1. Where the data 'lives' for each type of stock

Data is stored attached to alleles and is shown in the 'Nature of the Allele' section of the allele report

- RNAi alleles
  - data is in **mutagen** field on allele report
  - all alleles have mutagen 'in vitro construct – RNAi'

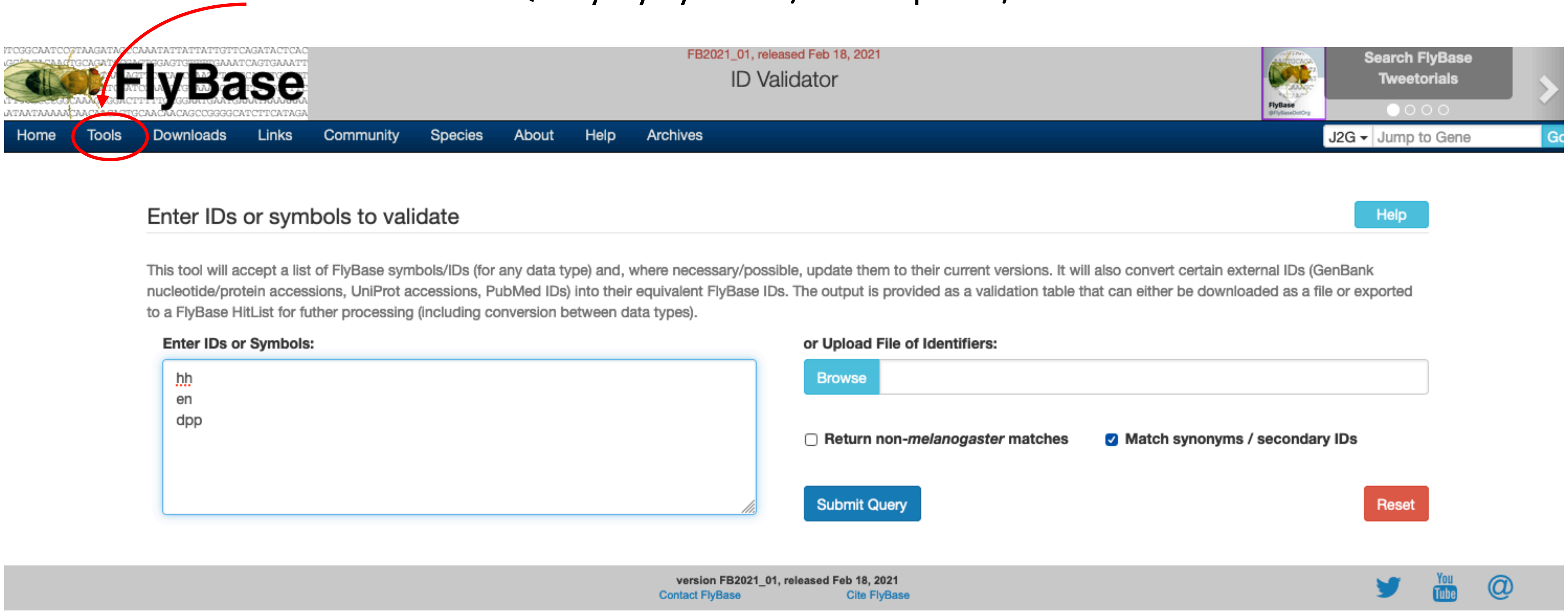
- CRISPR allele
  - data is in **mutagen** field on allele report
  - all allele have mutagen 'CRISPR/Cas9'

- UAS alleles
  - data is in **regulatory region(s)** field on allele report
  - all relevant alleles have UAS/UASt/UASp in this field
  - *most* alleles will have UAS as part of the superscripted part of the symbol
  - *note that this is filled in for* ***any*** *transgenic allele that is driven by UAS, so can include RNAi lines, or overexpression of non-wild type sequences*

2. put candidate gene list through ID Validator before starting

direct link: https://flybase.org/convert/id

Link from Blue NavBar: Tools->Query by symbols/IDs->Upload/Validate IDs



Enter IDs or symbols to validate

This tool will accept a list of FlyBase symbols/IDs (for any data type) and, where necessary/possible, update them to their current versions. It will also convert certain external IDs (GenBank nucleotide/protein accessions, UniProt accessions, PubMed IDs) into their equivalent FlyBase IDs. The output is provided as a validation table that can either be downloaded as a file or exported to a FlyBase HitList for futher processing (including conversion between data types).

Enter IDs or Symbols:

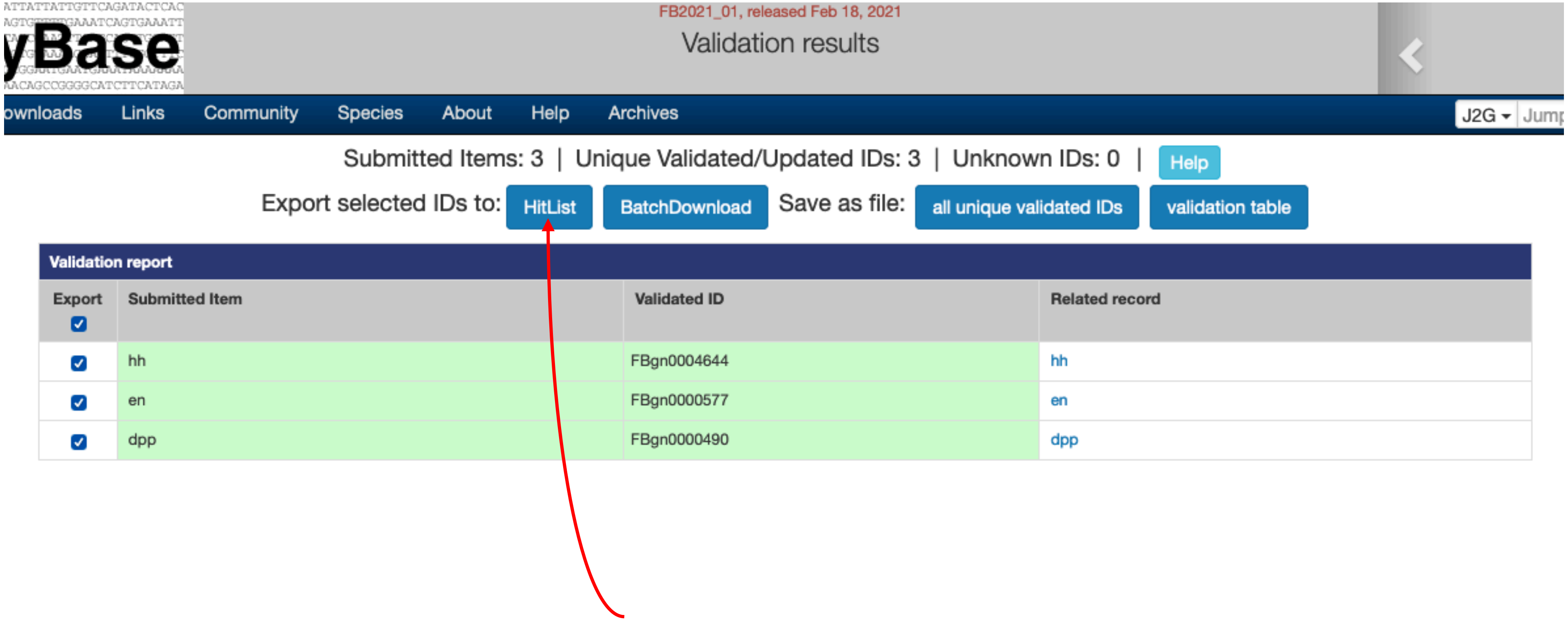
hh
en
dpp

or Upload File of Identifiers:

☐ **Return non-*melanogaster* matches** ☑ **Match synonyms / secondary IDs**

version FB2021_01, released Feb 18, 2021
Contact FlyBase Cite FlyBase

3. Turn your validated gene list into alleles



Validation results

Submitted Items: 3 | Unique Validated/Updated IDs: 3 | Unknown IDs: 0 |

Export selected IDs to: HitList BatchDownload Save as file: all unique validated IDs validation table

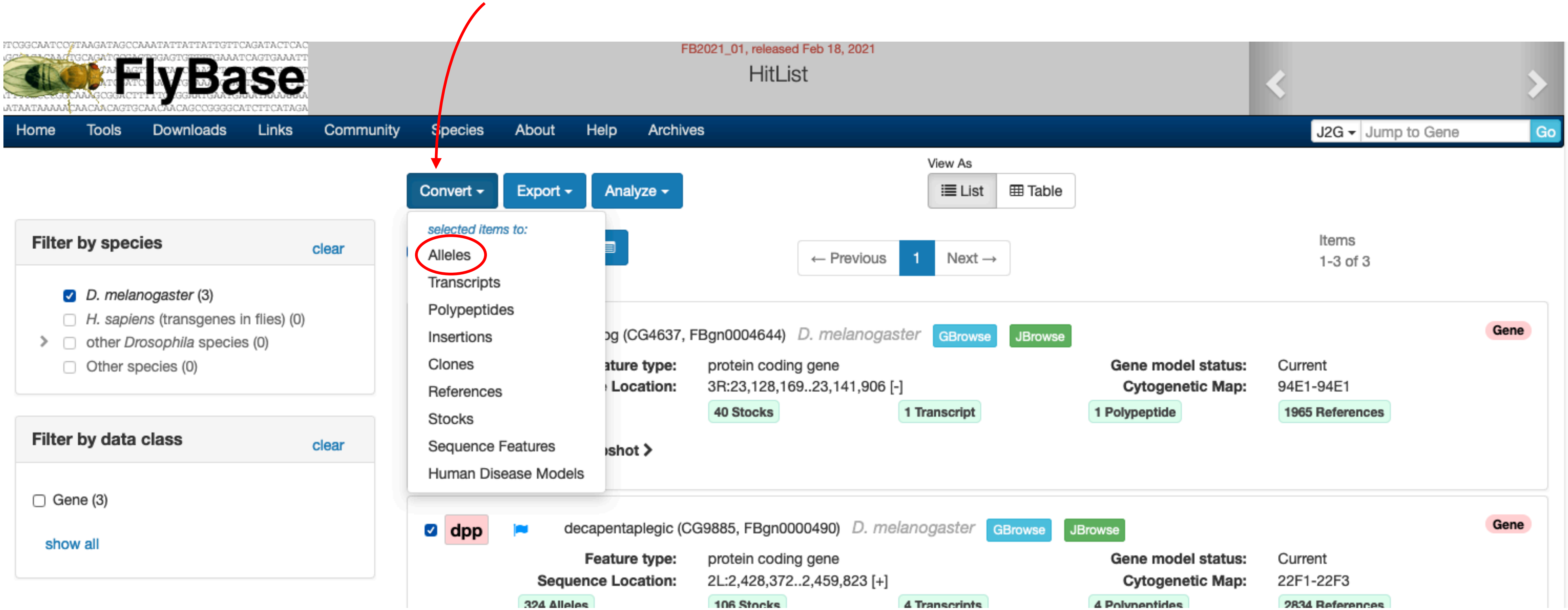
Validation report

Export ☑	Submitted Item	Validated ID	Related record
☑	hh	FBgn0004644	hh
☑	en	FBgn0000577	en
☑	dpp	FBgn0000490	dpp

1. Click on HitList in ID Validation results

3. Turn your validated gene list into alleles

2. Once on the HitList, use Convert button to change to alleles



Filter by species clear

☑ *D. melanogaster* (3)
☐ *H. sapiens* (transgenes in flies) (0)
☐ other *Drosophila* species (0)
☐ Other species (0)

Filter by data class clear

☐ Gene (3)

show all

og (CG4637, FBgn0004644) *D. melanogaster* GBrowse JBrowse **Gene**

ature type: protein coding gene **Gene model status:** Current
Location: 3R:23,128,169..23,141,906 [-] **Cytogenetic Map:** 94E1-94E1

40 Stocks **1 Transcript** **1 Polypeptide** **1965 References**

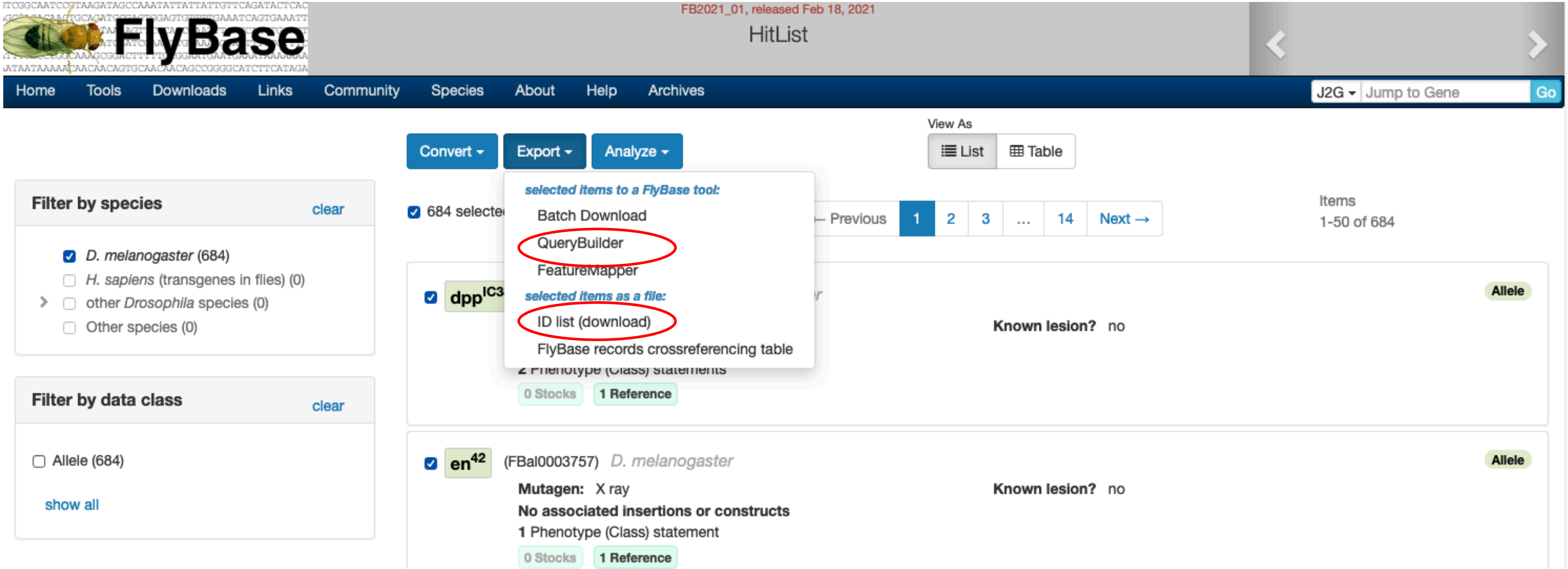
shot ›

☑ **dpp** decapentaplegic (CG9885, FBgn0000490) *D. melanogaster* GBrowse JBrowse **Gene**

Feature type: protein coding gene **Gene model status:** Current
Sequence Location: 2L:2,428,372..2,459,823 [+] **Cytogenetic Map:** 22F1-22F3

324 Alleles **106 Stocks** **4 Transcripts** **4 Polypeptides** **2834 References**

3. Turn your validated gene list into alleles



☑ **dpp**^{IC3}

Known lesion? no

2 Phenotype (Class) statements

0 Stocks 1 Reference

Allele

☑ **en**^{42} (FBal0003757) *D. melanogaster*

Mutagen: X ray

Known lesion? no

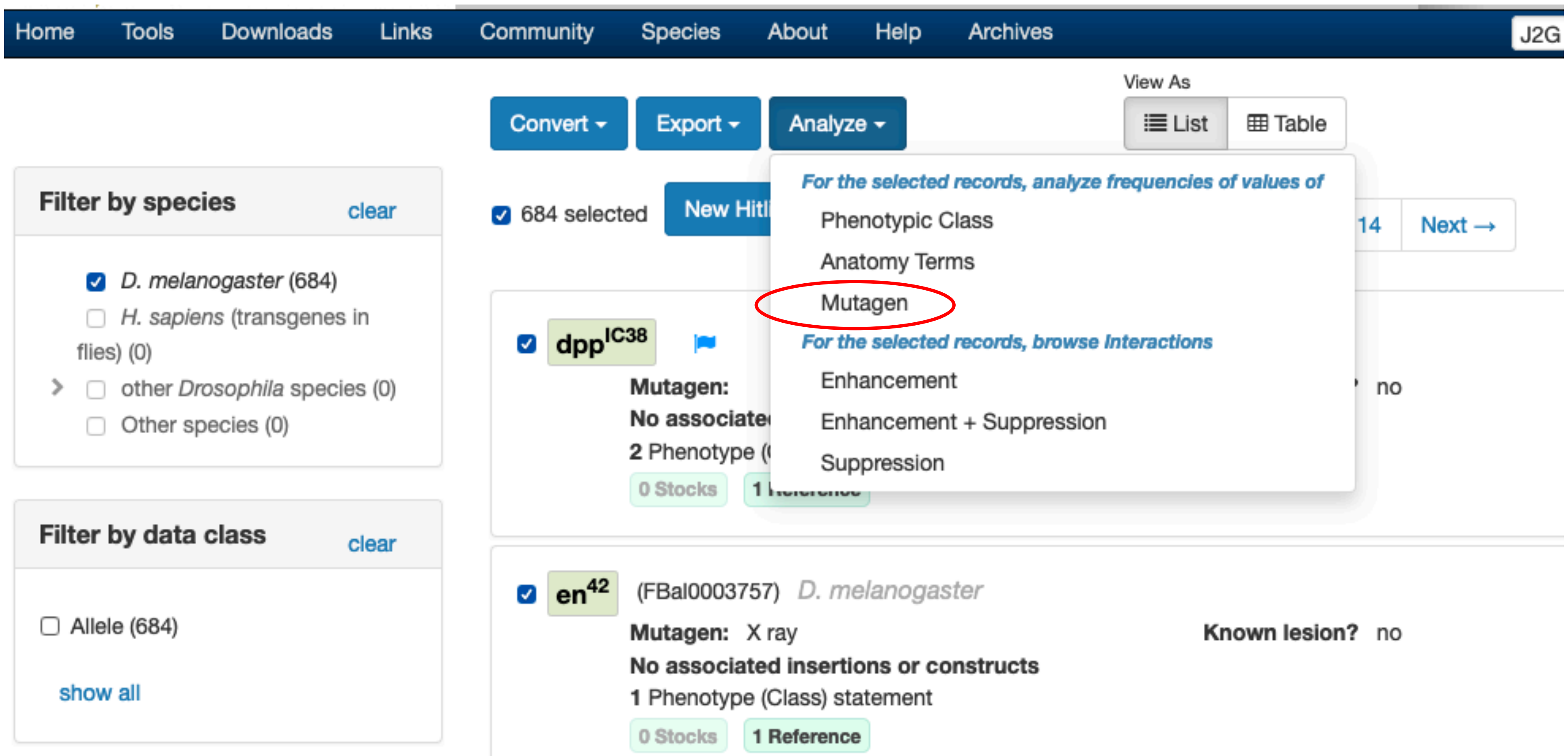
No associated insertions or constructs

1 Phenotype (Class) statement

0 Stocks 1 Reference

Allele

4. Trick for getting RNAi/CRISPR lines using the Analyze button



Filter by species

☑ *D. melanogaster* (684)
☐ *H. sapiens* (transgenes in flies) (0)
☐ other *Drosophila* species (0)
☐ Other species (0)

Filter by data class

☐ Allele (684)

☑ 684 selected

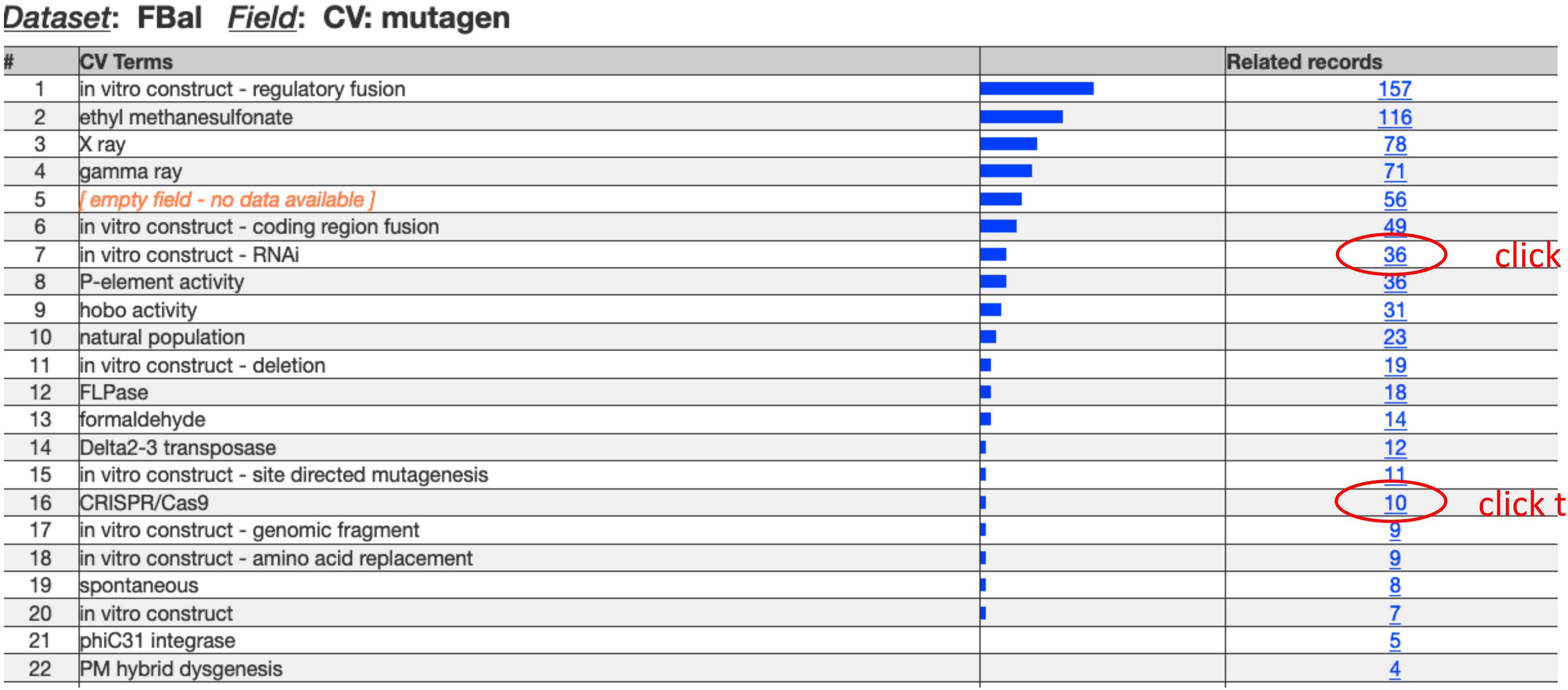
For the selected records, analyze frequencies of values of
- Phenotypic Class
- Anatomy Terms
- Mutagen

For the selected records, browse Interactions
- Enhancement
- Enhancement + Suppression
- Suppression

☑ **dpp^{IC38}**
Mutagen:
No associate
2 Phenotype (
no
0 Stocks
1

☑ **en^{42}** (FBal0003757) *D. melanogaster*
Mutagen: X ray
Known lesion? no
No associated insertions or constructs
1 Phenotype (Class) statement
0 Stocks
1 Reference

4. Trick for getting RNAi/CRISPR lines using the Analyze button



Dataset: **FBal** *Field*: **CV: mutagen**

#	CV Terms		Related records
1	in vitro construct - regulatory fusion		157
2	ethyl methanesulfonate		116
3	X ray		78
4	gamma ray		71
5	*[empty field - no data available]*		56
6	in vitro construct - coding region fusion		49
7	in vitro construct - RNAi		36
8	P-element activity		36
9	hobo activity		31
10	natural population		23
11	in vitro construct - deletion		19
12	FLPase		18
13	formaldehyde		14
14	Delta2-3 transposase		12
15	in vitro construct - site directed mutagenesis		11
16	CRISPR/Cas9		10
17	in vitro construct - genomic fragment		9
18	in vitro construct - amino acid replacement		9
19	spontaneous		8
20	in vitro construct		7
21	phiC31 integrase		5
22	PM hybrid dysgenesis		4

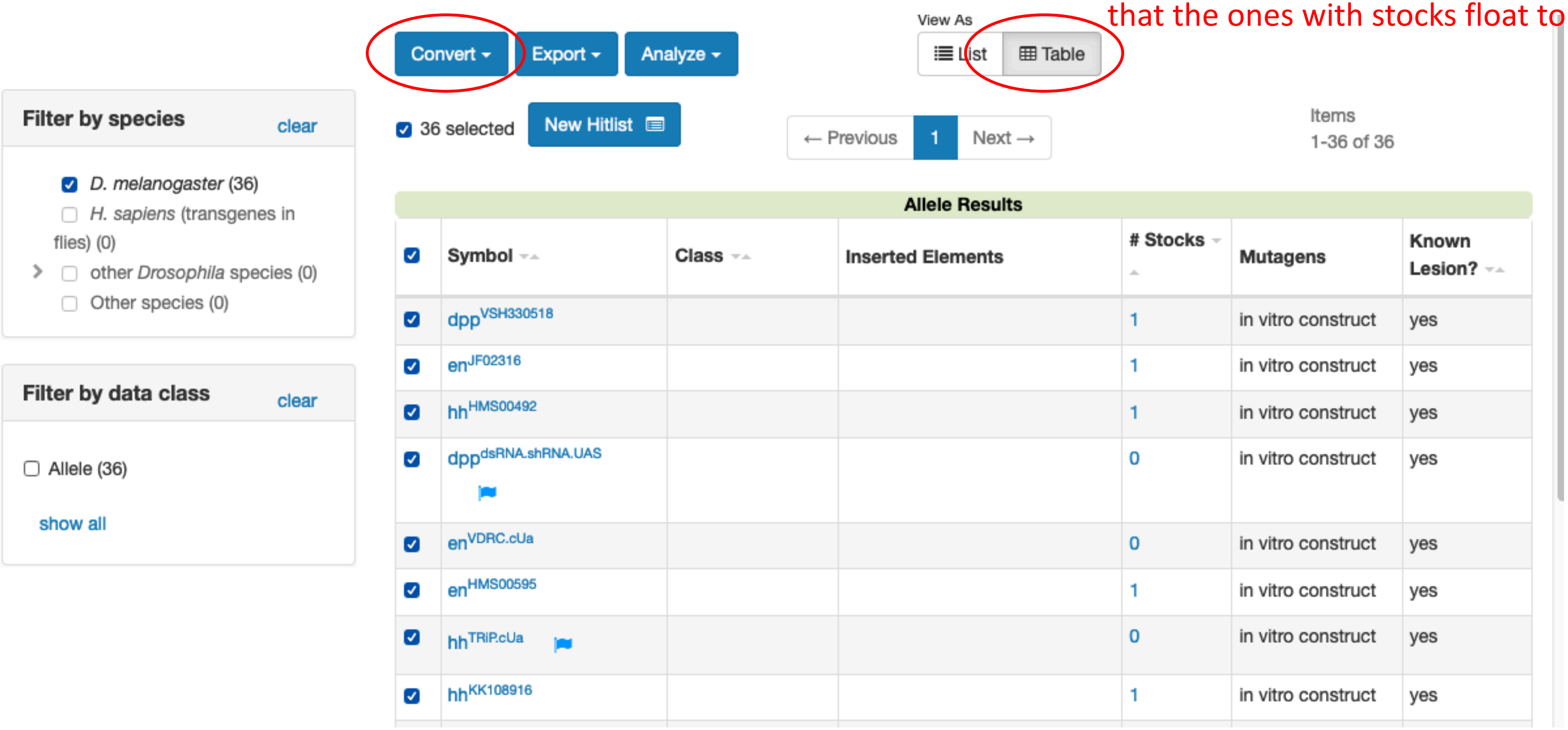
click to get list of RNAi alleles

click to get list of CRISPR alleles

4. Trick for getting RNAi/CRISPR lines using the Analyze button

You can use the 'Convert' button to convert the list to publicly available stocks

If you change the view to Table, you can click on the #Stocks column to sort by it so that the ones with stocks float to the top



Filter by species clear

☑ *D. melanogaster* (36)
☐ *H. sapiens* (transgenes in flies) (0)
☐ other *Drosophila* species (0)
☐ Other species (0)

Filter by data class clear

☐ Allele (36)

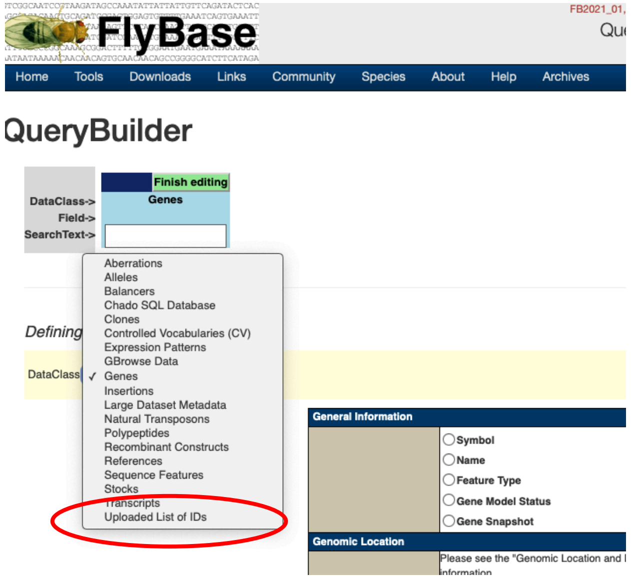
show all

☑ 36 selected

Allele Results

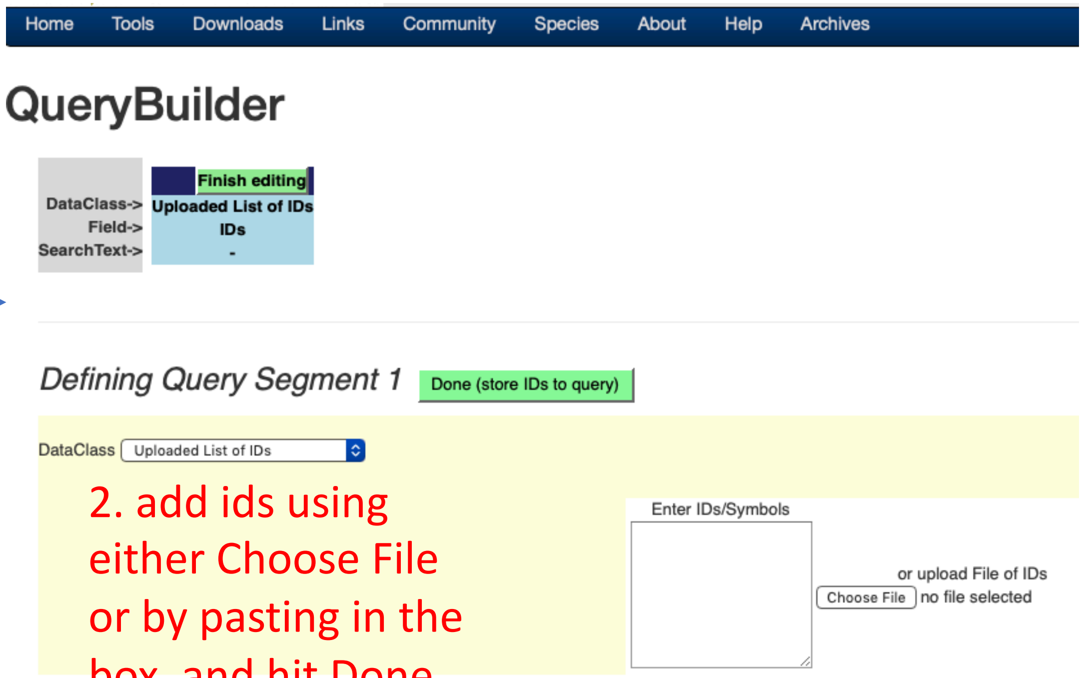
☑	Symbol	Class	Inserted Elements	# Stocks	Mutagens	Known Lesion?
☑	dpp^{VSH330518}			1	in vitro construct	yes
☑	en^{JF02316}			1	in vitro construct	yes
☑	hh^{HMS00492}			1	in vitro construct	yes
☑	dpp$^{dsRNA.shRNA.UAS}$ ⚑			0	in vitro construct	yes
☑	en$^{VDRC.cUa}$			0	in vitro construct	yes
☑	en^{HMS00595}			1	in vitro construct	yes
☑	hh$^{TRiP.cUa}$ ⚑			0	in vitro construct	yes
☑	hh^{KK108916}			1	in vitro construct	yes

5. Getting RNAi/CRISPR lines using the QueryBuilder (QB)



DataClass-> Genes
Field->
SearchText->

1. select 'Uploaded list' in DataClass

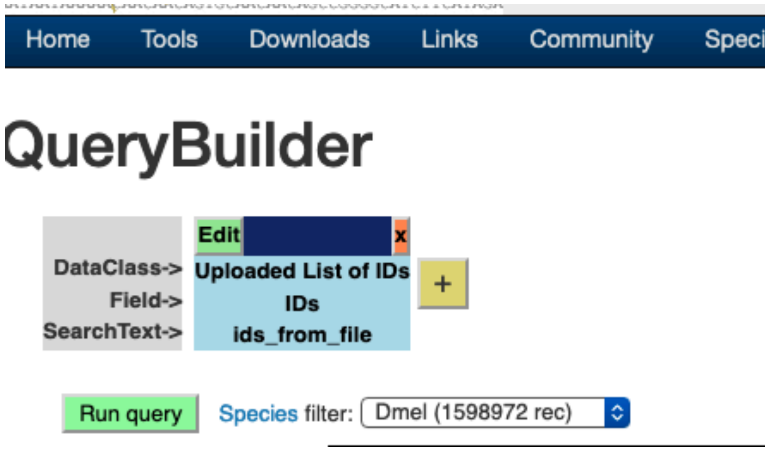


DataClass-> Uploaded List of IDs
Field-> IDs
SearchText-> -

DataClass: Uploaded List of IDs

no file selected

2. add ids using either Choose File or by pasting in the box, and hit Done

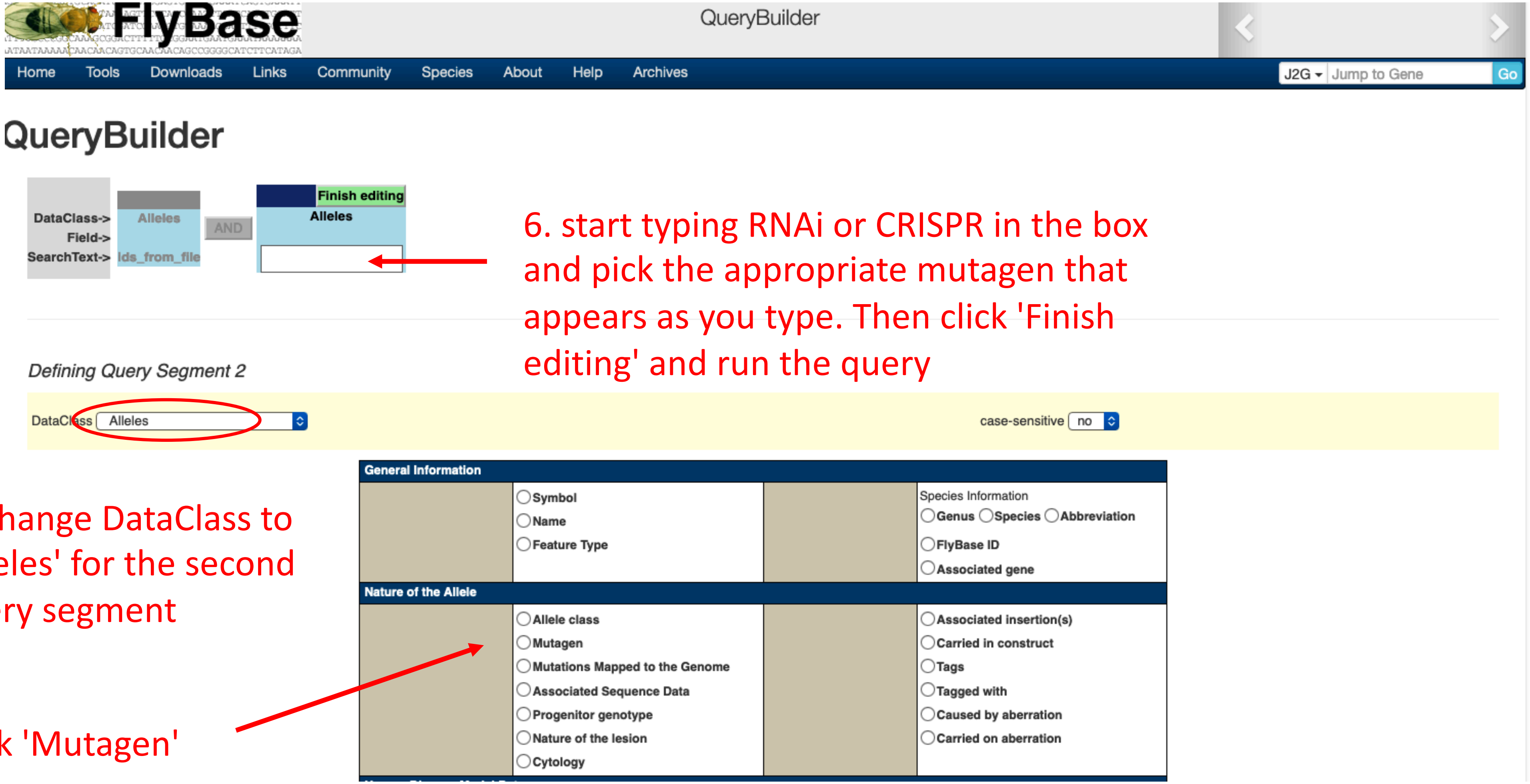


DataClass-> Uploaded List of IDs
Field-> IDs
SearchText-> ids_from_file

Species filter: Dmel (1598972 rec)

3. once the ids have been uploaded, you will see 'ids_from_file' in SearchText. You can now click on the + to add another part to the query (in this case mutagen)

5. Getting RNAi/CRISPR lines using the QueryBuilder (QB)



Defining Query Segment 2

DataClass: Alleles

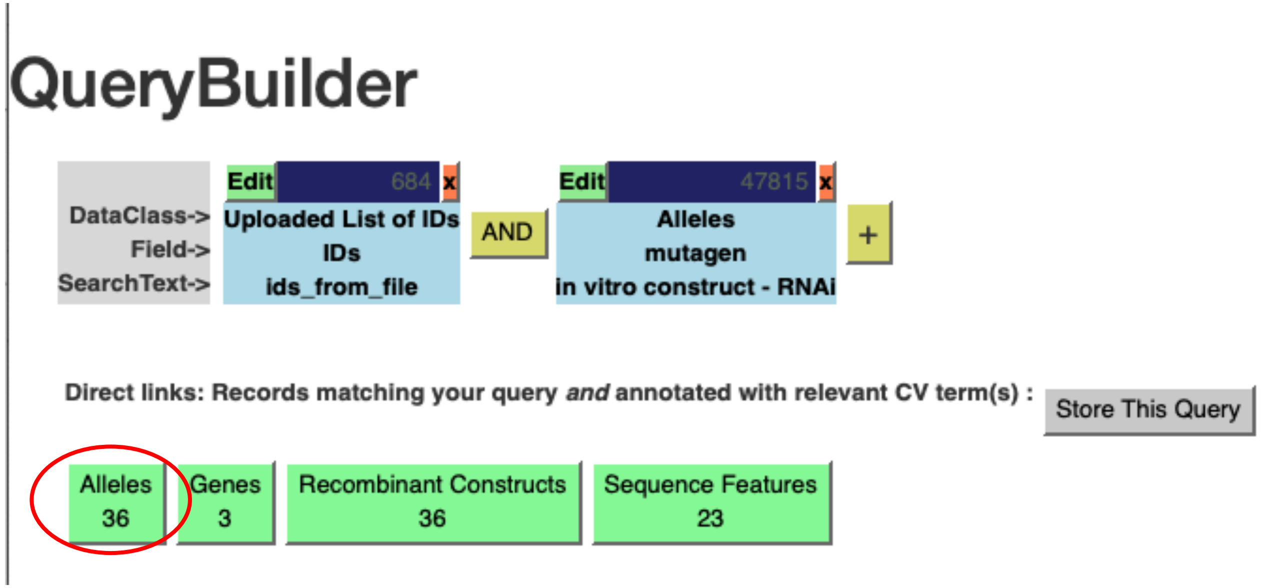
case-sensitive: no

4. change DataClass to 'Alleles' for the second query segment

5. pick 'Mutagen'

6. start typing RNAi or CRISPR in the box and pick the appropriate mutagen that appears as you type. Then click 'Finish editing' and run the query

5. Getting RNAi/CRISPR lines using the QueryBuilder (QB)



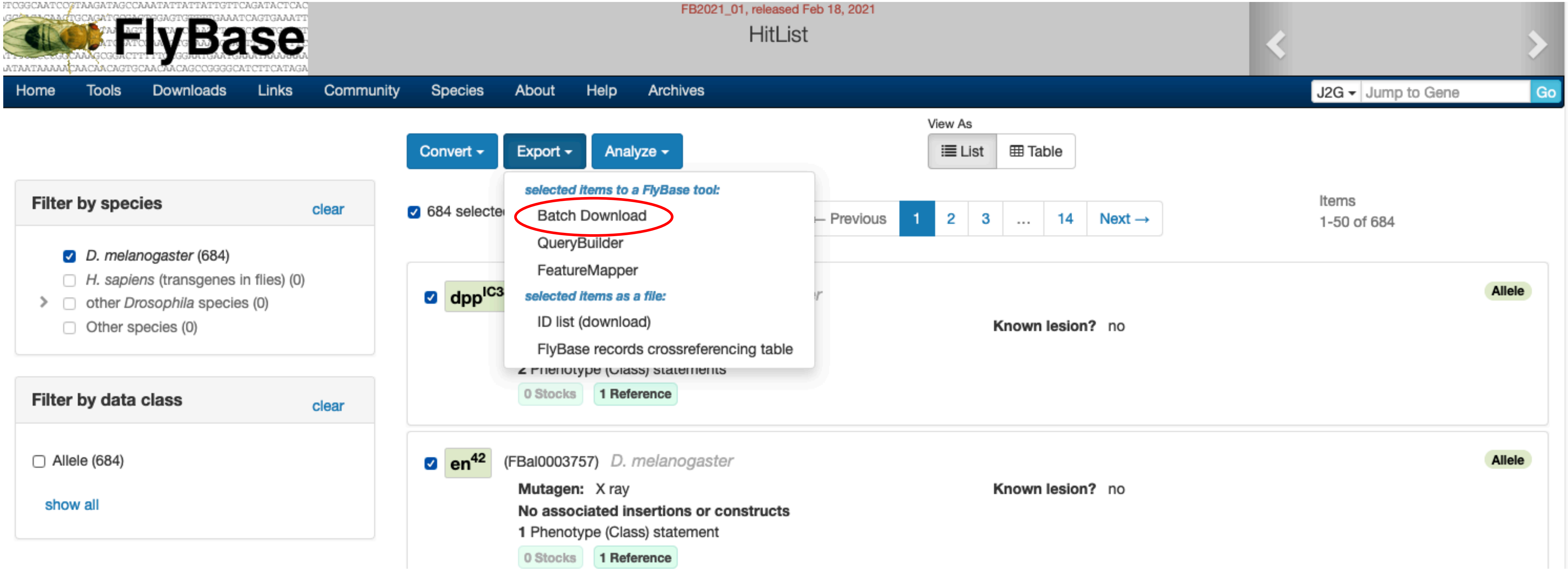
7. Click on Alleles to get to HitList of relevant alleles (and then to stocks as shown on slide 8)

6. Getting UAS overexpression lines

- UAS alleles
    - data is in **regulatory region(s)** field on allele report
    - all relevant alleles have UAS/UASt/UASp in this field
    - *most* alleles will have UAS as part of the superscripted part of the symbol
    - *note that this is filled in for **any** transgenic allele that is driven by UAS, so can include RNAi lines, or overexpression of non-wild type sequences*

- Unfortunately, the regulatory region field is quite new and so it has not been hooked up to the QueryBuilder (QB) or BatchDownload interface yet
- also, as noted above, getting the UAS regulatory region info doesn't distinguish between constructs that overexpress a wild-type or mutant version of the gene of interest
- (*adding both of the above features are on our to-do list)*
- If you end up with a small number of candidate genes, you could use the 'Transgenic Constructs' table in the 'Alleles, Insertions, Transgenic Constructs, and Aberrations ' section of the relevant genes, as you can easily filter for UAS constructs for a single gene (see https://flybase.org/commentaries/2019_08/tooltables.html for details)
- For a larger list of genes, I think that Batch Download to get the 'Nature of the lesion' text for the alleles is probably the best thing to do - I've outlined that strategy in the next few slides.

6. Getting UAS overexpression lines via BatchDownload (BD)



☑ 684 selected

Filter by species

☑ D. melanogaster (684)
☐ H. sapiens (transgenes in flies) (0)
☐ other Drosophila species (0)
☐ Other species (0)

Filter by data class

☐ Allele (684)

☑ dpp^{IC3}

Known lesion? no

2 Phenotype (Class) statements

☑ en^{42} (FBal0003757) D. melanogaster

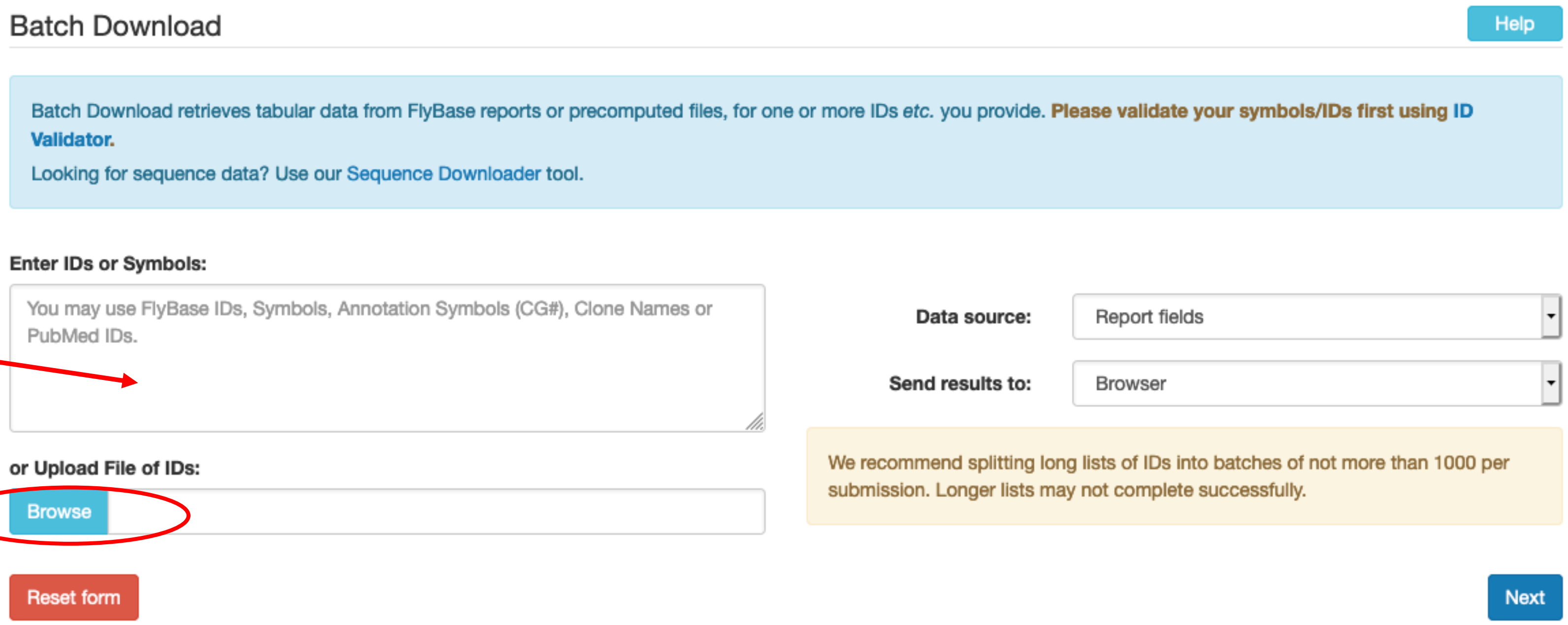
Mutagen: X ray

Known lesion? no

No associated insertions or constructs

1 Phenotype (Class) statement

6. Getting UAS overexpression lines via BatchDownload (BD)



Batch Download retrieves tabular data from FlyBase reports or precomputed files, for one or more IDs *etc.* you provide. **Please validate your symbols/IDs first using ID Validator.**

Looking for sequence data? Use our Sequence Downloader tool.

Enter IDs or Symbols:

You may use FlyBase IDs, Symbols, Annotation Symbols (CG#), Clone Names or PubMed IDs.

or Upload File of IDs:

Data source: Report fields

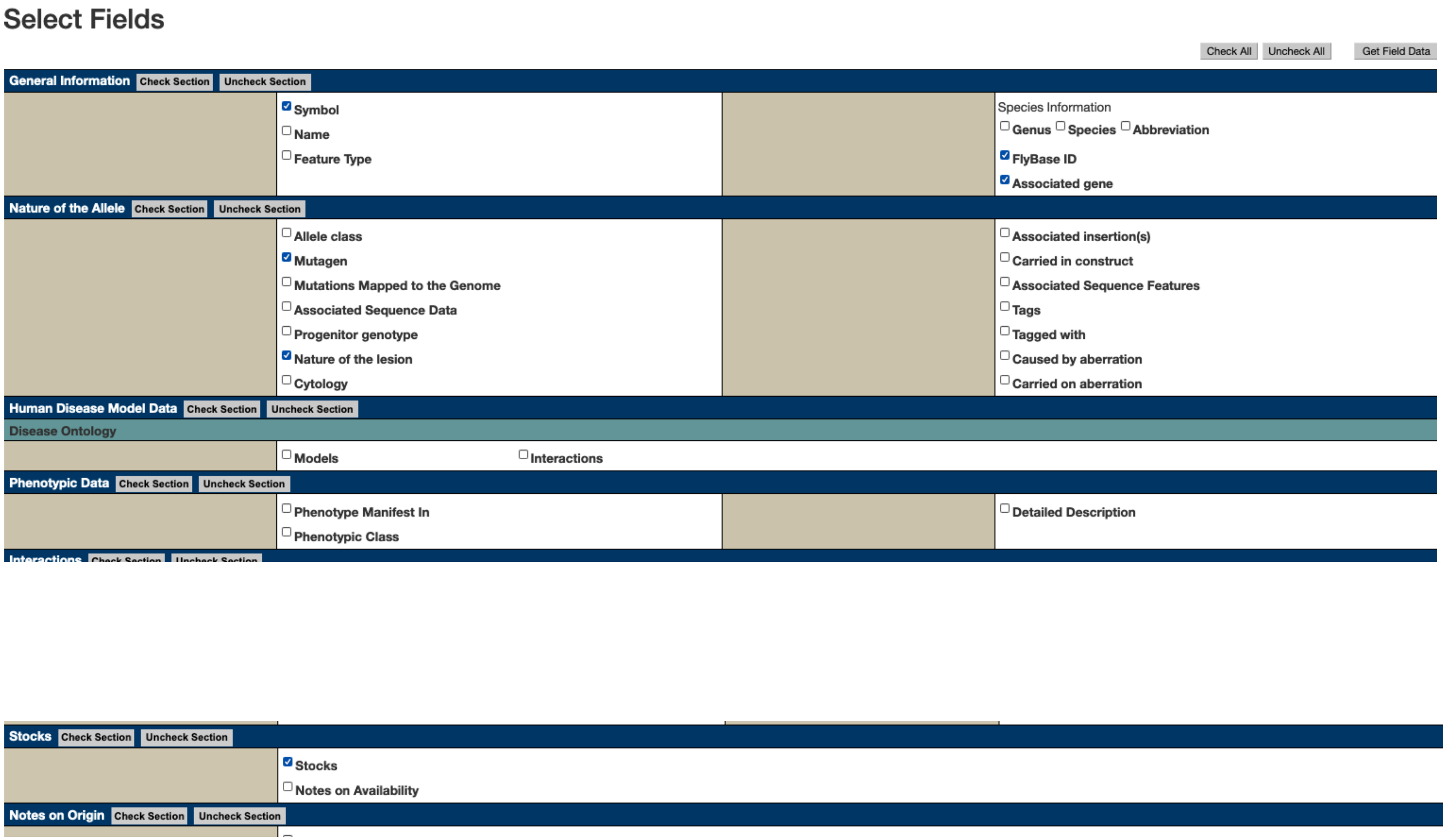
Send results to: Browser

We recommend splitting long lists of IDs into batches of not more than 1000 per submission. Longer lists may not complete successfully.

1. if you got to BD via a hit list, this box will already be filled in with your FBal ids

2. if you went to BD from the home page, add your FBal ids by either pasting in the box, or uploading the saved file

6. Getting UAS overexpression lines via BatchDownload (BD)



Select Fields

General Information

☑ Symbol
☐ Name
☐ Feature Type

Species Information
☐ Genus ☐ Species ☐ Abbreviation
☑ FlyBase ID
☑ Associated gene

Nature of the Allele

☐ Allele class
☑ Mutagen
☐ Mutations Mapped to the Genome
☐ Associated Sequence Data
☐ Progenitor genotype
☑ Nature of the lesion
☐ Cytology

☐ Associated insertion(s)
☐ Carried in construct
☐ Associated Sequence Features
☐ Tags
☐ Tagged with
☐ Caused by aberration
☐ Carried on aberration

Human Disease Model Data

Disease Ontology

☐ Models ☐ Interactions

Phenotypic Data

☐ Phenotype Manifest In
☐ Phenotypic Class

☐ Detailed Description

Interactions

Stocks

☑ Stocks
☐ Notes on Availability

Notes on Origin