Figure S18

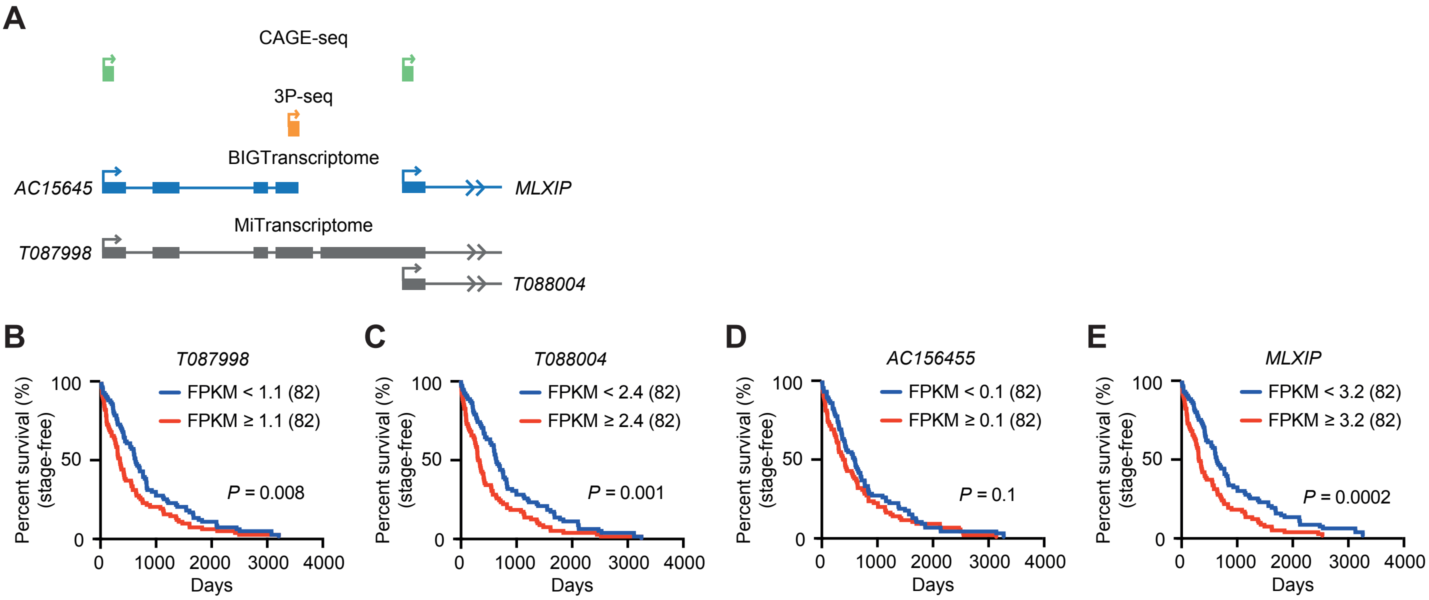

Figure S18. Survival analysis for liver cancer samples based on mis-annotated transcripts

(A) Gene models of a protein-coding gene, *MLXIP*, and a lncRNA, *AC156455*, in BIGTranscriptome and MiTranscriptome. (B-E) Survival analyses for TCGA liver cancer patient samples based on the gene models. 164 samples including termination events were divided into two groups, the top 50% and bottom 50%, according to the median FPKM values of *T087998* (B), *T088004* (C), *AC156455* (D), and *MLXIP* (E).