**Figure 10 – 10 scaffolds with the highest number of Chitinophagaceae genes.**

Genes with reciprocal best BLAST bits to genes from Chitinophagaceae bacteria were identified and enumerated by scaffold. The graph shows the number of Chitinophagaceae genes on the 10 scaffolds containing the highest number of Chitinophagaceae genes. In red are scaffolds that were removed from our raw assembly or retained in our post-filtered assembly (grey). Post-filtered scaffolds were not used for HGT analysis or other analysis in our original manuscript.