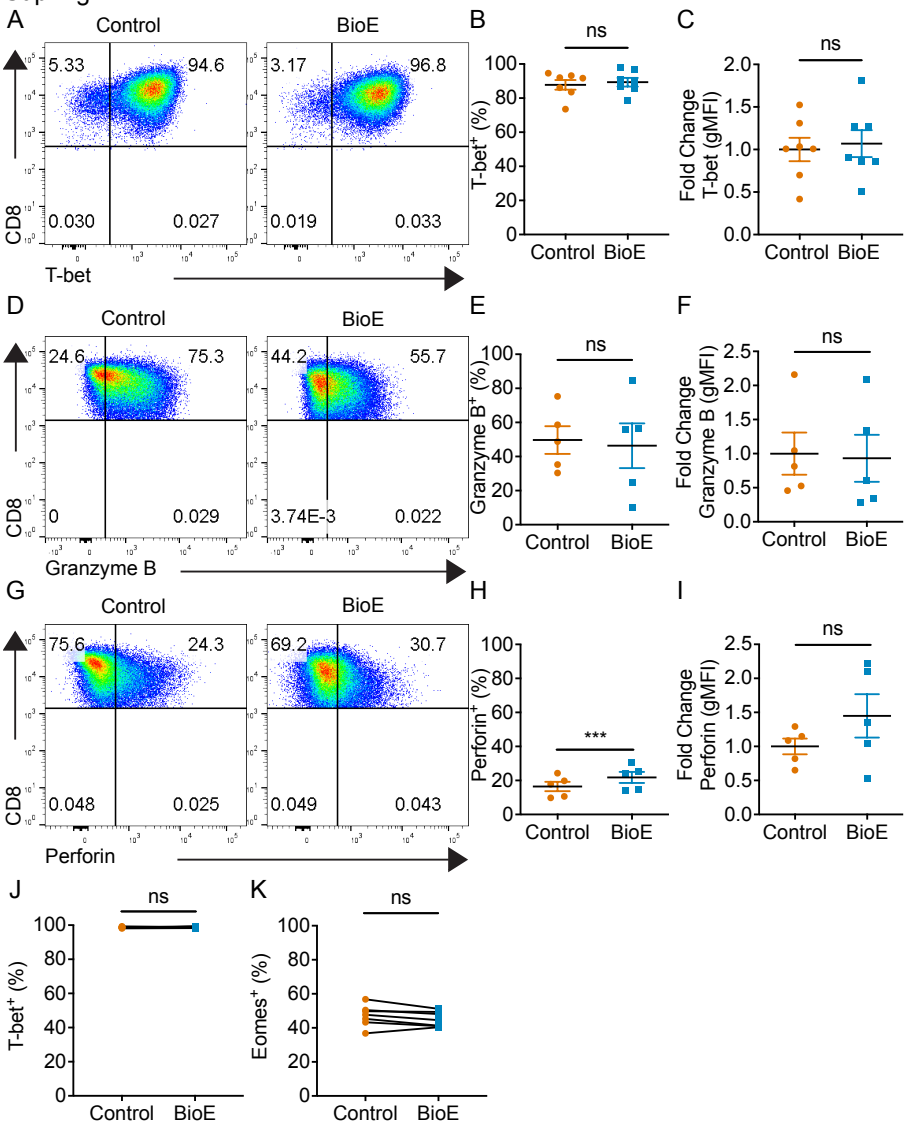
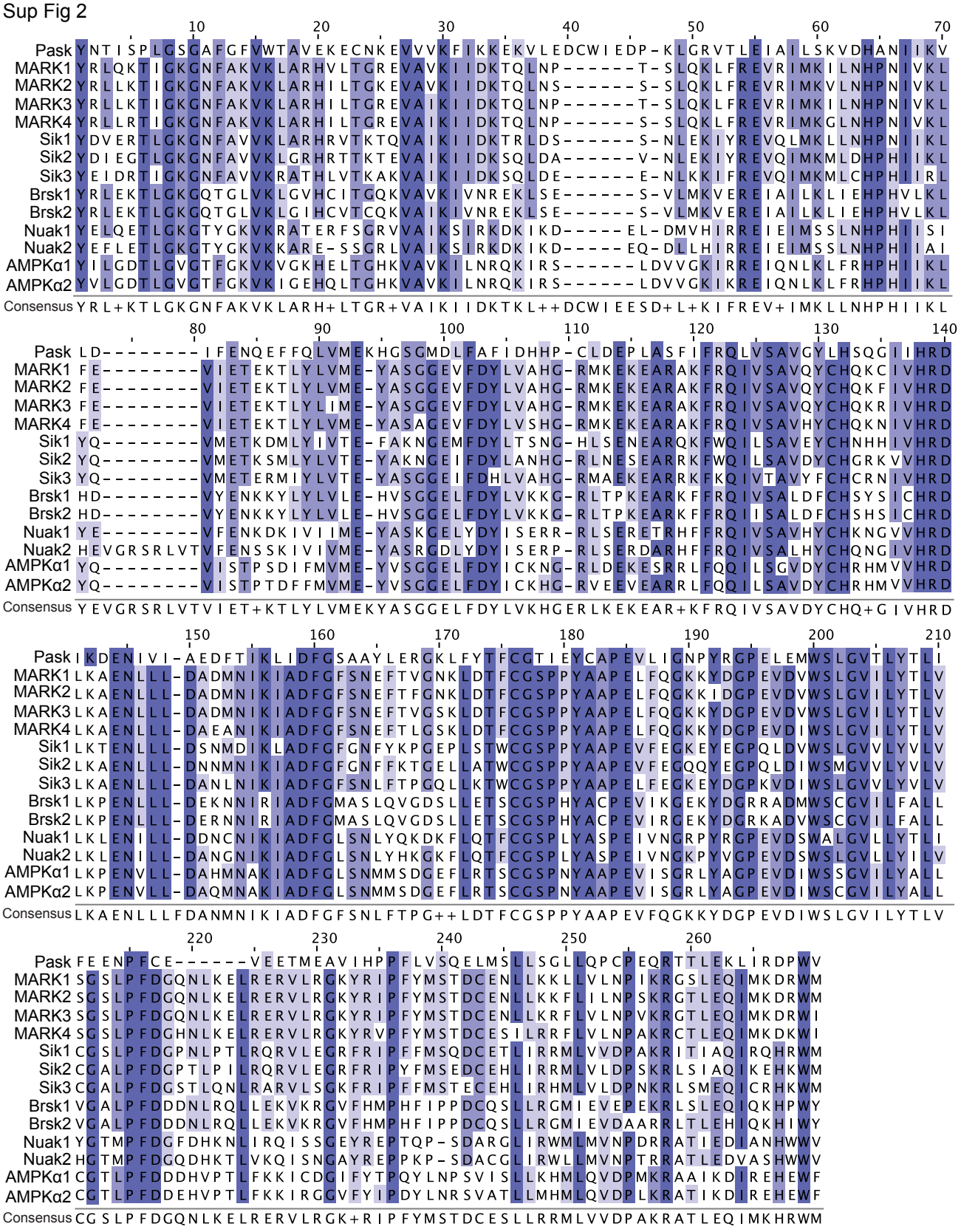
Sup Fig 1



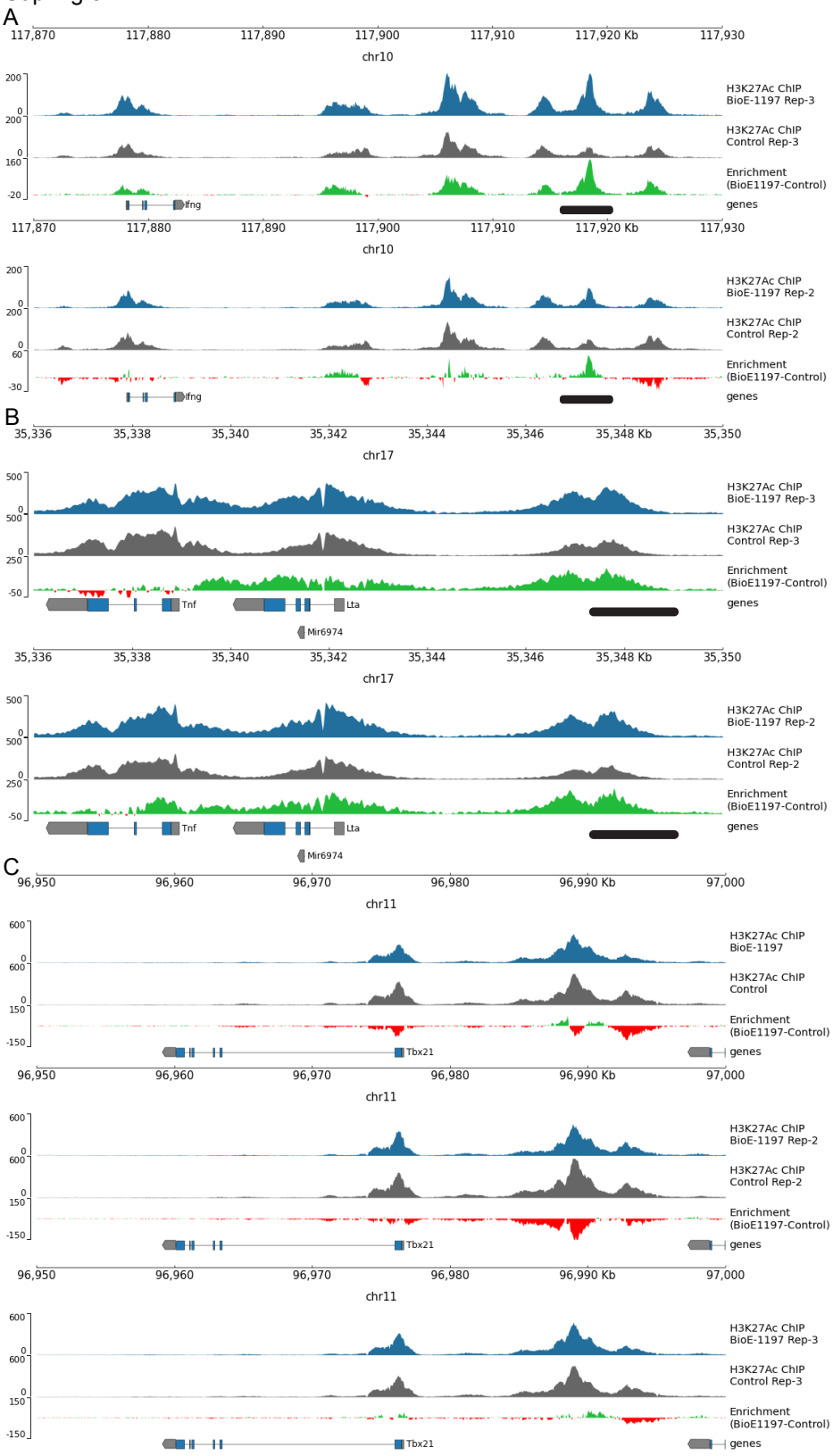
Supplemental Figure 1. Administration of BioE-1197 during T cell differentiation does not alter CD8$^+$ lineage specifying transcription factor or non-cytokine associated effector molecules. (A) Representative intracellular staining dot plots of T-bet in CD8$^+$ T cells on day six after activation and differentiation in control (DMSO) or BioE-1197 (50µM) conditions. (B) Quantification of the percent of T-bet positive cells represented in A across independent experiments. (C) Quantification of the fold change in gMFI of T-bet by CD8$^+$ T cells represented in A across independent experiments. (D) Representative intracellular staining dot plots of Granzyme B for CD8$^+$ T cells on day six after activation and differentiation in control (DMSO) or BioE-1197 (50µM) conditions. (E) Quantification of the percent of Granzyme B positive cells represented in D across independent experiments. (F) Quantification of the fold change in gMFI of Granzyme B by CD8$^+$ T cells represented in D across independent experiments. (G) Representative intracellular staining dot plots of Perforin for CD8$^+$ T cells on day six after activation and differentiation in control (DMSO) or BioE-1197 (50µM) conditions. (H) Quantification of the percent of Perforin positive cells represented in G across independent experiments. (I) Quantification of the fold change in gMFI of Perforin by CD8$^+$ T cells represented in G across independent experiments. (J) Quantification of the percent of T-bet positive cells across ten mice within one representative experiment. (K) Quantification of the percent of Eomes positive cells across ten mice within one representative experiment. Each dot represents values from an independent experiment, summary data are presented as the mean (black line) with SEM error bars (B-C, E-F, H-I). Each dot represents an individual mouse within one experiment and presented results are representative of one independent experiment (J-K). Paired t-test (B-C, E-F, H-K). *p ≤ 0.05, **p ≤ 0.01, ***p ≤ 0.001, ****p ≤ 0.0001, ns = not significant.

Sup Fig 2



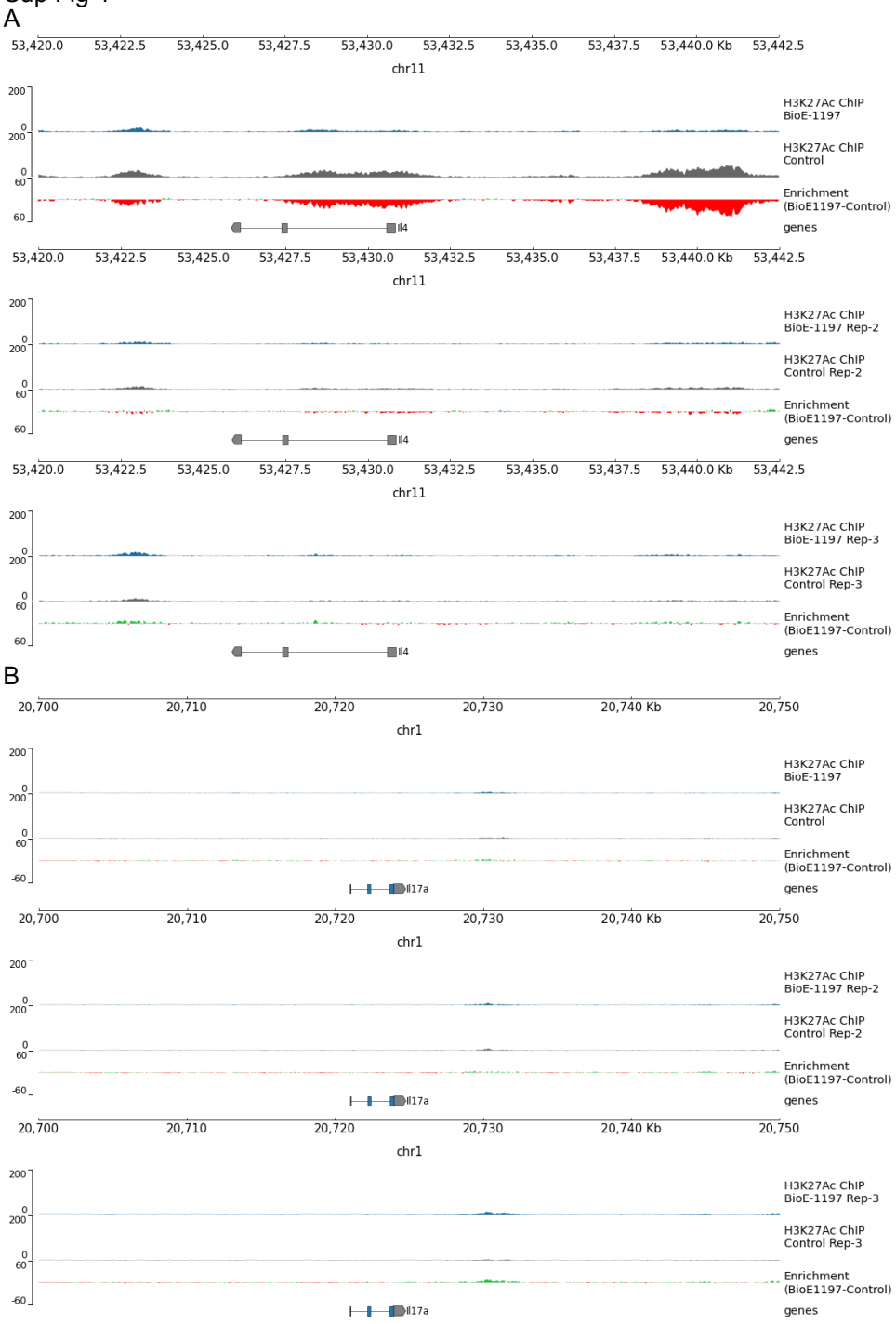
Supplemental Figure 2. Multiple sequence alignment of the kinase domains of PASK and LKB1 activated members of the ARK family. Coloring denotes percent identity.

Sup Fig 3



Supplemental Figure 3. H3K27Ac marks in CD8$^+$ T cell lineage specific genes. (A) H3K27Ac mark deposition within the *Ifng* loci in control and BioE-1197 (50μM) differentiated CD8$^+$ T cells on day six after activation and differentiation. (B) H3K27Ac mark deposition within the *Tnf* loci in control and BioE-1197 (50μM) differentiated CD8$^+$ T cells on day six after activation and differentiation. (C) H3K27Ac mark deposition within the *Tbx21* loci in control and BioE-1197 (50μM) differentiated CD8$^+$ T cells on day six after activation and differentiation.

Sup Fig 4



Supplemental Figure 4. H3K27Ac marks in CD8$^+$ T cell non-lineage associated cytokine genes. (A) H3K27Ac mark deposition within the *Il4* loci in control and BioE-1197 (50μM) differentiated CD8$^+$ T cells on day six after activation and differentiation. (B) H3K27Ac mark deposition within the *Il17a* loci in control and BioE-1197 (50μM) differentiated CD8$^+$ T cells on day six after activation and differentiation.