



Supplementary Figure 8. Illustration of HGT assay to detect HGT candidates. Figure shows the read coverage and z-score per position of scaffold jcf7180000797043 from *B. heterosporus* B8920. Z-score represents the number of standard deviations from the mean coverage per genic position; any gene model with a z-score greater than 2 or lower than -2 is removed from the analysis. BLAST results show that N168_01914 best hit is to alpha-proteobacteria from RefSeq. Coverage and z-scores for gene model N168_01914 do not show significant deviation of coverage (purple rectangle), making N168_01914 a plausible candidate for HGT origin.