Identification of biomarkers in keloids and folliculitis keloidalis nuchae (FKN) - Support #101

Secondary analysis: Transcription factor and pathway enrichment

10/04/2019 01:29 PM - Jon Ambler

Status:	New	**Start date:**	10/04/2019
Priority:	Normal	**Due date:**	
Assignee:	Jon Ambler	**% Done:**	0%
Category:		**Estimated time:**	0.00 hour
Target version:		**Spent time:**	0.00 hour

Description

Now that we have groups of candidate genes, we want to find out which genes will function better as biomarkers.

This includes:
Identifying those that are known transcription factors.
Identifying distinct clusters based on PPI and shared function.