

CCLE peripheral blood: 783 DEGs

Probeset ID	Entrez Gene	Gene Symbol	Chromosomal Location	Gene Title	p-value	FC (CCLE patients vs. Control)	Disease related pathways and processes												
							Apop	Oxid: Red	Cell adh	Cyto- chemo	Leu chem	NK	DC	TLR	TC	BC	IFN	Lys/Prot	
39463_at	22848	AAK1	chr2p14	AP2 associated kinase 1	0.027	-1.2											v		
35394_at	23460	ABC A6	chr17q24.3	ATP-binding cassette, sub-family A (ABC1), member 6	0.033	-1.2													
41681_at	22	ABC B7	chrXq13.3	ATP-binding cassette, sub-family B (MDR/TAP), member 7	0.014	-1.2													v
40294_at	23457	ABC B9	chr12q24	ATP-binding cassette, sub-family B (MDR/TAP), member 9	0.015	-1.2													
1930_at	8714	ABCC 3	chr17q22	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0.001	-1.4													
37261_g_at	10060	ABCC 9	chr12p12.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0.014	-1.2													
1635_at	25	ABL1	chr9q34.1	c-abl oncogene 1, non-receptor tyrosine kinase	0.047	1.2	v		v										v
39058_at	29	ABR	chr17p13.3	active BCR-related gene	0.030	1.3													
36417_s_at	30	ACAAJ	chr3p23-p22	acetyl-CoA acyltransferase 1	0.030	1.4			v										
39207_t_at	176	ACAN	chr15q26.1	aggrecan	0.046	-1.4			v										
37246_at	65057	ACD	chr16q22.1	adrenocortical dysplasia homolog (mouse)	0.033	-1.1													
41058_g_at	55856	ACOT13	chr6p22.3	acyl-CoA thioesterase 13	0.012	1.5													
34160_at	71	ACTG1	chr17q25	actin, gamma 1	0.028	1.2													
41654_at	100	ADA	chr20q13.12	adenosine deaminase	0.008	1.5			v		v						v	v	
37091_g_at	1587	ADAM3A	chr8p11.23	ADAM metallopeptidase domain 3A	0.012	-1.2													
36269_at	9508	ADAMTS3	chr4q13.3	ADAM metallopeptidase with thrombospondin type 1 motif, 3	0.041	-1.2													
33353_at	107	ADCY1	chr7p13-p12	adenylate cyclase 1 (brain)	0.042	-1.2			v										v
34686_at	108	ADCY2	chr5p15.3	adenylate cyclase 2 (brain)	0.036	-1.2			v										v
39383_at	1112	ADCY6	chr12q12-q13	adenylate cyclase 6	0.038	-1.2			v										v
34637_f_at	124	ADH1A	chr4q23	alcohol dehydrogenase 1A (class I), alpha polypeptide	0.029	-1.1			v										
31550_at	153	ADRBI	chr10q24-q26	adrenergic, beta-1, receptor	0.029	-1.5													
34315_at	10939	AFG3L2	chr18p11	AFG33 ATPase family gene 3-like 2 (S. cerevisiae)	0.043	1.4													
38852_at	116986	AGAP2	chr12q14.1	ArfGAP with GTase domain, ankyrin repeat and PH domain 2	0.042	-1.3													
31664_at	3268	AGFG2	chr7q22.1	ArfGAP with FG repeats 2	0.016	-1.3													
37880_at	189	AGXT	chr2q37.3	alanine-glyoxylate aminotransferase	0.030	-1.3													
34728_g_at	107678	AHCYLI	chr1p13.2	adenosylhomocysteinate-like 1	0.050	1.6													
36497_at	111346	AHNAK2	chr14q32.33	AHNAK nucleoprotein 2	0.004	-1.2													
34439_at	9447	AJM2	chr1q22	absent in melanoma 2	0.029	-1.1	v												v
41250_at	7965	AIMP2	chr7p22	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	0.006	1.4													
40685_at	221	ALDH3B1	chr1q13	aldehyde dehydrogenase 3 family, member B1	0.012	1.6													
678_at	251	ALPLPL2	chr2q37	alkaline phosphatase, placental-like 2	0.050	-1.4													
33532_at	8092	ALXI	chr12q21.31	ALX homeobox 1	0.014	-1.2			v										
41706_at	114899 /// 23600	AMACR /// CIOTNF3	chr5p13	alpha-methylacyl-CoA racemase // C1q and tumor necrosis factor related protein 3	0.000	-1.2													
35502_at	269	AMHR2	chr12q13	anti-Mullerian hormone receptor, type II	0.032	-1.2			v										
32919_at	347902	AMIGO2	chr12q13.11	adhesion molecule with Ig-like domain 2	0.012	-1.1	v												
36865_at	23357	ANGEL1	chr14q24.3	angel homolog 1 (Drosophila)	0.010	-1.2													
38199_at	90806	ANGEL2	chr13q2.3	angel homolog 2 (Drosophila)	0.028	-1.2													
40347_at	81611	ANP32E	chr1q21.2	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0.023	1.5													
37747_at	308	ANXA5	chr4q26-q28q42	annexin A5	0.020	1.9													
35593_at	314	AO2C	chr17q21	amine oxidase, copper containing 2 (retina-specific)	0.019	-1.3													
36161_at	163	AP2B1	chr17q11.2-q12	adaptor-related protein complex 2, beta 1 subunit	0.039	1.4													
32030_at	10239	AP3S2	chr15q26.1	adaptor-related protein complex 3, sigma 2 subunit	0.035	1.2													v
40148_at	323	APPBB2	chr4p13	amyloid beta (A4) precursor protein-binding, family B, member 2	0.025	-1.1													
39106_at	335	APOA1	chr11q23-q24	apolipoprotein A-I	0.047	-1.3											v		
261_s_at	338	APOB	chr2p24-p23	apolipoprotein B (including Agf(x) antigen)	0.018	-1.2													
41472_at	60489	APOBEC3G	chr2q13.1-q13.2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	0.018	2.4													
40430_at	375	ARFJ	chr1q42.13	ADP-ribosylation factor 1	0.048	-1.3													
34725_at	2909	ARHGAP35	chr19q13.3	glucocorticoid receptor binding factor 1	0.045	-1.2													
35505_at	8289	ARD1A	chr1p35.3	AT1 rich interactive domain 1A (SWI-like)	0.048	-1.4													v
31375_at	403	ARL3	chr10q23.3	ADP-ribosylation factor-like 3	0.049	-1.2													
39829_at	10123	ARL4C	chr2q37.1	ADP-ribosylation factor-like 4C	0.030	1.7													
32701_at	421	ARVCF	chr22q11.21	armadillo repeat gene deleted in velocardiofacial syndrome	0.013	-1.1			v										
31875_at	51665	ASB1	chr2q37	ankyrin repeat and SOCS box-containing 1	0.018	1.1	v												
287_at	467	AT73	chr1q32.3	activating transcription factor 3	0.002	1.2	v												v
41235_at	468	ATF4	chr22q13.1	activating transcription factor 4 (tax-responsive enhancer element B67)	0.039	1.6	v												
32439_at	496	ATPB4B	chr1q34	ATPase, H ⁺ /K ⁺ exchanging, beta polypeptide	0.033	-1.3													
34811_at	518	ATPSG3	chr2q31.1	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)	0.046	1.5													
36107_at	522	ATPSI	chr21q21.1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, subunit F6	0.024	1.5													
40134_at	9551	ATPS2	chr7q22.1	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit F2	0.029	1.5													
33854_at	51382	ATP6V1D	chr14q23-q24.2	ATPase, H ⁺ transporting, lysosomal 34kDa, VI subunit D	0.042	1.4													
37367_at	529	ATP6V1E1	chr22pter-q11.2[22q11.1]	ATPase, H ⁺ transporting, lysosomal 31kDa, VI subunit E1	0.034	1.2													
37395_at	9296	ATP6V1F	chr7q32	ATPase, H ⁺ transporting, lysosomal 14kDa, VI subunit F	0.044	1.3			v										
33741_at	51606	ATP6V1H	chr8q11.2	ATPase, H ⁺ transporting, lysosomal 50/57kDa, VI subunit H	0.012	1.2													v
33634_at	5205	ATPSB1	chr18q21-q22[18q21.31]	ATPase, aminophospholipid transporter, class I, type 8B, member 1	0.031	-1.2													
36142_at	6310	ATXN1	chr6p23	ataxin 1	0.041	1.6													
34487_at	6310	ATXN3	chr6p23	ataxin 3	0.017	-1.2													
39401_at	55289	ATXNL3B	chr12q21	ataxin 7-like 3B	0.010	1.2													
41582_at	10677	AVIL	chr12q14.1	avilin	0.012	-1.2													
1278_at	558	AXL	chr19q13.1	AXL receptor tyrosine kinase	0.017	1.4													
39432_at	8702	B4GALT4	chr3q13.3	UDP-Gal betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	0.004	1.5													
41115_s_at	8938	BAIAAP3	chr16p13.3	BAII-associated protein 3	0.026	-1.3													
1801_at	580	BARD1	chr2q24-q35	BRCA1 associated RING domain 1	0.034	2													
35425_at	8538	BAXR2	chr1q21	BAXR2 homeobox 2	0.007	-1.2			v										
1909_at	596	BC1L	chr18q21.33[18q21.3]	B-cell CLL/lymphoma 2	0.044	1.3	v		v								v		
31611_s_at	10018	BC12L11	chr22q13	BCL2-like 11 (apoptosis facilitator)	0.002	1.2	v		v										
1339_s_at	613	BCR	chr22q11(22q11.23	breakpoint cluster region	0.029	-1.1													
32127_at	636	BICDI	chr1p11.2-p11.1	bicaudal D homolog 1 (Drosophila)	0.023	1.1													
35266_at	10904	BLCAP	chr20q11.23	bladder cancer associated protein	0.012	1.3													
1544_at	641	BLM	chr15q26.1	Bloom syndrome, RecQL helicase-like	0.019	1.4			v								v		

35384	at	3269	<i>HRH1</i>	chr3p25	histamine receptor H1	0.049	-1.3											v		
41555	at	9957	<i>HS3ST1</i>	chr4p16	Heparan sulfate (glucosamine) 3-O-sulfotransferase 1	0.026	-1.3													
40778	at	3028	<i>HSD17B10</i>	chrXp11.2	hydroxysteroid (17-beta) dehydrogenase 10	0.017	-1.3													
202	at	3298	<i>HSF2</i>	chrq22.31	heat shock transcription factor 2	0.041	-1.3													
741	g	at	3359	<i>HTR3A</i>	chr11q23.1	5-hydroxytryptamine (serotonin) receptor 3A	0.040	-1.3												
34466	at	3360	<i>HTR4</i>	chr3q31.3-q33	5-hydroxytryptamine (serotonin) receptor 4	0.005	-1.4													
37176	at	3373	<i>HYAL1</i>	chr3p21.3-p21.2	hyaluronoglucosaminidase 1	0.005	-1.2											v		
40758	at	3396	<i>ICT1</i>	chr17q25.1	immature colon carcinoma transcript I	0.016	1.5													
39023	at	3417	<i>IDH1</i>	chr2q33.3	isocitrate dehydrogenase 1 (NADP+), soluble	0.023	1.5													
33155	at	3425	<i>IDUA</i>	chr4p16.3	iduronidase, alpha-L-	0.044	-1.2											v		
425	at	3429	<i>IFI27</i>	chr14q32	interferon, alpha-inducible protein 27	0.027	-14											v		
925	at	10437	<i>IFI30</i>	chr19p13.1	interferon, gamma-inducible protein 30	0.027	-2		v									v		
37641	at	10561	<i>IFI44</i>	chr1p31.1	interferon-induced protein 44	0.043	7.4											v		
36927	at	10964	<i>IFI44L</i>	chr1p31.1	interferon-induced protein 44-like	0.040	10.6											v		
1540	f	at	3442	<i>IFNA5</i>	chr9p22	interferon, alpha 5	0.012	-1.3		v	v	v						v		
1038	s	at	3459	<i>IFNGRI</i>	chr6q23.3	interferon gamma receptor 1	0.044	1.4		v	v	v						v		
34718	at	3480	<i>IGF1R</i>	chr15q26.3	insulin-like growth factor 1 receptor	0.037	-1.2	v												
1591	s	at	3481	// 723961 <i>IGF2//INS-IGF2</i>		chr1p15.5	insulin-like growth factor 2 (somatomedin A)	0.042	-1.3											
41420	at	3488	<i>IGFBP5</i>	chr2q33.4-q36	insulin-like growth factor binding protein 5	0.006	-1.2													
1736	at	3489	<i>IGFBP6</i>	chr12q13	insulin-like growth factor binding protein 6	0.033	-1.4													
31564	at	3500	<i>IGHG1</i>	chr14q32.33	Immunoglobulin heavy constant gamma 1 (G1m marker)	0.003	-1.2											v		
218	at	3550	<i>JK</i>	chr2p15-p14 5q31.3	IK cytokine, down-regulator of HLA II	0.049	1.5													
35659	at	3587	<i>IL10RA</i>	chr11q23	interleukin 10 receptor, alpha	0.047	1.3		v	v	v									
41848	f	at	11009	<i>IL24</i>	chr1q32	interleukin 24	0.032	-1.2		v										
36755	s	at	3568	<i>IL5RA</i>	chr3p26-p24	interleukin 5 receptor, alpha	0.019	-1.3		v										
938	at	3581	<i>IL9R</i>	chrXq28 and Yq12	interleukin 9 receptor	0.024	-1.2		v											
41406	at	65123	<i>INTS3</i>	chr1q21.3	integrator complex subunit 3	0.047	1.2													
35123	at	10526	<i>IP08</i>	chr12p11.21	importin 8	0.006	-1.2													
32957	g	at	124152	<i>IQCK</i>	chr16p12.3	iQ motif containing K	0.020	-1.2												
478	g	at	3663	<i>IRF5</i>	chr7q32	interferon regulatory factor 5	0.021	1.4	v								v	v		
41348	at	10265	<i>IRX5</i>	chr16q12.2	iroquois homeobox 5	0.032	-1.5													
1978	at	3673	<i>ITGA2</i>	chr5q11.2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	0.047	-1.2		v											
37918	at	3689	<i>ITGB2</i>	chr2q12.23	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	0.049	1.6		v	v	v	v						v		
1176	at	3690	<i>ITGB3</i>	chr17q21.32	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	0.031	-1.2		v											
40752	at	113177	<i>IZUMO4</i>	chr19p13.3	IZUMO family member 4	0.037	-1.2													
37468	at	3717	<i>JAK2</i>	chr9p24	Janus kinase 2	0.047	1.5	v	v	v	v							v		
36351	at	81621	<i>KAZALD1</i>	chr10q24.31	Kazal-type serine peptidase inhibitor domain 1	0.028	-1.1													
32344	r	at	3739	<i>KCN4A</i>	chr11p14	potassium voltage-gated channel, shaker-related subfamily, member 4	0.048	-1.2												
32709	at	7881	<i>KCNAB1</i>	chr3q26.1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	0.024	1.2													
31312	at	9312	<i>KCNB2</i>	chr8q13.2	potassium voltage-gated channel, Shab-related subfamily, member 2	0.005	-1.3													
32356	at	3762	<i>KCNJ5</i>	chr11q24	potassium inwardly-rectifying channel, subfamily J, member 5	0.003	-1.3													
40373	at	3778	<i>KCNM1</i>	chr10q22.3	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	0.007	-1.3													
36064	at	3785	<i>KCNQ2</i>	chr20q13.3	potassium voltage-gated channel, KQT-like subfamily, member 2	0.032	-1.4													
39479	g	at	154881	<i>KCTD7</i>	chr7q11.21	Potassium channel tetramerisation domain containing 7	0.019	-1.2												
41122	at	23028	<i>KDM1A</i>	chr1p36.12	lysine (K)-specific demethylase 1A	0.021	1.2	v										v		
40080	at	23065	<i>KIAA0090</i>	chr1p36.13	KIAA0090	0.015	-1.2													
35744	at	9812	<i>KIAA0141</i>	chr5q31.3	KIAA0141	0.005	1.2													
36970	at	23199	<i>KIAA0182</i>	chr16q24.1	KIAA0182	0.031	1.2													
36562	at	9811	<i>KIAA0427</i>	chr18q21.1	KIAA0427	0.039	-1.3													
37232	at	9786	<i>KIAA0586</i>	chr14q23.1	KIAA0586	0.027	-1.2													
36904	at	547	<i>KIF1A</i>	chr2q37.3	kinesin family member 1A	0.024	-1.2													
37171	at	9493	<i>KIF23</i>	chr5q23	kinesin family member 23	0.012	-1.1													
31978	at	3834	<i>KIF25</i>	chr6q27	kinesin family member 25	0.045	-1.3													
37778	at	22944	<i>KIN</i>	chr10p15-p14	KIN, antigenic determinant of recA protein homolog (mouse)	0.022	1.1													
36735	f	at	3811	// 3812 // 727787 <i>KIR3DL1</i> // <i>KIR3DE2</i>		chr19q13.4	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 // k	0.035	-1.4		v									
246	at	3816	<i>KLK1</i>	chr19q13.3	kalikrein 1	0.030	-1.2													
1805	g	at	354	<i>KLK3</i>	chr19q13.41	kalikrein-related peptidase 3	0.024	-1.4												
37554	at	5653	<i>KLK6</i>	chr19q13.3	kalikrein-related peptidase 6	0.045	-1.2													
32297	s	at	3821	// 3822 <i>KLRC1</i> // <i>KLRC2</i>		chr1p213	killer cell lectin-like receptor subfamily C, member 1 // killer cell lectin-like rece	0.017	-2.3			v					v	v		
32287	s	at	3821	<i>KLRC1</i> // <i>KLRC2</i> // <i>KLRC3</i>		chr1p213	killer cell lectin-like receptor subfamily C, member 1 // killer cell lectin-like rece	0.026	-2.8			v					v			
32288	r	at	3823	<i>KLRC3</i>	chr1p213	killer cell lectin-like receptor subfamily C, member 3	0.047	-1.7												
40407	at	3838	<i>KPN2</i>	chr17q24.2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	0.003	1.6	v										v		
35085	r	at	889	<i>KRT11</i>	chr7q21.2	KRT11, ankyrin repeat containing	0.048	1.1												
35766	at	3875	<i>KRT18</i>	chr12q13	keratin 18	0.007	-1.3													
34568	at	3884	<i>KRT33B</i>	chr17q21.2	keratin 33B	0.013	-1.3													
34244	r	at	26013	<i>L3MBTL1</i>	chr20q13.12	l(3)mbtl-like 1 (Drosophila)	0.047	-1.2	v											
40891	f	at	8270	<i>LAGE3</i>	chrXq28	L antigen family, member 3	0.040	1.1												
36917	at	3908	<i>LAMA2</i>	chr6q22-q23	laminin, alpha 2	0.017	-1.3		v											
41610	at	3911	<i>LAMAS</i>	chr20q13.2-q13.3	laminin, alpha 5	0.030	-1.3		v											
232	at	3915	<i>LAMCI</i>	chr1q31	laminin, gamma 1 (formerly LAMB2)	0.001	-1.2		v											
41485	at	3939	<i>LDHA</i>	chr1p15.4	lactate dehydrogenase A	0.003	1.8													
32855	at	3949	<i>LDLR</i>	chr19p13.3	low density lipoprotein receptor	0.006	1.9													
33412	at	3956	<i>LGALS1</i>	chr22q13.1	lectin, galactoside-binding, soluble, 1	0.025	2.1													
37456	at	3957	<i>LGALS2</i>	chr22q12-q13 22q13.1	lectin, galactoside-binding, soluble, 2	0.012	2													
37754	at	3959	<i>LGALS3BP</i>	chr17q25	lectin, galactoside-binding, soluble, 3 binding protein	0.002	2.8		v											
38091	at	3965	<i>LGALS9</i>	chr17q11.2	lectin, galactoside-binding, soluble, 9	0.037	1.5													
35378	at	3972	<i>LHB</i>	chr19q13.32	luteinizing hormone beta polypeptide	0.038	-1.2													
37542	at	10184	<i>LHFP12</i>	chr5q14.1	lipoma HMGIC fusion partner-like 2	0.010	1.8													
32475	at	11024	<i>LILRA1</i>	chr19q13.4	leucocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	0.047	1.5													
36753	at	11026	<i>LILRB4</i>	chr19q13.4	leucocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains)	0.019	2.1													

37782_at	6750	SST	chr3q28	somatostatin	0.020	-1.4												v	
34068_f_at	6756	SSX1	chrXp11.23	synovial sarcoma, X breakpoint 1	0.042	-1.2													
31462_f_at	6756	SSX5	chrXp11.23	synovial sarcoma, X breakpoint 5	0.026	-1.2													
38146_at	9705	ST18	chr8q11.23	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	0.045	-1.2													
32942_at	29906	ST8SIA5	chr18q21.1	ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 5	0.049	-1.1													
39391_at	10617	STAMBP	chr2p13.1	STAM binding protein	0.040	1.4													
32859_at	6772	STAT1	chr2q32.2	signal transducer and activator of transcription 1, 91kDa	0.043	2.2	v		v		v		v		v		v		
1244_at	6773	STAT2	chr12q13.3	signal transducer and activator of transcription 2, 113kDa	0.008	-1.2	v		v									v	
32043_at	8614	STC2	chr5q35.1	stannocalcin 2	0.037	-1.3													
207_at	10963	STIP1	chr11q13	stress-induced-phosphoprotein 1	0.004	1.2													
38685_at	23673	STX12	chr1p35.3	syntaxin 12	0.032	1.4													
39523_at	8675	STX16	chr20q13.32	syntaxin 16	0.024	-1.2													
33079_at	10228	STX6	chr1q25.3	syntaxin 6	0.039	-1.2													
31804_f_at	6817	SULT1A1	chr16p12.1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	0.046	1.9													
38738_at	6612	SUMO3	chr21q22.3	SM13 suppressor of mif two 3 homolog 3 (S. cerevisiae)	0.009	1.4												v	
36931_at	6876	TAGLN	chr11q23.2	transgelin	0.022	-1.3													
38473_at	6897	TARS	chr5p13.2	threonyl-tRNA synthetase	0.023	1.6													
32507_at	23216	TBC1D1	chr4p14	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	0.042	-1.3													
38223_at	11138	TBC1D8	chr2q11.2	TBC1 domain family, member 8 (with GRAM domain)	0.011	1.8													
39398_s_at	6904	TBCD	chr17q25.3	tubulin folding cofactor D	0.006	1.2													
33794_g_at	6942	TCF20	chr22q13.3;22q13.3	transcription factor 20 (AR1)	0.014	-1.2													
32256_r_at	7013	TERF1	chr8q13	telomeric repeat binding factor (NIMA-interacting) 1	0.045	1.2													
40767_at	7035	TFPI	chr2q32	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	0.019	-1.1													
971_s_at	7042	TGFBB2	chr1q41	transforming growth factor, beta 2	0.027	-1.3			v	v	v								
1767_s_at	7043	TGFBB3	chr14q24	transforming growth factor, beta 3	0.007	-1.2			v										
32868_at	7053	TGM3	chr20q11.2	transglutaminase 3 (E-peptidase, protein-glutamine-gamma-glutamyltransferase)	0.015	-1.4													
33001_s_at	9333	TGMS	chr15q15.2	transglutaminase 5	0.032	-1.2													
31827_s_at	10618	TGOLN2	chr2p11.2	trans-golgi network protein 2	0.029	1.2			v										
32124_at	57187	THOC2	chrXq25-q26.3	THO complex 2	0.029	1.2													
1428_at	7068	THR8	chr3p24.2	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog)	0.016	-1.3													
35230_at	148022	TICAMI	chr19p13.3	toll-like receptor adaptor molecule 1	0.037	1.3					v		v		v		v		
41626_at	8914	TIMELESS	chr12q12-q13	timeless homolog (Drosophila)	0.034	1.2													
32830_g_at	10440	TIMM17A	chr1q32.1	translocase of inner mitochondrial membrane 17 homolog A (yeast)	0.026	1.4			v										
1693_s_at	7076	TIMP1	chrXp11.3-p11.23	TIMP metalloendopeptidase inhibitor 1	0.024	1.5													
40837_at	7089	TLE2	chr19p13.3	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	0.031	-1.2													
31333_at	7092	TLL1	chr4q32-q33	tolloid-like 1	0.016	-1.2													
36950_at	54732	TMED9	chr5q35.3	transmembrane emp24 protein transport domain containing 9	0.005	1.2			v										
37934_at	161291	TMEM30B	chr14q23.1	transmembrane protein 30B	0.039	-1.2													
40437_at	23963	TMEM87A	chr15q15.1	transmembrane protein 87A	0.013	1.6													
32682_at	7112	TMPO	chr12q22	thymopoietin	0.023	-1.1													
34067_at	164656	TMPRSS6	chr22q12.3	transmembrane protease, serine 6	0.038	-1.3													
595_at	7128	TNFAIP3	chr6q23	tumor necrosis factor, alpha-induced protein 3	0.048	1.5	v										v		
31410_at	23495	TNFRSF13B	chr17p11.2	tumor necrosis factor superfamily, member 13B	0.025	-1.2			v	v	v								
35287_at	8741	TNFSF13	chr17p13.1	TNFSF12-TNFSF13 readthrough // tumor necrosis factor (ligand) superfamily, member 13	0.002	1.6			v										
41748_at	7125	TNNC2	chr20q12-q13.11	troponin C type 2 (fast)	0.038	-1.4													
38896_at	30000	TNP02	chr19p13.2	transportin 2	0.031	-1.4													
31377_r_at	23534	TNP03	chr7q32.2	transportin 3	0.010	-1.2													
34598_at	7143	TNR	chr1q24	tenascin R (restictin, janusin)	0.003	-1.1			v										
32360_s_at	8940	TOP3B	chr22q11.22	topoisomerase (DNA) III beta	0.045	-1.3													
1974_s_at	7157	TP53	chr17p13.1	tumor protein p53	0.036	-1.2	v		v		v		v		v		v		
32824_at	1200	TPP1	chr1p15	tripetidyl peptidase I	0.022	1.4											v		
33784_at	7186	TRAF2	chr9q34	TNF receptor-associated factor 2	0.036	-1.1	v		v		v		v		v		v		
36139_at	10758	TRAF3IP2	chr6q21	TRAF3 interacting protein 2	0.006	-1.2											v		
1468_at	10131	TRAP1	chr16p13.3	TNF receptor-associated protein 1	0.029	1.2	v										v		
36531_r_at	79090	TRAPPC6A	chr19q13.32	trafficking protein particle complex 6A	0.034	-1.3													
31322_at	6964	TRD9	chr14q11.2	T cell receptor delta locus	0.046	-1.1													
32955_at	51499	TRIAP1	chr12q24.31	TP53 regulated inhibitor of apoptosis 1	0.036	1.3	v												
36825_at	10346	TRIM22	chr1p15	tripartite motif-containing 22	0.033	2.4													
39412_at	7726	TRIM26	chr6p21.3	tripartite motif-containing 26	0.013	1.3													
34700_at	10612	TRIM3	chr1p15.5	tripartite motif-containing 3	0.040	-1.2													
41611_at	9325	TRIP4	chr15q22.31	thyroid hormone receptor interactor 4	0.005	1.3													
36806_at	55503	TRPV6	chr7q34	transient receptor potential cation channel, subfamily V, member 6	0.011	-1.2													
38469_at	7103	TSPAN8	chr12q14.1-q21.1	tetraspanin 8	0.038	-1.1													
36123_at	7263	TSZ1	chr22q13.1	thiosulfate sulfurtransferase (rhodanese)	0.023	-1.3													
31899_at	9694	TTC35	chr8q23.1	tetratricopeptide repeat domain 35	0.009	1.3													
39332_at	347733	TUBB2B	chr6p25	tubulin, beta 2B	0.035	-1.1													
40985_g_at	27729	TUBGCP4	chr15q15	tubulin, gamma complex associated protein 4	0.042	-1.2													
36992_at	7295	TXN	chr9q31	thioredoxin	0.015	1.4	v												
38089_at	988	UBAP2L	chr1q21.3	ubiquitin associated protein 2-like	0.004	1.4													
1725_s_at	7337	UBE3A	chr15q11.2	ubiquitin protein ligase E3A	0.040	1.5	v												
35161_at	22888	UBOX5	chr20p13	U-box domain containing 5	0.011	-1.2													
34422_r_at	7352	UCP3	chr11q13	uncoupling protein 3 (mitochondrial, proton carrier)	0.035	-1.4													
811_at	7353	UFDIL	chr22q11.21	ubiquitin fusion degradation 1 like (yeast)	0.009	1.2	v												
32392_s_at	54658	UGT1AI	chr2q37	UDP glucuronosyltransferase 1 family, polypeptide A1	0.025	-1.2													
32382_at	7348	UPK1B	chr3q13.32	uroplakin 1B	0.030	-1.2													
32448_at	7379	UPK2	chr11q23	uroplakin 2	0.036	-1.2													
283_at	7384	UQCRC1	chr3p21.3	ubiquinol-cytochrome c reductase core protein 1	0.024	1.4													
38561_at	27340	UTP20	chr12q23	UTP20, small subunit (SSU) processome component, homolog (yeast)	0.032	-1.3													
33780_at	6843	VAMP1	chr12p	vesicle-associated membrane protein 1 (synaptobrevin 1)	0.048	-1.2													
41757_at	9217	VAPB	chr20q13.33	VAMP (vesicle-associated membrane protein)-associated protein B and C	0.039	1.3											v	v	v
1704_at	7410	VAV2	chr9q34.1	vav 2 guanine nucleotide exchange factor	0.045	-1.2											v	v	v
38111_at	1462	VCAN	chr5q14.3	versican	0.010	1.2			v										
33818_at	7415	VCP	chr9p13.3	valosin-containing protein	0.016	1.2													
31607_at	7416	VDAC1	chr5q31	voltage-dependent anion channel 1	0.031	-1.4													
37697_s_at	7417	VDAC2	chr10q22	voltage-dependent anion channel 2	0.046														

Supplementary Table 1: CCLE DEGs (blood) associated with enriched disease-related pathways and processes. We delineate an extended 783 DEGs from a comparison of peripheral blood of 3 CCLE patients vs. 3 healthy control individuals (gold change (FC) = ±1, and $P < 0.05$). Eighty seven DEGs (**in bold**) are shared between the blood and our previously published skin expression profile (PMID: 24956118). Sixty of the 87 shared DEGs (**bold and underlined**) have corresponding genes in both tissues which are either synonymous or have similar functions. Disease-related pathways and processes that are associated with DEGs in both blood and skin profiles are marked with **V**.

Abbreviations used : FC, Fold change, CCLE, chronic cutaneous lupus erythematosus.

Disease related pathways and processes: **Apopt**: apoptosis; **Oxid Red**: oxidation/reduction; **Cell adh**: cell adhesion; **Cyto-chemo**: cytokine/chemokine; **Leu che**: leukocyte chemotaxis; **NK**: NK cells; **TLR**: Toll like receptor signaling; **DC**: Dendritic cells; **TC**: T cell; **BC**: B cell; **IFN**: Type I interferon and **Lys/Prot**: lysosome/ proteasome related.

Running title: Inter-stem analysis: Cutaneous leprosy, Das, Rao and Singla, 2018

Running title: Interactome analysis: Cutaneous lupus- Dey-Rao and Sinha, 2018