

SUPPLEMENTAL DATA

Belonging to the manuscript:

The ROK-family regulator Rok7B7 pleiotropically affects xylose utilization, carbon catabolite repression and antibiotic production in *Streptomyces coelicolor*

by

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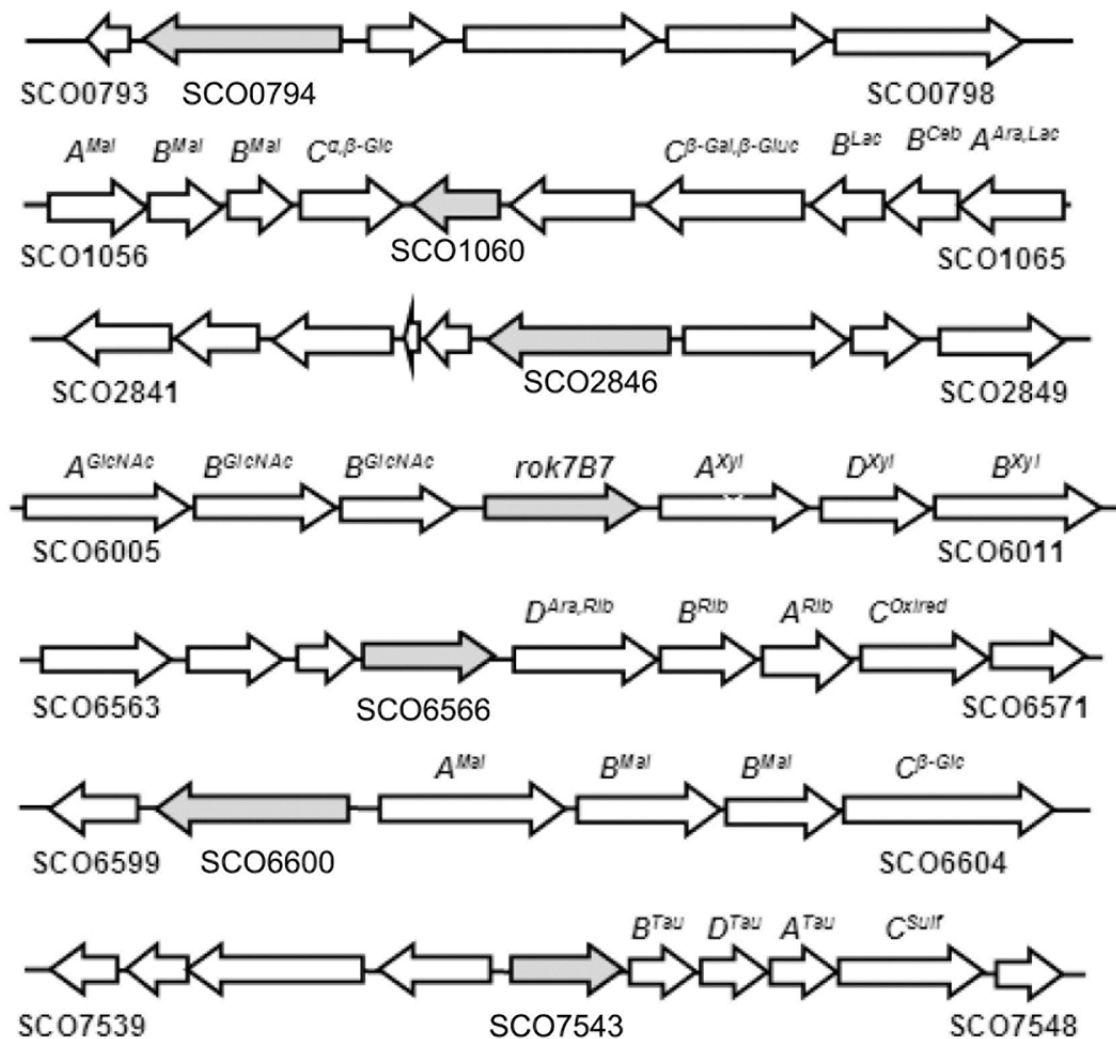


Figure S1. Genomic environment of the *rok* genes studied in this work. The genetic environments of SCO0794, SCO1060, SCO2846, SCO6008 (*rok7B7*), SCO6566, SCO6600 and SCO7543 (*rok* genes shaded in grey) are indicated, with ORFs represented by arrows. *S. coelicolor* reference numbers (SCO) for the ORFs are given for the first and last ORFs of each cluster of genes. Genes encoding substrate-binding proteins, membrane proteins, ATPases and catabolic enzymes are marked with suffixes A, B, C and D, respectively. The known or predicted substrates of the ABC transporters are indicated. Abbreviations: Mal – maltose; α,β -Glu - α,β -glucosidase; β -Gal – β -galactosidase; β -Glu - β -glucosidase; Lac – lactose; Ceb – cellobiose; Ara – arabinose; GlcNAc- *N*-acetylglucosamine; Xyl – xylose; Rib – ribose; Oxired – oxidoreductase; Tau – taurine; Sulf – sulfonate.

Table S1. Strains of *Streptomyces coelicolor* A3(2) described in this study.

Strain	Genotype #	Reference
M145	prototrophic SCP1 ⁻ SCP2 ⁻	(3)
GAM20	M145 SCO0794:: <i>aacC4</i> , Apr ^R	This work
GAM21	M145 SCO1060:: <i>aacC4</i> , Apr ^R	This work
GAM22	M145 SCO2846:: <i>aacC4</i> , Apr ^R	This work
GAM23	M145 SCO6008:: <i>aacC4</i> , Apr ^R	This work
GAM24	M145 SCO6566:: <i>aacC4</i> , Apr ^R	This work
GAM25	M145 SCO6600:: <i>aacC4</i> , Apr ^R	This work
GAM26	M145 SCO7543:: <i>aacC4</i> , Apr ^R	This work
GAM30	M145 Δ SCO0794 D	This work
GAM31	M145 Δ SCO1060 D	This work
GAM32	M145 Δ SCO2846 D	This work
GAM33	M145 Δ SCO6008 D	This work
GAM34	M145 Δ SCO6566 D	This work
GAM35	M145 Δ SCO6600 D	This work
GAM36	M145 Δ SCO7543 D	This work
DM9	M145 Δ <i>redD</i> Δ <i>actII</i> -ORF4	(2)

Apr, apramycin resistant; D, deletion mutant

Table S2. Plasmids constructs used in this study.

Plasmid	Description	Reference
pWHM3	Cloning vector, <i>colE1</i> replicon, pSG5 replicon, TsrR, AmpR	(4)
pUWLcre	pUWLoriT derivative with <i>cre(a)</i> gene under <i>ermE*</i> promoter	(1)
pGAM8	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO0794 with apraloxP_ <i>Xba</i> I inserted between them in pWHM3 <i>Eco</i> RI- <i>Hind</i> III	This work
pGAM9	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO1060 with apraloxP_ <i>Xba</i> I inserted between them in pWHM3 <i>Eco</i> RI- <i>Hind</i> III	This work
pGAM10	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO2846 with apraloxP_ <i>Xba</i> I inserted between them in pWHM3 <i>Eco</i> RI- <i>Hind</i> III	This work
pGAM11	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO6008 with apraloxP_ <i>Xba</i> I inserted between them in pWHM3 <i>Eco</i> RI- <i>Hind</i> III	This work
pGAM12	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO6566 with apraloxP_ <i>Xba</i> I inserted between them in pWHM3 <i>Eco</i> RI- <i>Hind</i> III	This work
pGAM13	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO6600 with apraloxP_ <i>Xba</i> I inserted between them in pWHM3 <i>Eco</i> RI- <i>Hind</i> III	This work
pGAM14	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO7543 with apraloxP_ <i>Xba</i> I inserted between them in pWHM3 <i>Eco</i> RI- <i>Hind</i> III	This work
pGAM15	pSET152 containing the <i>rok7B7</i> gene with its promoter and a C-terminal triple FLAG-tag epitope	This work

Table S3. Oligos used in this study. Restriction sites used for cloning are in bold and underlined. GGATTC, *Bam*HI; GAATTC, *Eco*RI; TCTAGA, *Xba*I; AAGCTT, *Hind*III; CATATG, *Nde*I; CTCGAG, *Xho*I. For scheme of primer design see image at the end of the table.

Name #	5'-3' sequence
0794LF-1497	gtcagaattc acc cggggattgaaccgcaggct
0794LR+6	gaagttatccatcacct ctagac gccatgtggctcctcccgta
0794RF+1285	gaagttatcgcgcatct ctagac actgaggtttcgccggtcgc
0794RR+2699	gtc caaag cttcgggcagcaaaatcgtggtcacg
1060LF-1387	gtcagaattc ggg ctgggacatcgaggcaccgct
1060LR+9	gaagttatccatcacct ctagag ttcatcatgggtgctgtcgag
1060RF+1228(48)	gaagttatcgcgcatct ctagac gggacgcggggctgacacgga
1060RR+2552(74)	gtc caaag cttgcgacacgctcgatctgggacacc
2846LF-1369	gtcagaattc ctt gcgggcgatccaggcgtcgt
2846LR+9	gaagttatccatcacct ctagac ctgttcacacccccattgtc
2846RF+1224	gaagttatcgcgcatct ctagac ggggggacggcgggctgagac
2846RR+2637	gtc caaag ctttcagacccgttccacgaggtcc
6008LF-848new	gtcagaattctgatcgtcgtgggtctcggcactg
6008LR+147new	gaagttatccatcacct ctagac ccggacgatgttcgagaccgctcg
6008RF+1201loxPnew	gaagttatcgcgcatct ctagac cttcaacttagagcacggatgg
6008RR+2675(97)	gtc caaag cttagctctacgctcggtagcgcct
6566LF-1406	gtcagaattc cg cgggacaagatgtccgaggtc
6566LR+6	gaagttatccatcacct ctagag gacacgacgaggccgcccgg
6566RF+1398	gaagttatcgcgcatct ctagac gctagccaccaccttcaact
6566RR+2677	gtc caaag cttagaccgacacgcttgccgggtgac
6600LF-1371	gtcagaattctcgaactgcgactcgtcgggca
6600LR+6	gaagttatccatcacct ctagag gccatccggcccctcccttt
6600RF+1321(41)	gaagttatcgcgcatct ctagag gatgaggccgtgcgcgcgggc
6600RR+2671(93)	gtc caaag ctttgcccgtgagctacgtcgacctg
7543LF-1253	gtcagaattc ac gggtgccgctcggcgttgac
7543LR+6	gaagttatccatcacct ctagag gtcaaggtagggaggctcga
7543RF+1270(90)	gaagttatcgcgcatct ctagac cttgacaagcggagtgccga
7543RR+2635(57)	gtc caaag ctttccatcagcaggatcgaggggtc
0794check-451	gtcagaattctgggtcaggcacagcgcgcacatg
0794check+1728(51)	gtc caaag cttagttcctgccccgactgcggcag
1060check-501	gtcagaattctcggcaccggcaaccagtgccag
1060check+1695(1718)	gtc caaag cttgccacggacaaccgctacgagg
2846check-687	gtcagaattc act cggcgtacacctgcgtgacc
2846check+1886(1907)	gtc caaag cttaccctcctcatgtcgggtgagc
6008check-689	gtcagaattctccagttgcagaacttcgggctg
6008check+1923(46)	gtc caaag ctttcaccttgccgtcgaggacggag
6566check-541	gtcagaattc ac accgagggctgggtcgatctg
6566check+1898(1921)	gtc caaag ctttcggctcgtgaccgaggtggacg
6600check-549	gtcagaattctcgaagttcttggcgtcccagg
6600check+1880(1901)	gtc caaag ctttggtagcgcgcccgggatctcg
7543check-626	gtcagaattc ag ccacacgaagatgccgtcg
7543check+1894(1917)	gtc caaag cttacgccccgaagatcgtggcgtc
xylG_for	tccgtctcgatcaacaggccgca
xylG_rev	aggcgatcggatgcggacgctc
RTgIcP1_for	agctgggtcaactggggctct

RTglcP1_rev	gtcgaagtccacgtccttg
rpsl_for	gagaccactcccagcagccgc
rpsl_rev	gtagcggttgtccagctcgagca

schematic representation of primer design for creating the knock-out constructs

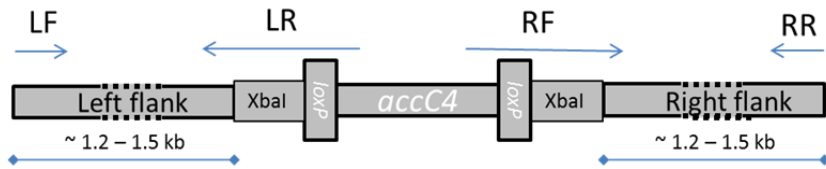


Table S4. Genes that show more than two-fold up- or down- regulation in transcription between *S. coelicolor* M145 and its *rok7B7* null mutant in MM mannitol solid-grown cultures. (*)

Gene	Name	Rok7B7/M145 ratio					
		14 h	24 h	30 h	36 h	42 h	54 h
SCO0007		1,050	0,832	0,943	0,938	0,420	1,856
SCO0013		1,137	0,800	1,001	0,838	0,407	0,965
SCO0022		1,389	1,203	1,199	1,252	1,222	2,618
SCO0045		0,809	1,387	0,889	0,768	2,038	1,013
SCO0056		1,185	0,993	0,917	1,012	0,727	2,008
SCO0182		0,842	0,906	1,034	1,029	0,483	1,464
SCO0190	<i>crtT</i>	2,091	1,703	1,538	1,360	0,931	0,958
SCO0194		1,199	1,019	0,886	2,152	0,872	1,974
SCO0251		1,895	0,692	0,751	0,825	0,204	2,823
SCO0436		0,864	0,737	1,335	0,871	1,207	2,109
SCO0527	<i>scoF</i>	1,304	1,080	0,939	1,062	0,486	2,048
SCO0779		0,950	0,716	0,954	0,882	0,337	1,498
SCO0861		1,212	1,238	1,353	2,037	1,707	0,961
SCO0949		1,057	0,871	1,010	0,974	0,491	1,194
SCO0989		0,933	0,665	0,983	0,768	0,394	1,077
SCO1027		1,053	1,099	0,993	0,878	0,393	2,787
SCO1082		1,045	1,152	1,025	0,431	1,119	0,610
SCO1255	<i>mug</i>	1,049	0,938	1,032	0,809	0,424	1,946
SCO1389	<i>cls</i>	1,104	1,182	0,967	1,110	1,225	2,570
SCO1426		0,973	0,982	1,107	1,461	2,096	0,697
SCO1431		1,024	0,845	1,158	0,757	0,437	2,868
SCO1480		0,945	0,978	1,124	1,117	0,625	2,264
SCO1599	<i>rpml</i>	1,421	1,100	1,008	1,130	0,337	4,874
SCO1675	<i>chpH</i>	1,622	1,107	1,072	0,988	0,542	4,044
SCO1721		0,989	0,870	1,055	1,083	0,427	1,726
SCO1800	<i>chpE</i>	1,869	1,281	1,084	0,988	0,555	4,642
SCO1828		0,995	1,050	1,127	1,407	0,513	2,893
SCO1839		1,536	1,347	1,125	0,930	0,474	2,984
SCO1914		1,394	1,012	0,999	0,898	0,154	8,244
SCO1978		1,224	0,886	0,969	0,779	0,387	2,856
SCO2113	<i>bfr</i>	0,400	0,605	0,996	1,386	0,779	0,907
SCO2156	<i>cox</i>	1,216	1,033	1,030	1,122	0,465	1,338
SCO2210	<i>glnII</i>	1,076	1,535	0,787	2,612	1,108	1,368
SCO2261		1,055	0,810	0,901	0,741	0,454	0,919
SCO2338		0,951	0,818	0,916	1,179	0,531	2,164
SCO2354		0,959	1,084	1,122	0,992	0,590	2,517
SCO2494		0,473	0,406	0,582	0,839	0,753	0,897
SCO2636		0,881	0,925	1,005	1,017	1,814	0,503
SCO2698		1,272	1,423	1,133	0,431	1,175	1,048
SCO2717	<i>chpD</i>	1,856	1,389	1,077	0,754	0,537	3,267
SCO2718	<i>rdIA</i>	1,789	1,717	1,056	0,996	0,279	8,120

SCO2719	<i>rdlB</i>	1,607	1,795	1,041	1,240	0,448	3,617
SCO2727		0,915	1,074	1,080	1,182	0,484	1,314
SCO3113		1,302	1,328	1,303	1,134	0,965	4,222
SCO3152		0,941	1,043	1,058	0,895	2,054	0,668
SCO3255	<i>spdB</i>	1,103	0,874	0,998	0,814	0,459	1,390
SCO3262		1,454	1,432	1,013	1,208	1,372	0,408
SCO3263		0,995	1,245	1,157	0,525	1,697	0,481
SCO3289		2,078	1,586	1,168	1,182	1,115	0,922
SCO3327		1,411	1,191	1,060	0,965	0,433	2,943
SCO3342		0,779	1,406	0,610	0,839	1,926	0,465
SCO3461		1,120	0,919	1,057	0,908	0,470	1,699
SCO3475		1,429	0,848	1,128	1,904	0,692	2,169
SCO3476		1,255	0,865	1,049	1,493	0,774	2,015
SCO3478		1,235	0,832	1,019	1,663	0,846	2,022
SCO3481		1,268	0,767	1,181	1,705	0,622	2,628
SCO3482		1,311	0,856	1,087	1,674	0,732	2,304
SCO3483		1,123	0,788	1,196	1,474	0,708	2,849
SCO3484		1,385	0,744	1,178	1,667	0,688	2,982
SCO3485		1,095	0,962	1,142	1,260	1,062	2,099
SCO3486		1,231	0,855	1,081	1,234	0,833	2,445
SCO3487		1,217	0,793	1,080	1,884	0,444	3,733
SCO3488		1,052	0,784	1,143	1,933	0,695	2,817
SCO3492		1,011	1,137	1,065	1,311	0,904	6,844
SCO3549	<i>bldG</i>	1,133	1,054	1,119	1,213	0,576	2,049
SCO3731	<i>scoF1</i>	1,458	1,117	0,960	0,893	0,516	2,024
SCO3748	<i>f40</i>	1,594	1,267	0,815	0,911	0,423	3,122
SCO3762		1,103	1,053	0,959	0,980	0,344	2,599
SCO3868		0,972	0,825	1,013	0,820	0,422	1,092
SCO3887	<i>parB</i>	0,964	0,965	1,074	1,090	0,465	2,004
SCO3906	<i>rpsF</i>	1,411	1,132	0,933	1,047	0,473	1,122
SCO3908	<i>rpsR</i>	1,489	1,164	0,983	1,088	0,437	1,305
SCO3938	<i>thiC</i>	1,144	0,914	1,036	1,118	0,197	4,461
SCO3990		1,049	1,146	0,857	0,606	2,213	0,785
SCO3992		1,381	1,624	1,180	0,843	2,708	0,921
SCO3993		1,065	1,430	1,245	0,948	2,192	0,529
SCO4005		0,941	1,218	0,940	1,027	1,640	0,483
SCO4011		0,950	0,903	1,024	0,738	1,491	0,439
SCO4063		1,174	1,070	0,965	0,565	2,092	0,669
SCO4212		1,102	0,547	0,968	0,512	0,048	2,180
SCO4225		1,039	0,940	1,014	0,686	1,630	0,450
SCO4261		1,176	0,832	0,954	0,885	0,306	1,570
SCO4289		0,752	1,241	0,879	0,928	2,713	0,369
SCO4424		1,009	0,887	0,937	1,237	1,735	0,480
SCO4442		1,452	1,129	1,310	0,909	0,338	3,005
SCO4635	<i>rpmG3</i>	1,315	0,991	1,095	1,028	0,404	2,221
SCO4652	<i>rpiI</i>	1,175	0,984	0,971	1,075	0,428	1,825

SCO4659	<i>rspL</i>	1,388	1,055	0,942	1,004	0,398	1,470
SCO4660	<i>rspG</i>	1,488	1,086	0,943	1,021	0,423	1,405
SCO4701	<i>rpsJ</i>	1,459	1,131	0,911	0,887	0,419	1,558
SCO4702	<i>rplC</i>	1,599	1,106	0,917	0,968	0,402	1,799
SCO4704	<i>rplW</i>	1,280	1,035	1,006	0,923	0,430	2,667
SCO4706	<i>rpsS</i>	1,651	1,075	0,942	1,001	0,327	2,397
SCO4711	<i>rpsQ</i>	1,364	1,086	1,033	0,894	0,272	4,002
SCO4712	<i>rplN</i>	1,386	1,115	0,983	0,900	0,418	1,893
SCO4713	<i>rplX</i>	1,325	1,076	0,998	0,878	0,440	0,995
SCO4714	<i>rplE</i>	1,461	1,070	0,927	0,929	0,344	1,793
SCO4715	<i>rpsN</i>	1,251	0,993	0,973	1,003	0,413	2,338
SCO4716	<i>rpsH</i>	1,322	1,035	0,913	0,951	0,480	1,548
SCO4717	<i>rplF</i>	1,341	0,996	0,977	1,000	0,493	1,485
SCO4720	<i>rpmD</i>	1,161	0,993	0,946	1,012	0,366	3,901
SCO4721	<i>rplO</i>	1,261	1,052	0,936	1,018	0,359	2,015
SCO4730	<i>rplQ</i>	1,390	1,047	0,918	0,963	0,475	2,452
SCO4761	<i>groES</i>	0,960	0,872	0,949	1,391	0,435	1,524
SCO4894		0,956	0,910	1,080	0,635	2,013	0,849
SCO4903		0,921	1,088	0,982	0,822	1,762	0,460
SCO5029		1,290	1,032	1,088	1,126	0,497	1,622
SCO5191		1,276	1,454	0,995	1,298	0,319	1,708
SCO5227	<i>nrdX</i>	0,812	0,782	1,033	0,985	0,529	2,819
SCO5240		1,519	1,201	0,936	1,328	0,484	2,311
SCO5326		0,966	1,569	1,012	0,490	2,565	0,477
SCO5490		1,127	0,921	0,909	0,768	0,386	1,260
SCO5578	<i>glcP1</i>	8,691	7,028	6,642	5,109	2,671	1,519
SCO5583	<i>amtB</i>	1,172	1,508	0,797	2,727	1,021	1,485
SCO5584	<i>glnK</i>	1,136	1,329	0,878	2,116	0,976	1,710
SCO5609		1,171	0,743	0,974	1,055	0,088	3,108
SCO5639		1,584	1,564	1,169	0,708	2,045	0,678
SCO5742		1,042	1,944	0,923	0,538	2,107	0,808
SCO5824		0,980	0,834	0,956	0,777	0,495	1,338
SCO5907		1,042	0,748	0,758	0,761	0,405	1,952
SCO5918		1,359	1,019	0,504	0,587	1,201	1,051
SCO5920		1,282	1,003	0,406	0,807	1,233	0,936
SCO5978		0,947	0,888	0,964	0,990	0,641	2,240
SCO5987		1,118	0,938	1,154	1,228	2,318	0,419
SCO6009	<i>xyIF</i>	3,530	2,202	1,982	2,337	1,105	1,803
SCO6010	<i>xyIG</i>	5,801	4,696	4,511	3,305	2,717	1,656
SCO6011	<i>xyIH</i>	2,056	1,566	1,464	1,459	1,295	1,110
SCO6026		0,903	1,209	0,939	0,465	0,973	1,031
SCO6027		0,906	1,076	0,895	0,435	0,954	0,973
SCO6045		0,996	0,992	0,990	0,984	1,363	0,476
SCO6290		1,327	1,050	1,055	1,100	0,333	1,675
SCO6338		0,984	1,337	1,123	0,356	1,516	0,551
SCO6403		1,136	1,129	0,681	0,726	0,498	1,125

SCO6480		1,250	1,042	0,698	0,700	0,438	1,762
SCO6499	<i>gvpO</i>	0,471	0,594	1,016	1,140	1,474	0,952
SCO6547		1,441	1,399	1,079	1,781	0,690	2,041
SCO6600	<i>rok8A6</i>	1,056	0,490	1,092	1,440	0,720	2,381
SCO6624		0,746	0,820	1,018	0,815	0,815	4,175
SCO6642		0,973	1,283	1,321	0,600	2,150	1,089
SCO6715	<i>wblH</i>	1,731	0,995	1,153	2,376	1,584	0,829
SCO6761		0,934	0,951	0,795	0,584	1,483	0,462
SCO6779		1,065	1,212	0,795	0,495	1,361	0,925
SCO6810		1,220	0,717	0,920	1,133	0,368	1,878
SCO6910		0,987	1,307	1,158	0,733	2,189	0,775
SCO6925		0,910	1,195	1,105	0,521	2,121	0,623
SCO6933		0,924	1,005	1,103	0,901	0,479	1,998
SCO7086		0,963	0,910	1,028	0,934	0,488	1,286
SCO7087		1,075	1,066	0,991	0,817	0,514	2,358
SCO7106		1,111	0,893	1,157	0,980	0,368	1,548
SCO7153	<i>glcP2</i>	8,047	6,510	6,128	4,418	3,350	1,514
SCO7217		1,123	0,996	0,975	1,172	1,063	2,339
SCO7528		0,953	0,792	0,966	0,858	0,456	2,030
SCO7552		1,196	1,083	0,959	1,174	0,383	2,315
SCO7636		1,155	1,099	1,034	0,631	0,345	1,305
SCO7645		0,939	0,866	0,944	0,867	0,462	1,254
SCO7742		1,283	1,149	1,019	1,291	0,475	2,133
SCO7752		1,009	0,933	1,045	1,029	0,466	1,625
SCO7774		1,119	0,955	0,924	0,928	0,436	1,223
SCO7800		1,009	1,781	1,172	0,590	2,237	0,833
SCO7833		1,254	0,934	0,918	0,823	0,488	1,442
SCO7836		1,107	0,976	0,987	1,203	0,413	3,370

SCO6659	2,05	0,58	2,58E-02	3	2,13	0,37	7,85E-02	2	0,01	2,09	4,25	glucose-6-phosphate isomerase 7395031:7396683 reverse MW:60424
SCO6660	1,84	0,02	5,77E-02	3	2,38	0,14	1,22E-03	3	0,08	2,11	4,32	hypothetical protein SC5A7.10c 7396676:7397611 reverse MW:33918
SCO6661	1,82	0,29	8,54E-03	3	2,48	0,19	1,06E-05	9	0,10	2,15	4,45	glucose-6-phosphate 1-dehydrogenase 7397608:7399386 reverse MW:65672
SCO6662	2,50	0,17	1,46E-03	3	2,81	0,46	9,00E-03	3	0,04	2,66	6,30	transaldolase 7399383:7400528 reverse MW:40407
SCO6663	2,45	0,04	6,94E-05	3	2,61	0,07	7,06E-02	3	0,02	2,53	5,77	transketolase 7400592:7402688 reverse MW:74588
SCO7638	1,22	0,12	8,53E-08	12	1,82	0,11	1,86E-06	10	0,12	1,52	2,86	enolase 8466854:8468158 reverse MW:45534
External												
SCO1230	2,12	0,05	1,10E-02	2	0,18	0,06	1,39E-02	5	0,45	1,15	2,22	putative secreted tripeptidylaminopeptidase 1304188:1305813 reverse MW:58517
SCO2383	1,68	0,10	0,00E+00	35	0,49	0,18	0,00E+00	51	0,32	1,09	2,12	putative secreted protein 2552256:2556893 forward MW:161489
SCO2920	2,37	0,19	5,21E-05	8	0,17	0,23	2,37E-02	13	0,46	1,27	2,40	putative secreted protease 3169338:3171683 reverse MW:85727
SCO3097	-0,77	0,16	9,33E-02	2	-1,41	0,03	1,01E-02	2	0,18	-1,09	0,47	putative secreted protein 3392082:3392816 reverse MW:24877
SCO4157	4,03	0,08	8,97E-03	2	1,05	0,15	6,43E-02	2	0,34	2,54	5,82	putative protease 4573947:4574990 reverse MW:34864
SCO6009	2,19	0,08	4,75E-04	3	2,47	0,15	1,28E-03	3	0,04	2,33	5,03	periplasmic solute-binding protein 6589575:6590690 forward MW:39215
SCO6281	-0,75	0,24	3,60E-04	8	-2,65	0,06	8,27E-03	5	0,33	-1,70	0,31	putative FAD-binding protein 6939907:6941544 forward MW:58522

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