

Table S7. Identification of promoters recognized by σ^E and σ^K

Promoters recognized by SigE-RNA polymerase holoenzyme

Gene		sense	TSS position	score	promoters
spacing 16-18 bp					
CD0106	<i>cwlD</i>	1	123155	2.66	TATATGGA ATA TTATAGTGTTTTTATAAG TATACATA TACA
CD0124	<i>spoIID</i>	1	169491	11.3	AGAAAGTT ATA AAATTAATAGGGTTGTT CATATACT TAAATA
CD0126	<i>spoIIID</i>	1	171391	44.64	AGCTTGTT ATA TTTTTGGTGTTTTT CATATATAT CATTA
CD0314		1	382298	1.74	AGTATGTT ATA AATGC'TTTGTGTAAAT CATATAAT AGTTTA
CD1167	<i>recV</i>	-1	1366292	3.54	TTTTTCCA TTA TATAATATTT CATT TATATTATATAATAAA
CD1192	<i>spoIIIAA</i>	1	1394269	9.67	TTTTGGTT ATA TCCTTGTCCTTTATA AA TAGAATTATATA
CD1198	<i>spoIIIAG</i>	1	1398222	9.72	TAATAGT ACT AAAAGAGAGGAAGAAA CA TAAACTCTAATG
CD1416		1	1640973	14.62	ACTTAGT AAT TAAATTAATAGGTTGTAT CATAAACT TCATTTA
CD1726		1	1999622	1.24	ATAAAT ACA TATAAGATATTTTT TAAG AATAAAATTTATTA
CD1746	<i>gltC</i>	-1	2023841	3.8	AATTAT ACT ACTGATCTTTTT TAAT ATACATTT ATTA ATA
CD1884		1	2190340	6.95	GATTGAGA ATAG GACAATTTTT TAAG ATACATA AAATA TAAAG
CD1940		-1	2238053	14.36	ATATAA AGATA TATTTTACTATTT AAAT GCATAT CAT TATA
CD2247	<i>cspBA</i>	-1	2604416	2.14	TCTAAT ACT TTTAGACTCACACAAA CA TATACATTAATA
CD2429.1		-1	2805180	1.04	ATTGAT GCATA TATAGTATTTTATACAAA ATATA AAATATTATATA
CD2629	<i>spoIVA</i>	-1	3039083	43.97	TTTTA AGATA TTAACCTTAACTCTAA ATATA ATTTTAATA
CD2864		-1	3350321	9.81	TTTTAT TCATA TATATAAAAT AA CCAT CATACAT TTTCTTG
CD2865		-1	3350950	3.51	TCTAAGTT ATA TGAAAAAGTTGTGAT GCATACA AA TTA ATA
CD3235	<i>ssb</i>	-1	3788231	3.85	GATTTG ATA AAAAATACATCCCTTATA AA TATATTTTATTA
CD3251		-1	3806139	3.41	TATAA AGCATA ATACAAGCTAATGAA ATA TATATTTATTTGTA
CD3457		-1	4051218	33.32	TTTAGAG CTA AGATAAGTTTATA AA AT CATATAT TTAGAA
CD3464		-1	4057317	11.98	ATGATATA ATA AAAGCTTTATACA ATGA ATAAACTGAAGTA
CD3494		-1	4084393	6.39	ATTTTAGA ATA AAATTAATAGTCCCT CTAG TATATTTAATAGTA
CD3542	<i>spmA</i>	-1	4137832	19.99	TTTCAAG TATA AGTATATAC CTA ACTAT CATA AAATTTATTTA
CD0129		-1	173974	4	AGTTAGG CTT TTTAAATGCTTTT TAT TCATATATTTTTTTG
CD0311		-1	373834	2.73	GAATGC ACATA TTATAAACTTTTT TA TATATATATTTATTA
CD1234		1	1437244	2.32	AAATAAG TATA AGACAAGTTTATGAGTT CATAT TTTATAACA
CD1319		1	1529627	10.44	TTTAGT GCATA AACAGAGCTTATTTTT TA AGTATTTAAATA
CD2000	<i>isp</i>	-1	2311655	7.84	TATGACT CTA AAAAATAAAAAATATAT CATA AAATATAAATA
CD2443		-1	2819700	1.52	CAATATG ATTAC CTTTTCTTGTTTAA ATA TATATTTAGATATTA
CD2445		-1	2821093	5.22	TTTTGG ATA ACGAGTCATATTTGAG CATAT CTATAATCA
CD2641		-1	3049708	27.8	TATAGT CAT TTTTTTTACTTCGAT ACATAT TTATTTTFA
CD2800		-1	3272107	3.07	TTAGTAA TTA AAAGCCTTTTCTCGAA TATATAT TAAATTTG
CD2816		1	3286453	4	TTATCTT ATA AAATATAGTTT AGAT TTATAATTTATAAA
CD3248		-1	3804051	10	TTACAG TACT TTTTTGAGCTGAAAA AAATA AAATTTTAAATA
CD3258		-1	3816903	1.85	AATAA TAAATA AAAAATAGTATCTTTG TAA ATATTTAAATA
CD3298		-1	3861389	17.82	AAGCTG ATA AAATCTTATAATAT GAATAT CTTAATTA
CD3483		-1	4070891	11.68	TTTAGG TATG TTATCATATTTCTATTT TATATA ATTTGTTA
CD3521		-1	4115392	3.76	TATTGAT ATA TTTAAATATTACACT ACA TATATCTTTG
CD3522		-1	4116812	8.44	AGAAGG TACT TTTTTTAATTTTGT TAA CATATATTTGTTA
CD3567	<i>sipL</i>	-1	4169365	1.75	TAGGTG ATA TTTTTTTTGCTCCTT AA TATAAAATATAGTG
CD3638		-1	4248132	7.13	TTTTAAG TAT CTTTTACATTAGATTT TATA AAATTTATTAATA

spacing 15 bp

CD3455		-1	4049892	46.84	TAAATG ATA AAAAATAACAGCTAG TAT CATATAATAATAATA
CD2833		-1	3311499	8.19	GAAAAG TATA TACAAGCTATCATA AGCATATA ATTCCTTA
CD0760		1	931632	4	GAAAA GCATAC ATCTTCACAACT GAAT TTTTTATTTAATA
CD1063		1	1255576	8.53	ATGTAG TATA AAAGTATATTTGAT GAATA AACTTTATTTG
CD1230	<i>sigK</i>	-1	1444808	4	TATATGTT TTA AAATCTAAAAATAT GCATAT TATTTTATTA
CD1511	<i>cotB</i>	-1	1748867	4.2	TAATAT ACATA AAATTTAAATAT TACGA ATAAAGTATTATA

found in silico for sigE

Promoters recognized by SigK-RNA polymerase holoenzyme

gene		sense	position +1	score	dRNA-seq
CD0120	<i>glmS</i>	1	163369	1.93	CTTATATG AC CTAACTCTAAAAATATATA ATA ATATTTTTAG
CD0551	<i>sleC</i>	-1	658278	3.55	ATTATTT ACA AAATTTCAAGCTATAT TCATAT CTTGAAATA
CD0896		1	1079040	1.77	AATCAT TAGC AAATAT TAC CCCTTAA ACATAG TATATTTTA
CD0902		1	1086288	19.98	TAGAA TGACA AGTACAACCAATTTT GA ATATAAAATATAGTA
CD1063.1		1	1256034	1.03	TAGA AGTACT TATCTGTCTAT TACTA CATATATTTAATTA
CD1063.2		1	1256423	1	ATCAC TAGC AAAATGGAAACCAAT GCATAG TATATGTTA
CD1067		1	1260209	3.78	AGCA AGTACA ATTAAGATTATA AAAGC CATAGTATTAATTA
CD1133		1	1332562	6.13	AATGACT ACAT TTCTTGAGCTTTTT GA ATATACTATAAATA
CD1433	<i>cotE</i>	-1	1664675	12.48	AAATAG TACA CTAATATGTATTAAT TA ATAGAATAAAATA
CD1613	<i>cotA</i>	-1	1868003	1.13	CTTTT GTA ACTTTTTTACATTATA AA TATAATATTACTA
CD1891		-1	2196837	3.7	TTTTT GTA ACTTACAATAAATTTTT TA ACTATATACTA

<u>CD1898</u>		-1	2201962	4.94	AAAAAGAA <u>AC</u> AAAATTCCTAGGTTATGCATATATTAATAG
<u>CD2144</u>		1	2480394	3.26	TATCTGTA <u>ACA</u> ATTTATCCATTTTACAACTATAACTAATA
<u>CD2409</u>		-1	2781176	6.06	TAAGTGAA <u>AC</u> GTATTTAATTATATTGCATATATATTGTA
<u>CD2664</u>	<i>murE</i>	-1	3078113	4.3	AACCATTC <u>AC</u> ATAGTAAAAAATTCCTAAATATAATATTATA
<u>CD2968</u>	<i>dpaA</i>	-1	3450268	7.42	TTTAGTGA <u>AC</u> CAATGTATTGATAAAAAACATATTGTATATAGTA
<u>CD3569</u>		-1	4170728	4	ATTAGGAA <u>AC</u> AAAGTTTATATCGAACATAGTATAAACTA
<u>CD3580</u>		-1	4180825	4	TACCATT <u>AC</u> ATTATTACTGTTTTAAGCATATTATATTGTA
<u>CD3613</u>		1	4219362	5.26	TAGATGTA <u>AC</u> AAAATCGCATCCATTTAAATATTGTATTTTA
CD0564		1	671798	5.24	GTATGATG <u>AC</u> TAATAATAAGAGTCTGTTTCATATACTTTAAT
CD1230	<i>sigK</i>	-1	1444765	4.63	TAACAGTCA <u>AC</u> TTGGATAAGTCTCCTTCATATAATTTAAAG
CD1518	<i>feoA</i>	-1	1760860	4	TAAAAGTA <u>AC</u> AAGGTAATAATAATAATGCATAGTTTAAATA
CD1927	<i>ytC</i>	-1	2225857	5.12	AAAATGGT <u>AC</u> AAATAGGTCATATTGTTAATAACATAATATA
CD2184		-1	2528930	5.2	CACGGAGA <u>AC</u> TTTTACCTTCTCAATTAAATATATTATTATTA
CD2459		-1	2837573	8.34	AAAAATTTGCATAGTGTAAACATTTTAAATATACTATATATATA

found in silico for sigK

candidates for SigK-dependent promoters

CD0332	tttac <u>AC</u> cagctaagccagtcaggAATAATTTaaagtg
CD3230	ttatc <u>AC</u> ataagaaattgtcgattCATATAATtatatag
CD3349	aggtc <u>AC</u> aatcataactaaatttgaCATATTATatata
CD1065	atatc <u>AC</u> tcacaattcaccacttcAATATTATttctata
CD2399	tagta <u>AC</u> gatttttaaatgattgAATATTATacactaga
CD0596	taaag <u>AC</u> ctattaaaactaccagtTATAATATagaacca

The transcriptional start sites and the -10 and -35 boxes are indicated in red and blue, respectively. The position of 5' start was identified by RNA-seq analysis with indicated score corresponding to the read length (51 bases) coverage ratio for TAP+ and TAP- sample. For σ^E and σ^K , the genes underlined are those validated by in silico analysis (see Materials and Methods) and listed in Table S8. TSS can be visualized at https://mmonot.eu/COV2HTML/visualisation.php?str_id=-14.