

Table S5: Assembly statistics and number of identified single-copy genes in the analysed genomes. The metrics follows the Quast manual. Gene recovery for the genome skimmed datasets after running Orthograph version 0.6.3 is given in the last two columns.

species	Number of raw reads	Assembly size [Mb]	Number of contigs	Largest contig [bp]	N50 [bp]	N75 [bp]	L50	L75	N's per 100 kbp	Number of identified orthologs (strict)	Number of identified orthologs used for target enrichment
<i>Heterogyna</i> sp. ("brown wings")	35,356,860	134	570,87	5166	632	554	12524	21000	1,21	3,061	186 / 195
<i>Heterogyna</i> sp. ("pale abdomen")	40,645,564	610	5,170,999	10884	773	612	40865	74243	0	3,104	188 / 195
<i>Eremiasphecium</i> sp.	37,012,072	179	102,65	64965	3125	1603	14203	33556	11,07	3,182	191 / 195
<i>Entomosericus concinnus</i>	34,429,846	451	4,802,285	3103	576	531	1639	2699	0	3,064	189 / 195