Transcriptomics Practical Setup

HackBio

April 7th 2021

Melyssa Minto

West Lab, Duke Neurobiology

Computational Biology and Bioinformatics

Transcriptomics pipeline/workflow

Preprocessing

Sample fastqs

transcriptome alignment

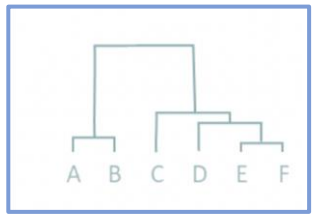
Sample bams

Generate gene counts

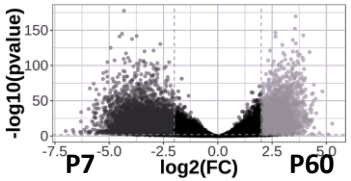
Gene Count matrix

Analyses

Clustering

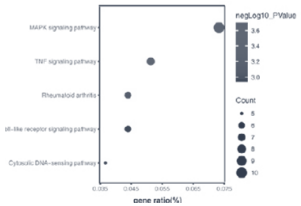


Differential Expression



DESeq2 limma Glimma edgeR

Functional Enrichment



GSEA Gene Set Enrichment Analysis

MetaCore

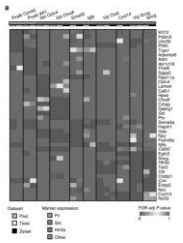
GREAT

KEGG Kyoto Encyclopedia of Genes and Genomes

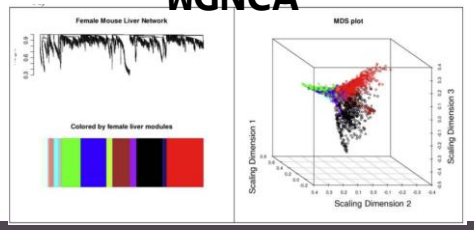
reactome

DAVID BIOINFORMATICS DATABASE

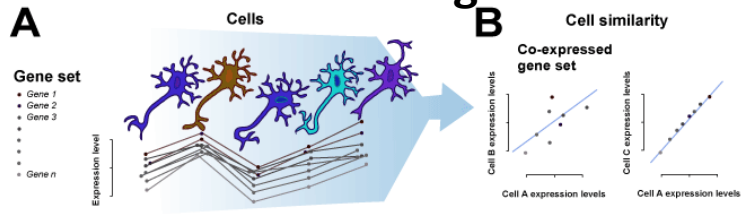
Coregulated Gene Expression



WGNCA



MetaNeighbor



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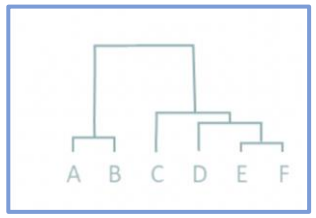

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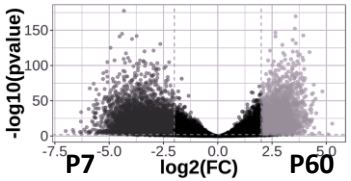

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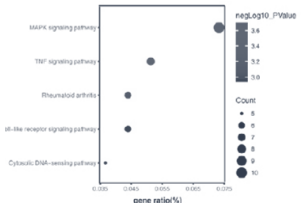

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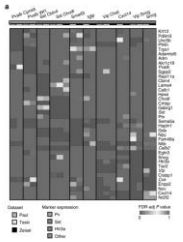

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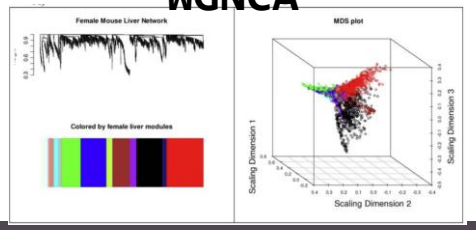

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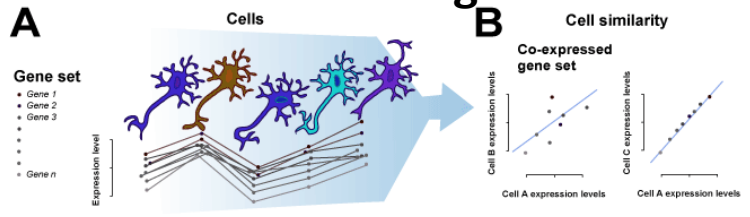

nature COMMUNICATIONS

ARTICLE

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

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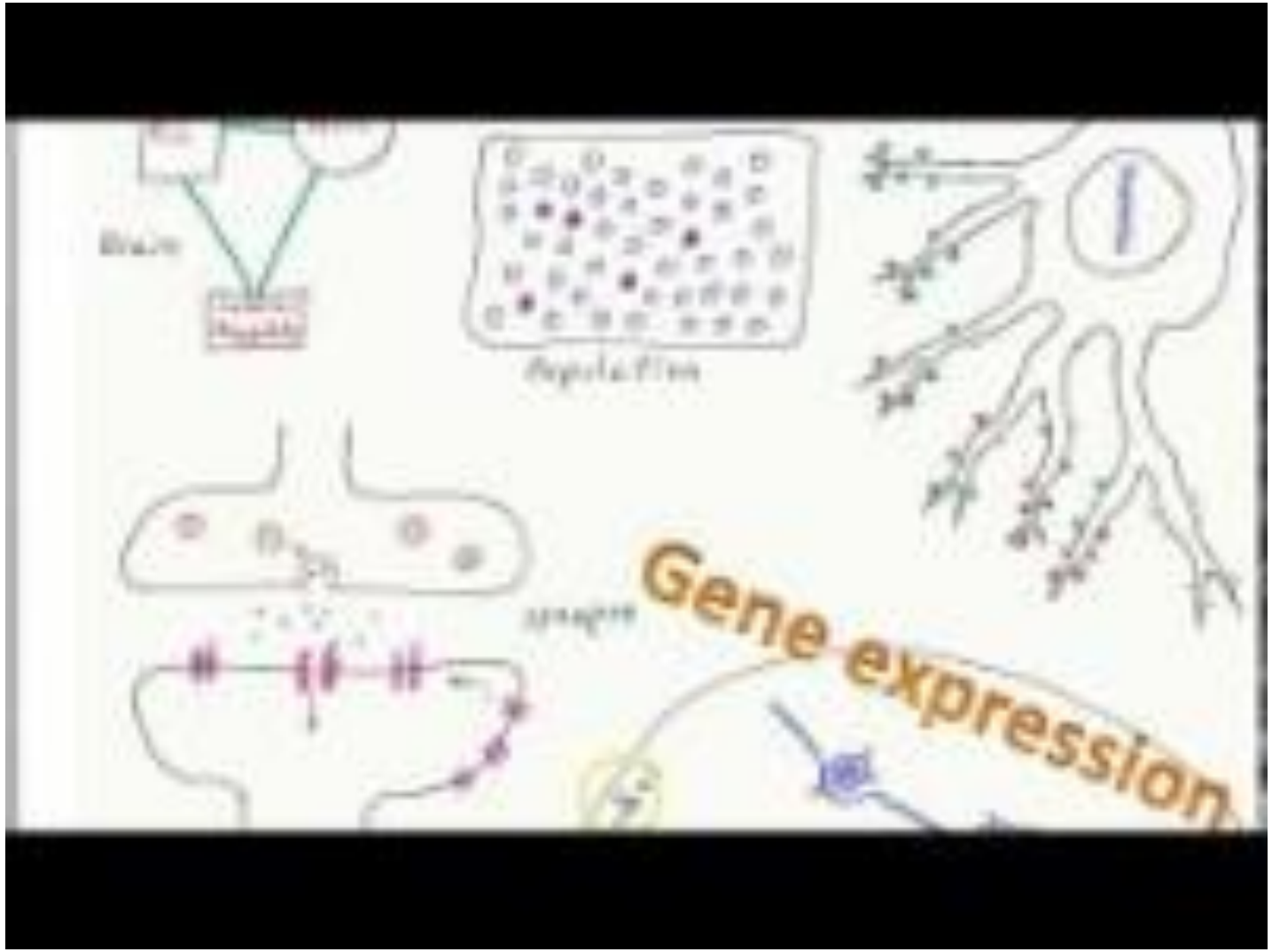
What is an engram??



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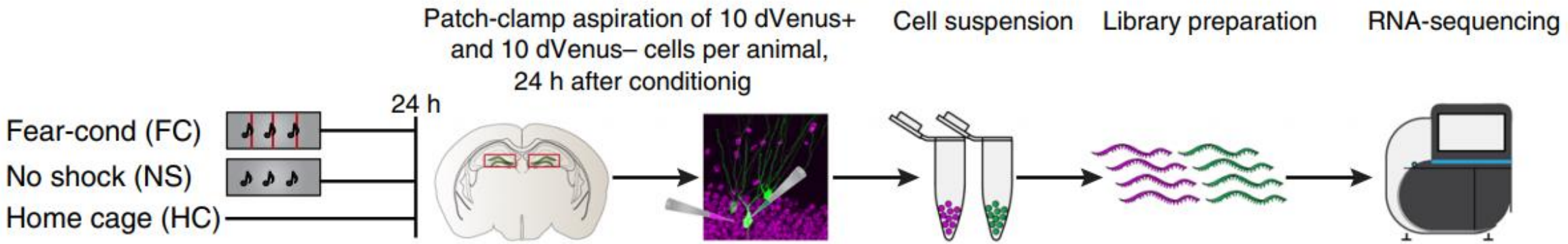
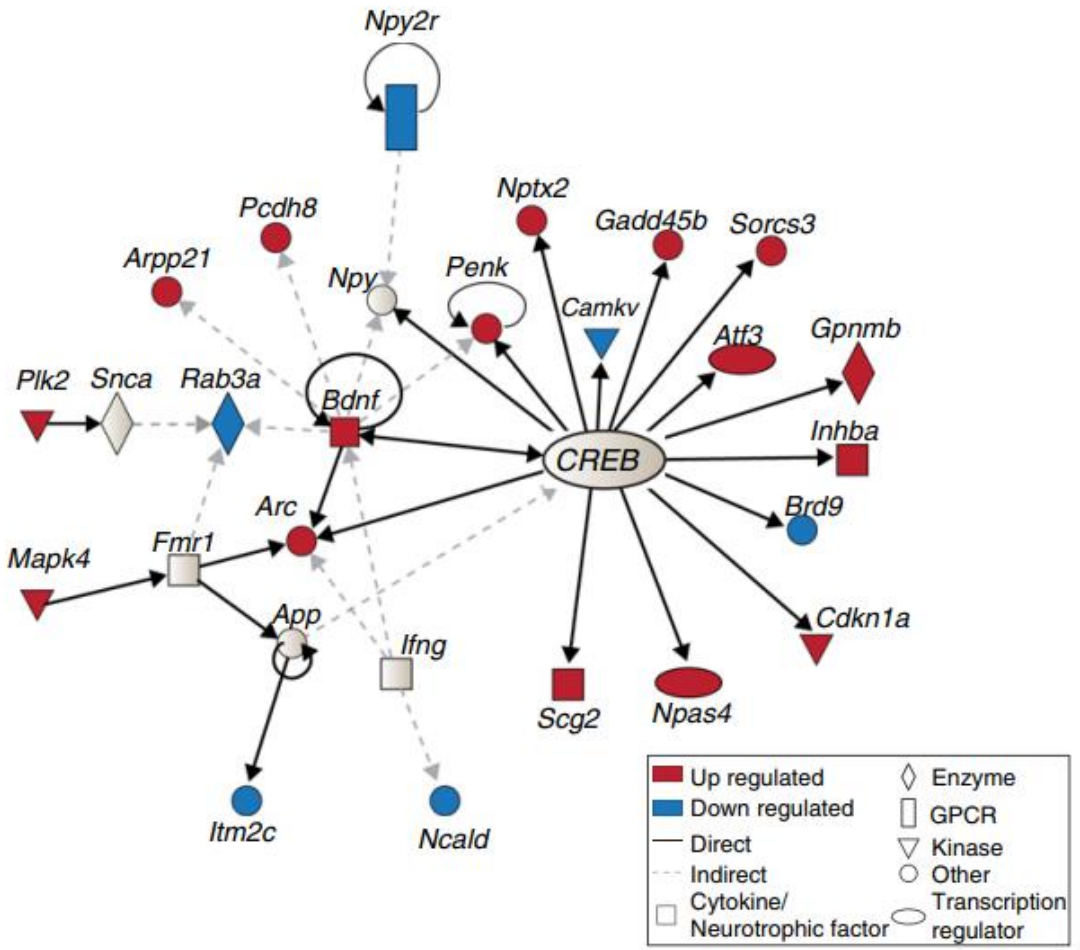
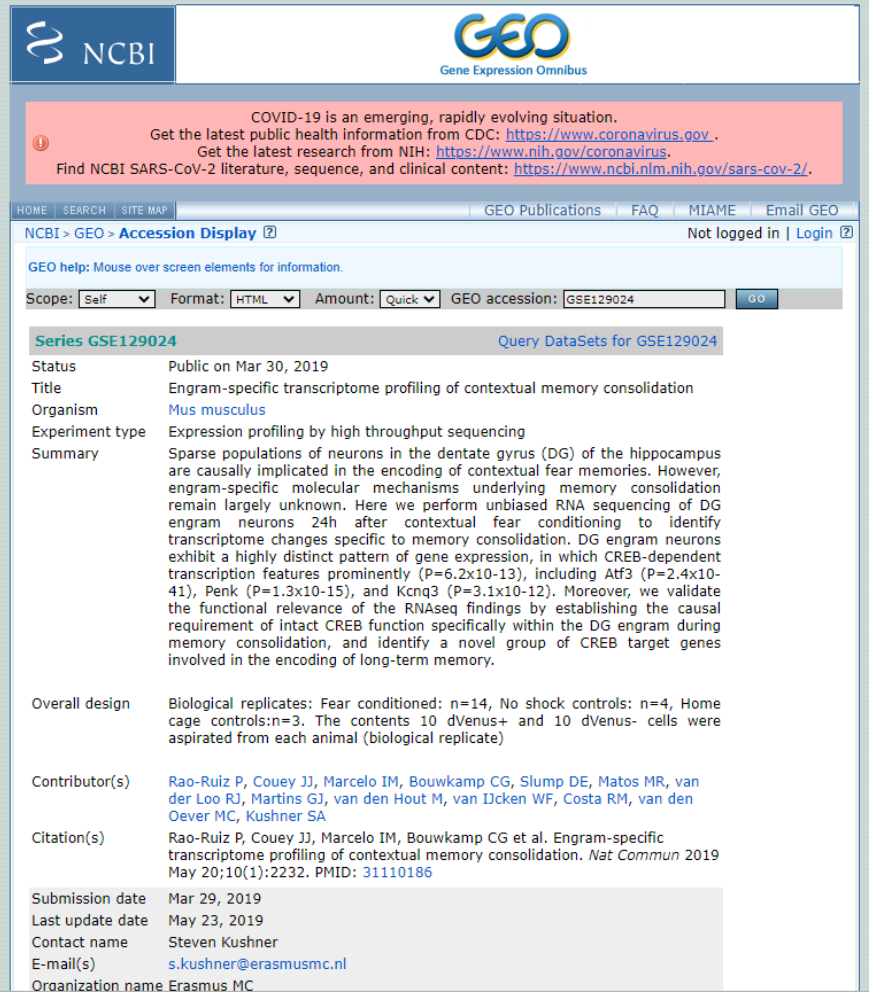
Experimental design to isolate engram cells that participate in fear learning



Novel target genes for CREB found that modulates fear memory learning



Accessing the data through NCBI GEO



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Series GSE129024 — Query DataSets for GSE129024

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Organism	Mus musculus
Experiment type	Expression profiling by high throughput sequencing
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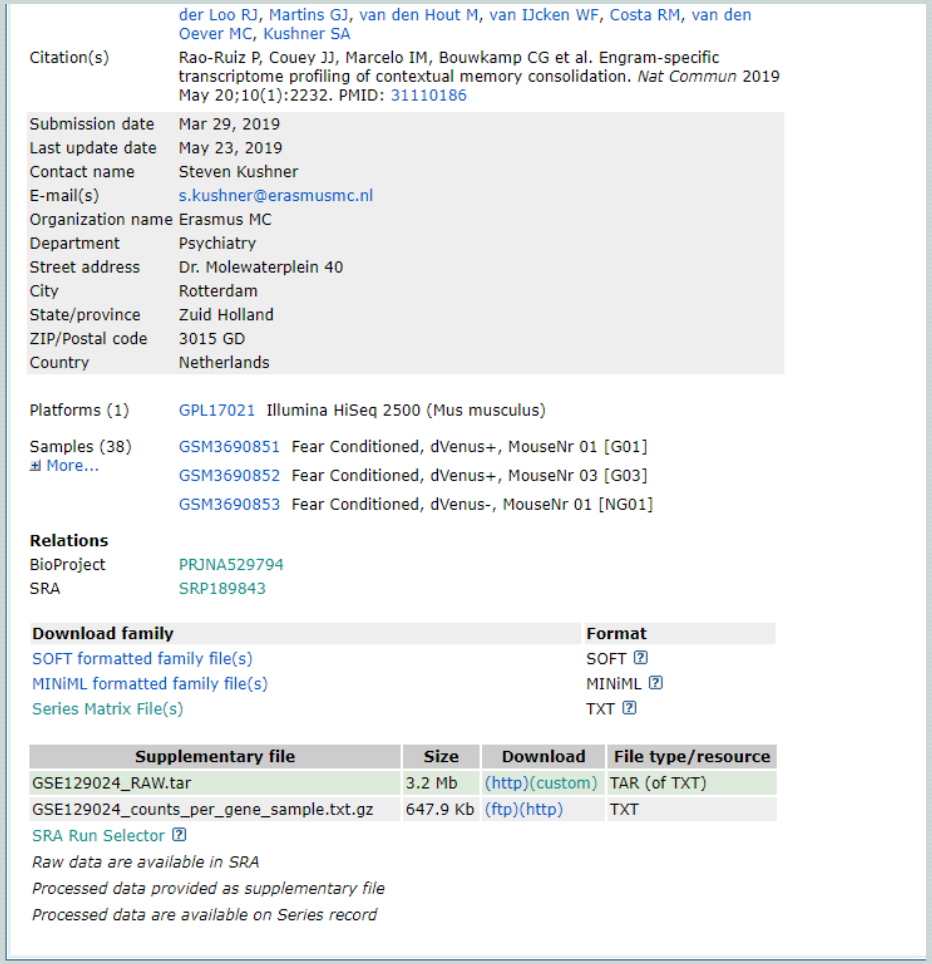
Contact name	Steven Kushner
E-mail(s)	s.kushner@erasmusmc.nl
Organization name	Erasmus MC



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Relations

BioProject	PRJNA529794
SRA	SRP189843

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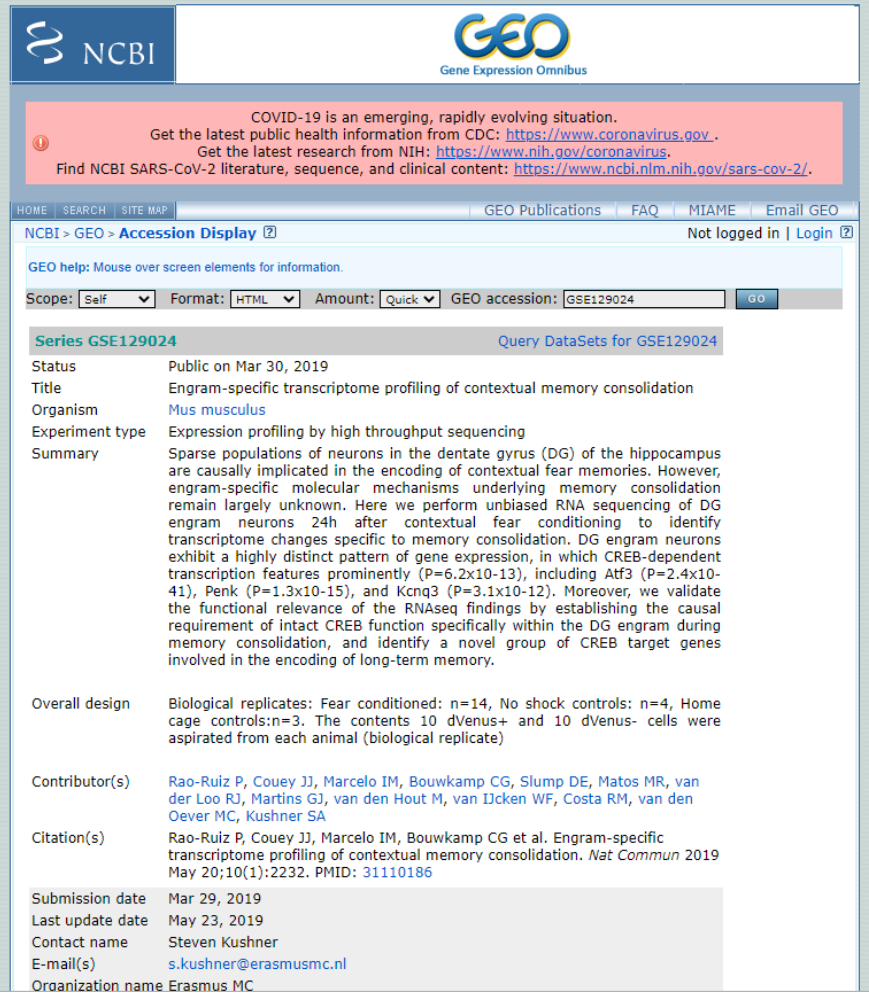

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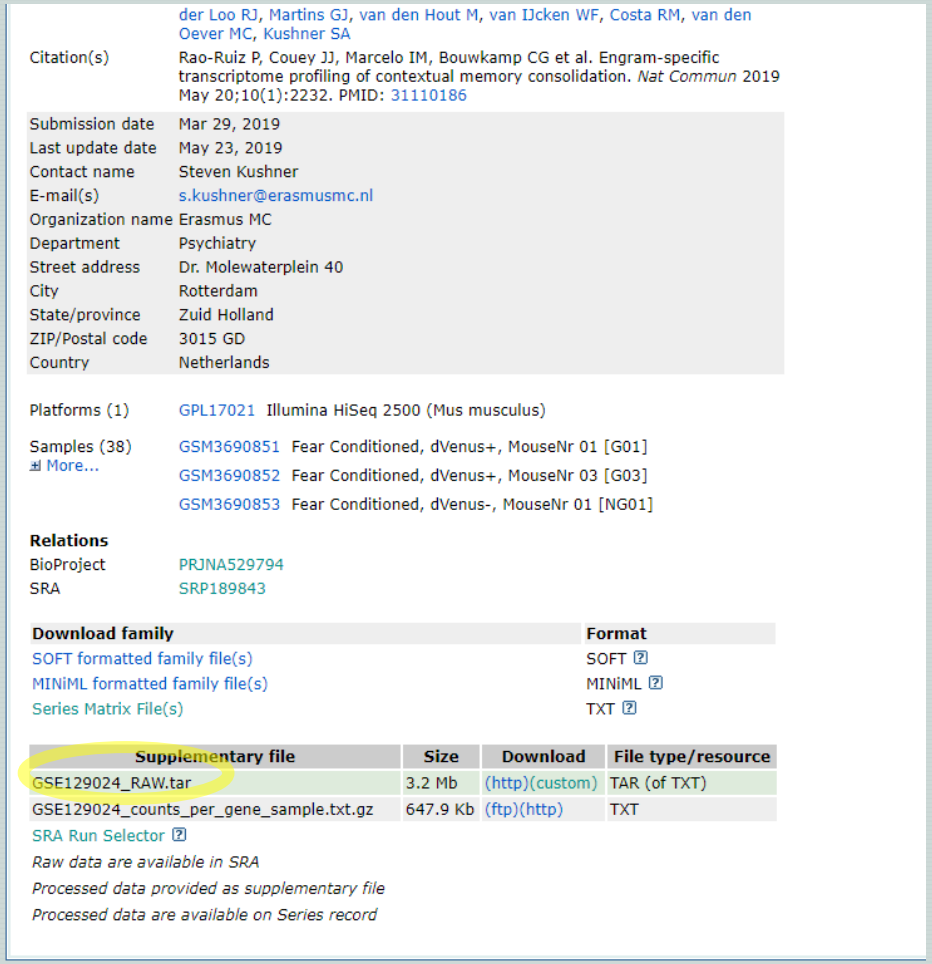

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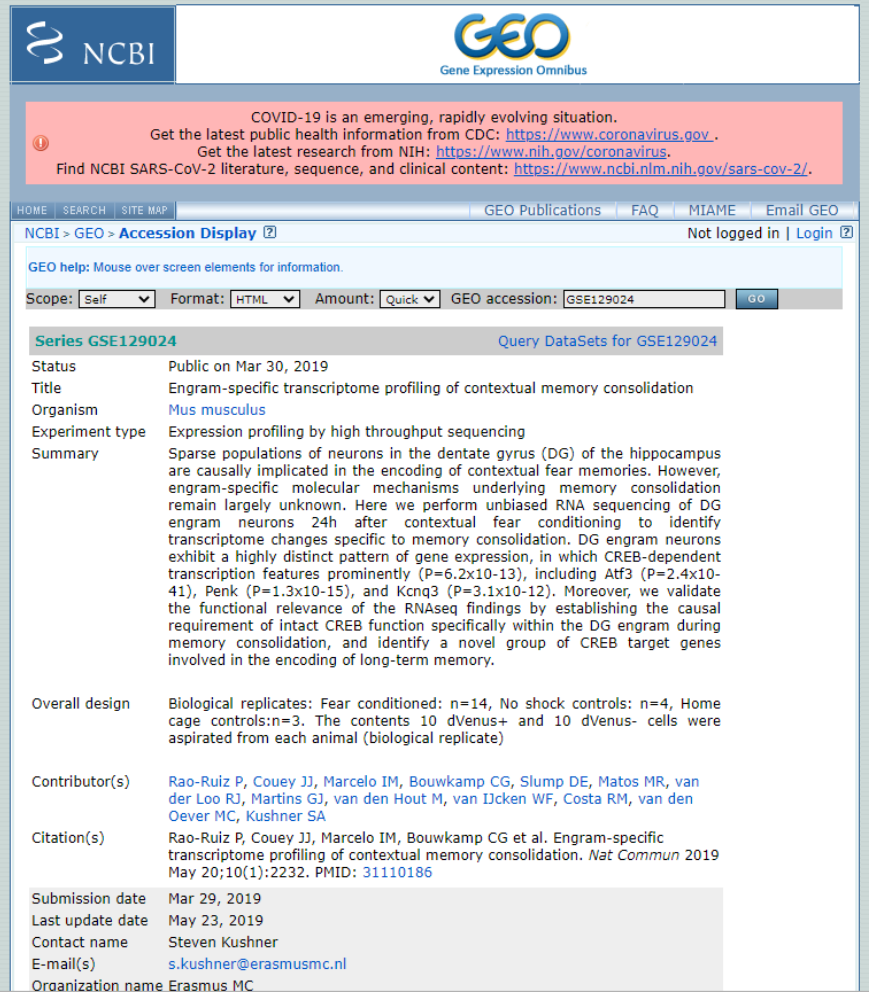

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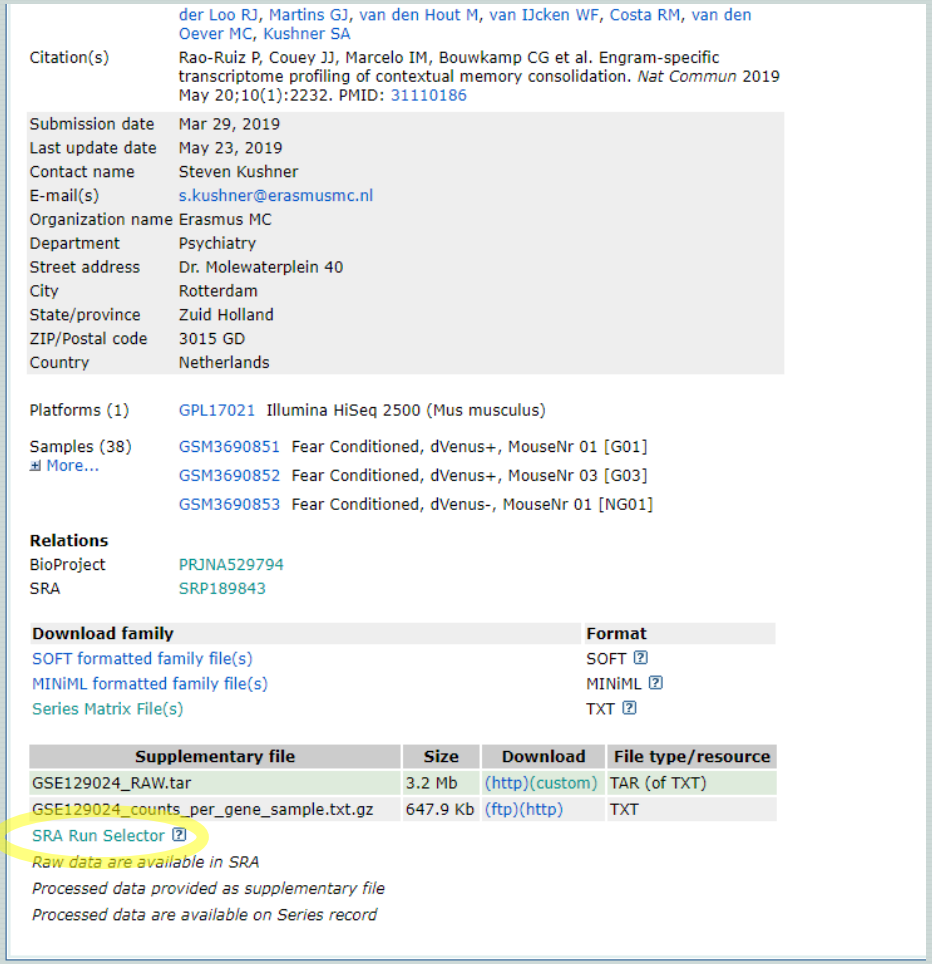

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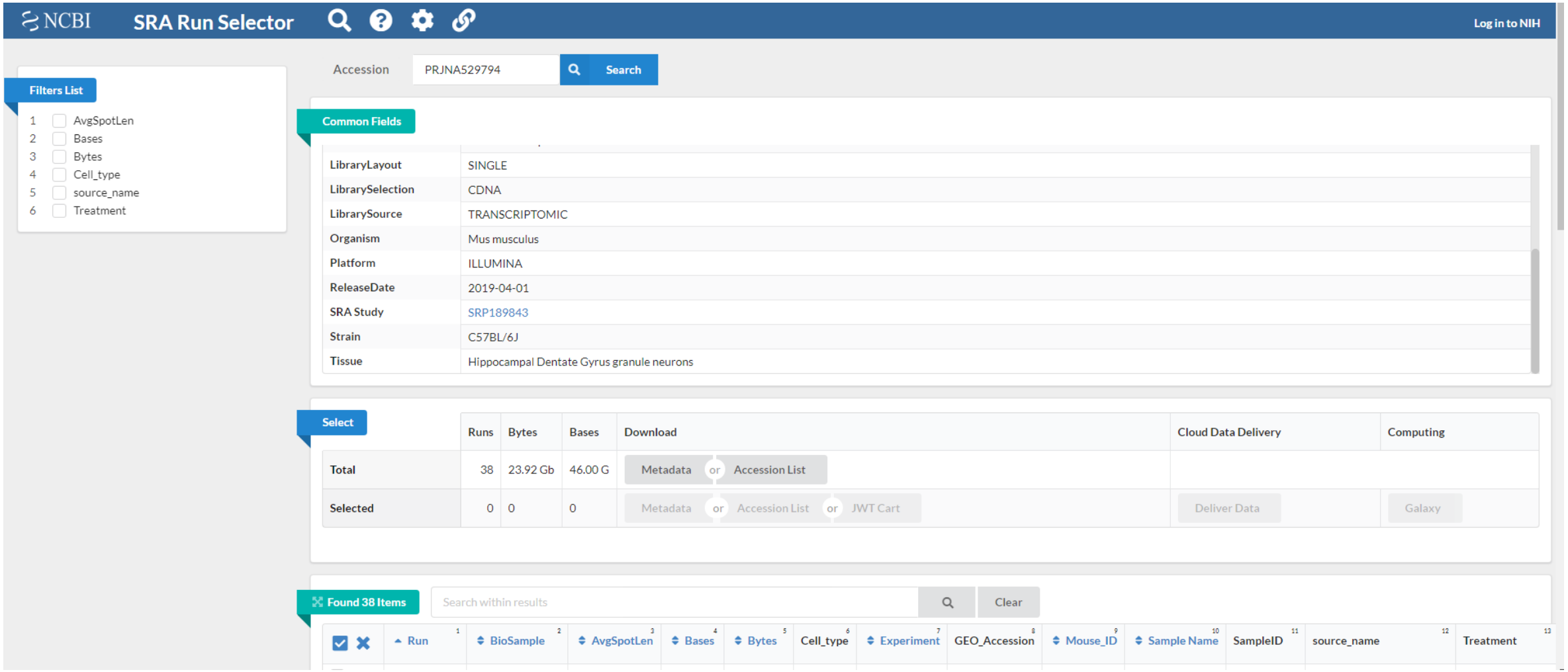

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