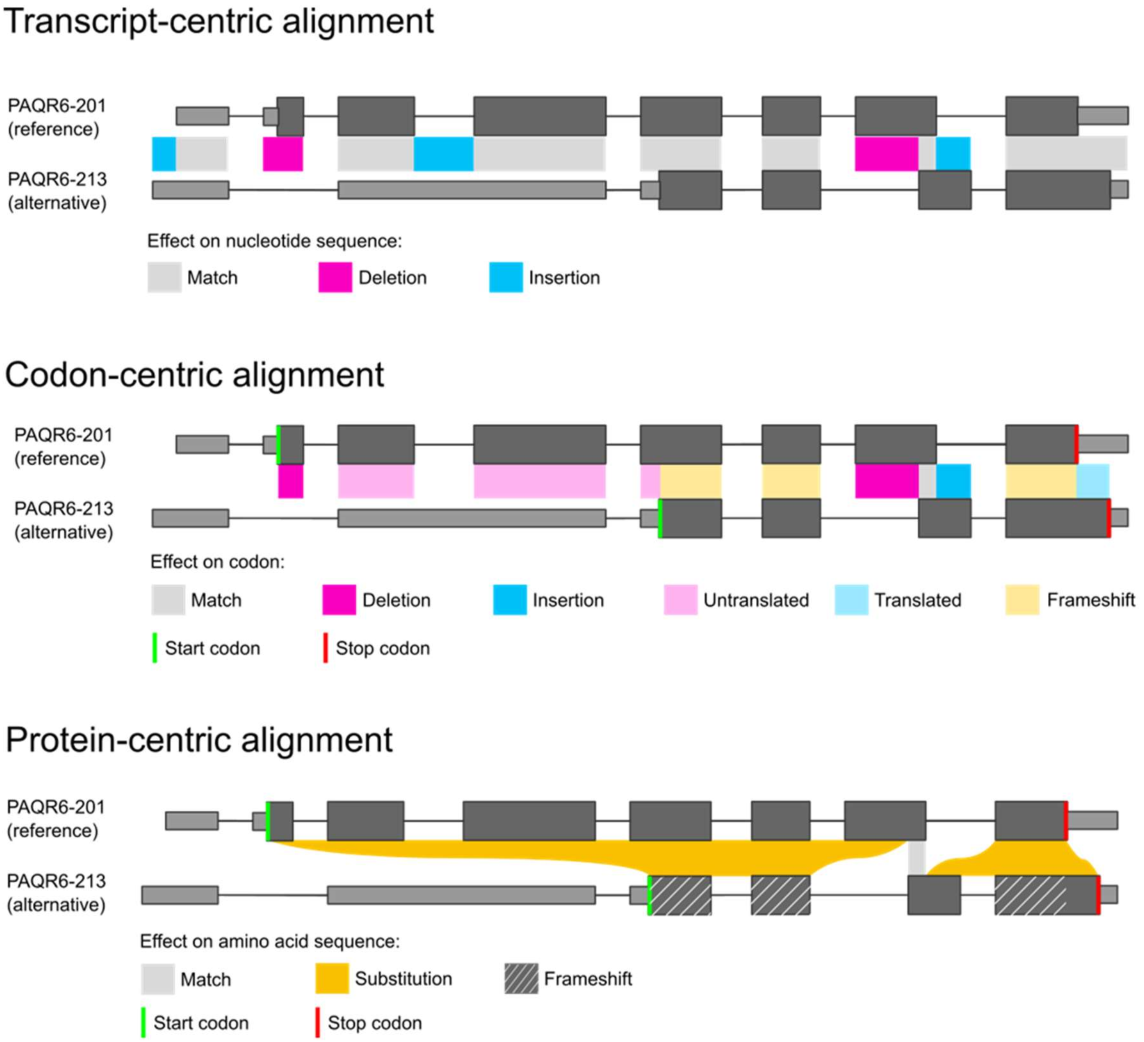

Transcript-centric alignment

Codon-centric alignment

Protein-centric alignment

Supplementary Figure S2: Biosurfer implements a multi-layered alignment to track source of protein alterations.

Biosurfer utilizes a multi-layered comparison that integrates both exon-intron structure and protein-centric perspectives for comparing isoforms. Here is shown a particularly complex example of the comparisons between *PAQRG* isoforms annotated in GENCODE, to illustrate the utility of Biosurfer. Note that though the terminology in each level is similar (Match, Deletion, etc.), they refer to different modes of comparison (e.g., nucleotides versus codons).