RNA-Seq analysis on chicken taste sensory organs:

An ideal system to study organogenesis

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Supplemental Table S2, Primers information and validation results of the 14 chosen differentially expressed genes (GE vs NGE) by qRT-PCR analysis.

Gene Name	Log2 FC by RNA-Seq	Log2 FC by qRT-PCR	Forward primer sequence	Reverse primer Sequence	Amplicon (bp)
USP13	-1.81	0.22	AGAAGGTACCAGGGGCATCT	TCACCAGTGCTGGTAACTCTTC	189
DHX30	-1.52	-0.53	AGAACCAGGTGGGATCCTCT	CGCTGGAAGATGTTCTGTTG	159
LAMP3	-1.47	-1.5	ATTCGCCAGCAGCATTTTAC	CGGGAACTGCCTTTGTACTT	190
ACE	-6.11	-6.54	CGGATCAAGGAGGACGAATA	CTGGATCACGAAGCTGACAA	168
CD36	2.27	0.98	TGCAATTTGCCAAAAGACTG	CCGACCGGTGACTTTATTTC	195
EYA2	2.38	1.37	ACGGCATACCTTCCTACAGC	ATTGGCTCCCTGGTAAATCC	164
LPP	1.83	-1.12	TTGAAAATCGGTGGGAACAT	CACTGGACATGGAAGTCACG	152
PCDH10	2.36	2.59	AAAATTCCAACGGCAGCAT	GCTCACTGTCTCCATGACCA	153
RHCG	1.53	1.56	ATCCTCCTCAACCTGCTTCA	GGGCCAGTACATCCACAGAT	198
GNAT3	5.5	1.8	GGTGCTGGAGAGTCAGGAAA	CAATTCTAGCGGGGTTTTCA	187
TRPM5	1.37	1	GACAATGGGGCCAACATAAC	TCTCCTGCTGTTGACCAGTG	157
TAS1R3	1.37	0.51	TGGGTGCTGCTGTGTATGAG	TACTGTCAGCTGTGCCCAAG	237
LGR5	4.84	6.18	CAAAGCAGACACATTCCGGC	GTAGCCCCGTCACAGGAAAA	161
KRT20	1.34	1.78	AGCTTGTCCTGCAGATCGAC	GCAGTCTGTCAACCTCCTCC	228
GAPDH as control			CGTCCTCTCTGGCAAAGTCC	TTCCCGTTCTCAGCCTTGAC	

Abbreviations: FC=fold change