А	Signal peptide cleavage	
Hp1033	1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYKETNQQVLKNLDEIFS	50
26695	1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS CagLHM	50
Hp1033	51 TTSPSANYEIGKEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF	100
26695		100
Hp1033	101 NTYMSSPELLLTYMKINPLDQETTEQQCGISDKVLVLYCEGKLKIEQEKQ	150
26695	•	150
Hp1033	151 NIRERLETSLKAYQSNIGGTASLITASQTLVESLKNKNFIKGIRKLMLAH	200
26695		200
Нр1033	201 NKVFLNYLEKLDALEISLEQSKRQYLQERQSSKIIVK 237	
26695	:	
В	Signal peptide	
B P12	Signal pcptide cleavage	50
2	Cleavage 1 MKTLVKNTISSFLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS 	50 50
P12	cleavage 1 MKTLVKNTISSFLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS 1 MKTLVKNTISSFLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS CagLHM 51 TTSPSANDKMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF	
P12 26695	Cleavage 1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS 	50
P12 26695 P12	cleavage   1 MKTLVKNTISSFLLSVLMÆDITSGLKQLDSTYQETNQQVLKNLDEIFS   1 MKTLVKNTISSFLLSVLMÆDITSGLKQLDSTYQETNQQVLKNLDEIFS   2 CagLHM   51 TTSPSANDKMGEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   1 ITSPSANNEMGEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   51 TTSPSANNEMGEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   51 TTSPSANNEMGEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   51 TTSPSANNEMGEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   51 TTSPSANNEMGEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF	50 100
P12 26695 P12 26695	cleavage   1 MKTLVKNTISSFLLSVLMÆDITSGLKQLDSTYQETNQQVLKNLDEIFS   1 MKTLVKNTISSFLLSVLMÆDITSGLKQLDSTYQETNQQVLKNLDEIFS   2 MKTLVKNTISSFLLSVLMÆDITSGLKQLDSTYQETNQQVLKNLDEIFS   CagLHM 51   51 TTSPSANDKMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   1 ITSPSANNEMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF	50 100 100
P12 26695 P12 26695 P12	Cleavage   1 MKTLVKNTISSFLLSVLMÆDITSGLKQLDSTYQETNQQVLKNLDEIFS   1 MKTLVKNTISSFLLSVLMÆDITSGLKQLDSTYQETNQQVLKNLDEIFS   2 CagLHM   51 TTSPSANDKMGEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   1 ITSPSANNEMGEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   51 TTSPSANNEMGEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   51 TTSPSANNEMGEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   51 TTSPSANNEMGEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   101 KTYMSSPELLLTYIKINPLDQKTAEQQCGISDKILVLYCEGKLKIEQEKQ   101 KTYMSSPELLLTYIKINPLDQKTAEQQCGISDKILVLYCEGKLKIEQEKQ	50 100 100 150
P12 26695 P12 26695 P12 26695	Cleavage   1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS   1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS   1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS   CagLHM   51 TTSPSANDKMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   1 INTSPSANNEMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   51 TTSPSANNEMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   101 KTYMSSPELLLTYIKINPLDQKTAEQQCGISDKILVLYCEGKLKIEQEKQ   101 KTYMSSPELLLTYMKINPLDQNTAEQQCGISDKVLVLYCEGKLKIEQEKQ	50 100 100 150 150
P12 26695 P12 26695 P12 26695 P12	Cleavage   1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS   1 MKTLVKNTISSFLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS   1 MKTLVKNTISSFLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS   CagLHM 51   51 TTSPSANDKMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   1 ::::::::::::::::::::::::::::::::::::	50 100 150 150 200
P12 26695 P12 26695 P12 26695 P12 26695 P12 26695	Cleavage   1 MKTLVKNTISSFLLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS   1 MKTLVKNTISSFLLSVLMAEDITSGLKQLDSTYQETNQQVLKNLDEIFS   CagLHM 1   51 TTSPSANDKMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   51 TTSPSANNEMGEEDALNIKKAAIALRGDLALLKANFEANELFFISEDVIF   51 KTYMSSPELLLTYIKINPLDQKTAEQQCGISDKVLVLYCEGKLKIEQEKQ   51 NIRERLETSLKAYQSNIGGTASLITASQTLVESLKNKNFIKGIRKLMLAQ   51 NIRERLETSLKAYQSNIGGTASLITASQTLVESLKNKNFIKGIRKLMLAH	50 100 150 150 200

## 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].