



**S1 Fig. Loss of Notch1 dimerization suppresses target gene expression in MK4 cells (supporting Fig 1, see S1 Data for raw data).** (A-B) EMSA data for purified proteins binding to probes containing two CSL (A) or SPS (B) sites. The number of balls marks the occupancy of sites, arrows below indicate orientation of binding sites in probes. (C-D) The average sites filled were plotted against RBPj concentrations to calculate the cooperativity factor “C” on CSL (C) and SPS (D) probes. (E) Relative expression of Notch target genes in mK4 cells overexpressing either N1ΔE or N1<sup>RA</sup>ΔE as determined by RNA Seq (all replicates are shown, values ranked per row. Green arrows indicate targets elevated more in N1<sup>RA</sup>ΔE, red arrows indicate targets repressed in N1<sup>RA</sup>ΔE relative to control. (F) Luciferase activation assays were used to analyze the homo and heterodimerization properties of Notch1 and Notch2 on a dimer-dependent reporter gene (Hes5-Luciferase) and a dimer-agnostic reporters (Hey2-Luciferase). As previously shown (Arnett et al., 2010), the dimer interface involves three amino acids, the Arg (R) mutated in this study, as well as the positively charged Lys (K1935, Notch1) and a negatively charged Glu (E1939, Notch1 or Asp (D1899) at the equivalent position in Notch2) that form salt bridges between NICD molecules. Dimer formation is critical for Notch-dependent activation of the Hes5 reporter, and mutating any of these amino acids abrogates activation. Notably, by co-expressing two Notch protein with complementary mutations, one in which K1935 was changed to E (N1KE), and a second in which D1899 was changed to K (N2DK) leads to strong enhancement in Luciferase expression, explained by achieving a more favorable conformation of the complementing mutant dimer. Note synergistic complementation between N1KE and N2DK, but not between N1KE and N2KD, providing strong evidence of a cooperative heterodimer. Significance tested by a student t test.