S1 Figure

Comparative genome analysis of *H. ducreyi* strains

- 5 CU strains (4 from Samoa and 1 from Vanuatu)
- 9 GU strains (5 class I and 4 class II strains)

Genome sequencing using Illumina MiSeq

- De novo assembly using Edena
- Annotation using RAST
- Contig ordering using Mauve

- Genome conservation analysis
- Genome rearrangements analysis
- SNP analysis
- Detection of recombination
- Evolutionary analysis
- Analysis of genes encoding known virulence determinants
- Antimicrobial susceptibility testing and identification of genes encoding antimicrobial resistance genes

- Diversity analysis
- Phylogenetic analysis
- Divergence time analysis
- Selection analysis