**Table S1 Genome assembly and annotation statistics for *P. caudatum*, as compared to *biaurelia* (McGrath *et al*., submitted), *tetraurelia* (AURY *et al.* 2006) and *sexaurelia* (McGrath *et al.,* submitted).**

| | *caudatum* | *biaurelia* | *tetraurelia* | *sexaurelia* |
|---|---|---|---|---|
| Average coverage | 186X | 45X | 13X | 42X |
| Number of scaffolds (total) | 1,202 | 2,362 | N/A* | 547 |
| Number of scaffolds (> 2 kb) | 274 | 1,426 | 697 | 230 |
| Average scaffold length (>2 kb scaffolds) | 109,242 | 53,140 | 103,448 | 294,183 |
| Largest scaffold length | 793,585 | 1,048,449 | 980,760 | 1,303,432 |
| Number of gaps | 1,412 | 1,459 | 419 | 1,298 |
| Assembly length with gaps (all scaffolds) | 30,525,943 | 76,976,592 | 72,102,941 | 68,020,722 |
| Number of genes | 18,509 | 39,242 | 39,521 | 34,939 |

* Only scaffolds > 2 kb are included in *tetraurelia* assembly