

**Table S4. Fold changes of the type III secretion system (T3SS) and alginate biosynthesis genes in HMM**

Locus tag	Description	$\Delta$ rsmA23/ PstDC3000	$\Delta$ rsmA23/ $\Delta$ rsmA3	$\Delta$ rsmA3/ PstDC3000
<b>Type III secretion system</b>				
PSPTO_1404	<i>hrpL</i> , RNA polymerase sigma factor HrpL	-504.9	-24.79	-20.37
PSPTO_1379	<i>hrpR</i> , type III transcriptional regulator HrpR	-6.82	-2.11	-3.24
PSPTO_1380	<i>hrpS</i> , type III transcriptional regulator HrpS	-7.05	-2.22	-3.18
PSPTO_0061	<i>hopY1</i> , type III effector HopY1	-80.53	-10.03	-8.03
PSPTO_0588	<i>hopH1</i> , type III effector HopH1	-117.78	-7.83	-15.05
PSPTO_0589	<i>hopC1</i> , type III effector HopC1	-75.79	-5.28	-14.35
PSPTO_1370	<i>hopN1</i> , type III effector HopN1	-43.08	-4.51	-9.56
PSPTO_1372	<i>hopAA1-1</i> , type III effector HopAA1-1	-62.9	-5.83	-10.79
PSPTO_1375	<i>hopM1</i> , type III effector HopM1	-29.03	-2.51	-11.54
PSPTO_1377	<i>avrE1</i> , type III effector protein AvrE1	-16.45	-2.79	-5.89
PSPTO_1406	<i>hopB1</i> , type III effector HopB1	-81.28	-6.58	-12.36
PSPTO_2678	<i>hopP1</i> , type III helper protein HopP1	-182.2	-10.69	-17.04
PSPTO_3087	<i>hopAB2</i> , type III effector HopAB2	-58.72	-5.41	-10.86
PSPTO_4001	<i>avrPto1</i> , type III effector protein AvrPto1	-84.14	-7.38	-11.4
PSPTO_4331	<i>hopE1</i> , type III effector HopE1	-213.12	-9.08	-23.46
PSPTO_4588	<i>hopS2</i> , type III effector HopS2	-47	-6.88	-6.83
PSPTO_4597	<i>hopS1</i> , type III effector HopS1	-140.87	-8.24	-17.09
PSPTO_4776	<i>hopI1</i> , type III effector HopI1	-75.24	-5.8	-12.98
PSPTO_5354	<i>hopA1</i> , type III effector HopA1	-69.62	-5.15	-13.53
PSPTO_0502	<i>hopF2</i> , type III effector HopF2	-15.08	/	-11.61
PSPTO_0877	<i>hopQ1-1</i> , type III effector HopQ1-1	-5.86	/	-4.24
PSPTO_0901	<i>hopAG1</i> , type III effector HopAG1	-2.37	/	-2.74
PSPTO_1568	<i>hopAF1</i> , type III effector HopAF1	-5.79	/	-3.33
PSPTO_4691	<i>hopAD1</i> , type III effector HopAD1	-15.83	/	-10.72
PSPTO_4718	<i>hopAA1-2</i> , type III effector HopAA1-2	-2.98	/	-1.83
PSPTO_4720	<i>hopV1</i> , type III effector HopV1	-8.73	/	-5.7
PSPTO_4722	<i>hopAO1</i> , type III effector HopAO1	-11.73	/	-8.71
PSPTO_4727	<i>hopG1</i> , type III effector HopG1	-18.6	/	-10.18
PSPTOA0012	<i>hopX1</i> , type III effector HopX1	-8.45	/	-5.99
PSPTOA0018	<i>hopO1-1</i> , type III effector HopO1-1	-3.14	/	-3.04
PSPTOA0019	<i>hopT1-1</i> , type III effector HopT1-1	-2.73	/	-2.45
PSPTO_1391	<i>hrpV</i> , negative regulator of <i>hrp</i> expression	-3.25	/	-3.37
PSPTOA0017	<i>shcO1</i> , type III chaperone ShcO1	-2.7	/	-1.95
PSPTO_1376	<i>shcE</i> , type III chaperone ShcE	-4.67	/	-4.36
PSPTO_0503	<i>shcF</i> , type III chaperone protein ShcF	-54.35	-3.06	-17.77
PSPTO_1369	<i>shcN</i> , type III chaperone protein ShcN	-38.18	-3.67	-10.39
PSPTO_1374	<i>shcM</i> , type III chaperone ShcM	-142.67	-7.78	-18.33
PSPTO_4589	<i>shcS2</i> , type III chaperone ShcS2	-14.13	-2.35	-6.02
PSPTO_4599	<i>shcS1</i> , type III chaperone ShcS1	-54.99	-3.33	-16.52

<i>PSPTO_4721</i>	<i>shcV</i> , type III chaperone ShcV	-32.76	-2.85	-11.51
<i>PSPTO_5353</i>	<i>shcA</i> , type III chaperone protein ShcA	-73.98	-6.06	-12.2
<i>PSPTO_1390</i>	<i>hrpT</i> , type III secretion protein HrpT	-10.4	/	-7.46
<i>PSPTO_1384</i>	<i>hrcJ</i> , type III secretion protein HrcJ	-176.38	-12.42	-14.2
<i>PSPTO_1400</i>	<i>hrcN</i> , type III secretion cytoplasmic ATPase	-192.15	-12.53	-15.33
<i>PSPTO_1397</i>	<i>hrcQa</i> , type III secretion protein HrcQa	-997.41	-70.41	-14.17
<i>PSPTO_1396</i>	<i>hrcQb</i> , type III secretion protein HrcQb	-263.65	-14.84	-17.76
<i>PSPTO_1395</i>	<i>hrcR</i> , type III secretion protein HrcR	-126.58	-7.75	-16.34
<i>PSPTO_1394</i>	<i>hrcS</i> , type III secretion protein HrcS	-276.6	-21.81	-12.68
<i>PSPTO_1393</i>	<i>hrcT</i> , type III secretion protein HrcT	-161.66	-13.21	-12.24
<i>PSPTO_1392</i>	<i>hrcU</i> , type III secretion protein HrcU	-58.37	-4.89	-11.94
<i>PSPTO_1402</i>	<i>hrcV</i> , type III secretion protein HrcV	-222.59	-13.68	-16.27
<i>PSPTO_1383</i>	<i>hrpB</i> , type III secretion protein HrpB	-464.83	-28.76	-16.16
<i>PSPTO_1385</i>	<i>hrpD</i> , type III secretion protein HrpD	-181.24	-12.29	-14.75
<i>PSPTO_1386</i>	<i>hrpE</i> , type III secretion protein HrpE	-215.99	-13.02	-16.59
<i>PSPTO_1387</i>	<i>hrpF</i> , type III secretion protein HrpF	-402.02	-26.78	-15.01
<i>PSPTO_1388</i>	<i>hrpG</i> , type III secretion protein HrpG	-959.23	-57.35	-16.73
<i>PSPTO_1403</i>	<i>hrpJ</i> , type III secretion protein HrpJ	-204.17	-12.87	-15.86
<i>PSPTO_1399</i>	<i>hrpO</i> , type III secretion protein HrpO	-239.83	-16.13	-14.87
<i>PSPTO_1398</i>	<i>hrpP</i> , type III secretion protein HrpP	-384.41	-24.48	-15.7
<i>PSPTO_1401</i>	<i>hrpQ</i> , type III secretion protein HrpQ	-327	-19.28	-16.96
<i>PSPTO_1378</i>	<i>hrpH</i> , lytic murein transglycosylase	-142.88	-11.74	-12.17
<i>PSPTO_1389</i>	<i>hrcC</i> , type III secretion protein HrcC	-226.35	-15.82	-14.31
<i>PSPTO_0852</i>	<i>hopAJI</i> , type III helper protein HopAJI	-24.47	-3.26	-7.51
<i>PSPTO_4101</i>	<i>hopAKI</i> , type III helper protein HopAKI	-55.64	-4.78	-11.65
<i>PSPTO_1381</i>	<i>hrpA1</i> , type III helper protein HrpA1	-1084.47	-53.6	-20.23
<i>PSPTO_1405</i>	<i>hrpK1</i> , type III helper protein HrpK1	-281.56	-17.75	-15.86
<i>PSPTO_1373</i>	<i>hrpW1</i> , type III helper protein HrpW1	-248.19	-18.86	-13.16
<i>PSPTO_1382</i>	<i>hrpZ1</i> , type III restriction system endonuclease	-883.37	-45.44	-19.44
<b>Alginate biosynthesis</b>				
<i>PSPTO_1235</i>	<i>algI</i> , alginate biosynthesis protein AlgI	20.27	2.03	10
<i>PSPTO_1236</i>	<i>algL</i> , alginate lyase AlgL	14.18	2.13	6.65
<i>PSPTO_1237</i>	<i>algX</i> , alginate biosynthesis protein AlgX	19.92	2.07	9.62
<i>PSPTO_1238</i>	<i>algG</i> , alginate biosynthesis protein AlgG	22.1	2.08	10.62
<i>PSPTO_1239</i>	<i>algE</i> , alginate biosynthesis protein AlgE	20.37	2.03	10.04
<i>PSPTO_1240</i>	<i>algK</i> , alginate biosynthesis protein AlgK	20.41	1.91	10.69
<i>PSPTO_1241</i>	<i>alg44</i> , alginate biosynthesis protein Alg44	22.14	2.11	10.47
<i>PSPTO_1232</i>	<i>algA</i> , alginate biosynthesis protein AlgA	27.6	2.51	11
<i>PSPTO_1233</i>	<i>algF</i> , alginate biosynthesis protein AlgF	24.71	3.12	7.91
<i>PSPTO_1234</i>	<i>algJ</i> , alginate biosynthesis protein AlgJ	22.26	2.13	10.47
<i>PSPTO_1242</i>	<i>alg8</i> , alginate biosynthesis protein Alg8	22.67	2.04	11.12
<i>PSPTO_1243</i>	<i>algD</i> , GDP-mannose 6-dehydrogenase AlgD	26.46	3.18	8.33

Differential expression in  $\Delta rsmA23$  versus *Pst*DC3000,  $\Delta rsmA23$  versus  $\Delta rsmA3$ , and  $\Delta rsmA3$  versus *Pst*DC3000 with fold change (FC) $\geq$ 1.5 or FC $\leq$ -1.5 and p-value <0.05. /: non-differentially expressed genes (DEGs); HMM: *hrp*-inducing minimum medium; *Pst*DC3000: *Pseudomonas syringae* pv. *tomato* DC3000;  $\Delta rsmA3$ : the *rsmA3* mutant;  $\Delta rsmA23$ : the *rsmA2/A3* double mutant.

**Table S5. Fold changes of the syringafactin biosynthesis genes in HMM**

Locus tag	Description	$\Delta rsmA23$	$\Delta rsmA23$	$\Delta rsmA3$
		/ <i>Pst</i> DC3000	/ $\Delta rsmA3$	/ <i>Pst</i> DC3000
<b>Syringafactin biosynthesis</b>				
<i>PSPTO_2828</i>	<i>syrR</i> , transcriptional regulator SyrR	12.93	-2.38	30.74
<i>PSPTO_2829</i>	<i>syfA</i> , non-ribosomal peptide synthetase SyfA	7.9	-7.37	58.2
<i>PSPTO_2830</i>	<i>syfB</i> , non-ribosomal peptide synthetase SyfB	4.56	-7.31	33.31
<i>PSPTO_2831</i>	<i>syfC</i> , syringafactin efflux protein SyfC	3.3	-5.39	17.77
<i>PSPTO_2832</i>	<i>syfD</i> , syringafactin efflux protein SyfD	2.6	-5.36	13.97

Differential expression in  $\Delta rsmA23$  versus *Pst*DC3000,  $\Delta rsmA23$  versus  $\Delta rsmA3$ , and  $\Delta rsmA3$  versus *Pst*DC3000 with fold change (FC) $\geq$ 1.5 or FC $\leq$ -1.5 and p-value <0.05. HMM: *hrp*-inducing minimum medium; *Pst*DC3000: *Pseudomonas syringae* pv. *tomato* DC3000;  $\Delta rsmA3$ : the *rsmA3* mutant;  $\Delta rsmA23$ : the *rsmA2/A3* double mutant.

**Table S6. Selected genes regulated mainly by RsmA2 in HMM**

Locus tag	Description	$\Delta rsmA23$	$\Delta rsmA23$	$\Delta rsmA3$
		/ <i>Pst</i> DC3000	/ $\Delta rsmA3$	/ <i>Pst</i> DC3000
<b>Positively regulated by RsmA2</b>				
<b>Sarcosine metabolism</b>				
<i>PSPTO_0457</i>	<i>soxG-1</i> , sarcosine oxidase, gamma subunit	-2.9	-3.91	/
<i>PSPTO_0458</i>	<i>soxA-1</i> , sarcosine oxidase, alpha subunit	-2.94	-4.21	/
<i>PSPTO_0459</i>	<i>soxD-1</i> , sarcosine oxidase subunit delta	-3.52	-4.21	/
<i>PSPTO_0460</i>	<i>soxB-1</i> , sarcosine oxidase, beta subunit	-3.13	-3.86	/
<b>Thiamine biosynthesis</b>				
<i>PSPTO_4798</i>	<i>thiD</i> , hydroxy-methylpyrimidine kinase	-2.05	-2.06	/
<i>PSPTO_4799</i>	<i>thiE</i> , thiamine-phosphate pyrophosphorylase	-2.1	-2.01	/
<b>Negatively regulated by RsmA2</b>				
<b>Oxidative stress response</b>				
<i>PSPTO_0066</i>	<i>oxyR</i> , oxidative stress regulatory OxyR	2.2	2.16	/
<b>Efflux pump</b>				
<i>PSPTO_3099</i>	<i>mexE</i> , multidrug efflux RND membrane fusion protein MexE	3.21	2.95	/
<i>PSPTO_3100</i>	<i>saxF</i> , aliphatic isothiocyanate resistance protein SaxF; AcrB/AcrD/AcrF family	3.28	3	/
<i>PSPTO_3101</i>	<i>oprN</i> , outer membrane efflux protein	3.89	3.3	/

Differential expression in  $\Delta rsmA23$  versus *Pst*DC3000,  $\Delta rsmA23$  versus  $\Delta rsmA3$ , and  $\Delta rsmA3$  versus *Pst*DC3000 with fold change (FC) $\geq$ 1.5 or FC $\leq$ -1.5 and p-value <0.05. /: non-differentially expressed genes (DEGs); HMM: *hrp*-inducing minimum medium; *Pst*DC3000: *Pseudomonas syringae* pv. *tomato* DC3000;  $\Delta rsmA3$ : the *rsmA3* mutant;  $\Delta rsmA23$ : the *rsmA2/A3* double mutant.

**Table S7. Selected genes regulated mainly by RsmA3 in HMM**

Locus tag	Description	$\Delta$ rsmA23	$\Delta$ rsmA23	$\Delta$ rsmA3
		/PstDC3000	/ $\Delta$ rsmA3	/PstDC3000
<b>Positively regulated by RsmA3</b>				
<b>Fatty acid biosynthesis/degradation</b>				
PSPTO_5093	acyl carrier protein	-3.51	/	-2.51
PSPTO_4860	<i>accB</i> , acetyl-CoA carboxylase, biotin carboxyl carrier protein	-1.96	/	-2.11
PSPTO_3706	acyl-CoA dehydrogenase	2.74	/	2.95
PSPTO_3857	acyl-CoA dehydrogenase	5.63	/	4.27
PSPTO_5020	acyl-CoA dehydrogenase family protein	2.15	/	2.09
PSPTO_0667	short-chain dehydrogenase	3.54	/	2.97
PSPTO_1056	short chain dehydrogenase	3.76	/	4.38
PSPTO_1119	short chain dehydrogenase	3.41	/	2.41
<b>Cellulose biosynthesis</b>				
PSPTO_1026	<i>wssA</i> , cell morphology protein	-3.27	/	-3.05
PSPTO_1027	<i>wssB</i> , cellulose synthase, catalytic subunit	-1.79	/	-1.96
PSPTO_1029	<i>wssD</i> , endoglucanase	-2.21	/	-1.64
<b>Two-component system</b>				
PSPTO_4373	<i>colS</i> , sensor histidine kinase ColS	-1.99	/	-1.64
PSPTO_4374	<i>colR</i> , response regulator ColR	-1.91	/	-1.86
<b>Negatively regulated by RsmA3</b>				
<b>Signal transduction</b>				
PSPTO_0073	<i>spoT</i> , guanosine-3',5'-bis(diphosphate,3'-pyrophosphohydrolase	-1.38	/	-1.75
PSPTO_0856	<i>fpRel</i> , hypothetical protein	1.93	/	2.3
PSPTO_0969	<i>dksA</i> , dnaK suppressor protein	2.13	/	2.11
PSPTO_3863	<i>psyR</i> , transcriptional regulator PsyR	3.45	/	2.1
PSPTO_3864	<i>psyI</i> , autoinducer synthesis protein PsyI	1.62	/	1.51
PSPTO_1499	<i>wspR</i> , GGDEF domain-containing protein	2.42	/	2.32
PSPTO_5477	<i>phoB</i> , phosphate regulon protein PhoB	3.02	/	2.43
PSPTO_5478	<i>phoR</i> , phosphate regulon sensor phoR	2.05	/	1.81
PSPTO_5483	<i>phoU</i> , phosphate transport system PhoU	3.17	/	1.99
PSPTO_5484	<i>pstB-2</i> , phosphate transporter ATP-binding protein	3.67	/	2.17
<b>Chemotaxis</b>				
PSPTO_0908	<i>cheB-1</i> , glutamate methylesterase CheB	13.42	/	17.54
PSPTO_0909	glutamine deamidase CheD	32.07	/	30.81
PSPTO_0910	<i>cheR-1</i> , chemotaxis protein CheR	123.62	/	97.38
PSPTO_0911	<i>cheW-1</i> , chemotaxis protein CheW	204.42	/	175.37
PSPTO_0912	methyl-accepting chemotaxis protein	144.44	/	101.24
PSPTO_0913	<i>cheA-1</i> , chemotaxis histidine kinase CheA	132.04	/	107.78
PSPTO_0915	<i>cheY-1</i> , chemotaxis protein CheY	176.81	/	119.59
PSPTO_0916	<i>methyl-accepting chemotaxis protein</i>	77.78	/	54.03

<i>PSPTO_1008</i>	methyl-accepting chemotaxis protein	16.67	/	11.48
<i>PSPTO_1493</i>	methyl-accepting chemotaxis protein	3.22	/	3.15
<i>PSPTO_1494</i>	chemotaxis protein CheW	2.93	/	2.9
<i>PSPTO_1495</i>	chemotaxis methyltransferase CheR	2.76	/	2.94
<i>PSPTO_1496</i>	chemotaxis protein CheW	2.84	/	3.25
<i>PSPTO_1928</i>	<i>cheR-2</i> , chemotaxis protein methyltransferase CheR	2.59	/	2.81
<i>PSPTO_2526</i>	methyl-accepting chemotaxis protein	2.88	/	5.74
<i>PSPTO_4541</i>	methyl-accepting chemotaxis protein	2.31	/	2.62
<i>PSPTO_4786</i>	methyl-accepting chemotaxis protein	2.54	/	2.12
<i>PSPTO_5159</i>	methyl-accepting chemotaxis protein	3.27	/	2.92
<b>Type VI secretion system</b>				
<i>PSPTO_3482</i>	Rhs element Vgr protein	2.1	/	1.92
<i>PSPTO_4385</i>	Rhs element Vgr protein	2.42	/	2.17
<i>PSPTO_5415</i>	Rhs element Vgr protein	1.75	/	1.99
<i>PSPTO_5418</i>	hypothetical protein PSPTO_5418	1.79	/	2.19
<i>PSPTO_5425</i>	clpB protein	1.95	/	2.36
<i>PSPTO_5435</i>	<i>hcp-2</i> , secreted protein Hcp	13.72	/	11.47
<i>PSPTO_5436</i>	Rhs element Vgr protein	6.38	/	7
<i>PSPTO_5438</i>	Rhs family protein	3.75	/	4.11
<b>Capsular polysaccharide</b>				
<i>PSPTO_3529</i>	<i>pslA</i> , capsular polysaccharide biosynthesis protein PslA	44.49	/	35.66
<i>PSPTO_3530</i>	<i>pslB</i> , mannose-6-phosphate isomerase PslB	34.38	/	29.57
<i>PSPTO_3531</i>	<i>pslD</i> , lipoprotein PslD	49.77	/	38.29
<i>PSPTO_3532</i>	<i>pslE</i> , exopolysaccharide biosynthesis PslE	55.35	/	43.74
<i>PSPTO_3533</i>	<i>pslF</i> , glycosyl transferase PslF	36.21	/	34.33
<i>PSPTO_3534</i>	<i>pslG</i> , glycosyl hydrolase, family 5 PslG	20.75	/	17.78
<i>PSPTO_3535</i>	<i>pslH</i> , glycosyl transferase PslH	25.99	/	23.63
<i>PSPTO_3536</i>	<i>pslI</i> , glycosyl transferase PslI	31.85	/	26.82
<i>PSPTO_3537</i>	<i>pslJ</i> , membrane protein PslJ	22.25	/	20.75
<i>PSPTO_3539</i>	<i>pslK</i> , membrane protein PslK	16.1	/	18.14
<b>Osmotic/Oxidative stress response</b>				
<i>PSPTO_0152</i>	<i>osmC</i> , osmotically inducible protein	4.81	/	3.77
<i>PSPTO_1338</i>	<i>sodC</i> , superoxide dismutase Cu-Zn	7.65	/	8.15
<i>PSPTO_4530</i>	<i>katG</i> , catalase/oxidase HPI	3.53	/	2.62
<i>PSPTO_5263</i>	<i>katE</i> , catalase	18.24	/	20.35

Differential expression in  $\Delta rsmA23$  versus *Pst*DC3000,  $\Delta rsmA23$  versus  $\Delta rsmA3$ , and  $\Delta rsmA3$  versus *Pst*DC3000 with fold change (FC)  $\geq 1.5$  or FC  $\leq -1.5$  and p-value  $< 0.05$ . /: non-differentially expressed genes (DEGs); HMM: *hrp*-inducing minimum medium; *Pst*DC3000: *Pseudomonas syringae* pv. *tomato* DC3000;  $\Delta rsmA3$ : the *rsmA3* mutant;  $\Delta rsmA23$ : the *rsmA2/A3* double mutant.

**Table S8. Fold changes of the chemotaxis genes in KB**

Locus tag	Description	$\Delta rsmA23$	$\Delta rsmA23$	$\Delta rsmA3$
		/ <i>PstDC3000</i>	/ <i>\Delta rsmA3</i>	/ <i>PstDC3000</i>
<b>Chemotaxis</b>				
<i>PSPTO_0117</i>	methyl-accepting chemotaxis protein	-5.45	-2.65	-2.05
<i>PSPTO_2480</i>	methyl-accepting chemotaxis protein	-4.84	-2.24	-2.16
<i>PSPTO_2511</i>	methyl-accepting chemotaxis protein	-5.29	-2.48	-2.13
<i>PSPTO_2616</i>	methyl-accepting chemotaxis protein	-5.2	-2.78	-1.87
<i>PSPTO_3680</i>	methyl-accepting chemotaxis protein	-5.07	-2.41	-2.11
<i>PSPTO_1323</i>	chemotaxis protein CheV	-2.92	-2.15	/
<i>PSPTO_1334</i>	methyl-accepting chemotaxis protein	-4.62	-3.05	/
<i>PSPTO_1495</i>	chemotaxis protein methyltransferase CheR	-2.62	-1.95	/
<i>PSPTO_1496</i>	chemotaxis protein CheW	-2.72	-2.22	/
<i>PSPTO_2441</i>	methyl-accepting chemotaxis protein	-2.59	-3.88	/
<i>PSPTO_2472</i>	methyl-accepting chemotaxis protein	-2.70	-2.28	/
<i>PSPTO_2475</i>	methyl-accepting chemotaxis protein	-1.99	-2.20	/
<i>PSPTO_2883</i>	methyl-accepting chemotaxis protein	-3.44	-2.31	/
<i>PSPTO_3237</i>	methyl-accepting chemotaxis protein	-3.65	-2.27	/
<i>PSPTO_3379</i>	methyl-accepting chemotaxis protein	-1.96	-1.85	/
<i>PSPTO_3480</i>	methyl-accepting chemotaxis protein	-2.30	-2.46	/
<i>PSPTO_3524</i>	chemotaxis protein CheV	-3.03	-2.04	/
<i>PSPTO_3577</i>	methyl-accepting chemotaxis protein	-2.67	-2.13	/
<i>PSPTO_3699</i>	methyl-accepting chemotaxis protein	-3.03	-2.30	/
<i>PSPTO_0466</i>	methyl-accepting chemotaxis protein	-4.07	/	-3.41
<i>PSPTO_1927</i>	chemotaxis protein CheV	-3.15	/	-1.80
<i>PSPTO_1928</i>	chemotaxis protein methyltransferase CheR	-3.01	/	-1.89
<i>PSPTO_4531</i>	methyl-accepting chemotaxis protein	-13.83	/	-7.17
<i>PSPTO_5553</i>	methyl-accepting chemotaxis protein	-5.37	/	-2.70

Differential expression in  $\Delta rsmA23$  versus *PstDC3000*,  $\Delta rsmA23$  versus  $\Delta rsmA3$ , and  $\Delta rsmA3$  versus *PstDC3000* with fold change (FC)  $\geq 1.5$  or  $FC \leq -1.5$  and p-value  $< 0.05$ . /: non-differentially expressed genes (DEGs); KB: King's B medium; *PstDC3000*: *Pseudomonas syringae* pv. *tomato* DC3000;  $\Delta rsmA3$ : the *rsmA3* mutant;  $\Delta rsmA23$ : the *rsmA2/A3* double mutant.

**Table S9. Fold changes of the ribosome genes in KB**

Locus tag	Description	$\Delta rsmA23$	$\Delta rsmA23$	$\Delta rsmA3$
		/ <i>PstDC3000</i>	/ <i>\Delta rsmA3</i>	/ <i>PstDC3000</i>
<b>Ribosome proteins</b>				
<i>PSPTO_0615</i>	<i>rplK</i> , 50S ribosomal protein L11	-1.9	1.79	-3.4
<i>PSPTO_0616</i>	<i>rplA</i> , 50S ribosomal protein L1	-1.94	1.87	-3.62
<i>PSPTO_0617</i>	<i>rplJ</i> , 50S ribosomal protein L10	-2.34	2.38	-5.58
<i>PSPTO_0618</i>	<i>rplL</i> , 50S ribosomal protein L7/L12	-2.29	2.88	-6.58
<i>PSPTO_0627</i>	<i>rplD</i> , 50S ribosomal protein L4	-1.77	2.15	-3.81

<i>PSPTO_0628</i>	<i>rplW</i> , 50S ribosomal protein L23	<b>-1.89</b>	<b>2.01</b>	<b>-3.78</b>
<i>PSPTO_0644</i>	<i>rpmD</i> , 50S ribosomal protein L30	<b>-1.81</b>	<b>2.47</b>	<b>-4.46</b>
<i>PSPTO_0648</i>	<i>rpsM</i> , 30S ribosomal protein S13	<b>-1.76</b>	<b>2.33</b>	<b>-4.1</b>
<i>PSPTO_0650</i>	<i>rpsD</i> , 30S ribosomal protein S4	<b>-1.79</b>	<b>2.29</b>	<b>-4.1</b>
<i>PSPTO_0652</i>	<i>rplQ</i> , 50S ribosomal protein L17	<b>-1.91</b>	<b>2.69</b>	<b>-5.13</b>
<i>PSPTO_0797</i>	<i>rplU</i> , 50S ribosomal protein L21	<b>-1.85</b>	<b>1.86</b>	<b>-3.43</b>
<i>PSPTO_0798</i>	<i>rpmA</i> , 50S ribosomal protein L27	<b>-1.78</b>	<b>2.01</b>	<b>-3.58</b>
<i>PSPTO_0619</i>	<i>rpoB</i> , RNA polymerase subunit beta	/	<b>3.25</b>	<b>-5.83</b>
<i>PSPTO_0621</i>	<i>rpsL</i> , 30S ribosomal protein S12	/	<b>1.74</b>	<b>-2.79</b>
<i>PSPTO_0622</i>	<i>rpsG</i> , 30S ribosomal protein S7	/	<b>1.91</b>	<b>-3.18</b>
<i>PSPTO_0625</i>	<i>rpsJ</i> , 30S ribosomal protein S10	/	<b>1.83</b>	<b>-3.07</b>
<i>PSPTO_0626</i>	<i>rplC</i> , 50S ribosomal protein L3	/	<b>1.98</b>	<b>-3.44</b>
<i>PSPTO_0629</i>	<i>rplB</i> , 50S ribosomal protein L2	/	<b>2.11</b>	<b>-3.34</b>
<i>PSPTO_0630</i>	<i>rpsS</i> , 30S ribosomal protein S19	/	<b>2.08</b>	<b>-3.63</b>
<i>PSPTO_0631</i>	<i>rplV</i> , 50S ribosomal protein L22	/	<b>2.14</b>	<b>-3.65</b>
<i>PSPTO_0632</i>	<i>rpsC</i> , 30S ribosomal protein S3	/	<b>2.43</b>	<b>-3.67</b>
<i>PSPTO_0633</i>	<i>rplP</i> , 50S ribosomal protein L16	/	<b>2.73</b>	<b>-4.1</b>
<i>PSPTO_0634</i>	<i>rpmC</i> , 50S ribosomal protein L29	/	<b>3.13</b>	<b>-4.63</b>
<i>PSPTO_0635</i>	<i>rpsQ</i> , 30S ribosomal protein S17	/	<b>3.21</b>	<b>-4.94</b>
<i>PSPTO_0636</i>	<i>rplN</i> , 50S ribosomal protein L14	/	<b>3.23</b>	<b>-5.04</b>
<i>PSPTO_0637</i>	<i>rplX</i> , 50S ribosomal protein L24	/	<b>3.18</b>	<b>-4.98</b>
<i>PSPTO_0638</i>	<i>rplE</i> , 50S ribosomal protein L5	/	<b>3.28</b>	<b>-5.92</b>
<i>PSPTO_0639</i>	<i>rpsN</i> , 30S ribosomal protein S14	/	<b>2.93</b>	<b>-5.13</b>
<i>PSPTO_0640</i>	<i>rpsH</i> , 30S ribosomal protein S8	/	<b>2.11</b>	<b>-3.52</b>
<i>PSPTO_0641</i>	<i>rplF</i> , 50S ribosomal protein L6	/	<b>2.32</b>	<b>-3.73</b>
<i>PSPTO_0642</i>	<i>rplR</i> , 50S ribosomal protein L18	/	<b>2.44</b>	<b>-3.75</b>
<i>PSPTO_0643</i>	<i>rpsE</i> , 30S ribosomal protein S5	/	<b>2.54</b>	<b>-3.98</b>
<i>PSPTO_0645</i>	<i>rplO</i> , 50S ribosomal protein L15	/	<b>2.52</b>	<b>-4.34</b>
<i>PSPTO_0647</i>	<i>rpmJ</i> , 50S ribosomal protein L36	/	<b>2.65</b>	<b>-4.68</b>
<i>PSPTO_0649</i>	<i>rpsK</i> , 30S ribosomal protein S11	/	<b>2.34</b>	<b>-4.21</b>
<i>PSPTO_1473</i>	<i>rpsP</i> , 30S ribosomal protein S16	/	<b>1.82</b>	<b>-2.99</b>
<i>PSPTO_1476</i>	<i>rplS</i> , 50S ribosomal protein L19	/	<b>2.22</b>	<b>-3.76</b>
<i>PSPTO_4930</i>	<i>rplI</i> , 50S ribosomal protein L9	/	<b>2.64</b>	<b>-4.4</b>
<i>PSPTO_4932</i>	<i>rpsR</i> , 30S ribosomal protein S18	/	<b>2.29</b>	<b>-3.98</b>
<i>PSPTO_4933</i>	<i>rpsF</i> , 30S ribosomal protein S6	/	<b>2.16</b>	<b>-3.75</b>

Differential expression in  $\Delta rsmA23$  versus *Pst*DC3000,  $\Delta rsmA23$  versus  $\Delta rsmA3$ , and  $\Delta rsmA3$  versus *Pst*DC3000 with fold change (FC) $\geq$ 1.5 or FC $\leq$ -1.5 and p-value <0.05. /: non-differentially expressed genes (DEGs); KB: King's B medium; *Pst*DC3000: *Pseudomonas syringae* pv. *tomato* DC3000;  $\Delta rsmA3$ : the *rsmA3* mutant;  $\Delta rsmA23$ : the *rsmA2/3* double mutant.

**Table S10. Selected genes regulated mainly by RsmA2 in KB**

Locus tag	Description	$\Delta rsmA23$	$\Delta rsmA23$	$\Delta rsmA3$
		/ <i>Pst</i> DC3000	/ $\Delta rsmA3$	/ <i>Pst</i> DC3000
<b>Positive regulated by RsmA2</b>				
<b>Capsular polysaccharide</b>				
<i>PSPTO_3529</i>	<i>pslA</i> , capsular polysaccharide biosynthesis protein PslA	-3.03	-2.27	/
<i>PSPTO_3530</i>	<i>pslB</i> , mannose-6-phosphate isomerase PslB	-2.5	-2.37	/
<i>PSPTO_3531</i>	<i>pslD</i> , lipoprotein <i>PslD</i>	-2.54	-2.94	/
<b>Mannitol metabolism</b>				
<i>PSPTO_2703</i>	<i>uxuB</i> , D-mannonate oxidoreductase	-3.76	-3.84	/
<i>PSPTO_2705</i>	mannitol ABC transporter permease	-3.94	-2.47	/
<i>PSPTO_2706</i>	mannitol ABC transporter permease	-4.73	-3.02	/
<i>PSPTO_2707</i>	mannitol ABC transporter	-2.83	-2.53	/
<b>Negatively regulated by RsmA2</b>				
<b>Alginate biosynthesis</b>				
<i>PSPTO_1232</i>	<i>algA</i> , alginate biosynthesis protein AlgA	3.11	2.38	/
<i>PSPTO_1236</i>	<i>algL</i> , alginate lyase	2.83	2.3	/
<i>PSPTO_1237</i>	<i>algX</i> , alginate biosynthesis protein AlgX	2.24	3.21	/
<i>PSPTO_1238</i>	<i>algG</i> , alginate biosynthesis protein AlgG	2.8	5.14	/
<i>PSPTO_1239</i>	<i>algE</i> , alginate biosynthesis protein AlgE	5.73	8.14	/
<i>PSPTO_1240</i>	<i>algK</i> , alginate biosynthesis protein AlgK	8.21	8.08	/
<i>PSPTO_1241</i>	<i>alg44</i> , alginate biosynthesis protein Alg44	8.14	3.98	/
<b>Phosphate regulation</b>				
<i>PSPTO_5477</i>	<i>phoB</i> , phosphate regulon transcriptional regulatory protein PhoB	6.19	6.65	/
<i>PSPTO_5478</i>	<i>phoR</i> , phosphate regulon sensor protein phoR	4.24	5.6	/
<i>PSPTO_5486</i>	phosphate ABC transporter permease	4.09	5	/
<i>PSPTO_5487</i>	phosphate ABC transporter substrate-binding protein	9.75	7.63	/

Differential expression in  $\Delta rsmA23$  versus *Pst*DC3000,  $\Delta rsmA23$  versus  $\Delta rsmA3$ , and  $\Delta rsmA3$  versus *Pst*DC3000 with fold change (FC) $\geq$ 1.5 or FC $\leq$ -1.5 and p-value <0.05. /: non-differentially expressed genes (DEGs); KB: King's B medium; *Pst*DC3000: *Pseudomonas syringae* pv. *tomato* DC3000;  $\Delta rsmA3$ : the *rsmA3* mutant;  $\Delta rsmA23$ : the *rsmA2/A3* double mutant.



**Table S11. Selected genes regulated mainly by RsmA3 in KB**

Locus tag	Gene description	$\Delta$ rsmA23	$\Delta$ rsmA23	$\Delta$ rsmA3
		/PstDC3000	/PstDC3000	/PstDC3000
<b>Positive regulated by RsmA3</b>				
<b>Fatty acid Biosynthesis /Degradation</b>				
PSPTO_3832	<i>fabG</i> , 3-ketoacyl-(acyl-carrier-protein) reductase	-1.94	/	-3.42
PSPTO_3833	<i>fabD</i> , malonyl CoA-acyl carrier protein transacylase	-2.06	/	-3.14
PSPTO_5093	acyl carrier protein	-4.48	/	-4.34
PSPTO_5094	acyl carrier protein	-3.39	/	-3.48
PSPTO_3834	fatty acid/phospholipid synthesis protein	-2.38	/	-2.96
PSPTO_4860	<i>accB</i> , acetyl-CoA carboxylase, biotin carboxyl carrier protein	-1.74	/	-2.26
PSPTO_0500	acyl-CoA dehydrogenase family protein	2.65	/	1.99
PSPTO_1056	short chain dehydrogenase	3.85	/	3.77
PSPTO_3706	acyl-CoA dehydrogenase	4.23	/	4.80
PSPTO_3857	acyl-CoA dehydrogenase	3.93	/	3.10
<b>Cellulose biosynthesis</b>				
PSPTO_1026	<i>wssA</i> , cell morphology protein	-2.52	/	-2.55
PSPTO_1027	<i>wssB</i> , cellulose synthase, catalytic subunit	-2.04	/	-4.49
PSPTO_1029	<i>wssD</i> , endoglucanase	-2.34	/	-4.47
<b>Two-component system</b>				
PSPTO_4373	<i>colS</i> , sensor histidine kinase ColS	-1.89	/	-2.24
PSPTO_4374	<i>colR</i> , DNA-binding response regulator ColR	-1.78	/	-1.48
<b>Negatively regulated by RsmA3</b>				
<b>Signal transduction</b>				
PSPTO_0073	<i>spoT</i> , guanosine-3',5'-bis(diphosphate),3'-pyrophosphohydrolase	-2.09	/	-2.12
PSPTO_0856	<i>fpRel</i> , hypothetical protein	2.41	/	2.67
PSPTO_3863	<i>psyR</i> , transcriptional regulator PsyR	1.81	/	2.18
PSPTO_3864	<i>psyI</i> , autoinducer synthesis protein PsyI	12.81	/	15.37
<b>Type VI secretion system</b>				
PSPTO_0373	Rhs family protein	3.08	/	3.63
PSPTO_4385	Rhs element Vgr protein	2.42	/	3.04
PSPTO_5435	<i>hcp-2</i> , secreted protein Hcp	3.83	/	4.08
PSPTO_5436	Rhs element Vgr protein	5.38	/	4.1
PSPTO_5438	Rhs family protein	2.11	/	1.71
<b>Syringafactin biosynthesis</b>				
PSPTO_2828	<i>syrR</i> , transcriptional regulator SyrR	5.02	-1.96	9.82
PSPTO_2829	<i>syfA</i> , non-ribosomal peptide synthetase	4.70	/	7.98
<b>Alginate biosynthesis</b>				
PSPTO_1234	<i>algJ</i> , alginate biosynthesis protein AlgJ	5.13	/	3.83

<i>PSPTO_1235</i>	<i>algI</i> , alginate biosynthesis protein AlgI	<b>4.8</b>	/	<b>3.04</b>
<i>PSPTO_1242</i>	<i>alg8</i> , alginate biosynthesis protein Alg8	<b>6.51</b>	/	<b>3.71</b>
<b>Capsular polysaccharide</b>				
<i>PSPTO_3536</i>	<i>psII</i> , glycosyl transferase PsII	<b>3.08</b>	/	<b>2.56</b>
<i>PSPTO_3537</i>	<i>psIJ</i> , membrane protein PsIJ	<b>3.29</b>	/	<b>2.64</b>
<b>Osmotic and oxidative stress response</b>				
<i>PSPTO_0152</i>	<i>osmC</i> , osmotically inducible protein	<b>1.89</b>	/	<b>2</b>
<i>PSPTO_1338</i>	<i>sodC</i> , superoxide dismutase, Cu-Zn	<b>2.45</b>	/	<b>2.29</b>
<i>PSPTO_3582</i>	<i>katB</i> , catalase	<b>4.31</b>	/	<b>4.38</b>
<i>PSPTO_5263</i>	<i>katE</i> , catalase	<b>8.28</b>	/	<b>8.56</b>

Differential expression in  $\Delta rsmA23$  versus *Pst*DC3000,  $\Delta rsmA23$  versus  $\Delta rsmA3$ , and  $\Delta rsmA3$  versus *Pst*DC3000 with fold change (FC)  $\geq 1.5$  or  $\text{FC} \leq -1.5$  and p-value  $< 0.05$ . /: non-differentially expressed genes (DEGs); KB: King's B medium; *Pst*DC3000: *Pseudomonas syringae* pv. *tomato* DC3000;  $\Delta rsmA3$ : the *rsmA3* mutant;  $\Delta rsmA23$ : the *rsmA2/A3* double mutant.