**S1 Table. Coverage analysis reports using the *H. pylori* 26695 genome (NC_000915.1) as reference.**

| Characteristics | Sample | |
|---|---|---|
| | **Wild type** | ***H. pylori*_Δ*glyA*** |
| **Number of mapped reads** | 219317 | 476251 |
| **Percent reads on target** | 100.00% | 100.00% |
| **Number of contigs** | 1 | 1 |
| **Average base coverage depth** | 32.06 | 76.78 |
| **Total base reads on target** | 53469632 | 128064498 |
| **Uniformity of base coverage** | 99.72% | 98.05% |