

Alterações moleculares no desenvolvimento da caquexia em pacientes com hepatocarcinomacelular

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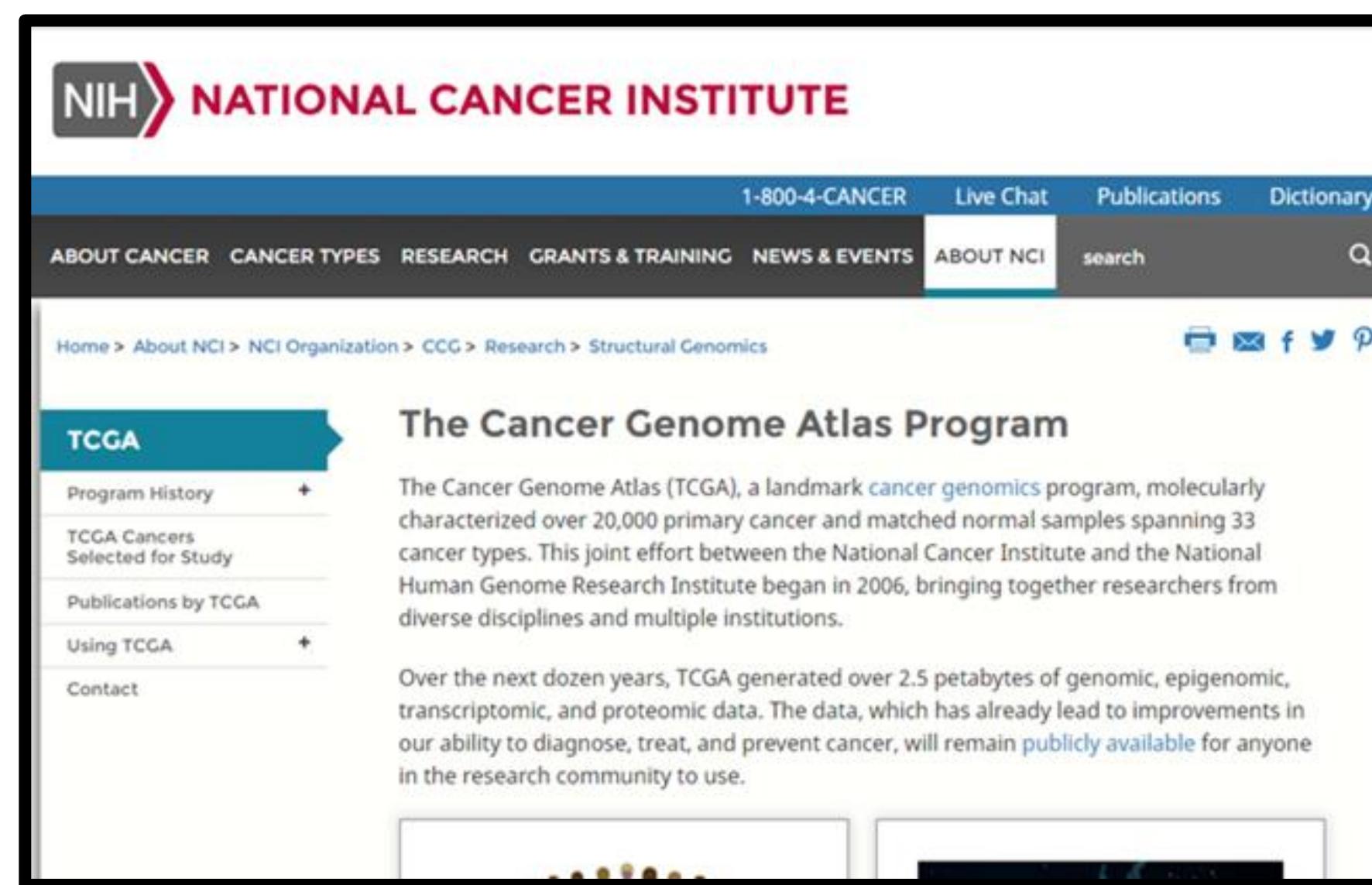
INTRODUÇÃO

O câncer de fígado no Brasil, apesar da baixa incidência, está entre os que apresentam a maior mortalidade. A caquexia do câncer é uma síndrome multifatorial caracterizada por perda de massa muscular, levando a uma perda de peso significativa que afeta a qualidade de vida do paciente, a tolerância ao tratamento, a resposta à terapia e a sobrevivência. A identificação da expressão no momento do diagnóstico pode ajudar a elaborar estratégias para minimizar os efeitos da caquexia em pacientes com câncer de fígado.

OBJETIVO

Avaliar os genes envolvidos na caquexia do hepatocarcinomacelular

METODOLOGIA



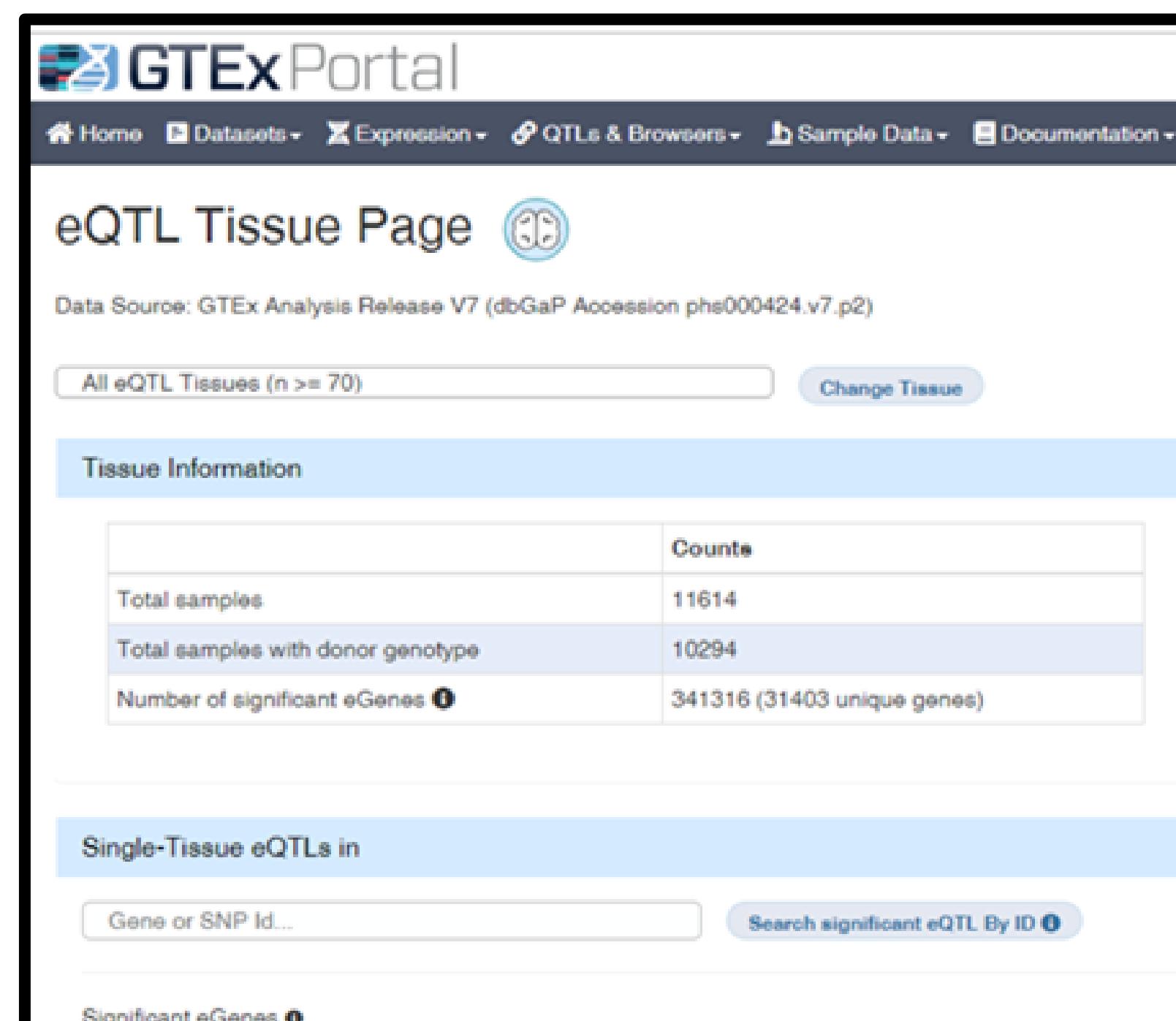
National Cancer Institute TCGA

The Cancer Genome Atlas Program

The Cancer Genome Atlas (TCGA), a landmark cancer genomics program, molecularly characterized over 20,000 primary and matched normal samples spanning 33 cancer types. This joint effort between the National Cancer Institute and the National Human Genome Research Institute began in 2006, bringing together researchers from diverse disciplines and multiple institutions.

Over the next dozen years, TCGA generated over 2.5 petabytes of genomic, epigenomic, transcriptomic, and proteomic data. The data, which has already lead to improvements in our ability to diagnose, treat, and prevent cancer, will remain publicly available for anyone in the research community to use.

National Cancer Institute TCGA
(<https://portal.gdc.cancer.gov/>)



eQTL Tissue Page

Data Source: GTEx Analysis Release V7 (dbGaP Accession phs000424 v7.p2)

All eQTL Tissues (n >= 70) Change Tissue

Tissue Information

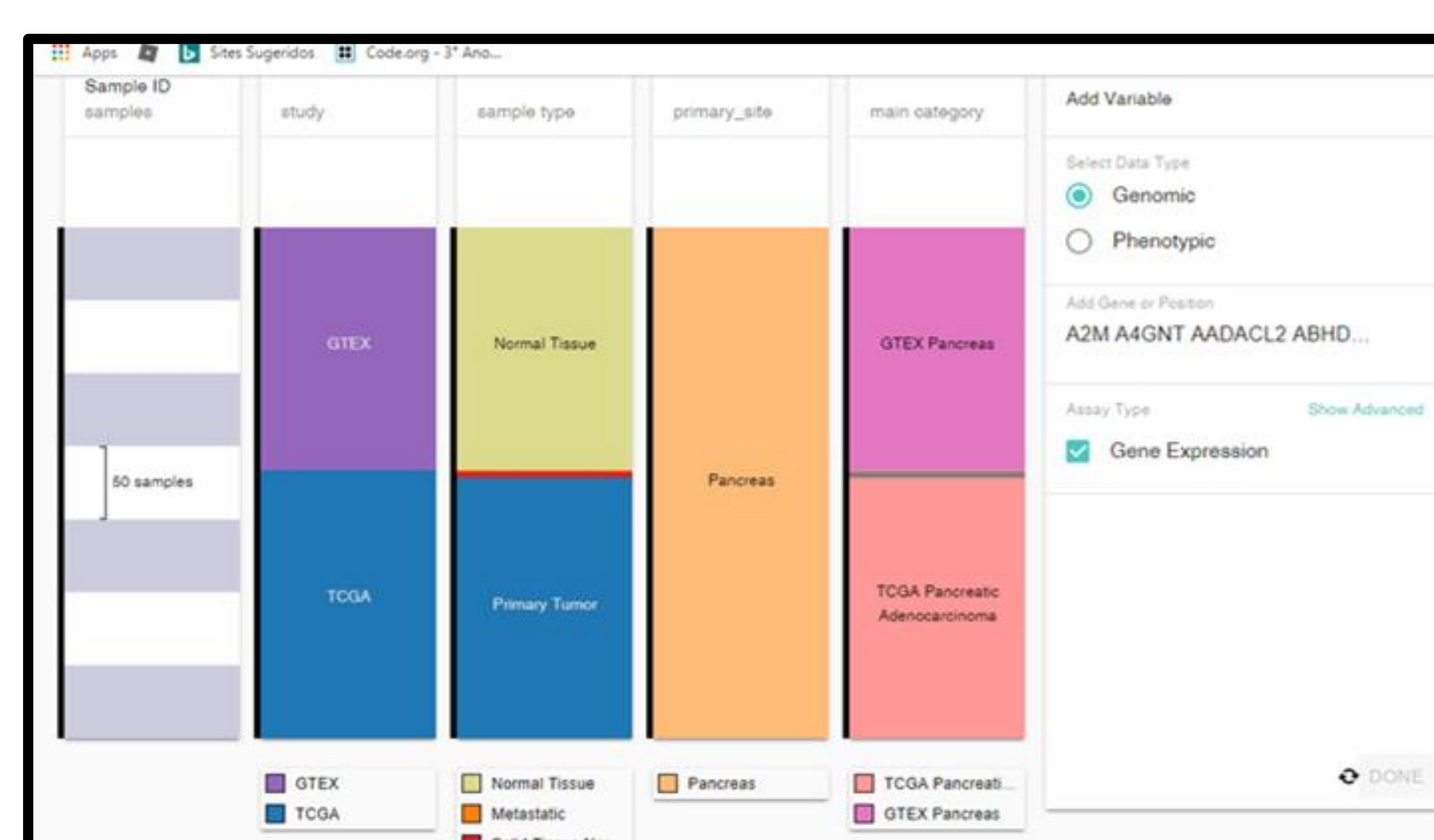
	Count
Total samples	11614
Total samples with donor genotype	10294
Number of significant eGenes	341316 (31403 unique genes)

Single-Tissue eQTLs in

Gene or SNP ID... Search significant eQTL By ID

Significant eGenes

Portal GTEx (<http://www.gtexportal.org/>)



Sample ID samples study sample type primary_site main category Add Variable

Select Data Type Genomic Phenotypic

Add Gene or Position A2M A4GNT ADAACL2 ABHD...

Assay Type Gene Expression Show Advanced

Legend: GTEx (Purple), TCGA (Blue), Normal Tissue (Yellow), Pancreas (Orange), TCGA Pancreas (Red), GTEx Pancreas (Pink)

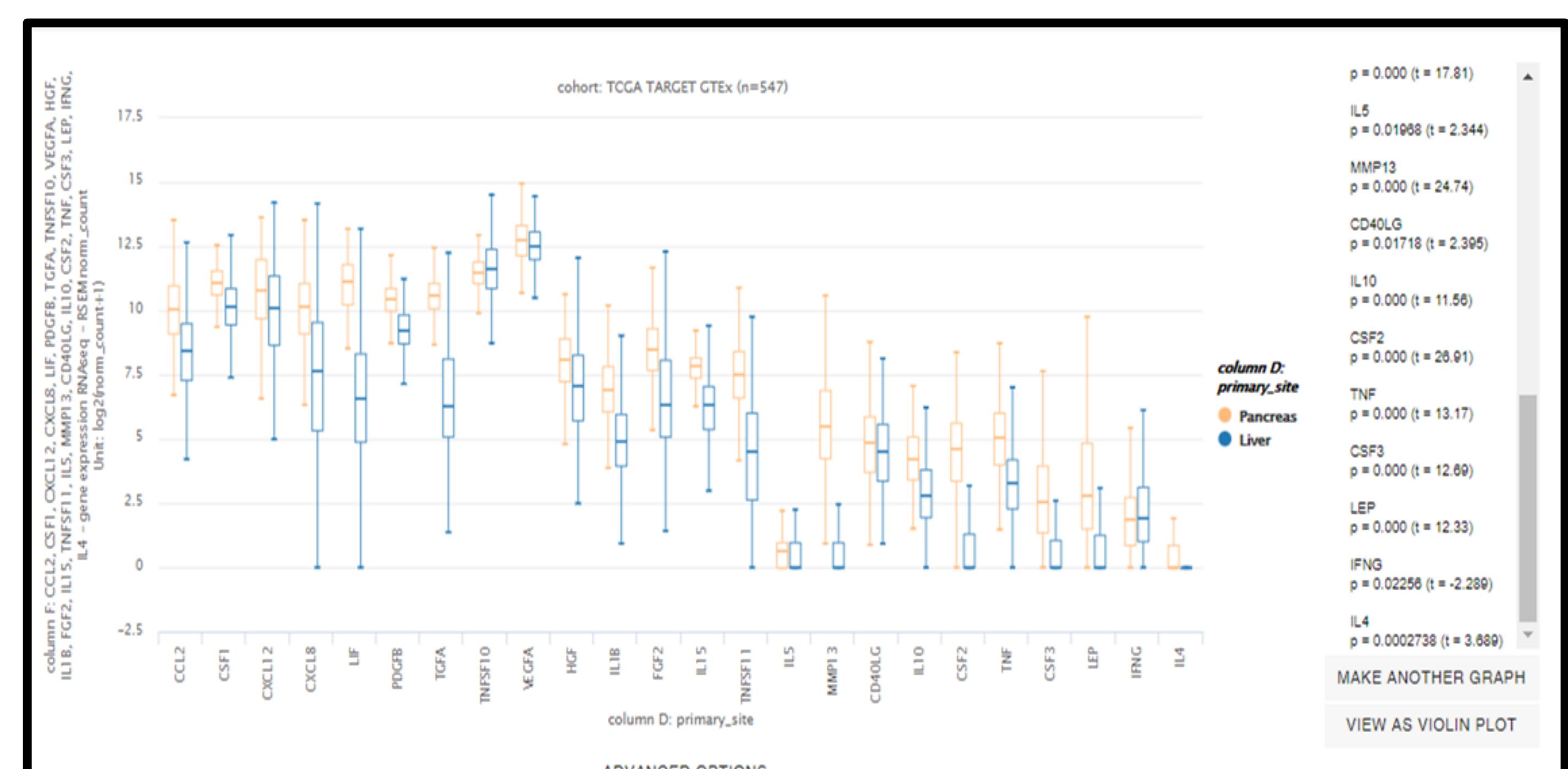
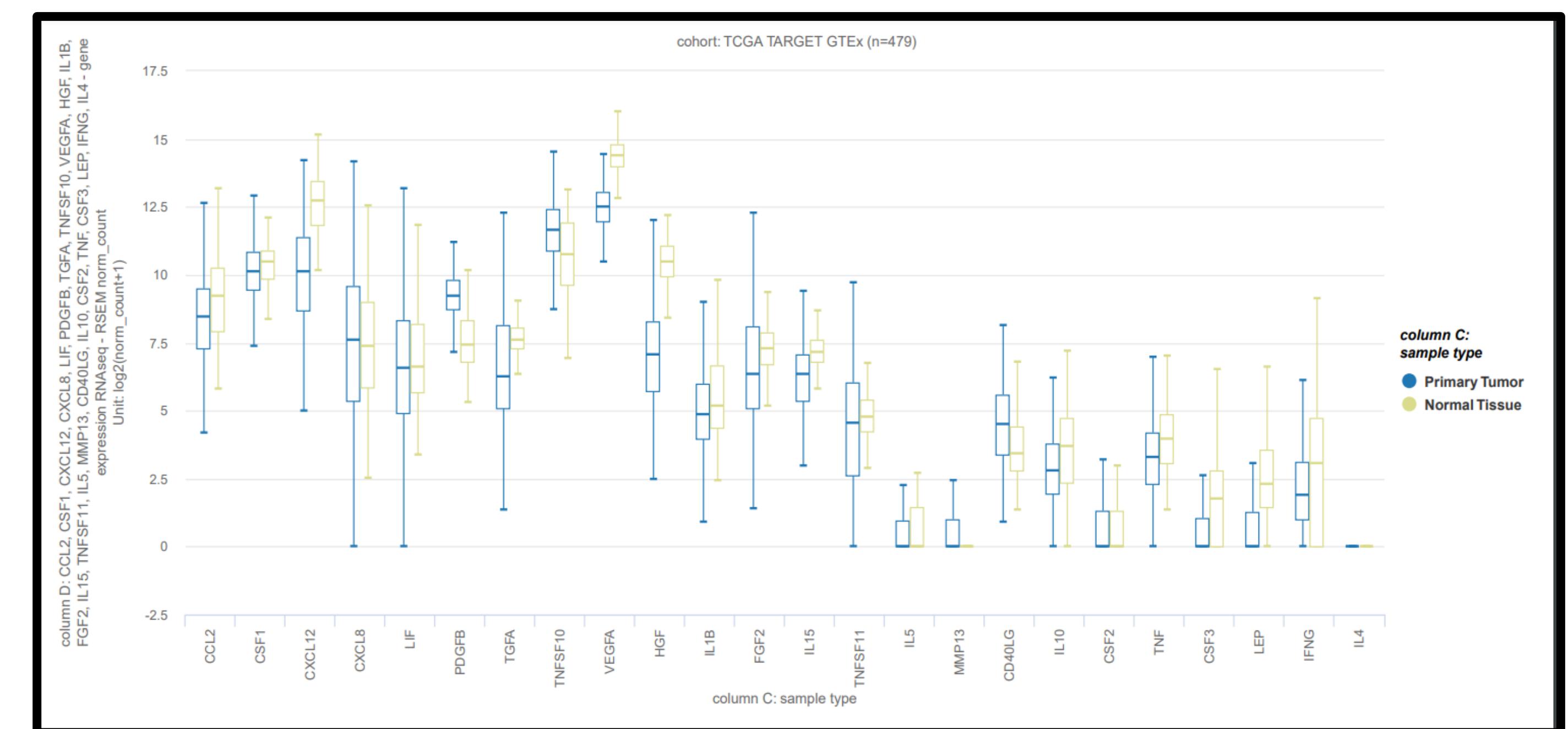
DONE

Xena Functional Genomics Explorer
(<http://xenabrowser.net>).

25 fatores caquéticos da literatura:

CCL2	TNFSF11
CSF1	IL6
CXCL12	MMP13
CXCL8	CD40LG
LIF	IL10
PDGFB	CSF2
TGFA	TNF
TNFSF10	CSF3
VEGFA	LEP
HGF	IFNG
IL1B	IL17A
FGF2	IL4
IL15	

RESULTADOS E DISCUSSÃO



CONCLUSÃO

Por tanto concluímos que a análise molecular demonstrou que o hepatocarcinoma celular não apresenta aumento relevante da expressão de fatores caquéticos. Logo a caquexia no hepatocarcinoma pode ser associada também a outros fatores que não a expressão desses fatores que não apenas pelo próprio tumor.

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