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 <br> (kb) | 277 | 260 | 27 | 73 | 53 |
| Singletons (\% genes) | $\begin{aligned} & 1613 \\ & (3.2 \%) \end{aligned}$ | $\begin{aligned} & 1246 \\ & (2.2 \%) \end{aligned}$ | 7583 (21.4\%) | $\begin{aligned} & 4704 \\ & (19.1 \%) \end{aligned}$ | 6029 (20.5\%) |
| Dispersed duplicates (\%) | $\begin{aligned} & 9153 \\ & (18.4 \%) \end{aligned}$ | $\begin{aligned} & 15198 \\ & (26.5 \%) \end{aligned}$ | 23418 (66.1\%) | $\begin{aligned} & 16090 \\ & (65.5 \%) \end{aligned}$ | 19149 (65.2\%) |
| Proximal duplicates (\%) | $\begin{aligned} & 588 \\ & (1.2 \%) \end{aligned}$ | $\begin{aligned} & 779 \\ & (1.4 \%) \end{aligned}$ | 252 (0.7\%) | $\begin{aligned} & 181 \\ & (0.7 \%) \end{aligned}$ | 265 (0.9\%) |
| Tandem duplicates (\%) | $\begin{aligned} & 1139 \\ & (2.3 \%) \end{aligned}$ | $\begin{aligned} & 1206 \\ & (2.1 \%) \end{aligned}$ | 1173 (3.3\%) | $\begin{aligned} & 717 \\ & (2.9 \%) \end{aligned}$ | 920 (3.1\%) |
| Segmental duplicates ${ }^{2}$ (\%) | $\begin{aligned} & 37342 \\ & (74.9 \%) \end{aligned}$ | $\begin{aligned} & 38961 \\ & (67.9 \%) \end{aligned}$ | 2998 (8.5\%) | $\begin{aligned} & 288 \mathrm{I} \\ & \text { (II.7\%) } \end{aligned}$ | 2988 (10.2\%) |
| Of which form homologs blocks (\%) | $\begin{aligned} & 36595 \\ & (73.4 \%) \end{aligned}$ | $\begin{aligned} & 37061 \\ & (64.5 \%) \end{aligned}$ | 0 | 0 | 0 |
| Of which form ohnologous blocks (\%) | $\begin{aligned} & \text { I705I } \\ & (34.2 \%) \end{aligned}$ | $\begin{aligned} & 15740 \\ & (27.4 \%) \end{aligned}$ | 2998 (8.5\%) | $\begin{aligned} & 2881 \\ & (100 \%) \end{aligned}$ | 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 I); ${ }^{2}$ 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 $\mathrm{Ks} \leq 0.3$ (A. vaga); ohnologous blocks defined as those with an average pairwise $\mathrm{Ks}>0.5$ (A. ricciae), Ks > 0.3 (A. vaga), and $K s>0.4$ for both $R$. macrura and R. magnacalcarata.

