

The effect of tadpole-tail blastema extract on rhabdomyosarcoma - Support #58

Pathway analysis

07/10/2018 11:17 AM - Katie Lennard

<b>Status:</b>	New	<b>Start date:</b>	07/10/2018
<b>Priority:</b>	Normal	<b>Due date:</b>	
<b>Assignee:</b>		<b>% Done:</b>	0%
<b>Category:</b>		<b>Estimated time:</b>	0.00 hour
<b>Target version:</b>		<b>Spent time:</b>	0.00 hour
<b>Description</b>			
Following differential abundance testing, the list of significant proteins were used as input for pathway analysis using the (new) R package pathfindR. Given the extremely clear difference between treated and untreated cells, with several proteins being completely absent from the treated group yet present in all untreated samples, Bridget suspected that the treatment was actually killing the cells, hence the extreme result. Pathway analysis supports this, with the only enriched pathways belonging to "Ubiquitin mediated proteolysis", "Mismatch repair", "DNA replication", "Nucleotide excision repair", "Ribosome biogenesis in eukaryotes". These pathways are also relevant in cancer research, but given that the majority of differentially abundant proteins are based on the absence of a large subset of proteins in the treated group, it seems like the treatment might be at too high a concentration, hence causing cell death instead of the desired anti-cancer activity.			