BUILDING SEX-SPECIFIC SYNTHETIC LETHALITY NETWORK IN CANCER - TEMP NAME

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Abstract

Introduction/Background Information

What are Synthetic Lethal Interactions?

Synthetic Lethal Interactions are Harnessed for Precision Oncology

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Building Pan-Cancer Synthetic Lethality Networks in a Sex Specific Manner

Materials and Methods

TCGA Data

RNA sequencing (RNA-seq) data was obtained from The Cancer Genome Atlas (TCGA). Raw STAR aligned counts for tumor tissue and healthy tissue samples were utilized. The Cancer Genome Atlas contains genomic information which spans 33 cancer types. For the purpose of this study, only 12 of the 33 cancer types were considered. We first filtered out sex-biased cancers which include breast invasive carcinoma (BRCA), cervical cell carcinoma (CESC), ovarian serous cystadenocarcinoma (OV), prostate adenocarcinoma (PRAD), testicular germ cell tumors (TGCT), uterine corpus endometrial carcinoma (UCEC), and uterine carcinosarcoma (UCS). Next, we filtered out blood cancers as well as cancers which lacked normal tissue gene expression samples. This included adrenocortical carcinoma (ACC), lymphoid neoplasm diffuse large b-cell lymphoma (DLBC), glioblastoma multiforme (GBM), acute myeloid leukemia (LAML), and brain lower grade glioma (LGG). Finally, we filtered out cancers that did not have any matching pairs of samples (NT and TP from same individual), as well as cancers that had extremely low numbers of matched sample pairs. This included mesothelioma (MESO), skin cutaneous melanoma (SKCM), thymoma (THYM), uveal melanoma (UVM), cholangiocarcinoma (CHOL), pancreatic adenocarcinoma (PAAD), pheochromocytoma and paraganglioma (PCPG), rectum adenocarcinoma (READ), and sarcoma (SARC).

Pre-filtering and Normalization of Raw RNA-seq Count Data

Data Quality Assessment (PCA, NPManova)

Differential Gene Expression Analysis with DESeq2

Results

Discussion

References

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