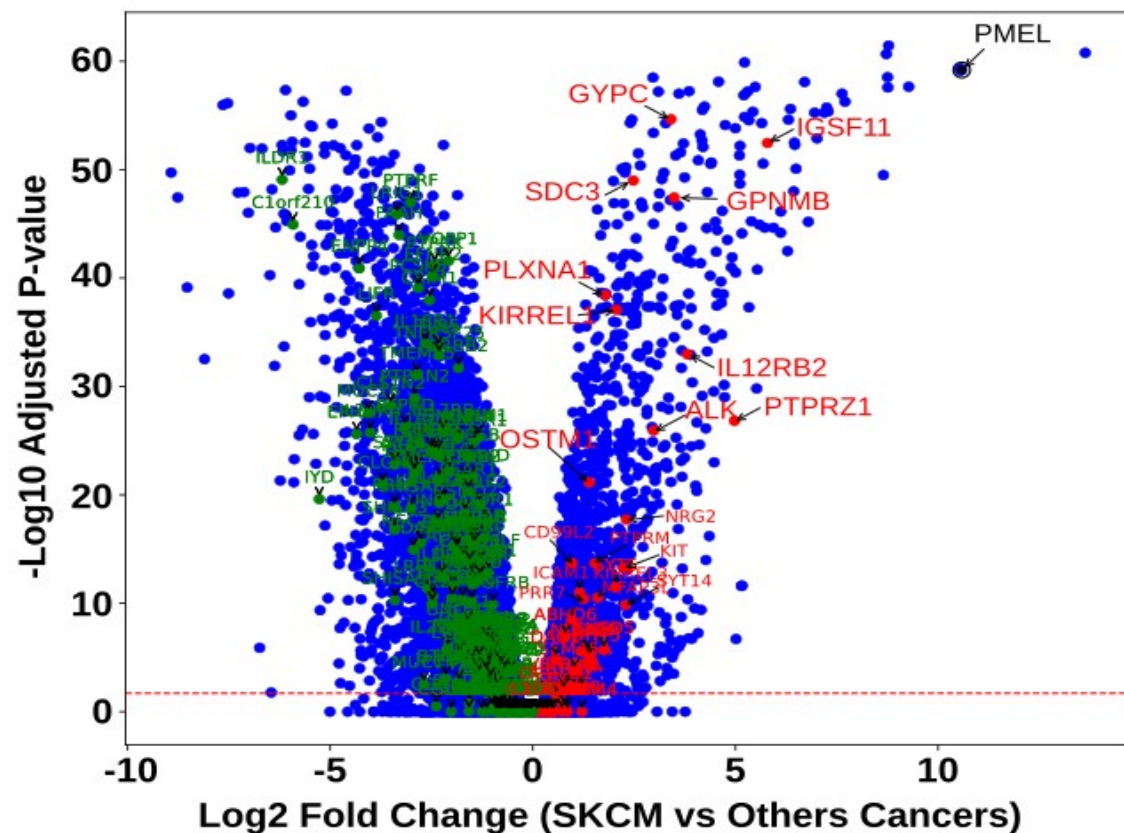


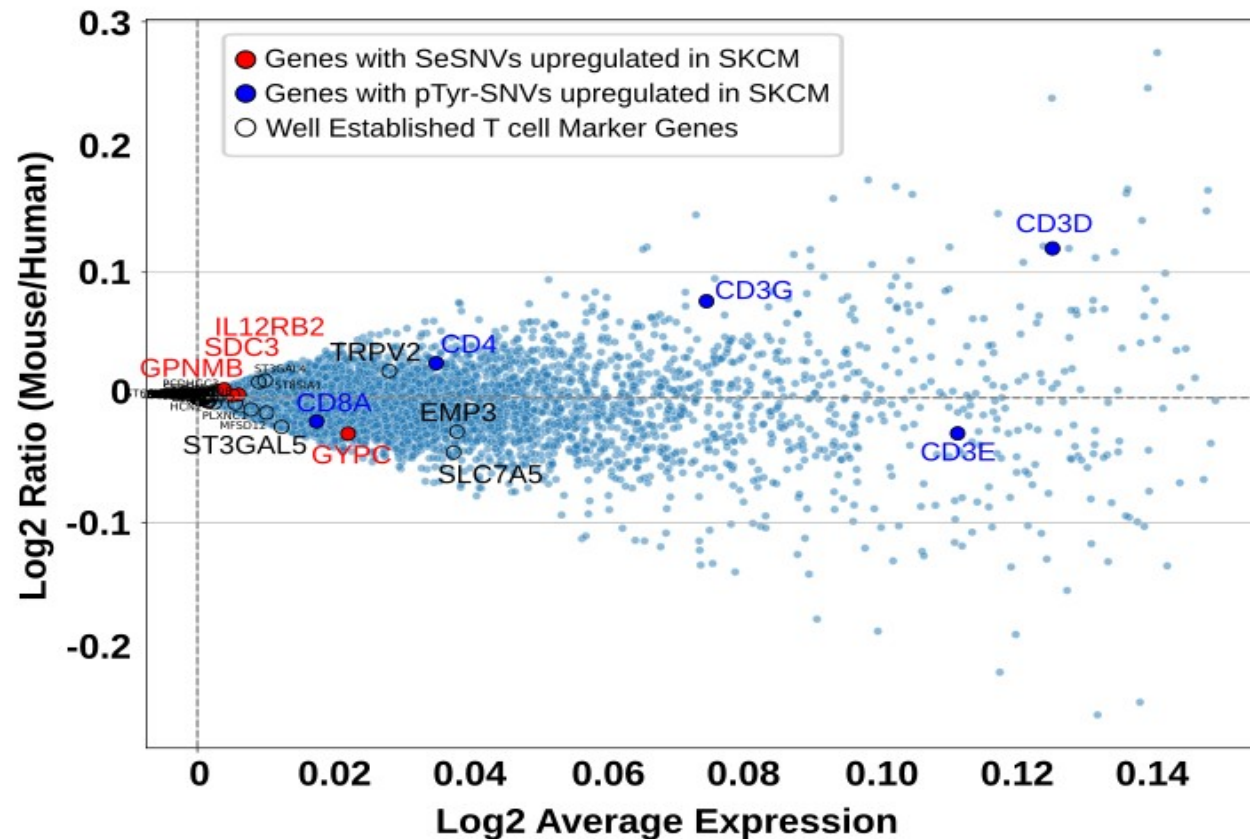
A

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 $-\log_{10}$ 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.