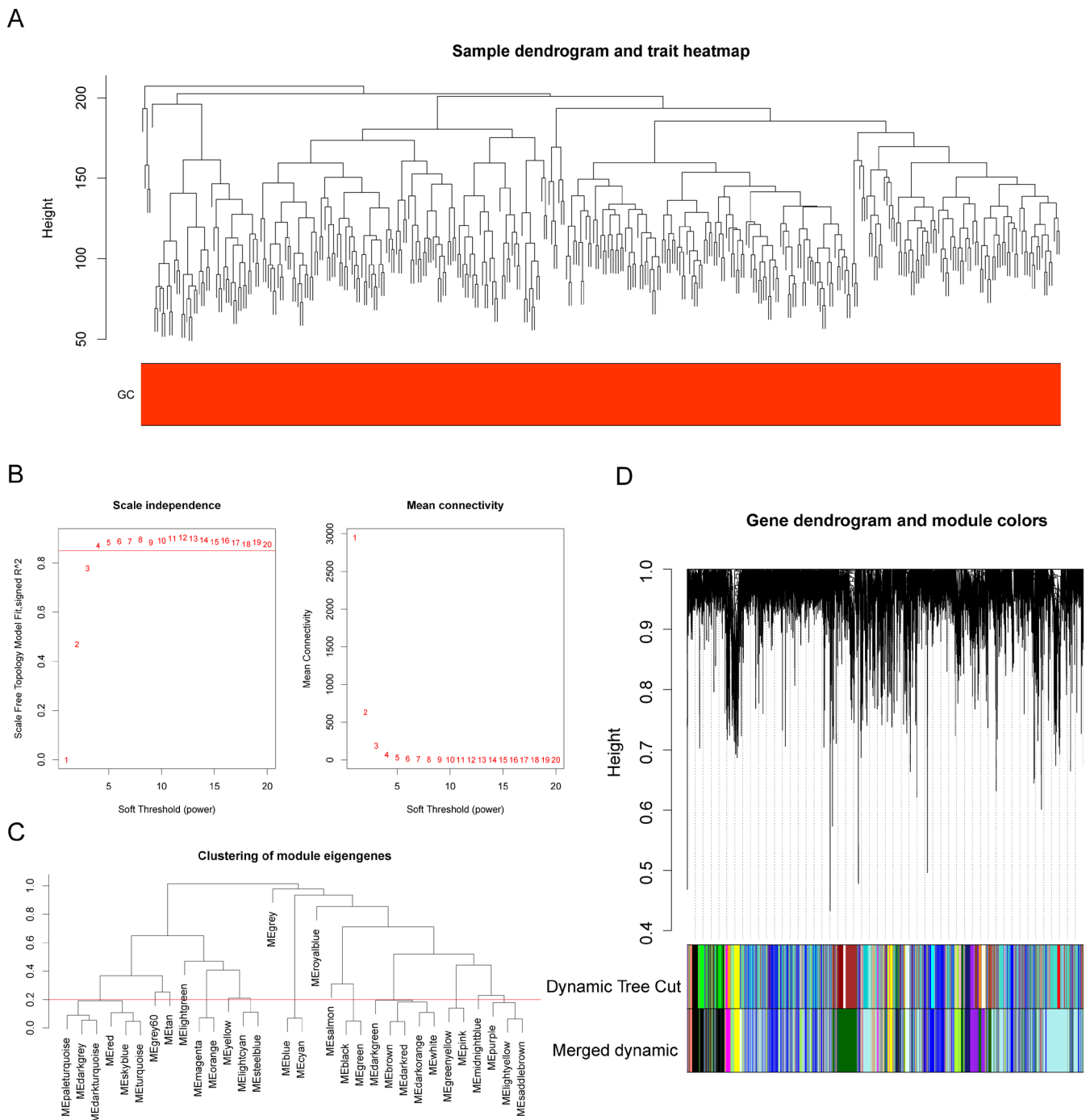


**Table S1** The sequences of primers

Primer	Sequences
AKAP12-F	AAGCAAATGGGGACTCGGAC
AKAP12-R	AGCCTGCGAATGAAGGAGAC
BST1-F	AGCTCTTACAGTGCGTGGAC
BST1-R	CAACATACAACCAAGCCAGCC
DCBLD1-F	GCGCAAGACAAGTCAAAGCA
DCBLD1-R	AAAGGCTGCAAAGATCCCCA
PDK4-F	AGAGGTGGAGCATTCTCGC
PDK4-R	GCTTTCTGGTCATCTGGGCT
SPART-F	CTTCAGAGCGATTGATCGTGG
SPART-R	AATGCAAGGTGCTGACAAGTG
internal reference-GAPDH-F	CGAAGGTGGAGTCAACGGATTT
internal reference-GAPDH-R	ATGGGTGGAATCATATTGGAAC



**Figure S1** Screen and score module genes closely related to phenotypes. (A) Hierarchical clustering analysis. (B) Selection of the soft threshold power value. The left panel represents the scale-free model fit index. The right panel represents the mean connectivity of these values. (C) Clustering of module eigengenes. (D) Cluster dendrogram of genes enriched based on dissimilarity measure and assignment modules. The upper half displays a hierarchical clustering dendrogram of genes, while the lower half shows the gene modules.

**Table S2** The F-statistics for the SNPs

id	P
AKAP12	0.864381045
BST1	0.4018357
CDO1	0.883307939
PDK4	0.889174946
F2R	0.876799224
SMARCD3	0.744012522
MSRB3	0.356487638
RASA4B	0.555865335
CCNA1	0.588297806
DCBLD1	0.45112296
CAND2	0.721423092
KCNMA1	0.250010548
DCLK2	0.726365909
CITED2	0.102476368
AS3MT	0.614918226
SPART	0.819920983

**Table S3** Results of horizontal pleiotropy test

outcome	exposure	Q	Q_df	Q_pval
GC	AKAP12	4.4932	2	0.1058
	BST1	3.1817	5	0.672
	DCBLD1	0.0506	2	0.975
	PDK4	2.2422	3	0.5237
	SPART	1.5937	5	0.902

**Table S4** The results of Leave-One-Out for 5 prognostic genes

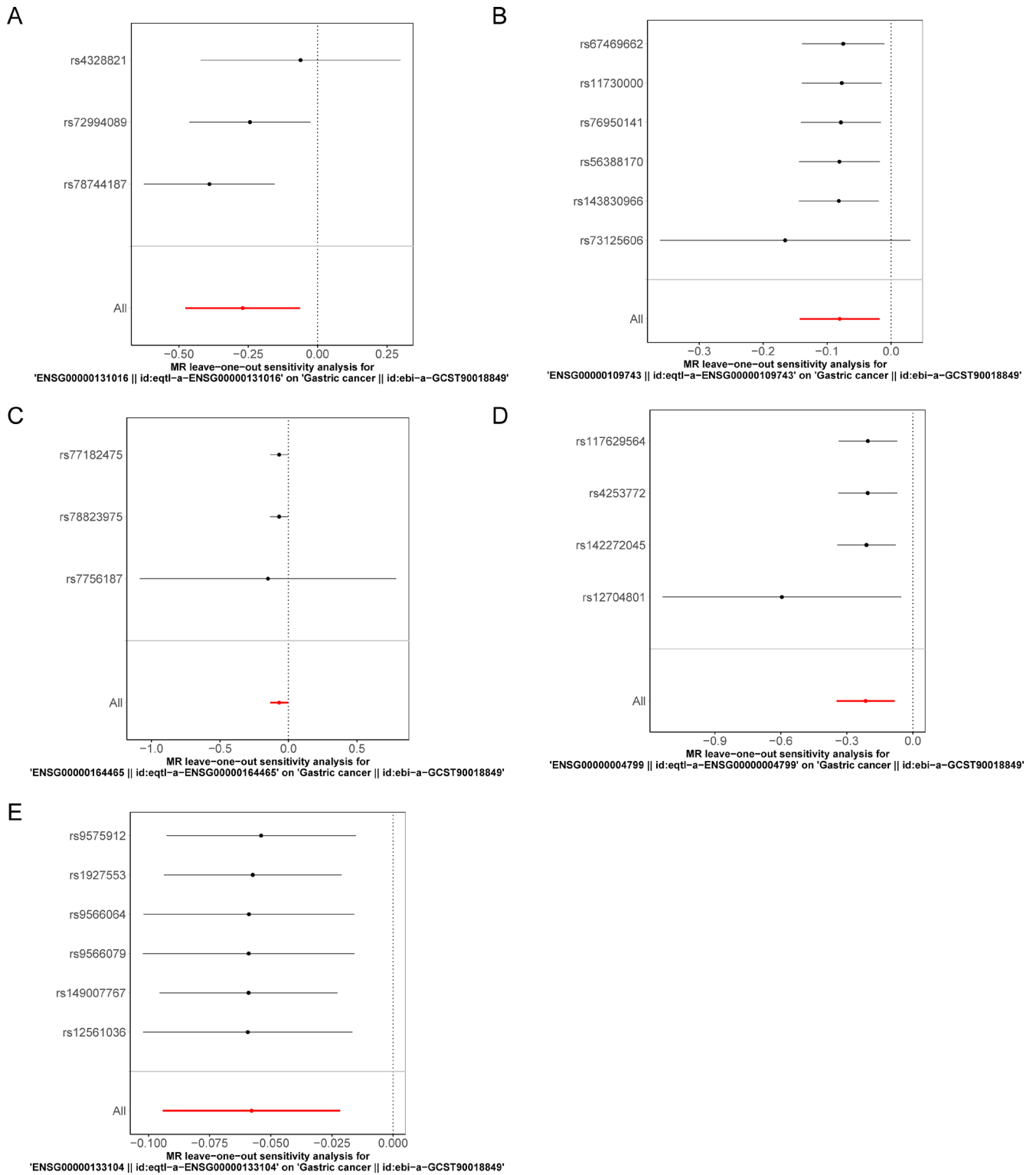
Outcome	Exposure	egger_intercept	se	Pval
GC	AKAP12	-0.0618	0.1127	0.6806
	BST1	0.0016	0.0228	0.9488
	DCBLD1	-0.0439	0.2241	0.8769
	PDK4	0.0037	0.2213	0.9883
	SPART	0.0016	0.0216	0.9443

**Table S5** The results of Steiger's direction test

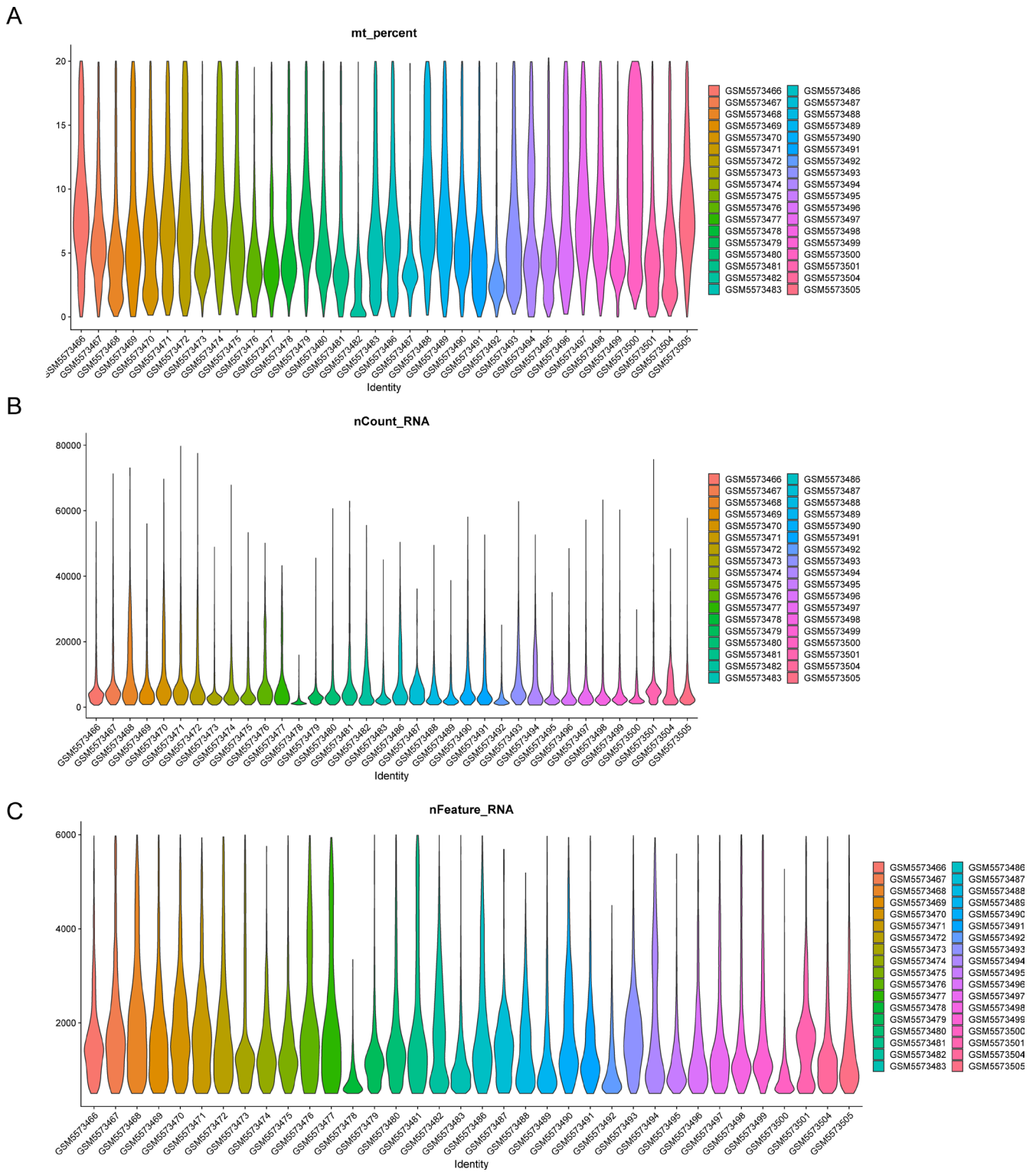
Outcome	Exposure	correct_causal_direction	steiger_pval
GC	AKAP12	TRUE	1.28E-60
	BST1	TRUE	5.38E-299
	DCBLD1	TRUE	1.53E-179
	PDK4	TRUE	1.29E-123
	SPART	TRUE	0

**Table S6** Quality control of single-cell sample data

id	P
riskScore	0.974734032
tumor_stage	0.127825766
pathologic_N	0.651430267
age	0.47890975
pathologic_T	0.481778087
gender	0.805381381



**Figure S2** Leave-one-out analysis of five key genes (AKAP12, BST1, DCBLD1, PDK4, and SPART).



**Figure S3** Quality control plots of single-cell sample data.

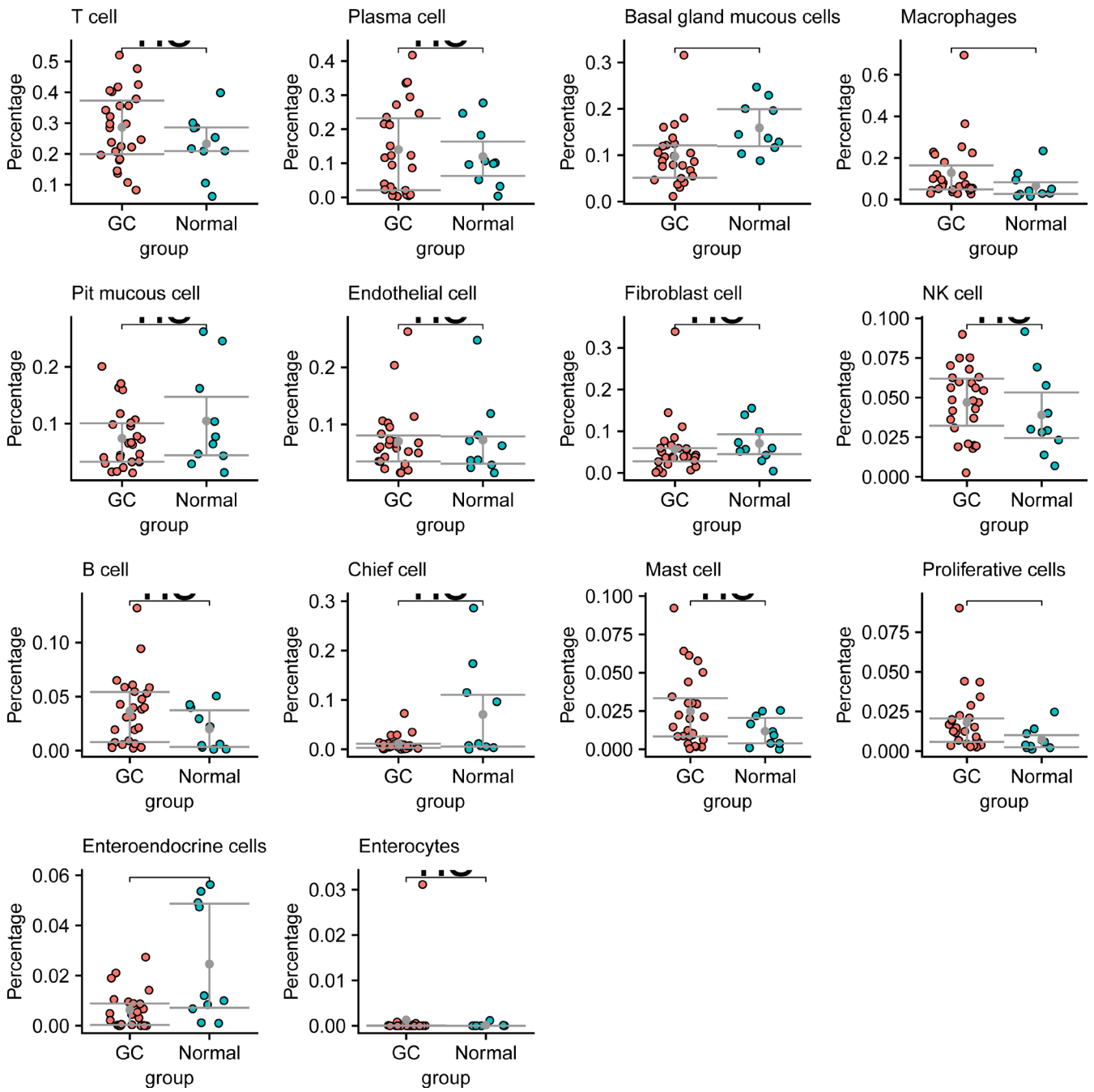
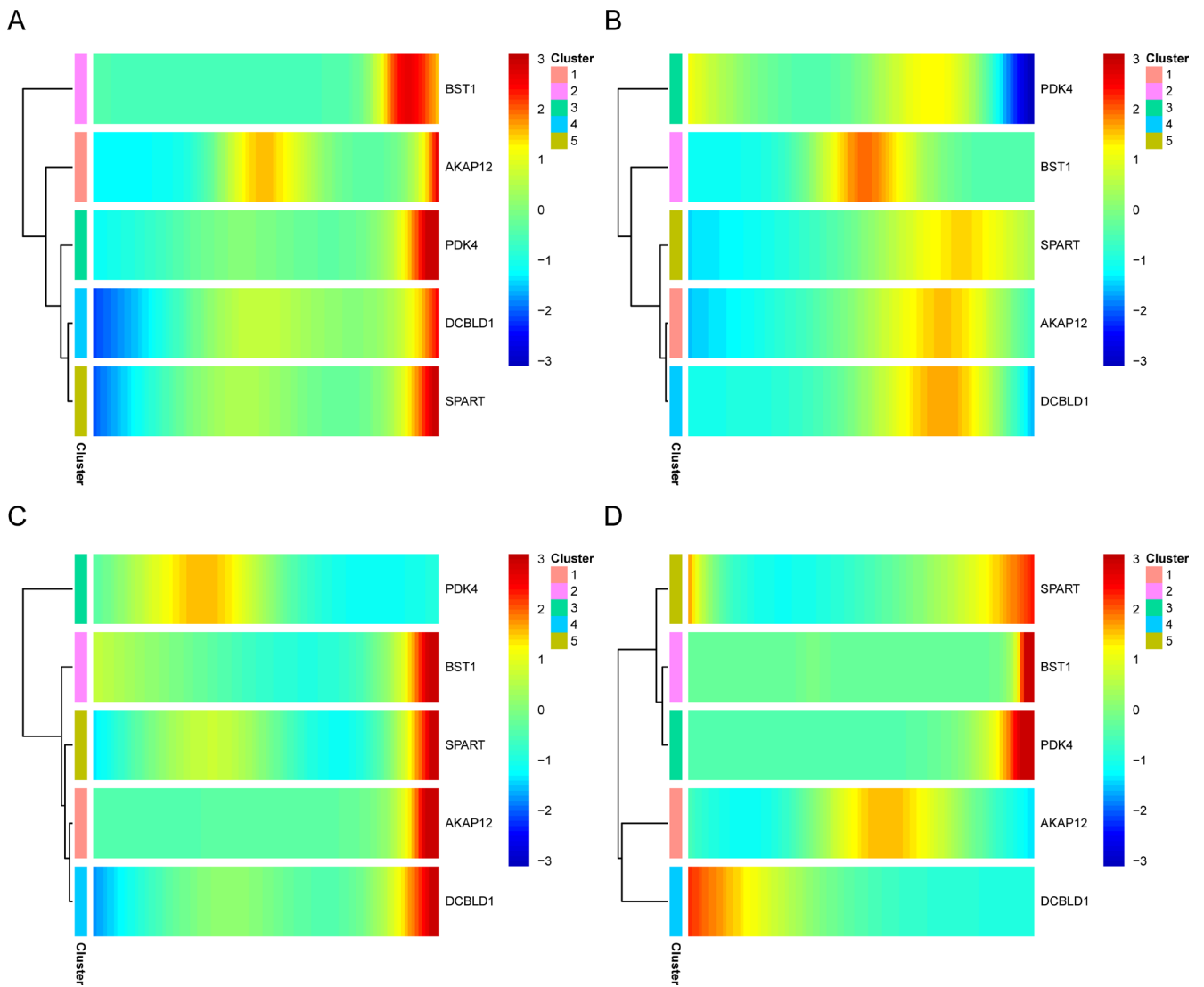


Figure S4 Key cell screening.



**Figure S5** Cell differentiation expression heatmaps of prognostic genes. (A) Expression heatmap of differentiation trajectory of prognostic genes in Basal gland mucous cells. (B) Expression heatmap of differentiation trajectory of prognostic genes in Enteroendocrine cells. (C) Expression heatmap of differentiation trajectory of prognostic genes in Macrophages. (D) Expression heatmap of differentiation trajectory of prognostic genes in Proliferative cells. Red indicates high expression and blue indicates low expression; the time of cell differentiation is from left to right.