Supplementary Figure 1. *RINT1* c.1334-5delA, c.1334-1_1335delGTT minigene assay

A) The genomic DNA region of interest that contains a putative splicing mutation found in the patient with breast cancer. Exonic and intronic sequences are in capital and small letters, respectively. Black squares denote the splice-acceptor site deletions. B) Schematic representation of minigene assay construct. The dark and light gray boxes represent SV40 promoter and 5 ′and 3 ′exons in pSPL3 vector, respectively. The white box represents *RINT1* exon10. Double parallel diagonal bars indicate the border of *RINT1* intron10 and pSPL3 intron. C) Agarose gel electrophoretic profile of RT-PCR products. Migration patterns of RT-PCR products from HEK293 cells and COS-7 cells with or without cycloheximide treatment are shown in the picture. The expected wild-type product size is 399bp, and there is no visible difference in size between wild-type and mutant RT-PCR products. D) Chromatograms derived using construct A. Left chromatograms show the intron-exon junction in wild-type and mutant construct A. Right chromatograms show the splicing outcomes of wild-type and mutant. The dashed lines indicate the sites of deletions. The same profiles were observed using construct B (data not shown).