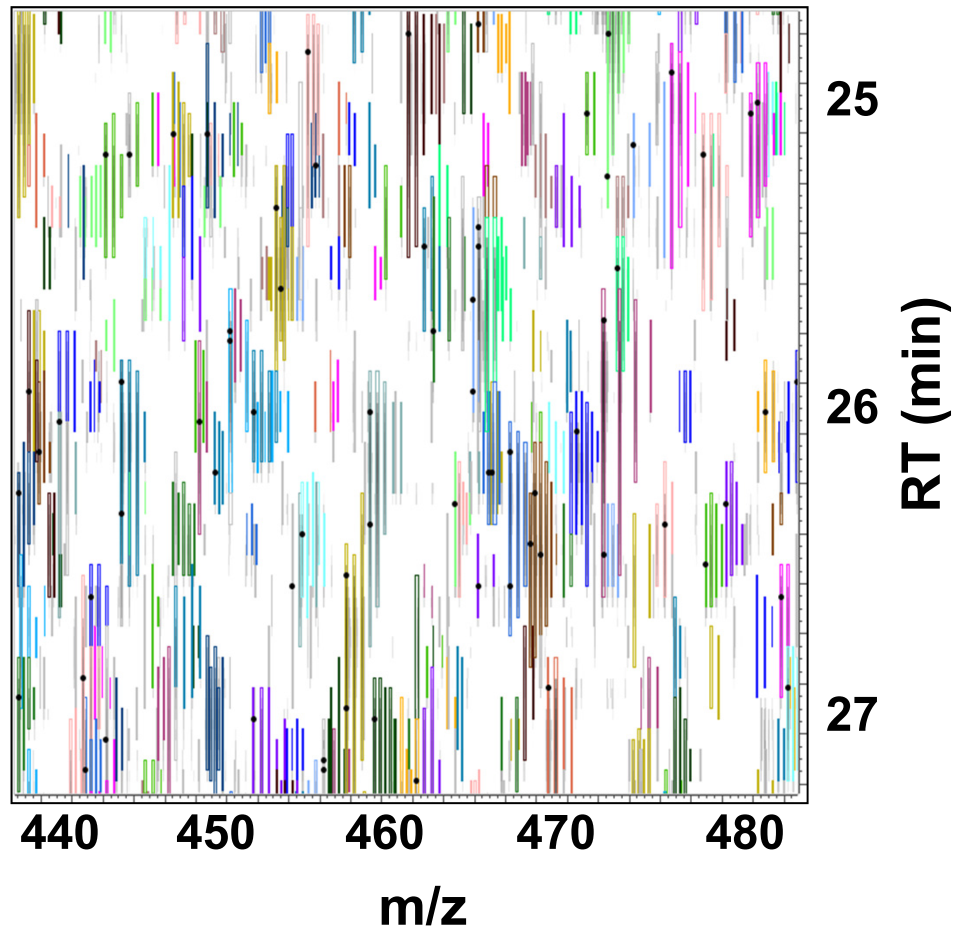
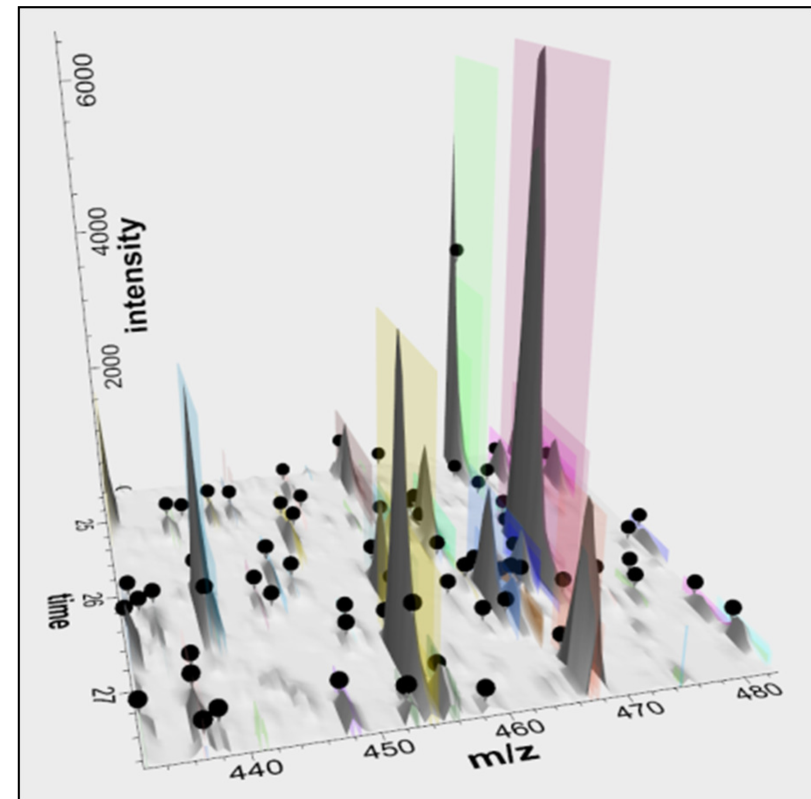
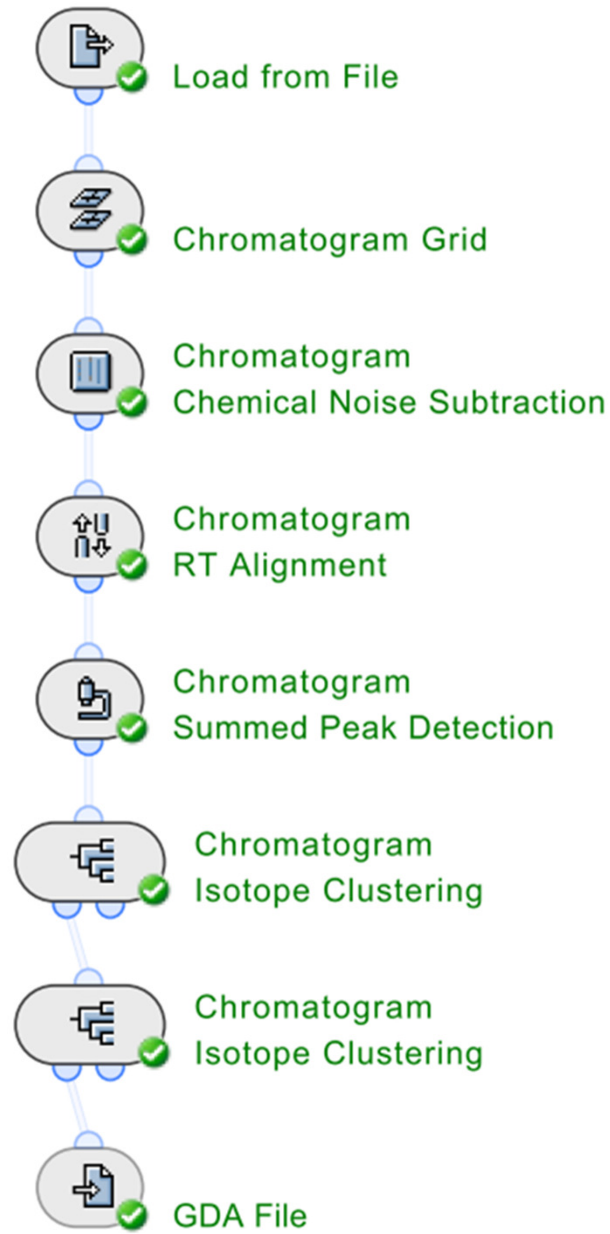
Supplementary Figure 1

(a)

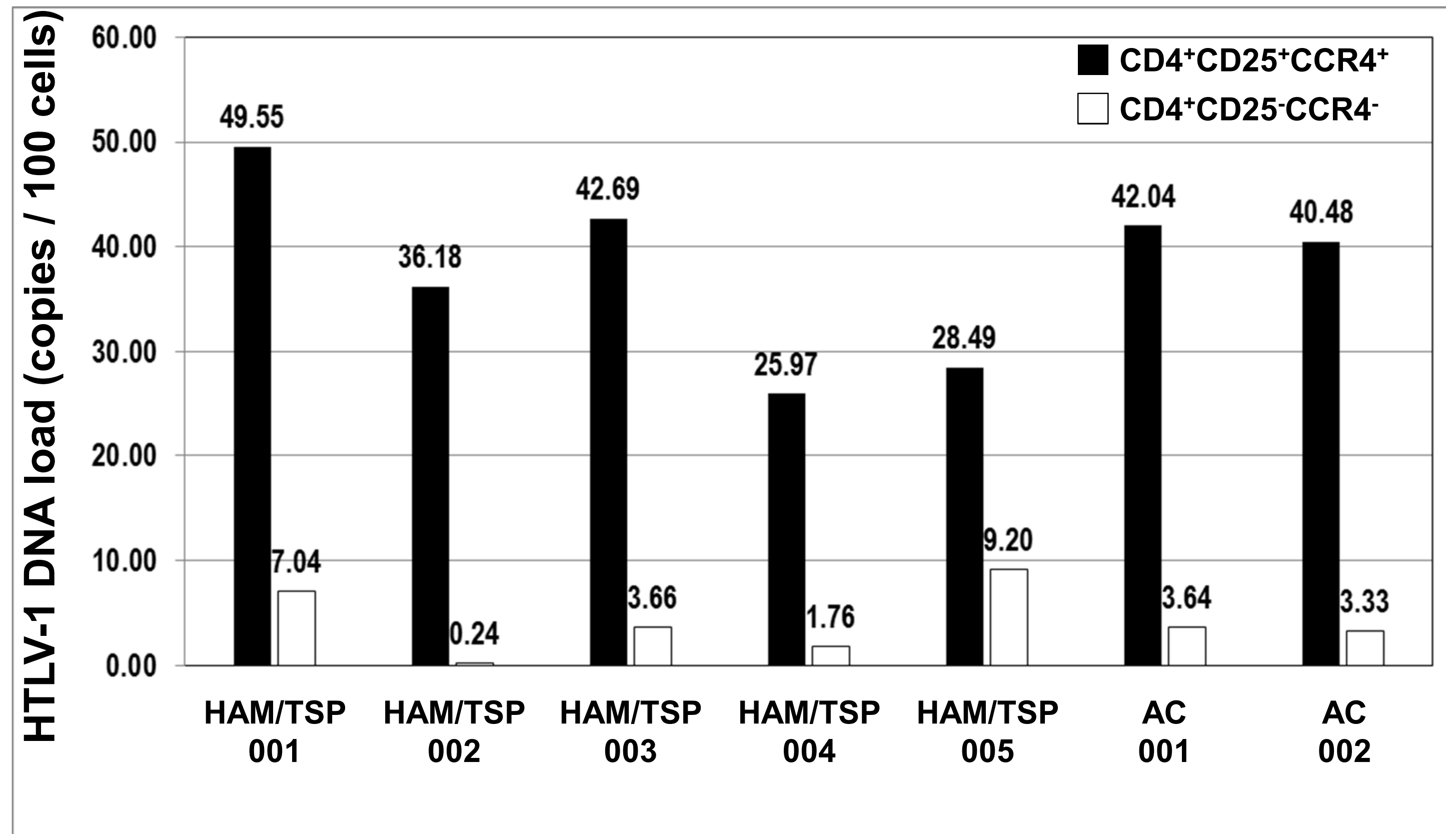




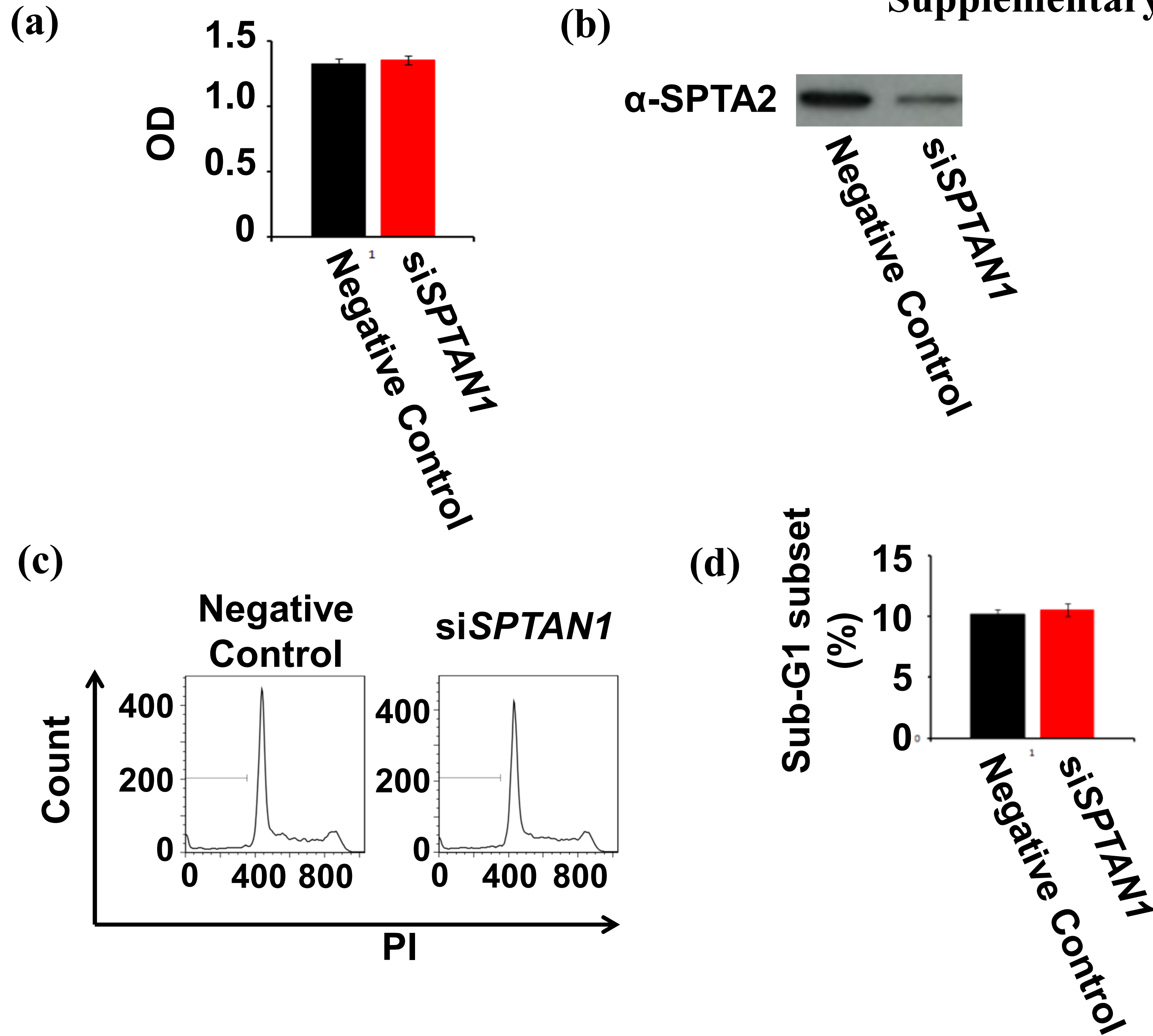
(b) **Supplementary Figure 1**



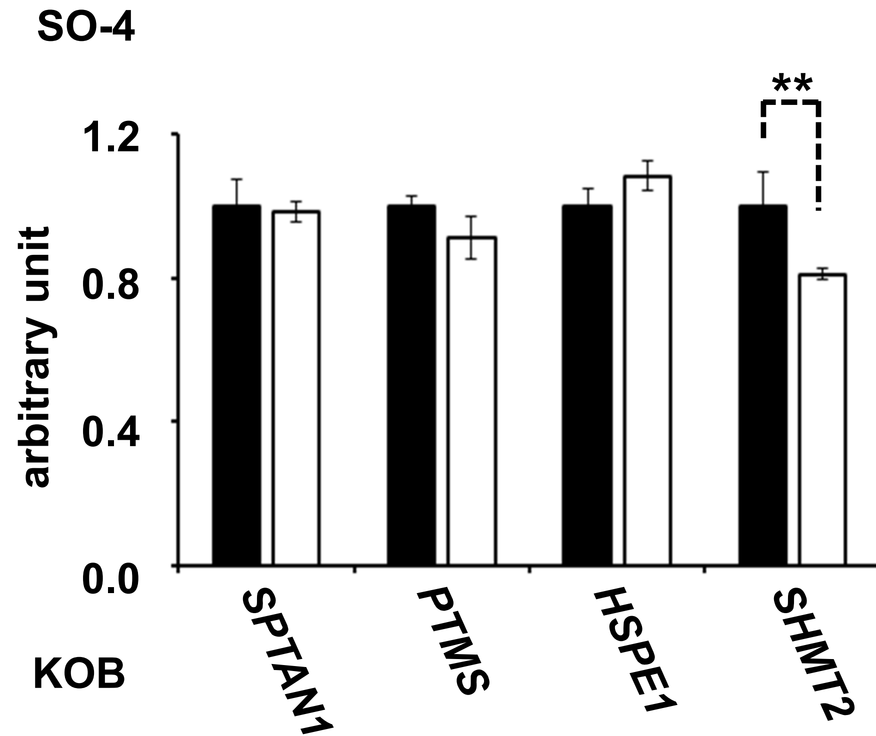
Supplementary Figure 2

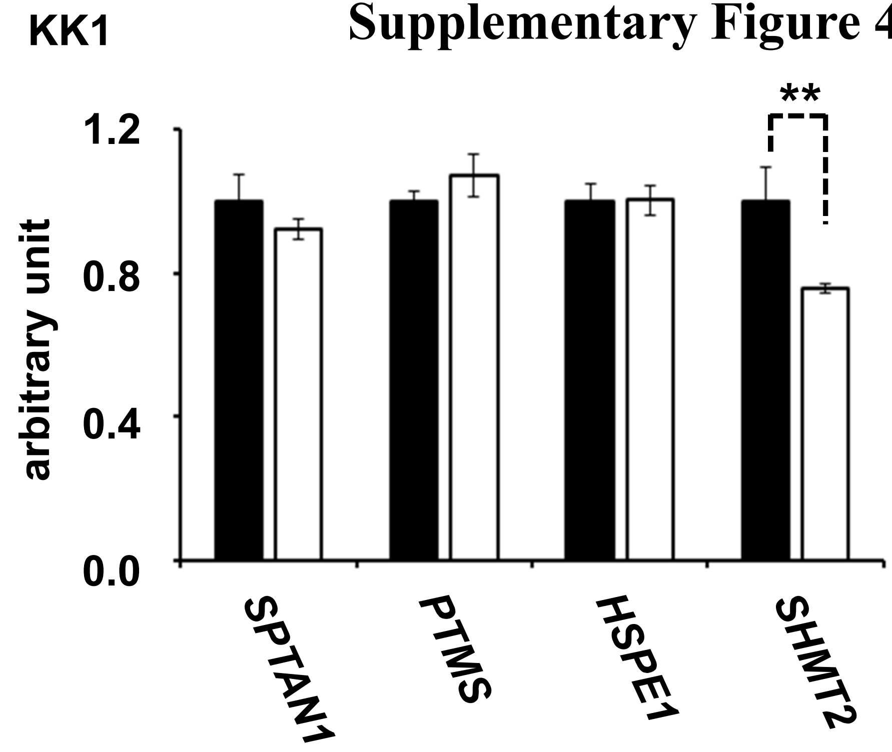


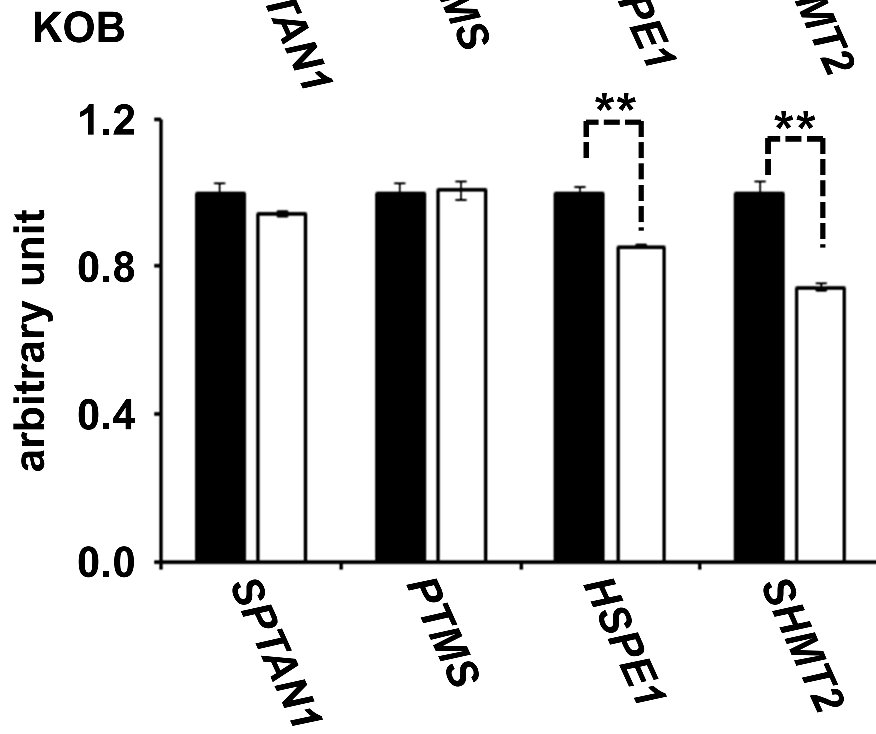
Supplementary Figure 3



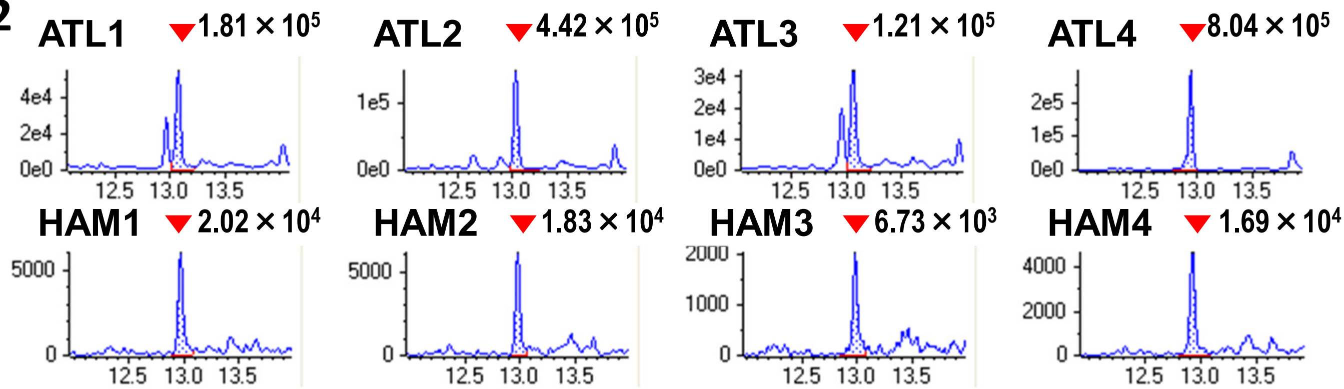
Supplementary Figure 4

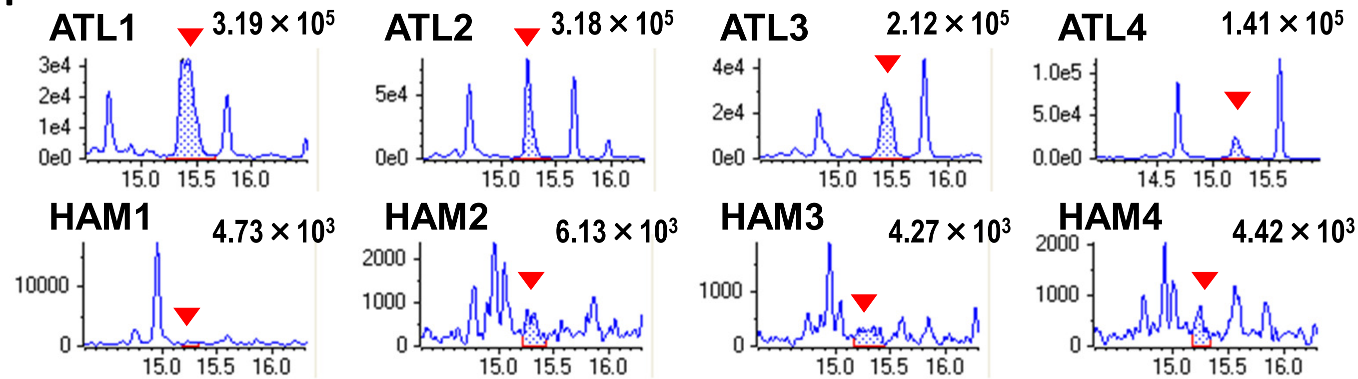


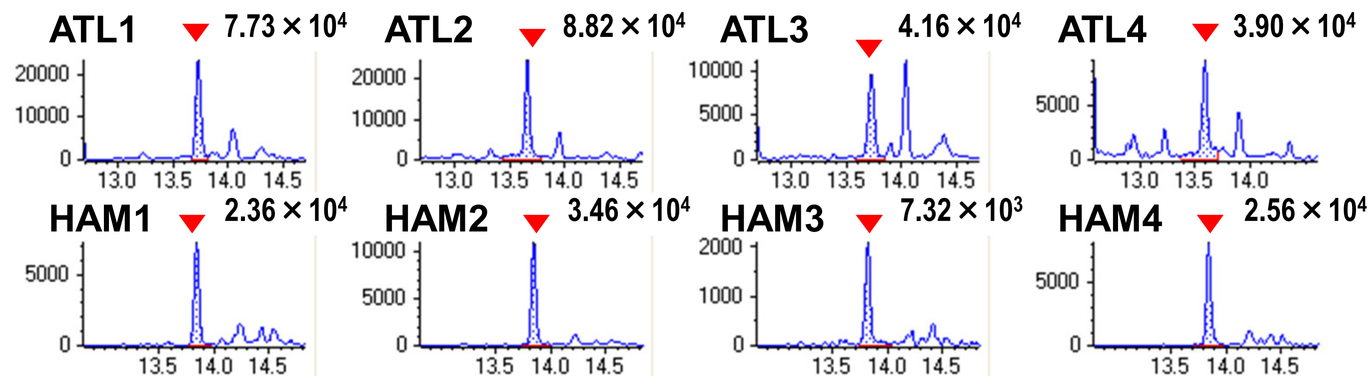




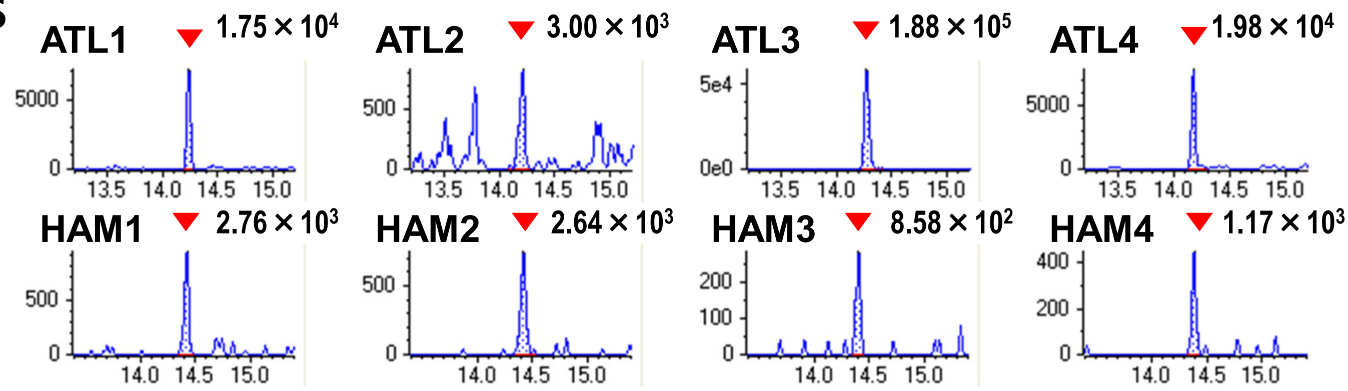
Supplementary Figure 5

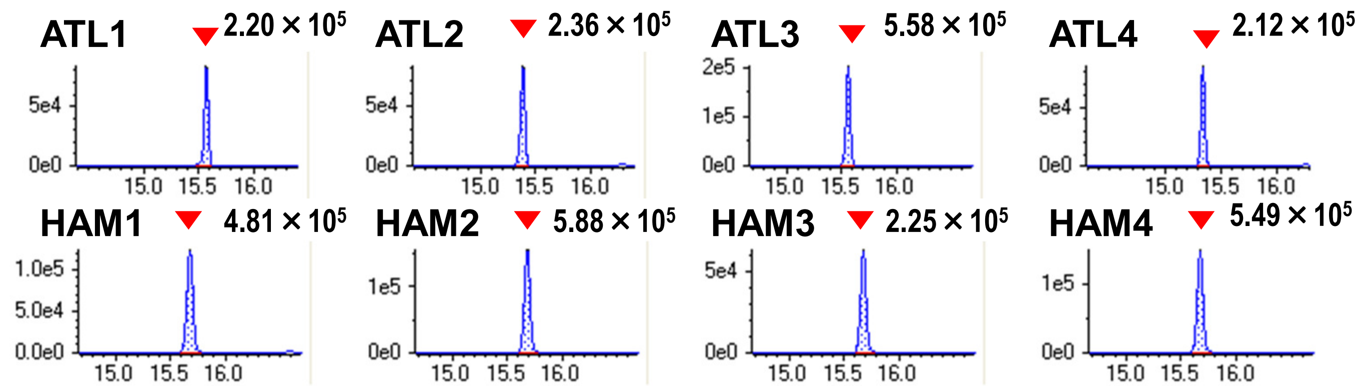




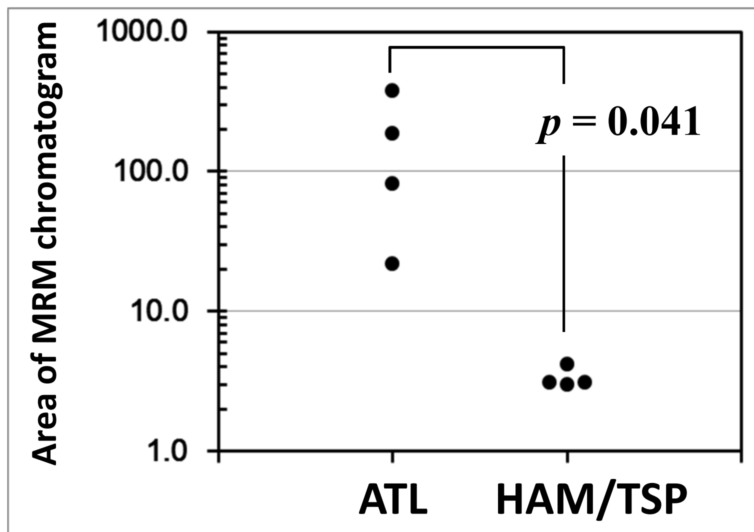


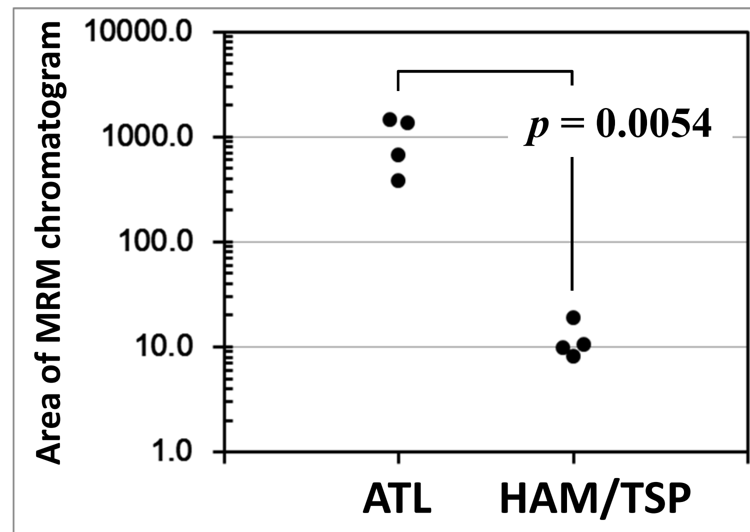
Supplementary Figure 5

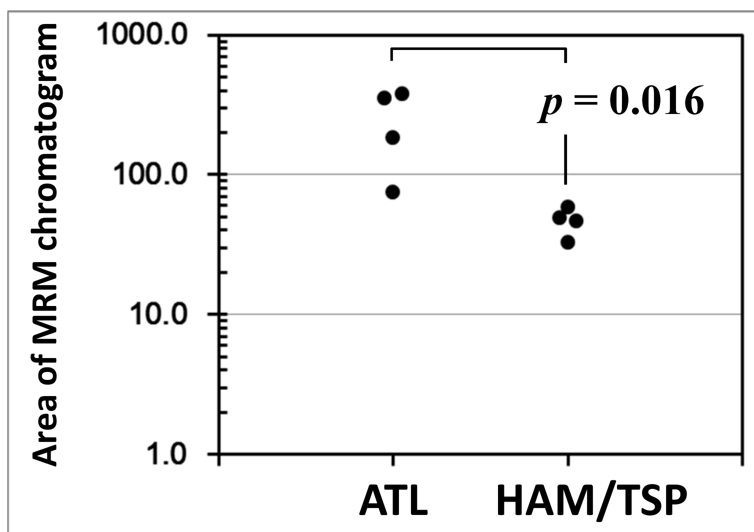


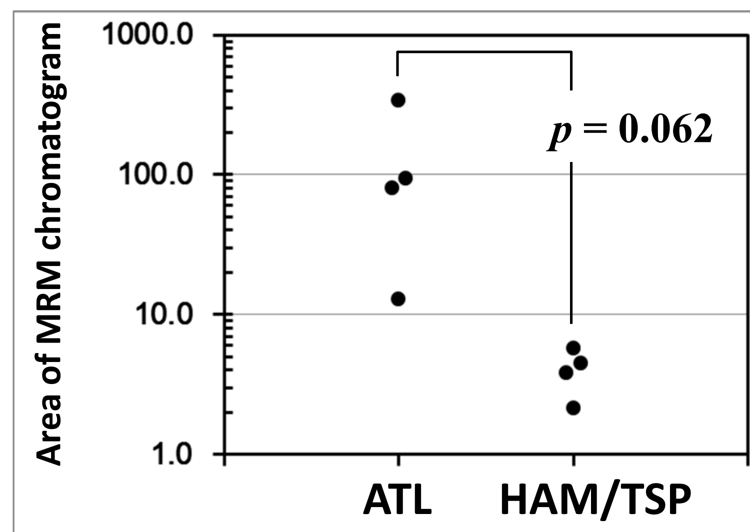


Supplementary Figure 6

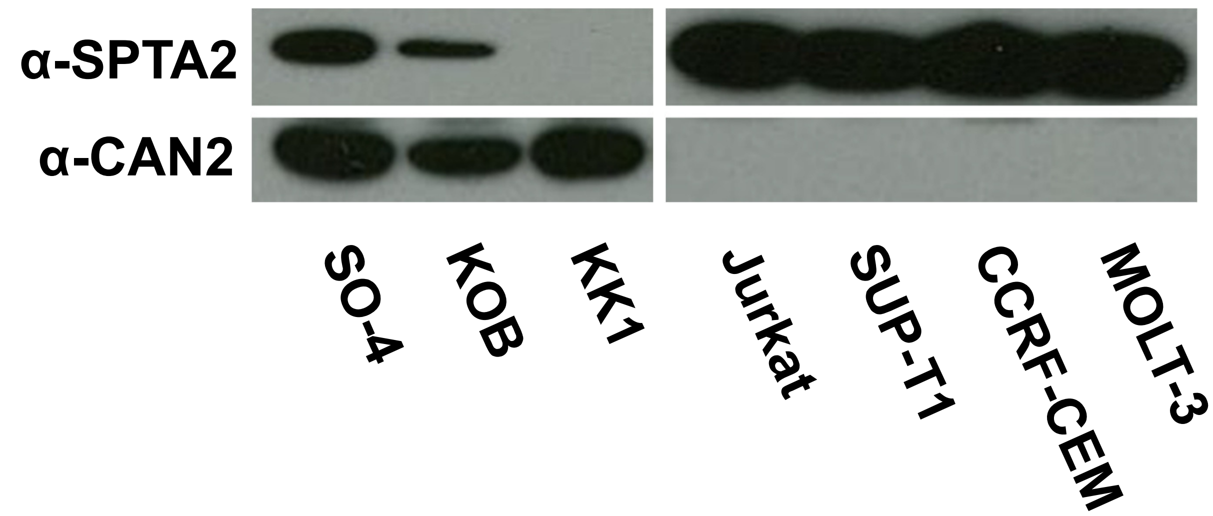








Supplementary Figure 7



Supplemental Figure 1 Data processing on the Expressionist RefinerMS module.

(A) Representative views of mass spectrometric data converted into 2-dimensional (left) or 3-dimensional (right) chromatograms on the Expressionist RefinerMS module. The black dots indicate the points at which MS/MS spectra were acquired. (B) The graphical user interface of processing work flow utilized in this study.

Supplemental Figure 2 Viral load analysis for $CD4^{+}CD25^{+}CCR4^{+}$ T-cells.

$CD4^{+}CD25^{+}CCR4^{+}$ (black bars) or $CD4^{+}CD25^{-}CCR4^{-}$ (white bars)T-cells were sorted from 7 PBMC samples and subjected to HTLV-1 viral DNA load analysis as described previously[10]. The values above bars indicate calculated viral load (copies/100 cells).

Supplemental Figure 3 Knockdown of alpha-II spectrin expression did not induce the cell death in ATL cells.

(A) The si*SPTAN1* did not alter SO4 cell growth in MTT assay 36 hours after transfection. (B) The effect of si*SPTAN1* was confirmed in protein level by immunoblot with anti-SPTA2. The si*SPTAN1* did not demonstrate any changes in cell cycle (C) and sub-G1 population (D) 24 hours after transfection.

Supplemental Figure 4 Cell proliferation assay for siRNA-treated ATL cell lines.

The siRNA specific to *SPTAN1*, *PTMS*, *HSPE1*, or *SHMT2* was transfected to SO-4, KK1, or KOB cells. Growth rate of cells was evaluated by MTT assay 36 hours after transfection in triplicated manner. MISSION siRNA Universal Negative Control oligo (Sigma) was used for negative controls. Astarisks indicate $p < 0.05$ by Student's t-test.

Supplemental Figure 5 Representative MRM chromatograms for 4 proteins upregulated in ATL cells.

Eight clinical samples (4 ATL patients and 4 HAM/TSP patients) were subjected to protein expression analysis by MRM (Multiple Reaction Monitoring). The MRM transitions m/z 409.7/375.2 for SPTA2, m/z 538.3/889.5 for PTMS, m/z 507.3/147.1 for CH10, m/z 490.3/147.1 for GLYM and m/z 581.3/919.5 for actin were simultaneously monitored by triple quadrupole mass spectrometer. The x- or y-axis shows retention time (minutes) or signal intensity (count per second), respectively. Arrow heads indicate MRM chromatogram peaks specific to each protein-derived peptide. Area used in quantification analysis was shown on each panel.

Supplemental Figure 6 Results of MRM-based quantification analysis for 4 proteins.

Area of MRM peak specific to SPTA2, GLYM, CH10, or PTMS was measured and subsequently normalized by that of actin. The normalized protein concentration values were plotted for 8 clinical samples. The *p*-values were calculated by Student's t-test and shown on each panel.

Supplemental Figure 7 Endogenous expression levels of calpain-2 and alpha-II spectrin.

Western blotting analysis was performed using anti-CAN2 or anti-SPTA2 antibody. The 10 μg of cell lysates from 7 cell lines were used.