Mouse Atlas DiscoverySpace Tutorial

DiscoverySpace 4

Example 1: Foregut vs. Hindgut

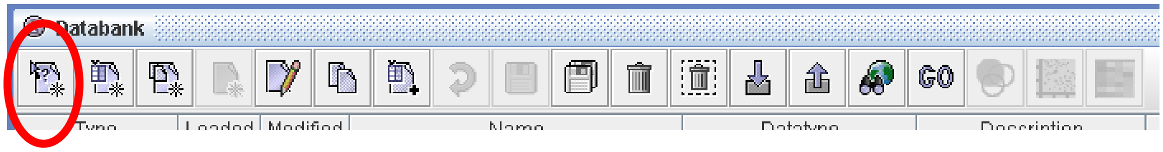
Example 2: Gene of Interest

Example 1: Foregut vs. Hindgut

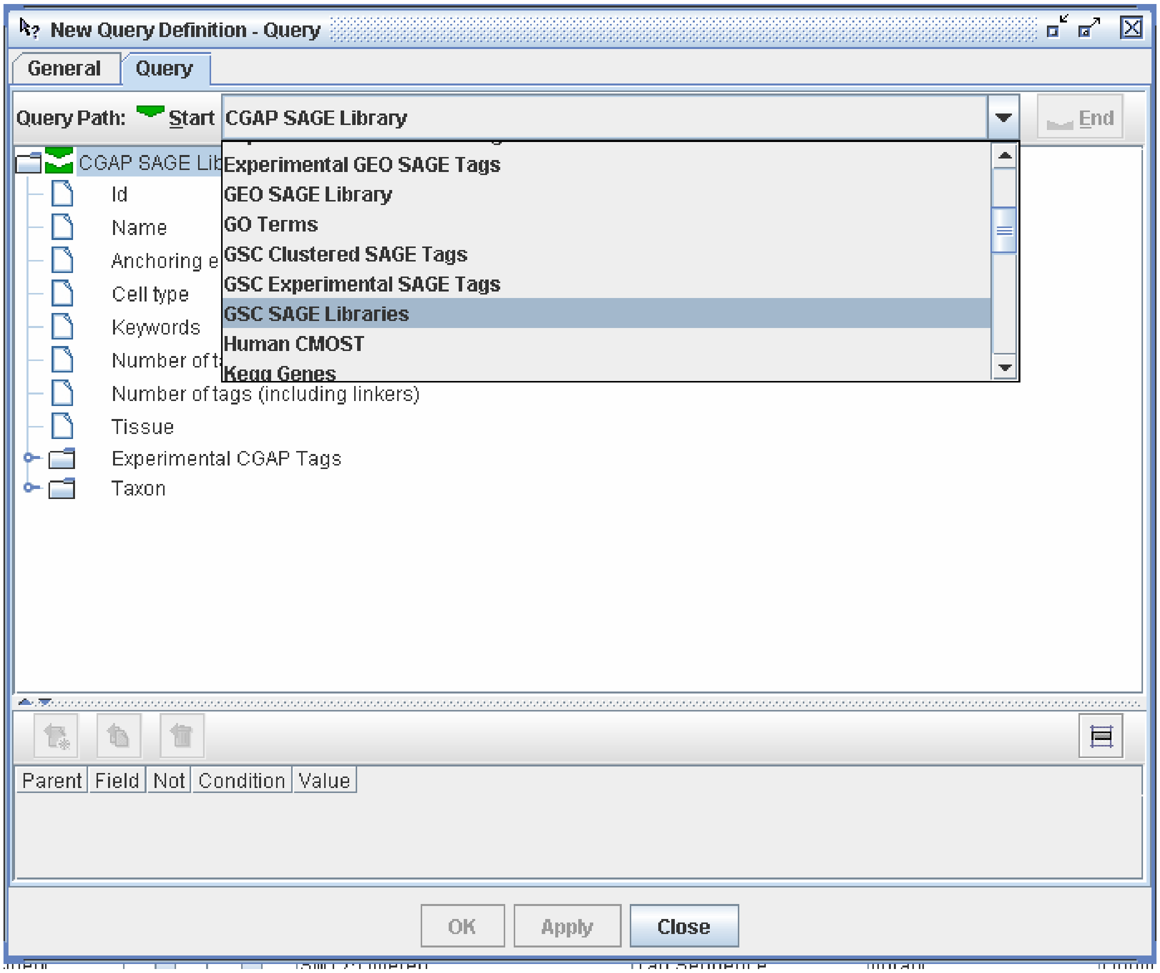
Task 1: find tags exclusively to hindgut and foregut libraries

1.1. Build query for Foregut (SM107)

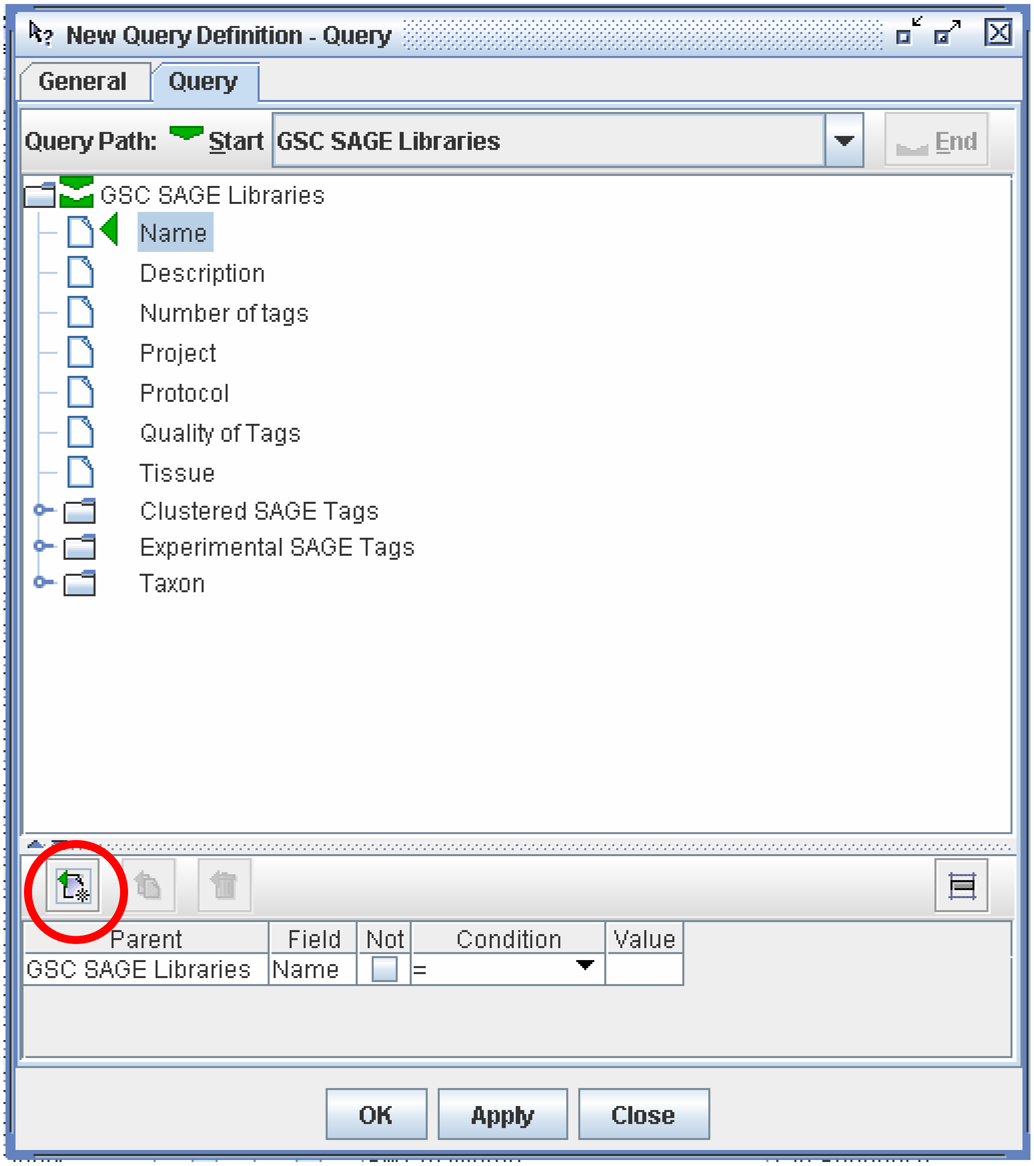
Create a new query by clicking the New Query button. This will open the Query Builder window.



Use the pull down menu to select GSC SAGE Libraries (Note: you must have set your user name and password to have access to these libraries. E-mail discoveryspace-support@bcgsc.ca if you do not have a password).



You can now begin to build your query. Understanding queries is crucial for successfully using DS4. It may feel overwhelming at first, but with a little practice, it will become clear.



Query Path: Start GSC SAGE Libraries

Parent	Field	Not	Condition	Value
GSC SAGE Libraries	Name	☐	=	

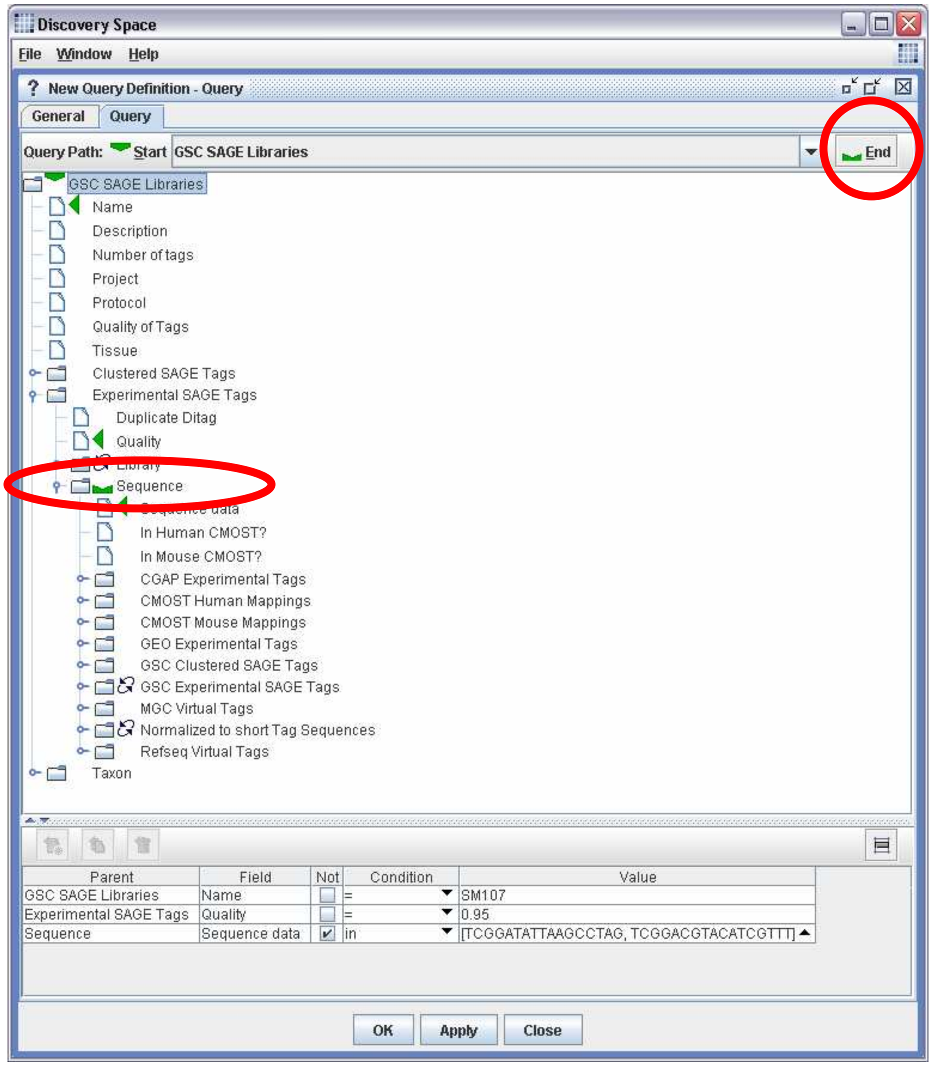
Click on each item you want to set a constraint for and click the "Set Parameter" button. In the bottom window you can set your constraint by selecting a condition and setting a value.

Parameters to set:

- GSC Libraries -> Name : set to library accession (SM107)
- Experimental SAGE Tags -> Quality : set to >= 0.95 (95%)
- Experimental SAGE Tags -> Sequence -> Sequence data: set to linkers using IN clause. Click NOT box to exclude linkers from your analysis.

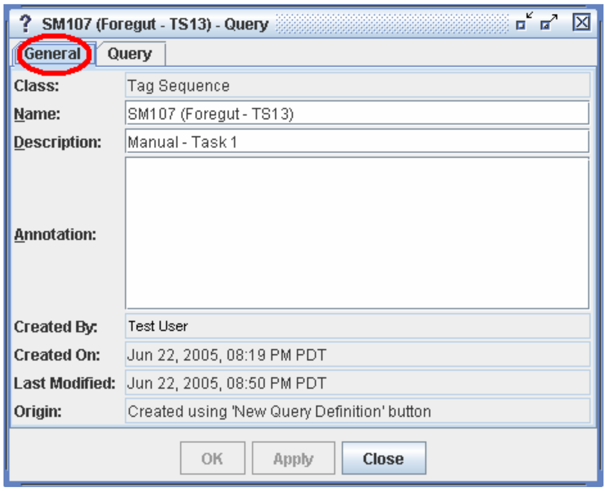
The final and VERY IMPORTANT step is to use the END button (on upper right hand side of the Query builder) to set what kind of data the query is going to return. In this case we set it to Sequence to return tags for our library.

Click Sequence, then click on the End button.



Parent	Field	Not	Condition	Value
GSC SAGE Libraries	Name	☐	=	SM107
Experimental SAGE Tags	Quality	☐	=	0.95
Sequence	Sequence data	☑	in	[TCGGATATTAAGCCTAG, TCGGACGTACATCGTTT]

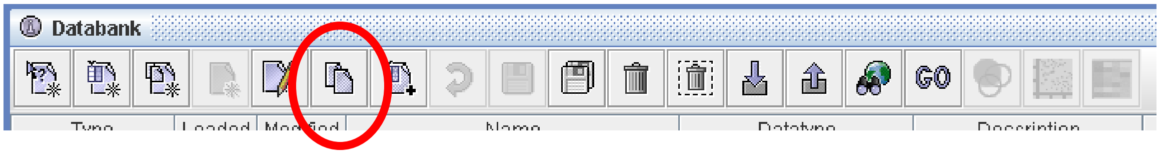
Our query is almost complete. Before clicking on "OK", make sure that you will be able to identify this query for future reference. You can do this by going to the General tab at the top of the query generator window and adding as much information as you think would be useful.

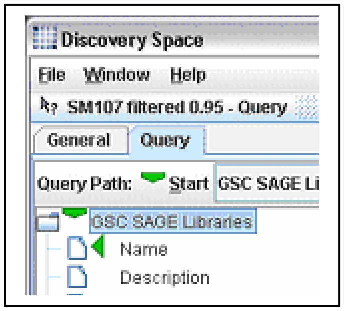


Class:	Tag Sequence
Name:	SM107 (Foregut - TS13)
Description:	Manual - Task 1
Annotation:	
Created By:	Test User
Created On:	Jun 22, 2005, 08:19 PM PDT
Last Modified:	Jun 22, 2005, 08:50 PM PDT
Origin:	Created using 'New Query Definition' button

The query is now complete. Click OK.

1.2. To create another query with the same parameters but for a different library, you can either repeat the previous step (1), or you can select your previous query in the databank and use the “Duplicate Selected Definitions” button on the databank to create an identical query for Hindgut (SM112).



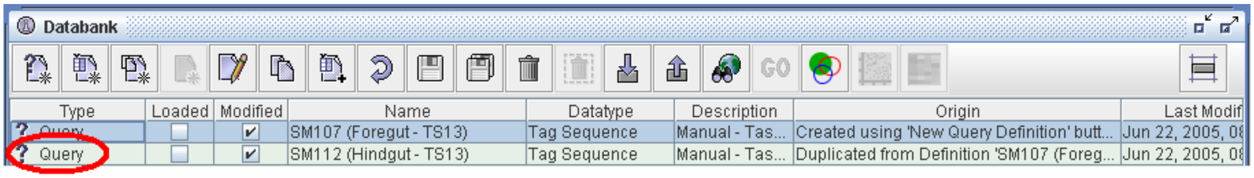


All you have to do is change the Name parameter to SM112. The other constraints will remain unchanged.

Again, you should save this query using an appropriate name by using the General tab.

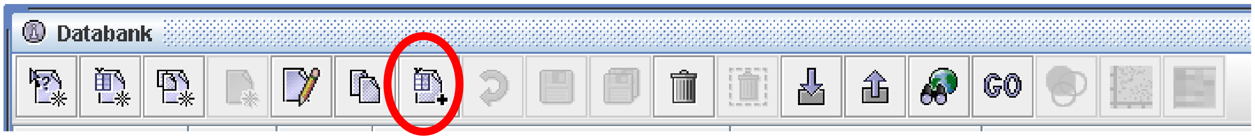
You now have two separate queries. One for Hindgut and one for Foregut.

Now go to the databank and look at the two queries. Notice they are both a query type. This indicates that if you work with this type of data you will be making a direct connection to the database. This is not necessarily a bad thing to do, but if many users are connecting in this fashion (using this data type) the queries will take a long time to return results.

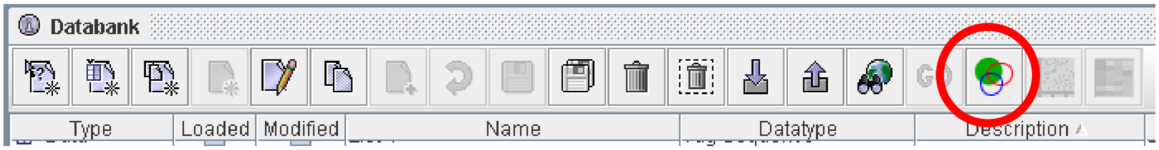


Type	Loaded	Modified	Name	Datatype	Description	Origin	Last Modif
? Query	☐	☑	SM107 (Foregut - TS13)	Tag Sequence	Manual - Tas...	Created using 'New Query Definition' butt...	Jun 22, 2005,
? Query	☐	☑	SM112 (Hindgut - TS13)	Tag Sequence	Manual - Tas...	Duplicated from Definition 'SM107 (Foreg...	Jun 22, 2005,

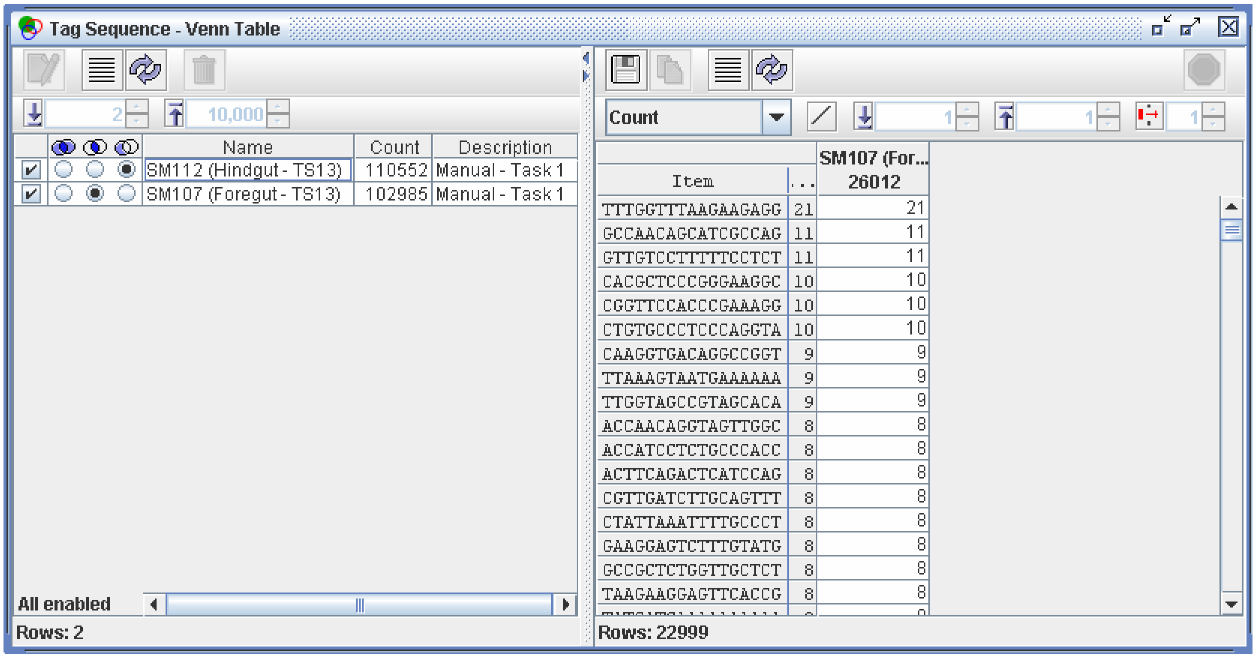
IMPORTANT: To speed up further analysis, you should create data definitions from your queries. Highlight your queries and select the Create Data Definition button. These definitions should be renamed for future reference. Click the General tab and enter identifying information. The data definitions will be used in subsequent analyses.



1.3. In the databank, select these two **data** definitions and click the Venn Diagram button.



The Venn widget will appear. You can extract tags exclusive to each library.



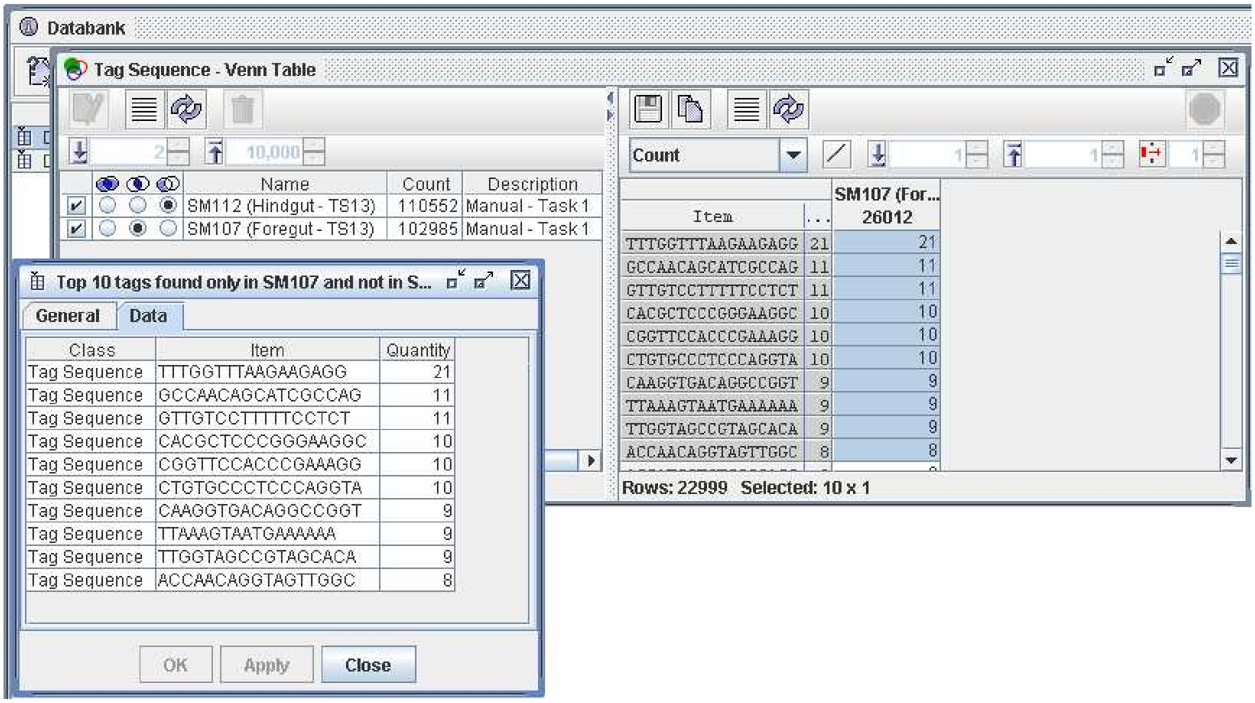
				Name	Count	Description
☑	○	○	●	SM112 (Hindgut - TS13)	110552	Manual - Task 1
☑	○	●	○	SM107 (Foregut - TS13)	102985	Manual - Task 1

Rows: 2

Item	...	SM107 (For... 26012
TTTGGTTTAAGAAGAGG	21	21
GCCAACAGCATCGCCAG	11	11
GTTGTCCTTTTTCCTCT	11	11
CACGCTCCCGGGAAGGC	10	10
CGGTTCCACCCGAAAGG	10	10
CTGTGCCCTCCCAGGTA	10	10
CAAGGTGACAGGCCGGT	9	9
TTAAAGTAATGAAAAAA	9	9
TTGGTAGCCGTAGCACA	9	9
ACCAACAGGTAGTTGGC	8	8
ACCATCCTCTGCCCACC	8	8
ACTTCAGACTCATCCAG	8	8
CGTTGATCTTGCAGTTT	8	8
CTATTAAATTTTGCCCT	8	8
GAAGGAGTCTTTGTATG	8	8
GCCGCTCTGGTTGCTCT	8	8
TAAGAAGGAGTTCACCG	8	8

Rows: 22999

You can drag your tags out anywhere on the desktop. This will create a data definition for those tags. Click the General tab to rename this data for future reference.



				Name	Count	Description
☑	○	○	●	SM112 (Hindgut - TS13)	110552	Manual - Task 1
☑	○	●	○	SM107 (Foregut - TS13)	102985	Manual - Task 1

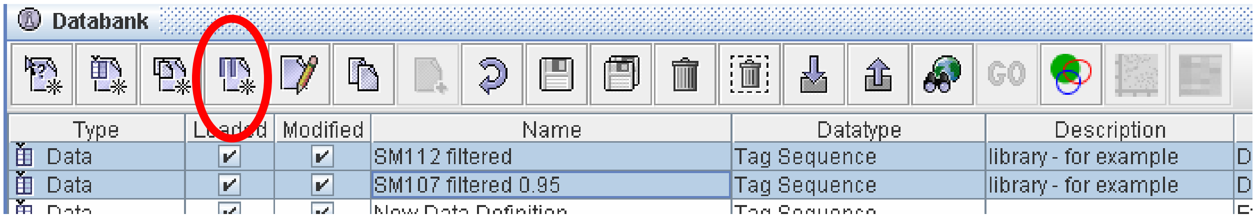
Class	Item	Quantity
Tag Sequence	TTTGGTTTAAGAAGAGG	21
Tag Sequence	GCCAACAGCATCGCCAG	11
Tag Sequence	GTTGTCCTTTTTCCTCT	11
Tag Sequence	CACGCTCCCGGGAAGGC	10
Tag Sequence	CGGTTCCACCCGAAAGG	10
Tag Sequence	CTGTGCCCTCCCAGGTA	10
Tag Sequence	CAAGGTGACAGGCCGGT	9
Tag Sequence	TTAAAGTAATGAAAAAA	9
Tag Sequence	TTGGTAGCCGTAGCACA	9
Tag Sequence	ACCAACAGGTAGTTGGC	8

Item	...	SM107 (For... 26012
TTTGGTTTAAGAAGAGG	21	21
GCCAACAGCATCGCCAG	11	11
GTTGTCCTTTTTCCTCT	11	11
CACGCTCCCGGGAAGGC	10	10
CGGTTCCACCCGAAAGG	10	10
CTGTGCCCTCCCAGGTA	10	10
CAAGGTGACAGGCCGGT	9	9
TTAAAGTAATGAAAAAA	9	9
TTGGTAGCCGTAGCACA	9	9
ACCAACAGGTAGTTGGC	8	8

Rows: 22999 Selected: 10 x 1

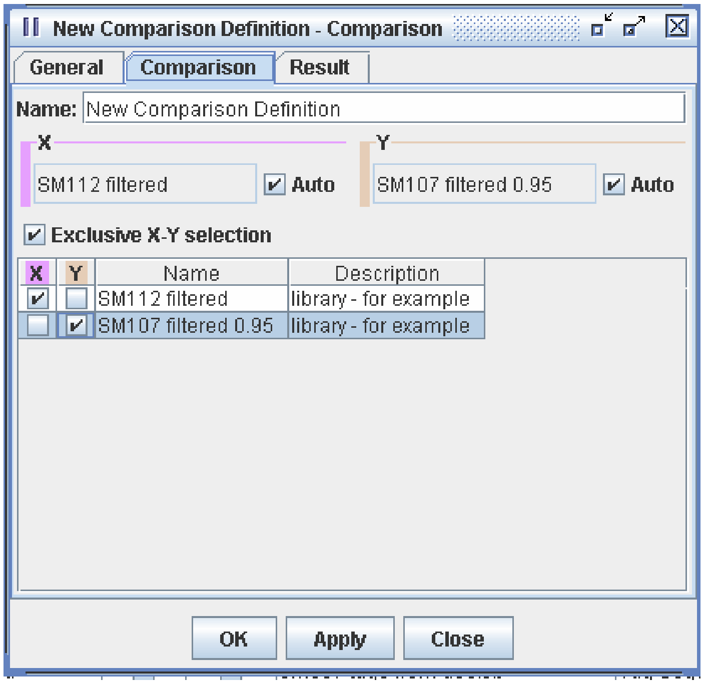
Task 2: find tags up regulated in Foregut vs. Hindgut

Highlight your two library tag Data Definitions and select the Comparison button.



Type	Loaded	Modified	Name	Datatype	Description
Data	☑	☑	SM112 filtered	Tag Sequence	library - for example
Data	☑	☑	SM107 filtered 0.95	Tag Sequence	library - for example

Select which library you want for each axis and rename the comparison. Close the widget.



Name: New Comparison Definition

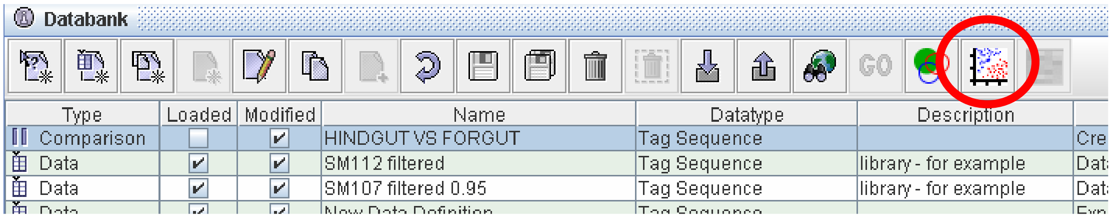
X: SM112 filtered ☑ Auto

Y: SM107 filtered 0.95 ☑ Auto

☑ Exclusive X-Y selection

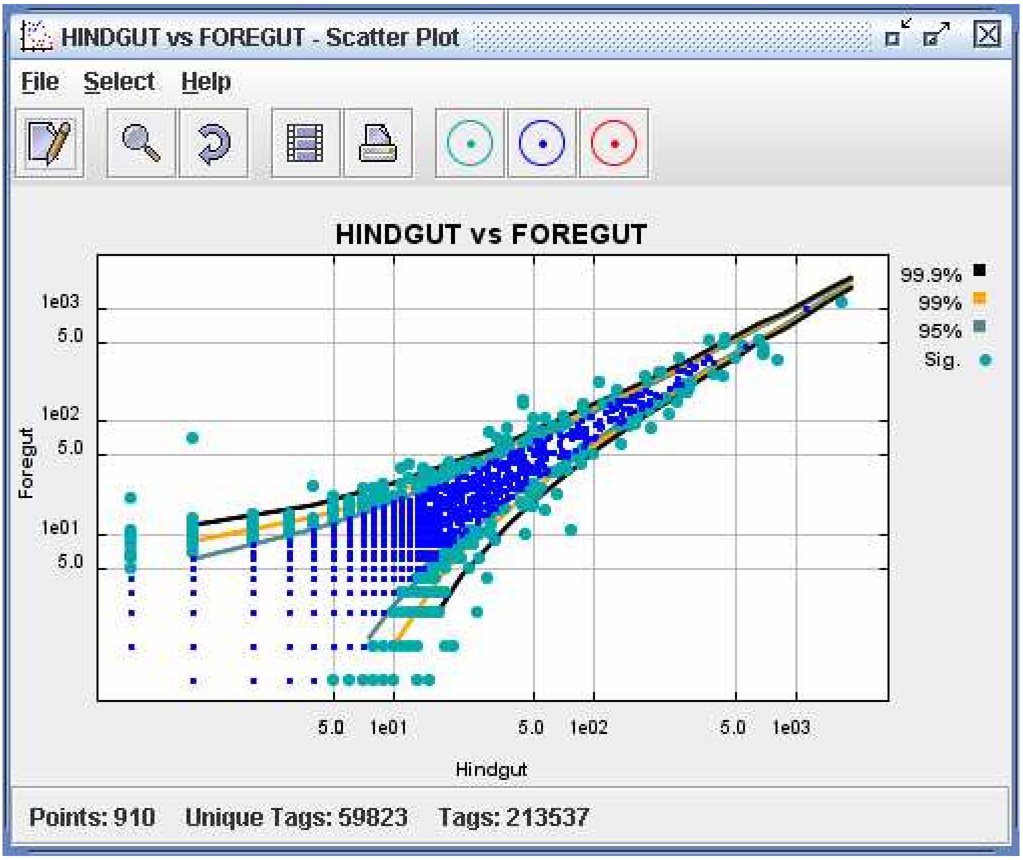
X	Y	Name	Description
☑	☐	SM112 filtered	library - for example
☐	☑	SM107 filtered 0.95	library - for example

Now highlight the comparison in the databank and select the Scatterplot button.



Type	Loaded	Modified	Name	Datatype	Description
Comparison	☐	☑	HINDGUT VS FORGUT	Tag Sequence	
Data	☑	☑	SM112 filtered	Tag Sequence	library - for example
Data	☑	☑	SM107 filtered 0.95	Tag Sequence	library - for example

This will open the scatterplot diagram. Selected tags of interest can be dragged anywhere on the desktop to create an additional data definition. Select the up regulated tags and save them as ‘UPREG’



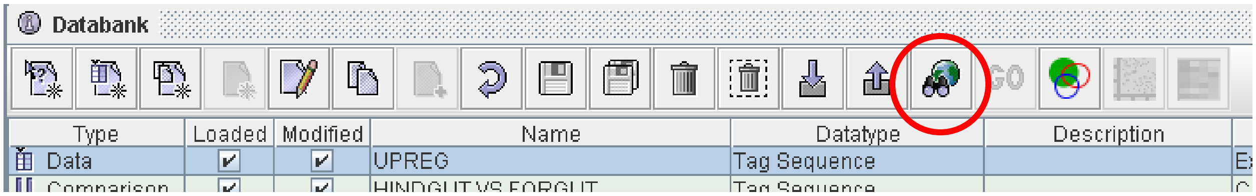
Points: 910 Unique Tags: 59823 Tags: 213537

Good job! By completing this example you have learned how to use the comparison widget and scatterplot.

Task 3: Map up regulated tags

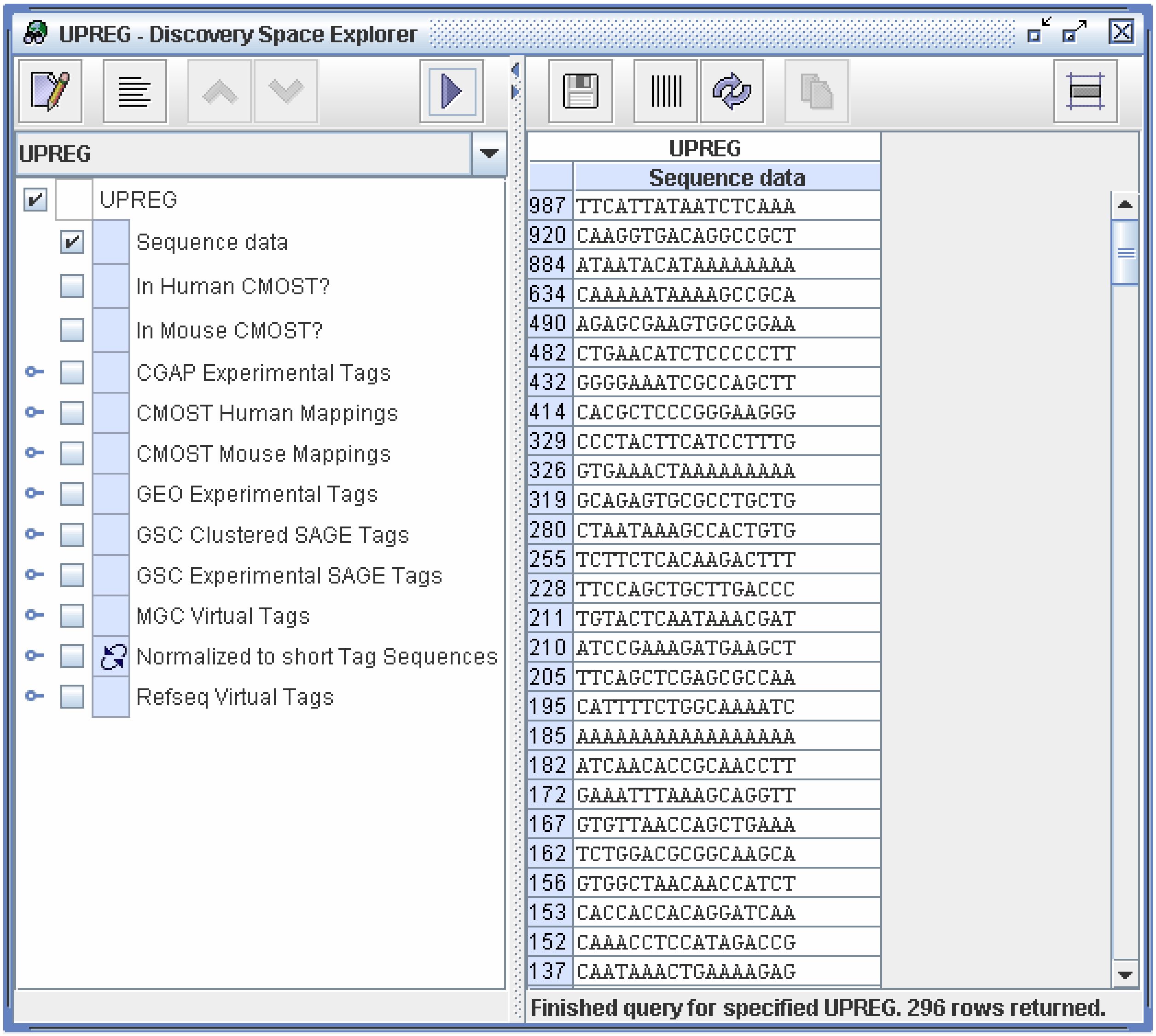
Ensure you have dragged tags out from the scatterplot into a data definition before you start this example.

Highlight your data definition and click the explorer button.



Type	Loaded	Modified	Name	Datatype	Description
Data	☑	☑	UPREG	Tag Sequence	
Comparison	☑	☑	HINDGUT VS FOREGUT	Tag Sequence	

This will open the Explorer widget which will allow you to map your tags. This widget is central to DS4.

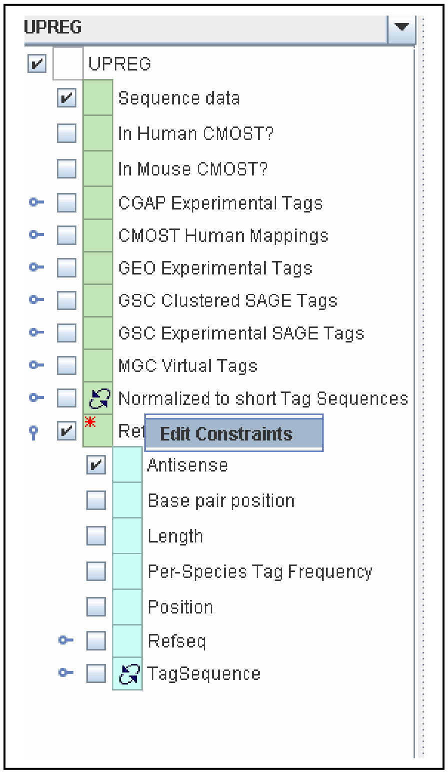


- ☑ UPREG
  - ☑ Sequence data
  - ☐ In Human CMOST?
  - ☐ In Mouse CMOST?
  - ☐ CGAP Experimental Tags
  - ☐ CMOST Human Mappings
  - ☐ CMOST Mouse Mappings
  - ☐ GEO Experimental Tags
  - ☐ GSC Clustered SAGE Tags
  - ☐ GSC Experimental SAGE Tags
  - ☐ MGC Virtual Tags
  - ☐ Normalized to short Tag Sequences
  - ☐ Refseq Virtual Tags

	UPREG
	Sequence data
987	TTCATTATAATCTCAAA
920	CAAGGTGACAGGCCGCT
884	ATAATACATAAAAAAAA
634	CAAAAATAAAAGCCGCA
490	AGAGCGAAGTGGCGGAA
482	CTGAACATCTCCCCCTT
432	GGGGAAATCGCCAGCTT
414	CACGCTCCCGGGAAGGG
329	CCCTACTTCATCCTTTG
326	GTGAAACTAAAAAAAAA
319	GCAGAGTGCGCCTGCTG
280	CTAATAAAGCCACTGTG
255	TCTTCTCACAAGACTTT
228	TTCCAGCTGCTTGACCC
211	TGTACTCAATAAACGAT
210	ATCCGAAAGATGAAGCT
205	TTCAGCTCGAGCGCCAA
195	CATTTTCTGGCAAAATC
185	AAAAAAAAAAAAAAAAA
182	ATCAACACCGCAACCTT
172	GAAATTTAAAGCAGGTT
167	GTGTTAACCAGCTGAAA
162	TCTGGACGCGGCAAGCA
156	GTGGCTAACAACCATCT
153	CACCACCACAGGATCAA
152	CAAACCTCCATAGACCG
137	CAATAAACTGAAAAGAG

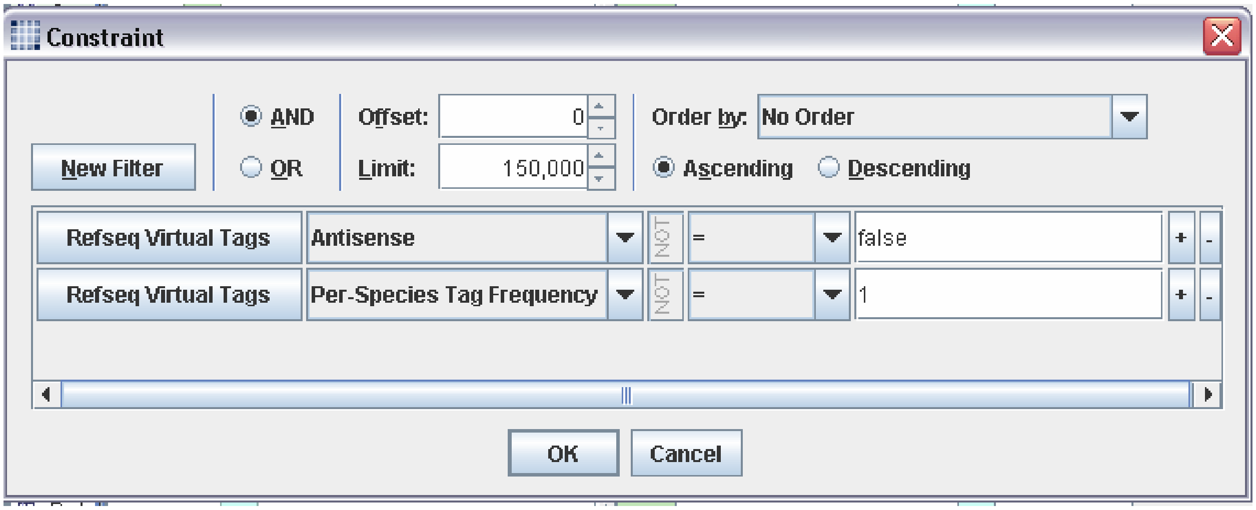
Finished query for specified UPREG. 296 rows returned.

In order to map our tags, we have to set some constraints similar to those set with the Query Builder.



Right click on RefSeq. This will allow you to open the constraints window.

You might want to exclude antisense mappings and only look at unambiguous matches.



● AND ○ OR

Offset: 0

Limit: 150,000

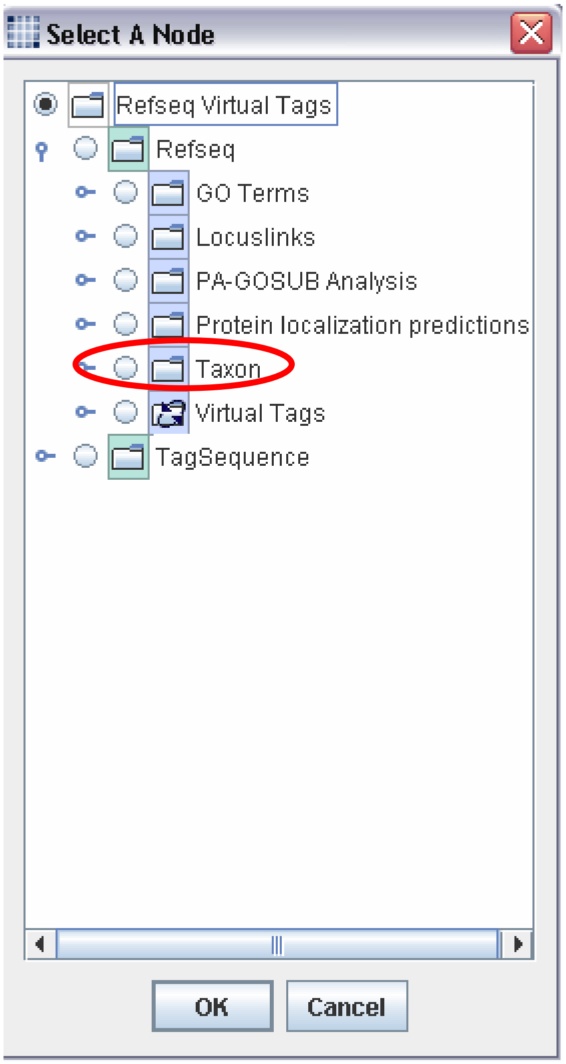
Order by: No Order

● Ascending ○ Descending

Refseq Virtual Tags	Antisense	NOT	=	false
Refseq Virtual Tags	Per-Species Tag Frequency	NOT	=	1

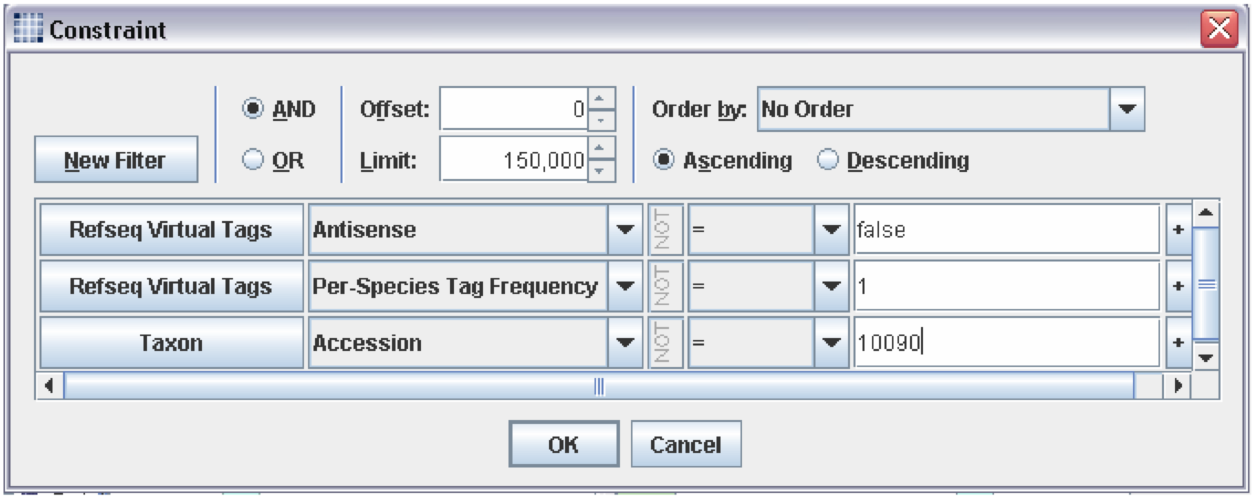
You also might want to only look at mouse matches. Click New Filter. Click the RefSeq Virtual Tags button.

This will open the Select a Node window.



By selecting the Taxon item you can narrow your mappings down by species.

In our case, we set the Taxon accession to 10090 for mouse.



● AND ○ OR

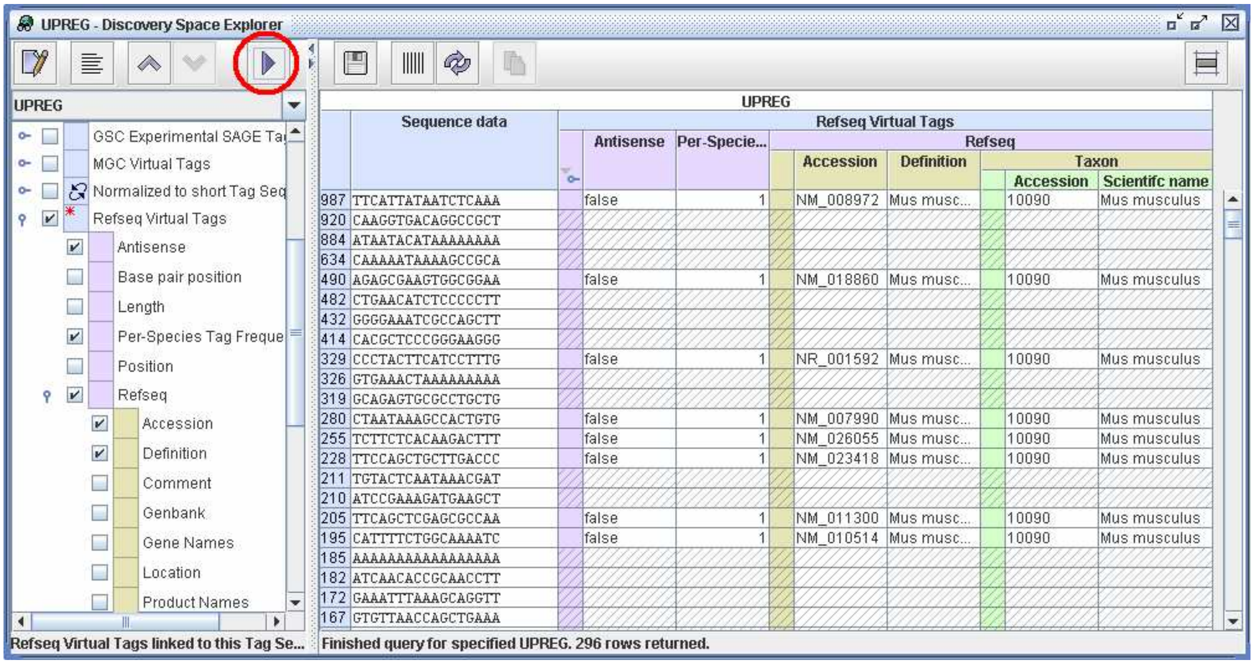
Offset: 0

Limit: 150,000

Order by: No Order

● Ascending ○ Descending

Refseq Virtual Tags	Antisense	NOT	=	false
Refseq Virtual Tags	Per-Species Tag Frequency	NOT	=	1
Taxon	Accession	NOT	=	10090



- ☐ GSC Experimental SAGE Ta
- ☐ MGC Virtual Tags
- ☐ Normalized to short Tag Seq
- ☑ Refseq Virtual Tags
  - ☑ Antisense
  - ☐ Base pair position
  - ☐ Length
  - ☑ Per-Species Tag Freque
  - ☐ Position
  - ☑ Refseq
    - ☑ Accession
    - ☑ Definition
    - ☐ Comment
    - ☐ Genbank
    - ☐ Gene Names
    - ☐ Location
    - ☐ Product Names

Refseq Virtual Tags linked to this Tag Se...

UPREG							
	Sequence data	Refseq Virtual Tags					
		Antisense	Per-Specie...	Refseq			
				Accession	Definition	Taxon	
						Accession	Scientifc name
987	TTCATTATAATCTCAAA	false	1	NM_008972	Mus musc...	10090	Mus musculus
920	CAAGGTGACAGGCCGCT						
884	ATAATACATAAAAAAAA						
634	CAAAAATAAAAGCCGCA						
490	AGAGCGAAGTGGCGGAA	false	1	NM_018860	Mus musc...	10090	Mus musculus
482	CTGAACATCTCCCCCTT						
432	GGGGAAATCGCCAGCTT						
414	CACGCTCCCGGGAAGGG						
329	CCCTACTTCATCCTTTG	false	1	NR_001592	Mus musc...	10090	Mus musculus
326	GTGAAACTAAAAAAAAA						
319	GCAGAGTGCGCCTGCTG						
280	CTAATAAAGCCACTGTG	false	1	NM_007990	Mus musc...	10090	Mus musculus
255	TCTTCTCACAAGACTTT	false	1	NM_026055	Mus musc...	10090	Mus musculus
228	TTCCAGCTGCTTGACCC	false	1	NM_023418	Mus musc...	10090	Mus musculus
211	TGTACTCAATAAACGAT						
210	ATCCGAAAGATGAAGCT						
205	TTCAGCTCGAGCGCCAA	false	1	NM_011300	Mus musc...	10090	Mus musculus
195	CATTTTCTGGCAAAATC	false	1	NM_010514	Mus musc...	10090	Mus musculus
185	AAAAAAAAAAAAAAAAA						
182	ATCAACACCGCAACCTT						
172	GAAATTTAAAGCAGGTT						
167	GTGTTAACCAGCTGAAA						

Finished query for specified UPREG. 296 rows returned.

Hit the run button and you will map your tags!!! As you can see, the tag counts are in the same table as the mappings.

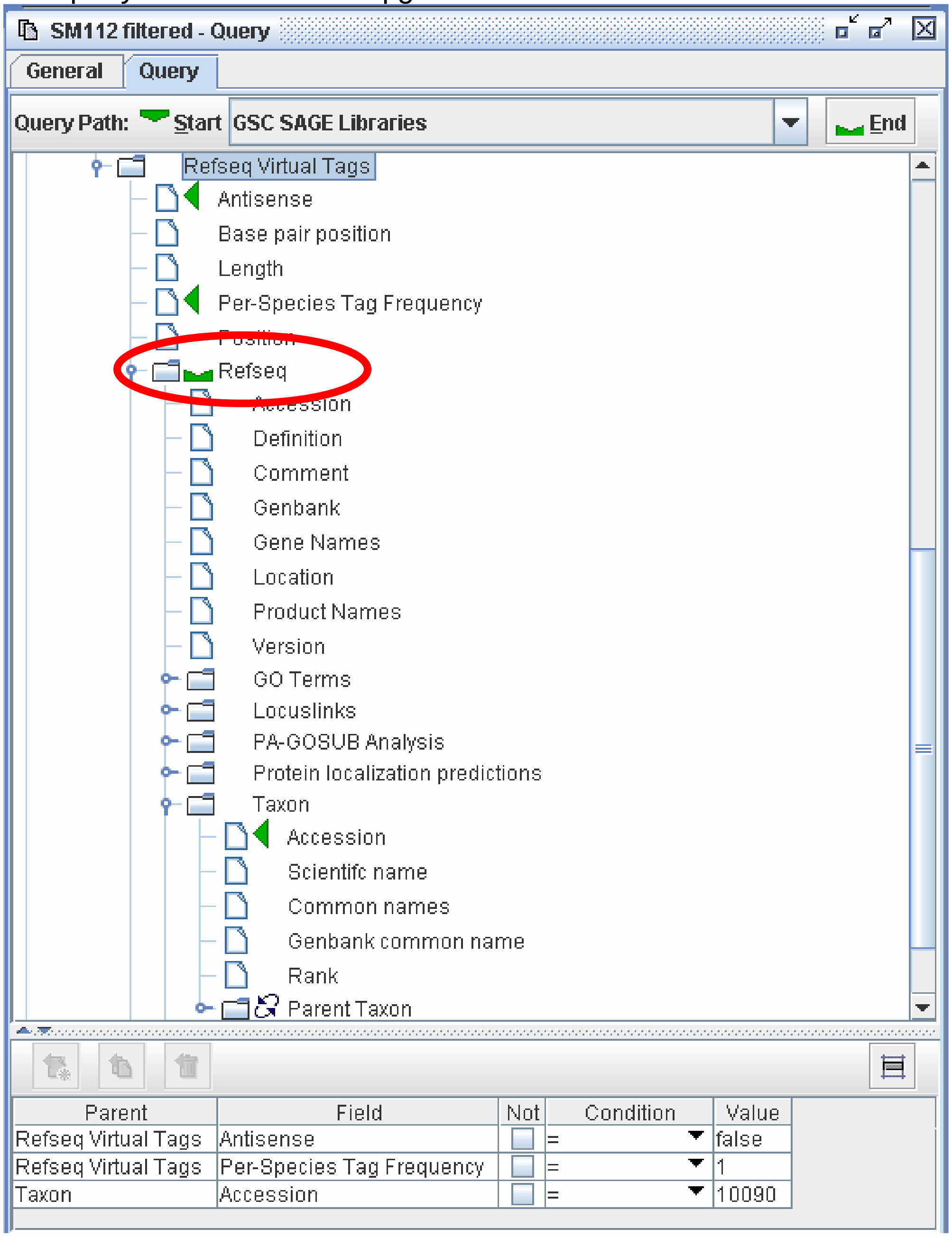
Task 4: Find GO Categories in Hindgut Library

In order to use the GO Browser, we must retrieve data that can be inputted into GO. As you may know, GO accepts RefSeq, MGC, and Ensembl accession numbers. Therefore, we do not want tag data, we want gene data.

Since we want to retrieve gene data for the Hindgut library, we can duplicate our query that retrieved the tag data for Hindgut and modify it to retrieve gene data.

4.1. Duplicate Hindgut query as in task 1. **<u>You must use your query definition NOT your data definition. The data definition only contains your tag data, you need the actual query so you can modify it.</u>**

4.2. Edit the query to retrieve RefSeq genes.



Parent	Field	Not	Condition	Value
Refseq Virtual Tags	Antisense	☐	=	false
Refseq Virtual Tags	Per-Species Tag Frequency	☐	=	1
Taxon	Accession	☐	=	10090

Since we are doing GO Analysis, we need to retrieve gene data. Therefore, set the END button to RefSeq.

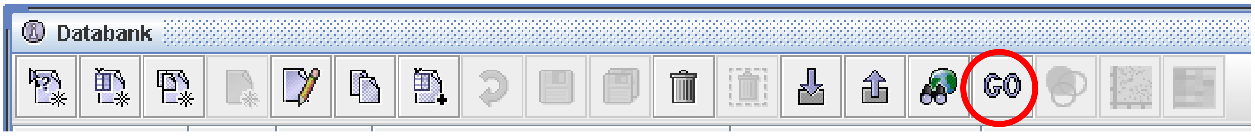
We need to narrow down the genes we return just as in Task 3. Therefore, we set the following parameters:

RefSeq Virtual Tags -> Antisense : set to “false”
RefSeq Virtual Tags -> Per-Species Tag Frequency : set to “1”
RefSeq Virtual Tags -> RefSeq -> Taxon -> Accession : set to 10090

This will return mouse genes that unambiguously map our tags. Make sure you rename this new query.

We are now ready to use the GO Browser!

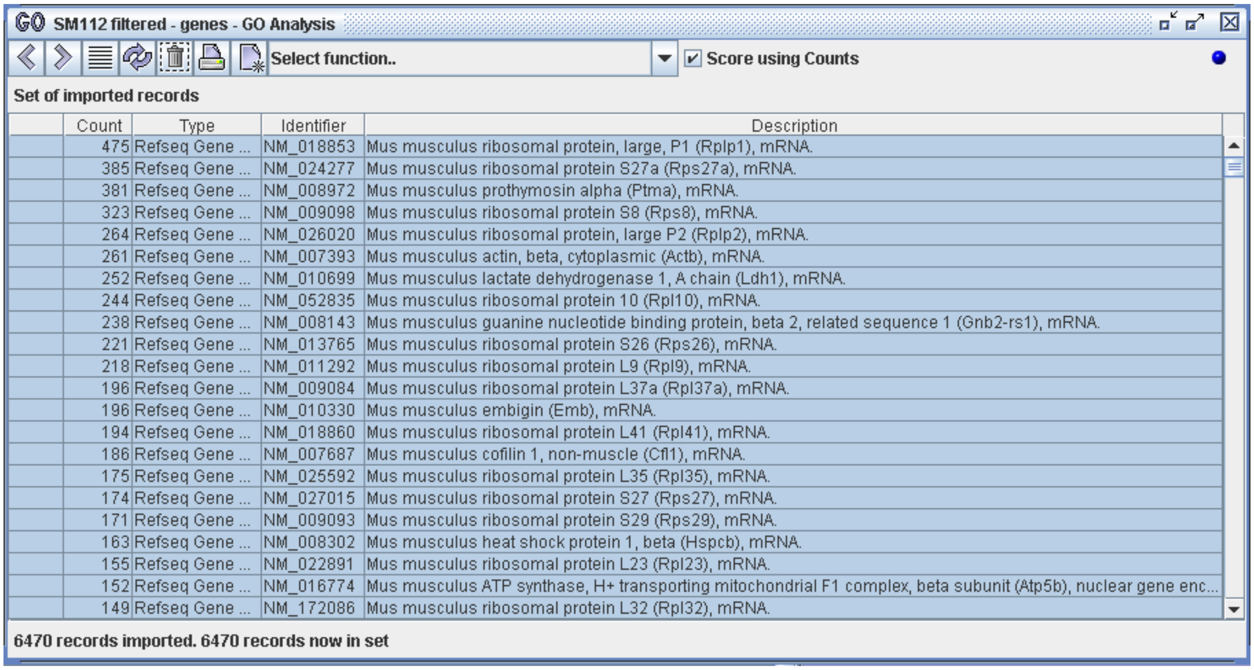
4.3. Highlight your new gene query and click the GO button.



This will open the GO Browser. Please refer to the GO Browser primer for detailed instructions of its use.

You will notice two things different in DS4.

1) Tag counts are imported into the GO Brower (left-most column)
2) There is an option to “Score using Counts”. This will calculate percentages based on tag counts. If you deselect this box, the percentages will be calculated based on number of genes.

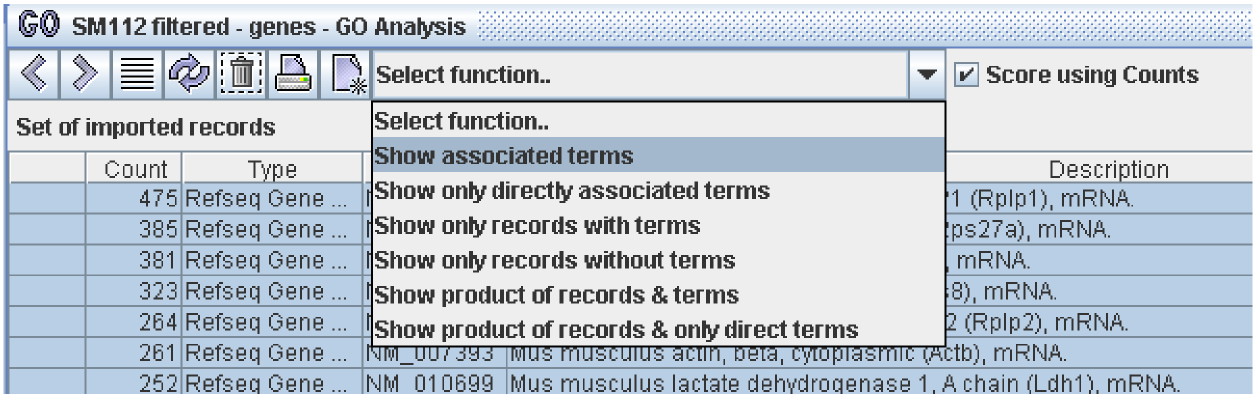


Set of imported records

	Count	Type	Identifier	Description
	475	Refseq Gene ...	NM_018853	Mus musculus ribosomal protein, large, P1 (Rplp1), mRNA.
	385	Refseq Gene ...	NM_024277	Mus musculus ribosomal protein S27a (Rps27a), mRNA.
	381	Refseq Gene ...	NM_008972	Mus musculus prothymosin alpha (Ptma), mRNA.
	323	Refseq Gene ...	NM_009098	Mus musculus ribosomal protein S8 (Rps8), mRNA.
	264	Refseq Gene ...	NM_026020	Mus musculus ribosomal protein, large P2 (Rplp2), mRNA.
	261	Refseq Gene ...	NM_007393	Mus musculus actin, beta, cytoplasmic (Actb), mRNA.
	252	Refseq Gene ...	NM_010699	Mus musculus lactate dehydrogenase 1, A chain (Ldh1), mRNA.
	244	Refseq Gene ...	NM_052835	Mus musculus ribosomal protein 10 (Rpl10), mRNA.
	238	Refseq Gene ...	NM_008143	Mus musculus guanine nucleotide binding protein, beta 2, related sequence 1 (Gnb2-rs1), mRNA.
	221	Refseq Gene ...	NM_013765	Mus musculus ribosomal protein S26 (Rps26), mRNA.
	218	Refseq Gene ...	NM_011292	Mus musculus ribosomal protein L9 (Rpl9), mRNA.
	196	Refseq Gene ...	NM_009084	Mus musculus ribosomal protein L37a (Rpl37a), mRNA.
	196	Refseq Gene ...	NM_010330	Mus musculus embigin (Emb), mRNA.
	194	Refseq Gene ...	NM_018860	Mus musculus ribosomal protein L41 (Rpl41), mRNA.
	186	Refseq Gene ...	NM_007687	Mus musculus cofilin 1, non-muscle (Cfl1), mRNA.
	175	Refseq Gene ...	NM_025592	Mus musculus ribosomal protein L35 (Rpl35), mRNA.
	174	Refseq Gene ...	NM_027015	Mus musculus ribosomal protein S27 (Rps27), mRNA.
	171	Refseq Gene ...	NM_009093	Mus musculus ribosomal protein S29 (Rps29), mRNA.
	163	Refseq Gene ...	NM_008302	Mus musculus heat shock protein 1, beta (Hspcb), mRNA.
	155	Refseq Gene ...	NM_022891	Mus musculus ribosomal protein L23 (Rpl23), mRNA.
	152	Refseq Gene ...	NM_016774	Mus musculus ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit (Atp5b), nuclear gene enc...
	149	Refseq Gene ...	NM_172086	Mus musculus ribosomal protein L32 (Rpl32), mRNA.

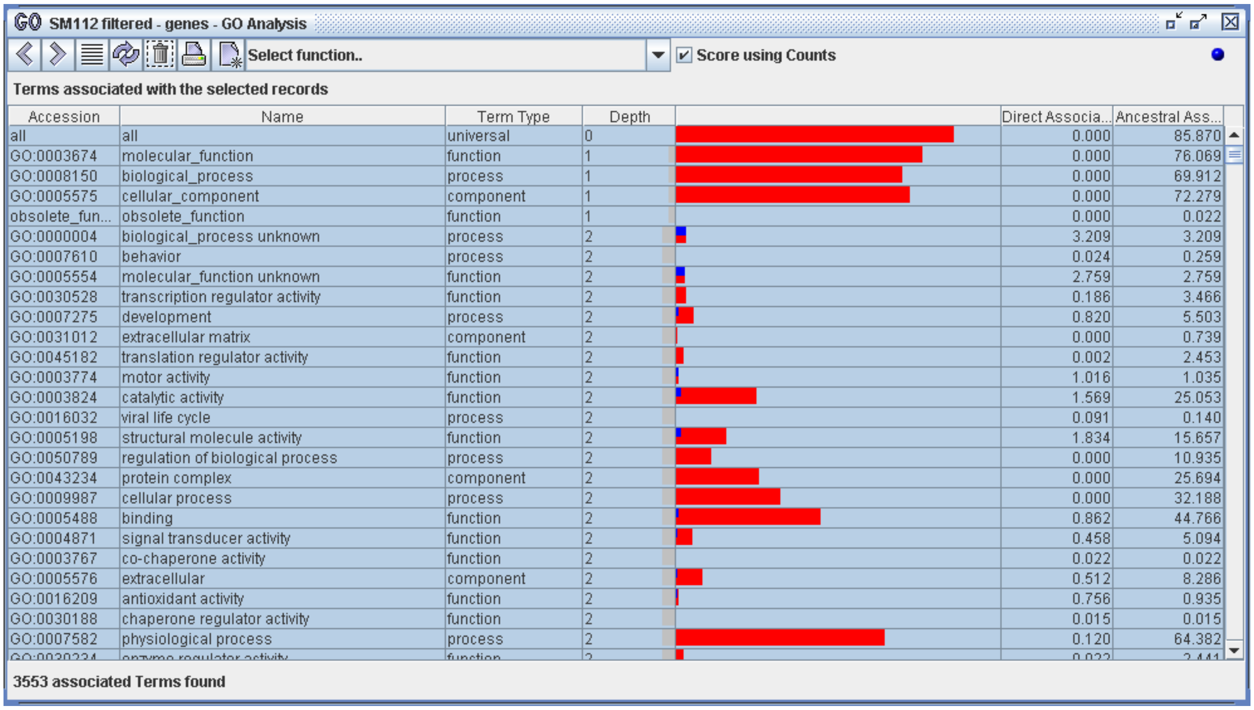
6470 records imported. 6470 records now in set

4.4. Select “Show associated terms” from the drop down menu.



This will display the GO categories and the percentage of transcripts in each category.

IMPORTANT:
Direct Association: the lowest branch a gene is categorized in
Ancestral Association: gene is in this category, but has also been put into lower branches
For example: a transcription factor (Direct Association) is also in DNA binding (Ancestral Association).



Terms associated with the selected records

Accession	Name	Term Type	Depth	Direct Associa...	Ancestral Ass...
all	all	universal	0	0.000	85.870
GO:0003674	molecular_function	function	1	0.000	76.069
GO:0008150	biological_process	process	1	0.000	69.912
GO:0005575	cellular_component	component	1	0.000	72.279
obsolete_fun...	obsolete_function	function	1	0.000	0.022
GO:0000004	biological_process unknown	process	2	3.209	3.209
GO:0007610	behavior	process	2	0.024	0.259
GO:0005554	molecular_function unknown	function	2	2.759	2.759
GO:0030528	transcription regulator activity	function	2	0.186	3.466
GO:0007275	development	process	2	0.820	5.503
GO:0031012	extracellular matrix	component	2	0.000	0.739
GO:0045182	translation regulator activity	function	2	0.002	2.453
GO:0003774	motor activity	function	2	1.016	1.035
GO:0003824	catalytic activity	function	2	1.569	25.053
GO:0016032	viral life cycle	process	2	0.091	0.140
GO:0005198	structural molecule activity	function	2	1.834	15.657
GO:0050789	regulation of biological process	process	2	0.000	10.935
GO:0043234	protein complex	component	2	0.000	25.694
GO:0009987	cellular process	process	2	0.000	32.188
GO:0005488	binding	function	2	0.862	44.766
GO:0004871	signal transducer activity	function	2	0.458	5.094
GO:0003767	co-chaperone activity	function	2	0.022	0.022
GO:0005576	extracellular	component	2	0.512	8.286
GO:0016209	antioxidant activity	function	2	0.756	0.935
GO:0030188	chaperone regulator activity	function	2	0.015	0.015
GO:0007582	physiological process	process	2	0.120	64.382

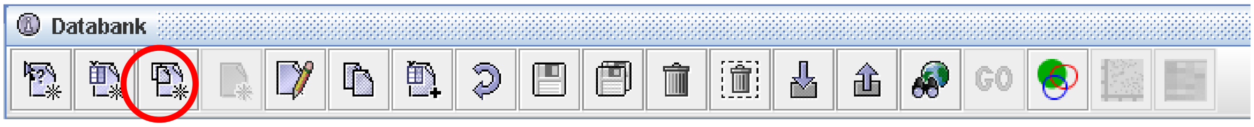
3553 associated Terms found

Example 2: Gene of Interest

Task 1: Retrieve tags for a gene of interest – FGF8

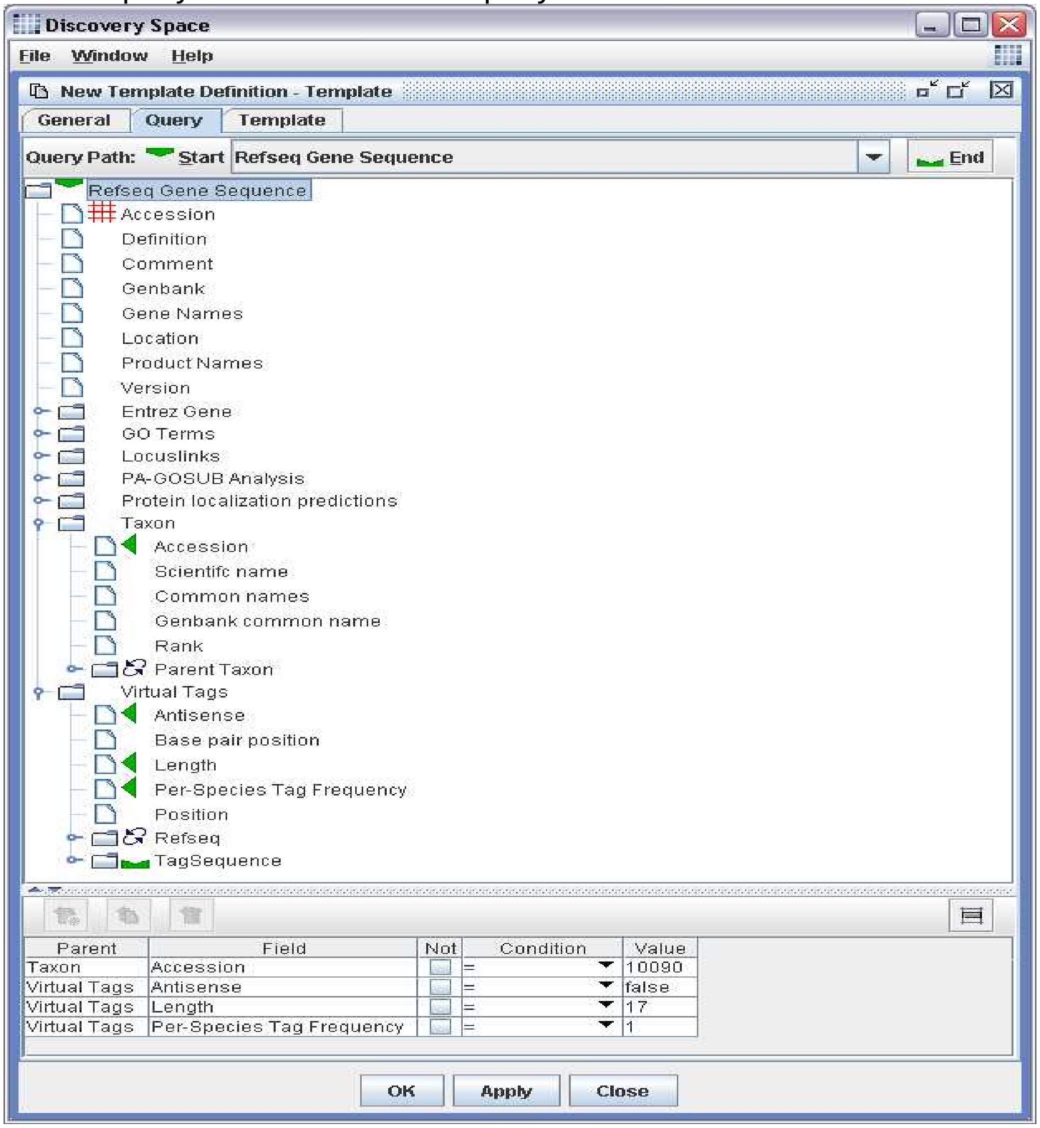
1.1 Build a query to return tags for a given gene. This time we will use the Template builder.

Click the Template button to create a Template.



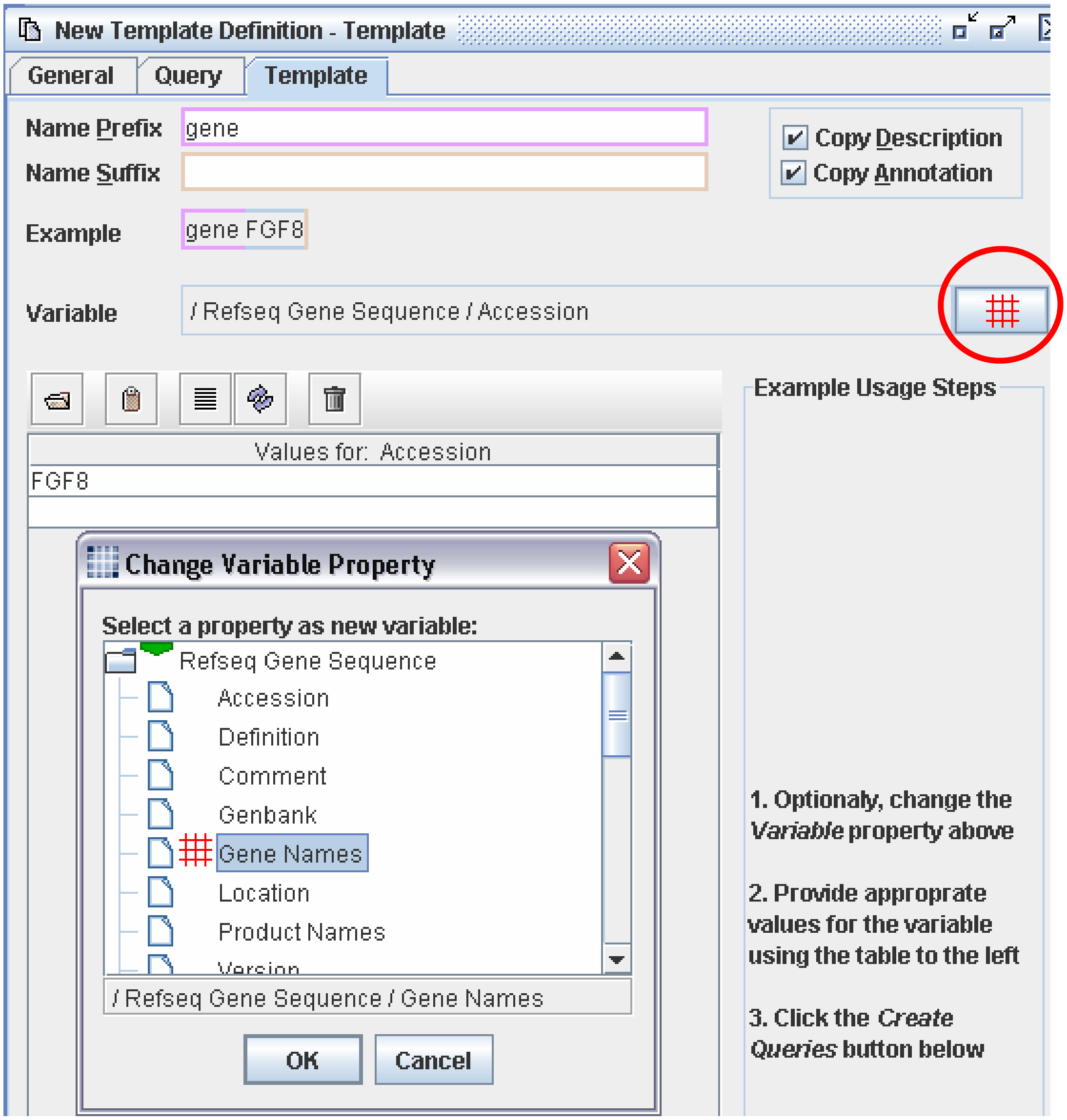
You should be comfortable with queries after completing Example 1. In this example we want to return tags from a given gene. We will use RefSeq Gene Sequence to retrieve all longSAGE mouse unambiguous tags. Notice the END function is on the TagSequence item.

Click the query tab and create this query:



Query Path: Start Refseq Gene Sequence End

Parent	Field	Not	Condition	Value
Taxon	Accession	☐	=	10090
Virtual Tags	Antisense	☐	=	false
Virtual Tags	Length	☐	=	17
Virtual Tags	Per-Species Tag Frequency	☐	=	1



Name Prefix: gene

Name Suffix:

Example: gene FGF8

Variable: / Refseq Gene Sequence / Accession

Values for: Accession

FGF8

Select a property as new variable:

- Refseq Gene Sequence
  - Accession
  - Definition
  - Comment
  - Genbank
  - Gene Names
  - Location
  - Product Names
  - Version

/ Refseq Gene Sequence / Gene Names

Example Usage Steps

1. Optionaly, change the *Variable* property above

2. Provide approprate values for the variable using the table to the left

3. Click the *Create Queries* button below

We have to set the variable. This allows us to run this query as many times as we like to create an identical query for different gene names. You can then input FGF8 into Values for: Gene Names column.

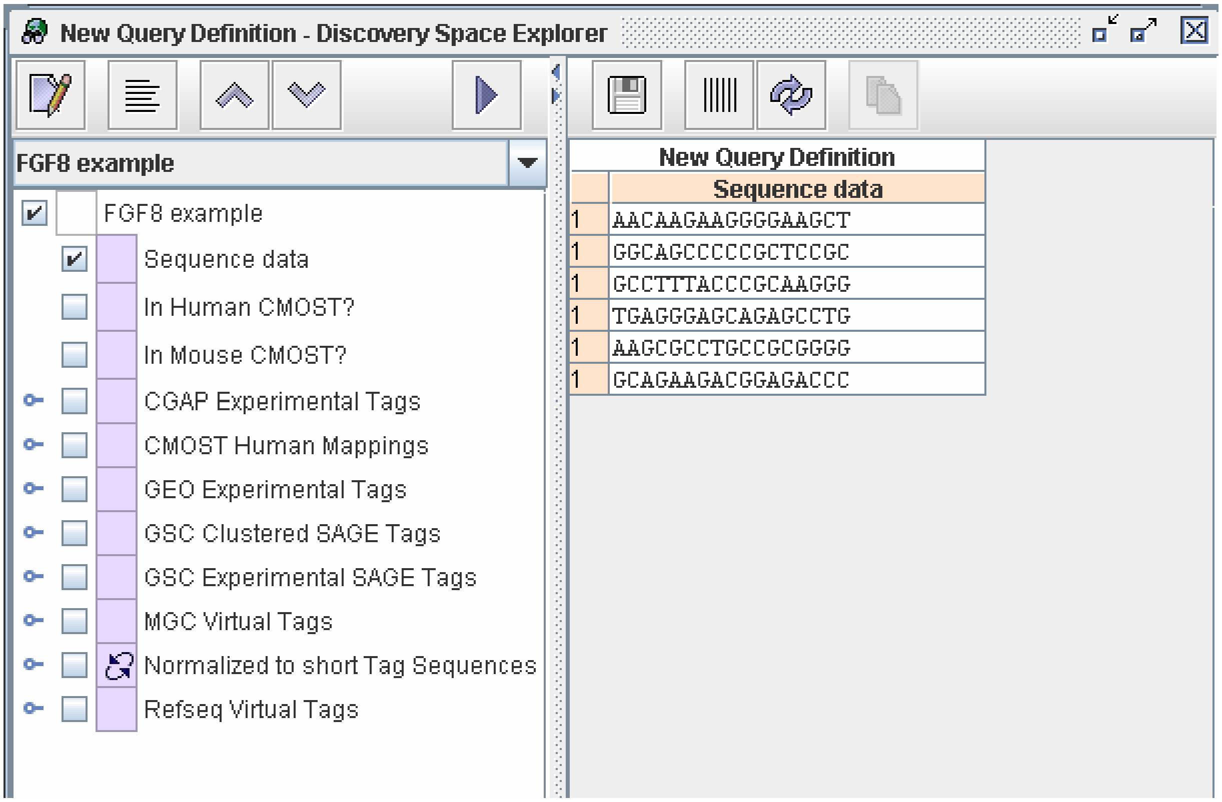
You can set Name Prefix and Name Suffix to help label your queries. In this example, the query will be named ‘gene FGF8’.

NOTE: We can now reuse this query over and over to retrieve tags for different genes!

Click Apply. Click Create queries.

This creates your specified queries in the Databank. Highlight your new query and select the Explorer button.

When the query is run, it will return tags.



- ☑ FGF8 example
  - ☑ Sequence data
  - ☐ In Human CMOST?
  - ☐ In Mouse CMOST?
  - ☐ CGAP Experimental Tags
  - ☐ CMOST Human Mappings
  - ☐ GEO Experimental Tags
  - ☐ GSC Clustered SAGE Tags
  - ☐ GSC Experimental SAGE Tags
  - ☐ MGC Virtual Tags
  - ☐ Normalized to short Tag Sequences
  - ☐ Refseq Virtual Tags

New Query Definition	
	Sequence data
1	AACAAGAAGGGGAAGCT
1	GGCAGCCCCCGCTCCGC
1	GCCTTTACCCGCAAGGG
1	TGAGGGAGCAGAGCCTG
1	AAGCGCCTGCCGCGGGG
1	GCAGAAGACGGAGACCC

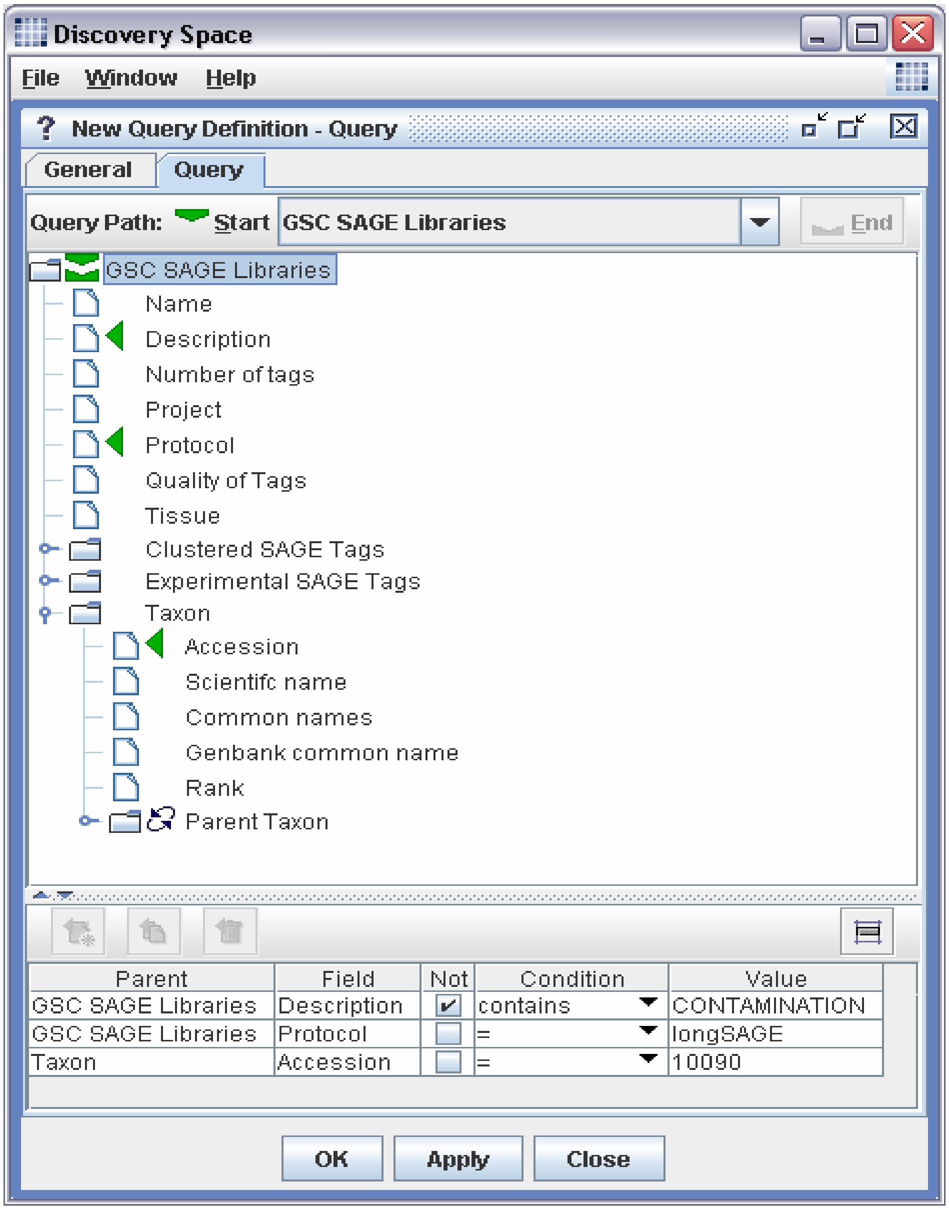
Task 2: Determine which libraries contain these tags

2.1. Create query of all available libraries

We need an additional query to return available libraries. This query will be used to open the Search For Tags in Libraries widget.

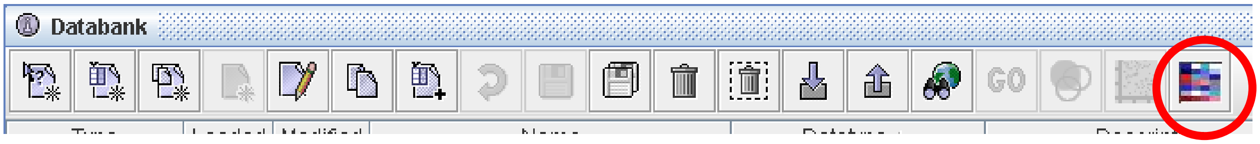
For our example, let's look at all longSAGE mouse libraries in the GSC Libraries.

Let's also remove the contaminated libraries.



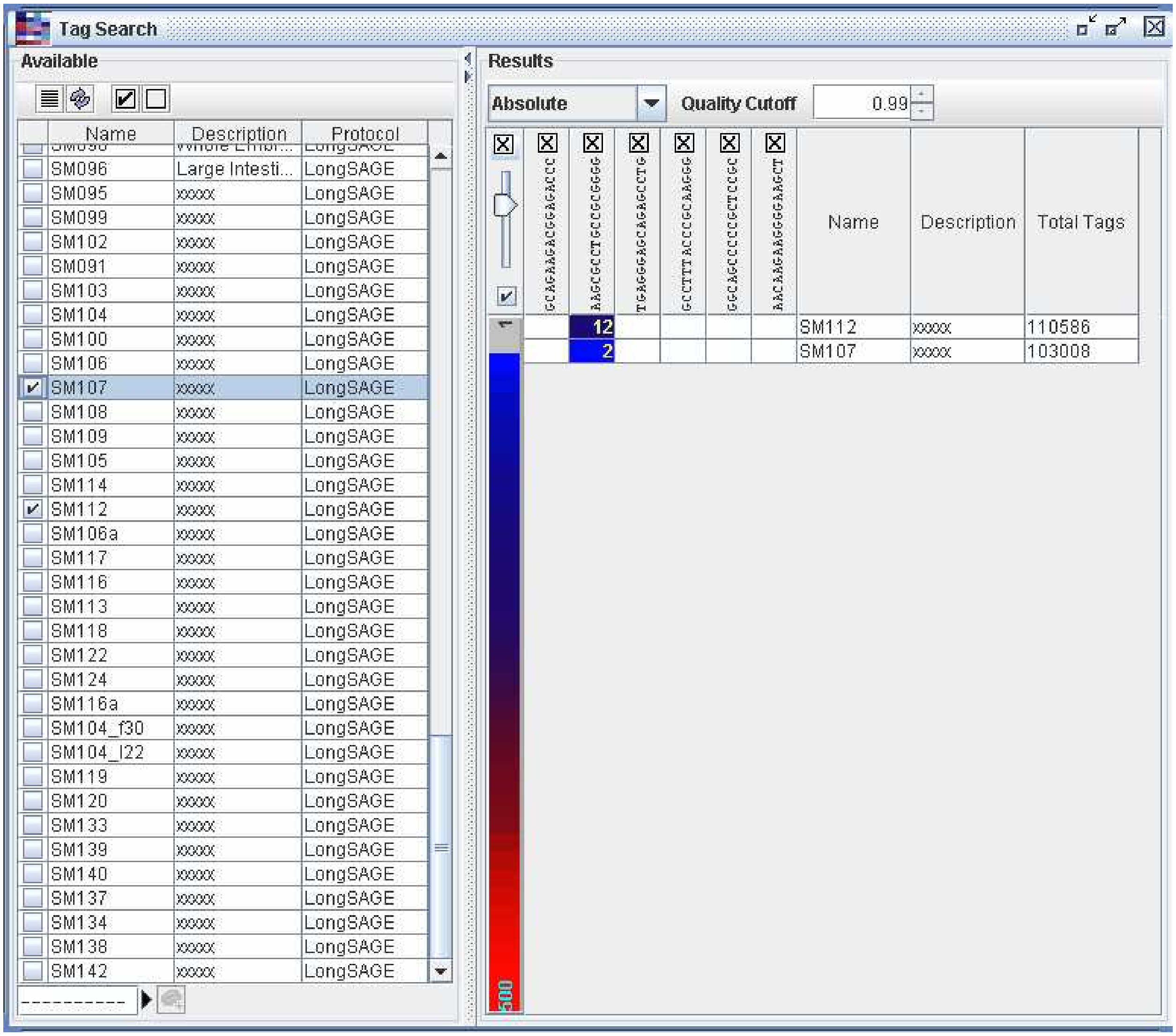
Parent	Field	Not	Condition	Value
GSC SAGE Libraries	Description	☑	contains	CONTAMINATION
GSC SAGE Libraries	Protocol	☐	=	longSAGE
Taxon	Accession	☐	=	10090

2.2. Highlight the GSC SAGE Libraries query and click the Search For Tags in Libraries button.



Now highlight the tags from your Tag Sequence query and drag them into the Search for Tags widget.

Click the libraries on the left column.

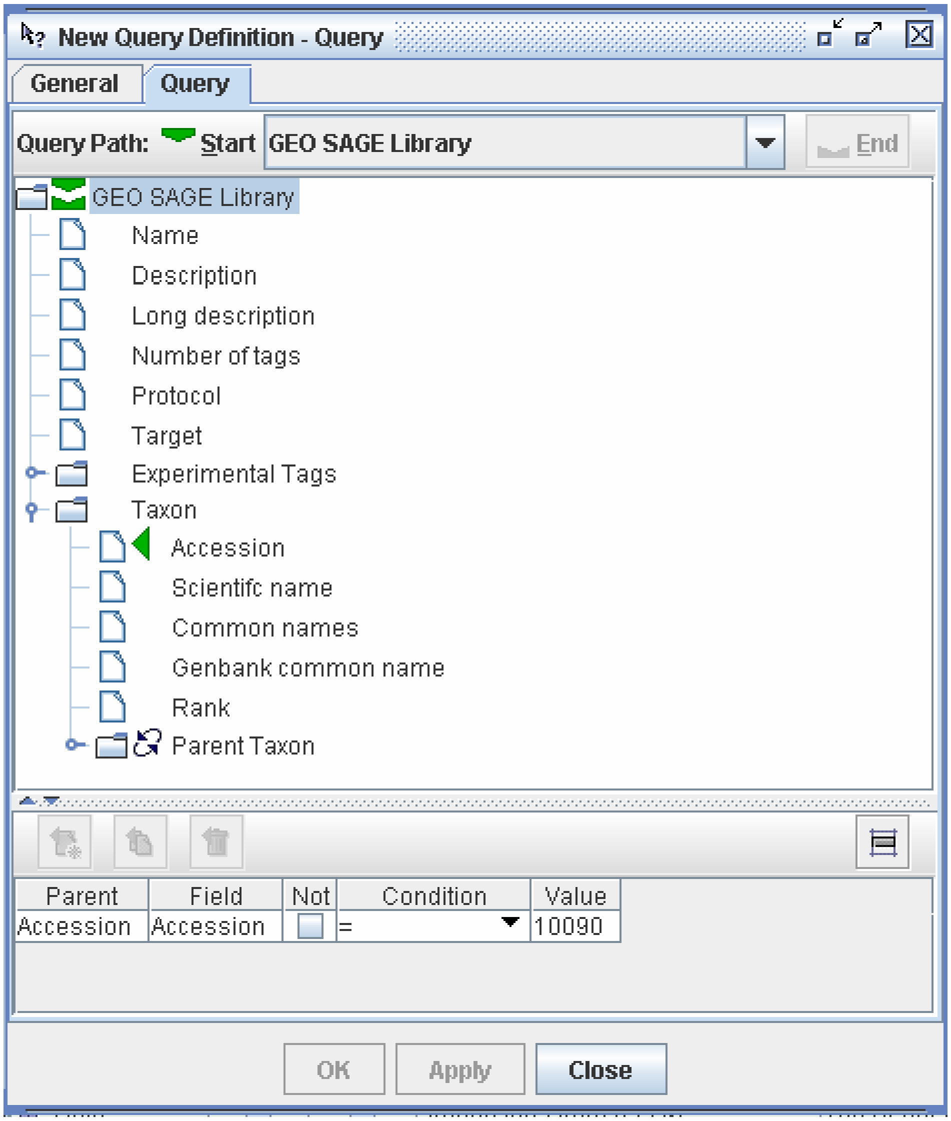


	Name	Description	Protocol
☐	SM096	Large Intesti...	LongSAGE
☐	SM095	xxxxx	LongSAGE
☐	SM099	xxxxx	LongSAGE
☐	SM102	xxxxx	LongSAGE
☐	SM091	xxxxx	LongSAGE
☐	SM103	xxxxx	LongSAGE
☐	SM104	xxxxx	LongSAGE
☐	SM100	xxxxx	LongSAGE
☐	SM106	xxxxx	LongSAGE
☑	SM107	xxxxx	LongSAGE
☐	SM108	xxxxx	LongSAGE
☐	SM109	xxxxx	LongSAGE
☐	SM105	xxxxx	LongSAGE
☐	SM114	xxxxx	LongSAGE
☑	SM112	xxxxx	LongSAGE
☐	SM106a	xxxxx	LongSAGE
☐	SM117	xxxxx	LongSAGE
☐	SM116	xxxxx	LongSAGE
☐	SM113	xxxxx	LongSAGE
☐	SM118	xxxxx	LongSAGE
☐	SM122	xxxxx	LongSAGE
☐	SM124	xxxxx	LongSAGE
☐	SM116a	xxxxx	LongSAGE
☐	SM104_f30	xxxxx	LongSAGE
☐	SM104_l22	xxxxx	LongSAGE
☐	SM119	xxxxx	LongSAGE
☐	SM120	xxxxx	LongSAGE
☐	SM133	xxxxx	LongSAGE
☐	SM139	xxxxx	LongSAGE
☐	SM140	xxxxx	LongSAGE
☐	SM137	xxxxx	LongSAGE
☐	SM134	xxxxx	LongSAGE
☐	SM138	xxxxx	LongSAGE
☐	SM142	xxxxx	LongSAGE

Absolute
Quality Cutoff 0.99

GCAGAAGACGGAGACCC	AAGCGCCTGCCGCGGGG	TGAGGGAGCAGAGCCTG	GCCTTTACCCGCAAGGG	GGCAGCCCCCGCTCCGC	AACAAGAAGGGGAAGCT	Name	Description	Total Tags
	12					SM112	xxxxx	110586
	2					SM107	xxxxx	103008

You might want to search public libraries for your tags. You can create a query for GEO libraries and repeat these steps.



Query Path: Start GEO SAGE Library

Parent	Field	Not	Condition	Value
Accession	Accession	☐	=	10090