

Variations in cag pathogenicity island genes of *Helicobacter pylori* from Latin American groups may influence neoplastic progression to gastric cancer

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Supplementary figure 1. Schematic alignment of the different patterns of EPIYA A, B or C motifs and CM motifs with number of observations in 72 sequenced Mexican and Colombian isolates. This analysis has been performed by extraction of Illumina reads of the *cagA* gene and realignment by the “de novo assemble” option of the same software. Subsequently, the consensus sequence of each isolate has been translated into amino acid sequence and aligned again.

