

## Supplementary material

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3	B.subtilis_168_ccpA	51	tcagctgtgc	cgattttgaa	acaagaaacg	catttgccag	tcTTTGTGTA		
4	MA3.3_ccpA_P2C	4	-----	-----	-----	-----	--TTTGTGTA		
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13	B.subtilis_168_ccpA	101	TGTTACGCAT	TCAACAGGCC	GCCGTGACCT	CtTGCTTCCG	ACAGCTAAAG		
14	MA3.3_ccpA_P2C	12	CGTCACACAC	TCAACAGGCC	GCCGCGATCT	CcTGCTTCCG	ACAGCAAAAG		
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23	B.subtilis_168_ccpA	151	CCGCTTTAGC	GATCGGTGCT	GAtGGCGTAA	TGGCTGAGGT	TCACCTGAT		
24	MA3.3_ccpA_P2C	62	CGGCGCTTGC	GATCGGCGCT	GAcGGCGTGA	TGGCCGAAGT	TCACCTGAT		
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33	B.subtilis_168_ccpA	201	CCGTCAGTCG	CaCTTTCTGA	CTCTGCTCAG	CAAATGGCGA	TTCCTGAATT		
34	MA3.3_ccpA_P2C	112	CCTTCCGTTG	CcCTTTCAGA	CTCTGCGCAG	CAGATGGATA	TACCTGAATT		
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43	B.subtilis_168_ccpA	251	CGaaAAATGG	CTGAATGAAC	TGAAGCCAAT	GGTGAAAGTC	AAcgcttaat		
44	MA3.3_ccpA_P2C	162	CGagAAATGG	CTGAACGAAT	TAAAGCCAAT	GCTGAAAGTA	AAagcataat		
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53	B.subtilis_168_ccpA	301	tgaacaatcc	a-----AAA	GGCCGCCGTG	CGGCCTTTTT	TTatgctttc		
54	MA3.3_ccpA_P2C	212	acaacgttcc	gctctttAAA	GGCCGCCTCG	CGCGGCTTTT	TTtctatct		
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59	B.subtilis_168_ccpA	345	tcg-TTTATT	TAGTTATAAA	AACCAAGTAT	ACGTTTTTCAT	CAtctatAAA		
60	MA3.3_ccpA_P2C	262	tcatTTTATT	TAATTATAAA	ATGAAAGTGA	ACGTTTTTCAT	CActgggAAA		
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4B.subtilis_168_ccpA      394  AACGTGTATA ATTTTCATGAG AAGTAATTAA ATTTGATGAA TAATGAAAAA
5MA3.3_ccpA_P2C          312  AACGTGTATA ATTTTCATGAG AGATATTTAA ATTTGATGAA TAATGAAAAA
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19B.subtilis_168_ccpA      444  TAATGTACAC TACTGACTTA CGCTTACaAA TCATAAACGA CATAAattcg
20MA3.3_ccpA_P2C          362  TAATGTACAC TACTGACTTA CGCTTAC-AA TCATAAACGA CAGAAatcgca
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34B.subtilis_168_ccpA      494  gacatTATGA CATTTCTCTA CATAAAGTGT TTATGCTATA GATAAGGATA
35MA3.3_ccpA_P2C          411  aatcgTACGA CATTTCTTTA CATAAAGTGT TTATGCTATA GATAAGGATA
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49B.subtilis_168_ccpA      544  AGTGTATCCA GTAAAAGGAG TGGTTTtagg aTGAGCAATA TTACGATCTA
50MA3.3_ccpA_P2C          461  AGTGTATCCA GTAAAAGGAG TGGTTTcag- -TGAGCAACA TTACGATATA
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64B.subtilis_168_ccpA      594  CGATGTAGCG AGAGAAGCtA ATGTAAGCAT GGCAACGTT TCCCGTGTCTG
65MA3.3_ccpA_P2C          509  CGATGTGGCC AGAGAAGCaA ATGTCAGTAT GGCGACTGTT TCCCGCGTCTG
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6B.subtilis_168_ccpA      644  TGAACGGCA
7MA3.3_ccpA_P2C          559  TGAACGGCA
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16B.subtilis_168_ccpA      1251  cggactcgaa  gcactgcagc  atctgatgag  cctggataaa  aaACCGACAG
17MA3.3_ccpA_P4C          1      -----  -----  -----  -----  --ACCGACGG
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31B.subtilis_168_ccpA      1301  CCATTCTTTC  TGCAACTGAT  GAAATGGCaC  TCGGCATTAT  CCATGCCGCT
32MA3.3_ccpA_P4C          9      CGATTCTTTC  TGCAACGGAT  GAAATGGCcC  TCGGCATTAT  CCATGCCGCC
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46B.subtilis_168_ccpA      1351  CAGGATCAGG  GcttatccAT  TCCGGAGGAT  CTCGACATTA  TCGGTTTTGA
47MA3.3_ccpA_P4C          59      CAAGATCAAG  GtctttcgAT  ACCTGATGAT  CTTGATATTA  TCGGTTTTGA
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59B.subtilis_168_ccpA      1401  TAATACaAGA  TTAAGCCTCA  TGGTTCGTCC  TCAGCTTTCA  ACAGTtggtC
60MA3.3_ccpA_P4C          109  CAATACgAGA  TTGAGCCTGA  TGGTCCGCCC  TCAGCTTTCA  ACAGTcgtgC
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6B.subtilis_168_ccpA      1451  AGCCGACATA  TGATATCGGC  GCCGTTGCGA  TGAGACTgcT  GACGAAGCTC
7MA3.3_ccpA_P4C          159  AGCCTACGTA  CGATATCGGC  GCCGTGGCGA  TGAGACTttT  GACAAAAC TG
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21B.subtilis_168_ccpA      1501  ATGAATAAAG  AGCCGTTTGA  AGAGCAtATC  GTCGAAGTGC  CGCACC GTAT
22MA3.3_ccpA_P4C          209  ATGAACAAAG  AGCCGTTTGA  AGAGCAgATC  GTCGAATTGC  CTCACC GCAT
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36B.subtilis_168_ccpA      1551  AGAGCTTAGA  aagTCAACCA  AGTCATAA GA  AAAACAAAGA  GCAAGCTTCA
37MA3.3_ccpA_P4C          259  CGAATTAA GA  caaTCAACCA  AGTCATAAAA  AAACGGAAAA  GCAAGCTTCA
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51B.subtilis_168_ccpA      1601  Ccttttat-GG  TGAATTCTTG  CTTTTTTcat  ggggagaaat  g-----ATGA
52MA3.3_ccpA_P4C          309  CtctgaggGG  TGAATCTTG  CTTTTTTact  tgagtaagga  gaagatATGA
53                                     ||||
54         *          **  *****  *****
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66B.subtilis_168_ccpA      1645  AACGTTTTGA  TTATCTTACA  CCTGTTGGAT  TTGTGTtagg  aacgATTATT
67MA3.3_ccpA_P4C          359  AACGTTTTGA  TTATCTGACG  CCCGTTGGCT  TTATGTtagg  ctgtATTATT
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13B.subtilis_168_ccpA      1695  ATTGTTATCG GGATTATTC AGGATCGGGA GTaagcggtt tccgcTCTTT
14MA3.3_ccpA_P4C          409  GTCGCAATCG GTATTCTGTC AGGGACGGGA CTggcgggaa tcagtTCATT
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16         *****
17         *****
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25B.subtilis_168_ccpA      1745  TCTTGATCTG ACCTCTTCTT TCATCGTAAC AGGgGGACTT TGC GCCGCTG
26MA3.3_ccpA_P4C          459  TTTAGATCTG ACTTCTTTTT TAATCGTCAC AGGcGGCCTT GCTGCGGCGA
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28         *****
29         *****
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31         *****
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37B.subtilis_168_ccpA      1795  TTTTATCAG TTTTCCGCCA AGtGAGCTGA AAAAAGCGCC CTCTGTGTTA
38MA3.3_ccpA_P4C          509  TCTTTATCAG CTTTCCGCCG AGgGATTAA AGAAAACCCC TTCTGTTCTG
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40         *****
41         *****
42         *****
43         *****
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46B.subtilis_168_ccpA      1845  AAGCAGGCAT tcatccgccca ggaagacaat gtgaaagatc ttgtgaaaac
47MA3.3_ccpA_P4C          559  AAACAGGTAT -----
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51 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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