Target Gene Notebook

User Guide
1.2

Target Gene Notebook allows the curation of persistent, editable, and distributable databases of genomic, biological, chemical, and other data that pertain to the local neighborhood around a gene of interest.

The current version draws heavily on the many harmonized data sources available through Ensembl[1].

1. Daniel R. Zerbino, Premanand Achuthan, Wasiu Akanni, M. Ridwan Amode, Daniel Barrell, Jyothish Bhai, Konstantinos Billis, Carla Cummins, Astrid Gall, Carlos García Giro´n, Laurent Gil, Leo Gordon, Leanne Haggerty, Erin Haskell, Thibaut Hourlier, Osagie G. Izuogu, Sophie H. Janacek, Thomas Juettemann, Jimmy Kiang To, Matthew R. Laird, Ilias Lavidas, Zhicheng Liu, Jane E. Loveland, Thomas Maurel, William McLaren, Benjamin Moore, Jonathan Mudge, Daniel N. Murphy, Victoria Newman, Michael Nuhn, Denye Ogeh, Chuang Kee Ong, Anne Parker, Mateus Patricio, Harpreet Singh Riat, Helen Schuilenburg, Dan Sheppard, Helen Sparrow, Kieron Taylor, Anja Thormann, Alessandro Vullo, Brandon Walts, Amonida Zadissa, Adam Frankish, Sarah E. Hunt, Myrto Kostadima, Nicholas Langridge, Fergal J. Martin, Matthieu Muffato, Emily Perry, Magali Ruffier, Dan M. Staines, Stephen J. Trevanion, Bronwen L. Aken, Fiona Cunningham, Andrew Yates, Paul Flicek
Ensembl 2018.
PubMed PMID: 29155950.

Target Gene Notebook was originally supported and created at Eisai Inc.’s Andover Innovative Medicine Institute in Andover, MA.

We encourage further development of this resource.

Target Gene Notebook team

Eisai (design, implementation and testing):
Andrew Kirby
Janna Hutz
Jamey Wierzbowski
Mary Pat Reeve

Massachusetts General Hospital (design input):
Mark Daly
Hailiang Huang

Requirements

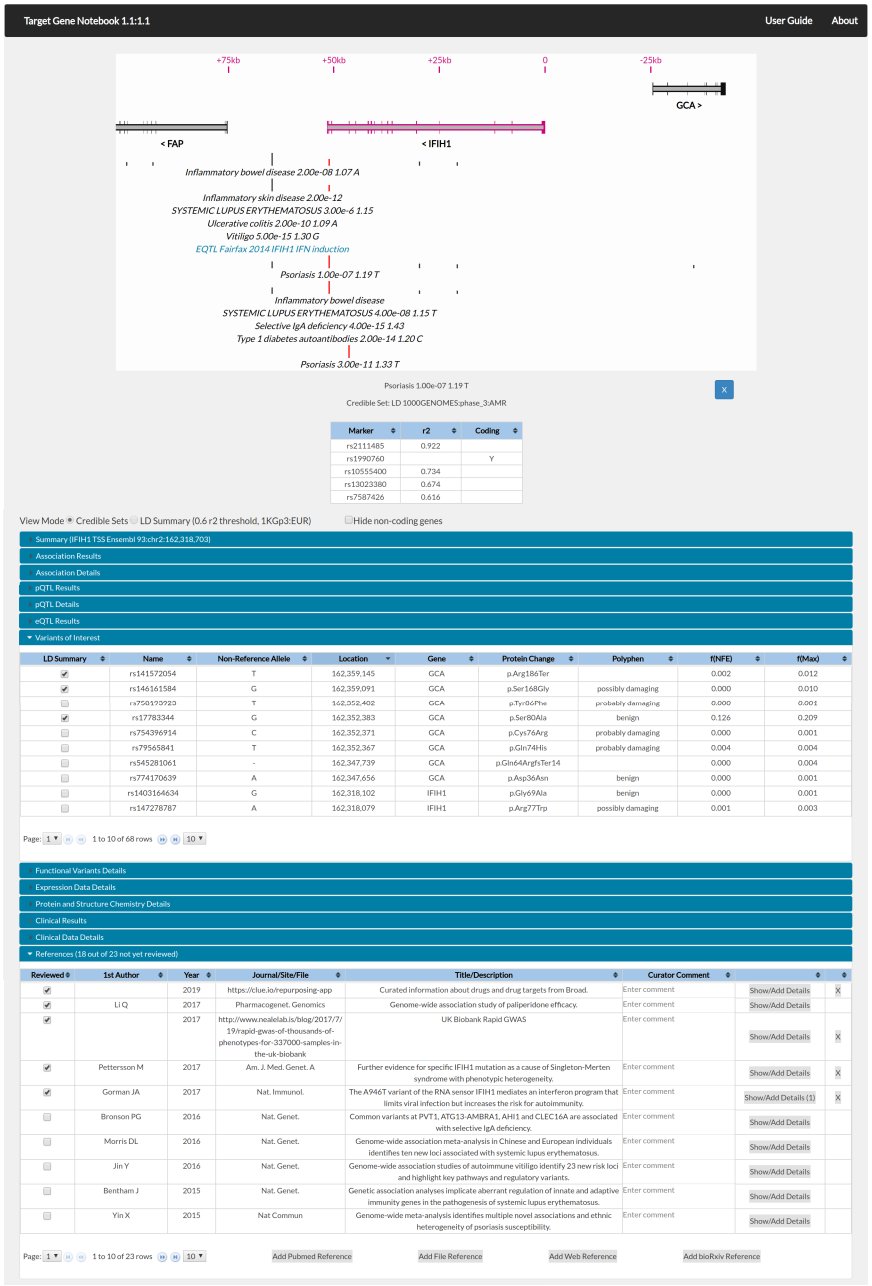
Server:
Java >= 1.7

Client:
Google Chrome
JavaScript enabled

Target Gene Notebook uses these frameworks/libraries:

Bootstrap 3.3.7 (MIT license)
FileSaver.js 1.3.2 (MIT license)
Huebee 2.0.0 (MIT license)
jQuery 2.2.4 (MIT license)
jQuery UI 1.12.1 (MIT license)
Lightbox2 2.9.0 (MIT license)
Select2 4.0.3 (MIT license)
tablesorter 2.28.14 (MIT license)
Spark micro framework (sparkjava.com, Apache 2 license)
Dependencies:
commons-io 2.4
commons-lang3 3.4
gson 2.7
jsoup 1.8.1
slf4j-simple 1.7.21
sqlite-jdbc 3.7.2

GUI Overview



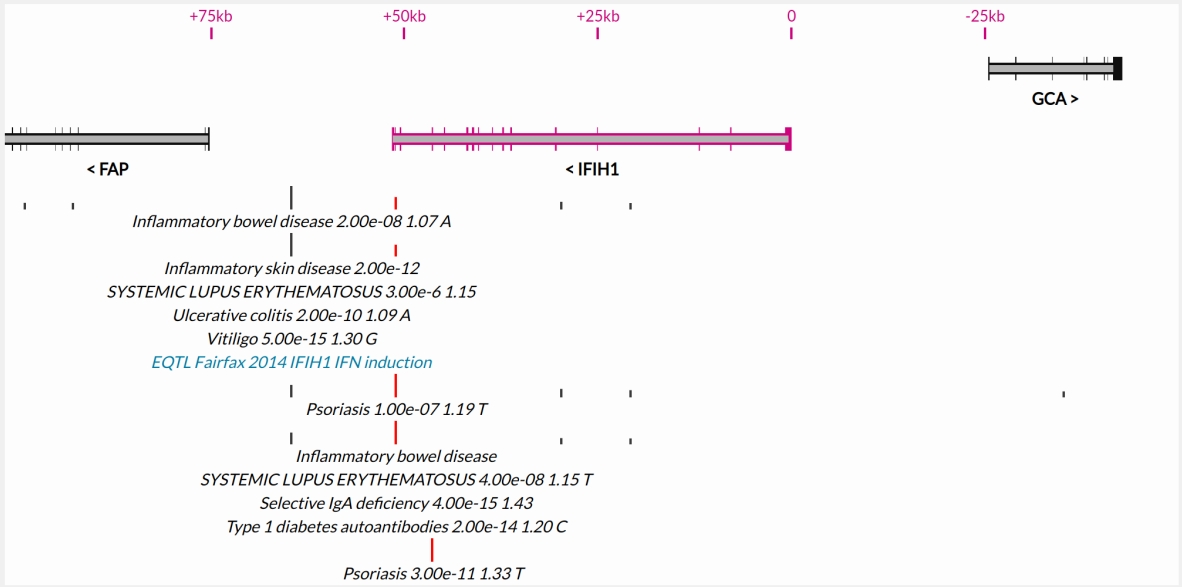
Interactive graphical view of curated data within a genomic context.

Text-based/tabular view of curated data.

Interactive graphical view of curated data within a genomic context…

Interactive graphical view of curated data within a genomic context.

Overview



Psoriasis 1.00e-07 1.19 T

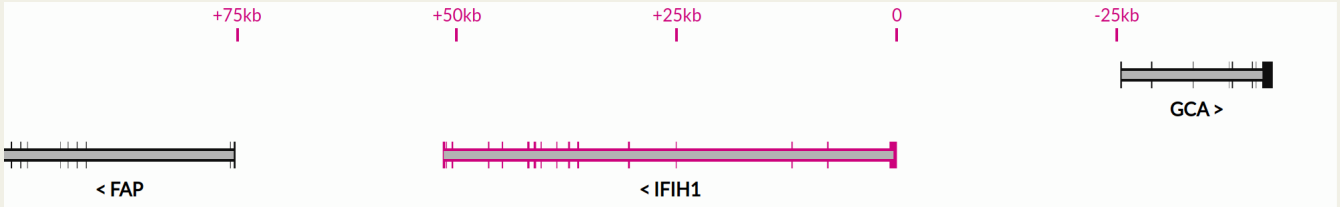
Credible Set: LD 1000GENOMES:phase_3:AMR

X

Marker	r2	Coding
rs2111485	0.922	
rs1990760		Y
rs10555400	0.734	
rs13023380	0.674	
rs7587426	0.616	

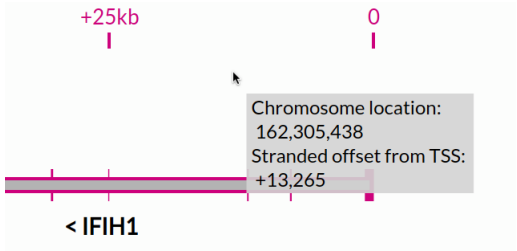
View Mode ◉ Credible Sets ○ LD Summary (0.6 r2 threshold, 1KGp3:EUR) ☐ Hide non-coding genes

Interactive graphical view of curated data within a genomic context.



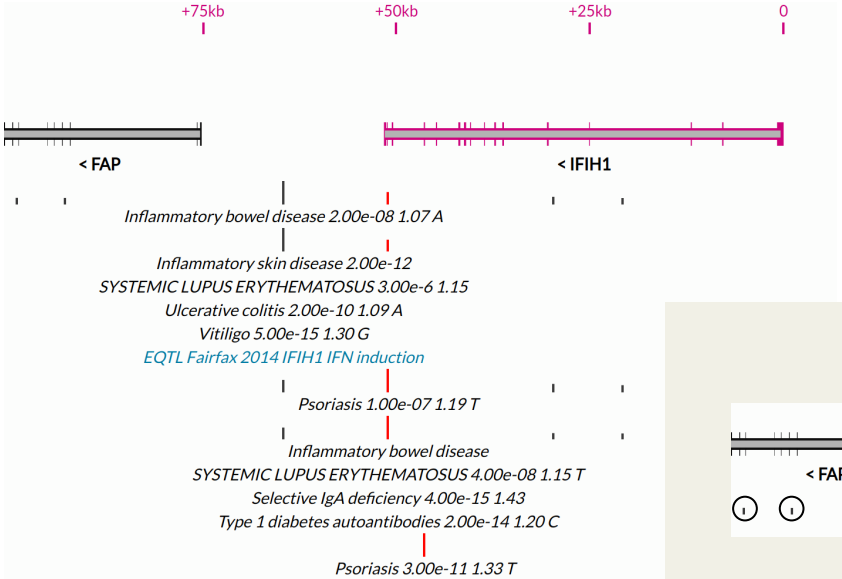
The display area shows a 50-kb neighborhood around the Ensembl canonical transcript for the target gene.

The genomic ruler is oriented relative to the start of the target-gene transcript.

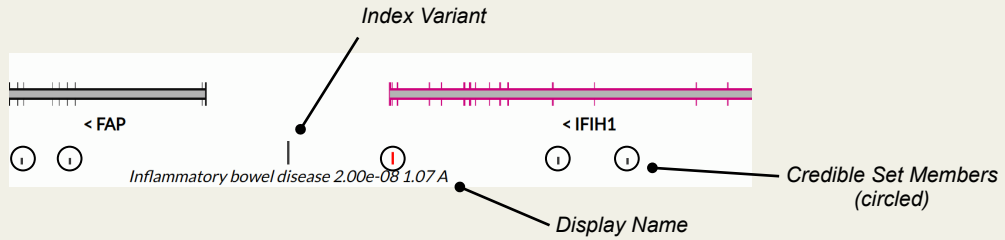


Clicking on the background of the display area will report the pointer's genomic position and strand-oriented distance from the transcript start site of the target gene.

Interactive graphical view of curated data within a genomic context.



Curated association/eQTL/pQTL results are shown below any gene annotations.

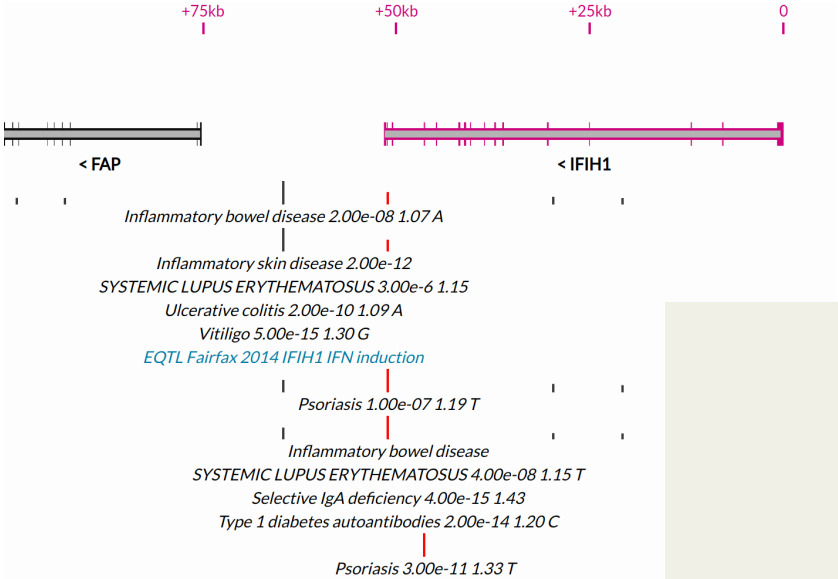


For any displayed result, that result's curated Display Name is shown directly below a set of tick marks. The tallest tick mark represents the index variant for the result. Other tick marks represent the "Credible Set" for that index variant: variants in high LD with the index variant, based on 1KG phase-3 data for selectable populations. The height of each member-variant's tick mark is proportional to its r^2 value to the index variant. A red tick mark indicates a coding/splice-impacting variant. When a user-defined Credible Set is being displayed, the height of each tick mark is proportional to the assigned posterior.

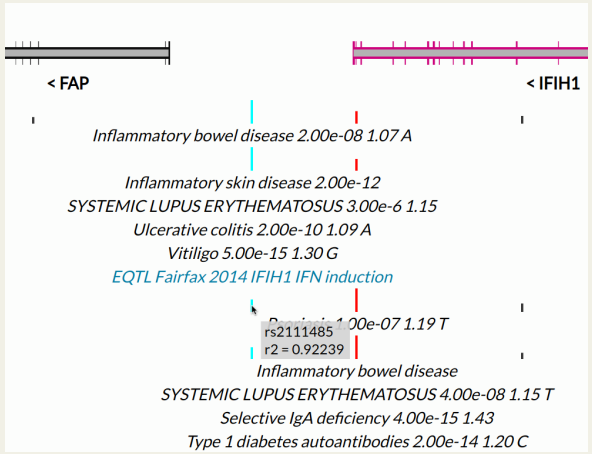
Credible Sets may offer useful insight into what variation is responsible for an association/eQTL/pQTL signal.

All results with the same index variant and Credible Set share a single set of tick marks.

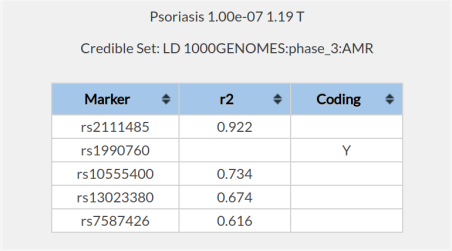
Interactive graphical view of curated data within a genomic context.



Curated association/eQTL/pQTL results are shown below any gene annotations.



Hovering the cursor over a variant's tick mark will display its name and its r^2 value to the index variant. Additionally, the same variant will be shaded teal where it appears in other association/ eQTL/pQTL results.

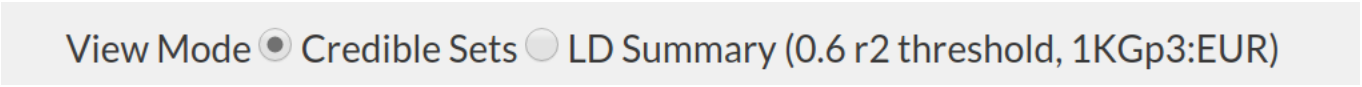


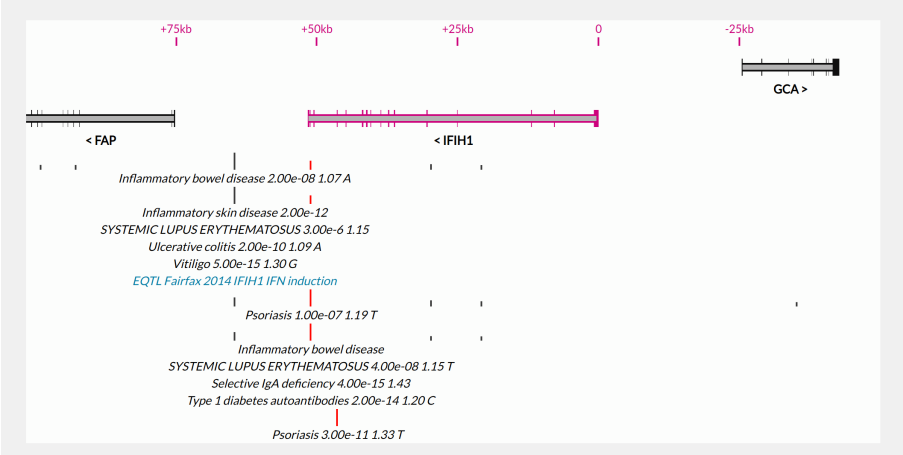
Marker	r2	Coding
rs2111485	0.922	
rs1990760		Y
rs10555400	0.734	
rs13023380	0.674	
rs7587426	0.616	

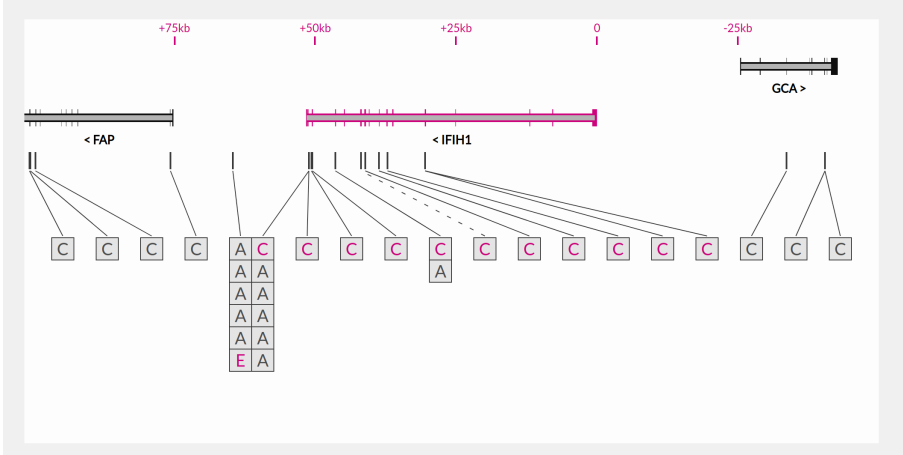
Clicking on the Display Name for an association/eQTL/pQTL result will reveal a dismissable table just below the display area summarizing the index variant and its Credible Set.

Interactive graphical view of curated data within a genomic context.

Two different graphical perspectives are available for the display area





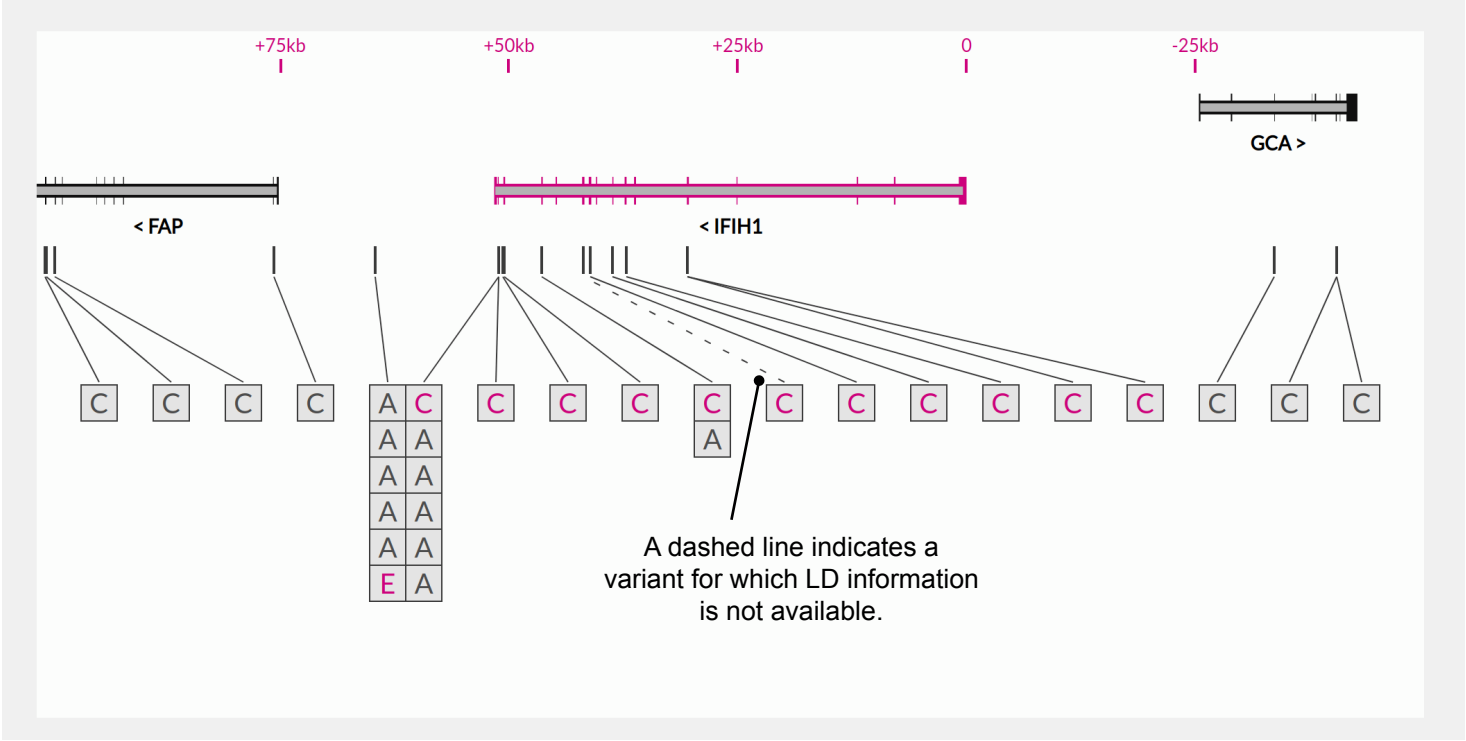


Credible Sets are shown for curated association, eQTL, and pQTL results.

Association, eQTL, and pQTL index variants, as well as other curated variants are shown in high-LD groups.

Interactive graphical view of curated data within a genomic context.

LD-summary graphical perspective



Each box represents a particular association result (A), allele coding impact (C), eQTL result (E), or pQTL result (P). Results for the same variant are stacked vertically.

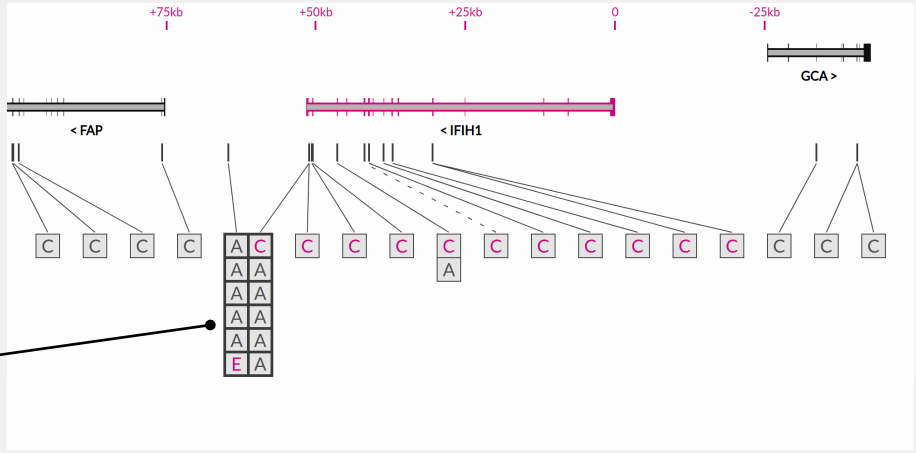
Variants are placed into groups where all members have r^2 >= 0.6 (1KGp3:EUR) to at least one other member of the group.

eQTL results and allele coding impacts assigned to the target gene are highlighted in magenta.

Interactive graphical view of curated data within a genomic context.

LD-summary graphical perspective

Clicking on an LD group will reveal a dismissable table below the display area summarizing the events in that group.



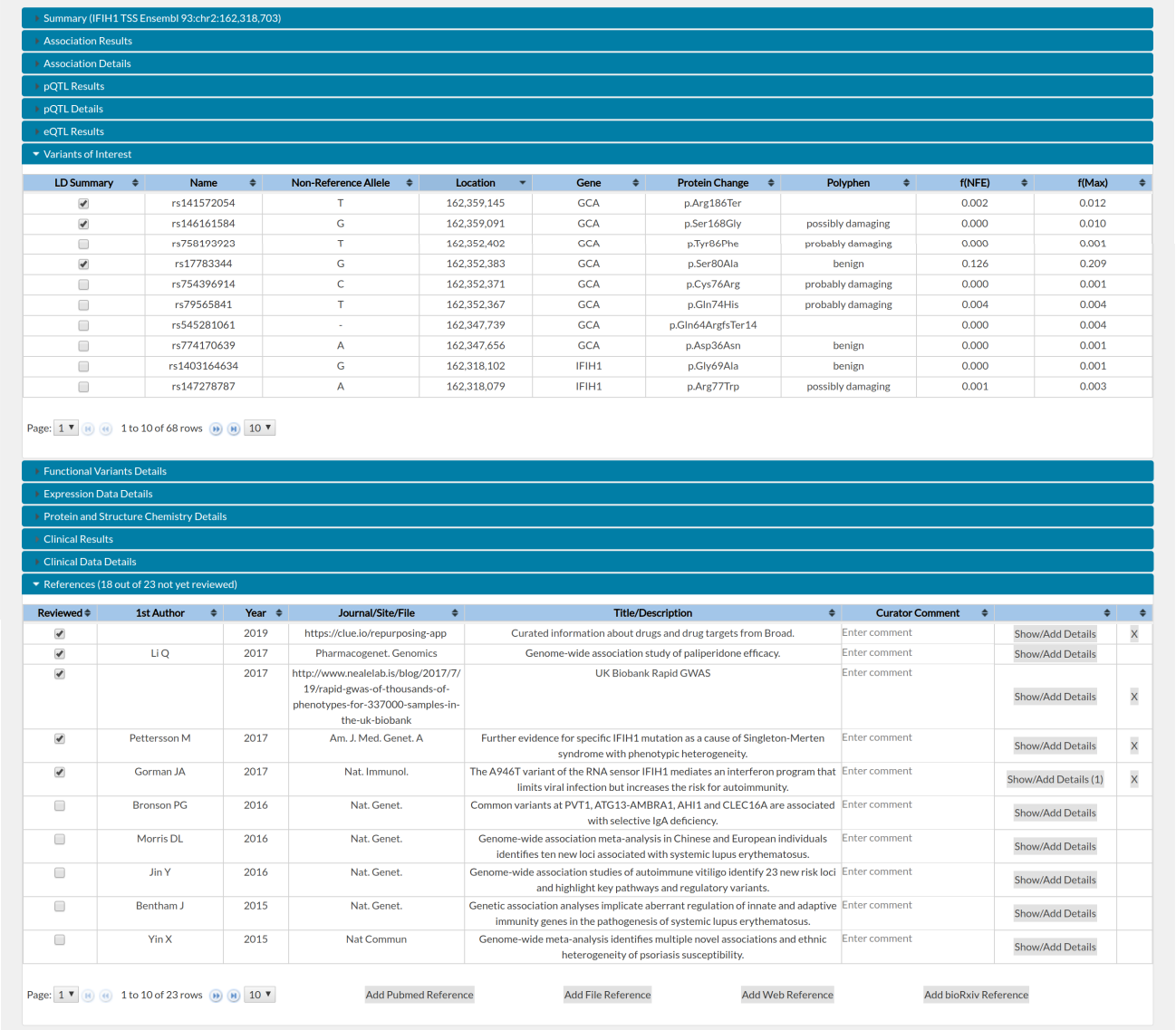
Marker	Finding	Allele	Gene	Coding Impact	Phenotype	Tissue	Freq	OR/Beta
rs2111485	Assoc.				Systemic lupus erythematosus		0.398 sum(MAF) 1KGp3:EUR	1.15
rs2111485	Assoc.	A			Ulcerative colitis		0.398 sum(MAF) 1KGp3:EUR	1.09
rs2111485	Assoc.				Inflammatory skin disease		0.398 sum(MAF) 1KGp3:EUR	
rs2111485	Assoc.	G			Vitiligo		0.398 sum(MAF) 1KGp3:EUR	1.30
rs2111485	Assoc.	A			Inflammatory bowel disease		0.398 sum(MAF) 1KGp3:EUR	1.07
rs2111485	eQTL		IFIH1			Monocytes	0.398 sum(MAF) 1KGp3:EUR	5.85
rs1990760	C. Variant	T	IFIH1	p.Ala946Thr			0.459 ExAC:ALL	
rs1990760	Assoc.				Selective IgA deficiency		0.395 sum(MAF) 1KGp3:EUR	1.43
rs1990760	Assoc.	T			Systemic lupus erythematosus		0.395 sum(MAF) 1KGp3:EUR	1.15
rs1990760	Assoc.				Inflammatory bowel disease		0.395 sum(MAF) 1KGp3:EUR	
rs1990760	Assoc.	T			Psoriasis		0.395 sum(MAF) 1KGp3:EUR	1.19
rs1990760	Assoc.	C			Type 1 diabetes autoantibodies		0.395 sum(MAF) 1KGp3:EUR	1.20

Interactive graphical view of curated data within a genomic context.

Text-based/tabular view of curated data…

Text-based/tabular view of curated data.

Overview



LD Summary	Name	Non-Reference Allele	Location	Gene	Protein Change	Polyphen	f(NFE)	f(Max)
☑	rs141572054	T	162,359,145	GCA	p.Arg186Ter		0.002	0.012
☑	rs146161584	G	162,359,091	GCA	p.Ser168Gly	possibly damaging	0.000	0.010
☐	rs758193923	T	162,352,402	GCA	p.Tyr86Phe	probably damaging	0.000	0.001
☑	rs17783344	G	162,352,383	GCA	p.Ser80Ala	benign	0.126	0.209
☐	rs754396914	C	162,352,371	GCA	p.Cys76Arg	probably damaging	0.000	0.001
☐	rs79565841	T	162,352,367	GCA	p.Gln74His	probably damaging	0.004	0.004
☐	rs545281061	-	162,347,739	GCA	p.Gln64ArgfsTer14		0.000	0.004
☐	rs774170639	A	162,347,656	GCA	p.Asp36Asn	benign	0.000	0.001
☐	rs1403164634	G	162,318,102	IFIH1	p.Gly69Ala	benign	0.000	0.001
☐	rs147278787	A	162,318,079	IFIH1	p.Arg77Trp	possibly damaging	0.001	0.003

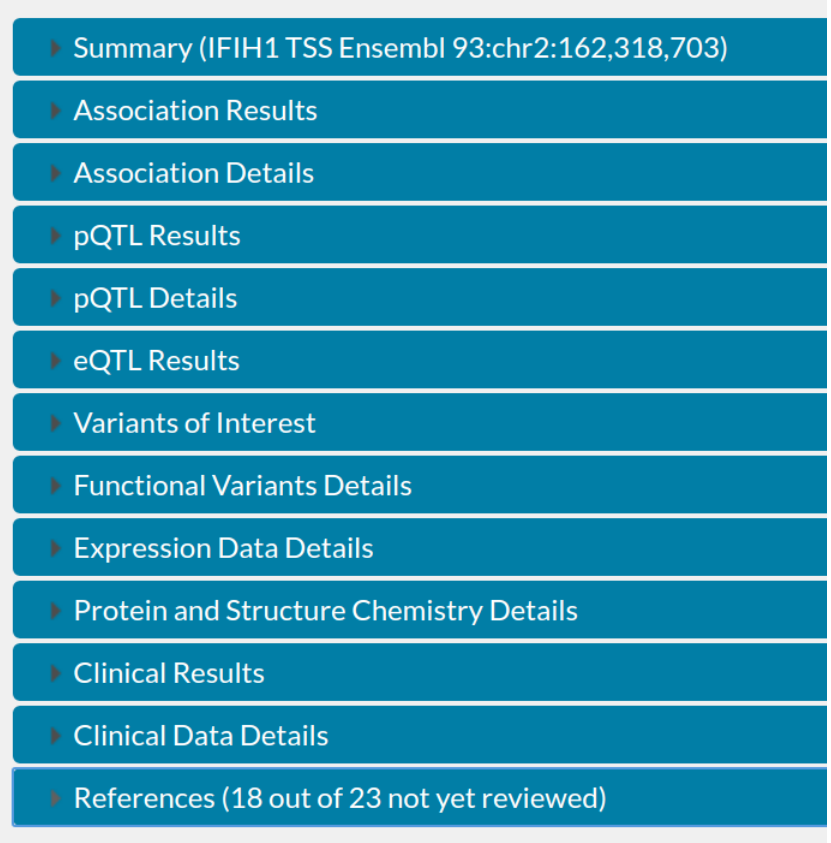
Page: 1 1 to 10 of 68 rows 10

Reviewed	1st Author	Year	Journal/Site/File	Title/Description	Curator Comment		
☑		2019	https://clue.io/repurposing-app	Curated information about drugs and drug targets from Broad.	Enter comment	Show/Add Details	X
☑	Li Q	2017	Pharmacogenet. Genomics	Genome-wide association study of paliperidone efficacy.	Enter comment	Show/Add Details	
☑		2017	http://www.nealelab.is/blog/2017/7/19/rapid-gwas-of-thousands-of-phenotypes-for-337000-samples-in-the-uk-biobank	UK Biobank Rapid GWAS	Enter comment	Show/Add Details	X
☑	Pettersson M	2017	Am. J. Med. Genet. A	Further evidence for specific IFIH1 mutation as a cause of Singleton-Merten syndrome with phenotypic heterogeneity.	Enter comment	Show/Add Details	X
☑	Gorman JA	2017	Nat. Immunol.	The A946T variant of the RNA sensor IFIH1 mediates an interferon program that limits viral infection but increases the risk for autoimmunity.	Enter comment	Show/Add Details (1)	X
☐	Bronson PG	2016	Nat. Genet.	Common variants at PVT1, ATG13-AMBRA1, AHI1 and CLEC16A are associated with selective IgA deficiency.	Enter comment	Show/Add Details	
☐	Morris DL	2016	Nat. Genet.	Genome-wide association meta-analysis in Chinese and European individuals identifies ten new loci associated with systemic lupus erythematosus.	Enter comment	Show/Add Details	
☐	Jin Y	2016	Nat. Genet.	Genome-wide association studies of autoimmune vitiligo identify 23 new risk loci and highlight key pathways and regulatory variants.	Enter comment	Show/Add Details	
☐	Bentham J	2015	Nat. Genet.	Genetic association analyses implicate aberrant regulation of innate and adaptive immunity genes in the pathogenesis of systemic lupus erythematosus.	Enter comment	Show/Add Details	
☐	Yin X	2015	Nat Commun	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility.	Enter comment	Show/Add Details	

Page: 1 1 to 10 of 23 rows 10

Text-based/tabular view of curated data.

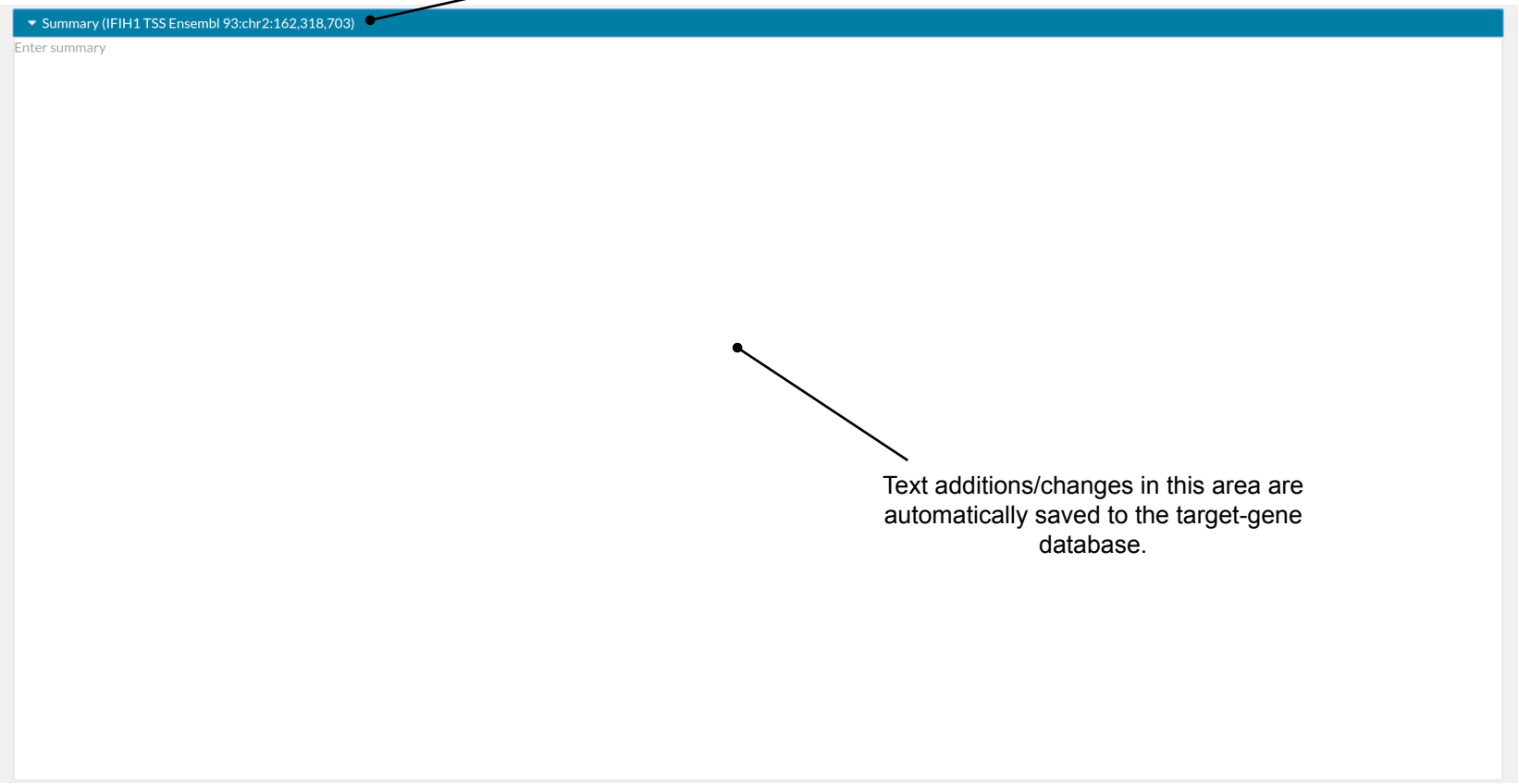
13 different sections hold curated data



Text-based/tabular view of curated data.

Summary section

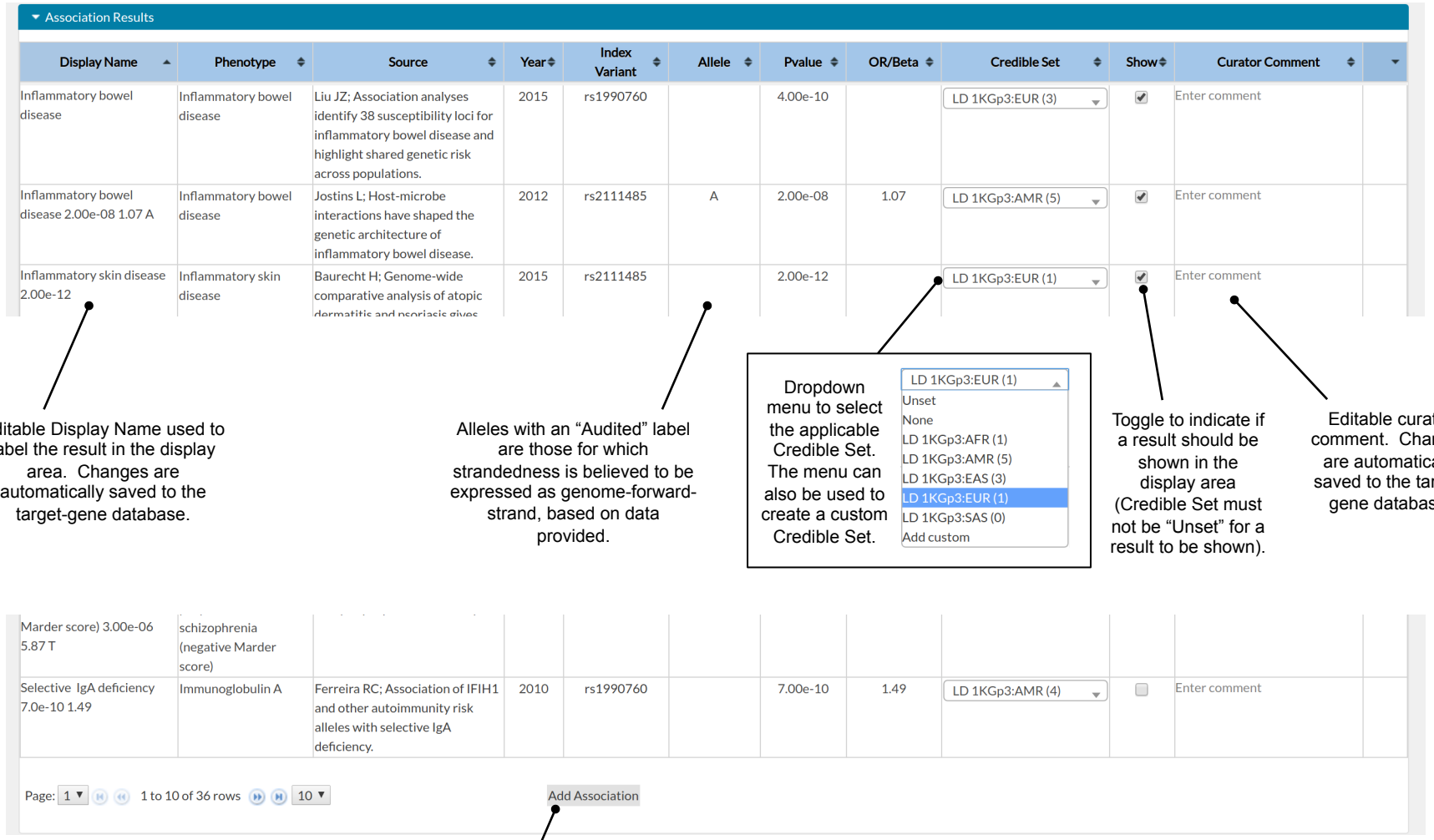
The Ensembl version against which the data were curated is shown here, along with the start position of the canonical transcript for the target gene.



Text additions/changes in this area are automatically saved to the target-gene database.

Text-based/tabular view of curated data.

Association Results section



Editable Display Name used to label the result in the display area. Changes are automatically saved to the target-gene database.

Alleles with an "Audited" label are those for which strandedness is believed to be expressed as genome-forward-strand, based on data provided.

Dropdown menu to select the applicable Credible Set. The menu can also be used to create a custom Credible Set.

Toggle to indicate if a result should be shown in the display area (Credible Set must not be "Unset" for a result to be shown).

Editable curator comment. Changes are automatically saved to the target-gene database.

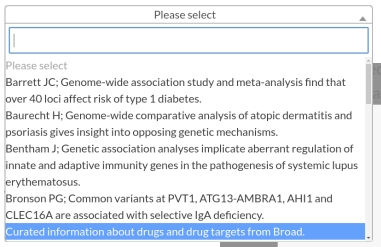
Button to add a new association result (see next page).

Text-based/tabular view of curated data.

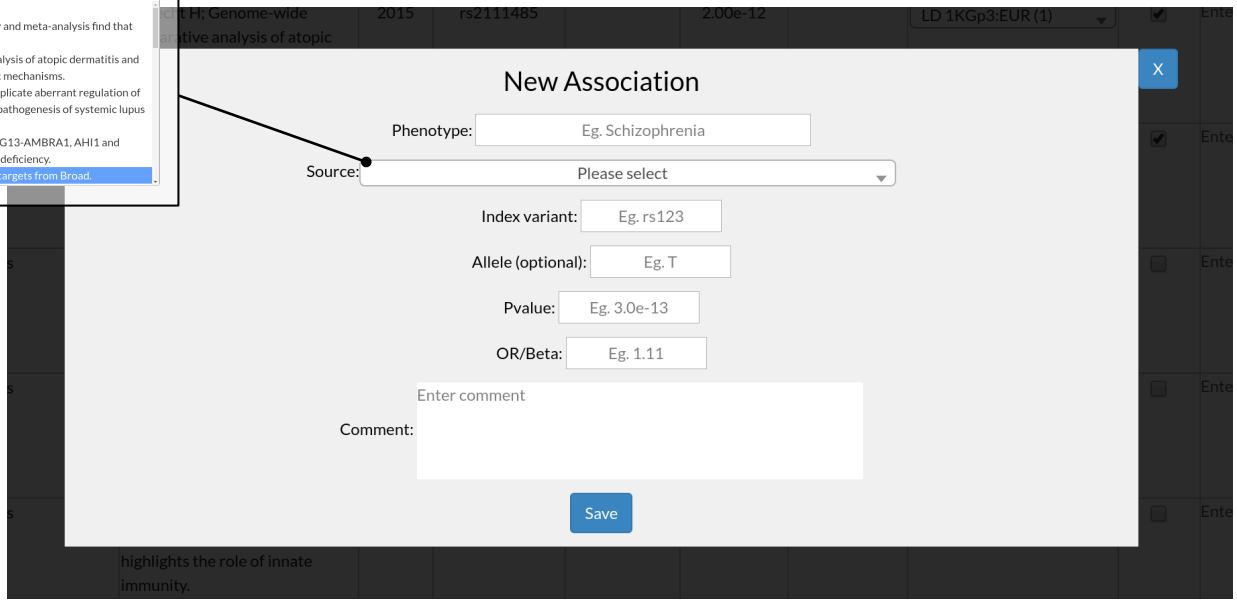
Association Results section

Adding an association result

Desired reference must already have been added to the References section to appear in the Source dropdown menu (see later description of the References section).



Add Association



Some new phenotype 1.00e-09 1.19 T	Some new phenotype	Curated information about drugs and drug targets from Broad.	2019	rs1990760	T	1.00e-09	1.19	Unset		This is a made-up example.	X

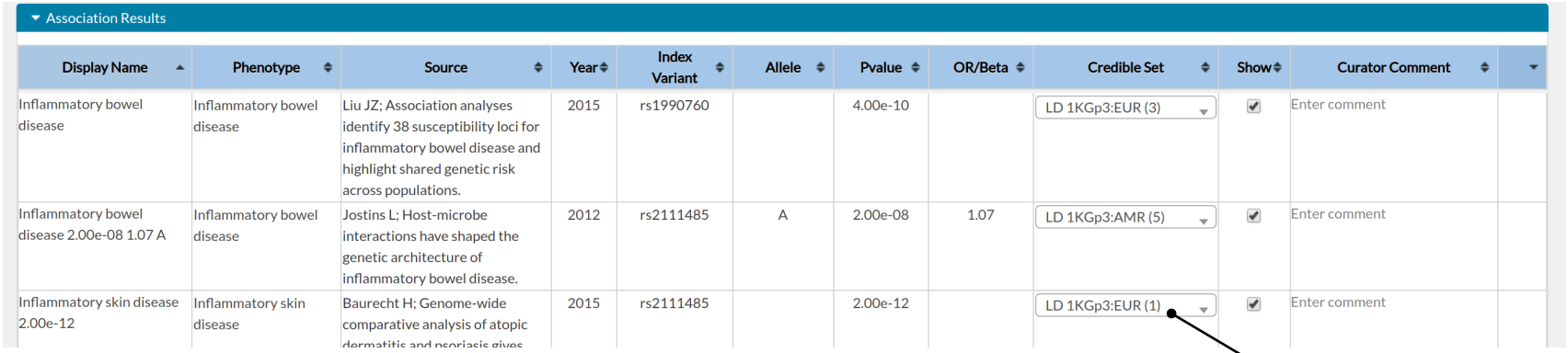
New row added to association-results table.

Button to remove association result.

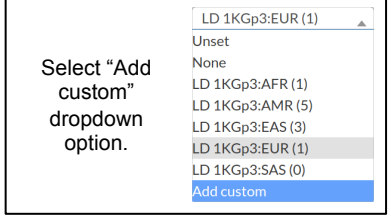
Text-based/tabular view of curated data.

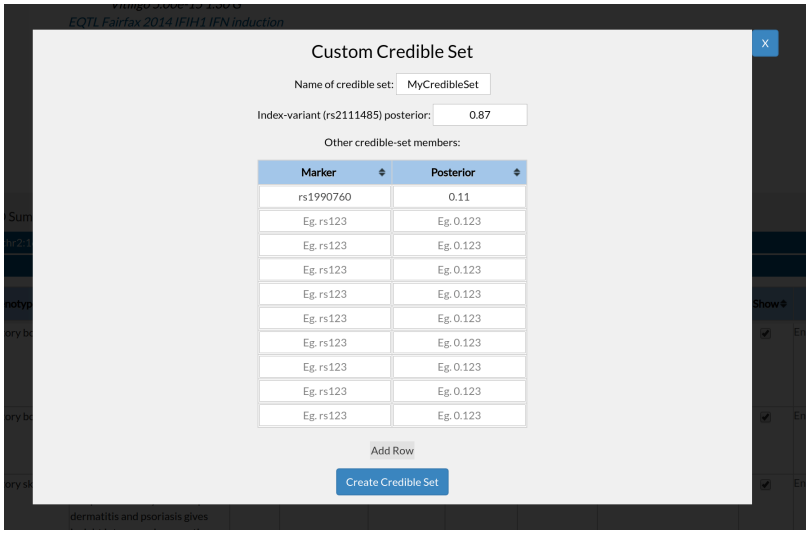
Association Results section

Creating a custom Credible Set

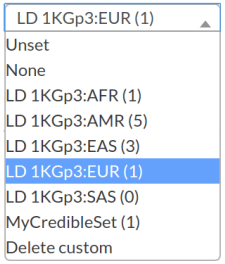


Select "Add custom" dropdown option.





Define custom Credible Set.



The custom Credible Set and ability to delete the custom Credible Set are now selectable options in the dropdown menu.

Text-based/tabular view of curated data.

pQTL Results and eQTL Results sections

These sections are very similar to the Association Results section

pQTL Results

eQTL Results

Display Name	Tissue	Gene	Source	Year	Index Variant	Pvalue	Beta	Effect Allele	Credible Set	Show	Curator Comment		
EQTL GTeX FAP Nerve Tibial 2.55e-05	Nerve Tibial	FAP	GTEx Consortium; Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans.	2015	rs3788967	2.55e-05	0.56		Unset		Tissue pval threshold = 4.11e-05		0
EQTL GTeX FAP Artery Tibial 5.19e-07	Artery Tibial	FAP	GTEx Consortium; Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans.	2015	rs3827491	5.19e-07	0.43		Unset		Tissue pval threshold = 3.54e-05		0
EQTL GTeX FAP Cells Transformed fibroblasts 1.67e-06	Cells Transformed fibroblasts	FAP	GTEx Consortium; Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans.	2015	rs6746339	1.67e-06	0.34		Unset		Tissue pval threshold = 3.54e-05		0
EQTL GTeX FAP Cells Transformed fibroblasts 7.80e-06	Cells Transformed fibroblasts	FAP	GTEx Consortium; Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans.	2015	rs12468578	7.80e-06	0.36		Unset		Tissue pval threshold = 3.54e-05		0
EQTL GTeX FAP Thyroid 2.67e-05	Thyroid	FAP	GTEx Consortium; Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans.	2015	rs2389683	2.67e-05	0.45		Unset		Tissue pval threshold = 3.29e-05		0
EQTL GTeX FAP Thyroid 2.91e-05	Thyroid	FAP	GTEx Consortium; Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans.	2015	rs11455810	2.91e-05	0.44		Unset		Tissue pval threshold = 3.29e-05		0
EQTL GTeX FAP Thyroid 4.53e-06	Thyroid	FAP	GTEx Consortium; Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans.	2015	rs16846600	4.53e-06	0.51		Unset		Tissue pval threshold = 3.29e-05		0
EQTL GTeX FAP Muscle Skeletal 1.58e-05	Muscle Skeletal	FAP	GTEx Consortium; Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans.	2015	rs35544136	1.58e-05	0.67		Unset		Tissue pval threshold = 1.85e-05		0
EQTL GTeX GCA Adrenal Gland 6.34e-06	Adrenal Gland	GCA	GTEx Consortium; Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans.	2015	rs34977319	6.34e-06	-0.77		Unset		Tissue pval threshold = 1.75e-05		0
EQTL Fairfax 2014 IFIH1 IFN induction	Monocytes	IFIH1	Fairfax BP; Innate immune activity conditions the effect of regulatory variants upon monocyte gene expression.	2014	rs2111485	1.19e-08	5.85		LD 1KGp3:EUR (1)	☑	Enter comment	X	10

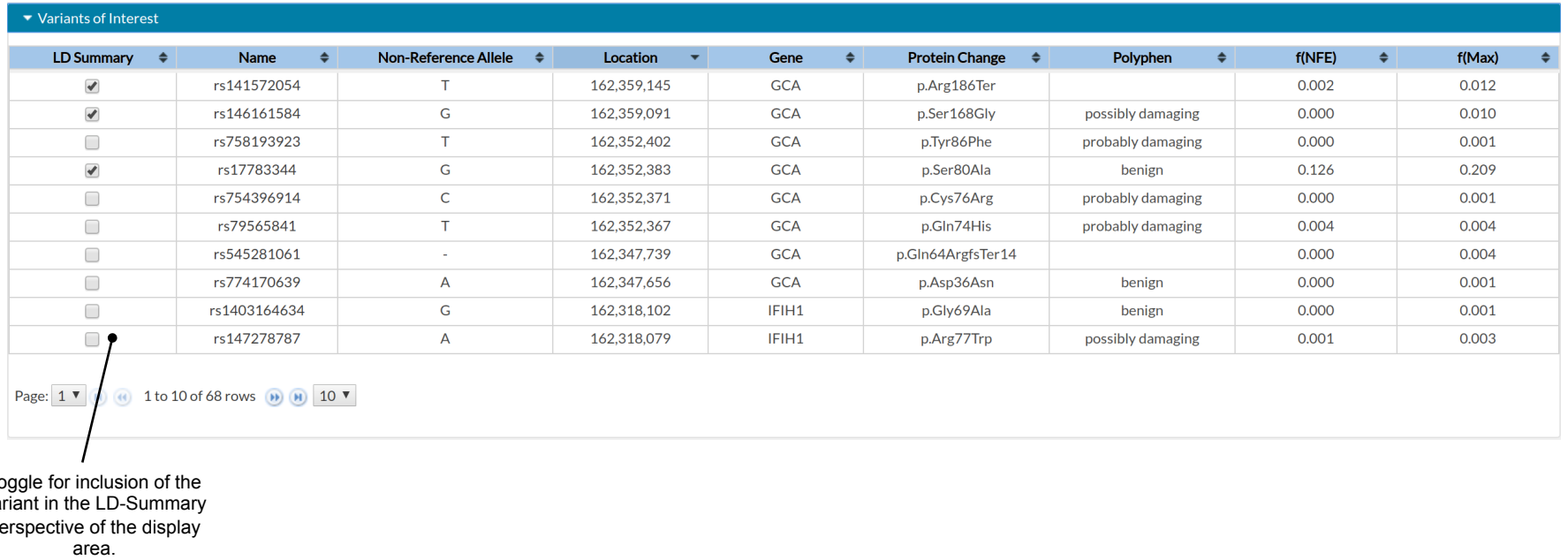
Page: 1 1 to 10 of 10 rows 10 Add eQTL

The eQTL Results table contains an extra column showing the count of displayed association and pQTL results that have intersecting Credible-Set members with the 1KGp3:EUR Credible Set of each eQTL result.

Text-based/tabular view of curated data.

Variants of Interest section

In this section are listed those variant alleles which confer a coding or likely splice change to any gene in the neighborhood of the target gene



Variants of Interest

LD Summary	Name	Non-Reference Allele	Location	Gene	Protein Change	Polyphen	f(NFE)	f(Max)
☑	rs141572054	T	162,359,145	GCA	p.Arg186Ter		0.002	0.012
☑	rs146161584	G	162,359,091	GCA	p.Ser168Gly	possibly damaging	0.000	0.010
☐	rs758193923	T	162,352,402	GCA	p.Tyr86Phe	probably damaging	0.000	0.001
☑	rs17783344	G	162,352,383	GCA	p.Ser80Ala	benign	0.126	0.209
☐	rs754396914	C	162,352,371	GCA	p.Cys76Arg	probably damaging	0.000	0.001
☐	rs79565841	T	162,352,367	GCA	p.Gln74His	probably damaging	0.004	0.004
☐	rs545281061	-	162,347,739	GCA	p.Gln64ArgfsTer14		0.000	0.004
☐	rs774170639	A	162,347,656	GCA	p.Asp36Asn	benign	0.000	0.001
☐	rs1403164634	G	162,318,102	IFIH1	p.Gly69Ala	benign	0.000	0.001
☐	rs147278787	A	162,318,079	IFIH1	p.Arg77Trp	possibly damaging	0.001	0.003

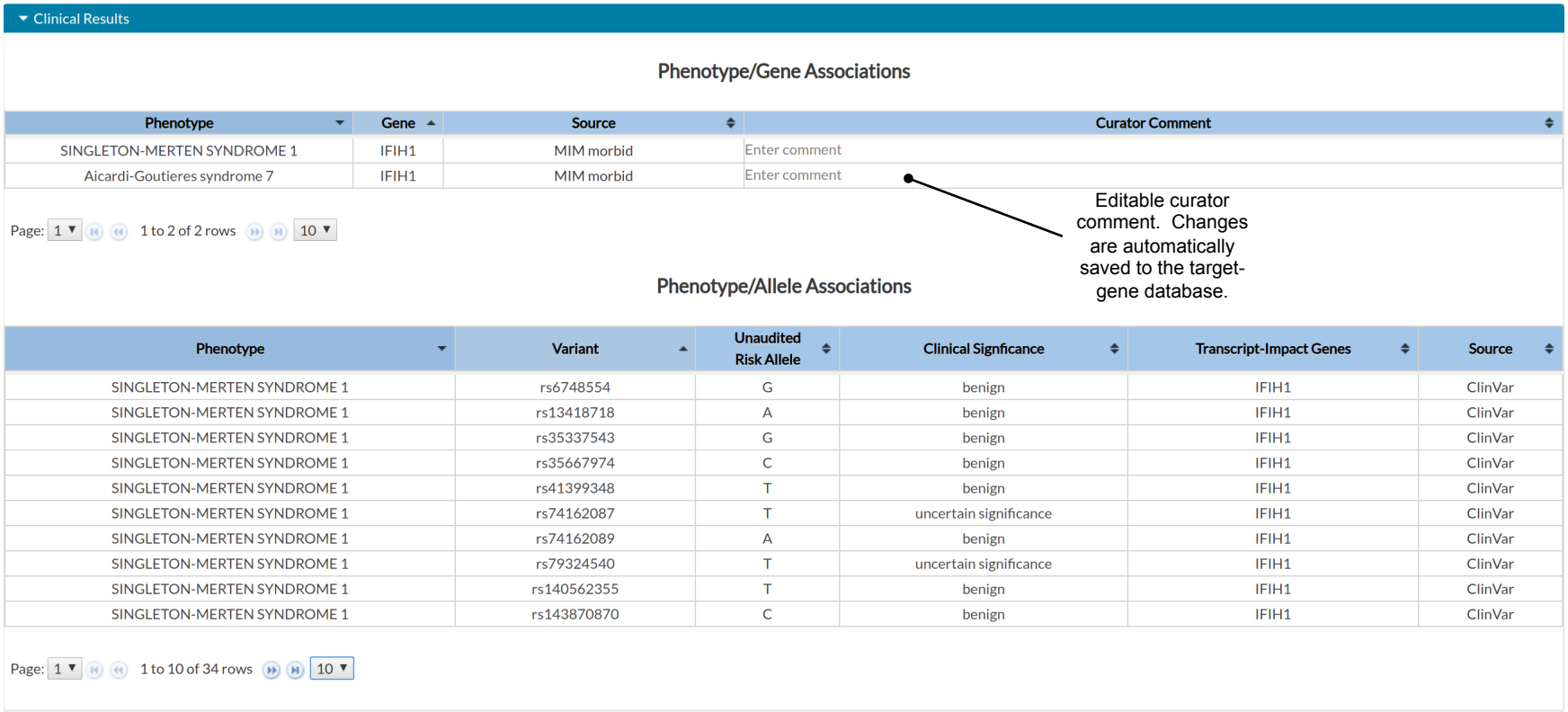
Page: 1 1 to 10 of 68 rows 10

Toggle for inclusion of the variant in the LD-Summary perspective of the display area.

To be included in this table, an allele must have a frequency of at least 0.001 in one of the ExAC sub-populations.

Text-based/tabular view of curated data.

Clinical Results section



Clinical Results

Phenotype/Gene Associations

Phenotype	Gene	Source	Curator Comment
SINGLETON-MERTEN SYNDROME 1	IFIH1	MIM morbid	Enter comment
Aicardi-Goutieres syndrome 7	IFIH1	MIM morbid	Enter comment

Page: 1 1 to 2 of 2 rows 10

Editable curator comment. Changes are automatically saved to the target-gene database.

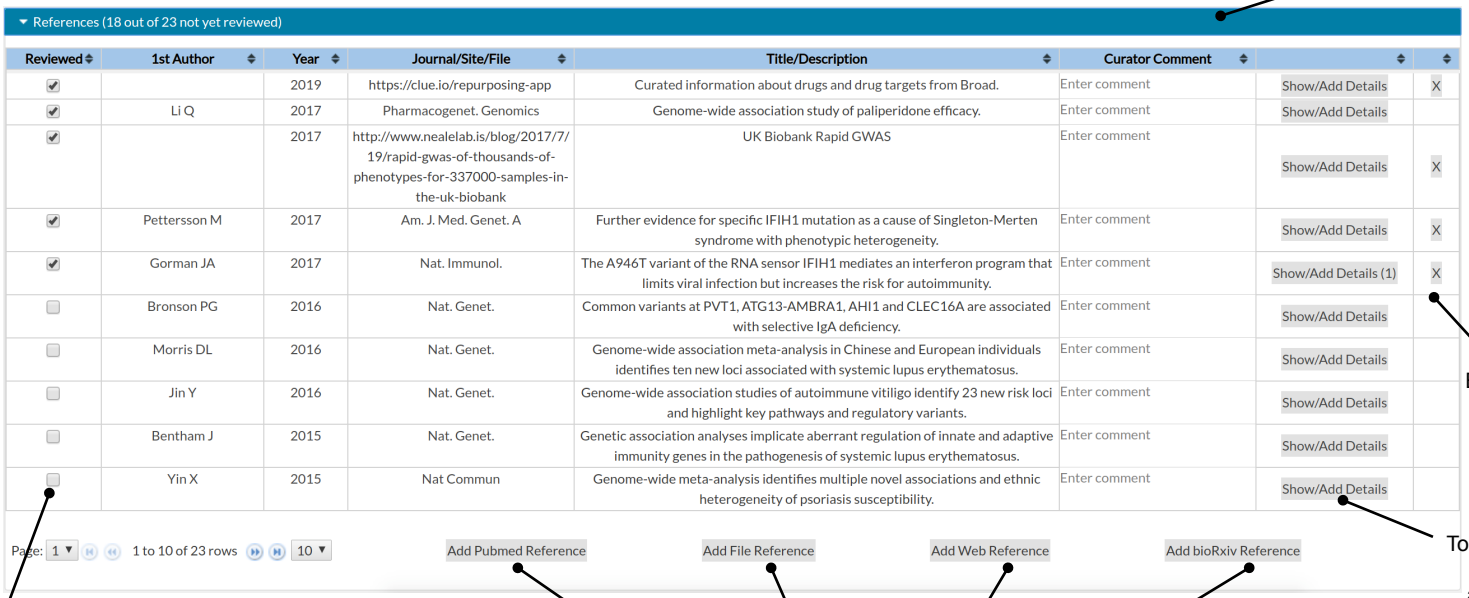
Phenotype/Allele Associations

Phenotype	Variant	Unaudited Risk Allele	Clinical Signficance	Transcript-Impact Genes	Source
SINGLETON-MERTEN SYNDROME 1	rs6748554	G	benign	IFIH1	ClinVar
SINGLETON-MERTEN SYNDROME 1	rs13418718	A	benign	IFIH1	ClinVar
SINGLETON-MERTEN SYNDROME 1	rs35337543	G	benign	IFIH1	ClinVar
SINGLETON-MERTEN SYNDROME 1	rs35667974	C	benign	IFIH1	ClinVar
SINGLETON-MERTEN SYNDROME 1	rs41399348	T	benign	IFIH1	ClinVar
SINGLETON-MERTEN SYNDROME 1	rs74162087	T	uncertain significance	IFIH1	ClinVar
SINGLETON-MERTEN SYNDROME 1	rs74162089	A	benign	IFIH1	ClinVar
SINGLETON-MERTEN SYNDROME 1	rs79324540	T	uncertain significance	IFIH1	ClinVar
SINGLETON-MERTEN SYNDROME 1	rs140562355	T	benign	IFIH1	ClinVar
SINGLETON-MERTEN SYNDROME 1	rs143870870	C	benign	IFIH1	ClinVar

Page: 1 1 to 10 of 34 rows 10

Text-based/tabular view of curated data.

References section



Editable curator comment. Changes are automatically saved to the target-gene database.

Button to remove user-added references.

Toggles to show/hide Detail elements attached to each reference (see next page). Number of Detail elements shown in parentheses.

Checkboxes to declare references having been reviewed.

Buttons to add new references of different types.

Text-based/tabular view of curated data.

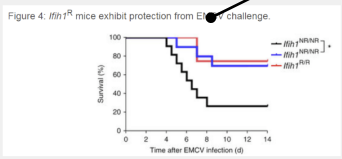
References section

Graphic elements (Details) can be saved with each reference

References (18 out of 23 not yet reviewed)

Reviewed	1st Author	Year	Journal/Site/File	Title/Description	Curator Comment		
☑		2019	https://clue.io/repurposing-app	Curated information about drugs and drug targets from Broad.	Enter comment	Show/Add Details	X
☑	Li Q	2017	Pharmacogenet. Genomics	Genome-wide association study of paliperidone efficacy.	Enter comment	Show/Add Details	
☑		2017	http://www.nealelab.is/blog/2017/7/19/rapid-gwas-of-thousands-of-phenotypes-for-337000-samples-in-the-uk-biobank	UK Biobank Rapid GWAS	Enter comment	Show/Add Details	X
☑	Pettersson M	2017	Am. J. Med. Genet. A	Further evidence for specific IFIH1 mutation as a cause of Singleton-Merten syndrome with phenotypic heterogeneity.	Enter comment	Show/Add Details	X
☑	Gorman JA	2017	Nat. Immunol.	The A946T variant of the RNA sensor IFIH1 mediates an interferon program that limits viral infection but increases the risk for autoimmunity.	Enter comment	Hide Details (1)	

Functional data linking rs1990760 (A946T) and protection from infection challenge in mice.



Zoomable thumbnail of Detail.

Section Assignment: Functional

Editable description field. Changes are automatically saved to the target-gene database.

Remove

X

Button to remove Detail

Button to add new Detail (see next page). Add Detail

Dropdown menu to select the applicable section in which the Detail should appear.

- Functional
- None
- Association
- Clinical
- Expression
- Functional
- PQTL
- Protein

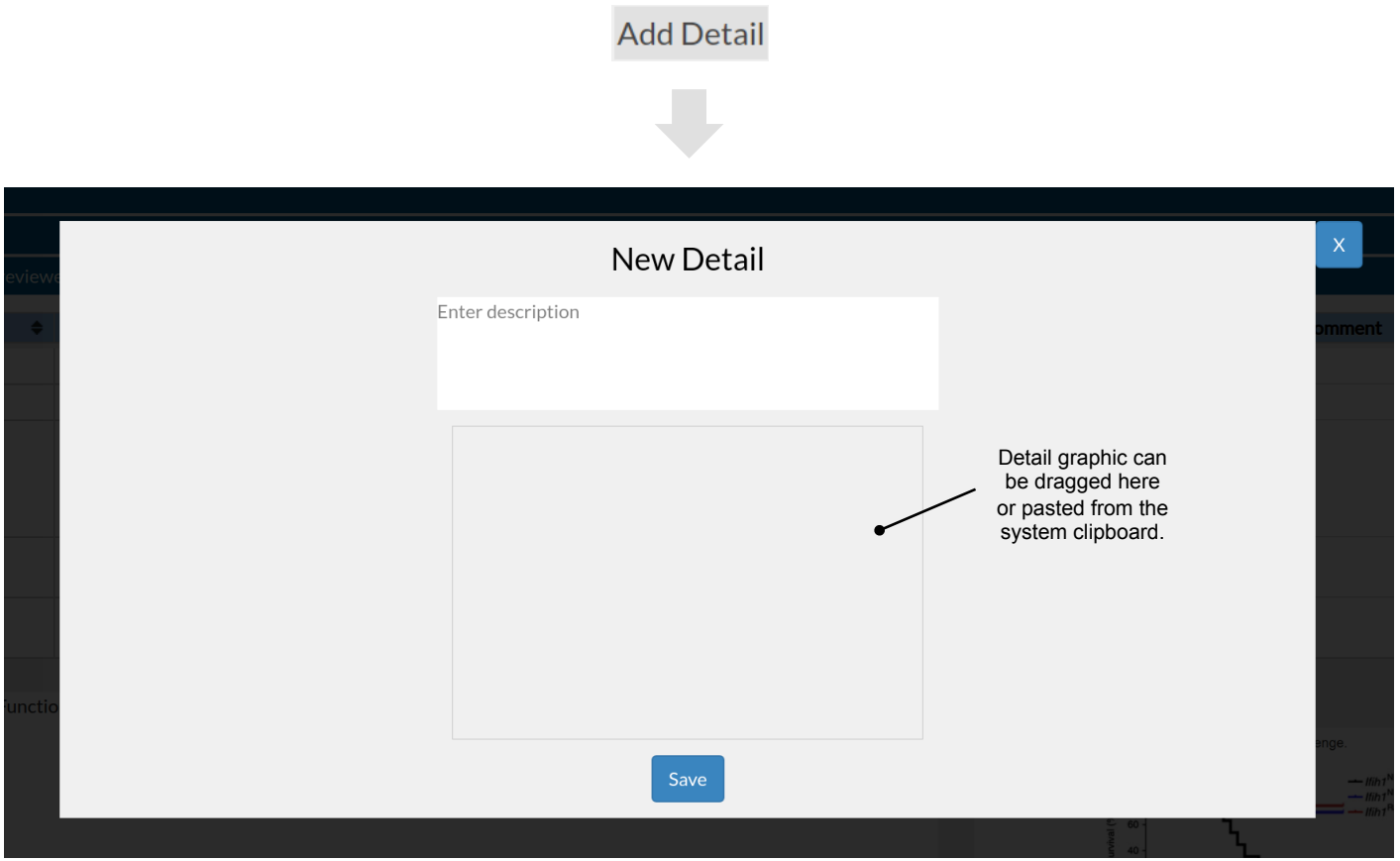
☐	Bronson PG	2016	Nat. Genet.	Common variants at PVT1, ATG13-AMBRA1, AHI1 and CLEC16A are associated with selective IgA deficiency.	Enter comment	Show/Add Details	
☐	Morris DL	2016	Nat. Genet.	Genome-wide association meta-analysis in Chinese and European individuals identifies ten new loci associated with systemic lupus erythematosus.	Enter comment	Show/Add Details	
☐	Jin Y	2016	Nat. Genet.	Genome-wide association studies of autoimmune vitiligo identify 23 new risk loci and highlight key pathways and regulatory variants.	Enter comment	Show/Add Details	
☐	Bentham J	2015	Nat. Genet.	Genetic association analyses implicate aberrant regulation of innate and adaptive immunity genes in the pathogenesis of systemic lupus erythematosus.	Enter comment	Show/Add Details	
☐	Yin X	2015	Nat Commun	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility.	Enter comment	Show/Add Details	

Page: 1 1 to 10 of 23 rows 10 Add Pubmed Reference Add File Reference Add Web Reference Add bioRxiv Reference

Text-based/tabular view of curated data.

References section

Adding a Detail



Text-based/tabular view of curated data.

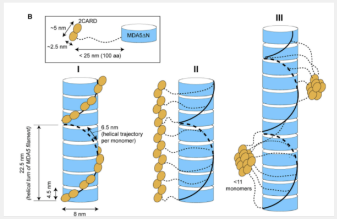
Association Details, pQTL Details, Functional Variants Details, Expression Data Details, Protein and Structure Chemistry Details, and Clinical Data Details sections

Each section contains those Details assigned to that particular section, organized by reference

▾ Protein and Structure Chemistry Details

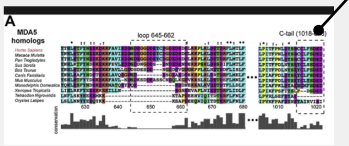
1st Author	Year	Journal/Site/File	Title/Description
Wu B	2013	Cell	Structural basis for dsRNA recognition, filament formation, and antiviral signal activation by MDA5.

Figure 7. Oligomerization of 2CARD in the Full-Length MDA5 Filament



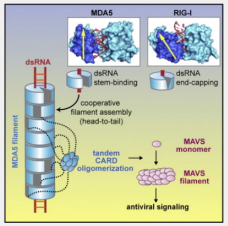
MDA5 homologs

Editable description field. Changes are automatically saved to the target-gene database.



Zoomable thumbnail of Detail

MDA5 filament formation



Page: 1 ▾ 1 to 1 of 1 rows 10 ▾

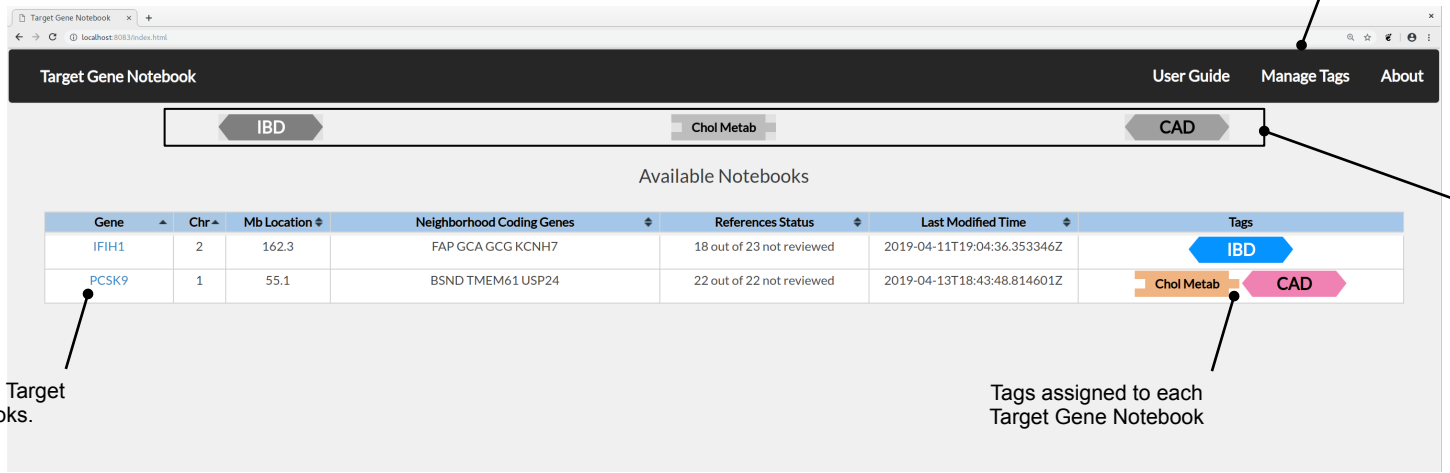
Text-based/tabular view of curated data.

Notebook utilities…

Notebook utilities.

Overview page of available Target Gene Notebooks

This is the TGN server's index.html page

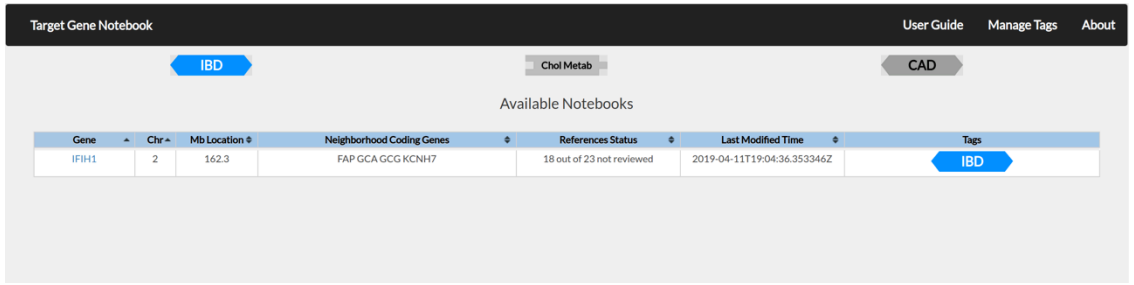


Link to Tag-management tools (see next page).

Toggles to filter TGN list according to assigned Tags.

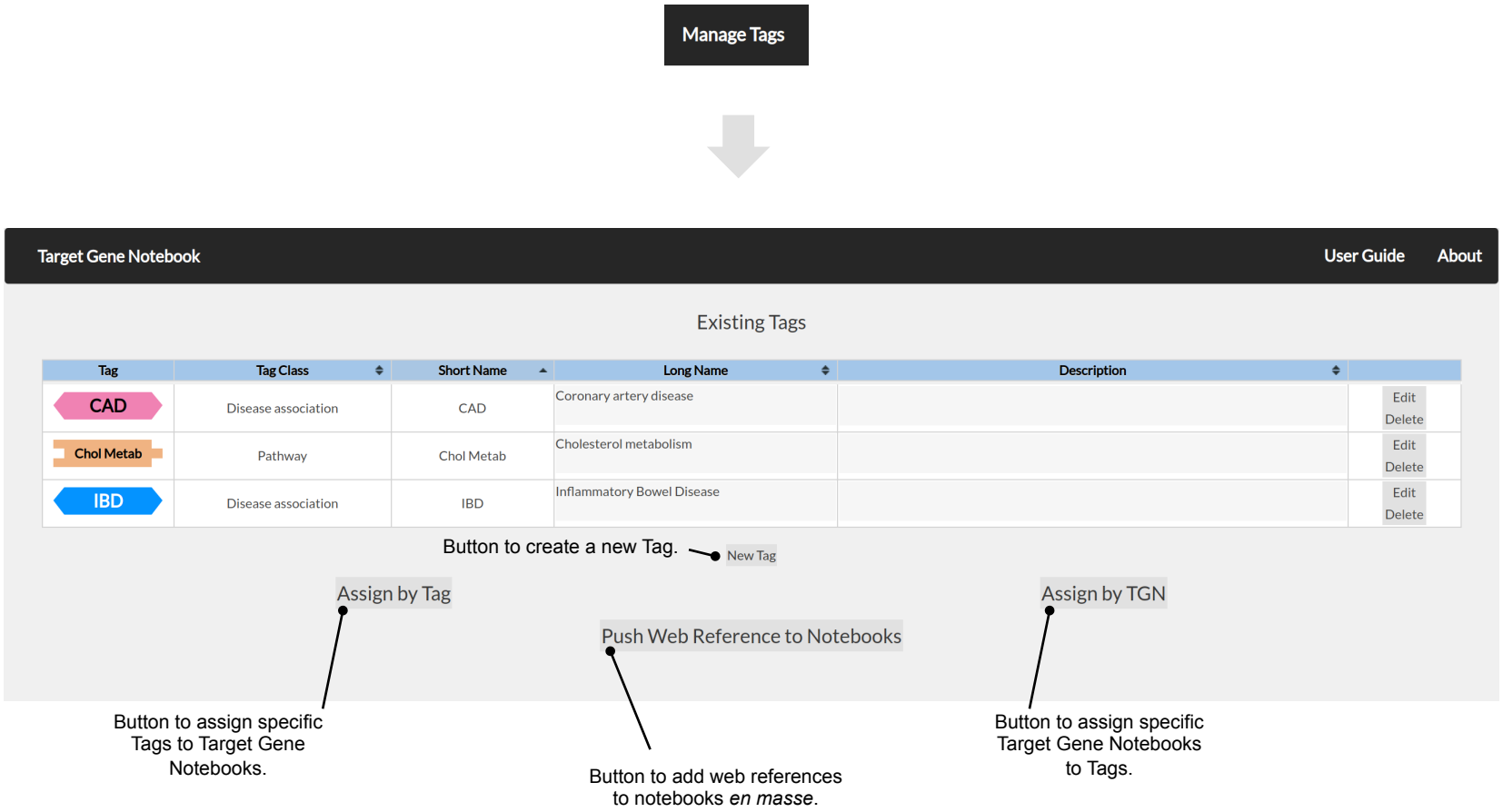
Links to available Target Gene Notebooks.

Tags assigned to each Target Gene Notebook



Notebook utilities.

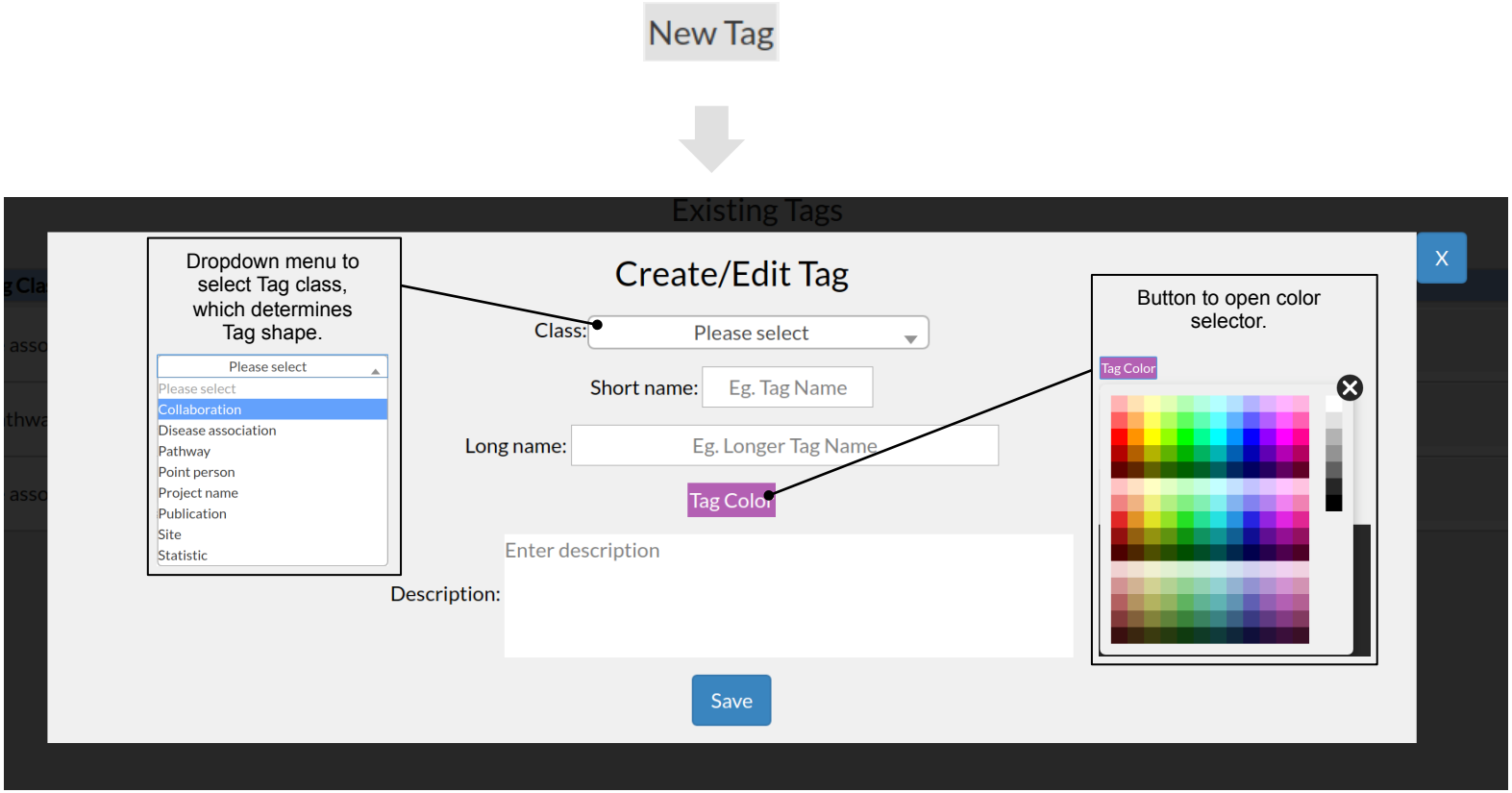
Tag-management tools



Notebook utilities.

Tag-management tools

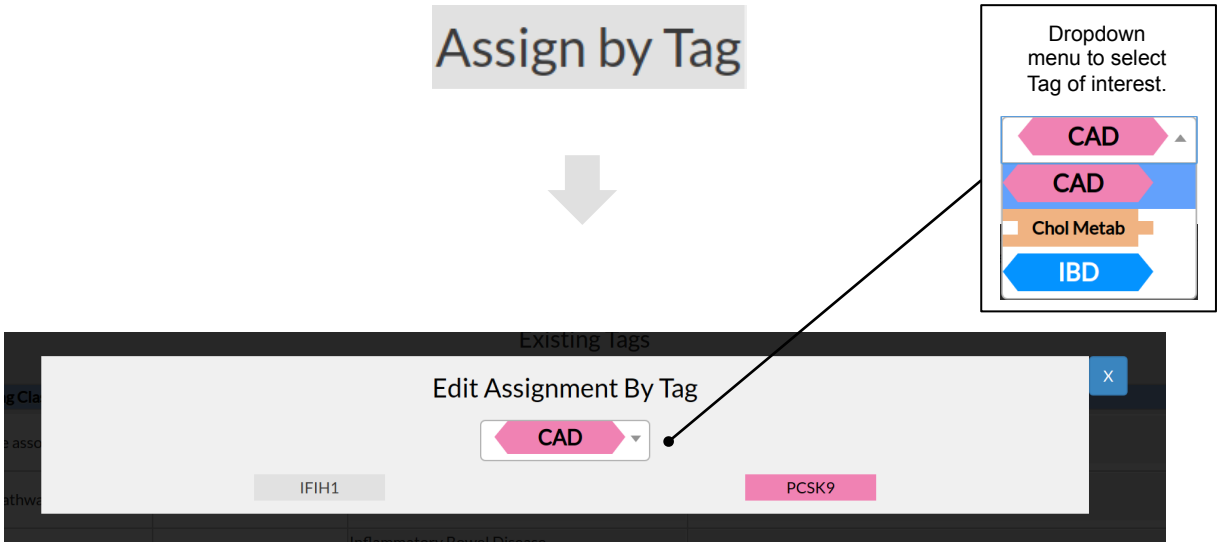
Creating a Tag



Notebook utilities.

Tag-management tools

Assigning specific Tags to Target Gene Notebooks

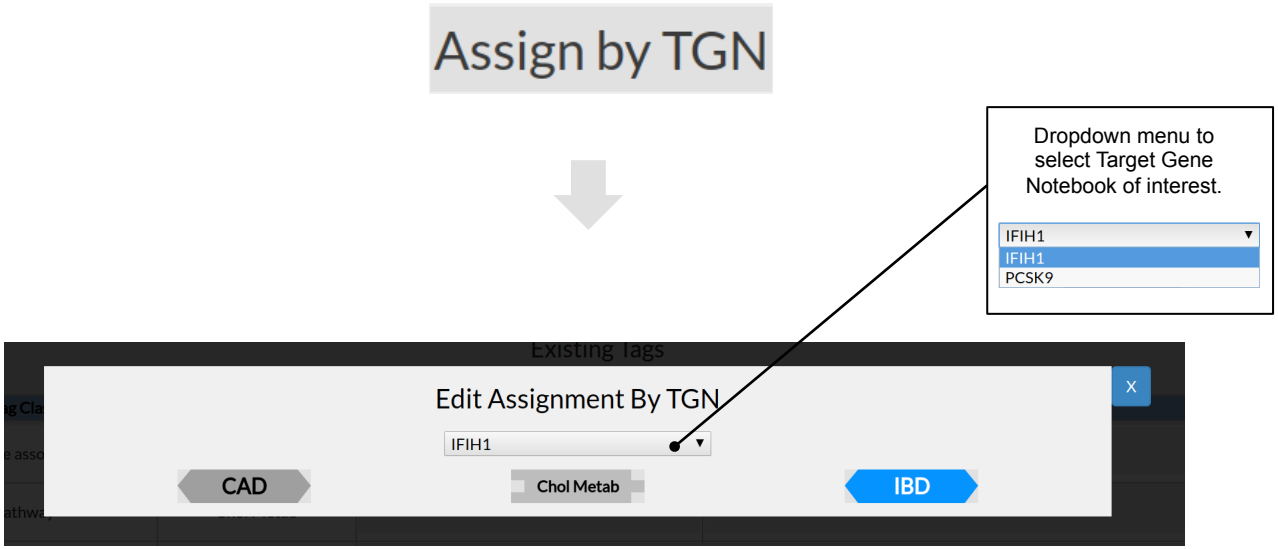


Use Notebook buttons to toggle Tag assignment: if the Notebook button is the same color as the Tag, then that Tag is assigned to the Notebook.

Notebook utilities.

Tag-management tools

Assigning specific Target Gene Notebooks to Tags



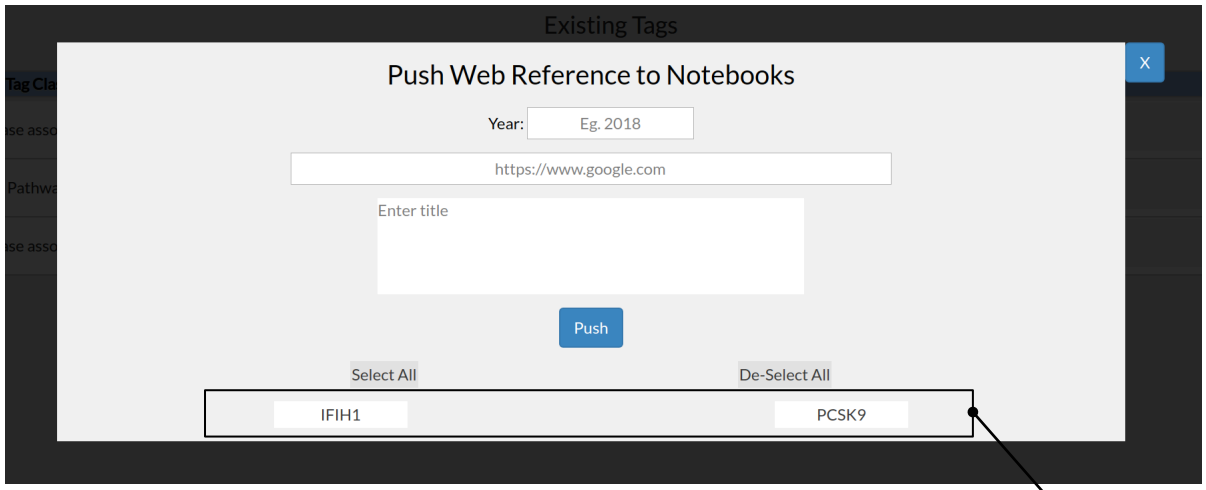
Use Tag buttons to toggle Tag assignment: if the Tag button is the same color as the Tag, then the Notebook is assigned to that Tag.

Tag-management tools

Pushing a web reference to existing Notebooks

(yes, we know this is technically not Tag management)

Push Web Reference to Notebooks



Toggle buttons to indicate Notebooks to receive the web reference. Those Notebooks shaded blue will be sent the reference.

Notebooks that already have the web reference will ignore the push.