J. Dairy Sci. 95:5657–5675
http://dx.doi.org/10.3168/jds.2011-5114

Supplement 3. List of genes affected by lactation 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. Fold effect and regulation columns consider the effects of lactation using the endometrium from non-lactating cows as the reference. (i.e. Down regulation means the endometrium from a non-lactating cow has a lower gene expression than the endometrium of a lactating cow)

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	**P-value**	**Fold Effect**	**Regulation**
retinyl ester hydrolase type 1	*BREH1*	497207	---	0.0028379	0.43	Down
dickkopf homolog 1 (Xenopus laevis)	*DKK1*	504445	0007275 // multicellular organismal development // inferred from electronic annotation /// 0030178 // negative regulation of Wnt receptor signaling pathway // inferred from electronic annotation	0.002016	0.52	Down
actin, alpha 2, smooth muscle, aorta	*ACTA2*	515610	0030240 // muscle thin filament assembly // inferred from sequence or structural similarity /// 0048741 // skeletal muscle fiber development // inferred from sequence or structural similarity	0.0068066	0.53	Down
carbonic anhydrase XI	*CA11*	326334	0006730 // one-carbon compound metabolic process // inferred from electronic annotation	0.000727	0.53	Down
hairy/enhancer-of-split related with YRPW motif-like	*HEYL*	538609	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0007219 // Notch signaling pathway // inferred from electronic	0.0007698	0.56	Down

J. Dairy Sci. 95:5657–5675
http://dx.doi.org/10.3168/jds.2011-5114

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value	Fold Effect	Regulation
			annotation /// 0007275 // m			
cell growth regulator with EF-hand domain 1	*CGREF1*	507586	---	0.0001387	0.57	Down
MAS-related GPR, member F	*MRGPRF*	615886	0007186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation	0.0030688	0.59	Down
transmembrane protein 88	*TMEM88*	507172	---	8.55E-06	0.59	Down
remodeling and spacing factor 1	*RSF1*	541248	---	0.0091683	0.59	Down
Dickkopf homolog 1 (Xenopus laevis)	*DKK1*	504445	---	0.0065874	0.60	Down
tenomodulin	*TNMD*	532034	---	0.0004339	0.60	Down
EGF-like-domain, multiple 8	*EGFL8*	782820	---	0.000844	0.61	Down
Fc fragment of IgG, low affinity IIb, receptor (CD32)	*FCGR2B*	282229	---	0.0007528	0.61	Down
chromosome 21 open reading frame 7 ortholog	*C1H21ORF7*	540879	---	0.0009234	0.63	Down
placental growth factor	*PGF*	280894	0001525 // angiogenesis // inferred from electronic annotation /// 0001658 // ureteric bud branching // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from	0.0008491	0.63	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value	Fold Effect	Regulation
			electronic annotation /// 0008283 // cell prol			
calponin 1, basic, smooth muscle	*CNN1*	534583	0031032 // actomyosin structure organization and biogenesis // inferred from electronic annotation	0.0057248	0.63	Down
tenomodulin	*TNMD*	781292	---	0.0077429	0.64	Down
proline rich 15	*PRR15*	538952	---	0.000313	0.64	Down
transmembrane protein 100	*TMEM100*	613987	---	0.0023752	0.64	Down
hypothetical LOC515053	*LOC515053*	515053	---	0.0031781	0.66	Down
major facilitator superfamily domain containing 2	*MFSD2*	512633	---	0.0053781	0.66	Down
Coiled-coil-helix-coiled-coil-helix domain containing 6	*CHCHD6*	615934	---	0.0024265	0.68	Down
hemicentin 1	*HMCN1*	521326	---	0.006747	0.69	Down
epoxide hydrolase 1, microsomal (xenobiotic)	*EPHX1*	535293	0009636 // response to toxin // inferred from electronic annotation	0.0063922	0.70	Down
FLYWCH family member 2	*FLYWCH2*	618572	---	0.0002608	0.70	Down
carbonic anhydrase VB, mitochondrial	*CA5B*	514494	0006730 // one-carbon compound metabolic process // inferred from electronic annotation	0.0054674	0.70	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value	Fold Effect	Regulation
tumor necrosis factor, alpha-induced protein 6	*TNFAIP6*	493710	0007155 // cell adhesion // inferred from electronic annotation	0.0001667	0.70	Down
microcephalin 1	*MCPH1*	100125236	---	0.0013684	0.71	Down
lectin, mannose-binding 2-like	*LMAN2L*	539289	0015031 // protein transport // inferred from electronic annotation	0.00377	0.72	Down
hypothetical LOC618094	*LOC618094*	618094	---	0.0005474	0.72	Down
folate receptor 2 (fetal)	*FOLR2*	507672	---	0.0036608	0.72	Down
phosphatidylethanolamine N-methyltransferase	*PEMT*	360197	0006644 // phospholipid metabolic process // inferred from electronic annotation /// 0008654 // phospholipid biosynthetic process // inferred from electronic annotation	0.0050417	0.72	Down
dimethylglycine dehydrogenase	*DMGDH*	504453	---	0.0062243	0.72	Down
fasciculation and elongation protein zeta 1 (zygin I)	*FEZ1*	511751	---	0.0082663	0.72	Down
S100 calcium binding protein A4	*S100A4*	282343	---	0.0010621	0.72	Down
similar to B0432.9	*LOC505636*	505636	---	0.0009182	0.73	Down
similar to nonclathrin coat	*LOC616222*	616222	---	0.0012836	0.73	Down

J. Dairy Sci. 95:5657–5675
http://dx.doi.org/10.3168/jds.2011-5114

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	**P-value**	**Fold Effect**	**Regulation**
protein zeta-COP						
Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	*FCGR3A*	281766	---	0.0013428	0.73	Down
BEX family member 5	*BEX5*	516056	---	0.0023283	0.73	Down
similar to RP5-860F19.3	*LOC506470*	506470	---	0.0010319	0.73	Down
chromosome 12 open reading frame 57 ortholog	*C5H12ORF57*	511545	---	0.000367	0.74	Down
sideroflexin 3	*SFXN3*	511755	0006812 // cation transport // inferred from electronic annotation	0.0068119	0.74	Down
XTP3-transactivated protein A	*XTP3TPA*	614103	---	0.0049676	0.75	Down
homeodomain interacting protein kinase 1	*HIPK1*	512233	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.0020695	0.75	Down
CDNA clone IMAGE:8067330	---	---	---	0.0009851	0.75	Down
similar to OB-cadherin-1 /// cadherin 11, type 2, OB-cadherin (osteoblast)	*CDH11 /// LOC535363*	535363 /// 785475	0007155 // cell adhesion // inferred from electronic annotation /// 0007156 // homophilic cell adhesion // inferred from electronic annotation	0.0041965	0.75	Down
GRP1 (general receptor for phosphoinositides 1)-	*GRASP*	507181	---	0.0060476	0.76	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	**P-value**	**Fold Effect**	**Regulation**
associated scaffold protein						
LATS, large tumor suppressor, homolog 2 (Drosophila)	*LATS2*	508208	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation	0.0031044	0.76	Down
potassium channel tetramerisation domain containing 11	*KCTD11*	539167	0001558 // regulation of cell growth // inferred from electronic annotation /// 0006813 // potassium ion transport // inferred from electronic annotation /// 0007049 // cell cycle // inferred from electronic annotation /// 0007275 // multicellular organis	0.0041659	0.76	Down
kallikrein 1	*KLK1*	493738	0006508 // proteolysis // inferred from electronic annotation	0.0066673	0.76	Down
similar to RCL	*LOC613560*	613560	---	0.0058554	0.77	Down
galactose-1-phosphate uridylyltransferase	*GALT*	506997	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0006012 // galactose metabolic process // inferred from electronic annotation	0.0001244	0.77	Down
hypothetical protein LOC783163	*LOC783163*	783163	---	0.0057849	0.78	Down
potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	*KCNN2*	404177	0006813 // potassium ion transport // inferred from electronic annotation	0.0098628	0.78	Down

J. Dairy Sci. 95:5657–5675
http://dx.doi.org/10.3168/jds.2011-5114

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value	Fold Effect	Regulation
tubulin, beta 6	*TUBB6*	534206	0007017 // microtubule-based process // inferred from electronic annotation /// 0007018 // microtubule-based movement // inferred from electronic annotation /// 0051258 // protein polymerization // inferred from electronic annotation	0.0012553	0.78	Down
hypothetical protein MGC128424	*MGC128424*	767924	---	0.0058502	0.78	Down
similar to tigger transposable element derived 5	*LOC540422*	540422	---	0.0008992	0.79	Down
minichromosome maintenance complex component 5	*MCM5*	506970	0006260 // DNA replication // inferred from electronic annotation /// 0006270 // DNA replication initiation // inferred from electronic annotation /// 0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcripti	0.0052936	0.79	Down
brain expressed X-linked 2	*BEX2*	768028	---	0.0060616	0.79	Down
hypothetical LOC535329	*LOC535329*	535329	---	0.0052257	0.79	Down
doublecortin-like kinase 1	*DCLK1*	613449	0007242 // intracellular signaling cascade // inferred from electronic annotation	0.0072226	0.79	Down
mediator complex subunit 29	*MED29*	614626	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic	0.0025694	0.79	Down

J. Dairy Sci. 95:5657–5675
http://dx.doi.org/10.3168/jds.2011-5114

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	**P-value**	**Fold Effect**	**Regulation**
			annotation			
Hypothetical protein LOC538173	*LOC538173*	538173	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation	0.0077394	0.79	Down
Zinc finger protein 45	*ZNF45*	540342	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.0035491	0.79	Down
transmembrane protein 119	*TMEM119*	510926	---	0.0031039	0.80	Down
ATP-binding cassette, sub-family D (ALD), member 1	*ABCD1*	515178	0006810 // transport // inferred from electronic annotation	0.0071784	0.80	Down
tumor suppressing subtransferable candidate 4	*TSSC4*	509559	---	0.0043477	0.80	Down
mitochondrial ribosomal protein L48	*MRPL48*	615873	0006412 // translation // inferred from electronic annotation	0.0026401	0.81	Down
Family with sequence similarity 33, member A	*FAM33A*	615847	0007049 // cell cycle // inferred from electronic annotation /// 0007067 // mitosis // inferred from electronic annotation /// 0051301 // cell division // inferred from electronic annotation	0.0013308	0.81	Down
brain protein 44-like	*BRP44L*	767977	---	0.0044743	0.81	Down
similar to NAC-beta splice /// NLR family, pyrin domain	*LOC528166 /// NLRP1*	528166 /// 790698	0006952 // defense response // inferred from electronic annotation	0.0013802	0.81	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value	Fold Effect	Regulation
containing 1						
lectin, galactoside-binding, soluble, 1 (galectin 1)	*LGALS1*	326598	0043123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from electronic annotation /// 0045445 // myoblast differentiation // inferred from electronic annotation	0.0009417	0.81	Down
Hypothetical LOC538666	*MGC139309*	538666	---	0.0037929	0.81	Down
Islet cell autoantigen 1, 69kDa	*ICA1*	535346	---	0.0055213	0.81	Down
Progestin and adipoQ receptor family member III	*PAQR3*	534876	---	0.0005713	0.82	Down
BCL2-associated athanogene 3	*BAG3*	782633	0006915 // apoptosis // inferred from electronic annotation	3.15E-05	0.82	Down
transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	*TGM2*	281528	0018149 // peptide cross-linking // inferred from electronic annotation	0.0084226	0.82	Down
DNL-type zinc finger	*DNLZ*	514124	0045449 // regulation of transcription // inferred from electronic annotation	0.0009163	0.82	Down
mediator complex subunit 11	*MED11*	511672	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.0062011	0.82	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	**P-value**	**Fold Effect**	**Regulation**
glyoxylate reductase/hydroxypyruvate reductase	*GRHPR*	504764	0008152 // metabolic process // inferred from electronic annotation	0.0071698	0.82	Down
KIAA0922-like	*LOC505156*	505156	---	0.0032555	0.82	Down
CDC28 protein kinase regulatory subunit 1B	*CKS1B*	615827	0007049 // cell cycle // inferred from electronic annotation /// 0051301 // cell division // inferred from electronic annotation	0.0055198	0.82	Down
chromosome 6 open reading frame 129 ortholog	*C23H6orf129*	507353	---	0.001545	0.82	Down
catechol-O-methyltransferase domain containing 1	*COMTD1*	514949	---	0.0090101	0.82	Down
nicolin 1	*NICN1*	614730	---	0.005362	0.82	Down
chromatin accessibility complex 1	*CHRAC1*	510942	---	0.0001791	0.83	Down
chromosome 6 open reading frame 145 ortholog /// hypothetical protein LOC782137	*C23H6orf145 /// LOC782137*	613986 /// 782137	0007154 // cell communication // inferred from electronic annotation	0.0094924	0.83	Down
ribonuclease H2, subunit C	*RNASEH2C*	505618	---	0.0071696	0.83	Down
hydroxymethylbilane synthase	*HMBS*	515614	0006779 // porphyrin biosynthetic process // inferred from electronic annotation /// 0006783 // heme biosynthetic process //	0.0040218	0.83	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	**P-value**	**Fold Effect**	**Regulation**
			inferred from electronic annotation /// 0033014 // tetrapyrrole biosynthetic process // inferred from electronic annotation			
mitochondrial ribosomal protein S26	*MRPS26*	516004	---	0.0031196	0.83	Down
hypothetical protein LOC613274	*LOC613274*	613274	---	0.0027544	0.83	Down
nucleosome assembly protein 1-like 5	*NAP1L5*	508508	0006334 // nucleosome assembly // inferred from electronic annotation	0.003815	0.84	Down
tetraspanin 6	*TSPAN6*	514741	---	0.0061109	0.84	Down
hypothetical LOC515954	*LOC515954*	515954	---	0.0036999	0.84	Down
coiled-coil domain containing 124	*CCDC124*	510778	---	0.0039946	0.84	Down
DnaJ (Hsp40) homolog, subfamily C, member 19	*DNAJC19*	513918	0006810 // transport // inferred from electronic annotation /// 0007601 // visual perception // inferred from electronic annotation /// 0015031 // protein transport // inferred from electronic annotation /// 0048806 // genitalia development // inferred fr	0.0033814	0.84	Down
four and a half LIM domains 3	*FHL3*	504795	---	0.0099134	0.84	Down

J. Dairy Sci. 95:5657–5675
http://dx.doi.org/10.3168/jds.2011-5114

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peroxisomal biogenesis factor 11 gamma	*PEX11G*	506518	0016559 // peroxisome fission // inferred from electronic annotation	0.004637	0.84	Down
Zinc finger protein 22 (KOX 15)	*ZNF22*	768051	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.0065009	0.85	Down
nudix (nucleoside diphosphate linked moiety X)-type motif 22	*NUDT22*	533578	---	0.0054617	0.85	Down
calmodulin /// calmodulin 3 (phosphorylase kinase, delta)	*CALM3 /// LOC407095*	407095 /// 520277	0007049 // cell cycle // inferred from electronic annotation /// 0043388 // positive regulation of DNA binding // inferred from electronic annotation	0.0067576	0.85	Down
MARVEL domain containing 1	*MARVELD1*	616867	---	0.0027277	0.85	Down
hypothetical LOC537248	*LOC537248*	537248	---	0.006393	0.85	Down
tumor suppressor candidate 1	*TUSC1*	539580	---	0.0079432	0.85	Down
hexamthylene bis-acetamide inducible 2	*HEXIM2*	614679	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.0092405	0.85	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value	Fold Effect	Regulation
hypothetical protein LOC788974	*LOC788974*	788974	---	0.0085347	0.85	Down
family with sequence similarity 32, member A	*FAM32A*	508634	---	0.0077942	0.85	Down
COMM domain containing 4	*COMMD4*	616960	---	0.0066121	0.85	Down
potassium channel tetramerisation domain containing 10	*KCTD10*	540881	0006813 // potassium ion transport // inferred from electronic annotation	0.0004138	0.85	Down
MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	*MID1IP1*	615572	---	0.0003568	0.85	Down
solute carrier family 35, member A4	*SLC35A4*	539354	0008643 // carbohydrate transport // inferred from electronic annotation	0.003682	0.85	Down
hypothetical LOC522040	*MGC143117*	522040	---	0.004216	0.85	Down
solute carrier family 39 (zinc transporter), member 13	*SLC39A13*	614946	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation /// 0006829 // zinc ion transport // inferred from electronic annotation /// 0030001 // metal ion transport // inferred from el	0.0004623	0.85	Down
microtubule-actin crosslinking factor 1	*MACF1*	506730	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0007050 // cell cycle arrest // inferred from	0.009649	0.85	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value	Fold Effect	Regulation
			electronic annotation			
nitrilase 1	*NIT1*	504199	0006807 // nitrogen compound metabolic process // inferred from electronic annotation	0.0025702	0.85	Down
similar to MAK31-like protein	*MGC133554*	538931	0016071 // mRNA metabolic process // inferred from electronic annotation	0.0007782	0.86	Down
similar to PO-GA	*LOC514842*	514842	---	0.005563	0.86	Down
cirrhosis, autosomal recessive 1A (cirhin)	*CIRH1A*	510315	---	0.0084049	0.86	Down
SIVA1, apoptosis-inducing factor	*SIVA1*	617931	0043065 // positive regulation of apoptosis // inferred from electronic annotation	0.006834	0.86	Down
amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)	*APBB1*	505096	---	0.0097578	0.86	Down
WD repeat domain 74	*WDR74*	505875	---	0.0029228	0.86	Down
WW domain binding protein 1	*WBP1*	509188	---	0.0010626	0.86	Down
Josephin domain containing 1	*JOSD1*	510781	---	0.0023964	0.86	Down
glutathione S-transferase pi	*GSTP1*	281806	0008152 // metabolic process // inferred from electronic annotation	0.0042726	0.86	Down
nudix (nucleoside diphosphate	*NUDT3*	618855	---	0.0037449	0.86	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	**P-value**	**Fold Effect**	**Regulation**
linked moiety X)-type motif 3						
SEC14-like 1 (S. cerevisiae)	*SEC14L1*	513449	0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation /// 0006810 // transport // inferred from electronic annotation	0.0064129	0.86	Down
RAB11 family interacting protein 5 (class I)	*RAB11FIP5*	535992	0008152 // metabolic process // inferred from electronic annotation	0.0099549	0.86	Down
Chromosome 3 open reading frame 60 ortholog	*C22H3orf60*	511968	---	0.0043558	0.87	Down
BTB (POZ) domain containing 10	*BTBD10*	505888	0006813 // potassium ion transport // inferred from electronic annotation	0.0028593	0.87	Down
mediator complex subunit 18	*MED18*	540695	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.0019681	0.87	Down
transaldolase 1	*TALDO1*	513453	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0006098 // pentose-phosphate shunt // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation	0.0021399	0.87	Down
transaldolase 1	*TALDO1*	513453	0005975 // carbohydrate metabolic process // inferred from electronic annotation ///	0.0021399	0.87	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	**P-value**	**Fold Effect**	**Regulation**
			0006098 // pentose-phosphate shunt // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation			
nuclear protein localization 4 homolog (S. cerevisiae)	*NPLOC4*	508519	---	0.0084807	0.87	Down
COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)	*COPS6*	512756	---	0.0033381	0.87	Down
flotillin 1	*FLOT1*	532573	---	0.0050366	0.87	Down
elaC homolog 1 (E. coli)	*ELAC1*	532568	0008033 // tRNA processing // inferred from electronic annotation	0.0031362	0.87	Down
clathrin, light polypeptide B (light chain B)	*CLTLB*	281698	0006461 // protein complex assembly // inferred from electronic annotation /// 0006886 // intracellular protein transport // inferred from electronic annotation /// 0016192 // vesicle-mediated transport // inferred from electronic annotation	0.0058922	0.87	Down
eukaryotic translation initiation factor 6	*EIF6*	286811	0006412 // translation // inferred from electronic annotation /// 0042256 // mature ribosome assembly // inferred from electronic annotation	0.006876	0.87	Down
chromosome 19 open reading frame 60 ortholog	*C7H19orf60*	511085	---	0.0009588	0.87	Down

J. Dairy Sci. 95:5657–5675
http://dx.doi.org/10.3168/jds.2011-5114

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ADP-ribosylation factor interacting protein 2 (arfaptin 2)	*ARFIP2*	514938	0030036 // actin cytoskeleton organization and biogenesis // inferred from electronic annotation	0.0009393	0.88	Down
NDRG family member 3	*NDRG3*	514399	---	0.0006719	0.88	Down
suppressor of Ty 4 homolog 1 (S. cerevisiae)	*SUPT4H1*	616425	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from electronic annotation /// 0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferre	0.0094645	0.88	Down
chromosome 3 open reading frame 10 ortholog	*C22H3ORF10*	540092	---	0.007623	0.88	Down
copper metabolism (Murr1) domain containing 1	*COMMD1*	534683	---	0.0072733	0.88	Down
chromosome 16 open reading frame 75 ortholog	*C25H16ORF75*	615553	---	0.0099042	0.88	Down
family with sequence similarity 125, member A	*FAM125A*	507199	---	0.0069884	0.88	Down
small nuclear ribonucleoprotein polypeptide N	*SNRPN*	780877	0016071 // mRNA metabolic process // inferred from electronic annotation	0.0066329	0.88	Down
peptidylprolyl isomerase	*PPIL1*	508179	0006397 // mRNA processing // inferred from electronic annotation /// 0006457 //	0.0028891	0.89	Down

J. Dairy Sci. 95:5657–5675
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(cyclophilin)-like 1			protein folding // inferred from electronic annotation /// 0008380 // RNA splicing // inferred from electronic annotation			
HCLS1 associated protein X-1	*HAX1*	506895	---	0.0064032	0.89	Down
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	*MLLT1*	504458	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.0090453	0.89	Down
RGP1 retrograde golgi transport homolog (S. cerevisiae)	*RGP1*	539393	---	0.0014906	0.89	Down
presenilin enhancer 2 homolog (C. elegans)	*PSENEN*	493993	0006509 // membrane protein ectodomain proteolysis // inferred from electronic annotation /// 0007219 // Notch signaling pathway // inferred from electronic annotation /// 0016485 // protein processing // inferred from electronic annotation /// 0043085 //	0.0035875	0.89	Down
CDC42 effector protein (Rho GTPase binding) 4	*CDC42EP4*	540152	---	0.0018496	0.89	Down
hypothetical LOC506622	*MGC138908*	506622	---	0.0060929	0.89	Down
COMM domain containing 5	*COMMD5*	504807	---	0.0096013	0.89	Down
similar to	*LOC616324*	616324	---	0.0062124	0.89	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value	Fold Effect	Regulation
OTTHUMP00000022229						
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	*NDUFB10*	327701	0006810 // transport // inferred from electronic annotation /// 0055114 // oxidation reduction // inferred from electronic annotation	0.0011604	0.89	Down
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	*NFKBIL1*	514369	---	0.004722	0.90	Down
ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)	*RPIA*	613376	0009052 // pentose-phosphate shunt, non-oxidative branch // inferred from electronic annotation	0.0080445	0.90	Down
hypothetical protein LOC777786	*LOC777786*	777786	---	0.0078997	0.90	Down
mitochondrial NADH:ubiquinone oxidoreductase ESSS subunit	*ESSS*	404161	0006810 // transport // inferred from electronic annotation /// 0055114 // oxidation reduction // inferred from electronic annotation	0.0092196	0.90	Down
synovial sarcoma translocation gene on chromosome 18-like 2	*SS18L2*	618689	---	0.0039869	0.90	Down
transmembrane protein 185A	*TMEM185A*	526189	---	0.004727	0.90	Down
chromosome 17 open reading frame 81 ortholog	*C19H17ORF81*	512976	---	0.0021741	0.90	Down

J. Dairy Sci. 95:5657–5675
http://dx.doi.org/10.3168/jds.2011-5114

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value	Fold Effect	Regulation
deoxynucleotidyltransferase, terminal, interacting protein 1	*DNTTIP1*	505524	---	0.0056551	0.90	Down
PDZ and LIM domain 4	*PDLIM4*	515410	---	0.0099966	0.90	Down
Hypothetical LOC507045	*LOC507045*	507045	---	0.0038383	0.91	Down
canopy 2 homolog (zebrafish)	*CNPY2*	506534	---	0.007249	0.91	Down
archaelysin family metallopeptidase 2	*AMZ2*	515126	---	0.0074735	0.91	Down
protein disulfide isomerase family A, member 2 /// Rho GDP dissociation inhibitor (GDI) gamma	*ARHGDIG /// PDIA2*	504356 /// 613745	0045454 // cell redox homeostasis // inferred from electronic annotation	0.0073757	0.91	Down
neural precursor cell expressed, developmentally down-regulated 8	*NEDD8*	286796	0000723 // telomere maintenance // inferred from electronic annotation /// 0006357 // regulation of transcription from RNA polymerase II promoter // inferred from sequence or structural similarity /// 0006464 // protein modification process // inferred fr	0.0075676	0.91	Down
exosome component 1	*EXOSC1*	506018	---	0.0092675	0.91	Down
cerebrum and skeletal muscle specific transcript 1	*LOC618598*	618598	---	0.0065798	0.91	Down
RNA binding motif protein	*RBM15B*	508868	0045449 // regulation of transcription //	0.0004059	0.91	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	**P-value**	**Fold Effect**	**Regulation**
15B			inferred from electronic annotation			
ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	*ATP6V1F*	282405	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation /// 0015986 // ATP synthesis coupled proton transport // inferred from electronic annotation /// 0015992 // proton transport //	0.0098168	0.91	Down
emerin (Emery-Dreifuss muscular dystrophy)	*EMD*	399681	---	0.0092171	0.91	Down
DnaJ (Hsp40) homolog, subfamily C, member 8	*DNAJC8*	614259	---	0.0074882	0.91	Down
TRM112-like	*TRM112L*	507833	---	0.0050655	0.92	Down
small nuclear RNA activating complex, polypeptide 2, 45kDa	*SNAPC2*	516078	---	0.0008313	0.92	Down
lactate dehydrogenase B	*LDHB*	281275	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0006096 // glycolysis // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation /// 0019642 // anaerobic glycolysis /	0.0014626	0.92	Down
similar to leucine-rich-domain inter-acting protein 1; LeR	*LOC515042*	515042	0006355 // regulation of transcription, DNA-dependent // inferred from electronic	0.0083649	0.94	Down

J. Dairy Sci. 95:5657–5675
http://dx.doi.org/10.3168/jds.2011-5114

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inter-acting protein 1; LEAP1			annotation			
similar to Serine/arginine repetitive matrix protein 2	*LOC534002*	534002	---	0.0067539	1.09	Up
adaptor-related protein complex 3, delta 1 subunit	*AP3D1*	281023	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	0.0067291	1.09	Up
suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	*ST13*	510494	0006950 // response to stress // inferred from electronic annotation	0.0003793	1.09	Up
similar to LBP-1a=transcription factor binding to initiation site of HIV-1 {alternatively spliced}	*LOC785419*	785419	---	0.0069641	1.09	Up
ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	*ARIH1*	508410	0006512 // ubiquitin cycle // inferred from electronic annotation	0.0037756	1.09	Up
pumilio homolog 2 (Drosophila)	*PUM2*	540170	---	0.0035776	1.09	Up
ubiquitin specific peptidase like 1	*USPL1*	788351	0006418 // tRNA aminoacylation for protein translation // inferred from	0.0060813	1.10	Up

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			electronic annotation			
zinc finger, FYVE domain containing 26	*ZFYVE26*	514402	---	0.0038088	1.10	Up
lipin 3	*LPIN3*	521637	---	0.0064708	1.10	Up
eukaryotic translation initiation factor 4E nuclear import factor 1	*EIF4ENIF1*	514108	---	0.0046419	1.10	Up
R3H domain containing 2	*R3HDM2*	613499	---	0.0067453	1.11	Up
NEDD4 binding protein 2-like 2	*N4BP2L2*	541201	---	0.0005451	1.11	Up
similar to KIAA0753	*LOC512933*	512933	---	0.0065387	1.12	Up
fragile X mental retardation, autosomal homolog 1	*FXR1*	536793	0007275 // multicellular organismal development // inferred from electronic annotation /// 0007519 // skeletal muscle development // inferred from electronic annotation /// 0030154 // cell differentiation // inferred from electronic annotation	0.003359	1.13	Up
Outer dense fiber of sperm tails 2	*ODF2*	539043	0007275 // multicellular organismal development // inferred from electronic annotation /// 0007283 // spermatogenesis // inferred from electronic annotation /// 0030154 // cell differentiation // inferred from electronic annotation	0.0045919	1.13	Up

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value	Fold Effect	Regulation
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	*ATP2A2*	540568	0006810 // transport // inferred from electronic annotation /// 0006812 // cation transport // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation	0.0059845	1.13	Up
heat shock 70kDa protein 4	*HSPA4*	536558	---	0.0056599	1.14	Up
protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	*PCMTD2*	505807	0006464 // protein modification process // inferred from electronic annotation	0.0013967	1.14	Up
Bardet-Biedl syndrome 4	*BBS4*	532120	0051297 // centrosome organization and biogenesis // inferred from sequence or structural similarity	0.0039836	1.15	Up
transmembrane protein 167	*TMEM167*	613669	---	0.0081252	1.15	Up
Fc fragment of IgG, receptor, transporter, alpha	*FCGRT*	338062	0006955 // immune response // inferred from electronic annotation /// 0019882 // antigen processing and presentation // inferred from electronic annotation	0.0099525	1.16	Up
Rho guanine nucleotide exchange factor (GEF) 11	*ARHGEF11*	511220	0007242 // intracellular signaling cascade // inferred from electronic annotation /// 0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation	0.0063696	1.16	Up
DnaJ (Hsp40) homolog,	*DNAJB6*	282215	0006457 // protein folding // inferred from	0.0044137	1.17	Up

Gene Title	Gene Symbol	Entrez Gene	Putative Function	P-value	Fold Effect	Regulation
subfamily B, member 6			electronic annotation			
Alstrom syndrome 1	*ALMS1*	533055	---	0.003775	1.17	Up
eukaryotic translation initiation factor 2C, 3	*EIF2C3*	406231	---	0.0076284	1.17	Up
SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	*SH3YL1*	534337	---	0.006273	1.17	Up
Similar to Nesprin-2 (Nuclear envelope spectrin repeat protein 2) (Syne-2) (Synaptic nuclear envelope protein 2) (Nucleus and actin connecting element protein) (Protein NUANCE)	*LOC540504*	540504	---	0.0074571	1.18	Up
A kinase (PRKA) anchor protein (yotiao) 9	*AKAP9*	520784	0008152 // metabolic process // inferred from electronic annotation	0.0029126	1.18	Up
centrosome and spindle pole associated protein 1	*CSPP1*	524180	---	0.0060966	1.19	Up
kinase insert domain receptor (a type III receptor tyrosine kinase)	*KDR*	407170	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // inferred from electronic annotation	0.0084445	1.19	Up
similar to carboxypeptidase D	*LOC532189*	532189	---	0.0002176	1.19	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	**P-value**	**Fold Effect**	**Regulation**
Bardet-Biedl syndrome 5	*BBS5*	528191	---	0.008851	1.19	Up
pericentriolar material 1	*PCM1*	525337	---	0.0071336	1.19	Up
NEDD4 binding protein 2-like 1	*N4BP2L1*	616069	---	0.0050615	1.20	Up
GRAM domain containing 1C	*GRAMD1C*	505581	---	0.0033702	1.20	Up
ganglioside induced differentiation associated protein 2	*GDAP2*	508774	---	0.0038183	1.20	Up
transmembrane 4 L six family member 1	*TM4SF1*	533038	---	0.0091551	1.21	Up
eukaryotic translation initiation factor 2C, 2 /// similar to EIF2C2 protein	*EIF2C2 /// LOC618754*	404130 /// 618754	0006412 // translation // inferred from electronic annotation /// 0031047 // gene silencing by RNA // inferred from electronic annotation	0.002324	1.22	Up
eukaryotic translation initiation factor 2C, 2 /// similar to EIF2C2 protein	*EIF2C2 /// LOC618754*	404130 /// 618754	0006412 // translation // inferred from electronic annotation /// 0031047 // gene silencing by RNA // inferred from electronic annotation	0.002324	1.22	Up
Mediator complex subunit 25	*MED25*	533865	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.0085425	1.22	Up

J. Dairy Sci. 95:5657–5675
http://dx.doi.org/10.3168/jds.2011-5114

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WNK lysine deficient protein kinase 1	*WNK1*	506433	---	0.0001584	1.22	Up
similar to Signal peptide peptidase-like 2A	*LOC530325*	530325	---	0.006624	1.22	Up
solute carrier family 1 (neutral amino acid transporter), member 5	*SLC1A5*	282355	0006810 // transport // inferred from electronic annotation /// 0006835 // dicarboxylic acid transport // inferred from electronic annotation	0.0084736	1.22	Up
human immunodeficiency virus type I enhancer binding protein 1	*HIVEP1*	529115	---	0.0084901	1.22	Up
Zinc finger, DHHC-type containing 23	*ZDHHC23*	512177	---	0.006518	1.22	Up
zinc finger protein 192	*ZNF192*	511794	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.0078616	1.23	Up
Rabaptin, RAB GTPase binding effector protein 2	*RABEP2*	511736	---	0.0023603	1.23	Up
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	*NFKBIZ*	282713	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic	0.0035535	1.23	Up

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			annotation			
neuroplastin	*NPTN*	540039	---	0.0035179	1.24	Up
similar to SEC14 and spectrin domains 1 /// SEC14 and spectrin domains 1	*LOC512176 /// SESTD1*	512176 /// 789054	---	0.0075638	1.24	Up
dihydrofolate reductase	*DHFR*	508809	0006545 // glycine biosynthetic process // inferred from electronic annotation /// 0006730 // one-carbon compound metabolic process // inferred from electronic annotation /// 0009165 // nucleotide biosynthetic process // inferred from electronic annotatio	0.0084086	1.25	Up
eukaryotic translation initiation factor 2-alpha kinase 3	*EIF2AK3*	535820	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.0025297	1.25	Up
Poly(A) polymerase gamma	*PAPOLG*	529071	0006350 // transcription // inferred from electronic annotation /// 0031123 // RNA 3'-end processing // inferred from electronic annotation /// 0043631 // RNA polyadenylation // inferred from electronic annotation	0.0017401	1.26	Up
suppressor of cytokine signaling 2	*SOCS2*	338437	0001558 // regulation of cell growth // inferred from electronic annotation /// 0006512 // ubiquitin cycle // inferred from electronic annotation /// 0007242 // intracellular signaling cascade // inferred	0.0043459	1.26	Up

J. Dairy Sci. 95:5657–5675
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			from electronic annotation /// 0009968 // negative			
Similar to sperm associated antigen 1	*LOC530104*	530104	---	0.0031703	1.26	Up
kinesin family member 27	*KIF27*	536335	---	0.0064639	1.27	Up
Rho-guanine nucleotide exchange factor	*LOC616969*	616969	0007242 // intracellular signaling cascade // inferred from electronic annotation /// 0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation	0.0082533	1.27	Up
Ubiquitin fusion degradation 1 like	*UFD1L*	507124	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation	0.0042013	1.28	Up
Transmembrane BAX inhibitor motif containing 4	*TMBIM4*	513242	---	0.0010393	1.28	Up
serine/threonine protein kinase MST4	*MST4*	539445	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.0030619	1.30	Up
eukaryotic translation initiation factor 4E family member 3	*EIF4E3*	616906	0006412 // translation // inferred from electronic annotation /// 0006413 // translational initiation // inferred from electronic annotation	0.0098587	1.32	Up
similar to carnitine O-palmitoyltransferase	*LOC506812*	506812	---	0.0017725	1.34	Up

J. Dairy Sci. 95:5657–5675
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SLAIN motif family, member 2	*SLAIN2*	534203	---	0.0067929	1.36	Up
angiopoietin-like 4	*ANGPTL4*	509963	0001525 // angiogenesis // inferred from electronic annotation /// 0007165 // signal transduction // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from electronic annotation /// 0030154 // cell differe	0.0090494	1.37	Up
PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	*PAN3*	519743	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.0042416	1.38	Up
Rho guanine nucleotide exchange factor (GEF) 3	*ARHGEF3*	782247	0007242 // intracellular signaling cascade // inferred from electronic annotation /// 0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation	0.0001497	1.41	Up
sperm specific antigen 2	*SSFA2*	538826	---	0.0051964	1.42	Up
RAS guanyl releasing protein 1 (calcium and DAG-regulated)	*RASGRP1*	533125	0051056 // regulation of small GTPase mediated signal transduction // inferred from electronic annotation	0.0063476	1.43	Up
breast carcinoma amplified sequence 1	*BCAS1*	504895	---	0.0063474	1.45	Up
malate dehydrogenase 1B,	*MDH1B*	527943	0005975 // carbohydrate metabolic process // inferred from electronic annotation ///	0.0067785	1.46	Up

J. Dairy Sci. 95:5657–5675
http://dx.doi.org/10.3168/jds.2011-5114

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NAD (soluble)			0006099 // tricarboxylic acid cycle // inferred from electronic annotation /// 0006108 // malate metabolic process // inferred from electronic annotation /// 0008152 // m			
hypothetical protein LOC784592	*LOC784592*	784592	---	0.0022122	1.48	Up
hydroxysteroid dehydrogenase like 2	*HSDL2*	404131	0008152 // metabolic process // inferred from electronic annotation	0.0006974	1.49	Up
pyruvate dehydrogenase kinase, isozyme 4	*PDK4*	507367	0007165 // signal transduction // inferred from electronic annotation /// 0018106 // peptidyl-histidine phosphorylation // inferred from electronic annotation	0.0033818	1.51	Up
aquaporin 4	*AQP4*	281008	0006810 // transport // inferred from electronic annotation	0.0065753	1.56	Up
tubulointerstitial nephritis antigen-like 1	*TINAGL1*	509642	0006508 // proteolysis // inferred from electronic annotation /// 0006810 // transport // inferred from electronic annotation	0.009497	1.56	Up
renal tumor antigen	*RAGE*	616277	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.0097608	1.63	Up
IQ motif containing with AAA domain	*IQCA*	618101	---	0.0074774	1.63	Up

J. Dairy Sci. 95:5657–5675
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SIX homeobox 1	*SIX1*	511371	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0045449 // regulation of transcription // inferred from electronic annotation	0.0004177	1.75	Up
coiled-coil domain containing 39	*CCDC39*	534432	---	0.0038289	1.79	Up
similar to axonemal dynein heavy chain DNAH5	*LOC783755*	783755	---	0.0077247	1.82	Up
IQ motif containing with AAA domain /// similar to IQ motif containing with AAA domain	*IQCA /// LOC787378*	618116 /// 787378	---	0.0083615	1.85	Up
WD repeat domain 16	*WDR16*	505885	---	0.0077216	1.85	Up
ropporin 1-like	*ROPN1L*	515565	0007165 // signal transduction // inferred from electronic annotation	0.0080679	1.85	Up
myostatin	*MSTN*	281187	0007179 // transforming growth factor beta receptor signaling pathway // inferred from electronic annotation /// 0040007 // growth // inferred from electronic annotation /// 0045941 // positive regulation of transcription // inferred from electronic annot	0.0012126	2.04	Up
T-cell receptor delta chain	*TRD@*	404176	---	0.0006777	2.07	Up

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similar to hydrocephalus inducing /// hydrocephalus inducing homolog (mouse)	*HYDIN /// LOC504406*	504406 /// 532419	---	0.0021916	2.13	Up
T-cell receptor delta chain	*TRD@*	404176	---	0.000896	2.48	Up
potassium channel regulator	*KCNRG*	404166	0006813 // potassium ion transport // inferred from electronic annotation	0.0063194	2.72	Up
immunoglobulin light chain, lambda gene cluster /// immunoglobulin lambda-like polypeptide 1	*IGL@ /// IGLL1*	505478 /// 789205	---	0.0018442	4.33	Up
immunoglobulin heavy constant gamma 1	*IGHG1*	281850	---	0.0015763	4.54	Up
immunoglobulin heavy constant gamma 1	*IGHG1*	281850	---	0.0004982	5.07	Up
IgG2a heavy chain constant region	*IgCgamma*	404109	---	0.000702	5.28	Up
immunoglobulin heavy constant gamma 1	*IGHG1*	281850	---	0.0002951	7.83	Up
Glutathione-S-transferase (GST) specific immunoglobulin light chain variable region (partial), anti-GST IgVL1	***	---	---	0.0027767	8.20	Up

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Ig kappa chain	*IGK*	506890	---	0.0006477	9.68	Up
immunoglobin light chain VJ region	*LOC404062*	404062	---	0.0003958	12.49	Up