Supplementary Figure S3 Gene abundance values of FACHB-83 calculated using six different mapping methodologies. (A) Gene abundance values calculated using Bowtie 2 with default parameters. (B) Abundance values calculated using Bowtie 2 with the parameter '--local'. (C) Abundance values calculated using BWA-MEM with default parameters. (D) Gene abundance values calculated using the 'Contig mapping' method proposed in this study. (E) Values of the TPM measure calculated using Salmon with the parameters '--meta --validateMappings'. (F) Values of the TPM measure calculated using Salmon with all contigs as decoy sequences.