

Position	Strand	Sequence	Score	Downstream ORF
189992	-	CCACGATGGTTCAGACAA	80.00	-N(126)- - SAV169 - - hypothetical protein
247377	-	CAGAGCTGGTGTAGACCG	80.00	-N(724)- - SAV211 - - hypothetical protein
801926	+	TGCCACTGTTGCAGACCA	81.45	-N(831)- - SAV644 - - hypothetical protein
1218178	+	CACGACTGGCCTGGACCA	80.63	-N(79)- - SAV957 - - hypothetical protein
1274359	+	ACAGTCGGGTCTAGACCA	84.12	-N(311)- - SAV1008 - - hypothetical protein
1329137	+	<i>TCAATTTGGTACGGACCA</i>	86.92	-N(21)- - SAV1053 - - putative sugar hydrolase
1613336	+	CCCTGGTGGTTTAGACCA	90.07	-N(25)- - SAV1305 - - putative GntR-family transcriptional regulator
1873454	-	AGATTCTGGTCTAGACCG	82.00	-N(93)- - SAV1530 - - putative secreted protein
2132244	+	CCTTACCGGTCTGGACCA	82.70	-N(81)- chiA2 SAV1751 - - putative chitinase A
2132285	+	CGTGATTGGTCCATACCA	87.70	-N(40)- chiA2 SAV1751 - - putative chitinase A
2947277	+	<i>GGACACTGGTCTAGACAA</i>	88.22	-N(12)- <i>hpr SAV2418 - - putative phosphocarrier protein</i>
2947283	-	CTCAGGTTGTCTAGACCA	85.00	-N(112)- - SAV2417 - - hypothetical protein
3179630	-	CCGAATTGGTCTGGACCA	93.00	-N(64)- chiB SAV2585 - - putative chitinase B
3345948	+	TACAATTGTTCTAGACAA	83.38	-N(100)- - SAV2728 - - putative transporter
3522866	+	GCGCACTGGTCCAGACCT	83.93	-N(95)- chiC SAV2878 - - putative chitinase C precursor
3522887	+	GACCTATGGTCCAGACCT	80.13	-N(74)- chiC SAV2878 - - putative chitinase C precursor
3773700	+	<i>ACATTGTGGACTAGACCA</i>	85.20	-N(254)- <i>gamA SAV3018 - - putative glucosamine-6-phosphate isomerase</i>
3773706	-	GGACCGTGGTCTAGTCCA	83.00	-N(257)- - SAV3017 - - putative two-component system sensor kinase
3773915	+	<i>CTAGATTGGTCTAAACCA</i>	92.69	-N(39)- <i>gamA SAV3018 - - putative glucosamine-6-phosphate isomerase</i>
3773921	-	CATATGTGGTTTAGACCA	91.00	-N(472)- - SAV3017 - - putative two-component system sensor kinase
3779785	+	GACCAATGGTGTAGACCA	93.18	-N(301)- - SAV3023 - - putative GntR-family transcriptional regulator
3779791	-	<i>CCGTACTGGTCTACACCA</i>	89.00	-N(65)- - SAV3022 - - putative sugar transporter sugar binding protein
3779809	+	GGAGCTTGGCCCAGACCA	80.57	-N(277)- - SAV3023 - - putative GntR-family transcriptional regulator
3779815	-	<i>GCCTATTGGTCTGGGCCA</i>	84.00	-N(89)- - SAV3022 - - putative sugar transporter sugar binding protein
3779955	+	GCGCGGTGGACTAGACCA	84.52	-N(131)- - SAV3023 - - putative GntR-family transcriptional regulator
3779961	-	<i>CCCTGTTGGTCTAGTCCA</i>	85.00	-N(235)- - SAV3022 - - putative sugar transporter sugar binding protein
3969427	-	GGCGATTGGTTCAGGCCA	80.00	-N(76)- - SAV3185 - - hypothetical protein
4053939	+	CCAGATTGGTCTGGACCA	93.91	-N(63)- chiA1 SAV3258 - - putative chitinase A
4053945	-	ACAAACTGGTCCAGACCA	94.00	-N(257)- - SAV3257 - - hypothetical protein
4410220	+	<i>GCGTACTGGCCTACACCA</i>	80.60	-N(480)- <i>glmU SAV3561 - - putative UDP-N-acetylglucosamine pyrophosphorylase</i>
4613717	-	TATCTGTGCTCTAGACCA	86.00	-N(498)- - SAV3727 - - hypothetical protein
4620849	-	GCATACTCGTATAGACGA	80.00	-N(107)- pra1 SAV3735 - - putative replication activator protein Pra
4763169	+	GCGCGCTGGTCCAGACCG	80.46	-N(37)- - SAV3856 - - hypothetical protein
4863930	-	CTTACGTGGTGTAGACCT	82.00	-N(69)- - SAV3939 - - putative secreted solute-binding protein
4912912	-	GCTTACTCGTATAGACGA	80.00	-N(111)- pra2 SAV3988 - - putative replication activator protein Pra
5569500	+	GGCCCATGGTCCGGACCA	82.66	-N(337)- sig40 SAV4561 - - putative RNA polymerase ECF-subfamily sigma factor
5615809	-	ACCCACAGGTCTAAACCA	82.00	-N(104)- acsA1 SAV4599 - - putative acetyl-CoA synthetase
6275198	-	<i>ACTGAGTGGTGTAGACCA</i>	94.00	-N(105)- - SAV5167 - - putative PTS transmembrane component
6275215	-	<i>TACAACAGGTCTACACCA</i>	81.00	-N(122)- - SAV5167 - - putative PTS transmembrane component
6276676	+	GACAGGTGGTGTAGACCA	90.69	-N(105)- - SAV5169 - - hypothetical protein

6276682	-	GGCAACTGGTCTACACCA	89.00	-N(53)-	- SAV5168 - - putative PTS transmembrane component
6308489	-	ACTCATTGGTCCAGAGCA	89.00	-N(370)-	- SAV5202 - - putative ATP-dependent helicase
6332002	+	GAGACTTGGTCTAGACCT	84.96	-N(40)-	chb SAV5223 - - putative chitin binding protein
6381466	+	GGAGAGTGGTCTATACCC	80.26	-N(58)-	hexA SAV5268 - - putative beta-N-acetylhexosaminidase
6816504	-	GACGAAAGGTCTGGACCA	80.00	-N(69)-	SAV5636 - - putative endochitinase
6816519	+	GTCAATAGGTCTGGACCA	84.25	-N(135)-	SAV5637 - - putative aldo/keto reductase
6816525	-	CCCCCTCTGGTCCAGACCT	81.00	-N(90)-	SAV5636 - - putative endochitinase
7722587	+	CCCCCTTGGTGGAGATCA	80.58	-N(67)-	SAV6446 - - hypothetical protein
8231292	+	GAAAGTTCGTCCGGACCA	80.09	-N(62)-	SAV6898 - - hypothetical protein
8236055	+	GCTAAGAGGACTAGACCA	80.18	-N(413)-	ribC SAV6902 - - putative riboflavin synthase
8236078	+	GTCAATAGGTATGGACCA	82.44	-N(390)-	ribC SAV6902 - - putative riboflavin synthase
8249843	+	TGCCAGTGGTCGGGACCA	85.99	-N(101)-	SAV6915 - - hypothetical protein
8253827	+	GGTCAATGGTTCGGACCA	84.28	-N(227)-	fadE2 SAV6919 - - putative acyl-CoA dehydrogenase
8253833	-	CGAAATGGTCCGAACCA	84.00	-N(117)-	chiD SAV6918 - - putative chitinase
8431857	+	GAGGATTGGTCTTGACCA	90.66	-N(83)-	SAV7069 - - putative GntR-family transcriptional regulator
8531318	+	GGCAATTAGTCCACACCA	80.73	-N(169)-	SAV7166 - - putative amidase
8531324	-	CGTCACTGGTGTGGACTA	80.00	-N(627)-	SAV7165 - - putative non-ribosomal peptide synthetase
8666568	+	GACTGCTCGTCCAGACCA	80.76	-N(71)-	SAV7268 - - hypothetical protein
8741829	+	CCGCATTGGTCCATACCA	89.60	-N(69)-	SAV7329 - - putative sugar transporter sugar binding protein
8741835	-	GGATTTTGGTATGGACCA	87.00	-N(89)-	SAV7328 - - hypothetical protein
8874611	-	AACTACTGGTCCGGACCA	86.00	-N(125)-	SAV7442 - - putative secreted hydrolase

Table 10. Sites in the *Streptomyces avermitilis* genome that match the sequence motif represented by matrix 2083. The non-coding regions of the *S. coelicolor* genome were searched against this matrix to find matches to the corresponding sequence motif. The scanning method assigned a score (maximum 100) to each match site. The minimum score threshold was chosen as 80. The position of the match site is given as the chromosomal sequence coordinate. Descriptions of potential target genes immediately downstream of the motifs were taken from the *S. avermitilis* genome annotation. The distance in nucleotides between the 3' end of the motif and the predicted translational start codon is given in parentheses. Genes encoding proteins that may be involved in degradation of polysaccharide are shown in bold and other genes implicated in carbohydrate transport and catabolism are italicised.