Table S1. Samples in NC superset to collect differentially expressed probes.

Accession number	Cancer (%)	Normal (%)	Year	Platform
GSE20916	91 (67.4)	44 (32.6)	2010	GPL570
GSE21510	19 (43.2)	25 (56.8)	2011	GPL570
GSE22598	17 (50.0)	17 (50.0)	2011	GPL570
GSE23878	35 (59.3)	24 (40.7)	2010	GPL570
GSE24514	34 (69.4)	15 (30.6)	2011	GPL96
GSE32323	17 (50.0)	17 (50.0)	2012	GPL570
GSE37364	27 (41.5)	38 (58.5)	2013	GPL570
GSE41258	186 (77.5)	54 (22.5)	2012	GPL96
Total	426 (64.5)	234 (35.5)	2010-2013	Affymetrix

Note: GPL570, HG-U133A Plus2; GPL96, Affymetrix HG-U133A

Table S2. Logistic regression analysis between 3 probe groups (A probes, V probes and V cycle probes) and 8 clinicopathological variables.

Variables	A probes		V probes		V cycle probes	
	OR (95% *CI*)	*P*	OR (95% *CI*)	*P*	OR (95% *CI*)	*P*
Age (n=867)	0.993 (0.984~1.003)	0.161	1.000 (0.991~1.010)	0.951	1.002 (0.992~1.011)	0.715
Gender (n=933)	1.257 (0.971~1.627)	0.082	1.193 (0.922~1.544)	0.179	0.921 (0.712~1.192)	0.530
Stage (n=928)	0.925 (0.715~1.197)	0.555	1.502 (1.159~1.945)	**0.002**	0.643 (0.496~0.833)	**8.320e-04**
Grade (n=278)	0.890 (0.455~1.740)	0.733	0.241 (0.110~0.529)	**3.825e-04**	3.068 (1.465~6.426)	**0.003**
AdjCTX (n=614)	1.013 (0.737~1.393)	0.935	0.520 (0.377~0.719)	**7.370e-05**	1.870 (1.355~2.583)	**1.426e-04**
T status (n=678)	0.890 (0.555~1.428)	0.630	0.458 (0.279~0.754)	**0.002**	1.922 (1.178~3.135)	**0.009**
N status (n=674)	0.822 (0.558~1.213)	0.324	0.529 (0.355~0.788)	**0.002**	2.053 (1.375~3.067)	**4.408e-04**
M status (n=677)	0.771 (0.504~1.179)	0.230	0.607 (0.395~0.935)	0.023	1.893 (1.224~2.930)	**0.004**

Note: The number of samples with clear description of each variable was appended to the corresponding variable name. Significant *p* values were in bold ($p<0.01$). For rank variables, the dichotomization was conducted as follows: Stage (III+IV/I+II); Grade (III/I+II); T status (T3+T4/T1+T2); N status (N2+N3/N0+N1). Abbreviations: *AdjCTX*, whether chemotherapy was used; *OR*, odds ratio; *CI*, confidence interval.

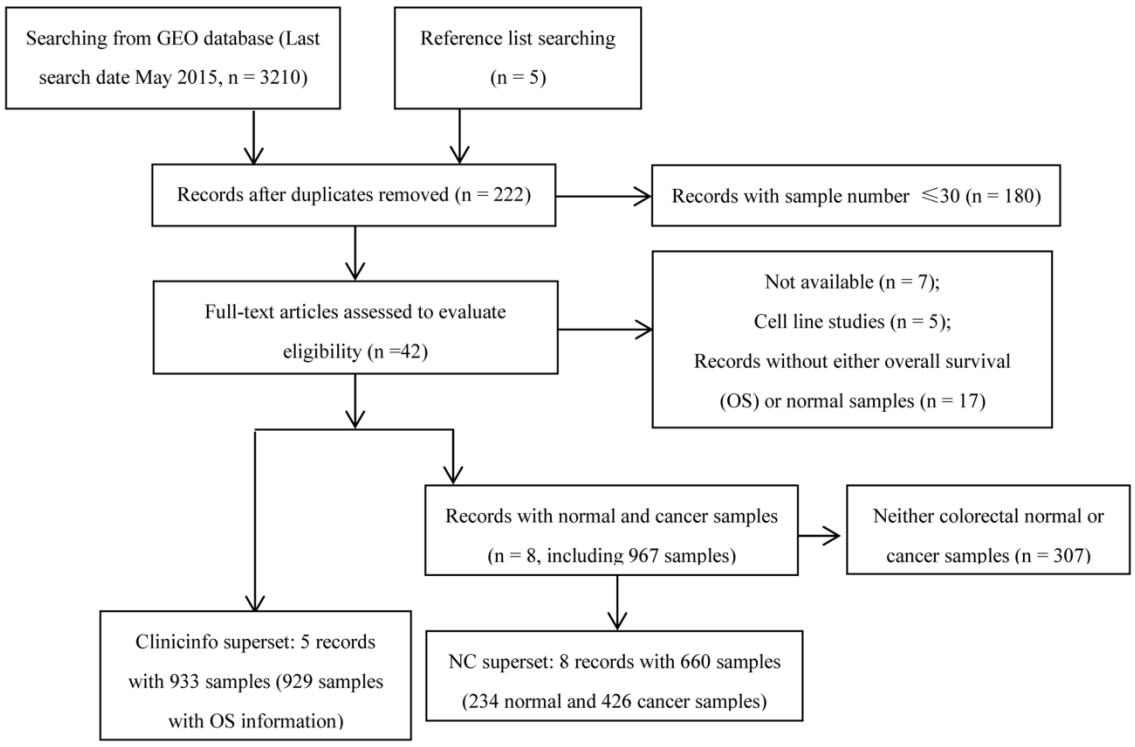

Fig. S1 Schematic diagram of meta-analysis literature searching

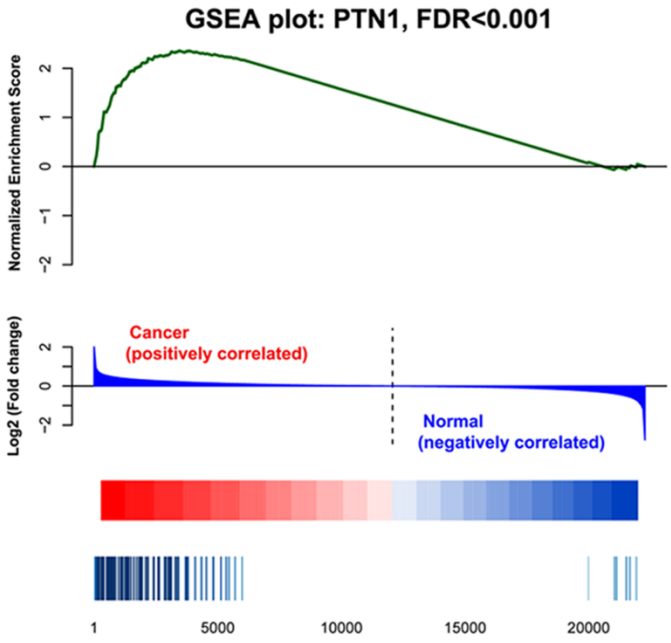

Fig. S2 GSEA analysis of PTN_1 in NC superset. PTN_1 belonged to 7 DDMs, containing DEPs generally being down-regulated along developmental time axis. GSEA analysis indicated that the DEPs within PTN_1 were significantly up-regulated in cancer with comparison to normal tissue, and therefore, PTN_1 was referred to as a significant DDM. Note: DEP represents differentially expressed probes; DDM represents developmental down-regulating modules; the significance criterion is FDR<0.001.

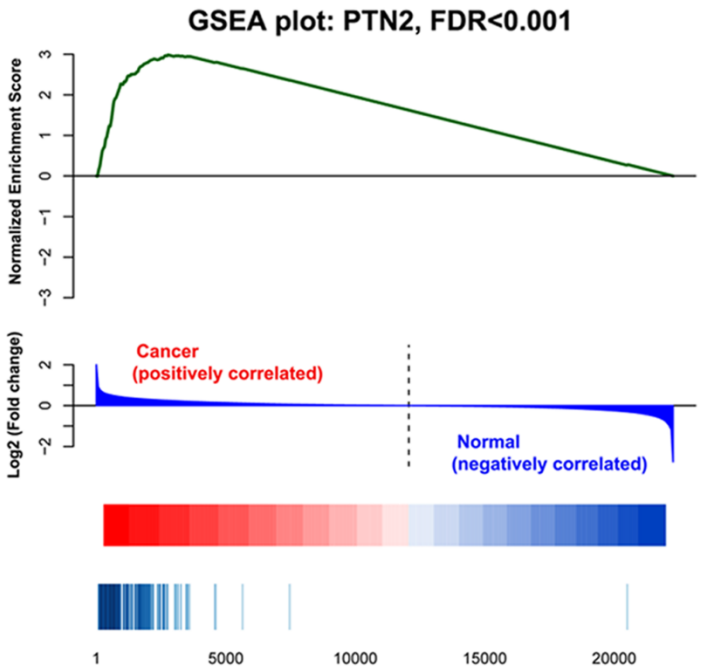

Fig. S3 GSEA analysis of PTN_2 in NC superset. PTN_2 belonged to 7 DDMs. GSEA analysis indicated that the DEPs within PTN_2 were significantly up-regulated in cancer with comparison to normal tissue, and therefore, PTN_2 was referred to as a significant DDM.

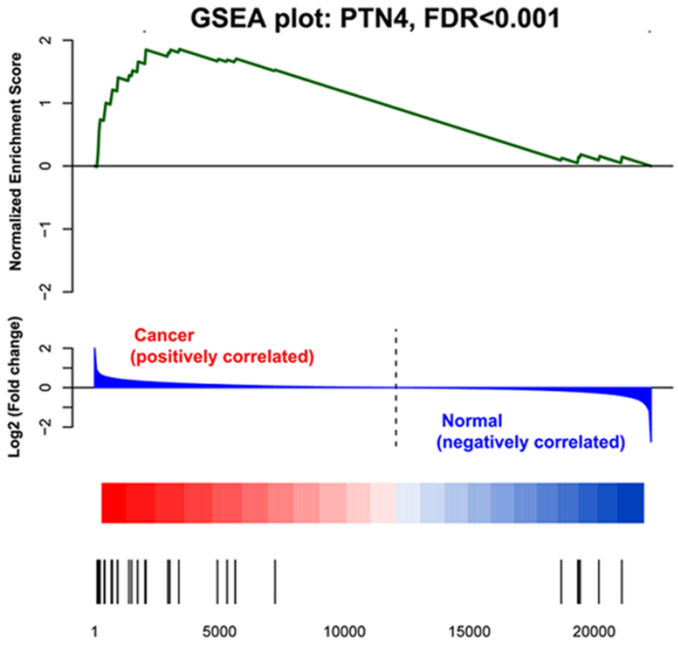

Fig. S4 GSEA analysis of PTN_4 in NC superset. PTN_4 belonged to 7 DDMs. GSEA analysis indicated that the DEPs within PTN_4 were significantly up-regulated in cancer with comparison to normal tissue, and therefore, PTN_4 was referred to as a significant DDM.

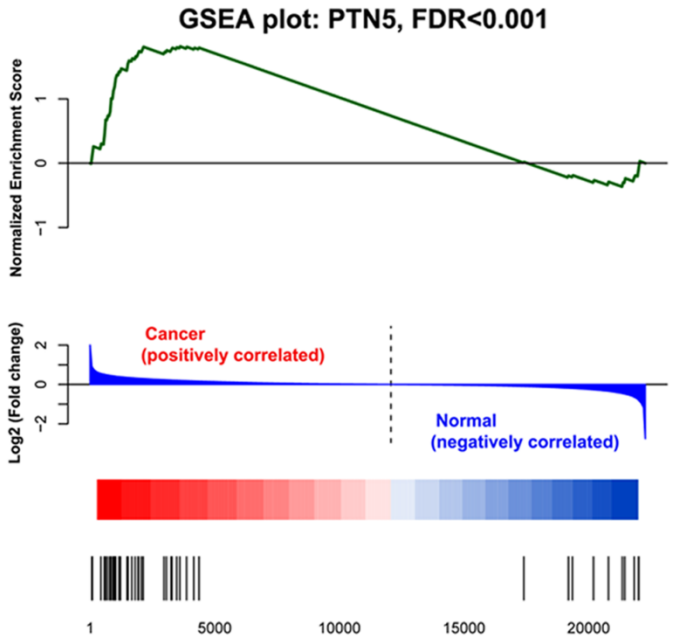

Fig. S5 GSEA analysis of PTN_5 in NC superset. PTN_5 belonged to 7 DDMs. GSEA analysis indicated that the DEPs within PTN_5 were significantly up-regulated in cancer with comparison to normal tissue, and therefore, PTN_5 was referred to as a significant DDM.

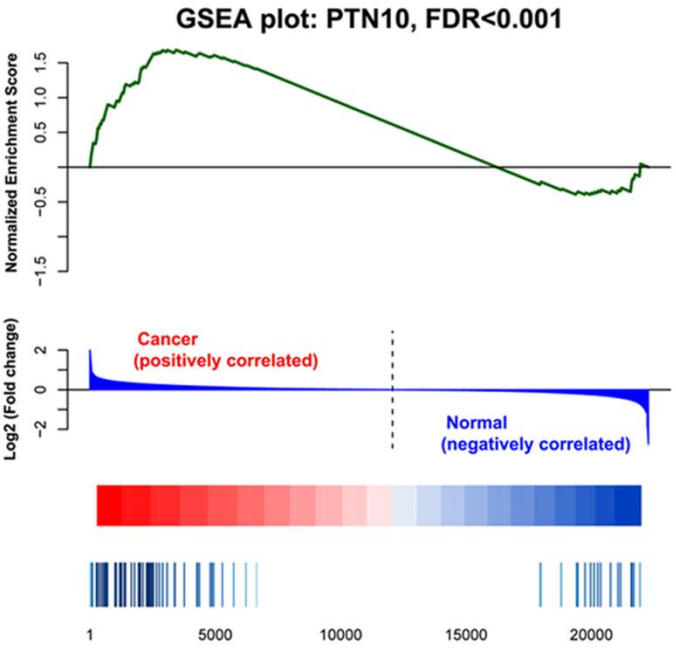

Fig. S6 GSEA analysis of PTN_10 in NC superset. PTN_10 belonged to 7 DDMs. GSEA analysis indicated that the DEPs within PTN_10 were significantly up-regulated in cancer with comparison to normal tissue, and therefore, PTN_10 was referred to as a significant DDM.

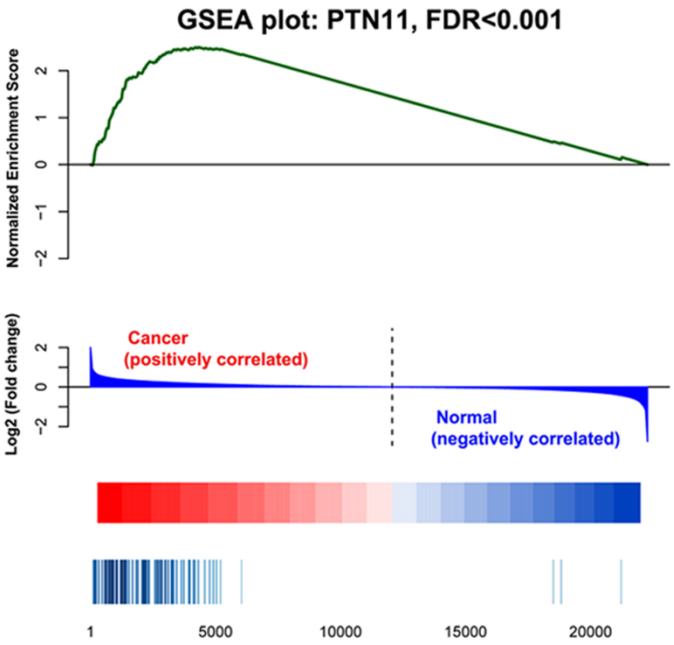

Fig. S7 GSEA analysis of PTN_11 in NC superset. PTN_11 belonged to 7 DDMs. GSEA analysis indicated that the DEPs within PTN_11 were significantly up-regulated in cancer with comparison to normal tissue, and therefore, PTN_11 was referred to as a significant DDM.

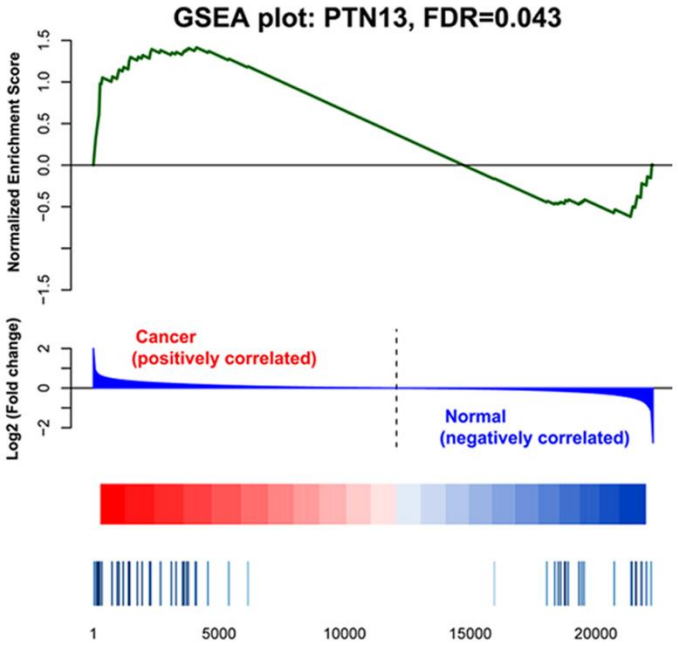

Fig. S8 GSEA analysis of PTN_13 in NC superset. PTN_13 belonged to 7 DDMs. GSEA analysis indicated that the DEPs within PTN_13 were not significantly up-regulated in cancer with comparison to normal tissue, and therefore, PTN_13 could not be referred to as a significant DDM.

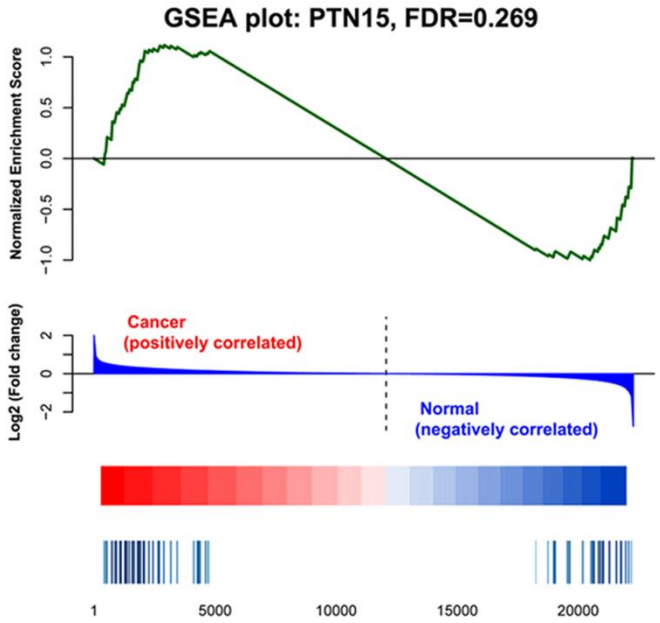

Fig. S9 GSEA analysis of PTN_15 in NC superset. PTN_15 belonged to 7 DUMs, containing DEPs generally being up-regulated along developmental time axis. GSEA analysis indicated that the DEPs within PTN_15 were not significantly down-regulated in cancer with comparison to normal tissue, and therefore, PTN_15 could not be referred to as a significant DUM. Note: DUM represents developmental up-regulating modules; the significance criterion is FDR<0.001.

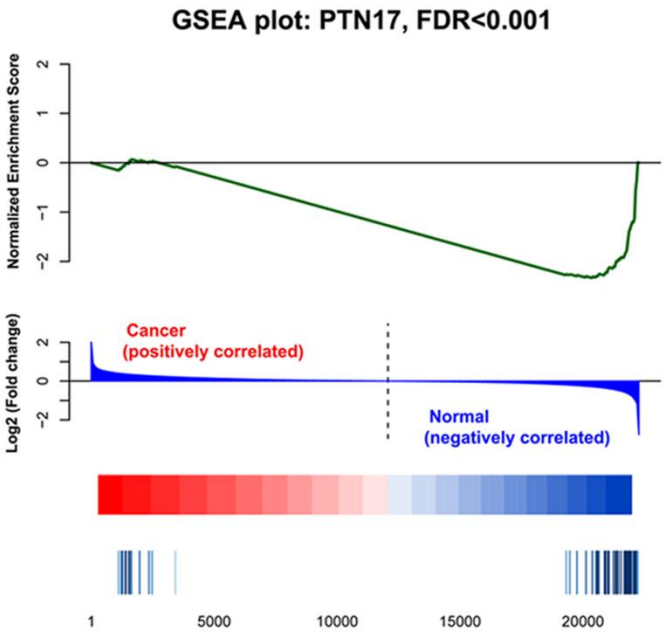

Fig. S10 GSEA analysis of PTN_17 in NC superset. PTN_17 belonged to 7 DUMs. GSEA analysis indicated that the DEPs within PTN_17 were significantly down-regulated in cancer with comparison to normal tissue, and therefore, PTN_17 was referred to as a significant DUM.

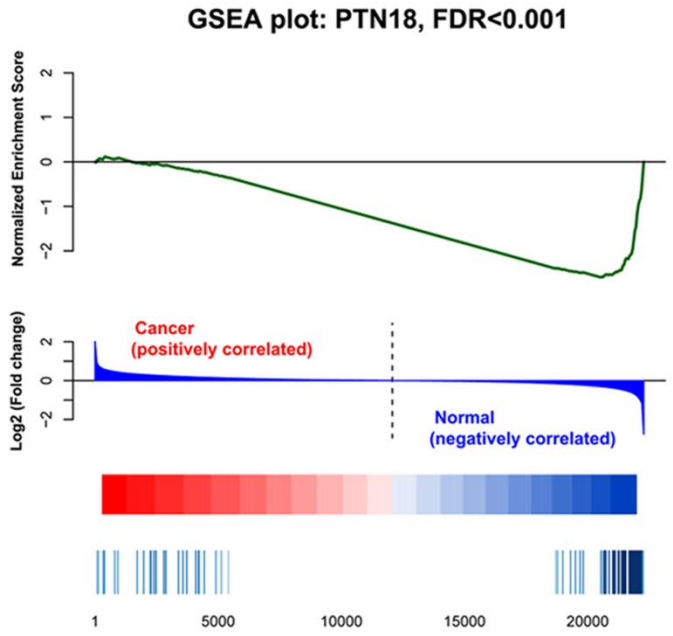

Fig. S11 GSEA analysis of PTN_18 in NC superset. PTN_18 belonged to 7 DUMs. GSEA analysis indicated that the DEPs within PTN_18 were significantly down-regulated in cancer with comparison to normal tissue, and therefore, PTN_18 was referred to as a significant DUM.

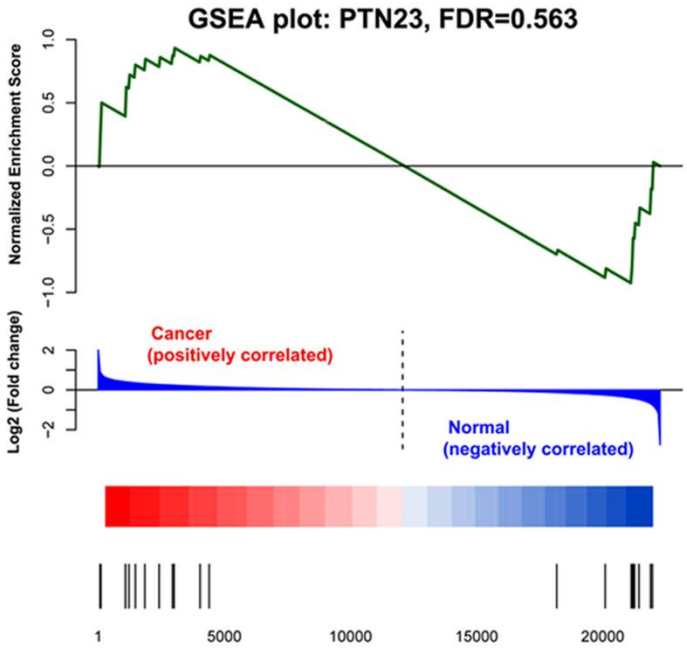

Fig. S12 GSEA analysis of PTN_23 in NC superset. PTN_23 belonged to 7 DUMs. GSEA analysis indicated that the DEPs within PTN_23 were not significantly down-regulated in cancer with comparison to normal tissue, and therefore, PTN_23 could not be referred to as a significant DUM.

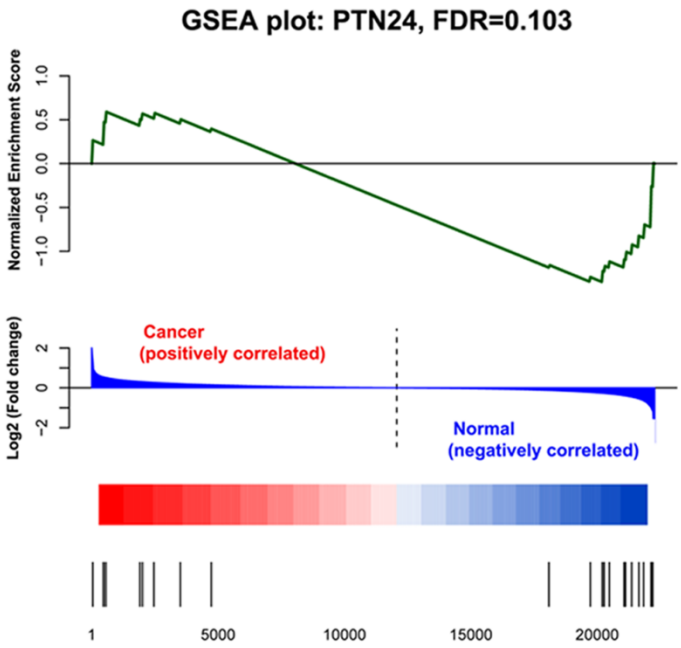

Fig. S13 GSEA analysis of PTN_24 in NC superset. PTN_24 belonged to 7 DUMs. GSEA analysis indicated that the DEPs within PTN_24 were not significantly down-regulated in cancer with comparison to normal tissue, and therefore, PTN_24 could not be referred to as a significant DUM.

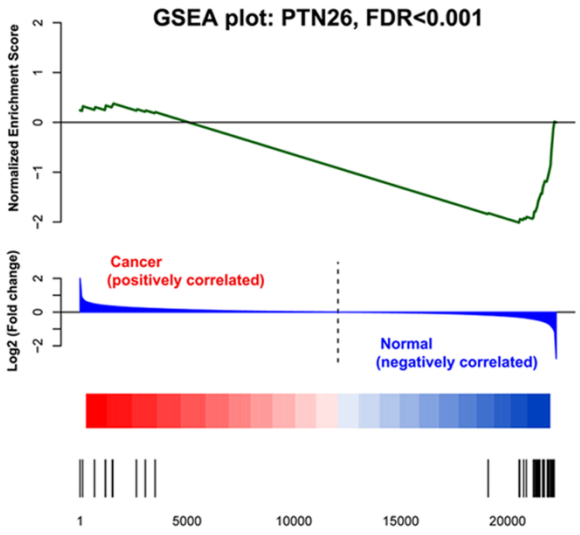

Fig. S14 GSEA analysis of PTN_26 in NC superset. PTN_26 belonged to 7 DUMs. GSEA analysis indicated that the DEPs within PTN_26 were significantly down-regulated in cancer with comparison to normal tissue, and therefore, PTN_26 was referred to as a significant DUM.

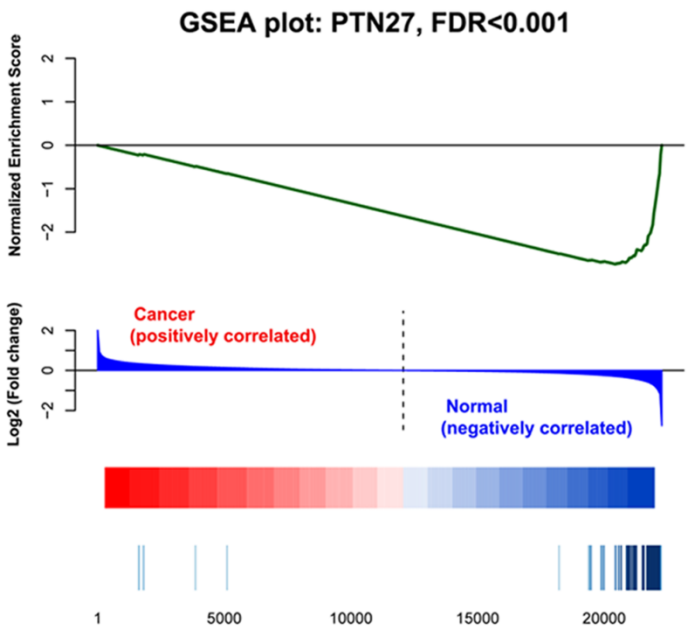

Fig. S15 GSEA analysis of PTN_27 in NC superset. PTN_27 belonged to 7 DUMs. GSEA analysis indicated that the DEPs within PTN_27 were significantly down-regulated in cancer with comparison to normal tissue, and therefore, PTN_27 was referred to as a significant DUM.

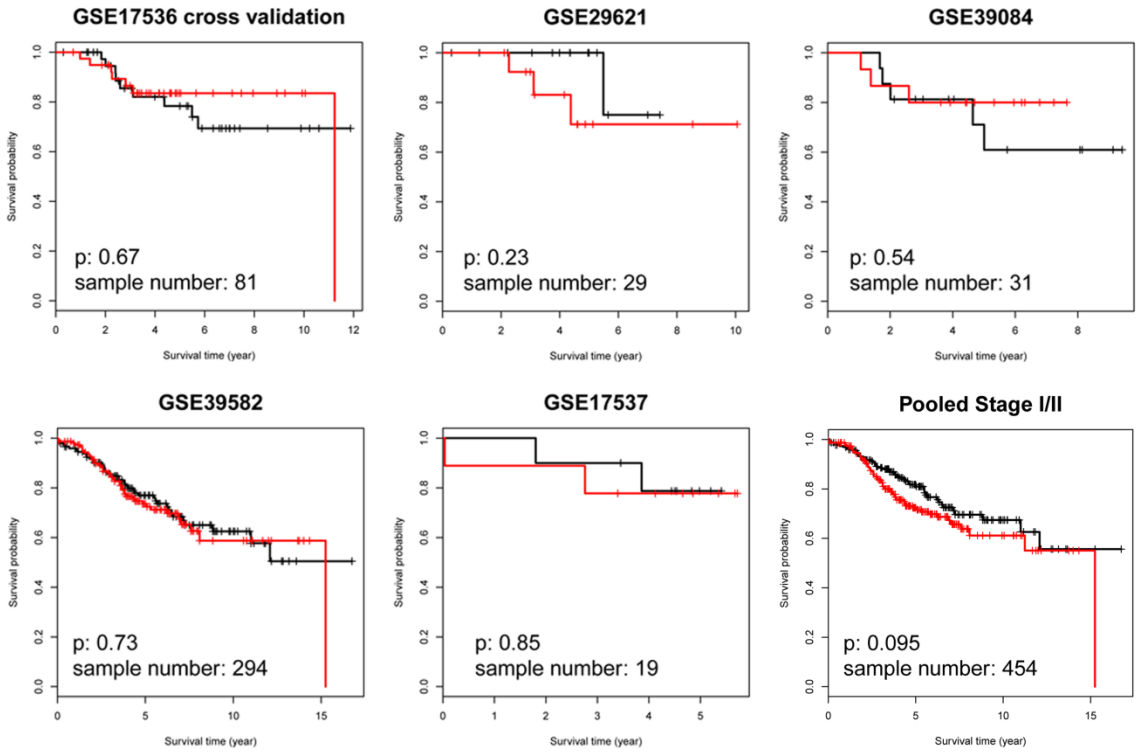

Fig. S16 Kaplan–Meier survival analysis of 28 V cycle probes with Stage I/II patients in 5 independent data sets of Clinicinfo superset.

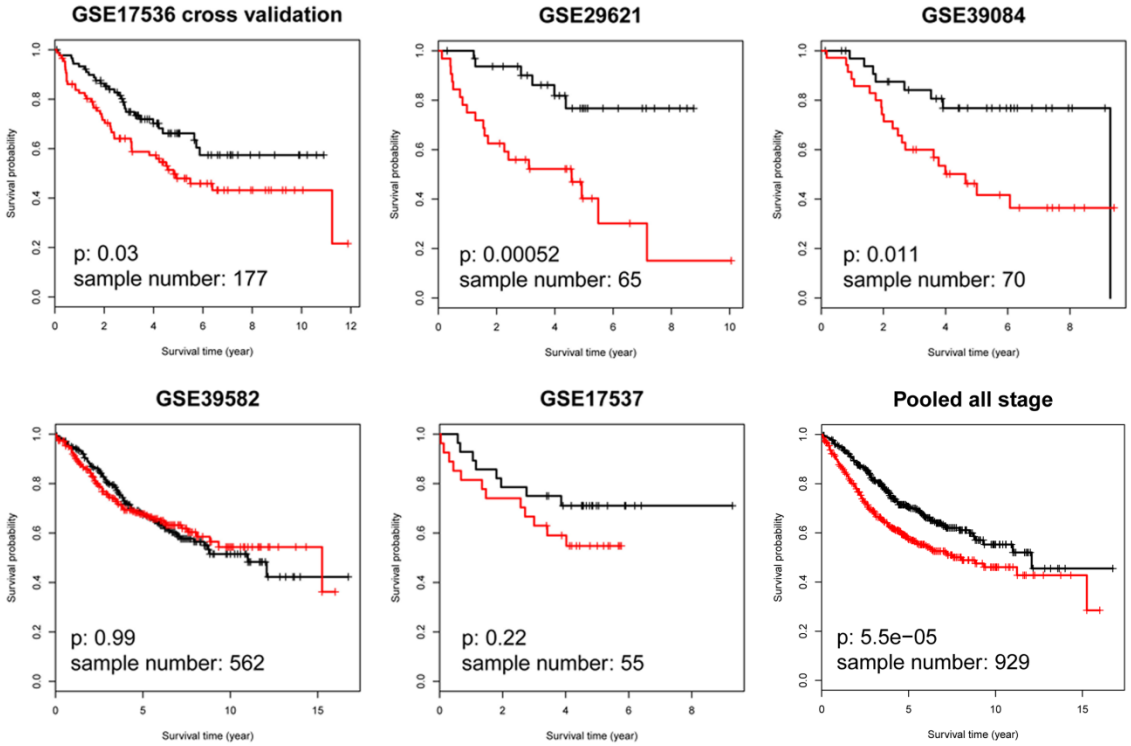

Fig. S17 Kaplan–Meier survival analysis of 28 V cycle probes with all stage patients in 5 independent data sets of Clinicinfo superset.

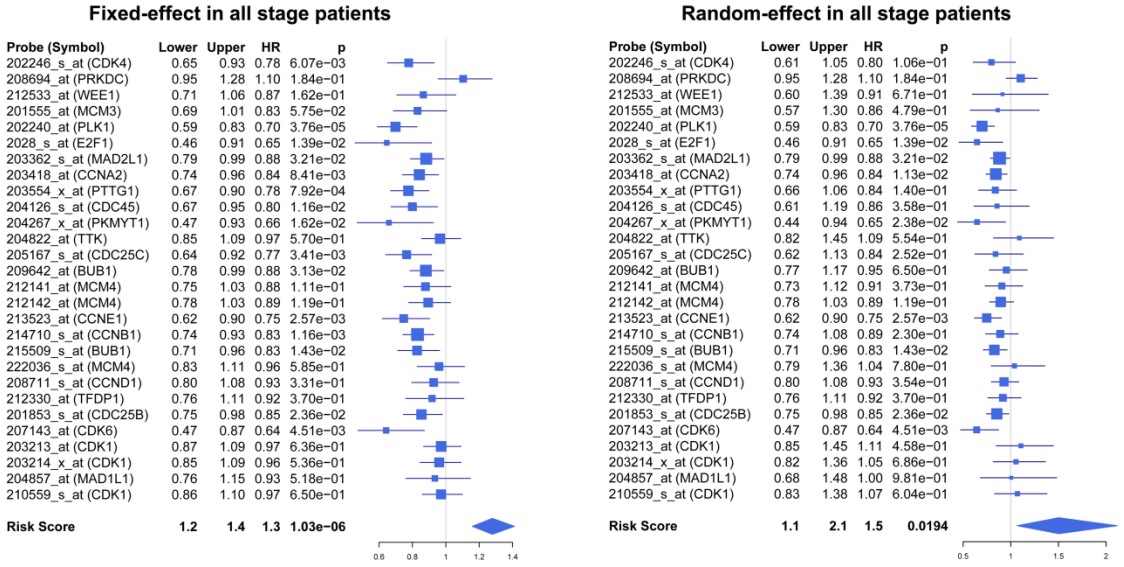

Fig. S18 Forest plot of 28 V cycle probes with fixed-effect and random-effect model in all stage patients.

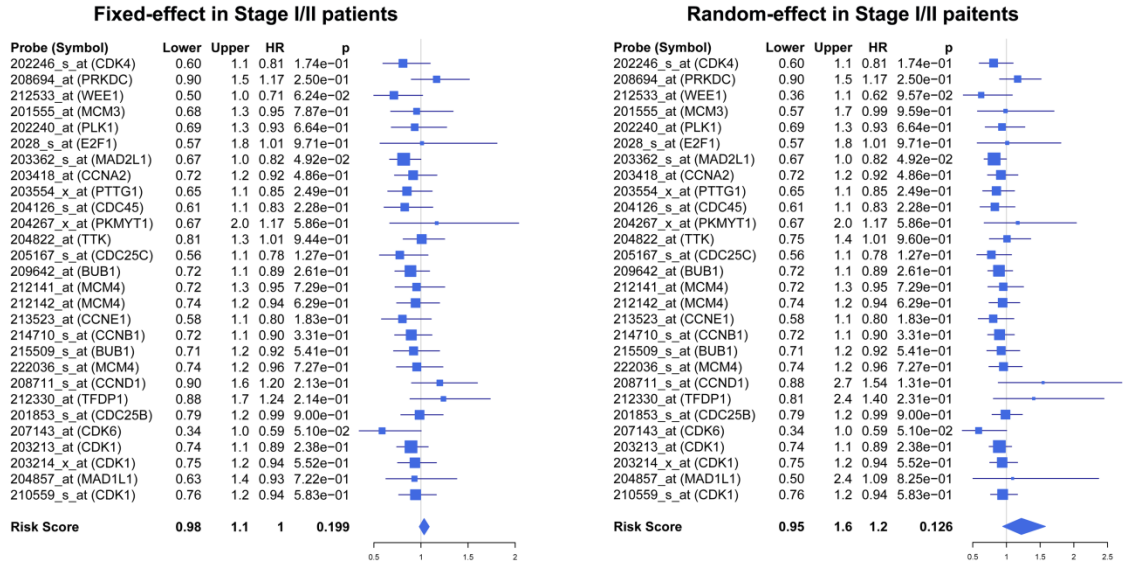

Fig. S19 Forest plot of 28 V cycle probes with fixed-effect and random-effect model in Stage I/II patients.