Equine Veterinary Journal

Supplementary Item 2: Differentially expressed genes at the OG1 vs. CON time.

Gene Name	Gene ID	Fold Change	p-value
syndecan binding protein (syntenin)	SDCBP	3.65	0.00001
biglycan; bone/cartilage proteoglycan I	BGN	-3.36	0.00008
dual specificity phosphatase and pro isomerase domain containing 1	DUPD1	>100	0.00010
heat shock 70kDa protein 8	HSPA8	3.67	0.00012
interleukin 4 receptor	IL4R	2.05	0.00013
tyrosinase-related protein 1	TYRP1	<-100	0.00019
vimentin	VIM	-2.46	0.00023
filamin A interacting protein 1-like; GIP130	FILIP1L	-2.04	0.00047
solute carrier family 26 (sulfate transporter), member 2	SLC26A2	2.54	0.00061
glucose-regulated protein	GRP94	2.50	0.00063
prostaglandin-endoperoxide synthase 1; COX-1	PTGS1	-6.35	0.00068
ubiquitin-conjugating enzyme E2D 1	UBE2D1	>100	0.00089
selenoprotein S	SELS	2.04	0.00111
S100 calcium binding protein A6; calcyclin	S100A6	2.50	0.00112
secreted protein, acidic, cysteine-rich (osteonectin)	SPARC	-2.38	0.00119
hemaglobin alpha chain complex	HBA	<-100	0.00123
mesencephalic astrocyte-derived neurotrophic factor	MANF	2.33	0.00177
gelsolin; actin-depolymerizing factor	GSN	-3.07	0.00179
ephrin B2; EPH-related receptor tyrosine kinase ligand	EFNB2	-3.31	0.00193
RAS protein activator like 2	RASAL2	-2.24	0.00204
thrombospondin 2	THBS2	-2.98	0.00217
prostaglandin E synthase	PTGES	3.94	0.00244
phosphodiesterase 4D, cAMP-specific	PDE4D	-6.88	0.00266
cytochrome c, somatic	CYCS	3.27	0.00339
toll-like receptor 2	TLR2	4.80	0.00360
fasciculation and elongation protein zeta 1 (zygin I)	FEZ1	-6.12	0.00390
beta-defensin-1	BD-1	35.73	0.00417
Yip1 interacting factor homolog A	YIF1A	2.58	0.00440
phosphoribosyl pyrophosphate amidotransferase	PPAT	2.59	0.00469
fibromodulin; keratan sulfate proteoglycan fibromodulin	FMOD	-2.80	0.00519

potassium voltage-gated channel, subfamily H, member 2	KCNH2	<-100	0.00550
prostaglandin F receptor (FP)	PTGFR	>100	0.00564
suppressor of cytokine signaling 3	SOCS3	>100	0.00598
dopamine beta-hydroxylase	DBH	<-100	0.00620
serine/arginine-rich splicing factor 5	SRSF5	-5.19	0.00638
selenoprotein X 1	SEPX1	5.38	0.00645
cortistatin	CORT	<-100	0.00662
C1q and tumor necrosis factor related protein 7	C1QTNF7	<-100	0.00677
hydroxyprostaglandin dehydrogenase 15-(NAD)	HPGD	<-100	0.00704
MAS-related GPR, member F; G protein-coupled receptor RTA	MRGPRF	<-100	0.00716
decorin	DCN	-3.89	0.00788
GM2 ganglioside activator	GM2A	-2.94	0.00893
matrix metallopeptidase 3 (stromelysin 1, progelatinase)	MMP3	>100	0.00899
aryl hydrocarbon receptor interacting protein	AIP	2.11	0.00959
family with sequence similarity 96, member A	FAM96A	>100	0.00992
transferrin receptor (p90, CD71)	TFRC	11.02	0.01031
selenoprotein P, plasma, 1	SEPP1	-3.33	0.01077
superoxide dismutase 2, mitochondrial	SOD2	46.16	0.01138
peptidyl arginine deiminase, type II	PADI2	-7.68	0.01249
non-metastatic cells 1, protein	NME1	5.49	0.01348
integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	ITGB3	2.26	0.01434
scleraxis	SCX	<-100	0.01447
chemokine (C-X-C motif) ligand 2; MIP-2a; GRO-2	CXCL2_dup1	>100	0.01543
calcitonin-related polypeptide alpha	CALCA	<-100	0.01806
kit oncogene	KIT	<-100	0.01811
tripartite motif containing 34	TRIM34	>100	0.01844
N-myc (and STAT) interactor	NMI	>100	0.01883
interleukin 1 receptor antagonist	IL1RN	5.69	0.01946
phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	>100	0.01957
chemokine (C-C motif) ligand 2; MCP-1	CCL2	>100	0.01962
thioredoxin reductase 1	TXNRD1	2.88	0.02002
caspase 1; ICE; IL-1 beta-converting enzyme	CASP1	>100	0.02133
PC4 and SFRS1 interacting protein 1	PSIP1	-3.52	0.02209
deafness, autosomal dominant 5	DFNA5	<-100	0.02283
chemokine (C-C motif) receptor 2; MCP-1 receptor	CCR2	<-100	0.02309
interleukin 12b; IL-12 p40	IL12B	>100	0.02400

glial fibrillary acidic protein	GFAP	2.57	0.02555
toll-like receptor 4	TLR4	4.17	0.02567
tumor necrosis factor (ligand) superfamily, member 12	TNFSF12	-3.79	0.02628
chemokine (C-X-C motif) ligand 6	CXCL6	>100	0.02632
tryptophan hydroxylase 2	TPH2	<-100	0.02729
aryl hydrocarbon receptor nuclear translocator-like	ARNTL	>100	0.02736
ADAM metallopeptidase with thrombospondin type 1 motif, 4	ADAMTS4	>100	0.02755
melanocortin 1 receptor	MC1R	>100	0.02796
matrix metallopeptidase 13 (collagenase 3)	MMP13	>100	0.02830
ISG12 protein-like; interferon, alpha-inducible protein 27	ISG12(A)	-2.19	0.02866
hexokinase 2	HK2	2.82	0.02917
solute carrier family 5 (sodium/glucose cotransporter), member 1	SLC5A1	2.42	0.02926
selectin E	SELE	>100	0.02935
steroidogenic acute regulatory protein	STAR	<-100	0.02972
tumor necrosis factor receptor superfamily, member 13	TNFRSF13C	<-100	0.03033
secretory Phospholipase A2	SPLA2	<-100	0.03126
COX-2; prostaglandin-endoperoxide synthase 2	PTGS2	9.27	0.03191
peripheral myelin protein 22	PMP22	5.77	0.03342
phosphofructokinase, muscle	PFKM	-2.23	0.03361
phosphorylase, glycogen, muscle	PYGM	<-100	0.03376
collagen, type XIV, alpha 1	COL14A1	-2.02	0.03420
chemokine (C-C motif) ligand 8; MCP-2	CCL8	>100	0.03455
COX10 homolog, cytochrome c oxidase assembly protein	COX10	3.06	0.03477
5-hydroxytryptamine (serotonin) receptor 2A, G protein-coupled	HTR2A	>100	0.03496
regulator of chromosome condensation 1	RCC1	2.15	0.03692
C25H9orf100 chromosome 9 open reading frame 100 ortholog	C25H9orf100	<-100	0.03894
serum amyloid A1	SAA1	68.00	0.03895
chemokine (C-C motif) ligand 13; MCP-4	CCL13	>100	0.03948
sphingosine-1-phosphate receptor 1	S1PR1	>100	0.03998
antimicrobial peptide NK-lysin	NKL	<-100	0.04002
DEFA35L Paneth cell-specific alpha-defensin 35L	DEFA35L	>100	0.04219
CD2 molecule; LFA-3 recpetor	CD2	<-100	0.04231
H19 fetal liver mRNA	H19	<-100	0.04253
fin bud initiation factor homolog	FIBIN	<-100	0.04282

TIMP metallopeptidase inhibitor 1	TIMP1	5.01	0.04343
erythropoietin	EPO	<-100	0.04563
CD1a6 molecule	CD1A6	>100	0.04640
fibroblast growth factor 1 (acidic)	FGF1	<-100	0.04802
TNNI3 interacting kinase	TNNI3K	<-100	0.04824
C13H16orf93 chromosome 16 open reading frame 93 ortholog	C13H16orf93	<-100	0.04832
bone morphogenetic protein 7	BMP7	-2.78	0.04850

*** Large fold change (Fc) values (either negative or positive) were obtained for some genes due to the fact that the value 0.001 was used in place of 0 for samples in which expression was undetectable via RNA Seq to allow for mathematical analysis of the results; >100 (for increases in Fc) or <-100 (for decreases in Fc) are used for genes in which this was performed.*