Electronic Supplementary Material (ESI) for Molecular Omics.

Supplementary files

Robust Determination of Differential Abundance in Shotgun Proteomics using Nonparametric Tests

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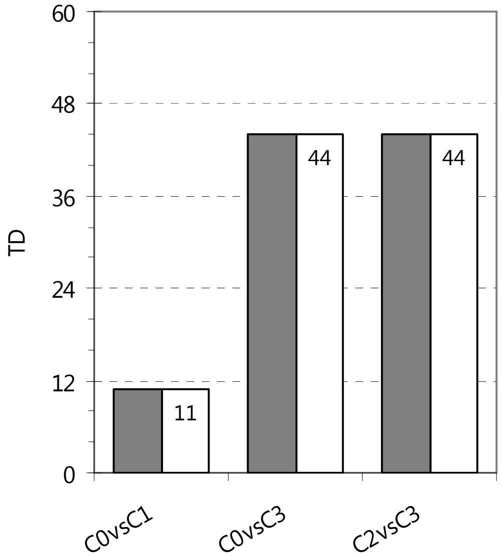
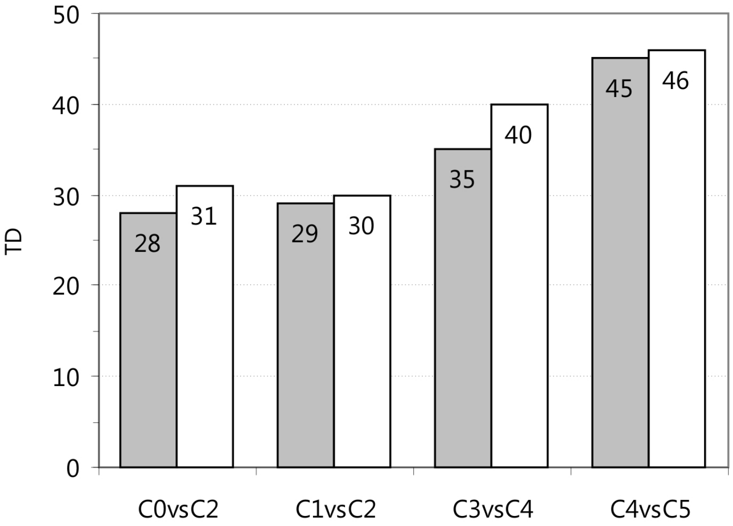
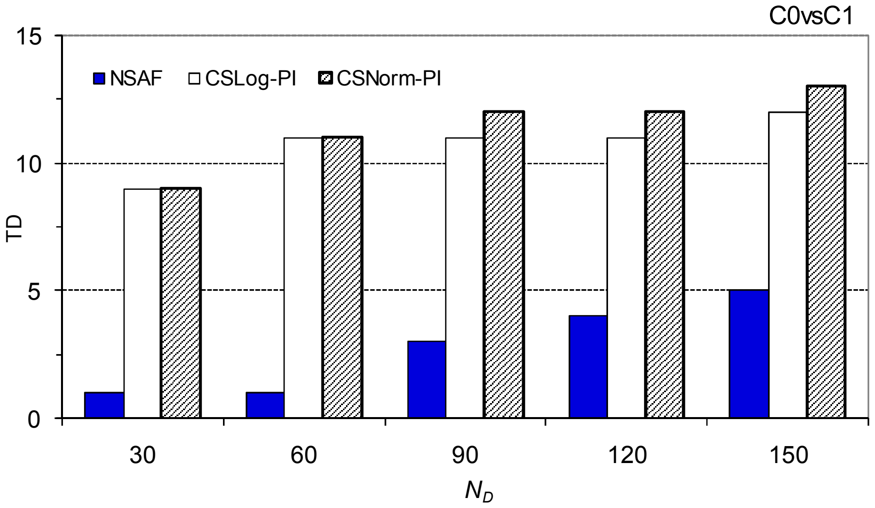
Supplementary Figure S1. Performances of CSLog-PI (gray) and CSNorm-PI (white) on differents pair of conditions with less discriminative power when setting the number of discoveries to N_D=60.

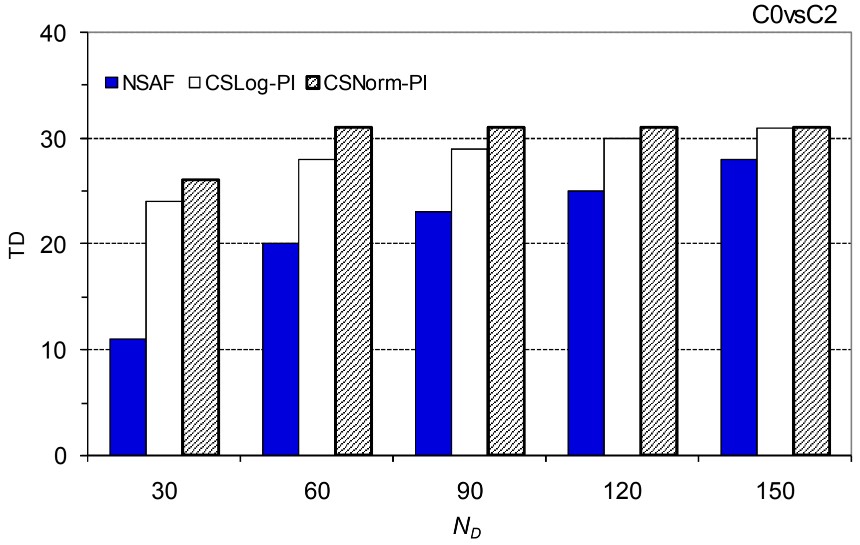


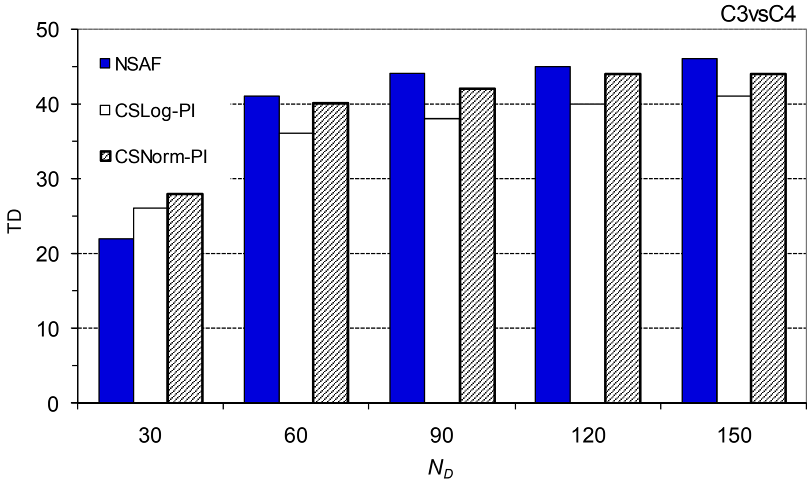
Supplementary Figure S2. Number of true discoveries obtained using CSNorm-SC (gray bars) at different numbers of discoveries N_D. Results obtained on CSNorm-PI (white bars) are shown for comparison.



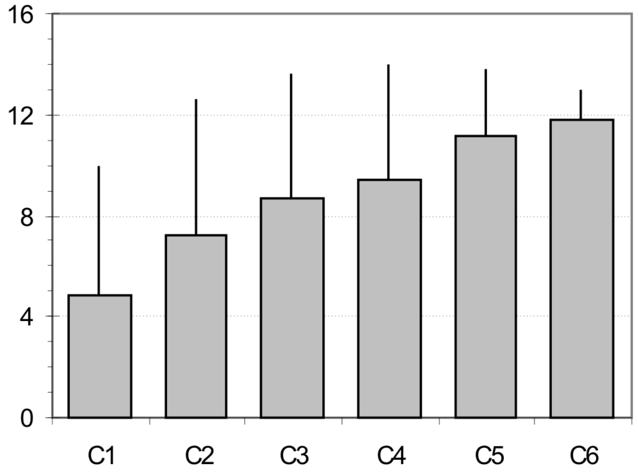
Supplementary Figure S3. Number of true discoveries TD obtained using method NSAF (blue bars) for comparisons C0vsC1 (top), C0vsC2 (middle) and C3vsC4 (bottom) at different number of discoveries N_D.



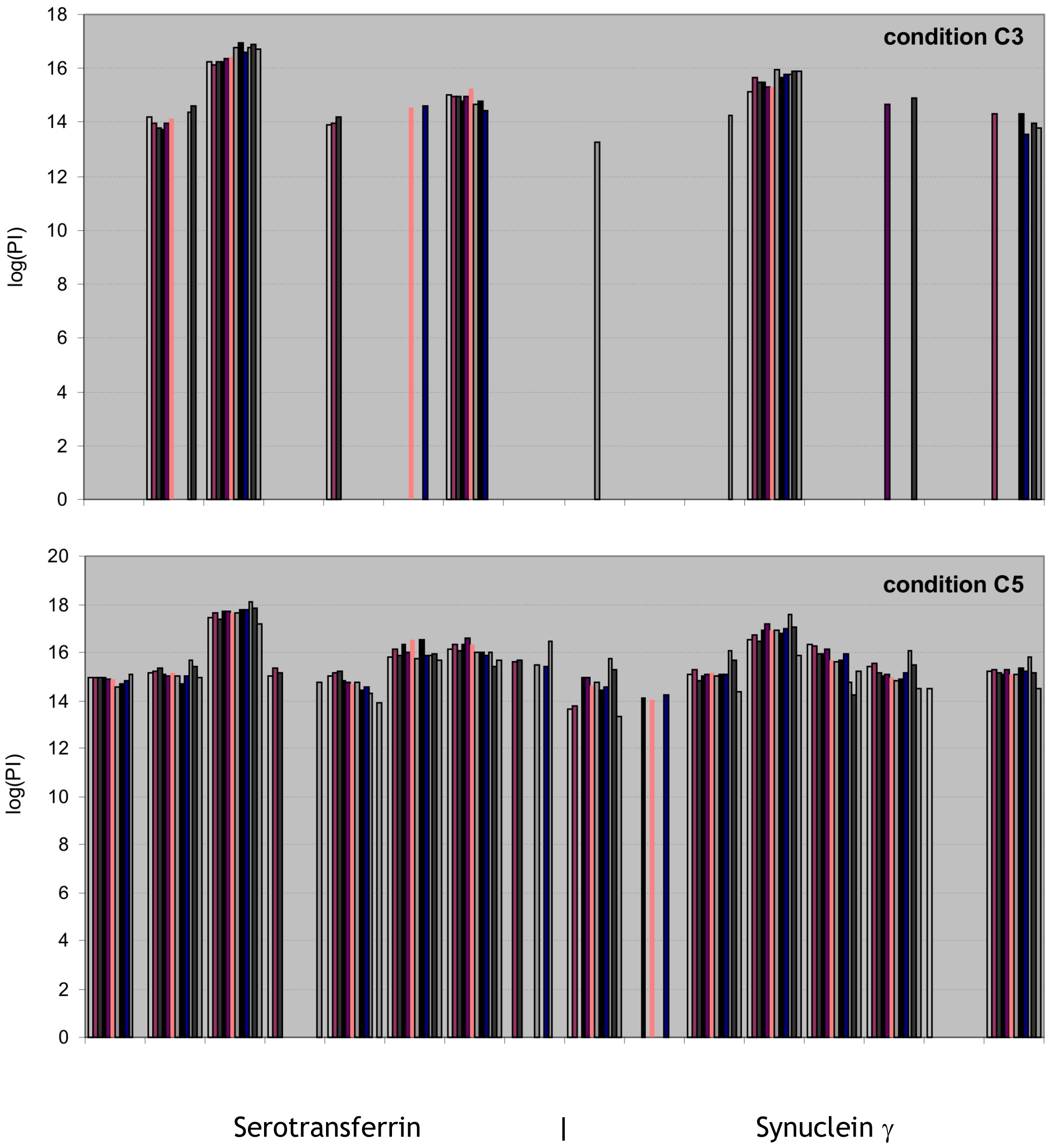



C3vsC4
NSAF
CSLog-PI
CSNorm-PI
TD
0
10
20
30
40
50
30
60
90
120
150
N_D

Supplementary Figure S4. Average number of null values among detected UPS1 peptides within each condition. Average over peptides + standard deviation is shown.



Supplementary figure S5. Values (log(PI)) obtained on 16 peptides from 2 UPS1 proteins for spike-in conditions C3 (top) and C5 (bottom). Eight peptides from Serotransferrin precursor protein (P02787; first eight group of bars, left) and eight peptides from Gamma-synuclein (O76070) are displayed. Each group of bars represents the values for the 12 samples of that condition.



Supplementary Table S1. Description of the dataset. Only peptides with single protein assignment are considered (87% of data). Note that 3 signals were assigned to UPS1 peptides in the yeast-only samples.

Condition	Average number of peptides	Number of observed UPS1 peptides
C0	3538	3
C1	3651	45
C2	3337	130
C3	3569	304
C4	3490	362
C5	3749	537
C6	3841	819

- **Additional files :**

All raw mass spectrometry data and database search results are provided for inspection via ProteomeXchange with identifier PXD006447. Summarized PSM results and data matrices used in this analysis are provided in the supplementary zip file.

MATLAB code.