Supplementary Data 1: Description of sequencing data and transcriptome assembly statistics of three replicate zooid samples.

Transcriptome feature	**Replicates**		
	Zooid 1	**Zooid 2**	**Zooid 3**
Raw reads (paired)	47,040,144	42,691,704	41,354,820
Paired reads after quality control	42,441,722	39,040,613	37,161,830
Duplicated reads	142,699 (0.34%)	119,997 (0.31%)	120,536 (0.32%)
Assembly parameter: *k-mer*/bubble size	35/300	35/300	35/300
Assembled contigs	92,581	83,011	74,811
Contigs after redundancy filtration	90,145	80,634	72,740
Average length (bp)	642	665	690
N50	919	1,015	1,108
GC content	51.8%	52.7%	52.9%
Trimmed reads mapped to respective replicate assembly	38,560,038 (90.8%)	35,722,612 (91.5%)	33,787,617 (90.9%)
Trimmed reads mapped to combined assembly (generated from all three zooid samples)	38,241,072 (90.1%)	35,140,999 (90%)	33,485,514 (90.1%)