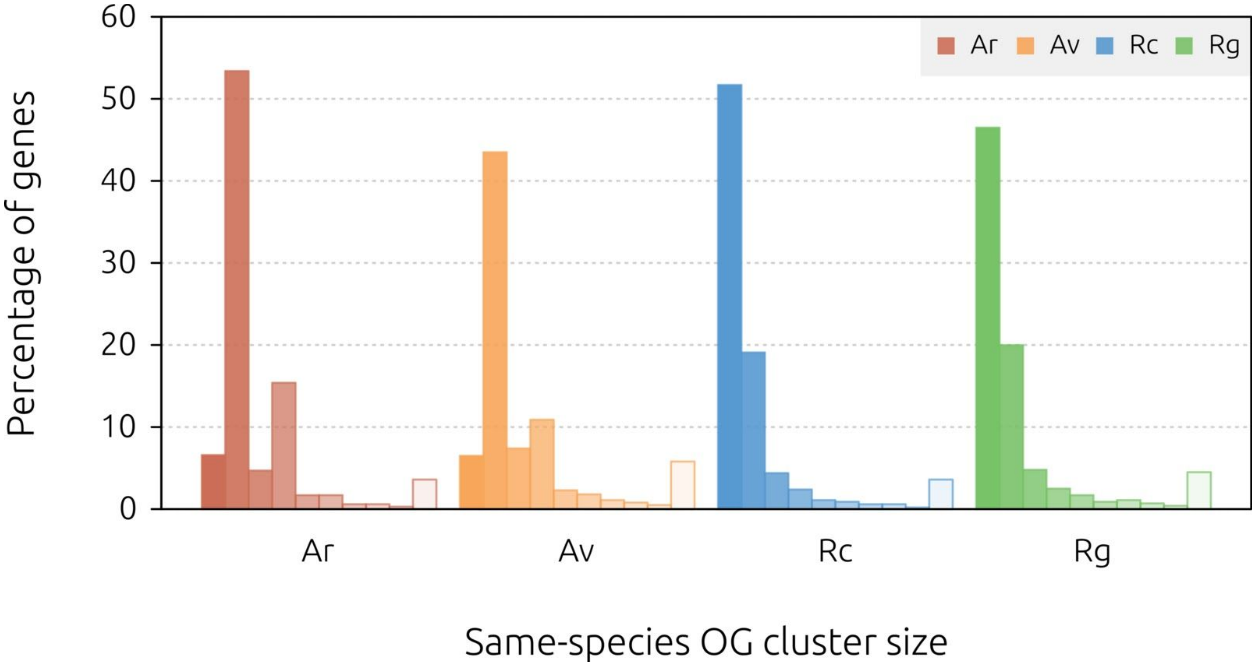

S12 Fig. Orthologous clustering within bdelloid genomes. Bars show the distribution of same-species co-orthologous cluster size, expressed as a proportion of each species genome (total number of CDS). Membership size ranges from one (i.e., singletons, left-hand bar) to 10+ (i.e., 10 co-orthologs from the same species, or more; right-hand bar).