1034	4043	4177	1176	3.90	4 03	1.10								
albD	3837575	3838885	+	937	3377	3537	1058	3.60	3.77	1.12								
albE	3838875	3840035	+	412	1659	1800	468	4.01	4.36	1.13								
albF	3840040	3841320	+	419	1327	1518	467	3.16	3.62	1.11								
albG	3841317	3842018	+	352	717	839	394	2.05	2.40	1.12								
ywhL	3842024	3843400	-	399	393	398	400	0.98	1.00	1.00								
ywhK	3843439	3844794	-	256	239	263	253	0.93	1.02	0.99	1120	<b>T</b> .	2044652	2045152	2011002	25.2 27.0		•
ranE	2845024	2846160		020	030	1003	1952	1.00	1 16	1.08	1130	Inter	3844652	3845152	3844902	25.3 27.0	<u> </u>	2
nhrF	3846153	3846272	+	3543	5697	6135	4020	1.00	1.10	1.56	1131	phrF	3846063	3846461	3846262	12.2 18.1	37 -0	4
ywhH	3846371	3846844	+	332	346	380	256	1.04	1.15	0.77		P	5010005	5010101	5010202	12.2	5.7 0.	
speB	3846876	3847748	-	5729	3728	3292	5248	0.65	0.57	0.92								
speE	3847809	3848639	-	6785	4628	3569	6296	0.70	0.53	0.93								
ywhE	3848841	3850784	+	230	199	213	248	0.87	0.93	1.09								
ywhD	3851208	3851726	-	6827	5782	5764	6490	0.85	0.84	0.95								
ywhC	3851740	3852399	-	3119	2781	2646	2877	0.89	0.85	0.92								
ywhB	3852508	3852696	+	5097	5464 1588	53/8	4320	1.08	1.07	0.84								
ywii/4 thr7	38532739	3855194	-	595	542	609	549	0.98	1.02	0.92								
mmr	3856039	3857439	-	1055	820	830	1037	0.78	0.79	0.92								
ywgB	3857439	3857909	-	883	589	571	808	0.67	0.65	0.90								
ywgA	3858021	3858521	-	2627	1805	1676	2427	0.69	0.64	0.93								
ywfO	3858557	3859858	-	3091	2415	2175	2946	0.78	0.71	0.95								
ywzC	3860020	3860244	-	1634	1378	1216	1497	0.85	0.75	0.91								
rsfA	3860459	3861235	+	325	856	954	318	2.63	2.92	0.98								
ywfM	3861379	3862269	-	2026	677	1880	2006	0.92	0.94	0.97								
ywjL wwf <b>F</b>	3802437	3864220	-	3020	1940	1889	1022	0.64	0.62	0.99								
уwјК	5805551	3804230	-	1215	823	870	1052	0.08	0.72	0.85	1134	Inter	3864287	3864464	3864376	41 65	22 0	0
eutD	3864377	3865348	-	15698	15181	14012	15072	0.97	0.89	0.96		inter	5001207	5001101	2001270		2.2 0.	
ywfI	3865633	3866382	+	6644	6378	6660	7155	0.97	1.01	1.08								
ywfH	3866515	3867294	+	535	2193	2855	527	4.11	5.36	0.98								
ywfG	3867309	3868508	-	641	1106	1202	661	1.73	1.89	1.02								
ywfF	3868509	3869693	-	900	1620	1789	951	1.80	1.99	1.06	1136	ywfF	3869370	3869530	3869450	0.5 0.7	1.3 5.	4
ywfE	3869690	3871108	-	754	1544	1750	810	2.07	2.35	1.07								
ywfD	3871127	3871894	-	687	1009	1107	641	1.47	1.61	0.93	1120		2072000	207221	2072152	10 17	1.1 -	0
ywfC wwfD	3872589	3872202	-	420	257	814	416	1.70	1.95	0.99	1138	ywiC	3872090	38/2216	38/2153	1.2 1.7	1.1 5.	U
уwjБ	3012388	36/3202	-	308	337	43/	542	0.97	1.19	0.93	1130	Inter	3873076	3873390	3872722	54 10.0	23 0	6
vwfA	3873354	3874592	-	736	647	725	752	0.88	0 99	1.02	1139	mer	5075070	2012209	3013233	3.4 10.0	2.3 0.	0
rocC	3874802	3876214	-	472	500	555	464	1.06	1.18	0.98	1140	rocC	3874980	3875140	3875060	0.1 0.6	0.6 4	5
rocB	3876214	3877914	-	328	507	544	299	1.56	1.66	0.91						510		_
rocA	3877988	3879535	-	870	7576	8784	880	8.71	10.11	1.01								
rocG	3879762	3881036	-	728	4868	6481	714	6.67	8.86	0.98								
yweA	3881213	3881677	-	1387	15543	17826	1475	11.18	12.83	1.06								
											1141	Inter	3881491	3882178	3881835	41.9 61.7	10.9 2.	5

Suppler	nentary Tab	de S1. Su	mma	ry of trar	scriptor	me and (	ChAP-ch	ip analys	es (contir	nued).				C	hAD ahin a	nolveie				
	gene			Sim	al intone	Trans		E analysis	raccion re	tio b	·			t	пар-спір а	inalysis	Dinding	intoncity	С	
			pu	Sign	iai intens	ity of KIN	A	Ext	Aahh	luo	PBR	ORF				Ał	orB	A	bh	Profile
name	start	end	strai	wild	∆abrB	∆abh ∆abrB	$\Delta abh$	∆abrB/ wild	∆abrB/ wild	<i>∆abh /</i> wild	ID	or Intergenic	start	end	center	wild -type	∆abh	wild -type	∆abrB	ID
spsL	3882001	3882456	-	497	404	452	497	0.81	0.91	1.00										
spsK	3882449	3883300	-	723	571	594	678	0.79	0.82	0.93	1142	spsK	3882851	3882994	3882923	3.1	2.8	4.5	3.0	
spsJ	3883314	3884261	-	602	502	495	609	0.84	0.83	1.01										
spsi spsG	3885026	3886045	-	460	356	391	490	0.79	0.79	1.07										
spsE	3886052	3886771	-	364	306	321	364	0.84	0.88	1.00										
spsE	3886764	3887885	-	318	280	272	343	0.88	0.86	1.08										
spsD	3887885	3888754	-	462	367	403	433	0.80	0.87	0.94										
spsC	3888755	3889924	-	394	317	340	404	0.81	0.87	1.04										
spsb spsA	3891368	3892138	-	193	165	177	198	0.87	0.89	1.04										
ywdL	3892458	3893003	+	191	166	153	216	0.88	0.80	1.18										
ywdK	3893076	3893417	-	3243	2564	2478	3448	0.79	0.76	1.06										
ywdJ	3893418	3894800	-	4593	3696	3889	4600	0.80	0.84	1.01			000 40 50				10.5		10	
ywdl mudu	3894820	3895137	-	4228	3090 577	3319	3613	0.73	0.78	0.86	1143	ywdl	3894853	3895217	3895035	16.2	13.7	7.7	1.8	
ywan ung	3896703	3897380	-	2601	1675	1704	2358	0.80	0.66	0.91										
ywdF	3897394	3898200	-	3681	2408	2473	3413	0.65	0.67	0.93										
ywdE	3898291	3898824	-	842	724	785	791	0.86	0.93	0.94										
ywdD	3898872	3899363	-	844	897	993	856	1.06	1.17	1.01										
ywdC thiD	3899406	3899834	+	293 5607	3923	4051	5557	1.05	0.72	1.12										
vwdA	3900888	3901136	_	3361	1877	2271	3473	0.55	0.66	1.04										
sacA	3901230	3902672	-	4272	2267	3178	4280	0.52	0.73	1.00	1145	sacA	3901109	3902102	3901606	65.3	79.0	60.5	18.1	P01
											1146	sacA	3902248	3902425	3902337	1.7	2.2	1.9	4.9	
sacP	3902669	3904054	-	2683	1186	1899	2798	0.43	0.67	1.05	1147	sacP	3903319	3903445	3903382	1.0	1.2	1.5	3.1	
ywcJ sacT	3904356	3905126	+	703	220	230	632	0.74	0.85	0.91										
vwcI	3906035	3906337	-	588	496	549	595	0.85	0.94	1.03										
vpr	3906867	3909287	+	313	411	476	323	1.32	1.54	1.04		*Broad	3906396	3913713						
ywcH	3909325	3910326	-	1356	912	1093	1406	0.68	0.82	1.03		I								
nfrA	3910500	3911249	-	5819	5616	6396	7059	0.97	1.10	1.21		ļ								
roaA vwcF	3911355	3912530	-	344	460	1210	2089	1.33	1.29	1.24		1								
qoxD	3913338	3913712	-	13738	11083	10176	12729	0.81	0.74	0.93		i								
qoxC	3913714	3914328	-	21464	18619	17799	20789	0.87	0.83	0.97		-								
qoxB	3914342	3916291	-	18530	15816	15059	18234	0.85	0.81	0.98										
qoxA	3916319	3917284	-	17200	13703	12907	16771	0.80	0.75	0.98										
yw2A galT	3918116	3919657	-	4191	3668	4322	4058	0.01	1.03	0.01										
galK	3919661	3920833	-	3581	2899	3255	3393	0.81	0.91	0.95										
ywcD	3920914	3921297	-	1683	1587	1554	2124	0.94	0.92	1.26										
ywcC	3921315	3921986	-	825	600	567	762	0.73	0.69	0.92										
ywcB ywcA	3922943	3923251	+	925 507	1025	958 485	862 507	1.11	1.04	0.93										
ywb0	3924819	3925421	_	2230	1729	1568	1965	0.78	0.71	0.88										
ywbN	3925705	3926955	-	7015	6199	6176	7078	0.88	0.88	1.01										
ywbM	3926974	3928131	-	8369	6993	7300	8132	0.84	0.88	0.97										
ywbL	3928128	3929573	-	3074	2528	2572	3080	0.82	0.84	1.00										
thiE thiM	3929730	3930398	-	2803	2790	2939	2873	0.89	0.94	1.00										
ywbI	3931221	3932126	-	1316	1186	1226	1479	0.90	0.93	1.13										
											1160	Inter	3932049	3932277	3932163	4.8	4.9	4.6	9.5	
ywbH	3932232	3932618	+	577	480	397	659	0.90	0.72	1.14										
ywbG	3932600	3933325	+	495	420	389	563	0.86	0.79	1.13	1121	Inter	3022102	302250/	3022245	22.0	21-1	- 26-1	17	PO2
vwbF	3933380	3934579	+	850	2289	2238	1122	2.70	2.63	1.32	1101	men	3733103	3733360	3733343	- 55.0	21.1	-20.1	1.7	r 02
ywbE	3934613	3934810	+	2371	3579	3613	2682	1.51	1.52	1.13										
ywbD	3934845	3936035	-	2293	1682	1662	2105	0.73	0.73	0.92										
ywbC	3936156	3936536	+	4717	4087	4325	4810	0.86	0.91	1.02										
ywbB	3936574	3937251	-	442	648 195	685 509	412	1.46	1.55	0.93										
ywoA epr	3938890	3940827	+	1632	465	1509	1731	0.79	0.83	1.10										
											1163	Inter	3940923	3941117	3941020	6.2	1.5	3.3	0.9	
sacX	3941255	3942634	+	817	670	664	838	0.83	0.82	1.02										
sacY	3942688	3943530	+	614	479	479	594	0.80	0.79	0.97										
gspA	3943581	3944441	-	3678	1796	3522	1528	0.49	0.95	0.42										
ywar ywaF	3944551	3945930	-+	530	534	907 495	898 530	0.82	0.97	0.93										
tyrZ	3946179	3947420	+	489	382	401	449	0.78	0.82	0.91										
ywaD	3947576	3948943	+	248	239	245	235	0.97	0.99	0.95										
ywaC	3948973	3949605	-	2570	2162	2651	2864	0.84	1.03	1.12										
menA	3949747	3950682	-	3509	2362	2108	3242	0.67	0.60	0.92										

pren	gene			, <b></b>		Trans	criptom	e analysis						Ch	AP-chip a	nalysis			
	gene			Sio	nal intens	ity of RN	A <sup>a</sup>	Exp	ession ra	tio <sup>b</sup>				0.11	ii ciipt	1111,515	Binding	intensity c	
	atant	and	pur	5181	an meens	4 11			∆ abh	4 11 /	PBR	ORF	atant	and	conton	Abr	B	Abh	Profile
name	start	ena	stra	wild	∆abrB	$\Delta abh$ $\Delta abrB$	$\Delta abh$	∆ abrB/ wild	∆abrB/	∆ abh /	ID	OF Intergenic	start	ena	center	wild	Aabh	wild A abr	, ID
						Aubib		wiid	wild	with		intergente				-type	auon	-type	J
dltA	3951296	3952807	+	14675	16862	16790	15543	1.15	1.15	1.06									
dltB dltC	3952804	3953991	+	12441	14039	13636	138/8	1.13	1.10	1.12									
dltD	3954244	3955422	+	15073	16998	17032	16028	1.13	1.13	1.12									
dltE	3955513	3956271	+	13531	15946	15582	14407	1.18	1.16	1.07									
ywaA	3956412	3957503	+	3326	3776	3870	3111	1.15	1.18	0.94									
licH	3957537	3958865	-	7138	3396	5680	6837	0.45	0.72	0.94									
licA	3958862	3959194	-	5730	2263	3879	4898	0.38	0.61	0.85									
licC licP	3959213	3960571	-	4040	1579	3115	3734	0.39	0.68	0.90									
licR	3961023	3962948	-	914	746	872	853	0.31	0.95	0.88									
vxzF	3963111	3963269	-	1401	870	1212	776	0.62	0.86	0.56									
yxlJ	3963298	3963888	-	675	564	653	594	0.84	0.97	0.88									
katX	3964017	3965660	+	742	691	940	527	0.94	1.25	0.75									
yxlH	3965765	3966967	+	1252	1015	1063	1257	0.81	0.85	1.00									
yxlG	3966960	3967739	-	1795	2671	3451	2442	1.50	1.95	1.35									
yxIF yxIF	3968630	3968818	-	186/	2595	32/5	2599	1.40	1.//	1.37									
vxlD	3968815	3969021	-	1182	1802	1935	1654	1.51	1.67	1.40									
yxlC	3969018	3969338	-	867	1101	1311	1316	1.37	1.66	1.54									
sigY	3969331	3969867	-	812	924	1230	1146	1.19	1.61	1.40									
yxlA	3970079	3971452	+	711	845	739	694	1.19	1.05	0.97									
yxk0	3971467	3972297	-	783	617	673	715	0.79	0.86	0.92									
cydD avdC	39/2383	3974110	-	549	425	459	547	0.78	0.84	1.00	1165	andC	2074270	2074452 2	074416	0.3	1.4	0.0 2	7
cyde cydB	3975810	3976826	-	861	766	816	978	0.84	0.80	1.03	1105	cyuc	3714317	3774433 3	5974410	0.5	1.4	0.9 2.	
cydA	3976810	3978216	-	1540	1070	1379	1540	0.70	0.88	0.99									
2											1166	Inter	3978000	3978464 3	3978232	15.5	8.0	26.5 4.	1
yxkJ	3978772	3980124	+	482	514	595	468	1.07	1.23	0.97									
yxkI	3980246	3981934	+	1342	2300	2435	1119	1.72	1.82	0.83						10.0	10 1		
E	2081002	2082102		1270	4516	1512	1054	2.26	2 70	1.41	1168	Inter	3981638	3982342 3	3981990	43.8	47.6	60.9 33.	2 P01
yx2E vxkH	3981992	3982192	+	546	4310	4343	496	1.30	5.28 1.05	0.90									
msmX	3983152	3984249	-	5042	3367	4884	4439	0.66	0.94	0.88									
yxkF	3984370	3985263	-	728	881	1037	653	1.21	1.42	0.90									
aldY	3985447	3986904	+	451	343	406	413	0.76	0.90	0.91									
yxkD	3986946	3987782	-	1070	1014	986	1065	0.95	0.92	1.00		-							-
hC	2000251	2000000		7152	14650	14276	12050	2.05	2.01	1.92	1169	Inter	3987775	3988530 3	3988153	47.2	64.7	52.4 17.	/
galE	3988967	3989986	-	8148	6139	6013	6346	0.75	0.74	0.78									
yxkA	3990101	3990607	-	390	305	311	398	0.78	0.80	1.02									
yxj0	3990737	3991612	+	663	469	434	633	0.71	0.65	0.95									
yxjN	3991690	3992163	+	1205	904	830	1133	0.75	0.68	0.94									
ухјМ	3992181	3993401	+	743	659	622	701	0.90	0.84	0.94									
yxjL T	3993388	3994044	+	549	530	544	527	0.97	0.99	0.96	1170	T	2005005	2005551 2	005210	20.7	25.0	26.5 52	D01
pepi	3994094	3993320	+	5512	3070	0547	3303	1.02	1.61	0.94	1170	Inter	3995085	3995551 3	3995518	22.2	27.9	15.1 17.	
vxiJ	3995848	3996111	+	2134	2547	2726	1855	1.20	1.28	0.87	1170	Inter	5775501	5775775 2	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	22.2	21.7	15.1 17.	<u> </u>
yxjI	3996240	3996728	+	1176	1122	1150	1104	0.95	0.99	0.94	1171	yxjI	3996241	3996707 3	3996474	20.3	19.8	5.0 1.0	5 P03
yxjH	3996983	3998005	+	999	853	972	842	0.85	0.97	0.85									_
yxjG	3998368	3999504	+	712	666	781	669	0.94	1.10	0.94	1172	yxjG	3998553	3998730 3	3998642	0.5	1.1	1.4 5.4	4
yxjF	3999557	4000330	-	427	331	343	453	0.77	0.80	1.06									
scob scoA	4000347 4000994	4001710	-	471 500	340 356	358 387	427 537	0.72	0.76	1.09									
vxiC	4001734	4003152	-	382	297	340	379	0.78	0.90	1.01									
yxjB	4003306	4004154	-	749	829	824	595	1.11	1.10	0.79									
											1175	Inter	4004180	4004918 4	4004549	25.4	44.8	10.6 2.3	5
yxjA	4004770	4005963	+	4992	5587	5052	6109	1.16	1.04	1.23									
yxiT	4006434	4006676	-	2088	2834	3369	1828	1.36	1.61	0.88									
yxiS ka+E	4006821	4007111	-	1646	1370	1588	1170	0.83	0.97	0.71									
киL citH	4009422	4010702	-+	1529 542	659 437	1203	748 508	0.05	0.98	0.55									
bglS	4010860	4011588	-	1862	885	1457	2168	0.30	0.74	1.13									
licT	4011884	4012717	-	2278	1728	2151	2663	0.75	0.94	1.16									
yxiP	4012813	4013493	-	407	487	487	436	1.20	1.21	1.07									_
											1178	Inter	4013292	4013928 4	013610	41.8	62.7	24.0 6.0	5
yxi0	4013700	4014986	+	578	824	818	633	1.42	1.41	1.09	1179	yxiO	4014669	4014931 4	4014800	3.5	2.1	4.4 9.3	3
deaD	4015005	4016444	-	5334	3684	3824	3836	0.69	0.72	0.72	1180	deaD	4016233	4016461 4	016347	1.4	1.2	2.1 8.	
yxiM yxiI	4016526	401/674	-	3668	2689	2766	2302	0.74	0.75	0.63									
yniL vxiK	4018166	4018627	-	4294	3768	3695	3263	0.85	0.82	0.07	1181	vxiK	4018120	4018620 4	018370	2.1	3.0	3.5 40	3 P04
yxiJ	4018643	4018939	-	2962	2099	2056	1836	0.71	0.69	0.62	. 101		.010120	.010020 4		2.1	5.0	3.3	. 07
yxiI	4018967	4019455	-	3270	2699	2586	2111	0.83	0.79	0.64									

Suppler	nentary Tal	de S1. Sur	nma	ry of trai	nscripto	me and (	hAP-ch	ip analyse	es (contin	ued).					h A D -him -					
	gene			Cia	a lintana	Trans		E analysis		tio b				t	пар-спір а	inalysis	Dinding	intonoite	с	
			ри	Sig	nai intens	ity of KIN	A	Exp	A abh	00	PBR	ORF				A	brB	Intensity	bh	Profile
name	start	end	stra	wild	∆abrB	∆abh ∆abrB	∆abh	∆abrB/ wild	∆abrB/ wild	∆abh / wild	ID	or Intergenic	start	end	center	wild -type	∆abh	wild -type	∆abrB	ID
yxzG	4019473	4019925	-	5555	4514	4404	3247	0.81	0.79	0.58										
yxiH	4019995	4020324	-	2350	1971	1885	1442	0.84	0.80	0.62										
yxiG yxiC	4020447	4020863	-	5426	4230	2000	2660	0.78	0.74	0.58										
vxiF	4020014	4021282	-	2974	2675	2530	1832	0.90	0.85	0.62										
yxxG	4022072	4022500	-	12633	10256	9775	9635	0.82	0.78	0.76										
wapA	4022562	4029566	-	15636	16436	15945	11612	1.05	1.02	0.74	1184	wapA	4023339	4023550	4023445	3.0	5.1	3.1	3.1	
											1184	wapA	4023560	4023958	4023759	7.2	21.6	7.3	7.4	
											1185	wapA Inter	4024053	4024519	4024286	12.5	15.4	23.0	37.2	
yxxF	4029728	4030663	-	865	1280	1217	800	1.48	1.41	0.92	1188 1188	yxxF Inter	4029765	4030214 4031013	4029990	20.5 20.6	39.5 35.8	1.7 1.7 4.2	2.1 1.9	P03 P03
yxiE	4030815	4031261	-	18601	17500	18816	19491	0.94	1.00	1.04										
bglH	4031364	4032773	-	19402	16621	17705	20686	0.85	0.91	1.06	1189	bglH	4031227	4031506	4031367	5.0	11.3	2.8	2.5	
bglP	4032796	4034625	-	17470	14342	15825	18364	0.81	0.89	1.04		-		100 50 10	100.10.40		20.2	140		
wrrF	4035008	4035316		1510	1353	1600	1358	0.80	1.05	0.91	1190	Inter	4034661	4035263	4034962	39.1	38.3	16.0	4.6	
vxxD	4035362	4035805	-	841	703	770	866	0.82	0.90	1.03	1191	vxxD	4035409	4035737	4035573	13.2	19.0	3.8	-0.1	
yxiD	4035802	4037511	-	1010	1557	1934	602	1.54	1.91	0.60	1191	yxiD	4035749	4036181	4035965	12.5	25.3	3.3	0.2	
											1191	yxiD	4036361	4036725	4036543	6.5	9.4	4.8	3.4	
		1005000			1000		100				1192	yxiD	4037330	4037473	4037402	2.4	4.2	2.0	0.8	
yxiC	4037531	4037800	-	716	1380	1752	430	1.95	2.42	0.61										
улів	4037812	4038177	-	390	1084	1514	265	1.80	2.18	0.48	1193	Inter	4038044	4038594	4038319	27.1	38.3	12.8	5.4	
yxiA	4038484	4039893	-	437	531	746	450	1.21	1.68	1.04	,,	inter	1050011	1020271	1050517		50.5	12.0	5.1	
hutP	4040501	4040956	+	1588	877	994	1454	0.61	0.67	0.95										
hutH	4041069	4042595	+	286	224	230	296	0.78	0.80	1.05										
hutU	4042592	4044250	+	392	284	321	371	0.72	0.82	0.95										
nut hutG	4044203	4045528	+	263	227	243	258	0.77	0.80	0.98										
hutM	4046556	4047983	+	444	384	419	439	0.86	0.94	0.98										
pdp	4048027	4049328	-	7993	3015	4695	7440	0.37	0.57	0.93										
nupC	4049358	4050539	-	11824	4799	6856	11325	0.40	0.56	0.95		_								
dra	4050655	4051200		11082	6120	7802	10021	0.51	0.65	0.01	1195	Inter	4050182	4051005	4050594	40.0	65.9	19.7	2.8	P02
deoR	4050055	4052337	-	11982	1101	1018	1374	0.75	0.05	0.91										
yxxB	4052428	4053297	-	565	369	422	510	0.65	0.75	0.90										
yxeR	4053370	4054482	-	1008	881	886	1016	0.88	0.88	1.01										
yxeQ	4054552	4055889	-	494	442	452	486	0.89	0.91	0.98										
yxeP	4055886	4057028	-	526	444	479	514	0.85	0.92	0.98										
yxe0 yxeN	4057807	4058481	-	655	593	626	616	0.90	0.92	0.94										
yxeM	4058504	4059298	-	363	281	311	318	0.77	0.86	0.88										
yxeL	4059323	4059820	-	373	302	304	425	0.82	0.83	1.18										
yxeK	4059834	4061159	-	388	323	341	372	0.83	0.88	0.97	1196	yxeK	4060314	4060406	4060360	1.8	2.8	1.2	0.7	
yxeJ yxeI	4061545	4061372	-	1606	1099	1594	1786	0.82	1.01	1.08	1197	vxeI	4061691	4061919	4061805	62	10.3	39	18	
yxeH	4062700	4063512	-	5527	6170	6155	5554	1.12	1.11	1.00	,	5/101	1001071	1001717	1001005	0.2	10.5	5.7	1.0	
yxeG	4063552	4064109	-	484	1113	1051	446	2.29	2.17	0.92										
yxeF	4064090	4064524	-	982	2422	2082	789	2.46	2.11	0.79										
yxeE	4064612	4064977	+	131	130	116	132	0.98	0.88	1.01	1198	Inter	4064734	4065251	4064993	17.7	29.0	3.7	1.3	
yxeD	4065225	4065578	+	130	289	371	98	2.23	2.88	0.76										
yxeC	4065622	4066020	-	5260	5075	4600	4699	0.97	0.88	0.90	1200	yxeC	4065840	4066169	4066005	11.1	12.7	7.2	13.2	
yxeB	4066198	4067157	+	13972	15622	15441	14072	1.12	1.11	1.00	1201	yxeB	4066927	4067087	4067007	2.7	5.7	2.0	1.8	
yxeA	4067204	4067551	-	714	502	534	708	0.70	0.75	0.99										
yxam yxdL	4067303	4009433	-	403	277	290	402	0.62	0.09	1.00										
yxdK	4070325	4071302	-	1339	960	948	1263	0.72	0.71	0.94										
yxdJ	4071299	4071988	-	1222	891	848	1193	0.73	0.69	0.98										
fbaB	4072097	4072969	-	2124	1512	1825	1989	0.73	0.88	0.94										
iolf iolH	4072990	4073826	-	2344	1519	1955	2169	0.66	0.85	0.92										
idh	4073912	4075835	-	3469	1977	2035	2403 3445	0.05	0.84	0.00										
iolF	4075858	4077177	-	2096	1152	1532	2063	0.55	0.72	0.98										
iolE	4077192	4078085	-	3077	1668	2362	3028	0.53	0.75	0.98										
iolD	4078102	4079844	-	3256	1536	2294	3061	0.47	0.69	0.94										
iolC	4080048	4081025	-	2192	957	1490	2070	0.43	0.66	0.94										
mmsA	4081049	4083402	-	2128	1053	1442	1850	0.41	0.01	0.99										
iolR	4083818	4084573	+	2940	1910	2011	2740	0.65	0.68	0.93										
iolS	4084627	4085559	+	8371	10949	11595	7818	1.31	1.39	0.93										
vxcE	4085821	4086471	+	2395	1755	1979	2454	0.73	0.82	1.02										

	gene					Trans	criptom	analysis		-7-				ChAP	chip a	analysis				
				Sigr	nal intens	ity of RN	$A^{a}$	Exp	ression ra	tio <sup>b</sup>		OPE				]	Binding	intensity	С	
name	start	end	strand	wild	∆abrB	∆abh ∧abrB	∆abh	∆abrB/ wild	∆abh ∆abrB/	∆abh / wild	PBR ID	or Intergenic	start	end ce	nter	Abı wild	rB Aabh	Awild	lbh ∕\abrB	Profile ID
wrcD.	4086475	4086783	+	1511	08/	1121	1/182	0.65	wild 0.74	0.08						-type		-type		
csbC	4087022	4088407	+	2167	896	1355	1126	0.42	0.65	0.51										
htpG	4088449	4090329	-	5359	9589	10372	5885	1.80	1.94	1.10										
	1000 107	1000710		2021	2271	2210	1000	1.77	1.50	0.02	1204	Inter	4090098	4090802 409	0450	24.7	38.1	5.0	-0.4	P03
yxcA yxbG	4090497	4090748	-+	2021	3361 405	533	1889 524	0.51	0.67	0.93										
yxbF	4091715	4092857	-	963	734	696	1049	0.76	0.72	1.09										
aldX	4093000	4094337	+	673	559	534	680	0.83	0.79	1.01										
yxbD	4094376	4094855	-	591	3555	3935	555	6.04	6.70	0.94	1205	Tester	4004416	4005275 400	1907	50.0	00 /	10.1	5.0	D02
yxbC	4094935	4095927	-	283	4746	5212	239	16.77	18.41	0.85	1203	mer	4094410	4093373 409	4690	32.2	00.0	10.1	5.0	P02
LD	1006126	4007170		125	1640	2000	209	2.05	4.02	0.01	1206	Inter	4095385	4096650 409	6018	55.6	100.0	34.5	2.7	P02
yxbB yxbA	4096436	409/170	+	435	1649 766	2088	398	3.85	4.92 6.30	0.91	1207	vxb A	4097170	4097296 409	7233	2.5	33	22	0.8	
yxnB	4097443	4097925	+	240	706	1000	182	2.95	4.18	0.76	1207	yxnB	4097374	4097805 409	7590	10.2	15.5	4.0	0.9	
asnH	4097946	4100189	+	333	570	687	318	1.72	2.07	0.95	1209	asnH	4098445	4098605 409	8525	3.8	2.8	5.1	2.7	
										4.00	1210	asnH	4099686	4099795 409	9741	2.9	1.3	0.8	-0.1	
ухаМ	4100186	4101385	+	410	644	776	418	1.58	1.92	1.00	1211	yxaM yxaM	4100349	4100/13 410	0531	11.3 25.0	13.2	17.4	5.5	
yxaL	4101449	4102681	-	1319	10381	10360	894	7.89	7.87	0.68	1213	yxaL	4101641	4101937 410	1789	4.8	7.5	3.9	1.5	
											1213	yxaL	4101947	4102396 410	2172	16.9	31.1	6.9	1.1	
											1213	Inter	4102406	4102991 410	2699	36.6	72.8	21.3	5.7	P02
yxa <b>J</b>	4102782	4103210	-	1612	7825	7803	1301	4.88	4.88	0.80	1213	Inter	4102899	4103858 410	3379	54.3	86.8	46.2	9.7	
yxaI	4103467	4103922	+	2936	1542	1503	1789	0.53	0.51	0.61		•								
yxaH	4103952	4105160	-	632	531	578	620	0.84	0.91	0.98	1214	yxaH	4104004	4104317 410	4161	8.4	13.4	5.5	1.6	
yxaG	4105268	4106281	-	485	375	413	449	0.77	0.85	0.93										
yxaF yxnA	4106375 4107081	4106950	-+	1570 740	6/8 413	574	551	0.43	0.37	0.85										
yxaD	4108208	4108639	-	868	636	662	863	0.73	0.76	0.99										
yxaC	4108866	4109933	+	466	337	355	467	0.72	0.76	1.00										
yxaB	4109973	4111004	-	1273	3676	4887	982	2.89	3.84	0.77										
yxaA	4111097	4112245	-	/62	2635	3841	/16	3.46	5.04	0.94	1215	Inter	4112045	4112612 411	2329	27.8	45.4	13.7	7.8	
gntR	4112441	4113172	+	4768	1579	2218	4323	0.35	0.45	0.87	1215	miler	4112045	4112012 411	2527	27.0	45.4	15.7	7.0	
gntK	4113165	4114706	+	7072	1650	3047	5936	0.23	0.40	0.81										
gntP	4114735	4116081	+	8712	2483	3854	7811	0.28	0.42	0.89										
gntZ	4110104	411/510	+	12059	4929	5849	11599	0.40	0.47	0.96	1217	Inter	4117843	4118053 411	7948	6.7	4.6	3.3	1.6	
ahpC	4117974	4118537	+	20500	21011	21407	20632	1.03	1.05	1.01										
ahpF	4118551	4120080	+	19272	20090	20722	19649	1.04	1.08	1.02										
bglA	4120190	4121629	-	8120	4860	5884	7053	0.59	0.70	0.85										
yyzE vvdK	4121043	4121873	+	1144	576	643	964	0.52	0.62	0.82		*Broad	4122721	4177332						
yydJ	4123244	4123966	-	896	6673	7320	1431	7.39	8.16	1.61		1								
yydI	4123987	4124616	-	908	7800	8804	1441	8.58	9.68	1.59		I								
yydH wydG	4124766	4125524	-	583	5566	6462	102	9.46	11.03	1.35										
yyaG vydF	4126522	4126671	-	616	19673	19736	1192	31.89	32.04	1.08		1								
fbp	4127053	4129068	+	4996	4770	5381	5746	0.96	1.08	1.15		Ì								
yydD	4129602	4131362	-	2529	1949	1981	2390	0.77	0.78	0.95		1								
yyaC vydR	4131362 4131753	4131760	-	1003	1128	669 1080	1072	0.74	0.67	1.07		1								
yydA	4133460	4133939	-	2250	1631	1534	2162	0.73	0.68	0.96		i								
yycS	4134376	4134789	+	568	499	470	527	0.88	0.83	0.93		I								
yycR	4134823	4136049	-	768	1301	1325	842	1.69	1.73	1.10		I								
yycQ yycP	4136387	4136635	-	370	466	500 324	365 328	1.28	1.36	0.99		1								
, ус <b>1</b> уусО	4137825	4138562	-	347	302	312	329	0.85	0.90	0.96		i								
yycN	4138704	4139174	-	479	841	940	490	1.76	1.96	1.02		i								
rapG	4139285	4140382	+	1081	4306	4226	930	4.05	3.97	0.86		I								
phrG rocF	4140383	4140499	+	3918 2562	11124 4386	11784 4216	3309 2445	2.84 1.74	3.01	0.84		1								
rocE	4141699	41431023	-	1462	2653	2582	1439	1.74	1.07	1.00		Ì								
rocD	4143325	4144530	-	1749	4492	4194	1834	2.64	2.48	1.09		i								
rocR	4144771	4146156	+	1180	760	.944	1095	0.64	0.80	0.93		I								
yyxA	4146591	4147793	-	5072	4525	4603	5254	0.90	0.91	1.03										
yycJ vycI	414/862 4148690	4148668	2	4821 4157	4005 3415	4294	4844 4392	0.83	0.89	1.00		1								
yycH	4149519	4150886	-	5513	4570	5026	5919	0.83	0.91	1.07		i								
yycG	4150876	4152711	-	4515	3546	4003	5111	0.78	0.88	1.13		I.								
yycF	4152719	4153426	-	2451	1889	2137	2825	0.77	0.87	1.15		I								
purA	4154457	4155749	-	9278	5238	5172	8182	0.57	0.57	0.89		I								

Supplem	entary Tal	de S1. Su	mma	ry of trai	nscriptor	me and (	hAP-ch	ip analyse	s (contin	ued).				<i>C</i> 1		<u> </u>		
	gene					Trans	criptom	e analysis		. b				Ch	AP-chip a	malysis		<u> </u>
			pu	Sigi	nal intens	ity of RN	A	Expi	ession rat	10	PBR	ORF				AbrB	Abh	Profile
name	start	end	stra	wild	∆abrB	∆abh ∆abrB	∆abh	⊿ <i>abrB</i> / wild	$\Delta abrB/$	⊿ <i>abh /</i> wild	ID	or Intergenic	start	end	center	wild <i>Aabh</i>	wild ∆ abrB	ID
yycE	4155955	4156374	-	423	403	517	415	0.95	1.22	0.98		1				-type	-type	
dnaC	4156495	4157859	-	2627	2067	2133	2684	0.79	0.81	1.02		1						
yycD	4158029	4158229	+	526	366	480	388	0.71	0.91	0.76								
yyzB yycC	4158277	4158480	-	244	3100	2924	227	0.73	0.73	0.92		1						
yyce yycB	4158814	4160022	+	4737	5199	5227	3586	1.10	1.12	0.38		1						
yycA	4160127	4162184	+	941	914	877	759	0.97	0.93	0.81		i						
rplI	4162221	4162670	-	7784	7238	6947	7316	0.93	0.90	0.94		I						
yybT	4162667	4164646	-	4171	4119	4025	4082	0.99	0.97	0.98								
yybS cotF	4166134	4165612	+	274	2881	2189	212	0.95	0.92	0.77		1						
yybR	4166646	4167023	-	402	342	455	393	0.85	1.13	0.98		i						
ppaC	4167228	4168157	+	15480	13114	13128	14588	0.85	0.85	0.94		Ì						
yybP	4168190	4168636	-	669	509	566	564	0.76	0.85	0.85		1						
yybO	4169069	4170376	+	575	380	452	412	0.66	0.79	0.71								
yybN vybM	4172689	4172373	++	1531	3457	3543	2449	2.82	2.82	1.52		1						
yybL	4173434	4174144	+	873	1740	1746	1266	1.98	2.00	1.45		i						
yybK	4174141	4174896	+	662	1322	1284	1010	1.97	1.94	1.54		1						
yybJ	4174893	4175549	+	1133	2895	2955	1700	2.57	2.64	1.51		1						
yybI	4175924	4176712	-	546	526	582	510	0.96	1.07	0.93								
yybH yybG	4170780	417/109	-	1559	1234	1326	020 1427	0.92	0.97	0.87		1						
yybG yybF	4178187	4179401	-	535	636	686	531	1.19	1.28	0.99		I						
yybE	4179630	4180466	+	539	372	399	487	0.69	0.74	0.90								
yybD	4180480	4180923	+	681	421	480	647	0.62	0.70	0.95								
yybC	4181006	4181485	+	1130	706	784	891	0.63	0.70	0.79								
yybB yybA	4181000	4182322	-	666	054 405	087 398	625	0.56	0.59	0.92								
vvaT	4183041	4183487	+	781	797	868	763	1.02	1.11	0.98								
yyaS	4183484	4184089	+	477	476	500	470	1.00	1.05	0.98								
yyaR	4184184	4184705	-	437	429	473	469	0.98	1.08	1.08								
yyaQ	4185116	4185472	+	1077	769	810	1121	0.71	0.75	1.05	1246	TWO D	4195701	4106101	1195056	96 141	16 00	
yyaP tetB	4185052	4180198	+	815 1954	480	1263	1840	0.59	0.62	0.95	1240	yyaP tetB	4185791	4180121	4185956	8.0 14.1 13.8 9.9	1.6 0.9	
1012	1100702	1100001		1701	1200	1200	1010	0.05	0.00	0.71	1248	tetB	4187610	4188161	4187886	13.2 21.9	9.7 2.6	
tetL	4188115	4188177	-	1073	615	631	1004	0.58	0.59	0.94								
yyaO	4188430	4188669	+	840	547	729	683	0.66	0.87	0.81		_						
waN	4188820	4180236	+	3/10	227	240	251	0.65	0.71	0.72	1249	Inter	4188579	4188942	4188761	7.9 19.3	1.2 1.0	
yyaN yyaM	4189233	4190150	+	405	283	338	450	0.05	0.84	1.10	1250	yyaN	4189786	4190115	4189951	10.0 10.0	3.4 1.4	
yyaL	4190222	4192291	+	2176	2076	2111	1901	0.95	0.97	0.87								
yyaK	4192288	4193187	-	2433	2420	2539	3476	0.99	1.04	1.43								
	4102412	1101760		524	150	40.2	530	0.05	0.01	0.00	1252	Inter	4192846	4193618	4193232	40.3 23.2	58.5 36.4	P01
yyaJ	4193413	4194/68	+	5 <i>5</i> 4	453	482	1103	0.85	0.91	0.98								
vvaH	4195374	4195754	-	662	665	648	629	1.01	0.98	0.95								
ccpB	4195810	4196745	-	469	494	530	409	1.05	1.13	0.87								
exoA	4196804	4197562	-	1109	681	668	969	0.62	0.60	0.87								
rpsR	4197627	4197866	-	11358	11077	10325	11602	0.98	0.91	1.02								
ssd rnsF	4197910	4198428	-	20551	20375	29511	20037	0.99	0.95	1.00		*Broad	4198711	4214630				
yyaF	4198867	4199967	-	9136	5677	5356	8397	0.62	0.59	0.92			1170/11	121 1050				
yyaE	4200094	4202097	-	2439	1322	1501	2526	0.54	0.62	1.03		Ì						
												1						
yyaD	4202448	4203464	-	418	344	396	435	0.83	0.95	1.04								
spo0.1	4203924	4205428	-	239 5628	4871	204 5325	244 5099	0.87	0.95	0.90		1						
soj	4205421	4206182	-	5902	5221	5420	5620	0.89	0.92	0.95		i						
yyaB	4206430	4206870	+	658	1223	1374	729	1.86	2.09	1.11		Ì						
yyaA	4206921	4207772	-	8924	9970	10095	8446	1.12	1.13	0.94		I						
gidB	4207894	4208613	-	8743	8095	7978	8554	0.93	0.91	0.97		I						
gidA	4208627	4210513	-	6549	5799	5804	6305	0.89	0.89	0.96		1						
trmE i	4210534	4211913	-	4161	3372	3363	4171	0.82	0.82	1.00		1						
jag	4212224	4212850	-	13967	12305	11380	15137	0.88	0.82	0.94		1						
sponij mpA	421284/	+210002	-	10320	5422	0202	6202	0.82	0.75	1.00		1						
rpmH	4214279	4214413	-	16909	16236	15697	16535	0.85	0.93	0.90								

*The approximate of the second s* 

		100 bp a	round	Б	consensus			100 bp a	round	consensus			100 bp a	round	consensus
attern	PBR ID -	top of p	beak	ID	sequence	pattern	PBK ID	top of j	Deak ID	sequence	pattern	PBR ID -	top of	peak ID	sequence
		Start	End					Start	End				Start	End	
P01	42	125834	125033 P01	1	TCCCACATTTCCTA	P02	20	69640	60730 P02 1	TATTACAAATTTCC	P03	217	678801	678000 P03_1	ATCCAACA
1 01	83	231160	231259 P01	2	TTCCTGTATTGGAA	1 02	109	303898	303997 P02_2	ND	105	235	724170	724269 P03_2	GAAAAGGG
	103	280007	280106 P01	3	ND		117.1	376211	376310 P02_3	ATACCCARATTCC		245.1	742880	742070 P03_3	CATCACCA
	105	200007	200100101		ND		117.1	570211	570510102_5	TATTGAAAACAATGA		240.1	742000	142515105_5	GAIGAGGA
	104	291687	291786 P01	_4	TCCTTTTTTTGTAA		211	658735	658834 P02_4	ND		246	744251	744350 P03_4	GAAAATGG
	107	300249	300348 P01	_5	TCCTATTTTTGGTG		328	1061805	1061904 P02_5	TTTATCCAAAATTAG		320	1018074	1018173 P03_5	AAAAACGA
	146	485528	485627 P01	_6	TTCCATTTGTGGAA		401	1336205	1336304 P02_6	AATTTCCAATATTTG		323	1044249	1044348 P03_6	AAGGAGGG
	236.1	725439	725538 P01	_7	TTCCATAATTGGAA		417	1391253	1391352 P02_7	TTTTTCCAAATTTGA		384	1276136	1276235 P03_7	AAAGAGGA
	272	843461	843560 P01	_8	ND		436	1447620	1447719 P02_8	ATTTAACAATATTTA		386	1278254	1278353 P03_8	GATGATGG
	316	970692	970791 P01	_9	ND		470	1594662	1594761 P02_9	AATAAACAAATATGA		471	1598405	1598504 P03_9	GAAAATGA
	352	1149308	1149407 P01	$_{10}$	ND		693	2305500	2305599 P02_10	AATTTAAAATACTGG		548	1910679	1910778 P03_10	GAGAAGGG
										ATTTTAAATGATTTG					
	357	1149308	1149407 P01	_11	ND		697	2324904	2325003 P02_11	ND		551	1914478	1914577 P03_1	GTTGATGG
	360.1	1185282	1185381 P01	_12	TTCCTATTTTGGAA		714	2364333	2364432 P02_12	ND		553	1920093	1920192 P03_12	GAAAAAGG
	387	1279823	1279922 P01	_13	TCCCATATTTGTCA		737	2445481	2445580 P02_13	ATTTTCCATCAGTGG TTTTTCCAAGCGTGA		565	1945141	1945240 P03_13	ATAAAGGG
	447	1492684	1492783 P01	14	ACCCAAATTTGGAA		781	2599153	2599252 P02 14	TTTATACAAAATTGA		608	2070054	2070153 P03 14	GAAGATGA
										TTTTTACAAAAAGTA					
	461	1544861	1544960 P01	15	TCCCTATAATGGAA		918	3036058	3036157 P02 15	TTGATCCAGAATTGA		677	2266253	2266352 P03 15	GAAAAGGA
										TATTTCAAGTATTTG					
	531.1	1862411	1862510 P01	_16	ND		1011	3426695	3426794 P02_16	TTTTAACAATATTGA		681	2272530	2272629 P03_10	AAGGAGGA
	598	2049845	2049944 P01	_17	ND		1077	3675985	3676084 P02_17	TATTTACAAACATGG		686.1	2280679	2280778 P03 1	GAAGATGA
	626	2115884	2115983 P01	18	TGCCATTTTTGGAA		1161	3933258	3933357 P02_18	TTTTTACATAAATGA		777	2587005	2587104 P03_18	GTGAAAGG
										CTTTTCAATAAGGGG					
	664	2220981	2221080 P01	_19	ND							796	2650769	2650868 P03_19	AAAGAAGG
	721	2388052	2388151 P01	_20	ND							809	2690795	2690894 P03_20	AAGGAGGG
	723.1	2399459	2399558 P01	_21	TTCCATTTATGGTA							819	2732619	2732718 P03_2	AAGGATGG
	860	2817528	2817627 P01	_22	TCCCATTTTTGGAT							831	2752888	2752987 P03_22	AAAAAGGG
	865	2826953	2827052 P01	_23	TCCCATTTTTGGAA							877	2883700	2883799 P03_23	GAAGACGG
	907	2988881	2988980 P01	_24	TGCCATTTTTGGAA							1171	3996469	3996568 P03_24	ATGGAGGG
	936	3116085	3116184 P01	_25	TTCCATTATTGGTT							1188.1	4029944	4030043 P03_25	ATGGATGA
	945	3152915	3153014 P01	_26	TTCCTTTTATGGTA							1188.2	4030714	4030813 P03_26	6 AAAGAGGA
	947	3161539	3161638 P01	_27	ND							1204	4090378	4090477 P03_22	GAGAATGA
	964	3194509	3194608 P01	_28	TTCCATTTATGGGA										
	968	3214653	3214752 P01	_29	TGGTATATTTGGAA										
	969	3216471	3216570 P01	_30	TACCATTTATGGTA						P04	97	277401	277500 P04_1	ATGGGCATACCA
	993	3343001	3343100 P01	_31	ND							322	1043346	1043445 P04_2	CAGGGAAATCCA
	1015	3449965	3450064 P01	_32	ND							355	1172252	1172351 P04_3	TTGGAAAATCCA
	1042	3581792	3581891 P01	_33	ND							415	1389362	1389461 P04_4	CTGCAAATTCCA
	1043	3589456	3589555 P01	_34	ND							524	1811449	1811548 P04_5	CTGGAAAATCCA
	1107	3746091	3746190 P01	_35	TGCCATTTTTAGAG							573	1970315	1970414 P04_6	CTGGAGCTTCCA
	1168	3981897	3981996 P01	_36	ND							703	2333355	2333454 P04_7	CTGGGAATACCA
	1170	3995386	3995485 P01	_37	ND							711	2361095	2361194 P04_8	CTGGAAAAACCG
												754	2511426	2511525 P04_9	ATGGGGAAAACA
												824	2743786	2743885 P04_10	CTGAAAATACCA
												886	2908862	2908961 P04_1	AAGGAAATTCCA
												1181	4018359	4018458 P04_12	AAGGGAATTCCA



















310 ,000 bp





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	ן איז ערעע איז	ي يايرييان بينا، بال يسايياتيا با با باينيان	իկ վվա անհանդերի անհանդերություններ		ւ - ս հանկեսի երկույի դեսի հանկես է ու ե	լ, այստեղակակություն երակակարություն
	ու հերկանություն հայուրը։ Ու հերկանություն	Աստասիսի է հետանակություն։ Աստանություն	իսի անդրանները է ներագրությունները է ներանությունները է ներանությունները է ներանությունները է ներանությունները ն	undinational to the condition of the second se	ւ ու հայրին անդերին կանությունը։	եսիների անդարերությունը։ Իստեսին անդարերին անդարություն











480,000bp			490,000bp
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	ունական գիներին կնկկովիցուի արաստաններինը, այս անգերինը ուրդ են Դուսի արդությունը արտ թուր ուրդ ընդերինը արդությունը էրությունը Դուսի արդությունը արտ թուր ուրդ էրությունը արդությունը են էրությունը էրությունը էրությունը էրությունը էրությունը		
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184	<u></u>	185 18	<u>36 (P02)</u>	187	188	<u></u>	189	<u></u>
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## 620,000bp































# 1,020,000bp











# 1,120,000bp







# 1,220,000bp

1,310,000bp





1,320,000bp

1,330,000bp	1,340,000bp
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ավորությունը՝ երկանությունը՝ հանդարանությունը՝ էր հանդարանությունը՝ էր հանդարանությունը՝ էր հանդարանությունը՝ հ Անհանդարանությունը՝ հանդարանությունը՝ հանդարանությունը՝ հանդարանությունը՝ էր հանդարանությունը՝ էր հանդարանությո		տուսու արտարությունը է արտարությունը հայտարանությունը։	



















		bb. uhu.
վ մահանու հմեստովետ հայտնակությունները		
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1,910,000bp





1,920,000bp













2,120,000bp









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# 177

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3,120,000bp



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3,310,000bp

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3,460,000bp



уvgР

*yvg*Q

уvgR

# Fig. S1-35

188

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	<b>Fig. S1-36</b> 189			

3,530,000bp

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	- t
1028	
wfG weT	
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3,540,000bp





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# Fig. S1-37 190

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3,670,000bp

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### 3,810,000bp



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					-սուսիս ինչ էն, ու ուսես է երերուսը -սուսիս ինչ ինչ է երերություն ու երերություն -սուսիս ինչ է երել է երերություն երերություն երերություն երերությու		 	
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				հեռում վետերինը, հաշերտերն Դուլի արտարություն		ովս.ս.ս.ս.ս.սնակներերերի ուորութորություրը		
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						Fi	<b>j. S1-3</b> 192	9













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	<u>հակես հմիս տեւնեւ</u> 	աղմուլուանդւնակովուկիրու 
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		ուն անագաններներուներուն, որ է որոշ ու է է որ լապապատասի թարություն որությունները 			
		որ արուսիրությունը հերուներ հերուներ			





Supplementary Figure S1. The entire dataset of AbrB and Abh binding profiles, and transcriptional profiles in wild-type and mutant cells. AbrB binding signals in wild-type and  $\Delta abh$  backgrounds, and Abh binding signals in wild-type and  $\Delta abrB$  cells, are shown above the schematic representation of gene arrangement, as in Figure 11A. PBRs are indicated by pink boxes, with ID numbers, below the binding profiles. Eight broad regions with contiguous binding signals are also indicated by gray boxes. Transcriptional signals in wild-type (168), OC003 ( $\Delta abrB$ ), OC005 ( $\Delta abrB\Delta abh$ ), and OC004 ( $\Delta abh$ ) cells are shown under the gene map, as in Figure 17 of the main text. Ribosomal RNA genes are indicated in red in the gene map. The raw and normalized data are available from the ArrayExpress database using the accession code E-MEXP-2774 and E-MEXP-2776 for ChAP-chip and transcriptome results respectively.