

Supplementary Information

The bacterial MtrAB two-component system regulates the cell wall homeostasis responding to environmental alkaline stress

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Figure S1

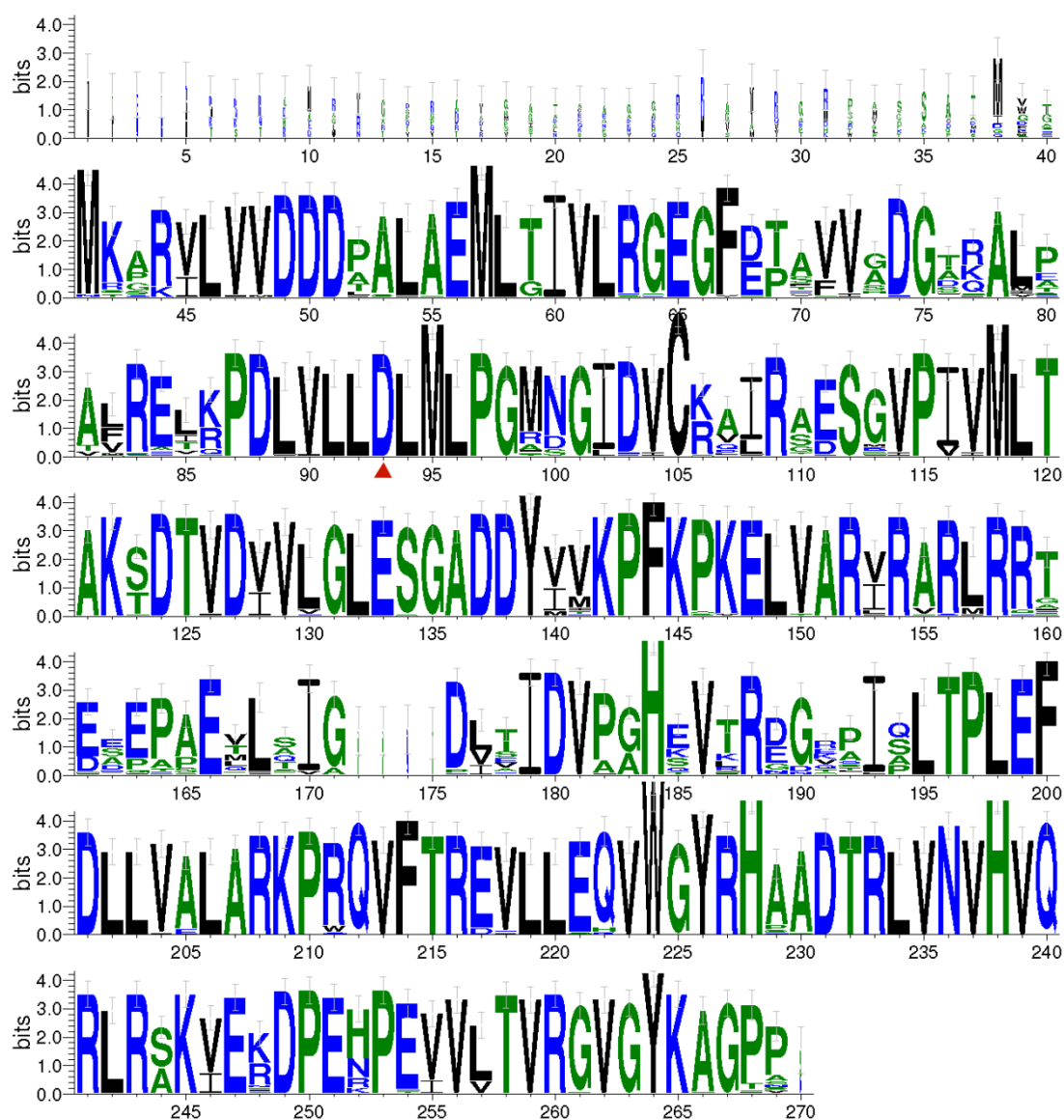
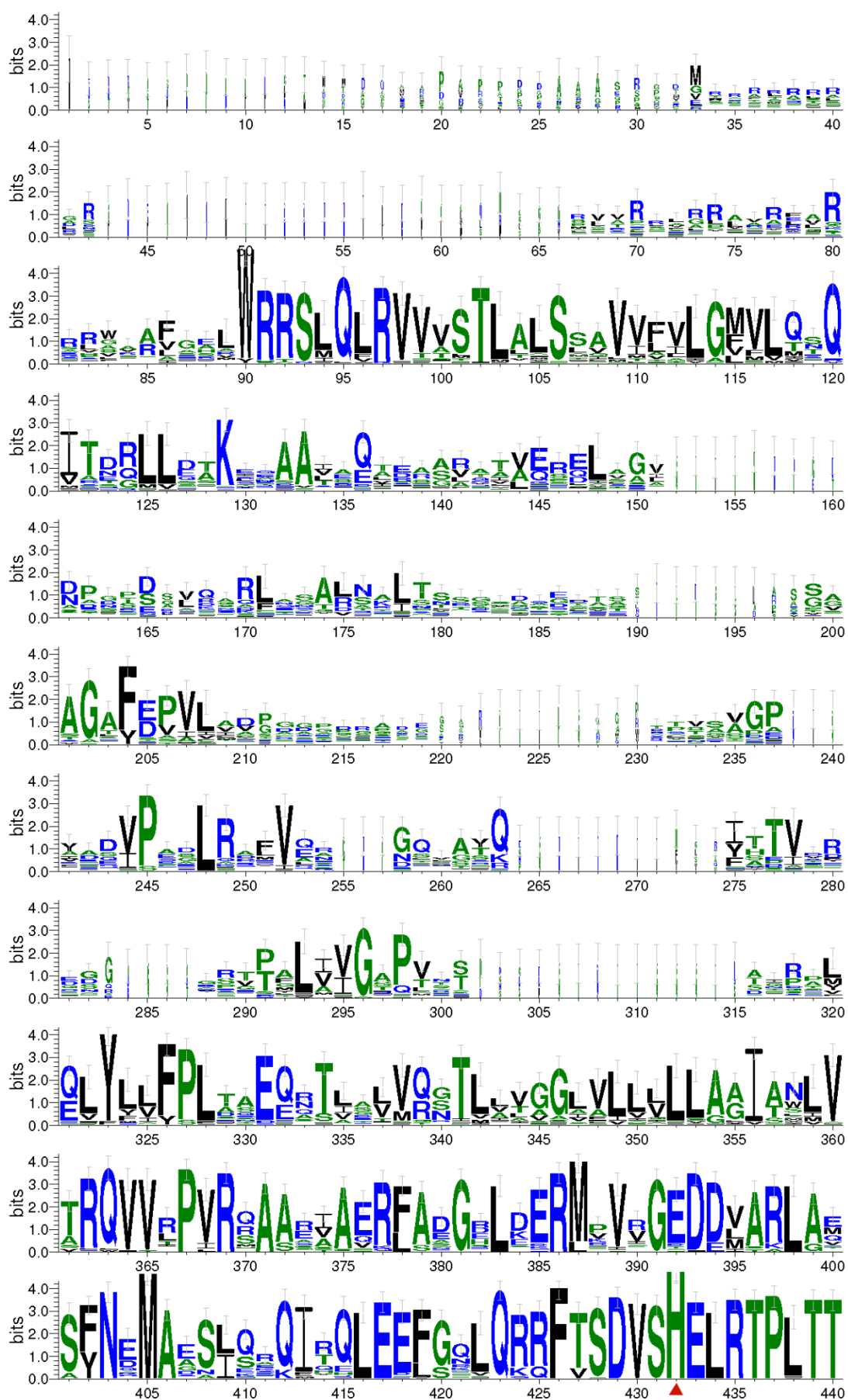
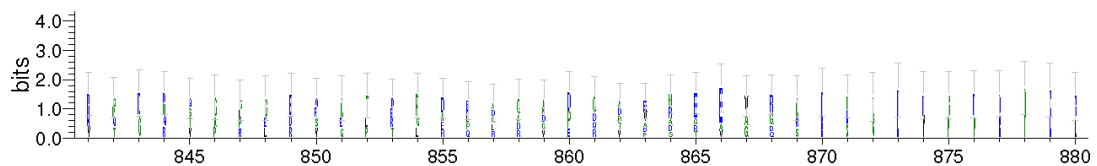
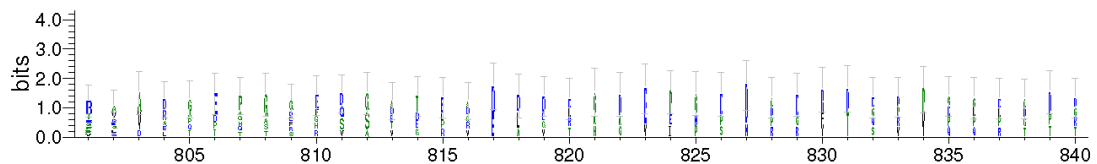
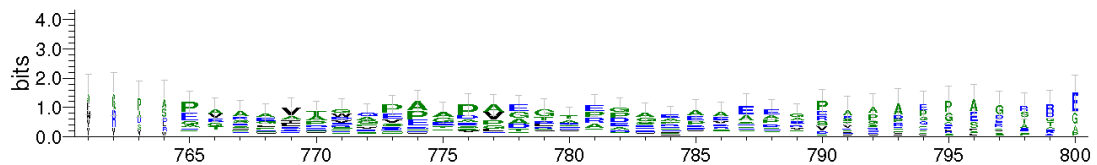
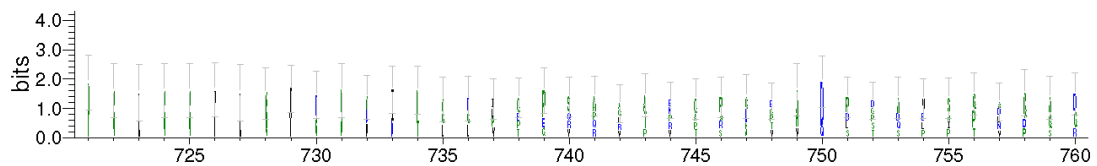
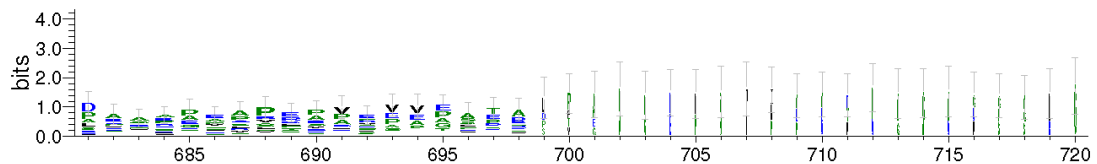
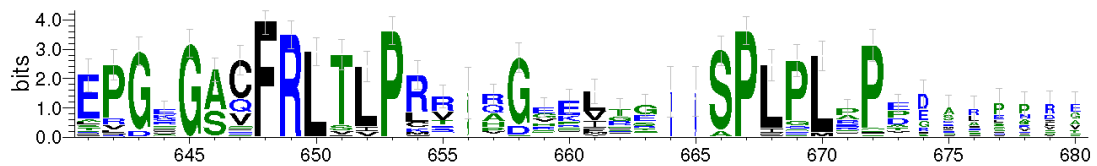
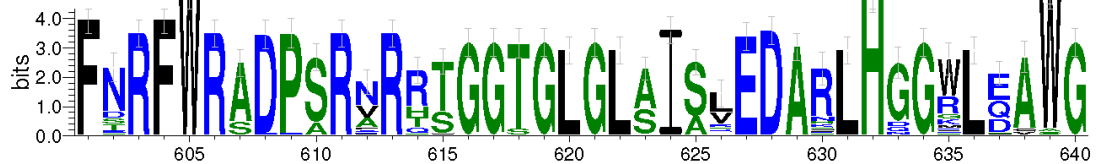
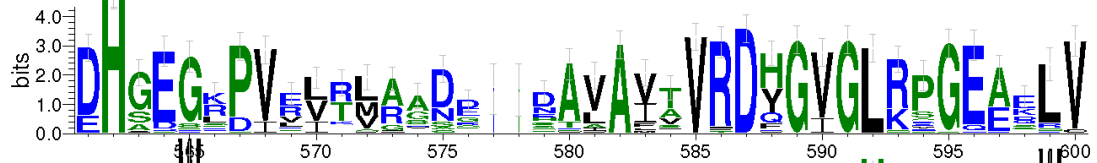
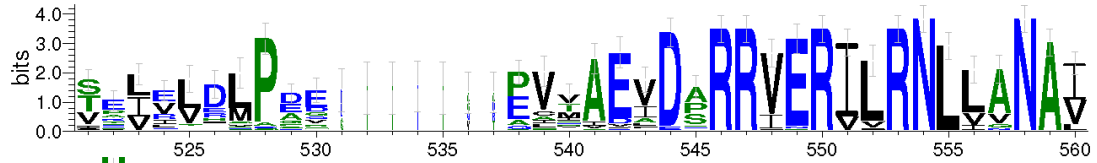
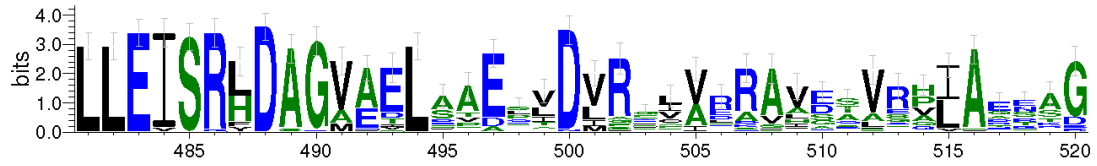
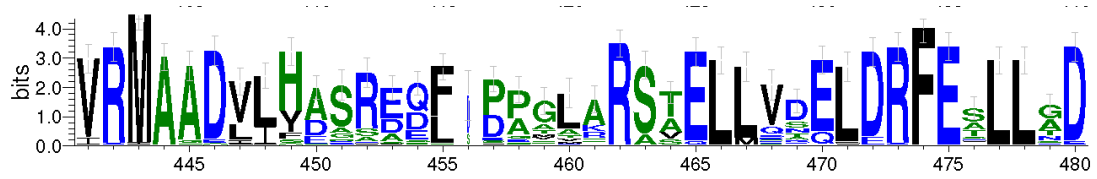


Fig S1. Comparison of the amino acid sequences of MtrA between *Dietzia* sp. DQ12-45-1b and other bacteria in Actinobacteria. The sequence logo was generated with WebLogo (<http://weblogo.threeplusone.com/create.cgi>). The red triangle represents the phosphorylation site.

Figure S2





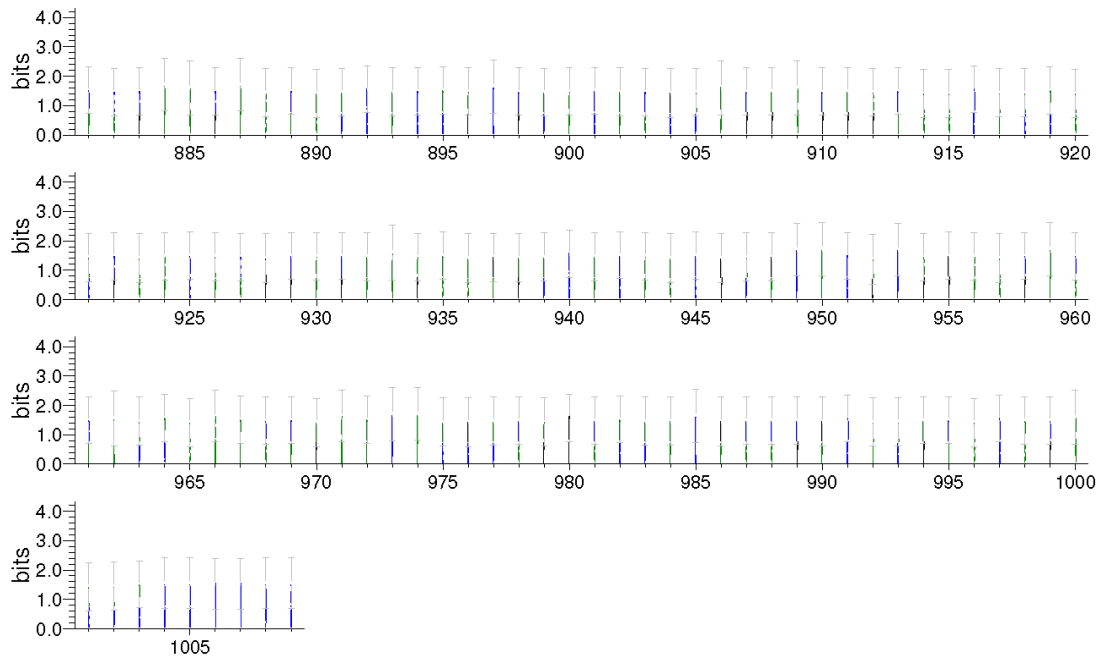


Fig S2. Comparison of the amino acid sequences of MtrB between *Dietzia* sp. DQ12-45-1b and other bacteria in Actinobacteria. The sequence logo was generated with WebLogo (<http://weblogo.threeplusone.com/create.cgi>). The red triangle represents the phosphorylation site.

Figure S3

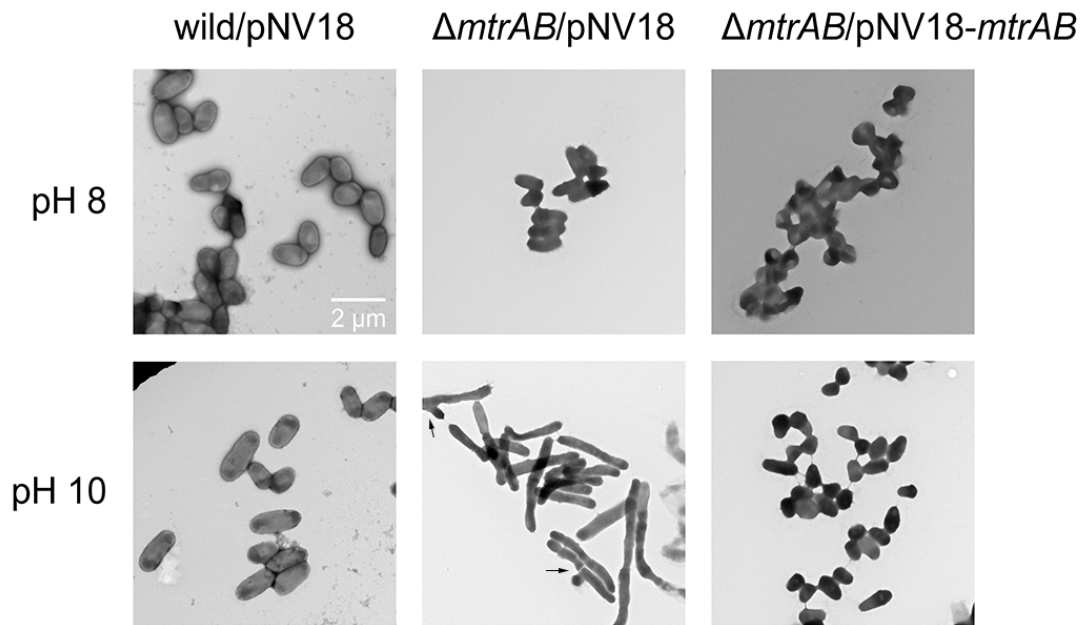


Fig S3. Cell morphology at different pH conditions. The representative micrographs of *Dietzia* sp. DQ12-45-1b wild/pNV18, $\Delta mtrAB/pNV18$, and $\Delta mtrAB/pNV18-mtrAB$ by transmission electron microscope. Bars show the length in microns. Note the branched phenotype (marked with arrows) present in $\Delta mtrAB/pNV18$ in pH 10.

Figure S4

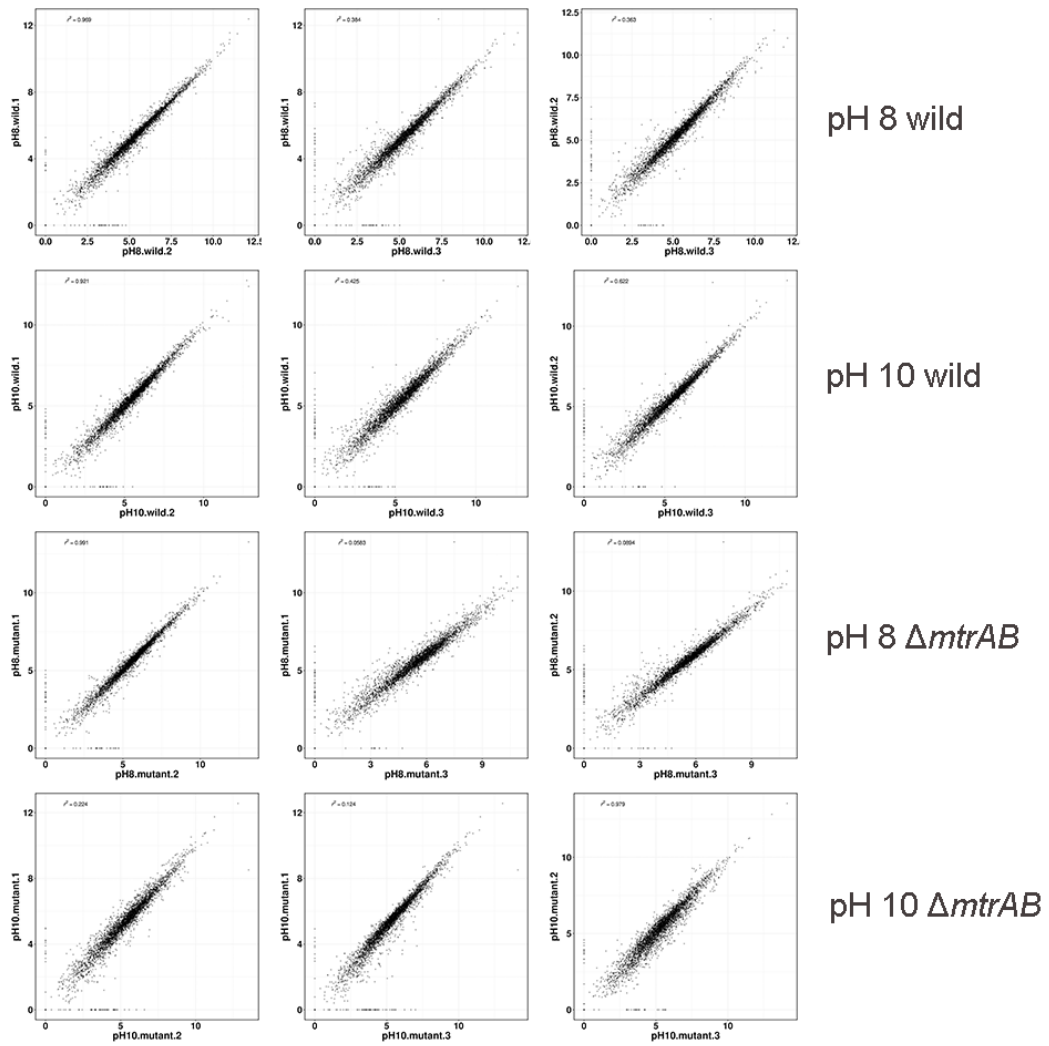
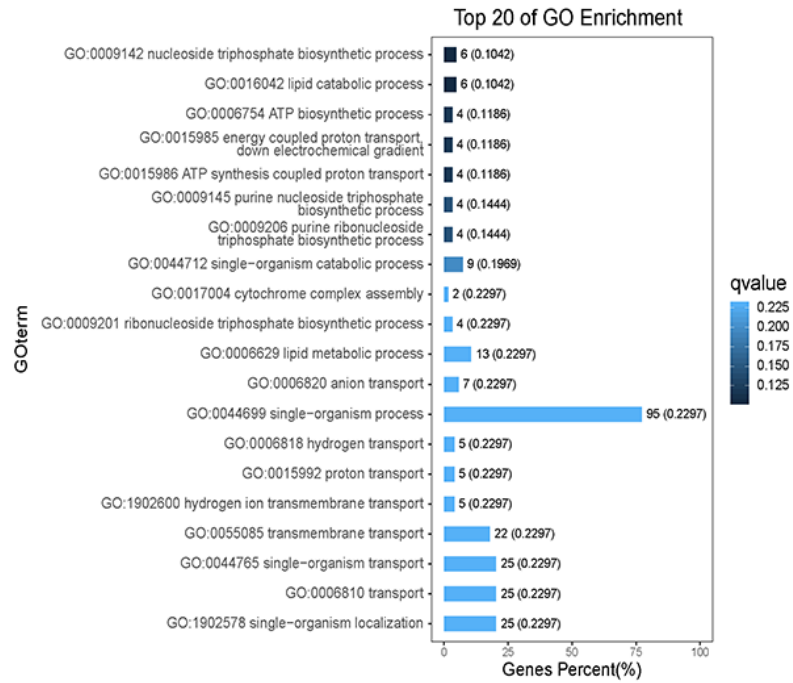


Fig S4. Scatter plots of consistency of transcriptomic data between parallel samples of *Dietzia* sp. DQ12-45-1b wild-type and $\Delta mtrAB$ mutant strains under the optimal and alkaline pH conditions.

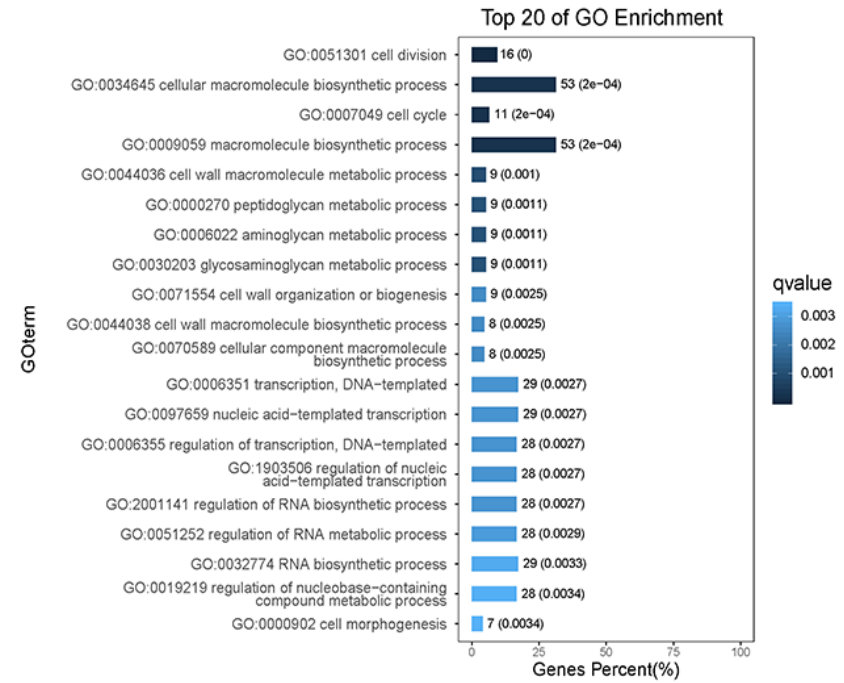
Figure S5

A pH 10 wild/pH 8 wild

Up-regulated genes

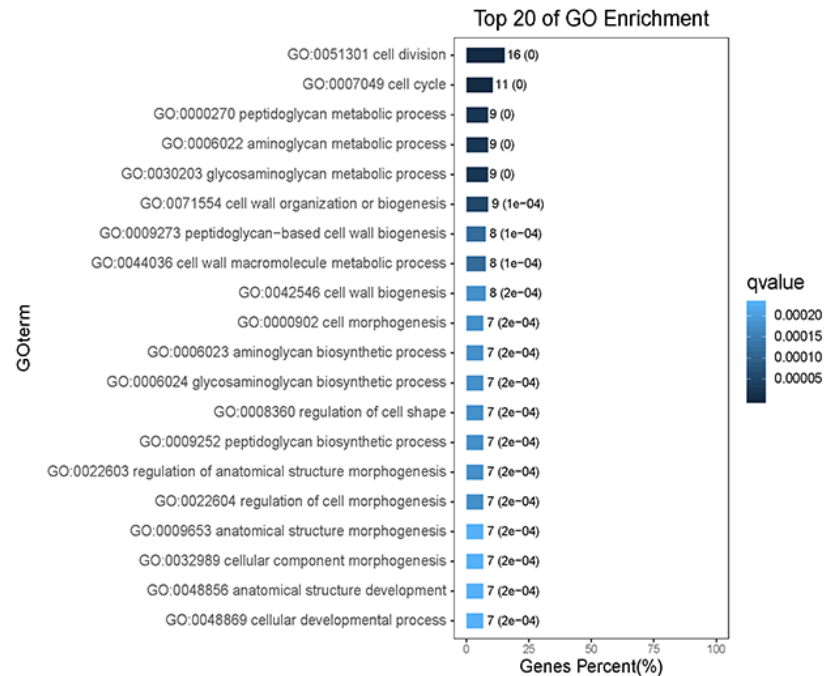


Down-regulated genes



B pH 10 $\Delta mtrAB$ /pH 10 wild

Up-regulated genes



Down-regulated genes

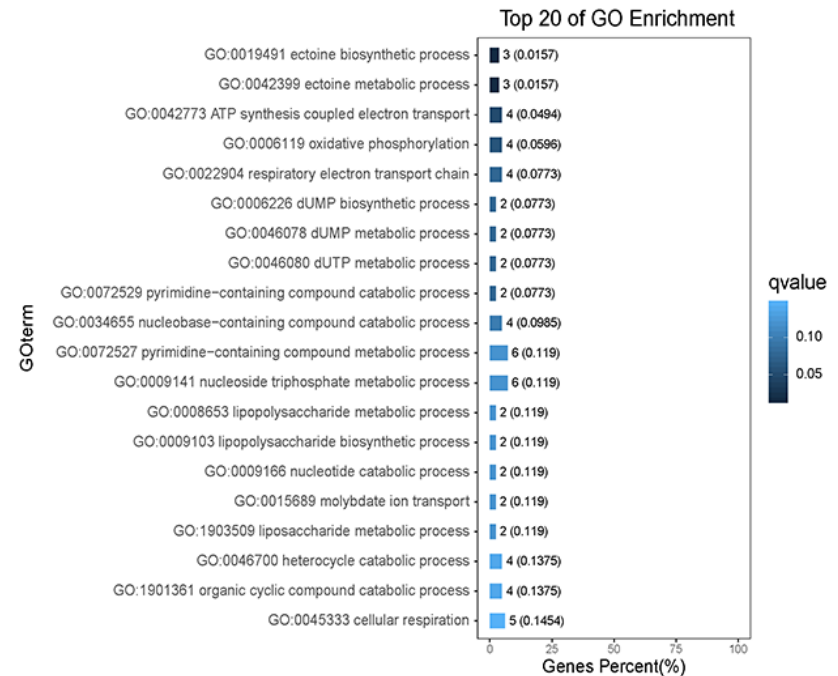
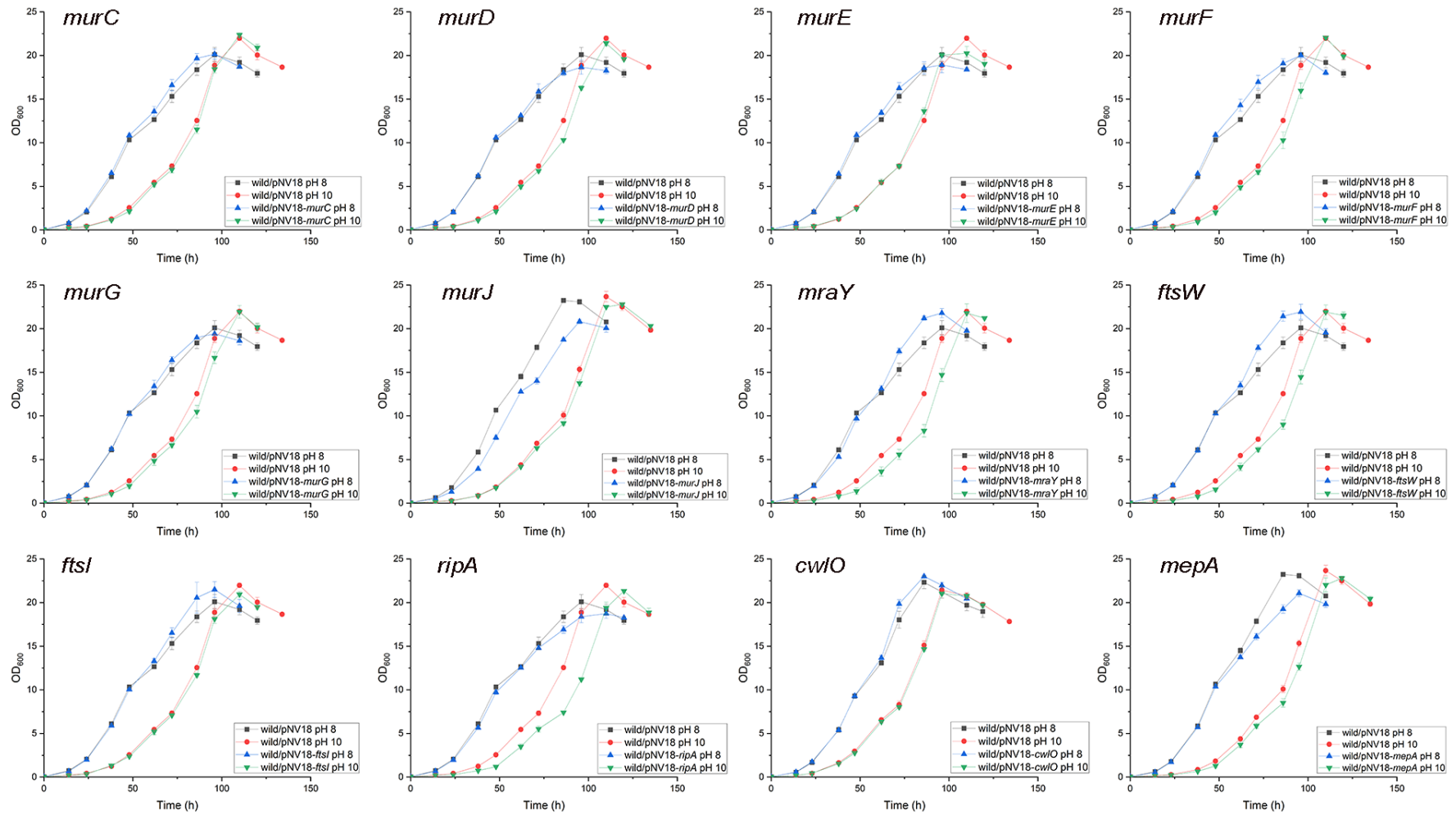


Fig S5. Gene Ontology (GO) classification and enrichment analysis. (A) Barplots of GO enriched from up-regulated genes and down-regulated genes of wild-type strain at pH 10 compared to pH 8 in Biological Process (BP) categories. (B) Barplots of GO enriched from up-regulated genes and down-regulated genes of $\Delta mtrAB$ mutant compared to wild-type strains at pH 10 in BP categories.

Figure S6



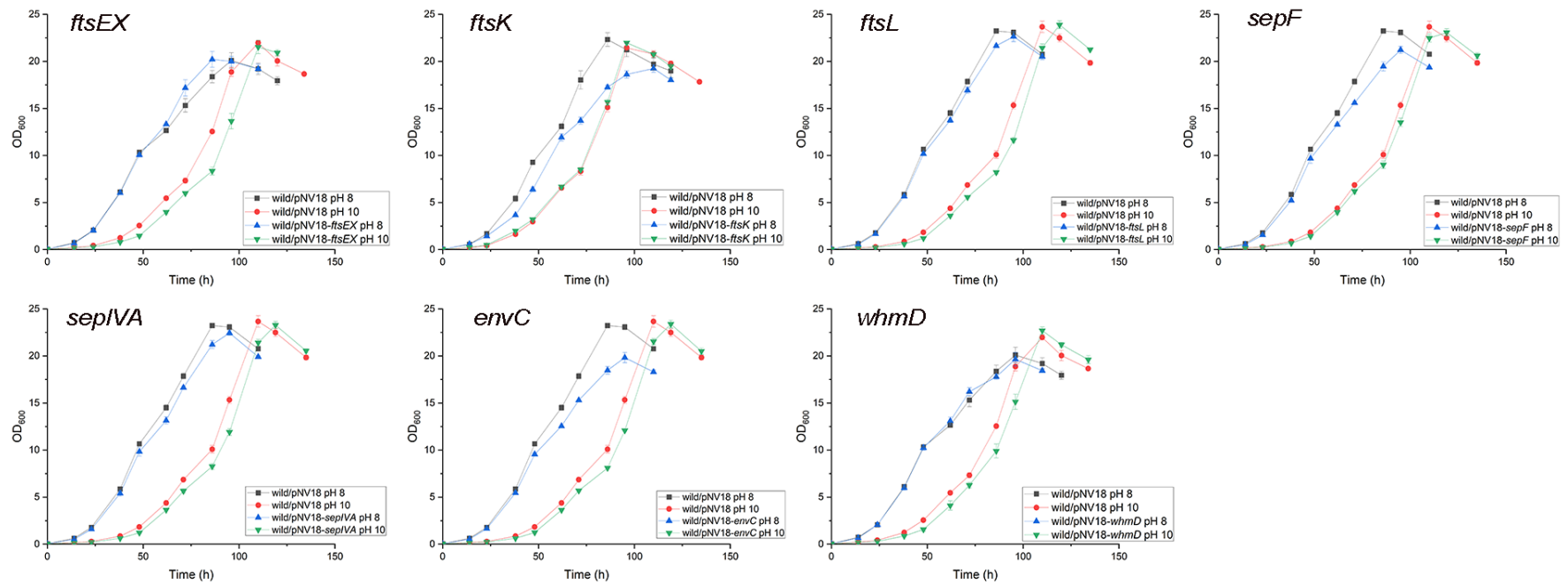


Fig S6. Growth curves of *Dietzia* sp. DQ12-45-1b wild-type strains overexpressing the genes involved in peptidoglycan homeostasis and cell division at different pH conditions. Black square and red circle represent wild-type strain carrying pNV18 at pH 8 and pH 10 respectively. Blue triangle and green inverted triangle mean wild/pNV18 with different genes at pH 8 and pH 10 respectively.

Figure S7

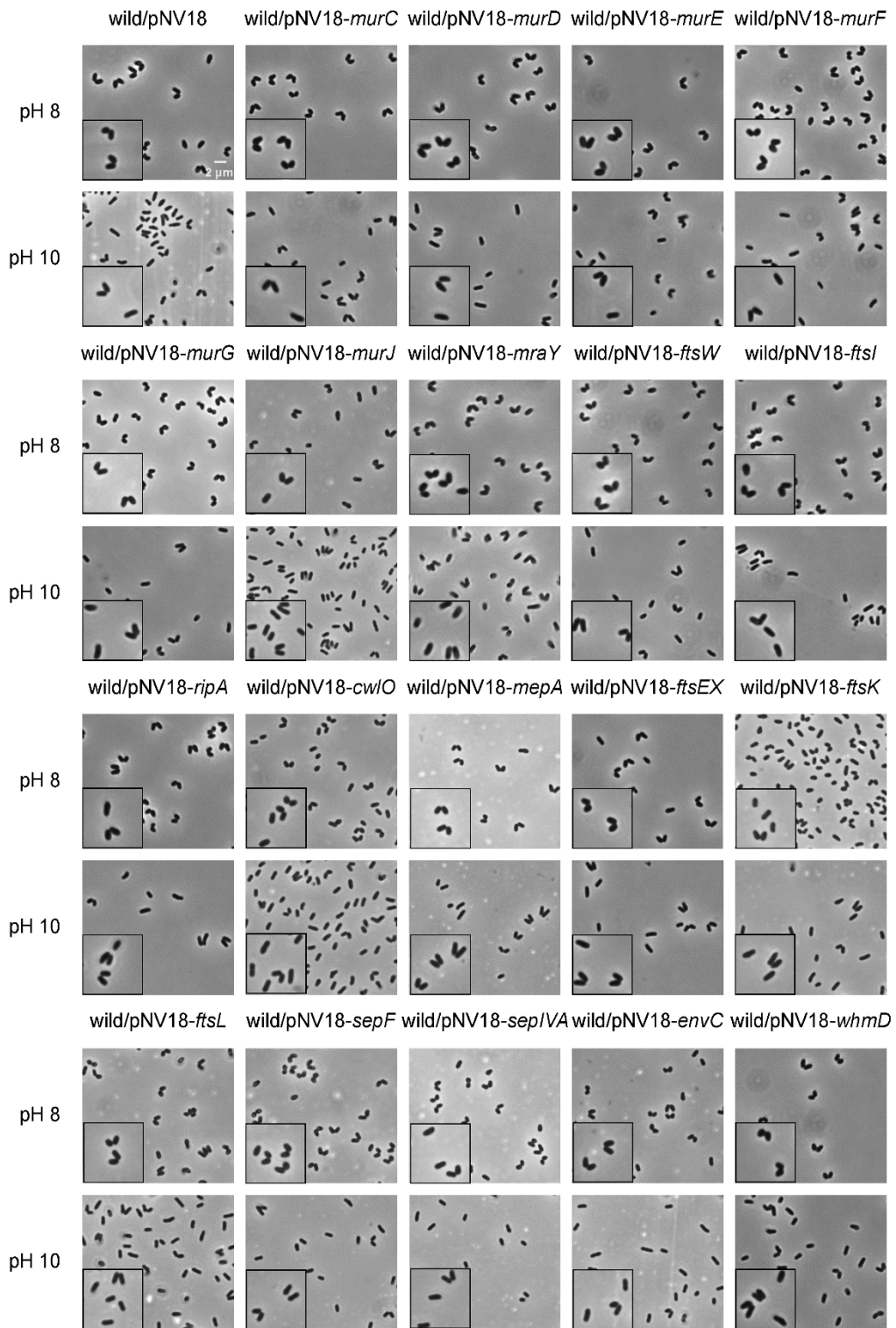


Fig S7. The representative micrographs of *Dietzia* sp. DQ12-45-1b wild-type strains overexpressing the genes involved in peptidoglycan homeostasis and cell division at different pH conditions.

Figure S8

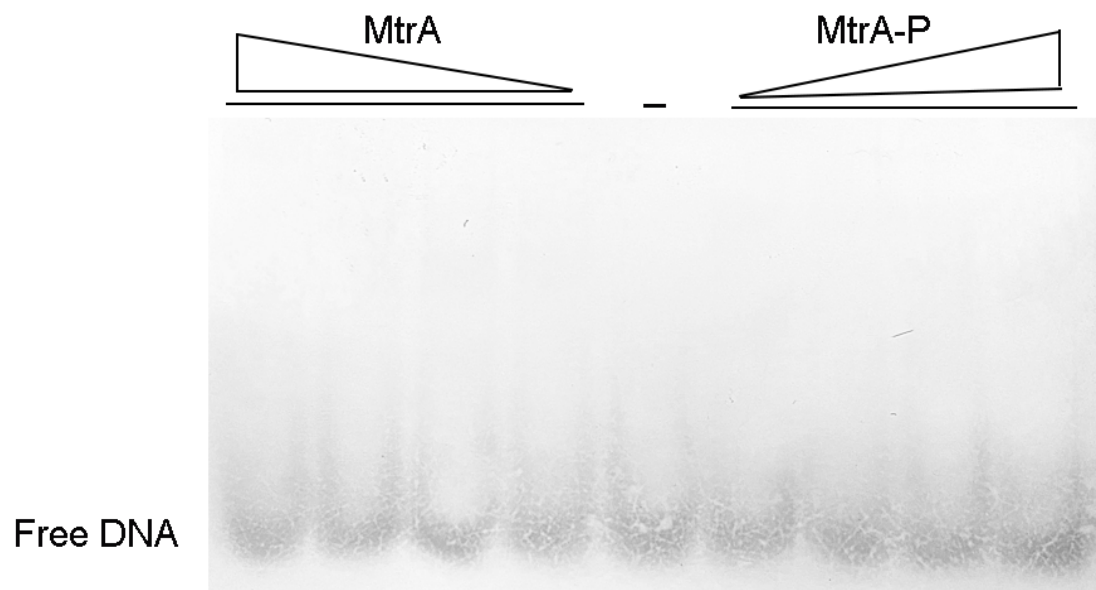


Fig S8. EMSA analysis of MtrA, MtrA-P binding to non-specific DNA (*Escherichia coli* DNA fragment) used as a negative control. MtrA, and MtrA~P at 0.5, 1, 2.5, and 5 μM concentration were incubated for 30 min with 0.1 μM of DIG-labeled DNA.

Table S1

Table S1 List of selected up- and down-regulated genes

Gene ID	Gene name	pH10 wild/pH8 wild		pH10 $\Delta mtrAB$ /pH10 wild		pH8 $\Delta mtrAB$ /pH8 wild		Gene product description
		Log ₂ FC	FDR	Log ₂ FC	FDR	Log ₂ FC	FDR	
Peptidoglycan synthesis								
GJR88_02065	<i>murE</i>	-1.45	0.000	2.44	0.000	0.21	0.326	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
GJR88_02066	<i>murF</i>	-1.55	0.000	2.93	0.000	0.45	0.021	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase
GJR88_02068	<i>mraY</i>	-1.34	0.000	2.85	0.000	0.52	0.003	phospho-N-acetylmuramoyl-pentapeptide-transferase
GJR88_02071	<i>murD</i>	-2.27	0.000	2.91	0.000	-0.46	0.028	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
GJR88_02073	<i>ftsW</i>	-2.70	0.000	2.64	0.000	-0.82	0.000	Cell division protein
GJR88_05430	<i>murJ</i>	-1.06	0.000	1.43	0.000	-0.10	0.676	Lipid II flippase
GJR88_02075	<i>murG</i>	-1.55	0.000	2.60	0.000	0.44	0.083	UDP-N-acetylglucosamine--N-acetylmuramyl-pyrophosphoryl-undecaprenol N-acetylglucosamine
GJR88_02077	<i>murC</i>	-1.53	0.000	2.65	0.000	0.56	0.003	UDP-N-acetylmuramate--L-alanine ligase

GJR88 _02062	<i>ftsI</i> (<i>pbpB</i>)	-1.58	0.000	2.61	0.000	-0.09	0.723	Penicillin-binding protein
Peptidoglycan hydrolysis								
GJR88 _02580	<i>ripA</i>	-2.39	0.000	1.85	0.000	1.63	0.000	Peptidoglycan endopeptidase
GJR88 _04713	NA	-2.59	0.000	3.89	0.000	1.06	0.000	1,4-beta-N-acetylmuramidase
GJR88 _02028	<i>cwlO</i>	-1.55	0.000	2.28	0.000	2.41	0.000	Peptidoglycan endopeptidase
GJR88 _00456	NA	-2.13	0.000	3.54	0.000	0.70	0.001	N-acetylmuramoyl-L-alanine amidase
GJR88 _03658	<i>mepA</i>	-0.41	0.125	1.84	0.000	2.09	0.000	Murein DD-endopeptidase
GJR88 _RS174 45	NA	-1.23	0.000	0.82	0.000	0.40	0.059	M23 peptidase domain-containing protein
GJR88 _03129	NA	-1.31	0.000	0.79	0.009	0.93	0.001	Membrane-bound lytic murein transglycosylase
Cell division								
GJR88 _02816	<i>ftsK</i>	-2.44	0.000	3.47	0.000	-0.43	0.032	Cell division protein
GJR88 _01576	<i>ftsE</i>	-1.55	0.000	1.24	0.000	-0.13	0.604	Cell division ATP-binding protein
GJR88 _01577	<i>ftsX</i>	-2.16	0.000	3.45	0.000	0.49	0.054	Cell division protein
GJR88	<i>ftsL</i>	-2.91	0.000	3.98	0.000	-0.32	0.137	Cell division protein

GJR88 _00770	<i>mrpE</i>	-1.33	0.000	0.81	0.012	-1.10	0.000	Putative monovalent cation/H ⁺ antiporter subunit E
GJR88 _00771	<i>mrpD</i>	-1.19	0.000	0.30	0.184	-1.07	0.000	Putative monovalent cation/H ⁺ antiporter subunit D
GJR88 _00774	<i>mrpC</i>	-1.31	0.000	0.04	0.947	-1.34	0.000	Putative monovalent cation/H ⁺ antiporter subunit C
GJR88 _00777	<i>mrpA</i>	0.42	0.039	-0.71	0.000	-0.16	0.456	Putative monovalent cation/H ⁺ antiporter subunit A
GJR88 _04437	<i>mrpA</i>	0.80	0.000	-0.35	0.140	0.28	0.200	Putative monovalent cation/H ⁺ antiporter subunit A
GJR88 _04438	<i>mrpC</i>	-0.59	0.064	0.41	0.277	-0.84	0.005	Putative monovalent cation/H ⁺ antiporter subunit C
GJR88 _04440	<i>mrpD</i>	-0.54	0.023	0.67	0.006	-0.77	0.001	Putative monovalent cation/H ⁺ antiporter subunit D
GJR88 _04442	<i>mrpE</i>	-0.45	0.100	0.44	0.142	-1.14	0.000	Putative monovalent cation/H ⁺ antiporter subunit E
GJR88 _04443	<i>mrpF</i>	-1.31	0.001	0.31	0.571	-1.97	0.000	Putative monovalent cation/H ⁺ antiporter subunit F
GJR88 _04444	<i>mrpG</i>	-0.01	0.990	0.00	1.000	-0.69	0.005	Putative monovalent cation/H ⁺ antiporter subunit G

Table S2

Table S2 Strains and plasmids used in the study.

Strain or plasmid	Genotype and description	Source and reference
<i>Dietzia</i> strains		
<i>Dietzia</i> sp. DQ12-45-1b (CGMCC 1.10709)	Wild-type	(1)
DQ12-45-1b/pNV18	Wild-type harboring pNV18; Km ^r	This study
DQ12-45-1bΔ <i>mtrAB</i>	DQ12-45-1b <i>mtrAB</i> deletion mutant; Sm ^r	This study
DQ12-45-1bΔ <i>mtrAB</i> /pNV18	DQ12-45-1b <i>mtrAB</i> deletion mutant harboring pNV18; Km ^r and Sm ^r	This study
DQ12-45-1bΔ <i>mtrAB</i> /pNV18- <i>mtrAB</i>	DQ12-45-1bΔ <i>mtrAB</i> harboring pNV18- <i>mtrAB</i> ; Km ^r and Sm ^r	This study
DQ12-45-1bΔ <i>mtrAB</i> /pNV18- <i>mtrA</i>	DQ12-45-1bΔ <i>mtrAB</i> harboring pNV18- <i>mtrA</i> ; Km ^r and Sm ^r	This study
DQ12-45-1bΔ <i>mtrAB</i> /pNV18- <i>mtrAD56E</i>	DQ12-45-1bΔ <i>mtrAB</i> harboring pNV18- <i>mtrAD56E</i> ; Km ^r and Sm ^r	This study
DQ12-45-1bΔ <i>mtrAB</i> /pNV18- <i>mtrAD56N</i>	DQ12-45-1bΔ <i>mtrAB</i> harboring pNV18- <i>mtrAD56N</i> ; Km ^r and Sm ^r	This study
DQ12-45-1b/pJV	Wild-type harboring pJV; Km ^r	This study
DQ12-45-1b/pJV- <i>mraZ</i>	Wild-type harboring pJV- <i>mraZ</i> ; Km ^r	This study

DQ12-45-1b Δ <i>mtrAB</i> /pJV	DQ12-45-1b Δ <i>mtrAB</i> harboring pJV; Km ^r and Sm ^r	This study
DQ12-45-1b Δ <i>mtrAB</i> /pJV- <i>mraZ</i> -AS	DQ12-45-1b Δ <i>mtrAB</i> harboring pJV- <i>mraZ</i> -AS; Km ^r and Sm ^r	This study
DQ12-45-1b/pNV18- <i>murC</i>	Wild-type harboring pNV18- <i>murC</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>murD</i>	Wild-type harboring pNV18- <i>murD</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>murE</i>	Wild-type harboring pNV18- <i>murE</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>murF</i>	Wild-type harboring pNV18- <i>murF</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>murG</i>	Wild-type harboring pNV18- <i>murG</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>murJ</i>	Wild-type harboring pNV18- <i>murJ</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>mraY</i>	Wild-type harboring pNV18- <i>mraY</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>ftsW</i>	Wild-type harboring pNV18- <i>ftsW</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>ftsI</i>	Wild-type harboring pNV18- <i>ftsI</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>ripA</i>	Wild-type harboring pNV18- <i>ripA</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>cwlO</i>	Wild-type harboring pNV18- <i>cwlO</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>mepA</i>	Wild-type harboring pNV18- <i>mepA</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>ftsEX</i>	Wild-type harboring pNV18- <i>ftsEX</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>ftsK</i>	Wild-type harboring pNV18- <i>ftsK</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>ftsL</i>	Wild-type harboring pNV18- <i>ftsL</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>sepF</i>	Wild-type harboring pNV18- <i>sepF</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>sepIVA</i>	Wild-type harboring pNV18- <i>sepIVA</i> ; Km ^r	This study

DQ12-45-1b/pNV18- <i>envC</i>	Wild-type harboring pNV18- <i>envC</i> ; Km ^r	This study
DQ12-45-1b/pNV18- <i>whmD</i>	Wild-type harboring pNV18- <i>whmD</i> ; Km ^r	This study
<i>Escherichia coli</i> strains		
BL21 (DE3)/pET-28a- <i>envZdel</i>	BL21 (DE3) harboring pET-28a- <i>envZdel</i> ; Km ^r	This study
BL21 (DE3)/pET-28a- <i>mtrA</i>	BL21 (DE3) harboring pET-28a- <i>mtrA</i> ; Km ^r	This study
BL21 (DE3)/pET-28a- <i>mtrAD56E</i>	BL21 (DE3) harboring pET-28a- <i>mtrAD56E</i> ; Km ^r	This study
BL21 (DE3)/pET-28a- <i>mtrAD56N</i>	BL21 (DE3) harboring pET-28a- <i>mtrAD56N</i> ; Km ^r	This study
Plasmids		
pNV18-DsRed.T4	<i>Dietzia-E.coli</i> shuttle vector (p45 promoter); Km ^r	(2)
pNV18	Cloned from pNV18-DsRed.T4 without DsRed; Km ^r	This study
pNV18- <i>mtrAB</i>	pNV18 + <i>mtrA</i> and <i>mtrB</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>mtrA</i>	pNV18 + <i>mtrA</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>mtrAD56E</i>	pNV18 + <i>mtrA</i> (phosphorylation-mimic) from DQ12-45-1b; Km ^r	This study
pNV18- <i>mtrAD56N</i>	pNV18 + <i>mtrA</i> (phosphorylation-defective) from DQ12-45-1b; Km ^r	This study
pJV53	<i>Dietzia-E.coli</i> shuttle vector (acetamide-inducible promoter); Km ^r	(3)
pJV	Cloned from pJV53 without Che9cp60 and Che9cp61; Km ^r	This study

pJV- <i>mraZ</i>	pJV + <i>mraZ</i> from DQ12-45-1b; Km ^r	This study
pJV- <i>mraZ</i> -AS	pJV + <i>mraZ</i> in antisense orientation from DQ12-45-1b; Km ^r	This study
pNV18- <i>murC</i>	pNV18 + <i>murC</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>murD</i>	pNV18 + <i>murD</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>murE</i>	pNV18 + <i>murE</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>murF</i>	pNV18 + <i>murF</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>murG</i>	pNV18 + <i>murG</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>murJ</i>	pNV18 + <i>murJ</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>mraY</i>	pNV18 + <i>mraY</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>ftsW</i>	pNV18 + <i>ftsW</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>ftsI</i>	pNV18 + <i>ftsI</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>ripA</i>	pNV18 + <i>ripA</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>cwlO</i>	pNV18 + <i>cwlO</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>mepA</i>	pNV18 + <i>mepA</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>ftsEX</i>	pNV18 + <i>ftsEX</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>ftsK</i>	pNV18 + <i>ftsK</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>ftsL</i>	pNV18 + <i>ftsL</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>sepF</i>	pNV18 + <i>sepF</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>sepIVA</i>	pNV18 + <i>sepIVA</i> from DQ12-45-1b; Km ^r	This study

pNV18- <i>envC</i>	pNV18 + <i>envC</i> from DQ12-45-1b; Km ^r	This study
pNV18- <i>whmD</i>	pNV18 + <i>whmD</i> from DQ12-45-1b; Km ^r	This study
pET-28a	Overexpression vector; Km ^r	Novagen
pET-28a- <i>envZ_{del}</i>	pET-28a + truncated <i>envZ</i> from <i>E.coli</i> ; Km ^r	This study
pET-28a- <i>mtrA</i>	pET-28a + <i>mtrA</i> from DQ12-45-1b; Km ^r	This study
pET-28a- <i>mtrA_{D56E}</i>	pET-28a + <i>mtrA_{D56E}</i> from pNV18- <i>mtrA_{D56E}</i> ; Km ^r	This study
pET-28a- <i>mtrA_{D56N}</i>	pET-28a + <i>mtrA_{D56N}</i> from pNV18- <i>mtrA_{D56N}</i> ; Km ^r	This study

Table S3

Table S3 Primers used in the study.

Primer	Sequence (5' → 3')	Application
mtrABLF	TGCTGTTCGCCCTGGACC	<i>ΔmtrAB</i> mutant strain
mtrABLR	CCTTCATCCGTTTCCACGGTTCGTCGTCGACGACGAGGA	
mtrABRF	AAGCGTGCATAATAAGCCCTCTCGACCACTCGGAGTCCAA	
mtrABRR	ACCGGACGGAGAGAAGGTGT	
SmF	ACCGTGGAAACGGATGAAGG	
SmR	AGGGCTTATTATGCACGCTT	
fusionF	GTCCTGCTCGACCGCTACGT	
fusionR	CAGCACGGTGGCGCAGATCG	
mtrAF	CCCAAGCTTCGACATACACGCCGACACAA	Complementary plasmids
mtrAR	CCCAAGCTTTCACGAGACCGGACCGGCCT	
mtrABR	CCCAAGCTTTCACGAACGGACCTCCTCGG	
pNVF	CCCAAGCTTGGCACTGGCCGTCG	
pNVR	CCCAAGCTTGTGCCCGCTGAACTTCTTC	
mraZF	TACGAGATCGGCGGCCGCATCTGATCCCAGGAGGTGGCGG	<i>mraZ</i> overexpression plasmid
mraZR	GTCGGAATTCGCCGGGGCGCTTAGAATTCGATCCCCAGGG	

pJVF	GCGCCCCGGCGAATTCCGACG	All acetamide-inducible plasmids
pJVR	ATGCGGCCCGCGATCTCGTAA	
mraZASF	TACGAGATCGGCGGCCGCATCCCCAGGGATGTGCCCTCCA	<i>mraZ</i> antisense expression vector
mraZASR	GTCGGAATTCGCCGGGGCGCGACCCCAACGACTCCGAGCG	
pNVF2	AAGCTTGTGCCCGCTGAACT	Overexpression plasmids carrying the genes involved in peptidoglycan homeostasis and cell division
pNVR2	GGCACTGGCCGTCGTTTTAC	
murcF	AGTTCAGCGGGCACAAGCTTGCCGCCGAAAGGCACGGCG	
murcR	GTAAAACGACGGCCAGTGCCTCATGACCCCGTCCCGCTCCC	
murdF	TTCAGCGGGCACAAGCTTCGAGCACATCGGGGTGACGGAC	
murdR	GTAAAACGACGGCCAGTGCCTCACCTCCCGGCGACCCGGCC	
mureF	AGTTCAGCGGGCACAAGCTTACGGAGAACGAGAGGCGGGT	
mureR	GTAAAACGACGGCCAGTGCCTCATGAGGTGTTGTCCTCCGT	
murfF	AGTTCAGCGGGCACAAGCTTCGGACGGAGGACAACACCTC	
murfR	GTAAAACGACGGCCAGTGCCTCATTCCGGACATCTCCTCACC	
murgF	AGTTCAGCGGGCACAAGCTTATCCACCGGGGACGGGAGCG	
murgR	GTAAAACGACGGCCAGTGCCTCAACGCCGTGCCTTTCCGGC	
murjF	AGTTCAGCGGGCACAAGCTTCGTGTCGAGGAGGTCTACGG	
murjR	GTAAAACGACGGCCAGTGCCTCACCGGGTGAGTTGTACCTC	
mrayF	AGTTCAGCGGGCACAAGCTTCGTGGTGAGGAGATGTCCGA	

mrayR	GTAAAACGACGGCCAGTGCCTCACCCCGATGTGCTCGCGAG
ftswF	AGTTCAGCGGGCACAAGCTTGGGTCGCCGGGAGGTAGGGC
ftswR	GTAAAACGACGGCCAGTGCCTCATCGCTCCCGTCCCCGGTG
ftsiF	AGTTCAGCGGGCACAAGCTTGACCTGCGAAAGGCCCTCG
ftsiR	GTAAAACGACGGCCAGTGCCTCACTGCGCCTGCAGGATCAG
ripaF	AGTTCAGCGGGCACAAGCTTCGGTTATCGGAAGGTGAAAC
ripaR	GTAAAACGACGGCCAGTGCCTCAGGTCAGCCGGACGACCAT
cwloF	AGTTCAGCGGGCACAAGCTTCCAGGAAGAAAGAGGAAATC
cwloR	GTAAAACGACGGCCAGTGCCTCAGTAGTAGCGGGTCGCACC
mepaF	AGTTCAGCGGGCACAAGCTTGCCGTTCTGGCCGTCGCCGC
mepaR	GTAAAACGACGGCCAGTGCCTCAGCTGCCGAAGGGGATGGA
ftsexF	AGTTCAGCGGGCACAAGCTTTTCGTGTGATCAGTGCTTCCC
ftsexR	GTAAAACGACGGCCAGTGCCTCACTGCCGAACCGTCACCCT
ftskF	AGTTCAGCGGGCACAAGCTTTCTGCGGGGTGGATGGGCGG
ftskR	GTAAAACGACGGCCAGTGCCTCAGCCCACCGGCGCCTCGTC
ftslF	AGTTCAGCGGGCACAAGCTTTCGTATCGACGGGAGAACCCC
ftslR	GTAAAACGACGGCCAGTGCCTCAGTAGAGCGGGCCGGGGAC
sepfF	AGTTCAGCGGGCACAAGCTTATCAGGAAGGTCCCCGGAAG
sepfR	GTAAAACGACGGCCAGTGCCTCAGCGACGGAACGCGCCGTT

sepivaF	AGTTCAGCGGGCACAAGCTTTGAAGGGACGAGTGTGTACC	
sepivaR	GTAAAACGACGGCCAGTGCCTCAGTAGTCCCCGTACCCGTC	
envcF	AGTTCAGCGGGCACAAGCTTACCGAACTCCGAGGTTTCCC	
envcR	GTAAAACGACGGCCAGTGCCTCAGACGGCGACACCCTGCGC	
whmdF	AGTTCAGCGGGCACAAGCTTCGTAACACGAGGGGATGACC	
whmdR	GTAAAACGACGGCCAGTGCCTCACATCACGGCGTCACGCTT	
mtrAD56NF	CCTGCTGAACCTCATGCTCC	MtrA phosphorylation-defective and - mimic vectors
mtrAD56EF	CCTGCTGGAGCTCATGCTCC	
mtrAD56NR	CGAGACCGGACCGGCCTTGTAC	
pNVD56NF	GTACAAGGCCGGTCCGGTCTCG	
pNVD56NR	GGAGCATGAGGTTTCAGCAGG	
pNVD56ER	GGAGCATGAGCTCCAGCAGG	
envZF	AAATGGGTGCGGGATCCGAATTCTTAAGCCATCAGATGGCGCA	EnvZ _{del} expression vector
envZR	GCTCGAGTGCGGCCGCAAGCTTTTACCCTTCTTTTGTCGTGCCC	
pETF	AAGCTTGCGGCCGCACTCGAGCA	
pETR	GAATTCGGATCCGCGACCCATTGTC	
mtrAF	GGGAATTC CATATGG TGACAATGACCCCGAAGAT	MtrA expression vector
mtrAR	CCCA AGCTT TACGAGACCGGACCGGCCT	
pETF2	CCCA AGCTT GCGGCCGCACTCGAGCACCACC	
pETR2	GGGAATTC CATATGG GCTGCCGCGCGGCACCAGGC	

mraZDIGF	AGGTGGGGAGAAGTGGGGCG (5'-Digoxigenin)	EMSA
mraZDIGR	CCGCCACCTCCTGGGATCAG	

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