TBro Demo Documentation

Release 1.1

Markus Ankenbrand

Jul 10, 2017

Contents

This tutorial leads you through the process of installing and loading transcriptomic data into TBro as well as analyzing it. If you read this on readthedocs.io, please be aware that Google Analytics is used.

CHAPTER 1

Cannabis sativa transcriptome

Original data published in:

Harm van Bakel et al. "The draft genome and transcriptome of Cannabis sativa." In: Genome biology 12.10 (Jan. 2011), R102. issn: 1465-6914. doi: 10.1186/gb- 2011-12-10-r102. url: http://genomebiology.com/2011/12/10/R102.

Installation

Docker

Installation of TBro is straightforward and easy using preconfigured docker containers. See docker documentation on how to install docker on your machine.

After installation of docker execute the following commands to pull the docker images:

```
docker pull greatfireball/generic_postgresql_db
docker pull tbroteam/generic_chado_db_reload
docker pull tbroteam/tbro_worker_ftp
docker pull tbroteam/tbro_worker
docker pull tbroteam/tbro_apache
# only required if predifined demo data should be loaded
docker pull tbroteam/tbro_demo
```

Now start the Chado database container and install the schema:

```
docker run -d -e DB_NAME=chado -e DB_USER=tbro -e DB_PW=tbro --name "Chado_DB_4_TBro_
↪official" greatfireball/generic_postgresql_db
sleep 60
docker run --rm -i -t --link Chado_DB_4_TBro_official:CHADO --name "Chado_DB_4_TBro_
↪load_official" tbroteam/generic_chado_db_reload
```

Now start the database container for the BLAST worker:

```
docker run -d -e DB_NAME=worker -e DB_USER=worker -e DB_PW=worker --name "Worker_DB_4_
↪TBro_official" greatfireball/generic_postgresql_db
```

Start an ftp server to host the BLAST databases:

```
docker run -d --name "Worker_FTP_4_TBro_official" -e FTP_USER="tbro" -e FTP_PW="ftp"␣
↪tbroteam/tbro_worker_ftp
```

Start a worker to execute the BLAST jobs:

```
docker run -d --link Worker_DB_4_TBro_official:WORKER --link Worker_FTP_4_TBro_
↪official:WORKERFTP --name "TBro_Worker_official" tbroteam/tbro_worker
docker exec -i -t TBro_Worker_official /home/tbro/worker_build_installation.sh
```

Finally start and install the main TBro container:

```
docker run -d --link Chado_DB_4_TBro_official:CHADO --link Worker_FTP_4_TBro_
↪official:WORKERFTP --link Worker_DB_4_TBro_official:WORKER --name "TBro_official" -
↪p 80:80 tbroteam/tbro_apache
docker exec -i -t TBro_official /home/tbro/build_installation.sh
```

You can now access the TBro web interface by pointing your browser to http://localhost However there is no data loaded, yet. To load data you can either perform the automatic demo installation (see next section), follow the step-by-step tutorial (next chapter) or load your own data.

Preload demo data

Run the following command to fill your TBro instance with demo data from *Cannabis sativa*.

```
docker run --rm -i -t --link Worker_DB_4_TBro_official:WORKER --link Worker_FTP_4_
↪TBro_official:WORKERFTP --link Chado_DB_4_TBro_official:CHADO --name "TBro_Demo_
↪official" tbroteam/tbro_demo
```

Congratulations, you have a full-featured TBro instance up and running.

Introduction

The aim of this manual is to teach you how to use the TBro. At first you will learn how to bring the data into the TBro. For this purpose you can follow the step by step guide using example data. When you work through this tutorial you have two options. You can either start from scratch, load the data from the original sources and perform the analyses yourself or you can just use the precomputed results in the example directory. In the manual it is assumed that you perform the analyses yourself so all commands that created the data are included. However the scope of this manual is not to teach you how to perform transcriptomic analyses and some of the methods may soon be out of date. The methods of importing and interpreting the data however will remain the same. If you choose to use the precomputed data just ignore all commands regarding their creation and use the accordingly named files in the example directory.

Data

The demo data consists of the published transcriptome of /Cannabis sativa/. And additional short read libraries of different samples.

Cannabis sativa

The raw data is available through NCBI. The transcriptome is described in @CSATIVA and has accession numbers (JP449145 - JP482359). Read data from different samples is available through the SRA at NCBI. The used samples are:

- Mature flower (SRR306868, SRR306869, SRR306870)
- Mature leaf (SRR306875, SRR306885, SRR306886)
- Entire root (SRR306861, SRR306862, SRR306863)

We analyzed the data in different ways and final results for each analysis are included in the example data. You can use this pregenerated results or generate it yourself, for this purpose each command for data creation along with program version is given. For an overview of the used programs and versions see table [tab:PROGRAMS].

[tab:PROGRAMS]

Task	Program	Version
Peptide prediction	Transdecoder	r2012-08-15
Repeat annotation	RepeatMasker	4.0.3
General annotations	InterproScan	5 RC5
GO/EC annotation	Blast2GO (B2G4Pipe)	2.5.0
General annotation	MapMan (Mercator)	2013/07/18
Count quantification	RSEM	1.2.5
Normalization / Differential expression	DESeq	1.12.1

Data creation and import into TBro is described as a workflow in the next section.

Bringing the data into TBro

For this tutorial it is assumed, that you have a fresh install of TBro as described in the installation section.

Attention: All commands are executed inside the TBro_official docker container. To enter this container do the following:

```
docker exec -it TBro_official /bin/bash
```

Alternatively you can download the tbro-cli tools to your local machine. But remember that you have to install them via phing and set the config.php properly (to point to the database in the docker container - find the ip via docker inspect)

No demo data has been loaded to the database yet. These are the manual steps to load the demo data (resembling the automatic installation via TBro_demo docker container). So lets start populating the database with our first transcriptome.

The Cannabis sativa transcriptome

Preparation

There is one preparation necessary before we can start importing data into TBro. We have to create the organism as is not part of the default `CHADO` repertoir.

```
tbro-db organism insert --genus Cannabis --species sativa\
 --common_name Weed --abbreviation C.sativa

tbro-db organism list
```

The last command shows us all organisms known to TBro. As we see the ID of is 13. We will need this ID for later commands. You have probably noticed that it is possible to use autocompletion for commands, subcommands and parameters. In addition the very useful `-help` option is present for every command and gives information on usage, and available parameters.

The Transcripts

Create a directory cannabis_sativa with subdirectory transcriptome

```
mkdir -p cannabis_sativa/transcriptome
cd cannabis_sativa/transcriptome
```

Note: The following documentation requires you to perform the search at NCBI yourself. It further assumes that you want to do all of the analyses manually again. If you just want to learn how to import the data files into TBro you can execute the following command:

```
git clone https://github.com/TBroTeam/DemoData
```

In the new `DemoData` folder you find all the pre-calculated files. So you only have to issue the `tbro-db` and `tbro-import` commands.

If you want to follow along with your own data instead you can copy your file into the docker container with this command (outside the docker container):

```
docker cp MyTranscriptome.fasta TBro_official:/
```

Please replace `MyTranscriptome.fasta` with your actual file name. It will be available in the root of the file system `/` inside the container.

Download the transcriptome from `NCBI`[1]. To do so, search for `74271[BioProject]` on http://www.ncbi.nlm.nih.gov/nuccore and download all hits as fasta. There should be sequences. Save those to the file cannabis_sativa_transcriptome.fasta in the newly created folder. As we have no isoform unigene relationship for those transcripts we treat all of them as separate isoforms. So the id file comes down to a simple list of all ids in the fasta.

```
grep ">" cannabis_sativa_transcriptome.fasta\
 | perl -pe 's/>(\S+).*/$1/'\
 >cannabis_sativa_transcriptome.ids
```

Now, it's time to import the sequence IDs into TBro. As we have no isoform - unigene relationship we import each transcript as a single isoform:

```
tbro-import sequence_ids --organism_id 13 --release 1.CasaPuKu\
 --file_type only_isoforms cannabis_sativa_transcriptome.ids
```

[1] In this case we start with a pre-assembled transcriptome. For your own data it might be necessary to do the assembly from the raw reads yourself. The SOS pipeline https://github.com/SchulzLab/SOS is great for that purpose.

We had to pass the previously given organism-id and a release name.

The release name can be selected freely and the release is automatically created upon first usage. The file-type was set to `only_isoforms` as we have no unigenes. Other possible values are `only_unigenes` and `map`. The last thing we pass is the path to the file containing the sequence-ids which we have just created. | TBro now knows about the sequence ids so lets feed it with the associated sequences:

```
tbro-import sequences_fasta --organism_id 13\
 --release 1.CasaPuKu cannabis_sativa_transcriptome.fasta
```

Now it's time to start up your browser and visit your TBro instance. Use the quick search field in the upper right corner to find `gi|351628922|gb|JP481805.1|`. You will see the isoform page with the basic information about this transcript. By now there is just the general info (date of import, organism, release) and the sequence together with a visualization as a horizontal bar. You can check back to this page after every successful import to watch how the new features are presentet. Of course you can choose any other isoform that is of interest to you.

Predicted Peptides

After we have the nucleotide sequences, the next step is to predict peptides and load this info into TBro. There are many tools available to predict peptides, we chose `Transdecoder` but the TBro does not restrict you to a certain tool.

```
mkdir -p ../peptids
cd ../peptids

transcripts_to_best_scoring_ORFs.pl -t \
 ../transcriptome/cannabis_sativa_transcriptome.fasta\
 -m 30 -v --CPU 4 >log >error.log
```

Note that we have set the minimum protein length to 30 and number of threads to 4, you can adjust those parameters to your own requirements. Unfortunatelly the output format for predicted peptides is not standardized. To make the peptide import generic and not rely on the output format of a special program the import into TBro is split into two steps. First a list of peptides is imported. This list has to be in tab delimited format and contain the following columns:

1. peptide id
2. isoform id
3. start position
4. end position
5. strand (+/-)

This file can easily be created from the output of every peptide prediction program. TBro contains a tool to get the table from the `Transdecoder` output so lets use that:

```
tbro-tools transToProt -o predicted_peptides.tbl\
 best_candidates.eclipsed_orfs_removed.pep
```

Lets have a look to see that the table has the desired format.

```
head -n5 predicted_peptides.tbl
m.243266        gi|351590686|gb|JP449145.1|     165     893     +
m.243259        gi|351590687|gb|JP449146.1|     1751    1894    +
m.243253        gi|351590687|gb|JP449146.1|     2       1684    +
```

```
m.243237        gi|351590688|gb|JP449147.1|     1       1986    +
m.243247        gi|351590688|gb|JP449147.1|     2173    2295    +
```

Now to import this peptide table issue the following command:

```
tbro-import peptide_ids --organism_id 13\
 --release 1.CasaPuKu predicted_peptides.tbl
```

TBro now knows about the predicted peptides and their locations. What's missing is the sequences. They are added the same way as the nucleotide sequences of the transcripts before. It is important, that the fasta IDs exactly match the IDs in the first column of the peptide table.

```
tbro-import sequences_fasta --organism_id 13\
 --release 1.CasaPuKu best_candidates.eclipsed_orfs_removed.pep
```

You might want to check back to the web interface to see our newly imported peptides.

RepeatMasker

Another basic type of annotation are repeats. So we create repeat annotations using `RepeatMasker` and import them.

```
mkdir -p ../analyses/repeats
cd ../analyses/repeats

RepeatMasker -pa 4 -dir . -xm -species viridiplantae\
 ../../transcriptome/cannabis_sativa_transcriptome.fasta
```

All we need to do now is tell TBro to import the generated file as `RepeatMasker` annotations:

```
tbro-import annotation_repeatmasker --organism_id 13\
 --release 1.CasaPuKu cannabis_sativa_transcriptome.fasta.out.xm
```

Interpro

`Interpro` is a usefull tool to annotate protein sequences with information from different databases. There exists a command line version of this tool called `InterproScan`. We use this tool to generate the interpro annotations for our transcriptome:

```
mkdir -p ../interpro
cd ../interpro

interproscan.sh --pa --iprlookup --goterms --fasta\
 ../../peptids/best_candidates.eclipsed_orfs_removed.pep\
 --output-file-base interpro >interpro.log
```

The results in the tsv format can be importet into TBro with the following command:

```
tbro-import annotation_interpro --organism_id 13\
 --release 1.CasaPuKu -i interproscan-5-RC5 interpro.tsv
```

Note that it is important to know the `InterproScan` version used as each version uses different versions of the underlying databases. Interpretation of the results requires knowledge of this versions so the `-i` switch taking the version is required for this import.

Blast2GO

Blast2GO uses BLAST to find sequence similarities to annotated sequences. The hits are then used to assign GO terms and EC numbers to the input sequences.

```
mkdir -p ../blast2go
cd ../blast2go

blastx -query ../../transcriptome/cannabis_sativa_transcriptome.fasta\
 -db /path/to/databases/NCBI/nr -evalue 1e-3 -outfmt 5\
 -num_alignments 250 -num_descriptions 250\
 -out cannabis_sativa_transcriptome.nr.xml\
 2> cannabis_sativa_transcriptome.nr.log

java -Xmx20G -cp *:ext/*: es.blast2go.prog.B2GAnnotPipe\
 -in cannabis_sativa_transcriptome.nr.xml\
 -out cannabis_sativa_transcriptome.blast2go.annot\
 -prop b2gPipe.properties -v -annot -dat -img\
 > cannabis_sativa_transcriptome.blast2go.log
```

First all sequences are blasted against a local copy of nr. The output format is set to 5 (xml output). The e-value cutoff was set to 10^{-3}. Afterwards the BLAST output is passed to the Blast2GO annotation pipeline. We can extract three different kinds of annotations from the Blast2GO output:

GO

Gene Ontology

```
grep "GO:" cannabis_sativa_transcriptome.blast2go.annot\
 >cannabis_sativa_transcriptome.blast2go.annot.go

tbro-import annotation_go --organism_id 13\
 --release 1.CasaPuKu cannabis_sativa_transcriptome.blast2go.annot.go
```

The lines containing “GO:” are selected and imported into TBro as annotation_go

EC

Enzyme Commission

```
grep "EC:" cannabis_sativa_transcriptome.blast2go.annot\
 >cannabis_sativa_transcriptome.blast2go.annot.ec

tbro-import annotation_ec --organism_id 13\
 --release 1.CasaPuKu cannabis_sativa_transcriptome.blast2go.annot.ec
```

The lines containing “EC:” are selected and imported into TBro as annotation_ec

Description

```
perl -ane 'print if(@F>2)'\
 cannabis_sativa_transcriptome.blast2go.annot.go\
 >cannabis_sativa_transcriptome.blast2go.annot.go.description
```

```
tbro-import annotation_description --organism_id 13 --release 1.CasaPuKu\
 cannabis_sativa_transcriptome.blast2go.annot.go.description
```

Descriptions are arbitrary text that describes a transcript. Some GO Terms contain a meaningful description so we import the lines containing such a description into TBro. However this is just an example, the source of the description does not matter. The format is a tab delimited format with the feature ID in the first column and the description in the second.

Mercator

Mercator is a tool to classify sequences into MapMan functional plant categories.

```
mkdir -p ../mercator
cd ../mercator
```

To perform the Mercator classification start up your browser and go to

http://mapman.gabipd.org/web/guest/mercator. | In the web interface you can upload the `cannabis_sativa_transcriptome.fasta`. Unfortunatelly, there is a restriction on the input file size. This limit is exceeded by our transcriptome. So you can either contact the people at MapMan to allow you the submission of a larger dataset or just split the input file into two parts. We split the file by sequence length but you can just as well open the file in a text editor and split it. Then run Mercator on each chunk and download the results afterwards. It is no problem to import the two reports, one after the other:

```
tbro-import annotation_mapman --organism_id 13\
 --release 1.CasaPuKu mercator.results_max1499.txt

tbro-import annotation_mapman --organism_id 13\
 --release 1.CasaPuKu mercator.results_min1500.txt
```

Expression Counts

Now we have all kinds of annotation for each transcript in the TBro so we can start with the fun part. Expression data and differential expression data in particular are the main prospects why we perform RNASeq experiments. So go ahead and download the SRA files listet above.

```
mkdir -p ../../samples
cd ../../samples

/path/to/sratoolkit/bin/fastq-dump *
```

In the samples directory we now have a `.fq` file for each downloaded `.sra` file. The SRA files are no longer required so you can delete them to save some space. The next step is the quantification by mapping the reads onto the transcripts. This quantification is done separately for each sample in the for loop:

```
rsem-prepare-reference cannabis_sativa_transcriptome.fasta\
 cannabis_sativa_transcriptome

for SAMPLE in *.fq
do
```

```
BASE=$(basename $SAMPLE .fq)
rsem-calculate-expression -p 4 $SAMPLE cannabis_sativa_transcriptome\
 $BASE >$BASE.log 2>$BASE.err
done
```

The results for each sample are aggregated into a single large table with the perl script `aggregator_Count.pl`.

```
perl aggregator_CountMat.pl --in_RSEM\
 SRR306868.isoforms.results SRR306869.isoforms.results\
 SRR306870.isoforms.results SRR306875.isoforms.results\
 SRR306885.isoforms.results SRR306886.isoforms.results\
 SRR306861.isoforms.results SRR306862.isoforms.results\
 SRR306863.isoforms.results\
 --labels_RSEM Flower.mature_L1 Flower.mature_L2 Flower.mature_L3\
 Leaf.mature_L1 Leaf.mature_L2 Leaf.mature_L3\
 Root.entire_L1 Root.entire_L2 Root.entire_L3\
 --out rsem_aggregated.mat
```

The resulting table could be imported into TBro as it is. However the data is not normalized yet. You should always(!) normalize your expression data. One way to do that is using the `DESeq` R-package provided by `Bioconductor`. So fire up `R` and install `DESeq` if you don't already have it. As we use `DESeq` also to create the differential expression data we will already do that and use the results in the next section.

```
# installing and loading DESeq
source("http://bioconductor.org/biocLite.R")
biocLite("DESeq")
library(DESeq)
# loading the expression data
cmat <- read.table(file="rsem_aggregated.mat", row.names=1, header=T)
cond <- sub("_L.*","",colnames(cmat))
# TMM normalization
cds <- newCountDataSet(round(cmat),cond)
cds <- estimateSizeFactors(cds)
write.table(file="rsem_aggregated_TMM.mat", counts(cds,normalized=T),
 quote=F, sep="\t")

# differential expressions
cds <- estimateDispersions(cds)
res.FvsR <- na.omit(nbinomTest(cds,"Flower","Root"))
res.FvsL <- na.omit(nbinomTest(cds,"Flower","Leaf"))
res.RvsL <- na.omit(nbinomTest(cds,"Root","Leaf"))
write.csv(res.FvsL, file="rsem_aggregated_TMM_diff_FvsL.mat", quote=F)
write.csv(res.FvsR, file="rsem_aggregated_TMM_diff_FvsR.mat", quote=F)
write.csv(res.RvsL, file="rsem_aggregated_TMM_diff_RvsL.mat", quote=F)
```

So now we have the expression counts in the file `rsem_aggregated_TMM.mat`. This file just lacks the header for the first column so we add it with the following command:

```
sed -i '1{s/^/ID\t/}' rsem_aggregated_TMM.mat
```

Before we can go ahead and import the data into TBro we have to make some preparations. Normally RNASeq experiments are performed on biomaterials in different conditions. To differentiate between biological signals and random noise it is mandatory to have replicates for each condition. Each replicate is called a sample. This hirarchical structure of biomaterial → condition → sample is also represented in the TBro. So lets tell TBro about our samples:

```
# Prepare database for Expression Data Import
# Add missing biomaterials (Flower and Root are already present)
```

```
tbro-db biomaterial insert --name Flower
tbro-db biomaterial insert --name Leaf
tbro-db biomaterial insert --name Root

# Add conditions
tbro-db biomaterial add_condition --name Flower.mature\
 --parent_biomaterial_name Flower
tbro-db biomaterial add_condition --name Leaf.mature\
 --parent_biomaterial_name Leaf
tbro-db biomaterial add_condition --name Root.entire\
 --parent_biomaterial_name Root

# Add samples
tbro-db biomaterial add_condition_sample --name Flower.mature_L1\
 --parent_condition_name Flower.mature
tbro-db biomaterial add_condition_sample --name Flower.mature_L2\
 --parent_condition_name Flower.mature
tbro-db biomaterial add_condition_sample --name Flower.mature_L3\
 --parent_condition_name Flower.mature
tbro-db biomaterial add_condition_sample --name Leaf.mature_L1\
 --parent_condition_name Leaf.mature
tbro-db biomaterial add_condition_sample --name Leaf.mature_L2\
 --parent_condition_name Leaf.mature
tbro-db biomaterial add_condition_sample --name Leaf.mature_L3\
 --parent_condition_name Leaf.mature
tbro-db biomaterial add_condition_sample --name Root.entire_L1\
 --parent_condition_name Root.entire
tbro-db biomaterial add_condition_sample --name Root.entire_L2\
 --parent_condition_name Root.entire
tbro-db biomaterial add_condition_sample --name Root.entire_L3\
 --parent_condition_name Root.entire
```

Also the experiments and analyses should be traceable. So we also have to include information about the experiment and the different steps in the analysis. Also the person who performed the analyses has to be specified:

```
# Add contact
tbro-db contact insert --name TBroDemo --description 'TBro Demo User'
# New item ID is 5.

#Add experiments
tbro-db assay insert --name SRX082027 --operator_id 4
# New item ID is 1.

# Add acquisitions (corresponding to experiments)
tbro-db acquisition insert --name SRX082027 --assay_id 1
# New item ID is 1.

# Add analyses
tbro-db analysis insert --name RSEM_TMM --program RSEM\
 --programversion 1.2.5 --sourcename Mapping\
 --description 'RSEM quantification with subsequent TMM normalization'
# New item ID is 50.
tbro-db analysis insert --name DESeq_isoform --program DESeq\
 --programversion 1.12.1 --sourcename Mapping_isoform
# New item ID is 51.

# Add quantifications
tbro-db quantification insert --name RSEM_SRX082027\
```

```
 --acquisition_id 1 --analysis_id 50
# New item ID is 1.
```

So we have created a contact, assay, acquisition, quantification and two analyses. Warning: It is important to use the right IDs. Those may differ in your case so carefully watch the output of each command and note the ID given. If you forget an ID you can always have a list of all available entries by issuing:

```
tbro-db <subcommand> list
```

After a lot of groundwork we are finaly there. Import the expression counts with this command:

```
tbro-import expressions -o 13 -r 1.CasaPuKu -q 1 -a 50\
 rsem_aggregated_TMM.mat
```

Differential Expression

Differential expression is the comparison of the expressions in two different conditions. When calculating differential expressions statistical methods are applied to correct for the multiple testing problem. We have already performed this analysis in the previous section. So if you have skipped the Expression section you have to use the R snippet there. We also already created the biomaterials, conditions, analyses, etc. Therefor we can go ahead and import the differential expression results:

```
tbro-import differential_expressions -o 13 -r 1.CasaPuKu --analysis_id\
 51 -A Flower.mature -B Leaf.mature rsem_aggregated_TMM_diff_FvsL.mat
tbro-import differential_expressions -o 13 -r 1.CasaPuKu --analysis_id\
 51 -A Flower.mature -B Root.entire rsem_aggregated_TMM_diff_FvsR.mat
tbro-import differential_expressions -o 13 -r 1.CasaPuKu --analysis_id\
 51 -A Root.entire -B Leaf.mature rsem_aggregated_TMM_diff_RvsL.mat
```

Blast DB

To search the transcriptome by homology. Lets add a blast database. To do so we create a nucleotide database and a protein database and zip them:

```
makeblastdb -in cannabis_sativa_transcriptome.fasta -dbtype nucl
makeblastdb -in cannabis_sativa_predpep.fasta -dbtype prot
zip cannabis_sativa_transcriptome.zip cannabis_sativa_transcriptome.fasta*
zip cannabis_sativa_predpep.zip cannabis_sativa_predpep.fasta*
md5sum *.zip
# b2ab466c7bfb7d41c27a89cf40837fb4  cannabis_sativa_predpep.zip
# 1f87bbeee5a623e6d2f8cab8f68c9726  cannabis_sativa_transcriptome.zip
```

This zip files should now be moved in a location where it can be reached from the worker machines. To tell TBro about the `BLAST` databases you should issue the following command in your directory containing the TBro source code (`/home/tbro/` in the docker container, but in the docker installation phing has already been executed, so you can skip this step, in case you want to execute it again make sure to run `source ~/.bash_profile` first, otherwise `phing` will not be found.):

```
phing queue-install-db
```

This will create a file called `queue_config.example.sql` in the current directory. Rename it to `queue_config.sql` and adjust the appropriate sections like this:

```
...

-- database files available. name is the name it will be referenced by, md5 is the␣
↪zip file's sum, download_uri specifies where the file can be retreived
INSERT INTO database_files
 (name, md5, download_uri) VALUES
 ('cannabis_sativa_transcriptome.fasta', '1f87bbeee5a623e6d2f8cab8f68c9726',
 'http://yourdomain/location/cannabis_sativa_transcriptome.zip'),
 ('cannabis_sativa_predpep.fasta', 'b2ab466c7bfb7d41c27a89cf40837fb4',
 'http://yourdomain/location/cannabis_sativa_predpep.zip');

-- contains information which program is available for which program.
-- additionally, 'availability_filter' can be used to e.g. restrict use for a␣
↪organism-release combination
INSERT INTO program_database_relationships
 (programname, database_name, availability_filter) VALUES
 ('blastn','cannabis_sativa_transcriptome.fasta', '13_1.CasaPuKu'),
 ('blastp','cannabis_sativa_predpep.fasta', '13_1.CasaPuKu'),
 ('blastx','cannabis_sativa_predpep.fasta', '13_1.CasaPuKu'),
 ('tblastn','cannabis_sativa_transcriptome.fasta', '13_1.CasaPuKu'),
 ('tblastx','cannabis_sativa_transcriptome.fasta', '13_1.CasaPuKu');

...
```

It is important that the name column in `database_files` matches the base filename of the blast database in the zip file.

The `availability_filter` column is very important it specifies for which organism and release the database is visible in the TBro interface. The form is `{organism_id}_{release}`. As we only have a single organism (id: 13) and release (1.CasaPuKu) we set it to `13_1.CasaPuKu`. If you want a single database to show up for multiple organisms or releases you have to specify multiple rows with different availability filters.

You have to specify a location that can be reached by your worker machine. If you just want to have a single worker on the same machine as the server you can specify the location in the local file system starting with `file://`. If you used the docker setup you can load the files into the docker ftp container with curl:

```
curl --data-binary --ftp-pasv --user $WORKERFTP_ENV_FTP_USER:$WORKERFTP_ENV_FTP_PW -T␣
↪cannabis_sativa_transcriptome.zip ftp://"$WORKERFTP_PORT_21_TCP_ADDR"/
curl --data-binary --ftp-pasv --user $WORKERFTP_ENV_FTP_USER:$WORKERFTP_ENV_FTP_PW -T␣
↪cannabis_sativa_predpep.zip ftp://"$WORKERFTP_PORT_21_TCP_ADDR"/
```

To perform the changes run the `queue_config.sql` commands in your queue database:

```
PGPASSWORD=$WORKER_ENV_DB_PW psql -U $WORKER_ENV_DB_USER -h $WORKER_PORT_5432_TCP_
↪ADDR -p $WORKER_PORT_5432_TCP_PORT <queue_config.sql
```

Now TBro knows about the database and shows it in the web interface.

To perform `BLAST` searches we need a worker to execute them. In case of the docker setup you already have a blast worker running. Otherwise you can create one with this command:

```
phing queue-build-worker
unzip unix-worker.zip
```

Modify the `config.php` to your needs. Most values should be preconfigured through your `build.properties`. After that you can start the worker (preferably in a screen):

```
screen -S blastworker
./worker.php config.php
```

Have fun blasting.

Synonym / Publication

Synonyms and publications can be added using the API key and internal name of your bibsonomy account. The structure of such a command is as follows:

```
tbro-db feature add_synonym -f 555 --synonym 'InterestingTranscript'\
 -b '[[publication/1adaa3fb03xxxxxxxxxxxxxaec4cef920/bibsonomy_username]]'
 -u 'bibsonomy_username' -t symbol -k 34a2149d8xxxxxxxxxxxxxbebd342aa
```

Pathways

To use TBros pathway feature we have to connect the imported data to pathways. As of now this connection is made via EC numbers and KEGG pathways. We have to import two tables containing descriptions for EC and KEGG identifiers in the simple formatL:

```
<Identifier><TAB><Description>
```

Additionally a mapping of which EC occurs in each KEGG pathway is required in the following format:

```
<EC number><TAB><KEGG ID>
```

We collected EC and KEGG information from ENZYME, Interpro and priam to get the descriptions and mapping. The resulting tables may not be complete and up to date so you might wish to create your own tables and mapping. For a quick start you find the three files `ec_info.tab`, `kegg_info.tab` and `ec_kegg_map.tab`

```
tbro-tools addECInformationToDB ec_info.tab
tbro-tools addPathwayInformationToDB kegg_info.tab
tbro-tools addEC2PathwayMapping ec_kegg_map.tab
```

Custom Annotations

Arbitrary key/value pairs can be added to isoforms and unigenes since TBro version 1.1.1 All you need is a tsv file with two columns (unigene/isoform identifier and value). The key is given as a command-line parameter for the whole file. Consider the file `custom.tsv`:

```
<Identifier><TAB><Value>
```

Importing this file into TBro with key `my_custom_annotation` you have to execute:

```
tpro-import annotation_custom --annotation-type my_custom_annotation custom.tsv
```

It is then possible to search via annotation search for custom annotations with key `my_custom_annotation`.

Any other transcriptome

With the description above it should be easy for you to import any transcriptome that interests you. The only thing that could differ significantly from the description above is if you have predicted unigenes for your transcriptome. This is common practice and if you use a de novo transcriptome assembler like `Trinity` you will get unigenes with corresponding isoforms. In this case the main difference is in the first step importing ids. Instead of importing a plain list of sequence IDs you import a map of the following format:

```
<Unigene ID><TAB><Isoform ID>
```

With a separate line for each isoform. The import command would then be:

```
tbro-import sequence_ids --organism_id 14 --release 1.0\
 --file_type map my_new_transcriptome.map
```

Of course you have to adjust the organism_id and release parameters. The use of unigenes brings a number of advantages. You can easily find isoforms that belong to the same unigene as each isoform contains a connection to its parent and on the unigene page you have a list of all corresponding isoforms. In addition you can now load expression and differential expression results on unigene level as well as on isoform level. Many programs like RSEM can readily handle that.

Exploring the imported Data

Feature annotations

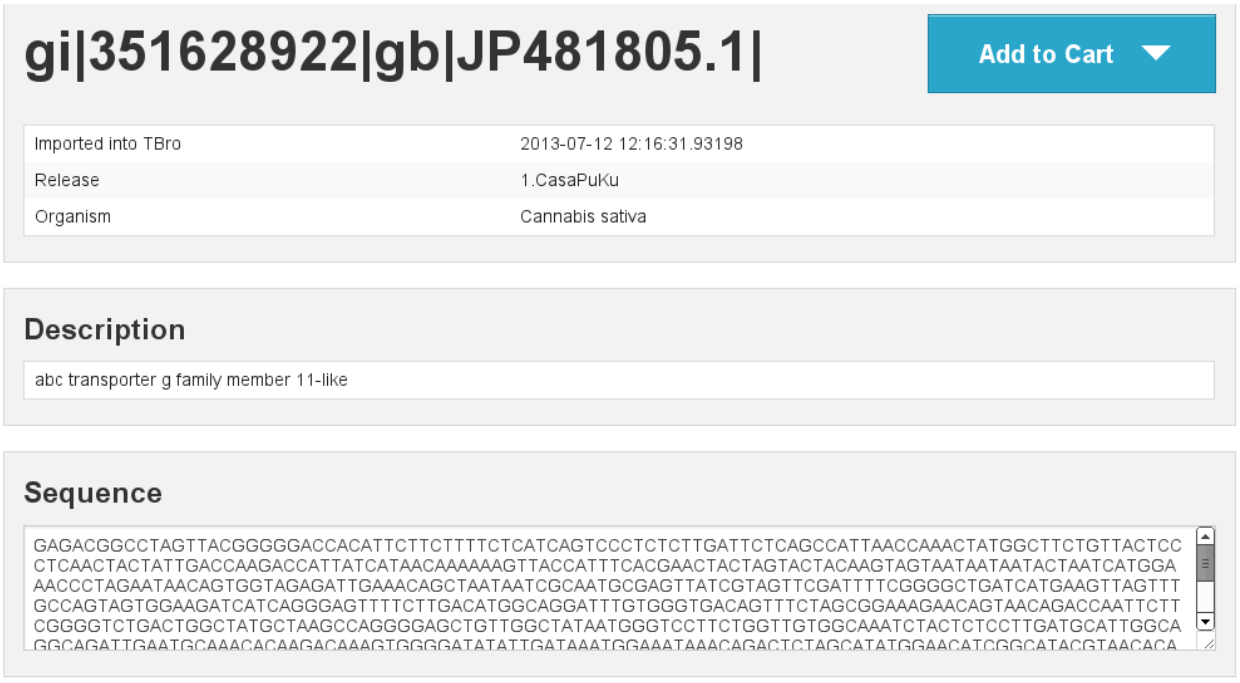


Fig. 1.1: Basic information

[fig:basic]

[fig:annotation]

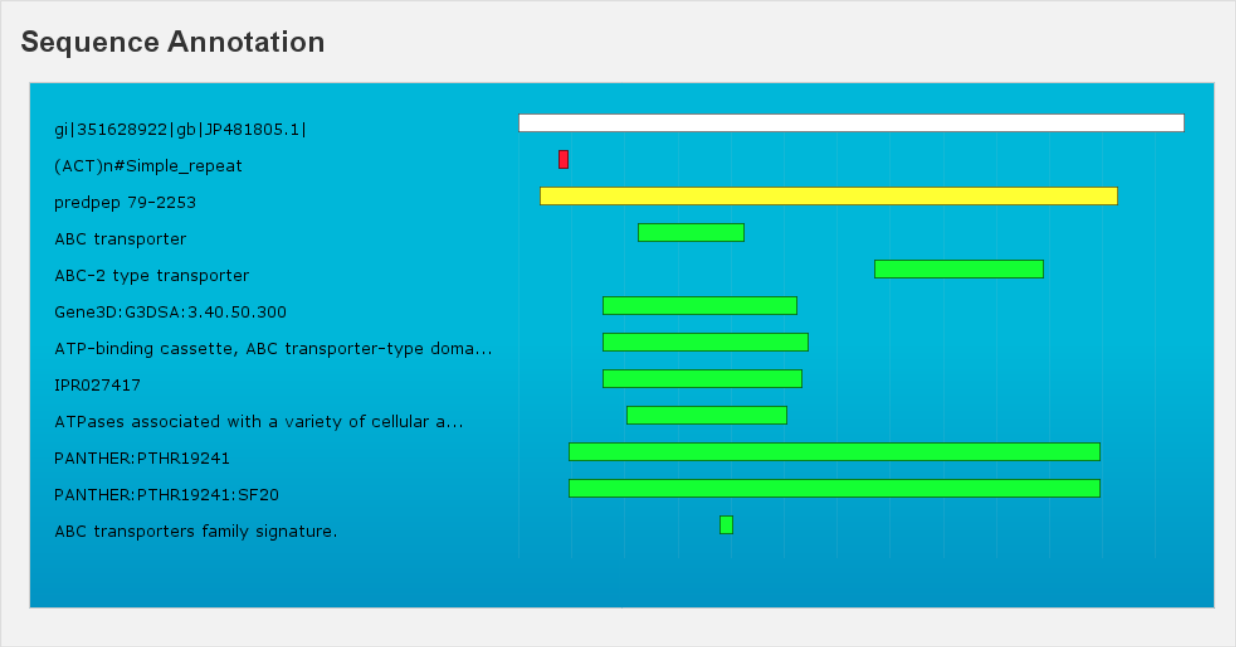


Fig. 1.2: Sequence Annotation

[fig:predpep]

[fig:go]

[fig:ec]

[fig:mapman]

[fig:repeatmasker]

Expressions

[fig:barplot:sub:*i*so]

[fig:barplot:sub:*c*art]

Differential Expressions

[fig:diffexp]

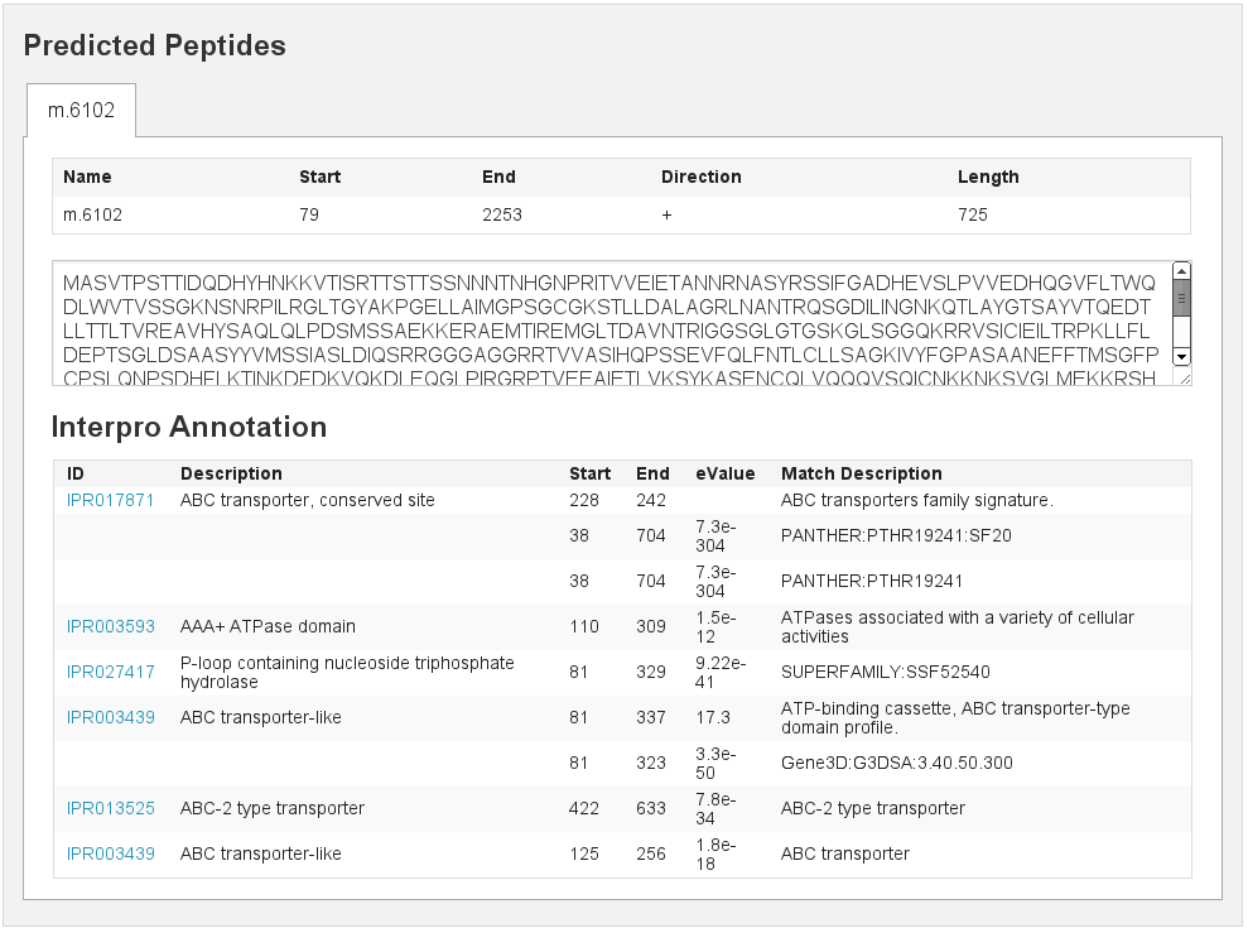
[fig:diffexp:sub:*r*esults]

Carts

[fig:carts]

Pathways

[fig:pathway]



Predicted Peptides

m.6102

Name	Start	End	Direction	Length
m.6102	79	2253	+	725

MASVTPSTTIDQDHYHNKKVTISRTTSTTSSNNNTNHGNPRITVVEIETANNRNASYRSSIFGADHEVSLPVVEDHQGVFLTWQ
DLWVTVSSGKNSNRPILRGLTGYAKPGELLAIMGPSGCGKSTLLDALAGRLNANTRQSGDILINGNKQTLAYGTSAYVTQEDT
LLTTLTVREAVHYSAQLQLPDSMSSAEKKERAEMTIREMGLTDAVNTRIGGSGLGTGSKGLSGGQKRRVSICIEILTRPKLLFL
DEPTSGLDSAASYYVMSSIASLDIQSRRGGGAGGRRTVVASIHQPSSEVFQLFNTLCLLSAGKIVYFGPASAANEFFTMSGFP
CPSLQNPSDHFLKTINKDFDKVQKDLEQGLPIRGRPTVFEAIFTLVKSYKASENCQLVQQQVSQICNKKNKSVGLMFKKRSH

Interpro Annotation

ID	Description	Start	End	eValue	Match Description
IPR017871	ABC transporter, conserved site	228	242		ABC transporters family signature.
		38	704	7.3e-304	PANTHER:PTHR19241:SF20
		38	704	7.3e-304	PANTHER:PTHR19241
IPR003593	AAA+ ATPase domain	110	309	1.5e-12	ATPases associated with a variety of cellular activities
IPR027417	P-loop containing nucleoside triphosphate hydrolase	81	329	9.22e-41	SUPERFAMILY:SSF52540
IPR003439	ABC transporter-like	81	337	17.3	ATP-binding cassette, ABC transporter-type domain profile.
		81	323	3.3e-50	Gene3D:G3DSA:3.40.50.300
IPR013525	ABC-2 type transporter	422	633	7.8e-34	ABC-2 type transporter
IPR003439	ABC transporter-like	125	256	1.8e-18	ABC transporter

Fig. 1.3: Predicted peptids

Gene Ontology

Molecular Function

GO:0005524 ATP binding

GO:0016887 ATPase activity

Biological Process

GO:0006200 ATP catabolic process

Cellular Component

GO:0016020 membrane

Fig. 1.4: GO

Fig. 1.5: EC

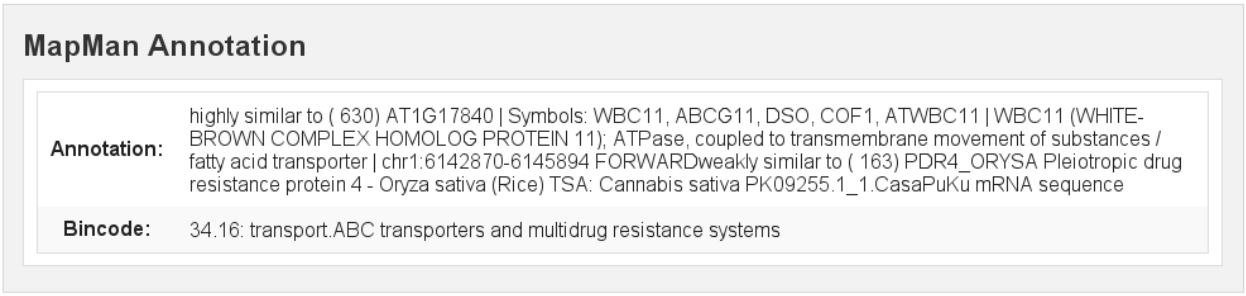


Fig. 1.6: Mapman Mercator

Fig. 1.7: RepeatMasker

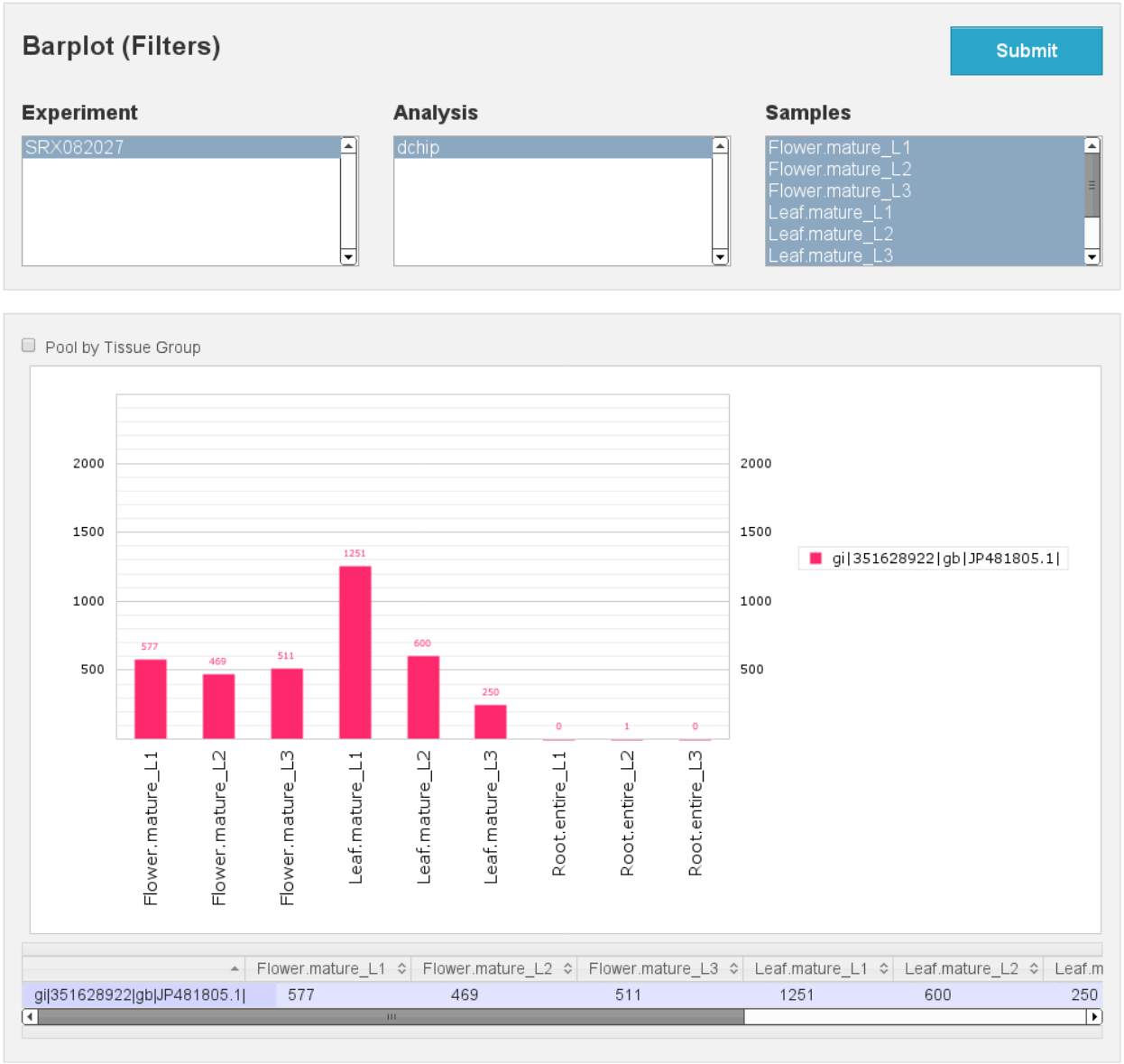


Fig. 1.8: Expression Barplot for a single Isoform

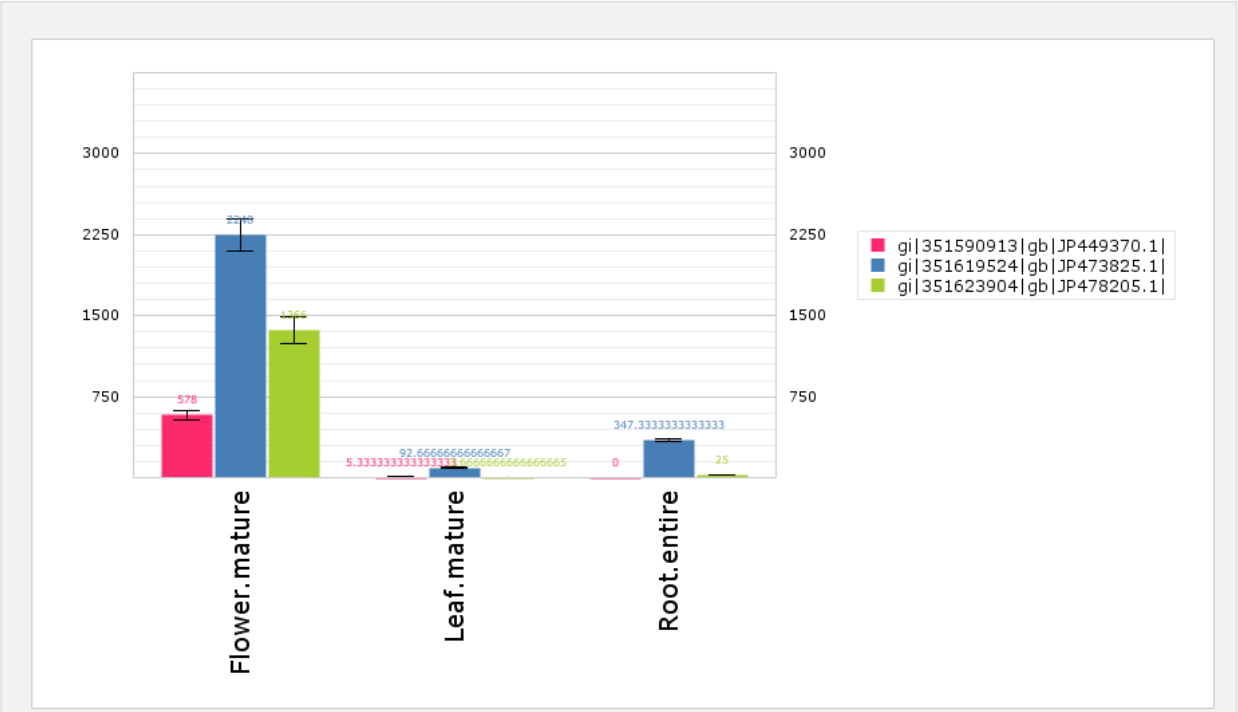


Fig. 1.9: Expression Barplot for all isoforms in a cart

Searches

[fig:combisearch]

[fig:multisearch]

Blast

[fig:blast]

[fig:blast:sub:*r*esults$_1$]

[fig:blast:sub:*r*esults$_2$]

Guides

Backup data

Backup your database with these commands:

```
docker exec Chado_DB_4_TBro_official pg_dump -U tbro -d chado | xz >tbro_backup_
↪$(date +%F_%T).sql.xz
docker exec Worker_DB_4_TBro_official pg_dump -U worker -d worker | xz >worker_backup_
↪$(date +%F_%T).sql.xz
```

You should keep a copy of you blast *.zip* files as well.

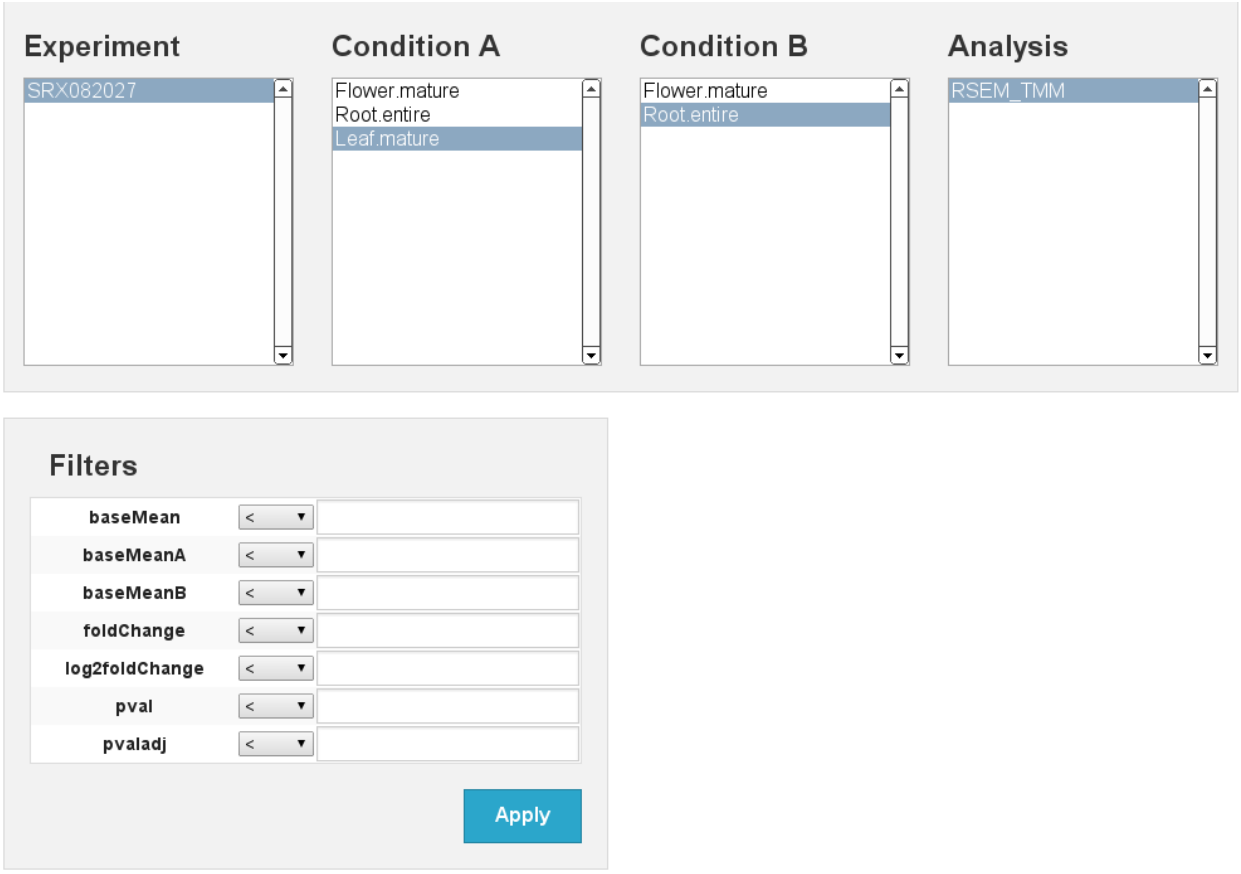


Fig. 1.10: Differential expression

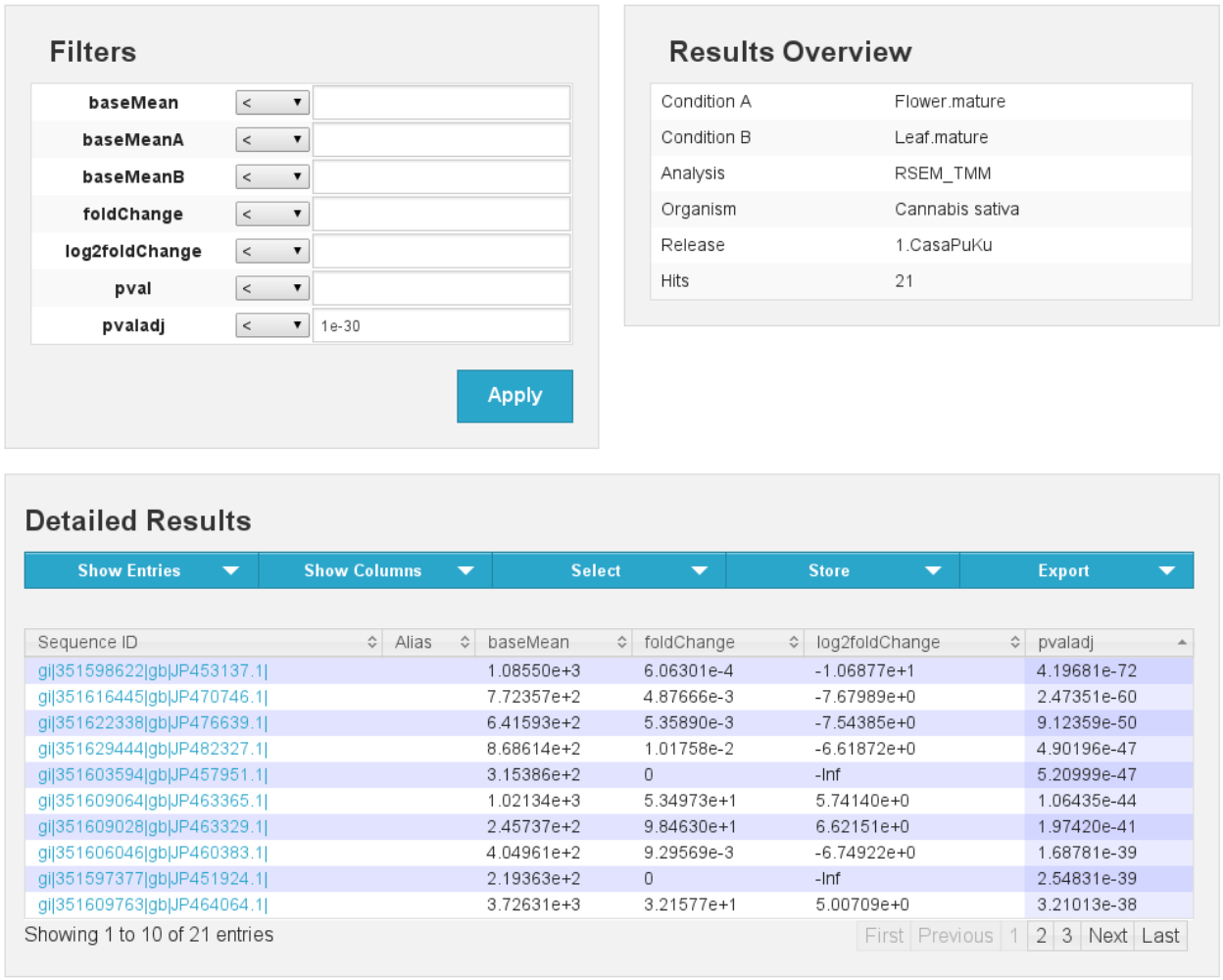
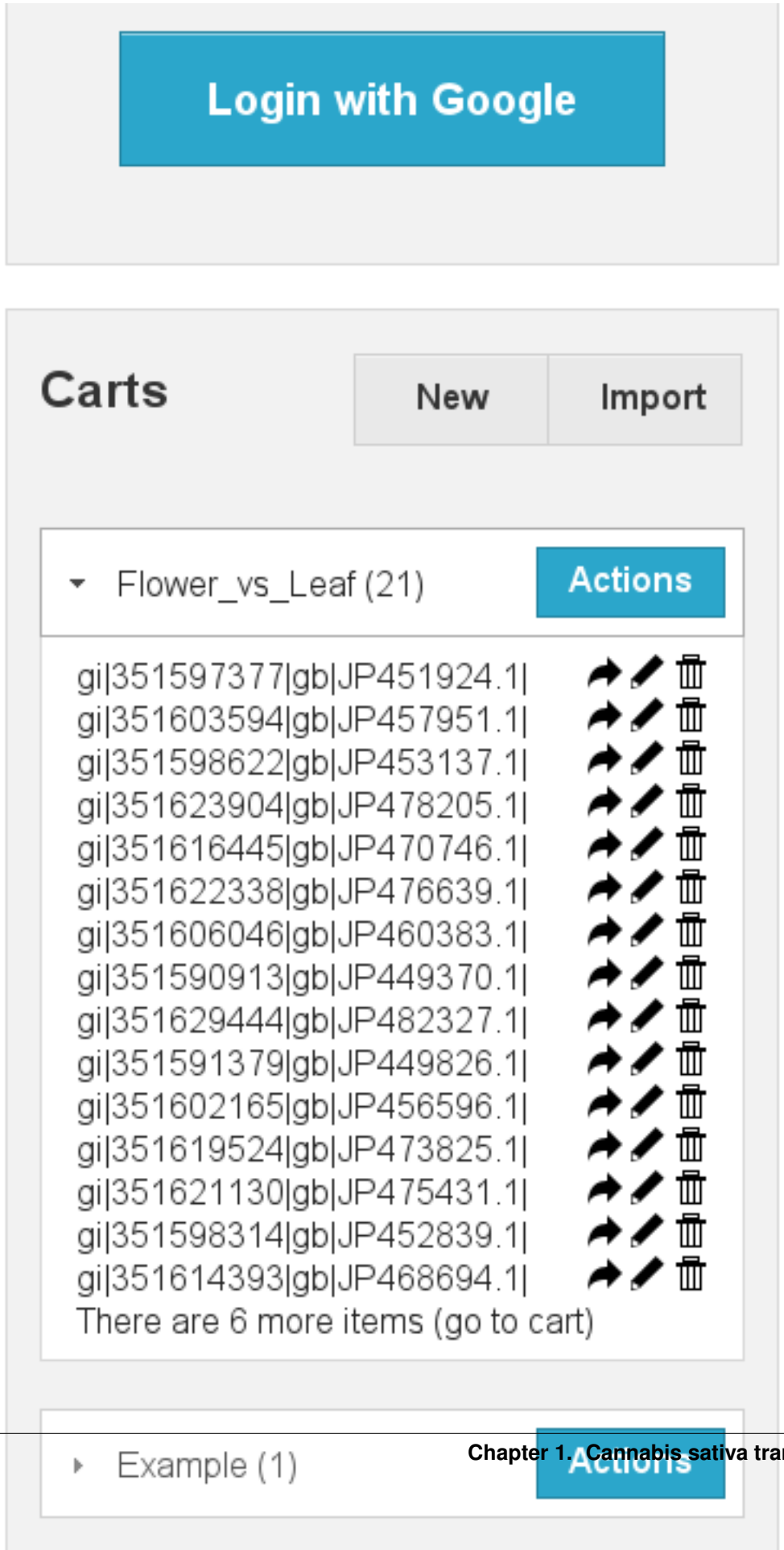


Fig. 1.11: Differential expression results Flower vs Leaf


Login with Google
Carts
New
Import
Flower_vs_Leaf (21)
Actions
gi|351597377|gb|JP451924.1|
gi|351603594|gb|JP457951.1|
gi|351598622|gb|JP453137.1|
gi|351623904|gb|JP478205.1|
gi|351616445|gb|JP470746.1|
gi|351622338|gb|JP476639.1|
gi|351606046|gb|JP460383.1|
gi|351590913|gb|JP449370.1|
gi|351629444|gb|JP482327.1|
gi|351591379|gb|JP449826.1|
gi|351602165|gb|JP456596.1|
gi|351619524|gb|JP473825.1|
gi|351621130|gb|JP475431.1|
gi|351598314|gb|JP452839.1|
gi|351614393|gb|JP468694.1|
There are 6 more items (go to cart)
Example (1)
Actions

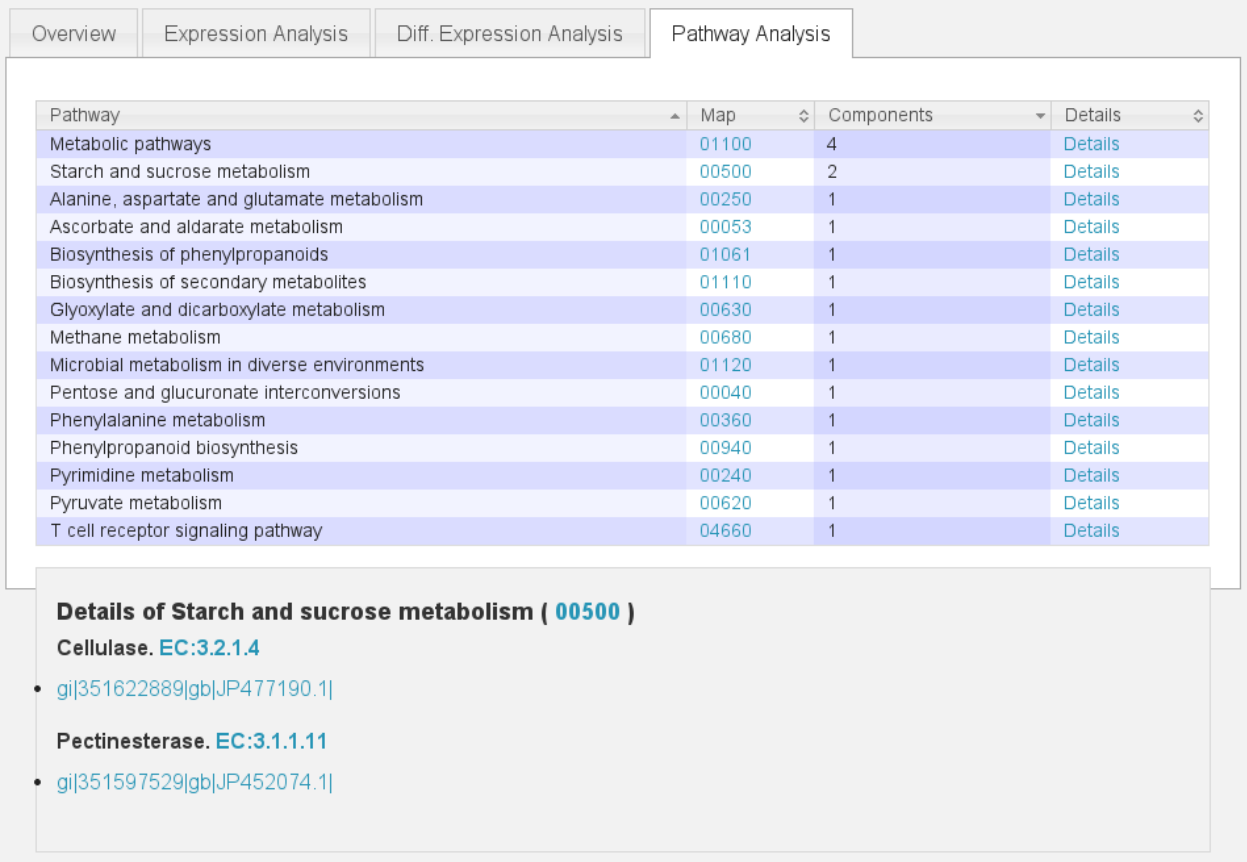


Fig. 1.13: List of Pathways in the cart

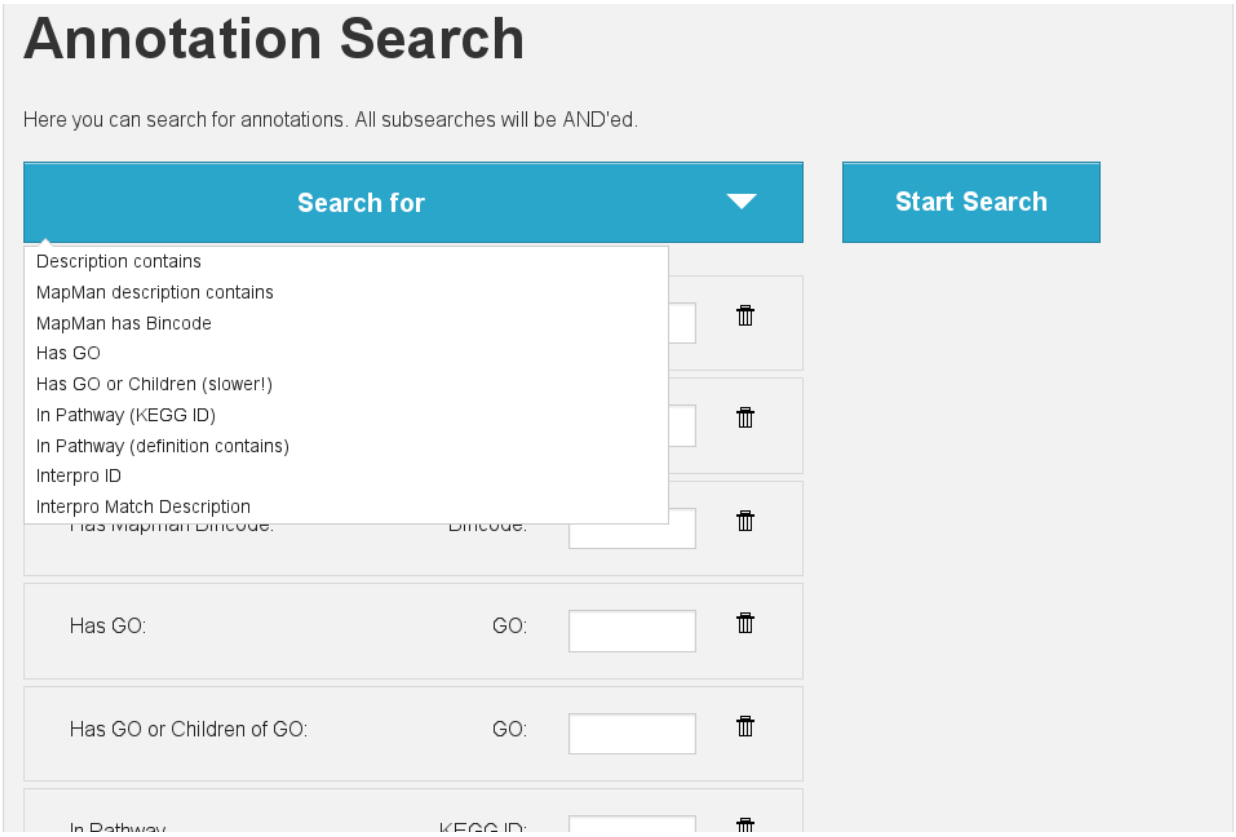


Fig. 1.14: Combisearch

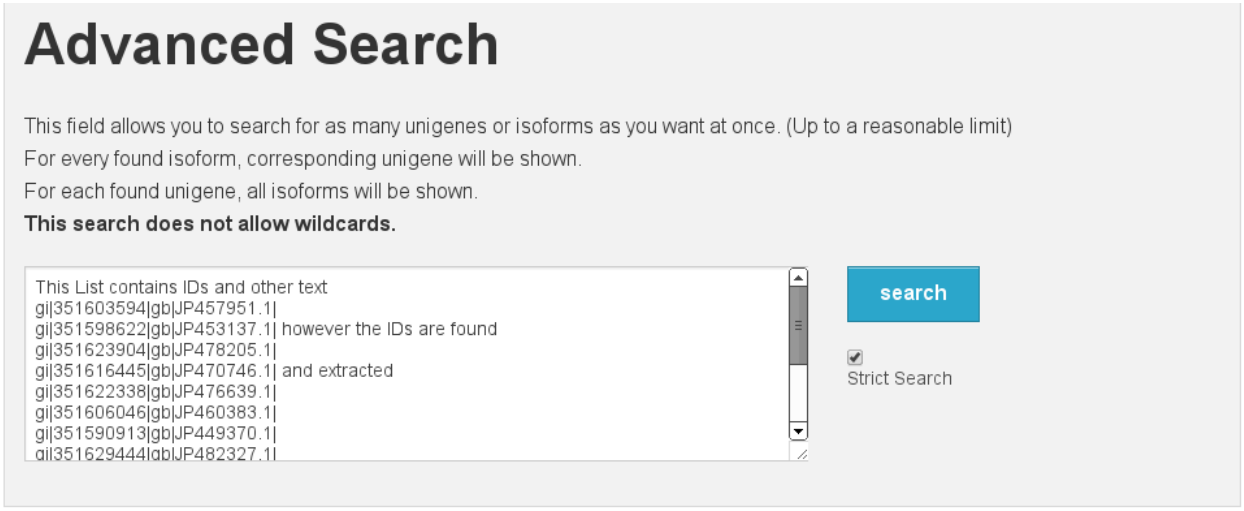


Fig. 1.15: Multisearch

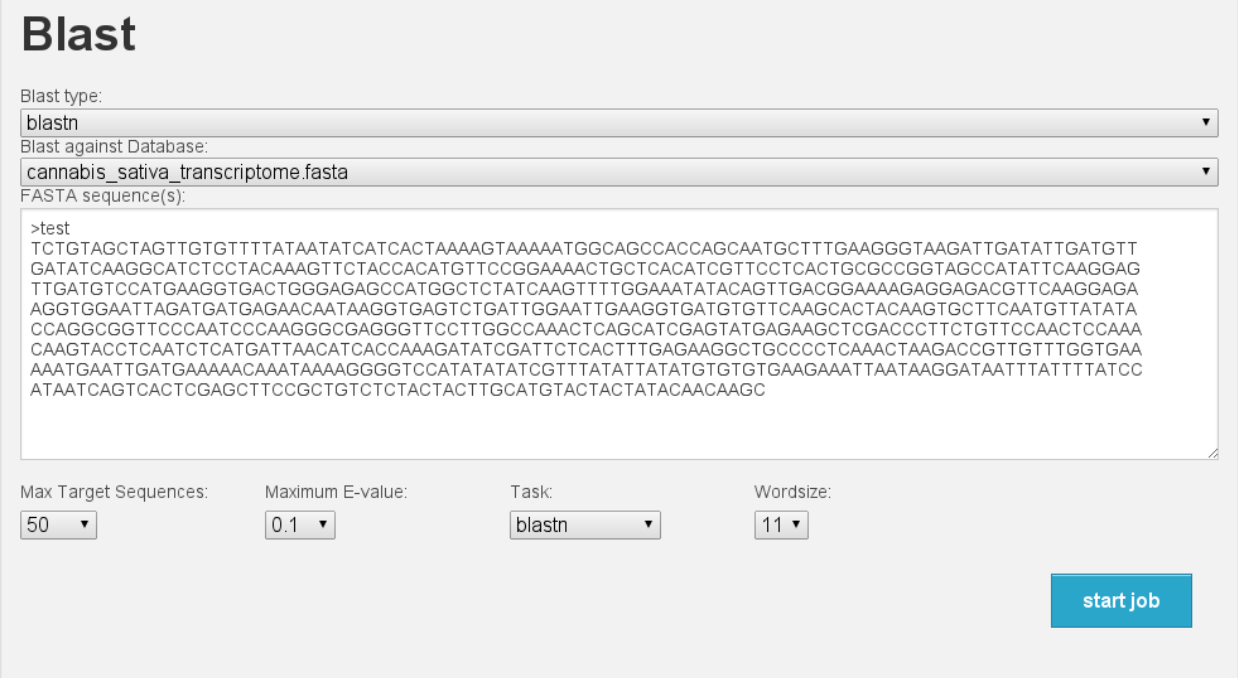


Fig. 1.16: Blast interface

Upgrade TBro

If you want to upgrade TBro to a new version (running docker) you have two options.

1. Replace the `tbro_apache` container
2. Upgrade in the existing container

Attention: Those methods will allow you to keep your databases and all of its content. However, before you upgrade check for breaking changes in the Changes section of the README. And always backup your data. You should do this regularly anyway but especially before performing an upgrade.

Choose option 1 if you did not modify anything inside the `tbro_apache` container. Just execute the following commands:

```
docker stop TBro_official
docker rm TBro_official
docker pull tbroteam/tbro_apache
docker run -d --link Chado_DB_4_TBro_official:CHADO --link Worker_FTP_4_TBro_
↪official:WORKERFTP --link Worker_DB_4_TBro_official:WORKER --name "TBro_official" -
↪p 80:80 tbroteam/tbro_apache
docker exec -i -t TBro_official /home/tbro/build_installation.sh
```

For option 2 follow these steps:

```
docker exec -it TBro_official /bin/bash
# inside the container
source ~/.bash_profile
cd /home
git clone https://github.com/TBroTeam/TBro.git
```

Fig. 1.17: Blast results

id	max score	total score	coverage	evalue	max identity
gi|351616445|gb|JP470746.1|	1402	1402	1.000	0	1.000
gi|351597369|gb|JP451917.1|	100	100	0.164	7.688e-18	0.774

Score	91 bits (100)
Expect	7.688e-18
Identities	89/115
Positives	89/115
Gaps	0/115
Query Frame	1
Hit Frame	1

```
Query    184 TTGATGTCCATGAAGGTGACTGGGAGAGCCATGGCTCTATCAAGTTTTGGAAATATACAGTTGACGGAAAAGAGGAGACGTTCAAGGAGAAGGTGGAATT 283
             ||||||| |||||||||||||||||| |  | ||||||| ||||| | ||||| ||||   | |  || || | ||||||| || ||||| || |||||  |
Subject  198 TTGATGTTCATGAAGGTGACTGGGAAACACCTGGCTCTGTCAAGCTCTGGAAGTATAACATCGGTGGGAAGGTGGAGACATTTAAGGAAAAAGTGGATGT 297

Query    284 AGATGATGAGAACAA                                                                              298
             ||||||| |||||
Subject  298 GGATGATGAAAACAA                                                                              312
```

gi|351622068|gb|JP476369.1|	46	46	0.104	0.003	0.726
gi|351607452|gb|JP461773.1|	44	44	0.039	0.012	0.926
gi|351622701|gb|JP477002.1|	44	44	0.057	0.012	0.825

Showing 1 to 5 of 5 entries

Fig. 1.18: Blast results

```
# you now have tbro (old) and TBro (new) in /home
cd TBro
# git checkout <branch> # if you want a specific branch instead of master
cp ../tbro/build.properties .
phing cli-install
phing web-install
phing database-update-modifications
```

Password protect TBro

See the write up by 000generic at https://github.com/TBroTeam/TBro/issues/48

TBro in Docker in Amazon's AWS Lightsail

Follow this protocol: https://benchling.com/s/prt-DHSo7HeddC5zM0x7x1Y4