Supplementary

Table S1 Primers of molecular targets used in this study

Genes	Sense (5'-3')	Anti-sense (3'-5')
NFKB2	ACACGTACCGACAGACAACC	TTCCTTCACCTCTGCTGTGC
BCL3	GCCTTGTCGTCCCCCTGG	GCAGTAAGGCTCCGGGGTAG
KLF3	CCCTGTCTCAGTGTCATACCC	CTTGTTCACCGTGAGGTCCA

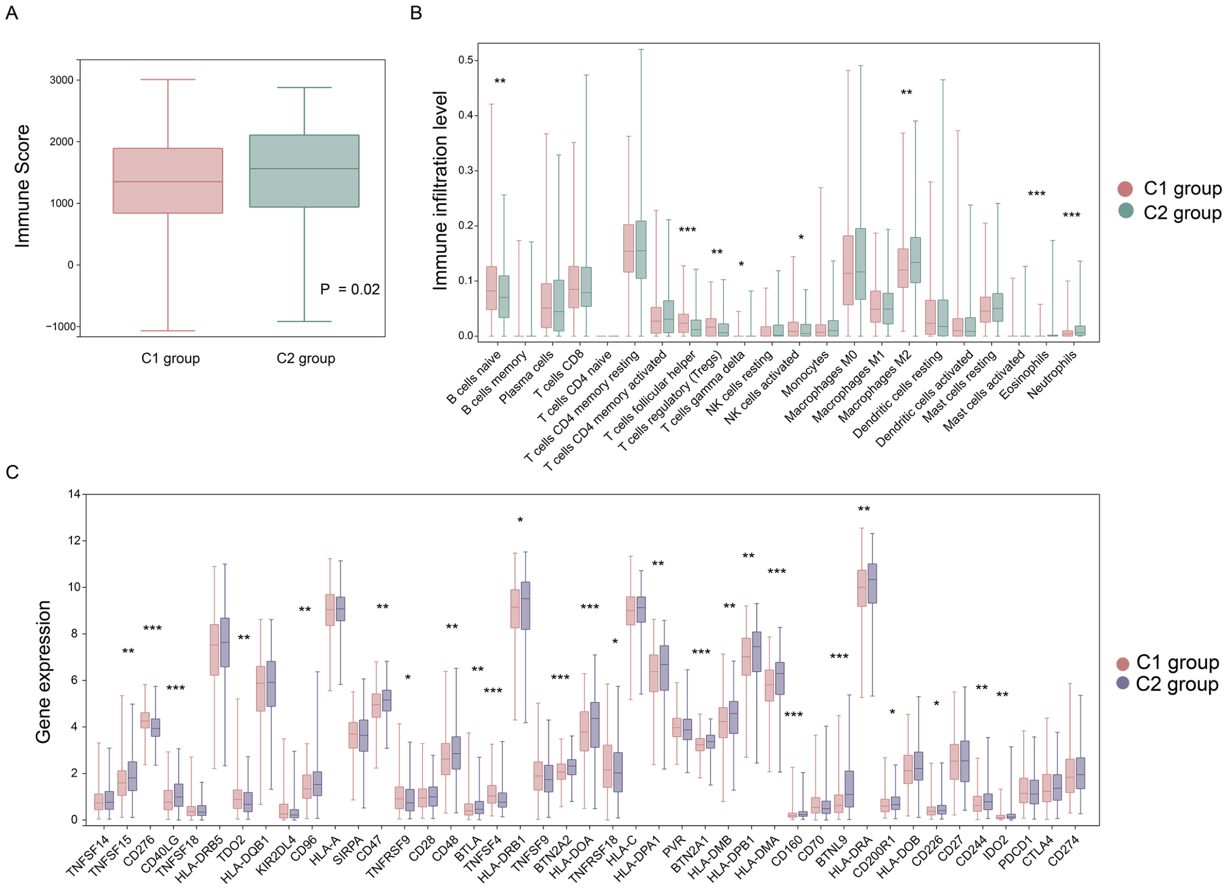

Figure S1 Correlation between MRIM subgroups and immune cell infiltration. (A) Immune scores across MRIM subtypes. (B) Comparison of tumor-infiltrating immune cell populations between the C1 and C2 groups. (C) Expression levels of immune checkpoint markers in the C1 and C2 groups. *, 0.01≤P<0.05; **, 0.001≤P<0.01; ***, P<0.001.

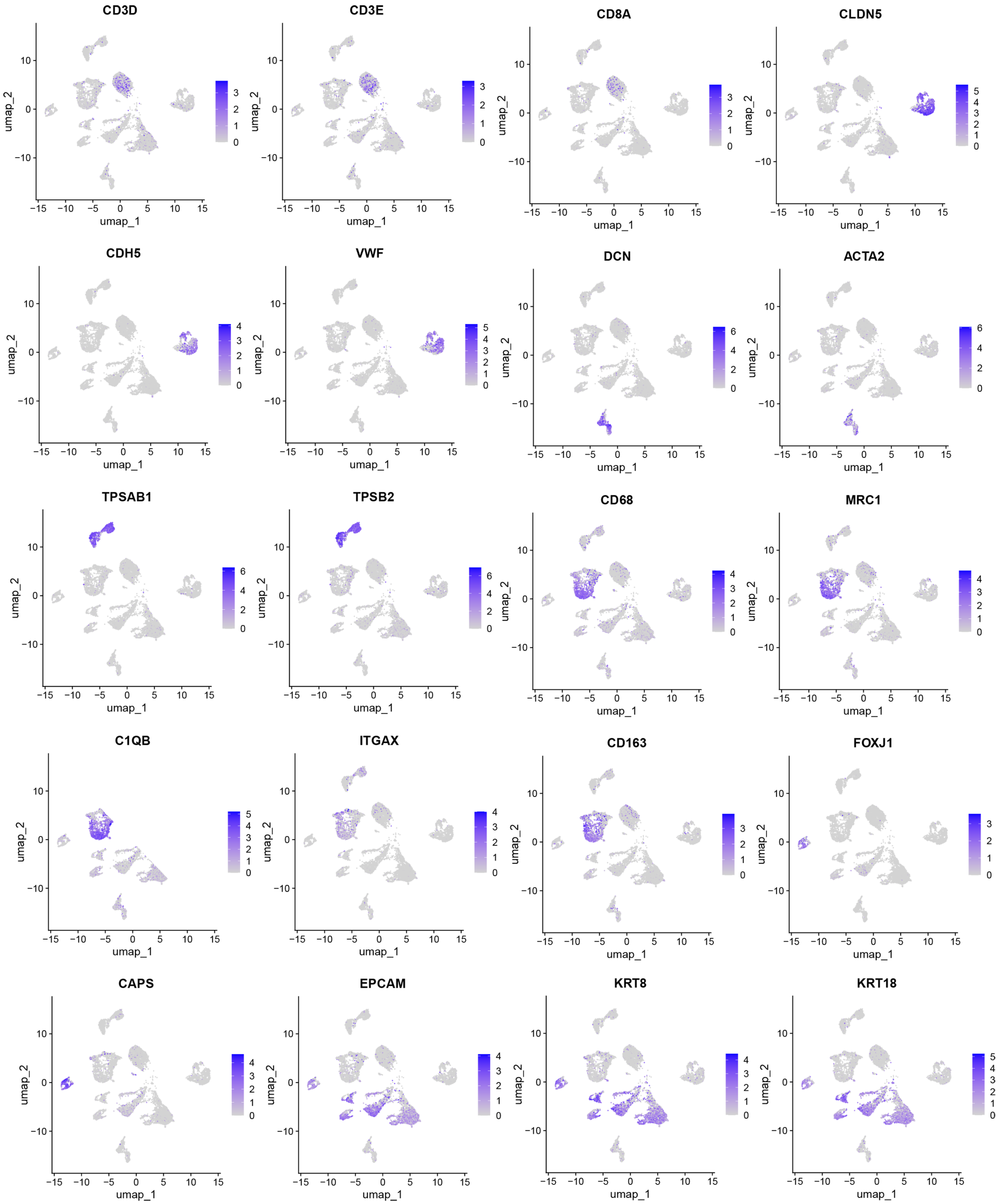

Figure S2 The expressions of cell type-specific marker genes in the UMAP dimension.

https://dx.doi.org/10.21037/tcr-2025-357

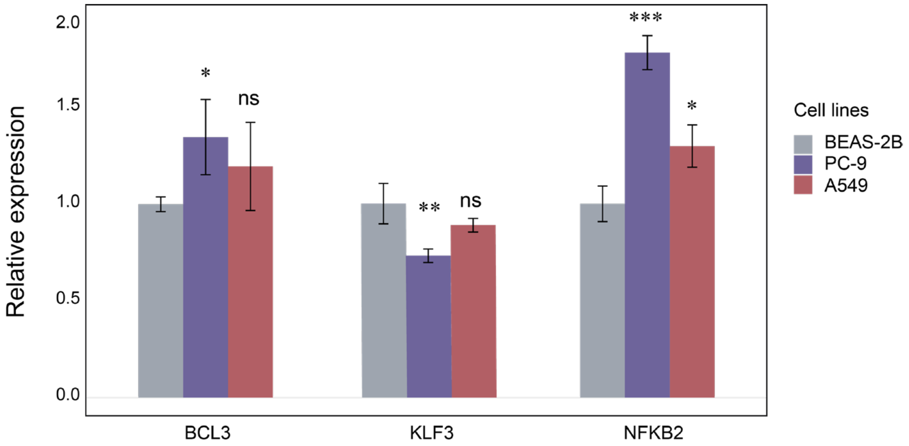

Figure S3 Relative expression levels of BCL3, KLF3, and NFKB2 in LUAD cell lines. *, 0.01≤P<0.05; **, 0.001 ≤P<0.01; ***, P<0.001.

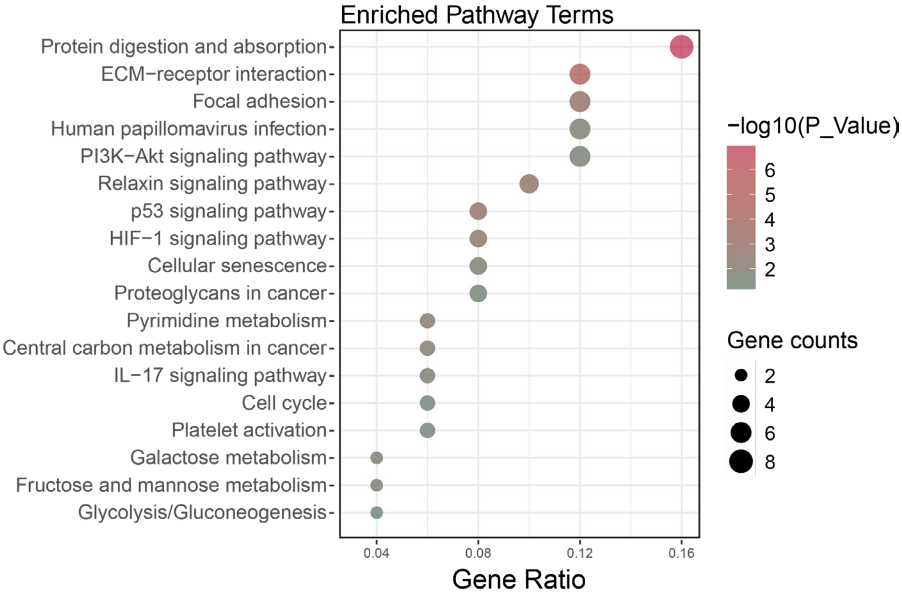

Figure S4 KEGG pathway enrichment analysis between C1 and C2 MRIM subtypes.

https://dx.doi.org/10.21037/tcr-2025-357

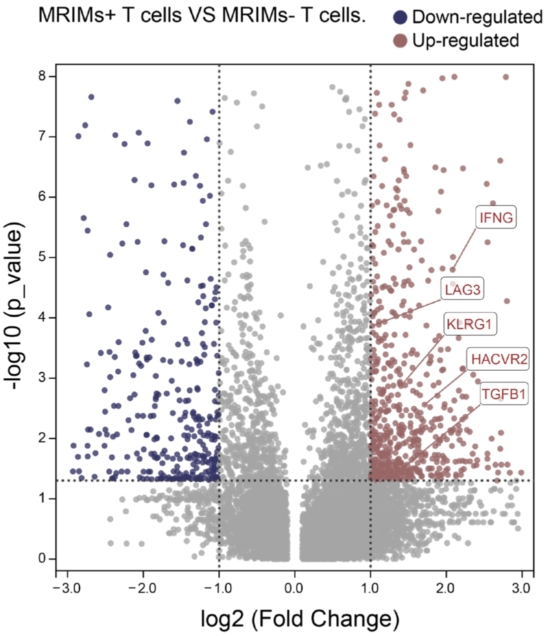

Figure S5 Volcano plot of differentially expressed genes between MRIMs+ and MRIMs− subclusters within T cells.

https://dx.doi.org/10.21037/tcr-2025-357