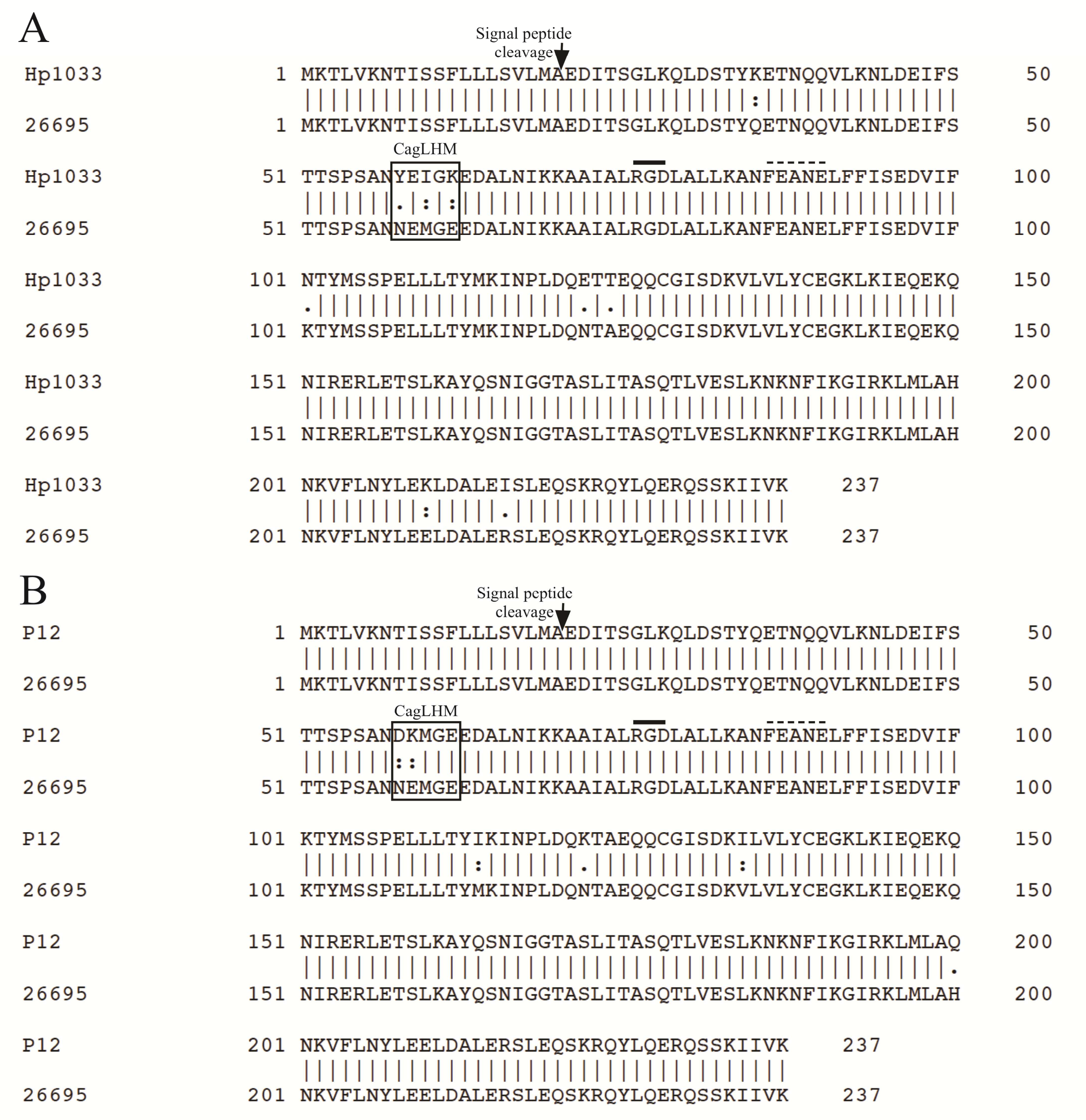

```
A
Hp1033             1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYKETNQQVLKNLDEIFS     50
                     ||||||||||||||||||||||||||||||||||:|||||||||||||||
26695              1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS     50

Hp1033            51 TTSPSANYEIGKEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF    100
                     |||||||.|:|:||||||||||||||||||||||||||||||||||||||
26695             51 TTSPSANNEMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF    100

Hp1033           101 NTYMSSPELLLTYMKINPLDQETTEQQCGISDKVLVLYCEGKLKIEQEKQ    150
                     .||||||||||||||||||||.|.||||||||||||||||||||||||||
26695            101 KTYMSSPELLLTYMKINPLDQNTAEQQCGISDKVLVLYCEGKLKIEQEKQ    150

Hp1033           151 NIRERLETSLKAYQSNIGGTASLITASQTLVESLKNKNFIKGIRKLMLAH    200
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
26695            151 NIRERLETSLKAYQSNIGGTASLITASQTLVESLKNKNFIKGIRKLMLAH    200

Hp1033           201 NKVFLNYLEKLDALEISLEQSKRQYLQERQSSKIIVK    237
                     |||||||||:|||||.|||||||||||||||||||||
26695            201 NKVFLNYLEELDALERSLEQSKRQYLQERQSSKIIVK    237

B
P12                1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
26695              1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS     50

P12               51 TTSPSANDKMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF    100
                     |||||||::|||||||||||||||||||||||||||||||||||||||||
26695             51 TTSPSANNEMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF    100

P12              101 KTYMSSPELLLTYIKINPLDQKTAEQQCGISDKILVLYCEGKLKIEQEKQ    150
                     |||||||||||||:|||||||.|||||||||||:||||||||||||||||
26695            101 KTYMSSPELLLTYMKINPLDQNTAEQQCGISDKVLVLYCEGKLKIEQEKQ    150

P12              151 NIRERLETSLKAYQSNIGGTASLITASQTLVESLKNKNFIKGIRKLMLAQ    200
                     |||||||||||||||||||||||||||||||||||||||||||||||||.
26695            151 NIRERLETSLKAYQSNIGGTASLITASQTLVESLKNKNFIKGIRKLMLAH    200

P12              201 NKVFLNYLEELDALERSLEQSKRQYLQERQSSKIIVK    237
                     |||||||||||||||||||||||||||||||||||||
26695            201 NKVFLNYLEELDALERSLEQSKRQYLQERQSSKIIVK    237
```

S6 Figure. Alignment of CagL amino acid sequences of *H. pylori* strains (A) Hp1033 versus 26695, and (B) P12 versus 26695.

In addition to sequence diversity within the CagL hypervariable motif (CagLHM; boxed), *H. pylori* strains (A) Hp1033 and 26695 also differ at residues 35, 101, 122, 124, 210 and 216; and (B) P12 and 26695 differ at residues 114, 122, 134 and 200. RGD motif – solid line; RGD helper motif – broken line. Hp1033 sequence translated from published nucleotide sequence [20]; P12 and 26695 accession numbers ACJ07700.1 and NP_208335.1, respectively; CagL sequences were verified for P12 and 26695 stocks used in this study. Protein alignments performed using Emboss Needle pairwise sequence alignment server [21].