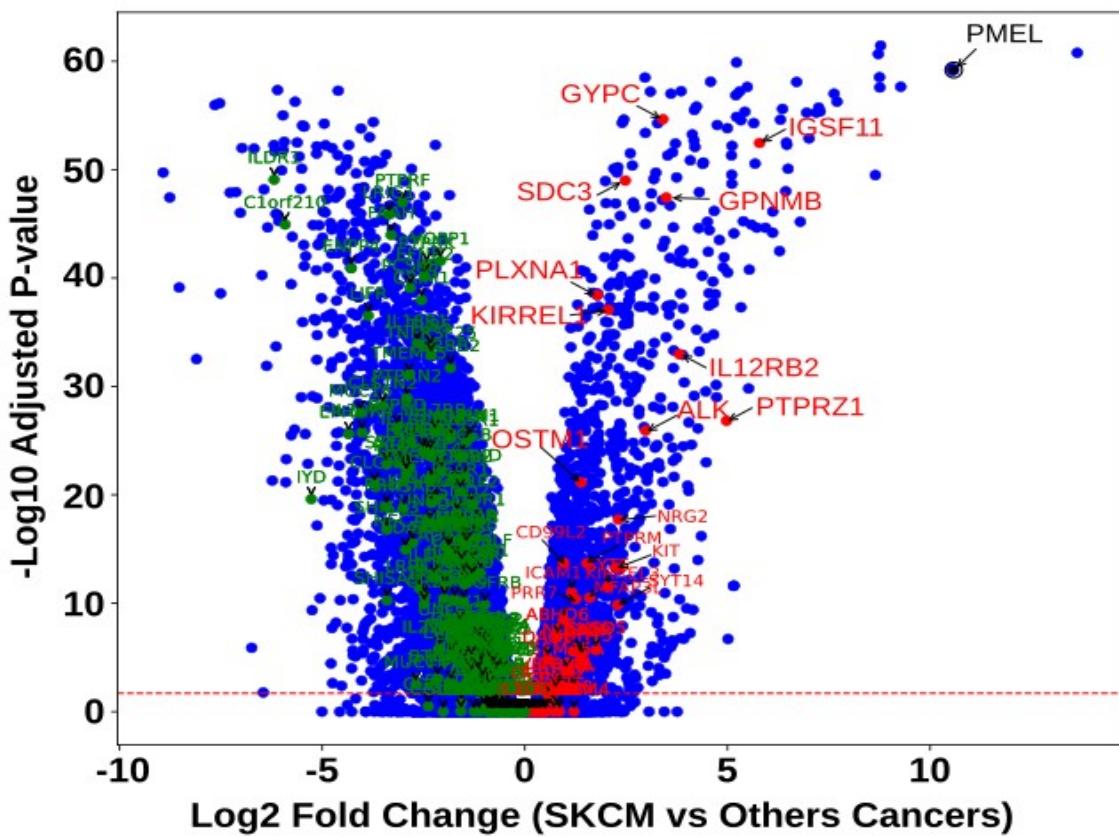


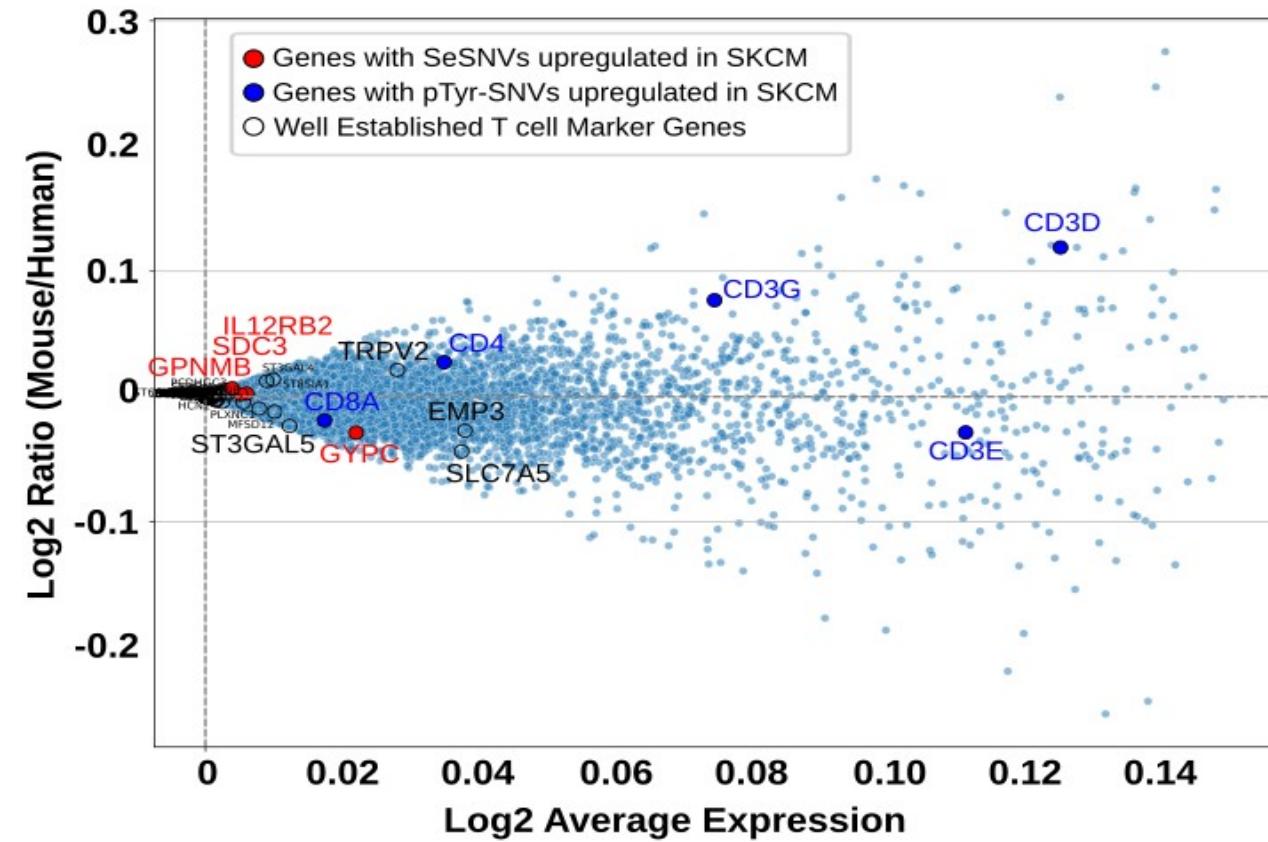
A

Volcano Plot: SKCM vs Other Cancer



B

MA Plot (Ratio vs. Average)



Online Figure-5. Assessing mRNA expression of membrane proteins enriched in melanoma tumors and T lymphocytes. (A) Volcano plot of RNA-Seq TCGA data showing gene expression enriched in tumours of skin cancers (n=103) (in red) over tumours from other cancer types (n=7831). The volcano plot displays the differential gene expression between SKCM and other cancer types. The x-axis represents the log₂ fold change in expression levels between SKCM and other cancers, while the y-axis shows the -log₁₀ of the adjusted p-values obtained from the Mann-Whitney U test. The p-values were adjusted for multiple comparisons using the Bonferroni correction. Genes with a significant difference in expression (adjusted p-value < 0.05) are highlighted above the red dashed line.

(B) MA plot showing evolutionarily conserved expression pattern of genes expressed in T lymphocytes. The MA plot visualises the RNA-Seq data log₂ fold change in gene expression geometric mean of multiple samples between mouse (n=150) and human (n=183) T lymphocytes. Each point represents a gene, with the x-axis showing the average log₂ expression level across species and the y-axis representing the log₂ ratio of expression between mouse and human. Genes known to harbour SeSNVs and upregulated in SKCM are highlighted in red, while other upregulated genes known to harbour pTyr-SNVs are shown in black. Genes well-established as T cell specific markers (CD8A, CD4, CD3D, CD3E, CD3G) are highlighted in blue.