

As previously mentioned, files resulting from the sequencer are stored at [varbank](#) server.

The following files from the bioinformatic process are available

**BAM** binary version of a SAM file

**SAM** a tab-delimited text file that contains sequence alignment data [SAM](#)

**BAM\_INDEX** bam index

**FUNC** functional annotation of variations

**FASTQ** gzip compressed FASTQ, containing raw sequence and quality scores [FASTQ](#)

**HS\_METRICS** Picard hybrid selection metrics

**EXONCOV\_ALL** total exon coverage statistics

**EXONCOV\_LOW** low coverage part of the EXONCOV\_ALL table

**VCF** row vcf (Variant Call Format) files from different variation callers [VCF](#)

In order to download files, select those files you are interested in by clicking on the left check box and next click on *Create and Send Download Links* located at the table foot. A window with download links will appear.

*We are interested in FASTQ files, the ones coming directly from the sequencing machine.*

Because there are many files and these are relatively large (3.5-4.1 Gb when compressed) it is best to download directly to local server using

wget and the links provided by the pop-up message from varbank, something like this:

```
wget
```

```
http://varbank.ccg.uni-koeln.de/downloads/2b3c87c39f158033283457199ef6e50a/SN7640211\_14143\_P1H03\_MND428\_1\_sequence.fq.gz
```

```
wget
```

```
http://varbank.ccg.uni-koeln.de/downloads/2b3c87c39f158033283457199ef6e50a/SN7640211\_14074\_P1A01\_MND1014\_1\_sequence.fq.gz
```

If we have many files to download, maybe it is best to copy all this links into a txt file (e.g. files-to-download.txt) and then download using

```
wget -i files-to-download.txt
```

where -i indicates -input-file, meaning that it reads URLs from a local or external file.

**It is very important NOT to close the varbank page since the download links are valid for the duration of a session - this is 14 days or until you log out.**

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