

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

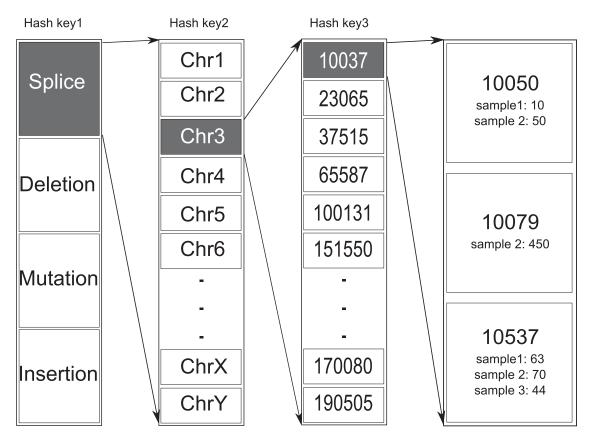


Figure S.2: Structure of hash table for accessing the original RNA-seq meta information

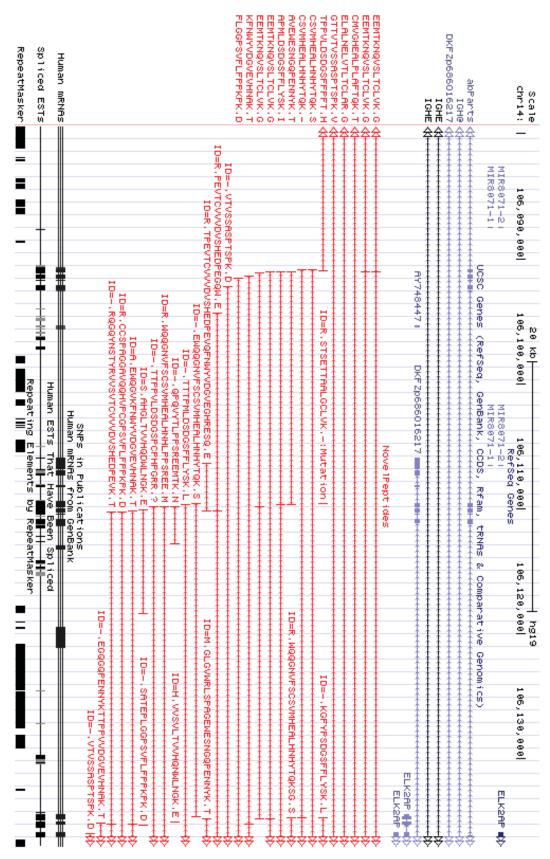


Figure S.3: UCSC genome browser plot of our novel peptide identifications within complex immunogloblin region rearrangements included in our peptide identification result.

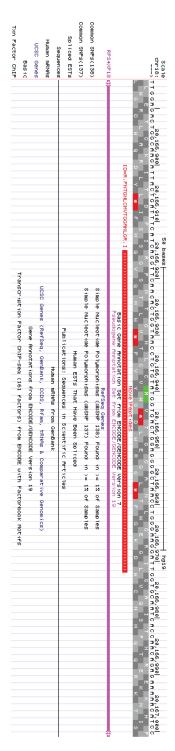


Figure S.4: UCSC genome browser plot of peptide identification in pseudo gene area.

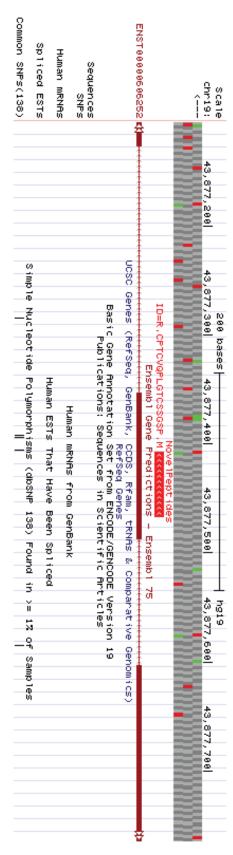


Figure S.5: UCSC genome browser plot of peptide identification in a possible novel gene area where a gene prediction method also reported as a possible gene.