



Figure S1. Workflow of processes and examples of NB patient OS using microarray data in cBioPortal (TARGET). (A) The list of 964 ECM-related genes was studied for patient OS using the 143 NB tissue sample RNA-sequencing datasets (TARGET) using the Z=2 setting and “auto-calculate” OS setting for TARGET-NBL dataset in PCAT (2-method selection). The 3-method selection featured the steps in the 2-method selection process in addition to the “mean” OS setting in the TARGET-NBL dataset deposited to PCAT. In the 2-method process, 12 genes (*AMBN*, *COLQ*, *ELFN1*, *HAS3*, *HSPE1*, *LMAN1*, *LRP5*, *MUC6*, *RAMP2*, *RUVBL2*, *SSBP1*, and *UMOD*) displayed significantly altered OS and were selected for further investigation. Specifically, the overexpression of 9 of 12 ECM-related genes (*AMBN*, *ELFN1*, *HSPE1*, *LRP5*, *MUC6*, *RAMP2*, *RUVBL2*, *SSBP1* and *UMOD*) correlated with the reduced patient OS using both methods. However, *COLQ*, *HAS3* and *LMAN1* were overexpressed in NB patients with increased OS based on auto-calculate OS setting for the TARGET-NBL dataset in PCAT, while the reverse was true for the 143 NB patient RNA-sequencing datasets (TARGET). OS was also estimated using a stricter 3-method selection workflow using the “mean” setting for the TARGET-NBL dataset in PCAT. Accordingly, 6 ECM-related genes (*i.e.*, *AMBN*, *HSPE1*, *MUC6*, *RAMP2*, *RUVBL2*, and *SSBP1*) showed significantly reduced OS using all 3 methods. (B) Based on the 249 microarray NB patient datasets in TARGET using Z=2 settings, overexpressing *LRP5* correlated with reduced patient OS (log-rank p -values: 7.98e-6).