

**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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<p>題目</p>	<p>Distribution of AbrB and Abh on the <i>Bacillus subtilis</i> genome and its implication on their function</p>
<p>AbrB is a global transcriptional regulator of <i>Bacillus subtilis</i> 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.</p> <p>Here, for the first time, we report the <i>in vivo</i> distribution of AbrB and Abh on the <i>B. subtilis</i> 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 <i>in vivo</i> and that hetero-complex were dominant to homo-complexes. ChAP- chip analysis of <i>abrB</i> and <i>abh</i> mutants indicated that AbrB/Abh binding regions contain various types of sequences with</p>	

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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LIST OF CONTENTS

LIST OF TABLES	iv
LIST OF FIGURES	iv
LIST OF SUPPLEMENTARY TABLES	vi
LIST OF SUPPLEMENTARY FIGURES	vi
INTRODUCTION	1
1. Regulation of the <i>abrB</i> expression	4
2. Mode of transcription regulation by AbrB	5
3. Structure of the AbrB protein	6
4. Characteristics of AbrB as a nucleoid associated protein	7
5. Conservation of AbrB protein in bacteria	8
MATERIALS and METHODS	11
1. Bacterial strains, and growth conditions	11
2. Primers	12
3. Construction of <i>B. subtilis</i> strains expressing AbrB C-terminally tagged with 12 histidines and a chitin-binding domain (AbrB-2HC), and an analogous form of Abh (Abh-2HC)	13
4. Construction of $\Delta abrB$, Δabh , and double mutant strains	14
5. Antibody production and purification	15
6. <i>In vivo</i> interaction of AbrB and Abh	17
7. Determination of the molecular numbers of AbrB and Abh molecules in <i>B. subtilis</i> cells	18
8. Analysis of AbrB and Abh interaction <i>in vitro</i> by Native-PAGE	20

LIST OF CONTENTS (continued)

9. ChAP-chip analysis	20
9.1 ChAP-chip procedure	20
9.2 Data normalization	21
9.3 Detection and quantitative analysis of AbrB/Abh binding sites	22
10. High-resolution transcriptome analysis	25
11. Overexpression of Abh in wild type 168 strain	25
11.1 Construction of $\Delta rsiX$ strains	25
11.2 Construction of plasmid for over-expression of Abh from the <i>spac</i> promoter	26
11.3 Determination of Abh expression in overexpressing cells (OC009) compared to that of in $\Delta rsiX$ strain (OC008)	26
RESULTS	27
1. AbrB and Abh form homodimers and heterodimers <i>in vivo</i>	27
2. AbrB and Abh interaction <i>in vitro</i>	33
3. Profiling of genome-wide AbrB and Abh binding sites	34
4. Most Abh binding sites overlap with those of AbrB in wild-type cells	39
5. AbrB markedly influences Abh-binding profile, whereas Abh has a minor effect on AbrB binding	39
6. A TGGNA motif identified <i>in vitro</i> acts as a determinant not only for AbrB but also for Abh binding <i>in vivo</i>	45
7. AbrB plays a major role in control of gene expression whereas Abh has a minor effect	49

LIST OF CONTENTS (continued)

8. Genome-wide correlation between AbrB/Abh binding and transcription levels	63
9. Overexpression of Abh counteracts the repression effect mediated by AbrB at the sublancin operon	65
DISCUSSION	68
ACKNOWLEDGEMENTS	80
REFERENCES	82
SUPPLEMENTARY DATA	90

LIST OF TABLES

Table 1.	<i>B. subtilis</i> strains used in this study	11
Table 2.	Primers used in this study	12
Table 3.	Classification of 160 PBRs with clear binding profiles	44
Table 4.	Coincidence of various paired TGGNA motifs with AbrB/Abh peaks on the <i>B. subtilis</i> genome	48
Table 5.	Possible TUs directly regulated by AbrB and/or Abh	53
Table 6.	Comparison of the data of the present study with previously reported information on AbrB- and/or Abh-regulated operons	62

LIST OF FIGURES

Figure 1.	AbrB regulation of transition state gene expression	3
Figure 2.	Secondary and quaternary structures of AbrB	7
Figure 3.	Alignment of AbrB and Abh	10
Figure 4.	Normalization of ChAP-chip results	23
Figure 5.	Detection of AbrB/Abh binding sites	24
Figure 6.	Western blot analysis of the cross-reactivity of AbrB and Abh antibody before and after purification	28
Figure 7.	Growth rates and transcriptosome profiles of OC001 (abrB-2HC) and OC002 (abh-2HC) cells	29
Figure 8.	AbrB and Abh interaction <i>in vivo</i>	31
Figure 9.	Determination of AbrB and Abh concentrations in exponentially growing wild-type cells	32

LIST OF FIGURES (continued)

Figure 10. Interaction of AbrB and Abh <i>in vitro</i>	34
Figure 11. AbrB and Abh binding signals on the <i>B. subtilis</i> genome	37
Figure 12. Quantitative evaluation of AbrB/Abh binding sites	38
Figure 13. Comparison of AbrB and Abh binding signals in various strains	41
Figure 14. Classification of PBRs according to AbrB and Abh binding profiles	43
Figure 15. Consensus sequences for AbrB/Abh binding	46
Figure 16. Transcriptome analysis in $\Delta abrB$ and Δabh deletion mutants	49
Figure 17. AbrB/Abh binding profile in the promoter region of gene repressed by AbrB	61
Figure 18. AbrB/Abh binding to actively transcribed regions	64
Figure 19. Abh expression level in <i>abh</i> -overexpressing cells compared to that of in $\Delta arsIX$ cells	66
Figure 20. Activation of sublancin operon in Abh overexpressing cell	67
Figure 21. Binding model of AbrB and Abh	73

LIST OF SUPPLEMENTARY TABLES

Table S1. Summary of transcriptome and ChAP-chip analyses	91
Table S2. Sequences used for motif extraction	153

LIST OF SUPPLEMENTARY FIGURES

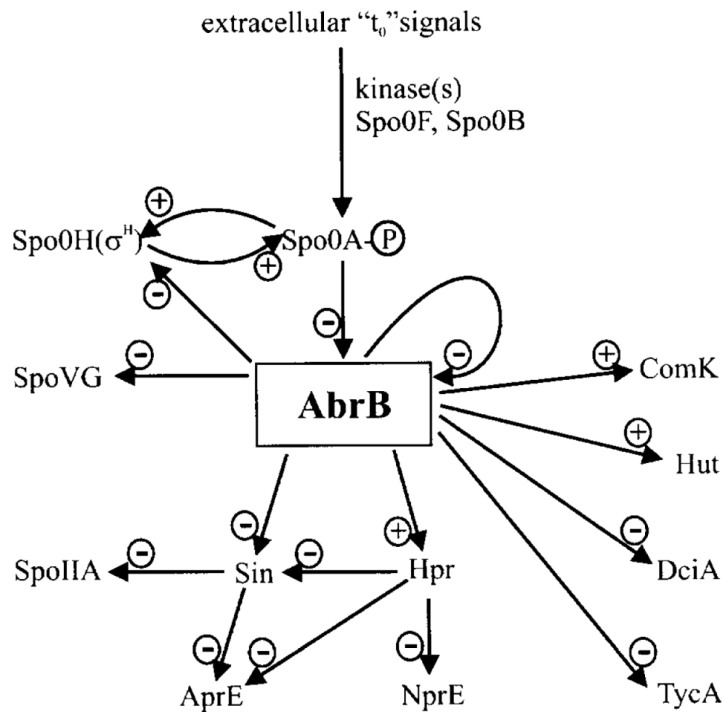
Figure S1. The entire dataset of AbrB and Abh binding profiles, and transcriptional profiles in wild-type and mutant cells	154
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INTRODUCTION

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 preceding 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.



<u>protein:</u>	<u>cellular function:</u>	<u>response:</u>
AbrB	major transition state regulator	growth state sensing
AprE	subtilisin protease	alternative resources
ComK	transcription of competence genes	competence development
DciA	ABC transporter for dipeptides	alternative resources
Hpr	transition state regulator	growth state sensing
Hut	histidase (histidine utilization)	alternative resources
NprE	neutral protease	alternative resources
Spo0A	major response regulator for sporulation	sporulation
Spo0H	alternative σ^H for sporulation	sporulation
SpoIIA	regulation of alternative σ^F	sporulation
SpoVG	maturation of spore cortex	sporulation
TycA	tyrocidine biosynthesis	secondary metabolite formation

Figure 1. AbrB regulation of transition state gene expression. (+), positive regulation; (-), negative regulation. The formation of the phosphorylated active form of Spo0A occurs at the end of exponential growth by a phosphorelay which is summarized here. t_0 means time zero according to the sporulation pathway. The components of this regulatory circuit and their cellular functions are summarized. From (Klein & Marahiel, 2002)

1. Regulation of the *abrB* expression

The *abrB* (Antibiotic resistance protein B) 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 AbbA, a 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 constitutive 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).

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 β -strands, one α -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 β 1 and β 2, and LP2, which connect α 1 and β 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.

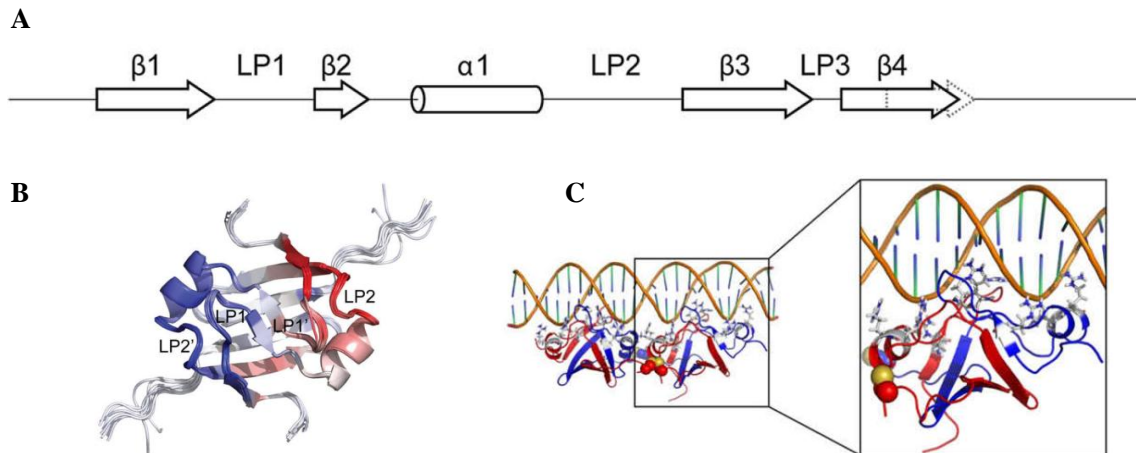


Figure 2. Secondary and quaternary structure of AbrB. (A) Schematic diagram showing the positions of the α -helical and β -strand secondary structure, as well as loop regions of AbrB N-terminal DNA binding domain. (B) The a swapped-hairpin barrel formed by of two molecules of AbrB N-terminal domain. (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, nucleoid-associated 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 nucleoid-associated 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, <http://mbgd.genome.ad.jp/>), 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.

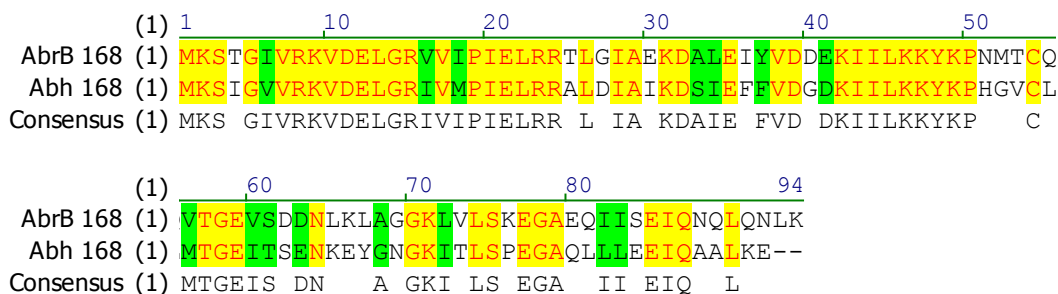


Figure 3. Alignment of AbrB and Abh. Identical residues are shown in yellow, similar residues are shown in green and dissimilar residues are shown in white.

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.

MATERIALS 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 µg/ml kanamycin (Km), 150 µg/ml spectinomycin (Spec), 0.5 µg/ml erythromycin (Erm), and/or 5 µg/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 OD₆₀₀ value of 0.01.

Table 1. *B. subtilis* strains used in this study

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

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

^b 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. Primers used in this study

Name	sequence ^{a b}	Position on <i>B. subtilis</i> genome or template DNA			Reference
		start	end	strand	
2H	TCAATAGTAAACAAAATGATTGACG	45,235	45,259	-	
abrB-FR-2HC	ggtgatgcatcctctcatTTAAGGTTTTGAAGCTGGTTTTG	44,849	44,872	+	
abrB-BF	cggaaggataactacatcctggCCTTAAATAATCATTCTTGTAC	44,833	44,855	-	
abrB-BR	AGAAAAGAAGAGGAGCTTGAAGCC	44,377	44,401	+	
abh-FF	TATCTTGAATCTTATAGAAAGCG	1,517,050	1,517,074	+	
abh-FR-2HC	ggtgatgcatcctctcatTCTTTTAAAGCGGCTTGAATTC	1,517,424	1,517,447	-	
abh-BF	cggaaggataactacatcctggCGCTTAAAGAATAAAATATGCG	1,517,435	1,517,458	+	
abh-BR	TTTTCTTAACCGCTGCTGTTTT	1,517,813	1,517,835	-	
abh2HC_CF	GGTGTGCGTCGGTAAAGAAATGTTTTTG	1,516,964	1,516,991	+	
abh2HC_CR	GCATTCGTTTGAATACGATTCCTGCG	1,517,900	1,517,926	-	
abrB2HC_CF	AAAGGATTTTAGTAGGATAATAGC	45,337	45,361	-	
abrB2HC_CR	GCATTACAGCTCTTATTGCTTCAGG	44,300	44,325	+	
abrB-metS-F	AGGACGAGAGCGGCGATAAG	45,569	45,588	-	
abrB-metS-R	gctcttctggaggagctctatccCATCTCTCCCAAGAGATAC	45,134	45,154	+	
abrB-yabC-F	cggaaggataactacatcctggAAACTTGCAGCGGTAATTTG	44,915	44,935	-	
abrB-yabC-R	GAGATCGGAAATTTGCTGTAACAC	44,487	44,510	+	
U-abh-F	CTGATGGTGTGCAACGACTACGTTCCG	1,516,567	1,516,594	+	
U-abh-R	gctcttctggaggagctctatccGGATGTACCTCAATATATCG	1,517,104	1,517,123	-	
D-abh-F	cggaaggataactacatcctggCTGCTTCTCGAAGAAATCAAGCC	1,517,411	1,517,435	+	
D-abh-R	AACCCGGTTTAGATGCCACGCTTGG	1,517,951	1,517,977	-	
abh-gwF	aaaaagcaggctcgCATCCTTAAACATTACATGAG	1,517,119	1,517,140	+	
abh-gw-r	agaaagctgggtcGCATAATTTTATCTTTTAAAGCGG	1,517,434	1,517,458	+	
abrB-B1-F	aaaaagcaggctcgATTTAAACAAATAAGTATCTCTTGG	45,144	45,168	-	
abrB-B1-R	AACTACACCTCCTAATTCATCAAC	45,080	45,103	+	
abrB-B2-F	CGTAAAGTTGATGAATTAGGAC	45,088	45,109	-	
pPAL7-abrB-F1	aagctttgAAATCTACTGGTATTGTACGTAAAGTTG	45,100	45,127	-	
pPAL7-abrB-R	aattcttaTGATTATTTAAGGTTTTGAAGCTGG	44,843	44,867	+	
pPAL7-abh-F	aagctttgAAATCAATAGGTGTGTGAGAAAAG	1,517,175	1,517,199	+	
pPAL7-abh-R	aattcttaGCATAATTTTATCTTTTAAAGCGG	1,517,434	1,517,458	-	
DrsIX-F-f	AGAAGACCTTCTCAAGAGGTTTATATCCG	2,414,287	2,414,316	-	
DrsIX-F-r	gctcttctggaggagctctatcc CCTGAGGCGAACGATGGTCTTTAACTGCCG	2,413,801	2,413,830	+	
DrsIX-B-f	cggaaggataactacatcctgg ATATGACATATCAGATGCAATTCGGTGGCC	2,412,810	2,412,839	+	
DrsIX-B-r	GGATTGCCGATTCAGCAAGCAAGATAGG	2,412,352	2,412,381	+	
sigX-u-F	TGAACGGAGGGGTTTCAAATGGAAGAAACC	2,414,394	2,414,423	-	
rsIX-d-r	AAGTCGTGATTTGACATCACCACATAGACG	2,412,234	2,412,263	+	
pPAL7-F	CAAATATGTAGACGCAGCTAGCGC	pPAL7			Bio-Rad
pPAL7-R	ATTGCTCAGCGGTGGCAGCAG	pPAL7			Bio-Rad
DC-2HC-F	ATGAGAGGATCCGATCACC	pMUTm2HC			This study
DC-2HC-R	gctcttctggaggagctctatccTCATCTATTTATTGAAGCTGC	pMUTm2HC			This study
rPCR-CmF2	ggatagactccaccagaagagcATCATCGGCAATAGTTACCC	pDLT3			Morimoto T. et al, 2002
rPCR-CmR2	ccaggatgtagtctcctccCGGCGTAGAGGATCTGGAGC	pDLT3			Morimoto T. et al, 2002
rPCR-KmF	ggatagactccaccagaagagcCGCAAGCTTACGATAAACCCAGC	pDG780			Guerout-Fleury AM et al, 1995
rPCR-KmR	ccaggatgtagtctcctccCGTAGTACTAAAACAATTCATCC	pDG780			Guerout-Fleury AM et al, 1995
rPCR-SpecF	ggatagactccaccagaagagcTCGAGTTCAAAAATATATGGAGATCG	pJL62			Ishikawa S et al, 2006
rPCR-SpecR	ccaggatgtagtctcctccCGTAGGTTATTGCAATAAAATAGCC	pJL62			Ishikawa S et al, 2006
rPCR-ermR	ggatagactccaccagaagagcAACAAATAGGGTTCCCGCGCA	pMUTm2HC			This study
rPCR-ermF	ccaggatgtagtctcctccCGTCATAGAATTTATCTCTCCG	pMUTm2HC			This study
pM12HisRattB2	ggggaccactttgtacaagaagctgggtcGAGCTCTCATCTATTTAATGG	pMUTmHis & pMUTm2HC			This study, Ishikawa S et al, 2006
Adapter-attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTCG	attB1 site			Invitrogen
Adapter-attB2	GGGGACCACCTTTGTACAAGAAAGCTGGGTC	attB2 site			Invitrogen
OidFNru3	CCTCTAGAGTCAAATGTGAG	pMUTmHis & pMUTm2HC			This study, Ishikawa S et al, 2006
TerRSmalb	cgcgccggggGGGTTATTGCTCATGAGCG	pMUTmHis & pMUTm2HC			This study, Ishikawa S et al, 2006
pDONR-F	TCCGTTAAGCGTAGCATGGATCTCG	pDONR201			Invitrogen
pDONR-R	GTGCTCAAATCTCTGATGTTAC	pDONR201			Invitrogen
2HC-F	<u>gccgctcgagcaattcccgggctcgag</u> ATGAGAGGATCGCATCACC	pO2HCGW			This study
2HC-R	<u>gccgagctcTCATCTATTTATTGATGCTGCACAGGCAGG</u>	pO2HCGW			This study

^a Lowercase letters indicate annealing sequences for recombinant PCR.

^b 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 chitin-binding 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 *StuI* 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 *SalI* and *SacI* 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 Δ *abrB*, Δ *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 Δ *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 Δ *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 DH5 α , respectively.

E. coli C600 cells harboring pO-abrB12xhis and DH5 α cells with plasmid pO-*abh12xhis* were grown in 400 ml aliquots of LB medium supplemented with 5 μ g/ml tetracycline, at 37°C with vigorous shaking. When cell cultures attained OD₆₀₀ 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 μ l 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 cross-reacted with AbrB and Abh or with other *B. subtilis*-encoded proteins. In brief, all proteins extracted from OC003 (Δ *abrB*) and OC004 (Δ *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 Δ *abrB* and Δ *abh* cells, respectively, were bound. Antibodies in the flow-through 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 OD₆₀₀ 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 µg/mL and RNase A to 200 µg/mL, respectively, for 30 min at 37°C in the presence of 10 mM MgCl₂. 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 β-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 anti-rabbit 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 eXactTM 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 Δ *abrB* and Δ *abh* mutants, were cultured to OD₆₀₀ values of 0.4 in LB medium, and harvested. Cells were washed once with chilled killing buffer [20mM Tris-HCl (pH. 7.5), 5mM MgCl₂, 20mM NaN₃] and store frozen 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 Δabh cells, respectively. Wild-type, $\Delta abrB$, and Δabh 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] β -mercaptoethanol, 0.01% [w/v] bromophenol blue) and boiled for 10 minutes at 95°C. To detect AbrB, cell lysates from 0.05 OD₆₀₀ units of wild-type and Δabh 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 OD₆₀₀ 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 OD₆₀₀ unit at OD₆₀₀ of 0.4 was determined by counting on bacteria counting chamber (Erma). The cells were cultured in the same manner as describe above. At OD₆₀₀ of 0.4, about two OD₆₀₀ 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 μ l 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 μ l 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 (2 μ g) 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 μ 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) Nadeoxycholate, 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 β -mercaptoethanol was added instead of 1 mM DTT). Dynabead Talon (100 μ 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 ≤ 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):

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

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 $\bar{Q}_{0.5}$ 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 Δabh (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 95th 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 40th percentile value; see Figure 4B).

1.5-fold the interquartile range of the 25th 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 40th and 90th percentile values, corresponding to probe intensities of 0.4 and 0.88, used as background and peak threshold values, respectively, are indicated.

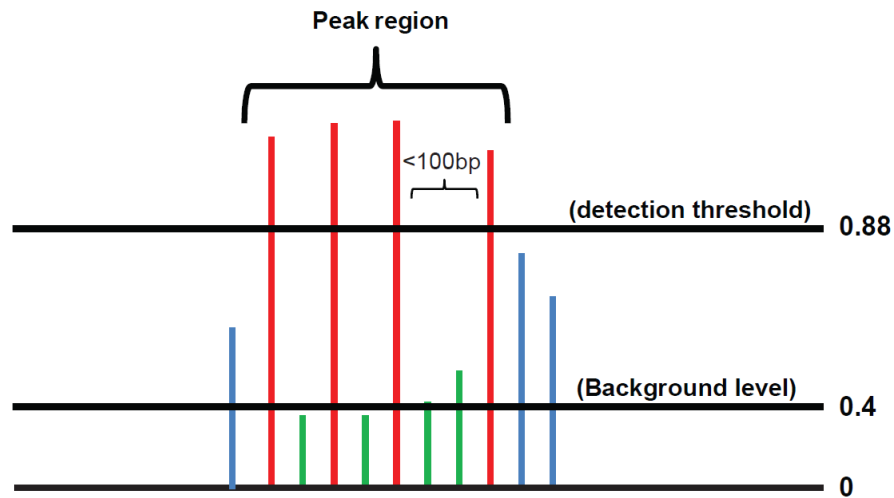


Figure 5. Detection of AbrB/Abh binding sites. Regions where at least four probes (indicated in red), with between-probe intervals of less than 100 bp, yielded signal intensities above the threshold value of 0.88 were computationally extracted for various strains (Peak regions). Next, regions overlapping 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 (OD₆₀₀ 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 Construction of Δ *rsiX* 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 Drs*iX*-F-f/Drs*iX*-F-r and Drs*iX*-B-f/Drs*iX*-B-r, respectively. A erythromycin-resistance gene with a promoter region was amplified from plasmid pMutiHis (Ishikawa et al, 2006) using primers rPCR-ermF and rPCR-ermR. The resulting three fragments were joined by recombinant PCR using primers Drs*iX*-F-f and Drs*iX*-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 Δ 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 OD₆₀₀ 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[®] SD Semi-Dry Electrophoretic 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 Δabh background (strain OC006) and Abh-2HC in a $\Delta abrB$ background (strain OC007).

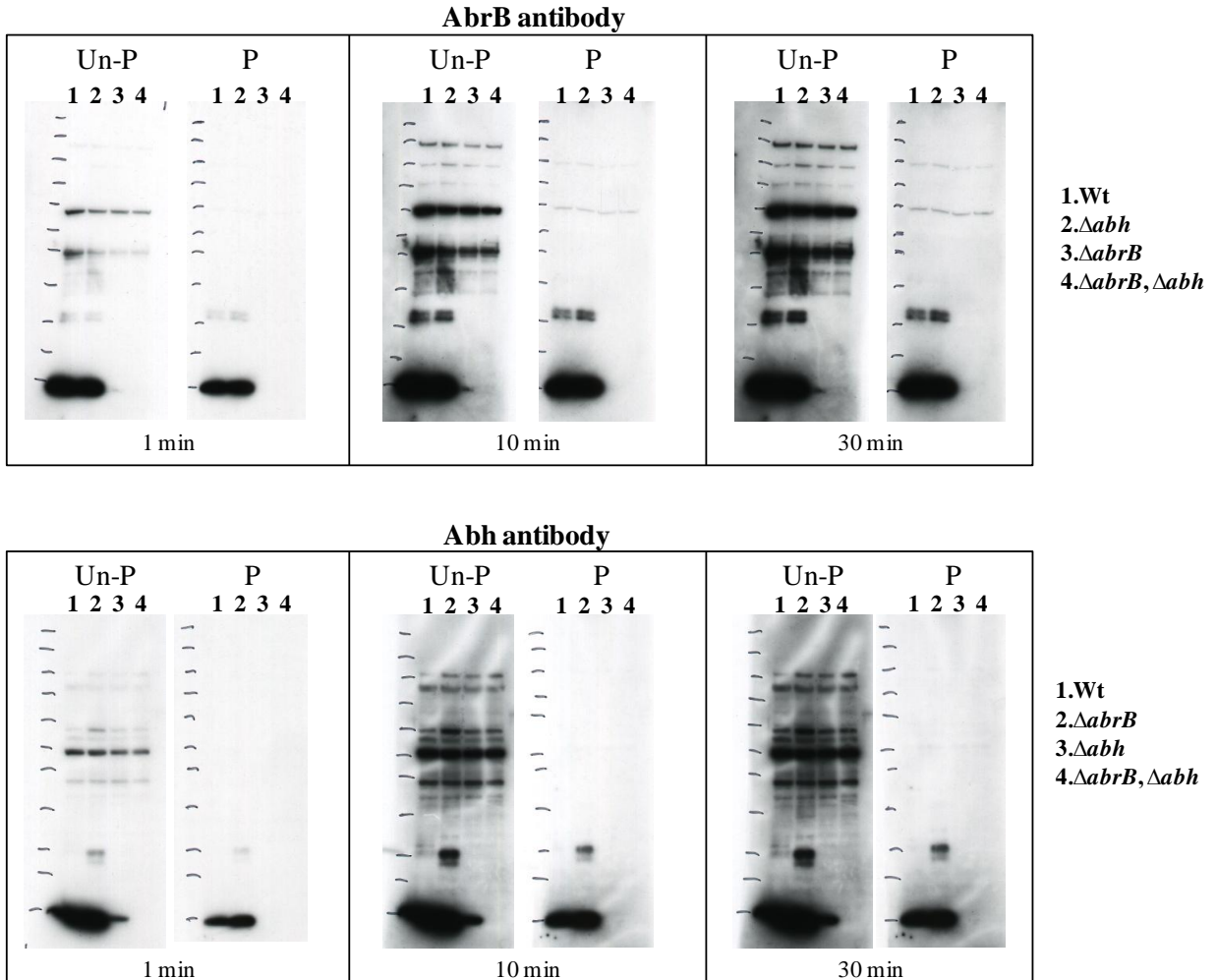


Figure 6. Western blot analysis of the cross-reactivity of AbrB and Abh antibody before and after purification. The same amount (0.1 OD₆₀₀ unit) of cell lysate of wild type *Bacillus subtilis* 168 (wt), $\Delta abrB$, Δabh and $\Delta abrB \Delta abh$ mutant strains were separated by SDS-PAGE in the 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.

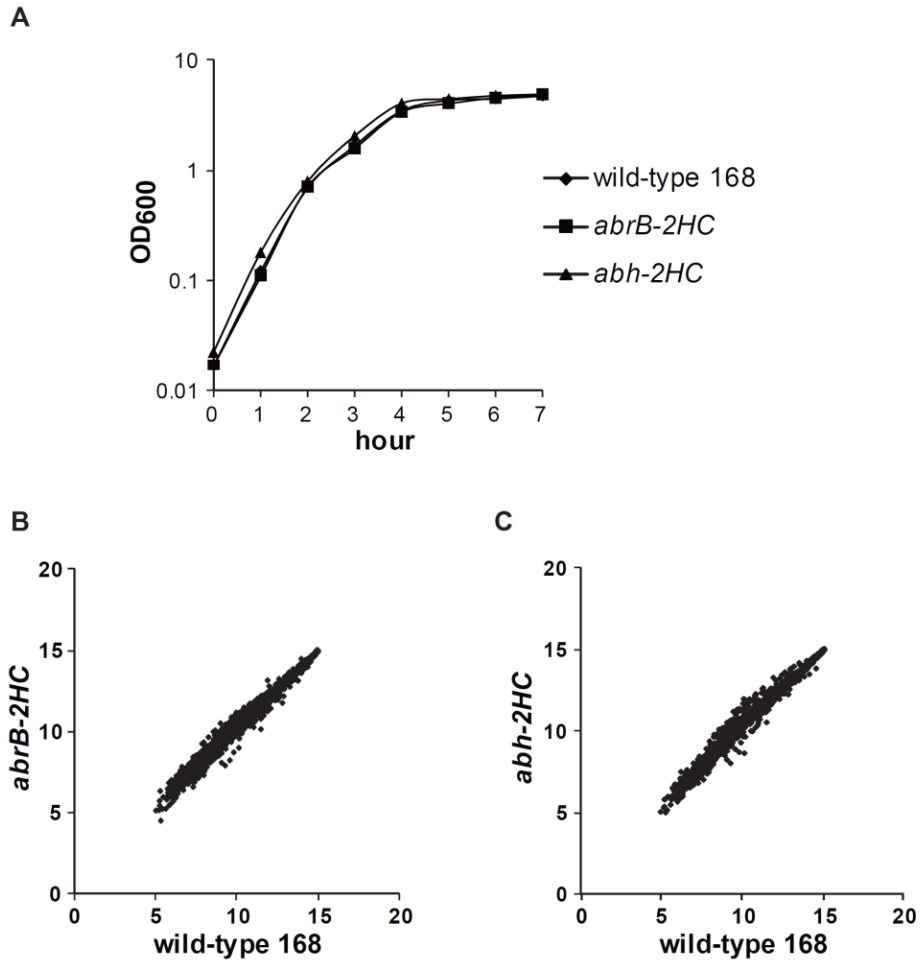


Figure 7. Growth rates and transcriptome profiles of OC001 (*abrB-2HC*) and OC002 (*abh-2HC*) cells. (A) Growth curves of *abrB-2HC*, *abh-2HC*, and wild-type cells in LB medium at 37°C. (B) A log-scale scatter plot of the transcriptional intensity of each gene in exponentially growing *abrB-2HC* (y-axis) 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 Δabh 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 C-terminal 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 Δabh 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 $32,700 \pm 6,500$ and $45,600 \pm 6,900$ 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 Δabh 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.

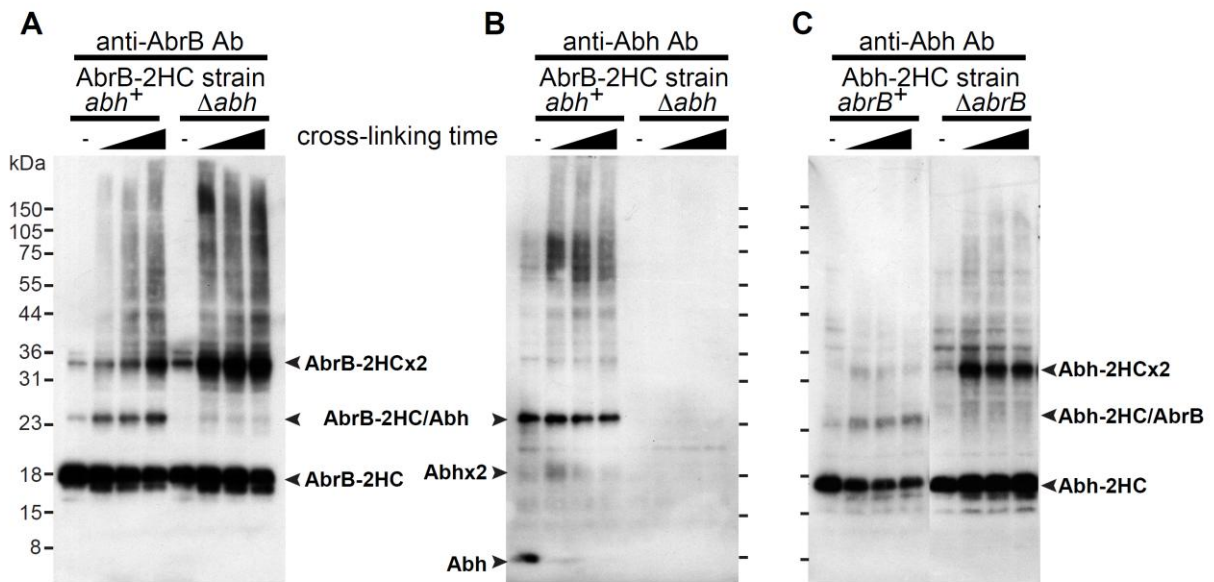


Figure 8. AbrB and Abh interaction *in vivo*. Western blot analysis of exponentially growing *B. subtilis* cells, either untreated or treated with 2 mM DSP for 5, 15, or 25 minutes. Lysates of cells expressing AbrB-2HC in the *abh*⁺ or Δabh background were probed using anti-AbrB antibody (A) or anti-Abh 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.

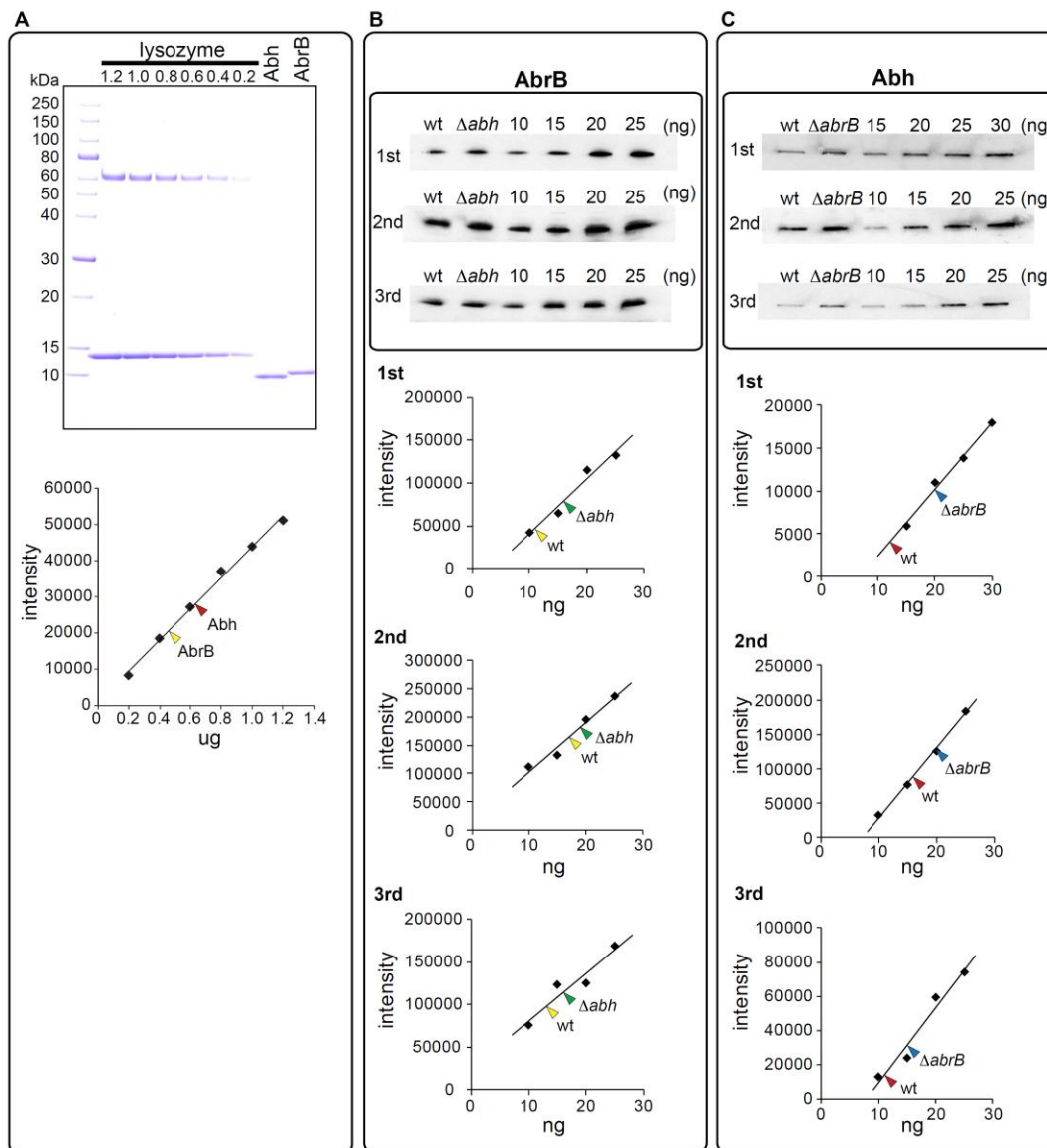


Figure 9. Determination of AbrB and Abh concentrations in exponentially growing wild-type cells. (A) Coomassie Brilliant Blue staining of purified tag free-AbrB and -Abh proteins (5 and 10 μ l amounts, respectively) separated by 10-20% (w/v) SDS-PAGE, together with various amounts (0.2-1.2 μ g) of lysozyme. The concentrations of purified AbrB and Abh proteins were determined to be 94.2 and 64.3 ng/ μ l, respectively, using the standard curve shown below the gel image. (B) In-gel chemiluminescence detection of AbrB in wild-type (wt) and Δabh cells using anti-AbrB antibody. The levels of AbrB in wild-type and Δabh cell lysates were determined using the standard curves indicated below the gel images. Protein molecular numbers per cell were calculated assuming that 1 OD₆₀₀ unit contained 2.41×10^8 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.

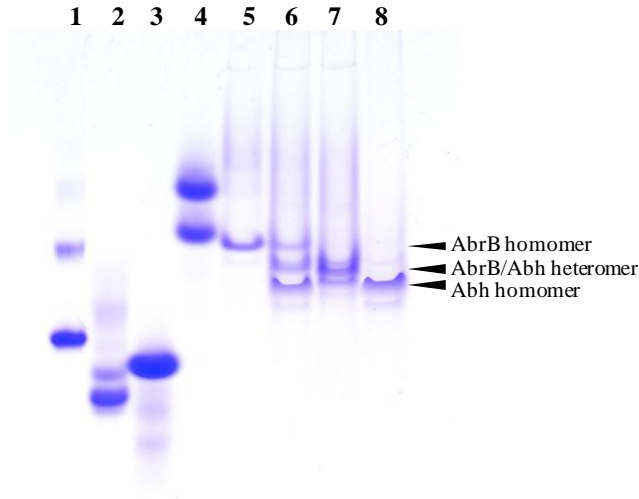


Figure 10. Interaction of AbrB and Abh *in vitro*. Native-PAGE analysis of AbrB and Abh; 1: BSA, 2: chicken egg albumin, 3 α -lactalbumin, 4: carbonic anhydrase, 5: AbrB, 6: AbrB and Abh mixture incubated at 25°C, 7: AbrB and Abh mixture incubated at 42°C, 8: Abh. Migration of AbrB homomer, AbrB/Abh 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*⁺), OC002 (*abh-2HC abrB*⁺), OC006 (*abrB-2HC Δ abh*), and OC007 (*abh-2HC Δ 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 Abh-binding 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 25th, 50th, 75th, and

100th 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.

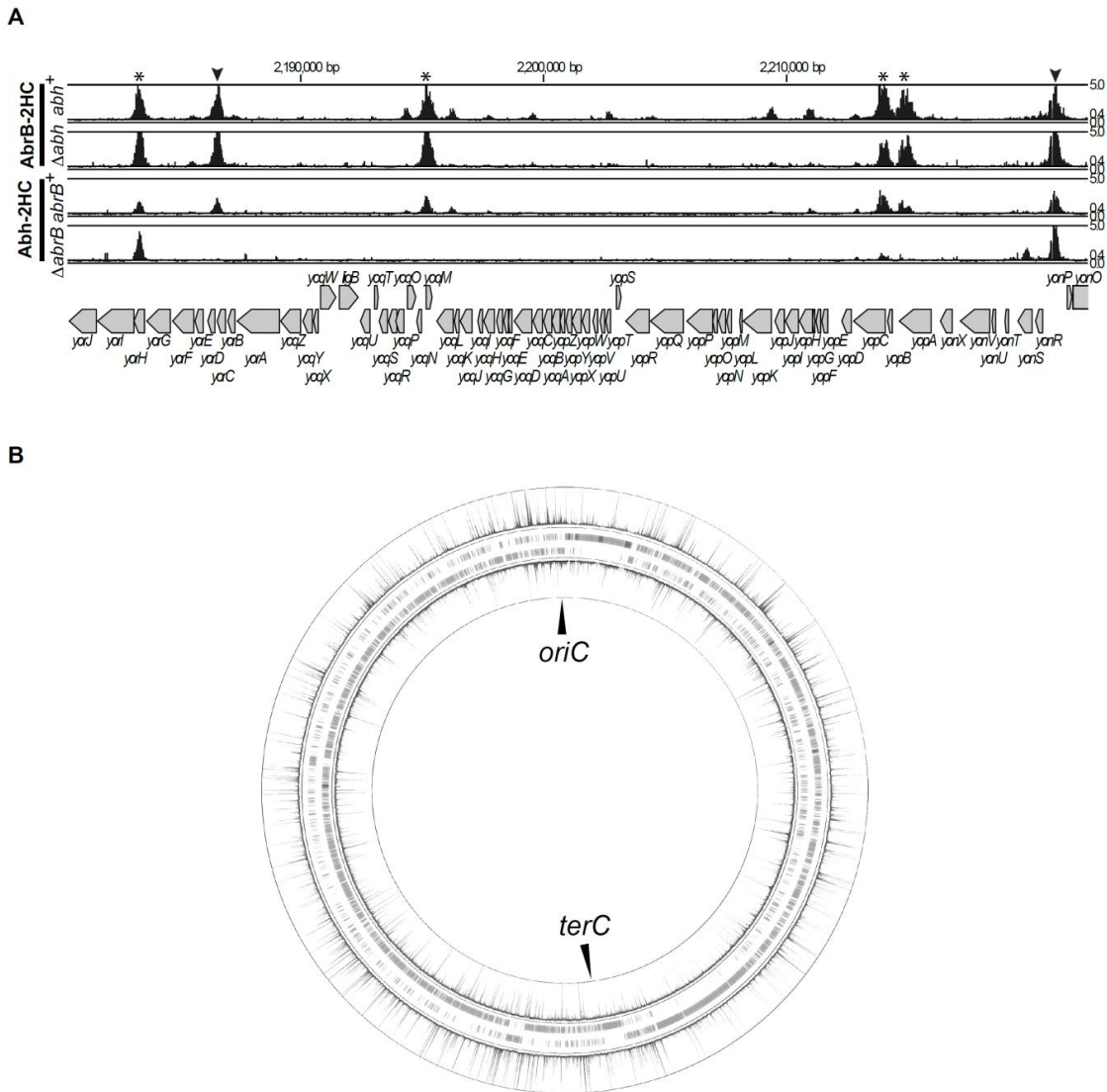


Figure 11. AbrB and Abh binding signals on the *B. subtilis* genome. (A) Distributions of AbrB binding signals in the *abh*⁺ and Δabh backgrounds, and Abh binding signals in *abrB*⁺ and $\Delta abrB$ backgrounds, in the 2,180,000 bp to 2,222,000 bp region of the genome, are shown. Protein-binding signals 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.

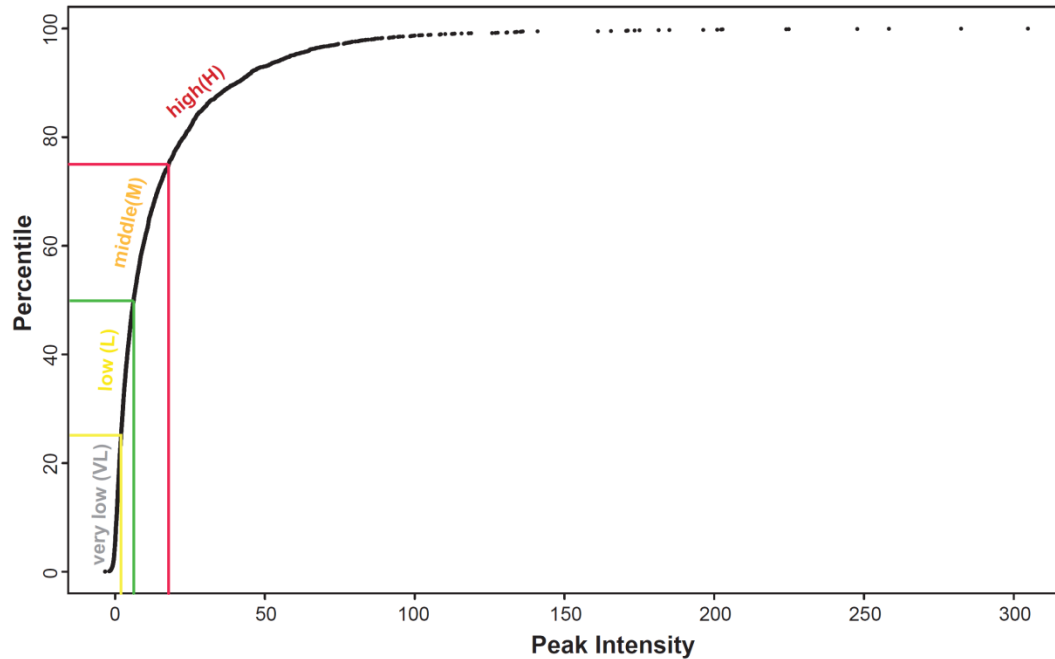


Figure 12. Quantitative evaluation of AbrB/Abh binding sites. Cumulative plots of the percentiles of number of PBRs (y-axis) against increasing AbrB or Abh binding intensities in the four strains (x-axis). The 25th, 50th, and 75th percentile values, corresponding to binding intensities of 2.0, 6.2, and 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 Δ *abh* cells and Abh binding in *abrB*⁺ and Δ *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

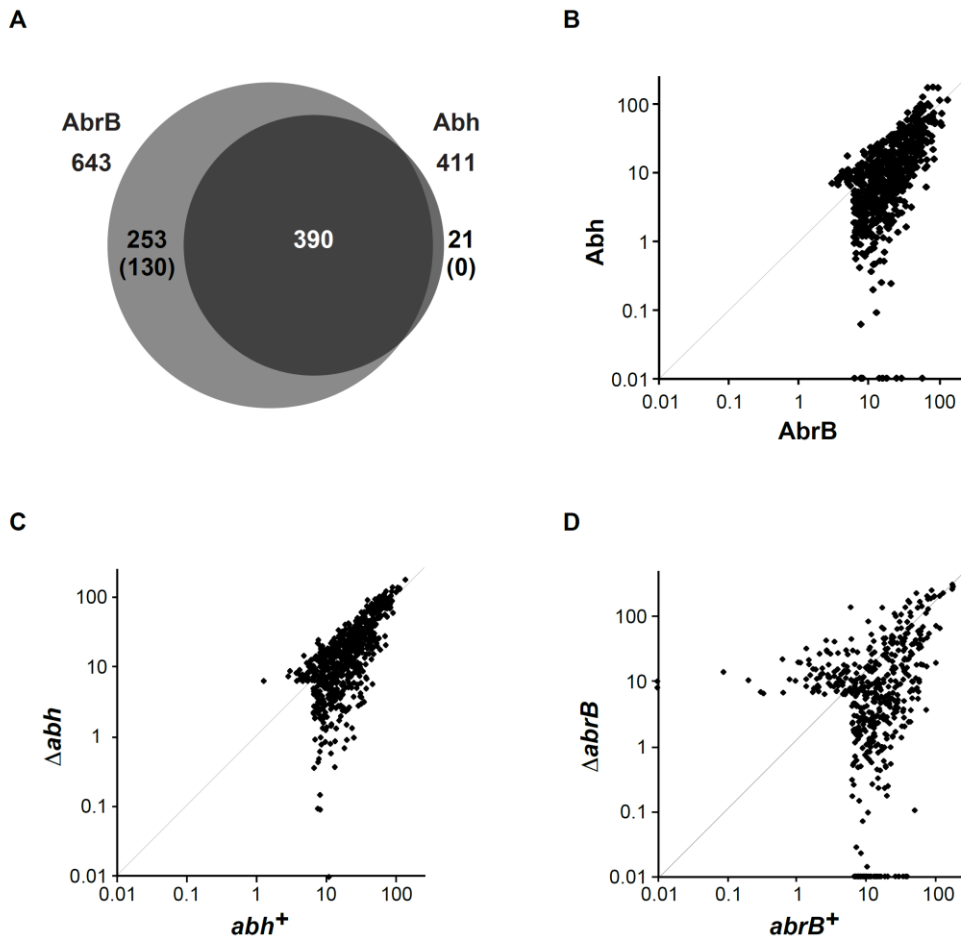


Figure 13. Comparison of AbrB and Abh binding signals in various strains. (A) A Venn diagram of overlapping binding sites for AbrB and Abh in a wild-type background. The numbers in parentheses indicate the levels of confidence associated with the identification of particular AbrB- and Abh-specific binding 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^+ (x-axis) and Δabh (y-axis) cells. (D) A log-scale scatter plot of Abh binding intensities in $abrB^+$ (x-axis) and $\Delta abrB$ 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.

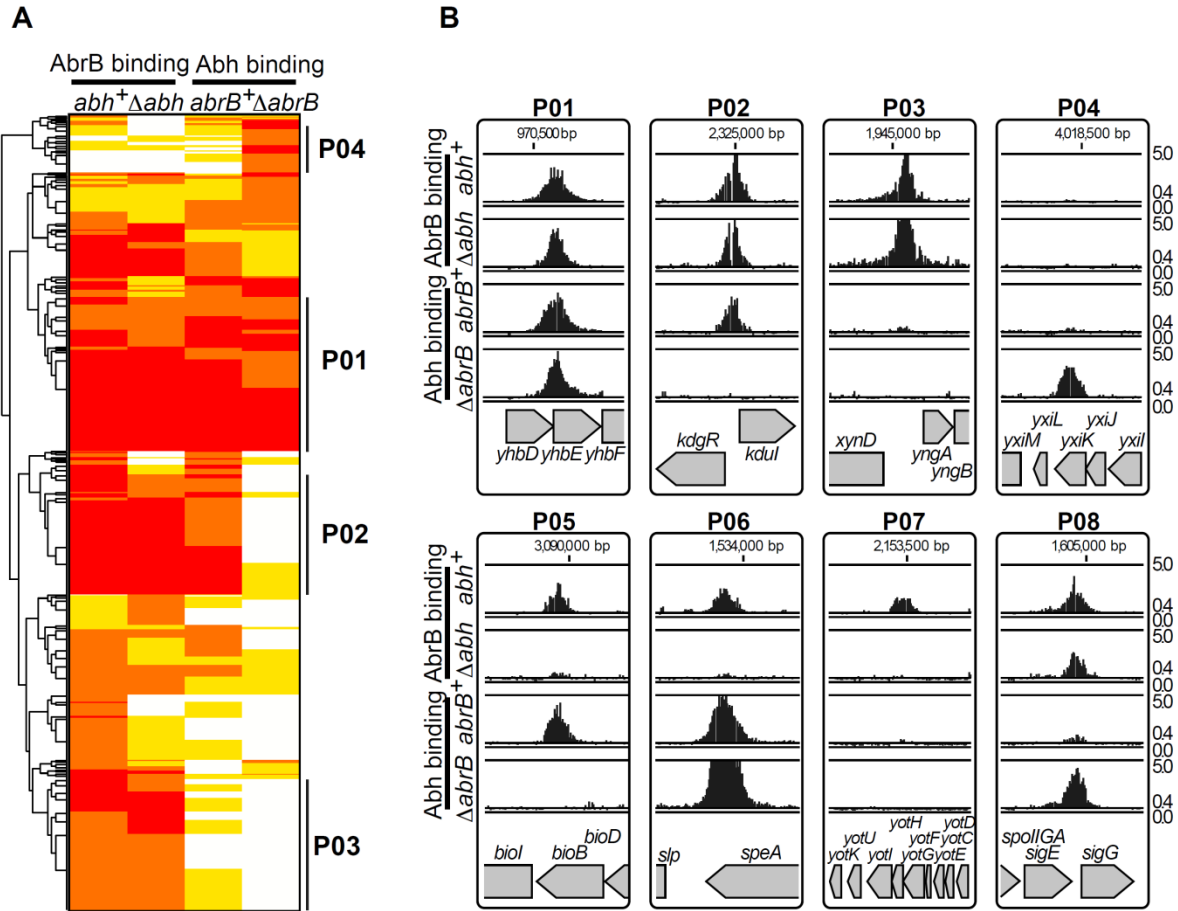


Figure 14. Classification of PBRs according to AbrB and Abh binding profiles. (A) A cluster diagram of 753 PBRs based on AbrB binding intensities (in various classes) in abh^+ and Δabh backgrounds, and Abh binding classes in $abrB^+$ and $\Delta abrB$ backgrounds. The VL, L, M, and H classes of AbrB/Abh 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.

Table 3 Classification of 160 PBRs with clear binding profiles

profile ID	Possible binding profiles				Molecules expected to be bound ^a			Assigned		Binding motif
	AbrB in wild	AbrB in Δabh	Abh in wild	Abh in $\Delta abrB$	AbrB homomer	AbrB/Abh heteromer	Abh homomer	number	%	
P01	•	•	•	•	•	•	•	60	37.3	TNCCA ^W WWWTGGNA
P02	•	•	•	-	•	•	-	46	28.6	WWWWWCCA ^W WWWTGG
P03	•	•	-	-	•	-	-	29	18	not clear
P04	-	-	-	•	-	-	• ($\Delta abrB$)	13	8.1	TGGNA ^W TNCCA
P05	•	-	•	-	-	•	-	5	3.1	
P06	•	-	•	•	-	•	•	4	2.5	
P07	•	-	-	-	• (wild)	-	-	3	1.9	
P08	•	•	-	•	•	-	• ($\Delta abrB$)	1	0.6	
P09	•	-	-	•	• (wild)	-	• ($\Delta abrB$)	0	0	
P10	-	•	•	•	• (Δabh)	-	•	0	0	
P11	-	•	•	-	• (Δabh)	-	• (wild)	0	0	
P12	-	•	-	•	• (Δabh)	-	• ($\Delta abrB$)	0	0	
P13	-	•	-	-	• (Δabh)	-	-	0	0	
P14	-	-	•	•	-	-	•	0	0	
P15	-	-	•	-	-	-	• (wild)	0	0	

^a 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.nbcrl.net>] (Bailey & Elkan, 1994). We suspected that the selected PBRs still included multiple AbrB/Abh-binding 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 4-bp 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 WWWWW-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.

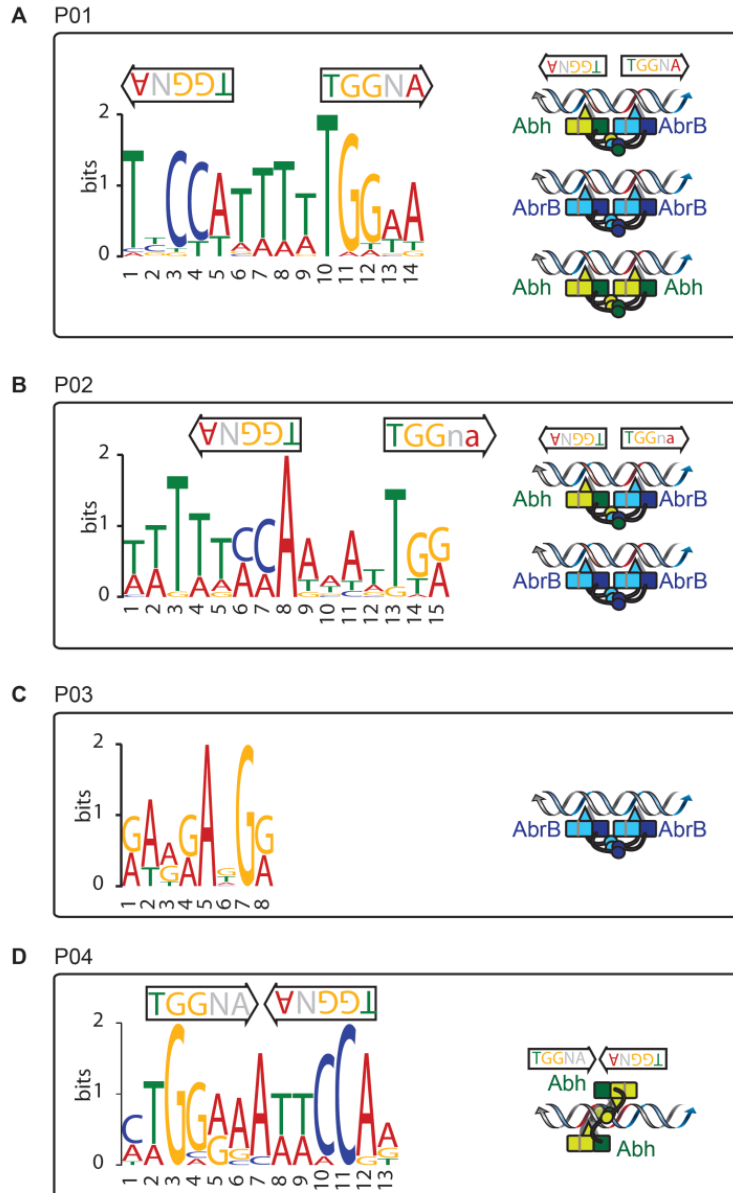


Figure 15. Consensus sequences for AbrB/Abh binding. Consensus sequences identified in selected PBRs belonging to classes P01 (A), P02 (B), P03 (C), and P04 (D) are presented, together with the position(s) and direction(s) of the TGGNA motif(s) in each sequence. Possible binding modes of AbrB/Abh homotetramers 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 base-pair mismatch resulted in loss of site enrichment in PBR regions.

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

Sequence ID	paired TGGNA motifs ^a		No. on genome ^b	No. in PBR ^c	coincidence (%) ^e	Enrichment (fold) ^d
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 WWWW	TGGNA	50	17	34.0	9.5
Pa1W6	TNCCA WWWW	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 WWWW	TNCCA	32	13	40.6	11.4
Pa2W6	TGGNA WWWW	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 WWWW	TGGNA	83	26	31.3	8.8
DrW6	TGGNA WWWW	TGGNA	113	15	13.3	3.7

^a Query sequences for searching paired TGGNA motifs.

^b Total number of sequences matched to query allowing 1 base mismatch.

^c Numbers of matched sequences located within 100 bp of centers of PBRs.

^d Proposed relevant sequences located in PBRs.

^e 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), Δabh (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).

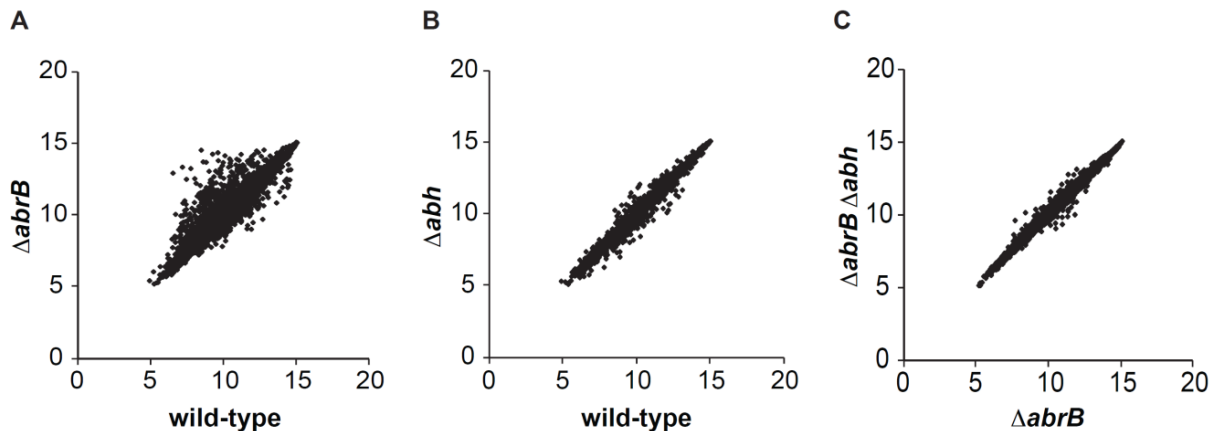


Figure 16. Transcriptome analysis in $\Delta abrB$ and Δabh mutants. Log-scale scatter plots of transcriptional intensities of each gene in $\Delta abrB$ (A, y-axis) and Δabh (B, y-axis) cells compared to those of wild-type cells (A and B, x-axis), and $\Delta abrB \Delta abh$ cells (C, y-axis), in comparison 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 *ΔabrB* 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*, *spo0E*, *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 *yvIABCD* 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 Δ *abrB* suggesting that AbrB might indirectly activate 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, *yfIA*, *ylaE*, *ctaCDEFG*, *yojL*, *ycaA* 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.

Table 5. Possible TUs directly regulated by AbrB and/or Abh^a

Operon	Gene/ PBR ID	Alternate Gene Name	Gene Function	Start	End	Strand/ Center position ^b	Expression ratio ^c				Signal intensity of RNA							
							<i>abrB</i>		Δ <i>abrB</i>		<i>Abh</i>		Wild		Δ <i>abrB</i>		Δ <i>abrB</i> Δ <i>abh</i>	
							Δ <i>abh</i>		Δ <i>abh</i>		Δ <i>abh</i>		Δ <i>abh</i>		Δ <i>abrB</i>		Δ <i>abh</i>	
							AbrB binding ^c		Abh Binding ^c		wild		Δ <i>abrB</i>		wild		Δ <i>abrB</i>	
wild		Δ <i>abh</i>		wild		Δ <i>abrB</i>		wild		Δ <i>abrB</i>		wild						
A: Repressed by AbrB																		
	25			55586	56001	55794	12.3	18.0	2.6	2.5								
1	<i>spoVG</i>		regulator required for spore cortex synthesis	55864	56157	+	3.36	3.42	1.29		7085	23826	24259	9115				
	54			155037	155452	155245	10.6	17.7	6.2	4.1								
2	<i>ybaJ</i>		putative methyltransferase	155155	155922	+	2.39	2.53	0.88		1873	4476	4735	1639				
	75			213445	214387	213916	56.7	72.2	27.9	6.1								
3	<i>ybcO</i>	<i>skfA</i>	sporulation killing factor A	213926	214093	+	8.96	11.20	1.11		879	7877	9837	972				
	<i>ybcP</i>	<i>skfB</i>	synthesis of sporulation killing factor A	214160	215392	+	8.55	10.25	0.98		456	3900	4677	448				
	<i>ybcS</i>	<i>skfC</i>	sporulation killing factor biosynthesis and export cell killing factor production.	215389	215946	+	7.10	8.29	1.06		423	2999	3503	449				
	<i>ybcT</i>	<i>skfD</i>	probable membrane-bound metalloprotease	215943	216878	+	6.75	7.82	1.06		528	3560	4123	560				
	<i>ybdA</i>	<i>skfE</i>	sporulation killing factor biosynthesis and export	216897	217616	+	7.96	8.79	1.21		407	3240	3579	493				
	<i>ybdB</i>	<i>skfF</i>	sporulation killing factor biosynthesis and export	217681	219027	+	4.23	4.65	1.11		435	1842	2021	482				
	<i>ybdD</i>	<i>skfG</i>	sporulation killing factor biosynthesis and export	219074	219487	+	5.45	6.02	1.13		518	2821	3116	584				
	<i>ybdE</i>	<i>skfH</i>	sibling killing effect; sporulation killing factor biosynthesis and export	219593	220018	+	4.87	4.98	1.23		141	687	702	174				
4	<i>ybdN</i>		putative phage protein	224063	224920	-	22.60	24.98	1.01		265	5990	6621	269				
	80			224495	225420	224958	36.5	59.9	20.9	5.1								
	80			224495	225420	224958	36.5	59.9	20.9	5.1								
5	<i>ybdO</i>		putative phage protein	225052	226236	+	7.64	7.29	1.16		388	2969	2833	451				
	92			249706	250104	249905	12.2	18.9	5.9	2.0								
6	<i>ybfO</i>		putative exported hydrolase	249967	251307	+	16.08	18.13	0.77		527	8471	9549	408				
	<i>ybfP</i>		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	<i>lip</i>		secreted alkaliphilic lipase	291757	292395	+	11.40	13.19	1.83		980	11178	12933	1791				
	167			544945	545292	545119	16.1	15.8	4.5	0.7								
8	<i>yddJ</i>		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	<i>yddT</i>		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	<i>ydeH</i>		putative integral inner membrane protein	567206	567652	+	3.24	2.61	1.24		397	1287	1036	494				
11	<i>ydeJ</i>			568834	569493	-	3.45	3.31	0.78		673	2322	2227	522				
	187		putative lipoprotein	569442	569704	569573	12.3	6.7	0.9	-0.3								
	215			670580	670859	670720	8.1	8.3	3.2	0.9								
12	<i>pspA</i>		phage shock protein A homolog	670793	671476	+	2.92	3.08	1.49		4246	12395	13066	6323				
	<i>ydjG</i>		putative phage replication protein	671542	672567	+	3.11	3.37	1.66		2648	8228	8924	4388				
	<i>ydjH</i>		conserved hypothetical protein	672567	673331	+	2.90	3.13	1.58		2557	7418	8012	4034				
	<i>ydjI</i>		putative phage protein	673362	674333	+	2.66	2.85	1.47		1885	5016	5368	2777				
13	<i>ydjL</i>	<i>bdhA</i>	acetoin reductase/2,3-butanediol 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	<i>yerI</i>		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	<i>rapH</i>		response regulator aspartate phosphatase	750293	751588	+	8.28	8.14	0.87		330	2730	2684	285				
16	<i>yfmI</i>		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								

Table 5. Possible TUs directly regulated by AbrB and/or Abh^a (continued)

Operon	Gene/ PBR ID	Alternate Gene Name	Gene Function	Start	End	Strand/ Center position ^b	Expression ratio ^c				Signal intensity of RNA			
							<i>abrB</i>	Δ <i>abrB</i>	Δ <i>abh</i>		Wild	Δ <i>abrB</i>	Δ <i>abrB</i>	Δ <i>abh</i>
							AbrB binding ^c		Abh Binding ^c					
							wild	Δ <i>abh</i>	wild	Δ <i>abrB</i>				
	265			819466	820408	819937	69.5	95.1	57.3	9.7				
17	<i>yfmH</i>		function unknown and unique	820066	820137	+	26.13	27.09	0.93		799	20880	21647	741
	<i>yfmG</i>		conserved hypothetical protein	820204	821667	+	44.97	46.47	1.00		219	9855	10184	218
18	272			842790	843800	843295	53.3	25.0	71.5	110.2				
	<i>yflC</i>		function unknown and unique	843587	843739	+	3.68	5.49	1.02		223	822	1226	227
	<i>yflB</i>		conserved hypothetical protein	843721	843981	+	4.03	7.41	1.18		152	613	1127	179
19	323			1044042	104457	1044250	24.5	23.1	5.4	2.0				
	<i>yheJ</i>		function unknown and unique	1044345	1044506	+	3.82	3.15	1.01		742	2835	2337	750
20	328			1061535	1062273	1061904	40.7	21.7	45.3	5.4				
	<i>yhaQ</i>		putative ABC-2 type transport system ATP-binding protein	1061899	1062795	+	3.67	3.55	1.76		2146	7869	7611	3784
	<i>yhaP</i>		putative ABC-2 type transport system permease protein	1062788	1064047	+	3.78	3.60	1.86		2342	8851	8442	4368
21	349.2			1128872	1129168	1129020	11.6	12.1	2.1	-0.4				
	<i>yhjM</i>	<i>ntdR</i>	transcriptional regulator of the ntd operon	1129020	1130009	+	6.53	6.14	1.35		172	1126	1058	232
22	<i>yjcM</i>		conserved hypothetical protein	1263014	1264243	-	3.04	2.97	1.38		3035	9227	9004	4202
	380			1263988	1264793	1264391	81.9	87.7	21.5	2.2				
23	<i>yjdB</i>		putative exported protein	1269045	1269392	-	35.41	32.81	0.90		394	13959	12934	355
	382			1269157	1269894	1269526	40.9	64.6	13.9	-0.4				
24	<i>yjdG</i>		putative acetyltransferase	1275650	1276156	-	5.13	4.17	0.95		370	1896	1544	352
	384			1275939	1276439	1276189	23.9	36.1	3.8	1.4				
25	<i>ctaO</i>		protoheme IX farnesyltransferase (heme O synthase)	1278825	1279814	-	6.03	11.96	1.21		210	1265	2511	255
	387			1279033	1280502	1279768	101.4	133.9	112.4	202.3				
26	427			1429772	1430136	1429954	19.0	18.8	9.7	1.7				
	<i>spo0E</i>		phosphatase acting on Spo0A-P	1429992	1430249	+	3.04	2.74	0.89		765	2330	2098	681
27	438			1466679	1467349	1467014	44.6	56.2	22.3	0.5				
	<i>ykuA</i>	<i>pbpH</i>	penicillin-binding protein for formation of rod-shaped peptidoglycan cell wall	1467109	1469166	+	3.10	3.19	0.76		1706	5288	5434	1301
28	446			1491193	1491829	1491511	54.8	63.4	14.7	0.8				
	<i>ykuU</i>		putative 2-cys peroxiredoxin	1491568	1492110	+	10.81	12.82	1.17		896	9689	11489	1051
	<i>ykuV</i>		thiol-disulfide isomerase	1492182	1492643	+	9.91	11.75	1.22		659	6529	7741	802
29	449			1502685	1503117	1502901	17.7	9.8	6.3	10.0				
	<i>yknW</i>		SdpC toxin resistance	1502889	1503584	+	3.76	4.28	1.53		4027	15157	17250	6150
	<i>yknX</i>		SdpC toxin resistance	1503589	1504722	+	3.42	4.01	1.44		3888	13306	15596	5605
	<i>yknY</i>		SdpC toxin resistance, probable ABC transport system ATP-binding protein	1504723	1505415	+	4.31	5.21	1.64		3241	13975	16877	5310
	<i>yknZ</i>		SdpC toxin resistance, probable ABC transport system permease protein	1505412	1506605	+	3.70	4.52	1.42		3401	12593	15366	4815
30	<i>nprE</i>		extracellular neutral metalloprotease	1539343	1540908	-	2.93	3.90	1.43		587	1719	2292	840
	459			1540714	1541180	1540947	21.4	11.8	4.0	-0.3				
31	<i>yIbA</i>		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				
32	474			1604600	1605032	1604816	24.7	26.5	6.1	44.2				
	<i>sigG</i>		sporulation-specific sigma factor	1604927	1605709	+	2.32	2.54	0.93		250	581	634	233
33	<i>yIqB</i>		conserved hypothetical protein	1670466	1670951	-	28.68	32.60	2.36		458	13128	14919	1081
	486			1670747	1671315	1671031	44.1	54.9	33.2	36.8				
34	<i>ymzB</i>		conserved hypothetical protein	1859209	1859565	-	4.87	6.66	0.89		322	1566	2142	286
	<i>ymaE</i>		putative hydrolase	1859644	1860342	-	6.65	8.91	1.33		158	1047	1403	210
35	530			1860178	1860729	1860454	35.6	41.7	10.9	0.6				
	<i>ymcM</i>		conserved hypothetical protein	1902720	1903472	-	4.32	4.57	0.86		1605	6931	7335	1374
36	546			1903188	1903841	1903515	27.3	15.0	7.2	0.0				
	<i>ymzD</i>		Spo0A-P phosphatase	1922050	1922223	-	4.71	3.05	0.99		155	731	473	154
	555			1922092	1922490	1922291	24.9	22.1	6.7	-1.3				

Table 5. Possible TUs directly regulated by AbrB and/or Abh^a (continued)

Operon	Gene/ PBR ID	Alternate Gene Name	Gene Function	Start	End	Strand/ Center position ^b	Expression ratio ^c				Signal intensity of RNA			
							<i>abrB</i>	Δ <i>abrB</i>	Δ <i>abh</i>	Δ <i>abh</i>	Wild	Δ <i>abrB</i>	Δ <i>abrB</i>	Δ <i>abh</i>
							AbrB binding ^c		Abh Binding ^c					
							wild	Δ <i>abh</i>	wild	Δ <i>abrB</i>				
37	<i>ynfF</i>	<i>xynC</i>	endo-xylanase	1941923	1943191	-	3.65	3.62	0.82		331	1207	1196	271
	<i>xynD</i>		endo-1,4-beta-xylanase (xylanase D)	1943322	1944863	-	3.22	3.06	0.84		196	630	599	164
	565			1944549	1945524	1945037	65.3	108.7	6.1	-3.3				
38	<i>ppsE</i>		plipastatin synthetase	1959407	1963246	-	1.87	1.89	1.00		209	390	394	208
	<i>ppsD</i>		plipastatin synthetase	1963254	1974065	-	2.27	2.25	0.98		190	432	427	186
	<i>ppsC</i>		plipastatin synthetase	1974090	1981757	-	3.49	3.45	1.03		169	590	583	173
	<i>ppsB</i>		plipastatin synthetase	1981774	1989456	-	3.89	4.05	1.09		158	616	641	173
	<i>ppsA</i>		plipastatin synthetase	1989481	1997166	-	4.38	4.71	1.05		136	596	642	142
	581			1996943	1997460	1997202	19.6	16.7	1.0	-1.5				
39	598			2049524	2050312	2049918	73.0	82.6	55.0	36.7				
	<i>yobB</i>		putative transcriptional regulator from bacteriophage	2049899	2050162	+	12.22	18.14	0.99		152	1858	2759	150
	602.2			2061084	2061584	2061334	30.4	19.2	9.8	-2.0				
40	<i>rapK</i>		response regulator aspartate phosphatase	2061361	2062476	+	6.54	8.53	1.31		154	1003	1310	201
	<i>phrK</i>		secreted regulator of phosphatase RapK	2062473	2062595	+	3.80	4.15	1.17		761	2891	3157	889
41	609			2075007	2075405	2075206	16.6	7.6	5.4	2.0				
	<i>yobO</i>		putative phage-related pre-neck appendage protein	2075417	2077837	+	2.87	4.62	1.05		177	509	820	186
42	616			2087264	2087543	2087404	7.8	15.8	0.1	0.1				
	<i>yocD</i>		putative carboxypeptidase	2087468	2088445	+	2.51	1.87	0.83		549	1377	1028	455
43	<i>phy</i>		phytase	2149306	2150454	-	2.98	3.32	1.08		136	405	451	146
	639			2150419	2150714	2150567	9.2	11.1	1.2	-0.6				
44	<i>yorD</i>		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	<i>yoqM</i>		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	<i>yomJ</i>		putative phage immunity protein; phage Spbeta	2247613	2248296	+	3.30	3.19	1.70		521	1720	1659	886
	680			2271272	2271653	2271463	14.5	21.0	0.5	-1.1				
47	<i>yoIC</i>		SP beta phage protein	2271352	2271687	+	3.40	3.89	0.83		136	463	530	113
48	<i>yoIB</i>		conserved hypothetical protein; phage Spbeta	2271730	2272086	-	4.30	3.77	0.62		545	2347	2054	339
	<i>yoIA</i>		exported protein of unknown 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	<i>yokL</i>		putative acetyltransferase; phage Spbeta	2273185	2273718	-	2.35	2.37	0.95		748	1754	1775	712
	<i>yokK</i>		conserved hypothetical protein; phage Spbeta	2273754	2274332	-	2.78	2.84	1.10		804	2234	2282	881
	<i>yokJ</i>		conserved hypothetical protein; phage Spbeta	2274396	2274893	-	3.30	3.51	1.10		1006	3324	3528	1108
	<i>yokI</i>		putative DNA wielding protein; 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	<i>qcrC</i>		menaquinol:cytochrome c oxidoreductase (cytochrome cc subunit)	2362307	2363074	-	4.42	4.44	2.01		1976	8737	8785	3975
	<i>qcrB</i>		menaquinol:cytochrome c oxidoreductase (cytochrome b subunit)	2363109	2363783	-	4.00	3.94	1.86		2703	10810	10640	5037
	<i>qcrA</i>		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	<i>yphF</i>		putative lipoprotein	2387051	2387785	-	2.27	2.57	1.65		735	1669	1891	1217
	<i>yphE</i>		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				

Table 5. Possible TUs directly regulated by AbrB and/or Abh^a (continued)

Operon	Gene/ PBR ID	Alternate Gene Name	Gene Function	Start	End	Strand/ Center position ^b	Expression ratio ^c				Signal intensity of RNA					
							<i>abrB</i>		Δ <i>abrB</i>		Δ <i>abh</i>		Wild	Δ <i>abrB</i>	Δ <i>abrB</i>	Δ <i>abh</i>
							AbrB binding ^c		Abh Binding ^c		wild	Δ <i>abrB</i>				
							wild	Δ <i>abh</i>	wild	Δ <i>abrB</i>						
52	<i>sigF</i>		sporulation-specific sigma factor(sigma-F)	2442618	2443385	-	3.17	3.38	1.30	283	897	956	369			
	<i>spoIIAB</i>		anti-sigma factor (antagonist of sigma(F)) andserine kinase	2443397	2443837	-	4.74	5.18	1.53	266	1261	1377	407			
	<i>spoIIAA</i>		anti-anti-sigma factor (antagonist of SpoIIAB)	2443834	2444187	-	4.47	4.68	1.46	518	2315	2426	759			
	<i>dacF</i>		D-alanyl-D-alanine carboxypeptidase (penicillinbinding protein)	2444283	2445452	-	2.10	2.65	1.05	175	369	466	185			
	737			2445284	2445818	2445551	52.2	24.6	43.4	3.6						
53	<i>tasA</i>		major biofilm matrix component	2552313	2553098	-	17.64	18.54	0.60	809	14267	14997	483			
	<i>sipW</i>		type I signal peptidase	2553162	2553734	-	12.58	13.65	0.88	344	4328	4695	304			
	<i>yqxM</i>		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	<i>yqzG</i>		putative exported protein	2554751	2555077	+	2.36	2.94	0.82	139	327	408	113			
55	<i>cccA</i>		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	<i>antE</i>		dnaG overlapping 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	<i>phrE</i>		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	<i>yqcG</i>		putative phage DNA manipulating enzyme; skin element	2660329	2661924	+	2.35	2.61	0.84	854	2007	2227	720			
59	<i>yqxJ</i>		hypothetical protein; skin element	2662778	2663140	-	3.77	4.57	0.73	437	1649	2000	319			
	<i>yqxI</i>		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	<i>yqaP</i>		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	<i>yrpD</i>		putative lipoprotein	2738712	2739419	+	4.60	4.75	0.86	4973	22864	23602	4301			
62	<i>csn</i>		chitinase	2747210	2748043	-	11.95	11.94	0.67	725	8664	8653	485			
	826			2747867	2748265	2748066	16.9	19.3	3.1	0.3						
63	<i>yrzI</i>		conserved hypothetical protein, induced by formaldehyde	2778150	2778299	-	4.76	3.97	1.20	279	1331	1109	335			
	842			2778332	2779001	2778667	51.5	61.6	55.9	6.9						
	897			2952377	2953064	2952721	42.1	60.6	40.5	21.8						
64	<i>yscB</i>		putative lipoprotein	2952869	2953501	+	3.93	3.52	1.47	446	1751	1570	657			
	961			3186072	3186776	3186424	38.0	64.0	6.4	0.5						
65	<i>yuaB</i>		conserved hypothetical protein	3186542	3187087	+	15.95	17.25	0.45	1128	17987	19456	513			
66	<i>tlpA</i>		methyl-accepting chemotaxis	3207319	3209307	-	7.55	7.31	1.04	178	1345	1303	185			
	967			3209005	3209794	3209400	63.1	92.9	11.5	1.0						
67	<i>dhbF</i>		dihydroxy-benzoyl-glycin biosynthesis	3279544	3286680	-	12.72	11.86	1.02	1022	13001	12124	1045			
	<i>dhbB</i>		dihydroxy-benzoyl-glycin biosynthesis	3286700	3287638	-	9.62	9.36	1.12	1467	14108	13733	1647			
	<i>dhbE</i>		dihydroxy-benzoyl-glycin biosynthesis	3287666	3289285	-	7.88	7.55	1.14	1939	15282	14633	2207			
	<i>dhbC</i>		dihydroxy-benzoyl-glycin biosynthesis	3289314	3290510	-	8.09	7.92	1.19	2378	19242	18821	2822			
	<i>dhbA</i>		dihydroxy-benzoyl-glycin biosynthesis	3290536	3291321	-	6.68	6.79	1.17	2153	14379	14620	2514			
	<i>yuil</i>		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	<i>yurI</i>	<i>bsn</i>	extracellular ribonuclease	3343140	3344006	+	2.67	3.17	1.68	394	1052	1247	662			

Table 5. Possible TUs directly regulated by AbrB and/or Abh^a (continued)

Operon	Gene/ PBR ID	Alternate Gene Name	Gene Function	Start	End	Strand/ Center position ^b	Expression ratio ^c				Signal intensity of RNA			
							<i>abrB</i>	Δ <i>abrB</i> <i>Abh</i>	<i>Abh</i>		Wild	Δ <i>abrB</i>	Δ <i>abrB</i> <i>Abh</i>	<i>Abh</i>
							AbrB binding ^c		Abh Binding ^c					
							wild -type	Δ <i>Abh</i>	wild -type	Δ <i>abrB</i>				
69	<i>yvqJ</i> 1005		putative efflux protein	3398118	3399386	-	3.83	4.66	1.16		263	1009	1226	305
				3399133	3399752	3399443	39.1	31.2	11.0	1.3				
70	<i>yvrN</i>		putative ABC transporter (ATP-binding protein)	3411158	3412408	-	3.56	3.64	1.13		1397	4977	5079	1575
	<i>yvrO</i>		putative ABC transporter (ATP-binding protein)	3412380	3413069	-	3.23	3.37	1.02		1638	5286	5521	1676
	<i>yvrP</i> 1008		putative ABC transporter component	3413053	3414246	-	3.11	3.14	1.10		1718	5343	5394	1881
				3414093	3414491	3414292	21.3	25.7	7.2	0.6				
	1011			3426384	3426867	3426626	35.0	45.7	25.1	5.1				
71	<i>yvgO</i>		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	<i>yvaW</i>	<i>sdpA</i>	export of SdpC killing factor	3463320	3463796	+	83.02	80.54	1.30		94	7811	7577	122
	<i>yvaX</i>	<i>sdpB</i>	export of SdpC killing factor	3463793	3464764	+	71.62	68.36	1.23		148	10565	10083	181
	<i>yvaY</i>	<i>spbC</i>	killing factor SdpC	3464807	3465418	+	65.94	60.61	1.27		360	23744	21826	456
73	<i>yvfF</i>	<i>epsO</i>	putative pyruvyl transferase	3513146	3514114	-	8.58	9.73	0.90		297	2551	2894	267
	<i>yvfE</i>	<i>epsN</i>	putative aminotransferase	3514093	3515259	-	7.60	8.27	0.96		476	3615	3937	455
	<i>yvfD</i>	<i>epsM</i>	putative O-acetyltransferase	3515264	3515914	-	4.79	5.37	1.06		400	1914	2144	425
	<i>yvfC</i>	<i>epsL</i>	putative phosphotransferase involved in extracellular matrix synthesis	3515911	3516519	-	4.76	5.55	1.06		449	2136	2490	477
	<i>yvfB</i>	<i>epsK</i>	putative extracellular matrix component exporter	3516516	3517553	-	5.43	6.39	1.06		386	2097	2470	409
	<i>yvfA</i>	<i>epsJ</i>	putative glycosyl transferase	3517703	3518032	-	3.70	4.38	0.88		1132	4188	4958	995
	<i>yveT</i>	<i>epsI</i>	putative polysaccharide pyruvyl transferase	3518029	3519063	-	7.27	8.33	0.97		568	4133	4736	552
	<i>yveS</i>	<i>epsH</i>	putative glycosyltransferase involved in biofilm formation	3519060	3520136	-	6.09	7.11	0.97		466	2840	3311	453
	<i>yveR</i>	<i>epsG</i>	biofilm extracellular matrix formation enzyme	3520141	3521175	-	6.95	7.77	1.10		452	3143	3512	498
	<i>yveQ</i>	<i>epsF</i>	putative glycosyltransferase involved in extracellular matrix formation	3521200	3522303	-	5.35	6.06	0.94		558	2983	3382	526
	<i>yveP</i>	<i>epsE</i>	putative glycosyltransferase	3522300	3523454	-	6.42	7.33	1.05		345	2216	2532	361
	<i>yveO</i>	<i>epsD</i>	putative extracellular matrix biosynthesis enzyme	3523447	3524283	-	6.39	7.07	0.99		382	2443	2700	380
	<i>yveN</i>	<i>epsC</i>	putative UDP-sugar epimerase	3524280	3525425	-	6.72	7.51	0.92		584	3924	4381	535
	<i>yveM</i>	<i>epsB</i>	protein tyrosine kinase	3525437	3527233	-	4.68	5.33	0.99		434	2029	2311	431
	<i>yveL</i>	<i>epsA</i>	modulator of protein tyrosine kinase EpsB	3527492	3528175	-	8.93	8.71	0.94		325	2903	2830	304
	<i>yveK</i> 1032	<i>slrR</i>	transcriptional regulator involved in biofilm formation	3528181	3528885	-	8.83	7.98	0.91		349	3084	2790	317
				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	<i>pnbA</i> 1049		para-nitrobenzyl esterase (intracellular esterase B)	3529665	3531134	+	10.02	11.25	1.72		787	7891	8855	1351
				3600906	3601134	3601020	3.8	8.0	0.8	0.3				
75	<i>yvnA</i>		putative transcriptional regulator	3601104	3601577	+	4.08	3.16	0.80		224	916	709	179
76	<i>cypX</i>		putative monooxygenase (cytochrome P450)	3601618	3602835	-	4.42	4.51	0.78		581	2568	2621	454
	<i>yvmC</i> 1050		conserved hypothetical protein	3602851	3603597	-	5.00	4.79	0.81		594	2970	2844	481
				3603609	3604075	3603842	14.3	33.1	1.5	-0.6				
77	<i>ywqE</i>	<i>ptpZ</i>	protein tyrosine-phosphatase	3730032	3730796	-	2.88	2.59	0.98		612	1765	1582	603
	<i>ywqD</i>	<i>ptkA</i>	protein tyrosine kinase, phosphorylating Ugd, TuaD and SSB	3730849	3731562	-	3.15	2.92	0.85		1723	5430	5038	1458
	<i>ywqC</i> 1100	<i>tkmA</i>	modulator of PtkA protein	3731552	3732298	-	4.33	3.60	0.97		607	2631	2186	591
				3732163	3732595	3732379	15.5	25.2	10.5	0.1				

Table 5. Possible TUs directly regulated by AbrB and/or Abh ^a (continued)

Operon	Gene/ PBR ID	Alternate Gene Name	Gene Function	Start	End	Strand/ Center position ^b	Expression ratio ^c				Signal intensity of RNA			
							<i>abrB</i>	Δ <i>abrB</i>	Δ <i>abh</i>		Wild	Δ <i>abrB</i>	Δ <i>abrB</i>	Δ <i>abh</i>
							AbrB binding ^c		Abh Binding ^c					
							wild -type	Δ <i>abh</i>	wild -type	Δ <i>abrB</i>				
78	1129			3834673	3835139	3834906	26.1	36.4	7.7	2.4				
	<i>sboA</i>		subtilisin A	3835081	3835212	+	10.54	11.78	0.98		562	5925	6624	553
	<i>sboX</i>		putative bacteriocin-like product	3835169	3835321	+	4.66	5.13	1.05		107	499	549	112
79	1129.1			3835149	3835666	3835408	32.4	46.3	18.6	1.5				
	<i>albA</i>		putative antilisterial bacteriocin (subtilisin) production enzyme	3835346	3836692	+	5.54	5.59	1.32		1502	8319	8398	1987
	<i>albB</i>		putative membrane component involved in subtilisin production	3836705	3836866	+	3.58	3.89	1.10		1906	6829	7409	2097
	<i>albC</i>		putative transporter involved in subtilisin production	3836863	3837582	+	3.91	4.04	1.14		1034	4043	4177	1176
	<i>albD</i>		putative integral inner membrane protein involved in subtilisin production and immunity	3837575	3838885	+	3.61	3.78	1.13		937	3377	3537	1058
	<i>albE</i>		putative hydrolase involved in subtilisin production	3838875	3840035	+	4.02	4.36	1.13		412	1659	1800	468
	<i>albF</i>		putative peptidase involved in subtilisin production	3840040	3841320	+	3.17	3.62	1.12		419	1327	1518	467
	<i>albG</i>		putative integral inner membrane protein involved in subtilisin production and immunity	3841317	3842018	+	2.03	2.38	1.12		352	717	839	394
80	<i>rocA</i>		delta-1-pyrroline-5 carboxylate dehydrogenase	3877988	3879535	-	8.71	10.10	1.01		870	7576	8784	880
	<i>rocG</i>		glutamate dehydrogenase	3879762	3881036	-	6.69	8.91	0.98		728	4868	6481	714
	<i>yweA</i>		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				
81	1161			3933103	3933586	3933345	33.0	21.1	26.1	1.7				
	<i>ywbF</i>		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	<i>yxzE</i>		putative bacteriocin	3981992	3982192	+	3.27	3.29	1.42		1379	4516	4543	1954
83	1198			4064734	4065251	4064993	17.7	29.0	3.7	1.3				
	<i>yxzD</i>		conserved hypothetical protein	4065225	4065578	+	2.23	2.86	0.76		130	289	371	98
84	<i>yxzD</i>		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	<i>yxzC</i>		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	<i>yxzB</i>		putative S-adenosylmethionine-dependent methyltransferase	4096436	4097170	+	3.79	4.80	0.91		435	1649	2088	398
	<i>yxzA</i>	<i>asIA</i>	D-aspartate ligase	4097170	4097439	+	4.45	6.10	0.87		172	766	1050	150
	<i>yxzB</i>		hypothetical protein	4097443	4097925	+	2.94	4.17	0.76		240	706	1000	182
87	<i>yxzL</i>		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	<i>yxzJ</i>		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	<i>yxzB</i>		putative exopolysaccharide pyruvyl transferase	4109973	4111004	-	2.89	3.84	0.77		1273	3676	4887	982
	<i>yxzA</i>	<i>glxK</i>	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				

Table 5. Possible TUs directly regulated by AbrB and/or Abh ^a (continued)

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

Table 5. Possible TUs directly regulated by AbrB and/or Abh ^a (continued)

Operon	Gene/ PBR ID	Alternate Gene Name	Gene Function	Start	End	Strand/ Center position ^b	Expression ratio ^c				Signal intensity of RNA			
							<i>abrB</i>	Δ <i>abrB</i> Δ <i>abh</i>	Δ <i>abh</i>		Wild	Δ <i>abrB</i>	Δ <i>abrB</i> Δ <i>abh</i>	Δ <i>abh</i>
							AbrB binding ^c		Abh Binding ^c					
							wild	Δ <i>abh</i>	wild	Δ <i>abrB</i>				
	1089			3700050	3700414	3700232	13.0	17.0	5.8	3.9				
5	<i>rbsR</i>		transcriptional repressor of the ribose operon	3700438	3701418	+	0.31	0.52	1.08	19128	5873	9899	20596	
	<i>rbsK</i>		ribokinase	3701420	3702301	+	0.33	0.54	1.04	20943	6849	11352	21813	
	<i>rbsD</i>		ribose ABC transporter (membrane bound ribose binding)	3702298	3702693	+	0.17	0.45	0.99	18453	3136	8237	18222	
	<i>rbsA</i>		ribose ABC transporter (ATP-binding protein)	3702709	3704190	+	0.29	0.53	1.00	24106	7008	12751	24152	
	<i>rbsC</i>		ribose ABC transporter (permease)	3704192	3705160	+	0.30	0.55	1.03	19886	6056	10947	20447	
	<i>rbsB</i>		ribose ABC transporter (ribose-binding lipoprotein)	3705172	3706089	+	0.44	0.62	1.07	25093	11068	15540	26837	
C: Repressed by AbrB and activated by Abh														
1	<i>bdbB</i>		thiol-disulfideoxidoreductase, sublancin biosynthesis	2264421	2264867	-	7.29	3.69	0.37	433	3155	1596	162	
	<i>yolJ</i>		putative glycosyltransferase, essential for sublancin production	2264864	2266132	-	6.87	4.00	0.33	505	3470	2017	167	
	<i>bdbA</i>		thiol-disulfideoxidoreductase,	2266132	2266545	-	5.90	3.02	0.28	495	2922	1493	136	
	<i>sunT</i>		sublancin 168 lantibiotic	2266542	2268659	-	6.56	3.21	0.33	240	1577	773	79	
	<i>sunA</i>		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: Additively repressed by AbrB and Abh														
	272.1			843810	844395	844103	33.5	26.0	34.5	40.8				
1	<i>yflA</i>		putative amino acid transporter	844106	845521	+	1.48	2.62	1.05	565	838	1477	595	
2	<i>ylaE</i>		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			1559142	1560032	1559587	71.5	51.3	64.8	17.7				
3	<i>ctaC</i>		cytochrome caa3 oxidase (subunit II)	1559773	1560843	+	5.43	5.88	2.43	658	3574	3868	1601	
	<i>ctaD</i>		cytochrome caa3 oxidase (subunit I)	1560876	1562744	+	4.94	5.35	2.47	928	4582	4963	2293	
	<i>ctaE</i>		cytochrome caa3 oxidase (subunit III)	1562744	1563367	+	6.01	6.04	2.92	531	3190	3209	1553	
	<i>ctaF</i>		cytochrome caa3 oxidase (subunit IV)	1563370	1563702	+	4.53	4.81	2.36	994	4504	4783	2347	
	<i>ctaG</i>		cytochrome aa(3) assembly factor	1563729	1564622	+	4.25	4.24	2.14	731	3105	3099	1563	
4	<i>yojL</i>	<i>cwlS</i>	peptidoglycan hydrolase (cell wall-binding, 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	<i>yedA</i>		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	<i>ywoF</i>		putative pectate lyase	3749790	3751196	-	3.72	3.63	3.02	779	2899	2824	2350	
	1108			3751050	3751499	3751275	31.4	15.9	20.7	8.2				
E: Repressed by Abh														
	117.1			375931	376635	376283	45.4	45.4	34.0	3.7				
1	<i>sfjAA</i>		surfactin synthetase	376525	387291	+	1.61	1.69	3.24	1120	1803	1888	3628	
	<i>sfjAB</i>		surfactin synthetase	387304	398067	+	1.83	1.91	3.46	1230	2254	2351	4254	
	<i>sfjAC</i>		surfactin synthetase	398104	401928	+	1.85	1.87	3.28	1163	2148	2173	3819	
	<i>sfjAD</i>		surfactin synthetase	401957	402685	+	1.95	1.97	3.46	814	1583	1600	2817	

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

^b Coding strand of genes or center position of PBRs are indicated.

^c Relative transcriptional signal intensities in Δ *abrB*, Δ *abrB* Δ *abh*, and Δ *abh* cells compared to that of wild-type cells are indicated for various genes. AbrB binding

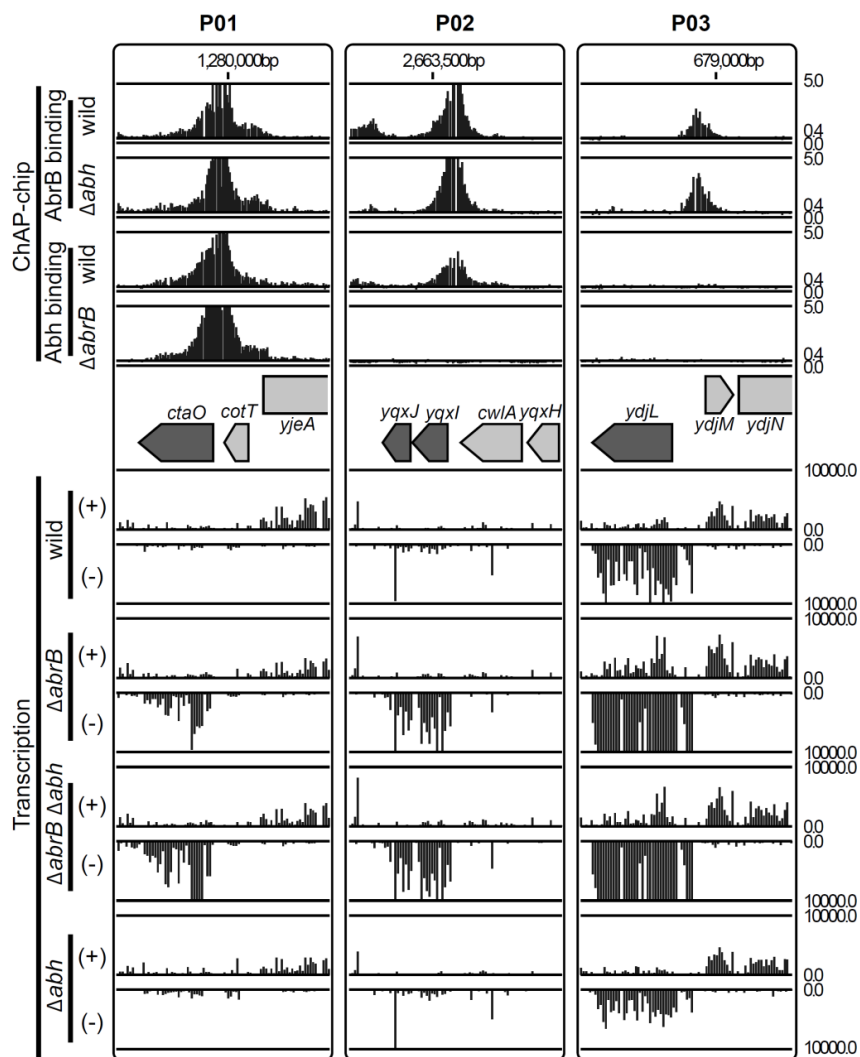


Figure 17. AbrB/Abh binding profile in the promoter region of gene repressed by AbrB. Examples of AbrB/Abh binding in the promoter region of genes regulated by AbrB. The AbrB/Abh binding profiles in four strains are depicted as in Figure 11A. The gene organization of selected regions is indicated in 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.

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

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

^a 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*, *tkl*, *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.

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 σ^X , and σ^X itself is inactivated by anti- σ^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- σ^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 σ^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 Δ *rsiX* cells. Western blot analysis of Abh in; (1) *abh*-overexpressing strain (OC009) induce with 75 μ M and (2) 50 μ M IPTG, (3) Δ *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.

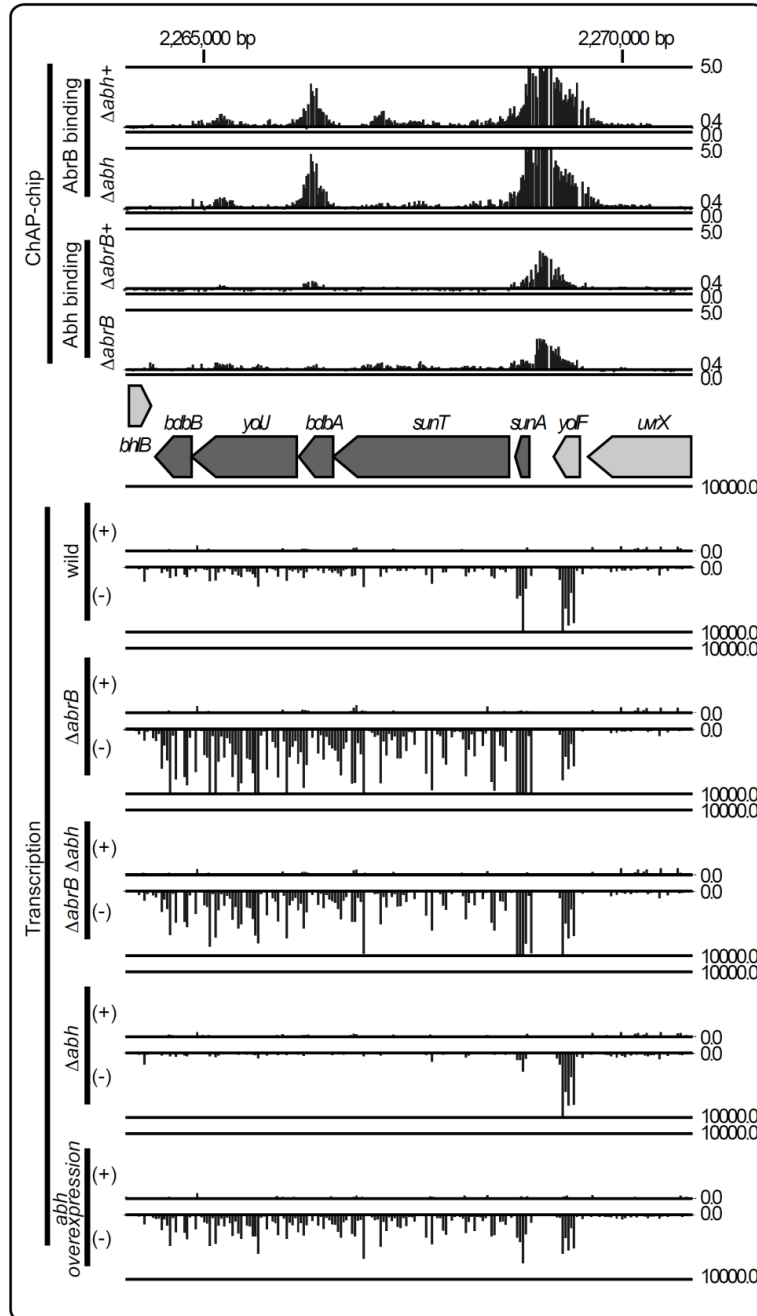


Figure 20. Activation of sublancin operon in Abh overexpressing cell. The *AbrB*/*Abh* binding profiles in four strains are depicted as in Figure 11A. The gene organization of selected regions is indicated in the middle and the sublancin operon is indicated in dark grey. Below the gene map, transcriptional 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 Δabh 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-WWWW-TGGNA for P01 sequences, WWWWW-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/Abh-binding, 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 mention, 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-4bp-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 4bp-spaced sequence has always longer, nearly twice, footprint protection region compared to 5bp-spaced 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 β -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.

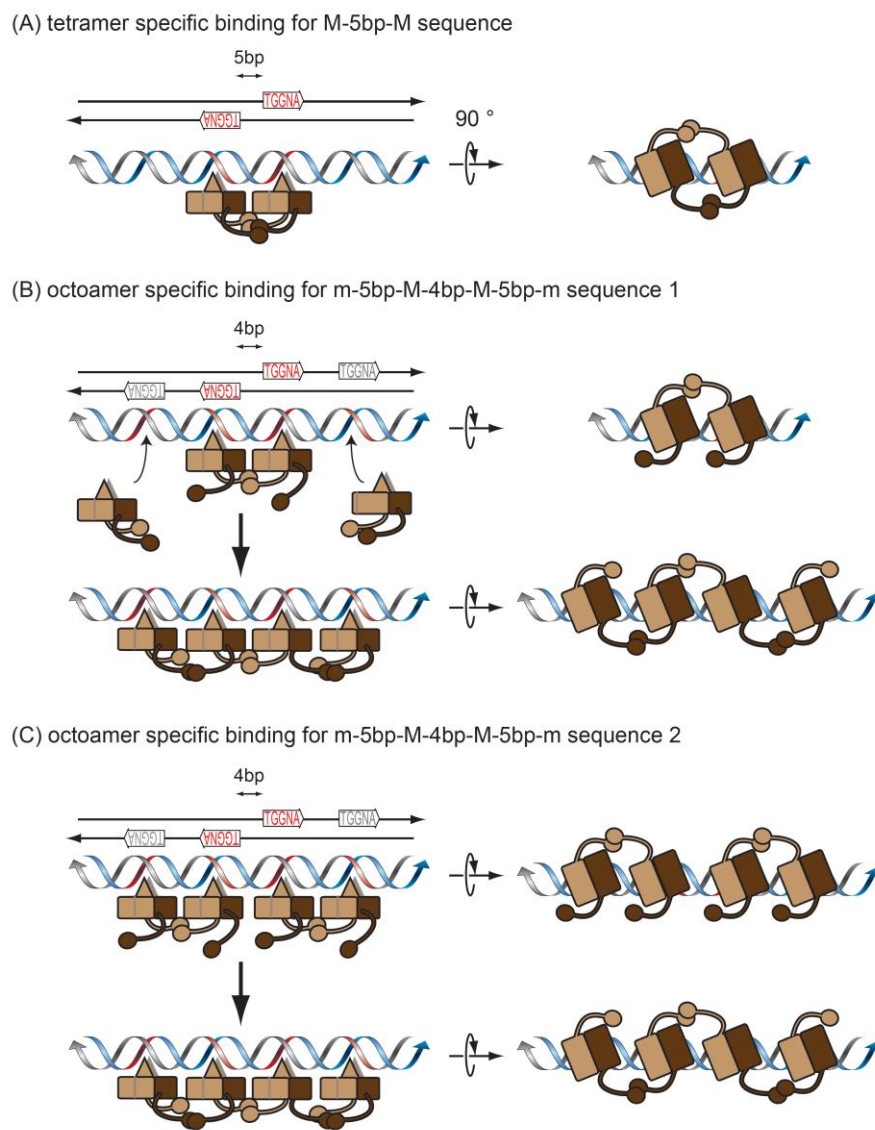


Figure 21. Binding model of AbrB and Abh. (A–C) Binding models for (A) tetramer specific binding for M-5bp-M sequence, (B) the first model of octamer specific binding for m-5bp-M-4bp-M-5bp-m sequence, and (C) the 2nd model of octamer specific binding for m-5bp-M-4bp-M-5bp-m sequence. Red coloration of 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 Δ *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*, *ycaA* 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 Δ *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 de-repress the gene expression (Strauch, 1995a). In our result, it seems to be clear that AbrB doesn'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 Δ *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 Δabh 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-NS-dependent (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.

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SUPPLEMENTARY DATA

Supplementary Table S1. Summary of transcriptome and ChAP-chip analyses.

gene				Transcriptome analysis						ChAP-chip analysis						Profile ID				
name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
				wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	Δabh wild	Δabh $\Delta abrB$ wild	Δabh wild							AbrB		Abh	
																wild -type	Δabh	wild -type	$\Delta abrB$	
<i>dnaA</i>	410	1750	+	7078	6317	5750	7267	0.90	0.81	1.03		*Broad	1	3629						
<i>dnaN</i>	1939	3075	+	5465	4876	4416	5247	0.91	0.81	0.95										
<i>yaaA</i>	3206	3421	+	4662	3989	3662	4420	0.85	0.78	0.94										
<i>recF</i>	3437	4549	+	6082	5370	4993	5632	0.88	0.82	0.93										
<i>yaaB</i>	4567	4725	+	7356	6416	6140	7508	0.87	0.84	1.02										
<i>gyrB</i>	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	
<i>gyrA</i>	6993	9458	+	8940	7550	7254	8606	0.85	0.81	0.96										
<i>yaaC</i>	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	
<i>guaB</i>	15913	17379	+	14698	10393	11161	13743	0.71	0.76	0.93										
<i>dacA</i>	17532	18863	+	8863	5643	4972	8512	0.64	0.56	0.96										
<i>yaaD</i>	19060	19944	+	11358	9844	9730	10360	0.87	0.86	0.91										
<i>yaaE</i>	19966	20556	+	10767	9489	9413	9737	0.88	0.87	0.90										
<i>serS</i>	20878	22155	+	9838	7030	7365	9434	0.71	0.75	0.96										
<i>tmsL-Ser</i>	22290	22382	+	12543	12042	12708	9641	0.90	1.01	0.82										
<i>dck</i>	22494	23147	-	4990	3025	3191	4992	0.61	0.64	0.92	10	dck	22781	23230	23006	11.9	10.9	22.3	39.2	
<i>dgk</i>	23144	23767	-	3704	2330	2247	3949	0.63	0.61	1.06										
<i>yaaH</i>	23866	25149	-	201	166	181	190	0.83	0.90	0.95										
<i>yaaI</i>	25219	25764	-	498	321	420	340	0.64	0.84	0.68										
<i>yaaJ</i>	25850	26335	+	1077	882	869	1003	0.82	0.81	0.94										
<i>scr</i>	26377	26730	+	12697	17971	17939	16077	1.39	1.39	1.26										
<i>dnaX</i>	26812	28503	+	4369	2916	2948	4162	0.67	0.67	0.95										
<i>yaaK</i>	28527	28850	+	15500	14269	14413	14814	0.92	0.93	0.96										
<i>recR</i>	28865	29461	+	6945	6574	6140	7091	0.95	0.89	1.02	11	recR	28901	29486	29194	10.7	7.0	23.3	46.6	
<i>yaaL</i>	29479	29703	+	5722	4843	4655	5498	0.85	0.81	0.97										
<i>bofA</i>	29770	30033	+	2171	1586	1548	2000	0.73	0.72	0.92										
<i>csfB</i>	35529	35723	+	331	322	355	290	0.98	1.07	0.89										
<i>xpaC</i>	35843	36457	+	1482	1179	1388	1735	0.80	0.94	1.17										
<i>yaaN</i>	36476	37636	+	1504	1263	1547	1629	0.84	1.04	1.09										
<i>yaaO</i>	37718	39160	+	2261	1709	1831	2340	0.76	0.82	1.04										
<i>tmk</i>	39157	39795	+	3098	2194	2303	3229	0.71	0.74	1.04										
<i>yaaQ</i>	39869	40198	+	6081	4657	4866	6236	0.76	0.80	1.02										
<i>yaaR</i>	40211	40651	+	5811	3975	4444	6155	0.69	0.77	1.06	13	yaaR	40082	40616	40349	44.6	18.3	34.6	5.0	
<i>holB</i>	40663	41652	+	4563	3099	3532	4788	0.68	0.77	1.05										
<i>yaaT</i>	41655	42482	+	6586	4558	5157	6633	0.69	0.78	1.01										
<i>yabA</i>	42497	42856	+	2822	1824	2051	3213	0.65	0.73	1.13										
<i>yabB</i>	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	
<i>yazA</i>	43645	43944	+	1810	759	835	1524	0.41	0.46	0.83										
<i>yabC</i>	43919	44797	+	2585	1406	1620	2373	0.55	0.63	0.92										
<i>abrB</i>	44846	45136	-	15102	52	46	14793	0.00	0.00	0.98										
<i>metG</i>	45631	47625	+	7112	6847	6826	7269	0.96	0.96	1.02	15	Inter	45199	45325	45262	4.7	2.3	0.7	2.0	
<i>yabD</i>	47704	48471	+	2706	2618	2664	2566	0.97	0.98	0.95		*Broad	45743	49864						
<i>yabE</i>	48627	49940	+	793	3208	2051	733	4.06	2.61	0.93										
<i>rmvV</i>	50085	50645	+	1925	1575	1230	1786	0.82	0.64	0.93										
<i>ksgA</i>	50638	51516	+	4063	3008	2628	3592	0.74	0.65	0.88										
<i>yabG</i>	51678	52550	+	482	355	371	437	0.74	0.77	0.91										
<i>veg</i>	52761	53021	+	10421	11411	10553	9289	1.10	1.01	0.89										
<i>sspF</i>	53181	53366	+	986	1280	1513	890	1.31	1.54	0.91										
<i>ipk</i>	53514	54383	+	5113	4804	4585	4985	0.94	0.90	0.97										
<i>purR</i>	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	
<i>yabJ</i>	55293	55670	+	8923	9278	9407	9362	1.04	1.05	1.05										
<i>spoVG</i>	55864	56157	+	7085	23826	24259	9115	3.38	3.45	1.28	25	Inter	55586	56001	55794	12.3	18.0	2.6	2.5	
<i>gcaD</i>	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	
<i>prs</i>	57743	58696	+	11962	8465	8204	12139	0.71	0.69	1.01										
<i>ctc</i>	58781	59395	+	18581	14563	15467	16073	0.78	0.83	0.86										
<i>spoVC</i>	59502	60068	+	3976	2375	2718	3322	0.60	0.69	0.83										
<i>yabK</i>	60128	60358	+	5427	3351	3727	4756	0.62	0.69	0.88										
<i>mfd</i>	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	
<i>spoVT</i>	64097	64633	+	3066	2365	2694	2741	0.77	0.88	0.89										
<i>yabM</i>	64815	66413	+	1749	1230	1302	1761	0.70	0.74	1.01	28	yabM	65055	65249	65152	5.4	2.5	0.6	0.0	
<i>yabN</i>	66403	67872	+	4762	4351	4614	4807	0.91	0.97	1.01										
<i>yabO</i>	67875	68135	+	4397	3774	4158	4342	0.86	0.95	0.99										
<i>yabP</i>	68214	68516	+	2867	2470	2425	3172	0.86	0.85	1.11										
<i>yabQ</i>	68513	69148	+	4872	4714	4756	5124	0.97	0.98	1.05										
<i>divIC</i>	69166	69543	+	6129	7178	6617	6492	1.17	1.08	1.06										
<i>yabR</i>	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	
<i>spoIIE</i>	70536	73019	+	419	322	346	373	0.77	0.82	0.89										
<i>yabS</i>	73104	73841	+	417	427	440	402	1.03	1.06	0.96										
<i>yabT</i>	73807	74823	+	533	496	521	492	0.93	0.98	0.92										
<i>yacA</i>	74927	76345	+	3602	3582	3604	4271	0.99	1.00	1.18										
<i>hprT</i>	76342	76884	+	6103	5116	5040	7175	0.84	0.82	1.17		*Broad	76463	79104						
<i>ftsH</i>	76982	78895	+	20524	20731	21287	20838	1.01	1.04	1.02										

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abhB$	Δabh	$\Delta abhB$ / wild	Δabh $\Delta abhB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abhB$																		
<i>yacB</i>	79090	79791	+	7006	3967	4807	7821	0.56	0.68	1.11											
<i>hslO</i>	79877	80752	+	6953	4557	5186	7982	0.65	0.74	1.15											
<i>yacD</i>	80799	81692	+	4812	2593	3208	5368	0.54	0.66	1.12											
<i>cysK</i>	81768	82694	+	9909	9268	10822	11090	0.93	1.09	1.12											
<i>pabB</i>	82861	84273	+	2932	2115	2197	2722	0.72	0.75	0.93											
<i>pabA</i>	84287	84871	+	4249	3470	3657	4184	0.82	0.86	0.98											
<i>pabC</i>	84871	85752	+	3764	3082	3047	3711	0.82	0.81	0.99											
<i>sul</i>	85734	86591	+	5775	4692	4783	5596	0.81	0.83	0.97											
<i>folB</i>	86584	86946	+	7284	6246	6213	7242	0.86	0.85	0.99											
<i>folK</i>	86943	87446	+	5953	4817	4891	5903	0.81	0.82	0.99											
<i>yazB</i>	87398	87607	+	6866	5729	5822	7306	0.83	0.85	1.06											
<i>yacF</i>	87631	88632	+	8106	7353	7139	7997	0.91	0.88	0.99											
<i>lysS</i>	88724	90223	+	10405	9315	9004	10242	0.90	0.87	0.98											
<i>trnJ-Leu1</i>	95646	95731	+	21683	24426	24548	20522	1.13	1.13	0.94											
<i>ctnR</i>	101446	101910	+	3501	3407	4086	4819	0.98	1.17	1.37											
<i>mesA</i>	101924	102481	+	3548	3746	4334	5106	1.09	1.25	1.44											
<i>mesB</i>	102481	103572	+	6600	7018	8052	8858	1.07	1.23	1.34											
<i>clpC</i>	103569	106001	+	8720	11082	12089	11232	1.28	1.40	1.28											
<i>radA</i>	106093	107469	+	3086	3873	4056	3965	1.27	1.33	1.28											
<i>yacL</i>	107473	108555	+	5467	5488	5879	6347	1.00	1.07	1.16											
<i>yacK</i>	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		
<i>ispD</i>	109786	110484	+	6417	5825	6056	6542	0.91	0.95	1.02											
<i>ispF</i>	110477	110953	+	5588	5017	5047	6144	0.90	0.90	1.10											
<i>glxX</i>	111044	112495	+	11759	10285	10161	12311	0.87	0.86	1.05											
<i>cysE</i>	112797	113450	+	4654	3170	3121	4268	0.68	0.67	0.92											
<i>cysS</i>	113447	114847	+	5450	3819	4085	5500	0.70	0.75	1.01											
<i>yazC</i>	114851	115282	+	4082	2947	3122	4260	0.72	0.77	1.05											
<i>yacO</i>	115266	116015	+	4567	3867	3769	4866	0.85	0.83	1.07											
<i>yacP</i>	116022	116534	+	5558	4176	4240	5527	0.75	0.76	0.99											
<i>sigH</i>	116597	117253	+	7373	10436	9935	7394	1.42	1.35	1.00	38	Inter	116396	116760	116578	13.1	16.1	9.2	4.0		
<i>rpmG_1</i>	117346	117495	+	5398	6384	6403	5249	1.18	1.18	0.97											
<i>secE</i>	117529	117708	+	4998	5815	5610	4921	1.21	1.14	1.01											
<i>nusG</i>	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		
<i>rpIK</i>	118588	119013	+	25543	24280	23122	25609	0.95	0.91	1.00	40	rpIK	118419	118953	118686	7.4	24.0	10.6	8.1		
<i>rpIA</i>	119107	119805	+	24092	22151	20805	24225	0.92	0.86	1.01	40.1	rpIA	118963	119293	119128	2.9	8.6	3.9	1.8		
<i>rpIJ</i>	120057	120557	+	25238	23925	22116	25027	0.95	0.88	0.99											
<i>rpIL</i>	120604	120975	+	18467	16829	15391	17600	0.91	0.83	0.95											
<i>yxbB</i>	121065	121670	+	5797	5856	4725	5251	1.07	0.82	0.87											
<i>rpoB</i>	121916	125497	+	13848	13696	13480	13538	0.99	0.97	0.98	41	Inter	121360	122081	121721	50.3	65.9	56.9	10.5		
<i>rpoC</i>	125559	129158	+	17243	17617	17268	16819	1.02	1.00	0.97	41.1	rpoB	122091	122385	122238	13.3	9.1	13.1	5.5		
<i>yxbF</i>	129339	129587	+	26440	25323	23367	25618	0.96	0.88	0.97	42	rpoC	125627	126263	125945	21.6	31.0	24.5	47.2	P01	
<i>rpsL</i>	129701	130117	+	28914	28704	27643	28294	0.99	0.96	0.98		*Broad	129520	132009							
<i>rpsG</i>	130159	130629	+	25900	26022	23227	26113	1.00	0.90	1.01											
<i>fusA</i>	130683	132761	+	30325	29173	28104	30108	0.96	0.93	0.99											
<i>tuf</i>	132881	134071	+	30935	30643	30129	31441	0.99	0.97	1.02											
<i>ybaC</i>	134170	135126	+	1048	721	716	1071	0.69	0.68	1.03											
<i>rpsJ</i>	135362	135670	+	30765	29417	29022	31131	0.96	0.94	1.01	45	Inter	135096	135477	135287	4.6	14.3	5.8	7.7		
<i>rpIC</i>	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		
<i>rpID</i>	136367	136990	+	26161	26196	24796	27056	1.00	0.95	1.03											
<i>rpIW</i>	136990	137277	+	30793	29478	28330	29378	0.96	0.92	0.95											
<i>rpIB</i>	137309	138142	+	29552	29483	28640	29696	1.00	0.97	1.01											
<i>rpsS</i>	138200	138478	+	23258	23484	21417	24263	1.02	0.92	1.04											
<i>rpIV</i>	138495	138836	+	31673	31879	30921	31279	1.01	0.98	0.99											
<i>rpsC</i>	138840	139496	+	24323	24773	22036	23941	1.02	0.91	0.98											
<i>rpIP</i>	139498	139932	+	26685	27217	25722	26806	1.02	0.96	1.00	47	rpIP	139789	139863	139826	0.6	2.3	0.9	0.6		
<i>rpmC</i>	139922	140122	+	24524	24143	21858	24512	0.98	0.89	1.00											
<i>rpsQ</i>	140145	140408	+	27588	25796	24332	27011	0.93	0.88	0.98											
<i>rpIN</i>	140449	140817	+	29582	28775	27733	28749	0.97	0.94	0.97											
<i>rpIX</i>	140855	141166	+	27565	26879	24697	27078	0.97	0.90	0.98											
<i>rpIE</i>	141193	141732	+	27393	26937	25348	27757	0.98	0.93	1.01											
<i>rpsN_1</i>	141755	141940	+	20981	19048	16950	20964	0.91	0.81	1.00											
<i>rpsH</i>	141972	142370	+	30272	29073	27961	29120	0.96	0.92	0.96											
<i>rpIF</i>	142400	142939	+	23487	22261	20462	23185	0.95	0.87	0.99											
<i>rpIR</i>	142972	143334	+	30357	29577	28215	29090	0.97	0.93	0.96											
<i>rpsE</i>	143359	143859	+	25653	24262	22491	24579	0.95	0.88	0.96											
<i>rpmD</i>	143873	144052	+	16375	12850	11020	15529	0.78	0.67	0.95											
<i>rpIO</i>	144083	144523	+	27726	26172	24154	26772	0.94	0.87	0.97											
<i>secY</i>	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		
<i>adk</i>	145875	146528	+	25010	23616	22049	24592	0.94	0.88	0.98											
<i>map</i>	146525	147271	+	22151	21058	18964	21778	0.95	0.86	0.98											

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID											
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c									
					wild	$\Delta abrB$	Δabh $\Delta abhB$	Δabh	$\Delta abhB$ / wild	Δabh $\Delta abhB$ / wild	Δabh / wild							AbrB		Abh							
wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh										
<i>ybdN</i>	224063	224920	-	265	5990	6621	269	22.51	25.01	1.01																	
<i>ybdO</i>	225052	226236	+	388	2969	2833	451	7.70	7.32	1.15	80	Inter	224495	225420	224958										P02		
<i>ybxG</i>	226554	227942	+	2810	1663	1812	2571	0.59	0.65	0.92																	
<i>csgA</i>	228054	228302	+	180	149	166	142	0.83	0.93	0.79																	
<i>ybxH</i>	228319	228510	+	480	419	495	427	0.87	1.03	0.89																	
<i>ybxI</i>	228537	229340	-	526	1135	1208	583	2.16	2.30	1.11	81	ybxI	228643	228939	228791												
<i>cypC</i>	229513	230766	+	731	561	714	542	0.77	0.98	0.74	82	Inter	229306	229619	229463												
<i>ybyB</i>	230807	231067	-	6685	4686	7705	2697	0.70	1.15	0.42																	
<i>ybeC</i>	231336	232955	+	6871	8206	7538	4769	1.20	1.10	0.70	83	Inter	230547	231863	231205												P01
<i>glpQ</i>	233002	233883	-	22513	4521	6528	18033	0.20	0.29	0.80	84	ybeC	231941	232084	232013												
<i>glpT</i>	233982	235316	-	21673	4030	5527	17219	0.19	0.26	0.80	85	glpQ	233760	233869	233815												
<i>ybeF</i>	235613	235861	+	889	742	884	880	0.83	0.99	0.97	86	ybeF	235477	235858	235668												
<i>ybfA</i>	235953	236870	+	1113	720	799	976	0.65	0.72	0.88																	
<i>ybfB</i>	236867	238117	+	885	631	736	798	0.71	0.84	0.90																	
<i>ybfE</i>	238152	238436	-	1773	998	1131	2013	0.56	0.64	1.13																	
<i>ybfF</i>	238632	239543	-	3131	1476	1746	3003	0.47	0.56	0.96	87	ybfF	238979	239377	239178												
<i>ybfG</i>	239632	241830	-	3516	1756	2112	2984	0.50	0.60	0.85																	
<i>ybfH</i>	241905	242825	-	942	815	857	988	0.86	0.91	1.05																	
<i>ybfI</i>	242822	243649	-	540	435	468	561	0.81	0.87	1.04																	
<i>purT</i>	243880	245034	+	5299	5437	6005	4610	1.03	1.13	0.87																	
<i>mpr</i>	245178	246119	+	522	945	989	491	1.82	1.90	0.94	89	Inter	244980	245225	245103												
<i>ybfJ</i>	246082	246480	+	205	448	466	220	2.19	2.27	1.07																	
<i>ybfK</i>	246646	247536	+	1411	2354	2112	1527	1.67	1.50	1.08	90	Inter	246374	246653	246514												
<i>pssA</i>	247732	248265	+	3213	4269	3740	3473	1.33	1.17	1.09	91	Inter	247411	247724	247568												
<i>ybfM</i>	248256	248744	+	3126	3508	3365	3235	1.13	1.08	1.04																	
<i>psd</i>	248737	249528	+	3561	4077	3925	3636	1.15	1.11	1.03																	
<i>ybfN</i>	249583	249861	+	914	893	906	849	0.98	0.99	0.93																	
<i>ybfO</i>	249967	251307	+	527	8471	9549	408	16.31	18.69	0.78	92	Inter	249706	250104	249905												
<i>ybfP</i>	251415	252302	+	547	4897	5443	536	8.96	9.99	0.99																	
<i>ybfQ</i>	252502	253470	+	8186	10412	11299	7840	1.27	1.38	0.96	93	Inter	252137	252603	252370												
<i>glpP</i>	253506	254750	-	860	1007	1238	745	1.18	1.43	0.86																	
<i>gamP</i>	254895	256790	-	4987	3695	4559	3619	0.75	0.92	0.73																	
<i>gamA</i>	256811	257560	-	5480	4328	5255	4019	0.79	0.96	0.73																	
<i>ybgA</i>	257779	258486	+	1293	843	934	1142	0.66	0.73	0.89																	
<i>ybgB</i>	258520	258795	+	2019	1636	1893	1864	0.81	0.93	0.92																	
<i>ybgE</i>	259004	260074	+	599	451	479	583	0.75	0.80	0.97																	
<i>ybgF</i>	260111	261523	-	425	354	385	408	0.83	0.91	0.96																	
<i>mmuM</i>	261644	262591	-	811	679	720	745	0.84	0.89	0.92																	
<i>ybgH</i>	262720	264111	-	576	490	535	622	0.85	0.93	1.08																	
<i>ybgJ</i>	264181	265164	-	281	210	235	274	0.75	0.84	0.98																	
<i>ycbA</i>	265536	266699	+	925	706	821	835	0.76	0.89	0.90																	
<i>ycbB</i>	266710	267654	+	1126	940	1060	1127	0.84	0.95	1.00																	
<i>ycbC</i>	267881	268807	+	392	308	328	371	0.78	0.84	0.95																	
<i>ycbD</i>	268837	270303	+	434	321	326	467	0.74	0.75	1.08																	
<i>ycbE</i>	270387	271754	+	400	333	355	430	0.83	0.89	1.09																	
<i>ycbF</i>	271791	273158	+	410	312	329	455	0.76	0.80	1.13																	
<i>ycbG</i>	273228	273929	+	1668	1606	1455	1403	0.96	0.87	0.84																	
<i>ycbH</i>	274020	275552	+	733	534	599	710	0.73	0.82	0.97																	
<i>ycbJ</i>	275829	276749	+	2220	11016	10665	1639	4.98	4.82	0.74	96	ycbJ	276294	276454	276374												
<i>yczA</i>	277151	277312	+	603	984	848	600	1.66	1.42	1.02																	
<i>ycbK</i>	277333	278271	+	1229	1475	1448	1075	1.20	1.18	0.87	97	ycbK	277246	277644	277445												
<i>ycbL</i>	278368	279048	+	443	369	381	391	0.83	0.86	0.88																	
<i>ycbM</i>	279050	279526	+	1289	1125	1109	1115	0.87	0.86	0.86																	
<i>ycbN</i>	279682	280521	+	833	670	635	679	0.80	0.76	0.81																	
<i>ycbO</i>	280640	281254	+	977	905	948	981	0.93	0.97	1.00																	
<i>ycbP</i>	281309	281695	-	1122	779	1096	698	0.70	0.97	0.63																	
<i>cwlJ</i>	282009	282437	+	361	371	371	34																				

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild	wild -type	Δabh	wild -type	$\Delta abrB$											
<i>lmrB</i>	288205	289644	-	1561	1667	1576	1650	1.11	1.03	1.05	876	ysxD	2878206	2878536	2878371	18.2	2.3	18.9	0.5	P05	
<i>lmrA</i>	289684	290250	-	1065	903	817	945	0.88	0.79	0.89	103	hnrB	288671	289527	289099	31.3	26.6	42.5	112.8	P01	
<i>yccC</i>	290467	291594	+	484	390	439	460	0.81	0.91	0.95											
<i>lip</i>	291757	292395	+	980	11178	12933	1791	11.41	13.20	1.83	104	Inter	291016	292315	291666	85.5	135.3	56.5	31.7	P01	
<i>yczC</i>	292433	292816	-	882	1242	1331	741	1.42	1.51	0.84	105	yczC	292512	293114	292813	23.6	23.3	15.5	3.5		
<i>yccF</i>	293051	294127	+	6074	5556	5577	5625	0.92	0.92	0.93											
<i>yccG</i>	294167	295123	-	1324	1207	1168	1219	0.91	0.88	0.92											
<i>yccH</i>	295136	295837	-	927	928	883	934	1.00	0.95	1.01											
<i>natA</i>	295981	296721	+	894	798	746	797	0.91	0.84	0.89	106	Inter	295827	295987	295907	4.7	6.0	0.2	-0.2		
<i>natB</i>	296722	297882	+	1202	1220	1130	1142	1.02	0.94	0.95											
<i>yccK</i>	298018	298950	+	818	1401	1497	859	1.72	1.84	1.05											
<i>ycaA</i>	298990	300054	-	422	1131	3205	926	2.68	7.50	2.19											
<i>ycaB</i>	300382	301800	+	560	927	931	641	1.67	1.67	1.13	107	Inter	299771	300798	300285	73.6	76.7	92.9	196.3	P01	
<i>ycaC</i>	301987	303348	+	772	542	528	668	0.71	0.69	0.86	108	ycaB	301080	301359	301220	5.6	2.7	8.5	8.1		
<i>ycaD</i>	303356	303859	-	371	443	438	443	1.19	1.18	1.19											
<i>rapJ</i>	303982	305103	+	1151	2436	2582	1697	2.14	2.27	1.47	109	Inter	303597	304198	303898	37.2	33.4	26.0	-0.5	P02	
<i>ycaF</i>	305210	305986	+	1297	805	1061	848	0.62	0.82	0.67											
<i>ycaG</i>	306011	307696	+	839	709	929	637	0.85	1.10	0.76											
<i>ycaH</i>	307884	308843	+	1446	548	599	1033	0.39	0.42	0.71											
<i>ycaI</i>	308899	309594	+	1956	999	910	1531	0.52	0.47	0.78											
<i>ycaA</i>	309552	310394	+	2546	1591	1439	2271	0.63	0.57	0.89											
<i>ycaB</i>	310432	311373	-	680	629	737	860	0.94	1.10	1.27											
<i>ycaC</i>	311711	312310	+	12296	14684	15677	14118	1.19	1.27	1.15											
<i>ycaD</i>	312332	312913	+	12887	15308	16923	14918	1.19	1.31	1.16											
<i>ycaE</i>	312948	313526	+	11650	13302	14335	13368	1.14	1.23	1.15											
<i>ycaF</i>	313577	314350	+	14128	15358	16236	15063	1.09	1.15	1.07											
<i>ycaG</i>	314435	316048	+	3869	4728	5353	4471	1.23	1.40	1.16											
<i>ycaH</i>	316064	317155	+	5254	6787	7466	5842	1.29	1.42	1.11											
<i>ycaI</i>	317277	318479	+	1958	1249	1317	1698	0.64	0.67	0.87											
<i>ycaJ</i>	318732	319904	-	373	321	340	376	0.86	0.91	1.01											
<i>ycaK</i>	319973	320275	-	1195	1378	1207	1008	1.26	1.03	0.90											
<i>opuAA</i>	320565	321821	+	3448	3742	3115	3458	1.08	0.90	1.00	110	Inter	320154	320552	320353	16.4	2.4	14.8	10.7		
<i>opuAB</i>	321823	322671	+	4556	5002	4300	4867	1.10	0.95	1.07	110	opuAA	320545	321130	320838	27.7	2.8	50.8	42.7	P06	
<i>opuAC</i>	322671	323552	+	4826	4945	4381	4841	1.03	0.91	1.00											
<i>anhX</i>	323571	324740	-	554	451	508	564	0.82	0.92	1.02											
<i>ycaA</i>	325133	326323	+	316	418	427	324	1.32	1.35	1.03											
<i>ycaB</i>	326439	327020	+	1155	632	762	1195	0.55	0.66	1.03											
<i>amyE</i>	327169	329151	+	3944	1178	2629	4614	0.29	0.61	1.16	111	Inter	326835	327233	327034	12.2	11.0	11.2	2.1		
<i>ldh</i>	329328	330293	+	15105	13890	15045	14145	0.92	0.99	0.93	112	amyE	327668	328049	327859	21.6	25.9	17.5	3.0		
<i>lciP</i>	330325	331950	+	2250	2312	2298	2346	1.02	1.01	1.04											
<i>mdr</i>	332258	333538	-	2015	1681	1622	1559	0.84	0.80	0.77											
<i>ycaE</i>	333651	334118	+	685	513	522	707	0.75	0.76	1.03											
<i>ycaF</i>	334192	334821	+	870	702	647	751	0.81	0.74	0.87											
<i>ycaG</i>	334891	335652	+	607	498	427	578	0.82	0.70	0.95											
<i>ycaH</i>	335684	336817	-	361	350	384	367	0.97	1.06	1.02											
<i>ycaI</i>	336984	337718	+	503	425	479	541	0.85	0.95	1.08											
<i>nadE</i>	337848	338666	+	10772	9897	10227	10572	0.92	0.95	0.98											
<i>tmrB</i>	338716	339309	-	396	418	381	376	1.08	0.97	0.97											
<i>aroK</i>	339585	340145	+	1659	938	1067	1459	0.57	0.64	0.88											
<i>ycaJ</i>	340173	340859	-	468	550	641	473	1.19	1.37	1.01											
<i>ycaK</i>	341052	342026	+	512	458	442	528	0.90	0.86	1.03											
<i>cah</i>	342098	343054	+	1354	1214	1314	1141	0.90	0.97	0.84											
<i>ycaL</i>	343138	343920	+	1678	1457	1513	1372	0.88	0.91	0.82											
<i>ycaM</i>	344111	345022	+	284	247	257	254	0.87	0.91	0.89											
<i>ycaN</i>	345039	346586	+	470	419	415	453	0.89	0.88	0.96											
<i>ycaO</i>	346782	348131	+	2101	1989	1887	1999	0.95	0.90	0.95	115	ycaO	347422	347599	347511	3.9	5.5	1.8	0.5		
<i>ycaP</i>	348284	349519	+	993	960	992	990	0.98	1.01	1.00	116	Inter	348119	348262	348191	4.8	1.3	0.1	-0.7		
<i>ycaQ</i>	349556	350413	-	2450	1905	2002	2500	0.78	0.82	1.02											
<i>ycaR</i>	350418	351302	-	1567	1117	1208	1677	0.71	0.78	1.07											
<i>ycaS</i>	351402	352256	-	243	221	232	254	0.91	0.95	1.04											
<i>ycaT</i>	352418	353428	+	5223	6373	6837	5472	1.22	1.31	1.05											
<i>nasF</i>	353460	354911	-	1598	1247	1184	1391	0.78	0.74	0.87											
<i>nasE</i>	354972	355292	-	1426	1177	1022	1231	0.83	0.72	0.87											
<i>nasD</i>	355324	357741	-	432	298	316	361	0.71	0.76	0.85											
<i>nasC</i>	357863	359995	-	283	242	256	278	0.86	0.91	0.99											

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$																		
<i>rsbT</i>	520167	520568	+	7451	7461	7829	6919	1.00	1.05	0.93											
<i>rsbU</i>	520580	521587	+	5290	5844	6194	5721	1.11	1.17	1.08											
<i>rsbV</i>	521649	521978	+	9592	8182	8899	7131	0.85	0.93	0.74											
<i>rsbW</i>	521975	522457	+	13929	10765	11789	9964	0.77	0.85	0.70											
<i>sigB</i>	522417	523211	+	6697	5838	6788	4471	0.89	1.05	0.66	156	sigB	522438	522767	522603	15.9	9.3	6.2	0.5		
<i>rsbX</i>	523211	523810	+	7298	7436	8101	4421	1.07	1.18	0.61											
											157	Inter	523780	524212	523996	12.0	22.5	2.7	29.8		
<i>ycdF</i>	524053	524346	+	554	364	383	513	0.64	0.69	0.91											
<i>ycdG</i>	524343	524783	+	891	872	862	865	0.99	0.98	0.97											
<i>ycdH</i>	524767	525210	+	518	449	465	491	0.87	0.91	0.94											
<i>ycdI</i>	525304	527463	+	3597	3194	3465	3991	0.89	0.97	1.11											
<i>ycdK</i>	527690	528142	+	642	543	556	698	0.85	0.87	1.08	159	ycdK	527809	528036	527923	7.6	4.0	2.3	0.8		
<i>tms-Leu1</i>	528735	528819	+	801	1111	1242	945	1.41	1.56	1.24											
<i>tms-Leu2</i>	528897	528983	+	1358	1512	1423	1384	1.12	1.06	1.06											
<i>ycdL</i>	529066	530172	-	314	427	521	285	1.35	1.64	0.91											
<i>ycdM</i>	530185	530694	-	593	626	719	492	1.06	1.20	0.84											
<i>ycdN</i>	530691	531074	+	836	620	709	718	0.75	0.83	0.86											
<i>sacV</i>	531348	531542	+	444	385	462	389	0.87	1.03	0.87											
<i>ycdO</i>	531853	532113	+	247	187	205	230	0.76	0.84	0.94											
<i>ycdP</i>	532483	532863	+	431	373	380	386	0.87	0.88	0.90											
<i>ycdQ</i>	532899	534341	+	138	119	129	137	0.86	0.93	0.99											
<i>ycdR</i>	534334	535392	+	180	169	182	175	0.94	1.01	0.97	164	ycdR	534609	534888	534749	11.1	2.5	9.8	16.1		
<i>ycdS</i>	535657	535926	+	395	359	409	371	0.91	1.04	0.94											
<i>ycdT</i>	535965	536231	+	351	332	330	309	0.94	0.94	0.88											
<i>yddA</i>	536248	536556	+	179	173	192	169	0.97	1.08	0.95											
<i>yddB</i>	536546	537610	+	167	125	149	144	0.75	0.89	0.86											
<i>yddC</i>	537622	537870	+	307	281	338	308	0.91	1.09	1.01											
<i>yddD</i>	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		
<i>yddE</i>	538295	540790	+	169	153	163	162	0.90	0.97	0.96											
<i>yddF</i>	540809	541135	+	169	139	152	168	0.84	0.93	0.99											
<i>yddG</i>	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		
<i>yddH</i>	543583	544572	+	365	306	321	353	0.84	0.88	0.97											
<i>yddI</i>	544587	545093	+	244	194	205	210	0.79	0.84	0.86											
											167	Inter	544945	545292	545119	16.1	15.8	4.5	0.7		
<i>yddJ</i>	545156	545536	+	243	605	830	261	2.49	3.41	1.07	167	yddJ	545302	545530	545416	7.5	6.0	0.4	1.0		
<i>yddK</i>	545727	546527	-	2615	2176	2361	4114	0.83	0.90	1.57											
											169	Inter	546373	547179	546776	77.5	89.2	28.4	3.9		
<i>rapI</i>	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		
<i>phrI</i>	547999	548118	+	1879	3151	3167	2086	1.71	1.70	1.12											
<i>yddM</i>	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		
<i>yddN</i>	549783	550802	-	219	185	199	224	0.85	0.91	1.02											
											172	Inter	550912	551106	551009	3.6	3.1	0.7	0.4		
<i>lrpA</i>	551062	551472	+	1072	833	843	1043	0.78	0.78	0.96											
											173	Inter	551286	551684	551485	7.4	6.3	1.5	21.1		
<i>lrpB</i>	551595	552044	-	207	188	192	238	0.91	0.93	1.16											
<i>yddQ</i>	552159	552701	+	908	424	445	985	0.47	0.49	1.08	174	yddQ	552102	552534	552318	26.4	27.0	8.4	7.2		
<i>yddR</i>	553254	554018	+	577	324	316	548	0.57	0.55	0.95											
<i>yddS</i>	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		
<i>yddT</i>	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		
<i>ydeA</i>	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		
											181	Inter	558443	558892	558668	31.3	29.3	14.5	8.4		
<i>cspC</i>	558808	559008	+	4075	5390	4181	3914	1.32	1.03	0.96											
											182	Inter	559106	559317	559212	5.9	3.0	0.5	0.4		
<i>ydeB</i>	559695	560156	-	835	1453	1792	1376	1.74	2.19	1.68											
											183	Inter	560092	560286	560189	4.7	0.8	3.5	5.0		
<i>ydeE</i>	560724	560960	-	846	714	845	742	0.84	1.00	0.88											
<i>ydeC</i>	561058	561933	-	359	288	318	331	0.81	0.89	0.93											
<i>ydeD</i>	562046	563005	+	334	306	317	311	0.91	0.95	0.93											
<i>ydeE</i>	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		
<i>ydeF</i>	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		
<i>ydeG</i>	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		
<i>ydeH</i>	567206	567652	+	397	1287	1036	494	3.20	2.59	1.26											
<i>ydeI</i>	567889	568482	+	584	611	628	582	1.05	1.07	1.00											
<i>ydeJ</i>	568834	569493	-	673	2322	2227	522	3.47	3.30	0.78											
											187	Inter	569442	569704	569573	12.3	6.7	0.9	-0.3		
<i>ydeK</i>	569915	570778	-	323	363	356	376	1.12	1.10	1.17											
											188	Inter	570734	570996	570865	9.4	1.2	3.9	0.0		
<i>ydeL</i>	570933	572324	+	285	284	308	283	0.99	1.08	0.99											

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$	Δabh / wild							AbrB		Abh	
wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh				
<i>ydeM</i>	572518	572943	+	1164	1061	1053	1071	0.91	0.90	0.92											
<i>ydeN</i>	572996	573568	-	848	790	848	884	0.95	1.02	1.06											
<i>ydzF</i>	573650	573979	-	890	811	857	907	0.92	0.97	1.01											
<i>ydeO</i>	574234	575106	+	2873	3199	3011	2853	1.12	1.05	0.99	189	ydeO	574423	574583	574503	4.5	2.3	1.2	0.4		
<i>ydeP</i>	575256	575642	-	902	408	468	875	0.45	0.52	0.97											
<i>ydeQ</i>	575753	576346	+	377	259	276	302	0.70	0.74	0.80											
<i>ydeR</i>	576490	577677	-	297	295	300	313	0.99	1.01	1.05											
<i>ydeS</i>	577881	578477	+	2176	1758	1667	2052	0.81	0.77	0.94											
<i>ydeT</i>	579085	579420	+	669	515	481	643	0.79	0.72	0.97											
<i>ydfA</i>	579433	580740	+	1867	1311	1259	1709	0.71	0.67	0.91											
<i>ydfB</i>	581238	582023	+	325	437	455	328	1.35	1.41	1.02											
<i>ydfC</i>	582080	583000	-	428	423	466	405	0.98	1.09	0.94											
<i>ydfD</i>	583133	584581	+	268	242	252	262	0.91	0.94	0.98											
<i>ydfE</i>	584699	585322	-	316	542	522	300	1.71	1.64	0.95											
<i>ydfF</i>	585412	586092	+	1225	1521	1514	1016	1.24	1.24	0.83											
<i>ydfG</i>	586172	586615	-	2123	2416	2497	2109	1.14	1.18	0.99											
<i>ydfH</i>	587288	588511	+	686	630	635	651	0.92	0.93	0.95											
<i>ydfI</i>	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		
<i>ydfJ</i>	589261	591435	+	276	244	254	259	0.88	0.92	0.94											
<i>nap</i>	591847	592749	-	1203	3213	2883	1293	2.70	2.42	1.08											
<i>ydfK</i>	592951	593640	-	366	342	344	344	0.95	0.95	0.95											
<i>ydfL</i>	593730	594542	-	516	479	486	516	0.93	0.95	1.00											
<i>ydfM</i>	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		
<i>ydfN</i>	596022	596642	+	238	196	205	263	0.83	0.86	1.10											
<i>ydfO</i>	596658	597596	+	423	360	375	441	0.85	0.89	1.04											
<i>ydfP</i>	597698	598087	+	647	606	566	653	0.94	0.87	1.01											
<i>ydfQ</i>	598273	598611	+	176	165	169	164	0.93	0.96	0.93											
<i>ydzH</i>	598651	598887	-	95	76	90	82	0.80	0.94	0.87											
<i>ydfR</i>	599773	600450	-	134	134	166	140	1.00	1.23	1.04											
<i>ydfS</i>	600563	601270	+	198	189	187	185	0.96	0.94	0.93											
<i>cotP</i>	601285	601716	-	129	144	140	129	1.11	1.08	0.99											
<i>ydgA</i>	601729	601971	-	190	163	180	155	0.86	0.95	0.82											
<i>ydgB</i>	601985	602257	-	192	186	194	150	0.97	1.01	0.78											
<i>ydgC</i>	602556	603143	+	4428	7922	7860	3764	1.82	1.80	0.85											
<i>ydgD</i>	603140	603484	+	1344	3195	3154	1378	2.50	2.47	1.07											
<i>ydgE</i>	603647	604120	+	932	1951	2009	885	2.18	2.26	0.95											
<i>expZ</i>	604280	605923	-	502	366	380	497	0.73	0.76	0.99											
<i>ydgF</i>	606243	607619	-	3272	2832	2642	3140	0.87	0.81	0.96											
<i>dinB</i>	607791	608309	-	2071	1770	1743	1906	0.86	0.84	0.92											
<i>ydgG</i>	608478	608936	+	624	551	528	532	0.93	0.89	0.85											
<i>ydgH</i>	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		
<i>ydgI</i>	611736	612365	-	1934	1477	1554	2070	0.79	0.82	1.08											
<i>ydgJ</i>	612381	612875	-	1459	1138	1217	1722	0.78	0.84	1.18											
<i>ydgK</i>	613186	614394	+	1432	804	845	1396	0.56	0.59	0.98											
<i>ydhB</i>	614389	615168	-	783	456	453	659	0.58	0.58	0.84											
<i>ydhC</i>	615417	616091	+	3478	2475	2691	3443	0.71	0.77	0.99											
<i>ydhD</i>	616218	617537	+	476	390	400	474	0.82	0.84	0.99											
<i>ydhE</i>	617683	618828	+	1812	1130	1223	1518	0.63	0.68	0.85											
<i>ydhF</i>	618867	619577	-	206	161	170	200	0.78	0.83	0.97	195	ydhF	619269	619497	619383	0.7	0.2	0.8	10.6		
<i>phoB</i>	619643	621031	-	328	268	268	316	0.82	0.82	0.96											
<i>ydhG</i>	621393	621764	+	2118	1982	1770	2192	0.94	0.84	1.04											
<i>ydhH</i>	621840	622337	-	968	854	997	880	0.88	1.03	0.91											
<i>ydhI</i>	622355	622837	-	516	450	535	538	0.87	1.04	1.05											
<i>ydhJ</i>	622920	623897	+	527	568	552	558	1.09	1.04	1.05											
<i>ydhK</i>	624039	624656	+	1521	734	934	941	0.49	0.63	0.61											
<i>ydhL</i>	624672	625838	-	4369	3428	2908	4275	0.78	0.66	0.98											
<i>ydhM</i>	626169	626480	+	6660	2284	2991	5476	0.34	0.44	0.83	196	Inter	625678	626177	625928	17.8	39.6	4.7	-1.3		
<i>ydhN</i>	626480	626812	+	3545	1036	1509	3399	0.29	0.42	0.95											
<i>ydhO</i>	626831	628159	+	3493	1179	1630	3075	0.33	0.45	0.88											
<i>ydhP</i>	628177	629574	+	3704	1197	1734	3493	0.32	0.46	0.94											
<i>ydhQ</i>	629717	630430	+	3457	1464	1877	3267	0.42	0.54	0.95											
<i>ydhR</i>	630459	631358	+	1852	778	993	1929	0.42	0.54	1.04											
<i>ydhS</i>	631355	632302	+	3438	1387	1745	3308	0.40	0.50	0.96											
<i>ydhT</i>	632321	633409	+	2289	904	1212	2116	0.40	0.54	0.93											
<i>ydhU</i>	633470	633925	-	138	128	151	134	0.93	1.10	0.97	198	ydhU	633345	633692	633519	7.5	2.5	11.6	20.0		
<i>thiL</i>	640209	641186	+	1200	907	831	1194	0.76	0.69	1.00											
<i>ydiB</i>	641201	641677	+	1245	910	927	1293	0.73	0.75	1.04											
<i>ydiC</i>	641658	642347	+	3917	2953	2992	3632	0.76	0.76	0.93											
<i>ydiD</i>	642357	642812	+	3828	2793	2714	3361	0.73	0.71	0.87											
<i>gcp</i>	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		
<i>ydiF</i>	644075	646003	-	2596	2248	2382	2807	0.87	0.92	1.08											
<i>moaC</i>	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		

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

gene	Transcriptome analysis										ChAP-chip analysis							Profile ID			
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center	Binding intensity ^c				
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild						AbrB		Abh		
wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh				
<i>yerD</i>	716119	717696	-	399	335	456	289	0.84	1.15	0.72	234	Inter	717535	717881	717708		11.6	5.7	8.3	3.9	
<i>pcrB</i>	717961	718647	+	2782	2392	1980	2715	0.86	0.71	0.97											
<i>pcrA</i>	718709	720928	+	5051	4243	4080	5015	0.84	0.81	0.99											
<i>ligA</i>	720952	722958	+	5131	4548	4336	5134	0.89	0.85	1.00											
<i>yerH</i>	722974	724164	+	7047	6521	6139	6991	0.93	0.87	0.99											
<i>yerI</i>	724326	725336	+	2600	11644	11104	2526	4.49	4.28	0.97	235	Inter	723994	724426	724210		30.2	26.7	5.3	5.1	P03
<i>sapB</i>	725374	726072	-	704	476	500	698	0.68	0.71	0.99	236	yerI	724572	724868	724720		3.0	3.6	5.1	11.1	
<i>opuE</i>	726179	727657	-	600	546	512	461	0.94	0.87	0.77	237	sapB	724878	726092	725485		58.4	64.8	125.8	224.9	P01
<i>gatC</i>	728071	728361	+	15376	13485	13122	14467	0.88	0.85	0.94											
<i>gatA</i>	728377	729834	+	12364	11684	11285	12569	0.95	0.91	1.02											
<i>gatB</i>	729848	731278	+	11993	11693	11324	11958	0.98	0.94	1.00											
<i>yerO</i>	731293	732162	-	452	369	344	395	0.82	0.76	0.87											
<i>yerP</i>	732255	735452	+	5697	10168	10084	4924	1.79	1.77	0.86											
<i>yerQ</i>	735775	736686	+	4536	4612	3871	4211	1.02	0.85	0.93											
<i>yefA</i>	736942	738321	+	2902	2720	2301	2457	0.95	0.79	0.84											
<i>yefB</i>	738334	739236	-	85	78	81	80	0.92	0.95	0.94											
<i>yefC</i>	739175	739552	+	632	545	473	572	0.92	0.77	0.87	241	yefC	739158	739369	739264		4.9	6.6	1.6	0.7	
<i>yeeA</i>	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	
											244	yeeA	741759	741885	741822		3.8	3.5	0.4	0.9	
<i>yeeB</i>	742278	744074	+	1590	1340	1278	1434	0.84	0.80	0.89	245	yeeB	742167	742547	742357		7.0	12.5	1.4	-0.4	
											246	yeeB	742558	743262	742910		33.7	60.1	3.2	-0.2	P03
<i>yeeC</i>	744187	745335	+	1348	1132	1052	1207	0.83	0.77	0.88	247	yeeC	744054	744520	744287		18.0	33.7	2.2	-0.2	P03
<i>yeeD</i>	745597	745902	-	86	69	71	63	0.80	0.83	0.74											
<i>yezA</i>	745969	746175	-	217	204	245	221	0.94	1.13	1.02											
<i>yeeF</i>	746415	748898	-	777	1478	1558	579	1.91	1.99	0.74											
<i>yeeG</i>	749034	750131	+	286	291	321	285	1.02	1.13	1.00											
<i>rapH</i>	750293	751588	+	330	2730	2684	285	8.23	8.01	0.87	249	Inter	750123	750351	750237		4.1	6.5	0.2	-0.3	
<i>yeeI</i>	751749	752468	+	8765	7749	7882	8383	0.89	0.90	0.96											
<i>yeeK</i>	752602	753039	+	397	402	405	436	1.03	1.03	1.10											
<i>yezE</i>	753154	753738	+	3846	4353	4514	3334	1.13	1.17	0.87											
<i>yesE</i>	753817	754260	+	741	695	737	706	0.95	1.00	0.94											
<i>yesF</i>	754257	755117	+	628	646	689	633	1.03	1.10	1.01											
<i>cotJA</i>	755244	755492	+	352	324	344	270	0.93	0.98	0.76											
<i>cotJB</i>	755437	755739	+	141	113	129	140	0.81	0.92	1.00											
<i>cotJC</i>	755754	756323	+	414	340	387	396	0.83	0.94	0.96											
<i>yesJ</i>	756448	756990	+	2623	1985	1907	2260	0.76	0.73	0.86											
<i>yesK</i>	756926	757315	+	1080	577	674	1040	0.53	0.62	0.98											
<i>yesL</i>	757430	758059	+	1213	700	1014	1243	0.58	0.81	1.02											
<i>yesM</i>	758056	759789	+	701	358	597	725	0.51	0.83	1.03											
<i>yesN</i>	759789	760895	+	441	268	377	429	0.61	0.86	0.97											
<i>yesO</i>	761044	762282	+	396	271	291	412	0.68	0.73	1.05											
<i>yesP</i>	762279	763208	+	372	292	310	390	0.78	0.83	1.05											
<i>yesQ</i>	763212	764102	+	477	383	453	460	0.80	0.95	0.96											
<i>yesR</i>	764118	765152	+	548	372	415	587	0.68	0.76	1.07											
<i>yesS</i>	765175	767460	+	421	343	367	452	0.81	0.87	1.08											
<i>yesT</i>	767474	768172	+	376	285	290	402	0.76	0.77	1.08											
<i>yesU</i>	768165	768827	+	281	222	243	317	0.79	0.86	1.14											
<i>yesV</i>	768824	769450	+	455	403	439	487	0.88	0.97	1.07											
<i>yesW</i>	769571	771433	+	241	200	208	279	0.83	0.86	1.16	251	Inter	769265	769816	769541		26.5	33.0	13.2	1.4	
<i>yesX</i>	771479	773317	+	323	254	268	382	0.78	0.83	1.20	252	yesW	770166	770496	770331		3.3	3.3	2.9	17.8	
<i>yesY</i>	773475	774128	+	326	263	274	321	0.81	0.84	0.99											
<i>yesZ</i>	774136	776127	+	359	296	312	405	0.82	0.87	1.14											
<i>yetA</i>	776171	778744	+	361	283	302	377	0.78	0.84	1.05											
<i>lplA</i>	778866	780374	+	454	260	291	465	0.57	0.64	1.03	254	lplA	779108	779285	779197		7.7	0.6	4.0	1.0	
<i>lplB</i>	780429	781385	+	443	293	317	422	0.66	0.71	0.95	256	lplB	780810	781308	781059		22.3	10.1	30.5	47.2	
<i>lplC</i>	781399	782286	+	514	367	400	564	0.71	0.77	1.10	257	lplC	781658	781784	781721		1.3	0.6	0.9	3.4	
<i>lplD</i>	782295	783635	+	460	315	355	491	0.68	0.77	1.07											
<i>yetF</i>	783718	784413	+	567	351	393	554	0.62	0.69	0.98											
<i>yetG</i>	784450	784827	-	8496	11727	12364	9814	1.38	1.46	1.16											
<i>yetH</i>	784880	785242	-	3794	2273	2586	3264	0.60	0.69	0.86											
<i>yetI</i>	785522	786607	+	1955	1189	1132	1908	0.61	0.58	0.97											
<i>yezB</i>	786613	786897	+	5380	2938	2774	5283	0.55	0.52	0.97											
<i>yezD</i>	787052	787219	+	105	105	104	122	1.01	0.99	1.16											
<i>yetJ</i>	787329	787973	+	6396	8237	7800	8483	1.29	1.22	1.32	259	Inter									

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$																		
<i>yetN</i>	790799	791869	-	1370	991	908	1270	0.73	0.67	0.93											
<i>yetO</i>	792019	795204	+	292	290	314	301	1.00	1.08	1.04											
<i>yfnI</i>	795651	797570	+	11995	11856	11780	12570	0.99	0.98	1.05											
<i>yfnH</i>	797806	798570	+	280	220	238	296	0.79	0.85	1.06											
<i>yfnG</i>	798640	799545	+	271	221	232	260	0.82	0.86	0.96											
<i>yfnF</i>	799569	800480	+	296	254	268	292	0.86	0.91	0.99											
<i>yfnE</i>	800509	801687	+	313	285	288	323	0.91	0.92	1.03											
<i>yfnD</i>	801688	802623	+	405	372	366	389	0.92	0.90	0.96											
<i>yfnC</i>	802654	803883	-	1185	1576	1565	868	1.33	1.32	0.73											
<i>yfnB</i>	803994	804701	-	736	880	863	710	1.20	1.17	0.97											
<i>yfnA</i>	804793	806178	-	1950	1396	1327	1748	0.71	0.68	0.89											
<i>yfnT</i>	806428	807885	+	3707	6483	6159	4021	1.76	1.67	1.08											
<i>yfmS</i>	807899	808759	+	3681	6489	6254	4010	1.79	1.72	1.09											
<i>yfmR</i>	808894	810783	+	3810	3761	3959	4009	0.99	1.04	1.05											
<i>yfmQ</i>	810906	811352	+	4178	3458	2913	2944	0.79	0.65	0.72	261	yfmQ	811136	811279	811208	3.5	3.7	1.4	0.3		
<i>yfmP</i>	811477	811899	+	845	868	719	712	1.01	0.84	0.83											
<i>yfmO</i>	811965	813155	+	584	394	411	568	0.67	0.70	0.97											
<i>yfmN</i>	813446	813601	+	149	122	119	150	0.83	0.82	1.06											
<i>yfmM</i>	813721	815277	-	3004	2153	1943	2763	0.72	0.65	0.92											
<i>yfmL</i>	815450	816580	+	3063	1952	1733	2679	0.64	0.57	0.88											
<i>yfmK</i>	816648	817094	+	757	1958	1926	617	2.62	2.55	0.81											
<i>yfmJ</i>	817147	818166	-	2538	4598	5513	2985	1.82	2.18	1.17											
<i>yfmI</i>	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>yfmH</i>	820066	820137	+	799	20880	21647	741	26.82	27.91	0.91	265	Inter	819466	820408	819937	69.5	95.1	57.3	9.7		
<i>yfmG</i>	820204	821667	+	219	9855	10184	218	44.96	46.46	1.00											
<i>yfmF</i>	822240	823040	-	5004	4008	3806	4670	0.80	0.76	0.93											
<i>yfmE</i>	823053	824054	-	2418	1936	1791	2346	0.80	0.74	0.97											
<i>yfmD</i>	824051	825052	-	2212	1675	1468	2173	0.76	0.66	0.98											
<i>yfmC</i>	825124	826071	-	11528	7933	7364	11136	0.68	0.64	0.96											
<i>yfmB</i>	826180	826548	-	85	97	106	83	1.16	1.25	0.99											
<i>yfmA</i>	826589	826756	+	201	244	211	229	1.23	1.05	1.15											
<i>yfIT</i>	826792	827139	+	2352	1688	3180	1048	0.77	1.36	0.52											
<i>pel</i>	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		
<i>yfIS</i>	828719	830155	+	584	373	375	550	0.64	0.64	0.94	268	Inter	830244	830319	830282	1.1	0.7	2.0	2.5		
<i>citS</i>	830282	831910	+	668	769	734	645	1.15	1.10	0.96											
<i>citT</i>	831882	832562	+	693	742	794	660	1.07	1.14	0.95											
<i>yfIP</i>	832745	833524	+	498	513	540	469	1.03	1.08	0.94											
<i>citM</i>	833720	835021	+	678	499	522	653	0.74	0.77	0.96											
<i>yfIN</i>	835077	835871	+	544	378	425	534	1.00	0.79	0.98											
<i>yfIM</i>	836071	837081	+	1371	1480	1374	1113	1.08	1.00	0.81											
<i>yfIL</i>	837072	837347	-	639	627	608	556	0.98	0.95	0.87											
<i>yfIK</i>	837414	838079	+	1453	1597	1592	1001	1.10	1.09	0.69											
<i>yfIJ</i>	838120	838257	-	1522	1263	1032	1264	0.83	0.68	0.84											
<i>yfII</i>	838414	838569	-	2222	1843	1633	2280	0.82	0.73	1.04											
<i>yfIH</i>	838676	838990	-	5461	4206	4634	5351	0.77	0.85	0.98											
<i>yfIG</i>	839072	839821	-	6407	5636	5694	6400	0.88	0.89	1.00											
<i>nagP</i>	839993	841351	+	5960	4488	5094	5622	0.75	0.85	0.94	271	Inter	839645	840060	839853	14.4	16.8	8.9	11.1		
<i>yfIE</i>	841384	843333	-	7684	7631	6819	6892	0.99	0.89	0.90	272	yfIE	842790	843800	843295	53.3	25.0	71.5	110.2	P01	
<i>yfID</i>	843434	843571	+	115	87	79	97	0.80	0.71	0.87											
<i>yfIC</i>	843587	843739	+	223	822	1226	227	3.65	5.50	1.02											
<i>yfIB</i>	843721	843981	+	152	613	1127	179	4.03	7.70	1.19	272	Inter	843810	844395	844103	33.5	26.0	34.5	40.8	P01	
<i>yfIA</i>	844106	845521	+	565	838	1477	595	1.49	2.69	1.04											
<i>yfKT</i>	845518	846594	-	246	262	290	237	1.06	1.18	0.96	273	yfKT	845765	846129	845947	16.4	4.5	16.6	0.9		
<i>yfKS</i>	846618	846818	-	206	218	240	253	1.06	1.17	1.22											
<i>yfKR</i>	846834	847988	-	189	166	180	196	0.88	0.95	1.03											
<i>yfKQ</i>	847969	849510	-	198	195	211	204	0.99	1.06	1.03											
<i>treP</i>	849703	851115	+	22408	11862	14973	22231	0.53	0.66	0.99											
<i>treA</i>	851186	852871	+	16922	10864	12779	16663	0.64	0.75	0.98											
<i>treR</i>	852892	853608	+	15214	11494	12429	14913	0.76	0.82	0.98											
<i>yfKO</i>	853748	854413	+	10238	5998	6450	8972	0.59	0.64	0.88											
<i>yfKN</i>	854450	858838	-	315	380	423	283	1.20	1.34	0.90											
<i>yfKM</i>	859081	859599	+	2043	1802	2564	1102	0.88	1.25	0.54											
<i>yfKL</i>	859639	860829	-	1108	768	765	1013	0.69	0.69	0.92											
<i>yfKK</i>	860922	861137	-	1304	1201	961	948	0.92	0.73	0.73											
<i>yfKJ</i>	861340	861810	+	2192	1646	2047	1524	0.75	0.93	0.69											
<i>yfKI</i>	861828	862148	+	2738	2528	2869	2181	0.92	1.05	0.78											
<i>yfKH</i>	862172	862999	+	2122	2096	2380	1804	0.99	1.13	0.84	279	yfKH	862816	863078	862947	9.9	7.0	10.6	1.1		
<i>yfKF</i>	863198	864373	-	689	1048	1019	587	1.52	1.48	0.85											

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$														
<i>yfkE</i>	864541	865596	+	745	464	555	448	0.65	0.80	0.60											
<i>yfkD</i>	865667	866461	+	737	527	589	396	0.72	0.83	0.53											
<i>yfkC</i>	866500	867342	-	2649	1817	1690	2464	0.69	0.64	0.93											
<i>yfkB</i>	867343	867804	-	3478	2259	2252	3374	0.65	0.65	0.97											
<i>yfkA</i>	867999	868463	-	1601	1072	933	1634	0.68	0.58	1.03											
<i>yjT</i>	868608	868793	+	1831	1712	1637	1803	0.94	0.89	0.99											
<i>yjS</i>	868894	869685	+	242	243	239	275	1.00	0.99	1.13											
<i>yjR</i>	869723	870508	-	1010	1717	2104	1073	1.73	2.13	1.06											
<i>yjQ</i>	870682	871641	-	1654	1757	1590	1612	1.06	0.96	0.97											
<i>yjP</i>	871760	872623	+	924	811	765	964	0.88	0.83	1.04											
<i>yjO</i>	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		
<i>yjN</i>	875761	876738	+	1725	2146	1931	1981	1.25	1.12	1.15	285	yjN	875872	876066	875969	6.3	4.0	4.8	4.9		
<i>yjM</i>	876934	877386	+	771	1269	1169	847	1.67	1.53	1.10											
<i>yjL</i>	877416	878105	+	1437	1866	1895	1392	1.31	1.32	0.97											
<i>acoA</i>	878337	879338	+	196	160	165	194	0.82	0.84	0.99											
<i>acoB</i>	879342	880370	+	343	271	284	349	0.79	0.83	1.03											
<i>acoC</i>	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		
<i>acoL</i>	881601	882977	+	412	329	342	419	0.80	0.83	1.01											
<i>acoR</i>	883093	884910	+	1122	408	641	1072	0.37	0.55	0.95											
<i>sspH</i>	884964	885143	+	2110	810	1550	1815	0.42	0.75	0.83											
<i>yjF</i>	885179	885508	-	1155	1197	1147	1014	1.04	0.99	0.88											
<i>yjE</i>	885558	886016	-	706	668	717	565	0.95	1.01	0.80											
<i>yjD</i>	886110	886667	-	418	372	393	362	0.89	0.93	0.87											
<i>yjC</i>	886699	887466	-	318	239	270	220	0.77	0.84	0.71											
<i>yjB</i>	887478	888701	-	375	269	288	311	0.71	0.76	0.82											
<i>yjA</i>	888707	889021	-	310	283	264	280	0.91	0.85	0.90											
											291	Inter	888894	889445	889170	28.1	15.9	23.6	20.0		
<i>malA</i>	889357	890706	+	1274	887	1064	1384	0.70	0.84	1.07											
<i>yfA</i>	890771	891535	+	807	623	762	787	0.78	0.95	0.98											
<i>malP</i>	891550	893133	+	956	549	735	936	0.58	0.76	0.98											
<i>yfB</i>	893239	894960	+	1108	1293	1500	1392	1.19	1.39	1.26											
<i>yfC</i>	894954	896768	+	1748	2201	2437	2236	1.29	1.43	1.28											
<i>yfD</i>	896923	897327	+	649	873	839	472	1.36	1.27	0.74											
<i>yfE</i>	897345	898202	+	782	994	935	600	1.27	1.18	0.76											
<i>yfF</i>	898296	899240	+	232	219	219	221	0.95	0.95	0.96											
<i>yfG</i>	899415	900863	+	485	338	389	468	0.70	0.80	0.97	292	yfG	899434	899730	899582	5.2	3.0	10.7	6.6		
<i>yfH</i>	900890	901831	+	469	273	309	474	0.58	0.66	1.00											
<i>yfI</i>	901841	903022	+	489	314	365	499	0.64	0.75	1.02											
											293	Inter	902919	903147	903033	10.0	4.8	1.5	0.0		
<i>yfJ</i>	903146	904348	+	902	1467	1208	870	1.63	1.34	0.97											
<i>yfK</i>	904345	905007	+	1034	1522	1279	892	1.46	1.22	0.86											
<i>yfL</i>	905151	906086	+	236	196	191	253	0.83	0.81	1.07											
<i>yfM</i>	906099	907289	+	267	249	248	285	0.93	0.93	1.07	294	yfM	906523	906785	906654	12.8	0.9	5.3	-0.6		
<i>yfN</i>	907303	908460	+	339	298	307	351	0.88	0.91	1.04											
<i>padR</i>	908533	909081	-	1000	769	648	995	0.77	0.65	1.00											
<i>lipB</i>	909354	909986	+	2104	1259	1323	1614	0.60	0.63	0.77											
<i>yfQ</i>	910175	911263	+	365	358	366	316	0.98	1.01	0.87	295	yfQ	910909	911086	910998	4.2	2.2	-0.2	0.2		
<i>yfR</i>	911299	911916	-	924	1018	1030	812	1.11	1.12	0.88											
<i>yfS</i>	911882	913135	-	507	679	713	415	1.34	1.40	0.82											
<i>yfT</i>	913259	913795	+	2167	2774	2762	1560	1.29	1.27	0.72											
<i>yfU</i>	913792	915348	-	262	259	287	270	0.99	1.10	1.03											
<i>yfV</i>	915459	915941	-	1097	1023	990	1129	0.95	0.92	1.04											
<i>yfW</i>	916113	916889	+	2389	3140	2962	2148	1.31	1.24	0.90											
<i>yfX</i>	916864	918684	+	2634	3497	3330	2257	1.33	1.27	0.86											
<i>yfY</i>	918702	919679	-	12160	11267	11051	12434	0.93	0.91	1.02											
<i>yfZ</i>	919810	920811	+	3076	3056	2727	3012	0.99	0.89	0.98											
<i>yfA</i>	920808	921839	+	4827	4589	4297	5045	0.95	0.90	1.04											
<i>yfB</i>	921954	922835	+	1573	3232	3294	1147	2.05	2.06	0.72											
<i>yfC</i>	922923	923507	+	11445	13732	13625	11433	1.20	1.19	0.99											
<i>yfD</i>	923546	923737	-	970	1357	1908	728	1.39	1.95	0.75											
<i>yfE</i>	923804	923914	-	902	897	1085	776	0.99	1.19	0.86	298	yfE	923744	924023	923884	9.4	2.8	1.6	12.3		
<i>yfF</i>	923969	924880	-	861	649	721	763	0.76	0.84	0.89											
<i>recX</i>	924969	925763	+	3057	2431	2393	2887	0.79	0.78	0.94											
<i>yfH</i>	925765	926079	+	2863	2363	2391	2610	0.83	0.84	0.91											
<i>yfI</i>	926222	927415	+	870	592	599	800	0.70	0.70	0.91											
<i>sspK</i>	927448	927600	-	166	177	199	204	1.20	1.34	1.29											
<i>yfJ</i>	927725	927994	+	1406	1377	1529	1593	1.01	1.11	1.13											
											299	Inter	927943	928222	928083	11.8	4.2	3.6	1.0		
<i>yfK</i>	928139	928657	+	2731	2530	3939	1476	0.96	1.52	0.51											
<i>yfL</i>	928742	929074	+	1161	1651	1969	963	1.52	1.92	0.85											

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

gene	Transcriptome analysis										ChAP-chip analysis						Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh				
<i>yhcV</i>	996509	996931	+	386	694	807	430	1.81	2.11	1.12											
<i>yhcW</i>	997058	997720	+	3595	3413	3931	4085	0.95	1.08	1.15											
<i>yhcX</i>	997736	999277	+	6795	7307	8141	7384	1.07	1.19	1.09											
<i>yhxA</i>	999697	1001049	+	1903	3353	3867	2030	1.76	2.03	1.07	317	Inter	999536	999713	999625		5.0	3.4	1.8	0.4	
<i>glpP</i>	1001077	1001655	+	3035	4160	4535	2915	1.37	1.49	0.96											
<i>glpF</i>	1001834	1002658	+	13070	1897	3495	10108	0.14	0.24	0.74	318	Inter	1001253	1002144	1001699		43.0	74.5	35.7	22.2	P01
<i>glpK</i>	1002677	1004167	+	17074	3991	6353	12887	0.23	0.35	0.74											
<i>glpD</i>	1004308	1005975	+	6746	837	1312	3449	0.13	0.19	0.49											
<i>yhxB</i>	1006107	1007804	+	8984	10493	10719	9690	1.17	1.20	1.08											
<i>yhcY</i>	1007953	1009092	+	607	856	877	505	1.40	1.43	0.83											
<i>yhcZ</i>	1009089	1009733	+	990	1724	1723	675	1.75	1.73	0.68											
<i>yhdA</i>	1009730	1010254	+	660	1054	1098	517	1.60	1.67	0.77											
<i>yhdB</i>	1010269	1010511	-	176	225	267	172	1.28	1.52	0.97											
<i>yhdC</i>	1010712	1011035	+	209	289	289	179	1.40	1.39	0.86											
<i>lytF</i>	1011076	1012542	-	3251	3647	3434	3803	1.16	1.08	1.18											
<i>yhdE</i>	1012695	1013135	-	1120	2726	2348	1059	2.44	2.09	0.94											
<i>ygxB</i>	1013238	1014896	-	463	488	691	410	1.07	1.48	0.91											
<i>spoVR</i>	1014927	1016333	+	143	117	124	137	0.82	0.87	0.96	319	spoVR	1015924	1016407	1016166		25.5	26.9	19.3	27.1	P01
<i>phoA</i>	1016363	1017748	-	321	446	475	313	1.38	1.47	0.96											
<i>lytE</i>	1018280	1019311	+	4210	4139	3609	5275	0.98	0.85	1.25	320	Inter	1017794	1018447	1018121		27.8	42.6	4.0	5.6	P03
<i>citR</i>	1019330	1020256	-	694	505	576	766	0.74	0.84	1.11											
<i>citA</i>	1020365	1021465	+	971	432	460	804	0.44	0.47	0.82											
<i>yhdF</i>	1021539	1022408	+	1192	641	741	965	0.54	0.62	0.81											
<i>yhdG</i>	1022658	1024055	+	334	320	349	392	0.96	1.05	1.18											
<i>yhdH</i>	1024173	1025528	+	2139	1637	1441	1890	0.77	0.67	0.88											
<i>yhdI</i>	1025563	1026972	-	579	556	557	504	0.96	0.96	0.87											
<i>yhdJ</i>	1027082	1027510	+	357	428	453	281	1.19	1.28	0.78											
<i>yhdK</i>	1027541	1027831	-	955	933	936	1218	0.98	0.98	1.27											
<i>yhdL</i>	1027819	1028895	-	3429	3213	3297	3898	0.94	0.96	1.14											
<i>sigM</i>	1028885	1029376	-	2020	2269	2140	2474	1.14	1.06	1.23	321	Inter	1029405	1029735	1029570		9.2	4.9	13.1	6.8	
<i>yhdN</i>	1029573	1030568	+	1484	852	1454	712	0.58	1.02	0.45											
<i>yhdO</i>	1030703	1031302	+	5234	5566	4307	5107	1.04	0.81	0.98											
<i>yhdP</i>	1031371	1032705	-	4078	3224	3598	4272	0.79	0.88	1.05											
<i>yhdQ</i>	1032766	1033197	-	3168	2795	2952	3412	0.88	0.93	1.08											
<i>yhdR</i>	1033354	1034535	+	1817	1902	2099	1684	1.05	1.16	0.92											
<i>yhdS</i>	1034675	1034785	-	217	261	249	224	1.22	1.16	1.04											
<i>yhdT</i>	1034862	1036247	+	2067	2380	2441	1936	1.15	1.18	0.94											
<i>ccrB</i>	1036614	1037009	-	873	895	846	782	1.03	0.97	0.89											
<i>yhdW</i>	1036996	1037727	-	873	979	860	851	1.12	0.97	0.96											
<i>yhdX</i>	1037961	1038068	+	446	389	533	244	0.87	1.17	0.55											
<i>yhdY</i>	1038217	1039332	+	1648	1502	1470	1845	0.92	0.90	1.11											
<i>yhdZ</i>	1039402	1040145	+	675	798	838	709	1.21	1.26	1.06											
<i>yheN</i>	1040169	1041017	-	3160	4109	3502	2480	1.32	1.12	0.80											
<i>dat</i>	1041302	1042150	+	1737	4933	5303	1505	2.84	3.04	0.85											
<i>nhaC</i>	1042193	1043554	-	2221	1809	1625	2302	0.81	0.73	1.04	322	nhaC	1043107	1043556	1043332		3.1	2.2	1.4	31.6	P04
<i>nhaX</i>	1043681	1044181	-	1493	867	1435	734	0.58	0.96	0.49											
<i>yheJ</i>	1044345	1044506	+	742	2835	2337	750	3.84	3.14	1.01	323	Inter	1044042	1044457	1044250		24.5	23.1	5.4	2.0	P03
<i>yheI</i>	1044626	1046383	+	433	947	1068	481	2.19	2.47	1.11											
<i>yheH</i>	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	
<i>yheG</i>	1048450	1049070	-	3388	2625	2664	3533	0.77	0.78	1.04											
<i>yheF</i>	1049109	1049234	-	133	176	196	143	1.31	1.48	1.05											
<i>sspB</i>	1049339	1049542	-	495	2081	2806	531	4.26	5.80	1.08											
<i>yheE</i>	1049751	1049969	-	347	338	348	285	0.97	1.00	0.82											
<i>yheD</i>	1050119	1051480	-	249	239	253	246	0.96	1.02	0.99	325	Inter	1049992	1050152	1050072		5.0	1.7	2.2	-0.3	
<i>yheC</i>	1051470	1052561	-	153	146	149	148	0.95	0.97	0.97											
<i>yheB</i>	1052828	1053961	+	2976	2460	2548	3265	0.83	0.86	1.09											
<i>yheA</i>	1054054	1054407	+	6418	5663	5394	6621	0.88	0.84	1.03	326	Inter	1053834	1054181	1054008		10.3	4.0	6.3	0.2	
<i>yhaZ</i>	1054451	1055524	-	640	944	983	503	1.48	1.53	0.79											
<i>yhaY</i>	1055717	1055968	-	397	450	405	375	1.13	1.02	0.94											
<i>yhaX</i>	1056011	1056877	+	434	273	272	376	0.63	0.63	0.87											
<i>hemZ</i>	1056989	1058494	+	1579	966	814	1371	0.62	0.51	0.87											
<i>yhaU</i>	1058512	1059738	-	786	880	1054	941	1.13	1.36	1.19											
<i>yhaT</i>	1059735	1060232	-	515	539	692	758	1.07	1.42	1.46											
<i>yhaS</i>	1060296	1060634	-	1379	1657	2008	1485	1.21	1.49	1.07											
<i>yhaR</i>	1060799	1061566	+	714	2008	2234	853	2.82	3.16	1.17											

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
wild	Δabh	-type	Δabh	-type	$\Delta abrB$	-type	Δabh	-type													
<i>yhaP</i>	1062788	1064047	+	2342	8851	8442	4368	3.78	3.61	1.87											
<i>yhaO</i>	1064154	1065380	+	1970	1800	1832	2033	0.92	0.94	1.03											
<i>yhaN</i>	1065385	1068276	+	2748	2366	2595	2911	0.86	0.95	1.06											
<i>yhaM</i>	1068350	1069294	+	6054	5558	5595	5967	0.92	0.93	0.99	329	yhaM	1069219	1069311	1069265	2.2	2.7	0.1	-0.3		
<i>yhaL</i>	1069419	1069631	+	445	379	336	494	0.85	0.76	1.11											
<i>prsA</i>	1069672	1070550	-	16781	17923	17600	16571	1.07	1.05	0.99	330	prsA	1070103	1070382	1070243	8.5	15.8	3.3	0.1		
<i>yhaK</i>	1071350	1071604	-	1263	853	785	1091	0.70	0.63	0.88											
<i>yhaJ</i>	1071628	1071867	-	509	399	360	531	0.79	0.71	1.06	331	Inter	1071446	1071793	1071620	6.8	14.1	2.5	3.9		
<i>yhaI</i>	1072075	1072416	+	546	646	606	595	1.16	1.10	1.08											
<i>hpr</i>	1072413	1073024	-	2707	3035	3094	2247	1.12	1.14	0.83											
<i>yhaH</i>	1073202	1073558	-	4498	5007	4780	4257	1.14	1.07	0.96											
<i>yhaG</i>	1073951	1074469	-	3398	3431	3612	2925	1.01	1.06	0.86											
<i>serC</i>	1074594	1075673	-	5726	5597	5874	4774	0.98	1.03	0.84											
<i>hit</i>	1075820	1076257	-	7332	8685	8927	7385	1.19	1.22	1.01											
<i>ecsA</i>	1076745	1077488	+	2241	2879	3012	2323	1.30	1.37	1.04											
<i>ecsB</i>	1077481	1078707	+	3626	4934	5465	3829	1.37	1.52	1.06											
<i>ecsC</i>	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		
<i>yhaA</i>	1079455	1080645	-	356	549	733	373	1.56	2.09	1.04											
<i>yhfA</i>	1080718	1082109	-	276	312	304	276	1.13	1.10	1.00											
<i>yhgB</i>	1082175	1082489	-	290	393	387	253	1.38	1.36	0.85											
<i>yhgC</i>	1082534	1083034	-	4198	7146	7455	5015	1.72	1.79	1.20											
<i>pbpF</i>	1083156	1085300	+	976	800	748	948	0.83	0.77	0.96											
<i>hemE</i>	1085422	1086483	+	3665	3172	3010	3495	0.89	0.83	0.96											
<i>hemH</i>	1086555	1087487	+	8285	7148	7145	8278	0.88	0.88	1.00											
<i>hemY</i>	1087502	1088914	+	4478	3981	3922	4440	0.92	0.90	1.00											
<i>yhgD</i>	1089060	1089635	+	2120	2649	2645	1772	1.22	1.19	0.84											
<i>yhgE</i>	1089706	1092033	+	2666	2524	2577	2265	0.94	0.95	0.85											
<i>fabHB</i>	1092075	1093052	-	746	1523	1084	860	1.96	1.41	1.11											
<i>yhfC</i>	1093178	1093954	+	326	746	715	373	2.28	2.19	1.14											
<i>yhfD</i>	1094045	1094248	-	222	219	228	208	0.99	1.03	0.94											
<i>yhfE</i>	1094367	1095407	+	2692	5064	5316	2998	1.92	2.01	1.11											
<i>yhfF</i>	1095420	1095827	+	3167	5880	6072	3401	1.87	1.93	1.07											
<i>glhT</i>	1095864	1097153	-	12605	12618	12104	12374	1.00	0.96	0.98	334	glhT	1095825	1096579	1096202	30.5	26.8	43.3	27.9	P01	
<i>yhfH</i>	1097424	1097564	-	4027	2754	2877	2130	0.74	0.75	0.51	335	Inter	1097167	1097581	1097374	15.8	7.3	5.0	0.8		
<i>yhfI</i>	1097716	1098450	+	5352	7907	8040	6851	1.48	1.51	1.28											
<i>yhfJ</i>	1098463	1099458	+	7471	10547	10918	9312	1.42	1.47	1.24											
<i>yhfK</i>	1099523	1100167	+	5475	8256	8311	6416	1.52	1.53	1.17											
<i>yhfL</i>	1100284	1101825	+	741	593	617	789	0.80	0.84	1.06											
<i>yhfM</i>	1101864	1102259	-	212	311	372	222	1.46	1.74	1.04	336	yhfM	1101808	1101934	1101871	3.8	1.0	0.2	-0.8		
<i>yhfN</i>	1102408	1103688	+	405	379	391	409	0.94	0.96	1.01											
<i>aprE</i>	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		
<i>yhfO</i>	1105307	1105756	+	1343	1238	1125	1234	0.92	0.83	0.92	338	Inter	1104800	1105130	1104965	18.0	11.8	1.9	-0.3		
<i>yhfP</i>	1105828	1106820	+	3527	4107	4328	3568	1.17	1.23	1.02											
<i>yhfQ</i>	1106962	1108008	+	10445	9472	8967	9559	0.91	0.86	0.92											
<i>yhfR</i>	1108040	1108621	-	3022	3093	3007	3312	1.06	1.02	1.12											
<i>yhfS</i>	1108692	1109786	-	546	595	591	512	1.10	1.09	0.93											
<i>yhfT</i>	1109783	1111222	-	790	804	832	706	1.02	1.06	0.88											
<i>yhfU</i>	1111229	1111789	-	238	234	245	247	0.98	1.03	1.04											
<i>hemAT</i>	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		
<i>yhfW</i>	1113361	1114890	-	170	227	234	160	1.34	1.39	0.94	340	Inter	1113113	1113409	1113261	7.8	11.4	-0.2	0.4		
<i>yhxC</i>	1115002	1115859	+	194	222	240	209	1.14	1.24	1.07											
<i>yhzC</i>	1115887	1116120	-	382	298	360	295	0.79	0.95	0.78											
<i>comK</i>	1116413	1116991	+	583	955	965	559	1.68	1.66	0.96	342	Inter	1116123	1116520	1116322	21.5	14.0	4.4	1.3		
<i>yhxD</i>	1117038	1117937	-	461	390	507	311	0.85	1.10	0.68											
<i>yhjA</i>	1118154	1118423	+	12987	20690	20589	9108	1.60	1.59	0.70	344	Inter	1117992	1118186	1118089	5.0	6.4	0.1	0.1		
<i>yhjB</i>	1118466	1119935	-	336	378	389	346	1.12	1.16	1.03											
<i>yhjC</i>	1119932	1120132	-	318	449	482	318	1.41	1.51	1.00											
<i>yhjD</i>	1120340	1120702	-	169	110	124	152	0.65	0.74	0.90											
<i>yhjE</i>	1120855	1121478	+	1155	1486	1404	1359	1.30	1.23	1.17											
<i>sipV</i>	1121480	1121986	+	2209	2494	2574	2377	1.13	1.17	1.07	345	Inter	1121970	1122181	1122076	1.2	6.2	4.4	5.0		
<i>yhjG</i>	1122166	1123665	+	527	791	844	495	1.50	1.60	0.93											
<i>yhjH</i>	1123742	1124269	+	825	1021	1098	704	1.26	1.35	0.85											
<i>glcP</i>	1124427	1125632	-	230	224	229	214	0.97	0.99	0.94	347	glcP	1124402	1124697	1124550	8.8	12.8	1.6	0.1		
											347	glcP	1124707	1125360	1125034	34.1	57.1	1.6	-0.8	P03	
											347	glcP	1125370	1125700	1125535	8.9	11.2	0.6	-1.0		
<i>yhjJ</i>	1125704	1126756	-	221	277	305	207	1.25	1.38	0.93	348	yhjJ	1126390	1126686	1126538	14.2	6.1	-0.1	-1.4		

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

gene	Transcriptome analysis										ChAP-chip analysis						Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$	wild	Δabh	wild	Δabh														
<i>argD</i>	1197406	1198563	+	199	180	179	230	0.90	0.90	1.16											
<i>carA</i>	1198634	1199695	+	243	221	238	286	0.91	0.98	1.18											
<i>carB_1</i>	1199688	1202780	+	226	205	212	238	0.91	0.94	1.05											
<i>argF</i>	1202768	1203727	+	284	259	263	297	0.91	0.93	1.04	365	<i>argF</i>	1202958	1203288	1203123	11.9	15.2	4.6	2.9		
<i>yjzC</i>	1203813	1203992	+	122	113	112	125	0.93	0.92	1.02											
<i>yjzD</i>	1204038	1204223	-	5466	5219	4687	5156	0.96	0.86	0.94											
<i>yjaU</i>	1204472	1205206	+	184	328	320	300	1.79	1.74	1.62	366	Inter	1204131	1204665	1204398	31.4	18.0	40.4	12.1		
<i>yjaV</i>	1205288	1205695	+	172	154	148	179	0.89	0.86	1.04											
<i>med</i>	1205937	1206890	+	2306	2564	2053	2223	1.11	0.89	0.96	368	<i>med</i>	1206018	1206484	1206251	17.6	16.1	27.7	38.4		
<i>comZ</i>	1206905	1207096	+	2883	3254	2583	3415	1.13	0.90	1.18											
<i>yjzB</i>	1207126	1207365	-	220	201	200	237	0.92	0.91	1.08											
<i>fabHA</i>	1207530	1208468	+	5872	7209	5553	6386	1.22	0.94	1.08											
<i>fabF</i>	1208491	1209732	+	10379	12116	10140	10787	1.17	0.97	1.04											
<i>yjaZ</i>	1209808	1210593	+	188	193	188	181	1.02	1.00	0.96	369	<i>yjaZ</i>	1210047	1210428	1210238	19.0	7.6	16.4	5.8		
											369	Inter	1210438	1210887	1210663	33.6	30.7	11.2	0.8		
<i>appD</i>	1210785	1211771	+	175	259	353	193	1.48	2.01	1.10											
<i>appF</i>	1211768	1212757	+	134	273	378	137	2.04	2.83	1.02											
<i>appA</i>	1212845	1214476	+	188	817	1092	211	4.29	5.69	1.12											
<i>appB</i>	1214552	1215505	+	246	466	619	258	1.89	2.48	1.06											
<i>appC</i>	1215522	1216433	+	231	413	519	214	1.78	2.23	0.92											
<i>yjBA</i>	1216639	1217391	+	251	396	468	253	1.58	1.86	1.00											
<i>trpS</i>	1217426	1218418	-	4775	4364	4440	4491	0.91	0.93	0.94	370	<i>trpS</i>	1217595	1217772	1217684	7.3	2.4	3.1	-0.1		
											371	Inter	1218445	1218639	1218542	5.2	6.2	2.1	1.5		
<i>oppA</i>	1219162	1220799	+	3262	7083	7824	2704	2.17	2.40	0.83											
<i>oppB</i>	1220907	1221842	+	657	1479	1584	555	2.19	2.31	0.83											
<i>oppC</i>	1221846	1222763	+	989	1979	2149	734	1.98	2.13	0.74											
<i>oppD</i>	1222768	1223844	+	1479	2974	3311	1114	1.98	2.20	0.75											
<i>oppF</i>	1223846	1224763	+	1797	3634	4088	1354	2.00	2.22	0.75											
<i>yjB</i>	1224870	1226087	+	297	740	719	304	2.49	2.42	1.02											
<i>yjC</i>	1226251	1226829	+	6244	5162	6559	6485	0.83	1.05	1.04											
<i>spxA</i>	1227010	1227405	+	13941	14672	16078	14236	1.05	1.15	1.02											
<i>yjE</i>	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		
<i>mecA</i>	1228381	1229037	+	2892	3365	3817	3230	1.16	1.32	1.12											
<i>yjF</i>	1229228	1230349	+	241	238	250	257	0.99	1.04	1.06											
<i>yjG</i>	1230579	1232408	+	5591	8914	9126	5876	1.60	1.64	1.05											
<i>yjH</i>	1232926	1233753	-	2933	2857	3414	3545	0.98	1.17	1.21											
<i>yjI</i>	1233822	1234220	-	1864	1968	2017	2165	1.06	1.09	1.16											
<i>yjJ</i>	1234475	1235020	-	1892	1682	1505	2079	0.91	0.80	1.11											
<i>yjK</i>	1235224	1235796	-	739	437	407	678	0.59	0.55	0.91											
<i>yjL</i>	1235921	1236289	+	8179	6073	6587	9055	0.74	0.80	1.11	375	<i>yjL</i>	1236143	1236319	1236231	5.8	2.6	1.5	0.4		
<i>yjM</i>	1236318	1236953	+	9881	7600	8683	10319	0.77	0.88	1.04											
<i>ppnK_1</i>	1236972	1237772	+	6940	6118	6850	8195	0.88	0.98	1.18											
<i>yjO</i>	1237835	1238686	+	6571	5973	6454	7427	0.91	0.98	1.13											
<i>yjP</i>	1238699	1239433	-	200	201	193	212	1.01	0.97	1.04	376	<i>yjP</i>	1238624	1238903	1238764	5.6	3.4	10.1	15.7		
<i>yjQ</i>	1239668	1241512	+	959	780	806	1053	0.88	0.88	1.07											
<i>tenA</i>	1241761	1242471	+	296	244	239	284	0.83	0.81	0.95											
<i>tenI</i>	1242446	1243063	+	393	351	335	389	0.90	0.85	0.97											
<i>goxB</i>	1243047	1244156	+	587	520	511	579	0.89	0.87	0.98											
<i>thiS</i>	1244156	1244356	+	574	493	424	553	0.86	0.74	0.97											
<i>thiG</i>	1244353	1245123	+	386	333	319	369	0.86	0.82	0.95											
<i>thiF</i>	1245120	1246130	+	519	450	423	500	0.87	0.81	0.96											
<i>yjV</i>	1246149	1246964	+	433	369	358	405	0.86	0.82	0.93											
<i>fabI</i>	1247100	1247876	+	7240	10818	8217	8373	1.50	1.13	1.17											
<i>yjX</i>	1247977	1248660	+	466	399	381	492	0.86	0.82	1.06											
<i>cotZ</i>	1248754	1249200	-	138	121	131	127	0.88	0.95	0.93											
<i>cotY</i>	1249328	1249816	-	115	124	127	121	1.07	1.10	1.05											
<i>cotX</i>	1249968	1250486	-	120	126	125	110	1.04	1.04	0.91											
<i>cotW</i>	1250585	1250902	-	146	99	108	107	0.68	0.73	0.73											
<i>cotV</i>	1250943	1251329	-	101	98	96	97	0.97	0.95	0.96											
<i>yjA</i>	1251489	1251845	+	379	370	382	413	0.98	1.01	1.07											
<i>yjB</i>	1252170	1252385	+	258	226	231	259	0.88	0.90	1.00											
<i>yjC</i>	1252649	1252951	+	157	141	134	130	0.90	0.86	0.83											
<i>yjD</i>	1253025	1255304	-	1611	758	677	1449	0.47	0.42	0.90											
<i>yjE</i>	1255385	1255687	-	301	311	303	260	1.04	1.01	0.86											
<i>yjF</i>	1255748	1256170	-	4288	6694	7353	4070	1.56	1.71	0.95											
<i>yjG</i>	1256174	1256689	-	5237	7711	9002	4979	1.47	1.72	0.95											
<i>yjH</i>	1256726	1257448	-	2766	4381	4731	2778	1.59	1.71	1.01											
<i>yjI</i>	1257804	1258925	+	539	542	706	487	1.01	1.31	0.90											
<i>yjJ</i>	1258918	1260090	+	418	432	538	419	1.03	1.29	1.01											
<i>yjK</i>	1260123	1260668	-	390	846	844	444	2.16	2.17	1.10											
<i>yjL</i>	1260738	1261928	-	343	315	335	399	0.92	0.98	1.17											

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

gene		Transcriptome analysis									ChAP-chip analysis							Profile ID		
name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center	Binding intensity ^c				
				wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild						AbrB			Abh	
														wild -type	Δabh	wild -type	$\Delta abrB$			
<i>xkdD</i>	1323110	1323460	+	365	170	187	298	0.47	0.51	0.82										
<i>xtrA</i>	1323457	1323663	+	1024	409	443	714	0.40	0.43	0.70										
<i>xpf</i>	1323779	1324288	+	579	216	232	411	0.37	0.40	0.71										
<i>xtmA</i>	1324404	1325201	+	3074	1200	1367	2305	0.39	0.44	0.75										
<i>xtmB</i>	1325198	1326499	+	2591	1094	1186	2062	0.42	0.46	0.80										
<i>xkdE</i>	1326503	1327990	+	3081	1351	1587	2461	0.44	0.52	0.80										
<i>xkdf</i>	1328010	1328837	+	7010	4118	4725	6111	0.58	0.67	0.87										
<i>xkdG</i>	1328863	1329798	+	5363	3360	3883	5384	0.62	0.72	1.00										
<i>xkdH</i>	1330202	1330558	+	4680	2637	3253	3895	0.56	0.69	0.83										
<i>xkdl</i>	1330555	1331040	+	6925	4004	4744	5708	0.57	0.68	0.83										
<i>xkdJ</i>	1331053	1331493	+	3783	2146	2530	3409	0.56	0.67	0.90										
<i>xkdK</i>	1331712	1333106	+	6850	4096	4822	6281	0.60	0.70	0.92										
<i>xkdm</i>	1333113	1333556	+	4927	2585	3113	4530	0.52	0.63	0.92										
<i>xkdn</i>	1333648	1334274	+	3868	1731	2021	3043	0.45	0.53	0.79										
<i>xkdo</i>	1334279	1338277	+	2461	1220	1398	1958	0.49	0.57	0.80	401	xkdO	1335915	1336483	1336199	30.7	48.3	19.0	0.5	P02
<i>xkdp</i>	1338222	1338929	+	3316	1566	1864	2413	0.47	0.57	0.73										
<i>xkdQ</i>	1338945	1339922	+	2630	1331	1656	2051	0.50	0.63	0.78										
<i>xkdr</i>	1339922	1340188	+	3006	1482	1683	2440	0.49	0.56	0.81										
<i>xkds</i>	1340245	1340670	+	3415	1764	2021	2716	0.52	0.59	0.80										
<i>xkdt</i>	1340663	1341709	+	2667	1399	1655	2135	0.52	0.62	0.80										
<i>xkdu</i>	1341693	1342271	+	1756	942	1083	1503	0.54	0.62	0.86										
<i>xkdv</i>	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	
<i>xkdW</i>	1344617	1344946	+	2283	1061	1324	1764	0.46	0.58	0.77										
<i>xkdx</i>	1344943	1345107	+	1610	732	891	1321	0.45	0.56	0.82										
<i>xepA</i>	1345151	1345990	+	2483	1309	1528	2082	0.53	0.62	0.84										
<i>xhlA</i>	1346043	1346312	+	6540	4012	5356	5926	0.61	0.82	0.91										
<i>xhlB</i>	1346325	1346588	+	5009	3009	4096	4650	0.60	0.82	0.93										
<i>xlyA</i>	1346601	1347494	+	4216	2883	3569	4349	0.68	0.85	1.03										
<i>spoIIISB</i>	1347754	1347924	-	751	1057	1010	694	1.40	1.33	0.92										
<i>spoIIISA</i>	1347924	1348670	-	1112	1491	1355	1179	1.34	1.22	1.06										
<i>pit</i>	1348794	1349780	-	14159	12418	11496	13821	0.88	0.81	0.98	404	pit	1348903	1349896	1349400	8.5	10.7	20.2	31.6	
<i>ykA</i>	1349793	1350410	-	9101	7260	6075	9744	0.80	0.67	1.07										
<i>ykBA</i>	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
											405	ykBA	1351555	1351834	1351695	0.9	0.0	5.4	7.1	
<i>ykCA</i>	1352391	1353341	+	1149	992	1067	1334	0.89	0.95	1.15										
<i>ykCB</i>	1353592	1355742	+	222	186	189	235	0.84	0.85	1.06	407	ykCB	1354377	1354707	1354542	1.7	1.8	4.0	10.9	
<i>ykC</i>	1355754	1356725	+	177	129	137	157	0.74	0.78	0.87										
<i>htrA</i>	1357243	1358592	-	1362	2629	2785	1699	1.99	2.08	1.26										
<i>proG</i>	1358761	1359579	+	1310	1223	1166	1214	0.93	0.89	0.92										
<i>dppA</i>	1359708	1360532	+	203	233	248	219	1.15	1.22	1.07										
<i>dppB</i>	1360549	1361475	+	141	145	158	134	1.03	1.12	0.95										
<i>dppC</i>	1361481	1362443	+	217	217	224	246	1.00	1.03	1.13										
<i>dppD</i>	1362448	1363455	+	375	367	358	471	0.99	0.96	1.29										
<i>dppE</i>	1363458	1365107	+	205	197	213	224	0.96	1.04	1.09										
<i>ykfA</i>	1365448	1366152	+	364	368	385	382	1.01	1.05	1.04										
<i>ykfB</i>	1366149	1367249	+	263	240	266	286	0.91	1.01	1.08										
<i>ykfC</i>	1367246	1368136	+	368	370	357	377	1.00	0.97	1.01										
<i>ykfD</i>	1368149	1369132	+	395	423	456	447	1.07	1.15	1.12										
<i>ykGB</i>	1369180	1370229	-	7873	10060	10440	8474	1.28	1.33	1.08										
<i>ykGA</i>	1370389	1371180	-	623	388	602	318	0.62	0.97	0.50										
<i>ykHA</i>	1371340	1371858	+	4653	2550	2805	4641	0.57	0.63	1.01										
<i>hmp</i>	1372097	1373296	+	755	253	266	707	0.36	0.37	0.95										
<i>ykZH</i>	1373373	1373597	-	160	137	148	115	0.86	0.92	0.72										
<i>ykJA</i>	1373742	1374473	+	316	284	270	316	0.90	0.86	1.00										
<i>ykKA</i>	1374565	1375092	+	195	622	563	215	3.23	2.91	1.09										
<i>ykKB</i>	1375082	1375600	+	219	445	427	280	2.03	1.95	1.27										
<i>ykKC</i>	1375823	1376161	+	830	714	644	805	0.86	0.78	0.97										
<i>ykKD</i>	1376161	1376478	+	433	396	355	405	0.91	0.82	0.93										
<i>purU</i>	1376549	1377451	+	3570	2671	2504	3192	0.75	0.70	0.90										
<i>proB</i>	1377802	1378899	+	3125	2203	2152	2900	0.71	0.69	0.93										
<i>proA</i>	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	
<i>ykIA</i>	1380284	1380709	+	2144	1439	1559	1835	0.67	0.72	0.86										
<i>ykMA</i>	1380740	1381183	+	1422	1210	1337	1268	0.85	0.94	0.89										
<i>ykZA</i>	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	
<i>guaD</i>	1381983	1382453	-	162	153	155	182	0.94	0.96	1.13										
<i>metE</i>	1382626	1384914	-	361	531	593	355	1.47	1.63	0.97										
<i>ispA</i>	1385330	1386289	-	164	166	168	155	1.01	1.02	0.95										
<i>ykOB</i>	1386512	1387345	+	8025	11099	11385	8546	1.38	1.42	1.06										
<i>ykOC</i>	1387376	1388140	-	371	326	347	373	0.89	0.94	1.01										
<i>ykOD</i>	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
<i>ykOE</i>	1389746	1390345	-	212	208	226	229	0.98	1.07	1.08										
											412	Inter	1382546	1382689	1382618	4.6	5.2	0.1	-0.3	
											413	Inter	1386218	1386667	1386443	33.4	34.8	7.5	-0.4	

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c				
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB /$ wild	$\Delta abh /$ $\Delta abrB /$ wild	$\Delta abh /$ wild							AbR		Abh		
-type	Δabh	-type	$\Delta abrB$																			
<i>ptsI</i>	1458959	1460671	+	23431	21910	21855	24855	0.94	0.93	1.06												
<i>splA</i>	1460762	1461001	+	1531	1240	1312	1367	0.81	0.85	0.89												
<i>splB</i>	1461079	1462107	+	989	756	820	901	0.75	0.82	0.90												
<i>ykwB</i>	1462280	1462801	-	112	125	142	120	1.11	1.26	1.07												
<i>mcpC</i>	1462936	1464900	+	1309	1720	1703	1514	1.33	1.31	1.15												
<i>ykwC</i>	1465037	1465903	+	7295	6075	6831	6428	0.84	0.94	0.88												
<i>ykwD</i>	1465942	1466715	-	576	568	682	515	0.98	1.18	0.88												
<i>ykuA</i>	1467109	1469166	+	1706	5288	5434	1301	3.14	3.24	0.77	438	Inter	1466679	1467349	1467014	44.6	56.2	22.3	0.5	P02		
<i>kinA</i>	1469330	1471150	+	447	1262	1315	501	2.87	3.00	1.10												
<i>patA</i>	1471161	1472339	-	4569	3475	3713	4501	0.76	0.81	0.99												
<i>cheV</i>	1472906	1473817	+	1246	1713	1455	1430	1.39	1.17	1.13												
<i>ykyB</i>	1473861	1474325	-	1752	2193	2021	1613	1.27	1.17	0.91												
<i>ykuC</i>	1474451	1475743	-	2154	2134	2060	2289	1.00	0.96	1.06												
<i>ykuD</i>	1475819	1476313	-	287	338	315	341	1.22	1.15	1.19												
<i>ykuE</i>	1476370	1477233	-	253	275	257	273	1.11	1.04	1.08												
<i>ykuF</i>	1477376	1478140	+	460	324	335	464	0.70	0.73	1.00												
<i>ykuG</i>	1478441	1480723	+	3074	1298	1527	2690	0.42	0.50	0.87	440	ykuG	1478291	1478671	1478481	13.8	7.2	5.2	13.6			
											441	ykuG	1479395	1479997	1479696	34.0	13.4	30.0	81.6			
<i>ykuH</i>	1480853	1481401	+	1130	989	925	1184	0.86	0.81	1.04												
<i>ykuI</i>	1481554	1482777	+	1211	1389	1398	1189	1.15	1.16	0.98												
<i>ykuJ</i>	1483423	1483662	+	9007	7835	7281	9530	0.87	0.81	1.06												
<i>ykuK</i>	1483772	1484290	+	8507	7830	6971	8786	0.92	0.82	1.03												
<i>ykzF</i>	1484424	1484621	+	9120	9256	8188	8889	1.02	0.90	0.98												
<i>ykuL</i>	1484759	1485202	+	2935	1030	1674	2670	0.35	0.56	0.91												
<i>ccpC</i>	1485351	1486232	+	4333	2051	2963	4002	0.47	0.68	0.92												
<i>ykuN</i>	1486344	1486820	+	4989	11487	11940	5205	2.31	2.40	1.04												
<i>ykuO</i>	1486810	1487703	+	4410	11831	12615	5117	2.69	2.87	1.16												
<i>ykuP</i>	1487719	1488255	+	4369	10930	11510	4462	2.53	2.66	1.03												
<i>ykuQ</i>	1488280	1488990	+	15452	14596	14824	15434	0.94	0.96	1.00	444	ykuQ	1488337	1489075	1488706	47.3	74.4	42.2	6.9			
<i>ykuR</i>	1489060	1490184	+	3918	3502	3823	4183	0.90	0.98	1.07												
<i>ykuS</i>	1490246	1490491	+	3990	4249	4815	4118	1.07	1.21	1.03	445	Inter	1490105	1490333	1490219	8.2	5.5	1.2	0.2			
<i>ykuT</i>	1490528	1491331	-	860	498	532	549	0.61	0.66	0.65												
<i>ykuU</i>	1491568	1492110	+	896	9689	11489	1051	11.17	13.32	1.16	446	Inter	1491193	1491829	1491511	54.8	63.4	14.7	0.8			
<i>ykuV</i>	1492182	1492643	+	659	6529	7741	802	10.09	12.03	1.21												
<i>rok</i>	1493094	1493669	+	5311	4600	4647	4679	0.87	0.88	0.88	447	Inter	1492383	1493376	1492880	71.3	67.4	55.1	58.4	P01		
<i>yknT</i>	1493710	1494675	-	120	99	102	104	0.82	0.85	0.87												
<i>mobA</i>	1494812	1495411	+	3347	2565	2451	3311	0.76	0.73	0.99												
<i>moeB</i>	1495462	1496481	+	2437	2085	1922	2521	0.86	0.79	1.03												
<i>moeA</i>	1496499	1497791	+	3313	2982	3001	3451	0.90	0.91	1.04												
<i>mobB</i>	1497752	1498273	+	3453	2909	3058	3408	0.84	0.89	0.99												
<i>moaE</i>	1498273	1498746	+	7091	6388	6286	6997	0.90	0.89	0.98												
<i>moaD</i>	1498739	1498972	+	1499	1315	1231	1644	0.88	0.82	1.09												
<i>yknU</i>	1499196	1500953	+	194	228	249	193	1.17	1.28	0.99	448	yknU	1499506	1500329	1499918	45.6	15.1	43.3	98.9			
<i>yknV</i>	1500965	1502779	+	212	220	235	219	1.04	1.11	1.04												
<i>yknW</i>	1502889	1503584	+	4027	15157	17250	6150	3.76	4.32	1.54	449	yknW	1502685	1503117	1502901	17.7	9.8	6.3	10.0			
<i>yknX</i>	1503589	1504722	+	3888	13306	15596	5605	3.42	4.02	1.44												
<i>yknY</i>	1504723	1505415	+	3241	13975	16877	5310	4.35	5.27	1.66												
<i>yknZ</i>	1505412	1506605	+	3401	12593	15366	4815	3.72	4.57	1.43												
<i>fruR</i>	1506885	1507640	+	2558	1245	1675	2592	0.51	0.67	1.00												
<i>fruK</i>	1507637	1508548	+	1382	511	693	1450	0.37	0.50	1.05												
<i>fruA</i>	1508563	1510470	+	2079	855	1091	2182	0.41	0.52	1.05												
<i>sipT</i>	1510615	1511196	+	1143	1267	1162	1414	1.11	1.03	1.24												
<i>ykoA</i>	1511230	1511499	-	920	983	815	946	1.06	0.88	1.03												
<i>ykpA</i>	1511680	1513302	+	8509	7324	6548	8393	0.86	0.77	0.99												
<i>ykpB</i>	1513359	1514270	+	2479	2112	2113	2202	0.85	0.85	0.89												
<i>ampS</i>	1514304	1515536	-	4689	5112	6369	5810	1.10	1.37	1.24	452	ampS	1514976	1515390	1515183	7.2	3.0	12.7	16.2			
<i>ykpC</i>	1515646	1515780	-	1141	1497	1863	1772	1.38	1.69	1.55												
<i>mreBH</i>	1515881	1516888	-	1317	1801	2302	2284	1.44	1.84	1.71	453	mreBH	1516013	1516513	1516263	15.0	10.9	23.4	49.8			
<i>abh</i>	1517172	1517450	+	15057	16595	28	94	1.10	0.00	0.01												
<i>kinC</i>	1517640	1518926	+	2432	2614	7215	5040	1.08	2.95	2.08												
<i>ykqA</i>	1518942	1519775	+	3502	3917	9189	6570	1.12	2.62	1.88												
<i>ykqB</i>	1519838	1520503	+	3166	3420	7085	4969	1.08	2.23	1.58												
<i>adeC</i>	1520658	1522391	+	3040	1843	1674	1824	0.61	0.55	0.60												
<i>ykqC</i>	1522425	1524092	-	9407	10251	9527	9827	1.09	1.01	1.05												
<i>ykzG</i>	1524098	1524307	-	6117	6883	5748	6037	1.12	0.93	0.98												
<i>ykrA</i>	1524693	1525466	+	4904	4281	4252	4943	0.88	0.87	1.01												
<i>def_1</i>	1525502	1526056	-	3328	2970	2556	3385	0.90	0.77	1.02												
<i>ykyA</i>	1526592	1527209	+	1343	2282	1776	1416	1.69	1.32	1.05	455	Inter	1526281	1526696	1526489	28.9	10.8	10.0	1.1			

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$	wild	Δabh												
<i>pdhA</i>	1527633	1528748	+	23262	18263	18192	23019	0.78	0.78	0.99											
<i>pdhB</i>	1528752	1529729	+	25046	20158	20288	25312	0.80	0.81	1.01											
<i>pdhC</i>	1529844	1531172	+	25310	22164	22463	25182	0.88	0.89	0.99											
<i>pdhD</i>	1531177	1532589	+	22660	19521	19753	22690	0.86	0.87	1.00											
<i>slp</i>	1532634	1533008	-	125	146	136	127	1.17	1.08	1.02											
<i>speA</i>	1533586	1535058	-	2801	1236	982	2305	0.45	0.35	0.84	456	<i>speA</i>	1533421	1534380	1533901	35.8	4.9	74.2	202.8	P06	
<i>yktA</i>	1535243	1535509	+	3142	2272	2187	2353	0.72	0.69	0.74											
<i>yktB</i>	1535542	1536180	+	5566	5848	6193	5870	1.05	1.12	1.05											
<i>ykzI</i>	1536420	1536608	+	1263	667	1088	485	0.52	0.84	0.37											
<i>yktC</i>	1536748	1537545	+	1447	1523	1781	1377	1.10	1.28	0.95											
<i>ykzC</i>	1537571	1537999	+	2387	2383	2668	2313	1.03	1.16	0.97											
<i>yktD</i>	1538077	1538991	-	176	279	302	184	1.57	1.69	1.06	457	<i>yktD</i>	1538572	1538749	1538661	5.5	2.0	3.4	4.7		
											458	Inter	1538844	1539412	1539128	24.7	17.8	6.5	1.8		
<i>nprE</i>	1539343	1540908	-	587	1719	2292	840	2.99	3.91	1.45	459	Inter	1540714	1541180	1540947	21.4	11.8	4.0	-0.3		
<i>ylaA</i>	1541193	1543133	+	270	267	263	287	1.00	0.98	1.07											
<i>ylaB</i>	1543123	1543392	+	401	418	354	365	1.05	0.88	0.93											
<i>ylaC</i>	1543392	1543913	+	348	368	335	396	1.08	0.98	1.13											
<i>ylaD</i>	1543910	1544203	+	358	386	386	417	1.08	1.08	1.15											
<i>ylaE</i>	1544243	1544854	-	134	207	793	200	1.55	5.91	1.48											
<i>ylaF</i>	1545127	1545315	-	4259	4181	4197	3475	0.98	0.98	0.82	461	Inter	1544352	1545549	1544951	37.4	38.3	39.8	171.0	P01	
<i>ylaG</i>	1545428	1547266	+	11482	7826	6546	10644	0.68	0.57	0.93	462	<i>ylaG</i>	1546375	1546535	1546455	0.9	2.0	0.6	4.1		
<i>ylaH</i>	1547323	1547640	+	5743	4315	3600	5365	0.75	0.62	0.93											
<i>ylaI</i>	1547696	1547905	-	4053	2920	3434	3706	0.72	0.84	0.91											
<i>ylaJ</i>	1547988	1548617	-	160	233	260	146	1.44	1.60	0.91											
<i>ylaK</i>	1548772	1550100	+	190	172	175	215	0.91	0.92	1.13											
<i>ylaL</i>	1550104	1550589	-	6073	7958	8260	7007	1.32	1.37	1.16											
<i>ylaM</i>	1550692	1551621	+	240	207	211	244	0.86	0.88	1.01											
<i>ylaN</i>	1551719	1552000	+	4448	4857	4742	4019	1.10	1.07	0.91											
<i>ftsW</i>	1552206	1553417	+	2477	2183	2054	2412	0.88	0.83	0.97											
<i>pycA</i>	1553492	1556938	+	8483	7793	7773	8433	0.92	0.92	0.99	463	<i>pycA</i>	1554076	1554474	1554275	12.4	9.6	23.0	25.7		
<i>ctaA</i>	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		
<i>ctaB</i>	1558616	1559533	+	6765	7577	6751	7178	1.11	0.99	1.07	465	Inter	1559142	1560032	1559587	71.5	51.3	64.8	17.7		
<i>ctaC</i>	1559773	1560843	+	658	3574	3868	1601	5.45	5.96	2.49											
<i>ctaD</i>	1560876	1562744	+	928	4582	4963	2293	4.96	5.40	2.49											
<i>ctaE</i>	1562744	1563367	+	531	3190	3209	1553	6.13	6.21	2.99											
<i>ctaF</i>	1563370	1563702	+	994	4504	4783	2347	4.59	4.90	2.41											
<i>ctaG</i>	1563729	1564622	+	731	3105	3099	1563	4.26	4.26	2.10											
<i>yhbA</i>	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		
<i>yhbB</i>	1565156	1565608	+	590	657	576	577	1.15	1.00	0.97											
<i>yhbC</i>	1565685	1566725	+	706	611	595	697	0.87	0.85	0.98											
<i>yhbD</i>	1566957	1567355	+	249	163	190	204	0.66	0.77	0.81											
<i>yhbE</i>	1567371	1567610	+	138	105	105	158	0.76	0.76	1.13											
<i>yhbF</i>	1567726	1568175	+	4649	5136	5062	4523	1.10	1.09	0.97											
<i>yhbG</i>	1568230	1568502	+	3346	3124	3357	3336	0.93	1.00	1.00											
<i>yhbH</i>	1568825	1569319	+	3674	2829	2793	3688	0.77	0.76	1.00											
<i>coaD</i>	1569383	1569868	+	4283	3629	3592	4150	0.85	0.84	0.97											
<i>yhbI</i>	1569879	1571105	-	197	189	204	197	0.96	1.04	1.00											
<i>yhbK</i>	1571286	1572068	+	1315	1580	1552	1257	1.22	1.21	0.94											
<i>yhbL</i>	1572070	1573122	+	1940	2263	2343	1885	1.18	1.23	0.97											
<i>yhbM</i>	1573111	1574358	-	584	405	435	522	0.70	0.74	0.89											
<i>yhbN</i>	1574568	1575086	+	17454	15801	13931	17470	0.90	0.80	1.00											
<i>rpmF</i>	1575108	1575287	+	29449	26679	26211	28718	0.91	0.89	0.98											
<i>yhbO</i>	1575433	1576014	+	462	353	330	456	0.76	0.71	0.98											
<i>yhbP</i>	1576071	1576553	-	842	2088	3253	874	2.52	3.98	1.03											
<i>yhbQ</i>	1576713	1577609	+	756	625	592	863	0.85	0.80	1.14											
<i>yhbA</i>	1577680	1579299	+	4005	3393	3572	4323	0.85	0.90	1.08	468	<i>yhbA</i>	1579151	1579260	1579206	2.8	2.0	0.0	0.1		
<i>yhbB</i>	1579425	1579856	+	4380	5548	4675	4657	1.26	1.07	1.06											
<i>mraW</i>	1579926	1580861	+	5834	7334	6341	5627	1.25	1.08	0.96											
<i>ftsL</i>	1580901	1581254	+	12330	12969	12078	11795	1.05	0.98	0.96											
<i>pbpB</i>	1581251	1583401	+	5061	4180	3813	4800	0.83	0.75	0.95	469	<i>pbpB</i>	1581191	1581538	1581365	13.6	4.8	14.9	0.2		
<i>spoVD</i>	1583518	1585455	+	227	185	185	246	0.81	0.81	1.07											
<i>murE</i>	1585631	1587115	+	7788	6523	5792	7323	0.84	0.74	0.94											
<i>mraY</i>	1587228	1588202	+	7806	6207	5545	7469	0.79	0.71	0.96											
<i>murD</i>	1588203	1589558	+	8894	7462	6671	8241	0.84	0.75	0.93											
<i>spoVE</i>	1589619	1590719	+	4642	3602	3236	4116	0.77	0.69	0.88											
<i>murG</i>	1590842	1591933	+	5309	4732	4122	5257	0.89	0.77	0.99											
<i>murB</i>	1591960	1592871	+	7913	7488	7514	8167	0.95	0.95	1.03											
<i>divIB</i>	1593002	1593793	+	4274	3565	3532	4400	0.83	0.83	1.03											

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID										
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c								
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh						
wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh									
<i>ylxW</i>	1593790	1594485	+	4925	4436	4359	4660	0.90	0.88	0.94																
<i>ylxX</i>	1594508	1595215	+	4095	3781	3799	4031	0.92	0.93	0.98	470	ybxX	1594434	1594951	1594693				37.8	35.1	26.1	4.9		P02		
<i>sbp</i>	1595233	1595598	+	4114	3208	3100	3915	0.78	0.75	0.95																
<i>ftsA</i>	1595772	1597094	+	8150	7728	7806	8501	0.95	0.96	1.04																
<i>ftsZ</i>	1597130	1598278	+	12294	13213	13552	12201	1.08	1.10	0.99																
<i>bpr</i>	1598580	1602881	+	200	185	193	207	0.92	0.96	1.02	471	Inter	1598260	1598691	1598476				26.0	29.9	1.3	-0.6		P03		
<i>spolIGA</i>	1603076	1604005	+	161	199	199	156	1.24	1.23	0.97	472	bpr	1600537	1600680	1600609				0.5	0.7	0.6	5.9				
<i>sigE</i>	1604068	1604787	+	166	229	216	152	1.37	1.30	0.91																
<i>sigG</i>	1604927	1605709	+	250	581	634	233	2.28	2.50	0.93																
<i>ylmA</i>	1605857	1606651	+	209	231	266	195	1.10	1.27	0.92																
<i>ylmB</i>	1606853	1608133	+	164	149	160	176	0.91	0.97	1.08																
<i>ylmC</i>	1608216	1608461	+	328	287	303	291	0.87	0.92	0.88																
<i>ylmD</i>	1608624	1609460	+	6087	4050	3851	5857	0.67	0.63	0.96																
<i>ylmE</i>	1609473	1610165	+	10742	7832	7735	10440	0.73	0.72	0.97																
<i>ylmF</i>	1610168	1610617	+	12274	9853	9834	11369	0.81	0.80	0.93																
<i>ylmG</i>	1610624	1610896	+	8583	8485	8232	8926	0.99	0.96	1.05																
<i>ylmH</i>	1610957	1611730	+	4305	3937	3826	4456	0.91	0.89	1.04																
<i>divIVA</i>	1611824	1612318	+	7061	6398	6226	6773	0.90	0.88	0.96																
<i>ileS</i>	1612660	1615425	+	9021	7217	6638	8159	0.80	0.74	0.90																
<i>ylxA</i>	1615503	1615946	+	149	127	135	143	0.85	0.91	0.96																
<i>lspA</i>	1616049	1616513	+	3401	2514	2323	3329	0.74	0.68	0.98																
<i>ylxB</i>	1616515	1617426	+	5085	4248	3865	5020	0.84	0.76	0.99																
<i>pyrR</i>	1617609	1618154	+	6427	6472	4261	6632	1.09	0.67	1.03																
<i>pyrP</i>	1618326	1619630	+	4978	3897	2259	5548	0.99	0.44	1.03																
<i>pyrB</i>	1619776	1620690	+	1747	1452	705	2387	1.32	0.40	1.15																
<i>pyrC</i>	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				
<i>pyrAA</i>	1621957	1623051	+	2728	2593	1370	3715	1.11	0.43	1.17																
<i>carB_2</i>	1623036	1626251	+	2622	2028	1165	3008	0.78	0.40	1.06																
<i>pyrK</i>	1626248	1627018	+	1899	1178	724	1880	0.60	0.36	0.96																
<i>pyrD</i>	1627018	1627953	+	2864	1643	1060	2578	0.57	0.36	0.89																
<i>pyrF</i>	1627922	1628641	+	3084	1421	1005	2569	0.46	0.33	0.83																
<i>pyrE</i>	1628620	1629270	+	2965	1231	863	2429	0.44	0.31	0.83																
<i>cysH</i>	1629682	1630383	+	690	667	742	532	0.93	1.03	0.75																
<i>cysP</i>	1630395	1631459	+	618	673	718	526	1.06	1.13	0.85																
<i>sat_2</i>	1631508	1632656	+	455	645	665	357	1.40	1.45	0.78	483	sat	1632429	1632555	1632492				4.1	1.5	2.8	0.0				
<i>cysC</i>	1632669	1633262	+	471	582	653	388	1.26	1.42	0.83																
<i>ylmD</i>	1633361	1634134	+	486	667	739	384	1.37	1.52	0.79																
<i>ylmE</i>	1634137	1634922	+	1317	1356	1481	1198	1.01	1.10	0.91																
<i>ylmF</i>	1634903	1635391	+	2155	2226	2493	2052	1.03	1.16	0.95																
<i>ylmA</i>	1635431	1637149	-	2686	2328	2353	2709	0.88	0.88	1.01																
<i>ylmB</i>	1637265	1639937	+	240	221	220	250	0.92	0.91	1.03																
<i>ylmC</i>	1640020	1640895	+	6962	7400	6680	7271	1.06	0.96	1.05																
<i>ylzA</i>	1640972	1641241	+	10702	10941	9816	11417	1.02	0.92	1.07																
<i>gmk</i>	1641249	1641863	+	6557	5909	5393	6980	0.90	0.82	1.06																
<i>rpoZ</i>	1641867	1642070	+	13902	11781	11533	12323	0.85	0.83	0.89																
<i>ylmI</i>	1642151	1643371	+	2228	1980	1882	2039	0.89	0.84	0.91																
<i>priA</i>	1643368	1645785	+	2132	1988	1912	1922	0.94	0.90	0.90																
<i>def_2</i>	1645812	1646294	+	2890	2611	2293	2637	0.90	0.79	0.91																
<i>fnt</i>	1646299	1647252	+	4601	3998	3832	4269	0.87	0.83	0.93																
<i>ylmM</i>	1647239	1648582	+	4574	4104	4013	4377	0.90	0.88	0.96																
<i>ylmN</i>	1648586	1649677	+	6664	5882	5774	6249	0.88	0.87	0.94																
<i>prpC</i>	1649684	1650448	+	4385	4171	3997	4250	0.95	0.91	0.97																
<i>prkC</i>	1650442	1652388	+	5632	4978	4960	5364	0.88	0.88	0.95																
<i>ylmQ</i>	1652403	1653299	+	5065	4507	4573	4656	0.89	0.90	0.92	485	ylmQ	1652438	1652666	1652552				8.5	3.4	5.5	2.7				
<i>rpe</i>	1653304	1653957	+	3918	3482	3545	3672	0.89	0.90	0.94																
<i>ylmS</i>	1654030	1654674	+	2476	1924	1907	2535	0.78	0.77	1.03																
<i>spoVM</i>	1654746	1654826	+	2645	1636	1745	1958	0.61	0.66	0.72																
<i>rpmB</i>	1654899	1655087	-	18604	16576	15613																				

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID						
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c				
					wild	Δ abrB	Δ abh Δ abrB	Δ abh	Δ abrB/ wild	Δ abh/ Δ abrB/ wild	Δ abh/ wild							AbrB		Abh		
wild	Δ abh	wild	Δ abh	wild	Δ abh	wild	Δ abh	wild	Δ abh	wild	Δ abh	wild	Δ abh	wild	Δ abh							
<i>yjxP</i>	1735448	1735726	+	17403	16288	15693	15371	0.93	0.90	0.88												
<i>rbfA</i>	1735743	1736096	+	6616	5904	5610	5437	0.90	0.85	0.82												
<i>truB</i>	1736178	1737107	+	3255	2392	2261	2690	0.73	0.69	0.83												
<i>ribC</i>	1737126	1738076	+	7041	5997	6341	7253	0.85	0.90	1.03												
<i>rpsO</i>	1738233	1738502	+	27126	27194	26529	27518	1.00	0.98	1.01												
<i>pppA</i>	1738675	1740792	+	11032	10570	9575	10513	0.96	0.87	0.95												
<i>yjxY</i>	1740910	1741869	+	2523	1766	1533	2072	0.72	0.61	0.80	504	ykY	1740991	1741218	1741105		8.3	3.8	1.3	-0.2		
<i>mlpA</i>	1741909	1743138	+	2399	1795	1534	2049	0.76	0.64	0.84												
<i>ymxH</i>	1743216	1743473	+	291	205	208	293	0.71	0.72	1.00												
<i>spoVFA</i>	1743659	1744552	+	120	102	108	127	0.85	0.89	1.05												
<i>spoVFB</i>	1744555	1745157	+	163	127	148	153	0.78	0.91	0.93												
<i>asd</i>	1745283	1746323	+	10094	8532	8463	9371	0.85	0.84	0.93												
<i>dapG</i>	1746415	1747629	+	9269	7568	7362	8617	0.82	0.79	0.93												
<i>dapA</i>	1747660	1748532	+	9557	8441	8232	9973	0.88	0.86	1.04												
<i>ymfA</i>	1748830	1750377	+	7186	6838	6141	6974	0.95	0.85	0.97	506	ymlA	1749219	1749600	1749410		19.6	7.1	5.7	1.4		
<i>tepA</i>	1750559	1751230	+	200	228	257	188	1.13	1.27	0.93												
<i>spoIIIE</i>	1751569	1753932	+	1540	1419	1300	1523	0.92	0.84	0.98												
<i>ymlC</i>	1754075	1754800	+	1798	2211	1890	1853	1.23	1.06	1.03												
<i>ymlD</i>	1754939	1755313	+	355	419	443	359	1.18	1.24	0.99												
<i>ymlE</i>	1755565	1756149	+	416	542	487	416	1.30	1.16	0.98	508	ymlE	1755492	1756009	1755751		11.4	3.1	11.8	52.1		
<i>ymlF</i>	1756424	1756756	+	6810	9343	9602	7310	1.40	1.43	1.07												
<i>ymlG</i>	1756821	1757543	+	6684	9351	9755	7682	1.41	1.47	1.15												
<i>ymlH</i>	1757626	1758873	+	5451	7862	7969	6506	1.46	1.48	1.19												
<i>fabG_2</i>	1758928	1759656	+	2695	2463	2392	2567	0.96	0.91	0.94												
<i>ymlJ</i>	1759737	1759994	+	1135	2079	2149	1583	1.90	1.91	1.45	509	ymlJ	1759640	1760157	1759899		25.5	23.6	9.5	6.0		
<i>ymlK</i>	1760138	1760638	+	2388	2267	2329	2303	0.95	0.98	0.96												
<i>ymlL</i>	1760526	1760912	+	6147	6055	6280	5677	0.99	1.02	0.92												
<i>ymlM</i>	1760979	1761620	+	4127	3843	3887	3740	0.93	0.94	0.91												
<i>pgsA</i>	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		
<i>cinA</i>	1762494	1763744	+	4942	4243	4264	4447	0.86	0.86	0.90												
<i>recA</i>	1763917	1764960	+	8500	7073	7087	8421	0.83	0.83	0.99												
<i>phpX</i>	1765128	1766303	+	6497	6408	6812	6230	0.99	1.05	0.96	512	phbX	1765573	1765699	1765636		2.6	4.5	0.9	0.6		
											513	phbX	1766117	1766379	1766248		9.8	6.0	2.5	1.2		
<i>ymlA</i>	1766580	1768142	+	15959	18293	17791	16045	1.15	1.12	1.01												
<i>ymlB</i>	1768211	1769005	+	3010	2949	2737	2655	0.98	0.91	0.88												
<i>spoVS</i>	1769205	1769465	+	8047	13719	14313	8163	1.71	1.79	1.01												
<i>tdh</i>	1769731	1770774	+	1959	2295	2648	1988	1.17	1.36	1.02												
<i>kbl</i>	1770787	1771965	+	2773	3017	3661	2836	1.09	1.32	1.02												
<i>ymcB</i>	1772113	1773642	+	7484	7300	7372	7365	0.98	0.99	0.98												
<i>ymcA</i>	1773644	1774075	+	4874	6031	6363	4750	1.25	1.31	0.97												
<i>cotE</i>	1774337	1774882	+	215	173	168	204	0.80	0.78	0.93												
<i>mutS</i>	1775015	1777591	+	1985	1689	1642	1947	0.85	0.83	0.98												
<i>mutL</i>	1777607	1779490	+	2682	2621	2614	2795	0.98	0.98	1.04												
<i>ymzD</i>	1779888	1780343	-	438	696	681	393	1.62	1.54	0.93												
<i>ymcC</i>	1780498	1781055	-	559	443	496	581	0.80	0.89	1.04												
<i>pkSA</i>	1781176	1781793	+	511	572	521	510	1.13	1.01	0.97												
<i>pkSB</i>	1781983	1782660	+	262	486	555	261	1.87	2.13	0.99												
<i>pkSC</i>	1783033	1783899	+	510	2168	2378	452	4.30	4.66	0.88	518	pkcC	1783066	1783294	1783180		2.5	1.5	0.6	6.6		
<i>pkSD</i>	1784403	1785293	+	176	1724	1842	168	9.81	10.43	0.95	519	pkcD	1784681	1784977	1784829		17.8	10.5	1.9	1.0		
<i>pkSE</i>	1785290	1787593	+	164	1295	1296	169	7.85	7.84	1.02												
<i>acpK</i>	1787654	1787902	+	137	1067	1201	128	7.91	8.90	0.94												
<i>pkSF</i>	1787880	1789130	+	123	509	523	162	4.15	4.28	1.32												
<i>pkSG</i>	1789131	1790393	+	208	922	921	235	4.43	4.41	1.13												
<i>pkSH</i>	1790381	1791160	+	103	373	362	114	3.63	3.53	1.11												
<i>pkSI</i>	1791200	1791949	+	112	351	349	128	3.13	3.09	1.13												
<i>pkSJ</i>	1791994	1807131	+	165	545	518	181	3.27	3.09	1.09	521	pkcJ	1791736	1792321	1792029		37.6	43.0	9.8	0.0		
											522	pkcJ	1794966	1795177	1795072		6.8	4.2	10.0	5.6		
<i>pkSL</i>	1807115	1820731	+	228	463	474	235	1.99	2.03	1.02	524	pkcL	1811065	1811854	1811460		4.2	0.8	5.9	136.1		P04
<i>pkSM</i>	1820747	1833535	+	215	288	293	218	1.32	1.34	1.00												
<i>pkSN</i>	1833603	1850069	+	203	370	400	223	1.80	1.94	1.08	527	pkcN	1845847	1845973	1845910		2.7	4.0	1.2	2.3		
<i>pkSR</i>	1850084	1857715	+	275	462	481	276	1.65	1.71	0.98	529	pkcR	1855537	1855680	1855609		0.1	0.6	-0.2	4.3		
<i>pkSS</i>	1857854	1858984	-	2577	2739	2813	2700	1.06	1.09	1.04												
<i>ymzB</i>	1859209	1859565	-	322	1566	2142	286	4.86	6.65	0.88												
<i>ymaE</i>	1859644	1860342	-	158	1047	1403	210	6.65	8.87	1.31												
<i>aprX</i>	1860580	1861908	-	128	119	122	134	0.92	0.95	1.04	530	Inter	1860178	1860729	1860454		35.6	41.7	10.9	0.6		
											531	aprX	1861759	1862038	1861899		7.3	3.1	4.7	17.7		
											531	Inter	1862048	1862888	1862468		45.8	27.3	41.5	161.3		P01
<i>ymaC</i>	1862644	1863351	+	516	350	364	471	0.70	0.72	0.89												
<i>ymaD</i>	1863421	1863873	+	1634	1956	1953	1795	1.21	1.21	1.09												
<i>ebrB</i>	1863887	1864240	-	397	322	328	389	0.83	0.84	0.99												
<i>ebrA</i>	1864254	1864571	-	231	192	204	263	0.83	0.89	1.14												

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$																		
<i>ynaG</i>	1864708	1865079	-	178	165	185	237	0.93	1.05	1.34											
<i>ynaF</i>	1865072	1865485	+	115	99	96	119	0.86	0.84	1.03											
<i>miaA</i>	1865584	1866528	+	1314	1014	931	1237	0.77	0.71	0.94											
<i>hfq</i>	1866568	1866789	+	1936	6233	6323	2340	3.18	3.25	1.18											
<i>ynzC</i>	1866985	1867257	+	548	1757	1869	601	3.26	3.41	1.08											
<i>ynzA</i>	1867339	1867569	+	2417	3290	3345	2509	1.38	1.40	1.02											
<i>nrpI_1</i>	1867812	1868204	+	2826	2635	2306	2670	0.95	0.82	0.95											
<i>nrpE</i>	1868164	1870266	+	5542	4299	3919	5317	0.78	0.70	0.96											
<i>nrpF_1</i>	1870284	1871273	+	4717	3544	3063	4325	0.75	0.64	0.92											
<i>ynaB</i>	1871323	1871943	+	3775	2692	2325	3136	0.72	0.61	0.82											
<i>cwlC</i>	1872007	1872774	-	121	116	109	128	0.96	0.90	1.05											
<i>spoVK</i>	1873398	1874366	+	202	135	137	173	0.67	0.68	0.84											
<i>ynbA</i>	1874587	1875591	+	2707	1905	1659	2316	0.70	0.61	0.86											
<i>ynbB</i>	1875779	1877044	+	2952	2232	2161	2676	0.76	0.73	0.91											
<i>glnR</i>	1877155	1877562	+	5436	4321	3967	4632	0.79	0.73	0.85	533	<i>glnR</i>	1877076	1877253	1877165	3.9	4.0	1.5	1.6		
<i>glnA</i>	1877623	1878957	+	15330	13058	13623	14055	0.85	0.89	0.92	534	<i>glnA</i>	1877365	1877966	1877666	53.3	77.8	22.2	1.0		P02
											535	Inter	1878691	1879854	1879273	84.5	86.4	15.6	2.8		
<i>ynxB</i>	1879285	1879575	+	294	594	635	300	2.02	2.20	1.02											
<i>ynzF</i>	1879821	1880165	+	296	732	790	312	2.48	2.67	1.07											
<i>ynzG</i>	1880296	1880547	+	74	127	141	69	1.71	1.90	0.92											
<i>ynaB</i>	1880867	1881178	+	758	2003	1789	857	2.62	2.39	1.11											
<i>ynaC</i>	1881248	1882039	+	557	1612	1625	537	2.93	3.02	0.97											
<i>ynaD</i>	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		
<i>ynaE</i>	1883446	1884087	+	158	304	301	183	1.90	1.90	1.15											
<i>ynaF</i>	1884176	1884529	+	318	529	535	357	1.64	1.69	1.13											
											538	Inter	1884352	1884784	1884568	20.8	15.8	0.2	3.4		
<i>ynaG</i>	1884573	1884848	+	444	699	712	482	1.56	1.61	1.09											
<i>ynaI</i>	1885265	1885735	+	95	121	102	92	1.24	1.05	0.97	539	<i>ynaI</i>	1885253	1885923	1885588	39.1	44.6	11.1	1.2		
<i>xynP</i>	1886560	1887951	+	529	402	442	524	0.76	0.83	0.99											
<i>xynB</i>	1887982	1889583	+	682	473	540	640	0.70	0.81	0.94	540	<i>xynB</i>	1889112	1889544	1889328	26.8	5.5	19.7	0.2		P05
<i>xylR</i>	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		
<i>xylA</i>	1891116	1892453	+	2451	3662	2901	2526	1.55	1.20	1.04											
<i>xylB</i>	1892604	1894103	+	1490	2444	1812	1571	1.75	1.25	1.05											
<i>yncB</i>	1894586	1895221	-	1267	454	534	1026	0.36	0.42	0.81											
											543	Inter	1895283	1895834	1895559	36.6	43.9	13.7	2.2		
<i>yncC</i>	1895632	1896891	+	237	176	191	280	0.75	0.81	1.19											
<i>yncD</i>	1897149	1898333	-	124	126	139	148	1.01	1.12	1.19											
<i>yncE</i>	1898797	1899258	+	1120	372	380	1007	0.33	0.34	0.90											
<i>yncF</i>	1899288	1899722	+	2363	1064	1135	2180	0.45	0.48	0.92											
											544	Inter	1899924	1900237	1900081	18.1	12.2	2.1	4.9		
<i>ynzH</i>	1900326	1900586	-	77	81	78	64	1.04	1.00	0.82											
											545	Inter	1900689	1900798	1900744	3.5	3.7	0.2	-0.3		
<i>thyA_1</i>	1901428	1902267	+	982	467	477	953	0.48	0.48	0.97											
<i>yncM</i>	1902720	1903472	-	1605	6931	7335	1374	4.38	4.57	0.85											
											546	Inter	1903188	1903841	1903515	27.3	15.0	7.2	0.0		
<i>cotC</i>	1904204	1904560	-	140	105	104	111	0.74	0.73	0.79											
<i>tatAC</i>	1904579	1904767	-	1214	991	979	1000	0.81	0.78	0.82											
<i>yndA</i>	1905018	1905416	+	106	114	112	105	1.07	1.05	0.99	547	<i>yndA</i>	1905177	1905490	1905334	7.7	4.4	10.5	17.1		
<i>yndB</i>	1905481	1905915	-	3329	3602	3445	3084	1.08	1.03	0.93											
<i>yndB</i>	1906222	1906410	+	184	120	115	129	0.65	0.62	0.70											
<i>yndD</i>	1906703	1908265	+	148	137	144	153	0.92	0.97	1.03											
<i>yndE</i>	1908295	1909386	+	127	129	141	163	1.02	1.11	1.28											
<i>yndF</i>	1909376	1910590	+	147	130	136	143	0.88	0.92	0.96											
											548	Inter	1910482	1910930	1910706	29.2	27.3	-0.1	-0.9		P03
<i>yndG</i>	1910737	1911543	+	924	1479	1398	881	1.60	1.51	0.95											
<i>yndH</i>	1911548	1912165	+	684	1050	961	728	1.52	1.40	1.06	549	<i>yndH</i>	1912028	1912171	1912100	2.1	5.1	-0.2	-0.5		
<i>yndJ</i>	1912162	1913802	+	775	1234	1149	766	1.60	1.47	0.98											
											550	Inter	1913575	1914041	1913808	16.8	8.8	3.3	-1.5		
<i>yndK</i>	1913839	1914204	+	1043	1648	1456	964	1.59	1.38	0.91											
<i>yndL</i>	1914430	1915188	+	135	125	128	126	0.93	0.96	0.95	551	<i>yndL</i>	1914187	1914772	1914480	32.1	43.9	3.7	1.7		P03
<i>yndM</i>	1915215	1915754	-	211	236	274	226	1.12	1.30	1.07											
<i>yndN</i>	1915872	1916306	+	2101	4463	5521	2360	2.16	2.70	1.13											
<i>lexA</i>	1916848	1917465	-	4224	4085	3466	4117	0.97	0.82	0.98											
<i>yneA</i>	1917615	1917932	+	325	245	239	317	0.76	0.74	0.98											
<i>yneB</i>	1917951	1918604	+	1092	597	637	946	0.55	0.58	0.86											
<i>ynzC</i>	1918668	1918901	+	2061	1313	1389	2076	0.64	0.67	1.01											
<i>tkf</i>	1919070	1921073	+	16550	16714	16934	17076	1.01	1.02	1.03	553	<i>tkf</i>	1919865	1920280	1920073	24.0	20.5	3.4	0.1		P03
											554	<i>tkf</i>	1920477	1920603	1920540	1.4	3.6	1.3	3.4		
<i>yneE</i>	1921226	1921672	+	343	233	262	337	0.68	0.77	0.94											
<i>yneF</i>	1921758	1921976	+	15432	10314	9866	14845	0.67	0.64	0.96											
<i>ynzD</i>	1922050	1922223	-	155	731	473	154	4.75	3.04	0.98											

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

gene		Transcriptome analysis									ChAP-chip analysis							Profile ID		
name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center	Binding intensity ^c				
				wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild						AbrB			Abh	
																wild -type	Δabh -type	wild -type	$\Delta abrB$ -type	
<i>ccdA</i>	1922443	1923150	+	420	706	739	454	1.71	1.76	1.06	555	Inter	1922092	1922490	1922291	24.9	22.4	6.7	-1.3	
<i>yneI</i>	1923239	1923601	+	1498	1935	1902	1479	1.28	1.26	0.97										
<i>yneJ</i>	1923680	1924171	+	2653	3261	3115	2877	1.23	1.18	1.09										
<i>yneK</i>	1924202	1924630	-	2514	2096	2052	1969	0.83	0.80	0.78										
<i>cotM</i>	1924864	1925256	-	72	85	85	64	1.19	1.20	0.92										
<i>sspP</i>	1925337	1925483	-	90	395	523	51	4.22	5.57	0.57										
<i>sspO</i>	1925515	1925661	-	132	397	569	106	3.05	4.39	0.80										
<i>citB</i>	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	
<i>yneN</i>	1928690	1929202	+	1077	6293	3908	1000	5.81	3.31	0.90										
<i>sspN</i>	1929473	1929619	+	144	584	953	152	4.04	6.60	1.05										
<i>tlp</i>	1929656	1929907	+	138	551	684	130	3.95	4.90	0.94										
<i>yneP</i>	1930043	1930408	+	1002	580	555	1060	0.59	0.58	1.05	558	yneP	1930065	1930208	1930137	2.3	4.5	0.9	-0.1	
<i>yneQ</i>	1930424	1930723	+	1923	1057	1149	1755	0.55	0.60	0.91										
<i>yneR</i>	1930754	1931041	-	4220	3811	3793	3926	0.90	0.90	0.93										
<i>yneS</i>	1931129	1931710	-	2828	2160	1690	2644	0.76	0.60	0.94										
<i>yneT</i>	1931880	1932287	+	2028	1943	2330	1895	0.96	1.15	0.93										
<i>parE</i>	1932686	1934653	+	4322	3110	3284	4224	0.72	0.76	0.98										
<i>parC</i>	1934657	1937077	+	4808	3730	3854	4647	0.78	0.80	0.96	559	parC	1935336	1935512	1935424	5.5	0.3	4.2	1.3	
<i>ynfC</i>	1937275	1937685	-	1616	1067	1099	1464	0.65	0.68	0.90										
<i>alsT</i>	1938134	1939531	+	4611	3542	2853	4087	0.77	0.62	0.89	561	alsT	1937970	1938334	1938152	23.6	3.7	12.6	1.2	
<i>bgIC</i>	1939834	1941333	+	263	243	260	273	0.92	0.99	1.03										
<i>ynfE</i>	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	
<i>ynfF</i>	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	
<i>xynD</i>	1943322	1944863	-	196	630	599	164	3.22	3.02	0.82	564	xynD	1943733	1943859	1943796	3.5	4.3	1.2	1.5	
											565	Inter	1944549	1945524	1945037	65.3	108.7	6.1	-3.3	
<i>yngA</i>	1945458	1945904	+	94	84	88	117	0.89	0.94	1.25										
<i>yngB</i>	1945911	1946804	+	558	520	501	554	0.93	0.90	0.99										
<i>yngC</i>	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	
<i>yngD</i>	1947522	1948721	-	152	140	143	153	0.92	0.94	1.00										
<i>yngE</i>	1948891	1950678	-	141	127	130	154	0.90	0.92	1.09										
<i>yngF</i>	1950437	1951219	-	99	93	86	105	0.95	0.88	1.14										
<i>yngG</i>	1951240	1952139	-	149	144	149	154	0.97	1.00	1.03										
<i>yngH</i>	1952390	1953724	-	138	116	112	152	0.84	0.81	1.10										
<i>yngI</i>	1953734	1955383	-	122	113	117	147	0.93	0.96	1.21										
<i>yngJ</i>	1955427	1956569	-	105	82	81	113	0.79	0.77	1.10										
<i>yngE</i>	1956660	1956965	-	109	128	143	128	1.17	1.31	1.19										
											570	Inter	1956874	1957255	1957065	16.1	12.7	28.8	29.6	
<i>yngK</i>	1957236	1958768	-	117	117	118	116	1.00	1.01	0.99										
<i>yngL</i>	1958904	1959296	-	127	120	140	136	0.95	1.11	1.07										
<i>ppsE</i>	1959407	1963246	-	209	390	394	208	1.80	1.81	0.98										
<i>ppsD</i>	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	
											573	ppsD	1970066	1970549	1970308	2.2	1.5	2.6	42.0	
<i>ppsC</i>	1974090	1981757	-	169	590	583	173	3.41	3.29	1.01										
<i>ppsB</i>	1981774	1989456	-	158	616	641	173	3.83	3.91	1.08	575	ppsB	1981762	1982075	1981919	15.4	2.8	12.9	2.4	
											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	
<i>ppsA</i>	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	
											581	Inter	1996943	1997460	1997202	19.6	16.7	1.0	-1.5	
<i>dacC</i>	1997549	1999024	-	360	1363	1463	456	3.85	4.17	1.22										
<i>yoxA</i>	1999058	2000035	-	320	1280	1354	438	4.25	4.45	1.34										
<i>yoeA</i>	2000169	2001560	-	646	4639	4696	683	7.30	7.35	1.04										
<i>yoeB</i>	2001846	2002391	+	7702	7094	6823	6933	0.96	0.92	0.90										
<i>trmSL-Arg</i>	2002484	2002559	-	705	3849	4041	677	4.88	5.13	0.96										
<i>yoeC</i>	2002869	2003156	-	556	440	446	472	0.80	0.82	0.85										
<i>yoeD</i>	2003472	2003702	-	304	331	271	311	1.08	0.88	1.00	582	Inter	2003046	2003733	2003390	43.0	78.7	38.2	21.4	
<i>ggt</i>	2003887	2005650	+	111	113	122	115	1.01	1.10	1.03										
<i>yofA</i>	2005751	2006608	-	218	471	457	273	2.18	2.09	1.22										
											583	Inter	2006616	2006759	2006688	4.9	1.4	3.0	-0.5	
<i>yogA</i>	2006736	2007725	+	186	253	279	176	1.35	1.47	0.93										
<i>gltD</i>	2007782	2009263	-	4197	714	1459	3202	0.17	0.35	0.76										
<i>gltA</i>	2009280	2013842	-	3875	517	1008	2865	0.13	0.26	0.74	584	gltA	2011614	2011774	2011694	2.2	1.3	4.0	5.1	
<i>gltC</i>	2013989	2014891	+	1427	698	749	1271	0.48	0.52	0.89										
<i>proJ</i>	2014943	2016058	-	723	672	715	681	0.93	1.01	0.91										
<i>proH</i>	2016055	2016948	-	745	718	702	722	0.99	0.99	0.95										
<i>rip</i>	2017095	2017463	-	366	482	567	334	1.33	1.58	0.90										
<i>fabG_3</i>	2017763	2018479	-	12238	10877	11053	13089	0.89	0.91	1.07										
<i>yoxC</i>	2018630	2018935	+	766	369	600	296	0.48	0.78	0.38										
<i>yoxB</i>	2019006	2019776	+	158	113	13														

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

gene	Transcriptome analysis										ChAP-chip analysis						Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$	Δabh / wild							AbrB		Abh	
wild	Δabh	-type	Δabh	-type	$\Delta abrB$	-type	Δabh	-type													
<i>yoaC</i>	2021771	2023234	-	157	122	137	153	0.77	0.87	0.98											
<i>yoaD</i>	2023252	2024286	-	221	150	178	219	0.68	0.80	0.99											
<i>yoaE</i>	2024610	2026643	+	447	439	503	384	0.98	1.13	0.85											
<i>yoaF</i>	2026720	2027013	+	1380	1552	1474	1172	1.08	1.06	0.86											
<i>yoaG</i>	2027386	2027790	-	1604	1954	2136	1764	1.22	1.35	1.11											
<i>yoaQ</i>	2028231	2028524	+	114	192	187	122	1.73	1.68	1.08											
<i>yoaH</i>	2028640	2030244	-	387	385	335	430	1.02	0.87	1.07											
<i>yoaI</i>	2030972	2032099	+	84	80	90	78	0.95	1.07	0.92											
<i>yoaJ</i>	2032136	2032834	-	898	1233	1359	891	1.37	1.50	0.98											
<i>yoaK</i>	2033104	2033781	-	354	473	516	414	1.34	1.45	1.16											
<i>pelB</i>	2033954	2034991	+	106	129	131	93	1.22	1.24	0.88											
<i>yoaM</i>	2035248	2035931	+	73	75	82	79	1.04	1.13	1.09											
<i>yoaN</i>	2036810	2037988	-	94	89	92	97	0.95	0.98	1.03											
<i>yoaO</i>	2038111	2038599	-	323	383	360	349	1.19	1.11	1.07											
<i>yoaP</i>	2038819	2039574	-	98	102	113	104	1.04	1.16	1.04											
<i>yoaQ</i>	2039882	2040238	+	140	131	142	124	0.94	1.02	0.89											
<i>yoaF</i>	2040786	2041037	-	93	97	124	68	1.05	1.32	0.74											
<i>yoaR</i>	2041138	2042049	-	133	131	139	149	0.98	1.04	1.12											
<i>yoaS</i>	2042396	2042878	+	394	314	325	387	0.80	0.82	0.98											
<i>yoaG</i>	2042888	2043142	+	634	433	440	604	0.68	0.68	0.92	595	yoaG	2042962	2043207	2043085	9.7	1.4	5.1	-0.8		
<i>yoaT</i>	2043248	2044042	+	702	587	631	683	0.85	0.91	0.95											
<i>yoaU</i>	2044166	2045038	-	274	234	256	271	0.85	0.94	0.97											
<i>yoaV</i>	2045139	2046017	+	186	168	163	191	0.90	0.87	1.02	596	Inter	2044919	2045179	2045049	8.5	6.0	3.3	0.7		
<i>yoaW</i>	2046190	2046621	-	93	216	251	79	2.31	2.65	0.84											
<i>yoaZ</i>	2046885	2047517	-	114	128	126	118	1.11	1.09	1.01											
<i>penP</i>	2047743	2048663	+	2180	2044	2191	1886	0.95	1.01	0.86	597	Inter	2047399	2047746	2047573	18.2	13.1	1.6	-0.6		
<i>yobA</i>	2049160	2049522	-	142	148	178	139	1.04	1.23	0.97											
<i>yobB</i>	2049899	2050162	+	152	1858	2759	150	12.10	17.45	0.99	598	yobB	2049524	2050312	2049918	73.0	82.6	55.0	36.7	P01	
<i>pps</i>	2050539	2051319	-	491	472	507	458	0.96	1.03	0.92											
<i>xynA</i>	2053809	2054450	-	4915	6872	6636	4578	1.39	1.35	0.93	599	Inter	2052992	2053594	2053293	46.0	64.0	14.2	3.0		
<i>yobD</i>	2055488	2055826	+	166	214	188	154	1.23	1.08	0.89	601	yobD	2055525	2055974	2055750	30.7	3.6	18.4	-1.1	P05	
<i>yoaH</i>	2055860	2056180	-	60	63	62	56	1.05	1.03	0.93											
<i>yoaI</i>	2056425	2056790	+	273	321	324	263	1.17	1.15	0.96											
<i>yobE</i>	2057012	2057671	+	481	282	373	523	0.60	0.79	1.09											
<i>yobF</i>	2057926	2058849	-	114	120	134	141	1.04	1.16	1.21											
<i>yoaJ</i>	2059448	2059903	-	134	128	144	134	0.95	1.07	0.98											
<i>rapK</i>	2061361	2062476	+	154	1003	1310	201	6.51	8.57	1.31											
<i>phrK</i>	2062473	2062595	+	761	2891	3157	889	3.98	4.30	1.16											
<i>yobH</i>	2062721	2063332	-	165	156	187	215	0.94	1.13	1.29											
<i>yoaK</i>	2063411	2063758	-	127	123	140	141	0.97	1.09	1.11											
<i>yoaL</i>	2063751	2064044	-	46	39	35	40	0.85	0.77	0.85											
<i>yoaM</i>	2064253	2064588	+	150	151	151	136	1.00	1.00	0.90											
<i>yobI</i>	2064635	2068240	-	806	755	740	763	0.93	0.91	0.95	604	yobI	2066218	2066463	2066341	7.7	7.2	0.9	-0.4		
<i>yobJ</i>	2069455	2070297	-	2009	2361	2471	2164	1.17	1.23	1.07	606	Inter	2068768	2069353	2069061	29.5	10.8	2.6	2.0		
<i>yobK</i>	2070497	2070955	-	809	1618	1668	779	1.99	2.07	0.95	608	yobJ	2069805	2070371	2070088	40.3	28.9	3.1	2.7	P03	
<i>yobL</i>	2070965	2072767	-	412	1052	1145	369	2.59	2.86	0.88											
<i>yobM</i>	2072869	2073357	-	538	2001	2137	466	3.74	4.00	0.86											
<i>yobN</i>	2073650	2074990	+	102	92	97	99	0.90	0.95	0.97											
<i>yobO</i>	2075417	2077837	+	177	509	820	186	2.90	4.82	1.03	609	Inter	2075007	2075405	2075206	16.6	7.6	5.4	2.0		
<i>csaA</i>	2078425	2078757	-	1151	1044	1088	986	0.91	0.95	0.85	610	yobO	2076520	2076867	2076694	6.4	0.4	5.4	25.6		
<i>yobQ</i>	2078822	2079547	-	631	554	620	542	0.89	1.00	0.85	611	Inter	2077727	2078159	2077943	18.1	12.4	-0.4	-0.9		
<i>yobR</i>	2079562	2080305	-	811	672	702	702	0.82	0.86	0.85											
<i>yobS</i>	2080383	2080958	-	382	296	301	343	0.77	0.78	0.88											
<i>yobT</i>	2080964	2081665	-	618	514	522	593	0.83	0.85	0.94											
<i>yobU</i>	2081742	2082224	-	130	142	146	119	1.09	1.12	0.91											
<i>yobV</i>	2082278	2083219	-	162	334	331	188	2.06	2.05	1.15											
<i>yobW</i>	2083425	2083970	+	150	151	149	153	1.01	1.00	1.02											
<i>yoaA</i>	2083997	2084320	-	1193	1173	1123	1191	1.02	0.96	1.03											
<i>yoaC</i>	2084514	2085191	+	3171	4960	4871	4078	1.58	1.55	1.28	613	yocA	2084918	2085197	2085058	10.4	3.9	3.1	-0.2		
<i>yoaB</i>	2085281	2085817	-	2446	2898	2160	2454	1.20	0.88	1.02											
<i>yobC</i>	2085954	2086736	-	200	285	408	176	1.42	2.04	0.87	614	yocB	2086312	2086506	2086409	6.6	0.9	1.8	0.1		
<i>yocC</i>	2086907	2087404	+	174	206	179	201	1.21	1.03	1.15	615	Inter	2086686	2086914	2086800	7.5	0.5	3.8	-0.8		
<i>yocD</i>	2087468	2088445	+	549	1377	1028	455	2.59	1.90	0.83	616	yocC	2087264	2087543	2087404	7.8	15.8	0.1	0.1		

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$														
<i>des</i>	2088607	2089665	+	1420	5580	4021	1224	3.94	2.84	0.87											
<i>yocF</i>	2089785	2090897	+	379	719	583	373	1.90	1.56	0.98											
<i>yocG</i>	2090916	2091515	+	881	1326	1165	802	1.51	1.33	0.90											
<i>yocH</i>	2092110	2092973	-	6180	5291	5781	6461	0.86	0.94	1.05											
<i>yocI</i>	2093221	2094996	-	983	676	666	917	0.68	0.68	0.92											
<i>acpD_1</i>	2095561	2096187	-	5354	3491	3397	5632	0.65	0.64	1.05	618	acpD	2095798	2096043	2095921	10.4	-0.1	4.7	0.2		
<i>yocK</i>	2096338	2096967	-	810	557	707	463	0.68	0.88	0.54											
<i>yocL</i>	2096904	2097236	-	314	406	331	276	1.31	1.05	0.84											
<i>yocM</i>	2097528	2098004	-	155	210	191	183	1.35	1.23	1.14	619	yocM	2097787	2098032	2097910	9.7	1.9	9.1	3.1		
<i>yozN</i>	2098071	2098334	+	93	95	100	96	1.02	1.08	1.03											
<i>yocZ</i>	2098339	2098572	+	112	117	120	106	1.06	1.06	0.94											
<i>yozO</i>	2098658	2099002	-	1843	2604	2276	1743	1.43	1.26	0.93											
<i>yozC</i>	2099359	2099562	-	2597	1470	1607	1958	0.58	0.63	0.76											
<i>dhaS</i>	2099792	2101279	+	1277	4266	5006	1451	3.37	3.97	1.13											
<i>sqhC</i>	2101380	2103278	+	121	129	131	133	1.06	1.08	1.09	621	sqhC	2102088	2102452	2102270	20.3	8.2	15.1	5.3		
<i>sodF</i>	2103268	2104113	+	155	128	132	182	0.82	0.85	1.17											
<i>yocR</i>	2104146	2105483	-	922	609	529	784	0.66	0.57	0.85	623	yocR	2105250	2105512	2105381	8.3	10.6	2.9	1.7		
<i>yocS</i>	2105702	2106667	+	154	150	164	165	0.98	1.06	1.07											
<i>odhB</i>	2106717	2107970	-	22224	23224	23954	21940	1.05	1.08	0.99											
<i>sucA</i>	2107986	2110811	-	19663	20751	21475	20105	1.06	1.09	1.02											
<i>yojO</i>	2111039	2113024	-	4971	4677	4909	5248	0.95	0.99	1.05											
<i>yojN</i>	2112966	2113880	-	3277	3034	3150	3658	0.94	0.97	1.12											
<i>yojM</i>	2113944	2114534	-	139	208	348	224	1.50	2.50	1.60											
<i>yojL</i>	2114627	2115871	-	390	1923	4452	1265	5.20	11.88	3.20											
<i>yojK</i>	2116253	2117470	-	363	666	788	395	1.88	2.20	1.06	626	Inter	2115365	2116392	2115879	46.7	29.8	76.3	181.5		P01
<i>yojJ</i>	2117706	2118329	-	132	107	119	144	0.81	0.91	1.05											
<i>yojI</i>	2118594	2119952	+	651	672	600	573	1.06	0.92	0.88	627	Inter	2118323	2118534	2118429	2.0	1.0	0.8	5.4		
<i>yojH</i>	2119968	2120816	+	1441	1386	1318	1191	0.97	0.91	0.83	628	yojI	2118816	2119197	2119007	12.8	3.3	10.2	0.0		
<i>yojG</i>	2120842	2121270	-	5309	6075	5043	5952	1.15	0.95	1.12											
<i>yojF</i>	2121524	2121874	-	5338	6514	4812	5693	1.22	0.90	1.07											
<i>yojE</i>	2122225	2123121	-	1721	1087	959	1594	0.64	0.56	0.93											
<i>yojR</i>	2123220	2123693	+	109	116	122	134	1.07	1.13	1.22											
<i>yojC</i>	2123586	2123819	-	94	103	108	78	1.10	1.16	0.84											
<i>yojB</i>	2123728	2123964	-	218	180	201	264	0.82	0.92	1.22											
<i>yojA</i>	2124049	2125383	-	320	232	261	326	0.73	0.82	1.03											
<i>yodA</i>	2125748	2126137	+	290	284	285	313	0.98	0.98	1.06											
<i>yodB</i>	2126544	2126882	-	536	620	566	474	1.15	1.04	0.86	630	Inter	2126245	2126490	2126368	6.9	4.4	5.0	4.3		
<i>yodC</i>	2127012	2127620	+	8524	10353	10748	8014	1.21	1.26	0.94											
<i>yodD</i>	2127663	2128265	-	205	147	167	308	0.71	0.82	1.42											
<i>yodE</i>	2128281	2129192	-	278	216	226	405	0.78	0.81	1.42											
<i>yodF</i>	2129576	2131066	+	266	311	352	272	1.16	1.31	1.02	632	Inter	2129305	2129533	2129419	8.5	1.8	6.9	1.8		
<i>ctpA</i>	2131101	2132501	-	5636	6246	6007	5748	1.11	1.07	1.02	633	yodF	2130767	2130876	2130822	0.1	0.3	0.4	3.8		
<i>yodH</i>	2132654	2133355	+	154	170	172	153	1.10	1.12	0.99											
<i>yodI</i>	2133443	2133694	+	295	277	283	334	0.94	0.96	1.13											
<i>yodJ</i>	2133765	2134586	-	8530	7483	7203	8544	0.88	0.85	1.00											
<i>deoD</i>	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		
<i>yodL</i>	2135737	2136054	-	672	545	503	578	0.81	0.74	0.85											
<i>yodM</i>	2136112	2136723	-	958	855	762	904	0.92	0.80	0.93											
<i>yozD</i>	2136801	2136977	-	172	145	143	195	0.84	0.81	1.08											
<i>yodN</i>	2137236	2137916	-	139	120	120	133	0.87	0.87	0.95											
<i>yozE</i>	2138067	2138291	-	922	873	944	876	0.96	1.03	0.95	635	Inter	2137924	2138101	2138013	4.6	1.9	5.6	4.7		
<i>kamA</i>	2138652	2140067	-	101	96	99	103	0.95	0.98	1.02											
<i>yodP</i>	2140096	2140923	-	86	80	86	95	0.93	1.01	1.09											
<i>yodQ</i>	2140901	2142211	-	125	109	118	137	0.88	0.95	1.11											
<i>yodR</i>	2142220	2142873	-	162	138	146	170	0.85	0.90	1.05											
<i>yodS</i>	2142858	2143547	-	144	114	120	179	0.79	0.84	1.24											
<i>yodT</i>	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		
<i>cgeE</i>	2145211	2145990	-	207	268	243	224	1.29	1.17	1.07											
<i>cgeD</i>	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		
<i>cgeC</i>	2147364	2147669	-	91	84	96	82	0.92	1.05	0.90											
<i>cgeA</i>	2147874	2148275	+	89	84	88	78	0.95	1.00	0.89											
<i>cgeB</i>	2148282	2149235	+	138	146	144	147	1.05	1.04	1.06											
<i>phy</i>	2149306	2150454	-	136	405	451	146	2.96	3.29	1.06											
<i>yodU</i>	2150824	2151249	+	104	153	157	103	1.48	1.51	1.00	639	Inter	2150419	2150714	2150567	9.2	11.1	1.2	-0.6		
<i>yotN</i>	2151284	2151460	-	86	74	84	86	0.87	0.98	1.00	640	yodU	2151116	2151344	2151230	5.2	7.0	6.8	8.4		
<i>yotM</i>	2151463	2152050	-	92	74	84	82	0.80	0.91	0.89											
<i>yotL</i>	2152125	2152367	+	38	66	59	39	1.78	1.55	1.05											

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

gene	Transcriptome analysis										ChAP-chip analysis							Profile ID			
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center	Binding intensity ^c				
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild						AbrB		Abh		
-type	Δabh	-type	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$	Δabh													
<i>yotK</i>	2152369	2152554	-	97	63	78	106	0.66	0.80	1.07											
<i>yotJ</i>	2152638	2152850	-	39	37	35	38	0.95	0.92	0.99											
<i>yotI</i>	2152916	2153278	-	62	56	58	54	0.90	0.94	0.87											
<i>yotH</i>	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	
<i>yotG</i>	2153464	2153781	-	80	76	77	80	0.94	0.96	1.00											
<i>yotF</i>	2153794	2153871	-	50	46	56	41	0.95	1.11	0.85											
<i>yotE</i>	2153903	2154049	-	118	82	93	104	0.70	0.78	0.88											
<i>yotD</i>	2154085	2154216	-	279	180	235	227	0.64	0.84	0.79											
<i>yotC</i>	2154256	2154447	-	68	52	55	76	0.76	0.80	1.10											
<i>yotB</i>	2154491	2155318	-	101	85	97	111	0.84	0.96	1.09											
<i>sspC</i>	2155437	2155655	+	74	162	178	73	2.15	2.36	0.99											
<i>yosZ</i>	2155846	2155911	-	927	603	730	733	0.65	0.78	0.77											
<i>yosX</i>	2155955	2156308	-	141	105	122	106	0.74	0.85	0.75											
<i>yosW</i>	2156539	2156880	-	109	102	113	112	0.93	1.04	1.03	642	yosW	2156454	2156648	2156551	5.8	1.4	-0.1	-0.4		
<i>yosV</i>	2157027	2157317	-	74	60	71	49	0.81	0.95	0.65	643	yosV	2156998	2157294	2157146	13.3	5.8	2.0	-0.8		
											643	Inter	2157321	2157770	2157546	32.2	8.6	6.2	5.5		
<i>yosU</i>	2157637	2157882	+	99	122	121	169	1.21	1.21	1.72											
<i>yosT</i>	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	
<i>yosS</i>	2158466	2158894	-	190	154	159	214	0.81	0.84	1.11											
<i>yosR</i>	2158940	2159182	-	134	120	142	134	0.90	1.06	1.00											
<i>nrdF_2</i>	2159179	2160976	-	134	114	132	131	0.85	0.98	0.98											
											644	Inter	2161214	2161323	2161269	1.9	1.1	-0.4	3.4		
<i>yosN</i>	2161306	2164812	-	96	86	93	96	0.89	0.97	0.99											
<i>nrdL_2</i>	2164775	2165164	-	74	57	61	72	0.77	0.82	0.96											
<i>yosL</i>	2165170	2165523	-	89	64	68	60	0.72	0.76	0.67											
<i>yosK</i>	2165611	2165811	-	88	57	65	74	0.65	0.73	0.83											
<i>yosJ</i>	2165856	2166050	-	139	124	152	106	0.89	1.10	0.76											
<i>yosI</i>	2166071	2166205	-	67	66	62	76	0.98	0.91	1.12											
<i>yosH</i>	2166237	2166707	-	150	130	144	160	0.86	0.96	1.06											
<i>yosG</i>	2166768	2167130	-	85	72	72	75	0.85	0.84	0.88											
<i>yosF</i>	2167173	2167298	-	105	81	85	84	0.78	0.82	0.81											
<i>yosE</i>	2167312	2167659	-	122	115	128	118	0.94	1.05	0.97											
<i>yosD</i>	2167674	2168069	-	123	85	83	88	0.69	0.67	0.71											
<i>yosC</i>	2168108	2168650	-	158	118	138	146	0.74	0.87	0.92											
<i>yosB</i>	2168695	2168874	-	82	71	84	90	0.91	1.11	1.19											
<i>yosA</i>	2169005	2169124	+	440	466	554	608	1.09	1.25	1.38											
<i>yorZ</i>	2169228	2169440	-	121	101	103	97	0.83	0.84	0.79											
<i>yorY</i>	2169507	2169689	-	81	67	76	85	0.83	0.94	1.05											
<i>yorX</i>	2169702	2169929	-	107	84	106	96	0.79	0.99	0.90											
<i>yorW</i>	2169969	2170334	-	106	98	107	95	0.93	1.01	0.90											
<i>yorV</i>	2170337	2170555	-	77	73	80	75	0.94	1.03	0.96											
<i>mitP</i>	2170599	2171930	-	147	121	132	138	0.82	0.90	0.94											
<i>yorT</i>	2171979	2172098	-	82	68	85	91	0.84	1.04	1.10											
<i>yorS</i>	2172130	2172648	-	61	61	63	61	1.00	1.02	0.99											
<i>yorR</i>	2172657	2173154	-	128	104	130	127	0.83	1.01	0.97											
<i>yorQ</i>	2173154	2173309	-	136	113	144	108	0.83	1.06	0.80											
<i>yorP</i>	2173302	2173517	-	132	145	143	121	1.09	1.09	0.91											
<i>yorO</i>	2173550	2173747	-	138	136	128	174	0.99	0.93	1.27											
<i>yorN</i>	2173783	2173932	-	177	198	210	205	1.15	1.19	1.19											
<i>yorM</i>	2174048	2174764	-	70	65	68	63	0.93	0.97	0.89	646	yorM	2173811	2174294	2174053	29.5	41.4	7.3	4.3		
											647	yorM	2174440	2174889	2174665	30.8	9.0	33.4	3.4		
<i>yorL</i>	2174792	2178709	-	98	81	91	86	0.83	0.93	0.88											
<i>yorK</i>	2178722	2180452	-	98	82	87	90	0.84	0.88	0.91											
<i>yorJ</i>	2180452	2181588	-	94	79	93	83	0.84	0.99	0.88											
<i>yorI</i>	2181604	2183118	-	77	68	73	73	0.88	0.95	0.94											
<i>yorH</i>	2183133	2183603	-	114	93	101	81	0.81	0.88	0.71	650	yorH	2182991	2183644	2183318	60.1	80.2	18.8	45.6	P01	
<i>yorG</i>	2183646	2184617	-	166	149	174	129	0.90	1.05	0.78											
<i>yorF</i>	2184700	2185614	-	103	124	136	78	1.20	1.32	0.76											
<i>yorE</i>	2185636	2186007	-	157	283	260	108	1.74	1.63	0.69											
<i>yorD</i>	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	
<i>yorC</i>	2186572	2186952	-	1043	1388	1604	666	1.33	1.54	0.63											
<i>yorB</i>	2187015	2187311	-	1433	1855	1880	835	1.28	1.30	0.58											
<i>yorA</i>	2187400	2189160	-	102	90	95	97	0.88	0.93	0.94											
<i>yoqZ</i>	2189157	2189981	-	147	141	161	130	0.96	1.09	0.88											
<i>yoqY</i>	2190080	2190475	-	119	111	119	135	0.94	1.00	1.14											
<i>yoqX</i>	2190530	2190751	-	112	81	87	143	0.75	0.78	1.24											
<i>yoqW</i>	2190822	2191496	+	183	173	217	214	0.94	1.18	1.18											
<i>ligB</i>	2191566	2192378	+	61	60	64	63	1.00	1.06	1.06											
<i>yoqU</i>	2192444	2192857	-	107	92	105	108	0.86	0.98	1.00											
<i>yoqT</i>	2193023	2193172	+	31	43	41	40	1.40	1.31	1.30											
<i>yoqS</i>	2193249	2193596	-	260	183	197	233	0.70	0.75	0.87											
<i>yoqR</i>	2193598	2193954	-	88	73	82	111	0.82	0.93	1.24											

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

gene	Transcriptome analysis										ChAP-chip analysis								Profile ID		
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center	Binding intensity ^c				
					wild	$\Delta abrB$	Δabh	Δabh	$\Delta abrB /$	Δabh	$\Delta abh /$						AbrB			Abh	
								wild	$\Delta abrB /$	Δabh	wild	-type	Δabh	wild	-type	$\Delta abrB$					
<i>yoqP</i>	2193914	2194255	-	164	127	133	178	0.77	0.81	1.07											
<i>yoqO</i>	2194369	2194743	+	423	630	690	390	1.52	1.66	0.93	654	Inter	2194194	2194456	2194325		11.2	1.4	2.5	0.8	
<i>yoqN</i>	2194760	2194978	-	186	159	171	181	0.86	0.92	0.97											
<i>yoqM</i>	2195182	2195460	+	164	2353	2651	142	13.96	15.77	0.86	655	yoqM	2194874	2195527	2195201		64.8	93.1	29.3	-1.4	
<i>yoqL</i>	2195585	2196277	-	133	102	111	108	0.76	0.83	0.80	656	yoqL	2196064	2196343	2196204		11.4	3.0	8.2	-1.3	
<i>yoqK</i>	2196317	2196520	-	161	109	116	135	0.67	0.72	0.83											
<i>yoqJ</i>	2196540	2197055	-	178	125	166	171	0.70	0.93	0.95											
<i>yoqI</i>	2197266	2197460	-	60	56	68	79	0.96	1.13	1.27											
<i>yoqH</i>	2197509	2197961	-	122	121	126	115	0.99	1.03	0.94											
<i>yoqG</i>	2198044	2198301	-	120	109	130	107	0.91	1.08	0.89											
<i>yoqF</i>	2198346	2198549	-	117	97	118	102	0.83	1.01	0.87											
<i>yoqE</i>	2198558	2198722	-	124	100	110	118	0.80	0.88	0.94											
<i>yoqD</i>	2198776	2199531	-	163	125	143	140	0.77	0.87	0.86											
<i>yoqC</i>	2199572	2199979	-	95	82	93	91	0.87	0.98	0.95	657	Inter	2199481	2199624	2199553		4.5	2.0	0.3	-0.1	
<i>yoqB</i>	2199986	2200324	-	75	60	65	66	0.80	0.86	0.88											
<i>yoqA</i>	2200321	2200671	-	195	163	195	178	0.83	1.00	0.91											
<i>yopZ</i>	2200684	2200887	-	218	187	192	158	0.86	0.88	0.73											
<i>yopY</i>	2200901	2201179	-	378	264	291	299	0.69	0.77	0.78											
<i>yopX</i>	2201176	2201580	-	142	116	133	133	0.82	0.94	0.94											
<i>yopW</i>	2201577	2201912	-	92	79	77	82	0.85	0.83	0.87											
<i>yopV</i>	2202001	2202195	-	171	107	122	129	0.61	0.70	0.73											
<i>yopU</i>	2202307	2202504	-	536	312	322	429	0.58	0.60	0.80											
<i>yopT</i>	2202574	2202792	-	379	196	183	269	0.49	0.46	0.68	658	yopT	2202560	2202786	2202673		6.3	2.1	0.9	-1.3	
<i>yopS</i>	2202975	2203199	+	810	1052	757	689	1.28	0.92	0.84											
<i>yopR</i>	2203388	2204365	-	1677	1236	1210	1607	0.73	0.72	0.95											
<i>yopQ</i>	2204389	2205771	-	1818	1332	1324	1796	0.73	0.73	0.99											
<i>yopP</i>	2205878	2206954	-	216	223	237	201	1.02	1.10	0.92											
<i>yopO</i>	2206944	2207156	-	299	275	306	252	0.91	1.02	0.83											
<i>yopN</i>	2207204	2207521	-	741	662	641	750	0.87	0.85	0.98											
<i>yopM</i>	2207524	2207724	-	212	187	156	202	0.84	0.72	0.94											
<i>yopL</i>	2208051	2208176	-	4667	7257	7411	4559	1.56	1.59	0.98											
<i>yopK</i>	2208190	2209350	-	125	193	185	141	1.50	1.46	1.14											
<i>yopJ</i>	2209527	2209943	-	472	1209	1150	620	2.59	2.41	1.30	659	Inter	2209171	2209535	2209353		16.6	5.5	2.5	-0.4	
<i>yopI</i>	2209945	2210478	-	153	293	261	170	1.85	1.66	1.08											
<i>yopH</i>	2210505	2211041	-	143	231	219	177	1.56	1.53	1.19	660	yopH	2210752	2211099	2210926		13.7	4.0	5.8	-0.6	
<i>yopG</i>	2211080	2211211	-	371	836	753	409	2.27	2.00	1.05											
<i>yopF</i>	2211222	2211437	-	143	265	252	152	1.79	1.74	1.05											
<i>yopE</i>	2211441	2211692	-	424	711	698	477	1.71	1.67	1.11											
<i>yopD</i>	2212279	2212674	-	1107	2181	2097	1164	1.95	1.87	1.06											
<i>yopC</i>	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	
<i>yopB</i>	2214168	2214395	-	81	92	104	76	1.16	1.29	0.93	662	yopC	2213557	2214431	2213994		86.9	58.4	51.2	11.1	
<i>yopA</i>	2214656	2215972	-	244	382	391	287	1.55	1.61	1.15	662	yopA	2214441	2215298	2214870		67.0	68.5	27.0	3.4	
<i>yonX</i>	2216329	2216835	-	91	75	83	86	0.82	0.91	0.94											
<i>yonV</i>	2217163	2218395	-	65	61	67	62	0.93	1.03	0.96											
<i>yonU</i>	2218477	2218665	-	1538	1601	1556	1139	1.04	1.01	0.74											
<i>yonT</i>	2218980	2219156	-	370	312	290	294	0.82	0.78	0.78											
<i>yonS</i>	2219531	2220142	-	534	667	503	592	1.27	0.94	1.11	663	yonS	2219711	2219973	2219842		3.2	1.9	2.4	13.0	
<i>yonR</i>	2220257	2220583	-	221	292	212	253	1.31	0.95	1.12											
<i>yonP</i>	2221536	2221730	+	89	88	86	68	0.98	0.97	0.76	664	Inter	2220306	2221452	2220879		58.7	92.5	39.9	64.1	
<i>yonO</i>	2221770	2224289	+	77	73	79	70	0.95	1.03	0.91	665	yonO	2223111	2223288	2223200		3.9	1.8	0.7	0.7	
<i>yonN</i>	2224533	2224811	+	432	228	242	263	0.53	0.56	0.61											
<i>yonK</i>	2226493	2226684	+	115	72	85	55	0.63	0.74	0.49											
<i>yonJ</i>	2226701	2227918	+	207	153	179	155	0.74	0.87	0.75											
<i>yonI</i>	2227952	2228362	-	1082	758	751	991	1.70	0.69	0.91											
<i>yonH</i>	2228581	2229081	+	112	79	96	87	0.72	0.87	0.79											
<i>yonG</i>	2229184	2230104	+	93	75	82	84	0.82	0.89	0.91											
<i>yonF</i>	2230091	2231860	+	88	78	82	80	0.88	0.93	0.91											
<i>yonE</i>	2231878	2233398	+	126	100	110	105	0.79	0.87	0.83											
<i>yonD</i>	2233429	2234865	+	379	294	373	217	0.78	0.99	0.58											
<i>yonC</i>	2234890	2235426	+	214	186	215	172	0.87	1.00	0.80											
<i>yonB</i>	2235465	2236481	+	354	290	383	179	0.82	1.08	0.50											
<i>yonA</i>	2236517	2236987	+	471	358	444	306	0.78	0.96	0.67											
<i>yomZ</i>	2237002	2237397	+	330	261	320	199	0.80	0.98	0.61											
<i>yomY</i>	2237394	2237648	+	350	242	300	192	0.71	0.88	0.57	667	yomY	2237459	2237720	2237590		7.9	3.3	-0.7	-0.8	
<i>yomX</i>	2237632	2238282	+	255	183	224	119	0.73	0.90	0.47											
<i>yomW</i>	2238279	2238785	+	259	198	260	162	0.77	1.01	0.63											
<i>yomV</i>	2238782	2239492	+	269	185	246	143	0.68	0.91	0.53											

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

gene	Transcriptome analysis										ChAP-chip analysis						Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
wild	Δabh -type	wild	Δabh -type																		
<i>yomU</i>	2239535	2240332	+	399	328	405	209	0.82	1.02	0.52											
<i>yomT</i>	2240961	2241188	+	184	146	180	149	0.79	0.96	0.79											
<i>yomS</i>	2241252	2241608	+	139	128	152	144	0.92	1.09	1.04											
<i>yomR</i>	2241610	2242827	+	167	138	162	103	0.83	0.97	0.62											
<i>yomQ</i>	2242838	2243188	+	192	162	175	147	0.85	0.91	0.77											
<i>yomP</i>	2243185	2243376	+	127	104	120	68	0.82	0.94	0.54											
<i>yomO</i>	2243426	2243926	+	147	110	141	96	0.74	0.96	0.65	668	yomO	2243171	2243705	2243438	43.4	31.4	9.0	-1.8		
<i>yomN</i>	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		
<i>yomM</i>	2244343	2245344	+	130	115	135	101	0.89	1.03	0.78											
<i>yoZP</i>	2245347	2245676	-	111	137	167	90	1.23	1.51	0.82											
<i>yomL</i>	2245852	2246538	-	894	3428	4105	635	5.01	5.67	1.18											
<i>yomK</i>	2247085	2247531	+	398	1502	1482	301	3.78	3.71	0.74	670	Inter	2246707	2246901	2246804	5.5	5.6	0.7	0.6		
<i>yomJ</i>	2247613	2248296	+	521	1720	1659	886	3.29	3.21	1.70	671	Inter	2247251	2247836	2247544	43.7	28.0	25.6	16.3		
<i>yomI</i>	2248350	2255207	+	98	86	90	80	0.88	0.92	0.82	672	yomI	2251433	2251746	2251590	10.0	18.2	1.3	0.3		
<i>yomH</i>	2255258	2256016	+	59	51	50	52	0.87	0.85	0.89	673	yomI	2253065	2253565	2253315	28.0	7.9	44.6	71.3		
<i>yomG</i>	2256028	2258655	+	133	115	125	114	0.86	0.94	0.86	674	yomG	2257502	2257730	2257616	8.1	6.2	-0.1	-1.0		
<i>yomF</i>	2258671	2259492	+	109	99	116	97	0.90	1.06	0.89	675	Inter	2258539	2258801	2258670	7.8	11.9	-0.4	-0.9		
<i>yomE</i>	2259529	2261463	+	110	93	101	88	0.85	0.92	0.80											
<i>yomD</i>	2261633	2262457	+	75	62	71	50	0.83	0.94	0.66											
<i>blyA</i>	2262685	2263788	+	154	131	148	118	0.85	0.96	0.76											
<i>bhlA</i>	2263876	2264088	+	83	70	75	61	0.85	0.91	0.74											
<i>bhlB</i>	2264099	2264365	+	101	76	90	74	0.78	0.90	0.75											
<i>bdbB</i>	2264421	2264867	-	433	3155	1596	162	7.15	3.57	0.38+											
<i>yoIJ</i>	2264864	2266132	-	505	3470	2017	167	6.79	3.87	0.35+	676	yoIJ	2265118	2265346	2265232	7.7	6.3	1.8	4.9		
<i>bdbA</i>	2266132	2266545	-	495	2922	1493	136	5.60	2.78	0.27+	677	bdbA	2266087	2266519	2266303	27.8	29.4	5.7	2.6		P03
<i>sunT</i>	2266542	2268659	-	240	1577	773	79	6.25	3.05	0.34+	678	sunT	2266988	2267284	2267136	9.3	2.2	0.7	4.0		
<i>sunA</i>	2268717	2268887	-	4390	19776	15215	1104	4.47	3.45	0.25+	679	Inter	2268518	2269715	2269117	108.3	130.6	48.3	38.4		P01
<i>yoIF</i>	2269184	2269501	-	5028	3081	3776	4558	0.62	0.76	0.92											
<i>uvrX</i>	2269603	2270853	-	219	169	185	225	0.77	0.84	1.02											
<i>yoID</i>	2270846	2271178	-	74	64	73	66	0.87	0.99	0.89											
<i>yoIC</i>	2271352	2271687	+	136	463	530	113	3.40	3.90	0.83	680	yoIC	2271272	2271653	2271463	14.5	21.0	0.5	-1.1		
<i>yoIB</i>	2271730	2272086	-	545	2347	2054	339	4.26	3.77	0.61											
<i>yoIA</i>	2272092	2272559	-	2374	9817	9171	1374	4.15	3.89	0.58											
<i>yokL</i>	2273185	2273718	-	748	1754	1775	712	2.31	2.36	0.94	681	Inter	2272343	2273165	2272754	57.5	85.7	-1.1	2.2		P03
<i>yokK</i>	2273754	2274332	-	804	2234	2282	881	2.75	2.84	1.08	682	Inter	2273550	2273914	2273732	20.3	30.0	8.8	0.9		
<i>yokJ</i>	2274396	2274893	-	1006	3324	3528	1108	3.33	3.54	1.10											
<i>yokI</i>	2274902	2276617	-	415	2142	2266	401	5.34	5.62	0.96											
<i>yokH</i>	2276717	2277274	-	984	2191	2207	883	2.17	2.24	0.91	684	Inter	2276593	2276804	2276699	6.3	6.5	-0.2	0.1		
<i>yokG</i>	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		
<i>yokF</i>	2279173	2280063	+	5973	6789	6213	3838	1.14	1.04	0.64											
<i>yokE</i>	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		
<i>yokD</i>	2280863	2281681	+	369	880	769	285	2.36	2.08	0.75	686	Inter	2280503	2281003	2280753	24.8	23.1	-0.9	-0.5		P03
<i>yokC</i>	2282332	2282847	-	146	149	152	159	1.00	1.03	1.08											
<i>yokB</i>	2283054	2283764	-	168	338	345	248	1.98	2.02	1.46	687	yokB	2283087	2283519	2283303	10.2	5.3	1.4	10.7		
<i>yokA</i>	2283967	2285604	+	407	477	453	403	1.15	1.09	0.98	687	Inter	2283529	2284131	2283830	66.7	55.3	15.3	3.8		
<i>ypqP</i>	2285626	2286249	+	451	542	498	424	1.22	1.10	0.96	688	Inter	2285501	2285814	2285658	8.1	13.8	13.7	18.5		
<i>ypqQ</i>	2286293	2286724	-	2861	3867	4641	3829	1.34	1.61	1.34											
<i>msrA</i>	2286725	2287258	-	2193	2713	3252	2729	1.24	1.49	1.24											
<i>ypoP</i>	2287390	2287815	+	2398	2718	2514	2419	1.12	1.04	1.02											
<i>ypnP</i>	2287865	2289202	-	537	372	386	508	0.70	0.72	0.92											
<i>ypmT</i>	2289274	2289468	-	2269	2082	2291	2129	0.94	1.02	0.93											
<i>ypmS</i>	2289481	2290044	-	2290	1763	1968	2077	0.77	0.86	0.90											
<i>ypmR</i>	2290054	2290821	-	1787	1790	1835	1739	1.00	1.03	0.97											
<i>ypmQ</i>	2290899	2291480	-	1028	1709	2023	1190	1.67	1.98	1.16											
<i>ypmP</i>	2291628	2291879	-	2088	3712	3338	1848	1.75	1.56	0.89											
<i>ibvA</i>	2291965	2293233	-	457	635	692	352	1.36	1.49	0.76											
<i>ypIP</i>	2293482	2294477	+	810	1025	779	776	1.23	0.94	0.96	691	ypIP	2294069	2294348	2294209	15.2	3.5	7.7	1.5		
<i>ypIQ</i>	2294498	2295139	+	852	993	870	763	1.14	1.01	0.89											
<i>ypkP</i>	2295178	2295798	-	2482	2211	2171	2705	0.89	0.87	1.09											
<i>dfvA</i>	2295799	2296305	-	2532	1958	1840	2506	0.77	0.72	0.98											
<i>thyA_2</i>	2296302	2297096	-	2482	1943	1849	2389	0.79	0.75	0.96											
<i>ypjQ</i>	2297180	2297713	-	5191	4778	5234	5148	0.92	1.01	0.99											

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$																		
<i>ypjP</i>	2297731	2298342	-	2165	2136	2143	2248	0.99	0.99	1.04											
<i>ypiP</i>	2298602	2299120	-	1954	1667	1575	1814	0.87	0.81	0.91											
<i>ypHP</i>	2299417	2299851	-	6202	6084	6224	6515	0.98	1.01	1.05											
<i>ihvD</i>	2299958	2301634	-	431	351	401	415	0.81	0.93	0.96											
<i>ypgR</i>	2301923	2303056	-	3725	4394	4712	4241	1.19	1.28	1.14											
<i>ypgQ</i>	2303116	2303733	-	1129	1647	2021	1287	1.46	1.79	1.13											
<i>bsaA</i>	2303749	2304231	-	698	941	1129	839	1.36	1.63	1.19											
<i>meta</i>	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	
<i>ugtP</i>	2305711	2306859	+	4888	3914	4080	4757	0.80	0.83	0.97											
<i>cspD</i>	2307102	2307302	+	28018	30340	31185	27750	1.08	1.11	0.99											
<i>degR</i>	2307354	2307536	-	643	508	468	614	0.79	0.72	0.95											
<i>ypzA</i>	2307692	2307961	+	179	496	434	166	2.68	2.33	0.94											
<i>ypeQ</i>	2307989	2308171	-	593	640	746	506	1.12	1.31	0.84											
<i>ypeP</i>	2308164	2308844	-	469	547	589	484	1.23	1.30	1.01											
											694	Inter	2308740	2308951	2308846	6.2	2.2	1.8	-0.2		
<i>ypdP</i>	2308927	2309616	+	527	412	389	593	0.77	0.74	1.12											
<i>ypdQ</i>	2309616	2310014	+	1346	1075	1029	1351	0.80	0.77	1.00											
<i>sspL</i>	2310056	2310184	+	731	897	773	578	1.25	1.04	0.81											
<i>ypcP</i>	2310192	2311082	-	1036	893	804	1027	0.87	0.78	0.99											
<i>ypbS</i>	2311404	2311661	-	3451	3328	3232	3026	0.97	0.94	0.88											
<i>ypbR</i>	2311726	2315307	-	1640	1355	1450	1433	0.83	0.88	0.87											
<i>ypbQ</i>	2315643	2316149	-	142	156	169	130	1.10	1.19	0.91											
<i>bcsA</i>	2316153	2317250	-	119	124	135	124	1.04	1.14	1.05											
<i>pbuX</i>	2317324	2318640	-	1641	1470	1243	2126	1.06	0.84	1.29											
<i>xpt</i>	2318637	2319221	-	1393	1289	1111	1828	1.15	0.93	1.31											
<i>ypwA</i>	2319552	2321057	-	6190	10158	10339	7903	1.65	1.68	1.27											
<i>kdgT</i>	2321169	2322161	-	934	642	764	854	0.69	0.83	0.92											
<i>kdgA</i>	2322206	2322796	-	474	332	380	488	0.70	0.80	1.03											
<i>kdgK</i>	2322798	2323772	-	991	803	943	896	0.81	0.95	0.90											
<i>kdgR</i>	2323810	2324829	-	967	906	942	856	0.93	0.97	0.88											
											697	Inter	2324686	2325203	2324945	47.3	47.2	38.4	-0.7	P02	
<i>kduI</i>	2325051	2325878	+	1205	1775	1994	1241	1.47	1.65	1.03											
<i>kduD</i>	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		
<i>ypvA</i>	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		
<i>yptA</i>	2328712	2328903	-	1808	1584	1225	1490	0.88	0.68	0.81											
<i>ypsC</i>	2329272	2330429	-	3902	3438	3062	3525	0.89	0.79	0.89											
<i>mpB</i>	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		
<i>ypsB</i>	2330976	2331272	-	9450	9136	9830	9711	0.97	1.04	1.03											
<i>ypsA</i>	2331350	2331892	-	2160	1747	1605	2032	0.83	0.75	0.94											
<i>cotD</i>	2331981	2332208	-	3739	4661	3816	3615	1.29	1.03	0.99											
<i>yprB</i>	2332521	2333762	-	1717	1510	1513	1425	0.88	0.88	0.83	703	yprB	2333220	2333533	2333377	2.3	2.0	1.1	19.4	P04	
<i>yprA</i>	2333778	2336027	-	1863	1677	1631	1658	0.90	0.87	0.89											
<i>ypqE</i>	2336130	2336636	-	7151	9960	10053	7167	1.41	1.42	1.00											
<i>ypqA</i>	2336774	2337193	+	108	91	93	100	0.84	0.87	0.94											
<i>yppG</i>	2337214	2337591	-	82	80	76	97	0.98	0.92	1.18											
<i>yppF</i>	2337779	2337967	+	2534	2104	2714	2148	0.83	1.07	0.85											
<i>yppE</i>	2338006	2338377	-	2171	2037	1975	1951	0.94	0.91	0.89											
<i>yppD</i>	2338423	2338668	-	120	211	221	139	1.75	1.84	1.15											
<i>sspM</i>	2338867	2338971	+	75	106	128	60	1.40	1.69	0.80											
<i>yppC</i>	2338996	2339958	-	222	216	188	222	0.97	0.85	1.00											
<i>recU</i>	2339999	2340619	+	4808	5445	5094	5579	1.13	1.06	1.16											
<i>ponA</i>	2340641	2343385	+	6381	6337	6171	6591	0.99	0.97	1.03											
<i>ypoC</i>	2343461	2343955	-	3619	2570	2548	2942	0.71	0.70	0.81											
<i>nth</i>	2343952	2344611	-	4011	2919	2870	3611	0.73	0.72	0.90											
<i>dnaD</i>	2344630	2345328	-	4736	3407	3374	4129	0.72	0.71	0.87											
<i>asnC</i>	2345421	2346713	-	14228	11672	11577	13651	0.82	0.81	0.96											
<i>aspB</i>	2346857	2348038	-	15403	14804	15001	15108	0.96	0.97	0.98											
<i>ypmB</i>	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		
<i>ypmA</i>	2348555	2348725	-	8640	7587	6644	8302	0.88	0.76	0.95											
											707	Inter	2348622	2348850	2348736	11.3	1.5	6.4	2.3		
<i>dinG</i>	2348868	2351663	-	3855	3635	3157	3728	0.95	0.82	0.97											
<i>panD</i>	2351789	2352172	-	4961	4381	4375	4844	0.88	0.88	0.97											
<i>panC</i>	2352174	2353034	-	8235	7640	7558	8490	0.93	0.92	1.03											
<i>panB</i>	2353036	2353869	-	7225	6732	6538	7327	0.93	0.91	1.01											
<i>birA</i>	2354115	2355092	-	3282	3061	2954	3379	0.95	0.90	1.02											
<i>cca</i>	2355077	2356270	-	6570	6630	6657	6613	1.01	1.02	1.00											
<i>ypjH</i>	2356275	2357408	-	5952	5856	5954	6304	0.99	1.00	1.06											
<i>ypjG</i>	2357440	2358114	-	5467	5086	5302	5668	0.94	0.97	1.03											
<i>mgsA</i>	2358107	2358520	-	7913	7818	7958	8280	1.00	1.01	1.05											
<i>dapB</i>	2358536	2359339	-	6741	6716	6664	7251	0.99	0.99	1.08											
<i>ypjD</i>	2359351	2359686	-	5415	4801	4755	5257	0.89	0.88	0.97											
<i>ypjC</i>	2360051	2360698	+	1756	2315	2282	1634	1.32	1.30	0.92											

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
wild	$\Delta abrB$	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$				
<i>ypjB</i>	2360740	2361534	-	932	996	886	926	1.08	0.93	0.97	711	ypjB	2360981	2361277	2361129	2.9	2.5	1.5	18.0	P04	
<i>ypjA</i>	2361603	2362160	-	659	808	715	686	1.24	1.07	1.03											
<i>qcrC</i>	2362307	2363074	-	1976	8737	8785	3975	4.43	4.47	2.03											
<i>qcrB</i>	2363109	2363783	-	2703	10810	10640	5037	3.99	3.93	1.86	713	Inter	2363038	2363147	2363093	1.7	2.2	3.9	1.9		
<i>qcrA</i>	2363785	2364288	-	3527	14753	14064	6325	4.18	3.98	1.79											
<i>ypjF</i>	2364431	2364877	-	1706	2300	3121	2159	1.36	1.82	1.28	714	Inter	2363990	2364626	2364308	51.4	67.0	42.9	2.4	P02	
<i>ypjB</i>	2364932	2365471	-	3348	4265	5012	3753	1.28	1.50	1.12	714	ypjF	2364637	2365068	2364853	37.2	18.2	21.8	4.0	P02	
<i>ypjA</i>	2365543	2366814	-	1623	1412	1430	1799	0.87	0.89	1.10											
<i>aroE_1</i>	2367150	2368436	-	5385	4249	4591	4789	0.79	0.85	0.89											
<i>tyrA</i>	2368447	2369562	-	5025	3794	3985	4511	0.75	0.79	0.90	715	tyrA	2368886	2369165	2369026	8.6	8.9	3.0	0.9		
<i>hisC</i>	2369611	2370693	-	5438	4506	4549	5003	0.83	0.84	0.92											
<i>trpA</i>	2370704	2371507	-	911	1244	1132	904	1.34	1.24	0.96											
<i>trpB</i>	2371500	2372702	-	207	306	291	212	1.47	1.40	1.02											
<i>trpF</i>	2372683	2373330	-	179	233	219	174	1.30	1.23	0.97											
<i>trpC</i>	2373335	2374087	-	131	183	165	150	1.38	1.26	1.12											
<i>trpD</i>	2374080	2375096	-	211	290	252	229	1.39	1.20	1.10											
<i>trpE</i>	2375068	2376615	-	254	538	406	237	2.03	1.58	0.92											
<i>aroH</i>	2376831	2377214	-	7280	5690	6172	6263	0.78	0.85	0.86											
<i>aroB</i>	2377211	2378299	-	5769	4899	5050	4887	0.86	0.88	0.85											
<i>aroF</i>	2378361	2379470	-	4580	3846	4035	3933	0.84	0.88	0.86											
<i>cheR</i>	2379545	2380315	-	1504	1001	1029	1216	0.66	0.68	0.81											
<i>ndk</i>	2380552	2381001	-	13103	11690	12391	13039	0.89	0.95	1.00											
<i>hepT</i>	2381117	2382163	-	9205	7517	7170	9397	0.82	0.78	1.02											
<i>ubiE</i>	2382105	2382806	-	9119	7989	7743	9052	0.88	0.85	0.99	718	ubiE	2382010	2382408	2382209	24.4	20.8	8.9	2.5		
<i>hepS</i>	2382813	2383568	-	5102	4015	3930	5538	0.79	0.77	1.09											
<i>mtrB</i>	2383731	2383958	-	8413	6621	6612	8403	0.79	0.79	1.00											
<i>folE</i>	2383980	2384552	-	7127	5872	5678	7094	0.82	0.80	1.00	719	folE	2384152	2384397	2384275	11.6	9.6	13.8	5.9		
<i>hbs</i>	2384740	2385018	-	31656	31367	31673	32619	0.99	1.00	1.03											
<i>spoIVA</i>	2385392	2386870	-	136	135	155	173	0.99	1.13	1.26	720	Inter	2385189	2385400	2385295	6.0	8.5	1.6	2.6		
<i>ypjF</i>	2387051	2387785	-	735	1669	1891	1217	2.27	2.60	1.65											
<i>ypjE</i>	2387807	2388010	-	585	1548	1325	907	2.57	2.23	1.51											
<i>gpsA</i>	2388348	2389385	-	5718	4433	4092	5397	0.78	0.72	0.95	721	Inter	2387824	2388358	2388091	25.1	18.7	34.1	29.1	P01	
<i>engA</i>	2389403	2390713	-	7339	5553	5131	6527	0.76	0.70	0.89											
<i>seaA</i>	2391058	2391951	-	238	254	250	253	1.07	1.05	1.04											
<i>ypjA</i>	2391948	2392547	-	323	326	330	317	1.01	1.02	0.98											
<i>ypjG</i>	2392799	2393857	-	2946	3789	3826	2744	1.29	1.31	0.93											
<i>rpsA</i>	2393861	2395009	-	15193	17151	17970	15396	1.13	1.18	1.01											
<i>cmk</i>	2395242	2395916	-	7258	5049	4421	6714	0.70	0.61	0.93											
<i>ypjB</i>	2395995	2396171	-	2352	1692	1694	2995	0.72	0.72	1.27											
<i>ypjA</i>	2396216	2396869	-	2368	1677	1604	2513	0.71	0.68	1.06											
<i>ypjB</i>	2396962	2398314	-	114	214	257	109	1.84	2.21	0.95											
<i>slxB</i>	2398349	2399266	-	143	179	215	130	1.25	1.49	0.91	723	slxB	2398500	2398898	2398699	3.9	4.0	8.0	16.3		
<i>ypjC</i>	2399405	2400061	-	748	1325	1047	694	1.75	1.40	0.91	723	ypjC	2398908	2400105	2399507	65.1	76.9	94.4	201.0	P01	
<i>ypjA</i>	2400181	2401155	-	4390	4504	4584	4582	1.03	1.05	1.04											
<i>gudB</i>	2401264	2402544	-	17579	18052	17913	17876	1.03	1.02	1.02	724	gudB	2402257	2402689	2402473	14.9	22.8	13.9	6.2		
<i>ypjH</i>	2402700	2403284	-	5004	4634	5355	5233	0.92	1.07	1.05											
<i>ypjG</i>	2403443	2404222	-	1454	1279	1432	1715	0.88	1.00	1.18											
<i>ypjF</i>	2404308	2404751	-	556	552	508	576	0.99	0.91	1.03	725	ypjF	2404246	2404916	2404581	52.4	48.7	20.2	-0.1	P02	
<i>ypjE</i>	2404814	2405536	-	2202	2102	1950	2089	0.96	0.88	0.95											
<i>ypjD</i>	2405487	2406056	-	1070	983	950	1104	0.91	0.89	1.03											
<i>recQ</i>	2406116	2407606	-	1575	1517	1581	1721	0.96	1.00	1.09											
<i>ypjB</i>	2407599	2408657	-	811	979	917	908	1.22	1.14	1.12											
<i>fer</i>	2408923	2409171	+	10667	8225	8320	9320	0.77	0.78	0.87											
<i>ypjA</i>	2409211	2409783	-	965	612	634	994	0.63	0.66	1.03											
<i>ypjE</i>	2409889	2410053	-	2704	2311	2381	2547	0.86	0.88	0.94											
<i>serA</i>	2410280	2411857	+	4982	5417	6161	4382	1.09	1.24	0.88	727	serA	2411131	2411376	2411254	13.2	2.6	9.6	2.5		
<i>aroD</i>	2411900	2412667	-	1706	1527	1463	1677	0.91	0.87	0.98	728	aroD	2412032	2412277	2412155	10.1	5.3	4.7	4.8		
<i>rsiX</i>	2412779	2413885	-	4493	5071	5071	4413	1.14	1.14	0.99											
<i>sigX</i>	2413821	2414405	-	2790	3167	2986	2823	1.14	1.09	1.02	729	sigX	2414242	2414487	2414365	8.5	1.3	6.7	1.8		
<i>resE</i>	2414609	2416378	-	7939	6211	6343	7150	0.78	0.80	0.90											
<i>resD</i>	2416375	2417097	-	7340	5660	5964	6514	0.76	0.81	0.89											
<i>resC</i>	2417178	2418236	-	5842	4502	4516	5132	0.77	0.78	0.88											
<i>resB</i>	2418372	2420000	-	5796	4502	4361	5381	0.77	0.75	0.93											
<i>resA</i>	2419997	2420542	-	6876	5872	5732	6609	0.85	0.83	0.96	730	resA	2420175	2420420	2420298	6.8</					

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$																		
<i>ypuI</i>	2423848	2424387	-	1847	1363	1137	1738	0.74	0.61	0.93											
<i>ypuH</i>	2424442	2425035	-	4960	4137	3449	4725	0.83	0.69	0.95											
<i>scpA</i>	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		
<i>ypuF</i>	2426061	2426585	+	369	268	254	360	0.72	0.69	0.97											
<i>ribT</i>	2426599	2426973	-	3210	3969	3415	2960	1.24	1.06	0.92											
<i>ribH</i>	2427086	2427550	-	2864	3036	3007	2665	1.06	1.05	0.93											
<i>ribA</i>	2427583	2428779	-	3092	3215	3294	2737	1.04	1.06	0.88											
<i>ribE</i>	2428794	2429441	-	1843	1917	1858	1598	1.04	1.01	0.87											
<i>ribD</i>	2429452	2430537	-	1846	2081	2047	1786	1.13	1.11	0.97											
<i>ypuE</i>	2430519	2430671	-	350	347	301	287	1.01	0.87	0.82											
<i>ypuD</i>	2430930	2431274	-	599	381	458	501	0.66	0.76	0.81											
<i>sipS</i>	2431509	2432063	-	3897	3881	3588	3914	1.00	0.93	1.01											
<i>ypzC</i>	2432330	2432566	+	140	139	151	114	0.99	1.08	0.82											
<i>ypuC</i>	2432969	2433358	-	418	407	447	396	0.98	1.08	0.95											
<i>ypuB</i>	2433336	2433539	-	237	199	228	326	0.84	0.96	1.37											
<i>ypzD</i>	2434205	2434417	+	60	59	67	55	0.99	1.11	0.91	732	Inter	2433452	2434173	2433813	63.5	74.4	38.2	16.1		
<i>ppiB</i>	2434553	2434984	-	13344	12717	12544	13176	0.95	0.94	0.99											
<i>ypuA</i>	2435238	2436110	+	11197	9625	11063	12086	0.86	0.99	1.08	733	ypuA	2435068	2435618	2435343	26.7	37.4	12.2	0.3		
<i>lysA</i>	2436139	2437458	-	2277	1627	1599	1856	0.71	0.70	0.81											
<i>spoVAF</i>	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		
<i>spoVAE</i>	2438993	2439964	-	206	245	266	205	1.18	1.28	0.99											
<i>spoVAD</i>	2439966	2440982	-	131	172	180	149	1.31	1.37	1.13											
<i>spoVAC</i>	2440995	2441447	-	122	154	174	124	1.26	1.42	1.01	735	spoVAC	2440507	2441619	2441063	104.6	130.8	53.1	7.8		
<i>spoVAB</i>	2441459	2441884	-	183	229	257	209	1.27	1.43	1.16											
<i>spoVAA</i>	2441894	2442496	-	64	85	101	66	1.32	1.57	1.03											
<i>sigF</i>	2442618	2443385	-	283	897	956	369	3.11	3.33	1.28											
<i>spolIAB</i>	2443397	2443837	-	266	1261	1377	407	4.67	5.12	1.46											
<i>spolIAA</i>	2443834	2444187	-	518	2315	2426	759	4.65	4.86	1.43											
<i>dacF</i>	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	
<i>punA</i>	2445607	2446422	-	10124	9924	10436	10702	0.98	1.03	1.06											
<i>drm</i>	2446435	2447619	-	11146	10511	10874	11248	0.94	0.98	1.01	739	drm	2447222	2447467	2447345	9.5	9.2	5.5	0.8		
<i>xerD</i>	2447780	2448670	-	2016	2142	1856	2062	1.06	0.92	1.02											
<i>fur</i>	2449029	2449478	-	3734	3184	3039	3684	0.86	0.82	0.99											
<i>spolIM</i>	2449591	2450235	-	147	143	170	162	0.98	1.16	1.10											
<i>yqkK</i>	2450336	2450551	-	342	222	204	316	0.65	0.60	0.93											
<i>mleA</i>	2450651	2451970	-	13928	10090	10610	13725	0.72	0.76	0.98											
<i>mleN</i>	2451988	2453394	-	13384	8801	8813	12916	0.66	0.66	0.96	740	mleN	2452441	2452771	2452606	9.0	17.2	4.9	1.9		
<i>aspA</i>	2453535	2454962	-	15882	13887	13450	15295	0.87	0.85	0.96											
<i>ansA</i>	2455007	2455996	-	16460	14547	13656	15643	0.88	0.83	0.95											
<i>ansR</i>	2456178	2456528	+	1133	1509	990	958	1.35	0.89	0.87											
<i>yqxK</i>	2456537	2457421	-	2084	2219	2282	2223	1.06	1.09	1.06	741	yqxK	2456913	2457259	2457086	15.7	8.4	9.8	2.5		
<i>nudF</i>	2457698	2458255	-	3842	3803	3966	3664	0.99	1.03	0.95											
<i>yqkF</i>	2458515	2459435	+	2469	3410	3622	2949	1.43	1.51	1.18											
<i>yqkE</i>	2459467	2459691	-	647	403	419	362	0.63	0.64	0.56											
<i>yqkD</i>	2459853	2460770	+	286	293	312	287	1.03	1.09	1.00											
<i>yqkC</i>	2460810	2461049	-	3730	3622	3555	3561	0.97	0.95	0.96											
<i>yqkB</i>	2461062	2461385	-	3602	3878	4009	3460	1.08	1.12	0.96											
<i>yqkA</i>	2461382	2462413	-	1106	1661	1833	791	1.49	1.65	0.71											
<i>yqjZ</i>	2462406	2462750	-	844	1260	1296	697	1.49	1.53	0.83											
<i>yqjY</i>	2462760	2463230	-	658	1100	978	563	1.67	1.48	0.86											
<i>yqjX</i>	2463416	2463754	-	249	181	194	259	0.73	0.78	1.03											
<i>yqjW</i>	2463751	2464989	-	190	139	145	212	0.73	0.76	1.12											
<i>yqzH</i>	2465155	2465361	+	734	729	664	590	0.99	0.87	0.80											
<i>yqjV</i>	2465910	2467142	+	380	849	770	341	2.23	2.01	0.89											
<i>yqjU</i>	2467160	2467351	+	585	1154	1057	476	1.99	1.84	0.83											
<i>yqjT</i>	2467348	2467734	-	4261	3393	3449	3915	0.80	0.81	0.92											
<i>coaA</i>	2467738	2468697	-	3196	2398	2456	3076	0.75	0.77	0.96											
<i>dsdA</i>	2468769	2470115	-	1749	1426	1450	1692	0.82	0.83	0.96											
<i>yqjQ</i>	2470191	2470970	-	1586	1381	1273	1577	0.88	0.81	0.99											
<i>yqjP</i>	2470976	2471935	-	417	363	338	426	0.87	0.82	1.00											
<i>proI</i>	2472340	2473176	+	861	607	516	741	0.74	0.61	0.87											
<i>yqjN</i>	2473217	2474860	-	688	809	921	746	1.17	1.33	1.07											
<i>yqjM</i>	2475032	2476048	+	1368	1583	1767	1563	1.17	1.29	1.14											
<i>yqjL</i>	2476158	2476919	+	4084	3887	4607	4701	0.95	1.13	1.15											
<i>yqjK</i>	2477195	2478118	-	1752	1211	1047	1554	0.69	0.60	0.88											
<i>zvf</i>	2478345	2479814	+	10793	10109	10764	11769	0.94	1.01	1.09	744	zvf	2478451	2478543	2478497	1.2	2.5	0.5	0.4		
<i>yqjI</i>	2479937	2481346	-	13937	12207	13522	14915	0.88	0.97	1.07											
<i>yqjH</i>	2481456	2482700	-	520	462	438	574	0.89	0.84	1.09											
<i>yqzJ</i>	2482773	2483060	+	1976	2230	2071	2187	1.13	1.05	1.11											
<i>yqjG</i>	2483091	2483918	+	2185	2304	2322	2537	1.05	1.06	1.16											
<i>yqjF</i>	2484098	2484826	+	173	164	160	162	0.95	0.93	0.93											

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$	Δabh													
<i>yqjE</i>	2484867	2485982	-	7215	8007	8168	7377	1.11	1.13	1.02											
<i>yqjD</i>	2486000	2487520	-	5058	6071	5766	5455	1.20	1.14	1.08											
<i>yqjC</i>	2487517	2487939	-	167	151	154	205	0.91	0.93	1.24											
<i>yqjB</i>	2488141	2488671	-	278	278	283	323	1.00	1.02	1.15	746	yqjB	2488345	2488488	2488417	3.5	1.2	4.4	0.6		
<i>yqjA</i>	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		
<i>yqiZ</i>	2489762	2490484	-	931	642	570	841	0.71	0.62	0.89											
<i>yqiY</i>	2490477	2491136	-	700	519	465	663	0.77	0.69	0.95											
<i>yqiX</i>	2491217	2491984	-	808	403	353	640	0.52	0.46	0.81	748	yqiX	2490946	2491548	2491247	50.7	21.4	18.2	0.2	P02	
<i>yqiW</i>	2492253	2492690	-	7177	7082	7395	7293	0.99	1.03	1.01											
<i>bmrU</i>	2492853	2493746	+	560	457	686	272	0.82	1.22	0.47											
<i>bmr</i>	2493847	2495016	+	731	844	833	685	1.16	1.15	0.94											
<i>bmrR</i>	2495089	2495925	+	428	351	408	397	0.83	0.95	0.92											
<i>bkdB</i>	2495987	2497261	-	4396	4566	4417	4138	1.04	1.00	0.94											
<i>bkdAB</i>	2497284	2498267	-	5663	5933	5814	5429	1.05	1.03	0.96											
<i>bkdAA</i>	2498281	2499273	-	5455	5858	5704	5323	1.08	1.04	0.97											
<i>lpdV</i>	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		
<i>buk</i>	2500741	2501832	-	3668	3814	3680	3795	1.04	1.00	1.03											
<i>bcd</i>	2501851	2502945	-	3334	3481	3404	3495	1.05	1.02	1.05											
<i>ptb</i>	2502957	2503856	-	2656	2691	2656	2741	1.02	1.00	1.03											
<i>bkdR</i>	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		
<i>yqzF</i>	2506212	2506448	+	524	1276	1213	483	2.44	2.29	0.92											
<i>yqiQ</i>	2506490	2507395	-	305	285	291	317	0.93	0.96	1.03											
<i>pppD</i>	2507413	2508831	-	184	168	178	197	0.91	0.97	1.05											
<i>mmgD</i>	2508846	2509964	-	201	189	192	225	0.94	0.95	1.12											
<i>mmgC</i>	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	P04	
<i>mmgB</i>	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		
<i>mmgA</i>	2512046	2513227	-	205	159	176	258	0.78	0.86	1.28											
<i>yqiK</i>	2513365	2514084	-	457	450	508	565	0.99	1.14	1.21											
<i>yqiL</i>	2514163	2514783	-	172	151	136	208	0.88	0.79	1.21											
<i>yqiH</i>	2514798	2515091	-	190	172	182	195	0.90	0.95	1.01											
<i>yqiG</i>	2515623	2516741	+	3081	2166	2243	3821	0.73	0.75	1.24											
<i>spoA</i>	2517257	2518060	-	2832	3394	3619	2722	1.20	1.28	0.96											
<i>spoIVB</i>	2518336	2519613	-	198	293	340	195	1.47	1.69	0.98	755	spoIVB	2518537	2519547	2519042	54.6	25.4	99.2	19.1	P01	
<i>recN</i>	2519788	2521518	-	3825	3140	3111	3752	0.83	0.81	0.97											
<i>ahrC</i>	2521555	2522004	-	3947	3137	2846	3618	0.80	0.72	0.90											
<i>yqxC</i>	2522139	2522948	-	6398	6669	6487	6055	1.04	1.02	0.94	756	yqxC	2522022	2522556	2522289	35.3	29.1	10.9	3.3		
<i>dxs</i>	2522945	2524846	-	4399	4700	4616	4428	1.07	1.05	1.00	757	dxs	2523127	2523236	2523182	1.4	1.2	2.6	1.5		
<i>yqiD</i>	2525093	2525911	-	2049	2058	1808	2063	1.05	0.91	1.01											
<i>yqiC</i>	2525901	2526065	-	4043	3937	3690	3509	1.00	0.92	0.85											
<i>xseA</i>	2526151	2527497	-	2569	2508	2240	2403	1.01	0.90	0.93											
<i>folD</i>	2527635	2528486	-	8250	7076	6758	7892	0.86	0.82	0.96	758	folD	2528125	2528336	2528231	8.1	1.8	6.3	2.2		
<i>nusB</i>	2528498	2528893	-	10002	8432	7930	9273	0.84	0.79	0.93											
<i>yqhY</i>	2529157	2529564	-	12036	12947	12344	12499	1.08	1.02	1.04											
<i>accC</i>	2529585	2530937	-	12163	12575	12308	12392	1.03	1.01	1.02											
<i>accB</i>	2530949	2531428	-	8994	9773	9179	9642	1.09	1.02	1.07											
<i>spoIIAH</i>	2531584	2532240	-	274	218	225	255	0.79	0.82	0.93											
<i>spoIIAG</i>	2532241	2532930	-	125	106	110	110	0.85	0.88	0.87											
<i>spoIIAF</i>	2532923	2533543	-	117	108	113	116	0.92	0.97	0.99											
<i>spoIIAE</i>	2533540	2534757	-	196	182	195	220	0.93	0.99	1.12											
<i>spoIIAD</i>	2534776	2535177	-	182	185	178	183	1.02	0.98	1.01											
<i>spoIIAC</i>	2535184	2535390	-	128	133	132	114	1.04	1.04	0.89											
<i>spoIIAB</i>	2535413	2535928	-	161	138	145	194	0.86	0.90	1.22	759	spoIIAB	2535436	2535595	2535516	0.4	0.1	1.3	4.5		
<i>spoIIAA</i>	2535922	2536845	-	151	135	131	179	0.89	0.86	1.18											
<i>yqhV</i>	2536921	2537202	-	83	84	85	85	1.01	1.03	1.03											
<i>efp</i>	2537347	2537904	-	12993	12943	12954	13072	1.00	1.00	1.01											
<i>yqhT</i>	2537929	2538990	-	14263	14946	14854	14552	1.05	1.04	1.02											
<i>yqhS</i>	2538987	2539433	-	7868	8981	9093	8397	1.14	1.16	1.07											
<i>yqhR</i>	2539520	2540056	-	142	151	147	151	1.07	1.04	1.07											
<i>yqhQ</i>	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		
<i>yqhP</i>	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		
<i>yqhO</i>	2541671	2542546	-	195	177	187	214	0.91	0.96	1.09											
<i>mntR</i>	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		
<i>yqhM</i>	2543200	2544036	-	4652	3814	3992	5197	0.82	0.87	1.12											
<i>yqhL</i>	2544227	2544607	+	3150	2707	2267	3054	0.87	0.72	0.98											
<i>gcvPB</i>	2544642	2546108	-	828	1315	1371	726	1.58	1.65	0.87											
<i>gcvPA</i>	2546101	2547447	-	1481	2437	2661	1234	1.64	1.79	0.83											
<i>gcvT</i>	2547477	2548565	-	1066	1807	1842	946	1.68	1.72	0.88											
<i>yqhH</i>	2549007	2550680	+	134	151	156	131	1.13	1.17	0.98											
<i>yqhG</i>	2550701	2551495	+	224	292	314	234	1.30	1.39	1.04											
<i>sinI</i>	2551678	2551851	+	1095	1859	2040	905	1.71	1.87	0.81	764	Inter	2551432	2551728	2551580	12.3	13.1	0.5	-0.6		
<i>sinR</i>	2551885	2552220	+	2771	2946	2622	2458	1.07	0.95	0.89	765	sinR	2551976	2552340	2552158	16.1	21.2	6.2	0.3		

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$														
<i>tasA</i>	2552313	2553098	-	809	14267	14997	483	17.60	18.43	0.59											
<i>sipW</i>	2553162	2553734	-	344	4328	4695	304	12.60	13.67	0.88											
<i>yqxM</i>	2553718	2554479	-	107	1119	1142	93	10.42	10.63	0.87											
<i>yqzG</i>	2554751	2555077	+	139	327	408	113	2.33	2.90	0.82	766	Inter	2554237	2555179	2554708		78.4	98.8	33.7	-3.4	P02
<i>yqzE</i>	2555060	2555299	-	79	73	74	67	0.92	0.93	0.85											
<i>comGG</i>	2555370	2555744	-	182	171	188	176	0.94	1.03	0.96											
<i>comGF</i>	2555745	2556128	-	209	193	209	227	0.92	1.00	1.08											
<i>comGE</i>	2556154	2556501	-	83	68	77	95	0.82	0.94	1.17											
<i>comGD</i>	2556485	2556916	-	66	59	62	76	0.90	0.95	1.13											
<i>comGC</i>	2556906	2557202	-	119	96	99	111	0.81	0.83	0.93											
<i>comGB</i>	2557216	2558187	-	158	164	182	148	1.03	1.15	0.93											
<i>comGA</i>	2558240	2559310	-	143	136	140	142	0.96	0.98	0.99											
<i>yqxL</i>	2559722	2560675	-	379	227	290	242	0.60	0.76	0.63											
<i>yqhB</i>	2560818	2562146	+	227	153	194	158	0.68	0.87	0.69											
<i>yqhA</i>	2562199	2563035	-	1002	399	426	347	0.44	0.51	0.32											
<i>trnSL-Gln</i>	2563122	2563195	+	2863	4528	4632	4454	1.65	1.70	1.45											
<i>yqzZ</i>	2563259	2563639	-	9055	5223	7294	3757	0.58	0.81	0.41											
<i>yqyY</i>	2563871	2564116	+	2644	6590	7280	4589	2.49	2.75	1.74	768	Inter	2563655	2563968	2563812		14.9	9.4	3.9	1.4	
<i>yqyX</i>	2564156	2564791	-	8876	9545	10244	9518	1.08	1.16	1.07											
<i>yqyW</i>	2564949	2565122	+	1235	2894	2963	1174	2.33	2.39	0.95	769	Inter	2564794	2565037	2564916		12.3	8.1	1.9	1.3	
<i>yqyV</i>	2565183	2565467	-	2376	2472	2264	2279	1.06	0.96	0.96											
<i>yqyU</i>	2565470	2566531	-	2826	2943	2860	3050	1.05	1.02	1.08	770	yqyU	2565967	2566195	2566081		2.8	0.2	-0.7	9.9	
<i>yqyT</i>	2566593	2567723	-	599	830	827	756	1.42	1.40	1.26											
<i>yqyS</i>	2567806	2569722	-	2653	3115	3300	2810	1.17	1.25	1.06	771	Inter	2567514	2567979	2567747		29.3	9.8	23.8	1.4	
<i>glcK</i>	2569838	2570803	-	2721	2510	2661	2836	0.92	0.98	1.04	773	glcK	2570540	2570835	2570688		10.1	11.6	3.1	0.6	
<i>yqyQ</i>	2570814	2571029	-	2137	1743	1919	2065	0.81	0.90	0.96											
<i>yqyP</i>	2571139	2572662	-	1195	1055	1023	1302	0.88	0.86	1.09											
<i>yqyO</i>	2572752	2572925	-	3712	2640	2651	3370	0.72	0.72	0.92											
<i>yqyN</i>	2572992	2573555	-	2906	2095	1978	2616	0.72	0.68	0.90											
<i>rpmG_2</i>	2573640	2573789	-	11475	9433	9089	11522	0.82	0.79	1.00											
<i>yqyM</i>	2573873	2574952	-	315	330	339	331	1.05	1.07	1.04											
<i>yqyL</i>	2574949	2575419	-	175	144	153	220	0.82	0.88	1.26											
<i>yqzD</i>	2575599	2575952	+	9355	8236	7666	9229	0.88	0.82	0.99											
<i>yqzC</i>	2575949	2576413	+	8898	8174	7587	8763	0.92	0.85	0.98											
<i>pstBB</i>	2576442	2577224	-	123	108	114	131	0.88	0.93	1.07											
<i>pstBA</i>	2577235	2578044	-	120	133	122	145	1.11	1.02	1.20											
<i>pstA</i>	2578065	2578949	-	180	196	186	183	1.10	1.03	1.02											
<i>pstC</i>	2578949	2579878	-	254	290	266	271	1.14	1.05	1.07											
<i>pstS</i>	2579947	2580849	-	241	389	270	233	1.58	1.11	0.97											
<i>pbpA</i>	2581003	2583153	-	7233	7143	6973	7458	0.99	0.96	1.03	775	pbpA	2581624	2581733	2581679		3.8	0.8	1.3	2.0	
<i>yqyE</i>	2583267	2584559	-	181	182	209	185	1.01	1.16	1.02											
<i>sodA</i>	2584666	2585274	-	22088	25943	25792	23476	1.18	1.17	1.07	776	sodA	2584582	2584844	2584713		7.0	7.5	1.3	1.5	
<i>yqyC</i>	2585453	2585935	-	1572	2235	2253	1141	1.42	1.43	0.72											
<i>yqyB</i>	2586045	2586803	+	2058	1359	1325	2055	0.66	0.65	1.00											
<i>yqyA</i>	2587229	2587657	-	14336	16408	15624	11946	1.14	1.09	0.83	777	Inter	2586860	2587359	2587110		22.5	22.0	1.9	2.7	P03
<i>yqfZ</i>	2587934	2588233	+	187	148	147	233	0.79	0.78	1.22	777	yqyA	2587370	2587819	2587595		14.4	19.6	3.5	4.8	
<i>ispG</i>	2588356	2589489	+	6568	5667	6010	6706	0.86	0.91	1.02											
<i>yqfX</i>	2589515	2589904	-	325	614	788	392	1.88	2.41	1.20											
<i>yqfW</i>	2590037	2590618	+	1818	1411	1276	2084	0.77	0.70	1.16	779	yqfW	2590022	2590318	2590170		4.5	1.4	2.3	15.7	
<i>zur</i>	2590661	2591098	-	2470	2318	2525	2456	0.94	1.02	0.99											
<i>yqfU</i>	2591236	2592117	-	1107	1379	1512	1221	1.28	1.38	1.10											
<i>yqfT</i>	2592233	2592487	+	155	153	172	147	0.99	1.11	0.95											
<i>yqfS</i>	2592514	2593407	-	4900	3913	3803	4511	0.80	0.78	0.92											
<i>yqfR</i>	2593417	2594733	-	5201	4093	3812	5004	0.79	0.73	0.96											
<i>yqfQ</i>	2594902	2595645	+	140	115	107	134	0.83	0.76	0.98	780	yqfQ	2595105	2595367	2595236		11.2	7.4	5.9	3.2	
<i>ispH</i>	2595768	2596712	+	3148	3003	2880	3153	0.97	0.93	1.01											
<i>yqfO</i>	2596735	2597856	-	5909	5358	5427	5741	0.91	0.92	0.97											
<i>yqfN</i>	2597849	2598499	-	3738	3493	3280	3561	0.93	0.88	0.95											
<i>cccA</i>	2598756	2599118	-	1261	3385	3219	1471	2.87	2.69	1.18											
<i>sigA</i>	2599447	2600562	-	9251	13118	12186	9245	1.43	1.33	1.00	781	Inter	2598862	2599685	2599274		78.4	67.5	54.9	5.4	P02
<i>dnaG</i>	2600761	2602572	-	4713	6686	6141	4904	1.42	1.30	1.04	782	sigA	2600375	2600654	2600515		12.1	6.1	4.9	0.2	
<i>antE</i>	2602212	2602508	+	358	1041	915	274	2.93	2.57	0.77	783	dnaG	2601854	2602490	2602172		44.3	58.1	19.2	4.5	P02
<i>yqxD</i>	2602606	2603196	-	4244	4003	3727	4274	0.94	0.88	1.00											
<i>yqfL</i>	2603354	2604166	-	4311	4424	4470	4														

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID						
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c					
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh			
wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh						
<i>recO</i>	2608179	2608946	-		4165	4165	4310	4355	1.00	1.03	1.05												
<i>era</i>	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		
<i>cdd</i>	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		
<i>dgkA</i>	2610689	2611033	-		3418	3215	2884	3803	0.94	0.84	1.11												
<i>yqfG</i>	2611040	2611513	-		3279	3180	3238	3521	0.97	0.99	1.07												
<i>yqfF</i>	2611514	2613649	-		3369	3341	3413	3327	0.99	1.01	0.99												
<i>phoH</i>	2613728	2614687	-		9078	9391	9871	8546	1.03	1.09	0.94												
<i>yqfD</i>	2614684	2615880	-		339	322	367	292	0.95	1.08	0.86												
<i>yqfC</i>	2615899	2616180	-		370	339	425	316	0.91	1.15	0.85												
<i>yqfB</i>	2616237	2616656	-		7744	9983	10667	6804	1.29	1.38	0.88												
<i>yqfA</i>	2616681	2617676	-		6601	9042	9487	6376	1.37	1.44	0.97												
<i>yqeZ</i>	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		
<i>yqeY</i>	2619142	2619588	-		22532	21445	21027	22921	0.96	0.93	1.02												
<i>rpsU</i>	2619603	2619776	-		24299	22007	21620	24168	0.91	0.89	1.00												
<i>yqeW</i>	2619940	2620872	+		241	235	254	254	0.97	1.05	1.05												
<i>yqeV</i>	2620909	2622264	-		6592	6247	5572	6630	0.96	0.85	1.00												
<i>yqeU</i>	2622264	2623034	-		3849	3149	2660	3593	0.83	0.70	0.93												
<i>prmA</i>	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		
<i>dnaJ</i>	2624017	2625135	-		9513	9307	8838	9315	0.99	0.93	0.98												
<i>dnaK</i>	2625335	2627170	-		17157	18934	18794	18720	1.11	1.10	1.09												
<i>grpE</i>	2627194	2627757	-		18979	19429	19983	20357	1.03	1.05	1.07												
<i>hrcA</i>	2627829	2628860	-		6015	4194	4758	7124	0.70	0.79	1.18	790	hrcA	2627762	2627905	2627834		3.5	2.9	1.0	0.0		
<i>hemN</i>	2628980	2630080	-		1818	1255	1170	1744	0.70	0.65	0.95												
<i>lepA</i>	2630133	2631971	-		4444	3559	3392	4253	0.80	0.77	0.96												
<i>yqxA</i>	2632105	2632443	-		115	131	150	103	1.14	1.30	0.89												
<i>spoIIP</i>	2632460	2633665	-		184	225	246	195	1.23	1.34	1.06												
<i>gpr</i>	2633728	2634834	-		155	201	221	178	1.30	1.43	1.15												
<i>rpsT</i>	2635038	2635304	+		20624	15428	16956	19656	0.76	0.82	0.95												
<i>hola</i>	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		
<i>comEC</i>	2636766	2639096	-		258	292	282	291	1.13	1.09	1.13												
<i>comEB</i>	2639100	2639669	-		1506	907	814	1475	0.60	0.54	0.98												
<i>comEA</i>	2639736	2640353	-		164	124	134	174	0.76	0.82	1.05												
<i>comER</i>	2640437	2641258	+		241	239	263	267	0.99	1.09	1.11												
<i>yqeM</i>	2641324	2642067	-		5497	5379	4286	5013	0.99	0.78	0.91												
<i>yqeL</i>	2642064	2642420	-		7801	7200	6349	7059	0.92	0.81	0.90												
<i>yqeK</i>	2642438	2642998	-		5718	5167	4468	4920	0.91	0.78	0.86												
<i>nadD</i>	2642988	2643557	-		6749	6184	5191	5928	0.92	0.77	0.87												
<i>yqeI</i>	2643569	2643859	-		6178	5571	4828	5461	0.90	0.78	0.88												
<i>aroE_2</i>	2643853	2644695	-		7552	6704	5767	6785	0.90	0.77	0.90												
<i>yqeH</i>	2644713	2645813	-		5476	4644	3977	5081	0.85	0.73	0.92	792	yqeH	2645068	2645483	2645276		20.6	14.2	4.5	0.0		
<i>yqeG</i>	2645817	2646335	-		3499	2933	2394	3271	0.85	0.69	0.92												
												793	Inter	2646122	2647047	2646585		50.7	73.7	21.2	6.4		
<i>sda</i>	2646679	2646837	+		491	1065	839	502	2.01	1.59	1.01												
<i>yqeF</i>	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		
<i>cwlH</i>	2648126	2648878	-		142	140	138	153	0.99	0.97	1.07												
<i>yqeD</i>	2649065	2649691	+		822	770	707	904	0.95	0.87	1.10												
<i>yqeC</i>	2649710	2650603	-		244	214	227	281	0.87	0.93	1.13												
												796	Inter	2650593	2651042	2650818		17.9	22.0	-0.2	-1.1		P03
<i>yqeB</i>	2650855	2651580	+		511	3312	3342	419	6.87	6.79	0.83												
<i>nucB</i>	2651613	2652023	-		141	134	132	175	0.95	0.94	1.24												
<i>spoIVCB</i>	2652219	2652689	+		121	177	190	113	1.46	1.57	0.93	797	spoIVCB	2652378	2652759	2652569		11.2	21.5	19.6	22.5		
<i>spoIVCA</i>	2652597	2654099	-		200	152	165	198	0.76	0.83	0.98												
<i>arsC</i>	2654548	2654967	-		1074	861	922	892	0.80	0.85	0.82												
<i>arsB</i>	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		
<i>yqcK</i>	2656042	2656482	-		132	102	109	117	0.75	0.82	0.87												
<i>arsR</i>	2656543	2656860	-		414	345	373	385	0.81	0.88	0.91												
<i>yqeI</i>	2657232	2657996	-		134	123	136	149	0.91	1.01	1.11	799	yqeI	2657512	2657672	2657592		0.8	0.6	0.1	5.2		
												800	Inter	2658124	2658641	2658383		23.6	18.2	2.9	9.2		
												801	rapE	2659178	2659729	2659454		55.3	68.4	32.0	17.6		
<i>rapE</i>	2658440	2659567	+		80	106	120	79															

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

gene		Transcriptome analysis									ChAP-chip analysis							Profile ID		
name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center	Binding intensity ^c				
				wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild						AbrB			Abh	
														wild -type	Δabh	wild -type	$\Delta abrB$			
<i>yqxG</i>	2665130	2666023	-	82	80	83	78	0.98	1.01	0.95										
<i>yqcE</i>	2666111	2666275	-	184	175	181	159	0.95	0.98	0.87										
<i>yqcD</i>	2666272	2666607	-	76	76	77	85	0.99	1.01	1.12										
<i>yqcC</i>	2666617	2667717	-	119	109	113	133	0.92	0.95	1.12										
<i>yqcB</i>	2667720	2667992	-	56	51	57	68	0.92	1.03	1.23										
<i>yqcA</i>	2667989	2668567	-	125	116	118	147	0.93	0.95	1.18										
<i>yqbT</i>	2668551	2669597	-	220	200	210	249	0.91	0.95	1.13										
<i>yqbS</i>	2669590	2670015	-	130	118	129	137	0.90	0.99	1.05										
<i>yqbR</i>	2670028	2670291	-	171	152	163	148	0.90	0.98	0.88										
<i>yqbQ</i>	2670288	2671268	-	140	122	128	131	0.87	0.92	0.95										
<i>yqbP</i>	2671281	2671940	-	159	135	136	131	0.85	0.86	0.83										
<i>yqbO</i>	2671933	2676690	-	138	119	124	143	0.87	0.90	1.03	805	<i>yqbO</i>	2674172	2674553	2674363	5.5	1.8	6.4	29.5	
<i>yqbN</i>	2676872	2677321	-	143	104	116	127	0.73	0.81	0.89	806	<i>yqbN</i>	2677011	2677205	2677108	5.1	2.0	7.2	1.7	
<i>yqdB</i>	2677467	2677646	+	132	162	137	146	1.22	1.04	1.11										
<i>yqbM</i>	2678369	2678812	-	221	177	175	223	0.80	0.79	1.01										
<i>yqbL</i>	2678815	2679219	-	153	151	165	129	0.99	1.08	0.85										
<i>yqbK</i>	2679297	2680214	-	182	160	154	209	0.88	0.84	1.14										
<i>yqbJ</i>	2680403	2680840	-	100	92	91	108	0.92	0.92	1.08										
<i>yqbl</i>	2680853	2681356	-	180	147	152	229	0.82	0.84	1.27										
<i>yqbH</i>	2681353	2681715	-	103	104	101	118	1.01	0.98	1.14										
<i>yqbG</i>	2681712	2682107	-	204	198	204	220	0.97	1.00	1.08										
<i>yqbF</i>	2682111	2682422	-	78	87	81	67	1.13	1.04	0.87										
<i>yqbE</i>	2682433	2683368	-	110	115	119	111	1.05	1.08	1.00										
<i>yqbD</i>	2683387	2684355	-	132	130	128	124	0.99	0.97	0.94										
<i>yqbC</i>	2684388	2685041	-	231	434	376	239	1.88	1.63	1.04										
<i>yqbB</i>	2685082	2685999	-	108	101	99	107	0.94	0.92	1.00	807	Inter	2684916	2685246	2685081	14.3	11.0	2.3	-0.2	
<i>yqbA</i>	2685996	2687528	-	150	143	150	152	0.96	1.00	1.01										
<i>yqaT</i>	2687532	2688827	-	133	123	129	143	0.93	0.97	1.07										
<i>yqaS</i>	2688820	2689539	-	107	102	112	110	0.95	1.04	1.03										
<i>yqaR</i>	2689607	2690071	-	118	138	134	125	1.16	1.14	1.06										
<i>yqaQ</i>	2690215	2690670	-	200	198	199	204	0.99	1.00	1.02	808	Inter	2689948	2690261	2690105	16.5	4.0	0.5	0.7	
<i>yqaP</i>	2690868	2691797	+	2458	8812	9186	2197	3.60	3.76	0.90	809	Inter	2690577	2691043	2690810	25.2	30.7	3.9	-1.7	
<i>yqaO</i>	2691871	2692077	-	126	140	127	141	1.11	1.01	1.12										
<i>yqaN</i>	2692159	2692587	-	201	174	187	197	0.87	0.94	0.99										
<i>yqaM</i>	2692823	2693764	-	111	98	108	94	0.89	0.98	0.85										
<i>yqaL</i>	2693646	2694347	-	115	100	111	116	0.87	0.97	1.01										
<i>yqaK</i>	2694399	2695253	-	129	111	115	115	0.86	0.89	0.89										
<i>yqaJ</i>	2695256	2696215	-	118	104	105	111	0.89	0.89	0.95										
<i>yqaI</i>	2696321	2696515	-	85	74	76	87	0.87	0.89	1.02										
<i>yqaH</i>	2696645	2696902	-	86	74	85	75	0.87	1.01	0.88										
<i>yqaG</i>	2696899	2697468	-	140	135	137	151	0.96	0.98	1.10										
<i>yqaD</i>	2697542	2697682	-	140	118	121	148	0.84	0.86	1.06										
<i>yqaF</i>	2697712	2697942	-	121	110	113	115	0.91	0.94	0.95										
<i>yqaE</i>	2698119	2698469	+	457	347	296	427	0.76	0.64	0.94										
<i>yqaD</i>	2698736	2698903	-	112	85	76	79	0.76	0.67	0.72	810	Inter	2698907	2699373	2699140	35.6	7.0	16.1	7.3	
<i>yqaC</i>	2699259	2699795	-	138	164	185	158	1.19	1.34	1.14										
<i>yqaB</i>	2700064	2700582	+	97	97	98	114	1.01	1.02	1.18										
<i>spoIIC</i>	2700564	2700980	+	217	153	175	259	0.71	0.82	1.18	811	<i>spoIIC</i>	2700454	2700733	2700594	10.1	14.8	11.2	16.2	
<i>yrkS</i>	2701205	2701369	-	231	199	203	246	0.87	0.88	1.05										
<i>yrkR</i>	2701914	2702333	-	291	243	268	308	0.86	0.94	1.07	812	Inter	2701355	2701872	2701614	27.4	44.0	19.0	5.9	
<i>yrkQ</i>	2702376	2703674	-	387	303	296	365	0.79	0.77	0.93										
<i>yrkP</i>	2703661	2704356	-	201	171	170	209	0.85	0.84	1.02										
<i>yrkO</i>	2704624	2705841	+	344	253	265	323	0.74	0.78	0.92										
<i>yrkN</i>	2706353	2706910	+	639	420	436	558	0.65	0.68	0.85	813	<i>yrkN</i>	2706812	2706989	2706901	4.8	2.4	0.5	-0.1	
<i>yrkM</i>	2706989	2707096	+	126	130	141	162	1.05	1.12	1.31										
<i>yrkL</i>	2707401	2707925	-	2146	3007	3197	2228	1.41	1.50	1.04	814	<i>yrkL</i>	2707288	2707686	2707487	26.0	22.3	10.2	0.7	
<i>yrkK</i>	2708169	2708645	-	386	368	332	427	0.95	0.86	1.11	814	Inter	2707696	2708519	2708108	108.4	127.0	72.1	3.6	
<i>yrkJ</i>	2709228	2710013	-	105	93	97	111	0.89	0.93	1.07										
<i>yrkI</i>	2710074	2710301	-	93	67	85	90	0.73	0.92	0.97										
<i>yrkH</i>	2710335	2711222	-	247	194	198	263	0.79	0.80	1.06										
<i>yrkG</i>	2711351	2711461	-	205	168	185	181	0.82	0.90	0.88										
<i>yrkF</i>	2711803	2712360	-	264	207	221	250	0.79	0.84	0.94										
<i>yrkE</i>	2712546	2713028	-	163	137	160	182	0.84	0.98	1.11										
<i>yrkD</i>	2713175	2713366	-	830	763	726	777	0.90	0.85	0.93										
<i>yrkC</i>	2714159	2714719	-	619	962	871	649	1.55	1.40	1.06	815	<i>yrkC</i>	2714462	2714722	2714592	11.2	3.6	2.5	-0.4	
<i>yrkB</i>	2714945	2715091	-	278	196	214	225	0.68	0.77	0.82										
<i>blrR</i>	2715261	2716082	-	279	219	218	291	0.78	0.79	1.04										

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB /$ wild	$\Delta abh /$ $\Delta abrB /$ wild	$\Delta abh /$ wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$																		
<i>blt</i>	2716199	2717401	+	260	242	246	247	0.93	0.95	0.95											
<i>bltD</i>	2717570	2718028	+	351	317	323	312	0.90	0.92	0.89											
<i>yrkA</i>	2718185	2719489	-	2303	1923	2117	2446	0.83	0.92	1.06											
<i>yrdR</i>	2719913	2720878	-	107	94	109	109	0.88	1.02	1.02											
<i>yrdQ</i>	2721004	2721870	+	675	492	503	651	0.73	0.75	0.97	816	yrdQ	2721109	2721286	2721198	5.8	0.5	5.4	-0.4		
<i>trkA</i>	2721993	2723030	-	156	149	148	152	0.95	0.94	0.96											
<i>czcD</i>	2723118	2724053	-	203	201	228	175	1.00	1.10	0.87											
<i>yrdN</i>	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		
<i>gltR</i>	2725063	2725953	+	350	283	284	331	0.82	0.83	0.96											
<i>yrkK</i>	2726111	2726428	-	898	765	729	862	0.86	0.81	0.97											
<i>brnQ</i>	2726386	2727708	-	848	614	638	847	0.72	0.75	1.00											
<i>acID</i>	2727873	2728205	-	1172	859	887	1238	0.73	0.75	1.07											
<i>acIC</i>	2728202	2728966	-	1175	880	994	1182	0.75	0.84	1.00	818	azC	2728521	2728749	2728635	0.6	0.2	-0.1	7.9		
<i>acIB</i>	2728979	2729452	-	861	546	612	776	0.63	0.71	0.90											
<i>yrdF</i>	2729786	2730061	-	106	89	84	96	0.84	0.79	0.90											
<i>cypA</i>	2730333	2731565	-	248	215	201	236	0.88	0.81	0.95											
<i>yrdD</i>	2731958	2732107	-	130	95	101	130	0.76	0.78	1.06											
<i>yrdC</i>	2732206	2732769	-	2446	2076	2108	2244	0.85	0.86	0.92	819	yrdC	2732380	2732965	2732673	27.2	30.9	2.6	-0.9		P03
<i>yrdB</i>	2732998	2733369	-	108	111	114	123	1.04	1.06	1.16											
											820	Inter	2733468	2734002	2733735	42.4	35.5	15.5	-1.6		
<i>yrdA</i>	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
<i>aadK</i>	2734908	2735762	-	519	583	612	537	1.13	1.18	1.04											
<i>yypB</i>	2736141	2737184	+	451	790	924	415	1.76	2.05	0.92											
<i>yypC</i>	2737534	2738331	+	218	182	184	230	0.83	0.85	1.06											
											822	Inter	2738500	2738779	2738640	15.2	13.6	0.2	-1.0		
<i>yypD</i>	2738712	2739419	+	4973	22864	23602	4301	4.62	4.76	0.86											
<i>yypE</i>	2740583	2741338	-	177	135	150	185	0.77	0.85	1.05											
<i>sigZ</i>	2741470	2742000	-	264	236	247	283	0.90	0.94	1.06											
<i>yypG</i>	2742165	2743115	+	329	317	334	362	0.96	1.01	1.08	823	yypG	2742869	2743046	2742958	0.3	0.2	0.3	6.8		
<i>yraO</i>	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
<i>yraN</i>	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		
											825	yraN	2745436	2745851	2745644	19.1	14.2	1.5	-1.9		
<i>yraM</i>	2745834	2746937	+	200	196	195	220	0.98	0.97	1.10											
<i>csn</i>	2747210	2748043	-	725	8664	8653	485	12.07	12.05	0.67											
											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		
<i>yraL</i>	2748486	2748749	+	1204	1265	1205	1385	1.05	1.01	1.15											
											828	Inter	2748734	2748945	2748840	7.8	0.1	1.5	0.3		
<i>yraK</i>	2748886	2749575	+	242	281	291	234	1.19	1.21	0.97											
<i>yraJ</i>	2750108	2750470	-	427	766	778	507	1.77	1.80	1.18											
<i>yraI</i>	2750517	2750951	-	876	1609	1716	893	1.83	1.93	1.01	829	yraI	2750604	2750764	2750684	4.3	2.7	1.5	0.6		
											829	Inter	2750774	2751206	2750990	26.6	14.8	6.6	0.3		
<i>yraH</i>	2751392	2751778	-	268	267	302	252	0.98	1.12	0.92											
<i>yraG</i>	2752027	2752272	+	148	188	230	131	1.26	1.54	0.89											
<i>yraF</i>	2752290	2752658	+	139	199	248	147	1.42	1.77	1.05											
<i>adhB</i>	2752677	2753813	+	149	199	239	163	1.34	1.61	1.10	831	adhB	2752712	2753093	2752903	21.5	20.0	3.7	3.1		P03
											832	adhB	2753749	2753875	2753812	2.1	0.9	1.8	3.7		
<i>yraE</i>	2753832	2754029	+	201	384	483	200	1.89	2.36	0.98											
<i>yraD</i>	2754045	2754344	+	161	257	309	156	1.61	1.93	0.97											
<i>yraB</i>	2754607	2755029	-	360	219	222	350	0.61	0.62	0.96											
<i>adhA</i>	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		
<i>yraA</i>	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		
<i>sacC</i>	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		
<i>levG</i>	2759458	2760285	-	758	896	1161	517	1.22	1.58	0.66											
<i>levF</i>	2760306	2761115	-	1056	1159	1482	745	1.10	1.42	0.69											
<i>levE</i>	2761132	2761620	-	879	1105	1433	597	1.30	1.68	0.66											
<i>levD</i>	2761620	2762060	-	1011	1160	1462	573	1.18	1.50	0.55											
<i>levR</i>	2762250	2765066	-	234	215	238	189	0.92	1.01	0.81											
<i>aapA</i>	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		
<i>yrhP</i>	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		
<i>yrhO</i>	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		
<i>sigV</i>	2769077	2769577	+	282	167	196	352	0.59	0.70	1.25											
<i>yrhM</i>	2769577	2770434	+	636	386	517	815	0.61	0.82	1.28											
<i>yrhL</i>	2770545	2772449	+	727	53																

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c				
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$	Δabh / wild							AbrB		Abh		
-type	Δabh	-type	$\Delta abrB$																			
<i>yrhF</i>	2779752	2780120	-		3904	1887	1810	3295	0.48	0.46	0.84											
<i>yrhE</i>	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	
<i>yrhD</i>	2783397	2783879	+		3246	2086	1820	3516	0.64	0.56	1.09											
<i>yrhC</i>	2783915	2784145	-		377	529	524	459	1.41	1.40	1.22											
<i>yrhB</i>	2784228	2785367	-		826	1186	1167	862	1.38	1.37	1.05											
<i>yrhA</i>	2785369	2786292	-		803	932	980	788	1.15	1.21	0.98											
<i>mtn</i>	2786357	2787052	-		5947	5349	5504	5724	0.90	0.93	0.96											
<i>yrhT</i>	2787073	2787714	-		875	775	784	945	0.89	0.90	1.08											
<i>yrzA</i>	2787907	2788110	+		3434	2454	2298	2844	0.72	0.67	0.83											
<i>yrhS</i>	2788147	2788848	-		4404	3890	3741	4599	0.89	0.85	1.05											
<i>yrhR</i>	2788913	2790667	-		549	461	456	555	0.86	0.84	1.00											
<i>greA</i>	2790721	2791194	-		10933	10844	10397	11200	0.99	0.95	1.02											
<i>udk</i>	2791445	2792080	-		6351	4572	4020	6310	0.73	0.64	1.00											
<i>yrhO</i>	2792087	2793355	-		7451	5318	4943	7162	0.72	0.66	0.96	849	yrhO	2792645	2793162	2792904		35.2	10.8	58.1	60.2	
<i>yrhN</i>	2793374	2794303	-		7298	4745	4307	7166	0.66	0.59	0.98											
<i>yrhM</i>	2794309	2794962	-		4976	3258	2777	4801	0.66	0.56	0.96											
<i>yrhL</i>	2795114	2796196	-		3944	4582	4452	3676	1.17	1.14	0.93											
<i>yrhK</i>	2796327	2796608	-		15569	15048	14246	16498	0.96	0.91	1.06											
<i>yrhJ</i>	2796626	2797042	-		10595	8045	8083	9965	0.76	0.76	0.94											
<i>yrhI</i>	2797050	2797316	-		8257	6247	5788	8160	0.76	0.70	0.99											
<i>alaS</i>	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	
<i>glnQ</i>	2800368	2801429	-		306	322	341	330	1.05	1.12	1.08											
<i>glnH</i>	2801585	2802313	+		120	106	108	129	0.88	0.90	1.08											
<i>glnM</i>	2802335	2803156	+		164	148	155	169	0.90	0.95	1.03											
<i>glnP</i>	2803217	2803867	+		201	215	211	209	1.07	1.05	1.04											
<i>glnR</i>	2803884	2804540	+		127	136	140	137	1.07	1.10	1.08											
<i>yrhD</i>	2804931	2805455	-		320	619	736	329	1.89	2.24	1.02	855	yrhD	2805021	2805198	2805110		7.2	7.3	1.4	-0.2	
<i>yrhC</i>	2805513	2807909	-		2837	2592	2328	2833	0.94	0.83	0.99	856	yrhC	2806908	2807170	2807039		5.0	2.7	8.2	1.7	
<i>yrhB</i>	2807934	2808554	-		3131	2888	2658	3216	0.94	0.86	1.02											
<i>mmmA</i>	2808640	2809764	-		7374	7208	6836	7622	0.98	0.93	1.03											
<i>yrhO</i>	2809786	2810925	-		5937	5921	5620	6155	1.00	0.95	1.04											
<i>yrhC</i>	2811027	2811362	-		2932	3037	3021	3043	1.04	1.04	1.04											
<i>yrhN</i>	2811562	2812827	+		1049	783	801	1042	0.75	0.77	0.99											
<i>yrhM</i>	2812869	2813633	-		2909	2039	1819	2411	0.70	0.63	0.83											
<i>aspS</i>	2813969	2815747	-		8287	7169	7059	7777	0.87	0.85	0.94											
<i>hisS</i>	2815761	2817035	-		5046	4381	4307	4808	0.87	0.85	0.95											
<i>yrhK</i>	2817417	2817587	-		74	98	91	79	1.34	1.25	1.04	860	yrhK	2817092	2817896	2817494		47.8	38.5	74.0	46.2	P01
<i>yrhJ</i>	2817720	2819276	+		2153	2271	2100	2287	1.08	0.97	1.07											
<i>yrhI</i>	2819303	2819701	-		6111	5034	4673	5331	0.83	0.77	0.87											
<i>relA</i>	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	
<i>apt</i>	2822127	2822639	-		7899	6667	6280	8003	0.84	0.80	1.01											
<i>yrhE</i>	2822645	2825005	-		6203	5644	5171	6304	0.91	0.84	1.02	862	yrhE	2824928	2825003	2824966		0.1	0.1	0.2	2.6	
<i>yrhD</i>	2825072	2825395	-		4307	3707	3862	3898	0.86	0.90	0.90											
<i>yrhC</i>	2825471	2825968	-		3659	3534	3402	3407	0.97	0.93	0.93	863	yrhC	2825234	2825768	2825501		22.2	16.9	11.8	6.6	
<i>secDF</i>	2826126	2828339	-		9705	9229	9300	9570	0.95	0.96	0.99	864	secDF	2825897	2826193	2826045		15.4	10.8	5.3	1.2	
<i>yrhD</i>	2828378	2828674	-		5821	6010	5371	5716	1.03	0.92	0.98	865	secDF	2826798	2827213	2827006		22.9	23.1	35.9	31.8	P01
<i>spoVB</i>	2828790	2830346	+		186	184	187	216	0.99	1.00	1.16											
<i>yrhG</i>	2830350	2831006	-		163	177	195	159	1.08	1.20	0.98											
<i>yrhE</i>	2831141	2831593	+		334	317	343	333	0.96	1.03	1.00											
<i>yajC</i>	2831650	2831919	-		14264	14086	13770	14022	0.99	0.97	0.98											
<i>tgt</i>	2831953	2833098	-		5550	4591	4242	5572	0.83	0.76	1.00											
<i>queA</i>	2833125	2834153	-		8579	6660	6324	7792	0.78	0.74	0.91											
<i>rvhB</i>	2834376	2835380	-		4354	3147	2903	4235	0.72	0.67	0.97											
<i>rvhA</i>	2835391	2835996	-		3101	1933	1783	2982	0.62	0.57	0.96											
<i>bofC</i>	2836135	2836647	-		727	374	532	461	0.52	0.77	0.63											
<i>csbX</i>	2836695	2838002	-		2299	930	1516	1721	0.40	0.66	0.75											
<i>yrhE</i>	2838073	2839098	-		3815	1339	2272	3705	0.36	0.58	0.97											
<i>yrhF</i>	2839336	2839728	+		1026	1170	1543	1244	1.14	1.51	1.21											
<i>yrhG</i>	2839761	2839982	+		1427	1678	2081	1860	1.17	1.44	1.30											
<i>yrhH</i>	2840394	2840525	+		581	409	331	526	0.71	0.58	0.89											
<i>yrhD</i>	2840836	2842290	+		276	236	247	299	0.86	0.90	1.08											
<i>yrhC</i>	2842331	2843053	-		1457	1538	1932	2060	1.08	1.35	1.41											
<i>coxA</i>	2843156	2843674	-		137	379	509	138	2.67	3.55												

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

gene	Transcriptome analysis										ChAP-chip analysis						Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$																		
<i>nifS</i>	2848794	2849981	+	127	124	128	135	0.98	1.01	1.06											
<i>yrxA</i>	2849941	2850477	+	1393	1784	1593	1391	1.34	1.17	1.02											
<i>pheA</i>	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		
<i>pheB</i>	2851383	2851826	-	3914	3932	3387	3508	1.00	0.86	0.89											
<i>obgE</i>	2851887	2853173	-	4652	5235	4462	4025	1.13	0.96	0.86											
<i>spoOB</i>	2853207	2853785	-	2516	3419	2481	2143	1.39	0.97	0.83											
<i>rpmA</i>	2854106	2854390	-	23818	22227	22325	23539	0.93	0.94	0.99											
<i>ysxB</i>	2854403	2854741	-	27512	26194	25103	27706	0.95	0.91	1.01											
<i>rplU</i>	2854744	2855052	-	26127	25238	23995	26530	0.97	0.92	1.02											
<i>spoIVFB</i>	2855199	2856065	-	403	396	412	400	0.98	1.02	0.99											
<i>spoIVFA</i>	2856058	2856852	-	250	214	208	229	0.86	0.83	0.90	873	spoIVFA	2856532	2856878	2856705	14.1	2.8	2.9	-0.4		
<i>minD</i>	2857003	2857809	-	12497	12974	12578	12116	1.04	1.01	0.97											
<i>minC</i>	2857811	2858491	-	10004	10454	9776	10052	1.04	0.98	1.00											
<i>mreD</i>	2858544	2859062	-	8210	7839	7422	8725	0.96	0.91	1.06	875	mreD	2858860	2859122	2858991	4.3	3.1	10.4	9.7		
<i>mreC</i>	2859059	2859931	-	13532	12894	12707	13244	0.95	0.94	0.98											
<i>mreB</i>	2859962	2860975	-	13169	13022	12366	13447	0.99	0.94	1.02											
<i>radC</i>	2861066	2861761	-	3753	4729	4301	4383	1.27	1.15	1.18											
<i>maf</i>	2861798	2862367	-	4650	5932	5369	4910	1.30	1.17	1.07											
<i>spoIIB</i>	2862520	2863518	-	180	155	160	184	0.86	0.89	1.02											
<i>comC</i>	2863652	2864398	-	382	394	404	395	1.03	1.06	1.03											
<i>folC</i>	2864538	2865830	-	4935	3470	3413	4492	0.71	0.70	0.91											
<i>valS</i>	2865890	2868532	-	9336	7179	6831	8648	0.77	0.73	0.93											
<i>ysxE</i>	2869029	2870054	-	202	197	187	198	0.97	0.93	0.97											
<i>spoVID</i>	2870087	2871814	-	185	160	161	194	0.86	0.87	1.04											
<i>hemL</i>	2871945	2873237	-	5157	4704	4642	4912	0.91	0.90	0.95											
<i>hemB</i>	2873267	2874241	-	4752	4658	4170	4717	0.99	0.88	0.99											
<i>hemD_2</i>	2874238	2875026	-	2970	2732	2622	2793	0.93	0.89	0.94											
<i>hemC</i>	2875016	2875960	-	2908	2583	2283	2809	0.88	0.78	0.95											
<i>hemX</i>	2875993	2876823	-	1748	1599	1412	1775	0.92	0.81	1.00											
<i>hemA</i>	2876831	2878198	-	4316	4150	4061	4304	0.96	0.94	1.00											
<i>ysxD</i>	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
<i>engB</i>	2878947	2879534	-	5669	5340	5319	5582	0.94	0.94	0.98											
<i>lonA</i>	2879531	2881855	-	4925	4718	4987	5204	0.96	1.01	1.06											
<i>lonB</i>	2882036	2883694	-	245	298	334	229	1.21	1.36	0.93											
<i>clpX</i>	2883846	2885108	-	11731	11461	12055	11929	0.98	1.03	1.02	877	Inter	2883493	2883925	2883709	21.6	25.8	2.4	0.0		P03
<i>tig</i>	2885381	2886655	-	23241	21750	21040	23007	0.94	0.91	0.99	878	Inter	2885108	2885285	2885197	2.8	4.1	4.3	5.4		
<i>ysoA</i>	2886883	2887815	-	1154	1056	991	1173	0.91	0.86	1.01	879	tig	2885381	2885540	2885461	2.9	1.0	4.3	3.1		
<i>leuD</i>	2888005	2888604	-	250	260	284	218	1.03	1.12	0.87											
<i>leuC</i>	2888617	2890035	-	295	336	399	301	1.13	1.32	1.02											
<i>leuB</i>	2890085	2891182	-	243	254	272	242	1.04	1.11	0.99											
<i>leuA</i>	2891203	2892759	-	236	270	341	214	1.13	1.42	0.91											
<i>ihvC</i>	2892746	2893774	-	359	411	476	351	1.14	1.32	0.97											
<i>ihvH</i>	2893791	2894315	-	214	301	336	216	1.40	1.55	1.01											
<i>ihvB</i>	2894312	2896036	-	238	308	343	241	1.28	1.41	1.00											
<i>ysnD</i>	2896852	2897187	+	107	87	95	112	0.81	0.88	1.04	881	Inter	2896532	2896912	2896722	14.4	11.0	1.4	-0.7		
<i>ysnE</i>	2897356	2897811	+	334	296	337	293	0.90	1.03	0.86											
<i>ysnF</i>	2897995	2898855	+	243	263	400	194	1.08	1.65	0.79											
<i>trnSL-Arg</i>	2898879	2898955	-	11441	16463	17220	11159	1.43	1.57	0.88											
<i>ysnB</i>	2899086	2899601	-	4612	4610	4782	4353	1.00	1.04	0.94											
<i>ysnA</i>	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		
<i>rph</i>	2900220	2900957	-	5287	5087	4880	5019	0.96	0.92	0.95											
<i>gerM</i>	2901068	2902168	-	267	209	230	281	0.78	0.86	1.05											
<i>racE</i>	2902284	2903102	-	5388	4125	3647	5358	0.76	0.68	0.99											
<i>ysmB</i>	2903110	2903550	-	5021	4355	3666	4626	0.87	0.73	0.92											
<i>gerE</i>	2903794	2904018	-	1764	1528	1865	1874	0.87	1.06	1.06	884	Inter	2903655	2903815	2903735	4.2	4.6	3.5	0.8		
<i>ysmA</i>	2904134	2904577	-	1521	1366	1461	1715	0.90	0.96	1.13											
<i>sdhB</i>	2904640	2905401	-	18695	16460	17919	19550	0.88	0.96	1.05											
<i>sdhA</i>	2905404	2907164	-	18898	15686	17102	19751	0.83	0.91	1.05	*Broad		2906256	2906450							
<i>sdhC</i>	2907198	2907806	-	15329	11536	13011	16587	0.75	0.84	1.08											
<i>ysIB</i>	2908099	2908545	+	12541	9028	9392	10932	0.72	0.75	0.87											
<i>lysC</i>	2908589	2909815	-	1305	918	858	1009	0.70	0.65	0.77	886	lysC	2908738	2909119	2908929	5.6	3.0	2.7	28.3		P04
<i>ask</i>	2909991	2910065	-	3844	4785	4006	3481	1.25	1.05	0.91											
<i>uvrC</i>	2910160	2911956	-	1070	889	940	1120	0.85	0.89	1.04											
<i>trxA</i>	2912092	2912406	-	15466	18006	17668	15984	1.17	1.15	1.03											
<i>xsa</i>	2912729	2914216	-	503	413	541	499	0.82	1.06	1.00	887	xsa	2913124	2913369	2913247	4.0	5.3	8.9	7.2		
<i>etfA</i>	2914433	2915410	-	3986	3248	3747	3790	0.81	0.94	0.95											
<i>etfB</i>	2915446	2916219	-	4906	3541	4198	4229	0.72	0.86	0.86											
<i>ysiB</i>	2916234	2917010	-	2531	1872	2195	2381	0.74	0.88	0.94											
<i>ysiA</i>	2917025	2917609	-	3540	2542	2879	3241	0.72	0.82	0.92	889	ysiA	2917426	2917568	2917497	1.4	0.5	3.3	4.7		

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
wild	$\Delta abrB$	wild	Δabh	wild	Δabh	wild	wild	Δabh	wild	Δabh	wild	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$					
<i>lefA</i>	2917714	2919396	-	1586	1676	1969	1422	1.06	1.25	0.90											
<i>yshE</i>	2919585	2919989	-	4353	4102	4013	3722	0.94	0.92	0.85											
<i>mutSB</i>	2920004	2922361	-	4066	4187	4147	3798	1.03	1.02	0.93											
<i>yshC</i>	2922382	2924094	-	3508	3567	3582	3434	1.02	1.02	0.98											
<i>yshB</i>	2924168	2924701	-	982	918	858	1122	0.93	0.89	1.14	891	yshB	2924174	2924555	2924365	24.6	11.1	6.6	0.5		
<i>yshA</i>	2924708	2924965	-	1262	1430	1236	1308	1.13	0.98	1.03	891	yshA	2924565	2925201	2924883	27.0	15.5	9.4	-0.5		
<i>rmhC</i>	2925099	2926040	+	1188	1435	1230	1342	1.21	1.04	1.14											
<i>pheT</i>	2926076	2928490	-	6821	5658	5375	6288	0.83	0.79	0.92											
<i>pheS</i>	2928506	2929540	-	5696	4953	4293	5283	0.87	0.75	0.93											
<i>ysgA</i>	2929895	2930641	-	1702	1273	1083	1514	0.74	0.63	0.89											
<i>sspI</i>	2930760	2930975	+	149	241	290	154	1.63	1.97	1.03											
<i>yafB</i>	2931044	2932150	+	518	462	423	540	0.89	0.81	1.04											
<i>yafC</i>	2932253	2933665	+	1517	12686	11100	1637	9.11	7.52	1.03											
<i>yafD</i>	2933662	2934996	+	979	9202	8100	1101	10.09	8.33	1.05											
<i>yafE</i>	2935035	2935277	-	2758	1661	2042	2797	0.60	0.73	1.01											
<i>cstA</i>	2935450	2937246	-	4455	2000	2912	4165	0.44	0.63	0.94	893	cstA	2936329	2936523	2936426	5.3	2.0	4.4	0.5		
<i>abfA</i>	2937398	2938900	-	276	320	374	286	1.17	1.37	1.03											
<i>araQ</i>	2938919	2939764	-	372	404	472	384	1.09	1.27	1.03											
<i>araP</i>	2939765	2940706	-	347	405	517	374	1.17	1.50	1.08											
<i>araN</i>	2940742	2942043	-	452	353	461	402	0.78	1.01	0.89											
<i>araM</i>	2942074	2943258	-	571	361	465	533	0.63	0.81	0.93											
<i>araL</i>	2943255	2944073	-	471	253	330	464	0.54	0.69	0.99											
<i>araD</i>	2944051	2944740	-	925	405	573	790	0.44	0.61	0.86											
<i>araB</i>	2944757	2946439	-	1183	510	740	1043	0.43	0.61	0.88											
<i>araA</i>	2946453	2947949	-	1335	567	789	1110	0.42	0.58	0.83	895	araA	2947277	2947488	2947383	1.4	1.0	3.4	8.2		
<i>abnA</i>	2948157	2949098	-	267	180	213	256	0.68	0.79	0.97											
<i>ysdC</i>	2949295	2950380	-	9020	10636	10836	9364	1.18	1.20	1.04											
<i>ysdB</i>	2950564	2950956	+	3595	3072	3661	3148	0.85	1.02	0.88											
<i>ysdA</i>	2950972	2951241	-	3012	1842	1600	2136	0.64	0.54	0.72											
<i>rpmI</i>	2951298	2951657	-	11511	11437	9292	11742	1.00	0.80	1.02											
<i>rpmL</i>	2951689	2951889	-	22339	21943	19747	21377	0.98	0.88	0.96											
<i>infC</i>	2951902	2952423	-	19589	18721	16293	19555	0.96	0.83	1.00											
<i>yycA</i>	2952595	2952819	+	43	39	40	35	0.90	0.92	0.82	897	yycA	2952377	2953064	2952721	42.1	60.6	40.5	21.8	P01	
<i>yycB</i>	2952869	2953501	+	446	1751	1570	657	3.98	3.52	1.47											
<i>yycB</i>	2953533	2954228	-	3598	972	1269	3591	0.27	0.34	0.99											
<i>yycB</i>	2954250	2954690	-	5320	1382	1767	5118	0.26	0.32	0.97											
<i>lytT</i>	2954824	2955549	-	2101	1659	1662	1861	0.79	0.80	0.89											
<i>lytS</i>	2955527	2957308	-	823	719	674	752	0.87	0.82	0.91											
<i>yycA</i>	2957475	2958257	+	4250	3839	3599	3800	0.90	0.85	0.89											
<i>thrS</i>	2958298	2960229	-	11848	9166	8800	11123	0.77	0.74	0.94											
											898	Inter	2960044	2960510	2960277	12.6	4.6	23.9	41.3		
<i>ytxC</i>	2960626	2961471	-	2519	1903	1825	2391	0.75	0.72	0.95											
<i>ytxB</i>	2961550	2962191	-	3763	3152	2920	3617	0.84	0.77	0.96											
<i>dnal</i>	2962225	2963160	-	2456	1888	1763	2357	0.77	0.72	0.96											
<i>dnab</i>	2963188	2964606	-	1166	865	801	1144	0.74	0.69	0.98											
<i>nrpR</i>	2964721	2965179	-	1336	1067	1126	1357	0.81	0.86	1.01											
<i>speD</i>	2965453	2965839	-	10226	6651	5817	9277	0.65	0.57	0.91											
											900	Inter	2965807	2965967	2965887	2.0	3.3	1.8	1.2		
<i>gapB</i>	2966072	2967094	-	1471	969	901	1209	0.65	0.60	0.81											
<i>ytcD</i>	2967300	2967680	-	657	485	482	657	0.75	0.74	1.01											
<i>ytbD</i>	2967864	2969054	+	495	244	247	490	0.50	0.50	0.99											
<i>ytbE</i>	2969078	2969920	+	647	300	297	598	0.46	0.46	0.92	902	ytbE	2969020	2969418	2969219	7.9	1.0	7.4	27.7		
<i>coaE</i>	2969962	2970555	-	3626	3513	3525	3643	0.97	0.97	1.00											
<i>yafF</i>	2970717	2971196	-	4867	5137	5342	5557	1.05	1.10	1.14											
<i>mutM</i>	2971368	2972204	-	3585	3725	3699	3825	1.04	1.03	1.07											
<i>polA</i>	2972221	2974863	-	3809	3527	3635	3898	0.93	0.96	1.02											
											903	Inter	2974953	2975096	2975025	6.5	1.8	1.3	-0.3		
<i>phoR</i>	2975107	2976846	-	4024	2902	3503	3768	0.72	0.87	0.94											
<i>phoP</i>	2976839	2977561	-	3244	2282	2793	2913	0.70	0.86	0.90											
<i>mdh</i>	2977773	2978711	-	16178	23143	23595	15166	1.43	1.46	0.93											
<i>icd</i>	2978755	2980026	-	17318	25070	25956	16650	1.45	1.50	0.96											
<i>ctzZ</i>	2980190	2981308	-	9485	17854	19155	9941	1.90	2.04	1.05											
<i>ytwI</i>	2981642	2982106	-	1361	651	642	1012	0.48	0.47	0.74											
<i>ytwI</i>	2982203	2983318	+	291	251	246	284	0.86	0.84	0.98											
<i>fxsA</i>	2983351	2983734	-	10795	7935	7950	10242	0.74	0.74	0.95	904	fxsA	2983623	2983749	2983686	2.1	3.3	0.6	0.2		
<i>pyk</i>	2983827	2985584	-	18563	14992	15215	18961	0.81	0.82	1.02	905	pyk	2984762	2984871	2984817	0.5	0.7	0.7	3.7		
<i>pfkA</i>	2985627	2986586	-	14378	10061	10203	14338	0.70	0.71	1.00											
<i>accA</i>	2986770	2987747	-	9866	9451	9028	9472	0.96	0.92	0.96	906	accA	2986768	2987387	2987078	56.4	76.9	45.4	26.0	P01	
											906	accA	2987397	2987795	2987596	22.1	33.2	12.5	2.9		
<i>accD</i>	2987732	2988520	-	9163	9022	8579	8860	0.99	0.94	0.97											
											907	Inter	2988570	2989121	2988846	43.3	40.8	65.3	42.8	P01	
<i>ytsJ</i>	2988939	2990171	-	8082	6512	6764	8313	0.81	0.84	1.03	907	ytsJ	2989131	2989665	2989398	8.4	7.5	13.1	27.8		
											908	ytsJ	2989845	2989954	2989900	2.1	1.2	3.4	1.4		

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c				
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	Δabh wild	Δabh $\Delta abrB$ wild	Δabh wild							AbrB		Abh		
wild	Δabh -type	wild	Δabh -type																			
<i>dnaE</i>	2990308	2993655	-	2001	1573	1558	1984	0.79	0.78	0.99												
<i>yirI</i>	2994133	2994636	+	146	116	122	124	0.80	0.84	0.85												
<i>yql</i>	2994947	2995888	-	3771	2828	3012	3870	0.75	0.80	1.03												
<i>ypl</i>	2996019	2996321	+	438	891	715	384	1.96	1.57	0.89												
<i>ytoI</i>	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			
<i>ytmM</i>	2997835	2998737	-	266	236	261	303	0.89	0.98	1.14												
<i>ytnL</i>	2998756	3000006	-	177	157	160	170	0.89	0.91	0.96	910	ytnL	2998685	2998862	2998774	7.3	0.4	0.9	-0.6			
											911	ytnL	2999467	2999865	2999666	22.4	1.3	32.3	2.0			P05
<i>ribR</i>	3000024	3000716	-	164	152	166	156	0.93	1.01	0.96												
<i>ytnJ</i>	3000763	3002091	-	162	146	158	178	0.90	0.97	1.10												
<i>ytnI</i>	3002088	3002369	-	311	272	282	326	0.87	0.91	1.05												
<i>ytmO</i>	3002384	3003388	-	238	228	234	272	0.96	0.98	1.15												
<i>ytmN</i>	3003385	3004164	-	217	203	200	263	0.94	0.92	1.23												
<i>ytmM</i>	3004161	3004868	-	234	245	260	235	1.04	1.11	1.00												
<i>ytmL</i>	3004898	3005617	-	158	148	156	161	0.93	0.98	1.02	912	ytmL	3005315	3005594	3005455	6.4	8.3	3.7	9.3			
<i>ytmK</i>	3005639	3006451	-	197	179	196	180	0.91	0.99	0.91												
<i>ytmJ</i>	3006465	3007274	-	166	145	144	165	0.88	0.87	1.01												
<i>ytmI</i>	3007288	3007824	-	148	143	148	173	0.96	1.00	1.17												
<i>ytlI</i>	3007977	3008903	+	185	171	176	178	0.92	0.95	0.96	913	ytlI	3007848	3008212	3008030	17.5	23.2	17.7	9.5			
<i>ytkL</i>	3008954	3009637	-	5074	6405	7105	5629	1.27	1.41	1.11												
<i>fabG_4</i>	3009700	3010467	-	3819	4958	5424	4874	1.30	1.42	1.28												
<i>yizD</i>	3010594	3010830	-	196	176	181	193	0.90	0.95	1.00												
<i>argH</i>	3010790	3012175	-	588	484	478	556	0.83	0.81	0.95												
<i>argG</i>	3012172	3013383	-	585	433	445	488	0.75	0.77	0.85												
<i>moaB</i>	3013553	3014065	-	3082	2741	2333	2572	0.90	0.75	0.82												
<i>ackA</i>	3014150	3015337	-	11593	12744	11156	10865	1.11	0.96	0.94												
<i>ytxK</i>	3015685	3016674	-	8150	8698	8717	8738	1.08	1.08	1.07												
<i>tpx</i>	3016735	3017238	-	14907	17332	17985	16927	1.16	1.21	1.14												
<i>ytfJ</i>	3017348	3017803	-	224	555	716	195	2.45	3.15	0.86												
<i>ytfI</i>	3017817	3018497	-	251	266	268	273	1.06	1.07	1.09												
<i>yteJ</i>	3018572	3019066	-	7316	10176	10495	7779	1.39	1.43	1.06												
<i>sppA</i>	3019079	3020086	-	8807	11938	12686	8766	1.36	1.44	1.00												
											914	Inter	3020089	3020435	3020262	15.2	16.3	8.3	0.0			
<i>ppnK_2</i>	3020272	3021075	+	4252	7263	8141	4762	1.72	1.92	1.12												
<i>ytcI</i>	3021107	3022696	-	4509	4040	4195	4842	0.90	0.93	1.07												
<i>ytcI</i>	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
<i>sspA</i>	3024484	3024693	-	4977	8174	9876	4595	1.64	1.99	0.92												
<i>ytbJ</i>	3024920	3025996	-	3267	2739	2688	3467	0.84	0.82	1.06												
<i>nifZ</i>	3026000	3027145	-	1684	1549	1452	1899	0.92	0.86	1.12												
<i>braB</i>	3027340	3028677	+	2056	1183	1064	1870	0.58	0.52	0.91												
<i>ezrA</i>	3028772	3030460	-	6273	6429	6170	5589	1.03	0.98	0.89												
<i>hisJ</i>	3030657	3031463	+	1103	789	789	1152	0.73	0.73	1.05												
<i>yttP</i>	3031460	3032083	-	198	234	204	173	1.19	1.03	0.88												
<i>ytsP</i>	3032464	3032700	+	5286	4393	4144	5233	0.83	0.78	0.99												
<i>ytrP</i>	3032738	3034477	-	1264	1107	1080	1210	0.88	0.86	0.96												
<i>rpsD</i>	3034772	3035374	+	19570	19015	17435	18827	0.97	0.89	0.96												
<i>tyrS</i>	3035645	3036913	-	7370	5803	5761	6956	0.79	0.78	0.95	918	tyrS	3035830	3036415	3036123	51.4	19.5	29.0	-0.2			P02
<i>acsA</i>	3037255	3038973	-	1810	2343	3059	1943	1.32	1.72	1.06												
<i>acuA</i>	3039134	3039766	+	2346	1092	1430	2016	0.47	0.60	0.86												
<i>acuB</i>	3039793	3040437	+	3301	1588	2187	3085	0.48	0.65	0.93												
<i>acuC</i>	3040434	3041597	+	2298	1284	1631	2295	0.56	0.71	1.00												
<i>ytxE</i>	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			
<i>ytxD</i>	3042326	3043144	-	2846	1572	1442	2610	0.56	0.51	0.91												
<i>ccpA</i>	3043207	3044211	-	5192	4568	4085	5071	0.88	0.79	0.98												
<i>aroA</i>	3044486	3045562	-	10065	9232	10002	9787	0.92	0.99	0.97												
<i>ytxJ</i>	3045798	3046124	-	4134	6434	6780	3361	1.56	1.65	0.81												
<i>ytxH</i>	3046148	3046606	-	6428	8257	8865	4596	1.29	1.39	0.71	923	ytxH	3046251	3046853	3046552	15.8	14.2	26.2	15.8			
<i>ytxG</i>	3046634	3047065	-	6936	8547	9428	4884	1.23	1.36	0.70												
<i>murC</i>	3047227	3048525	-	8834	8460	8059	9045	0.96	0.91	1.02												
<i>ytpT</i>	3048775	3050883	-	6904	5861	6010	7043	0.85	0.87	1.02												
<i>ytpS</i>	3050838	3051632	-	4793	3902	3873	4726	0.82	0.81	0.99												
<i>ytpR</i>	3051792	3052397	-	12476	11729	11472	12147	0.94	0.92	0.97												
<i>ytpQ</i>	3052413	3053222	-	9026	9424	9352	9379	1.04	1.04	1.04												
<i>ytpP</i>	3053237	3053560	-	6268	6361	6045	6466	1.01	0.96	1.02												
<i>ytoQ</i>	3053795	3054241	+	5687	8532	8464	5919	1.52	1.49	1.04												
<i>ytoP</i>	3054296	3055369	-	4456	3213	3348	4333	0.72	0.75	0.97												
<i>ytzB</i>	3055528	3055845	+	4388	7529	9006	4230	1.72	2.04	0.99												
<i>malS</i>	3055898	3057598	-	3769	4060	4322	3501	1.08	1.15	0.93												
<i>ytmP</i>	3057680	3058450	-	4239	4840	4916	4153	1.14	1.16	0.98												
<i>trmB</i>	3058596	3059237	-	4504	2251	1837	3930	0.50	0.41	0.87												
<i>ytxH</i>	3059444	3059722	+	167	256	283	157	1.57	1.75	0.93												
<i>ytmP</i>	3059723	3060532	-	2067	2215	1955	2154	1.08	0.95	1.04												
<i>amyX</i>	3060700	3062856	-	933	1180	1113	897	1.27	1.19	0.95												

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh				
<i>ytlR</i>	3062882	3063811	-	2138	2263	2079	2041	1.06	0.97	0.95											
<i>ytlQ</i>	3063860	3064774	-	2350	2157	2102	2350	0.92	0.89	1.00											
<i>ytlP</i>	3064800	3065351	-	2901	2447	2413	2832	0.85	0.84	0.98											
<i>ytkP</i>	3065500	3066435	+	3557	2435	2486	3579	0.69	0.70	1.00											
<i>ytlP</i>	3066469	3067860	-	3358	3907	3954	3488	1.16	1.18	1.03											
<i>ytlP</i>	3067957	3069255	+	1399	703	581	1314	0.55	0.44	0.93											
<i>ythQ</i>	3069294	3070451	-	2265	3131	3312	1988	1.38	1.46	0.88											
<i>ythP</i>	3070448	3071158	-	2272	3210	3542	1966	1.42	1.57	0.87											
<i>ytzE</i>	3071449	3071670	+	1459	1761	2959	1838	1.20	1.92	1.22											
<i>ytzF</i>	3071791	3072264	-	1501	1322	1293	1459	0.90	0.89	0.96											
<i>ytzG</i>	3072249	3072509	-	878	742	735	925	0.85	0.84	1.04											
<i>ytgP</i>	3072578	3074212	-	3032	2747	2588	3253	0.91	0.86	1.08											
<i>ytfP</i>	3074720	3075676	+	1392	1113	1103	1272	0.80	0.80	0.92											
<i>opuD</i>	3075865	3077403	+	2169	2177	2116	1999	1.01	0.98	0.92											
<i>yteV</i>	3077440	3077622	-	301	284	300	306	0.94	1.00	1.02											
<i>yteU</i>	3077690	3078358	-	571	559	592	628	0.98	1.04	1.10	926	yteU	3077599	3077793	3077696	0.1	0.2	-0.2	5.8		
<i>yteT</i>	3078380	3079666	-	312	258	286	333	0.83	0.92	1.07											
<i>yteS</i>	3079678	3080157	-	381	288	342	380	0.76	0.90	1.00											
<i>yteR</i>	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		
<i>yteQ</i>	3081307	3081798	-	225	182	207	286	0.81	0.92	1.28											
<i>yteP</i>	3081893	3082273	-	208	173	195	244	0.84	0.94	1.15											
<i>ytdP</i>	3082489	3084807	+	220	348	419	216	1.58	1.90	0.98											
<i>ytcQ</i>	3084848	3086317	-	836	344	451	775	0.41	0.54	0.93											
<i>ytcP</i>	3086370	3087230	-	567	382	381	602	0.67	0.67	1.06											
<i>yibQ</i>	3087437	3088042	-	308	273	286	302	0.89	0.93	0.97											
<i>bioI</i>	3088275	3089462	-	229	212	218	229	0.93	0.95	1.00											
<i>bioB</i>	3089531	3090538	-	254	234	255	261	0.92	1.00	1.02	929	bioB	3089618	3090084	3089851	30.1	5.8	49.3	0.1		P05
<i>bioD</i>	3090541	3091236	-	178	174	190	197	0.98	1.07	1.11	930	bioD	3091029	3091257	3091143	8.1	0.8	0.7	-0.2		
<i>bioF</i>	3091233	3092402	-	363	349	366	375	0.96	1.01	1.03											
<i>bioA</i>	3092392	3093738	-	258	243	256	262	0.94	0.99	1.02											
<i>bioW</i>	3093728	3094507	-	145	133	130	141	0.92	0.89	0.97											
<i>ytaP</i>	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		
<i>msmR</i>	3095831	3096865	+	1057	225	356	937	0.25	0.33	0.89											
<i>msmE</i>	3096899	3098179	+	330	149	236	277	0.48	0.69	0.81											
<i>amyD</i>	3098172	3099083	+	209	161	204	194	0.78	0.96	0.92											
<i>amyC</i>	3099080	3099910	+	278	233	318	244	0.84	1.13	0.87											
<i>melA</i>	3099930	3101228	+	486	367	467	418	0.76	0.95	0.87											
<i>ytfF</i>	3101250	3101456	-	2864	2778	2725	2812	0.97	0.95	0.98											
<i>leuS</i>	3101678	3104092	-	10072	8047	8104	10016	0.80	0.80	0.99											
<i>ytvB</i>	3104519	3104854	-	305	376	344	390	1.23	1.13	1.29											
<i>ytvA</i>	3105259	3106044	+	1481	1226	1368	1580	0.84	0.94	1.07	934	ytvA	3104850	3105112	3104981	9.3	9.5	1.9	1.3		
<i>yttB</i>	3106281	3107474	-	1111	862	800	973	0.81	0.73	0.88											
<i>yttA</i>	3107669	3108409	+	976	1315	1492	665	1.35	1.52	0.68											
<i>ytsD</i>	3108446	3110386	-	455	462	486	387	1.02	1.07	0.85											
<i>ytsC</i>	3110376	3111137	-	297	282	282	243	0.96	0.96	0.82											
<i>ytsB</i>	3111239	3112243	-	670	858	874	555	1.30	1.32	0.83											
<i>ytsA</i>	3112236	3112931	-	668	815	814	598	1.23	1.22	0.89											
<i>ytrF</i>	3113028	3114338	-	2670	2543	2266	2090	0.95	0.84	0.78											
<i>ytrE</i>	3114328	3115023	-	1668	1674	1522	1320	0.99	0.91	0.79											
<i>ytrD</i>	3115038	3116015	-	1733	1569	1392	1364	0.88	0.79	0.78											
<i>ytrC</i>	3116045	3117031	-	1539	1568	1299	1446	1.01	0.83	0.94	936	Inter	3115815	3116264	3116040	25.5	20.8	27.7	63.1		P01
<i>ytrB</i>	3117025	3117903	-	1443	1415	1188	1219	0.97	0.82	0.84	936	ytrC	3116274	3116655	3116465	25.6	30.2	13.3	15.2		
<i>ytrA</i>	3117896	3118288	-	1165	1078	870	919	0.91	0.74	0.78											
<i>ytzC</i>	3118614	3118886	-	520	539	651	406	1.01	1.22	0.78											
<i>ytaA</i>	3119048	3120016	+	1974	1771	1505	1958	0.90	0.76	0.99											
<i>ytaB</i>	3120013	3120597	+	3803	3343	3121	3419	0.89	0.82	0.90											
<i>ytpB</i>	3120587	3121690	-	4079	5192	5364	4771	1.30	1.34	1.18											
<i>ytpA</i>	3121711	3122490	-	5560	6942	6928	6024	1.26	1.27	1.08											
<i>ytoA</i>	3122539	3123054	+	569	737	741	649	1.30	1.30	1.15											
<i>ytnA</i>	3123299	3124690	-	7141	6559	6823	6476	0.92	0.96	0.91											
<i>asnB</i>	3124826	3126724	-	11795	10050	10197	12162	0.85	0.86	1.03	938	asnB	3126083	3126226	3126155	3.2	5.7	1.1	0.6		
<i>metK</i>	3126874	3128076	-	11583	9427	8254	11309	0.82	0.71	0.98											
<i>pckA</i>	3128579	3130162	+	3089	2689	2091	2681	0.88	0.66	0.87	939	Inter	3128123	3128283	3128203	2.7	4.5	0.6	0.6		
<i>ytmB</i>	3130201	3130443	-	3358	3059	3041	2667	0.91	0.91	0.79											
<i>ytmA</i>	3130495	3131268	-	992	861	860	994	0.87	0.87	0.99											
<i>ytlA</i>	3131419	3132108	+	236	216	231	274	0.91	0.98	1.17											
<i>ytlB</i>	3132105	3132422	+	116	116	135	104	1.01	1.17	0.90											
<i>ytlC</i>	3132435	3133217	+	161	137	146	179	0.86	0.91	1.12											

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB /$ wild	$\Delta abh /$ $\Delta abrB /$ wild	$\Delta abh /$ wild							AbrB		Abh	
wild	$\Delta abrB$	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$				
<i>ytlD</i>	3133192	3134004	+	277	294	283	298	1.06	1.03	1.08											
<i>ytkD</i>	3134031	3134507	-	811	592	502	692	0.73	0.62	0.85	941	ytkD	3133869	3134216	3134043		12.2	20.5	5.9	-0.7	
<i>ytkC</i>	3134716	3135120	-	315	282	362	274	0.90	1.15	0.87											
<i>dps</i>	3135286	3135723	-	9957	10632	12829	8020	1.07	1.29	0.80											
<i>ytkA</i>	3135986	3136423	-	4218	3861	4149	2842	0.92	0.99	0.67	943	Inter	3135586	3136052	3135819		25.7	8.3	9.6	0.7	
											944	Inter	3136351	3136562	3136457		3.9	9.0	0.8	-0.6	
<i>luxS</i>	3136543	3137016	-	4746	4416	4555	4683	0.93	0.96	0.99											
<i>yjiA</i>	3137145	3137372	+	656	565	522	595	0.86	0.79	0.91											
<i>yjiB</i>	3137369	3137932	-	4117	3105	3093	3719	0.76	0.75	0.90											
<i>rpmE2</i>	3138026	3138274	-	1089	661	920	542	0.61	0.85	0.49											
<i>ythA</i>	3138494	3139810	+	245	266	294	269	1.09	1.20	1.10											
<i>ythB</i>	3139854	3140894	+	394	475	518	375	1.20	1.31	0.95											
<i>ythC</i>	3140943	3141110	+	337	706	899	432	2.09	2.66	1.28											
<i>mntD</i>	3141125	3142012	-	1417	3606	3624	1442	2.51	2.51	1.01											
<i>mntC</i>	3142002	3143309	-	1676	4721	4733	1780	2.77	2.77	1.05											
<i>mntB</i>	3143315	3144067	-	1651	4882	4778	1726	2.92	2.85	1.04											
<i>mntA</i>	3144086	3145006	-	1560	4038	4009	1590	2.54	2.52	1.01											
<i>menC</i>	3145286	3146401	-	1227	969	1002	1199	0.79	0.82	0.97											
<i>menE</i>	3146398	3147858	-	1866	1556	1640	1803	0.84	0.88	0.96											
<i>menB</i>	3147949	3148764	-	13381	13128	13031	13429	0.98	0.97	1.00											
<i>ytxM</i>	3148799	3149623	-	2776	1782	1712	2703	0.64	0.62	0.97											
<i>menD</i>	3149611	3151353	-	3577	2216	2164	3417	0.62	0.61	0.95											
<i>menF</i>	3151350	3152765	-	5259	3431	3680	5212	0.65	0.70	0.99	945	Inter	3152552	3153239	3152896		61.6	94.6	59.3	44.1	P01
<i>yteA</i>	3153054	3153773	+	184	251	272	206	1.38	1.50	1.13											
<i>ytdA</i>	3153782	3154600	-	233	218	233	253	0.93	1.00	1.09											
<i>ytcA</i>	3154772	3156058	+	188	172	186	217	0.91	0.99	1.15											
<i>ytcB</i>	3156055	3157005	+	162	140	147	161	0.86	0.91	1.00											
<i>ytcC</i>	3157008	3158231	+	110	101	104	94	0.93	0.95	0.85	946	Inter	3158230	3158339	3158285		3.0	1.2	0.1	-0.4	
<i>ytxO</i>	3158305	3158736	-	123	97	101	102	0.79	0.82	0.83											
<i>cotS</i>	3158738	3159793	-	272	231	229	275	0.85	0.84	1.01											
<i>cotSA</i>	3159808	3160941	-	331	275	292	332	0.83	0.88	1.00											
<i>ytaA</i>	3161131	3162204	+	141	140	156	139	0.99	1.11	0.99	947	ytaA	3161103	3162096	3161600		57.7	81.0	83.7	185.0	P01
<i>ytaB</i>	3162284	3162751	+	394	271	324	294	0.69	0.82	0.74											
<i>glgP</i>	3162782	3165178	-	252	266	281	256	1.06	1.11	1.01											
<i>glgA</i>	3165165	3166619	-	322	338	361	330	1.05	1.12	1.02	948	glgA	3165693	3165802	3165748		0.4	0.6	0.7	3.9	
<i>glgD</i>	3166616	3167647	-	345	359	386	363	1.04	1.12	1.05											
<i>glgC</i>	3167671	3168813	-	240	247	265	254	1.03	1.10	1.06											
<i>glgB</i>	3168810	3170693	-	181	180	182	199	1.00	1.00	1.10	949	glgB	3170215	3170341	3170278		2.8	1.1	0.3	0.1	
<i>trmB-Ser2</i>	3171023	3171113	-	17668	20703	19996	17420	1.17	1.13	0.98											
<i>trmB-Ile2</i>	3171202	3171278	-	20103	27045	26053	18254	1.35	1.30	0.90											
<i>trmB-His</i>	3171378	3171453	-	5270	13564	11636	9571	2.52	2.22	1.71											
<i>trmB-Ser1</i>	3171741	3171832	-	12278	12685	13176	9760	0.98	1.06	0.85											
<i>trmB-Met1</i>	3171839	3171915	-	1906	1548	1270	1461	0.80	0.66	0.79											
<i>trmB-Leu1</i>	3172451	3172537	-	23732	22619	23692	19678	0.96	1.01	0.86											
<i>yuaJ</i>	3178345	3178923	+	1300	1016	833	1107	0.79	0.63	0.85											
<i>yuaI</i>	3178965	3179486	-	906	1323	1577	838	1.46	1.74	0.92	957	yuaI	3178847	3179092	3178970		13.9	7.9	3.5	-0.3	
<i>yuaG</i>	3179504	3181033	-	620	1314	1319	554	2.06	2.13	0.89											
<i>yuaF</i>	3181054	3181578	-	391	878	765	410	2.20	1.95	1.07											
<i>yuaE</i>	3181746	3182234	+	2761	3285	3780	2922	1.19	1.38	1.05											
<i>yuaD</i>	3182240	3182818	-	1448	2418	2339	1301	1.68	1.62	0.90	958	Inter	3182723	3182984	3182854		13.7	10.5	2.2	0.2	
<i>gbsB</i>	3182906	3184117	-	362	348	360	327	0.97	0.99	0.90											
<i>gbsA</i>	3184131	3185603	-	504	440	477	490	0.87	0.94	0.97											
<i>yuaC</i>	3185802	3186344	+	732	716	672	651	0.98	0.92	0.87	961	Inter	3186072	3186776	3186424		38.0	64.0	6.4	0.5	
<i>yuaB</i>	3186542	3187087	+	1128	17987	19456	513	16.49	17.66	0.46											
<i>yuaA</i>	3187453	3188121	+	527	574	615	500	1.07	1.17	0.96											
<i>yubG</i>	3188128	3189465	+	889	862	908	858	0.97	1.02	0.97											
<i>yubF</i>	3189501	3189764	-	11556	12520	12125	13309	1.08	1.05	1.15											
<i>yubE</i>	3189873	3190721	-	2225	2289	2170	2013	1.04	0.98	0.91	962	Inter	3189608	3190091	3189850		44.7	19.1	26.1	10.0	
											963	yubE	3190390	3190669	3190530		8.5	10.8	2.0	-0.7	
											963	Inter	3190680	3191060	3190870		19.8	10.9	14.5	-0.1	
<i>yubD</i>	3190882	3192417	-	553	383	400	562	0.71	0.73	1.01											
<i>yubC</i>	3192902	3193387	+	142	123	136	130	0.87	0.96	0.91											
<i>trnSL-Ala</i>	3193491	3193566	-	9920	12185	11824	10268	1.23	1.19	1.04											
<i>uppP</i>	3193674	3194504	-	3129	4585	5080	2916	1.49	1.66	0.93	964	Inter	3194250	3194834	3194542		46.2	68.9	59.8		

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

gene	Transcriptome analysis										ChAP-chip analysis						Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$																		
<i>yulD</i>	3198272	3198586	-	461	341	441	466	0.74	0.96	1.01											
<i>yulC</i>	3198604	3200061	-	1062	714	874	955	0.67	0.83	0.90											
<i>yulB</i>	3200066	3200842	-	1502	859	1021	1403	0.57	0.68	0.93											
<i>yuxG</i>	3200899	3202968	-	1276	579	760	1243	0.46	0.58	0.98											
<i>tlpB</i>	3203106	3205094	-	773	612	561	854	0.81	0.73	1.09											
<i>mcpA</i>	3205208	3207193	-	2567	4507	4086	2644	1.78	1.60	1.03											
<i>tlpA</i>	3207319	3209307	-	178	1345	1303	185	7.56	7.35	1.05	965	Inter	3207135	3207380	3207258	5.6	9.7	1.1	0.6		
											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		
<i>mcpB</i>	3209484	3211472	-	1866	2454	2280	1933	1.33	1.23	1.03											
<i>tgl</i>	3211630	3212367	+	303	256	259	285	0.85	0.85	0.95											
<i>yugU</i>	3212892	3213320	-	1033	1564	1582	856	1.51	1.53	0.81											
<i>yugT</i>	3213410	3215074	-	335	289	283	348	0.87	0.85	1.03	968	yugT	3214394	3214945	3214670	29.1	20.2	35.6	45.5		P01
<i>yugS</i>	3215201	3216505	-	358	309	337	359	0.87	0.94	1.00											
<i>yugP</i>	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
<i>yugO</i>	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		
<i>yugN</i>	3218875	3219279	-	2099	1791	2645	2204	0.85	1.25	1.05											
<i>yugM</i>	3219339	3219710	-	2038	1764	2415	2083	0.87	1.19	1.02											
<i>pgi</i>	3219769	3221124	-	15083	15067	15648	15834	1.00	1.04	1.05											
<i>yugK</i>	3221236	3222408	-	2722	2023	2147	2511	0.74	0.79	0.92											
<i>yugJ</i>	3222512	3223675	-	7745	10693	11063	8994	1.39	1.44	1.16											
<i>yuzA</i>	3223905	3224141	+	392	772	1089	337	1.99	2.80	0.87											
<i>yugI</i>	3224219	3224611	-	19585	16980	15293	18960	0.87	0.78	0.97											
<i>alaT</i>	3224813	3225973	-	7754	7073	7114	7056	0.91	0.92	0.91	972	akT	3224815	3225043	3224929	1.4	1.0	1.4	8.3		
<i>alaR</i>	3225974	3226474	-	6348	5630	5666	6041	0.89	0.89	0.95											
<i>yugF</i>	3226622	3227443	+	264	270	284	244	1.02	1.07	0.92											
<i>yugE</i>	3227472	3227738	-	3271	2305	2328	2734	0.71	0.71	0.84											
<i>patB</i>	3227819	3228982	+	4344	3926	4072	4206	0.91	0.94	0.97											
<i>kinB</i>	3229108	3230397	+	337	306	315	312	0.91	0.93	0.93											
<i>kapB</i>	3230443	3230829	+	2690	2749	2764	3028	1.03	1.03	1.13											
<i>kapD</i>	3230856	3231473	-	213	200	215	189	0.94	1.01	0.89											
<i>yuxJ</i>	3231684	3232862	+	217	232	237	225	1.08	1.10	1.05											
<i>pbpD</i>	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		
<i>yuxK</i>	3234850	3235263	+	2447	2243	1991	1919	0.92	0.82	0.78											
<i>yufK</i>	3235466	3236080	-	2576	2363	1905	2348	0.92	0.74	0.91											
<i>yufL</i>	3236201	3237802	+	1466	1115	1155	1571	0.76	0.79	1.07											
<i>yufM</i>	3237795	3238502	+	2804	2231	2200	2784	0.80	0.79	0.99											
<i>yufN</i>	3239001	3240053	+	177	179	182	209	1.01	1.03	1.19											
<i>yufO</i>	3240129	3241661	+	197	159	176	202	0.80	0.89	1.02											
<i>yufP</i>	3241654	3242700	+	265	262	273	294	0.99	1.03	1.11											
<i>yufQ</i>	3242701	3243660	+	361	351	360	422	0.97	1.00	1.16											
<i>maeN</i>	3243814	3245160	+	5755	1781	1903	5967	0.31	0.34	1.04											
<i>yufS</i>	3245196	3245411	-	561	509	561	546	0.91	1.00	0.98											
<i>mrpA</i>	3245642	3248047	+	3628	2627	2842	3443	0.72	0.78	0.95											
<i>mrpB</i>	3248040	3248471	+	3702	2775	2860	3617	0.75	0.77	0.98											
<i>mrpC</i>	3248471	3248812	+	3142	2452	2427	2946	0.78	0.77	0.94											
<i>mrpD</i>	3248805	3250286	+	3846	2990	3079	3625	0.78	0.80	0.94											
<i>mrpE</i>	3250292	3250768	+	2920	2104	2202	2925	0.72	0.76	1.00											
<i>mrpF</i>	3250768	3251052	+	2315	1644	1638	2226	0.71	0.71	0.96											
<i>mrpG</i>	3251036	3251410	+	1333	954	1027	1151	0.72	0.77	0.87											
<i>yuxO</i>	3251449	3251829	-	3395	3520	3360	3048	1.04	0.99	0.90											
<i>comA</i>	3251848	3252492	-	3694	4191	4007	3768	1.14	1.09	1.03											
<i>comP</i>	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		
<i>comX</i>	3254897	3255064	-	2441	1708	1658	3097	0.71	0.69	1.27											
<i>comQ</i>	3255052	3255951	-	2647	1880	1981	3214	0.71	0.75	1.22	980	comQ	3255024	3255303	3255164	6.6	2.7	3.9	15.2		
											981	Inter	3256027	3256170	3256099	4.3	1.2	0.7	-0.4		
<i>degQ</i>	3256136	3256276	-	201	138	155	163	0.69	0.77	0.82											
<i>yuzC</i>	3256737	3257105	+	658	490	492	701	0.75	0.75	1.08											
<i>yuxH</i>	3257081	3258310	-	3229	2482	2384	3224	0.77	0.74	0.99											
<i>yueK</i>	3258447	3259919	-	8069	7739	7902	8316	0.96	0.98	1.03											
<i>yueJ</i>	3259935	3260486	-	4830	4480	4638	5175	0.93	0.96	1.07											
<i>yueI</i>	3260583	3260981	-	3217	2554	2661	3362	0.80	0.84	1.05											
<i>yueH</i>	3261053	3261301	-	2815	2343	2351	2972	0.84	0.85	1.06											
<i>yueG</i>	3261374	3261595	-	2505	2036	2106	2459	0.81	0.84	0.98											
<i>yueF</i>	3261655	3262764	-	3736	3277	3219	3996	0.88	0.86	1.07											
<i>yuzE</i>	3262879	3263268	+	344	339	362	446	1.02	1.09	1.32											
<i>yuzF</i>	3263309	3263545	-	736	788	844	778	1.11	1.18	1.06											
<i>yueE</i>	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		
<i>yueD</i>	3264450	3265181	-	3688	4544	4596	3882	1.26	1.26	1.06											
<i>yueC</i>	3265244	3265699	-	1770	2939	2794	1716	1.73	1.60	0.97											
<i>yueB</i>	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		

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

gene	Transcriptome analysis									ChAP-chip analysis					Profile ID						
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start		end	center	Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$																		
<i>yukA</i>	3268958	3272581	-	1398	2121	2208	1360	1.57	1.60	0.96											
<i>yukB</i>	3272581	3273456	-	2099	2924	3182	2034	1.42	1.53	0.97											
<i>yukC</i>	3273484	3274839	-	1424	1750	2067	1389	1.25	1.47	0.97											
<i>yukD</i>	3274854	3275093	-	1724	2314	2835	1592	1.37	1.65	0.91											
<i>yukE</i>	3275237	3275479	-	17380	26177	27329	15749	1.51	1.57	0.91											
<i>yukF</i>	3275976	3277280	+	1022	839	840	960	0.83	0.83	0.94	984	Inter	3275288	3275975	3275632	56.7	64.5	19.7	4.5	P02	
<i>ald</i>	3277348	3278484	+	7869	14999	14701	7606	1.91	1.87	0.97	985	<i>yukF</i>	3276019	3276179	3276099	2.7	2.5	3.1	4.3		
<i>yuxI</i>	3278597	3278920	+	1740	4527	5503	2259	2.60	3.16	1.30											
<i>yukJ</i>	3278838	3279275	+	841	2287	2997	1073	2.72	3.57	1.28											
<i>dhbF</i>	3279544	3286680	-	1022	13001	12124	1045	12.72	11.77	1.02											
<i>dhbB</i>	3286700	3287638	-	1467	14108	13733	1647	9.62	9.33	1.12											
<i>dhbE</i>	3287666	3289285	-	1939	15282	14633	2207	7.88	7.55	1.14											
<i>dhbC</i>	3289314	3290510	-	2378	19242	18821	2822	8.09	7.92	1.19											
<i>dhbA</i>	3290536	3291321	-	2153	14379	14620	2514	6.68	6.79	1.17											
<i>yuiI</i>	3291515	3292459	-	1858	11557	11393	2225	6.22	6.14	1.20											
<i>yuiH</i>	3292598	3293194	-	593	996	884	569	1.68	1.48	0.95	987	Inter	3292237	3292737	3292487	35.7	41.9	8.2	1.5		
<i>yuiG</i>	3293295	3293897	+	1054	914	878	1011	0.87	0.83	0.96											
<i>yuiF</i>	3293967	3295295	-	872	580	564	734	0.66	0.65	0.84											
<i>pepA</i>	3295442	3296944	-	2913	3254	3294	2766	1.12	1.13	0.95											
<i>yuiD</i>	3297102	3297578	+	704	703	726	783	1.00	1.03	1.11											
<i>yuiC</i>	3297609	3298265	-	803	978	1032	662	1.21	1.27	0.81											
<i>yuiB</i>	3298369	3298689	-	1067	1820	1642	919	1.70	1.53	0.86											
<i>yuiA</i>	3298743	3298886	-	376	471	456	437	1.27	1.25	1.18											
<i>yumB</i>	3299059	3300279	-	652	1197	1332	640	1.87	2.06	1.02											
<i>yumC</i>	3300611	3301609	+	10904	10565	10473	11005	0.97	0.96	1.01											
<i>yuzG</i>	3301648	3301788	-	617	637	597	597	1.05	0.98	0.98											
<i>guaC</i>	3302067	3303047	+	1604	967	994	1599	0.68	0.68	1.00											
<i>paiB</i>	3303121	3303744	-	765	923	1018	775	1.20	1.32	1.01											
<i>paiA</i>	3303768	3304286	-	405	592	670	360	1.45	1.64	0.89											
<i>yutM</i>	3304624	3304986	-	9759	8769	9457	9432	0.90	0.97	0.97											
<i>dapF</i>	3305065	3305919	-	2986	1881	1830	2633	0.63	0.61	0.88											
<i>yutK</i>	3306042	3307256	-	3159	528	560	2471	0.17	0.18	0.78											
<i>yuzB</i>	3307393	3307629	-	722	540	528	676	0.75	0.73	0.94											
<i>yutJ</i>	3307892	3308884	+	5773	5628	4797	4921	0.99	0.83	0.86											
<i>yuzD</i>	3308986	3309312	-	1950	1709	1768	1629	0.88	0.90	0.83											
<i>yutI</i>	3309412	3309747	+	8689	8951	8814	8891	1.03	1.01	1.02											
<i>yuxL</i>	3309789	3311762	-	566	1180	1184	618	2.08	2.08	1.08											
<i>thrB</i>	3311870	3312799	-	1665	2491	2440	1425	1.49	1.44	0.85											
<i>thrC</i>	3312796	3313854	-	2190	3272	3129	1935	1.49	1.41	0.88											
<i>hom</i>	3313854	3315155	-	1443	2045	1890	1286	1.40	1.28	0.88											
<i>yutH</i>	3315356	3316375	-	248	239	240	243	0.97	0.97	0.98											
<i>yutG</i>	3316528	3317028	+	166	149	163	146	0.89	0.98	0.88											
<i>yutF</i>	3317055	3317825	-	7154	6101	6190	6954	0.85	0.86	0.97											
<i>yutE</i>	3317854	3318288	-	6726	5512	5389	6717	0.82	0.80	1.00											
<i>yutD</i>	3318312	3318620	-	5044	3793	3854	5144	0.75	0.77	1.02											
<i>yutC</i>	3318702	3319334	+	323	313	341	338	0.98	1.08	1.05											
<i>lipA</i>	3319350	3320246	-	11561	10426	10222	11250	0.90	0.88	0.97											
<i>yunA</i>	3320412	3321461	+	286	260	290	289	0.91	1.02	1.01	990	<i>yunA</i>	3320661	3320736	3320699	2.0	0.0	0.9	-0.1		
<i>yunB</i>	3321489	3322253	-	1122	950	932	1079	0.87	0.84	0.96											
<i>yunC</i>	3322326	3322631	-	1311	1370	1438	1446	1.06	1.11	1.11											
<i>yunD</i>	3322696	3324084	-	3211	3146	3497	3326	0.98	1.09	1.04											
<i>yunE</i>	3324104	3324925	-	2303	2145	2317	2459	0.93	1.01	1.07											
<i>yunF</i>	3324943	3325797	-	2056	2062	2266	2179	1.00	1.10	1.06											
<i>yunG</i>	3325829	3326176	-	1439	1230	1319	1605	0.85	0.92	1.12											
<i>pucH</i>	3326273	3327613	-	362	266	279	342	0.73	0.77	0.94											
<i>pucR</i>	3327788	3329383	+	390	351	353	341	0.91	0.91	0.88											
<i>pucJ</i>	3329528	3330877	+	341	327	328	351	0.96	0.96	1.03											
<i>pucK</i>	3330883	3332175	+	308	286	294	329	0.93	0.96	1.07											
<i>pucL</i>	3332188	3333672	+	295	260	255	300	0.88	0.86	1.02											
<i>pucM</i>	3333651	3334016	+	461	418	431	439	0.91	0.93	0.95											
<i>pucE</i>	3334777	3335298	-	247	171	172	258	0.69	0.70	1.04											
<i>pucD</i>	3335289	3337526	-	281	241	242	296	0.86	0.86	1.05											
<i>pucC</i>	3337527	3338360	-	253	211	222	286	0.84	0.88	1.14											
<i>pucB</i>	3338382	3338975	-	203	191	183	252	0.94	0.90	1.27											
<i>pucA</i>	3338972	3339964	-	160	142	149	172	0.89	0.93	1.09											
<i>yurG</i>	3340193	3341443	-	569	628	634	618	1.10	1.12	1.09											
<i>yurH</i>	3341460	3342698	-	347	329	332	388	0.95	0.96	1.13											
<i>yurI</i>	3343140	3344006	+	394	1052	1247	662	2.68	3.17	1.68	993	Inter	3342710	3343346	3343028	33.4	30.5	18.7	31.0	P01	
<i>yurJ</i>	3344040	3345143	-	903	791	777	917	0.88	0.86	1.01	994	Inter	3344852	3345539	3345196	21.7	17.4	16.6	66.8		

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c			
					wild	Δ abrB	Δ abh Δ abrB	Δ abh	Δ abrB/ wild	Δ abh/ Δ abrB/ wild	Δ abh/ wild							AbrB		Abh	
-type	Δ abh	-type	Δ abrB																		
yurK	3345265	3346053	+	943	788	900	931	0.84	0.96	1.00											
yurL	3346078	3346932	-	302	266	264	354	0.88	0.88	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	3348788	3350056	-	182	161	168	185	0.88	0.92	1.02											
yurP	3350137	3351123	-	307	259	253	264	0.84	0.82	0.86											
yurQ	3351339	3351713	-	4414	3312	3129	3770	0.75	0.71	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											
yurS	3353239	3353514	+	148	116	115	151	0.80	0.80	1.02											
yurT	3353578	3353961	-	2596	2053	1948	2541	0.78	0.74	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	3356471	3357691	-	11860	11944	12396	12077	1.01	1.05	1.02											
yurX	3357691	3359004	-	16456	16214	16736	16443	0.99	1.02	1.00											
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	3361632	3362300	-	9359	4864	4821	8752	0.52	0.51	0.93											
yusC	3362293	3363318	-	6884	3772	3704	6621	0.54	0.54	0.96											
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	3364418	3364858	-	1938	1858	2066	1992	0.96	1.07	1.03											
yusG	3364858	3365094	-	9553	10330	10127	9841	1.09	1.06	1.03											
gcvH	3365150	3365533	-	15723	17342	17292	17348	1.10	1.10	1.10											
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	3367866	3369041	-	956	643	722	899	0.67	0.76	0.94											
yusL	3369052	3371499	-	658	438	513	628	0.66	0.78	0.96											
yusM	3371767	3372675	-	229	192	219	242	0.84	0.96	1.06											
yusN	3373028	3373360	+	175	341	441	127	1.97	2.56	0.73											
yusO	3373519	3373986	+	1921	1552	1251	1487	0.81	0.64	0.77											
yusP	3373983	3375608	+	3429	2804	2460	2870	0.81	0.71	0.84	995 yusP	3374415	3374694	3374555	1.0	1.2	1.9	10.8			
yusQ	3375644	3376027	-	489	400	417	429	0.82	0.85	0.88											
yusR	3376046	3376435	-	352	307	311	377	0.87	0.88	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	3377827	3378114	-	1901	2773	2662	2077	1.46	1.39	1.09											
yusV	3378139	3378966	-	3378	5119	5094	4351	1.52	1.51	1.29	996 Inter	3379073	3379250	3379162	6.3	4.9	3.0	2.6			
yusW	3379184	3379621	-	320	302	359	299	0.94	1.12	0.94											
yusX	3379731	3381233	-	630	938	1245	658	1.49	1.99	1.03											
yusY	3381230	3381526	-	391	552	706	423	1.40	1.81	1.06											
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	3383692	81.4	102.5	175.0	282.4	PO1		
cssR	3384751	3385428	+	965	904	1028	1072	0.94	1.06	1.11											
cssS	3385425	3386780	+	1560	1405	1610	1734	0.90	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	3389809	3391257	+	187	192	194	195	1.03	1.04	1.04	1002 gerAB	3391177	3391320	3391249	5.0	0.3	1.3	0.3			
gerAB	3391226	3392323	+	223	227	256	232	1.02	1.15	1.04	1003 gerAB	3391772	3392357	3392065	13.9	6.1	17.7	63.3			
gerAC	3392320	3393441	+	171	159	161	159	0.93	0.94	0.93	1003 gerAC	3392367	3393003	3392685	33.9	51.9	15.2	8.2			
											1004 gerAC	3393200	3393547	3393374	8.7	16.2	3.1	1.2			
yvqC	3393449	3394084	-	1435	1287	1188	1276	0.89	0.83	0.88											
yvqE	3394062	3395144	-	1645	1551	1472	1661	0.94	0.89	1.01											
yvqF	3395141	3395866	-	1301	1394	1267	1309	1.08	0.97	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	3397576	3397956	-	1051	2029	2175	977	1.94	2.07	0.93											
yvqJ	3398118	3399386	-	263	1009	1226	305	3.84	4.66	1.16											
yvqK	3399563	3400144	-	1849	1213	1106	1685	0.66	0.60	0.91	1005 Inter	3399133	3399752	3399443	39.1	31.2	11.0	1.3			
yvrA	3400167	3401495	-	3002	1923	1752	2522	0.64	0.58	0.84											
yvrB	3401495	3402556	-	2110	1389	1305	1913	0.66	0.62	0.91											
yvrC	3402519	3403463	-	7748	5240	4730	6906	0.68	0.61	0.89											
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	3407379	3408488	-	533	445	415	518	0.84	0.78	0.96											
yvrI	3408492	3409067	-	255	271	278	262	1.06	1.09	1.03	1006 yvrI	3408534	3408813	3408674	7.7	5.6	11.9	8.9			
oxdC	3409496	3410653	+	547	1424	1456	660	2.64	2.69	1.18											
yvrL	3410714	3411124	+	406	673	678	484	1.70	1.68	1.20											

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID						
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c				
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh		
wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh					
<i>yvrN</i>	3411158	3412408	-	1397	4977	5079	1575	3.56	3.63	1.13												
<i>yvrO</i>	3412380	3413069	-	1638	5286	5521	1676	3.23	3.38	1.03												
<i>yvrP</i>	3413053	3414246	-	1718	5343	5394	1881	3.13	3.15	1.10												
<i>fhuC</i>	3414417	3415226	-	6261	7116	6566	5921	1.14	1.06	0.94	1008	Inter	3414093	3414491	3414292				21.3	25.7	7.2	0.6
<i>fhuG</i>	3415242	3416252	-	3674	3722	3511	3493	1.02	0.96	0.95												
<i>fhuB</i>	3416252	3417406	-	3787	4036	3649	3634	1.07	0.97	0.96												
<i>fhuD</i>	3417504	3418451	+	10017	10307	10190	9618	1.04	1.03	0.96												
<i>yvsH</i>	3418686	3420095	-	1347	759	628	1055	0.60	0.49	0.79	1009	yvsH	3419958	3420152	3420055				4.1	5.0	1.9	4.0
<i>sspJ</i>	3420495	3420635	-	106	342	463	102	3.49	4.73	0.98												
<i>yvsG</i>	3420802	3421284	+	1186	755	661	938	0.64	0.56	0.79												
<i>yvgJ</i>	3421384	3423237	+	1153	951	933	1076	0.83	0.81	0.93												
<i>yvgK</i>	3423265	3424191	-	2379	2168	1933	2298	0.91	0.81	0.97												
<i>yvgL</i>	3424302	3425084	+	2003	1420	1478	1841	0.70	0.74	0.92												
<i>yvgM</i>	3425188	3425748	+	1708	1394	1487	1597	0.81	0.87	0.94	1010	yvgM	3425245	3425405	3425325				2.3	2.0	1.7	6.8
<i>yvgN</i>	3425779	3426609	-	16196	20415	20532	18873	1.26	1.27	1.16												
<i>yvgO</i>	3426832	3427317	+	261	1900	3310	297	7.27	12.75	1.13	1011	Inter	3426384	3426867	3426626				35.0	45.7	25.1	5.1
<i>yvgP</i>	3427361	3429373	-	1819	2109	2275	2303	1.18	1.28	1.26												
<i>yvgQ</i>	3429628	3431343	-	1448	1375	1533	1347	0.95	1.06	0.93												
<i>yvgR</i>	3431369	3433186	-	1327	1176	1291	1212	0.89	0.97	0.91	1012	yvgR	3431501	3431797	3431649				7.0	3.6	11.1	14.7
<i>yvgS</i>	3433357	3435681	-	1319	1194	1253	1367	0.91	0.95	1.03												
<i>yvgT</i>	3435879	3436487	-	1957	883	800	1650	0.45	0.41	0.84												
<i>bdbC</i>	3436674	3437090	-	5934	4414	4252	4928	0.74	0.72	0.83												
<i>bdbD</i>	3437095	3437763	-	6459	4613	4517	5811	0.71	0.70	0.90												
<i>yvgW</i>	3437883	3439991	-	796	899	1029	924	1.15	1.29	1.14												
<i>yvgX</i>	3440151	3442562	-	1669	1275	1317	1515	0.77	0.79	0.90												
<i>yvgY</i>	3442643	3442852	-	1032	889	875	852	0.86	0.85	0.82												
<i>yvgZ</i>	3442926	3443231	-	2019	1561	1589	1482	0.78	0.78	0.72												
<i>yvaA</i>	3443359	3444435	+	9727	11846	14671	6956	1.22	1.51	0.72												
<i>acpD_2</i>	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
<i>yvaC</i>	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
<i>yvaD</i>	3447325	3447726	-	1120	1146	1218	943	1.02	1.09	0.84												
<i>yvaE</i>	3447723	3448082	-	1516	1540	1617	1300	1.02	1.07	0.86												
<i>yvaF</i>	3448079	3448651	-	734	721	747	678	0.98	1.02	0.92												
<i>yvaG</i>	3448762	3449556	-	1398	1543	1788	1114	1.10	1.28	0.79												
<i>ssrA</i>	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
<i>smgB</i>	3450278	3450748	-	4144	4810	4570	4012	1.17	1.10	0.96												
<i>mr</i>	3450893	3453232	-	4736	4485	4638	4215	0.95	0.98	0.89	1016	mr	3452309	3453013	3452661				38.0	23.3	47.1	7.2
											1016	mr	3453023	3453353	3453188				8.7	2.0	9.2	11.6
<i>yvaK</i>	3453251	3453997	-	4926	4259	4299	4424	0.86	0.87	0.90												
<i>secG</i>	3454123	3454353	-	16719	16382	15747	16596	0.98	0.94	0.99												
<i>yvaM</i>	3454502	3455272	+	241	476	477	231	1.97	1.98	0.95												
<i>yzcC</i>	3455312	3455545	-	300	276	292	316	0.92	0.98	1.06												
<i>yvaN</i>	3455697	3456104	+	1473	1248	1242	1049	0.84	0.84	0.71	1017	Inter	3455539	3455682	3455611				3.2	2.5	1.8	0.7
<i>yvaO</i>	3456134	3456553	+	1584	1714	1542	1401	1.08	0.97	0.88	1018	yvaP	3456237	3456634	3456436				22.1	5.0	20.9	21.4
<i>yvaP</i>	3456396	3457106	+	871	741	723	895	0.85	0.83	1.03	1018	yvaP	3456237	3456634	3456436				22.1	5.0	20.9	21.4
<i>yvaQ</i>	3457097	3458797	+	778	795	702	789	1.03	0.91	1.01												
<i>opuBD</i>	3458837	3459517	-	232	234	227	234	1.01	0.98	1.01												
<i>opuBC</i>	3459534	3460454	-	291	339	327	297	1.16	1.12	1.02												
<i>opuBB</i>	3460466	3461119	-	334	387	386	346	1.16	1.15	1.04												
<i>opuBA</i>	3461136	3462281	-	244	264	256	260	1.08	1.05	1.07												
<i>yvaV</i>	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
<i>yvaW</i>	3463320	3463796	+	94	7811	7577	122	82.89	80.41	1.30												
<i>yvaX</i>	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
<i>yvaY</i>	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
<i>yvaZ</i>	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
<i>yvbA</i>	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
<i>opuCD</i>	3466577	3467266	-	481	384	370	485	0.81	0.77	1.03												
<i>opuCC</i>	3467284	3468195	-	424	328	319	419	0.78	0.76	1.00												
<i>opuCB</i>	3468215	3468868	-	314	259	251	321	0.83	0.80	1.03												
<i>opuCA</i>	3468891	3470033	-	361	292	301																

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

gene				Transcriptome analysis							ChAP-chip analysis							Profile ID		
name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center	Binding intensity ^c				
				wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB /$ wild	$\Delta abh /$ $\Delta abrB /$ wild	$\Delta abh /$ wild						AbrB			Abh	
<i>yvbK</i>	3475074	3475541	+	1223	1631	1607	1654	1.35	1.31	1.36										
<i>eno</i>	3475586	3476878	-	18568	16553	17242	18027	0.89	0.93	0.97										
<i>pgm</i>	3476908	3478443	-	22065	20155	21195	21827	0.91	0.96	0.99										
<i>tpiA</i>	3478436	3479197	-	16935	15416	16148	17124	0.91	0.95	1.01										
<i>pgk</i>	3479228	3480412	-	19221	17608	18263	19534	0.92	0.95	1.02										
<i>gapA</i>	3480729	3481736	-	22951	17106	17978	22756	0.75	0.78	0.99										
<i>cggR</i>	3481783	3482805	-	5272	4057	4380	5878	0.78	0.83	1.11										
<i>araE</i>	3483103	3484497	-	591	443	553	514	0.75	0.93	0.88										
<i>araR</i>	3484635	3485789	+	2444	1799	1799	2324	0.74	0.74	0.95										
<i>yvbT</i>	3485838	3486848	-	1290	1170	1075	1304	0.91	0.84	1.01										
<i>yvbU</i>	3487005	3487883	-	292	293	257	351	1.00	0.88	1.19										
<i>yvbV</i>	3487983	3488900	+	573	426	418	558	0.74	0.73	0.97										
<i>yvbW</i>	3488941	3490284	-	821	637	644	717	0.78	0.79	0.88	1024	yvbW	3489930	3490090	3490010	2.7	3.1	5.6	4.3	
<i>yvbX</i>	3490686	3491720	-	1811	1620	1652	1659	0.91	0.91	0.92										
<i>yvbY</i>	3491828	3492550	-	14692	11386	13049	14090	0.78	0.89	0.96										
<i>yvfW</i>	3492550	3493989	-	11965	8862	10194	11770	0.74	0.85	0.98										
<i>yvfV</i>	3494016	3494732	-	10466	6991	8042	9948	0.67	0.77	0.95										
<i>yvfU</i>	3494907	3495509	-	889	1042	1099	798	1.17	1.24	0.89										
<i>yvfT</i>	3495526	3496512	-	664	1045	999	709	1.58	1.51	1.07										
<i>yvfS</i>	3496645	3497382	-	375	596	596	380	1.58	1.59	1.02										
<i>yvfR</i>	3497383	3498288	-	273	527	482	271	1.93	1.77	1.00										
											1025	Inter	3498243	3498590	3498417	16.0	14.8	13.7	8.9	
<i>rsbQ</i>	3498572	3499381	+	1650	1278	1165	1604	0.77	0.70	0.97										
<i>rsbP</i>	3499417	3500628	+	2442	1638	1517	2154	0.67	0.62	0.88										
<i>yvfO</i>	3500682	3501971	-	994	608	842	881	0.63	0.88	0.88										
<i>lacA</i>	3502051	3504114	-	1469	978	1535	1501	0.67	1.05	1.02										
<i>yvfM</i>	3504133	3504984	-	1218	683	1098	1252	0.56	0.91	1.03										
<i>yvfL</i>	3504988	3506244	-	1787	827	1318	1691	0.46	0.71	0.95										
<i>yvfK</i>	3506284	3507549	-	2449	781	1476	2107	0.32	0.57	0.86	1026	yvfK	3506539	3507226	3506883	6.3	2.7	10.6	82.3	
<i>lacR</i>	3507690	3508682	-	501	350	361	475	0.70	0.72	0.94										
<i>yvfI</i>	3508862	3509389	-	1927	1734	1582	1659	0.90	0.82	0.86										
<i>yvfH</i>	3509811	3511502	+	3262	2607	3650	2644	0.80	1.10	0.81										
<i>sigL</i>	3511529	3512839	-	3172	2418	3019	2991	0.77	0.94	0.94										
<i>yvfG</i>	3512918	3513136	+	5014	3814	3831	4677	0.76	0.76	0.93										
<i>yvfF</i>	3513146	3514114	-	297	2551	2894	267	8.58	9.71	0.90										
<i>yvfE</i>	3514093	3515259	-	476	3615	3937	455	7.57	8.24	0.95										
<i>yvfD</i>	3515264	3515914	-	400	1914	2144	425	4.80	5.39	1.07										
<i>yvfC</i>	3515911	3516519	-	449	2136	2490	477	4.75	5.52	1.06	1028	yvfC	3515957	3516253	3516105	2.2	0.4	1.7	15.3	
<i>yvfB</i>	3516516	3517553	-	386	2097	2470	409	5.43	6.40	1.06										
<i>yvfA</i>	3517703	3518032	-	1132	4188	4958	995	3.75	4.46	0.87										
<i>yveT</i>	3518029	3519063	-	568	4133	4736	552	7.29	8.36	0.97										
<i>yveS</i>	3519060	3520136	-	466	2840	3311	453	6.09	7.12	0.98										
<i>yveR</i>	3520141	3521175	-	452	3143	3512	498	6.95	7.78	1.10										
<i>yveQ</i>	3521200	3522303	-	558	2983	3382	526	5.41	6.13	0.94										
<i>yveP</i>	3522300	3523454	-	345	2216	2532	361	6.44	7.38	1.06										
<i>yveO</i>	3523447	3524283	-	382	2443	2700	380	6.41	7.09	1.00										
<i>yveN</i>	3524280	3525425	-	584	3924	4381	535	6.75	7.55	0.92	1029	yveN	3524270	3524447	3524359	3.9	1.7	4.8	1.1	
<i>yveM</i>	3525437	3527233	-	434	2029	2311	431	4.68	5.33	1.00										
<i>yveL</i>	3527492	3528175	-	325	2903	2830	304	8.99	8.80	0.94										
<i>yveK</i>	3528181	3528885	-	349	3084	2790	317	8.81	7.97	0.90										
											1032	Inter	3528707	3529292	3529000	18.8	19.9	4.7	-0.6	P03
<i>slr</i>	3529131	3529589	+	239	575	559	238	2.40	2.33	0.99										
<i>pnbA</i>	3529665	3531134	+	787	7891	8855	1351	10.08	11.32	1.71	1032	pnbA	3529302	3530142	3529722	45.5	62.1	25.8	8.0	
<i>padC</i>	3531355	3531840	-	545	749	956	629	1.41	1.78	1.13										
<i>yveG</i>	3531863	3532150	-	275	494	571	427	1.81	2.07	1.55										
<i>yveF</i>	3532226	3532318	-	344	603	782	497	1.85	2.33	1.46										
<i>racX</i>	3532449	3533132	-	1824	5104	5635	1678	2.82	3.12	0.92										
<i>pbpE</i>	3533148	3534503	-	1620	4813	5237	1673	2.97	3.26	1.04										
<i>sacB</i>	3535042	3536463	+	197	137	154	146	0.70	0.79	0.75	1033	sacB	3534845	3535412	3535129	23.8	5.9	8.9	-0.1	
<i>yveB</i>	3536537	3538087	+	246	209	221	241	0.85	0.90	0.98										
<i>yveA</i>	3538195	3539757	+	285	368	421	285	1.29	1.48	1.00										
<i>yvdT</i>	3539852	3540436	+	2597	1973	1936	2805	0.76	0.75	1.08										
<i>yvdS</i>	3540518	3540853	+	445	364	360	608	0.82	0.81	1.37										
<i>yvdR</i>	3540853	3541173	+	584	529	561	668	0.91	0.96	1.14										
<i>yvdQ</i>	3541209	3541721	-	361	581	671	387	1.65	1.91	1.10										
<i>yvdP</i>	3541973	3543316	-	245	227	233	246	0.93	0.95	1.00	1034	yvdP	3542494	3542925	3542710	16.7	5.9	17.6	10.6	
<i>yvdO</i>	3543672	3544634	+	180	187	181	210	1.04	1.00	1.17										
<i>trnQ-Arg</i>	3544916	3544994	-	11605	12184	13213	8282	1.05	1.14	0.69										
<i>clpP</i>	3545264	3545857	+	14661	18917	19167	17609	1.30	1.31	1.20										
<i>pgcM</i>	3545903	3546583	-	884	671	707	817	0.76	0.80	0.92										
<i>malL</i>	3546580	3548265	-	850	614	674	834	0.73	0.80	0.98										
<i>yvdK</i>	3548258	3550531	-	881	582	650	839	0.67	0.75	0.95	1035	yvdK	3548682	3548961	3548822	5.1	3.8	9.7	5.3	
<i>yvdJ</i>	3550509	3551393	-	725	493	557	700	0.68	0.77	0.96										

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$														
<i>yvdI</i>	3551399	3552235	-	676	454	550	643	0.68	0.82	0.95											
<i>yvdH</i>	3552236	3553543	-	535	385	448	554	0.72	0.84	1.04											
<i>yvdG</i>	3553583	3554836	-	584	379	437	568	0.65	0.75	0.97											
<i>yvdF</i>	3554932	3556701	-	403	374	444	398	0.93	1.10	0.99											
<i>yvdE</i>	3556814	3557764	-	273	267	310	280	0.98	1.14	1.03											
<i>yvdD</i>	3557970	3558545	-	4499	3293	3631	3953	0.73	0.81	0.88											
<i>yvdC</i>	3558662	3558982	+	2623	1826	1960	2048	0.69	0.74	0.78											
<i>yvdB</i>	3559009	3560601	-	611	526	552	605	0.86	0.91	0.99											
<i>yvdA</i>	3560620	3561213	-	326	250	277	311	0.77	0.85	0.95											
<i>yvcT</i>	3561596	3562573	+	6723	7887	8247	7401	1.17	1.23	1.11	1037 yvcT	3561925	3562289	3562107	8.0	1.9	12.0	25.9			
<i>yvcS</i>	3562611	3564551	-	1650	1998	1994	1288	1.21	1.21	0.78											
<i>yvcR</i>	3564526	3565305	-	2621	3392	3302	2072	1.30	1.26	0.79											
<i>yvcQ</i>	3565388	3566458	-	2005	2588	2522	1519	1.29	1.25	0.76											
<i>yvcP</i>	3566452	3567165	-	1618	2184	1937	1306	1.35	1.20	0.80											
<i>yvcN</i>	3567557	3568321	-	5167	5798	5543	5480	1.12	1.07	1.06											
<i>crh</i>	3568322	3568579	-	3044	2999	2907	3232	0.99	0.96	1.06											
<i>yvcL</i>	3568603	3569553	-	4537	4629	4689	4562	1.02	1.03	1.00											
<i>yvcK</i>	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			
<i>yvcJ</i>	3570531	3571418	-	4867	4926	5140	4935	1.01	1.06	1.01											
<i>yvcI</i>	3571443	3571919	-	4106	4060	3710	4193	0.99	0.90	1.02											
<i>trxB</i>	3572237	3573187	-	8299	7956	8251	9511	0.98	1.01	1.14	1040 Inter	3571887	3572166	3572027	10.9	13.7	0.8	0.2			
<i>yvcE</i>	3573393	3574814	-	12188	13696	12704	13202	1.12	1.04	1.08											
<i>yvcD</i>	3575195	3576649	-	3874	3522	3244	3388	0.91	0.84	0.88											
<i>yvcC</i>	3576775	3578544	-	2511	2639	2487	2236	1.05	0.99	0.89											
<i>yvcA</i>	3578709	3579068	-	555	1705	2381	556	3.08	4.09	0.99											
<i>yvcB</i>	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			
<i>yvcA</i>	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	
<i>hisI</i>	3581966	3582595	-	546	410	417	564	0.75	0.76	1.03											
<i>hisF</i>	3582592	3583350	-	379	278	313	358	0.73	0.83	0.94											
<i>hisA</i>	3583347	3584084	-	401	283	329	418	0.71	0.82	1.04											
<i>hisH</i>	3584081	3584719	-	680	519	557	645	0.77	0.82	0.97											
<i>hisB</i>	3584720	3585304	-	478	380	426	475	0.80	0.89	0.99											
<i>hisD</i>	3585301	3586584	-	330	253	277	327	0.76	0.84	0.99											
<i>hisG</i>	3586581	3587222	-	260	197	223	282	0.76	0.86	1.10											
<i>hisZ</i>	3587215	3588390	-	432	378	389	475	0.88	0.90	1.10											
<i>yvpB</i>	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	
<i>yvpA</i>	3589633	3590298	+	895	554	1349	904	0.62	1.51	1.01											
<i>yvoF</i>	3590318	3590836	-	3998	3384	3439	3989	0.85	0.86	1.00											
<i>hprP</i>	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			
<i>yvoD</i>	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	
<i>lgt</i>	3592449	3593258	-	4928	3848	3980	4767	0.78	0.81	0.97											
<i>hprK</i>	3593272	3594204	-	5318	4201	4334	5122	0.79	0.82	0.96											
<i>nagA</i>	3594386	3595576	+	2355	1988	2065	2046	0.84	0.88	0.87	1047 nagA	3594191	3594589	3594390	8.0	17.8	8.0	11.2			
<i>nagB</i>	3595573	3596301	+	3649	3192	3278	3039	0.87	0.90	0.83											
<i>yvoA</i>	3596319	3597050	+	2237	2255	2321	1969	1.01	1.04	0.88											
<i>yvnB</i>	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			
<i>yvnA</i>	3601104	3601577	+	224	916	709	179	4.08	3.13	0.84											
<i>cypX</i>	3601618	3602835	-	581	2568	2621	454	4.40	4.50	0.78											
<i>yvmC</i>	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			
<i>yvmB</i>	3604023	3604532	+	859	593	694	746	0.69	0.81	0.86											
<i>yvmA</i>	3604553	3605764	+	520	457	486	535	0.89	0.94	1.04											
<i>yvlD</i>	3605792	3606151	-	5547	7092	7719	5549	1.27	1.37	0.99											
<i>yvlC</i>	3606153	3606350	-	10451	12317	13572	10364	1.18	1.30	0.99											
<i>yvlB</i>	3606355	3607452	-	6045	7928	8681	6003	1.31	1.44	0.99											
<i>yvlA</i>	3607477	3607803	-	2830	4192	4278	2980	1.49	1.54	1.06											
<i>yvkN</i>	3608021	3608251	+	182	176	177	170	0.97	0.97	0.93											
<i>yvzB</i>	3608450	3608932	-	438	462	481	484	1.06	1.10	1.10											
<i>uvrA</i>	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			
<i>uvrB</i>	3611975	3613960	-	3096	2741	3611	3261	0.89	1.17	1.05											
<i>csbA</i>	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			
<i>yvkC</i>	3614823	3617318	+	282	737	791	266	2.62	2.81	0.94											
<i>yvkB</i>	3617394	3617963	+	940	1151	1137	847	1.22	1.21	0.90											
<i>yvkA</i>	3617994	3619328	+	570	645	655	544	1.13	1.15	0.96											
<i>minJ</i>	3619376	3620569	-	2022	1983	1852	2106	0.98	0.92	1.04											
<i>yvzD</i>	3620648	3620986	-	700	862	660	900	1.24	0.96	1.30											
<i>yvjB</i>	3621386	3622828	-	353	569	658	335	1.60	1.85	0.94	1053 Inter	3621204	3621449	3621327	8.3	6.7	-1.5	-0.4			

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

gene				Transcriptome analysis						ChAP-chip analysis						Profile ID				
name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
				wild	Δ abrB	Δ abh Δ abrB	Δ abh	Δ abrB/ wild	Δ abh/ Δ abrB/ wild	Δ abh/ wild							AbrB		Abh	
																	wild -type	Δ abh	wild -type	Δ abrB
<i>ftsX</i>	3622968	3623858	-	4539	4926	4479	4693	1.09	0.99	1.03	1054	Inter	3622785	3622928	3622857		4.7	2.3	0.7	0.3
<i>ftsE</i>	3623851	3624537	-	5513	5698	5200	5845	1.03	0.95	1.06	1055	<i>ftsE</i>	3623907	3624492	3624200		21.4	23.6	10.0	2.6
											1055	Inter	3624502	3624866	3624684		14.3	14.5	6.2	0.2
<i>cccB</i>	3624771	3625109	-	7688	7797	7497	6929	1.02	0.98	0.90										
<i>yvjA</i>	3625158	3626003	-	1197	2494	2193	1408	2.08	1.79	1.17										
<i>prfB</i>	3626169	3627270	-	8022	8393	8043	7981	1.05	1.00	1.00										
<i>secA</i>	3627340	3629865	-	8874	9308	9230	9036	1.05	1.04	1.02										
<i>yvyD</i>	3630033	3630602	-	6741	9578	11654	5269	1.42	1.73	0.77	1056	<i>yvyD</i>	3630282	3630476	3630379		1.9	3.8	5.0	7.1
<i>flhT</i>	3631180	3631521	-	4776	6890	6317	5300	1.46	1.33	1.12										
<i>flhS</i>	3631518	3631919	-	3491	5015	4841	3630	1.44	1.39	1.04										
<i>flhD</i>	3631941	3633437	-	4670	6700	6238	5267	1.44	1.34	1.13	1057	<i>flhD</i>	3632305	3632516	3632411		2.7	7.3	2.3	2.2
<i>yvyC</i>	3633455	3633784	-	1514	1774	1725	1726	1.17	1.14	1.14										
<i>hag</i>	3634017	3634931	-	21033	26756	26939	24024	1.27	1.28	1.14										
<i>csrA</i>	3635076	3635300	-	3586	2537	2444	3265	0.71	0.68	0.91										
<i>yviF</i>	3635294	3635725	-	1489	1057	1048	1460	0.71	0.70	0.98										
<i>yviE</i>	3635746	3636321	-	998	954	848	930	0.96	0.85	0.91										
<i>flgL</i>	3636368	3637264	-	4105	4584	4398	4254	1.12	1.07	1.03										
<i>flgK</i>	3637275	3638798	-	2076	2371	2152	2437	1.15	1.04	1.18										
<i>yvyG</i>	3638817	3639299	-	3845	4091	3737	4062	1.07	0.97	1.05										
<i>flgM</i>	3639315	3639581	-	4691	5758	5160	4721	1.25	1.10	1.00										
<i>yvyF</i>	3639662	3640081	-	1734	2207	1827	1816	1.28	1.04	1.04										
<i>comFC</i>	3640155	3640844	-	908	810	712	917	0.89	0.78	1.01										
<i>comFB</i>	3640841	3641137	-	1276	1042	1029	1210	0.82	0.81	0.95										
<i>comFA</i>	3641197	3642588	-	343	335	344	362	0.98	1.00	1.05										
<i>yviA</i>	3642694	3643539	-	2679	2109	1967	2574	0.79	0.73	0.96										
<i>degU</i>	3643637	3644326	-	5903	5674	5695	5274	0.96	0.96	0.89										
<i>degS</i>	3644409	3645566	-	3252	2777	2961	3147	0.85	0.91	0.97										
<i>yvyE</i>	3645783	3646436	+	2649	2367	1939	2664	0.89	0.73	1.00										
<i>yvhJ</i>	3646436	3647611	+	4833	4467	3984	4673	0.92	0.82	0.97	1059	<i>yvhJ</i>	3647435	3647578	3647507		1.9	1.7	2.4	3.5
<i>tagO</i>	3647684	3648760	-	3419	3300	2940	3753	0.97	0.86	1.10	1060	<i>tagO</i>	3647741	3647952	3647847		7.9	2.4	2.2	0.9
<i>tuaH</i>	3648905	3650098	-	365	372	382	375	1.02	1.05	1.03										
<i>tuaG</i>	3650127	3650885	-	475	418	446	460	0.89	0.94	0.96	1061	<i>tuaG</i>	3650155	3650349	3650252		8.2	6.1	1.9	0.1
<i>tuaF</i>	3650909	3651589	-	471	385	438	443	0.82	0.93	0.94										
<i>tuaE</i>	3651618	3653084	-	506	509	525	537	1.00	1.04	1.06	1062	<i>tuaE</i>	3651702	3652015	3651859		11.3	4.4	11.7	1.1
<i>tuaD</i>	3653169	3654554	-	486	434	474	460	0.89	0.98	0.95										
<i>tuaC</i>	3654616	3655785	-	264	238	239	282	0.90	0.91	1.07										
<i>tuaB</i>	3655782	3657233	-	450	458	477	434	1.02	1.06	0.96										
<i>tuaA</i>	3657383	3657922	-	157	161	166	153	1.03	1.06	0.97	1063	<i>tuaA</i>	3657788	3657999	3657894		3.6	6.2	0.9	0.1
<i>lytC</i>	3658149	3659639	-	2264	2529	2359	2944	1.12	1.04	1.29	1064	<i>lytC</i>	3658757	3658866	3658812		3.4	0.5	0.1	0.0
											1065	Inter	3659539	3659767	3659653		7.3	2.1	1.8	0.9
<i>lytB</i>	3659678	3661795	-	2745	2889	2533	3637	1.05	0.92	1.32	1066	<i>lytB</i>	3660185	3660600	3660393		15.4	2.0	6.1	2.4
											1067	<i>lytB</i>	3660696	3660957	3660827		0.5	-0.8	0.1	13.8
<i>lytA</i>	3661819	3662127	-	2907	2794	2549	3568	0.96	0.87	1.22										
											1068	Inter	3662210	3662334	3662272		5.0	2.5	0.7	0.7
<i>lytR</i>	3662311	3663231	+	6078	9151	9161	6360	1.51	1.51	1.05										
<i>yvyH</i>	3663271	3664413	-	3123	1798	1748	2803	0.58	0.56	0.90										
<i>gtaB</i>	3664659	3665537	+	11831	10012	10701	10693	0.85	0.90	0.90	1069	<i>gtaB</i>	3665336	3665666	3665501		5.1	3.4	7.4	6.4
											1070	Inter	3665948	3666210	3666079		6.6	9.4	1.4	2.0
<i>ggaB</i>	3666239	3668941	-	605	740	751	1238	1.20	1.22	2.02	1071	<i>ggaB</i>	3666917	3667264	3667091		9.0	11.3	2.4	3.6
											1072	<i>ggaB</i>	3667631	3667723	3667677		2.9	2.2	0.2	0.7
<i>ggaA</i>	3669065	3670405	-	439	509	490	774	1.15	1.11	1.75	1074	<i>ggaA</i>	3669416	3670137	3669777		43.9	23.4	13.7	2.9
											1074	<i>ggaA</i>	3670147	3670528	3670338		10.2	3.5	3.5	4.3
											1075	Inter	3670659	3671140	3670900		12.9	9.1	4.0	4.4
											1075	Inter	3671150	3671922	3671536		80.2	69.8	64.8	68.1
											1076	Inter	3672306	3672687	3672497		6.0	2.6	8.0	7.4
<i>tagH</i>	3672594	3674177	-	6598	6042	6020	6818	0.92	0.91	1.03										
<i>tagG</i>	3674197	3675024	-	4002	4057	3638	4516	1.02	0.91	1.13										
<i>tagF</i>	3675189	3677429	-	4292	3813	3471	4260	0.89	0.80	0.99	1077	<i>tagF</i>	3675757	3676359	3676058		37.4	19.6	25.1	2.7
											1078	<i>tagF</i>	3676692	3676903	3676798		5.9	2.5	1.7	0.0
											1079	<i>tagF</i>	3677151	3677668	3677410		16.8	15.2	0.7	-1.0
<i>tagE</i>	3677429	3679450	-	3955	3445	3128	4013	0.87	0.79	1.01										
<i>tagD</i>	3679611	3680000	-	6262	6943	6064	6169	1.11	0.97	0.98										
<i>tagA</i>	3680400	3681170	+	3152	2710	2472	2959	0.86	0.78	0.94	1080	Inter	3679837	3680524	3680181		26.2	43.0	12.7	1.5
<i>tagB</i>	3681203	3682348	+	1767	1363	1159	1716	0.78	0.66	0.98	1081	<i>tagA</i>	3680738	3681391	3681065		28.7	47.4	14.6	1.1
<i>tagC</i>	3682468	3683796	+	452	308	331	338	0.68	0.73</											

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh				
<i>ywtG</i>	3691560	3692933	-	1081	632	881	632	0.59	0.83	0.58	1085 Inter	3692961	3693307	3693134	10.9	15.9	0.4	-0.3			
<i>ywtF</i>	3693266	3694234	+	3198	3334	3238	3103	1.04	1.01	0.97											
<i>ywtE</i>	3694390	3695250	+	4994	3816	4290	5139	0.76	0.86	1.03											
<i>ywtD</i>	3695284	3696525	-	1803	2128	2087	2253	1.19	1.16	1.24											
<i>ywtC</i>	3696666	3696833	-	238	163	155	263	0.68	0.65	1.11											
<i>ywtB</i>	3696848	3697990	-	367	202	228	396	0.55	0.62	1.09											
<i>ywtA</i>	3698009	3698458	-	751	425	553	732	0.57	0.74	0.98											
<i>ywsC</i>	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			
<i>rhsR</i>	3700438	3701418	+	19128	5873	9899	20596	0.30	0.48	1.07	1090 rhsR	3701291	3701501	3701396	2.6	5.8	4.3	5.2			
<i>rhsK</i>	3701420	3702301	+	20943	6849	11352	21813	0.31	0.50	1.04											
<i>rhsD</i>	3702298	3702693	+	18453	3136	8237	18222	0.16	0.42	0.98											
<i>rhsA</i>	3702709	3704190	+	24106	7008	12751	24152	0.28	0.50	1.00											
<i>rhsC</i>	3704192	3705160	+	19886	6056	10947	20447	0.29	0.52	1.03											
<i>rhsB</i>	3705172	3706089	+	25093	11068	15540	26837	0.43	0.60	1.07	1091 rhsB	3705762	3706143	3705953	2.5	2.9	4.3	12.7			
<i>ywsB</i>	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			
<i>ywsA</i>	3706863	3707159	+	1415	485	673	1030	0.34	0.48	0.73											
<i>ywrO</i>	3707199	3707726	-	2975	6325	6068	3079	2.19	2.06	1.04											
<i>alsD</i>	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			
<i>alsS</i>	3708655	3710370	-	397	239	254	406	0.61	0.64	1.02											
<i>alsR</i>	3710525	3711433	+	898	1249	1243	939	1.42	1.40	1.05											
<i>ywrK</i>	3711644	3712972	+	327	332	349	329	1.01	1.07	1.00											
<i>ywrJ</i>	3713029	3713706	-	237	218	244	230	0.92	1.03	0.97											
<i>cotB</i>	3713766	3714908	-	241	211	226	219	0.88	0.94	0.92											
<i>cotH</i>	3715036	3716124	-	272	224	242	243	0.83	0.89	0.89											
<i>cotG</i>	3716265	3716852	+	289	230	280	224	0.80	0.97	0.77	1093 cotG	3716387	3716530	3716459	0.7	3.0	1.6	4.3			
<i>ywrF</i>	3717026	3717643	+	1731	2216	2747	2084	1.29	1.60	1.20											
											1094 Inter	3717543	3717822	3717683	9.4	14.2	4.6	2.6			
<i>ywrE</i>	3717821	3718156	+	1152	1831	1677	1197	1.60	1.48	1.05											
<i>ywrD</i>	3718161	3719738	-	223	183	188	245	0.82	0.84	1.12											
<i>ywrC</i>	3719952	3720428	+	1142	729	717	1003	0.64	0.63	0.88											
<i>ywrB</i>	3720442	3721035	+	933	760	747	928	0.82	0.81	1.00											
<i>ywrA</i>	3721032	3721568	+	1145	957	972	1084	0.84	0.85	0.95											
<i>ywqO</i>	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			
<i>ywqN</i>	3721813	3722358	-	372	333	352	384	0.89	0.94	1.03	1095 ywqN	3722014	3722616	3722315	27.4	31.3	34.8	21.2	P01		
<i>ywqM</i>	3722481	3723362	+	407	321	343	383	0.81	0.85	0.95											
<i>ywqL</i>	3723447	3724163	-	1927	3382	3613	1819	1.76	1.85	0.94											
<i>ywqK</i>	3724173	3724637	-	1430	3367	3286	1261	2.29	2.23	0.86											
<i>ywqJ</i>	3724627	3726435	-	878	2824	3405	603	3.21	3.76	0.68	1096 ywqJ	3724989	3725540	3725265	36.0	15.0	44.9	36.5			
<i>ywqI</i>	3726454	3726714	-	1686	4597	5677	894	2.77	3.28	0.52											
<i>ywqH</i>	3726724	3727146	-	1449	3628	4632	784	2.48	3.10	0.52											
<i>ywqG</i>	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			
<i>ywqF</i>	3728515	3729837	-	1368	2119	2068	1459	1.57	1.52	1.07											
<i>ywqE</i>	3730032	3730796	-	612	1765	1582	603	2.99	2.61	0.98											
<i>ywqD</i>	3730849	3731562	-	1723	5430	5038	1458	3.26	2.97	0.85											
<i>ywqC</i>	3731552	3732298	-	607	2631	2186	591	4.55	3.73	0.99											
											1100 Inter	3732163	3732595	3732379	15.5	25.2	10.5	0.1			
<i>ywqB</i>	3732879	3734489	+	1853	1481	1460	1652	0.81	0.79	0.89	1101 ywqB	3733710	3733904	3733807	6.2	4.9	1.1	1.6			
<i>ywqA</i>	3734476	3737244	+	2410	2220	2031	2116	0.94	0.85	0.88	1103 ywqA	3735206	3735366	3735286	0.9	1.6	1.0	5.7			
<i>ywpJ</i>	3737370	3738227	-	495	704	746	554	1.43	1.51	1.12											
<i>glcR</i>	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			
<i>ywpH</i>	3739233	3739574	-	1198	2456	2709	1240	2.14	2.34	1.05											
<i>ywpG</i>	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			
<i>ywpF</i>	3740209	3740619	+	3595	4138	4466	3351	1.15	1.24	0.93											
<i>ywpE</i>	3740758	3741066	-	366	306	279	290	0.84	0.76	0.79											
<i>ywpD</i>	3741410	3742246	+	257	232	242	249	0.90	0.94	0.97											
<i>mscL</i>	3742293	3742685	-	5108	3887	3751	4406	0.76	0.73	0.86											
<i>ywpB</i>	3742784	3743182	-	4456	3597	3275	4011	0.81	0.73	0.90											
<i>rapD</i>	3743374	3744438	+	2673	3851	4110	2522	1.44	1.53	0.94											
<i>flhP</i>	3744461	3745267	-	4459	4196	3673	4863	0.96	0.83	1.09											
<i>flhO</i>	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		
<i>mbl</i>	3746276	3747277	-	12237	12180	10292	11112	1.00	0.84	0.91											
<i>spolIID</i>	3747443	3747724	-	359	274	281	242	0.76	0.78	0.68											
<i>usd</i>	3747739	3747849	-	52	5																

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$																		
<i>spoOF</i>	3808573	3808947	-	1211	2139	1888	1299	1.81	1.57	1.08											
<i>ywjG</i>	3809113	3809634	+	1822	1677	1700	1702	0.92	0.93	0.93											
<i>pyrG</i>	3809716	3811323	-	15619	11223	10212	15316	0.72	0.65	0.98											
<i>rpoE</i>	3811565	3812086	-	9789	7793	7577	9204	0.80	0.77	0.94											
<i>acdA</i>	3812269	3813408	-	698	437	496	718	0.63	0.72	1.02	1125	acdA	3813083	3813396	3813240	3.4	3.4	5.5	14.2		
<i>ywjF</i>	3813405	3815522	-	659	424	488	645	0.64	0.74	0.98											
<i>ywjE</i>	3815677	3816873	+	359	357	378	377	1.00	1.05	1.05											
<i>uvsE</i>	3816886	3817848	+	245	245	275	225	1.00	1.12	0.92											
<i>ywjC</i>	3817929	3818201	+	4773	1871	3263	2014	0.40	0.69	0.44											
<i>ywjB</i>	3818243	3818767	-	4188	5496	5438	3189	1.31	1.30	0.76											
<i>ywjA</i>	3818777	3820504	-	3927	4649	4749	3025	1.18	1.21	0.77											
<i>ywiE</i>	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		
<i>narI</i>	3822581	3823252	-	492	415	469	486	0.84	0.95	0.99											
<i>narJ</i>	3823249	3823803	-	427	338	330	474	0.79	0.77	1.11											
<i>narH</i>	3823829	3825292	-	344	268	276	357	0.78	0.80	1.05											
<i>narG</i>	3825282	3828968	-	335	246	258	329	0.73	0.77	0.98											
<i>arfM</i>	3829164	3829640	-	336	318	340	316	0.95	1.01	0.94											
<i>ywiC</i>	3829784	3830503	+	1077	1041	1092	962	0.97	1.01	0.89											
<i>fnr</i>	3830535	3831251	-	869	742	723	760	0.83	0.81	0.88											
<i>narK</i>	3831350	3832537	-	524	446	476	510	0.85	0.91	0.97											
<i>argS</i>	3832673	3834343	-	6974	5153	4989	6628	0.74	0.72	0.95											
<i>ywiB</i>	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		
<i>sboA</i>	3835081	3835212	+	562	5925	6624	553	10.92	12.18	0.99											
<i>sboX</i>	3835169	3835321	+	107	499	549	112	4.27	4.77	1.12											
<i>albA</i>	3835346	3836692	+	1502	8319	8398	1987	5.52	5.58	1.32	1129	albA	3835149	3835666	3835408	32.4	46.3	18.6	1.5		
<i>albB</i>	3836705	3836866	+	1906	6829	7409	2097	3.57	3.88	1.10											
<i>albC</i>	3836863	3837582	+	1034	4043	4177	1176	3.90	4.03	1.13											
<i>albD</i>	3837575	3838885	+	937	3377	3537	1058	3.60	3.77	1.12											
<i>albE</i>	3838875	3840035	+	412	1659	1800	468	4.01	4.36	1.13											
<i>albF</i>	3840040	3841320	+	419	1327	1518	467	3.16	3.62	1.11											
<i>albG</i>	3841317	3842018	+	352	717	839	394	2.05	2.40	1.12											
<i>ywhL</i>	3842024	3843400	-	399	393	398	400	0.98	1.00	1.00											
<i>ywhK</i>	3843439	3844794	-	256	239	263	253	0.93	1.02	0.99											
											1130	Inter	3844652	3845152	3844902	25.3	27.0	11.2	-0.2		
<i>rapF</i>	3845024	3846169	+	939	939	1093	1853	1.00	1.16	1.98											
<i>phrF</i>	3846153	3846272	+	3543	5697	6135	4020	1.63	1.74	1.16	1131	phrF	3846063	3846461	3846262	12.2	18.1	3.7	-0.4		
<i>ywhH</i>	3846371	3846844	+	332	346	380	256	1.04	1.15	0.77											
<i>speB</i>	3846876	3847748	-	5729	3728	3292	5248	0.65	0.57	0.92											
<i>speE</i>	3847809	3848639	-	6785	4628	3569	6296	0.70	0.53	0.93											
<i>ywhE</i>	3848841	3850784	+	230	199	213	248	0.87	0.93	1.09											
<i>ywhD</i>	3851208	3851726	-	6827	5782	5764	6490	0.85	0.84	0.95											
<i>ywhC</i>	3851740	3852399	-	3119	2781	2646	2877	0.89	0.85	0.92											
<i>ywhB</i>	3852508	3852696	+	5097	5464	5378	4326	1.08	1.07	0.84											
<i>ywhA</i>	3852739	3853158	-	1626	1588	1515	1658	0.98	0.93	1.02											
<i>thrZ</i>	3853278	3855194	-	595	542	609	549	0.91	1.02	0.92											
<i>mmr</i>	3856039	3857439	-	1055	820	830	1037	0.78	0.79	0.98											
<i>ywgB</i>	3857439	3857909	-	883	589	571	808	0.67	0.65	0.90											
<i>ywgA</i>	3858021	3858521	-	2627	1805	1676	2427	0.69	0.64	0.93											
<i>ywfO</i>	3858557	3859858	-	3091	2415	2175	2946	0.78	0.71	0.95											
<i>ywzC</i>	3860020	3860244	-	1634	1378	1216	1497	0.85	0.75	0.91											
<i>rsfA</i>	3860459	3861235	+	325	856	954	318	2.63	2.92	0.98											
<i>ywfM</i>	3861379	3862269	-	736	677	689	715	0.92	0.94	0.97											
<i>ywfL</i>	3862437	3863282	-	3026	1940	1889	3006	0.64	0.62	0.99											
<i>ywfK</i>	3863331	3864230	-	1215	825	870	1032	0.68	0.72	0.85											
											1134	Inter	3864287	3864464	3864376	4.1	6.5	2.2	0.0		
<i>eutD</i>	3864377	3865348	-	15698	15181	14012	15072	0.97	0.89	0.96											
<i>ywfI</i>	3865633	3866382	+	6644	6378	6660	7155	0.97	1.01	1.08											
<i>ywfH</i>	3866515	3867294	+	535	2193	2855	527	4.11	5.36	0.98											
<i>ywfG</i>	3867309	3868508	-	641	1106	1202	661	1.73	1.89	1.02											
<i>ywfF</i>	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		
<i>ywfE</i>	3869690	3871108	-	754	1544	1750	810	2.07	2.35	1.07											
<i>ywfD</i>	3871127	3871894	-	687	1009	1107	641	1.47	1.61	0.93											
<i>ywfC</i>	3871891	3872598	-	420	710	814	416	1.70	1.95	0.99	1138	ywfC	3872090	3872216	3872153	1.2	1.7	1.1	5.0		
<i>ywfB</i>	3872588	3873202	-	368	357	437	342	0.97	1.19	0.93											
											1139	Inter	3873076	3873389	3873233	5.4	10.0	2.3	0.6		
<i>ywfA</i>	3873354	3874592	-	736	647	725	752	0.88	0.99	1.02											
<i>rocC</i>	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		
<i>rocB</i>	3876214	3877914	-	328	507	544	299	1.56	1.66	0.91											
<i>rocA</i>	3877988	3879535	-	870	7576	8784	880	8.71	10.11	1.01											
<i>rocG</i>	3879762	3881036	-	728	4868	6481	714	6.67	8.86	0.98											
<i>yweA</i>	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		

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh				
<i>spsL</i>	3882001	3882456	-	497	404	452	497	0.81	0.91	1.00											
<i>spsK</i>	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	
<i>spsJ</i>	3883314	3884261	-	602	502	495	609	0.84	0.83	1.01											
<i>spsI</i>	3884261	3885001	-	463	365	363	498	0.79	0.79	1.07											
<i>spsG</i>	3885026	3886045	-	460	356	391	462	0.78	0.85	1.00											
<i>spsF</i>	3886052	3886771	-	364	306	321	364	0.84	0.88	1.00											
<i>spsE</i>	3886764	3887885	-	318	280	272	343	0.88	0.86	1.08											
<i>spsD</i>	3887885	3888754	-	462	367	403	433	0.80	0.87	0.94											
<i>spsC</i>	3888755	3889924	-	394	317	340	404	0.81	0.87	1.04											
<i>spsB</i>	3889945	3891363	-	344	301	308	341	0.87	0.89	0.99											
<i>spsA</i>	3891368	3892138	-	193	165	177	198	0.86	0.92	1.04											
<i>ywdL</i>	3892458	3893003	+	191	166	153	216	0.88	0.80	1.18											
<i>ywdK</i>	3893076	3893417	-	3243	2564	2478	3448	0.79	0.76	1.06											
<i>ywdJ</i>	3893418	3894800	-	4593	3696	3889	4600	0.80	0.84	1.01											
<i>ywdI</i>	3894820	3895137	-	4228	3090	3319	3613	0.73	0.78	0.86	1143	ywdI	3894853	3895217	3895035		16.2	13.7	7.7	1.8	
<i>ywdH</i>	3895305	3896678	+	727	577	608	725	0.80	0.84	1.00											
<i>ung</i>	3896703	3897380	-	2601	1675	1704	2358	0.65	0.66	0.91											
<i>ywdF</i>	3897394	3898200	-	3681	2408	2473	3413	0.65	0.67	0.93											
<i>ywdE</i>	3898291	3898824	-	842	724	785	791	0.86	0.93	0.94											
<i>ywdD</i>	3898872	3899363	-	844	897	993	856	1.06	1.17	1.01											
<i>ywdC</i>	3899406	3899834	+	293	311	310	331	1.05	1.05	1.12											
<i>thiD</i>	3899983	3900798	+	5607	3923	4051	5557	0.70	0.72	0.99											
<i>ywdA</i>	3900888	3901136	-	3361	1877	2271	3473	0.55	0.66	1.04											
<i>sacA</i>	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	
											1147	sacP	3903319	3903445	3903382		1.0	1.2	1.5	3.1	
<i>sacP</i>	3902669	3904054	-	2683	1186	1899	2798	0.43	0.67	1.05											
<i>ywcJ</i>	3904356	3905126	+	703	518	599	632	0.74	0.85	0.91											
<i>sacT</i>	3905165	3905995	-	323	220	239	367	0.68	0.73	1.14											
<i>ywcI</i>	3906035	3906337	-	588	496	549	595	0.85	0.94	1.03											
<i>vpr</i>	3906867	3909287	+	313	411	476	323	1.32	1.54	1.04											
<i>ywcH</i>	3909325	3910326	-	1356	912	1093	1406	0.68	0.82	1.03											
<i>nfrA</i>	3910500	3911249	-	5819	5616	6396	7059	0.97	1.10	1.21											
<i>rodA</i>	3911355	3912536	-	1678	1202	1216	2089	0.72	0.72	1.24											
<i>ywcE</i>	3913032	3913295	+	344	460	447	394	1.33	1.29	1.14											
<i>qoxD</i>	3913338	3913712	-	13738	11083	10176	12729	0.81	0.74	0.93											
<i>qoxC</i>	3913714	3914328	-	21464	18619	17799	20789	0.87	0.83	0.97											
<i>qoxB</i>	3914342	3916291	-	18530	15816	15059	18234	0.85	0.81	0.98											
<i>qoxA</i>	3916319	3917284	-	17200	13703	12907	16771	0.80	0.75	0.98											
<i>ywzA</i>	3917895	3918044	+	2200	1314	2057	1277	0.61	0.93	0.61											
<i>galT</i>	3918116	3919657	-	4191	3668	4322	4058	0.87	1.03	0.97											
<i>galK</i>	3919661	3920833	-	3581	2899	3255	3393	0.81	0.91	0.95											
<i>ywcD</i>	3920914	3921297	-	1683	1587	1554	2124	0.94	0.92	1.26											
<i>ywcC</i>	3921315	3921986	-	825	600	567	762	0.73	0.69	0.92											
<i>ywcB</i>	3922943	3923251	+	925	1025	958	862	1.11	1.04	0.93											
<i>ywcA</i>	3923238	3924788	+	507	447	485	507	0.88	0.96	1.00											
<i>ywbO</i>	3924819	3925421	-	2230	1729	1568	1965	0.78	0.71	0.88											
<i>ywbN</i>	3925705	3926955	-	7015	6199	6176	7078	0.88	0.88	1.01											
<i>ywbM</i>	3926974	3928131	-	8369	6993	7300	8132	0.84	0.88	0.97											
<i>ywbL</i>	3928128	3929573	-	3074	2528	2572	3080	0.82	0.84	1.00											
<i>thiE</i>	3929730	3930398	-	3140	2790	2939	3122	0.89	0.94	1.00											
<i>thiM</i>	3930395	3931213	-	2803	2655	2836	2873	0.95	1.01	1.03											
<i>ywbI</i>	3931221	3932126	-	1316	1186	1226	1479	0.90	0.93	1.13											
<i>ywbH</i>	3932232	3932618	+	577	480	397	659	0.90	0.72	1.14	1160	Inter	3932049	3932277	3932163		4.8	4.9	4.6	9.5	
<i>ywbG</i>	3932600	3933325	+	495	420	389	563	0.86	0.79	1.13											
<i>ywbF</i>	3933380	3934579	+	850	2289	2238	1122	2.70	2.63	1.32	1161	Inter	3933103	3933586	3933345		33.0	21.1	26.1	1.7	P02
<i>ywbE</i>	3934613	3934810	+	2371	3579	3613	2682	1.51	1.52	1.13											
<i>ywbD</i>	3934845	3936035	-	2293	1682	1662	2105	0.73	0.73	0.92											
<i>ywbC</i>	3936156	3936536	+	4717	4087	4325	4810	0.86	0.91	1.02											
<i>ywbB</i>	3936574	3937251	-	442	648	685	412	1.46	1.55	0.93											
<i>ywbA</i>	3937328	3938662	-	612	485	508	668	0.79	0.83	1.10											
<i>epr</i>	3938890	3940827	+	1632	1535	1509	1731	0.97	0.93	1.06											
											1163	Inter	3940923	3941117	3941020		6.2	1.5	3.3	0.9	
<i>sacX</i>	3941255	3942634	+	817	670	664	838	0.83	0.82	1.02											
<i>sacY</i>	3942688	3943530	+	614	479	479	594	0.80	0.79	0.97											
<i>gspA</i>	3943581	3944441	-	3678	1796	3522	1528	0.49	0.95	0.42											
<i>ywaF</i>	3944551	3945264	-	941	778	907	898	0.82	0.97	0.93											
<i>ywaE</i>	3945415	3945930	+	539	534	495	530	0.99	0.92	0.99											
<i>tyrZ</i>	3946179	3947420	+	489	382	401	449	0.78	0.82	0.91											
<i>ywaD</i>	3947576	3948943	+	248	239	245	235	0.97	0.99	0.95											
<i>ywaC</i>	3948973	3949605	-	2570	2162	2651	2864	0.84	1.03	1.12											
<i>menA</i>	3949747	3950682	-	3509	2362	2108	3242	0.67	0.60	0.92											

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh	wild	Δabh				
<i>dltA</i>	3951296	3952807	+	14675	16862	16790	15543	1.15	1.15	1.06											
<i>dltB</i>	3952804	3953991	+	12441	14039	13636	13878	1.13	1.10	1.12											
<i>dltC</i>	3954008	3954244	+	15320	16845	16569	17118	1.10	1.08	1.12											
<i>dltD</i>	3954244	3955422	+	15073	16998	17032	16028	1.13	1.13	1.06											
<i>dltE</i>	3955513	3956271	+	13531	15946	15582	14407	1.18	1.16	1.07											
<i>ywaA</i>	3956412	3957503	+	3326	3776	3870	3111	1.15	1.18	0.94											
<i>licH</i>	3957537	3958865	-	7138	3396	5680	6837	0.45	0.72	0.94											
<i>licA</i>	3958862	3959194	-	5730	2263	3879	4898	0.38	0.61	0.85											
<i>licC</i>	3959213	3960571	-	4040	1579	3115	3734	0.39	0.68	0.90											
<i>licB</i>	3960587	3960895	-	1703	911	1872	1585	0.51	0.93	0.88											
<i>licR</i>	3961023	3962948	-	914	746	872	853	0.82	0.96	0.93											
<i>yxzF</i>	3963111	3963269	-	1401	870	1212	776	0.62	0.86	0.56											
<i>yxjI</i>	3963298	3963888	-	675	564	653	594	0.84	0.97	0.88											
<i>katX</i>	3964017	3965660	+	742	691	940	527	0.94	1.25	0.75											
<i>yxjH</i>	3965765	3966967	+	1252	1015	1063	1257	0.81	0.85	1.00											
<i>yxjG</i>	3966960	3967739	-	1795	2671	3451	2442	1.50	1.95	1.35											
<i>yxjF</i>	3967736	3968623	-	1887	2593	3275	2599	1.40	1.77	1.37											
<i>yxjE</i>	3968630	3968818	-	1864	2449	3293	2516	1.31	1.77	1.35											
<i>yxjD</i>	3968815	3969021	-	1182	1802	1935	1654	1.55	1.67	1.40											
<i>yxjC</i>	3969018	3969338	-	867	1101	1311	1316	1.37	1.66	1.54											
<i>sigY</i>	3969331	3969867	-	812	924	1230	1146	1.19	1.61	1.40											
<i>yxjA</i>	3970079	3971452	+	711	845	739	694	1.19	1.05	0.97											
<i>yxkO</i>	3971467	3972297	-	783	617	673	715	0.79	0.86	0.92											
<i>cydD</i>	3972383	3974110	-	549	425	459	547	0.78	0.84	1.00											
<i>cydC</i>	3974107	3975810	-	590	493	510	611	0.84	0.86	1.03	1165	cydC	3974379	3974453	3974416	0.3	1.4	0.9	2.7		
<i>cydB</i>	3975810	3976826	-	861	766	816	978	0.89	0.95	1.13											
<i>cydA</i>	3976810	3978216	-	1540	1070	1379	1540	0.70	0.88	0.99											
<i>yxkI</i>	3978772	3980124	+	482	514	595	468	1.07	1.23	0.97											
<i>yxkH</i>	3980246	3981934	+	1342	2300	2435	1119	1.72	1.82	0.83											
<i>yxzE</i>	3981992	3982192	+	1379	4516	4543	1954	3.26	3.28	1.41											
<i>yxkG</i>	3982206	3983045	-	546	704	579	496	1.30	1.05	0.90											
<i>msmX</i>	3983152	3984249	-	5042	3367	4884	4439	0.66	0.94	0.88											
<i>yxkF</i>	3984370	3985263	-	728	881	1037	653	1.21	1.42	0.90											
<i>aldY</i>	3985447	3986904	+	451	343	406	413	0.76	0.90	0.91											
<i>yxkD</i>	3986946	3987782	-	1070	1014	986	1065	0.95	0.92	1.00											
<i>yxkC</i>	3988251	3988892	+	7153	14658	14376	13050	2.05	2.01	1.82											
<i>galE</i>	3988967	3989986	-	8148	6139	6013	6346	0.75	0.74	0.78											
<i>yxkA</i>	3990101	3990607	-	390	305	311	398	0.78	0.80	1.02											
<i>yxjO</i>	3990737	3991612	+	663	469	434	633	0.71	0.65	0.95											
<i>yxjN</i>	3991690	3992163	+	1205	904	830	1133	0.75	0.68	0.94											
<i>yxjM</i>	3992181	3993401	+	743	659	622	701	0.90	0.84	0.94											
<i>yxjL</i>	3993388	3994044	+	549	530	544	527	0.97	0.99	0.96											
<i>pepT</i>	3994094	3995326	+	3512	5676	6347	3303	1.62	1.81	0.94	1170	pepT	3995085	3995551	3995318	30.7	35.9	36.5	52.8		P01
<i>yxjJ</i>	3995848	3996111	+	2134	2547	2726	1855	1.20	1.28	0.87	1170	Inter	3995561	3995993	3995777	22.2	27.9	15.1	17.8		
<i>yxjI</i>	3996240	3996728	+	1176	1122	1150	1104	0.95	0.99	0.94	1171	yxjI	3996241	3996707	3996474	20.3	19.8	5.0	1.6		P03
<i>yxjH</i>	3996983	3998005	+	999	853	972	842	0.85	0.97	0.85											
<i>yxjG</i>	3998368	3999504	+	712	666	781	669	0.94	1.10	0.94	1172	yxjG	3998553	3998730	3998642	0.5	1.1	1.4	5.4		
<i>yxjF</i>	3999557	4000330	-	427	331	343	453	0.77	0.80	1.06											
<i>scoB</i>	4000347	4000997	-	471	340	358	427	0.72	0.76	0.91											
<i>scoA</i>	4000994	4001710	-	500	356	387	537	0.71	0.77	1.09											
<i>yxjC</i>	4001734	4003152	-	382	297	340	379	0.78	0.90	1.01											
<i>yxjB</i>	4003306	4004154	-	749	829	824	595	1.11	1.10	0.79											
<i>yxjA</i>	4004770	4005963	+	4992	5587	5052	6109	1.16	1.04	1.23	1175	Inter	4004180	4004918	4004549	25.4	44.8	10.6	2.5		
<i>yxjT</i>	4006434	4006676	-	2088	2834	3369	1828	1.36	1.61	0.88											
<i>yxjS</i>	4006821	4007111	-	1646	1370	1588	1170	0.83	0.97	0.71											
<i>katE</i>	4007161	4009221	-	1329	859	1265	748	0.65	0.98	0.55											
<i>ctiH</i>	4009422	4010702	+	542	437	498	508	0.80	0.92	0.93											
<i>bgIS</i>	4010860	4011588	-	1862	885	1457	2168	0.46	0.74	1.13											
<i>licT</i>	4011884	4012717	-	2278	1728	2151	2663	0.75	0.94	1.16											
<i>yxjP</i>	4012813	4013493	-	407	487	487	436	1.20	1.21	1.07											
<i>yxjO</i>	4013700	4014986	+	578	824	818	633	1.42	1.41	1.09	1178	Inter	4013292	4013928	4013610	41.8	62.7	24.0	6.6		
<i>deaD</i>	4015005	4016444	-	5334	3684	3824	3836	0.69	0.72	0.72	1179	yxjO	4014669	4014931	4014800	3.5	2.1	4.4	9.8		
<i>yxjM</i>	4016526	4017674	-	3668	2689	2766	2302	0.74	0.75	0.63	1180	deaD	4016233	4016461	4016347	1.4	1.2	2.1	8.1		
<i>yxjL</i>	4017857	4018057	-	4948	4074	3974	3334	0.85	0.82	0.67											
<i>yxjK</i>	4018166	4018627	-	4294	3768	3695	3263	0.88	0.86	0.75	1181	yxjK	4018120	4018620	4018370	2.1	3.0	3.5	40.3		P04
<i>yxjI</i>	4018643	4018939	-	2962	2099	2056	1836	0.71	0.69	0.62											
<i>yxjI</i>	4018967	4019455	-	3270	2699	2586	2111	0.83	0.79	0.64											

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID					
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c				
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh		
-type	Δabh	-type	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$															
<i>yxzG</i>	4019473	4019925	-	5555	4514	4404	3247	0.81	0.79	0.58												
<i>yniH</i>	4019995	4020324	-	2350	1971	1885	1442	0.84	0.80	0.62												
<i>yniG</i>	4020447	4020863	-	5426	4230	4023	3128	0.78	0.74	0.58												
<i>yxzC</i>	4020914	4021282	-	4106	3186	2909	2660	0.77	0.71	0.65												
<i>yniF</i>	4021276	4021746	-	2974	2675	2530	1832	0.90	0.85	0.62												
<i>yxzG</i>	4022072	4022500	-	12633	10256	9775	9635	0.82	0.78	0.76												
<i>wapA</i>	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	4024053	4024519	4024286	12.5	15.4	23.6	37.2			
											1188	Inter	4029425	4029755	4029590	11.3	16.2	1.7	1.1			
<i>yxzF</i>	4029728	4030663	-	865	1280	1217	800	1.48	1.41	0.92	1188	yxzF	4029765	4030214	4029990	20.5	39.5	1.7	2.1			P03
											1188	Inter	4030496	4031013	4030755	20.6	35.8	4.2	1.9			P03
<i>yniE</i>	4030815	4031261	-	18601	17500	18816	19491	0.94	1.00	1.04												
<i>bglH</i>	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			
<i>bglP</i>	4032796	4034625	-	17470	14342	15825	18364	0.81	0.89	1.04												
											1190	Inter	4034661	4035263	4034962	39.1	38.2	16.0	4.6			
<i>yxzE</i>	4035008	4035316	-	1510	1353	1600	1358	0.89	1.05	0.91												
<i>yxzD</i>	4035362	4035805	-	841	703	770	866	0.82	0.90	1.03	1191	yxzD	4035409	4035737	4035573	13.2	19.0	3.8	-0.1			
<i>yniD</i>	4035802	4037511	-	1010	1557	1934	602	1.54	1.91	0.60	1191	yniD	4035749	4036181	4035965	12.5	25.3	3.3	0.2			
											1191	yniD	4036361	4036725	4036543	6.5	9.4	4.8	3.4			
											1192	yniD	4037330	4037473	4037402	2.4	4.2	2.0	0.8			
<i>yniC</i>	4037531	4037800	-	716	1380	1752	430	1.95	2.42	0.61												
<i>yniB</i>	4037812	4038177	-	590	1084	1314	283	1.86	2.18	0.48												
											1193	Inter	4038044	4038594	4038319	27.1	38.3	12.8	5.4			
<i>yniA</i>	4038484	4039893	-	437	531	746	450	1.21	1.68	1.04												
<i>hutP</i>	4040501	4040956	+	1588	877	994	1454	0.61	0.67	0.95												
<i>hutH</i>	4041069	4042595	+	286	224	230	296	0.78	0.80	1.00												
<i>hutU</i>	4042592	4044250	+	392	284	321	371	0.72	0.82	0.95												
<i>hutI</i>	4044263	4045528	+	528	407	448	540	0.77	0.86	1.02												
<i>hutG</i>	4045521	4046480	+	263	227	243	258	0.87	0.93	0.98												
<i>hutM</i>	4046556	4047983	+	444	384	419	439	0.86	0.94	0.98												
<i>pdp</i>	4048027	4049328	-	7993	3015	4695	7440	0.37	0.57	0.93												
<i>nupC</i>	4049358	4050539	-	11824	4799	6856	11325	0.40	0.56	0.95												
											1195	Inter	4050182	4051005	4050594	40.0	65.9	19.7	2.8			P02
<i>dra</i>	4050655	4051290	-	11982	6120	7893	10931	0.51	0.65	0.91												
<i>deor</i>	4051396	4052337	-	1466	1101	1018	1374	0.75	0.70	0.94												
<i>yxzB</i>	4052428	4053297	-	565	369	422	510	0.65	0.75	0.90												
<i>yxzR</i>	4053370	4054482	-	1008	881	886	1016	0.88	0.88	1.01												
<i>yxzQ</i>	4054552	4055889	-	494	442	452	486	0.89	0.91	0.98												
<i>yxzP</i>	4055886	4057028	-	526	444	479	514	0.85	0.92	0.98												
<i>yxzO</i>	4057045	4057794	-	498	425	454	444	0.86	0.92	0.90												
<i>yxzN</i>	4057807	4058481	-	655	593	626	616	0.90	0.96	0.94												
<i>yxzM</i>	4058504	4059298	-	363	281	311	318	0.77	0.86	0.88												
<i>yxzL</i>	4059323	4059820	-	373	302	304	425	0.82	0.83	1.18												
<i>yxzK</i>	4059834	4061159	-	388	323	341	372	0.83	0.88	0.97	1196	yxzK	4060314	4060406	4060360	1.8	2.8	1.2	0.7			
<i>yxzJ</i>	4061345	4061572	-	354	293	332	387	0.82	0.94	1.08												
<i>yxzI</i>	4061559	4062545	-	1606	1099	1594	1786	0.69	1.01	1.11	1197	yxzI	4061691	4061919	4061805	6.2	10.3	3.9	1.8			
<i>yxzH</i>	4062700	4063512	-	5527	6170	6155	5554	1.12	1.11	1.00												
<i>yxzG</i>	4063552	4064109	-	484	1113	1051	446	2.29	2.17	0.92												
<i>yxzF</i>	4064090	4064524	-	982	2422	2082	789	2.46	2.11	0.79												
<i>yxzE</i>	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			
<i>yxzD</i>	4065225	4065578	+	130	289	371	98	2.23	2.88	0.76												
<i>yxzC</i>	4065622	4066020	-	5260	5075	4600	4699	0.97	0.88	0.90	1200	yxzC	4065840	4066169	4066005	11.1	12.7	7.2	13.2			
<i>yxzB</i>	4066198	4067157	+	13972	15622	15441	14072	1.12	1.11	1.00	1201	yxzB	4066927	4067087	4067007	2.7	5.7	2.0	1.8			
<i>yxzA</i>	4067204	4067551	-	714	502	534	708	0.70	0.75	0.99												
<i>yxzM</i>	4067565	4069433	-	567	349	390	520	0.62	0.69	0.92												
<i>yxzL</i>	4069408	4070181	-	403	277	290	402	0.69	0.72	1.00												
<i>yxzK</i>	4070325	4071302	-	1339	960	948	1263	0.72	0.71	0.94												
<i>yxzJ</i>	4071299	4071988	-	1222	891	848	1193	0.73	0.69	0.98												
<i>fbzB</i>	4072097	4072969	-	2124	1512	1825	1989	0.73	0.88	0.94												
<i>iolI</i>	4072990	4073826	-	2344	1519	1955	2169	0.66	0.85	0.92												
<i>iolH</i>	4073912	4074781	-	2453	1569	2035	2465	0.65	0.84	1.01												
<i>idh</i>	4074801	4075835	-	3469	1977	2709	3445	0.57	0.79	0.99												
<i>iolF</i>	4075858	4077177	-	2096	1152	1532	2063	0.55	0.72	0.98												
<i>iolE</i>	4077192	4078085	-	3077	1668	2362	3028	0.53	0.75	0.98												
<i>iolD</i>	4078102	4079844	-	3256	1536	2294	3061	0.47	0.69	0.94												
<i>iolC</i>	4080048	4081025	-	2192	957	1490	2070	0.43	0.66	0.94												
<i>iolB</i>	4081049	4081864	-	1287	533	810	1293	0.41	0.61	0.99												
<i>mmsA</i>	4081939	4083402	-	2128	1053	1442	1850	0.49	0.66	0.87												
<i>iolR</i>	4083818	4084573	+	2940	1910	2011	2740	0.65	0.68	0.93												
<i>iolS</i>	4084627	4085559	+	8371	10949	11595	7818	1.31	1.39	0.93												
<i>yxzE</i>	4085821	4086471	+	2395	1755	1979	2454	0.73	0.82	1.02												

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

gene	Transcriptome analysis									ChAP-chip analysis						Profile ID						
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end		center	Binding intensity ^c				
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh / $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh		
-type	Δabh	-type	$\Delta abrB$	wild	Δabh	wild	$\Delta abrB$															
<i>ycx</i> D	4086475	4086783	+	1511	984	1121	1482	0.65	0.74	0.98												
<i>csb</i> C	4087022	4088407	+	2167	896	1355	1126	0.42	0.65	0.51												
<i>htp</i> G	4088449	4090329	-	5359	9589	10372	5885	1.80	1.94	1.10												
											1204 Inter	4090098	4090802	4090450				24.7	38.1	5.0	-0.4	P03
<i>ycx</i> A	4090497	4090748	-	2021	3361	3210	1889	1.66	1.59	0.93												
<i>yxb</i> G	4090865	4091686	+	791	405	533	524	0.51	0.67	0.66												
<i>yxb</i> F	4091715	4092857	-	963	734	696	1049	0.76	0.72	1.09												
<i>ald</i> X	4093000	4094337	+	673	559	534	680	0.83	0.79	1.01												
<i>yxb</i> D	4094376	4094855	-	591	3555	3935	555	6.04	6.70	0.94												
											1205 Inter	4094416	4095375	4094896				52.2	88.6	18.1	5.0	P02
<i>yxb</i> C	4094935	4095927	-	283	4746	5212	239	16.77	18.41	0.85												
											1206 Inter	4095385	4096650	4096018				55.6	100.0	34.5	2.7	P02
<i>yxb</i> B	4096436	4097170	+	435	1649	2088	398	3.85	4.92	0.91												
<i>yxb</i> A	4097170	4097439	+	172	766	1050	150	4.55	6.30	0.87	1207 <i>yxb</i> A	4097170	4097296	4097233				2.5	3.3	2.2	0.8	
<i>yxn</i> B	4097443	4097925	+	240	706	1000	182	2.95	4.18	0.76	1208 <i>yxn</i> B	4097374	4097805	4097590				10.2	15.5	4.0	0.9	
<i>asn</i> H	4097946	4100189	+	333	570	687	318	1.72	2.07	0.95	1209 <i>asn</i> H	4098445	4098605	4098525				3.8	2.8	5.1	2.7	
											1210 <i>asn</i> H	4099686	4099795	4099741				2.9	1.3	0.8	-0.1	
<i>yxa</i> M	4100186	4101385	+	410	644	776	418	1.58	1.92	1.00	1211 <i>yxa</i> M	4100349	4100713	4100531				11.3	13.2	17.4	5.5	
											1211 <i>yxa</i> M	4100723	4101172	4100948				25.0	10.7	35.3	2.0	
<i>yxa</i> L	4101449	4102681	-	1319	10381	10360	894	7.89	7.87	0.68	1213 <i>yxa</i> L	4101641	4101937	4101789				4.8	7.5	3.9	1.5	
											1213 <i>yxa</i> L	4101947	4102396	4102172				16.9	31.1	6.9	1.1	
											1213 Inter	4102406	4102991	4102699				36.6	72.8	21.3	5.7	P02
<i>yxa</i> J	4102782	4103210	-	1612	7825	7803	1301	4.88	4.88	0.80												
											1213 Inter	4102899	4103858	4103379				54.3	86.8	46.2	9.7	
<i>yxa</i> I	4103467	4103922	+	2936	1542	1503	1789	0.53	0.51	0.61												
<i>yxa</i> H	4103952	4105160	-	632	531	578	620	0.84	0.91	0.98	1214 <i>yxa</i> H	4104004	4104317	4104161				8.4	13.4	5.5	1.6	
<i>yxa</i> G	4105268	4106281	-	485	375	413	449	0.77	0.85	0.93												
<i>yxa</i> F	4106375	4106950	-	1570	678	574	1327	0.43	0.37	0.85												
<i>yxn</i> A	4107081	4108151	+	740	413	534	551	0.56	0.72	0.75												
<i>yxa</i> D	4108208	4108639	-	868	636	662	863	0.73	0.76	0.99												
<i>yxa</i> C	4108866	4109933	+	466	337	355	467	0.72	0.76	1.00												
<i>yxa</i> B	4109973	4111004	-	1273	3676	4887	982	2.89	3.84	0.77												
<i>yxa</i> A	4111097	4112245	-	762	2635	3841	716	3.46	5.04	0.94												
											1215 Inter	4112045	4112612	4112329				27.8	45.4	13.7	7.8	
<i>gnt</i> R	4112441	4113172	+	4768	1579	2218	4323	0.35	0.45	0.87												
<i>gnt</i> K	4113165	4114706	+	7072	1650	3047	5936	0.23	0.40	0.81												
<i>gnt</i> P	4114735	4116081	+	8712	2483	3854	7811	0.28	0.42	0.89												
<i>gnt</i> Z	4116104	4117510	+	12059	4929	5849	11599	0.40	0.47	0.96												
											1217 Inter	4117843	4118053	4117948				6.7	4.6	3.3	1.6	
<i>ahp</i> C	4117974	4118537	+	20500	21011	21407	20632	1.03	1.05	1.01												
<i>ahp</i> F	4118551	4120080	+	19272	20090	20722	19649	1.04	1.08	1.02												
<i>bgl</i> A	4120190	4121629	-	8120	4860	5884	7053	0.59	0.70	0.85												
<i>yyz</i> E	4121643	4121873	-	6514	3406	4198	5449	0.52	0.62	0.82												
<i>yxd</i> K	4122217	4122927	+	1144	576	643	964	0.50	0.56	0.84	*Broad	4122721	4177332									
<i>yxd</i> J	4123244	4123966	-	896	6673	7320	1431	7.39	8.16	1.61												
<i>yxd</i> I	4123987	4124616	-	908	7800	8804	1441	8.58	9.68	1.59												
<i>yxd</i> H	4124766	4125524	-	583	5566	6462	777	9.46	11.03	1.35												
<i>yxd</i> G	4125505	4126464	-	178	5917	6338	192	33.16	35.56	1.08												
<i>yxd</i> F	4126522	4126671	-	616	19673	19736	1197	31.89	32.04	1.94												
<i>fbp</i>	4127053	4129068	+	4996	4770	5381	5746	0.96	1.08	1.15												
<i>yxd</i> D	4129602	4131362	-	2529	1949	1981	2390	0.77	0.78	0.95												
<i>yxd</i> C	4131362	4131760	-	1003	746	669	1072	0.74	0.67	1.07												
<i>yxd</i> B	4131753	4133198	-	1476	1128	1080	1475	0.77	0.73	1.00												
<i>yxd</i> A	4133460	4133939	-	2250	1631	1534	2162	0.73	0.68	0.96												
<i>yye</i> S	4134376	4134789	+	568	499	470	527	0.88	0.83	0.93												
<i>yye</i> R	4134823	4136049	-	768	1301	1325	842	1.69	1.73	1.10												
<i>yye</i> Q	4136387	4136635	-	370	466	500	365	1.28	1.36	0.99												
<i>yye</i> P	4136651	4137814	-	380	315	324	328	0.83	0.85	0.86												
<i>yye</i> O	4137825	4138562	-	347	302	312	329	0.87	0.90	0.96												
<i>yye</i> N	4138704	4139174	-	479	841	940	490	1.76	1.96	1.02												
<i>rap</i> G	4139285	4140382	+	1081	4306	4226	930	4.05	3.97	0.86												
<i>phr</i> G	4140383	4140499	+	3918	11124	11784	3309	2.84	3.01	0.84												
<i>roc</i> F	4140735	4141625	-	2563	4386	4216	2445	1.74	1.67	0.97												
<i>roc</i> E	4141699	4143102	-	1462	2653	2582	1439	1.83	1.78	1.00												
<i>roc</i> D	4143325	4144530	-</																			

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

gene	Transcriptome analysis									ChAP-chip analysis							Profile ID				
	name	start	end	strand	Signal intensity of RNA ^a				Expression ratio ^b			PBR ID	ORF or Intergenic	start	end	center		Binding intensity ^c			
					wild	$\Delta abrB$	Δabh $\Delta abrB$	Δabh	$\Delta abrB$ / wild	Δabh $\Delta abrB$ / wild	Δabh / wild							AbrB		Abh	
-type	Δabh	-type	$\Delta abrB$																		
<i>yycE</i>	4155955	4156374	-	423	403	517	415	0.95	1.22	0.98											
<i>dnaC</i>	4156495	4157859	-	2627	2067	2133	2684	0.79	0.81	1.02											
<i>yycD</i>	4158029	4158229	+	526	366	480	388	0.71	0.91	0.76											
<i>yycB</i>	4158277	4158480	-	244	177	178	227	0.73	0.73	0.92											
<i>yycC</i>	4158601	4158741	+	2599	3100	2924	2268	1.20	1.12	0.88											
<i>yycB</i>	4158814	4160022	+	4737	5199	5227	3586	1.10	1.10	0.76											
<i>yycA</i>	4160127	4162184	+	941	914	877	759	0.97	0.93	0.81											
<i>rpmI</i>	4162221	4162670	-	7784	7238	6947	7316	0.93	0.90	0.94											
<i>yycT</i>	4162667	4164646	-	4171	4119	4025	4082	0.99	0.97	0.98											
<i>yycS</i>	4164683	4165612	-	3037	2881	2789	3090	0.95	0.92	1.02											
<i>cotF</i>	4166134	4166616	+	274	193	215	212	0.71	0.79	0.77											
<i>yycR</i>	4166646	4167023	-	402	342	455	393	0.85	1.13	0.98											
<i>ppaC</i>	4167228	4168157	+	15480	13114	13128	14588	0.85	0.85	0.94											
<i>yycP</i>	4168190	4168636	-	669	509	566	564	0.76	0.85	0.85											
<i>yycO</i>	4169069	4170376	+	575	380	452	412	0.66	0.79	0.71											
<i>yycN</i>	4172138	4172575	+	6210	17516	17533	9421	2.82	2.82	1.52											
<i>yycM</i>	4172689	4173444	+	1531	3457	3543	2449	2.25	2.32	1.59											
<i>yycL</i>	4173434	4174144	+	873	1740	1746	1266	1.98	2.00	1.45											
<i>yycK</i>	4174141	4174896	+	662	1322	1284	1010	1.97	1.94	1.54											
<i>yycJ</i>	4174893	4175549	+	1133	2895	2955	1700	2.57	2.64	1.51											
<i>yycI</i>	4175924	4176712	-	546	526	582	510	0.96	1.07	0.93											
<i>yycH</i>	4176780	4177169	-	716	654	692	626	0.92	0.97	0.87											
<i>yycG</i>	4177315	4178154	+	1559	1234	1326	1427	0.79	0.85	0.91											
<i>yycF</i>	4178187	4179401	-	535	636	686	531	1.19	1.28	0.99											
<i>yycE</i>	4179630	4180466	+	539	372	399	487	0.69	0.74	0.90											
<i>yycD</i>	4180480	4180923	+	681	421	480	647	0.62	0.70	0.95											
<i>yycC</i>	4181006	4181485	+	1130	706	784	891	0.63	0.70	0.79											
<i>yycB</i>	4181660	4182322	-	1165	654	687	1075	0.56	0.59	0.92											
<i>yycA</i>	4182469	4182921	-	666	405	398	625	0.62	0.61	0.97											
<i>yycT</i>	4183041	4183487	+	781	797	868	763	1.02	1.11	0.98											
<i>yycS</i>	4183484	4184089	+	477	476	500	470	1.00	1.05	0.98											
<i>yycR</i>	4184184	4184705	-	437	429	473	469	0.98	1.08	1.08											
<i>yycQ</i>	4185116	4185472	+	1077	769	810	1121	0.71	0.75	1.05											
<i>yycP</i>	4185632	4186198	+	815	480	508	758	0.59	0.62	0.93	1246	yycP	4185791	4186121	4185956	8.6	14.1	1.6	0.9		
<i>tetB</i>	4186705	4188081	-	1954	1265	1263	1840	0.65	0.65	0.94	1247	tetB	4186845	4187260	4187053	13.8	9.9	14.7	2.3		
											1248	tetB	4187610	4188161	4187886	13.2	21.9	9.7	2.6		
<i>tetL</i>	4188115	4188177	-	1073	615	631	1004	0.58	0.59	0.94											
<i>yycO</i>	4188430	4188669	+	840	547	729	683	0.66	0.87	0.81											
<i>yycN</i>	4188820	4189236	+	349	227	249	251	0.65	0.71	0.72	1249	Inter	4188579	4188942	4188761	7.9	19.3	1.2	1.0		
<i>yycM</i>	4189233	4190150	+	405	283	338	450	0.70	0.84	1.10	1249	yycN	4188953	4189503	4189228	11.1	17.9	4.5	2.7		
<i>yycL</i>	4190222	4192291	+	2176	2076	2111	1901	0.95	0.97	0.87	1250	yycM	4189786	4190115	4189951	10.0	10.0	3.4	1.4		
<i>yycK</i>	4192288	4193187	-	2433	2420	2539	3476	0.99	1.04	1.43											
<i>yycJ</i>	4193413	4194768	+	534	453	482	529	0.85	0.91	0.98	1252	Inter	4192846	4193618	4193232	40.3	23.2	58.5	36.4		P01
<i>maa</i>	4194802	4195356	-	1149	1106	1194	1103	0.96	1.04	0.96											
<i>yycH</i>	4195374	4195754	-	662	665	648	629	1.01	0.98	0.95											
<i>ccpB</i>	4195810	4196745	-	469	494	530	409	1.05	1.13	0.87											
<i>exoA</i>	4196804	4197562	-	1109	681	668	969	0.62	0.60	0.87											
<i>rpsR</i>	4197627	4197866	-	11358	11077	10325	11602	0.98	0.91	1.02											
<i>ssb</i>	4197910	4198428	-	26551	26375	25166	26637	0.99	0.95	1.00											
<i>rpsF</i>	4198469	4198756	-	30832	29461	29511	30497	0.96	0.96	0.99	*Broad		4198711	4214630							
<i>yycF</i>	4198867	4199967	-	9136	5677	5356	8397	0.62	0.59	0.92											
<i>yycE</i>	4200094	4202097	-	2439	1322	1501	2526	0.54	0.62	1.03											
<i>yycD</i>	4202448	4203464	-	418	344	396	435	0.83	0.95	1.04											
<i>yycC</i>	4203924	4204541	+	239	247	284	244	1.05	1.20	1.05											
<i>spoII</i>	4204580	4205428	-	5628	4871	5325	5099	0.87	0.95	0.90											
<i>soj</i>	4205421	4206182	-	5902	5221	5420	5620	0.89	0.92	0.95											
<i>yycB</i>	4206430	4206870	+	658	1223	1374	729	1.86	2.09	1.11											
<i>yycA</i>	4206921	4207772	-	8924	9970	10095	8446	1.12	1.13	0.94											
<i>gidB</i>	4207894	4208613	-	8743	8095	7978	8554	0.93	0.91	0.97											
<i>gidA</i>	4208627	4210513	-	6549	5799	5804	6305	0.89	0.89	0.96											
<i>trmE</i>	4210534	4211913	-	4161	3372	3363	4171	0.82	0.82	1.00											
<i>jag</i>	4212224	4212850	-	13967	12305	11380	13137	0.88	0.82	0.94											
<i>spoIII</i>	4212847	4213632	-	10526	8682	8262	10543	0.82	0.78	1.00											
<i>mpa</i>	4213777	4214127	-	6582	5422	4680	6292	0.83	0.71	0.96											
<i>rpmH</i>	4214279	4214413	-	16909	16236	15697	16535	0.96	0.93	0.97											

^a Average intensity of transcriptional signals from 2 independent experiments^b Average transcription signal ratio from 2 independent experiments^c Average binding signal intensity from 2 independent experiments

* Broad AbrB/Abh binding regions

Supplementary Table S2. Sequences used for motif extraction

pattern	PBR ID	100 bp around top of peak		ID	consensus sequence	pattern	PBR ID	100 bp around top of peak		ID	consensus sequence	pattern	PBR ID	100 bp around top of peak		ID	consensus sequence
		Start	End					Start	End					Start	End		
P01	42	125834	125933	P01_1	TCCACATTTGGTA	P02	29	69640	69739	P02_1	TATTACAAATTTGG	P03	217	678801	678900	P03_1	ATGGAAGA
	83	231160	231259	P01_2	TTCTGTATTGGAA		109	303898	303997	P02_2	ND		235	724170	724269	P03_2	GAAAAGGG
	103	289097	289196	P01_3	ND		117.1	376211	376310	P02_3	AATAGCCAAAATTTGG		245.1	742880	742979	P03_3	GATGAGGA
	104	291687	291786	P01_4	TCCTTTTTTGTAA	211	658735	658834	P02_4	ND	246	744251	744350	P03_4	GAAAATGG		
	107	300249	300348	P01_5	TCCTATTTTGGTG	328	1061805	1061904	P02_5	TTTATCCAAAATTAG	320	1018074	1018173	P03_5	AAAAACGA		
	146	485528	485627	P01_6	TTCCATTTGTGGAA	401	1336205	1336304	P02_6	AATTTCCAAATTTTG	323	1044249	1044348	P03_6	AAGGAGGG		
	236.1	725439	725538	P01_7	TTCCATAATTGGAA	417	1391253	1391352	P02_7	TTTTTCCAAATTTGA	384	1276136	1276235	P03_7	AAAGAGGG		
	272	843461	843560	P01_8	ND	436	1447620	1447719	P02_8	ATTTAACAAATTTTA	386	1278254	1278353	P03_8	GATGATGG		
	316	970692	970791	P01_9	ND	470	1594662	1594761	P02_9	AATAACAAATATGA	471	1598405	1598504	P03_9	GAAAATGA		
	352	1149308	1149407	P01_10	ND	693	2305500	2305599	P02_10	AATTTAAAATCTGG	548	1910679	1910778	P03_10	GAGRAAGGG		
	357	1149308	1149407	P01_11	ND	697	2324904	2325003	P02_11	ND	551	1914478	1914577	P03_11	GTGTATGG		
360.1	1185282	1185381	P01_12	TTCCATTTTGGAA	714	2364333	2364432	P02_12	ND	553	1920093	1920192	P03_12	GAAAAGGG			
387	1279823	1279922	P01_13	TTCCATATTTGTCA	737	2445481	2445580	P02_13	ATTTTCCATCAGTGG	565	1945141	1945240	P03_13	ATAAAGGG			
447	1492684	1492783	P01_14	ACCCAAATTTGGAA	781	2599153	2599252	P02_14	TTTTTCCAAAGCGTGA	608	2070054	2070153	P03_14	GAAGATGA			
461	1544861	1544960	P01_15	TTCCATAATGGAA	918	3036058	3036157	P02_15	TTTTTACAAAAGTGA	677	2266253	2266352	P03_15	GAAAAGGA			
531.1	1862411	1862510	P01_16	ND	1011	3426695	3426794	P02_16	TTTTTCAAGTATTGG	681	2272530	2272629	P03_16	AAGGAGGA			
598	2049845	2049944	P01_17	ND	1077	3675985	3676084	P02_17	TATTTACAAACATGG	686.1	2280679	2280778	P03_17	GAAGATGA			
626	2115884	2115983	P01_18	TGCCATTTTGGAA	1161	3933258	3933357	P02_18	TTTTTACATAAATGA	777	2587005	2587104	P03_18	GTGAAAGG			
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_21	AAGGATGG			
860	2817528	2817627	P01_22	TTCCATTTTGGAT						831	2752888	2752987	P03_22	AAAAGGGG			
865	2826953	2827052	P01_23	TTCCATTTTGGAA						877	2883700	2883799	P03_23	GAAGACGG			
907	2988881	2988980	P01_24	TGCCATTTTGGAA						1171	3996469	3996568	P03_24	ATGGAAGG			
936	3116085	3116184	P01_25	TTCCATTTTGGTT						1188.1	4029944	4030043	P03_25	ATGGATGA			
945	3152915	3153014	P01_26	TTCCATTTTGGTA						1188.2	4030714	4030813	P03_26	AAAAGAGGA			
947	3161539	3161638	P01_27	ND						1204	4090378	4090477	P03_27	GAGAATGA			
964	3194509	3194608	P01_28	TTCCATTTATGGGA													
968	3214653	3214752	P01_29	TGGTATATTTGGAA													
969	3216471	3216570	P01_30	TACCATTTATGGTA													
993	3343001	3343100	P01_31	ND													
1015	3449965	3450064	P01_32	ND													
1042	3581792	3581891	P01_33	ND													
1043	3589456	3589555	P01_34	ND													
1107	3746091	3746190	P01_35	TGCCATTTTGTAG													
1168	3981897	3981996	P01_36	ND													
1170	3995386	3995485	P01_37	ND													
												P04	97	277401	277500	P04_1	ATGGGCATACCAA
												322	1043346	1043445	P04_2	CAGGGAAATCCAA	
												355	1172252	1172351	P04_3	TTGGAAATCCAG	
												415	1389362	1389461	P04_4	CTGCAAAATCCAA	
												524	1811449	1811548	P04_5	CTGGAATCCAA	
												573	1970315	1970414	P04_6	CTGGAGCTCCAA	
												703	2333355	2333454	P04_7	CTGGAAATCCAT	
												711	2361095	2361194	P04_8	CTGGAARACCGA	
												754	2511426	2511525	P04_9	ATGGGAAACAG	
												824	2743786	2743885	P04_10	CTGAAAATCCAA	
												886	2908862	2908961	P04_11	AAGGAAATCCAG	
												1181	4018359	4018458	P04_12	AAGGAAATCCAT	

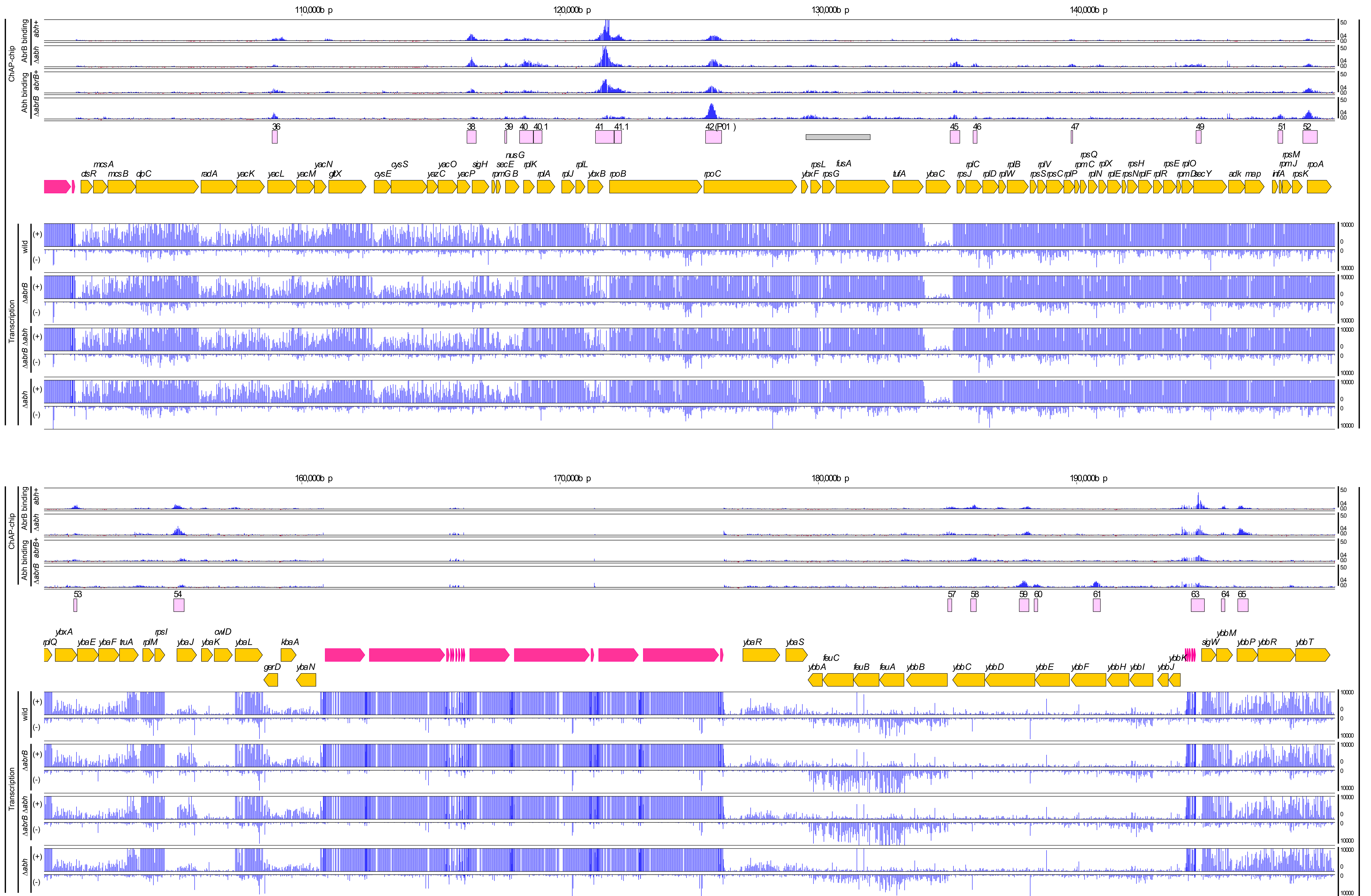


Fig.S1-2
155

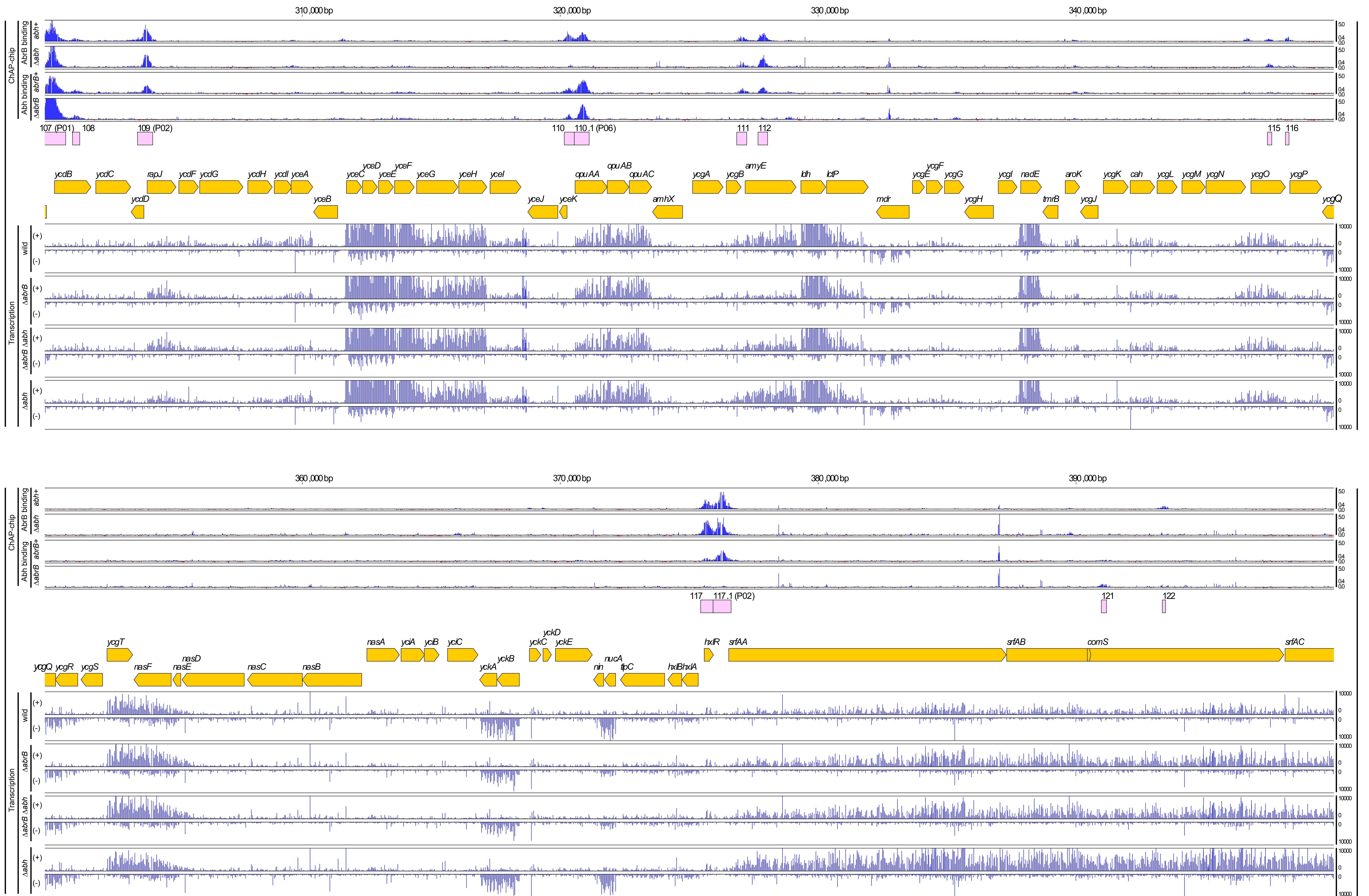


Fig.S14
157

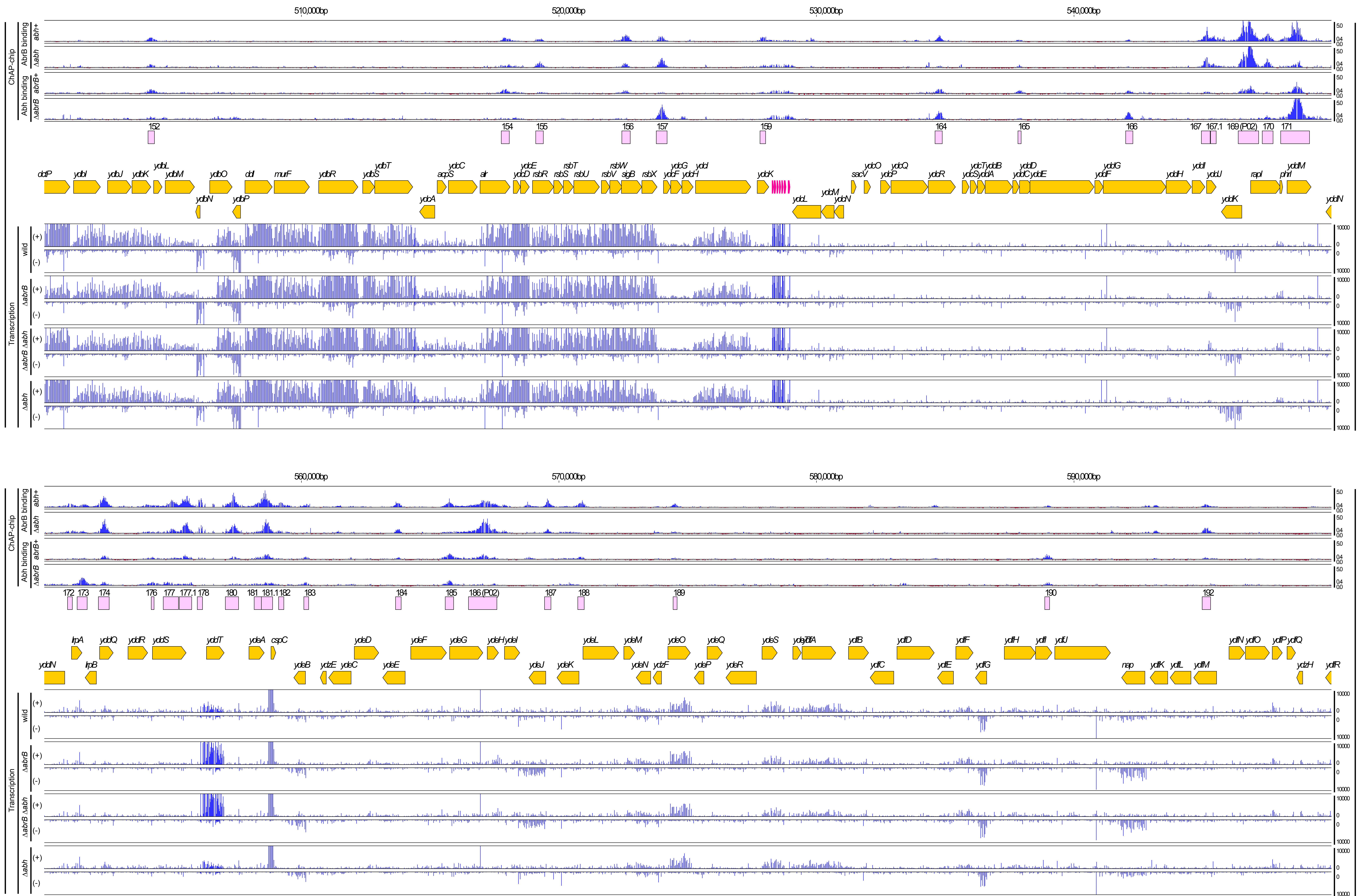


Fig.S16
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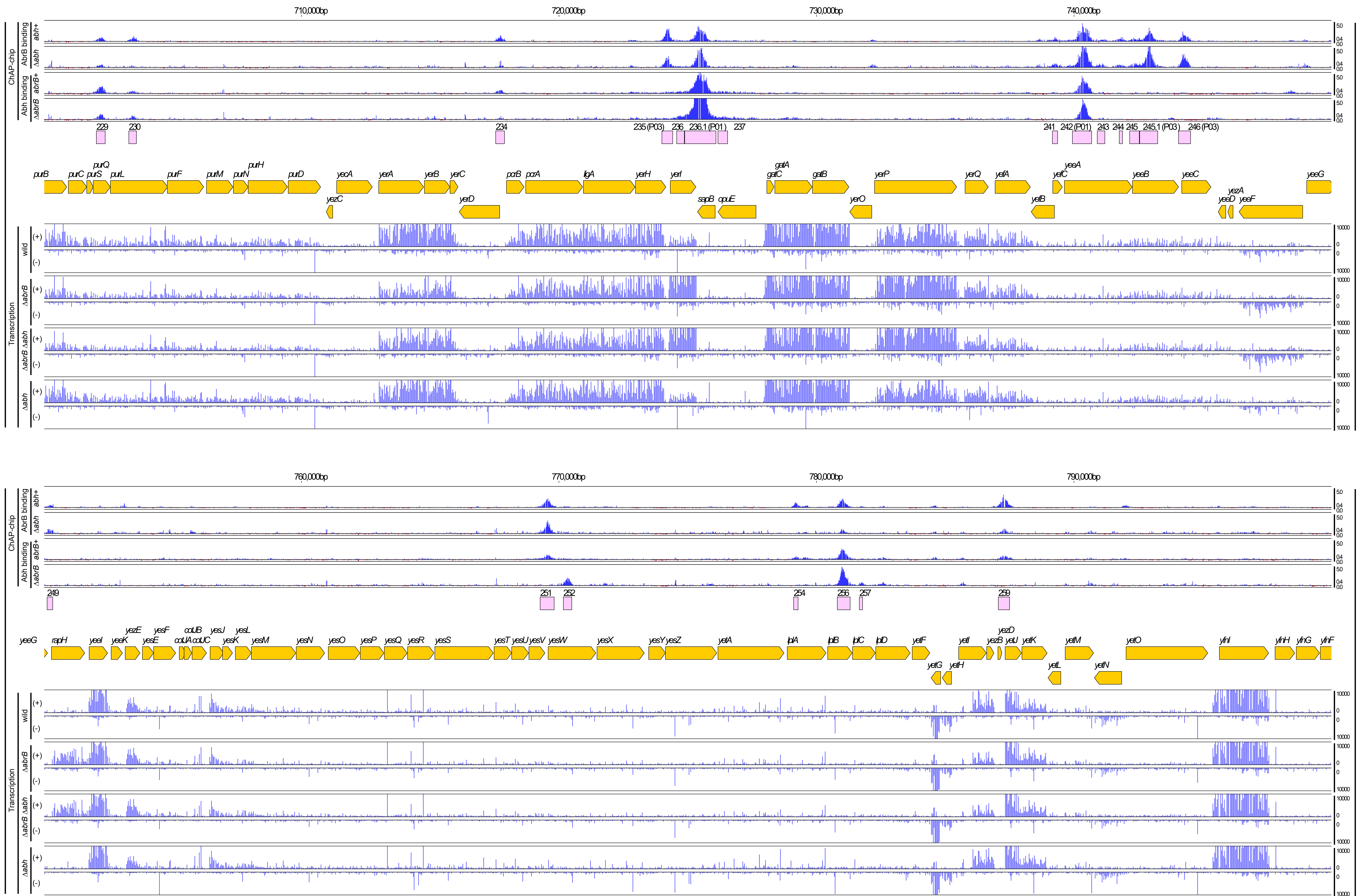


Fig.S18
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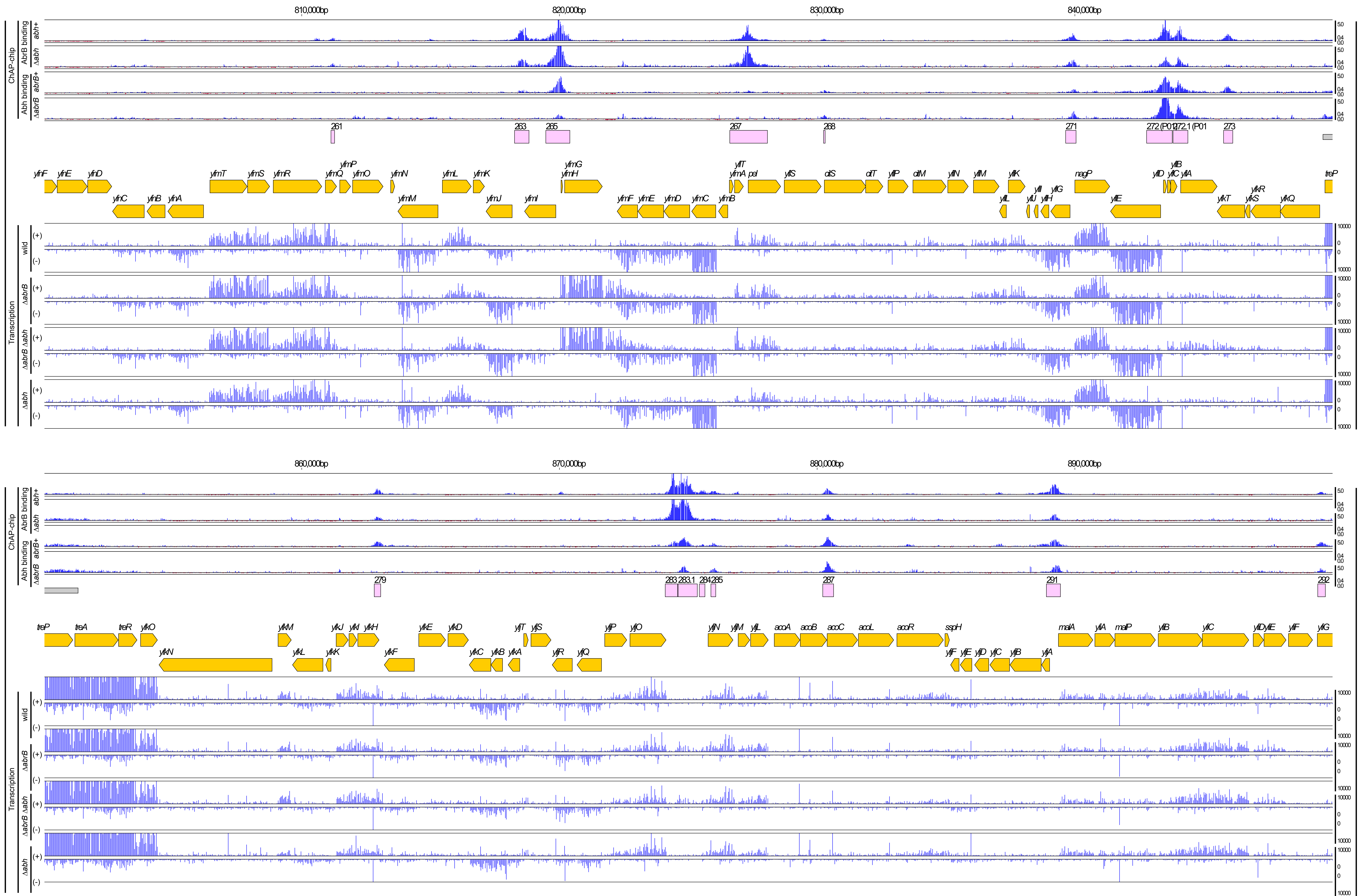


Fig.S1-9
162

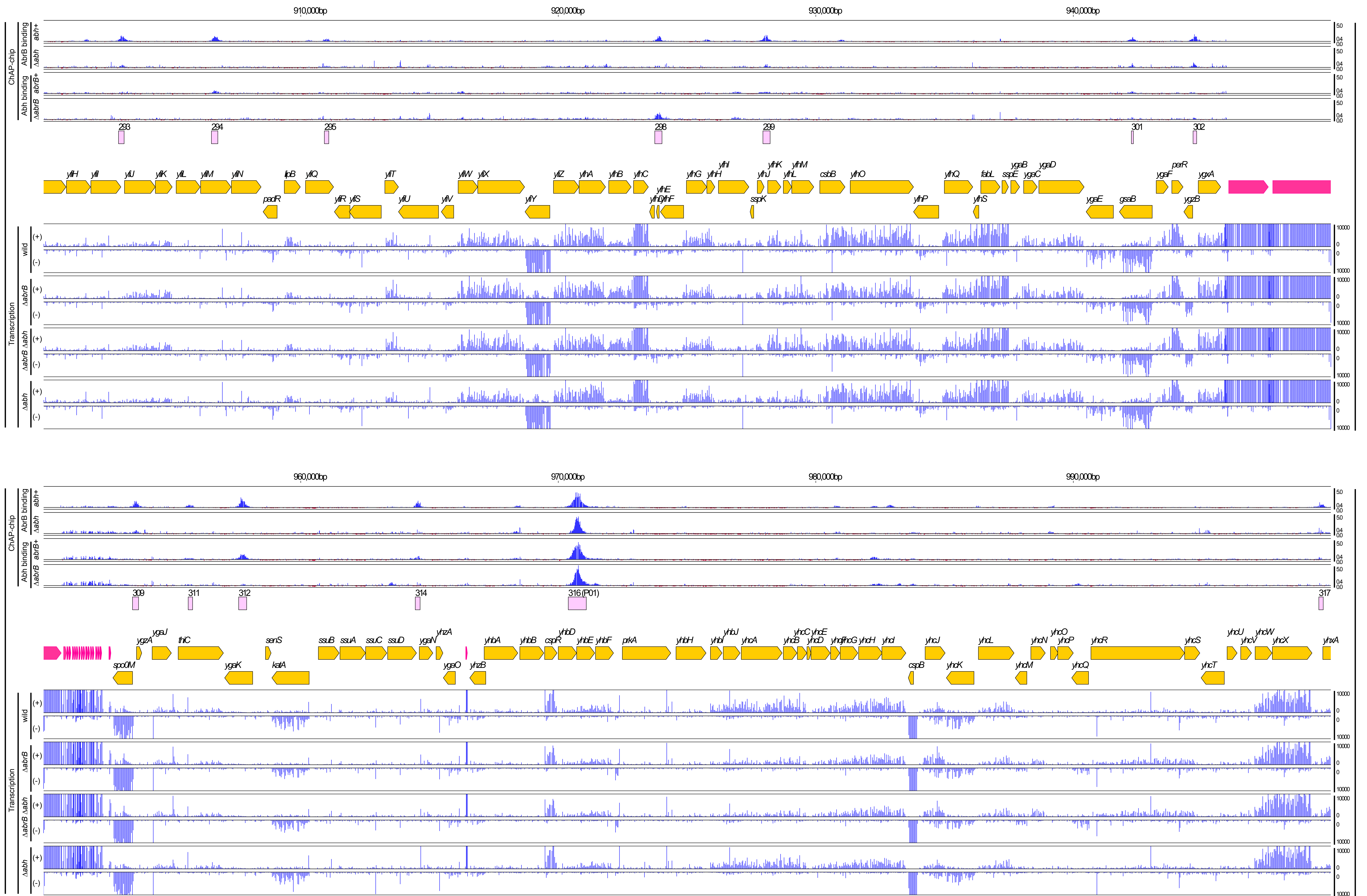


Fig.S1-10
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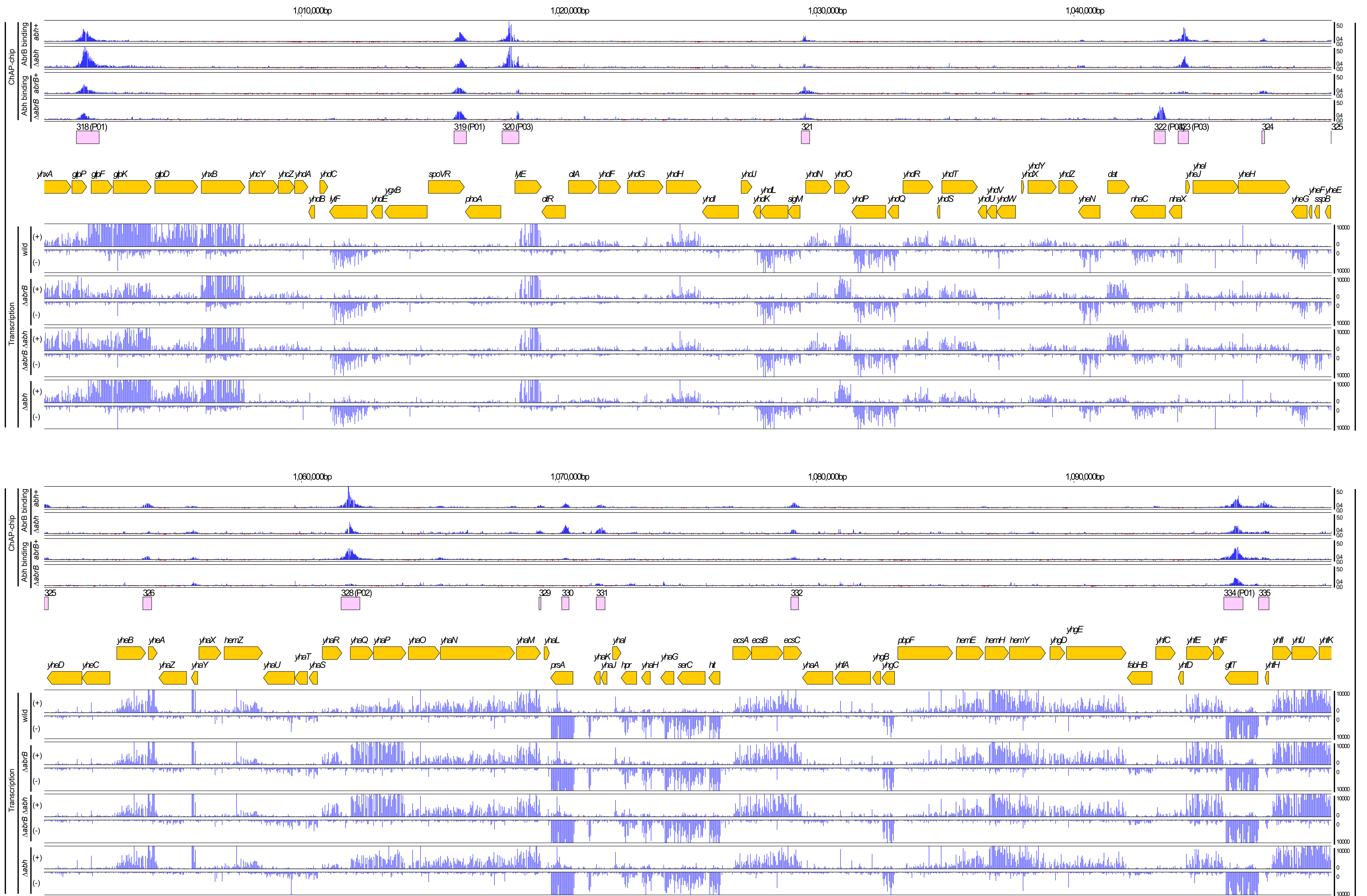


Fig.S1-11
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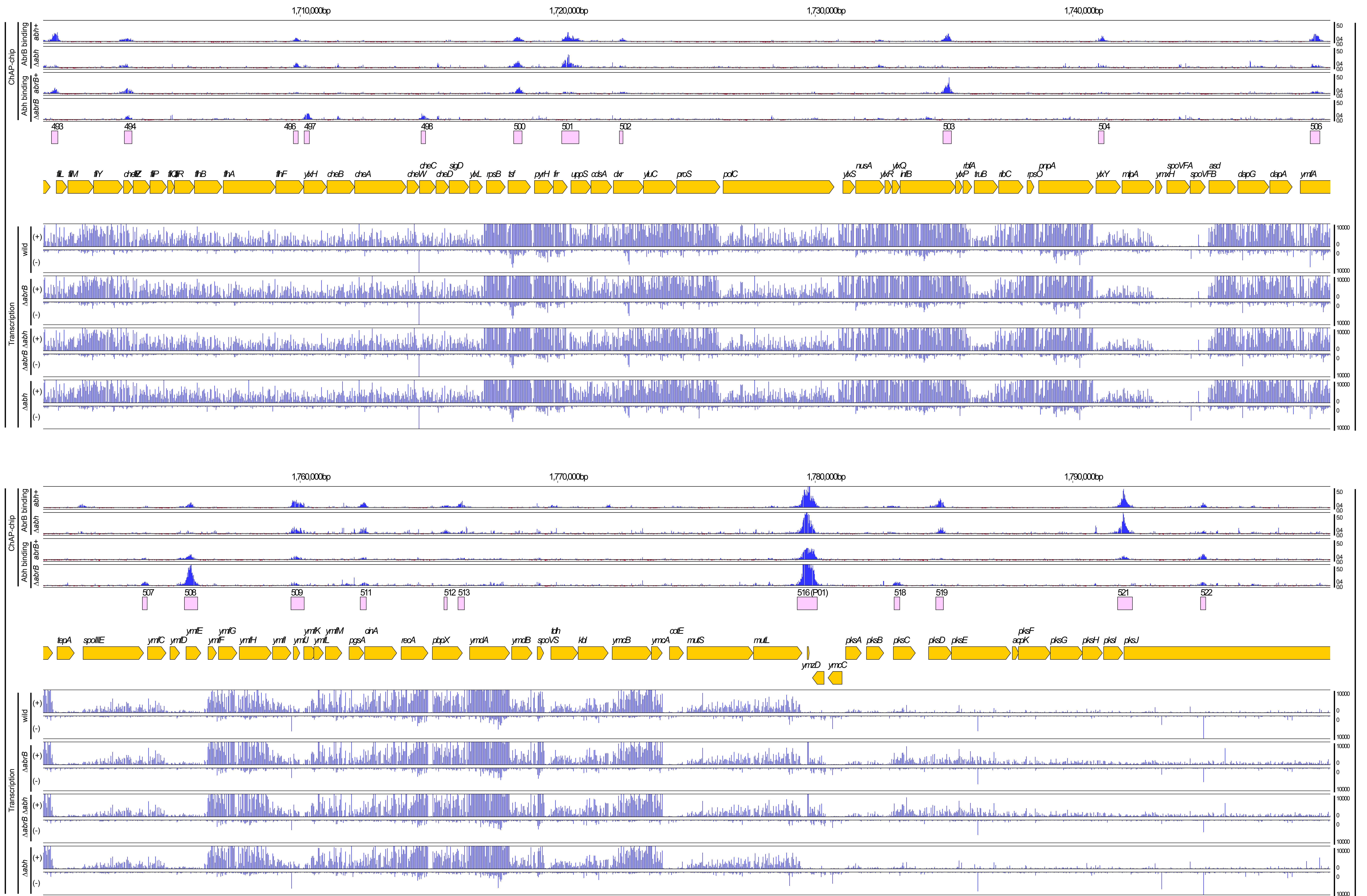


Fig.S1-18
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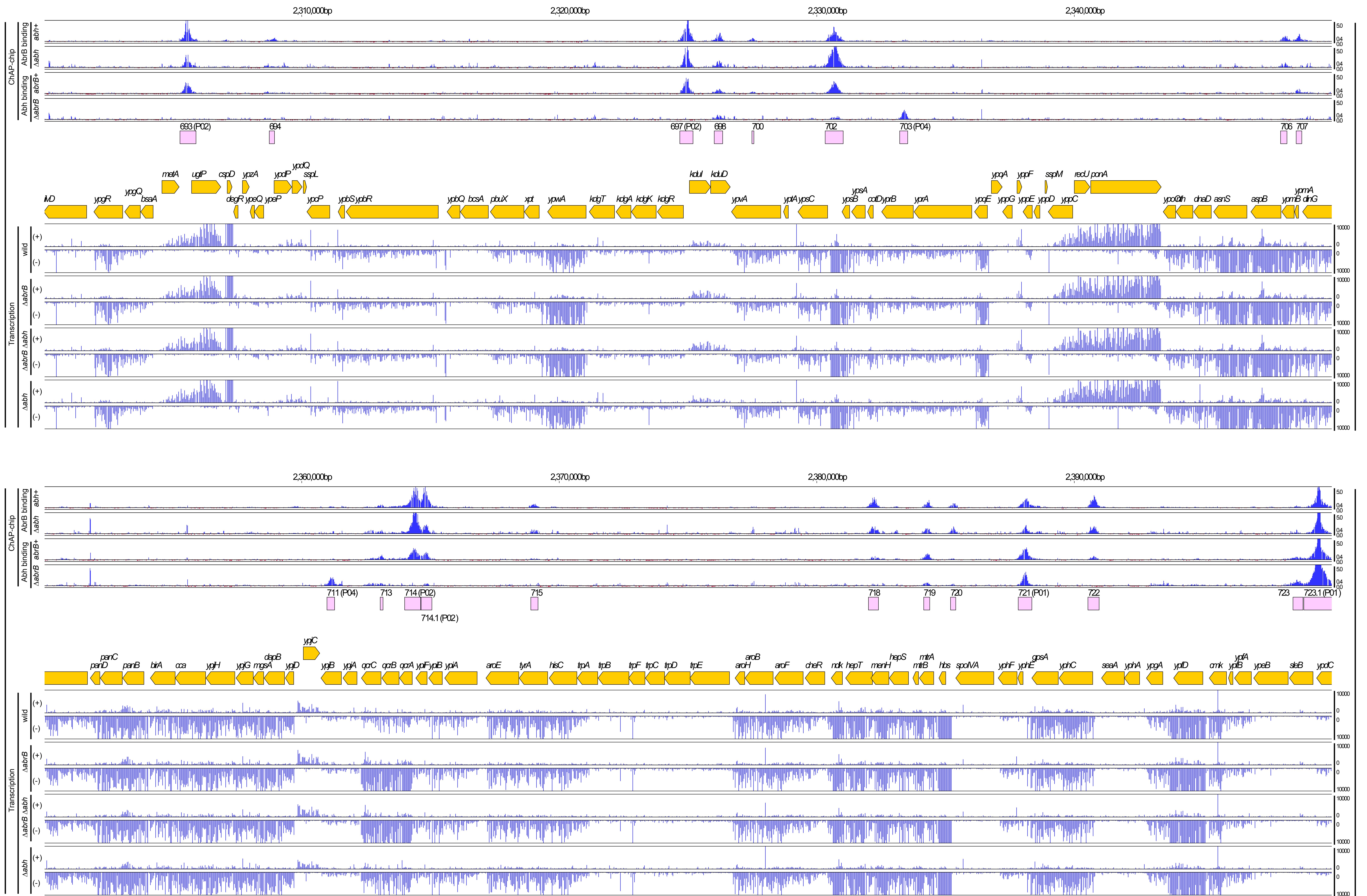


Fig.S1-24
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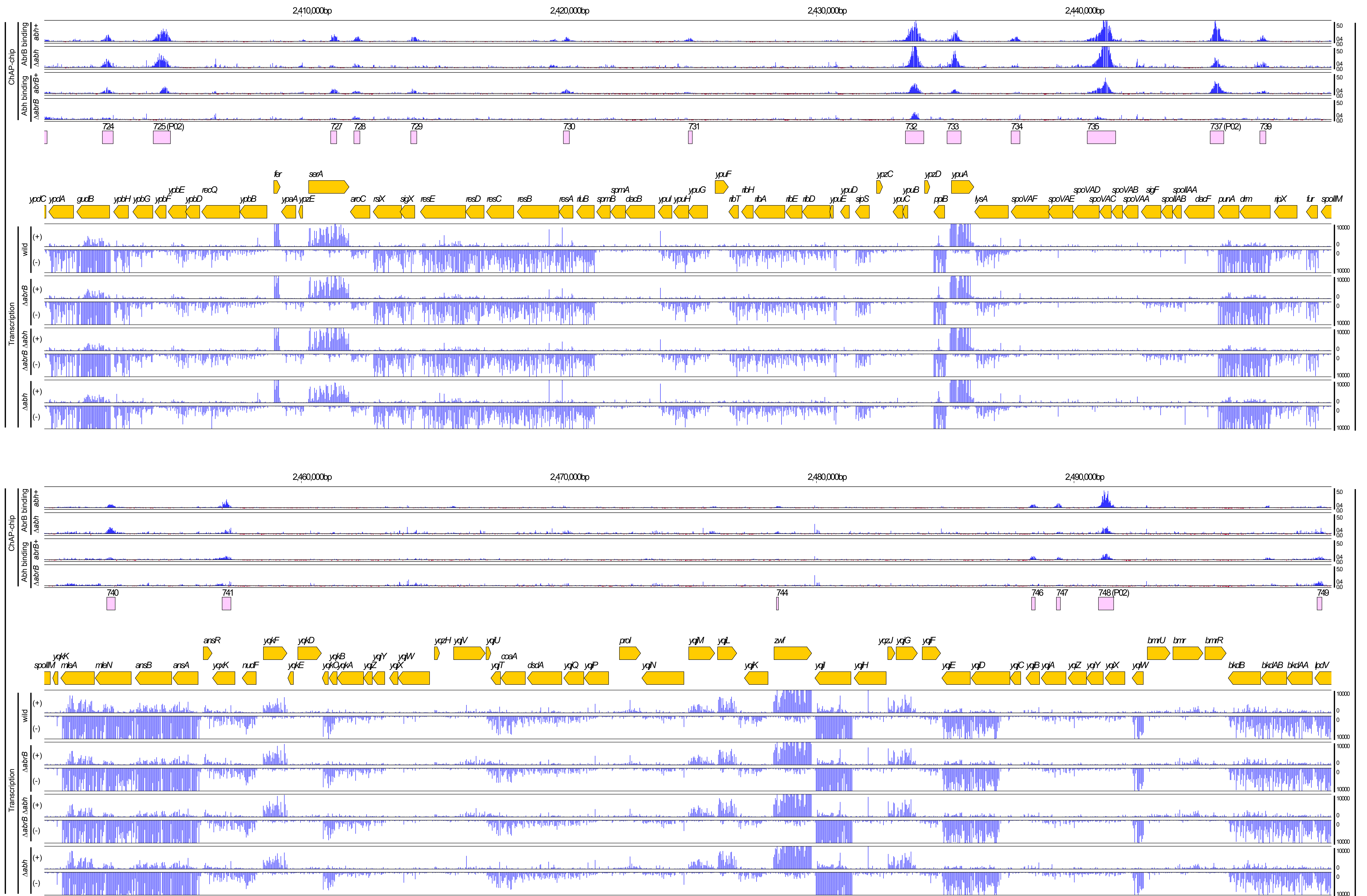


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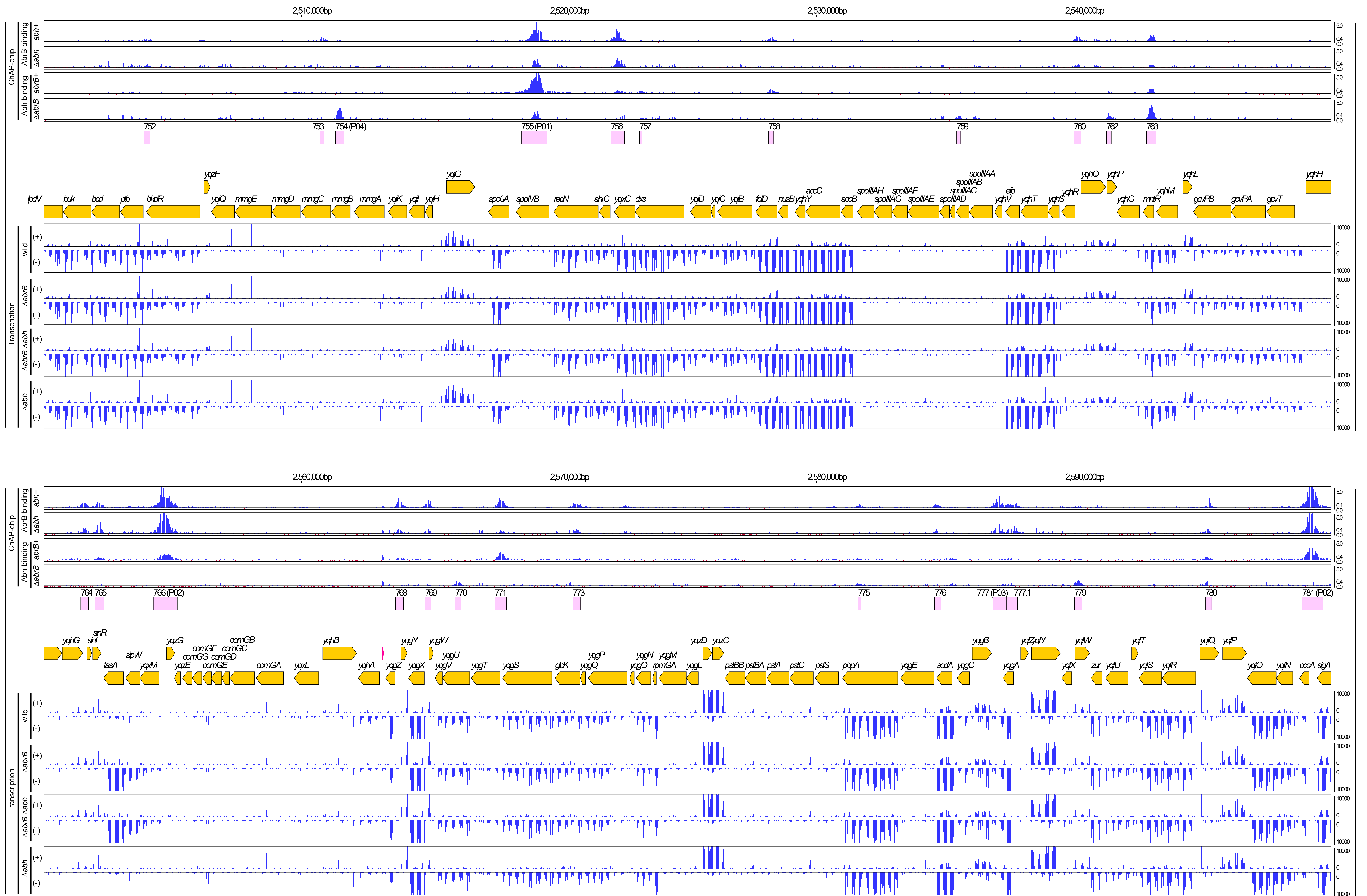


Fig.S1-26
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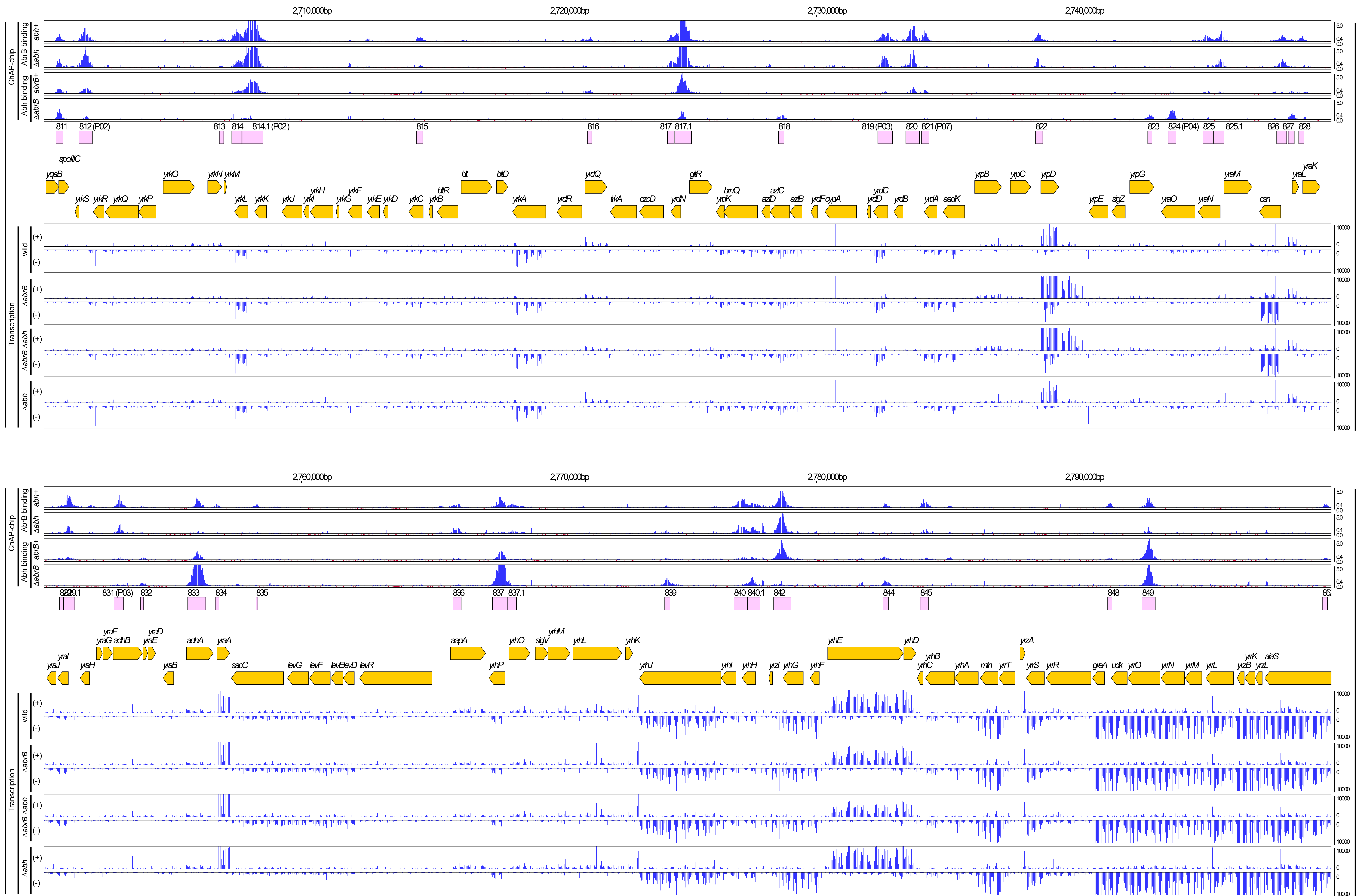


Fig.S1-28
181

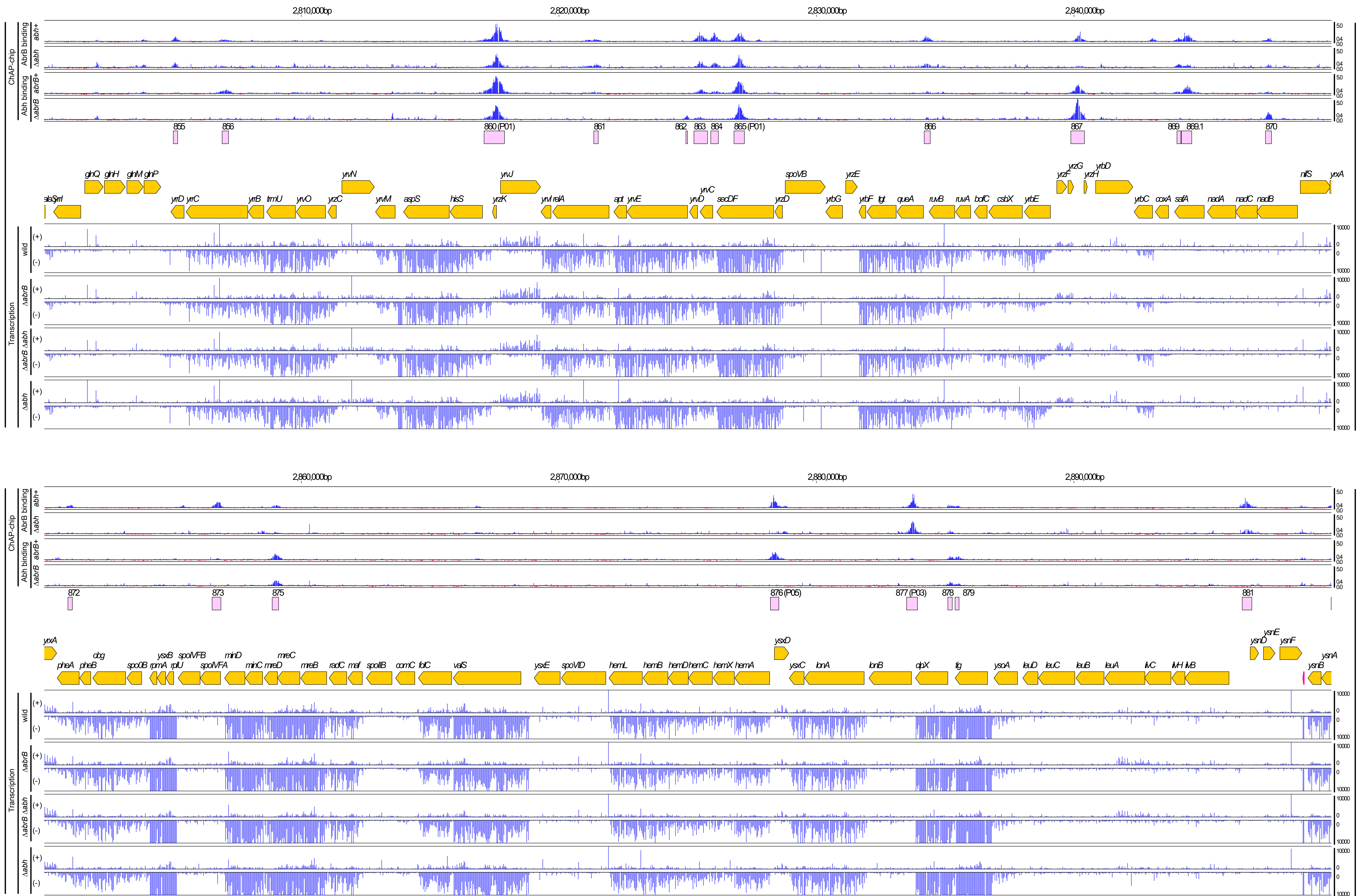


Fig.S1-29
182

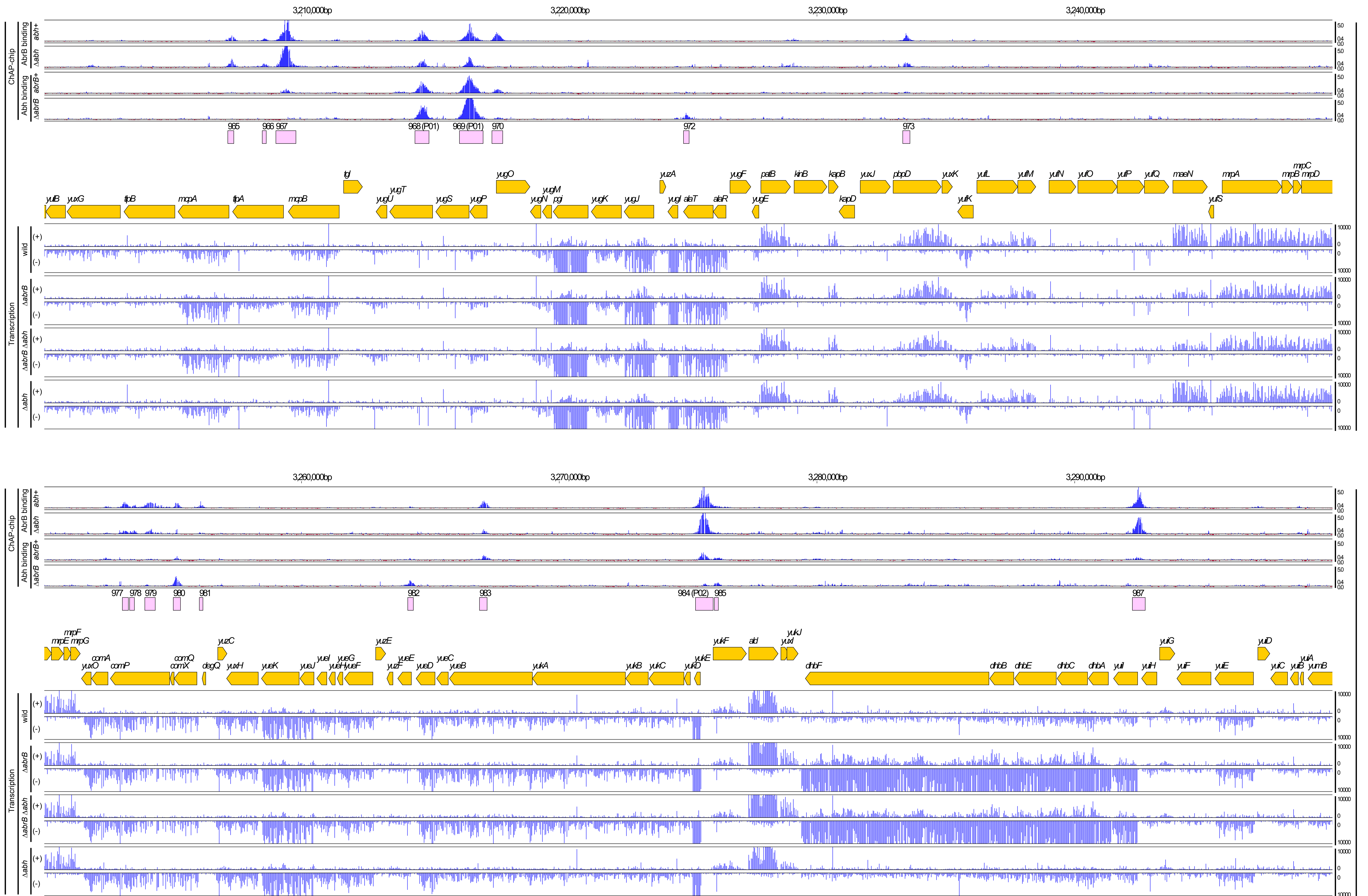


Fig.S1-33

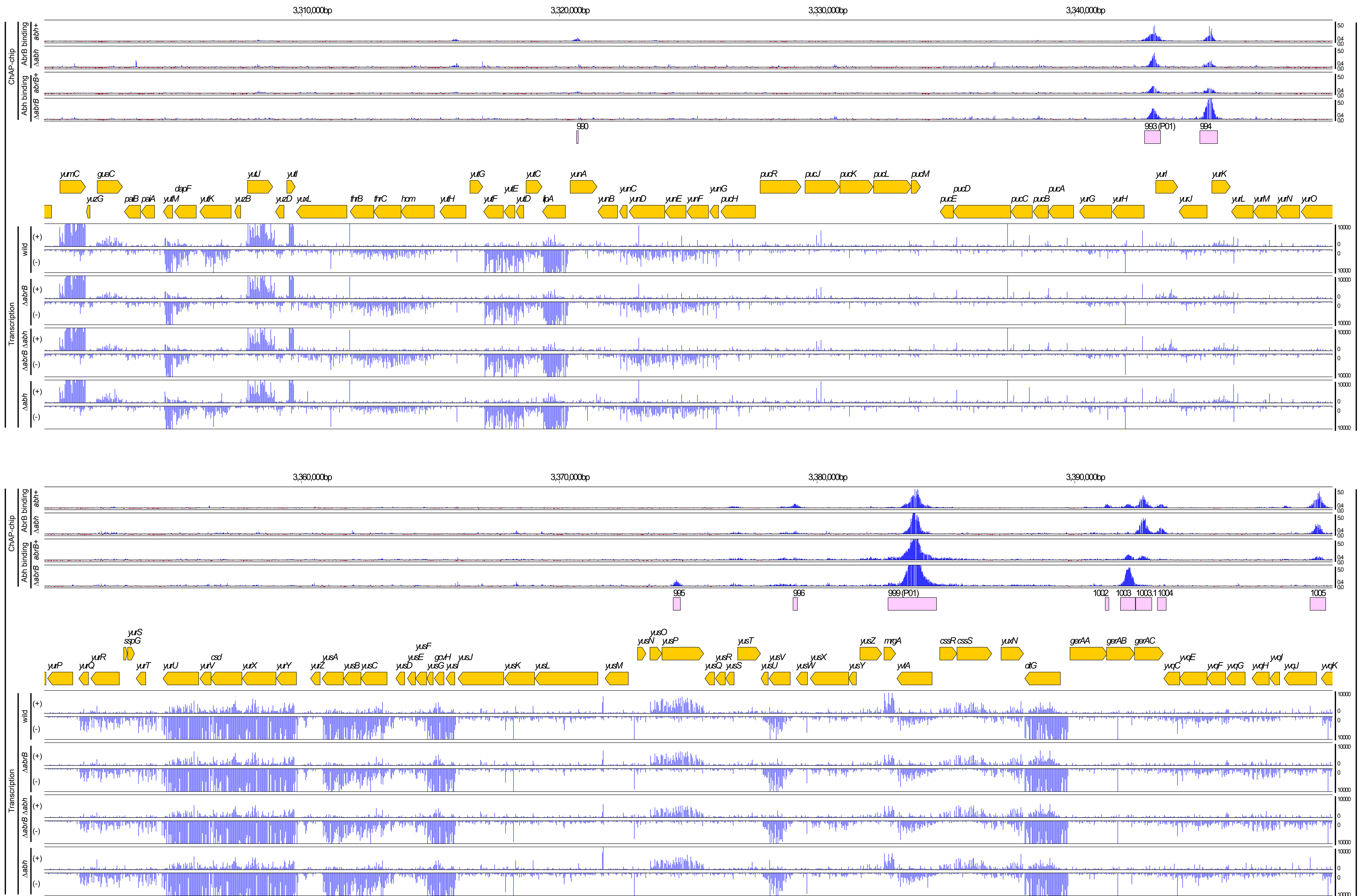


Fig.S1-34
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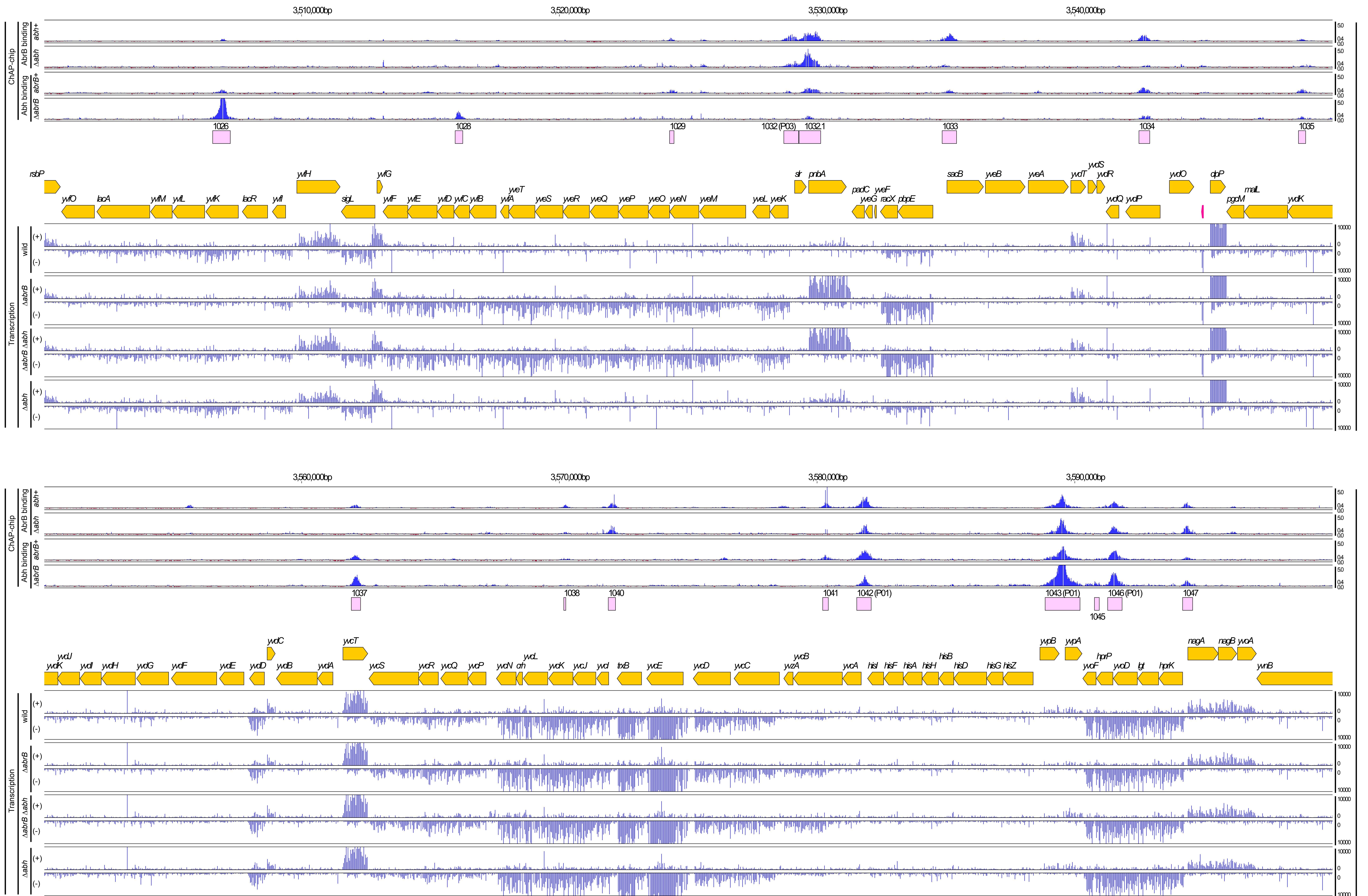


Fig.S1-36
189

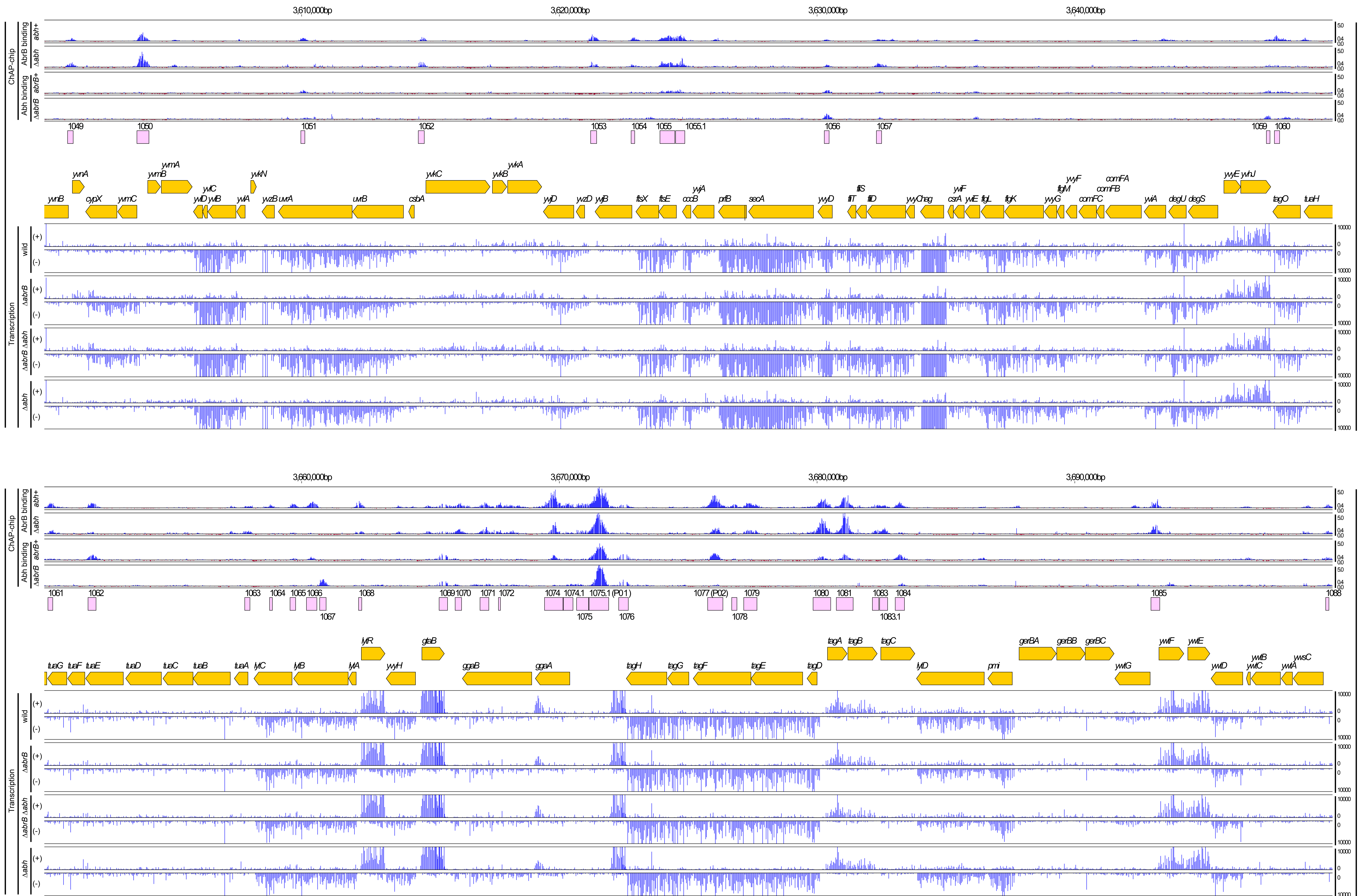


Fig.S1-37
190

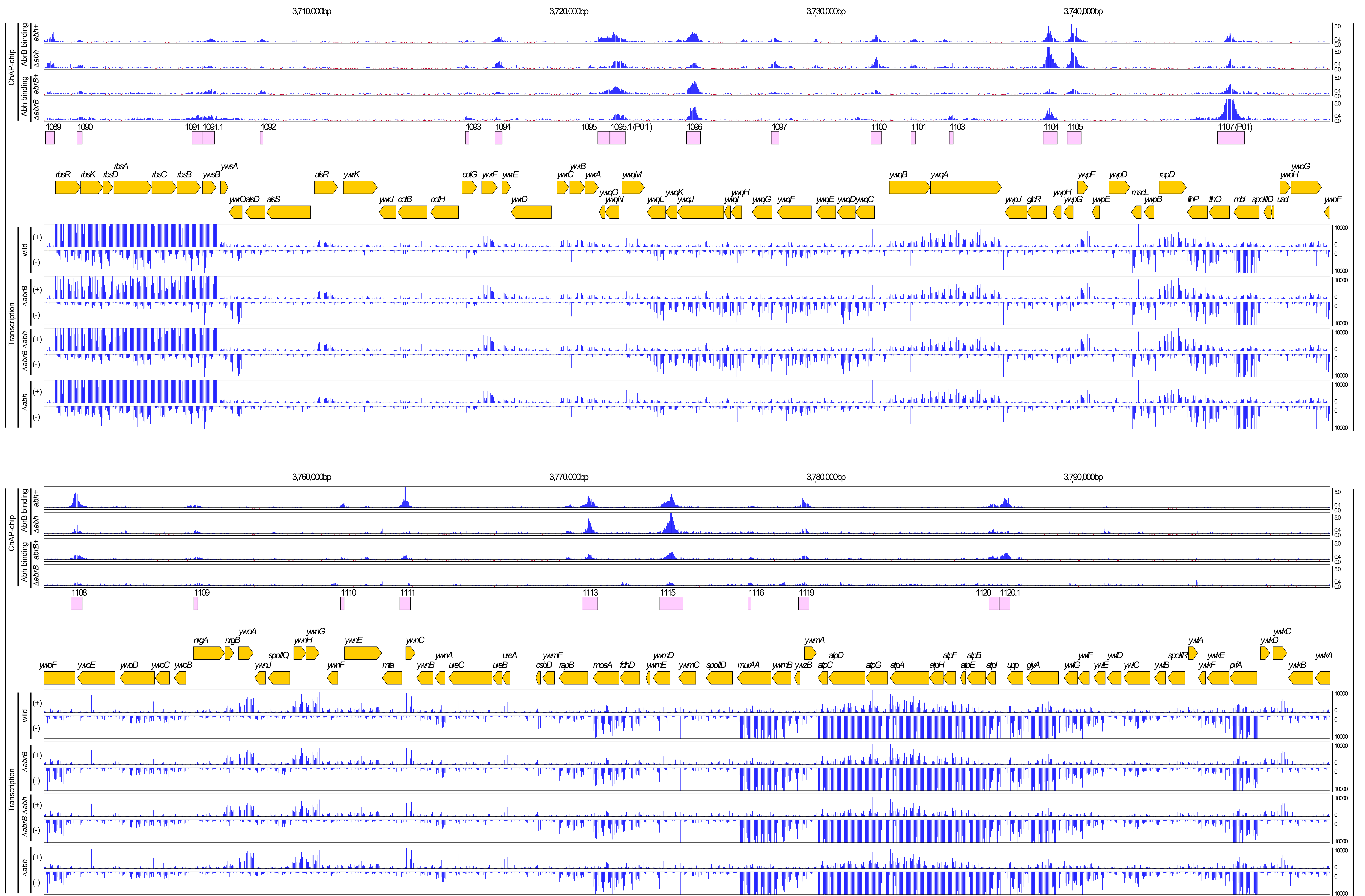
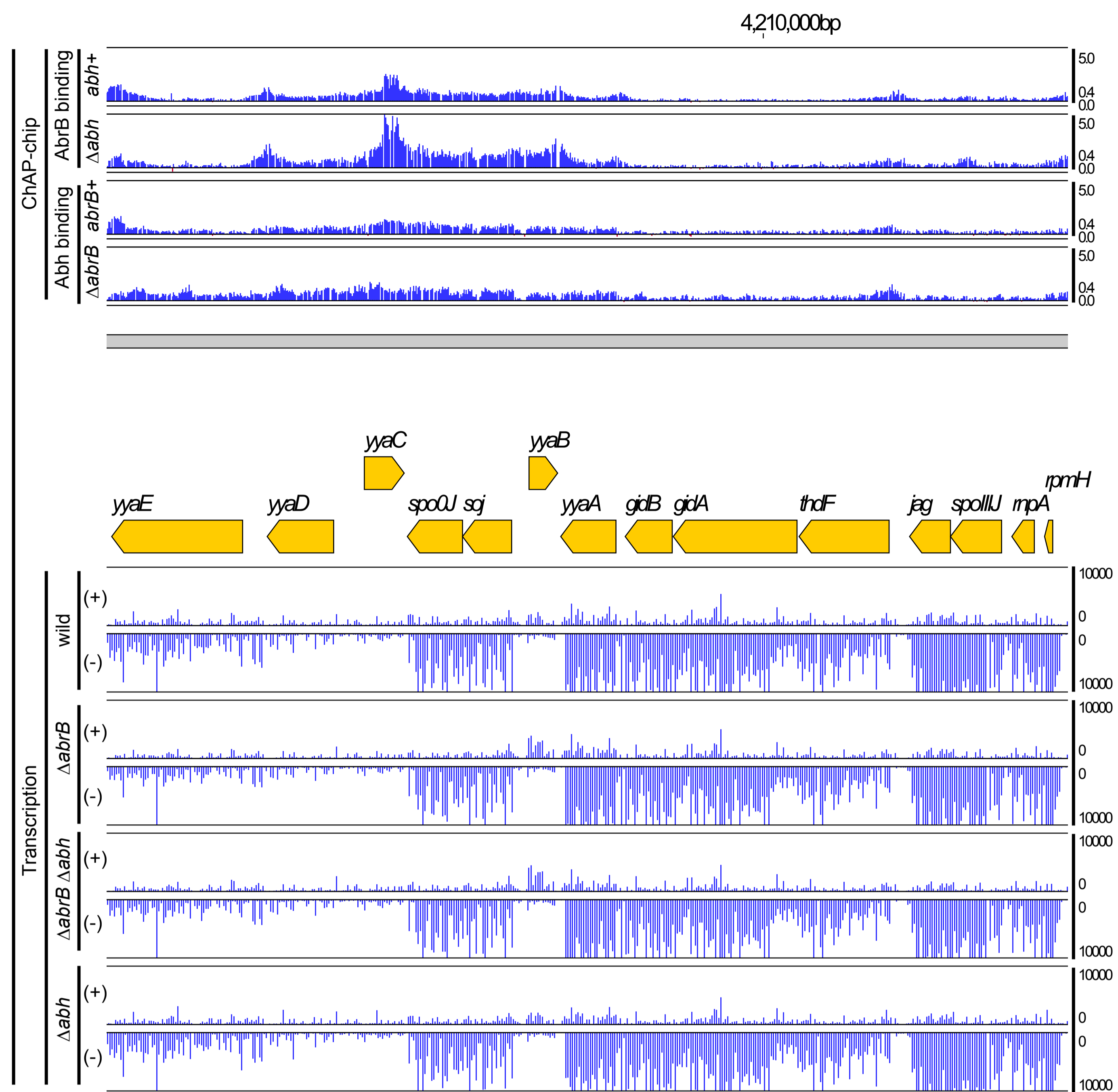


Fig.S1-38
191



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 Δabh 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 (Δabh) 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.