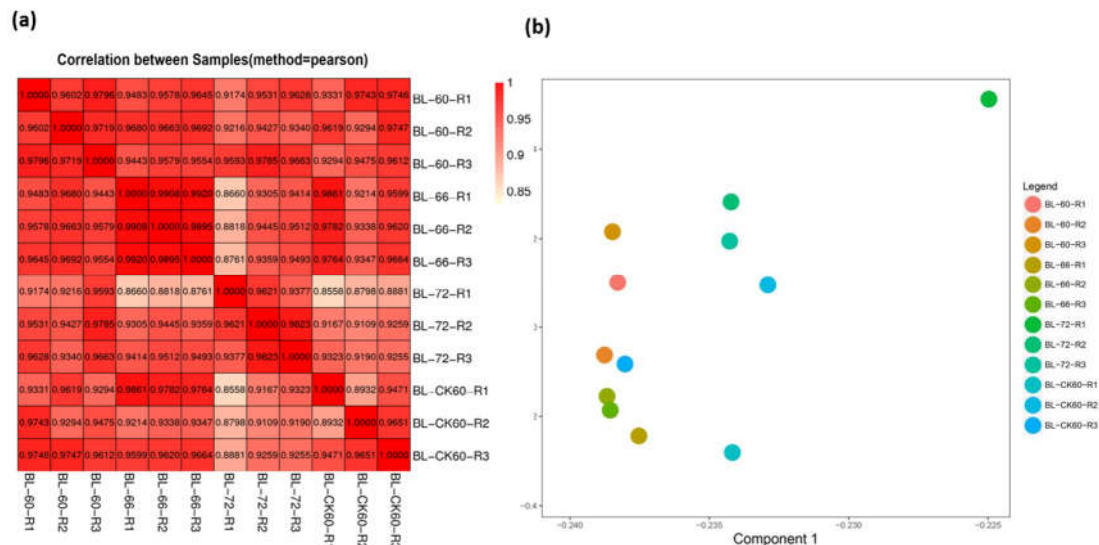
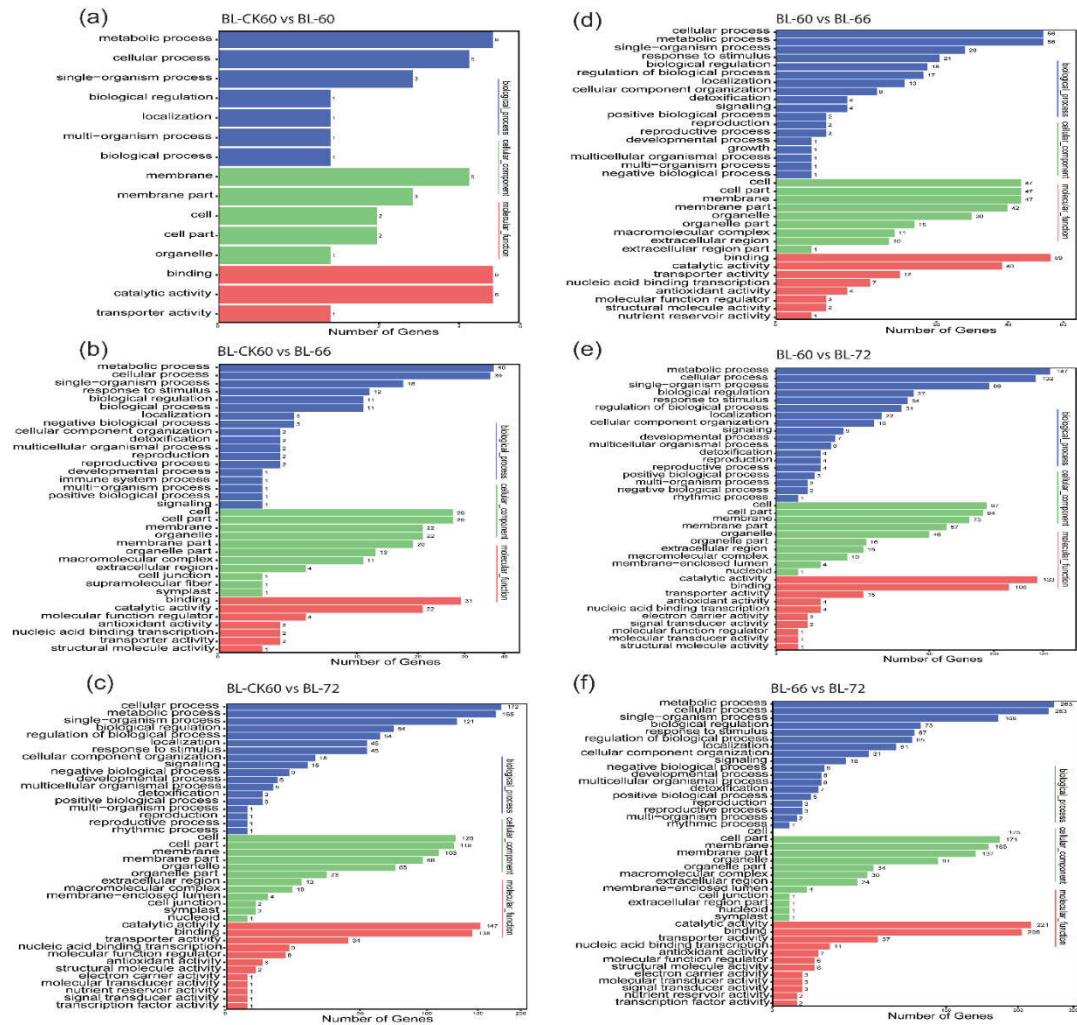


**Figure S1.** The distribution interval of gene expression in RNA-Seq data of each sample. X-axis shows number of genes and y-axis shows number of samples. Different colors show expression level of genes.



**Figure S2.** Correlation and principal component analysis; (a) Correlation of all samples. Bar is indication higher to lower expression values and samples are on x-axis and y-axis; (b) Principal component analysis; x-axis is component 1 and y-axis is component 2. Different colors showing different samples.



**Figure S3.** Gene ontology classification of DEGs among control and treatment and among treatment three time points (60h, 66h, and 72h); **(a-c)** Gene ontology classification of DEGs between control and treatment at tested time points (60h, 66h, and 72); **(d-f)** Gene ontology classification of DEGs among treatment tested time points (60h, 66h, and 72).