

Additional file 5 – Putative *S. coelicolor* AdpA-binding sites upstream from the *S. lividans* AdpA-dependent genes^a.

gene ^b	function ^c	cis-element ^c	score ^c	position ^c	gene ^d	Fc ^e	gene ^b	gene name ^f	Co-transcript gene ^g
SCO0169	hypothetical protein	tgacgtgatg	3.64	-7	SLI0098	0.621	-	-	-
SCO0171	nicotinate phosphoribosyltransferase	cggcgggaac	6.11	-119	SLI0101	0.615	-	-	-
SCO0197	hypothetical protein	cggcgagttc	4.39	-85	SLI0139	1.82	-	-	-
SCO0200	hypothetical protein	attccggcca	8.99	-9	SLI0142	1.656	-	-	SCO0199/ SCO0198
SCO0216	nitrate reductase subunit alpha NarG2	gttctggccc	5.0	-10	SLI0158	1.745	-	-	SCO0217/SCO0218/ /SCO0219
SCO0229	short chain dehydrogenase	aaaatcgaca	3.1	-72	SLI0172	1.988	-	-	SCO0230
SCO0231	hypothetical protein	ctaccggccc	4.07	-97	SLI0175	0.122	SGR4343	-	-
SCO0268	hypothetical protein	tggctcgttt	6.41	-114	SLI0220	0.1	-	-	-
SCO0379	catalase	gtccggaaac	3.87	-173	SLI0337	0.483	-	<i>katA</i>	-
SCO0382	UDP-glucose/GDP-mannose dehydrogenase	gaacgggtca	4.52	-9	SLI0340	0.491	-	-	-
SCO0384	hypothetical protein	gggcgaattc	3.13	-45	SLI0342	0.611	-	-	SCO0385/SCO0386
SCO0402*	hypothetical protein	attcgggcca	7.63	-151	SLI0360	0.578	-	-	-
SCO0453	solute-binding lipoprotein	ggtcccgcca	5.89	-84	SLI0411	1.876	-	-	-
SCO0494	iron-siderophore binding lipoprotein	tgtcggccca	4.36	-28	SLI0454	0.615	SGR6714	<i>cchF</i>	SCO0493
SCO0498	peptide monooxygenase	attcgagcca	6.91	-91	SLI0458	0.336	SGR6710	<i>cchB</i>	SCO0497/SCO0496/ SCO0495
SCO0499	formyltransferase	attcgagcca	6.91	-95	SLI0459	0.374	SGR6709	<i>cchA</i>	-
SCO0561	Fe regulatory protein	tggcgggcac	4.44	-84	SLI0523	0.613	-	<i>furS</i> . <i>fura</i>	SCO0560
SCO0592	hypothetical protein	gggcgcgtac	3.41	-105	SLI0556	0.624	-	-	-
SCO0643	cellulose-binding protein	gaatgagcca	5.28	-134	SLI0614	2.002	-	-	-
SCO0682	hypothetical protein	ttccggacg	5.03	-21	SLI0655	0.375	SGR4457	-	-
SCO0705	hypothetical protein	gggcggatc	6.53	-94	SLI0681	0.579	SGR92t SGR7047t	-	-
SCO0762	protease inhibitor protein	tggcgtgatc	7.19	-235	SLI0743	0.124	SGR551	<i>stil</i> <i>sgtA</i>	-
SCO0771	hypothetical protein	tggctgaacc	5.08	-10	SLI0752	0.612	-	-	SCO0770
SCO0774*	cytochrome P450	tggcgcgtatc	6.9	-180	SLI0755	0.075	SGR264	-	SCO0773
SCO0775*	hypothetical protein	tggcgcgtatc	6.9	-140	SLI0756	0.424	SGR1346	-	-
SCO0827	hypothetical protein	tgtctgctta	3.4	-68	SLI0811	0.516	-	-	-
SCO0863	hypothetical protein	gttccggccg	6.75	-141	SLI0848	0.225	-	-	SCO0862
SCO0864	ECF family RNA polymerase sigma factor	agtccccccg	4.45	-94	SLI0849	0.574	SGR6228	-	-

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SCO0865	hypothetical protein	catccgtaca	3.27	-18	SLI0850	0.621	-	-	-
SCO0919	hypothetical protein	tgtccgcac	5.1	-48	SLI1149	0.621	SGR6643	-	-
SCO0929	hypothetical protein	tggccggac	5.19	-201	SLI1160	0.419	SGR710	-	SCO0928
SCO1032*	putative ABC transport system ATP-binding	cggccgaact	4.36	#	SLI1304	2.138	-	-	SCO1033/SCO1032 /SCO1031
SCO1134*	oxidoreductase. iron-sulfur binding subunit	gattcggcca	8.17	-169	SLI1410	0.584	SGR6436	-	SCO1133/SCO1132 /SCO1131
SCO1179	hypothetical protein	gtacgggcc	4.05	-37	SLI1456	1.649	SGR3185	-	SCO1178
SCO1183	hypothetical protein	cgaccggaa	3.2	-18	SLI1460	1.682	SGR0892	-	SCO1184/SCO1185
SCO1186	Lacl family transcriptional regulator	gtatcgac	3.66	-35	SLI1464	1.657	-	-	-
SCO1196	hypothetical protein	tggccggacc	6.53	-95	SLI1475	0.493	SGR493	-	-
SCO1222	hypothetical protein	ctgcgggaac	3.76	-103	SLI1501	0.509	SGR5233	-	SCO1223
SCO1379	hypothetical protein	agtccggccc	4.56	-24	detected	1.8	SGR6150	-	-
SCO1407	hypothetical protein	tggcgactc	4.02	-10	SLI1704	0.617	SGR6124	-	-
SCO1430	TetR family transcriptional regulator	gggggggacc	3.52	-34	SLI1728	1.685	-	-	-
SCO1444	chitinase	catccggact	3.65	-320	SLI1742	1.984	SGR6088	-	-
SCO1565	glycerophosphoryl diester phosphodiesterase	cggccggaa	6.75	-82	SLI1868	0.531	SGR5973	<i>glpQ1</i>	-
SCO1593	transcriptional regulator	attcacggcc	5.44	-193	SLI1845	1.86	SGR5994	-	-
SCO1630	hypothetical protein	tgtcgggatc	6.71	-74	SLI1934	0.505	SGR1063	<i>cvn9. rarA</i>	SCO1629/SCO1628
SCO1674	hypothetical protein	cggccggaa	5.69	-154	SLI1979	0.564	SGR5829	<i>chpC</i>	-
SCO1684	hypothetical protein	gaatcgcc	5.36	-161	SLI1989	1.626	SGR5819	-	-
SCO1715	homogentisate 1,2-dioxygenase	gttccggta	6.38	-160	SLI2018	0.601	SGR5788	<i>hgd</i>	SCO1716/SCO1717
SCO1776*	CTP synthetase	cttcggcc	7.25	-170	SLI2080	1.744	SGR5721	<i>pyrG</i>	-
SCO1800	hypothetical protein	cggccggacc	4.69	-65	SLI2108	0.256	SGR5696	<i>chpE</i>	-
SCO1821	molybdenum cofactor biosynthesis protein A	cggccccgaa	5.39	-61	SLI2130	1.679	SGR5674	<i>moaA</i>	-
SCO1864	acetyltransferase	atttcgac	6.71	-203	SLI2175	2.903	SGR5635	<i>ectA</i>	-
SCO1865	diaminobutyrate--2-oxoglutarate aminotransferase	cggccgggac	3.24	-78	SLI2176	3.154	<u>SGR5634</u>	<i>ectB</i>	-
SCO1867	hydroxylase	gaagtggcca	4.62	-3	SLI2178	3.029	SGR5632	<i>ectD</i>	-
SCO1887	integral membrane transport protein	gttcgggtcg	3.18	-95	SLI2198	1.656	SGR210	-	SCO1886/SCO1885 /SCO1884/SCO188
SCO1968	hydrolase	cattcagcc	3.75	-92	SLI2284	0.537	SGR5556	<i>glpQ2</i>	SCO1969

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SCO2068*	alkaline phosphatase	tggccggttc	8.09	-91	SLI2391	0.621	-	-	-
SCO2174	transferase	gggccccgtac	5.41	-94	SLI2501	1.819	-	-	-
SCO2183	2-oxoacid dehydrogenase subunit E1	gttacagtc	3.68	-115	SLI2510	1.647	SGR5327	aceE1	-
SCO2212*	hypothetical protein	gttccggcca	8.59	-72	detected	0.516	-	-	-
SCO2396	hypothetical protein	cggcggttt	5.28	-57	SLI2728	1.734	SGR5099	-	-
SCO2424	hypothetical protein	cggccggtag	5.94	-113	SLI2756	1.617	SGR1042	SCO2425	
SCO2435	hypothetical protein	gatcggggcg	5.7	-156	SLI2769	0.526	-	SCO2436	
SCO2525	hypothetical protein	aatttggaca	5.8	-14	SLI2861	0.405	-	-	-
SCO2550	lipoprotein	catacggcca	5.58	-52	SLI2886	0.474	-	-	-
SCO2640	aspartate-semialdehyde dehydrogenase	gggcgggaag	4.24	-166	SLI2981	1.824	SGR4887	asd1	-
SCO2790	hypothetical protein	tgtccgggaa	3.36	-65	SLI3137	1.71	SGR4743	-	-
SCO2791*	hypothetical protein	gaaccggcca	8.09	-234	SLI3138	2.43	-	-	-
SCO2792*	AraC family transcription regulator	gaaccggcca	8.09	-148	SLI3139	0.383	SGR4742	<i>adpA</i> <i>bldH</i>	-
SCO2793	oligoribonuclease	aattcagccc	5.48	-133	SLI3140	1.966	SGR4741	<i>ornA</i>	-
SCO2797	cellobiose transport permease	gaacccggccg	6.25	-9	SLI3145	1.722	-	-	-
SCO2818	hypothetical protein	cttccagccg	4.69	-200	SLI3166	1.613	SGR4718	-	-
SCO2823	decarboxylase	agacaggccg	3.21	-185	SLI3172	0.489	-	SCO2822	
SCO2879	hypothetical protein	tttccggcca	7.69	-448	SLI3224	0.359	-	<i>cvnA12</i>	SCO2880/SCO2881
SCO2919	hypothetical protein	cgacccggca	3.74	-105	SLI3263	0.408	SGR4620	-	-
SCO2921*	hypothetical protein	tttgccgaca	4.62	-260	detected	0.196	SGR4618	<i>adbS3</i> - <i>orfA</i>	-
SCO2987	regulatory protein	gagcacgcca	3.68	-79	SLI3331	1.647	SGR6918	<i>ohrR</i>	-
SCO2997	transferase	ttggccgatt	5.59	-83	SLI3341	1.837	-	SCO2998	
SCO3061	hypothetical protein	attgacgcca	5.03	-36	SLI3411	1.632	SGR4476	-	-
SCO3123	ribose-phosphate pyrophosphokinase	tgaccggaaa	6.21	#	SLI3480	1.891	SGR4383	<i>prsA2</i>	-
SCO3167	TetR family transcriptional regulator	cgaccggAAC	4.54	-48	SLI3521	2.65	SGR4317	-	-
SCO3177*	hypothetical protein	tggctgatat	6.73	-75	SLI3531	1.618	SGR4301	-	-
SCO3202	RNA polymerase principal sigma factor	aatccggaca	7.75	-145	SLI3556	2.499	SGR4276	<i>hrdD</i>	-
SCO3323*	RNA polymerase sigma factor	gttccggte	6.38	-469	SLI3667	0.389	SGR4151	<i>bldN</i> . <i>adsA</i>	-
SCO3357	hypothetical protein	cggcgagtac	4.08	-14	SLI3699	1.656	SGR4124	<i>cseA</i>	-
SCO3495	aldolase	tgtcctgttc	5.47	-21	-	0.623	-	SCO3494	
SCO3579*	regulatory protein	tggcccgAAC	7.23	-135	SLI3822	0.31	SGR3340	<i>wblA</i>	-

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SCO3767	hypothetical protein	cttcccgta	4.4	-50	SLI4011	0.534	SGR3815		-
SCO3768	translocase	catcgcccc	3.83	-99	SLI4012	0.601	-		-
SCO3810	GntR family transcriptional regulator	tatccggacg	5.34	-57	SLI4061	1.762	SGR3772		SCO3809
SCO3811	D-alanyl-D-alanine carboxypeptidase	tatccggacg	5.34	-175	SLI4062	1.628	SGR3768	<i>dacA</i>	-
SCO3831	E1-alpha branched-chain alpha keto acid dehydrogenase	tggctacatg	3.37	-98	SLI4083	2.23	SGR3748	<i>bkdA2</i>	SCO3830/SCO3829
SCO3835	dehydrogenase	tgtcccgacc	3.62	-109	SLI4087	2.207	SGR3745		-
SCO3877	6-phosphogluconate dehydrogenase	gaacccgcgg	5.61	-55	SLI4134	2.02	SGR3702		SCO3876/SCO3875
SCO3917*	hypothetical protein	cttcggcca	6.52	-72	SLI4175	0.504	SGR3663		-
SCO3945	cytochrome oxidase subunit I	tgtcccgatt	6.39	-88	SLI4193	3.386	SGR3646	<i>cydA</i>	SCO3946
SCO3947	ABC transporter	catccgcgg	5.08	-30	SLI4195	2.653	SGR3644	<i>cydCD</i>	-
SCO3968*	hypothetical protein	tggcggttc	4.75	-10	SLI4216	0.443	SGR3623		-
SCO3971	hypothetical protein	tggccggtag	7.78	-465	SLI4220	1.631	SGR3620		-
SCO4032	marR regulatory protein	aaaaggccg	3.31	-73	SLI4266	1.807	SGR3555		SCO4031
SCO4034	RNA polymerase sigma factor	tgtcgcaac	4.15	-128	SLI4268	0.582	SGR3552	<i>sigN</i>	-
SCO4049*	antibiotic binding protein	tattcggcca	8.0	-62	SLI4283	1.708	SGR4229		SCO4050/SCO4051 /SCO4052
SCO4113	hydroxyglutarate oxidase	aaacccgtca	5.64	-52	SLI4344	0.568	SGR3901		-
SCO4114*	sporulation associated protein	tggcggttt	8.66	-117	SLI4345	0.487	SGR3902		-
SCO4164	thiosulfate sulfurtransferase	gttccggcca	5.7	-170	SLI4405	0.483	SGR3965	<i>cysA</i>	SCO4165
SCO4187*	hypothetical protein	tggcgagaag	5.39	-145	SLI4427	0.245	-		-
SCO4215	GntR family transcriptional regulator	gatgaggccc	3.74	-294	SLI4452	1.964	-	<i>xlnR</i>	-
SCO4293	threonine synthase	cggcccgatg	4.36	-145	SLI4530	0.362	SGR3228		SCO4294
SCO4295*	cold shock protein	attctcgcca	7.13	-193	SLI4532	0.217	SGR3226	<i>scoF4</i>	-
SCO4296	chaperonin GroEL	cggcccgatc	5.7	-210	SLI4533	0.566	SGR3225	<i>groEL2</i>	-
SCO4327	hypothetical protein	cgtcccgatc	3.34	-46	SLI4563	1.662	SGR3174		SCO4326
SCO4383	4-coumarate:CoA ligase	gatcaggccg	5.99	-122	SLI4617	1.81	SGR3091		SCO4384/SCO4385 /SCO4386
SCO4428	hypothetical protein	gateacggccg	5.35	-173	SLI4666	0.55	-		-
SCO4516	hypothetical protein	aattgcggccg	4.73	-184	SLI4797	0.374	-		SCO4515/SCO4514 /SCO4513/SCO4512/SCO4511
SCO4671	LysR family transcriptional regulator	aggctggtag	4.7	-47	SLI4944	1.734	SGR1131		-
SCO4761	co-chaperonin GroES	aaccccgccg	3.31	-197	SLI5031	0.401	SGR2770	<i>groES</i>	-
SCO4762	chaperonin GroEL	ttgccgtata	4.4	-44	SLI5032	0.44	SGR2769	<i>groEL1</i>	-
SCO4768	two-component regulator	aatctggccg	5.52	-292	SLI5039	0.586	SGR2759	<i>bldM</i>	-

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SCO4880	transferase	ggaccggcct	3.36	-138	SLI5154	0.597	SGR2660		SCO4881/ SCO4882
SCO4951	aldoketoreductase	tgtcccgttt	5.58	-120	SLI5223	0.44	SGR7003		-
SCO4952	TetR family transcriptional regulator	tgtcccgttt	5.58	-35	SLI5224	0.301	SGR7004		SCO4953
SCO4974	deaminase	tattcggccc	5.63	-121	SLI5246	1.826	-		-
SCO5012	hypothetical protein	cgaccagcca	3.66	-72	SLI5288	0.466	SGR2522		SCO5013/SCO5014 <i>/SCO5015</i>
SCO5029	hypothetical protein	ttacccgcgg	5.13	-377	SLI5306	0.566	SGR2504		-
SCO5050	nucleotide-sugar dehydrogenase	aaacctggcct	6.13	-37	SLI5327	1.852	-		SCO5051/SCO5052 <i>/SCO5053/SCO5054</i>
SCO5101	hypothetical protein	cggcgaaaac	6.11	-28	SLI5379	0.584	SGR2456		-
SCO5123	small membrane protein	atattggcca	6.23	-177	SLI5404	0.343	SGR2406		-
SCO5240*	hypothetical protein	tgtcccgatc	5.99	-170	SLI5531	2.246	SGR2274	<i>wblE</i>	-
SCO5249	nucleotide-binding protein	gtttcgacaa	6.31	-187	SLI5540	0.551	SGR2264		-
SCO5390	alkanal monooxygenase	gaatcgccgg	5.52	-119	SLI5659	0.608	SGR2147		-
SCO5512	acetolactate synthase 1 catalytic subunit	aatctcgcaa	5.09	-39	SLI5786	1.672	SGR2000	<i>ilvB</i>	SCO5513
SCO5555*	hypothetical protein	gtttcgacca	7.86	-241	SLI5832	2.828	SGR1927		-
SCO5556	histone-like DNA binding protein	ttgcggatata	3.76	-75	SLI5833	2.388	SGR1926	<i>hupS</i>	-
SCO5650	hypothetical protein	tgtcctttac	3.18	-14	SLI5907	0.578	SGR331		-
SCO5741	hypothetical protein	ggtcggatg	3.64	-90	SLI6001	2.502	SGR1779		-
SCO5742	hypothetical protein	ggactgaaat	3.69	-32	SLI6002	2.094	SGR1778		-
SCO5751	hypothetical protein	tggcgaaag	4.81	-97	SLI6012	0.613	SGR1770		-
SCO5790	hypothetical protein	ggcgaaatc	3.94	-35	SLI6052	1.704	-		SCO5789
SCO5862*	two-component regulator CutR	tggccgaaaa	7.69	-99	SLI6134	1.927	SGR1670	<i>cutR</i>	SCO5863
SCO6000	hypothetical protein	cggctggtc	5.53	-155	SLI6389	0.56	-		SCO6001
SCO6004	ATP/GTP binding protein	cggccgcatt	5.21	-292	SLI6392	0.603	SGR1503		-
SCO6009	solute-binding protein	cttccagcca	6.53	-52	SLI6398	1.736	SGR1498		-
SCO6073	cyclase	gggctgatc	4.27	-75	SLI6466	0.466	SGR6839	<i>geoA</i>	-
SCO6096*	lipoprotein	catcgccca	5.56	-147	SLI6490	0.557	SGR1397		SCO6095
SCO6099	adenylylsulfate kinase	tggccggtcc	5.72	-61	SLI6494	0.544	SGR1394	<i>cysC</i>	SCO6098/SCO6097
SCO6102	nitrite/sulfite reductase	cggccgaaaa	5.85	-366	SLI6496	0.532	SGR1391		SCO6101/SCO6100
SCO6174	hypothetical protein	ggacggaaac	4.01	-10	SLI6567	0.538	SGR1351		SCO6175
SCO6176	hypothetical protein	gaatcggct	5.0	-79	SLI6569	0.459	-		-
SCO6197	hypothetical protein	aattcagcca	7.85	-117	SLI6586	0.147	-		-
SCO6198	hypothetical protein	aattcagcca	7.85	-470	SLI6587	0.618	SGR4455		-

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SCO6376	hypothetical protein	cggccggacc	4.69	-59	-	0.603	-	-	-
SCO6384	integral membrane lysyl-tRNA synthetase	tggcaggatg	4.82	-122	-	0.59	-	-	-
SCO6482	hypothetical protein	tggcccgAAC	7.23	-37	SLI6829	0.538	SGR1161	-	-
SCO6509	hydrophobic protein	tttcccgtatt	4.04	-36	SLI6857	0.398	-	-	-
SCO6510	hypothetical protein	ttgtctttt	3.44	-69	SLI6858	0.406	SGR1146	-	-
SCO6685*	two-component system response regulator	gttcgggcca	7.23	-31	SLI7029	0.624	SGR2393	<i>ramR.</i> <i>amfR</i>	-
SCO6691	phospholipase C	cggccggttg	4.91	-41	SLI7035	0.414	SGR887	-	-
SCO6799	L-threonine 3-dehydrogenase	ggggccgcTT	3.47	-55	SLI7149	1.638	SGR1444	<i>tdh</i>	SCO6800/SCO6801 /SCO6802/SCO6803/SCO6804
SCO6808	transcription regulator ArsR	tggccggact	6.93	-77	SLI1107	0.268	-	-	-
SCO6820	oxidoreductase	tgtcgatAC	4.86	-287	SLI1095	0.338	-	-	-
SCO6831	hypothetical protein	gttccggCAA	6.24	-241	SLI1083	0.602	SGR6080	-	-
SCO6903	hypothetical protein	cgtcccgatC	4.15	-43	SLI0959	0.617	-	-	SCO6904
SCO6926	hypothetical protein	tggcttatac	5.26	-394	SLI0925	0.6	-	-	-
SCO6979	solute-binding lipoprotein	tatccggtec	4.15	-103	SLI7181	0.611	-	-	SCO6980/SCO6981 /SCO6982
SCO7070	hypothetical protein	tgacgcgatC	4.69	-24	SLI7275	1.649	SGR1238	-	-
SCO7221	polyketide synthase	tggccaagTC	3.44	-169	SLI7437	1.692	-	-	-
SCO7251	hypothetical protein	tggcgcatTC	5.36	-280	SLI7467	0.574	SGR6841	-	-
SCO7410	binding-protein dependent transport protein	tggcggcatG	4.67	-114	SLI7629	1.707	-	-	SCO7409
SCO7449	hypothetical protein	cggcgtgtTC	4.54	-131	SLI7668	1.634	-	-	-
SCO7477	hypothetical protein	caagaggCCA	3.43	-164	SLI7697	1.657	SGR1156	-	-
SCO7549	hypothetical protein	gttcccgCAG	3.76	-49	SLI7771	0.447	-	-	-
SCO7550	hydrolase	gaaccggTCA	5.88	-117	SLI7772	0.334	-	<i>glpQ3</i>	-
SCO7631*	hypothetical protein	tggcgtaAC	5.97	-123	SLI7859	0.355	-	-	-
SCO7657*	hypothetical protein	gatccggCCA	8.9	-139	SLI7885	0.033	SGR3840	<i>hyaS</i>	SCO7658
SCO7659*	oxidoreductase	gatcgaggCG	4.98	-25	SLI7886	0.511	-	-	-
SCO7697	hydrolase	tggccgtcac	3.1	-36	SLI7928	0.557	-	-	-
SCO7714	acetyltransferase	gaagtgcCCA	3.98	-110	SLI7945	0.516	-	-	-
SCO7774	hypothetical protein	cggcggaaAG	4.04	-540	SLI8023	0.589	-	-	SCO7775

- a.** Orthologs of *S. lividans* AdpA-dependent genes (listed in Additional file 2) were analysed *in silico* using the *S. coelicolor* genome database (version 1.2.3.0 of PREDetector software [39]). AdpA-binding sites upstream from *S. coelicolor* genes were identified and are presented in this Additional file with information about their *S. lividans* and *griseus* orthologs. Table 3 presents a selected subset of this complete compilation mainly genes whose orthologs are probably direct *S. griseus* AdpA-dependent genes (gene underlined) [12-15, 22].
- b.** Gene names are from the StrepDB database [7]. Genes in bold were identified as direct AdpA-targets. Genes underlined were described as AdpA-dependent, putative AdpA-binding sites have been found *in silico* in the promoter of genes indicated by a star [12-15, 22].
- c.** Function, cis-element sequence, score and position were searched in the “upstream region” of *S. coelicolor* genome as given by PREDetector software (version 1.2.3.0)[39]. When more than one putative AdpA-binding site was detected, only the one with the highest score was shown here. # Putative sites were searched in the “coding region” and were located in the following coding sequences: SCO1033 (at position 250th/285nt total length gene) and SCO3122 (1447th/1449nt).
- d.** Gene names were identified by searching *S. coelicolor* orthologs in the StrepDB database [7]. Genes in bold were identified as direct *S. lividans* AdpA-targets in our studies. No *S. lividans* orthologs were found for the following *S. coelicolor* genes: SCO3495, SCO6376, SCO6384, SCO7449 that had Fc values closed to our microarrays cut-off. By blast we detected putative *S. lividans* genes orthologs to SCO1379, SCO2212 and SCO2921 (97-100% nucleotide homology). As Fc-values are significant for SCO1379 and SCO2921, it is likely that *S. lividans* genome carried orthologs of these genes that are *S. lividans* AdpA-dependent.

- e. Gene expression fold change (Fc) in *S. lividans adpA* mutant compared to the wild-type strain 1326.
- f. Other *Streptomyces* gene names from StrepDB database [7].
- g. *S. coelicolor* co-transcript genes given by PREDetector software [39]. The genes in bold had no significant gene expression changes in *S. lividans adpA* mutant.