

supplementary Table 1: Summary of the sequence analyses Sample

Sample	Raw Reads	Clean reads	Clean bases	Error(%)	Q20(%)	Q30(%)	GC(%)
TM_0h1	49051962	47323406	7.1G	0.02	97.12	92.66	45.01
TM_0h2	53622654	51432524	7.71G	0.02	97.33	93.10	44.78
TM_0h3	51143430	49168870	7.38G	0.02	97.16	92.76	44.88
TM_6h1	48059140	46269170	6.94G	0.02	97.14	92.73	44.90
TM_6h2	50625418	48752916	7.31G	0.02	97.35	93.18	44.76
TM_6h3	49902314	47872316	7.18G	0.02	97.31	93.09	44.51
TM_14h1	49286802	47267348	7.09G	0.02	96.98	92.37	45.18
TM_14h2	63284274	60976736	9.15G	0.02	97.29	92.89	44.80
TM_14h3	55197834	53236974	7.99G	0.02	97.40	93.05	44.74
Summary	470173828	452300260	67.85G				

Sample name_1/2/3, Three biological repeats. Raw reads: The total number of reads. Clean reads: The number of reads after removing low-quality sequences. The subsequent analysis is based on clean reads. Error rate: Base error rate. Q20 and Q30, the percentage of bases with Phred values >20 and >30, respectively. GC content: the GC ratio of the total base number.

Supplementary Table 2: Success rate of gene annotation

	Number of unigenes	Percentage (%)
Annotated in Nr	120,165	61.24
Annotated in Nt	91,838	46.8
Annotated in KO	49,517	25.23
Annotated in SwissProt	87,173	44.42
Annotated in PFAM	81,101	41.33
Annotated in GO	82,680	42.13
Annotated in KOG	32,662	16.64
Annotated in all databases	19,657	10.01
Annotated in at least one database	131,652	67.09
Total unigenes	196,207	100

Annotated in Nr: The unigene number and annotation rate in the NR database.

Annotated in Nt: The unigene number and annotation rate in the NT database.

Annotated in KO: The unigene number and annotation rate in the KO database.

Annotated in SwissProt: The unigene number and annotation rate in the SwissPort database. Annotated in PFAM: The unigene number and annotation rate in the PFAM database. Annotated in GO: The unigene number and annotation rate in the GO database.

Annotated in KOG: The unigene number and annotation rate in the KOG database.

Annotated in all Databases: The unigene number and annotation rate in all seven databases. Annotated in at least one database: The unigene number and annotation rate in at least one database.

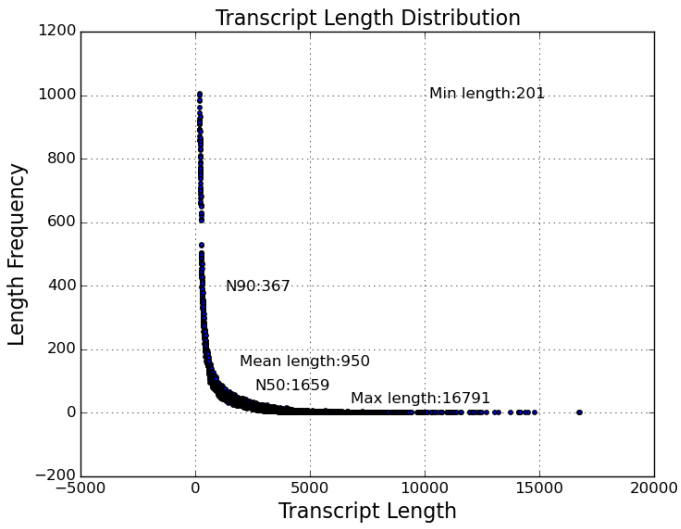


Figure S1. Length distribution of the assembled unigenes. A total of 268,621 transcripts were assembled with average and N50 length of 950 bp and 1659 bp, respectively.

**Table S3 | Primers
used in this study**

Gene_ID	Forward primer	Reverse primer
Cluster-29186.16026	TGGGTTTCAGTTCGGAAAAAC	TCGGAGTCGGTGACATCATA
Cluster-29186.98807	AAATCCGTCGAAGAAAAGCA	GACGACGATGAAGTTGACGA
Cluster-29186.148872	AGAAAGACTCGACCCAAGCA	CGTACGAGCAGCATTCTTCA
Cluster-29186.21713	GATAGCCTCGCCCTCTTCTT	GGTTGAGGACGGTGGATAGA
Cluster-29186.21846	AAGCGAGGCGAATCTTATCA	TCAGCAAGCCAAACATCAAG
Cluster-29186.30046	AAGCTCCTCCACACCTGAGA	GCTCCTATCGCCATTGAAAG
Cluster-29186.99722	CAACGATCTCGCGTATCTCA	TATCCCAATTTGGCGACAGT
Cluster-29186.152587	TTTACCGAAGGGTGCAAGTC	TCATTTCGTGCACTGCTTTTC
Cluster-29186.100002	TGTAACTTCAAGGGGCAACC	GCGGCTGTGGTTTCAGTATT
Cluster-29186.149462	CTTCAGTATGGGTGCTGCAA	GTCCAACGATTGCCCTTAGA
Cluster-29186.90009	AACATTATCCCCAGCAGCAC	GCCTGACAGTGAGGTCAACA
Cluster-29186.38298	CCTTGAGATCGGTCTTGTA	TTGAGGCGATTGGATAAAGG
Cluster-29186.24892	GAAGGCCAAAATCCAAGACA	TCTGAGCCGAAGAACCAAGT
Cluster-29186.146029	CCAATGTTCAAACCATGCAG	AAGCCCCCTGAGCATTTAAC
Cluster-12578.0	AAGCGTGCATTTGTTCACTG	TCTGCCCCTACTTCCTCGTA
Cluster-29186.78362	AGCTCGTCGAAAATGCAGAT	GGTCGCAGAAATCAAATGGT
Cluster-29186.107737	CTCTTCCAGCCTTCCTTCT	AGCACTGTGTTGGCGTACAG

Table S2 | Cq values of all samples in *Cyclocarya paliurus*.

	GAPDH	18sRNA	UBQ4	TUB	ACTF	ACT2	TUA2	
	TM-0h_1	16.07	22.07	28.21	18.37	23.84	23.02	20.56
	TM-6h_1	14.11	19.05	27.74	18.91	24.84	23.66	21.05
	TM-14h_1	13.54	18.51	27.57	18.91	24.98	24.11	21.52
	TM-0h_2	15.6	21.16	27.63	18.08	24.95	22.66	20.11
TM	TM-6h_2	14.3	18.9	27.55	18.49	26.18	23.44	20.86
	TM-14h_2	13.62	18.17	27.8	18.26	25.52	23.42	20.99
	TM-0h_3	15.53	22.12	26.59	18.03	22.85	22.81	19.92
	TM-6h_3	13.33	17.66	25.4	17.5	22.67	22.12	20.36
	TM-14h_3	14.19	18.35	27.1	18.7	23.75	23.3	20.9

Table S7 | Comparison the ranking of the candidate reference genes according to their stability value calculated by geNorm and NormFinder analysis.

Ranking	TM		PEG-6		NaCl-6		
	geNorm	NormFinder	geNorm	NormFinder	geNorm	NormFinder	geNorm
1	ACT2	UBQ4	ACT2	ACT2	18sRNA	GAPDH	ACT2
2	TUB	TUB	18sRNA	TUA2	GAPDH	ACT2	GAPDH
3	TUA2	ACT2	TUA2	18sRNS	ACT2	18sRNA	18sRNA
4	UBQ4	TUA2	UBQ4	GAPDH	TUA2	TUA2	TUA2
5	ACTF	GAPDH	TUB	UBQ4	ACTF	ACTF	UBQ4
6	GAPDH	ACTF	ACTF	TUB	TUB	TUB	TUB
7	18sRNA	18sRNA	GAPDH	ACTF	UBQ4	UBQ4	ACTF