Figure S1. Scatter plot of the mass error distribution of lysine modification sites. Import all mass error data of sites into Matlab, and use Matlab to plot a scatter plot of the mass error distribution of lysine acetylation (Kac) sites and lysine succinylation (Ksu) sites.
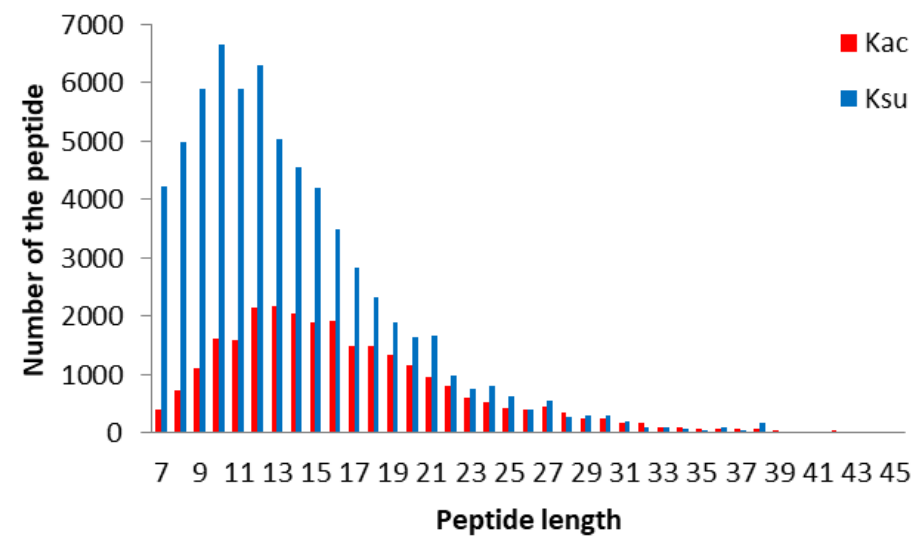
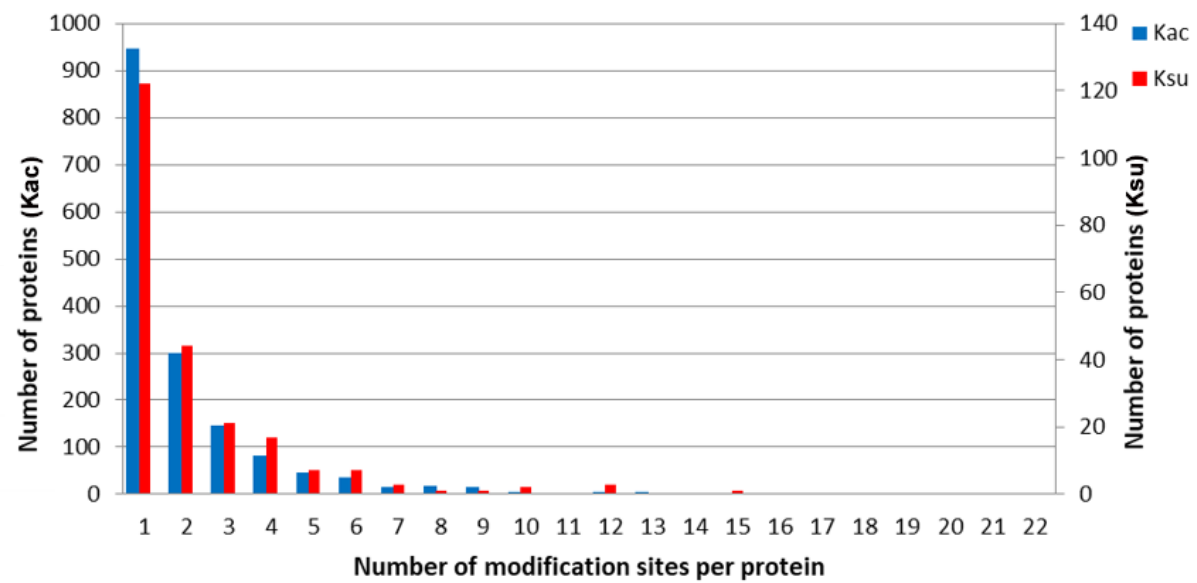**Figure S2.** Two-dimensional distribution map of the length of the peptide.

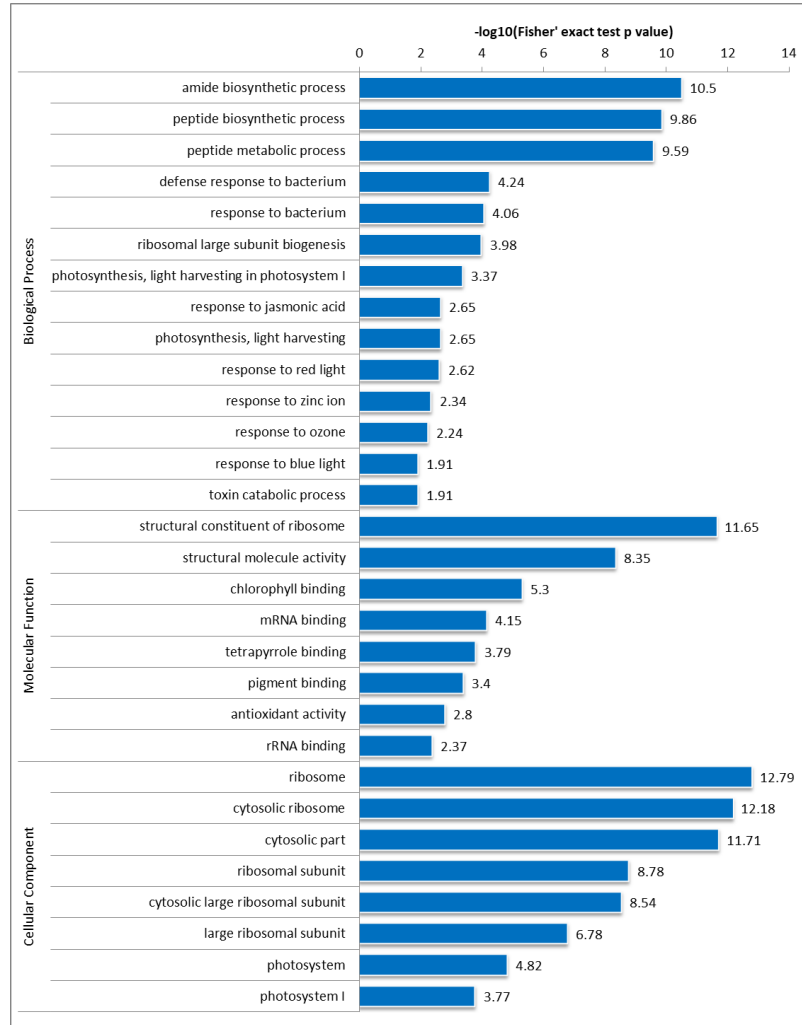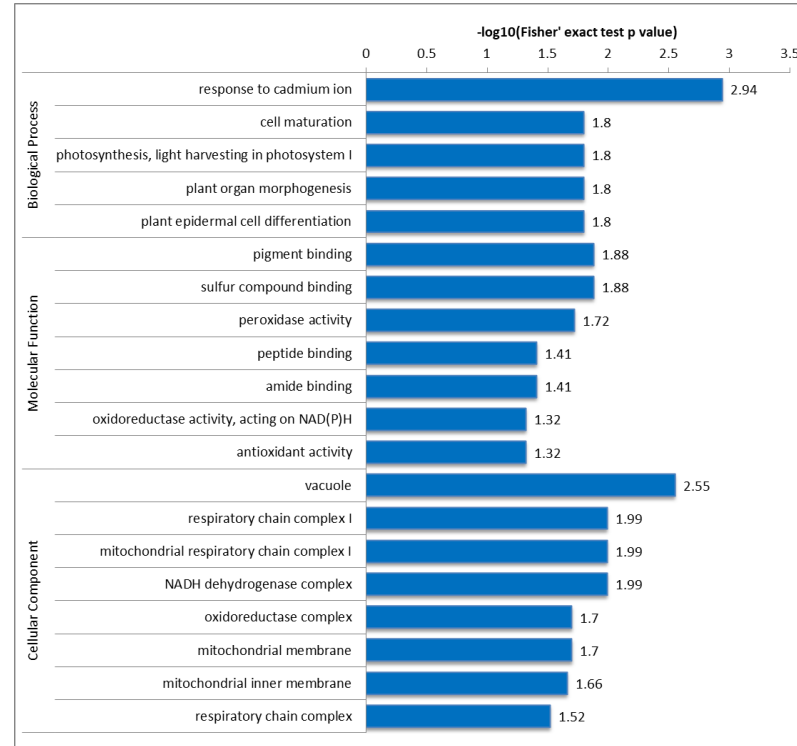**Figure S3.** Number distribution of modification sites per peptide.

Figure S4. GO-based enrichment analysis of identified downregulated differentially modified Kac (**A**) and Ksu (**B**) proteins.