Figure 1 Enrichment analysis of DEGs between clusters. (A) Volcano plot of the DEGs between 2 clusters (cluster 1 versus cluster 2). The *CHD5* gene is labeled. GO enrichment (B) and GSEA enrichment (C) results of the DEGs.

Table S1 Clinical information of samples in the GSE49710 dataset

Characteristic	Overall
N	498
Age (days), mean ± SD	758±1,031
Age group, n (%)	
<18 months	300 (60.2)
≥18 months	198 (39.8)
Status, n (%)	
Live	393 (78.9)
Death	105 (21.1)
Overall survival (days), mean ± SD	2,185.42±1,370.89
INSS stage, n (%)	
1	121 (24.3)
2	78 (15.7)
3	63 (12.7)
4	183 (36.7)
4S	53 (10.6)
MYCN status, n (%)	
Non-amplification	401 (80.5)
Amplification	92 (18.5)
No data	5 (1.0)
Sex, n (%)	
Female	211 (42.4)
Male	287 (57.6)

Table S2 Dormancy-associated genes with significantly different survival

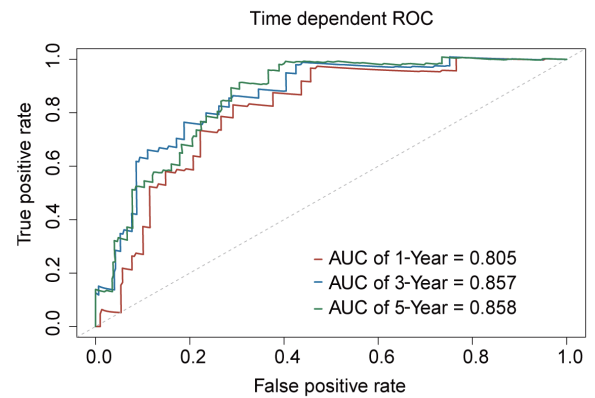| Gene	Log-rank P value
BHLHB3	1.78E-10
CDKN1B	3.84E-06
BMP7	5.05E-06
CDKN2A	0.000566
DYRK1B	0.000715
MAPK14	0.000737
CDKN2B	0.00207
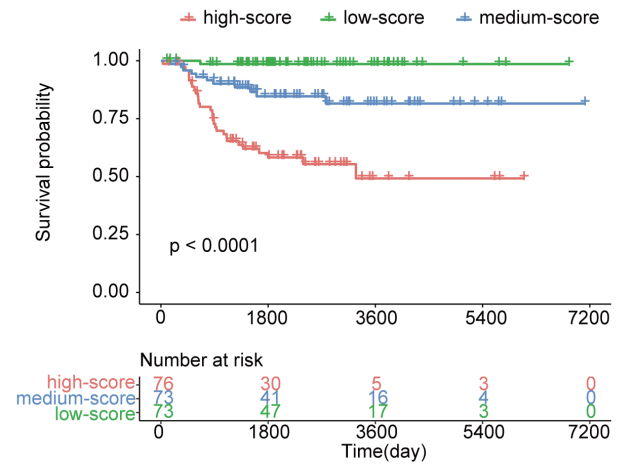
Figure S2 (A) Kaplan-Meier overall survival curves of the nomogram. Patients from the E-MTAB-8248 dataset were stratified into 3 groups according to the nomogram score. The P value was calculated by the log-rank test. (B) ROC curves for 1-, 3-, and 5-year overall survival predictions for the nomogram model in the E-MTAB-8248 dataset.
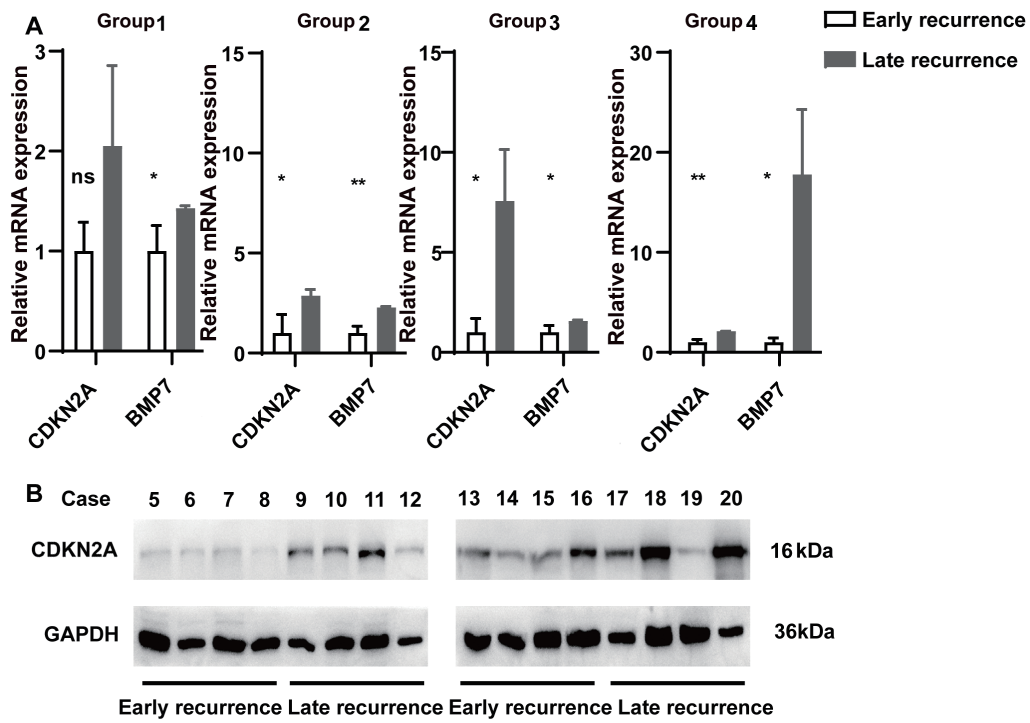
Figure S3 Verification of mRNA and protein expression of CDKN2A and/or BMP7 in human NB samples through RT-PCR and Western blotting. *, P<0.05; **, P<0.01; ns, not significant. One case of early recurrence and one case of late recurrence were randomly assigned in each group.