Figure S2

Peptide Spectral Matches (PSM)

PSM in %

Sequence Database

Sequence Database + Spectral Library
Figure S3. Agreement between peak ranks of three different LC-MS platforms (Ion-Trap, triple quadrupole (QQQ) and time-of-flight (TOF) analyzers) for identified S. pombe peptides. MS/MS spectra acquired by QQQ and TOF and the corresponding fragment ranks were obtained from SRM-Atlas (www.srmatlas.org).
Figure S4

A

B

C.
Figure S5: Distribution of annotated GO-terms of all identified proteins (blue bars) and all genes in the S. pombe database (red bars) according to table S5.
Correlation of emPAI and iBAQ calculated protein abundances

spearman correl=0.705
Figure S8

- Spearman correlation: 0.56
- Spearman correlation: 0.49
- Spearman correlation: 0.52