Table S1. Genes showing significantly different expression in summer granulosa cells

Genes showing reduced expression in summer granulosa cells

Probeset ID	Gene Symbol	Gene Description	Ctrl	Summ	Ratio Ctrl:Summ	Probes found in
Mmu.5409.1.S1_at	TMEM106B	transmembrane protein 106B	155	18	8.479	transcripts
MmugDNA.19043.1.S1_at	SHISA2	shisa homolog 2 (Xenopus laevis)	2932	444	6.600	genic&downstr. reg.
MmuMitochon.3.1.S1_s_at	ND2	NADH dehydrogenase subunit 2	7886	1207	6.536	transcripts
MmugDNA.15046.1.S1_at	HMCN1	hemicentin 1	343	58	5.942	transcripts
MmuMitochon.6.1.S1_s_at	ATP8	ATP synthase F0 subunit 8	2768	469	5.906	transcripts
MmuMitochon.10.1.S1_s_at	ND4L	NADH dehydrogenase subunit 4L	4125	740	5.574	transcripts
MmugDNA.32362.1.S1_at	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	224	44	5.113	transcripts
MmugDNA.34243.1.S1_at	KCNAB1	potassium voltage-gated channel,shaker-related subfamily,beta member 1	249	51	4.867	transcripts
MmuSTS.2065.1.S1_x_at	PYGL	phosphorylase,glycogen,liver	401	86	4.654	transcripts
MmugDNA.8704.1.S1_at	STC2	stanniocalcin 2	82	18	4.438	transcripts
Mmu.8081.1.S1_at	AKR1B10 /// AKR1B15	aldo-keto reductase family 1, member B10 (aldose reductase) /// aldo-keto reductase family 1, member B15	121	27	4.400	transcripts
Mmu.6025.1.S1_at	---	---	193	45	4.331	---
MmuSTS.2065.1.S1_at	PYGL	phosphorylase,glycogen,liver	352	83	4.249	transcripts
MmugDNA.14019.1.S1_at	FAM196A	family with sequence similarity 196,member A	401	95	4.220	transcripts
Mmu.8081.1.S1_x_at	AKR1B10 /// AKR1B15	aldo-keto reductase family 1, member B10 (aldose reductase) /// aldo-keto reductase family 1, member B15	127	30	4.207	transcripts
MmugDNA.23693.1.S1_at	PYGL	phosphorylase,glycogen,liver	77	19	4.060	transcripts
MmuSTS.1929.1.S1_at	MYCN	v-myc myelocytomatosis viral related oncogene,neuroblastoma derived (avian)	287	72	3.985	transcripts
MmugDNA.27799.1.S1_at	C8orf47	chromosome 8 open reading frame 47	670	181	3.709	transcripts
MmuSTS.2065.1.S1_s_at	PYGL	phosphorylase,glycogen,liver	203	56	3.604	transcripts
MmugDNA.37200.1.S1_at	SUSD3	sushi domain containing 3	744	208	3.580	transcripts
MmugDNA.27973.1.S1_at	VAT1L	vesicle amine transport protein 1 homolog (T. californica)-like	194	56	3.503	transcripts
MmugDNA.31819.1.S1_at	SLC26A2	solute carrier family 26 (sulfate transporter),member 2	2031	585	3.473	transcripts
Mmu.3044.13.S1_x_at	LOC100423785	ATP synthase subunit a-like	15638	4510	3.467	transcripts
MmugDNA.43522.1.S1_at	GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	93	27	3.438	transcripts
Mmu.3117.1.S1_at	---	---	4112	1248	3.296	---

MmugDNA.43592.1.S1_at	---	---	206	65	3.187	---
MmugDNA.32570.1.S1_at	LYZ	lysozyme (renal amyloidosis)	1311	429	3.057	transcripts
MmuSTS.345.1.S1_at	SVIL	supervillin	679	224	3.029	transcripts
Mmu.6867.1.S1_s_at	LOC100428825	uncharacterized LOC100428825	8041	3154	2.549	transcripts
MmuAffx.23.14.S1_s_at	---	---	19359	7630	2.537	---
Mmu.15402.1.A1_at	---	---	3394	1416	2.397	---
Mmu.13865.1.S1_s_at	---	---	4189	1754	2.388	---
Mmu.15402.10.S1_s_at	LOC100426925	uncharacterized LOC100426925	17356	7277	2.385	transcripts
MmugDNA.32338.1.S1_at	NAV1	neuron navigator 1	194	83	2.333	transcripts
MmugDNA.35652.1.S1_s_at	CCDC52	coiled-coil domain containing 52	345	151	2.294	transcripts
MmugDNA.35036.1.S1_at	---	---	2413	1061	2.275	---
MmugDNA.16268.1.S1_s_at	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	299	136	2.202	transcripts
MmugDNA.24286.1.S1_at	F2RL1	coagulation factor II (thrombin) receptor-like 1	5374	2479	2.168	transcripts
MmugDNA.33607.1.S1_at	MRPL36	mitochondrial ribosomal protein L36	2387	1109	2.152	transcripts
MmugDNA.10691.1.S1_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	1708	824	2.072	transcripts
MmugDNA.39768.1.S1_at	TMEM219	transmembrane protein 219	173	86	2.016	transcripts
MmugDNA.13478.1.S1_at	C11orf58	chromosome 11 open reading frame 58	591	310	1.907	transcripts
MmugDNA.9782.1.S1_at	ALAS1	aminolevulinate,delta-,synthase 1	1199	663	1.808	transcripts

Genes showing increased expression in summer granulosa cells

Probeset ID	Gene Symbol	Gene Description	Ctrl	Summ	Ratio Summ:Ctrl	Probes found in
MmuSTS.3686.1.S1_at	COL14A1	collagen,type XIV,alpha 1	39	627	16.268	transcripts
MmugDNA.42438.1.S1_at	ANKRD28	ankyrin repeat domain 28	35	502	14.490	genic&downstr. reg.
MmugDNA.11070.1.S1_at	SYNE1	spectrin repeat containing, nuclear envelope 1	12	127	10.560	transcripts
MmugDNA.6912.1.S1_at	GPM6A	glycoprotein M6A	23	212	9.170	transcripts
MmugDNA.34306.1.S1_at	TGFBR3	transforming growth factor, beta receptor III	17	131	7.770	genic&downstr. reg.
MmugDNA.28937.1.S1_at	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	20	147	7.454	genic&downstr. reg.
MmugDNA.11395.1.S1_at	FAM13A	family with sequence similarity 13, member A	40	290	7.283	genic&downstr. reg.
MmugDNA.13933.1.S1_at	HOPX	HOP homeobox	65	395	6.073	transcripts
MmugDNA.16061.1.S1_at	RBMS3	RNA binding motif, single stranded interacting protein 3	13	77	5.779	genic&downstr. reg.
MmugDNA.4885.1.S1_at	GPM6A	glycoprotein M6A	40	219	5.544	transcripts
MmugDNA.26075.1.S1_at	DENND1B	DENN/MADD domain containing 1B	15	83	5.464	genic&downstr. reg.
MmugDNA.8127.1.S1_at	TFG	TRK-fused gene	60	326	5.394	genic&downstr. reg.
MmugDNA.12544.1.S1_at	ACSL3	acyl-CoA synthetase long-chain family member 3	36	187	5.186	transcripts
MmugDNA.16839.1.S1_at	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	135	696	5.140	genic&downstr. reg.
MmugDNA.6175.1.S1_at	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	42	215	5.112	genic&downstr. reg.

MmugDNA.5795.1.S1_at	PTPRM	protein tyrosine phosphatase, receptor type, M	18	88	5.042	genic&downstr. reg.
MmugDNA.28171.1.S1_at	NEAT1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	190	887	4.674	transcripts
MmugDNA.38123.1.S1_at	DENND1B	DENN/MADD domain containing 1B	47	214	4.581	genic&downstr. reg.
MmugDNA.6058.1.S1_at	RORA	RAR-related orphan receptor A	281	1284	4.575	genic&downstr. reg.
MmugDNA.33749.1.S1_s_at	PGAP1	post-GPI attachment to proteins 1	555	2527	4.554	genic&downstr. reg.
MmuSTS.2906.1.S1_at	VWF	von Willebrand factor	226	971	4.290	transcripts
MmugDNA.20894.1.S1_at	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	21	90	4.228	genic&downstr. reg.
MmugDNA.27708.1.S1_at	TJP1	tight junction protein 1	69	278	3.998	genic&downstr. reg.
MmugDNA.11249.1.S1_at	KCTD12	potassium channel tetramerization domain containing 12	30	118	3.862	transcripts
MmugDNA.10709.1.S1_at	EZR	ezrin	27	103	3.788	genic&downstr. reg.
MmugDNA.21689.1.S1_at	GPM6A	glycoprotein M6A	23	80	3.504	transcripts
MmugDNA.2048.1.S1_at	REV3L	REV3-like, polymerase (DNA directed), zeta, catalytic subunit	48	154	3.223	genic&downstr. reg.
MmugDNA.6861.1.S1_at	H2AFY	H2A histone family, member Y	28	89	3.175	genic&downstr. reg.
MmuSTS.1361.1.S1_at	ANXA4	annexin A4	152	479	3.146	transcripts
MmugDNA.14309.1.S1_at	ALCAM	activated leukocyte cell adhesion molecule	48	151	3.139	transcripts
MmugDNA.30630.1.S1_at	---	---	67	209	3.111	---
MmugDNA.21716.1.S1_at	---	---	195	599	3.069	---
MmugDNA.37278.1.S1_at	EID3	EP300 interacting inhibitor of differentiation 3	109	329	3.027	transcripts
MmugDNA.31091.1.S1_at	MAP9	microtubule-associated protein 9	399	1197	3.004	transcripts
MmugDNA.2759.1.S1_at	USP15	ubiquitin specific peptidase 15	42	123	2.938	genic&downstr. reg.
MmugDNA.21432.1.S1_at	LOC729852	uncharacterized LOC729852	31	90	2.912	genic&downstr. reg.
MmugDNA.21050.1.S1_at	LOC100132013	hypothetical LOC100132013	49	139	2.812	transcripts
MmugDNA.2278.1.S1_at	A2BP1	ataxin 2-binding protein 1	115	310	2.686	transcripts
MmugDNA.25683.1.S1_at	ARID5B	AT rich interactive domain 5B (MRF1-like)	126	337	2.676	genic&downstr. reg.
MmugDNA.3305.1.S1_at	ZNF614	zinc finger protein 614	102	267	2.626	genic&downstr. reg.
MmuSTS.1355.1.S1_at	ALDH9A1	aldehyde dehydrogenase 9 family,member A1	722	1850	2.561	transcripts
MmunewRS.949.1.S1_at	MT3	metallothionein 3	204	515	2.530	transcripts
MmuSTS.3097.1.S1_at	MID1	midline 1 (Opitz/BBB syndrome)	62	157	2.524	transcripts
MmugDNA.7587.1.S1_at	MDH1	malate dehydrogenase 1, NAD (soluble)	59	147	2.487	genic&downstr. reg.
MmugDNA.36345.1.S1_at	AUTS2	autism susceptibility candidate 2	337	823	2.444	transcripts
MmugDNA.14310.1.S1_at	ALCAM	activated leukocyte cell adhesion molecule	1179	2839	2.409	transcripts
MmugDNA.43422.1.S1_s_at	CRIPT	cysteine-rich PDZ-binding protein	191	458	2.396	transcripts
MmugDNA.29455.1.S1_at	INPP4A	inositol polyphosphate-4-phosphatase,type I,107kDa	537	1274	2.374	transcripts
MmuSTS.138.1.S1_at	PRICKLE1	prickle homolog 1 (Drosophila)	209	492	2.353	transcripts

MmugDNA.38804.1.S1_at	INPP4A	inositol polyphosphate-4-phosphatase,type I,107kDa	174	409	2.350	transcripts
MmugDNA.43475.1.S1_at	INPP4A	inositol polyphosphate-4-phosphatase,type I,107kDa	160	368	2.298	transcripts
MmugDNA.25911.1.S1_at	---	---	40	90	2.244	---
MmuSTS.1357.1.S1_s_at	ANGPTL1	angiopoietin-like 1	75	164	2.187	transcripts
MmugDNA.28466.1.S1_at	NPTN	neuroplastin	159	348	2.182	genic&downstr. reg.
MmugDNA.1421.1.S1_at	PRICKLE2	prickle homolog 2 (Drosophila)	66	144	2.169	transcripts
MmugDNA.7673.1.S1_at	---	---	125	270	2.155	---
MmugDNA.11251.1.S1_at	KCTD12	potassium channel tetramerisation domain containing 12	1226	2618	2.136	transcripts
MmugDNA.36491.1.S1_s_at	AKR1C2	aldo-keto reductase family 1,member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase,type III)	974	2012	2.066	transcripts
MmugDNA.34028.1.S1_at	MARK1	MAP/microtubule affinity-regulating kinase 1	84	157	1.868	transcripts
MmugDNA.37092.1.S1_at	DR1	down-regulator of transcription 1,TBP-binding (negative cofactor 2)	64	112	1.747	transcripts
MmugDNA.11944.1.S1_at	TMEM87A	transmembrane protein 87A	406	694	1.709	transcripts
MmugDNA.35680.1.S1_at	CORO6	coronin 6	64	104	1.628	genic&downstr. reg.
MmugDNA.22282.1.S1_at	WDFY1	WD repeat and FYVE domain containing 1	280	444	1.586	transcripts