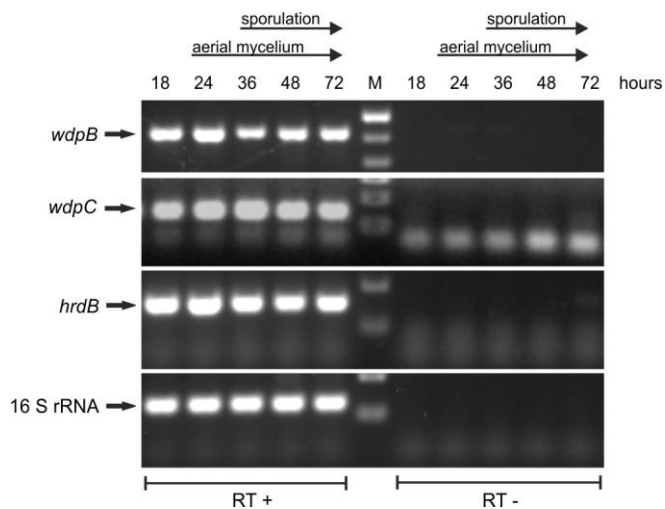
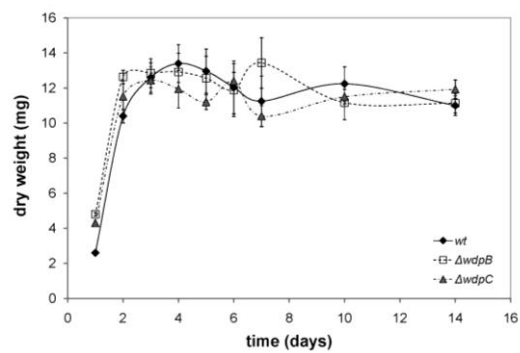


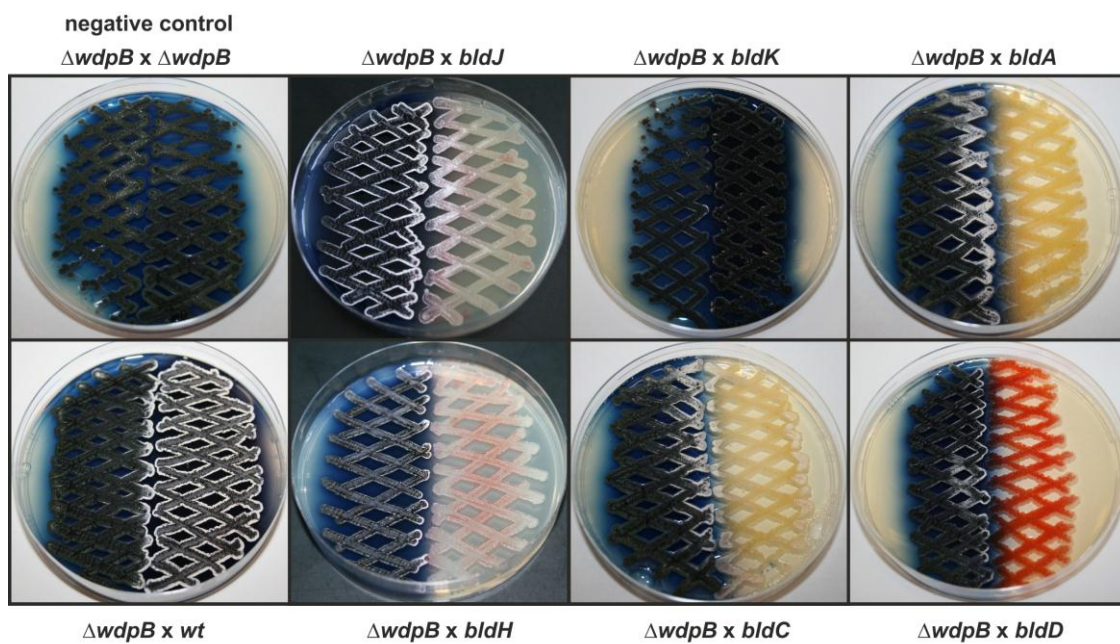
**Fig. S1** Organization of the *S. coelicolor* M145 chromosome near *wdpB* and *wdpC* genes and cotranscription analysis of SCO5951-3 and SCO2244-7 genes; schematic representation of *wdpB* and *wdpC* genome regions. DNA sequences deleted and replaced with apramycin resistance gene in both  $\Delta wdpB$  and  $\Delta wdpC$  mutant strains as well as DNA fragments that were cloned into vectors pWDB11, pWDB12, pWDB13, pMAL-WDB, pWDC622 and pMAL-WDC for overexpression and complementation experiments are represented by bars (panels **A** and **B**). To determine transcriptional organisation of *wdpB* and *wdpC* genome regions RNA was extracted from mycelium cultivated on modified R3 agar and harvested after 48 h. RT-PCR reactions containing primer pairs a+b, c+d and e+f (primer position is indicated in panel **A**) were used to detect the cotranscription of SCO5951-2 (a+b), SCO5952-3 (c+d) and SCO5953-4 (e+f), respectively (panel **C**). Similarly, RT-PCR reactions containing primer pairs 1+2, 3+4 and 5+6 (primer position is indicated in panel **B**) were used to detect the cotranscription of SCO2244-5 (1-2), SCO2245-6 (3-4) and SCO2246-7 (5-6), respectively (panel **D**). RT-PCR reactions were performed in the presence (+) or the absence (-) of reverse transcriptase (RT). Genomic DNA (gDNA) was used as a positive control for the PCR conditions. PCR products were separated on 1.5% agarose gel. The integrity of the cDNA samples was verified by the primer pair specific for the *hrdB* gene (data not shown). M – size marker.



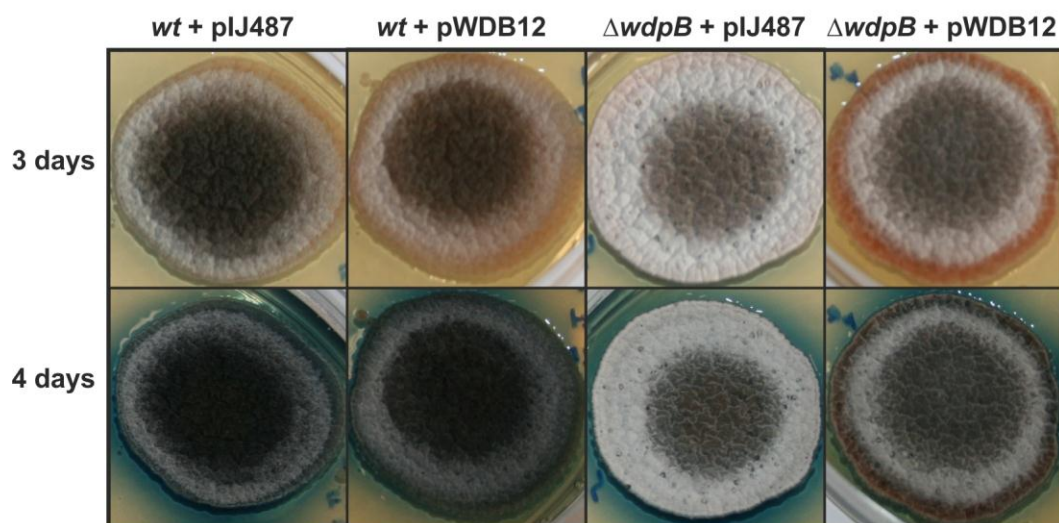
**Fig. S2** The presence of *wdpB* and *wdpC* transcripts determined by RT-PCR throughout development of *S. coelicolor* M145. The total RNA extracted from mycelium after 18, 24, 36, 48 and 72 hours of growth on modified R3 solid media was subjected to cDNA synthesis and subsequent RT-PCR. cDNA synthesized in presence (+) and absence (-) of reverse transcriptase (RT) was used for RT-PCR. *hrdB* and 16S rRNA genes were used as reference genes with constant gene expression during development (data not shown). PCR products were separated on a 1.5% agarose gel in TAE 1x buffer. M – size marker.



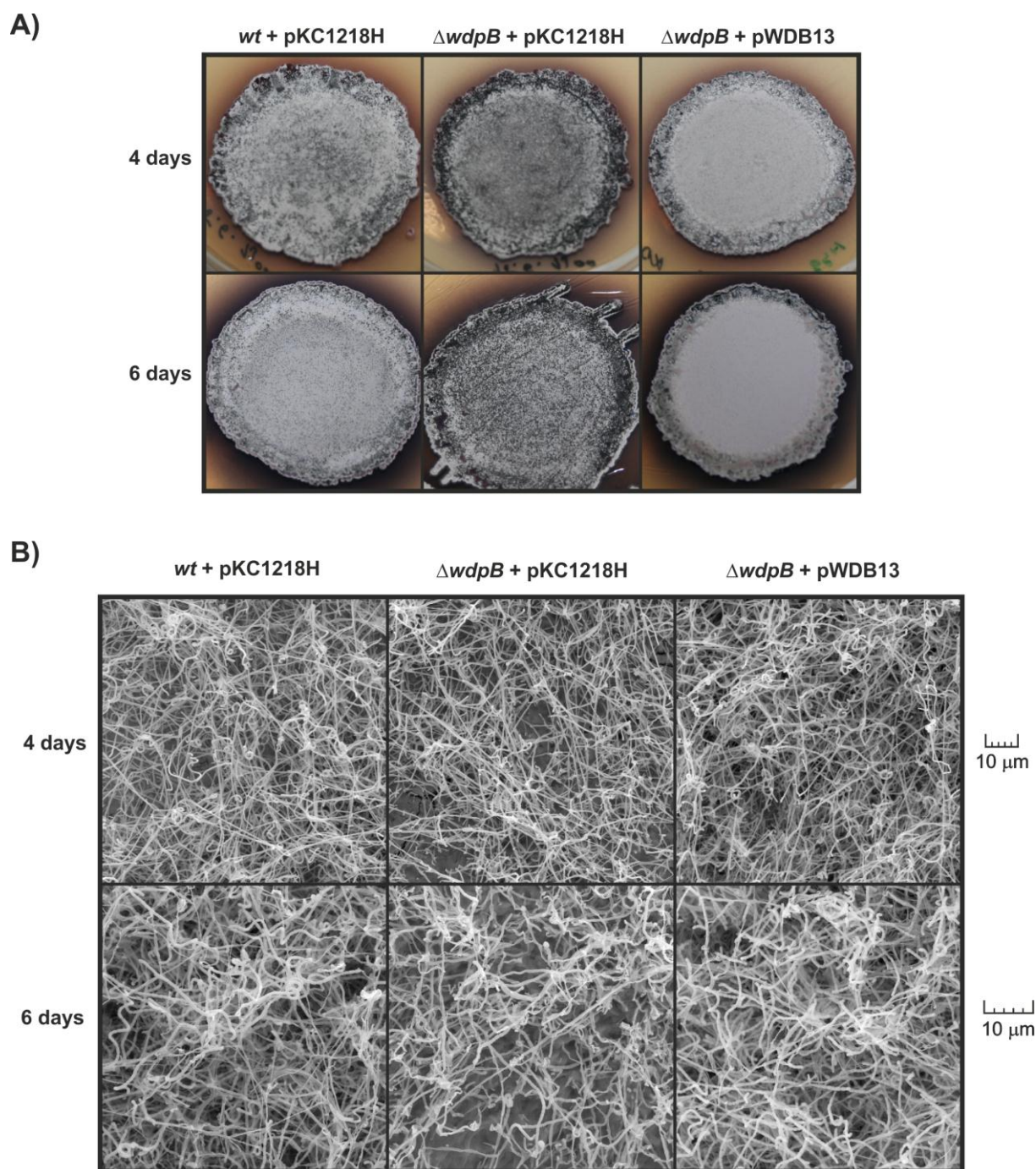
**Fig. S3** Growth kinetics of the  $\Delta wdpB$  and  $\Delta wdpC$  strains. The wild-type strain (*wt*) and both mutants were cultivated 14 days on modified R3 plates. The growth was calculated as mg of dry weight of mycelium. The standard errors of the means for four independent experiments are shown.



**Fig. S4** Extracellular complementation of the  $\Delta wdpB$  mutant and bald mutants. The  $\Delta wdpB$  mutant was grown in close proximity to the wild-type strain (positive control),  $\Delta wdpB$  mutant alone (negative control) and to the developmentally blocked *bldJ*, *bldK*, *bldA*, *bldH*, *bldC* and *bldD* mutants. Images were taken after 4 days of growth on R2YE agar plates.



**Fig. S5** Overexpression and genetic complementation of the  $\Delta wdpB$  mutant strain based on high-copy number vector pIJ487. The wild-type strain *wt* + pIJ487, mutant strain  $\Delta wdpB$  + pIJ487, *wdpB*-overexpression strain *wt* + pWDB12 and complemented strain  $\Delta wdpB$  + pWDB12 were cultivated on modified R3 solid plates. The images were taken after growth for 3 and 4 days. The overexpression strain *wt* + pWDB12 exhibited the same phenotype as wild-type strain *wt* + pIJ487. The complemented strain  $\Delta wdpB$  + pWDB12 showed recovery of the wild-type phenotype.



**Fig. S6** Genetic complementation of the  $\Delta wdpB$  mutant strain based on low-copy number vector pKC1218H. The wild-type strain *wt* + pKC1218H, mutant strain  $\Delta wdpB$  + pKC1218H and complemented strain  $\Delta wdpB$  + pWDB13 were cultivated on GYM solid plates. Macroscopic images (**A**) and scanning electron micrographs (**B**) were taken after growth for 4 and 6 days. The complemented strain  $\Delta wdpB$  + pWDB13 recovered the ability of aerial mycelium formation and sporulation similarly to that of the wild-type strain *wt* + pKC1218H.

**Table S1** *S. coelicolor* genes affected in the  $\Delta wdpB$  mutant compared to the wild-type strain M145 – comparison of gene transcript levels between microarray analysis and qRT-PCR analysis

Functional category	Gene no.	Gene product (gene)	DNA microarrays		qRT-PCR
			P-value	Fold change <sup>a</sup>	Fold change <sup>a</sup>
<b><u>1. wdpB gene and neighbouring SCO5954 gene</u></b>					
	SCO5953	putative membrane protein with WD-40 repetitive domains ( <i>wdpB</i> )	0.000	2.92	19.54 (± 3.74)
	SCO5954	probable chitinase (putative secreted protein)	0.001	12.43	34.51 (± 7.14)
<b><u>2. Aerial hyphae formation and its subsequent differentiation</u></b>					
<b>a) Chaplins</b>					
	SCO7257	<i>chpB</i>	0.032	-2.11	-1.12 (± 0.55)
	SCO1674	<i>chpC</i>	0.000	-3.40	-2.69 (± 0.60)
	SCO2717	<i>chpD</i>	0.000	-3.83	-3.55 (± 1.11)
	SCO1800	<i>chpE</i>	0.003	-1.76	-1.97 (± 0.20)
	SCO1675	<i>chpH</i>	0.000	-2.66	-10.24 (± 3.69)
<b>b) Rodlins</b>					
	SCO2718	<i>rdlA</i>	0.000	-13.50	-15.19 (± 7.95)
	SCO2719	<i>rdlB</i>	0.001	-6.29	-9.59 (± 3.14)
<b>c) ram gene cluster</b>					
	SCO6681	putative serine/threonine protein kinase ( <i>ramC</i> )	0.001	-3.87	-3.49 (± 0.61)
	SCO6682	surface-active peptide SapB ( <i>ramS</i> )	0.000	-5.95	-17.51 (± 7.15)
	SCO6683	probable ABC transporter ( <i>ramA</i> )	0.003	-2.20	
	SCO6684	probable ABC transporter ( <i>ramB</i> )	0.001	-2.42	
	SCO6685	two-component system response regulator ( <i>ramR</i> )	0.004	-2.25	-2.27 (± 0.51)
<b>d) nepA gene</b>					
	SCO4002	<i>nepA</i>	0.000	-2.61	-4.31 (± 0.59)
<b><u>3. Sporulation</u></b>					
	SCO4675	conserved hypothetical protein	0.000	-2.69	
	SCO4676	hypothetical protein	0.000	-2.00	
	SCO4677	putative regulatory protein; probably anti- $\sigma^F$ factor ( <i>ryfA</i> )	0.000	-2.04	-2.58 (± 0.46)
	SCO5321	polyketide hydroxylase ( <i>whiE</i> , <i>ORFVIII</i> )	0.011	-2.08	-1.15 (± 0.22)
	SCO5819	sporulation transcription factor ( <i>whiH</i> )	0.004	-2.64	-3.42 (± 0.01)
	SCO6029	two-component regulator ( <i>whiI</i> )	0.000	3.79	
<b><u>4. Secondary metabolism</u></b>					
	SCO6992	regulatory protein ( <i>absR1</i> )	0.013	-3.45	-8.95 (± 4.23)
<b>a) Calcium-dependent antibiotics</b>					
	SCO3210	probable 2-dehydro-3-deoxyheptonate aldolase	0.010	-2.20	
	SCO3214	probable anthranilate synthase component I ( <i>trpE2</i> )	0.018	-2.95	
	SCO3215	hypothetical protein	0.002	-2.07	
	SCO3217	transcriptional activator for the CDA biosynthesis cluster ( <i>cdaR</i> )	0.006	-1.40	-1.88 (± 0.63)
	SCO3218	putative small conserved hypothetical protein	0.003	-2.07	
	SCO3220	putative secreted protein	0.000	-2.90	
	SCO3221	probable oxidoreductase	0.000	-2.91	
	SCO3222	possible small secreted protein	0.000	-2.55	
	SCO3227	putative aminotransferase	0.001	-2.70	
	SCO3229	putative 4-hydroxyphenylpyruvic acid dioxygenase	0.000	-2.97	
	SCO3230	CDA peptide synthetase I ( <i>cdaPS1</i> )	0.004	-2.41	-2.27 (± 0.73)
	SCO3231	CDA peptide synthetase II ( <i>cdaPS2</i> )	0.005	-2.14	-2.67 (± 0.39)
	SCO3232	CDA peptide synthetase III ( <i>cdaPS3</i> )	0.016	-2.15	
	SCO3233	probable hydrolase	0.001	-2.32	
	SCO3234	possible phosphotransferase	0.000	-2.11	
	SCO3235	probable ABC transporter	0.000	-2.07	
	SCO3236	possible oxygenase	0.000	-2.36	-2.75 (± 0.39)
	SCO3237	conserved hypothetical protein	0.009	-2.26	

SCO3239	conserved hypothetical protein	0.001	-3.22	
SCO3241	possible isomerase	0.019	-2.14	
SCO3243	possible myo-inositol phosphate synthase	0.000	-2.10	
SCO3244	putative secreted protein	0.000	-2.30	
SCO3245	possible salicylate hydroxylase (putative secreted protein)	0.004	-2.28	
SCO3246	probable 3-oxoacyl-[acyl carrier protein] synthase III ( <i>fabH4</i> )	0.002	-3.12	
SCO3247	possible acyl CoA oxidase	0.002	-2.32	
SCO3248	probable 3-oxoacyl-[acyl carrier protein] synthase II ( <i>fabF3</i> )	0.000	-2.51	
SCO3249	probable acyl carrier protein	0.000	-2.32	
<b>b) Coelichelin</b>				
SCO0489	conserved hypothetical protein	0.007	-2.59	
SCO0490	putative esterase ( <i>cchJ</i> )	0.017	-2.33	
SCO0492	putative peptide synthetase ( <i>cchH</i> )	0.022	-2.07	-2.45 (± 0.33)
SCO0494	putative iron-siderophore binding lipoprotein ( <i>cchF</i> )	0.010	-1.98	
SCO0498	putative peptide monooxygenase ( <i>cchB</i> )	0.012	-2.60	-4.61 (± 1.70)
SCO0499	putative formyltransferase	0.018	-2.27	
<b>c) Carotenoids</b>				
SCO0191	probable lycopene cyclase ( <i>crtY</i> )	0.018	-2.18	
SCO0193	putative DNA-binding regulator ( <i>litR</i> )	0.000	-2.08	
SCO0194	putative sigma factor ( <i>litS</i> )	0.001	-5.58	-4.65 (± 0.92)
SCO0195	putative lipoprotein ( <i>litA</i> )	0.001	-3.64	
SCO0196	hypothetical protein ( <i>litB</i> )	0.002	-2.33	
<b>d) Methylisoborneol</b>				
SCO7699	nucleotide-binding protein ( <i>eshA</i> )	0.005	-2.65	
SCO7700	possible cyclase	0.002	-3.25	
SCO7701	2-methylgeranyl diphosphate synthase	0.035	-4.02	-3.34 (± 0.80)
<b>e) Geosmin</b>				
SCO6073	possible cyclase ( <i>geoA</i> )	0.001	-2.77	-3.32 (± 1.01)
<b>f) Undecylprodigiosin</b>				
SCO5877	specific transcriptional activator for RED biosynthesis cluster ( <i>redD</i> )	nd	nd	1.63 (± 0.44)
SCO5881	specific transcriptional activator for RED biosynthesis cluster ( <i>redZ</i> )	0.052	-1.22	1.20 (± 0.34)
<b>5. Primary metabolism</b>				
<b>a) Phosphorus metabolism</b>				
SCO4139	phosphate ABC transport system ATP-binding protein ( <i>pstB</i> )	0.004	-6.31	
SCO4140	phosphate ABC transport system permease protein ( <i>pstA</i> )	0.017	-4.08	
SCO4141	phosphate ABC transport system permease protein ( <i>pstC</i> )	0.025	-2.64	
SCO4142	phosphate-binding protein precursor ( <i>pstS</i> )	0.012	-4.08	-22.37 (± 10.08)
SCO4144	conserved hypothetical protein	0.022	-1.82	
SCO4145	polyphosphate kinase ( <i>ppk</i> )	0.000	-2.09	
SCO1845	low-affinity phosphate transport protein ( <i>pitH2</i> )	0.021	-2.20	-1.46 (± 0.70)
<b>b) Sulphur metabolism</b>				
SCO6095	probable ABC transporter ATP-binding protein	0.009	-3.04	
SCO6096	probable lipoprotein	0.008	-3.32	
SCO6099	adenylsulfate kinase ( <i>cysC</i> )	0.013	-2.24	-7.44 (± 3.95)
SCO6100	phosphoadenosine phosphosulfate reductase ( <i>cysH</i> )	0.050	-2.17	
SCO6102	probable nitrite/sulphite reductase	0.034	-5.42	
<b>c) Nitrogen metabolism</b>				
SCO2404	putative sugar-binding receptor	0.011	-2.61	
SCO2405	putative sugar-transport ATP binding protein	0.029	-2.28	
SCO2407	putative aldose 1-epimerase	0.026	-2.70	
<b>d) Arginine and proline metabolism</b>				
SCO5976	ornithine carbamoyltransferase ( <i>arcB</i> )	0.002	-2.05	
SCO5980	possible bifunctional hydroxylase/oxidoreductase	0.004	-2.04	
SCO5983	possible fatty acid-CoA ligase	0.000	-2.47	
SCO7034	aminotransferase; fragment	0.010	-2.84	
SCO7035	succinate-semialdehyde dehydrogenase; fragment ( <i>gabD</i> )	0.003	-3.32	-2.24 (± 0.17)
SCO7036	argininosuccinate synthase ( <i>argG</i> )	0.004	-1.82	
SCO2298	KHG/KDPG aldolase ( <i>kdgA</i> )	0.001	-1.99	
<b>e) Cluster of unknown function - putatively involved in saccharide metabolism</b>				



SCO3472	putative transposase remnant	0.019	-2.42	
SCO3473	putative aldolase	0.014	-3.47	
SCO3474	putative sugar kinase	0.022	-2.85	
SCO3475	putative isomerase	0.031	-2.92	
SCO3476	putative short-chain dehydrogenase	0.023	-3.07	-5.03 (± 2.89)
SCO3477	putative dehydrogenase	0.027	-3.02	
SCO3478	putative dehydrogenase	0.017	-3.27	
SCO3479	putative beta-galactosidase	0.029	-2.75	
SCO3480	putative racemase	0.028	-2.86	-4.46 (± 2.38)
SCO3481	hypothetical protein	0.032	-2.75	
SCO3482	putative sugar-permease	0.039	-2.99	
SCO3483	putative integral membrane transport protein	0.030	-3.07	-4.99 (± 3.15)
SCO3484	putative secreted sugar-binding protein	0.019	-3.21	
SCO3485	putative lacI-family transcriptional regulator	0.032	-1.65	
SCO3486	putative aldehyde dehydrogenase	0.018	-2.17	
SCO3487	putative hydrolase	0.044	-2.39	
SCO3496	putative lyase precursor	0.001	-3.24	

#### 6. Other and hypothetical genes

SCO3540	proteinase; putative secreted protein ( <i>slpD</i> )	0.006	-2.01	
SCO3595	probable D-alanine:D-lactate ligase ( <i>ddlA2</i> , <i>vanA</i> )	0.015	-3.74	
SCO4873	hypothetical protein	0.047	-2.19	
SCO4879	conserved hypothetical protein	0.042	-4.40	
SCO4881	putative polysaccharide biosynthesis related protein	0.030	-5.46	
SCO4882	hypothetical protein	0.004	-7.36	

<sup>a</sup> Fold changes represent the ratio of the expression levels in the comparison of *S. coelicolor*  $\Delta wdpB$  and wild type strain M145; positive or negative value indicate genes up- or down-regulated in the  $\Delta wdpB$  mutant. nd – not detected

**Table S2** *S. coelicolor* genes affected in the  $\Delta wdpC$  mutant compared to the wild-type strain M145 – comparison of gene transcript levels between microarray analysis and qRT-PCR analysis

Functiona l category	Gene no.	Gene product (gene)	DNA microarrays		qRT-PCR
			P-value	Fold change <sup>a</sup>	Fold change <sup>a</sup>
<b>1. <i>wdpC</i> gene</b>					
	SCO2244	probable serine/threonine protein kinase with WD-40 repetitive domains ( <i>wdpC</i> )	0.000	8.77	34.51 (± 6.64)
	SCO2245	hypothetical protein	0.001	-1.25	16.50 (± 4.86)
<b>2. Morphological differentiation</b>					
<b>a) Aerial hyphae formation</b>					
	SCO6681	probable SapB synthetase ( <i>ramC</i> )	0.024	-2.35	1.15 (± 0.52)
	SCO6682	peptide SapB ( <i>rams</i> )	0.000	-2.42	-2.35 (± 0.49)
<b>b) Sporulation</b>					
	SCO6029	two-component regulator ( <i>whiI</i> )	0.004	4.44	
<b>3. Components of <math>\sigma^U</math> regulon</b>					
	SCO0644	putative membrane protein.	0.012	2.98	
	SCO0930	putative lipoprotein	0.025	2.87	
	SCO2217	putative secreted protein	0.000	2.91	4.89 (± 0.70)
	SCO0828	putative alkaline phosphatase ( <i>phoC</i> )	0.009	3.05	-1.19 (± 0.27)
<b>4. Secondary metabolism</b>					
<b>a) Actinorhodin</b>					
	SCO5070	ORFB hydroxylacyl-CoA dehydrogenase ( <i>actVI ORF B</i> )	0.006	-2.44	
	SCO5071	ORFA hydroxylacyl-CoA dehydrogenase ( <i>actVI ORF A</i> )	0.000	-4.84	
	SCO5072	ORF1 hydroxylacyl-CoA dehydrogenase ( <i>actVI ORF 1</i> )	0.000	-3.88	
	SCO5073	putative oxidoreductase ( <i>actVI ORF 2</i> )	0.001	-3.86	
	SCO5074	putative dehydratase ( <i>actVI ORF 3</i> )	0.000	-4.41	-7.03 (± 3.20)
	SCO5075	possible oxidoreductase ( <i>actVI ORF 4</i> )	0.000	-3.76	
	SCO5076	integral membrane protein ( <i>actVA1</i> )	0.029	-2.68	
	SCO5077	hypothetical protein ( <i>actVA2</i> )	0.000	-2.25	
	SCO5078	hypothetical protein ( <i>actVA3</i> )	0.000	-3.32	
	SCO5079	conserved hypothetical protein ( <i>actVA4</i> )	0.000	-4.49	
	SCO5080	putative hydrolase ( <i>actVA5</i> )	0.001	-3.33	-6.33 (± 2.57)
	SCO5081	hypothetical protein ( <i>actVA6</i> )	0.002	-3.66	
	SCO5085	actinorhodin cluster activator ( <i>actII-ORF4</i> )	0.001	-3.43	-4.23 (± 0.68)
	SCO5086	ketoacyl reductase ( <i>actIII</i> )	0.000	-4.59	
	SCO5087	actinorhodin polyketide beta-ketoacyl synthase alpha subunit ( <i>actI-ORF1</i> )	0.005	-3.72	-6.93 (± 3.41)
	SCO5088	actinorhodin polyketide beta-ketoacyl synthase beta subunit ( <i>actI-ORF2</i> )	0.002	-4.66	
	SCO5089	actinorhodin polyketide synthase acyl carrier protein ( <i>actI-ORF 3</i> )	0.000	-6.16	
	SCO5090	actinorhodin polyketide synthase bifunctional ( <i>actVII</i> ) cyclase/dehydratase	0.000	-4.57	
	SCO5091	cyclase ( <i>actIV</i> )	0.002	-3.74	
	SCO5092	actinorhodin polyketide possible dimerase ( <i>actVB</i> )	0.018	-3.50	
<b>b) Calcium-dependent antibiotics</b>					
	SCO3217	transcriptional activator for the CDA biosynthesis cluster ( <i>cdaR</i> )	0.008	-1.41	-2.15 (± 0.64)
	SCO3218	putative small conserved hypothetical protein	0.001	-3.22	
	SCO3220	putative secreted protein	0.000	-3.41	
	SCO3221	probable oxidoreductase	0.001	-3.04	
	SCO3222	possible small secreted protein	0.000	-2.85	
	SCO3227	putative aminotransferase	0.021	-2.61	
	SCO3229	putative 4-hydroxyphenylpyruvic acid dioxygenase	0.005	-2.77	
	SCO3230	CDA peptide synthetase I ( <i>cdaPS1</i> )	0.010	-2.66	-3.00 (± 0.99)
	SCO3231	CDA peptide synthetase II ( <i>cdaPS2</i> )	0.013	-2.60	-4.55 (± 1.12)
	SCO3232	CDA peptide synthetase III ( <i>cdaPS3</i> )	0.022	-2.21	
	SCO3233	probable hydrolase	0.040	-2.43	

SCO3234	possible phosphotransferase	0.002	-2.98	
SCO3235	probable ABC transporter	0.003	-2.58	
SCO3236	possible oxygenase	0.003	-2.37	-3.42 (± 0.55)
SCO3244	putative secreted protein	0.000	-2.86	
SCO3245	possible salicylate hydroxylase (putative secreted protein)	0.035	-1.98	
SCO3247	possible acyl CoA oxidase	0.011	-2.42	
SCO3248	probable 3-oxoacyl-[acyl carrier protein] synthase II ( <i>fabF3</i> )	0.000	-2.40	
SCO3249	probable acyl carrier protein	0.000	-2.67	
<b>c) Coelichelin</b>				
SCO0489	conserved hypothetical protein	0.001	-2.90	
SCO0490	putative esterase ( <i>cchJ</i> )	0.011	-2.05	
SCO0492	putative peptide synthetase ( <i>cchH</i> )	0.007	-2.29	-2.18 (± 0.55)
SCO0498	putative peptide monooxygenase ( <i>cchB</i> )	0.010	-3.14	-1.48 (± 0.71)
SCO0499	putative formyltransferase	0.016	-2.25	
<b>d) Yellow pigment and a compound with antibacterial activity (product of <i>cpk</i> gene cluster)</b>				
SCO6272	possible secreted FAD-binding protein	0.044	-1.96	
SCO6273	probable type I polyketide synthase ( <i>cpkC</i> )	0.006	-2.40	-2.38 (± 0.08)
SCO6277	putative epoxide hydrolase ( <i>cpkE</i> )	0.004	-1.40	-2.07 (± 0.22)
SCO6279	putative diaminobutyrate-pyruvate aminotransferase ( <i>cpkG</i> )	0.049	-1.24	-2.24 (± 0.25)
<b>e) Grey polyketide spore pigment</b>				
SCO5318	polyketide beta-ketoacyl synthase alpha ( <i>whiE-ORFIII</i> )	0.000	-3.80	
<b>f) Undecylprodigiosin</b>				
SCO5877	specific transcriptional activator for RED biosynthesis cluster ( <i>redD</i> )	0.035	-1.27	-1.45 (± 0.65)
SCO5881	specific transcriptional activator for RED biosynthesis cluster ( <i>redZ</i> )	0.006	-1.46	-1.22 (± 0.06)
<b>5. Primary metabolism</b>				
<b>a) Phosphorus metabolism</b>				
SCO4139	phosphate ABC transport system ATP-binding protein ( <i>pstB</i> )	0.000	-2.44	
SCO4140	phosphate ABC transport system permease protein ( <i>pstA</i> )	0.019	-2.98	
SCO4141	phosphate ABC transport system permease protein ( <i>pstC</i> )	0.000	-1.97	
SCO4142	phosphate-binding protein precursor ( <i>pstS</i> )	0.004	-2.30	
SCO4145	polyphosphate kinase ( <i>ppk</i> )	0.002	-2.03	
<b>b) Sulphur metabolism</b>				
SCO6099	adenylylsulfate kinase ( <i>cysC</i> )	0.002	-2.27	
SCO6102	putative nitrite/sulphite reductase	0.022	-2.16	
<b>6. Other and hypothetical genes</b>				
SCO0162	conserved hypothetical protein	0.002	2.15	
SCO0163	conserved hypothetical protein	0.024	2.08	
SCO0168	possible regulator protein	0.001	2.03	
SCO0169	conserved hypothetical protein	0.000	2.03	
SCO0170	conserved hypothetical protein	0.001	2.40	
SCO0171	conserved hypothetical protein	0.002	2.01	
SCO0180	conserved hypothetical protein	0.018	2.06	
SCO0181	hypothetical protein	0.005	2.05	
SCO0184	conserved hypothetical protein	0.001	3.04	
SCO2828	probable amino acid ABC transporter protein, solute-binding component	0.016	-2.31	
SCO2829	amino acid ABC transporter protein, integral membrane component	0.014	-2.13	
SCO2830	probable amino acid ABC transporter protein, integral membrane component	0.000	-1.98	
SCO2831	probable amino acid ABC transporter protein, ATP-binding component	0.002	-1.97	
SCO3595	probable D-alanine:D-lactate ligase ( <i>ddlA2</i> , <i>vanA</i> )	0.001	-4.01	
SCO4173	hypothetical protein SCD66.10c	0.000	14.97	70.41 (± 1.10)
SCO4174	putative integral membrane protein	0.000	6.05	305.02 (± 90.89)
SCO4175	hypothetical protein SCD66.12c	0.000	16.75	243.8 (± 38.00)
SCO4176	conserved hypothetical protein	0.001	2.15	
SCO4214	putative AbaA-like regulatory protein	0.000	28.47	325.17 (± 56.75)

SCO4873	hypothetical protein	0.020	-2.39
SCO4874	possible integral membrane protein	0.002	-2.91
SCO4879	conserved hypothetical protein	0.001	-3.81
SCO4880	possible transferase	0.004	-2.06
SCO4881	possible polysaccharide biosynthesis related protein	0.002	-3.83
SCO4882	hypothetical protein	0.000	-6.02
SCO7511	glyceraldehyde 3-phosphate dehydrogenase ( <i>gap2</i> )	0.000	3.27

<sup>a</sup> Fold changes represent the ratio of the expression levels in the comparison of *S. coelicolor*  $\Delta wdpC$  and wild type strain M145; positive or negative value indicate genes up- or down-regulated in the  $\Delta wdpC$  mutant.

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**Table S3** Transcription profiles of selected genes in the  $\Delta wdpB$  mutant during *S. coelicolor* life cycle.

Gene no. (name)	Time of cultivation (h)			
	28	48	72	96
SCO0194 ( <i>litS</i> )	1,14 ( $\pm$ 0,01)	-4,65 ( $\pm$ 0,92)	-3,12 ( $\pm$ 0,74)	-2,04 ( $\pm$ 0,40)
SCO1674 ( <i>chpC</i> )	-3,46 ( $\pm$ 1,17)	-2,69 ( $\pm$ 0,60)	1,19 ( $\pm$ 0,59)	-1,72 ( $\pm$ 0,53)
SCO1675 ( <i>chpH</i> )	-3,73 ( $\pm$ 1,93)	-10,24 ( $\pm$ 3,69)	-6,54 ( $\pm$ 1,43)	-2,85 ( $\pm$ 1,92)
SCO1800 ( <i>chpE</i> )	-2,14 ( $\pm$ 0,98)	-1,97 ( $\pm$ 0,20)	-3,43 ( $\pm$ 0,63)	-1,99 ( $\pm$ 0,61)
SCO2718 ( <i>rdlA</i> )	-1,19 ( $\pm$ 0,71)	-15,19 ( $\pm$ 7,95)	1,17 ( $\pm$ 0,14)	-2,01 ( $\pm$ 0,87)
SCO2719 ( <i>rdlB</i> )	-1,13 ( $\pm$ 0,17)	-9,59 ( $\pm$ 3,14)	-1,4 ( $\pm$ 0,57)	-1,34 ( $\pm$ 0,60)
SCO3217 ( <i>cdaR</i> )	-1,05 ( $\pm$ 0,33)	-1,88 ( $\pm$ 0,63)	-1,34 ( $\pm$ 0,79)	-1,22 ( $\pm$ 0,01)
SCO3231 ( <i>cdaPS2</i> )	-1,84 ( $\pm$ 0,64)	-2,67 ( $\pm$ 0,39)	-1,7 ( $\pm$ 1,23)	-2,83 ( $\pm$ 0,35)
SCO4002 ( <i>nepA</i> )	-13,12 ( $\pm$ 2,61)	-4,31 ( $\pm$ 0,59)	nt	-3,59 ( $\pm$ 0,76)
SCO5819 ( <i>whiH</i> )	-1,02 ( $\pm$ 0,15)	-3,42 ( $\pm$ 0,01)	1,27 ( $\pm$ 0,68)	-1,38 ( $\pm$ 0,61)
SCO5953 ( <i>wdpB</i> )	40,86 ( $\pm$ 0,50)	19,54 ( $\pm$ 3,74)	13,47 ( $\pm$ 4,79)	14,33 ( $\pm$ 1,48)
SCO5954	20,88 ( $\pm$ 8,88)	34,51 ( $\pm$ 7,14)	16,94 ( $\pm$ 4,99)	30,70 ( $\pm$ 6,28)
SCO6073 ( <i>geoA</i> )	-2,85 ( $\pm$ 0,28)	-3,32 ( $\pm$ 1,01)	-1,14 ( $\pm$ 0,27)	-1,18 ( $\pm$ 0,06)
SCO6682 ( <i>ramS</i> )	-30,00 ( $\pm$ 14,84)	-17,52 ( $\pm$ 7,15)	-4,49 ( $\pm$ 1,07)	-3,11 ( $\pm$ 1,39)
SCO6685 ( <i>ramR</i> )	-3,28 ( $\pm$ 1,08)	-2,27 ( $\pm$ 0,51)	1,49 ( $\pm$ 0,93)	nt
SCO6992 ( <i>absR1</i> )	-1,20 ( $\pm$ 0,04)	-8,95 ( $\pm$ 4,23)	1,21 ( $\pm$ 0,17)	-1,07 ( $\pm$ 0,07)
SCO7701	-2,12 ( $\pm$ 1,09)	-3,34 ( $\pm$ 0,80)	-1,48 ( $\pm$ 1,31)	-1,86 ( $\pm$ 0,49)

Total RNA isolated from different development stages of life cycle (after 28, 48, 72 and 96 hours of cultivation on modified R3 plates) was transcribed into cDNA which was used as a template for qRT-PCR. The data represent the ratio of the expression levels in the comparison of *S. coelicolor*  $\Delta wdpB$  and wild type strain M145; positive or negative value indicate genes up- or down-regulated in the  $\Delta wdpB$  mutant. nt – not tested.

**Table S4** Transcription profiles of selected genes in the  $\Delta wdpC$  mutant during *S. coelicolor* life cycle.

Gene (name)	Time of cultivation (h)				
	28	48	64	72	96
SCO2244 ( <i>wdpC</i> )	13,77 ( $\pm$ 4,42)	27,33 ( $\pm$ 9,03)	34,51 ( $\pm$ 6,64)	29,2 ( $\pm$ 7,43)	25,00 ( $\pm$ 8,05)
SCO3231 ( <i>cdaPS2</i> )	1,14 ( $\pm$ 0,56)	-2,29 ( $\pm$ 0,45)	-4,55 ( $\pm$ 1,12)	-3,39 ( $\pm$ 0,41)	-1,73 ( $\pm$ 0,93)
SCO4174	4,08 ( $\pm$ 1,06)	45,70 ( $\pm$ 5,57)	305,02 ( $\pm$ 90,89)	7,88 ( $\pm$ 0,40)	6,93 ( $\pm$ 0,40)
SCO4214	10,80 ( $\pm$ 2,80)	30,69 ( $\pm$ 2,44)	325,17 ( $\pm$ 56,75)	18,65 ( $\pm$ 5,41)	7,63 ( $\pm$ 2,55)
SCO5085 ( <i>actII-ORF4</i> )	-1,03 ( $\pm$ 0,13)	-1,27 ( $\pm$ 0,19)	-4,23 ( $\pm$ 0,68)	-2,31 ( $\pm$ 0,27)	-2,64 ( $\pm$ 0,70)
SCO5087 ( <i>actI-ORF1</i> )	-1,36 ( $\pm$ 0,07)	1,18 ( $\pm$ 0,69)	-6,93 ( $\pm$ 3,41)	-4,59 ( $\pm$ 1,46)	-2,47 ( $\pm$ 0,08)
SCO6682 ( <i>ramS</i> )	-1,98 ( $\pm$ 0,03)	-1,60 ( $\pm$ 0,42)	-2,35 ( $\pm$ 0,49)	-2,03 ( $\pm$ 0,85)	-1,07 ( $\pm$ 0,07)
SCO6685 ( <i>ramR</i> )	-2,78 ( $\pm$ 1,68)	1,03 ( $\pm$ 0,06)	nt	1,63 ( $\pm$ 0,26)	nt

Total RNA isolated from different development stages of life cycle (after 28, 48, 72 and 96 hours of cultivation on modified R3 plates) was transcribed into cDNA which was used as a template for qRT-PCR. The data represent the ratio of the expression levels in the comparison of *S. coelicolor*  $\Delta wdpC$  and wild type strain M145; positive or negative value indicate genes up- or down-regulated in the  $\Delta wdpC$  mutant. nt – not tested.

**Table S5** List of primers used in cotranscription analyses

Oligonucleotide	Abbreviation	Sequence in direction 5' - 3'	PCR amplification product
SCO2245_F	1	ATGACCGGT AAGGACACACC	319 bp
R2wdpC_up	2	GTGCGTCCGAGGT AGACG	
SCO2246_F	3	TCCGGAAC T CAGTTTGTCC	536 bp
SCO2245_R	4	ACGAACATCGTCCAGGT CAC	
SCO2247_F	5	AAATCCCGGACAGGCT AATC	788 bp
SCO2246_R	6	CTC CACTTCCAGCAGGT GTT	
SCO5951_F	a	GT CGT CAGGACGCT CGAC	1043 bp
SCO5952_R	b	ATGGT GATCGCCAGGT ACTC	
SCO5952_F	c	ACTGAGCGAACT GACCTTCG	930 bp
wdpB_upR	d	CTCGAAGT ACCCCGACAGAC	
FwdpB	e	ATCACCT ACAACATGT CCGA	1334 bp
SCO5954R	f	GAGGT TCTCGAAGGCGT AGT	

**Table S6** List of primers used in qRT-PCR

Gene no.	Oligonucleotide	Sequence in direction 5' - 3'	Gene no.	Oligonucleotide	Sequence in direction 5' - 3'
SCO0194	SCO0194F	GT ACT CGACCGGT ACT GCT	SCO4214	SCO4214F2	ATCGACCGT TATCCGTGT G
	SCO0194R	GCGT CAGGT CCT CGT AGAAG		SCO4214R2	GCT GGT AGGGAGT GACGAAC
SCO0492	SCO0492F	TTCGTCTCCAGA ACTTCT	SCO4677	SCO4677F	GCT CACCCT GT ACGTCGT C
	SCO0492R	ACCCAGGT GAAGGGAT AGT G		SCO4677R	GT CGGAGGCAGGCT TTT
SCO0498	SCO0498F	ACAGCGGT GAT GGA CT AC	SCO5074	SCO5074F	CACCCGGT CT ACGACT ACG
	SCO0498R	ACCTTCTCCGGT ACATCTG		SCO5074R	CTGGT TGTACTCGGCGAAG
SCO0828	SCO0828F	GCGCT ACT CGCT CT ACAAGA	SCO5080	SCO5080F	GT CAGCGT CGT GGAT CACT
	SCO0828R	CGT AGT TGTCTCGGT CTCG		SCO5080R	CTGT CGACGAT CCCGT ACT
SCO1674	SCO1674F2	GGT GGGGACCACT CGAC	SCO5085	SCO5085F	TGGGACGT GT CCAT GT AATC
	SCO1674R2	GGCT TGT CCGGGT ATC		SCO5085R	CACAACT CCT CGATGAGCAC
SCO1675	SCO1675F	GGCAACGT CGT T CAGGT T	SCO5087	SCO5087F	AGGAGCT GT TCGATTGAAG
	SCO1675R	TCACTTGTGATGCAGACGT T		SCO5087R	GAGGT GAGCAGT TCCCAGA
SCO1800	SCO1800F	CCGGT GGCCT GAT CG	SCO5318	SCO5318F	GATGAGCT CCAT CAAGTCCA
	SCO1800R	GT T GACCGGGAT GT GGAT		SCO5318R	CGT AGT CCAGGT CGCACT C
SCO1845	SCO1845F	ACACGAT CT CCAAGGGT CTC	SCO5321	SCO5321F	CTCTTCCACAACGT CAGCAT
	SCO1845R	GT CAGGAGGT TCCAGAGGAT		SCO5321R	GT TCTCGT CCGTCAGGT AGC
SCO2217	SCO2217F	ACACAAGAAAACGCCGT ACA	SCO5819	SCO5819F	GAGGACGT CCAGCAGAGG
	SCO2217R	TAGAAGT TGGCCAGACCAG		SCO5819R	AGGGT GT GGA ACT CGGT ATC
SCO2244	wdpC_downF	CTCACCCACAAGT TCGTCAC	SCO5877	SCO5877F2	GACCT GGT GGACGA ACT GT
	wdpC_downR	GCCAGGT TCCACAGGAGT A		SCO5877R2	ACGCT CGT T GAGCACTTTC
SCO2245	SCO2245_F	ATGACCCGGT AAGGACACACC	SCO5881	SCO5881F	CATCAGAACCAT CACCGAAG
	SCO2245_R	ACGAACAT CGT CCAGGT CAC		SCO5881R	CCCT GGGT CAGT AAGAGGAG
SCO2717	SCO2717F	GGCAACGT CAT CCAGGT T	SCO5953	wdpB_upF	GCCAAGGAGAT CGAGT TCTG
	SCO2717R	CAGT CGT TCTCGCACTTGT T		wdpB_upR	CTCGAAGT ACCCCGACAGAC
SCO2718	SCO2718F	AGCT GT CGCT GGT CGAG	SCO5954	SCO5954F	CTCAAGGT CCGGT ACT TCGT
	SCO2718R	AGGACGT T GAT GT CCTGGAT		SCO5954R	GAGGT TCTCGAAGGCGT AGT
SCO2719	SCO2719F	GT ACT TCGGCAACT CGATGA	SCO6073	SCO6073F	ACTTCTTCGGCGT CGACT AT
	SCO2719R	ACCAGACCGAT GACACT GAC		SCO6073R	GAGAGCT GGAAGT CGT CGT A
SCO3217	SCO3217F	TGCGCT ACT ACCTGATGCT C	SCO6099	SCO6099F	GACCT GCGCAT CGAGT C
	SCO3217R	AGGT CCGT ACCCAGT TCAAG		SCO6099R	CAGTCCCCT TTCGGT GAG
SCO3230	SCO3230F	AACGT CGT ACGGCT CTCTC	SCO6273	SCO6273F	GAGAT GAT GACGT CGGACAC
	SCO3230R	CACACCGAGAAGT CGAAGG		SCO6273R	GGCCACAT ACT TCTCGAACA
SCO3231	SCO3231F	GAGAT CGAAACCACCT CAC	SCO6277	SCO6277F	CAACAACCT CCT CCGT GAC
	SCO3231R	CACGGT GT TCTCGT CGTATC		SCO6277R	GGT GACGT ACT CCT CCGT CT
SCO3236	SCO3236F	TTCCTGCCGGAAGAAGC	SCO6279	SCO6279F	GGT TCT TCGGCT ACT TCGTC
	SCO3236R	GT TCTCGT TGTGGAACGT CA		SCO6279R	TCTCTCGTCCGT GACATAC
SCO3476	SCO3476F	GATCATCAACCTCGCATCAC	SCO6681	SCO6681F	GAGACT GGCCGAGT ACACC
	SCO3476R	ATT CATTGCACAGAGCCTTG		SCO6681R	CAGGT CGT TGAAGACCACAC
SCO3480	SCO3480F	GGCT ACACCT ACACGGT CAA	SCO6682	SCO6682F	ACCTGCAGT CGATGGAGAC
	SCO3480R	TGACT GCCAT ATCTTCTCG		SCO6682R	TACAGGT GGT GAT GCTCAGG
SCO3483	SCO3483F	AACGCCT AT CCGCT CTCTA	SCO6685	SCO6685F	ACTGCT CAGATCCGACGAC
	SCO3483R	AAGGCGGT CGT GT AGT TCTC		SCO6685R	TCCGTCCACGACACAGAC
SCO4002	SCO4002_F	ACGACAACAACGGCAACT C	SCO6992	SCO6992F	GGACCT TCCACAACATCCTG
	SCO4002_R	CTGGT T GATCGACGT GAAG		SCO6992R	GGAGAACGGGT ACTCCATGA
SCO4142	SCO4142F2	CGAAGAAGGT CTGCAAGGAC	SCO7035	SCO7035F	CTGAT GACCT CCGAGATGG
	SCO4142R2	T TGGT GATCTTGCTGT CGAA		SCO7035R	GAGAACCAGCGGAAGA ACT C
SCO4173	SCO4173F	CTGCT GGA CT CGCT CCTG	SCO7257	SCO7257F	GAAGGAAGCGGAAAGGATTC
	SCO4173R	CCTCT GCACGAAGACCTG		SCO7257R	GAGT CGT TCGT CGACTCGT
SCO4174	SCO4174F	GACTGCCCT ACGAGGAGT G	SCO7701	SCO7701F	GCACAGCGAGT ACGAGAAGA
	SCO4174R	GGT GGT CCGGAT GGAAC		SCO7701R	GAGGT GGT CCAT GAGGAACT
SCO4175	SCO4175F	AACAGAACCGCCACCT AC	SCO5820	hrdBF	CGGT CAGCT TCACTGCT
	SCO4175R	AGCGGT CGGAGCAGCAC	(hrdB)	hrdBR	GT ACACCT TGCCGAT CTCGT