

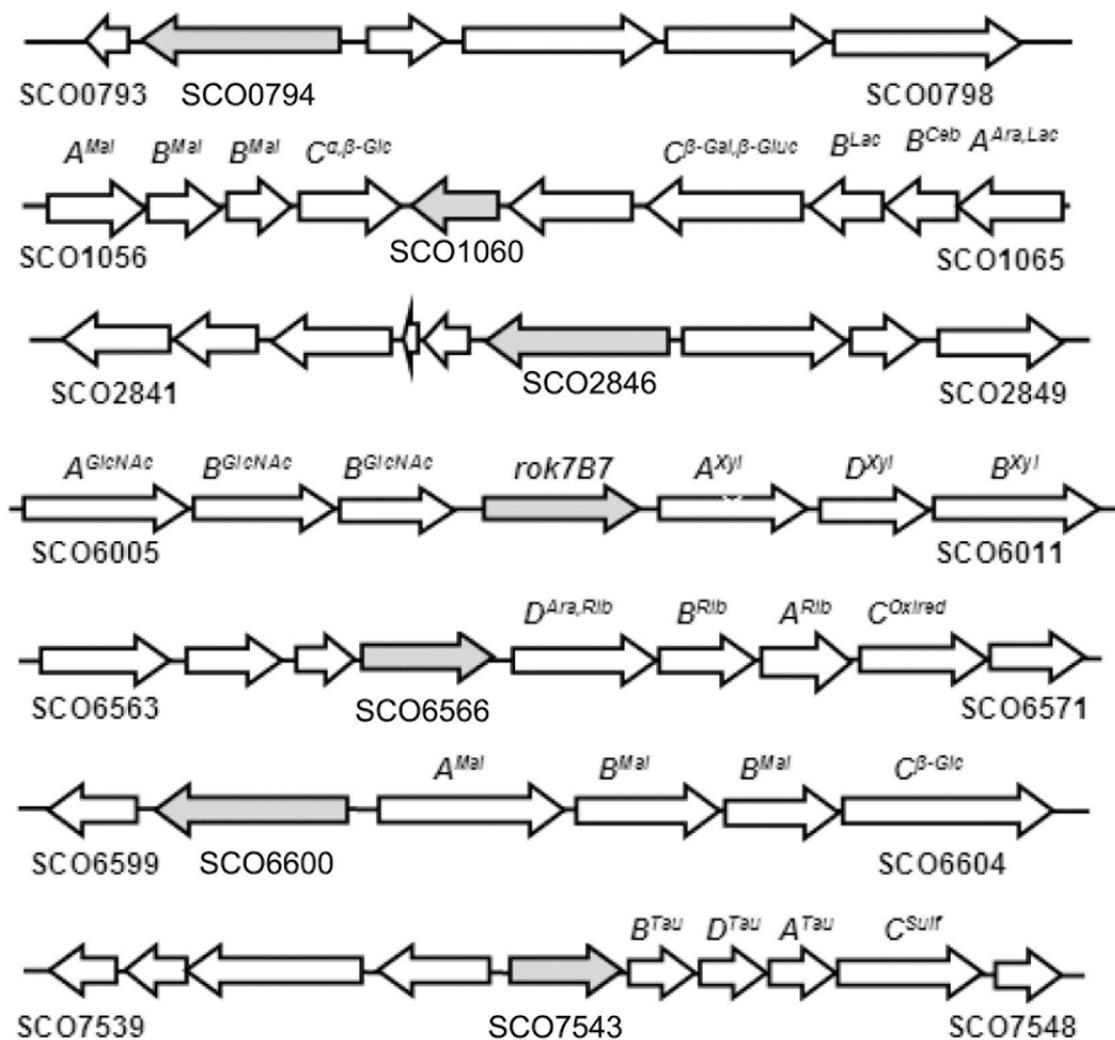
## SUPPLEMENTAL DATA

Belonging to the manuscript:

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

by

Magdalena A. Świątek, Jacob Gubbens, Giselda Bucca, Eunjung Song, Yung-Hun Yang, Emma Laing, Byung-Gee Kim, Colin P. Smith, and Gilles P. van Wezel



**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 <sup>-</sup> SCP2 <sup>-</sup>	(3)
GAM20	M145 SCO0794::aacC4, Apr <sup>R</sup>	This work
GAM21	M145 SCO1060::aacC4, Apr <sup>R</sup>	This work
GAM22	M145 SCO2846::aacC4, Apr <sup>R</sup>	This work
GAM23	M145 SCO6008::aacC4, Apr <sup>R</sup>	This work
GAM24	M145 SCO6566::aacC4, Apr <sup>R</sup>	This work
GAM25	M145 SCO6600::aacC4, Apr <sup>R</sup>	This work
GAM26	M145 SCO7543::aacC4, Apr <sup>R</sup>	This work
GAM30	M145 ΔSCO0794 D	This work
GAM31	M145 ΔSCO1060 D	This work
GAM32	M145 ΔSCO2846 D	This work
GAM33	M145 ΔSCO6008 D	This work
GAM34	M145 ΔSCO6566 D	This work
GAM35	M145 ΔSCO6600 D	This work
GAM36	M145 ΔSCO7543 D	This work
DM9	M145 ΔredDΔactII-ORF4	(2)

# Apr, apramycin resistant; D, deletion mutant

**Table S2. Plasmids constructs used in this study.**

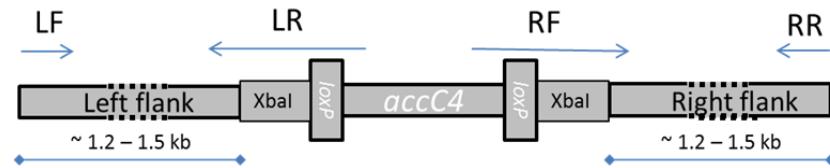
Plasmid	Description	Reference
pWHM3	Cloning vector, <i>colE1</i> replicon, pSG5 replicon, TsrR, AmpR	(4)
pUWLcre	pUWLoriT derivative with <i>cre(a)</i> gene under <i>ermE*</i> promoter	(1)
pGAM8	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO0794 with apraloxP_XbaI inserted between them in pWHM3 <i>EcoRI-HindIII</i>	This work
pGAM9	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO1060 with apraloxP_XbaI inserted between them in pWHM3 <i>EcoRI-HindIII</i>	This work
pGAM10	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO2846 with apraloxP_XbaI inserted between them in pWHM3 <i>EcoRI-HindIII</i>	This work
pGAM11	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO6008 with apraloxP_XbaI inserted between them in pWHM3 <i>EcoRI-HindIII</i>	This work
pGAM12	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO6566 with apraloxP_XbaI inserted between them in pWHM3 <i>EcoRI-HindIII</i>	This work
pGAM13	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO6600 with apraloxP_XbaI inserted between them in pWHM3 <i>EcoRI-HindIII</i>	This work
pGAM14	pWHM3 containing flanking regions of <i>S. coelicolor</i> SCO7543 with apraloxP_XbaI inserted between them in pWHM3 <i>EcoRI-HindIII</i>	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; GAATTTC, *Eco*RI; TCTAGA, *Xba*I; AAGCTT, *Hind*III; CATATG, *Nde*I; CTCGAG, *Xba*I. For scheme of primer design see image at the end of the table.

Name #	5'-3' sequence
0794LF-1497	<b>gtcagaatt<u>cacccggggatt</u>gaaccgcaggct</b>
0794LR+6	<b>gaagttat<u>ccatcacct</u>ctagacccatgtggctcccccgt</b> a
0794RF+1285	<b>gaagttat<u>cgcgcatct</u>ttagacactgaggttcgggtcg</b> c
0794RR+2699	<b>gtcaa<u>agcttcgggcagcaaaat</u>cgtggtcacg</b>
1060LF-1387	<b>gtcagaatt<u>cggctggacat</u>cgaggcaccgt</b>
1060LR+9	<b>gaagttat<u>ccatcacct</u>ttagagttcatcatggtgcgtcg</b> ag
1060RF+1228(48)	<b>gaagttat<u>cgcgcatct</u>ttagacgggacgcgggctgacacgg</b> a
1060RR+2552(74)	<b>gtcaa<u>agcttcgggaccgtcgat</u>tgggacacc</b>
2846LF-1369	<b>gtcagaatt<u>ccctgcggcgat</u>ccaggcgtcgt</b>
2846LR+9	<b>gaagttat<u>ccatcacct</u>ttagac<u>actgtt</u>acacccccattgtc</b>
2846RF+1224	<b>gaagttat<u>cgcgcatct</u>ttagacgggggacggcggctgagac</b>
2846RR+2637	<b>gtcaa<u>agcttcagaccgttccac</u>gagg</b> tcc
6008LF-848new	<b>gtcagaatt<u>tgtcggtgtctcg</u>gactg</b>
6008LR+147new	<b>gaagttat<u>ccatcacct</u>ttagac<u>ccggacgtt</u>cgagaccgtcg</b>
6008RF+1201loxPnew	<b>gaagttat<u>cgcgcatct</u>ttagac<u>gcctt</u>acttagacgacggatgg</b>
6008RR+2675(97)	<b>gtcaa<u>agcttagct</u>tacgtcggtgagcg</b> cct
6566LF-1406	<b>gtcagaatt<u>cgcgccgaca</u>agatgtccgagg</b> tc
6566LR+6	<b>gaagttat<u>ccatcacct</u>ttagaggacacgacgaggcccccgg</b>
6566RF+1398	<b>gaagttat<u>cgcgcatct</u>ttagagcgttagccaccac</b> ttcactt
6566RR+2677	<b>gtcaa<u>agcttagaccgac</u>acgttgcgggtgac</b>
6600LF-1371	<b>gtcagaatt<u>tgcgaact</u>gcactcg</b> tccggca
6600LR+6	<b>gaagttat<u>ccatcacct</u>ttagaggccatccggccccc</b> tttt
6600RF+1321(41)	<b>gaagttat<u>cgcgcatct</u>ttagaggatgaggccgtgcgcgcgg</b> c
6600RR+2671(93)	<b>gtcaa<u>agcttgcgcgt</u>agactacgtc</b> gacactg
7543LF-1253	<b>gtcagaatt<u>cacgggtccgtcg</u>gttgc</b>
7543LR+6	<b>gaagttat<u>ccatcacct</u>ttagagg</b> tcagggtcg
7543RF+1270(90)	<b>gaagttat<u>cgcgcatct</u>ttagac<u>ccct</u>gacaagcggagtgc</b> ga
7543RR+2635(57)	<b>gtcaa<u>agcttccatc</u>agcaggatcgagg</b> gttc
0794check-451	<b>gtcagaatt<u>tgtcg</u>aggcacagcg</b> cgccacatg
0794check+1728(51)	<b>gtcaa<u>agcttagttcg</u>gggactgcgg</b> cag
1060check-501	<b>gtcagaatt<u>tctggc</u>accggcaacc</b> agtgc
1060check+1695(1718)	<b>gtcaa<u>agcttgcc</u>acggacaacc</b> ctacgagg
2846check-687	<b>gtcagaatt<u>cactcg</u>gtacacc</b> tgcgtgacc
2846check+1886(1907)	<b>gtcaa<u>agcttacccgtcc</u>atgtcg</b> gtgagc
6008check-689	<b>gtcagaatt<u>tctcc</u>agg</b> ttgcagaacttcggctg
6008check+1923(46)	<b>gtcaa<u>agcttccat</u>ttgcgtcgaggacgg</b> ag
6566check-541	<b>gtcagaatt<u>cacacc</u>gagg</b> gtggtcgatctg
6566check+1898(1921)	<b>gtcaa<u>agcttcgg</u>ctgtgacc</b> aggagg
6600check-549	<b>gtcagaatt<u>tctcg</u>aa</b> ggttctggcg
6600check+1880(1901)	<b>gtcaa<u>agcttgg</u>ta</b> gcgcgggatctcg
7543check-626	<b>gtcagaatt<u>cagcc</u>acac</b> gaagatgcgtcg
7543check+1894(1917)	<b>gtcaa<u>agcttacgcgg</u>caagat</b> cg
xylG_for	<b>tccgtctcgat</b> caacaggccgca
xylG_rev	<b>aggcgatcggtatgcggacg</b> ctc
RTglcP1_for	<b>agctggta</b> actgggtct

RTglcP1_rev	gtcgaagtccacgtccttg
rpsl_for	gagaccactccc gagcagccgc
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 *rokB7* null mutant in MM mannitol solid-grown cultures. (\*)**

Gene	Name	RokB7/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>rpmI</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>rdlA</i>	1,789	1,717	1,056	0,996	0,279	8,120

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

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

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

**Table S5. Proteins that are significantly differentially expressed between *S. coelicolor* M145 and its *rokB7* null mutant in MM mannitol-grown liquid cultures as determined by quantitative proteomics experiments.**

14N:M145 / 15N RokB7				14N:RokB7 / 15N:M145							
ID	2log ratio	standard deviation	p-value	nr. Of peptides	2log ratio	standard deviation	p-value	nr. Of peptides	p-value	average ratio	average ratio
									label swap	2log(RokB7/wt)	RokB7/wt Description
<b>mycelial</b>											
SCO0492	1,96	0,15	8,88E-16	25	2,11	0,13	0,00E+00	27	0,02	2,03	4,09 putative peptide synthetase 513989:524920 reverse MW:389791
SCO0498	2,34	0,08	5,79E-02	3	2,43	0,19	2,72E-09	8	0,01	2,39	5,23 putative peptide monooxygenase 530970:532325 reverse MW:49851
SCO0499	2,01	0,17	2,45E-03	3	1,83	0,19	3,21E-09	14	0,03	1,92	3,78 putative formyltransferase 532501:533448 forward MW:35343
SCO1388	1,06	0,12	1,75E-02	4	1,52	0,15	5,65E-05	8	0,11	1,29	2,44 putative mannose-1-phosphate guanyltransferase 1465266:1467761 reverse MW:89609
SCO1623	1,24	0,02	5,86E-03	2	1,25	0,03	4,13E-03	5	0,00	1,24	2,37 hypothetical protein SCI41.06 1737167:1738009 forward MW:31483
SCO1648	1,06	0,10	1,60E-05	5	1,23	0,11	5,92E-02	3	0,05	1,15	2,21 AAA ATPase 1762040:1763806 reverse MW:65142
SCO2008	1,24	0,11	1,11E-07	7	1,63	0,14	3,25E-11	10	0,09	1,44	2,70 putative periplasmic branched chain amino acid binding protein 2149264:2150520 forward MW:43471
SCO2012	0,91	0,06	1,51E-03	3	1,56	0,12	2,11E-03	3	0,16	1,24	2,35 putative branched chain amino acid transport ATP-binding protein 2154331:2155047 forward MW:25593
SCO2026	0,62	0,09	0,00E+00	33	1,85	0,11	2,98E-12	20	0,29	1,24	2,36 putative glutamate synthase large subunit 2171840:2176384 reverse MW:162913
SCO2126	1,76	0,05	2,63E-04	3	1,56	0,03	5,77E-02	3	0,04	1,66	3,16 glucokinase 2285983:2286936 reverse MW:33062
SCO2179	-0,58	0,04	5,85E-02	3	-1,42	0,01	3,88E-03	2	0,25	-1,00	0,50 putative aminopeptidase 2342474:2344027 forward MW:51965
SCO2599	-1,45	0,22	1,84E-02	4	-2,11	0,16	4,35E-03	5	0,12	-1,78	0,29 hypothetical protein SCC88.10c 2814360:2818382 reverse MW:140415
SCO2776	1,49	0,10	1,40E-03	3	1,24	0,12	3,37E-03	3	0,06	1,36	2,57 acetyl/propionyl CoA carboxylase beta subunit 3027514:3029130 forward MW:57413
SCO2777	1,59	0,16	4,56E-02	2	1,46	0,09	7,30E-05	4	0,03	1,52	2,87 acetyl/propionyl CoA carboxylase alpha subunit 3029169:3031109 forward MW:68238
SCO2779	1,78	0,12	1,46E-03	3	1,47	0,24	6,27E-02	3	0,06	1,62	3,08 acyl-CoA dehydrogenase 3032065:3033225 forward MW:41726
SCO2785	2,25	0,33	6,92E-03	3	1,53	0,16	3,75E-03	3	0,12	1,89	3,71 hypothetical protein SCC105.16 3038895:3040682 forward MW:66590
SCO2884	1,01	0,04	1,89E-02	2	1,47	0,02	5,77E-02	3	0,12	1,24	2,36 putative cytochrome P450. 3138904:3140130 forward MW:44662
SCO3127	0,80	0,12	0,00E+00	29	1,26	0,13	0,00E+00	35	0,14	1,03	2,04 phosphoenolpyruvate carboxylase (EC 4.1.1.31) 3427131:3429866 reverse MW:101265
SCO3230	4,56	0,48	9,33E-11	21	4,51	0,59	0,00E+00	26	0,00	4,53	23,16 CDA peptide synthetase I 3543334:3565725 forward MW:798587
SCO3231	3,65	1,66	1,09E-09	22	4,84	0,29	4,29E-08	14	0,09	4,25	19,01 CDA peptide synthetase II 3565722:3576734 forward MW:394636
SCO3232	4,39	0,53	2,94E-06	10	5,03	0,18	3,06E-06	12	0,04	4,71	26,21 CDA peptide synthetase III 3576734:3583987 forward MW:258501
SCO3236	4,58	0,36	2,10E-03	3	3,14	1,05	3,57E-02	3	0,12	3,86	14,48 putative oxygenase 3587686:3588687 reverse MW:35981
SCO3285	1,23	0,09	2,66E-14	12	1,56	0,19	6,50E-05	8	0,07	1,40	2,63 putative large glycine/alanine rich protein 3628804:3634122 reverse MW:187287
SCO3286	1,24	0,07	1,08E-11	9	1,43	0,37	2,79E-06	9	0,05	1,33	2,52 hypothetical protein 3634208:3636241 reverse MW:74288
SCO3607	0,71	0,11	3,96E-11	13	1,30	0,15	6,79E-11	11	0,18	1,00	2,00 putative membrane protein 3983676:3985145 reverse MW:51612
SCO4092	-1,19	0,07	2,74E-02	2	-1,15	0,00	2,98E-04	2	0,01	-1,17	0,44 ATP-dependent helicase 4486638:4490621 reverse MW:150571
SCO4651	-2,06	0,22	3,54E-04	4	-1,92	0,07	4,16E-03	5	0,02	-1,99	0,25 putative lipoprotein 5075272:5076120 forward MW:30048
SCO4945	-0,77	0,26	2,83E-03	5	-2,51	0,15	3,22E-06	5	0,31	-1,64	0,32 putative dehydrogenase 5378898:5379938 forward MW:36494
SCO5166	-1,79	0,15	1,22E-05	5	-1,94	0,13	1,56E-03	3	0,02	-1,87	0,27 putative helicase 5612300:5614939 reverse MW:92468
SCO5357	-1,35	0,42	1,50E-09	16	-1,12	0,58	2,18E-03	7	0,06	-1,23	0,43 transcription terminator factor (fragment) 5826214:5828298 forward MW:75146
SCO5389	1,78	0,10	2,46E-06	5	1,72	0,10	2,68E-06	5	0,01	1,75	3,36 hypothetical protein 5858397:5858789 forward MW:14303
SCO5515	0,85	0,14	0,00E+00	21	1,34	0,25	1,57E-08	14	0,14	1,10	2,14 probable D-3-phosphoglycerate dehydrogenase 6006860:6008449 forward MW:55015
SCO5822	-1,30	0,11	1,36E-05	5	-1,39	0,14	4,53E-03	5	0,02	-1,34	0,39 undefined product 6371006:6373129 forward MW:77238
SCO5878	1,34	0,02	5,77E-02	3	1,46	0,18	5,34E-04	4	0,03	1,40	2,64 polyketide synthase RedX 6433668:6436616 forward MW:100927
SCO5879	1,64	0,07	5,80E-02	3	1,69	0,20	5,26E-02	2	0,01	1,66	3,17 acyl-coA dehydrogenase RedW 6436613:6437788 forward MW:41624
SCO5888	1,98	0,16	2,20E-03	3	1,90	0,14	5,86E-02	3	0,01	1,94	3,84 3-oxoacyl-[acyl-carrier-protein] synthase 6444587:6445594 forward MW:34665
SCO5890	2,22	0,29	5,54E-03	3	1,64	0,18	3,45E-08	8	0,10	1,93	3,81 transferase 6445914:6447836 forward MW:68062
SCO5891	2,37	0,17	3,21E-02	2	1,77	0,14	3,63E-02	2	0,09	2,07	4,20 peptide synthase 6447950:6449548 forward MW:56886
SCO5892	2,22	0,33	1,20E-04	5	2,02	0,14	4,96E-05	8	0,03	2,12	4,35 polyketide synthase 6449549:6456442 forward MW:241994
SCO5895	2,27	0,15	1,65E-02	4	1,54	0,15	1,97E-07	7	0,12	1,91	3,75 putative methyltransferase 6458306:6459394 forward MW:39394
SCO5896	2,10	0,01	5,34E-06	3	1,81	0,04	7,82E-02	3	0,05	1,95	3,88 phosphoenolpyruvate-utilizing enzyme 6459417:6462218 forward MW:102291
SCO6005	1,25	0,04	1,49E-02	2	2,57	0,05	7,05E-02	3	0,21	1,91	3,75 hypothetical protein SC7B7.02 6584624:6586033 forward MW:50611
SCO6009	3,33	0,14	4,23E-11	8	3,12	0,21	8,23E-11	9	0,02	3,22	9,33 periplasmic solute-binding protein 6589575:6590690 forward MW:39215
SCO6010	3,44	0,22	1,34E-03	3	3,39	0,13	1,87E-08	6	0,00	3,41	10,66 probable ABC-transport system ATP binding protein 6590859:6591641 forward MW:27896
SCO6198	1,82	0,07	3,66E-13	23	2,19	0,13	1,84E-14	23	0,06	2,00	4,01 putative secreted protein 6808799:6812269 forward MW:116719
SCO6431	1,57	0,06	2,18E-04	7	1,58	0,14	6,00E-10	9	0,00	1,57	2,98 hypothetical protein 7108264:7111779 forward MW:126560
SCO6436	1,88	0,07	4,03E-04	3	2,03	0,25	5,57E-02	2	0,02	1,96	3,88 putative tRNA synthetase 7118254:7119774 forward MW:55170

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
<b>External</b>											
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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