

IPD Project Details

Project ID: IPD3886

Project Title: Mining the meningioma lanscape to identify biomarkers using LFQ

Description: The project involved use of surgically resected meningioma tumor tissue and non tumor controls for performing global proteomic analysis on individual patient samples. The data generated was analysed using WHO grades and other radiological parameters inorder to identify markers that can aid in better patient prognostication.

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Sample Preparation: Tumor tissue were snap frozen in liquid nitrogen during surgery followed by washes using IX PBS to get rid of any blood or other fluids. The tumor tissue was then lysed using 8M urea buffer and sonicated at 40% Amplitude.

Peptide Separation: Centrifugation was done to get rid of debris and the lysates trypsinized using Trypsin. Peptides were further cleaned up using C18 tips and vaccuum dried. Prior to LC MS-MS peptides were reconstituted in 0.1 % Formic acid and 1ug of peptide was run in Q-Exactive Mass Spectrometer using nano-LC.

Protein Characterization: Data from intrument were .raw files these were further analysed using Proteome Discoverer 2.2 and the normalization was done using Total Peptide Intensity. The normalized abundances were further converted into Log2 scale and statistical analysis was done using ANOVA, student t test and FDR correction. Further bioinformatic analysis was done using REACTOME and NetworkAnalyst.

Experiment Type: Shutgun proteomics

Species: Homo sapiens - 9606

Tissue: Brain (bto:0000142)

Cell Type: Epithelial cell (bto:0000414)

Disease: Brain cancer (doid:1319)

Instrument Details: Q Exactive (MS:1001911)

Protein Modifications: iodoacetamide derivatized residue

PubMed ID: