	Fish signal number (reported as 2 if no abnormal population over cutoff)											Percentage of total cells with FISH signal number										
Patient ID	TP53	ARID1A	ZEB1	CDKN2A	DNMT3A	ATM	RB1	FAS	MYC	STAT3/5B	CARD11	TP53	ARID1A	ZEB1	CDK2NA	DNMT3A	ATM	RB1	FAS	MYC	STAT3/B	CARD11
1	1	2	2	2	2	2	2	2	4	2	2	85.0%	100.0%	100.0%	99.0%	100.0%	100.0%	100.0%	100.0%	86.0%	100.0%	100.0%
2	1	1	2	2	2	2	2	1	2	3	2	88.0%	42.5%	42.5%	98.0%	100.0%	88.0%	99.0%	88.0%	98.0%	42.5%	100.0%
3	1	2	2	1	2	1	2	2	3	3	2	100.0%	100.0%	100.0%	98.0%	100.0%	100.0%	100.0%	100.0%	97.0%	88.5%	100.0%
4	1	1	1	2	2	2	2	2	3	3	2	76.0%	58.5%	58.5%	95.5%	98.0%	100.0%	100.0%	98.0%	80.0%	58.5%	98.0%
5	1	2	1	1	1	2	2	1	2	2	2	34.5%	100.0%	11.0%	28.5%	36.0%	100.0%	99.0%	36.0%	94.0%	100.0%	100.0%
6	1	1	1	2	1	2	2	2	2	3	1	94.0%	84.0%	61.0%	99.0%	92.0%	94.0%	100.0%	92.0%	100.0%	23.0%	92.0%
7	1	2	0	2	1	2	1	2	3	3	3	73.5%	100.0%	64.0%	99.0%	94.0%	100.0%	71.0%	100.0%	50.6%	64.0%	94.0%
8	1	1	1	1	1	2	1	1	4	2	2	82.0%	54.0%	54.0%	36.0%	36.0%	100.0%	87.0%	36.0%	13.5%	100.0%	100.0%
9	1	2	1	2	1	2	2	1	3	3	3	59.9%	100.0%	64.0%	100.0%	47.0%	100.0%	100.0%	59.0%	59.0%	46.0%	59.0%
10	1	4	2	1	4	2	4	4	4	3,6	5	53.0%	39.5%	100.0%	87.0%	40.5%	100.0%	36.0%	40.5%	15.0%	52%,39.5%	40.5%
11	1	2	2	1	2	1	1	2	2	3	2	40.0%	90.0%	90.0%	56.0%	100.0%	70.0%	64.0%	100.0%	100.0%	90.0%	100.0%
12	1	1	2	2	2	1	2	2	3	3	3	99.5%	94.0%	96.0%	100.0%	99.5%	99.5%	100.0%	92.0%	52.0%	80.0%	99.5%
13	1	1	2	2	1	2	2	2	3	3	2	95.0%	80.5%	100.0%	100.0%	91.0%	95.0%	99.5%	100.0%	80.5%	80.5%	100.0%
14	2	2	2	2	2	2	2	2	3	1	2	100.0%	100.0%	100.0%	99.5%	100.0%	100.0%	100.0%	100.0%	62.0%	9.0%	100.0%
15	2	2	2	2	2	2	2	2	2	2	2	100.0%	100.0%	100.0%	98.5%	100.0%	100.0%	100.0%	100.0%	93.0%	100.0%	94.5%
16	2	2	2	2	2	2	2	2	2	2	2	100.0%	99.0%	99.0%	100.0%	100.0%	100.0%	99.0%	100.0%	99.0%	99.0%	100.0%
17	2	2	2	2	2	2	2	2	2	2	2	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
18	2	2	2	2	2	2	2	2	2	2	2	100.0%	99.5%	99.5%	99.5%	99.5%	100.0%	99.5%	100.0%	99.5%	99.5%	99.5%
19	2	2	2	2	2	2	2	2	2	2	2	99.0%	100.0%	100.0%	100.0%	100.0%	99.0%	100.0%	100.0%	100.0%	100.0%	100.0%
20	2	2	2	2	2	2	2	2	2	2	2	99.0%	100.0%	100.0%	100.0%	100.0%	99.0%	100.0%	100.0%	100.0%	100.0%	100.0%
21	2	2	2	2	2	2	2	2	2	2	2	99.0%	100.0%	100.0%	98.5%	98.5%	99.0%	99.5%	98.5%	99.5%	100.0%	98.5%
22	2	2	2	2	2	2	2	2	2	2	2	100.0%	100.0%	100.0%	100.0%	99.5%	100.0%	100.0%	99.5%	100.0%	100.0%	99.5%
23	2	2	2	2	2	2	2	2	2	2	2	100.0%	100.0%	100.0%	99.0%	100.0%	100.0%	99.0%	100.0%	100.0%	100.0%	100.0%
24	2	2	2	2	2	2	2	2	2	2	2	100.0%	100.0%	100.0%	99.0%	99.0%	100.0%	100.0%	99.0%	99.5%	100.0%	99.0%

	Patient Characteristics									
Patient ID	Diagnosis	Age	Sex	)7 ISCL blood le	PCR	CD4/CD8	CD3+ T Cell/µl	Percent CD26- of CD4+	Percent CD7- of CD4+	Sorted population
1	Sezary	69	M	B2	+	5.8	534	31.0%	33.8%	CD3+CD4+CD7-CD26-
2	Sezary	69	F	B2	+	13.5	2937	67.8%	98.0%	CD3+CD4+CD7+CD26-
3	Sezary	63	F	B2	- (Vbeta+)	8.6	533	19.1%	42.2%	CD3+CD4+CD26-VB7.2+
4	Sezary	79	F	B2	+	25.9	757	46.5%	3.8%	CD3+CD4+CD7-CD26-VB3+
5	Sezary	91	M	B2	+	6.1	1362	44.9%	50.7%	CD3+CD4+CD7-CD26-
6	Sezary	87	M	B2	+	3.6	454	40.4%	16.5%	CD3+CD4+CD26-
7	Sezary	73	F	B2	+	25.6	20235	90.3%	88.4%	non-sorted PBMC
8	Sezary	63	F	B2	+	6.6	838	63.8%	9.4%	CD3+CD4+CD7+CD26-
9	Sezary	76	M	B2	+	58.5	9764	90.7%	86.7%	non-sorted PBMC
10	Sezary	82	M	B2	+	10.4	3083	52.7%	62.7%	CD3+CD4+CD26-VB2+
11	ollicular M	72	M	B0	+	8.4	1437	14.1%	19.7%	CD3+CD4+CD7-CD26-VB20+
12	F with tum	61	M	B2	+	16.7	2967	29.8%	14.8%	CD3+CD4+CD26-
13	ch/plaque	60	M	B2	+	4.1	484	14.9%	53.0%	CD3dimCD4+CD7+CD26-
14	ch/plaque	51	M	B0	+	2.7	1141	29.8%	14.6%	CD3+CD4+CD26-
15	ollicular M	47	M	B0	+	1.1	553	5.0%	5.8%	VB2+
16	ch/plaque	61	F	B0	+	2.7	1415	10.4%	27.3%	CD3+CD4+CD7-CD26-
17	ch/plaque	82	F	B2	+	2.9	1071	21.8%	41.5%	CD3+CD4+CD7-CD26-
18	ch/plaque	86	M	B0	+	1.5	1110	20.8%	18.8%	CD3+CD4+CD26-
19	ch/plaque	76	M	B0	+	2.6	820	11.2%	14.6%	CD3+CD4+CD7-CD26-
20	ch/plaque	66	F	B0	NA	4.0	713	9.4%	6.1%	CD3+CD4+CD7-CD26-
21	ch/plaque	84	M	B0	+	1.5	1478	22.5%	18.0%	CD3+CD4+CD7-CD26-
22	ular mucii	37	M	B0	-	5.7	1493	23.4%	15.6%	CD3+CD4+CD26-
23	ch/plaque	74	F	B0	NA	1.9	505	17.0%	15.2%	CD3+CD4+CD26-
24	ematous	73	F	B0	+	1.3	367	23.6%	15.9%	CD3+CD4+CD26-

CD8+ Sorted Cells: Percentage of cells with normal (2x) signal of total counted (100 or 200) cells											
Patient ID	**TP53**	**ATM**	**MYC**	**RB1**	**CDKN2A**	**ARID1A**	**ZEB1**	**STAT3/5B**	**FAS**	**DMNT3A**	**CARD11**
1	97	98	93	92	84	97	97	94	95	98	98
2	94	99	94	95	94	94	97	97	98	97	95
3	99	98	96	100	97	98	94	96	97	97	98
4	97	96	97	97	99	94	98	99	97	97	99
8	97	96	95	99	95	97	97	96	94	98	98
11	96	95	99	94	97	97	100	93	99	99	98
15	96	95	94	91	94	96	95	99	98	99	100
18	98	96	93	96	96.5	94	96	97	97	97	99
Mean	96.750	96.625	95.125	95.500	94.563	95.875	96.750	96.375	96.875	97.750	98.125
STDV	1.488	1.506	2.100	3.162	4.594	1.642	1.832	2.134	1.642	0.886	1.458
99.00%	92.286	92.107	88.824	86.013	80.781	90.949	91.253	89.973	91.949	95.091	93.752
(M+/-3STDV)%	46.143	46.054	44.412	43.007	40.391	45.474	45.627	44.987	45.974	47.545	46.876
False Pos #	3.250	3.375	4.875	4.500	5.438	4.125	3.250	3.625	3.125	2.250	1.875
Normal 95% Cutoff	0.077	0.078	0.096	0.092	0.102	0.087	0.077	0.081	0.075	0.064	0.059
Normal 99% Cutoff	0.098	0.099	0.119	0.114	0.125	0.109	0.098	0.103	0.096	0.084	0.078

CTCL Exome Versus SS FISH Detected Gene Copy Number Alterations (GCNAs)												
Genes	**TP53**	**ARID1A**	**ZEB1**	**CDK2NA**	**DNMT3A**	**ATM**	**RB1**	**FAS**	**MYC**	**STAT3(/5B)**	**CARD11**	**Total Sezary patients**
Patients with GCNAs, exome study	35	23	24	16	14	11	10	16	17	25	9	40
Proportion Abnormal	0.875	0.575	0.600	0.400	0.350	0.275	0.250	0.400	0.425	0.625	0.225	
Standard Error	0.052	0.078	0.077	0.077	0.075	0.071	0.068	0.077	0.078	0.077	0.066	
Patients with GCNAs, FISH (separate cohort)	9	5	5	3	4	2	2	5	8	7	3	10
Proportion Abnormal	0.900	0.500	0.500	0.300	0.400	0.200	0.200	0.500	0.800	0.700	0.300	
Standard Error	0.095	0.158	0.158	0.145	0.155	0.126	0.126	0.158	0.126	0.145	0.145	

*Choi J, Goh G, Walradt T, *et al.* (2015) Genomic landscape of cutaneous T cell lymphoma. *Nat Genet* 47:1011-9.

Isolation of malignant T cells in leukemic CTCL

Approximately 45 mL of peripheral blood was obtained from each patient in Sodium Heparin Blood Collection Tubes (BD Vacutainer) and diluted with 90 mL PBS. Diluted blood was layered over 15 mL of ficoll (GE Healthcare Ficoll-Paque Premium or Isolymph from CTL Scientific Supply Corp.) in 50 mL conical tubes prior to centrifugation for 35 minutes at 1500 rpm. Buffy coats were isolated and washed with RPMI in 15 mL conical tubes, centrifuged for 10 minutes at 1400 rpm, resuspended in RPMI, rewashed in RPMI and centrifuged again for 8 minutes at 1100 rpm to minimize residual Ficoll. After RPMI resuspension, cells were counted (and if not immediately processed further were frozen in 90% RPMI 10% DMSO in liquid nitrogen). Malignant T cells were isolated from total mononuclear cells by either fluorescence-activated cell sorting (FACS) or magnetic bead sorting.

For samples sorted by FACS, mononuclear cells were first stained with: anti-CD3-BV-421 (clone OKT3, Biolegend, San Diego, CA), anti-CD4-PerCP (clone RPA-T4, Biolegend), anti-CD7-APC (clone CD7-6B7, Biolegend), anti-CD8-PE-Cy7 (clone SK1, Biolegend), anti-CD26-PE (clone BA5b, Biolegend). For patients with a known V-beta clone, cells were also stained with corresponding anti-V-beta-PE (Beckman Coulter, Inc.). After washing twice with stain buffer, cells were sorted (BD FACSAria) with gates to identify population previously defined as abnormal by clinical flow cytometry. In most cases, lymphocytes were gated from forward- and side-scatter followed by subsequent gating on CD3+CD4+CD8- cells to allow visualization of CD4+ T cells. (If V-beta antibody was present, V-beta positive CD4+ T cells were further gated thereafter.) A scatter plot of CD4+ (and V-beta+ if present) T cells along CD26 and CD7 axes allowed for sorting of the previously defined abnormal populations, whether CD26-CD7-, CD26-CD7+/-, or CD26+/-CD7-. In cases where previous studies demonstrated an abnormal population with atypical markers, such as CD3 dim or CD4 dim, corresponding adjustments in gating were made. For controls, CD3+CD8+ lymphocytes were sorted simultaneously.

For samples sorted by magnetic beads, mononuclear cells were stained with T Cell Biotin-Antibody Cocktail as well as anti-CD26-biotin (eBioscience) and/or anti-CD7-biton (eBioscience) and incubated with anti-biotin microbeads according to the manufacturer's instructions to isolate populations previously identified as abnormal by flow cytometry; in most cases this population was CD4+CD26-CD7- or CD4+CD26-CD7+/-.

Fixation

Sorted cells were pelleted in a 5 ml centrifuge tube and gently resuspended in 4.5 ml hypotonic solution (0.075M KCl). After 16 minutes incubation at room temperature, 300 ul fresh fixative (3 parts methanol to 1 part acetic acid) was added to each sample, followed by gentle inversion and 10 minutes incubation at room temperature. Next cells were centrifuged at 1100 rpm for 10 minutes, resuspended in 4 ml fixative, incubated at room temperature for 10 minutes, and centrifuged again at 1100 rpm for 10 minutes. After resuspension in 1 ml fixative, samples were stored at 34 for up to 1 month before performing FISH.

Hybridization

For both commercially available and custom probes, fixed samples underwent overnight FISH hybridization using probes for TP53, ATM, MYC, RB, and CDKN2A (P53/ATM Probe Combination LPH 052, cMYC Breakapart LPH 010, RB1 Deletion LPS 011, P16 Deletion LPH 009-A; Cytocell Aquarius) and newly developed probes for ARID1A, ZEB1, STAT3/5B, DNMT3A, CARD11, and FAS (Cytocell myProbes Custom Probes). Hybridization for all probes was performed according to standard manufacturer instructions for CytoCell Aquarius probes.

Probe visualization and quantification

Probes were quantified using a fluorescent light microscope (BX-60 or BX-43, Olympus; or Axio Observer Z1, Zeiss) running CytoVision (Version 7.4, Leica Biosystems) or TissueFAXs (Version 4.2, TissueGnostics) software. For each probe, signals in 100 or 200 nuclei were examined.