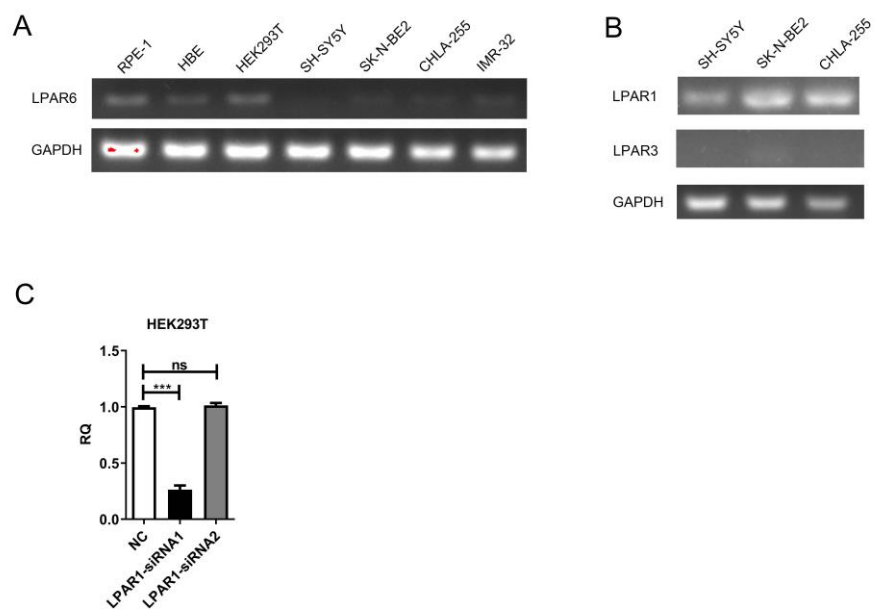


**Figure S1.** The expression pattern of FN1, PIK3R5 and LPAR6 in NB. The R2 database view-a-gene was used to analyze the expression pattern of screened genes based on the average mRNA expression of the 498 NB SEQC dataset, with  $p < 0.05$  regarded as the critical point with statistical significance. (A–C) The association between the FN1 expression and the NB INSS stage (A), likelihood of being high-risk (B) and likelihood of a death event (C). (D–F). The association between the PIK3R5 expression and the NB INSS stage (D), likelihood of being high-risk (E) and likelihood of a death event (F). (G–I) The association between the LPAR6 expression and the NB INSS stage (G), likelihood of being high-risk (H) and likelihood of a death event (I).



**Figure S2.** The expression of LPAR1, LPAR3 and LPAR6 in NB cell lines and non-malignant cell lines. (A–B) The LPAR6 (A), LPAR1 and LPAR3 (B) expression were detected by PCR. (C) The knockdown efficiency of LPAR1 siRNAs was detected in HEK293T cells by real-time PCR.