

Table S1 Statistics of the transcriptome data generated after Illumina sequencing in *B. ciliata*

Category	Items	Number
Raw reads	Total raw read	21,490,725
Clean reads	Total clean reads	21,277,286
	Total clean nucleotides (nt)	1,33,174,507
	Q20 percentage	98.02%
	Q30 percentage	93.98%
	GC percentage	44.71%
Unigenes	Total sequence number	65,010
	Total sequence base	66,576,757
	Largest	6,531
	Smallest	301
	Average	1,024
	N50 (bp)	1,349
	N90 (bp)	494
EST-SSR	Total number of examined sequences	65,010
	Total size of examined sequences (bp)	66,576,757
	Total number of identified SSRs	18,226
	Number of SSR-containing sequences	14,497
	Number of sequences containing more than one SSR	2,913
	Number of SSRs present in compound formation	1,468