

## GET-Evidence - Feature #9241

### Add "Genes for Good" support for genome report

05/19/2016 04:50 PM - Abram Connelly

<b>Status:</b>	New	<b>Start date:</b>	05/19/2016
<b>Priority:</b>	Normal	<b>Due date:</b>	
<b>Assigned To:</b>		<b>% Done:</b>	0%
<b>Category:</b>		<b>Estimated time:</b>	0.00 hour
<b>Target version:</b>		<b>Totalhours:</b>	
<b>Billable:</b>		<b>Resolution:</b>	
<b>Estimatedhours:</b>			
<b>Hours:</b>			

#### Description

Some participants are uploading [Genes for Good](#) files. The format is very similar to 23andMe with some minor differences (difference header text, not all lines have rsids).

It would be nice to add functionality to the GET-Evidence reports to accommodate the "Genes for Good" format.

#### History

##### #1 - 05/19/2016 04:52 PM - Abram Connelly

There is gtg branch on [github.com/abeconnelly/GETEvidenceReport](https://github.com/abeconnelly/GETEvidenceReport) that implements this feature. Currently this repo is being used for Veritas VCF reports only. We might be able to replace just this component (job) in the current pipeline being used by the GET-Evidence machine without having to replace the whole pipeline.

Participant [hu76380E](#) has uploaded their [Genes for Good dataset](#) which can be used as a reference.