

S4 Table. Alignment of experimentally confirmed and putative *sigI* promoters from different *Bacillales* species, including the experimentally confirmed *sigI*-dependent promoters of the *B. subtilis bcrC* and *mreBH* genes.

Species	Promoter sequences (5'→3')
<i>B. subtilis sigI</i> ^{a,b}	aa <u>ACCCCC</u> ttAAttcttttagaaaggca <u>CGAA</u> atcaT
<i>B. subtilis bcrC</i> ^b	atc <u>CCCCC</u> agAAaccgcgattcctctt <u>CGAA</u> ttctc
<i>B. subtilis mreBH</i> ^b	ac <u>ACCCCC</u> aaAAatcgcagatatttctga <u>GAA</u> acttT
<i>B. licheniformis</i> ATCC 14580 ^b	aa <u>ACCCCC</u> ttAAtcgtcaaacagatca <u>CGAA</u> ttgtT
<i>B. thuringiensis</i> sv. Israelensis ATCC 35646 ^b	tg <u>ACCCCC</u> atAAaactatgtattcctc <u>CGAA</u> tatgT
<i>Bacillus</i> sp. NRRL B-14911 ^b	cc <u>ACCCCC</u> aaAAgctcctctttccggg <u>CGAA</u> gcttT
<i>Bacillus tequilensis</i>	aa <u>ACCCCC</u> ttAAttcttttagaaagaca <u>CGAA</u> atcaT
<i>Bacillus</i> sp TH008	aa <u>ACCCCC</u> ctAAtcctcaaagatatat <u>CGAA</u> ttgaT
<i>Bacillus vallismortis</i>	aa <u>ACCCCC</u> ttAAttctcttagaaaggca <u>CGAA</u> atcaT
<i>Bacillus sonorensis</i>	aa <u>ACCCCC</u> ctAAtcaacaagtaaataa <u>CGAA</u> ttgaT
<i>Geobacillus thermoglucosidasus</i>	tg <u>ACC</u> aaCaaAAatccgctatgatgta <u>CGAA</u> tgata
<i>Bacillus</i> sp NSP91	aa <u>ACCCCC</u> ttAAtcgtcaaagaaacaa <u>CGAA</u> ttgtT
<i>Bacillus mojavensis</i>	aa <u>ACCCCC</u> aaAAttctctttaagggca <u>CGAA</u> atccT
<i>Bacillus stratophericus</i> LAMA 587	at <u>ACCCCC</u> ttAtttcttttgcttttaaa <u>CGAA</u> acgtT
<i>Bacillus xiamenensis</i>	at <u>ACCCCC</u> ttAtttcttttgcttttaaa <u>CGAA</u> acgtT
<i>Salinibacillus aidingensis</i> MSP4	aa <u>ACCCCC</u> aaAAttctctttaagggca <u>CGAA</u> atccT
<i>Bacillus amyloliquefaciens</i> FZB42	aa <u>ACCCCC</u> ttAAttctgcatgggggca <u>CGAA</u> atcaT
<i>Bacillus pumilus</i> ATCC 7061	at <u>ACCCCC</u> ttAtttctttgcattaga <u>CGAA</u> acacT
<i>Bacillus mycoides</i> Rock1-4	tg <u>ACCCCC</u> atAAaatttttatttcctt <u>CGAA</u> atgT
<i>Bacillus pseudomycooides</i> DSM 12442	tg <u>ACCCCC</u> atAAaatttttatttcctc <u>CGAA</u> atgT
<i>Bacillus weihenstephanensis</i> KBAB4	tg <u>ACCCCC</u> atAAaattatttgttcctt <u>CGAA</u> tataT
<i>Bacillus cereus</i> ATCC 10987	tg <u>ACCCCC</u> atAAacgatgtattcctc <u>CGAA</u> tataT
<i>Bacillus anthracis</i> strain Ames	cg <u>ACCCCC</u> atAAaactttgtattcctc <u>CGAA</u> atgT
<i>Bacillus thuringiensis</i> subsp. konkukian	tg <u>ACCCCC</u> atAAaactttgtattcctc <u>CGAA</u> atgT
<i>Bacillus</i> sp. SG-1	gt <u>ACCCCC</u> acAAgctattggaagtctt <u>CG</u> tAacttT

<i>Bacillus coahuilensis</i> m4-4	tt ACCCCT ta AA actaattttatcatc CGtA tgтта
<i>Geobacillus kaustophilus</i> HTA426	aat CCCC tttg A acgacggtcataatttg GA ttgcga
<i>Geobacillus stearothermophilus</i> NUB3621	ta ACC a CC ag A tttccgttaagatgta CGAA tgata
Consensus	ACCCCT--AA 15 (N) CGAA----T

The most conserved bases are shown in bold capital fonts. Underlined are the -35 and -10 promoter elements proposed by Tseng and Shaw [34].

^a Promoter sequence confirmed experimentally by Asai and co-workers [17].

^b Promoter sequence confirmed experimentally by Tseng and Shaw [34].