



Figure A1: Neighbour-Joining tree of *hsdS* alleles for different loci queried by the microarray. The tree shows that there is no consistent nomenclature or sequence similarity among the different *hsdS* alleles, which is why they were excluded from our *in silico* typing scheme. *hsdS1/2/3/x* represent the different *hsdS* loci, the ascending numbers 01-05 represent the different allelic variants. Evolutionary analyses were conducted in MEGA v5.0 (1) using the entire gene. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree.

References

1. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, and Kumar S. 2011. MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Mol Biol Evol* **28**:2731-2739.