

S2 Table. BUSCO report for transcriptome assemblies.

Assembly	BUSCOs found	Database (total number of records)							
		Eukaryotes (303)		Metazoa (978)		Bacteria (148)		Fungi (290)	
<i>H. dujardini</i>	Complete	295	97.36%	899	91.92%	135	91.22%	266	91.72%
	Single-copy	267	88.12%	815	83.33%	45	30.41%	222	76.55%
	Duplicated	28	9.24%	84	8.59%	90	60.81%	44	15.17%
	Fragmented	2	0.66%	27	2.76%	6	4.05%	18	6.21%
	Missing	6	1.98%	52	5.32%	7	4.73%	6	2.07%
<i>H. panicea</i>	Complete	300	99.01%	954	97.55%	146	98.65%	280	96.55%
	Single-copy	118	38.94%	529	54.09%	15	10.14%	94	32.41%
	Duplicated	182	60.07%	425	43.46%	131	88.51%	186	64.14%
	Fragmented	2	0.66%	15	1.53%	1	0.68%	10	3.45%
	Missing	1	0.33%	9	0.92%	1	0.68%	0	0.00%