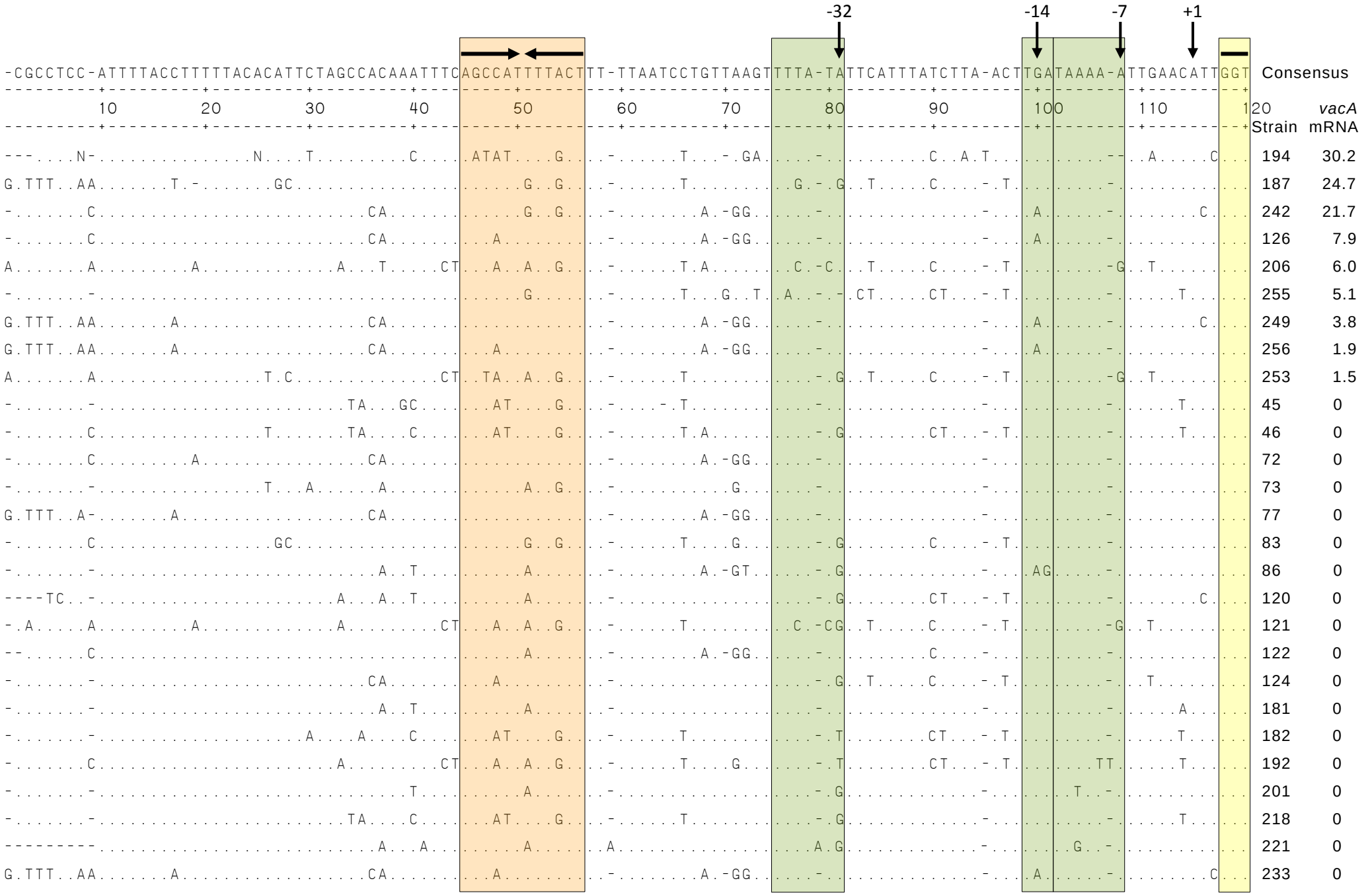
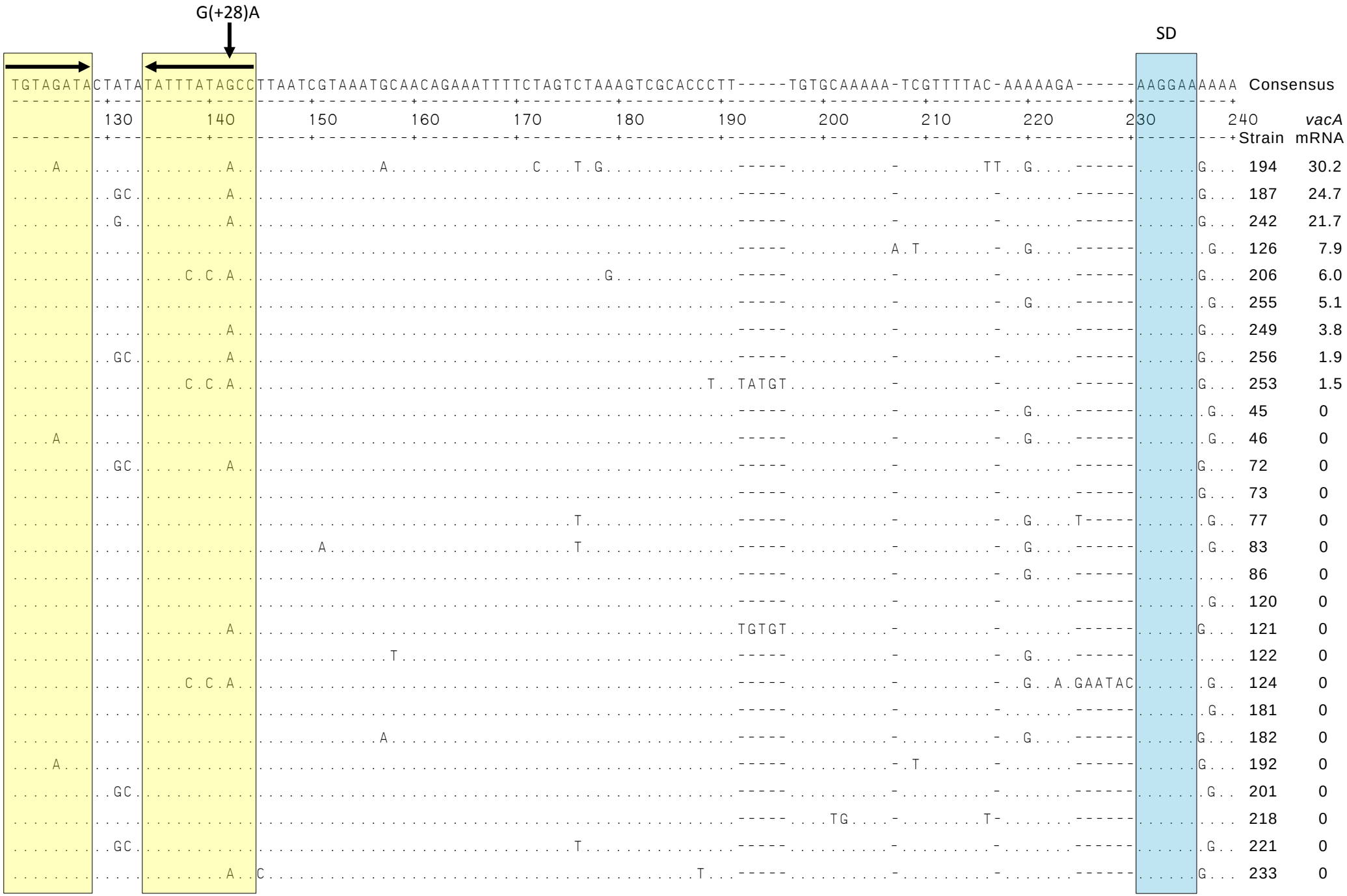

-32
-14
-7
+1
-CGCCTCC-ATTTTACCTTTTTACACATTCTAGCCACAAATTTCAGCCATTTTACTTT-TTAATCCTGTTAAGTTTTA-TATTCATTTATCTTA-ACTTGATAAAA-ATTGAACATTGGT Consensus
10 20 30 40 50 60 70 80 90 100 110 120
Strain
vacA mRNA
194 30.2
187 24.7
242 21.7
126 7.9
206 6.0
255 5.1
249 3.8
256 1.9
253 1.5
45 0
46 0
72 0
73 0
77 0
83 0
86 0
120 0
121 0
122 0
124 0
181 0
182 0
192 0
201 0
218 0
221 0
233 0


G(+28)A
SD
TGTAGATACTATATATTTATAGCCTTAATCGTAAATGCAACAGAAATTTTCTAGTCTAAAGTCGCACCCTT-----TGTGCAAAAA-TCGTTTTAC-AAAAAGA------AAGGAAAAAA Consensus
130 140 150 160 170 180 190 200 210 220 230 240
Strain
vacA mRNA
194 30.2
187 24.7
242 21.7
126 7.9
206 6.0
255 5.1
249 3.8
256 1.9
253 1.5
45 0
46 0
72 0
73 0
77 0
83 0
86 0
120 0
121 0
122 0
124 0
181 0
182 0
192 0
201 0
218 0
221 0
233 0

Supplementary Figure 1. Sequence alignment of the *cysS-vacA* intergenic region of 27 *H. pylori* clinical isolates ranked in order of in vivo relative *vacA* mRNA level from highest (top) to lowest (bottom). Relative in vivo *vacA* mRNA level (shown in the right-hand column) was quantified by reverse transcriptase quantitative polymerase chain reaction (RT-qPCR) using cDNA synthesised from total RNA purified from patient gastric biopsies. *H. pylori 16S rRNA* was used as a reference gene, and *vacA* mRNA level was measured relative to that of a comparator biopsy cDNA sample included in each run (assigned an arbitrary value of 100). The following features described in the Results section are annotated: an upstream inverted repeat (orange shading); the -35 and -10 promoter sequences (green shading); the 5' untranslated region stem loop (yellow shading); and the Shine-Dalgarno sequence (blue shading). The start of the *vacA* transcript is labelled +1, and the polymorphisms at nucleotides -32, -14, -7 and G(+28)A, described in the Results section, are indicated by arrows. Nucleotide identity to the consensus sequence is shown by a dot, and gaps in the alignment are indicated by a dash.