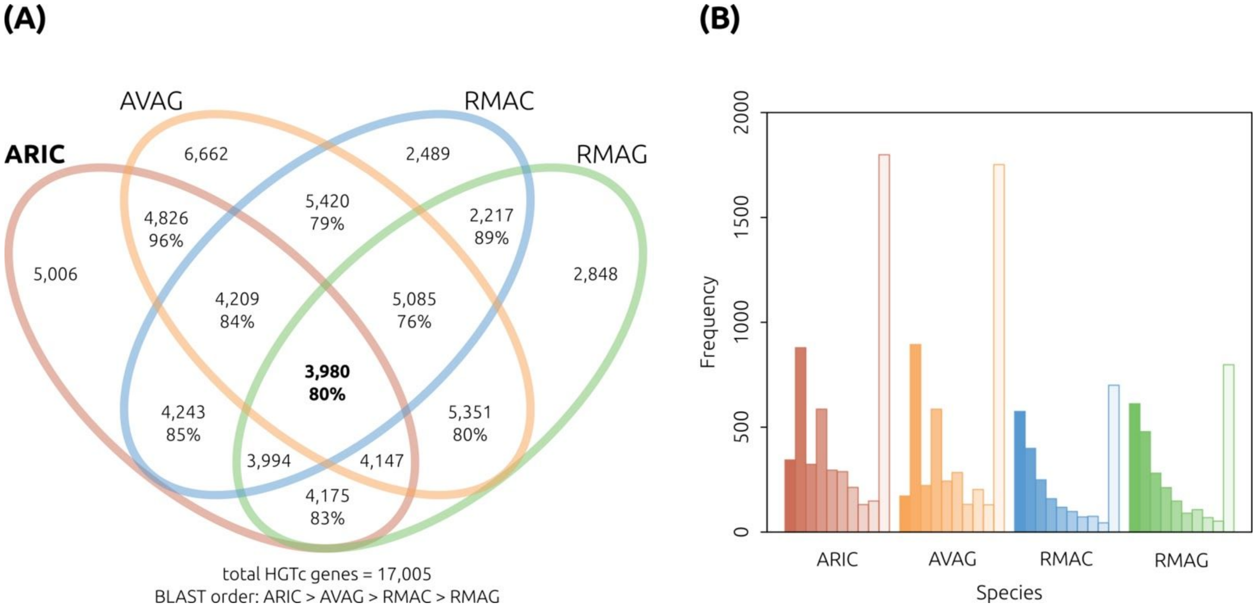

S13 Fig. Evidence for ancient origin for most HGT_C genes in bdelloids. (A). Sequential BLAST analysis of HGT_C genes. Values within overlapping segments represent the number/proportion HGT_C present in each set, based on TBLASTN analysis (*E*-value ≤ 1e−5, accepting hits showing ≥ 60% query coverage). All values are relative, based on the order *A. ricciae* (ARIC) > *A. vaga* (AVAG) > *R. macrura* (RMAC) > *R. magnacalcarata* (RMAG). Thus, 3,980 (80%) of *A. ricciae* HGT_C genes are found in all four species; 5,085 (76%) of *A. vaga* HGT_C genes are found in *R. macrura* and *R. magnacalcarata*, etc. (B) OG membership distribution for HGT_C genes. For each species, bars from left to right represent the number of co-orthologous genes for HGT_C genes (based on BLASTP hits showing ≥ 60% query coverage as above). The shape of each distribution reflects that of all genes (**S12 Fig**), except many HGT_C genes show 10+ hits to other proteins, suggesting that some HGT_C genes may have undergone substantial duplication after domestication.