–35
TTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATAT
AATTTTTATATTGCATAGTCTTTTTTTGCTTTAAAATTAACAAAAATGTTGCAAAATTTGAAAATAAGAGTATTAGT
CGTTAAGATTTTTATTGATAGGTGAAATTTTGGCTT TTAAAGTAGCCATTTGTTGGAAAAGGGA AATTTTTTAAAAA TTAAAGTAGCCATTTGTTGGAGAATGGA GCTTAAAGTCATT
-10 GTATAATACTATTATAAGAAAATAAAGTTTTTATAAACATTGAGATGCAAAATATAAACCTTTTGTAACAATAT TTCACTTATAAATTTATTATTTTTCTAGAAACTTGTCTATTGGCTAGTTTGAGTA <u>TTGATT</u> TATATGATTTATATGG -35 TSS3
ATTTACCAAAATAATACAATTTATTTTATATTATAACCATATAAATCATATAAATCAATACTCAAACTAGCCAATAG TTATAATATAA
ACAAGTTTCTAGAAAAATAATAAATTTATAAGTGAAAATGACTTTAAGC TCCATTCTCCAACAATCGGAGACTTTAA TAAAAACTTTATTTTCTTATTATAATAGTATTATACTTTTTAAAAAATT TCCCTTTTTCCAACAATCGGAGACTTTAA
-35 TTAGTATTTAATAATAATCTTAATGTTCAATACAATATTCAAGAATTGTTCAAAAATACTTAAGTATTA <u>TAGTCT</u> A
-10 TSS4 GTTTGTAAAGATATTA <u>TAAAAAT</u> AATAAT <mark>A</mark> CTAGTTATATATGAAAATAAAACATTATAATTTGTAATAATTATAAAA
CTTGAGATTATGATTAAAATACCTTTGAATGGAGTGGTGTA <mark>ATG</mark>

Fig S3. Identification and mapping of multiple transcriptional start sites upstream

of *cmrRST*. Map of transcriptional start sites (TSS) identified by 5' RACE in *recV cmr*-ON, *recV cmr*-OFF and *recV cmr*-OFF pDccA. Gray highlight indicates the Cdi-2-2 riboswitch sequence. Red and blue text denote the OFF and ON orientations of the *cmr* switch, respectively. Bold text indicates the inverted repeats. Green highlights mark TSS. Underlined text indicates putative -10/-35 sites. Yellow highlight denotes the *cmrR* start codon.