LabBook_24_02_2017

Claire Green

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## Warning: package 'knitr' was built under R version 3.3.2
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Monday

Wenbin and I worked out that the reasons for the differences between mine and Sandeep's results is probably due to the fact that he used the transcript matrix rather than the gene IDs. This meant that I was looking at expression across a gene rather than each individual transcript. The thing is, I still can't generate a list that has anywhere near as many ALS genes as Sandeep's list. I think I'm going to have to ask for his script so I can see what his methods were.

I have done the translatome analysis in Limma, DESeq2 and EnrichR and the overlap is a little disconcerting.

	DESeq2	EdgeR	Overlap
TRL	510	159	137

	DESeq2	Limma	Overlap
TRL	510	2391	476

	EdgeR	Limma	Overlap
TRL	159	2391	111

Enrichment with DEGs

	DESeq2	Limma	EdgeR	SA_DESeq2	LC_Bitseq_EdgeR
overlap	4	20	2	19	40
pval	0.17	0.17	0.15	0.015	3e-24

Enrichment in pathways

DESeq2: SIDS susceptibility pathways - 0.03

Limma: Nothing

EdgeR: SIDS susceptibility pathways - 0.004

SA_DESeq2: Nothing

LC_Bitseq_EnrichR Nothing

THINGS HAVE CHANGED

Sandeep realised he sent me the transcripts instead of the gene output and sent me the genes instead. The transcript analysis was done using Sailfish.

These are the numbers for significance (adj p val $< .05$)

.	CG(deseq2)	SA (deseq2)	LC (bitseq)
TRL	510	1308	3400
CYT	2741	323	3116
WCT	1604	4085	2652

	CG(deseq2)	SA (deseq2)	Overlap
TRL	510	1308	101
CYT	2741	323	163
WCT	1604	4085	621