

## Description of Additional Supplementary Files

**Supplementary Data 1: Whole gene expression and alternative splicing changes upon Tax expression.** Whole gene expression threshold was set to  $\log_2(\text{FC}) = 0.6$ ,  $p < 0.05$  (glm and Wald test). For differential splicing, deltaPsi threshold was set to 1.1  $p < 0.05$  (Fisher test). Tax-induced splicing regulation identified in RNA-seq datasets derived from carriers and ATLL samples (EGAS00001001296). Alternative splicing profiles of each clinical sample was assessed using Farline analysis, with peripheral blood CD4+ T-cells used as a control. The table lists 452 Tax-induced splicing regulations identified at least once across 56 clinical samples. The sheet “samples EGAS00001001296” lists primary cell samples published by Kataoka and colleagues<sup>24</sup>. The sheet “PSI\_donors\_carriers\_ATLL” presents the psi values for exons expressed in donors, asymptomatic carriers, and ATL patients.

**Supplementary Data 2: Sequence features of exons regulated by Tax.**

**Supplementary Data 3: Genes modified in splicing by Tax in a DDX5/17-dependent manner.** Tax splicing targets responsive to DDX5/17 were attributed to splicing events lost upon DDX5/17 depletion.

**Supplementary Data 4: Protein features encoded by Tax-regulated exons.**

**Supplementary Data 5: List of oligonucleotides, siRNAs, sgRNAs, and TALE sequences.**