Panel of genes: design and analysis for clinical applications. TEAM

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GDA

International Course on Genomic Data Analysis

PRINCIPE FELIPE
CENTRO DE INVESTIGACION

Introduction

- **Development of high throughput sequencing technologies**:
  - Fast and economical genome sequencing
  - Disease targeted sequencing: powerful and cost-effective application

- **Vast amount of biological knowledge available**:
  - HGMD-public, HUMSAVAR, ClinVar, COSMIC

- We need a tool to connect **sequencing data and biological knowledge for diagnostic:**
  - TEAM (**T**argeted **E**nrichment **A**nalysis and **M**anagement)

Introduction

Sequencing data

Biological knowledge

GWAS

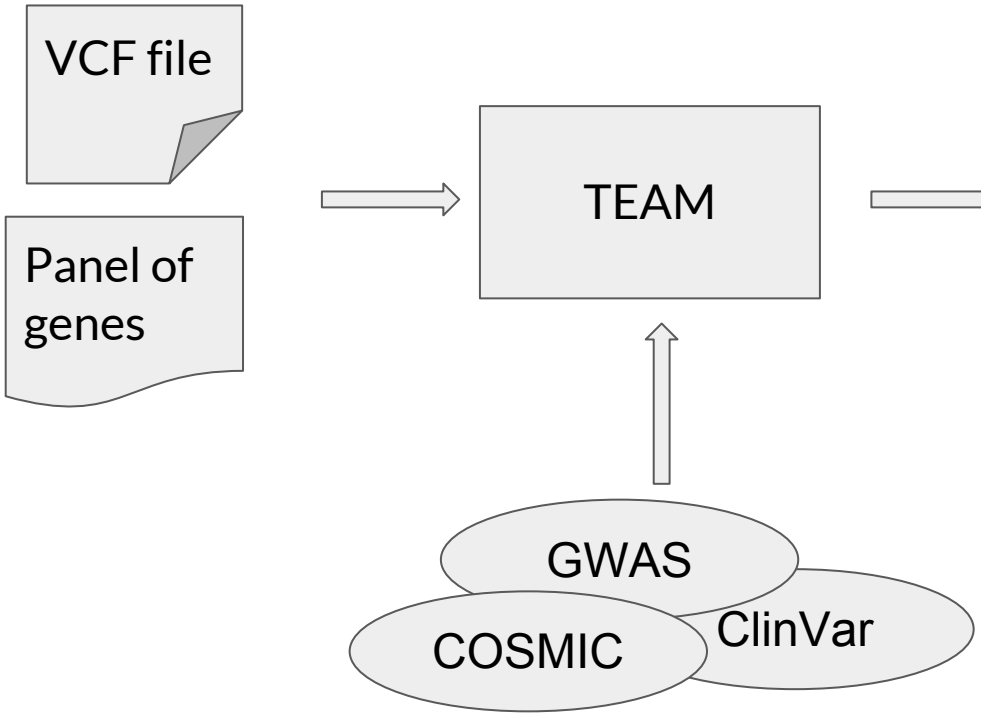
COSMIC

ClinVar

TEAM

Diagnostic

How does TEAM work?



Diagnostic

Chr	Pos	Ref	Alt	SNP Id
9	135786112	T	C	rs6597586
9	135786904	A	G	rs1073123
19	55453134	G	A	rs775886

Getting information

ClinVar

ClinVar aggregates information about genomic variation and its relationship to human health.

COSMIC
Catalogue of somatic mutations in cancer

GWAS Catalog

The NHGRI-EBI Catalog of published genome-wide association studies

Getting information: SIFT & PolyPhen

- **SIFT**
  - SIFT predicts whether an amino acid substitution affects protein function
  - **Interpretation:** 1 (tolerated) to 0 (deleterious)

http://sift.jcvi.org/

- **PolyPhen**
  - Polymorphism Phenotyping is a tool which predicts possible impact of an amino acid substitution on the structure and function of a human protein.
  - **Interpretation:** 1 (probably damage) to 0 (bening)

http://genetics.bwh.harvard.edu/pph2/index.shtml

Getting information: Conservation

- **Phylop**
  - PhyloP scores measure evolutionary conservation at individual alignment sites. The scores are interpreted as follows compared to the evolution expected under neutral drift:
    - Positive scores -- Measure conservation, which is slower evolution than expected, at sites that are predicted to be conserved.
    - Negative scores -- Measure acceleration, which is faster evolution than expected, at sites that are predicted to be fast-evolving.
- **PhastCons**
  - PhastCons is a program for identifying evolutionarily conserved elements in a multiple alignment, given a phylogenetic tree.
  - PhastCons essentially does three things:
    - It produces base-by-base conservation scores (as displayed in the conservation tracks in the UCSC browser)
    - It produces predictions of discrete conserved elements (as displayed in the "most conserved" tracks in the browser)
    - It estimates free parameters.

Getting information: Effect

e!Ensembl BLAST/BLAT | BioMart | Tools | Downloads | Help & Documentation | Blog | Mirrors

Using this website | Annotation and prediction | Data access | API & software | About us

In this section

- Web interface
  - Input form
  - Results
- VEP script
  - Tutorial
  - Download and install
  - Running the script
  - Caches and databases
  - Filtering results
  - Custom annotations
  - Plugins
  - Examples and use cases
  - Other information
- Data formats
- FAQ

Search documentation…

Go

Help & Documentation > API & Software > Ensembl Tools > Variant Effect Predictor

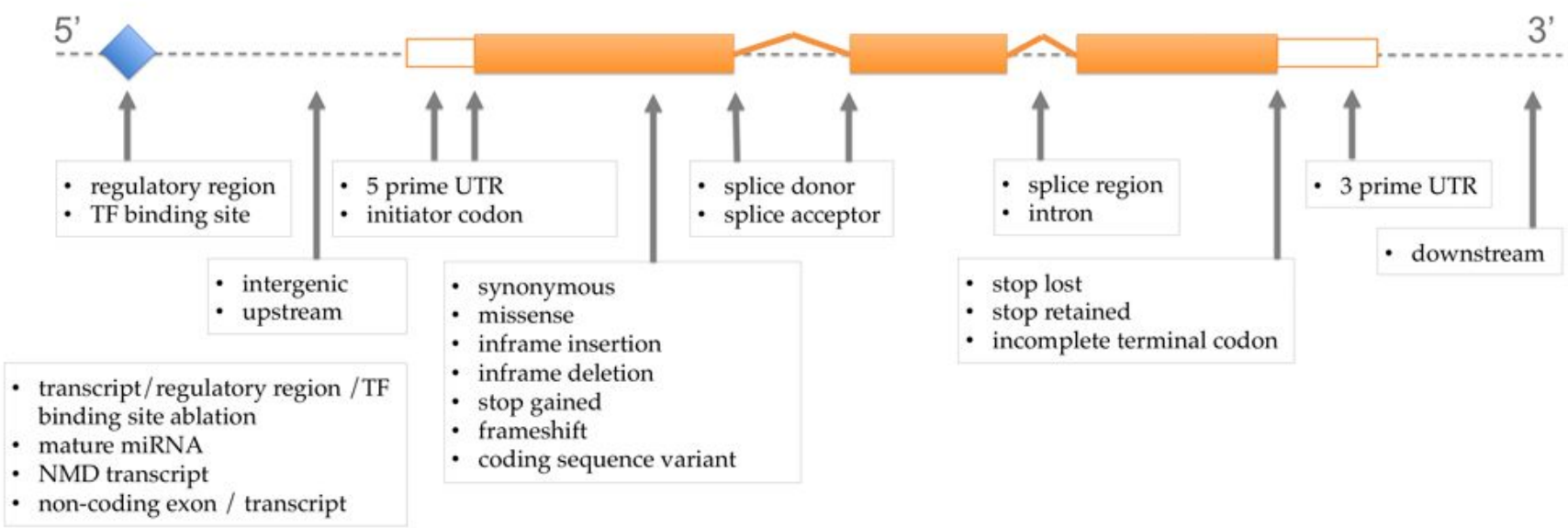
Variant Effect Predictor

The VEP determines the effect of your variants (SNPs, insertions, deletions, CNVs or structural variants) on genes, transcripts, and protein sequence, as well as regulatory regions. Simply input the coordinates of your variants and the nucleotide changes to find out the:

- **genes** and **transcripts** affected by the variants
- **location** of the variants (e.g. upstream of a transcript, in coding sequence, in non-coding RNA, in regulatory regions)
- **consequence** of your variants on the protein sequence (e.g. stop gained, missense, stop lost, frameshift)
- **known variants** that match yours, and associated minor allele frequencies from the **1000 Genomes Project**
- **SIFT** and **PolyPhen** scores for changes to protein sequence
- ... And more!

Launch VeP

Getting information: Effect



http://www.ensembl.org/info/genome/variation/predicted_data.html

Inputs: Panel + VCF

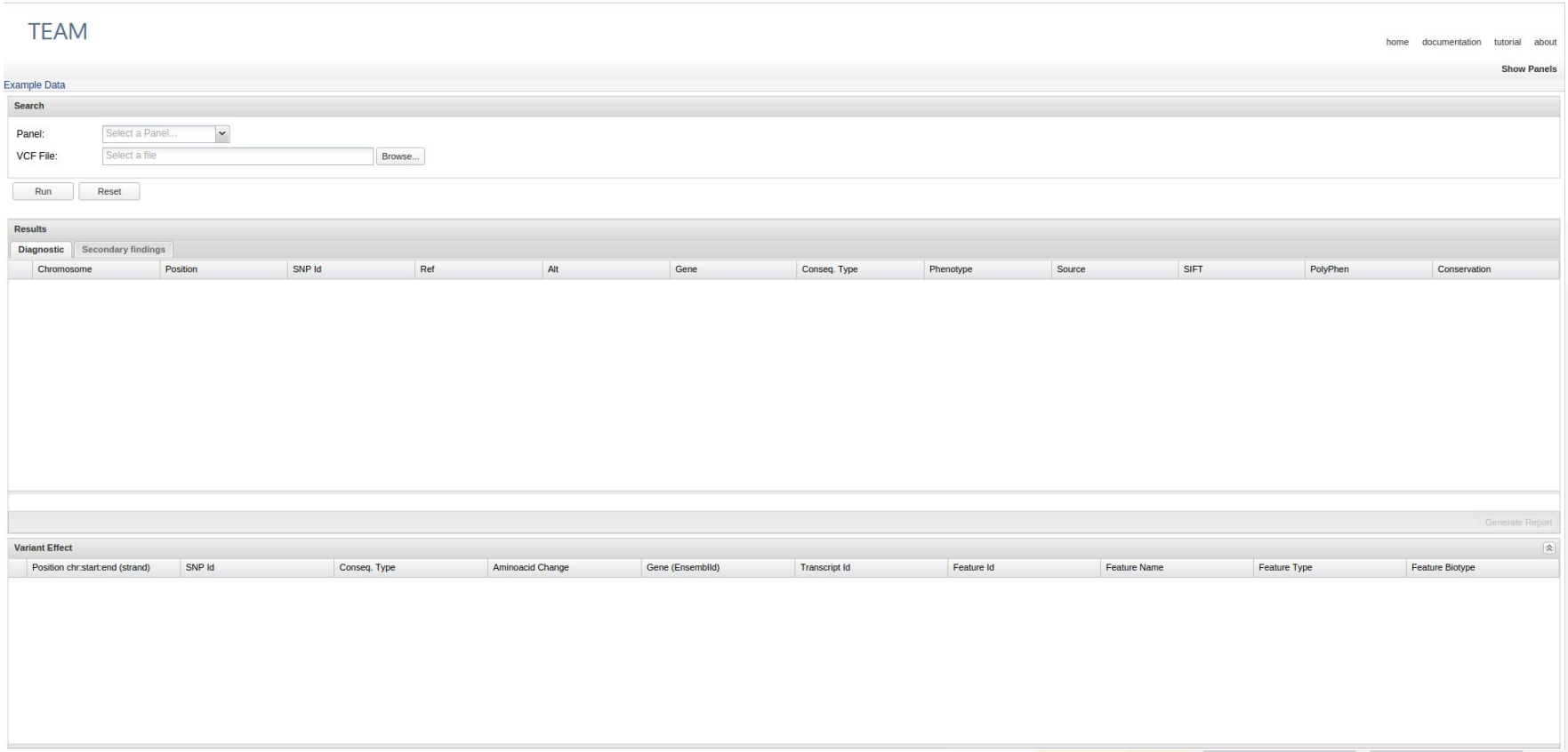
TEAM needs a:

1. **VCF file**:
   - The VCF file needs to be stored/indexed in our database.
   - This file could be already added if we used BiERapp (both tools are compatible)

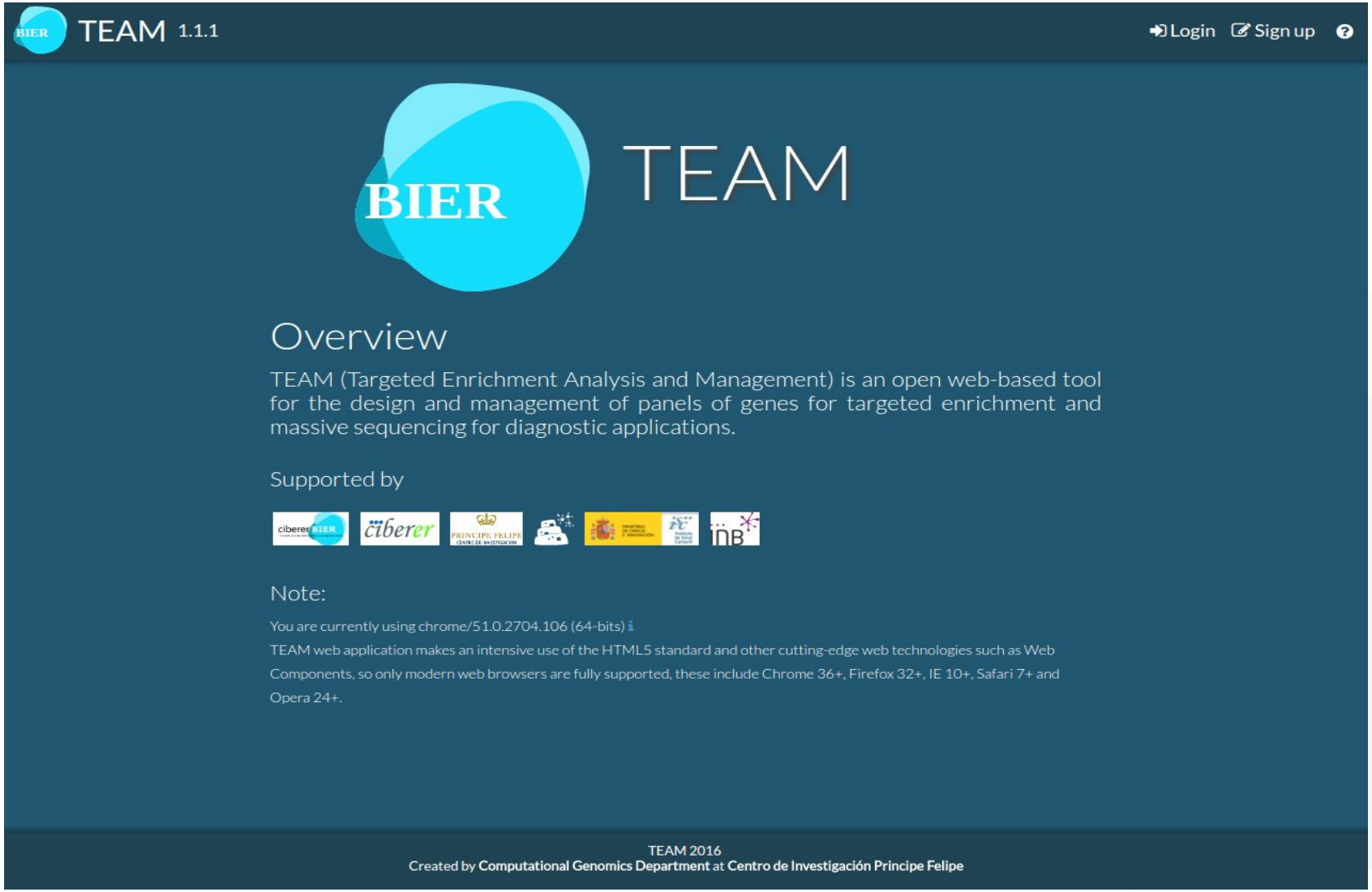
2. **Panel of genes**:
   - TEAM works with virtual panel of genes.
   - You can design/create/manage these panels using TEAM.
   - These panels contains:
     - Phenotypes
     - Genes
     - Mutations

Tool interface: Official release

http://team.babelomics.org/



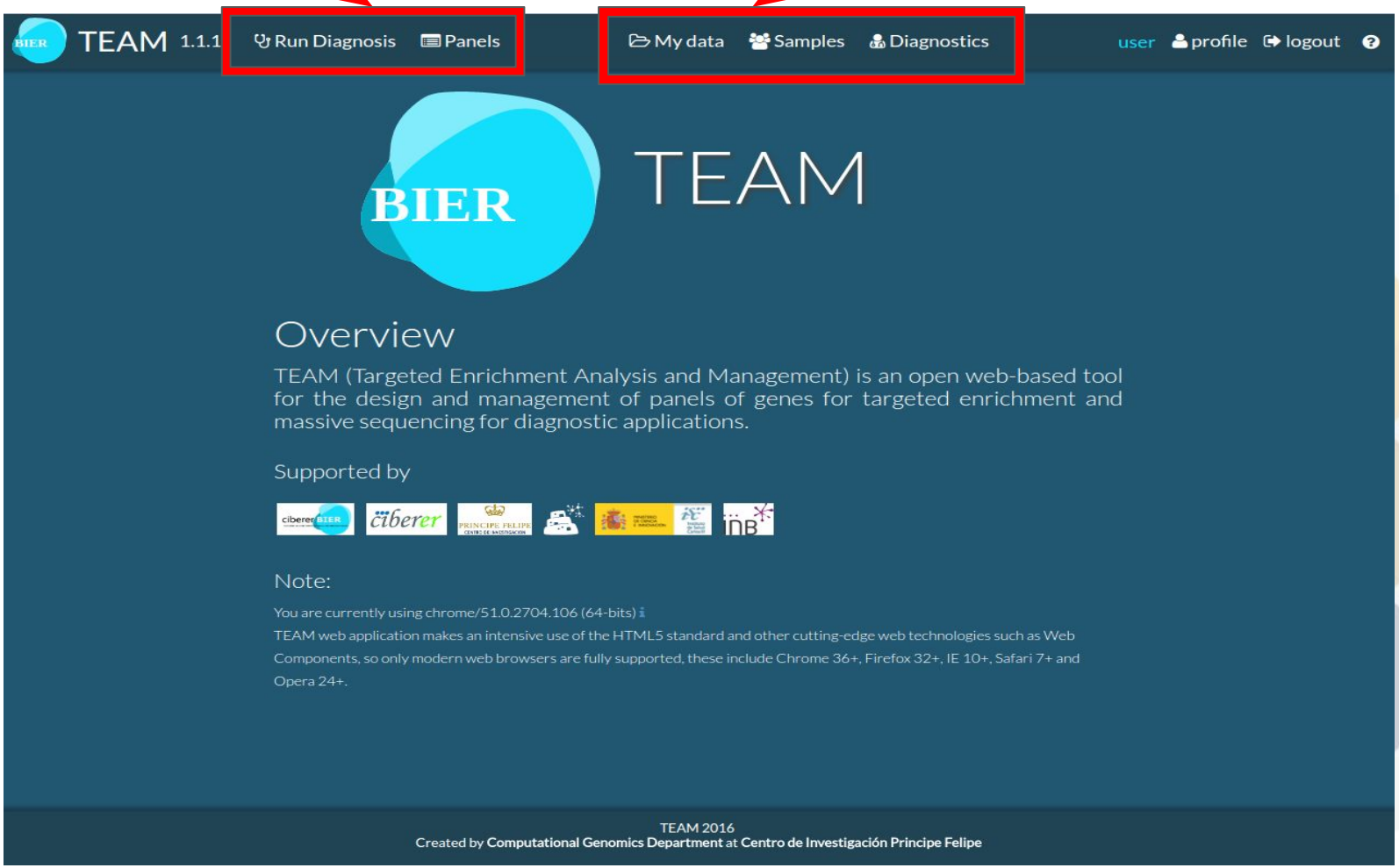
Tool interface: Beta



Tool interface: Beta

Design/Manage Panels

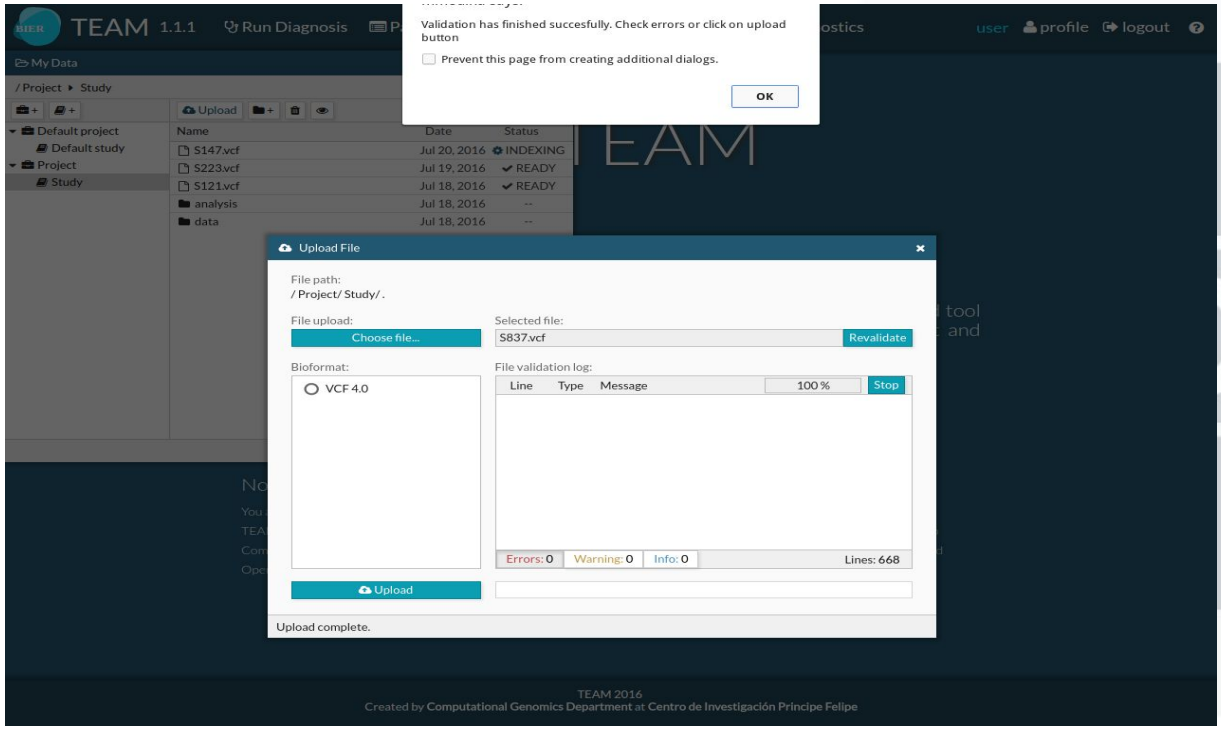
Data & Diagnoses



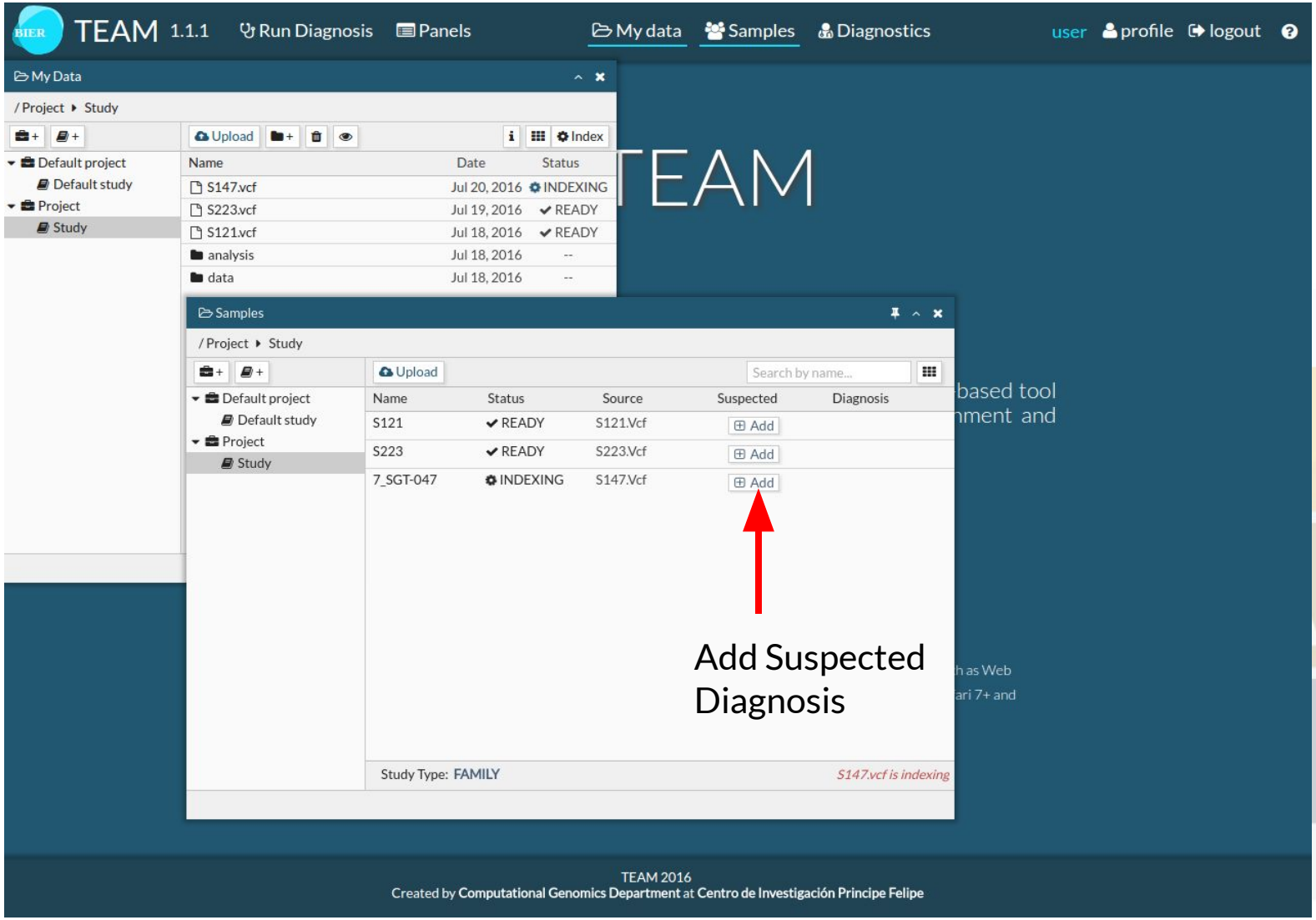
Loading Samples

From “My data” or from “My Samples” you can:

- Create a Project
- Create a Study
- Upload Files: The input is a VCF file: individual VCF file for only one sample or multisample VCF file for several samples at the same time.



Loading Samples



Add Suspected Diagnosis

Panel Manager

You can manage your panels using “Panels”

Search Panel

Edit Panel

Archive Panel

View Panel

TEAM 1.1.1 | Run Diagnosis | Panels | My data | Samples | Diagnostics | test | profile | logout

User Panel List

Main | Archived

Search by name...

- asthma
- cardiac
- retinitis
- CMT
- hypercolesterolemia
- cataratas
- Hyperammonaemia
- osteogenesis
- fanconi
- Ketotic

Example Panel List

- retinitis

+ New Panel

Export panel to PDF/Print

Panel Preview

Name: retinitis
Author: aaleman
Version: 1
Description:

Diseases | Genes/Regions | Mutations

Name	Chr	Start	End
RP1L1	8	10463859	10569697
ZFYVE26	14	68194091	68283307
PRPF31	19	54618837	54635140
SNRNP200	2	96940074	96971297
PRPF6	.	.	.
MERTK	2	112656056	112787138
RP1	8	55528627	55543394
C2orf71	2	29283842	29297127
MYO7A	11	76839310	76926284
MAK	6	10762956	10838764
NR2E3	15	72084977	72110600
CRX	19	48322703	48346587
RPE65	1	68894505	68915642
TOPORS	9	32540542	32552551
TULP1	6	35465651	35480715
PRPH2	6	42664340	42690312
PDE6B	4	619373	664571
LOC102723833	.	.	.
RDH12	14	68168603	68201169

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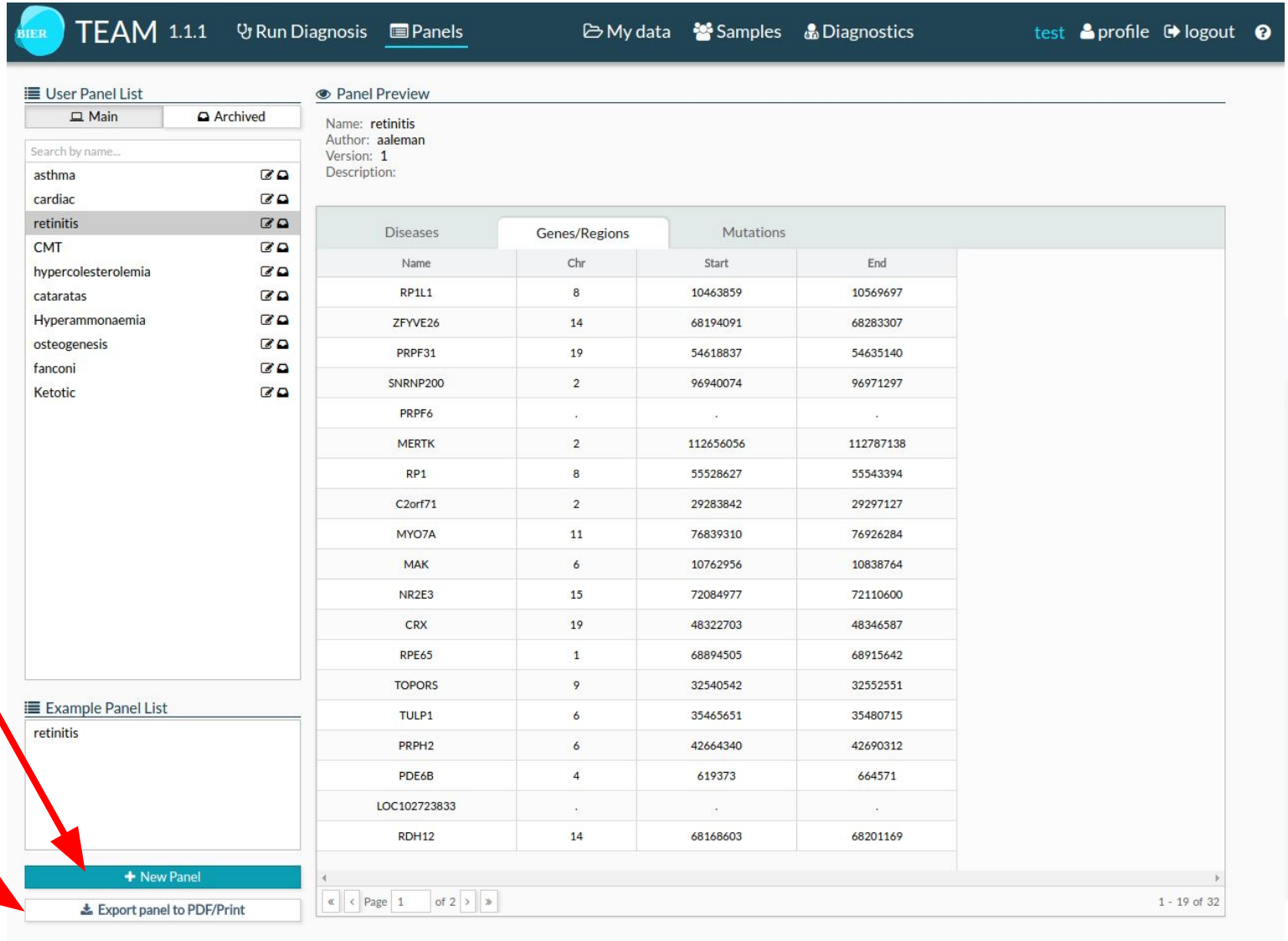
Panel Manager: Create a Panel



Name	Chr	Start	End
RP1L1	8	10463859	10569697
ZFYVE26	14	68194091	68283307
PRPF31	19	54618837	54635140
SNRNP200	2	96940074	96971297
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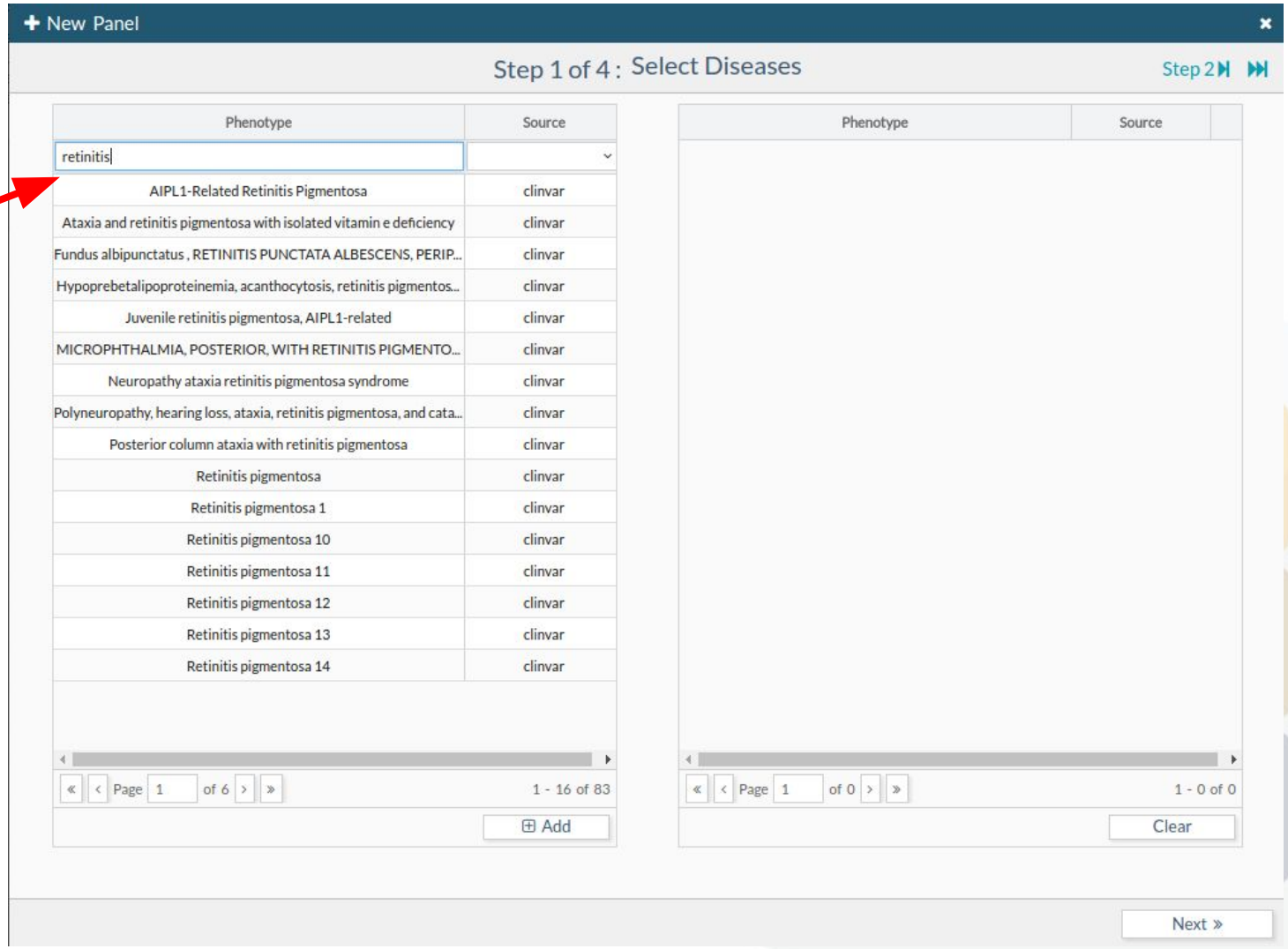
PRPH2	6	42664340	42690312
PDE6B	4	619373	664571
LOC102723833	.	.	.
RDH12	14	68168603	68201169

Create a New Panel

Export or Print a Panel

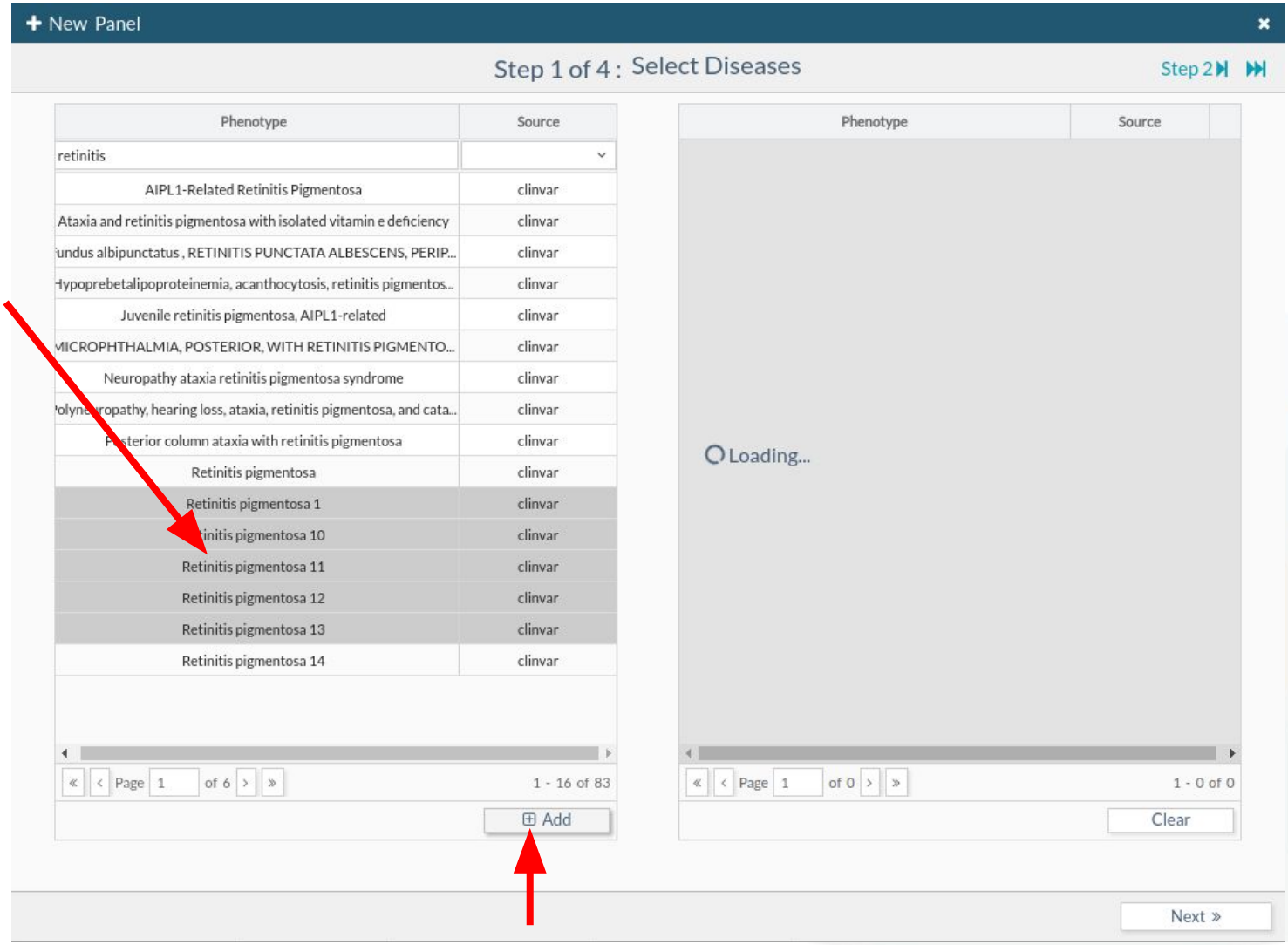
Panel Designer: Diseases

Write the phenotypes you are interested in.



Panel Designer: Diseases

Select the phenotypes you want to add to the virtual panel. That will add the associated genes and mutations



Click “Add”

Panel Designer: Diseases

New Panel

Step 1 of 4 : Select Diseases

Step 2

Phenotype	Source
retinitis	
AIPL1-Related Retinitis Pigmentosa	clinvar
Ataxia and retinitis pigmentosa with isolated vitamin e deficiency	clinvar
Fundus albipunctatus , RETINITIS PUNCTATA ALBESCENS, PERIP...	clinvar
Hypoprebetalipoproteinemia, acanthocytosis, retinitis pigmentos...	clinvar
Juvenile retinitis pigmentosa, AIPL1-related	clinvar
MICROPHTHALMIA, POSTERIOR, WITH RETINITIS PIGMENTO...	clinvar
Neuropathy ataxia retinitis pigmentosa syndrome	clinvar
Polyneuropathy, hearing loss, ataxia, retinitis pigmentosa, and cata...	clinvar
Posterior column ataxia with retinitis pigmentosa	clinvar
Retinitis pigmentosa	clinvar
Retinitis pigmentosa 1	clinvar
Retinitis pigmentosa 10	clinvar
Retinitis pigmentosa 11	clinvar
Retinitis pigmentosa 12	clinvar
Retinitis pigmentosa 13	clinvar
Retinitis pigmentosa 14	clinvar

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⊞ Add

Phenotype	Source	
Retinitis pigmentosa 1	clinvar	✖
Retinitis pigmentosa 10	clinvar	✖
Retinitis pigmentosa 11	clinvar	✖
Retinitis pigmentosa 12	clinvar	✖
Retinitis pigmentosa 13	clinvar	✖

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Clear

Next »

Next Step

Panel Designer: Genes

Selected Diseases in previous step.

These genes have been added by previous step.
These genes are related to the selected diseases

New Panel

Step 1 | Step 2 of 4 : Select Genes | Step 3

Diseases Selected:
- Retinitis pigmentosa
- Retinitis pigmentosa 1
- Retinitis pigmentosa 10
- Retinitis pigmentosa 11
- Retinitis pigmentosa 12
- Retinitis pigmentosa 13

Genes/Regions

BRCA2 , PPL

Add Genes

Import from BED

Import

Import from other Panel

View Panel | Import

Import from external App

- Panel App | Import

Name	Chr	Start	End
RP1L1	8	10463859	10569697
ZFYVE26	14	68194091	68283307
PRPF31	19	54618837	54635140
SNRNP200	2	96940074	96971297
PRPF6	.	.	.
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MAK	6	10762956	10838764
NR2E3	15	72084977	72110600
CRX	19	48322703	48346587
RPE65	1	68894505	68915642
TOPORS	9	32540542	32552551
TULP1	6	35465651	35480715

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Clear

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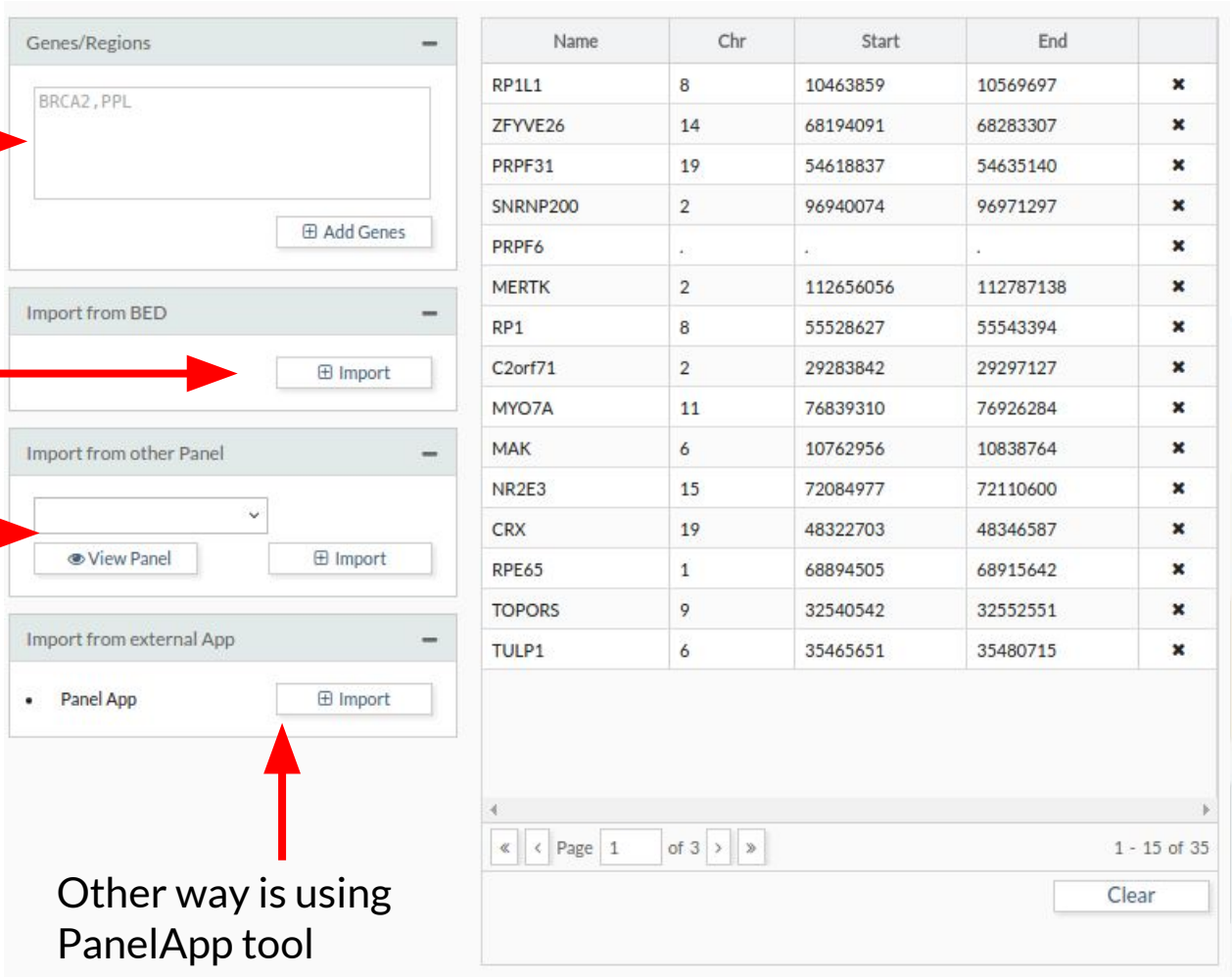
Panel Designer: Genes

We can add new genes typing the name or the region.

Adding regions through a BED file is also supported

We can import genes from other virtual panels already created.

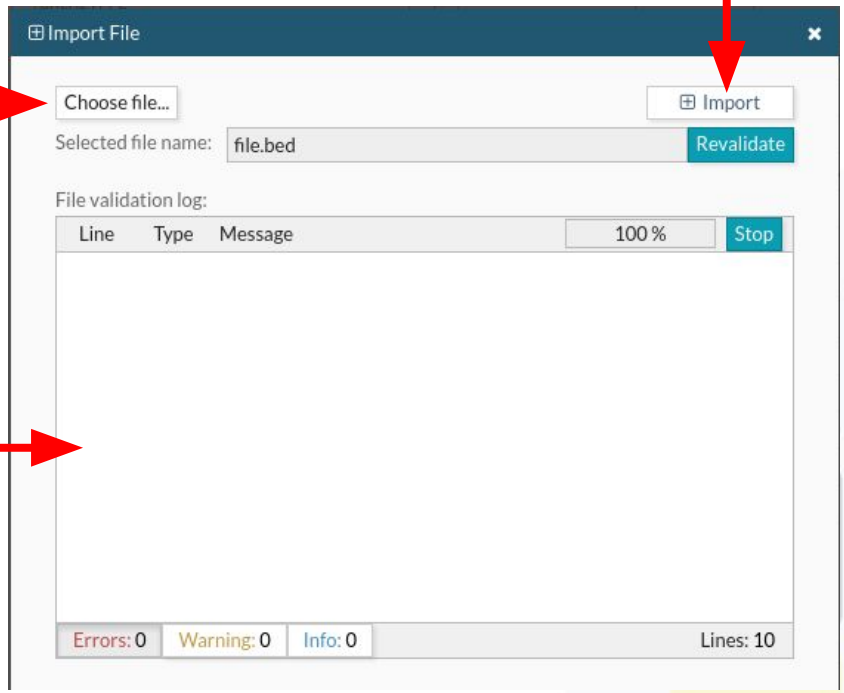


Other way is using PanelApp tool

Panel Designer: Genes (BED file)

Import genes

Choose a BED file



Check errors or warnings

Panel Designer: Genes (PanelApp)

⊞ Import From PanelApp

Disease	N°Genes	Version
conge	filter by N°Genes	filter by Version
Congenital myopathy	66	0.3
Congenital myaesthenia	17	0.0
Congenital neutropaenia	15	1.16
Congenital hearing impairment (profound/s...	348	1.5
Paediatric congenital malformation-dysmor...	62	1.2
Congenital muscular dystrophy	38	0.0
Congenital adrenal hypoplasia	18	0.36
Autosomal recessive congenital ichthyosis	12	1.0
Beckwith-Wiedemann syndrome (BWS) and...	9	1.8
Congenital heart disease	19	0.5
Congenital hypothyroidism or thyroid agene...		0.0

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>>More info <<

Gene	Level Of Confidence
CHAT	HighEvidence
CHRNA1	HighEvidence
CHRNB1	HighEvidence
CHRND	HighEvidence
CHRNE	HighEvidence
DOK7	HighEvidence
GFPT1	HighEvidence
MUSK	HighEvidence
RAPSN	HighEvidence
SCN4A	HighEvidence
COLQ	ModerateEvidence
DPAGT1	ModerateEvidence
AGRN	LowEvidence
ALG2	LowEvidence

Total: 17

⊞ Add Genes

https://bioinfo.extge.co.uk/crowdsourcing/PanelApp/

Panel Designer: Genes (PanelApp)

Genomics England PanelApp

A crowdsourcing tool to allow gene panels to be shared, downloaded, viewed and evaluated by the Scientific Community

Reviews are assessed by Genomics England Curators to establish a final virtual gene panel

Each gene is either…	Evidence Level
Green	High, diagnostic-grade gene that will be used to Interpret genomes.
Red	Low/moderate evidence, genes that currently cannot be used to report clinically, more evidence may arise in the future.

https://bioinfo.extge.co.uk/crowdsourcing/PanelApp/

Figure 1: The curation process for the initial establishment of gene panels for each rare disease category

Genomics England Rare Disease List

Disease Group (Level 2 title) e.g. Cardiovascular disorders	Disease Subgroup (Level 3 title) e.g. Cardiac arrhythmia	**Specific Disease (Level 4 title)** e.g. Brugada Syndrome

A Genomics England Curator searches for the specific disease (and other phenotypes in the eligibility statement description) in information from 4 sources to create an initial gene list.

1. Radboud University Medical Center
2. Illumina Trugenome Predisposition Screen
3. Emory Genetics Laboratory
4. UKGTN

The virtual gene panel is added to PanelApp, with genes colour-coded using a traffic light system to indicate the number of sources.

The gene is on a panel from…		Evidence Level
1 of 4 of the sources + genes from eligibility statements or from experts	Red	Low
2 of 4 of the sources	Amber	Moderate
3 or 4 of 4 of the sources	Green	High

Panel Designer: Mutations

Selected Diseases in previous step.

These mutations have been added by the first step. They are related to the selected diseases

New Panel

Step 2 | Step 3 of 4 : Select Mutations | Step 4

Diseases Selected:
- Retinitis pigmentosa
- Retinitis pigmentosa 1
- Retinitis pigmentosa 10
- Retinitis pigmentosa 11
- Retinitis pigmentosa 12
- Retinitis pigmentosa 13

Genomic Pos.
Chr: Pos:
Ref: Alt:
Phe:
Open Genome Browser | Add

Import VCF
Phe:
Import

Import CSV
Separator: ;
Ignore first line (header):
Choose File No file chosen
Import

Import from other Panel
View Panel | Import

Chr	Pos	Ref	Alt	Phenotype	Source	
20	3899342	G	A	Retinitis pigmentosa	clinvar	✖
20	3899364	C	T	Retinitis pigmentosa	clinvar	✖
20	25282958	G	A	Retinitis pigmentosa	clinvar	✖
2	27601023	A	G	Retinitis pigmentosa	clinvar	✖
2	62067454	G	A	Retinitis pigmentosa	clinvar	✖
2	62063210	G	A	Retinitis pigmentosa	clinvar	✖
2	29296527	T	A	Retinitis pigmentosa	clinvar	✖
2	29296572	G	A	Retinitis pigmentosa	clinvar	✖
6	65146137	C	A	Retinitis pigmentosa	clinvar	✖
6	64430522	A	T	Retinitis pigmentosa	clinvar	✖
7	23180394	G	A	Retinitis pigmentosa	clinvar	✖
7	2318049[illegible]	[illegible]	A	Retinitis pigmentosa	clinvar	✖
16	53720436	C	T	Retinitis pigmentosa	clinvar	✖
17	74536228	G	A	Retinitis pigmentosa	clinvar	✖
1	21303215	A	G	Retinitis pigmentosa	clinvar	✖

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Clear

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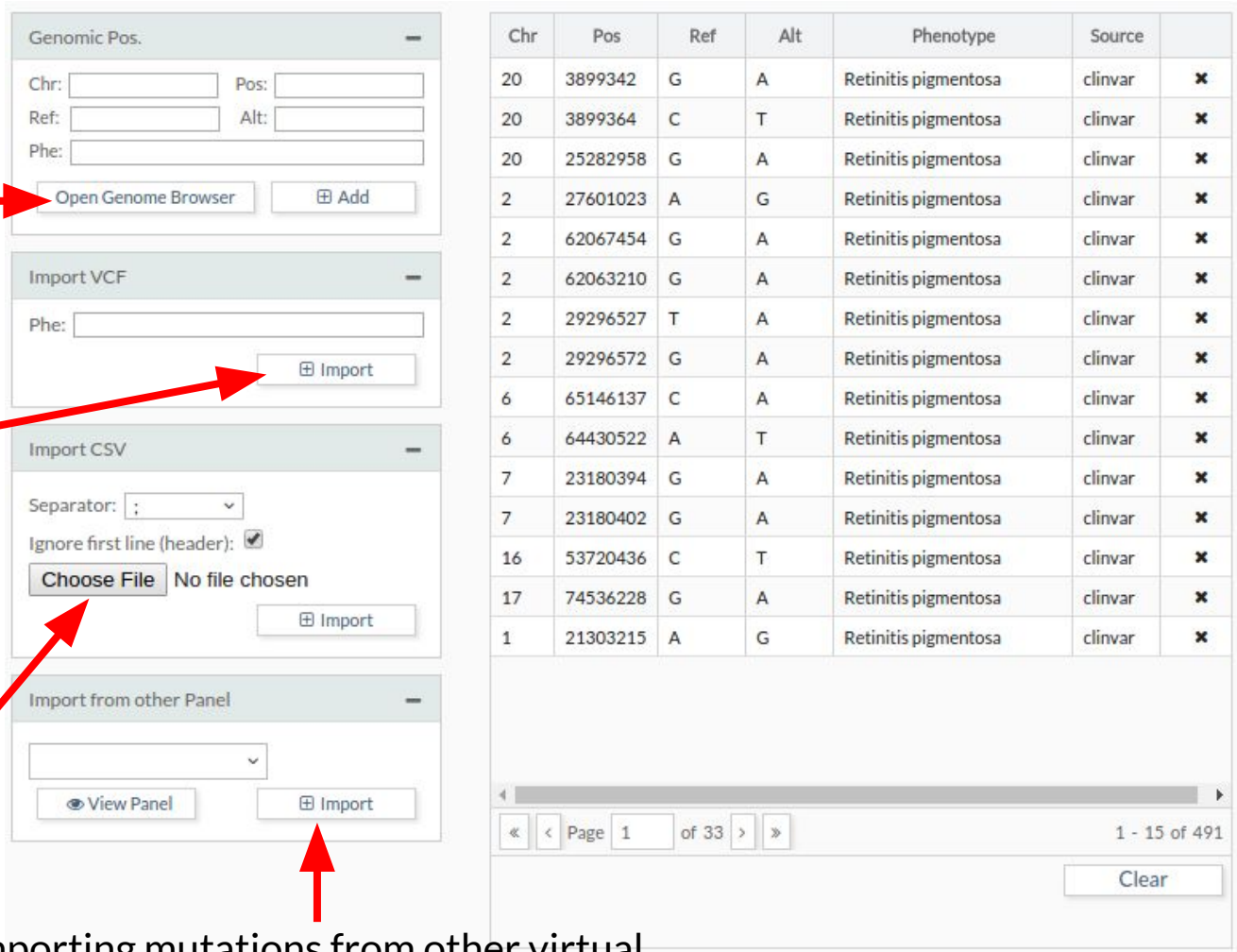
Panel Designer: Mutations

We add our custom mutations by writing the genomic position and the change (ref-alt).
Or we can use the Genome Browser to find the specific position

You can import mutations from a VCF file

Or you can import them from a CSV file with the next format:
CHR POS REF ALT PHE



Chr	Pos	Ref	Alt	Phenotype	Source	
20	3899342	G	A	Retinitis pigmentosa	clinvar	✖
20	3899364	C	T	Retinitis pigmentosa	clinvar	✖
20	25282958	G	A	Retinitis pigmentosa	clinvar	✖
2	27601023	A	G	Retinitis pigmentosa	clinvar	✖
2	62067454	G	A	Retinitis pigmentosa	clinvar	✖
2	62063210	G	A	Retinitis pigmentosa	clinvar	✖
2	29296527	T	A	Retinitis pigmentosa	clinvar	✖
2	29296572	G	A	Retinitis pigmentosa	clinvar	✖
6	65146137	C	A	Retinitis pigmentosa	clinvar	✖
6	64430522	A	T	Retinitis pigmentosa	clinvar	✖
7	23180394	G	A	Retinitis pigmentosa	clinvar	✖
7	23180402	G	A	Retinitis pigmentosa	clinvar	✖
16	53720436	C	T	Retinitis pigmentosa	clinvar	✖
17	74536228	G	A	Retinitis pigmentosa	clinvar	✖
1	21303215	A	G	Retinitis pigmentosa	clinvar	✖

Importing mutations from other virtual panels is supported too.

Panel Designer: Mutations

Import mutation

Search mutation

View Mutation

Chr: 1 Pos: 1004553 Ref: C Alt: G Disease Name: My Disease

Reset Check Add Mutation

Min Max 77 1:1004515-1004591 Go!

Region overview Window size: 615 nts

1004246 1004553 1004860

Detailed information Window size: 77 nts

1004515 1004553 1004591

Sequence

CATCAGCAGCCCCGCCCCTGCCTGCCGGCACCTTCCCCCCATCCGTAGCCCCTCCCCAAGCGCGCTTGTCCGCAGGG(

Gene

SNP

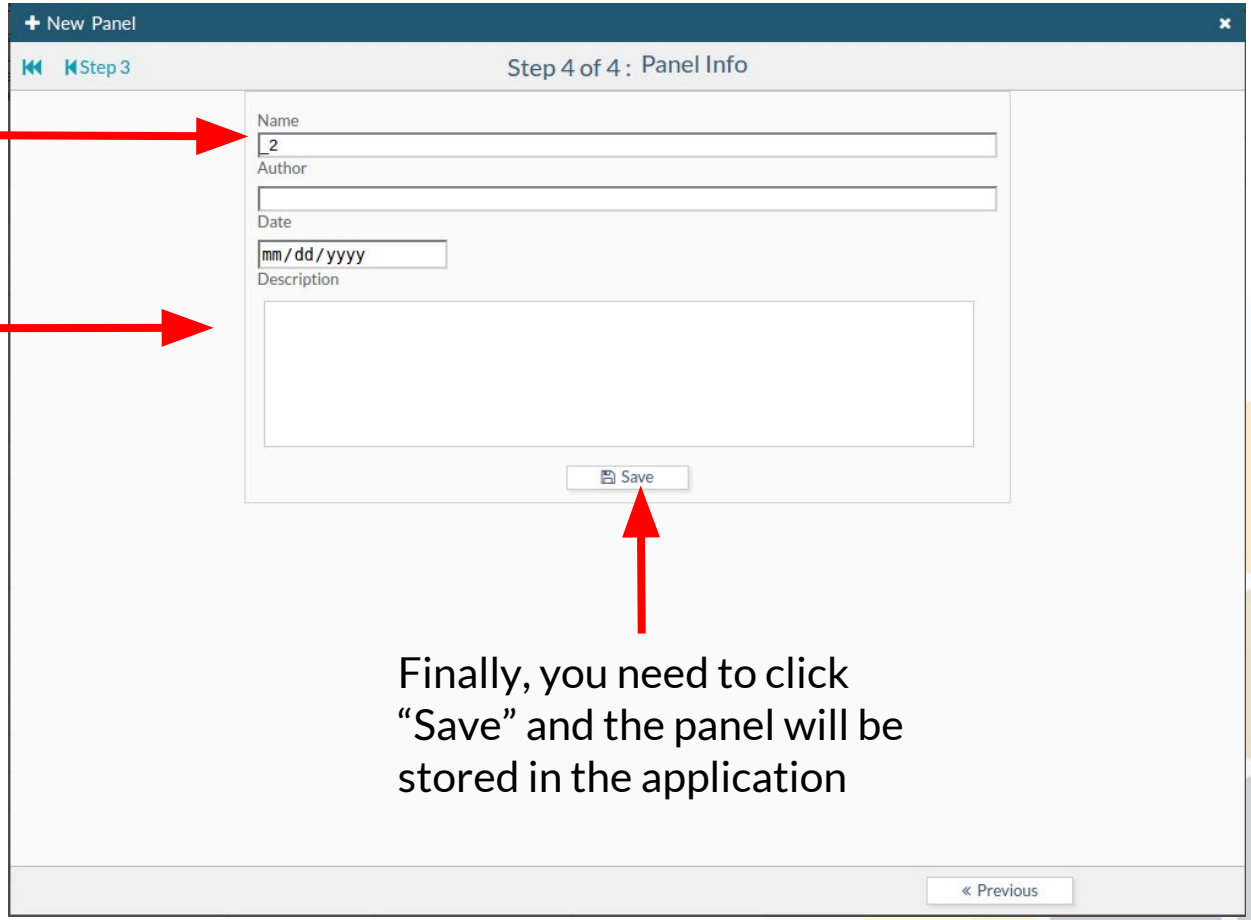
rs189753683 rs371314094 rs75134978

Powered by Genome Maps C 1:1004583

Panel Designer: Panel info

The name of the Panel

The author/ date/ description



Finally, you need to click "Save" and the panel will be stored in the application

New Diagnosis

Click "Run Diagnosis"

Choose a Study. And then a sample/s in **Ready** status and with **Suspected diagnosis** added.

BIER TEAM 1.1.1 | Run Diagnosis | Panels | My data | Samples | Diagnostics | test | profile | logout

Step 1 of 3 : Choose a Sample — Step 2

/ family ▸ fam1

Upload | Search by name...

- Default project
  - Default study
- family
  - fam1
- family2
  - fam2
- family3
  - fam3
- TEAM
  - RET
  - ret2
- gda
  - gda
- asdf
  - asdf
- asdfasdf
  - asdfasdfasd
- fda
  - fda
- aaa
  - aaa
- a
  - a
- acci
  - acci
  - acci2
- acci2
  - vcfPrueba
  - ngsl

Name	Status	Source	Suspected	Diagnosis
HG01500	✔ READY	HG01500_HG0150...	Retinitis	
HG01501	✔ READY	HG01500_HG0150...	Retinitis	
HG01500_HG0...	✔ READY	HG01500_HG0150...	Retinitis	
HG01500_HG0...	✔ READY	HG01500_HG0150...	⊞ Add	
HG01500_HG0...	✔ READY	HG01500_HG0150...	⊞ Add	

Study Type: FAMILY

Next Step

Next »

New Diagnosis

Step 1 | Step 2 of 3 : Choose a Panel | Step 3

User Panel List

- asthma
- cardiac
- retinitis
- CMT
- hypercolesterolemia
- cataratas
- Hyperammonaemia
- osteogenesis
- fanconi
- Ketotic

Example Panel List

- retinitis

+ New Panel

Panel Preview

Name: retinitis
Author: aaleman
Version: 1
Description:

Diseases | Genes/Regions | Mutations

Chr	Pos	Ref	Alt	Phenotype	Source
20	3899342	G	A	Retinitis pigmentosa	clinvar
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6	65146137	C	A	Retinitis pigmentosa	clinvar
6	64430522	A	T	Retinitis pigmentosa	clinvar
7	23180394	G	A	Retinitis pigmentosa	clinvar
7	23180402	G	A	Retinitis pigmentosa	clinvar
16	53720436	C	T	Retinitis pigmentosa	clinvar
17	74536228	G	A	Retinitis pigmentosa	clinvar
1	213032155	A	G	Retinitis pigmentosa	clinvar
1	213032515	G	A	Retinitis pigmentosa	clinvar

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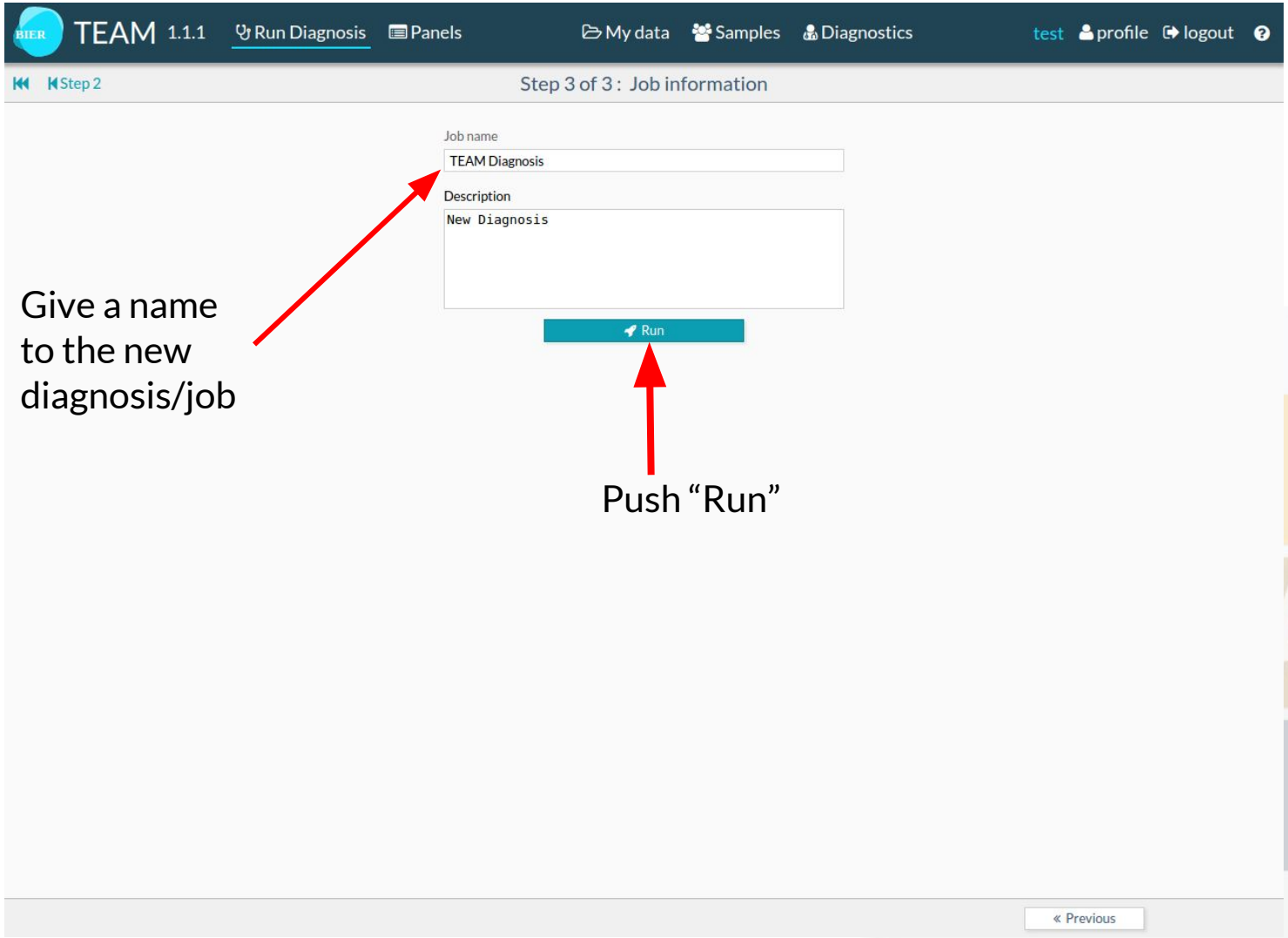
Select the panel to be used.

Next Step

New Diagnosis



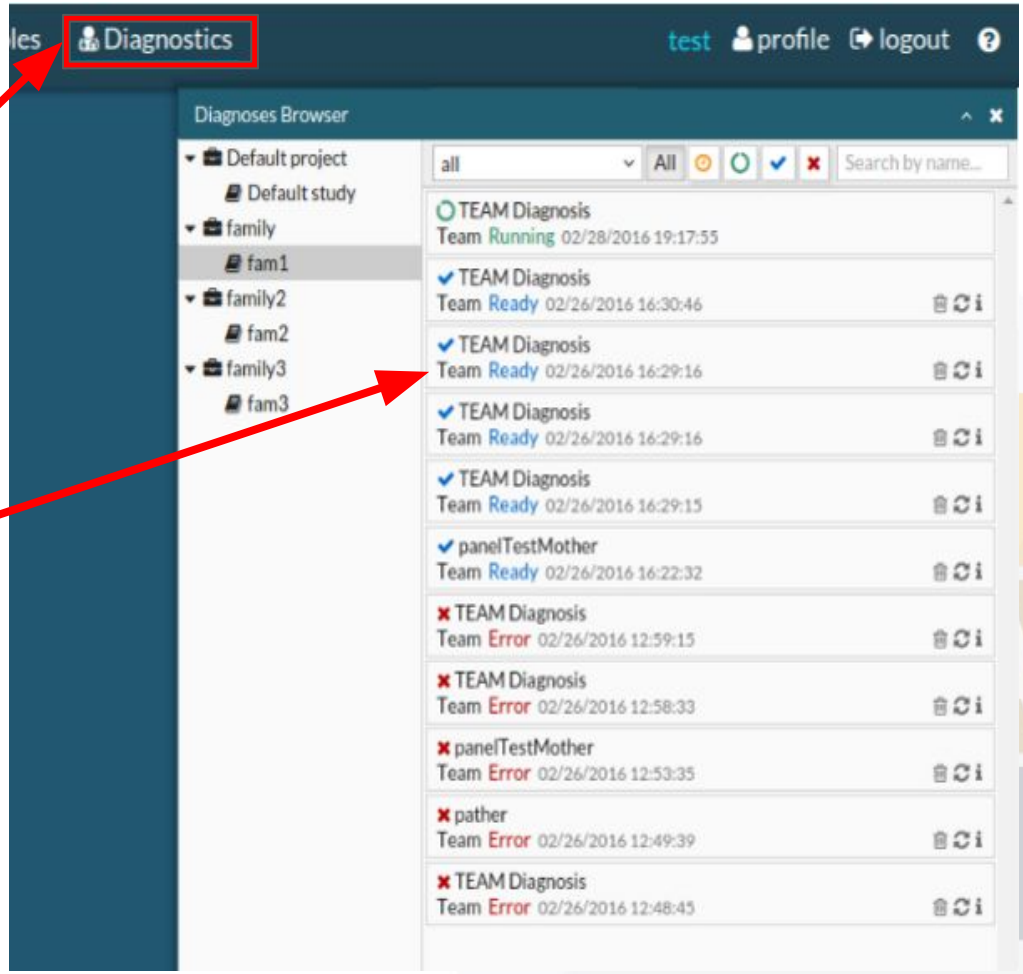
Give a name to the new diagnosis/job

Push “Run”

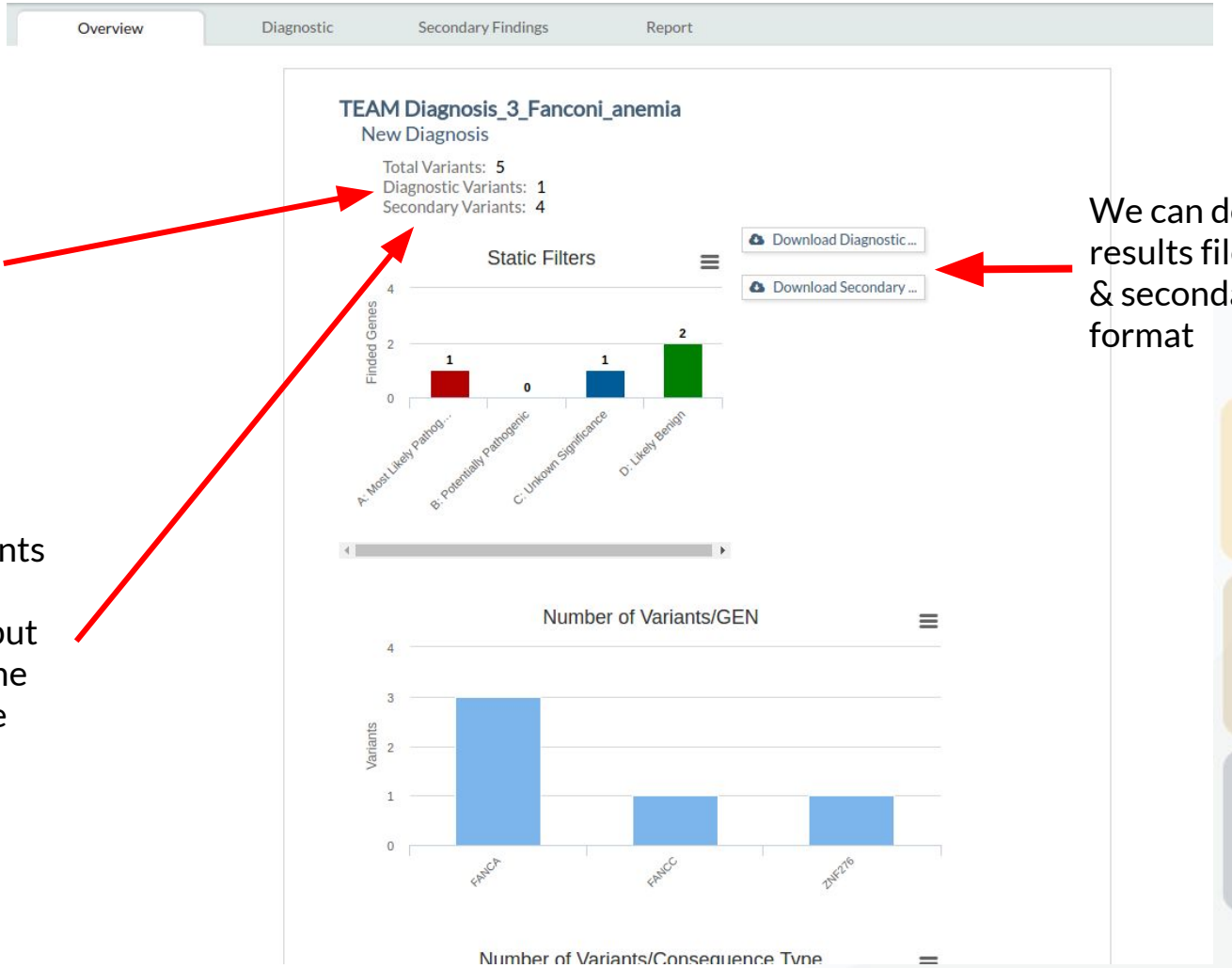
Diagnoses

This view shows the status of the current/past diagnoses.
The different status are: QUEUED, RUNNING, READY, ERROR

If you select a specific Diagnoses you will access to the results of that diagnoses.



Results: Overview

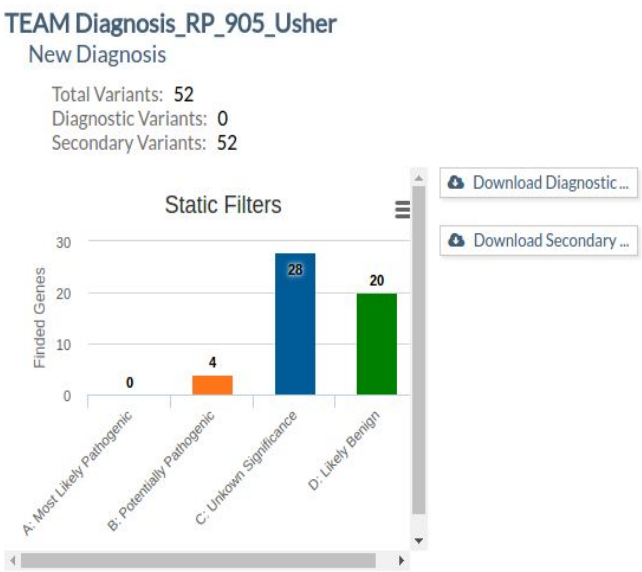


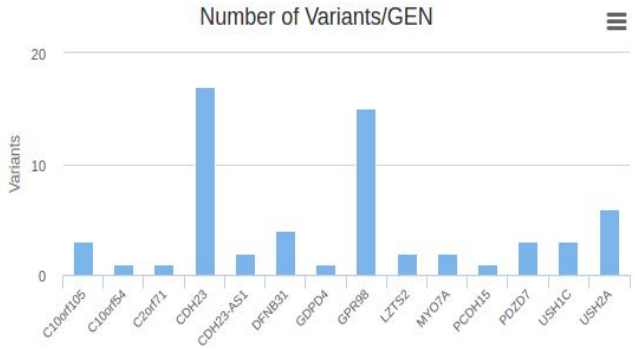
We got one diagnostic variant

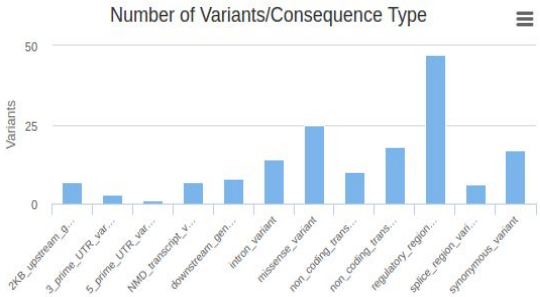
Secondary findings: 4
These variants are not diagnostic but are inside the genes of the panel

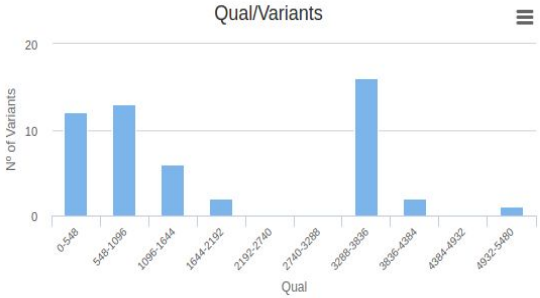
We can download the results files (diagnostic & secondary) in CSV format

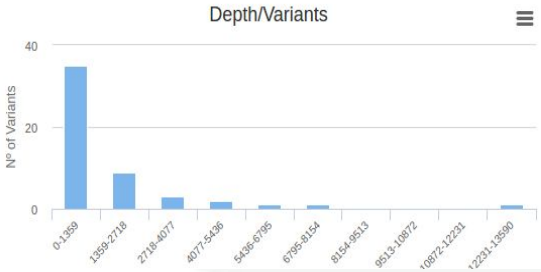
Results: Overview











Results: Diagnostic Variants

Overview | Diagnostic | Secondary Findings | Report

Diagnostic

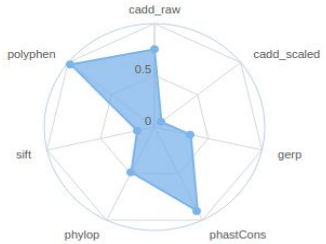
Chr	Pos	Ref	Alt	Gt	Gene	Conseq. Type	phyloP	Phastco...	SIFT	Polyphen	MAF 10...	ESP 6500	Beacon	OMIM	Phenotype	Source
X	38240670	C	T	1|1	TM4SF2,OTC	missense_variant,non_coding_transcript_exon_variant,non_c...	0.486	0.902	0.16	0.03	0.0003	0.0001			Hyperammonaemia	clinvar

« ‹ Page 1 of 1 › » 1 - 1 of 1

Variant Data

Overview | Comments | Frequencies | Genome Viewer

X:38240670:C:T

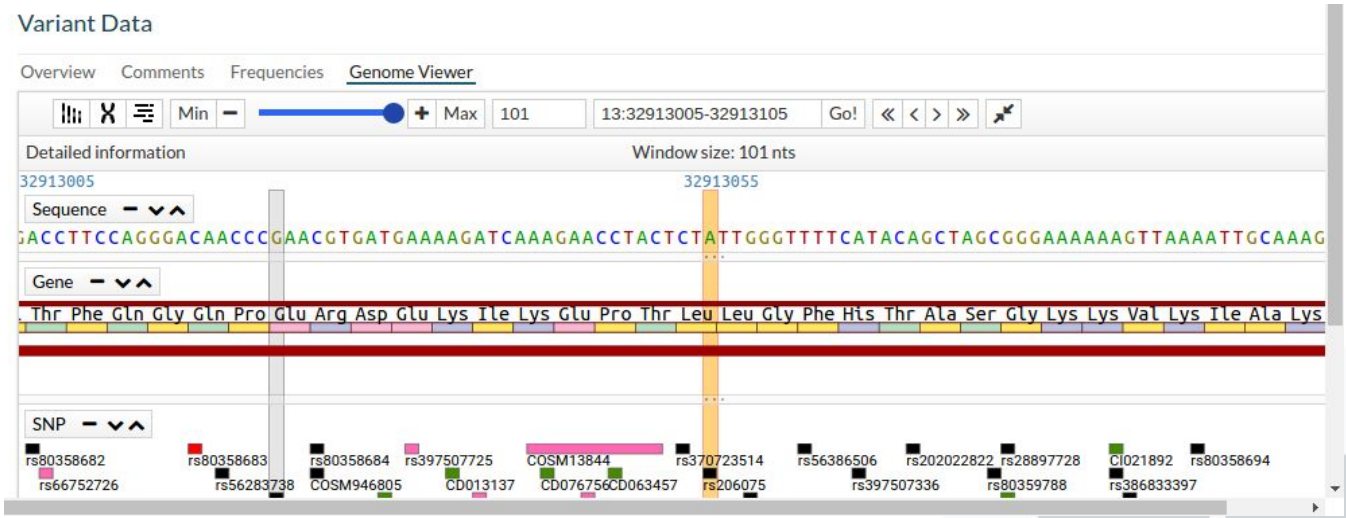


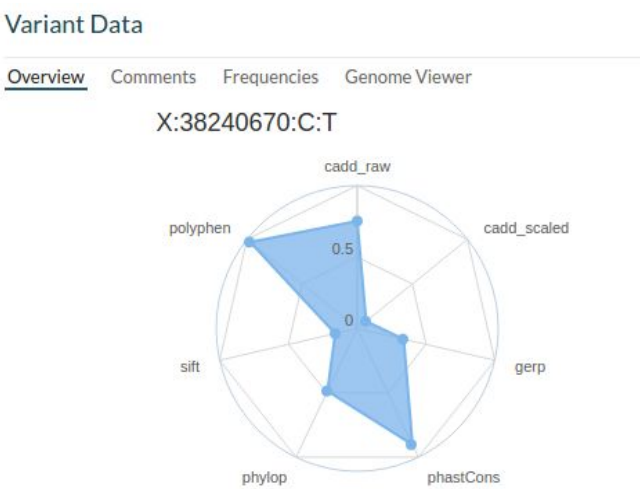
- All values are normalized between zero and one.
- Values closest to zero are deleterious and closest to one are benign.
- Polyphen and Sift are opposed, but in this case, Polyphen has been calculated as 1 - Polyphen.

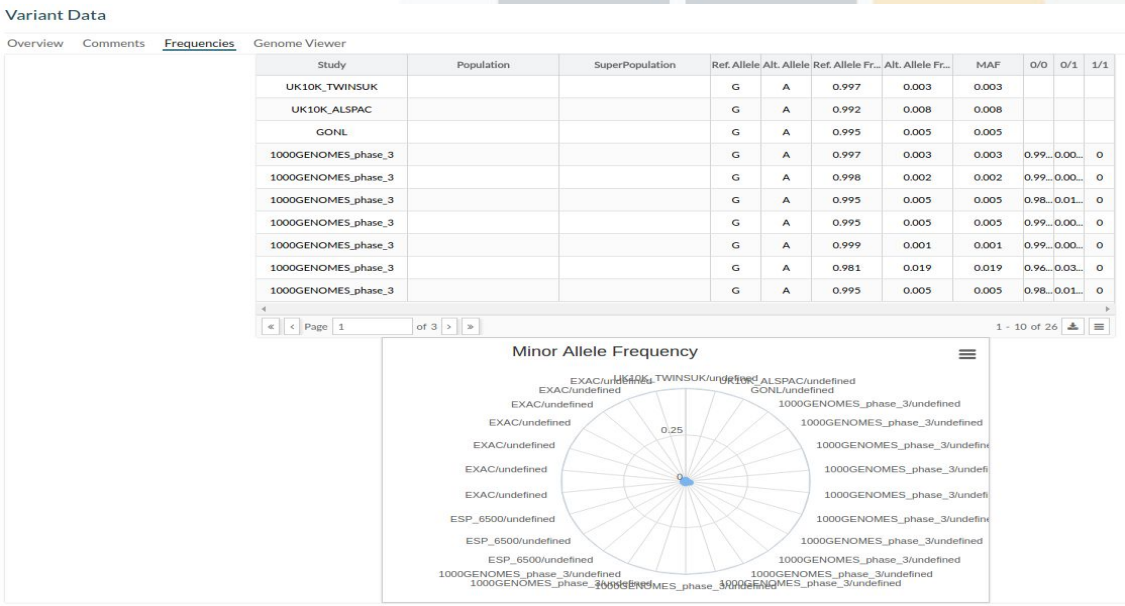
We found a diagnostic variant. It appears in Clinvar.

These are the variants in our sample that are within the regions and appear in the list of mutations of our panel.

Results: Variant Data







Study	Population	SuperPopulation	Ref. Allele	Alt. Allele	Ref. Allele Fr...	Alt. Allele Fr...	MAF	0/0	0/1	1/1
UK10K_TWINSUK			G	A	0.997	0.003	0.003			
UK10K_ALSPAC			G	A	0.992	0.008	0.008			
GONL			G	A	0.995	0.005	0.005			
1000GENOMES_phase_3			G	A	0.997	0.003	0.003	0.99...	0.00...	0
1000GENOMES_phase_3			G	A	0.998	0.002	0.002	0.99...	0.00...	0
1000GENOMES_phase_3			G	A	0.995	0.005	0.005	0.98...	0.01...	0
1000GENOMES_phase_3			G	A	0.995	0.005	0.005	0.99...	0.00...	0
1000GENOMES_phase_3			G	A	0.999	0.001	0.001	0.99...	0.00...	0
1000GENOMES_phase_3			G	A	0.981	0.019	0.019	0.96...	0.03...	0
1000GENOMES_phase_3			G	A	0.995	0.005	0.005	0.98...	0.01...	0

Page 1 of 3 1 - 10 of 26

Results: Secondary Findings

These are the variants that are within the regions of our panel, but not in the list of mutations.

Overview | Diagnostic | Secondary Findings | Report

Variant Filters

Static Filters | Custom Filters

- Without Filters 4
- A: Most Likely Pathogenic 1
- B: Potentially Pathogenic 0
- C: Unkown Significance 1
- D: Likely Benign 2

Secondary Findings

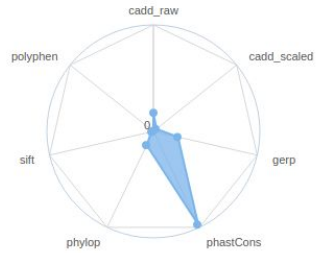
Chr	Pos	Ref	Alt	Gt	SNP Id	Qual	Gene	Conseq. Type	phyloP	Phastc...	SIFT	Polyp...	MAF 1000G Phas...	ESP 6500	Spanish MAF	EXAC	Beacon	OMIM	Clinvar
9	98011497	G	A	1|0	rs1800361	100.000	FANCC	missense_variant,non_coding_transcript_exon...	-0.143	0.971	0.02	0.998	0.0026	0.005	0.007	0.0047			Hereditary ca
16	89806347	A	T	1|0	rs7195906	100.000	ZNF276,FANCA	2KB_upstream_gene_variant,non_coding_tran...	0.555	0.009	.	.	0.2935	.	0.344	0.4773			.
16	89836323	C	T	1|1	rs7195066	100.000	FANCA	missense_variant,2KB_upstream_gene_varian...	-0.385	0.002	0.3	0	0.3333	0.4307	0.327	0.469			.
16	89866043	T	C	1|1	rs7190823	100.000	FANCA	missense_variant,2KB_upstream_gene_varian...	0.555	0.145	1	0	0.3095	0.494	0.357	0.4834			.

« ‹ Page 1 of 1 › » 1 - 4 of 4

Variant Data

Overview | Comments | Frequencies | Genome Viewer

9:98011497:G:A



- All values are normalized between zero and one.
- Values closest to zero are deleterious and closest to one are benign.
- Polyphen and Sift are opposed, but in this case, Polyphen has been calculated as 1 - Polyphen.

We have static filters for categorize Secondary findings variants in four levels.

We also found 4 variants within the genes defined in our panel.
Maybe we can discover an interesting variant here.

Results: Secondary Findings

Custom filters

You can see filters used previously in Filters History

Overview | Diagnostic

Variant Filters

Static Filters | Custom Filters

Clear | Search

- Position +
- Population Freqs. +
- Genotype +
- Quality +
- Protein Substitution Scores +
- Conservation +
- Consequence Type +

Static Filters | Custom Filters

Clear | Search

Chr	Pos	Ref	Alt	Gt	SNP Id	Qual
17	41251931	G	A	1/1	rs799923	17483.0
						14325.0

Clear

Date	Name	Found
20/7 16:14	Qual > 10000	2
20/7 16:14	Consequence Types: splice_acceptor_variant,splice_...	0
20/7 16:13	GT=het AND MAF 1000GP3 < 0.025	1
20/7 16:13	Chromosomal Location: (13) AND Genes: (BRCA2) ...	5

QUAL

Variant Data

Overview | Comments | Frequencies | Genome

Search variants with selected params

Results: Secondary Findings (Filters)

Position

Chromosomal location:
1:1-1000000,2:1-1000000

Gene:
BRCA2,PPL

SNPId:
rs9988179,rs140361978

Genotype

- [x] Heterozygous 5
- [ ] Homozygous 5

Quality

QUAL
> 10000

DP
< 0

If our VCF contains QUAL & DP we can filter using them.

Population Freqs.

1000G Phase 3
< 0.01

ESP 6500
< 0

Spanish MAF
< 0.225

EXAC
< 0

Protein Substitution Scores

SIFT
< 0.05

Polyphen
> 0.7

CADD
< 0.075

Conservation

PhyloP
< 0

PhastCons
< 0.003000

Consequence Type

» High

» Moderate
- [ ] inframe_insertion 0
- [ ] inframe_deletion 0
- [ ] missense_variant 25
- [ ] inframe_insertion 0
- [ ] inframe_deletion 0
- [ ] missense_variant 3

» Low
- [ ] splice_region_variant 6
- [ ] synonymous_variant 17
- [ ] stop_retained_variant 0
- [ ] splice_region_variant 0
- [ ] synonymous_variant 2
- [ ] stop_retained_variant 0

» Modifier

Number of variants found in each category

Results: Report

We can choose which sections we want to print

Complete the information about patient and save the report for a next view

The report can be downloaded as PDF

Confirmed diagnosis

Overview | Diagnostic | Secondary Findings | Report

Select to Show

- [x] Patient data
- [x] Generic data
- [x] Static filter resume
- [x] Custom filter resume
- [ ] Editable conslusions
- [x] Diagnostic table
- [ ] Most pathogenic table
- [ ] Secondary findinds (with last custom filter used)
- [x] Panel used

Save report

Export report to PDF/Print

Export panel to PDF/Print

Team report

Cellbase v4 9/16/2016, 3:23:05 PM

Job name: TEAM Diagnosis_3_Fanconi_anemia

Job description: *New Diagnosis*

Patient data

Patient ID: 1234

Instrument: Ilumina

Analyzed by: test

Sample Origin:

Patient Suspected Diagnosis: **b**

Patient Diagnosis: Fanconi anemia, complementation group q

Generic data

Total Variants: **5**

Diagnostic Variants: **1**

Secondary Variants: **4**

Static filter resume

Variants found with static filters:

A: Most Likely Pathogenic: **1**

B: Potentially Pathogenic: **0**

C: Unkown Significance: **1**

D: Likely Benign: **2**

Static filters description:

A: Most Likely Pathogenic: *Sift least than **0.05** and Polyphen bigger than **0.95***

Who is using TEAM?

ciberer isciii

Centro de Investigación Biomédica en Red
Enfermedades Raras

IT4Innovations
national!$11€0
supercomputing
center1001$1$0

ivo
FUNDACIÓN
INSTITUTO VALENCIANO DE ONCOLOGÍA

GDA

Conclusions

- TEAM is a **free and easy-to-use web tool** that fills the gap between the enormous amount of data in targeted enrichment sequencing analysis and the **biological knowledge** available.

- TEAM **provides an intuitive environment for the clinicians** in which unprocessed data on patient's genomic variation can easily be transformed in a **diagnostic**.

- All data is stored in a Server so you can access to you diagnostics in anywhere you want.

More info: publication

Nucleic Acids Research Advance Access published May 26, 2014

Nucleic Acids Research, 2014 **1**
doi: 10.1093/nar/gku472

A web tool for the design and management of panels of genes for targeted enrichment and massive sequencing for clinical applications

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More info: TEAM behind the scenes