



Fig. S7. Comparison of performance between a phylogenomic approach and two BLAST-based approaches (HGTector (Zhu et al., 2014) and HGTpropor). Panel a shows a Venn diagram of the number of HGT orthogroups identified by each approach. Panel b shows a grouped barplot that compares the *true positive* and *false positive* rates of HGTector and HGTpropor. The *true* set is considered as the number of HGT orthogroups identified by well-supported final phylogenetic analyses after improvement of taxon sampling and curation of translations and frame-shift errors. HGTpropor outperforms HGTector in having a slightly higher true positive rate and much lower false positive rate.

References

Zhu, Q., Kosoy, M. & Dittmar, K. HGTector: an automated method facilitating genome-wide discovery of putative horizontal gene transfers. *BMC Genomics* 15, 717, doi:10.1186/1471-2164-15-717 (2014).