Figure S1. Copy number variants analysis by single nucleotide polymorphism-array. (A) Genomic profile of patients with NB using single nucleotide polymorphism-microarrays confirming 3q13.31 breakpoints, as indicated by red arrows. (B) Closer view of investigated patients with NB showing breakpoints inside *LSAMP*. (C) Focal alterations of *LSAMP* in NB cell lines. The cell lines on the right have *LSAMP* rearrangements, whereas those on the left do not. *LSAMP*, limbic system-associated membrane protein; NB, neuroblastoma.

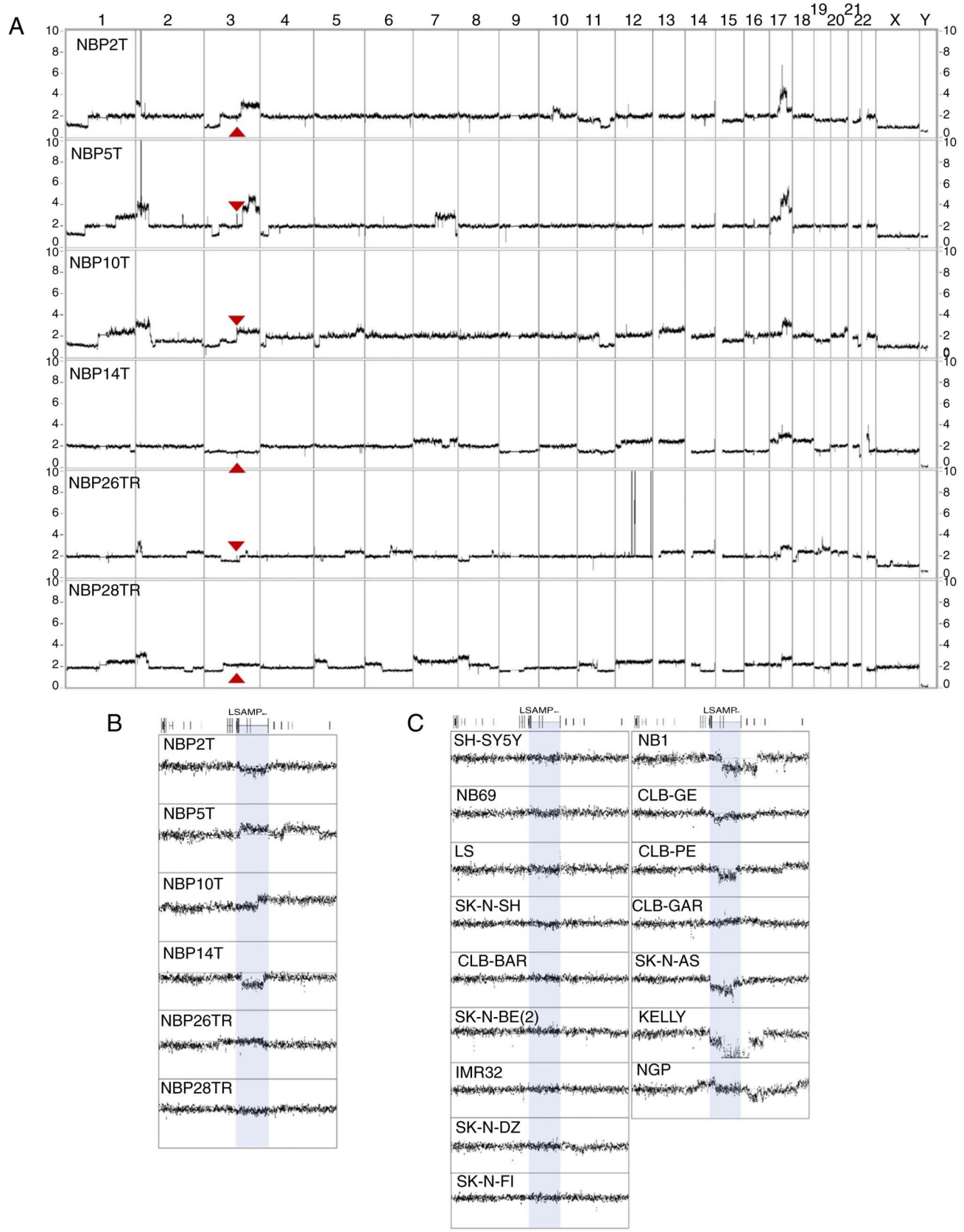

Figure S2. Verification of detected aberrations by Sanger sequencing. New structures formed in the breakpoint region. The segmental alterations involving *LSAMP* usually occur within the same chromosome as a focal deletion or as a tandem duplication and, in NBP5T also in combination with a translocation. The specific breakpoints associated with the *LSAMP* aberrations are indicated above the respective electropherogram, whereas the extended sequence with fusion region indicated by underlining is shown below each panel. *LSAMP*, limbic system-associated membrane protein.

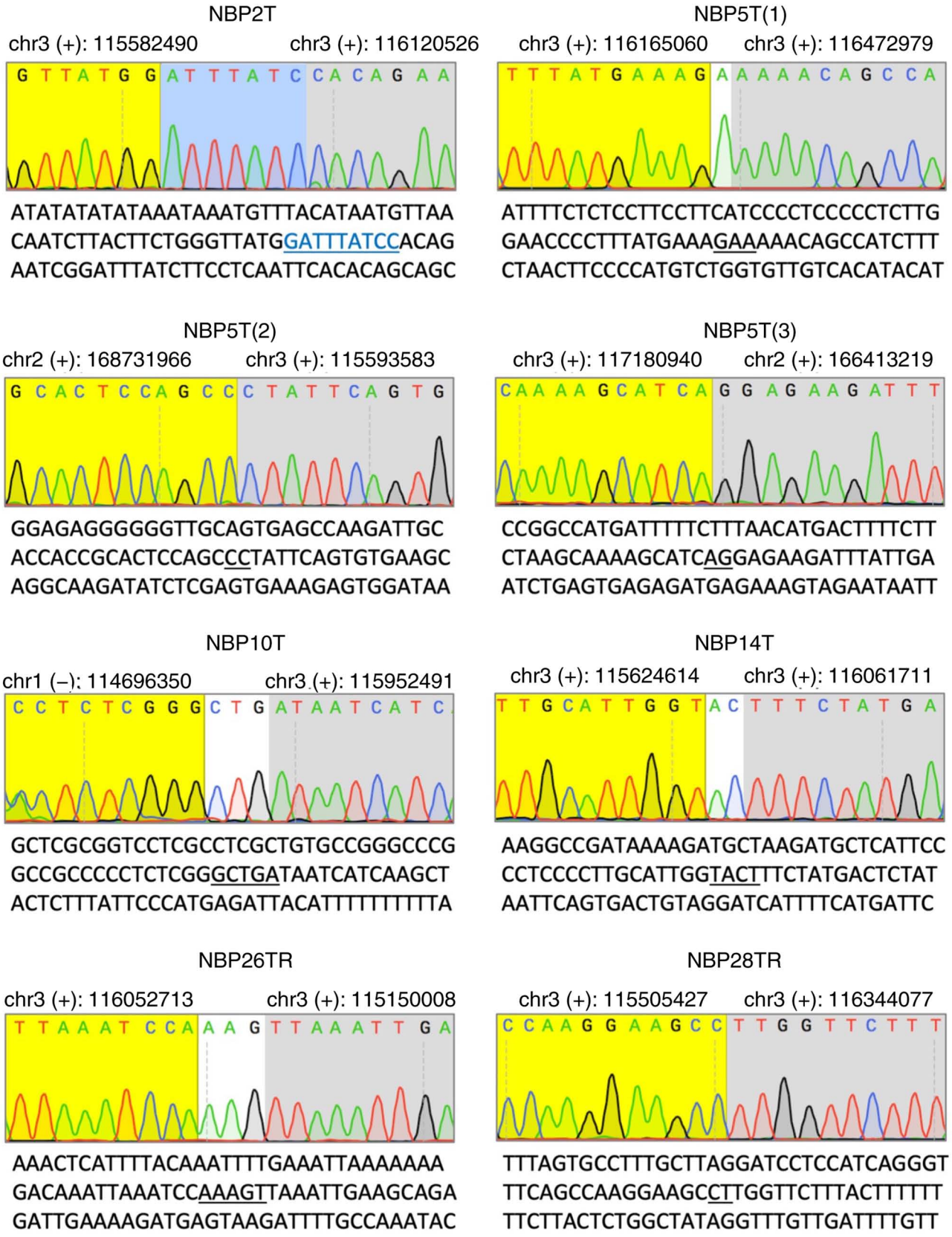

Figure S3. *LSAMP* expression levels. *LSAMP*, limbic system-associated membrane protein; sh, short hairpin; SVs, structural variants. (A) Expression levels of *LSAMP* from three different exon boundaries in neuroblastoma cell lines. (B) *LSAMP* expression levels after silencing (left panel) and overexpression (right panel), indicating the efficiency of the transfection and transduction. (C) Different transcripts of *LSAMP* in blue; the TaqMan probes used in green. (D) Viability of KELLY cells normalized against control after *LSAMP* re-expression at 96 h; data were statistically analyzed using two-sided unpaired t-test. *LSAMP*, limbic system-associated membrane protein; sh, short hairpin. ***P<0.001.

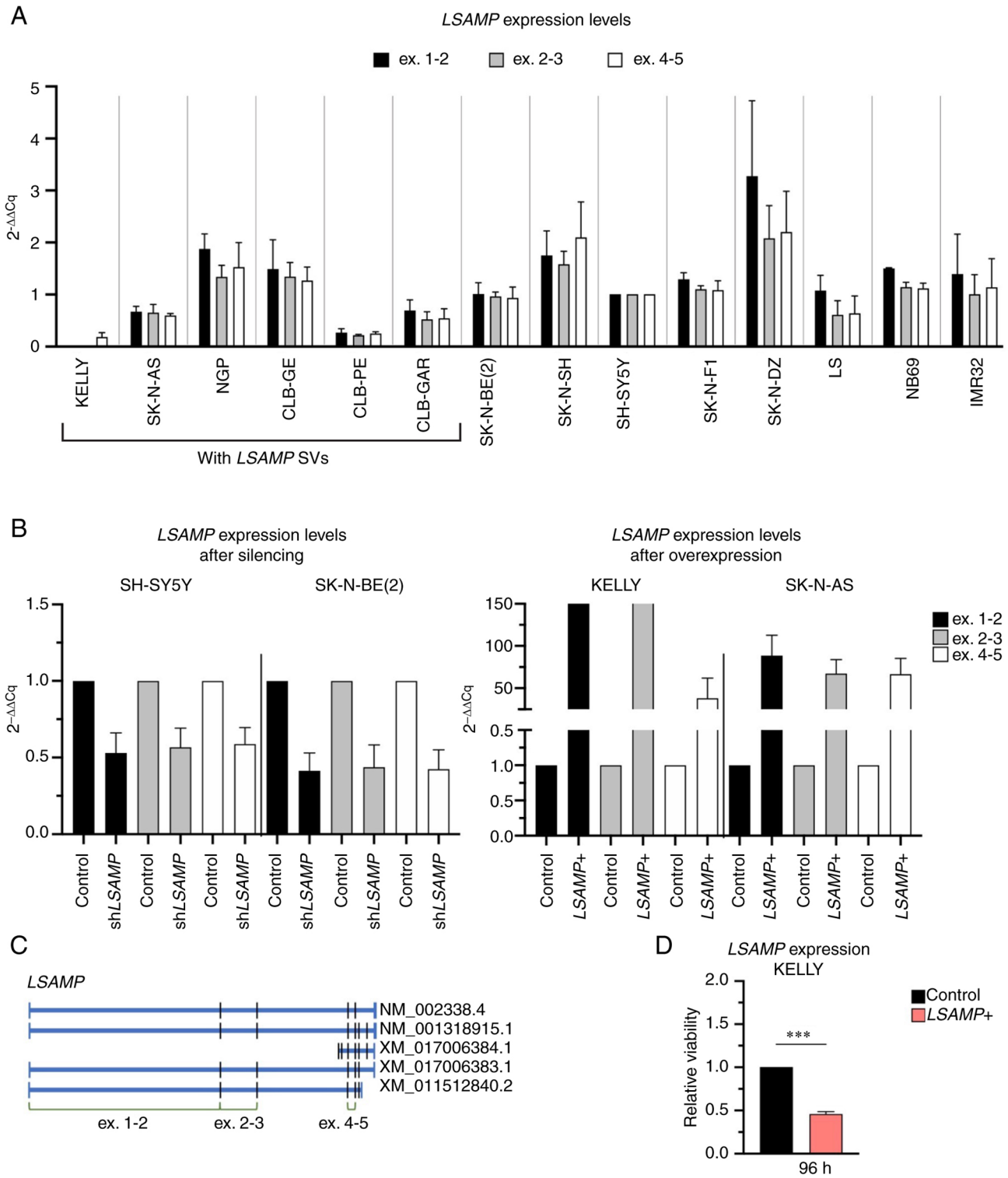

Figure S4. Effect of *LSAMP* knockdown on neurite extension. No marked impact on neurite extension could be seen in standard medium or in the presence of RA after *LSAMP* knockdown. Cells viewed under x40 magnification. *LSAMP*, limbic system-associated membrane protein; RA, retinoic acid; sh, short hairpin.

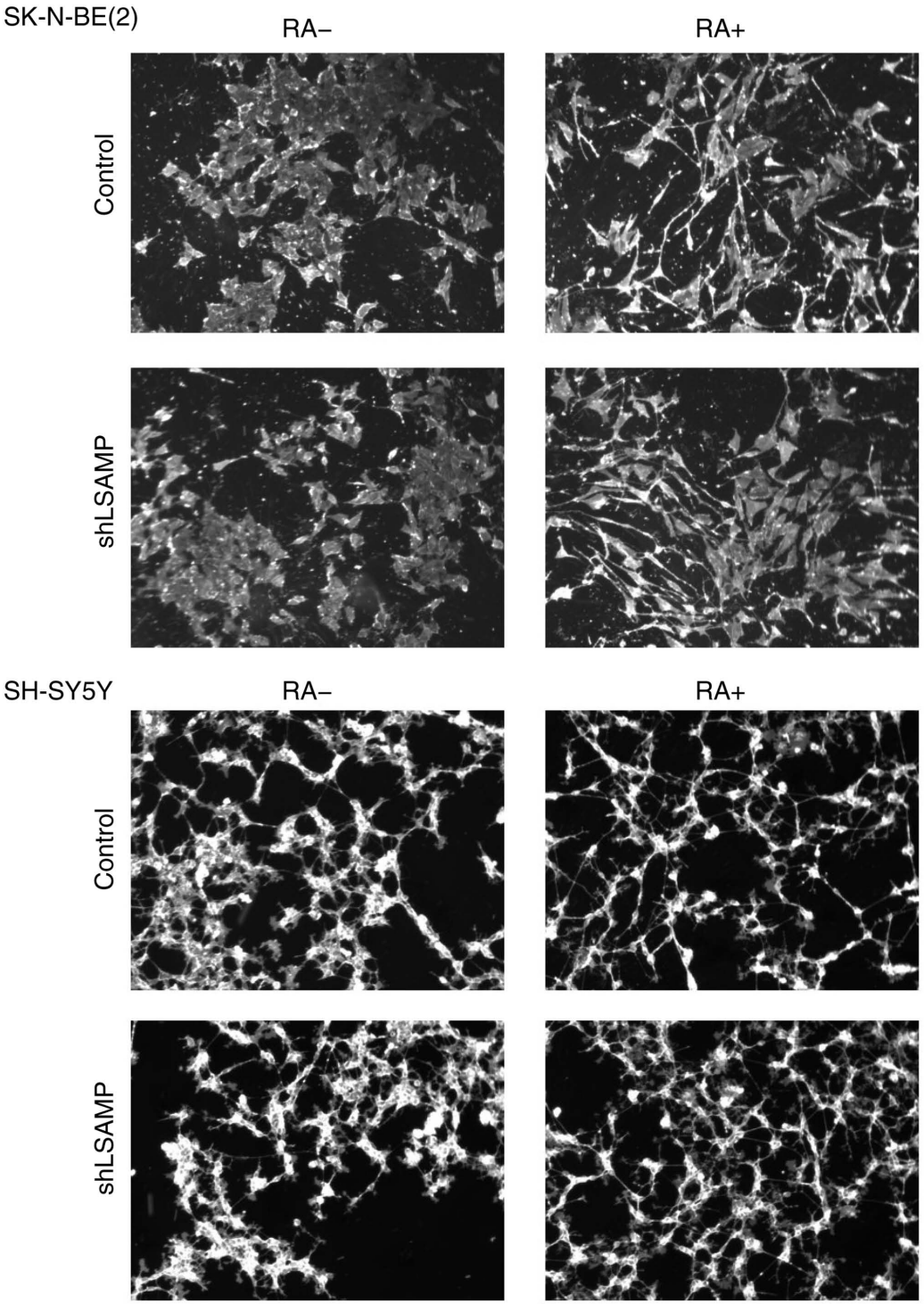

Figure S5. *LSAMP* expression and survival in relation to MNA. (A) Low *LSAMP* expression (indicated in red) was associated with poor overall and event-free survival when considering the entire cohort (left panels) and non-MNA cases (middle panels), and to a lesser extent in MNA cases (right panels). The survival curves were made using the Kaplan-scan cutoff method. (B) No statistical difference using one-way ANOVA was apparent in *LSAMP* expression levels when comparing MNA and non-MNA cases. Log2-transformed expression levels are shown. (C) Distribution of *LSAMP* levels over all 498 cases. *LSAMP*, limbic system-associated membrane protein; MNA, *MYCN*-amplified; Raw, unadjusted P-value; Corr, Bonferroni corrected P-value.

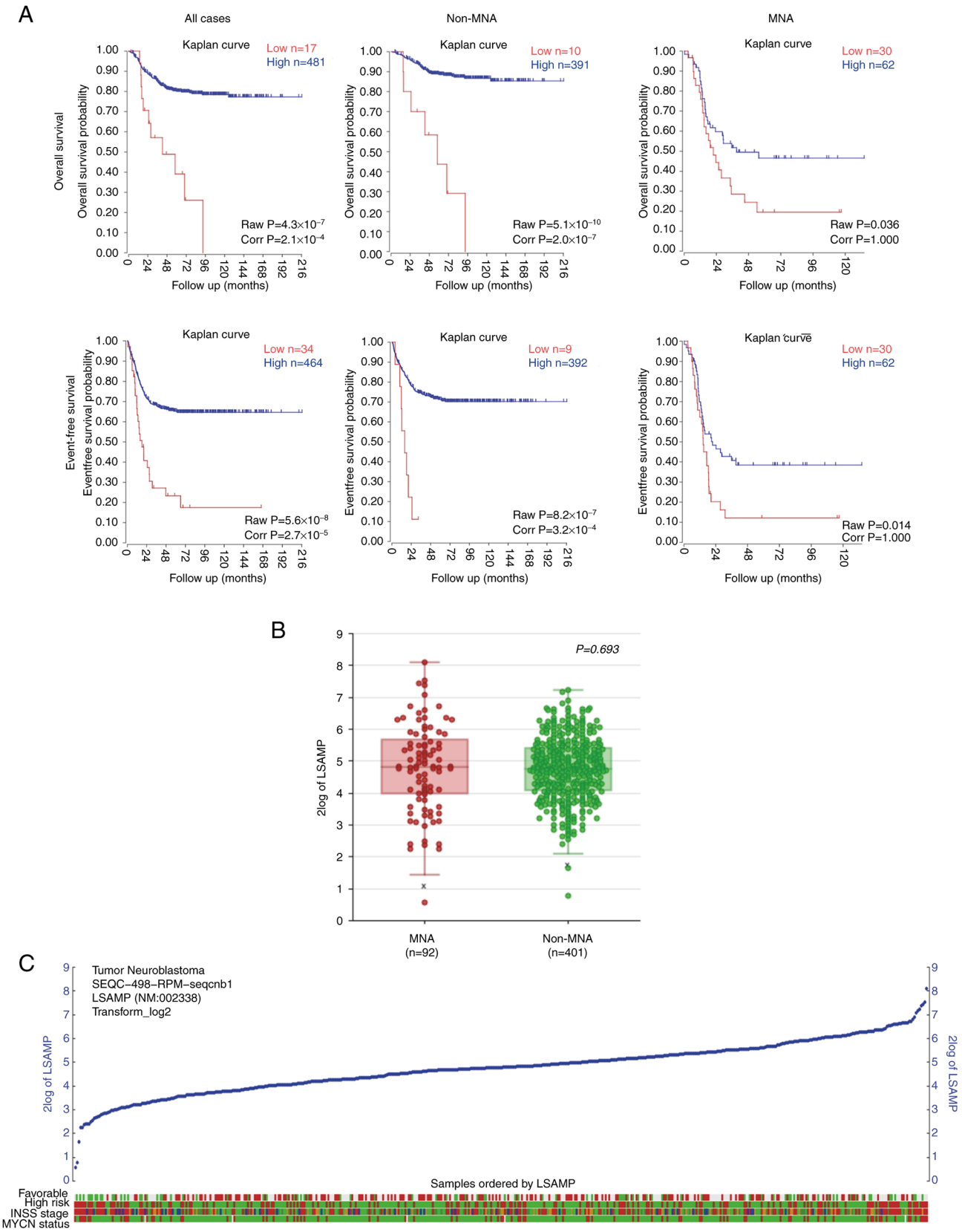

Figure S6. Survival in relation to gene expression of other members of the IgLON family and correlation between the expression levels of each IgLON family member. (A) Low expression (indicated in red) was associated with poor overall survival (upper panels) and poor event-free survival (lower panels) for other members of the IgLON family, *OPCML, NTM, IGLON5* and *NEGR1*. (B) Correlation between the expression levels of the different members of the IgLON family. *IGLON5*, Ig-like cell adhesion 5; *LSAMP*, limbic system-associated membrane protein; *NEGR1*, neuronal growth regulator 1; *NTM*, neurotrimin; *OPCML*, opioid-binding protein/cell adhesion molecule like; Raw, unadjusted P-value; Corr, Bonferroni corrected P-value.