



### Flowchart for application of in silico codes PP3, BP4, and BP7

\*AND no predicted differences in splicing (SpliceAI < 0.2)

\*Including silent, and apparent “missense” or “single amino acid in-frame deletions” for which there is a predicted splice effect

††Excluding ± 1,2 positions

\*\*Core splice motif includes last three nucleotides and first nucleotide of the exon