

SAV4189, a MarR-family Regulator in *Streptomyces avermitilis*, Activates Avermectin Biosynthesis

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Supplementary Figures:

FIGURE S1: Schematic methods for deletion of *sav_4189* (A) and *sav_4190* (B).

FIGURE S2: Confirmation of transcriptional unit *sav_4189-sav_4190* by RT-PCR.

FIGURE S3: Amino acid sequence alignment of SAV4189 and its homologs in eight *Streptomyces* species.

FIGURE S4: Effects of *sav_4189* deletion and overexpression on morphological differentiation.

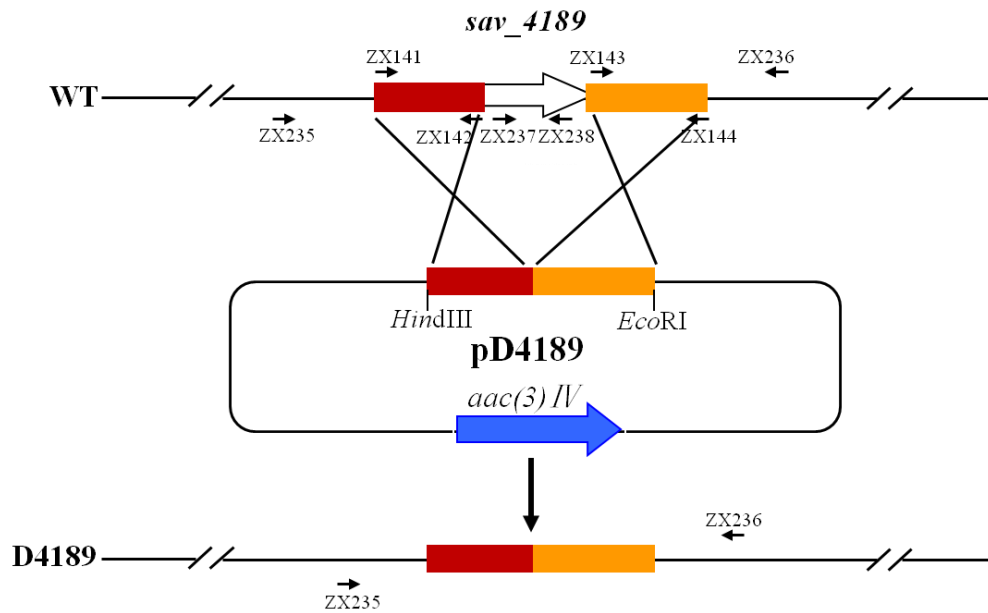
Supplementary Tables:

TABLE S1: Primers used in this study.

TABLE S2: Putative targets of SAV4189.

FIGURE S1

A



B

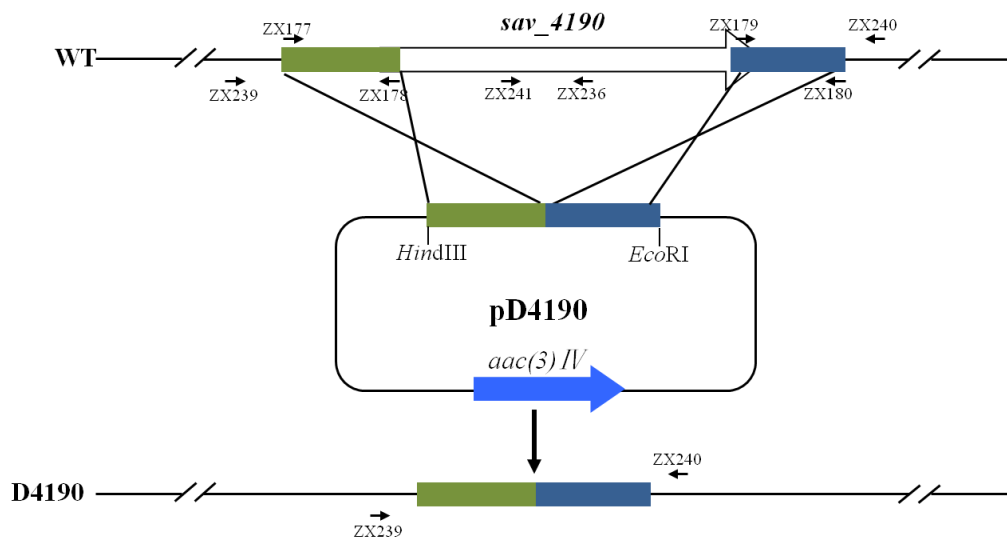


FIGURE S1 | Schematic methods for deletion of *sav_4189* (A) and *sav_4190* (B).

Large arrows: genes and their directions. Small arrows: positions of primers used for amplifying exchange regions and confirming gene deletions. Blocks: homologous exchange regions used for gene deletions.

FIGURE S2

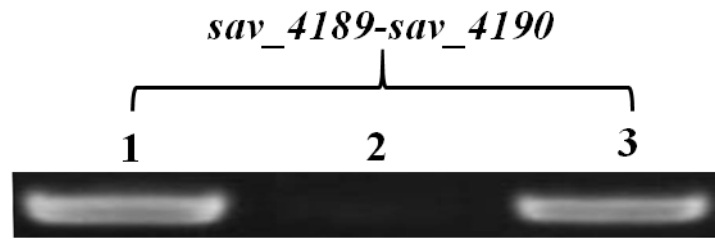


FIGURE S2 | Confirmation of transcriptional unit *sav_4189-sav_4190* by RT-PCR. Lane 1: positive control with WT genomic DNA as template. Lane 2: negative control with WT RNAs (reverse transcriptase omitted) as template. Lane 3: RT-PCR analysis. Primers used for amplifying *sav_4189-sav_4190* intergenic region were ZX226 and ZX227.

FIGURE S3

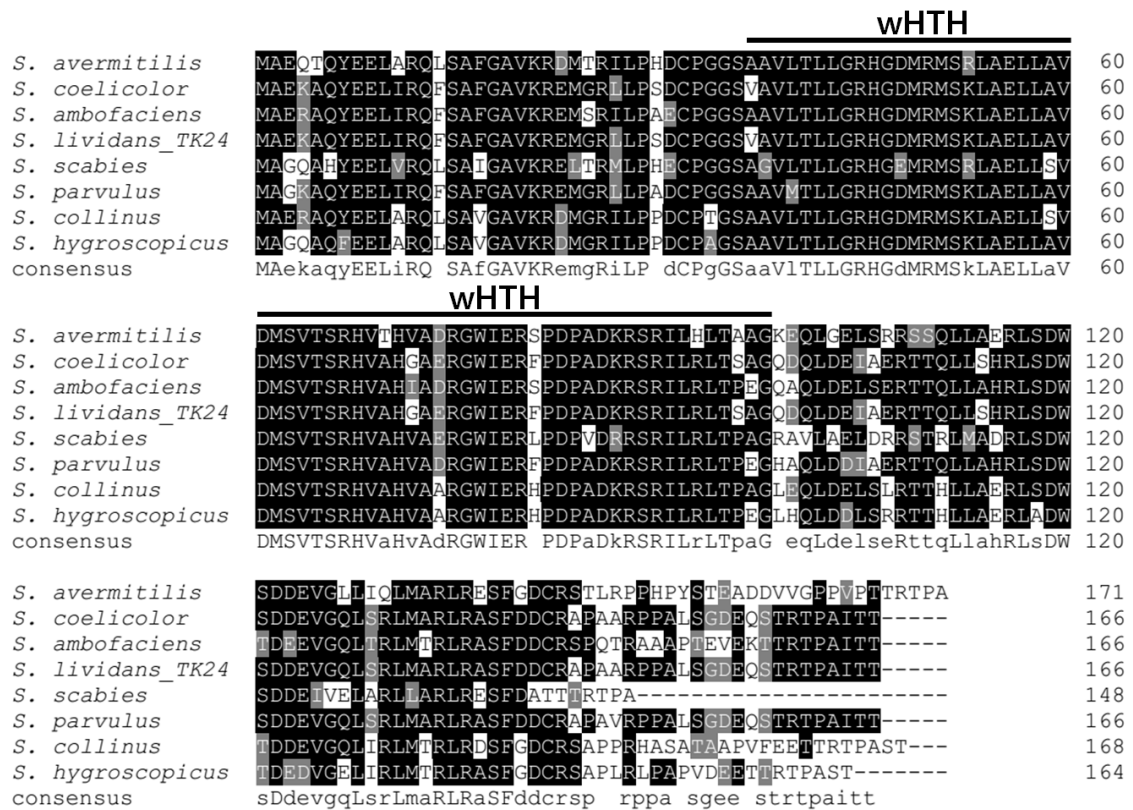


FIGURE S3 | Amino acid sequence alignment of SAV4189 and its homologs in eight *Streptomyces* species. *S. avermitilis* SAV4189 showed high identity with its homologs in the other species, as follows: *S. coelicolor* (77%), *S. ambofaciens* (79%), *S. lividans* (77%), *S. scabies* (72%), *S. parvulus* (77%), *S. collinus* (80%), *S. hygroscopicus* (77%). Black line at top: wHTH domain.

FIGURE S4

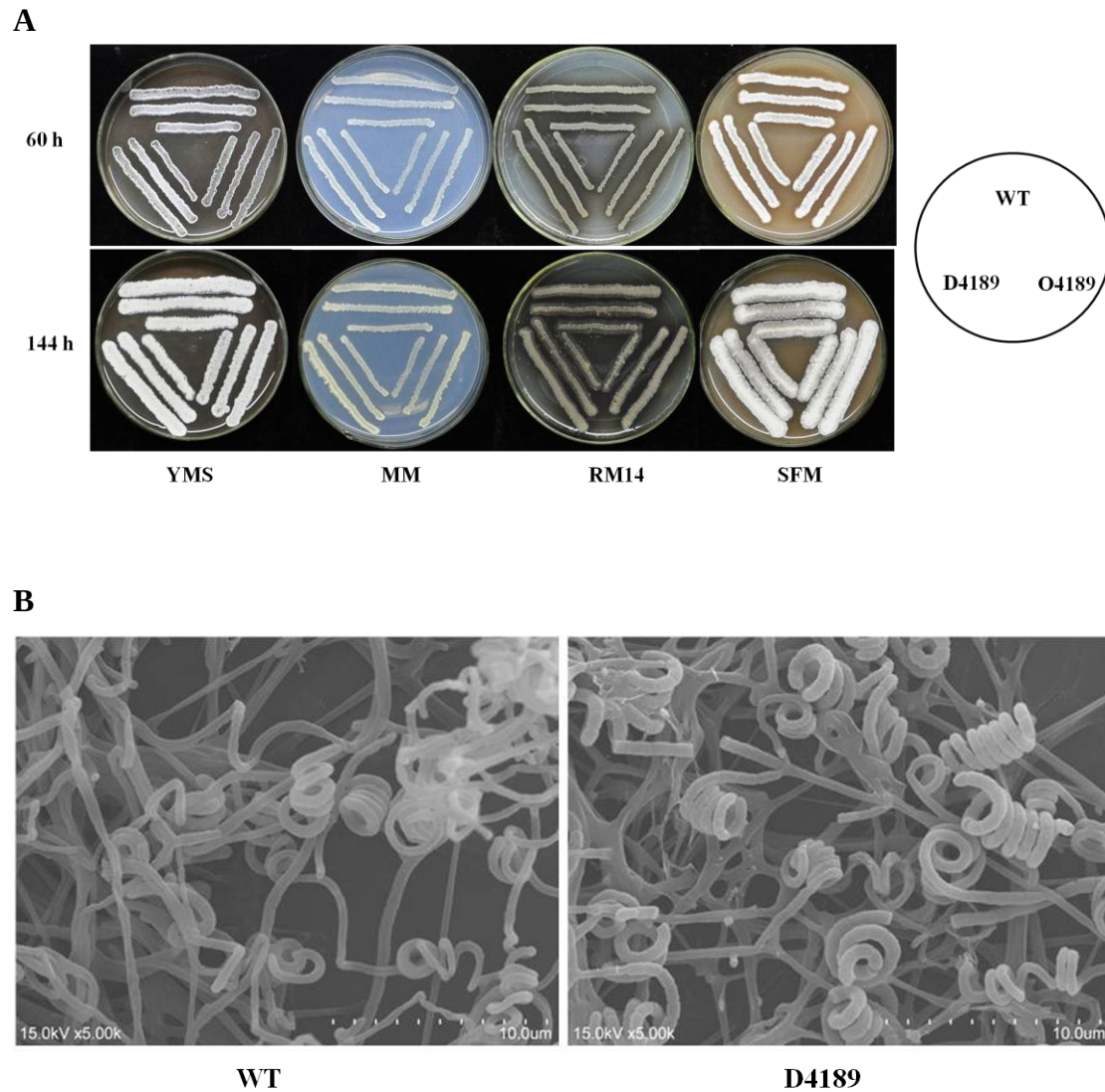


FIGURE S4 | Effects of *sav_4189* deletion and overexpression on morphological differentiation. (A) Phenotypes of WT, *sav_4189* deletion mutant (D4189), and *sav_4189* overexpression strain (O4189) grown on YMS, MM, RM14, and SFM plates at 28 °C. **(B)** SEM images showing aerial hyphae and spores of WT and D4189 grown on SFM for 4 d.

TABLE S1 | Primers used in this study.

Primer purpose/ primer	DNA sequence (5'-3')	Use
Gene deletion, complementation, and overexpression		
ZX141	CTGA <u>AAGCTT</u> ACGAAGGCACGGAACATCT, <i>HindIII</i>	Deletion of <i>sav_4189</i>
ZX142	GTGTCTTATGCGGGTGTACGCTGGTCACCGACATGTCCAC	
ZX143	GTGGACATGTCGGTGACCAGCGTACACCCGCATAAGACAC	
ZX144	GCTGA <u>AATTC</u> CCGAGGTAGCCGGAGTAAC, <i>EcoRI</i>	
ZX235	GACGATGCCGACGATCAG	Confirmation of <i>sav_4189</i>
ZX236	GTAGGTCTGCCACGAGATCC	deletion in D4189
ZX237	GACGCAGTACGAGGAACTGG	
ZX238	ATGAGCTGGATGAGCAGACC	
ZX149	ACATG <u>CATGCG</u> CAACGAATACGGGAGGTG, <i>SphI</i>	Complementation of
ZX150	GCT <u>CTAGAG</u> TGCTTGCGTGAGAGCC, <i>XbaI</i>	<i>sav_4189</i> in D4189 and overexpression of <i>sav_4189</i> in <i>Streptomyces</i>
ZX177	CTGA <u>AAGCTT</u> TGTGAAGCGGGACATGACG, <i>HindIII</i>	Deletion of <i>sav_4190</i>
ZX178	GGTGTACTCGCCGCTGTCTGAGAGGGCCTCCATGATCT	
ZX179	AGATCATGGAGGCCCTCTCGACAGCGGCGAGTACACC	
ZX180	GCTGA <u>AATTC</u> GGAGATCCCCAGGTGCTG, <i>EcoRI</i>	
ZX239	TAAGCAACGAATACGGGAGGT	Confirmation of <i>sav_4190</i>
ZX240	ATAGGTGATCTGCGGGTACG	deletion in D4190
ZX241	TCCAGATAGCCCTCGTCATC	
ZX236	GTAGGTCTGCCACGAGATCC	
ZX205	AACC <u>CATATG</u> CCCGAGCAGACGCAG, <i>NdeI</i>	Overexpression of
ZX206	GCTGA <u>AATTC</u> CGTGAGAGCCCCGCACAC, <i>EcoRI</i>	His ₆ -SAV4189 in <i>E. coli</i>
EMSAs		
YQ1	GCCTGGTCCTCCGAACTCC	Probe <i>aveRp</i>
YQ2	GGTGCAGACAGGAACTCCCT	
ZX73	CGACCGCTCCTGACCTCC	Probe <i>4189p</i>
ZX74	CATCACACCTCCCGTATTCTG	
GJ91	CCAAGGGCTACAAGTTCTCC	Probe <i>hrdB</i>
GJ92	TTGATGACCTCGACCATGTG	
ZX63	GTACGCCACCTGGTGGTGCCAATACTTGCCTTT GCCAAGTTTTGCCATGGCCGACCAGG	Probe A
ZX64	CCTGGTCGGCCATGGCAAACTTGCAAAGG CAAGTATTGGCACCACCAGGTGGCGTAC	
ZX61	CACGTACGCCACCTGGTGGTAGTTTGCTGCGGC AACCAAGCCATGGCCGACCAGGCC	Probe B1
ZX62	GGGCCTGGTCGGCCATGGCTTGTTGCCGCAGGC AAACTACCACCAGGTGGCGTACGTG	
ZX65	CACGTACGCCACCTGGTGGATGGTTGCCCTA	Probe B2

	AGCAACGAAGCCATGGCCGACCAGGCC	
ZX66	GGGCCTGGTCGGCCATGGCTTCGTTGCTTA GGGCAACCATCCACCAGGTGGCGTACGTG	
ZX243	TCGGTCAGCCTTGCGTAG	Probe 2073p
ZX244	TCCGGACTTGACTGATCT	
ZX245	AATTGCTGGCCGAAGCCC	Probe <i>olmRII</i> p
ZX246	CGAGGACCACACCGCCTT	
ZX247	GACGATCTCACCCGCACC	Probe 5653p
ZX248	CCTTCCGTTTCATGCACAC	
ZX249	GTCCTAAACGAGCCATCTACC	Probe <i>pks1-3</i> p
ZX250	GCATCGGATTCTGTGTG	
ZX251	CGGACGATCAGGAGGGTC	Probe <i>aspB1</i> p
ZX252	GACTGCCGGAACCTCCATG	
ZX253	TGACCCCTCCCGCCACTTC	Probe <i>ectAp</i>
ZX254	GCGTCGATAACCCCCATTTTGTC	
ZX255	CGAAGGACTGACGTTTTTC	Probe <i>add4</i> p
ZX256	GTACGTGCTCCATTCCAG	
ZX257	TGTGGTTCGAGCTGGCGG	Probe <i>prpM3</i> p
ZX258	ACATACTCCCAGTCTTCTA	
ZX259	GATCAACGTTGCCAAGGC	Probe <i>savR1</i> p
ZX260	GACGACTCATATGCGGCA	
ZX261	ACGGACAGCGGGGCGGACAT	Probe <i>hmuOp</i>
ZX262	TCATGGGATCTCCGGTGC	
ZX263	GATGTCGTCGAACTCGTC	Probe 1959p
ZX264	TCTTGCGTGCGTGTCCTCA	
ZX265	GTCAACTCTCGGTGCTTC	Probe <i>xylF</i> p
ZX266	CGTGTTCACTTCAGAAAC	
ZX267	CGTGCGTTCGATGTTGCT	Probe <i>ngcEp</i>
ZX268	AAGTCCTCGCCTTCTCCA	
ZX269	TGCCATACGTTGAATATGT	Probe <i>ccrA2</i> p
ZX270	CGTCCAGGATTTCCTTCAC	
DNase I footprinting assay		
FAM-89footS	ACGAAGGCACGGAACATCT	<i>sav_4189</i> promoter region
89footAS	CTGGTCACCGACATGTCCAC	
qRT-PCR		
GJ97	CAGAAGAACTCACGCTCGTC	<i>aveR</i> ORF
GJ98	ACTCTTTCCACAGCCCATTTC	
ZX9	GAATACGGGAGGTGTGATGG	<i>sav_4189</i> ORF
ZX10	CGTCATGTCCCGCTTCAC	
ZX11	GGATCTCGTGGCAGACCTAC	<i>sav_4190</i> ORF
ZX12	ATGGAGGAGAGGGTGATGGT	
RT-PCR		
ZX226	AGGTCGGTCTGCTCATCCAG	Amplification of
ZX227	GCCGATCCCAGCACATAGAT	<i>sav_4189-sav_4190</i>

		intergenic region
5' RACE analysis		
4189SP1	GGCGAGCAGCTCGGCGAG	Determination of <i>sav_4189</i>
4189SP2	CCTGCTCATCCGCATGTC	TSS
4189SP3	GAGCAGCGTGAGCACGGC	
Oligo (dT)	GACCACGCGTATCGATGTCGACTTTTTTTTTTTTTTV	
anchor primer		
Anchor	GACCACGCGTATCGATGTCGAC	
primer		

TABLE S2 | Putative targets of SAV4189.

#	Accession number	Gene	Function	Score
Regulatory function (49)				
1	SAV_82		putative TetR-family transcriptional regulator	7.7
2	SAV_86		putative erythropoiesis-stimulating protein	8.6
3	SAV_146		putative TetR-family transcriptional regulator	7.6
4	SAV_151		putative TetR-family transcriptional regulator	8.2
5	SAV_431		putative TetR-family transcriptional regulator	7
6	SAV_458	<i>hspR18_1</i>	putative hsp18 transcriptional regulator	7.1
7	SAV_520		putative transcriptional regulator	10.3
8	SAV_537		putative Sir2-family regulator protein	8
9	SAV_554		putative LacI-family transcriptional regulator	7.3
10	SAV_566		putative TetR-family transcriptional regulator	8.3
11	SAV_663	<i>sig6</i>	putative RNA polymerase ECF-subfamily sigma factor	7.3
12	SAV_729		putative LysR-family transcriptional regulator	7.4
13	SAV_1087	<i>sig14</i>	putative RNA polymerase sigma factor	7.6
14	SAV_1091		putative anti-sigma factor antagonist	7.1
15	SAV_1252	<i>cvnA1</i>	putative sensor-like histidine kinase	7.4
16	SAV_1362		putative transcriptional regulator	7.6
17	SAV_1612		putative two-component system response regulator	9.3
18	SAV_1644		putative regulatory protein	7.8
19	SAV_1984		putative GntR-family transcriptional regulator	7.1
20	SAV_2007		putative transcriptional regulator	9.6
21	SAV_2073		putative GntR-family transcriptional regulator	9.8
22	SAV_2301		putative regulatory protein	7
23	SAV_2652		putative regulatory protein	8
24	SAV_2689		putative MerR-family transcriptional regulator	8
25	SAV_2901	<i>olmRII</i>	LuxR-family transcriptional regulator	8.4
26	SAV_2914		putative transcriptional regulator	7
27	SAV_3053	<i>catR</i>	putative hydrogen peroxide sensitive repressor	7.3
28	SAV_3481		putative two-component system response regulator	7.1
29	SAV_3631		putative two-component system sensor kinase	7.4
30	SAV_3632		putative regulatory protein	7.4
31	SAV_3970		putative CarD-like transcriptional regulator	7.6
32	SAV_4130	<i>bldC</i>	putative MerR-family transcriptional regulator	7.1
33	SAV_4189		putative MarR-family transcriptional regulator	13.9
34	SAV_4328		putative regulatory protein	8.4
35	SAV_4361		putative AsnC-family transcriptional regulator	7.2
36	SAV_4735	<i>bds</i>	putative RNA polymerase ECF-subfamily sigma factor (BldN)	7.4
37	SAV_4758		putative transcriptional regulator	7.6
38	SAV_5006	<i>pkn19</i>	putative serine/threonine protein kinase	8
39	SAV_5013		putative DNA-binding protein	9.9

40	SAV_5014		putative regulatory protein	9.9
41	SAV_5068		putative two-component system response regulator	7.4
42	SAV_5220		putative GntR-family transcriptional regulator	7.4
43	SAV_5333		putative TetR-family transcriptional regulator	7.3
44	SAV_5653		putative ROK-family transcriptional regulator	11.1
45	SAV_5974		putative LysR-family transcriptional regulator	8.2
46	SAV_6131		putative DNA-binding protein	8
47	SAV_6889		putative sensor-like histidine kinase	8.8
48	SAV_6954		putative IclR-family transcriptional regulator	7.6
49	SAV_7270		putative LacI-family transcriptional regulator	8.2
Secondary metabolism (1)				
50	SAV_7362	<i>pks1-3</i>	putative modular polyketide synthase	7.3
Metabolism of amino acids and related molecules (6)				
51	SAV_2008	<i>aspB1</i>	putative aspartate aminotransferase	9.6
52	SAV_2111	<i>mmuM</i>	putative homocysteine S-methyltransferase	7
53	SAV_4243	<i>pheA</i>	putative prephenate dehydratase	7.8
54	SAV_4244	<i>serS1</i>	putative seryl-tRNA synthetase	8.4
55	SAV_5075	<i>gdhA1</i>	putative NAD-specific glutamate dehydrogenase	7.1
56	SAV_5451	<i>valS</i>	putative valyl-tRNA synthetase	9.1
Carbohydrate metabolism (15)				
57	SAV_887		putative glycosyl hydrolase, secreted	8.3
58	SAV_967		putative glycosyl hydrolase, secreted	8.5
59	SAV_1307	<i>dexA</i>	putative oligo glucosidase	7.6
60	SAV_1641	<i>agaB3</i>	putative alpha-galactosidase	7.8
61	SAV_1918	<i>glxK</i>	putative glycerate kinase	7.6
62	SAV_2024	<i>gip</i>	putative hydroxypyruvate isomerase	7.1
63	SAV_2258	<i>acnA</i>	putative aconitase	7.4
64	SAV_3533	<i>eno</i>	putative enolase	7
65	SAV_4362	<i>bkdA</i>	putative 3-methyl-2-oxobutanoate dehydrogenase	7.2
66	SAV_5359		putative glycosyltransferase	7.6
67	SAV_6398	<i>ectA</i>	diaminobutyrate acetyltransferase	9.3
68	SAV_6953	<i>adhA10</i>	putative alcohol dehydrogenase	9.4
69	SAV_7181	<i>xylB1</i>	xylulose kinase	7.1
70	SAV_7182	<i>xylA</i>	xylose isomerase	7.1
71	SAV_7442	<i>lamA2</i>	putative secreted glucanase	7.9
Fatty acid and lipid metabolism (5)				
72	SAV_524	<i>cdh</i>	putative CDP-diacylglycerol phosphatidylhydrolase	7.1
73	SAV_665	<i>fabG1</i>	putative 3-oxoacyl-ACP reductase	7.6
74	SAV_1831	<i>fabH2</i>	putative 3-oxoacyl-ACP synthase III	7.1
75	SAV_1911	<i>ccrA2</i>	putative crotonyl-CoA reductase	8
76	SAV_7008	<i>fabG8</i>	putative 3-oxoacyl-ACP reductase	7.3
Nucleotide metabolism (3)				
77	SAV_404	<i>pntA</i>	putative pyridine nucleotide transhydrogenase alpha subunit	7.3

78	SAV_4906	<i>add4</i>	putative adenosine deaminase	9.1
79	SAV_6662	<i>mtnK</i>	putative 5-methylthioribose kinase	7.6
Protein synthesis, folding, and modification (10)				
80	SAV_1000	<i>sprC</i>	putative streptogrisin C (secreted serine protease)	8.4
81	SAV_1128	<i>zmp2</i>	putative griselysin (secreted neutral zinc metalloprotease)	7.4
82	SAV_1642	<i>ptpA2</i>	putative conventional protein tyrosine phosphatase	7.8
83	SAV_2764		putative metallopeptidase, secreted	8.8
84	SAV_3185	<i>prpM3</i>	putative magnesium or manganese-dependent protein phosphatase	9.7
85	SAV_3931	<i>groEL2</i>	putative class I heat-shock protein	7.1
86	SAV_4229	<i>prpB7</i>	putative magnesium or manganese-dependent protein phosphatase	7.2
87	SAV_4329	<i>ppiA</i>	putative peptidyl-prolyl cis-trans isomerase	8.4
88	SAV_5411	<i>pepG</i>	putative aminopeptidase G	7.5
89	SAV_6682	<i>prcA</i>	putative 20S proteasome alpha-subunit	7.4
DNA synthesis, repair, recombination, modification, and packaging (5)				
90	SAV_2928		putative DNA repair helicase	7.6
91	SAV_3309	<i>savR1</i>	putative Mrr restriction system protein	9.5
92	SAV_3728	<i>int8</i>	putative tyrosine-family recombinase/integrase	7.4
93	SAV_5202		putative ATP-dependent helicase	9.5
94	SAV_6833	<i>ruvC</i>	putative Holliday junction nuclease	8.2
RNA synthesis and modification (1)				
95	SAV_2475	<i>miaA</i>	putative delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase	8.2
Membrane bioenergetics (1)				
96	SAV_589		putative F420-dependent dehydrogenase	7.3
Metabolism of cofactors and vitamins (4)				
97	SAV_412	<i>pteD</i>	cytochrome P450 hydroxylase	7.1
98	SAV_3517	<i>pobA</i>	putative p-hydroxybenzoate hydroxylase	8
99	SAV_5930	<i>hmuO</i>	putative heme oxygenase	10
100	SAV_7469	<i>cyp28</i>	cytochrome P450 hydroxylase	7.3
Detoxification and adaptation to atypical conditions (8)				
101	SAV_459	<i>hsp18_1</i>	putative heat shock protein	7.1
102	SAV_565	<i>bphC</i>	putative dihydroxybiphenyl dioxygenase	8.3
103	SAV_1959		putative acyl esterase, secreted	10.1
104	SAV_3052	<i>katA1</i>	putative catalase	7.3
105	SAV_3675	<i>pacB1</i>	putative penicillin acylase, secreted	7.5
106	SAV_3932	<i>cspB2</i>	putative cold shock protein	7.4
107	SAV_3947	<i>terD2</i>	putative tellurium resistance protein	7
108	SAV_4697	<i>clpC2</i>	putative ATP-dependent Clp protease	7.1
Cell wall and cell envelope (1)				
109	SAV_5913	<i>dacF</i>	putative D-alanyl-D-alanine carboxypeptidase	8.9
Cell division and differentiation (1)				
110	SAV_4664	<i>tilS</i>	putative tRNA(Ile)-lysine synthase	7.5

Transport and binding proteins (19)

111	SAV_145		putative membrane transport protein	7.6
112	SAV_610		putative MFS transporter protein	8
113	SAV_891		putative quaternary amine transporter	7.1
114	SAV_1508	<i>pbuX1</i>	putative xanthine/uracil permease	7.4
115	SAV_1558	<i>ssuC2</i>	putative ABC transporter permease protein	8.6
116	SAV_1560	<i>ssuA2</i>	putative ABC transporter substrate-binding protein	7.4
117	SAV_1828	<i>rbsA1</i>	putative simple sugar ABC transporter ATP-binding protein	9.1
118	SAV_2066		putative xanthine/uracil permease	7.3
119	SAV_2247	<i>xylF</i>	putative simple sugar ABC transporter substrate-binding protein	7.2
120	SAV_2251	<i>ngcE</i>	putative ABC transporter substrate-binding protein	9
121	SAV_3370		putative simple sugar ABC transporter substrate-binding protein	9.2
122	SAV_3482		putative di-tripeptide transporter	7.6
123	SAV_3676		putative sodium/proton antiporter	7.5
124	SAV_5175		putative osmoprotectant transporter	7.9
125	SAV_5912		putative ABC transporter permease protein	8.9
126	SAV_6276		putative integral membrane export protein	7.2
127	SAV_6665	<i>glpF1</i>	putative glycerol uptake facilitator protein	8.2
128	SAV_7200	<i>glpF3</i>	putative glycerol uptake facilitator protein	7.4
129	SAV_7271		putative multiple sugar ABC transporter substrate-binding protein	8.2

Gas vesicle (1)

130	SAV_599	<i>gvpO1</i>	putative gas vesicle synthesis protein	7.5
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Mobile and extrachromosomal element functions (5)

131	SAV_273		putative DNA invertase/recombinase	7.2
132	SAV_309		putative IS3 family ISVisp1-like transposase	7.3
133	SAV_3722		putative IS701 family ISAzvi8-like transposase	8.1
134	SAV_7545		putative ISL3 family ISFsp1-like transposase	7.3
135	SAV_7548		putative ISL3 family ISFsp1-like transposase	7.3

Unknown or unclassified genes (115)

136	SAV_14		putative membrane protein	8
137	SAV_83		hypothetical protein	7.7
138	SAV_87		hypothetical protein	8.6
139	SAV_152		putative dehydrogenase	8.2
140	SAV_164		hypothetical protein	7.1
141	SAV_169		hypothetical protein	7.4
142	SAV_304		hypothetical protein	8.3
143	SAV_305		putative membrane protein	8.3
144	SAV_307		hypothetical protein	7.1
145	SAV_362		putative secreted protein	10.7
146	SAV_432		putative secreted protein	7
147	SAV_493		putative secreted protein	8.8
148	SAV_506		hypothetical protein	7.2

149	SAV_521		putative secreted protein	10.3
150	SAV_536		hypothetical protein	8
151	SAV_539		hypothetical protein	8.2
152	SAV_553		hypothetical protein	7.3
153	SAV_649	<i>ard</i>	putative phosphotransferase	7.3
154	SAV_662		hypothetical protein	7.3
155	SAV_712		hypothetical protein	7.5
156	SAV_730		hypothetical protein	7.4
157	SAV_756		putative secreted protein	9.3
158	SAV_761		hypothetical protein	9.5
159	SAV_762		putative methyltransferase	9.5
160	SAV_777		hypothetical protein	7
161	SAV_866		hypothetical protein	10
162	SAV_886		hypothetical protein	8.3
163	SAV_892		hypothetical protein	7.4
164	SAV_902		hypothetical protein	7.8
165	SAV_999		putative carboxylase-amine ligase	7.8
166	SAV_1003		putative dehydrogenase	7.6
167	SAV_1004		hypothetical protein	7.6
168	SAV_1052		hypothetical protein	8
169	SAV_1053		putative sugar hydrolase	8
170	SAV_1090		putative secreted protein	7.1
171	SAV_1160		hypothetical protein	7.8
172	SAV_1161		putative isomerase	7.8
173	SAV_1220		hypothetical protein	8.3
174	SAV_1248		hypothetical protein	7.6
175	SAV_1306		putative methyltransferase	7.6
176	SAV_1353		putative secreted protein	8
177	SAV_1363		putative secreted protein	7.6
178	SAV_1557		hypothetical protein	8.6
179	SAV_1613		putative dehydrogenase	9.3
180	SAV_1806		putative secreted protein	7.4
181	SAV_1872		putative secreted protein	7.1
182	SAV_1919		hypothetical protein	7.6
183	SAV_1921		putative integral membrane protein	7.6
184	SAV_1964		hypothetical protein	8
185	SAV_1965		putative secreted protein	8
186	SAV_1985		putative oxidoreductase	7.1
187	SAV_2074		hypothetical protein	9.8
188	SAV_2149		putative copper amine oxidase	7.5
189	SAV_2252		putative alpha mannosidase	9
190	SAV_2426		hypothetical protein	9.7
191	SAV_2451		putative secreted protein	8.7
192	SAV_2476		hypothetical protein	8.2

193	SAV_2653	hypothetical protein	8
194	SAV_2688	hypothetical protein	8
195	SAV_2934	hypothetical protein	8.4
196	SAV_3222	hypothetical protein	7
197	SAV_3399	hypothetical protein	8.9
198	SAV_3668	hypothetical protein	7.8
199	SAV_3901	hypothetical protein	7.6
200	SAV_3904	putative lipoprotein	7.6
201	SAV_3944	hypothetical protein	7.2
202	SAV_3945	<i>thiX2</i> putative flavin-dependent reductase	7.2
203	SAV_3946	hypothetical protein	7
204	SAV_4080	putative lipoprotein	10.2
205	SAV_4097	hypothetical protein	8.6
206	SAV_4153	putative amidase	8.2
207	SAV_4165	hypothetical protein	8.2
208	SAV_4188	putative membrane protein	13.9
209	SAV_4228	hypothetical protein	7.2
210	SAV_4325	putative secreted protein	7.8
211	SAV_4373	hypothetical protein	8.2
212	SAV_4392	putative pirin-like protein	8
213	SAV_4630	hypothetical protein	8.2
214	SAV_4696	putative proline-rich protein	7.8
215	SAV_4750	putative membrane protein	7.1
216	SAV_4759	putative dehydrogenase	7.6
217	SAV_4862	putative secreted protein	12.6
218	SAV_4897	putative peptidase amidohydrolase	10.1
219	SAV_5011	putative secreted protein	7.1
220	SAV_5019	hypothetical protein	9.5
221	SAV_5221	hypothetical protein	7.4
222	SAV_5266	hypothetical protein	7.3
223	SAV_5334	putative membrane protein	7.3
224	SAV_5405	putative secreted protein	7.6
225	SAV_5412	hypothetical protein	7.5
226	SAV_5432	hypothetical protein	7.3
227	SAV_5450	putative membrane protein	9.1
228	SAV_5591	putative secreted protein	7.1
229	SAV_5652	hypothetical protein	11.1
230	SAV_5761	putative protocatechuate dioxygenase	7.1
231	SAV_5874	hypothetical protein	7.8
232	SAV_5875	putative NGG1-interacting factor	7.8
233	SAV_5885	hypothetical protein	7.1
234	SAV_5973	hypothetical protein	8.2
235	SAV_6248	putative integral membrane protein	7.5
236	SAV_6622	hypothetical protein	8.9

237	SAV_6640		putative oxidoreductase	7.4
238	SAV_6641		putative FMN-dependent monooxygenase	7.4
239	SAV_6848		putative secreted protein	8.2
240	SAV_6857		hypothetical protein	7.4
241	SAV_6888		hypothetical protein	8.8
242	SAV_6911		putative ATPase	8.2
243	SAV_6916		hypothetical protein	8.2
244	SAV_6955	<i>hcaC2</i>	putative ferredoxin subunit of phenylpropionate dioxygenase	7.6
245	SAV_6967		hypothetical protein	7.4
246	SAV_6968		putative MutT-like protein	7.4
247	SAV_7099		putative NLP/P60-family secreted protein	9
248	SAV_7291		hypothetical protein	7.3
249	SAV_7298		putative membrane protein	7.1
250	SAV_7299		putative glycine-rich protein	7.1

Total: 250

Yellow highlighting: putative targets selected and confirmed experimentally by EMSAs.