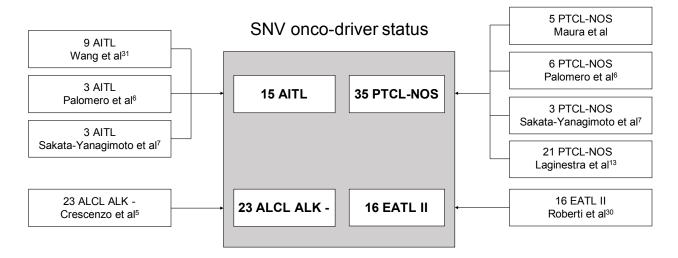
## **Supplementary Figures and Tables**

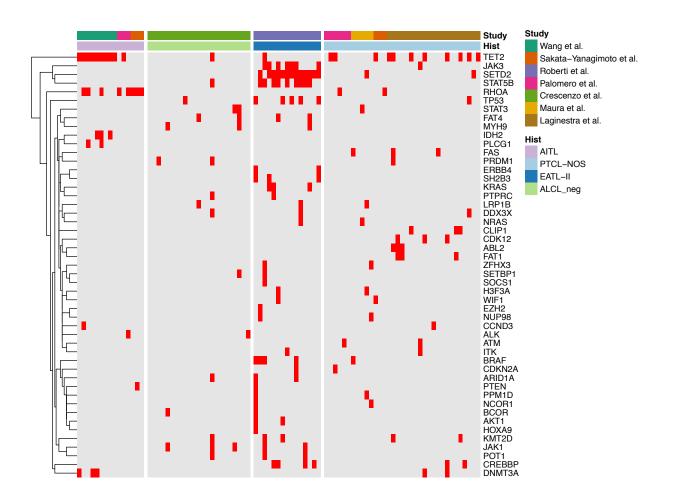
CDKN2A deletion is a frequent event associated with poor outcome in patients with peripheral T-cell lymphoma not otherwise specified (PTCL-NOS)

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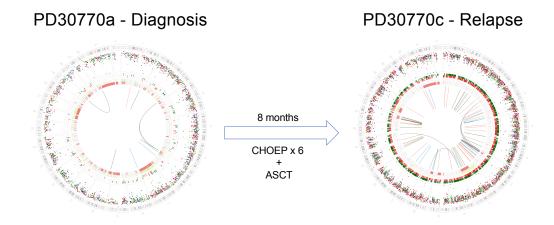
**Supplementary Figure 1**. Summary of whole exome sequencing data used to investigate the prevalence of mutations in driver genes in PTCLs.



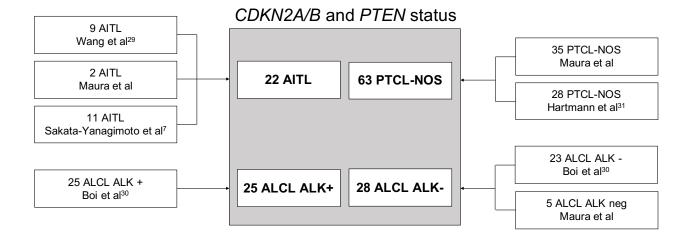
## **Supplementary Figure 2**. Number of driver mutations per patient across different PTCLs.



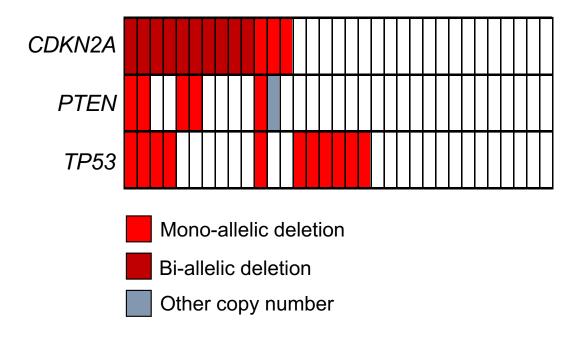
**Supplementary Figure 3**. Genome plots at diagnosis (PD30770a) and at relapsed (PD30770c) after treatment in the only patient where 2 samples were collected at different time points. In this patient, at relapse, several novel SV were observed, including complex events (i.e on chromosome 16). From the external ring to the internal: mutations, (vertically plotted according to their inter-mutational distance and where the color of each dot represents the mutation class), indels (dark green = insertion; and brown = deletion); copy number variants (red = deletions, green = gain), rearrangements (blue = inversion, red = deletions, green = ITD, black=translocations).



**Supplementary Figure 4.** Summary of copy number data used to investigate the prevalence of CDKN2A and PTEN deletion across different PTCLs.



**Supplementary Figure 5.** The prevalence of *TP53*, *PTEN* and *CDKN2A* deletions among PTCL-NOSs samples with available ASCAT copy number data (SNP array or WGS data).



Supplementary Table 1. Sample characteristics and summary of the WGS
<b>Supplementary Table 2</b> . All PTCL patients included in the study and evaluated for CDKN2A and PTEN status.