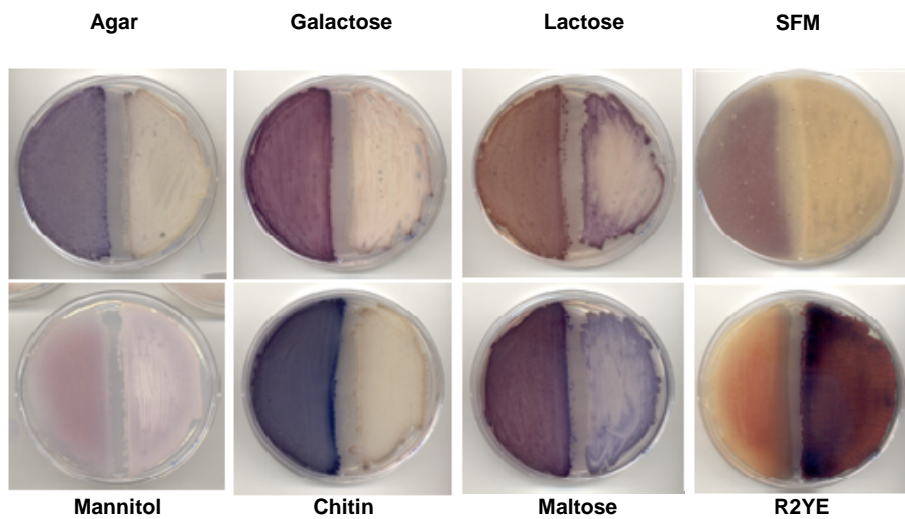


## Supplementary Figure S1

**Effect of *dasR* deletion on antibiotic production in *S. coelicolor*.** Enhanced production of pigmented antibiotics in a *dasR* mutant (BAP29, left part of the plates) compared to the parental *S. coelicolor* M145 (right part of the plates) on minimal medium with several nonrepressing carbon sources (allowing morphological differentiation of both strains). Note that *reduced* antibiotic production by BAP29 is observed on the R2YE plate, which does not allow development of BAP29.



## Supplementary Table S1.

Construction of the DasR binding site position weight matrix for the prediction of DasR-responsive elements (for details see Hiard *et al.*, *Biochem Biophys Res Commun* 357, 861-864 (2007)).

**A Multiple Alignment**

Genes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	Scores
<i>crr-ptsI</i>	T	G	T	G	G	T	C	T	A	G	A	C	C	T	C	T	15.55
<i>malX2</i>	A	C	T	G	G	T	G	T	A	G	A	C	C	A	G	T	17.88
<i>nagE2</i> (1)	A	C	A	G	G	T	C	T	A	C	A	C	C	A	C	T	16.47
<i>nagE2</i> (2)	A	G	T	G	G	T	G	T	A	G	A	C	C	A	C	C	16.03
<i>ptsH</i> (1)	A	C	T	G	G	T	C	T	A	G	A	C	A	A	C	T	19.55
<i>ptsH</i> (2)	A	C	T	G	G	T	C	T	A	G	A	C	A	A	G	A	18.07
<i>nagB</i>	A	T	T	G	G	T	C	T	A	A	A	C	C	A	C	A	17.87
Consensus	A	C	T	G	G	T	C	T	A	G	A	C	C	A	C	T	19.52

(1) and (2) are for the first and second *dres*. Scores are in unit of bit.

**B Alignment Matrix**

positions	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
<b>A</b>	6	0	1	0	0	0	0	0	7	1	7	0	2	6	0	2
<b>C</b>	0	4	0	0	0	0	5	0	0	1	0	7	5	0	5	1
<b>G</b>	0	2	0	7	7	0	2	0	0	5	0	0	0	0	2	0
<b>T</b>	1	1	6	0	0	7	0	7	0	0	0	0	0	1	0	4

Each line displays the number of occurrence of the given nucleotide at the 16 different positions. Numbers enclosed in boxes indicate the number of occurrence of nucleotides that constitute the consensus sequence.

**C Weight Matrix**  
(Maximum score: 19.55 bits ; Minimun score: -33.28 bits)

positions	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
<b>A</b>	1.70	-2.08	0.02	-2.08	-2.08	-2.08	-2.08	-2.08	1.85	0.20	1.85	-2.08	0.65	1.7	-2.08	0.65
<b>C</b>	-2.08	0.41	-2.08	-2.08	-2.08	-2.08	0.62	-2.08	-2.08	-0.75	-2.08	0.94	0.62	-2.08	0.62	-0.75
<b>G</b>	-2.08	-0.20	-2.08	0.94	0.94	-2.08	-0.20	-2.08	-2.08	0.62	-2.08	-2.08	-2.08	-2.08	-0.20	-2.08
<b>T</b>	0.02	0.02	1.70	-2.08	-2.08	1.85	-2.08	1.85	-2.08	-2.08	-2.08	-2.08	-2.08	0.02	-2.08	1.31

Each line displays the weight of the given nucleotide at the 16 different positions. Scores are in unit of bit. Values enclosed in boxes indicate the scores of nucleotides that constitute the consensus sequence.

## Supplementary Table S2. Computational prediction of the DasR regulon of *Streptomyces coelicolor*

Numbers highlighted in yellow indicates genes validated experimentally (*in vitro* and/or *in vivo*) as part of the DasR regulon of *Streptomyces coelicolor*. The prediction has been performed with PREDetector using the position weight matrix shown in supplemental Table S1.

#	GENE ID	FUNCTION	<i>dre</i>	POSITION	SCORE	CO-TRANSC GENE(S)	CO-TRANSC FUNCTION(S)
1	SCO5841c, <i>ptsH</i>	PTS phosphocarrier protein HPr	agttgtctagaccagt	-51	19.55	-	-
	SCO5842	conserved hypothetical protein SC9B10.09	tcttgtctagaccagt	-168			
2	SCO2905c, <i>malX2</i>	PTS <sup>GlcNAc</sup> EIIB component		-134	17.88	SCO2904c, <i>rph</i>	putative ribonuclease PH
	SCO2906, <i>nagE1</i>	putative PTS transmembrane component	actgggtctacaccagt	-41		-	-
3	SCO5236c, <i>nagB</i>	Glucosamine-6-phosphate isomerase	tgtggtttagaccaat	-68	17.87	-	-
4	SCO1390, <i>crr</i>	putative PTS system sugar phosphotransferase component IIA	tgtgggtctagacctct	-130	16.57	SCO1391, <i>ptsI</i>	phosphoenolpyruvate-protein phosphotransferase
5	SCO2907, <i>nagE2</i>	PTS <sup>GlcNAc</sup> EIIC component	acagggtctacaccact	-49	16.47	-	-
			agtgggtgtagaccacc	-32	16.03		
			caagggtgtagacctct	-236	9.07		
6	SCO7056c	GntR-family transcriptional regulator	attgggtctaaaccagc	-79	15.65	-	-
7	SCO5232, <i>dasA</i>	Chitobiose ABC transporter, sugar binding protein	actgggtctacaccatt cttgggtctagtcata	-106 -322	15.45 8.06	SCO5233, <i>dasB</i> /SCO5234, <i>dasC</i> /SCO5235, <i>dasD</i>	chitobiose transporter integral membrane protein/chitobiose transporter integral membrane protein/intracellular $\beta$ -N-acetylglucosaminidase
8	SCO7224c	putative integral membrane protein	ccttgtctagaccaat tcagggtctagacctgt tatgggtctagacctga	-159 -293 -272	14.95 14.68 12.8	-	-
	SCO7225	secreted chitin-binding protein		-168 -34 -55			
9	SCO3679	hypothetical protein	tgttgtctagtccaat	-314	14.57	-	-
10	SCO3563, <i>acsA</i>	acetyl-coenzyme A synthetase	acagggtctaaaccatt	-102	14.54	-	-
11	SCO1433	hypothetical protein SC6D7.06c.		-205	14.38	-	-
	SCO1432c	putative membrane protein.	attgggtgtcgaccact	-86			
12	SCO5239	histidine kinase	agtgggtctagtcacaca	-335	14.32	-	-
13	SCO6300c	secreted $\beta$ -N-acetylglucosaminidase	atagggtctagacaaaa	-131	14.12	-	-
			agagggtctagacaaaa	-116	13.9		

14	SCO1444	putative chitinase precursor	actggtctagtcctct attggtccataacctat	-53 -75	13.91 8.12	-	-
15	SCO4286	putative solute-binding protein (putative secreted protein)	agaggtctagtcacct	-81 -63	13.3	SCO4287	hypothetical protein SCD95A.20
	SCO4285c, <i>nagK</i>	N-acetylglucosamine kinase	ggtggtgtagacctta	-83 -101	10.24	SCO4284c, <i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase
16	SCO5003c, <i>chiA</i>	chitinase A (family 18-B)	ggtggtccagaccaat	-77	13.14	-	-
	SCO5004	hypothetical protein SCK15.06		-258		-	-
17	SCO4442	hypothetical protein SCD6.20	attggcgtaaaccaca	-41	13.12	-	-
18	SCO6486, <i>dppA</i>	D-ala-D-ala aminopeptidase	agtgggtccagaccacc	-71	12.92	SCO6487/SCO6488/SCO6489/SCO6490	putative aminoacylase/putative acyl-peptide hydrolase/conserved hypothetical protein/putative acetyltransferase
19	SCO4315	putative homeostasis protein	attggactagacctgt	-39	12.7	-	-
20	SCO2672	putative membrane protein	agaggtctggacaaca	-32	12.67	-	-
21	SCO1429, <i>chiD</i>	chitinase D (family 18-A)	actggtctagtcctcc	-96	11.85	-	-
	SCO1428c	acyl-CoA dehydrogenase		-312		-	-
22	SCO5673, <i>chiB</i>	Chitinase B (family 18-B)	attggtctggacccaaa	-63	11.84	-	-
23	SCO7250c	N-acetylmuramoyl-L-alanine amidase	agtggcgtagacctgt	-213	11.72	-	-
24	SCO7263, <i>chiF</i>	Chitinase F (family 19)	actggtctacaccctt actggtacagacccaaa	-172 -155	11.67 10.0	SCO7264	putative oxidoreductase
25	SCO6013	probable 1-deoxyxylulose-5-phosphate synthase	aatggtctggaccaga	-274 -258	11.62	-	-
	SCO6012c, <i>chiH</i>	Chitinase H (family 18-C)	atgggactagaccaat	-111 -127	8.72	-	-
26	SCO5580	putative prokaryotic docking protein	tttgggtggaaaccaca	-37	11.44	-	-
	SCO5579c	putative transmembrane protein		-134		-	-
27	SCO6004c	putative secreted ATP/GTP binding protein	agtggactataacctgt	-244	11.21	-	-
	SCO6005, <i>ngcE</i>	NgcE, putative GlcNAc/chitobiose ABC transporter		-334		SCO6006, <i>ngcF</i> /SCO6007, <i>ngcG</i>	ABC transmembrane transport protein/ABC transmembrane transport protein
28	SCO4393c	conserved hypothetical protein	tgcggtctggaccagt	-55	11.15	-	-
	SCO4394	iron repressor		-184		-	-
29	SCO5376c, <i>chiC</i>	chitinase C (family 18-A)	ataggtctggaccaat aaaggtctggaccata	-109 -88	10.82 8.06	-	-
	30	SCO2946c	Putative ABC sugar transporter sugar-binding protein	agaggtctgaaccaat	-112	10.82	SCO2945c/SCO2944c/S CO2943c
31	SCO2833c, <i>chb</i>	secreted chitin binding protein.	gcaggtctagaccaag acatgtccataccaaa	-70 -110	10.79 8.35	-	-
32	SCO2503, <i>chiJ</i>	Chitinase J (family 18-B)	aaaggtctggaccaca cttgggtccagacctct	-78 -99	10.76 9.74	-	-

33	SCO5716c	putative peptide transport system secreted peptide binding protein	attggcgcagaccact	-197	10.45	SCO5715c/SCO5714c/S CO5713c/SCO5712c	putative peptide transport system permease/putative peptide transport permease/putative peptide transport ATP-binding protein/putative peptide transport ATP-binding protein
34	SCO4506	conserved hypothetical protein	agaggtcaagatcact	-103	10.28	SCO4507	putative serine/threonine protein kinase
	SCO4505c	cold shock protein		-206			
35	SCO1117c	putative secreted protein	cgcggctctagacccaaa	-131	10.28	-	-
36	SCO5881c, <i>redZ</i>	Red cluster pathway-specific activator (via <i>redD</i> )	agtgggtttccacctca	-201	10.2	-	-
37	SCO4841c	putative short-chain dehydrogenase	actgctccagacatgt	-3	10.1	-	-
38	SCO6149	putative ATP GTP-binding protein	ggaggtgtcgaccaat	-140	10.09	SCO6150/SCO6151	putative ADA-like regulatory protein/putative methylated-DNA-protein-cysteine methyltransferase
39	SCO4671c	putative lysR-family regulatory protein	gctggtagacagaccagt	-55	10.01	-	-
40	SCO0764c	putative hydrolase	attgggtgtgtacctct	-80	10.0	-	-
41	SCO4240c, <i>msiK</i>	ABC transporter ATP-binding protein	ggtgggtgtagtccaca	-75	9.87	-	-
42	SCO2753	putative LacI-family transcriptional regulator.		-120	9.75	SCO2751c/SCO2750c	conserved hypothetical protein SCC57A.22c./conserved hypothetical protein SCC57A.21c.
	SCO2752c	putative oxidoreductase	ggtgggtctggacaaga	-127			
43	SCO7591c	putative regulatory protein	tgtgctgttcaccagt	-5	9.72	SCO7593	hypothetical protein SC7H9.05
	SCO7592	conserved hypothetical protein		-124			
44	SCO2655c	conserved hypothetical protein SC8E4A.25c	agtgttttcgaccaca	-124	9.68	-	-
	SCO2656	putative membrane protein		-110			
45	SCO2549c	possible protease	agaggtttggatcact	-45	9.68	-	-
46	SCO3975c	putative regulator	tgtggctcgagaccgga	-86	9.47	-	-
47	SCO2221	conserved hypothetical protein SC10B7.16	actggcgtcaacaagt	-64	9.45	SCO2222	putative iron-sulfur oxidoreductase (putative secreted protein)
48	SCO4107	putative integral membrane protein	agtgggtgaacacaacg	-133	9.43	-	-
49	SCO7587	putative integral membrane protein	acaagtgaagaccaca	-4	9.41	-	-
50	SCO5012	putative integral membrane protein	acaggagaagacaact	-242	9.19	SCO5013/SCO5014/SC O5015	putative secreted protein/putative secreted protein/putative secreted protein
51	SCO4646	preprotein translocase SecE subunit	actgggtctccaaaacc	-156	9.17	SCO4647	transcription antitermination protein
	SCO4645c	aspartate aminotransferase		-281			
52	SCO1906c	putative secreted protein	actggcggagacctct	-128	9.16	-	-
53	SCO6345	Chitin-binding protein	gtaggtctagacctgc	-94	9.11	-	-
			taaggtctagacctgc	-114			
	SCO6344c	putative secreted amidase		-153			
				-133			
54	SCO1262c	putative gntR-family transcriptional regulator	cttgggtcaagaccaat	-113	9.11	-	-
55	SCO1226c	Chitinase	cttgggtccagacctgt	-188	8.92	-	-
56	SCO6266	ScbA protein	agtagttttgatcaat	12	8.88	-	-

57	SCO0528	putative lipoprotein	agtggctctagctatga	-45	8.83	-	-
	SCO0527c	cold shock protein		-302		-	-
58	SCO7815	putative TetR-family transcriptional regulator	agtggctctcgatcgggt	-346	8.79	-	-
59	SCO7726	putative hydrolase	cgtggctcgagacgaat	-327	8.79	-	-
60	SCO7069c	chitinase	acaggtccgaccaat	-61	8.77	-	-
	SCO7070	chitosanase		-50		-	-
61	SCO5954, <i>chiE</i>	chitinase E (family 18-A)	attgggtccagaccttc	-95	8.76	-	-
			acagggcgcagaccacc	8	7.1	-	-
62	SCO6033	hypothetical protein SC1C3.21	cttggctctagtccatt	-278	8.72	-	-
	SCO6032c	$\beta$ -Nacetylglucosaminidase		-154		-	-
63	SCO5261	putative malate oxidoreductase	ggttctttacaccct	-162	8.66	-	-
64	SCO6231c	probable sugar transport system sugar-binding lipoprotein SC2H4.13c	tcaggactagaccggt	-202	8.65	SCO6230c/SCO6229c	putative sugar transport system permease protein/putative sugar transport system permease protein
	SCO6232	putative beta-mannosidase		-86		SCO6233	putative transcriptional regulator
65	SCO5230c	putative integral membrane protein	tctggctctagtccctgg	-118	8.65	SCO5229c/SCO5228c/SCO5227c/SCO5226c/SCO5225c	putative permease/putative acetyltransferase/putative redoxin/ribonucleotide-diphosphate reductase large chain/ribonucleotide-diphosphate reductase small chain
66	SCO1634c	putative small membrane protein	tgatgtcgagactaga	-16	8.58	-	-
67	SCO5430c	putative extracellular solute-binding lipoprotein	aatggctctagtcagggt	-81	8.53	SCO5429c/SCO5428c	putative integral membrane transport protein/putative integral membrane transport protein
68	SCO6319	putative lipoprotein	attggctctgaaccatg	-30	8.51	-	-
69	SCO3490	transposase	aatcgtcaagacctgt	-118	8.51	-	-
70	SCO2529	putative metalloprotease.	agtgcggtataccact	-120	8.44	SCO2530/SCO2531	hypothetical protein SCC117.03./putative beta-glucosidase.
	SCO2528c	2-isopropylmalate synthase		-259		-	-
71	SCO5819	sporulation transcription factor, WhiH	tgtgcttttcacccaaa	-55	8.42	-	-
72	SCO3131c	conserved hypothetical protein	cgtggctcgagaccggt	6	8.42	-	-
73	SCO2119c	6-phosphofruktokinase	ggtggttgaggccact	-40	8.39	SCO2118c	putative D-lactate dehydrogenase
74	SCO1798c	putative ABC transporter ATP-binding subunit	tgtcgcgtacacctgt	-56	8.36	SCO1797c	putative integral membrane protein
	SCO1799	hypothetical protein		-114		-	-
75	SCO2426	possible regulatory protein	agagatgtacaacaca	-144	8.34	-	-
76	SCO5366	ATP synthase protein I	agaggtaaagacctca	-172	8.26	-	-
77	SCO2835c	putative membrane protein.	agttggttagagcagc	-227	8.22	SCO2834c	putative membrane protein
78	SCO1953c	ABC excision nuclease subunit C	ggatgtgaagacctct	-268	8.22	SCO1952c/SCO1951c/SCO1950c/SCO1949c/SCO1948c	conserved hypothetical protein/conserved hypothetical protein/hypothetical protein/small hypothetical protein/putative zinc-binding carboxypeptidase
	SCO1954	hypothetical protein		-101		-	-
79	SCO4722	preprotein translocase SecY subunit	gctcgtctgaaccact	-266	8.19	SCO4723	adenylate kinase

80	SCO3366c	putative exporter	agttgtctactactggg	-72	8.15	-	-
	SCO3367	putative tetR-family regulator		-103		-	-
81	SCO6755	putative transferase	tctgggtgaacaccagg	33	8.14	SCO6756	putative glycosyltransferase
82	SCO2978	putative secreted protein	cctggcgctacaccaga	-67	8.14	SCO2979/SCO2980	putative integral membrane transport protein/putative integral membrane transport protein
83	SCO2261c	putative membrane protein.	actggtagaccgaccagt	17	8.14	-	-
84	SCO7477	putative membrane protein	ataggttagagaccaat	-187	8.12	-	-
	SCO7476c	putative secreted protein		-86		-	-
85	SCO0915	hypothetical protein SCM10.03	tttgggtatggaccatt	-98	8.12	-	-
	SCO0914c	putative lipoprotein		-127		-	-
86	SCO7628	conserved hypothetical protein	attgggtctgggcctga	-146	8.11	SCO7629/SCO7630	probable starvation sensing protein/putative isomerase
87	SCO5231c, <i>dasR</i>	DasR, GlcNAc regulon transcriptional regulator	cttgggtctagtcata	-150	8.06	-	-
88	SCO0481, <i>chb3</i>	secreted chitin binding protein	tatgggtctagtcacaac	-201	8.06	-	-
89	SCO1211c	putative polypeptide deformylase	tgaggtccacaccacg	-5	8.04	-	-
	SCO1212	putative ligase		-76		SCO1213	conserved hypothetical protein
90	SCO5085, <i>actII-4</i>	actinorhodin cluster activator protein	tgttgagtaggctgt	-59	7.98	-	-
91	SCO4526	putative protein kinase	accgctgtcgaccact	4	7.97	SCO4527/SCO4528/SCO4529/SCO4530/SCO4531/SCO4532/SCO4533/SCO4534/SCO4535/SCO4536/SCO4537	putative integral membrane protein/putative integral membrane protein/putative membrane protein/putative septum determining protein/putative membrane protein/hypothetical protein/putative membrane protein/putative integral membrane protein/hypothetical protein/putative integral membrane protein/hypothetical protein 2SCD4.08
92	SCO4516c	hypothetical protein SCD35.23c	actgggtctggatccgt	-20	7.97	SCO4515c/SCO4514c/SCO4513c/SCO4512c/SCO4511c/SCO4510c	putative membrane protein/putative integral membrane protein/hypothetical protein SCD35.20c/hypothetical protein SCD35.19c/putative integral membrane protein/hypothetical protein SCD35.17
93	SCO1648, <i>arc</i>	AAA ATPase	agtgttcaaacaccgct	-196	7.97	-	-
	SCO1649	putative ferredoxin		-66		-	-
94	SCO5609c	hypothetical protein SC2E1.26c	actggctcaggaccgct	-133	7.88	-	-
95	SCO2438	putative secreted protein	tgtcgcgttagagcagt	2	7.84	-	-
96	SCO3091c	cyclopropane-fatty-acyl-phospholipid synthase	atagctgtacacacca	-115	7.83	-	-
97	SCO0409c, <i>sapA</i>	spore-associated protein precursor	agatgtttacgactgt	-125	7.82	-	-
98	SCO4394, <i>desR</i>	iron repressor	actgatcgacaccacg	9	7.81	-	-
99	SCO7458	putative membrane protein.	tgatctgttagacgaaa	2	7.73	-	-
100	SCO7784	putative oxidoreductase	aggggtgtcgacgact	-337	7.68	SCO7785	putative transcriptional regulator
101	SCO4735	30S ribosomal protein S9	cgtggccgagaccact	-1	7.66	-	-
102	SCO1600c	putative translation initiation factor IF-3	tgttcgttagacctaa	-72	7.59	-	-
	SCO1601	hypothetical protein SCI35.23		-328		-	-
103	SCO7053c	hypothetical protein	tgtggagtagagtagt	-50	7.52	-	-
	SCO7054	conserved hypothetical protein		-47		SCO7055	putative methyltransferase
104	SCO0790	putative hydrolase	cctcgtcgacaccaat	36	7.47	-	-

105	SCO4635, rpmG	50S ribosomal protein L33	agcgggtgtagctcagt	-164	7.42	SCO4636/SCO4637	hypothetical protein SCD82.07/conserved hypothetical protein
106	SCO0072c	putative secreted protein	ccaggttcagacctgt	-309	7.42	-	-
	SCO0073	hypothetical protein		-219		SCO0074/SCO0075	hypothetical protein/hypothetical protein
107	SCO2024	putative chitosanase (putative secreted protein)	agaggtgtccccaat	-14	7.4	-	-
108	SCO6445	putative inositol monophosphatase	acgcgtgtacacctga	-88	7.37	SCO6446	hypothetical protein SC9B5.13
109	SCO4689	hypothetical protein SCD31.14	gcatgtctacatcagc	-145	7.37	SCO4690/SCO4691/SCO4692/SCO4693/SCO4694/SCO4695/SCO4696	putative membrane protein/putative membrane protein/conserved hypothetical protein SCD31.17/putative membrane protein/hypothetical protein SCD31.19/hypothetical protein SCD31.20/hypothetical protein SCD31.21
110	SCO6021	conserved hypothetical protein SC1C3.09		-227	7.34	SCO6022/SCO6023/SCO6024/SCO6025	hypothetical protein SC1C3.10/conserved hypothetical protein SC1C3.11/putative transferase/hypothetical protein
	SCO6020c	putative transcriptional regulator	actgctgttgacagca	-233		-	-
111	SCO5329	hypothetical protein	tgtggttgagacctca	-183	7.34	-	-
112	SCO4062	putative transposase	tgacgtctcaaccaca	-32	7.34	-	-
	SCO4061c	hypothetical protein 2SCD60.27c		-2		-	-
113	SCO3905c	putative membrane protein		-40	7.34	-	-
	SCO3906, <i>rpsF</i>	putative 30S ribosomal protein S6	tgtgttttagccctca	-252		SCO3907.ssb /SCO3908, rpsR/SCO3909, rplI	putative single-strand DNA-binding protein/putative 30S ribosomal protein S18/50S ribosomal protein L9
114	SCO6593c	hypothetical protein	agtgcctctatagaagc	-146	7.32	SCO6592c	-putative secreted protein
115	SCO7070	hypothetical protein SC4G1.36	acaggtccggaccaat	-50	7.28	-	-
116	SCO5046, <i>wblI</i>	hypothetical protein	tcaggagtagacctgt	-14	7.28	-	-
117	SCO3914c	putative transcriptional regulator		-35	7.28	SCO3913c	conserved hypothetical protein
	SCO3915	putative transmembrane efflux protein	agtggctgagaccagg	-122		-	-
118	SCO3185	putative Na <sup>+</sup> /H <sup>+</sup> antiporter		-52	7.28	-	-
	SCO3184c	putative penicillin acylase (EC 3.5.1.11).	accgggtgtacgcctca	-279		-	-
119	SCO5490c	conserved hypothetical protein	agtggctcttcgtcact	-36	7.21	SCO5489c	hypothetical protein
	SCO5491	conserved hypothetical protein		-63		SCO5492	putative oxidoreductase
120	SCO6350c	hypothetical protein SC3A7.18c	gcttgtgtcgacctat	-1	7.2	-	-
	SCO6351	hypothetical protein SC3A7.19		-95		-	-
121	SCO2920c	putative secreted protease	acgcgtgtagtcaagt	-91	7.18	-	-
122	SCO1006c	hypothetical protein	tgtggccgacagcagt	-197	7.16	-	-
123	SCO7290c	putative dehydrogenase	acaggtgtaaacgggc	-49	7.06	SCO7289c	putative regulator
124	SCO5330	hypothetical protein SC6G9.03c	gctggcgtagcccact	-54	7.06	-	-
125	SCO2787	conserved hypothetical protein SCC105.18		-61	7.06	SCO2788/SCO2789	hypothetical protein SCC105.19/glucosamine-fructose-6-phosphate aminotransferase
	SCO2786c	beta-N-acetylhexosaminidase	acgggtgcggaccact	-70		-	-
126	SCO5252	conserved hypothetical protein	agtggccaacatgaga	-27	7.05	SCO5253	hypothetical protein 2SC7G11.15
127	SCO0021	hypothetical protein	acttttctccccaggt	34	7.03	-	-
128	SCO7173	putative transcriptional regulator	agaggtgtgcagcaga	-110	7.02	-	-



### Supplementary Table S3.

#### Oligonucleotides used in this work.

For doublestranded (ds) oligonucleotides used in electromobility shift assays (EMSAs) only the top strand oligo is given. Forward and reverse oligos are indicated with 'for' and 'rev', respectively. Predicted *dre* sites in bold face and italicized.

Oligonucleotide	Sequence (5' to 3')	Position #
<b>RT PCR</b>		
<i>actII-4-RTfor</i>	GCTGCAGACGTACGTGTACCACAC	+185
<i>actII-4-RTrev</i>	GCGTCGATACGGAGCTGCATTCC	+495
<i>kasO-RTfor</i>	GCGGGATGCTCAGTGAGCACGG	+211
<i>kasO-RTrev</i>	GACGAGGTCGGCGAGGACGGG	+440
<i>redD-RTfor</i>	TCATGGGAGTGCGGAGAACGCG	+123
<i>redD-RTrev</i>	CGCCCCACAGTTCGTCCACCAG	+384
<i>redZ-RTfor</i>	CGACATGAAAGTGCAGGTGG	+74
<i>redZ-RTrev</i>	TCGGGCTTGGTCAGCAAAGC	+241
<i>rpsI-RTfor</i>	GAGACCACTCCCGAGCAGCCGC	+7
<i>rpsI-RTrev</i>	GTAGCGGTTGTCCAGCTCGAGCA	+299
<b>EMSAs (ds oligos)</b>		
<i>actII-4-dre</i>	CACATTGAAATCT <b><i>GTTTGAGTAGGCCTGTT</i></b> TATTGTGCGCCCC	-71
<i>crr-dre</i>	CCGTGAGGAGT <b><i>GTGGTCTAGACCTCT</i></b> AATCGGAACA	-140
<i>redZ-dre</i>	ACAAGATCTTCT <b><i>TGAGGTGGAAACCACT</i></b> TTCGTATCAGTCT	-212
<i>crp-cis</i>	TGCGGCATCCTTGTGACAGATCACACTGTTTGGACT	-116
<b>EMSAs (fragments)</b>		
<i>ptsH_upFor</i>	GCTTCCCAGTGGGCGGGTACTC	-249
<i>ptsH_upRev</i>	ATCGTCACCGGGACGCCTGTGG	+103
<i>actII-4_upFor</i>	TCGGAAGCCTCGACCACTGC	-134
<i>actII-4_upRev</i>	AGCAGCACCAGGAGCTGGGTTCG	+97
<i>redZ_upFor</i>	TGCACGTGTCCTTCTGAGCGGAG	-280
<i>redZ_upRev</i>	TGTCGTGCCGCTCCAGCAATGC	+78

# Refers to the nt position of the 5' end of the oligonucleotide relative to the translational start site of the gene.