

**Supplement 4.** List of genes with a lactation by pregnancy interaction effect in the intercaruncular endometrium on d 17 of the cycle or pregnancy. Genes were selected based on an absolute expression value > 40 and P-value <0.01

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value
thyroid hormone receptor interactor 12	<i>TRIP12</i>	<a href="#">514387</a>	0006464 // protein modification process // inferred from electronic annotation /// 0006512 // ubiquitin cycle // inferred from electronic annotation	0.00017
Alanine-glyoxylate aminotransferase 2-like 2	<i>AGXT2L2</i>	<a href="#">537241</a>	---	0.00022
uridine-cytidine kinase 1-like 1	<i>UCKL1</i>	<a href="#">534046</a>	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0006952 // defense response // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation	0.00024
ral guanine nucleotide dissociation stimulator-like 2	<i>RGL2</i>	<a href="#">504334</a>	0007165 // signal transduction // inferred from electronic annotation /// 0007264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 0051056 // regulation of small GTPase mediated signal transduction // inferred from e	0.00024
HemK methyltransferase family member 1	<i>HEMK1</i>	<a href="#">515459</a>	0006306 // DNA methylation // inferred from electronic annotation /// 0006479 // protein amino acid methylation // inferred from electronic annotation /// 0032259 // methylation // inferred from electronic annotation	0.00071
sorting and assembly machinery component 50 homolog	<i>SAMM50</i>	<a href="#">618777</a>	---	0.00074

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ubiquitin specific peptidase 20	<i>USP20</i>	<a href="#">505839</a>	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation /// 0006512 // ubiquitin cycle // inferred from electronic annotation	0.00075
Werner helicase interacting protein 1	<i>WRNIP1</i>	782711 /// 788824	0006270 // DNA replication initiation // inferred from electronic annotation /// 0006275 // regulation of DNA replication // inferred from electronic annotation /// 0006281 // DNA repair // inferred from electronic annotation	0.00076
cyclin G associated kinase	<i>GAK</i>	<a href="#">511296</a>	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.0008
alpha-kinase 1	<i>ALPK1</i>	<a href="#">524375</a>	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.00081
Similar to Zinc finger and BTB domain containing 8	<i>LOC521943</i>	<a href="#">521943</a>	---	0.00099
Rho GTPase activating protein 17	<i>ARHGAP17</i>	<a href="#">504245</a>	0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation /// 0007165 // signal transduction // inferred from electronic annotation	0.00129
chromosome 9 open reading frame 100 ortholog	<i>C9orf100</i>	<a href="#">780881</a>	0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation	0.00135
syntaxin 5	<i>STX5</i>	<a href="#">510312</a>	0006810 // transport // inferred from electronic annotation /// 0006886 // intracellular protein transport // inferred from electronic annotation /// 0016192 // vesicle-mediated transport // inferred from electronic annotation	0.00202
suppressor of var1, 3-like 1	<i>SUPV3L1</i>	<a href="#">505988</a>	---	0.00231

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(S. cerevisiae)				
synaptotagmin-like 1	<i>SYTL1</i>	<a href="#">527641</a>	0006810 // transport // inferred from electronic annotation /// 0006886 // intracellular protein transport // inferred from electronic annotation	0.00262
ribosomal protein S15a	<i>RPS15A</i>	<a href="#">337888</a>	0006412 // translation // inferred from electronic annotation	0.00288
Sphingomyelin phosphodiesterase 4, neutral membrane (neutral sphingomyelinase-3)	<i>SMPD4</i>	<a href="#">507207</a>	---	0.003
tubulin tyrosine ligase-like family, member 12	<i>TLL12</i>	<a href="#">511319</a>	0006464 // protein modification process // inferred from electronic annotation	0.00306
nuclear receptor subfamily 4, group A, member 1	<i>NR4A1</i>	<a href="#">528390</a>	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.00308
solute carrier family 15, member 4	<i>SLC15A4</i>	<a href="#">510499</a>	0006857 // oligopeptide transport // inferred from electronic annotation	0.00331
chondroitin sulfate proteoglycan 5 (neuroglycan C)	<i>CSPG5</i>	<a href="#">505866</a>	---	0.00333
zinc finger, FYVE domain containing 26	<i>ZFYVE26</i>	<a href="#">514402</a>	---	0.00354
glucocorticoid modulatory element binding protein 2	<i>GMEB2</i>	<a href="#">508301</a>	---	0.00367

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Biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen)	<i>BPHL</i>	<a href="#">505457</a>	---	0.00375
AT rich interactive domain 5A (MRF1-like)	<i>ARID5A</i>	<a href="#">524118</a>	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.00382
reelin	<i>RELN</i>	<a href="#">281450</a>	0000904 // cellular morphogenesis during differentiation // inferred from sequence or structural similarity /// 0001764 // neuron migration // inferred from sequence or structural similarity /// 0007417 // central nervous system development // inferred fr	0.00383
solute carrier family 38, member 2	<i>SLC38A2</i>	<a href="#">338044</a>	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation /// 0006814 // sodium ion transport // inferred from electronic annotation /// 0006865 // amino acid transport // inferred from	0.00384
DPH2 homolog (S. cerevisiae)	<i>DPH2</i>	<a href="#">768224</a>	---	0.00388
dachsous 1 (Drosophila)	<i>DCHS1</i>	<a href="#">515576</a>	0007156 // homophilic cell adhesion // inferred from electronic annotation	0.00394
transforming, acidic coiled-coil containing protein 2	<i>TACC2</i>	<a href="#">533768</a>	---	0.00413
transforming growth factor, beta receptor associated protein 1	<i>TGFBRAP1</i>	<a href="#">514660</a>	---	0.00417

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CDNA clone IMAGE:8433672	---	---	---	0.00417
hypothetical protein LOC508334	<i>LOC508334</i>	<a href="#">508334</a>	---	0.00443
hect domain and RLD 2	<i>HERC2</i>	<a href="#">535440</a>	0006464 // protein modification process // inferred from electronic annotation /// 0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0006512 // ubiquitin cycle // inferred from electronic annotation	0.00465
NLR family member X1	<i>NLRX1</i>	<a href="#">539974</a>	---	0.0049
chromosome 15 open reading frame 44 ortholog	<i>C10H15orf4</i> 4	<a href="#">534159</a>	---	0.00508
similar to FLJ10769 protein	<i>LOC613996</i>	<a href="#">613996</a>	---	0.00526
GTP binding protein 1	<i>GTPBP1</i>	<a href="#">513922</a>	0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation	0.0054
polymerase (RNA) I polypeptide A, 194kDa	<i>POLR1A</i>	<a href="#">536316</a>	---	0.00541
similar to poly-(ADP- ribose) polymerase II /// similar to poly (ADP- ribose) polymerase 2	<i>LOC505828</i> /// <i>LOC783580</i>	505828 /// 783580	0006471 // protein amino acid ADP-ribosylation // inferred from electronic annotation /// 0006508 // proteolysis // inferred from electronic annotation	0.00541
similar to putative E3 ubiquitin ligase	<i>LOC540077</i>	<a href="#">540077</a>	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation /// 0030071 // regulation of mitotic	0.00556

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			metaphase/anaphase transition // inferred from electronic annotation	
zinc finger protein 142	<i>ZNF142</i>	<a href="#">511573</a>	---	0.00562
similar to Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	<i>LOC514916</i>	<a href="#">514916</a>	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.00576
HECT domain containing 3	<i>HECTD3</i>	<a href="#">513646</a>	0006464 // protein modification process // inferred from electronic annotation /// 0006512 // ubiquitin cycle // inferred from electronic annotation /// 0030071 // regulation of mitotic metaphase/anaphase transition // inferred from electronic annotation	0.00586
similar to AIM1	<i>LOC526200</i>	<a href="#">526200</a>	---	0.00617
replication initiator 1	<i>REPIN1</i>	<a href="#">511510</a>	0006260 // DNA replication // inferred from electronic annotation	0.00635
dual specificity phosphatase 12	<i>DUSP12</i>	<a href="#">505302</a>	0006470 // protein amino acid dephosphorylation // inferred from electronic annotation /// 0016311 // dephosphorylation // inferred from electronic annotation	0.00644
adaptor-related protein complex 3, delta 1 subunit	<i>AP3D1</i>	<a href="#">281023</a>	0006461 // protein complex assembly // inferred from electronic annotation /// 0006810 // transport // inferred from electronic annotation /// 0006886 // intracellular protein transport // inferred from electronic annotation /// 0015031 // protein transpo	0.00659
centrobin, centrosomal BRCA2 interacting protein	<i>CNTROB</i>	<a href="#">539106</a>	---	0.00672
sialic acid acetyltransferase	<i>SIAE</i>	<a href="#">507461</a>	---	0.00702

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transformation/transcription domain-associated protein	<i>TRRAP</i>	<a href="#">507169</a>	---	0.00716
ADP-ribosylation factor-like 2	<i>ARL2</i>	<a href="#">511349</a>	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation	0.00723
Microtubule associated monooxygenase, calponin and LIM domain containing 2	<i>MICAL2</i>	<a href="#">534041</a>	0006725 // aromatic compound metabolic process // inferred from electronic annotation	0.00735
ectonucleoside triphosphate diphosphohydrolase 4	<i>ENTPD4</i>	<a href="#">531411</a>	---	0.00752
mahogunin, ring finger 1	<i>MGRN1</i>	<a href="#">616130</a>	---	0.0076
isovaleryl Coenzyme A dehydrogenase	<i>IVD</i>	<a href="#">510440</a>	0008152 // metabolic process // inferred from electronic annotation /// 0055114 // oxidation reduction // inferred from electronic annotation	0.00772
kelch domain containing 3	<i>KLHDC3</i>	<a href="#">541138</a>	0007126 // meiosis // inferred from electronic annotation	0.00778
hypothetical LOC618886	<i>LOC618886</i>	<a href="#">618886</a>	---	0.00788
kinesin family member 3B	<i>KIF3B</i>	<a href="#">508404</a>	0007018 // microtubule-based movement // inferred from electronic annotation	0.00792
crooked neck pre-mRNA splicing factor-like 1 (Drosophila)	<i>CRNKL1</i>	<a href="#">526536</a>	---	0.00802
minichromosome maintenance complex	<i>MCM3AP</i>	<a href="#">534293</a>	---	0.00803

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component 3 associated protein				
nuclear receptor binding protein 2	<i>NRBP2</i>	<a href="#">504664</a>	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.00837
coenzyme Q6 homolog, monooxygenase (S. cerevisiae)	<i>COQ6</i>	<a href="#">511624</a>	0006725 // aromatic compound metabolic process // inferred from electronic annotation /// 0006744 // ubiquinone biosynthetic process // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation /// 0055114	0.00878
hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	<i>HEXDC</i>	<a href="#">506184</a>	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation	0.00882
2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	<i>DERA</i>	<a href="#">534558</a>	0008152 // metabolic process // inferred from electronic annotation /// 0009264 // deoxyribonucleotide catabolic process // inferred from electronic annotation	0.00894
similar to hexokinase II	<i>LOC614107</i>	<a href="#">614107</a>	0006096 // glycolysis // inferred from electronic annotation	0.00898
adenylate cyclase 6	<i>ADCY6</i>	<a href="#">509936</a>	0007242 // intracellular signaling cascade // inferred from electronic annotation /// 0009190 // cyclic nucleotide biosynthetic process // inferred from electronic annotation	0.00902
similar to Ras-GTPase-activating protein SH3-domain-binding protein	<i>LOC783166</i>	<a href="#">783166</a>	---	0.00904
COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	<i>COPS7B</i>	<a href="#">617995</a>	---	0.00918



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jumonji domain containing 1A	<i>JMJD1A</i>	<a href="#">536073</a>	0007242 // intracellular signaling cascade // inferred from electronic annotation	0.00919
ribosomal protein L21	<i>RPL21</i>	<a href="#">326584</a>	0006412 // translation // inferred from electronic annotation	0.00919
Arginine and glutamate rich 1	<i>ARGLU1</i>	<a href="#">540543</a>	---	0.0092
WD repeat domain 5	<i>WDR5</i>	<a href="#">100125836</a>	---	0.00938
spastic paraplegia 11 (autosomal recessive)	<i>SPG11</i>	<a href="#">507819</a>	---	0.00947