

Figure Legends

Figure S1. The heatmap of 118 DE-DRGs in TCGA.

Figure S2. Forest plot of 36 survival-related DRGs from TCGA-CRC by univariate Cox regression analysis.

Figure S3. Stratification analysis of various clinical features by Kaplan-Meier survival curves for the patients with CRC in the TCGA dataset. A-B. age; C-D. gender; E-F. T stage; G-H. N stage; I-J. M stage; K-L. AJCC stage.

Figure S4. External validation of the 9 DE-DRGs signature in the GEO datasets.

A. The distribution of risk score and patient's survival time. B. The distribution of risk score and patient's survival status. C. The high-risk score was related to poorer OS. D. ROC analysis of the sensitivity and specificity of the OS. E. Heatmap of the DNA repair-related gene expression profiles in prognostic signature for TCGA. F-G. Forest plot of the association between risk factors and survival of TCGA-CRC by univariate and multivariate Cox regression analysis.

Figure S5. Gene expression between Tumor and Normal tissues in TCGA-CRC cohort. *P<0.001**

Figure S6. The protein expression of 7 DRGs between colorectal normal and tumor tissues of in HPA (ESCO2 and MC1R cannot be found in HPA).

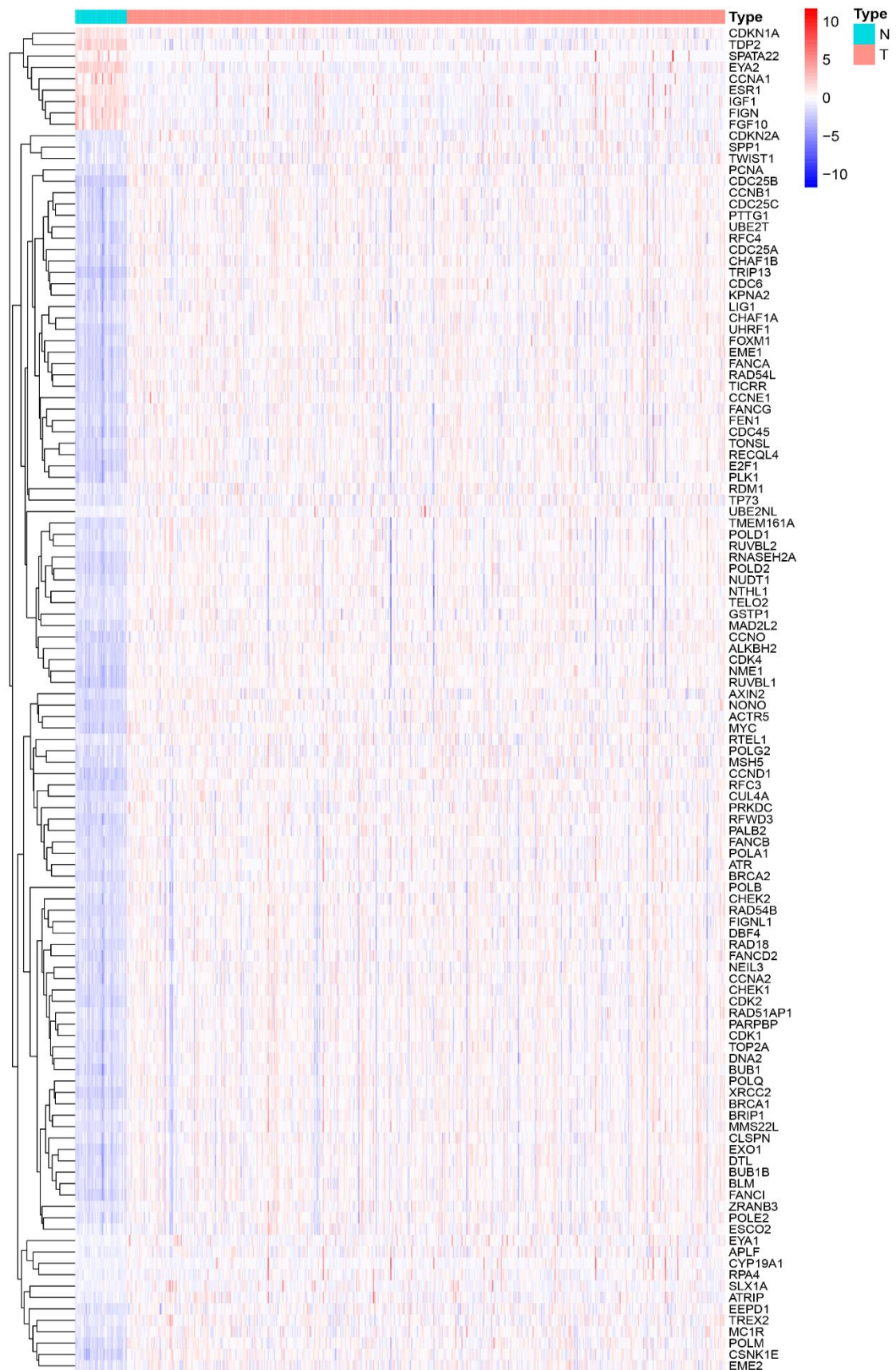


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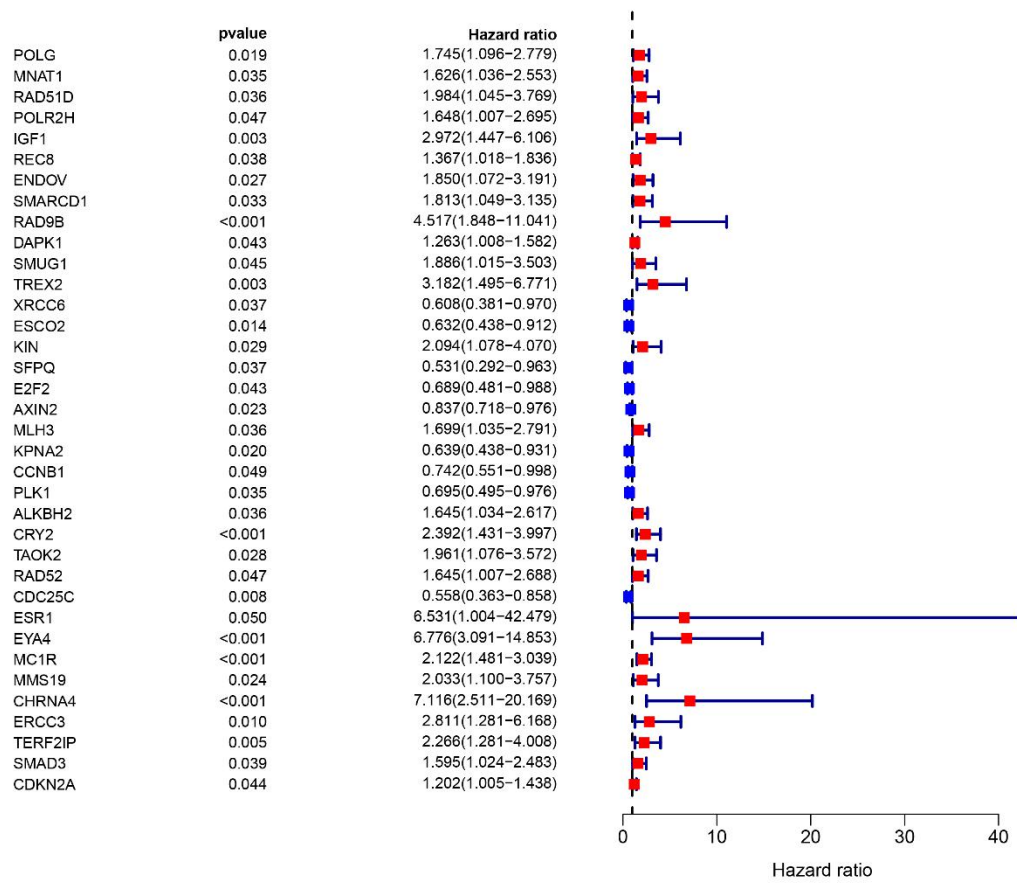


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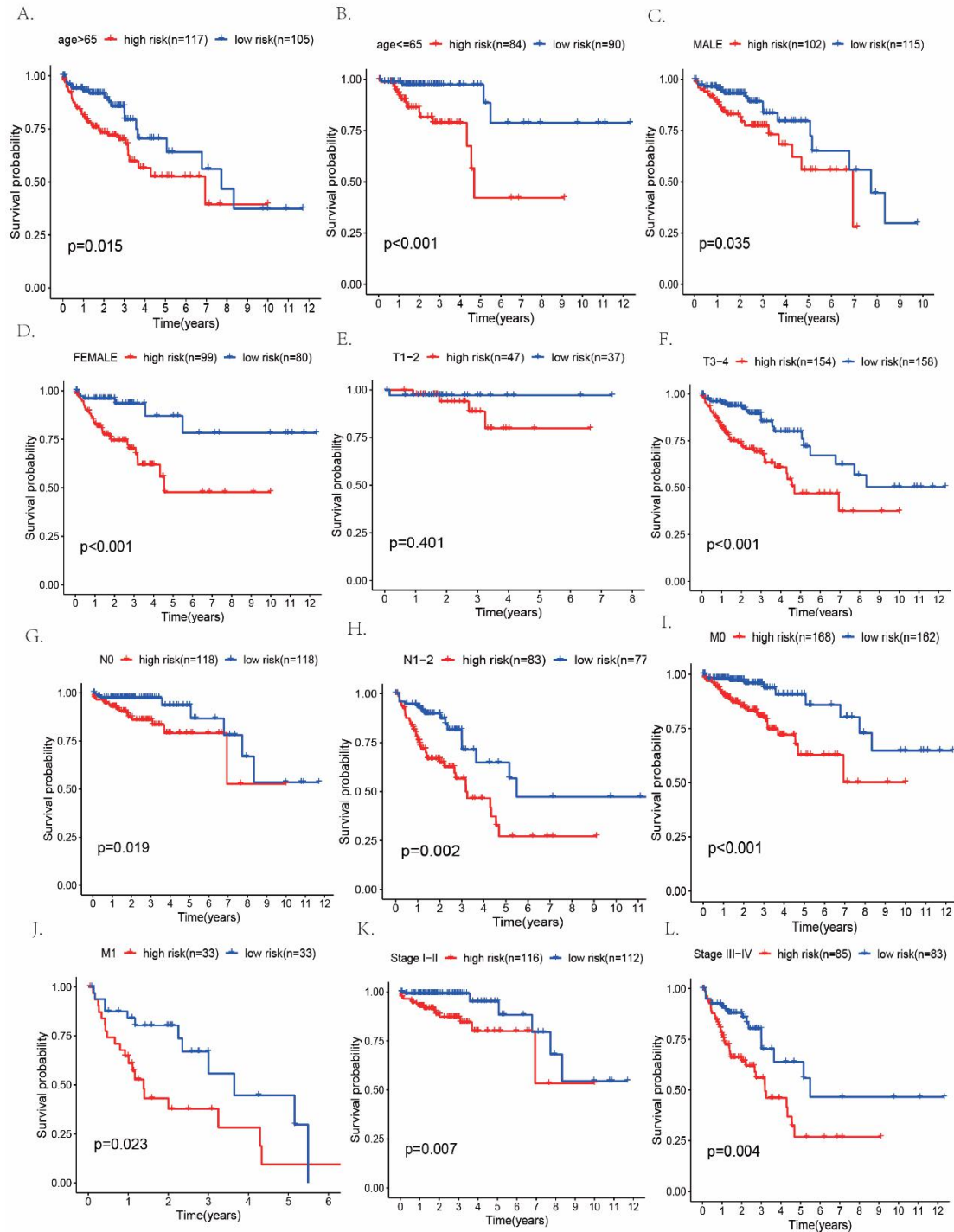


Figure S3. Stratification analysis of various clinical features by Kaplan-Meier survival curves for the patients with CRC in the TCGA dataset. A-B. age; C-D. gender; E-F. T stage; G-H. N stage; I-J. M stage; K-L. AJCC stage.

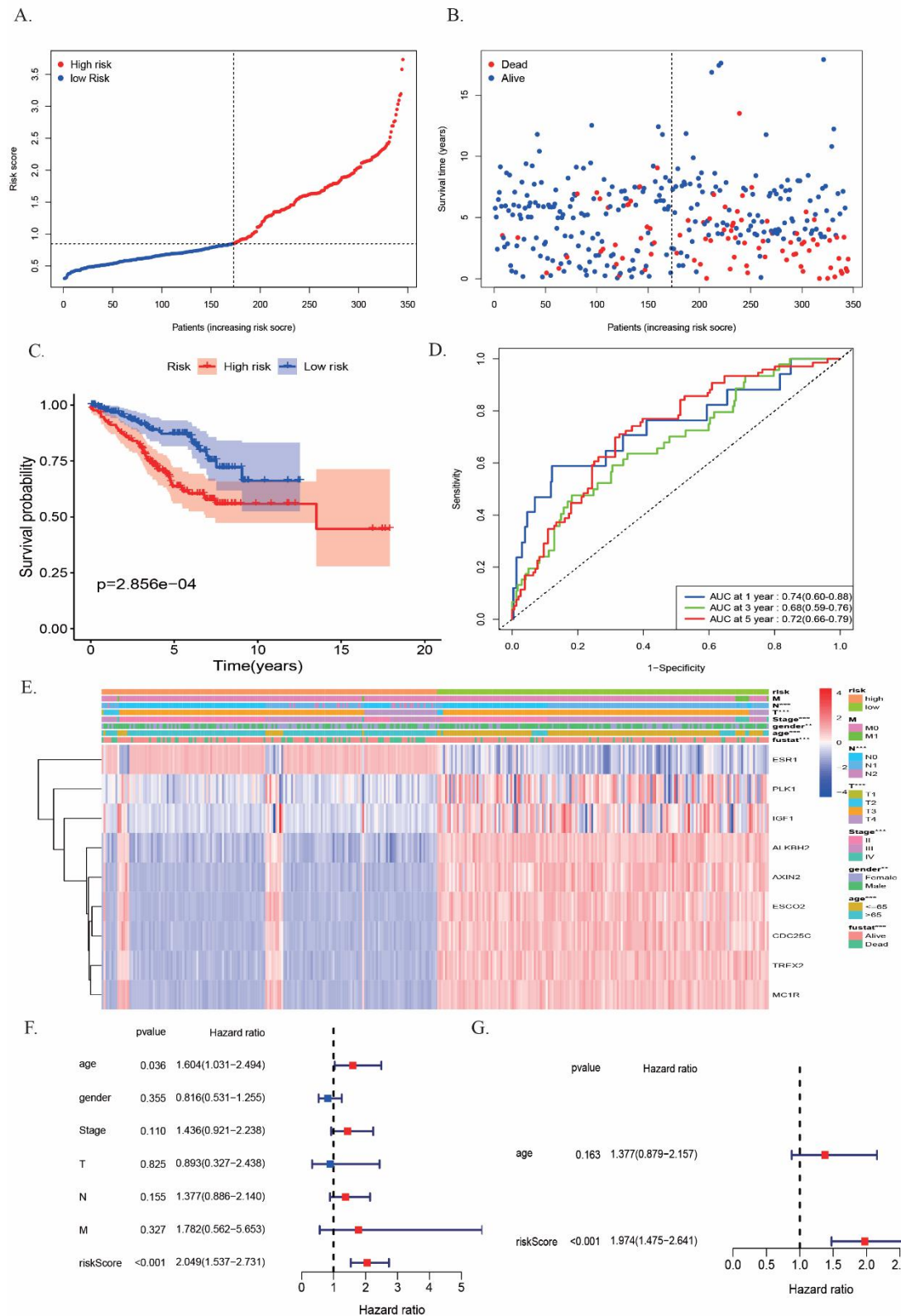


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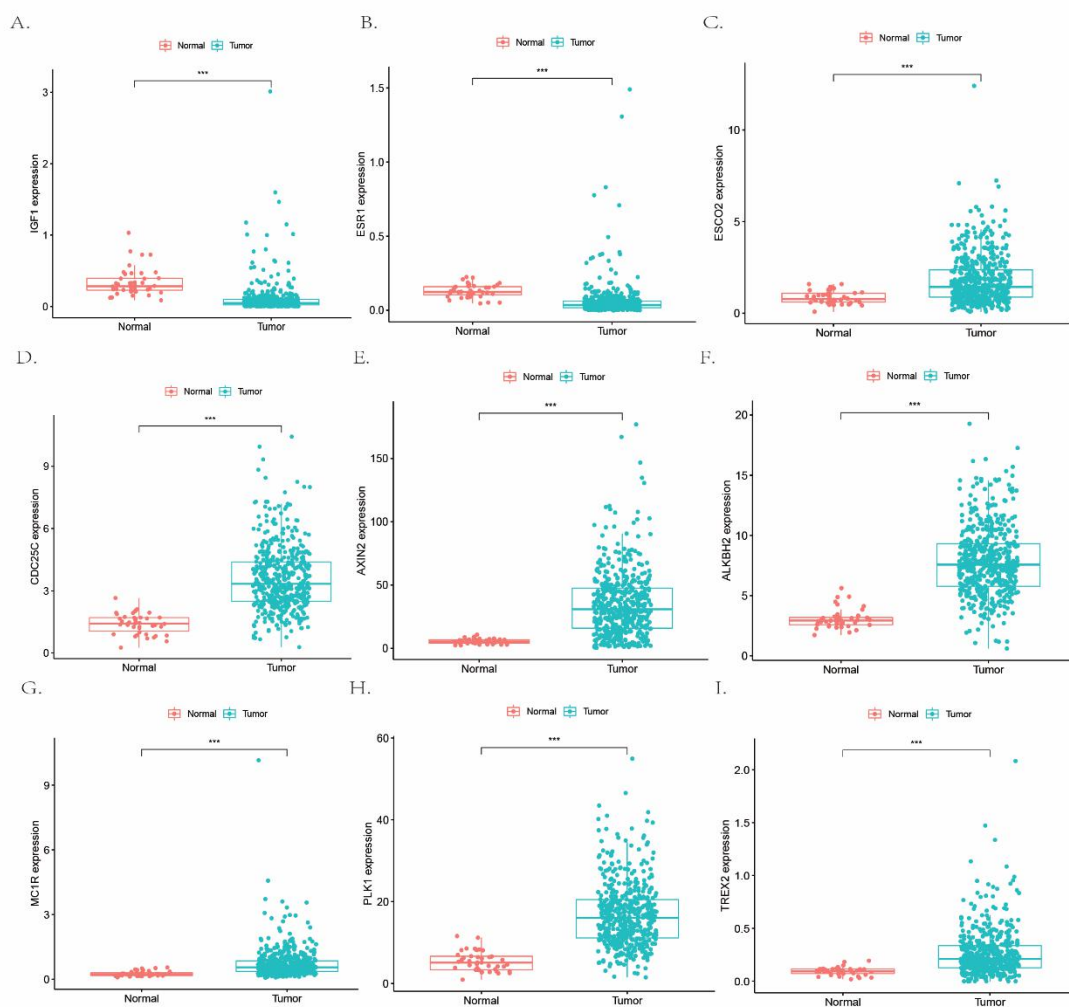


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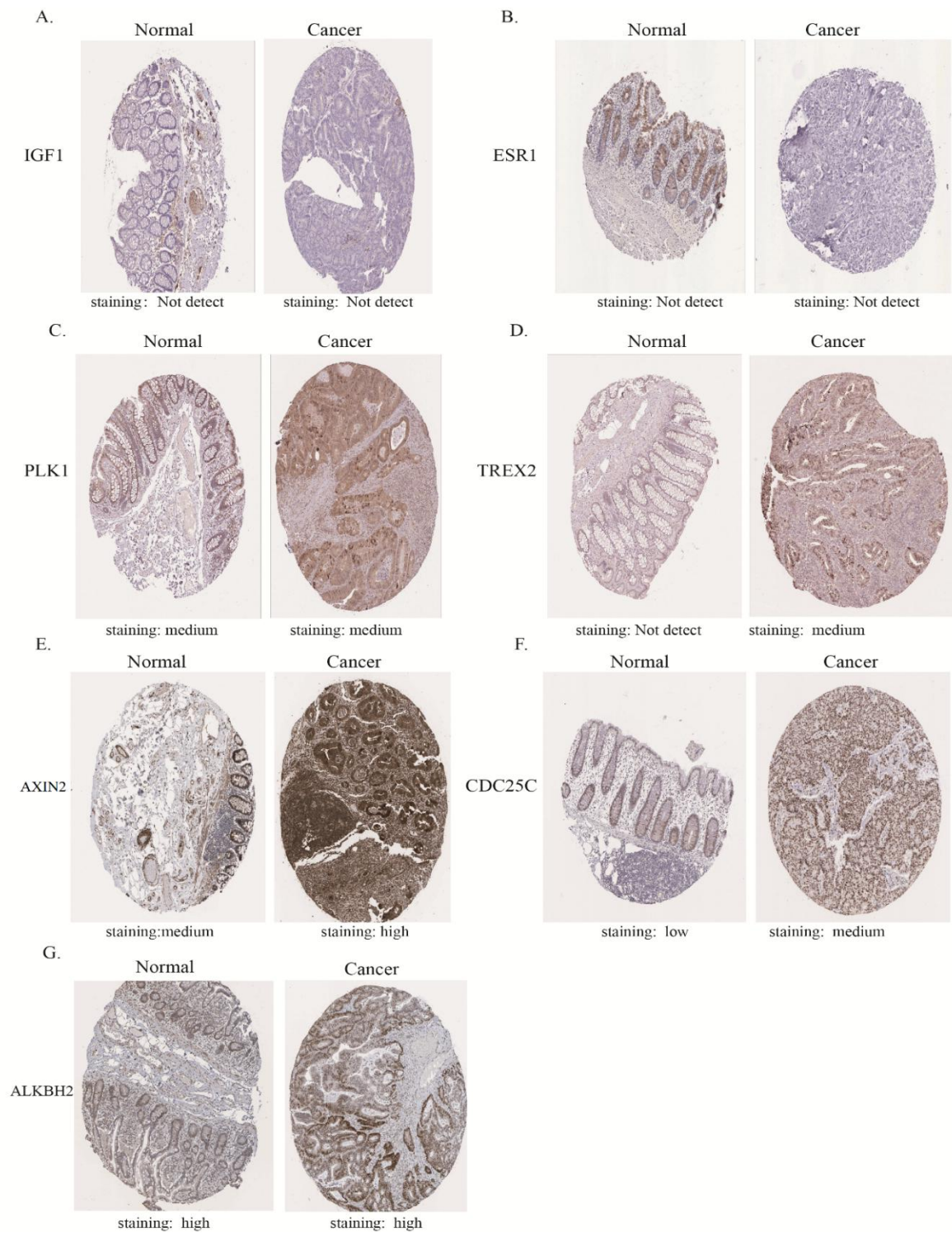


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