

TABLE S1**Primers used for RT-PCR, PCR and for primer extension**

primer	sequence	size of PCR product
rps1	5'-CAA GCACGACCACCACTCCC-3'	
+16R	5'-TTCGGCGTAGTGGGTCTCGT-3'	460 bp
ramR F1	5'-GAGATGGTTCGT ATTGCCGT-3'	
ramR R1	5'-GCA CGATGCGGATCGCGTCGA-3'	583 bp
SCPMPF3	5'-TGGCCCCCGGGGGCAGATCCC-3'	
pnpB1	5'-CTCGTCGCGGGATCCGACGTG-3'	2560 bp
SCO3982F1	5'- GTG-CCC-GCT-TCG-CGA-GTG-AGC-3'	
SCO3982R1	5'-TCA-GCT-CTC-CCT-GCC-CTC-GAC-3'	2449 bp
SCINTLF1 (SC05737)	5'-GCCGAGGGCCTCGGACACCTG-3'	
3987R2 (SCO3987)	5'-GGATTTGTCATCCGTGCAACA-3'	
3988R1 (SCO3988)	5'-TCA GCTCTCCCTGCCCTCGAC-3'	

Table S2 - RNA-seq RESULTS BY GENE TYPE

Listings in **red** represent genes whose transcripts increased by \geq two-fold in *S. coelicolor* JSE1880 as compared to M145. Listings in black represent genes whose transcripts decreased by \geq two-fold in JSE1880. Listings in **blue** indicate transcripts that were present in the BARD. Ribosomal RNA genes are listed in black even though some of the transcripts from those genes changed by less than two-fold in JSE1880.

PUTATIVE REGULATORY PROTEINS

[SCO0168](#) (2.41) - possible regulator protein
[SCO0772](#) (2.46) - putative regulatory protein
SCO3217 (-2.18) – CdaR, putative transcriptional regulator
[SCO3982](#) (2.31) – weak similarity to ROK family of transcriptional regulators, *S. clavuligerus*
[SCO3983](#) (2.14) – weak similarity to putative transcriptional regulator, *Nocardia farcinica*
[SCO3984](#) (2.23) – putative transmembrane protein
[SCO3985](#) (2.61) – GntR regulator family (?), conserved in other streptomycetes
[SCO3986](#) (2.20) - putative GntR-family transcriptional regulator
[SCO4229](#) (2.15) - putative sensor kinase (*phoR*)
[SCO5190](#) (3.92) - putative DNA-binding protein
[SCO5338](#) (2.67) - putative regulatory protein
[SCO5341](#) (3.70) - SpdA2 protein
[SCO5342](#) (3.51) - SpdB2 protein
SCO5344 (4.16) - SpdD2 protein
[SCO5607](#) (2.43) - putative transcriptional regulator
SCO6280 (-2.00) – KasO, possible regulatory protein
[SCO6823](#) (2.31) - putative ArsR-family transcriptional regulator

ABC TRANSPORTERS

[SCO1558](#) (2.08) - putative ABC transporter permease protein
SCO3223 (-13.76) - putative ABC transporter integral membrane protein
SCO3224 (-9.71) – putative ABC transporter ATP-binding protein
[SCO4140](#) (2.39) - phosphate ABC transport system permease protein
[SCO4141](#) (3.14) - phosphate ABC transport system permease protein
[SCO5112](#) (2.56) - BldKA, putative ABC transport system integral membrane protein
[SCO5113](#) (2.21) - BldKB, putative ABC transport system lipoprotein
[SCO5114](#) (2.22) - BldKC, putative ABC transport system integral membrane protein
[SCO5479](#) (2.14) - oligopeptide ABC transporter ATP-binding protein

NITROGEN AND PHOSPHORUS METABOLISM

[SCO0209](#) (2.01) - urease β subunit
[SCO0216](#) (2.45) - nitrate reductase alpha chain NarG2
[SCO0217](#) (2.02) - probable nitrate reductase beta chain
[SCO0218](#) (2.41) - putative nitrate reductase delta chain NarJ2
[SCO0219](#) (2.18) - putative nitrate reductase delta chain NarI2
[SCO1234](#), [5526](#) (2.23) - urease α subunit
[SCO2198](#) (2.09) - glutamine synthetase I
[SCO4142](#) (3.59) – phosphate binding protein precursor

[SCO4145](#) (2.34) – polyphosphate kinase
[SCO4947](#) (3.23) - nitrate reductase alpha chain NarG3
[SCO4948](#) (3.77) - nitrate reductase beta chain NarH3
[SCO4949](#) (3.37) - nitrate reductase delta chain NarJ3
[SCO4950](#) (2.54) - nitrate reductase gamma chain NarI3

CARBOHYDRATE METABOLISM

[SCO0199](#) (2.70) - putative alcohol dehydrogenase
[SCO0773](#) (2.63) - putative ferredoxin
[SCO4283](#) (2.06) - probable sugar kinase
[SCO4857](#), 4858, 5106, 5107 (3.16) - putative succinate dehydrogenase membrane subunit
[SCO4875](#) (2.13) - putative sugar transferase
[SCO4878](#) (2.00) - possible glycosyltransferase
[SCO4880](#) (3.91) - possible transferase
[SCO4881](#) (3.99) – putative polysaccharide biosynthesis related protein
[SCO5578](#) (2.40) - putative sugar transporter
[SCO7511](#) (2.37) - glyceraldehyde 3-phosphate dehydrogenase

ATP-GTP BINDING PROTEINS

SCO1627 (-2.63)
SCO6797 (-2.06)

CYTOCHROMES

SCO1626 (-2.60) - putative cytochrome P450
[SCO0774](#) (3.87) - putative cytochrome P450
[SCO0924](#) (2.61) - putative cytochrome B subunit

MEMBRANE ATPases

SCO3216 (-4.81)

OTHER MEMBRANE PROTEINS

[SCO0201](#) (2.78) - putative integral membrane protein
[SCO0863](#) (2.21) - putative integral membrane protein
SCO1630 (-2.26) - putative integral membrane protein, possible histidine sensor kinase
[SCO1700](#) (2.11) - putative membrane protein
[SCO1710](#) (2.08) - putative integral membrane transport protein
[SCO2197](#) (2.47) - putative integral membrane protein
SCO4225 (2.04) - possible integral membrane protein
[SCO4843](#) (2.20) - putative integral membrane protein
[SCO5476](#) (3.11) - oligopeptide transport integral membrane protein
[SCO5477](#) (2.18) - putative oligopeptide-binding lipoprotein
[SCO5478](#) (2.54) - oligopeptide transport system integral membrane protein
SCO6278 (-4.06) – integral membrane transport protein
[SCO6728](#) (2.14) - putative membrane protein
SCO7536 (-2.33) – possible integral membrane protein

TRANSPOSASES AND OTHER MOBILE ELEMENTS

SCO3113 (-3.76) – transposase remnant

[SCO4698 \(11.32\)](#) - putative insertion element IS1652 transposase

[SCO5339 \(2.93\)](#) - plasmid transfer protein

[SCO6015 \(2.01\)](#) – prophage gene

[SCO6396 \(-3.23\)](#) - probable transposase for IS1648

GLYCEROL UTILIZATION AND METABOLISM

[SCO1659 \(-2.63\)](#) - *glpF*, probable glycerol uptake facilitator protein

[SCO1660 \(-2.67\)](#) – glycerol kinase

LIPID METABOLISM

[SCO1565 \(2.15\)](#) - putative glycerophosphoryl diester phosphodiesterase

[SCO1661 \(-2.20\)](#) - probable glycerol-3-phosphate dehydrogenase

RIBOSOMAL RNAs

[rrnA1 \(-1.01\)](#) [rrnD1 \(-1.14\)](#)

[rrnA2 \(1.33\)](#) [rrnD2 \(-1.38\)](#)

[rrnA3 \(8.41\)](#) [rrnD3 \(-1.04\)](#)

[rrnB1 \(4.36\)](#) [rrnE1 \(-1.38\)](#)

[rrnB2 \(-1.69\)](#) [rrnE2 \(-1.27\)](#)

[rrnB3 \(-1.49\)](#) [rrnE3 \(-1.02\)](#)

[rrnC1 \(2.33\)](#) [rrnF1 \(-1.52\)](#)

[rrnC2 \(-1.69\)](#) [rrnF2 \(-2.04\)](#)

[rrnC3 \(-1.35\)](#) [rrnF3 \(-1.69\)](#)

RIBOSOMAL PROTEINS

[SCO1150 \(2.03\)](#) – *rpmE*, ribosomal protein L31

[SCO5595 \(2.23\)](#) - 50S ribosomal protein L19

tRNAs

[SCOt23 \(-2.35\)](#) - tRNA_{leu} (TAG)

[SCOt39 \(-2.25\)](#) – tRNA_{gly} (GCC)

[SCOt12 \(2.00\)](#) – tRNA_{asn} (GTT)

[SCOt13 \(3.31\)](#) – tRNA_{asn} (GTT)

[SCOt17 \(2.10\)](#) – tRNA_{gly} (TCC)

[SCOt26 \(3.63\)](#) – tRNA_{ala} (CGC)

[SCOt36 \(2.10\)](#) – tRNA_{arg} (ACG)

[SCOt37 \(3.40\)](#) – tRNA_{ser} (CGA)

[SCOt55 \(2.17\)](#) – tRNA_{arg} (CCG)

[SCOt62 \(4.71\)](#) - tRNA_{leu} (GAG)

OTHER MISCELLANEOUS PROTEINS

[SCO0494 \(-2.14\)](#) - probable iron-siderophore binding lipoprotein

[SCO1906 \(2.44\)](#) - putative twin-arginine pathway signal protein

[SCO3132 \(2.26\)](#) - putative trans-aconitate methyltransferase

[SCO3236 \(-3.02\)](#) – possible antibiotic oxygenase

SCO3244 (-4.19) - putative secreted protein
[SCO3783](#) (2.16) - putative lipoprotein
[SCO4095](#) (2.00) - possible lipoprotein
[SCO4145](#) (2.34) - polyphosphate kinase
[SCO5142](#) (2.06) - possible secreted protein
[SCO5347](#) (3.54) - replication initiation protein
[SCO5353](#) (3.26) - diaminopimelate decarboxylase
[SCO5464](#) (2.07) - possible calcium-binding protein
[SCO5520](#) (2.46) - delta-1-pyrroline-5-carboxylate dehydrogenase
[SCO6009](#) (2.44) - solute-binding protein
[SCO6276](#) (-4.89) – epoxide hydrolase
[SCO6277](#) (-4.95) – putative secreted protein
[SCO6279](#) (-2.13) - probable diaminobutyrate-pyruvate aminotransferase
[SCO6282](#) (-15.73) - probable 3-oxoacyl-[acyl-carrier protein] reductase
[SCO6284](#) (-2.39) – putative decarboxylase
[SCO7391](#) (2.08) - possible phytoene dehydrogenase, pseudogene

HYPOTHETICAL PROTEINS

[SCO0074](#) (2.30)
[SCO0169](#) (2.00) – possible regulator (?)
[SCO0198](#) (2.76)
[SCO0200](#) (3.74) – universal stress protein family
[SCO0209](#) (2.01) – urease β subunit
[SCO0268](#) (3.27)
[SCO0499](#) (-2.14) – formyltransferase (?)
[SCO0500](#) (2.82) – formyltransferase (?)
[SCO0536](#) (2.23)
[SCO0955](#) (2.06)
[SCO1374](#) (3.42)
[SCO1628](#) (-2.19) – ATP/GTP binding protein (?)
[SCO2072](#) (2.11)
[SCO3003](#) (2.18)
[SCO3141](#) (2.13)
[SCO3142](#) (2.23)
[SCO3152](#) (2.73)
[SCO4144](#) (2.06) – contains TTA, high G+C content
[SCO4227](#) (2.33)
[SCO4249](#) (2.40)
[SCO4748](#) (2.34)
[SCO4879](#) (3.66)
[SCO4882](#) (3.05)
[SCO4925](#) (2.11)
[SCO5145](#) (2.08)
[SCO5163](#) (3.35)
[SCO5189](#) (2.96)
[SCO5191](#) (2.69)
[SCO5340](#) (4.94)
[SCO5345](#) (3.52)

SCO5346 (3.54)
SCO5519 (2.38) – delta-1-pyrroline-5-carboxylate dehydrogenase (?)
SCO5521 (2.81)
SCO5536 (3.43)
SCO5606 (5.16) – possible prophage, low G+C content (?)
SCO5608 (2.74) – possible transcriptional regulator
SCO5757 (2.61)
SCO6283 (-2.56)
SCO6317 (2.09)
SCO6682 (-3.80)
SCO6716 (-3.23) – acyl-[acyl carrier protein] desaturase (?)
SCO7348 (-2.42)
SCO7658 (-2.14) – oxidoreductase (?)

TABLE S3

Genes whose transcript levels changed by \geq two-fold in the mRNA pool from JSE1880 as compared with M145 and whose enrichment ratio in the BARD was \geq 1.0

GENE ID NUMBER	FUNCTION	FOLD INCREASE IN JSE1880	ENRICHMENT RATIO
SCO0168	possible transcriptional regulator	2.41	100
SCO0198	hypothetical protein	2.70	47.6
SCO0200	universal stress protein family	3.74	24.3
SCO0209	urease β subunit	2.01	33.8
SCO0216	nitrate reductase alpha chain NarG2	2.45	13.8
SCO0217	possible nitrate reductase β chain	2.02	8.4
SCO0218	putative nitrate reductase δ chain NarJ2	2.41	5.2
SCO0219	putative nitrate reductase δ chain NarJ2	2.18	30
SCO0494	probable iron-siderophore binding lipoprotein	-2.14	19
SCO0499	formyltransferase	2.10	24.4
SCO0772	regulatory protein	2.46	3.0
SCO0773	ferredoxin	2.6	5.4
SCO0863	putative integral membrane protein	2.21	18.4
SCO0924	cytochrome B subunit	2.61	7.2
SCO1626	cytochrome P450	-2.60	22.8
SCO2198	glutamine synthetase I	2.09	12.4
SCO3982	hypothetical protein, contains TTA codon	2.31	1.4
SCO3983	hypothetical protein, contains TTA codon	2.14	1.5
SCO3985	hypothetical protein	2.61	13.7
SCO4140	phosphate ABC transporter permease	2.39	2.1
SCO4225	putative integral membrane protein	2.04	1.3
SCO4227	hypothetical protein	2.33	1.3
SCO4878	glycosyltransferase	2.00	1.6
SCO4882	hypothetical protein	3.05	4.8
SCO5112	ABC transporter integral membrane protein BldKA	2.56	1.4
SCO5142	hypothetical protein	2.06	20.5
SCO5520	delta-1-pyrroline-5-carboxylate dehydrogenase	2.46	2.1
SCO5608	possible transcriptional regulator	2.74	4.2