

The effect of tadpole-tail blastema extract on rhabdomyosarcoma - Support #57

Perform proteomics differential abundance testing

07/05/2018 11:18 AM - Katie Lennard

Status:	New	Start date:	07/05/2018
Priority:	Normal	Due date:	
Assignee:		% Done:	90%
Category:		Estimated time:	0.00 hour
Target version:		Spent time:	0.00 hour
Description			
<p>MS/MS data was sent by Bridget Calder for analysis. The data included N=5 untreated (PBS) and N=5 treated (tadpole extract) samples.</p> <p>Relevant info from Bridget:</p> <p>"So there are 2 groups, 'PBS' and 'Tad' for control and experimental, respectively. There are 5 replicates in each. In the protein groups file, I usually use the 'majority protein ID' column as the identifier for the protein, and then the 'LFQ intensity [sample name]' column for the quantitative measure. In this case I think LFQ is preferable because it is a cell culture so we expect to see the same proteins in each sample (unlike in my samples!).</p> <p>I haven't filtered this data at all so it still contains entries for contaminants (CON) and reverse hits (REV) which should be filtered out prior to analysis. I've had a quick look at the summary.txt (attached) file and in terms of QC all the runs seem fine, perhaps the sample 'Tad2' is a bit of an outlier (just fyi). I can generate QC graphs for the mass spec results as metadata which might help with interpretation if there's anything strange happening in the analysis"</p> <p>Analysis was performed in R using the edgeR package with log2-transformed LFQ values as input. The data was first filtered to exclude very sparse rows (at least 3 of the 10 total samples had to have data for a given row to be included for downstream analyses). Multiple testing correction was performed using "BH" method at q=0.05 and a fold change of 2.</p> <p>The results are very strong with clear differences between treated and untreated samples! The results were summarized in table format as well as annotated heatmaps and have been sent to Jenna.</p>			

Files

edgeR_significant_heatmap_gene_symbols.pdf	21.5 KB	07/05/2018	Katie Lennard
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