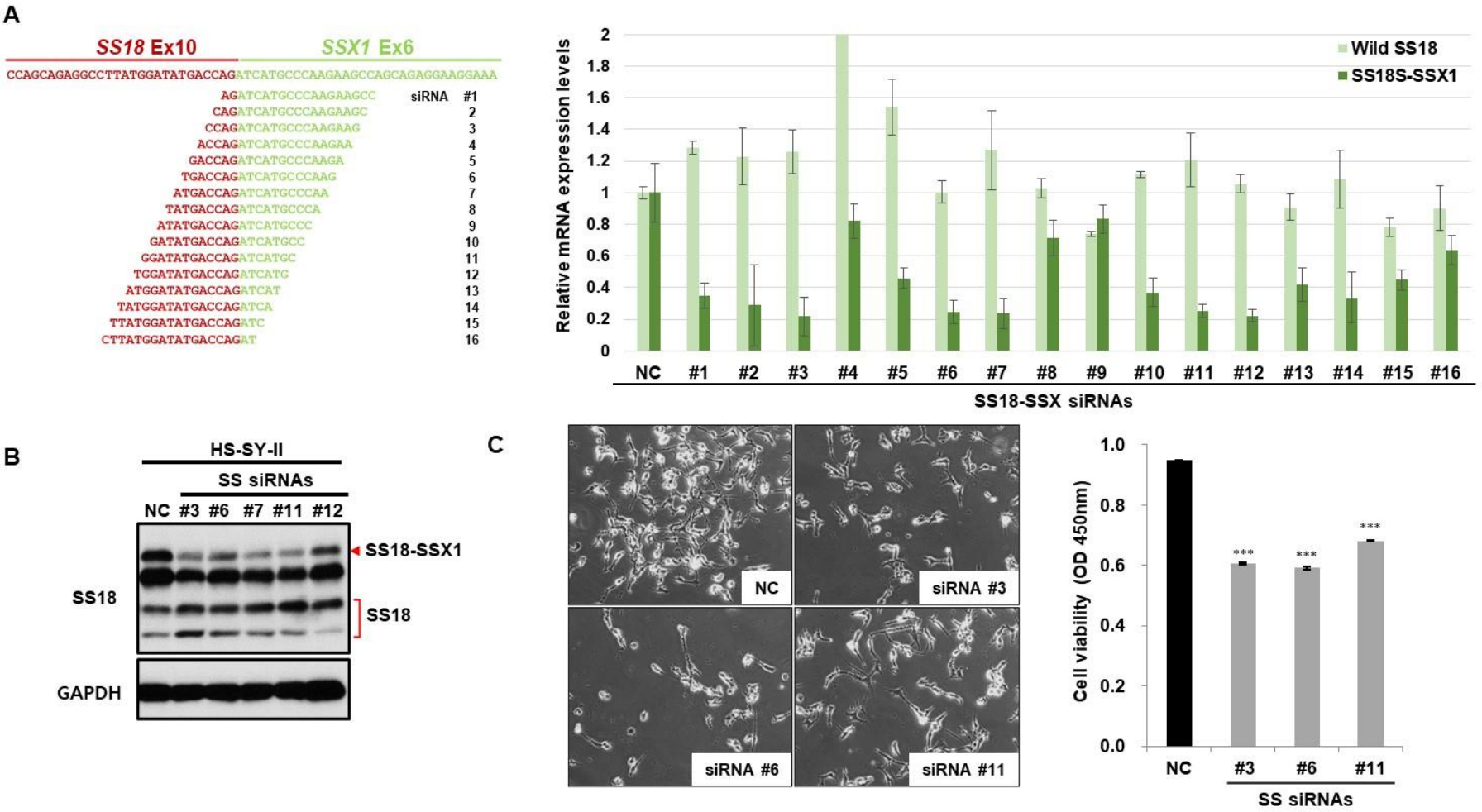

S6 Fig. Silencing effect of siRNAs targeting the junction region of *SS18-SSX* fusion. (A) The left panel shows the scheme of the junction sequence of *SS18-SSX* (*SS*) mRNA and the 16 siRNA candidates targeting the junction region, while the right panel shows the relative *SS* mRNA level upon *SS* siRNA treatment. HS-SY-II cells were treated with *SS* siRNAs Nos. 1 to 16 at a concentration of 50 nM. After 72 hours, analysis was done with the RNA extracted from the cells. Wild-type SS18 (SYT) level was analyzed using a primer pair targeting the SS18 C-terminal region, and mRNA level of *SS* fusion was determined using

a primer pair targeting the junction region of the fusion gene. *GUSB* was used as an internal control for the quantitative reverse transcription polymerase chain reaction reaction. The bar graphs illustrate the average value of triplicates, and error bars represent the standard deviation. (B) Immunoblots show the expression of SS fusion (red arrowhead) and SS18 (red bracket) proteins in cells transfected with the siRNAs. *SS* siRNAs Nos. 3, 7, and 11 attenuated SS18 expression, as compared to the negative control, scrambled siRNA control. (C) Growth rate assay upon *SS* siRNA treatment. HY-SY-II cells (1×10^5) expressing SS fusion gene were seeded into a 6-well plate and then treated with 50 nM siRNA. Twenty-four hours later, the cells were replated into the 96-well plates with 5,000 cells per well in 100 μL media in triplicate. After 48 hours, the cell growth was measured using WST assay (right panel) and representative images were acquired (left panel).