Identification of biomarkers in keloids and folliculitis keloidalis nuchae (FKN) - Support #100

Time seres analysis

10/04/2019 01:19 PM - Jon Ambler

Status:	Resolved		**Start date:**	10/04/2019
Priority:	High		**Due date:**	
Assignee:	Jon Ambler		**% Done:**	100%
Category:			**Estimated time:**	0.00 hour
Target version:			**Spent time:**	40.00 hours

Description

Looking at the time series data for the samples, we needed to compare the expression of the different conditions (FKN, Scar, Keloid) to skin at time points do, d14, d28.

History

#1 - 10/04/2019 01:21 PM - Jon Ambler

- Status changed from New to In Progress

- % Done changed from 0 to 30

Time series analysis was done using deseq2, and saved as an R script.

Exported the results to csv files

#2 - 10/04/2019 01:25 PM - Jon Ambler

- Status changed from In Progress to Resolved

- % Done changed from 30 to 100

A python script to profile the time series data was created.

This script takes in the expression info from the different time points and determines if they show significant changes in direction.

For example:
d0: up, d14, up, d28 no change.

These were used to create profiles that grouped genes by similar expression patterns and times.

GSEA of these sets showed that the sets had distinct pathways.

Results exported and sent to Relebohile.