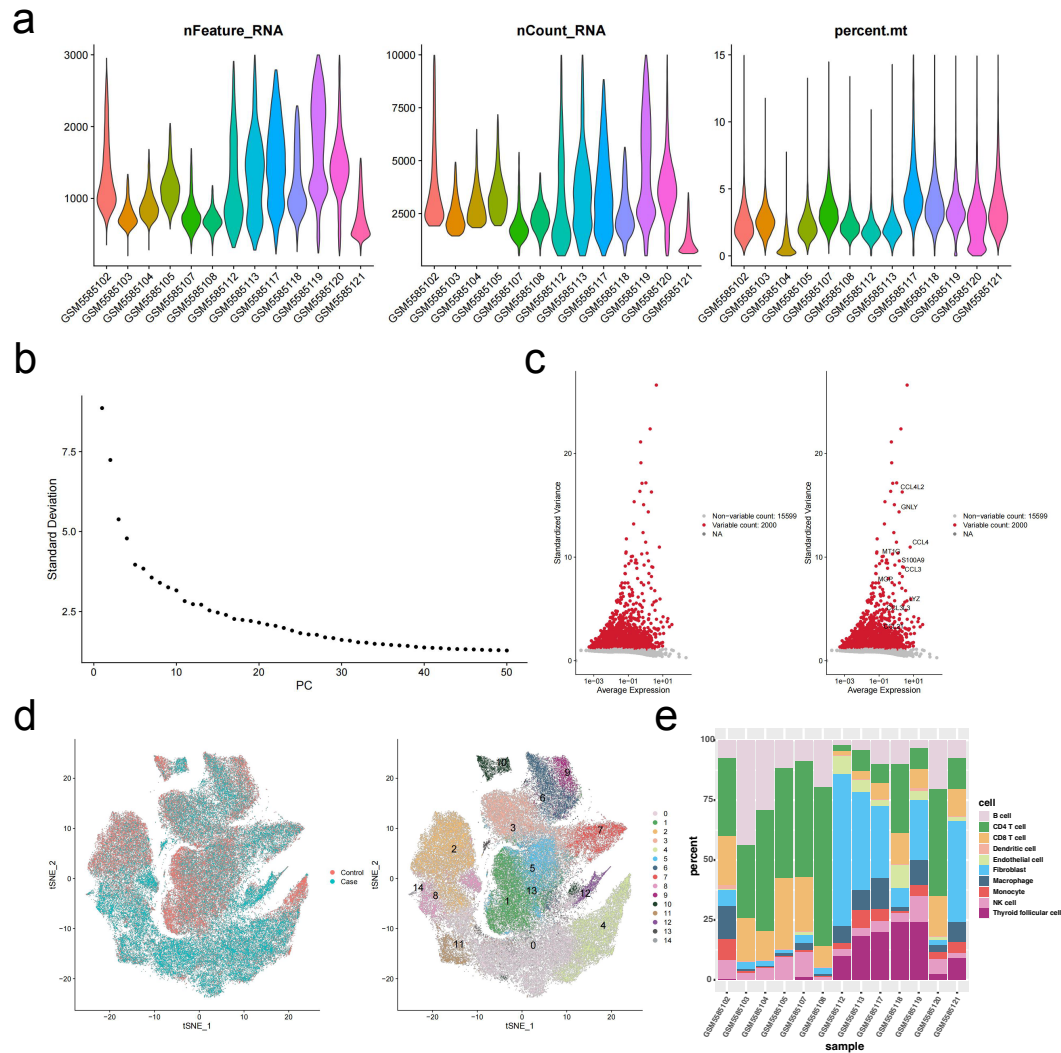


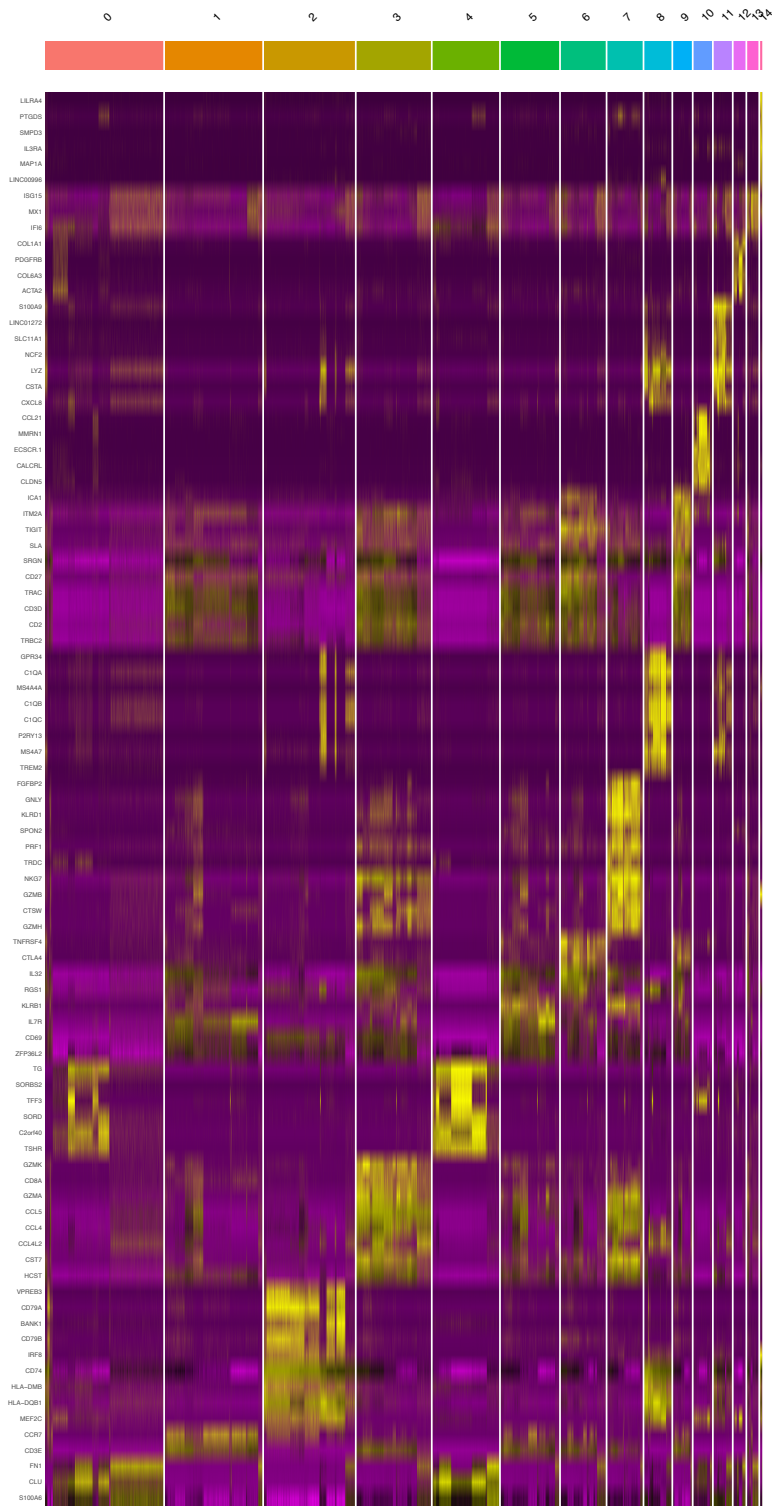
1 Supplementary Figures



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3 **Figure S1. Quality control and cell proportion analysis of single-cell RNA-seq** 4 **data.**

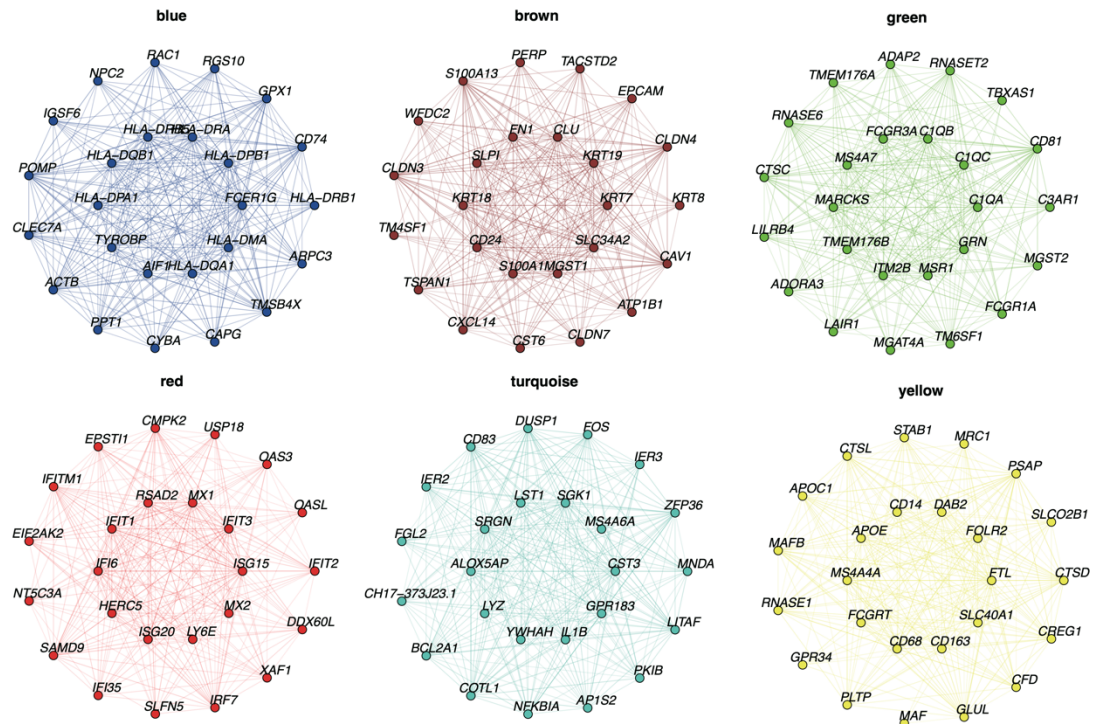
5 (a–d) Quality control metrics of single-cell data, including filtering thresholds, gene
6 counts per cell, and mitochondrial gene content. (e) Stacked bar plot showing the
7 distribution of ten annotated cell types across all samples. The y-axis indicates the
8 relative proportion of each cell type, and the x-axis represents individual samples.



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10 **Figure S2. Heatmap of top marker genes across identified cell clusters.**

11 Expression heatmap showing representative marker genes used to annotate the ten
 12 major cell types identified in the single-cell dataset. indicates relative gene expression
 13 levels.



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15 **Figure S3. Co-expression networks of the six gene modules identified by**
 16 **hdWGCNA.**

17 Network visualization of the top hub genes in each of the six modules (blue, brown,
 18 green, red, turquoise, and yellow) constructed via hdWGCNA. Each node represents
 19 a gene, and each edge represents a significant co-expression relationship. The density
 20 and connectivity within each module reflect the degree of intra-modular co-regulation.

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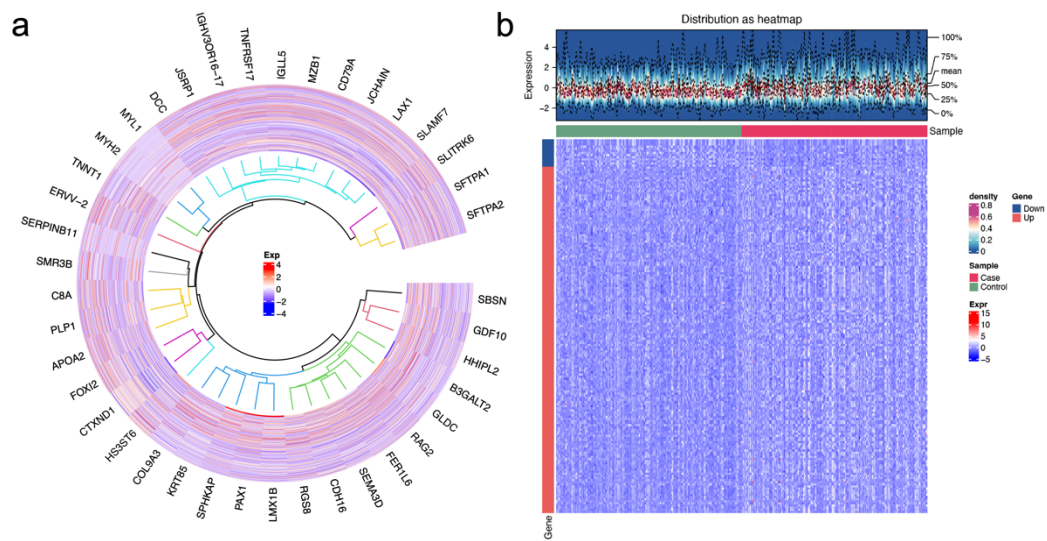
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33 **Figure S4. Visualization of differentially expressed genes between high- and low-**
 34 **risk groups.**

35 (a) Circular dendrogram of DEGs based on hierarchical clustering. Colors represent
 36 gene expression levels, with red indicating upregulation and blue indicating
 37 downregulation in the high-risk group. (b) Heatmap showing the expression profiles of
 38 DEGs across samples.

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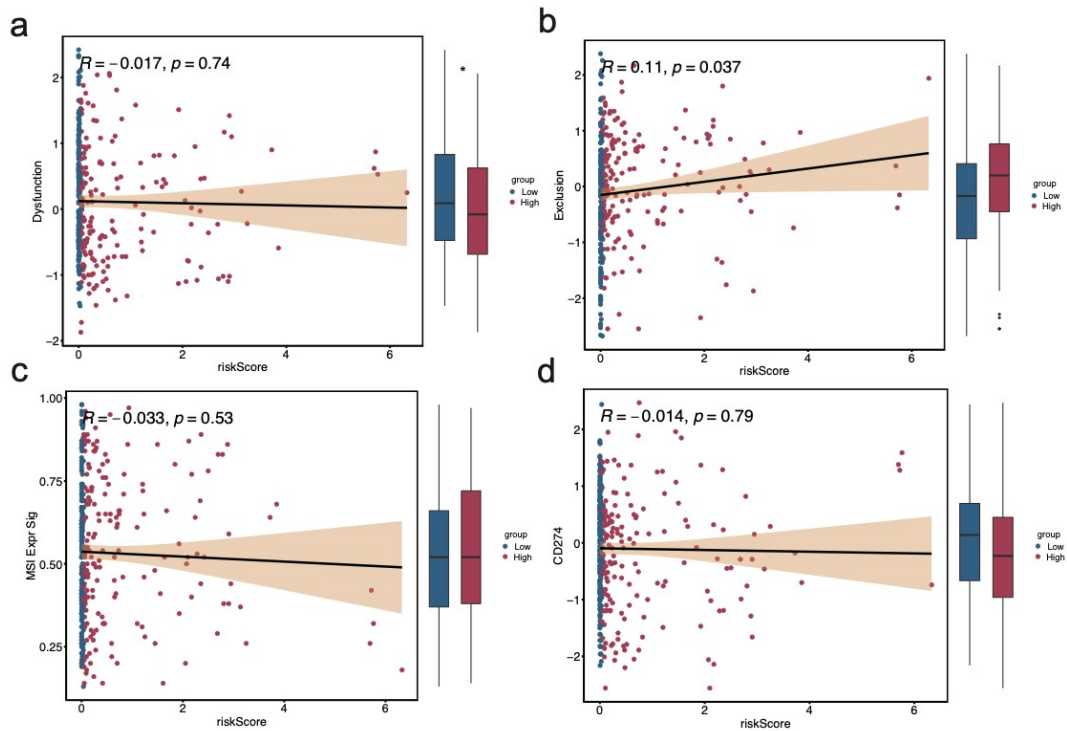
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53 **Figure S5. Correlation between risk score and immunotherapy response**
 54 **indicators.**

55 (a) No significant correlation was observed between risk score and T cell dysfunction
 56 score ($R = -0.017$, $p = 0.74$). (b) A weak but significant positive correlation was found
 57 between risk score and T cell exclusion score ($R = 0.11$, $p = 0.037$). (c) No significant
 58 association was detected between risk score and microsatellite instability (MSI)
 59 expression signature ($R = -0.033$, $p = 0.53$). (d) Risk score was not correlated with
 60 CD274 (PD-L1) expression ($R = -0.014$, $p = 0.79$).

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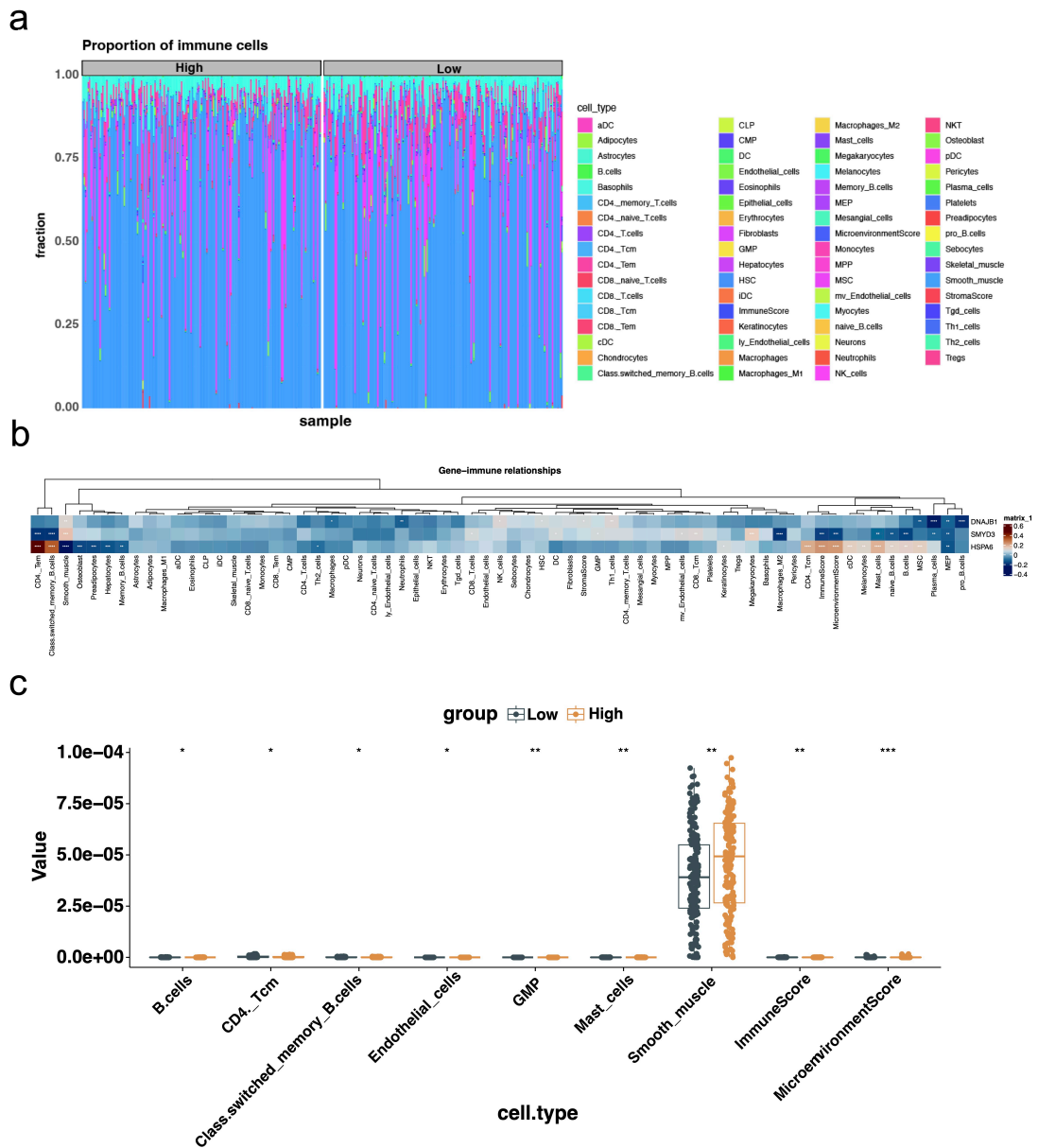
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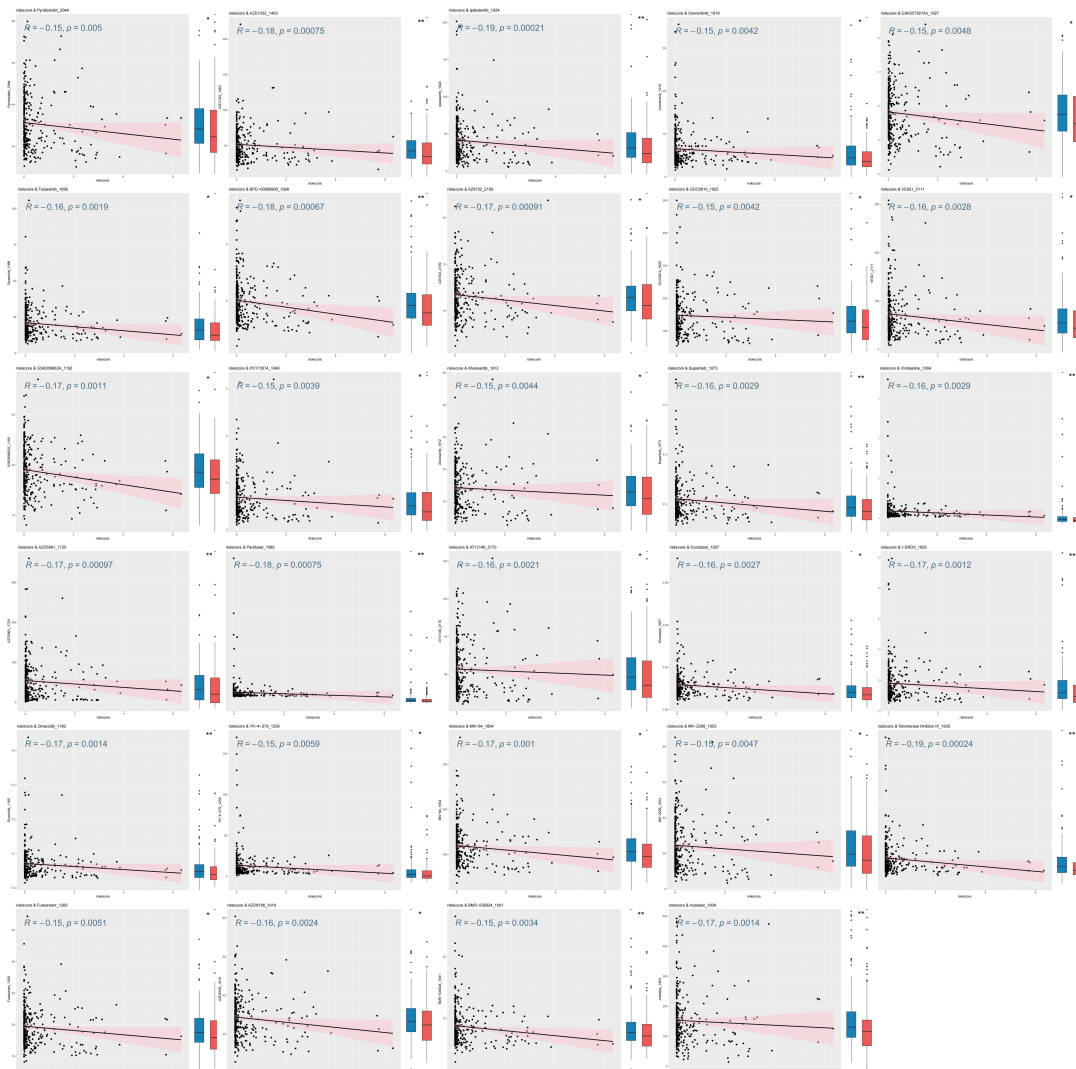
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75 high- and low-risk groups. Significant differences were observed in several immune
76 cell types and microenvironment scores. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

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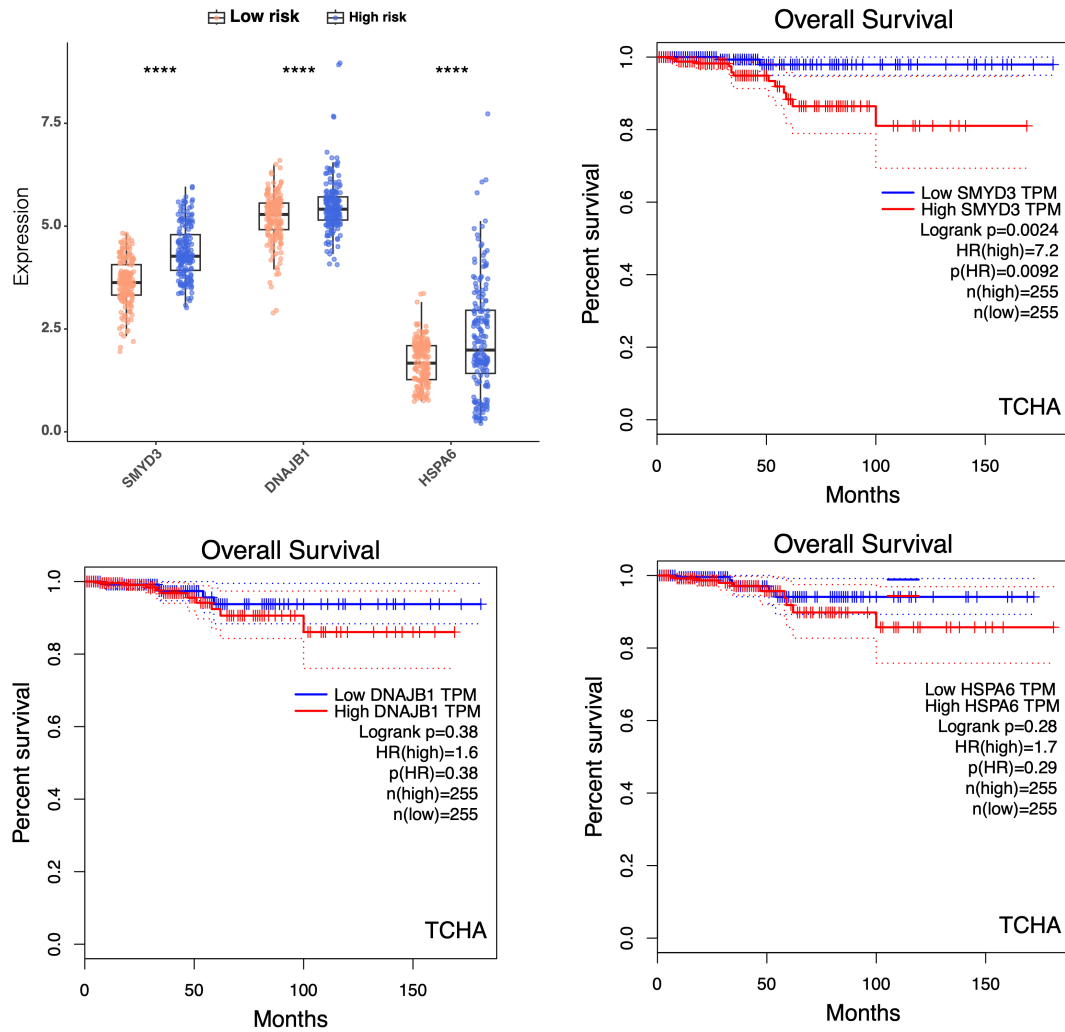


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79 **Figure S7. Expanded drug sensitivity analysis in high- and low-risk groups.**

80 Scatter plots showing the correlation between risk score and predicted IC50 values for

81 29 candidate compounds based on GDSC2 data.



82

83 **Figure S8. Expression patterns and prognostic significance of SMYD3,**
 84 **DNAJB1, and HSPA6 in thyroid cancer.**

85 (a) Boxplots showing the expression levels of SMYD3, DNAJB1, and HSPA6 between
 86 low- and high-risk groups. SMYD3 exhibited significantly higher expression in the high-
 87 risk group compared to the low-risk group. (b–d) Kaplan–Meier survival curves
 88 stratified by the median expression levels of SMYD3 (b), DNAJB1 (c), and HSPA6 (d)
 89 in TCGA-THCA patients. High SMYD3 expression was significantly associated with
 90 poor overall survival (log-rank $p = 0.0024$), while DNAJB1 and HSPA6 showed no
 91 statistically significant prognostic value.