Equine Veterinary Journal

Supplementary Item 3: Differentially expressed genes at the OG1 vs. DEV time.

Gene Name	Gene ID	Fold Change	p-value
inducible nitric oxide synthase	INOS	<-100	0.0001
heat shock 70kDa protein 8	HSPA8	6.27	0.0002
gelsolin; actin-depolymerizing factor; brevin	GSN	-4.17	0.0002
tumor protein p53	TP53	2.03	0.0005
cytochrome c, somatic	CYCS	2.21	0.0006
scleraxis	SCX	<-100	0.0006
Yip1 interacting factor homolog A	YIF1A	4.18	0.0006
secreted protein, acidic, cysteine-rich (osteonectin)	SPARC	-2.24	0.0007
aryl hydrocarbon receptor interacting protein	AIP	7.98	0.0010
isocitrate dehydrogenase 1 (NADP+), soluble	IDH1	-2.23	0.0011
serine/arginine-rich splicing factor 5	SRSF5	-6.20	0.0011
glucose-regulated protein	GRP94	2.77	0.0014
matrix metallopeptidase 1 (interstitial collagenase)	MMP1	>100	0.0019
pleckstrin homology domain containing, family A	PLEKHA8	>100	0.0022
prostaglandin E synthase	PTGES	3.96	0.0029
bone morphogenetic protein 7	BMP7	-3.19	0.0029
selenoprotein I	SELI	2.18	0.0037
serine/arginine-rich splicing factor 7	SRSF7	4.47	0.0038
toll-like receptor 2	TLR2	6.54	0.0039
TNNI3 interacting kinase	TNNI3K	<-100	0.0041
prostaglandin F receptor (FP)	PTGFR	4.93	0.0043
mesencephalic astrocyte-derived neurotrophic factor	MANF	2.11	0.0052
beta-defensin-1	BD-1	48.00	0.0064
cortistatin	CORT	>100	0.0065
COX10 homolog, cytochrome c oxidase assembly protein	COX10	3.04	0.0067
syndecan binding protein (syntenin)	SDCBP	2.53	0.0072
thioredoxin reductase 1	TXNRD1	>100	0.0072
cadherin 11	CDH11	>100	0.0076
prostaglandin-endoperoxide synthase 1; COX-1	PTGS1	-4.16	0.0090
synaptojanin 2 binding protein	SYNJ2BP	>100	0.0092
thrombospondin 2	THBS2	-2.34	0.0094
protein kinase, AMP-activated, alpha 1 catalytic subunit	PRKAA1	2.65	0.0097
N-myc (and STAT) interactor	NMI	>100	0.0105
hydroxyprostaglandin dehydrogenase 15-(NAD)	HPGD	<-100	0.0109

S100 calcium binding protein A6	S100A6	2.01	0.0111
C1q and tumor necrosis factor related protein 7	C1QTNF7	<-100	0.0111
matrix metallopeptidase 3 (stromelysin 1, progelatinase)	MMP3	>100	0.0116
CD2 molecule; T-cell surface antigen CD2	CD2	<-100	0.0124
nuclear receptor subfamily 5, group A, member 1; steroidogenic factor-1	NR5A1	<-100	0.0126
caspase 1; interleukin 1 beta-converting enzyme; ICE-1	CASP1	>100	0.0129
interleukin 1 receptor antagonist	IL1R1	2.16	0.0129
tyrosinase-related protein 1	TYRP1	<-100	0.0156
GM2 ganglioside activator	GM2A	-2.90	0.0162
interleukin 1 receptor antagonist	IL1RN	>100	0.0167
ADP-ribosylation factor 4	ARF2	>100	0.0174
biglycan; bone/cartilage proteoglycan I	BGN	-3.15	0.0175
colony stimulating factor 3 (granulocyte)	CSF3	<-100	0.0176
integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	ITGB3	7.30	0.0200
lipopolysaccharide-induced TNF factor	LITAF	-3.64	0.0202
integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	ITGA2B	-4.02	0.0203
superoxide dismutase 2, mitochondrial	SOD2	32.04	0.0205
vitamin D (1,25- dihydroxyvitamin D3) receptor	VDR	2.89	0.0210
solute carrier family 2 (facilitated glucose transporter), member 1; GLUT1	SLC2A1	-2.24	0.0211
selenoprotein P, plasma, 1	SEPP1	-2.72	0.0225
phosphoribosyl pyrophosphate amidotransferase	PPAT	>100	0.0228
solute carrier family 5 (inositol transporters), member 3	SLC5A3	3.16	0.0231
24-dehydrocholesterol reductase	DHCR24	2.19	0.0239
2'-5'-oligoadenylate synthetase 2, 69/71kDa	OAS2	>100	0.0240
transferrin receptor (p90, CD71)	TFRC	19.32	0.0250
striatin, calmodulin binding protein 3	STRN3	2.15	0.0250
apolipoprotein B mRNA-editing enzyme-catalytic polypeptide-like 3Z1b	APOBEC3Z1B	<-100	0.0250
inhibin, beta A	INHBA	<-100	0.0253
fibroblast growth factor 1 (acidic)	FGF1	<-100	0.0266
interleukin 6	IL6	>100	0.0277
serine/threonine kinase 31	STK31	<-100	0.0284
cytochrome p450 3A93	CYP3A93	<-100	0.0299
CD1c molecule	CD1C	<-100	0.0300
beta-2 microglobulin	B2M	2.01	0.0305
endothelin receptor type A	EDNRA	>100	0.0309
hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	HSD3B1	<-100	0.0327

melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	MC1R	>100	0.0329
fasciculation and elongation protein zeta 1 (zygin I)	FEZ1	-4.22	0.0344
cytochrome P450 2C92	CYP2C92	<-100	0.0349
suppressor of cytokine signaling 3	SOCS3	>100	0.0352
chemokine (C-C motif) ligand 13; MCP_4	CCL13	>100	0.0358
matrix metallopeptidase 13 (collagenase 3)	MMP13	55.41	0.0365
amiloride-sensitive cation channel 3	ACCN3	<-100	0.0366
Fc fragment of IgE, low affinity II, receptor for (CD23)	FCER2	<-100	0.0373
chemokine (C-X-C motif) ligand 2; MIP-2a	CXCL2_dup1	>100	0.0374
killer cell lectin-like receptor	LY49C	<-100	0.0375
estrogen receptor 1	ESR1	<-100	0.0377
secretory Phospholipase A2	SPLA2	>100	0.0386
hemoglobin, alpha 1	HBA_dup1	<-100	0.0401
toll-like receptor 4	TLR4	5.11	0.0402
endothelin 2	EDN2	<-100	0.0406
TIMP metallopeptidase inhibitor 1	TIMP1	7.41	0.0409
phosphofructokinase, muscle	PFKM	-2.59	0.0415
CD14 molecule	CD14	5.51	0.0417
fibroblast growth factor 2 (basic); heparin-binding growth factor 2	FGF2	<-100	0.0420
regulator of chromosome condensation 1	RCC1	2.25	0.0420
non-metastatic cells 1, protein (NM23A)	NME1	4.17	0.0434
myxovirus (influenza virus) resistance 1, interferon-inducible protein p78	MX1	>100	0.0437
deafness, autosomal dominant 5	DFNA5	<-100	0.0438
interferon delta 1	IFND1	<-100	0.0447
transient receptor potential cation channel, subfamily V, member 5	TRPV5	>100	0.0450
steroid sulfatase (microsomal), isozyme S	STS	<-100	0.0458
inhibin, alpha	INHA	<-100	0.0458
solute carrier family 11 , member 1	SLC11A1	>100	0.0461
leptin	LEP	>100	0.0462
prostaglandin-endoperoxide synthase 2; COX-2	PTGS2	9.51	0.0463
eukaryotic translation initiation factor 2-alpha kinase 2	EIF2AK2	>100	0.0463
chondroadherin-like	CHADL	>100	0.0486
phosphorylase, glycogen, muscle	PYGM	<-100	0.0494
chemokine (C-C motif) ligand 2; MCP-1	CCL2	>100	0.0495

*** 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.*