Table S2. Genes showing significantly different expression in summer cumulus cells

Genes showing reduced expression in summer cumulus cells

Probeset ID	Gene Symbol	Gene Description	Ctrl	Summ	Ratio Ctrl:Summ	Probes found in
MmuMitochon.6.1.S1_s_at	ATP8	ATP synthase F0 subunit 8	2293	53	43.185	transcripts
MmuMitochon.10.1.S1_s_at	ND4L	NADH dehydrogenase subunit 4L	2117	77	27.330	transcripts
MmuMitochon.3.1.S1_s_at	ND2	NADH dehydrogenase subunit 2	6547	402	16.300	transcripts
MmugDNA.8704.1.S1_at	STC2	stanniocalcin 2	1153	100	11.547	transcripts
MmuSTS.4178.1.S1_at	CTSL2	cathepsin L2	251	30	8.312	transcripts
Mmu.6025.1.S1_at	---	---	184	25	7.480	---
Mmu.6867.1.A1_at	---	---	2795	376	7.438	---
MmugDNA.19043.1.S1_at	SHISA2	shisa homolog 2 (Xenopus laevis)	1643	226	7.283	genic&downstr. reg.
MmugDNA.21615.1.S1_at	STC2	stanniocalcin 2	444	65	6.886	transcripts
MmugDNA.42645.1.S1_at	---	---	364	65	5.558	---
Mmu.3117.1.S1_at	---	---	4096	848	4.827	---
MmugDNA.38441.1.S1_at	GUCY1A3	guanylate cyclase 1,soluble,alpha 3	122	30	4.009	transcripts
MmugDNA.9861.1.S1_at	ACTN2	actinin,alpha 2	186	50	3.715	transcripts
MmugDNA.3526.1.S1_at	---	---	216	59	3.688	---
MmugDNA.32328.1.S1_at	LHFP	lipoma HMGIC fusion partner	567	162	3.502	transcripts
MmugDNA.27799.1.S1_at	C8orf47	chromosome 8 open reading frame 47	462	137	3.374	transcripts
MmugDNA.35476.1.S1_at	MCC	mutated in colorectal cancers	159	49	3.252	transcripts
MmuSTS.1688.1.S1_at	UGT1A9	UDP glucuronosyltransferase 1 family,polypeptide A9	805	249	3.227	transcripts
Mmu.3064.4.S1_s_at	---	---	18738	5834	3.212	---
MmugDNA.21104.1.S1_at	LHCGR	luteinizing hormone/choriogonadotropin receptor	157	50	3.166	transcripts
MmugDNA.25149.1.S1_at	ZNF879	zinc finger protein 879	119	39	3.053	transcripts
MmugDNA.40336.1.S1_at	COL5A1	collagen, type V, alpha 1	271	89	3.033	transcripts
MmugDNA.28033.1.S1_at	SIDT1	SID1 transmembrane family,member 1	230	77	2.982	transcripts
MmugDNA.7989.1.S1_at	ANGPT2	angiopoietin 2	98	34	2.905	transcripts
MmugDNA.36098.1.S1_at	ANKRD37	ankyrin repeat domain 37	1053	364	2.892	transcripts
MmuSTS.2135.1.S1_at	SAP30	Sin3A-associated protein,30kDa	129	45	2.861	transcripts
MmuSTS.2065.1.S1_s_at	PYGL	phosphorylase,glycogen,liver	259	91	2.853	transcripts
MmugDNA.27973.1.S1_at	VAT1L	vesicle amine transport protein 1 homolog (T. californica)-like	888	320	2.774	transcripts
MmugDNA.15364.1.S1_at	OPN3	opsin 3	373	136	2.744	transcripts
MmuSTS.3605.1.S1_at	DYNC1I1	dynein,cytoplasmic 1,intermediate chain 1	493	180	2.742	transcripts
MmugDNA.13626.1.S1_at	PTGIS	prostaglandin I2 (prostacyclin) synthase	190	70	2.736	transcripts
MmugDNA.20560.1.S1_at	TRIM9	tripartite motif-containing 9	96	35	2.731	transcripts
MmugDNA.42278.1.S1_s_at	SGMS2	sphingomyelin synthase 2	424	156	2.724	transcripts
MmugDNA.19504.1.S1_at	SORBS2	sorbin and SH3 domain containing 2	1326	487	2.719	genic&downstr. reg.

Mmu.3044.13.S1_x_at	LOC100423785	ATP synthase subunit a-like	14663	5407	2.712	transcripts
MmugDNA.19923.1.S1_at	RFTN2	raftlin family member 2	143	53	2.707	transcripts
MmugDNA.40338.1.S1_s_at	COL5A1	collagen,type V,alpha 1	191	71	2.693	transcripts
MmuSTS.2065.1.S1_x_at	PYGL	phosphorylase,glycogen,liver	638	237	2.686	transcripts
MmugDNA.33613.1.S1_at	---	---	366	140	2.610	---
MmuSTS.3872.1.S1_at	SLC2A1	solute carrier family 2 (facilitated glucose transporter),member 1	603	232	2.595	transcripts
MmuSTS.3980.1.S1_at	SH3BGR	SH3 domain binding glutamic acid-rich protein	528	204	2.591	transcripts
MmuSTS.2065.1.S1_at	PYGL	phosphorylase,glycogen,liver	602	233	2.587	transcripts
MmugDNA.33494.1.S1_at	ELAVL2	ELAV (embryonic lethal,abnormal vision,Drosophila)-like 2 (Hu antigen B)	814	316	2.581	transcripts
MmugDNA.9064.1.S1_at	---	---	255	99	2.572	---
MmugDNA.16704.1.S1_at	COX4I1	cytochrome c oxidase subunit IV isoform 1	347	137	2.528	transcripts
MmuSTS.4136.1.S1_at	ENO2	enolase 2 (gamma,neuronal)	389	155	2.508	transcripts
MmuSTS.4189.1.S1_s_at	OLFM4	olfactomedin 4	2554	1021	2.502	transcripts
MmugDNA.33613.1.S1_x_at	---	---	262	106	2.458	---
MmuSTS.3600.1.S1_at	DAPK1	death-associated protein kinase 1	265	108	2.458	transcripts
MmugDNA.28658.1.S1_at	PELP1	proline, glutamate and leucine rich protein 1	178	72	2.454	genic&downstr. reg.
Mmu.6048.2.S1_at	---	---	97	40	2.419	---
MmugDNA.357.1.S1_at	DCLK1	doublecortin-like kinase 1	156	65	2.412	transcripts
MmugDNA.39180.1.S1_at	JAKMIP2	janus kinase and microtubule interacting protein 2	254	105	2.409	transcripts
MmuAffx.23.14.S1_s_at	---	---	18850	7898	2.387	---
MmugDNA.31648.1.S1_at	PID1	phosphotyrosine interaction domain containing 1	176	74	2.369	transcripts
MmuSTS.921.1.S1_at	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	120	51	2.360	transcripts
MmugDNA.27981.1.S1_at	LRRC49	leucine rich repeat containing 49	187	80	2.349	transcripts
MmugDNA.29470.1.S1_at	---	---	356	152	2.339	---
MmuSTS.2655.1.S1_at	ABCA8	ATP-binding cassette,sub-family A (ABC1),member 8	141	61	2.326	transcripts
MmugDNA.20507.1.S1_at	---	---	371	160	2.326	---
MmugDNA.579.1.S1_at	RHPN2	rhophilin,Rho GTPase binding protein 2	236	102	2.303	transcripts
MmugDNA.23054.1.S1_at	SLC22A23	solute carrier family 22,member 23	497	216	2.302	transcripts
MmugDNA.8421.1.S1_at	PDZRN3	PDZ domain containing ring finger 3	431	188	2.294	transcripts
MmuSTS.2101.1.S1_at	RIN2	Ras and Rab interactor 2	478	210	2.279	transcripts
MmuSTS.4406.1.S1_at	COL5A1	collagen,type V,alpha 1	359	158	2.268	transcripts
MmugDNA.39722.1.S1_at	FRMD5	FERM domain containing 5	99	44	2.249	genic&downstr. reg.
Mmu.15402.1.A1_at	---	---	3095	1396	2.217	---
MmunewRS.356.1.S1_s_at	CRIP1	cysteine-rich protein 1 (intestinal)	459	209	2.198	transcripts
MmugDNA.32938.1.S1_at	CBWD3	COBW domain containing 3	113	51	2.197	transcripts
MmuSTS.4660.1.S1_at	TNFAIP6	tumor necrosis factor,alpha-induced protein 6	1318	611	2.156	transcripts

MmuSTS.1837.1.S1_at	UST	uronyl-2-sulfotransferase	328	153	2.143	transcripts
MmugDNA.17750.1.S1_at	ATP2B1	ATPase,Ca transporting,plasma membrane 1	466	219	2.127	transcripts
MmugDNA.36416.1.S1_at	KLHL23 /// PHOSPHO2-KLHL23	PHOSPHO2-KLHL23 readthrough /// kelch-like family member 23	336	159	2.110	genic&downstr. reg.
MmugDNA.18785.1.S1_at	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	962	457	2.104	transcripts
MmugDNA.35629.1.S1_at	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	1593	757	2.103	transcripts
MmugDNA.34243.1.S1_at	KCNAB1	potassium voltage-gated channel,shaker-related subfamily,beta member 1	299	143	2.093	transcripts
MmugDNA.5413.1.S1_at	---	---	112	54	2.086	---
MmuSTS.3163.1.S1_at	RGS7	regulator of G-protein signaling 7	215	103	2.081	transcripts
MmugDNA.31819.1.S1_at	SLC26A2	solute carrier family 26 (sulfate transporter),member 2	681	331	2.055	transcripts
MmugDNA.31856.1.S1_at	RIF1	RAP1 interacting factor homolog (yeast)	285	138	2.055	genic&downstr. reg.
MmuSTS.813.1.S1_at	DDIT4	DNA-damage-inducible transcript 4	386	189	2.036	transcripts
Mmu.4442.1.S1_s_at	---	---	991	487	2.036	---
MmugDNA.7835.1.S1_at	PABPC4L	poly(A) binding protein,cytoplasmic 4-like	120	59	2.028	transcripts
MmugDNA.28101.1.S1_at	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	441	218	2.022	transcripts
MmugDNA.32170.1.S1_at	C20orf160	chromosome 20 open reading frame 160	395	195	2.021	transcripts
MmugDNA.34151.1.S1_at	DYNLT3	dynein,light chain,Tctex-type 3	636	318	1.999	transcripts
MmugDNA.327.1.S1_at	PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	882	443	1.989	genic&downstr. reg.
MmugDNA.27864.1.S1_at	COL12A1	collagen,type XII,alpha 1	96	48	1.988	transcripts
MmugDNA.34279.1.S1_at	RYR2	ryanodine receptor 2 (cardiac)	188	94	1.987	transcripts
MmugDNA.3351.1.S1_at	NSG1	neuron specific gene family member 1	537	271	1.982	transcripts
MmugDNA.37334.1.S1_at	---	---	144	73	1.970	---
MmugDNA.39542.1.S1_at	GUCY1B3	guanylate cyclase 1,soluble,beta 3	94	48	1.966	transcripts
MmugDNA.10449.1.S1_at	---	---	636	325	1.956	---
MmugDNA.21052.1.S1_at	---	---	320	165	1.940	---
MmugDNA.40984.1.S1_at	STON1	stonin 1	100	52	1.938	transcripts
MmuSTS.809.1.S1_at	ASAP2	ArfGAP with SH3 domain,ankyrin repeat and PH domain 2	222	115	1.929	transcripts
MmugDNA.22711.1.S1_at	RARS2	arginyl-tRNA synthetase 2,mitochondrial	481	250	1.925	transcripts
MmuSTS.3429.1.S1_at	COL12A1	collagen,type XII,alpha 1	536	279	1.919	transcripts
MmuSTS.1273.1.S1_at	DCLK1	doublecortin-like kinase 1	1557	818	1.904	transcripts
MmuSTS.1232.1.S1_at	CPNE4	copine IV	111	58	1.897	transcripts
MmugDNA.20015.1.S1_at	GGPS1	geranylgeranyl diphosphate synthase 1	154	81	1.895	transcripts
MmugDNA.32827.1.S1_at	TMEM90B	transmembrane protein 90B	157	83	1.882	transcripts

MmugDNA.2140.1.S1_at	INSIG2	insulin induced gene 2	199	106	1.879	transcripts
MmugDNA.8112.1.S1_at	---	---	637	340	1.874	---
MmuSTS.4685.1.S1_at	TYMS	thymidylate synthetase	273	146	1.872	transcripts
MmugDNA.13752.1.S1_at	SPATA7	spermatogenesis associated 7	201	108	1.872	transcripts
MmugDNA.15777.1.S1_at	TRMT61B	tRNA methyltransferase 61 homolog B (S. cerevisiae)	418	224	1.868	transcripts
MmuSTS.3178.1.S1_at	RNF144A	ring finger protein 144A	604	324	1.865	transcripts
MmugDNA.39440.1.S1_at	CDR2	cerebellar degeneration-related protein 2,62kDa	185	99	1.864	transcripts
MmuSTS.4341.1.S1_at	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	108	58	1.864	genic&downstr. reg.
MmugDNA.21828.1.S1_at	BDH2	3-hydroxybutyrate dehydrogenase,type 2	134	72	1.861	transcripts
MmugDNA.10370.1.S1_at	ARV1	ARV1 homolog (S. cerevisiae)	245	132	1.853	transcripts
MmugDNA.877.1.S1_at	SORBS2	sorbin and SH3 domain containing 2	765	413	1.851	genic&downstr. reg.
Mmu.5288.1.S1_at	LOC100423814	cytochrome c oxidase subunit 7C, mitochondrial-like	4156	2247	1.850	transcripts
MmugDNA.42808.1.S1_at	ZEB1	zinc finger E-box binding homeobox 1	310	168	1.849	transcripts
MmugDNA.36175.1.S1_at	SLC26A2	solute carrier family 26 (sulfate transporter),member 2	1026	556	1.845	transcripts
MmugDNA.7590.1.S1_at	SH3D19	SH3 domain containing 19	173	94	1.845	transcripts
MmugDNA.12017.1.S1_at	FANK1	fibronectin type III and ankyrin repeat domains 1	137	74	1.839	transcripts
MmugDNA.1672.1.S1_at	TNFAIP6	tumor necrosis factor,alpha-induced protein 6	392	214	1.837	transcripts
MmugDNA.13968.1.S1_at	GCOM1 /// MYZAP	GRINL1A complex locus 1 /// myocardial zonula adherens protein	971	529	1.837	transcripts
MmugDNA.21575.1.S1_at	IRX3	iroquois homeobox 3	474	259	1.831	transcripts
MmugDNA.25037.1.S1_at	ARL5A	ADP-ribosylation factor-like 5A	432	236	1.831	genic&downstr. reg.
MmugDNA.7522.1.S1_at	---	---	160	88	1.820	---
MmugDNA.13217.1.S1_at	IKBIP	IKBKB interacting protein	488	269	1.819	transcripts
MmugDNA.12912.1.S1_at	---	---	278	153	1.818	---
MmugDNA.9983.1.S1_at	SEPT11	septin 11	231	127	1.816	genic&downstr. reg.
MmugDNA.5448.1.S1_at	---	---	111	61	1.810	---
MmugDNA.9106.1.S1_at	LARP6	La ribonucleoprotein domain family, member 6	81	45	1.803	transcripts
MmugDNA.15046.1.S1_at	HMCN1	hemicentin 1	290	161	1.797	transcripts
MmugDNA.13156.1.S1_at	CAV1	caveolin 1,caveolae protein,22kDa	790	440	1.797	transcripts
MmugDNA.8435.1.S1_at	PROSC	proline synthetase co-transcribed homolog (bacterial)	147	82	1.783	transcripts
MmugDNA.8778.1.S1_at	ASAP1	ArfGAP with SH3 domain,ankyrin repeat and PH domain 1	312	176	1.770	transcripts
MmugDNA.15092.1.S1_at	CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	226	128	1.767	transcripts
MmuSTS.4562.1.S1_at	TCEA3	transcription elongation factor A (SII),3	669	380	1.760	transcripts

MmugDNA.15417.1.S1_at	CDK8	cyclin-dependent kinase 8	181	103	1.758	genic&downstr. reg.
MmugDNA.37811.1.S1_at	ETAA1	Ewing tumor-associated antigen 1	218	124	1.754	transcripts
MmugDNA.3425.1.S1_at	---	---	175	100	1.742	---
MmuSTS.2903.1.S1_at	VEGFC	vascular endothelial growth factor C	94	54	1.735	transcripts
MmugDNA.8340.1.S1_at	C13orf36	chromosome 13 open reading frame 36	1741	1004	1.735	transcripts
MmugDNA.40534.1.S1_s_at	SKP2	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase	106	61	1.734	genic&downstr. reg.
MmugDNA.12399.1.S1_at	TMX1	thioredoxin-related transmembrane protein 1	2097	1213	1.728	transcripts
MmugDNA.5051.1.S1_s_at	CDCA7L	cell division cycle associated 7-like	372	215	1.726	genic&downstr. reg.
MmugDNA.21010.1.S1_at	ZSCAN29	zinc finger and SCAN domain containing 29	236	137	1.723	transcripts
MmugDNA.9349.1.S1_at	CKLF /// CKLF-CMTM1	CKLF-CMTM1 readthrough /// chemokine-like factor	536	311	1.722	genic&downstr. reg.
MmugDNA.18610.1.S1_at	MIR210 /// MIR210HG	MIR210 host gene (non-protein coding) /// microRNA 210	364	212	1.719	genic&downstr. reg.
MmuSTS.1414.1.S1_at	CAV2	caveolin 2	1143	665	1.719	transcripts
MmugDNA.37206.1.S1_at	SMAD7	SMAD family member 7	139	81	1.718	transcripts
MmugDNA.3502.1.S1_at	GLCE	glucuronic acid epimerase	738	430	1.715	transcripts
MmugDNA.13821.1.S1_s_at	CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	1142	668	1.708	transcripts
MmugDNA.18194.1.S1_at	MAP2K6	mitogen-activated protein kinase kinase 6	109	64	1.707	transcripts
MmugDNA.4477.1.S1_at	CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	359	211	1.700	transcripts
MmugDNA.30425.1.S1_at	ALG9	asparagine-linked glycosylation 9,alpha-1,2-mannosyltransferase homolog (S. cerevisiae)	443	260	1.699	transcripts
MmugDNA.33877.1.S1_at	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	772	455	1.697	transcripts
MmugDNA.33296.1.S1_at	JUB	jub,ajuba homolog (Xenopus laevis)	1134	669	1.694	transcripts
MmugDNA.8964.1.S1_s_at	ZNF627	zinc finger protein 627	355	209	1.694	transcripts
MmugDNA.30648.1.S1_at	IFT81	intraflagellar transport 81 homolog (Chlamydomonas)	137	81	1.692	transcripts
MmugDNA.17479.1.S1_at	---	---	1142	677	1.687	---
MmugDNA.18859.1.S1_at	LOC707289	endothelial zinc finger protein induced by tumor necrosis factor alpha-like	123	73	1.686	genic&downstr. reg.
MmugDNA.43133.1.S1_at	NME5	NME/NM23 family member 5	165	98	1.683	transcripts
MmugDNA.26960.1.S1_at	DCAF13	DDB1 and CUL4 associated factor 13	398	237	1.682	transcripts
MmugDNA.31556.1.S1_at	TES	testis derived transcript (3 LIM domains)	1502	894	1.681	transcripts
MmugDNA.30627.1.S1_s_at	AJUBA	ajuba LIM protein	727	433	1.680	transcripts
MmugDNA.18285.1.S1_at	PON2	paraoxonase 2	115	68	1.679	genic&downstr. reg.
MmugDNA.28771.1.S1_at	---	---	178	106	1.679	---
MmugDNA.21209.1.S1_at	LRRC27	leucine rich repeat containing 27	165	98	1.678	transcripts
MmugDNA.23750.1.S1_at	PARP11	poly (ADP-ribose) polymerase family,member 11	873	524	1.669	transcripts

MmugDNA.22887.1.S1_s_at	MRPL30	mitochondrial ribosomal protein L30	148	89	1.666	transcripts
MmugDNA.27852.1.S1_at	RIMKLB	ribosomal modification protein rimK-like family member B	408	245	1.665	transcripts
MmugDNA.34216.1.S1_at	ZBTB8A	zinc finger and BTB domain containing 8A	91	55	1.665	transcripts
MmugDNA.617.1.S1_at	PLEKHH1	pleckstrin homology domain containing,family H (with MyTH4 domain) member 1	139	84	1.664	transcripts
MmugDNA.14289.1.S1_at	KCTD1	potassium channel tetramerisation domain containing 1	1054	635	1.661	transcripts
MmugDNA.3538.1.S1_at	RIMS2	regulating synaptic membrane exocytosis 2	173	104	1.657	transcripts
MmuSTS.1223.1.S1_at	POSTN	periostin,osteoblast specific factor	1775	1073	1.654	transcripts
MmugDNA.2116.1.S1_at	HMGB1	high-mobility group box 1	187	113	1.652	transcripts
MmugDNA.29009.1.S1_at	---	---	310	188	1.651	---
MmunewRS.149.1.S1_at	C9orf91	chromosome 9 open reading frame 91	323	196	1.648	transcripts
MmugDNA.35114.1.S1_at	ZNF350	zinc finger protein 350	385	235	1.637	transcripts
MmugDNA.28179.1.S1_at	PDE7B	phosphodiesterase 7B	192	118	1.623	transcripts
MmuSTS.3856.1.S1_at	SLC26A2	solute carrier family 26 (sulfate transporter),member 2	87	54	1.601	transcripts
MmugDNA.33041.1.S1_at	---	---	98	61	1.598	---
MmuSTS.555.1.S1_at	BHMT	betaine--homocysteine S-methyltransferase	155	98	1.584	transcripts
MmuSTS.2151.1.S1_at	BCAT1	branched chain aminotransferase 1,cytosolic	1719	1086	1.583	transcripts
MmugDNA.42233.1.S1_s_at	STYXL1	serine/threonine/tyrosine interacting-like 1	495	314	1.576	transcripts
MmugDNA.26751.1.S1_at	ZNF12	zinc finger protein 12	345	219	1.574	transcripts
MmugDNA.29113.1.S1_at	LMBR1	limb reg. 1 homolog (mouse)	430	273	1.573	transcripts
MmugDNA.28933.1.S1_at	SEPT11	septin 11	1193	759	1.572	transcripts
Mmu.4512.2.S1_at	MRPS10	mitochondrial ribosomal protein S10	193	123	1.568	transcripts
MmugDNA.4207.1.S1_at	KIAA1430	KIAA1430	518	331	1.566	transcripts
MmugDNA.28405.1.S1_at	---	---	334	215	1.555	---
MmuSTS.1578.1.S1_at	NIN	ninein (GSK3B interacting protein)	132	86	1.533	transcripts
MmugDNA.30295.1.S1_at	MRPL44	mitochondrial ribosomal protein L44	234	153	1.524	transcripts
MmugDNA.42921.1.S1_at	H3F3B	H3 histone,family 3B (H3.3B)	1106	726	1.523	transcripts
MmugDNA.43063.1.S1_s_at	C9orf30	chromosome 9 open reading frame 30	135	90	1.497	transcripts
MmugDNA.33751.1.S1_at	RASD1	RAS,dexamethasone-induced 1	1436	960	1.497	transcripts
MmuSTS.3342.1.S1_at	SMYD3	SET and MYND domain containing 3	231	155	1.484	transcripts
MmugDNA.15847.1.S1_at	RABEP1	rabaptin, RAB GTPase binding effector protein 1	421	287	1.465	genic&downstr. reg.
MmugDNA.11063.1.S1_at	ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	422	289	1.459	genic&downstr. reg.
MmugDNA.33378.1.S1_s_at	EGLN1	egl nine homolog 1 (C. elegans)	520	366	1.423	transcripts
MmugDNA.31015.1.S1_at	CCBL1	cysteine conjugate-beta lyase,cytoplasmic	278	196	1.421	transcripts
MmugDNA.16094.1.S1_at	CANX	calnexin	1060	752	1.409	transcripts

Genes showing increased expression in summer cumulus 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	31	384	12.200	transcripts
MmugDNA.11070.1.S1_at	SYNE1	spectrin repeat containing, nuclear envelope 1	34	255	7.438	transcripts
Mmu.10186.1.S1_at	DEFB122	defensin, beta 122 (pseudogene)	31	230	7.367	transcripts
Mmu.5303.1.S1_at	---	---	57	418	7.277	---
MmugDNA.34451.1.S1_at	NOV	nephroblastoma overexpressed	23	122	5.310	transcripts
MmugDNA.42438.1.S1_at	ANKRD28	ankyrin repeat domain 28	35	179	5.079	genic&downstr. reg.
MmuSTS.2906.1.S1_at	VWF	von Willebrand factor	154	761	4.935	transcripts
MmugDNA.17507.1.S1_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	35	162	4.653	genic&downstr. reg.
MmugDNA.393.1.S1_at	---	---	161	689	4.280	---
MmuSTS.1361.1.S1_at	ANXA4	annexin A4	178	720	4.057	transcripts
MmugDNA.28171.1.S1_at	NEAT1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	231	922	3.987	transcripts
MmugDNA.11872.1.S1_at	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	60	237	3.982	genic&downstr. reg.
MmugDNA.6058.1.S1_at	RORA	RAR-related orphan receptor A	181	702	3.875	genic&downstr. reg.
MmugDNA.11251.1.S1_at	KCTD12	potassium channel tetramerisation domain containing 12	545	2013	3.693	transcripts
MmugDNA.26082.1.S1_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	59	217	3.663	transcripts
MmugDNA.14309.1.S1_at	ALCAM	activated leukocyte cell adhesion molecule	38	139	3.622	transcripts
MmuSTS.1357.1.S1_s_at	ANGPTL1	angiopoietin-like 1	24	85	3.597	transcripts
MmugDNA.17754.1.S1_at	---	---	105	369	3.526	---
MmugDNA.18778.1.S1_s_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	91	295	3.243	transcripts
MmuSTS.3135.1.S1_at	RGS4	regulator of G-protein signaling 4	131	423	3.237	transcripts
MmuSTS.2617.1.S1_at	---	---	288	879	3.058	---
MmuSTS.2426.1.S1_at	GPR116	G protein-coupled receptor 116	40	123	3.036	transcripts
MmugDNA.11395.1.S1_at	FAM13A	family with sequence similarity 13, member A	52	154	2.978	genic&downstr. reg.
MmugDNA.12998.1.S1_at	---	---	185	549	2.964	---
MmugDNA.28937.1.S1_at	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	28	83	2.950	genic&downstr. reg.
MmugDNA.28587.1.S1_at	---	---	642	1875	2.921	---
MmugDNA.6268.1.S1_at	DST	dystonin	28	82	2.893	genic&downstr. reg.
MmugDNA.16839.1.S1_at	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	216	615	2.848	genic&downstr. reg.
MmugDNA.2118.1.S1_at	MAML2	mastermind-like 2 (Drosophila)	62	176	2.846	genic&downstr. reg.
MmugDNA.18778.1.S1_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	115	324	2.813	transcripts
MmugDNA.14310.1.S1_at	ALCAM	activated leukocyte cell adhesion molecule	993	2687	2.707	transcripts
Mmu.15280.1.S1_at	---	---	443	1191	2.688	---

MmugDNA.39582.1.S1_at	SLC7A2	solute carrier family 7 (cationic amino acid transporter,y system),member 2	75	192	2.565	transcripts
MmugDNA.38804.1.S1_at	INPP4A	inositol polyphosphate-4-phosphatase,type I,107kDa	134	340	2.538	transcripts
Mmu.7053.1.S1_at	AKR1C1	aldo-keto reductase family 1,member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	41	102	2.483	transcripts
MmugDNA.7064.1.S1_at	---	---	173	429	2.480	---
MmugDNA.14528.1.S1_s_at	DCN	decorin	199	492	2.474	transcripts
MmugDNA.36292.1.S1_at	FAM110B	family with sequence similarity 110, member B	106	263	2.472	genic&downstr. reg.
MmugDNA.18446.1.S1_s_at	AKR1C2	aldo-keto reductase family 1,member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase,type III)	2731	6685	2.448	transcripts
MmugDNA.41363.1.S1_at	FOXO1	forkhead box O1	95	231	2.438	genic&downstr. reg.
MmugDNA.1995.1.S1_at	SND1	staphylococcal nuclease and tudor domain containing 1	70	171	2.427	genic&downstr. reg.
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)	1775	4299	2.422	transcripts
MmugDNA.14736.1.S1_at	---	---	144	346	2.404	---
MmugDNA.37278.1.S1_at	EID3	EP300 interacting inhibitor of differentiation 3	108	256	2.371	transcripts
MmuSTS.1355.1.S1_at	ALDH9A1	aldehyde dehydrogenase 9 family,member A1	846	1997	2.359	transcripts
MmuSTS.2738.1.S1_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	294	685	2.332	transcripts
MmuSTS.138.1.S1_at	PRICKLE1	prickle homolog 1 (Drosophila)	146	339	2.326	transcripts
MmugDNA.26078.1.S1_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	59	136	2.316	transcripts
MmugDNA.22489.1.S1_at	MYST3	MYST histone acetyltransferase (monocytic leukemia) 3	615	1406	2.286	transcripts
MmugDNA.27647.1.S1_at	BMPR1B	bone morphogenetic protein receptor,type IB	55	126	2.284	transcripts
MmugDNA.13802.1.S1_at	DCN	decorin	206	468	2.267	transcripts
MmuSTS.1244.1.S1_at	PKN2	protein kinase N2	40	91	2.255	transcripts
Mmu.1738.2.S1_at	SPAG11A /// SPAG11B	sperm associated antigen 11A /// sperm associated antigen 11B	90	202	2.248	transcripts
MmugDNA.6354.1.S1_at	---	---	115	259	2.242	---
MmugDNA.20967.1.S1_at	PABPC1	poly(A) binding protein, cytoplasmic 1	77	173	2.236	genic&downstr. reg.
MmugDNA.33327.1.S1_s_at	COL4A3	collagen,type IV,alpha 3 (Goodpasture antigen)	106	235	2.214	transcripts
MmuSTS.837.1.S1_at	DPP8	dipeptidyl-peptidase 8	225	493	2.193	transcripts

MmugDNA.4591.1.S1_at	---	---	53	114	2.164	---
MmugDNA.881.1.S1_at	---	---	918	1972	2.148	---
MmugDNA.38765.1.S1_at	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	61	130	2.147	genic&downstr. reg.
MmugDNA.38484.1.S1_at	KCNJ8	potassium inwardly-rectifying channel,subfamily J,member 8	359	770	2.145	transcripts
MmugDNA.6175.1.S1_at	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	51	109	2.141	genic&downstr. reg.
MmugDNA.789.1.S1_at	RORA	RAR-related orphan receptor A	254	541	2.130	transcripts
MmuSTS.1717.1.S1_at	AKAP4	A kinase (PRKA) anchor protein 4	41	86	2.124	transcripts
MmugDNA.26193.1.S1_at	RORA	RAR-related orphan receptor A	890	1863	2.092	transcripts
MmugDNA.24173.1.S1_at	MAML2	mastermind-like 2 (Drosophila)	156	326	2.088	genic&downstr. reg.
MmuSTS.46.1.S1_at	ALG6	asparagine-linked glycosylation 6,alpha-1,3-glucosyltransferase homolog (S. cerevisiae)	129	268	2.078	transcripts
MmugDNA.30781.1.S1_at	C9orf95	chromosome 9 open reading frame 95	1063	2201	2.071	transcripts
MmugDNA.18731.1.S1_at	TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	43	90	2.066	genic&downstr. reg.
MmugDNA.606.1.S1_at	RHOQ	ras homolog gene family,member Q	119	244	2.052	transcripts
MmugDNA.32965.1.S1_at	DCN	decorin	80	162	2.017	transcripts
MmugDNA.738.1.S1_at	BTC	betacellulin	419	843	2.012	genic&downstr. reg.
MmugDNA.33589.1.S1_at	CHODL	chondrolectin	887	1758	1.982	transcripts
MmugDNA.41838.1.S1_x_at	MT1X	metallothionein 1X	307	602	1.961	transcripts
MmugDNA.41838.1.S1_at	MT1X	metallothionein 1X	286	560	1.955	transcripts
MmugDNA.43209.1.S1_at	ACPP	acid phosphatase,prostate	3570	6937	1.943	transcripts
MmugDNA.13537.1.S1_s_at	CYP2B6	cytochrome P450,family 2,subfamily B,polypeptide 6	100	192	1.927	transcripts
MmugDNA.36345.1.S1_at	AUTS2	autism susceptibility candidate 2	245	469	1.914	transcripts
MmuSTS.2094.1.S1_at	RBMS3	RNA binding motif,single stranded interacting protein	315	598	1.900	transcripts
MmugDNA.28098.1.S1_at	---	---	151	286	1.892	---
MmuSTS.2560.1.S1_at	TOX	thymocyte selection-associated high mobility group box	131	245	1.873	transcripts
MmugDNA.8802.1.S1_at	SHC4	SHC (Src homology 2 domain containing) family,member 4	1227	2294	1.869	transcripts
Mmu.7287.1.S1_at	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	66	122	1.845	genic&downstr. reg.
MmugDNA.2278.1.S1_at	A2BP1	ataxin 2-binding protein 1	158	290	1.833	transcripts
MmugDNA.18400.1.S1_at	RORA	RAR-related orphan receptor A	131	239	1.825	transcripts
MmugDNA.17758.1.S1_at	KCNG3	potassium voltage-gated channel,subfamily G,member 3	842	1536	1.825	transcripts

MmuSTS.1880.1.S1_at	COL4A2	collagen,type IV,alpha 2	653	1190	1.822	transcripts
MmugDNA.19859.1.S1_at	TMEM144	transmembrane protein 144	51	89	1.754	transcripts
MmugDNA.40814.1.S1_at	ACPL2	acid phosphatase-like 2	1532	2631	1.718	transcripts
MmugDNA.7355.1.S1_at	---	---	168	286	1.705	---
MmugDNA.23310.1.S1_at	SEPT6	septin 6	927	1574	1.698	transcripts
MmugDNA.9695.1.S1_at	NAA25	N(alpha)-acetyltransferase 25, NatB auxiliary subunit	69	107	1.557	genic&downstr. reg.