

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

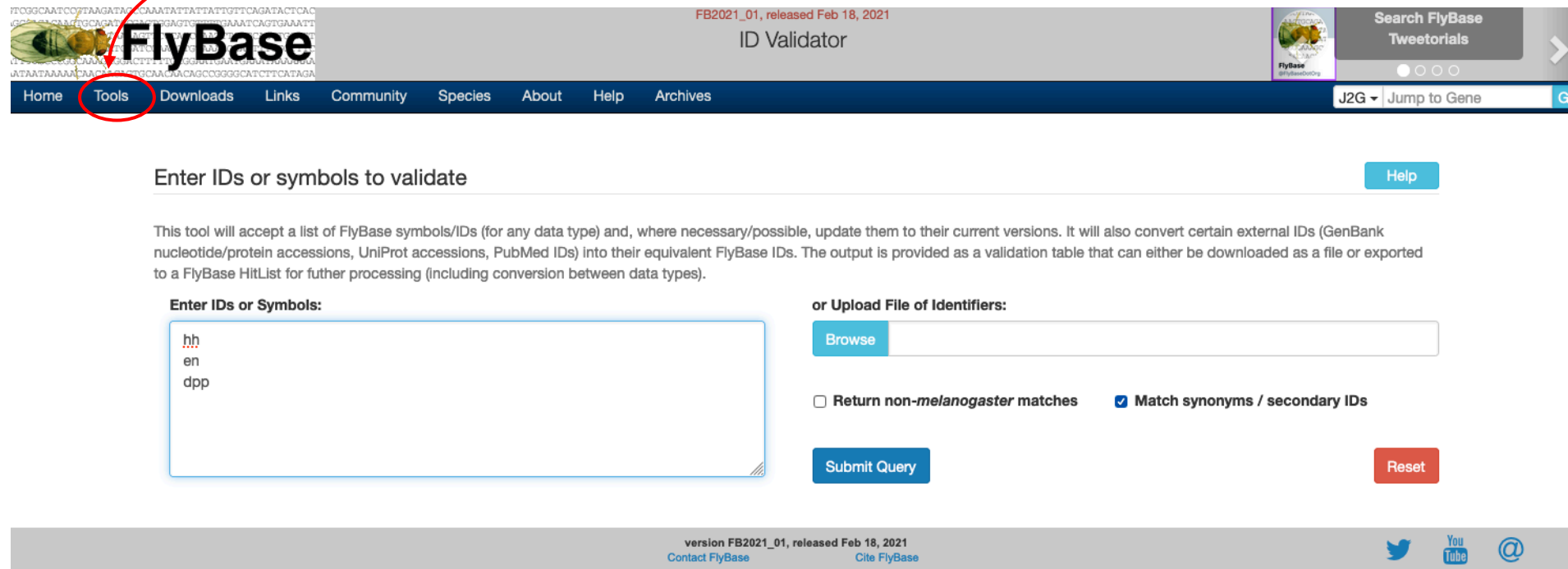
Data is stored attached to alleles and is shown in the 'Nature of the Allele' section of the allele report

- 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/UAS^t/UAS^p 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



The screenshot shows the FlyBase ID Validator tool interface. At the top, the FlyBase logo is on the left, and the text "FB2021_01, released Feb 18, 2021" and "ID Validator" are in the center. A blue navigation bar contains links for Home, Tools (circled in red), Downloads, Links, Community, Species, About, Help, and Archives. On the right of the navigation bar, there is a search box for "Search FlyBase" and "Tweeterials", and a "Jump to Gene" button. Below the navigation bar, the main content area has the heading "Enter IDs or symbols to validate" and a "Help" button. A paragraph explains the tool's function: "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 further processing (including conversion between data types)." There are two input methods: "Enter IDs or Symbols:" with a text area containing "hh", "en", and "dpp"; and "or Upload File of Identifiers:" with a "Browse" button. Below these are two checkboxes: "Return non-melanogaster matches" (unchecked) and "Match synonyms / secondary IDs" (checked). At the bottom of the input section are "Submit Query" and "Reset" buttons. The footer contains the version information "version FB2021_01, released Feb 18, 2021", links for "Contact FlyBase" and "Cite FlyBase", and social media icons for Twitter, YouTube, and a general social media icon.

3. Turn your validated gene list into alleles

FB2021_01, released Feb 18, 2021

Validation results

Downloads Links Community Species About Help Archives J2G Jump

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

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

Validation report			
Export	Submitted Item	Validated ID	Related record
<input checked="" type="checkbox"/>	hh	FBgn0004644	hh
<input checked="" type="checkbox"/>	en	FBgn0000577	en
<input checked="" type="checkbox"/>	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

The screenshot shows the FlyBase HitList interface. At the top, the FlyBase logo is on the left, and the text 'FB2021_01, released Feb 18, 2021' and 'HitList' are on the right. Below the logo is a navigation bar with links: Home, Tools, Downloads, Links, Community, Species, About, Help, Archives. A search bar on the right contains 'J2G' and a 'Jump to Gene' button with a 'Go' button next to it. Below the navigation bar are three buttons: 'Convert', 'Export', and 'Analyze'. A red arrow points from the text above to the 'Convert' button. A dropdown menu is open from the 'Convert' button, showing a list of options: 'Alleles' (circled in red), 'Transcripts', 'Polypeptides', 'Insertions', 'Clones', 'References', 'Stocks', 'Sequence Features', and 'Human Disease Models'. The main content area shows a list of genes. The first gene is 'log (CG4637, FBgn0004644) D. melanogaster'. It has buttons for 'GBrowse' and 'JBrowse', and a 'Gene' label. Below the gene name are details: 'Feature 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', and '1965 References'. The second gene is 'dpp (CG9885, FBgn0000490) D. melanogaster'. It also has 'GBrowse' and 'JBrowse' buttons and a 'Gene' label. Details include: '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', and '2834 References'. On the left side, there are two filter panels. The first is 'Filter by species' with a 'clear' button. It has a checked box for 'D. melanogaster (3)', and unchecked boxes for 'H. sapiens (transgenes in flies) (0)', 'other Drosophila species (0)', and 'Other species (0)'. The second is 'Filter by data class' with a 'clear' button. It has an unchecked box for 'Gene (3)' and a 'show all' button below it.

3. Turn your validated gene list into alleles

The screenshot shows the FlyBase HitList interface. At the top, there is a navigation bar with links for Home, Tools, Downloads, Links, Community, Species, About, Help, and Archives. A search bar on the right contains 'J2G' and a 'Jump to Gene' button. Below the navigation bar, there are three main sections: 'Filter by species', 'Filter by data class', and a list of gene entries. The 'Filter by species' section shows 'D. melanogaster (684)' selected. The 'Filter by data class' section shows 'Allele (684)' selected. The gene list shows two entries: 'dpp^{IC3}' and 'en⁴² (FBal0003757) D. melanogaster'. A dropdown menu is open over the 'Export' button, showing options for 'selected items to a FlyBase tool' (Batch Download, QueryBuilder, Featuremapper) and 'selected items as a file' (ID list (download), FlyBase records crossreferencing table). The 'QueryBuilder' and 'ID list (download)' options are circled in red. The page also shows a 'View As' section with 'List' and 'Table' options, and a pagination bar with 'Previous', '1', '2', '3', '...', '14', and 'Next' buttons. The total number of items is 684, and the current view shows items 1-50 of 684.

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

The screenshot shows a web interface with a dark blue navigation bar at the top containing links: Home, Tools, Downloads, Links, Community, Species, About, Help, Archives, and a user profile 'J2G'. Below the navigation bar, there are buttons for 'Convert', 'Export', and 'Analyze'. The 'Analyze' button is open, showing a dropdown menu with two sections: 'For the selected records, analyze frequencies of values of' and 'For the selected records, browse Interactions'. The 'Mutagen' option in the first section is circled in red. The interface also shows filter panels for species and data class, and a list of records with details for 'dpp^{IC38}' and 'en⁴²'.

Home Tools Downloads Links Community Species About Help Archives J2G

View As List Table

Convert Export Analyze

Filter by species clear

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

Filter by data class clear

- Allele (684)

show all

684 selected New Hit

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 associated mutations 2 Phenotype (Class) statements 0 Stocks 1 Reference

en⁴² (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 it so that the ones with stocks float to the top

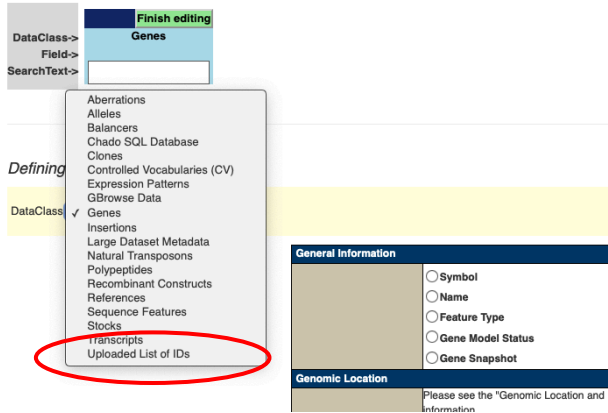
The screenshot shows a web interface for managing alleles. On the left, there are two filter panels: 'Filter by species' and 'Filter by data class'. The 'Filter by species' panel shows 'D. melanogaster (36)' selected. The 'Filter by data class' panel shows 'Allele (36)' selected. In the top navigation area, the 'Convert' button is circled in red. To its right are 'Export' and 'Analyze' buttons. Further right, the 'View As' section shows 'List' and 'Table' buttons, with 'Table' circled in red. Below the navigation, there are '36 selected' and 'New Hitlist' buttons, and a pagination control showing '1' of 36 items. The main content is a table titled 'Allele Results' with the following columns: Symbol, Class, Inserted Elements, # Stocks, Mutagens, and Known Lesion?. The table contains 9 rows of data, with the first three rows having 1 stock and the last three rows having 0 stocks.

	Symbol	Class	Inserted Elements	# Stocks	Mutagens	Known Lesion?
<input checked="" type="checkbox"/>	dpp ^{VSH330518}			1	in vitro construct	yes
<input checked="" type="checkbox"/>	en ^{JF02316}			1	in vitro construct	yes
<input checked="" type="checkbox"/>	hh ^{HMS00492}			1	in vitro construct	yes
<input checked="" type="checkbox"/>	dpp ^{dsRNA.shRNA.UAS}			0	in vitro construct	yes
<input checked="" type="checkbox"/>	en ^{VDRC.cUa}			0	in vitro construct	yes
<input checked="" type="checkbox"/>	en ^{HMS00595}			1	in vitro construct	yes
<input checked="" type="checkbox"/>	hh ^{TRIP.cUa}			0	in vitro construct	yes
<input checked="" type="checkbox"/>	hh ^{KK108916}			1	in vitro construct	yes

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



QueryBuilder



1. select 'Uploaded list' in DataClass



QueryBuilder

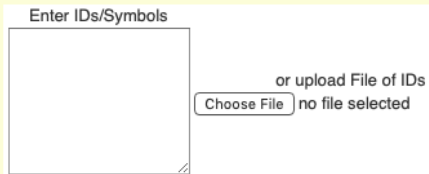


Defining Query Segment 1

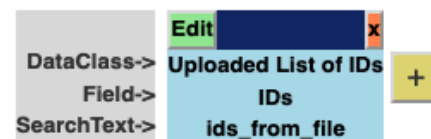
Done (store IDs to query)

DataClass: Uploaded List of IDs

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



QueryBuilder



Run query 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)

The screenshot shows the FlyBase QueryBuilder interface. At the top, there is a navigation bar with 'FlyBase' logo, 'QueryBuilder' title, and navigation arrows. Below this is a menu with 'Home', 'Tools', 'Downloads', 'Links', 'Community', 'Species', 'About', 'Help', and 'Archives'. A search bar contains 'J2G' and a 'Jump to Gene' button with a 'Go' button.

The main area is titled 'QueryBuilder' and shows a query segment definition. On the left, a 'DataClass->' dropdown is set to 'Alleles', and a 'Field->' dropdown is set to 'ids_from_file'. A 'SearchText->' input field is empty. To the right, a 'Finish editing' button is visible. A red arrow points to the 'Finish editing' button.

Below the query segment definition, there is a section titled 'Defining Query Segment 2'. It shows a 'DataClass' dropdown set to 'Alleles' (circled in red) and a 'case-sensitive' dropdown set to 'no'.

At the bottom, there is a table of filters for the 'Alleles' data class. The table is divided into two sections: 'General Information' and 'Nature of the Allele'. The 'Nature of the Allele' section is highlighted with a red arrow.

General Information	
<input type="radio"/> Symbol	<input type="radio"/> Species Information
<input type="radio"/> Name	<input type="radio"/> Genus <input type="radio"/> Species <input type="radio"/> Abbreviation
<input type="radio"/> Feature Type	<input type="radio"/> FlyBase ID
	<input type="radio"/> Associated gene

Nature of the Allele	
<input type="radio"/> Allele class	<input type="radio"/> Associated insertion(s)
<input type="radio"/> Mutagen	<input type="radio"/> Carried in construct
<input type="radio"/> Mutations Mapped to the Genome	<input type="radio"/> Tags
<input type="radio"/> Associated Sequence Data	<input type="radio"/> Tagged with
<input type="radio"/> Progenitor genotype	<input type="radio"/> Caused by aberration
<input type="radio"/> Nature of the lesion	<input type="radio"/> Carried on aberration
<input type="radio"/> Cytology	

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

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

5. pick 'Mutagen'

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

QueryBuilder

The QueryBuilder interface shows two conditions connected by an AND operator. The first condition is 'Uploaded List of IDs' with a search text of 'ids_from_file' and an 'Edit' button showing 684 records. The second condition is 'Alleles mutagen in vitro construct - RNAI' with an 'Edit' button showing 47815 records. A plus sign button is visible to the right of the second condition.

Direct links: Records matching your query *and* annotated with relevant CV term(s) : [Store This Query](#)

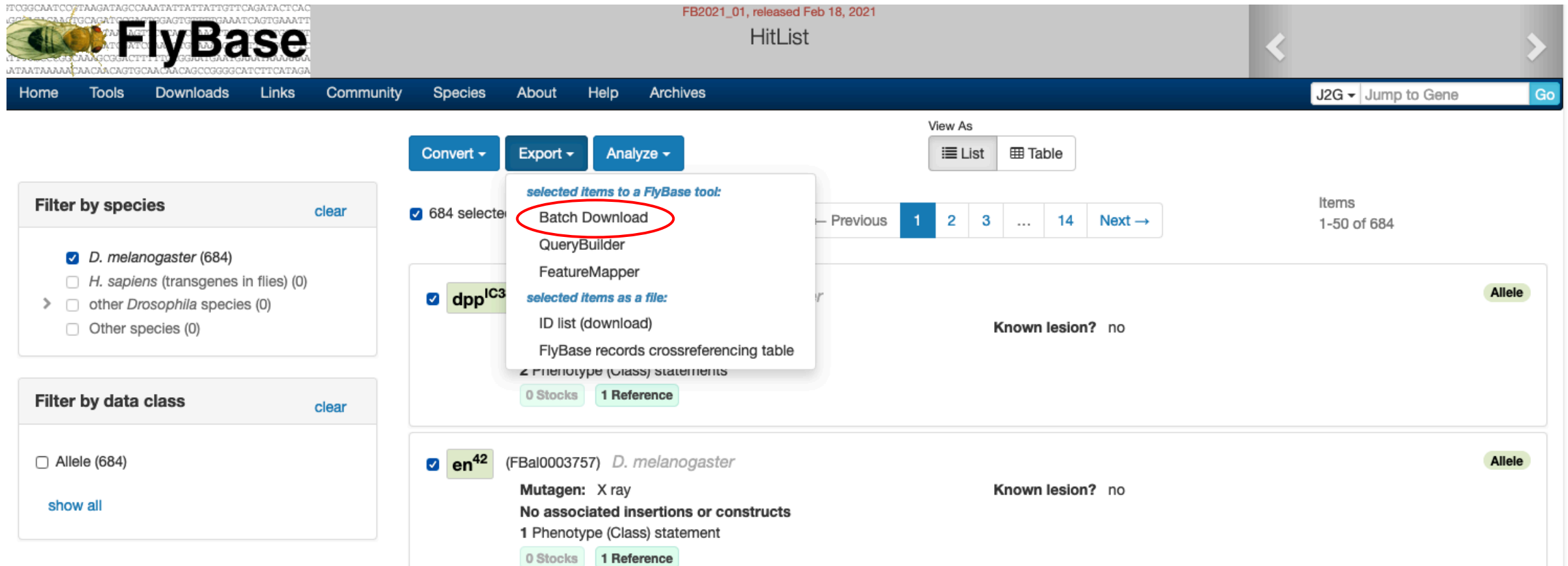
Alleles 36	Genes 3	Recombinant Constructs 36	Sequence Features 23
---------------	------------	------------------------------	-------------------------

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/UAS^t/UAS^p 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)



The screenshot displays the FlyBase HitList interface. At the top, the FlyBase logo is visible on the left, and the text "HitList" is centered. A navigation bar includes links for Home, Tools, Downloads, Links, Community, Species, About, Help, and Archives. On the right of the navigation bar, there is a "J2G" dropdown menu, a "Jump to Gene" input field, and a "Go" button. Below the navigation bar, there are three main buttons: "Convert", "Export", and "Analyze". The "Export" button is highlighted, and a dropdown menu is open, showing options for "selected items to a FlyBase tool:" (Batch Download, QueryBuilder, FeatureMapper) and "selected items as a file:" (ID list (download), FlyBase records crossreferencing table). The "Batch Download" option is circled in red. The main content area shows a list of items, with the first item being "dpp^{IC3}" and the second being "en⁴² (FBal0003757) D. melanogaster". The "Batch Download" option is circled in red.

FB2021_01, released Feb 18, 2021

HitList

Home Tools Downloads Links Community Species About Help Archives

J2G Jump to Gene Go

View As List Table

Convert Export Analyze

Filter by species clear

- D. melanogaster* (684)
- H. sapiens* (transgenes in files) (0)
- other *Drosophila* species (0)
- Other species (0)

Filter by data class clear

- Allele (684)

show all

684 selected

Batch Download

QueryBuilder

FeatureMapper

selected items as a file:

ID list (download)

FlyBase records crossreferencing table

0 Stocks 1 Reference

1

2 3 ... 14 Next →

Items 1-50 of 684

Allele

Known lesion? no

en⁴² (FBal0003757) *D. melanogaster*

Mutagen: X ray

No associated insertions or constructs

1 Phenotype (Class) statement

0 Stocks 1 Reference

6. Getting UAS overexpression lines via BatchDownload (BD)

Batch Download Help

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:
Browse

Reset form

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.

Next

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

[Check All](#) [Uncheck All](#) [Get Field Data](#)

General Information Check Section Uncheck Section	
<input checked="" type="checkbox"/> Symbol <input type="checkbox"/> Name <input type="checkbox"/> Feature Type	Species Information <input type="checkbox"/> Genus <input type="checkbox"/> Species <input type="checkbox"/> Abbreviation <input checked="" type="checkbox"/> FlyBase ID <input checked="" type="checkbox"/> Associated gene
Nature of the Allele Check Section Uncheck Section	
<input type="checkbox"/> Allele class <input checked="" type="checkbox"/> Mutagen <input type="checkbox"/> Mutations Mapped to the Genome <input type="checkbox"/> Associated Sequence Data <input type="checkbox"/> Progenitor genotype <input checked="" type="checkbox"/> Nature of the lesion <input type="checkbox"/> Cytology	<input type="checkbox"/> Associated insertion(s) <input type="checkbox"/> Carried in construct <input type="checkbox"/> Associated Sequence Features <input type="checkbox"/> Tags <input type="checkbox"/> Tagged with <input type="checkbox"/> Caused by aberration <input type="checkbox"/> Carried on aberration
Human Disease Model Data Check Section Uncheck Section	
Disease Ontology	
<input type="checkbox"/> Models	<input type="checkbox"/> Interactions
Phenotypic Data Check Section Uncheck Section	
<input type="checkbox"/> Phenotype Manifest In <input type="checkbox"/> Phenotypic Class	<input type="checkbox"/> Detailed Description
Interactions Check Section Uncheck Section	
Stocks Check Section Uncheck Section	
<input checked="" type="checkbox"/> Stocks <input type="checkbox"/> Notes on Availability	
Notes on Origin Check Section Uncheck Section	