

CCLE peripheral blood: 783 DEGs							Disease related pathways and processes											
Probeset ID	Entrez Gene	Gene Symbol	Chromosomal Location	Gene Title	p-value	FC (CCLE patients vs. Control)	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											✓	
35390 at	23460	ABCA6	chr17q24.3	ATP-binding cassette, sub-family A (ABC1), member 6	0.033	-1.2												
41681 at	22	ABCB7	chrXq13.3	ATP-binding cassette, sub-family B (MDR/TAP), member 7	0.014	1.2												
40294 at	23457	ABCB9	chr12q24	ATP-binding cassette, sub-family B (MDR/TAP), member 9	0.015	-1.2		✓										✓
1930 at	8714	ABCC3	chr17q22	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0.001	-1.4												
37261 g at	10060	ABCC9	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	✓		✓								✓	
39058 at	29	ABR	chr17p13.3	active BCR-related gene	0.030	1.3												
36417 s at	30	ACAA1	chr3p23-p22	acetyl-CoA acyltransferase 1	0.030	1.4		✓										
39207 t at	176	ACAV	chr15q26.1	aggrecan	0.046	-1.4			✓									
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			✓		✓				✓		✓	
37091 g at	1587	ADAM3A	chr8p11.23	ADAM metalloproteinase domain 3A	0.012	-1.2												
36269 at	9508	ADAMTS3	chr4q13.3	ADAM metalloproteinase with thrombospondin type 1 motif, 3	0.041	-1.2												
33353 at	107	ADCY1	chr7p13-p12	adenylate cyclase 1 (brain)	0.042	-1.2				✓							✓	
34686 at	108	ADCY2	chr5p15.3	adenylate cyclase 2 (brain)	0.036	-1.2				✓							✓	
39383 at	112	ADCY6	chr12q12-q13	adenylate cyclase 6	0.038	-1.2				✓							✓	
34637 t at	124	ADH1A	chr4q23	alcohol dehydrogenase 1A (class I), alpha polypeptide	0.029	-1.1		✓										
31550 at	153	ADRB1	chr10q24-q26	adrenergic, beta-1-, receptor	0.029	-1.5												
34315 at	10939	AFG3L2	chr18p11	AFG3 ATPase family gene 3-like 2 (S. cerevisiae)	0.043	1.4												
38852 at	116986	AGAP2	chr12q14.1	ArfGAP with GTPase 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	10768	AHCYL1	chr1p13.2	adenosylhomocysteinease-like 1	0.050	1.6												
36497 at	113146	AHNAK2	chr14q32.33	AHNAK nucleoprotein 2	0.004	-1.2												
34439 at	9447	AIM2	chr1q22	absent in melanoma 2	0.029	-1.1	✓										✓	
41250 at	7965	AIMP2	chr7p22	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	0.006	1.4												
40685 at	221	ALDH3B1	chr11q13	aldehyde dehydrogenase 3 family, member B1	0.012	1.6												
678 at	251	ALPLP2	chr2q37	alkaline phosphatase, placental-like 2	0.050	-1.4												
33532 at	8092	ALX1	chr12q21.31	ALX homeobox 1	0.014	-1.2			✓									
41706 at	114899 /// 23600	AMACR /// C1QTNF3	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				✓								
32919 at	347902	AMIGO2	chr12q13.11	adhesion molecule with Ig-like domain 2	0.012	-1.1			✓									
36865 at	23357	ANGEL1	chr14q24.3	angel homolog 1 (Drosophila)	0.010	-1.2												
38199 at	90806	ANGEL2	chr1q32.3	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-q28/q27	annexin A5	0.020	1.9												
35593 at	314	AOC2	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												✓
40148 at	323	APBB2	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							✓					
261 s at	338	APOB	chr2p24-p23	apolipoprotein B (including Ag(x) antigen)	0.018	-1.2												
41472 at	60489	APOBEC3G	chr22q13.1-q13.2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	0.018	2.4												
40430 at	375	ARF1	chr1q42.13	ADP-ribosylation factor 1	0.048	-1.3												
34725 at	2909	ARHGAP35	chr19q13.3	glucocorticoid receptor DNA binding factor 1	0.045	-1.2												
35505 at	8289	ARID1A	chr1p35.3	AT rich interactive domain 1A (SWI-like)	0.048	-1.4											✓	
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			✓									
31875 at	51665	ASB1	chr2q37	ankyrin repeat and SOCS box-containing 1	0.018	1.1	✓											
287 at	467	ATF3	chr1q32.3	activating transcription factor 3	0.002	1.2	✓										✓	
41235 at	468	ATF4	chr22q13.1	activating transcription factor 4 (tax-responsive enhancer element B67)	0.039	1.6	✓										✓	
32439 at	496	ATP4B	chr13q34	ATPase, H ⁺ /K ⁺ exchanging, beta polypeptide	0.033	-1.3												
34811 at	518	ATP5G3	chr2q31.1	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)	0.046	1.5												
36107 at	522	ATP5J	chr21q21.1	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit F6	0.024	1.5												
40134 at	9551	ATP5J2	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, V1 subunit D	0.042	1.4												
37367 at	529	ATP6V1E1	chr22pter-q11.22q11.1	ATPase, H ⁺ transporting, lysosomal 31kDa, V1 subunit E1	0.034	1.2												
37395 at	9296	ATP6V1F	chr7q32	ATPase, H ⁺ transporting, lysosomal 14kDa, V1 subunit F	0.044	1.3		✓										
33741 at	51606	ATP6V1H	chr8q11.2	ATPase, H ⁺ transporting, lysosomal 50/57kDa, V1 subunit H	0.012	1.2												✓
33634 at	5205	ATP8B1	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	552889	ATXN7L3B	chr12q21	ataxin 7-like 3B	0.010	1.2												
41582 at	10677	AVIL	chr12q14.1	advillin	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-beta-GlcNAc beta 1,4- galactosyltransferase, polypeptide 4	0.004	1.5												
41115 s at	8938	BAIAP3	chr16p13.3	BAI1-associated protein 3	0.026	-1.3												
1801 at	580	BARD1	chr2q34-q35	BRCA1 associated RING domain 1	0.034	2												
35425 at	8538	BARX2	chr11q25	BARX homeobox 2	0.007	-1.2			✓									
1909 at	596	BCL2	chr18q21.33/18q21.3	B-cell CLL/lymphoma 2	0.044	1.3	✓		✓		✓				✓		✓	
31611 s at	10018	BCL2L11	chr2q13	BCL2-like 11 (apoptosis facilitator)	0.002	1.2	✓		✓									
1339 s at	613	BCR	chr22q11/22q11.23	breakpoint cluster region	0.029	-1.1												
32127 at	636	BICD1	chr12p11.2-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, RecQ helicase-like	0.019	1.4					✓				✓			

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36102_at	7419	<i>VDAC3</i>	chr8p11.2	voltage-dependent anion channel 3	0.040	1.3												
334_s_at	7432	<i>VIP</i>	chr6q25	vasoactive intestinal peptide	0.041	-1.3												
40001_r_at	23230	<i>VPS13A</i>	chr9q21	vacuolar protein sorting 13 homolog A (S. cerevisiae)	0.027	1.2												
35779_at	11311	<i>VPS45</i>	chr1q21.2	vacuolar protein sorting 45 homolog (S. cerevisiae)	0.024	1.4												
34281_at	7447	<i>VSNL1</i>	chr2p24.3	visinin-like 1	0.017	-1.1												
38987_at	79084	<i>WDR77</i>	chr1p13.2	WD repeat domain 77	0.012	-1.2												
35164_at	7466	<i>WFS1</i>	chr4p16	Wolfram syndrome 1 (wolframin)	0.034	-1.3	✓											
33392_at	26100	<i>WIP2</i>	chr7p22.1	WD repeat domain, phosphoinositide interacting 2	0.018	1.3												
32359_at	8840	<i>WISP1</i>	chr8q24.22	WNT1 inducible signaling pathway protein 1	0.011	-1.2				✓								
32358_at	8838	<i>WISP3</i>	chr6q21	WNT1 inducible signaling pathway protein 3	0.005	-1.3												
33718_at	58525	<i>WIZ</i>	chr19p13.1	widely interspaced zinc finger motifs	0.033	-1.2												
35305_at	7511	<i>XPNPEP1</i>	chr10q25.3	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	0.036	1.2												
40824_at	23039	<i>XPO7</i>	chr8p21	exportin 7	0.021	1.5												
38977_at	8565	<i>YARS</i>	chr1p35.1	tyrosyl-tRNA synthetase	0.009	1.4												
31922_l_at	9189	<i>ZBED1</i>	chrXp22.33 and Yp11	zinc finger, BED-type containing 1	0.017	-1.2												
38532_at	9880	<i>ZBTB39</i>	chr12q13.3	zinc finger and BTB domain containing 39	0.009	-1.1												
32587_at	678	<i>ZFP36L2</i>	chr2p22.3-p21	zinc finger protein 36, C3H type-like 2	0.032	1.6												
35611_at	7539	<i>ZFP37</i>	chr9q32	zinc finger protein 37 homolog (mouse)	0.050	-1.2												
37943_at	23503	<i>ZFYVE26</i>	chr14q24.1	zinc finger, FYVE domain containing 26	0.018	1.4												
34611_at	7745	<i>ZKSCAN8</i>	chr6p21.3	zinc finger with KRAB and SCAN domains 8	0.006	-1.1												
37116_at	23613	<i>ZMYND8</i>	chr20q13.12	zinc finger, MYND-type containing 8	0.007	-1.1												
36392_at	7694	<i>ZNF135</i>	chr19q13.4	zinc finger protein 135	0.018	-1.2												
41393_at	7748	<i>ZNF195</i>	chr11p15.5	zinc finger protein 195	0.003	1.3												
35838_at	57862	<i>ZNF410</i>	chr14q24.3	zinc finger protein 410	0.022	1.3												

Supplementary Table 1. CCLE DEGs (blood) associated with enriched, disease-related pathways and processes. We delineated an extended 783 DEGs from a comparison of peripheral blood of 3 CCLE patients vs. 3 healthy control individuals (fold change (FC) ≥ ±1.1 and p-value at <0.05). Eighty seven DEGs (in **bold**) are shared between the blood and our previously published skin expression profile (PMID: 24956118). Six of the 87 shared DEGs (**bold and underlined**) have corresponding genes in both lists 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 ✓.

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