Supplementary Table 2. Statistics of the transcriptome assembly

	Number of paired-end reads*[1]			Transcriptome assembly*[2]		
	Library 1	Library 2	Library 3	N50	No. contig*[3]	Total base
Pseudotrichonympha grassii	23,169,867	20,874,582	30,215,345	1,175	39,825	35,619,360
Holomastigotoides hartmanni	25,488,617	26,149,361	28,319,743	837	108,262	76,841,851
Holomastigotoides minor	28,291,610	49,604,672	27,702,408	1,018	70,088	58,009,961
Cononympha leidyi	40,348,124	28,828,635	33,194,456	1,213	51,266	47,901,578

*[1] The number of paired-reads after removal of adapter and quality filtering.

*[2] These statistics are calculated after removal of contamination

*[3] Contigs longer than ≥ 300bp are shown