

Table S1. The key DEGs and DEMs of *P. vannamei* under cold stress.

Pathway	Genes/Metabolites	Description	log2 FC(T2/CK)	log2 FC(T4/T2)	log2 FC(T4/CK)
Amino acid metabolism	M104T376_NEG	L-serine	-0.962606017	0	0
	M105T328_NEG	Glycerate/Glyceric acid	0	0	-3.537351536
	M74T358_NEG	Glycine	-0.898461040	0	-0.952692699
	M118T357_NEG	L-Threonine	-1.353407689	0	-1.954460693
	M135T330_NEG	L-threonate	-1.295326495	0	-1.302054740
	M128T370_NEG	L-pyrogutamic acid	0	0.596884107	0.775056740
	M132T344_2_POS	Alanine betaine	0	-0.483044274	0
	M88T339_NEG	Alanine	0	1.766475732	1.418774223
	M169T434_POS	L-Glutamine	-2.459652441	3.341647945	0.881995504
	M146T409_NEG	Glutamate/Glutamic acid	0	-0.742869950	0
	M116T446_POS	D-ornithine	0.459155890	0	0
	M175T515_POS	Arginine	-0.637661019	0	-1.290435941
	M114T304_2_NEG	Proline	0	1.212791422	1.706985977
	M131T383_2_NEG	Asparagine	0	0.686283997	0
	M206T348_POS	4-acetamidobutanoate	0.866689421	-0.751423202	0
	ROT61431.1(AMT)	Aminomethyl transferase	0	0	1.416311402
	ROT66029.1(SHMT1)	Serine hydroxymethyltransferase, cytosolic	0	0	-1.235863583
	ROT81872.1(ASL)	Argininosuccinate lyase	0	0	-1.559335374
	ROT77699.1(Aldh3a1)	Aldehyde dehydrogenase, dimeric NADP-preferring	0	-3.040157126	0
	ROT78477.1(Aldh16a1)	Aldehyde dehydrogenase family 16 member A1	0	-1.089878050	-1.393638984
Lipid metabolism	M199T45_NEG	Dodecanoic acid	0	-0.421400477	0
	M283T679_NEG	Stearic acid	0	1.185139086	0

Carbohydrate metabolism	M749T147_POS	Phosphatidylethanolamine	0	0	-0.167627755
	M104T376_POS	Choline	0	0	-1.068152551
	M204T298_POS	Acetylcarnitine	0	1.390580893	0
	M400T169_POS	L-Palmitoylcarnitine	-1.189203211	0	-1.405969717
	ROT63220.1(FACL4)	Long-chain-fatty-acid--CoA ligase 4	0	0	3.205548911
	ROT60937.1(LPLAT1)	Lysophospholipid acyltransferase 1	0	0	1.629447887
	ROT75541.1(ELOVL7)	Elongation of very long chain fatty acids protein 7	0	1.353792105	1.238642227
	ROT71423.1(CPT2)	Carnitine O-palmitoyltransferase 2, mitochondrial	0	0	-1.643188979
	M165T370_2_NEG	D-Arabinonate/Arabinonic acid	-1.346771979	-1.519635895	-2.866407873
	M149T300_NEG	D-Lyxose	-0.475546392	0	-0.535164768
	ROT73830.1(PGM1)	Phosphoglucomutase-1	0	0	-1.338331553
	ROT82509.1(G6PC)	Glucose-6-phosphatase	0	0	-1.464092025
	ROT60920.1(FBP1)	Fructose-1,6-bisphosphatase 1	0	-3.365004518	-3.258636567
	ROT62958.1(PCK1)	Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	4.489384841	0	0
Nucleotide metabolism	M211T300_NEG	D-ribose 1-phosphate	0	-1.373672238	-1.795190468
	M191T475_NEG	Citrate	0	0	-0.080839076
	M61T100_POS	Urea	0	-1.596034142	-1.890633305
	M129T474_POS	Barbiturate/Barbituric acid	0	0	-0.148757439
	M136T168_POS	3-Hydroxypropanoate/3-hydroxyanthranilic acid	0	0.818527098	0
	M113T383_NEG	Dihydrouracil	0	0.702801827	0
	M157T182_NEG	L-dihydroorotate	-0.713557079	0	-1.359309104
	M569T379_POS	Xanthosine	1.418689730	1.217766302	2.636456032

	M267T211_NEG	Inosine	0	0.814250348	0.846113982
	M137T211_2_POS	Hypoxanthine	0	0.483399199	0.535425471
	M251T178_NEG	Deoxyinosine	0	-0.619173081	-1.324054963
	ROT68566.1(DPYS)	Dihydropyrimidinase	0	-1.279738226	-1.398811185
	ROT70986.1(DPYD)	Dihydropyrimidine dehydrogenase	0	0	1.120657214
	ROT62010.1(NT5E)	5'-Nucleotidase	0	0	1.294674486
	MSTRG.3682(HPRT1)	Hypoxanthine-guanine phosphoribosyltransferase	0	-1.819147701	-1.958813862
	ROT81136.1(HPRT1)	Hypoxanthine-guanine phosphoribosyltransferase	0	-1.170513496	-1.672736928
Antioxidation	ROT68062.1(GPX)	Glutathione peroxidase	0	-2.799747589	-1.671245701
	ROT61838.1(Trx-2)	Thioredoxin, mitochondrial	0	0	-1.740866530
	ROT65492.1(Txndc12)	Thioredoxin domain-containing protein 12	0	0	-1.149943188
Immunity	ROT81705.1(LYZ)	Lysozyme	0	-2.152693976	-2.033366191
	ROT63690.1(CTL2)	C-type lectin 2	0	-1.105598270	0
	MSTRG.21167(CTL2)	C-type lectin 2	0	-1.741861301	0
Osmoregulation	ROT72182.1(ATP2C1)	Calcium-transporting ATPase type 2C member 1	0	1.757938577	1.560783447
	ROT61630.1(ATP2B3)	plasma membrane calcium-transporting ATPase 2	0	0	1.618198830
	ROT61631.1(ATP2B3)	Plasma membrane calcium-transporting ATPase 2	0	0	1.769777042
	ROT75121.1(SLO)	Calcium-activated potassium channel	0	0	-1.053295585

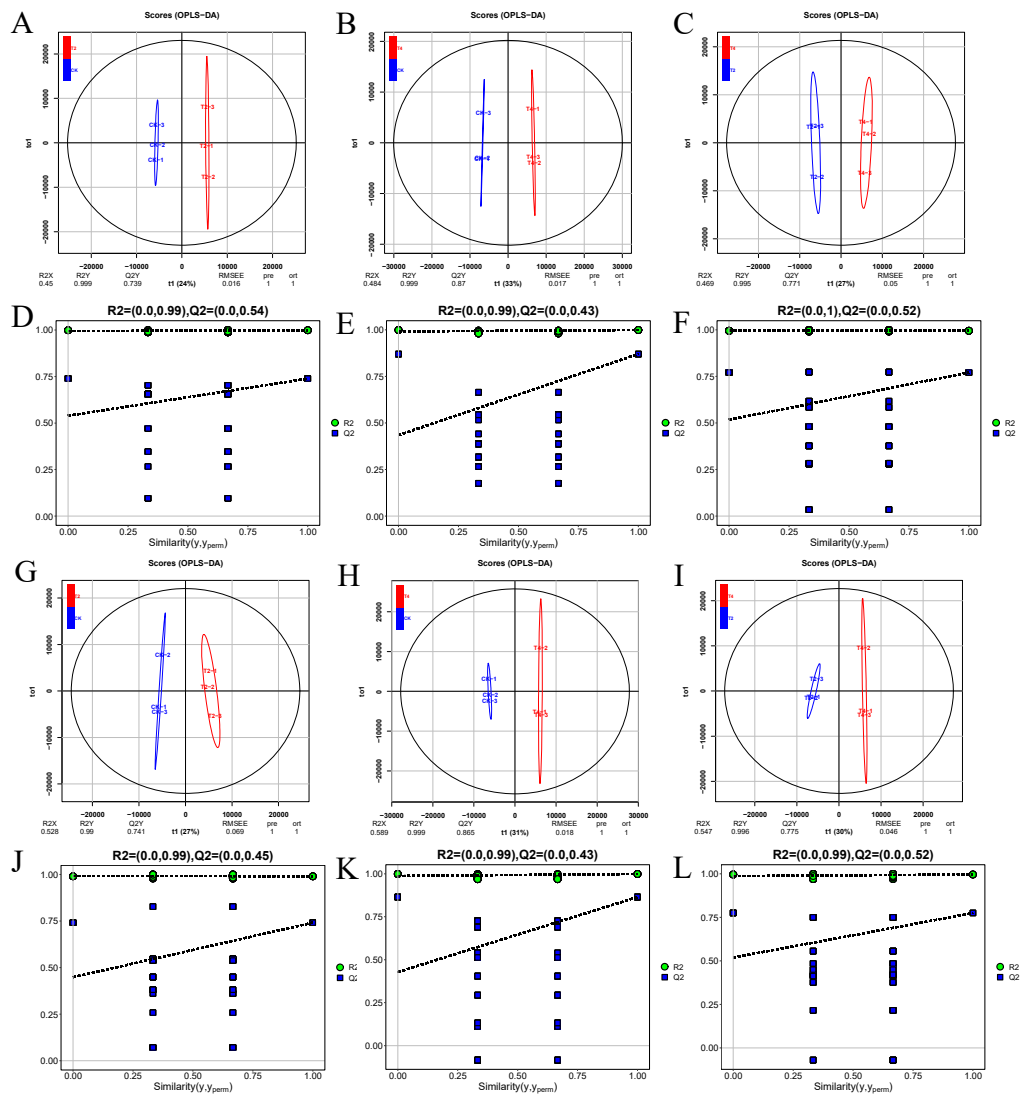


Figure. S1 OPLS-DA score plots and OPLS-DA permutation test.

Positive OPLS-DA score plots of CK vs T2 (A), CK vs T4 (B), and T2 vs T4 (C) and permutation tests of CK vs T2 (D), CK vs T4 (E), T2 vs T4 (F); Negative OPLS-DA score plots of CK vs T2 (G), CK vs T4 (H) and T2 vs T4 (I) and permutation tests of CK vs T2 (J), CK vs T4 (K), T2 vs T4 (L).