

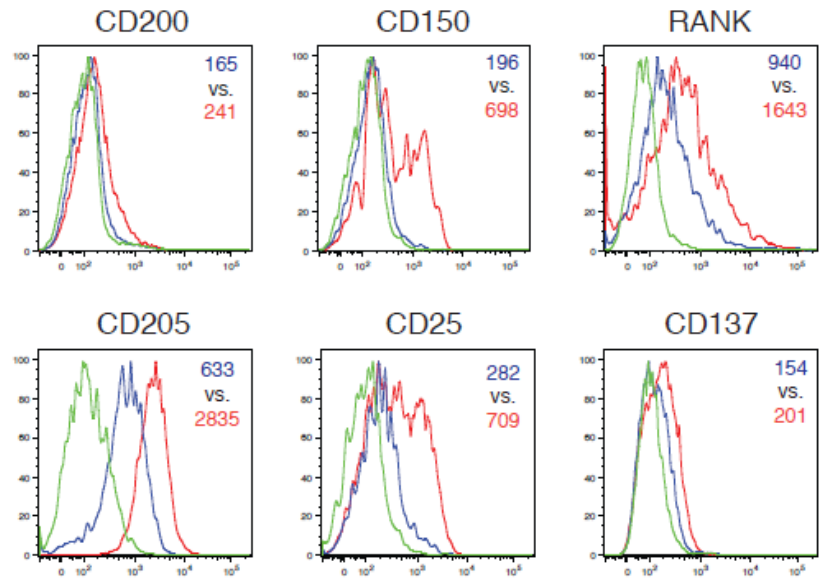
normal skin were cultured with CFSE-labeled allogeneic T cells +/- 25% TSN. Percentages of proliferating cells within live CD3<sup>+</sup>CD4<sup>+</sup> and CD3<sup>+</sup>CD8<sup>+</sup> cells were determined by CFSE dilution. (B) FACS histograms of CFSE dilution assay using LCs and TSN. Numbers show percentages of proliferating cells. (C) Effect of TSN on production of IFN- $\gamma$ , IL-4, IL-17, and IL-22 by CD4<sup>+</sup> and CD8<sup>+</sup> T cells. n.s., not significant. (D) Dot plot analysis of IFN- $\gamma$ , IL-4, IL-17, and IL-22 expression in proliferating CD4<sup>+</sup> and CD8<sup>+</sup> T cells stimulated by LCs +/-TSN. Numbers show percent gated cells.

**Figure 4:** TSN enhances proliferation and IFN- $\gamma$  response by CD4<sup>+</sup> and CD8<sup>+</sup> T cells induced by in vitro-generated LCs, but suppresses those by monocyte-derived DCs. (A) CD1a<sup>+</sup>CD14<sup>-</sup> LC-type DCs derived from CD34<sup>+</sup> hematopoietic progenitors, or, monocyte-derived DCs were cultured with CFSE-labeled T cells +/- 25% TSN. Percentages of proliferating cells were determined by CFSE dilution. (B) FACS histograms of CFSE dilution assay. Numbers show percentages of proliferating cells. (C) Effect of TSN on in vitro generated LC or DC driven production of IFN- $\gamma$ , IL-4, IL-17, or IL-22, by CD4<sup>+</sup> and CD8<sup>+</sup> T-cells. n.s., not significant. (D) Dot plot analysis of IFN- $\gamma$ , IL-4, IL-17, and IL-22 expression in proliferating CD4<sup>+</sup> and CD8<sup>+</sup> T cells stimulated by LC-type DCs or mono-DCs, +/- TSN. Numbers show percent gated cells.

**Supplementary Figure 1:** Flow cytometric analysis of surface molecules expressed on LCs from SCC and peritumoral non-lesional skin. HLA-DR<sup>+</sup>CD207<sup>+</sup> LCs in the epidermal cell suspensions from SCC and peritumoral non-lesional skin were subjected to the

analysis of cell surface expression of CD200, CD25, CD137, CD205, CD150, and receptor activator of nuclear factor  $\kappa$ B (RANK). Target molecules were selected from the gene list shown in Supplementary Table 2. Green lines, isotype controls; blue lines, LCs from SCC; red lines, LCs from SCC. Mean fluorescence intensity values are shown in the upper right hand of each histogram. Data represent 1 of 3 independent experiments.

**Supplementary Figure 2:** Flow cytometric analysis of surface molecules on in vitro-generated LC-type DCs. LC-type DCs were FACS-sorted as CD1a+CD14<sup>-</sup> cells from CD34<sup>+</sup> hematopoietic progenitors cultured for 8 days with GM-CSF, TNF $\alpha$ , and Flt3L. CD1a+CD14<sup>-</sup> cells from CD34<sup>+</sup> hematopoietic progenitors were subjected to the analysis of cell surface expression of HLA-DR and CD207. Shaded areas indicate isotype controls. Data are representative of three independent experiments.



Supplementary Figure 1

Supplementary Figure S2

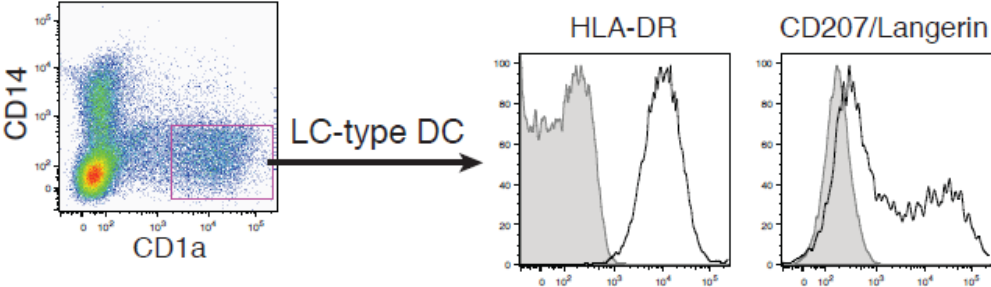


Table S1 Genomic expression differences between SCC-derived LCs and PTNL skin-derived LCs

Probe	Symbol	Description	Fold Change	P value	FDR
<b>Upregulated genes in LCs from SCC</b>					
202350_s_at	MATN2	matrilin 2	10.088	0.001	0.08
238790_at	LOC374443	CLR pseudogene	9.65	<0.0001	0.01
1552365_at	SCIN	scinderin	9.271	0.001	0.09
209583_s_at	CD200	CD200 molecule	8.291	<0.0001	<0.0001
242586_at	FSD1L	fibronectin type III and SPRY domain containing 1-like	7.433	0.001	0.07
227985_at			7.404	<0.0001	0.04
217553_at	MGC87042	STEAP family protein MGC87042	6.878	<0.0001	0.03
202833_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	6.722	0.004	0.15
206336_at	CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	6.442	0.004	0.14
205816_at	ITGB8	integrin, beta 8	6.409	<0.0001	0.01
227646_at	EBF1	early B-cell factor 1	6.36	<0.0001	0.06
204161_s_at	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	6.352	<0.0001	0.06
229504_at			6.284	<0.0001	0.03
202436_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	5.851	0.004	0.15
218469_at	GREM1	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	5.79	0.004	0.14
210146_x_at	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	5.726	<0.0001	0.03
203397_s_at	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	5.684	<0.0001	0.02
227290_at			5.606	<0.0001	0.06
200832_s_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	5.565	0.001	0.08
220643_s_at	FAIM	Fas apoptotic inhibitory molecule	5.507	0.001	0.07
203874_s_at	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	5.475	<0.0001	0.01
211429_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	5.398	<0.0001	0.06
235318_at	FBN1	fibrillin 1	5.395	<0.0001	0.05
206181_at	SLAMF1	signaling lymphocytic activation molecule family member 1	5.308	0.003	0.13
226925_at	ACPL2	acid phosphatase-like 2	5.269	0.001	0.09
225763_at	RCSD1	RCSD domain containing 1	5.14	<0.0001	<0.0001
1552394_a_at	ENTHD1	ENTH domain containing 1	5.078	0.004	0.14
221019_s_at	COLEC12	collectin sub-family member 12	4.96	0.003	0.13
211423_s_at	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	4.957	<0.0001	0.01
228152_s_at	DDX60L	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	4.891	0.001	0.07
206118_at	STAT4	signal transducer and activator of transcription 4	4.881	<0.0001	0.04
224724_at	SULF2	sulfatase 2	4.859	0.002	0.1
226390_at	STARD4	StAR-related lipid transfer (START) domain containing 4	4.797	<0.0001	0.04
223159_s_at	NEK6	NIMA (never in mitosis gene a)-related kinase 6	4.77	0.001	0.07
220132_s_at	CLEC2D	C-type lectin domain family 2, member D	4.768	<0.0001	0.04

1552393_at	ENTHD1	ENTH domain containing 1	4.742	0.005	0.16
224833_at	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	4.737	<0.0001	0.02
211056_s_at	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	4.736	<0.0001	<0.0001
212325_at	LIMCH1	LIM and calponin homology domains 1	4.727	<0.0001	0.03
205767_at	EREG	epiregulin	4.719	0.005	0.16
212190_at	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	4.696	0.002	0.11
203158_s_at	GLS	glutaminase	4.673	<0.0001	0.02
203373_at	SOCS2	suppressor of cytokine signaling 2	4.638	<0.0001	0.03
217371_s_at	IL15	interleukin 15	4.629	0.001	0.08
204849_at	TCFL5	transcription factor-like 5 (basic helix-loop-helix)	4.628	0.002	0.11
205222_at	EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	4.605	0.001	0.08
1569599_at	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	4.537	0.007	0.18
228933_at	NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	4.518	<0.0001	0.05
224444_s_at	C1orf97	chromosome 1 open reading frame 97	4.514	0.001	0.08
200965_s_at	ABLIM1	actin binding LIM protein 1	4.512	0.004	0.14
211144_x_at			4.508	0.003	0.13
223463_at	RAB23	RAB23, member RAS oncogene family	4.506	<0.0001	0.02
202925_s_at	PLAGL2	pleiomorphic adenoma gene-like 2	4.487	<0.0001	0.04
236600_at	SPG20	spastic paraplegia 20 (Troyer syndrome)	4.474	0.001	0.09
214660_at			4.469	0.002	0.12
204160_s_at	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	4.457	0.001	0.07
202437_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	4.388	0.002	0.11
230904_at	FSD1L	fibronectin type III and SPRY domain containing 1-like	4.373	0.001	0.09
206003_at	CEP135	centrosomal protein 135kDa	4.359	<0.0001	0.01
235678_at	GM2A	GM2 ganglioside activator	4.322	<0.0001	0.04
238846_at	TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFkB activator	4.314	<0.0001	0.04
219718_at	FGGY	FGGY carbohydrate kinase domain containing	4.3	<0.0001	0.04
224443_at	C1orf97	chromosome 1 open reading frame 97	4.289	<0.0001	0.05
243087_at	WDR63	WD repeat domain 63	4.267	0.001	0.07
235304_at			4.251	0.007	0.18
226556_at			4.25	<0.0001	0.01
231303_at	NCRNA00158	non-protein coding RNA 158	4.244	0.006	0.17
230864_at	MGC42105	serine/threonine-protein kinase NIM1	4.238	0.003	0.12
233500_x_at	CLEC2D	C-type lectin domain family 2, member D	4.237	<0.0001	0.03
222108_at	AMIGO2	adhesion molecule with Ig-like domain 2	4.197	0.003	0.13
213093_at	PRKCA	protein kinase C, alpha	4.177	0.002	0.12
209146_at	SC4MOL	sterol-C4-methyl oxidase-like	4.145	<0.0001	0.01
224800_at	WDFY1	WD repeat and FYVE domain containing 1	4.123	0.006	0.17
216575_at			4.119	0.002	0.11
213430_at	RUFY3	RUN and FYVE domain containing 3	4.11	<0.0001	0.01
202007_at	NID1	nidogen 1	4.09	<0.0001	0.02
225525_at	KIAA1671	KIAA1671	4.057	0.004	0.15

223423_at	GPR160	G protein-coupled receptor 160	4.029	<0.0001	0.03
223839_s_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	4.023	0.006	0.17
239413_at	CEP152	centrosomal protein 152kDa	4.019	<0.0001	0.05
238513_at	PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	4.016	0.001	0.07
203086_at	KIF2A	kinesin heavy chain member 2A	4.013	0.001	0.08
234284_at	GNG8	guanine nucleotide binding protein (G protein), gamma 8	4.01	<0.0001	0.03
202539_s_at	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	3.985	0.002	0.11
210073_at	ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	3.973	0.008	0.19
213552_at	GLCE	glucuronic acid epimerase	3.958	0.004	0.15
204205_at	APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	3.955	<0.0001	0.05
1559776_at	GM2A	GM2 ganglioside activator	3.951	<0.0001	0.06
215016_x_at	DST	dystonin	3.913	0.001	0.09
204526_s_at	TBC1D8	TBC1 domain family, member 8 (with GRAM domain)	3.901	0.002	0.1
205668_at	LY75	lymphocyte antigen 75	3.901	<0.0001	0.05
203139_at	DAPK1	death-associated protein kinase 1	3.896	0.002	0.1
225205_at	KIF3B	kinesin family member 3B	3.893	<0.0001	0.01
1554519_at	CD80	CD80 molecule	3.889	0.001	0.08
228333_at			3.889	0.001	0.08
232231_at	RUNX2	runt-related transcription factor 2	3.86	0.006	0.17
239401_at	S1PR1	sphingosine-1-phosphate receptor 1	3.794	0.005	0.16
202786_at	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	3.764	0.001	0.09
219675_s_at	UXS1	UDP-glucuronate decarboxylase 1	3.755	<0.0001	0.02
225583_at	UXS1	UDP-glucuronate decarboxylase 1	3.755	<0.0001	0.02
209813_x_at			3.745	0.007	0.17
204820_s_at			3.738	0.006	0.17
229670_at			3.715	0.001	0.09
215389_s_at	TNNT2	troponin T type 2 (cardiac)	3.69	0.004	0.15
209406_at	BAG2	BCL2-associated athanogene 2	3.689	<0.0001	0.06
209582_s_at	CD200	CD200 molecule	3.68	0.001	0.08
202270_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	3.666	0.004	0.15
1559500_at	VPS8	vacuolar protein sorting 8 homolog (S. cerevisiae)	3.66	0.005	0.16
211339_s_at	ITK	IL2-inducible T-cell kinase	3.645	0.008	0.19
205899_at	CCNA1	cyclin A1	3.636	0.003	0.13
215806_x_at			3.625	0.004	0.15
239870_at			3.606	<0.0001	0.04
223324_s_at	TRPM7	transient receptor potential cation channel, subfamily M, member 7	3.601	0.001	0.08
228286_at	GEN1	Gen homolog 1, endonuclease (Drosophila)	3.593	<0.0001	0.04
238559_at			3.593	0.001	0.09
203875_at	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	3.585	<0.0001	0.01
213800_at	CFH	complement factor H	3.581	0.001	0.09
212254_s_at	DST	dystonin	3.578	0.001	0.07
224358_s_at	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	3.571	0.002	0.11

229146_at	C7orf31	chromosome 7 open reading frame 31	3.57	<0.0001	0.06
235052_at	ZNF792	zinc finger protein 792	3.569	<0.0001	0.06
212350_at	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	3.564	<0.0001	0.01
212298_at	NRP1	neuropilin 1	3.561	0.006	0.17
1555355_a_at	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	3.559	<0.0001	0.01
201791_s_at	DHCR7	7-dehydrocholesterol reductase	3.559	0.004	0.15
219543_at	PBLD	phenazine biosynthesis-like protein domain containing	3.545	0.005	0.16
228438_at	LOC100132891	hypothetical protein LOC100132891	3.506	0.002	0.12
210959_s_at	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	3.502	<0.0001	0.01
203913_s_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	3.5	0.008	0.19
235522_at	CLEC2D	C-type lectin domain family 2, member D	3.498	0.004	0.15
209459_s_at	ABAT	4-aminobutyrate aminotransferase	3.458	0.001	0.09
207037_at	TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFkB activator	3.457	<0.0001	0.05
213208_at	KIAA0240	KIAA0240	3.448	0.002	0.1
205676_at	CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	3.445	0.007	0.17
206710_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	3.429	0.003	0.12
1560156_at			3.425	<0.0001	0.01
207266_x_at	RBMS1	RNA binding motif, single stranded interacting protein 1	3.404	0.002	0.11
230650_at			3.397	0.002	0.1
209460_at	ABAT	4-aminobutyrate aminotransferase	3.384	<0.0001	0.05
228551_at	DENND5B	DENN/MADD domain containing 5B	3.38	0.004	0.15
221561_at	SOAT1	sterol O-acyltransferase 1	3.331	0.006	0.17
225984_at	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	3.33	0.001	0.07
219895_at	FAM70A	family with sequence similarity 70, member A	3.329	<0.0001	0.05
219631_at	LRP12	low density lipoprotein-related protein 12	3.32	0.006	0.17
206026_s_at	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	3.319	0.001	0.07
209198_s_at	SYT11	synaptotagmin XI	3.304	0.001	0.08
244706_at	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	3.303	0.001	0.08
204497_at	ADCY9	adenylate cyclase 9	3.302	0.001	0.09
227611_at	TARSL2	threonyl-tRNA synthetase-like 2	3.299	0.001	0.09
226122_at	PLEKHG1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	3.298	0.002	0.11
243871_at	LOC100130476	similar to hCG2036711	3.295	0.001	0.08
212867_at			3.284	0.006	0.17
218842_at	RPAP3	RNA polymerase II associated protein 3	3.282	0.001	0.08
203789_s_at	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	3.246	<0.0001	0.06
218596_at	TBC1D13	TBC1 domain family, member 13	3.245	0.008	0.19
1555274_a_at	SELI	selenoprotein I	3.242	0.006	0.17
209943_at	FBXL4	F-box and leucine-rich repeat protein 4	3.238	<0.0001	0.04
200887_s_at	STAT1	signal transducer and activator of transcription 1, 91kDa	3.236	0.007	0.18
226045_at	FRS2	fibroblast growth factor receptor substrate 2	3.236	0.006	0.17
219629_at	FAM118A	family with sequence similarity 118, member A	3.231	0.005	0.16
211269_s_at	IL2RA	interleukin 2 receptor, alpha	3.204	0.001	0.08



212750_at	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	3.199	0.006	0.17
209868_s_at	RBMS1	RNA binding motif, single stranded interacting protein 1	3.198	0.006	0.16
202269_x_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	3.17	0.008	0.19
230362_at	INPP5F	inositol polyphosphate-5-phosphatase F	3.157	0.002	0.1
208962_s_at	FADS1	fatty acid desaturase 1	3.152	0.001	0.09
215388_s_at			3.152	0.003	0.13
1569183_a_at	CHM	choroideremia (Rab escort protein 1)	3.146	0.005	0.16
213268_at	CAMTA1	calmodulin binding transcription activator 1	3.138	<0.0001	0.03
235683_at	SESN3	sestrin 3	3.137	<0.0001	0.06
205992_s_at	IL15	interleukin 15	3.131	0.004	0.15
1552644_a_at	PHC3	polyhomeotic homolog 3 (Drosophila)	3.108	0.002	0.11
226251_at	ASXL2	additional sex combs like 2 (Drosophila)	3.095	0.003	0.14
211776_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	3.091	<0.0001	0.02
212741_at	MAOA	monoamine oxidase A	3.089	0.004	0.15
229487_at	EBF1	early B-cell factor 1	3.089	<0.0001	0.04
206877_at	MXD1	MAX dimerization protein 1	3.086	0.004	0.15
235231_at	ZNF789	zinc finger protein 789	3.086	<0.0001	0.06
227395_at	TBCEL	tubulin folding cofactor E-like	3.074	0.003	0.12
203943_at	KIF3B	kinesin family member 3B	3.059	<0.0001	0.03
228083_at	CACNA2D4	calcium channel, voltage-dependent, alpha 2/delta subunit 4	3.058	0.001	0.07
218911_at	YEATS4	YEATS domain containing 4	3.05	0.001	0.09
228386_s_at	DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	3.05	0.003	0.13
244461_at	CYT5B	cytospin B	3.049	0.004	0.14
1555689_at	CD80	CD80 molecule	3.04	0.006	0.17
230015_at	PRCD	progressive rod-cone degeneration	3.039	0.006	0.17
212397_at	RDX	radixin	3.032	<0.0001	0.02
219584_at	PLA1A	phospholipase A1 member A	3.032	<0.0001	0.05
218445_at	H2AFY2	H2A histone family, member Y2	3.028	0.001	0.08
229064_s_at	RCAN3	RCAN family member 3	3.025	<0.0001	0.05
202540_s_at	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	3.022	0.001	0.07
235707_at	LOC221710	hypothetical protein LOC221710	3.019	0.005	0.15
221962_s_at	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	3.009	0.004	0.15
230256_at	C1orf104	chromosome 1 open reading frame 104	3.005	0.006	0.17
209649_at	STAM2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	3.002	0.007	0.18
217767_at	C3	complement component 3	3.002	0.002	0.1
235051_at	CCDC50	coiled-coil domain containing 50	2.982	0.004	0.15
241435_at			2.968	0.008	0.19
221828_s_at	FAM125B	family with sequence similarity 125, member B	2.964	0.002	0.11
52975_at	FAM125B	family with sequence similarity 125, member B	2.962	0.001	0.09
225837_at	C12orf32	chromosome 12 open reading frame 32	2.961	<0.0001	0.05
219501_at	ENOX1	ecto-NOX disulfide-thiol exchanger 1	2.959	<0.0001	0.06
46665_at	SEMA4C	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic	2.945	0.001	0.09

		domain, (semaphorin) 4C			
203685_at	BCL2	B-cell CLL/lymphoma 2	2.944	<0.0001	0.03
242181_at			2.935	0.006	0.17
210375_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	2.931	0.002	0.1
204584_at	L1CAM	L1 cell adhesion molecule	2.922	0.003	0.13
209686_at	S100B	S100 calcium binding protein B	2.921	0.007	0.17
223465_at	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	2.912	0.006	0.17
226962_at	ZBTB41	zinc finger and BTB domain containing 41	2.911	0.005	0.16
221449_s_at	ITFG1	integrin alpha FG-GAP repeat containing 1	2.908	0.006	0.17
225888_at	C12orf30	chromosome 12 open reading frame 30	2.898	0.008	0.18
204301_at	KBTBD11	kelch repeat and BTB (POZ) domain containing 11	2.89	0.008	0.19
204935_at	PTPN2	protein tyrosine phosphatase, non-receptor type 2	2.888	<0.0001	0.04
224359_s_at	HOOK3	hook homolog 3 (Drosophila)	2.881	0.002	0.11
220984_s_at	SLCO5A1	solute carrier organic anion transporter family, member 5A1	2.869	<0.0001	0.04
229865_at	FNDC3B	fibronectin type III domain containing 3B	2.859	0.007	0.18
204642_at	S1PR1	sphingosine-1-phosphate receptor 1	2.856	0.001	0.09
244487_at			2.855	0.008	0.19
214455_at	HIST1H2BC	histone cluster 1, H2bc	2.844	0.001	0.09
241379_at	APLF	aprataxin and PNKP like factor	2.835	0.001	0.07
228829_at	ATF7	activating transcription factor 7	2.831	0.003	0.13
1558102_at			2.83	0.002	0.1
227481_at	CNKSR3	CNKSR family member 3	2.828	0.002	0.11
214681_at	GK	glycerol kinase	2.827	0.002	0.11
44696_at	TBC1D13	TBC1 domain family, member 13	2.825	0.003	0.13
213454_at			2.823	0.001	0.07
203748_x_at	RBMS1	RNA binding motif, single stranded interacting protein 1	2.821	0.003	0.12
203379_at	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	2.818	0.001	0.08
238335_at	DNAJC21	DnaJ (Hsp40) homolog, subfamily C, member 21	2.818	0.001	0.07
219321_at	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	2.815	0.001	0.09
209360_s_at	RUNX1	runt-related transcription factor 1	2.811	0.003	0.13
210950_s_at	FDFT1	farnesyl-diphosphate farnesyltransferase 1	2.801	0.001	0.08
209037_s_at	EHD1	EH-domain containing 1	2.8	0.001	0.07
226632_at	CYGB	cytoglobin	2.795	<0.0001	0.06
228983_at			2.79	0.008	0.19
204421_s_at	FGF2	fibroblast growth factor 2 (basic)	2.788	0.002	0.1
205401_at	AGPS	alkylglycerone phosphate synthase	2.779	0.001	0.09
216693_x_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	2.778	0.001	0.09
203159_at	GLS	glutaminase	2.777	0.001	0.09
201063_at	RCN1	reticulocalbin 1, EF-hand calcium binding domain	2.774	0.001	0.08
213437_at	RUFY3	RUN and FYVE domain containing 3	2.768	<0.0001	0.05
225113_at	AGPS	alkylglycerone phosphate synthase	2.762	0.001	0.08
215294_s_at	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	2.759	0.003	0.13

213353_at	ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5	2.758	0.001	0.08
207387_s_at	GK	glycerol kinase	2.757	0.001	0.08
209526_s_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	2.751	0.004	0.15
202245_at	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	2.745	0.002	0.1
202886_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	2.743	<0.0001	0.04
222514_at	RRAGC	Ras-related GTP binding C	2.737	0.001	0.09
218502_s_at	TRPS1	trichorhinophalangeal syndrome I	2.736	0.003	0.13
205026_at	STAT5B	signal transducer and activator of transcription 5B	2.732	0.005	0.16
218656_s_at	LHFP	lipoma HMGIC fusion partner	2.732	0.005	0.16
239559_at			2.732	0.007	0.18
203275_at	IRF2	interferon regulatory factor 2	2.728	<0.0001	0.03
207956_x_at	PDS5B	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	2.727	<0.0001	0.01
226089_at	RABL3	RAB, member of RAS oncogene family-like 3	2.725	<0.0001	0.05
242023_at	ABHD4	abhydrolase domain containing 4	2.724	<0.0001	0.01
221752_at	SSH1	slingshot homolog 1 (Drosophila)	2.717	0.001	0.08
218627_at	DRAM1	DNA-damage regulated autophagy modulator 1	2.702	<0.0001	0.05
203869_at	USP46	ubiquitin specific peptidase 46	2.696	0.008	0.19
202763_at	CASP3	caspase 3, apoptosis-related cysteine peptidase	2.695	<0.0001	0.02
225078_at	EMP2	epithelial membrane protein 2	2.693	0.004	0.14
219649_at	ALG6	asparagine-linked glycosylation 6, alpha-1,3-glucosyltransferase homolog (S. cerevisiae)	2.692	0.005	0.16
229844_at			2.69	0.005	0.16
204866_at	PHF16	PHD finger protein 16	2.684	0.006	0.17
221564_at	PRMT2	protein arginine methyltransferase 2	2.677	0.001	0.07
203117_s_at	PAN2	PAN2 poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	2.676	<0.0001	0.06
238035_at	SP3	Sp3 transcription factor	2.675	<0.0001	0.03
211786_at	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	2.665	<0.0001	0.03
36564_at	RNF19B	ring finger protein 19B	2.665	0.008	0.19
1560520_at	LOC401312	hypothetical LOC401312	2.66	0.005	0.16
236140_at	GCLM	glutamate-cysteine ligase, modifier subunit	2.657	0.006	0.17
221935_s_at	C3orf64	chromosome 3 open reading frame 64	2.654	0.004	0.15
227638_at	KIAA1632	KIAA1632	2.649	0.003	0.13
202176_at	ERCC3	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	2.648	0.004	0.15
230416_at			2.644	0.007	0.18
222730_s_at	ZDHHC2	zinc finger, DHHC-type containing 2	2.641	0.001	0.08
225331_at	CCDC50	coiled-coil domain containing 50	2.631	<0.0001	0.02
202321_at	GGPS1	geranylgeranyl diphosphate synthase 1	2.628	0.005	0.16
214887_at	N4BP2L1	NEDD4 binding protein 2-like 1	2.619	0.005	0.16
200770_s_at	LAMC1	laminin, gamma 1 (formerly LAMB2)	2.618	0.001	0.09
217197_x_at	N4BP2L1	NEDD4 binding protein 2-like 1	2.613	<0.0001	0.06
218816_at	LRRC1	leucine rich repeat containing 1	2.61	0.005	0.15
1553954_at	ALG14	asparagine-linked glycosylation 14 homolog (S. cerevisiae)	2.599	<0.0001	0.05

202924_s_at	PLAGL2	pleiomorphic adenoma gene-like 2	2.592	0.003	0.12
226264_at	SUSD1	sushi domain containing 1	2.586	<0.0001	0.05
220999_s_at	CYFIP2	cytoplasmic FMR1 interacting protein 2	2.583	0.001	0.09
212956_at	TBC1D9	TBC1 domain family, member 9 (with GRAM domain)	2.582	0.007	0.17
204037_at	LPAR1	lysophosphatidic acid receptor 1	2.581	0.001	0.09
228486_at	SLC44A1	solute carrier family 44, member 1	2.576	<0.0001	0.05
223250_at	KLHL7	kelch-like 7 (Drosophila)	2.569	0.001	0.08
212623_at	TMEM41B	transmembrane protein 41B	2.565	0.008	0.19
222209_s_at	TMEM135	transmembrane protein 135	2.565	0.001	0.09
204675_at	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	2.564	<0.0001	0.03
210277_at	AP4S1	adaptor-related protein complex 4, sigma 1 subunit	2.564	0.001	0.07
206412_at	FER	fer (fps/fes related) tyrosine kinase	2.555	0.001	0.08
204036_at	LPAR1	lysophosphatidic acid receptor 1	2.554	0.007	0.17
243016_at			2.536	0.005	0.16
214632_at	NRP2	neuropilin 2	2.534	0.004	0.15
202074_s_at	OPTN	optineurin	2.531	0.001	0.08
203336_s_at	ITGB1BP1	integrin beta 1 binding protein 1	2.531	0.001	0.08
200974_at	ACTA2	actin, alpha 2, smooth muscle, aorta	2.53	0.002	0.12
226189_at	ITGB8	integrin, beta 8	2.522	0.001	0.07
213038_at	RNF19B	ring finger protein 19B	2.521	0.005	0.16
218992_at	C9orf46	chromosome 9 open reading frame 46	2.517	0.005	0.16
209271_at	BPTF	bromodomain PHD finger transcription factor	2.515	<0.0001	0.05
218079_s_at	GGNBP2	gametogenetin binding protein 2	2.512	0.003	0.13
214860_at	SLC9A7	solute carrier family 9 (sodium/hydrogen exchanger), member 7	2.509	<0.0001	0.03
220987_s_at			2.508	0.003	0.13
212526_at	SPG20	spastic paraplegia 20 (Troyer syndrome)	2.507	<0.0001	0.04
1556378_a_at	LOC440896	hypothetical LOC440896	2.501	0.004	0.15
220672_at	PPP4R4	protein phosphatase 4, regulatory subunit 4	2.5	0.004	0.15
202562_s_at	C14orf1	chromosome 14 open reading frame 1	2.499	0.002	0.11
220636_at	DNAI2	dynein, axonemal, intermediate chain 2	2.498	0.008	0.19
235625_at	VPS41	vacuolar protein sorting 41 homolog (S. cerevisiae)	2.495	<0.0001	0.06
217540_at	FAM55C	family with sequence similarity 55, member C	2.493	0.006	0.17
235938_at			2.486	0.007	0.18
210849_s_at	VPS41	vacuolar protein sorting 41 homolog (S. cerevisiae)	2.485	<0.0001	0.06
221685_s_at	CCDC99	coiled-coil domain containing 99	2.485	0.001	0.09
204369_at	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	2.484	0.003	0.12
238950_at			2.478	0.005	0.16
204618_s_at	GABPB1	GA binding protein transcription factor, beta subunit 1	2.477	0.005	0.15
224596_at	SLC44A1	solute carrier family 44, member 1	2.477	0.001	0.08
214830_at	SLC38A6	solute carrier family 38, member 6	2.475	0.003	0.14
203925_at	GCLM	glutamate-cysteine ligase, modifier subunit	2.474	0.002	0.11
1556194_a_at			2.472	0.004	0.14

213149_at	DLAT	dihydrolipoamide S-acetyltransferase	2.472	0.002	0.11
209338_at	TFCP2	transcription factor CP2	2.471	0.004	0.15
202529_at	PRPSAP1	phosphoribosyl pyrophosphate synthetase-associated protein 1	2.469	0.001	0.08
203716_s_at	DPP4	dipeptidyl-peptidase 4	2.466	0.004	0.15
224436_s_at	NIPSNAP3A	nipsnap homolog 3A (C. elegans)	2.463	0.002	0.11
216060_s_at	DAAM1	dishevelled associated activator of morphogenesis 1	2.462	0.001	0.09
201619_at	PRDX3	peroxiredoxin 3	2.457	0.004	0.15
200771_at	LAMC1	laminin, gamma 1 (formerly LAMB2)	2.455	0.004	0.15
219904_at	ZSCAN5A	zinc finger and SCAN domain containing 5A	2.455	0.006	0.17
209043_at	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	2.449	0.001	0.08
221751_at	SLC2A3P1	solute carrier family 2 (facilitated glucose transporter), member 3 pseudogene 1	2.44	0.004	0.15
202625_at	LYN	v-src-1 Yamaguchi sarcoma viral related oncogene homolog	2.434	<0.0001	0.02
1405_i_at	CCL5	chemokine (C-C motif) ligand 5	2.431	0.007	0.17
230363_s_at	INPP5F	inositol polyphosphate-5-phosphatase F	2.43	<0.0001	0.06
1552486_s_at	LACTB	lactamase, beta	2.428	0.006	0.17
230446_at			2.426	0.001	0.08
211018_at	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	2.421	0.004	0.15
217762_s_at	RAB31	RAB31, member RAS oncogene family	2.421	0.001	0.08
235310_at	GCET2	germinal center expressed transcript 2	2.419	0.001	0.08
1555370_a_at	CAMTA1	calmodulin binding transcription activator 1	2.417	0.006	0.17
201559_s_at	CLIC4	chloride intracellular channel 4	2.415	<0.0001	0.06
225585_at	RAP2A	RAP2A, member of RAS oncogene family	2.415	<0.0001	0.04
235457_at	MAML2	mastermind-like 2 (Drosophila)	2.411	0.007	0.18
221830_at	RAP2A	RAP2A, member of RAS oncogene family	2.408	<0.0001	0.02
227816_at	NTN1	netrin 1	2.407	0.001	0.08
210473_s_at	GPR125	G protein-coupled receptor 125	2.406	0.006	0.17
225859_at	XIAP	X-linked inhibitor of apoptosis	2.406	0.004	0.14
232267_at	GPR133	G protein-coupled receptor 133	2.4	0.002	0.11
204067_at	SUOX	sulfite oxidase	2.399	0.006	0.17
224603_at			2.398	0.002	0.11
206385_s_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	2.397	0.003	0.13
223400_s_at	PBRM1	polybromo 1	2.396	0.006	0.17
213393_at	MFSD9	major facilitator superfamily domain containing 9	2.395	<0.0001	0.05
232539_at			2.391	0.007	0.18
214672_at	TTLL5	tubulin tyrosine ligase-like family, member 5	2.387	0.001	0.08
212681_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	2.384	0.006	0.17
208881_x_at	IDI1	isopentenyl-diphosphate delta isomerase 1	2.383	0.002	0.12
226685_at	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	2.382	0.001	0.08
223276_at	MST150	MSTP150	2.38	<0.0001	0.06
201537_s_at	DUSP3	dual specificity phosphatase 3	2.378	0.001	0.09
209442_x_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	2.378	0.004	0.15
211488_s_at	ITGB8	integrin, beta 8	2.378	0.006	0.17

226190_at			2.367	0.001	0.08
1555638_a_at	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	2.361	0.001	0.07
226713_at	CCDC50	coiled-coil domain containing 50	2.354	0.007	0.18
226270_at	EXOC2	exocyst complex component 2	2.352	0.002	0.1
227940_at	LOC339803	hypothetical protein LOC339803	2.351	0.005	0.16
202158_s_at	CUGBP2	CUG triplet repeat, RNA binding protein 2	2.349	0.003	0.14
239250_at	ZNF542	zinc finger protein 542	2.346	0.008	0.19
205411_at	STK4	serine/threonine kinase 4	2.345	<0.0001	0.04
224484_s_at	BRMS1L	breast cancer metastasis-suppressor 1-like	2.342	0.003	0.14
225836_s_at	C12orf32	chromosome 12 open reading frame 32	2.34	0.003	0.12
226468_at			2.336	0.002	0.1
202599_s_at	NRIP1	nuclear receptor interacting protein 1	2.334	0.001	0.07
203414_at	MMD	monocyte to macrophage differentiation-associated	2.332	0.001	0.08
213361_at	TDRD7	tudor domain containing 7	2.331	0.001	0.08
223268_at	C11orf54	chromosome 11 open reading frame 54	2.331	0.005	0.16
230536_at	PBX4	pre-B-cell leukemia homeobox 4	2.331	0.001	0.1
226726_at	MBOAT2	membrane bound O-acyltransferase domain containing 2	2.328	<0.0001	0.03
242329_at			2.328	0.003	0.13
203315_at	NCK2	NCK adaptor protein 2	2.326	<0.0001	0.02
228667_at	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	2.326	0.005	0.16
203087_s_at	KIF2A	kinesin heavy chain member 2A	2.323	0.001	0.1
208315_x_at	TRAF3	TNF receptor-associated factor 3	2.322	<0.0001	0.02
222735_at	TMEM38B	transmembrane protein 38B	2.322	0.007	0.18
221750_at	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	2.318	0.001	0.09
227802_at	RUFY3	RUN and FYVE domain containing 3	2.318	0.002	0.1
227231_at	KIAA1211	KIAA1211	2.317	0.005	0.15
1554569_a_at	CUGBP2	CUG triplet repeat, RNA binding protein 2	2.315	0.001	0.08
219279_at	DOCK10	dedicator of cytokinesis 10	2.312	0.001	0.08
224990_at	C4orf34	chromosome 4 open reading frame 34	2.312	0.003	0.13
220649_at	AGBL3	ATP/GTP binding protein-like 3	2.309	0.003	0.13
226853_at	BMP2K	BMP2 inducible kinase	2.304	0.002	0.11
33494_at	ETFDH	electron-transferring-flavoprotein dehydrogenase	2.302	0.002	0.11
226046_at	MAPK8	mitogen-activated protein kinase 8	2.298	0.003	0.13
1568957_x_at	SRGAP2P1	SLIT-ROBO Rho GTPase activating protein 2 pseudogene 1	2.292	0.006	0.17
224504_s_at	BUD13	BUD13 homolog (S. cerevisiae)	2.291	0.003	0.12
228954_at	LYSMD4	LysM, putative peptidoglycan-binding, domain containing 4	2.288	0.001	0.08
243894_at	SLC41A2	solute carrier family 41, member 2	2.288	0.005	0.15
227840_at	C2orf76	chromosome 2 open reading frame 76	2.279	0.005	0.16
209481_at	SNRK	SNF related kinase	2.278	0.007	0.17
214906_x_at	N4BP2L1	NEDD4 binding protein 2-like 1	2.275	0.003	0.13
217986_s_at	BAZ1A	bromodomain adjacent to zinc finger domain, 1A	2.274	0.008	0.19
225594_at	CREBZF	CREB/ATF bZIP transcription factor	2.273	0.004	0.14

228243_at			2.273	0.001	0.07
219499_at	SEC61A2	Sec61 alpha 2 subunit ( <i>S. cerevisiae</i> )	2.272	0.001	0.08
243601_at	LOC285957	hypothetical protein LOC285957	2.27	0.005	0.16
219551_at	EAF2	ELL associated factor 2	2.263	<0.0001	0.04
239277_at			2.261	0.003	0.13
219366_at	AVEN	apoptosis, caspase activation inhibitor	2.26	0.004	0.14
223498_at	CYTSB	cytospin B	2.257	0.005	0.15
223351_at	C17orf80	chromosome 17 open reading frame 80	2.256	0.005	0.16
211763_s_at	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	2.255	0.004	0.15
1563111_a_at	PIGX	phosphatidylinositol glycan anchor biosynthesis, class X	2.251	<0.0001	0.06
239186_at	MGC39372	hypothetical protein MGC39372	2.251	0.008	0.19
239431_at	TICAM2	toll-like receptor adaptor molecule 2	2.25	<0.0001	0.06
228042_at	ADPRH	ADP-ribosylarginine hydrolase	2.249	<0.0001	0.03
223790_at	KATNAL1	katanin p60 subunit A-like 1	2.248	<0.0001	0.04
202314_at	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	2.247	<0.0001	0.04
226142_at	GLIPR1	GLI pathogenesis-related 1	2.243	0.003	0.14
225023_at	GOPC	golgi associated PDZ and coiled-coil motif containing	2.242	0.004	0.15
225048_at	PHF10	PHD finger protein 10	2.24	0.004	0.15
207090_x_at	ZFP30	zinc finger protein 30 homolog (mouse)	2.239	0.004	0.15
208328_s_at	MEF2A	myocyte enhancer factor 2A	2.237	0.006	0.17
210048_at	NAPG	N-ethylmaleimide-sensitive factor attachment protein, gamma	2.236	0.002	0.11
238493_at	ZNF506	zinc finger protein 506	2.233	0.005	0.16
204542_at	ST6GALNAC2	ST6 (alpha-N-acetyl-neuraminy1-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	2.23	0.002	0.12
203603_s_at	ZEB2	zinc finger E-box binding homeobox 2	2.228	0.001	0.08
238336_s_at	DNAJC21	Dnaj (Hsp40) homolog, subfamily C, member 21	2.225	0.001	0.09
227637_at	TFCP2	transcription factor CP2	2.224	0.003	0.13
208070_s_at	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	2.222	0.003	0.13
212453_at	KIAA1279	KIAA1279	2.22	0.006	0.17
210715_s_at	SPINT2	serine peptidase inhibitor, Kunitz type, 2	2.217	0.007	0.17
219129_s_at	SAP30L	SAP30-like	2.217	0.001	0.1
208875_s_at	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	2.213	0.007	0.18
1556385_at			2.211	<0.0001	0.04
236347_at	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	2.211	0.004	0.15
1554465_s_at			2.207	0.003	0.12
224831_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	2.207	0.007	0.18
203010_at	STAT5A	signal transducer and activator of transcription 5A	2.206	0.001	0.08
231929_at	IKZF2	IKAROS family zinc finger 2 (Helios)	2.206	0.006	0.17
212742_at	RNF115	ring finger protein 115	2.202	0.003	0.14
204500_s_at	AGTPBP1	ATP/GTP binding protein 1	2.201	0.004	0.15
230219_at	NDE1	nudE nuclear distribution gene E homolog 1 ( <i>A. nidulans</i> )	2.201	0.001	0.07
211383_s_at	WDR37	WD repeat domain 37	2.198	0.006	0.17

204460_s_at	RAD1	RAD1 homolog (S. pombe)	2.197	0.002	0.12
219358_s_at	ADAP2	ArfGAP with dual PH domains 2	2.195	0.001	0.09
206695_x_at	ZNF43	zinc finger protein 43	2.193	0.007	0.18
220147_s_at	FAM60A	family with sequence similarity 60, member A	2.193	0.003	0.12
227006_at	PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	2.193	0.003	0.13
202422_s_at	ACSL4	acyl-CoA synthetase long-chain family member 4	2.188	0.009	0.19
231975_s_at	MIER3	mesoderm induction early response 1, family member 3	2.187	0.005	0.15
203265_s_at	MAP2K4	mitogen-activated protein kinase kinase 4	2.186	0.002	0.11
214684_at	MEF2A	myocyte enhancer factor 2A	2.185	0.002	0.11
205801_s_at	RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	2.181	0.004	0.14
228385_at	DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	2.181	0.005	0.16
212377_s_at	NOTCH2	Notch homolog 2 (Drosophila)	2.179	0.004	0.15
224968_at	CCDC104	coiled-coil domain containing 104	2.179	0.001	0.08
203556_at	ZHX2	zinc fingers and homeoboxes 2	2.174	0.004	0.15
228785_at	ZNF281	zinc finger protein 281	2.172	0.001	0.09
243350_at			2.171	0.007	0.18
226725_at			2.17	0.007	0.17
203598_s_at	WBP4	WW domain binding protein 4 (formin binding protein 21)	2.165	0.002	0.11
224891_at	FOXO3	forkhead box O3	2.165	0.001	0.08
220952_s_at	PLEKHA5	pleckstrin homology domain containing, family A member 5	2.164	0.007	0.17
204615_x_at	IDI1	isopentenyl-diphosphate delta isomerase 1	2.163	0.004	0.15
208964_s_at	FADS1	fatty acid desaturase 1	2.162	<0.0001	0.06
202604_x_at	ADAM10	ADAM metallopeptidase domain 10	2.158	0.005	0.16
225440_at	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	2.158	0.001	0.09
201503_at	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	2.153	0.003	0.14
227516_at	SF3A1	splicing factor 3a, subunit 1, 120kDa	2.153	<0.0001	0.05
231853_at	TUBD1	tubulin, delta 1	2.153	0.008	0.19
225829_at	PDZD8	PDZ domain containing 8	2.152	0.002	0.12
202466_at	POLS	polymerase (DNA directed) sigma	2.15	0.001	0.09
201297_s_at	MOBKL1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	2.147	0.001	0.08
221522_at	ANKRD27	ankyrin repeat domain 27 (VPS9 domain)	2.146	0.001	0.09
224695_at	C2orf29	chromosome 2 open reading frame 29	2.146	0.001	0.09
209608_s_at	ACAT2	acetyl-Coenzyme A acetyltransferase 2	2.143	0.008	0.19
216941_s_at	TAF1B	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	2.142	0.004	0.15
232535_at			2.137	0.002	0.12
223211_at	HACL1	2-hydroxyacyl-CoA lyase 1	2.135	<0.0001	0.04
225123_at			2.135	<0.0001	0.05
227124_at	LOC221710	hypothetical protein LOC221710	2.132	0.005	0.16
204715_at	PANX1	pannexin 1	2.13	0.001	0.07
205055_at	ITGAE	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	2.128	<0.0001	0.06
209524_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	2.127	0.003	0.12
212390_at	PDE4DIP	phosphodiesterase 4D interacting protein	2.125	0.002	0.11



202569_s_at	MARK3	MAP/microtubule affinity-regulating kinase 3	2.123	0.001	0.07
219565_at	CYP20A1	cytochrome P450, family 20, subfamily A, polypeptide 1	2.122	0.004	0.14
225346_at	MTERFD3	MTERF domain containing 3	2.122	0.002	0.11
213645_at	ENOSF1	enolase superfamily member 1	2.121	0.002	0.11
219109_at	SPAG16	sperm associated antigen 16	2.121	0.001	0.08
230009_at	FAM118B	family with sequence similarity 118, member B	2.12	0.001	0.07
203506_s_at	MED12	mediator complex subunit 12	2.119	0.008	0.19
216607_s_at	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	2.119	0.003	0.12
58367_s_at	ZNF419	zinc finger protein 419	2.116	0.008	0.19
224492_s_at	ZNF627	zinc finger protein 627	2.111	0.005	0.15
226152_at	TTC7B	tetratricopeptide repeat domain 7B	2.11	0.005	0.16
207900_at	CCL17	chemokine (C-C motif) ligand 17	2.109	<0.0001	0.06
229028_s_at	ARL17	ADP-ribosylation factor-like 17	2.109	0.006	0.17
225114_at	AGPS	alkylglycerone phosphate synthase	2.108	0.002	0.11
1569791_at	STK4	serine/threonine kinase 4	2.105	0.006	0.17
226159_at	C5orf51	chromosome 5 open reading frame 51	2.105	0.001	0.08
203519_s_at	UPF2	UPF2 regulator of nonsense transcripts homolog (yeast)	2.103	<0.0001	0.03
235911_at	LOC440995	hypothetical protein LOC440995	2.103	0.003	0.13
244110_at	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	2.101	0.005	0.16
1556588_at	C15orf37	chromosome 15 open reading frame 37	2.1	0.002	0.11
220754_at	ARMC9	armadillo repeat containing 9	2.098	0.004	0.15
226413_at	LOC400027	hypothetical protein LOC400027	2.098	0.006	0.17
203446_s_at	OCRL	oculocerebrorenal syndrome of Lowe	2.097	<0.0001	0.06
208647_at	FDFT1	farnesyl-diphosphate farnesyltransferase 1	2.097	0.002	0.1
202469_s_at	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa	2.09	0.003	0.13
229437_at	MIR155HG	MIR155 host gene (non-protein coding)	2.09	0.001	0.09
207176_s_at	CD80	CD80 molecule	2.089	0.001	0.07
218852_at	PPP2R3C	protein phosphatase 2 (formerly 2A), regulatory subunit B", gamma	2.087	<0.0001	0.01
204143_s_at	ENOSF1	enolase superfamily member 1	2.086	0.006	0.17
229126_at	TMEM19	transmembrane protein 19	2.086	<0.0001	0.06
212403_at	UBE3B	ubiquitin protein ligase E3B	2.081	0.007	0.18
200638_s_at	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	2.074	0.001	0.08
213415_at	CLIC2	chloride intracellular channel 2	2.072	0.004	0.15
209799_at	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	2.071	0.002	0.11
228747_at	SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae)	2.068	0.005	0.16
225049_at	BLOC1S2	biogenesis of lysosomal organelles complex-1, subunit 2	2.066	0.007	0.18
221881_s_at	CLIC4	chloride intracellular channel 4	2.065	<0.0001	0.06
201560_at	CLIC4	chloride intracellular channel 4	2.064	0.007	0.18
201824_at	RNF14	ring finger protein 14	2.062	0.001	0.08
221732_at	CANT1	calcium activated nucleotidase 1	2.057	0.002	0.11
210216_x_at	RAD1	RAD1 homolog (S. pombe)	2.055	<0.0001	0.05
200906_s_at	PALLD	palladin, cytoskeletal associated protein	2.052	0.004	0.15

224790_at	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	2.052	0.004	0.15
203633_at	CPT1A	carnitine palmitoyltransferase 1A (liver)	2.051	0.003	0.14
205530_at	ETFDH	electron-transferring-flavoprotein dehydrogenase	2.05	0.003	0.13
233040_at	PLEKHA5	pleckstrin homology domain containing, family A member 5	2.049	0.008	0.19
234351_x_at	TRPS1	trichorhinophalangeal syndrome I	2.048	0.004	0.15
209892_at	FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	2.047	0.007	0.18
212200_at	ANKLE2	ankyrin repeat and LEM domain containing 2	2.047	0.004	0.15
1552264_a_at	MAPK1	mitogen-activated protein kinase 1	2.046	0.003	0.13
206756_at	CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	2.043	0.001	0.07
226188_at	HSPC159	galectin-related protein	2.043	0.001	0.09
202156_s_at	CUGBP2	CUG triplet repeat, RNA binding protein 2	2.042	0.001	0.08
202334_s_at	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	2.04	0.005	0.15
213305_s_at	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform	2.04	<0.0001	0.03
228245_s_at			2.038	0.008	0.19
210458_s_at	TANK	TRAF family member-associated NFkB activator	2.034	0.003	0.14
205681_at	BCL2A1	BCL2-related protein A1	2.033	0.003	0.13
224791_at	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	2.032	0.006	0.17
222113_s_at	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	2.031	0.007	0.18
223548_at	C1orf26	chromosome 1 open reading frame 26	2.031	0.001	0.08
212549_at	STAT5B	signal transducer and activator of transcription 5B	2.027	0.004	0.15
226261_at	ZNRF2	zinc and ring finger 2	2.027	0.003	0.12
224445_s_at	ZFYVE21	zinc finger, FYVE domain containing 21	2.023	0.002	0.11
212166_at	XPO7	exportin 7	2.022	0.004	0.15
211758_x_at	TXNDC9	thioredoxin domain containing 9	2.02	0.001	0.07
224675_at	MESDC2	mesoderm development candidate 2	2.018	0.001	0.09
1552291_at	PIGX	phosphatidylinositol glycan anchor biosynthesis, class X	2.015	0.001	0.09
201132_at	HNRNP2	heterogeneous nuclear ribonucleoprotein H2 (H')	2.015	0.005	0.15
212780_at	SOS1	son of sevenless homolog 1 (Drosophila)	2.014	0.005	0.15
203097_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	2.01	0.006	0.17
206862_at	ZNF254	zinc finger protein 254	2.008	<0.0001	0.04
217690_at			2.006	0.003	0.13
219495_s_at	ZNF180	zinc finger protein 180	2.006	0.002	0.11
229429_x_at	LOC728855	hypothetical LOC728855	2.006	0.006	0.17
203578_s_at	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	2.005	0.008	0.19
212410_at	EFHA1	EF-hand domain family, member A1	2.005	0.003	0.13
203375_s_at	TPP2	tripeptidyl peptidase II	2.001	0.001	0.08

#### Downregulated genes in LCs from SCC

214414_x_at			0.497	0.006	0.17
203092_at	TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)	0.495	0.007	0.17
209535_s_at			0.491	0.002	0.11
205103_at	C1orf61	chromosome 1 open reading frame 61	0.488	0.002	0.1
213766_x_at	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	0.487	<0.0001	0.06

222233_s_at	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, <i>S. cerevisiae</i> )	0.487	0.001	0.08
209048_s_at	ZMYND8	zinc finger, MYND-type containing 8	0.486	0.002	0.1
203126_at	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	0.481	0.008	0.19
237157_at			0.474	0.008	0.19
218066_at	SLC12A7	solute carrier family 12 (potassium/chloride transporters), member 7	0.472	0.001	0.08
232311_at	B2M	beta-2-microglobulin	0.463	<0.0001	0.06
239794_at			0.463	0.002	0.12
242794_at	MAML3	mastermind-like 3 ( <i>Drosophila</i> )	0.463	0.005	0.16
241916_at			0.458	0.001	0.07
232551_at	SLC26A6	solute carrier family 26, member 6	0.457	0.002	0.12
220221_at	VPS13D	vacuolar protein sorting 13 homolog D ( <i>S. cerevisiae</i> )	0.456	<0.0001	0.05
218002_s_at	CXCL14	chemokine (C-X-C motif) ligand 14	0.453	0.006	0.17
232826_at			0.453	0.006	0.17
219534_x_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	0.45	0.005	0.16
214805_at	EIF4A1	eukaryotic translation initiation factor 4A, isoform 1	0.449	0.006	0.17
203973_s_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	0.447	0.002	0.11
242014_at			0.447	0.004	0.15
221815_at	ABHD2	abhydrolase domain containing 2	0.442	0.003	0.13
239811_at			0.44	0.002	0.11
227093_at	USP36	ubiquitin specific peptidase 36	0.438	0.003	0.12
238157_at			0.438	0.004	0.15
225618_at	ARHGAP27	Rho GTPase activating protein 27	0.435	0.006	0.17
236439_at			0.435	0.006	0.17
231108_at	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	0.433	0.006	0.17
203240_at			0.432	0.006	0.17
238672_at			0.431	<0.0001	0.03
244204_at			0.43	0.004	0.15
230529_at	HECA	headcase homolog ( <i>Drosophila</i> )	0.424	0.007	0.18
239049_at			0.423	0.003	0.13
242946_at	CD53	CD53 molecule	0.418	0.001	0.08
1552482_at	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	0.417	0.007	0.18
204687_at	DKFZP564O0823	prostatic androgen-repressed message-1	0.415	0.003	0.13
1568780_at	LOC649305	hypothetical LOC649305	0.413	0.002	0.11
237180_at	PSME4	proteasome (prosome, macropain) activator subunit 4	0.413	0.006	0.17
235730_at			0.412	0.001	0.07
231252_at	C2orf67	chromosome 2 open reading frame 67	0.41	0.005	0.16
230207_s_at	DOCK5	dedicator of cytokinesis 5	0.405	<0.0001	0.05
205349_at	GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	0.399	0.006	0.17
61734_at	RCN3	reticulocalbin 3, EF-hand calcium binding domain	0.396	0.001	0.09
1556814_a_at			0.39	0.005	0.16
238967_at			0.386	0.001	0.07
202005_at	ST14	suppression of tumorigenicity 14 (colon carcinoma)	0.384	0.005	0.16

217988_at	CCNB1IP1	cyclin B1 interacting protein 1	0.381	0.004	0.14
242325_at	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	0.381	0.002	0.11
216905_s_at	ST14	suppression of tumorigenicity 14 (colon carcinoma)	0.378	0.002	0.11
235589_s_at			0.378	0.008	0.19
212123_at	TCTN3	tectonic family member 3	0.374	0.004	0.15
228487_s_at			0.374	<0.0001	0.01
230494_at	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	0.37	0.006	0.17
217996_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	0.364	<0.0001	0.04
226907_at	PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	0.349	0.001	0.08
238715_at	LOC646014	hypothetical protein LOC646014	0.346	<0.0001	0.01
216682_s_at	FAM48A	family with sequence similarity 48, member A	0.343	0.005	0.16
221704_s_at	VPS37B	vacuolar protein sorting 37 homolog B (S. cerevisiae)	0.342	0.008	0.19
227998_at	S100A16	S100 calcium binding protein A16	0.342	0.004	0.15
210380_s_at	CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit	0.339	0.001	0.07
229041_s_at			0.333	0.004	0.15
237690_at	GPR115	G protein-coupled receptor 115	0.325	0.001	0.09
212384_at	BAT1	HLA-B associated transcript 1	0.324	0.004	0.15
222549_at	CLDN1	claudin 1	0.317	<0.0001	0.03
225251_at	RAB24	RAB24, member RAS oncogene family	0.316	0.006	0.17
230233_at			0.307	0.008	0.18
219377_at	FAM59A	family with sequence similarity 59, member A	0.303	0.001	0.07
212188_at	KCTD12	potassium channel tetramerisation domain containing 12	0.302	<0.0001	0.06
226213_at	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	0.301	0.003	0.13
204446_s_at	ALOX5	arachidonate 5-lipoxygenase	0.296	0.001	0.09
201131_s_at	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	0.289	0.005	0.16
222670_s_at	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	0.288	0.001	0.09
204595_s_at	STC1	stanniocalcin 1	0.286	0.004	0.15
218644_at	PLEK2	pleckstrin 2	0.282	0.001	0.08
201596_x_at	KRT18	keratin 18	0.28	0.001	0.07
201656_at	ITGA6	integrin, alpha 6	0.279	0.005	0.16
229396_at	OVOL1	ovo-like 1(Drosophila)	0.273	0.001	0.08
212086_x_at	LMNA	lamin A/C	0.269	0.001	0.07
227404_s_at	EGR1	early growth response 1	0.264	<0.0001	0.06
1565579_at			0.263	0.001	0.08
225173_at	ARHGAP18	Rho GTPase activating protein 18	0.249	0.006	0.17
242664_at			0.248	0.005	0.16
243797_at	STK17B	serine/threonine kinase 17b	0.247	0.007	0.17
219799_s_at	DHRS9	dehydrogenase/reductase (SDR family) member 9	0.246	0.002	0.12
213338_at	TMEM158	transmembrane protein 158	0.24	0.001	0.08
201695_s_at	NP	nucleoside phosphorylase	0.226	0.003	0.13
213848_at			0.223	0.002	0.12
215813_s_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	0.206	<0.0001	0.06

231849_at	KRT80	keratin 80	0.206	<0.0001	0.05
205220_at	NIACR2	niacin receptor 2	0.204	0.007	0.18
230206_at	DOCK5	dedicator of cytokinesis 5	0.204	<0.0001	0.06
204268_at	S100A2	S100 calcium binding protein A2	0.195	<0.0001	0.06
238017_at	SDR16C5	short chain dehydrogenase/reductase family 16C, member 5	0.189	0.002	0.11
205128_x_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	0.168	<0.0001	0.05
206726_at	HPGDS	hematopoietic prostaglandin D synthase	0.124	0.003	0.13
204952_at	LYPD3	LY6/PLAUR domain containing 3	0.121	0.002	0.11

**Table S2: Antibodies used for flow cytometry**

<b>Antigen-fluorophor</b>	<b>Manufacturer</b>	<b>Clone<sup>a</sup></b>	<b>Isotype</b>	<b>Dilution</b>
HLA-DR-Alexa Fluor 700	BioLegend	L243	IgG2a	1:1000
CD207- Phycoerythrin	Immunotech	DCGM4	IgG1	1:100
CD207- Alexa 647	IMGENEX	DCGM4/122D5.03	IgG1	1:50
CD40-FITC	BD Pharmingen	5C3	IgG1	1:20
CD80-FITC	BD Pharmingen	L307.4	IgG1	1:20
CD83-Allophycocyanin	BD Pharmingen	HB15e	IgG1	1:33
CD86-Allophycocyanin	BD Pharmingen	2331(FUN-1)	IgG1	1:100
CD3-Allophycocyanin	BD Pharmingen	SK7	IgG1	1:500
CD3-Pacific Blue	eBioscience	500A2	IgG2a	1:40
CD4-Phycoerythrin-Cy7	eBioscience	RPA-T4	IgG1	1:200
CD8-PerCp-Cy5.5	BD Pharmingen	RPA-T7	IgG1	1:50
IFN- $\gamma$ -Alexa Fluor 700	BD Pharmingen	L243	IgG1	1:200
IL-4-Phycoerythrin	BD Pharmingen	8D4-8	IgG1	1:20
IL-17-Alexa Fluor 488	eBioscience	eBio17B7	IgG1	1:20
IL-22-Allophycocyanin	R & D systems	142928	IgG1	1:20
CD1a- Phycoerythrin	BD Pharmingen	HI149	IgG1	1:33
CD14- Allophycocyanin	BD Pharmingen	M $\phi$ P9	IgG2b	1:33
CD150-FITC	BioLegend	A12(7D4)	IgG1	1:20
CD25-FITC	BD Pharmingen	2A3	IgG1	1:20
CD137- Allophycocyanin	BD Pharmingen	4B4-1	IgG1	1:20

CD200-FITC	AbD Serotec	OX2	IgG1	1:20
CD205- Alexa Fluor 647	BD Pharmingen	MMRI-7	IgG1	1:20
RANK- Phycoerythrin	Abcam	9A725	IgG1	1:20

<sup>a</sup>All are murine monoclonals.