



An Annotation in GeneTalk is user-generated content specific genomic position about, for example, a genetic disorder. Users can provide more details such as links to a scientific articles. Other users can rate annotations in the subjects *Medical Relevance* and *Scientific Evidence*. Users can comment annotations to provide additional information or start a discussion.

Annotation

1 Position	chr4 : 77476772	Link	http://genomebiology.com/2011/12/9/R91
2 Genotype	T/T	OMIM-ID	604570
3 Gene	SHROOM3 (Entrez-ID: 57619)	Pubmed Links	Pubmed Article 21936905
4 HGVS DNA code	c.179G>T	MutationTaster	
4 HGVS protein code	p.G60V		
5 Author:	Knaus		
6 Text:	The missense mutation was shown to be disease-causing in homzygous state in the recessive heterotaxy syndrome. <small>Created at August 19, 2013 11:26, Last update October 10, 2013 17:25</small>		
7 Voting			
Medical relevance	★★★★★ Disease causing		
Scientific evidence	★★★★☆ Medium (e.g., functional assays)		
8 Votes			
	Stars	Medical relevance	Scientific evidence
9	5	4 votes	0 votes
	4	0 votes	0 votes
	3	0 votes	3 votes
	2	0 votes	1 vote
	1	0 votes	0 votes

10 Rate this variant! Medical relevance ★★★★★ Scientific evidence ★★★★★ **Vote**

Comments

11 [Alexej](#) October 09, 2013 09:47
Although this is a rare dbSNP entry (rs144435434) it only occurred in heterozygous state in the 1kGP.

12 Your comment

Add comment

- | | | |
|--|---|--|
| 1 Genomic position | 7 Majority vote for <i>Medical Relevance</i> | 13 Link to external source or website |
| 2 Genotype or allele | 8 Majority vote for <i>Scientific Evidence</i> | 14 OMIM-ID |
| 3 Gene name and Entrez ID
Click to open the gene info | 9 Votes (score list) | Click to open a link to http://omim.org |
| 4 HGVS codes for DNA and protein level | 10 Your votes | 15 Link to publication in Pubmed |
| 5 Author of annotation | 11 Comment from a user
Click the mail button to contact the user | Click to open a link to www.ncbi.nlm.nih.gov |
| 6 Annotation Text | 12 Add your comment here | 16 Link to MutationTaster |
| | | Click to evaluate disease-causing potential |
| | | 17 Click the VOTE button to apply your vote |

How to Find Annotations

There are several ways to find annotations in GeneTalk.

- ① Open a VCF file in the VCF file viewer (Manage Files → List →). An expert icon , a patient icon , or a star rating show that there are annotations for a variant. Just click the stars or the icons to open a list of annotations for this variant.
- ② Search for a gene (Search Genetalk → Genes) to find all annotations for a gene.
- ③ Search by genomic position(Search Genetalk → Annotations)

How to Add Annotations

In the VCF Viewer, just click the *Annotate* button to add an annotation. You can choose, whether your annotation is visible just for you, for a selected group of GeneTalk users, or publicly visible.

Votes for Annotations

The votes for *Medical Relevance* and *Scientific Evidence* range from one star (irrelevant/artifact and very low, respectively) to five stars (disease causing and very high, respectively). New annotations must have initial votes for both medical relevance and scientific evidence.

The total votes for an annotation in both subjects are fixed by the majority of the users' votes. Users can revise their vote. A majority vote changes as soon as a new majority of users is found.

Genetalk's Knowledgebase

GeneTalk combined annotations from publicly available databases to set up its knowledgebase. For example, annotations from ClinVar defined as "disease causing" are initialized in GeneTalk's medical relevance ranking with 5 stars. Sequence variants that were encountered as common artifacts in the 1000 genomes project were classified as medically irrelevant. However, especially for the variants of unknown clinical significance, VUCS, we count on the wisdom of the crowd. In a wiki like approach we encourage the GeneTalk user community to contribute their own ranking so that the status of each VUCS will be as up to date as possible.

Filtering Variants Using Annotation Votes

You can set GeneTalk's *annotation filter* to any level of medical relevance and scientific evidence. If, for example, the filter is set to two stars in medical relevance, all sequencing artifacts and irrelevant variants will be removed. As a first approach in diagnostic filtering it might be reasonable to start with a five star rating for medical relevance and at least a two star rating for scientific evidence. Removing variants without annotations will result in a short list of variants with additional information in GeneTalk. This setting can be used to check if there are variants in a data set with known mutations. If a patient cannot be diagnosed using this setting, it is a more elaborated research question and other filtering parameters have to be chosen.

Chrom	Pos	dbSNP ID	Gene	Ref	465 (Affected)	466 (Unaffected)	467 (Unaffected)	Effect	Medical Relevance	Scientific Evidence
1	145296451	rs140256918	NBPF10	G	C/G	C/G	G/G	missense		
1	145368518	rs61813437	NBPF10	C	C/T	C/C	C/T	missense		
9	35090263	rs142164373	PIGO	G	A/G	A/G	G/G	missense		
9	35091529		PIGO	G	G/GG	G/G	G/GG	frameshift-insertion		

Annotations							show filter
User	Chrom	Pos	Genotype	Gene	Comment	OMIM-ID	Actions
Alexej	9	35091529	G/GG	PIGO	HPRMS Hyperphosphatasia with mental r...		

Annotate

Visibility:

- Visible to all GeneTalk users
- Restricted visibility

Medical Relevance

- Irrelevant or artifact
- Suspicious
- Disease associated
- Disease modifying
- Disease causing

Scientific Evidence

- Very low (e.g. incidental finding)
- Low (e.g. multiple cases)
- Medium (e.g. functional assays)
- High (e.g. animal models)
- Very high (e.g. therapy studies)

dbSNP clinically precious (ca. 100.000)	
Medical relevance	Disease causing (initial rating: 5)
Scientific evidence	Very high (initial rating: 5)
ClinVar disease causing	
Medical relevance	Disease causing (initial rating: 5)
Scientific evidence	Very high (initial rating: 5)
Sequencing artifacts from 1kGP (ca. 600.000)	
Medical relevance	Irrelevant or artifact (initial rating: 1)
Scientific evidence	Very high (initial rating: 5)

File Annotation

Filter for annotations

Medical relevance at least Suspicious

Scientific evidence at least Very low (incidental finding)

Keep variants without annotation