

Supplementary Table S1 Output statistics of the sequencing reads for each sample.

Sample	Raw reads	Clean reads	Clean bases(G)	Error rate(%)	Q20(%)	Q30(%)	GC(%)
C1	78545122	78347416	10.9	0.2	97.52	93.05	45.52
C2	75705446	75532868	10.51	0.19	97.73	93.58	45.56
C3	81726938	81504264	11.34	0.24	97.35	92.77	45.42
P1	76628834	76379484	10.62	0.28	97.24	92.57	46.36
P2	81128982	80933782	11.24	0.22	97.8	93.80	46.53
P3	75737372	75535648	10.51	0.23	97.62	93.34	46.59
P+Q1	81143544	80901170	11.27	0.26	97.43	92.98	46.24
P+Q2	85956418	85723402	11.93	0.24	97.62	93.37	45.99
P+Q3	98378380	98107478	13.66	0.25	97.51	93.13	46.00

Supplementary Table S2 The 14 mRNA differentially expressed among the three groups

Genbank#	Accession number	Symbol
ENSSSCG00000004751	100621371	CHP1
ENSSSCG00000006580	HGNC:10492	S100A2
ENSSSCG00000009560	100621036	TFDP1
ENSSSCG00000011264	100519275	CSRNP1
ENSSSCG00000013433	100512586	ADAMTSL5
ENSSSCG00000013457	100738665	DOT1L
ENSSSCG00000014335	100520367	REEP2
ENSSSCG00000016438	100517250	NUB1
ENSSSCG00000016991	100522469	DUSP1
ENSSSCG00000021569	100626072	MMP25
ENSSSCG00000030209	102161832	MFNG
ENSSSCG00000031262	733688	TXNIP
ENSSSCG00000031342	110261334	-
ENSSSCG00000033126	110257088	FAM168B