

Doctoral Dissertation

**Functional analysis of the protein Veg that
stimulates biofilm formation
in *Bacillus subtilis***

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Abstract

Biofilm is a complex aggregate of cells that adhere to each other and produce an extracellular matrix. In *Bacillus subtilis*, an extracellular polysaccharide (EPS) and amyloid fiber (TasA), synthesized by *epsA-O* and *tapA-sipW-tasA* operons, respectively, are the primary components of the extracellular matrix. I investigated the functional role of the previously uncharacterized *veg* gene in *B. subtilis*. It has been known that the *veg* gene, encoding a highly conserved small protein among gram-positive bacteria, is highly transcribed. However, I discovered that the protein level is kept at very low level by rapid proteolysis, in part, with LonA, ClpYQ and MlpA. Therefore I overproduced Veg, and found that overproduction of Veg stimulated biofilm formation via inducing transcription of the *epsA-O* and *tapA-sipW-tasA* operons. Moreover overproduced Veg restored the impairment of biofilm formation in deletion mutants of *sinI*, *slrA* or *slrR*, encoding an antirepressor of SinR that acts as the master regulator of biofilm formation, while biofilm morphology in the absence of SinR was not affected by either additional *veg* deletion or overproduction, indicating that Veg negatively regulates SinR activity independently of the known antirepressors. Expression of *sinR* was not affected in Veg-overproducing cells, and SinR amounts were similar in cells expressing different levels of Veg, strongly suggesting that Veg modulates the repressor activity of SinR. Interestingly, the results of *in vivo* pull-down assay of the SinR complex indicated that Veg inhibits the interactions between SinR and SlrR. Based on these findings, I propose that Veg or a Veg-induced protein acts as an antirepressor of SinR to regulate biofilm formation. In this study, I will discuss how Veg activity is regulated and what Veg controls other than biofilm formation via the newly identified pathway.

Keywords:

Bacillus subtilis, Veg, biofilm formation, EPS, TasA, SinR.

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1. INTRODUCTION

Bacillus subtilis is able to differentiate into a variety of cellular states in response to environmental changes. When nutrients are abundant, cells grow as a free-floating planktonic form. Under nutrient-limiting conditions, developmental cellular differentiation processes, such as competence of DNA uptake, sporulation and biofilm formation, proceed appropriately in response to different environments. These processes are accompanied by dramatic changes in gene expression, i.e., a new set of genes is turned on and nonessential genes for differentiation are turned off. Thus, *B. subtilis* presents a good model organism to study these physiological mechanisms in complex lifestyles.

1.1 Biofilms

In natural environments, microorganisms do not live as simple state of single cells but instead tend to form surface-attached multicellular communities, so-called biofilms, as one of the most important survival strategies (Yang *et al.*, 2011). Biofilms present in our daily lives, such as in natural and industrial settings, surfaces of dead tissues and medical devices; they can also impact our bodies to cause diseases, as in the case of infection (Hall-Stoodley *et al.*, 2004). Cells in biofilms are embedded by a biofilm extracellular matrix that consists of extracellular polymeric substances, including peptidoglycan, lipids, phospholipids and all major classes of macromolecules, such as exopolysaccharides, proteins and nucleic acids, mostly produced by organisms themselves (Flemming & Wingender, 2010; Yang *et al.*, 2011). The matrix is not only responsible for adhesion of the planktonic cells to surfaces, cohesion in the biofilm and

stabilization of the three-dimensional architecture of the biofilm, but also serves as a nutrient source to provide carbon-, nitrogen- and phosphorus-containing compounds for utilization by the biofilm community (Flemming & Wingender, 2010; Abee *et al.*, 2011). Additionally, the matrix functions as a signal to trigger sporulation in spore-forming bacteria, allowing these matrix-producing cells to continue the sporulation development at the tips of aerial structure in the mature biofilms (Aguilar *et al.*, 2010).

In addition, the matrix plays an important role in the protection from diverse environmental stresses, as well to various antimicrobial agents and host defenses (Fux *et al.*, 2005; Anderson & O'toole, 2008; López *et al.*, 2010). This broad resistance makes it difficult to remove biofilms and results in serious problems for public health and industrial processes. On the other hand, there are also benefits that a bacterial community might obtain from the formation of biofilms. For example, it can be used for the removal of organic pollutants and ammonia from wastewater, and hydrocarbons and heavy metals from the environment; it is also used in industrial plants to help in immobilization and degradation of pollutants (Wuertz *et al.*, 2003; Singh *et al.*, 2006).

1.2 Processes in biofilm development

Biofilm formation is a developmental process in which bacteria switch from a free-living state to a surface-associated multicellular state, and then subsequent growth results in a three-dimensional structured communities and cellular differentiation (Kuchma & O'Toole, 2000; Stoodley *et al.*, 2002; Lemon *et al.*, 2008). The stages involved in *B. subtilis* growth cycle of a biofilm are shown in Figure 1.

Stage I is the cell attachment phase that is induced by environmental signals. Various environmental signals regulate bacterial biofilm formation including variations changes

in pH, availability of nutrients, temperature, oxygen concentration, osmolality and iron (Aparna *et al.*, 2008). This stage is reversible as some planktonic cells can adhere to a surface; some cells also can detach from it. During this stage, cells exhibit a logarithmic growth rate.

Stage II is microcolonies formation phase. After adhering to the surface, cells begin to multiply through cell-cell intercellular signals and communications to form monolayer colonies. Once the signal intensity exceeds a certain threshold level, the genetic system of biofilm extracellular matrix productions is activated, and then the matrix supports structured microcolonies formation in which there can be extensive cellular differentiation. The interactions involved in cell-cell communication and matrix production are also important for biofilm formation and development (Stanley & Lazazzera, 2004; Aparna *et al.*, 2008; Simões *et al.*, 2010). During this stage, cell aggregation is formed and motility is decreased.

Stage III is biofilm maturation phase. Accompanied by cell division and differentiation, biofilms form three-dimensional architecture. Near the top of the aerial structures, cells differentiate to spores (Branda *et al.*, 2001). Meanwhile, this complicated structure is encased in the extracellular matrix that protects cells within it from various environmental stresses. During this stage, a lot of genes encoding proteins involved in sporulation, metabolism, membrane transport and/or secretion, and gene regulation are activated in mature biofilm (Stoodley *et al.*, 2002). In *B. subtilis*, Stanley *et al.* (Stanley *et al.*, 2003) used DNA microarray technology to compare the genes differentially expressed during biofilm formation. They observed that transcriptional factors Spo0A- and SigH- activated genes were upexpressed under biofilm formation conditions. In a separate study, Branda *et al.* (Branda *et al.*, 2004) identified several

genes encoding biofilm matrix, ABC transporter subunits and regulatory proteins, which were upregulated during biofilm formation.

Stage IV is cell dispersion and spore germination phase. Active cell dispersal is initiated via a highly regulated process. Changes in environment conditions, such as nutrition level and oxygen depletion, whether favorable or unfavorable, can lead to biofilm dispersal; since it is beneficial to increase the biofilm at nearby locations when nutrient are plentiful and beneficial to colonize further locations when nutrients are scarce (Karatan & Watnick, 2009; Kaplan, 2010; Wood *et al.*, 2011). In addition to cell dispersal, released spores can germinate to planktonic cells under certain conditions (Setlow, 2003).

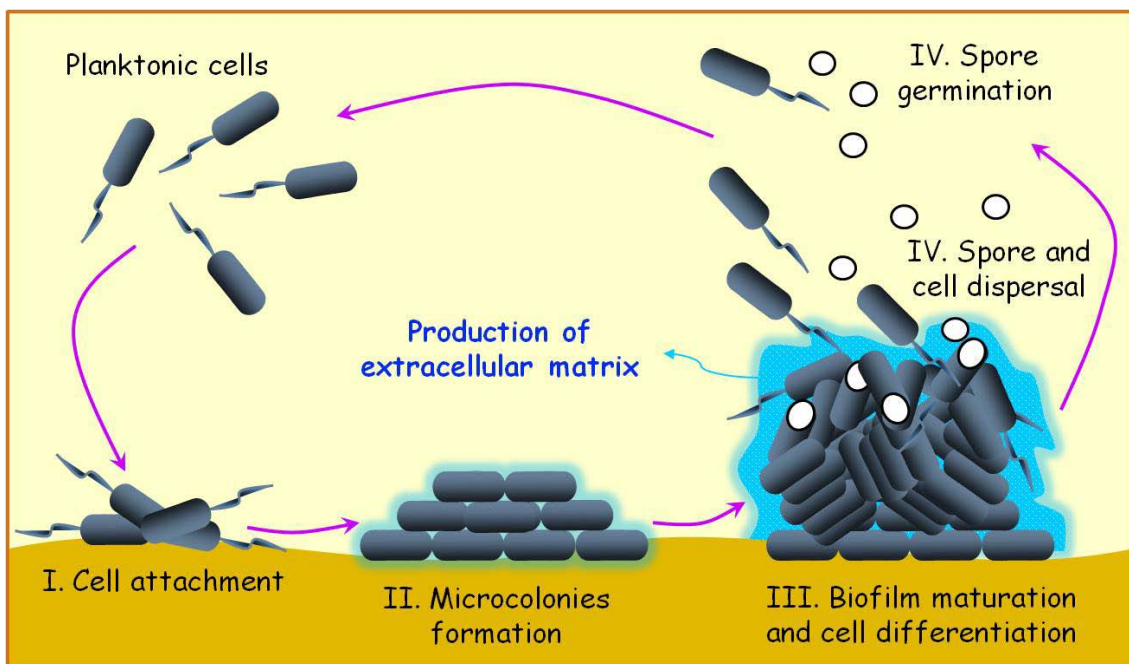


Figure 1. Model showing growth cycle of a biofilm in *B. subtilis* (O'Toole *et al.*, 2000).

1.3 The genetic regulation of *B. subtilis* biofilm formation

In *B. subtilis*, an extracellular polysaccharide (EPS) synthesized from the *epsA-O* 15-gene operon (*eps*) and amyloid fiber formed by TasA protein encoded by the *tapA-sipW-tasA* operon (*tasA*) bind cells together in biofilm, and constitute the primary components of the extracellular matrix (Branda *et al.*, 2006). *B. subtilis* matrix production during biofilm formation is governed by multiple physiological and population signals (Figure 2). AbrB and SinR, the main repressors, bind promoters of the *eps* and *tasA* operons independently to block biofilm formation (Hamon *et al.*, 2004; Kearns *et al.*, 2005; Chu *et al.*, 2008; Chumsakul *et al.*, 2011). These repressors are under the negative control of phosphorylated Spo0A (Spo0A~P), the key factor in the decision-making process for spore formation or biofilm formation (Hamon & Lazazzera, 2001; López *et al.*, 2009b). This phosphorylation is governed by the activity of five histidine sensor kinases (KinA-E) via a multicomponent phosphorelay consisting of the phosphorelay proteins Spo0F and Spo0B. The phosphorelay starts with Spo0F, and then passes its phosphoryl group to Spo0B, which goes on to phosphorylate Spo0A (Figure 2) (LeDeaux *et al.*, 1995; Jiang *et al.*, 2000). Two of these kinases, KinA and KinB, have high activity and are required to achieve the high levels of Spo0A~P necessary for sporulation (Grossman, 1995; LeDeaux *et al.*, 1995; Piggot & Hilbert, 2004); while KinC and KinD moderate low levels of Spo0A~P at the onset of stationary phase to trigger biofilm extracellular matrix production (López *et al.*, 2009a; López & Kolter, 2010; Aguilar *et al.*, 2010). However, the nature of the signal and the mechanism of kinase activation remain to be elucidated.

Activation of Spo0A via phosphorylation suppresses expression of *abrB* and induces the antirepressor, AbbA, which binds to AbrB and prevents interactions with DNA

(Strauch *et al.*, 1990; Banse *et al.*, 2008). On the other hand, the small protein antagonist of SinR, SinI, that lacks the N-terminal DNA binding domain but contains a C-terminal oligomerization domain similar to SinR, binds directly to SinR via protein-protein interactions to derepress the SinR regulon, and its transcription is directly switched on by Spo0A~P. In addition to the Spo0A/SinI pathway, YwcC/SlrA, another pathway of SinR regulation, has been identified (Kobayashi, 2008; Chai *et al.*, 2009; Chai *et al.*, 2012). YwcC is a TetR-type repressor that suppresses the divergently transcribed *slrA* gene, while SlrA is a SinI paralog that functions as another antirepressor of SinR. Based on observation that mutations of late-flagellar genes such as *motA* affect expression of SlrR/SlrA-regulated genes, the pathway is proposed to be related to flagellar-associated regulation (Kobayashi, 2008), although the precise underlying mechanisms remain to be clarified.

Furthermore, SinR activity is regulated by SlrR (Figure 2). SlrR is a SinR homolog composed of both the C-terminal oligomerization and N-terminal DNA-binding domains. Its transcription is repressed by SinR (Chu *et al.*, 2008; Kobayashi, 2008; Colledge *et al.*, 2011). Importantly, when *slrR* expression is derepressed via inactivation of SinR by SinI and/or SlrA, induced SlrR binds to SinR and inhibits the ability of SinR to bind to the control region of *slrR*. Thus, SinR, *slrR* and SlrR form a self-reinforcing, double-negative feedback loop in which SlrR antagonizes SinR, thereby stimulating derepression of *slrR* (Figure. 2) (Chai *et al.*, 2010). SlrR is additionally involved in the regulation of motility and cell separation as a repressor via direct interactions with regulatory regions of *hag*, *lytABC* operon and *lytF* genes, although these interactions are substantially stimulated by the presence of SinR (Chai *et al.*, 2010).

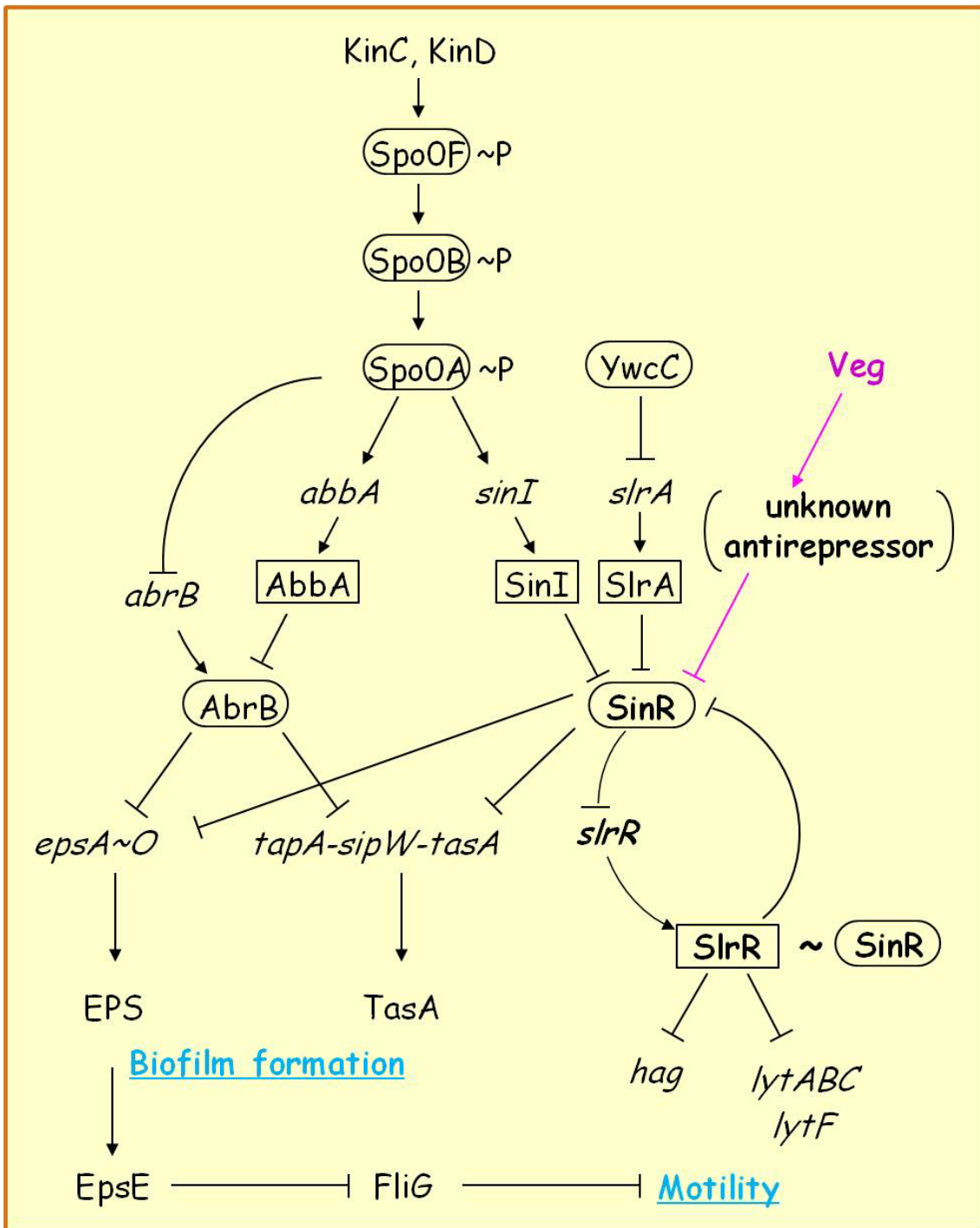


Figure 2. Regulatory pathways for biofilm formation and motility in *B. subtilis*. Arrows indicate activation and T bars indicate repression. Transcription regulators and antirepressors are encircled by ellipses and squares, respectively.

1.4 Motility in *B. subtilis*

Biofilm formation and motility are mutually exclusive lifestyles of *B. subtilis*: cells within a biofilm are nonmotile and aggregated by the extracellular matrix. Therefore, biofilm formation and motility are coordinately and oppositely controlled by the master regulator SinR (Blair *et al.*, 2008; Diethmaier *et al.*, 2011). SinR not only controls biofilm formation but is also involved in the regulation of motility. First, one of the proteins expressed in the *eps* operon, EpsE, interacts with the flagellar motor switch protein FliG to prevent the rotation of the flagellum (Figure 2) (Blair *et al.*, 2008). In this way, motility is directly inhibited when *epsE* expression is derepressed via inactivation of SinR. Second, in an alternative complex with the transcription factor SlrR, SinR triggers the DNA binding activity of this regulator, resulting in repression of autolysis and motility genes. On the other hand, in complex with SlrR, SinR can no longer repress the biofilm operons (Chai *et al.*, 2009; Chai *et al.*, 2010). Thus, SinR is the very important key to govern the balance between biofilm formation and motility.

1.5 Previous study of Veg in *B. subtilis*

The *B. subtilis veg* gene encoding a small, conserved protein is transcribed at high levels during both exponential growth and sporulation, and thus widely applied for investigation of the transcription mechanism (Ollington & Losick, 1981; Grice *et al.*, 1986). A previous study showed that deletion of Veg results in delayed spore germination during the sporulation phase, although the exact function is yet to be elucidated (Fukushima *et al.*, 2003). Interestingly, in the previous report for Veg, I noticed that Veg-GFP fusion proteins seemed to be localized on the whole nucleoid in exponential growing cells (Fukushima *et al.*, 2003). Thus, in my previous study, a

Veg-GFP expressing strain was constructed to reconfirm the nucleoid localization (Figure 3). Since the low molecular mass of Veg is highly expressing and localized to the nucleoid, which are analogous to those of nucleoid-associated proteins, I suspected that Veg could also be a new nucleoid-associated protein. Hence, ChAP (Chromatin affinity precipitation)-chip analysis (Ishikawa *et al.*, 2007) was performed to determine the distribution of Veg protein on the *B. subtilis* genome by using a strain expressing Veg C-terminally tagged with 12His or 2HC (twelve histidines plus a chitin-binding domain) (Veg2HC). The VegHis or Veg2HC expressing strain showed normal growth and spore germination, indicating that the fusion protein retains function of Veg. ChAP-chip result showed that distribution of Veg on the whole *B. subtilis* genome during exponential growth phase was detected non-specific (Figure 4). I concluded that the nucleoid interaction of Veg might be indirect. Thus, the role of Veg in *B. subtilis* was still unclear.

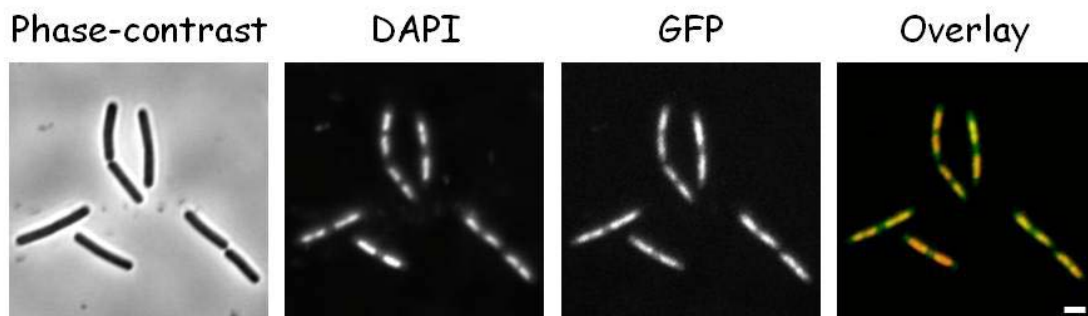


Figure 3. Localization of the Veg-GFP protein. LY067 (*veg-gfp*) strain was cultured to mid-logarithmic phase in LB medium at 37°C, and localization of Veg-GFP was visualized by fluorescence microscopy with DNA staining by DAPI. Overlay is a DAPI image overlaid on a GFP image with DNA shown in red and Veg-GFP in green. The scale bar is 2 μ m.

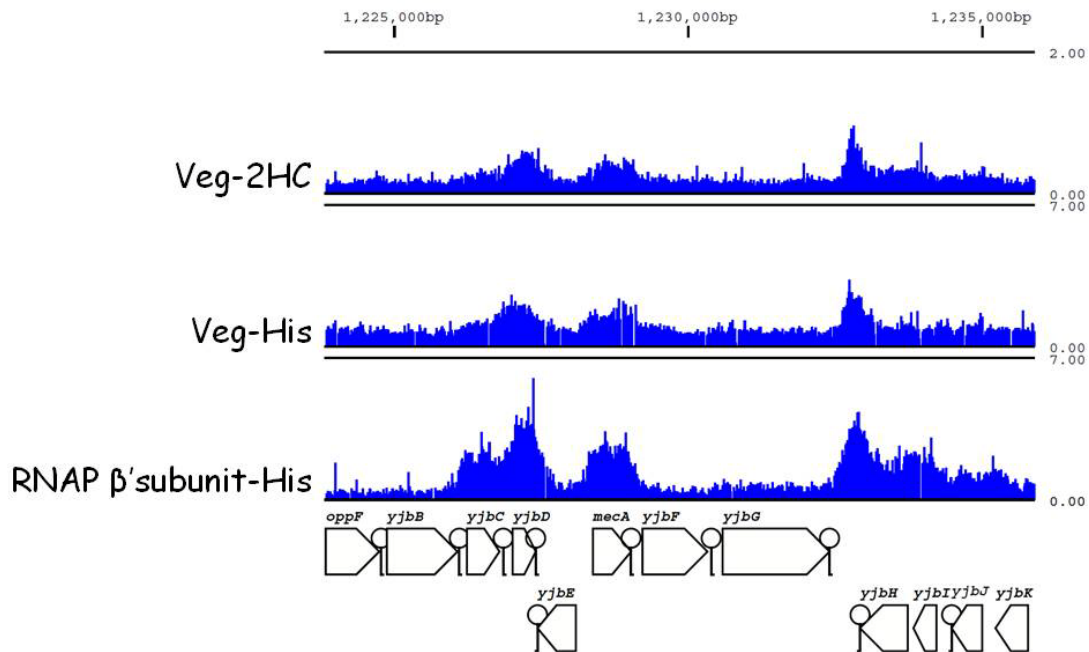


Figure 4. Veg binding signals on the *B. subtilis* genome. Distribution of Veg and RNA polymerase (RNAP) β subunit binding signals in the 1,225,000 bp to 1,235,000 bp region of the genome, are shown. Strains used for ChAP-chip analysis are indicated on the left. Protein-binding signals for each probe in the region are indicated alongside the genomic coordinates. The gene organization is schematically shown at the bottom.

1.6 Conservation of Veg protein in bacteria

The *veg* gene of *B. subtilis* encodes an 86-amino-acid polypeptide (Moran *et al.*, 1982), with no significant motif in the amino acid sequence (Fukushima *et al.*, 2003). According to the Microbial Genome Database (MBGD) (Uchiyama *et al.*, 2010), *veg* is highly conserved in two phyla, Firmicutes (low GC Gram-positive bacteria) and Synergistetes (anaerobic Gram-negative bacteria), as well as a family of Actinobacteria (Coriobacteridae), indicating that conservation of *veg* is not restricted to spore-forming bacteria (such as *Bacillus* and *Clostridium*), but also extends to non-spore-forming bacteria (*Lactobacillus* and *Synergistetes*). This finding further suggests an important role of Veg during growth phases other than sporulation

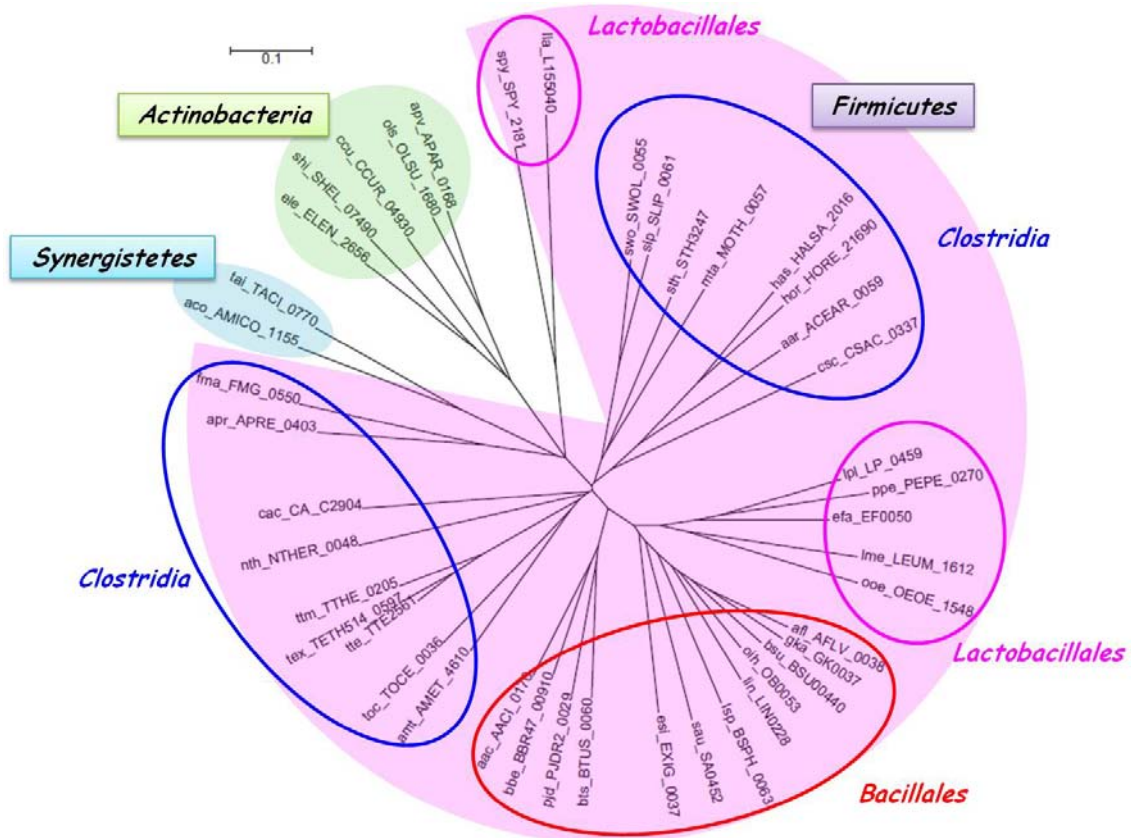


Figure 5. Phylogenetic trees based on Veg amino-acid sequence.

In the present study, I demonstrate that Veg is an additional regulatory protein to contribute to the control of biofilm matrix production. My results indicate that Veg is unstable in the wild-type cells, and partially degraded by LonA, ClpYQ and MlpA proteases. When Veg protein is increased to detectable levels, it stimulates biofilm development by transcriptional activation of the matrix genes through repression of SinR activity independently on SinI, SlrA and SlrR pathways. Overproduction of Veg also prevents SlrR binding to SinR, and inhibits cell motility probably through inactivation of SinR.

2. MATERIALS AND METHODS

2.1 Bacterial strains and culture conditions

The *B. subtilis* strains used in the present study, specifically, the laboratory strain 168 BFA, undomesticated wild-type strain NCIB3610 and derivatives, are listed in Table 1. The procedures used to construct mutant strains are described below. Plasmids and primers used in the present study are listed in Tables 2 and 3, respectively. The *E. coli* strains, DH5 α and C600, were used for plasmid construction. All bacterial strains were grown in Luria-Bertani (LB), MSgg (Branda *et al.*, 2006), or Spizizen's minimal medium (SMM) (Spizizen, 1958), at 37°C or 30°C as indicated. Antibiotics were used at the following concentrations: ampicillin, 50 $\mu\text{g ml}^{-1}$; chloramphenicol, 5 $\mu\text{g ml}^{-1}$; kanamycin, 10 $\mu\text{g ml}^{-1}$; spectinomycin, 100 $\mu\text{g ml}^{-1}$; tetracycline, 10 $\mu\text{g ml}^{-1}$; and erythromycin plus lincomycin, 0.5 $\mu\text{g ml}^{-1}$ and 25 $\mu\text{g ml}^{-1}$; respectively.

Table 1. <i>B. subtilis</i> strains used in this study.		
Strain	Relevant genotype and description ^a	Reference and source ^b
168 BFA	<i>trpC2</i>	Laboratory stock
NCIB3610	undomesticated wild type	Laboratory stock
DS1882	3610 <i>epsH::tet amyE::P_{eps}-lacZ cat</i>	Kearns & Losick, 2003
DS3352	3610 <i>epsH::tet amyE::P_{tapA}-lacZ cat</i>	Chu <i>et al.</i> , 2006
OC003	168 <i>abrB::spec</i>	Chumsakul <i>et al.</i> , 2011
TMO310	168 <i>aprE::spec lacI P_{spac}-mazF</i>	Morimoto <i>et al.</i> , 2009
QB4756	168 <i>clpC::spec</i>	Msadek <i>et al.</i> , 1998
RIK741	<i>trpC2 lys1 nprE18 nprR2 aprEΔ3 clpP::spec spo0E::erm</i>	Nanamiya <i>et al.</i> , 2000
RIK770	<i>trpC2 lys1 nprE18 nprR2 aprEΔ3 clpX::neo</i>	Nanamiya <i>et al.</i> , 2003
LY001	168 <i>veg::pMUTinHisΔveg</i>	pMUTinHisΔveg → 168 BFA
LY002	168 <i>veg::pMUTin2HCΔveg</i>	pMUTin2HCΔveg → 168 BFA
LY011	168 <i>veg::cat</i>	PCR product → 168 BFA
LY012	168 <i>sinR::kan</i>	PCR product → 168 BFA
LY013	168 <i>slrR::kan</i>	PCR product → 168 BFA
LY014	168 <i>sinI</i> (no marker)	PCR product → 168 BFA (removal of <i>erm</i> cassette)
LY015	168 pO-MCS <i>tet</i>	pO-MCS → 168 BFA
LY016	168 pO-veg <i>tet</i>	pO-veg → 168 BFA
LY017	168 <i>veg::cat sinR::kan</i>	LY012 → LY011
LY018	168 <i>veg::cat slrR::kan</i>	LY013 → LY011
LY019	168 <i>veg::cat sinI</i>	LY011 → LY014
LY020	168 <i>slrR::kan sinI</i>	LY013 → LY014
LY021	168 <i>veg::cat slrR::kan sinI</i>	LY013 → LY019
LY022	168 <i>sinR::kan</i> pO-MCS <i>tet</i>	LY012 → LY015
LY023	168 <i>sinR::kan</i> pO-veg <i>tet</i>	LY012 → LY016
LY024	168 <i>slrR::kan</i> pO-MCS <i>tet</i>	pO-MCS → LY013
LY025	168 <i>slrR::kan</i> pO-veg <i>tet</i>	pO-veg → LY013
LY026	168 <i>sinI</i> pO-MCS <i>tet</i>	pO-MCS → LY014
LY027	168 <i>sinI</i> pO-veg <i>tet</i>	pO-veg → LY014
LY028	168 <i>slrR::kan sinI</i> pO-MCS <i>tet</i>	pO-MCS → LY020
LY029	168 <i>slrR::kan sinI</i> pO-veg <i>tet</i>	pO-veg → LY020
LY030	168 <i>veg::erm</i>	pCm:Em → LY011
LY031	168 <i>epsH::tet amyE::P_{eps}-lacZ cat</i>	DS1882 → 168 BFA
LY032	168 <i>epsH::tet amyE::P_{tapA}-lacZ cat</i>	DS3352 → 168 BFA
LY033	168 <i>epsH::spec amyE::P_{tapA}-lacZ cat</i>	pTc::Sp → LY032
LY034	168 <i>epsH::spec</i>	LY033 → 168 BFA
LY035	168 <i>epsH::spec amyE::P_{eps}-lacZ cat</i>	LY034 → LY031
LY036	168 <i>epsH::spec amyE::P_{eps}-lacZ cat</i> pO-MCS <i>tet</i>	pO-MCS → LY035
LY037	168 <i>epsH::spec amyE::P_{eps}-lacZ cat</i> pO-veg <i>tet</i>	pO-veg → LY035
LY038	168 <i>epsH::spec amyE::P_{tapA}-lacZ cat</i> pO-MCS <i>tet</i>	pO-MCS → LY033
LY039	168 <i>epsH::spec amyE::P_{tapA}-lacZ cat</i> pO-veg <i>tet</i>	pO-veg → LY033
LY040	168 <i>veg::erm epsH::tet amyE::P_{eps}-lacZ cat</i>	LY030 → LY031
LY041	168 <i>veg::erm epsH::tet amyE::P_{tapA}-lacZ cat</i>	LY030 → LY032
LY042	168 <i>sinR::kan epsH::tet amyE::P_{eps}-lacZ cat</i>	LY012 → LY031
LY043	168 <i>sinR::kan epsH::tet amyE::P_{tapA}-lacZ cat</i>	LY012 → LY032
LY044	168 <i>slrR::kan epsH::tet amyE::P_{eps}-lacZ cat</i>	LY013 → LY031
LY045	168 <i>slrR::kan epsH::tet amyE::P_{tapA}-lacZ cat</i>	LY013 → LY032
LY046	168 <i>sinI epsH::tet amyE::P_{eps}-lacZ cat</i>	LY031 → LY014

Table 1. <i>B. subtilis</i> strains used in this study.		
Strain	Relevant genotype and description ^a	Reference and source ^b
LY047	168 <i>sinI epsH::tet amyE::P_{tapA}-lacZ cat</i>	LY032 → LY014
LY048	3610 <i>veg::cat</i>	LY011 → NCIB3610
LY057	3610 pO-MCS <i>tet</i>	pO-MCS → LY015
LY058	3610 pO-veg <i>tet</i>	pO-veg → LY016
LY066	168 <i>abrB::kan</i>	pSp::Km → OC003
LY067	168 <i>veg-gfp tet</i>	PCR product → 168 BFA
LY068	168 <i>abrB::kan epsH::tet amyE::P_{eps}-lacZ cat</i>	LY066 → LY031
LY069	168 <i>abrB::kan epsH::tet amyE::P_{tapA}-lacZ cat</i>	LY066 → LY032
LY070	168 <i>veg::cat abrB::kan</i>	LY066 → LY011
LY071	168 <i>abrB::kan</i> pO-MCS <i>tet</i>	pO-MCS → LY066
LY072	168 <i>abrB::kan</i> pO-veg <i>tet</i>	pO-veg → LY066
LY073	168 <i>lonA::cat</i>	PCR product → 168 BFA
LY074	168 <i>clpYQ::kan</i>	PCR product → 168 BFA
LY075	168 <i>lonA::cat</i> pO-veg <i>tet</i>	pO-veg → LY073
LY076	168 <i>clpYQ::kan</i> pO-veg <i>tet</i>	pO-veg → LY074
LY077	168 <i>clpC::spec</i>	QB4756 → 168 BFA
LY078	168 <i>clpP::spec</i>	RIK741 → 168 BFA
LY079	168 <i>clpX::neo</i>	RIK770 → 168 BFA
LY080	168 <i>clpC::spec</i> pO-veg <i>tet</i>	LY077 → LY016
LY081	168 <i>clpP::spec</i> pO-veg <i>tet</i>	LY078 → LY016
LY082	168 <i>clpX::neo</i> pO-veg <i>tet</i>	LY079 → LY016
LY083	168 <i>sinR-2hc cat</i>	PCR product → 168 BFA
LY084	168 <i>sinR-2hc cat</i> pO-MCS <i>tet</i>	LY083 → LY015
LY085	168 <i>sinR-2hc cat</i> pO-veg <i>tet</i>	LY083 → LY016
LY086	168 <i>sinR-2hc cat veg::erm</i>	LY083 → LY030
LY087	168 <i>mlpA::kan</i>	PCR product → 168 BFA
LY088	168 <i>mlpA::kan</i> pO-veg <i>tet</i>	pO-veg → LY087
LY089	168 <i>mlpA::erm</i>	pKm::Em → LY087
LY090	168 <i>lonA::cat clpYQ::kan mlpA::erm</i>	LY074 and LY089 → LY073
LY091	168 <i>slrA::kan</i>	PCR product → 168 BFA
LY092	168 <i>slrA::kan epsH::tet amyE::P_{eps}-lacZ cat</i>	LY091 → LY031
LY093	168 <i>slrA::kan epsH::tet amyE::P_{tapA}-lacZ cat</i>	LY091 → LY032
LY094	168 <i>veg^{hy}_01::spec</i>	PCR product → 168 BFA
LY095	168 <i>veg^{hy}_02::spec</i>	PCR product → 168 BFA
LY096	168 <i>veg^{hy}_03::spec</i>	PCR product → 168 BFA
LY099	168 <i>veg^{hy}_06::spec</i>	PCR product → 168 BFA
LY100	168 <i>veg^{hy}_07::spec</i>	PCR product → 168 BFA
LY101	168 <i>veg^{hy}_08::spec</i>	PCR product → 168 BFA
LY102	168 <i>veg^{hy}_09::spec</i>	PCR product → 168 BFA
LY103	168 <i>veg^{hy}_10::spec</i>	PCR product → 168 BFA
LY104	168 <i>veg^{hy}_11::spec</i>	PCR product → 168 BFA
LY105	168 <i>veg^{hy}_12::spec</i>	PCR product → 168 BFA
LY106	168 <i>veg^{loss}_01::spec</i>	PCR product → 168 BFA
LY107	168 <i>veg^{loss}_02::spec</i>	PCR product → 168 BFA
LY108	168 <i>veg^{loss}_03::spec</i>	PCR product → 168 BFA
LY109	168 <i>veg^{loss}_04::spec</i>	PCR product → 168 BFA
LY110	168 <i>veg^{loss}_05::spec</i>	PCR product → 168 BFA

Plasmid	Description	Reference and source
pO-MCS	A shuttle vector in <i>E. coli</i> and <i>B. subtilis</i> carrying the multiple cloning site sequence of pUC19	Okumura <i>et al.</i> , 2012
pO-veg	A shuttle vector in <i>E. coli</i> and <i>B. subtilis</i> carrying the insert sequence of <i>veg</i>	This study
pXT-gfp-MCS	A shuttle vector in <i>E. coli</i> and <i>B. subtilis</i> carrying the <i>gfp</i> sequence of pGFPuv4 under a xylose-inducible promoter P _{xyI} at <i>amyE</i> locus	This study
pO-vegx12his	A shuttle vector in <i>E. coli</i> and <i>B. subtilis</i> carrying the insert sequence of <i>vegx12his</i>	This study
pCm::Em	An antibiotic-resistance cassette switching vector from chloramphenicol to erythromycin	Yoshimura unpublished
pTc::Sp	An antibiotic-resistance cassette switching vector from tetracycline to spectinomycin	Yoshimura unpublished
pSp::Km	An antibiotic-resistance cassette switching vector from spectinomycin to kanamycin	Yoshimura unpublished
pKm::Em	An antibiotic-resistance cassette switching vector from kanamycin to erythromycin	Yoshimura unpublished

Primers	Sequence (5' -> 3') ^a	Location			Description	Reference
		start	end	strand		
Construction of pO-veg and pO-vegx12his						
attB1-SD-veg-F	aaaaagcaggctcgttgggaggaggtgaagcATGGC GAAGACGTTGTCCGATATTTAAAAG	52761	52789	+	Genome of 168 BFA	This study
attB2-veg-R	agaaagctgggtcTTAAAA TGCCACTGAGCTTGC GGCG	53021	52997	-	Genome of 168 BFA	This study
pM12HisRattB2	ggggaccacttgtacaagaagctgggtcGAGCTCTCA TCTATTTAATGG				12 x His	Chumsakul <i>et al.</i> , 2011
pUCMCS-F-adapter	aaaaagcaggctcgtTGTAAAACGACGGCCAGTG				pUC19	This study
pUCMCS-R-adapter	agaaagctgggtcTGACCA TGA TTA CGCCAAGC				pUC19	This study
A adapter-attB1	GGGGACAAAGTTTGTACAAAAAGCAGGCTC G	<i>attB1</i> site				Invitrogen
A adapter-attB2	GGGGACCACTTTGTACAAAGAAAGCTGGGTC	<i>attB2</i> site				Invitrogen
pDONR-F	TCGCGTTAA CGCTAGCATGGATCTCG				pDONR201	Invitrogen
pDONR-R	GTGTCTCAAAA TCTCTGATGTTAC				pDONR201	Invitrogen
OidFNrul3	CCTCTAGAGTCAAA TGTGAG				pMUTinHis	Ishikawa <i>et al.</i> , 2006
TerRSmalb	cgcgcccgggGGGTTA TTGTCTCATGAGCG				pMUTinHis	Ishikawa <i>et al.</i> , 2006
Deletion of <i>veg</i> from the <i>B. subtilis</i> genome						
veg-Fr-f	GAAACAGTTCAAACAGCCCCAAAAAAGATC CCTCAC	52245	52280	+	Genome of 168 BFA	This study
veg-Fr-r	gctcttctggggagctatccATTGTACAAACGAGC CCATTTTTGTC	52739	52713	-	Genome of 168 BFA	This study
veg-Ba-f	cggaaggatactacatcctggGAGCTGACATTTAATG ATGACGCCGC	52977	53002	+	Genome of 168 BFA	This study
veg-Ba-r	CATTGATCACA TTTGAAGTACAGGATGAAC ATATCC	53475	53439	-	Genome of 168 BFA	This study

Table S3. Primers used in this study.						
Primers	Sequence (5' -> 3') ^a	Location			Description	Reference
		start	end	strand		
Deletion of <i>lonA</i> from the <i>B. subtilis</i> genome						
lonA-Fr-f	GATGGGCCGTCA GCA GGCA TTGCG	2882371	2882348	-	Genome of 168 BFA	This study
lonA-Fr-r	gctcttctggtggagtctatccGACTTTAGTATGAAACC ATTATAATACAAC	2881873	2881901	+	Genome of 168 BFA	This study
lonA-Ba-f	cggaaggatactacatcctggGCCTTAGTAGGAGAG AAGAAA TGAAAAG	2879554	2879528	-	Genome of 168 BFA	This study
lonA-Ba-r	CGGACAACTTCGCGTGTGGTCC	2879056	2879080	+	Genome of 168 BFA	This study
Deletion of <i>clpYQ</i> from the <i>B. subtilis</i> genome						
clpQ_Y-Fr-f	GCTGCTCTATGCCACTGGAA TGAGGG	1686909	1686934	+	Genome of 168 BFA	This study
clpQ_Y-Fr-r	gctcttctggtggagtctatccGGCCTCCTTTAATTTTT CTTAAATGC	1687410	1687384	-	Genome of 168 BFA	This study
clpQ_Y-Ba-f	cggaaggatactacatcctggCGAAGAAAAGCTCGG AACGATAGCC	1689322	1689346	+	Genome of 168 BFA	This study
clpQ_Y-Ba-r	CGACA ACTGTTGCGCCGTATTCAGC	1689869	1689845	-	Genome of 168 BFA	This study
Deletion of <i>mlpA</i> from the <i>B. subtilis</i> genome						
mlpA-Fr-f	GAAGGCAATTGGGTGAGAAACAATG	1741399	1741423	+	Genome of 168 BFA	This study
mlpA-Fr-r	gctcttctggtggagtctatccACAAGCTGCCTTCATCT GTTACTTC	1741887	1741863	-	Genome of 168 BFA	This study
mlpA-Ba-f	cggaaggatactacatcctggCGTCTTAAAAAGGAA AGCCTGCCCC	1743131	1743155	+	Genome of 168 BFA	This study
mlpA-Ba-r	TGGA TCTCTAGTTGTAAAGCTCCCC	1743630	1743606	-	Genome of 168 BFA	This study
Deletion of <i>sinR</i> from the <i>B. subtilis</i> genome						
sinR-Fr-F	GAATACCA TCTAGAAAACAGGCGC	2551388	2551412	+	Genome of 168 BFA	This study
sinR-Fr-R	gctcttctggtggagtctatccGTGATATTATAGCACAT TCAGAAAAGG	2551868	2551843	-	Genome of 168 BFA	This study
sinR-Ba-F	cggaaggatactacatcctggGGGTA TCGAAAAA CAATTCGTG	2552149	2552173	+	Genome of 168 BFA	This study
sinR-Ba-R	GTCTGCTAAAAATGATGCA GCGGC	2552676	2552653	-	Genome of 168 BFA	This study
Deletion of <i>slrR</i> from the <i>B. subtilis</i> genome						
slrR-Fr-F	GATTCA GATAGGTGCAATCCGCGC	3528593	3528616	+	Genome of 168 BFA	This study
slrR-Fr-R	gctcttctggtggagtctatccGTCGTTATTCGTTCAAT ATAAGG	3529106	3529083	-	Genome of 168 BFA	This study
slrR-Ba-F	cggaaggatactacatcctggGGAAGATGATGATCG GTTAAAGGGC	3529581	3529605	+	Genome of 168 BFA	This study
slrR-Ba-R	GACAA TGA CTCTCCCTGTGCGC	3530057	3530034	-	Genome of 168 BFA	This study
Deletion of <i>slrA</i> from the <i>B. subtilis</i> genome						
slrA-Fr-F	TGCTCCTTTGCTGTACCCGGCGGC	3921843	3921866	+	Genome of 168 BFA	This study
slrA-Fr-R	gctcttctggtggagtctatccAATGTTTTCTGCAACA TGCGGGC	3922321	3922298	-	Genome of 168 BFA	This study
slrA-Ba-F	cggaaggatactacatcctggACCGTCCGGCAAGAC TAGTCCGAAC	3922483	3922507	+	Genome of 168 BFA	This study
slrA-Ba-R	AGCTTGAAAAGACGCGGTTGCA GC	3922993	3922970	-	Genome of 168 BFA	This study

Table S3. Primers used in this study.						
Primers	Sequence (5' -> 3') ^a	Location			Description	Reference
		start	end	strand		
Deletion of <i>sinI</i> from the <i>B. subtilis</i> genome						
sinI-Fr-F	GAAGA TTTCAAAGCAAGCTGACCC	2551154	2551178	+	Genome of 168 BFA	This study
sinI-Fr-R	gctcttctggtggagtctatccTTA TGTA TTTCA GCCAG TCCGGCC	2551651	2551628	-	Genome of 168 BFA	This study
sinI-Ba-F	cggaaggatactacatcctggTCTGCTCA TCCTGGTC CGGCAGCC	2551801	2551824	+	Genome of 168 BFA	This study
sinI-Ba-R	GAAAA TGAAAAAGCGCATAGCGAGG	2552348	2552324	-	Genome of 168 BFA	This study
sinI-Fr-r	ggctgccggaccaggatgagcagaTTA TGTA TTTCA G CCA GTCCGGCC	2551651	2551628	-	Genome of 168 BFA	This study
sinI-Ba-f	TCTGCTCA TCCTGGTCCGGCAGCC	2551801	2551824	+	Genome of 168 BFA	This study
sinI-Ba-r	gcttgagtcaattccgctgtcgAAAA TGAAAAAGCG CATAGCGAGG	2552348	2552324	-	Genome of 168 BFA	This study
sinI-Fr-F2	AATGTCACGATTTCA TACCA GTCCG	2551070	2551094	+	Genome of 168 BFA	This study
pAPNC-F	CGACAGCGGAA TTGA CTCAAGC				Genome of TMO310	Morimoto et al., 2009
chpA-R	CGCGGATCCTACCCAATCA GTACGTTA TTTTG				Genome of TMO310	Morimoto et al., 2009
emD-F2	acgtactgattgggtaggatccgcGAGTGAAAAAGT ACTCAACC				Genome of TMO310 and	This study
Erm-R	cacccgccagcctaaccgatCTAACA TTCCTTTA GTAA CGTGTAAC				pMUTinNC	Morimoto et al., 2002
Construction of <i>veg</i> mutant strains						
veg-f5	CAATAAA TGTA GTGA GGTGGATGCAATG	52736	52763	+	Genome of 168 BFA	This study
veg-r5	gctcttctggtggagtctatccCAGTAAACAAAAGGTT CACTGCCCG	53046	53022	-	Genome of 168 BFA	This study
veg-Fr-f3	GCA TGGAGATGAA GTCA GGCTGATTGC	51788	51814	+	Genome of 168 BFA	This study
veg-Fr-r3	TGCA TCCACCTCACTACA TTTA TTGTAC	52760	52733	-	Genome of 168 BFA	This study
veg-Ba-f4	cggaaggatactacatcctggCTTTTTGTTTTGCCCTTT TTTGGTTTCC	53047	53074	+	Genome of 168 BFA	This study
veg-Ba-r3	ATGACCCAGCAGTGCGGAGGCGTGTC	54013	53989	-	Genome of 168 BFA	This study
Construction of GFP-HBsu and native GFP strains						
tet2F	ggaggatccgaattcctcgaqCAGGTGATATGAAC AGC				pBEST307	This study
tetR-TerF	ggcagttccctactctcgcaTTAACGATTTAGAAATC CCTTTGAG				pBEST307	This study
Ter-F	TGCGAGAGTAGGGA ACTGCC				pMUTinNC	This study
TerR-SmaI	cgcgcccgggGGGTTA TTGTCTCATGAGCG				pMUTinNC	This study
SPCF	aagaacttCAAAAA TTA TATGGAGATCTGTATA AT				pAPNC213	This study
specR-ESKSBX	gactctagaggatcccgggtaccgagctcgaattGTTAT TGCAATAAAA TTAGCC				pAPNC213	This study
yfpGWSp-F(XbaI)	gcgctctagaTGGGA TTACACA TGGCATGG				pUC19-yfpGWSp	This study
yfpGWSp-R(BglII)	cgcgagatctCTGATATCA CCACTTTGTACAAG				pUC19-yfpGWSp	This study
xyIR-BglII	ggcagatctGATTTAAGTGAACAA GTTTATCC				pXTiGW	This study
attR'1F-SpeI	ggcactagtGAACTA TACAAAACA GTTTGTAC				pXTiGW	This study
gfp4*-BhSD	aaaggaggtgccacagaATGAGTAAAGGAGAAAG AACTTTTC				pGFPuv4	This study
gfp4*-linker-SpeI	ggcactagctcgatccaccagaaccgccagaaccgccTTT GTAGACTCA TCCATGCCATG				pGFPuv4	This study

Table S3. Primers used in this study.						
Primers	Sequence (5' -> 3') ^a	Location			Description	Reference
		start	end	strand		
Construction of GFP-HBsu and native GFP strains						
gfp-f	CAAGAGTGCCATGCCCGAAGG				pGFPuv4	This study
gfp-r	CGATCCACCAGAACCGCCAG				pGFPuv4	This study
gfp-erm-r	gtgctagaggatcaattctgaaTTATTTGTAGAGCTCA TCCATGCCATGTG				pGFPuv4	This study
hbs-f	ctggcggttctggtggatcgAACAAAAACAGAACTTAT CAATGCCGG	2385015	2384991	-	Genome of 168 BFA	This study
hbs-r	gtgctagaggatcaattctgaaTTATTTCCGGCAACT GCGTC	2384740	2384760	+	Genome of 168 BFA	This study
Erm-F2	TTCAAGAA TTGATCCTCTAGCAC				Genome of MU02	This study
amyE-backR	GTTGACTGCTAATGGAA CGCACG				Genome of MU02	This study
gfp-f2	TTATGTACAGGAACGCACTATA TC				pGFPuv4	This study
amyE-R2	ATCAAAGCCAGGCTGATTCTGACCG				Genome of MU02	This study
Construction of Veg-, Veg^{hy}-, Veg^{loss}-GFP strains						
veg_GFPHis-Fr-f	GAGGAGTTCTGAGAA TTGGTATGCC	52510	52534	+	Genome of 168 BFA	This study
veg mut-GFP-Fr-r	ggtgatgcatcctctcatAAA TGCCA CTGAGCTTGC GGCGTC	53018	52995	-	Genome of 168 BFA	This study
gfp-F	ATGAGTAAAGGAGAAGAACTTTTC				pGFPuv4	This study
12His-GFP-R	gctcttctggtggagtctatcctaTTTGTAGAGCTCATC CATGCCATGTG					This study
sinR-6his-r	gtgatggtgatggtgatgcatcctctcatCTCCTCTTTTTG GGATTTTCTCC	2552217	2552195	-	Genome of 168 BFA	This study
sinR-Cm-Ba-f2	cggaaggatactacatcctggCACTAACTCCTCTTTTTG TCAA TAACC	2552235	2552260	+	Genome of 168 BFA	This study
sinR-Cm-Ba-r	GTTGACAGTTGGAAAAGAGGGCGGC	2552760	2552736	-	Genome of 168 BFA	This study
DC-2HC-F	ATGAGAGGATCGCATCAACC				pMUTin2HC	Chumsakul et al., 2011
DC-2HC-R	gctcttctggtggagtctatcTCA TCTATTTATTGAAG CTGC				pMUTin2HC	Chumsakul et al., 2011
Antibiotics cassette						
rPCR-tetF	ggatagactccaccagaagagcCAGGTCGATATGAA CAGC				pUC19	Okumura et al., 2012
rPCR-tetR	ccaggatgtagtaccctccgGGGTTATTGTCTCATGA GCG				pUC19	Okumura et al., 2012
rPCR-CmF2	ggatagactccaccagaagagcATCA TCGGCAATAG TTAACC				pDLT3	Morimoto et al., 2002
rPCR-CmR2	ccaggatgtagtaccctccgCGGCGTAGAGGATCTG GAGC				pDLT3	Morimoto et al., 2002
rPCR-CmNoPTR	ccaggatgtagtaccctccgTTA TCTCA TATTA TAAA AGCCA GTC				pDLT3	This study
rPCR-KmF	ggatagactccaccagaagagcCGCAA GCTTACGAT AAACCCAGC				pDG780	Guerout-Fleury et al., 1995
rPCR-KmR	ccaggatgtagtaccctccgCTAGGTA CTA AAAACAA TTCA TCC				pDG780	Guerout-Fleury et al., 1995
rPCR-ermF	ggatagactccaccagaagagcAACAAA TAGGGGT TCCGCGCA				pMUTin2HC	Chumsakul et al., 2011
rPCR-ermR	ccaggatgtagtaccctccgCTCATA GAAATTA TTTCC TCCCG				pMUTin2HC	Chumsakul et al., 2011
a Capital and low er-case letters correspond to sequences annealed to a template and attached tag sequence, and underlined letters indicate an endonuclease recognition site.						

2.2 Construction of the plasmids pO-veg, pO-veg12His and pO-MCS

Expression plasmids for Veg (pO-veg), Veg-12His (pO-veg12His) and a negative control plasmid (pO-MCS) were created using the Gateway cloning system (Invitrogen), as described previously (Ishikawa *et al.*, 2006). To construct pO-veg, the *veg* gene was amplified from *B. subtilis* 168 BFA chromosomal DNA using primers attB1-SD-veg-F, in which the SD sequence of the *hbs* gene and half of the *attB1* sequence are attached at the 5' end, and attB2-veg-R, in which half of *attB2* sequence is attached at the 5' end. To construct pO-veg12His, a *veg* gene translationally fused with a coding sequence of twelve histidines (*veg-12xhis*) was amplified from chromosomal DNA of strain LY001 (168; *veg::pMUTinHisΔveg*) using the primers attB1-SD-veg-F and pM12HisR-attB2. To construct pO-MCS, the multi-cloning site was amplified from pUC19 using primers pUCMCS-F-adapter and pUCMCS-R-adapter. Next, entire recombination sites for BP clonase, *attB1* and *attB2*, were attached to the first PCR products in the second PCR using the adapter primers, Adapter-attB1 and Adapter-attB2. Fragments were cloned into an entry vector, pDONR201 (Invitrogen), with BP clonase to create entry clones, followed by transfer to a pOGW destination vector (Ishikawa *et al.*, 2006), according to Gateway technology instructions. For transformation of *B. subtilis* strains, the resulting plasmids were amplified in *E. coli recA*⁺ strain, C600.

2.3 Construction of deletion mutant by replacement with antibiotic cassette

To construct strains in which a gene was deleted, an antibiotic resistance cassette flanked by the regions upstream and downstream of the gene sequence was amplified with the gene-Fr-F/gene-Fr-R and gene-Ba-F/gene-Ba-R primer sets, respectively

(Table 3). The resulting three fragments were ligated using recombinant PCR, and integrated into the *B. subtilis* strain 168 BFA genome via double crossover recombination with selection for antibiotic resistance. To construct a deletion mutant of NCIB3610, the strain was transformed with chromosomal DNA from newly generated strain 168 BFA deletion mutants. To obtain double-deletion mutant strains, chromosomal DNA of one deletion mutant was transferred into the other deletion mutant strain.

2.4 Deletion of *sinI* gene using a marker-free gene disruption method

For deletion of the *sinI* gene, we performed a method of marker-free gene disruption comprising three steps (Morimoto *et al.*, 2009).

In the first step, *sinI* was replaced with an erythromycin resistance cassette amplified from a pMUTin2HC plasmid using the primer set rRCP-ermF/rRCP-ermR, as described above.

In the second step, a cassette in which *mazF* (a toxin gene encoding endoribonuclease that cleaves free mRNAs) under control of IPTG-inducible *spac* promoter, fused with the flanking sequences of the *sinI* region, was inserted between the front and internal sequence of the erythromycin resistance gene to remove the entire marker region in single-crossover recombination via counter-selection. Upstream (fragment A) and downstream (fragment B) sequences of the *sinI* region were amplified from *B. subtilis* 168 BFA genomic DNA using the primer sets, sinI-Fr-F/sinI-Fr-r and sinI-Ba-f/sinI-Ba-r, respectively. The *mazF* cassette was amplified using primers pAPNC-F and chpA-R from genomic DNA of *B. subtilis* TMO310 (168, *aprE::spec^R*, *lacI*, *Pspac-mazF*). An internal sequence in the

erythromycin resistance region (fragment C) was amplified using primers emD-F2 and Erm-R. PCR products were fused using recombinant PCR in the order A-B-*mazF*-cassette-C, using primers sinI-Fr-F and Erm-R, and integrated into the *sinI* deletion strain generated in the first step through homologous recombination between fragment A and C loci. The resulting recombinants were selected for spectinomycin resistance in the absence of IPTG.

In the last step, the inserted *mazF* cassette was removed to obtain marker-free *sinI* disruption. The primary transformant achieved in the second step was cultivated in the presence of IPTG (i.e., *mazF* toxin-inducing conditions), and clones in which the *mazF* cassette had been removed by intramolecular homologous recombination at region B were selected.

2.5 Construction of Veg mutant strains

To construct a Veg mutant strain, the method of error-prone PCR mutagenesis was carried with KAPA2G Robust PCR Kits (KAPA BIOSYSTEMS) (KAPA2G Buffer A, was used), followed with 0, 0.1 and 0.2 mM MnCl₂. Mutagenic PCR reactions were performed in Veriti 96-well Thermal cycler (Applied Biosystems) for 30 cycles: 15 sec at 95°C, 30 sec at 58°C and 30 sec at 72°C using *B. subtilis* 168 BFA genomic DNA as a template and primers veg-f5 and veg-r5. Then, a spectinomycin resistance cassette, amplified from a pUC19 plasmid using primers rRCP-SpecF and rRCP-SepcR, front and back regions of the *veg* gene were amplified by veg-Fr-f3/veg-Fr-r3 and veg-Ba-f4/veg-Ba-r3 primer sets respectively. The resulting four fragments were joined by recombinant PCR using primers veg-Fr-f3 and veg-Ba-r3 with KOD-Plus-Neo kits (TOYOBO) and integrated into the strain LY011 genome by double crossover

recombination with selection for the spectinomycin resistance on SMM medium plates. Mutant screens were performed with comparison of colony morphology formed between the Veg mutants and wild-type strain. Finally, the sequence of each obtained mutant was determined by ABI PRISM 3100 Genetic Analyzer (Applied Biosystems).

2.6 Construction of other strains

2.6.1 SinR2HC (LY083) strain

To construct a *B. subtilis* strain expressing SinR C-terminally tagged with twelve histidines and a chitin-binding domain (SinR-2HC), the *sinR* gene without the stop codon was amplified from *B. subtilis* 168 BFA genomic DNA using primers sinI-Ba-f and sinR-6his-r. The coding sequence of the *2hc* tag and a chloramphenicol resistance gene were amplified from plasmids pMUTin2HC and pDLT3 using the DC-2HC-F/DC-2HC-R and rPCR-CmF2/rPCR-CmR2 primer sets, respectively. The downstream region of *sinR* was amplified from *B. subtilis* 168 BFA genomic DNA with the sinR-Cm-Ba-f2 and sinR-Cm-Ba-r primers. Subsequently, the four fragments were ligated with recombinant PCR using primers sinI-Ba-f and sinR-Cm-Ba-r, and employed to transform *B. subtilis* 168 BFA cells, followed by double-crossover recombination with selection for chloramphenicol resistance to create LY083 strain.

2.6.2 GFP-HBsu (LY112) and native GFP (LY121) strains

Integration of *gfp*-fusion gene under xylose-inducible promoter P_{xyl} into *amyE* locus on the *B. subtilis* 168 BFA chromosome was carried out by use of pXT-Ngfp. To construct this Destination vector, pXTt was firstly constructed from pX (Kim *et al.*,

1996) by exchange of the chloramphenicol-resistance gene between two *EcoRV* sites on pX with tetracycline-resistance gene fused with strong terminator that was created by recombinant PCR between tetracycline resistance gene, amplified from pBEST307 (Itaya, 1992) with tet2F and tetT-TerF primers, and transcriptional terminator of *E. coli* *rrnB*, amplified from pMUTinNC (Morimoto *et al.*, 2002) with Ter-F and TerR-SmaI primers. Then, the pXTt was converted to Destination vector by insertion of Gateway cassette amplified with yfpGWSpF(Xba) and yfpGWSpR(BglII) primers from pUC19-yfpGWsp (a plasmid which chloramphenicol resistance gene, an antibiotic maker of Gateway cassette, between two *BamHI* sites on pUC19-yfpGW (Ishikawa *et al.*, 2006) was substituted by a spectinomycin resistance gene amplified from pAPNC213 with SPCF (Morimoto *et al.*, 2002) and specR-ESKSBX primers), into the *XbaI*-*BglII* sites, to create pXTtGW. Finally, entire pXTtGW was PCR-amplified with xylR-*BglII* and attR'1F-*SpeI* primers, digested with *BglII*, blunt-ended with Mung Bean Nuclease, digested with *SpeI*, and then ligated with *gfp* gene, which was amplified from pGFPuv4 (Ito *et al.*, 1992) with *gfp4**-BhSD and *gfp4**-linker-*SpeI*r primers, to create Destination vector pXT-*Ngfp*. Next, plasmid pXT-*Ngfp* was converted to pXT-*Ngfp*-MCS by recombination reaction with pENTR-MCS, a Gateway entry clone with multiple cloning site (MCS) (Okumura *et al.*, 2012). Plasmid pXT-*Ngfp*-MCS was amplified in *E. coli* *recA*⁺ strain and C600, and then, the resulting plasmid was transformed to *B. subtilis* 168 BFA cells, and created LY111 strain.

To construct *B. subtilis* strain expressing HBSu N-terminally fused with GFP or native GFP under xylose-inducible promoter P_{xyl} at *amyE* locus, the *gfp* gene (fragment A), the *hbs* gene (fragment B) and an erythromycin resistance gene connected with the back part of the *amyE* gene (fragment C) were amplified from plasmid

pXT-Ngfp-MCS, *B. subtilis* 168 BFA genomic DNA, and *B. subtilis* MU02 (*amyE::P_{xyI}-dnaA erm*) (Okumura *et al.*, 2012) using primer sets of gfp-f/gfp-r (for LY112 strain) or gfp-f/gfp-erm-r (for LY121 strain), hbs-f/hbs-r and Erm-F2/amyE-backR, respectively. Then, the three fragments (A, B and C) and two fragment (A and C) were joined by recombinant PCR using primer sets gfp-f2/amyE-R2 and gfp-f/amyE-backR, and used to transform to LY111 cells followed by double crossover recombination with selection for the erythromycin plus lincomycin resistance to create LY112 and LY121 strains, respectively.

2.6.3 Veg-GFP and Veg^{hy}-, Veg^{loss}-GFP strains

To construct *B. subtilis* strain expressing Veg or Veg mutants C-terminally fused with GFP, the wild-type *veg* gene, *veg*^{hy} and *veg*^{loss} mutants without stop codon were amplified from genomic DNA of *B. subtilis* 168 BFA and 168 BFA-derived *veg* mutants using primers veg_GFPHis-Fr-f and veg mut-GFP-Fr-r. The coding sequence of the *gfp* gene and a tetracycline resistance gene were amplified from plasmids pXT-Ngfp-MCS and pUC19 using primer sets of gfp-F/12His-GFP-R and rPCR-tetF/rPCR-tetR, respectively. The downstream region of the *veg* gene was amplified from *B. subtilis* 168 BFA genomic DNA using primers veg-Ba-f4 and veg-Ba-r. Then, the four fragments were joined by recombinant PCR using primers veg_GFPHis-Fr-f and veg-Ba-r and employed to transform *B. subtilis* 168 BFA cells followed by double crossover recombination with selection for the tetracycline resistance, to create LY067 and LY113-120 strains.

2.7 Assays of colony formation, pellicle formation and motility

Strains were grown in LB to OD₆₀₀ of 1.0. For the colony assay, 3 µl of culture was spotted onto LB, SMM or MSgg agar (1.5% agar), and plates incubated at 30°C for the indicated times. For the pellicle assay, 9 µl of culture was added to 9 ml of MSgg medium contained within a well of a 6-well microtiter dish (BD Falcon), and the dishes incubated without agitation at 30°C for the indicated times. Photographs were obtained using a Nikon camera (D70S).

For motility assays, cells, previously grown on LB broth-2% agar plates with appropriate antibiotic, were seeded onto the center of 9.0-cm plates containing freshly prepared LB broth plus 0.2% and 0.7% agar to evaluate swimming and swarming motility, respectively. Swimming and swarming plates were incubated at 30°C, when appropriate, 1 mM IPTG was added; diameters of halos due to bacterial migration were recorded 13 or 15 h post-inoculation, as indicated.

2.8 Fluorescence microscopy

Live cells were examined on agarose slides (Price and Losick, 1999). Cell morphology and nucleoid distribution were examined by fluorescence microscopy after 5 ng ml⁻¹ DAPI (4', 6-diamidino-2-phenylindole) staining using a filter set (Cube A4, Leica Microsystems), as described previously (Hassan *et al.*, 1997). Fluorescence was detected using fluorescence microscopy (DMRE-HC, Leica Microsystems), a cooled digital CCD camera (model 1300Y, Roper Scientific), and a GFP filter set (Cube L5, Leica Microsystems). Images were uploaded and analyzed to determine the intracellular locations of the signals using Meta-Morph software (Universal Imaging).

2.9 β -Galactosidase assays

β -galactosidase-specific activity was calculated as previously described (Youngman *et al.*, 1985). Cells were grown in LB medium at 37°C with shaking. 1 ml of culture was collected at each time point. Cells were suspended in 1 ml of Z-buffer (60 mM Na_2HPO_4 , 40 mM NaH_2PO_4 , 10 mM KCl, 1 mM MgSO_4 , 1 mM DTT). Each sample was diluted in Z-buffer to a final volume of 1 ml supplemented with 0.25 mg ml⁻¹ lysozyme and 5 $\mu\text{g ml}^{-1}$ DNase I mixture solution, followed by incubation at 37°C for 5 mins. Triton-X100 was added to each sample to a final concentration of 1% before measurement. Reactions were started with addition of 200 μl of 4 mg ml⁻¹ ONPG (o-nitrophenyl β -D-galactoside) and stopped with addition of 400 μl of 1 M Na_2CO_3 . OD_{420} values of the reaction mixture were measured. The β -Galactosidase-specific activity was calculated according to the equation: $1000 \times \text{OD}_{420} / (\text{reaction time} \times \text{OD}_{600} \text{ unit of cells})$. Assays were conducted in 3 times.

To monitor β -galactosidase activity on solid medium, colonies were grown as described above on MSgg plates containing 40 $\mu\text{g ml}^{-1}$ X-Gal (5-bromo-4-chloro-3-indolyl- β -D-galactopyranoside) for the indicated times at 30°C and photographs were taken using a EPSON scanner (GT-X900) or Nikon camera (D70S).

2.10 Transcriptome analysis

Cells from 50 ml aliquots of exponentially growing cultures (total 20 OD_{600} for each sample) were collected by centrifugation at 6000 g for 5 min 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. Isolation of total RNA, synthesis of complementary

DNA, terminal labeling and hybridization with the tiling array were performed according to the Affymetrix instruction manual. Processing of hybridization signal data, background correction, data normalization and calculation of expression levels of individual genes, were all performed as previously described (Morimoto *et al.*, 2008). Duplicates of biologically independent experiments were carried out.

2.11 Antibody production

E. coli DH5 α cells harboring pO-veg12his were grown in 400 ml aliquots of LB medium supplemented with 5 $\mu\text{g ml}^{-1}$ tetracycline, at 37°C with vigorous shaking. When cell cultures attained OD₆₀₀ values of 1.0, IPTG was added to a final concentration of 1mM, 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 [pH7.5], with 150 mM NaCl). Cells were disrupted by sonication on ice using an Astrason Ultrasonic Processor XL (Misonix) for 10 min (4 sec “ON” and 10 sec “OFF”, at output level 5) in 12 ml UT buffer (100 mM HEPES [pH7.5], 0.5 M NaCl, 50 mM imidazole [pH 7.5], 8 M urea, 0.3% [v/v] Triton-X100, 1 mM DTT and 1 mM PMSF). After removal of cell debris by centrifugation, 900 μl amounts of MagneHis (Promega) were added to supernatants, followed by incubation at room temperature for 2 h 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-Veg antibody was raised in rabbits by injection of purified Veg-12xHis at the facilities of the Medical & Biological Laboratories Co., Ltd, Japan.

2.12 Protein stability of Veg

Cells expressing Veg from the P_{spac} promoter on the pO-veg plasmid were grown in LB in the presence of 1 mM IPTG at 37°C with shaking. When cell cultures attained OD_{600} of 0.4-0.5, protein synthesis was inhibited by the addition of chloramphenicol to a final concentration of 200 $\mu\text{g ml}^{-1}$. Samples (10 ml) taken at the indicated times were harvested by centrifugation at 8000 rpm for 3 min, washed once with 1 ml chilled killing buffer, and stored at -80°C. Cells were resuspended in lysis buffer (25 mM Tris-HCl [pH 8.0], 10 mM EDTA, 50 mM glucose, 1 mM DTT, 1x protease inhibitor cocktail [Roche]), and incubated for 10 min at 37°C. After mixing with SDS sample buffer, followed by centrifugation to remove cell debris, proteins in the supernatant equivalent to 0.02 OD_{600} units were separated on 10-20% (w/v) Tris-tricine polyacrylamide gel and transferred to Immobilon-PSQ membranes (Millipore) for 1 h at 10 V in a semi-dry transfer apparatus (Bio-Rad). Transferred proteins were detected using anti-Veg at 1/20000 dilution as the primary antibody, followed by secondary anti-rabbit IgG antibody (Bio-Rad) at 1/8000 dilution conjugated to horseradish peroxidase. Proteins were detected, as described above. The signal intensities of protein bands on X-ray films were quantified using the NIH-Imagine program (Rasband & Bright, 1995). To estimate relative abundance, standard curves were determined by loading two-fold serial dilutions of the sample ($t=0$) on each gel, and the levels of other samples estimated by comparing protein band intensities with the linear range of the standard curve.

2.13 Western blot analysis

Cells were grown in SMM to OD_{600} of 0.4-0.5, and 10 ml culture harvested by

centrifugation at 6000 g for 5 min. Cells were washed once with 1 ml chilled killing buffer (Völker *et al.*, 1994), resuspended in lysis buffer (25 mM Tris-HCl [pH 8.0], 10 mM EDTA, 50 mM glucose, 0.1 mg ml⁻¹ lysozyme, 1 mM PMSF), and incubated for 10 min at 37°C. The cell lysates were separated on a precast polyacrylamide gel, specifically, 16% (w/v) Novex Tricine Gel (Life Technologies) for SinR/SlrR detection and 10-20% (w/v) SuperSep Ace (Wako) for Veg detection, and transferred to Immobilon-P^{SQ} membranes (Millipore) for 1 h at 10 V in a semi-dry transfer apparatus (Bio-Rad). Transferred proteins were examined by incubation with anti-SinR at 1/8000 dilution (a generous gift from R. Losick) (Chai *et al.*, 2009) or anti-Veg antibody (1/20,000 dilution) as the primary antibody, followed by secondary anti-rabbit (1/8000 dilution) conjugated to horseradish peroxidase. Detection of proteins was performed using the ECL-Plus system (Amersham), followed by exposure to X-ray film.

2.14 *In vivo* pull-down assay of protein complex

To cross-link proteins, cells were treated with formaldehyde (0.1% final concentration) for 30 min at OD₆₀₀ of 0.4-0.5 and stored at -80°C after washing twice with Tris-buffer saline (50 mM Tris-HCl [pH 7.5], 0.15 M NaCl). Cells were disrupted by sonication on ice using an Astrason Ultrasonic Processor XL (Misonix) for 10 min (4 sec “ON” and 10 sec “OFF” at an output level 5.0) in 3 ml of UT buffer (0.1 M HEPES, 0.5 M NaCl, 10 mM imidazole [pH 7.5], 8 M urea, 1% [v/v] Triton X-100, 1 mM PMSF). After centrifugation at 6000 g for 15 min at 4°C, 100 μl of MagneHis beads (Promega) were added to the supernatant, followed by overnight incubation at room temperature with gentle rotating. MagneHis beads were washed five times with 1.5 ml UT buffer. Bound proteins were eluted with elution buffer (0.1 M Tris-HCl [pH

7.5], 0.5 mM imidazole [pH 7.5], 1% [w/v] SDS, 10 mM DTT). Cross-linked proteins were dissociated by heating for 40 min at 90°C and separated on a 16% (w/v) Tricine-gel.

2.15 Chromatin immunoprecipitation method

Cells were grown in MSgg medium to an OD₆₀₀ of 0.4-0.5, the culture was treated with formaldehyde (0.1% final concentration) for 30 min and harvested by centrifugation. Cells were washed twice with Tris-buffer saline (50 mM Tris-HCl [pH 7.5], 0.15 M NaCl) and stored at -80°C for overnight. Collected cells were disrupted by sonication on ice for 10 min (4 sec “ON” and 10 sec “OFF” at output level 4.0) in IP buffer II (50 mM HEPES-KOH [pH 7.5], 0.5 M NaCl, 1 mM EDTA, 1% [v/v] Triton-X100, 5% [v/v] glycerol, 0.2 mg ml⁻¹ RNase A, 1x protease inhibitor cocktail free EDTA [Roche], 1 mM PMSF). After centrifugation at 13,500 g for 15 min at 4°C, anti-GFP magnetic beads (MBL) were added to the supernatant, followed by incubation for overnight at 4°C with gentle rotating. Anti-GFP magnetic beads were washed three times with IP buffer I (50 mM HEPES-KOH [pH 7.5], 0.5 M NaCl, 1 mM EDTA, 1% [v/v] Triton-X100, 0.1% [w/v] Na-dexycolate, 0.1% [w/v] SDS, 20% [v/v] glycerol), and then washed three times with wash buffer (10 mM Tris-HCl [pH 8.0], 0.25 M LiCl, 1 mM EDTA, 0.5% [v/v] Nonidet P-40, 0.5% [w/v] Na-dexycolate). Bound proteins were eluted with elution buffer (0.1 M Tris-HCl [pH 7.5], 0.1% [w/v] SDS, 10 mM DTT). Cross-linked proteins were dissociated by heating for 40 min at 90°C and separated by 16% (w/v) Tricine-gel. Interacting proteins with Veg-GFP was analyzed by SDS-PAGE and visualized by silver staining.

3. RESULTS

3.1 Veg is an unstable protein susceptible to proteolysis

Previous study demonstrated that disruption of *veg* led to poor germination in *B. subtilis*, however, molecular mechanism of Veg on the process is still obscure (Fukushima *et al.*, 2003). Since Veg is a highly conserved protein even in nonspore-forming bacteria according to the MBGD database (Uchiyama *et al.*, 2010) and the gene is highly transcribed during the exponential growth phase in *B. subtilis* as well as the sporulation phase, I expected that Veg should have important function(s) besides the sporulation phase. In a first attempt to identify the function, growth properties of a *veg* deletion strain (Δveg) was examined during the exponential growth phase in liquid culture, and showed that growth rate and cell morphology of the Δveg mutant were similar to those of the parent strain. Interestingly, although *veg* gene is highly transcribed, the translated Veg protein in wild-type cells was barely detectable with Western blot analysis. To reconcile this apparent conflict, I hypothesized that Veg might be subject to rapid degradation by some protease(s) and thus to be unstable. To address this hypothesis, Veg proteins were overexpressed from multi-copy plasmid, pO-veg, in which expression is inducible by IPTG. For the first time, Veg protein became detectable in Veg-overexpressing cells grown in rich (LB), minimum (SMM) or biofilm-inducing (MSgg) medium containing IPTG (Figure 6A). Additionally, the stability of Veg protein during the mid-logarithmic phase in LB medium was monitored after chloramphenicol treatment to inhibit protein synthesis (Figure 6B-D). As expected, Veg proteins were rapidly degraded, with a half-life of approximately 5 min.

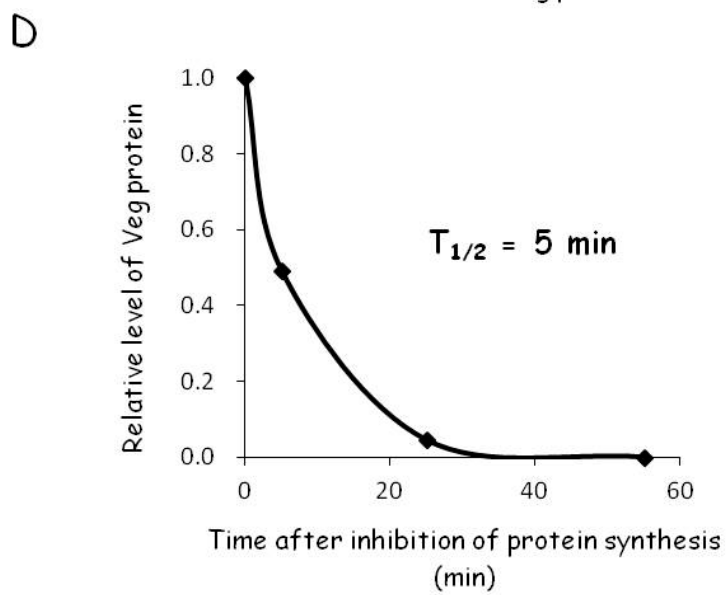
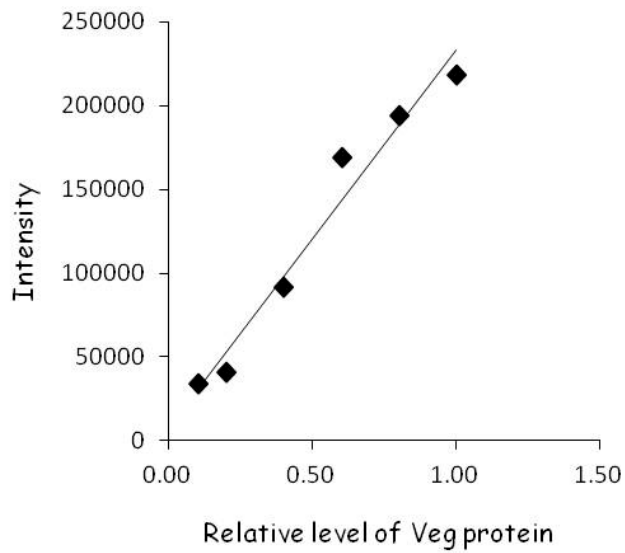
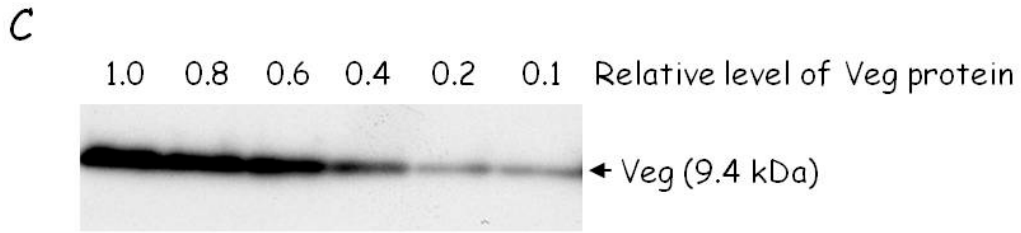
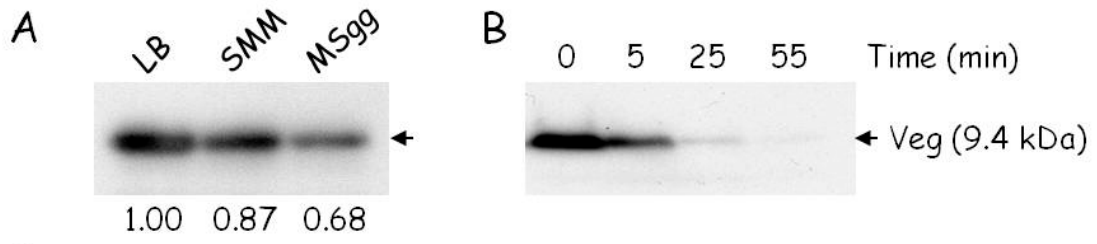


Figure 6. Stability of Veg protein. (A) Cells of LY016 (168 BFA strain harboring pO-veg) strain were grown to the mid-logarithmic phase in LB, SMM or MSgg medium in the presence of 1mM IPTG at 37°C, and Veg in cells equivalent to 0.02 OD600 units detected by Western blotting with anti-Veg antibody. The signal intensities of Veg bands on X-ray films were quantified using the NIH-Imagine program and the signal intensities relative to that of cells cultivated in LB are shown below the bands. (B) Cells of LY016 were grown to mid-logarithmic phase in the presence of 1 mM IPTG in LB medium at 37°C and treated with chloramphenicol to block protein synthesis. Samples were taken at the indicated times and Veg proteins remaining in the cells with 0.02 OD₆₀₀ units were detected by Western blotting with use of anti-Veg antibody. (C) The sample shown in (B) at the 0 min time point was diluted to the indicated concentration. Standard curve shown below was determined based on the gel imagine. (D) Protein levels of Veg at each time point shown in (B) were determined using the standard curve indicated (C) and plotted in a chart. The half-life of Veg was calculated based on the chart.

3.2 LonA, ClpYQ and MlpA are responsible for degradation of Veg

Next, protease(s) involved in the proteolysis of Veg were investigated. In my previous study, Veg-GFP fusion proteins were confirmed to localize on the whole nucleoid in exponential growing cells (Figure 3). Thus, I presumed that some protease(s), which localize in the intracellular region, might control the level of Veg protein. In *B. subtilis*, several ATP-dependent proteases have been characterized, such as Clp and Lon. They are often referred to as protein quality control system, whose function is crucial and becomes essential under certain condition to activate stress response (Turgay, 2007). It has been reported that LonA and ClpC are coincident with the nucleoid during the normal growth. ClpXP are responsible for proteolysis with SpX that is an RNA-binding protein (Nakano *et al.*, 2002), although they localize mostly near cell poles that are not occupied by the nucleoid (Simmons *et al.*, 2008). Moreover,

ClpYQ and MlpA, whose exact functions in *B. subtilis* are not known, are also localized to intracellular region (Turgay, 2007). Thus, the amount of Veg proteins was determined in a single deletion mutant with *lonA*, *clpC*, *clpP*, *clpX*, *clpYQ* or *mlpA* by Western blotting. As a result, Veg protein was still undetectable in the absence of any of these proteases. It was possible that the increased level of Veg proteins was below the limits of detection. Therefore, Veg proteins were overexpressed from the multi-copy plasmid (pO-veg) in the absence of these proteases. The result showed that accumulation of Veg was noticeably detected in the absence of LonA, ClpYQ or MlpA compared with the control strain, but no in the absence of ClpC, ClpP or ClpX (Figure 7A). To further confirm the degradation rate of Veg, the levels of Veg proteins in the deletion of *lonA*, *clpYQ* or *mlpA* were detected at different time points after inhibition protein synthesis, as described above. The result showed that the degradation rate of Veg was reduced in all of the three deletion mutant strains (Figure 7B). However, when protein synthesis was blocked after 15 min, the levels of Veg proteins were gradually reduced. These results indicate that Veg is not only degraded by one protease. Thus, I asked whether Veg would be stable in a triple deletion mutant of *lonA*, *clpYQ* and *mlpA*. However, Veg was still undetectable in the triple deletion mutant (Figure 11A).

In summary, LonA, ClpYQ and MlpA are required for the rapid proteolysis of Veg proteins, although other as-yet unidentified protease(s) might still exist.

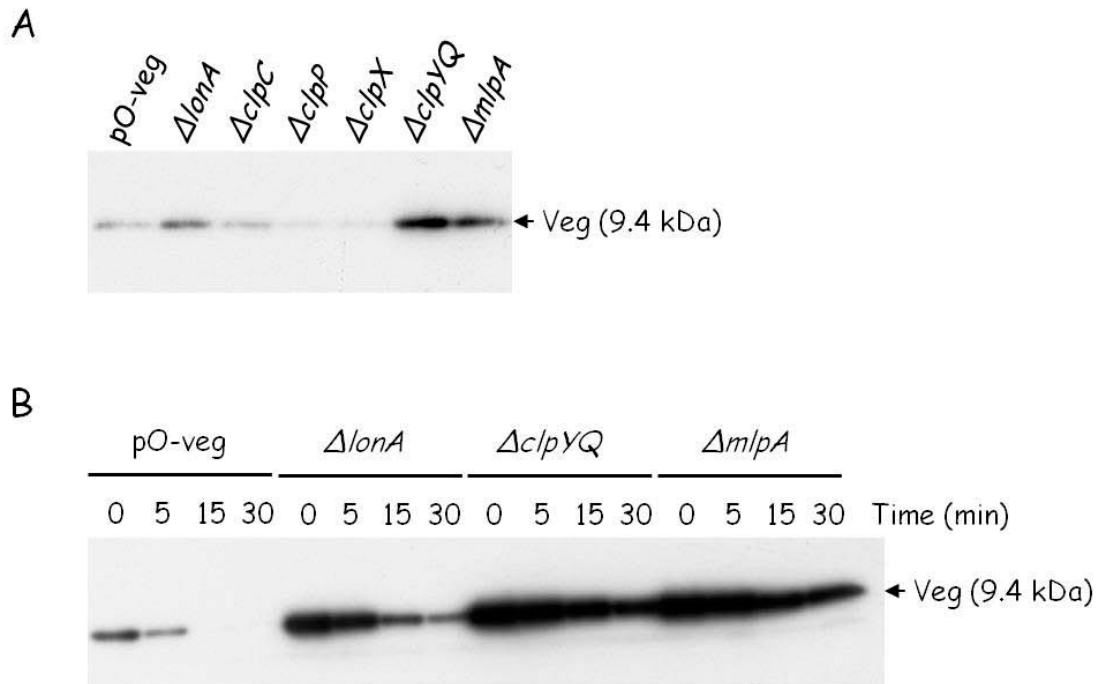


Figure 7. Proteolytic regulation of Veg protein by deletion of single protease. Veg proteins in $\Delta lonA$ (LY075), $\Delta clpC$ (LY080), $\Delta clpP$ (LY081), $\Delta clpX$ (LY082), $\Delta clpYQ$ (LY076) and $\Delta mlpA$ (LY088) mutant strains harboring plasmid pO-veg were compared to that in the wild-type strain pO-veg (LY016). (A) Cells were grown to OD_{600} of 0.4-0.5 in the presence of 1 mM IPTG in LB medium at 37°C. Veg proteins remaining in the cells with 0.02 OD_{600} units were detected by Western blotting with use of anti-Veg antibody. (B) Cells were grown to mid-logarithmic phase in the presence of 1 mM IPTG in LB medium at 37°C and treated with chloramphenicol to a final concentration of 200 $\mu g ml^{-1}$ to block protein synthesis. Samples were taken at the indicated times and Veg proteins were detected with anti-Veg antibody.

3.3 Biofilm formation is stimulated by overproduction of Veg and inhibited in its absence

In several bacteria, Lon protease is involved not only in general quality control by degradation of abnormal proteins but also in specific control of several regulatory proteins (Tsilibaris *et al.*, 2006). In *B. subtilis*, it has been shown that LonA degrades

σ^H and σ^G to prevent initiation of sporulation and inappropriate synthesis of σ^G , respectively (Schmidt *et al.*, 1994; Liu *et al.*, 1999). Interestingly, Lon protease has been known to have an ability to control biofilm formation negatively in *E. coli* (Belik *et al.*, 2008) and *Pseudomonas aeruginosa* (Marr *et al.*, 2007). Thus, I first examined the phenotype formed by deletion of *B. subtilis lonA* ($\Delta lonA$) on the agar plate of LB, SMM or MSgg medium. Absence of LonA induced a thicker and more wrinkled colony structure than that in the presence (Figure 8), suggesting that *B. subtilis* LonA plays the same role in the control of biofilm formation as reported in *E. coli* and *P. aeruginosa*. Since LonA is, in part, responsible for the instability of Veg, I suspected that stabilized Veg might be involved in biofilm formation and responsible for the phenotype of the $\Delta lonA$ mutant.

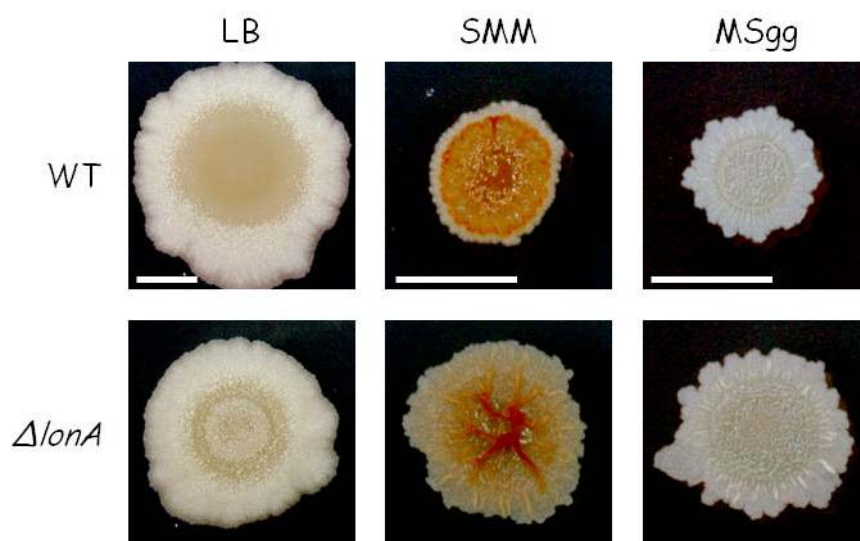


Figure 8. Effects of *lonA* deletion mutant on the architecture of colonies. WT (168 BFA) and $\Delta lonA$ (LY073) strains were grown in the indicated media for 72 h at 30°C. The scale bar is 0.5 cm.

In agreement with this prediction, phenotype of a Veg-overproducing strain was formed a thick and complicated colony morphology on various solid media as the *AlonA* mutant did, which was clearly distinguishable from those of the wild-type 168 BFA strain and a strain harboring a control plasmid without insert of *veg* gene (pO-MCS) (Figure 9). The strain 168 BFA harbors no substitution in the *epsC* gene that often contains a null mutation impairing EPS production in other 168 strains (Branda *et al.*, 2001), and forms biofilm architecture on solid MSgg medium as previously described (McLoon *et al.*, 2011). Assessment of colony morphology revealed for the first time a clear phenotype of the *Δveg* mutant deficient in steric structure, compared with the wild-type strain (Figure 9). Additionally, the formation of pellicle, another biofilm form that develops at the liquid-air interface of standing cultures, was investigated (Branda *et al.*, 2001). Pellicle formation at the surface of a standing MSgg culture was severely impaired in the *Δveg* strain, while the effect of Veg overproduction on pellicle formation seemed to form a more wrinkled appearance than that of the parental strain, although the effect was not clear compared to that of *veg* deletion (Figure 9). It is possible that expression levels of biofilm formation genes are already elevated in the biofilm-inducing condition and thus their further increase was not induced by Veg overproduction.

Some laboratory 168 strains have been reported to lose the ability to form clear biofilm architecture, compared to the undomesticated wild-type NCIB3610 strain (Branda *et al.*, 2001; Stanley & Lazazzera, 2005; McLoon *et al.*, 2011). Therefore, we examined biofilm formation using strains derived from NCIB3610 (Figure 9). In the NCIB3610 genetic background, the *Δveg* mutant strain also showed reduced biofilm formation on MSgg plates and pellicle formation in standing culture, albeit to a

moderate extent, compared to the 168 BFA-derived strain (Figure 9). These results demonstrate that Veg impacts biofilm formation, even in the NCIB3610 genetic background. However, the clear inhibition of biofilm formation observed in the 168 BFA-derived Δveg strain appeared to be partly masked by strong biofilm formation ability in the NCIB3610 genetic background. In addition, introduction of the control plasmid (pO-MCS) resulted in reduced pellicle formation, and thus, the precise effects of Veg overproduction could not be examined (Figure 9). Although the exact reason is unclear at present, it is proposed that the pO-MCS plasmid acts negatively on the 80 kb plasmid harboring a gene related to colony morphology in the NCIB3610 strain (McLoon *et al.*, 2011). Thus, in subsequent experiments, we used derivatives of the 168 BFA strain.

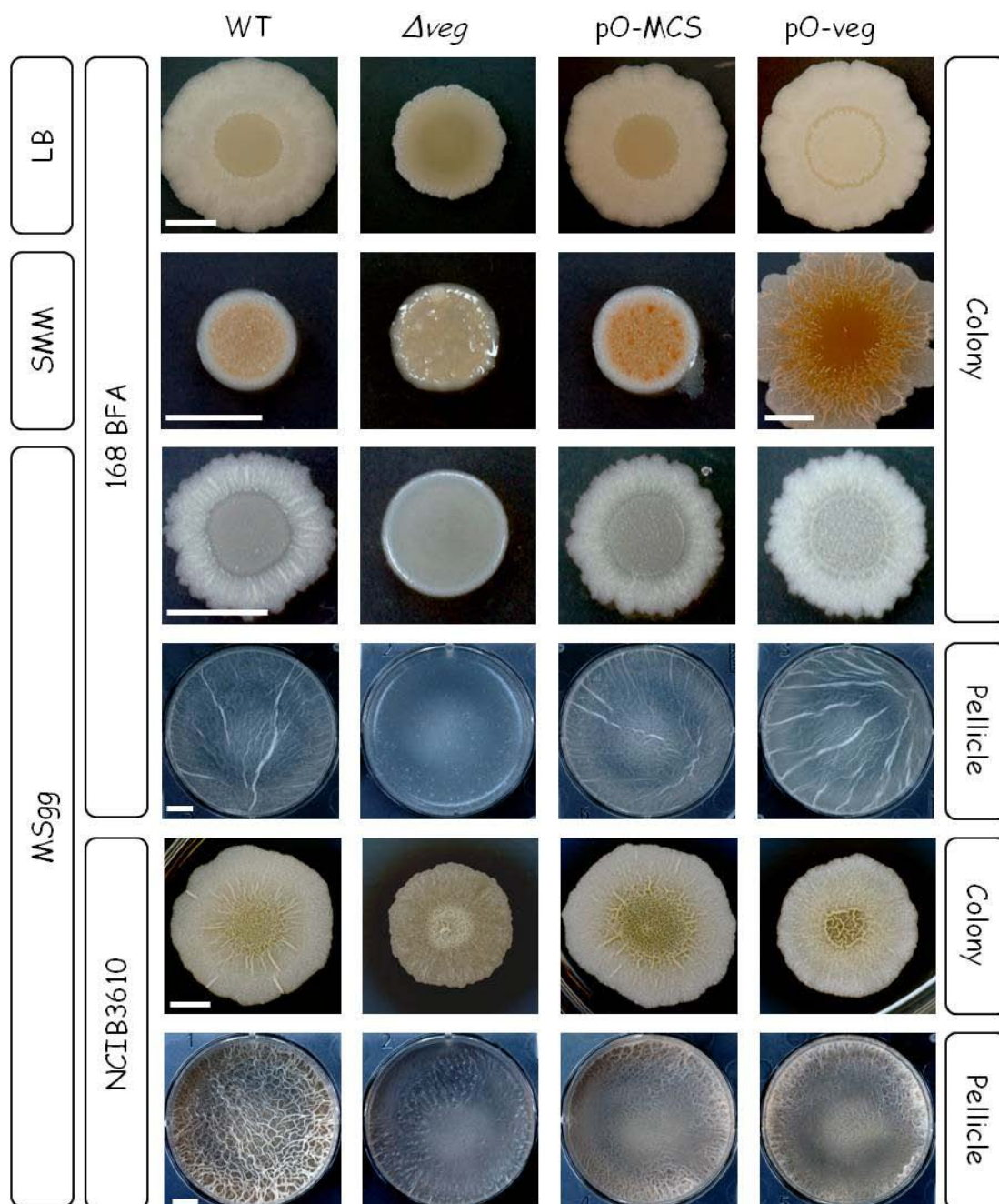


Figure 9. Effects of Veg inactivation and overproduction on the architecture of colonies and pellicles. WT (168 BFA or NCIB3610), Δveg (LY011; 168 BFA harboring Δveg or LY048; NCIB3610 harboring Δveg), pO-veg (LY016; 168 BFA harboring pO-veg or LY058; NCIB3610 harboring pO-veg) and pO-MCS (LY015; 168 BFA harboring pO-MCS or LY057; NCIB3610 harboring pO-MCS) strains were grown in the indicated media for 72 h (168 BFA background strains) or 48 h (NCIB3610 background strains) at 30°C. LY015, LY016, LY057 and LY058 strains were grown in the presence of 1 mM IPTG. The scale bar is 0.5 cm.

3.4 Stabilization of Veg contributes to biofilm development

In the present study, I have shown that Veg protein is extremely unstable and undetectable by Western blotting (Figure 6 and 11), and that overproduction of Veg protein leads to induction of biofilm formation (Figure 9). Based on these observations, I asked whether a hyper biofilm-producing phenotype by a Veg mutant would increase the amount of Veg protein levels. Thus, the method of error-prone PCR mutagenesis containing various concentrations of MnCl_2 was applied to obtain random point mutations within the *veg* gene. The error-prone PCR fragments of *veg* were introduced to its original position to create *veg* mutant strains to express the mutant Veg protein as well as the wild-type. Sixty-four clones with hyper-wrinkled colony morphology phenotype (hyper mutants) on SMM plates out of ~10,000 colonies were collected, and sequencing analysis was performed to confirm the mutations in the *veg* region. Twelve hyper mutants carrying single, double or triple amino-acid mutations within the coding region were selected. Positions of these mutations were shown in Figure 10A. Various levels of biofilm formation of these mutants were reconfirmed on MSgg plates (Figure 10C).

According to the screening of hyper mutants, I found that mutation frequency was elevated with increasing Mn^{2+} concentration, but still enough to introduce single mutation in the absence of Mn^{2+} (Figure 10A). Since a high mutation frequency makes it difficult to determine which mutation is responsible for the phenotype, error-prone PCR mutagenesis was performed without MnCl_2 to obtain Veg loss-of-function mutants. Out of ~10,000 colonies, one hundred and twenty-eight clones forming smooth colonies as the Δveg did (loss-of-function mutants) on SMM plates were isolated. Among these Veg mutants, five loss-of-function mutants carrying single

amino-acid mutation were selected to simplify the analysis. Positions of the mutations were mapped in Figure 10B. Colony structures of these mutants were reconfirmed on MSgg plates (Figure 10D).

These results showed that mutations of the hyper mutants located in non-conserved amino-acids of Veg, while mutations of the loss-of-function mutants were found in conserved amino-acids, suggesting that the conserved regions are very important for Veg function. Since the five loss-of-function mutations are scattered in the two terminal regions of the complete polypeptide, both of N- and C-terminus of Veg are probably very important for its function, although the structure of Veg protein has been not reported. Therefore, these mutants are expected to be beneficial for structure analysis in the future.

A Veg hyper mutants

Clone No.	MnCl ₂ (mM)	MAKTLSDIKRSLDGNL GKRLTLKANGGRKTIERSGILAE TYP SVFVIQLDQDENSFERVSYSYADILTE IVELTFNDDAASSVAF
1	0	V
2	0	T
3	0.1	G
4	0.1	K
5	0.2	V
6	0.2	A
7	0.2	V
8	0.2	G
9	0.2	G
10	0.2	G
11	0.2	V
12	0.2	L

B Veg loss-of-function mutants

Clone No.	MnCl ₂ (mM)	MAKTLSDIKRSLDGNL GKRLTLKANGGRKTIERSGILAE TYP SVFVIQLDQDENSFERVSYSYADILTE IVELTFNDDAASSVAF
1	0	A
2	0	S
3	0	D
4	0	N
5	0	G

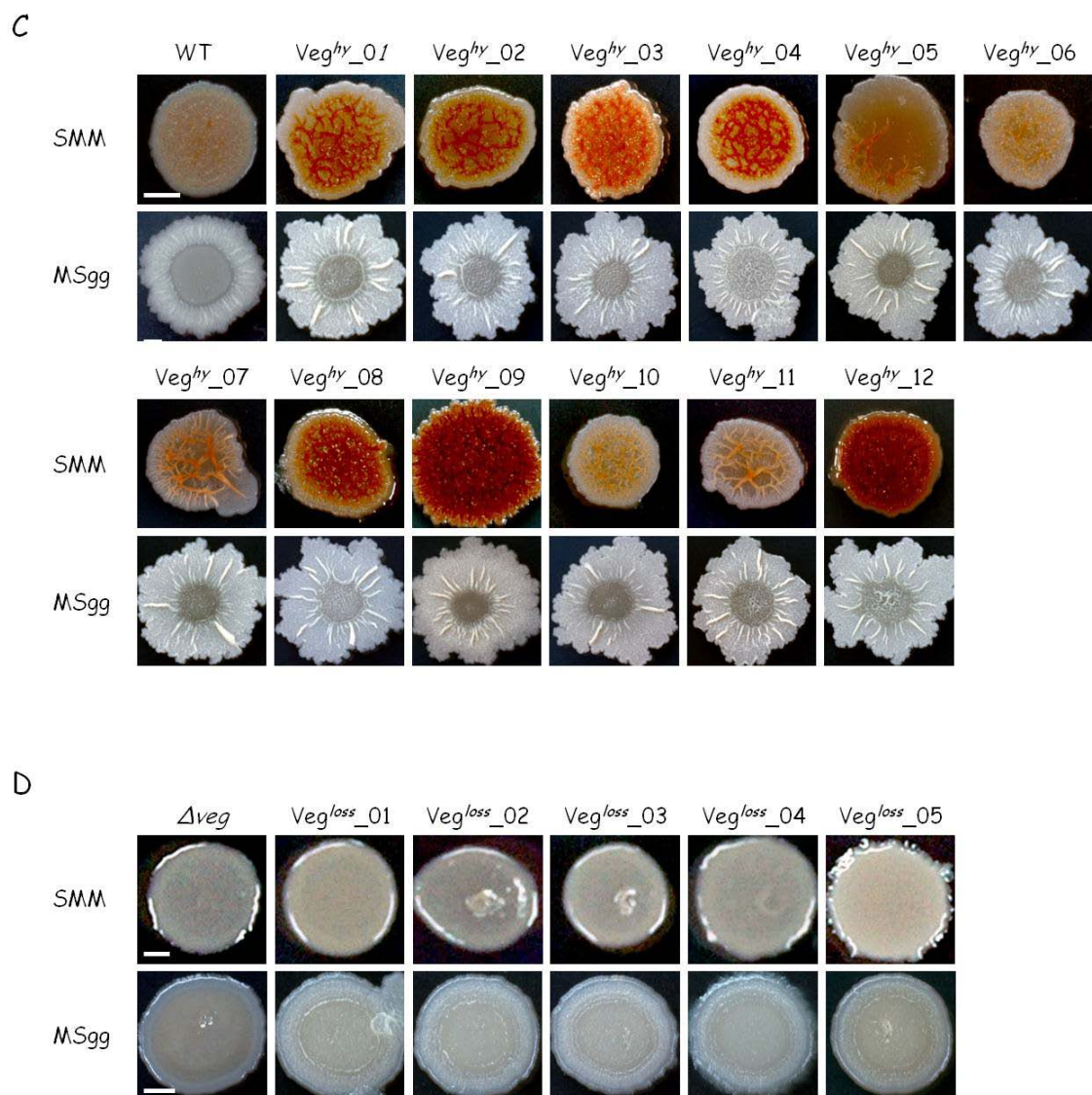


Figure 10. Screening for Veg hyper and loss-of-function mutants. (A) and (B) indicate the sequences of Veg hyper (LY094-105) and loss-of-function (LY106-110) mutants, respectively. Amino-acid sequence of Veg was shown in the upper line. Locations of identified mutations were shown in the lower lines. Conserved amino acids were shown by magenta. Mutants containing single, double or triple amino-acid mutations are indicated by green, pink and blue, and mutants carrying the same mutations are indicated by red. Veg hyper (C) and loss-of-function (D) mutants were selected from SMM plates and phenotypes were reconfirmed on MSgg plates for 72 h at 30°C. The scale bar is 0.25 cm.

All of the Veg hyper mutants formed similar colony architectures on MSgg plates, but Veg^{hy}_05, 06 and 10 mutants seemed to exhibit weaker biofilm structures than other hyper mutants. Thus, the amounts of Veg proteins in Veg hyper mutants except for Veg^{hy}_05, 06 and 10 were examined by Western blotting in LB medium during exponential growth phase. As a result, in the three hyper mutants (Veg^{hy}_01, 02 and 11), the bands approximately 9.4-kDa which are coincident with the wild-type Veg were detected by anti-Veg antibody without overproduction (Figure 11), although these proteins showed different mobilities on SDS-PAGE from the wild-type Veg proteins overproduced from the pO-veg. It is probable that changes of amino-acids by the mutants may alter the amount of SDS molecules bound to each Veg mutant protein, and thus negative charge of the denatured Veg polypeptide that affects migration on the gel. These results reveal that these hyper mutant Veg proteins are stabilized and certainly stimulate biofilm development. These results also suggest that proteolysis of Veg is required to repress biofilm formation during the exponential phase and its stabilization may be important for cell differentiation at the correct time. Nevertheless, the protein levels of hyper mutant Veg were less than overproduced Veg, suggesting that these mutant proteins were partly stabilized and still degraded by some protease(s).

In my previous study, Veg-GFP fusion proteins were shown to be localized on the nucleoid with weak fluorescence intensity. Such low fluorescence intensity might be due to instability of the Veg-GFP protein (Figure 5 and 12A). Hence, the question was, if Veg protein was stabilized, the fluorescence intensity on the nucleoid would increase or Veg-GFP would show a different localization? To address this question, I made use of strains that carry GFP fusion with the three Veg hyper mutants and express under

the control of the native P_{veg} promoter. In addition, Veg loss-of-function mutants with GFP fusions were also constructed to identify whether Veg localization would lose in the nucleoid or not, if Veg did not work in the Veg loss-of-function mutants. As a control, nucleoid-associated protein HBSu-GFP was investigated, because HBSu in *B. subtilis* has been shown to be localized on the nucleoid *in vivo* (Kohler & Maeahiel, 1997). As shown in Figure 12B, localization of HBSu-GFP coincides with the DAPI-stained region, reconfirming the previous report that HBSu is associated with the nucleoid. Stabilization of Veg in the Veg hyper mutants did not change its nucleoid localization but significantly increased the whole intensity (Figure 12C to E), suggesting that Veg function might be largely associated with the nucleoid distribution. On the other hand, specific localization of the loss-of-function Veg mutants was not observed, instead showing non-specific whole-cell fluorescence (Figure 12F-J). This result may support the above mentioned idea, however; assuming if Veg-GFP proteins with the loss-of-function mutants is more unstable than wild-type fusion protein, it is also possible that the diffused localization in the cells may simply indicate free GFP produced as a result of the proteolysis.

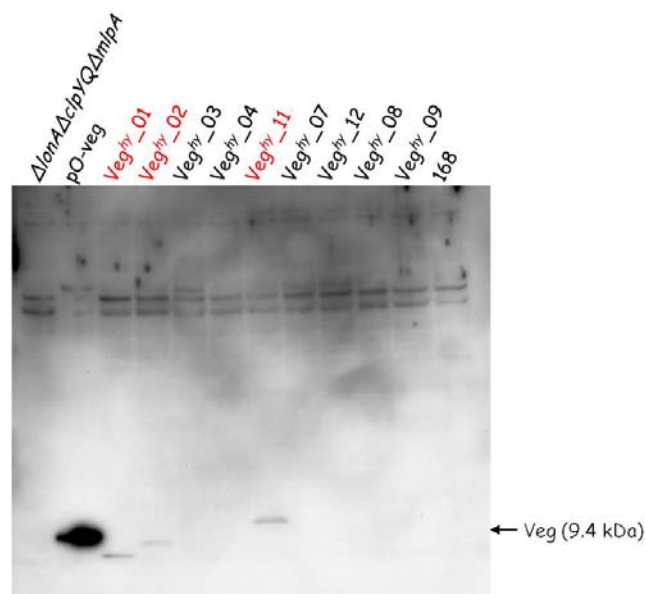
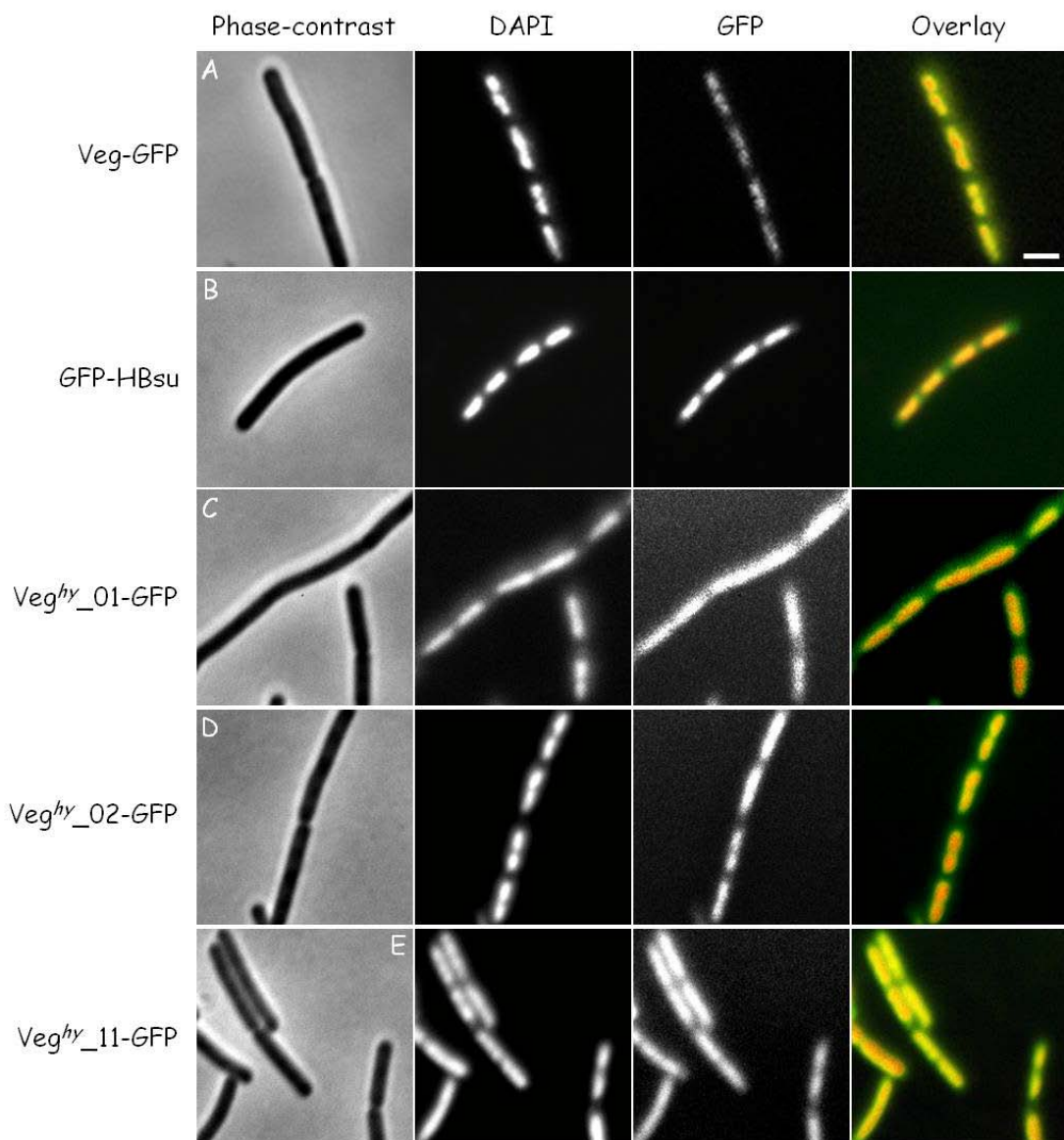


Figure 11. Stability of Veg protein in Veg hyper mutants and a triple deletion mutant of $\Delta lonA\Delta clpYQ\Delta mlpA$. Cells were grown to OD_{600} of 0.4-0.5 in LB medium at 37°C. Veg proteins in the cells with 0.1 OD_{600} units (pO-veg sample containing 1 mM IPTG with 0.02 OD_{600} units) were detected by Western blotting with use of anti-Veg antibody. The following strains were used; Veg^{hy}_01-04, 07-09 and 11-12 (LY094-097, 100-102 and 104-105), $\Delta lonA\Delta clpYQ\Delta mlpA$ (LY090) and pO-veg (LY016).



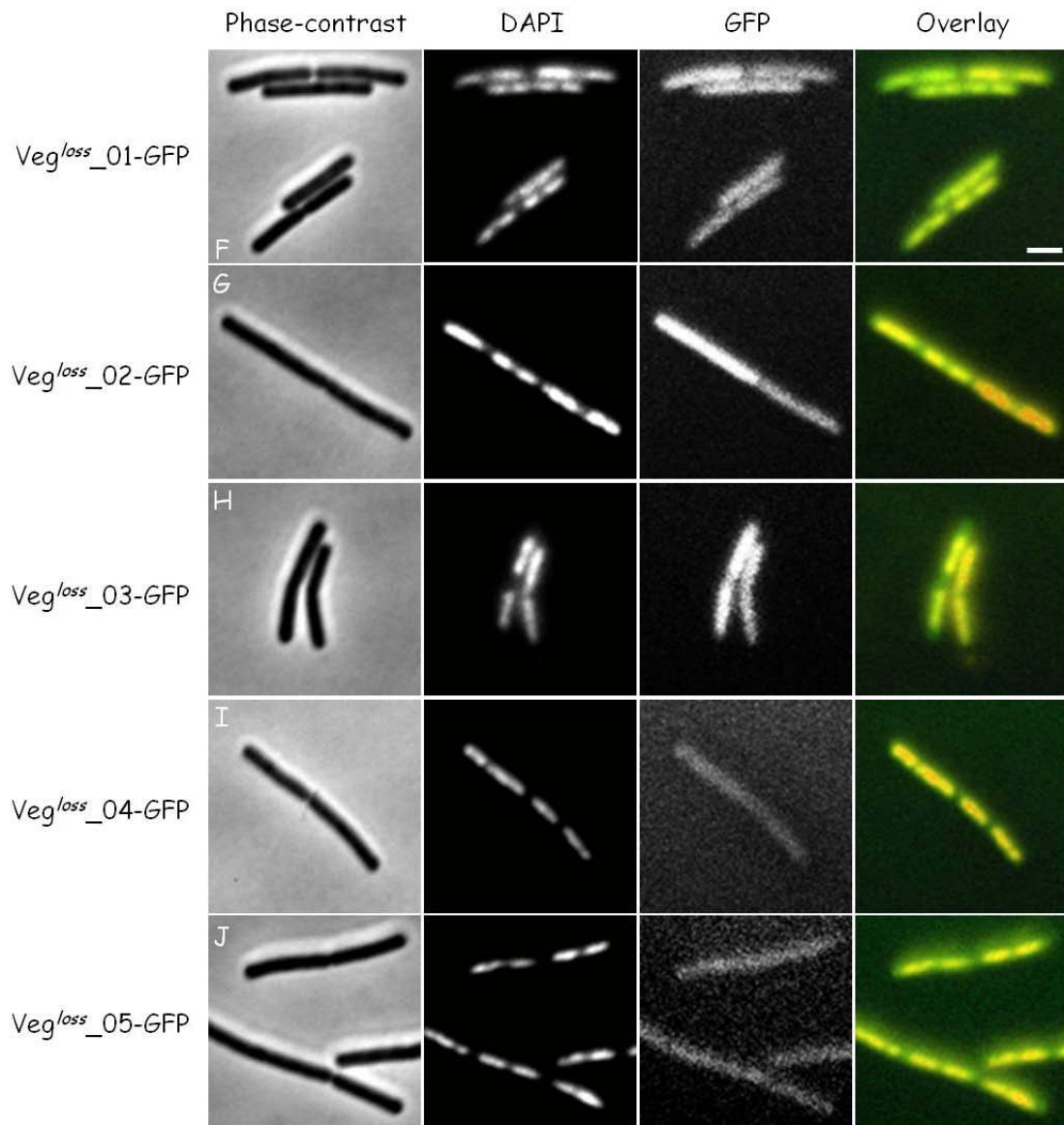


Figure 12. Localization of the Veg mutant proteins with GFP fusion. GFP strains were cultured to mid-logarithmic phase (OD_{600} of 0.3-0.5) in LB medium at 37°C, and localization of GFP fusions were visualized by fluorescence microscopy with DNA staining by DAPI. Overlay is a DAPI image overlaid on a GFP image with DNA shown in red and GFP in green. The following strains were used; Veg-GFP (LY067), GFP-HBsu (LY112), Veg^{hy}_01, 02 and 11-GFP (LY113-115) and Veg^{loss}_01-05-GFP (LY116-120). The scale bar is 2 μ m.

3.5 Transcription of *epsA-O* and *tapA-sipW-tasA* operons is induced by overproduction of Veg and reduced in its absence

Since increased protein levels in the Veg hyper mutants was not high enough as compared to that in the Veg overproducing cells (Figure 11), Veg-overexpressing strain was used in the following experiments. To identify the genes that might contribute to the induced biofilm formation by Veg overproduction, genome-wide transcriptional profiles were compared in the Veg-overexpressing strain and its control strain during the mid-exponential-phase, using the Affymetrix tiling chip. Based on the colony morphology shown in Figure 9, the difference between Veg overexpressing strain and its control strain was the most distinct on SMM plates, and thus, transcriptome analysis was conducted in SMM liquid medium. The scatter plots of gene expressions in the two strains obtained from two independent experiments are shown in Figure 13A and B. As a result, transcriptional profiles of genes in the two strains were essentially the same, except for several genes. Searching genes which expression levels are reproducibly changed more than 2-fold by overproduction of Veg in the two independent experiments, twelve up-regulated and seven down-regulated operons were identified (marked by red and green dots in Figure 13, and listed in Table 4). Interestingly, expressions of *epsA-O* and *tapA-sipW-tasA* operons, which encode biofilm extracellular matrix components, EPS and TasA, respectively (Branda *et al.*, 2006), were specifically up-regulated by overproduction of Veg. Additionally, several genes in the prophage regions of PBSX and SP β were also upexpressed. Although the exact effect of the induction of prophage genes was unclear at present, it may represent another general phenotype of bacteria in biofilms.

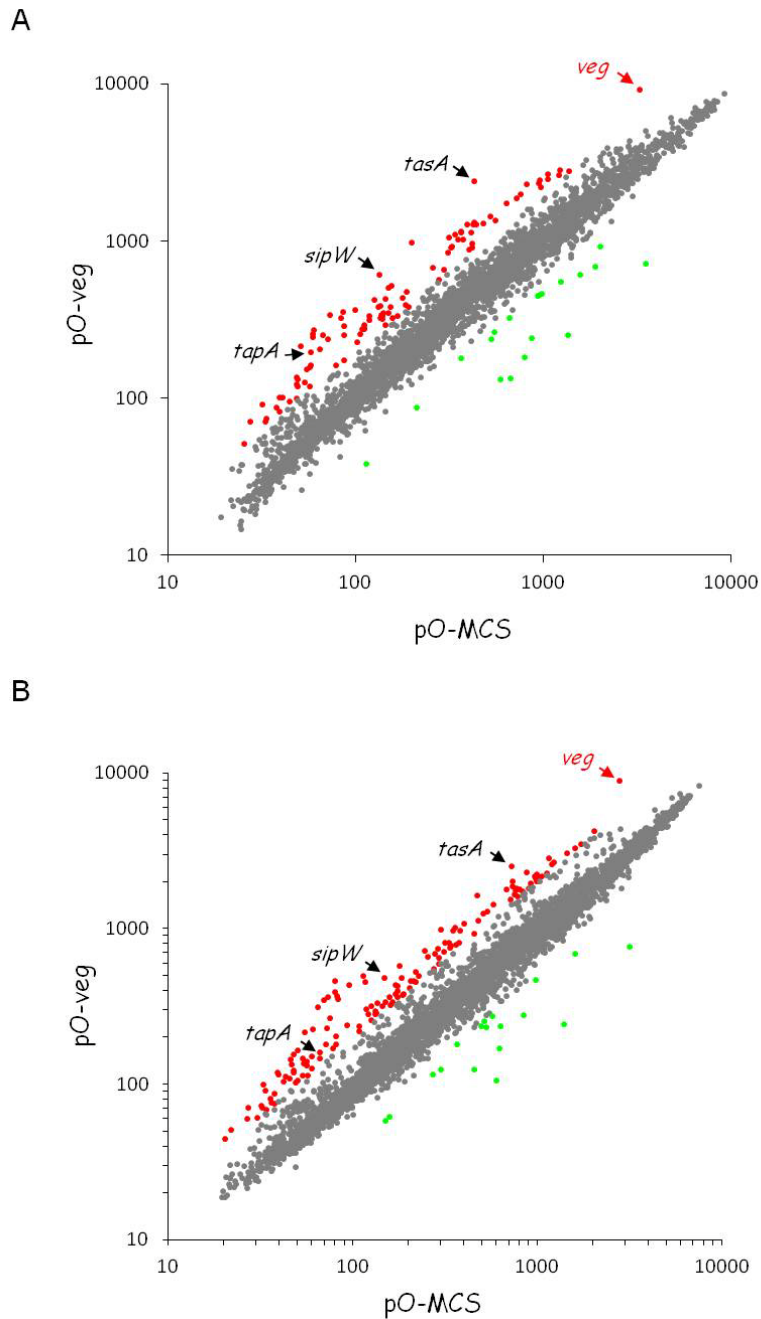


Figure 13. Comparison of gene expressions in cells with and without overproduction of Veg. Log-scale scatter plots of the transcriptional intensities of genes in the cells with (LY016; 168 harboring pO-veg) and without (LY015; 168 harboring pO-MCS) overproduction of Veg is indicated. Genes up- and down-regulated more than 2-fold are indicated as red and green dots, respectively. *tapA-sipW-tasA* operon and *veg* gene are also pointed out by black and red arrows, respectively. (A) and (B) are indicated two independent experiments.

Table 4. Genes up- or down- regulated in Veg overexpression cells (pO-veg) more than 2-fold compared with its control cells (pO-MCS).

Transcription unites	Gene name	Location			Expression ratio ^a	Gene function
		start	end	strand		
Up-regulated						
1	<i>ydaE</i>	472143	472646	+	2.7 ± 0.9	unknown
2	<i>ydcO</i>	531853	532113	+	2.6 ± 0.5	unknown
	<i>ydcT</i>	535965	536231	+	2.3 ± 0.4	unknown
3	<i>xlyB</i>	1316849	1317802	+	2.3 ± 0.2	N-acetylmuramoyl-L-alanine amidase, peptidoglycan hydrolase
4	<i>xk dB</i>	1321325	1322158	+	2.0 ± 0.0	PBSX prophage protein
	<i>xk dD</i>	1323110	1323460	+	2.3 ± 0.3	PBSX prophage protein
	<i>xpf</i>	1323779	1324288	+	2.3 ± 0.2	RNA polymerase PBSX sigma factor, PBSX prophage protein
	<i>xk dH</i>	1330202	1330558	+	2.4 ± 0.4	PBSX prophage protein
	<i>xk dI</i>	1330555	1331040	+	2.3 ± 0.3	PBSX prophage protein
	<i>xk dJ</i>	1331053	1331493	+	2.1 ± 0.2	PBSX prophage protein
	<i>xk dO</i>	1334279	1338277	+	2.5 ± 0.6	PBSX prophage protein
	<i>xk dP</i>	1338222	1338929	+	2.6 ± 0.8	PBSX prophage protein
	<i>xk dQ</i>	1338945	1339922	+	2.6 ± 0.6	PBSX prophage protein
	<i>xk dR</i>	1339922	1340188	+	2.8 ± 0.7	PBSX prophage protein
	<i>xk dS</i>	1340245	1340670	+	2.5 ± 0.4	PBSX prophage protein
	<i>xk dT</i>	1340663	1341709	+	2.4 ± 0.5	PBSX prophage protein
	<i>xk dU</i>	1341693	1342271	+	2.5 ± 0.5	PBSX prophage protein
	<i>xk dV</i>	1342542	1344605	+	2.5 ± 0.6	PBSX prophage protein
	<i>xk dW</i>	1344617	1344946	+	2.6 ± 0.7	PBSX prophage protein
	<i>xk dX</i>	1344943	1345107	+	3.0 ± 0.6	PBSX prophage protein
	<i>xepA</i>	1345151	1345990	+	2.5 ± 0.3	lytic exoenzyme associated with PBSX prophage
	<i>xhIA</i>	1346043	1346312	+	2.3 ± 0.3	involved in cell lysis upon induction of PBSX
	<i>xlyA</i>	1346601	1347494	+	2.4 ± 0.4	N-acetylmuramoyl-L-alanine amidase, peptidoglycan hydrolase (PBSX prophage-mediated lysis)
5	<i>yosJ</i>	2165856	2166050	-	2.4 ± 0.2	SP-beta protein
	<i>yorZ</i>	2169228	2169440	-	2.5 ± 0.5	SP-beta protein
	<i>yorW</i>	2169969	2170334	-	2.3 ± 0.1	SP-beta protein
	<i>yorV</i>	2170337	2170555	-	2.5 ± 0.6	SP-beta protein
	<i>mtbP</i>	2170599	2171930	-	2.2 ± 0.2	modification methylase bsu, SP-beta protein
	<i>yorG</i>	2183646	2184617	-	2.4 ± 0.1	SP-beta protein
	<i>yorF</i>	2184700	2185614	-	2.5 ± 0.3	SP-beta protein
6	<i>yonN</i>	2224533	2224811	+	2.2 ± 0.2	histone-like protein, SP-beta protein
	<i>yonK</i>	2226493	2226684	+	2.6 ± 0.1	SP-beta protein
	<i>yonJ</i>	2226701	2227918	+	3.0 ± 0.3	SP-beta protein
	<i>yonH</i>	2228581	2229081	+	2.8 ± 0.5	SP-beta protein
	<i>yonE</i>	2231878	2233398	+	2.3 ± 0.2	SP-beta protein
	<i>yonD</i>	2233429	2234865	+	3.8 ± 0.1	SP-beta protein
	<i>yonC</i>	2234890	2235426	+	3.8 ± 0.6	SP-beta protein
	<i>yonB</i>	2235465	2236481	+	4.2 ± 0.5	SP-beta protein
	<i>yonA</i>	2236517	2236987	+	4.2 ± 0.2	SP-beta protein
	<i>yomZ</i>	2237002	2237397	+	4.5 ± 0.5	SP-beta protein
	<i>yomY</i>	2237394	2237648	+	4.7 ± 0.3	SP-beta protein
	<i>yomX</i>	2237632	2238282	+	4.7 ± 0.4	SP-beta protein
	<i>yomW</i>	2238279	2238785	+	5.2 ± 0.9	SP-beta protein

Table 4. Genes up- or down- regulated in Veg overexpression cells (pO-veg) more than 2-fold compared with its control cells (pO-MCS).

Transcription unites	Gene name	Location			Expression ratio ^a		Gene function
		start	end	strand	pO-veg/ pO-MCS		
Up-regulated							
6	<i>yomV</i>	2238782	2239492	+	4.5 ± 0.6	SP-beta protein	
	<i>yomU</i>	2239535	2240332	+	4.1 ± 0.5	SP-beta protein	
	<i>yomS</i>	2241252	2241608	+	2.9 ± 0.5	similar to phage-related lytic exoenzyme, SP-beta	
	<i>yomR</i>	2241610	2242827	+	3.3 ± 0.8	similar to phage-related protein, SP-beta protein	
	<i>yomQ</i>	2242838	2243188	+	3.4 ± 0.3	SP-beta protein	
	<i>yomP</i>	2243185	2243376	+	2.9 ± 0.1	similar to phage-related protein, SP-beta protein	
	<i>yomO</i>	2243426	2243926	+	2.8 ± 0.4	SP-beta protein	
	<i>yomN</i>	2243910	2244329	+	3.2 ± 0.7	SP-beta protein	
	<i>yomM</i>	2244343	2245344	+	2.9 ± 0.6	integrase/recombinase, SP-beta protein	
	<i>yomD</i>	2261633	2262457	+	2.3 ± 0.4	SP-beta protein	
7	<i>tasA</i>	2552313	2553098	-	4.5 ± 1.5	major biofilm matrix component	
	<i>sipW</i>	2553162	2553734	-	3.9 ± 0.9	type I signal peptidase	
	<i>tapA</i> (<i>yqxM</i>)	2553718	2554479	-	2.9 ± 0.7	lioprotein for biofilm formation	
8	<i>yqeF</i>	2647143	2647874	-	2.1 ± 0.1	unknown	
9	<i>yrhK</i>	2772583	2772873	+	2.5 ± 0.0	unknown	
10	<i>epsO</i> (<i>yvfF</i>)	3513146	3514114	-	2.6 ± 0.4	putative pyruvyl transferase	
	<i>epsN</i> (<i>yvfE</i>)	3514093	3515259	-	3.0 ± 0.5	putative amino transferase	
	<i>epsM</i> (<i>yvfD</i>)	3515264	3515914	-	2.3 ± 0.3	putative O-acetyl transferase	
	<i>epsL</i> (<i>yvfC</i>)	3515911	3516519	-	2.5 ± 0.5	putative phosphotransferase involved inextracellular matrix synthesis	
	<i>epsK</i> (<i>yvfB</i>)	3516516	3517553	-	2.6 ± 0.3	putative extracellular matrix component exporter	
	<i>epsK</i> (<i>yvfA</i>)	3517703	3518032	-	2.9 ± 0.5	putative extracellular matrix component exporter	
	<i>epsJ</i> (<i>yveT</i>)	3518029	3519063	-	2.5 ± 0.1	putative glycosyl transferase	
	<i>epsI</i> (<i>yveS</i>)	3519060	3520136	-	2.3 ± 0.1	putative polysaccharide pyruvyl transferase	
	<i>epsG</i> (<i>yveQ</i>)	3521200	3522303	-	2.7 ± 0.3	biofilm extracellular matrix formation enzyme	
	<i>epsF</i> (<i>yveP</i>)	3522300	3523454	-	2.1 ± 0.1	putative phosphotransferase involved inextracellular matrix formation	
	<i>epsE</i> (<i>yveO</i>)	3523447	3524283	-	2.3 ± 0.5	putative glycosyl transferase	
	<i>epsD</i> (<i>yveN</i>)	3524280	3525425	-	2.3 ± 0.3	putative extracellular matrix biosynthesis enzyme	
	<i>epsB</i> (<i>yveL</i>)	3527492	3528175	-	2.4 ± 0.4	protein tyrosine kinase	
	<i>epsA</i> (<i>yveK</i>)	3528181	3528885	-	2.8 ± 0.8	modulator of protein tyrosine kinase EpsB	

Table 4. Genes up- or down- regulated in Veg overexpression cells (pO-veg) more than 2-fold compared with its control cells (pO-MCS).

Transcription unites	Gene name	Location			Expression ratio ^a pO-veg/ pO-MCS	Gene function
		start	end	strand		
Up-regulated						
11	<i>tagC</i>	3682468	3683796	+	2.3 ± 0.1	teichoic acid biosynthesis protein C
12	<i>yxiT</i>	4006434	4006676	-	2.0 ± 0.0	unknown
Down-regulated						
1	<i>gamP</i>	254895	256790	-	0.5 ± 0.0	PTS glucosamine-specific enzyme IICBA component
2	<i>ydbN</i>	505883	506062	-	0.5 ± 0.0	unknown
3	<i>yrhP</i>	2767269	2767901	-	0.4 ± 0.0	RhtB subfamily of amino-acid-efflux protein
4	<i>yurJ</i>	3344040	3345143	-	0.3 ± 0.0	similar to multiple sugar transport system ATP-binding protein
	<i>yurL</i>	3346078	3346932	-	0.3 ± 0.0	probable sugar kinase
	<i>yurM</i>	3346946	3347848	-	0.2 ± 0.0	multiple sugar transport system permease protein
	<i>yurN</i>	3347852	3348730	-	0.2 ± 0.0	multiple sugar transport system permease protein
	<i>yurO</i>	3348788	3350056	-	0.2 ± 0.0	multiple sugar transport system substrate-binding protein
	<i>yurP</i>	3350137	3351123	-	0.2 ± 0.0	probable phosphosugar isomerases
5	<i>yvaB</i>	3444472	3445107	-	0.4 ± 0.0	acyl carrier protein phosphodiesterase
6	<i>yvbA</i>	3466085	3466357	-	0.4 ± 0.1	transcriptional regulator (ArsR family), inducing the <i>atp</i> and <i>yusL</i> KJ operon
7	<i>bglH</i>	4031364	4032773	-	0.5 ± 0.0	beta-glucosidase

^a Average ratio of transcription signals in two independent experiments.

In order to confirm the transcriptional effect brought about by Veg, transcriptional activity of biofilm extracellular matrix operons, *epsA-O* (*eps*) and *tapA-sipW-tasA* (*tasA*) operons, was examined on solid MSgg medium containing X-Gal (Figure 14). I introduced into the 168 BFA strain, the *lacZ* gene under control of P_{eps} or P_{tapA} at the *amyE* locus (*amyE::P_{eps}-lacZ* or *amyE::P_{tapA}-lacZ*) to monitor expression of *eps* and *tasA* operon promoters, and *epsH* deletion mutation to suppress the aerial structure that interferes with color comparison in the colonies (Chu *et al.*, 2006). The Δveg mutation, Veg overexpression (pO-veg), and control plasmid (pO-MCS) were introduced into the resultant strains. For comparison, LacZ activities in deletion mutants of known biofilm regulators, *abrB*, *sinR*, *slrR*, *sinI*, and *slrA* were examined.

Since the master repressors, AbrB and SinR, act in an additive manner to repress matrix operons (Chu *et al.*, 2008), intensity of the blue color of colonies containing P_{tapA} -*lacZ* and P_{eps} -*lacZ* reporters in $\Delta sinR$ and the $\Delta abrB$ strains increased, indicating derepression of *eps* and *tasA* in the absence of SinR or AbrB (Figure 14). In addition, colonies containing either of the reporters were not colored in the deletion mutant of *sinI* encoding an antagonist of SinR. Thus, it appears that deletion leads to constitutive repression of these operons (Kearns *et al.*, 2005; Hamon *et al.*, 2004; Chai *et al.*, 2008). The $\Delta slrA$ strain color for P_{tapA} -*lacZ* reporter was slightly weaker (Figure 14), indicating that SlrA plays a minor role in suppressing the expression of matrix genes, as observed in the NCIB3610 strain (Chai *et al.*, 2009). SlrR has been shown to induce transcription of *tasA*, but not the *eps* operon (Chu *et al.*, 2008). Consistently, the $\Delta slrR$ strain containing the P_{eps} -*lacZ* reporter was faint blue in color, similar to the wild-type background, while P_{tapA} -*lacZ* expression was markedly impaired (Figure 14). Thus, effects of transcriptional regulators on *eps* and *tasA* operons appear essentially similar in both 168 BFA and NCIB3610 strains. Consistent with the finding that the inactivation of Veg impairs biofilm formation, its deletion resulted in severe blockage of P_{tapA} -*lacZ* expression (Figure 14). Conversely, overproduction of Veg enhance the expression of P_{tapA} -*lacZ* to some extent (Figure 14, see also Figure 17B). However, the transcriptional effect of P_{eps} -*lacZ* was not clearly detected in the absence or overproduction of Veg under this condition (Figure 14). On the other hand, both expressions of P_{tapA} -*lacZ* and P_{eps} -*lacZ* were reduced by the *veg* deletion in the NCIB3610 strain (Figure 14). Thus, although expression of P_{eps} -*lacZ* that was not affected in the 168 BFA strain in the absence or overproduction of Veg, it is reduced by the *veg* deletion in the NCIB3610 background.

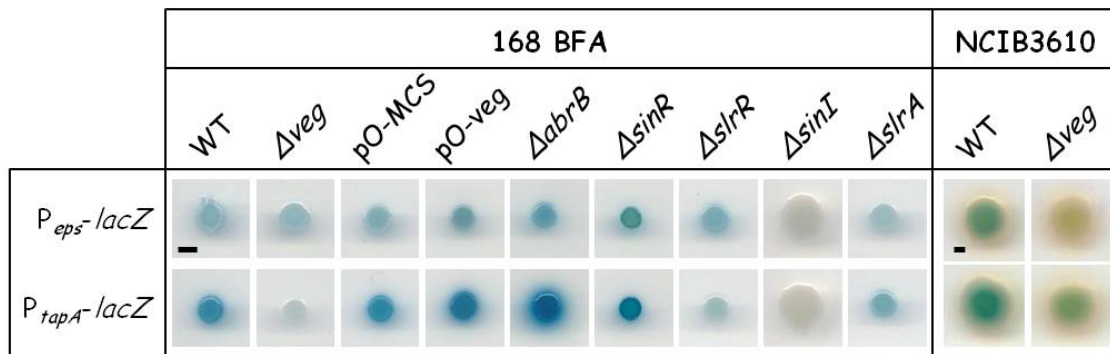
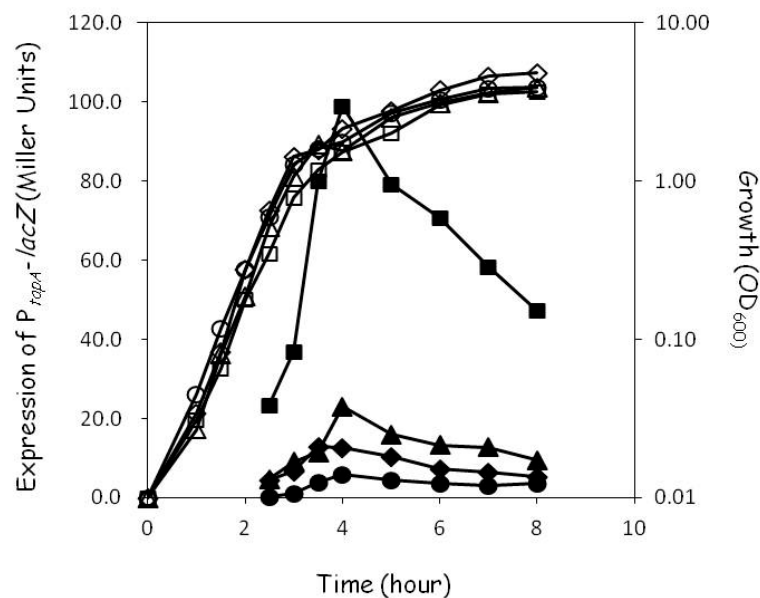


Figure 14. Overproduction and deletion of Veg induces and suppresses transcription of *eps* and *tasA* operons. Expressions of $P_{eps^-} lacZ$ and $P_{tapA^-} lacZ$ were compared after cultivation for 72 h (168 BFA background strains) or 24 h (NCIB3610 background strains) at 30°C on solid MSgg medium containing X-Gal and 1 mM IPTG, for strains with mutation(s) and/or plasmid, indicated at the upper side of each picture. All strains contain an *epsH* mutation in order to abolish cell aggregation, and strains in the up and bottom panels have insertion of $P_{eps^-} lacZ$ and $P_{tapA^-} lacZ$ at the *amyE* loci, respectively. The scale bar is 0.2 cm.

To quantitatively evaluate the effects of Veg on transcriptional activity of the *tasA* operon from the exponential to stationary phase, expression levels of $P_{tapA^-} lacZ$ were measured in the Veg-overproducing and deletion strains. Liquid LB medium was selected, since *tasA* is not highly induced in LB, and the effect was thus expected to be clearly detectable (López *et al.*, 2009b). Consistent with the LacZ plate assay data, transcriptional activity of *tasA* in LB liquid medium was dramatically increased upon overproduction of Veg from the exponential growth phase (Figure 15A). On the other hand, *tasA* expression in the Δveg mutant was decreased, but only to a slight extent, since *tasA* is induced at a very low level in LB liquid medium (Figure 15A). To clearly observe effect of the deletion of *veg*, LacZ activity of *tasA* was examined in biofilm-inducing medium, MSgg, in which transcription of *tasA* operon is known to be highly induced. The result showed that the Δveg mutant strongly decreased the

expression of *tasA* after transition to stationary phase (Figure 15B). Based on the transcriptome result and LacZ assay data, I conclude that Veg promotes biofilm formation through transcriptional activation of *eps* and *tasA* operons. Prevention of biofilm formation in the Δveg strain is caused mainly by transcriptional block of the *tasA* operon in the 168 BFA background, while transcription of both *eps* and *tasA* operons is repressed in the absence of Veg in the NCIB3610 background.

A



B

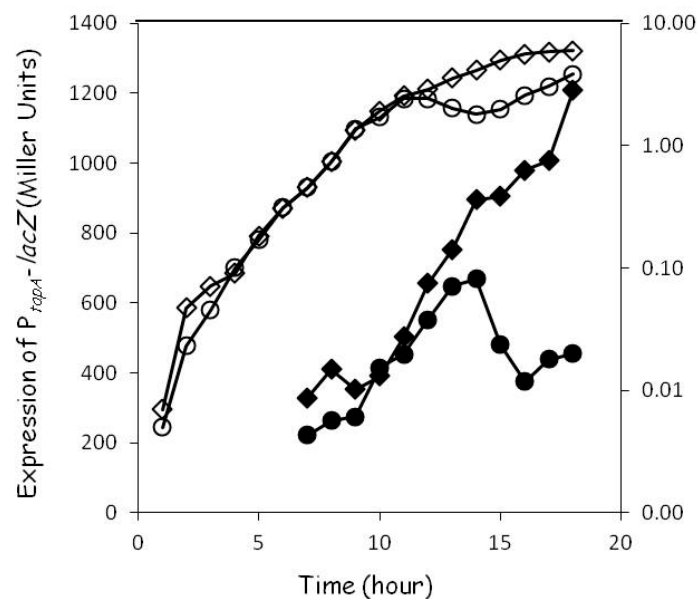


Figure 15. Expression of *tasA* operon was measured in Veg overproduction and deletion cells. Growth and expression of P_{tapA} -*lacZ* in wild-type (LY032, diamonds), Δveg (LY041, circles), pO-veg (LY039, squares) and pO-MCS (LY038, triangles) strains in LB (A) and MSgg (B) liquid media were measured and indicated by open and closed symbols, respectively. All strains have an *epsH* mutation in order to abolish cell aggregation. LY038 and LY039 strains were grown in the presence of 1 mM IPTG.

3.6 Veg induces biofilm formation independently of AbrB

Biofilm formation is governed by two master repressors, AbrB and SinR. Accordingly, we investigated whether Veg regulates biofilm formation via repression of either of these repressors. To this end, I examined effects of *veg* deletion and Veg overproduction on colony architecture and pellicle formation (Figure 16) and P_{eps} -*lacZ* and P_{tapA} -*lacZ* expression (Figure 17) in mutants of regulators for biofilm formation.

On biofilm-inducing medium, expression of P_{eps} -*lacZ* and P_{tapA} -*lacZ* was increased in the $\Delta abrB$ strain (Figure 17). Also the center of the colony showed more complicated structure compared to the parent strain, although modulation of pellicle formation was not clearly observed (Figure 16A). In contrast, both transcription of the *eps* and *tasA* operons and biofilm formation on solid and liquid medium were suppressed upon additional deletion of *veg* (Figure 16B). These results are similar to the genetic relationship previously reported in the $\Delta abrB$ - $\Delta sinI$ double mutant ((Kearns *et al.*, 2005). These results strongly suggest that Veg induces biofilm formation through up-regulation of matrix genes independently of AbrB. The effect of Veg on P_{eps} -*lacZ* expression was not detected in the presence of AbrB, suggesting that Veg function in regulation of the *eps* promoter was masked by AbrB in the Δveg strain.

The effect of Veg-overproduction was examined by comparing mutants harboring

the control plasmid (pO-MCS) and mutants carrying the Veg-overexpressing plasmid (pO-Veg) (Figure 16 and 17). For unknown reason, the $\Delta abrB$ strain harboring the control plasmid showed a different colony morphology and decrease in P_{iapA} -*lacZ* expression compared to the parent strain (Figure 16C). When Veg-overexpressing plasmid was introduced into the $\Delta abrB$ strain, its colony size doubled and surface of the colony was colored compared to the $\Delta abrB$ strain harboring the control plasmid (Figure 16D). However, the effect of Veg-overproduction on expression of matrix genes was not evident (Figure 17). It is possible that slightly increased matrix gene expression undetectable by the LacZ assay leads to the alteration of colony morphology. However, it seems to be more plausible that in the absence of AbrB, expression levels of matrix genes are elevated close to the maximum level on the biofilm-inducing medium and thus their further increase was not induced by Veg overproduction. If this hypothesis is correct, Veg might affect colony morphology in the absence of AbrB through direct regulation of unknown gene(s), as discussed later.

Additionally, the effects of Veg overproduction on other AbrB-regulated genes were examined by comparing the transcriptome result in both overexpressing and control strains during the mid-exponential phase. Transcriptome analysis revealed that transcription of *eps* and *tasA* operons, which is not induced in the control strain, was induced (Table 4), while other AbrB regulons were not affected by Veg overexpression in exponentially growing cells (Table S1). These results further indicated that Veg has an ability to induce matrix genes independently of AbrB.

3.7 Veg induces biofilm formation through inhibition of SinR activity

Next, I examined the possibility that Veg inhibits the ability of SinR to suppress expressions of *eps* and *tasA* operons, either directly or indirectly. In the absence of SinR, transcriptional levels of *eps* and *tasA* operons were increased, leading to highly structured colonies and pellicles in the NCIB3610 genetic background (Kearns *et al.*, 2005). In the 168 BFA background, the $\Delta sinR$ strain also enhanced expressions of these matrix genes (Figure 17A). However, unexpectedly, the induction of matrix genes expression by the *sinR* deletion did not enhance biofilm formation in the 168 BFA background. Instead, the $\Delta sinR$ strain formed smaller colony compared to the parent strain, having smaller structured periphery and covered by transparent mucoïd on the central area. Furthermore, pellicle formation was impaired (Figure 16A). While the precise reason for the apparent biofilm-deficient phenotype of the $\Delta sinR$ mutant in the 168 BFA background is unclear, it is possible that this phenotype is related to mutation of *sfp*, *swrA* and *degQ* in the 168 strain that impair not only biofilm formation but also swarming motility (McLoon *et al.*, 2011). For example, the phenotype may be caused by further impairment of motility enhanced by *sinR* deletion even in the presence of increased matrix materials (Kearns *et al.*, 2005; Fredrick & Helmann, 1996). Downsizing of colony was also observed in the reporter strains and affected intensities of the blue color of the colonies. To avoid this problem, the colony color intensities of the $\Delta sinR$ strains were compared after cultivation for 24 h before the time of the apparent morphological change among the strains. The $\Delta sinR$ strain showed highly induced transcription of matrix genes at this stage without apparent difference in colony structure (Figure 17B).

Next, I compared the phenotypes of the $\Delta sinR$ and $\Delta sinR\text{-}\Delta veg$ double mutants.

Colony morphology of the double mutant was similar to that of the $\Delta sinR$ mutant (Figure 16A and B), indicating that the deficiency of biofilm formation in the absence of Veg is partially restored by additional deletion of *sinR* through derepression of transcription of *eps* and *tasA* operons (Figure 17). Conversely, transcriptional levels of *eps* and *tasA* operons and colony morphology in the $\Delta sinR$ mutant were not affected by additional overproduction of Veg (Figure 16C-D and 17). Similarly, additional inactivation or overproduction of Veg had no impact on pellicle formation of the $\Delta sinR$ mutant, although pellicle formation was stimulated by introduction of the control plasmid (Figure 16). These results strongly suggest that Veg is involved in negative control of the SinR activity.

The transcriptome result showed that the *sinR* expression is not affected in Veg-overexpressing cells (Table S1). Furthermore, wild-type, Δveg , Veg-overexpressing and control strain cells displayed similar protein levels during the exponential growth phase (Figure 18). Interestingly, SlrR, whose transcription is blocked by SinR under these conditions, was induced only upon overproduction of Veg (Figure 18). Consistently, the *slrR* expression was elevated in Veg-overexpressing cells (Table S1). Thus, all biofilm-associated genes repressed by SinR (not only *eps* and *tasA* operons but also *slrR*) were derepressed upon overexpression of Veg, with no corresponding alterations in the SinR levels, strongly suggesting that Veg inhibits the repressor activity of SinR either directly or indirectly.

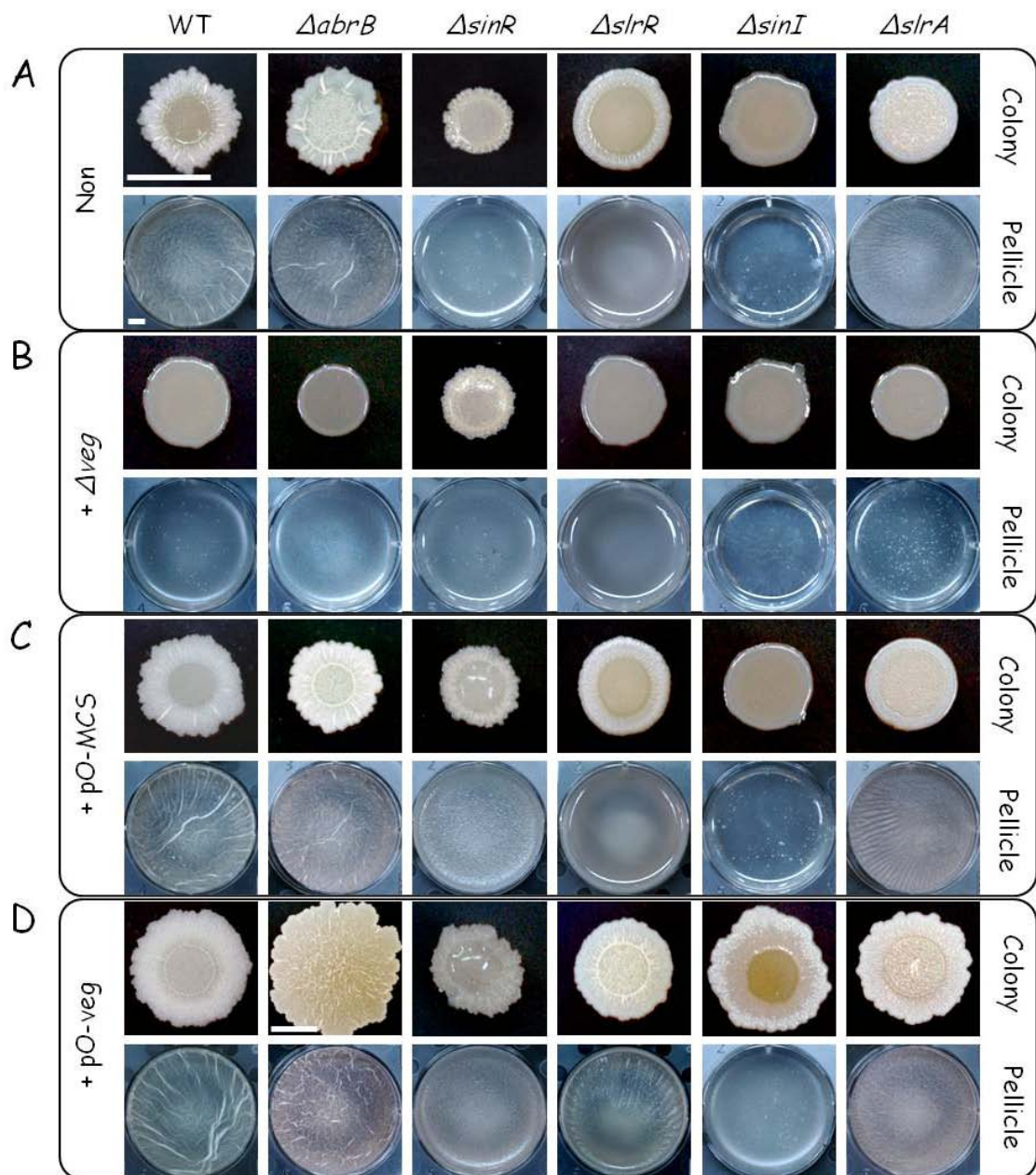


Figure 16. Comparison of the architecture of colonies and pellicles formed by mutants of regulators involved in biofilm formation additional with deletion and overproduction of Veg. (A) Colonies and pellicles of strains with mutation(s) as indicated at the upper side of each picture were formed on solid and liquid MSgg mediums for 72 h at 30°C. Strains with additional Δveg mutation (B), introduction of pO-MCS (as a negative control for pO-veg) (C) and pO-veg (D) were also examined. Strains harboring plasmid were cultured in the presence of 1mM IPTG. The scale bar is 0.5 cm.

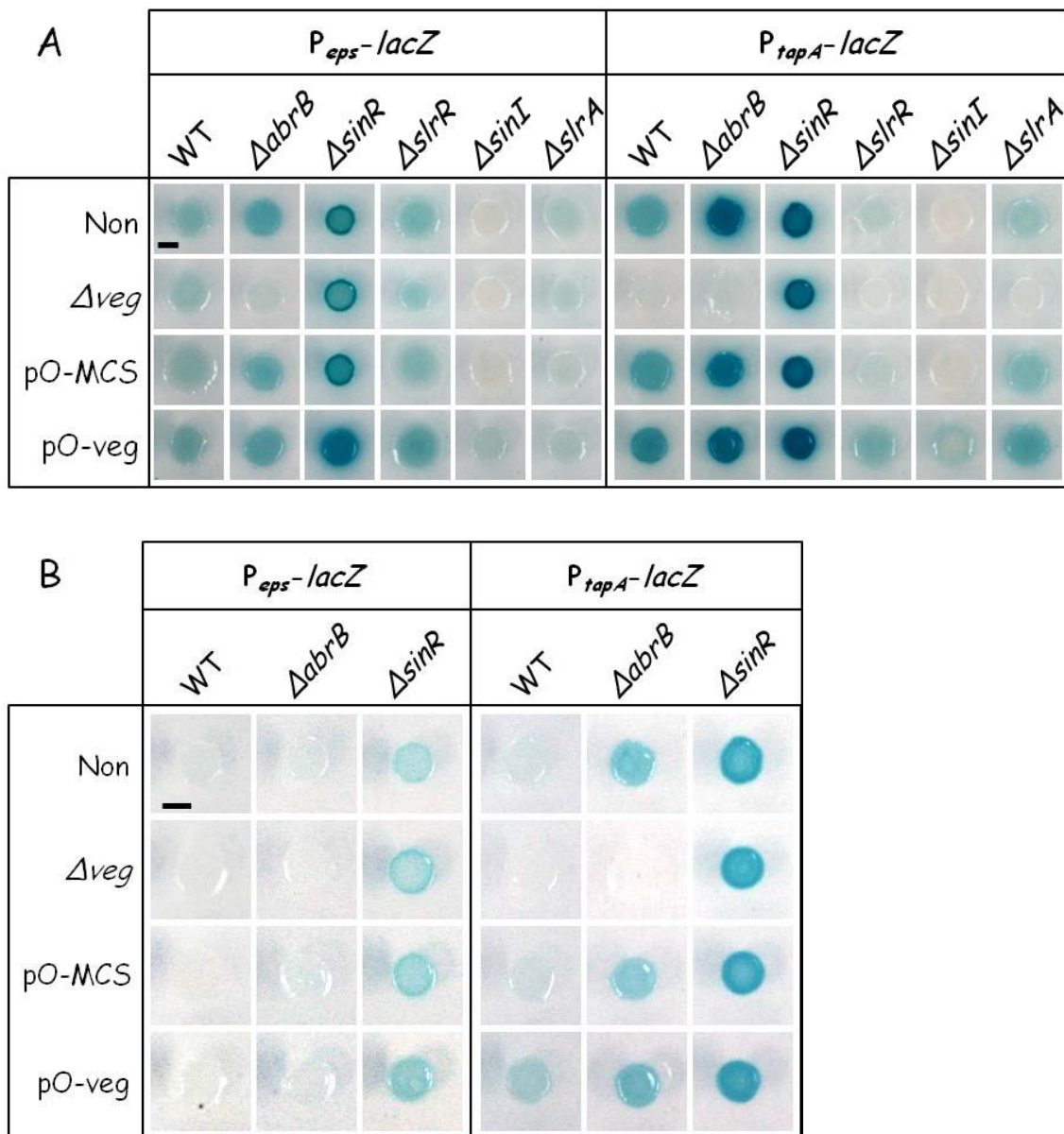


Figure 17. Transcription levels of *eps* and *tasA* operons were compared with mutants of regulators for biofilm formation additional with deletion or overproduction of Veg. Expressions of $P_{eps-lacZ}$ and $P_{tapA-lacZ}$ were compared after cultivation for 48 h (A) or 24 h (B) at 30°C on solid MSgg medium containing X-Gal and 1 mM IPTG. All strains contain an *epsH* mutation, and strains in the left and right panels have insertion of $P_{eps-lacZ}$ and $P_{tapA-lacZ}$ at the *amyE* loci, respectively. The scale bar is 0.2 cm.

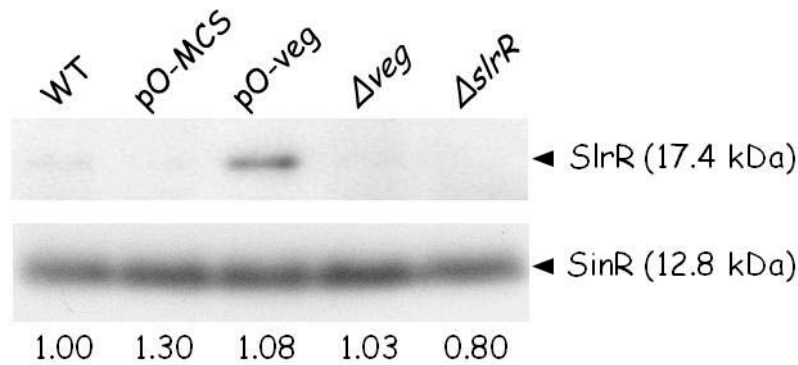


Figure 18. Induction of SlrR by overproduction of Veg. WT (168 BFA), Δveg (LY011), pO-veg (LY016), pO-MCS (LY015) and $\Delta slrR$ (LY013) strains were grown to mid-logarithmic phase in SMM medium at 37°C, and SinR in the cells equivalent to 0.1 OD₆₀₀ units was detected by Western blotting with anti-SinR antibody that cross-reacts with SlrR (Chai *et al.*, 2009). LY015 and LY016 strains were grown in the presence of 1 mM IPTG. The signal intensities of SinR bands on X-ray films were quantified using the NIH-Imagine program and the signal intensities relative to that of WT cells are shown below the bands.

3.8 Veg inhibits SinR activity independently of known antirepressors

SinI, SlrA and SlrR are antirepressors of SinR, which exert their activities via protein-protein interactions (Kearns *et al.*, 2005; Chu *et al.*, 2008; Kobayashi, 2008; Chai *et al.*, 2009). To determine the relationship between Veg and known antirepressors, I next determined whether the Veg-induced increase in transcription of *slrR* is responsible for inhibition of SinR activity. Deletion of *slrR* led to partial biofilm deficient phenotypes, formation of weak structured colonies, and thin and flat pellicles, possibly owing to the remaining inhibitory activities of SinI and SlrA on SinR (Figure 16A). Similar to the Δveg mutant, a double mutant of $\Delta slrR$ and Δveg reduced expression of P_{tapA} -*lacZ* and exhibited a more severe biofilm-deficient colony

morphology compared to the $\Delta slrR$ mutant (Figure 16B and 17A). Conversely, overproduction of Veg induced transcription of $P_{eps-lacZ}$ and $P_{tapA-lacZ}$ rescued the biofilm-deficient phenotype of the $\Delta slrR$ strain, forming a more complicated colony structure and hyper-wrinkled pellicles (Figure 16C and D). These results imply that Veg inhibits SinR activity independently of SlrR.

Deletion of SinI leads to a more severe biofilm-deficient phenotype than single deletion of other anti-repressors of SinR (Kearns *et al.*, 2005; Chu *et al.*, 2006). Consistently, the $\Delta sinI$ and $\Delta sinI-\Delta veg$ double mutant strains showed the most severe biofilm-deficient phenotype, i.e., transcription of *eps* and *tasA* operons was almost completely blocked (Figure 17A), thus forming smooth and featureless colonies and no pellicles (Figure 16A and B). Overproduction of Veg derepressed the expressions of $P_{eps-lacZ}$ and $P_{tapA-lacZ}$ (Figure 17A), and partially restored biofilm deficiency of the $\Delta sinI$ mutant, leading to the formation of a complicated structure in the peripheral zones of colonies and thin pellicles (Figure 16C and D). These results imply that Veg functions independently of SinI.

Consistent with the results of the LacZ assay for matrix genes (Figure 17A), deletion of *slrA* impaired biofilm formation mildly to form a colony with moderate structure and thick but less wrinkled pellicles (Figure 16A). The $\Delta slrA$ and Δveg double mutant severely reduced the expression of $P_{tapA-lacZ}$ (Figure 17A) and displayed severely impaired colony and pellicle morphology, similar to the Δveg mutant (Figure 16B). Overproduction of Veg derepressed the expression of $P_{tapA-lacZ}$ (Figure 17A) and bypassed the biofilm formation deficiency in the $\Delta slrA$ cells (Figure 16C and D), indicating that Veg inhibits SinR activity independently of SlrA.

Based on the collective results, I conclude that Veg controls SinR activity, not

through effects on the known antirepressors, SlrR, SinI or SlrA, but via a novel unknown pathway.

3.9 Examination of physical interaction between Veg and SinR

While my results showed that SinR-repressed genes, including biofilm matrix genes (*eps* and *tasA* operons) and *slrR*, are induced by Veg independently of antirepressors, it was unclear whether SinR activity is directly or indirectly inhibited by Veg. To resolve this issue, proteins interacting with SinR in Veg-overproducing and control cells were examined. In brief, cells expressing SinR-2HC (SinR C-terminally tagged with twelve histidines plus a chitin-binding domain [totally 8.2 kDa]) were grown to the mid-exponential growth phase in minimal medium, and treated with formaldehyde to stabilize complexes among proteins, followed by affinity purification of SinR complexes, as described previously (Ishikawa *et al.*, 2006). Notably, the expression level of SlrR seemed to be higher in the SinR-2HC-expressing cells (Figure 19) compared to that in the 168 BFA cells (Figure 18), suggesting that the repressor activity of SinR is partly impaired by the C-terminal 2HC-tag fusion. However, the SinR-2HC-expressing strain formed an intermediated colony morphology between those observed for the wild-type and the $\Delta sinR$ strains (Figure 20), indicating that the SinR-2HC retained the repressor activity, albeit partially.

Upon examination of SinR complexes with the anti-Veg antibody, Veg was not detected despite its clear presence in the Veg-overexpressing cells (Figure 19), suggesting that Veg does not interact directly with SinR. Interestingly, SlrR was clearly detected in the SinR complexes purified from the control cells, but not in the complex

purified from the Veg-overexpressing cells (Figure 19), suggesting that Veg prevents SlrR binding to SinR directly or indirectly.

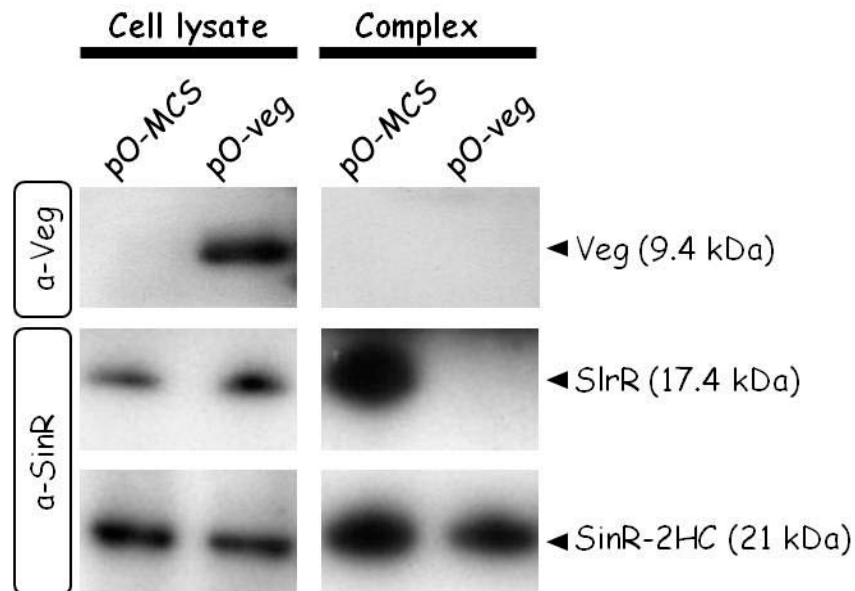


Figure 19. Examination of physical interaction between Veg and SinR. SinR-2HC harboring plasmid pO-veg (LY085) and pO-MCS (LY084) strains were grown to mid-logarithmic phase in SMM medium at 37°C in the presence of 1 mM IPTG. SinR-2HC complexes were purified as described in MATERIALS AND METHODS, and detected by Western blotting, together with crude cell lysates, with anti-Veg (α -Veg) and anti-SinR (α -SinR) antibodies. SinR complexes and crude cell lysates equivalent to 0.8 and 0.1 OD₆₀₀ units respectively, were applied on SDS-PAGE.

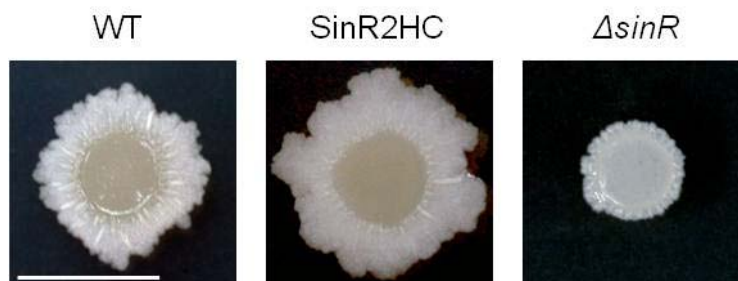


Figure 20. Effects of SinR2HC on the architecture of colonies. The architecture of colonies formed by WT (168 BFA), SinR2HC (LY083) and Δ *sinR* (LY012) strains were grown on MSgg plates for 3 days at 30°C. The scale bar is 0.5 cm.

3.10 *In vivo* complex analysis of Veg

Here, I demonstrated that Veg-GFP showed nucleoid-associated fluorescence and Veg hyper mutants increased the fluorescence intensities. These results suggest that Veg function may be related to the nucleoid localization (Figure 12A, C-E). However, ChAP-chip results reveal that the nucleoid interaction of Veg may be indirectly (Figure 4). It seems reasonable to hypothesize that localization of Veg on the nucleoid region is dependent on an unknown factor via interaction with Veg directly. This unknown factor might also be involved in biofilm formation. To identify the factor, Veg mutants C-terminally fused with GFP strains were used for complex analysis *in vivo*, because the hyper mutant (Veg^{hy}_11) was partially stabilized to induce development of biofilms, while the loss-of-function mutants (Veg^{loss}_01, 03, 05) failed to form biofilms.

As a precise negative control, a GFP expression strain, in which the *gfp* gene was placed under control of the *xyl* inducible promoter at the *amyE* locus, was also constructed, since free GFP protein itself may interact with other proteins in *B. subtilis* cells. To control the expression levels to be a similar extend to that of wild-type Veg-GFP protein. Thus, optimum concentration of xylose was investigated by Western blotting. As a result, I found that addition of 0.01% and 0.1% (w/v) xylose induced GFP proteins to similar levels with Veg-GFP and Veg^{hy}_11-GFP proteins, respectively (Figure 21).

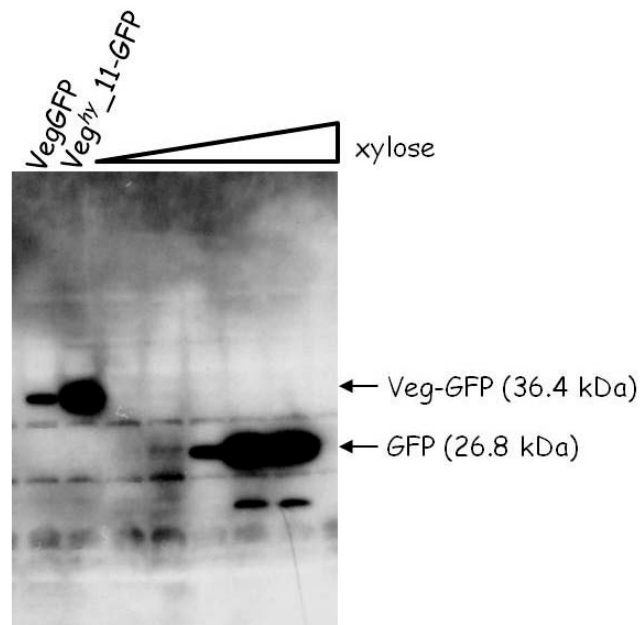


Figure 21. Examination of GFP protein levels in the *gfp* strain with various concentrations of xylose. The *gfp* expressing strain (LY121) was grown to mid-logarithmic phase in LB medium at 37°C, addition with increasing concentration of xylose (0%, 0.001%, 0.01%, 0.1% and 1%). GFP proteins equivalent to 0.1 OD₆₀₀ units were detected by Western blotting, together with that in VegGFP (LY067) and Veg^{hy}_11-GFP (LY115) cells, using anti-GFP antibody.

Next, GFP fusion proteins in Veg-GFP expressing strains and the negative control *gfp* strain were purified by anti-GFP magnetic beads using chromatin immunoprecipitation method described previously (Grainger *et al.*, 2004). The protein patterns of the purified GFP complexes were compared after SDS-PAGE and silver staining (Figure 22A). Unfortunately, no specific bands copurified with Veg-GFP and/or Veg^{hy}_11-GFP were detected, comparing to that with the negative control GFP. In addition, in the Veg^{loss}_01, 03, 05-GFP strains, Veg-GFP band was not detected. Here arises a question. Was purification of Veg-GFP complexes unsuccessful or Veg proteins completely degraded in these mutant strains? In agreement with the increased

fluorescence image of Veg^{hy}-GFP, the increased amount compared to the wild-type Veg-GFP was confirmed by Western blotting (Figure 21). Since clear localization of the Veg^{loss}-GFP was not observed, the amount was examined by Western blotting with anti-GFP antibody. As shown in Figure 22B, neither Veg-GFP protein nor free GFP were detectable in the loss-of-function mutants, indicating that Veg^{loss}-GFP proteins become unstable by the loss-of-function mutations to be degraded more easily, producing small amount of free GFP proteins expanding to whole cells (Figure 12F-J).

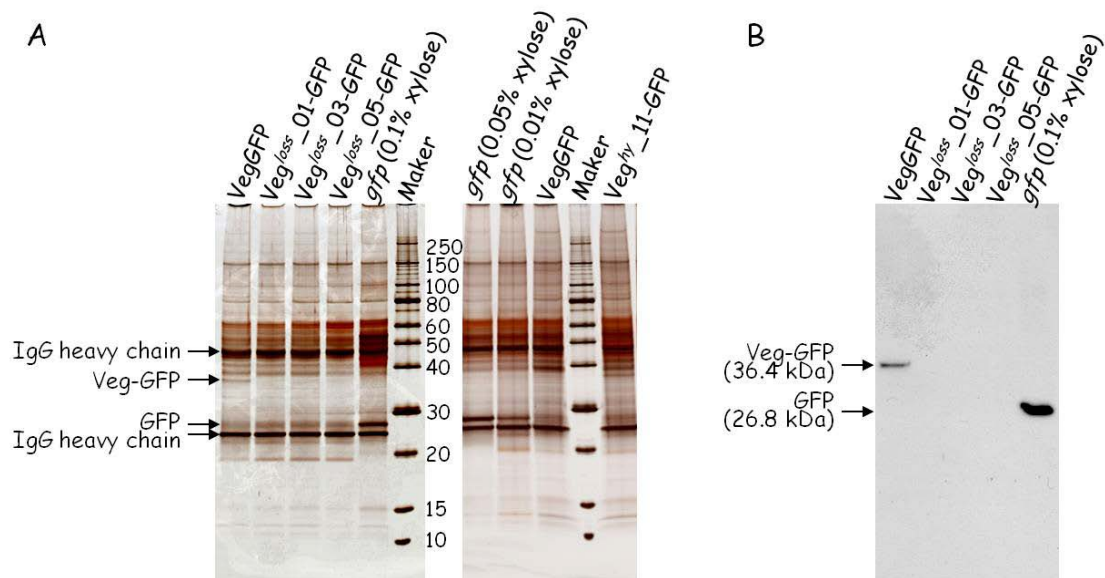


Figure 22. *In vivo* complex analysis with GFP fusion proteins. VegGFP (LY067), Veg^{loss}_01, 03, 05-GFP (LY116, 118 and 120), Veg^{hy}_11-GFP (LY115) strains were grown to mid-logarithmic phase in MSgg medium at 37°C. The *gfp* strain (LY121) grown in the presence of xylose (0.01%, 0.05% and 0.1%) was also examined. (A) Veg-GFP complexes were purified as described in the MATERIALS AND METHODS, and then separated by SDS-PAGE and visualized by silver staining. (B) Veg-GFP proteins in cells with 0.1 OD₆₀₀ units were detected by Western blotting with anti-GFP antibody.

3.11 Motility is inhibited by overproduction of Veg

Motility and matrix synthesis are often coordinately and oppositely regulated. Bacteria have two types of surface motility, swimming and swarming motility. Both of them require the production of functional flagella, but many factors appear to distinguish the two forms of movement. Flagella allow bacteria to swim as individual behavior independently perceiving chemical signals that trigger adaptive chemotactic responses. Swarming regarded as a multicellular behavioral in addition requires the production of a surfactant to reduce surface tension rapidly and colonize nutrient-rich solid substrates (Shapiro, 1998; Harshey, 2003; Calvio *et al.*, 2005; Kearns *et al.*, 2005; Patrick & Kearns, 2012). In *B. subtilis*, motility is positively controlled by SinR, the master repressor of biofilm formation. Deletion of *sinR* blocked motility on a solid surface (Kearns *et al.*, 2005). As previous discussed, Veg stimulates biofilm formation through inhibition of the SinR activity. Thus, I asked whether Veg would be associated with regulation of motility.

Plates containing less than 0.5% agar are called 'swim plates' because motile bacteria swim through the porous medium and create a large zone of colonization. Plates fortified with more than 0.5% agar are called 'swarm plates' as the reduced pore size and extensive colonization of the plate can only occur by bacterial migration over the agar surface (Kearns & Losick, 2003). Thus, swimming and swarming plate assays were performed in wild-type 168 BFA, Δveg , Veg-overexpressing and its control strain with LB medium supplemented with a low (0.2%) and high (0.7%) concentration of agar. Strains were incubated on the center of the surface with a toothpick and incubated at 30°C for 13 or 15 h. On swimming plates, motility was reduced by overproduction of Veg as compared to its control stain (Figure 22A), suggesting that Veg apparently

has a negative effect on motility. However, the Δveg strain showed a similar swimming ability as compared to the wild strain 168 BFA (Figure 23A), revealing that the effect of Δveg mutant cannot be detectable on the plates with low concentration of agar.

On the other hand, it has been reported that laboratory strains (eg. 168), carrying a mutation in the region of *sfp* gene that impairs surfactin synthesis and a frameshift mutation in the *swrA* region that encodes a master regulator of flagellar gene expression, have a non-swarming phenotype (Kearns & Losick, 2003; Calvio *et al.*, 2005; Calvio *et al.*, 2008, Osera *et al.*, 2009). Hence, the wild strain 168 BFA, Veg overproduction (pO-veg) and together with its control strain (pO-MCS) showed no swarming ability on the plates with high concentration agar (Figure 23B). Surprisingly, deletion of *veg* resulted better motility than other strains, leading to migration of dendrites on LB medium (Figure 23B and C). Since deletion of *veg* increased motility in the 168 BFA genetic background lacking surfactin and SwrA-associated activation of flagellar genes, these observations revealed that deletion of *veg* simply increased swimming motility. In total, I conclude that Veg not only plays a positive role in biofilm formation, but also negatively regulates motility in *B. subtilis*.

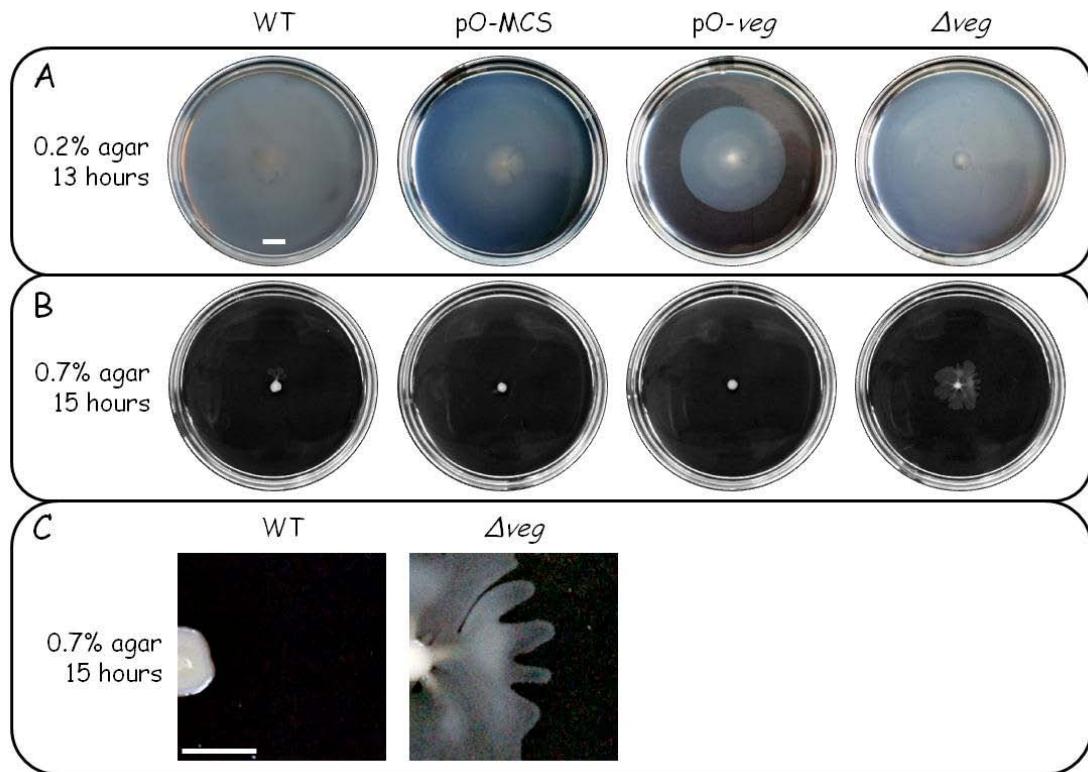


Figure 23. Effects of Veg inactivation and overproduction on motility. Swimming (A) and swarming (B and C) patterns on LB medium with 0.2% and 0.7% agar, respectively, formed by the following strains. WT (168 BFA), pO-MCS (LY015), pO-veg (LY016), Δveg (LY011) strains were grown at indicated times at 30°C. LY015 and LY016 strains were cultivated in the presence of 1 mM IPTG. The scale bar is 1 cm (A and B) and 0.5 cm (C).

4. DISCUSSION

In the present investigation, comprehensive analysis of the genetic interactions of regulators of biofilm formation in *B. subtilis* revealed that Veg stimulates biofilm formation by inhibiting SinR repressor activity to induce gene expression for matrix synthesis. Additionally, SinR activity is inhibited by Veg through a novel pathway that is independent of the three known antirepressors, SlrR, SinI and SlrA. Accordingly, Veg suppresses motility probably owing to inhibition of SinR activity, as well.

4.1 Proteolytic regulation of Veg

The *veg* gene is constitutively transcribed at high level not only during the exponential phase but also in the stationary phase in rich (LB) and minimum (SMM) media (Morimoto *et al.*, 2008). However, in the present study, I showed that Veg protein was extremely unstable (Figure 6B and D) and undetectable by Western blotting (Figure 11 and 19) in cells growing during exponential phase. Deletion of intracellular protease LonA, ClpYQ or MlpA resulted much more increased amount of Veg proteins (Figure 7), suggesting that LonA, ClpYQ and MlpA are required for the rapid degradation of Veg. However, Veg protein was still undetectable when deletion of these three proteases (Figure 11). These observations indicate that there are other unknown protease(s) responsible for Veg proteolysis. Thus, identification of unknown protease(s) contributing to the Veg instability will be the future work.

In the present study, I also showed that deletion of *lonA* formed complicated colony structure as well as overproduction of Veg and Veg hyper mutants did (Figure 8, 9 and 10C). These results reveal that the phenotype formed by deletion of *lonA* is most likely

due to partially stabilized Veg, which then stimulates biofilm formation. Nevertheless, the effect of deletion of *lonA* seems stronger than the Veg hyper mutants, in which Veg proteins can be detected but not in the $\Delta lonA$ mutant. These results indicate that *B. subtilis* LonA also regulates other unknown proteins involved in biofilm formation by proteolysis. In addition, several Veg hyper mutants exhibited hyper biofilm phenotype similar to others, but stabilization of Veg was undetectable in them. It is probable because the increased amount of Veg is below the limit of detection by Western blotting. Another possibility is that Veg mutant proteins could not be detectable with the anti-Veg antibody purified from wild-type strain.

Since Veg is degraded by more than one protease, the questions arise as to (i) why Veg is strikingly unstable; (ii) whether the proteolysis of Veg is necessary or not. When Veg was overproduced, transcription of the matrix genes, which should have been repressed by SinR and AbrB during exponential phase, was activated (Figure 13-14, and 15A, see also Table 4). Thereby, increased *veg* expression to a detectable level leads to induce biofilm development, resulting in differentiation during exponential phase. The results suggest that rather than transcriptional induction of the *veg* gene, stabilization of Veg protein leads to activation of genes that promote biofilm development. Thus, I hypothesize that proteolysis of Veg is required to avoid inappropriate differentiation as cells were grown in the medium with plentiful nutrients. Moreover, deletion of *veg* clearly showed a deficiency in biofilm formation and decreased expression of *tasA* after transition to stationary phase (Figure 9, 14 and 15B). Hence, it is expected that activity of protease(s) responsible for Veg degradation is decreased during the biofilm development process to regulate biofilm formation in response to unknown signal(s).

It has been known that proteolysis is an important mechanism used by bacteria to rapidly modulate protein levels during adaptive responses to changing environmental conditions, cell cycle progression, and development (Dougan *et al.*, 2002; Gottesman, 2003; Jenal & Hengge-Aronis, 2003; Skerker & Laub, 2004). In *B. subtilis*, protease-dependent regulation of protein activity has been found for the Spx protein. Spx protein is known as a global transcriptional regulator to control transcriptions through its interaction with the C-terminal domain of the RNA polymerase α subunit (α -CTD) and the amount is kept at very low level by the ClpXP protease (Zuber, 2004). However, under disulfide stress conditions, Spx concentration increases due in part to a reduction in ClpXP-catalyzed proteolysis to activate genes for detoxification of the stress and induce Spx-dependent transcriptional repression. Although all of the protease(s) involved in proteolysis of Veg are yet to be identified, one possible explanation is that in order to survive stress conditions, an unknown signal stabilizes Veg protein to stimulate biofilm formation. The specific protease(s) contributing to Veg instability and times of Veg stabilization are currently under investigation.

4.2 Veg negatively regulates the activity of SinR in a new pathway

In the case of the known antirepressors, all of these are homologous to entire of SinR (SlrR) or C-terminal of SinR (SinI and SlrA) and directly interact with SinR to antagonize SinR activity. According to comparison of phenotypes, the biofilm morphology in the absence of SinR was not affected by either *veg* deletion or overproduction, whereas the biofilm-deficient phenotype of *sinI*, *slrA* or *slrR* deletion mutants was partially restored by Veg overproduction (Figure 16), supporting to the theory that Veg controls the ability of SinR to induce biofilm formation independently

of the antirepressors. This conclusion was further supported by transcriptome analysis showing that transcription of the Spo0A regulon, including not only *sinI* and *abrB*, but also other genes, such as *spoIIIGA-sigE*, *spoIIIE* and *spoIIAA-spoIIAB-sigF* involved in sporulation (Molle *et al.*, 2003), was not affected by overexpression of Veg (Table S1). Earlier studies have reported that transcription of *slrA* is regulated by YwcC (Kobayashi, 2008; Chai *et al.*, 2009), and increased transcription induces the genes required for biofilm formation and reduces the entire σ^D regulon (Cozy *et al.*, 2012). However, in our experiments, Veg overproduction did not alter expression of *ywcC*, *slrA* or the σ^D regulon (Table S1) (Serizawa *et al.*, 2004). These results collectively suggest that Veg controls SinR activity through a novel mechanism independent of Spo0A-*sinI*-SinI and YwcC-*slrA*-SlrA pathways (Figure 2).

I found that not only deletion of *veg* but also single deletion of *slrR* and *slrA* specifically reduce transcription of the *tasA* operon but not that of the *eps* operon (Figure 14 and 17A). Thus, the differential effect on the expression of matrix genes will be common for antirepressor of SinR. On the other hand, transcriptome analysis demonstrated that Veg overexpression induces transcription of the *eps* and *tasA* operons in cells exponentially growing in SMM medium (Table 4). Furthermore, I found that *veg* deletion decreases both P_{tapA} -*lacZ* and P_{eps} -*lacZ* expression in the Δ *abrB* mutant (Figure 17). These results may suggest that transcriptional regulation of biofilm extracellular matrix genes are modulated by the expression levels of regulators. Further systematic and quantitative expression analyses of regulators involved in biofilm formation are necessary to understand the complex regulatory system for biofilm formation.

Expression of *sinR* was not affected in Veg-overproducing cells (Table S1) and SinR

protein levels were similar in cells expressing different levels of Veg (Figure 18), strongly suggesting that Veg modulates the repressor activity of SinR. Interestingly, although Veg was not detected in the SinR complex purified from Veg-overproducing cells, interactions between SinR and SlrR were inhibited upon overexpression of Veg. These results suggest that an unknown antirepression factor for SinR is induced or activated by Veg that competes with SlrR via direct binding to SinR. However, considering that Veg is extremely unstable, it is possible that the protein interacts directly with SinR and is degraded due to proteolysis during the purification process.

4.3 *In vivo* complex analysis of Veg

Fluorescence microscopy analysis of Veg and Veg hyper mutants fused with GFP showed that Veg localized on the nucleoid (Figure 12A and C-E), revealing that Veg function is associated with the nucleoid. Additionally, Veg plays a function on inhibition of SinR activity via the unknown antirepression factor induced by Veg. Thus, we hypothesized that this factor might be the important key to explain localization of Veg and clarify the mechanism of interaction between Veg and SinR.

To identify the factor induced by Veg, complex analysis of Veg^{hy}-GFP was performed in the Veg^{hy}_11-GFP cells, in which Veg is functional, compared to that in the wild-type and loss of its function cells. Unfortunately, any specific band interacting with Veg failed to be detected (Figure 21A). It is probable that the level of Veg proteins in the hyper mutant is not high enough, leading to the induced level of the unknown antirepressor below the limit of detection by silver staining. Hence, in the future, I will use a strain overexpressing Veg-GFP for complex analysis.

On the other hand, a fundamental question remains to be explored. Dose Veg

activate the target protein(s) through induction of their expressions or modulate their activities through protein-protein interactions? Since no specific bands interacting with Veg were detected, Veg might be involved in the control of genes expressions. The transcriptome result showed that in addition to the matrix genes and prophage genes, there are seven other genes upregulated in the Veg-overexpressing cells (Table 4). The target of Veg might be included in these seven genes. Additionally, the preliminary ChAP-chip analysis showed that the binding sites of Veg distributed throughout the *B. subtilis* genome and the pattern is mostly similar to that of RNA polymerase even after RNase treatment (Figure 4). This result suggests that Veg might bind to RNA polymerase not DNA. Therefore, another possibility is that the target protein of Veg might be RNA polymerase, like Spx as discussed above.

4.4 Veg negatively regulates motility

It has been reported that motility and biofilm formation are often coordinately and oppositely regulated (Blair *et al.*, 2008). According to motility assays, motility was reduced by overproduction of Veg and increased by deletion of it (Figure 23), indicating that Veg has ability to control motility negatively. The mechanism by which Veg inhibits motility may be involved in regulation of SinR. In *B. subtilis* biofilms, motility is inhibited by EpsE, which acts as a clutch on the flagella rotor to inhibit motility, and which is encoded within the 15 gene *eps* operon required for EPS production. Previous study showed that EpsE fusion with GFP failed to localize as puncta represented sites of flagellar basal bodies in the presence of FliG that rendered the flagellum insusceptible to inhibition by EpsE. Accordingly, EpsE is thought to interact directly with FliG to inhibit the motility (Blair *et al.*, 2008; Guttenplan *et al.*,

2010). Overproduction of Veg prevents the activity of SinR, resulting in derepression of *eps* operon including *epsE*. When EpsE is induced, it interacts with FliG directly and affects its three-dimensional structure to alter FliG interaction with MotA, which provides power for flagellum rotation (Blair & Berg, 1990; Lloyd *et al.*, 1996; Zhou *et al.*, 1998; Kojima & Blair, 2001; Berg, 2003; Thomas *et al.*, 2006), leading to the flagella behave as though they are unpowered rather than immobilized (Blair *et al.*, 2008) (Figure 24).

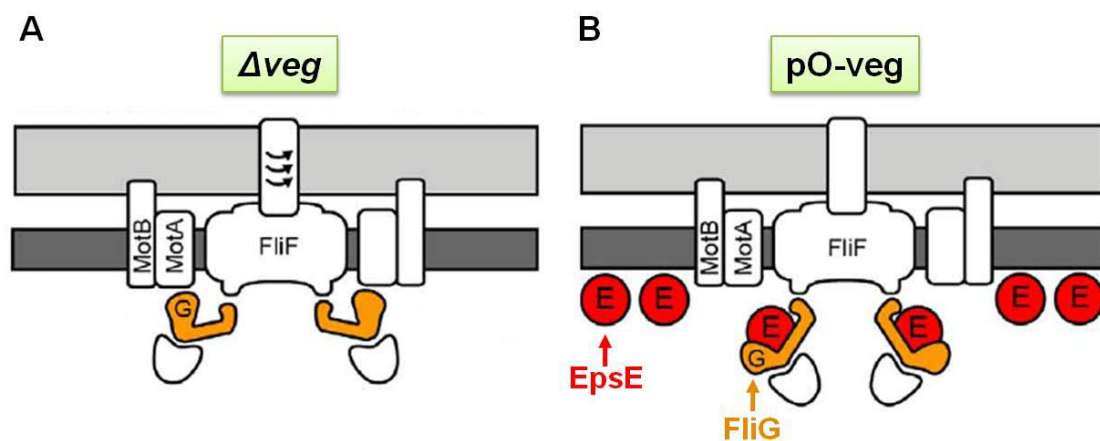


Figure 24. The mechanism of motility regulation by Veg. Cross-section diagrams of the *B. subtilis* flagellar basal body are indicated (Guttenplan *et al.*, 2010). Dark grey rectangles indicate the plasma membrane while light grey rectangles indicate the peptidoglycan cell wall. “G” indicates the rotor FliG. “E” indicates EpsE. (A) Cells in absence of *veg* are incapable of EPS biosynthesis. FliG interacts with MotA to drive flagellar motor rotation. (B) Cells in overproduction of Veg induce EPS biosynthesis. EpsE binds to FliG directly and disables flagellar rotation by disrupting the FliG-MotA interaction.

In addition, motility is also related to the flagellin filament (*hag*), and autolysins LytC (an *N*-acetylmuramoyl-L-alanine amidase) and LytF (a γ -D-glutamate meso-diaminopimelate muropeptidase), which are under the regulation of σ^D . Based on the transcriptome result, transcription of σ^D regulon was not changed by

overproduction of Veg. Thus, the motility inhibition of Veg is probable mainly due to repression of SinR activity. On the other hand, the reason why swarming assays showed the increase of motility in the absence of Veg in the 168 genetic background is still unclear. It has been reported that SwrA and DegU cooperatively drive the *fla/che* operon encoding flagella components, which is regarded as the primary event in the development of motility (Kearns & Losick, 2005; Tsukahara & Ogura, 2008). A low concentration of phospho-DegU (DegU-P) is sufficient to activate transcription of flagellar genes to increase swarming motility in undomesticated and laboratory strains of *B. subtilis*, whereas a high concentration of DegU-P inhibits swarming motility (Verhamme *et al.*, 2007; Kobayashi 2007; Calvio *et al.*, 2008). Furthermore, the laboratory strain 168 has a frameshift mutation in the *swrA* region, leading to lose the induction of flagellar gene expression dependently of SwrA (Kearns *et al.*, 2004; Calvio *et al.*, 2005; Patrick & Kearns, 2009). Therefore, it is possible that deletion of *veg* might be related to keep the low concentration of DegU-P to improve motility and/or induce transcription of flagellar genes through an unknown mechanism.

4.5 Other functions of Veg

It should be noted that Veg should be also involved in maintenance of cell robustness at the entry into stationary growth phase in the biofilm-inducing medium, because the Δveg cells abruptly lysed in this timing, while the wild-type strain did not (Figure 15B). Although exact reason for the cell lysis is now under investigation, these results clearly suggest that Veg is activated being coupled with growth phase to develop not only biofilm but also to maintain cell robustness. When planktonic cells transit to biofilm cells, the matrix genes together with *slrR* will be derepressed from

SinR through inhibition of SinR activity in the wild-type strain. While in the absence of Veg, part of SinR activity will be insusceptible, resulting to sustaining repression of *slrR* that suppresses autolysin genes (*lytC* and *lytF*) (Chai *et al.*, 2010). Thus, it is expected that autolysin genes will be derepressed and resulted in cell lysis the Δveg cells.

In addition, the transcriptome result also showed that, in addition to biofilm matrix genes, several genes in the prophage regions of PBSX and SP β are induced by Veg (Table 4). Interestingly, the same gene clusters on PBSX are highly expressed in biofilm-inducing cells (Stanley *et al.*, 2003), but not induced in *sinR* deletion mutant cells (Chu *et al.*, 2006). My results suggest that during biofilm formation, the gene cluster on PBSX may be induced in a Veg-dependent, SinR-independent manner. Earlier reports have demonstrated that phage genes are induced in a *Pseudomonas aeruginosa* biofilm and proposed that the phage induction participates in gene transfer or exclusion of other strains (Whiteley *et al.*, 2001). Although the exact biological roles of phage-related genes in *B. subtilis* cells have not been established yet, one possibility is a similar function to that reported for *P. aeruginosa*. Another proposal is that restricted phage-related genes are induced to develop a defense machinery to protect against phage infection for survival. Furthermore, Veg has been shown to play an important role during the sporulation phase in mature spore development for normal germination (Fukushima *et al.*, 2003). Thus, Veg appears to function in the regulation of other genes in addition to SinR.

4.6 Conclusion remark

In summary, in addition to the two known pathways, Spo0A-*sinI*-SinI and

YwcC-*slrA*-SlrA, we have identified a novel third pathway triggered by Veg to induce biofilm formation (Figure 2). All three pathways act in parallel, leading to inhibition of SinR to stimulate a self-reinforcing double-negative feedback loop of SinR-*slrR*-SlrR and derepress SinR-repressed *eps* and *tasA* operons, which facilitates biofilm development. Moreover, we suggest that Veg is involved in the regulation of genes other than SinR during biofilm and spore formation, although further studies are necessary to elucidate the entire spectrum of Veg-induced gene activities.

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Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>dnaA</i>	410	1750	+	741.89	590.61	1.26	917.68	1159.36	0.79	Spo0A regulon
<i>dnaN</i>	1939	3075	+	397.84	278.97	1.43	686.83	729.38	0.94	
<i>yaaA</i>	3206	3421	+	698.78	674.4	1.04	783.26	986.53	0.79	
<i>recF</i>	3437	4549	+	1411.36	1196.25	1.18	1214.2	1377.84	0.88	
<i>yaaB</i>	4567	4725	+	1584.67	1301.09	1.22	1414.2	1551.81	0.91	
<i>gyrB</i>	4866	6782	+	1780.89	1591.68	1.12	2160.89	2257.27	0.96	
<i>gyrA</i>	6993	9458	+	1527.8	1249.83	1.22	1910.44	1939.5	0.99	
<i>yaaC</i>	14845	15792	-	51.13	36.89	1.39	29.87	30.35	0.98	
<i>guaB</i>	15913	17379	+	1621.67	1676.1	0.97	2065.4	2078.53	0.99	
<i>dacA</i>	17532	18863	+	814.77	729.71	1.12	1175.31	1388.61	0.85	
<i>yaaD</i>	19060	19944	+	3198.17	2738.63	1.17	3257.04	3347.41	0.97	Spo0A regulon
<i>yaaE</i>	19966	20556	+	3246.68	2767.31	1.17	3061.63	2974.25	1.03	
<i>serS</i>	20878	22155	+	2051.37	1831.23	1.12	1614.81	1508.06	1.07	
<i>dck</i>	22494	23147	-	493.37	384.62	1.28	556.93	557.88	1.00	
<i>dgk</i>	23144	23767	-	466.85	366.4	1.27	601.75	602.35	1.00	
<i>yaaH</i>	23866	25149	-	544.24	274.45	1.98	169.52	77.67	2.18	
<i>yaaI</i>	25219	25764	-	1883.71	1021.99	1.84	576.67	178.52	3.23	
<i>yaaJ</i>	25850	26335	+	248.95	238.42	1.04	251.72	282.71	0.89	
<i>dnaX</i>	26812	28503	+	479.76	367.68	1.30	606.84	664.12	0.91	
<i>yaaK</i>	28527	28850	+	1958.21	1446.56	1.35	2185.61	2475.13	0.88	
<i>recR</i>	28865	29461	+	807.31	530.15	1.52	1094.43	1030.46	1.06	
<i>yaaL</i>	29479	29703	+	421.21	297.37	1.42	510.58	543.95	0.94	
<i>bofA</i>	29770	30033	+	162.17	100.11	1.62	170.55	179	0.95	
<i>csfB</i>	35529	35723	+	113.05	83.59	1.35	90.27	60.86	1.48	
<i>xpaC</i>	35843	36457	+	367.45	340.04	1.08	290.01	304.87	0.95	
<i>yaaN</i>	36476	37636	+	380.58	374.7	1.02	490.57	463.18	1.06	
<i>yaaO</i>	37718	39160	+	219.25	175.75	1.25	268.87	292.56	0.92	
<i>tmk</i>	39157	39795	+	756.87	444.76	1.70	690.24	611.9	1.13	
<i>yaaQ</i>	39869	40198	+	1627.23	1380.23	1.18	1440.68	1300.76	1.11	
<i>yaaR</i>	40211	40651	+	1578.95	1345	1.17	1320.12	1236.46	1.07	
<i>holB</i>	40663	41652	+	1214.78	966.77	1.26	1000.41	965.8	1.04	
<i>yaaT</i>	41655	42482	+	1272.34	963.3	1.32	1225.6	1266.82	0.97	
<i>yabA</i>	42497	42856	+	305.47	275.45	1.11	446.92	461.71	0.97	
<i>yabB</i>	42915	43658	+	294.97	224.99	1.31	364.47	387.5	0.94	
<i>yazA</i>	43645	43944	+	197.84	166.3	1.19	373.77	392.62	0.95	
<i>yabC</i>	43919	44797	+	353.45	271.58	1.30	567.91	556.25	1.02	
<i>abrB</i>	44846	45136	-	2790.27	3429.5	0.81	1529.1	1681.59	0.91	Spo0A regulon
<i>metS</i>	45631	47625	+	901.51	897.47	1.00	1311.89	1452.79	0.90	Spo0A regulon
<i>yabD</i>	47704	48471	+	344.96	340.43	1.01	700.41	641.61	1.09	
<i>yabE</i>	48627	49940	+	623.53	816.45	0.76	765.76	1199	0.64	
<i>rnmV</i>	50085	50645	+	286.27	255.22	1.12	330.9	398.5	0.83	
<i>ksgA</i>	50638	51516	+	356.73	281.62	1.27	461.3	494.39	0.93	
<i>yabG</i>	51678	52550	+	63.13	63.98	0.99	59.57	65.27	0.91	
<i>veg</i>	52761	53021	+	9228.78	3265.94	2.83	8853.78	2773.25	3.19	Spo0A regulon
<i>sspF</i>	53181	53366	+	130.98	191.68	0.68	91.21	141.86	0.64	
<i>ispE</i>	53514	54383	+	814.99	816.15	1.00	1068.33	1166.56	0.92	
<i>purR</i>	54439	55296	+	1617.51	1618.63	1.00	1788.64	1794.49	1.00	
<i>yabJ</i>	55293	55670	+	2111.22	2056.02	1.03	2153.07	2007.23	1.07	
<i>spoVG</i>	55864	56157	+	3895.02	4865.21	0.80	3645.04	4045.46	0.90	AbrB regulon
<i>gcaD</i>	56350	57720	+	796.43	720.27	1.11	1455.26	1704.13	0.85	
<i>prs</i>	57743	58696	+	840.45	631.56	1.33	1496.73	1542.86	0.97	
<i>ctc</i>	58781	59395	+	5904.8	6724.45	0.88	3760.09	3335.98	1.13	
<i>spoVC</i>	59502	60068	+	1326.54	1433.26	0.93	793.06	761.05	1.04	
<i>yabK</i>	60128	60358	+	1085.56	1106.93	0.98	686.1	683.25	1.00	
<i>mfd</i>	60428	63961	+	826.71	753.51	1.10	845.21	762.12	1.11	
<i>spoVT</i>	64097	64633	+	402.02	388.73	1.03	617.58	514.59	1.20	
<i>yabM</i>	64815	66413	+	175.48	144.31	1.22	286.72	244.8	1.17	

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<i>yabN</i>	66403	67872	+	905.64	810.9	1.12	1138.31	1041.51	1.09	
<i>yabO</i>	67875	68135	+	1541.01	1469.37	1.05	1786.79	1690.55	1.06	
<i>yabP</i>	68214	68516	+	955.87	847.88	1.13	1051.25	955.72	1.10	
<i>yabQ</i>	68513	69148	+	1622.56	1079.07	1.50	1180.82	1038.88	1.14	
<i>diviC</i>	69166	69543	+	1943.49	1399.56	1.39	1673.92	1880.43	0.89	
<i>yabR</i>	69624	70010	+	2718.25	2138.48	1.27	2119.08	2517.7	0.84	
<i>spolIE</i>	70536	73019	+	146.15	111.41	1.31	99.9	87.91	1.14	Spo0A regulon
<i>yabS</i>	73104	73841	+	263	174.75	1.51	169.22	164.5	1.03	
<i>yabT</i>	73807	74823	+	332.81	212.53	1.57	196.31	127.83	1.54	
<i>yacA</i>	74927	76345	+	1269.57	937.98	1.35	1044.81	1106.29	0.94	
<i>hprT</i>	76342	76884	+	1578.27	1182.09	1.34	1584.47	1708.24	0.93	
<i>ftsH</i>	76982	78895	+	3021.7	2695.72	1.12	2911.34	3020.35	0.96	
<i>yacB</i>	79090	79791	+	531.07	479.29	1.11	611.52	616.09	0.99	
<i>yacC</i>	79877	80752	+	493.68	414.09	1.19	689.7	679.35	1.02	
<i>yacD</i>	80799	81692	+	289.79	312.49	0.93	490.63	570.53	0.86	
<i>cysK</i>	81768	82694	+	2799.36	2238.63	1.25	3064.84	3425.96	0.89	
<i>pabB</i>	82861	84273	+	604.36	528.37	1.14	714.62	674.6	1.06	
<i>pabA</i>	84287	84871	+	834.12	885.44	0.94	1002.53	1029.39	0.97	
<i>pabC</i>	84871	85752	+	504.09	438.31	1.15	643.29	716.87	0.90	
<i>sul</i>	85734	86591	+	743.92	647.55	1.15	962.74	1043.56	0.92	
<i>folB</i>	86584	86946	+	1135.92	1061.58	1.07	1506.21	1610.62	0.94	
<i>folK</i>	86943	87446	+	926.32	840.04	1.10	1207.62	1299.82	0.93	
<i>yazB</i>	87398	87607	+	971.85	828.01	1.17	1350.73	1479.44	0.91	
<i>yacF</i>	87631	88632	+	1441.84	1275.46	1.13	1946.55	1923.3	1.01	
<i>lysS</i>	88724	90223	+	1554.11	1380.45	1.13	2159.6	1977.03	1.09	
<i>ctsR</i>	101446	101910	+	2924.88	2793.7	1.05	1458.77	1021.71	1.43	
<i>mcsA</i>	101924	102481	+	2872.44	2493.65	1.15	975.23	758.91	1.29	
<i>mcsB</i>	102481	103572	+	3526.85	2915.33	1.21	1355.51	1187	1.14	
<i>clpC</i>	103569	106001	+	4646.35	3613.81	1.29	2404.61	2058.37	1.17	
<i>radA</i>	106093	107469	+	1844.57	1291.47	1.43	1083.81	922.98	1.17	
<i>yacK</i>	107473	108555	+	1919.65	1448.72	1.33	1423.9	1276.14	1.12	
<i>yacL</i>	108671	109771	+	2035.29	1899.33	1.07	1413.51	1299.76	1.09	
<i>yacM</i>	109786	110484	+	1443.43	1262.99	1.14	1128.53	1064.23	1.06	
<i>yacN</i>	110477	110953	+	940.94	693.79	1.36	843.07	867.44	0.97	
<i>gltX</i>	111044	112495	+	1889.1	1704.43	1.11	2033.53	2210.34	0.92	
<i>cysE</i>	112797	113450	+	611.37	485	1.26	866.11	874.32	0.99	
<i>cysS</i>	113447	114847	+	850.8	774.92	1.10	1078.08	1027.17	1.05	
<i>yazC</i>	114851	115282	+	644.49	632.06	1.02	775.51	815.68	0.95	
<i>yacO</i>	115266	116015	+	1056.12	1028.11	1.03	1383.43	1311.68	1.05	
<i>yacP</i>	116022	116534	+	783.53	715.58	1.09	983.8	970.35	1.01	
<i>sigH</i>	116597	117253	+	2247.23	2439.33	0.92	2032.03	2539.99	0.80	
<i>secE</i>	117529	117708	+	665.25	836.54	0.80	1223.32	1626.09	0.75	
<i>nusG</i>	117887	118420	+	1031.5	945.48	1.09	1013.09	1400.84	0.72	
<i>rplK</i>	118588	119013	+	4108.21	4452.84	0.92	4694.88	4908.64	0.96	
<i>rplA</i>	119107	119805	+	3197.48	3508.18	0.91	4093.94	4360.74	0.94	
<i>rplJ</i>	120057	120557	+	3400.8	3954.29	0.86	4602.3	4495.61	1.02	
<i>rplL</i>	120604	120975	+	1801.25	2226.45	0.81	3185.71	3237.8	0.98	
<i>ybxB</i>	121065	121670	+	568.4	670.12	0.85	1025.66	1188.26	0.86	
<i>rpoB</i>	121916	125497	+	2625.56	2872.49	0.91	3289.97	3524.87	0.93	
<i>rpoC</i>	125559	129158	+	3201.02	3754.8	0.85	3747.17	3813.61	0.98	
<i>ybxF</i>	129339	129587	+	5745.36	5779.29	0.99	6169.25	5939.17	1.04	
<i>rpsL</i>	129701	130117	+	6364.81	6753.06	0.94	6754.7	6301.46	1.07	
<i>rpsG</i>	130159	130629	+	5467.99	5991.25	0.91	5664.79	5619.43	1.01	
<i>fusA</i>	130683	132761	+	6389.52	6916.3	0.92	6237.41	5959.1	1.05	
<i>tufA</i>	132881	134071	+	6956.21	7376.38	0.94	6275.82	5852.47	1.07	
<i>ybaC</i>	134170	135126	+	150.98	132.06	1.14	171.82	175.33	0.98	
<i>rpsJ</i>	135362	135670	+	6127.24	6617.59	0.93	5275.13	5292.05	1.00	
<i>rplC</i>	135710	136339	+	5923.1	6594.16	0.90	5804.89	5588.26	1.04	

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<i>rplD</i>	136367	136990	+	6009	6518.54	0.92	5544.6	5167.5	1.07	
<i>rplW</i>	136990	137277	+	6655.43	6955.36	0.96	6568.76	6384.67	1.03	
<i>rplB</i>	137309	138142	+	6484.39	7081.32	0.92	5858.6	5674.26	1.03	
<i>rpsS</i>	138200	138478	+	6230.39	7027.13	0.89	6503.43	6246.43	1.04	
<i>rplV</i>	138495	138836	+	6598.97	7112.84	0.93	6388.18	6280.55	1.02	
<i>rpsC</i>	138840	139496	+	5299.49	5971.06	0.89	5752.59	5499.77	1.05	
<i>rplP</i>	139498	139932	+	5984.33	6461.49	0.93	5845.2	5703.06	1.02	
<i>rpmC</i>	139922	140122	+	5999.92	6126.7	0.98	4925.72	5104.24	0.97	
<i>rpsQ</i>	140145	140408	+	6161.9	6745.95	0.91	6019.75	5709.77	1.05	
<i>rplN</i>	140449	140817	+	7023.36	7902.55	0.89	6932.3	6646.46	1.04	
<i>rplX</i>	140855	141166	+	6422.89	7003.76	0.92	6037.52	5577.4	1.08	
<i>rplE</i>	141193	141732	+	6268.45	6791.94	0.92	5484.52	5095.29	1.08	
<i>rpsN</i>	141755	141940	+	5567.6	5656.46	0.98	4859.43	4399.98	1.10	
<i>rpsH</i>	141972	142370	+	6958.42	7571.17	0.92	6368.24	5816.82	1.09	
<i>rplF</i>	142400	142939	+	6201.04	6745.33	0.92	5705.22	5308.48	1.07	
<i>rplR</i>	142972	143334	+	7284.62	8034.06	0.91	6594.66	6111.3	1.08	
<i>rpsE</i>	143359	143859	+	6342.16	6910.76	0.92	5663.55	5371.46	1.05	
<i>rpmD</i>	143873	144052	+	3344.57	3637.86	0.92	2928.54	3128.29	0.94	
<i>rplO</i>	144083	144523	+	7037.7	7480.28	0.94	5898.08	5565.94	1.06	
<i>secY</i>	144525	145820	+	6802.5	7283.58	0.93	5699	5377.81	1.06	
<i>adk</i>	145875	146528	+	6645.77	6987.78	0.95	5538.35	5201.19	1.06	
<i>map</i>	146525	147271	+	6169.69	6557.28	0.94	5504.73	5236.54	1.05	
<i>infA</i>	147583	147801	+	6105.83	4767.18	1.28	5161.42	4907.19	1.05	
<i>rpsM</i>	147971	148336	+	5969.79	6389.31	0.93	5445.77	5052.72	1.08	
<i>rpsK</i>	148357	148752	+	6135.97	6539.82	0.94	5338.27	5055.95	1.06	
<i>rpoA</i>	148929	149873	+	6881.2	7291.48	0.94	6210.84	5811.47	1.07	
<i>rplQ</i>	149951	150313	+	3845.59	3982.37	0.97	3423.74	3382.33	1.01	
<i>ybxA</i>	150441	151286	+	750.19	746.42	1.01	1072.42	1024.5	1.05	
<i>ybaE</i>	151301	152131	+	492.54	481.19	1.02	662.26	650.14	1.02	
<i>ybaF</i>	152128	152925	+	603.09	540.57	1.12	659.69	652.02	1.01	
<i>truA</i>	152935	153678	+	941.84	759.49	1.24	1469	1286.81	1.14	
<i>rplM</i>	153841	154278	+	4880.23	5244.4	0.93	5585.54	5531.49	1.01	
<i>rpsI</i>	154299	154691	+	2539.37	2946.67	0.86	3790.58	3793.18	1.00	
<i>ybaJ</i>	155155	155922	+	248.53	269.28	0.92	440.03	505.38	0.87	AbrB regulon
<i>ybaK</i>	156108	156551	+	36.08	37.1	0.97	41.53	48.56	0.86	
<i>cwD</i>	156611	157324	+	53.68	56.02	0.96	50.94	59.12	0.86	
<i>ybaL</i>	157420	158478	+	2247.28	2438.63	0.92	2339.14	2362.25	0.99	
<i>gerD</i>	158514	159071	-	32.24	36.29	0.89	33.96	33.77	1.01	
<i>kbaA</i>	159181	159777	+	237.98	297.53	0.80	282.49	407.03	0.69	
<i>ybaN</i>	159778	160542	-	29.13	33.53	0.87	27.5	31.39	0.88	
<i>ybaR</i>	177082	178518	+	279.84	253.66	1.10	425.61	407.29	1.04	
<i>ybaS</i>	178733	179584	+	189.2	148.82	1.27	244.16	222.65	1.10	
<i>ybaA</i>	179594	180163	-	183.22	205	0.89	122.08	162.23	0.75	
<i>feuC</i>	180168	181352	-	239.2	267.5	0.89	146.31	186.87	0.78	
<i>feuB</i>	181345	182349	-	231.47	258.07	0.90	114.52	142.08	0.81	
<i>feuA</i>	182368	183321	-	592.04	705.96	0.84	322.27	425.27	0.76	
<i>ybbB</i>	183412	185001	-	290.75	304.28	0.96	209.25	254.76	0.82	
<i>ybbC</i>	185192	186436	-	84.43	96.19	0.88	91.55	109.27	0.84	
<i>ybbD</i>	186450	188378	-	96	107.72	0.89	100.66	118.41	0.85	
<i>ybbE</i>	188406	189731	-	106.9	112.9	0.95	116.46	142.54	0.82	
<i>ybbF</i>	189788	191155	-	90.34	91.24	0.99	89	108.18	0.82	
<i>ybbH</i>	191181	192032	-	135.55	135.71	1.00	184.83	210.57	0.88	
<i>ybbI</i>	192049	192963	-	177.07	186.83	0.95	263.12	291.34	0.90	
<i>ybbJ</i>	193134	193553	-	97.95	122.1	0.80	107.31	106.99	1.00	
<i>ybbK</i>	193566	194021	-	268.95	346.17	0.78	281.62	280.5	1.00	
<i>sigW</i>	194838	195401	+	2999.68	2721.56	1.10	3712.16	3555.8	1.04	
<i>ybbM</i>	195415	196041	+	1415.87	1286.86	1.10	2111.83	1951.6	1.08	
<i>ybbP</i>	196202	197023	+	717.57	700.28	1.02	782.55	867.39	0.90	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ybbR</i>	197016	198467	+	841.09	733.16	1.15	1142.99	1288.66	0.89	
<i>ybbT</i>	198486	199832	+	734.87	647.47	1.13	1078.29	1195.92	0.90	
<i>glmS</i>	200263	202065	+	873.11	835.87	1.04	1102.82	1312.06	0.84	
<i>alkA</i>	202533	203444	-	111.99	109.89	1.02	137.73	139.77	0.99	
<i>adaA</i>	203715	204350	+	46.18	57.8	0.80	37.55	35.11	1.07	
<i>adaB</i>	204337	204876	+	59.32	63.24	0.94	42.39	46.09	0.92	
<i>ndhF</i>	205395	206912	+	101.03	77.08	1.31	48.12	46.77	1.03	
<i>ybcC</i>	206927	207169	+	81.86	62.58	1.31	31.19	37.22	0.84	
<i>ybcD</i>	207166	209430	+	203.52	132.53	1.54	58.75	57.37	1.02	
<i>ybcF</i>	209619	210146	+	242.15	164.11	1.48	53.6	50.36	1.06	
<i>ybcH</i>	210210	210500	+	268.91	199.3	1.35	60.08	57.99	1.04	
<i>ybcI</i>	210558	210932	+	289.48	215.44	1.34	73.48	73.26	1.00	
<i>ybcL</i>	211845	213017	+	68.32	68.59	1.00	81.84	80.45	1.02	
<i>ybcM</i>	213141	213455	+	61.75	61.62	1.00	56.23	74	0.76	
<i>ybcO</i>	213926	214093	+	1321.14	1589.5	0.83	1666.2	2253.43	0.74	Spo0A and AbrB regulon
<i>ybcP</i>	214160	215392	+	639.53	817.42	0.78	889.19	1092.69	0.81	AbrB regulon
<i>ybcS</i>	215389	215946	+	514.94	685.34	0.75	781.42	947.51	0.82	AbrB regulon
<i>ybcT</i>	215943	216878	+	446.91	535.85	0.83	614.85	740.1	0.83	AbrB regulon
<i>ybdA</i>	216897	217616	+	498.12	581.46	0.86	674.35	793.8	0.85	AbrB regulon
<i>ybdB</i>	217681	219027	+	286.44	320.18	0.89	370.2	447.59	0.83	AbrB regulon
<i>ybdD</i>	219074	219487	+	377.94	424.84	0.89	564.88	626.92	0.90	AbrB regulon
<i>ybdE</i>	219593	220018	+	195.65	232.97	0.84	357.05	438.19	0.81	AbrB regulon
<i>ybdG</i>	220264	221154	+	118.86	114.26	1.04	178.98	158.85	1.13	
<i>ybdJ</i>	221246	221917	+	228.17	186.95	1.22	282.03	251.88	1.12	
<i>ybdK</i>	221938	222900	+	291.88	237.2	1.23	395.28	397.16	1.00	
<i>ybdL</i>	222970	223164	+	723.92	762.14	0.95	1141.98	1131.75	1.01	
<i>ybdM</i>	223207	223977	-	115.14	108.56	1.06	108.7	106.37	1.02	
<i>ybdN</i>	224063	224920	-	675.69	728.76	0.93	734.65	693.19	1.06	AbrB regulon
<i>ybdO</i>	225052	226236	+	1024.59	1621.97	0.63	908.44	1229.61	0.74	AbrB and SigD regulon
<i>ybxG</i>	226554	227942	+	411.92	509.68	0.81	541.66	586.94	0.92	
<i>csgA</i>	228054	228302	+	50.48	39.28	1.29	44.08	36.78	1.20	
<i>ybxH</i>	228319	228510	+	20.66	22.32	0.93	30.56	23.48	1.30	
<i>ybxI</i>	228537	229340	-	177.37	187.66	0.95	200.59	208.93	0.96	
<i>cypC</i>	229513	230766	+	1369.96	1039.25	1.32	592.31	292.57	2.02	
<i>ybyB</i>	230807	231067	-	8762.8	10016.5	0.87	5769.63	4327.93	1.33	
<i>ybeC</i>	231336	232955	+	1255.43	1471.12	0.85	994.44	1203.74	0.83	
<i>glpQ</i>	233002	233883	-	105.27	126.02	0.84	99.71	131.07	0.76	
<i>glpT</i>	233982	235316	-	77.53	100.9	0.77	69.83	99.05	0.70	
<i>ybeF</i>	235613	235861	+	33.92	37.93	0.89	44.35	42.17	1.05	
<i>ybfA</i>	235953	236870	+	184.81	179.64	1.03	186.65	194.89	0.96	
<i>ybfB</i>	236867	238117	+	131.41	117.79	1.12	133.89	135.43	0.99	
<i>ybfE</i>	238152	238436	-	100.09	73.3	1.37	160.08	173.85	0.92	
<i>ybfF</i>	238632	239543	-	196.72	137.56	1.43	332.82	268.06	1.24	
<i>ybfG</i>	239632	241830	-	1348.97	558.86	2.41	2187.32	1125.51	1.94	
<i>ybfH</i>	241905	242825	-	113.15	143.94	0.79	132.07	157.51	0.84	
<i>ybfI</i>	242822	243649	-	160.12	209.23	0.77	136.44	184.63	0.74	
<i>purT</i>	243880	245034	+	1126.46	1070.97	1.05	1518.48	1433.06	1.06	
<i>mpr</i>	245178	246119	+	584.16	618.65	0.94	676.4	649.61	1.04	
<i>ybfJ</i>	246082	246480	+	154.21	156.42	0.99	185.1	202.52	0.91	
<i>ybfK</i>	246646	247536	+	591.13	498.11	1.19	568.96	651.43	0.87	
<i>pssA</i>	247732	248265	+	452.47	401.31	1.13	537.18	614.28	0.87	
<i>ybfM</i>	248256	248744	+	358.18	285.91	1.25	438.98	469.86	0.93	
<i>psd</i>	248737	249528	+	421.49	342.99	1.23	443.47	483.18	0.92	
<i>ybfN</i>	249583	249861	+	63.74	69.58	0.92	64.76	71.41	0.91	
<i>ybfO</i>	249967	251307	+	662.42	542.91	1.22	1090.21	960.28	1.14	AbrB regulon
<i>ybfP</i>	251415	252302	+	220.22	185.27	1.19	407.49	344.27	1.18	AbrB regulon
<i>ybfQ</i>	252502	253470	+	1191.33	1133.22	1.05	1342.17	1205.94	1.11	
<i>glpP</i>	253506	254750	-	144.68	155.16	0.93	133.98	137.65	0.97	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>gamP</i>	254895	256790	-	265.66	550.13	0.48	235.68	494.93	0.48	
<i>gamA</i>	256811	257560	-	326.7	663.63	0.49	338.77	625.02	0.54	
<i>ybgA</i>	257779	258486	+	183.22	170.98	1.07	209.98	212.13	0.99	
<i>ybgB</i>	258520	258795	+	69	68.6	1.01	113.89	106.15	1.07	
<i>ybgE</i>	259004	260074	+	446.69	473.67	0.94	667.38	579.48	1.15	
<i>ybgF</i>	260111	261523	-	336.47	239.15	1.41	618.53	528.37	1.17	
<i>ybgG</i>	261644	262591	-	251.05	262.8	0.96	315.31	342.92	0.92	
<i>ybgH</i>	262720	264111	-	93.37	93.76	1.00	69.25	72.65	0.95	
<i>ybgJ</i>	264181	265164	-	57.18	64.44	0.89	48.58	57.34	0.85	
<i>ycbA</i>	265536	266699	+	139.6	127.38	1.10	134.26	151.31	0.89	
<i>ycbB</i>	266710	267654	+	134.14	112.35	1.19	165.53	175.27	0.94	
<i>ycbC</i>	267881	268807	+	84.09	85.32	0.99	76.51	96.25	0.79	
<i>ycbD</i>	268837	270303	+	120.71	130.98	0.92	107.21	134.12	0.80	
<i>ycbE</i>	270387	271754	+	76.71	78.73	0.97	64.73	75.01	0.86	
<i>ycbF</i>	271791	273158	+	131.2	139.91	0.94	103.18	124.83	0.83	
<i>ycbG</i>	273228	273929	+	245.02	232.41	1.05	423.32	454.52	0.93	
<i>ycbH</i>	274020	275552	+	118.11	118.03	1.00	123.22	138.5	0.89	
<i>ycbJ</i>	275829	276749	+	824.53	807.77	1.02	870.04	986.21	0.88	
<i>yczA</i>	277151	277312	+	95.12	115.1	0.83	151.39	142.82	1.06	
<i>ycbK</i>	277333	278271	+	178.8	182	0.98	171.5	180.45	0.95	
<i>ycbL</i>	278368	279048	+	98.16	97.16	1.01	98.2	117.51	0.84	
<i>ycbM</i>	279050	279526	+	165.6	175.32	0.94	252.05	272.98	0.92	
<i>ycbN</i>	279682	280521	+	118.82	109.61	1.08	161.12	177.44	0.91	
<i>ycbO</i>	280640	281254	+	145.44	116.44	1.25	241.52	236.85	1.02	
<i>ycbP</i>	281309	281695	-	2850.56	1822.16	1.56	1678.77	848.03	1.98	
<i>cwJ</i>	282009	282437	+	71.43	68.76	1.04	60.75	72.69	0.84	
<i>ycbR</i>	282543	283274	+	93.35	89.66	1.04	94.58	111.1	0.85	
<i>phoD</i>	283553	285223	+	80.88	79.9	1.01	59.28	69.01	0.86	
<i>tatAD</i>	285318	285530	+	58.28	62.36	0.93	55.71	51.04	1.09	
<i>tatCD</i>	285591	286328	+	45.79	51.2	0.89	40.82	46.6	0.88	
<i>pcp</i>	286325	286972	-	422.27	364.55	1.16	428.77	380.65	1.13	
<i>ycbU</i>	287051	288163	+	342.33	287.75	1.19	312.71	287.31	1.09	
<i>lmrB</i>	288205	289644	-	161.23	134.07	1.20	313.17	341.94	0.92	
<i>lmrA</i>	289684	290250	-	169.25	186.37	0.91	264.84	308.05	0.86	
<i>yccC</i>	290467	291594	+	105.93	131.5	0.81	78.73	89.69	0.88	
<i>lip</i>	291757	292395	+	1120.12	1087.64	1.03	2629.49	2541.77	1.03	AbrB regulon
<i>yczC</i>	292433	292816	-	142.39	134.14	1.06	140.57	118.73	1.18	
<i>yccF</i>	293051	294127	+	507.55	449.48	1.13	646.55	724.83	0.89	
<i>yccG</i>	294167	295123	-	149.97	134.08	1.12	157.32	170.31	0.92	
<i>yccH</i>	295136	295837	-	133.57	122.59	1.09	172.04	182.8	0.94	
<i>natA</i>	295981	296721	+	108.83	95.53	1.14	118.42	116.54	1.02	
<i>natB</i>	296722	297882	+	129.15	100.98	1.28	192.96	156.44	1.23	
<i>yccK</i>	298018	298950	+	272.95	262.33	1.04	319.86	309.91	1.03	
<i>ycdA</i>	298990	300054	-	1001.77	599.58	1.67	1244.21	890.82	1.40	AbrB regulon
<i>ycdB</i>	300382	301800	+	148.47	140.01	1.06	208.64	181.62	1.15	
<i>ycdC</i>	301987	303348	+	140.55	114.22	1.23	169.33	170.83	0.99	
<i>ycdD</i>	303356	303859	-	152.15	132.08	1.15	150.63	151.15	1.00	
<i>rapJ</i>	303982	305103	+	746.11	640.5	1.16	664.69	724.24	0.92	
<i>ycdF</i>	305210	305986	+	3691.05	2442.01	1.51	1655.41	747.57	2.21	
<i>ycdG</i>	306011	307696	+	3876.33	2445.94	1.58	1427.82	577.67	2.47	
<i>ycdH</i>	307884	308843	+	321.11	207.82	1.55	183.89	181.48	1.01	
<i>ycdI</i>	308899	309594	+	201.67	196.77	1.02	187	190.05	0.98	
<i>yceA</i>	309552	310394	+	178.62	141.58	1.26	252.42	211.54	1.19	
<i>yceB</i>	310432	311373	-	108.97	99.02	1.10	119.13	120.81	0.99	
<i>yceC</i>	311711	312310	+	3220.38	2891.26	1.11	3730.39	3694.05	1.01	
<i>yceD</i>	312332	312913	+	3413.47	3105.47	1.10	3947.09	3648.26	1.08	
<i>yceE</i>	312948	313526	+	3028.97	2967.68	1.02	3731.69	3584.93	1.04	
<i>yceF</i>	313577	314350	+	3200.9	3000.22	1.07	3557.65	3415.6	1.04	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yceG</i>	314435	316048	+	1351.81	1199.26	1.13	1815.6	1621.45	1.12	
<i>yceH</i>	316064	317155	+	1752.9	1527.76	1.15	2303.23	2036.26	1.13	
<i>yceI</i>	317277	318479	+	911.47	681.77	1.34	827.53	820.6	1.01	
<i>yceJ</i>	318732	319904	-	46.55	46.7	1.00	43.8	47.11	0.93	
<i>yceK</i>	319973	320275	-	154.14	150.72	1.02	178.28	365.67	0.49	
<i>opuAA</i>	320565	321821	+	1600.22	1170.6	1.37	2765.87	3192.29	0.87	
<i>opuAB</i>	321823	322671	+	1963.87	1644.49	1.19	3752.97	3746.77	1.00	
<i>opuAC</i>	322671	323552	+	1617.93	1522.94	1.06	3214.79	3305.6	0.97	
<i>amhX</i>	323571	324740	-	1469.56	1350.52	1.09	1324.07	1212.3	1.09	
<i>ycgA</i>	325133	326323	+	296.63	267.45	1.11	165.61	163.98	1.01	
<i>ycgB</i>	326439	327020	+	220.94	198.21	1.11	146.84	142.18	1.03	
<i>amyE</i>	327169	329151	+	230.41	247.87	0.93	214.43	196.19	1.09	AbrB regulon
<i>ldh</i>	329328	330293	+	9799.43	10347.4	0.95	5501.92	4794.88	1.15	
<i>lctP</i>	330325	331950	+	7025.39	7487.25	0.94	1492.24	938.18	1.59	
<i>mdr</i>	332258	333538	-	198.91	242.17	0.82	269.62	413.74	0.65	
<i>ycgE</i>	333651	334118	+	137.07	131.64	1.04	118.29	178.23	0.66	
<i>ycgF</i>	334192	334821	+	168.17	142.14	1.18	161.51	214.77	0.75	
<i>ycgG</i>	334891	335652	+	123.1	109.41	1.13	124.61	169.2	0.74	
<i>ycgH</i>	335684	336817	-	58.57	61.36	0.95	51.16	60.67	0.84	
<i>ycgI</i>	336984	337718	+	52.26	51.57	1.01	52.94	68.43	0.77	
<i>nadE</i>	337848	338666	+	3556.86	2595.32	1.37	2234.96	1643.53	1.36	
<i>tmrB</i>	338716	339309	-	127.39	113.28	1.12	184.3	159.66	1.15	
<i>aroK</i>	339585	340145	+	102.69	112.62	0.91	154.25	161.23	0.96	
<i>ycgJ</i>	340173	340859	-	121.01	131.42	0.92	122.04	125.51	0.97	
<i>ycgK</i>	341052	342026	+	82.81	91.06	0.91	95.66	123.65	0.77	
<i>cah</i>	342098	343054	+	137.51	144.93	0.95	260.23	335.45	0.78	
<i>ycgL</i>	343138	343920	+	154.25	132.35	1.17	370.15	385.34	0.96	
<i>ycgM</i>	344111	345022	+	120.87	139.97	0.86	200.38	190.99	1.05	Spo0A regulon
<i>ycgN</i>	345039	346586	+	214.13	220.08	0.97	328.13	322.99	1.02	
<i>ycgO</i>	346782	348131	+	716.19	481.36	1.49	1054.31	946.21	1.11	
<i>ycgP</i>	348284	349519	+	136.43	155.08	0.88	150.69	158.38	0.95	
<i>ycgQ</i>	349556	350413	-	109.45	106.14	1.03	208.32	208.24	1.00	
<i>ycgR</i>	350418	351302	-	117.95	103.93	1.13	146.62	159.13	0.92	
<i>ycgS</i>	351402	352256	-	61.07	70.56	0.87	84.54	86.61	0.98	
<i>ycgT</i>	352418	353428	+	575.24	804.76	0.71	457.25	676.44	0.68	
<i>nasF</i>	353460	354911	-	1595.3	829.11	1.92	514.47	388.61	1.32	
<i>nasE</i>	354972	355292	-	2562.76	1327.44	1.93	494.97	302.6	1.64	
<i>nasD</i>	355324	357741	-	2621.01	1215.51	2.16	394.99	207.34	1.91	
<i>nasC</i>	357863	359995	-	105.03	100.23	1.05	83.22	96.5	0.86	
<i>nasB</i>	360002	362314	-	100.55	92.55	1.09	78.62	81.81	0.96	
<i>nasA</i>	362494	363759	+	153.4	130.56	1.17	106.28	115.75	0.92	
<i>yciA</i>	363815	364732	+	36.54	39.25	0.93	34.53	37.63	0.92	
<i>yciB</i>	364729	365313	+	39.4	44.44	0.89	38.88	47.78	0.81	
<i>yciC</i>	365622	366815	+	67.68	67.42	1.00	45.13	55.92	0.81	
<i>yckA</i>	366864	367544	-	92.28	107.63	0.86	183.25	207.06	0.89	
<i>yckB</i>	367554	368417	-	247.19	279.02	0.89	379.56	508.92	0.75	
<i>yckC</i>	368795	369250	+	223.24	141.21	1.58	146.27	114.59	1.28	
<i>yckD</i>	369332	369664	+	48.73	53.3	0.91	46.83	49.17	0.95	
<i>yckE</i>	369818	371251	+	73.02	73.95	0.99	83.31	87.94	0.95	
<i>nin</i>	371288	371686	-	674.58	709.03	0.95	572.03	851.01	0.67	
<i>nucA</i>	371713	372156	-	1344.1	1345.2	1.00	1395.13	1656.87	0.84	
<i>tipC</i>	372330	374051	-	464.32	366.33	1.27	404.7	347.95	1.16	SigD regulon
<i>hxlB</i>	374162	374719	-	996.59	1235.82	0.81	249.94	252.86	0.99	
<i>hxlA</i>	374725	375357	-	1012.34	1265.43	0.80	245.42	273.45	0.90	
<i>hxlR</i>	375589	375951	+	368.13	419.99	0.88	480.96	561.12	0.86	
<i>srfAA</i>	376525	387291	+	5448.95	6398.36	0.85	5098.43	5310.52	0.96	
<i>srfAB</i>	387304	398067	+	6856.85	8150.04	0.84	5966.75	6009.73	0.99	
<i>srfAC</i>	398104	401928	+	6739.91	7876.8	0.86	5979.66	6048.31	0.99	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>srfAD</i>	401957	402685	+	4807.49	6034.99	0.80	4409.34	4527.67	0.97	
<i>ycxA</i>	402786	404015	+	392.27	514.2	0.76	368.37	487.09	0.76	
<i>ycxB</i>	404030	404587	-	104.41	94.27	1.11	134.38	129.6	1.04	
<i>ycxC</i>	404641	405579	-	96.39	85.85	1.12	65.25	78.76	0.83	
<i>ycxD</i>	405703	407037	+	77.23	78.02	0.99	73.85	85.28	0.87	
<i>sfp</i>	407210	407707	-	182.76	182.69	1.00	237.98	232.65	1.02	
<i>yczE</i>	407812	408459	-	126.07	142	0.89	169.25	176.08	0.96	
<i>ycKI</i>	408777	409520	-	668.43	348.63	1.92	700.41	446.79	1.57	
<i>ycxJ</i>	409534	410238	-	499.26	254.94	1.96	535.94	342.97	1.56	
<i>ycxK</i>	410225	411031	-	858.86	492.58	1.74	928.21	604.38	1.54	
<i>yclA</i>	411146	412018	-	266.52	194.63	1.37	181.31	108.92	1.66	
<i>yclB</i>	412108	412722	+	86.88	94.72	0.92	66.36	77.88	0.85	
<i>yclC</i>	412725	414146	+	60.55	71.67	0.84	67.81	77.22	0.88	
<i>yclD</i>	414163	414852	+	68.63	78.36	0.88	74.96	87.13	0.86	
<i>yclE</i>	414918	415763	+	137.54	135.21	1.02	116.01	117.96	0.98	
<i>yclF</i>	415803	417281	-	63.64	68.55	0.93	61.65	72.96	0.84	
<i>yclG</i>	417561	419315	+	59.91	57.3	1.05	46.38	51.99	0.89	
<i>yczF</i>	419331	419552	-	29.04	31.95	0.91	38.79	36.66	1.06	
<i>gerKA</i>	419678	421312	+	100.59	96.24	1.05	77.71	95.85	0.81	
<i>gerKC</i>	421302	422525	+	98.34	88.26	1.11	94.39	91.86	1.03	
<i>gerKB</i>	422550	423671	+	85.21	80.51	1.06	89.85	86.91	1.03	
<i>yclH</i>	423776	424456	-	74.17	72.02	1.03	61.15	69.49	0.88	
<i>yclI</i>	424472	425932	-	95.34	87.33	1.09	69.18	89.71	0.77	
<i>yclJ</i>	426145	426828	+	325.33	301.18	1.08	281.27	258.63	1.09	
<i>yclK</i>	426815	428236	+	587.25	480.21	1.22	565.46	532.86	1.06	
<i>rapC</i>	428399	429547	+	1372.09	1351.5	1.02	1101.78	1398.3	0.79	
<i>yclM</i>	430191	431555	-	444.04	496.86	0.89	745	687.34	1.08	
<i>yclN</i>	431940	432890	+	535.37	432.99	1.24	529.31	628.93	0.84	
<i>yclO</i>	432883	433830	+	607.04	428.31	1.42	600.05	692.35	0.87	
<i>yclP</i>	433824	434582	+	1136.06	792.47	1.43	1110.36	1306.81	0.85	
<i>yclQ</i>	434604	435557	+	1253.13	874.85	1.43	1382.52	1665.19	0.83	
<i>ycnB</i>	435604	437022	-	294.12	230.35	1.28	390.57	341.68	1.14	
<i>ycnC</i>	437042	437920	-	466.37	411.27	1.13	494.28	485.3	1.02	
<i>ycnD</i>	438084	438833	-	483.54	733.89	0.66	551.59	820.74	0.67	
<i>ycnE</i>	438850	439137	-	456.49	793.33	0.58	865.42	1198.36	0.72	
<i>yczG</i>	439277	439591	+	152.11	174.7	0.87	221.91	222.56	1.00	
<i>gabR</i>	439593	441032	-	63.93	67.15	0.95	75.95	78.91	0.96	
<i>gabT</i>	441139	442449	+	108.96	112.94	0.96	94.26	100.05	0.94	
<i>gabD</i>	442518	443906	+	978.09	832.15	1.18	891.45	754.04	1.18	
<i>glcU</i>	444029	444892	+	53.91	60.46	0.89	41.64	58.63	0.71	
<i>gdh</i>	444912	445697	+	84.73	84.49	1.00	67.89	78.12	0.87	
<i>ycnI</i>	445742	446356	-	557.1	495.69	1.12	295.02	283.75	1.04	
<i>ycnJ</i>	446369	447994	-	730.13	588.59	1.24	347.59	344.2	1.01	
<i>ycnK</i>	448029	448601	-	770.61	574.99	1.34	406.03	372.82	1.09	
<i>ycnL</i>	448766	449119	+	202.32	169.44	1.19	190.17	206.88	0.92	
<i>mtlA</i>	449292	451124	+	123.49	199.71	0.62	133.31	201.72	0.66	
<i>mtlD</i>	451177	452277	+	154.89	248.16	0.62	143.19	230.36	0.62	
<i>ycsA</i>	452385	453449	+	218.32	262	0.83	215.26	277.43	0.78	
<i>sipU</i>	453584	454147	+	108.23	141.24	0.77	138.48	204.86	0.68	
<i>yczH</i>	454257	454814	-	400.65	348.25	1.15	336.98	312.07	1.08	
<i>ycsD</i>	454900	455292	+	248.91	241.9	1.03	168.19	213.15	0.79	
<i>ycsE</i>	455622	456371	+	477.36	427.96	1.12	630.81	644.08	0.98	
<i>ycsF</i>	456576	457349	+	451.95	627.81	0.72	446.64	476.37	0.94	
<i>ycsG</i>	457364	458578	+	287	478.93	0.60	460.36	495.8	0.93	
<i>ycsI</i>	458584	459375	+	182.79	258.9	0.71	278.85	312.5	0.89	
<i>kipl</i>	459419	460141	+	243.62	331.21	0.74	423.99	440.71	0.96	
<i>kipA</i>	460144	461157	+	216.15	257.43	0.84	360.06	378.02	0.95	
<i>kipR</i>	461173	461913	+	267.38	285.39	0.94	425.25	475.81	0.89	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ycaK</i>	461988	462629	+	115.78	121.25	0.95	227.77	258.47	0.88	
<i>yczI</i>	462802	463047	+	682.08	589.06	1.16	1342.89	1343.33	1.00	
<i>yczJ</i>	463053	463340	-	755.5	739.82	1.02	648.57	563.36	1.15	
<i>pbpC</i>	463491	465497	+	1670.65	1338.18	1.25	1946.74	1791.4	1.09	
<i>ycaN</i>	465599	466501	+	1405.95	1389.68	1.01	1511.78	1513.45	1.00	
<i>mtlR</i>	466687	468771	+	193.77	238.73	0.81	220.14	290.76	0.76	
<i>ydaB</i>	468982	470379	+	265.43	178.27	1.49	138.31	117.55	1.18	
<i>ydaC</i>	470514	471059	-	440.64	251.9	1.75	150.05	59.79	2.51	
<i>ydaD</i>	471267	472127	+	3277.05	1694.53	1.93	1632.68	471.76	3.46	
<i>ydaE</i>	472143	472646	+	2799.14	1365.67	2.05	976.92	297.7	3.28	
<i>ydaF</i>	472731	473282	+	708.68	733.84	0.97	645.39	668.11	0.97	
<i>ydaG</i>	473360	473782	+	7103.5	6456.31	1.10	4366.66	2814.57	1.55	
<i>ydaH</i>	474288	475097	+	125.51	97.41	1.29	212.31	186.88	1.14	
<i>ydzA</i>	475141	475431	-	489.01	392.91	1.24	222	202.91	1.09	
<i>lrpC</i>	475616	476050	+	234.63	236.38	0.99	190.94	202.24	0.94	
<i>topB</i>	476115	478298	+	829.93	629.5	1.32	897.46	881.3	1.02	
<i>ydaJ</i>	478501	479589	+	376.38	270.93	1.39	179.65	128.51	1.40	
<i>ydaK</i>	479570	480421	+	286.53	164.57	1.74	122.06	97.86	1.25	
<i>ydaL</i>	480432	482141	+	333.11	166.68	2.00	144.66	110.54	1.31	
<i>ydaM</i>	482134	483396	+	294.76	154.8	1.90	152.68	117.46	1.30	
<i>ydaN</i>	483402	485513	+	244.66	142.91	1.71	192.12	133.25	1.44	
<i>ydaO</i>	485989	487812	+	180.64	164.12	1.10	204.23	223.74	0.91	
<i>mutT</i>	487871	488320	+	104.26	76.54	1.36	83.32	75.19	1.11	
<i>ydaP</i>	488387	490111	+	3986.02	2842.53	1.40	2075.54	1020.41	2.03	
<i>ydaQ</i>	490288	490578	+	150.4	115.62	1.30	86.13	71.6	1.20	
<i>mntH</i>	490702	491979	-	1263.57	1219.34	1.04	1049.17	1129.17	0.93	
<i>ydaS</i>	492209	492466	-	3094.79	2607.99	1.19	1813.7	772.31	2.35	
<i>ydaT</i>	492544	492996	-	2520.96	1709.41	1.47	1114.87	474.56	2.35	
<i>ydbA</i>	493114	493932	+	223.98	215.69	1.04	228.42	258.36	0.88	
<i>gsiB</i>	494061	494432	+	8725.02	9205.19	0.95	7339.65	5942.07	1.24	
<i>ydbB</i>	494564	494905	+	437.65	377.39	1.16	477.51	439.47	1.09	
<i>ydbC</i>	494899	495258	+	352.02	276	1.28	392.34	353.93	1.11	
<i>ydbD</i>	495295	496116	-	2043.43	1963	1.04	1486.01	789.32	1.88	
<i>dctB</i>	496207	497259	-	143.14	173.24	0.83	190.13	250.4	0.76	
<i>dctS</i>	497329	498936	+	142.22	141.01	1.01	172	221.7	0.78	
<i>dctR</i>	498926	499606	+	142	151.26	0.94	189.29	262.69	0.72	
<i>dctP</i>	499727	500992	+	109.09	117.83	0.93	151.1	188.5	0.80	
<i>ydbI</i>	501140	502192	+	381.91	330.55	1.16	482.28	506.19	0.95	
<i>ydbJ</i>	502469	503395	+	626.27	460.8	1.36	754.37	707.03	1.07	
<i>ydbK</i>	503415	504155	+	537.28	356.82	1.51	553.73	508.78	1.09	
<i>ydbL</i>	504250	504585	+	1273.58	1363.31	0.93	703.65	549.3	1.28	
<i>ydbM</i>	504713	505858	+	942.79	887.53	1.06	681.46	614.65	1.11	
<i>ydbN</i>	505883	506062	-	924.88	2020.13	0.46	274.09	569.59	0.48	
<i>ydbO</i>	506427	507299	+	443.67	323.12	1.37	639.55	611.75	1.05	
<i>ydbP</i>	507314	507634	-	694.62	681.25	1.02	696.91	598.34	1.16	
<i>ddl</i>	507809	508873	+	891.34	764.9	1.17	1079.19	989.32	1.09	
<i>murF</i>	508945	510318	+	503.26	382.12	1.32	740.7	579.03	1.28	
<i>ydbR</i>	510667	512202	+	2612.63	2152.61	1.21	2761.98	3044.62	0.91	
<i>ydbS</i>	512375	512854	+	1093.17	979.47	1.12	1767.84	1850.57	0.96	
<i>ydbT</i>	512844	514325	+	659.58	614.17	1.07	1236.42	1352.5	0.91	
<i>ydcA</i>	514577	515176	-	161.53	154.27	1.05	137.35	176.06	0.78	
<i>acpS</i>	515271	515636	+	278.12	257.64	1.08	472.83	490.07	0.96	
<i>ydcC</i>	515697	516818	+	213.59	199.74	1.07	386.17	413.81	0.93	
<i>alr</i>	516933	518102	+	537.37	477.13	1.13	891.27	831.21	1.07	
<i>ydcD</i>	518218	518499	+	3520.97	3652.95	0.96	5337.68	5638.72	0.95	
<i>ydcE</i>	518504	518854	+	1397.55	1495.62	0.93	2841.17	3074.14	0.92	
<i>rsbR</i>	518969	519793	+	541.83	499.41	1.08	843.51	894.71	0.94	
<i>rsbS</i>	519798	520163	+	683.15	611.19	1.12	1162.94	1129.79	1.03	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>rsbT</i>	520167	520568	+	753.99	718.11	1.05	1497.24	1393.53	1.07	
<i>rsbU</i>	520580	521587	+	710.26	707.46	1.00	1420.13	1310.19	1.08	
<i>rsbV</i>	521649	521978	+	6079.64	6754.49	0.90	4161.5	3609.14	1.15	
<i>rsbW</i>	521975	522457	+	7109.82	7593.35	0.94	4396.19	3926.53	1.12	
<i>sigB</i>	522417	523211	+	6981.93	7503.4	0.93	3774.23	3383.07	1.12	
<i>rsbX</i>	523211	523810	+	7201.67	7515.75	0.96	4241.92	3909.23	1.09	
<i>ycdF</i>	524053	524346	+	148.53	155.1	0.96	96	125.75	0.76	
<i>ycdG</i>	524343	524783	+	261.09	266.03	0.98	211.21	236.21	0.89	
<i>ycdH</i>	524767	525210	+	119.29	120.59	0.99	87.03	93.29	0.93	
<i>ycdI</i>	525304	527463	+	363.27	267.58	1.36	599.84	507.57	1.18	
<i>ycdK</i>	527690	528142	+	243.79	207.44	1.18	241.48	274.13	0.88	
<i>ycdL</i>	529066	530172	-	212.5	184.56	1.15	363.31	421.42	0.86	
<i>ycdM</i>	530185	530694	-	256.44	216.15	1.19	361.2	422.65	0.85	
<i>ycdN</i>	530691	531074	-	174.42	173.24	1.01	238.63	270.16	0.88	
<i>sacV</i>	531348	531542	+	848.67	308.97	2.75	1078.98	654.65	1.65	
<i>ycdO</i>	531853	532113	+	430.9	143.54	3.00	701.77	311.03	2.26	
<i>ycdP</i>	532483	532863	+	928.69	327.73	2.83	1192.42	616.52	1.93	
<i>ycdQ</i>	532899	534341	+	326.8	135.53	2.41	430.26	241.21	1.78	
<i>ycdR</i>	534334	535392	+	339.89	137.57	2.47	526.15	274.3	1.92	
<i>ycdS</i>	535657	535926	+	326.1	157.11	2.08	571.46	326.61	1.75	
<i>ycdT</i>	535965	536231	+	674.8	259.08	2.60	929.48	455.13	2.04	
<i>yddA</i>	536248	536556	+	319.74	139.43	2.29	573.58	317.45	1.81	
<i>yddB</i>	536546	537610	+	351.5	150.19	2.34	604.17	318.79	1.90	
<i>yddC</i>	537622	537870	+	373.56	218.27	1.71	745.53	335.83	2.22	
<i>yddD</i>	537883	538407	+	275.12	108.85	2.53	351.46	199.54	1.76	
<i>yddE</i>	538295	540790	+	175.81	87	2.02	258.57	153.28	1.69	
<i>yddF</i>	540809	541135	+	119.22	57.11	2.09	270.96	142.02	1.91	
<i>yddG</i>	541139	543586	+	196.11	105.21	1.86	310.18	176.56	1.76	
<i>yddH</i>	543583	544572	+	173.24	105.72	1.64	241.56	154.91	1.56	
<i>yddI</i>	544587	545093	+	136.02	74.36	1.83	207.85	113.58	1.83	
<i>yddJ</i>	545156	545536	+	618.39	487.34	1.27	671.57	464.12	1.45	AbrB regulon
<i>yddK</i>	545727	546527	-	207.78	201.77	1.03	270.93	324.16	0.84	
<i>rapI</i>	546867	548042	+	297.18	199.4	1.49	293.79	225.55	1.30	
<i>yddM</i>	548271	549212	+	260.27	184.21	1.41	334.99	276.13	1.21	
<i>yddN</i>	549783	550802	-	56.21	49.77	1.13	62.04	59.54	1.04	
<i>IrpA</i>	551062	551472	+	95.51	89.61	1.07	148.1	179.84	0.82	
<i>IrpB</i>	551595	552044	-	28.98	33.36	0.87	36.67	36.58	1.00	
<i>yddQ</i>	552159	552701	+	77.67	74.62	1.04	113.11	105.47	1.07	
<i>yddR</i>	553254	554018	+	84.14	81.69	1.03	81.94	76.04	1.08	
<i>yddS</i>	554212	555522	+	121.55	120.21	1.01	119.24	111.83	1.07	
<i>yddT</i>	556306	556992	+	960.37	933.41	1.03	1452.92	1181.5	1.23	AbrB regulon
<i>ydeA</i>	557952	558545	+	97.74	92.56	1.06	116.29	104.89	1.11	
<i>cspC</i>	558808	559008	+	997.39	1149.23	0.87	1749.65	2266.61	0.77	
<i>ydeB</i>	559695	560156	-	1296.9	1157.29	1.12	781.48	1036.81	0.75	
<i>yzdE</i>	560724	560960	-	60.16	56.75	1.06	70.05	78.76	0.89	
<i>ydeC</i>	561058	561933	-	73.32	78.4	0.94	80.03	93.65	0.85	
<i>ydeD</i>	562046	563005	+	43.95	57.04	0.77	48.44	53.74	0.90	
<i>ydeE</i>	563158	564030	-	76.2	73.48	1.04	98.39	103.7	0.95	
<i>ydeF</i>	564248	565645	+	75.66	87.16	0.87	91.17	102.52	0.89	
<i>ydeG</i>	565755	567047	+	54.14	63.06	0.86	59.11	66.09	0.89	
<i>ydeH</i>	567206	567652	+	81.55	69.54	1.17	174.8	185.47	0.94	AbrB regulon
<i>ydeI</i>	567889	568482	+	87.96	103.16	0.85	90.2	104.61	0.86	
<i>ydeJ</i>	568834	569493	-	378.66	396.21	0.96	372.51	444.14	0.84	AbrB regulon
<i>ydeK</i>	569915	570778	-	93.49	108.55	0.86	76.41	83.48	0.92	
<i>ydeL</i>	570933	572324	+	73.27	68.15	1.08	85.95	91.8	0.94	
<i>ydeM</i>	572518	572943	+	362.45	268.38	1.35	408.79	451.81	0.90	
<i>ydeN</i>	572996	573568	-	201.24	198.42	1.01	232.11	214.74	1.08	
<i>yzdF</i>	573650	573979	-	229.68	225.09	1.02	213.6	191.94	1.11	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ydeO</i>	574234	575106	+	632.4	422.36	1.50	827.63	778.54	1.06	
<i>ydeP</i>	575256	575642	-	114.67	94.34	1.22	129.22	160.41	0.81	
<i>ydeQ</i>	575753	576346	+	202.71	183.07	1.11	138.58	113.58	1.22	
<i>ydeR</i>	576490	577677	-	41.3	44.7	0.92	40.27	44.09	0.91	
<i>ydeS</i>	577881	578477	+	254	221.6	1.15	256.8	314.32	0.82	
<i>ydeT</i>	579085	579420	+	108.57	131	0.83	151.78	175.25	0.87	
<i>ydfA</i>	579433	580740	+	135.04	143.04	0.94	202.41	228.9	0.88	
<i>ydfB</i>	581238	582023	+	60.28	56.59	1.07	67.4	60.06	1.12	
<i>ydfC</i>	582080	583000	-	30.71	33.36	0.92	28.99	31.88	0.91	
<i>ydfD</i>	583133	584581	+	54.16	61.4	0.88	67.7	70.42	0.96	
<i>ydfE</i>	584699	585322	-	68.51	73.46	0.93	78.45	105.66	0.74	
<i>ydfF</i>	585412	586092	+	210.27	197.54	1.06	223.91	235.73	0.95	
<i>ydfG</i>	586172	586615	-	375.06	430.15	0.87	613.17	590.06	1.04	
<i>ydfH</i>	587288	588511	+	142.47	124.88	1.14	173.04	170.63	1.01	
<i>ydfI</i>	588504	589145	+	135.22	116	1.17	195.14	203.46	0.96	
<i>ydfJ</i>	589261	591435	+	51.91	56.37	0.92	53.54	57.72	0.93	
<i>nap</i>	591847	592749	-	561.75	397.29	1.41	405.44	420.02	0.97	
<i>ydfK</i>	592951	593640	-	35.08	39.36	0.89	41.14	40.29	1.02	
<i>ydfL</i>	593730	594542	-	125.51	126.98	0.99	144.88	139.32	1.04	
<i>ydfM</i>	594653	595546	-	38.08	41.12	0.93	45.78	46.27	0.99	
<i>ydfN</i>	596022	596642	+	120.85	126.79	0.95	120.16	183.45	0.66	
<i>ydfO</i>	596658	597596	+	250.34	180.4	1.39	135.14	209.41	0.65	
<i>ydfP</i>	597698	598087	+	177.81	156.84	1.13	135.99	197.15	0.69	
<i>ydfQ</i>	598273	598611	+	44.25	44.06	1.00	43.96	39.62	1.11	
<i>ydzH</i>	598651	598887	-	24.56	30.63	0.80	22.57	21.25	1.06	
<i>ydfR</i>	599773	600450	-	36.55	43.87	0.83	32.94	42.17	0.78	
<i>ydfS</i>	600563	601270	+	46.18	50.17	0.92	49.64	52.86	0.94	
<i>cotP</i>	601285	601716	-	27.07	31.95	0.85	27.11	27.9	0.97	
<i>ydgA</i>	601729	601971	-	19.88	25.24	0.79	22.72	26.36	0.86	
<i>ydgB</i>	601985	602257	-	21.05	29.65	0.71	23.15	26.24	0.88	
<i>ydgC</i>	602556	603143	+	610.15	470.32	1.30	1189.69	1252.24	0.95	
<i>ydgD</i>	603140	603484	+	337.66	278.19	1.21	832.39	728.94	1.14	
<i>ydgE</i>	603647	604120	+	240.37	227.26	1.06	552.56	526.69	1.05	
<i>expZ</i>	604280	605923	-	345.56	445.22	0.78	244.23	253.83	0.96	
<i>ydgF</i>	606243	607619	-	317.32	307.34	1.03	344.97	348.1	0.99	
<i>dinB</i>	607791	608309	-	1467.33	991.84	1.48	1399.97	965.9	1.45	
<i>ydgG</i>	608478	608936	+	51.57	51.38	1.00	98.97	107.74	0.92	
<i>ydgH</i>	608933	611590	+	160.7	139.33	1.15	236.37	208.78	1.13	
<i>ydgl</i>	611736	612365	-	117.12	116.19	1.01	189.91	212.58	0.89	
<i>ydgJ</i>	612381	612875	-	155.07	170.44	0.91	221.23	254.64	0.87	
<i>ydgK</i>	613186	614394	+	109.15	102.76	1.06	149.43	161.85	0.92	
<i>ydhB</i>	614389	615168	-	259.85	197.16	1.32	130.99	119.09	1.10	
<i>ydhC</i>	615417	616091	+	333.5	354.08	0.94	297.57	365.28	0.81	
<i>ydhD</i>	616218	617537	+	99.31	86.91	1.14	78.9	83.72	0.94	
<i>ydhE</i>	617683	618828	+	281.29	251.47	1.12	168.81	179.3	0.94	
<i>ydhF</i>	618867	619577	-	45.77	45.36	1.01	42.92	40.09	1.07	
<i>phoB</i>	619643	621031	-	92.32	90.96	1.01	81.83	86.89	0.94	
<i>ydhG</i>	621393	621764	+	279.29	268.21	1.04	416.21	383.6	1.09	
<i>ydhH</i>	621840	622337	-	165.8	159.12	1.04	151.53	163.62	0.93	
<i>ydhl</i>	622355	622837	-	143.22	139.87	1.02	109.59	116.22	0.94	
<i>ydhJ</i>	622920	623897	+	209.12	159.98	1.31	222.85	186.12	1.20	
<i>ydhK</i>	624039	624656	+	3966	3356.55	1.18	2076.2	1847.91	1.12	
<i>ydhL</i>	624672	625838	-	66.65	71.76	0.93	46.17	53.99	0.86	
<i>ydhM</i>	626169	626480	+	83.81	86.74	0.97	87.17	96.23	0.91	AbrB regulon
<i>ydhN</i>	626480	626812	+	51	53.68	0.95	42.39	48.96	0.87	AbrB regulon
<i>ydhO</i>	626831	628159	+	73.02	76.95	0.95	65.16	75.05	0.87	AbrB regulon
<i>ydhP</i>	628177	629574	+	83.97	88.34	0.95	72.85	84.32	0.86	AbrB regulon
<i>ydhQ</i>	629717	630430	+	188.17	141.9	1.33	139.19	146.59	0.95	AbrB regulon

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ydhR</i>	630459	631358	+	186.43	156.42	1.19	146.54	158.98	0.92	AbrB regulon
<i>ydhS</i>	631355	632302	+	161.29	118.22	1.36	121.4	129	0.94	AbrB regulon
<i>ydhT</i>	632321	633409	+	150.07	113.29	1.32	116.08	118	0.98	AbrB regulon
<i>ydhU</i>	633470	633925	-	25.95	31.12	0.83	32.07	33.12	0.97	
<i>thiL</i>	640209	641186	+	268.95	243.24	1.11	349.71	362.81	0.96	
<i>ydiB</i>	641201	641677	+	192.45	173.45	1.11	356.06	367.1	0.97	
<i>ydiC</i>	641658	642347	+	360.13	282.85	1.27	520.86	498	1.05	
<i>ydiD</i>	642357	642812	+	432.25	336.85	1.28	738.03	667.02	1.11	
<i>gcp</i>	642805	643845	+	463.98	360.51	1.29	684.04	584.54	1.17	
<i>ydiF</i>	644075	646003	-	567.04	455.93	1.24	593.95	441.67	1.34	
<i>ydiG</i>	646129	646641	+	565.19	464.22	1.22	617.34	666.95	0.93	
<i>ydiH</i>	646638	647285	+	727.38	637.46	1.14	701.65	745.49	0.94	
<i>tatAY</i>	647307	647480	+	602.29	526.04	1.14	661.97	963.29	0.69	
<i>tatCY</i>	647487	648251	+	683.07	695.09	0.98	507.68	581.04	0.87	
<i>ydiK</i>	648289	648480	-	84.59	112.47	0.75	220.03	293.3	0.75	
<i>ydiL</i>	648477	649211	-	391.65	347.24	1.13	365.75	408.43	0.90	
<i>groES</i>	649450	649734	+	4070.79	4356.59	0.93	4947.72	4652.26	1.06	
<i>groEL</i>	649781	651415	+	2937.49	3164.83	0.93	3505.55	3521.83	1.00	
<i>ydiM</i>	652979	653359	+	197.37	153.3	1.29	251.73	195.88	1.29	
<i>ydiN</i>	654526	654741	+	275.48	207.73	1.33	340.54	269.02	1.27	
<i>ydiO</i>	654771	656054	+	711.63	498.36	1.43	659.88	547.74	1.20	
<i>ydiP</i>	656076	657245	+	1073.87	692.08	1.55	1075.29	891.1	1.21	
<i>ydiQ</i>	657731	657919	+	37.42	30.2	1.24	28.68	32.11	0.89	
<i>ydiR</i>	659171	660112	+	718.3	611.78	1.17	944.05	950.39	0.99	
<i>ydiS</i>	660144	661175	+	872.93	654.14	1.33	1129.86	1091.93	1.03	
<i>ydjA</i>	661178	662575	+	610.12	468.62	1.30	852.91	854.66	1.00	
<i>ydjB</i>	663149	663484	+	76.93	70.24	1.10	162.12	169.41	0.96	
<i>ydjC</i>	663867	664217	+	46.61	44.14	1.06	68.44	70.24	0.97	
<i>gutR</i>	664323	666812	-	228.36	236.67	0.96	263.98	265.73	0.99	
<i>gutB</i>	667014	668075	+	163.66	166.87	0.98	140.94	159.39	0.88	
<i>gutP</i>	668149	669540	+	63.53	64.59	0.98	73.83	72.25	1.02	
<i>ydjE</i>	669635	670597	+	1006.78	933.63	1.08	1237.05	1120.7	1.10	
<i>pspA</i>	670793	671476	+	1624.68	1423.28	1.14	2697.58	2563.08	1.05	AbrB regulon
<i>ydjG</i>	671542	672567	+	1107.67	903.37	1.23	2258.07	2332.47	0.97	AbrB regulon
<i>ydjH</i>	672567	673331	+	1025.01	808.45	1.27	2223.72	2258.6	0.98	AbrB regulon
<i>ydjI</i>	673362	674333	+	1041.45	850.92	1.22	1929.4	1939.21	0.99	AbrB regulon
<i>ydjJ</i>	674380	675405	-	965.92	622.32	1.55	237.86	93.34	2.55	
<i>ydjK</i>	675990	677411	+	59.51	58.51	1.02	51.91	58.25	0.89	
<i>ydjL</i>	677459	678499	-	4727.35	4573.9	1.03	4125.98	3608.24	1.14	AbrB regulon
<i>ydjM</i>	678938	679309	+	184.89	116.47	1.59	457.18	481.92	0.95	
<i>ydjN</i>	679375	680421	+	304.56	186.8	1.63	759.5	694.76	1.09	
<i>ydjO</i>	680803	681012	-	4405.89	3972.43	1.11	4369.77	4068.58	1.07	
<i>ydjP</i>	681095	681910	-	532.3	426.81	1.25	911.8	831.66	1.10	
<i>yeaA</i>	681923	682912	-	372.62	337.59	1.10	660.86	611.48	1.08	
<i>cotA</i>	683010	684551	-	144.46	144.89	1.00	122.75	133.73	0.92	
<i>gabP</i>	684703	686112	-	1111.15	1126.45	0.99	1009.68	1107.79	0.91	
<i>yeaB</i>	686510	687382	+	105.33	111.46	0.95	109.16	127.89	0.85	
<i>yeaC</i>	687535	688497	+	283.53	240.86	1.18	280.23	294.41	0.95	
<i>yeaD</i>	688881	689693	+	356.68	240.72	1.48	507.62	457.35	1.11	
<i>yebA</i>	689890	691857	+	350.53	246.65	1.42	555.03	495.61	1.12	
<i>guaA</i>	692090	693631	+	1204.89	1088.77	1.11	1590.28	1710.1	0.93	
<i>pbuG</i>	694011	695333	+	118.9	140.01	0.85	313.12	505.14	0.62	
<i>yebC</i>	695535	696338	+	278.77	259.63	1.07	362.9	320.95	1.13	
<i>yebD</i>	696497	696790	+	93.01	99.26	0.94	66.38	50.32	1.32	
<i>yebE</i>	696880	697434	+	920.95	875.24	1.05	461.92	213.98	2.16	
<i>yebG</i>	697434	697631	+	772.45	724.29	1.07	392.81	318.7	1.23	
<i>purE</i>	697954	698442	+	492.01	519.65	0.95	918.34	1289.42	0.71	
<i>purK</i>	698435	699574	+	561.95	554.46	1.01	1375.76	1765.01	0.78	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>purB</i>	699571	700866	+	1040.16	1006.05	1.03	2300.52	2698.08	0.85	
<i>purC</i>	700939	701664	+	1441.53	1492.57	0.97	2944.88	3243.86	0.91	
<i>purS</i>	701657	701911	+	1179.51	1218.82	0.97	2506.97	2960.48	0.85	
<i>purQ</i>	701908	702591	+	1028.21	1063.07	0.97	2110.1	2641.38	0.80	
<i>purL</i>	702575	704803	+	1656.82	1835.58	0.90	2776.98	3173.77	0.87	
<i>purF</i>	704779	706209	+	2247.1	2596.25	0.87	3060.96	3427.42	0.89	
<i>purM</i>	706311	707351	+	2018.98	2234.79	0.90	2679.92	2967.4	0.90	
<i>purN</i>	707348	707935	+	2063.84	2239.69	0.92	2411.09	2705.39	0.89	
<i>purH</i>	707932	709470	+	2746.18	3005.09	0.91	3023.3	3342.43	0.90	
<i>purD</i>	709486	710754	+	2090.68	2291.57	0.91	2359.12	2545.7	0.93	
<i>yezC</i>	710957	711214	-	179.58	189.06	0.95	173.33	201.92	0.86	
<i>yecA</i>	711358	712749	+	84.97	95.61	0.89	77.49	84.76	0.91	
<i>yerA</i>	713003	714745	+	658.36	644.81	1.02	455.52	418.57	1.09	
<i>yerB</i>	714772	715767	+	1315.36	1417.27	0.93	1752.16	1940.77	0.90	Spo0A regulon
<i>yerC</i>	715770	716084	+	76.72	100.92	0.76	179.6	176.65	1.02	
<i>yerD</i>	716119	717696	-	2278.41	1324.71	1.72	733.89	288.06	2.55	
<i>pcrB</i>	717961	718647	+	377.63	327.79	1.15	533.32	621.41	0.86	
<i>pcrA</i>	718709	720928	+	576.37	391.92	1.47	999.9	905.83	1.10	
<i>ligA</i>	720952	722958	+	674.09	519.53	1.30	1211.65	996.86	1.22	
<i>yerH</i>	722974	724164	+	675.43	571.19	1.18	1316.77	1116.73	1.18	
<i>yerI</i>	724326	725336	+	1960.88	1744.94	1.12	2164.53	2138.2	1.01	AbrB regulon
<i>sapB</i>	725374	726072	-	264.84	220.08	1.20	228.23	226.39	1.01	
<i>opuE</i>	726179	727657	-	1551.28	1102.19	1.41	1092.5	1024.37	1.07	
<i>gatC</i>	728071	728361	+	1885.72	1957.55	0.96	2852.84	3148.18	0.91	
<i>gatA</i>	728377	729834	+	1599.92	1580.19	1.01	2432.66	2517.59	0.97	
<i>gatB</i>	729848	731278	+	1470.52	1592.51	0.92	2252.85	2336.43	0.96	
<i>yerO</i>	731293	732162	-	89.25	99.66	0.90	95.1	121.66	0.78	
<i>yerP</i>	732255	735452	+	936.05	828.64	1.13	2079.53	2224.87	0.93	
<i>yerQ</i>	735775	736686	+	481.66	450	1.07	580.26	648.15	0.90	
<i>yefA</i>	736942	738321	+	316.09	263.71	1.20	467.31	468.67	1.00	
<i>yefB</i>	738334	739236	-	33.83	38.49	0.88	37.83	37.42	1.01	
<i>yefC</i>	739175	739552	+	59.48	50.7	1.17	108.34	100.23	1.08	
<i>yeeA</i>	739627	742266	+	119.28	93.02	1.28	195.55	173.04	1.13	
<i>yeeB</i>	742278	744074	+	403.76	290.89	1.39	608.94	476.8	1.28	
<i>yeeC</i>	744187	745335	+	399.26	332.47	1.20	561.21	481.49	1.17	
<i>yeeD</i>	745597	745902	-	63.93	58.73	1.09	53.97	53.2	1.01	
<i>yezA</i>	745969	746175	-	83.94	73.96	1.13	60.49	74.6	0.81	
<i>yeeF</i>	746415	748898	-	473.7	436.28	1.09	551.73	521.25	1.06	
<i>yeeG</i>	749034	750131	+	52.5	61.18	0.86	52.3	61.28	0.85	
<i>rapH</i>	750293	751588	+	2072.24	1753.48	1.18	2141.09	1839.36	1.16	AbrB regulon
<i>yeeI</i>	751749	752468	+	1687.54	1530.16	1.10	2175.64	2243.11	0.97	
<i>yeeK</i>	752602	753039	+	96.38	98.37	0.98	108.03	111.4	0.97	
<i>yezE</i>	753154	753738	+	594.41	670.93	0.89	883.26	985.89	0.90	
<i>yesE</i>	753817	754260	+	95.94	114.08	0.84	130.18	162.52	0.80	
<i>yesF</i>	754257	755117	+	125.14	126.06	0.99	133.41	141.74	0.94	
<i>cotJA</i>	755244	755492	+	41.06	57.33	0.72	47.01	64.86	0.72	
<i>cotJB</i>	755437	755739	+	34.57	43.03	0.80	35.1	38.02	0.92	
<i>cotJC</i>	755754	756323	+	215.64	210.17	1.03	119.81	151	0.79	
<i>yesJ</i>	756448	756990	+	346.85	327.57	1.06	407.11	402.81	1.01	
<i>yesK</i>	756926	757315	+	98.24	94.38	1.04	65.59	86.03	0.76	
<i>yesL</i>	757430	758059	+	89.61	95.43	0.94	91.87	104.57	0.88	
<i>yesM</i>	758056	759789	+	77.56	83.1	0.93	72.32	86.54	0.84	
<i>yesN</i>	759789	760895	+	94.98	91.69	1.04	78.66	88.02	0.89	
<i>yesO</i>	761044	762282	+	96.77	103.92	0.93	76.59	89.11	0.86	
<i>yesP</i>	762279	763208	+	84.12	90.19	0.93	71.91	87.83	0.82	
<i>yesQ</i>	763212	764102	+	78.13	79.61	0.98	61.89	70.19	0.88	
<i>yesR</i>	764118	765152	+	146.31	147.8	0.99	127.83	172.4	0.74	
<i>yesS</i>	765175	767460	+	127.08	127.01	1.00	103.42	111.58	0.93	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yesT</i>	767474	768172	+	105.28	111.31	0.95	89	107.01	0.83	
<i>yesU</i>	768165	768827	+	97.35	85.54	1.14	62.59	73.87	0.85	
<i>yesV</i>	768824	769450	+	89.4	80.29	1.11	64.6	67.41	0.96	
<i>yesW</i>	769571	771433	+	118.33	122.62	0.97	83.99	106.77	0.79	
<i>yesX</i>	771479	773317	+	131.37	127	1.03	95.72	122.61	0.78	
<i>yesY</i>	773475	774128	+	88.39	89.34	0.99	64.44	76.1	0.85	
<i>yesZ</i>	774136	776127	+	116.55	114.88	1.01	86.05	99.88	0.86	
<i>yetA</i>	776171	778744	+	173.29	170.17	1.02	130.33	156.41	0.83	
<i>lplA</i>	778866	780374	+	125.66	111.15	1.13	88.29	103.88	0.85	
<i>lplB</i>	780429	781385	+	42.85	46.77	0.92	41.86	42.75	0.98	
<i>lplC</i>	781399	782286	+	84.9	83.37	1.02	83.43	84.52	0.99	
<i>lplD</i>	782295	783635	+	80.11	81.69	0.98	76.44	80.78	0.95	
<i>yetF</i>	783718	784413	+	81.89	86.93	0.94	69.9	85.73	0.82	
<i>yetG</i>	784450	784827	-	1945.88	2408.38	0.81	1132.45	1570.29	0.72	
<i>yetH</i>	784880	785242	-	601.62	591.18	1.02	433.88	431.32	1.01	
<i>yetI</i>	785522	786607	+	172.01	210.68	0.82	155.48	181.58	0.86	
<i>yezB</i>	786613	786897	+	155.62	190.55	0.82	150.45	180.58	0.83	
<i>yezD</i>	787052	787219	+	34.7	24.07	1.44	58.3	149.05	0.39	
<i>yetJ</i>	787329	787973	+	782.76	609.39	1.28	1156.03	1143.3	1.01	
<i>yetK</i>	787973	788965	+	539.38	492.17	1.10	844.47	923.6	0.91	
<i>yetL</i>	788989	789492	-	71.34	84.25	0.85	66.9	79.22	0.84	
<i>yetM</i>	789655	790764	+	107.68	107.42	1.00	82.31	99.79	0.82	
<i>yetN</i>	790799	791869	-	146.89	136.27	1.08	182.7	183.04	1.00	
<i>yetO</i>	792019	795204	+	478.26	245.72	1.95	150.6	116.21	1.30	
<i>yfnI</i>	795651	797570	+	801.5	705.85	1.14	1347.23	1417.83	0.95	
<i>yfnH</i>	797806	798570	+	76.34	75.76	1.01	62.9	66.64	0.94	
<i>yfnG</i>	798640	799545	+	84.72	92.72	0.91	72.36	85.81	0.84	
<i>yfnF</i>	799569	800480	+	59.25	57.03	1.04	53.17	53.51	0.99	
<i>yfnE</i>	800509	801687	+	67.38	65.07	1.04	64.38	67.87	0.95	
<i>yfnD</i>	801688	802623	+	89.71	88.06	1.02	86.73	99.83	0.87	
<i>yfnC</i>	802654	803883	-	467.28	411.25	1.14	384.31	363.75	1.06	
<i>yfnB</i>	803994	804701	-	276.46	269.28	1.03	208.44	241.6	0.86	
<i>yfnA</i>	804793	806178	-	118.42	125.18	0.95	317.45	344.89	0.92	
<i>yfmT</i>	806428	807885	+	3183.89	3300.63	0.96	2003.38	2084.92	0.96	SigD regulon
<i>yfmS</i>	807899	808759	+	3030.33	2993.48	1.01	1556.14	1738.78	0.89	
<i>yfmR</i>	808894	810783	+	619.9	552.73	1.12	655.48	611.6	1.07	
<i>yfmQ</i>	810906	811352	+	2160.41	1415.22	1.53	831.01	678.62	1.22	
<i>yfmP</i>	811477	811899	+	208.95	173.47	1.20	198.64	261.31	0.76	
<i>yfmO</i>	811965	813155	+	81.63	81.75	1.00	73.07	79.22	0.92	
<i>yfmM</i>	813721	815277	-	329.29	324	1.02	447.33	481.63	0.93	
<i>yfmL</i>	815450	816580	+	403.6	396.6	1.02	517.76	446.26	1.16	
<i>yfmK</i>	816648	817094	+	242.78	227.52	1.07	290.45	316.73	0.92	
<i>yfmJ</i>	817147	818166	-	288.99	360.49	0.80	406.15	480.45	0.85	
<i>yfmI</i>	818648	819868	-	114.17	138.56	0.82	154.87	191.56	0.81	Spo0A and AbrB regulon
<i>yfmG</i>	820204	821667	+	885.92	846.74	1.05	1565.38	1624.12	0.96	AbrB regulon
<i>yfmF</i>	822240	823040	-	700.18	613.98	1.14	737.98	724.78	1.02	
<i>yfmE</i>	823053	824054	-	383.06	314.79	1.22	428.5	428.55	1.00	
<i>yfmD</i>	824051	825052	-	294.21	257.75	1.14	331.53	333.54	0.99	
<i>yfmC</i>	825124	826071	-	1348.28	1518.18	0.89	1224.71	1316.43	0.93	
<i>yfmB</i>	826180	826548	-	496.19	607.73	0.82	325.18	298.17	1.09	
<i>yfmA</i>	826589	826756	+	40.93	41.14	0.99	47.95	60.86	0.79	
<i>yfIT</i>	826792	827139	+	5253.2	6105.84	0.86	3757.64	2477.4	1.52	
<i>pel</i>	827330	828592	+	2528.92	2963.21	0.85	2812.16	3084.08	0.91	
<i>yfIS</i>	828719	830155	+	369.23	332.51	1.11	186.46	158.71	1.17	
<i>citS</i>	830282	831910	+	389.33	335.33	1.16	444.24	481.11	0.92	
<i>citT</i>	831882	832562	+	362.23	291.19	1.24	408.12	479.49	0.85	
<i>yfIP</i>	832745	833524	+	286.16	239.18	1.20	325.29	381.96	0.85	
<i>citM</i>	833720	835021	+	380.59	406.17	0.94	537.72	490.55	1.10	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yfiN</i>	835077	835871	+	204.25	236.97	0.86	214.06	284.32	0.75	
<i>yfiM</i>	836071	837081	+	372.89	325.96	1.14	522.33	487.86	1.07	
<i>yfiL</i>	837072	837347	-	165	154.38	1.07	147.27	172.65	0.85	
<i>yfiK</i>	837414	838079	+	410.62	314.31	1.31	476.6	403.18	1.18	
<i>yfiI</i>	838414	838569	-	856.46	582.93	1.47	474.85	470.62	1.01	
<i>yfiH</i>	838676	838990	-	1041.32	906.96	1.15	789.75	599.73	1.32	
<i>yfiG</i>	839072	839821	-	1006.51	843.98	1.19	1099.1	1045.27	1.05	
<i>nagP</i>	839993	841351	+	808.16	763.13	1.06	567.14	566.02	1.00	
<i>yfiE</i>	841384	843333	-	576.35	760.33	0.76	866.39	1032.66	0.84	
<i>yfiB</i>	843721	843981	+	158.17	112.04	1.41	125.29	118.97	1.05	AbrB regulon
<i>yfiA</i>	844106	845521	+	3815.91	3339.01	1.14	1527.85	852.82	1.79	AbrB regulon
<i>yfkT</i>	845518	846594	-	24.89	30.55	0.81	30.37	30.88	0.98	
<i>yfkS</i>	846618	846818	-	19.1	27.35	0.70	23.74	23	1.03	
<i>yfkR</i>	846834	847988	-	56.51	65.92	0.86	49	54.25	0.90	
<i>yfkQ</i>	847969	849510	-	48.18	51.96	0.93	40.89	48.94	0.84	
<i>treP</i>	849703	851115	+	86.83	78.15	1.11	73.39	77.71	0.94	
<i>treA</i>	851186	852871	+	96.5	91.26	1.06	74.79	78.18	0.96	
<i>treR</i>	852892	853608	+	252.15	263.46	0.96	340.03	440.77	0.77	
<i>yfkO</i>	853748	854413	+	228.81	250.77	0.91	275.21	318.16	0.87	
<i>yfkN</i>	854450	858838	-	339.38	291.95	1.16	438.85	395.62	1.11	
<i>yfkM</i>	859081	859599	+	3924.98	3219.14	1.22	1995.34	1031.3	1.93	
<i>yfkL</i>	859639	860829	-	183.27	154.19	1.19	212.96	233.92	0.91	
<i>yfkK</i>	860922	861137	-	376.06	342.38	1.10	475.63	479.89	0.99	
<i>yfkJ</i>	861340	861810	+	3594.22	2255.54	1.59	2167.28	966.45	2.24	
<i>yfkI</i>	861828	862148	+	5016.68	3511.16	1.43	2663.85	1404.1	1.90	
<i>yfkH</i>	862172	862999	+	3854.59	2589.63	1.49	1717.87	825.84	2.08	
<i>yfkF</i>	863198	864373	-	99.96	110.85	0.90	116.2	153.95	0.75	
<i>yfkE</i>	864541	865596	+	1346.93	916.88	1.47	537.5	304.91	1.76	
<i>yfkD</i>	865667	866461	+	1149.33	755.86	1.52	514.06	301.02	1.71	
<i>yfkC</i>	866500	867342	-	126.96	111.28	1.14	201.6	187.96	1.07	
<i>yfkB</i>	867343	867804	-	191.17	178.86	1.07	347.91	353.93	0.98	
<i>yfkA</i>	867999	868463	-	168.45	161.44	1.04	240.61	255.97	0.94	
<i>yfiT</i>	868608	868793	+	121.24	144.42	0.84	266.57	375.25	0.71	
<i>yfiS</i>	868894	869685	+	67.62	77.33	0.87	80.96	103.61	0.78	
<i>yfiR</i>	869723	870508	-	302.27	307.49	0.98	426.76	441.81	0.97	
<i>yfiQ</i>	870682	871641	-	221.53	183.7	1.21	352.01	357.65	0.98	
<i>yfiP</i>	871760	872623	+	225.56	258.16	0.87	196.48	252.2	0.78	
<i>yfiO</i>	872737	874137	+	345.42	369.2	0.94	428.7	557.97	0.77	
<i>yfiN</i>	875761	876738	+	171.25	157.08	1.09	341.98	325.18	1.05	
<i>yfiM</i>	876934	877386	+	179.89	187.5	0.96	238.63	245.11	0.97	
<i>yfiL</i>	877416	878105	+	235.34	228.12	1.03	371.74	380.67	0.98	
<i>acoA</i>	878337	879338	+	51.22	57.35	0.89	47.56	55.32	0.86	
<i>acoB</i>	879342	880370	+	76.44	79.33	0.96	62.87	75.72	0.83	
<i>acoC</i>	880384	881580	+	103.61	104.92	0.99	105.44	115.36	0.91	
<i>acoL</i>	881601	882977	+	128.44	135.44	0.95	109.85	129.16	0.85	
<i>acoR</i>	883093	884910	+	94.06	93.85	1.00	88.71	111.26	0.80	
<i>sspH</i>	884964	885143	+	66.66	88.4	0.75	128.82	150	0.86	
<i>yfiF</i>	885179	885508	-	211.48	158.79	1.33	139.87	167.1	0.84	
<i>yfiE</i>	885558	886016	-	296.74	196.59	1.51	166.48	181.11	0.92	
<i>yfiD</i>	886110	886667	-	248.45	181.71	1.37	187.02	186.4	1.00	
<i>yfiC</i>	886699	887466	-	128.23	118.43	1.08	103.85	125.8	0.83	
<i>yfiB</i>	887478	888701	-	145.17	173.7	0.84	106.79	124.55	0.86	
<i>yfiA</i>	888707	889021	-	96.99	133.57	0.73	65.91	77.64	0.85	
<i>malA</i>	889357	890706	+	158.5	171.41	0.92	136.83	162.24	0.84	
<i>yfiA</i>	890771	891535	+	164.77	152.98	1.08	151.18	141.06	1.07	
<i>malP</i>	891550	893133	+	154.49	157.19	0.98	109.02	129.05	0.84	
<i>yfiB</i>	893239	894960	+	172.28	155.27	1.11	202.16	213.05	0.95	
<i>yfiC</i>	894954	896768	+	250.51	229.04	1.09	356.73	349.72	1.02	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yfiD</i>	896923	897327	+	60.33	67.61	0.89	56.12	81.29	0.69	
<i>yfiE</i>	897345	898202	+	67.61	76.63	0.88	66.87	85.69	0.78	
<i>yfiF</i>	898296	899240	+	64.34	80.43	0.80	68.01	80.67	0.84	
<i>yfiG</i>	899415	900863	+	75.5	78.24	0.96	61.41	70.62	0.87	
<i>yfiH</i>	900890	901831	+	97.54	102.35	0.95	93.07	97.01	0.96	
<i>yfiI</i>	901841	903022	+	90.34	96.66	0.93	83.72	99.62	0.84	
<i>yfiJ</i>	903146	904348	+	216.22	208.61	1.04	233.72	267.71	0.87	
<i>yfiK</i>	904345	905007	+	201.76	190.51	1.06	228.58	242.86	0.94	
<i>yfiL</i>	905151	906086	+	97.59	89.51	1.09	63.43	75.37	0.84	
<i>yfiM</i>	906099	907289	+	63.35	59.55	1.06	54.14	56.94	0.95	
<i>yfiN</i>	907303	908460	+	119.91	131.13	0.91	85.54	99.28	0.86	
<i>padR</i>	908533	909081	-	321.74	287.82	1.12	259.52	306.84	0.85	
<i>lipB</i>	909354	909986	+	205.42	196.18	1.05	346.09	351.74	0.98	
<i>yfiQ</i>	910175	911263	+	60.51	66.71	0.91	59.17	64.44	0.92	
<i>yfiR</i>	911299	911916	-	187.9	162.96	1.15	247.13	261.74	0.94	
<i>yfiS</i>	911882	913135	-	79.88	89.36	0.89	71.39	98.17	0.73	
<i>yfiT</i>	913259	913795	+	584.52	554.6	1.05	669.96	649.78	1.03	
<i>yfiU</i>	913792	915348	-	74.49	73.91	1.01	81.67	92.3	0.88	
<i>yfiV</i>	915459	915941	-	144.2	156.4	0.92	163.35	193.53	0.84	
<i>yfiW</i>	916113	916889	+	573.67	432.87	1.33	747.66	667.27	1.12	
<i>yfiX</i>	916864	918684	+	425.9	305.15	1.40	772.53	633.94	1.22	
<i>yfiY</i>	918702	919679	-	850.94	943.98	0.90	1165.3	1593.46	0.73	
<i>yfiZ</i>	919810	920811	+	380.96	338.5	1.13	464.79	483.35	0.96	
<i>yfhA</i>	920808	921839	+	496.32	465.13	1.07	559.25	611.91	0.91	
<i>yfhB</i>	921954	922835	+	1792.29	1647.68	1.09	1874.71	1732.96	1.08	
<i>yfhC</i>	922923	923507	+	1746.17	2147.11	0.81	1926.02	2207.59	0.87	
<i>yfhD</i>	923546	923737	-	1099.13	751.2	1.46	511.52	296.89	1.72	
<i>yfhF</i>	923969	924880	-	1358.69	915.71	1.48	656.69	255.23	2.57	
<i>yfhG</i>	924969	925763	+	754.45	701.85	1.07	769.65	772.93	1.00	
<i>yfhH</i>	925765	926079	+	380.63	392.56	0.97	507.57	543.28	0.93	
<i>yfhI</i>	926222	927415	+	126.83	121.04	1.05	122.57	109.99	1.11	
<i>sspK</i>	927448	927600	-	28.85	33.26	0.87	26.33	24.44	1.08	
<i>yfhJ</i>	927725	927994	+	536.8	423.09	1.27	408.09	311.75	1.31	
<i>yfhK</i>	928139	928657	+	6617.03	6734.47	0.98	3733	2474.06	1.51	
<i>yfhL</i>	928742	929074	+	2896.23	2946.52	0.98	1316.13	971.63	1.35	
<i>yfhM</i>	929061	929921	+	3174.71	3172.7	1.00	1566.5	1255.68	1.25	
<i>csbB</i>	930154	931143	+	1200.92	1277.67	0.94	932.77	676.16	1.38	
<i>yfhO</i>	931340	933799	+	602.72	442.07	1.36	383.56	356.36	1.08	
<i>yfhP</i>	933792	934775	-	422.42	349.85	1.21	305.63	271.33	1.13	
<i>yfhQ</i>	934991	936100	+	354.39	281.58	1.26	667.93	553.78	1.21	
<i>yfhS</i>	936108	936332	-	25.34	29.54	0.86	23.98	29.47	0.81	
<i>fabL</i>	936414	937166	+	1439.5	1145.08	1.26	1989.97	1666.11	1.19	
<i>sspE</i>	937235	937489	+	755.59	622.21	1.21	1330.75	1113.17	1.20	
<i>ygaB</i>	937578	937922	+	69.72	82.86	0.84	108.45	133.71	0.81	
<i>ygaC</i>	938066	938596	+	696.21	553.41	1.26	763.3	751.94	1.02	
<i>ygaD</i>	938657	940426	+	348.17	255.4	1.36	454.75	406.16	1.12	
<i>ygaE</i>	940503	941564	-	385.17	338.63	1.14	211.46	166.03	1.27	
<i>gsaB</i>	941784	943073	-	668.98	601.56	1.11	891.15	915.73	0.97	
<i>ygaF</i>	943226	943699	+	288.24	246.48	1.17	472.4	554.73	0.85	
<i>perR</i>	943822	944259	+	1795.48	1696.23	1.06	1549.86	1696.75	0.91	
<i>ygzB</i>	944294	944647	-	850.03	810.87	1.05	575.3	578.21	0.99	
<i>ygxA</i>	944855	945739	+	880.28	960.14	0.92	783.93	851.17	0.92	
<i>spoOM</i>	952707	953483	-	1519.94	1588.58	0.96	2517.01	2684.17	0.94	
<i>ygaZ</i>	953625	953828	+	60.81	53.39	1.14	63.7	76.44	0.83	
<i>ygaJ</i>	954225	954980	+	475.92	435.93	1.09	531.81	464.66	1.14	
<i>thiC</i>	955231	957003	+	2521.86	3095.27	0.81	3038.69	3359.65	0.90	
<i>ygaK</i>	957041	958144	-	40.48	45.39	0.89	34.66	39.74	0.87	
<i>senS</i>	958626	958844	+	37.03	35.16	1.05	33.38	37.06	0.90	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>katA</i>	958871	960322	-	1031.84	796.73	1.30	969.39	886.05	1.09	
<i>ssuB</i>	960686	961498	+	48.63	55.08	0.88	40.6	53.12	0.76	
<i>ssuA</i>	961516	962514	+	55.12	57.95	0.95	48.57	58.93	0.82	
<i>ssuC</i>	962511	963341	+	69.88	72.63	0.96	52.59	63.69	0.83	
<i>ssuD</i>	963364	964494	+	76.61	77.93	0.98	60.6	74.76	0.81	
<i>ygaN</i>	964598	965134	+	153.27	150.44	1.02	139.99	152.92	0.92	
<i>yhzA</i>	965246	965515	+	69.1	67.72	1.02	65.94	67.93	0.97	
<i>ygaO</i>	965533	966006	-	311.87	293.57	1.06	320.12	267.52	1.20	Spo0A regulon
<i>yhbB</i>	966566	967189	-	168.07	181.97	0.92	181.54	180.84	1.00	
<i>yhbA</i>	967125	968432	+	87.29	81.9	1.07	87.21	89.87	0.97	
<i>yhbB</i>	968499	969434	+	53	75.65	0.70	50.94	56.66	0.90	
<i>cspR</i>	969472	969954	+	292.45	240.22	1.22	536.39	561.64	0.96	
<i>yhbD</i>	970004	970720	+	89.16	91.7	0.97	114.13	138.53	0.82	
<i>yhbE</i>	970711	971424	+	201.68	205.82	0.98	299.98	350.39	0.86	
<i>yhbF</i>	971436	972143	+	229.06	227.55	1.01	313.42	345.68	0.91	
<i>prkA</i>	972493	974388	+	123.23	127.05	0.97	113.36	122.52	0.93	
<i>yhbH</i>	974568	975746	+	79.46	76.38	1.04	87.46	83.53	1.05	
<i>yhbI</i>	975906	976370	+	200.94	127.79	1.57	183.51	140.79	1.30	
<i>yhbJ</i>	976406	977071	+	500.52	319.37	1.57	477.32	286.29	1.67	
<i>yhcA</i>	977112	978710	+	441.06	256.67	1.72	317.56	196.85	1.61	
<i>yhcB</i>	978733	979263	+	447.39	271.18	1.65	287.26	194.57	1.48	
<i>yhcC</i>	979276	979650	+	227.53	167.54	1.36	136.73	107.43	1.27	
<i>yhcE</i>	979810	980571	+	82.09	86.56	0.95	133.92	149.42	0.90	
<i>yhcF</i>	980574	980939	+	137.61	135.79	1.01	254.62	317.13	0.80	
<i>yhcG</i>	980941	981639	+	170.6	153.06	1.11	312.41	368.06	0.85	
<i>yhcH</i>	981656	982573	+	233.22	212.92	1.10	467.39	529.99	0.88	
<i>yhcI</i>	982566	983507	+	213.27	203.9	1.05	384.15	390.84	0.98	
<i>cspB</i>	983599	983802	-	6555.04	6481.4	1.01	4629.53	4689.69	0.99	
<i>yhcJ</i>	984238	985029	+	522.85	442.36	1.18	567.86	850.57	0.67	
<i>yhcK</i>	985070	986149	-	233.41	216.6	1.08	409.61	360.87	1.14	
<i>yhcL</i>	986322	987713	+	215.37	178.76	1.20	341.31	419.99	0.81	
<i>yhcM</i>	987753	988208	-	1896.37	1508.63	1.26	802.02	329.3	2.44	
<i>yhcN</i>	988358	988927	+	53.11	69.48	0.76	83.18	83.17	1.00	
<i>yhcO</i>	989107	989406	+	26.7	35.01	0.76	27.62	35.94	0.77	
<i>yhcP</i>	989397	990014	+	51.76	51.64	1.00	40.6	53.4	0.76	
<i>yhcQ</i>	989946	990599	-	46.1	51.64	0.89	46.48	53.23	0.87	
<i>yhcR</i>	990682	994335	+	260.18	291.12	0.89	323.13	339.87	0.95	
<i>yhcS</i>	994332	994928	+	241.31	255.68	0.94	288.16	287.29	1.00	
<i>yhcT</i>	994958	995866	-	112.19	99.04	1.13	119.76	120.77	0.99	
<i>yhcU</i>	995977	996372	+	95.85	88.79	1.08	107.25	101.96	1.05	
<i>yhcV</i>	996509	996931	+	90.3	86	1.05	64.29	71.65	0.90	
<i>yhcW</i>	997058	997720	+	563.52	552.79	1.02	622.72	653.34	0.95	
<i>yhcX</i>	997736	999277	+	1067.53	972.61	1.10	1404.18	1317.63	1.07	
<i>yhxA</i>	999697	1001049	+	428.44	516.95	0.83	396.11	543	0.73	
<i>glpP</i>	1001077	1001655	+	348.63	429.86	0.81	419.8	599.69	0.70	
<i>glpF</i>	1001834	1002658	+	123.6	151.36	0.82	183.57	239.6	0.77	AbrB regulon
<i>glpK</i>	1002677	1004167	+	1526.44	1300.14	1.17	949.45	705.96	1.34	AbrB regulon
<i>glpD</i>	1004308	1005975	+	766.38	708.84	1.08	312.76	380.47	0.82	AbrB regulon
<i>yhxB</i>	1006107	1007804	+	1895.13	1428.05	1.33	1906.88	1552.45	1.23	
<i>yhcY</i>	1007953	1009092	+	257.98	219.1	1.18	311.33	324	0.96	
<i>yhcZ</i>	1009089	1009733	+	346.12	285.34	1.21	453.49	451.69	1.00	
<i>yhdA</i>	1009730	1010254	+	251.3	210.94	1.19	358.76	333.3	1.08	
<i>yhdB</i>	1010269	1010511	-	27.03	31.95	0.85	28.52	36.58	0.78	
<i>yhdC</i>	1010712	1011035	+	51.33	46.17	1.11	62.37	58.63	1.06	
<i>lytF</i>	1011079	1012542	-	1625.94	2256.83	0.72	1463.72	2011.95	0.73	SigD regulon
<i>yhdE</i>	1012695	1013135	-	567.51	591.05	0.96	593.32	743.21	0.80	
<i>yqxB</i>	1013238	1014896	-	2035.93	1874.06	1.09	1167.53	687.11	1.70	
<i>spoVR</i>	1014927	1016333	+	61.06	65.97	0.93	59.86	65.42	0.92	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>phoA</i>	1016363	1017748	-	132.82	110.91	1.20	131.04	127.18	1.03	
<i>lytE</i>	1018280	1019311	+	1099	865.56	1.27	1315.52	1644.08	0.80	Spo0A regulon
<i>citR</i>	1019330	1020256	-	156.84	144.33	1.09	127.04	130.83	0.97	
<i>citA</i>	1020365	1021465	+	212.73	180.85	1.18	198.35	182.87	1.08	
<i>yhdF</i>	1021539	1022408	+	1811.89	1004.06	1.80	958.65	378.49	2.53	
<i>yhdG</i>	1022658	1024055	+	346.86	366.87	0.95	702.17	515.68	1.36	
<i>yhdH</i>	1024173	1025528	+	197.91	166.23	1.19	343.36	278.72	1.23	
<i>yhdI</i>	1025563	1026972	-	97.92	98.59	0.99	95.73	106.7	0.90	
<i>yhdJ</i>	1027082	1027510	+	254.41	264.28	0.96	225.26	225.37	1.00	
<i>yhdK</i>	1027541	1027831	-	62.86	68.71	0.91	128.58	129.88	0.99	
<i>yhdL</i>	1027819	1028895	-	579.17	551.75	1.05	626.82	660.32	0.95	
<i>sigM</i>	1028885	1029376	-	380.56	418.91	0.91	382.37	455.72	0.84	
<i>yhdN</i>	1029573	1030568	+	2381.27	2935.89	0.81	1417.51	1171.61	1.21	
<i>yhdO</i>	1030703	1031302	+	1251.11	1381.34	0.91	930.89	1138.56	0.82	
<i>yhdP</i>	1031371	1032705	-	740.76	689.48	1.07	1314.87	1312.49	1.00	
<i>yhdQ</i>	1032766	1033197	-	1048.65	974.96	1.08	1499.24	1503.03	1.00	
<i>yhdR</i>	1033354	1034535	+	404.01	391.38	1.03	800.94	922.36	0.87	
<i>yhdT</i>	1034862	1036247	+	1140.44	1440.79	0.79	1008.76	1297.46	0.78	
<i>yhdU</i>	1036261	1036617	-	106.59	81.78	1.30	154.48	148.64	1.04	
<i>yhdV</i>	1036614	1037009	-	295.83	243.39	1.22	309.69	315.55	0.98	
<i>yhdW</i>	1036996	1037727	-	439.89	370.32	1.19	559.03	541.47	1.03	
<i>yhdY</i>	1038217	1039332	+	169.69	133.78	1.27	165.63	140.76	1.18	
<i>yhdZ</i>	1039402	1040145	+	260.45	258.84	1.01	289.71	327.09	0.89	
<i>yheN</i>	1040169	1041017	-	799.99	724.25	1.10	971.03	1113.23	0.87	
<i>dat</i>	1041302	1042150	+	2410.6	2408.61	1.00	2524.41	2640.36	0.96	
<i>nhaC</i>	1042193	1043554	-	183.17	190.71	0.96	196.47	207.79	0.95	
<i>nhaX</i>	1043681	1044181	-	4101.43	5315.62	0.77	2119.7	1251.89	1.69	
<i>yheI</i>	1044626	1046383	+	611.97	878.49	0.70	371.12	437.86	0.85	
<i>yheH</i>	1046380	1048401	+	576.47	710.15	0.81	404.25	467.17	0.87	
<i>yheG</i>	1048450	1049070	-	275.39	363.99	0.76	431.36	541.45	0.80	
<i>sspB</i>	1049339	1049542	-	62.18	84.25	0.74	89.56	112.86	0.79	
<i>yheE</i>	1049751	1049969	-	86.35	98.47	0.88	81.1	82.43	0.98	
<i>yheD</i>	1050119	1051480	-	73.03	68.22	1.07	80.94	78.5	1.03	
<i>yheC</i>	1051470	1052561	-	45.88	53.25	0.86	48.32	50.8	0.95	
<i>yheB</i>	1052828	1053961	+	273.43	258.64	1.06	365.81	413.59	0.88	
<i>yheA</i>	1054054	1054407	+	783.51	775.62	1.01	722.95	653.97	1.11	
<i>yhaZ</i>	1054451	1055524	-	229.61	163.14	1.41	268.59	218.09	1.23	
<i>yhaY</i>	1055717	1055968	-	23.91	26.7	0.90	25.23	27.32	0.92	
<i>yhaX</i>	1056011	1056877	+	47.49	49.99	0.95	47.62	60.45	0.79	
<i>hemZ</i>	1056989	1058494	+	134.67	136.56	0.99	213.99	241.62	0.89	
<i>yhaU</i>	1058512	1059738	-	202.96	147.93	1.37	237.91	198.56	1.20	
<i>yhaT</i>	1059735	1060232	-	158.23	108.36	1.46	195.53	154.51	1.27	
<i>yhaS</i>	1060296	1060634	-	348.77	216.56	1.61	461.53	329.08	1.40	
<i>yhaR</i>	1060799	1061566	+	147.07	193.27	0.76	124.02	169.45	0.73	
<i>yhaQ</i>	1061899	1062795	+	547.88	444.2	1.23	1128.03	998.58	1.13	AbrB regulon
<i>yhaP</i>	1062788	1064047	+	386.09	327.98	1.18	966.12	841.12	1.15	AbrB regulon
<i>yhaO</i>	1064154	1065380	+	326.84	252.84	1.29	411.33	373.84	1.10	
<i>yhaN</i>	1065385	1068276	+	613.09	365.48	1.68	532.66	416.72	1.28	
<i>yhaM</i>	1068350	1069294	+	1362.53	1036.89	1.31	1247.77	1172.24	1.06	
<i>yhaL</i>	1069419	1069631	+	55.94	55.14	1.01	89.09	126.28	0.71	
<i>prsA</i>	1069672	1070550	-	2446.22	2104.58	1.16	3476.98	3263.27	1.07	
<i>yhaK</i>	1071350	1071604	-	64.91	87.96	0.74	60.53	65.18	0.93	
<i>yhaJ</i>	1071628	1071867	-	59.64	91.32	0.65	70.52	84.03	0.84	
<i>yhaI</i>	1072075	1072416	+	156.97	154.85	1.01	222.93	219.58	1.02	
<i>hpr</i>	1072413	1073024	-	1489.13	1381.68	1.08	1318.32	1430.9	0.92	
<i>yhaH</i>	1073202	1073558	-	1116.74	1146.61	0.97	1035.03	1213.14	0.85	
<i>yhaG</i>	1073951	1074469	-	936.41	883.39	1.06	1225.63	1177.99	1.04	
<i>serC</i>	1074594	1075673	-	2163.5	1960.86	1.10	1938.36	1963.61	0.99	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>hit</i>	1075820	1076257	-	912.82	985.27	0.93	1552.89	1608.09	0.97	
<i>ecsA</i>	1076745	1077488	+	367.42	317.19	1.16	420.13	451.98	0.93	
<i>ecsB</i>	1077481	1078707	+	475.33	340.5	1.40	643.34	650.65	0.99	
<i>ecsC</i>	1078727	1079437	+	405.98	308.61	1.32	563.48	571.07	0.99	
<i>yhaA</i>	1079455	1080645	-	1106.01	1135.82	0.97	1245.83	1291.53	0.96	
<i>yhfA</i>	1080718	1082109	-	73.99	72.72	1.02	65.87	74.14	0.89	
<i>yhgB</i>	1082175	1082489	-	124.12	120.35	1.03	100.61	117.61	0.86	
<i>yhgC</i>	1082534	1083034	-	1527.01	1750.43	0.87	1948.2	1861.71	1.05	
<i>pbpF</i>	1083156	1085300	+	265.01	215.56	1.23	336.2	287.68	1.17	
<i>hemE</i>	1085422	1086483	+	1472.89	971.52	1.52	955.88	727.46	1.31	
<i>hemH</i>	1086555	1087487	+	2701.09	1910.49	1.41	1757.55	1352.56	1.30	
<i>hemY</i>	1087502	1088914	+	1454.26	1018.59	1.43	855.75	686.14	1.25	
<i>yhgD</i>	1089060	1089635	+	423.51	395.52	1.07	657.88	465.2	1.41	
<i>yhgE</i>	1089706	1092033	+	436.78	394.3	1.11	780.96	572.43	1.36	
<i>fabHB</i>	1092075	1093052	-	2025.01	2019.15	1.00	1230.39	994.56	1.24	
<i>yhfC</i>	1093178	1093954	+	321.49	336.54	0.96	319.13	272.36	1.17	
<i>yhfD</i>	1094045	1094248	-	26.31	35.45	0.74	33.85	30.67	1.10	
<i>yhfE</i>	1094367	1095407	+	861.61	825.5	1.04	1057.48	931.38	1.14	
<i>yhfF</i>	1095420	1095827	+	690.05	735.61	0.94	954.04	833.05	1.15	
<i>glfT</i>	1095864	1097153	-	1441.83	1734.92	0.83	1360.59	1889.75	0.72	
<i>yhfI</i>	1097716	1098450	+	648.49	525.77	1.23	707.46	658.99	1.07	
<i>yhfJ</i>	1098463	1099458	+	1242.77	970.85	1.28	1413.69	1271.34	1.11	
<i>yhfK</i>	1099523	1100167	+	921.72	798.86	1.15	880.65	782.61	1.13	
<i>yhfL</i>	1100284	1101825	+	177.83	129.85	1.37	185.13	146.35	1.26	
<i>yhfM</i>	1101864	1102259	-	162.45	128.67	1.26	127.48	94.82	1.34	
<i>yhfN</i>	1102408	1103688	+	204.75	169.57	1.21	207.97	184.92	1.12	
<i>aprE</i>	1103727	1104872	-	264	341.72	0.77	205.99	278.79	0.74	
<i>yhfO</i>	1105307	1105756	+	128.9	122.98	1.05	167.22	188.4	0.89	
<i>yhfP</i>	1105828	1106820	+	509.03	438.58	1.16	656.4	569.06	1.15	
<i>yhfQ</i>	1106962	1108008	+	851.06	1175.52	0.72	729.91	1018.83	0.72	
<i>yhfR</i>	1108040	1108621	-	659.85	737.95	0.89	1396.57	1678.81	0.83	
<i>yhfS</i>	1108692	1109786	-	514.87	600.77	0.86	976.17	1212.53	0.81	
<i>yhfT</i>	1109783	1111222	-	498.03	565.04	0.88	893.62	1139.88	0.78	
<i>yhfU</i>	1111229	1111789	-	252.49	352.97	0.72	464.43	672.83	0.69	
<i>hemAT</i>	1111924	1113222	-	1800.66	1840.83	0.98	1597.42	1835.07	0.87	SigD regulon
<i>yhfW</i>	1113361	1114890	-	72	77.24	0.93	61.08	82.41	0.74	
<i>yhxC</i>	1115002	1115859	+	92.09	91.51	1.01	62.35	76.68	0.81	
<i>yhzC</i>	1115887	1116120	-	2466.08	3196.94	0.77	1279.11	1366.5	0.94	
<i>comK</i>	1116413	1116991	+	669.7	733.04	0.91	978.41	1204.2	0.81	Spo0A regulon
<i>yhxD</i>	1117038	1117937	-	3030.94	1634.86	1.85	1854.79	727.33	2.55	
<i>yhjA</i>	1118154	1118423	+	2439.87	2520.57	0.97	2907.38	2547.92	1.14	
<i>yhjB</i>	1118466	1119935	-	999.97	889.7	1.12	1005.39	766.87	1.31	
<i>yhjC</i>	1119932	1120132	-	1730.66	1539.39	1.12	1856.37	1431.04	1.30	
<i>yhjD</i>	1120340	1120702	-	49.73	43.95	1.13	56.55	39.85	1.42	
<i>yhjE</i>	1120855	1121478	+	467.66	334.48	1.40	459.84	376.76	1.22	
<i>sipV</i>	1121480	1121986	+	415.92	304.75	1.36	455.4	387.89	1.17	
<i>yhjG</i>	1122166	1123665	+	202.98	224.8	0.90	179.14	230.82	0.78	
<i>yhjH</i>	1123742	1124269	+	167.49	163.04	1.03	177.46	195.66	0.91	
<i>glcP</i>	1124427	1125632	-	45.85	45.35	1.01	51.5	55.5	0.93	
<i>yhjJ</i>	1125704	1126756	-	90.28	81.84	1.10	100.09	100.06	1.00	
<i>yhjK</i>	1126759	1127619	-	71.17	68.92	1.03	83.04	91.1	0.91	
<i>yhjL</i>	1127591	1128916	-	45.59	50.11	0.91	47.75	56.76	0.84	
<i>yhjM</i>	1129020	1130009	+	359.86	323.57	1.11	455.53	562.14	0.81	AbrB regulon
<i>yhjN</i>	1130223	1131377	-	133.12	135.87	0.98	161.78	170.37	0.95	
<i>yhjO</i>	1131484	1132689	-	76.24	75.03	1.02	48.76	57.12	0.85	
<i>yhjP</i>	1132803	1134530	+	144.49	119.14	1.21	158.19	149.48	1.06	
<i>yhjQ</i>	1134560	1134886	-	76.6	79.07	0.97	55.32	46.89	1.18	
<i>yhjR</i>	1135004	1135441	-	40.72	40.89	1.00	34.63	38.93	0.89	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>addB</i>	1135625	1139125	+	547.73	436.84	1.25	653.97	603.2	1.08	
<i>addA</i>	1139112	1142810	+	726.28	652.29	1.11	1093.89	954.57	1.15	
<i>sbcD</i>	1142882	1144057	+	507.78	486.4	1.04	770	659.36	1.17	
<i>yirY</i>	1144054	1147446	+	718.06	692.38	1.04	1212.52	1027.75	1.18	
<i>yisB</i>	1147460	1147762	+	520.82	526.91	0.99	1006.77	839.84	1.20	
<i>gerPF</i>	1147799	1148026	-	35.08	32.82	1.07	45.29	39.3	1.15	
<i>gerPE</i>	1148049	1148450	-	47.07	57.33	0.82	43.14	49.12	0.88	
<i>gerPD</i>	1148450	1148626	-	54.58	54.7	1.00	57.36	61.34	0.94	
<i>gerPC</i>	1148623	1149240	-	104.95	112.85	0.93	86.94	98.21	0.89	
<i>gerPB</i>	1149263	1149505	-	37.29	39.97	0.93	31.5	35.3	0.89	
<i>gerPA</i>	1149511	1149732	-	44.7	48.87	0.91	44.04	54.31	0.81	
<i>yisI</i>	1150155	1150325	-	52.24	45.51	1.15	64.41	77.16	0.83	
<i>yisJ</i>	1150471	1151394	-	61.54	61.62	1.00	39.22	49	0.80	
<i>yisK</i>	1151549	1152454	+	651.75	862.46	0.76	752.23	983.55	0.76	
<i>yisL</i>	1152570	1152926	+	345.46	433.77	0.80	446.01	553.85	0.81	
<i>wprA</i>	1153094	1155778	+	4000.18	4478.37	0.89	4756.71	4907.61	0.97	
<i>yisN</i>	1155809	1156396	-	42.91	41.01	1.05	38.18	41.76	0.91	
<i>asnO</i>	1156542	1158386	+	74.66	76.95	0.97	60.71	75.51	0.80	
<i>yizA</i>	1158516	1158995	-	81.82	95.11	0.86	66.71	77.53	0.86	
<i>yisP</i>	1159227	1160051	+	635.19	431.2	1.47	350.12	234.28	1.49	
<i>yisQ</i>	1160081	1161448	-	52	59.35	0.88	45.12	51.72	0.87	
<i>yisR</i>	1161572	1162435	+	425.17	264.05	1.61	245.33	230.58	1.06	
<i>degA</i>	1162453	1163466	+	836.54	539.27	1.55	530.56	487.56	1.09	
<i>yisS</i>	1163675	1164703	+	89.16	85.89	1.04	98.73	107.78	0.92	
<i>yisT</i>	1164754	1165263	-	725.9	803.14	0.90	517.37	474.02	1.09	
<i>yisU</i>	1165313	1165975	-	63.54	64.01	0.99	52.75	63.13	0.84	
<i>yisV</i>	1166042	1167496	+	159.37	153.03	1.04	150.9	167.82	0.90	
<i>yisX</i>	1167504	1168142	-	248.3	271.92	0.91	283.22	293.94	0.96	
<i>yisY</i>	1168348	1169154	+	132.89	130.99	1.01	169.2	166.6	1.02	
<i>yisZ</i>	1169182	1169781	-	52.57	55.68	0.94	47.2	54.45	0.87	
<i>yitA</i>	1169778	1170947	-	90.71	95.8	0.95	82.49	100.55	0.82	
<i>yitB</i>	1171060	1171770	-	150.09	151.47	0.99	104.54	120.4	0.87	
<i>yitC</i>	1171955	1172641	+	81.11	86.52	0.94	70.93	74.91	0.95	
<i>yitD</i>	1172638	1173396	+	67.16	65.33	1.03	53	63.42	0.84	
<i>yitE</i>	1173441	1174070	-	38.88	42.01	0.93	32.78	39.46	0.83	
<i>yitF</i>	1174166	1175281	-	71.88	76.99	0.93	52.56	62.62	0.84	
<i>yitG</i>	1175290	1176558	-	75.96	81.17	0.94	67.98	81.18	0.84	
<i>yitH</i>	1176670	1177518	-	309.58	325.1	0.95	350.5	418.73	0.84	
<i>yitI</i>	1177523	1177987	-	300.33	308.14	0.97	335.87	462.38	0.73	
<i>yitJ</i>	1178062	1179900	-	458.01	508.86	0.90	814.31	1015.13	0.80	
<i>yitK</i>	1180214	1180705	-	670.98	663.06	1.01	616.5	701.67	0.88	
<i>yitL</i>	1180804	1181700	+	435.6	394.29	1.10	445.66	472.1	0.94	
<i>yitM</i>	1181753	1182337	-	455.97	478.27	0.95	307.61	372.55	0.83	
<i>yitN</i>	1182334	1182702	-	64.52	70.02	0.92	60.1	67.33	0.89	
<i>yitO</i>	1182834	1183046	-	32.49	35.45	0.92	44.04	41.69	1.06	
<i>yitP</i>	1183247	1183783	-	50.26	57.08	0.88	57.08	65.66	0.87	
<i>yitQ</i>	1184155	1184892	+	219.48	185.92	1.18	200.72	237.28	0.85	
<i>yitR</i>	1184912	1185205	+	147.2	116.59	1.26	133.15	144.73	0.92	
<i>nprB</i>	1185341	1186957	+	104.9	107	0.98	103.7	116.96	0.89	
<i>yitS</i>	1187004	1187855	-	604.8	499.41	1.21	539.7	494.36	1.09	
<i>yitT</i>	1187993	1188835	+	2593.34	1645.74	1.58	1282.07	531.21	2.41	
<i>ipi</i>	1188950	1189309	+	1172.23	736.83	1.59	318.6	172.61	1.85	
<i>yitU</i>	1189794	1190606	-	479.26	428.86	1.12	550.8	641.43	0.86	
<i>yitV</i>	1190727	1191494	+	462.08	375.35	1.23	498.01	533.06	0.93	
<i>yitW</i>	1191558	1191866	+	2066.82	1860.57	1.11	2144.62	1991.57	1.08	
<i>yitY</i>	1192162	1193592	+	162.3	159.01	1.02	319.67	386.74	0.83	
<i>yitZ</i>	1193637	1194131	+	79.77	80.21	0.99	165.96	191.18	0.87	
<i>argC</i>	1194338	1195378	+	194.25	187.03	1.04	831.2	1379.33	0.60	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>argJ</i>	1195398	1196618	+	337.05	434.89	0.78	1471.76	2007.03	0.73	
<i>argB</i>	1196633	1197409	+	329.84	445.93	0.74	1180.93	1600.9	0.74	
<i>argD</i>	1197406	1198563	+	406.32	511.32	0.79	1063.92	1417.41	0.75	
<i>carA</i>	1198634	1199695	+	628.22	778.77	0.81	1347.62	1741.79	0.77	
<i>carB</i>	1199688	1202780	+	992.72	1193.75	0.83	1460.6	1832.5	0.80	
<i>argF</i>	1202768	1203727	+	1245.91	1543.29	0.81	1510.03	1841.89	0.82	
<i>yjzC</i>	1203813	1203992	+	40.15	58.64	0.68	39.96	47.45	0.84	
<i>yjzD</i>	1204038	1204223	-	567.99	679.21	0.84	634.23	684.37	0.93	
<i>yjaU</i>	1204472	1205206	+	85.7	79.6	1.08	92.1	104.42	0.88	
<i>yjaV</i>	1205288	1205695	+	47.41	48.09	0.99	47.13	53.08	0.89	
<i>med</i>	1205937	1206890	+	872.58	827.68	1.05	616.38	570.13	1.08	Spo0A regulon
<i>comZ</i>	1206905	1207096	+	174.26	249.89	0.70	294.78	229.08	1.29	
<i>yjzB</i>	1207126	1207365	-	89.14	103.72	0.86	98.1	93.29	1.05	
<i>fabHA</i>	1207530	1208468	+	2298.42	2412.96	0.95	1835.96	2241.49	0.82	
<i>fabF</i>	1208491	1209732	+	3099.39	3126.59	0.99	3051.58	3167.74	0.96	
<i>yjaZ</i>	1209808	1210593	+	76.8	85.89	0.89	66.07	69.67	0.95	
<i>appD</i>	1210785	1211771	+	913.27	1199.11	0.76	787.06	981.29	0.80	
<i>appF</i>	1211768	1212757	+	1358.49	1488.16	0.91	1156.92	1483.12	0.78	
<i>appA</i>	1212845	1214476	+	3890.49	4672.14	0.83	3033.37	3577.02	0.85	
<i>appB</i>	1214552	1215505	+	1871.49	2427.12	0.77	1472.69	1960.93	0.75	
<i>appC</i>	1215522	1216433	+	1658.15	2187.96	0.76	1279.98	1706.35	0.75	
<i>yjBA</i>	1216639	1217391	+	127.02	147.12	0.86	159.38	254.13	0.63	
<i>trpS</i>	1217426	1218418	-	891.97	889.45	1.00	1004.42	1049.52	0.96	
<i>oppA</i>	1219162	1220799	+	2803.34	3150.42	0.89	1875.51	2102.38	0.89	
<i>oppB</i>	1220907	1221842	+	650	564.49	1.15	399.34	453.74	0.88	
<i>oppC</i>	1221846	1222763	+	859.28	758.9	1.13	602.79	643.36	0.94	
<i>oppD</i>	1222768	1223844	+	1185.2	1137.84	1.04	894.94	985.99	0.91	
<i>oppF</i>	1223846	1224763	+	1104.65	1128.51	0.98	929.6	976.83	0.95	
<i>yjBB</i>	1224870	1226087	+	82.85	78.45	1.06	118.84	108.12	1.10	
<i>yjBC</i>	1226251	1226829	+	1907.06	2025.15	0.94	1798.2	1425.17	1.26	
<i>yjBD</i>	1227010	1227405	+	1955.74	2062.31	0.95	1263.05	1250.24	1.01	
<i>yjBE</i>	1227448	1228104	-	49.14	54.18	0.91	47.16	52.75	0.89	
<i>mecA</i>	1228381	1229037	+	1257.77	1414.36	0.89	915.81	780.19	1.17	
<i>yjBF</i>	1229228	1230349	+	156.71	136.33	1.15	186	170.58	1.09	
<i>yjBG</i>	1230579	1232408	+	1822.09	1847.02	0.99	1939.76	1760.97	1.10	
<i>yjBH</i>	1232926	1233753	-	368.67	341.01	1.08	395.79	425.26	0.93	
<i>yjBI</i>	1233822	1234220	-	500.06	426.42	1.17	346.56	439.23	0.79	
<i>yjBJ</i>	1234475	1235020	-	1141.98	1787.05	0.64	1024.45	1300.24	0.79	SigD regulon
<i>yjBK</i>	1235224	1235796	-	330.1	301.16	1.10	263.97	247.92	1.06	
<i>yjBL</i>	1235921	1236289	+	549.61	513.66	1.07	747.6	868.74	0.86	
<i>yjBM</i>	1236318	1236953	+	773.64	736.34	1.05	932.74	976.58	0.96	
<i>yjBN</i>	1236972	1237772	+	770.91	726.7	1.06	850.49	925.05	0.92	
<i>yjBO</i>	1237835	1238686	+	704.09	671.69	1.05	770.37	821.75	0.94	
<i>yjBP</i>	1238699	1239433	-	94.23	96.01	0.98	125.87	127.43	0.99	
<i>yjBQ</i>	1239668	1241512	+	94.14	103.1	0.91	197.54	220.37	0.90	
<i>tenA</i>	1241761	1242471	+	1243.69	1497.48	0.83	1884.08	2355.3	0.80	
<i>tenI</i>	1242446	1243063	+	1932.82	2392.34	0.81	3172.38	3484.82	0.91	
<i>goxB</i>	1243047	1244156	+	2033.16	2396.75	0.85	2822.64	3171.31	0.89	
<i>thiS</i>	1244156	1244356	+	2194.57	2715.1	0.81	3417.49	3706.51	0.92	
<i>thiG</i>	1244353	1245123	+	2249.73	2823.36	0.80	2928.59	3182.44	0.92	
<i>thiF</i>	1245120	1246130	+	2310.35	2817.72	0.82	2914.92	3181.67	0.92	
<i>yjBV</i>	1246149	1246964	+	2295.45	2859.52	0.80	3033.87	3252.28	0.93	
<i>fabI</i>	1247100	1247876	+	2987.27	3691.79	0.81	1850.2	2549.96	0.73	
<i>yjBX</i>	1247977	1248660	+	159.47	179.65	0.89	122.21	158.93	0.77	
<i>cotZ</i>	1248754	1249200	-	47.78	62.48	0.76	44.98	56.39	0.80	
<i>cotY</i>	1249328	1249816	-	33.06	56.76	0.58	30.94	37.57	0.82	
<i>cotX</i>	1249968	1250486	-	42.28	82.79	0.51	39.66	45.27	0.88	
<i>cotW</i>	1250585	1250902	-	73.68	103.11	0.71	57.36	76.97	0.75	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>cotV</i>	1250943	1251329	-	38.79	61.76	0.63	33.15	37.92	0.87	
<i>yjcA</i>	1251489	1251845	+	70.56	65.96	1.07	67.5	74.08	0.91	
<i>yjcB</i>	1252170	1252385	+	39.96	45.95	0.87	46.54	40.5	1.15	
<i>yjcC</i>	1252649	1252951	+	28.61	33.61	0.85	23.7	30.67	0.77	
<i>yjcD</i>	1253025	1255304	-	131.79	111.36	1.18	198.08	188.64	1.05	
<i>yjcE</i>	1255385	1255687	-	20.12	28.27	0.71	29.34	48.98	0.60	
<i>yjcF</i>	1255748	1256170	-	1664.1	2210.23	0.75	2231.31	2865.31	0.78	
<i>yjcG</i>	1256174	1256689	-	2005.41	2614.52	0.77	2120.74	3108.84	0.68	
<i>yjcH</i>	1256726	1257448	-	1647.92	2106.17	0.78	1504.22	2364.5	0.64	
<i>yjcl</i>	1257804	1258925	+	575.23	774.78	0.74	1041.39	1662.5	0.63	
<i>yjcJ</i>	1258918	1260090	+	588.21	839.65	0.70	874.22	1267.88	0.69	
<i>yjcK</i>	1260123	1260668	-	172.43	235.25	0.73	167.44	211.61	0.79	
<i>yjcL</i>	1260738	1261928	-	206.03	279.72	0.74	178.67	227.5	0.79	
<i>yjCM</i>	1263014	1264243	-	1082.42	1054.31	1.03	1520.78	1922.66	0.79	AbrB regulon
<i>yjCN</i>	1264369	1264689	+	1254.41	1494.62	0.84	1132.39	1455.57	0.78	
<i>yjCO</i>	1265199	1265660	+	280.13	337.11	0.83	364.93	402.19	0.91	
<i>yjCP</i>	1265926	1266429	+	934.94	940.13	0.99	1115.7	1128.97	0.99	Spo0A and SigD regulon
<i>yjCQ</i>	1266441	1266725	+	352.21	347.16	1.01	522.92	533.52	0.98	
<i>yjCR</i>	1266886	1267413	+	34.8	37.36	0.93	35.26	36.55	0.96	
<i>yjCS</i>	1267587	1267904	+	678.37	631.15	1.07	679.83	734.45	0.93	
<i>yjDA</i>	1268141	1268896	+	695.31	660.52	1.05	650.37	583.83	1.11	
<i>yjDB</i>	1269045	1269392	-	243.84	179.65	1.36	172.7	147.13	1.17	AbrB regulon
<i>manR</i>	1269943	1271889	+	59.32	55.02	1.08	59.74	66.79	0.89	
<i>manP</i>	1272037	1273806	+	66.09	71.13	0.93	57.08	71.81	0.79	
<i>manA</i>	1274005	1274952	+	42.23	54.47	0.78	43.98	49.32	0.89	
<i>yjDF</i>	1275122	1275604	+	316.2	279.89	1.13	528.71	469.13	1.13	
<i>yjDG</i>	1275650	1276156	-	376.01	369.48	1.02	338.76	403.31	0.84	AbrB regulon
<i>yjDH</i>	1276388	1276792	-	67.34	70.84	0.95	59	79.26	0.74	
<i>yjDL</i>	1276997	1277476	+	421.06	397.59	1.06	408.74	385.12	1.06	
<i>yjDJ</i>	1277876	1278205	-	145.49	130.94	1.11	153.93	164.67	0.93	
<i>ctaO</i>	1278825	1279814	-	344.83	263.96	1.31	225.67	326.39	0.69	AbrB regulon
<i>cotT</i>	1279937	1280260	-	61.92	112.55	0.55	41.92	56.07	0.75	
<i>yjEA</i>	1280439	1281842	+	268.29	459.6	0.58	135.34	173.59	0.78	
<i>yjFA</i>	1281882	1282355	-	745.48	687.7	1.08	480.21	404.77	1.19	
<i>yjFB</i>	1282480	1282647	-	4137.69	3844.64	1.08	3275.51	2517.49	1.30	SigD regulon
<i>yjFC</i>	1282774	1283703	+	53.2	58.04	0.92	46.47	57.33	0.81	
<i>yjGA</i>	1283681	1284079	-	131.71	110.5	1.19	95.56	95.37	1.00	
<i>yjGB</i>	1284180	1284755	-	398.11	302.31	1.32	235.83	107.79	2.19	
<i>yjGC</i>	1284901	1287858	+	3421.48	2016.91	1.70	1780.67	679.93	2.62	
<i>yjGD</i>	1287851	1288411	+	3913.41	2193.91	1.78	2280.64	873.67	2.61	
<i>yjHA</i>	1288608	1289249	+	279.72	237.05	1.18	493.56	465.61	1.06	
<i>yjHB</i>	1289442	1289954	+	150.05	133.52	1.12	169.51	165.25	1.03	
<i>yjIA</i>	1289985	1290263	-	53.21	62.14	0.86	73.23	92.61	0.79	
<i>yjIB</i>	1290654	1291844	+	258.99	242.76	1.07	347.29	331.52	1.05	
<i>yjIC</i>	1291867	1293045	+	239.75	216.25	1.11	421.47	362.33	1.16	
<i>yjJA</i>	1293448	1294260	+	442.85	387.7	1.14	597.06	615.36	0.97	
<i>yjKA</i>	1294306	1295058	-	108.59	100.39	1.08	149.9	140.71	1.07	
<i>yjKB</i>	1295058	1295810	-	100.34	99.1	1.01	127.31	141.62	0.90	
<i>yjLA</i>	1295930	1296904	-	226.48	171.95	1.32	220.69	214.04	1.03	
<i>yjLB</i>	1297036	1297533	+	1268.83	720	1.76	684.86	276.91	2.47	
<i>yjLC</i>	1297922	1298344	+	3338.38	3488.4	0.96	2686.12	3036.16	0.88	
<i>yjLD</i>	1298384	1299562	+	3306.19	3461.9	0.96	3096.2	3458.77	0.90	
<i>uxaC</i>	1299760	1301181	+	61.98	67.42	0.92	44.87	56.98	0.79	
<i>yjMB</i>	1301249	1302628	+	68.76	73.3	0.94	60.94	61.17	1.00	
<i>yjMC</i>	1302733	1303746	+	79.29	82.07	0.97	61.08	92.62	0.66	
<i>yjMD</i>	1303752	1304771	+	123.04	126.43	0.97	92.55	112.84	0.82	
<i>uxuA</i>	1304796	1305875	+	78.34	80.32	0.98	61.66	74.66	0.83	
<i>yjMF</i>	1305872	1306708	+	109.48	115.62	0.95	98.66	116.31	0.85	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>exuT</i>	1306756	1308024	+	65.01	66.81	0.97	53.35	64.29	0.83	
<i>exuR</i>	1308112	1309113	+	256.23	268.32	0.95	255.25	324.97	0.79	
<i>uxaB</i>	1309190	1310632	+	71.49	78.36	0.91	53.57	61.7	0.87	
<i>uxaA</i>	1310629	1312122	+	56.75	60.18	0.94	50.39	55.69	0.90	
<i>yjnA</i>	1312161	1312925	-	240.59	151.2	1.59	289.24	406.67	0.71	
<i>yjoA</i>	1313150	1313614	-	3023.9	2590.11	1.17	2350.87	1872.04	1.26	
<i>yjoB</i>	1313763	1315034	+	264.33	220.66	1.20	486.07	542.48	0.90	
<i>rapA</i>	1315179	1316315	+	4045.34	5313.11	0.76	2750.05	3115.2	0.88	Spo0A regulon
<i>yjpA</i>	1316470	1316712	-	150.09	133.77	1.12	296.51	248.89	1.19	
<i>xlyB</i>	1316849	1317802	+	971.92	416.5	2.33	1609.31	774.21	2.08	
<i>yjqA</i>	1317839	1318216	-	316.32	290.28	1.09	613.74	524.78	1.17	
<i>yjqB</i>	1318322	1318924	+	224.48	160.68	1.40	306.1	217.21	1.41	
<i>yjqC</i>	1319001	1319837	+	196.61	140.02	1.40	302.33	225.58	1.34	
<i>xkdA</i>	1319881	1320477	-	239.97	130.13	1.84	197.76	120.87	1.64	
<i>xre</i>	1320640	1320981	-	366.38	351.2	1.04	507.91	585.56	0.87	
<i>xkdB</i>	1321325	1322158	+	293.1	144.29	2.03	378.54	188.51	2.01	
<i>xkdC</i>	1322058	1322858	+	393.53	185.09	2.13	593.9	299.78	1.98	
<i>xkdD</i>	1323110	1323460	+	281.52	111.6	2.52	413.88	201.44	2.05	
<i>xtrA</i>	1323457	1323663	+	444.99	252.3	1.76	787.49	450.97	1.75	
<i>xpf</i>	1323779	1324288	+	349.01	140.72	2.48	645.51	293.39	2.20	
<i>xtmA</i>	1324404	1325201	+	1269.83	392.49	3.24	1842.35	936.05	1.97	
<i>xtmB</i>	1325198	1326499	+	1057.11	316.41	3.34	1451.02	757.3	1.92	
<i>xkdE</i>	1326503	1327990	+	1028.6	372.64	2.76	1566.69	847.1	1.85	
<i>xkdF</i>	1328010	1328837	+	2826.15	1221.2	2.31	3943.75	2176.58	1.81	
<i>xkdG</i>	1328863	1329798	+	2494.49	1054.36	2.37	3731.3	1937.29	1.93	
<i>xkdH</i>	1330202	1330558	+	1861.34	725.35	2.57	2659.48	1223.32	2.17	
<i>xkdl</i>	1330555	1331040	+	2445.66	964.07	2.54	3291.07	1606.35	2.05	
<i>xkdJ</i>	1331053	1331493	+	2195.54	964.99	2.28	3450.66	1727.85	2.00	
<i>xkdK</i>	1331712	1333106	+	2665.61	1062.17	2.51	3820.02	2018	1.89	
<i>xkdM</i>	1333113	1333556	+	1978.23	753.32	2.63	2966.41	1608.46	1.84	
<i>xkdN</i>	1333648	1334274	+	1309.03	429.53	3.05	2330.67	1320.01	1.77	
<i>xkdO</i>	1334279	1338277	+	1020.3	351.57	2.90	1791.48	895.64	2.00	
<i>xkdP</i>	1338222	1338929	+	1140.61	363.88	3.13	2147.38	1060.49	2.02	
<i>xkdQ</i>	1338945	1339922	+	1269.39	423.91	2.99	2105.93	980.41	2.15	
<i>xkdR</i>	1339922	1340188	+	1096.31	339.82	3.23	1739.54	763.08	2.28	
<i>xkdS</i>	1340245	1340670	+	1429.82	520.74	2.75	2582.98	1194.13	2.16	
<i>xkdT</i>	1340663	1341709	+	1143.4	414.53	2.76	2083.99	984.21	2.12	
<i>xkdU</i>	1341693	1342271	+	916.38	322.74	2.84	1521.39	710.17	2.14	
<i>xkdV</i>	1342542	1344605	+	1279.46	438.03	2.92	2251.52	1118.65	2.01	
<i>xkdW</i>	1344617	1344946	+	1150.4	365.79	3.14	1955.34	918.24	2.13	
<i>xkdX</i>	1344943	1345107	+	523.16	155.36	3.37	807.24	314.87	2.56	
<i>xepA</i>	1345151	1345990	+	1288.15	481.31	2.68	2211.26	992.74	2.23	
<i>xhlA</i>	1346043	1346312	+	2349.78	946.61	2.48	4219.56	2033.45	2.08	
<i>xhlB</i>	1346325	1346588	+	2316.78	813.79	2.85	3374.12	1847.26	1.83	
<i>xlyA</i>	1346601	1347494	+	1744.71	636.12	2.74	3045.6	1444.59	2.11	
<i>spolISB</i>	1347754	1347924	-	369.95	312.04	1.19	416.55	396.82	1.05	
<i>spolISA</i>	1347924	1348670	-	517.57	378.26	1.37	466.25	477.07	0.98	
<i>pit</i>	1348794	1349780	-	1097.02	890.61	1.23	1196.31	1193.57	1.00	
<i>ykaA</i>	1349793	1350410	-	1207.29	1129.29	1.07	1174.49	1188.3	0.99	Spo0A regulon
<i>ykbA</i>	1350686	1352002	-	149.91	135.1	1.11	103.81	130.7	0.79	
<i>ykcA</i>	1352391	1353341	+	182.54	230.54	0.79	275.52	381.76	0.72	
<i>ykcB</i>	1353592	1355742	+	96.92	98.65	0.98	79.73	91.33	0.87	
<i>ykcC</i>	1355754	1356725	+	49.46	53.34	0.93	50.99	56.53	0.90	
<i>htrA</i>	1357243	1358592	-	645.89	708.56	0.91	2184.13	2918.62	0.75	
<i>proG</i>	1358761	1359579	+	317.32	282.28	1.12	448.82	401.75	1.12	
<i>dppA</i>	1359708	1360532	+	1231.35	1483.65	0.83	1010.48	1452.46	0.70	
<i>dppB</i>	1360549	1361475	+	879.18	961.64	0.91	443.78	708.12	0.63	
<i>dppC</i>	1361481	1362443	+	829.01	921.92	0.90	429.34	723.85	0.59	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>dppD</i>	1362448	1363455	+	1044.9	1231.12	0.85	593.79	947.57	0.63	
<i>dppE</i>	1363458	1365107	+	1101.46	1360.8	0.81	738.88	1165.51	0.63	
<i>ykfA</i>	1365448	1366152	+	449.96	542.53	0.83	339.18	525.74	0.65	
<i>ykfB</i>	1366149	1367249	+	434.85	546.59	0.80	400.97	554.79	0.72	
<i>ykfC</i>	1367246	1368136	+	402.63	510.46	0.79	432	623.74	0.69	
<i>ykfD</i>	1368149	1369132	+	392.87	522.54	0.75	416.12	594.54	0.70	
<i>ykgB</i>	1369180	1370229	-	3304.51	3015.74	1.10	2350.21	2038.32	1.15	
<i>ykgA</i>	1370389	1371180	-	2889.61	2456.85	1.18	1008.41	356.33	2.83	
<i>ykhA</i>	1371340	1371858	+	477.19	386.95	1.23	548.57	497.37	1.10	
<i>hmp</i>	1372097	1373296	+	977.88	199.81	4.89	116.19	68.39	1.70	
<i>ykhH</i>	1373373	1373597	-	32.88	35.59	0.92	27.58	29.07	0.95	
<i>ykjA</i>	1373742	1374473	+	99.87	70.95	1.41	44.39	51.11	0.87	
<i>ykkA</i>	1374565	1375092	+	233.44	205.21	1.14	269.48	217.14	1.24	
<i>ykkB</i>	1375082	1375600	+	201.69	183.29	1.10	243.19	197.93	1.23	
<i>ykkC</i>	1375823	1376161	+	197.52	173.89	1.14	172.7	178.44	0.97	
<i>ykkD</i>	1376161	1376478	+	115.78	107.92	1.07	129.2	117.03	1.10	
<i>ykkE</i>	1376549	1377451	+	424.41	433.37	0.98	503.79	521.46	0.97	
<i>proB</i>	1377802	1378899	+	457.27	479.63	0.95	802.89	921.05	0.87	
<i>proA</i>	1378911	1380158	+	811.54	876.41	0.93	1130.91	1283.94	0.88	
<i>yklA</i>	1380284	1380709	+	178.85	367.03	0.49	282.66	545.76	0.52	
<i>ykmA</i>	1380740	1381183	-	254.6	231.12	1.10	260.1	232.06	1.12	
<i>ykzA</i>	1381326	1381736	+	6778.08	6620.19	1.02	4006.65	2450.88	1.63	
<i>guaD</i>	1381983	1382453	-	87.11	106.93	0.81	144.13	179.45	0.80	
<i>metE</i>	1382626	1384914	-	2119.04	2394.02	0.89	3555.54	3837.57	0.93	
<i>ispA</i>	1385330	1386289	-	172.23	237.78	0.72	131.43	147.51	0.89	
<i>ykoB</i>	1386512	1387345	+	756.85	794.14	0.95	1210.67	1216.58	1.00	
<i>ykoC</i>	1387376	1388140	-	1336.37	1267.56	1.05	1631.75	1425.34	1.14	
<i>ykoD</i>	1388287	1389759	-	1045.75	981.45	1.07	1283.9	1150.61	1.12	
<i>ykoE</i>	1389746	1390345	-	1279.71	1264.33	1.01	1584.93	1397.9	1.13	
<i>ykoF</i>	1390347	1390949	-	1310.59	1329.54	0.99	1636.25	1436.27	1.14	
<i>ykoG</i>	1391260	1391946	+	167.94	156.78	1.07	183.5	202.9	0.90	
<i>ykoH</i>	1391950	1393314	+	143.72	123.11	1.17	215.91	224.95	0.96	
<i>ykoI</i>	1393311	1393991	+	124.54	102.06	1.22	225.11	222.44	1.01	
<i>ykoJ</i>	1394083	1394595	+	789.84	1399.08	0.56	1813.74	2848.65	0.64	
<i>ykdD</i>	1394678	1394815	+	18.32	29.32	0.62	44.66	48.88	0.91	
<i>ykoK</i>	1395321	1396676	+	598.65	587.15	1.02	696.26	689.17	1.01	
<i>tnrA</i>	1396719	1397051	-	212.65	263.6	0.81	169.41	194.18	0.87	
<i>ykbB</i>	1397246	1397401	+	54.58	52.08	1.05	69.11	54.63	1.27	
<i>ykoL</i>	1397489	1397671	+	21.83	24.51	0.89	23.27	27.32	0.85	
<i>ykoM</i>	1397804	1398268	+	470.18	537.9	0.87	637.85	831.16	0.77	
<i>ykoN</i>	1398283	1399404	-	58.97	60.62	0.97	52.46	56.19	0.93	
<i>ykoP</i>	1399496	1400047	+	32.81	37.13	0.88	34.28	36.3	0.94	
<i>ykoQ</i>	1400075	1400887	-	53.86	55.36	0.97	47.98	56.24	0.85	
<i>ykoS</i>	1401080	1402774	+	66.59	62.8	1.06	55.83	61.83	0.90	
<i>ykoT</i>	1402787	1403800	+	61.43	54.4	1.13	53.54	49.75	1.08	
<i>ykoU</i>	1403826	1405661	-	99.67	85.96	1.16	88.83	107.23	0.83	
<i>ykoV</i>	1405665	1406600	-	120.67	99	1.22	87	99.6	0.87	
<i>ykoW</i>	1406637	1408886	-	328.67	358.45	0.92	254.53	349.66	0.73	
<i>ykoX</i>	1409220	1409885	+	143.29	141.77	1.01	230.84	267.15	0.86	
<i>ykoY</i>	1409962	1410936	+	143.15	157.76	0.91	158.72	201.34	0.79	
<i>sigI</i>	1411200	1411955	+	287.02	210.02	1.37	304.04	269.72	1.13	
<i>ykrI</i>	1411952	1413097	+	242.46	176.95	1.37	485.17	458.86	1.06	
<i>sspD</i>	1413108	1413302	-	86.74	117.07	0.74	87.45	93.93	0.93	
<i>ykrK</i>	1413433	1414134	-	183.68	229.65	0.80	231.55	319.09	0.73	
<i>ykrL</i>	1414305	1415201	+	585.1	499.64	1.17	683.42	633.94	1.08	
<i>ykrM</i>	1415375	1416724	+	80.59	82.32	0.98	121.87	114.18	1.07	
<i>ykrP</i>	1417246	1418268	-	179.9	109.27	1.65	186.84	112.7	1.66	
<i>kinE</i>	1418521	1420737	+	314.48	296.94	1.06	431.72	377.44	1.14	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ogt</i>	1420734	1421231	+	487.49	443.46	1.10	587.92	478.53	1.23	
<i>ykrS</i>	1421480	1422541	-	4249.04	5045.47	0.84	5109.86	5417.03	0.94	
<i>ykrT</i>	1422549	1423748	-	4046.72	4710.2	0.86	4493.21	5022.94	0.89	
<i>ykrU</i>	1424075	1424854	-	476.68	540.04	0.88	717.69	848.82	0.85	
<i>ykrV</i>	1424949	1426145	+	841.7	1005.2	0.84	1177.46	1304.45	0.90	
<i>ykrW</i>	1426342	1427586	+	527.89	635.86	0.83	755.7	1081.14	0.70	
<i>ykrX</i>	1427583	1428290	+	1099.7	1215.01	0.91	1713.6	2231.35	0.77	
<i>ykrY</i>	1428248	1428877	+	1622.37	1793.7	0.90	2223.75	2853.34	0.78	
<i>ykrZ</i>	1428892	1429428	+	1301.91	1599.64	0.81	1876.23	2319.52	0.81	
<i>ykva</i>	1429469	1429789	-	523.35	541.43	0.97	420.31	434.12	0.97	
<i>spo0E</i>	1429992	1430249	+	1617.71	1898.47	0.85	1240.36	1093.29	1.13	AbrB regulon
<i>eag</i>	1430335	1430766	+	186.43	196.4	0.95	141.98	127.53	1.11	
<i>kinD</i>	1430794	1432314	-	672.39	523.67	1.28	622.15	590.83	1.05	
<i>ykve</i>	1432507	1432944	+	343.7	228.79	1.50	376.69	284.19	1.33	
<i>motB</i>	1432984	1433769	-	2660.07	3026.31	0.88	1536.07	1792.52	0.86	
<i>motA</i>	1433741	1434553	-	2757.47	3447.35	0.80	1657.4	1826.32	0.91	SigD regulon
<i>clpE</i>	1434936	1437035	-	180.57	164.63	1.10	131.53	127.33	1.03	
<i>ykvl</i>	1437400	1438443	+	80.29	78	1.03	65.96	70.88	0.93	
<i>ykvw</i>	1438756	1439415	+	126.18	126.42	1.00	230.59	252.28	0.91	
<i>ykvk</i>	1439408	1439857	+	171.35	165.04	1.04	310.14	318.01	0.98	
<i>ykvl</i>	1439850	1440581	+	180.08	170.53	1.06	306.48	314.39	0.97	
<i>ykvm</i>	1440599	1441096	+	290	278.46	1.04	460.19	428.88	1.07	
<i>ykvn</i>	1441655	1442011	-	121.95	110.36	1.11	140.97	181.72	0.78	
<i>ykvo</i>	1442180	1442926	+	47.95	51.37	0.93	61.3	59.45	1.03	
<i>ykvp</i>	1443407	1444606	+	66.25	53.57	1.24	57.47	45.26	1.27	
<i>ykvq</i>	1444946	1445644	+	75.9	57.33	1.32	70.43	66.5	1.06	
<i>ykvr</i>	1446559	1446849	+	67.52	66.52	1.02	68.74	77.06	0.89	
<i>ykvs</i>	1446970	1447401	-	211.68	186.24	1.14	294.62	389.26	0.76	
<i>ykvt</i>	1447814	1448440	+	49.77	50.01	1.00	45.48	55.5	0.82	
<i>ykvu</i>	1448558	1449895	+	46.91	51.2	0.92	45.68	50.77	0.90	
<i>ykvv</i>	1449946	1450443	+	72.4	69.66	1.04	88.47	91.75	0.96	
<i>ykvw</i>	1450679	1452592	+	156.26	128.65	1.21	150.24	139.67	1.08	
<i>ykvy</i>	1452999	1454090	+	473.17	487.37	0.97	561.98	714.17	0.79	
<i>yk vz</i>	1454372	1455337	+	99.35	112.98	0.88	176.49	226.91	0.78	
<i>glcT</i>	1455400	1456257	+	282.91	316.89	0.89	330.47	421.39	0.78	
<i>ptsG</i>	1456496	1458595	+	3253.1	3407.32	0.95	3261.51	3292.62	0.99	
<i>ptsH</i>	1458693	1458959	+	4473.6	4823.78	0.93	3735.31	3988.15	0.94	
<i>ptsI</i>	1458959	1460671	+	5018.33	5509.97	0.91	4170.45	4298.69	0.97	
<i>splA</i>	1460762	1461001	+	298.74	329.39	0.91	284.91	319.18	0.89	
<i>splB</i>	1461079	1462107	+	210.13	228.53	0.92	225.6	248.96	0.91	
<i>ykwB</i>	1462280	1462801	-	615.22	549.56	1.12	436.33	397.3	1.10	
<i>mcpC</i>	1462936	1464900	+	2427.75	2795.39	0.87	1576.17	1847.43	0.85	SigD regulon
<i>ykwC</i>	1465037	1465903	+	2040.02	1688.59	1.21	2717.29	2386	1.14	
<i>ykwD</i>	1465942	1466715	-	178.24	153.45	1.16	219.19	183.83	1.19	
<i>ykuA</i>	1467109	1469166	+	585.7	653.72	0.90	553.04	698.38	0.79	AbrB regulon
<i>kinA</i>	1469330	1471150	+	298.77	296.71	1.01	297.02	338.57	0.88	Spo0A regulon
<i>patA</i>	1471161	1472339	-	1003.02	953.43	1.05	925.28	907.06	1.02	
<i>cheV</i>	1472906	1473817	+	1075.14	1721.04	0.62	839.74	1272.55	0.66	SigD regulon
<i>ykyB</i>	1473861	1474325	-	1076.84	977.33	1.10	897.46	921.5	0.97	
<i>ykuC</i>	1474451	1475743	-	198.68	151.28	1.31	318.37	320.18	0.99	
<i>ykuD</i>	1475819	1476313	-	72.3	64.61	1.12	80.31	90.53	0.89	
<i>ykuE</i>	1476370	1477233	-	106.42	101.59	1.05	97.97	116.09	0.84	
<i>ykuF</i>	1477376	1478140	+	426.89	308	1.39	367.31	302.27	1.22	
<i>ykuG</i>	1478441	1480723	+	889.44	404.59	2.20	1389.59	785.35	1.77	
<i>ykuH</i>	1480853	1481401	+	472.19	310.68	1.52	663.03	652.91	1.02	
<i>ykuI</i>	1481554	1482777	+	558.7	424.52	1.32	707.25	669.63	1.06	
<i>ykuJ</i>	1483423	1483662	+	1117.26	874.98	1.28	1363.27	1291.26	1.06	
<i>ykuK</i>	1483772	1484290	+	1398.05	1118.84	1.25	1540.15	1599.95	0.96	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yzkF</i>	1484424	1484621	+	2185.21	2344.86	0.93	3141.98	3376.55	0.93	Spo0A regulon
<i>ykuL</i>	1484759	1485202	+	312.39	335.72	0.93	341.12	314.12	1.09	Spo0A regulon
<i>ccpC</i>	1485351	1486232	+	202.89	202.19	1.00	327.58	428.64	0.76	
<i>ykuN</i>	1486344	1486820	+	824.11	1412.69	0.58	230.48	529.36	0.44	
<i>ykuO</i>	1486810	1487703	+	648.61	1042.62	0.62	123.59	297.72	0.42	
<i>ykuP</i>	1487719	1488255	+	497.17	802.77	0.62	114.56	269.54	0.43	
<i>ykuQ</i>	1488280	1488990	+	3422.3	3215.37	1.06	3551.98	3009.23	1.18	
<i>ykuR</i>	1489060	1490184	+	1031.4	1049.56	0.98	1221.15	1092.12	1.12	
<i>ykuS</i>	1490246	1490491	+	1266.37	1238.73	1.02	1337.33	1175.12	1.14	
<i>ykuT</i>	1490528	1491331	-	424.1	263.02	1.61	290.6	219.38	1.32	
<i>ykuU</i>	1491568	1492110	+	1366.98	1224.36	1.12	1688.37	1439.5	1.17	AbrB regulon
<i>ykuV</i>	1492182	1492643	+	603.85	526.08	1.15	816.31	717.15	1.14	Spo0A and AbrB regulon
<i>rok</i>	1493094	1493669	+	306.56	329.61	0.93	488.05	606.88	0.80	Spo0A regulon
<i>yknT</i>	1493710	1494675	-	53.59	58.79	0.91	43.51	52.46	0.83	
<i>mobA</i>	1494812	1495411	+	482.82	382.36	1.26	731.15	574.1	1.27	
<i>moeB</i>	1495462	1496481	+	506.74	432.76	1.17	795.43	660.15	1.20	
<i>moeA</i>	1496499	1497791	+	509.99	411.42	1.24	815.34	638.32	1.28	
<i>mobB</i>	1497752	1498273	+	607.91	465.03	1.31	962.91	786.06	1.22	
<i>moaE</i>	1498273	1498746	+	1206.38	982.14	1.23	1856.61	1589.57	1.17	
<i>moaD</i>	1498739	1498972	+	83.55	84.61	0.99	313.12	243.46	1.29	
<i>yknU</i>	1499196	1500953	+	92.71	92.8	1.00	97.05	102.2	0.95	
<i>yknV</i>	1500965	1502779	+	109.65	105.81	1.04	106.42	114.47	0.93	
<i>yknW</i>	1502889	1503584	+	2536.85	2494.5	1.02	3192.01	3237.72	0.99	AbrB regulon
<i>yknX</i>	1503589	1504722	+	1072.62	1064.12	1.01	2758.78	3092.84	0.89	AbrB regulon
<i>yknY</i>	1504723	1505415	+	1018.32	1013.21	1.01	2580.04	2653.3	0.97	AbrB regulon
<i>yknZ</i>	1505412	1506605	+	1066.09	1053.36	1.01	2303.08	2399.54	0.96	AbrB regulon
<i>fruR</i>	1506885	1507640	+	800.5	933.58	0.86	559.71	387.79	1.44	Spo0A regulon
<i>fruK</i>	1507637	1508548	+	508.09	613.85	0.83	235.91	187.93	1.26	
<i>fruA</i>	1508563	1510470	+	528.85	640.61	0.83	358.58	338.62	1.06	
<i>sipT</i>	1510615	1511196	+	407.92	367.55	1.11	408.38	464.69	0.88	
<i>ykoA</i>	1511230	1511499	-	33.92	42.01	0.81	129.17	149.53	0.86	
<i>ykpA</i>	1511680	1513302	+	916.3	900.6	1.02	1116.75	1406.3	0.79	
<i>ykpB</i>	1513359	1514270	+	453.56	519.34	0.87	424.64	566.16	0.75	
<i>ampS</i>	1514304	1515536	-	479.38	418.3	1.15	849.82	832.16	1.02	
<i>mreBH</i>	1515881	1516888	-	416.67	240.46	1.73	737.68	451.16	1.64	
<i>abh</i>	1517172	1517450	+	1333.62	1133.26	1.18	2048.07	1612.43	1.27	
<i>kinC</i>	1517640	1518926	+	564.05	490.42	1.15	681.32	674.85	1.01	Spo0A regulon
<i>ykqA</i>	1518942	1519775	+	578.14	488.78	1.18	684.4	716	0.96	
<i>ykqB</i>	1519838	1520503	+	752.98	717.52	1.05	790.06	801.05	0.99	
<i>adeC</i>	1520658	1522391	+	360.07	316.81	1.14	561.85	504.96	1.11	
<i>ykqC</i>	1522425	1524092	-	1855.93	1924.37	0.96	2288.5	2711.39	0.84	
<i>yzkG</i>	1524098	1524307	-	1754.77	2125.46	0.83	1766.18	2279.31	0.77	
<i>ykrA</i>	1524693	1525466	+	553.91	490.54	1.13	651.67	594.22	1.10	
<i>ykrB</i>	1525502	1526056	-	274.31	213.13	1.29	485.15	551.34	0.88	
<i>ykyA</i>	1526592	1527209	+	402.56	359.05	1.12	526.09	558.46	0.94	
<i>pdhA</i>	1527633	1528748	+	3416.56	2763.03	1.24	3139.11	3290.98	0.95	
<i>pdhB</i>	1528752	1529729	+	3957.21	3635.85	1.09	3370.66	3478.31	0.97	
<i>pdhC</i>	1529844	1531172	+	5242.75	5234.5	1.00	4564.94	4587.15	1.00	
<i>pdhD</i>	1531177	1532589	+	3962.11	4055.48	0.98	3473.88	3464.3	1.00	
<i>slp</i>	1532634	1533008	-	43.42	42.89	1.01	64.82	64.16	1.01	
<i>speA</i>	1533586	1535058	-	133.5	168.86	0.79	200.95	209.34	0.96	
<i>yktA</i>	1535243	1535509	+	383.79	372.76	1.03	721.2	761.53	0.95	
<i>yktB</i>	1535542	1536180	-	759.78	629.93	1.21	1082.81	978.5	1.11	
<i>yzkI</i>	1536420	1536608	+	2960.78	3298.69	0.90	2204.04	1227.6	1.80	
<i>yktC</i>	1536748	1537545	+	1180.91	1355.98	0.87	861.31	689.99	1.25	
<i>yzkC</i>	1537571	1537999	+	621.22	610.75	1.02	488.74	455.18	1.07	
<i>yktD</i>	1538077	1538991	-	161.11	123.51	1.30	152.67	119.14	1.28	
<i>nprE</i>	1539343	1540908	-	148.72	149.25	1.00	201.39	224	0.90	AbrB regulon

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ylaA</i>	1541193	1543133	+	54.77	60.16	0.91	64.18	66.67	0.96	
<i>ylaB</i>	1543123	1543392	+	49.51	39.53	1.25	63.47	57.03	1.11	
<i>ylaC</i>	1543392	1543913	+	76.31	65.94	1.16	100.3	94.29	1.06	
<i>ylaD</i>	1543910	1544203	+	65.39	62.8	1.04	82.51	83.03	0.99	
<i>ylaE</i>	1544243	1544854	-	331.94	441.29	0.75	287.19	365.19	0.79	AbrB regulon
<i>ylaF</i>	1545127	1545315	-	2541.71	2394.75	1.06	1875.41	1611.71	1.16	
<i>ylaG</i>	1545428	1547266	+	1060.04	1023.37	1.04	1173.8	1546.06	0.76	
<i>ylaH</i>	1547323	1547640	+	173.16	171.9	1.01	372.36	448.67	0.83	
<i>ylaI</i>	1547696	1547905	-	389.18	444.78	0.87	450.24	572.22	0.79	
<i>ylaJ</i>	1547988	1548617	-	61.65	68.62	0.90	55.04	68.79	0.80	
<i>ylaK</i>	1548772	1550100	+	75.84	66.91	1.13	63.94	69.33	0.92	
<i>ylaL</i>	1550104	1550589	-	1448.66	1705.07	0.85	1504.51	1613.5	0.93	
<i>ylaM</i>	1550692	1551621	+	123.39	115.8	1.07	114.92	125.1	0.92	
<i>ylaN</i>	1551719	1552000	+	1202.01	1621.53	0.74	1066.76	1503.59	0.71	
<i>ftsW</i>	1552206	1553417	+	468.98	418.12	1.12	587.57	607.08	0.97	
<i>pycA</i>	1553492	1556938	+	2358.47	2092.18	1.13	2870.41	2549.64	1.13	
<i>ctaA</i>	1557341	1558261	-	1066.99	1027.32	1.04	342.78	340.77	1.01	
<i>ctaB</i>	1558616	1559533	+	1420.13	1696.98	0.84	1161.22	1319.79	0.88	
<i>ctaC</i>	1559773	1560843	+	776.58	1175.55	0.66	512.54	807.11	0.64	AbrB regulon
<i>ctaD</i>	1560876	1562744	+	703.72	1117.55	0.63	521.35	805.12	0.65	AbrB regulon
<i>ctaE</i>	1562744	1563367	+	551.06	948.89	0.58	463.4	738.32	0.63	AbrB regulon
<i>ctaF</i>	1563370	1563702	+	534.59	861.05	0.62	367.42	680.61	0.54	AbrB regulon
<i>ctaG</i>	1563729	1564622	+	322.36	556.12	0.58	273.6	433.92	0.63	AbrB regulon
<i>ylbA</i>	1564654	1565016	-	1155.97	1603.25	0.72	1232.86	1640.13	0.75	AbrB regulon
<i>ylbB</i>	1565156	1565608	+	226.32	218.72	1.03	244.63	273.28	0.90	
<i>ylbC</i>	1565685	1566725	+	444.96	377.79	1.18	573.37	483.4	1.19	
<i>ylbD</i>	1566957	1567355	+	94.24	88.07	1.07	89.33	119.93	0.74	
<i>ylbE</i>	1567371	1567610	+	49.25	50.91	0.97	56.73	61.34	0.92	
<i>ylbF</i>	1567726	1568175	+	602.47	577.15	1.04	771.61	889.06	0.87	
<i>ylbG</i>	1568230	1568502	+	366.64	357.99	1.02	491.54	593.79	0.83	
<i>ylbH</i>	1568825	1569319	+	334.83	304.99	1.10	611.4	696.74	0.88	
<i>ylbI</i>	1569383	1569868	+	286.02	252.69	1.13	492.85	565.32	0.87	
<i>ylbJ</i>	1569879	1571105	-	41.8	46.27	0.90	38.24	48.64	0.79	
<i>ylbK</i>	1571286	1572068	+	204.03	181.41	1.12	268.9	308.06	0.87	
<i>ylbL</i>	1572070	1573122	+	281.79	267.27	1.05	444.15	504.31	0.88	
<i>ylbM</i>	1573111	1574358	-	144.37	160.04	0.90	168.85	196.43	0.86	
<i>ylbN</i>	1574568	1575086	+	2400.01	2271.37	1.06	2733.23	3156.49	0.87	
<i>rpmF</i>	1575108	1575287	+	3434.24	4011.38	0.86	4200.28	4116.03	1.02	
<i>ylbO</i>	1575433	1576014	+	171.8	182.56	0.94	157.86	196.6	0.80	
<i>ylbP</i>	1576071	1576553	-	1032.82	1505.6	0.69	927.93	1293.2	0.72	
<i>ylbQ</i>	1576713	1577609	+	201.32	184.78	1.09	268.09	321.76	0.83	
<i>ylIA</i>	1577680	1579299	+	294.51	278.2	1.06	564.28	634.02	0.89	
<i>ylIB</i>	1579425	1579856	+	1627.86	1867.06	0.87	1782.79	2194.48	0.81	
<i>ylxA</i>	1579926	1580861	+	1041.55	1126.55	0.92	1212.69	1540.37	0.79	
<i>ftsL</i>	1580901	1581254	+	1406.84	1934.65	0.73	1850.1	2326.43	0.80	
<i>pbpB</i>	1581251	1583401	+	373.05	483.46	0.77	696.9	907.8	0.77	
<i>spoVD</i>	1583518	1585455	+	109.01	102.13	1.07	114.44	123.97	0.92	
<i>murE</i>	1585631	1587115	+	859.21	582.3	1.48	1351.6	1328.42	1.02	
<i>mraY</i>	1587228	1588202	+	667.31	415.55	1.61	1086.21	1014.55	1.07	
<i>murD</i>	1588203	1589558	+	953.36	669.57	1.42	1760.62	1630.78	1.08	
<i>spoVE</i>	1589619	1590719	+	461.33	305.02	1.51	748.25	709.75	1.05	
<i>murG</i>	1590842	1591933	+	459.66	339.34	1.35	1137.45	939.64	1.21	
<i>murB</i>	1591960	1592871	+	610.34	481.72	1.27	1348.29	1130.31	1.19	
<i>divIB</i>	1593002	1593793	+	537.58	454.15	1.18	894.32	821.03	1.09	
<i>ylxW</i>	1593790	1594485	+	535.53	453.09	1.18	1023.24	908.42	1.13	
<i>ylxX</i>	1594508	1595215	+	570.81	562.08	1.02	949.78	929.52	1.02	
<i>sbp</i>	1595233	1595598	+	184.72	218.53	0.85	534.09	604.17	0.88	
<i>ftsA</i>	1595772	1597094	+	2008.05	2034.88	0.99	2003.61	2053.48	0.98	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ftsZ</i>	1597130	1598278	+	3083.62	2932.72	1.05	3350.62	3117.14	1.07	
<i>bpr</i>	1598580	1602881	+	116.62	122.77	0.95	130.18	127.78	1.02	
<i>spollGA</i>	1603076	1604005	+	39.17	40.97	0.96	43.44	49.07	0.89	Spo0A regulon
<i>sigE</i>	1604068	1604787	+	47.08	44.18	1.07	58.91	63.66	0.93	
<i>sigG</i>	1604927	1605709	+	50.74	54.87	0.92	56.86	70.73	0.80	AbrB regulon
<i>ylmA</i>	1605857	1606651	+	391.47	321.92	1.22	709	732.75	0.97	
<i>ylmB</i>	1606853	1608133	+	426.94	401.42	1.06	759.98	705.08	1.08	
<i>ylmC</i>	1608216	1608461	+	652.84	627.57	1.04	1105	1079.91	1.02	
<i>ylmD</i>	1608624	1609460	+	1685.89	1520.83	1.11	1787.19	1751.46	1.02	Spo0A regulon
<i>ylmE</i>	1609473	1610165	+	2546.63	2001.5	1.27	2545.75	2349.67	1.08	
<i>ylmF</i>	1610168	1610617	+	2548.26	2122.89	1.20	2788.39	2529.23	1.10	
<i>ylmG</i>	1610624	1610896	+	1391.02	1149.02	1.21	1799.13	1639.15	1.10	
<i>ylmH</i>	1610957	1611730	+	728.99	650.57	1.12	1136.24	1197.27	0.95	
<i>divIVA</i>	1611824	1612318	+	938.82	926.12	1.01	1526.95	1794.66	0.85	Spo0A regulon
<i>ileS</i>	1612660	1615425	+	858.26	881.47	0.97	1522.56	1599.47	0.95	
<i>ylyA</i>	1615503	1615946	+	28.24	33.94	0.83	33.43	35.2	0.95	
<i>lspA</i>	1616049	1616513	+	271.48	265.16	1.02	386.51	474.94	0.81	
<i>ylyB</i>	1616515	1617426	+	363.41	305.64	1.19	606.32	669.32	0.91	
<i>pyrR</i>	1617609	1618154	+	236.73	530.31	0.45	748.51	1054.71	0.71	
<i>pyrP</i>	1618326	1619630	+	342.17	370.44	0.92	725.72	914.72	0.79	
<i>pyrB</i>	1619776	1620690	+	192.85	205.73	0.94	582.2	728.29	0.80	
<i>pyrC</i>	1620674	1621960	+	309.65	338.36	0.92	1013.75	1226.85	0.83	
<i>pyrAA</i>	1621957	1623051	+	532.89	612.32	0.87	1392.81	1682.78	0.83	
<i>pyrAB</i>	1623036	1626251	+	1060.32	1180.55	0.90	1565.74	1786.03	0.88	
<i>pyrK</i>	1626248	1627018	+	1040.79	1216.22	0.86	1263.95	1460.95	0.87	
<i>pyrD</i>	1627018	1627953	+	1719.76	1861.19	0.92	1714.72	1910.53	0.90	
<i>pyrF</i>	1627922	1628641	+	1631.67	1792.92	0.91	1609.46	1813.72	0.89	
<i>pyrE</i>	1628620	1629270	+	1426.14	1511.04	0.94	1180.07	1384.52	0.85	
<i>cysH</i>	1629682	1630383	+	3643.86	3150.57	1.16	3315.19	3543.23	0.94	
<i>cysP</i>	1630395	1631459	+	2937	2414	1.22	2859.81	2999.63	0.95	
<i>sat</i>	1631508	1632656	+	3577.69	3141.82	1.14	3852.74	3803.49	1.01	
<i>cysC</i>	1632669	1633262	+	3174.75	2898.72	1.10	3035.06	2872	1.06	
<i>ylnD</i>	1633361	1634134	+	3283.15	3118.75	1.05	3306.2	3301.38	1.00	
<i>ylnE</i>	1634137	1634922	+	3358.62	3132.01	1.07	3260.29	3104.8	1.05	
<i>ylnF</i>	1634903	1635391	+	2640.5	2571.9	1.03	3361.64	3159.4	1.06	
<i>yloA</i>	1635431	1637149	-	359.02	349.35	1.03	432.83	503.45	0.86	
<i>yloB</i>	1637265	1639937	+	111.92	117.42	0.95	123.21	135.91	0.91	
<i>yloC</i>	1640020	1640895	+	1353.89	1159.74	1.17	1409.45	1601.65	0.88	
<i>ylzA</i>	1640972	1641241	+	1562.26	1238.84	1.26	1580.98	1743.75	0.91	
<i>gmk</i>	1641249	1641863	+	1208.56	1001.75	1.21	1665.04	1803.83	0.92	
<i>yloH</i>	1641867	1642070	+	1737.88	1277.46	1.36	1841.56	2084.73	0.88	
<i>yloI</i>	1642151	1643371	+	242.09	200.59	1.21	473.73	464.69	1.02	
<i>priA</i>	1643368	1645785	+	296.15	285.31	1.04	541.21	543.3	1.00	
<i>def</i>	1645812	1646294	+	362.74	355.49	1.02	669.63	682.16	0.98	
<i>fmt</i>	1646299	1647252	+	607.34	588.69	1.03	950.38	1052.17	0.90	
<i>yloM</i>	1647239	1648582	+	639.17	602.95	1.06	1018.82	1041.5	0.98	
<i>yloN</i>	1648586	1649677	+	965.13	973.48	0.99	1425.23	1390.18	1.03	
<i>prpC</i>	1649684	1650448	+	546.61	640.87	0.85	1064.54	1146.34	0.93	
<i>prkC</i>	1650442	1652388	+	554.47	656.33	0.84	1178.21	1361.94	0.87	
<i>yloQ</i>	1652403	1653299	+	1157.45	910.38	1.27	1099.76	1090.57	1.01	
<i>rpe</i>	1653304	1653957	+	796.46	627.34	1.27	704.44	736.38	0.96	
<i>yloS</i>	1654030	1654674	+	437.24	315.68	1.39	456.86	504.23	0.91	
<i>rpmB</i>	1654899	1655087	-	227.66	331.29	0.69	1880.11	1970.19	0.95	
<i>yloU</i>	1655364	1655726	+	1305.03	1305.84	1.00	1952.12	2068.04	0.94	
<i>yloV</i>	1655742	1657403	+	978.59	1005.51	0.97	1435.96	1465.12	0.98	
<i>sdaAB</i>	1657542	1658204	+	533.76	491.9	1.09	420.56	379.31	1.11	
<i>sdaAA</i>	1658230	1659132	+	824.16	694.17	1.19	707.44	626.92	1.13	
<i>recG</i>	1659110	1661158	+	616.42	451.61	1.36	555.77	475.03	1.17	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ylpC</i>	1661267	1661833	+	3237.47	3696.04	0.88	2657.41	2993.98	0.89	
<i>plsX</i>	1661847	1662848	+	2174.68	2412.05	0.90	1827.17	2271.01	0.80	
<i>fabD</i>	1662867	1663820	+	2526.2	2544.47	0.99	2560.14	2977.55	0.86	
<i>fabG</i>	1663813	1664553	+	3794.07	3652.35	1.04	3499.45	4024.04	0.87	
<i>acpA</i>	1664637	1664870	+	4068.43	4536.54	0.90	5020.53	4877.47	1.03	
<i>rnc</i>	1665010	1665759	+	1338.16	1003.73	1.33	1463.12	1597.36	0.92	
<i>smc</i>	1665860	1669420	+	397.33	337.6	1.18	675.44	673.29	1.00	
<i>ftsY</i>	1669440	1670429	+	389.15	344.97	1.13	728.92	661.04	1.10	
<i>ylqB</i>	1670466	1670951	-	3772.56	4902.41	0.77	3709.54	4263.26	0.87	AbrB and SigD regulon
<i>ylxM</i>	1671128	1671460	+	4095.39	3918.23	1.05	3481.82	3985.99	0.87	
<i>ffh</i>	1671474	1672814	+	3188.14	3336.04	0.96	2909.24	3271.61	0.89	
<i>rpsP</i>	1672920	1673192	+	3512.69	4032.6	0.87	2684.41	2853.69	0.94	
<i>ylqC</i>	1673192	1673437	+	2743.39	2795.33	0.98	1359.35	1401.32	0.97	
<i>ylqD</i>	1673559	1673945	+	522.77	564.55	0.93	880.38	1084.61	0.81	
<i>rimM</i>	1673950	1674474	+	1071.26	1094.6	0.98	1201.5	1528.52	0.79	
<i>trmD</i>	1674471	1675202	+	1126.8	966.17	1.17	1127.35	1175.12	0.96	
<i>rplS</i>	1675333	1675689	+	7148.82	8018.19	0.89	6668.48	6386.26	1.04	
<i>ylqF</i>	1675832	1676680	+	313.48	330.1	0.95	441.96	600.98	0.74	
<i>rnhB</i>	1676751	1677518	+	1341.78	1365.5	0.98	1092.49	1271.79	0.86	
<i>ylqG</i>	1677550	1679280	+	1261.43	1186.22	1.06	849.95	1022.48	0.83	
<i>ylqH</i>	1679277	1679558	+	779.96	675.05	1.16	599.91	775.9	0.77	
<i>sucC</i>	1679731	1680888	+	4609.67	5112.24	0.90	4597.09	4688.07	0.98	
<i>sucD</i>	1680917	1681819	+	4474.54	5133.21	0.87	4491.92	4662.4	0.96	
<i>smf</i>	1681880	1682773	+	343.22	429.86	0.80	511.03	744.78	0.69	
<i>topA</i>	1682961	1685036	+	869.01	863.03	1.01	1194.4	1350.82	0.88	
<i>gid</i>	1685112	1686419	+	382.36	306.4	1.25	741.3	678.09	1.09	
<i>codV</i>	1686487	1687401	+	1121.04	867.89	1.29	1538.15	1393.68	1.10	
<i>clpQ</i>	1687414	1687959	+	985.43	787.71	1.25	1523.74	1451.6	1.05	
<i>clpY</i>	1687976	1689379	+	1576.74	1245.99	1.27	2045.45	1870.42	1.09	
<i>codY</i>	1689419	1690198	+	1390.23	1109.02	1.25	1765.66	1569.78	1.12	
<i>flgB</i>	1690578	1690967	+	1484.87	1645.08	0.90	1124.35	1408.21	0.80	Spo0A and SigD regulon
<i>flgC</i>	1690967	1691419	+	2517.28	2861.37	0.88	2093.4	2313.23	0.90	
<i>fliE</i>	1691430	1691750	+	1547.12	1810.43	0.85	1450.16	1614.91	0.90	
<i>fliF</i>	1691796	1693406	+	2404.63	2526.68	0.95	2131.24	2398.93	0.89	
<i>fliG</i>	1693419	1694435	+	2517.35	2538.6	0.99	2196.5	2421.27	0.91	
<i>fliH</i>	1694553	1695179	+	2613.13	2696.69	0.97	2389.63	2613.15	0.91	
<i>fliI</i>	1695166	1696488	+	1993.22	2101.44	0.95	2033.02	2228.03	0.91	
<i>fliJ</i>	1696491	1696934	+	2556.67	2663.18	0.96	2374.29	2717.94	0.87	
<i>ylxF</i>	1696946	1697587	+	1836.37	1872.47	0.98	2047.08	2178.76	0.94	
<i>fliK</i>	1697748	1699037	+	1457.05	1530.04	0.95	1747.05	1795.72	0.97	
<i>ylxG</i>	1699034	1699456	+	1424.84	1503.87	0.95	1800.29	1767.95	1.02	
<i>flgE</i>	1699478	1700272	+	2187.06	2312.69	0.95	2741.23	2788.65	0.98	
<i>fliL</i>	1700524	1700946	+	1770.01	1745.8	1.01	1972.06	2163.12	0.91	
<i>fliM</i>	1700980	1701978	+	2552.58	2805.25	0.91	2848.31	2794.79	1.02	
<i>fliY</i>	1701968	1703104	+	2415.43	2629.28	0.92	2736.22	2762.82	0.99	
<i>cheY</i>	1703130	1703492	+	2214.12	2356.31	0.94	2485.66	2444.01	1.02	
<i>fliZ</i>	1703507	1704166	+	1970.31	2147.35	0.92	2151.42	2295.9	0.94	
<i>fliP</i>	1704159	1704824	+	1657.23	1791.48	0.93	1916.97	2081.79	0.92	
<i>fliQ</i>	1704839	1705108	+	1434	1541.25	0.93	1729.43	1891.59	0.91	
<i>fliR</i>	1705116	1705895	+	1216.01	1323.41	0.92	1444.02	1599.45	0.90	
<i>flhB</i>	1705895	1706977	+	1345.1	1512.39	0.89	1645.75	1814.65	0.91	
<i>flhA</i>	1707010	1709043	+	1208.45	1331.03	0.91	1489.73	1656.54	0.90	
<i>flhF</i>	1709043	1710143	+	1198.51	1372.7	0.87	1607.55	1700.18	0.95	
<i>ylxH</i>	1710134	1711030	+	941.77	1064.19	0.88	1292.64	1386.99	0.93	
<i>cheB</i>	1711032	1712105	+	1211.81	1347.09	0.90	1665.24	1743.71	0.95	
<i>cheA</i>	1712111	1714126	+	1699.68	1960.67	0.87	1983.13	2010.3	0.99	
<i>cheW</i>	1714148	1714618	+	2062.56	2507.8	0.82	2603.56	2618.29	0.99	
<i>cheC</i>	1714637	1715266	+	1980.94	2239.14	0.88	1952.95	1969.54	0.99	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>cheD</i>	1715263	1715763	+	1515.21	1716.25	0.88	1636.15	1633.89	1.00	
<i>sigD</i>	1715786	1716550	+	2202.95	2435.11	0.90	2402.24	2344.86	1.02	
<i>ylxL</i>	1716579	1717082	+	1855.18	1969.52	0.94	1855.84	1810.99	1.02	
<i>rpsB</i>	1717226	1717966	+	3967.72	4000.68	0.99	4024.71	4069.03	0.99	
<i>tsf</i>	1718068	1718949	+	3057.32	3164.95	0.97	3873.1	4131.84	0.94	
<i>pyrH</i>	1719095	1719817	+	1137.01	1049.89	1.08	2026	2306.76	0.88	
<i>frr</i>	1719819	1720376	+	592.42	545.08	1.09	1190.06	1344.25	0.89	
<i>uppS</i>	1720507	1721289	+	845.01	811.68	1.04	1107.29	1256.74	0.88	
<i>cdsA</i>	1721293	1722102	+	429.56	370.02	1.16	707.22	833.25	0.85	
<i>dxr</i>	1722164	1723330	+	782.32	661.96	1.18	1336.87	1445.86	0.92	
<i>yluC</i>	1723321	1724589	+	1143.59	999.38	1.14	1693.88	1759.25	0.96	
<i>proS</i>	1724622	1726316	+	876.4	781.77	1.12	1506.4	1464.92	1.03	
<i>polC</i>	1726425	1730738	+	426.67	394.2	1.08	713.7	731.74	0.98	
<i>ylxS</i>	1731068	1731538	+	1237.56	1212.65	1.02	1934.6	2331.74	0.83	
<i>nusA</i>	1731573	1732688	+	1759.64	1714.4	1.03	2517.21	2903.65	0.87	
<i>ylxR</i>	1732702	1732977	+	1810.77	1951.09	0.93	3155.74	3413.21	0.92	
<i>ylxQ</i>	1732979	1733281	+	2016.68	2170.33	0.93	3545.46	3614.49	0.98	
<i>infB</i>	1733301	1735451	+	2157.57	2449.33	0.88	2837.15	3004.82	0.94	
<i>ylxP</i>	1735448	1735726	+	4356.19	4284.9	1.02	3291.49	3150.1	1.04	
<i>rbfA</i>	1735743	1736096	+	527.05	531.73	0.99	566.84	533.24	1.06	
<i>truB</i>	1736178	1737107	+	781.12	719.25	1.09	665.13	743.44	0.89	
<i>ribC</i>	1737126	1738076	+	1387.08	1214.35	1.14	1292.96	1305.85	0.99	
<i>rpsO</i>	1738233	1738502	+	1596.76	2088.62	0.76	3644.1	3771.93	0.97	
<i>pnpA</i>	1738675	1740792	+	1823.19	1772.03	1.03	2182.05	2394.26	0.91	
<i>ylxY</i>	1740910	1741869	+	167.4	155.09	1.08	404.58	434.5	0.93	
<i>mlpA</i>	1741909	1743138	+	239.71	231.96	1.03	504.76	523.64	0.96	
<i>ymxH</i>	1743216	1743473	+	37.16	47.12	0.79	49.84	48.4	1.03	
<i>spoVFA</i>	1743659	1744552	+	44.25	48.78	0.91	34.19	41.17	0.83	
<i>spoVFB</i>	1744555	1745157	+	58.92	62.33	0.95	46.07	48.27	0.95	
<i>asd</i>	1745283	1746323	+	2119.83	1959.59	1.08	2396.12	2734.91	0.88	
<i>dapG</i>	1746415	1747629	+	1194.13	961.16	1.24	1856.45	1743.07	1.07	
<i>dapA</i>	1747660	1748532	+	1837.8	1598.27	1.15	2444.14	2226.02	1.10	
<i>ymfA</i>	1748830	1750377	+	1666.77	1435.78	1.16	2157.14	2118.83	1.02	
<i>tepA</i>	1750559	1751230	+	76.95	73.09	1.05	93.97	98.28	0.96	
<i>spolIII</i>	1751569	1753932	+	599.43	539	1.11	556.06	592.21	0.94	
<i>ymfC</i>	1754075	1754800	+	728.21	847.83	0.86	811.39	1068.5	0.76	
<i>ymfD</i>	1754939	1755313	+	88.83	98.47	0.90	83.22	110.98	0.75	
<i>ymfE</i>	1755565	1756149	+	55.29	58.1	0.95	80.39	83.07	0.97	
<i>ymfF</i>	1756424	1756756	+	894.41	771.55	1.16	1078.36	1325.68	0.81	
<i>ymfG</i>	1756821	1757543	+	1061.31	1028.39	1.03	1554.63	1623.95	0.96	
<i>ymfH</i>	1757626	1758873	+	846.69	869.93	0.97	1297.32	1267.22	1.02	
<i>ymfI</i>	1758928	1759656	+	178.89	180.87	0.99	261.76	226.71	1.15	
<i>ymfJ</i>	1759737	1759994	+	100.28	115.54	0.87	219.79	176.12	1.25	
<i>ymfK</i>	1760138	1760638	+	741.53	817.23	0.91	488.78	601.98	0.81	
<i>ymfL</i>	1760526	1760912	+	1200.49	1322.76	0.91	907.15	1189.38	0.76	
<i>ymfM</i>	1760979	1761620	+	813.02	935.1	0.87	875.41	977.19	0.90	
<i>pgsA</i>	1761895	1762476	+	316.84	258.61	1.23	541.46	521.35	1.04	
<i>cinA</i>	1762494	1763744	+	624.93	510.68	1.22	1050.13	951.32	1.10	
<i>recA</i>	1763917	1764960	+	2125.72	1936.35	1.10	2366.26	2383.02	0.99	
<i>bbpX</i>	1765128	1766303	+	171.1	163.75	1.04	431.66	421.61	1.02	
<i>ymdA</i>	1766580	1768142	+	4079.88	4158.32	0.98	3992.4	4062.52	0.98	
<i>ymdB</i>	1768211	1769005	+	510.74	509.94	1.00	732.59	804.2	0.91	
<i>spoVS</i>	1769205	1769465	+	1109.37	1138.4	0.97	1344.85	1485.79	0.91	
<i>tdh</i>	1769731	1770774	+	111.52	141.45	0.79	120.93	148.92	0.81	
<i>kbl</i>	1770787	1771965	+	104.19	135.33	0.77	98.78	123.51	0.80	
<i>ymcB</i>	1772113	1773642	+	1436.3	1260.5	1.14	1772.27	1711.77	1.04	
<i>ymcA</i>	1773644	1774075	+	798.57	915.59	0.87	1203.93	1083.1	1.11	
<i>cotE</i>	1774337	1774882	+	80.27	79.5	1.01	82.75	85.27	0.97	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>mutS</i>	1775015	1777591	+	318.61	253.59	1.26	454.67	519.55	0.88	
<i>mutL</i>	1777607	1779490	+	497.23	438.76	1.13	763.11	746.52	1.02	
<i>ymzD</i>	1779888	1780343	-	251.14	305.57	0.82	256.49	336.38	0.76	
<i>ymcC</i>	1780498	1781055	-	62.37	66.85	0.93	73.3	79.87	0.92	
<i>pksA</i>	1781176	1781793	+	149.28	152.64	0.98	181.01	265.06	0.68	
<i>pksB</i>	1781983	1782660	+	333.11	272.84	1.22	298.92	292.85	1.02	
<i>pksC</i>	1783033	1783899	+	443.44	454.54	0.98	525.24	578.66	0.91	
<i>pksD</i>	1784403	1785293	+	294.59	240.8	1.22	308.61	359.52	0.86	
<i>pksE</i>	1785290	1787593	+	387.41	308.71	1.25	432.74	512.16	0.84	
<i>acpK</i>	1787654	1787902	+	268.85	215.9	1.25	307.95	354.8	0.87	
<i>pksF</i>	1787880	1789130	+	260.86	231.74	1.13	319.1	341.18	0.94	
<i>pksG</i>	1789131	1790393	+	212.59	206.64	1.03	334.96	367.69	0.91	
<i>pksH</i>	1790381	1791160	+	173.52	173.97	1.00	260.02	289.54	0.90	
<i>pksI</i>	1791200	1791949	+	126.33	128.35	0.98	210.55	257.6	0.82	
<i>pksJ</i>	1791994	1807131	+	288.08	301.54	0.96	361.53	355.08	1.02	
<i>pksL</i>	1807146	1820731	+	459.13	453.42	1.01	471.19	437.59	1.08	
<i>pksM</i>	1820747	1833535	+	339.05	335.71	1.01	357.38	327.03	1.09	
<i>pksN</i>	1833603	1850069	+	390.14	380.75	1.02	450.61	388.61	1.16	
<i>pksR</i>	1850084	1857715	+	477.98	443.97	1.08	533.96	448.18	1.19	
<i>pksS</i>	1857854	1858984	-	664.25	538.91	1.23	606.07	601.72	1.01	
<i>ymzB</i>	1859209	1859565	-	831.45	577.9	1.44	677.17	445.7	1.52	AbrB regulon
<i>ymaE</i>	1859644	1860342	-	409.21	390.58	1.05	694.88	580.96	1.20	AbrB regulon
<i>aprX</i>	1860580	1861908	-	85.57	85.06	1.01	73.62	82.46	0.89	
<i>ymaC</i>	1862644	1863351	+	97.09	100.14	0.97	110.54	124.99	0.88	
<i>ymaD</i>	1863421	1863873	+	107.59	118.16	0.91	220.92	195.85	1.13	
<i>ebrB</i>	1863887	1864240	-	76.69	80.78	0.95	62.6	64.49	0.97	
<i>ebrA</i>	1864254	1864571	-	54.58	61.44	0.89	55.67	59.33	0.94	
<i>ymaG</i>	1864708	1865079	-	40.04	41.83	0.96	38.42	45.32	0.85	
<i>ymaF</i>	1865072	1865485	+	46.83	46.39	1.01	41.61	51.28	0.81	
<i>miaA</i>	1865584	1866528	+	348.97	251.03	1.39	331.35	297.36	1.11	
<i>ymaH</i>	1866568	1866789	+	461.17	502.19	0.92	751.06	958.5	0.78	
<i>ymzC</i>	1866985	1867257	+	251.25	213.79	1.18	306.77	318.1	0.96	
<i>ymzA</i>	1867339	1867569	+	439.6	426.4	1.03	645.67	650.98	0.99	
<i>ymaA</i>	1867812	1868204	+	463.23	365.86	1.27	865.74	1083.44	0.80	
<i>nrdE</i>	1868164	1870266	+	757.54	580.87	1.30	1457.6	1602.28	0.91	
<i>nrdF</i>	1870284	1871273	+	677.09	596.08	1.14	1313.37	1346.36	0.98	
<i>ymaB</i>	1871323	1871943	+	319.3	294.73	1.08	733.24	708.36	1.04	
<i>cwlC</i>	1872007	1872774	-	44.14	50.11	0.88	52.5	51.73	1.01	
<i>spoVK</i>	1873398	1874366	+	82.93	83.55	0.99	89.05	95.26	0.93	
<i>ynbA</i>	1874587	1875591	+	476.96	394.43	1.21	629.49	617.27	1.02	
<i>ynbB</i>	1875779	1877044	+	473.62	328.54	1.44	811.87	672.98	1.21	
<i>glnR</i>	1877155	1877562	+	1561.48	1783.04	0.88	1153.09	1151.33	1.00	
<i>glnA</i>	1877623	1878957	+	4131.37	4792.31	0.86	4123.72	4290.71	0.96	
<i>ynxB</i>	1879285	1879575	+	126.05	141.65	0.89	120.2	111.03	1.08	
<i>ynzF</i>	1879821	1880165	+	412.64	367.34	1.12	414.32	364.59	1.14	
<i>ynzG</i>	1880296	1880547	+	72.22	64.66	1.12	60.06	58.83	1.02	
<i>ynaB</i>	1880867	1881178	+	519.8	404.99	1.28	627.36	495.26	1.27	
<i>ynaC</i>	1881248	1882039	+	338.05	274.98	1.23	463.75	391.73	1.18	
<i>ynaD</i>	1882374	1882886	+	40.19	43.25	0.93	69.35	75.16	0.92	
<i>ynaE</i>	1883446	1884087	+	139.95	143.22	0.98	150.85	190.23	0.79	
<i>ynaF</i>	1884176	1884529	+	101.47	98.91	1.03	100.41	130.9	0.77	
<i>ynaG</i>	1884573	1884848	+	117.24	104.81	1.12	131.99	141.02	0.94	
<i>ynaI</i>	1885265	1885735	+	47.65	45.56	1.05	55.69	63.31	0.88	
<i>xynP</i>	1886560	1887951	+	34.84	44.54	0.78	38.06	42.03	0.91	
<i>xynB</i>	1887982	1889583	+	58.47	57.72	1.01	57.3	60.53	0.95	
<i>xylR</i>	1889720	1890772	-	168.31	155.86	1.08	183.5	182.86	1.00	
<i>xylA</i>	1891116	1892453	+	82.87	143.42	0.58	84.65	105	0.81	
<i>xylB</i>	1892604	1894103	+	84.14	93.4	0.90	86.35	90.88	0.95	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yncB</i>	1894586	1895221	-	120.58	123.14	0.98	168.02	158.57	1.06	
<i>yncC</i>	1895632	1896891	+	54.36	69.4	0.78	52.37	61.61	0.85	
<i>yncD</i>	1897149	1898333	-	67.4	76.7	0.88	59.6	73.68	0.81	
<i>yncE</i>	1898797	1899258	+	89.57	87.72	1.02	138.01	129.45	1.07	
<i>yncF</i>	1899288	1899722	+	183.7	170.58	1.08	261.51	284.51	0.92	
<i>ynzH</i>	1900326	1900586	-	28.36	35.23	0.80	34.44	37.5	0.92	
<i>thyA</i>	1901428	1902267	+	139	130.44	1.07	191.46	207.63	0.92	
<i>yncM</i>	1902720	1903472	-	1301.94	1443.74	0.90	1212.88	1276.11	0.95	AbrB regulon
<i>cotC</i>	1904204	1904560	-	31.69	36.2	0.88	44.33	48.27	0.92	
<i>tatAC</i>	1904579	1904767	-	310.5	328.23	0.95	282.09	290.9	0.97	
<i>yndA</i>	1905018	1905416	+	31.33	36.71	0.85	37.14	39.78	0.93	
<i>yndB</i>	1905481	1905915	-	393.78	406.62	0.97	485.48	569.47	0.85	
<i>ynzB</i>	1906222	1906410	+	52.63	56.46	0.93	76.16	85.79	0.89	
<i>yndD</i>	1906703	1908265	+	64.07	57.63	1.11	43.67	46.89	0.93	
<i>yndE</i>	1908295	1909386	+	55.91	50.45	1.11	44.01	46.44	0.95	
<i>yndF</i>	1909376	1910590	+	96.8	99.6	0.97	86.89	95.49	0.91	
<i>yndG</i>	1910737	1911543	+	209.42	159.55	1.31	336.7	282.81	1.19	
<i>yndH</i>	1911548	1912165	+	198.04	142.82	1.39	268.77	242.92	1.11	
<i>yndJ</i>	1912162	1913802	+	189.56	137.85	1.38	322.96	265.7	1.22	
<i>yndK</i>	1913839	1914204	+	211.85	154.17	1.37	324.2	286.45	1.13	
<i>yndL</i>	1914430	1915188	+	56.27	64.5	0.87	46.15	64.27	0.72	
<i>yndM</i>	1915215	1915754	-	25.83	31.25	0.83	31.3	30.87	1.01	
<i>yndN</i>	1915872	1916306	+	553.81	468.93	1.18	774.15	617.21	1.25	
<i>lexA</i>	1916848	1917465	-	1195.51	1285.25	0.93	884.81	1206.13	0.73	
<i>yneA</i>	1917615	1917932	+	200.67	116.96	1.72	186.88	146.65	1.27	
<i>yneB</i>	1917951	1918604	+	233.15	158.57	1.47	329.04	274.55	1.20	
<i>ynzC</i>	1918668	1918901	+	104.61	109.26	0.96	151.86	201.76	0.75	
<i>tkk</i>	1919070	1921073	+	1790.5	1746.89	1.02	2315.97	2301.51	1.01	Spo0A regulon
<i>yneE</i>	1921226	1921672	+	64.97	81.5	0.80	77.42	84.77	0.91	Spo0A regulon
<i>yneF</i>	1921758	1921976	+	598.39	646.17	0.93	1716.03	1689.11	1.02	
<i>ynzD</i>	1922050	1922223	-	136.05	122.98	1.11	262.34	306.72	0.86	AbrB regulon
<i>ccdA</i>	1922443	1923150	+	212.14	176.26	1.20	244.78	237.14	1.03	
<i>ynel</i>	1923239	1923601	+	551.22	461.64	1.19	689.1	704.15	0.98	
<i>yneJ</i>	1923680	1924171	+	357.09	395.84	0.90	496.85	557.99	0.89	
<i>yneK</i>	1924202	1924630	-	526.66	406.42	1.30	458.08	439.68	1.04	
<i>cotM</i>	1924864	1925256	-	23.22	28.38	0.82	31.84	36.7	0.87	
<i>citB</i>	1925889	1928618	+	2896.95	3674.44	0.79	3726.66	4118.6	0.90	
<i>yneN</i>	1928690	1929202	+	359.6	549.87	0.65	745.39	1081.97	0.69	
<i>tlp</i>	1929656	1929907	+	225.32	166.74	1.35	216.85	108.55	2.00	
<i>yneP</i>	1930043	1930408	+	117.84	93.4	1.26	123.45	122.14	1.01	
<i>yneQ</i>	1930424	1930723	+	143.38	136.19	1.05	256.42	237.13	1.08	
<i>yneR</i>	1930754	1931041	-	253.88	266.08	0.95	542.31	461.88	1.17	
<i>yneS</i>	1931129	1931710	-	445.25	427	1.04	453.15	558.88	0.81	
<i>yneT</i>	1931880	1932287	+	612.48	701.97	0.87	747.71	856.18	0.87	
<i>parE</i>	1932686	1934653	+	471.26	359.45	1.31	839.99	769.31	1.09	
<i>parC</i>	1934657	1937077	+	697.32	557.74	1.25	1226.97	1041.16	1.18	
<i>ynfC</i>	1937275	1937685	-	1634.33	1941.85	0.84	703.93	584.2	1.20	
<i>alsT</i>	1938134	1939531	+	322.29	332.82	0.97	508.46	670.4	0.76	
<i>bglC</i>	1939834	1941333	+	175.94	169.97	1.04	160.14	154.33	1.04	
<i>ynfE</i>	1941401	1941664	+	30.93	32.24	0.96	32.28	34.19	0.94	
<i>ynfF</i>	1941923	1943191	-	349.14	251.23	1.39	383.28	297.77	1.29	AbrB regulon
<i>xynD</i>	1943322	1944863	-	251.6	180.16	1.40	312.27	265.3	1.18	AbrB regulon
<i>yngA</i>	1945458	1945904	+	47.99	42.6	1.13	37.09	37.91	0.98	
<i>yngB</i>	1945911	1946804	+	349.26	267.95	1.30	322.24	329.35	0.98	
<i>yngC</i>	1946877	1947473	+	568.92	419.79	1.36	838.78	633.71	1.32	
<i>yngD</i>	1947522	1948721	-	63.4	66.72	0.95	59.16	62.43	0.95	
<i>yngE</i>	1948891	1950678	-	81.4	79.59	1.02	66.62	75.53	0.88	
<i>yngF</i>	1950437	1951219	-	56.72	57.66	0.98	45.68	48.24	0.95	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yngG</i>	1951240	1952139	-	63.7	60.01	1.06	44.44	59.68	0.74	
<i>yngH</i>	1952390	1953724	-	76.27	80.54	0.95	59.6	71.59	0.83	
<i>yngI</i>	1953734	1955383	-	69.07	69.9	0.99	49.45	57.88	0.85	
<i>yngJ</i>	1955427	1956569	-	82.9	80.95	1.02	55.01	64.86	0.85	
<i>ynzE</i>	1956660	1956965	-	25.34	35.1	0.72	25.2	29.91	0.84	
<i>yngK</i>	1957236	1958768	-	72.3	78.36	0.92	53.83	75.92	0.71	
<i>yngL</i>	1958904	1959296	-	45	50.83	0.89	38.82	51.42	0.75	
<i>ppsE</i>	1959407	1963246	-	375.87	406	0.93	407.91	419.29	0.97	AbrB regulon
<i>ppsD</i>	1963254	1974065	-	458.5	494.8	0.93	461.78	471.8	0.98	AbrB regulon
<i>ppsC</i>	1974090	1981757	-	489.68	534.22	0.92	494.4	518.92	0.95	AbrB regulon
<i>ppsB</i>	1981774	1989456	-	271.52	305.45	0.89	329.01	365.89	0.90	AbrB regulon
<i>ppsA</i>	1989481	1997166	-	417.3	437.29	0.95	389.08	432.15	0.90	AbrB regulon
<i>dacC</i>	1997549	1999024	-	355.55	359.27	0.99	429.22	443.74	0.97	
<i>yoxA</i>	1999058	2000035	-	286.39	304.44	0.94	360.09	378.09	0.95	
<i>yoeA</i>	2000169	2001560	-	427.07	410.44	1.04	589.72	487.04	1.21	
<i>yoeB</i>	2001846	2002391	+	3963.47	5630.05	0.70	1746.59	1508	1.16	
<i>yoeC</i>	2002869	2003156	-	105.45	75.49	1.40	91.68	118.73	0.77	
<i>yoeD</i>	2003472	2003702	-	77.38	72.65	1.07	102.02	105.43	0.97	
<i>ggt</i>	2003887	2005650	+	94.99	106.75	0.89	80.7	92.51	0.87	
<i>yofA</i>	2005751	2006608	-	111.7	84.36	1.32	165.18	171.5	0.96	
<i>yogA</i>	2006736	2007725	+	77.98	76.62	1.02	86.3	91.96	0.94	
<i>gltB</i>	2007782	2009263	-	3244.86	3739.73	0.87	3851.7	3812.86	1.01	
<i>gltA</i>	2009280	2013842	-	1960.66	2175.52	0.90	2818.7	2960.83	0.95	
<i>gltC</i>	2013989	2014891	+	268.12	257.48	1.04	202.37	273.59	0.74	
<i>proJ</i>	2014943	2016058	-	298.65	158.5	1.88	856.8	687.08	1.25	
<i>proH</i>	2016055	2016948	-	418.98	229.86	1.82	1125.53	915.15	1.23	
<i>rtp</i>	2017095	2017463	-	79.3	96.66	0.82	116.6	118.99	0.98	
<i>yoxD</i>	2017763	2018479	-	586.77	596.42	0.98	1227	1262.03	0.97	
<i>yoxC</i>	2018630	2018935	+	3940.98	3113.26	1.27	2015.8	987.06	2.04	
<i>yoxB</i>	2019006	2019776	+	1771.28	1166.12	1.52	457.58	205.57	2.23	
<i>yoaA</i>	2019820	2020317	+	1137.43	684.34	1.66	332.05	175.71	1.89	
<i>yoaB</i>	2020433	2021677	-	181.39	244.05	0.74	375.09	442.23	0.85	
<i>yoaC</i>	2021771	2023234	-	168.7	216.01	0.78	531.77	627.58	0.85	
<i>yoaD</i>	2023252	2024286	-	101.37	112.46	0.90	263.32	321.49	0.82	
<i>yoaE</i>	2024610	2026643	+	329.88	341.22	0.97	633.18	675.03	0.94	
<i>yoaF</i>	2026720	2027013	+	431.23	381.79	1.13	631.31	875.49	0.72	
<i>yoaG</i>	2027386	2027790	-	162.61	155.03	1.05	385.99	446.84	0.86	
<i>yozQ</i>	2028231	2028524	+	86.64	93.11	0.93	120.12	125.2	0.96	
<i>yoaH</i>	2028640	2030244	-	635.78	746.87	0.85	508.82	473.1	1.08	SigD regulon
<i>yoaI</i>	2030972	2032099	+	61.61	51.64	1.19	40.19	40.08	1.00	
<i>yoaJ</i>	2032136	2032834	-	201.13	236	0.85	178.51	195.92	0.91	
<i>yoaK</i>	2033104	2033781	-	71.75	73.06	0.98	97.79	98.19	1.00	
<i>pelB</i>	2033954	2034991	+	53.23	53.78	0.99	56.63	54.38	1.04	
<i>yoaM</i>	2035248	2035931	+	34.7	44.53	0.78	37.55	46.04	0.82	
<i>yoaN</i>	2036810	2037988	-	46.09	52.8	0.87	45.68	50.04	0.91	
<i>yoaO</i>	2038111	2038599	-	131.55	111.84	1.18	209.9	175.1	1.20	
<i>yoaP</i>	2038819	2039574	-	62.46	59.22	1.05	58.82	56.02	1.05	
<i>yoaQ</i>	2039882	2040238	+	33.08	34.95	0.95	32.98	35.33	0.93	
<i>yozF</i>	2040786	2041037	-	49.22	42.78	1.15	41.26	38.94	1.06	
<i>yoaR</i>	2041138	2042049	-	51.22	53.09	0.96	36.69	43.26	0.85	
<i>yoaS</i>	2042396	2042878	+	157.34	179.65	0.88	104.98	109.36	0.96	
<i>yozG</i>	2042888	2043142	+	297.35	326.04	0.91	247.77	260.47	0.95	
<i>yoaT</i>	2043248	2044042	+	126.2	148.08	0.85	135.72	133.84	1.01	
<i>yoaU</i>	2044166	2045038	-	63.97	61.5	1.04	59.6	70.24	0.85	
<i>yoaV</i>	2045139	2046017	+	45.49	51.28	0.89	48.34	52.89	0.91	
<i>yoaW</i>	2046190	2046621	-	64.41	39.63	1.63	69.27	47.71	1.45	
<i>yoaZ</i>	2046885	2047517	-	49.45	50.95	0.97	62.87	61.75	1.02	
<i>penP</i>	2047743	2048663	+	464.48	455.48	1.02	652.38	615.21	1.06	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yobA</i>	2049160	2049522	-	65.43	74.47	0.88	104.76	94.49	1.11	
<i>yobB</i>	2049899	2050162	+	98.5	118.02	0.83	115.34	138.66	0.83	AbrB regulon
<i>pps</i>	2050539	2053139	-	129.36	142.95	0.90	214.89	213.52	1.01	
<i>xynA</i>	2053809	2054450	-	1535.4	1398.57	1.10	1597.27	1455.61	1.10	
<i>yobD</i>	2055488	2055826	+	61.33	73.23	0.84	106.17	176.76	0.60	
<i>yoZH</i>	2055860	2056180	-	22.68	21.59	1.05	20.45	19.81	1.03	
<i>yoZI</i>	2056425	2056790	+	54.32	71.41	0.76	98.18	152.72	0.64	
<i>yobE</i>	2057012	2057671	+	113.93	146.39	0.78	116.83	134.48	0.87	
<i>yobF</i>	2057926	2058849	-	176.8	175.47	1.01	172.91	190.45	0.91	
<i>yoZJ</i>	2059448	2059903	-	41.76	37.47	1.11	55.36	66.56	0.83	
<i>rapK</i>	2061361	2062476	+	494.94	433.8	1.14	751.33	864.37	0.87	AbrB regulon
<i>yobH</i>	2062721	2063332	-	54.1	55.63	0.97	48.76	50.96	0.96	
<i>yoZK</i>	2063411	2063758	-	22.81	25.38	0.90	24.04	26.96	0.89	
<i>yoZL</i>	2063751	2064044	-	15.59	24.29	0.64	18.69	19.41	0.96	
<i>yoZM</i>	2064253	2064588	+	116.88	143.33	0.82	135.95	151.68	0.90	
<i>yobI</i>	2064635	2068240	-	600.4	373.65	1.61	573.64	588.98	0.97	
<i>yobJ</i>	2069455	2070297	-	360.67	270.28	1.33	874.42	1102.75	0.79	
<i>yobK</i>	2070497	2070955	-	215.53	173.35	1.24	394.03	408.64	0.96	
<i>yobL</i>	2070965	2072767	-	312.4	287.89	1.09	428.64	564.85	0.76	
<i>yobM</i>	2072869	2073357	-	421.41	381.62	1.10	579.98	517.44	1.12	
<i>yobN</i>	2073650	2074990	+	37.67	41.32	0.91	31.33	36.56	0.86	
<i>yobO</i>	2075417	2077837	+	178.37	186	0.96	171.36	150.72	1.14	AbrB regulon
<i>csaA</i>	2078425	2078757	-	266.65	340.7	0.78	433.79	606.97	0.71	
<i>yobQ</i>	2078822	2079547	-	167.44	197.25	0.85	354.02	527.06	0.67	
<i>yobR</i>	2079562	2080305	-	210.05	240.21	0.87	346.25	494.78	0.70	
<i>yobS</i>	2080383	2080958	-	59.64	65.81	0.91	101.99	119.81	0.85	
<i>yobT</i>	2080964	2081665	-	96.65	95.16	1.02	117.8	141.11	0.83	
<i>yobU</i>	2081742	2082224	-	81.83	80.48	1.02	68.03	72.41	0.94	
<i>yobV</i>	2082278	2083219	-	94.29	104.61	0.90	129.6	132.41	0.98	
<i>yobW</i>	2083425	2083970	+	35.6	43.58	0.82	35.54	38.74	0.92	
<i>yoZA</i>	2083997	2084320	-	331.75	359.01	0.92	343.36	353.37	0.97	
<i>yoCA</i>	2084514	2085191	+	775.95	531.29	1.46	1456.48	1322.92	1.10	
<i>yoZB</i>	2085281	2085817	-	1097.71	819.58	1.34	701.34	644.15	1.09	
<i>yoCB</i>	2085954	2086736	-	3620.13	2079.03	1.74	2010.96	732.75	2.74	
<i>yoCC</i>	2086907	2087404	+	74.14	73.56	1.01	134.46	110.45	1.22	
<i>yoCD</i>	2087468	2088445	+	317.65	338.42	0.94	489.95	514.65	0.95	AbrB regulon
<i>des</i>	2088607	2089665	+	320.72	384.41	0.83	295.81	377.4	0.78	
<i>yoCF</i>	2089785	2090897	+	178.75	155.54	1.15	144.82	130.42	1.11	
<i>yoCG</i>	2090916	2091515	+	236.49	195.31	1.21	217.91	193.62	1.13	
<i>yoCH</i>	2092110	2092973	-	2335.23	1672.71	1.40	3900.98	3488.27	1.12	Spo0A regulon
<i>yoCI</i>	2093221	2094996	-	217.21	199.43	1.09	310.16	324.2	0.96	
<i>yoCJ</i>	2095561	2096187	-	784.03	799.85	0.98	805.67	776.51	1.04	
<i>yoCK</i>	2096338	2096967	-	2890	2564.4	1.13	1218.62	675.57	1.80	
<i>yoCL</i>	2096904	2097236	-	128.64	93.33	1.38	267.63	323.61	0.83	
<i>yoCM</i>	2097528	2098004	-	97.58	72.39	1.35	141.47	181.01	0.78	
<i>yoZN</i>	2098071	2098334	+	53.21	54.49	0.98	46.07	47.21	0.98	
<i>yoCN</i>	2098339	2098572	+	45.35	39.39	1.15	49.21	42.01	1.17	
<i>yoZO</i>	2098658	2099002	-	453.44	363.53	1.25	610.17	787.72	0.77	
<i>yoZC</i>	2099359	2099562	-	398.6	319.91	1.25	451.1	451.45	1.00	
<i>dhaS</i>	2099792	2101279	+	910.93	1422.35	0.64	782.97	1110	0.71	
<i>sqhC</i>	2101380	2103278	+	68.18	74.31	0.92	61.26	74.7	0.82	
<i>sodF</i>	2103268	2104113	+	92.23	97.75	0.94	80.7	94.2	0.86	
<i>yoCR</i>	2104146	2105483	-	286.63	309.22	0.93	353.58	408.58	0.87	
<i>yoCS</i>	2105702	2106667	+	479.25	606.86	0.79	523.35	520.98	1.00	
<i>odhB</i>	2106717	2107970	-	4012.53	4813.7	0.83	4439.42	4784.53	0.93	
<i>odhA</i>	2107986	2110811	-	3084.69	3750.17	0.82	3623.03	3988.68	0.91	
<i>yoJO</i>	2111039	2113024	-	312.63	249.96	1.25	619.8	608.18	1.02	
<i>yoJN</i>	2112966	2113880	-	258.9	218.24	1.19	425.99	454.07	0.94	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yojM</i>	2113944	2114534	-	292.49	315.17	0.93	417.96	527.58	0.79	
<i>yojL</i>	2114627	2115871	-	1156.81	1358.01	0.85	1573.95	2013.08	0.78	AbrB regulon
<i>yojK</i>	2116253	2117470	-	178.54	161.9	1.10	279.4	267.03	1.05	
<i>yojJ</i>	2117706	2118329	-	131.45	105.03	1.25	74.53	50.51	1.48	
<i>yojI</i>	2118594	2119952	+	116.12	108.32	1.07	203	197.72	1.03	
<i>yojH</i>	2119968	2120816	+	216.49	189.87	1.14	335.4	315.27	1.06	
<i>yojG</i>	2120842	2121270	-	945.64	823.36	1.15	1570.11	1321.89	1.19	
<i>yojF</i>	2121524	2121874	-	925.98	762.07	1.22	1222.85	1132.94	1.08	
<i>yojE</i>	2122225	2123121	-	183.65	205.38	0.89	147.36	190.35	0.77	
<i>yoZR</i>	2123220	2123693	+	44.87	53.57	0.84	37.24	44.76	0.83	
<i>yojC</i>	2123586	2123819	-	24.04	26.7	0.90	26.01	28.12	0.92	
<i>yojB</i>	2123728	2123964	-	44.05	49.89	0.88	42.78	51.76	0.83	
<i>yojA</i>	2124049	2125383	-	101.64	108.32	0.94	86.31	98.05	0.88	
<i>yodA</i>	2125748	2126137	+	74.01	74.52	0.99	85.3	97.97	0.87	
<i>yodB</i>	2126544	2126882	-	233.96	238.44	0.98	170.27	233.47	0.73	
<i>yodC</i>	2127012	2127620	+	938.05	1132.39	0.83	1017.7	1132.19	0.90	
<i>yodD</i>	2127663	2128265	-	145.74	196.19	0.74	114.04	176.26	0.65	
<i>yodE</i>	2128281	2129192	-	181.34	215.18	0.84	188.04	286.48	0.66	
<i>yodF</i>	2129576	2131066	+	720.51	796.38	0.90	1183.2	1277.76	0.93	
<i>ctpA</i>	2131101	2132501	-	1405.2	1268.51	1.11	1916.85	1887.39	1.02	
<i>yodH</i>	2132654	2133355	+	57.21	56.51	1.01	60.3	56.82	1.06	
<i>yodI</i>	2133443	2133694	+	85.11	94.53	0.90	89.48	92.18	0.97	
<i>yodJ</i>	2133765	2134586	-	542.96	443.44	1.22	931.81	786.37	1.18	
<i>deoD</i>	2134669	2135370	-	739.64	752.24	0.98	1172.22	1192.25	0.98	
<i>yodL</i>	2135737	2136054	-	234.29	183.37	1.28	260.18	218.92	1.19	
<i>yodM</i>	2136112	2136723	-	161.81	105.16	1.54	179.7	132.65	1.35	
<i>yoZD</i>	2136801	2136977	-	65.88	61.27	1.08	56.89	54.63	1.04	
<i>yodN</i>	2137236	2137916	-	52.63	57.82	0.91	52.77	54.16	0.97	
<i>yoZE</i>	2138067	2138291	-	240.66	243.03	0.99	380.03	290.11	1.31	
<i>kamA</i>	2138652	2140067	-	54.59	58.51	0.93	46.29	52.76	0.88	
<i>yodP</i>	2140096	2140923	-	52.82	53.35	0.99	52.63	53.05	0.99	
<i>yodQ</i>	2140901	2142211	-	60.28	60.59	0.99	47.86	57.62	0.83	
<i>yodR</i>	2142220	2142873	-	106.4	97.24	1.09	111.14	144.32	0.77	
<i>yodS</i>	2142858	2143547	-	56.89	60.81	0.94	45.13	56.83	0.79	
<i>yodT</i>	2143554	2144888	-	73.39	78.17	0.94	57.95	72.75	0.80	
<i>cgeE</i>	2145211	2145990	-	541.56	507.11	1.07	305.25	344.76	0.89	
<i>cgeD</i>	2146019	2147299	-	275.84	294.66	0.94	171.7	192.71	0.89	
<i>cgeC</i>	2147364	2147669	-	22.06	26.17	0.84	24.73	24.92	0.99	
<i>cgeA</i>	2147874	2148275	+	26.17	51.81	0.51	28.86	34.03	0.85	
<i>cgeB</i>	2148282	2149235	+	82.45	98.69	0.84	71.42	87	0.82	
<i>phy</i>	2149306	2150454	-	71.14	63.02	1.13	69.58	64.47	1.08	AbrB regulon
<i>yodU</i>	2150824	2151249	+	64.41	72.16	0.89	70.63	78.44	0.90	
<i>yotN</i>	2151284	2151460	-	26.12	29.76	0.88	30.09	21.57	1.39	
<i>yotM</i>	2151463	2152050	-	63.79	36.14	1.77	77.37	39.61	1.95	
<i>yotL</i>	2152125	2152367	+	38.59	53.68	0.72	64.25	57.83	1.11	
<i>yotK</i>	2152369	2152554	-	66.27	43.33	1.53	103.43	42.17	2.45	
<i>yotJ</i>	2152638	2152850	-	35.47	21.88	1.62	50.54	21.81	2.32	
<i>yotI</i>	2152916	2153278	-	51.24	33.01	1.55	74.55	37.31	2.00	
<i>yotH</i>	2153275	2153448	-	68.61	57.33	1.20	79.45	56.55	1.40	
<i>yotG</i>	2153464	2153781	-	45.09	33.19	1.36	50.7	30.59	1.66	
<i>yotC</i>	2154256	2154447	-	61.01	44.86	1.36	62.53	41.22	1.52	
<i>yotB</i>	2154491	2155318	-	69.85	44.93	1.55	79.61	42.17	1.89	
<i>sspC</i>	2155437	2155655	+	35.28	44.64	0.79	40.43	46.49	0.87	
<i>yosX</i>	2155955	2156308	-	91.89	52.83	1.74	124.99	60.04	2.08	
<i>yosW</i>	2156539	2156880	-	55.88	40.26	1.39	62.69	45.53	1.38	
<i>yosV</i>	2157027	2157317	-	46.94	33.61	1.40	63	33.93	1.86	
<i>yosU</i>	2157637	2157882	+	29.63	30.53	0.97	40.9	37.62	1.09	
<i>yosT</i>	2157922	2158371	-	163.81	119.21	1.37	177.34	123.07	1.44	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yosS</i>	2158466	2158894	-	140.47	75.47	1.86	139.89	71.78	1.95	
<i>yosR</i>	2158940	2159182	-	92.52	51.2	1.81	118.48	47.77	2.48	
<i>yosP</i>	2159182	2160976	-	268.78	190.13	1.41	442.18	344.46	1.28	
<i>yosN</i>	2161309	2164812	-	88.94	53.9	1.65	113.78	56.57	2.01	
<i>yosM</i>	2164775	2165164	-	37.94	31.8	1.19	54.85	31.71	1.73	
<i>yosL</i>	2165170	2165523	-	51.79	31.88	1.62	68.37	33.68	2.03	
<i>yosK</i>	2165611	2165811	-	85.18	46.17	1.84	145.75	53.44	2.73	
<i>yosJ</i>	2165856	2166050	-	87.32	38.07	2.29	122.24	47.45	2.58	
<i>yosH</i>	2166237	2166707	-	105.06	54.92	1.91	146.36	66.23	2.21	
<i>yosG</i>	2166768	2167130	-	97.35	49.2	1.98	139.9	55.8	2.51	
<i>yosE</i>	2167312	2167659	-	54.63	30.76	1.78	60.45	30.26	2.00	
<i>yosD</i>	2167674	2168069	-	84.69	43.49	1.95	113.48	53.14	2.14	
<i>yosC</i>	2168108	2168650	-	79.33	46.35	1.71	103.82	56.03	1.85	
<i>yosB</i>	2168695	2168874	-	97.07	54.27	1.79	88.86	60.86	1.46	
<i>yorZ</i>	2169228	2169440	-	71.53	33.04	2.16	115.19	39.54	2.91	
<i>yorY</i>	2169507	2169689	-	27.68	27.13	1.02	44.19	20.13	2.20	
<i>yorX</i>	2169702	2169929	-	70.56	39.61	1.78	102.49	48.88	2.10	
<i>yorW</i>	2169969	2170334	-	74.26	33.33	2.23	107.82	45.13	2.39	
<i>yorV</i>	2170337	2170555	-	81.99	39.39	2.08	133.05	46.49	2.86	
<i>mtbP</i>	2170599	2171930	-	99.25	48.67	2.04	131.83	55.87	2.36	
<i>yorS</i>	2172130	2172648	-	56.79	42.96	1.32	88.78	46.13	1.92	
<i>yorR</i>	2172657	2173154	-	131.33	104.16	1.26	158.58	87.75	1.81	
<i>yorQ</i>	2173154	2173309	-	235.46	206.13	1.14	308.89	187.39	1.65	
<i>yorP</i>	2173302	2173517	-	162.95	143.33	1.14	181.95	122.69	1.48	
<i>yorO</i>	2173550	2173747	-	208.95	150.33	1.39	203.1	142.82	1.42	
<i>yorM</i>	2174048	2174764	-	56.42	38.22	1.48	75.13	48.21	1.56	
<i>yorL</i>	2174792	2178709	-	67.03	46.44	1.44	70.31	49.01	1.43	
<i>yorK</i>	2178722	2180452	-	52.93	36.22	1.46	66.97	41.32	1.62	
<i>yorJ</i>	2180452	2181588	-	52.49	33	1.59	68.25	37.48	1.82	
<i>yorI</i>	2181604	2183118	-	73.17	42.14	1.74	90.36	46.02	1.96	
<i>yorH</i>	2183133	2183603	-	74.15	40.26	1.84	105.59	49.99	2.11	
<i>yorG</i>	2183646	2184617	-	126.47	53.72	2.35	180.67	71.39	2.53	
<i>yorF</i>	2184700	2185614	-	131.81	49.03	2.69	179.19	80.78	2.22	
<i>yorE</i>	2185636	2186007	-	135.27	48.64	2.78	208.61	137.96	1.51	
<i>yorD</i>	2186181	2186495	-	1393.98	1468.85	0.95	1864.36	2305.35	0.81	AbrB regulon
<i>yorC</i>	2186572	2186952	-	355.47	184.81	1.92	414.4	280.02	1.48	
<i>yorB</i>	2187015	2187311	-	1456.26	779.96	1.87	1423.7	996.36	1.43	
<i>yorA</i>	2187400	2189160	-	178.23	104.51	1.71	131.8	73.58	1.79	
<i>yoqZ</i>	2189157	2189981	-	161.66	108.75	1.49	150.05	77.14	1.95	
<i>yoqY</i>	2190080	2190475	-	38.74	36	1.08	52.01	35.82	1.45	
<i>yoqX</i>	2190530	2190751	-	32.88	32.24	1.02	42.94	30.83	1.39	
<i>yoqW</i>	2190822	2191496	+	127.85	163.38	0.78	128.67	151.49	0.85	
<i>ligB</i>	2191566	2192378	+	28.36	29.28	0.97	31.01	31.25	0.99	
<i>yoqU</i>	2192444	2192857	-	43.47	33.64	1.29	53.19	40.86	1.30	
<i>yoqT</i>	2193023	2193172	+	17.54	19.26	0.91	19.28	20.61	0.94	
<i>yoqS</i>	2193249	2193596	-	77.13	48.7	1.58	85.23	65.45	1.30	
<i>yoqR</i>	2193598	2193954	-	64.78	37.42	1.73	76.32	48.96	1.56	
<i>yoqP</i>	2193914	2194255	-	65.1	51.55	1.26	71.93	54.63	1.32	
<i>yoqO</i>	2194369	2194743	+	111.77	144.92	0.77	211.97	192.52	1.10	
<i>yoqN</i>	2194760	2194978	-	90.25	59.52	1.52	81.1	66.14	1.23	
<i>yoqM</i>	2195182	2195460	+	298.51	267.51	1.12	170.78	150.72	1.13	AbrB regulon
<i>yoqL</i>	2195585	2196277	-	58.09	43	1.35	69.23	55.44	1.25	
<i>yoqK</i>	2196317	2196520	-	73.87	45.08	1.64	77.1	53.92	1.43	
<i>yoqJ</i>	2196540	2197055	-	97.35	61.63	1.58	93.05	66.44	1.40	
<i>yoqI</i>	2197266	2197460	-	69	44.64	1.55	59	47.69	1.24	
<i>yoqH</i>	2197509	2197961	-	67.66	53.29	1.27	71.1	51.65	1.38	
<i>yoqG</i>	2198044	2198301	-	81.09	54.49	1.49	90.39	71.29	1.27	
<i>yoqF</i>	2198346	2198549	-	59.25	54.05	1.10	66.53	44.33	1.50	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yqE</i>	2198558	2198722	-	115.78	70.02	1.65	106.72	99.2	1.08	
<i>yqD</i>	2198776	2199531	-	75.97	59.15	1.28	90.56	72.95	1.24	
<i>yqC</i>	2199572	2199979	-	51.24	46.58	1.10	67.3	50.8	1.32	
<i>yqB</i>	2199986	2200324	-	57.31	44.27	1.29	73.97	53.68	1.38	
<i>yqA</i>	2200321	2200671	-	98.68	75.71	1.30	118.07	84.35	1.40	
<i>yopZ</i>	2200684	2200887	-	85.18	60.39	1.41	74.75	73.09	1.02	
<i>yopY</i>	2200901	2201179	-	174.1	127.7	1.36	164.55	138.12	1.19	
<i>yopX</i>	2201176	2201580	-	91.44	74.4	1.23	85.5	79.76	1.07	
<i>yopW</i>	2201577	2201912	-	56.72	43.54	1.30	57.83	48.16	1.20	
<i>yopV</i>	2202001	2202195	-	54.58	51.2	1.07	98.73	104	0.95	
<i>yopU</i>	2202307	2202504	-	104.87	71.33	1.47	120.36	129.4	0.93	
<i>yopT</i>	2202574	2202792	-	313.23	187.75	1.67	332.63	309.83	1.07	
<i>yopS</i>	2202975	2203199	+	50.55	45.66	1.11	71.78	98.73	0.73	
<i>yopR</i>	2203388	2204365	-	419.98	395.9	1.06	575.07	583.11	0.99	
<i>yopQ</i>	2204389	2205771	-	454.94	435.46	1.04	534.53	628.99	0.85	
<i>yopP</i>	2205878	2206954	-	203.36	194.23	1.05	165.3	240.28	0.69	
<i>yopO</i>	2206944	2207156	-	122.8	98.91	1.24	84.16	100.16	0.84	
<i>yopN</i>	2207204	2207521	-	182.99	178.38	1.03	240.15	279.31	0.86	
<i>yopM</i>	2207524	2207724	-	138.78	105.47	1.32	128.35	154.32	0.83	
<i>yopK</i>	2208190	2209350	-	130.23	116.34	1.12	148.14	169.89	0.87	
<i>yopJ</i>	2209527	2209943	-	256.61	192.94	1.33	385.93	419.88	0.92	
<i>yopI</i>	2209945	2210478	-	355.6	270.06	1.32	336.97	373.68	0.90	
<i>yopH</i>	2210505	2211041	-	279.61	240.15	1.16	226.73	284.71	0.80	
<i>yopF</i>	2211222	2211437	-	146.97	132.6	1.11	168.55	233.39	0.72	
<i>yopE</i>	2211441	2211692	-	238.19	182.17	1.31	185	284.07	0.65	
<i>yopD</i>	2212279	2212674	-	555.66	472.05	1.18	550.78	573.42	0.96	
<i>yopC</i>	2212732	2214060	-	328.87	289.95	1.13	358.6	407.5	0.88	
<i>yopB</i>	2214168	2214395	-	51.07	49.89	1.02	61.59	67.09	0.92	
<i>yopA</i>	2214656	2215972	-	274.12	228.88	1.20	281.25	243.18	1.16	
<i>yonX</i>	2216329	2216835	-	47.06	35.81	1.31	45.22	35.07	1.29	
<i>yonV</i>	2217163	2218395	-	34.87	34.07	1.02	38.54	34.69	1.11	
<i>yonU</i>	2218477	2218665	-	1104.59	1105.47	1.00	1176.3	1068.96	1.10	
<i>yonT</i>	2218980	2219156	-	58.86	90.59	0.65	60.65	72.37	0.84	
<i>yonS</i>	2219531	2220142	-	297.44	296.53	1.00	530.02	610.67	0.87	
<i>yonR</i>	2220257	2220583	-	189.38	212.17	0.89	200.19	254.29	0.79	
<i>yonP</i>	2221536	2221730	+	47.17	29.76	1.59	72.17	31.63	2.28	
<i>yonO</i>	2221770	2224289	+	48.88	29.33	1.67	64.54	33.25	1.94	
<i>yonN</i>	2224533	2224811	+	161.98	78.34	2.07	278.56	120.17	2.32	
<i>yonK</i>	2226493	2226684	+	71.34	27.57	2.59	90.27	33.55	2.69	
<i>yonJ</i>	2226701	2227918	+	156.86	57.3	2.74	229.37	72.47	3.17	
<i>yonI</i>	2227952	2228362	-	209.78	202.24	1.04	234.02	244.54	0.96	
<i>yonH</i>	2228581	2229081	+	101.07	40.7	2.48	143.22	45.57	3.14	
<i>yonG</i>	2229184	2230104	+	46.71	38.42	1.22	52.94	33.96	1.56	
<i>yonF</i>	2230091	2231860	+	60.18	36.6	1.64	80.26	35.82	2.24	
<i>yonE</i>	2231878	2233398	+	96.24	44.49	2.16	134.92	54.23	2.49	
<i>yonD</i>	2233429	2234865	+	365.02	99.12	3.68	453.3	116.88	3.88	
<i>yonC</i>	2234890	2235426	+	238.53	71.53	3.33	348.53	82.64	4.22	
<i>yonB</i>	2235465	2236481	+	322.42	83.73	3.85	431.16	95.66	4.51	
<i>yonA</i>	2236517	2236987	+	354.71	86.13	4.12	493.18	112.91	4.37	
<i>yomZ</i>	2237002	2237397	+	214.35	51.27	4.18	311.91	64.01	4.87	
<i>yomY</i>	2237394	2237648	+	271.84	59.81	4.55	389.75	79.4	4.91	
<i>yomX</i>	2237632	2238282	+	258.15	59.05	4.37	363.23	72.69	5.00	
<i>yomW</i>	2238279	2238785	+	338.69	73.48	4.61	461	79.29	5.81	
<i>yomV</i>	2238782	2239492	+	244.93	59.44	4.12	344.42	69.29	4.97	
<i>yomU</i>	2239535	2240332	+	253.49	66.94	3.79	364.79	81.52	4.47	
<i>yomT</i>	2240961	2241188	+	73.81	43.76	1.69	111.27	42.81	2.60	
<i>yomS</i>	2241252	2241608	+	122.6	48.36	2.54	154.05	47.69	3.23	
<i>yomR</i>	2241610	2242827	+	161.33	58.08	2.78	215.31	54.95	3.92	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yomQ</i>	2242838	2243188	+	205.57	64.62	3.18	265.63	74.68	3.56	
<i>yomP</i>	2243185	2243376	+	91.61	31.95	2.87	98.73	32.59	3.03	
<i>yomO</i>	2243426	2243926	+	101.2	39.47	2.56	119.04	38.82	3.07	
<i>yomN</i>	2243910	2244329	+	152.23	54.81	2.78	224.14	60.51	3.70	
<i>yomM</i>	2244343	2245344	+	119.22	49.33	2.42	163.85	49.84	3.29	
<i>yoZP</i>	2245347	2245676	-	47.4	53.48	0.89	74.66	76.68	0.97	
<i>yomL</i>	2245852	2246538	-	868.76	854.23	1.02	1371.66	1120.38	1.22	
<i>yomK</i>	2247085	2247531	+	2114.11	2081.89	1.02	1273.52	1425.18	0.89	
<i>yomJ</i>	2247613	2248296	+	1201.44	1210.97	0.99	941.98	1070.07	0.88	AbrB regulon
<i>yomI</i>	2248350	2255207	+	60.34	42.77	1.41	70.42	44.2	1.59	
<i>yomH</i>	2255258	2256016	+	37.64	24.65	1.53	59.32	26.84	2.21	
<i>yomG</i>	2256028	2258655	+	72.82	49.36	1.48	90.91	53.64	1.69	
<i>yomF</i>	2258671	2259492	+	56.88	32.6	1.74	76.09	36.06	2.11	
<i>yomE</i>	2259529	2261463	+	61.6	38.12	1.62	86.38	37.46	2.31	
<i>yomD</i>	2261633	2262457	+	51.4	25.62	2.01	70.03	27.1	2.58	
<i>blyA</i>	2262685	2263788	+	51.24	32.16	1.59	69.99	32.08	2.18	
<i>bhlA</i>	2263876	2264088	+	37.81	24.95	1.52	38.08	27.8	1.37	
<i>bhlB</i>	2264099	2264365	+	22.61	23.63	0.96	25.15	20.37	1.23	
<i>bdbB</i>	2264421	2264867	-	188.81	199.66	0.95	395.71	479.51	0.83	AbrB regulon
<i>yoJ</i>	2264864	2266132	-	500.2	371.65	1.35	673.11	815.56	0.83	AbrB regulon
<i>bdbA</i>	2266132	2266545	-	301.84	179.24	1.68	386.59	550.45	0.70	AbrB regulon
<i>sunT</i>	2266542	2268659	-	261.84	171.55	1.53	394.47	522.87	0.75	AbrB regulon
<i>sunA</i>	2268717	2268887	-	4302.2	4130.85	1.04	6892.81	5381.96	1.28	AbrB regulon
<i>yoIF</i>	2269184	2269501	-	1089.39	1343.44	0.81	1072.87	1395.33	0.77	
<i>uvrX</i>	2269603	2270853	-	49.46	54.7	0.90	53.33	49.56	1.08	
<i>yoID</i>	2270846	2271178	-	25.11	28.88	0.87	30.84	28.08	1.10	
<i>yoIC</i>	2271352	2271687	+	188.22	188.26	1.00	220.89	245.3	0.90	AbrB regulon
<i>yoIB</i>	2271730	2272086	-	1620.73	1919.62	0.84	1603.51	1822.26	0.88	AbrB regulon
<i>yoIA</i>	2272092	2272559	-	4303.84	4868.8	0.88	3785.57	4257.12	0.89	AbrB regulon
<i>yokL</i>	2273185	2273718	-	249.07	207	1.20	374.94	420.9	0.89	AbrB regulon
<i>yokK</i>	2273754	2274332	-	377.54	302.41	1.25	552.78	592.31	0.93	AbrB regulon
<i>yokJ</i>	2274396	2274893	-	418.75	359.82	1.16	683.42	789.15	0.87	AbrB regulon
<i>yokI</i>	2274902	2276617	-	488.06	427.85	1.14	722.81	864.83	0.84	AbrB regulon
<i>yokH</i>	2276717	2277274	-	512.34	455.23	1.13	759.95	666.89	1.14	
<i>yokG</i>	2277798	2278871	-	1881.66	1607.68	1.17	1657.66	1447.27	1.15	
<i>yokF</i>	2279173	2280063	+	576.42	549	1.05	920.61	869.66	1.06	
<i>yokE</i>	2280077	2280559	+	164.67	126.04	1.31	254.77	233.78	1.09	
<i>yokD</i>	2280863	2281681	+	386.57	261.04	1.48	383.07	374.02	1.02	
<i>yokC</i>	2282332	2282847	-	103.59	105.31	0.98	105.23	123.73	0.85	
<i>yokB</i>	2283054	2283764	-	212.21	224.69	0.94	211.81	249.6	0.85	
<i>yokA</i>	2283967	2285604	+	127.02	103.42	1.23	231.59	285.38	0.81	
<i>ypqP</i>	2285626	2286249	+	110.96	93.53	1.19	230.64	239.01	0.96	
<i>ypqQ</i>	2286293	2286724	-	496.6	538.44	0.92	645.56	701.83	0.92	
<i>msrA</i>	2286725	2287258	-	662.5	679.61	0.97	551.22	625.29	0.88	
<i>ypoP</i>	2287390	2287815	+	470.48	490.1	0.96	456.57	620.03	0.74	
<i>ypnP</i>	2287865	2289202	-	67	67.37	0.99	78.03	89.56	0.87	
<i>ypmT</i>	2289274	2289468	-	104.87	101.97	1.03	187.12	170.61	1.10	
<i>ypmS</i>	2289481	2290044	-	360.01	383.55	0.94	461.84	568.23	0.81	
<i>ypmR</i>	2290054	2290821	-	454.24	527.98	0.86	556.6	776.7	0.72	
<i>ypmQ</i>	2290899	2291480	-	598.45	670.68	0.89	666.33	909.65	0.73	
<i>ypmP</i>	2291628	2291879	-	1243.31	1355.8	0.92	1811.78	2059.01	0.88	
<i>ilvA</i>	2291965	2293233	-	1043.87	1267.26	0.82	1244.42	1668.03	0.75	
<i>ypIP</i>	2293482	2294477	+	545.16	483.19	1.13	297.87	477.33	0.62	
<i>ypIQ</i>	2294498	2295139	+	792.76	716.94	1.11	407.62	543.08	0.75	
<i>ypkP</i>	2295178	2295798	-	308.54	262.87	1.17	450.24	459.28	0.98	
<i>dfirA</i>	2295799	2296305	-	303.33	240.22	1.26	377.29	405.2	0.93	
<i>thyB</i>	2296302	2297096	-	309.16	310.31	1.00	404.42	453.94	0.89	
<i>ypjQ</i>	2297180	2297713	-	705.86	836.87	0.84	781.26	917.36	0.85	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ypjP</i>	2297731	2298342	-	1013.04	996.31	1.02	729.2	895.41	0.81	
<i>ypiP</i>	2298602	2299120	-	246.09	234.45	1.05	282.77	285.68	0.99	
<i>ypbP</i>	2299417	2299851	-	646.65	565.43	1.14	963.49	952.48	1.01	
<i>ilvD</i>	2299958	2301634	-	1415.15	1797.41	0.79	2105.24	2405.42	0.88	
<i>ypgR</i>	2301923	2303056	-	743.38	629.74	1.18	1108.12	1031.54	1.07	
<i>ypgQ</i>	2303116	2303733	-	397.27	381.62	1.04	639.9	528.2	1.21	
<i>bsaA</i>	2303749	2304231	-	270.23	261.75	1.03	423.56	378.87	1.12	
<i>metA</i>	2304574	2305248	+	254.72	292.49	0.87	283.44	444.42	0.64	
<i>ugtP</i>	2305711	2306859	+	581.56	566.17	1.03	718.58	970.83	0.74	
<i>cspD</i>	2307102	2307302	+	5299.39	5873.09	0.90	7133.05	6563.31	1.09	
<i>degR</i>	2307354	2307536	-	437.98	387.96	1.13	609.31	466.07	1.31	SigD regulon
<i>ypzA</i>	2307692	2307961	+	76.11	88.51	0.86	58.53	78.72	0.74	
<i>ypeQ</i>	2307989	2308171	-	99.41	91.9	1.08	169.25	180.68	0.94	
<i>ypeP</i>	2308164	2308526	-	247.04	235.26	1.05	275.3	245.1	1.12	
<i>ypdP</i>	2308927	2309616	+	191.21	189.5	1.01	155.06	176.33	0.88	
<i>ypdQ</i>	2309616	2310014	+	312.6	280.03	1.12	337.8	358.36	0.94	
<i>ypcP</i>	2310192	2311082	-	299.89	274.54	1.09	244.24	336.65	0.73	
<i>ypbS</i>	2311404	2311661	-	840.38	1102.52	0.76	1389.99	1426.48	0.97	
<i>ypbR</i>	2311726	2315307	-	316.35	290.5	1.09	651.32	546.79	1.19	
<i>ypbQ</i>	2315643	2316149	-	35.86	45.87	0.78	45.01	51.19	0.88	
<i>bcsA</i>	2316153	2317250	-	35	38.67	0.91	35.58	45.32	0.79	
<i>pbuX</i>	2317324	2318640	-	380.01	458.18	0.83	866.13	1113.31	0.78	
<i>xpt</i>	2318637	2319221	-	572.66	674.84	0.85	1278.72	1583.84	0.81	
<i>ypwA</i>	2319552	2321057	-	1346.55	1271.26	1.06	1512.88	1265.95	1.20	
<i>kdgT</i>	2321169	2322161	-	160.36	194.5	0.82	127.2	162.58	0.78	
<i>kdgA</i>	2322206	2322796	-	150.03	198.72	0.75	150.45	187.15	0.80	
<i>kdgK</i>	2322798	2323772	-	229.04	287.51	0.80	262.52	313.29	0.84	
<i>kdgR</i>	2323810	2324829	-	288.19	325.38	0.89	298.63	404.32	0.74	
<i>kdul</i>	2325051	2325878	+	580.59	717.6	0.81	646.38	822	0.79	
<i>kduD</i>	2325880	2326644	+	275.96	348.36	0.79	279.92	360.58	0.78	
<i>ypvA</i>	2326685	2328610	-	366.3	314.27	1.17	501.27	479.97	1.04	
<i>yptA</i>	2328712	2328903	-	107.2	105.03	1.02	194.17	196.49	0.99	
<i>ypsC</i>	2329272	2330429	-	579.14	505	1.15	744.41	854.26	0.87	
<i>ypsB</i>	2330976	2331272	-	2515.52	2576.98	0.98	2376.68	2377.55	1.00	
<i>ypsA</i>	2331350	2331892	-	366.48	281.77	1.30	473.04	471.34	1.00	
<i>colD</i>	2331981	2332208	-	1096.41	739.82	1.48	1080.87	957.78	1.13	Spo0A regulon
<i>yprB</i>	2332521	2333762	-	1046.13	621.83	1.68	901.4	588.17	1.53	
<i>yprA</i>	2333778	2336027	-	379.02	242.51	1.56	659.3	483.65	1.36	
<i>ypqE</i>	2336130	2336636	-	1350.63	1001.75	1.35	1971.75	1785.2	1.10	
<i>ypqA</i>	2336774	2337193	+	38.38	36.76	1.04	31.6	36.58	0.86	
<i>yppG</i>	2337214	2337591	-	29.96	33.01	0.91	36.13	34.57	1.05	
<i>yppF</i>	2337779	2337967	+	161.78	221.88	0.73	103.9	158.15	0.66	Spo0A regulon
<i>yppE</i>	2338006	2338377	-	164.51	131.54	1.25	301.09	308.91	0.97	
<i>yppD</i>	2338423	2338668	-	44.83	49.74	0.90	41.53	52.4	0.79	Spo0A regulon
<i>yppC</i>	2338996	2339958	-	48.92	51.35	0.95	43.63	48.9	0.89	
<i>recU</i>	2339999	2340619	+	1071.01	669.87	1.60	1273.02	1197.33	1.06	
<i>ponA</i>	2340641	2343385	+	1480.33	1106.36	1.34	2112.59	1814	1.16	
<i>ypoC</i>	2343461	2343955	-	301.73	295.48	1.02	441.42	458.9	0.96	
<i>nth</i>	2343952	2344611	-	531.24	503.72	1.05	692.99	688.07	1.01	
<i>dnaD</i>	2344630	2345328	-	802.59	763.44	1.05	946.56	946.16	1.00	
<i>asnS</i>	2345421	2346713	-	1551.16	1541.29	1.01	1920.73	2095.63	0.92	
<i>aspB</i>	2346857	2348038	-	1703.52	1669.25	1.02	2800.4	2756.61	1.02	
<i>ypmB</i>	2348061	2348546	-	2264.42	2114.27	1.07	3055.48	3227.5	0.95	
<i>ypmA</i>	2348555	2348725	-	665.45	456.46	1.46	1092.15	1270.01	0.86	
<i>dinG</i>	2348868	2351663	-	440.93	341.89	1.29	833.71	924.26	0.90	
<i>panD</i>	2351789	2352172	-	928.29	868.44	1.07	863.07	838.74	1.03	
<i>panC</i>	2352174	2353034	-	1454.5	1385.97	1.05	1945.4	1684.86	1.15	
<i>panB</i>	2353036	2353869	-	1440.39	1401.12	1.03	1945.06	1721.22	1.13	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>birA</i>	2354115	2355092	-	366.51	283.68	1.29	969.52	834.29	1.16	
<i>cca</i>	2355077	2356270	-	466.32	344	1.36	1037.7	910.9	1.14	
<i>ypjH</i>	2356275	2357408	-	443.27	336.19	1.32	1024.35	923.5	1.11	
<i>ypjG</i>	2357440	2358114	-	419.75	294.58	1.42	928.19	859.92	1.08	
<i>mgsA</i>	2358107	2358520	-	565.4	415.21	1.36	1090.39	981.14	1.11	
<i>dapB</i>	2358536	2359339	-	484.03	351.05	1.38	997.75	897.38	1.11	
<i>ypjD</i>	2359351	2359686	-	478.07	393	1.22	844.38	836.69	1.01	
<i>ypjC</i>	2360051	2360698	+	238.37	204	1.17	379.09	337.61	1.12	
<i>ypjB</i>	2360740	2361534	-	226.86	204.28	1.11	322.97	317.92	1.02	
<i>ypjA</i>	2361603	2362160	-	207.85	191.79	1.08	236.48	233.11	1.01	
<i>qcrC</i>	2362307	2363074	-	1509.82	2021.13	0.75	1371	1764.46	0.78	
<i>qcrB</i>	2363109	2363783	-	1677.48	2190.43	0.77	1554.1	1963.15	0.79	
<i>qcrA</i>	2363785	2364288	-	2146.28	2803.78	0.77	2159.98	2557.66	0.84	
<i>ypjF</i>	2364431	2364877	-	354.62	530.03	0.67	432.22	622.17	0.69	
<i>ypjB</i>	2364932	2365471	-	1345.15	1897.01	0.71	1059.36	1179.71	0.90	
<i>ypjA</i>	2365543	2366814	-	426.7	322.67	1.32	480.83	401.99	1.20	
<i>aroE</i>	2367150	2368436	-	759.72	883.59	0.86	1720.77	1936.78	0.89	
<i>tyrA</i>	2368447	2369562	-	486.82	553.16	0.88	1826.27	2153.33	0.85	
<i>hisC</i>	2369611	2370693	-	802.94	734.32	1.09	1624.47	1996.55	0.81	
<i>trpA</i>	2370704	2371507	-	502	399.82	1.26	871.92	1205.23	0.72	
<i>trpB</i>	2371500	2372702	-	148.97	164.25	0.91	178.34	199.99	0.89	
<i>trpF</i>	2372683	2373330	-	149.25	158.92	0.94	172.42	189.14	0.91	
<i>trpC</i>	2373335	2374087	-	118.05	120.42	0.98	108.89	124.18	0.88	
<i>trpD</i>	2374080	2375096	-	144.5	146.26	0.99	109.79	134.15	0.82	
<i>trpE</i>	2375068	2376615	-	143.2	136.36	1.05	122.41	183.38	0.67	
<i>aroH</i>	2376831	2377214	-	1086.58	1281.09	0.85	2020.48	2459.23	0.82	
<i>aroB</i>	2377211	2378299	-	1042.11	1256.66	0.83	2204.48	2672.63	0.82	
<i>aroF</i>	2378361	2379470	-	777.59	978.52	0.79	1903.74	2391.83	0.80	
<i>cheR</i>	2379545	2380315	-	295.78	397.5	0.74	387.5	488.73	0.79	
<i>ndk</i>	2380552	2381001	-	1116.87	1788.91	0.62	1111.06	1541.8	0.72	
<i>hepT</i>	2381117	2382163	-	549.85	506.96	1.08	902.83	1293.95	0.70	
<i>menH</i>	2382105	2382806	-	883.48	829.79	1.06	1180.65	1577.18	0.75	
<i>hepS</i>	2382813	2383568	-	575.81	621.95	0.93	844.7	1254.57	0.67	
<i>mtrB</i>	2383731	2383958	-	1078.08	1141.58	0.94	1139.16	1474.41	0.77	
<i>mtrA</i>	2383980	2384552	-	1149.14	1220.1	0.94	1243.82	1369.29	0.91	
<i>hbs</i>	2384740	2385018	-	4989.47	5375.84	0.93	4469.11	4399.69	1.02	
<i>spoIVA</i>	2385392	2386870	-	69.72	82.13	0.85	75.91	89.88	0.84	
<i>yphF</i>	2387051	2387785	-	417.55	495.82	0.84	581.41	745.18	0.78	AbrB regulon
<i>yphE</i>	2387807	2388010	-	590.4	657.99	0.90	821.11	1017.68	0.81	AbrB regulon
<i>gpsA</i>	2388348	2389385	-	1181.21	1070.34	1.10	1482.86	1365.32	1.09	
<i>yphC</i>	2389403	2390713	-	1068.05	907.79	1.18	1263.85	1232.55	1.03	
<i>seaA</i>	2391058	2391951	-	129	110.42	1.17	106.81	106.63	1.00	
<i>yphA</i>	2391948	2392547	-	115.47	99.37	1.16	90.74	82.64	1.10	
<i>ypgA</i>	2392799	2393437	-	595.02	548.15	1.09	688.54	788.08	0.87	
<i>ypfD</i>	2393861	2395009	-	4551.34	4719.63	0.96	4350.11	4289.14	1.01	
<i>cmk</i>	2395242	2395916	-	572.91	652.05	0.88	635.17	907.1	0.70	
<i>ypfB</i>	2395995	2396171	-	135.66	125.16	1.08	166.2	189.3	0.88	
<i>ypfA</i>	2396216	2396869	-	297.91	314.81	0.95	380.88	461.1	0.83	
<i>ypeB</i>	2396962	2398314	-	71.74	68.26	1.05	61.82	68.15	0.91	
<i>sleB</i>	2398349	2399266	-	57.9	58.61	0.98	47.08	54.47	0.86	
<i>ypdC</i>	2399405	2400061	-	216.94	190.81	1.14	260.96	330.2	0.79	
<i>ypdA</i>	2400181	2401155	-	608.12	554.3	1.10	891.34	1031.78	0.86	
<i>gudB</i>	2401264	2402544	-	2068.41	1938.45	1.07	2487.9	2356.2	1.06	
<i>yphH</i>	2402700	2403284	-	1060.26	1260.23	0.84	878.99	936.82	0.94	
<i>yphG</i>	2403443	2404222	-	142.07	150.67	0.94	285.4	242.77	1.18	
<i>yphF</i>	2404308	2404751	-	218.61	207.25	1.05	241.76	325.84	0.74	
<i>yphE</i>	2404814	2405536	-	787.37	742.98	1.06	882.3	1078.17	0.82	
<i>yphD</i>	2405487	2406056	-	396.11	322.58	1.23	399.67	495.41	0.81	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>recQ</i>	2406116	2407606	-	611.19	534.18	1.14	672.12	767.1	0.88	
<i>ypbB</i>	2407599	2408657	-	255.15	243.16	1.05	272.89	348.47	0.78	
<i>fer</i>	2408923	2409171	+	1279.33	1451.42	0.88	1362.01	1530	0.89	
<i>ypaA</i>	2409211	2409783	-	379.25	481.16	0.79	182.02	203.75	0.89	
<i>ypzE</i>	2409889	2410053	-	785.51	922.98	0.85	225.67	300.01	0.75	
<i>serA</i>	2410280	2411857	+	1925.65	2410.53	0.80	3176.91	3835.65	0.83	
<i>aroC</i>	2411900	2412667	-	379.45	326.68	1.16	386.71	387.16	1.00	
<i>rsiX</i>	2412779	2413885	-	555.75	550.73	1.01	752.67	866.48	0.87	
<i>sigX</i>	2413821	2414405	-	676.04	767.83	0.88	953.46	1085.82	0.88	
<i>resE</i>	2414609	2416378	-	1361.42	1318.63	1.03	1012.17	1001.31	1.01	
<i>resD</i>	2416375	2417097	-	1564.7	1482.64	1.06	989.05	1048.68	0.94	
<i>resC</i>	2417178	2418236	-	970.14	860.08	1.13	446.34	505.08	0.88	
<i>resB</i>	2418372	2420000	-	907.06	749.9	1.21	622.62	716.37	0.87	
<i>resA</i>	2419997	2420542	-	913.41	796.28	1.15	912.2	968.52	0.94	
<i>rluB</i>	2420674	2421363	-	889.39	807.75	1.10	1102.46	949.17	1.16	
<i>spmB</i>	2421455	2421994	-	34.11	36.47	0.94	38.4	44.49	0.86	
<i>spmA</i>	2421999	2422589	-	86.54	82.68	1.05	81.3	100.27	0.81	
<i>dacB</i>	2422577	2423725	-	61.28	58.48	1.05	74.66	78.25	0.95	
<i>ypul</i>	2423848	2424387	-	192.9	152.01	1.27	252	270.86	0.93	
<i>ypuH</i>	2424442	2425035	-	410.67	312.71	1.31	590.5	650.78	0.91	
<i>ypuG</i>	2425025	2425780	-	295.41	261.38	1.13	476.9	538.22	0.89	
<i>ypuF</i>	2426061	2426585	+	90.64	85.67	1.06	82.12	90.94	0.90	
<i>ribT</i>	2426599	2426973	-	1166.83	1180.06	0.99	1420.85	1574.13	0.90	
<i>ribH</i>	2427086	2427550	-	1072.2	895.62	1.20	1236.77	1158.25	1.07	
<i>ribA</i>	2427583	2428779	-	1011.59	809.26	1.25	1026.42	1004.6	1.02	
<i>ribE</i>	2428794	2429441	-	853.21	701.97	1.22	978.69	908.75	1.08	
<i>ribD</i>	2429452	2430537	-	929.6	846.89	1.10	947.28	872.85	1.09	
<i>ypuD</i>	2430930	2431274	-	521.21	540.77	0.96	530.56	275.25	1.93	
<i>sipS</i>	2431509	2432063	-	658.82	580.27	1.14	805.99	893.36	0.90	
<i>ypzC</i>	2432330	2432566	+	20.53	28.01	0.73	21.63	21.57	1.00	
<i>ypuC</i>	2432969	2433358	-	119.51	89.84	1.33	82.81	74.08	1.12	
<i>ypuB</i>	2433336	2433539	-	81.67	84.9	0.96	79.22	66.62	1.19	
<i>ypzD</i>	2434205	2434417	+	14.62	24.51	0.60	18.57	20.13	0.92	
<i>ppiB</i>	2434553	2434984	-	1157.56	1053.28	1.10	1449.75	1384.13	1.05	
<i>ypuA</i>	2435238	2436110	+	468.83	399.36	1.17	985.6	899.9	1.10	
<i>lysA</i>	2436139	2437458	-	735.53	615.84	1.19	1305.1	1217.33	1.07	
<i>spoVAF</i>	2437564	2439042	-	140.88	120.51	1.17	171.71	156.03	1.10	
<i>spoVAE</i>	2438993	2439964	-	65.54	66.21	0.99	71.27	72.81	0.98	
<i>spoVAD</i>	2439966	2440982	-	57.2	59	0.97	47	54.73	0.86	
<i>spoVAC</i>	2440995	2441447	-	26.68	30.54	0.87	25.23	26.94	0.94	
<i>spoVAB</i>	2441459	2441884	-	40.74	47.59	0.86	33.2	40.02	0.83	
<i>spoVAA</i>	2441894	2442496	-	19.52	25.41	0.77	22.73	23.11	0.98	
<i>sigF</i>	2442618	2443385	-	325.16	350.23	0.93	272.63	297.72	0.92	AbrB regulon
<i>spollAB</i>	2443397	2443837	-	336.47	369.37	0.91	279.63	287.44	0.97	AbrB regulon
<i>spollAA</i>	2443834	2444187	-	495.22	574.84	0.86	447.89	435.56	1.03	Spo0A and AbrB regulon
<i>dacF</i>	2444283	2445452	-	66.71	70.08	0.95	54.1	66.04	0.82	AbrB regulon
<i>punA</i>	2445607	2446422	-	538.32	508.16	1.06	1054.33	1003.69	1.05	
<i>drm</i>	2446435	2447619	-	616.39	536.83	1.15	920.15	913.59	1.01	
<i>ripX</i>	2447780	2448670	-	595.01	471.24	1.26	676.86	742.66	0.91	
<i>fur</i>	2449029	2449478	-	643.85	556.28	1.16	532.35	560.39	0.95	
<i>spollM</i>	2449591	2450235	-	29.94	32.01	0.94	34.04	36.68	0.93	
<i>yqkK</i>	2450336	2450551	-	80.31	78.12	1.03	103.2	93.21	1.11	
<i>mleA</i>	2450651	2451970	-	225.89	262.04	0.86	261.32	299.39	0.87	
<i>mleN</i>	2451988	2453394	-	134.11	164.7	0.81	168.6	189.68	0.89	
<i>ansB</i>	2453535	2454962	-	254.31	230.47	1.10	294	291.11	1.01	
<i>ansA</i>	2455007	2455996	-	274.08	260.06	1.05	388.28	378.03	1.03	
<i>ansR</i>	2456178	2456528	+	156.97	148.58	1.06	120.44	153.68	0.78	
<i>yqxK</i>	2456537	2457421	-	675.03	592.98	1.14	613.11	547.69	1.12	

<i>ypbG</i>	2403443	2404222	-	142.07	150.67	0.94	285.4	242.77	1.18	
<i>ypbF</i>	2404308	2404751	-	218.61	207.25	1.05	241.76	325.84	0.74	
<i>ypbE</i>	2404814	2405536	-	787.37	742.98	1.06	882.3	1078.17	0.82	
<i>ypbD</i>	2405487	2406056	-	396.11	322.58	1.23	399.67	495.41	0.81	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>recQ</i>	2406116	2407606	-	611.19	534.18	1.14	672.12	767.1	0.88	
<i>ypbB</i>	2407599	2408657	-	255.15	243.16	1.05	272.89	348.47	0.78	
<i>fer</i>	2408923	2409171	+	1279.33	1451.42	0.88	1362.01	1530	0.89	
<i>ypaA</i>	2409211	2409783	-	379.25	481.16	0.79	182.02	203.75	0.89	
<i>ypzE</i>	2409889	2410053	-	785.51	922.98	0.85	225.67	300.01	0.75	
<i>serA</i>	2410280	2411857	+	1925.65	2410.53	0.80	3176.91	3835.65	0.83	
<i>aroC</i>	2411900	2412667	-	379.45	326.68	1.16	386.71	387.16	1.00	
<i>rsiX</i>	2412779	2413885	-	555.75	550.73	1.01	752.67	866.48	0.87	
<i>sigX</i>	2413821	2414405	-	676.04	767.83	0.88	953.46	1085.82	0.88	
<i>resE</i>	2414609	2416378	-	1361.42	1318.63	1.03	1012.17	1001.31	1.01	
<i>resD</i>	2416375	2417097	-	1564.7	1482.64	1.06	989.05	1048.68	0.94	
<i>resC</i>	2417178	2418236	-	970.14	860.08	1.13	446.34	505.08	0.88	
<i>resB</i>	2418372	2420000	-	907.06	749.9	1.21	622.62	716.37	0.87	
<i>resA</i>	2419997	2420542	-	913.41	796.28	1.15	912.2	968.52	0.94	
<i>rluB</i>	2420674	2421363	-	889.39	807.75	1.10	1102.46	949.17	1.16	
<i>spmB</i>	2421455	2421994	-	34.11	36.47	0.94	38.4	44.49	0.86	
<i>spmA</i>	2421999	2422589	-	86.54	82.68	1.05	81.3	100.27	0.81	
<i>dacB</i>	2422577	2423725	-	61.28	58.48	1.05	74.66	78.25	0.95	
<i>ypuL</i>	2423848	2424387	-	192.9	152.01	1.27	252	270.86	0.93	
<i>ypuH</i>	2424442	2425035	-	410.67	312.71	1.31	590.5	650.78	0.91	
<i>ypuG</i>	2425025	2425780	-	295.41	261.38	1.13	476.9	538.22	0.89	
<i>ypuF</i>	2426061	2426585	+	90.64	85.67	1.06	82.12	90.94	0.90	
<i>ribT</i>	2426599	2426973	-	1166.83	1180.06	0.99	1420.85	1574.13	0.90	
<i>ribH</i>	2427086	2427550	-	1072.2	895.62	1.20	1236.77	1158.25	1.07	
<i>ribA</i>	2427583	2428779	-	1011.59	809.26	1.25	1026.42	1004.6	1.02	
<i>ribE</i>	2428794	2429441	-	853.21	701.97	1.22	978.69	908.75	1.08	
<i>ribD</i>	2429452	2430537	-	929.6	846.89	1.10	947.28	872.85	1.09	
<i>ypuD</i>	2430930	2431274	-	521.21	540.77	0.96	530.56	275.25	1.93	
<i>sipS</i>	2431509	2432063	-	658.82	580.27	1.14	805.99	893.36	0.90	
<i>ypzC</i>	2432330	2432566	+	20.53	28.01	0.73	21.63	21.57	1.00	
<i>ypuC</i>	2432969	2433358	-	119.51	89.84	1.33	82.81	74.08	1.12	
<i>ypuB</i>	2433336	2433539	-	81.67	84.9	0.96	79.22	66.62	1.19	
<i>ypzD</i>	2434205	2434417	+	14.62	24.51	0.60	18.57	20.13	0.92	
<i>ppiB</i>	2434553	2434984	-	1157.56	1053.28	1.10	1449.75	1384.13	1.05	
<i>ypuA</i>	2435238	2436110	+	468.83	399.36	1.17	985.6	899.9	1.10	
<i>lysA</i>	2436139	2437458	-	735.53	615.84	1.19	1305.1	1217.33	1.07	
<i>spoVAF</i>	2437564	2439042	-	140.88	120.51	1.17	171.71	156.03	1.10	
<i>spoVAE</i>	2438993	2439964	-	65.54	66.21	0.99	71.27	72.81	0.98	
<i>spoVAD</i>	2439966	2440982	-	57.2	59	0.97	47	54.73	0.86	
<i>spoVAC</i>	2440995	2441447	-	26.68	30.54	0.87	25.23	26.94	0.94	
<i>spoVAB</i>	2441459	2441884	-	40.74	47.59	0.86	33.2	40.02	0.83	
<i>spoVAA</i>	2441894	2442496	-	19.52	25.41	0.77	22.73	23.11	0.98	
<i>sigF</i>	2442618	2443385	-	325.16	350.23	0.93	272.63	297.72	0.92	AbrB regulon
<i>spollAB</i>	2443397	2443837	-	336.47	369.37	0.91	279.63	287.44	0.97	AbrB regulon
<i>spollAA</i>	2443834	2444187	-	495.22	574.84	0.86	447.89	435.56	1.03	Spo0A and AbrB regulon
<i>dacF</i>	2444283	2445452	-	66.71	70.08	0.95	54.1	66.04	0.82	AbrB regulon
<i>punA</i>	2445607	2446422	-	538.32	508.16	1.06	1054.33	1003.69	1.05	
<i>drm</i>	2446435	2447619	-	616.39	536.83	1.15	920.15	913.59	1.01	
<i>ripX</i>	2447780	2448670	-	595.01	471.24	1.26	676.86	742.66	0.91	
<i>fur</i>	2449029	2449478	-	643.85	556.28	1.16	532.35	560.39	0.95	
<i>spollM</i>	2449591	2450235	-	29.94	32.01	0.94	34.04	36.68	0.93	
<i>yqkK</i>	2450336	2450551	-	80.31	78.12	1.03	103.2	93.21	1.11	
<i>mleA</i>	2450651	2451970	-	225.89	262.04	0.86	261.32	299.39	0.87	
<i>mleN</i>	2451988	2453394	-	134.11	164.7	0.81	168.6	189.68	0.89	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>spoIVB</i>	2518336	2519613	-	69.53	72.26	0.96	65.75	79.58	0.83	
<i>recN</i>	2519788	2521518	-	421.17	406.47	1.04	771.3	806.66	0.96	
<i>ahrC</i>	2521555	2522004	-	517.54	495.89	1.04	894.17	910.96	0.98	
<i>yqxC</i>	2522139	2522948	-	755.74	685.39	1.10	1284.31	1470.31	0.87	
<i>dxs</i>	2522945	2524846	-	1261.96	1194.75	1.06	1600.72	1685.53	0.95	
<i>yqiD</i>	2525093	2525911	-	538.4	418.71	1.29	881.34	790.95	1.11	
<i>yqiC</i>	2525901	2526065	-	902.85	644.2	1.40	1300.42	1366.34	0.95	
<i>yqiB</i>	2526151	2527497	-	547.01	365.63	1.50	762.82	745.61	1.02	
<i>folD</i>	2527635	2528486	-	1606.15	1361.72	1.18	1663.02	1732.03	0.96	
<i>nusB</i>	2528498	2528893	-	1815.34	1659.21	1.09	2107.73	2112.8	1.00	
<i>yqhY</i>	2529157	2529564	-	3102.63	3108.7	1.00	3252	3195.21	1.02	
<i>accC</i>	2529585	2530937	-	3699.04	3508.56	1.05	3436.4	3267.13	1.05	
<i>accB</i>	2530949	2531428	-	2011.27	1970.72	1.02	2202.44	2575.87	0.86	
<i>spolIIAH</i>	2531584	2532240	-	77.67	78.2	0.99	72.52	84.11	0.86	
<i>spolIIAG</i>	2532241	2532930	-	50.19	49.54	1.01	39.79	47.27	0.84	
<i>spolIIAF</i>	2532923	2533543	-	45.81	44.98	1.02	37.11	39.95	0.93	
<i>spolIIAE</i>	2533540	2534757	-	58.72	60.71	0.97	46.56	51.43	0.91	
<i>spolIIAD</i>	2534776	2535177	-	24.61	32.22	0.76	27.09	26.9	1.01	
<i>spolIIAC</i>	2535184	2535390	-	19.88	29.76	0.67	30.09	30.67	0.98	
<i>spolIIAB</i>	2535413	2535928	-	78.43	80.05	0.98	67.4	70.84	0.95	
<i>spolIIAA</i>	2535922	2536845	-	63.14	63.89	0.99	47.71	56.97	0.84	
<i>yqhV</i>	2536921	2537202	-	22.45	30.2	0.74	28.11	30.96	0.91	
<i>efp</i>	2537347	2537904	-	1557.77	1712.51	0.91	2347.24	2433.3	0.96	
<i>yqhT</i>	2537929	2538990	-	2307.65	2413.27	0.96	2661.43	2742.7	0.97	
<i>yqhS</i>	2538987	2539433	-	1648.04	1615.22	1.02	1613.44	1644.46	0.98	
<i>yqhR</i>	2539520	2540056	-	77.74	80.27	0.97	85.8	66.7	1.29	
<i>yqhQ</i>	2540283	2541239	+	990.71	915.81	1.08	443.13	443.42	1.00	
<i>yqhP</i>	2541279	2541674	+	1097.72	1189.66	0.92	387.87	461.1	0.84	
<i>yqhO</i>	2541671	2542546	-	63.76	64.17	0.99	58.34	67.77	0.86	
<i>mntR</i>	2542672	2543100	-	467.89	406.22	1.15	829.23	913.98	0.91	
<i>yqhM</i>	2543200	2544036	-	447.71	362.28	1.24	754.14	793.84	0.95	
<i>yqhL</i>	2544227	2544607	+	403.7	342.54	1.18	507.69	629.73	0.81	
<i>gcvPB</i>	2544642	2546108	-	633.08	795.07	0.80	636.61	717.13	0.89	
<i>gcvPA</i>	2546101	2547447	-	786.33	987.69	0.80	839.03	928.18	0.90	
<i>gcvT</i>	2547477	2548565	-	606.09	737.81	0.82	746.76	888.99	0.84	
<i>yqhH</i>	2549007	2550680	+	48.41	53.91	0.90	42.45	50.75	0.84	
<i>yqhG</i>	2550701	2551495	+	194.57	156.81	1.24	177.88	150.94	1.18	
<i>sinI</i>	2551678	2551851	+	351.24	309.85	1.13	376.12	566.95	0.66	Spo0A regulon
<i>sinR</i>	2551885	2552220	+	243.65	282.64	0.86	365.62	428.13	0.85	
<i>tasA</i>	2552313	2553098	-	2398.42	427.18	5.61	2500.21	718.97	3.48	AbrB regulon
<i>sipW</i>	2553162	2553734	-	612.46	134.32	4.56	482.59	147.94	3.26	AbrB regulon
<i>yqxM</i>	2553718	2554479	-	196.5	57.84	3.40	158.54	65.66	2.41	AbrB regulon
<i>yqzG</i>	2554751	2555077	+	39.7	42.45	0.94	53.05	45.53	1.17	AbrB regulon
<i>yqzE</i>	2555060	2555299	-	88.49	125.75	0.70	250.12	398.89	0.63	
<i>comGG</i>	2555370	2555744	-	250.89	353.55	0.71	708.24	1062.7	0.67	
<i>comGF</i>	2555745	2556128	-	412.5	636.57	0.65	878.37	1295.82	0.68	
<i>comGE</i>	2556154	2556501	-	327.2	476.22	0.69	696.44	988.61	0.70	
<i>comGD</i>	2556485	2556916	-	330.77	482.33	0.69	665.49	914.95	0.73	
<i>comGC</i>	2556906	2557202	-	547.48	746.61	0.73	1064.41	1433.34	0.74	
<i>comGB</i>	2557216	2558187	-	581.13	718.44	0.81	797.12	1067.11	0.75	
<i>comGA</i>	2558240	2559310	-	799.44	1009.33	0.79	1318.29	1682.85	0.78	
<i>yqxL</i>	2559722	2560675	-	1557.11	1231.04	1.26	715.78	245.81	2.91	
<i>yqhB</i>	2560818	2562146	+	894.52	564.83	1.58	316.65	143.46	2.21	
<i>yqhA</i>	2562199	2563035	-	481.26	484.86	0.99	466.19	392.23	1.19	
<i>yqgZ</i>	2563259	2563639	-	6757.59	6656.46	1.02	4370.94	3813.86	1.15	
<i>yqgY</i>	2563871	2564116	+	1898.58	2489.17	0.76	1366.6	1843.07	0.74	
<i>yqgX</i>	2564156	2564791	-	907.12	990.14	0.92	1251.43	1243.01	1.01	
<i>yqgW</i>	2564949	2565122	+	959.38	1397.37	0.69	1455.57	1760.76	0.83	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yqgV</i>	2565183	2565467	-	603.46	505.47	1.19	936.88	864.2	1.08	
<i>yqgU</i>	2565470	2566531	-	385.27	324.79	1.19	673.67	657.78	1.02	
<i>yqgT</i>	2566593	2567723	-	156.85	140.42	1.12	307.44	327.38	0.94	
<i>yqgS</i>	2567806	2569722	-	586.35	588.96	1.00	959.17	1149.44	0.83	
<i>glcK</i>	2569838	2570803	-	581.13	602.59	0.96	755.96	761.49	0.99	
<i>yqgQ</i>	2570814	2571029	-	221.04	226.84	0.97	333.8	447.62	0.75	
<i>yqgP</i>	2571139	2572662	-	205.31	219.01	0.94	246.76	333.97	0.74	
<i>yqgO</i>	2572752	2572925	-	368.39	375.93	0.98	380.82	500.34	0.76	
<i>yqgN</i>	2572992	2573555	-	262.07	289.1	0.91	300.42	352.77	0.85	
<i>rpmGA</i>	2573640	2573789	-	875.18	1129.54	0.77	1555.24	1402.28	1.11	
<i>yqgM</i>	2573873	2574952	-	116.32	105.17	1.11	120.29	127.75	0.94	
<i>yqgL</i>	2574949	2575419	-	87.01	92.87	0.94	91.49	93.88	0.97	
<i>yqzD</i>	2575599	2575952	+	1783.32	1470.46	1.21	1932.7	1804.92	1.07	Spo0A regulon
<i>yqzC</i>	2575949	2576413	+	895.32	766.16	1.17	1164.86	1066.86	1.09	
<i>pstBB</i>	2576442	2577224	-	62.6	58.41	1.07	54.56	59.91	0.91	
<i>pstBA</i>	2577235	2578044	-	53.49	53.28	1.00	49.25	52.05	0.95	
<i>pstA</i>	2578065	2578949	-	54.03	52.87	1.02	46.63	51.3	0.91	
<i>pstC</i>	2578949	2579878	-	54.71	55.82	0.98	47.52	51.38	0.92	
<i>pstS</i>	2579947	2580849	-	42.97	48.92	0.88	38.25	40.21	0.95	
<i>pbpA</i>	2581003	2583153	-	1586.92	1315.05	1.21	1611.98	1544.44	1.04	
<i>yqgE</i>	2583267	2584559	-	73.52	74.36	0.99	54.77	62.13	0.88	
<i>sodA</i>	2584666	2585274	-	7473.24	7778.68	0.96	6025.22	5392.95	1.12	
<i>yqgC</i>	2585453	2585935	-	1619.02	1108.14	1.46	773.62	716.81	1.08	
<i>yqgB</i>	2586045	2586803	+	406.96	344.44	1.18	442.56	387.18	1.14	
<i>yqgA</i>	2587229	2587657	-	2605.08	2875.32	0.91	3279.74	3613.59	0.91	
<i>yqfZ</i>	2587934	2588233	+	46.29	47.37	0.98	46.31	57.99	0.80	
<i>yqfY</i>	2588356	2589489	+	701.9	671.41	1.05	797.9	871.54	0.92	
<i>yqfX</i>	2589515	2589904	-	80.65	90.92	0.89	77.81	93.57	0.83	
<i>yqfW</i>	2590037	2590618	+	454.34	373.64	1.22	609.85	577.13	1.06	
<i>zur</i>	2590661	2591098	-	362.07	384.59	0.94	259.62	274.82	0.94	
<i>yqfU</i>	2591236	2592117	-	604.56	559.18	1.08	589.09	701.16	0.84	
<i>yqfT</i>	2592233	2592487	+	38.2	37.93	1.01	35.57	31.15	1.14	
<i>yqfS</i>	2592514	2593407	-	1044.28	1283.23	0.81	925.39	1229.56	0.75	
<i>yqfR</i>	2593417	2594733	-	1148.21	1366.28	0.84	925.82	1234.74	0.75	
<i>yqfQ</i>	2594902	2595645	+	94.95	101.6	0.93	74.81	89.03	0.84	
<i>yqfP</i>	2595768	2596712	+	549.55	437.62	1.26	517.32	572.43	0.90	
<i>yqfO</i>	2596735	2597856	-	640.55	574.88	1.11	904.46	872.63	1.04	
<i>yqfN</i>	2597849	2598499	-	449.74	422.61	1.06	693.37	671.97	1.03	
<i>cccA</i>	2598756	2599118	-	909.2	963.24	0.94	791.93	877.16	0.90	AbrB regulon
<i>sigA</i>	2599447	2600562	-	2316.32	2484.04	0.93	2541.2	2689.08	0.95	SigD regulon
<i>dnaG</i>	2600761	2602572	-	1192.44	1256.72	0.95	1404.82	1692.45	0.83	Spo0A regulon
<i>antE</i>	2602212	2602508	+	78.04	75.89	1.03	77.95	102.27	0.76	AbrB regulon
<i>yqxD</i>	2602606	2603196	-	1031.72	1042.92	0.99	1133.22	1350.56	0.84	
<i>yqfL</i>	2603354	2604166	-	473.42	482.48	0.98	695.22	793.11	0.88	
<i>yqzB</i>	2604192	2604830	-	566.56	643.56	0.88	799.28	845.14	0.95	
<i>glyS</i>	2604963	2607002	-	758.84	857.81	0.88	1328.52	1336.35	0.99	
<i>glyQ</i>	2606995	2607882	-	565.72	558.34	1.01	1011.6	1083.89	0.93	
<i>recO</i>	2608179	2608946	-	1098.06	909.13	1.21	1354.91	1632.93	0.83	
<i>era</i>	2609274	2610179	-	1565.16	1383.39	1.13	1897.61	2016.47	0.94	Spo0A regulon
<i>cdd</i>	2610160	2610570	-	1187.63	1071.77	1.11	1473.67	1554.08	0.95	
<i>dgkA</i>	2610689	2611033	-	719.05	451.64	1.59	694.01	615.59	1.13	
<i>yqfG</i>	2611040	2611513	-	863.71	623.98	1.38	1033.52	844.15	1.22	
<i>yqfF</i>	2611514	2613649	-	884.57	642.18	1.38	883.32	789.22	1.12	
<i>phoH</i>	2613728	2614687	-	1943.35	1466.82	1.32	1649.7	1494.62	1.10	
<i>yqfD</i>	2614684	2615880	-	125.53	110.44	1.14	152.95	152.91	1.00	
<i>yqfC</i>	2615899	2616180	-	62.84	65.03	0.97	140.29	143.87	0.98	
<i>yqfB</i>	2616237	2616656	-	2263.24	2410.75	0.94	2980.04	3329.82	0.89	
<i>yqfA</i>	2616681	2617676	-	2299.75	2357.63	0.98	3188.42	3404.54	0.94	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yqeV</i>	2620909	2622264	-	643.44	565.3	1.14	1301.39	1353.99	0.96	
<i>yqeU</i>	2622264	2623034	-	384.01	287.41	1.34	715.17	812.65	0.88	
<i>yqeT</i>	2623057	2623992	-	507.07	408.83	1.24	947.43	1074.81	0.88	
<i>dnaJ</i>	2624017	2625135	-	1042.19	1005	1.04	1720.07	1739.85	0.99	
<i>dnaK</i>	2625335	2627170	-	3271.76	3042.35	1.08	3852.23	3540.37	1.09	
<i>grpE</i>	2627194	2627757	-	2820.98	2360.95	1.19	3168.53	3022.77	1.05	
<i>hrcA</i>	2627829	2628860	-	899.35	783.59	1.15	882.97	732.57	1.21	
<i>hemN</i>	2628980	2630080	-	236.88	211.64	1.12	354.1	339.48	1.04	
<i>lepA</i>	2630133	2631971	-	693.25	591.52	1.17	899.99	995.85	0.90	
<i>yqxA</i>	2632105	2632443	-	52.04	47.7	1.09	48.97	49.92	0.98	
<i>spolIP</i>	2632460	2633665	-	92.82	85.02	1.09	79.59	99.89	0.80	
<i>gpr</i>	2633728	2634834	-	85.81	83.28	1.03	77.66	86.98	0.89	
<i>rpsT</i>	2635038	2635304	+	583.71	780.89	0.75	786.71	733.57	1.07	
<i>yqeN</i>	2635319	2636362	-	252.67	250	1.01	335.86	428.7	0.78	
<i>comEC</i>	2636766	2639096	-	105.02	124.87	0.84	146.76	242.44	0.61	
<i>comEB</i>	2639100	2639669	-	340.26	360.69	0.94	465.33	650.38	0.72	
<i>comEA</i>	2639736	2640353	-	285.55	306.53	0.93	404.93	669.48	0.60	
<i>comER</i>	2640437	2641258	+	78.91	75.84	1.04	56.17	61.09	0.92	
<i>yqeM</i>	2641324	2642067	-	686.84	512.93	1.34	1206.26	1049.61	1.15	
<i>yqeL</i>	2642064	2642420	-	1091.14	830.42	1.31	1943.9	1780.97	1.09	
<i>yqeK</i>	2642438	2642998	-	639	460.83	1.39	1250.2	1101.95	1.13	
<i>yqeJ</i>	2642988	2643557	-	926.54	639.35	1.45	1444.14	1318.74	1.10	
<i>yqeI</i>	2643569	2643859	-	962.26	726.13	1.33	1934.65	1726.25	1.12	
<i>aroD</i>	2643853	2644695	-	805.77	604.38	1.33	1554.18	1432.4	1.09	
<i>yqeH</i>	2644713	2645813	-	485.34	345	1.41	986.35	929.21	1.06	
<i>yqeG</i>	2645817	2646335	-	343.02	254.51	1.35	535.97	621.15	0.86	
<i>sda</i>	2646679	2646837	+	179.71	123.41	1.46	246.36	463.91	0.53	
<i>yqeF</i>	2647143	2647874	-	908.57	416.61	2.18	371.73	184.35	2.02	
<i>cwlH</i>	2648126	2648878	-	150.95	129.61	1.16	153.79	124.29	1.24	
<i>yqeD</i>	2649065	2649691	+	97.33	62.12	1.57	75.38	70.74	1.07	
<i>yqeC</i>	2649710	2650603	-	96.57	93.04	1.04	81.21	82.5	0.98	
<i>yqeB</i>	2650855	2651580	+	403.78	289.41	1.40	615.75	452.58	1.36	
<i>nucB</i>	2651613	2652023	-	64.47	71.72	0.90	61.77	72.13	0.86	
<i>spoIVCB</i>	2652219	2652689	+	50.76	52.25	0.97	71.93	67.24	1.07	
<i>spoIVCA</i>	2652597	2654099	-	67.51	66	1.02	88.72	97.17	0.91	
<i>arsC</i>	2654548	2654967	-	179.76	192.51	0.93	235.13	243.34	0.97	
<i>arsB</i>	2654979	2656019	-	131.17	137.98	0.95	134.27	147.78	0.91	
<i>yqcK</i>	2656042	2656482	-	49.9	59.03	0.85	58.56	69.12	0.85	
<i>arsR</i>	2656543	2656860	-	68.38	73.61	0.93	95.63	112.82	0.85	
<i>yqcI</i>	2657232	2657996	-	30.21	34.77	0.87	29.15	34.96	0.83	
<i>rapE</i>	2658440	2659567	+	137.89	151.71	0.91	182.87	166.55	1.10	
<i>yqzI</i>	2659801	2659959	+	86.54	101.97	0.85	97.79	98.25	1.00	
<i>yqcG</i>	2660329	2661924	+	624.92	512.49	1.22	725.88	703.69	1.03	Spo0A and AbrB regulon
<i>yqcF</i>	2661939	2662517	+	444.44	327.86	1.36	516.76	461.3	1.12	
<i>yqxJ</i>	2662778	2663140	-	602.35	532.67	1.13	758.95	627.13	1.21	AbrB regulon
<i>yqxI</i>	2663156	2663635	-	1571.96	1361.93	1.15	1633	1391.45	1.17	Spo0A and AbrB regulon
<i>cwlA</i>	2663800	2664618	-	55.88	56.41	0.99	61.99	59.55	1.04	
<i>yqxH</i>	2664663	2665085	-	29.54	32.63	0.91	29.2	28.12	1.04	
<i>yqxG</i>	2665130	2666023	-	26.15	29.62	0.88	27.12	28.69	0.95	
<i>yqeE</i>	2666111	2666275	-	28.46	28.88	0.99	35.26	29.23	1.21	
<i>yqcD</i>	2666272	2666607	-	26.12	32.31	0.81	29.46	25.56	1.15	
<i>yqcC</i>	2666617	2667717	-	56.83	49.8	1.14	75.19	59.94	1.25	
<i>yqcB</i>	2667720	2667992	-	30.02	38.29	0.78	29.27	31.27	0.94	
<i>yqcA</i>	2667989	2668567	-	52.96	49.82	1.06	35.08	40.59	0.86	
<i>yqbT</i>	2668551	2669597	-	62.75	72.63	0.86	56.29	69.3	0.81	
<i>yqbS</i>	2669590	2670015	-	39.24	48.14	0.82	34.01	36.53	0.93	
<i>yqbR</i>	2670028	2670291	-	23	29.32	0.78	28.44	30.91	0.92	
<i>yqbQ</i>	2670288	2671268	-	60.88	53.99	1.13	53.73	51.68	1.04	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yqbM</i>	2678369	2678812	-	141.25	88.84	1.59	73.71	56.34	1.31	
<i>yqbL</i>	2678815	2679219	-	145.12	80.42	1.80	66.17	43.43	1.52	
<i>yqbK</i>	2679297	2680214	-	59.93	63.21	0.95	63.69	68.82	0.93	
<i>yqbJ</i>	2680403	2680840	-	36.47	41.87	0.87	39.86	44.57	0.89	
<i>yqbI</i>	2680853	2681356	-	54.62	60.44	0.90	51.67	51.28	1.01	
<i>yqbH</i>	2681353	2681715	-	30.96	34.64	0.89	37.34	36.9	1.01	
<i>yqbG</i>	2681712	2682107	-	60.08	75.38	0.80	68.99	73.8	0.93	
<i>yqbF</i>	2682111	2682422	-	33.04	39.28	0.84	41.96	38.1	1.10	
<i>yqbE</i>	2682433	2683368	-	40.69	41.47	0.98	50.48	46.09	1.10	
<i>yqbD</i>	2683387	2684355	-	73.73	77.92	0.95	71.61	82.3	0.87	
<i>yqbC</i>	2684388	2685041	-	148.45	166.04	0.89	175.55	185.47	0.95	
<i>yqbB</i>	2685082	2685999	-	62.83	55.28	1.14	63.57	60.66	1.05	
<i>yqbA</i>	2685996	2687528	-	53.96	51.78	1.04	53.44	52.51	1.02	
<i>yqaT</i>	2687532	2688827	-	49.35	56.49	0.87	46.32	57.89	0.80	
<i>yqaS</i>	2688820	2689539	-	66.39	93.58	0.71	73.07	85.42	0.86	
<i>yqaR</i>	2689607	2690071	-	165.2	207	0.80	261.51	321.15	0.81	
<i>yqaQ</i>	2690215	2690670	-	33.83	46.58	0.73	37.56	42.39	0.89	
<i>yqaP</i>	2690868	2691797	+	2016.2	1884.94	1.07	2069.11	2093.64	0.99	AbrB regulon
<i>yqaO</i>	2691871	2692077	-	25.53	28.88	0.88	24.92	21.57	1.16	
<i>yqaN</i>	2692159	2692587	-	47.39	51.45	0.92	53.07	50.96	1.04	
<i>yqaM</i>	2692823	2693764	-	34.03	36.89	0.92	32.44	34.67	0.94	
<i>yqaL</i>	2693646	2694347	-	61.96	65.55	0.95	46.91	52.48	0.89	
<i>yqaK</i>	2694399	2695253	-	47.23	46.49	1.02	37.48	42.95	0.87	
<i>yqaJ</i>	2695256	2696215	-	23.84	27.95	0.85	25.49	27.58	0.92	
<i>yqaI</i>	2696321	2696515	-	24.56	34.57	0.71	26.33	22.05	1.19	
<i>yqaH</i>	2696645	2696902	-	26.51	30.09	0.88	21.51	26.72	0.81	
<i>yqaG</i>	2696899	2697468	-	31.12	38.04	0.82	30.36	34.75	0.87	
<i>yqaD</i>	2697542	2697682	-	41.32	42.45	0.97	52.19	51.28	1.02	
<i>yqaF</i>	2697712	2697942	-	19.49	25.53	0.76	21.78	22.68	0.96	
<i>yqaE</i>	2698119	2698469	+	257.68	249.82	1.03	233.74	246.97	0.95	
<i>yqaD</i>	2698736	2698903	-	23	29.32	0.78	34.79	33.55	1.04	
<i>yqaC</i>	2699259	2699795	-	89.76	84.35	1.06	80.83	70.13	1.15	
<i>yqaB</i>	2700064	2700582	+	29.66	36.09	0.82	34.79	37.95	0.92	
<i>spolIIC</i>	2700564	2700980	+	83.33	80.85	1.03	60.88	81.89	0.74	
<i>yrkS</i>	2701205	2701369	-	40.93	44.2	0.93	36.2	48.88	0.74	
<i>yrkR</i>	2701914	2702333	-	131.76	73.19	1.80	96.26	70.39	1.37	
<i>yrkQ</i>	2702376	2703674	-	189	128.38	1.47	155.78	130.58	1.19	
<i>yrkP</i>	2703661	2704356	-	92.17	99.59	0.93	98.52	93	1.06	
<i>yrkO</i>	2704624	2705841	+	89.77	74.79	1.20	82.2	80.3	1.02	
<i>yrkN</i>	2706353	2706910	+	95.9	83.69	1.15	96.42	93.27	1.03	
<i>yrkL</i>	2707401	2707925	-	606.87	507.33	1.20	529.89	512.56	1.03	
<i>yrkK</i>	2708169	2708645	-	89.88	92.78	0.97	81.81	91.27	0.90	
<i>yrkJ</i>	2709228	2710013	-	35.23	36.81	0.96	36.5	33.27	1.10	
<i>yrkI</i>	2710074	2710301	-	30.02	29.91	1.00	42.63	39.94	1.07	
<i>yrkH</i>	2710335	2711222	-	82.24	79.41	1.04	80.29	93.06	0.86	
<i>yrkF</i>	2711803	2712360	-	54.77	57.08	0.96	54.97	54.75	1.00	
<i>yrkE</i>	2712546	2713028	-	38.59	44.55	0.87	35.26	35.99	0.98	
<i>yrkD</i>	2713175	2713366	-	257.48	302.63	0.85	362.48	476.61	0.76	
<i>yrkC</i>	2714159	2714719	-	155.36	129.14	1.20	201.98	225.98	0.89	
<i>yrkB</i>	2714945	2715091	-	75.24	57.33	1.31	101.55	80.03	1.27	
<i>bltR</i>	2715261	2716082	-	49.76	53.63	0.93	69.91	78.76	0.89	
<i>blt</i>	2716199	2717401	+	42.3	48.56	0.87	42.37	47.89	0.88	
<i>bltD</i>	2717570	2718028	+	27.25	33.8	0.81	39.75	41.8	0.95	
<i>yrkA</i>	2718185	2719489	-	413.4	514.2	0.80	250.66	328.19	0.76	
<i>yrdR</i>	2719913	2720878	-	34.42	37.45	0.92	30.91	31.44	0.98	
<i>yrdQ</i>	2721004	2721870	+	168.16	159.16	1.06	197.33	182.09	1.08	
<i>trkA</i>	2721993	2723030	-	325.81	466.71	0.70	123.45	172.93	0.71	
<i>czcD</i>	2723118	2724053	-	519.8	861.44	0.60	242.27	303.14	0.80	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>aziD</i>	2727873	2728205	-	151.26	144.16	1.05	226.23	211.44	1.07	
<i>aziC</i>	2728202	2728966	-	123.54	118.05	1.05	159.8	169.88	0.94	
<i>aziB</i>	2728979	2729452	-	109.78	108.4	1.01	162.53	147.56	1.10	
<i>yrdF</i>	2729786	2730061	-	32.65	34.03	0.96	45.84	38.34	1.20	
<i>cypA</i>	2730333	2731565	-	67.71	55.55	1.22	94.24	80.98	1.16	
<i>yrdC</i>	2732206	2732769	-	189.1	189.13	1.00	354.76	450.73	0.79	
<i>yrdB</i>	2732998	2733369	-	45.33	56.14	0.81	82.01	99.14	0.83	
<i>yrdA</i>	2734179	2734682	-	571.74	385.08	1.48	366.46	397.95	0.92	
<i>aadK</i>	2734908	2735762	-	288.44	254.23	1.13	266.25	308.66	0.86	
<i>yrpB</i>	2736141	2737184	+	474.31	427.94	1.11	366.44	322.06	1.14	
<i>yrpC</i>	2737534	2738331	+	61.5	69.41	0.89	66.5	68.01	0.98	
<i>yrpD</i>	2738712	2739419	+	2047.63	2391.79	0.86	2447.25	2605.17	0.94	AbrB regulon
<i>yrpE</i>	2740583	2741338	-	32.4	33.4	0.97	48.15	46.13	1.04	
<i>sigZ</i>	2741470	2742000	-	65.62	60.98	1.08	74.83	68.49	1.09	
<i>yrpG</i>	2742165	2743115	+	99.85	95	1.05	92.32	93.31	0.99	
<i>yraO</i>	2743389	2744705	-	140.63	176.14	0.80	167.29	206.06	0.81	
<i>yraN</i>	2744820	2745689	-	205.79	256.46	0.80	285.2	329.11	0.87	
<i>yraM</i>	2745834	2746937	+	55.58	64.53	0.86	63.92	68.19	0.94	
<i>csn</i>	2747210	2748043	-	1433.58	1088.28	1.32	1081.74	878.14	1.23	AbrB regulon
<i>yraL</i>	2748486	2748749	+	602.03	445.37	1.35	609	626.54	0.97	
<i>yraK</i>	2748886	2749575	+	122.38	115.51	1.06	120.83	122.18	0.99	
<i>yraJ</i>	2750108	2750470	-	443.37	299.42	1.48	315.62	236.27	1.34	
<i>yraI</i>	2750517	2750951	-	1003.87	718.93	1.40	883.58	625.9	1.41	
<i>yraH</i>	2751392	2751778	-	262.8	194.19	1.35	194.17	180.75	1.07	
<i>yraG</i>	2752027	2752272	+	58.18	43.22	1.35	38.9	28.99	1.34	
<i>yraF</i>	2752290	2752658	+	72.56	60.27	1.20	52.92	41.9	1.26	
<i>adhB</i>	2752677	2753813	+	85.43	71.43	1.20	67.51	52.01	1.30	
<i>yraE</i>	2753832	2754029	+	114.22	77.9	1.47	76.63	54.63	1.40	
<i>yraD</i>	2754045	2754344	+	58.94	48.67	1.21	53.31	37.67	1.42	
<i>yraB</i>	2754607	2755029	-	97.75	88.24	1.11	85.04	85.67	0.99	
<i>adhA</i>	2755537	2756586	+	124.66	121.55	1.03	131.69	116.97	1.13	
<i>yraA</i>	2756717	2757226	+	1451.77	1727.95	0.84	1742.7	1918.48	0.91	
<i>sacC</i>	2757268	2759301	-	204.56	131.22	1.56	130.95	113.41	1.15	
<i>levG</i>	2759458	2760285	-	475.25	247.11	1.92	319.13	223.62	1.43	
<i>levF</i>	2760306	2761115	-	473.76	245.93	1.93	328.49	213.98	1.54	
<i>levE</i>	2761132	2761620	-	479.73	244.03	1.97	361.82	240.92	1.50	
<i>levD</i>	2761620	2762060	-	433.54	228.98	1.89	300.16	192.76	1.56	
<i>levR</i>	2762250	2765066	-	176.96	113.2	1.56	193.58	130.65	1.48	
<i>aapA</i>	2765783	2767162	+	73.81	71.18	1.04	78.53	83.82	0.94	
<i>yrhP</i>	2767269	2767901	-	87.87	212.92	0.41	61.5	157.29	0.39	
<i>yrhO</i>	2768054	2768881	+	148.76	130.15	1.14	176.19	192.42	0.92	
<i>sigV</i>	2769077	2769577	+	33.63	39.27	0.86	37.23	42	0.89	
<i>yrhM</i>	2769577	2770434	+	49.58	51.6	0.96	52.54	56.67	0.93	
<i>yrhL</i>	2770545	2772449	+	81.86	75.85	1.08	97.12	93.28	1.04	
<i>yrhK</i>	2772583	2772873	+	274.36	111.07	2.47	203.48	80.42	2.53	
<i>yrhJ</i>	2773117	2776281	-	210.8	217.65	0.97	401.5	329.73	1.22	
<i>yrhI</i>	2776297	2776881	-	84.08	75.04	1.12	140.97	114.21	1.23	
<i>yrhH</i>	2777104	2777646	-	68.51	76	0.90	95.28	106.03	0.90	
<i>yrzI</i>	2778150	2778299	-	1687.59	2162.36	0.78	732.49	847.31	0.86	AbrB regulon
<i>yrhG</i>	2778689	2779489	-	174.55	151.73	1.15	226.26	186.72	1.21	
<i>yrhF</i>	2779752	2780120	-	165.57	150.8	1.10	283.9	259.41	1.09	
<i>yrhE</i>	2780436	2783378	+	142.21	146.27	0.97	119.73	134.4	0.89	
<i>yrhD</i>	2783397	2783879	+	90.68	98.73	0.92	65.3	72.89	0.90	
<i>yrhC</i>	2783915	2784145	-	59.38	64.48	0.92	47.64	44.73	1.07	
<i>yrhB</i>	2784228	2785367	-	254.7	256.44	0.99	306.3	379.9	0.81	
<i>yrhA</i>	2785369	2786292	-	287.26	262.07	1.10	337.81	424.61	0.80	
<i>mtn</i>	2786357	2787052	-	870.28	814.52	1.07	1140.34	1215.73	0.94	
<i>yrpT</i>	2787073	2787714	-	410.55	356.03	1.15	422.91	551.77	0.77	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>udk</i>	2791445	2792080	-	367.04	325.81	1.13	762.58	782.74	0.97	
<i>yrrO</i>	2792087	2793355	-	480.54	404.83	1.19	984.66	948.04	1.04	
<i>yrrN</i>	2793374	2794303	-	488.44	394.31	1.24	857	913.51	0.94	
<i>yrrM</i>	2794309	2794962	-	291.44	259.05	1.13	574.33	627.24	0.92	
<i>yrrL</i>	2795114	2796196	-	691.77	544.42	1.27	975.82	805.45	1.21	Spo0A regulon
<i>yrzB</i>	2796327	2796608	-	3241.17	3390.59	0.96	2933.94	2863.75	1.02	
<i>yrrK</i>	2796626	2797042	-	1986.2	1805.36	1.10	2101.67	1921.97	1.09	
<i>yrzL</i>	2797050	2797316	-	1793.72	1575.71	1.14	1863.89	1714.99	1.09	
<i>alaS</i>	2797401	2800037	-	1214.06	995.98	1.22	1690.73	1490.93	1.13	
<i>yrrI</i>	2800368	2801429	-	67.11	62.55	1.07	58.46	65.71	0.89	
<i>glnQ</i>	2801585	2802313	+	117.6	117.8	1.00	107.32	121.04	0.89	
<i>glnH</i>	2802335	2803156	+	76.61	55.01	1.39	37.67	38.99	0.97	
<i>glnM</i>	2803217	2803867	+	74.28	65.85	1.13	45.42	53.8	0.84	
<i>glnP</i>	2803884	2804540	+	42.8	35.51	1.21	31.25	30.7	1.02	
<i>yrrD</i>	2804931	2805455	-	43.17	50.17	0.86	55.65	54.24	1.03	
<i>yrrC</i>	2805513	2807909	-	223.21	201.78	1.11	405.15	432.66	0.94	
<i>yrrB</i>	2807934	2808554	-	259.94	235.65	1.10	536.75	547.46	0.98	
<i>trmU</i>	2808640	2809764	-	728.8	705.67	1.03	929.79	1179.46	0.79	
<i>yrvO</i>	2809786	2810925	-	769.92	727.22	1.06	930.09	1243.47	0.75	
<i>yrzC</i>	2811027	2811362	-	362.03	354.27	1.02	361.86	602.42	0.60	
<i>yrvN</i>	2811562	2812827	+	197.84	177.87	1.11	205.17	195.97	1.05	
<i>yrvM</i>	2812869	2813633	-	295.6	369.32	0.80	272.81	375.08	0.73	
<i>aspS</i>	2813969	2815747	-	1295.33	1570.2	0.82	1759.48	1964.14	0.90	
<i>hisS</i>	2815761	2817035	-	770.24	857.2	0.90	1070.75	1397.39	0.77	
<i>yrzK</i>	2817417	2817587	-	23.78	28.01	0.85	40.9	43.61	0.94	
<i>yrvJ</i>	2817720	2819276	+	1012.53	971.82	1.04	1383.68	1318.18	1.05	
<i>yrvI</i>	2819303	2819701	-	1024.59	876.4	1.17	1539.53	1399.2	1.10	
<i>relA</i>	2819755	2821959	-	1402.56	1242.35	1.13	1523.96	1535.55	0.99	
<i>apt</i>	2822127	2822639	-	880.53	709.81	1.24	1318.93	1404.63	0.94	
<i>yrvE</i>	2822645	2825005	-	687.66	619.3	1.11	1040.29	1120.11	0.93	
<i>yrvD</i>	2825072	2825395	-	1129.74	1212.18	0.93	896.72	659.05	1.36	
<i>yrvC</i>	2825471	2825968	-	338.27	358.86	0.94	461.68	633.31	0.73	
<i>secDF</i>	2826126	2828339	-	1514.18	1550.65	0.98	1539.93	1768.51	0.87	
<i>yrzD</i>	2828378	2828674	-	1375.04	1420.57	0.97	1612.25	2008.53	0.80	
<i>spoVB</i>	2828790	2830346	+	59.19	64.73	0.91	52.87	63.47	0.83	
<i>yrbG</i>	2830350	2831006	-	55.49	63.75	0.87	46.76	52.94	0.88	
<i>yrzE</i>	2831141	2831593	+	70.01	57.94	1.21	67.28	55.07	1.22	
<i>yrbF</i>	2831650	2831919	-	2593.37	2446.94	1.06	2056.06	2083.53	0.99	
<i>tgt</i>	2831953	2833098	-	759.93	589.83	1.29	1158.16	1045.34	1.11	
<i>queA</i>	2833125	2834153	-	905.31	677.46	1.34	1227.64	1156.5	1.06	
<i>ruvB</i>	2834376	2835380	-	568.14	471.12	1.21	713.84	763.52	0.93	
<i>ruvA</i>	2835391	2835996	-	541.78	400.97	1.35	474.95	626.55	0.76	
<i>bofC</i>	2836135	2836647	-	1054.5	700.66	1.51	427.88	264.59	1.62	
<i>csbX</i>	2836695	2838002	-	1941.8	1477.79	1.31	731.72	449.64	1.63	
<i>yrbE</i>	2838073	2839098	-	228.77	235.33	0.97	233.5	285.93	0.82	
<i>yrzF</i>	2839336	2839728	+	514.97	505.09	1.02	387.99	406.34	0.95	
<i>yrzG</i>	2839761	2839982	+	505.22	521.88	0.97	283.26	321.34	0.88	
<i>yrbD</i>	2840836	2842290	+	132.02	136.5	0.97	94.61	106.05	0.89	
<i>yrbC</i>	2842331	2843053	-	210.19	204.14	1.03	264.25	239.4	1.10	
<i>coxA</i>	2843156	2843674	-	362.15	354.3	1.02	495.26	489.59	1.01	
<i>safA</i>	2843900	2845063	-	3235.46	3539.64	0.91	2888.12	2994.54	0.96	
<i>nadA</i>	2845180	2846286	-	4229.09	4270.49	0.99	3634.81	3682.68	0.99	
<i>nadC</i>	2846273	2847142	-	2946.66	2577.2	1.14	2468.91	2592.44	0.95	
<i>nadB</i>	2847096	2848691	-	2521.91	1815.34	1.39	2212.16	2542.45	0.87	
<i>nifS</i>	2848794	2849981	+	1202.56	792.72	1.52	1102.76	1302.92	0.85	
<i>yrxA</i>	2849941	2850477	+	1560.11	1172.27	1.33	1725.86	1969.67	0.88	
<i>pheA</i>	2850509	2851366	-	352.69	375.89	0.94	655.14	675.65	0.97	
<i>pheB</i>	2851383	2851826	-	875.26	864.92	1.01	1194.95	1211.17	0.99	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>rplU</i>	2854744	2855052	-	6299	7465.03	0.84	5887.07	5916.8	0.99	
<i>spolVFB</i>	2855199	2856065	-	76.89	64.91	1.18	95.14	75.83	1.25	
<i>spolVFA</i>	2856058	2856852	-	88.49	66.84	1.32	119.64	82.83	1.44	
<i>minD</i>	2857003	2857809	-	1551.25	1335.39	1.16	2107.76	2063.47	1.02	
<i>minC</i>	2857811	2858491	-	1728.69	1468.19	1.18	2271.69	2359.4	0.96	
<i>mreD</i>	2858544	2859062	-	1158.8	908.61	1.28	1670	1751.87	0.95	
<i>mreC</i>	2859059	2859931	-	1374.55	1156.59	1.19	2606.81	2587.62	1.01	
<i>mreB</i>	2859962	2860975	-	1308.36	1173.22	1.12	2004.66	2110.25	0.95	
<i>radC</i>	2861066	2861761	-	500.94	491.79	1.02	849.96	949.87	0.89	
<i>maf</i>	2861798	2862367	-	734.19	733.33	1.00	1271.86	1288.62	0.99	
<i>spolIB</i>	2862520	2863518	-	118.77	110.21	1.08	130.81	165.82	0.79	
<i>comC</i>	2863652	2864398	-	149.74	145.22	1.03	203.73	291.81	0.70	
<i>folC</i>	2864538	2865830	-	523.74	594.92	0.88	985.34	993.81	0.99	
<i>valS</i>	2865890	2868532	-	673.48	639.25	1.05	1406.02	1504.74	0.93	
<i>ysxE</i>	2869029	2870054	-	72.64	75.86	0.96	62.8	78.28	0.80	
<i>spoVID</i>	2870087	2871814	-	95.7	98.92	0.97	79.39	85.77	0.93	
<i>hemL</i>	2871945	2873237	-	1615.61	1241.23	1.30	1439.66	1139.29	1.26	
<i>hemB</i>	2873267	2874241	-	1657.81	1187.91	1.40	1517.55	1244.07	1.22	
<i>hemD</i>	2874238	2875026	-	1103.99	679.72	1.62	902.88	712.72	1.27	
<i>hemC</i>	2875016	2875960	-	1122.36	684.65	1.64	766.24	606.13	1.26	
<i>hemX</i>	2875993	2876823	-	586.66	375.08	1.56	415.38	359.82	1.15	
<i>hemA</i>	2876831	2878198	-	1715.05	1349.02	1.27	1121.04	1073.97	1.04	
<i>ysxD</i>	2878362	2878925	+	76.8	82.06	0.94	104.57	106.75	0.98	
<i>ysxC</i>	2878947	2879534	-	1093.03	854.06	1.28	1395.21	1138.25	1.23	
<i>lonA</i>	2879531	2881855	-	1588.73	1266.86	1.25	1518.42	1233.68	1.23	
<i>lonB</i>	2882036	2883694	-	130.14	104.38	1.25	85.49	94.73	0.90	
<i>clpX</i>	2883846	2885108	-	2186.05	2012.94	1.09	2185.88	2322.09	0.94	
<i>tig</i>	2885381	2886655	-	2232.86	1990.75	1.12	3463.58	3784.58	0.92	
<i>ysoA</i>	2886883	2887815	-	558.08	634.81	0.88	744.83	986.37	0.76	
<i>leuD</i>	2888005	2888604	-	1006.88	1504.53	0.67	1629.93	2052.59	0.79	
<i>leuC</i>	2888617	2890035	-	2909.58	3903.36	0.75	3602.06	4322.83	0.83	
<i>leuB</i>	2890085	2891182	-	2714.83	3637.96	0.75	3598.8	4308.75	0.84	
<i>leuA</i>	2891203	2892759	-	2749.39	3631.94	0.76	3349.93	4039.72	0.83	
<i>ilvC</i>	2892746	2893774	-	4119.65	5246.46	0.79	4522.78	5069.34	0.89	
<i>ilvH</i>	2893791	2894315	-	3083.26	3915.38	0.79	3737.23	4204.75	0.89	
<i>ilvB</i>	2894312	2896036	-	2256.75	2677.71	0.84	2840.12	3467.56	0.82	
<i>ysnD</i>	2896852	2897187	+	63.41	64.55	0.98	48.9	53.44	0.92	
<i>ysnE</i>	2897356	2897811	+	103.26	107.46	0.96	128.4	125.14	1.03	
<i>ysnF</i>	2897995	2898855	+	2698.46	2692.51	1.00	1736.81	929.76	1.87	
<i>ysnB</i>	2899086	2899601	-	2157.63	1488.88	1.45	1543.21	1176.79	1.31	
<i>ysnA</i>	2899611	2900207	-	2485.58	1700.29	1.46	1819.28	1474.91	1.23	
<i>rph</i>	2900220	2900957	-	2121.04	1428.01	1.49	1442.08	1192.45	1.21	
<i>gerM</i>	2901068	2902168	-	144.43	132.54	1.09	87.26	98.74	0.88	
<i>racE</i>	2902284	2903102	-	516.66	493.38	1.05	639.22	718.55	0.89	
<i>ysmB</i>	2903110	2903550	-	755.5	721.13	1.05	937.63	1142.48	0.82	
<i>gerE</i>	2903794	2904018	-	151.06	155.58	0.97	222.61	279.16	0.80	
<i>ysmA</i>	2904134	2904577	-	227.19	323.32	0.70	368.28	517.11	0.71	
<i>sdhB</i>	2904640	2905401	-	2442.65	2861.63	0.85	2758.21	2933.8	0.94	
<i>sdhA</i>	2905404	2907164	-	2357.17	2697.76	0.87	3084.82	3347.1	0.92	
<i>sdhC</i>	2907198	2907806	-	1714.4	1727.45	0.99	2263.11	2563.02	0.88	
<i>ysiB</i>	2908099	2908545	+	961.37	862.97	1.11	1131.33	860.04	1.32	
<i>lysC</i>	2908589	2909815	-	1327.22	1406.17	0.94	1436.85	1835.97	0.78	
<i>uvrC</i>	2910160	2911956	-	461.25	324.66	1.42	332.79	343.11	0.97	
<i>trxA</i>	2912092	2912406	-	4848.67	4159.65	1.17	3549.13	3589.09	0.99	
<i>xsa</i>	2912729	2914216	-	93.93	102.77	0.91	85.68	106.06	0.81	
<i>etfA</i>	2914433	2915410	-	260.51	375.6	0.69	315.33	461.04	0.68	
<i>etfB</i>	2915446	2916219	-	376.54	482.09	0.78	476.6	643.63	0.74	
<i>ysiB</i>	2916234	2917010	-	264.03	327.52	0.81	316.77	422.22	0.75	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yshC</i>	2922382	2924094	-	565.12	540.06	1.05	749.03	777.07	0.96	
<i>yshB</i>	2924168	2924701	-	156.06	165.83	0.94	133.6	166.74	0.80	
<i>yshA</i>	2924708	2924965	-	319.53	317.58	1.01	421.25	574.94	0.73	
<i>rnhC</i>	2925099	2926040	+	280.53	247.37	1.13	305.93	343.46	0.89	
<i>pheT</i>	2926076	2928490	-	901.37	983.21	0.92	1333.7	1337.23	1.00	
<i>pheS</i>	2928506	2929540	-	830.61	785.14	1.06	1412.57	1485.58	0.95	
<i>ysgA</i>	2929895	2930641	-	314.83	276.95	1.14	301.55	349.88	0.86	
<i>sspl</i>	2930760	2930975	+	37.03	45.95	0.81	35.73	36.42	0.98	
<i>ysfB</i>	2931044	2932150	+	130.82	114.9	1.14	152.21	160.98	0.95	
<i>ysfC</i>	2932253	2933665	+	350.52	245.36	1.43	359.33	373.78	0.96	
<i>ysfD</i>	2933662	2934996	+	289.28	214.54	1.35	238.27	245.07	0.97	
<i>ysfE</i>	2935035	2935277	-	384.25	413.57	0.93	398.53	430.05	0.93	
<i>cstA</i>	2935450	2937246	-	227.08	251.48	0.90	238.33	270.92	0.88	
<i>abfA</i>	2937398	2938900	-	80.2	81.83	0.98	69.69	85.03	0.82	
<i>araQ</i>	2938919	2939764	-	51.42	51.93	0.99	45.29	49.41	0.92	
<i>araP</i>	2939765	2940706	-	74.24	74.93	0.99	64.31	72.43	0.89	
<i>araN</i>	2940742	2942043	-	73.59	76.4	0.96	68.47	74.72	0.92	
<i>araM</i>	2942074	2943258	-	69.55	68.8	1.01	60.29	71.06	0.85	
<i>araL</i>	2943255	2944073	-	65.65	68.73	0.96	55.83	64.87	0.86	
<i>araD</i>	2944051	2944740	-	57.79	62.06	0.93	57.24	65.33	0.88	
<i>araB</i>	2944757	2946439	-	130.88	139.87	0.94	134.23	138.44	0.97	
<i>araA</i>	2946453	2947949	-	145.37	142.26	1.02	127.63	152.23	0.84	
<i>abnA</i>	2948157	2949098	-	42.47	43.15	0.98	33.97	37.67	0.90	
<i>ysdC</i>	2949295	2950380	-	1223.55	1096.01	1.12	1554.25	1466.21	1.06	
<i>ysdB</i>	2950564	2950956	+	1170.45	1439.7	0.81	955.87	960.76	0.99	
<i>ysdA</i>	2950972	2951241	-	55.26	68.82	0.80	128.82	134.43	0.96	
<i>rplT</i>	2951298	2951657	-	718.66	1010.14	0.71	1373.14	1596.54	0.86	
<i>rpml</i>	2951689	2951889	-	4590.09	5265.65	0.87	4704.04	4813.33	0.98	
<i>infC</i>	2951902	2952423	-	4238.2	4788.9	0.89	4362.78	4414.49	0.99	
<i>yscA</i>	2952595	2952819	+	16.57	24.51	0.68	24.68	21.57	1.14	
<i>yscB</i>	2952869	2953501	+	2047.99	2290.72	0.89	1736.85	1691.3	1.03	AbrB and SigD regulon
<i>ysbB</i>	2953533	2954228	-	100.67	109.63	0.92	69.99	96.12	0.73	
<i>ysbA</i>	2954250	2954690	-	48.08	52.03	0.92	48.11	52.03	0.92	
<i>lytT</i>	2954824	2955549	-	223.86	173.92	1.29	337.09	329.78	1.02	
<i>lytS</i>	2955527	2957308	-	164.57	146.12	1.13	174.12	200.02	0.87	
<i>ysaA</i>	2957475	2958257	+	667.17	623.19	1.07	903.99	1113.65	0.81	
<i>thrS</i>	2958298	2960229	-	770.17	832.76	0.92	1297.42	1376.15	0.94	
<i>ytxC</i>	2960626	2961471	-	293.14	236.34	1.24	388.03	404.53	0.96	
<i>ytxB</i>	2961550	2962191	-	420.66	328.2	1.28	598.53	575.99	1.04	
<i>dnal</i>	2962225	2963160	-	343.91	285.12	1.21	460.16	497.78	0.92	
<i>dnaB</i>	2963188	2964606	-	205.83	197.4	1.04	265.51	331.76	0.80	
<i>ytCG</i>	2964721	2965179	-	137.65	151.08	0.91	226.51	242.23	0.94	
<i>speD</i>	2965453	2965839	-	1061.42	1449.18	0.73	1112.83	1234.9	0.90	
<i>gapB</i>	2966072	2967094	-	75.48	75.73	1.00	76.63	87.7	0.87	
<i>ytCD</i>	2967300	2967680	-	89.55	83.46	1.07	115.66	118.1	0.98	
<i>ytdD</i>	2967864	2969054	+	67.49	64.37	1.05	51.12	55.45	0.92	
<i>ytdE</i>	2969078	2969920	+	90.39	89.13	1.01	88.61	92.72	0.96	
<i>ytdG</i>	2969962	2970555	-	596.53	421.21	1.42	879.21	740.92	1.19	
<i>ytdF</i>	2970717	2971196	-	842.16	615.05	1.37	1378.56	1076.34	1.28	
<i>mutM</i>	2971368	2972204	-	833.61	641.08	1.30	1228.29	964.43	1.27	
<i>polA</i>	2972221	2974863	-	735.63	504.14	1.46	925.06	815.62	1.13	
<i>phoR</i>	2975107	2976846	-	479.82	453.88	1.06	537.01	594.65	0.90	
<i>phoP</i>	2976839	2977561	-	441.96	476.64	0.93	444.43	546.63	0.81	
<i>mdh</i>	2977773	2978711	-	6217.58	6825.9	0.91	5291.25	5258.04	1.01	
<i>icd</i>	2978755	2980026	-	7020.17	7499.56	0.94	6242.13	6092.87	1.02	
<i>citZ</i>	2980190	2981308	-	5717.28	6244.82	0.92	4840.96	4803.08	1.01	
<i>ytdW</i>	2981642	2982106	-	130.83	140.39	0.93	207.33	221.89	0.93	
<i>ytdV</i>	2982203	2983318	+	42.56	44.64	0.95	33.92	41.96	0.81	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>accD</i>	2987732	2988520	-	1607.26	1573.42	1.02	2283.75	2377.3	0.96	Spo0A regulon
<i>ytsJ</i>	2988939	2990171	-	1090.66	1092.16	1.00	1261.34	1372.54	0.92	
<i>dnaE</i>	2990308	2993655	-	479.69	440.03	1.09	436.32	426.81	1.02	
<i>ytrI</i>	2994133	2994636	+	31.04	33.54	0.93	35.69	36.12	0.99	
<i>ytqI</i>	2994947	2995888	-	339.82	360.61	0.94	619.14	730.67	0.85	
<i>ytpl</i>	2996019	2996321	+	596.83	478.25	1.25	405.08	437.36	0.93	
<i>ytol</i>	2996340	2997659	-	244.85	248.78	0.98	255.29	310.5	0.82	
<i>ytnM</i>	2997835	2998737	-	66.02	68.53	0.96	57.74	63.37	0.91	
<i>ytnL</i>	2998756	3000006	-	57.66	57.83	1.00	57.27	57.41	1.00	
<i>ribR</i>	3000024	3000716	-	51.82	51.48	1.01	56.18	52.3	1.07	
<i>ytnJ</i>	3000763	3002091	-	60.99	67.01	0.91	58.93	62.82	0.94	
<i>ytnI</i>	3002088	3002369	-	69.29	68.27	1.01	79.22	79.32	1.00	
<i>ytmO</i>	3002384	3003388	-	92.8	94.56	0.98	79.91	95.3	0.84	
<i>ytmN</i>	3003385	3004164	-	122.67	120.49	1.02	90.29	118.02	0.77	
<i>ytmM</i>	3004161	3004868	-	45.54	45.44	1.00	40.76	43.81	0.93	
<i>ytmL</i>	3004898	3005617	-	41.89	40.7	1.03	40.2	44.28	0.91	
<i>ytmK</i>	3005639	3006451	-	59.84	53.09	1.13	51.29	61.92	0.83	
<i>ytmJ</i>	3006465	3007274	-	70.44	63.87	1.10	58.16	70.31	0.83	
<i>ytml</i>	3007288	3007824	-	48.52	43.21	1.12	43.85	56.2	0.78	
<i>ytlI</i>	3007977	3008903	+	71.96	54.76	1.31	94.5	153.12	0.62	
<i>ytkL</i>	3008954	3009637	-	2853.19	2179.02	1.31	1701.34	1330.36	1.28	
<i>ytkK</i>	3009700	3010467	-	589.93	494.89	1.19	758.95	846.97	0.90	
<i>ytzD</i>	3010594	3010830	-	263.27	300.07	0.88	996.55	1284.23	0.78	
<i>argH</i>	3010790	3012175	-	835.12	905.45	0.92	2398.07	2747.35	0.87	
<i>argG</i>	3012172	3013383	-	477.02	454.38	1.05	1954.91	2373.13	0.82	
<i>moaB</i>	3013553	3014065	-	246.09	191.8	1.28	391.67	336.52	1.16	
<i>ackA</i>	3014150	3015337	-	733.63	590.84	1.24	1311.16	1159.38	1.13	
<i>ytxK</i>	3015685	3016674	-	636.6	617.23	1.03	684.87	666.75	1.03	
<i>tpx</i>	3016735	3017238	-	3340.52	3579.87	0.93	2866.76	2731.48	1.05	
<i>ytfJ</i>	3017348	3017803	-	46.74	51.84	0.90	50.83	56.98	0.89	
<i>ytfI</i>	3017817	3018497	-	65.22	67.45	0.97	77.99	76.56	1.02	
<i>yteJ</i>	3018572	3019066	-	986.19	1154.83	0.85	2593.48	2606.26	1.00	
<i>sppA</i>	3019079	3020086	-	901.89	923.31	0.98	1766.34	1936.29	0.91	
<i>ytdI</i>	3020272	3021075	+	838.84	1125.84	0.75	1092.48	1159.47	0.94	
<i>ytcJ</i>	3021107	3022696	-	660.55	572.42	1.15	1068.24	928.27	1.15	
<i>ytcl</i>	3022716	3024311	-	630.84	486.39	1.30	1133.43	1042.53	1.09	
<i>sspA</i>	3024484	3024693	-	189.07	155.65	1.21	286.63	267.1	1.07	
<i>ytbJ</i>	3024920	3025996	-	285.59	220.79	1.29	512.86	473.36	1.08	
<i>niZ</i>	3026000	3027145	-	209.28	189.38	1.11	267.25	263.89	1.01	
<i>braB</i>	3027340	3028677	+	86.38	75.21	1.15	231.31	183.55	1.26	
<i>ezrA</i>	3028772	3030460	-	1229.43	1289.73	0.95	1298.53	1590.39	0.82	
<i>hisJ</i>	3030657	3031463	+	464.54	491.49	0.95	415	511.41	0.81	
<i>yttP</i>	3031460	3032083	-	58.73	68.33	0.86	65.79	77.78	0.85	Spo0A regulon
<i>ytsP</i>	3032464	3032700	+	296.92	298.61	0.99	579.85	625.1	0.93	
<i>ytrP</i>	3032738	3034477	-	458.41	319.19	1.44	257.71	271.81	0.95	
<i>rpsD</i>	3034772	3035374	+	825.16	1051.44	0.78	1496.55	1737.17	0.86	
<i>tyrS</i>	3035645	3036913	-	487.27	481.16	1.01	1162.77	1310.61	0.89	
<i>acsA</i>	3037255	3038973	-	832.7	997.67	0.83	1091.3	1381.89	0.79	
<i>acuA</i>	3039134	3039766	+	409.46	310.32	1.32	413.22	417.15	0.99	
<i>acuB</i>	3039793	3040437	+	433.57	328.17	1.32	464.41	495.42	0.94	
<i>acuC</i>	3040434	3041597	+	470.02	387.1	1.21	522.83	537.03	0.97	
<i>ytxE</i>	3041608	3042336	-	90.44	99.88	0.91	178.9	240.47	0.74	
<i>ytxD</i>	3042326	3043144	-	76.84	86.24	0.89	196.38	216.84	0.91	
<i>ccpA</i>	3043207	3044211	-	489.39	493.74	0.99	822.41	905.82	0.91	
<i>aroA</i>	3044486	3045562	-	1886.79	1856.94	1.02	3398.7	3408.74	1.00	
<i>ytxJ</i>	3045798	3046124	-	4710.09	5239.31	0.90	2277.07	1915.8	1.19	
<i>ytxH</i>	3046148	3046606	-	6707.04	7459.08	0.90	3928.96	3556.18	1.10	
<i>ytxG</i>	3046634	3047065	-	6740.09	7410.02	0.91	4003.76	3358.36	1.19	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ytpQ</i>	3052413	3053222	-	1048.87	755.08	1.39	1649.95	1438.61	1.15	
<i>ytpP</i>	3053237	3053560	-	877.9	611.31	1.44	1354.41	1326.48	1.02	
<i>ytoQ</i>	3053795	3054241	+	751.94	780.55	0.96	1220.39	1260.21	0.97	
<i>ytoP</i>	3054296	3055369	-	741.56	746.98	0.99	839.73	896.71	0.94	
<i>ytzB</i>	3055528	3055845	+	2058.24	1892.95	1.09	2297.98	2077.54	1.11	
<i>malS</i>	3055898	3057598	-	3385.26	2698.25	1.25	3026.79	2266.74	1.34	
<i>ytnP</i>	3057680	3058450	-	3792.32	2993.39	1.27	3385.13	2573.62	1.32	
<i>ytmQ</i>	3058596	3059237	-	256.35	300.01	0.85	327.25	423.62	0.77	
<i>ytzH</i>	3059444	3059722	+	22.32	27.02	0.83	24.8	27.08	0.92	
<i>ytmP</i>	3059723	3060532	-	444.51	455.05	0.98	477.06	564.53	0.85	
<i>amyX</i>	3060700	3062856	-	597.51	433.32	1.38	580.54	576.37	1.01	
<i>ytiR</i>	3062882	3063811	-	1136.67	861.88	1.32	975.61	938.04	1.04	
<i>ytiQ</i>	3063860	3064774	-	1111.41	988.84	1.12	1049.26	916.06	1.15	
<i>ytlP</i>	3064800	3065351	-	608.56	515.02	1.18	772.79	658.44	1.17	
<i>ytkP</i>	3065500	3066435	+	203.95	196.81	1.04	284.79	321.78	0.89	
<i>ytjP</i>	3066469	3067860	-	1062.76	833.96	1.27	1362.76	1058.71	1.29	
<i>ytiP</i>	3067957	3069255	+	106.99	87.41	1.22	115.93	120.12	0.97	
<i>ythQ</i>	3069294	3070451	-	451.67	398.99	1.13	656.29	657.05	1.00	
<i>ythP</i>	3070448	3071158	-	704.98	608.7	1.16	1000.47	938.96	1.07	
<i>ytzE</i>	3071449	3071670	+	649.2	886.94	0.73	305.59	319.66	0.96	
<i>ytzF</i>	3071791	3072264	-	206.65	164.46	1.26	240.62	237.66	1.01	
<i>ytzG</i>	3072249	3072509	-	195.31	172.87	1.13	230.37	245.54	0.94	
<i>ytgP</i>	3072578	3074212	-	312.04	266.35	1.17	358.99	421.41	0.85	
<i>ytiP</i>	3074720	3075676	+	540.89	434.84	1.24	527.41	457.32	1.15	
<i>opuD</i>	3075865	3077403	+	747.52	557.67	1.34	515.33	449.45	1.15	
<i>yteV</i>	3077440	3077622	-	21.83	33.26	0.66	23.98	26.84	0.89	
<i>yteU</i>	3077690	3078358	-	58.79	57.52	1.02	69.26	62.99	1.10	
<i>yteT</i>	3078380	3079666	-	98.87	98.49	1.00	82.5	90.1	0.92	
<i>yteS</i>	3079678	3080157	-	51.5	49.45	1.04	42.17	50.42	0.84	
<i>yteR</i>	3080178	3081299	-	91.51	93.96	0.97	63.53	77.24	0.82	
<i>yteQ</i>	3081307	3081798	-	90.36	89.15	1.01	72.83	91.15	0.80	
<i>yteP</i>	3081893	3082273	-	34.97	38.95	0.90	33.58	35.26	0.95	
<i>ytdP</i>	3082489	3084807	+	112.74	115.75	0.97	110.81	106.59	1.04	
<i>ytcQ</i>	3084848	3086317	-	161.56	140.99	1.15	109.94	110.89	0.99	
<i>ytcP</i>	3086370	3087230	-	89.62	88.76	1.01	55.12	61.12	0.90	
<i>ytbQ</i>	3087437	3088042	-	1067.86	1032.01	1.03	1359.73	1323.96	1.03	
<i>bioI</i>	3088275	3089462	-	947.47	1002.5	0.95	1557.46	1505.51	1.03	
<i>bioB</i>	3089531	3090538	-	1837.99	1843.5	1.00	2686.75	2663.39	1.01	
<i>bioD</i>	3090541	3091236	-	1954.51	1814.36	1.08	2441.58	2271.38	1.07	
<i>bioF</i>	3091233	3092402	-	3340.56	3115.57	1.07	3685.58	3390.89	1.09	
<i>bioA</i>	3092392	3093738	-	3169.35	2930.89	1.08	3214.74	2989.73	1.08	
<i>bioW</i>	3093728	3094507	-	2556.85	2393.37	1.07	2959.77	2712.27	1.09	
<i>ytaP</i>	3094714	3095613	-	68.03	72.77	0.93	68.58	72.11	0.95	
<i>msmR</i>	3095831	3096865	+	88.19	92.26	0.96	84.43	101.71	0.83	
<i>msmE</i>	3096899	3098179	+	81.88	102.9	0.80	85.74	115.95	0.74	
<i>amyD</i>	3098172	3099083	+	57.1	73.92	0.77	65	84.81	0.77	
<i>amyC</i>	3099080	3099910	+	73.93	83.59	0.88	68.62	92.57	0.74	
<i>melA</i>	3099930	3101228	+	136.65	142.99	0.96	153.93	182.03	0.85	
<i>ytwF</i>	3101250	3101456	-	258.07	184.9	1.40	305.83	302.17	1.01	
<i>leuS</i>	3101678	3104092	-	1015.95	838.01	1.21	1522.46	1449.71	1.05	
<i>ytvB</i>	3104519	3104854	-	204.4	153.54	1.33	152.33	172.21	0.88	
<i>ytvA</i>	3105259	3106044	+	250.83	192.15	1.31	287.43	228.83	1.26	
<i>yttB</i>	3106281	3107474	-	70.74	61.38	1.15	63.06	64.2	0.98	
<i>ytiA</i>	3107669	3108409	+	356.47	329.77	1.08	445.37	513.92	0.87	
<i>ytsD</i>	3108446	3110386	-	118.21	102.42	1.15	112.46	115.86	0.97	
<i>ytsC</i>	3110376	3111137	-	103.8	93.22	1.11	100.85	111.69	0.90	
<i>ytsB</i>	3111239	3112243	-	296.29	271.56	1.09	372.11	373.16	1.00	
<i>ytsA</i>	3112236	3112931	-	222.64	212.51	1.05	239.8	265.22	0.90	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ytrB</i>	3117025	3117903	-	264.55	279.47	0.95	394.07	584.16	0.67	
<i>ytrA</i>	3117896	3118288	-	232.4	252.7	0.92	306.27	506.7	0.60	
<i>ytzC</i>	3118614	3118886	-	137.22	137.75	1.00	90.27	67.21	1.34	
<i>ytqA</i>	3119048	3120016	+	308.48	332.2	0.93	410.53	568.12	0.72	
<i>ytqB</i>	3120013	3120597	+	346.65	352.2	0.98	564.68	669.62	0.84	
<i>ytpB</i>	3120587	3121690	-	1034.42	802.25	1.29	1138.88	904.62	1.26	
<i>ytpA</i>	3121711	3122490	-	1326.13	966.35	1.37	1345.53	1117.46	1.20	
<i>ytoA</i>	3122539	3123054	+	187.05	221.72	0.84	255.08	306.02	0.83	
<i>ytnA</i>	3123299	3124690	-	437.09	392.25	1.11	783.2	809.9	0.97	
<i>asnB</i>	3124826	3126724	-	673.83	527.94	1.28	1192.58	1265.92	0.94	
<i>metK</i>	3126874	3128076	-	1042.15	993.15	1.05	1349.14	1594.97	0.85	
<i>pckA</i>	3128579	3130162	+	156.42	164.03	0.95	177.09	231.81	0.76	
<i>ytmB</i>	3130201	3130443	-	582.15	497.74	1.17	309.51	378.29	0.82	
<i>ytmA</i>	3130495	3131268	-	189.4	150.5	1.26	200.18	193.01	1.04	
<i>ytlA</i>	3131419	3132108	+	50.43	56.48	0.89	47.07	52	0.91	
<i>ytlB</i>	3132105	3132422	+	36.38	42.23	0.86	27.35	28.68	0.95	
<i>ytlC</i>	3132435	3133217	+	42.2	42.4	1.00	37.29	39.95	0.93	
<i>ytlD</i>	3133192	3134004	+	37.94	41.02	0.92	34.62	34.81	0.99	
<i>ytkD</i>	3134031	3134507	-	320.87	316.15	1.01	282.79	306.19	0.92	
<i>ytkC</i>	3134716	3135120	-	143.79	128.85	1.12	70.99	61.55	1.15	
<i>dps</i>	3135286	3135723	-	7706.61	8265.5	0.93	5263.86	4484.17	1.17	
<i>ytkA</i>	3135986	3136423	-	1188.12	1021.83	1.16	670.06	553.53	1.21	
<i>luxS</i>	3136543	3137016	-	1283.88	1178.73	1.09	1206.39	1054.63	1.14	
<i>ytiA</i>	3137145	3137372	+	189.2	226.26	0.84	130.86	206.72	0.63	
<i>ytiB</i>	3137369	3137932	-	784.8	736.69	1.07	706.55	786.17	0.90	
<i>ytiA</i>	3138026	3138274	-	2347.97	1869.29	1.26	1786.4	803.86	2.22	
<i>ythA</i>	3138494	3139810	+	65.01	66.8	0.97	49.47	60.39	0.82	
<i>ythB</i>	3139854	3140894	+	54.58	50.52	1.08	55.53	52.17	1.06	
<i>ythC</i>	3140943	3141110	+	126.31	113.35	1.11	87.45	117.9	0.74	
<i>mntD</i>	3141125	3142012	-	1857.31	1619.67	1.15	2161.71	1883.56	1.15	
<i>mntC</i>	3142002	3143309	-	2561.4	2207.43	1.16	3101.9	2772.59	1.12	
<i>mntB</i>	3143315	3144067	-	2708.79	2277.05	1.19	3460.57	3220.93	1.07	
<i>mntA</i>	3144086	3145006	-	2674.17	1984.42	1.35	3707.73	3576.13	1.04	
<i>menC</i>	3145286	3146401	-	1104.36	748.9	1.47	636.51	423.34	1.50	
<i>menE</i>	3146398	3147858	-	1107.75	816.38	1.36	696.47	498.71	1.40	
<i>menB</i>	3147949	3148764	-	2419.87	2033.7	1.19	2203.83	1824.43	1.21	
<i>ytxM</i>	3148799	3149623	-	577.89	400.24	1.44	555.03	410.4	1.35	
<i>menD</i>	3149611	3151353	-	400.38	286.68	1.40	439.61	361.48	1.22	
<i>menF</i>	3151350	3152765	-	466.37	335.68	1.39	672.52	619.03	1.09	
<i>yteA</i>	3153054	3153773	+	35.45	39.63	0.89	32.62	37.46	0.87	
<i>ytdA</i>	3153782	3154600	-	68.01	64.42	1.06	60.58	63.21	0.96	
<i>ytcA</i>	3154772	3156058	+	105.47	101.09	1.04	65.18	76.29	0.85	
<i>ytcB</i>	3156055	3157005	+	44.2	44.64	0.99	35.73	43.45	0.82	
<i>ytcC</i>	3157008	3158231	+	40.34	42.93	0.94	34.59	38.01	0.91	
<i>ytxO</i>	3158305	3158736	-	47.69	58.69	0.81	55.95	54.26	1.03	
<i>cotS</i>	3158738	3159793	-	126.74	137.97	0.92	122.85	143.6	0.86	
<i>cotSA</i>	3159808	3160941	-	155.81	148.16	1.05	126.92	138.22	0.92	
<i>ytaA</i>	3161131	3162204	+	36.99	42.28	0.87	38.3	40.56	0.94	
<i>ytaB</i>	3162284	3162751	+	1024.52	719.91	1.42	429.2	169.85	2.53	
<i>glgP</i>	3162782	3165178	-	100.13	96	1.04	110.61	112.13	0.99	
<i>glgA</i>	3165165	3166619	-	114.14	112.93	1.01	118.21	128.83	0.92	
<i>glgD</i>	3166616	3167647	-	91.94	91.16	1.01	95.69	100.09	0.96	
<i>glgC</i>	3167671	3168813	-	66.76	65.25	1.02	69.21	75.47	0.92	
<i>glgB</i>	3168810	3170693	-	49.05	55.33	0.89	48.97	56.63	0.86	
<i>yuaJ</i>	3178345	3178923	+	1058.49	1147.25	0.92	939.46	985.08	0.95	
<i>yuaI</i>	3178965	3179486	-	1571.98	1520.79	1.03	1867.08	2009.14	0.93	
<i>yuaG</i>	3179504	3181033	-	1603.15	1533.33	1.05	2194.24	2425.8	0.90	
<i>yuaF</i>	3181054	3181578	-	964.48	880.41	1.10	1301.15	1520.74	0.86	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yuaC</i>	3185802	3186344	+	83.55	83.55	1.00	135.28	205.52	0.66	
<i>yuaB</i>	3186542	3187087	+	541.74	397.85	1.36	704.67	532.6	1.32	AbrB regulon
<i>yuaA</i>	3187453	3188121	+	143.68	133.18	1.08	142.66	144.28	0.99	
<i>yubG</i>	3188128	3189465	+	122.74	109.23	1.12	119.31	118.79	1.00	
<i>yubF</i>	3189501	3189764	-	1171.94	1290.48	0.91	2172.07	2096.59	1.04	
<i>yubE</i>	3189873	3190721	-	181.24	194.33	0.93	254.33	315.6	0.81	
<i>yubD</i>	3190882	3192417	-	315.85	254.23	1.24	210.28	218.02	0.96	
<i>yubC</i>	3192902	3193387	+	26.2	30.42	0.86	28.82	30.77	0.94	
<i>yubB</i>	3193674	3194504	-	353.02	299.8	1.18	541.68	499.08	1.09	
<i>yubA</i>	3194597	3195763	-	506.47	408	1.24	507.35	529.15	0.96	
<i>yulF</i>	3195945	3196931	+	405.16	338.12	1.20	584.69	544.08	1.07	
<i>yulE</i>	3196972	3198246	-	79.71	84.7	0.94	81.81	91.27	0.90	
<i>yulD</i>	3198272	3198586	-	68.94	66.74	1.03	92.78	90.82	1.02	
<i>yulC</i>	3198604	3200061	-	155.27	141.14	1.10	187.88	203.66	0.92	
<i>yulB</i>	3200066	3200842	-	166.85	156.79	1.06	203.92	209.94	0.97	
<i>yuxG</i>	3200899	3202968	-	77.78	85.81	0.91	83.08	106.37	0.78	
<i>tlpB</i>	3203106	3205094	-	905.85	677.83	1.34	853.46	543.65	1.57	SigD regulon
<i>mcpA</i>	3205208	3207193	-	2341.27	2982.14	0.79	1699.45	1948.29	0.87	SigD regulon
<i>tlpA</i>	3207319	3209307	-	777.97	790.1	0.98	698.28	700.87	1.00	AbrB and SigD regulon
<i>mcpB</i>	3209484	3211472	-	2298.18	2752.26	0.84	1389.2	1540.44	0.90	SigD regulon
<i>tgl</i>	3211630	3212367	+	62.96	67.79	0.93	62.9	66.48	0.95	
<i>yugU</i>	3212892	3213320	-	1668.75	1352.35	1.23	917.2	528.88	1.73	
<i>yugT</i>	3213410	3215074	-	78.92	71.85	1.10	75.93	75.52	1.01	
<i>yugS</i>	3215201	3216505	-	65.77	74.74	0.88	60.8	70.22	0.87	
<i>yugP</i>	3216533	3217210	-	206.59	217.51	0.95	257.77	283.65	0.91	
<i>yugO</i>	3217562	3218878	+	195.07	130.26	1.50	63.95	67.6	0.95	
<i>yugN</i>	3218875	3219279	-	210.56	234.68	0.90	175.36	211.83	0.83	
<i>yugM</i>	3219339	3219710	-	269.88	321.29	0.84	299.55	327.26	0.92	
<i>pgi</i>	3219769	3221124	-	1578.39	1505.81	1.05	2217.59	2031.72	1.09	
<i>yugK</i>	3221236	3222408	-	288.59	314.76	0.92	399.06	354.18	1.13	
<i>yugJ</i>	3222512	3223675	-	1649.86	1886.57	0.87	1775.57	1668.85	1.06	
<i>yuzA</i>	3223905	3224141	+	735.1	484.61	1.52	428.77	174.29	2.46	
<i>yugI</i>	3224219	3224611	-	2049.19	1971.62	1.04	2709.58	3103.48	0.87	
<i>alaT</i>	3224813	3225973	-	1037.35	1050.02	0.99	1322.94	1608.65	0.82	
<i>alaR</i>	3225974	3226474	-	1356.8	1458.36	0.93	1676.5	2049.05	0.82	
<i>yugF</i>	3226622	3227443	+	80.27	69.78	1.15	64.48	66.06	0.98	
<i>yugE</i>	3227472	3227738	-	293.74	233.37	1.26	323.46	289.11	1.12	
<i>patB</i>	3227819	3228982	+	260.37	311.8	0.84	397.77	541.31	0.73	
<i>kinB</i>	3229108	3230397	+	261.21	144.91	1.80	270.57	249.8	1.08	
<i>kapB</i>	3230443	3230829	+	559.26	396.99	1.41	834.74	712.7	1.17	
<i>kapD</i>	3230856	3231473	-	123.19	105.56	1.17	130.23	142.88	0.91	
<i>yuxJ</i>	3231684	3232862	+	106.26	101.27	1.05	93.17	91.97	1.01	
<i>pbpD</i>	3232955	3234829	+	576.52	510.61	1.13	700.17	709.96	0.99	
<i>yuxK</i>	3234850	3235263	+	366.15	290.32	1.26	404.03	386.75	1.04	
<i>yufK</i>	3235466	3236080	-	139.84	120.94	1.16	166.33	178.04	0.93	
<i>yufL</i>	3236201	3237802	+	443.29	419.47	1.06	392.8	406.88	0.97	
<i>yufM</i>	3237795	3238502	+	572.45	434.14	1.32	515.75	498.36	1.03	
<i>yufN</i>	3239001	3240053	+	2053.27	2004.02	1.02	1649.46	1561.02	1.06	
<i>yufO</i>	3240129	3241661	+	1005.34	873.03	1.15	934.13	778.5	1.20	
<i>yufP</i>	3241654	3242700	+	730.11	568.54	1.28	626.29	509	1.23	
<i>yufQ</i>	3242701	3243660	+	493.53	384.99	1.28	400.49	347.06	1.15	
<i>maeN</i>	3243814	3245160	+	103.65	108.66	0.95	98.63	98.54	1.00	
<i>yufS</i>	3245196	3245411	-	63.54	55.8	1.14	49.37	55.83	0.88	
<i>mrpA</i>	3245723	3248047	+	399.66	361.35	1.11	571.42	590.76	0.97	
<i>mrpB</i>	3248040	3248471	+	375.26	338.24	1.11	617.89	585.58	1.06	
<i>mrpC</i>	3248471	3248812	+	256.25	238.15	1.08	392.1	359.6	1.09	
<i>mrpD</i>	3248805	3250286	+	385.56	356.02	1.08	588.56	555.34	1.06	
<i>mrpE</i>	3250292	3250768	+	343.6	337.11	1.02	515.33	448.19	1.15	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>comP</i>	3252573	3254882	-	884.79	804.67	1.10	660.94	809	0.82	
<i>comX</i>	3254897	3255064	-	1691.1	1691.03	1.00	1415.61	1655.32	0.86	
<i>comQ</i>	3255052	3255951	-	668.06	679.75	0.98	632.88	627.54	1.01	
<i>yuzC</i>	3256737	3257105	+	122.41	128.23	0.95	99.91	141.46	0.71	
<i>yuxH</i>	3257081	3258310	-	517.06	481.37	1.07	446.12	477.62	0.93	
<i>yueK</i>	3258447	3259919	-	1447.24	1429.6	1.01	1781.92	1696.74	1.05	
<i>yueJ</i>	3259935	3260486	-	1243.83	1259.34	0.99	1347.83	1326.36	1.02	
<i>yueI</i>	3260583	3260981	-	467.26	347.59	1.34	496.12	490.15	1.01	
<i>yueH</i>	3261053	3261301	-	426.09	351.71	1.21	466.85	436.44	1.07	
<i>yueG</i>	3261374	3261595	-	157.75	124.87	1.26	275.04	223.01	1.23	
<i>yueF</i>	3261655	3262764	-	383.43	305.91	1.25	406.89	383.71	1.06	
<i>yuzE</i>	3262879	3263268	+	44.88	45.68	0.98	51.42	57.57	0.89	
<i>yuzF</i>	3263309	3263545	-	726.78	850.47	0.85	400.72	423.02	0.95	
<i>yueE</i>	3263722	3264252	-	1095.2	1282.46	0.85	709.21	730.97	0.97	
<i>yueD</i>	3264450	3265181	-	649.97	617.61	1.05	1120.08	1027.57	1.09	
<i>yueC</i>	3265244	3265699	-	540.89	522.23	1.04	1204.8	1108.21	1.09	
<i>yueB</i>	3265731	3268961	-	410.01	411.43	1.00	1281.71	1167.64	1.10	
<i>yukA</i>	3268958	3272581	-	347.17	292.13	1.19	884.86	769.73	1.15	
<i>yukB</i>	3272581	3273456	-	347.38	255.32	1.36	678.44	644.96	1.05	
<i>yukC</i>	3273484	3274839	-	399.77	312.14	1.28	714.11	681.63	1.05	
<i>yukD</i>	3274854	3275093	-	529.65	453.39	1.17	847.52	752.74	1.13	
<i>yukE</i>	3275237	3275479	-	7698.68	7361.2	1.05	6843.75	6048.6	1.13	
<i>yukF</i>	3275976	3277280	+	200.69	170.5	1.18	311.41	255.82	1.22	
<i>aid</i>	3277348	3278484	+	1043.74	1684.28	0.62	401.93	771.94	0.52	
<i>yuxI</i>	3278597	3278920	+	873.88	1141.94	0.77	608.06	628.37	0.97	
<i>yukJ</i>	3278838	3279275	+	289	382.35	0.76	365.38	284.43	1.28	
<i>dhbF</i>	3279544	3286680	-	456.72	670.86	0.68	288.89	429.37	0.67	AbrB regulon
<i>dhbB</i>	3286700	3287638	-	361.72	525.82	0.69	215.48	362.09	0.60	AbrB regulon
<i>dhbE</i>	3287666	3289285	-	335.58	426.94	0.79	200.37	322.42	0.62	AbrB regulon
<i>dhbC</i>	3289314	3290510	-	468.05	557.22	0.84	228.35	375.31	0.61	AbrB regulon
<i>dhbA</i>	3290536	3291321	-	451.94	505.95	0.89	211.96	357.57	0.59	AbrB regulon
<i>yuiI</i>	3291515	3292459	-	737.52	689.48	1.07	427.72	594.03	0.72	AbrB regulon
<i>yuiH</i>	3292598	3293194	-	167.81	135.5	1.24	163.72	157.56	1.04	
<i>yuiG</i>	3293295	3293897	+	1499.9	1398.59	1.07	1906.48	1548.71	1.23	
<i>yuiF</i>	3293967	3295295	-	477.91	380.72	1.26	530.65	641.71	0.83	
<i>yuiE</i>	3295442	3296944	-	741.79	681.37	1.09	888.75	846.39	1.05	
<i>yuiD</i>	3297102	3297578	+	271.75	316.06	0.86	216.74	171.62	1.26	
<i>yuiC</i>	3297609	3298265	-	219.61	275.07	0.80	229.12	374.07	0.61	
<i>yuiB</i>	3298369	3298689	-	1025.65	1244.71	0.82	748	1035.1	0.72	
<i>yuiA</i>	3298743	3298886	-	2780.29	3625.38	0.77	1398.21	1920.83	0.73	
<i>yumB</i>	3299059	3300279	-	511.88	508.82	1.01	413.76	460.14	0.90	
<i>yumC</i>	3300611	3301609	+	1054.72	1095.58	0.96	1210.83	1741.74	0.70	
<i>guaC</i>	3302067	3303047	+	372.46	376.96	0.99	146.72	169.65	0.86	
<i>paiB</i>	3303121	3303744	-	183.48	206.65	0.89	199.4	275.47	0.72	
<i>paiA</i>	3303768	3304286	-	98.01	125.97	0.78	126.67	194.02	0.65	
<i>yutM</i>	3304624	3304986	-	1882.39	1876.02	1.00	1913.76	1871.19	1.02	
<i>dapF</i>	3305065	3305919	-	326.4	409.25	0.80	385.22	459.14	0.84	
<i>yutK</i>	3306042	3307256	-	66.26	78.06	0.85	97.76	97.6	1.00	
<i>yuzB</i>	3307393	3307629	-	29.89	36.03	0.83	61.9	67.89	0.91	
<i>yutJ</i>	3307892	3308884	+	972.62	1107.26	0.88	997.72	1231.57	0.81	
<i>yuzD</i>	3308986	3309312	-	274.75	278.77	0.99	265.91	327.61	0.81	
<i>yutI</i>	3309412	3309747	+	990.44	1184.97	0.84	992.09	1067.69	0.93	
<i>yuxL</i>	3309789	3311762	-	126.08	153.3	0.82	141.17	172.16	0.82	
<i>thrB</i>	3311870	3312799	-	1963.57	2283.65	0.86	2489.54	2717.15	0.92	
<i>thrC</i>	3312796	3313854	-	2616.52	3105.37	0.84	3156.87	3448.34	0.92	
<i>hom</i>	3313854	3315155	-	1606.64	2197.72	0.73	1881.72	2299.28	0.82	
<i>yutH</i>	3315356	3316375	-	114.66	112.79	1.02	134.48	131.63	1.02	
<i>yutG</i>	3316528	3317028	+	58.58	56.97	1.03	41.71	51.32	0.81	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>lipA</i>	3319350	3320246	-	1393.41	1271.65	1.10	2334.44	2235	1.04	
<i>yunA</i>	3320412	3321461	+	79.76	80.27	0.99	69.42	77.85	0.89	
<i>yunB</i>	3321489	3322253	-	158.05	137.69	1.15	227.18	237.46	0.96	
<i>yunC</i>	3322326	3322631	-	400.12	348.53	1.15	518.57	528.13	0.98	
<i>yunD</i>	3322696	3324084	-	669.02	535.9	1.25	737.62	699.31	1.05	
<i>yunE</i>	3324104	3324925	-	573.44	499.53	1.15	647.39	616.15	1.05	
<i>yunF</i>	3324943	3325797	-	601.79	531.37	1.13	651.64	660.61	0.99	
<i>yunG</i>	3325829	3326176	-	451.69	441.14	1.02	392.26	397.46	0.99	
<i>pucH</i>	3326273	3327613	-	153	150.57	1.02	144.23	144.92	1.00	
<i>pucR</i>	3327788	3329383	+	130.3	122.6	1.06	104.6	101.61	1.03	
<i>pucJ</i>	3329528	3330877	+	105.79	102.66	1.03	98.7	104.05	0.95	
<i>pucK</i>	3330883	3332175	+	95.34	91.94	1.04	69.53	80.25	0.87	
<i>pucL</i>	3332188	3333672	+	122.2	115.9	1.05	109.5	113.89	0.96	
<i>pucM</i>	3333651	3334016	+	128.84	112.4	1.15	155.54	140.34	1.11	
<i>pucE</i>	3334777	3335298	-	85.63	77.39	1.11	61.75	70.41	0.88	
<i>pucD</i>	3335289	3337526	-	126.64	126.09	1.00	104.11	110.37	0.94	
<i>pucC</i>	3337527	3338360	-	69.72	72.17	0.97	54.38	60.11	0.90	
<i>pucB</i>	3338382	3338975	-	74.76	81.74	0.91	61.15	83.01	0.74	
<i>pucA</i>	3338972	3339964	-	65.01	71.75	0.91	49.59	64.33	0.77	
<i>yurG</i>	3340193	3341443	-	245.9	251.74	0.98	224.64	254.12	0.88	
<i>yurH</i>	3341460	3342698	-	154.59	171.46	0.90	137.18	172.19	0.80	
<i>yurI</i>	3343140	3344006	+	336.39	329.39	1.02	304.36	337.14	0.90	AbrB regulon
<i>yurJ</i>	3344040	3345143	-	242.66	871.48	0.28	275.59	838.22	0.33	
<i>yurK</i>	3345325	3346053	+	232.16	411.71	0.56	235.96	631.34	0.37	
<i>yurL</i>	3346078	3346932	-	183.52	791.77	0.23	169.81	623.11	0.27	
<i>yurM</i>	3346946	3347848	-	131.46	594.46	0.22	123.32	452.22	0.27	
<i>yurN</i>	3347852	3348730	-	134.24	667.34	0.20	105.33	596.03	0.18	
<i>yurO</i>	3348788	3350056	-	254.19	1360.19	0.19	241.07	1391.2	0.17	
<i>yurP</i>	3350137	3351123	-	717.59	3521.45	0.20	764.59	3165.59	0.24	
<i>yurQ</i>	3351339	3351713	-	297.11	303.09	0.98	644.1	634.73	1.01	
<i>yurR</i>	3351816	3352934	-	474.72	404.74	1.17	486.91	480.09	1.01	
<i>yurS</i>	3353239	3353514	+	26.61	35.67	0.75	23.86	26.24	0.91	
<i>yurT</i>	3353578	3353961	-	205.59	173.09	1.19	365.89	384.12	0.95	
<i>yurU</i>	3354620	3356017	-	2662.36	2808.94	0.95	3200.29	3329.6	0.96	
<i>yurV</i>	3356038	3356481	-	2893.77	2955.46	0.98	3316.51	3264.75	1.02	
<i>csd</i>	3356471	3357691	-	2423.84	2416.32	1.00	2885.8	2966.7	0.97	
<i>yurX</i>	3357691	3359004	-	3263.38	3158.59	1.03	3666.9	3759.94	0.98	
<i>yurY</i>	3359022	3359807	-	2652.33	2317.66	1.14	2707.19	3004.05	0.90	
<i>yurZ</i>	3360332	3360709	-	49.68	54.52	0.91	52.52	68.19	0.77	
<i>yusA</i>	3360794	3361618	-	1214.64	1553.24	0.78	2298.4	3110.47	0.74	
<i>yusB</i>	3361632	3362300	-	449.28	594.09	0.76	872.21	1356.75	0.64	
<i>yusC</i>	3362293	3363318	-	467.25	649.96	0.72	1003.76	1485.98	0.68	
<i>yusD</i>	3363645	3363989	-	376.77	337.42	1.12	389.91	409.04	0.95	
<i>yusE</i>	3364096	3364416	-	260.1	237.81	1.09	301.27	301.35	1.00	Spo0A regulon
<i>yusF</i>	3364418	3364858	-	513.41	478.05	1.07	766.23	714.03	1.07	
<i>yusG</i>	3364858	3365094	-	1111.41	1181.77	0.94	1948.75	1855.17	1.05	
<i>gcvH</i>	3365150	3365533	-	4598.81	4724.66	0.97	5102.96	4622.97	1.10	
<i>yusI</i>	3365600	3365956	-	742.05	687.38	1.08	1609.39	1672.58	0.96	
<i>yusJ</i>	3366067	3367851	-	133.23	128.93	1.03	138.24	136.83	1.01	
<i>yusK</i>	3367866	3369041	-	186.33	189.89	0.98	188.72	219.59	0.86	
<i>yusL</i>	3369052	3371499	-	156.18	140.29	1.11	174.74	188.41	0.93	
<i>yusM</i>	3371767	3372675	-	74.2	73.81	1.01	52.39	66.16	0.79	
<i>yusN</i>	3373028	3373360	+	38.79	39.24	0.99	41.29	38.18	1.08	
<i>yusO</i>	3373519	3373986	+	495.01	441.71	1.12	557.87	564.27	0.99	
<i>yusP</i>	3373983	3375608	+	440.54	335.19	1.31	528.54	477.18	1.11	
<i>yusQ</i>	3375644	3376027	-	78.75	84.57	0.93	65.82	74.04	0.89	
<i>yusR</i>	3376046	3376435	-	100.43	104.16	0.96	81.63	93.93	0.87	
<i>yusS</i>	3376457	3376786	-	80.5	96.57	0.83	86.04	91.94	0.94	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yusX</i>	3379731	3381233	-	847.72	944.33	0.90	969.13	1060.28	0.91	
<i>yusY</i>	3381230	3381526	-	672.27	704.92	0.95	623.53	716	0.87	
<i>yusZ</i>	3381660	3382502	+	191.69	212.38	0.90	240.49	266.99	0.90	
<i>mrgA</i>	3382592	3383053	+	656.99	702.98	0.93	952.56	1220.07	0.78	
<i>yvtA</i>	3383097	3384473	-	1669.21	1271.17	1.31	2390.35	2808.1	0.85	
<i>cssR</i>	3384751	3385428	+	408.4	409.19	1.00	554.68	518.91	1.07	
<i>cssS</i>	3385425	3386780	+	607.33	568.44	1.07	817.98	805	1.02	
<i>yuxN</i>	3387140	3388015	+	232.16	190.01	1.22	262.36	290.4	0.90	
<i>citG</i>	3388051	3389439	-	1582.81	1947.48	0.81	2370.4	2608.8	0.91	
<i>gerAA</i>	3389809	3391257	+	53.68	60.21	0.89	45	53.2	0.85	
<i>gerAB</i>	3391226	3392323	+	25.77	32.97	0.78	31.15	33.69	0.92	
<i>gerAC</i>	3392320	3393441	+	49.21	56.24	0.88	47.99	53.79	0.89	
<i>yvqC</i>	3393449	3394084	-	334.98	279.96	1.20	369.8	381.86	0.97	
<i>yvqE</i>	3394062	3395144	-	343.67	292.98	1.17	367.02	413.71	0.89	
<i>yvqF</i>	3395141	3395866	-	302.63	266.26	1.14	314.72	346.16	0.91	
<i>yvqG</i>	3395900	3396622	-	288.94	259.96	1.11	371.36	449.65	0.83	
<i>yvqH</i>	3396872	3397549	-	308.92	222.89	1.39	513.49	260.8	1.97	
<i>yvqI</i>	3397576	3397956	-	204.91	128.5	1.59	237.25	145.75	1.63	
<i>yvqJ</i>	3398118	3399386	-	296.74	288.63	1.03	322.95	304.6	1.06	AbrB regulon
<i>yvqK</i>	3399563	3400144	-	212.73	209.76	1.01	299.48	312.51	0.96	
<i>yvrA</i>	3400167	3401495	-	282.47	255.24	1.11	388.61	402.56	0.97	
<i>yvrB</i>	3401495	3402556	-	157.81	156.81	1.01	249.05	256.36	0.97	
<i>yvrC</i>	3402519	3403463	-	574.89	604.78	0.95	839.88	944.22	0.89	
<i>yvrD</i>	3403861	3404652	+	364.99	371.35	0.98	522.16	511.08	1.02	
<i>yvrE</i>	3404690	3405568	-	2214.2	1738.31	1.27	1314.75	802.88	1.64	
<i>yvrG</i>	3405640	3407361	-	582.37	405.79	1.44	818.17	709.19	1.15	
<i>yvrH</i>	3407379	3408488	-	156.74	153.75	1.02	158.32	160.63	0.99	
<i>yvri</i>	3408492	3409067	-	64.92	83.29	0.78	73.34	85.53	0.86	
<i>oxdC</i>	3409496	3410653	+	465.15	988.49	0.47	436.68	802.91	0.54	
<i>yvrL</i>	3410714	3411124	+	61.5	88.84	0.69	79.57	111.49	0.71	
<i>yvrN</i>	3411158	3412408	-	908.24	801.12	1.13	1214.34	1279.31	0.95	AbrB regulon
<i>yvrO</i>	3412380	3413069	-	1080.84	978.72	1.10	1498.94	1673.93	0.90	AbrB regulon
<i>yvrP</i>	3413053	3414246	-	911.68	1027.59	0.89	1198.01	1516.78	0.79	AbrB regulon
<i>fhuC</i>	3414417	3415226	-	571.62	561.28	1.02	487.05	600.07	0.81	
<i>fhuG</i>	3415242	3416252	-	342.68	298.55	1.15	259.01	315.36	0.82	
<i>fhuB</i>	3416252	3417406	-	334.77	327.35	1.02	216.82	298.67	0.73	
<i>fhuD</i>	3417504	3418451	+	1720.89	2133.53	0.81	851.08	1295.43	0.66	
<i>yvsH</i>	3418686	3420095	-	274.62	228.8	1.20	495.56	559.37	0.89	
<i>sspJ</i>	3420495	3420635	-	81.48	79.21	1.03	64.88	46.97	1.38	
<i>yvsG</i>	3420802	3421284	+	136.95	103.24	1.33	158.86	148.42	1.07	
<i>yvgJ</i>	3421384	3423237	+	236	165.36	1.43	353.49	281.41	1.26	
<i>yvgK</i>	3423265	3424191	-	588.9	520.08	1.13	592.3	527.74	1.12	
<i>yvgL</i>	3424302	3425084	+	194.16	173.97	1.12	168.71	202.14	0.83	
<i>yvgM</i>	3425188	3425748	+	99.41	97.34	1.02	107.04	128.04	0.84	
<i>yvgN</i>	3425779	3426609	-	1566.76	1783.68	0.88	1724.92	1799.84	0.96	
<i>yvgO</i>	3426832	3427317	+	4317.65	2901.01	1.49	2799.55	1150.37	2.43	AbrB regulon
<i>yvgP</i>	3427361	3429373	-	559.07	438.5	1.27	667.25	622.76	1.07	
<i>yvgQ</i>	3429628	3431343	-	2418.62	2401.76	1.01	2769.8	2930.74	0.95	
<i>yvgR</i>	3431369	3433186	-	1754.13	1665.39	1.05	2282.8	2510.29	0.91	
<i>yvgS</i>	3433357	3435681	-	316.18	243.33	1.30	439.56	356.04	1.23	
<i>yvgT</i>	3435879	3436487	-	153.23	167.08	0.92	141.25	163.87	0.86	
<i>bdbC</i>	3436674	3437090	-	927.67	856.46	1.08	716.45	787.03	0.91	
<i>bdbD</i>	3437095	3437763	-	1716.1	1568.32	1.09	1212.82	1338.86	0.91	
<i>yvgW</i>	3437883	3439991	-	1051.78	1363.1	0.77	454.82	537.02	0.85	
<i>yvgX</i>	3440151	3442562	-	2606.19	1847.78	1.41	730.47	775.81	0.94	
<i>yvgY</i>	3442643	3442852	-	2054.62	1499.34	1.37	539.73	527.89	1.02	
<i>yvgZ</i>	3442926	3443231	-	919.77	758.77	1.21	573.11	432.95	1.32	
<i>yvaA</i>	3443359	3444435	+	4329.63	4405.27	0.98	3471.74	2943.32	1.18	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yvaF</i>	3448079	3448651	-	149.91	153.68	0.98	150.34	151.81	0.99	
<i>yvaG</i>	3448762	3449556	-	407.4	361.97	1.13	388.61	309.19	1.26	
<i>smpB</i>	3450278	3450748	-	1956.61	1153.61	1.70	998.03	1144.78	0.87	
<i>rnr</i>	3450893	3453232	-	3235.82	2006.15	1.61	1471.52	1100.96	1.34	
<i>yvaK</i>	3453251	3453997	-	2104.36	1436.52	1.46	1439.69	1074.05	1.34	
<i>secG</i>	3454123	3454353	-	1787	2022.47	0.88	1076.32	1189.65	0.90	
<i>yvaM</i>	3454502	3455272	+	105.85	95.31	1.11	101.33	87.85	1.15	
<i>yzc</i>	3455312	3455545	-	32.75	30.34	1.08	31.34	31.47	1.00	
<i>yvaN</i>	3455697	3456104	+	255.44	269.37	0.95	303.66	368.18	0.82	
<i>yvaO</i>	3456134	3456553	+	139.32	142.83	0.98	188.53	223.45	0.84	
<i>yvaP</i>	3456396	3457106	+	181.39	167.45	1.08	187.41	210.87	0.89	
<i>yvaQ</i>	3457097	3458797	+	719.4	849.49	0.85	415.19	374.4	1.11	
<i>opuBD</i>	3458837	3459517	-	155.32	201.42	0.77	325.43	498.9	0.65	
<i>opuBC</i>	3459534	3460454	-	166.81	222.43	0.75	696.51	1100.67	0.63	
<i>opuBB</i>	3460466	3461119	-	118.38	150.17	0.79	508.54	785.14	0.65	
<i>opuBA</i>	3461136	3462281	-	147.68	147.97	1.00	581.46	968.21	0.60	
<i>yvaV</i>	3462556	3463098	+	238.08	178.68	1.33	273.15	317.7	0.86	
<i>yvaW</i>	3463320	3463796	+	497.08	549.93	0.90	1157.92	1925.76	0.60	Spo0A and AbrB regulon
<i>yvaX</i>	3463793	3464764	+	457.33	441.26	1.04	1192.74	1898.87	0.63	
<i>yvaY</i>	3464807	3465418	+	4063.04	4814.1	0.84	5164.82	5062.41	1.02	
<i>yvaZ</i>	3465465	3466088	-	610.79	1579.99	0.39	367.69	586.29	0.63	
<i>yvbA</i>	3466085	3466357	-	688.84	1886.21	0.37	253.17	514.11	0.49	
<i>opuCD</i>	3466577	3467266	-	1504.49	1747.95	0.86	2144.69	2504.07	0.86	
<i>opuCC</i>	3467284	3468195	-	1914.42	1960.91	0.98	2868.59	3430.96	0.84	
<i>opuCB</i>	3468215	3468868	-	1205.1	1120.38	1.08	1933.83	2410.36	0.80	
<i>opuCA</i>	3468891	3470033	-	1507.96	1166.03	1.29	2362.51	3127.3	0.76	
<i>yvbF</i>	3470297	3470854	+	334.77	283.08	1.18	544.94	722.95	0.75	
<i>yvbG</i>	3470872	3471507	-	296.33	261.06	1.14	117.98	82.53	1.43	
<i>yvbH</i>	3471657	3472271	+	294.56	308.84	0.95	592.35	721.2	0.82	
<i>yvbI</i>	3472403	3473101	+	132.83	160.85	0.83	264.47	429.25	0.62	
<i>yvbJ</i>	3473137	3474954	-	606.18	679.11	0.89	1205.2	1455.69	0.83	
<i>yvbK</i>	3475074	3475541	+	356.31	331.25	1.08	467.94	479.01	0.98	
<i>eno</i>	3475586	3476878	-	4366.19	4807.32	0.91	4171.12	3902.7	1.07	
<i>pgm</i>	3476908	3478443	-	5803.38	6150.08	0.94	5248.04	4819.84	1.09	
<i>tpiA</i>	3478436	3479197	-	4684.17	4812.76	0.97	3758.27	3422.61	1.10	
<i>pgk</i>	3479228	3480412	-	5609.67	5895.53	0.95	4899.34	4496.84	1.09	
<i>gapA</i>	3480729	3481736	-	7884	8202.79	0.96	6172.54	5695.41	1.08	
<i>cggR</i>	3481783	3482805	-	2391.91	2496.01	0.96	2140.14	2225.28	0.96	
<i>araE</i>	3483103	3484497	-	67.84	66.82	1.02	49.33	56.36	0.88	
<i>araR</i>	3484635	3485789	+	297.81	248.36	1.20	334.13	350.57	0.95	
<i>yvbT</i>	3485838	3486848	-	176.76	171.2	1.03	211.04	238.65	0.88	
<i>yvbU</i>	3487005	3487883	-	59.89	61.92	0.97	63.58	69.88	0.91	
<i>yvbV</i>	3487983	3488900	+	105.46	109.01	0.97	76.51	92.58	0.83	
<i>yvbW</i>	3488941	3490284	-	161.83	182.44	0.89	193.22	249.78	0.77	
<i>yvbX</i>	3490686	3491720	-	1353.73	1654.69	0.82	1308.99	1483.94	0.88	
<i>yvbY</i>	3491828	3492550	-	5824.71	5409.02	1.08	5045.19	4745.33	1.06	
<i>yvfW</i>	3492550	3493989	-	4589.98	4365.75	1.05	4822.1	4494.15	1.07	
<i>yvfV</i>	3494016	3494732	-	3708.53	3489.2	1.06	4255.1	4167.57	1.02	
<i>yvfU</i>	3494907	3495509	-	180.63	157.11	1.15	173.99	214.05	0.81	
<i>yvfT</i>	3495526	3496512	-	195.62	171.83	1.14	189	211.21	0.89	
<i>yvfS</i>	3496645	3497382	-	71.84	70.97	1.01	68.75	84.64	0.81	
<i>yvfR</i>	3497383	3498288	-	77.15	75.99	1.02	66.76	72.04	0.93	
<i>rsbQ</i>	3498572	3499381	+	308.2	264.44	1.17	276.26	324.43	0.85	
<i>rsbP</i>	3499417	3500628	+	378.4	300.26	1.26	394.01	420.96	0.94	
<i>yvfO</i>	3500682	3501971	-	91.08	91.32	1.00	69.72	92.71	0.75	
<i>lacA</i>	3502051	3504114	-	107.83	119.87	0.90	108.29	132.63	0.82	
<i>yvfM</i>	3504133	3504984	-	83.98	93.51	0.90	79.5	108.54	0.73	
<i>yvfL</i>	3504988	3506244	-	62	70.98	0.87	68.11	83.04	0.82	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>sigL</i>	3511529	3512839	-	1022.79	1076.61	0.95	836.19	815.46	1.03	
<i>yvfG</i>	3512918	3513136	+	457.4	379.29	1.21	517.94	484.68	1.07	
<i>yvfF</i>	3513146	3514114	-	380.4	132.64	2.87	336.76	149.95	2.25	AbrB regulon
<i>yvfE</i>	3514093	3515259	-	507.12	149.95	3.38	477.92	182.69	2.62	AbrB regulon
<i>yvfD</i>	3515264	3515914	-	383.75	154.02	2.49	335.37	163.49	2.05	AbrB regulon
<i>yvfC</i>	3515911	3516519	-	386.91	135.2	2.86	362.85	173.04	2.10	AbrB regulon
<i>yvfB</i>	3516516	3517553	-	333.32	118.89	2.80	329.99	135.44	2.44	AbrB regulon
<i>yvfA</i>	3517703	3518032	-	289.32	87.38	3.31	300.34	117.66	2.55	AbrB regulon
<i>yveT</i>	3518029	3519063	-	475.58	186.48	2.55	524	217.27	2.41	AbrB regulon
<i>yveS</i>	3519060	3520136	-	333.81	139.11	2.40	359.14	157.18	2.28	AbrB regulon
<i>yveR</i>	3520141	3521175	-	350.6	189.55	1.85	494.05	227.25	2.17	AbrB regulon
<i>yveQ</i>	3521200	3522303	-	251.63	86.91	2.90	314.3	125.36	2.51	AbrB regulon
<i>yveP</i>	3522300	3523454	-	227.99	101.52	2.25	257.77	125.72	2.05	AbrB regulon
<i>yveO</i>	3523447	3524283	-	294.3	110.68	2.66	320.62	159.13	2.01	AbrB regulon
<i>yveN</i>	3524280	3525425	-	434.59	177.48	2.45	454.9	219.37	2.07	AbrB regulon
<i>yveM</i>	3525437	3527233	-	384.08	191.73	2.00	316.9	183.62	1.73	AbrB regulon
<i>yveL</i>	3527492	3528175	-	316.71	118.52	2.67	286.68	133.54	2.15	AbrB regulon
<i>yveK</i>	3528181	3528885	-	422.58	125.9	3.36	376.44	170.82	2.20	AbrB regulon
<i>slr</i>	3529131	3529589	+	140.69	79.96	1.76	150.49	88.09	1.71	
<i>pnbA</i>	3529665	3531134	+	557.84	390.47	1.43	944.14	804.13	1.17	AbrB regulon
<i>padC</i>	3531355	3531840	-	98.43	96.46	1.02	124.73	135	0.92	
<i>yveG</i>	3531863	3532150	-	86.15	86	1.00	100.49	93.93	1.07	
<i>racX</i>	3532449	3533132	-	3310.49	2326.64	1.42	3172.22	2275.65	1.39	
<i>pbpE</i>	3533148	3534503	-	3043.1	2063.85	1.47	2913	2090.79	1.39	
<i>sacB</i>	3535042	3536463	+	44.45	52.15	0.85	43.79	48.78	0.90	
<i>yveB</i>	3536537	3538087	+	78.35	77.89	1.01	57.19	64.9	0.88	
<i>yveA</i>	3538195	3539757	+	46.23	45.1	1.03	36.63	39.12	0.94	
<i>yvdT</i>	3539852	3540436	+	582.19	543.89	1.07	351.23	360.67	0.97	
<i>yvdS</i>	3540518	3540853	+	120	105.62	1.14	67.31	75.4	0.89	
<i>yvdR</i>	3540853	3541173	+	129.03	108.62	1.19	90.08	94.32	0.96	
<i>yvdQ</i>	3541209	3541721	-	106	96.48	1.10	78.73	109.27	0.72	
<i>yvdP</i>	3541973	3543316	-	95.15	70.67	1.35	74.95	72.35	1.04	
<i>yvdO</i>	3543672	3544634	+	55.42	54.85	1.01	52.83	56.19	0.94	
<i>clpP</i>	3545264	3545857	+	3455.36	3239.79	1.07	2754.98	2471.6	1.11	
<i>pgcM</i>	3545903	3546583	-	147.36	121.47	1.21	119.18	118.28	1.01	
<i>mall</i>	3546580	3548265	-	154.19	137.35	1.12	149.84	142.06	1.05	
<i>yvdK</i>	3548258	3550531	-	138.49	131.33	1.05	128.31	138.78	0.92	
<i>yvdJ</i>	3550509	3551393	-	66.61	69.52	0.96	69.63	72.71	0.96	
<i>yvdI</i>	3551399	3552235	-	68.41	77.96	0.88	65.4	73.17	0.89	
<i>yvdH</i>	3552236	3553543	-	72.95	85.43	0.85	66.79	81.09	0.82	
<i>yvdG</i>	3553583	3554836	-	98.8	104.48	0.95	101.34	111.94	0.91	
<i>yvdF</i>	3554932	3556701	-	78.17	80.54	0.97	67.27	72.57	0.93	
<i>yvdE</i>	3556814	3557764	-	67.25	71.12	0.95	64.1	59.87	1.07	
<i>yvdD</i>	3557970	3558545	-	1413.3	1299.48	1.09	2043	2022.98	1.01	
<i>yvdC</i>	3558662	3558982	+	637.77	600.88	1.06	893.09	1071.02	0.83	
<i>yvdB</i>	3559009	3560601	-	127.65	132.83	0.96	116.03	123.23	0.94	
<i>yvdA</i>	3560620	3561213	-	126.25	133.65	0.94	95.08	102.85	0.92	
<i>yvcT</i>	3561596	3562573	+	1207.72	1075.45	1.12	2072.42	1772.72	1.17	
<i>yvcS</i>	3562611	3564551	-	208.96	208.41	1.00	272.82	290.11	0.94	
<i>yvcR</i>	3564526	3565305	-	423.83	400.62	1.06	594.71	655.61	0.91	
<i>yvcQ</i>	3565388	3566458	-	267.6	264.14	1.01	380.68	429.39	0.89	
<i>yvcP</i>	3566452	3567165	-	252.59	263.69	0.96	318.62	372.94	0.85	
<i>yvcN</i>	3567557	3568321	-	1100.24	959.91	1.15	1073.5	1025.3	1.05	
<i>crh</i>	3568322	3568579	-	1340.34	1153.61	1.16	1348.38	1436.67	0.94	
<i>yvcL</i>	3568603	3569553	-	1154.75	1002.52	1.15	1249.55	1245.73	1.00	
<i>yvcK</i>	3569576	3570529	-	1144.14	924.07	1.24	1149.82	1074.32	1.07	
<i>yvcJ</i>	3570531	3571418	-	1205.7	967.56	1.25	1015.77	989.78	1.03	
<i>yvcI</i>	3571443	3571919	-	946.2	765.34	1.24	1016.03	1000.67	1.02	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yvzA</i>	3578709	3579068	-	351.5	208.9	1.68	621.45	484.36	1.28	
<i>yvcB</i>	3579083	3580993	-	634.62	407.73	1.56	624.24	488.64	1.28	
<i>yvcA</i>	3580995	3581720	-	337.62	371.31	0.91	309.56	256.31	1.21	
<i>hisI</i>	3581966	3582595	-	2513.56	2925.85	0.86	1809.36	1903.13	0.95	
<i>hisF</i>	3582592	3583350	-	2885.2	3107.78	0.93	1657	1823.91	0.91	
<i>hisA</i>	3583347	3584084	-	2636.18	2833.11	0.93	1695.19	1784.27	0.95	
<i>hisH</i>	3584081	3584719	-	3363.14	3674.46	0.92	2245.76	2435.54	0.92	
<i>hisB</i>	3584720	3585304	-	2903.21	3264.37	0.89	2247.44	2300.36	0.98	
<i>hisD</i>	3585301	3586584	-	1941.89	1872.22	1.04	1212.49	1266.19	0.96	
<i>hisG</i>	3586581	3587222	-	1869.77	1742.2	1.07	1416.42	1401.16	1.01	
<i>hisZ</i>	3587215	3588390	-	1195.83	889.44	1.34	965.27	1014.46	0.95	
<i>yvpB</i>	3588641	3589393	+	232.59	266.38	0.87	165.79	218.61	0.76	
<i>yvpA</i>	3589633	3590298	+	161.73	183.75	0.88	159.07	194.99	0.82	
<i>yvoF</i>	3590318	3590836	-	679.02	585.45	1.16	811.12	874.59	0.93	
<i>hprP</i>	3590840	3591490	-	1017.7	820.28	1.24	1171.63	1158.85	1.01	
<i>yvoD</i>	3591487	3592425	-	1002.62	821.94	1.22	1155.25	1138.8	1.01	
<i>lgt</i>	3592449	3593258	-	653.59	546.98	1.19	739.12	741.76	1.00	
<i>hprK</i>	3593272	3594204	-	721.47	667.98	1.08	750.24	842.12	0.89	
<i>nagA</i>	3594386	3595576	+	463.49	465.86	0.99	391.59	387.5	1.01	
<i>nagB</i>	3595573	3596301	+	763.4	679.16	1.12	551.61	515.03	1.07	
<i>yvoA</i>	3596319	3597050	+	589.71	540.24	1.09	401.64	375.41	1.07	
<i>yvmB</i>	3597070	3600939	-	137.31	125.84	1.09	140.99	146.35	0.96	
<i>yvmA</i>	3601104	3601577	+	293.86	252.12	1.17	260.51	312.47	0.83	AbrB regulon
<i>cypX</i>	3601618	3602835	-	254.71	227.73	1.12	243.35	244.23	1.00	AbrB regulon
<i>yvmC</i>	3602851	3603597	-	360.57	317.68	1.14	407.88	386.25	1.06	AbrB regulon
<i>yvmB</i>	3604023	3604532	+	111.42	104.04	1.07	137.2	133.01	1.03	
<i>yvmA</i>	3604553	3605764	+	120.31	114.61	1.05	136.34	123.69	1.10	
<i>yvID</i>	3605792	3606151	-	1180.93	876.88	1.35	1276.05	1089.49	1.17	
<i>yvIC</i>	3606153	3606350	-	3279.67	2581.62	1.27	2946.87	2543.61	1.16	
<i>yvIB</i>	3606355	3607452	-	1878.61	1582.48	1.19	2540.3	2394.07	1.06	
<i>yvIA</i>	3607477	3607803	-	682.01	558.13	1.22	1271.9	1299.32	0.98	
<i>yvkN</i>	3608021	3608251	+	67.05	74.25	0.90	87.13	79.87	1.09	
<i>yvzB</i>	3608450	3608932	-	2074.41	2169.21	0.96	1406.38	1354.88	1.04	
<i>uvrA</i>	3609094	3611967	-	1761.79	1452.27	1.21	1488.31	1095.63	1.36	
<i>uvrB</i>	3611975	3613960	-	1252.92	1065.73	1.18	901.59	701.84	1.28	
<i>csbA</i>	3614146	3614376	-	319.14	297.16	1.07	332.24	292.82	1.13	
<i>yvkC</i>	3614823	3617318	+	117.51	103.92	1.13	196.02	162.08	1.21	
<i>yvkB</i>	3617394	3617963	+	134.37	131.43	1.02	250.12	205.34	1.22	
<i>yvkA</i>	3617994	3619328	+	94.85	89.88	1.06	136.05	116.1	1.17	
<i>yvjD</i>	3619376	3620569	-	835.24	844.84	0.99	598	662.52	0.90	
<i>yvzD</i>	3620648	3620986	-	854.12	1202.63	0.71	782.17	906.02	0.86	
<i>yvjB</i>	3621386	3622828	-	73.15	82.4	0.89	71.72	90.82	0.79	
<i>ftsX</i>	3622968	3623858	-	309.78	259.94	1.19	573.86	597.91	0.96	
<i>ftsE</i>	3623851	3624537	-	1142.02	898.17	1.27	1344.7	1448.62	0.93	Spo0A regulon
<i>cccB</i>	3624771	3625109	-	1021.56	817.87	1.25	1058.77	995.16	1.06	
<i>yvjA</i>	3625158	3626003	-	212.44	171.66	1.24	164.55	140.37	1.17	
<i>prfB</i>	3626169	3627270	-	1633.08	1528.49	1.07	1845.56	1829.45	1.01	
<i>secA</i>	3627340	3629865	-	2456.88	2321.68	1.06	2061.51	2108.99	0.98	
<i>yvyD</i>	3630033	3630602	-	6016.41	6920.15	0.87	4101.05	3652.1	1.12	Spo0A regulon
<i>fliT</i>	3631180	3631521	-	4706.52	4527.94	1.04	3692.92	3676.95	1.00	
<i>fliS</i>	3631518	3631919	-	4479.77	4379.43	1.02	3612.72	3338.21	1.08	
<i>fliD</i>	3631941	3633437	-	4300.65	4411.51	0.97	3289.21	3238.71	1.02	
<i>yvyC</i>	3633455	3633784	-	1471.49	1654.56	0.89	1101.16	1191.01	0.92	SigD regulon
<i>hag</i>	3634017	3634931	-	10338.2	11308.5	0.91	8217.53	7537.18	1.09	SigD regulon
<i>csrA</i>	3635076	3635300	-	755.3	783.81	0.96	743.54	890.2	0.84	
<i>yviF</i>	3635294	3635725	-	461.26	466.91	0.99	318.65	423.71	0.75	
<i>yviE</i>	3635746	3636321	-	1154.09	1187.17	0.97	781.2	1003.25	0.78	
<i>flgL</i>	3636368	3637264	-	3941.96	3956.67	1.00	2361.54	2748.82	0.86	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>comFC</i>	3640155	3640844	-	680.79	887.42	0.77	722.94	1086.52	0.67	
<i>comFB</i>	3640841	3641137	-	949.09	1211.9	0.78	927.41	1395.38	0.66	
<i>comFA</i>	3641197	3642588	-	903.57	1145.79	0.79	987.7	1432.47	0.69	
<i>yviA</i>	3642694	3643539	-	370.43	353.76	1.05	487.47	587.95	0.83	
<i>degU</i>	3643637	3644326	-	1308.28	1267.72	1.03	1615.16	1703.79	0.95	
<i>degS</i>	3644409	3645566	-	792.82	688.23	1.15	880.44	987.24	0.89	
<i>yvyE</i>	3645783	3646436	+	468.92	430.58	1.09	598.71	716	0.84	Spo0A regulon
<i>yvhJ</i>	3646436	3647611	+	504.34	434.08	1.16	895.48	1003.7	0.89	
<i>tagO</i>	3647684	3648760	-	851.89	750.14	1.14	626.77	792.5	0.79	
<i>tuaH</i>	3648905	3650098	-	82.48	69.25	1.19	101.85	89.98	1.13	
<i>tuaG</i>	3650127	3650885	-	113.24	102.84	1.10	126.99	125.84	1.01	
<i>tuaF</i>	3650909	3651589	-	120.07	107.3	1.12	150.36	133.5	1.13	
<i>tuaE</i>	3651618	3653084	-	83.05	80.14	1.04	99.18	89.45	1.11	
<i>tuaD</i>	3653169	3654554	-	127.88	106.94	1.20	136.05	133.06	1.02	
<i>tuaC</i>	3654616	3655785	-	115.94	106.87	1.08	97.06	98.01	0.99	
<i>tuaB</i>	3655782	3657233	-	70.55	69.31	1.02	68.52	74.81	0.92	
<i>tuaA</i>	3657383	3657922	-	54.12	56.31	0.96	45.45	53	0.86	
<i>lytC</i>	3658149	3659639	-	2619.67	2430.57	1.08	1931.46	2242.52	0.86	
<i>lytB</i>	3659678	3661795	-	2289.36	2127.47	1.08	1849.66	2420.15	0.76	
<i>lytA</i>	3661819	3662127	-	1980.82	2242.54	0.88	1863.75	2299.15	0.81	SigD regulon
<i>lytR</i>	3662311	3663231	+	2244.76	2206.55	1.02	1963.37	1901.64	1.03	
<i>yvyH</i>	3663271	3664413	-	333.88	315.73	1.06	316.11	322.89	0.98	
<i>gtaB</i>	3664659	3665537	+	4537.31	4632.65	0.98	2531.92	2218.6	1.14	
<i>ggaB</i>	3666239	3668941	-	90.69	95.54	0.95	433.77	446.22	0.97	
<i>ggaA</i>	3669065	3670405	-	40.12	36.73	1.09	111.32	148.81	0.75	
<i>tagH</i>	3672594	3674177	-	375.35	317.05	1.18	703.79	727.05	0.97	
<i>tagG</i>	3674197	3675024	-	389.64	366.54	1.06	635.71	654.85	0.97	
<i>tagF</i>	3675189	3677429	-	359.06	281.68	1.27	657.49	746.99	0.88	
<i>tagE</i>	3677429	3679450	-	484.6	418.12	1.16	669.24	779.83	0.86	
<i>tagD</i>	3679611	3680000	-	1037.18	1206.31	0.86	943.78	1321.43	0.71	
<i>tagA</i>	3680400	3681170	+	860.95	866.52	0.99	778.69	1039.04	0.75	
<i>tagB</i>	3681203	3682348	+	370.58	341.37	1.09	389.38	482.87	0.81	
<i>tagC</i>	3682468	3683796	+	257.33	106.45	2.42	393.57	174.88	2.25	
<i>lytD</i>	3683856	3686498	-	1722.42	1710.47	1.01	1451.93	1412.92	1.03	SigD regulon
<i>pmi</i>	3686627	3687577	-	699.44	707.88	0.99	674.52	751.62	0.90	
<i>gerBA</i>	3687842	3689290	+	51.27	54.09	0.95	46.69	49.72	0.94	
<i>gerBB</i>	3689296	3690402	+	44.93	48.01	0.94	49.94	54	0.92	
<i>gerBC</i>	3690399	3691523	+	69.13	65.59	1.05	67.31	72.28	0.93	
<i>ywtG</i>	3691560	3692933	-	2728.83	1892.03	1.44	962.64	349.28	2.76	
<i>ywtF</i>	3693266	3694234	+	696.88	618.54	1.13	568.07	533.52	1.06	
<i>ywtE</i>	3694390	3695250	+	625.13	528.98	1.18	735.6	720.95	1.02	
<i>ywtD</i>	3695284	3696525	-	4121.25	3358.49	1.23	3690.23	2910.33	1.27	
<i>ywtC</i>	3696666	3696833	-	48.73	42.89	1.14	60.18	51.28	1.17	
<i>ywtB</i>	3696848	3697990	-	79.03	77.02	1.03	73.94	85.79	0.86	
<i>ywtA</i>	3698009	3698458	-	48.43	40.65	1.19	41.58	42.97	0.97	
<i>ywsC</i>	3698473	3699654	-	50.72	49.47	1.03	46.3	48.34	0.96	
<i>rbsR</i>	3700438	3701418	+	206.29	206.46	1.00	243.87	295.52	0.83	AbrB regulon
<i>rbsK</i>	3701420	3702301	+	189.51	218.8	0.87	255.8	328.5	0.78	AbrB regulon
<i>rbsD</i>	3702298	3702693	+	70.8	98.8	0.72	126.18	152.94	0.83	AbrB regulon
<i>rbsA</i>	3702709	3704190	+	120.36	160.5	0.75	163.34	221.22	0.74	AbrB regulon
<i>rbsC</i>	3704192	3705160	+	89.66	123.52	0.73	90.72	130.53	0.70	AbrB regulon
<i>rbsB</i>	3705172	3706089	+	216.14	279.36	0.77	207.64	289.8	0.72	AbrB regulon
<i>ywsB</i>	3706171	3706707	+	5562.56	5680.6	0.98	3027.44	1825.24	1.66	
<i>ywsA</i>	3706863	3707159	+	158.95	260.83	0.61	68.29	50.68	1.35	
<i>ywrO</i>	3707199	3707726	-	782.64	523.89	1.49	1283.88	1093.95	1.17	
<i>alsD</i>	3707826	3708593	-	173.39	149.07	1.16	174.99	134.72	1.30	
<i>alsS</i>	3708655	3710370	-	165.51	120.2	1.38	150.66	128.81	1.17	
<i>alsR</i>	3710525	3711433	+	263.53	298.72	0.88	279.94	329.89	0.85	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>cotG</i>	3716265	3716852	+	38.05	114.59	0.33	36.06	47.26	0.76	
<i>ywrF</i>	3717026	3717643	+	489.84	508.33	0.96	428.37	363.11	1.18	
<i>ywrE</i>	3717821	3718156	+	308.1	262.44	1.17	451.57	477.57	0.95	
<i>ywrD</i>	3718161	3719738	-	78.07	83.07	0.94	64.16	73.08	0.88	
<i>ywrC</i>	3719952	3720428	+	231.77	265.53	0.87	153.74	180.98	0.85	
<i>ywrB</i>	3720442	3721035	+	143.39	157.22	0.91	118.01	120.73	0.98	
<i>ywrA</i>	3721032	3721568	+	108.31	110.83	0.98	99.67	113.74	0.88	
<i>ywqO</i>	3721595	3721816	-	41.45	43.62	0.95	56.57	47.45	1.19	
<i>ywqN</i>	3721813	3722358	-	68.32	57.77	1.18	84.35	79	1.07	
<i>ywqM</i>	3722481	3723362	+	106.58	123.23	0.86	90.91	119.18	0.76	
<i>ywqL</i>	3723447	3724163	-	504.12	329.72	1.53	548.22	491.48	1.12	
<i>ywqK</i>	3724173	3724637	-	710	412.82	1.72	671.79	628.53	1.07	
<i>ywqJ</i>	3724627	3726435	-	725.9	475.46	1.53	644.25	518.54	1.24	
<i>ywqI</i>	3726454	3726714	-	1060.25	802.3	1.32	990.36	728.22	1.36	
<i>ywqH</i>	3726724	3727146	-	858.63	646.73	1.33	710.65	569.24	1.25	
<i>ywqG</i>	3727538	3728323	-	439.96	350.36	1.26	724.77	691.25	1.05	
<i>ywqF</i>	3728515	3729837	-	196.25	154.07	1.27	324.08	293.15	1.11	
<i>ywqE</i>	3730032	3730796	-	112.93	96.6	1.17	159.95	147.41	1.09	AbrB regulon
<i>ywqD</i>	3730849	3731562	-	336.24	270.12	1.24	496.81	525.76	0.94	AbrB regulon
<i>ywqC</i>	3731552	3732298	-	214.99	225.8	0.95	376.93	426.74	0.88	Spo0A and AbrB regulon
<i>ywqB</i>	3732879	3734489	+	209	180.54	1.16	212.34	262.98	0.81	
<i>ywqA</i>	3734476	3737244	+	382.56	282.16	1.36	484.1	460.4	1.05	
<i>ywpJ</i>	3737370	3738227	-	252.19	278.36	0.91	504.68	663.11	0.76	
<i>glcR</i>	3738233	3739009	-	214.96	247.79	0.87	360.63	518.9	0.69	
<i>ywpH</i>	3739233	3739574	-	3282.27	3801.6	0.86	3531.66	4101.89	0.86	
<i>ywpG</i>	3739651	3740034	-	48.68	56.89	0.86	129.47	127.18	1.02	
<i>ywpF</i>	3740209	3740619	+	1841.52	1689.99	1.09	1284.97	1363.58	0.94	
<i>ywpE</i>	3740758	3741066	-	38.05	36.32	1.05	53.97	50.51	1.07	
<i>ywpD</i>	3741410	3742246	+	45.36	45.73	0.99	48.47	51.47	0.94	
<i>mscL</i>	3742293	3742685	-	564.19	540.75	1.04	659.5	743.19	0.89	
<i>ywpB</i>	3742784	3743182	-	223.93	243.33	0.92	290.89	349.17	0.83	
<i>rapD</i>	3743374	3744438	+	384.15	303.11	1.27	510.36	489.79	1.04	
<i>flhP</i>	3744461	3745267	-	1352.33	1877.64	0.72	1155.67	1548.24	0.75	
<i>flhO</i>	3745301	3746113	-	1339.04	2311.37	0.58	1147.43	1486.65	0.77	
<i>mbI</i>	3746276	3747277	-	981.51	921.44	1.07	1097.54	1594.83	0.69	
<i>spolIID</i>	3747443	3747724	-	27.29	41.47	0.66	30.56	40.02	0.76	
<i>ywoH</i>	3748074	3748487	+	60.03	58.59	1.02	63.41	99.56	0.64	
<i>ywoG</i>	3748509	3749699	+	79.27	73.86	1.07	97.68	108.25	0.90	
<i>ywoF</i>	3749790	3751196	-	613.83	507.04	1.21	755.93	797.65	0.95	AbrB regulon
<i>ywoE</i>	3751302	3752774	-	62.23	64.53	0.96	54.77	60.39	0.91	
<i>ywoD</i>	3752955	3754313	-	169.23	149.3	1.13	184.43	169.64	1.09	
<i>ywoC</i>	3754313	3754882	-	295.14	275.97	1.07	376.35	385.52	0.98	
<i>ywoB</i>	3755066	3755530	-	234.16	235.11	1.00	324.71	341.28	0.95	
<i>nrgA</i>	3755812	3757026	+	312.13	321.44	0.97	168.27	157.81	1.07	
<i>nrgB</i>	3757038	3757388	+	851.84	861.33	0.99	1195.85	830.26	1.44	
<i>ywoA</i>	3757569	3758150	+	451.25	320.18	1.41	495.17	451.3	1.10	
<i>ywnJ</i>	3758191	3758613	-	80.79	66.25	1.22	96.38	73.74	1.31	
<i>spolIQ</i>	3758724	3759575	-	72.04	105.16	0.69	69.58	81.84	0.85	
<i>ywnH</i>	3759716	3760207	+	468.11	477.07	0.98	489.33	620.1	0.79	
<i>ywnG</i>	3760204	3760722	+	369.56	340.96	1.08	429.63	477.21	0.90	
<i>ywnF</i>	3761009	3761443	-	554.15	431.73	1.28	216.21	203.14	1.06	
<i>ywnE</i>	3761686	3763134	+	211.92	175.16	1.21	255.46	250.32	1.02	
<i>mta</i>	3763155	3763928	-	149.11	137.83	1.08	143.5	127.16	1.13	
<i>ywnC</i>	3764073	3764456	+	88.1	80.71	1.09	140.3	141.65	0.99	
<i>ywnB</i>	3764491	3765132	-	191.51	221.01	0.87	251.75	302.5	0.83	
<i>ywnA</i>	3765200	3765601	-	323.85	332.28	0.97	376	434.86	0.86	
<i>ureC</i>	3765736	3767445	-	570.32	479.7	1.19	491.74	386.38	1.27	
<i>ureB</i>	3767442	3767816	-	694.4	563.05	1.23	659.88	509.65	1.29	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>moaA</i>	3771348	3772373	-	902.63	673.32	1.34	1163.18	858.52	1.35	
<i>fdhD</i>	3772389	3773177	-	670.86	439.18	1.53	704.38	539.79	1.30	
<i>ywmD</i>	3773678	3774352	-	312.04	238.92	1.31	306.39	290.33	1.06	
<i>ywmC</i>	3774676	3775359	-	197.43	172.7	1.14	140.1	153.48	0.91	
<i>spolID</i>	3775745	3776776	-	190.27	194.06	0.98	132.94	135.87	0.98	Spo0A regulon
<i>murAA</i>	3776972	3778282	-	2148.79	1780.49	1.21	1887.94	2052.13	0.92	
<i>ywmB</i>	3778316	3779056	-	1689.22	1256.59	1.34	1318.64	1406.26	0.94	
<i>ywzB</i>	3779185	3779415	-	1497.87	1130.56	1.32	1110.17	1050.19	1.06	
<i>ywmA</i>	3779585	3780058	+	79.18	93.57	0.85	59.24	61.1	0.97	
<i>atpC</i>	3780092	3780490	-	4800.16	4765.59	1.01	3214.33	3187.66	1.01	
<i>atpD</i>	3780514	3781935	-	3249.19	3926.6	0.83	3225.97	3477.77	0.93	
<i>atpG</i>	3781961	3782824	-	3431.85	4131.85	0.83	4093.13	4309.13	0.95	
<i>atpA</i>	3782901	3784409	-	3018.22	3229.26	0.93	3345.48	3657.88	0.91	
<i>atpH</i>	3784426	3784971	-	3179.12	3402.52	0.93	3691.27	3909.95	0.94	
<i>atpF</i>	3784968	3785480	-	4081.41	4420.57	0.92	4376.8	4743.34	0.92	
<i>atpE</i>	3785643	3785855	-	2254.6	2410.94	0.94	3064.88	3505.46	0.87	
<i>atpB</i>	3785901	3786635	-	2634.35	2876.72	0.92	2819.08	3179.9	0.89	
<i>atpI</i>	3786643	3787026	-	1416.17	1481.29	0.96	1251.41	1641.55	0.76	
<i>upp</i>	3787449	3788078	-	718.51	751.54	0.96	1304.34	1519.86	0.86	
<i>glyA</i>	3788213	3789460	-	2740.04	3009.52	0.91	2545.27	2890.87	0.88	
<i>ywlG</i>	3789667	3790209	-	695.23	679.32	1.02	646.69	610.88	1.06	
<i>ywlF</i>	3790222	3790671	-	1009.06	984.29	1.03	913.44	932.3	0.98	
<i>ywlE</i>	3790828	3791280	-	492.92	491.03	1.00	372.09	392.19	0.95	
<i>ywlD</i>	3791356	3791913	-	71.22	64.16	1.11	63.76	67.98	0.94	
<i>ywlC</i>	3791992	3793032	-	313.65	306.41	1.02	316.25	295.24	1.07	
<i>ywlB</i>	3793189	3793632	-	583.28	349.23	1.67	230.84	137.44	1.68	
<i>spolIR</i>	3793699	3794373	-	591.11	352.87	1.68	249.12	130.45	1.91	
<i>ywlA</i>	3794514	3794876	+	143.4	135.04	1.06	177.51	179.38	0.99	
<i>ywkF</i>	3794893	3795180	-	214.33	168.58	1.27	255.67	251.03	1.02	
<i>ywkE</i>	3795240	3796106	-	337.56	245.93	1.37	435.95	418.43	1.04	
<i>prfA</i>	3796108	3797178	-	1284.04	1159.01	1.11	1435.83	1367.85	1.05	
<i>ywkD</i>	3797304	3797690	+	223.99	189.75	1.18	263.28	198.41	1.33	
<i>ywkC</i>	3797812	3798366	+	433.14	428.59	1.01	544.04	480.45	1.13	Spo0A regulon
<i>ywkB</i>	3798400	3799359	-	83.95	65.94	1.27	55.87	44.38	1.26	
<i>ywkA</i>	3799441	3801189	-	100.68	79.12	1.27	106.16	72.7	1.46	
<i>tdk</i>	3801428	3802015	-	194.16	236.98	0.82	202.2	277.14	0.73	
<i>rpmE</i>	3802104	3802304	-	1546.08	2103.5	0.74	3367.65	3811.7	0.88	
<i>rho</i>	3802423	3803706	-	1628.2	1357.23	1.20	1655.41	1656.59	1.00	
<i>ywjI</i>	3804113	3805078	-	1102.7	1370.77	0.80	1547.76	2289.5	0.68	
<i>murAB</i>	3805109	3806398	-	1236.63	1424.8	0.87	1639.73	2361.27	0.69	
<i>ywjH</i>	3806777	3807415	-	2923.25	3799.44	0.77	3299.05	4103.77	0.80	
<i>fbaA</i>	3807535	3808392	-	3303.22	4012.09	0.82	3542.93	4124.41	0.86	
<i>spo0F</i>	3808573	3808947	-	742.29	739.99	1.00	604.31	810.77	0.75	Spo0A regulon
<i>ywjG</i>	3809113	3809634	+	241.59	239.47	1.01	267.73	267.73	1.00	
<i>pyrG</i>	3809716	3811323	-	493.27	498.8	0.99	918.47	997.13	0.92	
<i>rpoE</i>	3811565	3812086	-	957.56	1013.57	0.94	1013.12	1331.03	0.76	
<i>acdA</i>	3812269	3813408	-	147.63	128.78	1.15	153.22	147.78	1.04	
<i>ywjF</i>	3813405	3815522	-	145.46	130.44	1.12	149.23	158.41	0.94	
<i>ywjE</i>	3815677	3816873	+	56.61	60.01	0.94	43.28	53.18	0.81	
<i>ywjD</i>	3816886	3817848	+	50.1	49.09	1.02	37.93	44.11	0.86	
<i>ywjC</i>	3817929	3818201	+	1697.33	2317.07	0.73	2126.94	1166.37	1.82	
<i>ywjB</i>	3818243	3818767	-	1582.97	1475.55	1.07	946.06	978.36	0.97	
<i>ywjA</i>	3818777	3820504	-	1864.77	1803.83	1.03	945.8	997.8	0.95	
<i>ywiE</i>	3820593	3822095	-	1347.65	1632.07	0.83	988.21	778.35	1.27	
<i>narI</i>	3822581	3823252	-	59.38	61.73	0.96	55.89	62.99	0.89	
<i>narJ</i>	3823249	3823803	-	112.47	114.15	0.99	91.4	106.95	0.85	
<i>narH</i>	3823829	3825292	-	124.75	118.34	1.05	84.63	111.52	0.76	
<i>narG</i>	3825282	3828968	-	96.6	93.8	1.03	70.95	88.09	0.81	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>argS</i>	3832673	3834343	-	918.32	848.89	1.08	927.38	1082.28	0.86	
<i>ywiB</i>	3834340	3834768	-	509.25	517.68	0.98	560.73	733.78	0.76	
<i>albA</i>	3835346	3836692	+	3725.12	2917.96	1.28	2365.84	1962.31	1.21	AbrB regulon
<i>albB</i>	3836705	3836866	+	3152.97	2376.81	1.33	1724.49	1474.17	1.17	AbrB regulon
<i>albC</i>	3836863	3837582	+	2003.35	1172.76	1.71	1017.48	911.31	1.12	AbrB regulon
<i>albD</i>	3837575	3838885	+	1512.17	869.07	1.74	709.91	669.72	1.06	AbrB regulon
<i>albE</i>	3838875	3840035	+	1138.61	655.58	1.74	497.81	475.56	1.05	AbrB regulon
<i>albF</i>	3840040	3841320	+	899.84	587.06	1.53	371.54	372.16	1.00	AbrB regulon
<i>albG</i>	3841317	3842018	+	416.87	282.02	1.48	149.04	154.52	0.96	AbrB regulon
<i>ywhL</i>	3842024	3843400	-	60.27	60.03	1.00	58.3	61.5	0.95	
<i>ywhK</i>	3843439	3844794	-	44.15	47.02	0.94	44.15	46.91	0.94	
<i>rapF</i>	3845024	3846169	+	2507.48	2361.04	1.06	2765.08	2820.67	0.98	
<i>ywhH</i>	3846371	3846844	+	272.1	199.82	1.36	395.72	359.96	1.10	
<i>speB</i>	3846876	3847748	-	234.13	247.48	0.95	479.55	473.04	1.01	
<i>speE</i>	3847809	3848639	-	406.47	531.17	0.77	613.9	762.16	0.81	
<i>ywhE</i>	3848841	3850784	+	82.96	83.43	0.99	63.5	81.73	0.78	
<i>ywhD</i>	3851208	3851726	-	776	663.24	1.17	1091.87	1081.1	1.01	
<i>ywhC</i>	3851740	3852399	-	527.74	475.44	1.11	594.03	648.36	0.92	
<i>ywhB</i>	3852508	3852696	+	287.31	297.37	0.97	431.36	438.27	0.98	
<i>ywhA</i>	3852739	3853158	-	308.14	302.12	1.02	330.3	337.55	0.98	
<i>thrZ</i>	3853278	3855194	-	142.37	140.59	1.01	150.07	154.53	0.97	
<i>mmr</i>	3856039	3857439	-	172.43	168.14	1.03	182.7	206.09	0.89	
<i>ywgB</i>	3857439	3857909	-	87.56	93.35	0.94	110.58	127.62	0.87	
<i>ywgA</i>	3858021	3858521	-	306.44	269.11	1.14	475.53	538.02	0.88	
<i>ywfO</i>	3858557	3859858	-	551.64	533.72	1.03	773.04	853.02	0.91	
<i>ywzC</i>	3860020	3860244	-	281.26	335.23	0.84	170.9	238.91	0.72	
<i>rsfA</i>	3860459	3861235	+	89.99	102.73	0.88	64.16	78.52	0.82	
<i>ywfM</i>	3861379	3862269	-	95.77	84.74	1.13	91.25	86.66	1.05	
<i>ywfL</i>	3862437	3863282	-	165.49	172.1	0.96	217.81	262.65	0.83	
<i>ywfK</i>	3863331	3864230	-	158.68	166.64	0.95	168.8	182.25	0.93	
<i>pta</i>	3864377	3865348	-	1082.57	959.03	1.13	1581.45	1399.05	1.13	
<i>ywfI</i>	3865618	3866382	+	1014	797.2	1.27	698.48	643.42	1.09	
<i>ywfH</i>	3866515	3867294	+	1029.04	933.25	1.10	946.58	1040.98	0.91	
<i>ywfG</i>	3867309	3868508	-	268.12	265.72	1.01	382.43	408.61	0.94	
<i>ywfF</i>	3868509	3869693	-	406.77	382.17	1.06	676.3	691.52	0.98	
<i>ywfE</i>	3869690	3871108	-	593.52	547.68	1.08	930.62	952.68	0.98	
<i>ywfD</i>	3871127	3871894	-	549.11	489.37	1.12	742.61	794.27	0.93	
<i>ywfC</i>	3871891	3872598	-	429.11	431.97	0.99	629.97	708.42	0.89	
<i>ywfB</i>	3872588	3873202	-	251.47	267.5	0.94	239.7	290.76	0.82	
<i>ywfA</i>	3873354	3874592	-	125.86	114.44	1.10	92.03	99.16	0.93	
<i>rocC</i>	3874802	3876214	-	235.58	234.08	1.01	203.36	194.55	1.05	
<i>rocB</i>	3876214	3877914	-	212.87	329.89	0.65	180.36	189.69	0.95	
<i>rocA</i>	3877988	3879535	-	448.36	939.22	0.48	304.89	434.06	0.70	AbrB regulon
<i>rocG</i>	3879762	3881036	-	310.35	418.08	0.74	280.65	351.16	0.80	Spo0A and AbrB regulon
<i>yweA</i>	3881213	3881677	-	2652.93	3229.85	0.82	2077.95	2278.4	0.91	AbrB regulon
<i>spsL</i>	3882001	3882456	-	95.73	77.9	1.23	120.88	112.2	1.08	
<i>spsK</i>	3882449	3883300	-	173.57	142.44	1.22	186.04	175.29	1.06	
<i>spsJ</i>	3883314	3884261	-	112.94	99.29	1.14	140.51	122.91	1.14	
<i>spsI</i>	3884261	3885001	-	119.79	114.07	1.05	120.66	125.68	0.96	
<i>spsG</i>	3885026	3886045	-	102.14	97.9	1.04	99.07	100.59	0.98	
<i>spsF</i>	3886052	3886771	-	71.64	69.28	1.03	71.57	68.84	1.04	
<i>spsE</i>	3886764	3887885	-	108.87	109.32	1.00	97	96.18	1.01	
<i>spsD</i>	3887885	3888754	-	67.14	62.66	1.07	65.69	69.99	0.94	
<i>spsC</i>	3888755	3889924	-	105.45	108.32	0.97	86.77	108.92	0.80	
<i>spsB</i>	3889945	3891363	-	44.49	47.51	0.94	40.06	42.65	0.94	
<i>spsA</i>	3891368	3892138	-	46.3	55.04	0.84	36.39	44.34	0.82	
<i>ywdL</i>	3892458	3893003	+	53.11	62.11	0.86	36.67	43.69	0.84	
<i>ywdK</i>	3893076	3893417	-	710.34	589.64	1.20	568.17	520.3	1.09	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location		strand	Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end		pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>ywdF</i>	3897394	3898200	-	357.91	279.87	1.28	572.59	515.89	1.11	
<i>ywdE</i>	3898291	3898824	-	74.65	76.84	0.97	102.1	125.08	0.82	
<i>ywdD</i>	3898872	3899363	-	65.45	68.23	0.96	108.98	165.58	0.66	
<i>ywdC</i>	3899406	3899834	+	28.51	33.97	0.84	31.44	33.85	0.93	
<i>thiD</i>	3899983	3900798	+	509.37	547.05	0.93	742.19	864.92	0.86	
<i>ywdA</i>	3900888	3901136	-	345.65	444.2	0.78	197.93	215.34	0.92	
<i>sacA</i>	3901230	3902672	-	318.44	399.49	0.80	292.22	395.1	0.74	
<i>sacP</i>	3902669	3904054	-	141.64	175.97	0.80	134.21	182.39	0.74	
<i>ywcJ</i>	3904356	3905126	+	1009.42	831.14	1.21	192.22	167.08	1.15	
<i>sacT</i>	3905165	3905995	-	102.1	135.19	0.76	118.32	142.34	0.83	
<i>ywcl</i>	3906035	3906337	-	82.8	99.34	0.83	81.24	135.34	0.60	
<i>vpr</i>	3906867	3909287	+	456.35	416.33	1.10	697.77	598.4	1.17	
<i>ywcH</i>	3909325	3910326	-	186.76	171.57	1.09	175.76	156.47	1.12	Spo0A regulon
<i>nfrA</i>	3910500	3911249	-	1009.78	995.4	1.01	988.85	817.84	1.21	Spo0A and SigD regulon
<i>rodA</i>	3911355	3912536	-	113.12	136.97	0.83	167.62	201.03	0.83	
<i>ywcE</i>	3913032	3913295	+	67.73	81.18	0.83	144.8	252.92	0.57	
<i>qoxD</i>	3913338	3913712	-	479.1	587.25	0.82	1153.8	998.55	1.16	
<i>qoxC</i>	3913714	3914328	-	4661.74	4617.54	1.01	3688.29	3412.32	1.08	
<i>qoxB</i>	3914342	3916291	-	4303.48	4292.01	1.00	3454.4	3159.97	1.09	
<i>qoxA</i>	3916319	3917284	-	3774.86	3832.21	0.99	2744.37	2835.73	0.97	
<i>ywzA</i>	3917895	3918044	+	2439.19	2195.19	1.11	1412.79	720.79	1.96	
<i>galT</i>	3918116	3919657	-	1131.5	882.19	1.28	665.51	588.23	1.13	
<i>galK</i>	3919661	3920833	-	903.39	737.81	1.22	607.3	459.22	1.32	
<i>ywcD</i>	3920914	3921297	-	188.07	184.25	1.02	200.15	230.31	0.87	
<i>ywcC</i>	3921315	3921986	-	142.63	155.83	0.92	125.18	144.46	0.87	
<i>slrA</i>	3922342	3922500	+	520.43	415.32	1.25	498.82	431.32	1.16	
<i>ywcB</i>	3922943	3923251	+	116.25	98.99	1.17	129.95	117.42	1.11	
<i>ywcA</i>	3923238	3924788	+	81.82	79.39	1.03	71.13	78.29	0.91	
<i>ywbO</i>	3924819	3925421	-	154.37	146.67	1.05	141.25	193.45	0.73	
<i>ywbN</i>	3925705	3926955	-	723.87	761.9	0.95	606.55	748.15	0.81	
<i>ywbM</i>	3926974	3928131	-	713.86	802.3	0.89	598.9	864.79	0.69	
<i>ywbL</i>	3928128	3929573	-	302.17	368.79	0.82	236.32	350.62	0.67	
<i>thiE</i>	3929730	3930398	-	635.92	520.76	1.22	564.94	525.26	1.08	
<i>thiM</i>	3930395	3931213	-	717.23	564.2	1.27	653.57	576.61	1.13	
<i>ywbI</i>	3931221	3932126	-	378.07	279.79	1.35	333.89	307.81	1.08	
<i>ywbH</i>	3932232	3932618	+	164.4	116.1	1.42	186.38	280.84	0.66	
<i>ywbG</i>	3932600	3933325	+	167.72	130.06	1.29	121.63	183.3	0.66	
<i>ywbF</i>	3933380	3934579	+	293.87	286.85	1.02	391.01	396.45	0.99	AbrB regulon
<i>ywbE</i>	3934613	3934810	+	364.88	348.36	1.05	619.89	653.7	0.95	
<i>ywbD</i>	3934845	3936035	-	389.73	336.66	1.16	379.18	380.21	1.00	
<i>ywbC</i>	3936156	3936536	+	518.19	447.81	1.16	672.9	666.16	1.01	
<i>ywbB</i>	3936574	3937251	-	93.54	74.32	1.26	87.48	89.53	0.98	
<i>ywbA</i>	3937328	3938662	-	101.74	104.32	0.98	85.02	106.95	0.79	
<i>epr</i>	3938890	3940827	+	2588.43	2029.35	1.28	1982.55	1706.1	1.16	SigD regulon
<i>sacX</i>	3941255	3942634	+	108.24	99.8	1.08	168.01	175.91	0.96	
<i>sacY</i>	3942688	3943530	+	67.73	72.63	0.93	143.21	153.89	0.93	
<i>gspA</i>	3943581	3944441	-	6590.66	6290.69	1.05	3481.81	1800.73	1.93	
<i>ywaF</i>	3944551	3945264	-	61.75	61.6	1.00	50	56.72	0.88	
<i>ywaE</i>	3945415	3945930	+	207.46	227.05	0.91	218.7	248.43	0.88	
<i>tyrZ</i>	3946179	3947420	+	85.2	100.19	0.85	98.83	112.88	0.88	
<i>ywaD</i>	3947576	3948943	+	108.34	106.91	1.01	90.2	91.25	0.99	
<i>ywaC</i>	3948973	3949605	-	215.83	262.02	0.82	340.96	346.02	0.99	
<i>menA</i>	3949747	3950682	-	523.99	638.13	0.82	503.91	646.4	0.78	
<i>dltA</i>	3951296	3952807	+	1883.39	1591.75	1.18	2538.08	2331	1.09	Spo0A and SigD regulon
<i>dltB</i>	3952804	3953991	+	1776.08	1400.86	1.27	2768.46	2503.18	1.11	
<i>dltC</i>	3954008	3954244	+	2692.97	1950.55	1.38	3594.58	3190.2	1.13	
<i>dltD</i>	3954244	3955422	+	2223.04	1646.49	1.35	3091.21	2856.94	1.08	
<i>dltE</i>	3955513	3956271	+	1607.26	1255.94	1.28	2683.96	2438.18	1.10	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>licB</i>	3960587	3960895	-	69.85	111.6	0.63	96.07	119.81	0.80	
<i>licR</i>	3961023	3962948	-	228.9	236.12	0.97	201.28	268.86	0.75	
<i>yxjJ</i>	3963298	3963888	-	631.95	373.59	1.69	360.13	205.26	1.75	
<i>katX</i>	3964017	3965660	+	1601.18	857.31	1.87	1243.07	510.55	2.43	
<i>yxjH</i>	3965765	3966967	+	99.18	92.59	1.07	109.6	111.87	0.98	
<i>yxjG</i>	3966960	3967739	-	345.35	315.44	1.09	408.06	341.33	1.20	
<i>yxjF</i>	3967736	3968623	-	455.63	394.35	1.16	490.36	435.72	1.13	
<i>yxjE</i>	3968630	3968818	-	391	354.92	1.10	447.34	321.34	1.39	
<i>yxjD</i>	3968815	3969021	-	360.99	300.44	1.20	445.46	352.73	1.26	
<i>yxjC</i>	3969018	3969338	-	212.46	191.95	1.11	244.19	212.98	1.15	
<i>sigY</i>	3969331	3969867	-	173.3	162.48	1.07	228.15	227.86	1.00	
<i>yxjA</i>	3970079	3971452	+	179.64	139.84	1.28	309.42	324.76	0.95	
<i>yxkO</i>	3971467	3972297	-	583.26	383.02	1.52	378.47	275.93	1.37	
<i>cydD</i>	3972383	3974110	-	1737.55	1563.67	1.11	110.22	85.89	1.28	
<i>cydC</i>	3974107	3975810	-	2997.94	2639.92	1.14	171.36	102.18	1.68	
<i>cydB</i>	3975810	3976826	-	3676.02	3192.91	1.15	282.09	132.73	2.13	
<i>cydA</i>	3976810	3978216	-	2609.87	2183.9	1.20	511.85	392.01	1.31	
<i>yxkJ</i>	3978772	3980124	+	761.37	872.2	0.87	436.2	516.02	0.85	
<i>yxkI</i>	3980246	3981934	+	339.51	322.29	1.05	368.89	437.14	0.84	
<i>yxzE</i>	3981992	3982192	+	382.04	405.69	0.94	732.02	670.95	1.09	AbrB regulon
<i>yxkH</i>	3982206	3983045	-	368.28	434.28	0.85	377.28	358.32	1.05	
<i>msmX</i>	3983152	3984249	-	312.17	426.96	0.73	356.49	499.63	0.71	
<i>yxkF</i>	3984370	3985263	-	176.33	190.39	0.93	143.67	199.48	0.72	
<i>aldY</i>	3985447	3986904	+	913.25	738.33	1.24	322.36	200.2	1.61	
<i>yxkD</i>	3986946	3987782	-	119.23	130.66	0.91	139	178.9	0.78	
<i>yxkC</i>	3988251	3988892	+	4081.97	4453.65	0.92	4278.55	4278.28	1.00	SigD regulon
<i>galE</i>	3988967	3989986	-	1153.4	1181.72	0.98	1294.85	1444.1	0.90	
<i>yxkA</i>	3990101	3990607	-	71.61	61.09	1.17	71.56	57.75	1.24	
<i>yxjO</i>	3990737	3991612	+	113.97	124.51	0.92	105.23	138.31	0.76	
<i>yxjN</i>	3991690	3992163	+	158.35	210.11	0.75	177.1	252.61	0.70	
<i>yxjM</i>	3992181	3993401	+	104.52	110.28	0.95	115.29	136.35	0.85	
<i>yxjL</i>	3993388	3994044	+	133.71	140.28	0.95	152.48	190.2	0.80	
<i>pepT</i>	3994094	3995326	+	1065.41	1452.5	0.73	1209.87	1441.68	0.84	
<i>yxjJ</i>	3995848	3996111	+	3026.92	3154.34	0.96	2511.83	1643.82	1.53	
<i>yxjI</i>	3996240	3996728	+	430.61	376.67	1.14	494.31	461.37	1.07	
<i>yxjH</i>	3996983	3998005	+	850.02	885.37	0.96	1071.69	1248.87	0.86	
<i>yxjG</i>	3998368	3999504	+	1178.15	1468.93	0.80	1537.17	1906.66	0.81	
<i>yxjF</i>	3999557	4000330	-	71.86	70.02	1.03	62.16	67.49	0.92	
<i>scoB</i>	4000347	4000997	-	115.86	118.1	0.98	98.48	107.7	0.91	
<i>scoA</i>	4000994	4001710	-	66.57	72.36	0.92	67.67	71.35	0.95	
<i>yxjC</i>	4001734	4003152	-	78.38	74.87	1.05	55.25	66.1	0.84	
<i>yxjB</i>	4003306	4004154	-	136.5	118.58	1.15	152.37	160.94	0.95	
<i>yxjA</i>	4004770	4005963	+	61.33	86.38	0.71	209.58	232.74	0.90	
<i>yxjT</i>	4006434	4006676	-	564.48	277.02	2.04	547.72	274.45	2.00	
<i>yxjS</i>	4006821	4007111	-	1853.42	1248.23	1.48	1022.94	577.88	1.77	
<i>katE</i>	4007161	4009221	-	4019.21	2846.45	1.41	1616.86	832.43	1.94	
<i>citH</i>	4009422	4010702	+	51.5	53.96	0.95	40.99	45.43	0.90	
<i>bglS</i>	4010860	4011588	-	105.73	141.02	0.75	104.06	134.99	0.77	
<i>licT</i>	4011884	4012717	-	565.93	663.42	0.85	505.34	561.22	0.90	
<i>yxjP</i>	4012813	4013493	-	336.57	338.13	1.00	305.1	341.49	0.89	
<i>yxjO</i>	4013700	4014986	+	265.28	255.37	1.04	219.03	243.49	0.90	
<i>deaD</i>	4015005	4016444	-	750.96	846.26	0.89	669.69	836.84	0.80	
<i>yxjM</i>	4016526	4017674	-	711.34	851.99	0.83	604.09	776.51	0.78	
<i>yxjL</i>	4017857	4018057	-	481.05	502.84	0.96	344.85	438.99	0.79	
<i>yxjK</i>	4018166	4018627	-	896.58	1058.38	0.85	693.7	891.88	0.78	
<i>yxjJ</i>	4018643	4018939	-	937.55	1107.05	0.85	827.36	1002.68	0.83	
<i>yxjI</i>	4018967	4019455	-	897.9	1082.8	0.83	884.02	992.72	0.89	
<i>yxzG</i>	4019473	4019925	-	1143.69	1330.63	0.86	1054.35	1218.63	0.87	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yxxG</i>	4022072	4022500	-	3248.92	3354.65	0.97	2398.33	2849.67	0.84	
<i>wapA</i>	4022562	4029566	-	3615.92	4367.31	0.83	3830.51	4224.28	0.91	
<i>yxxF</i>	4029728	4030663	-	267.48	220.91	1.21	346.48	350.91	0.99	
<i>yxiE</i>	4030815	4031261	-	1463.43	1826.7	0.80	996.08	1189.28	0.84	
<i>bglH</i>	4031364	4032773	-	453.89	963.47	0.47	466.11	978.65	0.48	
<i>bglP</i>	4032796	4034625	-	364.66	682.38	0.53	337.97	638.84	0.53	
<i>yxxE</i>	4035008	4035316	-	102.37	60.22	1.70	149.79	125.85	1.19	
<i>yxxD</i>	4035362	4035805	-	226.16	132.85	1.70	299.35	216.76	1.38	
<i>yxD</i>	4035802	4037511	-	349.45	205.15	1.70	367.88	283.41	1.30	
<i>yxiC</i>	4037531	4037800	-	418.49	330.31	1.27	336.98	210.51	1.60	
<i>yxiB</i>	4037812	4038177	-	434.11	457.46	0.95	331.25	233.67	1.42	
<i>yxiA</i>	4038484	4039893	-	120.34	111.44	1.08	144.49	141.31	1.02	
<i>hutP</i>	4040501	4040956	+	396.85	621.27	0.64	438.36	468.56	0.94	
<i>hutH</i>	4041069	4042595	+	75.9	83.32	0.91	55.73	68.29	0.82	
<i>hutU</i>	4042592	4044250	+	87.37	93.18	0.94	80.5	88.87	0.91	
<i>hutI</i>	4044263	4045528	+	115.36	119.73	0.96	107.73	108.76	0.99	
<i>hutG</i>	4045521	4046480	+	77.07	80	0.96	81.98	77.74	1.05	
<i>hutM</i>	4046556	4047983	+	108.29	89.25	1.21	90.13	82	1.10	
<i>pdp</i>	4048027	4049328	-	681.97	705.9	0.97	523.16	581.59	0.90	
<i>nupC</i>	4049358	4050539	-	739.38	691.64	1.07	543.15	555.51	0.98	
<i>dra</i>	4050655	4051290	-	1736.48	1404.56	1.24	1286.05	1046.51	1.23	
<i>deoR</i>	4051396	4052337	-	350.9	421.94	0.83	269.8	398.3	0.68	
<i>yxxB</i>	4052428	4053297	-	393.53	410.13	0.96	201.63	137.25	1.47	
<i>yxeR</i>	4053370	4054482	-	383.49	281.96	1.36	420.62	341.67	1.23	
<i>yxeQ</i>	4054552	4055889	-	378.04	259.78	1.46	422.16	297.54	1.42	
<i>yxeP</i>	4055886	4057028	-	683.46	417.84	1.64	689.88	487.48	1.42	
<i>yxeO</i>	4057045	4057794	-	539.3	297.96	1.81	677.7	482.3	1.41	
<i>yxeN</i>	4057807	4058481	-	608.9	307.6	1.98	676.51	475.12	1.42	
<i>yxeM</i>	4058504	4059298	-	658.76	297.29	2.22	897.86	640.99	1.40	
<i>yxeL</i>	4059323	4059820	-	427.75	246.63	1.73	634.7	474.02	1.34	
<i>yxeK</i>	4059834	4061159	-	286.45	180.03	1.59	444.49	382.06	1.16	
<i>yxeJ</i>	4061345	4061572	-	23.58	33.26	0.71	34.32	35.46	0.97	
<i>yxeI</i>	4061559	4062545	-	70.97	70.2	1.01	107.1	109.86	0.97	
<i>yxeH</i>	4062700	4063512	-	590.73	443.85	1.33	925.74	861.64	1.07	
<i>yxeG</i>	4063552	4064109	-	204.21	151.31	1.35	302.3	306.48	0.99	
<i>yxeF</i>	4064090	4064524	-	368.59	270.3	1.36	529.5	567.61	0.93	
<i>yxeE</i>	4064612	4064977	+	66.99	76.73	0.87	36.75	45.21	0.81	
<i>yxD</i>	4065225	4065578	+	29.3	39.31	0.75	25.62	28.6	0.90	AbrB regulon
<i>yxeC</i>	4065622	4066020	-	540.03	581.37	0.93	645.64	718.39	0.90	
<i>yxeB</i>	4066198	4067157	+	943.54	1437.29	0.66	461.72	864.5	0.53	
<i>yxeA</i>	4067204	4067551	-	98.52	100.22	0.98	97.86	115.91	0.84	
<i>yxDM</i>	4067565	4069433	-	79.07	79.18	1.00	69.56	75.41	0.92	
<i>yxDL</i>	4069408	4070181	-	68.18	70.68	0.96	68.33	72.5	0.94	
<i>yxDK</i>	4070325	4071302	-	166.99	145.65	1.15	172.04	170.55	1.01	
<i>yxDJ</i>	4071299	4071988	-	201.47	179.68	1.12	196.7	196.4	1.00	
<i>fbaB</i>	4072097	4072969	-	148.72	181.24	0.82	181.71	213.68	0.85	
<i>iolI</i>	4072990	4073826	-	104.2	137.19	0.76	129.29	172.46	0.75	
<i>iolH</i>	4073912	4074781	-	89.87	121.33	0.74	101.01	144.46	0.70	
<i>idH</i>	4074801	4075835	-	128.85	157.7	0.82	155.29	233.5	0.67	
<i>iolF</i>	4075858	4077177	-	120.63	141.34	0.85	108.42	147.88	0.73	
<i>iolE</i>	4077192	4078085	-	106.99	140.16	0.76	108.07	155.43	0.70	
<i>iolD</i>	4078102	4079844	-	133.7	174.73	0.77	149.51	219.19	0.68	
<i>iolC</i>	4080048	4081025	-	104.05	144.53	0.72	124.76	175.29	0.71	
<i>iolB</i>	4081049	4081864	-	52.9	82.87	0.64	89.07	120.2	0.74	
<i>mmsA</i>	4081939	4083402	-	115.75	144.02	0.80	159.39	225.89	0.71	
<i>iolR</i>	4083818	4084573	+	225.49	262.4	0.86	325.02	368.29	0.88	
<i>iolS</i>	4084627	4085559	+	644.51	665.57	0.97	1221.38	1094.62	1.12	
<i>yxcE</i>	4085821	4086471	+	363.25	409.02	0.89	330.36	279.72	1.18	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yxbG</i>	4090865	4091686	+	1636.07	1435.25	1.14	680.28	346.54	1.96	
<i>yxbF</i>	4091715	4092857	-	120.33	113.54	1.06	129.26	142.69	0.91	
<i>aldX</i>	4093000	4094337	+	133.05	137.31	0.97	121.21	138.62	0.87	
<i>yxbD</i>	4094376	4094855	-	271.36	268.03	1.01	715.86	806.58	0.89	AbrB regulon
<i>yxbC</i>	4094935	4095927	-	1806.66	2140.2	0.84	1969.74	2155.89	0.91	Spo0A and AbrB regulon
<i>yxbB</i>	4096436	4097170	+	2054.95	2436.97	0.84	2288.95	2715.17	0.84	AbrB regulon
<i>yxbA</i>	4097170	4097439	+	1481.27	1801.2	0.82	1874.94	2152.9	0.87	AbrB regulon
<i>yxnB</i>	4097443	4097925	+	1257.17	1580	0.80	1605.69	2019.36	0.80	AbrB regulon
<i>asnH</i>	4097946	4100189	+	470.63	607.04	0.78	790.15	1134.31	0.70	
<i>yxalM</i>	4100186	4101385	+	363.54	531.79	0.68	599.16	892.9	0.67	
<i>yxalL</i>	4101449	4102681	-	1356.87	1021.29	1.33	965.11	852.55	1.13	AbrB regulon
<i>yxalJ</i>	4102782	4103210	-	438.08	336.27	1.30	641.51	570.9	1.12	AbrB regulon
<i>yxalI</i>	4103467	4103922	+	198.46	243.28	0.82	362.53	475.7	0.76	
<i>yxalH</i>	4103952	4105160	-	148.06	181.06	0.82	163.13	234.26	0.70	
<i>yxalG</i>	4105268	4106281	-	194.15	251.15	0.77	260.7	389.89	0.67	
<i>yxalF</i>	4106375	4106950	-	62.49	62.51	1.00	83.87	96.07	0.87	
<i>yxalA</i>	4107081	4108151	+	2137.14	1683.43	1.27	767.57	338.54	2.27	
<i>yxalD</i>	4108208	4108639	-	83.81	87.09	0.96	79.98	110.12	0.73	
<i>yxalC</i>	4108866	4109933	+	83.48	70.4	1.19	70.98	69.9	1.02	
<i>yxalB</i>	4109973	4111004	-	1142.47	731.68	1.56	783.66	361.78	2.17	AbrB regulon
<i>yxalA</i>	4111097	4112245	-	235.32	187.45	1.26	280.38	232.93	1.20	AbrB regulon
<i>gntR</i>	4112441	4113172	+	220.06	200.39	1.10	553.15	374.64	1.48	AbrB regulon
<i>gntK</i>	4113165	4114706	+	281.53	253.52	1.11	312.68	281.5	1.11	AbrB regulon
<i>gntP</i>	4114735	4116081	+	279.7	222.74	1.26	338.13	314.98	1.07	AbrB regulon
<i>gntZ</i>	4116104	4117510	+	452.59	326.32	1.39	774.74	683.24	1.13	AbrB regulon
<i>ahpC</i>	4117974	4118537	+	5697.44	4845.31	1.18	5545.37	4931.21	1.12	
<i>ahpF</i>	4118551	4120080	+	4890.11	4316.18	1.13	4409.15	3848.03	1.15	
<i>bglA</i>	4120190	4121629	-	121.3	120.03	1.01	135.5	153.38	0.88	
<i>yyzE</i>	4121643	4121873	-	138	131.73	1.05	138.54	170.93	0.81	
<i>yydK</i>	4122217	4122927	+	166.83	162.08	1.03	147.13	171.63	0.86	
<i>yydJ</i>	4123244	4123966	-	486.62	457.42	1.06	888.21	1144.24	0.78	AbrB regulon
<i>yydI</i>	4123987	4124616	-	975.33	918.63	1.06	1386.36	1775.75	0.78	AbrB regulon
<i>yydH</i>	4124766	4125524	-	488.74	457.92	1.07	1011.59	1389.62	0.73	AbrB regulon
<i>yydG</i>	4125505	4126464	-	291.37	262.56	1.11	1063.67	1470.7	0.72	AbrB regulon
<i>fbp</i>	4127053	4129068	+	371.22	342.46	1.08	669.89	694.89	0.96	
<i>yydD</i>	4129602	4131362	-	1359.16	958.03	1.42	1053.24	1004.31	1.05	
<i>yydC</i>	4131362	4131760	-	1125.79	762.42	1.48	746.36	636.08	1.17	
<i>yydB</i>	4131753	4133198	-	1074.21	890.39	1.21	879.12	799.36	1.10	
<i>yydA</i>	4133460	4133939	-	547.36	557.02	0.98	538.74	509.06	1.06	
<i>yycS</i>	4134376	4134789	+	144.02	119.96	1.20	118.27	119.49	0.99	
<i>yycR</i>	4134823	4136049	-	489.72	366.7	1.34	351.04	306.18	1.15	
<i>yycQ</i>	4136387	4136635	-	38.07	54.41	0.70	47.33	55.43	0.85	
<i>yycP</i>	4136651	4137814	-	76.45	82.64	0.93	72.01	85.59	0.84	
<i>yycO</i>	4137825	4138562	-	104.09	102.09	1.02	84.68	95.32	0.89	
<i>yycN</i>	4138704	4139174	-	197.61	182.67	1.08	194.22	206.89	0.94	
<i>rapG</i>	4139285	4140382	+	596.04	638.48	0.93	763.32	883.34	0.86	
<i>rocF</i>	4140735	4141625	-	553.01	573.24	0.96	892.49	749.5	1.19	
<i>rocE</i>	4141699	4143102	-	425.55	485.35	0.88	660.79	557.13	1.19	
<i>rocD</i>	4143325	4144530	-	750.23	897.5	0.84	749.47	634.48	1.18	
<i>rocR</i>	4144771	4146156	+	172.22	166.49	1.03	237.04	277.01	0.86	Spo0A regulon
<i>yyxA</i>	4146591	4147793	-	512.51	382.55	1.34	926.03	753.44	1.23	
<i>yycJ</i>	4147862	4148668	-	545.99	405.32	1.35	896.86	715.14	1.25	
<i>yycI</i>	4148690	4149532	-	692.83	494.15	1.40	1238.72	1059.18	1.17	
<i>yycH</i>	4149519	4150886	-	675.57	485.53	1.39	1101.86	931.41	1.18	
<i>yycG</i>	4150876	4152711	-	677.99	514.91	1.32	873.22	747.75	1.17	
<i>yycF</i>	4152719	4153426	-	699.98	608.7	1.15	817.53	677.71	1.21	
<i>purA</i>	4154457	4155749	-	1780.45	1696.34	1.05	1285.34	1673.87	0.77	
<i>yycE</i>	4155955	4156374	-	34.26	39.82	0.86	45.49	51.52	0.88	

Table S1. Transcriptome analysis in Veg overexpression cells (pO-veg) compared with its control cells (pO-MCS).

Gene name	Location			Signal intensity of RNA		Expression ratio	Signal intensity of RNA		Expression ratio	Description ^a
	start	end	strand	pO-veg_01	pO-MCS_01	pO-veg/pO-MCS_01	pO-veg_02	pO-MCS_02	pO-veg/pO-MCS_02	
<i>yycA</i>	4160127	4162184	+	338.24	312.86	1.08	358.52	337.2	1.06	
<i>rplI</i>	4162221	4162670	-	1149.49	1106.1	1.04	1328.11	1473.53	0.90	
<i>yybT</i>	4162667	4164646	-	995.65	720.97	1.38	964.9	1003.31	0.96	
<i>yybS</i>	4164683	4165612	-	599.24	411.16	1.46	515.63	551.85	0.93	
<i>cotF</i>	4166134	4166616	+	29.66	36.01	0.82	27.44	30.89	0.89	
<i>yybR</i>	4166646	4167023	-	122.07	90.34	1.35	126.33	141.45	0.89	
<i>ppaC</i>	4167228	4168157	+	1922.52	2142.56	0.90	2053.74	2422.29	0.85	
<i>yybP</i>	4168190	4168636	-	146.11	136.85	1.07	122.8	130.36	0.94	
<i>yybO</i>	4169069	4170376	+	760.95	389.12	1.96	294.47	131.77	2.23	
<i>yybN</i>	4172138	4172575	+	3420.48	3365.28	1.02	3150.29	3686.06	0.85	
<i>yybM</i>	4172689	4173444	+	553.12	492.2	1.12	539.7	799.84	0.67	
<i>yybL</i>	4173434	4174144	+	169.34	135.32	1.25	276.23	527.91	0.52	
<i>yybK</i>	4174141	4174896	+	154.35	136.46	1.13	230.81	454.21	0.51	
<i>yybJ</i>	4174893	4175549	+	404.21	352.39	1.15	547.5	840.35	0.65	
<i>yybI</i>	4175924	4176712	-	142.43	160.66	0.89	135.95	137.95	0.99	
<i>yybH</i>	4176780	4177169	-	167.71	186	0.90	157.71	183.87	0.86	
<i>yybG</i>	4177315	4178154	+	235.89	227.61	1.04	243.67	250.92	0.97	
<i>yybF</i>	4178187	4179401	-	94.69	89.62	1.06	143.29	165.82	0.86	
<i>yybE</i>	4179630	4180466	+	73.77	80.21	0.92	76.34	98.22	0.78	
<i>yybD</i>	4180480	4180923	+	112.23	120.11	0.93	117.48	139.83	0.84	
<i>yybC</i>	4181006	4181485	+	67.13	63.46	1.06	79.74	91.87	0.87	
<i>yybB</i>	4181660	4182322	-	336.17	265.76	1.26	248.39	231.86	1.07	
<i>yybA</i>	4182469	4182921	-	206.3	195.01	1.06	211.52	239.77	0.88	
<i>yyaT</i>	4183041	4183487	+	92.61	124.05	0.75	113.46	166.57	0.68	
<i>yyaS</i>	4183484	4184089	+	36.03	48.95	0.74	52.82	73.67	0.72	
<i>yyaR</i>	4184184	4184705	-	54.72	50.65	1.08	85.18	75.98	1.12	
<i>yyaQ</i>	4185116	4185472	+	271	220.5	1.23	236.4	199.21	1.19	
<i>yyaP</i>	4185632	4186198	+	118.48	108.94	1.09	138.89	133.79	1.04	
<i>tetB</i>	4186705	4188081	-	1353.66	1460.52	0.93	930.25	978.08	0.95	
<i>yyaO</i>	4188430	4188669	+	367.52	361.27	1.02	269.75	186.19	1.45	
<i>yyaN</i>	4188820	4189236	+	34.6	38.46	0.90	38.9	45.59	0.85	
<i>yyaM</i>	4189233	4190150	+	49.19	44.58	1.10	57.03	52.82	1.08	
<i>yyaL</i>	4190222	4192291	+	614.7	480.94	1.28	522.31	455.38	1.15	
<i>yyaK</i>	4192288	4193187	-	737.58	599.98	1.23	810.18	727.19	1.11	
<i>yyaJ</i>	4193413	4194768	+	101.39	95.61	1.06	92.75	99.47	0.93	
<i>maa</i>	4194802	4195356	-	225.1	218.96	1.03	227.71	235.91	0.97	
<i>yyaH</i>	4195374	4195754	-	202.65	237.56	0.85	266.49	282.36	0.94	
<i>ccpB</i>	4195810	4196745	-	132.42	126.08	1.05	120.3	114.1	1.05	
<i>exoA</i>	4196804	4197562	-	114.48	114.9	1.00	153.48	155.38	0.99	
<i>rpsR</i>	4197627	4197866	-	901.42	1117.87	0.81	1541.14	1415.7	1.09	
<i>ssb</i>	4197910	4198428	-	6594.91	7206.48	0.92	6355.09	6093.51	1.04	
<i>rpsF</i>	4198469	4198756	-	7759.43	8461.6	0.92	7059.59	6696.42	1.05	
<i>yyaF</i>	4198867	4199967	-	1091.89	1215.65	0.90	1593.17	2104.93	0.76	
<i>yyaE</i>	4200094	4202097	-	234.46	209.34	1.12	300.94	300.11	1.00	
<i>yyaD</i>	4202448	4203464	-	52.25	56.98	0.92	54.59	64.37	0.85	
<i>yyaC</i>	4203924	4204541	+	61.89	63.36	0.98	52.91	69.45	0.76	
<i>spoJ</i>	4204580	4205428	-	1215.74	1052.91	1.15	1308.01	1157.93	1.13	
<i>soj</i>	4205421	4206182	-	1342.95	1173.43	1.14	1281.98	1222.86	1.05	Spo0A regulon
<i>yyaB</i>	4206430	4206870	+	174.78	190.96	0.92	182.1	176.2	1.03	
<i>yyaA</i>	4206921	4207772	-	1223.65	1194.79	1.02	1879.62	1637.89	1.15	
<i>gidB</i>	4207894	4208613	-	1002.15	768.77	1.30	1718.71	1504.19	1.14	
<i>gidA</i>	4208627	4210513	-	897.45	685.98	1.31	1467.73	1277.57	1.15	
<i>thdF</i>	4210534	4211913	-	554.66	441.75	1.26	717.95	703.76	1.02	
<i>jag</i>	4212224	4212850	-	1174.15	1122.57	1.05	1896.67	2478.43	0.77	
<i>spoIIIJ</i>	4212847	4213632	-	1148.39	1086.61	1.06	1471.78	1924.69	0.76	
<i>rnpA</i>	4213777	4214127	-	426.76	415.5	1.03	884.08	1340.18	0.66	

^a Spo0A, AbrB and SigD regulons shown here are described in Molle *et al.*, 2003, Chumsakul *et al.*, 2011 and Serizawa *et al.*, 2004, respectively.