Figure S4. H-B-01 sample output figure of IMonitor. (A) Sequence length distribution. (B) Saturation curve, rarefaction studies of sequences. Sub-sequences are randomly selected and observed unique CDR3 number and predicted CDR3 number (Chao1 corrected algorithm) are calculated. (C) CDR3 nucleotide length distribution. (D) CDR3 abundance distribution. (E) CDR3 amino acid frequencies sectional content. (F) Top ten frequency of CDR3 amino acid. (G) Length distribution of V/D/J gene in CDR3 region. (H) Deletion length distribution of V/D/J gene. (I) Insertion length distribution of between V and D gene, D and J gene. (J) Hyper-mutation, Only for Ig. (K), J gene usage. (L) V gene usage. (M) Three-dimensional graph of V-J pairing.