

PROTEOGENOMICS SHARED RESOURCE

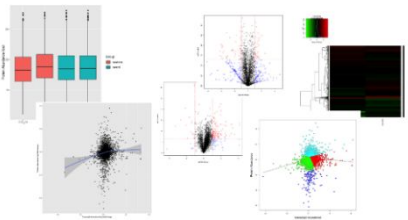


PROTEOGENOMICS

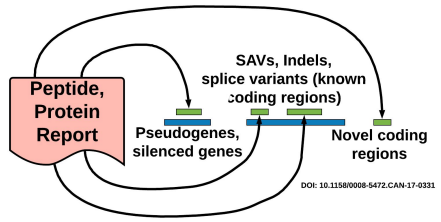
INTEGRATE RNA-SEQ AND MS-BASED PROTEOMICS DATA TO IDENTIFY EXPRESSED VARIANTS AND MECHANISMS OF FUNCTIONAL REGULATION

- IDENTIFY FUNCTIONAL DRIVERS AND BIOMARKERS
- PATHWAY ANALYSIS OF CANCER DEVELOPMENT, PROGRESSION AND INTERVENTION
- PEPTIDE NEOANTIGEN IDENTIFICATION

RNA – PROTEIN RESPONSE



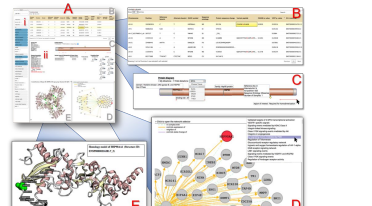
NOVEL PEPTIDE MAPPING



RESULTS VISUALIZATION



IMPACT ANALYSIS OF VARIANTS



POWERED BY:



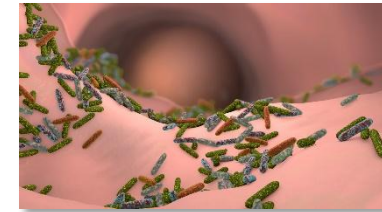
HIGH RESOLUTION MS



NEXT-GEN SEQUENCING



CUSTOMIZED
BIOINFORMATICS

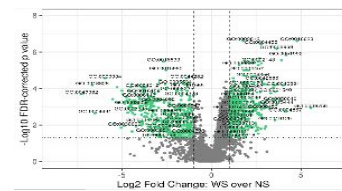


METAPROTEOMICS

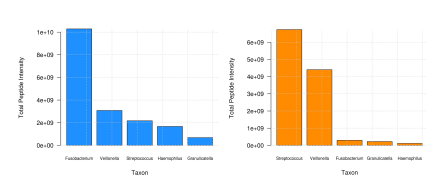
INTEGRATE METAGENOMICS AND PROTEOMICS DATA TO STUDY DYNAMIC HOST-MICROBIOME INTERACTIONS

- IDENTIFY FUNCTIONAL MARKERS EXPRESSED BY MICROBES AND HOST
- FUNCTIONAL VERSUS TAXONOMY RESPONSE UNDER DIFFERENT CONDITIONS
- FUNCTIONAL-TAXONOMIC INTERACTIONS

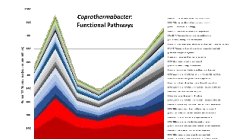
DIFFERENTIAL EXPRESSION



TAXONOMIC ABUNDANCE



FUNCTION-TAXONOMY INTERACTION



STATISTICAL ANALYSIS

