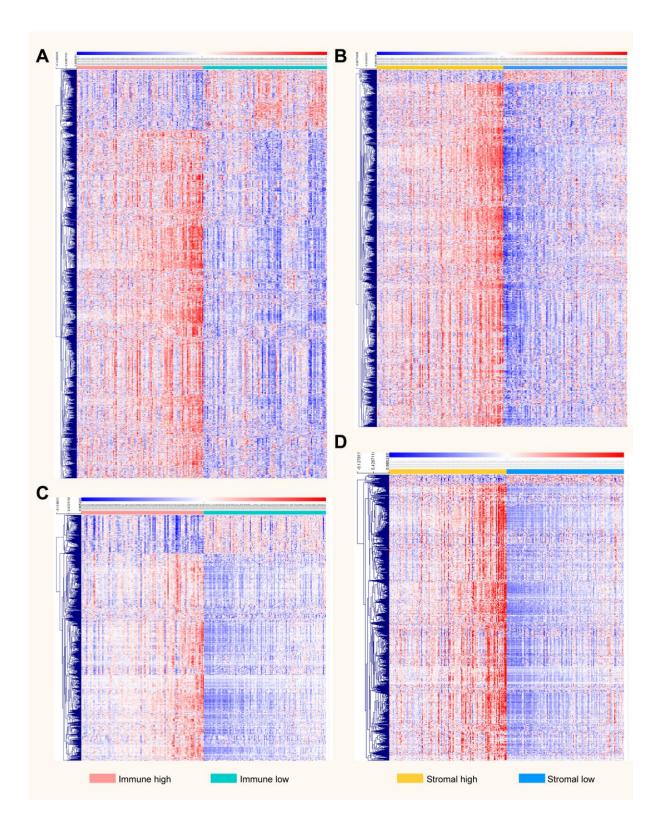
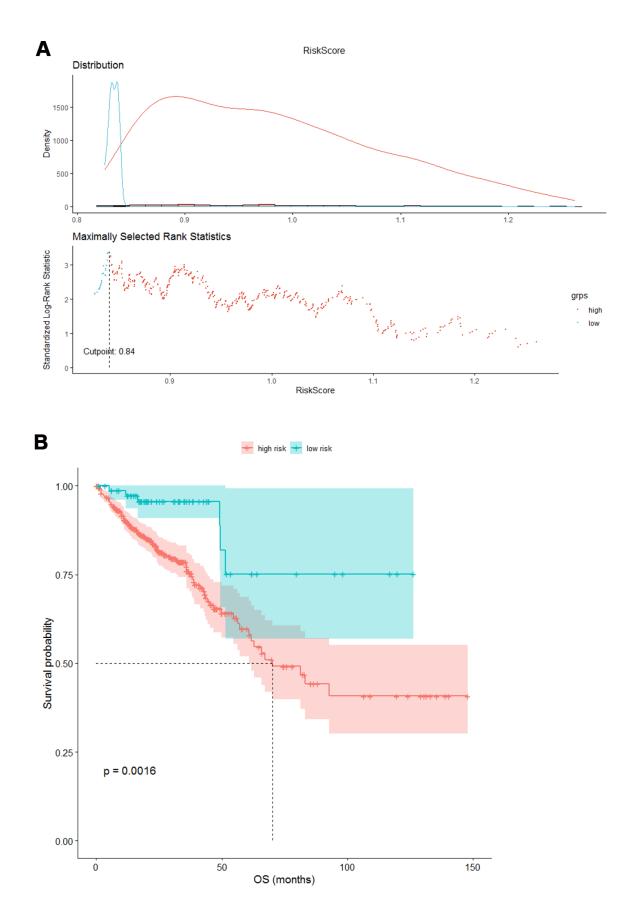
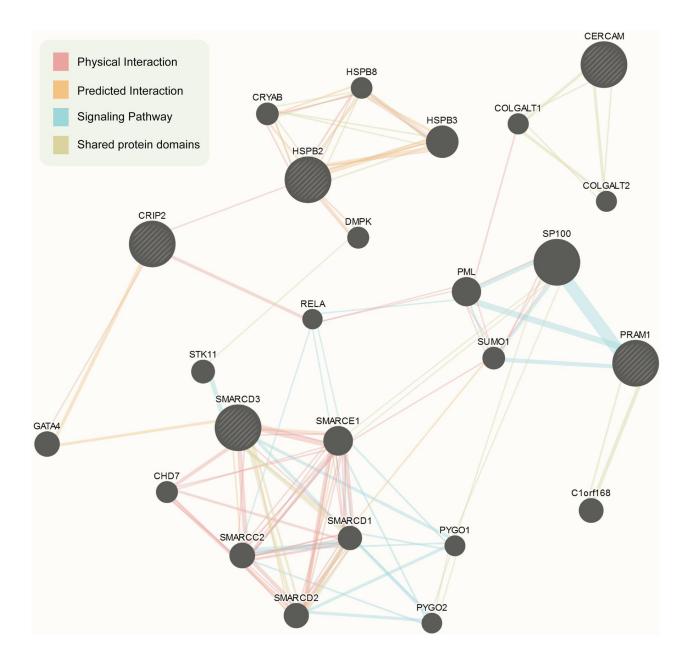
SUPPLEMENTARY FIGURES



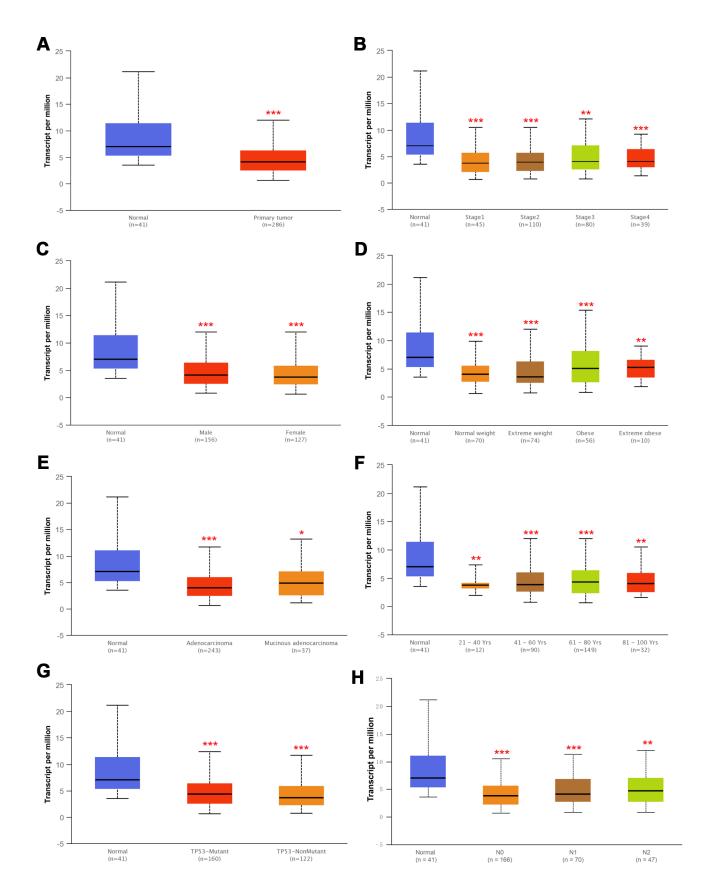
Supplementary Figure 1. Heat map of TME related genes. DEGs computed based on immune (A) or stromal score (B) using HNSC Agilent microarray data. DEGs computed based on immune (C) or stromal score (D) using HNSC RNAseq data.



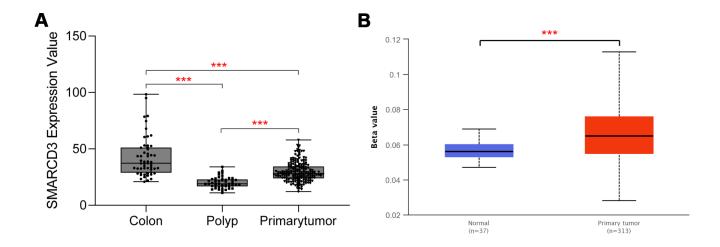
Supplementary Figure 2. (A) Upper graph: the distribution of risk scores; lower graph: cutoff point selection based on log rank statistics. (B) Kaplan-Meier survival analysis of high risk and low risk groups.



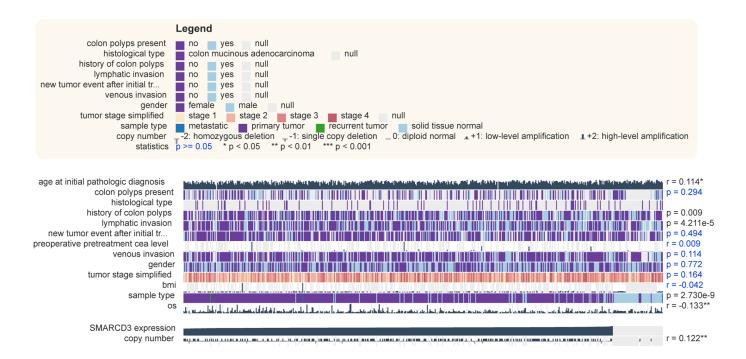
Supplementary Figure 3. Protein-Protein interaction network of SMARCD3, CRIP2, PRAM1, HSPB2 and CERCAM.



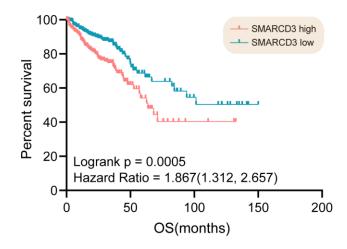
Supplementary Figure 4. SMARCD3 expression in different clinical subgroups. (A) SMARCD3 expression in colon cancer and normal controls. SMARCD3 expression in different cancer stage (B), gender (C), body weight (D), sample type (E), age (F), TP53 mutation status (G) and nodal metastasis status (H).



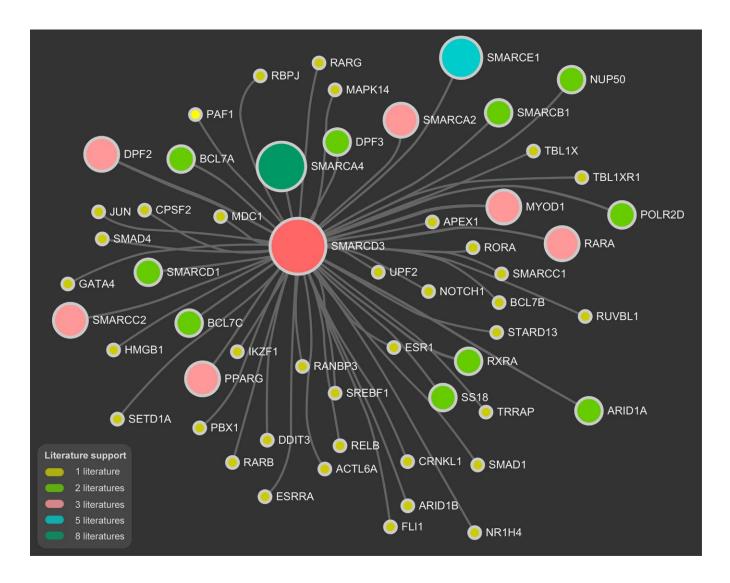
Supplementary Figure 5. (A) SMARCD3 expression in normal control, polyps and primary tumor. (B) the methylation level of SMARCD3 in primary tumor is significantly higher than normal control.



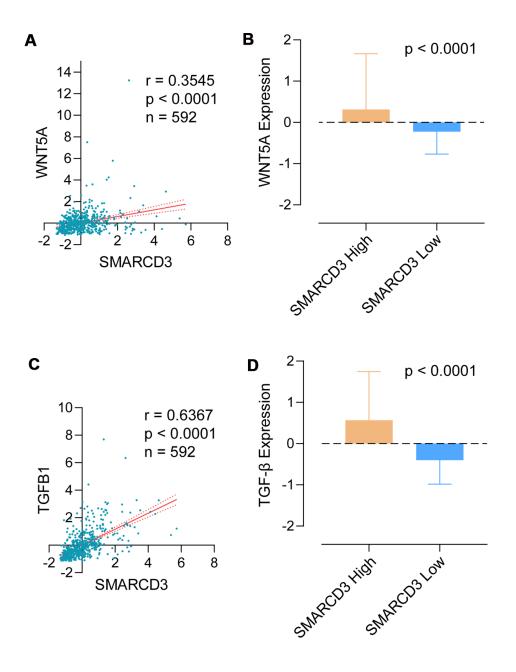
Supplementary Figure 6. Association between SMARCD3 expression levels and clinical features.



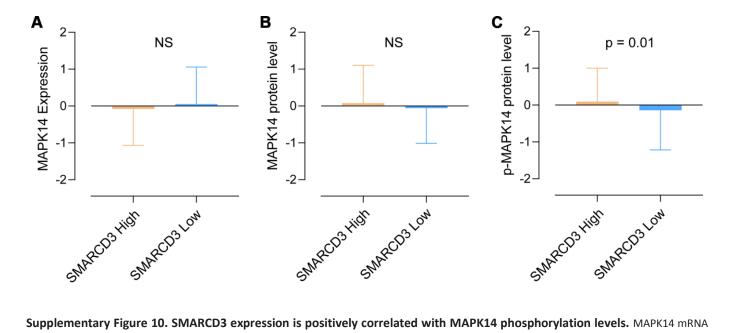
Supplementary Figure 7. Kaplan-Meier survival analysis based on SMARCD3 expression values using TCGA COAD RNAseq data (N = 592).



Supplementary Figure 8. Protein-Protein interaction network of SMARCD3 based on data from CTDbase.



Supplementary Figure 9. SMARCD3 expression is positively correlated with WNT5A and TGF- β . (A) Correlation plot of WNT5A and SMARCD3. (B) WNT5A mRNA expression in SMARCD3 high and low groups. (C) Correlation plot of TGFB1 and SMARCD3. (D) TGFB1 mRNA expression in SMARCD3 high and low groups.



Supplementary Figure 10. SMARCD3 expression is positively correlated with MAPK14 phosphorylation levels. MAPK14 mRNA (A), MAPK14 protein (B) and p-MAPK14 protein (C) expression levels in SMARCD3 high and low groups.