Supplementary Table 2. Meta-analysis simulation results with different overlap percentages ( in quantified proteins between studies (q-value threshold of 5%, and n = 6). The average numbers of detected differential proteins were reported. The average true integration-drive discovery rates (tIDR) and the average true integration revision rates (tIRR) were shown in parentheses. The results were based on 1,000 simulations.

|  |  |  |  |
| --- | --- | --- | --- |
| Meta Analysis | =0.75 | =0.50 | =0.25 |
| Pearson’s test | 322.10 (8.20%, 2.63%) | 346.75 (5.26%, 2.79%) | 383.18% (2.88%, 1.97%) |
| Stouffer’s test | 355.05 (14.66%, 1.55%) | 376.34 (10.27%, 1.05%) | 400.04 (5.39%, 0.78%) |