

PREDetector Regulon prediction report

Analysis Summary

Date: 2016-11-01

Template sequence

- Streptomyces scabiei 87.22 strain=87.22 [FN554889_1]
- Source: ncbi [2016-10-01]
- Taxid: 680198

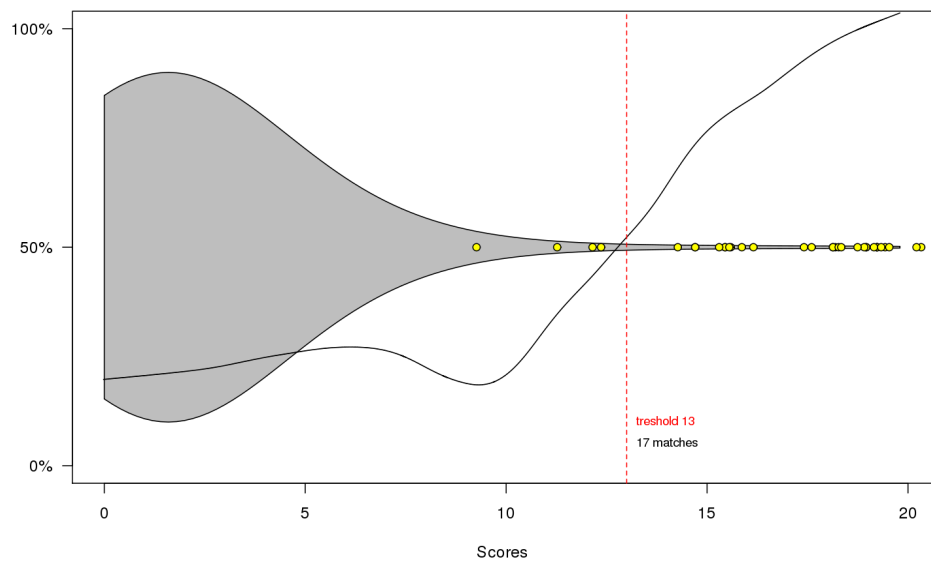
Matrix sequences

- CelR_Actinomycetales.fasta
- 35 sequences.
- 2016-10-01

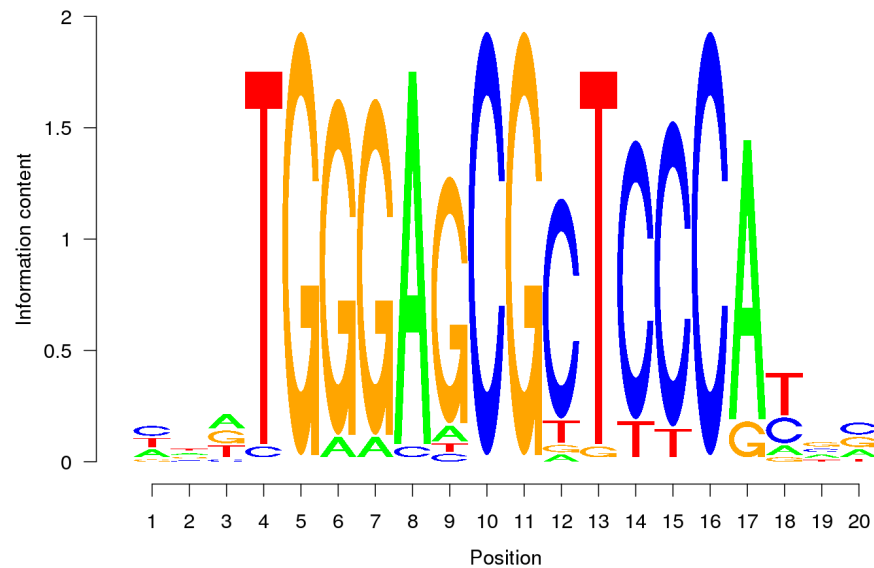
Parameters

- Cutoff score: 13.00
- Selected regions: Upstream Regulatory Coding
- Co-transcribed genes: -10 150
- Regulatory bounds: -350 to 50

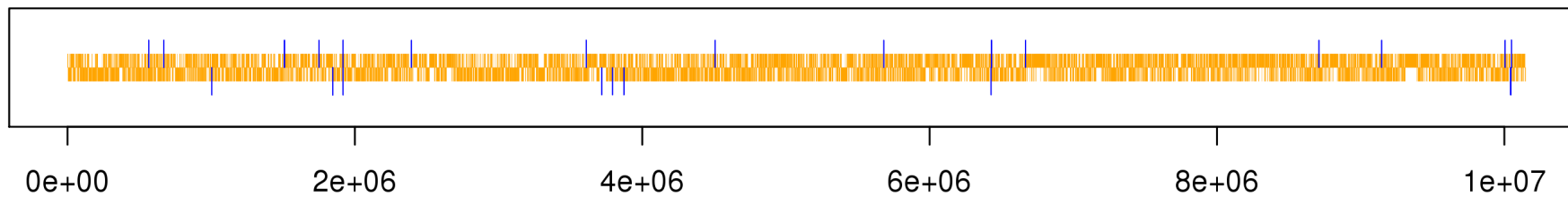
Cut-off plot



Matrix Logo



Genomic Context



Prediction results

PREDICTION RESULTS

Gene	Product	Sequence	Position	Score	Co-transc. genes	Co-transc. products
SCAB_78881	putative secreted glycosylhydrolase	TCATGGGAGCGCTCCCATGA	-88	19.8	NA	NA
celB	putative secreted cellulase B precursor	AAATGGGAGCGCTCCCAAAG	-85	19.4	NA	NA
SCAB_5971	conserved hypothetical protein	AAATGGGAGCGCTCCCAAAG	-559	19.4	NA	NA
SCAB_90091	putative secreted cellulase	CAGTGGGAGCGCTCCCATGA	-108	19.2	NA	NA
SCAB_90101	putative secreted cellulase	CAGTGGGAGCGCTCCCATGA	-764	19.2	NA	NA
SCAB_17011	putative secreted cellulase	ATATGGGAGCGCTCCCCTG	-133	19	NA	NA
SCAB_17001	putative secreted cellulase	ATATGGGAGCGCTCCCCTG	-314	19	NA	NA
SCAB_51081	putative secreted cellulase	TGATGGGAGCGCTCCCACG	-57	18.9	NA	NA
SCAB_57721	putative beta-glucosidase	GCATGGAAGCGCTCCCATTG	-16	18.7	NA	NA
celI	secreted endoglucanase	AAGTGGGAGCGCTCCCAATT	-93	18.3	NA	NA
SCAB_8891	hypothetical protein	AAGTGGGAGCGCTCCCAATT	-854	18.3	NA	NA
SCAB_16431	putative POSSIBLE CELLULASE CELA1 (ENDOGLUCANASE) (ENDO-1%2C4-BETA-GLUCANASE) (FI-CMCASE) (CARBOXYMETHYL CELLULASE)	CAATGGGAGCGCTCCCACCT	-116	18	NA	NA
SCAB_16421	putative LacI-family transcriptional regulator	CAATGGGAGCGCTCCCACCT	-251	18	NA	NA
SCAB_57751	putative secreted cellobiose-binding (transport system associated)	CTGTGGGAGCGCTCCCACGA	-133	17.9	NA	NA
SCAB_57761	putative cellobiose transport regulator	CTGTGGGAGCGCTCCCACGA	-499	17.9	SCAB_57771	conserved hypothetical protein
SCAB_90081	putative secreted cellulase B precursor	GATTGGGAGCGCTCCCAAGA	-63	17.7	NA	NA
SCAB_90061	putative cellulase	GACTGGGAGCGCTCCCAAAA	-204	17.6	NA	NA
SCAB_21081	putative secreted cellulose/chitin binding protein	ACATGGGAGCGCTCCCACCC	-180	17.5	NA	NA
SCAB_4971	conserved hypothetical protein	CCATGGGAGCGCTCCCACCC	-161	16.9	NA	NA
SCAB_4961	putative secreted protein	CCATGGGAGCGCTCCCACCC	-69	16.9	NA	NA
SCAB_89741	putative secreted cellulose-binding protein.	CTATGGGAGCGCTCCAGCG	-119	16.5	NA	NA
SCAB_82431	hypothetical protein	GTGTGGGAGCGCTTCCATGG	118	16.3	NA	NA
SCAB_15711	putative secreted glucosidase	TTTTGAGAGCGCTCTCAGGA	-140	14.7	NA	NA
txtR	cellobiose-dependent regulator TxtR	AAGCGGGAGCGCTCCCACAG	-789	14.3	NA	NA
txtA	thaxtomin synthetase A	AAGCGGGAGCGCTCCCACAG	-902	14.3	txtB	thaxtomin synthetase B
SCAB_16431	putative POSSIBLE CELLULASE CELA1 (ENDOGLUCANASE) (ENDO-1%2C4-BETA-GLUCANASE) (FI-CMCASE) (CARBOXYMETHYL CELLULASE)	TACTGGAAGCGCTTCCAATG	-131	14.1	NA	NA
SCAB_16421	putative LacI-family transcriptional regulator	TACTGGAAGCGCTTCCAATG	-236	14.1	NA	NA
SCAB_90101	putative secreted cellulase	AATCGGGAGCGCTCCCAGAA	-195	14.1	NA	NA
SCAB_90091	putative secreted cellulase	AATCGGGAGCGCTCCCAGAA	-677	14.1	NA	NA
SCAB_40131	conserved hypothetical protein	TTCTGAGAGCGCTCTCAAAC	-66	14	NA	NA

Gene	Product	Sequence	Position	Score	Co-transc. genes	Co-transc. products
SCAB_59891	putative regulatory protein phosphatase	TTCTGGGATCGCTCCCACCG	691	13.9	NA	NA
SCAB_32951	putative lambdoid prophage protein	CCATGGAAACGTTCTCAAAG	488	13.5	NA	NA
SCAB_17011	putative secreted cellulase	TGGTGGAAACCGCTCCCCTG	-286	13.3	NA	NA
SCAB_17001	putative secreted cellulase	TGGTGGAAACCGCTCCCCTG	-161	13.3	NA	NA
SCAB_33591	conserved hypothetical protein	CGATGGGATCGCTCCCAGCG	1625	13.2	NA	NA
SCAB_34281	putative regulatory protein	GAACGGGACCGCTCCCCTCT	2277	13.2	NA	NA
SCAB_13491	putative secreted sugar hydrolase	TCTTGAGAGCGCTCTCAGTC	-120	13	NA	NA
SCAB_13481	putative transcriptional regulator	TCTTGAGAGCGCTCTCAGTC	-280	13	NA	NA

Matrix sequences

>cebE |NC_003155:6369965-6369946 [Streptomyces avermitilis MA-4680]
 TtgTGGGAGCGCTCCCAcGg
 >bgIC2 |NC_003155:6366430-6366411 [Streptomyces avermitilis MA-4680]
 cgATGGGAGCGCTtCCATGc
 >celA1 |NC_003155:702283-702302 [Streptomyces avermitilis MA-4680]
 TttTGGGAGCGCTCCCAaGA
 >celA1 |NC_003155:702428-702447 [Streptomyces avermitilis MA-4680]
 gaATGGGAGCGCTCCCAcct
 >celA1 |NC_003155:702452-702471 [Streptomyces avermitilis MA-4680]
 TgATGGGAGCGCTCCGaac
 >SAV1695 |NC_003155:2074290-2074271 [Streptomyces avermitilis MA-4680]
 gCtcGGGAGCGCTCtCAacg
 >guxA3 |NC_003155:2274155-2274174 [Streptomyces avermitilis MA-4680]
 TgATGGaAtCGCTCCCActg
 >guxA3 |NC_003155:2274298-2274317 [Streptomyces avermitilis MA-4680]
 atATGGGAGCGCTCCCActg
 >SAV5257 |NC_003155:6369946-6369965 [Streptomyces avermitilis MA-4680]
 cCgTGGGAGCGCTCCCAcaA
 >lamA1 |NC_003155:2155004-2155023 [Streptomyces avermitilis MA-4680]
 TCtTGaGAGCGCTCtCAaGg
 >celA2 |NC_003155:2274317-2274298 [Streptomyces avermitilis MA-4680]
 cagTGGGAGCGCTCCCATat
 >celA2 |NC_003155:2274174-2274155 [Streptomyces avermitilis MA-4680]
 cagTGGGAGCGaTtCCATcA
 >celS2 |NC_003155:2750245-2750226 [Streptomyces avermitilis MA-4680]
 aggTGGGAGCGCTCCCATat
 >SCO2795 |NC_003888:3051111-3051130 [Streptomyces coelicolor A3(2)]
 TtgTGGGAGCGCTCCCAcac
 >SCO2798 |NC_003888:3054654-3054673 [Streptomyces coelicolor A3(2)]
 ctATGGGAGCGCTtCCATGc
 >SCO1187 |NC_003888:1259374-1259393 [Streptomyces coelicolor A3(2)]
 aagTGGGAGCGCTCCCATcA
 >SCO1187 |NC_003888:1259400-1259419 [Streptomyces coelicolor A3(2)]

agtTGGGAGCGCTCCCgcac
>SCO7555 |NC_003888:8377139-8377158 [Streptomyces coelicolor A3(2)]
cggTGGGAaCGtgCCCAccA
>SCO7555 |NC_003888:8377160-8377179 [Streptomyces coelicolor A3(2)]
aatTGGGcaCGtTCCCAccc
>SCO6546 |NC_003888:7243948-7243929 [Streptomyces coelicolor A3(2)]
TgATGGaAcCGTCCCActg
>SCO6546 |NC_003888:7243806-7243787 [Streptomyces coelicolor A3(2)]
ctATGGGAGCGCTCCCActg
>SCO6548 |NC_003888:7243787-7243806 [Streptomyces coelicolor A3(2)]
cagTGGGAGCGCTCCCAtag
>SCO6548 |NC_003888:7243929-7243948 [Streptomyces coelicolor A3(2)]
cagTGGGAGCGgTtCCATcA
>SCO7637 |NC_003888:8466370-8466351 [Streptomyces coelicolor A3(2)]
cttTGGGAGCGCTCCCATcg
>SCO0765 |NC_003888:812469-812450 [Streptomyces coelicolor A3(2)]
attTGGGAGCGCTCCCATtc
>SCO0643 |NC_003888:685169-685150 [Streptomyces coelicolor A3(2)]
cCtTGGGAGCGCTCCCATGc
>SCO6665 |NC_003888:7405316-7405297 [Streptomyces coelicolor A3(2)]
ctcTGaGAGCGCTcAGaA
>Tfu_0934 |NC_007333:1098697-1098716 [Thermobifida fusca YX]
TCtTGGGAGCGCTCCCATGc
>Tfu_1959 |NC_007333:2289619-2289638 [Thermobifida fusca YX]
TacTGGGAGCGCTCCG TGA
>Tfu_1959 |NC_007333:2289713-2289732 [Thermobifida fusca YX]
TCATGGGAGCGCTCCCATGc
>Tfu_0620 |NC_007333:721594-721575 [Thermobifida fusca YX]
TttTGGGAGCGCTCCCGTGc
>Tfu_0620 |NC_007333:721493-721474 [Thermobifida fusca YX]
aagTGGGAGCGCTCCCAgcc
>Tfu_0901 |NC_007333:1064168-1064149 [Thermobifida fusca YX]
atATGGGAGCGCTCCCAtag
>Tfu_1627 |NC_007333:1890516-1890497 [Thermobifida fusca YX]
aaATGGGAGCGCTCCCATGg
>Tfu_1268 |NC_007333:1473429-1473410 [Thermobifida fusca YX]
gCATGGGAGCGtTCCCATGc