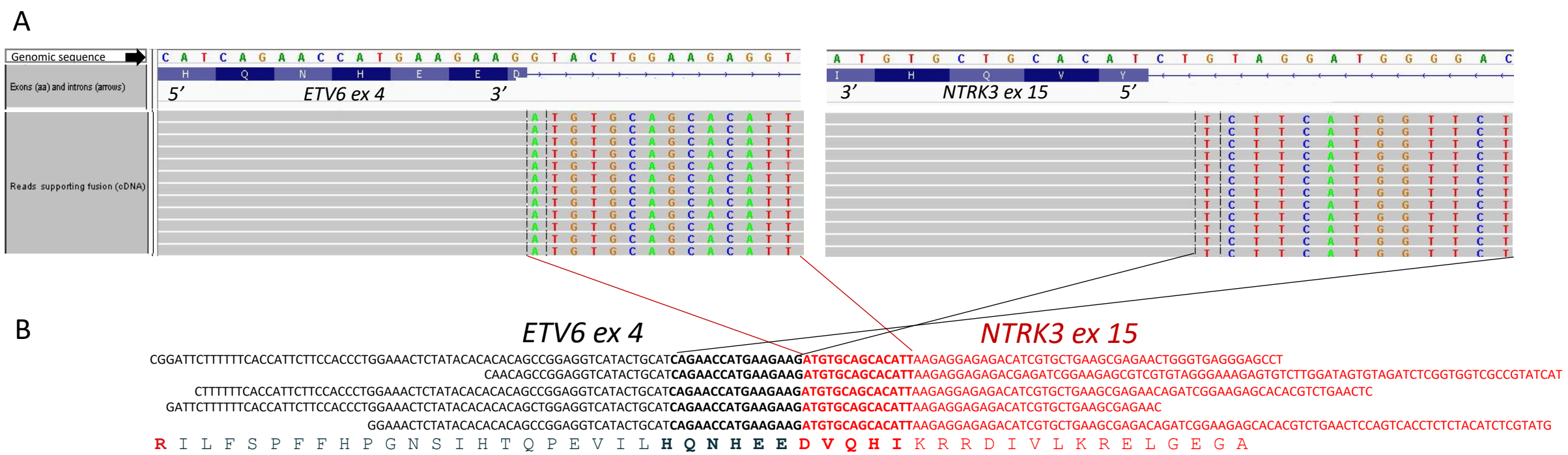

Supplemental Figure 1: Genomic alignment of the sequenced cDNA reads revealing a *ETV6-NTRK3* fusion. (A) Screenshot from the Integrated Genome Viewer (IGV) showing a split view of the genomic alignment of selected reads containing *ETV6-NTRK3* fusion transcripts. Each grey horizontal bar represents a single sequenced molecule that aligns to that genomic region. The portion of each read that does not align to the same genomic region is shown as a sequence of readable nucleotides. The readable sequence of nucleotides after *ETV6* exon 4 aligns to *NTRK3*exon 15 and the readable sequence of nucleotides before *NTRK3* exon 15 aligns to *ETV6* exon 4. (Exons are represented by the sequence of amino acids they encode for (single letters in blue rectangles); introns as a sequence of arrows). (B) Five representative of ~2000 sequenced reads from cDNA containing the fusion transcripts and corresponding amino acid sequence.