

GET-Evidence - Feature #1080

Add non-reference variant counts to metadata

08/14/2012 05:28 PM - Anonymous

Status:	New	Start date:	
Priority:	Normal	Due date:	
Assigned To:	Madeleine Ball	% Done:	0%
Category:		Estimated time:	0.00 hour
Target version:		Totalhours:	
Billable:		Resolution:	
Estimatedhours:			
Hours:			

Description

Add counts of number of variants to metadata information.

We'd like to use the metadata (metadata.json) to generate aggregate reports on our genomic data. VCF files (e.g. produced for 23andme exomes) don't show up as having much "coverage" due to the lack of reference annotation, but they do have many non-reference variant calls. So, in addition to coverage statistics, we'd like to have metadata reporting the number of non-reference variants in a genetic data file. It might also be useful to create whole genome and coding numbers (as with the coverage).