



Supplementary Figure 9. Distribution and number of introns for the genes from the HGT assay identified in *Basidiobolus meristosporus* CBS 931.73. Distribution of quantiles is represented by the boxplots, where bold lines represent the median number of introns per genic origin. The violin plot represents the raw distribution of the data. Colors represent origin. A higher number of genes with no introns are found in genes of presumptive HGT origin than in fungal genes.