

Hackathon P1RCC

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Research topic: Analyze the gene expression signature and come up with a treatment regimen

Background

P1RCC

Hereditary papillary renal carcinoma (HPRC) is a hereditary condition that increases the risk of the papillary type of renal cell carcinoma (kidney cancer). The tumors in HPRC are a specific type of papillary cancer called type 1 papillary renal cell cancer. Individuals with HPRC have an increased risk of multiple kidney tumors and an increased risk of developing tumors on both kidneys, called bilateral tumors. Currently, no other types of cancer or noncancerous health problems are known to be related to HPRC. (www.cancer.net)

CMAP

The Connectivity Map, or CMap, is a resource that uses transcriptional expression data to probe relationships between diseases, cell physiology, and therapeutics. The changes in gene expression, or “signatures,” that arise from a disease, genetic perturbation (knockdown or overexpression of a gene) or treatment with a small molecule are compared for similarity to all perturbational signatures in the database. Perturbations that elicit highly similar, or highly dissimilar, expression signatures are termed “connected”; their related transcriptional effects suggest they confer related physiological effects on the cell. The goal of CMAP is to use these connections to uncover novel treatments for a variety of diseases, including cancers, neurological diseases, and infectious diseases. ([CMAP](http://cmap.kgi.edu/))

Goal

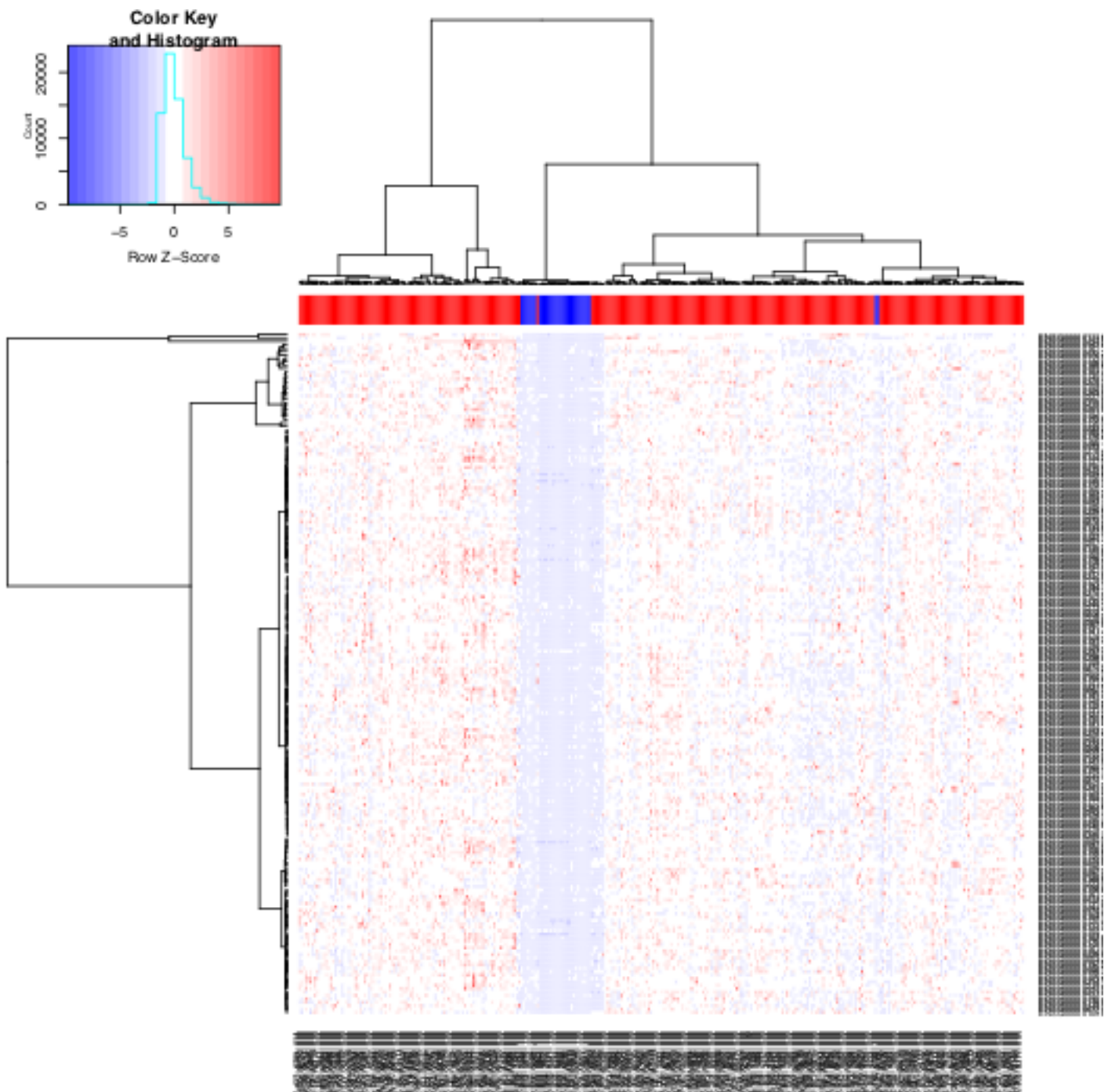
We will first identify gene expression signatures in P1RCC, then feed the genes into CMAP to check if there's any potential drug for the disease.

Data preprocessing

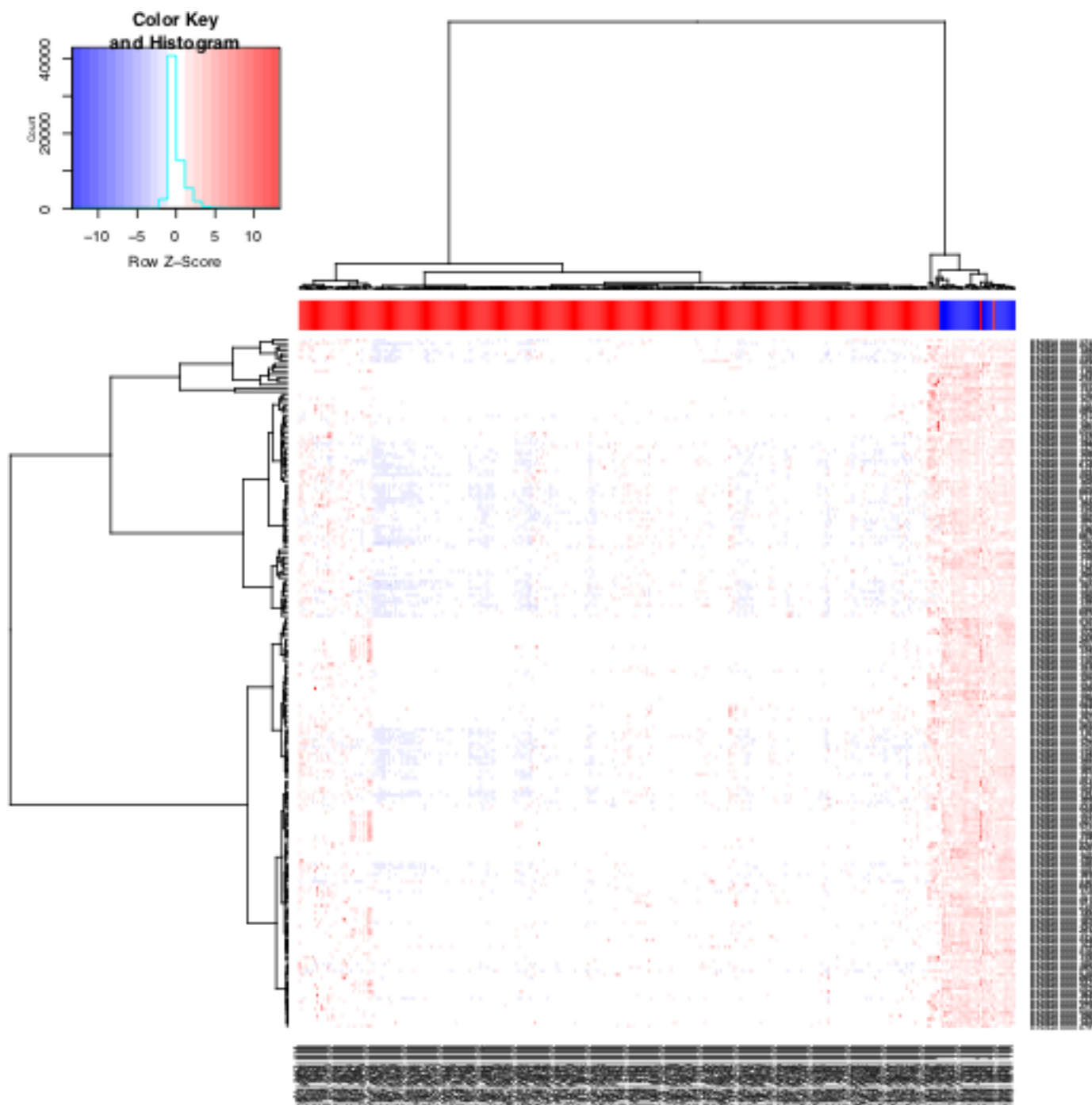
- Download data from TCGA
- 321 samples
- 288 tumors tissues
- 32 normal tissues
- 1 "additional primary tissues" was removed
- Used FPKM data to represent gene expression value

Perform differential expression analysis

Top 200 differential expressed genes in P1RCC (all up-regulated in P1RCC)



Top 200 down-regulated genes in P1RCC



Top up-regulated genes in P1RCC

	hgnc_symbol	entrezgene	description
1	DBNDD1	79007	dysbindin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:28455]
2	TMEM98	26022	transmembrane protein 98 [Source:HGNC Symbol;Acc:HGNC:24529]
3	ELAC2	60528	elaC ribonuclease Z 2 [Source:HGNC Symbol;Acc:HGNC:14198]
4	LRRC23	10233	leucine rich repeat containing 23 [Source:HGNC Symbol;Acc:HGNC:19138]
5	MVP	9961	major vault protein [Source:HGNC Symbol;Acc:HGNC:7531]
6	VIM	7431	vimentin [Source:HGNC Symbol;Acc:HGNC:12692]

Top down-regulated genes in P1RCC

	hgnc_symbol	entrezgene	description
1	FBXL3	26224	F-box and leucine rich repeat protein 3 [Source:HGNC Symbol;Acc:HGNC:26224]
2	CSDE1	7812	cold shock domain containing 1 [Source:HGNC Symbol;Acc:HGNC:7812]
3	SEMA3G	56920	semaphorin 3G [Source:HGNC Symbol;Acc:HGNC:56920]
4	PIK3C2A	5286	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 alpha [Source:HGNC Symbol;Acc:HGNC:5286]
5	SLC30A9	10463	solute carrier family 30 member 9 [Source:HGNC Symbol;Acc:HGNC:10463]
6	CNTN1	1272	contactin 1 [Source:HGNC Symbol;Acc:HGNC:1272]

Drug discovery at Connectivity Map (CMAP)

Input:

- 134 up-regulated genes
- 140 down-regulated genes

Output:

Top positively associated signatures



Top negatively associated signatures



Potential drugs

According to the top negatively associated signatures, here's the potential drug list

- AKT inhibitor

- HDAC inhibitor
- PI3K inhibitor ...