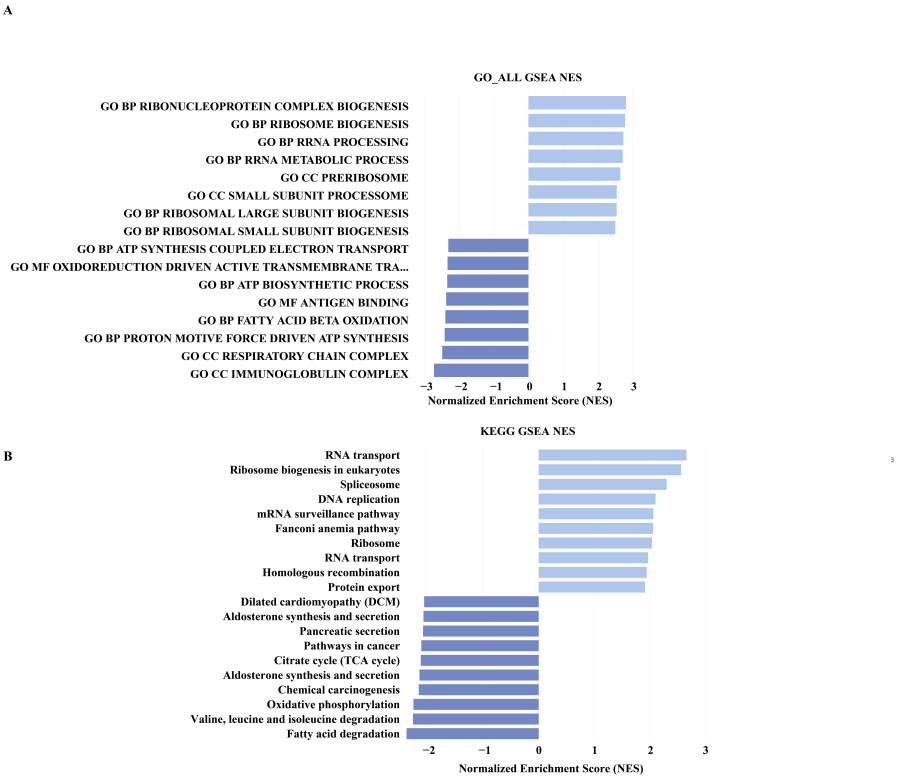

Fig. S1 Additional GSEA results along the N-A-T continuum. (A) Gene Ontology (GO)-based gene set enrichment analysis (GSEA) of genes showing monotonic changes along the normal–adjacent–tumor (N-A-T) continuum. (B) Kyoto Encyclopedia of Genes and Genomes (KEGG)-based GSEA of genes showing monotonic changes along the N-A-T continuum.

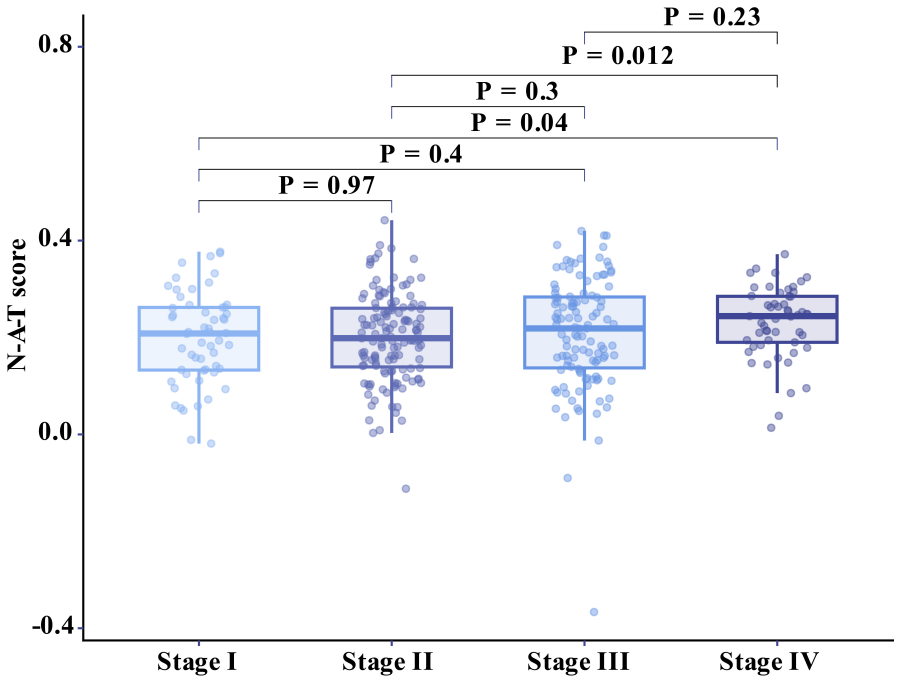

Fig. S2 Associations between the N-A-T score and clinical stage in TCGA colorectal cancer samples. Comparison of N-A-T scores among different pathological stages in the TCGA colorectal cancer cohort.

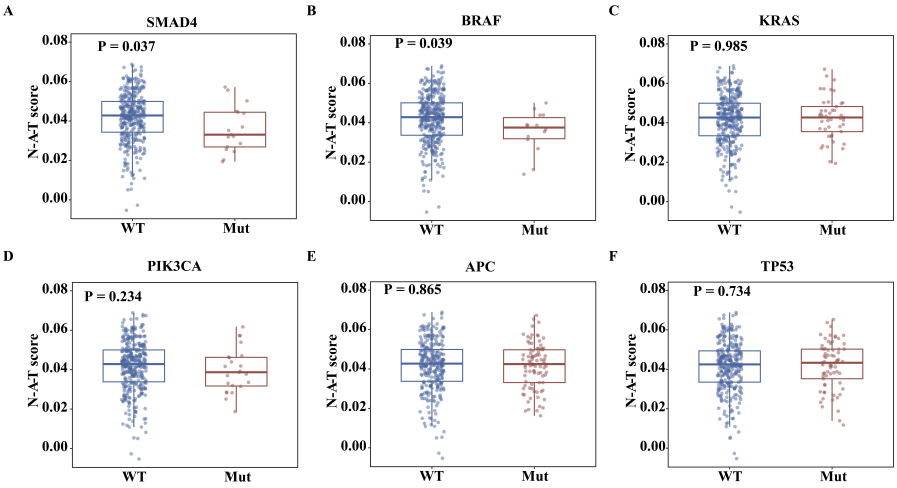

Fig. S3 Associations between the N-A-T score and common driver gene alterations in CRC. Comparisons of N-A-T scores according to mutation status of representative CRC driver genes, including SMAD4, BRAF, KRAS, PIK3CA, APC, and TP53.

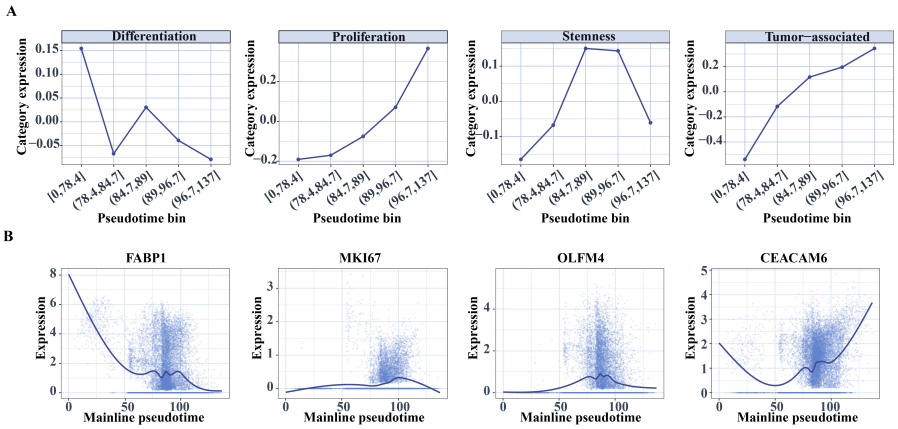

Fig. S4 Dynamic epithelial programs and representative marker-gene expression along pseudotime. (A) Dynamic changes in representative biological programs along epithelial-cell pseudotime. (B) Dynamic expression patterns of representative epithelial marker genes along pseudotime.

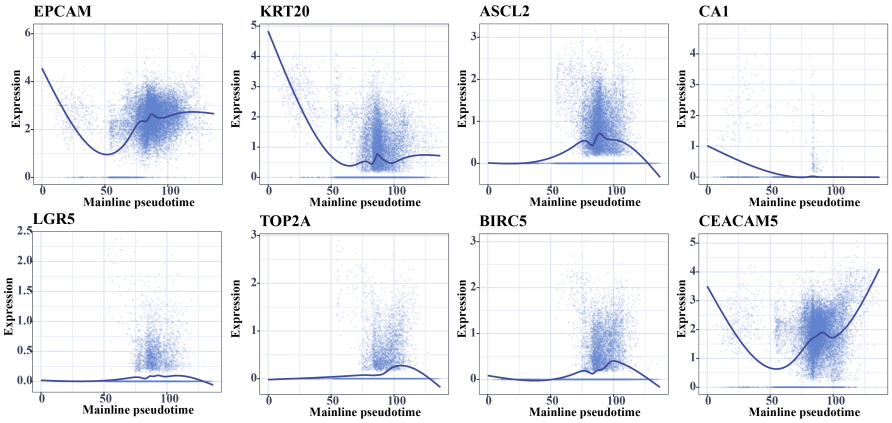

Fig. S5 Dynamic expression changes of additional epithelial marker genes along pseudotime. Dynamic expression patterns of representative epithelial marker genes along epithelial-cell pseudotime reconstructed using Slingshot.