S2 Table. MCScanX collinearity metrics within genomes.

Species	***A. ricciae***	***A. vaga***	***A. vaga* (collapsed)**	***R. macrura***	***R. magnacalcarata***
Genes[1]	49857	57431	35424	24594	29359
Assembly N50 (kb)	277	260	27	73	53
Singletons (% genes)	1613 (3.2%)	1246 (2.2%)	7583 (21.4%)	4704 (19.1%)	6029 (20.5%)
Dispersed duplicates (%)	9153 (18.4%)	15198 (26.5%)	23418 (66.1%)	16090 (65.5%)	19149 (65.2%)
Proximal duplicates (%)	588 (1.2%)	779 (1.4%)	252 (0.7%)	181 (0.7%)	265 (0.9%)
Tandem duplicates (%)	1139 (2.3%)	1206 (2.1%)	1173 (3.3%)	717 (2.9%)	920 (3.1%)
Segmental duplicates[2] (%)	37342 (74.9%)	38961 (67.9%)	2998 (8.5%)	2881 (11.7%)	2988 (10.2%)
Of which form homologs blocks (%)	36595 (73.4%)	37061 (64.5%)	0	0	0
Of which form ohnologous blocks (%)	17051 (34.2%)	15740 (27.4%)	2998 (8.5%)	2881 (100%)	2988 (100%)
Total # blocks					
Homologous	475	905	0	0	0
Ohnologous	903	923	184	175	187
Median block size (# genes)					
Homologous	24	13	NA	NA	NA
Ohnologous	11	9	5	11	12

[1] Curated gene sets for reference genomes were used in this analysis (see Table 1); [2] Total genes forming collinear blocks. Note that the a gene may contribute to multiple collinear blocks. Homologous blocks defined as those with an average pairwise $Ks \leq 0.5$ (*A. ricciae*) and $Ks \leq 0.3$ (*A. vaga*); ohnologous blocks defined as those with an average pairwise $Ks > 0.5$ (*A. ricciae*), $Ks > 0.3$ (*A. vaga*), and $Ks > 0.4$ for both *R. macrura* and *R. magnacalcarata*.