

Table S1

Top Upregulated				
Gene ID	Gene Description	E3 Counts	E4 Counts	padj
LOC119745626	uncharacterized	41528	80	1.78E-49
LOC119746463	eukaryotic translation initiation factor 5A-1-like	4529	1	5.64E-48
LOC119741506	cyclic AMP-dependent transcription factor ATF-3-like	21718	83	1.33E-42
LOC119735925	matrix metalloproteinase-18-like	5793	22	1.43E-39
LOC119722448	beta-1,3-glucan-binding protein-like	1582	0	1.60E-38
LOC119737579	chromobox protein homolog 8-like	17058	128	3.27E-36
LOC119736918	uncharacterized	6029	42	2.47E-35
LOC119738310	high choriolytic enzyme 1-like	2543	12	4.30E-35
LOC119740974	reticulocyte binding protein 2 homolog b-like	1795	5	5.10E-35
LOC119727425	uncharacterized	1083	0	7.78E-35
LOC119738421	uncharacterized	1081	0	7.78E-35
LOC119737034	cytochrome P450 3A6-like	3584	24	2.78E-34
LOC119743565	adenylate cyclase type 10-like	1001	0	4.21E-34
LOC119746280	highly reducing polyketide synthase ZEA2-like	10182	97	9.57E-34
LOC119730869	development-specific protein LVN1.2a	959	0	1.04E-33

Top Downregulated				
Gene ID	Gene Description	E3 Counts	E4 Counts	padj
LOC119722077	uncharacterized	0	653	3.03E-29
LOC119741163	Acetylcholine receptor subunit alpha	6	1076	1.05E-28
LOC119725586	uncharacterized LOC119725586	108	4920	4.78E-24
LOC119722078	putative glutamate synthase [NADPH]	1	396	4.04E-23
LOC119730635	T-box transcription factor TBX2-like	11	772	2.13E-22
LOC119723130	phospholipase A2 AP-PLA2-I-like	2	405	2.32E-22
LOC119735275	protein mesh-like	0	306	4.22E-22
LOC119744245	fibrillin-2-like	56	2073	2.37E-21
LOC119728568	protein mab-21-like 2	7	556	3.36E-21
LOC119727609	heart- and neural crest derivatives-expressed protein 2-like	3	349	4.14E-20
LOC119734622	protein PERCC1-like	0	242	5.91E-20
LOC119735654	zinc finger protein 567-like	0	239	7.67E-20
LOC119723154	integrase/recombinase xerD homolog	0	236	9.07E-20
LOC119737744	development-specific protein LVN1.2b	10	553	1.01E-19
LOC119746085	homeobox protein HB1-like	4	344	3.19E-19

Table S2

#	Gene	LOC	RT-qPCR Primer Sequence	In situ Primer Sequence
1	PmFibrillin2_F PmFibrillin2_R	LOC119744245	CATCGATGAGTGCCGTATTG GTTGATGCACTGACCACCAC	GCACAGCTGAGTACAATTTACTGTGCCCAAGAGGTC GATCATTAGGTGACACTATAGCGCCATCGTGCACTCATCAATATCCAGACAACCTG
2	PmBATMAN_F PmBATMAN_R	LOC119745626	ATCGGTTGGGTCTCTGAGTG GAAGCTGGAAGTCGGTTTTG	GAGGTTACCGGGGACGAGGACGTGGGCGTGGG GATCATTAGGTGACACTATAGGATCTGCGTCTTCATCTTGCCACCTTGCTCTG
3	PmEIF5A1_F PmEIF5A1_R	LOC119746463	CACGTCAAGCGTGAGGATTA TTGGGCAGTTTCTTCAAACC	CGAGGAAGACTAAAGCGAGTAAGAAGACGCAGAAAG GATCATTAGGTGACACTATAGGGTGCCGAGCTCTCCCTCCGGCAAACGAATGTCGC
4	PmLvN1.2_F PmLvN1.2_R	LOC119730869	GTCTACCTGGGCGACCATAA AGGCACCGTGAAGTATTTGG	GAGTTTCATTTCTATCCGCAAATCCGGCCAGGCAATTC GATCATTAGGTGACACTATAGCGATTTGTTCTACCGTCACCCGTCGGGATGAATGTG
5	PmATF3_F PmATF3_R	LOC119741506	CCGCCCAAACCTCAGTATAA TTTCGTTCTGCAGCTTTTCA	GCGCTGGCGACATATCTACTGGTCAAAACACCTTAC GATCATTAGGTGACACTATAGCAGAGTTACTTTATTTCTGAAAATAATCTGTGTTAGTA
6	PmLOX2A_F PmLOX2A_R	LOC119735518	Not tested	AGGTAGTGTGCCGTCAGCTT GATCATTAGGTGACACTATAGGCCACCAGATTGTCTGGATT
7	PmHSPG_F PMHSPG_R	LOC119744428	GACTTTCACTGACGGGGTGT GTTATCTCCCCTGATCCAA	GGGTTGCGAGCCCAATGAGTACCGGTGTGCCAGC GATCATTAGGTGACACTATAGGTTCCCTTCCAGGACGATGTCCGGCGTGAGGTCC
8	PmVasa_F PmVasa_R	LOC119728304	See table S3	CGGTCCAGAAGTACGGGATA TAATACGACTCACTATAGGGGTAGAAGCTGGTTGCCTTGC

Table S3

Gene	qPCR Primer Sequence
PmNanos3qF PmNanos3qR	CCGAAGAGTTGACGAGGAAG CAACTCCAAGCACCCACAG
PmPiwi_qF PmPiwi_qR	AAAAGAACCGCTTCCAGGAT CGCTCATCCTTCTTCTTTGG
PmWnt3_qF PmWnt3_qR	CTGATCTACTACGACCCGTCACC CTGGCACCCATCTATGGCGT
PmWnt8_qF PmWnt8_qR	GGGCAGAAACCCAGAACGAC TACAGCTCCGTGCTTCCCAC
PmVasa_qF PmVasa_qR	TGGCTGATGCTCAACAAGAC AAAGTTTCCGCCTCCGTAAT
PmFoxA_qF PmFoxA_qR	GTCTCTCAGTGGCGCAAGAT TGGCGCATATAATCCTCACC
PmNodal_qF PmNodal_qR	CCAACACGGCATGGAGTTTG AGTTGGTCTCGGATGTGCTG
PmUbi_qF PmUbi_qR	TTCGGTGAAAGCCAAGATTC CCCACCTCTCATGGCTAGAA
PmBMP2/4_qF PmBMP2/4_qR	TCGCAGACATCCTCTGTACG TGGGGACTGGCTGAGTTTAC
PmMYP_qF PmMYP_qR	CCATCAGCACAAAGAAAGCA TCTTGACAGCATCCGTCTTG
PmErg_qF PmErg_qR	AAGATGACCGACCCGGACGA TGCCGTGGACCTTGGTCATA