SUPPLEMENTARY MATERIALS

Materials and Methods.

Patient Selection.

Inclusion criteria:

1. CTCL patients age ≥18 and ≤90.
2. At least T2 skin involvement and flow cytometric blood involvement after analysis by CD3+, CD4+, CD8+, CD4+CD7+, CD4+CD7-, CD4+CD26+, CD4+CD26-, CD25+, CD4+CD25+, CD45RO, CD4/CD8 ratios, positive PCR for TCR β/γ, and a panel of Vα or Vβ (Vonderheid et al, 2005; Vonderheid et al,2006; Rappl et al, 2001).

Exclusion criteria:

1. Previous use of immunosuppressive regimens including multi-drug chemotherapy within 3 months.
2. Known HIV or HTLV-1 positive patients.
3. Pregnant or nursing mothers.

1. Vonderheid EC, Boselli CM, Conroy M, et al (2005). Evidence for restricted Vβ usage in the leukemic phase of cutaneous T cell lymphoma. *J Invest Dermatol* 124(3):651-61.
2. Vonderheid EC (2006). On the diagnosis of erythrodermic cutaneous T-cell lymphoma. *J Cutan Pathol* 33 Suppl 1:27-42.
3. Rappl G, Muche JM, Abken H, *et al* (2001). CD4(+)CD7(-) T cells compose the dominant T-cell clone in the peripheral blood of patients with Sézary syndrome. *J Am Acad Dermatol* 44(3):456-61.

Patients were selected from a pool of CTCL patients with the above inclusion and exclusion criteria based on clinical assessment and with evidence of blood involvement from FACS data, and who received treatment with photopheresis. At the same time, a reasonable diversity of clinical phenotypes and molecular markers on FACS analysis (such as CD4/CD8 ratios) ranging from predominantly early to late stage disease was also desired. Approval was received from Yale School of Medicine Human Investigation Committee (HIC protocols: 25269 and 23636).

Clinical Data Collection. Patient's current status, skin disease, PET/CT results and lymph node status on physical exam were categorized into "Improved," "Stable," or "Worsened." Current status was determined by physician global assessment. Skin disease was assessed taking into account changes over one year in body surface area and whether lesions were patches, plaques, tumors, or erythrodermic.

Isolation of Malignant Cells From each CTCL patient. 10 mL of lymphocyte-enriched blood was drawn in the final cycle of leukapheresis prior to 8-methoxypsoralen exposure. For the four normal controls, 50 mL of whole blood were drawn from volunteers chosen as most similar to the patient population based on age and sex. The blood sample was immediately layered on 4 mL of Isolymph (per 10 mL of blood, CTL Scientific Supply Corp.; Deer Park, NY) and processed as described by the manufacturer. Wash steps used 10 mL of RPMI (Gibco; Carlsbad, CA) with 1% penicillin-streptomycin followed by 10 min centrifugation at 1200 RPM, 20°C. An extra incubation at 4°C in lysis buffer (Sigma; St. Louis, MO) prior to the final centrifugation was performed on samples with a visible amount of red blood cells. Negative selection using CD7 and/or CD26 mAb conjugated to biotin (eBiosciences; San Diego, CA; Miltenyi Biotech; Auburn, CA) and anti-biotin microbeads (Miltenyi Biotech) was performed first followed by positive selection using anti-CD4 Microbeads (Miltenyi Biotech). Following manufacturer's instructions, populations were isolated using a Magnetic-bead Antibody Cell Sorting LS column and magnet (Miltenyi Biotech). Washes were done using filtered RPMI (Gibco) with 10% AB serum, 1% pencillin-streptomycin and 2mM EDTA.

Affymetrix Human SNP 6.0 and Gene 1.0 ST array assay details. 500ng of genomic DNA was input in the PCR based Affymetrix Human SNP 6.0 assay so approximately

225ug of fragmented and labeled PCR product was hybridized to the human SNP 6.0 arrays (Affymetrix). Total RNA (300ng) was input in the Affymetrix Whole Transcript assay utilizing in vitro transcription and a second round of first strand cDNA synthesis to create the sense targeted single stranded DNA needed for hybridization. The sscDNA was fragmented, labeled and approximately 2.5ug was hybridized to the human Gene 1.0 ST arrays (Affymetrix) at the Keck Microarray Core facility according to manufacturer specifications.

Genomic Data Quality Controls. Affymetrix Expression Console software using the gene level RMA algorithm on all samples as a batch was used to assess quality metrics for hybridization and assay performance for the Affymetrix human Gene 1.0 ST array. Perfect mean match were found to be in an acceptable range (298.2-402.7) compared to background values. Positive versus negative area under the ROC curve values to assess overall data quality were also acceptable (0.836-0.886). All samples run on the Affymetrix Human Genome wide SNP6.0 arrays were found to have acceptable contrast QC values (1.56-3.30) indicating sufficient contrast resolution quality for genotyping.

Genomic Data Access. All genomic data will be available in the GEO database (Accession number pending). Temporarily, the raw genomic data may be downloaded at: Login information: Username: WGEO Passcode: ctcl. Please click on "SIMPLE MENU," then "Download Affy, Illumina, Nimblegen Files from Keck." From there, click on individual CEL files to save them to a local directory. CTCL cell line data is available in 2 parts temporarily at:
http://medapps12.med.yale.edu/MARR_Database/KeckaffyLab/batch/WGEO_group_1_18671.zip and
http://medapps12.med.yale.edu/MARR_Database/KeckaffyLab/batch/WGEO_group_2_18671.zip

GISTIC Parameters. genome build: hg18, amplifications threshold: 0.1, deletions threshold: 0.1, join.segment.size: 8, qv.thresh: 0.25, remove.X: 1. Copy number variants were removed as part of the GISTIC algorithm based on a University of Toronto database of genomic variants (file: variation.hg18.v8.txt)

Comparative Marker Selection Parameters. test.direction = 2, test.statistic = 0, number.of.permutations = 1000, complete = false, balanced = false, random.seed = 779948241, smooth.p.values = true.

Hierarchical Clustering of GISTIC lesions. In a particular cell, no amplification or deletion was assigned a value of 0, a low-level amplification or deletion (0.1< log2(copy number in region-1) <0.9) was assigned a value of 1, and high level amplification or deletion (0.9< log2(copy number in region-1)) was assigned a value of 2.

Supplementary Table 1. Significant regions of DNA copy number amplifications and deletions in leukemic CTCL based upon GISTIC analysis of 23 patient samples.

Supplementary Table 2. Summary of study characteristics used in the consensus analysis

Supplementary Table 3. Details about individual cell lines including origin, culture media, and references.

Supplementary Table 4. Significant regions of DNA copy number amplifications and deletions in leukemic CTCL based upon GISTIC analysis of 5 patient samples.

Supplementary Table 5. FACS data from 24 patients with leukemic CTCL.

Supplementary Table 1a: Significant regions of DNA copy number amplification in CTCL

Rank	Cytoband	Q-Value	Number of Samples	Region	Genes in region	Genes of interest related to region
1	8q23.3	3.44E-08	14	chr8:112360671-115742135	1 gene: CSMD3	***MYC****
2	17q25.1	1.84E-05	8	chr17:40531449-75546555	371 genes	**NGFR, PHB, RPS6KB1, BPTF, GRB2, ITGB4,** MIR21, *PRKAR1A, USP32*
3	1p36.13	0.000945	5	chr1:19256834-19274554	1 gene: UBR4	-
4	3p11.1	0.00429	8	chr3:90106010-96880237	5 genes: PROS1, NSUN3, ARL13B, DHFRL1, STX19	**POU1F1***
5	6p21.1	0.00596	2	chr6:43979350-43993064	1 gene: C6orf223	***VEGFA****
6	8p23.3	0.00950	8	chr8:577114-1646102	2 genes: DLGAP2, ERICH1	-
7	10p13	0.0128	3	chr10:4275516-17978213	75 genes: PFKFB3, PTPLA, ST8SIA6, STAM, OLAH, AKR1C3, CDC123, GATA3, SEC61A2, NUDT5, ACBD7, PRKCQ, VIM, SFMBT2, IL2RA, OPTN, FBXO18, USP6NL, RBM17, HSPA14, TAF3, AKR1CL1, tAKR, PHYH, TRDMT1, KIN, C10orf31, MCM10, ANKRD16, CALML5, ECHDC3, AKR1CL2, AKR1C2, CAMK1D, DHTKD1, C10orf111, IL15RA, DCLRE1C, MEIG1, ITGA8, LOC439951, FLJ45983, RPP38, PRPF18, ASB13, RSU1, TCEB1P3, FAM107B, CUGBP2, FRMD4A, AKR1C1, SEPHS1, ATP5C1, AKR1C4, GDI2, C10orf18, C10orf97, CUBN, SUV39H2, C10orf49, C10orf47, ARMETL1, UCN3, C1QL3, ITIH2, UPF2, TUBAL3, LOC100128356, NMT2, LOC389936, CALML3	*GATA3*
8	5p15.33	0.0204	5	chr5:2179815-3322657	2 genes: C5orf38, IRX2	**TERT***
9	10p12.33	0.0204	3	chr10:1-135374737	717 genes	-
10	22q11.23	0.0320	9	chr22:20471826-21907111	13 genes: hsa-mir-650, BCR, GNAZ, MAPK1, VPREB1, TOP3B, RAB36, PPM1F, PRAME, RTDR1, GGTLC2, ZNF280A, ZNF280B	**CRKL***
11	7q35	0.0362	5	chr7:142856201-158821424	103 genes: hsa-mir-595, hsa-mir-153-2, hsa-mir-671, ABP1, CDK5, DPP6, EN2, EZH2, GBX1, MNX1, HTR5A, INSIG1, KCNH2, NOS3, PTPRN2, RARRES2, RHEB, SHH, SLC4A2, SMARCD3, VIPR2, XRCC2, ARHGEF5, ZNF212, ZNF282, CUL1, ACCN3, PDIA4, UBE3C, FAM115A, DNAJB6, ABCF2, FASTK, ABCB8, PAXIP1, SSPO, CNTNAP2, GIMAP2, OR2F1, TPK1, ZNF777, TMEM176B, REPIN1, PRKAG2, NUB1, CSGlcA-T, NCAPG2, WDR60, GIMAP4, GIMAP5, TMEM176A, ACTR3B, FAM62B, ZNF398, MLL3, GALNT11, LMBR1, NOM1, LRRC61, ZNF767, TMUB1, KRBA1, C7orf29, CENTG3, NOBOX, OR2A14, OR6B1, OR2F2, ZNF786, ASB10, RNF32, GIMAP8, CRYGN, ZNF425, ZNF783, ZNF746, ATP6V0E2, CCT8L1, RBM33, GALNTL5, GIMAP7, ZNF467, GIMAP1, C7orf33, TAS2R41, CNPY1, FAM139A, ZNF775, ATG9B, CTAGE6, OR2A12, OR2A1, WDR86, OR2A25, OR2A5, OR2A7, OR2A42, LOC402715, LOC441294, OR2A2, FLJ43692, GIMAP6, LOC643641	
12	1q42.3	0.0410	2	chr1:232738038-232763374	1 gene: IRF2BP2	-
13	4q12	0.0467	4	chr4:55224058-55239617	1 gene: KIT	***KIT***
14	7p11.2	0.0531	3	chr7:54899474-65012069	20 genes: CCT6A, EGFR, GBAS, PHKG1, PSPH, ZNF138, ZNF273, SUMF2, CHCHD2, ZNF117, MRPS17, ZNF107, LANCL2, ECOP, ZNF479, VKORC1L1, ZNF92, ZNF680, 14-Sep, ZNF713	***EGFR***
15	4q13.1	0.0780	9	chr4:63139114-63362224	1 gene: LPHN3	-
16	20q13.2	0.0894	1	chr20:1-62435964	520 genes	**ZNF217**
17	21q22.3	0.156	1	chr21:39772858-46944323	88 genes: ADARB1, AIRE, PTTG1IP, C21orf2, CBS, COL6A1, COL6A2, CRYAA, CSTB, DSCAM, PRMT2, ITGB2, LSS, MX1, MX2, NDUFV3, PCNT, PCP4, PDE9A, PFKL, PKNOX1, PWP2, S100B, SH3BGR, SLC19A1, SUMO3, TFF1, TFF2, TFF3, TMEM1, TMPRSS2, TRPM2, U2AF1, UBE2G2, C21orf33, PDXK, RRP1, MCM3AP, ABCG1, B3GALT5, WDR4, FTCD, HSF2BP, RRP1B, DIP2A, POFUT2, ICOSLG, BACE2, C2CD2, DNMT3L, ZNF295, UBASH3A, SLC37A1, PCBP3, C21orf58, C21orf57, C21orf29, FAM3B, RIPK4, AGPAT3, PRDM15, TMPRSS3, COL18A1, LRRC3, C21orf56, C21orf70, RSPH1, UMODL1, IGSF5, SNF1LK, PLAC4, KRTAP12-2, KRTAP12-1, KRTAP10-10, C21orf123, KRTAP10-4, KRTAP10-6, KRTAP10-7, KRTAP10-9, KRTAP10-1, KRTAP10-11, KRTAP10-2, KRTAP10-5, KRTAP10-8, KRTAP10-3, KRTAP12-3, KRTAP12-4, KRTAP10-12	-

1. Rank according to Q-value. Q-value are false-discovery rate corrected.
2. Cytoband from the middle of the minimal common region.
3. Region represents the wider area that results when the samples defining each border of the minimal common region are left out.
4. Genes of interest related to region:
   Genes in bold represent significantly amplified genes in cancer from Beroukhim *et al.* (PMID: 20164920, Supplementary Table 2: GISTIC analysis of 3,131 cancer specimens of 26 tumor types).
   Genes in italics represent genes that are in the region that are mentioned in the text
   Genes with * represent genes adjacent to the region

Supplementary Table 1b: Significant regions of DNA copy number deletion in CTCL

Rank	Cytoband	Q-value	Number of samples	Region	Genes in region	Genes of interest related to region
1	17p12	1.73E-07	10	chr17:15524281-15794764	4 genes: ADORA2B, TRIM16, ZNF286A, TBC1D26	**MAP2K4*, ZNF18***
2	17q25.3	1.73E-07	12	chr17:78226063-78242141	1 gene: RAB40B	**ZNF750***
3	10p11.22	6.79E-06	4	chr10:30673943-31410094	4 genes: MAP3K8, PAPD1, LYZL2, ZNF438	-
4	7q21.2	1.74E-05	7	chr7:91195291-91198925	1 gene: MTERF	-
5	17p13.3	1.74E-05	14	chr17:2109320-2748547	10 genes: MNT, PAFAH1B1, SGSM2, GARNL4, KIAA0664, SMG6, TSR1, SRR, METT10D, LOC284009	***TP53*, ATP1B2***
6	16p12.3	1.86E-05	6	chr16:19711348-19743071	1 gene: IQCK	-
7	1q31.2	0.000481	5	chr1:191421896-191426345	2 genes: B3GALT2, CDC73	-
8	8p11.21	0.000481	7	chr8:42269520-42277830	1 gene: IKBKB	**C8orf4*, ZMAT4***
9	10q23.33	0.00288	4	chr10:60671322-97354704	211 genes	***PTEN***
10	10p11.23	0.00346	7	chr10:29478793-30143973	4 genes: hsa-mir-938, hsa-mir-604, SVIL, LYZL1	-
11	9p21.3	0.00376	3	chr9:21790514-22605798	4 genes: CDKN2A, CDKN2B, MTAP, DMRTA1	***CDKN2A***
12	2q37.1	0.0121	3	chr2:232785309-232823401	1 gene: DIS3L2	TMEM16G, ING5
13	12q15	0.0121	3	chr12:66948191-66954650	1 gene: IL22	-
14	12q21.1	0.0121	3	chr12:69853599-69876390	1 gene: TSPAN8	-
15	4p13	0.0128	4	chr4:43100100-43137404	1 gene: LOC389207	-
16	8p23.2	0.0133	4	chr8:3570501-12646620	57 genes: hsa-mir-598, hsa-mir-124a-1, hsa-mir-597, ANGPT2, BLK, CTSB, DEFA1, DEFA3, DEFA4, DEFA5, DEFA6, DEFB1, DEFB4, FDFT1, GATA4, MSRA, TNKS, MFHAS1, SPAG11B, PINX1, AGPAT5, DEFB103A, CSMD1, MTMR9, MCPH1, PPP1R3B, SOX7, C8orf13, AMAC1L2, FAM86B1, THEX1, LONRF1, RP1L1, CLDN23, DEFB104A, PRAGMIN, UNQ9391, C8orf74, DEFB105A, DEFB106A, DEFB107A, DEFB130, NEIL2, XKR6, DUB3, XKR5, DEFB103B, DEFB107B, DEFB104B, DEFB106B, DEFB105B, DEFB136, DEFB137, DEFB134, SPAG11A, LOC728358, LOC728957,	**CSMD1**
17	22q11.23	0.0144	6	chr22:22564665-23056324	10 genes: DDT, GGT5, GSTT1, GSTT2, MIF, SPECC1L, CABIN1, SUSD2, GSTT2B, DDTL	**VPREB1***
18	7p21.1	0.0150	3	chr7:16820392-17640380	2 genes: AHR, AGR3	-
19	9q21.2	0.0184	5	chr9:80289820-92881841	43 genes: hsa-mir-7-1, CKS2, CTSL1, DAPK1, EDG3, GAS1, HNRPK, NTRK2, SYK, TLE1, TLE4, SEMA4D, GADD45G, SPIN1, AGTPBP1, CCRK, UBQLN1, GOLM1, SHC3, DIRAS2, KIF27, MAK10, SLC28A3, SECISBP2, ZCCHC6, RMI1, GKAP1, ISCA1, C9orf64, NXNL2, RASEF, FRMD3, C9orf47, C9orf79, LOC286238, C9orf164, FLJ46321, C9orf153, CTSL3, FLJ45537, FAM75B, C9orf103, CHCHD9	-
20	13q21.1	0.0184	4	chr13:54591155-54593583	1 gene: FLJ40296	***RB1****
21	12p13.2	0.0399	7	chr12:10860835-11642691	18 genes: PRB1, PRB3, PRB4, PRH1, PRH2, PRR4, TAS2R13, TAS2R10, TAS2R14, TAS2R43, TAS2R44, TAS2R46, TAS2R47, TAS2R48, TAS2R49, TAS2R50, TAS2R42, PRB2	**ETV6***
22	6q24.1	0.0596	3	chr6:141733503-163657589	99 genes: ACAT2, ESR1, FUCA2, GRM1, HIVEP2, IGF2R, LPA, MAS1, MAP3K4, NMBR, OPRM1, PARK2, PCMT1, PLAGL1, PLG, SLC22A1, SLC22A3, SLC22A2, SOD2, TCP1, DYNLT1, UTRN, EZR, VIP, EPM2A, PEX3, STX11, SYNJ2, LATS1, WTAP, AKAP12, PHACTR2, UST, RAB32, KATNA1, RBM16, MAP3K7IP2, SASH1, SYNE1, MTHFD1L, PIP3-E, TIAM2, FBXO5, RGS17, MRPL18, CLDN20, NOX3, TFB1M, AIG1, SNX9, VTA1, MTRF1L, RMND1, AGPAT4, TULP4, GPR126, PLEKHG1, ARID1B, TMEM181, ZBTB2, ULBP3, C6orf211, ZDHHC14, C6orf103, C6orf97, MYCT1, ULBP2, ULBP1, LPAL2, PPP1R14C, SF3B5, RSPH3, FBXO30, FNDC1, LRP11, LTV1, SERAC1, PPIL4, SYTL3, C6orf72, TAGAP, ADAT2, STXBP5, PACRG, RAET1E, CNKSR3, RAET1L, PNLDC1, LOC202459, SHPRH, ZC3H12D, NUP43, RAET1G, C6orf98, SUMO4, SAMD5, IYD, LOC389435, GTF2H5,	-
23	10q21.1	0.0596	4	chr10:50229783-58152761	27 genes: hsa-mir-605, CHAT, ERCC6, MBL2, MSMB, PRKG1, SLC18A3, NCOA4, PARG, TIMM23, ZWINT, DKK1, CSTF2T, A1CF, FAM21B, OGDHL, ASAH2, PCDH15, SGMS1, PGBD3, C10orf53, FAM21A, CTGLF3, DRGX, CTGLF4, ASAH2B, CTGLF5	-
24	19p13.3	0.0596	11	chr19:3178103-5466792	54 genes: hsa-mir-7-3, hsa-mir-637, DAPK3, EEF2, MATK, NFIC, MAP2K2, PTPRS, SH3GL1, TBXA2R, APBA3, CHAF1A, EBI3, M6PRBP1, HMG20B, SEMA6B, JMJD2B, ZFR2, PIP5K1C, TJP3, ITGB1BP3, UHRF1, ZBTB7A, FZR1, SIRT6, PIAS4, FEM1A, STAP2, CCDC94, C19orf10, SHD, C19orf29, BRUNOL5, FSD1, UBXD1, DOHH, CREB3L3, HDGF2, RAX2, MPND, ATCAY, DPP9, MRPL54, LRG1, TMIGD2, TNFAIP8L1, C19orf28, GIPC3, TICAM1, ZNRF4, ANKRD24, LSDP5, ARRDC5, KIAA1881	**GZMM*, THEG*, PPAP2C*, C19orf20***
25	10p15.1	0.0610	3	chr10:3931317-3941491	1 gene: KLF6	-
26	3q11.2	0.0676	2	chr3:99583690-99616246	1 gene: OR5K3	-
27	3q13.2	0.0849	2	chr3:113854947-124236792	70 genes: hsa-mir-198, hsa-mir-568, ADPRH, ATP6V1A, CASR, CD80, CD86, CSTA, DRD3, GAP43, GOLGB1, GSK3B, GTF2E1, HCLS1, HGD, KPNA1, LSAMP, NDUFB4, SLC15A2, UPK1B, ZNF80, B4GALT4, NR1I2, STXBP5L, IQCB1, COX17, POLQ, FSTL1, C3orf17, ZBTB20, C3orf28, GTPBP8, C3orf1, PLA1A, FBXO40, SEMA5B, WDR5B, PARP14, GRAMD1C, SIDT1, TMEM39A, WDR52, EAF2, KTELC1, CDGAP, KIAA1407, POPDC2, HSPBAP1, QTRTD1, NAT13, PARP9, DIRC2, C3orf15, BOC, LRRC58, CCDC58, CD200R1, DTX3L, CCDC52, IGSF11, C3orf30, PARP15, GPR156, VSTM3, KIAA2018, ZDHHC23, RABL3, ILDR1, CD200R2, ARGFX	**LSAMP**

28	6p21.1	0.0877	4	chr6:41292490-41342376	1 gene: TREML4	-
29	16p13.12	0.0877	2	chr16:14139929-14166178	1 gene: MKL2	-
30	2p11.2	0.125	2	chr2:85892717-85927786	1 gene: ST3GAL5	-
31	13q32.3	0.133	1	chr13:1-114142980	302 genes	***RB1*, LATS2**
32	1p36.13	0.149	2	chr1:19552461-19610776	1 gene: CAPZB	-
33	4p12	0.153	2	chr4:47936218-47954681	1 gene: TEC	-
34	1p36.11	0.155	3	chr1:25408676-28385091	64 genes: CD52, EXTL1, EYA3, FGR, IFI6, SFN, GPR3, HMGN2, STMN1, PAFAH2, PPP1R8, PTAFR, RHCE, RHD, RPA2, RPS6KA1, SLC9A1, SLC30A2, ARID1A, NR0B2, FCN3, MAP3K6, C1orf38, WASF2, CNKSR1, NUDC, WDTC1, TMEM50A, STX12, SYF2, LDLRAP1, AHDC1, SMPDL3B, ZNF593, ATPBD1B, AIM1L, XKR8, TMEM57, PIGV, FAM54B, C1orf63, MAN1C1, SEPN1, GPATCH3, CCDC21, C1orf135, LIN28, GRRP1, DHDDS, SH3BGRL3, C1orf160, ZDHHC18, TRIM63, SYTL1, UBXD5, FAM46B, C1orf172, PDIK1L, PAQR7, FAM76A, ZNF683, CATSPER4, LOC388610, CD164L2	**SFN**
35	8q12.3	0.155	2	chr8:60048458-67666248	23 genes: hsa-mir-124a-2, ASPH, CA8, CRH, MYBL1, PDE7A, RAB2A, TTPA, GGH, CYP7B1, MTFR1, TOX, RRS1, BHLHB5, ARMC1, CHD7, TRIM55, DNAJC5B, ADHFE1, RLBP1L1, YTHDF3, C8orf46, NKAIN3	-
36	14q11.2	0.155	6	chr14:19800971-22103068	43 genes: ANG, APEX1, HNRNPC, NP, RNASE1, RNASE2, RNASE3, RNASE4, RNASE6, SALL2, TEP1, TOX4, PARP2, FAM12A, SUPT16H, OR10G3, OR10G2, OR4E2, SLC39A2, ZNF219, OSGEP, FLJ10357, METTL3, RPGRIP1, NDRG2, CHD8, CCNB1IP1, FAM12B, METT11D1, RNASE7, RAB2B, TMEM55B, TTC5, RNASE11, TPPP2, RNASE8, KLHL33, RNASE10, OR6S1, RNASE9, OR5AU1, RNASE13, RNASE12	**ZNF219, NDRG2**
37	11q22.3	0.163	3	chr11:103469638-116739377	89 genes: hsa-mir-34c, ACAT1, APOA1, APOA4, APOC3, ATM, CASP1, CASP4, CASP5, CRYAB, DDX10, DLAT, DRD2, FDX1, GRIA4, GUCY1A2, HSPB2, HTR3A, IL18, NCAM1, NNMT, NPAT, PAFAH1B2, POU2AF1, PPP2R1B, PTS, RDX, SDHD, SLN, TAGLN, ZBTB16, CUL5, ZNF259, PCSK7, HTR3B, ZW10, RBM7, CEP164, EXPH5, SNF1LK2, KIAA0999, BACE1, CADM1, REXO2, TIMM8B, SIDT2, C11orf71, SLC35F2, RAB39, BTG4, FAM55D, TTC12, C11orf57, ELMOD1, TEX12, ARHGAP20, USP28, ICEBERG, AASDHPPT, C11orf1, ALG9, PDGFD, TMPRSS5, BCDO2, KIAA1826, BUD13, DIXDC1, ZC3H12C, ALKBH8, LOC91893, C11orf52, COP1, APOA5, PIH1D2, FAM55A, KBTBD3, CWF19L2, KDELC2, LAYN, C11orf65, ANKK1, RNF214, C11orf53, LOC399947, FLJ45803, FLJ46266, INCA, LOC643923, LOC644672	**ATM, CADM1**
38	8q22.1	0.169	4	chr8:95625564-95627290	1 gene: KIAA1429	-
39	5q33.1	0.205	2	chr5:151480736-151502520	1 gene: GLRA1	-
40	4q31.3	0.223	2	chr4:153897161-153915365	1 gene: TIGD4	-

1. Rank according to Q-value. Q-value are false-discovery rate corrected.
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   Genes in italics represent genes that are in the region that are mentioned in the text
   Genes with * represent genes adjacent to the region

Supplementary Table 2 - Summary of studies used in consensus analysis

STUDIES	Year of Publication	Number of Samples	Genomic Array	Resolution	Regions Defined
Mao et al.	2002	10	CGH	Low	From Table 1
Mao et al.	2003	9	CGH	Low	From Table 1
Fischer et al.	2004	4	CGH	Low	From Table 1
Vermeer et al.	2008	20	CGH	3.5K	By Authors
Caprini et al.	2009	26	SNP	10K	By Authors
Laharanne et al.	2010	16	CGH	105K	By Authors
Lin et al.	current study	23	SNP	1800K	By Authors

Supplementary Table 3: Leukemic CTCL cell lines

Cell Line Name	HUT78	HUT78	Myla	SeAx	HH	Pno	Sez4
Other Designation	HUT-Foss	HUT-Lars	-	-	-	-	SZ-4
Obtained From	Francine Foss (Yale University; New Haven, CT, USA)	Emmanuel Contassot and Lars French (University Hospital Zurich; Zurich, Switzerland)	Emmanuel Contassot and Lars French (University Hospital Zurich; Zurich, Switzerland)	Emmanuel Contassot and Lars French (University Hospital Zurich; Zurich, Switzerland)	Francine Foss (Yale University; New Haven, CT, USA)	Martine Bagot, Armand Bensussan, Anne Marie-Cardine (INSERM; Paris, France)	Eric Vonderheid and Alain Rook (University of Pennsylvania; Philadelphia, PA, USA)
Culture Media	IMDM, 20% FCS, L-Glutamine, Pen/Strep	IMDM, 20% FCS, L-Glutamine, Pen/Strep	RPMI 1640, 10% FCS, L-Glutamine, Pen/Strep	RPMI 1640, 10% FCS, L-Glutamine, Pen/Strep; 20ng/ml IL2 (R&D Systems)	RPMI 1640, 10% FCS, L-Glutamine, Pen/Strep	RPMI 1640, 10% human serum, Na Pyruvate, L-Glutamine, Pen/Strep, 20 ng/ml IL2 (R&D Systems), 5 ng/mL IL7 (R&D Systems)	RPMI 1640, 10% FCS, L-Glutamine, Pen/Strep; 20ng/ml IL2 (R&D Systems)
Origin	PBMC	PBMC	plaque biopsy	PBMC	PBMC	PBMC	Sez4
Reference	Gazdar et al., Blood 55 (3): 409, 1980	Gazdar et al., Blood 55 (3): 409, 1980	Kaltoft et al., In Vitro Cell. Dev. Biol. 28A:161, 1992	Kaltoft et al., Arch Dermatol Res (1987) 279:293.	Starkebaum et al., Int. J. Cancer: 49:246 (1991)	Poszepczynska et al., Blood 96 (3): 1056 (2000)	Abrams et al., J Invest Dermatol 96:31 (1991)

Supplementary Table 4a: Significant regions of DNA copy number amplification in leukemic CTCL cell lines

Rank	Cytoband	Q-Value	Number of Samples	Region	Genes in region	Genes of interest related to region
1	8q24.21	0.11	4	chr8:126774747-134898335	*17 genes: ADCY8, KCNQ3, MYC, ST3GAL1, SLA, TG, WISP1, NDRG1, EFR3A, LRRC6, DDEF1, PHF20L1, FAM49B, MLZE, TMEM71, FAM84B, OC9*	***MYC***
2	4q24	0.12	2	chr4:97279410-104277847	*32 genes: ADH1A, ADH1B, ADH1C, ADH4, ADH5, ADH6, ADH7, CENPE, EIF4E, H2AFZ, MANBA, MTTP, NFKB1, PPP3CA, RAP1GDS1, UBE2D3, MAP2K1IP1, TSPAN5, METAP1, DAPP1, EMCN, BANK1, BDH2, SLC39A8, DNAJB14, C4orf17, RG9MTD2, DDIT4L, NHEDC2, NHEDC1, C4orf37, CISD2*	-
3	4q25	0.12	2	chr4:1-191273063	722 genes	-
4	4q26	0.12	2	chr4:116980729-130457903	*44 genes: ANXA5, CCNA2, FABP2, FGF2, IL2, MAD2L1, EXOSC9, TRPC3, PRSS12, PDE5A, NDST3, SEC24D, SPRY1, PGRMC2, PLK4, PRDM5, NUDT6, HSPA4L, INTU, MYOZ2, USP53, LARP2, BBS7, ANKRD50, KIAA1627, IL21, C4orf31, FAT4, TNIP3, PHF17, C4orf29, SLC25A31, GPR103, KIAA1109, SCLT1, C4orf33, TMEM155, ADAD1, TRAM1L1, SPATA5, BBS12, SYNPO2, MFSD8, LOC401152*	-
5	8q21.3	0.14	4	chr8:82816542-105436183	*94 genes: hsa-mir-875, ATP6V1C1, OSGIN2, CA1, CA2, CA3, CALB1, RUNX1T1, CDH17, COX6C, DECR1, E2F5, GEM, KCNS2, MATN2, MMP16, NBN, ODF1, POLR2K, RPL30, SDC2, SPAG1, STK3, KLF10, UQCRB, YWHAZ, FZD6, RIPK2, CPNE3, CCNE2, RIMS2, PTDSS1, HRSP12, PGCP, POP1, WWP1, RAD54B, WDSOF1, RNF19A, KIAA1429, RGS22, PABPC1, RRM2B, MTERFD1, FAM82B, ZNF706, UBR5, AZIN1, OTUD6B, PPM2C, CNGB3, RBM35A, LAPTM4B, TMEM55A, INTS8, SNX16, NECAB1, PLEKHF2, NPAL2, BAALC, GRHL2, SLC25A32, TM7SF4, NCALD, LRRCC1, TSPYL5, PSKH2, TMEM67, MTDH, CHMP4C, TP53INP1, SLC26A7, CTHRC1, OSR2, FAM92A1, C8orf38, WDR21C, RALYL, ANKRD46, C8orf37, VPS13B, SLC7A13, CNBD1, SNX31, TMEM64, C8orf47, ATP6V0D2, REXO1L1, DPY19L4, FBXO43, CA13, RBM12B, GDF6, C8orf59*	-
6	20q11.21	0.17	1	chr20:1-62435964	524 genes	***CRKL***

1. Rank according to Q-value. Q-value are false-discovery rate corrected.
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   Genes in bold represent significantly amplified genes in cancer from Beroukhim *et al.* (PMID: 20164920, Supplementary Table 2: GISTIC analysis of 3,131 cancer specimens of 26 tumor types).
   Genes in italics represent genes that are in the region that are mentioned in the text
   Genes with * represent genes adjacent to the region

Supplementary Table 4b: Significant regions of DNA copy number deletion in leukemic CTCL cell lines

Rank	Cytoband	Q-value	Number of samples	Region	Genes in region	Genes of interest related to region
1	9p21.3	2.99E-05	4	chr9:20944461-22057275	*23 genes: hsa-mir-31, CDKN2A, CDKN2B, IFNA1, IFNA2, IFNA4, IFNA5, IFNA6, IFNA7, IFNA8, IFNA10, IFNA13, IFNA14, IFNA16, IFNA17, IFNA21, IFNB1, IFNW1, MTAP, KIAA1797, KLHL9, IFNE1, PTPLAD2*	***CDKN2A***
2	4q35.1	0.12267	3	chr4:171099753-185609300	*34 genes: AGA, DCTD, GPM6A, HMGB2, HPGD, ING2, IRF2, VEGFC, GLRA3, SAP30, HAND2, MFAP3L, MORF4, ADAM29, SCRG1, FBXO8, AADAT, GALNT7, CLDN22, NEIL3, CDKN2AIP, ODZ3, STOX2, SPCS3, C4orf41, WWC2, KIAA1712, WDR17, SPATA4, ENPP6, ASB5, RWDD4A, LOC285501, GALNT17*	***FRG2*, TUBB4Q****
3	6q21	0.21278	3	chr6:103244744-113499286	*53 genes: hsa-mir-587, AIM1, AMD1, PRDM1, FOXO3, FYN, GPR6, LAMA4, PREP, REV3L, SMPD2, NR2E1, DDO, SNX3, CD164, WISP3, WASF1, ATG5, ZBTB24, FIG4, TRAF3IP2, BVES, SEC63, CDC2L6, SESN1, OSTM1, TUBE1, C6orf203, CDC40, SOBP, QRSL1, PDSS2, HACE1, KIAA1553, POPDC3, MICAL1, ARMC2, BXDC1, RTN4IP1, SLC22A16, KIAA1919, GTF3C6, SLC16A10, C6orf199, C6orf224, LACE1, SCML4, C6orf182, PPIL6, LIN28B, FLJ42177, RFPL4B, LOC619208*	***GTF3C6, TUBE1, ROS1***
4	10q23.31	0.21951	3	chr10:89718107-95455172	*44 genes: hsa-mir-107, ACTA2, FAS, CYP26A1, HHEX, HTR7, IDE, IFIT2, IFIT1, IFIT3, KIF11, LIPA, PDE6C, PPP1R3C, PTEN, RBP4, LIPF, CH25H, BTAF1, MPHOSPH1, RPP30, CPEB3, IFIT5, FER1L3, ANKRD1, PANK1, EXOC6, MARCH5, CEP55, C10orf59, STAMBPL1, TNKS2, PCGF5, C10orf4, ANKRD22, LIPJ, HECTD2, FGFBP3, GPR120, CYP26C1, SLC16A12, IFIT1L, LIPK, LIPN*	***PTEN***, *FAS*

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Supplementary Table 5 - FACS data from leukemic CTCL patients

Name	Population Isolated	CD4+/CD8+Ratio	%CD3	%CD4	%CD8	%CD4+CD26+	%CD4+CD26-	%CD4+CD7+	%CD4+CD7-	%CD25(IL2R)	%CD4+CD25+	%CD45RO	%Vbeta
REFERENCE		*0.8-3.5*	*58-86*	*25-65*	*12.0-44*	*10.0-54*	*2.0-18*	*32-55*	*4.0-6*	*0-4*	*1.0-10*	*15-40*	*N/A*
Patient 01	CD4+	1.7	-	46	-	22	10	44	9	41	11	61	N/A
Patient 02	CD4+CD7-CD26-	1.6	64	62	39.81	11	45	16	51	25	10	65	N/A
Patient 03	CD4+	2.9	53	52	17.67	28	15	32	18	27	9	35	Valpha12.1 7% REF(2-4.8)
Patient 04	CD4+CD7-	38	32	85	2.24	76	12	26	58	25	40	73	N/A
Patient 05	CD4+CD7-CD26-	100	-	100	-	0	100	1	99	9	2	99	N/A
Patient 06	CD4+	2.3	-	48	-	21	12	43	12	34	12	50	N/A
Patient 07	CD4+	0.79	-	27	-	11	5	29	4	19	4	29	N/A
Patient 08	CD4+	0.28	-	10	-	6	2	19	4	11	1	49	VB8A 7% REF(1.8-4.2)
Patient 09	CD4+	1.2	-	33	-	15	11	34	13	35	8	63	N/A
Patient 10	CD4+CD26-	19.7	86	89	4.53	4	84	71	18	51	43	53	VB2 79% REF(1.5-7.5)
Patient 11	CD4+CD7-CD26-	3.5	-	50	-	15	32	23	25	13	8	44	N/A
Patient 12	CD4+CD7-CD26-	2.8	85	47	16.54	8	24	16	55	31	8	57	N/A
Patient 13	CD4+	1.6	54	39	24	9	13	32	15	18	2	40	N/A
Patient 14	CD4+CD26-	40.8	-	64	-	6	60	57	17	44	59	70	N/A
Patient 15	CD4+	1.4	51	24	17.06	8	4	33	6	26	2	41	VB5a 41%; REF(0-1.3)
Patient 16	CD4+CD7-CD26-	4.9	79	68	13.92	13	55	18	50	30	14	73	VB5a 7% REF(0-1.3)
Patient 17	CD4+	3.3	-	59	-	35	15	58	9	45	16	46	N/A
Patient 18	CD4+CD26-	3.6	-	58	-	7	38	53	6	39	9	58	VB5c 38% REF(1.6-7.2)
Patient 19	CD4+	3.1	-	45	-	24	10	52	6	23	7	33	N/A
Patient 20	CD4+CD7-CD26-	3.4	83	56	16.59	9	34	32	32	28	1	53	VB3 10% REF(0-5.9); VB13.3 5% REF(0.5-1.7)
Patient 21	CD4+CD7-CD26-	7.5	44	41	5.5	34	17	3	48	12	19	69	N/A
Patient 22	CD4+	7.6	-	62	-	38	7	64	3	55	27	24	VB5c 6% REF(0-1.3)
Patient 24	CD4+	3.1	-	44	-	14	1	49	2	9	1	12	N/A
Patient 25	CD4+	1.2	-	45	-	37	10	49	2	7	4	22	N/A