Missing proteins as potential biomarkers in cancers

Objective: This study explored potential expressd missing proteins in cancer cells and their distributions in different cancer types and components. The missing proteins detected were further examined for their power as biomarkers in cancer detection and cancer classification.

Biological Methods: sample preparation, experiments

Peptide Spectra Matching Methods

# Statistical Methods

After peptide spectral matching (PSM), the raw spectral count was acquired for each protein for each sample (uniquely identified by an IPAS number). Raw spectral count (SpC) data for cell components such as total cell extraction (TCE), media, nuclear, exosome, and surface were available. The availability of samples in data of different components was different (see supplementary table 1 for more details).

## Data normalization

The normalized spectral abundance factors (NSAFs) were calculated using the raw spectral count data (Zybailov et al., 2006). The NSAF for a given protein , is calculated by:

The length-adjusted spectral count for protein k is the total number of spectral counts matched to the protein divided by the amino acids length of the protein. This value is then divided by the sum of length-adjusted spectral counts of all N proteins in a sample to get NASF. The NASF used in this study was scaled by , which didn’t change the property and the reason for doing this will be mentioned later. The NASF can be used to measure the relative abundance of proteins within a sample and the relative abundance of a specific protein between samples, since it is normalized based on the sequencing depth of each sample and the length of the proteins (Neilson et al., 2013).

## Missing proteins distribution for components

## Due to the less reliable detection of low-abundance proteins for the SpCs-based label-free proteomics technique (Lundgren et al., 2010), a pre-filtering was applied to control the false discovery rate (FDR) by only keeping proteins with valid count reads in a certain number of samples (Bourgon et al., 2010). The application of pre-filtering is highly recommended in widely used high-throughput count data analysis packages, such as the edgeR (Yunshun Chen, 2022) and DESeq2 (Michael I. Love, 2022). Considering the number of samples in total and in each cancer type are different for different cell line component datasets, the pre-filtering approach we used needed to control for those factors to make expressed proteins from different component datasets comparable. For example, the pre-filtering in DESeq2 only keeps rows with a total sum greater than 10. For the same truly expressed protein in different component datasets, the dataset with more samples in it is obviously more likely to keep the protein left after pre-filtering using this approach than the component dataset with far fewer samples. The pre-filtering we used for this section was keeping a protein if only it had a valid abundance value (NSAF > 0) in at least N samples, where N was the number of samples in the smallest cancer type group in that dataset (Yunshun Chen, 2022).

## For each cell line component data,

## Correlation between RNA-Seq data

# Result

# Supplementary statistical methods

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