TABLE S1. Strains and plasmids used in this study

Strains and Plasmids	Relevant characteristic(s)[a]	Reference or source
Sphingobium		
lignivorans SYK-6	Wild type; Nal^r Sm^r	1
Δ*ligS*	SYK-6 derivative; Δ*ligS*; Nal^r Sm^r	This study
Δ*ligL*	SYK-6 derivative; Δ*ligL*; Nal^r Sm^r	2
Δ*ligLN*	Δ*ligL* derivative; Δ*ligL ligN*; Nal^r Sm^r	2
Δ*ligDLN*	Δ*ligLN* derivative; Δ*ligD ligL ligN*; Nal^r Sm^r	This study
Δ*ligI*	SYK-6 derivative; Δ*ligI*; Nal^r Sm^r	3
Δ*ligI ligS*	Δ*ligI* derivative; Δ*ligI ligS*; Nal^r Sm^r	This study
Escherichia coli		
BL21(DE3)	F^- *ompT* $hsdS_B(r_B^-\ m_B^-)$ *gal dcm* (DE3); T7 RNA polymerase gene under the control of the *lacUV5* promoter	4
HB101	*recA13 supE44 hsd20 ara-14 proA2 lacY1 galK2 rpsL20 xyl-5 mtl-1*	5
NEB 10-beta	*araD 139* Δ(*ara-leu*)*7697 fhuA lacX74 galK* (ϕ80 Δ*lacZ* ΔM15) *recA1 endA1 nupG rpsL* (Sm^r) Δ(*mrr-hsdRMS-mcrBC*)	New England Biolabs
Plasmid		
pRK2013	Tra^+ Mob^+ ColE1 replicon; Km^r	6
pSEVA225	RK2 cloning vector, Km^r	SEVA
pET-16b	Expression vector; T7 promoter, Ap^r	Novagen
pMAL-cX5	pMB1 ori cloning vector; Taq promoter, *lacI*, *malE*, Ap^r	New England Biolabs
pAK405	Plasmid for allelic exchange and markerless gene deletions in Sphingomonads; Km^r	7
pAK405GFP	pAK405 with synthesized promoter and codon-optimized superfolder GFP gene	8
pJB861	RK2 broad-host-range expression vector; P_m *xylS*; Km^r	9
pD1	pSEVA225 with a PCR amplified fragment of -269 to +30 relative to the *ligD* start codon	This study
pD2	pSEVA225 with a PCR amplified fragment of -173 to +30 relative to the *ligD* start codon	This study
pD3	pSEVA225 with a PCR amplified fragment of -108 to +30 relative to the *ligD* start codon	This study
pD2m35	pD2 with the mutation at TRM site (TTGA to CCAG) in *ligD* promoter	This study
pD2m2	pD2 with the mutation at LigS binding site (TGT to CAC) in *ligD* promoter	This study
pD2m3	pD2 with the mutation at LigS binding site (GGAAATG to AGGGATA) in *ligD* promoter	This study
pL1	pSEVA225 with a PCR amplified fragment of -119 to +30 relative to the *ligL* start codon	This study
pL2	pSEVA225 with a PCR amplified fragment of -64 to +30 relative to the *ligL* start codon	This study
pL1m35	pL1 with the mutation at TRM site (TTGA to CCAG) in *ligL* promoter	This study
pL1m2	pL1 with the mutation at LigS binding site (TGT to CAC) in *ligL* promoter	This study
pL1m3	pL1 with the mutation at LigS binding site (GGAACGG to AGGGCGA) in *ligL* promoter	This study
pP1	pSEVA225 with a PCR amplified fragment of -116 to +27 relative to the *ligP* start codon	This study
pP2	pSEVA225 with a PCR amplified fragment of -75 to +27 relative to the *ligP* start codon	This study
pP1m35	pP1 with the mutation at TRM site (TCGATG to CCAGTC) in *ligP* promoter	This study
pP1m1	pP1 with the mutation at LigS binding site (TTGA to CCAG) in *ligP* promoter	This study
pP1m2	pP1 with the mutation at LigS binding site (TGT to CAC) in *ligP* promoter	This study
pP1m3	pP1 with the mutation at LigS binding site (GGAAACG to AGGGACA) in *ligP* promoter	This study
pZ1	pSEVA225 with a PCR amplified fragment of -173 to +30 relative to the *hpvZ* start codon	This study
pZ2	pSEVA225 with a PCR amplified fragment of -108 to +30 relative to the *hpvZ* start codon	This study
pZ3	pSEVA225 with a PCR amplified fragment of -62 to +30 relative to the *hpvZ* start codon	This study
pZ2m35	pZ2 with the mutation at TRM site (TTGA to CCAG) in *hpvZ* promoter	This study
pZ2m2	pZ2 with the mutation at LigS binding site (TGT to CAC) in *hpvZ* promoter	This study
pZ2m3	pZ2 with the mutation at LigS binding site (GAAAAAG to AAAGGAA) in *hpvZ* promoter	This study
pA1	pSEVA225 with a PCR amplified fragment of -71 to +19 relative to the *ldpA* start codon	This study
pA2	pSEVA225 with a PCR amplified fragment of -26 to +19 relative to the *ldpA* start codon	This study
pET*ligS*	pET-16b with a 1.6 kb PCR amplified deletion fragment of *ligS*	This study
pETdTetR	pET-16b with a 0.6 kb PCR amplified deletion fragment of dTetR	This study

pMAL*ligS*	pMAL-cX5 with a 1.6 kb PCR amplified deletion fragment of *ligS*	This study
pMALdTetR	pMAL-cX5 with a 0.6 kb PCR amplified deletion fragment of dTetR	This study
pMALdMarR	pMAL-cX5 with a 1.0 kb PCR amplified deletion fragment of dMarR	This study
pAK*ligD*	pAK405 with a 2.3 kb PCR amplified deletion fragment of *ligD*	[2]
pAK*ligS*	pAK405GFP with a 2.0 kb PCR amplified deletion fragment of *ligS*	This study
pJB*ligS*	pJB861 with a 1.6-kb BamHI fragment carrying *ligS*	This study
pJBMBP*ligS*	pJB861 with a 2.8-kb BamHI fragment carrying MBP*ligS*	This study
pJBMBPdMarR	pJB861 with a 2.2-kb BamHI fragment carrying MBPdMarR	This study

[a]Nal^r, Sm^r, Ap^r, and Km^r indicate resistance to nalidixic acid, streptomycin, ampicillin, and kanamycin, respectively.

TABLE S2. Primers used in this study

Purpose	primer	sequences (5′to 3′)
For the construction of a plasmid for *ligS* disruption		
pAK*ligS*	dis*ligS*_topF	AGCTCGGTACCCGGGTGTTGCCCTATCCCGAGTTC
	dis*ligS*_topR	GATTTTCTACTCCCGGCTCG
	dis*ligS*_botF	CGAGCCGGGAGTAGAAAATCGCTTTCGCGGTGCGATTGCG
	dis*ligS*_botR	AGGTCGACTCTAGAGTGCCTGATAGAATGAGGCGA
For the construction of reporter plasmid		
pD1	pD1_F	ACCTGCAGGCATGCAGAGCGGAGATGACGGCGTCC
	pD_R	TCATATGTTTTTCCTCCTAGAACGCGACCTGATCCTGGAAATC
pD2	pD2_F	ACCTGCAGGCATGCAGTCGATCGCGCGGGGCGTCG
	pD_R	TCATATGTTTTTCCTCCTAGAACGCGACCTGATCCTGGAAATC
pD3	pD3_F	ACCTGCAGGCATGCAGCAGATGGCGCGGGCATCGT
	pD_R	TCATATGTTTTTCCTCCTAGAACGCGACCTGATCCTGGAAATC
pD2m35	pD2m35_topF	ACCTGCAGGCATGCAGTCGATCGCGCGGGGCGTCGGGTCTTTGCCAGCATTGT
	pD2m35_topR	CTTGAAGCGGGTTTCCACTCATTTCCGGACAATGCTGG
	pD2m35_botF	GAGTGGAAACCCGCTTCAAG
	pD_R	TCATATGTTTTTCCTCCTAGAACGCGACCTGATCCTGGAAATC
pD2m2	pD2m2_topF	ACCTGCAGGCATGCAGTCGATCGCGCGGGGCGTCGGGTCTTTGTTGACATCAC
	pD2m2_topR	CTTGAAGCGGGTTTCCACTCATTTCCGGGTGG
	pD2m2_botF	GAGTGGAAACCCGCTTCAAG
	pD_R	TCATATGTTTTTCCTCCTAGAACGCGACCTGATCCTGGAAATC
pD2m3	pD2m3_topF	ACCTGCAGGCATGCAGTCGATCGCGCGGGGCGTCGGGTCTTTGTTGACATTGTTTAAGG
	pD2m3_topR	CTTGAAGCGGGTTTCCACTCATCCTTAA
	pD2m3_botF	GAGTGGAAACCCGCTTCAAG
	pD_R	TCATATGTTTTTCCTCCTAGAACGCGACCTGATCCTGGAAATC
pL1	pL1_F	ACCTGCAGGCATGCAGGGACTGACTGCGGATCAGG
	pL_R	TCATATGTTTTTCCTCCTAGATGAACGCCGTGGTCCCTG
pL2	pL2_F	ACCTGCAGGCATGCAGTGCAACGATCATGGGCTTC
	pL_R	TCATATGTTTTTCCTCCTAGATGAACGCCGTGGTCCCTG
pL1m35	pL1m35_topF	ACCTGCAGGCATGCAGGGACTGACTGCGGATCAGGCATACGCCAGTTTTGT
	pL1m35_topR	GGCTTATGCGCCGTTCCGGACAAAACTGGCGTATG
	pL1m35_botF	TCCGGAACGGCGCATAAGCC
	pL_R	TCATATGTTTTTCCTCCTAGATGAACGCCGTGGTCCCTG
pL1m2	pL1m2_topF	ACCTGCAGGCATGCAGGGACTGACTGCGGATCAGGCATACGTTGATTTCAC
	pL1m2_topR	GGCTTATGCGCCGTTCCGGGTGGAATCAAC
	pL1m2_botF	TCCGGAACGGCGCATAAGCC
	pL_R	TCATATGTTTTTCCTCCTAGATGAACGCCGTGGTCCCTG
pL1m3	pL1m3_topF	ACCTGCAGGCATGCAGGGACTGACTGCGGATCAGGCATACGTTGATTTTGTTTAAGG
	pL1m3_topR	GGCTTATGCGCCGCCTTAAA
	pL1m3_botF	TCCGGAACGGCGCATAAGCC
	pL_R	TCATATGTTTTTCCTCCTAGATGAACGCCGTGGTCCCTG
pP1	pP1_F	ACCTGCAGGCATGCACCGCTCGTTTCCAGACATTA
	pP_R	TCATATGTTTTTCCTCCTAGATGGTGATCTTGTTGTCTT
pP2	pP2_F	ACCTGCAGGCATGCAGCCAAAATCAACTAGCACTG
	pP_R	TCATATGTTTTTCCTCCTAGATGGTGATCTTGTTGTCTT
pP1m35	pP1_F	ACCTGCAGGCATGCACCGCTCGTTTCCAGACATTA
	pP1m35_topR	CATTCGTTCCCGGATCGTTG
	pP1m35_mid	CAACGATCCGGGAACGAATGGCCAAAATCAATCGATGCTGACCGCCGGTTGCGCTTA
	pP1m35_mid	TAAGCGCAACCGGCGGTCAGCATCGATTGATTTTGGCCATTCGTTCCCGGATCGTTG
	pP1m35_botF	CTGACCGCCGGTTGCGCTTA

	pP_R	TCATATGTTTTTCCTCCTAGATGGTGATCTTGTTGTCTT
pP1m1	pP1m1_topF	ACCTGCAGGCATGCACCGCTCGTTTCCAGACATTACTGG
	pP1m1_topR	CAGTGCTAGTTGATTTTGGCCATTCGTTCCCGGATCGCCAGTAA
	pP1m1_botF	GCCAAAATCAACTAGCACTG
	pP_R	TCATATGTTTTTCCTCCTAGATGGTGATCTTGTTGTCTT
pP1m2	pP1m2_topF	ACCTGCAGGCATGCACCGCTCGTTTCCAGGTGTTATCAA
	pP1m2_topR	CAGTGCTAGTTGATTTTGGCCATTCGTTCCCGGATCGTTGATAACACCTG
	pP1m2_botF	GCCAAAATCAACTAGCACTG
	pP_R	TCATATGTTTTTCCTCCTAGATGGTGATCTTGTTGTCTT
pP1m3	pP1m3_topF	ACCTGCAGGCATGCACCGCTCGTCCTTAAACATTA
	pP1m3_topR	CAGTGCTAGTTGATTTTGGCCATTCGTTCCCGGATCGTTGATAATGTTTAAGG
	pP1m3_botF	GCCAAAATCAACTAGCACTG
	pP_R	TCATATGTTTTTCCTCCTAGATGGTGATCTTGTTGTCTT
pZ1	pZ1_F	ACCTGCAGGCATGCAAGGACGAGGGGCTGAAGCTC
	pZ_R	TCATATGTTTTTCCTCCTACACATAGTCGACCGTTCTG
pZ2	pZ2_F	ACCTGCAGGCATGCAGCGATCCTCTGGTTGACTTTG
	pZ_R	TCATATGTTTTTCCTCCTACACATAGTCGACCGTTCTG
pZ3	pZ3_F	ACCTGCAGGCATGCACCGATGGAGTCAATGCAGCG
	pZ_R	TCATATGTTTTTCCTCCTACACATAGTCGACCGTTCTG
pZ2m35	pZ2m35_topF	ACCTGCAGGCATGCAGCGATCCTCTGGCCAGCTTTGT
	pZ2m35_topR	CCGCTACAAGGCGGTCTTTTTCGAACAAAGCTGGC
	pZ2m35_botF	AAAAGACCGCCTTGTAGCGG
	pZ_R	TCATATGTTTTTCCTCCTACACATAGTCGACCGTTCTG
pZ2m2	pZ2m2_topF	ACCTGCAGGCATGCAGCGATCCTCTGGTTGACTTCAC
	pZ2m2_topR	CCGCTACAAGGCGGTCTTTTTCGAGTGGAG
	pZ2m2_botF	AAAAGACCGCCTTGTAGCGG
	pZ_R	TCATATGTTTTTCCTCCTACACATAGTCGACCGTTCTG
pZ2m3	pZ2m3_topF	ACCTGCAGGCATGCAGCGATCCTCTGGTTGACTTTGTTTAAGG
	pZ2m3_topR	CCGCTACAAGGCGGTCTTCCTTAA
	pZ2m3_botF	AAAAGACCGCCTTGTAGCGG
	pZ_R	TCATATGTTTTTCCTCCTACACATAGTCGACCGTTCTG
pA1	pA1_F	ACCTGCAGGCATGCAATGGCGTTTCCTCTCGAT
	pA_R	TCATATGTTTTTCCTCCTAGCGTTTCCACATCAGCCATT
pA2	pA2_F	ACCTGCAGGCATGCATTGCAGACAAGGAGAGAG
	pA_R	TCATATGTTTTTCCTCCTAGCGTTTCCACATCAGCCATT
For the construction of expression plasmid		
pET*ligS*	pET*ligS*_F	TCGAAGGTCGTCATATGACGGGCGGAAAGGCCGT
	pET*ligS*_R	GTTAGCAGCCGGATCCTCAGTCCCGGTCCATCTCCT
pETdTetR	pETdTetR_F	TCGAAGGTCGTCATATGACGGGCGGAAAGGCCGT
	pETdTetR_R	GTTAGCAGCCGGATCTCACTGGAAGCGACGCAGCCGGT
pMAL*ligS*	pM*ligS*_F	ATCGAGGGAAGGATTTCACATATGACGGGCGGAAAGGCCGT
	pM*ligS*_R	GAGCCTTTCGTTTTATTTGATCAGTCCCGGTCCATCTCCT
pMALdTetR	pMdTetR_F	ATCGAGGGAAGGATTTCACATATGACGGGCGGAAAGGCCGT
	pMdTetR_R	GAGCCTTTCGTTTTATTTGATCACTGGAAGCGACGCAGCCGGT
pMALdMarR	pMdMarR_F	ATCGAGGGAAGGATTTCACATATGTCAAGCCTCTGGGTGTT
	pMdMarR_R	GAGCCTTTCGTTTTATTTGATCAGTCCCGGTCCATCTCCT
For the construction of complementary plasmid		
pJB*ligS*	pJB*ligS*_F	ATGGGAAGCTTCGTGAAAGGAGGTATATATAATGACGGGCGGAAAGGCCGT
	pJB*ligS*_R	TCCTGCAGGATATCTGTCAGTCCCGGTCCATCTCC
pJBMBP*ligS*	pJBMBP_F	ATGGGAAGCTTCGTGAAAGGAGGTATATATAATGAAAATCGAAGAAGGTAA
	pJB*ligS*_R	TCCTGCAGGATATCTGTCAGTCCCGGTCCATCTCC
pJBMBPdMarR	pJBMBP_F	ATGGGAAGCTTCGTGAAAGGAGGTATATATAATGAAAATCGAAGAAGGTAA
	pJB*ligS*_R	TCCTGCAGGATATCTGTCAGTCCCGGTCCATCTCC

For confirmation of gene disruption		
Δ*ligD*	dis*ligD*_confF	GCCTCATCTATGAACTGAAT
	dis*ligD*_confR	CTCGAACAGCATGGGGCGAT
Δ*ligS*	dis*ligS*_confF	GGAGAAATATGGCAATACCG
	dis*ligS*_confR	CAATCGCGCCGCGACTGTTC
For RT-PCR		
RT0863-*ligD*	0863-*ligD*_F	CGCAGCACGGCAACAACAAT
	0863-*ligD*_R	CATCATAAGTGGTCTTCTCG
RT*ligD*-*ligF*	*ligD*-*ligF*_F	CGAGAAGACCACTTATGATG
	ligD-*ligF*_R	AGATATTCGCAGATCACCGT
RT*ligF*-*ligE*	*ligF*-*ligE*_F	ACGGTGATCTGCGAATATCT
	ligF-*ligE*_R	AGGATATAGCAGCGGAACCA
RT*ligF*-*ligG*	*ligE*-*ligG*_F	TGGTTCCGCTGCTATATCCT
	ligE-*ligG*_R	CAGGATGACCATGCTTTCCT
RT*ligG*-0868	*ligG*-0868_F	AGGAAAGCATGGTCATCCTG
	ligG-0868_R	GCCATCACGAGGATATTGTC
RT1263-*ldpB*	1263-*ldpB*_F	CCTTCAGCAGATCGACAAGC
	1263-*ldpB*_R	ACATCTACGAAACCAGCCTC
RT*ldpA*-1266	*ldpA*-1266_F	TGGTTCCAGAATCGCTTCAC
	ldpA-1266_R	GATATAATCTTCCGCCACCC
RT1266-1267	1266-1267_F	GGGTGGCGGAAGATTATATC
	1266-1267_R	TCCCAATGCTCCACGATCTT
RT1267-1268	1267-1268_F	AAGATCGTGGAGCATTGGGA
	1267-1268_R	TCGATGAACACATTGTCCTT
RT1268-*ldpC*	1268-*ldpC*_F	AAGGACAATGTGTTCATCGA
	1268-*ldpC*_R	TTCATCGCCATGCCTCGCTT
RT*ldpC*-1270	*ldpC*-1270_F	AAGCGAGGCATGGCGATGAA
	ldpC-1270_R	TCCTCGGCGGAGATATCCGC
RT1280-1282	1280-1282_F	CGCCACCATGTTCGG
	1280-1282_R	GCGGCAGTGAGAACA
RT1282-*hpvZ*	1282-*hpvZ*_F	CGTCACCTTCGGCAT
	1282-*hpvZ*_R	CTTTCCACCGCACCT
RT3257-3258	3257-3258_F	CCCAGGCATCCAAGCTCGAT
	3257-3258_R	ACTTCCTGGTTCCAGCCAAA
RT3258-3259	3258-3259_F	CTGAGCTTCACGTACAAGGG
	3258-3259_R	CACCTGCACGGAGAGCTTCT
RT3259-*ligP*	3259-*ligP*_F	ACGTCACTTACCGCCTCTAT
	3259-*ligP*_R	CACCCATTTCCCGTCATCGA
RT3365-*ligL*	3365-*ligL*_F	TCCTTGAGAGTCGAGAAATC
	3365-*ligL*_R	TGGCGGACAACTGGATGGAA
RT*ligL*-3367	*ligL*-3367_F	GCTCCTCGAAGAACTGCCTG
	ligL-3367_R	ATGAGATGGTGGCGAGGGGA
RT3367-3368	3367-3368_F	TCCCCTCGCCACCATCTCAT
	3367-3368_R	CGGTCGTCCTCTATTTCTTC
RT3589-*ligN*	3589-*ligN*_F	TGACCTGTTCAACCTGCAAG
	3589-*ligN*_R	AGGACATGGATGTTGCCGAA
RT*ligN*-3591	*ligN*-3591_F	CAGTTCGGCACCCTCATGTA
	ligN-3591_R	GGCTGTCATATACTGCATCC
RT3591-3592	3591-3592_F	GGATGCAGTATATGACAGCC
	3591-3592_R	CAGGCAGTCATGGCAGGGAA

For qRT-PCR		
ligD	q*ligD*_F	CTGGAAGGGCTCGGGATCAC
	q*ligD*_R	ATAGGCCTCGCGGTCCATGA
ligL	q*ligL*_F	GCGCGGCTGGTGCTT
	q*ligL*_R	GAAGAACTGCCTGGCTTCGT
ligN	q*ligN*_F	CAGGACGCCCTCGATCAG
	q*ligN*_R	GGAGTGAACGGCAAGATTGG
ligF	q*ligF*_F	CAAGCGCGCCGAAATG
	q*ligF*_R	ACGCACCAGCAGAAATATTCATC
ligE	q*ligE*_F	TCCGGCTGCACGATCAG
	q*ligE*_R	CCTTGTGCTTGAGCGCATATT
ligP	q*ligP*_F	GAGCGGTGCGACGATCA
	q*ligP*_R	TGTGCGCGATGGCATATT
ligG	q*ligG*_F	AGTTCCGCTCCAACCTGATG
	q*ligG*_R	ATCGTTGAGTGTCTTGCCGA
ligQ	q*ligQ*_F	AGGAACTGACGATCTATCAC
	q*ligQ*_R	GCATGATTTCCACACGCTCG
ligO	q*ligO*_F	AGCACCCCATCCAGCTCTATT
	q*ligO*_R	CGAGCATGATGGTGACTTTCTG
ldpB	q*ldpB*_F	CATCCGGCAGGACCATCTC
	q*ldpB*_R	GCGACATTCTTCTGGCTGAAA
ldpA	q*ldpA*_F	CATTCGCTGATGCTGCAGAT
	q*ldpA*_R	TTGACCAGCACATGGCATTT
For the construction of probes used in EMSAs		
Dp1	Dp1_F	GAGCGGAGATGACGGCGT
	Dp_R	GAACGCGACCTGATCCTG
Dp2	Dp2_F	TCTCCTGATTTCTACGGC
	Dp_R	GAACGCGACCTGATCCTG
Dp3	Dp3_F	CCTGTCATGGGCGATCCC
	Dp_R	GAACGCGACCTGATCCTG
Dp4	Dp4_F	CTTGAAGCGGGTTTCCAC
	Dp_R	GAACGCGACCTGATCCTG
Dp5	Dp5_F	CGAGAGCCGGAACAGACG
	Dp_R	GAACGCGACCTGATCCTG
Dp6	Dp4_F	CTTGAAGCGGGTTTCCAC
	Dp6_R	GTCGATCGCGCGGGGCGTCG
Dp6m1	pD6m1_F	GTCGATCGCGCGGGGCGTCGGGTCTTTGCCAG
	pD6m1_R	CTTGAAGCGGGTTTCCACTCATTTCCGGACAATGCTGG
Dp6m2	pD6m2_F	GTCGATCGCGCGGGGCGTCGGGTCTTTGTTGACACCAC
	pD6m2_R	CTTGAAGCGGGTTTCCACTCATTTCCGGGTGG
Dp6m3	pD6m3_F	GTCGATCGCGCGGGGCGTCGGGTCTTTGTTGACATTGTTTAAGG
	pD6m3_R	CTTGAAGCGGGTTTCCACTCATCCTTAA
Lp1		Gene synthesis (Twist Bioscience)
Lp2	Lp2_F	GGGACAACGGACCTTATC
	Lp_R	GATGAACGCCGTGGTCCC
Lp3	Lp3_F	ATCTGGCAAGGGCGTTTC
	Lp_R	GATGAACGCCGTGGTCCC
Lp4	Lp4_F	GGGACTGACTGCGGATCA
	Lp_R	GATGAACGCCGTGGTCCC
Lp5	Lp5_F	GTGCAACGATCATGGGCT
	Lp_R	GATGAACGCCGTGGTCCC
Lp6	Lp4_F	GGGACTGACTGCGGATCA
	Lp6_R	GGCTTATGCGCCGTTC

Lp6m1	Lp6m1_F	GGGACTGACTGCGGATCAGGCATACGCCAGTTTTG
	Lp6m1_R	GGCTTATGCGCCGTTCCGGACAAAACTGGCGTATG
Lp6m2	Lp6m2_F	GGGACTGACTGCGGATCAGGCATACGTTGATTCCACCCGG
	Lp6m2_R	GGCTTATGCGCCGTTCCGGGTGGAATCAAC
Lp6m3	Lp6m3_F	GGGACTGACTGCGGATCAGGCATACGTTGATTTTGTTTAAGG
	Lp6m3_R	GGCTTATGCGCCGCCTTAAA
Pp1	Pp1_F	CCGCTCGTTTCCAGACATTA
	Pp_R	GATGGTGATCTTGTTGTCTT
Pp2	Pp2_F	GCCAAAATCAACTAGCACTG
	Pp_R	GATGGTGATCTTGTTGTCTT
Pp3	Pp2_F	GCCAAAATCAACTAGCACTG
	Pp3_R	CAGTGCTAGTTGATTTTGGC
Pp3m1	Pp3m1_F	CCGCTCGTTTCCAGACATTACTGGCGA
	Pp3m1_R	CAGTGCTAGTTGATTTTGGCCATTCGTTCCCGGATCGCCAGTAA
Pp3m2	Pp3m2_F	CCGCTCGTTTCCAGGTGTTA
	Pp3m2_R	CAGTGCTAGTTGATTTTGGCCATTCGTTCCCGGATCGTTGATAACACCTG
Pp3m3	Pp3m3_F	CCGCTCGTCCTTAAACATTA
	Pp3m3_R	CAGTGCTAGTTGATTTTGGCCATTCGTTCCCGGATCGTTGATAATGTTTAAGG
Zp1		Gene synthesis (Twist Bioscience)
Zp2	Zp2_F	CCCCATCGTCATCCTGCT
	Zp_R	CACATAGTCGACCGTTCT
Zp3	Zp3_F	AGGACGAGGGGCTGAAGC
	Zp_R	CACATAGTCGACCGTTCT
Zp4	Zp4_F	GCGATCCTCTGGTTGACT
	Zp_R	CACATAGTCGACCGTTCT
Zp5	Zp5_F	CCGATGGAGTCAATGCAG
	Zp_R	CACATAGTCGACCGTTCT
Zp6	Zp4_F	GCGATCCTCTGGTTGACT
	Zp6_R	CCGCTACAAGGCGGTCTTTT
Zp6m1	Zp6m1_F	GCGATCCTCTGGCCAGCTTTGTTCG
	Zp6m1_R	CCGCTACAAGGCGGTCTTTTTCGAACAAAGCTGGC
Zp6m2	Zp6m2_F	GCGATCCTCTGGTTGACTCCACTCG
	Zp6m2_R	CCGCTACAAGGCGGTCTTTTTCGAGTGGAG
Zp6m3	Zp6m3_F	GCGATCCTCTGGTTGACTTTGTTTAAGG
	Zp6m3_R	CCGCTACAAGGCGGTCTTCCTTAA
Ap1	Ap1_F	GGCATTGTTGACCAGCACAT
	Ap_R	AGCGATTCTGGAACCATGTG
Ap2	Ap2_F	GGGGCGATCCGTGACATC
	Ap_R	AGCGATTCTGGAACCATGTG
Ap3	Ap3_F	CAATGCCGAAGCCGATGC
	Ap_R	AGCGATTCTGGAACCATGTG
Ap4	Ap4_F	ATGGCGTTTCCTCTCGAT
	Ap_R	AGCGATTCTGGAACCATGTG
Ap5	Ap5_F	TTGCAGACAAGGAGAGAG
	Ap_R	AGCGATTCTGGAACCATGTG

TABLE S3. dTetR and dMarR nucleotide sequences and amino acid sequences.

Name	Sequence (5′to 3′) or (N- to C-terminal)
dTetR nucleotide	ATGACGGGCGGAAAGGCCGTGCTGGACCGCTTTGCGGTGGGGGTCGACAAGGACGCGATCATCGCGGCTGCGCTGGCGCTGC AGGCGAAACATGGGCTGGCGGGCTGCACGCTCGCTGCAGTCGCGGAACGGCTGCGCGTCGACGAGACGCAGGTGAGCCGACA TTTCGCTGATCGCGCGGACCTGCTGACGGCCATGGCGCGCGAGATTGCCCGCGGCGTCCGCGCCACGCCGCCCGCGCAGGGCT GGCGGGCGCAGCTCGTCCAGCGCGCCAGTGCCGGGCGCCAGCTGATGCTTTCCCGGCGGGACGGCGCATTGCTGTTCGCGCAC ATGCCGTCTCTCTTCCCGCCTGGAGGAACAGGCTTCGACTGTGTGCCGGCCCTTTGCGAGGTGGGTTTTTCTCCGGCCGATGCG CGCGCCGCCGTGGCGCTCGTCGATCGGTTCACGGTCGGTTTCGCGGTGGCCGAGCAGGCCGCGCCGGCCAGTGCGGAGACGTC GGCAAGCTTCGAGAGCCAGCTTGACATTGTCCTGTCCGGACTTGCCTCCGCCCGCCCCGACGGCCTGGTGGCGCAGCGGGACG ACCGGCTGCGTCGCTTCCAGTCAAGCCTCTGGGTGTTCCTGCGCGATGCGTGA
dTetR amino acid	MTGGKAVLDRFAVGVDKDAIIAAALALQAKHGLAGCTLAAVAERLRVDETQVSRHFADRADLLTAMAREIARGVRATPPAQGWRA QLVQRASAGRQLMLSRRDGALLFAHMPSLFPPGGTGFDCVPALCEVGFSPADARAAVALVDRFTVGFAVAEQAAPASAETSASFESQ LDIVLSGLASARPDGLVAQRDDRLRRFQSSLWVFLRDA
dMarR nucleotide	ATGGCGCGCGAAAGCGCCAACATCTCCTTTGCGCGGACTGTCCACATCAACGAACTGGATCGCCGCATCCTACTGCTGCTTCAG GCGCAGGGCGACATGACGCTTGCCGCGATTTCCCTGTCCACGGGGGTGGACAAGGCGCAGGTGAGCCGCGCGATCAAGCGCAT GACGGAGATCTCGCTGCTCGCCCGCGGCGGCATCCGCAGCCCGATCCGCCTGAGTGCGAGCGGCCGCCAGCTTGCCGAGCGCT TGCTGCGGCAGGCTGAGCTGCGCAATCGTGAGCTGACGTTCGGCATCACGGACGAGCAGATCGTCACGCTGTTCGGCGTGCTG GACACGCTGCTGACCCGCGCCGTCGCGCTGTTCGAGAAGGAGCGCAAGCTCGTCGCGTCCAACCAGCGGCAGGAACCGGTCG ATTTCCAGGATCTGGTCGCGGAGGGCCTGCCGGACGAGAACGGGATTGCCGTGGATCGCTCGCGCATCCTTCCGCCGTTCATTA CGCTGTGTTCGTACATGCTGCGGGGCGGGGCGCTCGCTCACAAGCGGCGCACCGGGCTTTCCAACTTCGAGAGCTGGGTCATT GCCGAGATCTGCCGCAATCCGCCAATCAGCTGGCCGCAGCTGGTGCTGGCCCTCTATCGCGACCAGAGCCAGGCAGGGCGAAC GGTCAATCATCTGGTGGAGAGCGGCCTTGTCGAGCGCACCGGCAAGCCGGGGCGGCGCCATGGCTTCTTCGCGCCGACCGAGG AGGGCCGGCGGATCAGCGACATCATTCGCGACACCGCCGCGCGGCGCAGCGAATTCCTCTTCCAGGGCATCCCGCCCCCGCAG CTCGACAGCTTCATGGACGCGTTCGACATTCTTTCGCGCAATGCCGAAGTGCAGCTCGCCCGGGAAAAGGCGATCCAGGAGAT GGACCGGGACTGA
dMarR amino acid	MARESANISFARTVHINELDRRILLLLQAQGDMTLAAISLSTGVDKAQVSRAIKRMTEISLLARGGIRSPIRLSASGRQLAERLLRQAE LRNRELTFGITDEQIVTLFGVLDTLLTRAVALFEKERKLVASNQRQEPVDFQDLVAEGLPDENGIAVDRSRILPPFITLCSYMLRGGALA HKRRTGLSNFESWVIAEICRNPPISWPQLVLALYRDQSQAGRTVNHLVESGLVERTGKPGRRHGFFAPTEEGRRISDIIRDTAARRSEFL FQGIPPPQLDSFMDAFDILSRNAEVQLAREKAIQEMDRD

TABLE S4. Synthesized genes used for EMSA in this study.

Name	Sequence (5′to 3′)
Zp1	CGGCGACCTGCGCACCGCGATCCTCAGCGTGAACTGGGTCGCGATCCCCATCGTCATCCTGCTGCTGGTGCTGGTGTTCCGGATCCG CAAGGACGAGGGGCTGAAGCTCGAGCGGGCGCGGGCGGGCGGCGAACCCGTCTGACCCGGCCCGGCCGGCCTGCGCGATCCTCT GGTTGACTTTGTTCGAAAAAGACCGCCTTGTAGCGGCCGATGGAGTCAATGCAGCGCACAGCCAAATCGTGCGCGCGGGGTGAGA GGAAAGACAGGCCAATGGTTGATGTCAGAACGGTCGACTATGTG
Lp1	TTGTCCGCCAGGGCTGGGCCGTGAGCGGCGATGGCCGGGACAACGGACCTTATCGGACCGAGCAAGCGACCGCGCGGGCGGCTGG CCGGGGCATCTGGCAAGGGCGTTTCGATCGGCCGGGTGACTGGCGCGCGGCAAACCGGCACCCGCGGGACTGACTGCGGATCAGG CATACGTTGATTTTGTCCGGAACGGCGCATAAGCCGTGCAACGATCATGGGCTTCACCGCCCGGCAGCAAGCGATCGGTTCGAACA GGAGAGGAAGCATCATGGACATCGCAGGGACCACGGCGTTCATC

TABLE S5. RNA-Seq analysis of SYK-6 grown in the presence and absence of GGE

Gene	SYK-6 SEMP (TPM)	SEMP + GGE (TPM)	Fold (GGE + SEMP/SEMP)
GGE catabolism genes			
ligD[*]	19	740	39
ligL[*]	21	59	2.8
ligN[*]	25	156	6.2
ligF	27	681	25
ligE	11	436	40
ligP	27	1099	41
ligG	10	198	20
ligQ	1145	1717	1.5
hpvZ	30	394	13
SLG_20400	439	220	0.5
vceA	158	256	1.6
vceB	144	177	1.2
DGPD catabolism genes			
ligO	14	60	4.3
ldpB	6	61	10
ldpC	18	68	3.8
ldpA	9	149	17

[*] Genes involved in both GGE and DGPD catabolism.

TABLE S6. Orthologs of LigS and catabolic enzymes of GGE and DGPD in bacteria

Strains (ANI%)	Group	LigS E value	LigS Per. ident	LigS Accession	LigD E value	LigD Per. ident	LigD Accession	LigL E value	LigL Per. ident	LigL Accession	LigN E value	LigN Per. ident	LigN Accession	LigF E value	LigF Per. ident	LigF Accession
Sphingobium lignivorans B1D3A (96.37)		0	99.61	WP_184156215.1	0	99.02	WP_184150528.1	0	98.96	WP_184155832.1	0	99.36	WP_184156221.1	0	99.22	WP_184150531.1
Sphingobium xanthum NL9 (78.56)		0	73.45	WP_221714856.1	0	87.54	WP_221712134.1	8e-165	78.55	WP_221711867.1	6e-176	77.49	WP_221714853.1	1e-178	91.02	WP_221712135.1
Sphingobium nicotianae H33 (78.35)		0	70.92	WP_214622404.1	0	85.57	WP_214624314.1	0	82.35	WP_214622484.1	4e-170	77.49	WP_214622401.1	9e-180	90.23	WP_214624315.1
Sphingobium sp. B7D2B (78.07)		0	64.53	WP_264612266.1	0	82.78	WP_264575394.1	0	84.38	WP_264595009.1	0	89.39	WP_264612264.1	1e-175	88.33	WP_264573239.1
Sphingobium sp. B12D2B (78.08)		0	64.53	WP_264593633.1	0	82.78	WP_264575394.1	0	84.38	WP_264595009.1	0	89.07	WP_264577161.1	1e-175	88.33	WP_264573239.1
Sphingobium sp. B11D3B (78.28)		0	64.53	WP_264585926.1	0	82.78	WP_264585427.1	0	84.03	WP_181558876.1	0	88.75	WP_264585928.1	3e-174	87.94	WP_264585426.1
Sphingobium sp. B8D3D (78.2)		0	64.34	WP_264577611.1	0	82.12	WP_264578489.1	0	83.68	WP_264578320.1	0	89.07	WP_181561233.1	5e-176	88.72	WP_264575395.1
Sphingobium sp. B8D3A (78.01)		0	64.34	WP_264577611.1	0	82.12	WP_264578489.1	0	83.68	WP_264578320.1	0	89.07	WP_181561233.1	5e-176	88.72	WP_264575395.1
Sphingobium sp. B8D3C (78.11)	Group 1	0	64.15	WP_181561235.1	0	83.11	WP_181560166.1	0	84.03	WP_181558876.1	0	89.07	WP_181561233.1	6e-176	88.72	WP_181560165.1
Sphingobium sp. B8D3B (78.23)		0	64.15	WP_181561235.1	0	83.11	WP_181560166.1	0	84.03	WP_181558876.1	0	89.07	WP_181561233.1	6e-176	88.72	WP_181560165.1
Sphingobium sp. B2D3D (77.92)		0	64.15	WP_181561235.1	0	83.11	WP_181560166.1	0	84.03	WP_181558876.1	0	89.07	WP_181561233.1	6e-176	88.72	WP_181560165.1
Sphingobium sp. B2D3A (77.86)		0	64.15	WP_264573863.1	0	82.45	WP_264573240.1	0	84.38	WP_264574592.1	0	88.42	WP_264573865.1	1e-175	88.33	WP_264573239.1
Sphingobium sp. B1D7B (77.94)		0	64.15	WP_264604630.1				0	84.38	WP_264595009.1	0	88.75	WP_264604628.1	1e-175	88.33	WP_264573239.1
Sphingobium sp. B11D3D (78.03)		0	64.15	WP_264573863.1	0	83.11	WP_181560166.1	0	83.68	WP_264592784.1	0	88.42	WP_264573865.1	2e-174	87.94	WP_264593195.1
Sphingobium sp. B11D3A (78.23)		0	64.15	WP_181561235.1	0	83.11	WP_181560166.1	0	84.03	WP_264569602.1	0	89.07	WP_181561233.1	2.00E-176	87.94	WP_264570839.1
Sphingobium sp. B10D7B (78.16)		0	64.15	WP_181561235.1	0	83.11	WP_181560166.1	0	84.03	WP_264569602.1	0	89.07	WP_181561233.1	2.00E-176	87.94	WP_264570839.1
Sphingobium sp. B10D3B (78.14)		0	64.15	WP_264577163.1	0	82.78	WP_264575394.1	0	84.72	WP_264603880.1	0	89.07	WP_264577161.1	5e-176	88.72	WP_264575395.1
Sphingobium xanthum B10D3A(78.08)		0	64.15	WP_264577163.1	0	82.78	WP_264575394.1	0	84.72	WP_264576417.1	0	89.07	WP_264577161.1	5e-176	88.72	WP_264575395.1
Sphingobium sp. B2D3C (77.98)		0	63.76	WP_264588043.1	0	83.11	WP_181560166.1	0	84.38	WP_264586689.1	0	89.39	WP_264588045.1	1e-175	88.33	WP_264573239.1
Sphingobium sp. B2D3B (78.06)		0	63.76	WP_264588043.1	0	83.11	WP_181560166.1	0	84.38	WP_264595009.1	0	89.39	WP_264588045.1	1e-175	88.33	WP_264573239.1
Erythrobacter sp. SG61-1L		3e-56	51.5	WP_156313532.1	6e-55	40.28	WP_054529235.1	6e-97	50.75	WP_054528944.1	1e-149	68.59	WP_054529846.1	3e-110	63.11	WP_054529921.1
Altererythrobacter lauratis Y-8		2e-92	50.62	WP_336917268.1										7e-107	59.02	WP_336917312.1
Altererythrobacter sp. CC-YST694		4e-104	47.84	WP_226793390.1				5e-94	50	WP_226796119.1	4e-71	43.28	WP_226794229.1	5e-57	41.94	WP_226795285.1
Altericroceibacterium spongiae HN-Y73		5e-89	47.81	WP_120323437.1	3e-112	55.56	WP_120323434.1	2e-94	50.37	WP_183029928.1	6e-154	69.77	WP_120325606.1	5e-109	61.48	WP_120323395.1
Aurantiacibacter xanthus CCTCC AB 2015396		6e-93	47.63	WP_119591858.1										2e-110	61.89	WP_119591529.1
Altererythrobacter fulvus KACC 19119		3e-101	47.24	WP_336977150.1				9e-94	50	WP_336981246.1	4e-143	68.91	WP_336977148.1	5e-110	63.52	WP_336977288.1
Altererythrobacter sp. Root672		6e-92	47.18	WP_055918889.1				3e-95	49.1	WP_055921433.1				2e-116	63.82	WP_055919008.1
Croceibacterium aestuarii D39		1e-98	46.58	WP_305096110.1				1e-96	50.18	WP_305096787.1	2e-56	41.2	WP_305096787.1	7e-112	61.38	WP_305096062.1
Altererythrobacter palmitatis KCTC52607		2e-83	46.44	WP_336924945.1										3e-108	59.84	WP_336924981.1
Aurantiacibacter suaedae GH3-15		1e-92	46.3	WP_137679304.1										8e-109	60.66	WP_137679268.1
Croceibacterium selenioxidans LX-88		1e-98	46.3	WP_214534979.1				8e-91	46.93	WP_214537776.1				2e-116	63.82	WP_214535039.1
Altererythrobacter segetis YJ20		8e-98	46.17	WP_166175673.1	3e-113	55.89	WP_166175669.1	2e-94	49.46	WP_166181083.1	3e-57	40.65	WP_166175669.1	3e-104	59.43	WP_166176688.1
Aurantiacibacter sp. DGU5		6e-91	46.01	WP_346784571.1										6e-107	59.43	WP_346784609.1
Croceibacterium salegens MCCC 1K01500		2e-101	45.79	WP_159794201.1				3e-97	50.18	WP_159798294.1	2e-58	41.2	WP_159798294.1	1e-104	58.61	WP_159794271.1
Altericroceibacterium indicum DSM 18604		9e-96	45.45	WP_160738402.1	3e-111	55.1	WP_160738399.1	6e-94	48.2	WP_160738757.1	1e-150	68.71	WP_211371425.1	2e-108	63.03	WP_160738361.1
Aurantiacibacter sp. MUD11	Group 2	2e-95	45.41	WP_269101125.1										3e-110	61.89	WP_269101078.1
Altericroceibacterium endophyticum LMG 29518		2e-92	44.5	WP_237437587.1	3e-104	51.7	WP_160734846.1	3e-96	49.82	WP_160736709.1	1e-154	69.23	WP_160734837.1	4e-105	61.76	WP_160734880.1
Aurantiacibacter sp. 219JJ12-13		2e-94	44.5	WP_305958720.1										2e-109	62.3	WP_305958675.1
Aurantiacibacter odishensis KCTC 23981		3e-97	44.36	WP_120078629.1										1e-107	60.25	WP_276309496.1
Alteraurantiacibacter aestuarii JCM 16339		2e-99	44.22	GAA0279405.1				1e-58	40.22	WP_160590025.1	8e-71	44.41	WP_160590027.1	7e-106	58.2	WP_343807278.1
Erythrobacter westpacificensis JCM18014		3e-97	43.88	WP_346033271.1										3e-107	60.66	WP_346033310.1
Altericroceibacterium xinjiangense CCTCC AB 207166		2e-107	43.76	WP_126172622.1				6e-95	49.82	WP_164549797.1				7e-110	63.52	WP_126172788.1
Alteraurantiacibacter buctensis M0322		3e-97	43.54	WP_160772164.1										3e-104	57.79	WP_160772131.1
Aurantiacibacter sp. DGU6		2e-93	43.54	WP_341672726.1										4e-110	62.7	WP_341672779.1
Croceibacterium soli MCCC 1K02066		1e-96	43.52	WP_160747193.1				2e-92	48.74	WP_160747354.1	1e-68	42.16	WP_160745958.1	8e-112	64.75	WP_160747672.1
Aurantiacibacter rhizosphaerae GH3-10		9e-96	43.51	MWV27948.1										5e-107	60.66	WP_160485639.1
Altererythrobacter sp. B11		1e-89	43.34	WP_119083232.1				9e-93	49.28	WP_119084013.1	9E-73	45.42	WP_119082788.1	9e-121	66.26	WP_119083264.1
Aurantiacibacter arachoides RC4-10-4		3e-93	43.33	WP_160731819.1												
Croceibacterium atlanticum 26DY36		3e-89	43.3	AKH41525.1				5e-93	49.63	WP_046902213.1				6e-123	66.94	WP_235979777.1
Aurantiacibacter sp. H149		3e-97	42.99	WP_338245033.1										8e-108	61.07	WP_338244947.1
Altererythrobacter sp. KTW20L		3e-92	42.46	WP_249704121.1										6e-105	59.43	WP_249702777.1
Alteraurantiacibacter aquimixticola SSKS-13		2e-98	41.54	WP_136693152.1										6e-108	60.66	WP_136693114.1
Croceibacterium xixiisoli S36		5e-80	41.19	WP_161391630.1				7e-88	50.2	WP_161389953.1	4e-104	53.95	WP_161392239.1	4e-138	72.98	WP_161390046.1

Strains (ANI%)	LigE E value	LigE Per. ident	LigE Accession	LigP E value	LigP Per. ident	LigP Accession	LigG E value	LigG Per. ident	LigG Accession	LigQ E value	LigQ Per. ident	LigQ Accession	HpvZ E value	HpvZ Per. ident	HpvZ Accession
Sphingobium lignivorans B1D3A (96.37)	0	99.29	WP_184150534.1	0	99.29	WP_184155674.1	0	97.74	WP_184150537.1	0	98.66	WP_184149499.1	0	99.46	WP_184151413.1
Sphingobium xanthum NL9 (78.56)	0	92.17	WP_221712136.1	0	95.02	WP_221715071.1	8e-177	89.66	WP_221712137.1	2e-172	80.49	WP_221715304.1	0	88.41	WP_221712747.1
Sphingobium nicotianae H33 (78.35)	0	89.96	WP_214624316.1	0	93.93	WP_214621644.1	7e-177	88.46	WP_214624317.1	1e-170	79.58	WP_214622575.1	0	90.05	WP_214622792.1
Sphingobium sp. B7D2B (78.07)	1e-127	63.84	WP_264572128.1	0	88.97	WP_264572128.1	4e-175	87.69	WP_264610762.1	0	86.74	WP_181558444.1	0	90.58	WP_181559906.1
Sphingobium sp. B12D2B (78.08)	1e-127	63.84	WP_264572128.1	0	88.97	WP_264572128.1	1e-175	88.08	WP_264593194.1	0	86.74	WP_264593690.1	0	90.4	WP_264594352.1
Sphingobium sp. B11D3B (78.28)	1e-127	63.84	WP_264572128.1	0	88.97	WP_264572128.1	7e-175	87.31	WP_264585425.1	0	86.74	WP_264573797.1	0	90.4	WP_264575633.1
Sphingobium sp. B8D3D (78.2)	5e-127	63.47	WP_181558791.1	0	88.61	WP_181558791.1	7e-175	87.31	WP_264578490.1	0	86.74	WP_264573797.1	0	90.22	WP_264579080.1
Sphingobium sp. B8D3A (78.01)	5e-127	63.47	WP_181558791.1	0	88.61	WP_181558791.1	7e-175	87.31	WP_264578490.1	0	86.74	WP_264573797.1	0	90.22	WP_264579080.1
Sphingobium sp. B8D3C (78.11)	5e-127	63.47	WP_181558791.1	0	88.61	WP_181558791.1	7e-175	87.69	WP_181560164.1	0	86.74	WP_181558444.1	0	90.58	WP_181559906.1
Sphingobium sp. B8D3B (78.23)	5e-127	63.47	WP_181558791.1	0	88.61	WP_181558791.1	7e-175	87.69	WP_181560164.1	0	86.74	WP_181558444.1	0	90.58	WP_181559906.1
Sphingobium sp. B2D3D (77.92)	5e-127	63.47	WP_181558791.1	0	88.61	WP_181558791.1	7e-175	87.69	WP_181560164.1	0	86.74	WP_181558444.1	0	90.58	WP_181559906.1
Sphingobium sp. B2D3A (77.86)	1e-127	63.84	WP_264572128.1	0	88.97	WP_264572128.1	1e-173	86.54	WP_264573238.1	0	86.74	WP_264573797.1	0	90.58	WP_181559906.1
Sphingobium sp. B1D7B (77.94)	1e-127	63.84	WP_264572128.1	0	88.97	WP_264572128.1	1e-175	88.08	WP_264593194.1	0	86.74	WP_264593690.1	0	90.58	WP_181559906.1
Sphingobium sp. B11D3D (78.03)	1e-127	63.84	WP_264572128.1	0	88.97	WP_264572128.1	1e-175	88.08	WP_264593194.1	0	86.74	WP_264573797.1	0	90.58	WP_181559906.1
Sphingobium sp. B11D3A (78.23)	1e-127	63.84	WP_264572128.1	0	88.97	WP_264572128.1	1e-175	87.64	WP_264570838.1	0	86.38	WP_264571849.1	0	90.58	WP_181559906.1
Sphingobium sp. B10D7B (78.16)	1e-127	63.84	WP_264572128.1	0	88.97	WP_264572128.1	1e-175	87.64	WP_264570838.1	0	86.38	WP_264571849.1	0	90.58	WP_181559906.1
Sphingobium sp. B10D3B (78.14)	5e-127	63.47	WP_181558791.1	0	88.61	WP_181558791.1	3e-174	86.54	WP_264575396.1	0	84.69	WP_264577229.1	0	90.4	WP_264575633.1
Sphingobium xanthum B10D3A(78.08)	5e-127	63.47	WP_181558791.1	0	88.61	WP_181558791.1	3e-174	86.54	WP_264575396.1	0	84.69	WP_264577229.1	0	90.4	WP_264575633.1
Sphingobium sp. B2D3C (77.98)	1e-127	63.84	WP_264572128.1	0	88.97	WP_264572128.1	8e-178	88.46	WP_264587540.1	0	86.38	WP_264587989.1	0	90.58	WP_264587349.1
Sphingobium sp. B2D3B (78.06)	1e-127	63.84	WP_264572128.1	0	88.97	WP_264572128.1	8e-178	88.46	WP_264587540.1	0	86.38	WP_264587989.1	0	90.58	WP_264587349.1
Erythrobacter sp. SG61-1L	2e-132	66.42	WP_054530343.1	5e-169	80.8	WP_054530343.1				3e-112	60.58	WP_054530291.1	0	73.13	WP_054531597.1
Altererythrobacter lauratis Y-8	1e-105	55.8	WP_336918772.1	7e-121	60.65	WP_336918772.1				4e-110	58.97	WP_336920450.1			
Altererythrobacter sp. CC-YST694	7e-114	59.71	WP_226795769.1	2E-132	66.06	WP_226795769.1				8e-115	61.31	WP_226792749.1	0	72.95	WP_226796439.1
Altericroceibacterium spongiae HN-Y73	6e-131	66.3	WP_120323457.1	2e-161	75.89	WP_120323457.1				3e-118	61.68	WP_120324443.1	0	71.06	WP_120323894.1
Aurantiacibacter xanthus CCTCC AB 2015396	2e-111	56.79	WP_119591893.1	6e-121	59.35	WP_119591893.1				2e-119	62.64	WP_119592861.1			
Altererythrobacter fulvus KACC 19119	2e-134	67.9	WP_336978096.1	5e-167	79.71	WP_336978096.1				2e-113	60.95	WP_336978088.1	0	73.51	WP_336982025.1
Altererythrobacter sp. Root672	9e-124	64.07	WP_055921561.1	8e-161	76.16	WP_055921561.1				1e-119	62.41	WP_055917904.1	0	71.79	WP_055925360.1
Croceibacterium aestuarii D39	9e-105	56.04	WP_305095466.1	2e-128	62.99	WP_305095466.1				7e-121	62.64	WP_305095588.1	0	70.11	WP_305097058.1
Altererythrobacter palmitatis KCTC52607	2e-106	57.41	WP_336926247.1	7e-120	60.29	WP_336926247.1				3e-111	59.12	WP_336927381.1			
Aurantiacibacter suaedae GH3-15	2e-108	56.79	WP_137681416.1	7e-118	58.76	WP_137681416.1				4e-119	61.9	WP_137679603.1			
Croceibacterium selenioxidans LX-88	2e-126	65.56	WP_214537737.1	1e-161	76.16	WP_214537737.1				1e-118	61.31	WP_214534554.1	0	71.43	WP_214536513.1
Altererythrobacter segetis YJ20	4e-110	58.24	WP_166179040.1	1e-127	63.21	WP_166179040.1				4e-112	59.35	WP_166175069.1	0	71.22	WP_166180642.1
Aurantiacibacter sp. DGU5	7e-111	57.3	WP_346784300.1	3e-120	61.11	WP_346784300.1				3e-118	61.9	WP_346783354.1			
Croceibacterium salegens MCCC 1K01500	2e-105	56.78	WP_328598029.1	9e-129	63.7	WP_328598029.1				1e-116	62.27	WP_159793633.1	0	70.79	WP_159793117.1
Altericroceibacterium indicum DSM 18604	4e-133	67.53	WP_160738791.1	2e-161	76.6	WP_160738791.1	7e-124	65.5	WP_246204857.1	3e-116	60.95	WP_160739969.1	0	71.59	WP_160739415.1
Aurantiacibacter sp. MUD11	1e-113	57.35	WP_269101606.1	8e-125	61.9	WP_269101606.1				5e-112	59.49	WP_269100414.1			
Altericroceibacterium endophyticum LMG 29518	5e-135	67.53	WP_160736792.1	1e-162	78.49	WP_160736792.1	4e-121	64.86	WP_237437588.1	6e-118	60.81	WP_160737263.1	0	70.15	WP_160735609.1
Aurantiacibacter sp. 219JJ12-13	5e-102	52.01	WP_305959048.1	2e-115	58.82	WP_305959048.1				2e-112	59.85	WP_305958951.1	0	55.37	WP_305960133.1
Aurantiacibacter odishensis KCTC 23981	9e-102	54.85	WP_120076741.1	1e-115	58.89	WP_120076741.1				1e-111	59.56	WP_120078097.1	7E-118	40.84	WP_120077822.1
Alteraurantiacibacter aestuarii JCM 16339	8e-110	56.83	WP_343808752.1	7e-127	62.82	WP_343808752.1				5e-109	59.71	WP_160589805.1			
Erythrobacter westpacificensis JCM18014	3e-103	53.99	WP_346033700.1	4E-117	59.26	WP_346033700.1				1e-108	59.56	WP_346032295.1	5e-121	41.03	WP_346032410.1
Altericroceibacterium xinjiangense CCTCC AB 207166	2e-123	63.1	WP_126174227.1							3e-116	60.07	WP_126171910.1	0	73.62	WP_126173134.1
Alteraurantiacibacter buctensis M0322	2e-113	58.01	WP_160771940.1	6e-126	61.54	WP_160771940.1				2e-115	60.81	WP_160771283.1			
Aurantiacibacter sp. DGU6	2e-104	55.16	WP_341672239.1	1e-120	61.11	WP_341672239.1				1e-110	58.57	WP_341673277.1			
Croceibacterium soli MCCC 1K02066	2e-119	59.36	WP_160746401.1	4e-130	64.96	WP_160746401.1				4e-116	60.44	WP_160745935.1	0	70.48	WP_160745313.1
Aurantiacibacter rhizosphaerae GH3-10	2e-104	54.32	WP_160485184.1	7e-118	58.61	WP_160485184.1				5e-111	59.12	WP_160486056.1			
Altererythrobacter sp. B11	5e-115	60.44	WP_119083884.1	8e-136	66.19	WP_119083884.1				3e-116	60.07	WP_119082622.1	0	72.53	WP_119082169.1
Aurantiacibacter arachoides RC4-10-4										5e-108	56.79	WP_131452941.1			
Croceibacterium atlanticum 26DY36	8e-117	60	WP_046903179.1	3e-144	68.33	WP_046903179.1				5e-113	59.71	WP_046903092.1	0	72.34	WP_046904276.1
Aurantiacibacter sp. H149	5e-103	55.22	WP_338240764.1	2e-117	59.33	WP_338240764.1				5e-113	60.22	WP_338243999.1			
Altererythrobacter sp. KTW20L	4e-109	57.2	WP_249702488.1	1e-127	62.64	WP_249702488.1				8e-111	58.24	WP_249704464.1			
Alteraurantiacibacter aquimixticola SSKS-13	8e-111	57.3	WP_136692365.1	2e-124	61.54	WP_136692365.1				4e-112	60.44	WP_136693502.1			
Croceibacterium xixiisoli S36	3e-122	64.49	MXP00500.1	1e-141	68.21	WP_161389921.1				2e-113	59.71	WP_161391429.1	0	71.14	WP_161391987.1

Strains (ANI%)	LigO E value	LigO Per. ident	LigO Accession	LdpC E value	LdpC Per. ident	LdpC Accession	LdpB E value	LdpB Per. ident	LdpB Accession	LdpA E value	LdpA Per. ident	LdpA Accession
Sphingobium lignivorans B1D3A (96.37)	0	99.66	WP_184156219.1	3e-177	97.59	WP_184151381.1	0	98.03	WP_184151373.1	0	98.35	WP_184049978.1
Sphingobium xanthum NL9 (78.56)	0	89.23	WP_221714854.1	2e-157	87.15	WP_221712762.1	0	86.8	WP_221712776.1	4e-168	90	WP_221712775.1
Sphingobium nicotianae H33 (78.35)	0	87.21	WP_214622402.1	4e-159	87.95	WP_214622778.1	0	87.46	WP_214622763.1	1e-167	90.34	WP_214622764.1
Sphingobium sp. B7D2B (78.07)	5e-76	41.13	WP_264575394.1	2e-147	84.74	WP_264605215.1	0	84.82	WP_264611090.1	3e-160	86.25	WP_264611089.1
Sphingobium sp. B12D2B (78.08)	5e-76	41.13	WP_264575394.1	7e-147	84.34	WP_264594476.1	0	84.82	WP_264594501.1	4e-162	88.19	WP_264575811.1
Sphingobium sp. B11D3B (78.28)	2e-75	40.78	WP_264585427.1	9e-148	84.74	WP_264585048.1	0	84.82	WP_264585023.1	7e-162	87.08	WP_264570266.1
Sphingobium sp. B8D3D (78.2)	3e-76	41.13	WP_264578489.1	7e-147	84.34	WP_264578888.1	0	85.15	WP_264578857.1	2e-161	86.67	WP_264578858.1
Sphingobium sp. B8D3A (78.01)	3e-76	41.13	WP_264578489.1	7e-147	84.34	WP_264578888.1	0	85.15	WP_264578857.1	2e-161	86.67	WP_264578858.1
Sphingobium sp. B8D3C (78.11)	7e-76	40.78	WP_181560166.1	3e-145	83.94	WP_181559660.1	0	85.15	WP_181559623.1	2e-160	86.25	WP_181559624.1
Sphingobium sp. B8D3B (78.23)	7e-76	40.78	WP_181560166.1	3e-145	83.94	WP_181559660.1	0	85.15	WP_181559623.1	2e-160	86.25	WP_181559624.1
Sphingobium sp. B2D3D (77.92)	7e-76	40.78	WP_181560166.1	3e-145	83.94	WP_181559660.1	0	85.15	WP_181559623.1	2e-160	86.25	WP_181559624.1
Sphingobium sp. B2D3A (77.86)	2e-75	40.78	WP_264573240.1	3e-151	84.34	WP_264572831.1	0	85.81	WP_264572795.1	4e-161	86.67	WP_264572796.1
Sphingobium sp. B1D7B (77.94)				2e-147	84.74	WP_264605215.1						
Sphingobium sp. B11D3D (78.03)	7e-76	40.78	WP_181560166.1	3e-151	84.34	WP_264572831.1	0	85.81	WP_264572795.1	4e-161	86.67	WP_264572796.1
Sphingobium sp. B11D3A (78.23)	7e-76	40.78	WP_181560166.1	4e-147	83.94	WP_264570300.1	0	85.15	WP_181559623.1	7e-162	87.08	WP_264570266.1
Sphingobium sp. B10D7B (78.16)	7e-76	40.78	WP_181560166.1	4e-147	83.94	WP_264570300.1	0	85.15	WP_181559623.1	7e-162	87.08	WP_264570266.1
Sphingobium sp. B10D3B (78.14)	5e-76	41.13	WP_264575394.1	1e-147	83.94	WP_264575779.1	0	84.49	WP_264575812.1	4e-162	88.19	WP_264575811.1
Sphingobium xanthum B10D3A(78.08)	5e-76	41.13	WP_264575394.1	1e-147	83.94	WP_264575779.1	0	84.49	WP_264575812.1	4e-162	88.19	WP_264575811.1
Sphingobium sp. B2D3C (77.98)	7e-76	40.78	WP_181560166.1	4e-148	84.34	WP_264587217.1	0	85.48	WP_264587190.1	7e-162	87.08	WP_264570266.1
Sphingobium sp. B2D3B (78.06)	7e-76	40.78	WP_181560166.1	4e-148	84.34	WP_264587217.1	0	85.48	WP_264587190.1	7e-162	87.08	WP_264570266.1
Erythrobacter sp. SG61-1L	1e-71	43.77	WP_054529846.1	1e-118	71.54	WP_054531106.1	3e-145	67.88	WP_054531093.1	3e-119	71.68	WP_054531094.1
Altererythrobacter lauratis Y-8				3e-120	69.64	WP_336919016.1	7e-144	68.54	WP_336919006.1	4e-118	72.65	WP_336919007.1
Altererythrobacter sp. CC-YST694	1e-68	41.79	WP_226794229.1	4e-120	72.06	WP_226795286.1	1e-144	67.88	WP_226795299.1	6e-118	72.32	WP_226795298.1
Altericroceibacterium spongiae HN-Y73	3e-172	79.73	WP_120323440.1	3e-100	60.32	WP_120324048.1	4e-142	65.23	WP_120324971.1	2e-119	70.35	WP_120324970.1
Aurantiacibacter xanthus CCTCC AB 2015396				8e-120	68.44	WP_119594550.1	5e-138	66.01	WP_119594541.1	3E-119	71.24	WP_119594542.1
Altererythrobacter fulvus KACC 19119	1E-66	42.09	WP_336982050.1	8e-117	70.33	WP_336979596.1	7e-145	67.88	WP_336979616.1	5e-118	72.12	WP_336979615.1
Altererythrobacter sp. Root672	8e-65	40.27	WP_055921430.1	6e-122	68.83	KRA80744.1	2e-145	68.21	WP_055925709.1	6e-119	70.85	WP_055925707.1
Croceibacterium aestuarii D39	3e-66	42.42	WP_305097046.1	3e-112	68.67	WP_305097957.1	7e-143	65.56	WP_305097973.1	1e-117	71.3	WP_305097972.1
Altererythrobacter palmitatis KCTC52607				8e-119	69.23	WP_336927055.1	3e-144	67.88	WP_336927064.1	3e-117	70.35	WP_336927063.1
Aurantiacibacter suaedae GH3-15				2e-119	69.26	WP_137680792.1	1e-134	64.69	WP_137680802.1	4e-117	69.91	WP_137680801.1
Croceibacterium selenioxidans LX-88				2e-124	70.45	WP_250893821.1	1e-141	66.89	WP_214536396.1	9e-121	72.65	WP_214536397.1
Altererythrobacter segetis YJ20	4e-85	48.13	WP_166175669.1	1e-111	68.83	WP_166180104.1	1e-149	69.54	WP_166180646.1	2e-115	69.96	WP_166180648.1
Aurantiacibacter sp. DGU5				4e-118	67.62	WP_346785377.1	2e-135	65.35	WP_346785365.1	3e-118	70.8	WP_346785366.1
Croceibacterium salegens MCCC 1K01500	5e-65	41.41	WP_159793093.1	1e-117	68.27	MXO61215.1	1e-138	64.03	WP_159798099.1	4e-114	70.4	WP_159798097.1
Altericroceibacterium indicum DSM 18604	1e-168	78.45	WP_160738405.1	7e-92	60.73	WP_160740204.1	3e-137	66.78	WP_343033341.1	4e-118	70.35	WP_160740210.1
Aurantiacibacter sp. MUD11				2e-125	71.72	WP_269099027.1	9e-141	65.79	WP_269099012.1	1e-131	75	WP_269099015.1
Altericroceibacterium endophyticum LMG 29518	3e-174	78.04	WP_160734840.1	2e-96	62.35	WP_160735789.1	5e-148	68.21	WP_160735781.1	2e-116	70.8	WP_160735782.1
Aurantiacibacter sp. 219JJ12-13				1e-121	69.96	WP_305957517.1	2e-141	66.45	WP_305957525.1	8e-134	76.15	WP_305957524.1
Aurantiacibacter odishensis KCTC 23981				1e-122	70.04	WP_120077291.1	1e-139	65.68	WP_120077283.1	1e-135	77.82	WP_120077284.1
Alteraurantiacibacter aestuarii JCM 16339				5e-123	70.45	WP_160590455.1	3e-143	67	WP_160590437.1	1e-117	70.8	WP_160590439.1
Erythrobacter westpacificensis JCM18014				3e-123	70.45	WP_346032804.1	8e-139	65.68	WP_346032796.1	2e-135	77.41	WP_346032797.1
Altericroceibacterium xinjiangense CCTCC AB 207166	4e-65	42.09	WP_126173125.1	5e-127	70.68	WP_241233568.1	9e-157	69.87	WP_126173043.1	2e-119	71.75	WP_126173042.1
Alteraurantiacibacter buctensis M0322				6e-113	69.23	WP_337192852.1	4e-131	65.35	WP_160770607.1	2e-115	69.47	WP_160770608.1
Aurantiacibacter sp. DGU6				2e-116	67.89	WP_341674665.1	2e-134	64.47	WP_341671590.1	3e-138	78.24	WP_341671589.1
Croceibacterium soli MCCC 1K02066	9e-69	41.37	WP_160745955.1	5e-118	68.27	MXP40529.1	4e-149	68.54	WP_160745359.1	7e-121	72.65	WP_160745358.1
Aurantiacibacter rhizosphaerae GH3-10				1e-76	55.06	WP_160484350.1	5e-139	65.13	WP_160484359.1	7e-132	75.73	WP_160484358.1
Altererythrobacter sp. B11	2e-67	41.79	WP_119082788.1	7e-123	72.06	WP_119081448.1	3e-149	69.54	WP_119081459.1	3e-118	70.4	WP_119081457.1
Aurantiacibacter arachoides RC4-10-4												
Croceibacterium atlanticum 26DY36	1E-63	41.91	WP_053833306.1	1e-122	68.83	WP_046903632.1	1e-149	69.21	WP_046903625.1	2e-121	72.2	WP_046903626.1
Aurantiacibacter sp. H149	5e-63	40.79	WP_338240942.1	2e-119	69.64	WP_338241671.1	2e-137	64.8	WP_338241659.1	3e-135	76.99	WP_338241660.1
Altererythrobacter sp. KTW20L				2e-119	68.83	WP_249700649.1	4e-144	68.21	WP_249704401.1	7e-120	72.57	WP_249704400.1
Alteraurantiacibacter aquimixticola SSKS-13				9e-120	68.02	WP_246021798.1	4e-143	66.89	WP_136694380.1	8e-117	70.31	WP_136694381.1
Croceibacterium xixiisoli S36	1e-64	43.9	WP_161391998.1	1e-50	40.55	WP_161389286.1	7e-148	68.54	WP_161389475.1	3e-118	69.51	WP_161389474.1

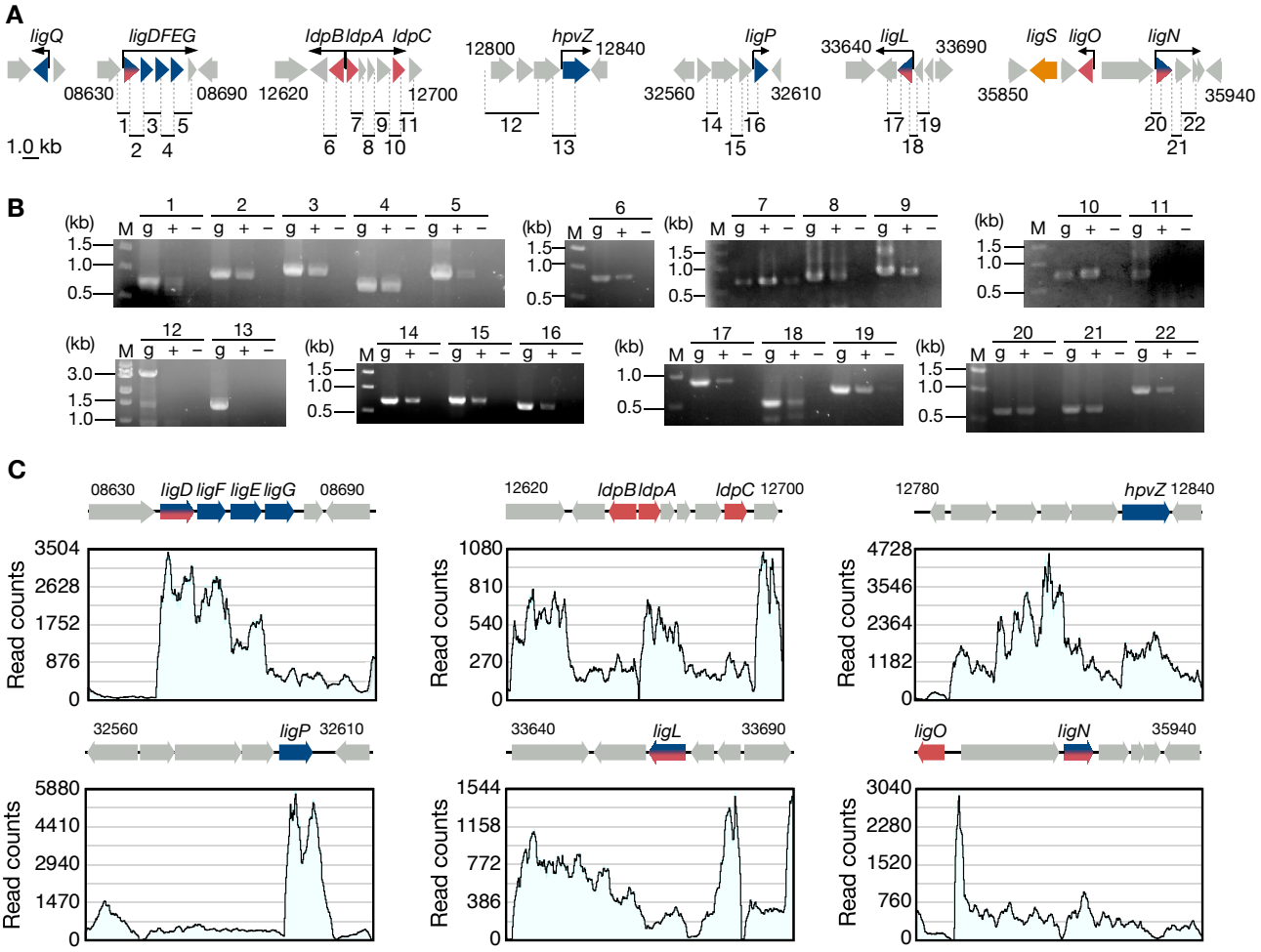


Fig. S1. Identification of transcription units for GGE and DGPD catabolism genes.

(A) Organization of the GGE and DGPD catabolism genes. The bars with numbers below the map indicate the regions to be amplified and correspond to the numbering in panel B. (B) Agarose gel electrophoresis of RT-PCR assays with primers amplifying the regions shown in panel A. Total RNAs isolated from SYK-6 cells grown in Wx-SEMP + 5 mM GGE were used as templates for cDNA synthesis. Lanes: M, molecular size markers; g, control PCR with the SYK-6 genomic DNA; + and -, RT-PCR with or without reverse transcriptase, respectively. (C) RNA-Seq read coverage of the GGE and DGPD catabolism genes. RNAseq was performed using RNA obtained from SYK-6 cells grown in Wx-SEMP + 5 mM GGE.

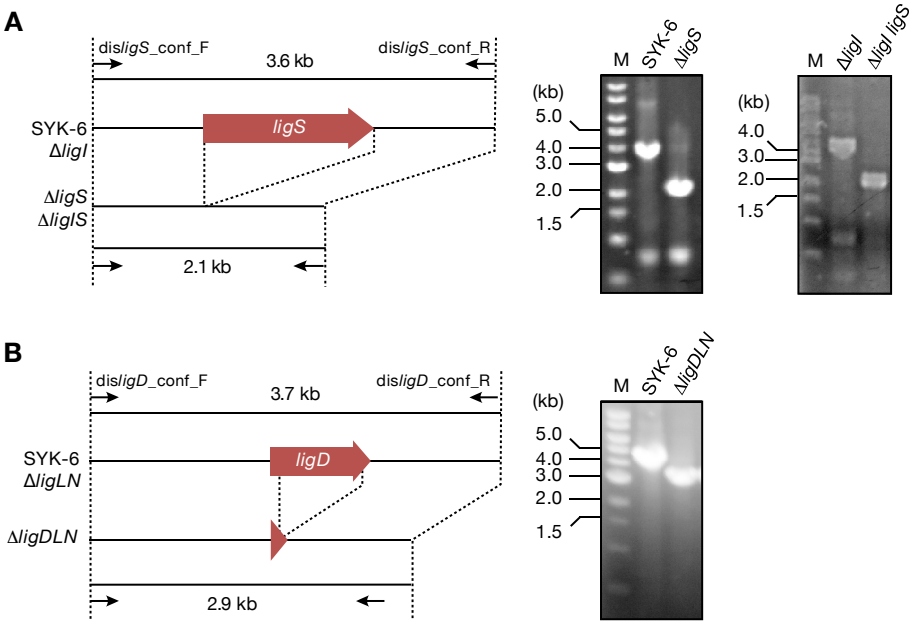


Fig. S2. Construction of *ligS* mutants and *ligD ligL ligN* triple mutant.

The left panels show schematic representations of the disruption of *ligS* in SYK-6 and Δ*ligI* (A) and the disruption of *ligD* in Δ*ligLN* (B). The disruption of the genes was examined by colony PCR analyses (right side panels). The primer pairs used for colony PCR analyses are shown in Table S2. M, molecular size markers.

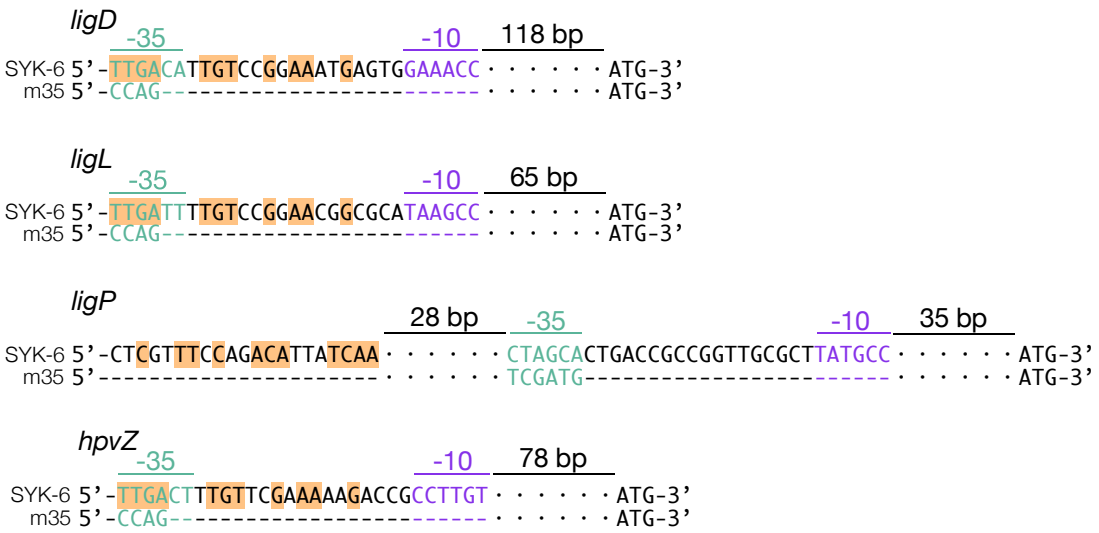


Fig. S3. Mutation into the putative *ligD*, *ligL*, *ligP*, and *hpvZ* promoter sequences.
The putative –35 and –10 elements are shown in green and violet, respectively. LigS binding sequences were highlighted in yellow. Mutations in the –35 element are shown as m35.

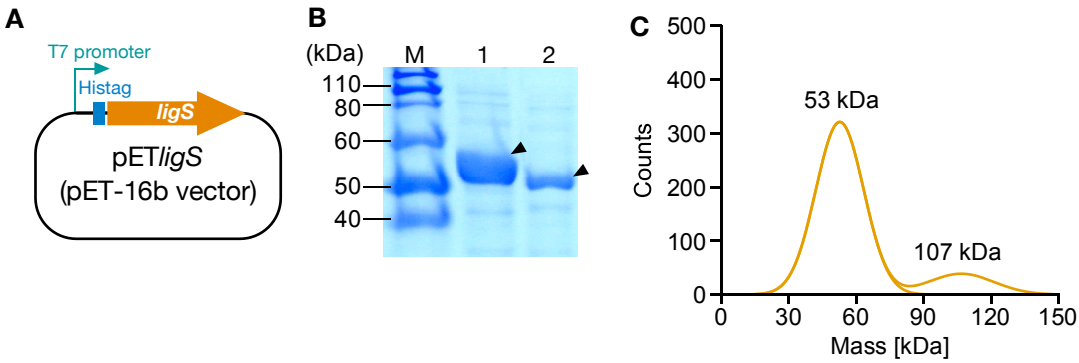
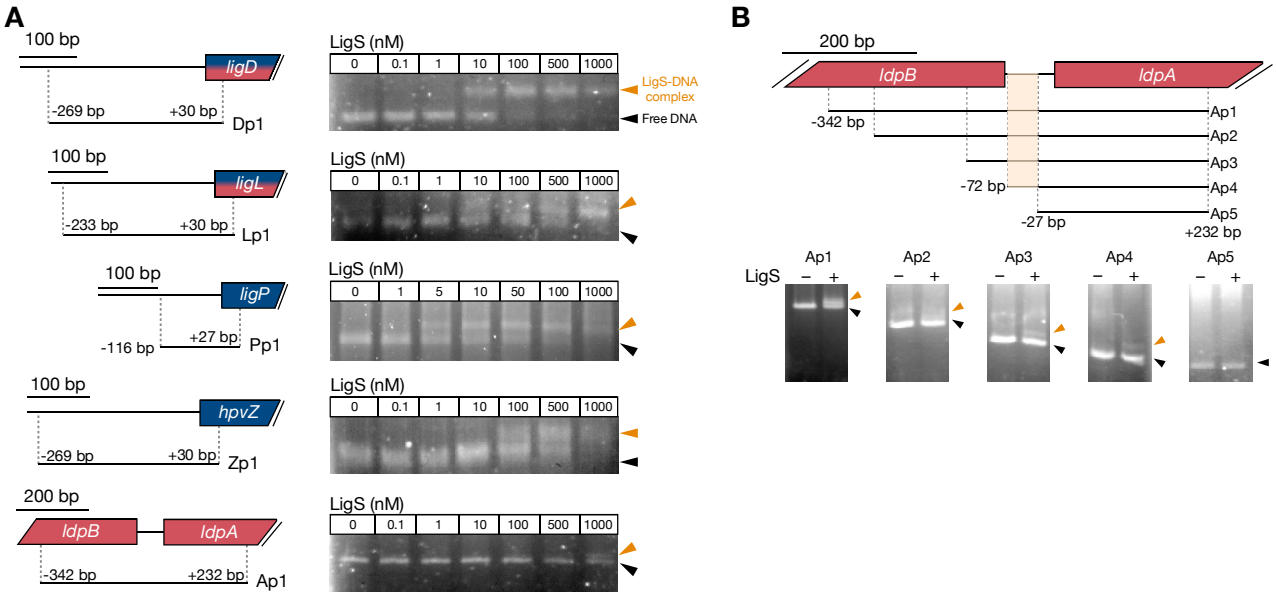


Fig. S4. Purification and molecular mass analysis of LigS.

(A) A plasmid construction of pET*ligS*. (B) SDS-PAGE of purified LigS. Lanes: M, molecular size markers; 1, His-LigS (2 µg); 2, LigS with His-tag removed by Factor Xa (2 µg). (C) Molecular mass analysis of LigS using Mass photometry.



C

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ligD  GTCGATCGCGCGGGGCGTCGGGTCTTTG-TTGACATTGTCCGGAAATGAGTGGAAACCCGCTTCAAG 60 bp
ligL  --GGGACTGACTGCGGATCAGGCATACG-TTGATTTTGTCCGGAACGGCGCATAAGCC--------- 55 bp
ligP  ------------CATTCGTTCCCGGATCGTTGATAATGTCTGGAAACGAGCGG-------------- 41 bp
hpvZ  -----------------GCGATCCTCTGGTTGACTTTGTTCGAAAAAGACCGCCTTGTAGCGG---- 46 bp
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Fig. S5. Identification of LigS binding region.

(A) EMSAs of LigS (0–1000 nM) binding to Dp1, Lp1, Pp1, Zp1, and Ap1 probes (40 fmol). (B) EMSA of LigS (1000 nM) binding to stepwise shortened *ldpA* probes (40 fmol). Each probe was incubated in the presence (+) and absence (-) of purified LigS. (C) Alignment of LigS binding regions upstream of *ligD*, *ligL*, *ligP*, and *hpvZ*. Alignment was performed using Clustal W.

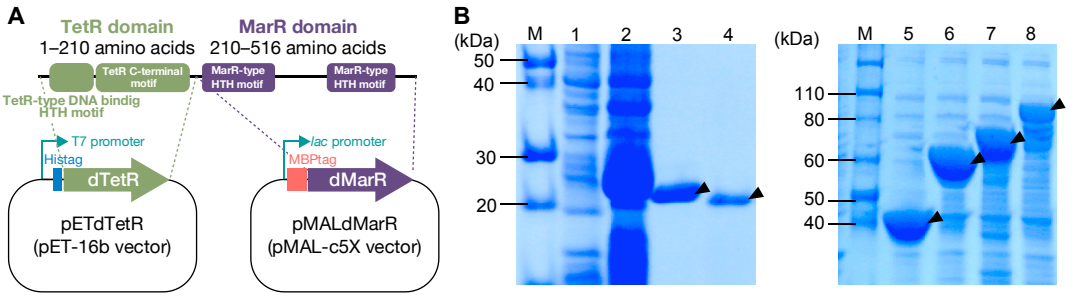

Fig. S6. Expression plasmids for coding regions of TetR and MarR domains.

(A) Plasmids construction of pETdTetR and pMALdMarR. dTetR uses amino acid residues from position 1 to 210 of LigS, and dMarR uses amino acid residues from position 210 to 516. dTetR and dMarR have a stop codon (TGA) and a start codon (ATG) added, respectively. (B) SDS-PAGE of dTetR and dMarR. Lanes: M, molecular size markers; 1, cell extracts of *E. coli* harboring pET-16b (10 μg); 2, cell extracts of *E. coli* harboring pETdTetR (10 μg); 3, purified His-dTetR (2 μg); 4, purified dTetR with His-tag removed by Factor Xa (2 μg); 5, cell extracts of *E. coli* harboring pMAL-c5X (MBP; 10 μg); 6, cell extracts of *E. coli* harboring pMALdTetR (MBP-dTetR; 10 μg); 7, cell extracts of *E. coli* harboring pMALdMarR (MBP-dMarR; 10 μg); 8, cell extracts of *E. coli* harboring pMALLigS (MBP-LigS; 10 μg).

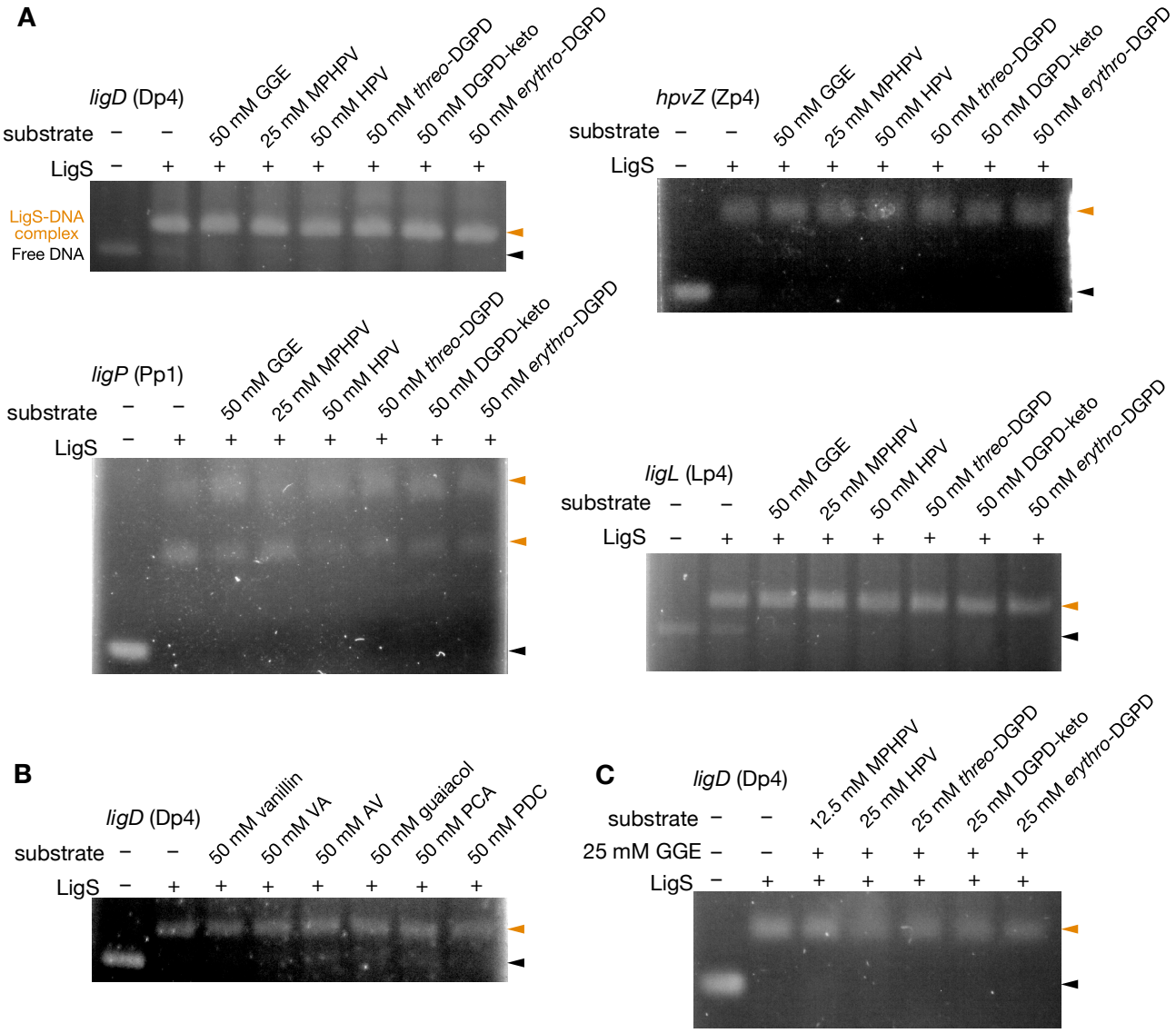

Fig. S7. Search for effector molecules of LigS.

(A) EMSAs of LigS (100–1000 nM) binding to Dp4, Lp4, Pp1, and Zp4 (40 fmol) in the presence of GGE, DGPD, and their metabolites. (B) EMSAs of LigS (100 nM) binding to Dp4 (40 fmol) in the presence of downstream metabolites. (C) EMSAs of LigS (100 nM) binding to Dp4 (40 fmol) in the presence of GGE plus MPHPV, HPV, *threo*-DGPD, DGPD-keto, or *erythro*-DGPD. Abbreviations: VA, vanillic acid; AV, acetovanillone; PCA, protocatechuic acid; PDC, 2-pyrone-4,6-dicarboxylic acid; HPV, β-hydroxypropiovanillone. Each probe was incubated in the presence (+) and absence (-) of purified LigS.

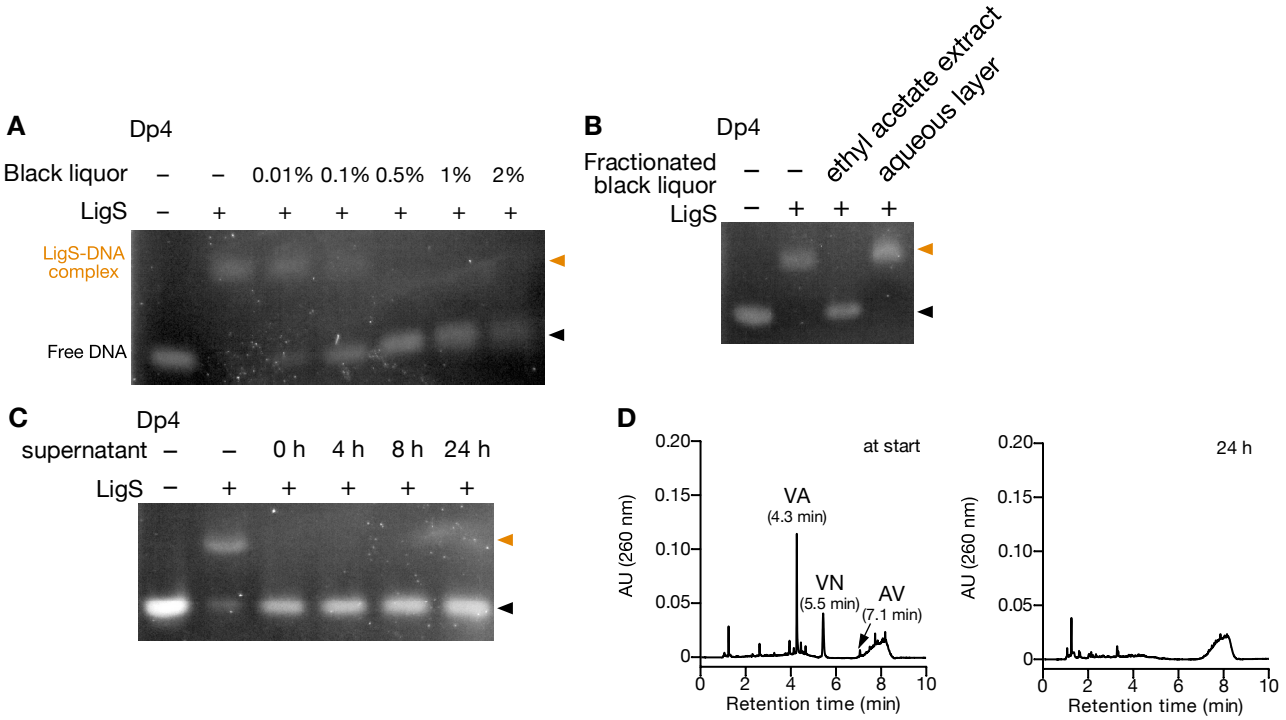

Fig. S8. Search for effector molecules of LigS from black liquor.

(A) EMSAs of LigS (100 nM) binding to Dp4 (40 fmol) in the presence of neutralized black liquor. (B) EMSAs of LigS (100 nM) binding to Dp4 (40 fmol) in the presence of ethyl acetate extract of black liquor and aqueous layer after ethyl acetate extraction. (C) EMSAs of LigS (100 nM) binding to Dp4 (40 fmol) in the presence of black liquor incubated with SYK-6 for 4, 8, and 24 h. Each probe was incubated with (+) or without (-) purified LigS. (D) HPLC analysis of black liquor incubated with SYK-6 for 24 h. SYK-6 cells were incubated with 5% neutralized black liquor in Wx-SEMP. Portions of the culture were collected at the start and 24 h and analyzed using HPLC. HPLC analysis was performed with the ACQUITY UPLC system (Waters). The sample solution was filtered through a PTFE filter (Captiva Econofilter, Agilent) with a pore size of 0.20 µm and using CORTECS UPLC T3 column (particle size, 1.6 µm; 2.1 × 150 mm, Waters). The mobile phase was a mixture of solution A (acetonitrile containing 0.1% formic acid) and B (water containing 0.1% formic acid) under the following conditions: 0–3.0 min, linear gradient from 1 to 20% A; 3.0–5.0 min, decreasing gradient from 20 to 7% A; 5.0–6.1 min, linear gradient from 7 to 30% A; 6.1–7.1 min, linear gradient from 30 to 50% A; 7.1–7.5 min, decreasing gradient from 50 to 1% A; 7.5–10 min, 1% A. The flow rate was 0.3 mL/min, and the column temperature was 40°C. Abbreviations: VA, vanillic acid; VN, vanillin; AV, acetovanillone.

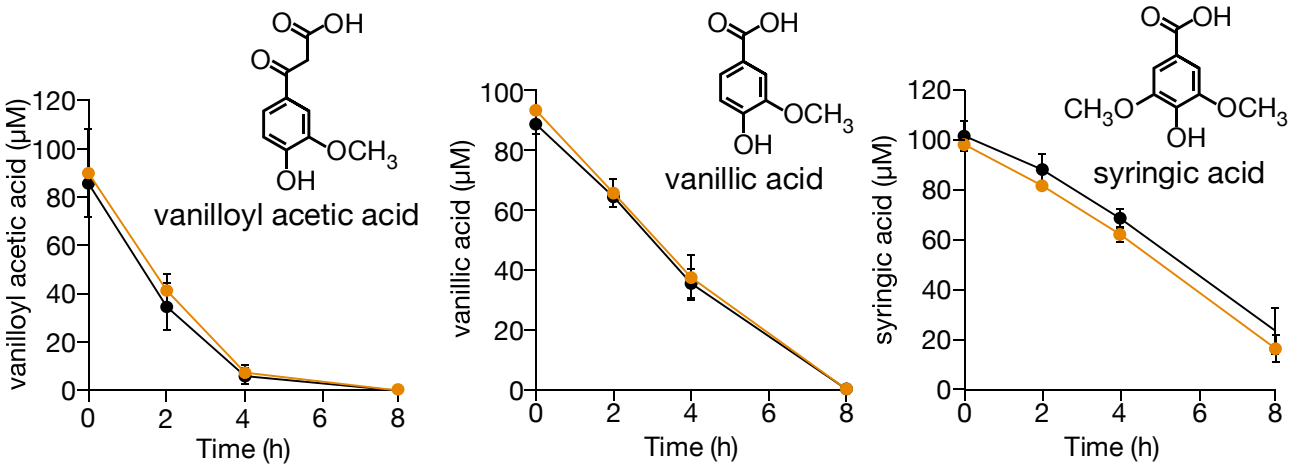

Fig. S9. Conversion of vanilloyl acetic acid, vanillic acid, and syringic acid by resting cells of SYK-6 and Δ*ligS*.

Cells of SYK-6 (black) and Δ*ligS* (orange) with an OD_{600} of 0.5 vanilloyl acetic acid and 1.0 (vanillic acid and syringic acid), respectively, were incubated with 100 μM vanilloyl acetic acid, vanillic acid, and syringic acid.

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