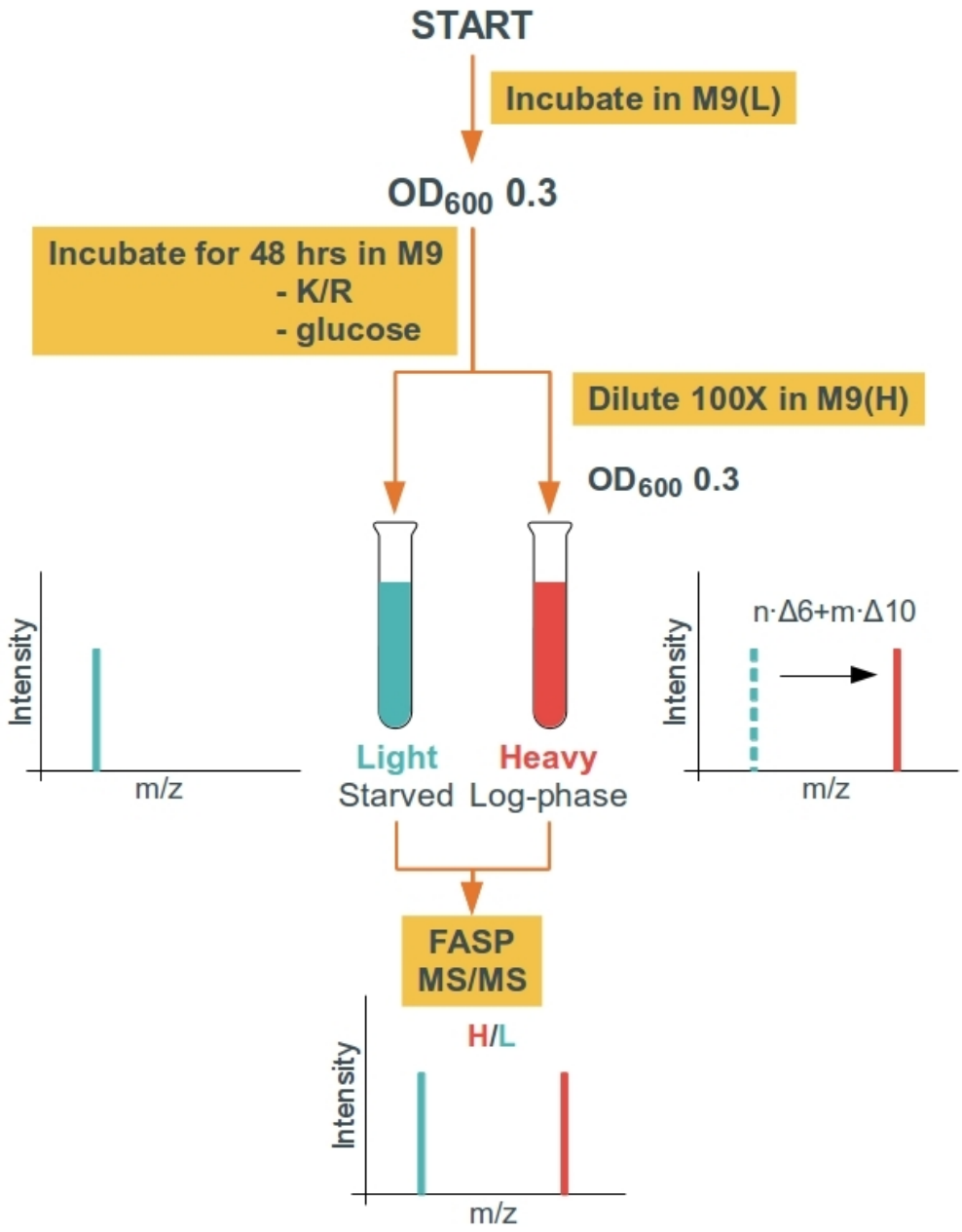

Figure S1. The experimental workflow of the study. The *Escherichia coli* SLE1 strain cells were grown in M9 medium supplemented with 'light' lysine/arginine amino acids and glucose until the culture reached OD_{600} 0.3. The cells then were transferred to and incubated in M9 devoid of the carbon source for 48 hours. On the day of the harvest, the portion of the starved culture was diluted 100 times in M9 containing 'heavy' lysine/arginine supplement as well as glucose, and was allowed to grow until late log-phase (OD_{600} 0.3). The two cultures were harvested simultaneously, and the cells processed as described in Materials and methods. For the label-free analysis, the pre-harvest cells were diluted in 'light' M9.

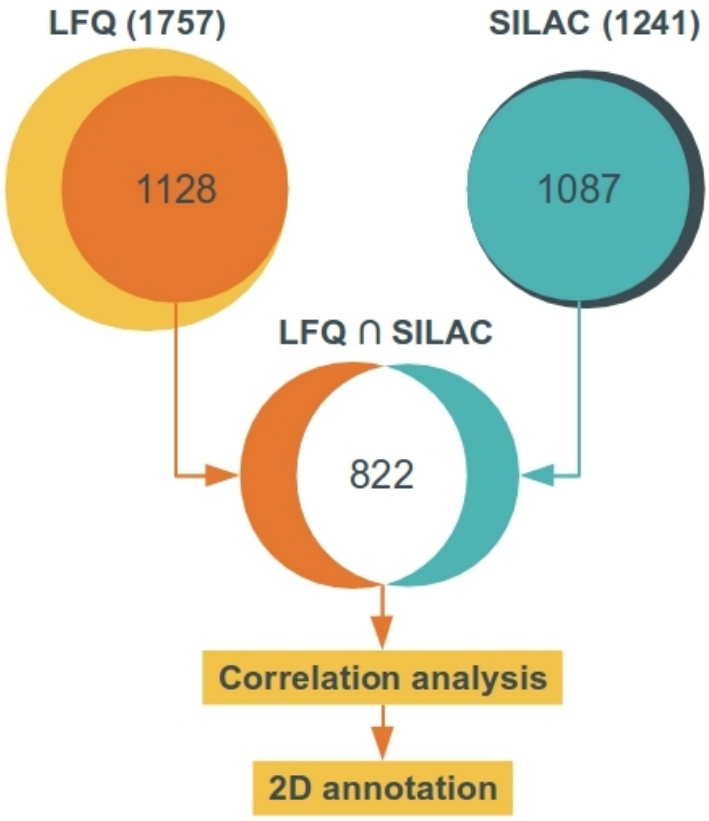

Figure S2. The statistical data analysis workflow of the study. Of 1,757 LFQ and 1,241 SILAC protein groups 1,128 and 1,087 had quantifiable ratios respectively. Of the groups with quantified ratios 822 were present in both datasets. These 822 groups were used for the determination of the correlation between the quantification techniques and 2D Gene Ontology annotation enrichment.