Transcriptomics Practical Setup

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Faculty Member, Sa'adu Zungur University

@babasaraky

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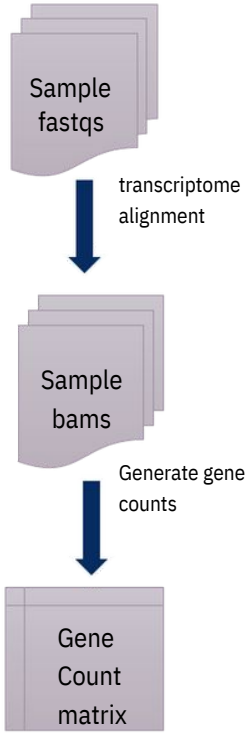
Transcriptomics pre-proccesing workflow

Preprocessing



Transcriptomics pipeline/workflow

Preprocessing

Sample fastqs

transcriptome alignment

Sample bams

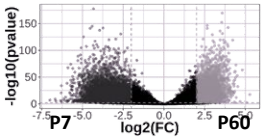
Generate gene counts

Gene Count matrix

Analyses

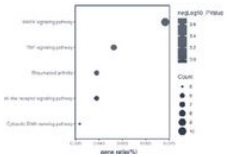
Clustering

Differential Expression



DESeq2 limma Glimma edgeR

Functional Enrichment



GSEA Gene Set Enrichment Analysis

MetaCore

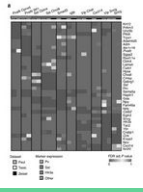
GREAT

KEGG

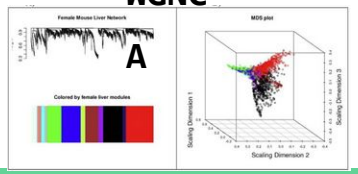
reactome

DAVID BIOINFORMATICS DATABASE

Coregulated Gene Expression



WGNC



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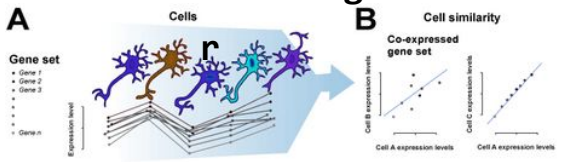

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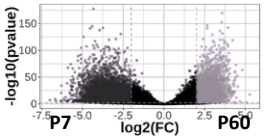

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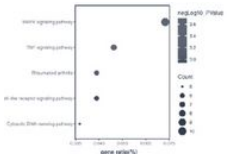

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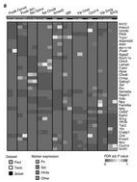

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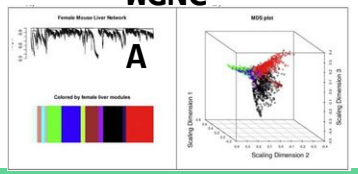

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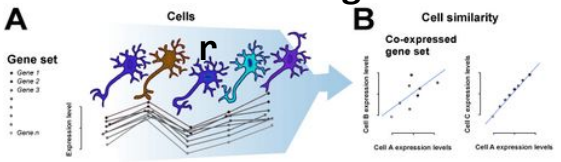


nature COMMUNICATIONS

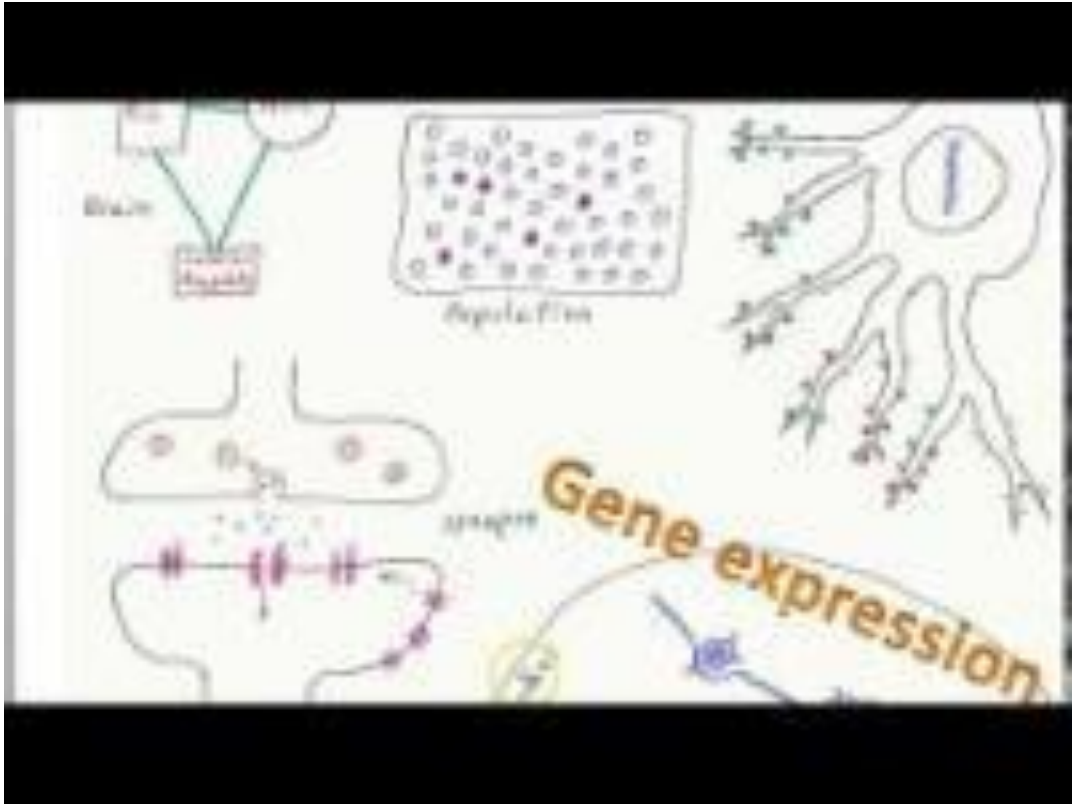
ARTICLE

https://doi.org/10.1038/s41467-019-09960-x OPEN

Engram-specific transcriptome profiling of contextual memory consolidation

Priyanka Rao-Ruiz[1,2], Jonathan J. Couey[1], Ivo M. Marcelo[1,3], Christian G. Bouwkamp[1], Denise E. Slump[1], Mariana R. Matos[2], Rolinka J. van der Loo[2], Gabriela J. Martins[3,4], Mirjam van den Hout[5], Wilfred F. van IJcken[5], Rui M. Costa[3,4], Michel C. van den Oever[2] & Steven A. Kushner[1]

What is an engram??



https://www.youtube.com/watch?v=4ZmWzDKeCs0&list=PLCBaYkVpZFBd0DDS_iOA7w1fDv1ONh169

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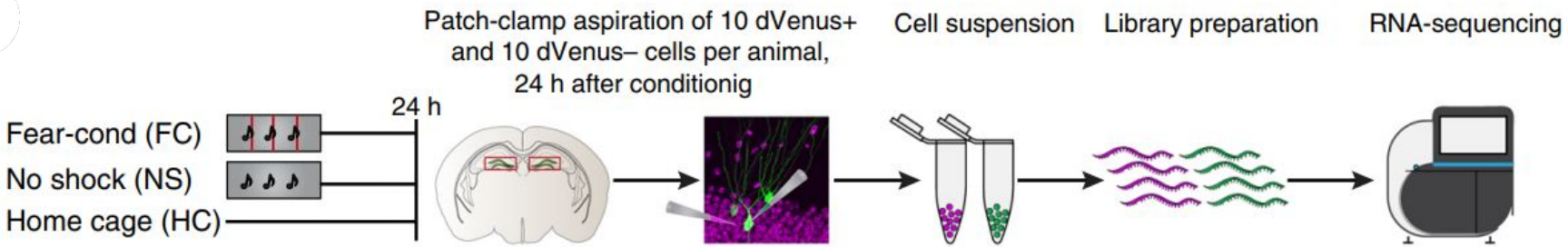
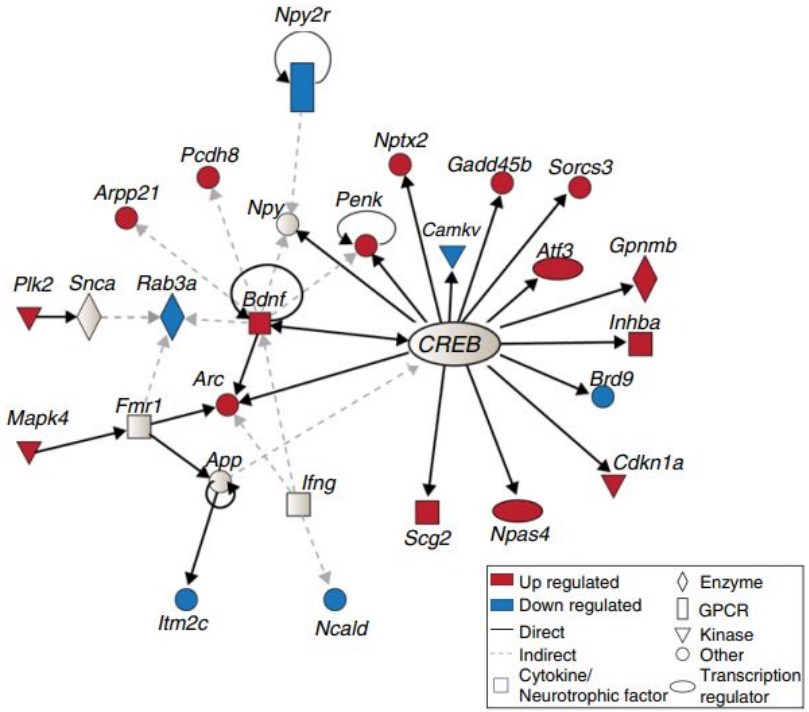
Experimental design to isolate cells that participate in fear learning engram

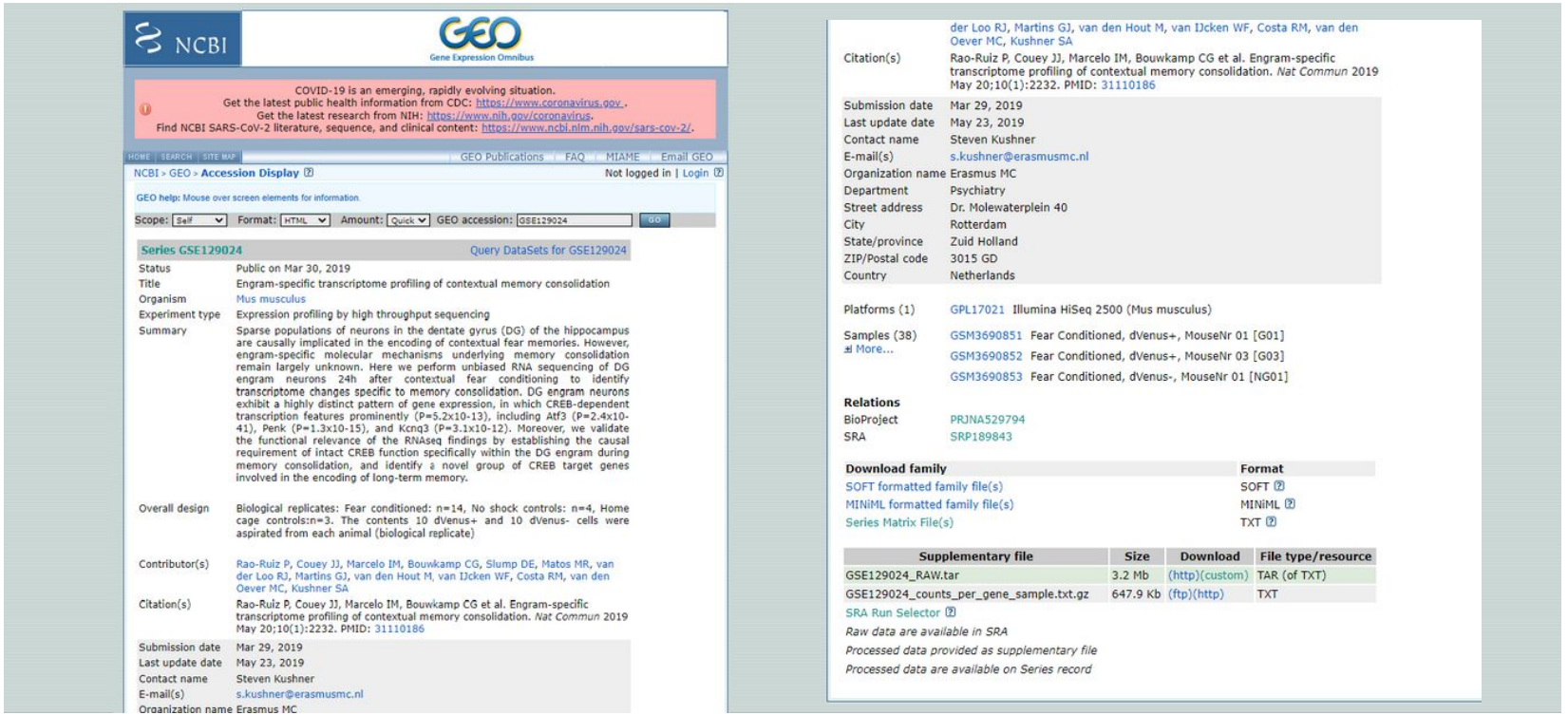


Novel target genes for CREB found that modulates fear memory learning



Rao-Ruiz et al. Nat Comm. 2019

Accessing the data through NCBI GEO



NCBI

GEO Gene Expression Omnibus

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Scope: Self Format: HTML Amount: Quick GEO accession: GSE129024 GO

Series GSE129024 Query DataSets for GSE129024

Status	Public on Mar 30, 2019
Title	Engram-specific transcriptome profiling of contextual memory consolidation
Organism	Mus musculus
Experiment type	Expression profiling by high throughput sequencing
Summary	Sparse populations of neurons in the dentate gyrus (DG) of the hippocampus are causally implicated in the encoding of contextual fear memories. However, engram-specific molecular mechanisms underlying memory consolidation remain largely unknown. Here we perform unbiased RNA sequencing of DG engram neurons 24h after contextual fear conditioning to identify transcriptome changes specific to memory consolidation. DG engram neurons exhibit a highly distinct pattern of gene expression, in which CREB-dependent transcription features prominently (P=5.2x10-13), including Atf3 (P=2.4x10-41), Penk (P=1.3x10-15), and Kcnq3 (P=3.1x10-12). Moreover, we validate the functional relevance of the RNAseq findings by establishing the causal requirement of intact CREB function specifically within the DG engram during memory consolidation, and identify a novel group of CREB target genes involved in the encoding of long-term memory.
Overall design	Biological replicates: Fear conditioned: n=14, No shock controls: n=4, Home cage controls:n=3. The contents 10 dVenus+ and 10 dVenus- cells were aspirated from each animal (biological replicate)
Contributor(s)	Rao-Ruiz P, Couey JJ, Marcelo IM, Bouwkamp CG, Slump DE, Matos MR, van der Loo RJ, Martins GJ, van den Hout M, van IJcken WF, Costa RM, van den Oever MC, Kushner SA
Citation(s)	Rao-Ruiz P, Couey JJ, Marcelo IM, Bouwkamp CG et al. Engram-specific transcriptome profiling of contextual memory consolidation. *Nat Commun* 2019 May 20;10(1):2232. PMID: 31110186
Submission date	Mar 29, 2019
Last update date	May 23, 2019
Contact name	Steven Kushner
E-mail(s)	s.kushner@erasmusmc.nl
Organization name	Erasmus MC

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Organization name	Erasmus MC
Department	Psychiatry
Street address	Dr. Molewaterplein 40
City	Rotterdam
State/province	Zuid Holland
ZIP/Postal code	3015 GD
Country	Netherlands

Platforms (1) GPL17021 Illumina HiSeq 2500 (Mus musculus)

Samples (38) GSM3690851 Fear Conditioned, dVenus+, MouseNr 01 [G01]
GSM3690852 Fear Conditioned, dVenus+, MouseNr 03 [G03]
GSM3690853 Fear Conditioned, dVenus-, MouseNr 01 [NG01]
More...

Relations

BioProject	PRJNA529794
SRA	SRP189843

Download family	Format
SOFT formatted family file(s)	SOFT
MINiML formatted family file(s)	MINiML
Series Matrix File(s)	TXT

Supplementary file	Size	Download	File type/resource
GSE129024_RAW.tar	3.2 Mb	(http)(custom)	TAR (of TXT)
GSE129024_counts_per_gene_sample.txt.gz	647.9 Kb	(ftp)(http)	TXT

SRA Run Selector

Raw data are available in SRA
Processed data provided as supplementary file
Processed data are available on Series record

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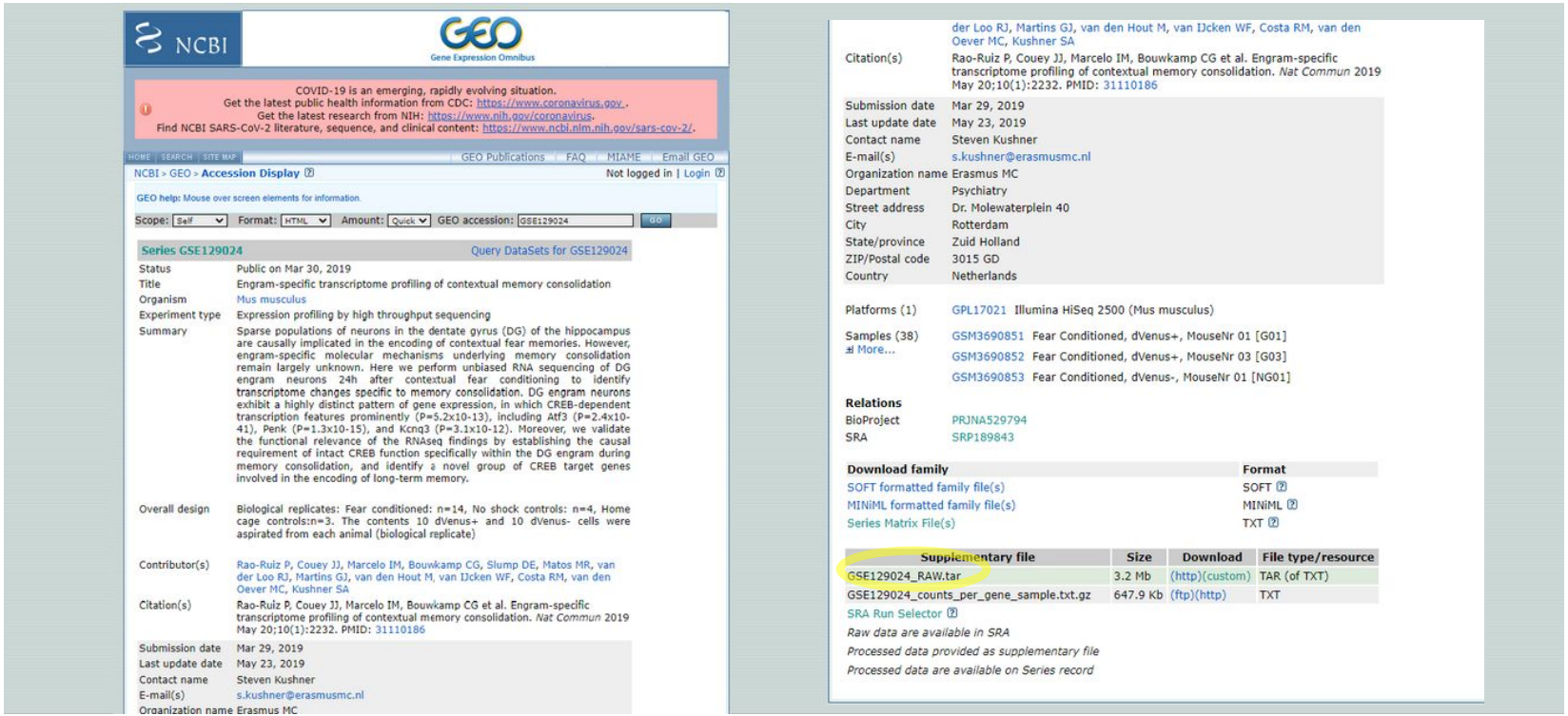

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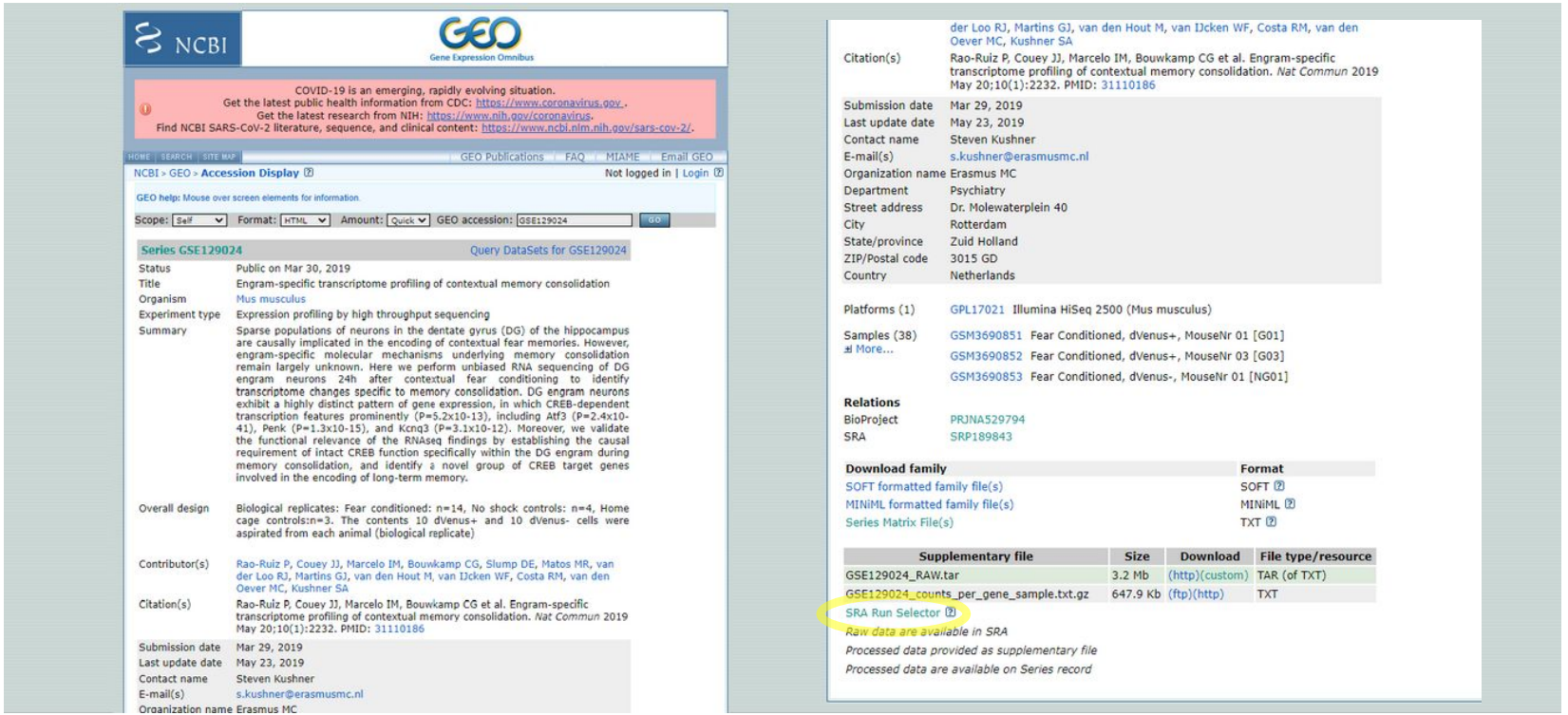

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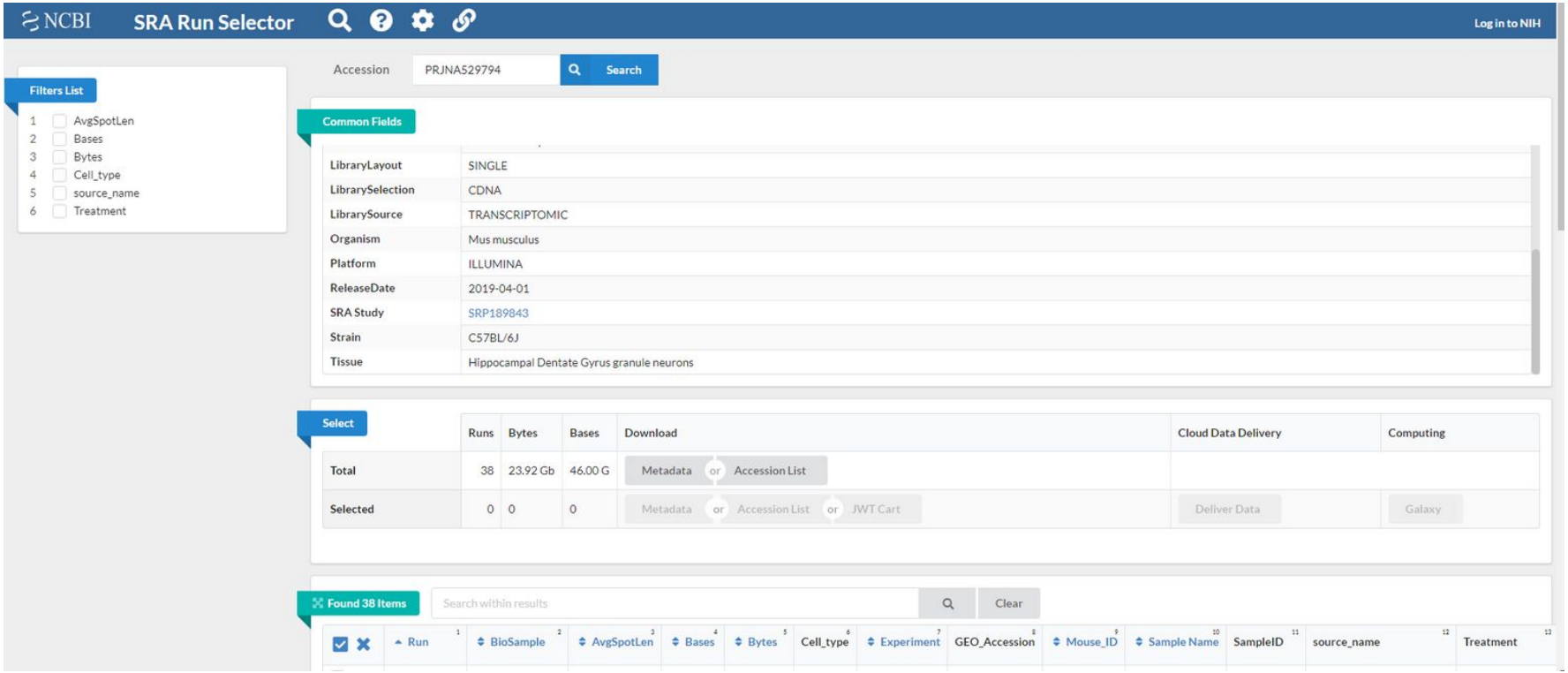

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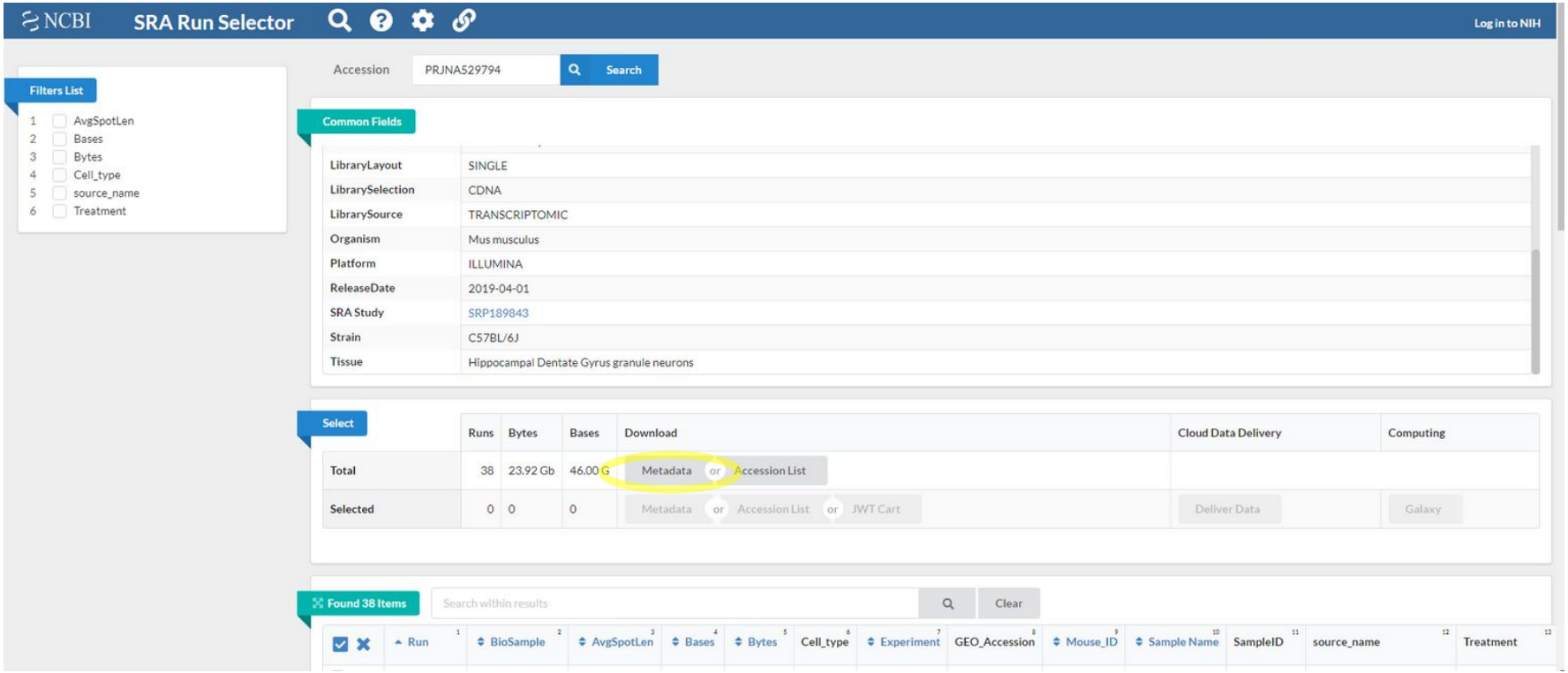

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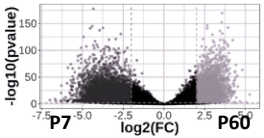

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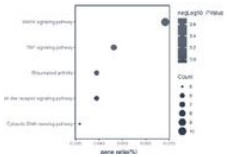

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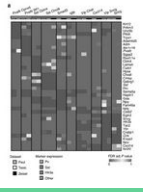

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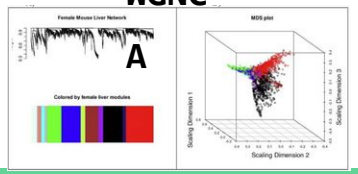

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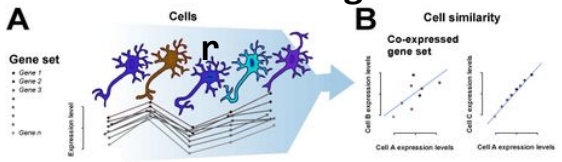

Questions?

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