Figure S1. KEGG pathway analysis of differentially expressed genes in human umbilical vein endothelial cells following lncRNA-antisense noncoding RNA in the INK4 locus overexpression. The top 10 Gene Ontology pathways of upregulated gene sets are presented. KEGG, Kyoto Encyclopedia of Genes and Genomes.

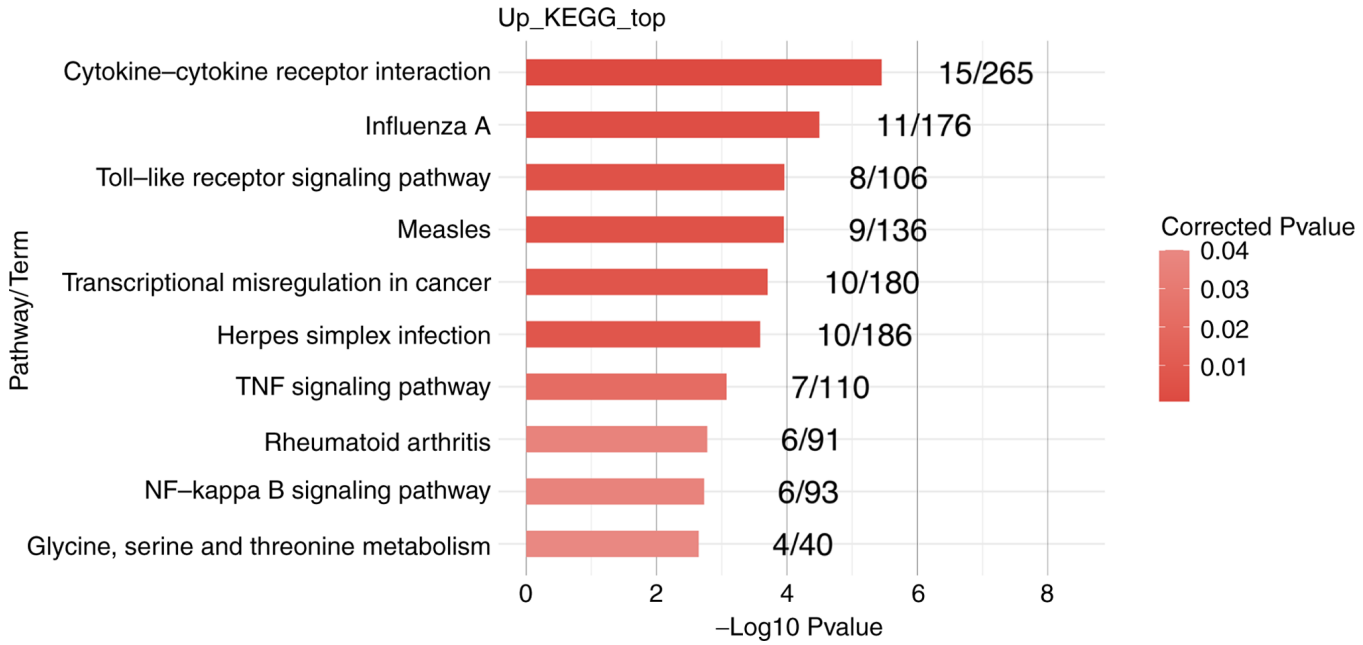

Figure S2. KEGG pathway analysis of differentially expressed genes in human umbilical vein endothelial cells following lncRNA-antisense non-coding RNA in the INK4 locus overexpression. Top 10 Gene Ontology pathways of downregulated gene sets are presented. KEGG, Kyoto Encyclopedia of Genes and Genomes.

Figure S3. AS pattern analysis following ANRIL overexpression in HUVECs. Integrative Genomics Viewer-sashimi plots of ANRIL-regulated ES of (A) ATP13A2, (B) SIGIRR and (C) HDAC7 demonstrate AS changes in ANRIL overexpression and Ctrl cells. The transcripts for the gene are presented below The schematic diagrams depicts the structures of ASEs, AS1 (purple) and AS2 (green). The exon sequences were denoted by boxes and intron sequences by the horizontal line. RNA-seq quantification and RT-qPCR of RNA validation of ASEs were presented in the histogram. The altered ratio of ASEs in RNA-seq was calculated using as follows: AS1 junction reads/(AS1 junction reads + AS2 junction reads). The altered ratio of ASEs in qPCR was calculated as follows: AS1 transcript level/AS2 transcript level. Student's t test was performed to compare ANRIL-OE and Ctrl cells. **P<0.01 vs. Ctrl. HUVECs, human umbilical vein endothelial cells; ANRIL, lncRNA-antisense non-coding RNA in the INK4 locus; A3SS, alternative 3' splice site; ES, exon skipping; ASEs, alternative splicing events; RT-q, reverse transcription-quantitative; Ctrl, control; RNA-seq, RNA-sequencing.