

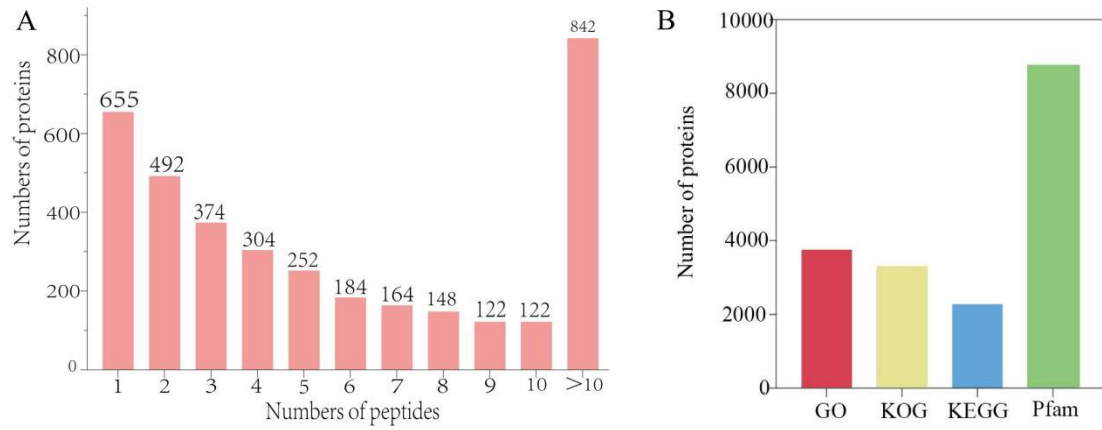
**Table S1.** Primer pairs applied for qRT-PCR.

Gene name	Primer sequences(5'-3')	Annealing temperature(°C)	Product length(bp)
PAK1	F:GACATTTGGTCCTTGGGC	51	296
	R:TTGTTCTTGCTTGCTTCC		
ITGA3	F:GCGGAAGGACTGGGATT	51	175
	R:CTGGCTCAGCAAAAAGA		
GNAI1	F:AATGTTTGATGTGGGA	45	382
	R:CGTGAAGTGGGTGTAT		
PDLIM1	F:GTGACAGAGGAAGGGAA	51	379
	R:GCAAAACCAGGAATGAA		
PIP4K2C	F:GAAAGTGAAGGCAGTG	45	114
	R:GTGGTAGTTGGACAGG		
IQGAP2	F:AACGCTAAGAAACCCAAACG	53	328
	R:ATACATCGCAGCAGCAAAAG		
TMSB4X	F:GACAAACCCGATATGGC	48	119
	R:CCTGCTTGCTTCTCCTG		
PRKCI	F:GAACAGGCATCCAATCATCC	51	252
	R:TCCTTCAGAGTCCAGCAACA		
ACSL1	F:CCAGAGGGGCTTACAC	51	266
	R:CTTCAGTTCCGAGGGT		
ELOVL5	F:CCCCACTTTGGTCTGTTC	51	168
	R:TCCATACTCCCGTCACT		
COL14A1	F:CCTTCAGTCTCAAGCCATGGTG	60	262
	R:CGAGTGGCTGGGAATCTGGTTA		
SERPINH1	F:TCTGGATGGGCAAGATGCAGAA	59.5	480
	R:CTGTAAGTCGTGGGTCACCTCC		
CD81	F:ACCTGCCTGGTGATCCTCTTTG	60	144
	R:GCTTCACATCCTTGGCGATCTG		
SLC23A2	F:ATGCCATGTGTGTGGGGTATGA	59.5	124
	R:AACAGGGGTAACCTGCATCCAA		
TAGLN	F:AATGGCGTGATTCTGAGCAAGC	59	172
	R:TGCTCCATCTGCTTGAAGACCA		
S100A13	F:GTTGCCTCACCTGCTCAAGGAT	60	168
	R:TCTCCAGGCCTTCTCTTTCCT		

**Table S2.** Sequencing statistics for each replicate. GC: the percentage of G and C bases in the clean data with respect to the total bases;  $\geq Q20\%/\geq Q30\%$ : percentage of bases in the clean data above the Q20/Q30 threshold; Mapped Reads: successfully mapped paired-end reads.

Group	Sample ID	Clean reads	GC(%)	$\geq Q20(\%)$	$\geq Q30(\%)$	Mapped Reads
L	LW1	40896120	2928446761 (48.02%)	5891857314(96.61%)	5560566739 (91.18%)	285118
	LW2	44090358	3219267208 (48.88%)	6373795371(96.77%)	6032781788 (91.59%)	1078872
	LW3	39981692	2914559503 (48.79%)	5732259738(95.97%)	5364762265 (89.81%)	286774

	HW1	41314794	2970527282 (48.10%)	5934462590(96.08%)	5561329403 (90.04%)	592122
H	HW2	39669232	2719049218 (45.98%)	5716080046(96.66%)	5392739623 (91.19%)	654458
	HW2	41652334	2969106092 (47.74%)	6010604034(96.63%)	5669578197 (91.15%)	610786



**Figure S1.** The distribution of peptide numbers and annotated protein numbers in different databases. (A) Distribution map of peptide number. (B) Protein database distribution.