Supplementary

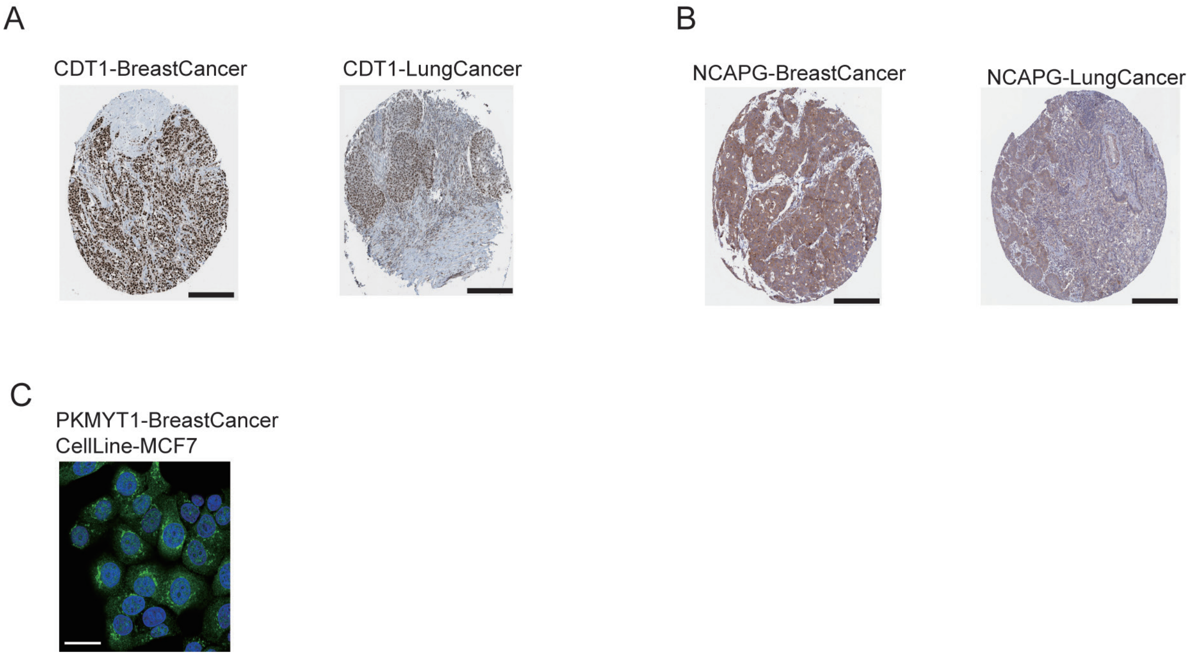

Figure S1 Representative protein-level validation of prognostic genes from the Human Protein Atlas. (A) Immunohistochemistry (IHC) staining of CDT1 in breast and lung cancer tissues shows nuclear localization (scale bar =200 µm). (B) IHC staining of NCAPG reveals cytoplasmic and membranous expression in breast and lung cancer (scale bar =200 µm). (C) Immunofluorescence (IF) staining of PKMYT1 in MCF7 breast cancer cells shows perinuclear and Golgi localization (scale bar = 20 µm).

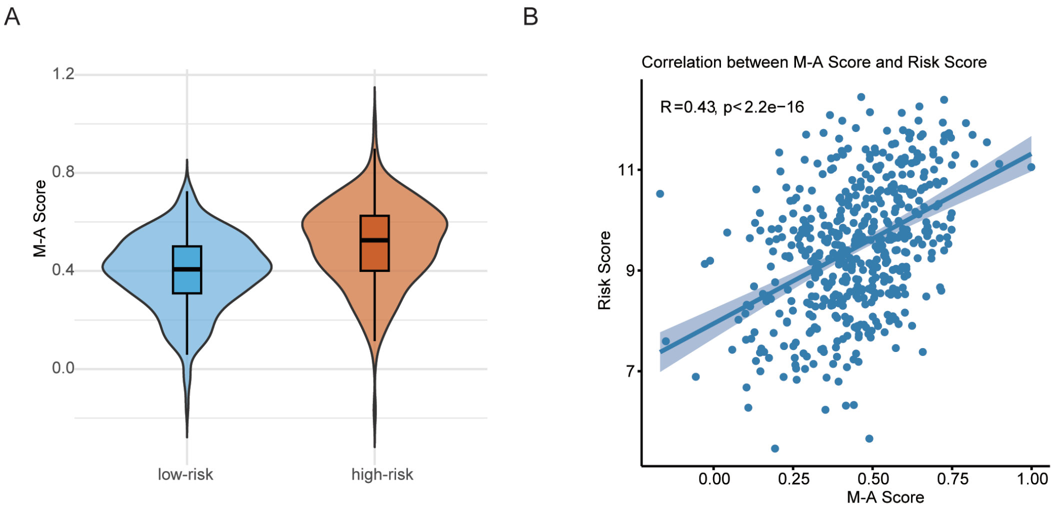

Figure S2 Association between MES/ADRN transcriptomic identity and RiskScore. (A) Distribution of MES-ADRN (M-A) ssGSEA scores in high- and low-risk groups defined by the three-gene model. High-risk patients exhibit significantly elevated M-A scores. (B) Scatter plot showing the positive correlation between M-A score and RiskScore. Each dot represents one patient in the GSE49710 cohort.

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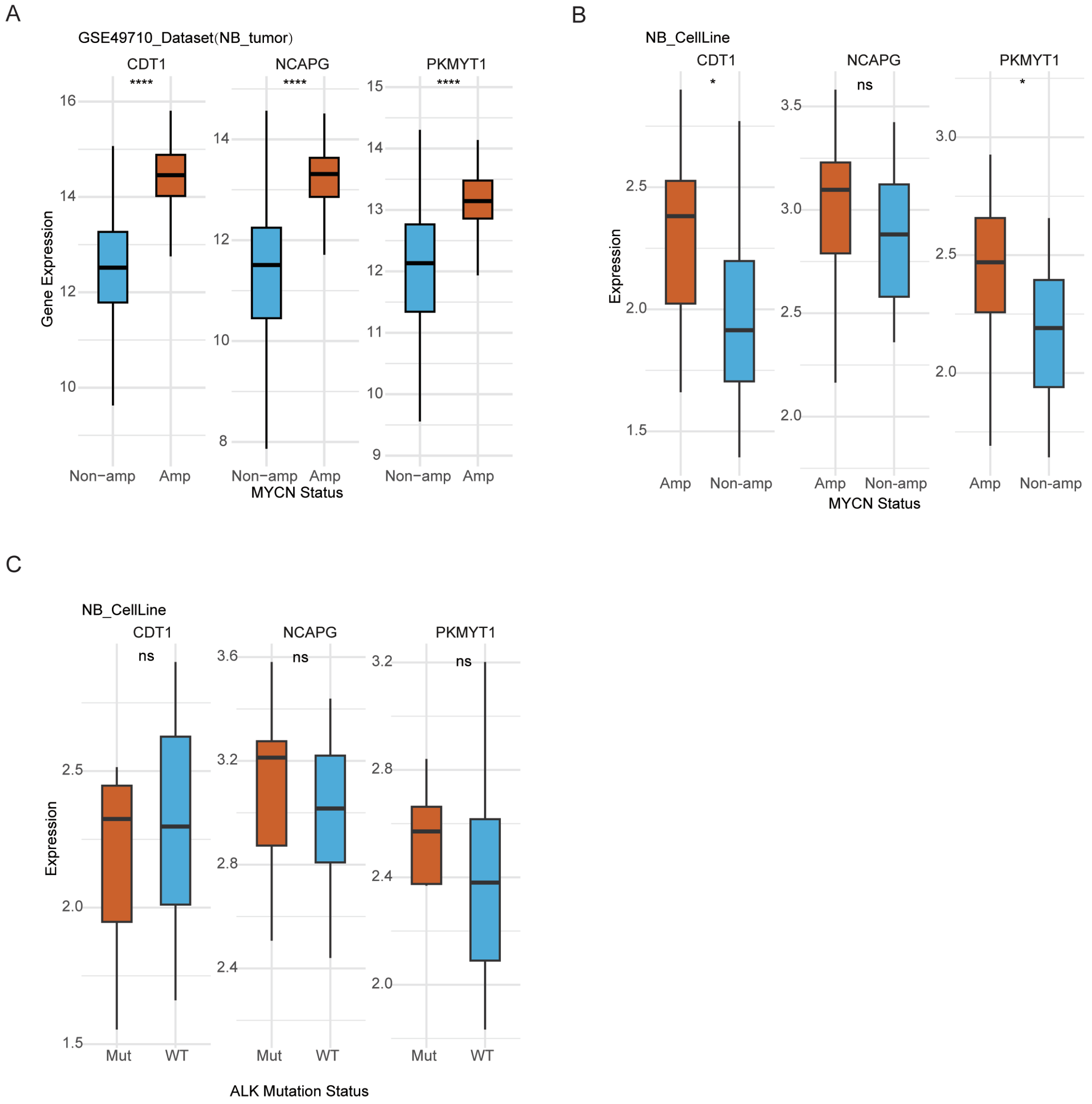

Figure S3 Expression of model genes in MYCN- and ALK-defined subgroups. (A) GSE49710 dataset (patients): All three genes are significantly upregulated in MYCN-amplified tumors. (B) GSE89413 dataset (neuroblastoma cell lines): PKMYT1 and CDT1 show significantly higher expression in MYCN-amplified lines; NCAPG shows a similar trend without statistical significance. (C) GSE89413: No significant differences in gene expression observed between ALK-mutant and wild-type neuroblastoma cell lines. ns: not significant. Asterisks indicate statistical significance: $P<0.05$ (*), $P<0.0001$ (****).

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