**Table S1.** The related parameters used in identification and quantitative analyses by mass spectrometry

|  |  |
| --- | --- |
| **Item** | **Value** |
| Protein Database | Uniprot\_HomoSapiens\_161584\_20180123Download link：<http://www.uniprot.org/> |
| Enzyme | Trypsin |
| Max Missed Cleavages | 2 |
| Instrument | ESI-TRAP |
| Precursor Mass Tolerance | ± 20 ppm |
| Fragment Mass Tolerance | 0·1 Da |
| Use Average Precursor Mass | False |
| Modification Groups from Quan Method | iTRAQ 4 plex |
| Dynamic modifications | Oxidation (M), Acetyl (Protein N-term), Deamidated (NQ) |
| Static modifications | Carbamidomethyl (C) |
| Database pattern | Decoy |
| Peptide FDR | ≤0.01 |