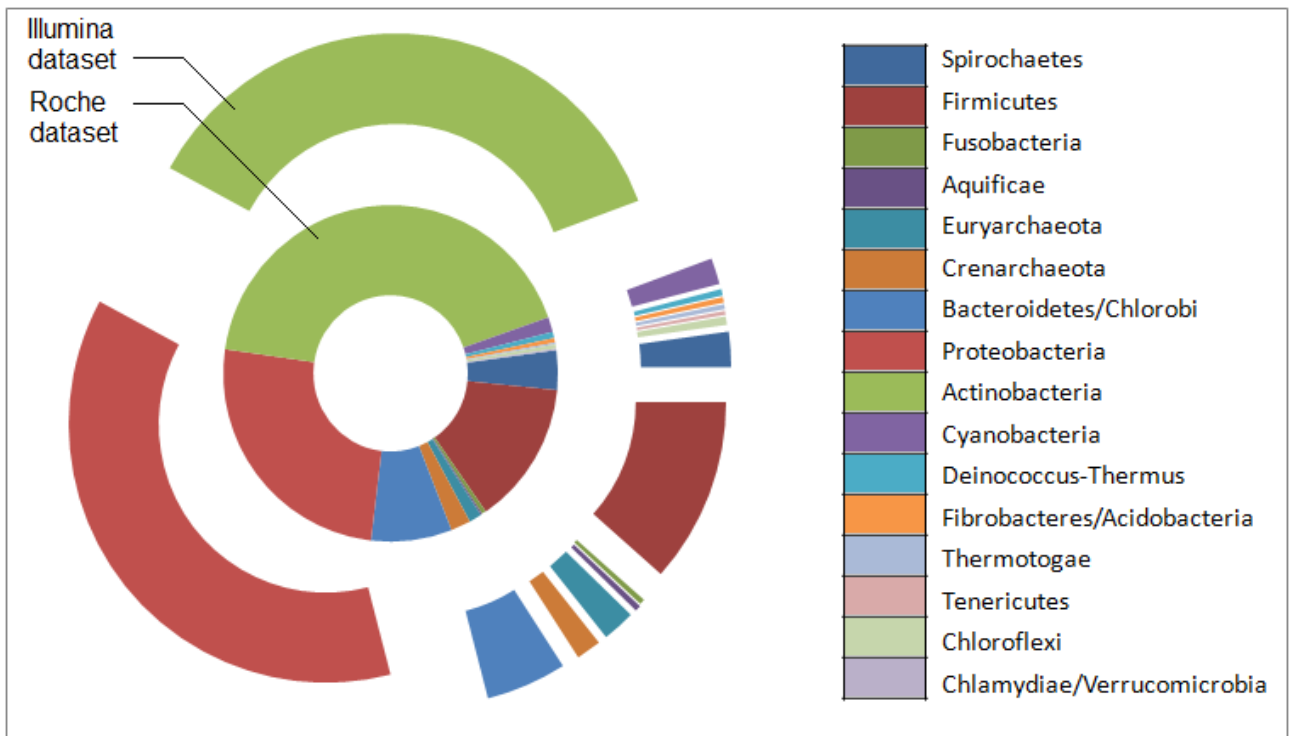**Figure S1**: Evaluation of the 'Binpairs' strategy for a real metagenomic dataset

Comparison of binning results of the Oral metagenome dataset. The 'Roche' reads (~400 bp in length) constituting this metagenome were binned with SPHINX. Equivalent volume of simulated 'Illumina' mate-paired reads (see Methods) were binned using 'Binpairs' strategy SII in combination with SPHINX.