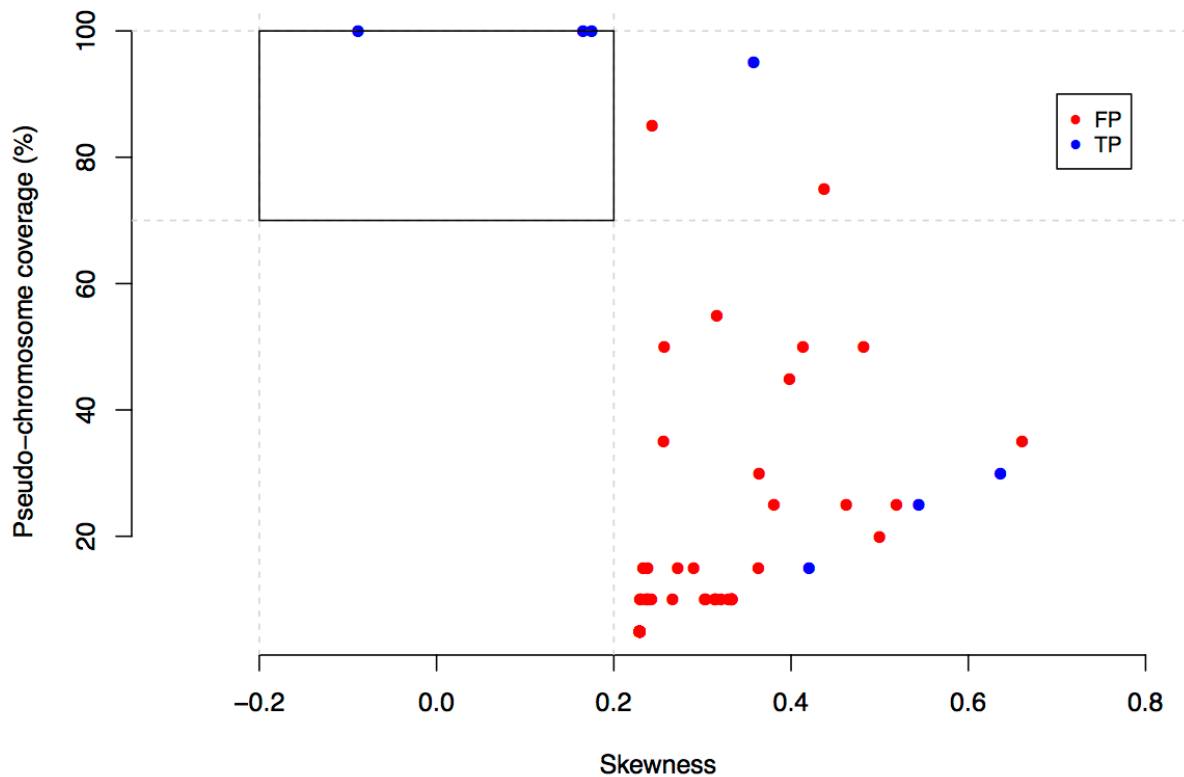


### Skewness vs Percent Pseudo-chromosome Coverage for ERR675624



S1 Fig. Evaluation of cut-offs for FindFungi species identification.

Species identified by FindFungi from dataset ERR675624 before cut-offs were applied were categorized as true positives (TP, blue) or false positives (FP, red) by comparing 10 randomly selected reads from each species prediction against the NCBI nt/nr database (BLASTn and BLASTx). Reads that supported the FindFungi prediction (same species or a close relative), were deemed to be true positives. The boxed region shows skewness cut-offs range from -0.2 to 0.2 and chromosome coverage cut-off ranges from 70-100%. These cut-offs were applied to subsequent predictions by FindFungi.