**Kidney Transplant Proteomic Data**

**iTRAQ Dataset**

“iTRAQ-labeled peptides were identified based on tandem MS/MS spectra. MS/MS spectra were converted to peak lists using DeconMSn (version 2.2.2.2, <http://omics.pnl.gov/software/DeconMSn.php>) (v1) using default parameters. The database used was SEQUEST v27. The protein database from Uniprot was downloaded (released May 5, 2010) with 20,776 total entries. The considerations in Sequest searches were used carbamidomethylation of cysteine and iTRAQ labeling (+304.2022) as static modification and oxidation of methionine as a dynamic modification. Both fully and partially tryptic peptides were considered with two missed cleavages allowed. The mass tolerance for precursor ions was 50 ppm and fragmentation tolerance for HCD were 0.05 Da. All peptides were identified with <0.1% False Discovery Rate by using a MS-Generating Function Score (MS-GF) <1E-10 and a decoy database searching strategy. The reporter ion intensities for each peptide were summed for all identified spectra for each channel in each biological condition. Relative abundances at the peptide level were rolled-up to the protein level using the software tool DAnTE with the abundances being log2 transformed and normalized by the central tendency approach. For each eight-plex iTRAQ experiment, a global mean (*i.e.* average abundance) was calculated for each protein across the eight channels in to serve as a baseline for normalization across the three iTRAQ experiments. All protein abundances (log2 transformed) in the three iTRAQ experiments were normalized against the global mean (*i.e.*subtracting by the global mean) obtained from their respective iTRAQ experiment to identify increased or decreased protein abundances in each phenotype.” – From Sigdel, T.K. et al. (2014)

**Label-free Dataset**

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| Parameter Value  Version 1.5.3.30  Fixed modifications Carbamidomethyl (C)  Decoy mode revert  Special AAs KR  Include contaminants True  MS/MS tol. (FTMS) 20 ppm  Top MS/MS peaks per 100 Da. (FTMS) 12  MS/MS deisotoping (FTMS) True  MS/MS tol. (ITMS) 0.5 Da  Top MS/MS peaks per 100 Da. (ITMS) 8  MS/MS deisotoping (ITMS) False  MS/MS tol. (TOF) 40 ppm  Top MS/MS peaks per 100 Da. (TOF) 10  MS/MS deisotoping (TOF) True  MS/MS tol. (Unknown) 0.5 Da  Top MS/MS peaks per 100 Da. (Unknown) 8  MS/MS deisotoping (Unknown) False  PSM FDR 0.01  Protein FDR 0.01  Site FDR 0.01  Use Normalized Ratios For Occupancy True  Min. peptide Length 7  Min. score for unmodified peptides 0  Min. score for modified peptides 40  Min. delta score for unmodified peptides 0  Min. delta score for modified peptides 6  Min. unique peptides 0  Min. razor peptides 1  Min. peptides 1  Use only unmodified peptides and True  Modifications included in protein quantification Oxidation (M);Acetyl (Protein N-term)  Peptides used for protein quantification Razor  Discard unmodified counterpart peptides True  Min. ratio count 2  Use delta score False  iBAQ False  iBAQ log fit False  Match between runs True  Matching time window [min] 0.7  Alignment time window [min] 20  Find dependent peptides False  Fasta file SAME AS iTRAQ  Site tables Oxidation (M)Sites.txt  Decoy mode revert  Special AAs KR  Include contaminants True  RT shift False  Advanced ratios True  AIF correlation 0  First pass AIF correlation 0  AIF topx 0  AIF min mass 0  AIF SIL weight 0  AIF ISO weight 0  AIF iterative False  AIF threshold FDR 0 |