

Supplementary Figure S5 for M.E. Wall *et al.*, Genome majority vote improves gene predictions, *PLoS Computational Biology* (2011).

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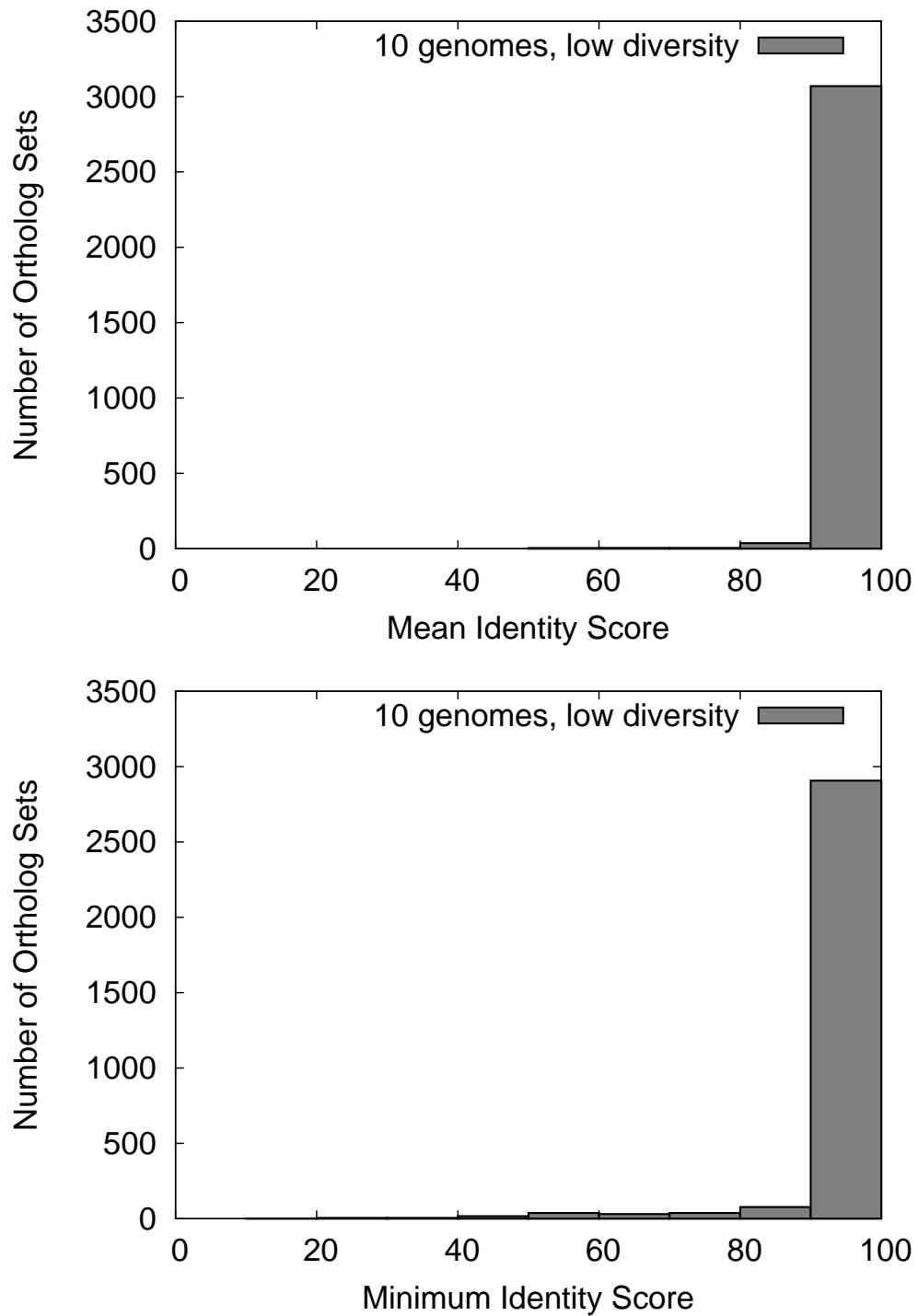


Figure S5: Histogram of mean (top) and minimum (bottom) identity score between genes in ortholog sets derived from the low diversity, 10 genome set.