

Supplementary Figure 1. Gene content tree of completely sequenced prokaryotes. The tree was composed using the SHOT algorithm (Korbel *et al.* 2002) to calculate distances between genomes, and BioNJ (Gascuel 1997) to make a neighbor-joining tree.

Gascuel, O. 1997. BIONJ: an improved version of the NJ algorithm based on a simple model of sequence data. Mol Biol Evol **14**:685-695.

Korbel, J. O., B. Snel, M. A. Huynen, and P. Bork. 2002. SHOT: a web server for the construction of genome phylogenies. Trends Genet **18**:158-162.