

Table S1. Primers information of the 8 chosen differentially expressed genes by qRT-PCR analysis

Ensemble gene ID	Forward primer sequence	Reverse primer Sequence	Amplicon (bp)
ENSAPLG000000530 4	GGCTCTGTATCTGCTTCGTG	CGCCGCTTTGCCAGTTTT	267
ENSAPLG000000159 4	CGTGCTGCCCTGCCACTTGTC CCT	TGACCAACTCTGTTCTCCC	158
ENSAPLG000000119 6	CCAGAAGGGCAAGGACAT	GAGAAGGGGTGAGACAG A	206
ENSAPLG000000755 8	TGTAGCCGCAGTCCTTCT	GACCTGGTTCTCCCTTG	170
ENSAPLG000000807 9	CACTGCCTATGTGCTGTCA	GAGGGTCTCATCGTTCCA	172
ENSAPLG000000968 0	CGCCATCAAAGCCAACAA	CATCGGGCAAGTAGCAGA A	218
ENSAPLG0000001175 0	TATGATGGGAGTTGAGTG	AACCCTGTGGTCCTATTT	132
ENSAPLG000000883 5	CTCATCGCCACGACAGAAT	CAGGGTAGCCGCAGTTCA	235
ENSAPLG000000462 8	GACCAGTATGGCTATGACGG	TCCTCCTCCCACTTCCTCT	100
ENSAPLG000000961 3	ATGGTGGGCTCCGTCCTA	GACCAGCTCGATGCTTTG G	183
ENSAPLG0000001360 5	CTGCTGTGGACGGATGCT	TGCTGTAGCGGCTGTTT	158
ENSAPLG000000197 2	GCAGGAGGAGAACCAGGGCTA C	TCGGTGATGATGGCTGTG AG	117
ENSAPLG000000516 8 (<i>β-actin</i> as control)	GCTATGTCGCCCTGGATTTC	CACAGGACTCCATACCCA AGAA	168

Table S2. Summary statistics for sequence quality and alignment information of six samples

Samples	HRFI1	HRFI2	HRFI3	LRFI1	LRFI2	LRFI3
Raw Reads	123,870,722	104,465,292	124,365,626	88,346,404	113,403,496	111,689,750
Clean Reads	122,086,104	102,420,080	122,345,718	87,366,606	110,605,622	110,253,048
Clean Reads Rate (%)	98.56	98.04	98.38	98.89	97.53	98.71
rRNA Mapping Reads	1276,794	1064,744	1437,049	2266,460	1855,299	3424,483
rRNA Mapping Rate (%)	1.05	1.04	1.17	2.59	1.68	3.11
Total Clean Reads	120,708,088	101,283,174	120,839,342	84,980,878	108,640,352	106,676,626

Total Q30(%) ^a	93.47	92.5	92.78	95.64	92.6	94.32
Mapped Reads	86,219,119	69,504,059	81,736,548	59,436,909	77,087,093	70,782,609
Mapping Rate	0.71	0.69	0.68	0.70	0.71	0.66

¹Q30 represent the proportion of bases with a Phred quality score greater than 30.

Table S3.[AU: please provide the title of Table S3.]

GO Term	GO Subterm	Up_Cou		Down_Co	
		nt	Up_Percent	unt	Down_Percent
biological_process	cellular process	8	0.6154	8	0.4706
biological_process	biological regulation	8	0.6154	4	0.2353
biological_process	single-organism process	7	0.5385	9	0.5294
biological_process	metabolic process	6	0.4615	7	0.4118
biological_process	response to stimulus	6	0.4615	2	0.1176
biological_process	localization	4	0.3077	2	0.1176
biological_process	multicellular organismal process	3	0.2308	2	0.1176
biological_process	immune system process	3	0.2308	1	0.0588
biological_process	multi-organism process	2	0.1538	0	0.0000
biological_process	developmental process	2	0.1538	1	0.0588
biological_process	cellular component organization or biogenesis	2	0.1538	0	0.0000
biological_process	signaling	1	0.0769	0	0.0000
biological_process	behavior	1	0.0769	0	0.0000
biological_process	biological adhesion	1	0.0769	1	0.0588
cellular_component	cell part	11	0.8462	13	0.7647
cellular_component	organelle	7	0.5385	4	0.2353
cellular_component	macromolecular complex	6	0.4615	5	0.2941
cellular_component	membrane part	5	0.3846	10	0.5882
cellular_component	extracellular region part	4	0.3077	3	0.1765
cellular_component	membrane	4	0.3077	6	0.3529
cellular_component	organelle part	3	0.2308	6	0.3529
cellular_component	extracellular region	2	0.1538	0	0.0000
cellular_component	collagen trimer	1	0.0769	0	0.0000
cellular_component	synapse	1	0.0769	0	0.0000
molecular_function	binding	7	0.5385	6	0.3529
molecular_function	transporter	4	0.3077	1	0.0588
molecular_function	catalytic	4	0.3077	5	0.2941
molecular_function	molecular transducer	2	0.1538	2	0.1176
molecular_function	antioxidant	1	0.0769	0	0.0000
molecular_function	nutrient reservoir	1	0.0769	0	0.0000
molecular_function	structural molecule	1	0.0769	1	0.0588