Figure 1s

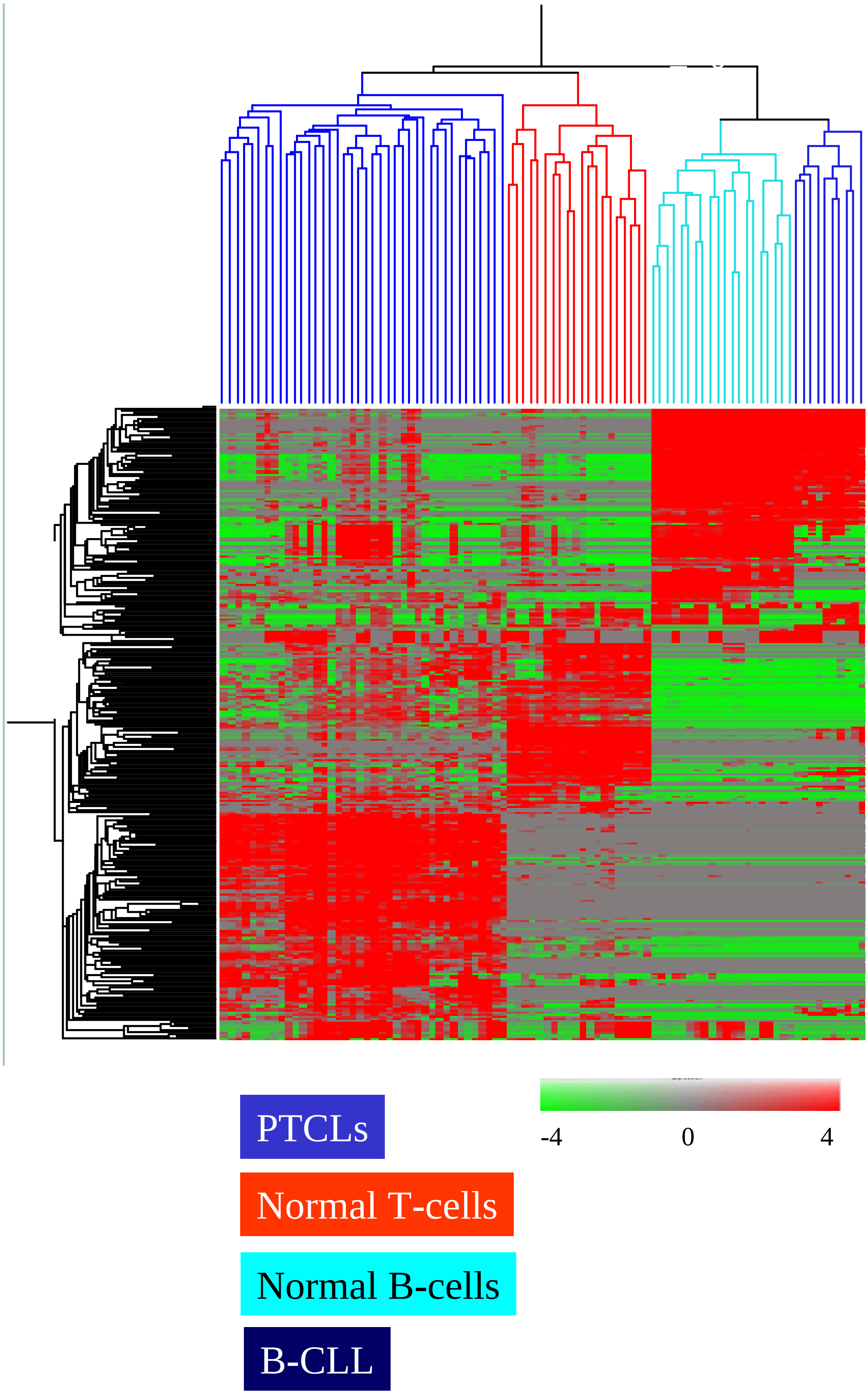


Figure 2s

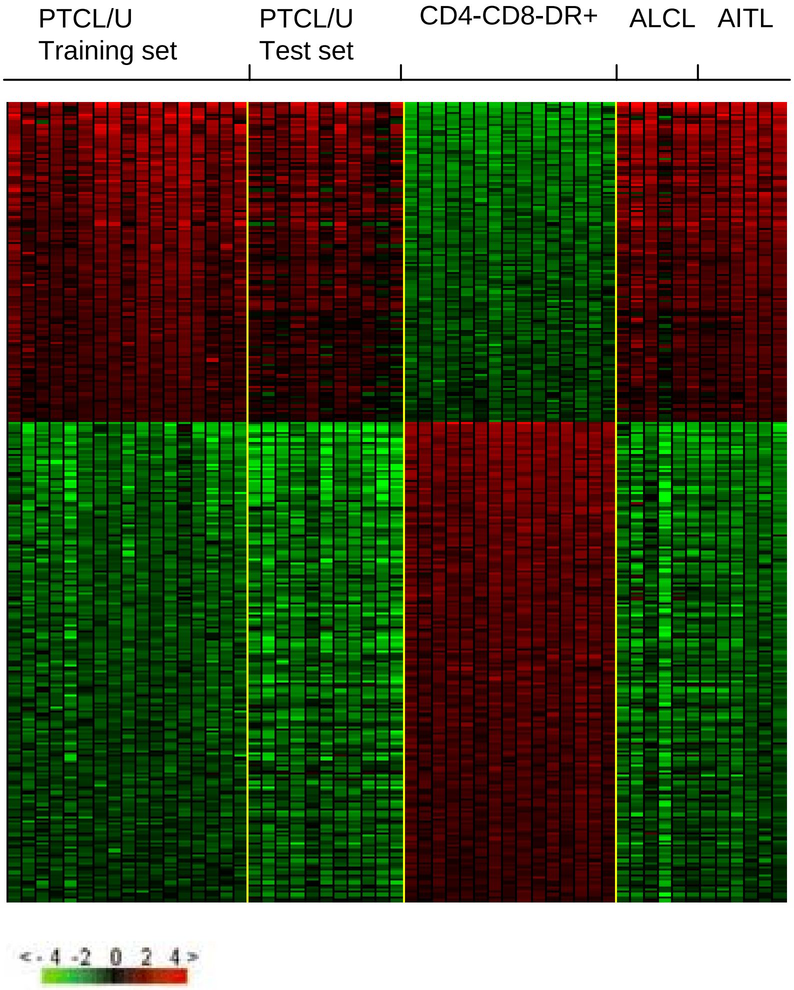
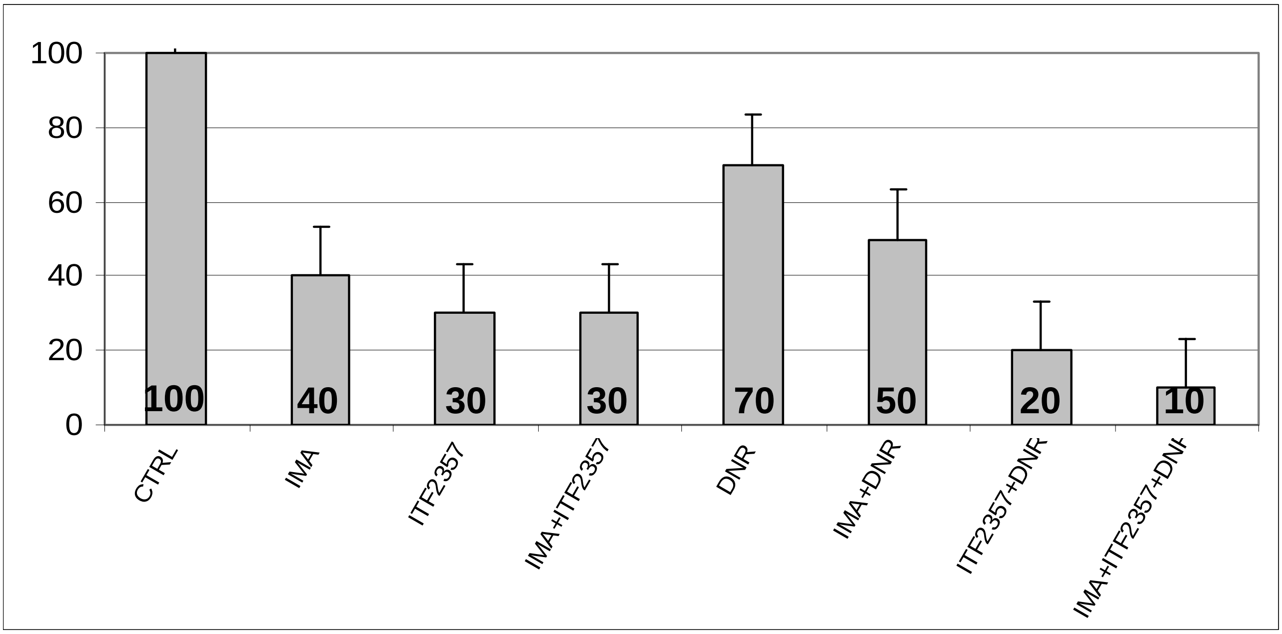


Figure 3s



100
80
60
40
20
0
100
40
30
30
70
50
20
10
CTRL
IMA
ITF2357
IMA+ITF2357
DNR
IMA+DNR
ITF2357+DNR
IMA+ITF2357+DNR

Figure 1s. **Unsupervised hierarchical clustering distinguishes PTCLs, B-CLL and normal B and T-lymphocytes.**

Unsupervised hierarchical clustering of gene expression profiles generated from PTCL/U (28), AITL (6), ALCL (6), B-CLL (10) and normal T- (20) and B-lymphocytes (20). The 90 samples are clustered according to their expression of 327 genes. Such approach promptly distinguished between T- and B-cell populations. Within each group, the samples clustered on the basis of their nature (i.e. B-cells vs. B-CLL and T-lymphocytes vs. PTCLs).

Figure 2s. Supervised analysis of PTCL/U and other PTCLs identifies differentially expressed genes.

Unsupervised analysis identified 155 genes that are differentially expressed in PTCL/U versus CD4, CD8 and HLA-DR+ lymphocytes (Figure 4). The expression of the 155 genes was then investigated in AITL and ALCL cases (represented on the right side of the matrix). The signature was largely shared by PTCL/U, AITL and ALCL.

Figure 3s. Effects of imatinib, ITF2357, daunorubicin and their combinations on PTCL/U primary cells viability.

PTCL/U primary cells were incubated for 48 hours in media containing 10% FBS with or without imatinib, ITF2357, and daunorubicin at 1, 0.5, and 5 μM concentration respectively. Furthermore, all the possible combinations were tested using the same doses of each compound. While “double” combinations did not determine significant benefit, the association of the three drugs induced a striking effect on cell viability.

Table 1s. Gene categories differentially expressed in the two PTCL subgroups identified by unsupervised analysis (Figure 1). All five categories were over-represented in Group 1. The categories have been selected according to the Gene Ontology (GO) database and compared with the EASE software (see Methods section for details).

GO System	**Gene Category**	**P value**
Biological Process	response to biotic stimulus	6.59e-004
Biological Process	immune response	7.58e-004
Biological Process	response to external stimulus	2.96e-003
Biological Process	defense response	2.99e-003
Biological Process	response to stress	9.54e-003

Table 2s. Genes differentially expressed in HLA-DR+ vs. HLA-DR- non-neoplastic T-lymphocytes

Probe set	***Common name***	***GeneBank***	***Description***
39402_at	*IL1B*	M15330	interleukin 1, beta
239704_at	*IBRDC2*	BE274992	IBR domain containing 2
233555_s_at	*SULF2*	AL034418	
231899_at	*KIAA1726*	AB051513	KIAA1726 protein
230689_at		AA825243	Transcribed sequences
230446_at		AI627850	Transcribed sequences
230276_at	*DKFZP566A1524*	AI934342	hypothetical protein DKFZp566A1524
228585_at	*ENTPD1*	AI301948	ectonucleoside triphosphate diphosphohydrolase 1
228056_s_at	*NAP1L*	AI763426	napsin B pseudogene
228055_at	*NAP1L*	AI763426	napsin B pseudogene
227970_at	*GPR157*	AK026883	Similar to RIKEN cDNA F730108M23 gene (LOC400734), mRNA
227867_at	*LOC129293*	AA005361	hypothetical protein LOC129293
227140_at		AI343467	CDNA FLJ11041 fis, clone PLACE1004405
226841_at	*MPEG1*	BF590697	macrophage expressed gene 1
226818_at	*MPEG1*	T64884	macrophage expressed gene 1
226694_at	*AKAP2*	BG540494	paralemmin 2
226517_at	*BCAT1*	AL390172	Homo sapiens mRNA; cDNA DKFZp547I204 (from clone DKFZp547I204).
226433_at	*RNF157*	BF056204	ring finger protein 157
226397_s_at		BG502771	CDNA: FLJ21028 fis, clone CAE07155
226218_at	*IL7R*	BE217880	interleukin 7 receptor
225897_at	*MARCKS*	AI709406	myristoylated alanine-rich protein kinase C substrate

225710_at		H99792	CDNA FLJ34013 fis, clone FCBBF2002111
225285_at	*BCAT1*	AK025615	branched chain aminotransferase 1, cytosolic
224795_x_at		AW575927	Immunoglobulin kappa light chain mRNA, partial cds
224724_at	*SULF2*	AL133001	sulfatase 2
224654_at	*DDX21*	BG164358	602341831F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4452270 5', mRNA sequence.
224583_at	*COTL1*	AL565621	coactosin-like 1 (Dictyostelium)
224428_s_at	*CDCA7*	AY029179	cell division cycle associated 7
224356_x_at	*MS4A6A*	AF237908	membrane-spanning 4-domains, subfamily A, member 6A
223484_at	*NMES1*	AF228422	normal mucosa of esophagus specific 1
223344_s_at	*MS4A7*	AB026043	membrane-spanning 4-domains, subfamily A, member 7
223343_at	*MS4A7*	AI301935	membrane-spanning 4-domains, subfamily A, member 7
222862_s_at	*AK5*	BG169832	adenylate kinase 5
222680_s_at	*RAMP*	AK001261	RA-regulated nuclear matrix-associated protein
222496_s_at	*FLJ20273*	AW241742	RNA-binding protein
222146_s_at	*TCF4*	AK026674	transcription factor 4
221841_s_at	*KLF4*	BF514079	Kruppel-like factor 4 (gut)
221724_s_at	*CLECSF6*	AF200738	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 6
221671_x_at		M63438	Immunoglobulin kappa light chain mRNA, partial cds
221651_x_at	*IGKC*	BC005332	Homo sapiens cDNA clone MGC:12418 IMAGE:3934658, complete cds.
221059_s_at	*CHST6*	NM_021615	carbohydrate (N-acetylglucosamine 6-O)

			sulfotransferase 6
220266_s_at	*KLF4*	NM_004235	Kruppel-like factor 4 (gut)
219947_at	*CLECSF6*	NM_016184	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 6
219593_at	*SLC15A3*	NM_016582	solute carrier family 15, member 3
219584_at	*PLA1A*	NM_015900	phospholipase A1 member A
218039_at	*NUSAP1*	NM_016359	nucleolar and spindle associated protein 1
218035_s_at	*FLJ20273*	NM_019027	RNA-binding protein
217979_at	*TM4SF13*	NM_014399	transmembrane 4 superfamily member 13
217764_s_at	*RAB31*	AF183421	RAB31, member RAS oncogene family
217763_s_at	*RAB31*	NM_006868	RAB31, member RAS oncogene family
217762_s_at	*RAB31*	BE789881	RAB31, member RAS oncogene family
217678_at	*SLC7A11*	AA488687	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
217478_s_at	*HLA-DMA*	X76775	
217414_x_at	*HBA2*	V00489	Human alpha-globin gene with flanks.
217388_s_at	*KYNU*	D55639	kynureninase (L-kynurenine hydrolase)
216243_s_at	*IL1RN*	BE563442	interleukin 1 receptor antagonist
215633_x_at	*LST1*	AV713720	AV713720 DCB Homo sapiens cDNA clone DCBBJA12 5', mRNA sequence.
215537_x_at	*DDAH2*	AJ012008	
215193_x_at	*HLA-DRB3*	AJ297586	major histocompatibility complex, class II, DR beta 3
215177_s_at	*ITGA6*	AV733308	integrin, alpha 6
214945_at	*NY-REN-7*	AW514267	NY-REN-7 antigen
214414_x_at	*HBA2*	T50399	hemoglobin, alpha 2

214390_s_at	*BCAT1*	AI652662	branched chain aminotransferase 1, cytosolic
213975_s_at	*LYZ*	AV711904	AV711904 DCA Homo sapiens cDNA clone DCAAIE08 5', mRNA sequence.
213891_s_at	*TCF4*	AI927067	transcription factor 4
213566_at	*RNASE6*	NM_005615	ribonuclease, RNase A family, k6
213533_at	*D4S234E*	M98528	Homo sapiens neuron-specific protein gene, last exon, clone D4S234.
213479_at	*NPTX2*	U26662	neuronal pentraxin II
213415_at	*CLIC2*	AI768628	chloride intracellular channel 2
213258_at	*TFPI*	BF511231	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
213002_at	*MARCKS*	AA770596	myristoylated alanine-rich protein kinase C substrate
212822_at	*HEG*	AA121502	HEG homolog
212681_at	*EPB41L3*	AI770004	erythrocyte membrane protein band 4.1-like 3
212671_s_at	*HLA-DQA1*	BG397856	major histocompatibility complex, class II, DQ alpha 1
212592_at	*IGJ*	AV733266	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides
212387_at	*TCF4*	BG495771	transcription factor 4
212386_at	*TCF4*	BF592782	transcription factor 4
212385_at	*TCF4*	AU118026	transcription factor 4
212382_at	*TCF4*	BF433429	transcription factor 4
211991_s_at	*HLA-DPA1*	M27487	major histocompatibility complex, class II, DP alpha 1
211990_at	*HLA-DPA1*	M27487	major histocompatibility complex, class II, DP alpha 1
211745_x_at	*HBA2*	BC005931	hemoglobin, alpha 2
211699_x_at	*HBA2*	AF349571	hemoglobin, alpha 2

211506_s_at	*IL8*	AF043337	Homo sapiens interleukin 8 C-terminal variant (IL8) mRNA, complete cds.
210982_s_at	*HLA-DRA*	M60333	major histocompatibility complex, class II, DR alpha
210895_s_at	*CD86*	L25259	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)
210664_s_at	*TFPI*	AF021834	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
210663_s_at	*KYNU*	BC000879	kynureninase (L-kynurenine hydrolase)
210512_s_at	*VEGF*	AF022375	vascular endothelial growth factor
210340_s_at	*CSF2RA*	BC002635	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)
210146_x_at	*LILRB2*	AF004231	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2
210118_s_at	*IL1A*	M15329	interleukin 1, alpha
210073_at	*SIAT8A*	L32867	sialyltransferase 8A (alpha-N-acetylneuraminate: alpha-2,8-sialyltransferase, GD3 synthase)
209921_at	*SLC7A11*	AB040875	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
209901_x_at	*AIF1*	U19713	allograft inflammatory factor 1
209871_s_at	*APBA2*	AB014719	amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)
209774_x_at	*CXCL2*	M57731	chemokine (C-X-C motif) ligand 2

209684_at	*RIN2*	AL136924	Ras and Rab interactor 2
209683_at	*DKFZP566A1524*	AA243659	hypothetical protein DKFZp566A1524
209619_at	*CD74*	K01144	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)
209458_x_at	*HBA2*	AF105974	hemoglobin, alpha 2
209312_x_at	*HLA-DRB1*	U65585	major histocompatibility complex, class II, DR beta 3
209191_at	*MGC4083*	BC002654	tubulin beta MGC4083
209184_s_at	*IRS2*	BF700086	602127569F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284401 5', mRNA sequence.
209116_x_at	*HBB*	M25079	Human sickle cell beta-globin mRNA, complete cds.
208949_s_at	*LGALS3*	BC001120	lectin, galactoside-binding, soluble, 3 (galectin 3)
208894_at	*HLA-DRA*	M60334	major histocompatibility complex, class II, DR alpha
208890_s_at	*PLXNB2*	BC004542	plexin B2
208864_s_at	*TXN*	AF313911	thioredoxin
208594_x_at	*ILT8*	NM_024318	synonym: LILRB6; immunoglobulin-like transcript 8; Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 6 (ILT8), mRNA.
208306_x_at	*HLA-DRB3*	NM_021983	major histocompatibility complex, class II, DR beta 3
208146_s_at	*CPVL*	NM_031311	carboxypeptidase, vitellogenic-like
207850_at	*CXCL3*	NM_002090	chemokine (C-X-C motif) ligand 3
207697_x_at	*LILRB2*	NM_005874	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2

207540_s_at	*SYK*	NM_003177	spleen tyrosine kinase
207085_x_at	*CSF2RA*	NM_006140	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)
206710_s_at	*EPB41L3*	NM_012307	erythrocyte membrane protein band 4.1-like 3
206632_s_at	*APOBEC3B*	NM_004900	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B
206488_s_at	*CD36*	NM_000072	CD36 antigen (collagen type I receptor, thrombospondin receptor)
206380_s_at	*PFC*	NM_002621	properdin P factor, complement
206157_at	*PTX3*	NM_002852	pentaxin-related gene, rapidly induced by IL-1 beta
205997_at	*ADAM28*	NM_021778	a disintegrin and metalloproteinase domain 28
205859_at	*LY86*	NM_004271	lymphocyte antigen 86
205767_at	*EREG*	NM_001432	epiregulin
205559_s_at	*PCSK5*	NM_006200	proprotein convertase subtilisin/kexin type 5
205237_at	*FCN1*	NM_002003	ficolin (collagen/fibrinogen domain containing) 1
205207_at	*IL6*	NM_000600	interleukin 6 (interferon, beta 2)
205159_at	*CSF2RB*	AV756141	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
205067_at	*IL1B*	NM_000576	interleukin 1, beta
204971_at	*CSTA*	NM_005213	cystatin A (stefin A)

204793_at	*GASP*	NM_014710	
204777_s_at	*MAL*	NM_002371	mal, T-cell differentiation protein
204748_at	*PTGS2*	NM_000963	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
204670_x_at	*HLA-DRB3*	NM_002125	major histocompatibility complex, class II, DR beta 3
204614_at	*SERPINB2*	NM_002575	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2
204249_s_at	*LMO2*	NM_005574	LIM domain only 2 (rhombotin-like 1)
204112_s_at	*HNMT*	NM_006895	histamine N-methyltransferase
204018_x_at	*HBA2*	NM_000558	hemoglobin, alpha 2
203932_at	*HLA-DMB*	NM_002118	major histocompatibility complex, class II, DM beta
203888_at	*THBD*	NM_000361	thrombomodulin
203887_s_at	*THBD*	NM_000361	thrombomodulin
203753_at	*TCF4*	NM_003199	transcription factor 4
203509_at	*SORL1*	NM_003105	sortilin-related receptor, L(DLR class) A repeats-containing
203413_at	*NELL2*	NM_006159	NEL-like 2 (chicken)
202949_s_at	*FHL2*	NM_001450	four and a half LIM domains 2
202933_s_at	*YES1*	NM_005433	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
202932_at	*YES1*	NM_005433	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
202897_at	*PTPNS1*	AB023430	protein tyrosine phosphatase, non-receptor type substrate 1
202503_s_at	*KIAA0101*	NM_014736	KIAA0101 gene product
202391_at	*BASP1*	NM_006317	brain abundant, membrane attached signal protein 1

202345_s_at	*FABP5*	NM_001444	fatty acid binding protein 5 (psoriasis-associated)
202286_s_at	*TACSTD2*	J04152	GA733-1 protein precursor; Human gastrointestinal tumor-associated antigen GA733-1 protein gene, complete cds, clone 05516.
202283_at	*SERPINF1*	NM_002615	serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1
202262_x_at	*DDAH2*	NM_013974	dimethylarginine dimethylaminohydrolase 2
202241_at	*TRIB1*	NM_025195	phosphoprotein regulated by mitogenic pathways
202085_at	*TJP2*	NM_004817	tight junction protein 2 (zona occludens 2)
201887_at	*IL13RA1*	NM_001560	interleukin 13 receptor, alpha 1
201820_at	*KRT5*	NM_000424	keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)
201798_s_at	*FER1L3*	NM_013451	fer-1-like 3, myoferlin (C. elegans)
201710_at	*MYBL2*	NM_002466	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
201670_s_at	*MARCKS*	M68956	myristoylated alanine-rich protein kinase C substrate
201669_s_at	*MARCKS*	NM_002356	myristoylated alanine-rich protein kinase C substrate
201656_at	*ITGA6*	NM_000210	integrin, alpha 6
201506_at	*TGFBI*	NM_000358	transforming growth factor, beta-induced, 68kDa
201489_at	*PPIF*	BC005020	peptidylprolyl isomerase F (cyclophilin F)
201425_at	*ALDH2*	NM_000690	aldehyde dehydrogenase 2 family (mitochondrial)
201422_at	*IFI30*	NM_006332	interferon, gamma-inducible protein 30
201360_at	*CST3*	NM_000099	cystatin C (amyloid angiopathy and cerebral

			hemorrhage)
201292_at	*TOP2A*	AL561834	topoisomerase (DNA) II alpha 170kDa
201212_at	*LGMN*	D55696	legumain
201137_s_at	*HLA-DPB1*	NM_002121	major histocompatibility complex, class II, DP beta 1
200871_s_at	*PSAP*	NM_002778	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
200866_s_at	*PSAP*	M32221	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
200839_s_at	*CTSB*	NM_001908	cathepsin B
200838_at	*CTSB*	NM_001908	cathepsin B
200788_s_at	*PEA15*	NM_003768	phosphoprotein enriched in astrocytes 15
200736_s_at	*GPX1*	NM_000581	glutathione peroxidase 1
200678_x_at	*GRN*	NM_002087	granulin
1569110_x_at	*PDCD6*	BC020552	programmed cell death 6
1567628_at	*CD74*	M28590	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)
1558662_s_at	*BANK1*	BG200452	B-cell scaffold protein with ankyrin repeats 1
1556346_at		AJ227860	Partial mRNA; ID YG39-1A
1555745_a_at	*LYZ*	U25677	lysozyme (renal amyloidosis)
1554899_s_at	*FCER1G*	BC020763	Homo sapiens Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide, mRNA (cDNA clone MGC:22620 IMAGE:4704425), complete cds.
1552519_at	*ACVR1C*	NM_145259	activin A receptor, type IC

Table 3s. Genes differentially expressed in CD4+ vs. CD8+ non-neoplastic T-lymphocytes

Probe set	***Common name***	***GeneBank***	***Description***
39402_at	*IL1B*	M15330	interleukin 1, beta
37145_at	*GNLY*	M85276	Homo sapiens NKG5 gene, complete cds.
36711_at	*MAFF*	AL021977	Human DNA sequence from clone CTA-447C4 on chromosome 22q12.2-13.2, complete sequence.
242385_at	*RORB*	R18374	RAR-related orphan receptor B
236782_at	*SAMD3*	AI129628	sterile alpha motif domain containing 3
231776_at	*EOMES*	NM_005442	eomesodermin homolog (Xenopus laevis)
231093_at	*FCRH3*	BF514552	Fc receptor-like protein 3
230508_at	*DKK3*	AL569601	dickkopf homolog 3 (Xenopus laevis)
229309_at	*ADRB1*	AI625747	adrenergic, beta-1-, receptor
226731_at	*ITGA1*	AA156873	integrin, alpha 1
226694_at	*AKAP2*	BG540494	paralemmin 2
225496_s_at	*SYTL2*	N21426	yx58d01.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:265921 3', mRNA sequence.
223280_x_at	*MS4A6A*	AF253977	membrane-spanning 4-domains, subfamily A, member 6A
221127_s_at	*RIG*	NM_006394	
220646_s_at	*KLRF1*	NM_016523	killer cell lectin-like receptor subfamily F, member 1
220307_at	*CD244*	NM_016382	CD244 natural killer cell receptor 2B4
219666_at	*MS4A6A*	NM_022349	membrane-spanning 4-domains, subfamily A, member 6A
219033_at	*FLJ21308*	NM_024615	hypothetical protein FLJ21308
219013_at	*GALNT11*	NM_022087	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)
216920_s_at	*TRGV9*	M27331	T cell receptor gamma locus
216676_x_at	*KIR2DS2*	AC006293	
216191_s_at	*TRD@*	X72501	T cell receptor delta locus
215894_at	*PTGDR*	AI460323	prostaglandin D2 receptor (DP)

215806_x_at	*TRGV9*	M13231	T cell receptor gamma locus
214660_at	*ITGA1*	X68742	integrin, alpha 1
214567_s_at	*XCL1*	NM_003175	chemokine (C motif) ligand 2
214450_at	*CTSW*	NM_001335	cathepsin W (lymphopain)
214247_s_at	*DKK3*	AU148057	dickkopf homolog 3 (Xenopus laevis)
213975_s_at	*LYZ*	AV711904	AV711904 DCA Homo sapiens cDNA clone DCAAIE08 5', mRNA sequence.
213915_at	*NKG7*	NM_005601	natural killer cell group 7 sequence
213385_at	*CHN2*	AK026415	chimerin (chimaerin) 2
212240_s_at	*PIK3R1*	AI679268	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)
211144_x_at	*TRGV9*	M30894	T cell receptor gamma locus
210690_at	*KLRC4*	U96845	killer cell lectin-like receptor subfamily C, member 4
210606_x_at	*KLRD1*	U30610	killer cell lectin-like receptor subfamily D, member 1
210354_at	*IFNG*	M29383	Human mRNA for HuIFN-gamma interferon.
210140_at	*CST7*	AF031824	cystatin F (leukocystatin)
209993_at	*ABCB1*	AF016535	ATP-binding cassette, sub-family B (MDR/TAP), member 1
209813_x_at	*TRGV9*	M16768	T-cell receptor (V-J-C) precursor; Human T-cell receptor gamma chain VJCI-CII-CIII region mRNA, complete cds.
208983_s_at	*PECAM1*	M37780	platelet/endothelial cell adhesion molecule (CD31 antigen)
208982_at	*PECAM1*	AW574504	UI-HF-BK0-aab-h-05-0-UI.s1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053409 3', mRNA sequence.
207979_s_at	*CD8B1*	NM_004931	CD8 antigen, beta polypeptide 1 (p37)
207840_at	*CD160*	NM_007053	CD160 antigen
207795_s_at	*KLRD1*	AB009597	killer cell lectin-like receptor subfamily D, member 1

207723_s_at	*KLRC3*	NM_002261	synonyms: NKG2E, NKG2-E; isoform NKG2-E is encoded by transcript variant NKG2-E; go_component: integral to membrane [goid 0016021] [evidence IEA]; go_function: transmembrane receptor activity [goid 0004888] [evidence TAS] [pmid 9683661]; go_function: lectin [goid 0005530] [evidence IEA]; go_function: sugar binding [goid 0005529] [evidence IEA]; go_process: cellular defense response [goid 0006968] [evidence TAS] [pmid 9683661]; go_process: heterophilic cell adhesion [goid 0007157] [evidence IEA]; Homo sapiens killer cell lectin-like receptor subfamily C, member 3 (KLRC3), transcript variant NKG2-E, mRNA.
207314_x_at	*KIR2DL3*	NM_006737	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1
207001_x_at	*DSIPI*	NM_004089	delta sleep inducing peptide, immunoreactor
206914_at	*CRTAM*	NM_019604	class-I MHC-restricted T cell associated molecule
206785_s_at	*KLRC1*	NM_002260	killer cell lectin-like receptor subfamily C, member 2
206666_at	*GZMK*	NM_002104	granzyme K (serine protease, granzyme 3; tryptase II)
206366_x_at	*XCL1*	U23772	chemokine (C motif) ligand 1
206365_at	*XCL1*	NM_002995	chemokine (C motif) ligand 1
206267_s_at	*MATK*	NM_002378	megakaryocyte-associated tyrosine kinase
206118_at	*STAT4*	NM_003151	signal transducer and activator of transcription 4
205821_at	*KLRK1*	NM_007360	killer cell lectin-like receptor subfamily K, member 1
205758_at	*CD8A*	AW006735	CD8 antigen, alpha polypeptide (p32)

205495_s_at	*GNLY*	NM_006433	granulysin
205336_at	*PVALB*	NM_002854	parvalbumin
204655_at	*CCL5*	NM_002985	chemokine (C-C motif) ligand 5
204011_at	*SPRY2*	NM_005842	sprouty homolog 2 (Drosophila)
203413_at	*NELL2*	NM_006159	NEL-like 2 (chicken)
202806_at	*DBN1*	NM_004395	drebrin 1
202196_s_at	*DKK3*	NM_013253	dickkopf homolog 3 (Xenopus laevis)
201506_at	*TGFBI*	NM_000358	transforming growth factor, beta-induced, 68kDa
201161_s_at	*CSDA*	NM_003651	cold shock domain protein A
201160_s_at	*CSDA*	AL556190	cold shock domain protein A
1555938_x_at	*VIM*	AI520969	Vimentin
1555759_a_at	*CCL5*	AF043341	chemokine (C-C motif) ligand 5
1555691_a_at	*KLRK1*	AF439512	killer cell lectin-like receptor subfamily K, member 1
1405_i_at	*CCL5*	M21121	chemokine (C-C motif) ligand 5

Table 4s. Histologic, and immunophenotypic characteristics of the 28 PTCLs/U studied by gene expression profiling

Case	Percentage of neoplastic cells	Reactive cells	Immuno-phenotype	Closest normal counterpart*
1	≥90%	Reactive CD4 and CD8 <5%., HEV, and rare epithelioid histiocytes.	DN	CD4
2	≥90%	Reactive CD8 <5%. HEV, rare eosinophils and epithelioid histiocytes; scattered CD20+ B-lymphocytes.	CD4	CD4
3	≥90%	Reactive CD4 and CD8.	DN	CD4
4	≥90%	Reactive CD8 <5%. HEV; rare histiocytes; scattered CD20+ B-lymphocytes.	CD4	CD4
5	≥80%	Reactive CD8 5%. HEV, moderate amount of histiocytes, rare eosinophils, and CD20+ B-lymphocytes at times in small aggregates.	CD4	CD4
6	≥90%	Reactive CD8 <2%. Rare HEV and histiocytes.	CD4	CD4
7	≥90%	Reactive CD8. HEV, epithelioid histiocytes, and eosinophils.	CD4	CD4
8	≥90%	Reactive CD4 and CD8. HEV, epithelioid histiocytes and eosinophils.	DN	CD4
9	≥90%	Reactive CD8. HEV and epithelioid histiocytes.	CD4	CD4
10	≥90%	Reactive CD8 <5%. Abundant HEV, rare epithelioid histiocytes.	DN	CD4
11	≥90%	Reactive CD8. HEV, epithelioid histiocytes, and eosinophils.	CD8	CD4
12	≥90%	Reactive CD8 <10%. Rare HEV, epithelioid histiocytes and eosinophils.	CD4	CD4
13	≥90%	Reactive CD8 <5%.	CD4	CD8
14	≥90%	Reactive CD4 and CD8. HEV.	DN	CD8
15	≥90%	HEV, epithelioid histiocytes and eosinophils.	DP	CD8
16	≥80%	CD20 10%. Some HEV.	DN	CD8
17	≥90%	Reactive CD8 2-3%. HEV.	CD4	CD8
18	≥70%	Reactive CD8 <20%. HEV and epithelioid histiocytes.	CD4	CD4
19	≥70%	Reactive CD4 and CD8.	DN	CD4
20	≥80%	Reactive CD8 <10%. Rare HEV, epithelioid histiocytes and eosinophils.	DP	CD4
21	≥70%	Reactive CD8 <15%. Rare HEV and histiocytes.	CD4	CD4
22	≥70%	Reactive CD4 and CD8. Some histiocytes.	DN	CD4

23	≥70%	Reactive CD8 <20%.	CD4	CD4
24	≥80%	Reactive CD8 <15%. HEV and eosinophils.	CD4	CD4
25	≥80%	Reactive CD4 and CD8 <15%. HEV and rare epithelioid histiocytes.	DN	CD4
26	≥90%	Reactive CD4 >10%. HEV.	CD8	CD4
27	≥70%	Reactive CD8 <20%. Rare HEV and histiocytes.	CD4	CD4
28	≥80%	Reactive CD8 <10%. HEV, some histiocytes and scattered CD20+ B-lymphocytes	DN	CD4

HEV = high endothelium venules
DN=double negative
DP=double positive
* as found by gene expression analysis

Table 5s. Genes over-expressed in PTCL/U vs. normal T-lymphocytes (corresponding to CD4+, CD8+ and HLA-DR+ elements)

Over-expression (Z score)	**Probe set**	**Description**	**Common**	**GeneBank**
6,94	215076_s_at	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	*COL3A1*	AU144167
5,35	209687_at	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	*CXCL12*	U19495
5,14	203868_s_at	vascular cell adhesion molecule 1	*VCAM1*	NM_001078
4,83	201289_at	cysteine-rich, angiogenic inducer, 61	*CYR61*	NM_001554
4,54	202237_at	nicotinamide N-methyltransferase	*NNMT*	NM_006169
4,04	208782_at	follistatin-like 1	*FSTL1*	BC000055
3,75	212667_at	secreted protein, acidic, cysteine-rich (osteonectin)	*SPARC*	AL575922
3,51	225664_at	collagen, type XII, alpha 1	*COL12A1*	AA788946
8,666	211719_x_at	fibronectin 1	*FN1*	BC005858
6,502	208747_s_at	complement component 1, s subcomponent	*C1S*	M18767
6,424	218541_s_at	chromosome 8 open reading frame 4	*C8orf4*	NM_020130
6,419	225575_at	leukemia inhibitory factor receptor	*LIFR*	AI680541
6,361	205890_s_at	ubiquitin D	*UBD (FAT10)*	NM_006398
6,152	211161_s_at			AF130082
5,982	217757_at	alpha-2-macroglobulin	*A2M*	NM_000014
5,967	201163_s_at	insulin-like growth factor binding protein 7	*IGFBP7*	NM_001553
5,891	209183_s_at	chromosome 10 open reading frame 10	*C10orf10*	AL136653
5,891	212077_at	caldesmon 1	*CALD1*	AL583520
5,806	218232_at	complement component 1, q subcomponent, alpha polypeptide	*C1QA*	NM_015991
5,666	209120_at	nuclear receptor subfamily 2, group F, member 2	*NR2F2*	AL037401
5,627	219134_at	EGF, latrophilin and seven transmembrane domain containing 1	*ELTD1*	NM_022159
5,471	200795_at	SPARC-like 1 (mast9, hevin)	*SPARCL1*	NM_004684
5,429	204416_x_at	apolipoprotein C-I	*APOC1*	NM_001645
5,426	211980_at	collagen, type IV, alpha 1	*COL4A1*	AI922605
5,384	202403_s_at	collagen, type I, alpha 2	*COL1A2*	AA788711
5,341	200986_at	serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)	*SERPING1*	NM_000062
4,966	202404_s_at			NM_000089
4,925	215388_s_at	H factor (complement)-like 1	*HFL1*	X56210
4,758	202411_at	interferon, alpha-inducible protein 27	*IFI27 (p27)*	NM_005532
4,615	211964_at	collagen, type IV, alpha 2	*COL4A2*	X05610
4,563	204112_s_at	histamine N-methyltransferase	*HNMT*	NM_006895

4,484	235229_at	olfactory receptor, family 2, subfamily I, member 6	*OR2I6*	AI694413
4,445	201645_at	tenascin C (hexabrachion)	*TNC*	NM_002160
4,389	223204_at	hypothetical protein DKFZp434L142	*DKFZp434L142*	AF260333
4,291	217853_at	tensin-like SH2 domain containing 1	*TENS1*	NM_022748
4,234	212067_s_at	complement component 1, r subcomponent	*C1R*	AL573058
4,202	209289_at	nuclear factor I/B	*NFIB*	AI700518
4,053	202133_at	transcriptional co-activator with PDZ-binding motif (TAZ)	*TAZ*	BF674349
4,031	203131_at	platelet-derived growth factor receptor, alpha polypeptide	*PDGFRA*	NM_006206
3,985	201667_at	gap junction protein, alpha 1, 43kDa (connexin 43)	*GJA1*	NM_000165
3,934	202800_at	solute carrier family 1 (glial high affinity glutamate transporter), member 3	*SLC1A3*	NM_004172
3,923	201505_at	laminin, beta 1	*LAMB1*	NM_002291
3,916	212698_s_at	septin 10	*SEPT10*	BF966021
3,858	201279_s_at	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	*DAB2*	BC003064
3,854	221748_s_at	tensin	*TNS*	AL046979
3,823	228220_at	hypothetical protein BC014311	*LOC115548*	AI627666
3,765	222453_at	cytochrome b reductase 1	*CYBRD1*	AL136693
3,739	209210_s_at	pleckstrin homology domain containing, family C (with FERM domain) member 1	*PLEKHC1*	Z24725
3,695	212724_at	ras homolog gene family, member E	*ARHE*	BG054844
3,667	207173_x_at	cadherin 11, type 2, OB-cadherin (osteoblast)	*CDH11*	D21254
3,644	224894_at	Yes-associated protein 1, 65kDa	*YAP1*	BF247906
3,638	202766_s_at	fibrillin 1 (Marfan syndrome)	*FBN1*	NM_000138
3,482	226621_at	fibrinogen, gamma polypeptide	*FGG*	AI133452
3,434	225040_s_at	ribulose-5-phosphate-3-epimerase	*RPE*	AV699857
3,415	210986_s_at	tropomyosin 1 (alpha)	*TPM1*	Z24727
3,353	209656_s_at	transmembrane 4 superfamily member 10	*TM4SF10*	AL136550
3,247	203910_at	PTPL1-associated RhoGAP 1	*PARG1*	NM_004815
3,204	226022_at	SAM and SH3 domain containing 1	*SASH1*	AU144882
3,196	226837_at	sprouty-related, EVH1 domain containing 1	*SPRED1*	BE967019
3,194	203324_s_at	caveolin 2	*CAV2*	NM_001233
3,131	202878_s_at	complement component 1, q subcomponent, receptor 1	*C1QR1*	NM_012072
3,042	202011_at	tight junction protein 1 (zona occludens 1)	*TJP1*	NM_003257
2,854	225202_at	Rho-related BTB domain containing 3	*RHOBTB3*	BE620739
2,623	240481_at	Transcribed sequences		BE502509

Table 6s. Genes down-regulated in PTCL/U vs. normal T-lymphocytes (corresponding CD4+, CD8+ and HLA-DR+ elements)

Over-expression (Z score)	**Probe set**	**Description**	**Common**	**GeneBank**
8.006	242832_at	period homolog 1 (Drosophila)	*PER1*	AI743776
6.542	204621_s_at	nuclear receptor subfamily 4, group A, member 2	*NR4A2*	AI935096
6.105	230511_at	cAMP responsive element modulator	*CREM*	AI800640
6.003	209959_at	Human mitogen induced nuclear orphan receptor (MINOR) mRNA, complete cds.	*NR4A3*	U12767
5.878	242904_x_at	qr06h10.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1940131 3' similar to contains MER22.t1 TAR1 repetitive element ;, mRNA sequence.	*MGC8721*	AI351653
5.583	1555832_s_at	MRNA; cDNA DKFZp564C2063 (from clone DKFZp564C2063)		BU683415
5.582	218723_s_at	response gene to complement 32	*RGC32*	NM_014059
5.544	217783_s_at	yippee protein	*CGI-127*	NM_016061
5.438	238633_at	enhancer of polycomb homolog 1 (Drosophila)	*EPC1*	W93523
5.335	212225_at	putative translation initiation factor	*SUI1*	AL516854
5.314	225557_at	AXIN1 up-regulated 1	*AXUD1*	AI091372
5.302	219228_at	zinc finger protein 331	*ZNF331*	NM_018555
5.256	224606_at	602363024F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4471541 5', mRNA sequence.		BG250721
5.211	222408_s_at	yippee protein	*CGI-127*	BC000836
5.209	208961_s_at	core promoter element binding protein	*COPEB*	AB017493
5.155	225951_s_at	chromodomain helicase DNA binding protein 2	*CHD2*	AV756026
4.943	1556873_at	Homo sapiens hypothetical protein LOC51320, mRNA (cDNA clone IMAGE:4828930), partial cds.	*RKHD2*	BC032952
4.809	202643_s_at	tumor necrosis factor, alpha-induced protein 3	*TNFAIP3*	AI738896
4.778	201464_x_at	v-jun sarcoma virus 17 oncogene homolog (avian)	*JUN*	BG491844

4.778	37028_at	protein phosphatase 1, regulatory (inhibitor) subunit 15A	*PPP1R15A*	U83981
4.742	209795_at	CD69 antigen (p60, early T-cell activation antigen)	*CD69*	L07555
4.582	36711_at	Human DNA sequence from clone CTA-447C4 on chromosome 22q12.2-13.2, complete sequence.	*MAFF*	AL021977
4.467	230380_at	hypothetical protein DKFZp564I0422	*DKFZP564I0422*	AW235671
4.456	1557257_at	B-cell CLL/lymphoma 10	*BCL10*	AA994334
4.308	204794_at	dual specificity phosphatase 2	*DUSP2*	NM_004418
4.289	202147_s_at	interferon-related developmental regulator 1	*IFRD1*	NM_001550
4.246	228562_at	zinc finger and BTB domain containing 10	*ZBTB10*	N29918
4.195	1555411_a_at	cyclin L1	*CCNL1*	AF367476
4.169	1559975_at	Hypothetical protein LOC256021 (LOC256021), mRNA	*BTG1*	BC009050
4.14	228097_at	myosin regulatory light chain interacting protein	*MYLIP*	AW292746
4.08	203752_s_at	jun D proto-oncogene	*JUND*	NM_005354
4.045	217741_s_at	zinc finger protein 216	*ZNF216*	AW471220
4.043	241985_at	junction-mediating and regulatory protein	*JMY*	AI814405
4.037	201751_at	KIAA0063 gene product	*KIAA0063*	NM_014876
3.966	202704_at	transducer of ERBB2, 1	*TOB1*	AA675892
3.94	207574_s_at	growth arrest and DNA-damage-inducible, beta	*GADD45B*	NM_015675
3.935	200730_s_at	602135085F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290141 5', mRNA sequence.	*PTP4A1*	BF576710
3.935	209069_s_at	H3 histone, family 3B (H3.3B)	*H3F3B*	BC001124
3.922	230048_at	Transcribed sequence with moderate similarity to protein pdb:1LBG (E. coli) B Chain B, Lactose Operon Repressor Bound To 21-Base Pair Symmetric Operator Dna, Alpha Carbons Only		BF061555
3.91	1554306_at	inositol 1,4,5-trisphosphate 3-kinase B	*ITPKB*	BC015009
3.862	230233_at	RasGEF domain family, member 1B	*RASGEF1B*	BF110534
3.857	211840_s_at	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	*PDE4D*	U50157

3.847	231182_at	Wiskott-Aldrich syndrome protein interacting protein	*WASPIP*	BF446719
3.838	226153_s_at	CCR4-NOT transcription complex, subunit 6-like	*CNOT6L*	AW514857
3.817	1568665_at	ring finger protein 103	*RNF103*	BC022477
3.764	227558_at	chromobox homolog 4 (Pc class homolog, Drosophila)	*CBX4*	AI570531
3.752	203725_at	growth arrest and DNA-damage-inducible, alpha	*GADD45A*	NM_001924
3.712	209510_at	ring finger 139	*RNF139*	AF064801
3.683	221763_at	thyroid hormone receptor interactor 8	*JMJD1C*	AI694023
3.65	212665_at	TCDD-inducible poly(ADP-ribose) polymerase	*TIPARP*	AL556438
3.627	208706_s_at	eukaryotic translation initiation factor 5	*EIF5*	AK026933
3.611	224569_s_at	interferon regulatory factor 2 binding protein 2	*IRF2BP2*	AW242432
3.575	236213_at	Transcribed sequence with strong similarity to protein ref:NP_060117.2 (H.sapiens) FtsJ homolog 3		AI809760
3.574	205214_at	serine/threonine kinase 17b (apoptosis-inducing)	*STK17B*	NM_004226
3.57	226650_at	hypothetical protein LOC90637	*LOC90637*	AI984061
3.566	222044_at	chromosome 20 open reading frame 67	*C20orf67*	AI199589
3.544	228812_at	Transcribed sequence with weak similarity to protein ref:NP_060265.1 (H.sapiens) hypothetical protein FLJ20378 [Homo sapiens]		AI652899
3.541	211999_at	H.sapiens hH3.3B gene for histone H3.3.	*H3F3B*	Z48950
3.519	226970_at	F-box only protein 33	*FBXO33*	AI690694
3.517	214683_s_at	CDC-like kinase 1	*CLK1*	AI251890
3.506	205281_s_at	phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria)	*PIGA*	NM_002641
3.488	1569136_at	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme A	*MGAT4A*	BC031487
3.481	210054_at	hypothetical protein MGC4701	*C4orf15*	BC003648
3.47	1554036_at	zinc finger protein 450	*ZBTB24*	BC036731
3.466	205027_s_at	mitogen-activated protein kinase kinase kinase 8	*MAP3K8*	NM_005204
3.465	218319_at	pellino homolog 1 (Drosophila)	*PELI1*	NM_020651
3.441	1554089_s_at	Shwachman-Bodian-Diamond syndrome pseudogene	*SBDS*	BC010183
3.377	223394_at	SERTA domain containing 1	*SERTAD1*	BC002670

3.325	238893_at	Hypothetical protein LOC338758, mRNA (cDNA clone IMAGE:5299152), partial cds	*LOC338758*	AI377324
3.297	204243_at	rearranged L-myc fusion sequence	*RLF*	NM_012421
3.268	238389_s_at	Transcribed sequences		AI458208
3.239	210426_x_at	RAR-related orphan receptor A	*RORA*	U04897
3.183	231863_at	inhibitor of growth family, member 3	*ING3*	AF161419
3.181	209184_s_at	602127569F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284401 5', mRNA sequence.	*IRS2*	BF700086
3.177	216027_at	hypothetical protein DJ971N18.2	*DJ971N18.2*	AI005473
3.138	218603_at	headcase homolog (Drosophila)	*HECA*	NM_016217
3.134	223287_s_at	forkhead box P1	*FOXP1*	AF146696
3.124	208810_at	DnaJ (Hsp40) homolog, subfamily B, member 6	*DNAJB6*	AF080569
3.08	202393_s_at	TGFB inducible early growth response	*TIEG*	NM_005655
3.071	224836_at		*C20orf110*	AL109824
3.064	212493_s_at	huntingtin interacting protein B	*HYPB*	AI761110
3.06	212293_at	homeodomain interacting protein kinase 1	*HIPK1*	BG111260
2.921	227650_at	likely ortholog of mouse heat shock protein, 70 kDa 4	*HSPA14*	AV757332
2.882	212508_at	modulator of apoptosis 1	*MOAP1*	AK024029
2.87	210281_s_at	zinc finger protein 198	*ZNF198*	AL136621
2.867	206374_at	dual specificity phosphatase 8	*DUSP8*	NM_004420
2.796	1552542_s_at	T-cell activation GTPase activating protein	*TAGAP*	NM_138810
2.794	202302_s_at	similar to splicing factor, arginine/serine-rich 4	*FLJ11021*	NM_023012
2.671	200694_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	*DDX24*	NM_020414
2.665	229106_at	dynein light chain 2	*Dlc2*	AA401429
2.632	218205_s_at	MAP kinase-interacting serine/threonine kinase 2	*MKNK2*	NM_017572

Table 7s. Top 10 categories of genes up-regulated in PTCL/U vs. normal T-lymphocytes (corresponding to CD4+, CD8+ and HLA-DR+ elements), ranked according with analysis performed with EASE

System	*Gene Category*	*List Hits*	*List Total*	*Population Hits*	*Population Total*	*Fisher Exact test probability*	*Bonferroni*	*Gene identifiers*	*Affymetrix probesets*
GO Biological Process	cell adhesion	13	48	596	12580	2,22E-07	8,34E-05	390; 1009; 1278; 1282; 1303; 2335; 3371; 3491; 3912; 6387; 7412; 10979; 22918	201289_AT; 201505_AT; 201645_AT; 202403_S_AT; 202404_S_AT; 202878_S_AT; 203868_S_AT; 207173_X_AT; 209210_S_AT; 209687_AT; 211719_X_AT; 211980_AT; 212724_AT; 225664_AT
GO Biological Process	circulation	6	48	113	12580	4,15E-06	1,56E-03	710; 1281; 2266; 2697; 6387; 7168	200986_AT; 201667_AT; 209687_AT; 210986_S_AT; 215076_S_AT; 226621_AT
GO Biological Process	complement activation\, classical pathway	4	48	31	12580	5,44E-06	2,05E-03	710; 712; 715; 716	200986_AT; 208747_S_AT; 212067_S_AT; 218232_AT
GO Biological Process	complement activation	4	48	41	12580	1,70E-05	6,40E-03	710; 712; 715; 716	200986_AT; 208747_S_AT; 212067_S_AT; 218232_AT
GO Biological Process	humoral defense mechanism (sensu Vertebrata)	5	48	128	12580	0,000121606	4,57E-02	710; 712; 715; 716; 10537	200986_AT; 205890_S_AT; 208747_S_AT; 212067_S_AT; 218232_AT
GO Biological Process	response to pest/pathogen/parasite	8	48	463	12580	0,000327109	1,23E-01	710; 712; 715; 716; 2335; 6387; 10537; 22918	200986_AT; 202878_S_AT; 205890_S_AT; 208747_S_AT; 209687_AT; 211719_X_AT; 212067_S_AT; 218232_AT
GO Biological Process	humoral immune response	5	48	170	12580	0,000454773	1,71E-01	710; 712; 715; 716; 10537	200986_AT; 205890_S_AT; 208747_S_AT; 212067_S_AT; 218232_AT
GO Biological Process	immune response	9	48	724	12580	0,001458541	5,48E-01	710; 712; 715; 716; 2335; 3429; 6387; 10537; 22918	200986_AT; 202411_AT; 202878_S_AT; 205890_S_AT; 208747_S_AT; 209687_AT; 211719_X_AT; 212067_S_AT; 218232_AT
GO Biological Process	skeletal development	4	48	135	12580	0,001712203	6,44E-01	1009; 1278; 1303; 2200	202403_S_AT; 202404_S_AT; 202766_S_AT; 207173_X_AT; 225664_AT

GO Biological Process	defense response	9	48	814	12580	0,003250129	1,00E+00	710; 712; 715; 716; 2335; 3429; 6387; 10537; 22918	200986_AT; 202411_AT; 202878_S_AT; 205890_S_AT; 208747_S_AT; 209687_AT; 211719_X_AT; 212067_S_AT; 218232_AT

Table 8s. Top 10 categories of genes down-regulated in PTCL/U vs. normal T-lymphocytes (corresponding to CD4+, CD8+ and HLA-DR+ elements , ranked according with analysis performed with EASE

System	*Gene Category*	*List Hits*	*List Total*	*Population Hits*	*Population Total*	*Fisher Exact test probability*	*Bonferroni*	*Gene identifiers*	*Affymetrix probesets*
GO Biological Process	regulation of transcription\, DNA-dependent	21	60	1981	12580	0,000196281	5,91E-02	1316; 1390; 3725; 3727; 4780; 4929; 5187; 6018; 6095; 7071; 7750; 8013; 8535; 23764; 27086; 29072; 29950; 51696; 54556; 55422; 221037	201464_X_AT; 202393_S_AT; 203752_S_AT; 204243_AT; 204621_S_AT; 208961_S_AT; 209959_AT; 210281_S_AT; 210426_X_AT; 212493_S_AT; 218603_AT; 219228_AT; 221763_AT; 223287_S_AT; 223394_AT; 227558_AT; 230511_AT; 231863_AT; 236213_AT; 242832_AT; 36711_AT
GO Biological Process	transcription	22	60	2139	12580	0,000200953	6,05E-02	1316; 1390; 3725; 3727; 4780; 4929; 5187; 6018; 6095; 7071; 7750; 8013; 8535; 23764; 27086; 29072; 29950; 51696; 54556; 55422; 80314; 221037	201464_X_AT; 202393_S_AT; 203752_S_AT; 204243_AT; 204621_S_AT; 208961_S_AT; 209959_AT; 210281_S_AT; 210426_X_AT; 212493_S_AT; 218603_AT; 219228_AT; 221763_AT; 223287_S_AT; 223394_AT; 227558_AT; 230511_AT; 231863_AT; 236213_AT; 238633_AT; 242832_AT; 36711_AT
GO Biological Process	regulation of transcription	21	60	2013	12580	0,000246752	7,43E-02	1316; 1390; 3725; 3727; 4780; 4929; 5187; 6018; 6095; 7071; 7750; 8013; 8535; 23764; 27086; 29072; 29950; 51696; 54556; 55422; 221037	201464_X_AT; 202393_S_AT; 203752_S_AT; 204243_AT; 204621_S_AT; 208961_S_AT; 209959_AT; 210281_S_AT; 210426_X_AT; 212493_S_AT; 218603_AT; 219228_AT; 221763_AT; 223287_S_AT; 223394_AT; 227558_AT; 230511_AT; 231863_AT; 236213_AT; 242832_AT; 36711_AT
GO Biological Process	transcription\, DNA-dependent	21	60	2066	12580	0,000356077	1,07E-01	1316; 1390; 3725; 3727; 4780; 4929; 5187; 6018; 6095; 7071; 7750; 8013; 8535; 23764; 27086; 29072; 29950; 51696; 54556; 55422; 221037	201464_X_AT; 202393_S_AT; 203752_S_AT; 204243_AT; 204621_S_AT; 208961_S_AT; 209959_AT; 210281_S_AT; 210426_X_AT; 212493_S_AT; 218603_AT; 219228_AT; 221763_AT; 223287_S_AT; 223394_AT; 227558_AT; 230511_AT; 231863_AT; 236213_AT; 242832_AT; 36711_AT
GO Biological Process	regulation of CDK activity	3	60	39	12580	0,000834283	2,51E-01	1647; 28984; 29950	203725_AT; 218723_S_AT; 223394_AT
GO Biological Process	nucleobase\, nucleoside\, nucleotide and nucleic acid metabolism	26	60	3085	12580	0,001058108	3,18E-01	1316; 1390; 1647; 3021; 3725; 3727; 4780; 4929; 5187; 6018; 6095; 7071; 7750; 8013; 8535; 23764; 27086; 29072; 29950; 51696; 54556; 55422; 57062; 65117; 80314; 221037	200694_S_AT; 201464_X_AT; 202302_S_AT; 202393_S_AT; 203725_AT; 203752_S_AT; 204243_AT; 204621_S_AT; 208961_S_AT; 209069_S_AT; 209959_AT; 210281_S_AT; 210426_X_AT; 211999_AT; 212493_S_AT; 218603_AT; 219228_AT; 221763_AT; 223287_S_AT; 223394_AT; 227558_AT; 230511_AT; 231863_AT; 236213_AT; 238633_AT; 242832_AT; 36711_AT
GO Biological Process	protein kinase cascade	5	60	168	12580	0,001208136	3,64E-01	1844; 1850; 2872; 4616; 9262	204794_AT; 205214_AT; 206374_AT; 207574_S_AT; 218205_S_AT
GO Biological Process	G2/M transition of mitotic cell cycle	3	60	46	12580	0,00135333	4,07E-01	1647; 28984; 29950	203725_AT; 218723_S_AT; 223394_AT
GO Biological Process	MAPKKK cascade	3	60	52	12580	0,001930725	5,81E-01	1844; 1850; 4616	204794_AT; 206374_AT; 207574_S_AT

GO Biological Process	inactivation of MAPK	2	60	15	12580	0,002256925	6,79E-01	1844; 1850	204794_AT; 206374_AT

Table 9s. Genes differentially expressed in PTCL/U vs. the other PTCLs (i.e. AITL *plus* ALCL). Notably, all these genes are down-regulated in PTCL/U.

Zscore	Gene	Common	GeneBank	Description
3.707	212859_x_at	*MT1E*	BF217861	metallothionein 2A
2.449	210524_x_at	*MT1F*	AF078844	C-terminus similar to human metallothionein-IF: Swiss-Prot Accession Number P04733; Homo sapiens hqp0376 protein mRNA, complete cds.
2.354	202424_at	*MAP2K2*	NM_030662	mitogen-activated protein kinase kinase 2
2.286	215001_s_at	*GLUL*	AL161952	glutamate-ammonia ligase (glutamine synthase)
2.222	1558836_at		BQ024490	UI-1-BB1p-aut-f-08-0-UI.s1 NCI_CGAP_Pl6 Homo sapiens cDNA clone UI-1-BB1p-aut-f-08-0-UI 3', mRNA sequence.
2.068	217762_s_at	*RAB31*	BE789881	RAB31, member RAS oncogene family
2.046	222670_s_at	*MAFB*	AW135013	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
2.035	202759_s_at	*AKAP2*	BE879367	paralemmin 2
1.998	206359_at	*SOCS3*	BG035761	suppressor of cytokine signaling 3
1.933	203973_s_at	*CEBPD*	NM_005195	KIAA0146 protein
1.898	1558837_a_at		BQ024490	UI-1-BB1p-aut-f-08-0-UI.s1 NCI_CGAP_Pl6 Homo sapiens cDNA clone UI-1-BB1p-aut-f-08-0-UI 3', mRNA sequence.
1.85	204166_at	*KIAA0963*	NM_014963	
1.82	212527_at	*D15Wsu75e*	BF057059	DNA segment, Chr 15, Wayne State University 75, expressed
1.766	213733_at	*MYO1F*	BF740152	myosin IF
1.754	221484_at	*B4GALT5*	BF691447	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5
1.751	231241_at		AW469714	Transcribed sequence with moderate similarity to protein ref:NP_055224.1 (H.sapiens) PCAF associated factor 65 beta [Homo sapiens]
1.75	234973_at	*SLC38A5*	BG325630	solute carrier family 38, member 5
1.732	204908_s_at	*BCL3*	NM_005178	B-cell CLL/lymphoma 3
1.732	206540_at	*GLB1L*	NM_024506	galactosidase, beta 1-like
1.687	221006_s_at	*SNX27*	NM_030918	sorting nexin family member 27
1.645	225922_at	*KIAA1450*	BE501838	KIAA1450 protein
1.554	228325_at	*KIAA0146*	AI363213	KIAA0146 protein
1.534	212506_at	*PICALM*	AL135735	phosphatidylinositol binding clathrin assembly protein
1.419	222303_at		AV700891	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)

1.343	242188_at		AI743332	Transcribed sequences
1.306	212606_at	*WDFY3*	AL536319	AL536319 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF015YG13 3-PRIME, mRNA sequence.
1.303	209234_at	*KIF1B*	BF939474	kinesin family member 1B
1.293	225415_at	*BBAP*	AA577672	rhysin 2

Supplementary Methods

Generation of Gene Expression Profiles

Total RNA was extracted using the TRIzol reagent (Invitrogen and Life Technologies) and purified using the Rneasy Kit (QIAGEN). Double-strand cDNA was generated from 5 μg of total RNA using the Super-Script Choice System (Invitrogen and Life Technologies) and a poly-dT oligonucleotide that contained a T7 RNA polymerase initiation site. The double-strand cDNA was used as template to generate biotinylated cRNA by in vitro transcription using MEGAscript T7 High Yield Transcription kit (Ambion), biotin-11-CTP, and biotin-11-UTP (PerkinElmer). The biotinylated cRNA was purified by the RNeasy Kit (QIAGEN) and fragmented according to the Affymetrix, Inc. protocol. 15 μg of fragmented cRNA was hybridized to HG-U133 2.0 plus microarrays (Affymetrix, Inc.). The gene expression values were determined by MAS 5 algorithm in GCOS 1.2; Affymetrix, Inc.

Gene Expression Profiles Analysis

The dendrogram (Figure 1 and 1s) was generated using a hierarchical clustering algorithm based on the average-linkage method (Hartigan et al, 1975; Eisen et al, 1998). Only genes displaying a twofold average change in the expression level across the whole panel were chosen to generate the hierarchical clustering. The expression value of each selected gene is normalized to have a zero mean value and unit standard deviation. The distance between two individual samples was calculated by Pearson distance with the normalized expression values. To perform the supervised gene expression analysis (Figures 2-5), we used the Genes@Work software platform, which is a gene expression analysis tool based on the pattern discovery algorithm and structural pattern localization analysis by sequential histograms (Califano, 2000; Califano et al, 2000). In the matrix, each column represents a sample and each row represents a gene. The color scale bar shows the relative gene expression changes normalized by the standard deviation (0 is the mean expression level of a given gene). The classification method used for the cell type classification (Figures 2-4) was described previously (Klein et al, 2001). In brief, the classifier is a scoring function based on the values of a set of genes (gene cluster), which are differentially expressed in two sets of cell types, and thus, can be used for cell type classification. The higher the score, the more likely it is that a cell type is related to the phenotype set.

The EASE software was applied in order to establish whether specific cell functions and biological processes, defined according to gene ontology (Jenssen et al, 2001;Hosack et al, 2003), were significantly represented among the deregulated genes.