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# myVCF Documentation

*Release latest*

Oct 09, 2017



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## Contents

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<b>1</b>	<b>Want to try myVCF?</b>	<b>3</b>
<b>2</b>	<b>Documentation contents</b>	<b>5</b>
2.1	How to install myVCF . . . . .	5
2.2	Setup the application . . . . .	10
2.3	myVCF features . . . . .	15
2.4	FAQ . . . . .	25
2.5	How to cite myVCF . . . . .	25



Welcome to **myVCF** manual page!

myVCF is a user-friendly platform that helps end-users, without programming skills, to analyze and visualize mutations in an easy and flexible manner. Helping decision making for further downstream analysis.

myVCF will manage **VCF (Variant Call Format)** files (the standard format for storing NGS mutations data) deriving from different NGS applications (Whole Exome/Genome sequencing, Public database...)

myVCF will help end-users to browse and analyze VCF coming from exome and targeted sequencing projects. myVCF can handle multiple-sample VCF and multiple projects can be created as separate environment in order to manage different VCFs with the same application.



# CHAPTER 1

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Want to try myVCF?

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You can download **myVCF** package from:

- Project [homepage](#) (.zip and tar.gz)
- [GitHub project](#) (cloning the project)

and follow the instructions contained in the *[installation page](#)*





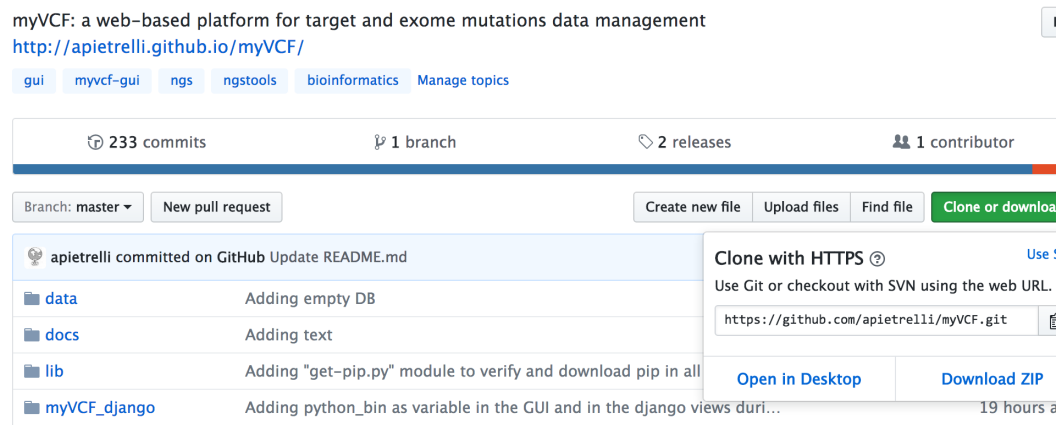
## How to install myVCF

### Download myVCF

You can download **myVCF** package from:

- **Compressed ZIP package**

1. Go to [myVCF homepage](http://apietrelli.github.io/myVCF/)
2. Click on Clone or Download button



3. Click on **Download ZIP**
4. Extract the compressed file in your working directory
5. At the end of the process you will have a directory named `myVCF-master/` containing the desktop application
  - **git command line**

If you have GitHub installed on your computer, you can clone the project directly on your working directory

1. Open the terminal and type:

**Note:** For MAC users, you can find the terminal app by searching through Spotlight and type `terminal` and click on the application

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```
$> cd path/to/working/dir
$> git clone https://github.com/apietrelli/myVCF.git
```

The command will create a directory named `myVCF/` containing the desktop application

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**Note:** To download `git` tool for Unix/MAC operating systems

---

```
# Ubuntu/Debian Unix OS
$> sudo apt-get install git
# MAC
$> brew install git
```

for Windows users, you can download the `git` software from the [Git homepage](#) and use the same command as for Unix/MAC user by using [GitBASH](#)

---

**Warning:** Remember the path to myVCF application, as it is necessary for installation and *VCF file loading*

## Installation requirements

The application is developed using the [Python/Django](#) framework and the [sqlite](#) database platform. Please verify the installation of `python2.7` and `sqlite` on your computer.

### Python 2.7

myVCF tool is based on **Python 2.7** language. Please verify that you have `python` installed.

If you are not sure or you need to install it, please follow the notes below about the installation depending on your operating system.

#### Unix (Ubuntu/Debian system)

Using the terminal, install `python2.7` using `apt-get`

```
$> sudo apt-get install python2.7
```

#### MAC

Open the terminal and install `python2.7` with `brew`

---

**Note:** You can find the shell terminal in MAC OS by typing `terminal` in the Spotlight textbox and click on the application.

---

```
# Terminal application
$> brew install python2.7
```

You can test the installation in the terminal

---

```
$> python
Python 2.7.5 (default, Mar  9 2014, 22:15:05)
[GCC 4.2.1 Compatible Apple LLVM 5.0 (clang-500.0.68)] on darwin
Type "help", "copyright", "credits" or "license" for more information.
>>>
>>>quit()
```

## Windows

You can download the `python2.7` package from the [Python project site](#)

Follow the installation process pointing out this two requirements to let myVCF full compatible with your system:

- By default Python2.7 will be installed in `C:\Python27`. Please **DO NOT** modify the Python path and leave the default installation destination directory.

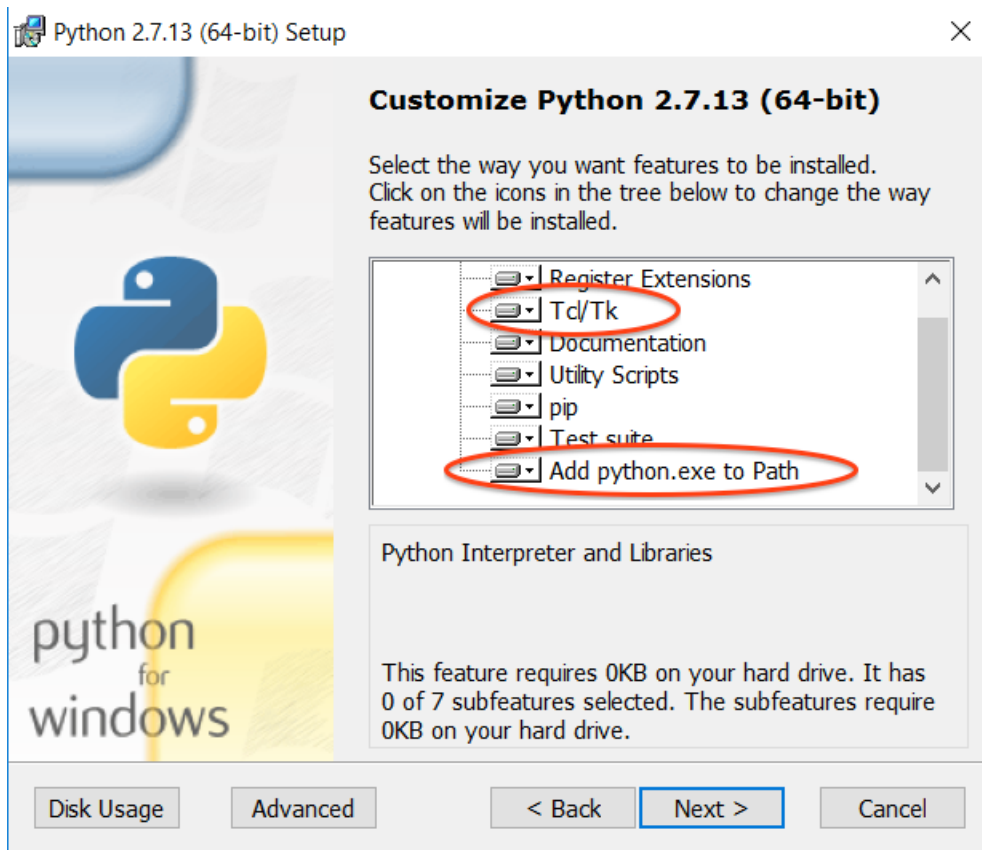
**Warning:** Please download the **Python2.7** package **NOT** Python3.x

- Please verify that the options:

- **Add Python to PATH**
- **Tcl/Tk**

are selected during the installation step.

This will allow the **myVCF\_GUI.py** launcher to be functional with no errors.



## sqlite

The storage of VCF file has been implemented by using `sqlite` as the backend database. This cross-platform solution allows the end-user to workaround some complex configuration setups which are mandatory with other database system.

Please follow these instructions to install `sqlite` according to your operating system

### Unix (Ubuntu/Debian system)/MAC

1. Open the terminal
2. Install `sqlite3` package

```
# Ubuntu/Debian Unix OS
$> sudo apt-get install sqlite3
# MAC OS
$> brew install sqlite3
```

3. Launch `sqlite3` from the shell

```
$> sqlite3
SQLite version 3.7.13 2012-07-17 17:46:21
Enter ".help" for instructions
Enter SQL statements terminated with a ";"
sqlite>
# Quit from the sqlite3 shell
sqlite> .q
```

### Windows

We tested different version of Windows (XP, 7, 10) and in all the Windows systems the `sqlite` library was already installed by default.

If you have troubles in launching myVCF application, follow this procedure to install the `sqlite` necessary files.

1. Go to the `sqlite` web site <https://sqlite.org/download.html> and download precompiled binaries from the Windows section.
  - `sqlite-dll-win32-x86-*.zip`or
  - `sqlite-dll-win64-x64-*.zip`

**Warning:** Check what Windows version you have installed (32 or 64 bit) on your computer to correctly download the right `sqlite3` package from the web site

To check your system version click on:

**Start > Control panel > System**

and check the version.

2. Unpack the `.zip` file and follow the default installation instructions

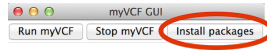
## Python library dependencies

Now that all the major components have been installed, let's proceed with the last step of the installation process regarding Python library dependencies.

## Install packages with myVCF\_GUI

The easiest way to satisfy the myVCF Python dependencies is to use the myVCF GUI.

1. Open the GUI menu by double-clicking the icon relative to your system for launching the GUI
2. Click on the button “**Install packages**”



3. The system will install all the dependencies to start **myVCF** properly

## Install packages with terminal

If the `python2.7` installation doesn't fail, you should have also installed `pip` which is the Python command for library installation.

Now we are going to install all the dependencies using just one command-line using `pip`

- **Unix (Ubuntu/Debian system)/MAC**

1. Open the terminal
2. Go to `myVCF/` directory
3. Execute this command:

```
pip install -r requirements.txt
```

Verify the installation by typing:

```
python manage.py shell
```

If you see something like..

```
Python 2.7.5 (default, Mar  9 2014, 22:15:05)
Type "copyright", "credits" or "license" for more information.
>>>
```

..everything went well! :) Now exit from the python shell.

```
>>> quit
```

- **Windows**

1. Open the MS-DOS prompt (`cmd.exe`)

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**Note:** To open CMD shell in Windows click on

**Start** > type on the search box “**cmd**” > click on **cmd.exe**

---

2. Go to the `myVCF/` directory
3. Execute this command:

```
# MS-DOS Prompt
$> C:\Python27\python.exe pip -m install -r requirements.txt
```

**Warning:** If you followed the *Python 2.7 Windows installation chapter*, you should have all the Python command in `C:/Python27/`

## Launch the application

Finally, you're ready to start the application:

### With GUI

- Open the **myVCF GUI**:
  1. Double-click on **myVCF\_GUI.py** (Windows)
  2. Double-click on **myVCF\_launcher** (MAC/Unix)
- Click on “**Run myVCF**”



- Wait few second for browser loading the homepage

**Note:** If you are on Windows and the double-click on **myVCF\_GUI.py** does not open the application, try to open the file with

**Right mouse click -> Open with -> Choose default program**

and browse the directory to find Python executable `python.exe` in `C:/Python27/`

---

### With Terminal

```
# UNIX on terminal
$> cd path/to/myVCF/
$> python manage.py runserver

# Windows on MS-DOS cmd
$> cd C:\path\to\myVCF\
$> C:\Python27\python.exe manage.py runserver
```

Visit <http://127.0.0.1:8000/> in your browser to see how it looks.

## Setup the application

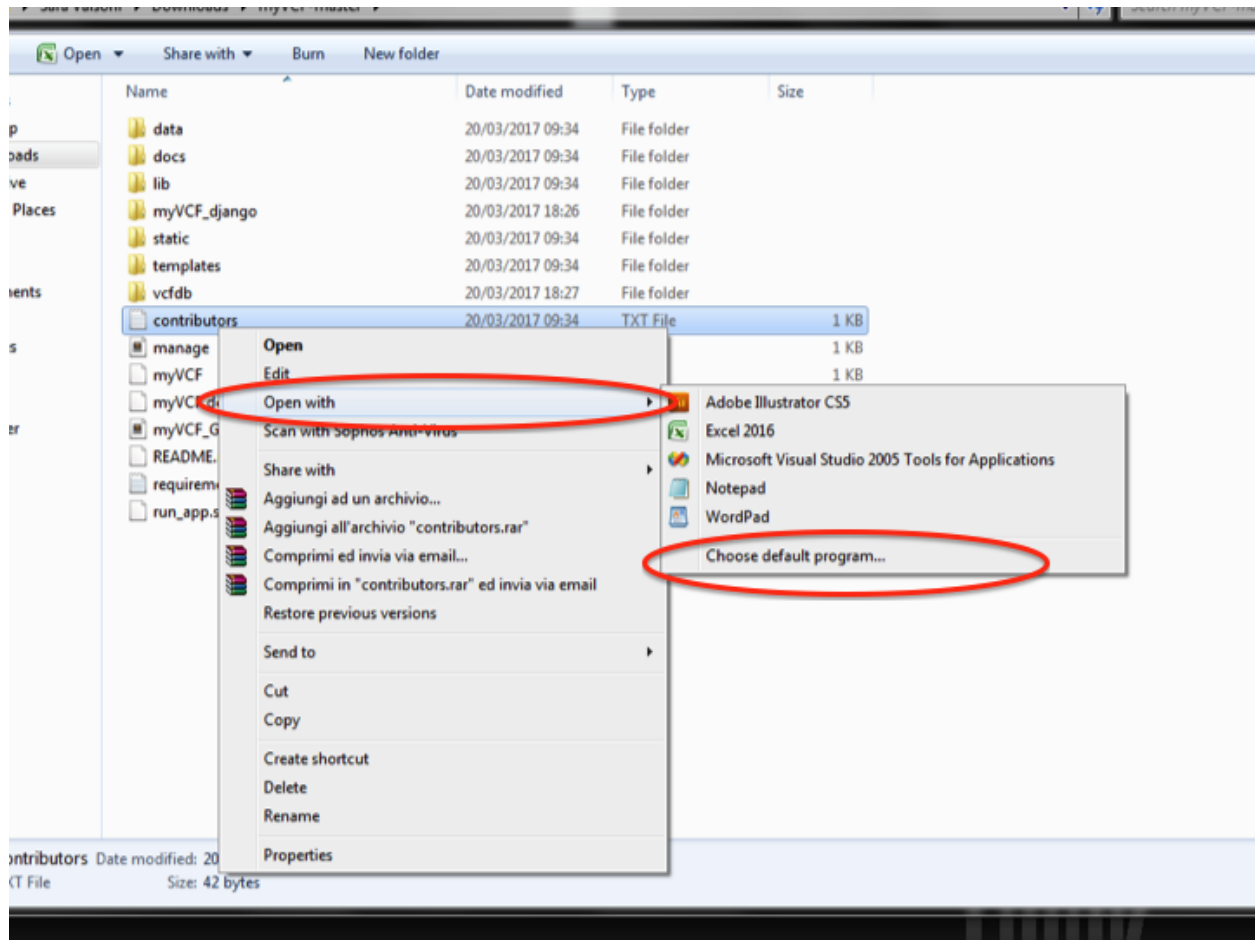
Now you are ready to load all your VCF files and start to analyze your data with myVCF.

myVCF is designed for human annotated VCF files, but it accepts any type VCF coming from different species with or without annotations.

For more information about **not-annotated** or **non-human** VCF file, please follow this [link](#)

myVCF manages **annotated VCF** files with specific fields that are mandatory in order to load and visualize the data correctly.

To verify if your `.vcf` file is compatible with myVCF, please read the following section.



myVCF

[About](#)
[Contact Developer](#)
[myVCF Page](#)

## MyVCF Homepage

web-based platform for browsing VCF data

Upload page

[Upload new project](#)

Available DB

Project name	# Samples	Annotation software	ENSEMBL version	Delete?
★ <a href="#">testAnnovar</a>	80	annovar	75	<a href="#">Delete</a>
★ <a href="#">epidemicVEP</a>	80	vep	84	<a href="#">Delete</a>

Created by Alessandro Pietrelli

## VCF fields and requirements

myVCF can read VCF files deriving from **Annotvar** or **VEP** annotation systems. These software are the most common tools used for VCF annotation after the SNP calling step.

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**Note:** If you are not sure if your VCF file respect the mandatory field and requirements, try to load it by following the [Load new data section](#)

---

Let's define which are the mandatory fields that a VCF must contains for myVCF

- Since myVCF is a tool to browse and visualize mutations genotyped with NGS technologies, the VCF file **must** contain at least 1 genotyped sample

See example below:

```
...
##contig=<ID=17,length=81195210,assembly=b37>
##contig=<ID=18,length=78077248,assembly=b37>
##contig=<ID=19,length=59128983,assembly=b37>
##contig=<ID=20,length=63025520,assembly=b37>
##contig=<ID=21,length=48129895,assembly=b37>
##contig=<ID=22,length=51304566,assembly=b37>
##contig=<ID=X,length=155270560,assembly=b37>
##contig=<ID=Y,length=59373566,assembly=b37>
##contig=<ID=MT,length=16569,assembly=b37>
##INFO=<ID=Func_ensGene,Number=.,Type=String,Description="Func_ensGene annotation_
↳provided by ANNOVAR">
##INFO=<ID=Gene_ensGene,Number=.,Type=String,Description="Gene_ensGene annotation_
↳provided by ANNOVAR">
##INFO=<ID=GeneDetail_ensGene,Number=.,Type=String,Description="GeneDetail_ensGene_
↳annotation provided by ANNOVAR">
##INFO=<ID=ExonicFunc_ensGene,Number=.,Type=String,Description="ExonicFunc_ensGene_
↳annotation provided by ANNOVAR">
#CHROM      POS      ID      REF      ALT      QUAL      FILTER  INFO      FORMAT  Sample1
1          762273   rs3115849      G      A      123.7     LowQual  AC=2;AF=1;AN=2;Func_
↳ensGene=ncRNA_exonic;Gene_ensGene=ENSG00000225880;GeneDetail_ensGene=.;ExonicFunc_
↳ensGene=. GT:AD:DP:GQ:PL  1/1:0,63:63:99:1550,188,0
```

This is part of a VCF file in which one sample has been genotyped (Sample1) for one mutation.

- For **Annotvar** annotated VCF files, the mandatory fields would be:
  1. Gene\_ensGene
  2. ExonicFunc\_ensGene
- For **VEP** annotated VCF files, the mandatory field would be:
  1. CSQ

This field is added by default during VEP annotation

---

**Note:** To verify the necessary fields for the annotation part, you should see in the HEADER part of the VCF file the following lines:

```
# Annotvar fields
##INFO=<ID=Gene_ensGene,Number=.,Type=String,Description="Gene_ensGene annotation_
↳provided by ANNOVAR">
##INFO=<ID=ExonicFunc_ensGene,Number=.,Type=String,Description="ExonicFunc_ensGene_
↳annotation provided by ANNOVAR">
```



```
# VEP: CSQ field
##INFO=<ID=CSQ,Number=.,Type=String,Description="Consequence annotations from Ensembl_
↳VEP. Format: Allele|Consequence|IMPACT|SYMBOL|Gene|Feature_
↳type|Feature|BIOTYPE|EXON|INTRON|HGVS|HGVS|cDNA_position|CDS_position|Protein_
↳position|Amino_acids|Codons|Existing_variation|DISTANCE|STRAND|VARIANT_CLASS|SYMBOL_
↳SOURCE|HGNC_ID|CANONICAL>
```

or copy the VCF in myVCF/data/VCFs/ directory and try to load the VCF through the [Upload page](#)

## How to annotate your VCF

If you don't have the genomic/transcript annotation for your VCF file, or the VCF is not suitable for myVCF please consider to annotate it using the following instructions.

### How to install the annotation tools

#### Annovar

The installation of Annovar is very well-described on [ANNOVAR Manual pages](#)

Since *Annovar* is a perl script, the software can be run on different operating systems including Unix and Windows.

#### VEP

The installation of VEP is described on [VEP main page](#)

Please follow the instructions below to install the software based on your operating system.

#### Unix (Ubuntu/Debian system)/MAC

For UNIX/MAC users, there is a [tutorial](#) available that describes the download and the installation steps in a simple manner.

#### Windows

Please follow these [instructions](#) to install and configure VEP for Windows.

---

**Note:** The easiest way is the **Cygwin** installation procedure.

---

### Launch the code for annotation

Here we reported the *minimum code* to run a correct annotation that is compatible with myVCF. The tutorial contains both the *Annovar* and *VEP* annotation procedure.

For **Windows users** please launch the commands using **Cygwin** downloaded in the previous section or **CMD shell** (*find CMD*)

## Annovar

1. Download the ENSEMBL transcript reference database required for myVCF compatibility.

```
# Download the ensembl DB (example: hg19)
# buildver = hg19/hg38 depending on what reference assembly you used during the read_
↳mapping
table_annovar.pl -downdb -webfrom annovar -buildver hg19 ensGene

## Optional but useful annotation
# dbSNP147
table_annovar.pl -downdb -webfrom annovar -buildver hg19 avsnpl47
# dbnsfp30a - non-synonymous variants annotation compendium (it takes lot for_
↳download)
#http://annovar.openbioinformatics.org/en/latest/user-guide/filter/#ljb42-dbnsfp-non-
↳synonymous-variants-annotation
table_annovar.pl -downdb -webfrom annovar -buildver hg19 dbnsfp30a
```

2. Launch the annotation process. The command line is based on [Annovar tutorial](#).

```
# Launch the annotation
table_annovar.pl example/ex2.vcf humandb/ -buildver hg19 -out myanno -remove -
↳protocol ensGene,avsnpl42,dbnsfp30a -operation g,f,f -nastring . -vcfinput
```

---

**Note:** To download additional databases to enrich the annotation for your mutations, please see [this link](#) and modify the **Launch the annotation** command line by adding the name of the database in `-protocol` and an `f` in `-operation` for every database you want to add.

---

## VEP

A simpler approach than Annovar, can be to use the following command. Once downloaded the tool and the human assembly containing the annotations, launch this command to annotate your VCF file

```
perl variant_effect_predictor.pl -i example.vcf --cache --force_overwrite --vcf -o_
↳example_VEP.vcf
```

At the end of the process you will have file named `example_VEP.vcf` with all the information suitable for myVCF

## Load Data

In myVCF package there are two annotated VCF files that you can use for a trial run. This can be done by loading these files directly from the myVCF upload page by clicking on the dropdown menu **VCF File**:

- `mini_annovar.vcf` (annotated with *Annovar*)
- `mini_vep.vcf` (annotated with *VEP*)

These files reported ~ 1000 mutations in 80 samples and they are stored in `/path/to/myVCF/data/VCFs`

1. Copy/move the VCF files you want to load into myVCF in `/path/to/myVCF/data/VCFs`
2. Launch the application (See how to [launch the app](#)) and load <http://127.0.0.1:8000/> in your browser
3. Click on the **Upload new project** link in the myVCF homepage

4. Give a name to the project and select the VCF to load

myVCF [About](#) [Contact Developer](#) [myVCF Page](#)

---

# UPLOAD PAGE

Start page for VCF project

## Setup a new project

Project name

This will be the name showed in myVCF home page

VCF file

This dropdown menu shows the VCFs directory listing

The VCF is good!

Annotation system: vep

Annotation software

Annotation version

☒ ENSEMBL 75

☐ ENSEMBL 84

Fig. 2.1: New project upload page example. `mini_VEP.vcf` is the mutation file to upload into `test` project using ENSEMBL75 as the transcript reference.

**Note:** If you don't find your VCF in the dropdown menu, please verify that you have copied the file into the directory `myVCF/data/VCFs` and restart the application

5. Click on submit button for saving the project

**Warning:** Don't panic if the saving process takes very long time. Do **NOT refresh** the page until the **Upload completed** page will appear.

## myVCF features

myVCF is designed as a tool for browsing and visualizing mutational data coming from NGS technologies, including Whole-Exome and -Genome sequencing as well as target resequencing.

Several features have been implemented to help the end-user in the navigation and the exploration of his project. In the next paragraphs you will find the description of principal features available in myVCF.

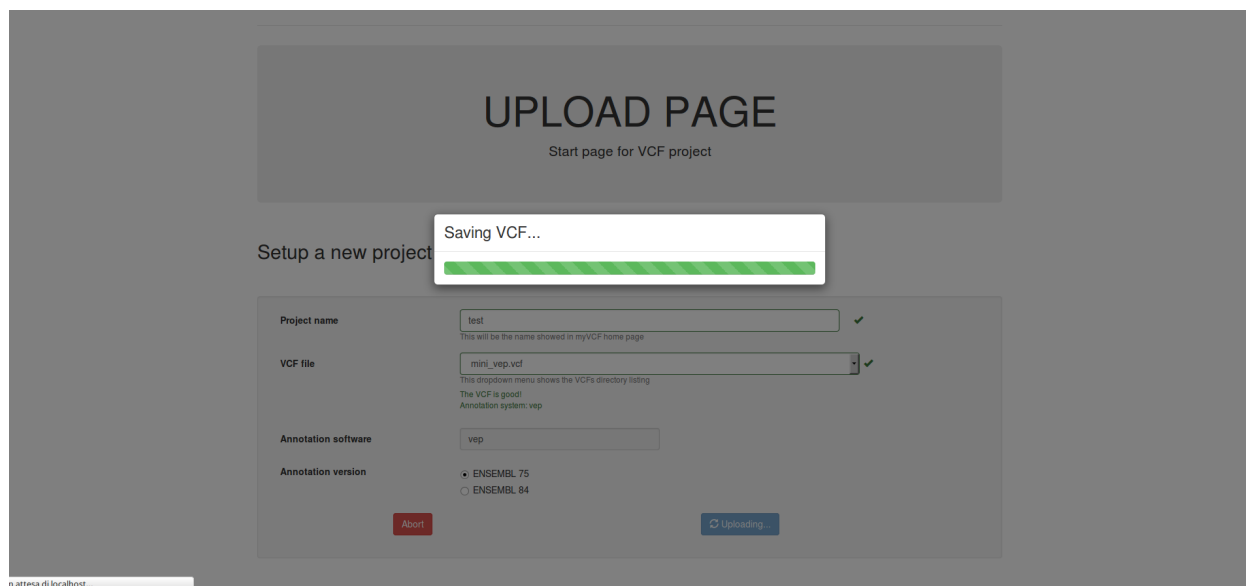


Fig. 2.2: The storing process of very large VCF files (above 50 MB) will take a long time.

## How to query a project database?

The search engine in myVCF is very versatile. Once you are in a project homepage, you can query the database by searching for:

1. Gene name (Official Gene Symbol)
2. Genomic region (1:20000-200100)
3. dbSNP ID (rs324239)
4. Variant (1-456783-456783-A-T)

### Gene/Region view

Basic gene/region search will generate a **Gene page** composed by:

- **Table** containing the mutations found in the gene/region
- **Mutation plot** showing the distribution of the mutations grouped by their functional consequence.

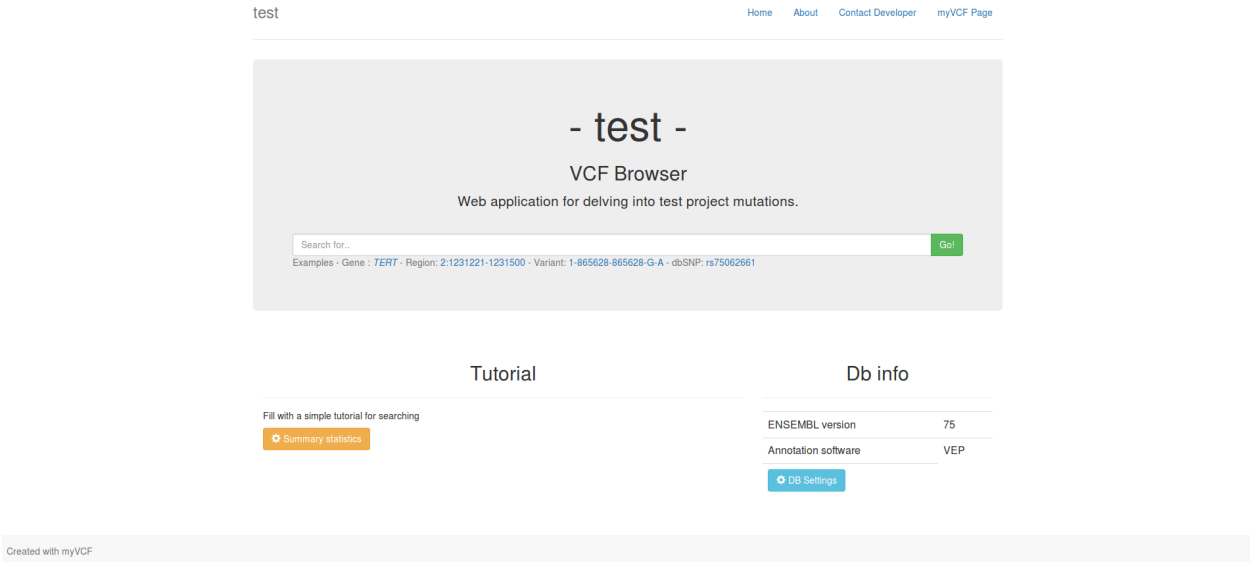
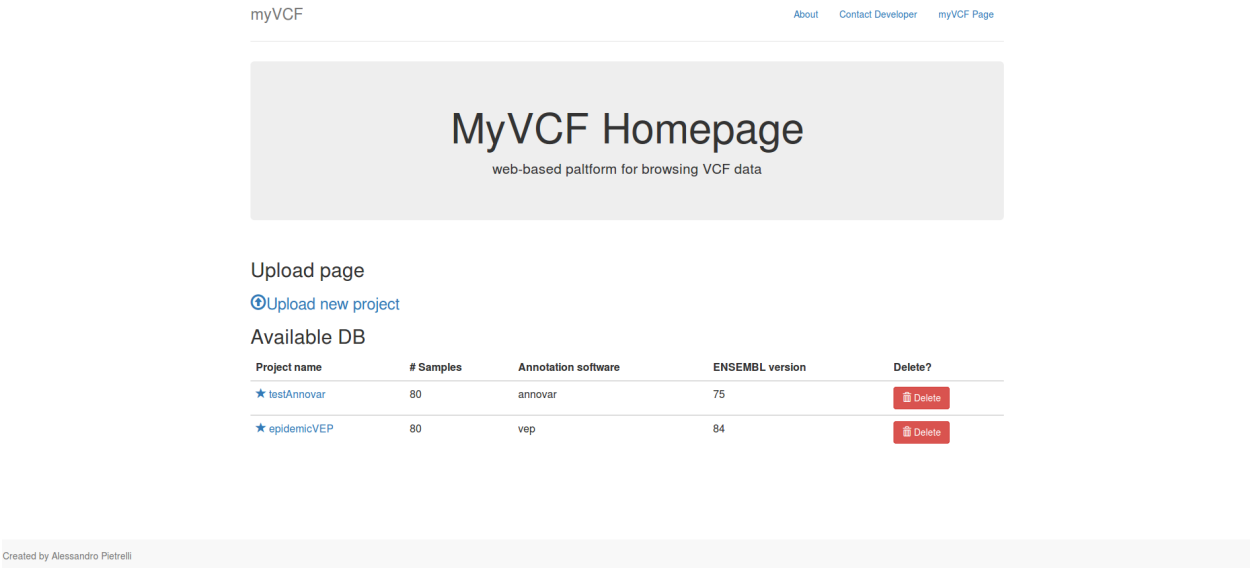
Here we described a simple gene search example

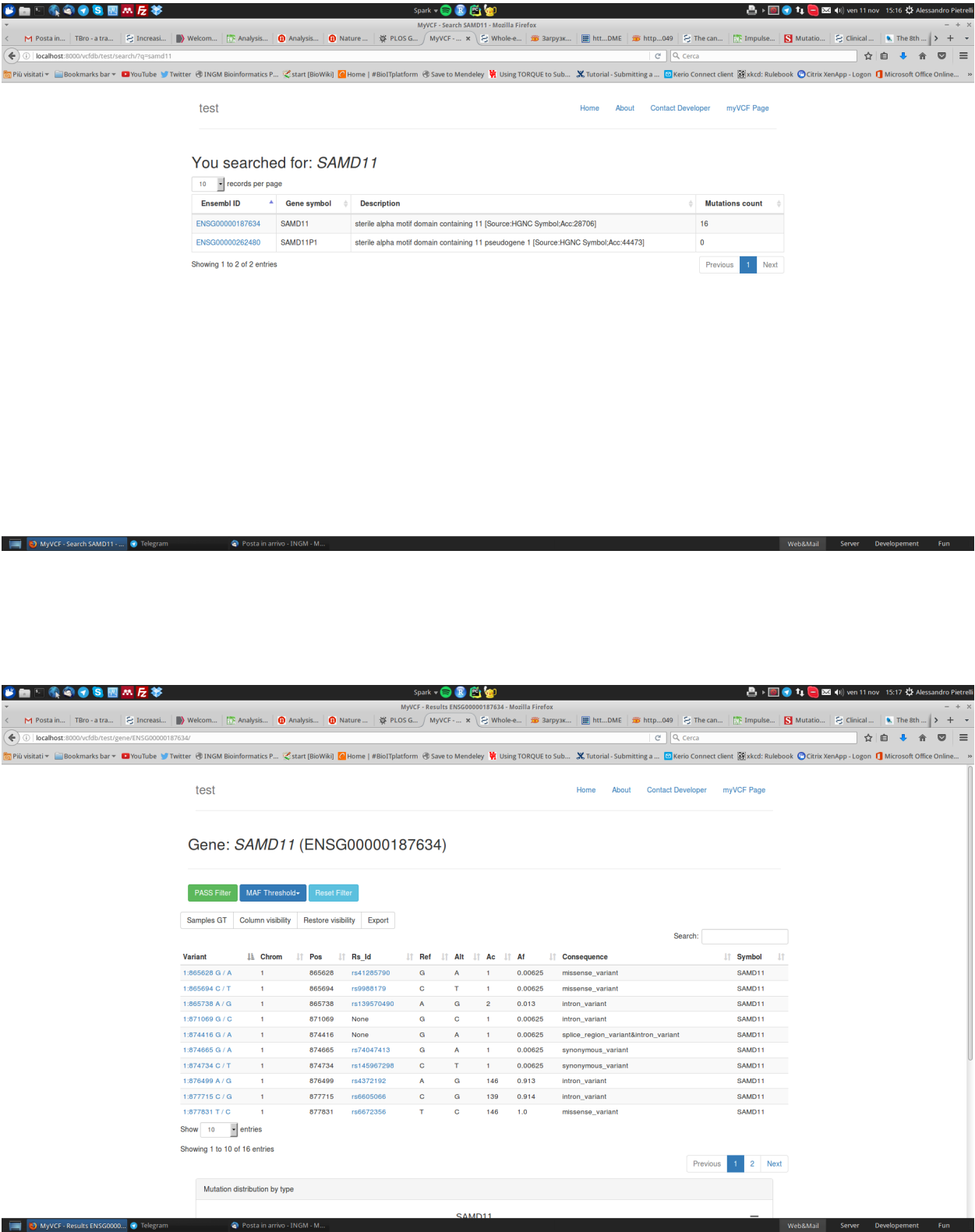
### Example for SAMD11 gene search:

- Launch myVCF application (see how to [launch here](#))
- Click on the project name you want to explore
- Fill the text box with `SAMD11` and click **GO!**

We searched for `SAMD11` gene. The system will output all genes containing the name you searched for. So in this case, together with `SAMD11`, the pseudogene `SAMD11P1` is also reported.

- To display the mutation list for `SAMD11` – `ENSG00000187634` just click on the **ENSEMBL Gene ID** link and you will be directed to the **SAMD11 gene page**





PASS Filter

MAF Threshold ▾

Reset Filter

You can filter the mutations by using the *Filter buttons*

- **PASS Filter** - Only PASS mutations will be showed. This filter acts on the `FILTER` field in the VCF file
- **MAF Threshold** - Only mutations with an Allele Frequency (AF) lower than the MAF threshold you have selected will be reported. This filter acts on the `AF` field in the VCF file.
- **Reset Filters** - Reset all filters. All mutations will be displayed.

You can also modify the visualization aspect by using the following *Display buttons*

Samples GT

Column visibility

Restore visibility

Export

- **Samples GT** - All the genotypes of the samples (stored in the VCF file) will be showed in the table
- **Column visibility** - Toggle On/Off the columns by selecting them from a dropdown menu
- **Restore visibility** - Restore the default column visualization
- **Export** - Save the table in different formats including XLS, PDF and CSV

---

**Hint:** The function to export the table will recapitulate the browser visualization. If the Sample genotype columns are showed in the table, they will be exported in the file.

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**Note:** This visualization (Gene view) and all the entire features described in this paragraph are available to search for **Gene** (as in the example), **Region** and **dbSNP ID**

---

## Variant view

Variant view directly connects the single variant with the additional information contained in the VCF file uploaded and stored in myVCF database.

The variant page links additional information about the allele frequency of the searched variation by interrogating all the principal population frequency database:

- **ExAC**
- **ESP**
- **1000Genomes**

Data from those database will be automatically displayed in the page.

## Example for variant search:

- You can search directly for single variant by using the format:

**CHR-Position-Position-Ref-Alt**

from the project home page.

In this example we are going to search for the **1-878314-878314-G-C** variant.

## - testvcp -

### VCF Browser

Web application for delving into testvcp project mutations.

Examples - Gene : [TERT](#) - Region: [2:1231221-1231500](#) - Variant: [1-865628-865628-G-A](#) - dbSNP: [rs75062661](#)

## Tutorial

## Db info

- If the variant exists in the VCF file, the **variant page** will retrieve information from the VCF regarding:
  - **Variant quality**
  - **Variant annotation**
  - **Zigosity distribution** across samples

testvcp

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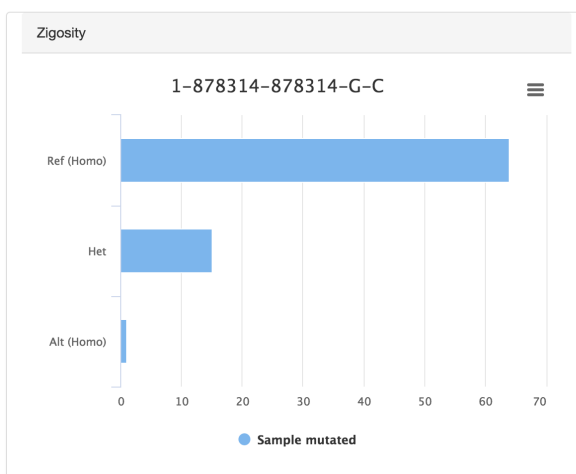
## Variant: 1:878314 G / C

### Variant information

Filter	PASS
dbSNP	<a href="#">rs142558220</a>
Allele Frequency	0.106
Allele count	17 / 160
UCSC	<a href="#">1-878314-878314-G-C</a>
ClinVar	<a href="#">Click to search for variant in ClinVar</a> <a href="#">Q</a>

### Annotations from VCF

Gene name	SAMD11
ENSEMBL Gene ID	<a href="#">ENSG00000187634</a>
Consequence	synonymous_variant
Gene description	sterile alpha motif domain containing 11 [Source:HGNC Symbol;Acc:28706]



- In the bottom part of the **variant page**, you will find the variant frequency distribution according to major public databases.



## Population frequencies

ExAC (GRCh37/hg19)

Populations	Allele Count	Allele Number	Number of Homozygous	Allele Frequency
European (Non-Finnish)	1109	6260	51	0.177157
South Asian	386	6190	9	0.062359
Latino	51	378	2	0.134921
European (Finnish)	39	154	1	0.253247
African	30	1100	0	0.027273
Other	16	148	1	0.108108
East Asian	1	1058	0	0.000945
<b>Total</b>	<b>1632</b>	<b>15288</b>	<b>64</b>	<b>0.106750</b>

ESP Database (GRCh37/hg19)

Populations	Allele Frequency
EA - European American	0.0669
AA - African American	0.0134
<b>Mean</b>	<b>0.040150</b>

1000G Phase 3 Database (GRCh37/hg19)

Populations	Allele Frequency
European	0.1193
American (Ad Mixed)	0.0778
South Asian	0.0317
African	0.0083
East Asian	0
<b>Mean</b>	<b>0.118550</b>

**Important:** Since all the linked public database are mapped on **GRCh37/hg19** human assembly, if you load and query variation from GRCh38 assembly the frequency showed won't be correct!

**Hint:** Every variation in the **gene table view** (described before) is a link to its variant page.

**Note:** Internet connection is needed to retrieve the frequency information from public databases.

## VCF metrics summary

myVCF can also generate a global VCF summary report considering several metrics and information.

You can generate this report by clicking on the *Summary button*

 Summary statistics

**Hint:** The first time you load the summary statistics the process will take several minutes, especially for exome/genome projects. All following loadings will be very fast thanks to the system saving in the cache that speeds-up the process. Cache memory will be removed once the application is closed.

The VCF quality report consists of several statistics and plots all-in-one page. You can export separately each plot as single images.

Here, some example of the statistics generated:

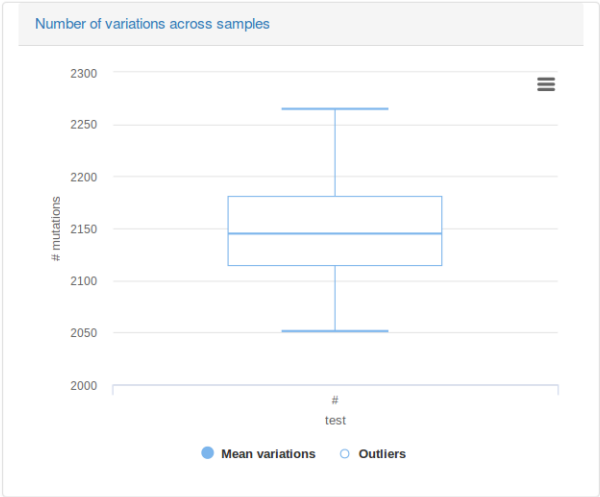
- Number of variants and the distribution of mutation across samples
- Variant quality distribution
- Variant distribution across chromosomes stratified by functional consequence
- Variant functional consequence distribution as pie chart

test

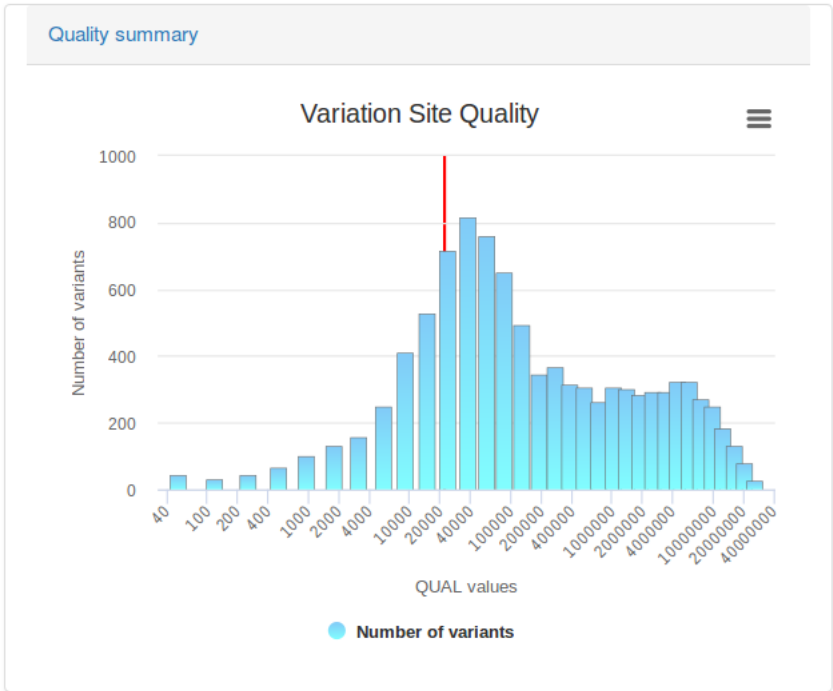
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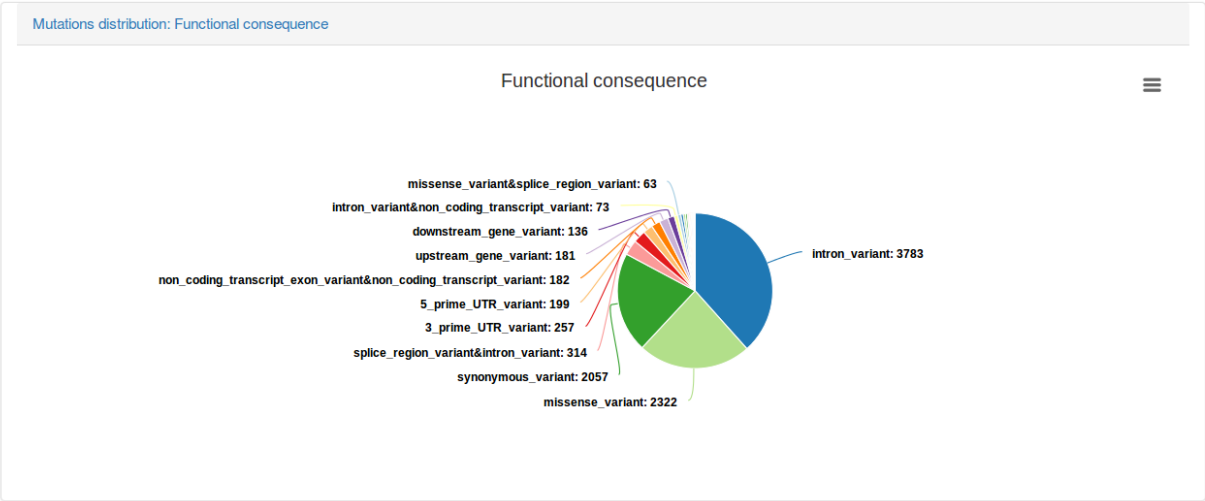
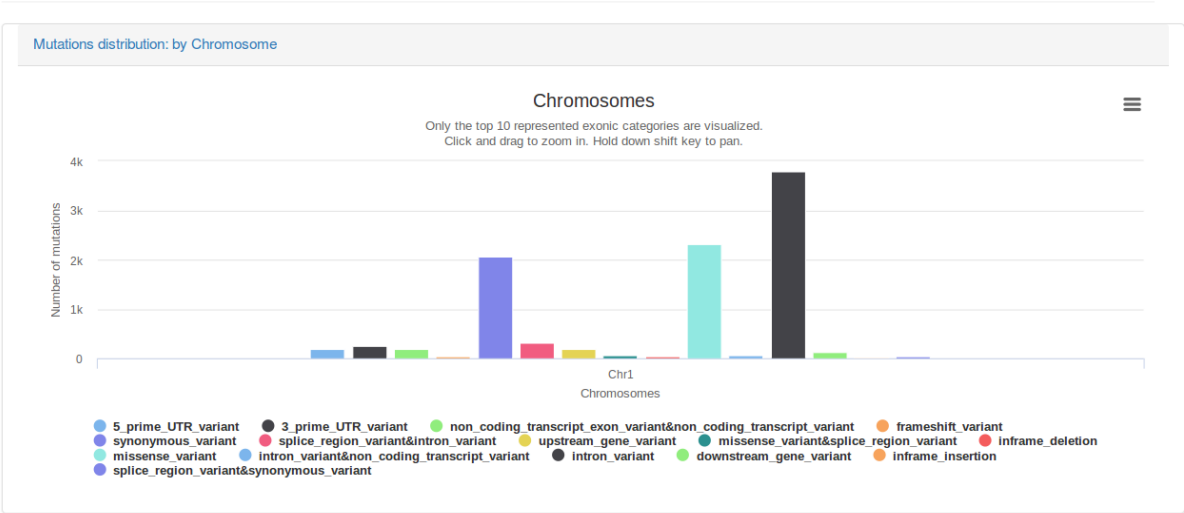
## Summary statistics

Project name	test
Software annotation	vep
Number of samples	80
Number of records	9857



## Summary statistics VCF





## Add sample groups

Most of the times, exome and target sequencing projects, are performed to understand the genetic difference between two or more group of samples that belong to a particular phenotype or hold some features of interest according to clinical data.

With myVCF you can easily define samples groups in order to filter and export mutations that are present only in certain samples defined by the group.

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**Hint:** This feature is available **only for human-based and annotated projects**

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To define and add groups in specific project, follow these steps:

1. Click on *DB settings page* from the project homepage
2. Go to **Setup Groups** section
3. Define a *group name* and select the *sample ID* that you want to include in the group

4. Save group by clicking on **Save group** button
5. You can verify the correct group definition by looking at the *Available group lists* table.

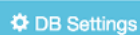
Available group lists		
Name	Samples list	Delete?
HealthyControl	C11,C12,C13,C14	Delete

Now you can apply filters on mutations/region results by your sample group definition.

## Change default columns view

By default myVCF visualizes a set of columns in the gene/region view composed by the principal annotation given by the VCF file.

You can change the default view by accessing to the *DB settings page*



You will be redirected to the preferences page and you can select which columns will be displayed in the Gene/Region table.

## Database preferences

Default columns  
visibility

ChromPosRs\_idRefAltSymbolAcAfConsequence

Add other columns

Other columns available

Qual	Filter	An	Baseqranksum	Ccc	Clippingranksum	Db	Dp	Ds	End	Fs	Gq_mean
Gq_stddev	Hwp	HaplotypeScore	Inbreedingcoeff	Mleac	Mleaf	Mq	Mq0	Mqranksum	Ncc		
Negative_train_site	Positive_train_site	Qd	Readposranksum	Sor	Vqslod	Culprit	Allele	Impact	Gene		
Feature_type	Feature	Biotype	Exon	Intron	Hgvsc	Hgvsp	Cdna_position	Cds_position			
Protein_position	Amino_acids	Codons	Existing_variation	Distance	Strand	Variant_class	Symbol_source				
Hgnc_id	Canonical	Tsl	Appris	Ccids	Ensp	Swissprot	Trembl	Uniparc	Gene_pheno	Sift	
Polyphen	Domains	Hgvs_offset	Gmaf	Afr_maf	Amr_maf	Eas_maf	Eur_maf	Sas_maf	Aa_maf		
Ea_maf	Exac_maf	Exac_adj_maf	Exac_afr_maf	Exac_amr_maf	Exac_eas_maf	Exac_fin_maf	Exac_nfe_maf				
Exac_oth_maf	Exac_sas_maf	Clin_sig	Somatic	Pheno	Pubmed	Motif_name	Motif_pos	High_inf_pos			
Motif_score_change											

To save the column view modified by the user, click on *Save changes*

Save changes

## FAQ

### 1. What if my VCF file is not annotated or is not human-based?

Don't worry! myVCF can handle VCF from any type and automatically detect the format of your file.

You can still upload the VCF, create the project, query for available region according to your species chromosomes names and export the mutation and the genotype data.

Since the application is designed for human-based VCF, some of the available features such as, gene query or allele frequency/in-silico predictors annotation, will be disabled.

## How to cite myVCF

Paper under review!!

Update will be available soon. Fingers crossed :)