**File descriptions**

**INPUTS AND PARAMS DIRECTORIES**

**Diaumpire\_se\_orbi\_strict.txt –** parameters file used for DIA-Umpire signal extraction from urine dataset

**Diaumpire\_se.params**– parameters file used for DIA-Umpire signal extraction module used for the acetyl dataset including the variable window definition

**20150810.mouse.cc.iRT.fasta –** database file used for MS-GF+ database searches of the acetyl dataset and for populating Skyline document

**20161213.human.fasta** – database file used for MS-GF+ database searches of the urine dataset and for populating the Skyline document

**20150810.mouse.cc.iRT\_DECOY.fasta –** database file used for COMET and X! Tandem database searches of the acetyl dataset

**20161213.human\_DECOY.fasta** – database file used for the COMET and X! Tandem database searches of the urine dataset

**Comet.Kac.DIA.params –** Comet database search parameters file used for acetyl dataset

**Comet64.params.orbi.new** – Comet database search parameters file used for urine dataset

**taxonomy.xml** – File required for X! Tandem database searches specifying the location of the database file used for the acetyl dataset

**human\_taxonomy.xml** – File required for X! Tandem database searches specifying the location of the database file used for the urine dataset

**xTandem\_Kac\_params.xml** – X! Tandem database search parameters file used for the acetyl dataset

**xTandem\_pSTY\_orbi\_params.xml** – X! Tandem database search parameters file used for the urine dataset

**ACETYLLYSINE DATASET RESULTS FILES: OUTPUTS\ACETYL\_MOUSE\_LIVER\**

**fullDIA.final.interact.ptm.pep.xls.xlsx** – iProphet-filtered peptide identification results

**fullDIA.final.interact.ptm.pep.xml** – final peptide identification results in pep.xml format

**fullDIA.pt99.mProph.features.csv** – complete list of mProphet feature scores produced within Skyline

**default\_empty.sky** – ‘empty’ Skyline document containing all appropriate settings

**2016\_0826\_mapDIA.skyr** – custom Skyline report file

**2016\_0826\_mapDIA.csv** – Skyline report before mapDIA filtering for interferences and reformatting

**mapDIA\_Input.txt** – Filtered and reformatted Skyline report used for input to mapDIA

**site\_level\_areas.txt** – mapDIA site-level area report containing areas used for calculation of CV values in figure 1c.

**mapDIA\_analysis\_output.txt** – raw mapDIA output results with site-level fold changes and probabilities used to generate figure 1d.

**URINE PHOSPHORYLATION DATASET RESULTS FILES: OUTPUTS\URINE\**

**ptmProphet-output-file.ptm.pep.xml.zip** – compressed PTM prophet output

**iPro-output-file.pep.xml** – combined iProphet results from used for input to PTMProphet

**noCor\_analysis\_output.txt** – site-level mapDIA output using no normalization used to produce supplemental figure 3A.

**proteinlevels.txt** – protein-level quantities used for protein-level correction of site-level changes used to produce supplemental figure 3B.

**protlvlCor\_noTICcor\_analysis\_output.txt** - site-level mapDIA output using protein-level normalization but not local TIC normalization used to produce supplemental figure 3C.

**TICcor\_noProtCor\_analysis\_output.txt** - site-level mapDIA output using local TIC normalization but not protein-level normalization used to produce supplemental figure 3D.

**bothCor\_analysis\_output.txt** – site-level mapDIA output using both local TIC normalization and protein-level correction used to produce supplemental figure 3E.