SUPPORTING INFORMATION

Temporal proteomic profiling of SH-SY5Y differentiation with retinoic acid using FAIMS and Real-Time Searching

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Supplemental Figure 1: Protein differences in the time course dataset.

Supplemental Table 1: Proteins quantified in the end-point TMT6 dataset.

**Supplemental Table 2: Proteins quantified in the time course TMTpro16 dataset.**

Supplemental Table 3: Peptides quantified in end-point TMT6-plex dataset.

Supplemental Table 4: Peptides quantified in the time course TMT16pro dataset.

Supplemental Table 5: Expanded gene ontology classifications for differentially abundant proteins.

Supplemental Table 6: Expanded KEGG pathway classifications for differentially abundant proteins.

Supplemental Figure 1:

A)
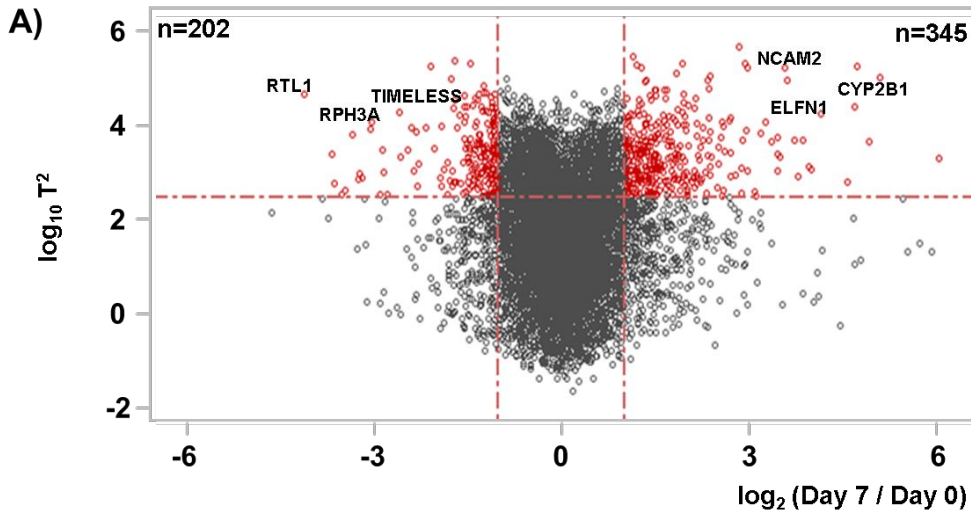
B) Proteins with increased abundance

Catagory	Term	Count	%	FDR
BP	cell adhesion	30	8.82	4.43E-05
BP	cell migration	17	5.00	4.29E-04
BP	extracellular matrix organization	20	5.88	1.61E-05
CC	actin cytoskeleton	17	5.00	4.32E-03
CC	cell surface	38	11.18	1.05E-08
CC	cell-cell junction	16	4.71	1.02E-03
CC	extracellular exosome	158	46.47	2.02E-39
CC	extracellular matrix	21	6.18	9.48E-04
CC	extracellular space	52	15.29	1.02E-03
CC	focal adhesion	47	13.82	7.99E-21
CC	membrane raft	19	5.59	7.70E-05
CC	plasma membrane	131	38.53	2.89E-08

C) Proteins with decreased abundance

Catagory	Term	Count	%	FDR
BP	cell division	27	13.64	8.15E-12
BP	DNA repair	13	6.57	1.24E-02
BP	DNA replication	26	13.13	1.68E-19
BP	DNA replication initiation	12	6.06	2.31E-11
BP	mitotic nuclear division	20	10.10	2.80E-08
CC	cytoplasm	95	47.98	5.94E-07
CC	nuclear chromosome, telomeric region	10	5.05	1.04E-02
CC	nucleus	111	56.06	1.44E-13
MF	chromatin binding	17	8.59	7.07E-03
MF	structural molecule activity	13	6.57	2.06E-02

Supplemental Figure 1: Protein differences in the time course dataset. A) Volcano plot illustrating the $\log_{10}T^2$-statistic plotted against the $\log_2$ values the fold changes of Day7/Day0. Highlighted on the volcano plot are six of the most altered proteins resulting from retinoic acid treatment. These are the same proteins that are highlighted in **Figure 2** and **Figure 3**. Gene ontology classifications for **B)** up-regulated (n=345) and **C)** down-regulated (n=202) differentially abundant proteins as determined from the T^2-statistic and fold change in panel **A)**.