

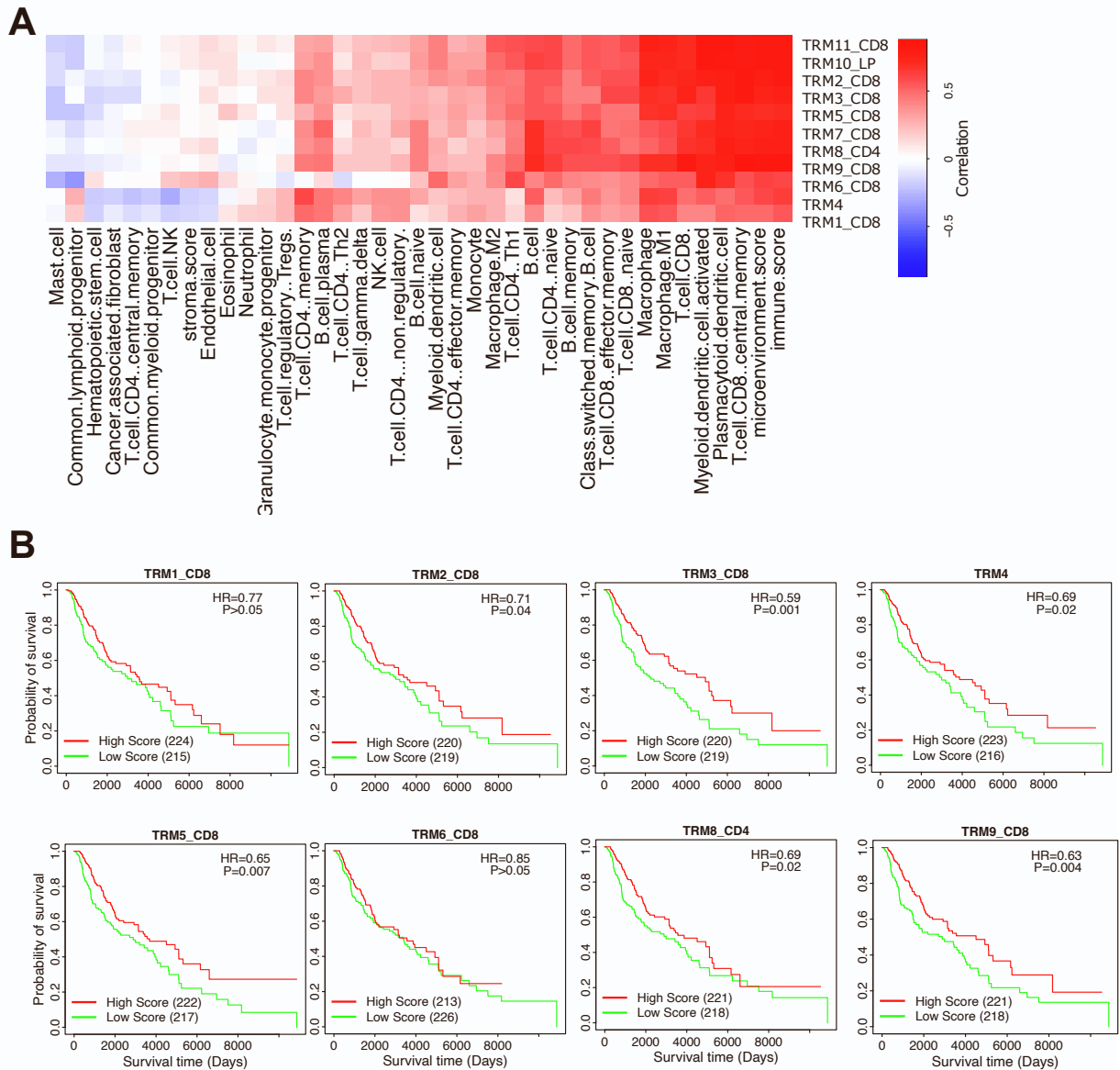
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**Supplemental information**

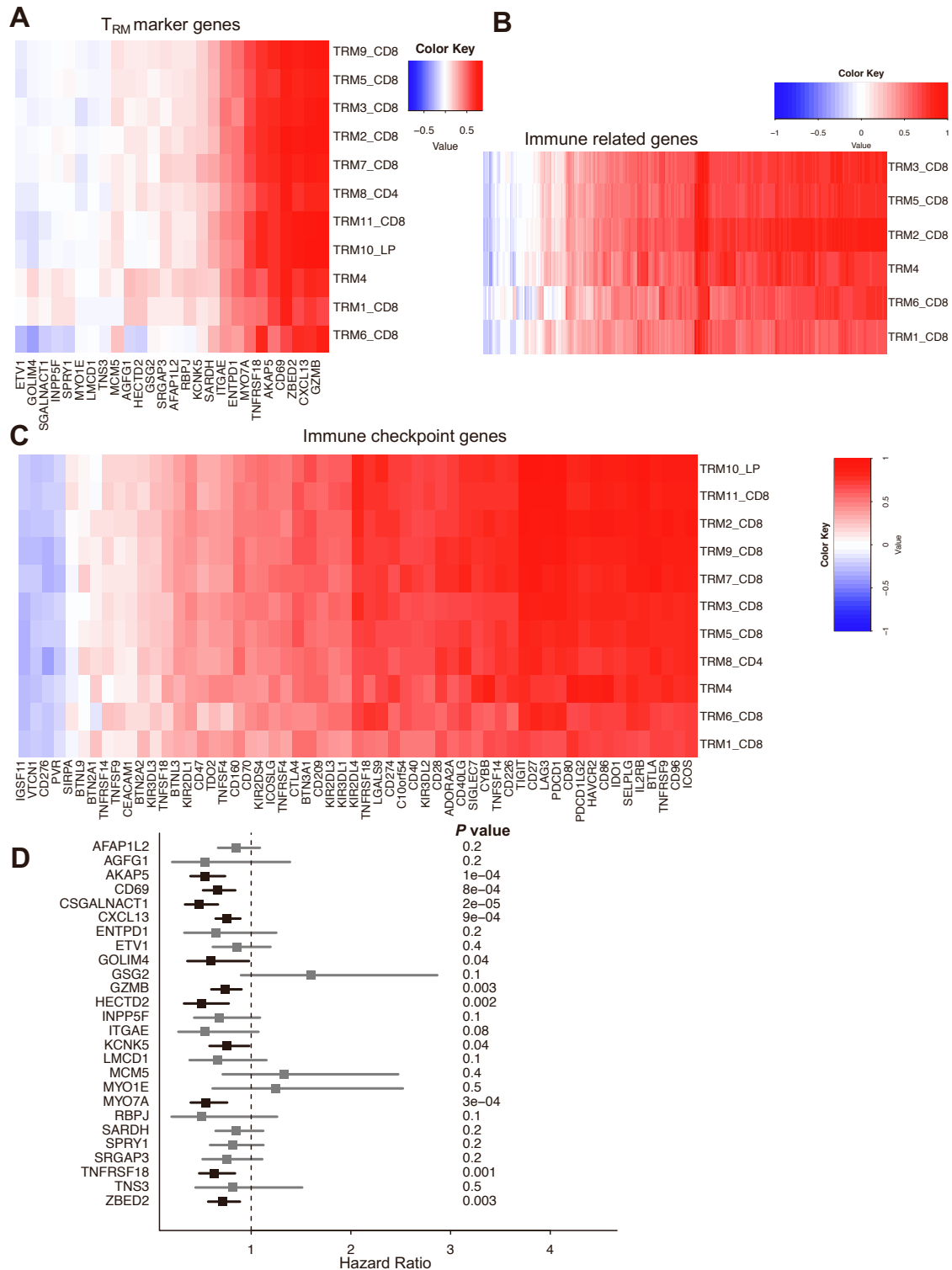
**Tissue-resident memory T cell signatures  
from single-cell analysis associated  
with better melanoma prognosis**

**Chongming Jiang, Cheng-Chi Chao, Jianrong Li, Xin Ge, Aidan Shen, Vadim Jucaud, Chao Cheng, and Xiling Shen**

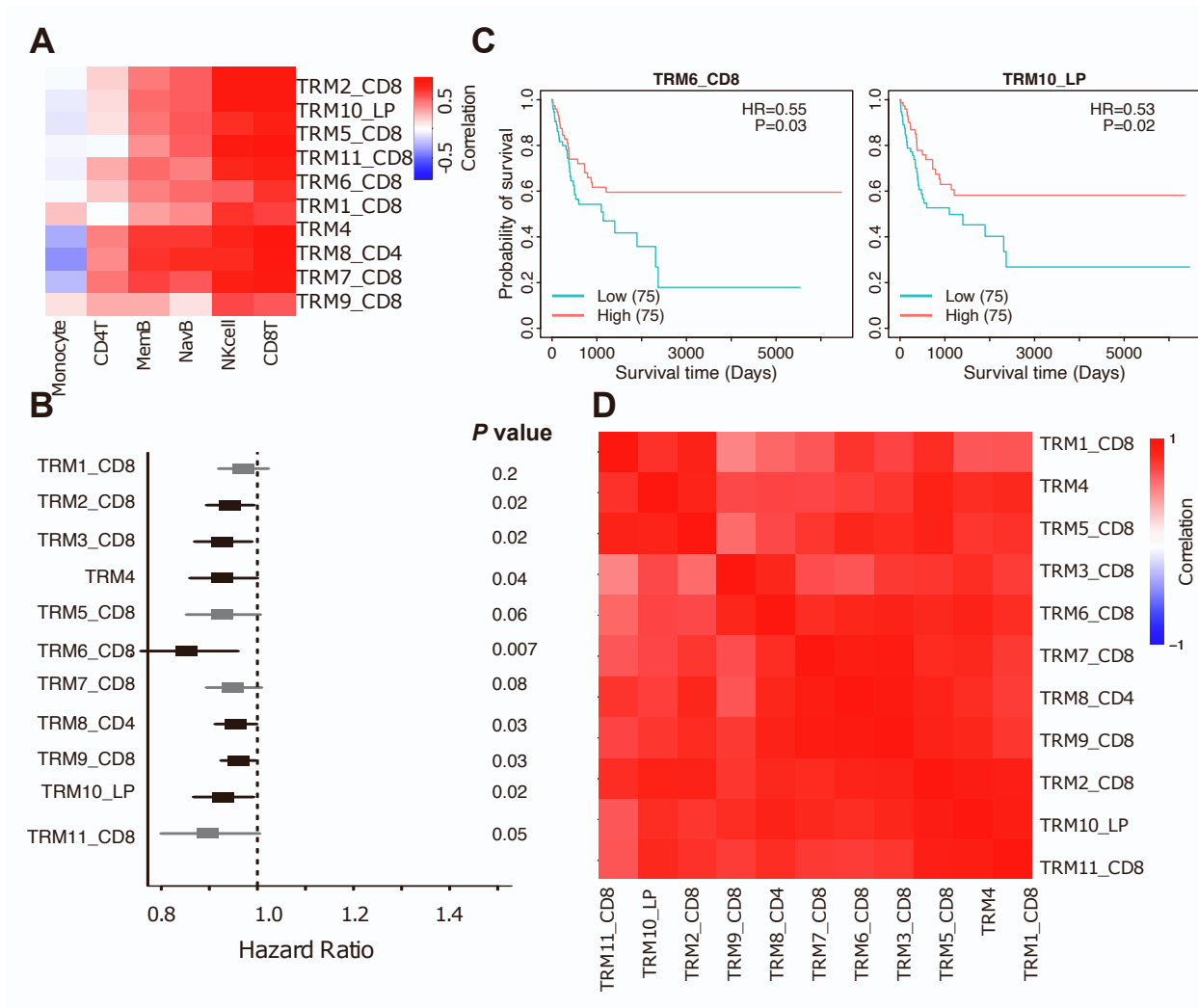
## Supplementary Figures



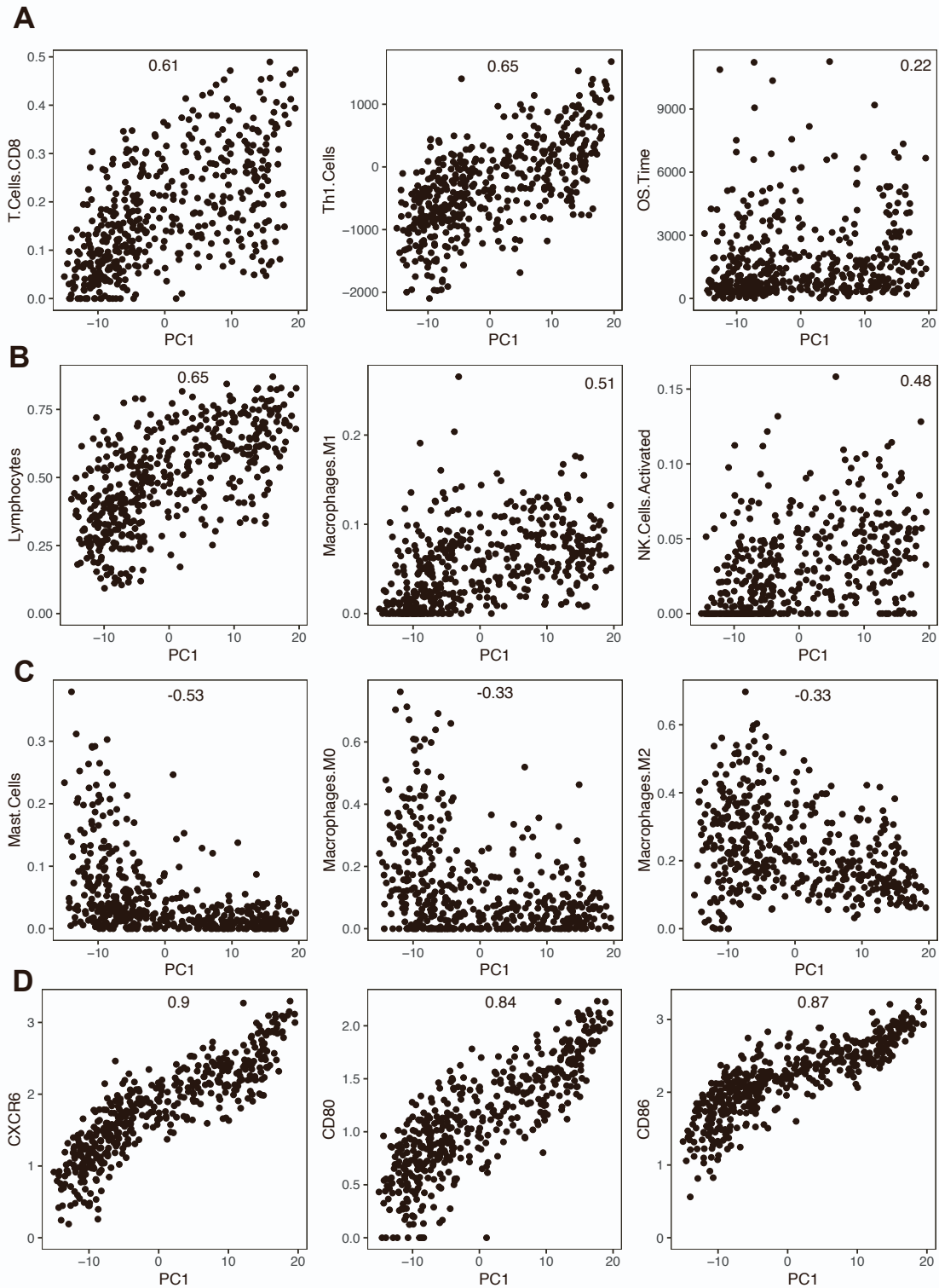
**Figure S1.  $T_{RM}$  signatures are in high correlation with the CD8 T and CD4 T cells in TCGA-SKCM by all three tumor infiltration methods, related to Figure 3. A. xCell method. B. Survival analysis for all 11  $T_{RM}$  signatures.**



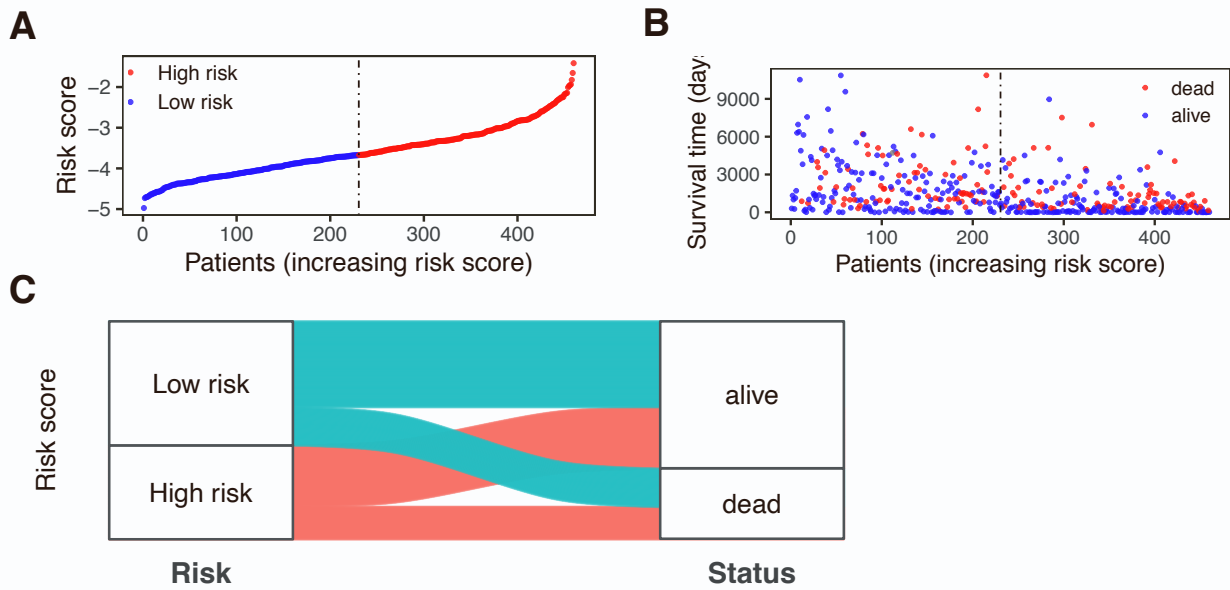
**Figure S2. The correlation of  $T_{RM}$  abundance with the  $T_{RM}$  marker genes, immune checkpoint genes, and immune related genes, related to Figure 3. A.** The correlation of  $T_{RM}$  abundance with the  $T_{RM}$  marker genes. **B.** The correlation of  $T_{RM}$  abundance with significant immune related genes. **C.** The correlation of  $T_{RM}$  abundance with immune checkpoint genes. **D.** Forest plot showing that many of the  $T_{RM}$  marker genes were associated with good prognosis.



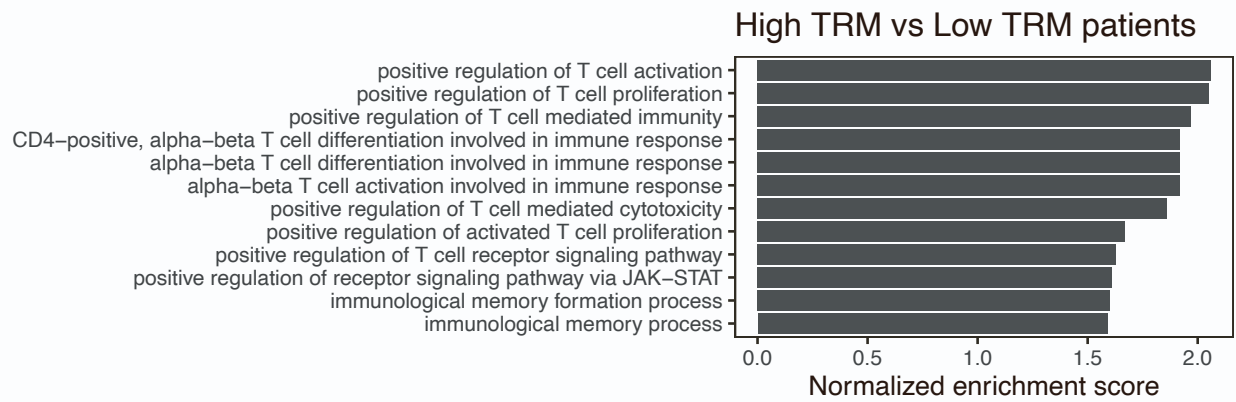
**Figure. S3. T<sub>RM</sub> abundance is positively associated with melanoma prognosis in melanoma datasets. GSE65904, related to Figure 3.** A. The correlation of T<sub>RM</sub> signatures with immune infiltration in GSE65904. B. The forest plot shows that T<sub>RM</sub> signatures were associated with good prognosis. C. Survival analysis for two individual T<sub>RM</sub> signatures. D. The correlation of the T<sub>RM</sub> signatures with each other.



**Figure S4. The correlation of  $T_{RM}$  cells and immune cells in the melanoma, related to Figure 4. A.** SCC between PC1 and CD8+ T cells, Th1 cells, and patients' survival time. **B.** SCC between PC1 and lymphocytes, M1 macrophages, and activated NK cells. **C.** SCC between PC1 and mast cells, M0 and M2 macrophages. **D.** SCC between PC1 and resident NK cell marker gene, CXCR6, M1-like tumor associate macrophage marker genes, CD80 and CD86.



**Figure S5. Survival analysis of the 20-gene risk score model in malignant melanoma patients, related to Figure 5.** A. The risk score distribution in high- and low-risk groups. B. The survival status distribution with the risk score. C. The relationships among the risk score and survival status in melanoma patients.



**Figure S6. GSEA analysis of high  $T_{RM}$  vs low  $T_{RM}$  patients, related to Figure 7.** High  $T_{RM}$  patients with significant up-regulated memory T cell and immune related pathways in the melanoma.