Description of Additional Supplementary Files:

Supplementary Data 1: A systematic annoation of XB1826LQ project data provided by the Jingjie PTM Biolabs. The relative abundances of each protein (column AX to BE) corresponds to exactly the data of LFQ intensity (column AP to AW). It is obtained by using the LFQ intensity of each condition to be normalized by the average of the LFQ intensity of all conditions of each protein.

Supplementary Data 2: Absolute abundance of each individual protein wtih the information of iBaq intensity of the XB1826LQ project. Maxquant raw data gives the information of iBAQ intensity, which is a proxy of the copy number of each protein. We then use the iBAQ intensity of each protein to multiply its molecular weight (MW) to obtain the iBAQ mass. The proteome fraction of each protein (or a protein function sector) is obainted by normalizing its value by the sum of the whole proteome.

Supplementary Data 3: The proteome fraction of each proteome function sector using the information of iBAQ mass in supplementary table 2 for DK1042 strain and DS7906 strain growing in mannose medium.

Supplementary Data 4: The proteome fraction of each proteome function sector using the information of iBAQ mass in supplementary table 2 for DK1042 strain and DS7906 strain growing in ribose medium.

Supplementary Data 5: A systematic annoation of XB1827LQ project data provided by the Jingjie PTM Biolabs. The relative abundances of each protein (column AD to AG) corresponds to exactly the data of LFQ intensity (column Z to AC). It is obtained by using the LFQ intensity of each condition to be normalized by the average of the LFQ intensity of all conditions of each protein.

Supplementary Data 6: Absolute abundance of each individual protein wtih the information of iBaq intensity of the XB1827LQ project. Maxquant raw data gives the information of iBAQ intensity, which is a proxy of the copy number of each protein. We then use the iBAQ intensity of each protein to multiply its molecular weight (MW) to obtain the iBAQ mass. The proteome fraction of each protein (or a protein function sector) is obainted by normalizing its value by the sum of the whole proteome.

Supplementary Data 7: The proteome fraction of each proteome function sector using the information of iBAQ mass in supplementary table 6.