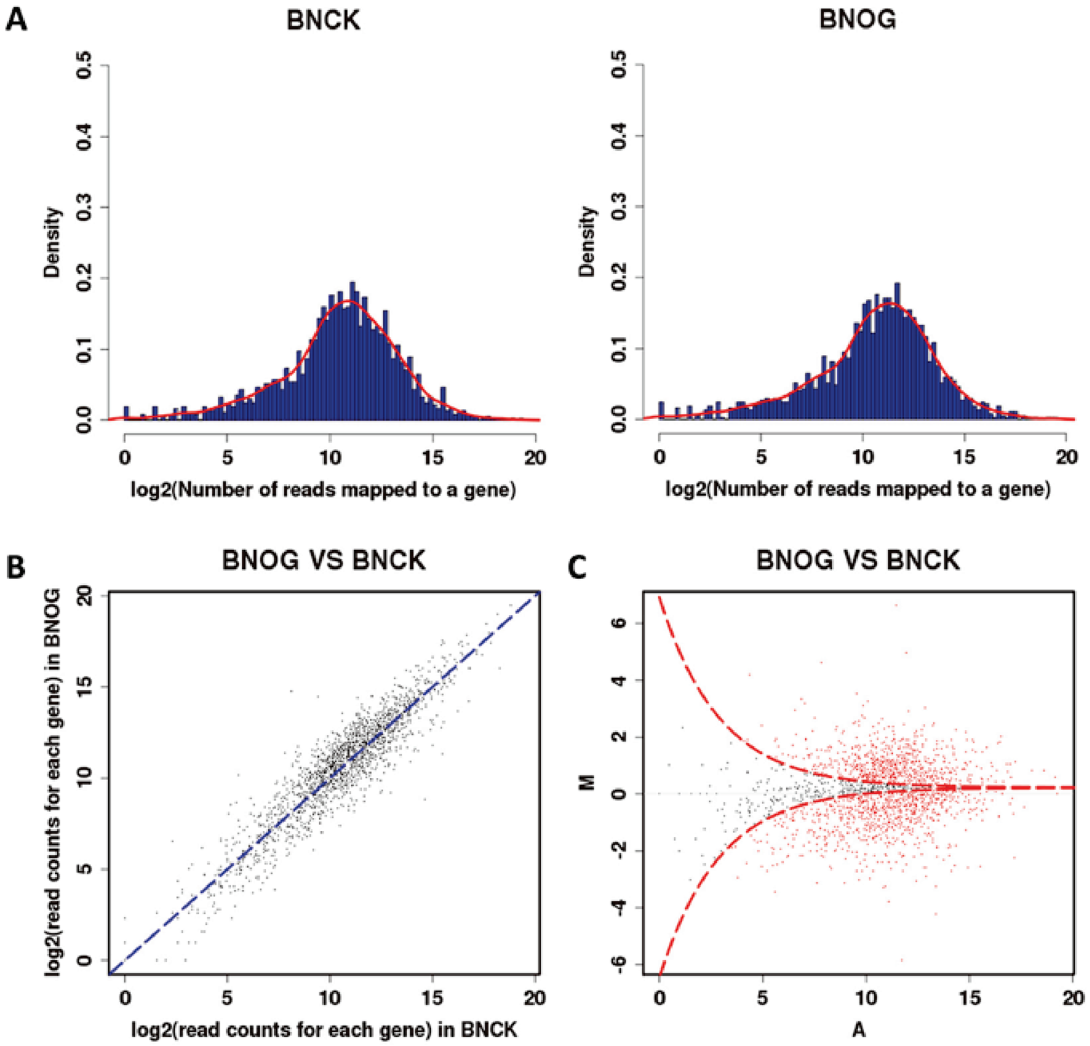

Fig. S2. Comparing RNA-seq data and identifying differentially expressed genes *in B. longum* BBMN68. (A) Effective unique-mapping-reads distribution. (B) Scatterplot comparing the number of reads for each gene. (C) Differentially expressed genes (red points) identified by the MA-plot-based method with random sampling model at a false discovery rate of 0.001. BNCK, *B. longum* BBMN68 grown without bile; BNOG, *B. longum* BBMN68 grown in the presence of 0.75 g l^{-1} ox-bile.