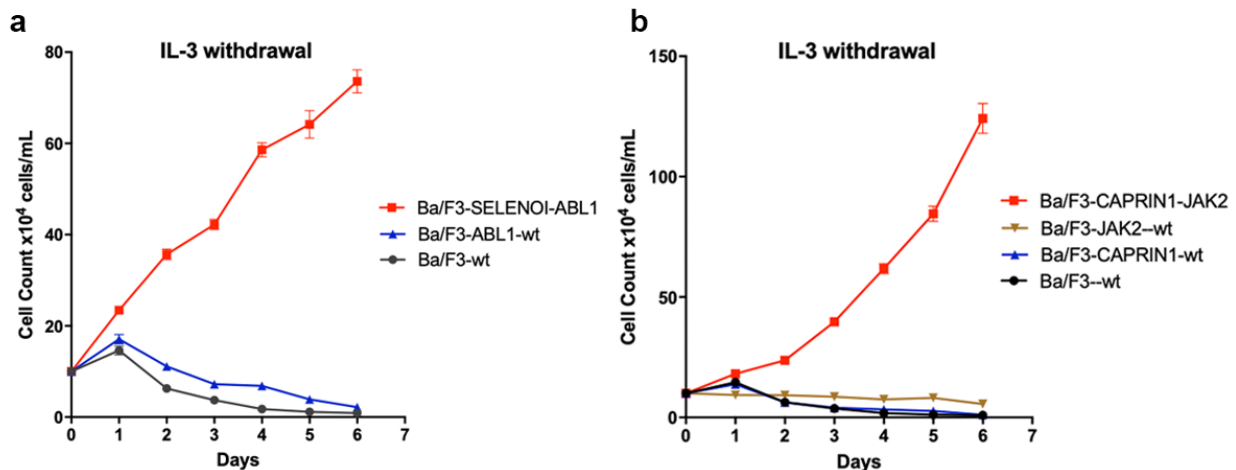
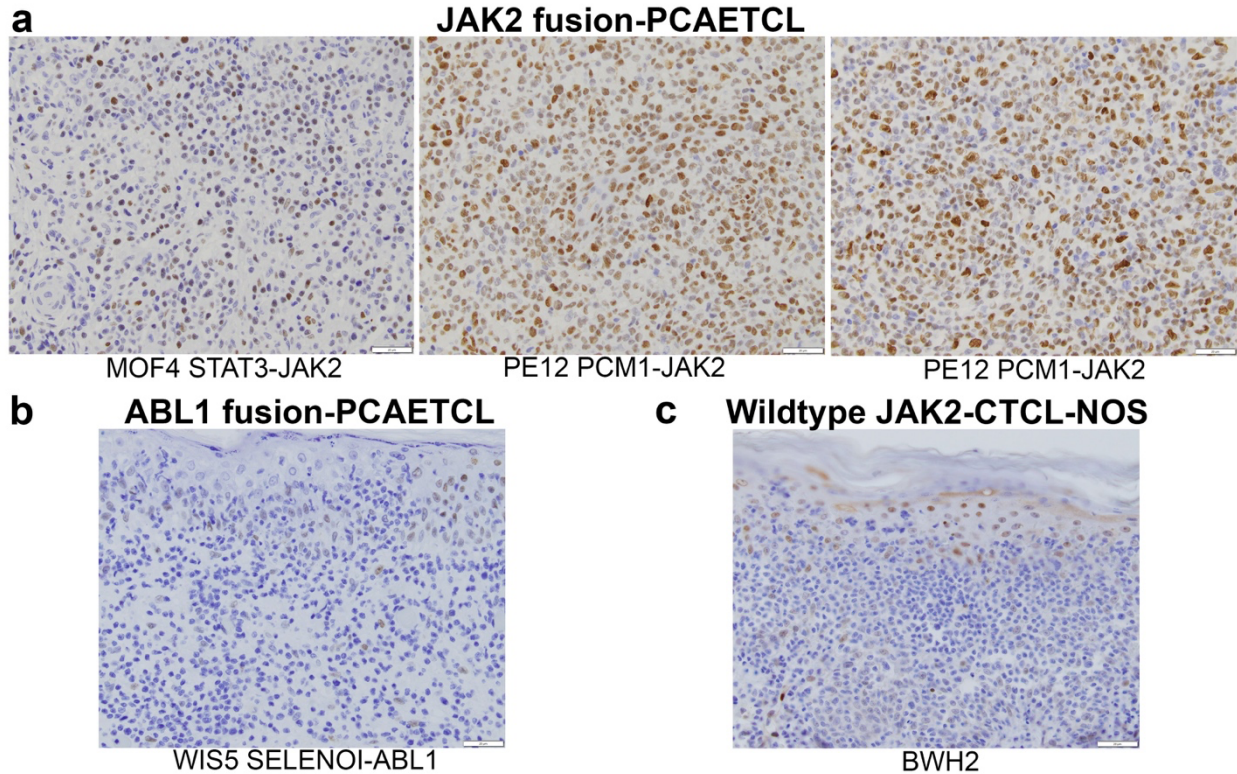


Supplemental Figure 1. Histological features of primary cutaneous CD8+ aggressive epidermotropic T cell lymphoma. The hematoxylin & eosin-stained and immuno-stained slides for case MGH6 reveals pagetoid epidermotropism. The lymphocytic infiltrate is CD3+, CD8+, CD4-, weakly CD2+, CD56+, and granzyme B positive.



Supplemental Figure 2. Kinase fusions confer IL-3 independent growth.

a. Retroviruses encoding SENENOI-ABL1, wildtype ABL1, and empty vector controls were transduced into Ba/F3 cells. Stable cells were seeded without IL-3 at 10^5 cells/mL. Viable cells were manually counted daily. **b.** Retroviruses encoding CAPRIN1-JAK2, wildtype JAK2, wildtype CAPRIN1, and empty vector were transduced into Ba/F3. Stable cells were seeded without IL-3 at 10^5 cells/mL, and viable cells were manually counted daily. All assays were performed in triplicate.



Supplemental Figure 3. JAK2 fusion positive PCAETCLs are positive for pSTAT3. **a.** Three JAK2 fusion positive PCAETCL, **b.** 1 ABL1 fusion positive PCAETCL, and **c.** a wildtype JAK2 CTCL-NOS were selected for immunohistochemistry with phospho-STAT3 (**pSTAT3**). Formalin-fixed paraffin-embedded sections (4 microns in thickness) from each sample were subjected to dewaxing, rehydration, and staining for phospho-STAT3 on a Leica Bond III automated immunostainer. Following antigen retrieval in EDTA buffer for 20 min at 100°C, pSTAT3 staining was performed using a rabbit monoclonal (Cell Signaling Technology, clone D3A7) diluted 1:100 in Bond Primary Diluent. Primary antibody was applied for 30 min and staining was then developed using the Leica Biosystems Refine Detection Kit. Sections were counterstained with hematoxylin. PCAETCL cases with JAK2 fusions were positive for pSTAT3. The PCAETCL with SELENOI-ABL1 and the CTCL-NOS, BWH2, were negative for pSTAT3.

Supplemental Table 1. List of somatic single nucleotide variants from PCAETCL and CTCL-NOS. Position refers to amino acid position. AA change = amino acid change.
* = stop codon

Sample	Gene	Position	AA Change	Alteration Type
UT22	JAK3	906	p.P906S	nonsynonymous SNV
NU9	STAT3	661	p.D661Y	nonsynonymous SNV
NU9	JUNB	282	p.A282V	nonsynonymous SNV
NU11	STAT3	714	p.P714L	nonsynonymous SNV
NU14	JAK1	1097	p.G1097D	nonsynonymous SNV
UT22	KMT2D	3967	p.Q3967*	nonsense
NU1	CDKN2A	80	p.R80*	nonsense
NU1	CREBBP	160	p.G160fs	frameshift deletion
NU4	KMT2D	353	p.Q353*	nonsense
NU6	NR3C1	479	p.R479*	nonsense
NU11	SH2B3	None	splicing	splice site
NU7	SOCS1	108	p.Q108*	nonsense
NU7	CDKN1B	53	p.E53*	nonsense