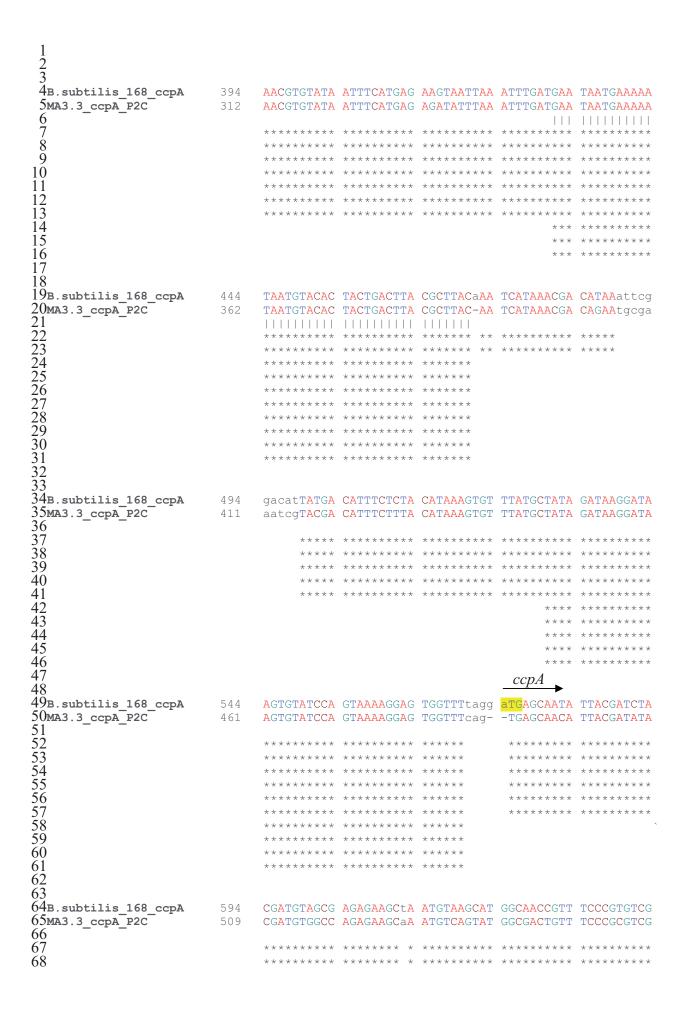
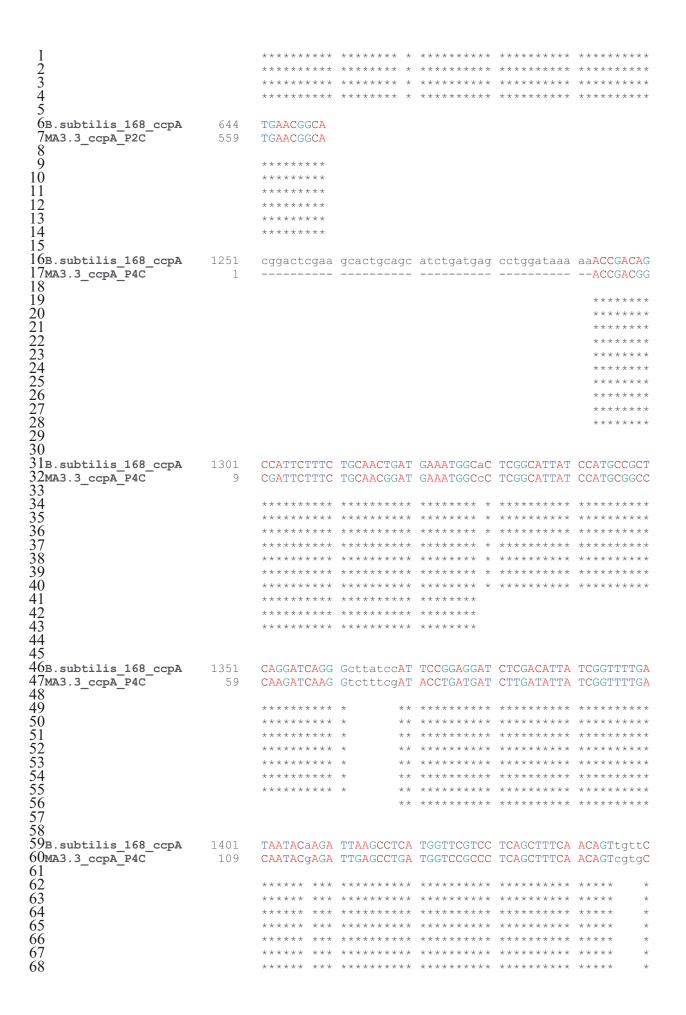
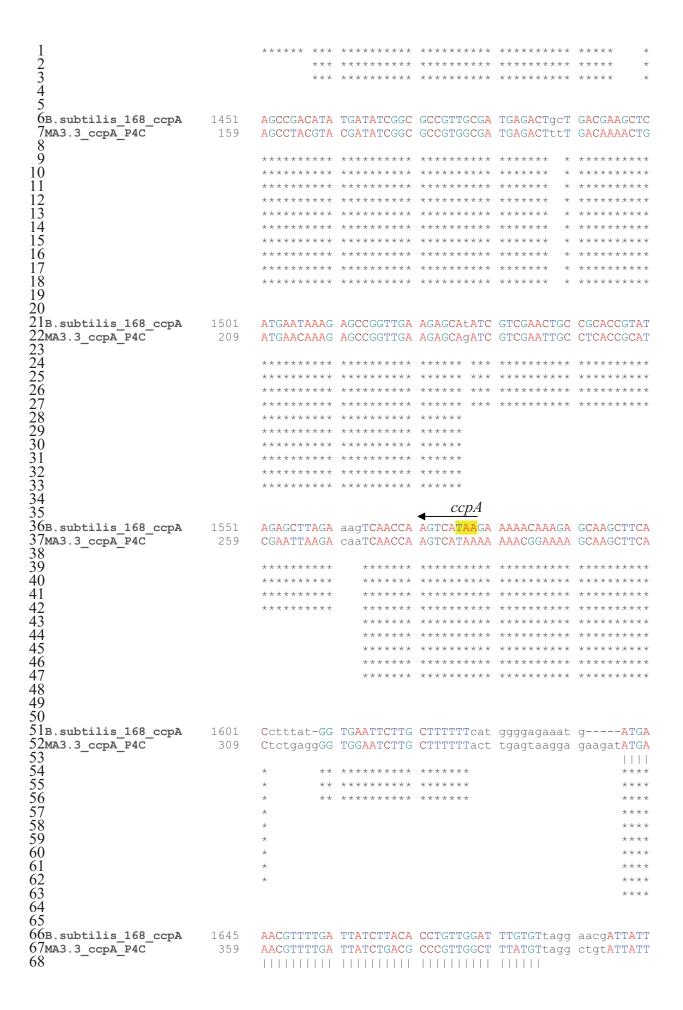
1 Supplementary material						
3B.subtilis_168_ccpA 4MA3.3_ccpA_P2C 5 6 7	51 4	tcagctgtgc			catttgccag	
8 9 10 11 12	101					****** ****** ****
13B.subtilis_168_ccpA 14MA3.3_ccpA_P2C 15	101 12				CtTGCTTCCG CcTGCTTCCG	
16		******	******	*****	* ******	******
17		******	******	*****	* ******	*****
18		******	******	******	* ******	******
19		******	******	*****	* ******	*****
20 21 22		*****	*****	*****	* *****	*****
23B.subtilis_168_ccpA 24MA3.3_ccpA_P2C 25	151 62				TGGCTGAGGT TGGCCGAAGT	
26		******	******	** ******	******	******
27		******	******	** ******	*****	*****
28		*****	******	** ******	******	*****
29 30		******	******	** ******	*****	*****
31 32		*****	*****	** *****	*****	*****
33B.subtilis_168_ccpA 34MA3.3_ccpA_P2C 35	201 112	CCTTCCGTTG	CcCTTTCAGA	CTCTGCGCAG	CAAATGGCGA CAGATGGATA	TACCTGAATT
36					*****	
37					*****	
38					*****	
39					*****	
40 41 42					*****	
43B.subtilis_168_ccpA 44MA3.3_ccpA_P2C 45	251 162	C Gag <mark>AAA</mark> TGG	CTGAACGAAT	TAAAGCCAAT	GGTGAAAGTC GCTGAAAGTA	AAagcataat
46					*****	
47					*****	
48					******	
49						
50 51 52		** *****	****	****	*****	**
53B.subtilis_168_ccpA 54MA3.3_ccpA_P2C 55	301 212				CGCCCTTTTT CGCGGCTTTT	
56 57 58			***	*****	*****	**
59B.subtilis_168_ccpA 60MA3.3_ccpA_P2C 61	345 262	-			ACGTTTTCAT ACGTTTTCAT	
62		*****	*****	*****	******	** ***
63		*****	*****	*****	******	** ***
64		*****	*****	*****	*****	** ***
65		*****	*****	******	******	** ***
66		*****	*****	*****	*****	** ***
67						***
68						***







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                     ****** *** ***** *****
                     ******* ***** *****
13B.subtilis 168 ccpA 1695 ATTGTTATCG GGATTATTTC AGGATCGGGA GTaagcggtt tccgctCTTT
14ma3.3_ccpA_P4C
                409 GTCGCAATCG GTATTCTGTC AGGGACGGGA CTggcgggaa tcagtTCATT
15
16
                     ******* ****** ****** **
176
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25B.subtilis_168_ccpA
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                     ******* ****** **
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                     ******* ****** **
46B.subtilis 168 ccpA 1845 AAGCAGGCAT tcatccgcca ggaagacaat gtgaaagatc ttgtgaaaac
47ma3.3_ccpa_P4C
                559
                    AAACAGGTAT ------
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                     *****
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- S1 Sequence alignment of ccpA flanking region from B. subtilis 168 and Bacillus sp. MA3.3
- 52 (using primers P2C and P4C).

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