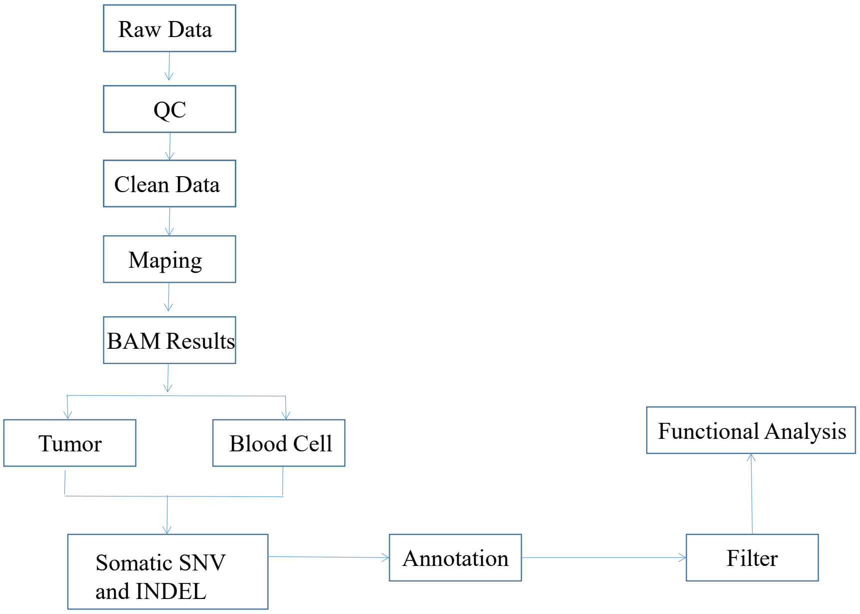

Figure S1 Analysis flow chart of the sequencing results. QC, quality control; BAM, binary sequence alignment/map format; SNV, single-nucleotide variants; INDEL, insertion-deletion.

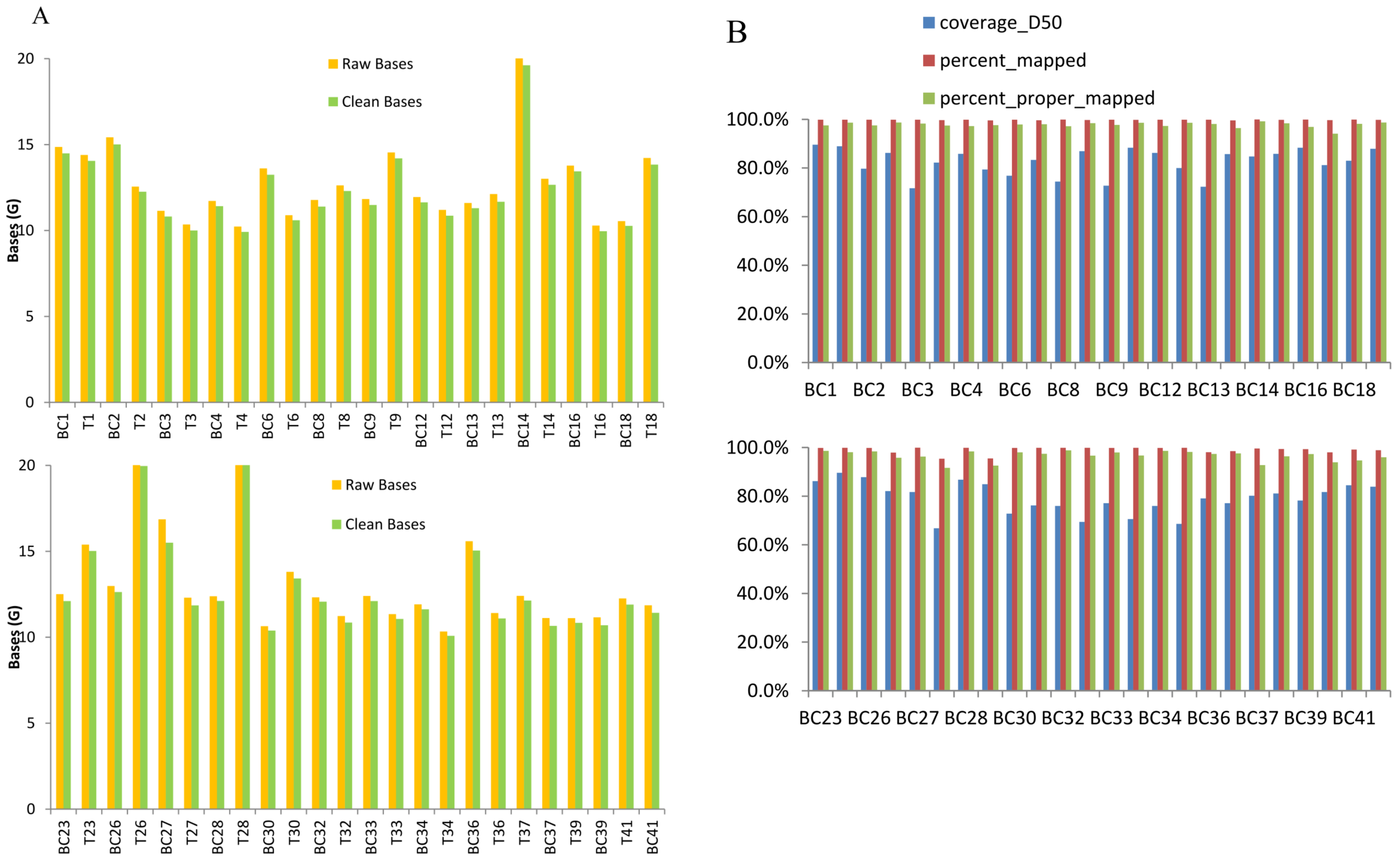

Figure S2 Quality control and comparison results. (A) Total number of read bases in each sample. The total number of read base groups in each sample was higher than 10 Gb, which met the requirements for whole-exome sequencing analysis. (B) The proportion of reads mapped to the reference genome in each sample. BC, blood cell, T, tumor.