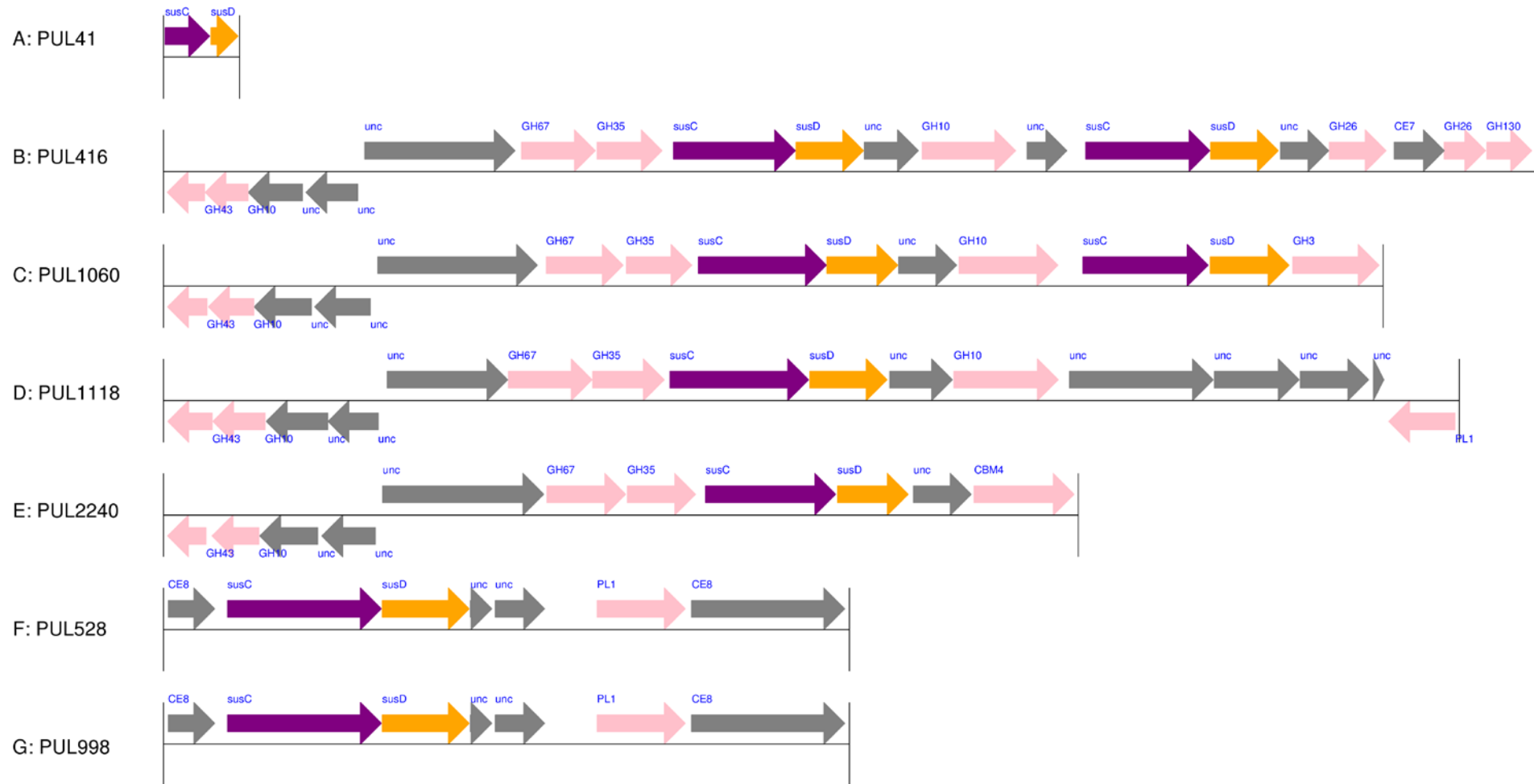
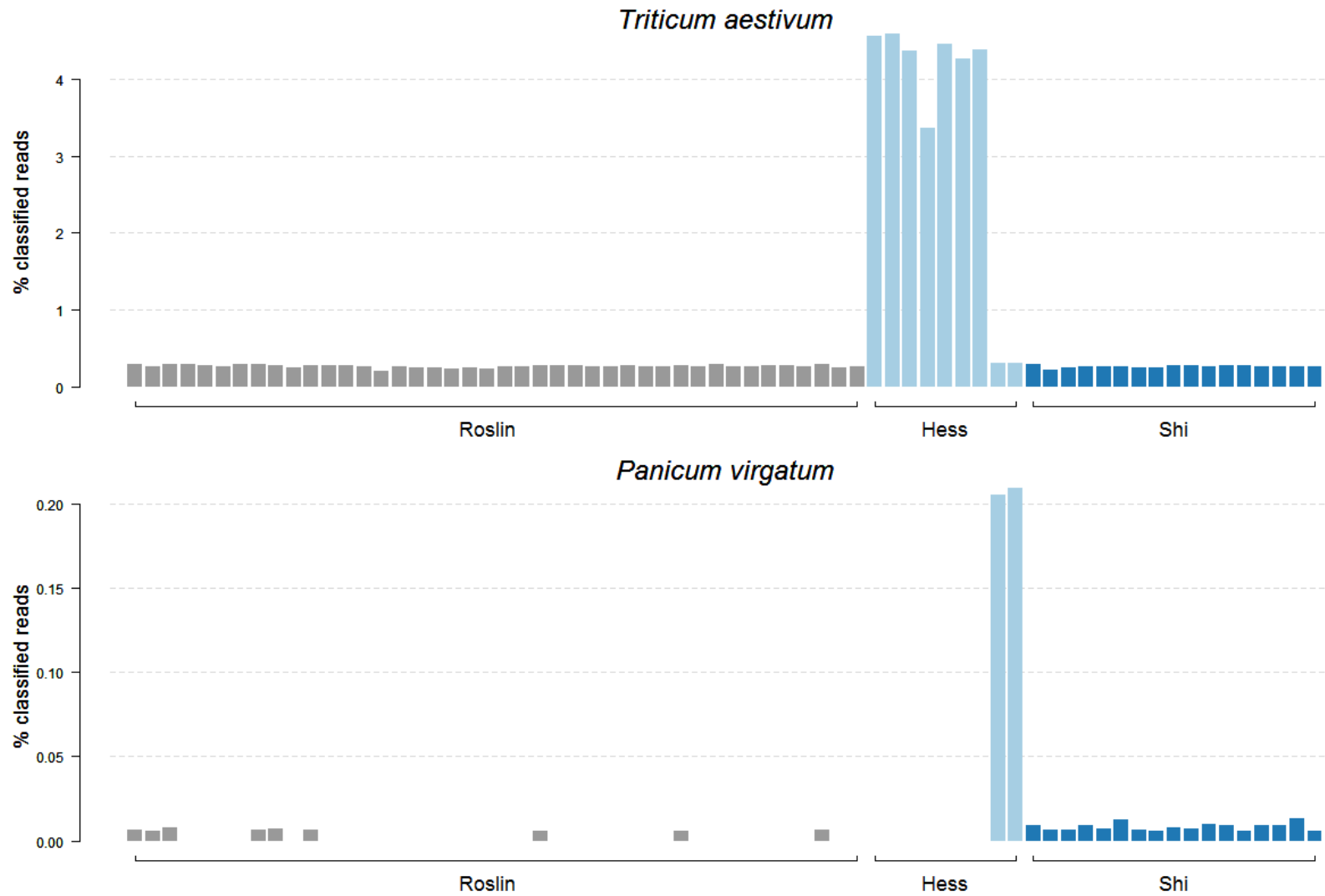


Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen

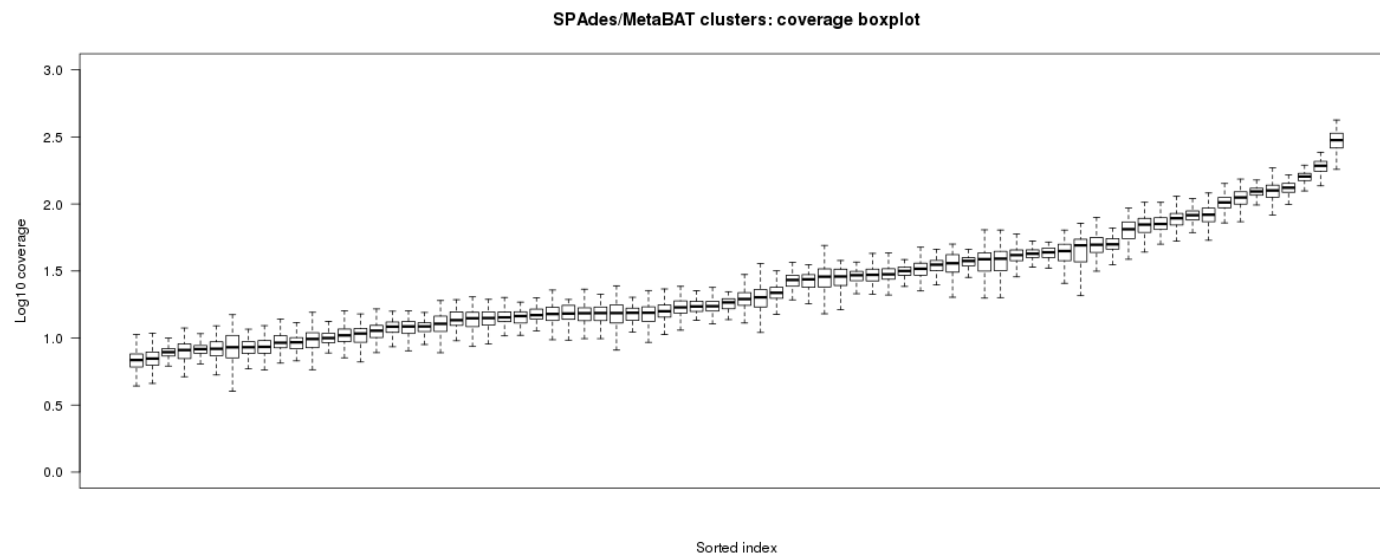
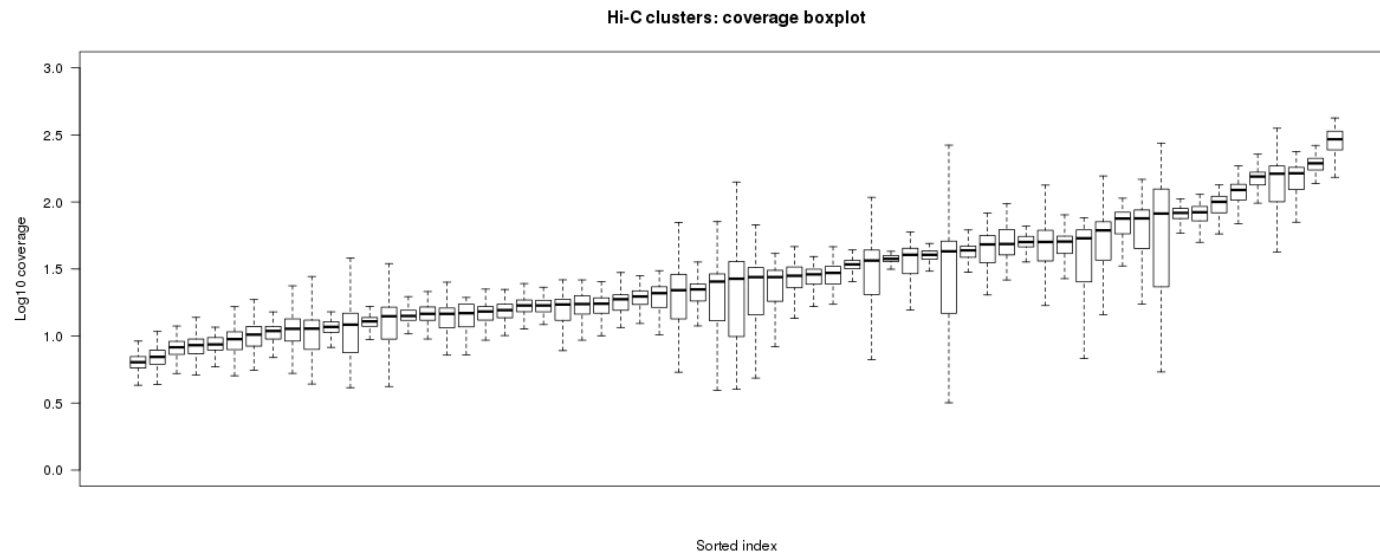
Stewart *et al*



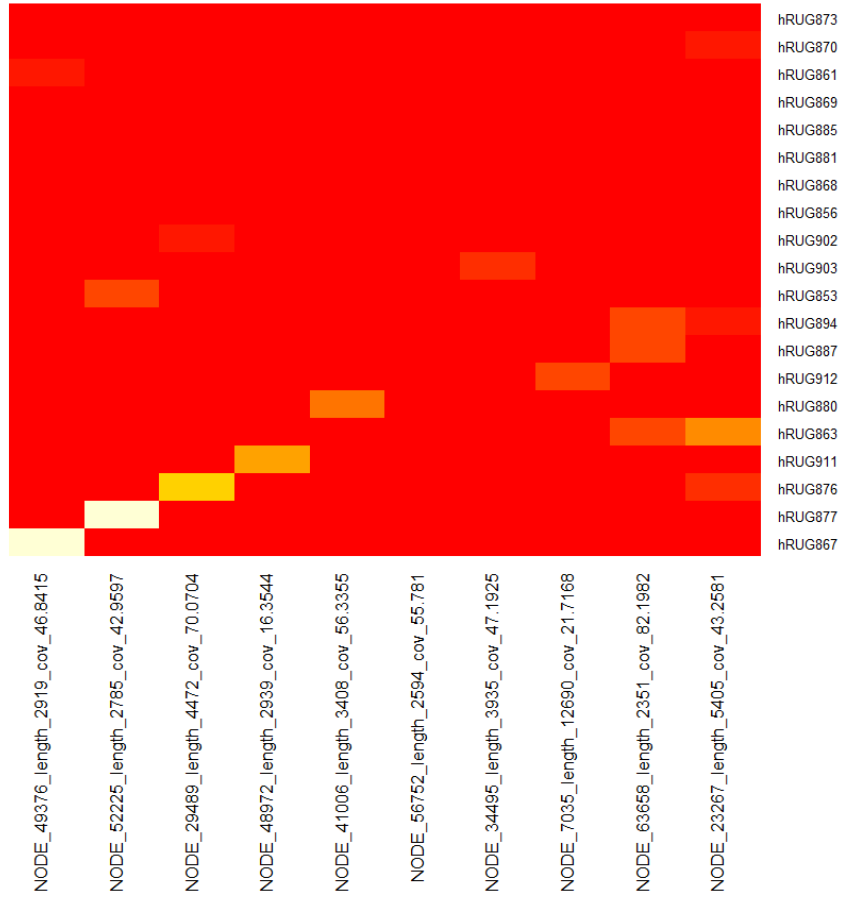
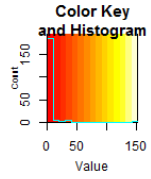
Supplementary Figure 1 A selection of predicted PULs. A: the most common, a simple *susC*/*susD* pair; B-E: a variety of PULs with similar configurations involved in xylan degradation; F-G: two identical PULs involved in pectin degradation



Supplementary Figure 2 Predicted contamination from plants in our data and the Hess and Shi data (using Centrifuge).



Supplementary Figure 4 Range of coverage values for contigs within bins from the 63 Hi-C genomes and the 76 metaSPAdes/MetaBAT genomes



Supplementary Figure 5 Heatmap of the number of Hi-C links between 10 high coverage contigs with plasmid BLAST hits and 63 high quality hRUG genomes