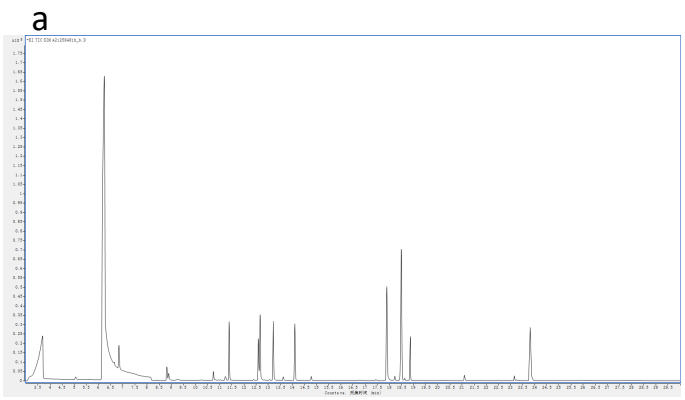

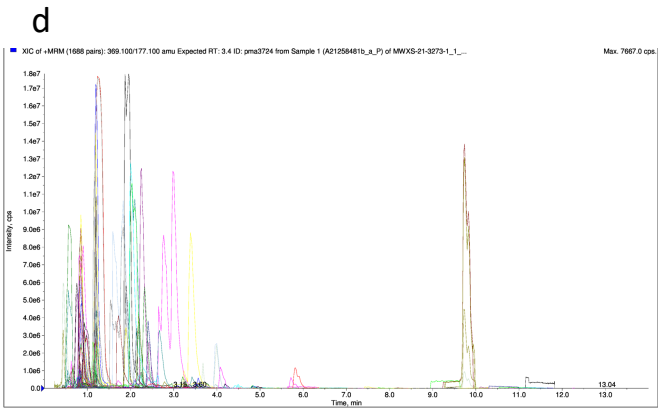

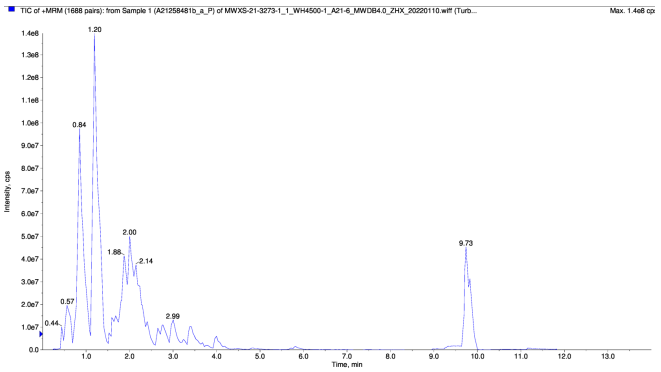

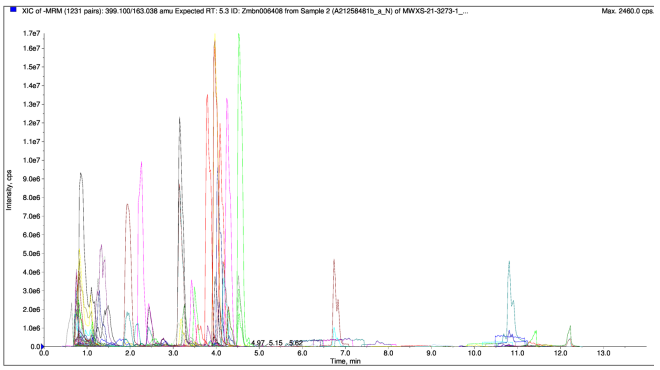

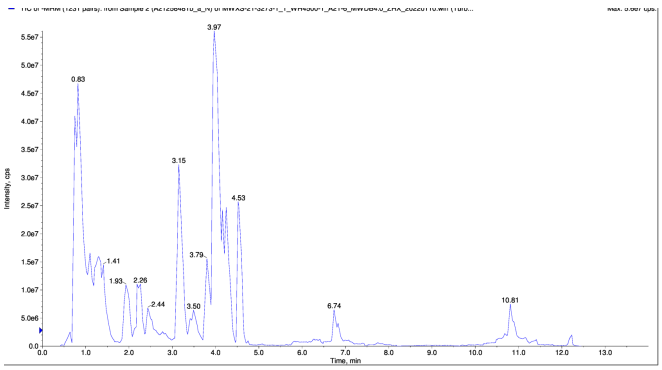

Figure S1 Quality control of data from widely targeted metabolome. a b and c. Total ion current of one quality control sample,as revealed by mass spectrometry detection. d and e. A multi-peak detection plot of the metabolites in the multiple reaction monitoring mode.Each mass spectrum peak with a different color represents a detected metabolite .

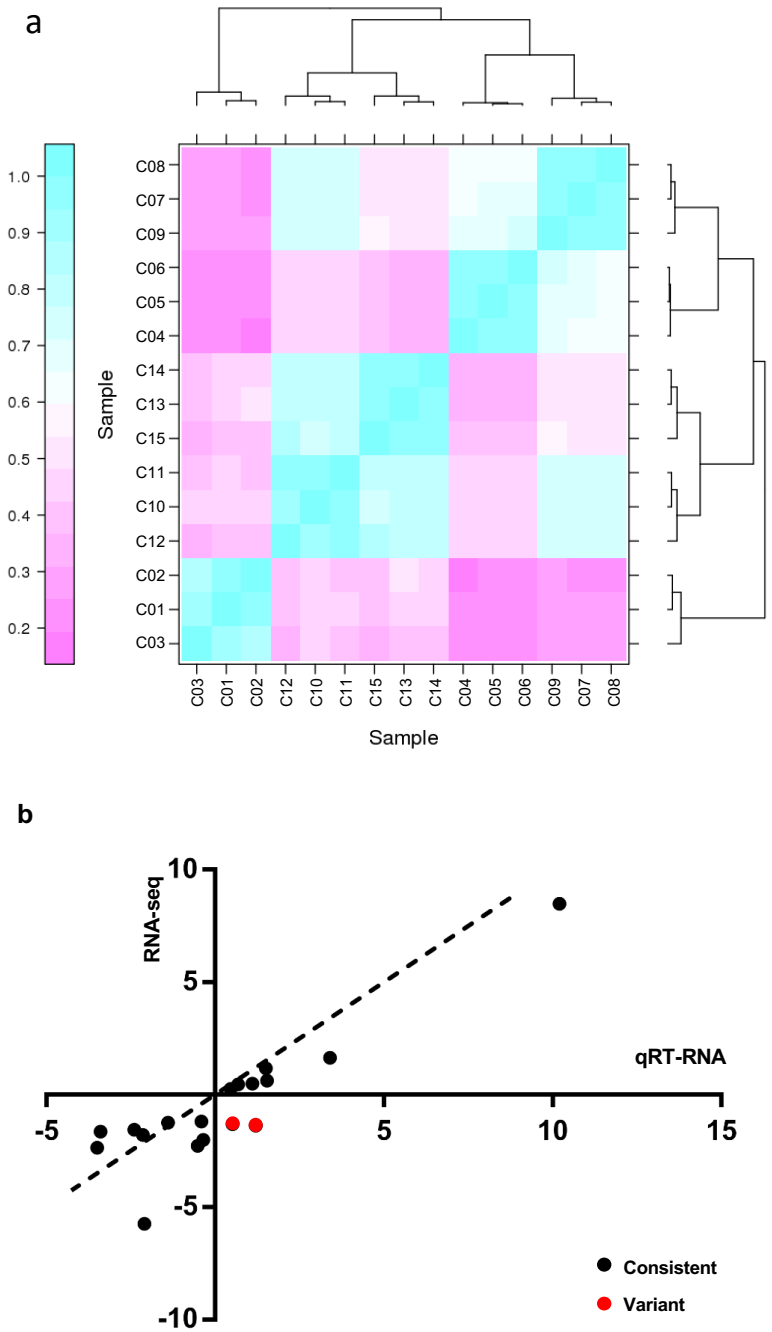

Figure S2 Quality control of data from RNA-seq. a.The hierarchical cluster analysis of all the replications. Replications of each treatment for RNA are shown below: 0 h (C01, C02 and C03); 3 h (C04, C05 and C06); 12 h (C07, C08 and C09); 36 h (C10, C11 and C12); and 60 h (C13, C14 and C15). Given the log2(fold change), expression levels of genes were clustered. b.Comparison of expression levels of the randomly selected genes between the RNA-seq and qRT-PCR. Consistent represents the consistency of results for RNA-seq and qRT-RNA.Variant represents an inconsistency in the results of RNA-seq and qRT-RNA. The ratios of values of log2(fold change) of 18 genes from RNA-seq and qRT-PCR after treatment for 3 h. The 18 selected genes included CTRG_00166, CTRG_00173, CTRG_00423, CTRG_00627, CTRG_00770, CTRG_01068, CTRG_01142, CTRG_01327, CTRG_01443, CTRG_01732, CTRG_01733, CTRG_01777, CTRG_02168, CTRG_02702, CTRG_03453, CTRG_03911, CTRG_03917, and CTRG_03930. The primers for RT-

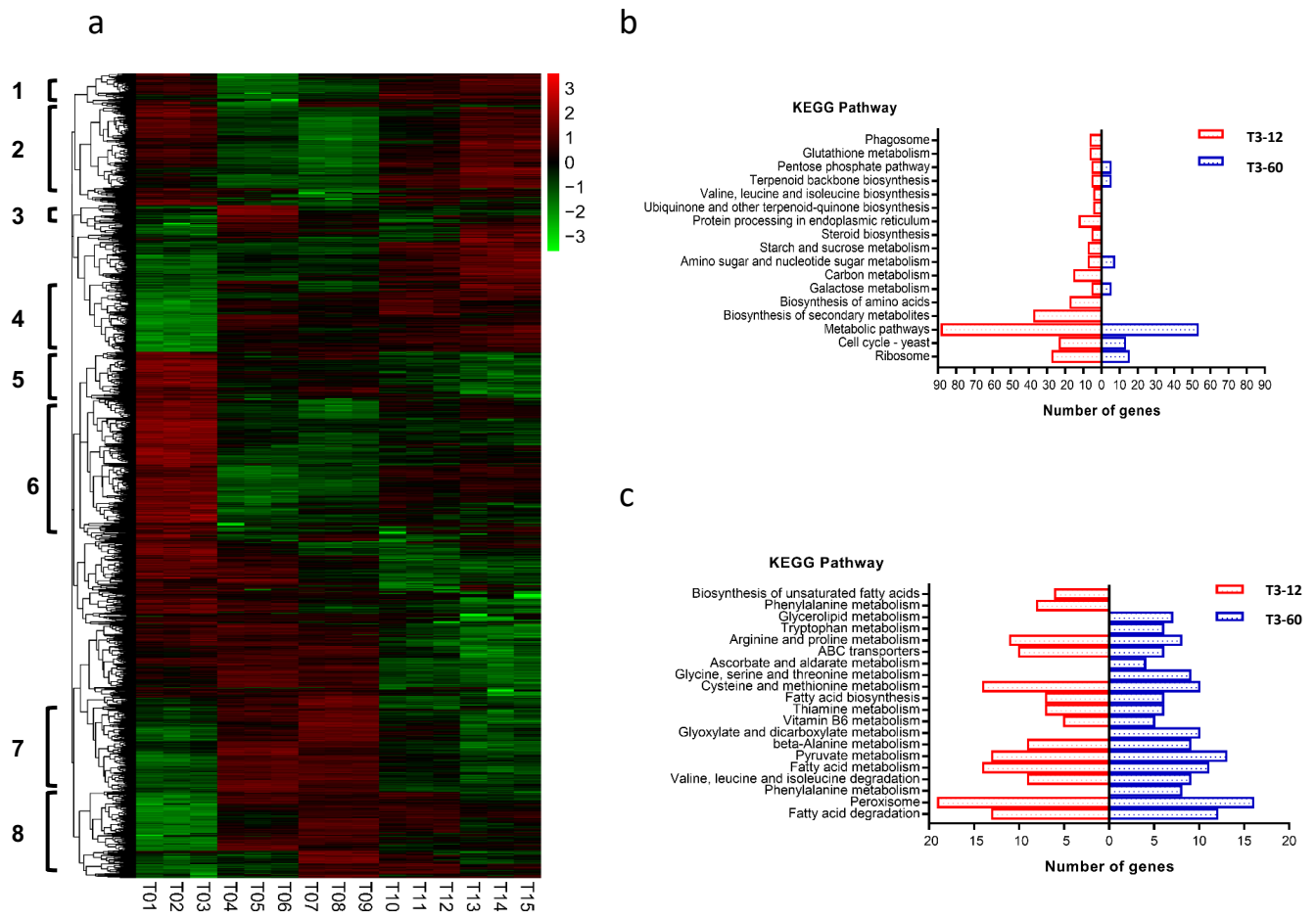

Figure S3 Transcriptome and proteome response to hydrolysate after the treatment for 0, 3, 12, 36, 60 h. a. The cluster analysis of differentially expressed genes on transcription level. Color represents the log2(fold change) of gene in the sample. Genes in clusters 1-8 related to the hydrolysate tolerance of the strain. b. KEGG enrichment analysis of up-regulated genes in sample T3-12 (cluster 3 and cluster 7) and T3-60 (cluster 4 and cluster 8). T3-6 represents the samples treated for 3 and 12 h. T3-60 represents the samples treated for 3 to 60 h. c. KEGG enrichment analysis of down-regulated genes in sample T3-12 (cluster 1 and cluster 2) and T3-60 (cluster 5 and cluster 6).

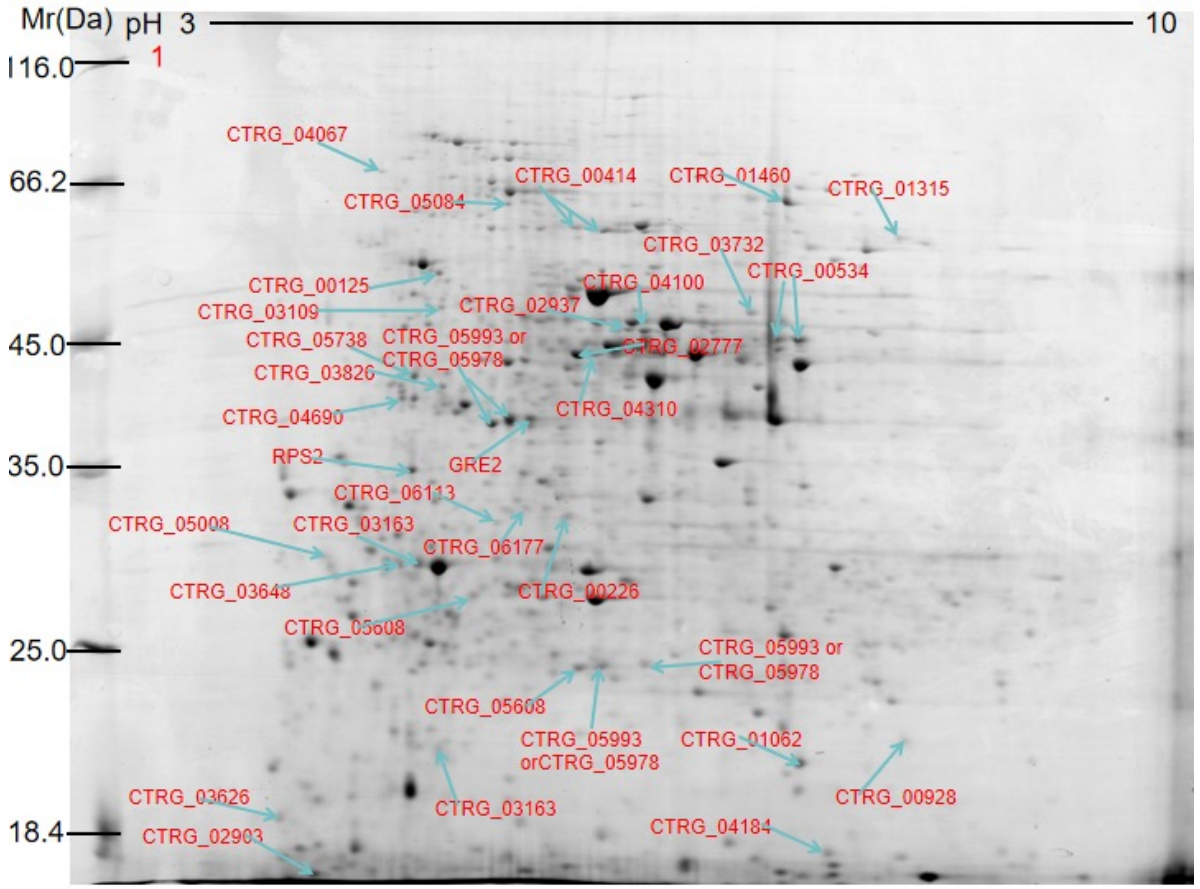

Figure S4 Proteome response to hydrolysate after the treatment for 3 hours. dimensional gel electrophoresis of the up-regulated proteins (33 proteins).

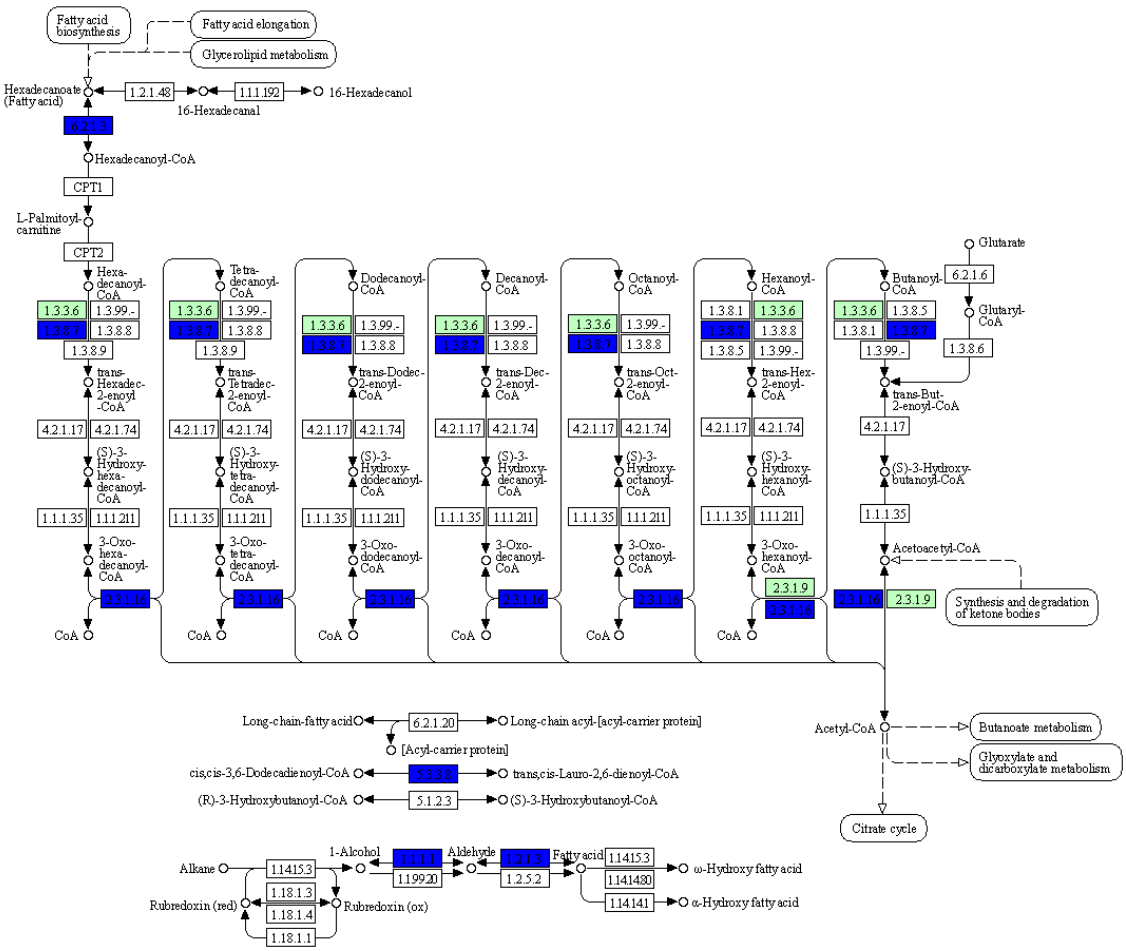

Figure S5 Fatty acid degradation pathway. Blue EC number of proteins were down-regulated by 2-fold in the presence of hydrolysate for 3 and/or 6 h and protein genes listed in **Table S8**.

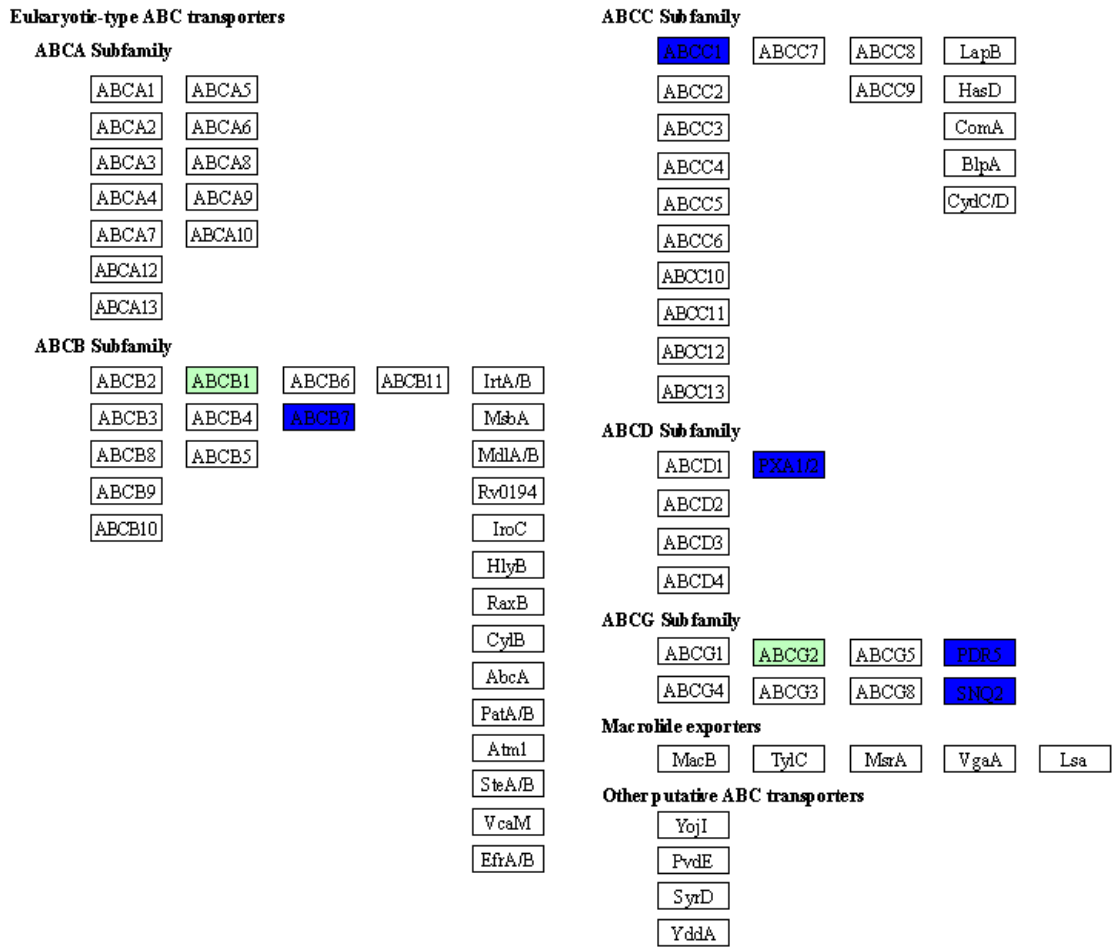

Figure S6 ABC transporters pathway. Bluee EC number of proteins were down-regulated by 2-fold in the presence of hydrolysate for 3 and/or 6 h and protein genes listed in **Table S8**.

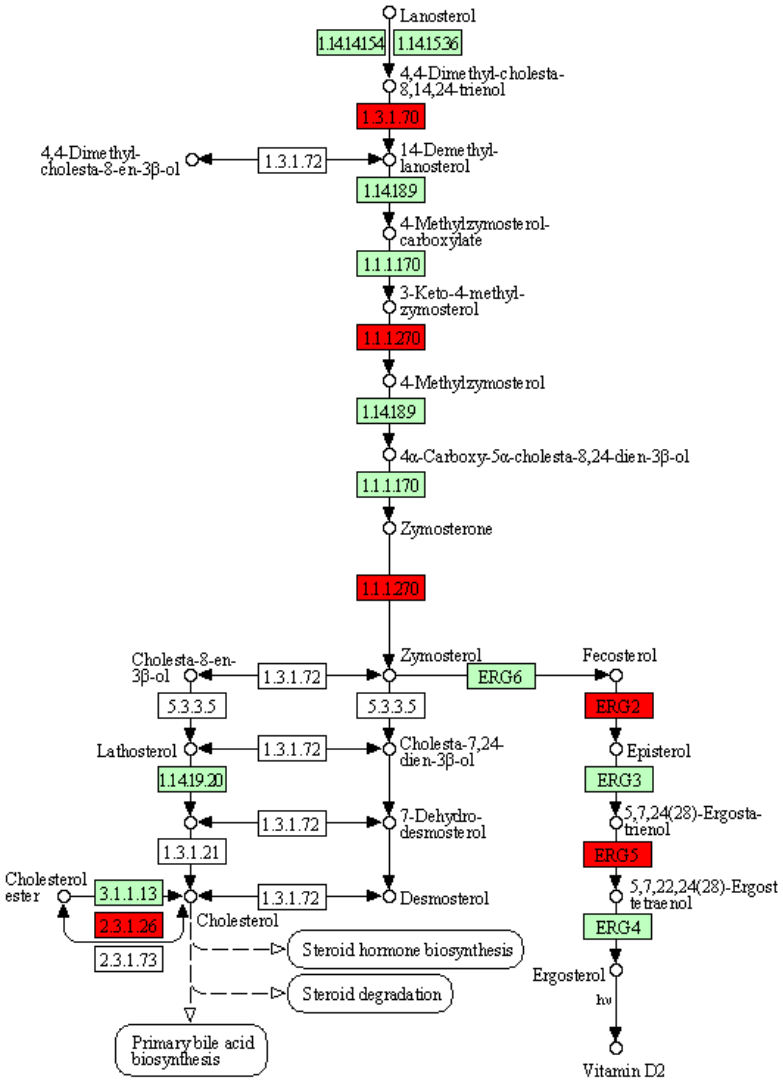

Figure S7 Steroid biosynthesis pathway. Red EC number of proteins were up-regulated by 2-fold in the presence of hydrolysate for 3 and/or 6 h and protein genes listed in **Table S8**.

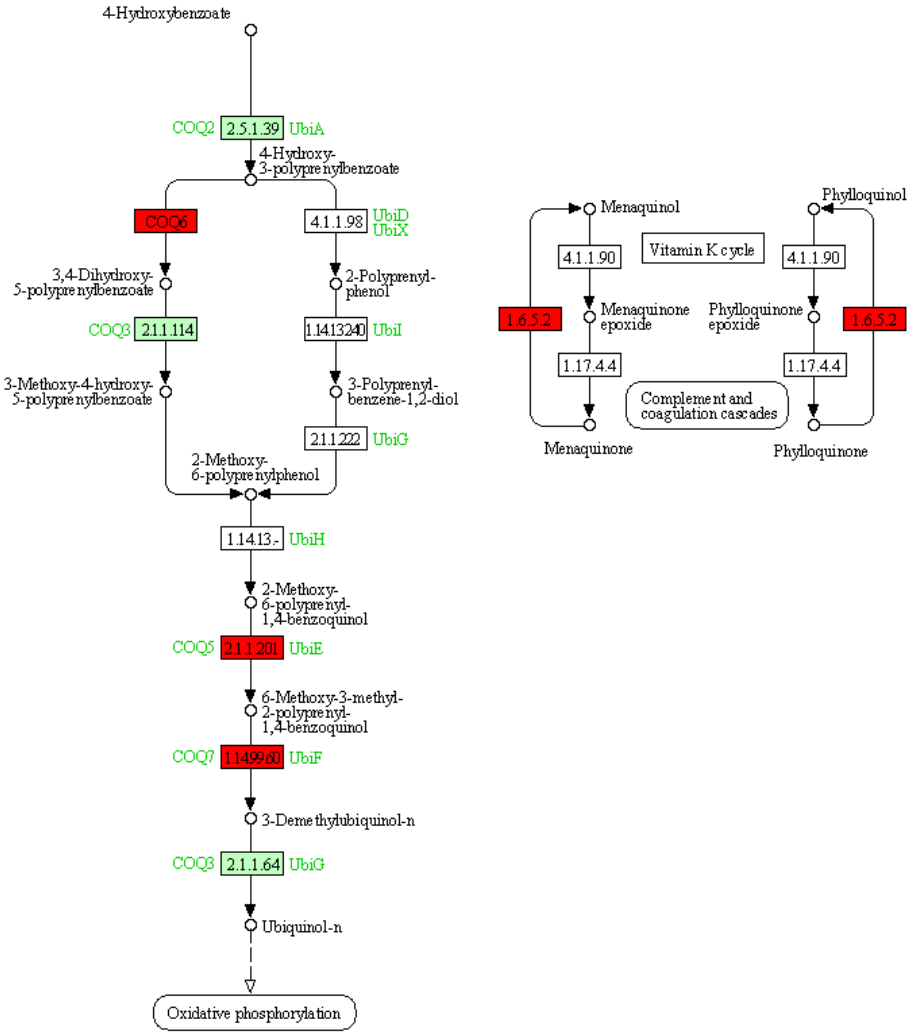

Figure S8 Ubiquinone and other terpenoid-quinone biosynthesis pathway. Rede EC number of proteins were up-regulated by 2-fold in the presence of hydrolysate for 3 and/or 6 h and protein genes listed in **Table S8**.