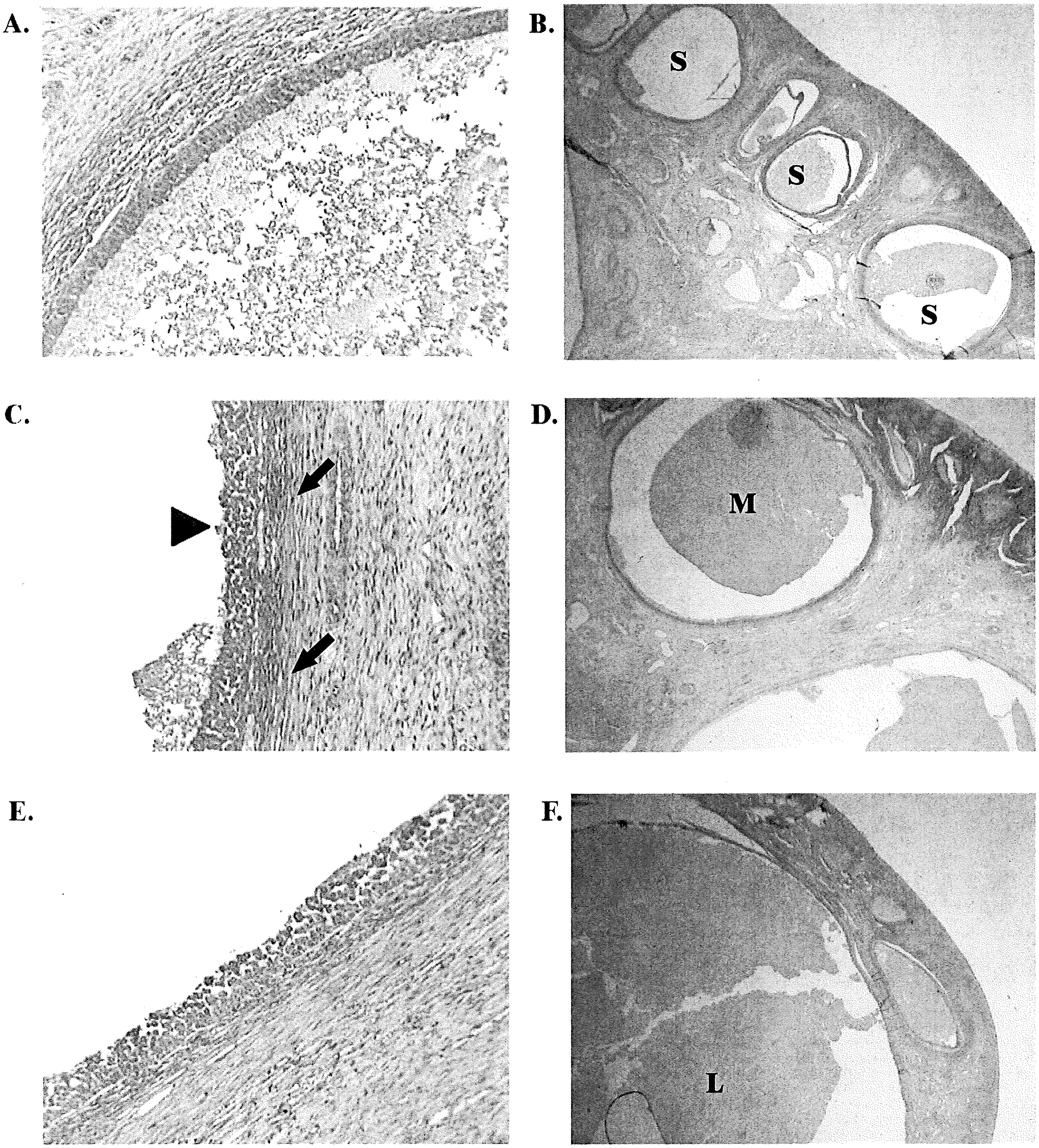
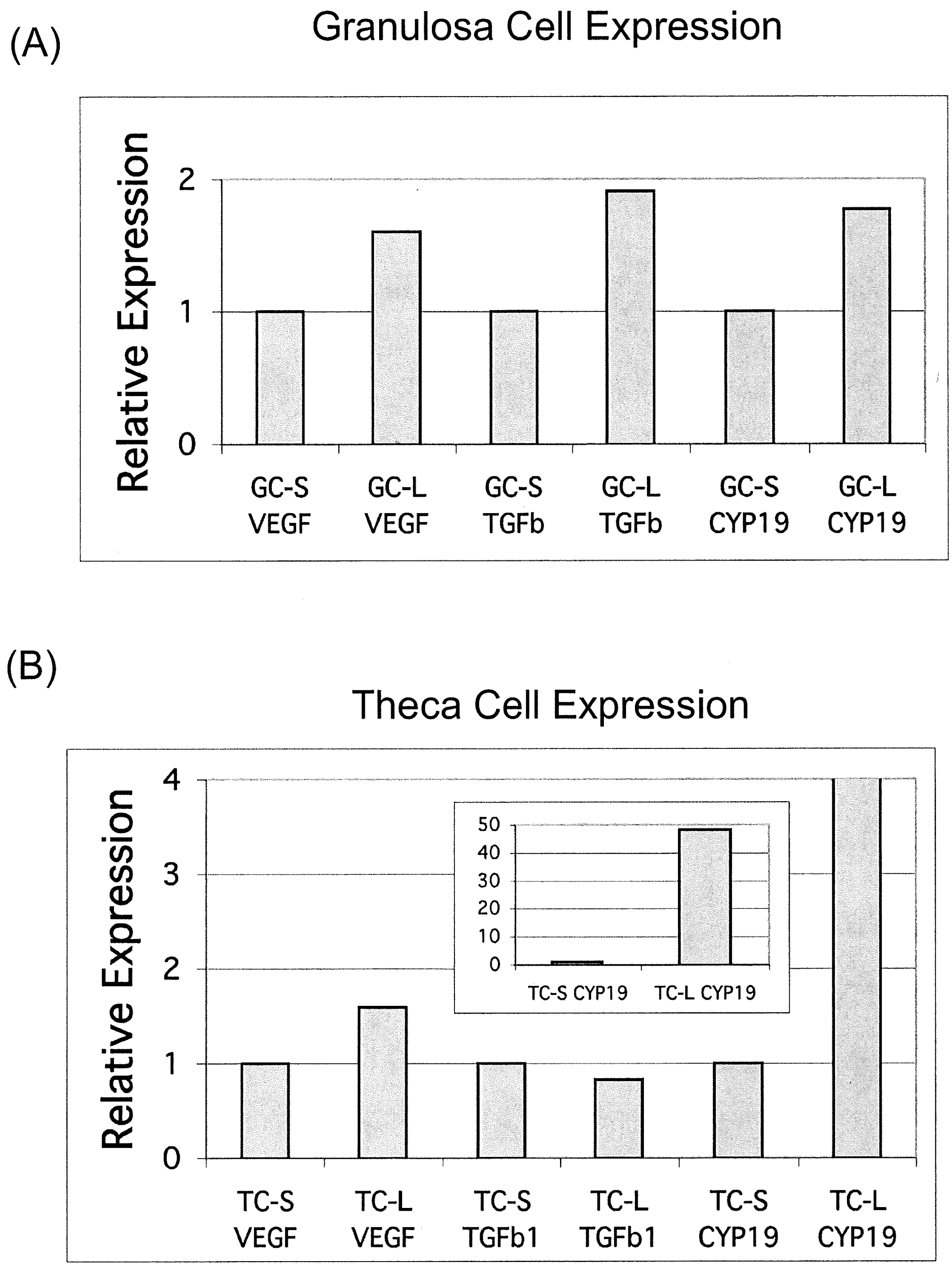
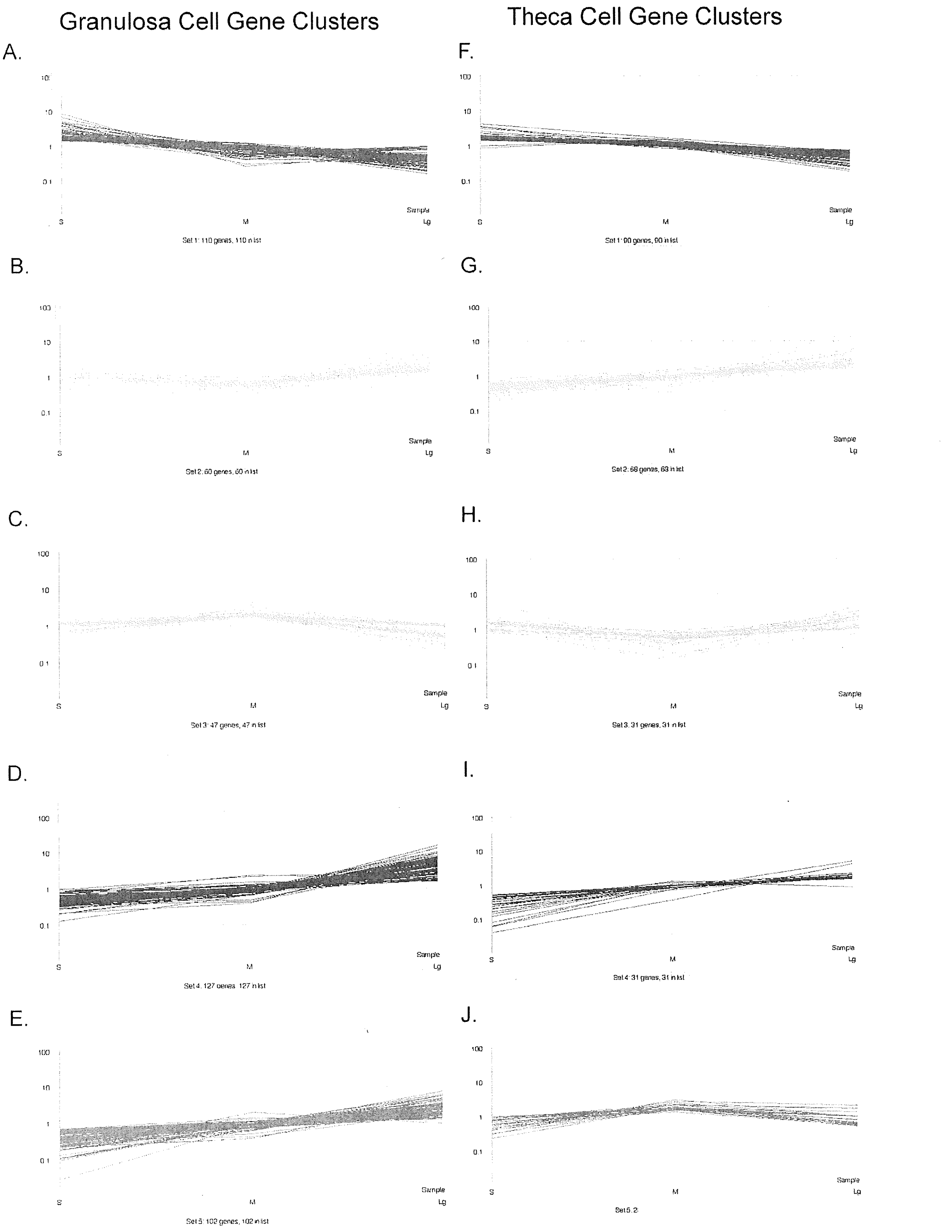


Supplemental Figure S1 (color): Bovine antral follicle morphology for the (A, B) small (S), (C, D) medium (M) and (E, F) large (L) antral follicles. The theca cell layer is indicated with an arrow and granulosa cells with an arrowhead. The follicles A, C and E are at 100X magnification and follicles B, D and F are at 10X magnification. The histology represents the type of follicles used for analysis.



Supplemental Figure S2. Real-time PCR for VEGF, TGFbeta (TGFb) and aromatase (cyp19) in granulosa cell (GC) and theca cells (TC) from small (S) or large (L) follicles. Data was normalized with the constitutively expressed gene S2 and relative expression is presented in comparison with small follicle expression. The mean from pooled follicle samples and two independent sets of RNA are presented.



Supplemental Figure S3: Regulated gene clusters for granulosa cell (A-E) and theca cell (F-J) for small (S), medium (M) and large (Lg) follicle cell isolation. The number of genes are listed for each cluster set with relative expression presented.

Supplmental Table S1

Bovine Granulosa Cell Regulated Genes

Category/Gene Symbol	Microarray Signal				
Apoptosis	S	M	L	GenBank	Description
Casp4	**19**	**45**	**128**	**NM_176638.2**	**caspase 4, apoptosis-related cysteine protease**
Loc509600	**58**	**147**	**1013**	**CB433486**	**similar to glycoprotein (transmembrane) nmb isoform a precursor+F49**
Loc525159	**29**	**50**	**259**	**CK774234**	**similar to UNC-112 related protein 2 short form (LOC525159), predicted**
---	103	64	33	CB437307	Transcribed locus, strongly similar to NP_005698.1 programmed cell death 7
Peg3	417	105	188	CB166978	paternally expressed gene 3
Mgc128158	247	628	383	BE751816	similar to optineurin
Cell Cycle	S	M	L	GenBank	Description
Aif1	**54**	**112**	**742**	**NM_173985.2**	**allograft inflammatory factor 1**
Mgc127947	469	274	89	CB432953	similar to Septin-4 (Peanut-like protein 2) (Brain protein H5) (MGC127947)
Loc512632	57	122	38	CK772111	similar to suppression of tumorigenicity 5 (LOC512632), predicted
---	829	143	324	AW463731	Transcribed locus, moderately similar to XP_341967.1 similar to p57kip2
Development	S	M	L	GenBank	Description
Ncf1	**23**	**47**	**286**	**NM_174119.2**	**neutrophil cytosolic factor 1 (47kDa, chronic granulomatous disease)**
Ncf2	**19**	**31**	**113**	**NM_174120.2**	**neutrophil cytosolic factor 2 [65kD, human : chronic granulomatous**
Loc505318	**14**	**29**	**84**	**CK957752**	**similar to Olfactomedin-like protein 3 precursor (HNOEL-iso) (hOLF44)**
---	**106**	**175**	**275**	**CB438214**	**Transcribed locus, moderately similar to NP_150280.1 epithelial stromal**
---	**34**	**54**	**106**	**CK772701**	**Canis familiaris similar to origin recognition complex subunit 5 isoform 1**
---	**18**	**49**	**530**	**CK950711**	**Transcribed locus, moderately similar to NP_057703.1 placenta-specific**
Mog	85	47	19	CK941863	Myelin oligodendrocyte glycoprotein
Eed	251	140	89	BE722433	Embryonic ectoderm development protein
---	580	291	193	CB455803	Transcribed locus, moderately similar to NP_060019.1 upregulated
---	753	433	126	CK772110	Transcribed locus, strongly similar to XP_513604.1 HMT1 hnRNP
Loc509575	41	27	89	CK957152	similar to Junctional adhesion molecule-like precursor (Dendritic-cell
---	50	32	77	BE723501	Transcribed locus, strongly similar to XP_511686.1 similar to unc-13
Electron Transport	S	M	L	GenBank	Description
Cybb	**38**	**115**	**302**	**NM_174035.2**	**cytochrome b-245, beta polypeptide [chronic granulomatous disease]**
Maob	94	33	21	CK775534	Monoamine oxidase B
Ecm/ Cytoskeleton	S	M	L	GenBank	Description
Loc507126	**4**	**12**	**81**	**CB435689**	**similar to basement membrane-induced gene (LOC507126), predicted**
Vcam1	**48**	**104**	**252**	**AB052747.1**	**vascular cell adhesion molecule 1**
Tnfaip6	**31**	**50**	**342**	**CB442867**	**Tumor necrosis factor, alpha-induced protein 6**
Scin	**42**	**86**	**455**	**NM_174177.2**	**scinderin**
Postn	**138**	**275**	**448**	**BF231198**	**Periostin, osteoblast specific factor**
Lum	**278**	**525**	**875**	**NM_173934.1**	**lumican**
Fn1	**27**	**49**	**93**	**AF260304.1**	**fibronectin 1**
Coro1a	**55**	**83**	**828**	**NM_174521.2**	**coronin, actin binding protein, 1A**
Cald1	**59**	**124**	**220**	**NM_174258.2**	**caldesmon, smooth muscle**
Loc511869	**36**	**54**	**97**	**CB456256**	**similar to transmembrane 4 superfamily member 5, transcript variant 1**
Loc505687	**187**	**391**	**625**	**CK777314**	**similar to plastin 3, transcript variant 3**
Lrrc33	**7**	**23**	**94**	**CK775761**	**leucine rich repeat containing 33 (LRRC33), NM_001034391.1**
Itgal	**11**	**31**	**175**	**BI681282**	**Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated**
Itgb2	**41**	**63**	**526**	**NM_175781.1**	**integrin, beta 2 (antigen CD18 subunit (p95), lymphocyte function-associated**
Itga5	**69**	**109**	**189**	**CK945847**	**Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)**
Loc511711	**14**	**34**	**175**	**CK941183**	**similar to Fibroleukin precursor (Fibrinogen-like protein 2) (pT49),**
Acta1	208	51	30	NM_174225	actin, alpha 1, skeletal muscle
Loc538668	416	241	137	BM480879	similar to transmembrane 4 superfamily member 9 (LOC538668)
Loc530050	904	481	120	CK972362	similar to smooth muscle myosin heavy chain 11 isoform SM1 (LOC530050)
Loc511602	122	59	31	CB421028	similar to alpha 5 type IV collagen isoform 2, precursor
Loc537784	85	48	22	CK979703	similar to plakophilin 2 isoform 2a
Itga2	152	94	33	L25886.1	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
Mfap2	516	144	308	NM_174388.2	microfibrillar-associated protein 2
F5	35	21	97	NM_173879.2	coagulation factor V (proaccelerin, labile factor)
Des	123	53	185	CK948671	desmin
Amelx	107	69	167	M63631.1	amelogenin (X chromosome)
Mcam	172	267	97	CK773680	melanoma adhesion molecule (MCAM), predicted
Loc522371	119	36	66	CK769482	similar to tetraspanin 15, transcript variant 1 (LOC522371),
---	53	35	80	CK774709	Transcribed locus, strongly similar to NP_037373.1 formin homology 2 domain
Golgi Apparatus	S	M	L	GenBank	Description
Loc520900	**15**	**33**	**233**	**CK946016**	**similar to mannose receptor C1**
Loc537017	**19**	**66**	**123**	**AW478320**	**similar to cytidine monophospho-N-acetylneuraminic acid hydroxylase**
Loc504309	**39**	**92**	**904**	**CB459865**	**similar to C-type lectin domain family 2, member e (LOC504309)**
Loc533653	9	130	33	AV615565	similar to melanoma-associated chondroitin sulfate proteoglycan 4
Growth Factors	S	M	L	GenBank	Description
Vegf	**44**	**83**	**134**	**NM_174216.1**	**vascular endothelial growth factor**
Spp1	**627**	**1935**	**6851**	**NM_174187.2**	**secreted phosphoprotein 1 [osteopontin, bone sialoprotein I**
Ifitm3	**1157**	**1803**	**3438**	**CB443586**	**Interferon induced transmembrane protein 3 (1-8U)**
Ccl8	**8**	**15**	**105**	**NM_174007.1**	**chemokine (C-C motif) ligand 8**

Supplmental Table S1

Bovine Granulosa Cell Regulated Genes

Ccl5	**3**	**22**	**427**	**NM_175827.2**	**chemokine (C-C motif) ligand 5**
Ccl3l1	**50**	**77**	**305**	**NM_174511.2**	**chemokine (C-C motif) ligand 3-like 1**
Ccl3l1	**49**	**101**	**271**	**NM_174511.2**	**Chemokine (C-C motif) ligand 3-like 1**
Ccl2	**63**	**166**	**611**	**NM_174006.2**	**chemokine (C-C motif) ligand 2**
Loc511671	**109**	**176**	**1054**	**CK770974**	**similar to chemokine (C-X-C motif) ligand 16, transcript variant 1**
Gmfg	**40**	**81**	**435**	**CK771942**	**glia maturation factor, gamma (GMFG), NM_001024537.1**
Loc511671	**35**	**64**	**405**	**BF775515**	**similar to chemokine (C-X-C motif) ligand 16, transcript variant 3**
Loc613811	**37**	**72**	**115**	**CK771033**	**similar to stromal cell derived factor 1 isoform beta precursor**
Loc414347	**25**	**57**	**338**	**CB463807**	**putative MIP1-beta protein (LOC414347), predicted**
---	**8**	**26**	**90**	**CK772450**	**Transcribed locus, moderately similar to NP_032740.2**
Igfbp2	293	151	76	NM_174555.1	insulin-like growth factor binding protein 2, 36kDa
Loc617915	101	46	20	CK959718	similar to Angiopoietin-4 precursor (ANG-4) (ANG-3) (LOC617915), predicted
Igfbp4	74	259	167	NM_174557.2	insulin-like growth factor-binding protein 4
Igfbp3	152	87	259	NM_174556.1	insulin-like growth factor binding protein 3
Igf1r	119	185	38	BM482617	insulin-like growth factor 1 receptor
Gdf8	81	13	34	BF652431	growth differentiation factor 8
Cxcr4	96	53	460	NM_174301.2	chemokine (C-X-C motif) receptor 4
Tdgf1	75	9	15	CB468433	teratocarcinoma-derived growth factor 1 (TDGF1)
Loc504526	56	35	111	CK771963	similar to growth arrest-specific 6 (LOC504526), predicted

Hormones	S	M	L	GenBank	Description
Ttr	**5**	**26**	**100**	**AB009591.1**	**transthyretin [prealbumin, amyloidosis type I]**
Amh	645	373	186	NM_173890.1	anti-Mullerian hormone
Gal	98	10	15	NM_173914.2	galanin
Inhbb	52	148	26	NM_176852.1	inhibin, beta B (activin AB beta polypeptide)

Immune Response	S	M	L	GenBank	Description
Fcgr1a	**38**	**78**	**322**	**NM_174538.2**	**Fc fragment of IgG, high affinity Ia, receptor for (CD64)**
C1qa	**85**	**154**	**1922**	**CB168331**	**complement component 1, q subcomponent, alpha polypeptide**
Loc509968	**24**	**39**	**697**	**CK771390**	**similar to Complement C1q subcomponent, C chain precursor**
Loc507549	**5**	**51**	**459**	**CK771045**	**similar to T-cell immunoglobulin and mucin domain containing**
Loc510910	**5**	**17**	**95**	**CK772231**	**similar to CD84 antigen (leukocyte antigen) (LOC510910), predicted**
Loc414345	**9**	**20**	**117**	**AY533858.1**	**CD86**
Mx2	**15**	**27**	**93**	**NM_173941.2**	**myxovirus (influenza virus) resistance 2 (mouse)**
Loc404109	**25**	**46**	**83**	**CK973343**	**IgG2a heavy chain constant region**
Igj	**20**	**30**	**218**	**NM_175773.1**	**immunoglobulin J chain**
Gnly	**21**	**33**	**289**	**CB454206**	**Granulysin**
Gnly	**27**	**43**	**291**	**CB435234**	**granulysin (GNLY), predicted**
Defb1	**50**	**96**	**272**	**NM_175703.2**	**defensin, beta 1 (enteric)**
Cd86	**4**	**6**	**89**	**AJ291475.1**	**CD86 antigen**
Cd45	**3**	**15**	**86**	**BM363771**	**membrane tyrosine phosphatase**
Cd3g	**11**	**19**	**139**	**CB421951**	**Antigen CD3G, gamma polypeptide**
Cd14	**35**	**63**	**290**	**NM_174008.1**	**CD14 antigen**
Bnbd-5	**4**	**128**	**454**	**BM106372**	**Neutrophil beta-defensin 5**
Bnbd-4	**84**	**216**	**421**	**BM106372**	**neutrophil beta-defensin 4**
Loc615930	**172**	**356**	**1459**	**CK771078**	**similar to interferon gamma inducible protein 30, transcript variant 1**
Loc504960	**92**	**166**	**1824**	**CK774183**	**similar to CD68 antigen, transcript variant 2 (LOC504960)**
Loc509597	**56**	**89**	**660**	**AV617024**	**similar to HLA class I histocompatibility antigen, A-11 alpha chain precursor**
Mgc128288	**61**	**110**	**389**	**CK776832**	**similar to lymphocyte cytosolic protein 1 (predicted) (MGC128288)**
Loc540824	**70**	**115**	**177**	**CF930575**	**similar to B cell lymphoma/leukemia 10(B-cell CLL/lymphoma 10)**
Bola-Dqa1	**15**	**26**	**170**	**D50454.1**	**histocompatibility complex, class II, DQ alpha, type1 (BOLA-DQA1)**
Loc617034	**16**	**25**	**77**	**BE755445**	**similar to CD83 antigen precursor (Cell surface protein HB15)**
Fcnb	**25**	**55**	**382**	**BF776071**	**ficolin B (FCNB), NM_001010996.1**
Loc525727	**7**	**20**	**84**	**BI849171**	**similar to HLA class II histocompatibility antigen, DO alpha chain precursor**
Loc510910	**10**	**19**	**91**	**BM089070**	**similar to CD84 antigen (leukocyte antigen) (LOC510910), predicted**
Loc513266	**2**	**19**	**86**	**BM365324**	**similar to CD209 antigen (LOC513266), predicted**
Loc616818	**35**	**65**	**726**	**BM433957**	**similar to Calgranulin A (Migration inhibitory factor-related protein 8)**
Loc508386	**16**	**43**	**329**	**CB423230**	**similar to B-lymphocyte activation marker BLAST-1 precursor**
Loc528593	**10**	**37**	**612**	**CB426639**	**similar to CD5 antigen-like (LOC528593), predicted**
Bola-Dqa2	**2**	**12**	**95**	**CB444277**	**mRNA for MHC class II DQA2**
Bola-Dmb	**15**	**30**	**263**	**CK773078**	**major histocompatibility complex, class II, DM beta-chain, expressed**
Loc614262	**29**	**66**	**368**	**CK816899**	**similar to V-set and immunoglobulin domain containing protein 4**
Loc615744	**12**	**27**	**141**	**CK775301**	**similar to Leukocyte specific transcript 1 protein (B144 protein)**
Loc539605	**36**	**65**	**271**	**CK770528**	**similar to properdin P factor, complement**
Loc614044	**15**	**28**	**110**	**CK981542**	**similar to Leukocyte immunoglobulin-like receptor subfamily A member**
Nkg7	**15**	**28**	**121**	**CK775256**	**natural killer cell group 7 sequence (NKG7), NM_001035279.1**
Bla-Dqb	**8**	**16**	**481**	**D37953.1**	**MHC class II antigen, NM_001034668.1**
---	**40**	**66**	**223**	**CK773094**	**Transcribed locus, moderately similar to NP_004224.1 CD83 antigen**
Loc537167	630	353	123	CB464823	similar to Core histone macro-H2A.2 (Histone macroH2A2) (mH2A2)
Loc511486	56	30	281	CK960422	similar to T-cell receptor alpha chain C region (LOC511486), predicted
Loc407206	14	9	80	CK772383	T cell receptor gamma chain variable region BVG7
Cd3z	28	16	135	NM_174012.2	antigen CD3Z, zeta polypeptide
Cd36	297	193	825	NM_174010.2	CD36 antigen [collagen type I receptor, thrombospondin receptor]
Bola	242	104	428	AB008573.1	MHC class I antigen (BoLA), predicted

Loc510398	34	21	137	CK849860	similar to Ig gamma-1 chain C region, membrane-bound form
Loc617975	44	131	27	BI682571	similar to Histone H1.0 (H1(0)) (Histone H1), transcript variant 1
Agp	106	15	37	CB530461	alpha-1 acid glycoprotein (AGP), predicted
Loc528926	6	2	93	CK958366	similar to lymphocyte antigen 9 (LOC528926), predicted
Loc615844	39	23	128	CK943316	similar to Endoglin precursor (CD105 antigen) (LOC615844), predicted
---	42	119	79	CK946910	Transcribed locus, strongly similar to NP_005233.3 coagulation factor II

Metabolism	S	M	L	GenBank	Description
Loc512512	**10**	**19**	**100**	**CK950056**	**similar to Deoxyribonuclease gamma precursor (DNase gamma)**
Slc2a5	**29**	**70**	**248**	**CK777297**	**solute carrier family 2 (facilitated glucose/fructose transporter), member 5**
Xdh	**7**	**26**	**133**	**NM_173972.2**	**xanthene dehydrogenase**
Slco2b1	**6**	**20**	**96**	**CK954377**	**Organic anion transporting polypeptide 2b1**
Slc2a5	**13**	**33**	**114**	**AF308830.1**	**solute carrier family 2 (facilitated glucose/fructose transporter), member 5**
Rgn	**29**	**73**	**128**	**NM_173957.2**	**regucalcin (senescence marker protein-30)**
Lyz	**29**	**49**	**755**	**L19980.1**	**lysozyme, macrophage**
Hbb	**13**	**23**	**314**	**NM_173917.1**	**hemoglobin, beta [beta globin]**
Ggta1	**33**	**61**	**95**	**NM_177511.1**	**alpha-galactosyltransferase 1 (glycoprotein)**
Fabp5	**42**	**109**	**770**	**CK969096**	**Fatty acid binding protein 5**
Fabp4	**111**	**213**	**2236**	**NM_174314.2**	**fatty acid-binding protein, adipocyte**
Ctss	**71**	**228**	**1513**	**CK848234**	**cathepsin S**
Ctsc	**266**	**581**	**1640**	**CK848620**	**cathepsin C**
Apn	**9**	**14**	**104**	**CK769810**	**Aminopeptidase N**
Ang	**29**	**107**	**852**	**NM_173891.1**	**angiogenin**
Aldh1a1	**36**	**62**	**319**	**NM_174239.2**	**aldehyde dehydrogenase 1 family, member A1**
Oas1	**112**	**236**	**531**	**CK960499**	**2'-5'-oligoadenylate synthetase 1 (OAS1), NM_178108**
Loc509003	**49**	**81**	**149**	**CB166446**	**similar to Nucleobindin 2 precursor (DNA-binding protein NEFA)**
Loc511644	**71**	**119**	**191**	**CB168603**	**similar to Thiopurine S-methyltransferase (Thiopurine methyltransferase)**
Mgc128896	**14**	**24**	**119**	**CK946616**	**similar to GTPase, IMAP family member 7 (MGC128896), NM_001034771.1**
Loc532964	**10**	**20**	**120**	**BF075879**	**similar to myosin IF (LOC532964), predicted**
Loc528288	**21**	**34**	**81**	**BF601649**	**similar to GTPase, IMAP family member 6 isoform 1 (LOC528288), predicted**
Loc512863	**15**	**24**	**89**	**BF706229**	**similar to sialic acid binding immunoglobulin-like lectin-like protein 1 isoform b**
Loc512863	**13**	**21**	**175**	**CB453710**	**similar to sialic acid binding immunoglobulin-like lectin-like protein 1 I**
Loc507865	**18**	**45**	**152**	**CB166927**	**similar to axotrophin, transcript variant 3 (LOC507865), predicted**
Loc512938	**44**	**71**	**953**	**CB171496**	**similar to ubiquitin D, transcript variant 2 (LOC512938), predicted**
Loc512867	**4**	**7**	**78**	**CB420233**	**similar to GTPase, IMAP family member 1 (LOC512867), predicted**
Loc510988	**17**	**28**	**320**	**CK778198**	**similar to GTPase, IMAP family member 7 (LOC510988), predicted**
Loc530077	**6**	**22**	**171**	**CK770886**	**similar to GTPase, IMAP family member 5, (LOC530077), predicted**
Loc540329	**40**	**72**	**121**	**CB428002**	**similar to protein phosphatase 1K (PP2C domain containing)**
Pla2g2d1	**10**	**17**	**171**	**CB437801**	**calcium-dependent phospholipase A2 PLA2G2D1 (PLA2G2D1)**
Loc505394	**9**	**16**	**135**	**CB530133**	**similar to Apolipoprotein A-II precursor (Apo-AII) (ApoA-II) (LOC505394)**
Loc525813	**29**	**54**	**129**	**CK777442**	**similar to malic enzyme 3, NADP(+)-dependent, mitochondrial (LOC525813), pred**
Loc507597	**17**	**37**	**119**	**CK775223**	**similar to N-acetylneuraminate pyruvate lyase (LOC507597), predicted**
Ace2	**16**	**32**	**83**	**CK948184**	**angiotensin I converting enzyme 2 precursor**
Loc518062	**34**	**59**	**123**	**CK771026**	**similar to Putative transporter C20orf59 (LOC518062), predicted**
Birc4bp	**27**	**50**	**132**	**CK770588**	**XIAP associated factor-1 (BIRC4BP), NM_001035075.1**
Loc512486	**27**	**63**	**189**	**CK957199**	**similar to Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1)**
Pc	313	136	85	NM_177946.2	pyruvate carboxylase
Ltf	1434	281	133	NM_180998.2	lactoferrin [lactotransferrin]
Phgdh	613	298	185	CK771294	phosphoglycerate dehydrogenase (PHGDH), NM_001035017.1
Loc511449	253	168	103	AW356212	similar to 5-nucleotidase, cytosolic III, transcript variant 8 (LOC511449), predic
Loc510504	341	222	81	CK940736	similar to glycosyltransferase-like 1B transcript variant 2 (LOC510504), predict
Loc510372	114	75	43	CK776058	similar to importin 4, transcript variant 5 (LOC510372), predicted
Loc504250	83	40	20	AV589549	similar to Dihydropyrimidinase-related protein 1 (DRP-1) (Collapsin response me
Cpxm	95	57	37	BE754081	carboxypeptidase X (CPXM), NM_001015642.1
Loc521064	124	55	22	CB464666	similar to proline rich 6 (LOC521064), predicted
Loc614203	92	40	10	CK769376	similar to UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltrar
Ddo	115	35	9	NM_173908.2	D-aspartate oxidase
---	434	667	250	CK848432	Transcribed locus, moderately similar to NP_056174.1 solute carrier family 39 (zinc tran
Slc11a1	24	15	472	NM_174652.2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
Scd	1374	2139	787	AY241933.1	stearoyl-coenzyme A desaturase
Pnmt	106	15	43	NM_177505.2	phenylethanolamine N-methyltransferase
Kpnb2	114	287	183	AY298813.1	karyopherin (importin) beta 2
Ece1	230	352	144	Z35306.1	endothelin converting enzyme 1
Ca2	448	270	888	NM_178572.2	carbonic anhydrase II
Ahsg	15	9	81	CB537901	alpha-2-HS-glycoprotein
Loc511053	76	278	146	CK770053	similar to solute carrier family 27 member 3, transcript variant 1
Loc512468	344	731	214	CB444175	similar to Glutamate--cysteine ligase catalytic subunit
Loc540066	589	1046	331	CK769427	similar to carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8,
Loc514105	69	236	141	CB538971	similar to Carboxypeptidase D precursor (Metallocarboxypeptidase D)
Loc512464	96	146	55	CB530449	similar to solute carrier family 11 (proton-coupled divalent metal ion
Loc515918	73	141	42	CK976676	similar to carbonic anhydrase VIII (LOC515918), predicted
Mgc128502	55	35	147	AU097767	similar to tRNA splicing 2 phosphotransferase 1 (MGC128502)
Cacna1h	134	37	57	AW481855	calcium channel, voltage-dependent, alpha 1H subunit (CACNA1H)
Loc613869	52	30	88	BF651608	similar to arachidonate 5-lipoxygenase activating protein

Supplmental Table S1

Bovine Granulosa Cell Regulated Genes

Loc511617	11	6	82	BI775718	similar to GTPase, IMAP family member 5 (LOC511617), predicted
Loc514346	38	19	233	BM251912	similar to serine dehydratase (LOC514346), predicted
Loc515161	76	20	36	CF615708	similar to Sodium/potassium-transporting ATPase alpha-2 chain precursor
Loc528735	64	35	99	CK770139	similar to S-100 protein, alpha chain (S100 calcium-binding protein A1)
Loc505721	126	16	38	CK849612	similar to regulator of telomere elongation helicase 1 isoform 2
Loc514105	94	309	203	AW465202	similar to Carboxypeptidase D precursor (Metallocarboxypeptidase D)
Hmox1	1108	721	2719	CK770847	heme oxygenase (decyclizing) 1 (HMOX1), NM_001014912.1
Cyp51	124	304	202	CK961820	cytochrome P450, family 51, subfamily A, polypeptide 1 (CYP51)
---	102	67	215	CK769509	Transcribed locus, moderately similar to NP_057457.1 WW domain containing
---	49	25	89	CB464568	Transcribed locus, moderately similar to NP_002601.1 pyruvate dehydrogenase

Protease	S	M	L	GenBank	Description
Loc617313	**10**	**17**	**182**	**CK776010**	**similar to Granzyme H precursor (Cytotoxic T-lymphocyte proteinase)**
Serpinb2	**675**	**2271**	**4058**	**AF416234.1**	**serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2**
Serpinb2	**17**	**71**	**173**	**AF416234.1**	**serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2**
Loc404103	**45**	**153**	**532**	**NM_205786.1**	**spleen trypsin inhibitor**
Serping1	158	15	80	NM_174821.2	serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1,
Serpina3 /// Loc49720	386	1144	680	CB530241	serine (or cysteine) proteinase inhibitor, clade A

Receptors	S	M	L	GenBank	Description
Il2rg	**24**	**36**	**223**	**NM_174359.1**	**interleukin 2 receptor, gamma**
Loc509418	**11**	**39**	**250**	**CB446844**	**similar to colony stimulating factor 1 receptor precursor,**
Loc529800	**20**	**36**	**83**	**CK769532**	**similar to ephrin receptor EphB6 precursor (LOC529800), predicted**
Loc505292	**9**	**17**	**114**	**CK776540**	**G-protein-coupled receptor GPR34**
Olr1	**197**	**510**	**1243**	**NM_174132.2**	**oxidised low density lipoprotein (lectin-like) receptor 1**
oc407150 /// Loc4080	459	256	129	AJ488553.1	insulin receptor /// insulin receptor
---	69	40	128	CB421632	Transcribed locus, moderately similar to NP_058934.1 vasoactive

Signaling	S	M	L	GenBank	Description
Loc538835	**15**	**30**	**140**	**CB429928**	**similar to Rho GTPase activating protein 30 isoform 1, transcript**
S100a12	**75**	**139**	**1289**	**NM_174651.1**	**S100 calcium binding protein A12 (calgranulin C)**
Loc507427	**20**	**38**	**109**	**CK848566**	**similar to receptor-interacting serine-threonine kinase 3**
Loc510102	**54**	**99**	**586**	**BP106985**	**similar to retinoic acid receptor responder (tazarotene induced)**
Loc507329	**8**	**18**	**118**	**CK963233**	**similar to SH2 containing inositol phosphatase isoform b**
Mgc128725	**3**	**8**	**95**	**CK952709**	**similar to SH2 domain protein 1A (MGC128725), NM_001034733.1**
Loc541093	**34**	**55**	**103**	**CK846284**	**similar to neurexophilin 3 (LOC541093), predicted**
Tlr2	**27**	**54**	**251**	**NM_174197.2**	**toll-like receptor 2**
Tgfb1	**66**	**107**	**232**	**BM251237**	**transforming growth factor, beta 1 (Camurati-Engelmann disease)**
Rap1a	**90**	**139**	**255**	**NM_174448.2**	**RAP1A, member of RAS oncogene family**
Adcy7	**19**	**35**	**149**	**NM_174230.2**	**adenylate cyclase 7**
Loc510549	**52**	**80**	**163**	**CK849639**	**similar to Ras association domain family 4 isoform a, transcript variant**
Cd53	**31**	**89**	**508**	**CK849015**	**CD53 antigen (CD53), NM_001034232.1**
Ms4a7	**14**	**23**	**153**	**AV598285**	**membrane-spanning 4-domains, subfamily A, member 7 (MS4A7)**
Loc618035	**39**	**67**	**103**	**AW336381**	**similar to RAB27A protein (LOC618035), predicted**
Fes	**6**	**14**	**93**	**BF602813**	**feline sarcoma viral (v-fes) oncogene (FES), predicted**
Loc540836	**15**	**53**	**416**	**CB170921**	**similar to Regulator of G-protein signaling 1 (RGS1) (Early response protein**
Loc532569	**8**	**21**	**178**	**CB417812**	**similar to Calgranulin B (Migration inhibitory factor-related protein 14)**
C3	**8**	**19**	**165**	**CB461274**	**complement component 3 (C3), predicted**
Loc534996	**10**	**19**	**82**	**CF764664**	**similar to Yamaguchi sarcoma viral (v-yes-1) oncogene homolog**
Loc514076	**8**	**21**	**80**	**CK769662**	**similar to Complement factor B precursor (C3/C5 convertase)**
Loc514616	**19**	**30**	**128**	**CK770042**	**similar to docking protein 2 isoform a (LOC514616), predicted**
Loc513244	**13**	**24**	**93**	**CK846023**	**similar to Lymphocyte cytosolic protein 2 (SH2 domain-containing**
Mgc128111	**14**	**26**	**244**	**CB464071**	**similar to SAM-domain protein SAMSN-1 (SAM domain, SH3 domain**
Loc534171	**15**	**31**	**253**	**CK970569**	**similar to SAM-domain protein SAMSN-1 (SAM domain, SH3 domain**
Loc512312	**13**	**35**	**157**	**CK849706**	**src homology 2 domain-containing phosphatase-1, (LOC512312), predicted**
---	**24**	**76**	**200**	**CB430850**	**Transcribed locus, strongly similar to NP_005019.2**
---	**31**	**99**	**350**	**CB468195**	**Transcribed locus, strongly similar to NP_005019.2**
---	**15**	**40**	**370**	**CK956156**	**Transcribed locus, moderately similar to XP_514081.1**
---	335	218	107	CK729758	Transcribed locus, strongly similar to NP_037407.3 ankyrin repeat
Stc1	1286	821	345	NM_176669.2	stanniocalcin 1
Loc506627	505	318	183	AW336328	similar to Dickkopf-related protein 3 precursor (Dkk-3)
Rasl11b	228	113	29	CK977446	RAS-like family 11, member B (RASL11B), NM_001015635.1
Loc539768	232	136	73	CK776838	similar to phosphodiesterase 8B isoform 1 (LOC539768), predicted
Loc539201	385	107	57	CB437887	similar to Diphosphoinositol polyphosphate phosphohydrolase
Loc532856	89	54	29	AV600334	similar to ankyrin repeat domain 11 (LOC532856), predicted
Loc516303	122	70	27	CB456788	similar to mitogen-inducible gene 6 protein (LOC516303), predicted
---	125	55	22	CK772945	Transcribed locus, strongly similar to XP_511363.1 similar to TNF
Loc511989	53	15	104	CK948223	similar to FYVE, RhoGEF and PH domain containing 2
Mgat4a	45	23	105	CK849000	Mannosyl (alpha-1,3-)-glycoprotein beta-1,
Mgc126900	31	20	96	AW289293	similar to Proto-oncogene tyrosine-protein kinase LCK
Loc504585	59	89	34	BI847915	similar to Sperm-associated antigen 5 (Astrin)
Ppp1r1b	95	3	7	NM_174647.2	protein phosphatase 1, regulatory (inhibitor) subunit 1B
Lrp8	36	391	243	CB166058	low density lipoprotein receptor-related protein 8
Cart	1805	129	292	BM288295	Cocaine and amphetamine responsive transcript

Lgals9	155	99	259	CK849539	lectin, galactoside-binding, soluble, 9 (galectin 9)
Loc614644	148	47	89	CK773279	similar to BMP and activin membrane-bound inhibitor homolog precursor
Loc514282	20	11	82	AV594085	similar to Apolipoprotein-L3 (Apolipoprotein L-III) (ApoL-III)
Loc616759	57	103	35	CB439542	similar to FAS-associated factor 1 (FAF1 protein) (LOC616759), predicted
Loc533332	28	122	67	CF765405	similar to RAB38 (LOC533332), predicted
---	49	20	173	CB464749	Transcribed locus, strongly similar to NP_005864.1 regulator of G-protein

Steroidogenesis	S	M	L	GenBank	Description
Cyp19	**120**	**2467**	**2477**	**NM_174305.1**	**cytochrome P450, subfamily XIX (aromatase)**
Cyp17	**33**	**70**	**139**	**NM_174304.1**	**cytochrome P450, subfamily XVII**
Ptges	187	24	99	NM_174443.2	prostaglandin E synthase

Transcription	S	M	L	GenBank	Description
Snai2	**163**	**274**	**518**	**CK846343**	**Snail homolog 2 (Drosophila)**
Ostf1	**224**	**378**	**721**	**NM_174409.2**	**osteoclast stimulating factor 1**
Loc540789	**50**	**81**	**127**	**CK964890**	**similar to poly (ADP-ribose) polymerase family, member 14**
Loc617673	**5**	**22**	**145**	**CB420213**	**similar to Vav proto-oncogene (LOC617673), predicted**
Loc507100	**28**	**50**	**234**	**CB431054**	**similar to Transcription factor PU.1 (31 kDa transforming protein)**
Loc617628	**4**	**11**	**77**	**CB440072**	**similar to ATF-like basic leucine zipper transcription factor B-ATF**
Irf5	**33**	**57**	**228**	**CK771035**	**interferon regulatory factor 5 isoform b (IRF5), NM_001035465.1**
Loc515564	255	163	101	CK776693	similar to Zinc finger protein 197 (ZnF20), transcript variant 5
Loc533826	295	194	108	BP106791	similar to Cullin-associated NEDD8-dissociated protein 2
Loc510050	593	365	242	CB420255	similar to TG-interacting factor isoform a (LOC510050), predicted
Loc534213	173	100	61	CK834868	similar to zinc finger protein 521 isoform 1 (LOC534213), predicted
Loc527574	293	122	69	CK770186	similar to sal-like 2 (LOC527574), predicted
Loc516156	160	97	53	CK729854	similar to Zinc finger protein 331 (Zinc finger protein 463)
Loc506114	80	53	31	CK769584	similar to Transcription factor Dp-2 (E2F dimerization partner 2
Loc514174	135	56	31	CK775981	similar to cytoplasmic polyadenylation element binding protein 1
Loc521364	133	47	17	CK775529	similar to Frizzled 9 precursor (Frizzled-9) (Fz-9) (mFz9) (mFz3)
Rpl6	251	144	402	AV601026	Ribosomal protein L6
Rpl24	327	515	141	CK775524	Ribosomal protein L24
Foxl2	73	124	36	AY116404.1	forkhead box L2
Loc514246	467	298	786	BE664618	similar to Transcription factor jun-B (LOC514246), predicted
---	175	325	78	X15543.1	RF-36-DNA-binding protein
Loc617975	75	155	41	CF765300	similar to Histone H1.0 (H1(0)) (Histone H1), transcript variant 1
Mgc128169	67	102	26	AW447459	similar to zinc finger protein 36 (MGC128169), NM_001035368.1
Loc520842	39	23	77	CB165826	similar to Kruppel-like factor 4 (Epithelial zinc-finger protein EZF)
Loc541088	73	144	47	CB444034	similar to BCoR protein (BCL-6 corepressor), transcript variant 3
Loc614909	65	41	184	CK958835	similar to interferon regulatory factor 8 (LOC614909), predicted
Loc617975	171	281	100	CB420587	similar to Histone H1.0 (H1(0)) (Histone H1), transcript variant 1
---	75	28	115	AW464305	Transcribed locus, strongly similar to NP_084520.2 immediate early

Translation	S	M	L	GenBank	Description
Rnase6	43	119	1172	NM_174594.2	ribonuclease k6

Unknown Function	S	M	L	GenBank	Description
Loc404122	**701**	**1086**	**1709**	**CK978279**	**Hypothetical protein LOC404122**
Loc507138	**355**	**1027**	**1856**	**CB456756**	**similar to putative ISG12(a) protein (LOC507138), predicted**
Loc512361	**129**	**205**	**1337**	**CK774666**	**similar to Lysosomal-associated multitransmembrane protein**
Icam3	**18**	**32**	**276**	**NM_174349.1**	**intercellular adhesion molecule 3**
Evi2b	**10**	**15**	**81**	**CB538192**	**Ecotropic viral integration site 2B**
Loc504773	**66**	**142**	**1445**	**CB530693**	**regakine-1 protein (LOC504773), NM_001034220.1**
Mgc127454	**18**	**35**	**195**	**AW658502**	**similar to Hematopoietic lineage cell specific protein**
Loc507801	**32**	**50**	**76**	**BF039068**	**similar to splicing factor, arginine/serine-rich 12**
Loc617446	**25**	**38**	**191**	**BF601096**	**hypothetical protein LOC617446 (LOC617446), predicted**
Mgc127869	**10**	**15**	**82**	**CB424390**	**similar to testis expressed sequence 12 (MGC127869), NM_001034263.1**
Plac8	**2**	**7**	**132**	**CB425639**	**placenta-specific 8 (PLAC8), NM_001025325.1**
Loc513939	**28**	**51**	**109**	**CK846668**	**similar to Gasdermin domain containing protein 1 (FKSG10 protein)**
Flj14213	**30**	**53**	**108**	**CK771521**	**hypothetical protein FLJ14213**
Loc510773	**7**	**16**	**97**	**CK848741**	**similar to CG8312-PA, isoform A (LOC510773), predicted**
Loc493778	4035	2574	1661	CB532123	Up-regulated during vascular calcification
Loc513556	772	435	259	CB444311	similar to CG12093-PA (LOC513556), predicted
Mgc128811	2000	1225	670	CB168739	similar to Protein C10orf58 precursor (MGC128811), NM_001034599.1
Loc617091	1410	847	445	CB421708	similar to Ectoderm-neural cortex-1 protein (ENC-1)
Loc515133	2483	766	435	CK776308	similar to esophageal cancer related gene 4 protein
Loc511591	691	326	191	CK951333	similar to sortilin 1 preproprotein (LOC511591), predicted
Loc525051	160	88	52	CK776192	similar to bromodomain containing protein 3 (LOC525051), predicted
Loc540275	277	183	54	CA035043	similar to Chordin-like protein 1 precursor (Neuralin) (Ventroptin)
Loc538109	91	48	24	CB455153	similar to CG9913-PB, isoform B (LOC538109),
C20orf55	78	41	14	CK729276	chromosome 20 open reading frame 55 (C20orf55), NM_001014961.1
Trb2	1394	3293	2180	CK982437	TRB-2 protein
Loc614391	133	398	242	CK952483	similar to Arg/Abl-interacting protein 2 isoform 1, transcript variant 4
Loc539911	168	110	311	CB461411	hypothetical LOC539911, transcript variant 4 (LOC539911), predicted

Loc617312	208	409	138	CK846089	similar to centrosomal protein 72 kDa (LOC617312), predicted
Mgc127874	533	925	343	CK958497	hypothetical LOC508617 (MGC127874), NM_001034325.1
Loc504975	293	457	95	CK775855	similar to tolloid-like 2, transcript variant 1 (LOC504975), predicted
Loc539087	51	26	157	CK775676	hypothetical LOC539087, transcript variant 1 (LOC539087), predicted
Loc511970	53	89	27	CK833514	similar to CG5965-PA, transcript variant 6 (LOC511970), predicted
Loc511219	146	23	42	CB429630	hypothetical LOC511219 (LOC511219), predicted
Loc533184	71	37	125	CK770048	similar to tweety 2 isoform 1 (LOC533184), predicted
Loc508790	50	33	98	CK770695	similar to transmembrane protein induced by tumor necrosis factor alpha
Loc618286	49	83	12	CK952023	similar to TBC1 domain family, member 14 (LOC618286), predicted
Loc513551	46	110	70	CK952083	hypothetical LOC513551, predicted

Ests	S	M	L	GenBank	Description
---	**182**	**287**	**554**	**CK846622**	**Transcribed locus, strongly similar to NP_005070.1 tumor protein**
---	**153**	**258**	**502**	**CB460448**	**Transcribed locus**
---	**284**	**481**	**1036**	**CB450086**	**Transcribed locus, moderately similar to XP_291663.3 lipase-like,**
---	**98**	**209**	**374**	**CK846663**	**Transcribed locus**
---	**97**	**161**	**384**	**CK948196**	**Transcribed locus**
---	**67**	**173**	**1087**	**BP105987**	**Transcribed locus**
---	**73**	**116**	**215**	**CK959800**	**Transcribed locus**
	69	**155**	**291**	**CK980839**	**Transcribed locus**
---	**61**	**101**	**237**	**CB535138**	**Transcribed locus**
---	**66**	**186**	**1106**	**CK947002**	**Transcribed locus**
---	**56**	**106**	**530**	**CK848334**	**Transcribed locus**
---	**56**	**124**	**303**	**CB425083**	**Transcribed locus**
---	**22**	**35**	**82**	**AW670030**	**Transcribed locus**
---	**15**	**32**	**220**	**BF440340**	**Transcribed locus**
---	**39**	**68**	**338**	**BM251338**	**Transcribed locus**
---	**18**	**33**	**282**	**BM255348**	**Transcribed locus**
---	**4**	**14**	**122**	**BM366388**	**Transcribed locus, weakly similar to NP_067004.3 SLAM family**
---	**15**	**30**	**84**	**BP102940**	**Transcribed locus**
---	**10**	**22**	**105**	**CB421639**	**Transcribed locus, moderately similar to XP_521353.1 similar to MGC16121**
---	**25**	**48**	**107**	**CB433662**	**Transcribed locus**
---	**34**	**53**	**128**	**CB452350**	**Transcribed locus, moderately similar to XP_521353.1 similar to MGC16121**
---	**11**	**37**	**92**	**CB459939**	**---**
---	**21**	**57**	**158**	**CB464048**	**Transcribed locus**
---	**22**	**41**	**100**	**CB465263**	**Transcribed locus**
---	**6**	**18**	**104**	**CK729527**	**Transcribed locus**
---	**3**	**21**	**153**	**CK769342**	**Transcribed locus**
---	**7**	**19**	**86**	**CK769793**	**Transcribed locus**
---	**12**	**20**	**119**	**CK978314**	**Transcribed locus**
---	**35**	**53**	**264**	**CK773226**	**Transcribed locus**
---	**44**	**66**	**108**	**CK848032**	**Transcribed locus**
---	**25**	**54**	**125**	**CK960947**	**Transcribed locus**
---	**11**	**26**	**136**	**CK957284**	**Transcribed locus**
---	**8**	**19**	**87**	**CK961132**	**Transcribed locus**
---	**31**	**67**	**173**	**CK773493**	**Transcribed locus**
---	**9**	**23**	**99**	**CK778710**	**Transcribed locus**
---	**16**	**35**	**81**	**CK950136**	**Transcribed locus**
---	377	180	106	CK973831	Transcribed locus
---	313	197	115	CK975775	Transcribed locus
	245	145	90	CF930523	Transcribed locus
---	692	441	231	AW481945	Transcribed locus
---	1567	521	269	CK847032	Transcribed locus
---	314	164	103	AV599401	---
---	575	355	195	CK775474	Transcribed locus, moderately similar to XP_488839.1
---	794	311	201	AV612255	Transcribed locus
---	269	172	113	CK955739	Transcribed locus, weakly similar to XP_529728.1 LOC453731 [Pan troglodytes]
---	2078	1360	392	BM483521	Transcribed locus, moderately similar to XP_328828.1 Neurospora crassa
---	519	297	110	CK957216	Transcribed locus
---	664	337	165	CK769502	Transcribed locus
---	134	76	48	CB421837	Transcribed locus
---	180	117	72	CB421746	Transcribed locus, weakly similar to XP_531051.1 LOC463585 [Pan troglodytes]
---	162	81	29	BP109863	Transcribed locus
---	134	79	51	CB453664	Transcribed locus
---	171	111	62	CB444243	---
---	186	105	58	CB430887	Transcribed locus
---	81	51	33	AV601907	Transcribed locus, weakly similar to XP_529728.1 LOC453731 [Pan troglodytes]
---	110	20	13	AW307709	Transcribed locus
---	125	44	21	BE752516	Transcribed locus
---	149	51	22	BM107097	Transcribed locus, weakly similar to XP_517689.1 adaptor-related protein
---	85	51	30	BM287472	Transcribed locus, strongly similar to XP_375848.2 KIAA0792 gene
---	150	56	33	BP107025	Transcribed locus
---	81	43	20	CB451852	Transcribed locus
---	107	54	35	CB534769	---
---	106	55	32	CK817083	Transcribed locus
---	139	72	43	CK968818	Transcribed locus

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---	123	53	14	CK954380	Transcribed locus, strongly similar to NP_777619.1 hypothetical protein
---	96	54	31	CK950652	Transcribed locus
---	97	63	17	CK849085	Transcribed locus
---	308	195	513	AFFX-r2-Bs-thr-M	---
---	155	93	233	AFFX-LysX-3	---
---	193	118	345	AFFX-r2-Bs-phe-	---
---	304	188	502	AFFX-ThrX-3	---
---	437	245	663	AFFX-r2-Bs-thr-3	---
---	806	523	1228	AFFX-r2-Bs-dap-	---
---	1016	662	1554	AFFX-DapX-M	---
---	258	423	159	BE217509	Transcribed locus, moderately similar to NP_003934.1 genethonin
---	81	272	138	CK975625	Transcribed locus
---	210	880	423	CK951444	Transcribed locus, strongly similar to NP_694958.1 transmembrane protein
---	101	64	169	CK776305	Transcribed locus
---	108	67	169	AFFX-LysX-M	---
---	123	223	74	CK961923	---
---	82	135	40	BM286259	Transcribed locus
---	35	19	80	AV597441	Transcribed locus, moderately similar to NP_081019.1 RIKEN cDNA
---	88	28	42	BE758306	Transcribed locus
---	259	26	40	CB226640	Transcribed locus
---	134	35	54	CB451799	Transcribed locus
---	10	6	86	CB537957	---
---	50	78	24	CK849442	Transcribed locus, weakly similar to NP_065140.1 Rhesus blood group
---	107	20	71	CK950562	Transcribed locus

Bolded genes are increased for all three antral follicle sizes.

Supplemental Table S2

Bovine Theca Cell Regulated Genes

Category/Gene Symbol	Microarray Signal				
Cell Cycle	S	M	Lg	Genbank	Description
Gadd45b	**343**	**534**	**961**	**CK964359**	**growth arrest and DNA-damage-inducible, beta**
Loc614739	78	4	8	CK771969	similar to reprimo, TP53 dependant G2 arrest mediator
---	259	137	86	CK967918	Transcribed locus, moderately similar to NP_212132.1 dedicator of
Development	S	M	Lg	Genbank	Description
Mgc128098	42	105	67	CB456431	similar to anterior pharynx defective 1a homolog
---	172	105	25	CK777690	Transcribed locus, strongly similar to NP_061928.4 roundabout homolog
---	121	37	203	CK948890	Transcribed locus, moderately similar to NP_114433.1 regenerating
Ecm & Cytoskeleton	S	M	Lg	Genbank	Description
Loc514273	**27**	**52**	**112**	**CK965841**	**similar to amphoterin induced gene 2 (LOC514273)**
Mgc128478	**24**	**67**	**154**	**BF076836**	**similar to claudin 11 (MGC128478), NM_001035055.1**
Tnfaip6	**10**	**39**	**650**	**CB442867**	**Tumor necrosis factor, alpha-induced protein 6**
---	**45**	**68**	**125**	**BE722311**	**Transcribed locus, strongly similar to NP_002282.1 laminin, beta 1**
Bgn	488	272	178	NM_178318.2	biglycan
Col18a1	1173	619	203	CK773859	Collagen, type XVIII, alpha 1
Loc512343	553	252	126	BE482398	similar to alpha 1 type XVI collagen precursor
Loc512343	1723	829	397	BE482398	similar to alpha 1 type XVI collagen precursor
Loc513668	872	378	157	AV617451	similar to collagen, type XXVII, alpha 1
Loc513668	120	79	19	BE237617	similar to collagen, type XXVII, alpha 1
Loc537532	497	328	84	CK833035	similar to alpha 1 type XV collagen precursor
Magp2	58	545	169	NM_174386.2	microfibril-associated glycoprotein-2
Tnnt1	211	92	580	NM_174474.1	troponin T1, skeletal, slow
---	95	146	55	CB436656	Transcribed locus, strongly similar to NP_005564.1 lamin B1
---	1980	1051	364	BE758040	Transcribed locus, weakly similar to NP_000486.1 collagen,
Electron Transport	S	M	Lg	Genbank	Description
Maob	**34**	**82**	**208**	**NM_177944.1**	**monoamine oxidase B**
Golgi Apparatus	S	M	Lg	Genbank	Description
Loc510504	76	42	11	CK940736	similar to glycosyltransferase-like 1B transcript variant 2
Mgat4a	419	251	108	CK849000	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-
Clp-1	27	107	42	CK849654	Chitinase-like protein 1 (CLP-1)
Loc511430	76	18	7	CK773758	similar to Mucin-13 precursor
Growth Factors	S	M	Lg	Genbank	Description
Ccl2	**83**	**159**	**252**	**NM_174006.2**	**chemokine (C-C motif) ligand 2**
Spp1	**55**	**129**	**674**	**NM_174187.2**	**secreted phosphoprotein 1 [osteopontin, bone sialoprotein I,**
Xcl1	**269**	**855**	**1606**	**NM_175716.2**	**chemokine (C motif) ligand 1**
Ang	**93**	**269**	**501**	**NM_173891.1**	**angiogenin**
Loc508666	1193	697	2794	CB465019	similar to Small inducible cytokine A23 precursor (CCL23)
Loc614833	160	95	45	CK772942	similar to EGF-like-domain, multiple 7 (LOC614833)
---	118	77	28	CB431697	Transcribed locus, moderately similar to XP_524353.1
Immune Response	S	M	Lg	Genbank	Description
F3	**17**	**37**	**108**	**NM_173878.2**	**coagulation factor III [thromboplastin, tissue factor]**
Loc509597	**46**	**71**	**152**	**AB008623.1**	**similar to HLA class I histocompatibility antigen**
Loc404109	56	167	102	CK973343	IgG2a heavy chain constant region
Loc505478	129	465	232	CK977367	similar to Immunoglobulin lambda-like polypeptide
Loc507549	50	32	79	CK771045	similar to T-cell immunoglobulin and mucin domain
Loc512972	81	48	24	CB531703	similar to minor histocompatibility antigen HA-1 (LOC512972)
Loc528593	12	2	80	CB426639	similar to CD5 antigen-like (LOC528593), predicted
Loc617435	239	144	392	CB435760	similar to complement component 1, q subcomponent
Mgc128080	170	104	39	BP107529	similar to CD200 antigen isoform a precursor
---	119	37	70	CB165744	Transcribed locus, weakly similar to NP_002107.3 major
Hormones	S	M	Lg	Genbank	Description
Oxt	**38**	**70**	**353**	**NM_176855.1**	**oxytocin**
Pthlh	**23**	**77**	**128**	**NM_174753.1**	**parathyroid hormone-like hormone**
Bcar3	**93**	**156**	**244**	**CK770175**	**breast cancer antiestrogen resistance 3**
Inhba	**153**	**1901**	**4189**	**NM_174363.1**	**inhibin, beta A (activin A, activin AB alpha polypeptide)**
Metabolism	S	M	Lg	Genbank	Description
Art3	**19**	**31**	**104**	**BM256348**	**mono (ADP-ribosyl)transferase**
Bcat2	**260**	**394**	**765**	**CK951109**	**branched chain aminotransferase 2, mitochondrial**
Ca2	**38**	**89**	**263**	**NM_178572.2**	**carbonic anhydrase II**
Clic4	**426**	**759**	**1144**	**BP104059**	**Chloride intracellular channel 4**
Fdft1	**99**	**237**	**466**	**CK982401**	**farnesyl-diphosphate farnesyltransferase 1**
Gpt	**70**	**106**	**251**	**CK772830**	**glutamic-pyruvate transaminase (GPT), predicted**
Idh1	**201**	**545**	**911**	**NM_181012.2**	**isocitrate dehydrogenase 1 (NADP+), soluble**
Idh3a	**192**	**336**	**829**	**NM_174644.2**	**isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A)**
Loc407176	**28**	**44**	**77**	**L26101.1**	**calcium activated potassium channel beta subunit**
Loc505394	**8**	**12**	**308**	**CB530133**	**similar to Apolipoprotein A-II precursor (Apo-AII)**
Loc505472	**157**	**276**	**446**	**CK959696**	**similar to liver glycogen phosphorylase**

Loc505472	**165**	**321**	**501**	**CK977645**	**similar to liver glycogen phosphorylase**
Loc509696	**69**	**115**	**195**	**CK970946**	**similar to trans-prenyltransferase**
Loc511053	**30**	**50**	**92**	**CK770053**	**similar to solute carrier family 27 member 3**
Loc513376	**38**	**72**	**166**	**BI539693**	**similar to Genethonin 1 (GENX-3414)**
Loc532778	**864**	**1425**	**2500**	**CK969786**	**similar to ADP-ribosylation factor GTPase activating**
Loc533186	**35**	**59**	**89**	**BE237450**	**similar to citrate lyase beta like**
Loc540923	**43**	**71**	**122**	**BF652540**	**similar to plasma glutamate carboxypeptidase**
Mgc:129011	**143**	**247**	**409**	**CK848365**	**similar to Sulfite oxidase, mitochondrial precursor**
Oas1	**178**	**292**	**592**	**CK960499**	**2'-5'-oligoadenylate synthetase 1 (OAS1), NM_178108**
Rgn	**67**	**104**	**783**	**NM_173957.2**	**regucalcin (senescence marker protein-30)**
Peg3	1239	575	339	CB429880	paternally expressed gene 3
Tcn2	522	292	191	BM364701	Transcobalamin II; macrocytic anemia
Mest	616	280	139	CK773236	Mesoderm-specific transcript
	343	227	131	BP108175	Transcribed locus, strongly similar to NP_066188.1 amylase
Kdr	227	121	59	CB426507	Kinase insert domain receptor (a type III receptor tyrosine kinase)
Loc515013	91	55	35	CK769953	similar to secernin 2, (LOC515013), predicted
---	161	80	31	CB420635	Transcribed locus, weakly similar to NP_877585.1 IQ motif
Loc510299	101	63	29	BG689826	similar to cytoglobin (LOC510299), predicted
Loc514194	106	49	14	BM362809	similar to Ceruloplasmin precursor (Ferroxidase
Scg2	328	210	2612	NM_174176.2	secretogranin II (chromogranin C)
Tf	168	51	362	NM_177484.2	transferrin
Loc505315	35	18	104	CK848241	similar to T12A2.1 (LOC505315), predicted
Pgdh	214	324	99	CF764344	hydroxyprostaglandin dehydrogenase 15-(NAD)
Mgc127515	46	147	96	CB446157	similar to transmembrane 4 superfamily member
Loc507503	63	142	94	CK772874	similar to THAP domain protein 4 (LOC507503)
Mgc127657	28	99	43	CB461257	similar to plasmalemma vesicle associated protein
Aqp1	47	126	30	NM_174702.2	aquaporin 1

Protease	S	M	Lg	Genbank	Description
Loc613577	**896**	**1409**	**2122**	**CK848260**	**similar to homocysteine-inducible, endoplasmic reticulum**
Serpinb2	**71**	**519**	**1627**	**AF416234.1**	**serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2**
Serpine1	**64**	**285**	**474**	**NM_174137.2**	**serine (or cysteine) proteinase inhibitor, clade E**
Loc514813	102	274	174	CB456244	similar to ubiquitin specific protease 7 (herpes virus-associated)

Receptors	S	M	Lg	Genbank	Description
Il4r	**30**	**48**	**80**	**AV666299**	**interleukin-4 receptor alpha chain,(IL4R), predicted**
	720	339	144	CB421632	Transcribed locus, moderately similar to NP_058934.1
Loc507783	229	136	46	AV603307	similar to Parathyroid hormone/parathyroid hormone-related
Loc512018	76	49	33	CK774341	similar to brother of CDO (LOC512018), predicted
Loc527140	57	97	34	CF931289	similar to Calcitonin gene-related peptide type 1 receptor

Signaling	S	M	Lg	Genbank	Description
Loc515156	**56**	**88**	**133**	**CB424830**	**similar to Six transmembrane epithelial antigen of prostate 1**
Loc533562	**20**	**64**	**100**	**CB419946**	**similar to Transmembrane 9 superfamily protein member 4**
Loc538437	**327**	**522**	**1115**	**CB170392**	**similar to GTP-binding protein GEM (GTP-binding mitogen-induced**
Cryab	**53**	**103**	**203**	**NM_174290.2**	**crystallin, alpha polypeptide 2**
Isg15	**169**	**260**	**437**	**NM_174366.1**	**interferon-stimulated protein, 15 kDa**
Loc516303	**28**	**66**	**104**	**CB456788**	**similar to mitogen-inducible gene 6 protein (LOC516303), predicted**
Loc534658	**27**	**55**	**92**	**CK941373**	**similar to WNT1 inducible signaling pathway protein 2 precursor**
Loc613697	**51**	**113**	**178**	**BI682659**	**similar to Rho GTPase activating protein 10 (LOC613697), predicted**
Lrp8	**5**	**70**	**348**	**CB166058**	**low density lipoprotein receptor-related protein 8**
Mgc128138	**25**	**61**	**278**	**CF614403**	**similar to cardiac ankyrin repeat protein (MGC128138)**
Olr1	**23**	**107**	**346**	**NM_174132.2**	**oxidised low density lipoprotein (lectin-like) receptor 1**
Pik3r1	**20**	**84**	**194**	**NM_174575.1**	**phosphoinositide-3-kinase, regulatory subunit, polypeptide 1**
---	**38**	**62**	**105**	**CK775786**	**Transcribed locus, strongly similar to NP_055104.2 calpain 6**
	335	**598**	**938**	**CK770721**	**Transcribed locus, strongly similar to XP_523795.1**
Lec3	77	34	19	CB534322	Latrophilin 3
Loc525795	500	316	142	BE752701	similar to agrin (LOC525795), predicted
Loc540153	140	80	46	CB426404	similar to tensin like C1 domain containing phosphatase isoform 2
Loc613547	213	105	44	CB456927	similar to receptor (calcitonin) activity modifying protein 3,
Mgc128924	116	72	31	CK774019	similar to ankyrin repeat and SOCS box-containing protein 2 (predicted)
Loc538507	99	56	36	CB423270	similar to Frizzled 2 precursor (Frizzled-2) (Fz-2) (hFz2) (FzE2)
Loc616055	141	85	50	CB456064	similar to Ran GTPase-activating protein 1, transcript variant 3
Tm7sf2	96	33	204	NM_174622.2	transmembrane 7 superfamily member 2
Loc504437	24	82	46	CK978780	similar to Serine/threonine-protein kinase 6 (Serine/threonine kinase 15)
Loc514787	144	84	230	CB427601	similar to serine/threonine kinase 38 like, transcript variant 1
Aurkb	64	109	40	CB538063	Aurora kinase B
Loc521162	19	116	45	CK778554	similar to Slit homolog 2 protein precursor (Slit-2)
Loc533332	48	91	30	CF765405	similar to RAB38 (LOC533332), predicted
Mgc128911	55	475	212	CK848780	similar to secreted frizzled-related protein 2 precursor (MGC128911)
Rfrp	32	240	130	NM_174168.1	RFamide-related peptide precursor

Steroidogenesis	S	M	Lg	Genbank	Description
Cyp19	**37**	**548**	**2956**	**NM_174305.1**	**cytochrome P450, family XIX (conversion of androgen to estrogen)**

Supplemental Table S2

Bovine Theca Cell Regulated Genes

Transcription	S	M	Lg	Genbank	Description
Loc614673	**103**	**162**	**260**	**CK848830**	**similar to Nuclear protein 1 (Protein p8) (Candidate of metastasis 1)**
Bhlhb2	**34**	**102**	**231**	**CB167431**	**differentiated embryo chondrocyte expressed gene 1 (BHLHB2)**
Cited1	**85**	**156**	**619**	**AF362075.1**	**transactivator, with Glu/Asp-rich carboxy-terminal domain, 1**
Eif4e	**21**	**37**	**78**	**CB427688**	**eukaryotic translation initiation factor 4E (EIF4E)**
Fos	**102**	**189**	**339**	**NM_182786.1**	**murine FBJ osteosarcoma viral (v-fos) oncogene homolog**
Loc505549	**31**	**53**	**80**	**AW461342**	**similar to PHD finger protein 22 (LOC505549), predicted**
Loc511939	**47**	**83**	**131**	**AW482178**	**similar to Pirin, transcript variant 3 (LOC511939), predicted**
Loc525888	**56**	**105**	**354**	**BE217422**	**similar to thymus high mobility group box protein TOX**
Loc541305	**68**	**102**	**226**	**BI680153**	**similar to nuclear receptor subfamily 5, group A, member 2 isoform 2**
Loc617269	**48**	**80**	**129**	**CF615274**	**similar to ankyrin repeat and SOCS box-containing 8 (**
Zfp36	**93**	**160**	**285**	**NM_174493.1**	**zinc finger protein homologous to Zfp-36 in mouse**
Loc506470	274	177	97	CK776908	similar to Transcription factor COE4 (Early B-cell factor 4)
Loc510013	644	420	210	CK776799	similar to nuclear receptor co-repressor 2 (LOC510013), predicted
Loc515303	207	122	73	BE236505	similar to HMG-box transcription factor TCF-3 (LOC515303), predicted
Loc527574	260	166	107	CK770186	similar to sal-like 2 (LOC527574), predicted
Loc532209	105	63	36	CK776496	similar to ecotropic viral integration site 1 (LOC532209), predicted
Loc540142	104	46	8	CK776938	similar to forkhead-like 18 (LOC540142), predicted
Loc540251	81	48	21	BM481287	similar to homeo box D10 (LOC540251), predicted
Xist	1088	682	319	CK848330	X (inactive)-specific transcript (XIST) on chromosome X
Loc504585	117	210	73	CK774460	similar to Sperm-associated antigen 5 (Astrin) (Mitotic spindle
Loc514918	132	48	87	CK982002	similar to GC-rich sequence DNA-binding factor homolog
Loc538474	63	103	42	CK966337	similar to Nuclear factor 1 B-type (Nuclear factor 1/B)
Loc541088	50	133	79	CB444034	similar to BCoR protein (BCL-6 corepressor), transcript variant 3
Loc617976	195	293	101	CB533092	similar to LIM domain binding 2 (LOC617976), predicted

Translation	S	M	Lg	Genbank	Description
18s Rrna	1576	252	92	5823437	18S ribosomal RNA gene
Mtif2	76	27	44	CB444297	mitochondrial translational initiation factor 2 (MTIF2)
---	69	26	135	CK774193	Transcribed locus, weakly similar to XP_484324.1

Misc	S	M	Lg	Genbank	Description
Peg3	343	198	85	AW461515	paternally expressed gene 3
Ahsg	40	8	89	CB537901	alpha-2-HS-glycoprotein

Unknown Function	S	M	Lg	Genbank	Description
16-Jun	**430**	**838**	**1558**	**CB461321**	**similar to putative 6-16 protein, transcript variant 1 (6-16), predicted**
Loc505854	**538**	**827**	**1426**	**CK970588**	**similar to Protein C10orf57 homolog,(LOC505854), predicted**
Loc508699	**71**	**113**	**173**	**CB450089**	**hypothetical protein LOC508699 (LOC508699), NM_001031754.1**
Loc511583	**93**	**192**	**417**	**CK941057**	**hypothetical LOC511583 (LOC511583), predicted**
Loc513234	**142**	**329**	**1017**	**CK778634**	**similar to ovary-specific acidic protein (LOC513234), predicted**
Loc529235	**593**	**904**	**1968**	**CK846550**	**similar to RTP801, transcript variant 1 (LOC529235), predicted**
Loc539199	**30**	**46**	**96**	**CK773180**	**similar to MAM domain containing 2 (LOC539199), predicted**
Mgc128138	**103**	**202**	**949**	**CB168998**	**similar to cardiac ankyrin repeat protein (MGC128138)**
Mgc128158	**26**	**95**	**150**	**AV605192**	**similar to optineurin (MGC128158), NM_001034602.1**
Plap-1	**188**	**523**	**829**	**CF765170**	**similar to Asporin precursor**
Cathl5	168	35	10	NM_174510.2	cathelicidin 5
Loc504245	115	69	40	CB425779	similar to nadrin isoform 1 (LOC504245), predicted
Loc504741	603	317	198	CK728198	similar to collectin sub-family member 12 isoform II
Loc509964	82	52	20	CB468388	similar to ankyrin repeat domain 47 (LOC509964), predicted
Loc510926	677	437	264	AW658522	hypothetical LOC510926
Loc515133	941	324	186	CK776308	similar to esophageal cancer related gene 4 protein
Loc518495	194	111	53	CB438670	similar to Apolipoprotein-L3 (Apolipoprotein L-III) (ApoL-III)
Loc616994	157	64	40	CB430275	similar to leucine rich repeat (in FLII) interacting protein 1
Loc507172	117	199	56	CB426994	hypothetical LOC507172 (LOC507172), predicted
Loc507432	32	156	95	AV599674	similar to microtubule-associated protein 1 light chain 3 gamma
Loc508175	82	263	139	BM088163	similar to Plexin B2 precursor (MM1), (LOC508175), predicted
Loc508562	205	120	315	BI848980	similar to CG14120-PA (LOC508562), predicted
Loc513195	51	87	34	CK769492	hypothetical LOC513195, predicted
Loc514940	3115	1132	1803	CK779293	similar to influenza virus NS1A binding protein isoform 2
Loc515235	25	88	52	AV665925	similar to steroid-sensitive protein 1, (LOC515235), predicted
Loc515676	312	170	657	CK973550	similar to CG33196-PB (LOC515676), predicted
Loc521424	120	200	65	CK973730	similar to Epithelial membrane protein 1 (EMP-1)
Mgc127998	53	20	207	CB456384	similar to Calmegin precursor (MGC127998), NM_001034205.1
Mgc127998	75	26	209	CB531852	similar to Calmegin precursor (MGC127998), NM_001034205.1

Ests	S	M	Lg	Genbank	Description
	159	**300**	**457**	**CK771023**	**Transcribed locus, moderately similar to NP_775149.1**
---	**69**	**119**	**182**	**CK772599**	**Transcribed locus**
---	**151**	**249**	**423**	**CK948835**	**Transcribed locus**
---	**54**	**92**	**183**	**CK772076**	**Transcribed locus, moderately similar to NP_997259.1**
---	**72**	**115**	**196**	**CB452156**	**Transcribed locus, strongly similar to NP_080943.2**
---	**27**	**83**	**127**	**CB537905**	**---**
---	**67**	**108**	**183**	**CB466824**	**---**
---	**98**	**1937**	**3291**	**CK773598**	**Transcribed locus**

---	**96**	**190**	**333**	**CK778134**	**Transcribed locus, strongly similar to XP_059689.3**
---	**86**	**141**	**294**	**CK774867**	**Transcribed locus**
---	**53**	**94**	**156**	**CK974214**	**Transcribed locus**
---	**99**	**204**	**368**	**CK846849**	**Transcribed locus**
---	**72**	**150**	**287**	**CK970634**	**Transcribed locus**
	59	**144**	**311**	**BE217509**	**Transcribed locus, moderately similar to NP_003934.1**
---	**66**	**119**	**244**	**BI540104**	**Transcribed locus**
---	**37**	**62**	**101**	**BI540137**	**---**
	261	166	106	CK955810	Transcribed locus, moderately similar to NP_036271.1
---	122	77	40	CA035817	Transcribed locus
---	86	47	23	CB170964	Transcribed locus
---	107	52	30	CB437846	Transcribed locus
---	203	111	67	CB431739	Transcribed locus
	109	51	33	CB430887	Transcribed locus
---	106	49	33	CB533238	---
	266	162	106	CK773136	Transcribed locus, weakly similar to XP_328828.1
	274	176	106	CB531827	Transcribed locus
	1842	1070	615	BF603163	Transcribed locus
---	120	63	32	CB445425	---
---	110	65	30	AW425901	Transcribed locus
---	282	143	93	BE808552	Transcribed locus
---	157	101	56	CK848002	Transcribed locus, moderately similar to XP_510678.1
---	152	41	16	CA923335	Transcribed locus
	315	110	68	CB421639	Transcribed locus, moderately similar to XP_521353.1
	227	136	85	BI541767	Transcribed locus, strongly similar to XP_232372.2
---	214	128	79	BF601695	Transcribed locus, moderately similar to XP_223730.2
---	141	87	43	CK773285	Transcribed locus
---	458	277	145	CK729536	Transcribed locus
---	80	39	25	CK769590	Transcribed locus, strongly similar to XP_375469.1 ProSAPiP2
---	116	74	40	CK777757	---
---	126	61	34	CK776385	Transcribed locus
---	115	61	32	AV616558	Transcribed locus, weakly similar to NP_277055.1 chromosome 19
---	111	71	35	CK769253	Transcribed locus
---	117	71	34	CK770333	Transcribed locus, strongly similar to NP_598684.2 RIKEN cDNA
	288	156	93	CB446249	Transcribed locus
---	142	71	36	CK952296	Transcribed locus
---	75	30	18	CB456691	Transcribed locus
---	136	79	41	AV616245	---
---	353	198	124	BE683785	Transcribed locus
---	444	284	135	BE663820	Transcribed locus
---	110	71	20	BF046170	Transcribed locus
---	163	89	40	AV617450	Transcribed locus
---	187	55	110	CB536259	Transcribed locus
---	163	66	101	CK831507	Transcribed locus
---	92	23	46	AU276024	Transcribed locus
---	58	37	92	CK944968	Transcribed locus
---	239	367	132	CK772779	---
---	175	39	68	CB461365	Transcribed locus
---	54	112	34	CK846762	Transcribed locus
---	665	418	1149	CK944387	Transcribed locus
---	206	69	116	CB433831	Transcribed locus
---	204	129	328	CB170513	Transcribed locus
---	219	78	141	CK975790	Transcribed locus
---	140	42	72	CB466120	Transcribed locus
---	134	50	82	BI536928	Transcribed locus
---	2076	577	1196	CB165272	Transcribed locus, strongly similar to NP_008917.2 melanoma antigen

Bolded genes are increased for all three antral follicle sizes (S<M<L).