

Supplementary Table S1. Genes comprised in the main categories displayed in Figure 2B of gene ontology classification of biological processes of up-regulated and down-regulated genes.

GO term	Regulation	Number of annotated genes	Gene symbols
Cellular process	Up	36	<i>AFP, ANO3, BORCS6, CBLC, CCL20, CDK1, CDK3, CLDN6, CXCL10, CXCL8, ENPEP, FOXG1, HTRA3, IFIT2, IFIT3, INHBB, ISG15, KCTD14, LIF, LOC100157935, LOC100516302, LOC110255217, MLC1, PKP3, PLP1, PLPPR2, PPP1R1B, RGS5, RSAD2, SDCBP2, SEMA3A, SERPINB2, SLITRK5, SPRY3, SYCE1L, TMIGD3</i>
	Down	10	<i>APOD, CA3, CRABP1, DEFB1, KCNJ3, LOC100621701, NPSR1, PIWIL2, RASL10A, SYT17</i>
Biological regulation	Up	28	<i>AFP, ANO3, CBLC, CCL20, CDK1, CDK3, CXCL10, CXCL8, ENPEP, FOXG1, HTRA3, IFIT3, INHBB, ISG15, LIF, LOC100516302, LOC110255217, MLC1, PKP3, PLP1, PLPPR2, RGS5, RSAD2, SEMA3A, SERPINB2, SLITRK5, SPRY3, TMIGD3</i>
	Down	7	<i>APOD, CRABP1, DEFB1, NPSR1, PIWIL2, RASL10A, SYT17</i>
Regulation of biological process	Up	26	<i>AFP, CBLC, CCL20, CDK1, CDK3, CXCL10, CXCL8, FOXG1, HTRA3, IFIT3, INHBB, ISG15, LIF, LOC100516302, LOC110255217, MLC1, PKP3, PLP1, PLPPR2, RGS5, RSAD2, SEMA3A, SERPINB2, SLITRK5, SPRY3, TMIGD3</i>
	Down	7	<i>APOD, CRABP1, DEFB1, NPSR1, PIWIL2, RASL10A, SYT17</i>
Response to stimulus	Up	25	<i>AFP, CBLC, CCL20, CDK1, CDK3, CXCL10, CXCL8, FOXG1, IFIT2, IFIT3, INHBB, ISG15, LIF, LOC100153139, LOC106504372, LOC110255217, MLC1, OASL, PLP1, PLPPR2, RGS5, RSAD2, SEMA3A, SLITRK5, SPRY3</i>
	Down	5	<i>APOD, CRABP1, DEFB1, LOC100525396, RASL10A</i>
Metabolic process	Up	20	<i>AFP, CBLC, CCL20, CDK1, CDK3, CXCL8, ENPEP, FOXG1, INHBB, ISG15, LIF, LOC100157935, LOC100516302, LOC100526118, MMP1, PKP3, PLP1, PLPPR2, RSAD2, TMIGD3</i>
	Down	5	<i>APOD, CA3, CRABP1, PIWIL2, SQLE</i>
Localization	Up	18	<i>AFP, ANO3, BORCS6, CCL20, CDK1, CXCL10, CXCL8, ENPEP, FOXG1, INHBB, LIF, LOC100157935, MLC1, PKP3, RSAD2, SEMA3A, SYCE1L, TMIGD3</i>
	Down	5	<i>APOD, DEFB1, KCNJ3, NPSR1, SYT17</i>
Multicellular organismal process	Up	16	<i>AFP, CDK1, CDK3, CXCL10, CXCL8, ENPEP, FOXG1, GUCA1A, INHBB, ISG15,</i>

			<i>LIF, PLP1, RSAD2, SEMA3A, SLITRK5, SPRY3</i>
	Down	6	<i>APOD, CRABP1, DEFB1, LOC100621701, PIWIL2, SYT17</i>
Signaling	Up	17	<i>AFP, CBLC, CCL20, CDK3, CXCL10, CXCL8, INHBB, LIF, LOC110255217, PLP1, PLPPR2, PPP1R1B, RGS5, RSAD2, SEMA3A, SLITRK5, SPRY3</i>
	Down	5	<i>APOD, CRABP1, DEFB1, LOC100621701, RASL10A</i>
Developmental process	Up	14	<i>AFP, CDK1, CDK3, CXCL10, CXCL8, FOXG1, INHBB, ISG15, LIF, PLP1, RSAD2, SEMA3A, SLITRK5, SPRY3</i>
	Down	6	<i>APOD, CRABP1, DEFB1, LOC100621701, PIWIL2, SYT17</i>
Positive regulation of biological process	Up	16	<i>CCL20, CDK1, CDK3, CXCL10, CXCL8, FOXG1, INHBB, ISG15, LIF, LOC110255217, MLC1, PKP3, PLP1, RSAD2, SEMA3A, SLITRK5</i>
	Down	4	<i>DEFB1, NPSR1, PIWIL2, SYT17</i>
Negative regulation of biological process	Up	16	<i>CBLC, CDK1, CXCL10, CXCL8, FOXG1, IFIT3, INHBB, ISG15, LIF, LOC100516302, PKP3, RGS5, RSAD2, SEMA3A, SERPINB2, TMIGD3</i>
	Down	3	<i>APOD, NPSR1, PIWIL2,</i>
Immune system process	Up	11	<i>CCL20, CXCL10, CXCL8, IFIT3, ISG15, LIF, LOC100153139, LOC106504372, LOC110255217, OASL, RSAD2</i>
	Down	3	<i>APOD, DEFB1, LOC100525396</i>
Interspecies interaction among organisms	Up	9	<i>CCL20, CXCL10, CXCL8, IFIT3, ISG15, LOC110255217, OASL, RSAD2, SYCE1L</i>
	Down	1	<i>DEFB1</i>
Locomotion	Up	7	<i>CCL20, CXCL8, CXCL10, ENPEP, FOXG1, SEMA3A, TMIGD3</i>
	Down	2	<i>APOD, DEFB1</i>
Reproduction	Up	5	<i>AFP, CDK1, INHBB, LIF, SEMA3A</i>
	Down	2	<i>DEFB1, PIWIL2</i>
Reproductive process	Up	5	<i>AFP, CDK1, INHBB, LIF, SEMA3A</i>
	Down	2	<i>DEFB1, PIWIL2</i>
Multi-organism process	Up	4	<i>AFP, CDK1, INHBB, LIF</i>
	Down	2	<i>DEFB1, PIWIL2</i>
Growth	Up	2	<i>HTRA3, SEMA3A</i>
	Down	2	<i>APOD, SYT17</i>
Biological adhesion	Up	1	<i>CXCL8</i>
	Down	2	<i>APOD, LOC100621701</i>
Behavior	Up	1	<i>SLITRK5</i>
	Down	-	-
Biom mineralization	Up	1	<i>ISG15</i>
	Down	-	-
Rhythmic process	Up	1	<i>AFP</i>
	Down	-	-

Supplementary Table S2. Genes comprised in the main categories displayed in Figure 2C of gene ontology classification of cellular processes of genes.

GO term	Regulation	Number of annotated genes	Gene symbols
Cellular anatomical entity	Up	41	<i>AFP, ANO3, BORCS6, CBLC, CCL20, CDK1, CDK3, CLDN6, CXCL10, CXCL8, ENPEP, FOXG1, GUCA1A, HTRA3, IFIT3, INHBB, ISG15, LIF, LOC100153139, LOC100157935, LOC100516302, LOC106504372, LOC110255217, MLC1, MMP1, NRM, PI15, PKP3, PLP1, PLPPR2, RGS5, RSAD2, SDCBP2, SEMA3A, SERPINB2, SERPINB7, SLITRK5, SPRY3, SYCE1L, TMEM45B, TMIGD3</i>
	Down	15	<i>APOD, CA3, CPNE4, CRABP1, DEFB1, KCNJ3, LOC100525396, LOC100621701, NPSR1, PIWIL2, RASL10A, SHISA3, SQLE, SYT17, TECTB</i>
Intracellular	Up	21	<i>AFP, BORCS6, CBLC, CCL20, CDK1, CDK3, CXCL8, ENPEP, FOXG1, IFIT3, INHBB, LIF, LOC100157935, LOC110255217, MLC1, NRM, PKP3, RGS5, RSAD2, SDCBP2, SYCE1L</i>
	Down	7	<i>APOD, CA3, CRABP1, DEFB1, PIWIL2, SQLE, SYT17</i>
Protein-containing complex	Up	8	<i>BORCS6, CDK1, CDK3, LOC100153139, LOC100157935, LOC106504372, PKP3, SLITRK5</i>
	Down	3	<i>APOD, KCNJ3, PIWIL2</i>

Supplementary Table S3. Genes comprised in the main categories displayed in Figure 2D according to Kyoto Encyclopedia of Genes and Genomes (KEGG).

Pathways	Number of annotated genes	Differentially expressed genes
Viral myocarditis	5	<i>LOC110256649, LOC106504372, LOC100153139, LOC110258821</i> and <i>BGI_novel_G000045</i>
Hepatitis C	5	<i>IFIT1, IFIT3, IFIT2, CXCL8</i> and <i>CLDN6</i>
Chemokine signaling	6	<i>CXCL10, BGI_novel_G000048, LOC100525396, CCL20, CXCL8</i> and <i>LOC110255211</i>
Herpes infection	8	<i>IFIT1, IFIT3, IFIT2, LOC106504372, LOC100153139, CDK1, MAP3K7CL</i> and <i>SHISA3</i>
NOD-like receptor	5	<i>GVIN1, BGI_novel_G000048, LOC100525396, CXCL8</i> and <i>MAP3K7CL</i>
Influenza A	5	<i>CXCL10, RSAD2, LOC106504372, LOC100153139</i> and <i>CXCL8</i>

Supplementary Table S4. Characteristics of primers used in RT-qPCR according to MIQE guidelines.

Gene symbol	Accession		Sequence	Amplicon length	Exons	[Primer]	Efficiency
<i>Sus scrofa</i>							
<i>PPP1R1B</i>	XM_021067044.1	Sense	GGCACCACCTCAAGTCGAAG	99	NA	0.08 μ M	99%
	XM_021067045.1	Antisense	TGATGGACTGCAGGTGAGAC				
	XM_021067046.1						
	XM_021067047.1						
<i>OASL</i>	NM_001031790.1	Sense	GTGTGGTTGGTCGAGGAAGT	98	2	0.08 μ M	101%
		Antisense	CTGTAGGCAGGCATGATGGT				
<i>PPP4R4</i>	XM_021099655.1	Sense	ATATGCCTGTCTCCCACACG	115	NA	0.2 μ M	97 %
	XM_021099656.1	Antisense	TGAAGCTGCCTTTTGCACAG				
	XM_021099657.1						
	XM_021099658.1						
	XM_021099659.1						
	XM_021099660.1						
	XM_021099661.1						
	XM_021099662.1						
<i>HES4</i>	XM_003481929.4	Sense	GAAAGAGAGTTCCCGCCACT	181	NA	0.2 μ M	99 %
		Antisense	GACCAGGAATCGGTTACCT				
<i>NEURL3</i>	XM_003124839.5	Sense	CATGGATCCTACAGCCAGCG	203	NA	0.2 μ M	102%
		Antisense	GGCATTGGCCGTGTCTTTG				
<i>HTD2</i>	XM_003132274.4	Sense	GTGGGGTTGGACTGAATGCT	97	NA	0.2 μ M	98%
	XM_021069097.1	Antisense	ATGTCCAAGGGTAAGGCAGC				
	XM_021069098.1						
	XM_003132275.4						
<i>CYP2C32</i>	XM_013983597.2	Sense	GCCCGCATGGAGCTATTTTT	115	NA	0.08 μ M	96%
		Antisense	CGTGGCTGAACCCACTATAAA				
<i>AFP</i>	NM_214317.1	Sense	AGAGGAACAACCTTGAGGCCG	107	13/14	0.1 μ M	101%
		Antisense	TCAGTGCTGGACCCCTCTCT				
<i>TMEM45B</i>	XM_021063152.1	Sense	TTGTGCTGGAGCTTTTCCGA	109	NA	0.2 μ M	98%
	XM_021063153.1	Antisense	TTCTGGTCCCATTGAGGTGC				
	XM_021063154.1						
	XM_021063155.1						

XM_021063156.1							
<i>ENPEP</i>	NM_214017.1	Sense	TATCTGTGCAGCGGTAGTGG	286	1	0.1 µM	102%
		Antisense	GGAGATGTTCACTGTCCCCG				
<i>LOC110256649</i>	XM_021072807.1	Sense	ACAACACGGCTGAAGGTAGG	199	NA	0.2 µM	102%
		Antisense	TCTGAGGTGGGATCAAAAGG				
<i>CYP2J34</i>	NM_001244633.1	Sense	AGCGGTTTGACTACCAGGATG	91	4/5	0.2 µM	100%
		Antisense	AGCTGGACCTGCACTGATGTG				
<i>LOC100526118</i>	XM_003128792.4	Sense	GGTTATCCGGTGGCTTCTGG	152	NA	0.1 µM	101%
		Antisense	TCTGGACCAACTTCATGCCA				
<i>SI00A2</i>	XM_001929556.5	Sense	GGTTGCCACCTTCCACAAGTA	203	NA	0.08 µM	102%
		Antisense	CCAGGAAAACGGCATACTCC				
<i>SPRY3</i>	XM_013986552.2	Sense	CAGCATTACGCCCTCACCTT	96	NA	0.2 µM	100%
	XM_003135510.5	Antisense	GCTTCTCCCTTCAGAGCACC				
<i>FOXG1</i>	XM_021099188.1	Sense	TATGAGAAGCCGCCGTTTCAG	171	NA	0.2 µM	100%
		Antisense	GAGGGACAGATTGTGGCGAA				
<i>GTSF1</i>	XM_003126205.6	Sense	AGCCCTGCAAGCAACATAGT	87	NA	0.2 µM	98%
	XM_005663861.3	Antisense	TGGCAGAACATACGGCAGAG				
<i>SQLE</i>	NM_001101026.1	Sense	GCAGCTATTCTCCAGGCCAA	191	8/10	0.2 µM	99%
		Antisense	AGCGCAACTGGACCACTAAT				
<i>CHL1</i>	XM_021069243.1	Sense	CTGCAAACAATGACCCTGTGT	154	NA	0.2 µM	102%
	XM_021069244.1	Antisense	GGAGGCAGCCCAGAAAGAAT				
	XM_021069246.1						
	XM_013981901.2						
	XM_021069247.1						
	XM_021069248.1						
	XM_021069249.1						
	XM_021069250.1						
<i>UBA52</i>	NM_214211.1	Sense	CTGCCGCAAGTGTTATGCTC	100	4/5	0.2 µM	102%
		Antisense	TTTGACCTTCTTCTTGGGGCG				

NA, Not Applicable

Gene symbol	Accession		Sequence	Amplicon length	Exon	[Primer]	Efficiency
<i>Homo sapiens</i> genes							
<i>PP1R1B</i>	NM_032192	Sense	GGGCACCATCTCAAGTCGAA	126	4/5	0.2 µM	92%
	NM_181505	Antisense	TGAGGCCTGGTTCTCATTCA				
<i>AFP</i>	NM_001134.3	Sense	CTTTGGGCTGCTCGCTATGA	176	5/6	0.2 µM	91%
	NM_001354717	Antisense	ATGGCTTGGAAGTTCGGGT		6/7		
<i>TMEM45B</i>	NM_001331210.2	Sense	CTCTGTTCGGAGGGTGTGTT	158	5/6	0.2 µM	95%
	NM_138788.5	Antisense	GTCCCATTGCGGTGTTCCAA		4/5		
	NM_001331211.2				5/6		
	NM_001331212.2				5/6		
<i>ENPEP</i>	NM_001977.4	Sense	GAAGAGCTTACCCCCAGCAG	120	1	0.4 µM	100%
	NM_001379611.1	Antisense	GACTTGTCCGTTCTCCGTGT				
	NM_001379612.1						
	NM_001379613.1						
<i>SPRY3</i>	NM_005840.4	Sense	TGAACAGCTGCGCTCTACTC	237	2	0.4 µM	98%
	NM_001304990.2	Antisense	GCAGTGGTGCTATGGGACAT		3		
	NM_001394353.1				4		
	NM_001394354.1				4		
	NM_001394355.1				4		
<i>SQLE</i>	NM_003129.4	Sense	GCCTGCCTTTCATTGGCTTC	90	1/2	0.2 µM	99%
		Antisense	TTCCTTTTCTGCGCCTCCTG				
<i>GAPDH</i>				132	4/5	0.2 µM	95%
	NM_002046.7	Sense	CAAATTCCATGGCACCGTCA		3/4		
	NM_001256799.3	Antisense	GACTCCACGACGTACTCAGC		4/5		
	NM_001289745.3				3/4		
	NM_001289746.2						

Gene symbol	Accession		Sequence	Amplicon length	Exon	[Primer]	Efficiency
Mouse genes							
<i>Ppp1r1b</i>	NM_144828.2	Sense	CCCAACCCCTGTGCCTATAC	119	4/5	0.3 µM	90%
	NM_001313970.1	Antisense	TCCCGAAGCTCCCCTAACTC				
<i>Afp</i>	NM_007423.4	Sense	AGTTTCCAGAACCTGCCGAG	145	4/5	0.1 µM	100%
		Antisense	ACCTTGTCGTACTGAGCAGC				
<i>Tmem45b</i>	NM_144936.1	Sense	TCGGGATAACATCGTGCTGG	115	4/5	100 µM	0.2%
		Antisense	GTCCCATTTCTGGCCTTCCAA				
<i>Enpep</i>	NM_007934.3	Sense	GCAAACCCACTCGTGACCTA	188	1	0.2 µM	97%
		Antisense	CAGCCGATAGACACTGTCCC				
<i>Spry3</i>	NM_001030293.3	Sense	GCTCTCCCACGCAGTATCAG	111	4	0.2 µM	98%
	NM_001401849.1	Antisense	TTGATCAGAGGCAGTGGTGC				
	NM_001401850.1						
	NM_001401851.1						
<i>Sqle</i>	NM_009270.3	Sense	TACCTCAGTGTGCGACCTCGT	92	2	0.2 µM	99%
		Antisense	TGGAGAGAACTGCTGCCAAG				
<i>Ppib</i>	NM_011149.2	Sense	GGAGATGGCACAGGAGGAA	72	3/4	0.1 µM	103%
		Antisense	GTAGTGCTTCAGCTTGAAGTTCTCAT				