

**Table1: *H. pylori* strains used and their characteristic virulence factors**

<b><i>H. pylori</i> strains</b>	<b>Virulence Factors</b>
<b>60190</b> *(isogenic mutants CagA, CagE)	-s1/m1 isoform of <i>vacA</i> toxin - <i>cag</i> pathogenicity island (CagPAI) positive
<b>251</b> *(isogenic mutant CagM)	-unknown <i>vacA</i> isoform -Cag PAI positive -genetics of bacterial strain remains largely unknown
<b>G27</b> *(isogenic EPISA mutant)	-Cag PAI positive -five EPIYA tyrosine phosphorylation motifs repeated within <i>cagA</i> gene -s1/m1 <i>b</i> isoform
<b>7.13</b> *(isogenic 7.13 CagA mutant)	-rodent adapted form of <i>H. pylori</i> B128 strain -developed via passage through gerbil model -Cag PAI positive -s1/m1 <i>vacA</i> isoform

\* isogenic mutants to corresponding wildtype bacterial strain indicated in the representative table

**Table 2: Concentration of cytokines detected in cells**

Treatment	Concentration (pg/ml)		
	IL-6	IL-11	LIF
Control	ND	ND	ND
<i>H. pylori</i> infected	19.22	ND	ND