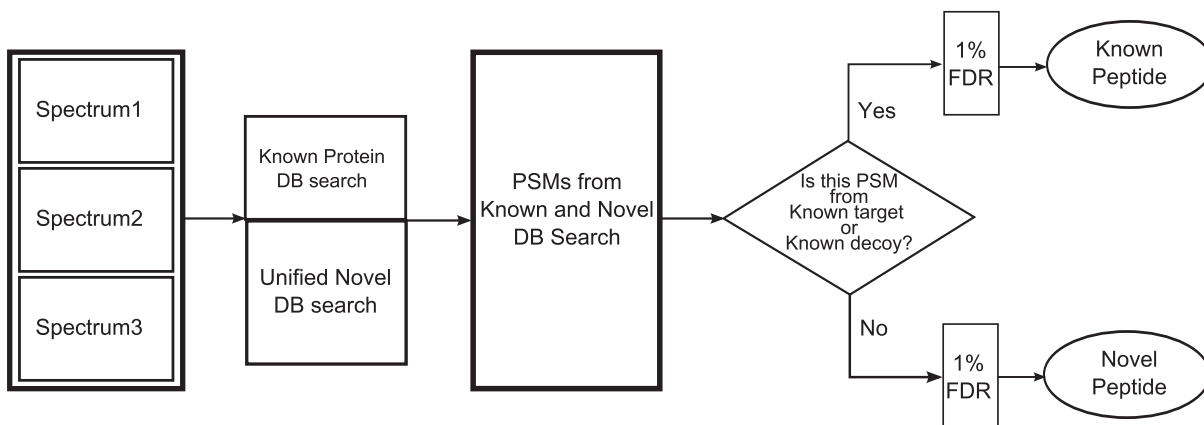
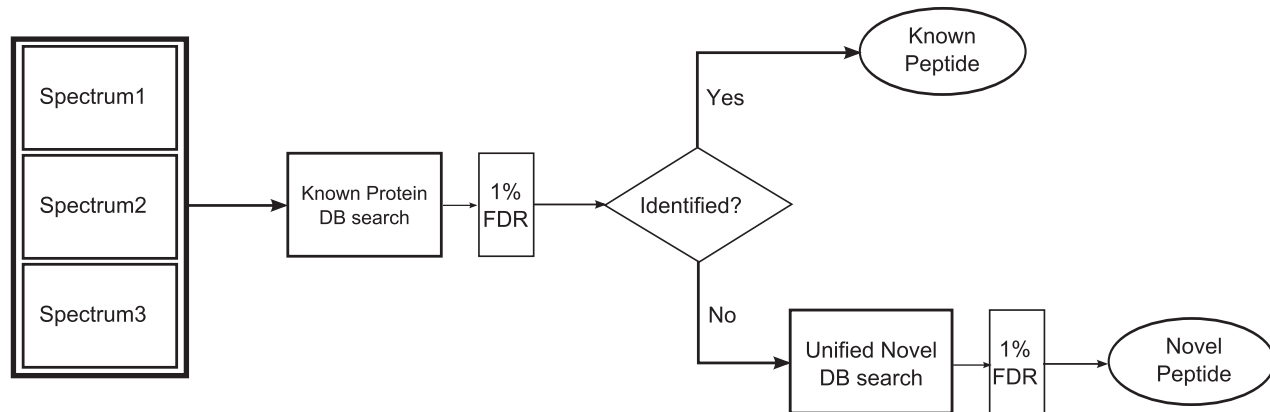


(a) Combined-FDR



(b) Separate-FDR



(c) Two-Stage-FDR

Figure S.1: Diagram describing different FDR based error control strategies applied in this study.

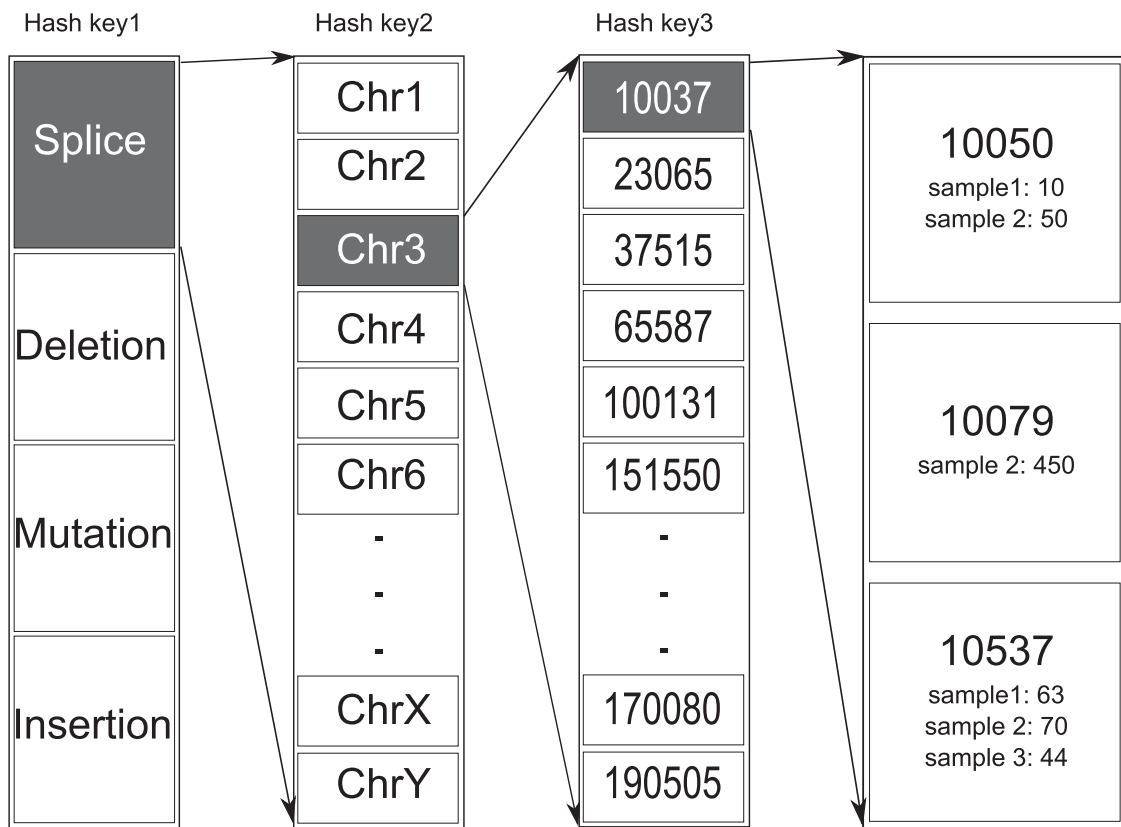


Figure S.2: Structure of hash table for accessing the original RNA-seq meta information





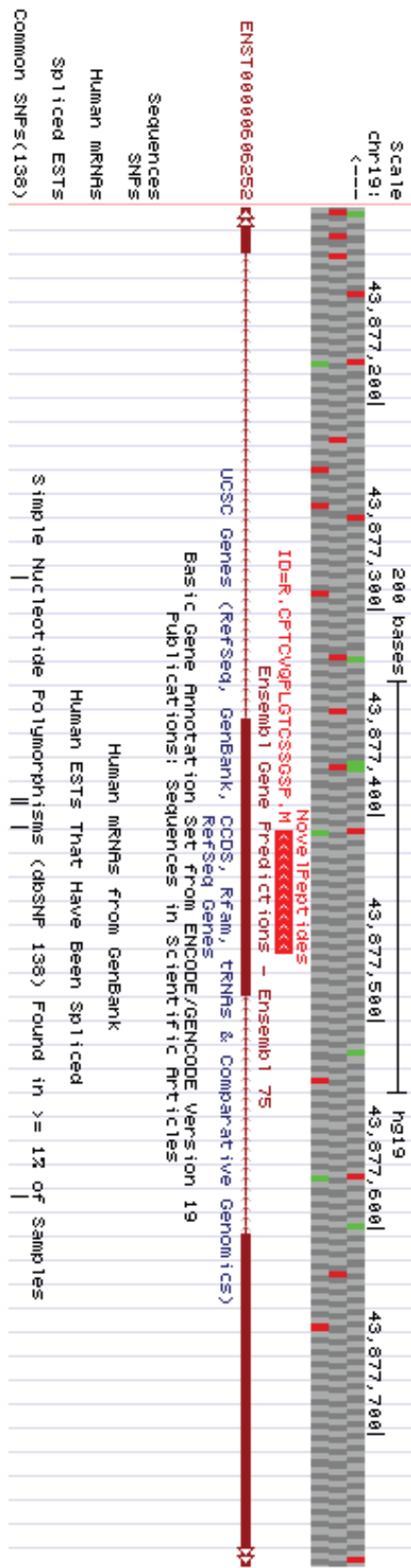


Figure S.5: UCSC genome browser plot of peptide identification in a possible novel gene area where a gene prediction method also reported as a possible gene.