Supplemental Material

Temperature differentially affects gene expression in Antarctic thraustochytrid *Oblongichytrium* sp. RT2316-13

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1. Table S1 to S3.
2. Figure S1.
3. Excel file Paredes_et_al.xlsx.

Table S1. Sequencing results. The initial amount of reads (total reads) and the number of reads that passed quality control filters (HQ reads).

Condition	ID	Total reads	HQ reads	HQ reads (%)
Control	GM1595-1	30,853,728	30,688,242	99.46
Control	GM1595-2	47,592,052	47,358,355	99.51
Control	GM1595-3	21,876,024	21,759,224	99.47
Treatment	GM1595-4	25,468,998	25,337,912	99.49
Treatment	GM1595-5	24,655,850	24,529,757	99.49
Treatment	GM1595-6	24,124,200	23,985,768	99.43

Table S2. Total number of high quality (HQ) reads that were mapped to a sequence in RT2316-13 transcriptome, concordantly one or more times (properly aligned), and the total number of reads aligned (overall aligned), with their respective mapping rate (%).

ID	HQ reads	Properly aligned	Overall aligned	Properly aligned mapping rate (%)	Overall mapping rate (%)
GM1595-1	30,688,242	27,437,849	30,383,019	89.41	99.01
GM1595-2	47,358,355	42,773,627	46,999,661	90.32	99.24
GM1595-3	21,759,224	19,310,940	21,553,763	88.75	99.06
GM1595-4	25,337,912	24,353,793	25,094,881	96.12	99.04
GM1595-5	24,529,757	23,699,786	24,327,830	96.61	99.18
GM1595-6	23,985,768	21,237,876	23,773,688	88.55	99.12
			Average	91.63	>99.0

Table S3. Primers used for identifying genes related to production of fatty acids.

Gene	Gene abbreviation[§]	Sequence	T_m (℃)
Malic enzyme	Me_F	AAGCCTGCCAAGAGTTCCA	56.9
	Me_R	GCCAGTTGTTCACGAGAGTC	55.9
Acetyl-CoA	ACC_F	GAGACCACTTACCGCCTGTT	57.0
carboxylase	ACC_R	CGCCAATGAGCACAAGGAAG	56.8
PKS subunit A	Pfaa_F	AGCCTCCTTGATAGCCTTCTC	56.2
	Pfaa_R	TCTGGTGCGTGTTCTTGGT	56.9
PKS subunit C	Pfac_F	CTGGTGGTGGTGTTGGATG	56.1
	Pfac_R	GCTGCTTGCGGACATTGT	56.6
18S rRNA	18s_F	TGCCGACTTGCGATTGTTG	56.4
	18s_R	TTCAGCCTTGCGACCATACT	56.5

[§]Forward primers (_F) and reverse primers (_R). The sequences were obtained from Ma et al. [29]. T_m = melting temperature.

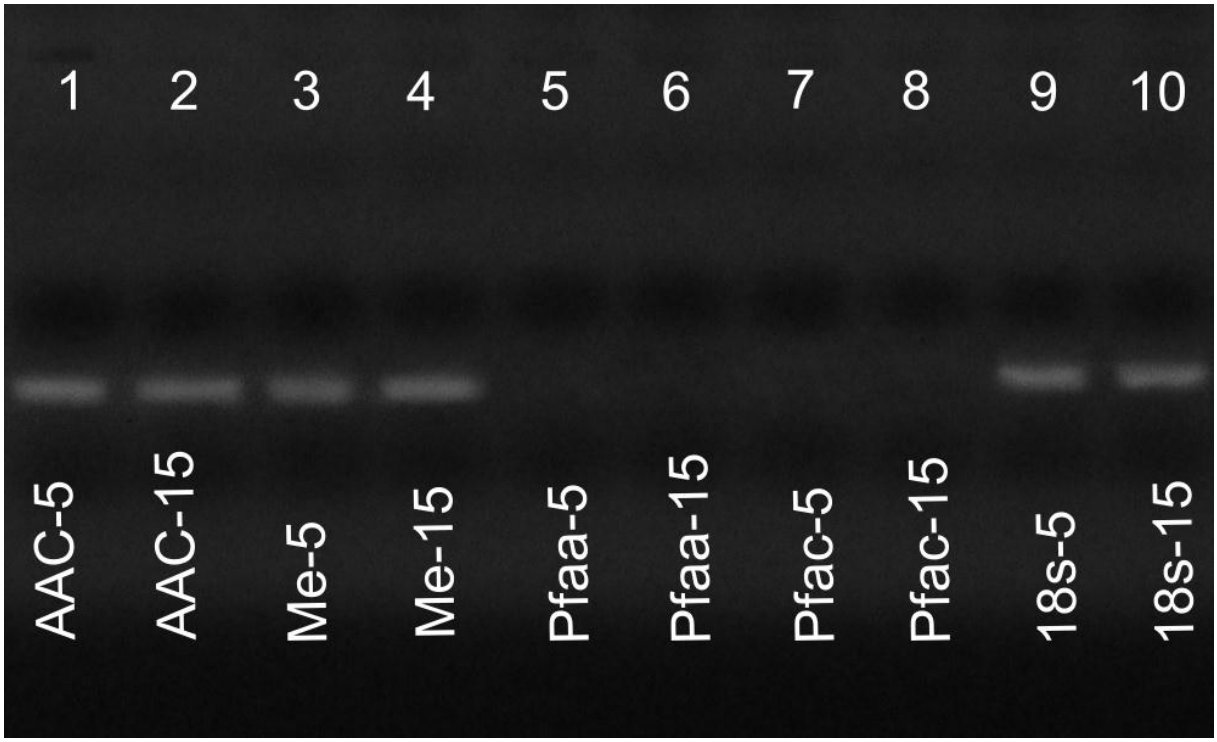

Figure S1. Amplification of cDNA segments. AAC, acetyl-CoA carboxylase; Me, malic enzyme; Pfaa, subunit A of PKS gene; Pfac, subunit C of PKS gene; 18s, 18S subunit of RNA. xx-5 and xx-15 denote cDNA of cells grown at 5 and 15 ℃, respectively.