



Figure 2. Relative abundance of major bacterial families in P30 and NP30 communities estimated using ContigEval analysis pipeline. Height of the colored boxes represents a number of identities in all contigs assigned to a given taxon related to a number of identities in all contigs assigned to all taxa. The boxes are ordered by a taxon abundance averaged for P30 and NP30 cultures. For each culture, only the most abundant families contributing to the 90 % of cumulative percentage are shown.