

Table 4: Classification of *Streptomyces coelicolor* genes with a putative SFBS $CGTAA N_{\{18\ 19\}}GTT$ in their upstream region

0.0.0	Unknown function, no known homologs (1049)		
	SCO3324 SCE68.22	hypothetical protein	cgtaaccaagtgccgcccgtcggt
	SCO3374 SCE94.25	hypothetical proline-rich protein	cgtaaccgagcgctcttcgactggt
	SCO6909 SC1B2.15	hypothetical protein SC1B2.15	cgtaattcactaagtgcagtgccggt
0.0.2	Conserved in organism other than <i>Escherichia coli</i> (1322)		
	SCO4398 SCD10.30c	conserved hypothetical protein	cgtaacccccgggtgggcccgggagtt
	SCO4543 2SCD4.14c	hypothetical protein	cgtaagcggtacagggacaggtgagtt
	SCO5581 SC7A1.25c	conserved hypothetical protein	cgtaaccgcccgtgcgtcggaccggt
1.5.0	Transport/binding proteins (520)		
	SCO2422 SCC42.03c	putative ABC-transporter ATP-binding protein	cgtaacgtgccgggtgcgggtgctcggt
	SCO6483 SC9C7.19	putative efflux protein	cgtaactcgtcgcacttgttcgcagtt
2.1.3	Degradation of polysaccharides (92)		
	SCO2430 SCC24.01	putative sugar hydrolase (fragment) (putative secreted protein)	cgtaaccgggcccacggcctacgggtt
	SCO7019 aml	putative secreted beta-galactosidase (fragment) secreted alpha-amylase.	cgtaagagattttctgcaactttccggt
2.2.1	Amino acyl tRNA syn; tRNA modific'n (34)		
	SCO1595 pheS	putative phenylalanyl-tRNA synthetase alpha chain	cgtaatccggttccacagccccggt
2.2.4	Glycoprotein (11)		
	SCO2981 SCE50.09	putative glycosyl transferase	cgtaaccaagcgggtccaccggccggt
2.2.10	Proteins - translation and modification (36)		
	SCO1528 SCL2.18	putative elongation factor	cgtaaaaaatgcacgcgcgtacttggt
3.6.0	Fatty acid biosynthesis (3)		
	SCO6473 SC9C7.09c	crotonyl CoA reductase	cgtaaagatttcatctgagaagagtt
3.8.0	Secondary metabolism (165)		
	SCO5799 SC4H2.20	putative aminotransferase	cgtaacccccgtgaacggtcctcggt

4.1.6	Gram +ve membrane (836)		
	SCO1540 SCL2.30c	putative membrane protein	cgtaactcttccggccgatggaccggt
4.1.7	Gram +ve exported/lipoprotein (439)		
	SCO5202 2SC3B6.26	putative secreted protein	cgtaacccgcccccgcggtgagcgtt
5.1.2	Phage-related functions and prophages (25)		
	SCO5612 SC2E1.29	putative ATP binding protein	cgtaagcggctcctccgtctcctggt
6.3.5	LacI (34)		
	SCO7014 SC1H10.03c	probable LacI-family transcriptional regulatory protein	cgtaacggggatcggcaacgactggt
6.3.8	TetR (122)		
	SCO3367 SCE94.18	putative tetR-family regulator	cgtaactagccggcggtcaagtaagtt
6.3.11	LuxR (GerR) (23)		
	SCO4768 SC6G4.46	putative two-component regulator	cgtaactctttcgagtgaccatcggt
	Not known according to classification		
	SCP1.28c SCP1.167 SCP1.230 mmyB SCP1.326		cgtaagccggaggaagaggacgtagtt cgtaacagcgcggtggacatcaccggt cgtaagccccggtttaactctccggt cgtaagccggaggaagaggacgtagtt