

Visual Breakdown of Shiny Apps

- This document serves as a visual walkthrough/breakdown of the Gene and Cluster and Cluster Enrichment shiny apps.
- This document will walk through how to access the apps using the code available in Text S3, how to use the different app features available in the sidebars, and breakdown each app's output.
- This guide is broken down into sections, with the first section walking through the Gene and Cluster app and the second walking through the Cluster Enrichment app.

Gene and Cluster App Breakdown

To access shiny apps, paste code available in Text S3 into R script, install necessary packages, and read in shiny package.

The image shows a screenshot of an RStudio environment and a Notepad window. The RStudio window displays a script titled 'Untitled1*' with the following R code:

```
1 #Paste the following into a R script to have access to our interactive shiny apps.
2
3 #R Script to access Gene Identification and Cluster enrichment Shiny apps
4 #Created: 8/22/2024
5
6 #You will need the following packages:
7 #Install if needed
8 install.packages("shiny")
9 install.packages("bslib")
10 install.packages("tidyverse")
11 install.packages("rms")
12 install.packages("DT")
13
14 library(shiny)
15
16 #Run the following to have access to our Gene and Cluster app.
17 #This allows users to look up specific genes, and receive information regarding their
18 #expression trajectory, cluster placement, and identification in young vs old analyses.
19 runGitHub("Gene_and_Cluster_Shiny", "Hanson19")
20
21
22 #Run the following to have access to our Cluster enrichment app.
23 #This allows users to view a cluster's enriched term, and have the ability to compare
24 #clusters and their enriched terms. You can select specific clusters you are interested in,
25 #and choose which types of terms you want shown.
26 runGitHub("Enrichment_Shiny", "Hanson19")
```

The RStudio console shows the following output:

```
> library(shiny)
> #Run the following to have access to our Gene and Cluster app.
> #This allows users to look up specific genes, and receive information regarding their
> #expression trajectory, cluster placement, and identification in young vs old analyses.
> runGitHub("Gene_and_Cluster_Shiny", "Hanson19")
Downloading https://github.com/Hanson19/Gene_and_Cluster_Shiny/archive/HEAD.tar.gz
```

The Notepad window, titled 'Shiny app R Script text - Notepad', contains the same R code as the RStudio script.

To access the Gene and Cluster app, run `runGitHub("Gene_and_Cluster_Shiny", "Hanson19")` on line 19 of the screenshot.

A new window should pop up and look like this.
We have provided a brief description for each part of the app.

Submit gene with FBgn or Gene symbol

FBgn0024248

Choose Timeframe

Day

Changes the x-axis to survival, day or sampling point timeframe

Gene Trajectories

After typing in a gene's symbol or FBgn number the app will inform whether the gene was identified in our analyses, plot the gene's cluster's expression trajectories with a representative curve, plot the individual gene's expression trajectory with all sampling point and normalized read counts, inform if the gene was identified in our Young vs Old Analysis, and list the published Young vs Old studies used in our paper that the gene was identified in.

IDs validated with FlyBase version FB2024_03 on July 19th, 2024

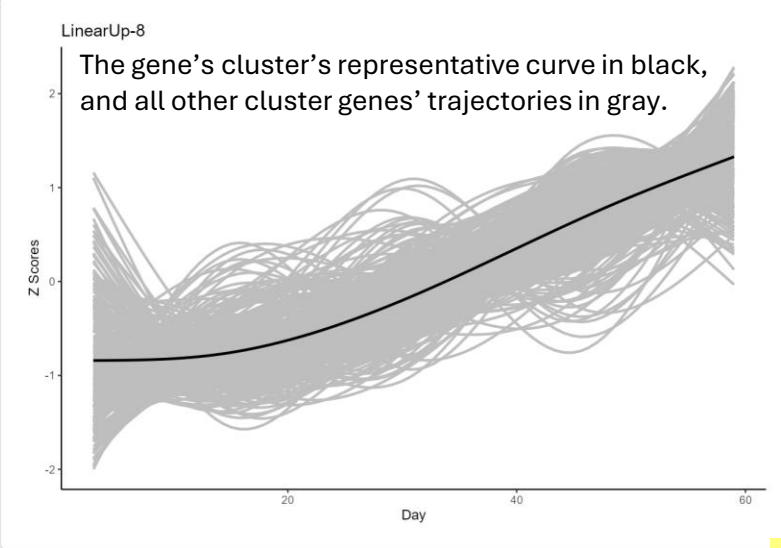
If Gene Symbol has special characters, use FBgn Number.

FBgn Number or Gene Symbol

chico's (FBgn0024248) expression changes with aging and is in LinearUp-8. Identified in survival analysis, day analysis and sampling point analysis.

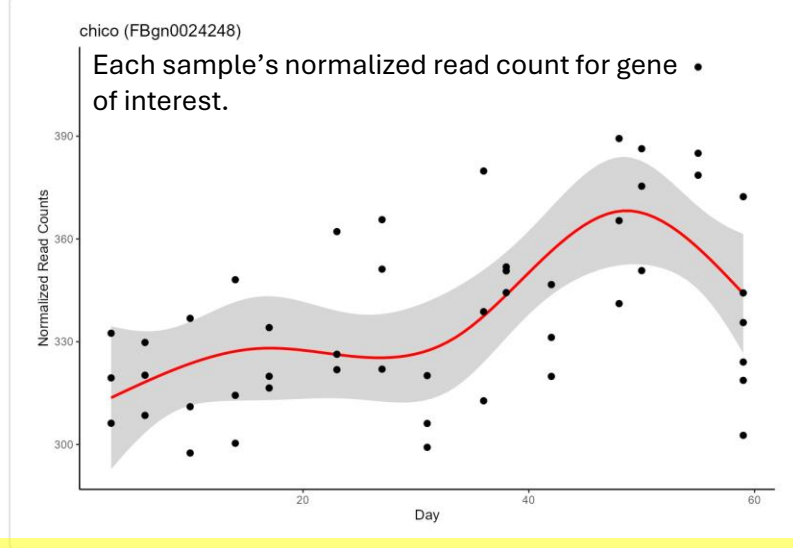
LinearUp-8

The gene's cluster's representative curve in black, and all other cluster genes' trajectories in gray.



chico (FBgn0024248)

Each sample's normalized read count for gene of interest.



Information on if gene was identified in our analysis, what analyses it was identified in, and what cluster it is a part of.

FBgn0024248 was not identified in our Young v Old Analysis.

If the gene was identified in our YvO analysis using Day 59 samples as old

validated_id	current_symbol	Official_ID	First_Author	Year	PMID	website_address
FBgn0024248	chico	LinearUp-8	Carnes	2015	26378456	https://pubmed.ncbi.nlm.nih.gov/26378456/

Listed if the gene was identified in any of the previously published YvO analyses we used for comparisons.

Additional example now using Gene symbol and a different timeframe

Gene Trajectories

Aftering typing in a gene's symbol or FBgn number the app will inform whether the gene was identified in our anlyses, plot the gene's cluster's expression trajectories with a representative curve, plot the individual gene's expression trajectory with all sampling point and normalized read counts, inform if the gene was identified in our Young vs Old Analysis, and list the published Young vs Old studies used in our paper that the gene was identified in.

IDs validated with FlyBase version FB2024_03 on July 19th, 2024

If Gene Symbol has special characters, use FBgn Number.

FBgn Number or Gene Symbol

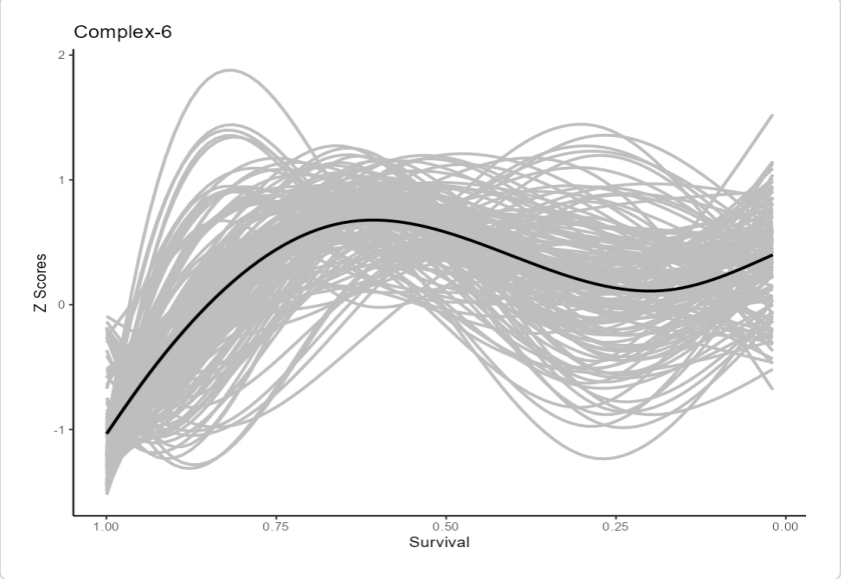
Indy

Choose Timeframe

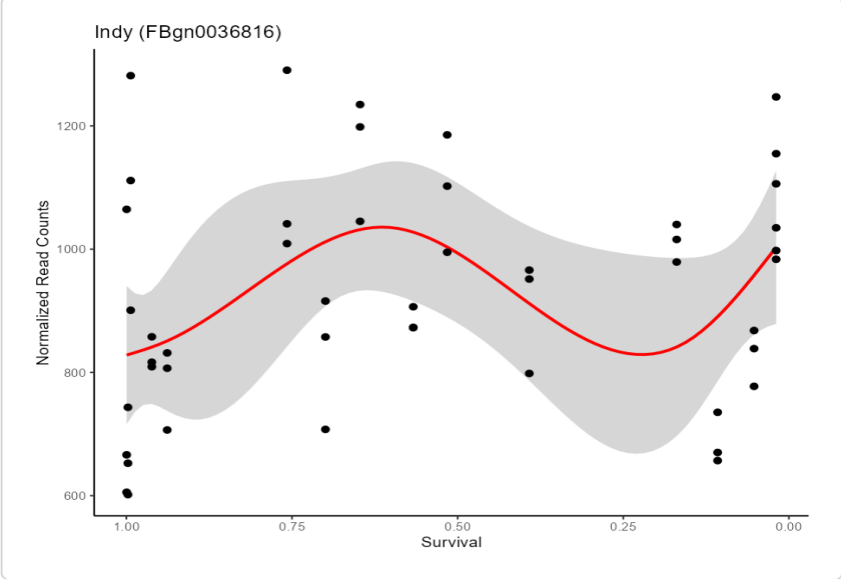
Survival

Indy's (FBgn0036816) expression changes with aging and is in Complex-6. Identified in sampling point analysis.

Complex-6



Indy (FBgn0036816)



Indy (FBgn0036816) was identified in our Young v Old Analysis.

validated_id	current_symbol	Official_ID	First_Author	Year	PMID	website_address
FBgn0036816	Indy	Complex-6	Carnes	2015	26378456	https://pubmed.ncbi.nlm.nih.gov/26378456/
FBgn0036816	Indy	Complex-6	Giradot	2006	16584578	https://pubmed.ncbi.nlm.nih.gov/16584578/
FBgn0036816	Indy	Complex-6	Highfill	2016	27485207	https://pubmed.ncbi.nlm.nih.gov/27485207/
FBgn0036816	Indy	Complex-6	Lai	2007	17196240	https://pubmed.ncbi.nlm.nih.gov/17196240/

If a gene's expression does not significantly change with aging, the app will still plot the gene's expression trajectory.

Gene Trajectories

After typing in a gene's symbol or FBgn number the app will inform whether the gene was identified in our analyses, plot the gene's cluster's expression trajectories with a representative curve, plot the individual gene's expression trajectory with all sampling point and normalized read counts, inform if the gene was identified in our Young vs Old Analysis, and list the published Young vs Old studies used in our paper that the gene was identified in.

IDs validated with FlyBase version FB2024_03 on July 19th, 2024

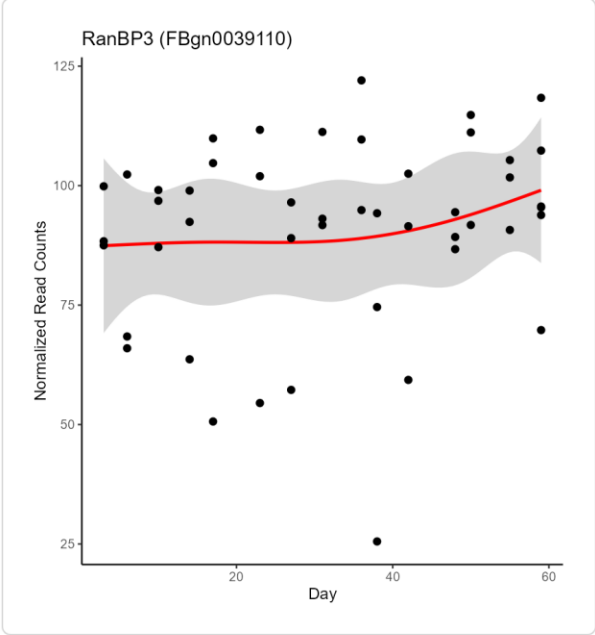
If Gene Symbol has special characters, use FBgn Number.

FBgn Number or Gene Symbol

Choose Timeframe

Day

RanBP3's (FBgn0039110) expression does not significantly change with aging.



RanBP3 was not identified in our Young v Old Analysis.

If the submitted gene symbol or FBgn is not found within our data, the app will state that it was not identified. We do suggest to double check the spelling of the submitted ID to be sure. If using a gene symbol, we also suggest to try the gene’s FBgn in case the gene symbol has changed. As a reminder IDs were validated with FlyBase version FB2024_03 on July 19th, 2024.

Gene Trajectories

Aftering typing in a gene's symbol or FBgn number the app will inform whether the gene was identified in our anlyses, plot the gene's cluster's expression trajectories with a representative curve, plot the individual gene's expression trajectory with all sampling point and normalized read counts, inform if the gene was identified in our Young vs Old Analysis, and list the published Young vs Old studies used in our paper that the gene was identified in.

IDs validated with FlyBase version FB2024_03 on July 19th, 2024

If Gene Symbol has special characters, use FBgn Number.

FBgn Number or Gene Symbol

Choose Timeframe

Day

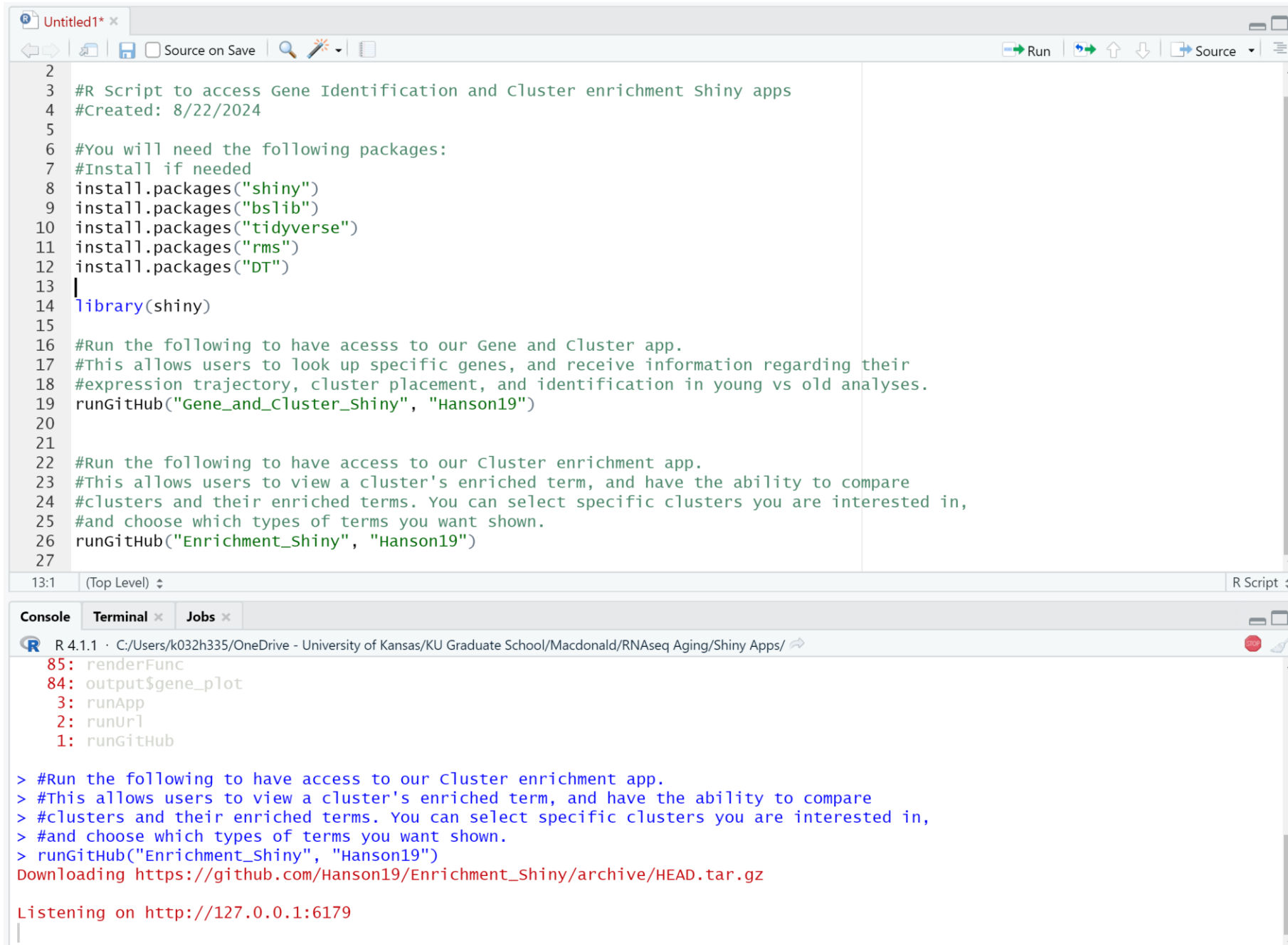
docs was not identified in our analysis. Check spelling of submitted ID to be sure.



docs was not identified in our Young v Old Analysis.

Cluster Enrichment App Breakdown

To access the cluster enrichment app , run `runGitHub("Enrichment_Shiny", Hanson19)` on line 26 of the screenshot.



The screenshot displays the RStudio environment. The top pane shows an R script file named 'Untitled1*' with the following content:

```
2
3 #R Script to access Gene Identification and Cluster enrichment Shiny apps
4 #Created: 8/22/2024
5
6 #You will need the following packages:
7 #Install if needed
8 install.packages("shiny")
9 install.packages("bslib")
10 install.packages("tidyverse")
11 install.packages("rms")
12 install.packages("DT")
13 |
14 library(shiny)
15
16 #Run the following to have access to our Gene and Cluster app.
17 #This allows users to look up specific genes, and receive information regarding their
18 #expression trajectory, cluster placement, and identification in young vs old analyses.
19 runGitHub("Gene_and_Cluster_Shiny", "Hanson19")
20
21
22 #Run the following to have access to our Cluster enrichment app.
23 #This allows users to view a cluster's enriched term, and have the ability to compare
24 #clusters and their enriched terms. You can select specific clusters you are interested in,
25 #and choose which types of terms you want shown.
26 runGitHub("Enrichment_Shiny", "Hanson19")
27
```

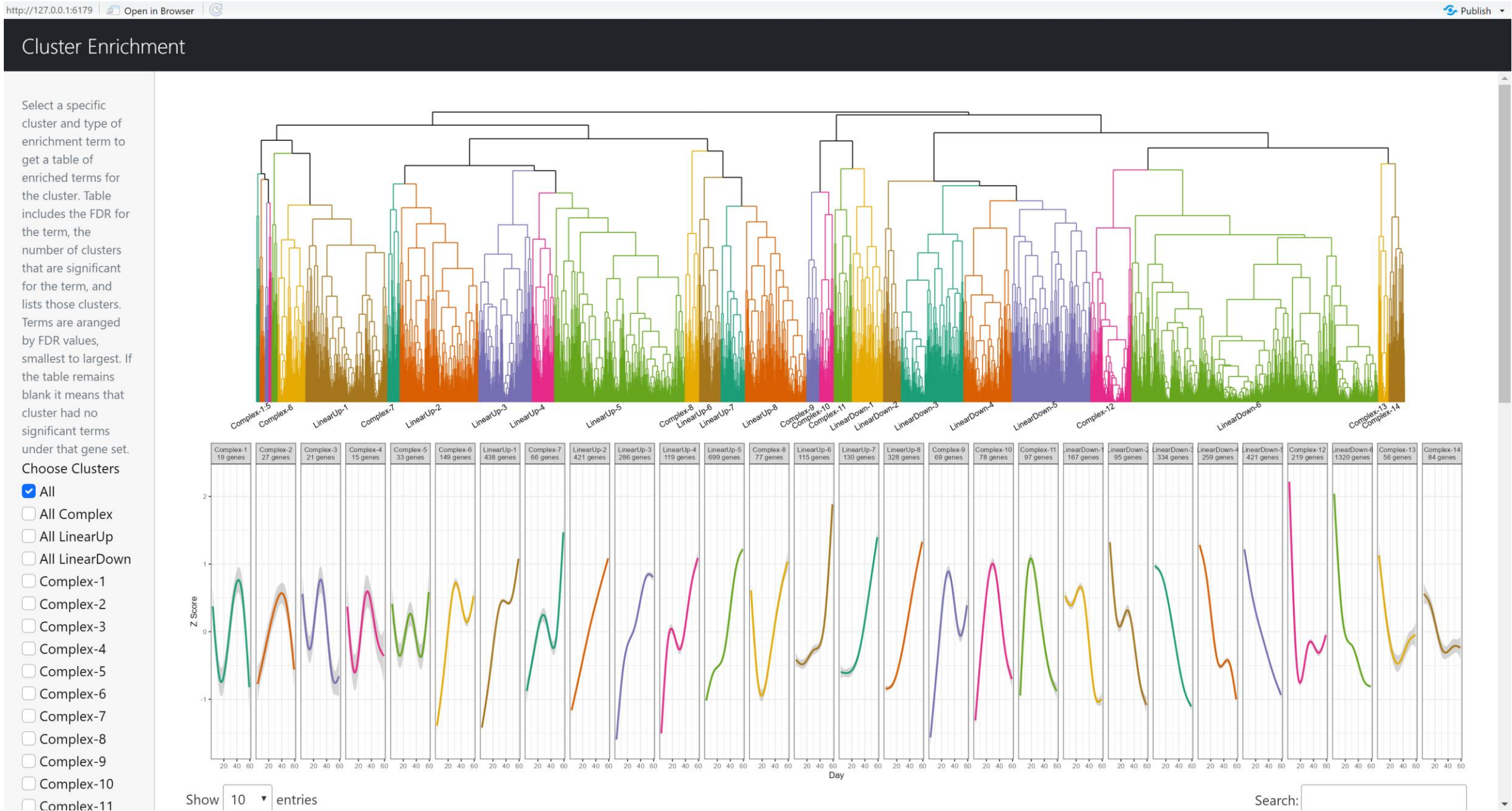
The bottom pane shows the R console output for the script execution:

```
R 4.1.1 · C:/Users/k032h335/OneDrive - University of Kansas/KU Graduate School/Macdonald/RNAseq Aging/Shiny Apps/
85: renderFunc
84: output$gene_plot
3: runApp
2: runUrl
1: runGitHub

> #Run the following to have access to our Cluster enrichment app.
> #This allows users to view a cluster's enriched term, and have the ability to compare
> #clusters and their enriched terms. You can select specific clusters you are interested in,
> #and choose which types of terms you want shown.
> runGitHub("Enrichment_Shiny", "Hanson19")
Downloading https://github.com/Hanson19/Enrichment_Shiny/archive/HEAD.tar.gz

Listening on http://127.0.0.1:6179
```

A window that looks like this should pop up. The output of this app is a lot bigger than that of the gene and cluster app so it may not all fit on one page and require scrolling.



Sidebar features:

Select which clusters you want to see enriched terms for. You can choose to look at multiple clusters at the same time. App defaults to “All”.

Cluster Enrichment

Choose Clusters

☒ All

☐ All Complex

☐ All LinearUp

☐ All LinearDown

☐ Complex-1

☐ Complex-2

☐ Complex-3

☐ Complex-4

☐ Complex-5

☐ Complex-6

☐ Complex-7

☐ Complex-8

☐ Complex-9

☐ Complex-10

☐ Complex-11

☐ Complex-12

☐ Complex-13

☐ Complex-14

☐ LinearUp-1

☐ LinearUp-2

☐ LinearUp-3

☐ LinearUp-4

☐ LinearUp-5

☐ LinearUp-6

☐ LinearUp-7

☐ LinearUp-8

☐ LinearDown-1

☐ LinearDown-2

☐ LinearDown-3

☐ LinearDown-4

☐ LinearDown-5

☐ LinearDown-6

Select what type of terms you want to see. Can look at multiple types at the same time.

Select All Enrichment Term Types

☒ SLIM2 GO BP

☐ SLIM2 GO CC

☐ SLIM2 GO MF

☐ DRSC GLAD Gene Group

☐ FlyBase Gene Group

☐ REACTOME pathway

If multiple clusters are selected, you can choose to show all terms the clusters are enriched. You can also compare clusters by either only showing terms that are shared between selected clusters or terms that are unique to one of the selected clusters.

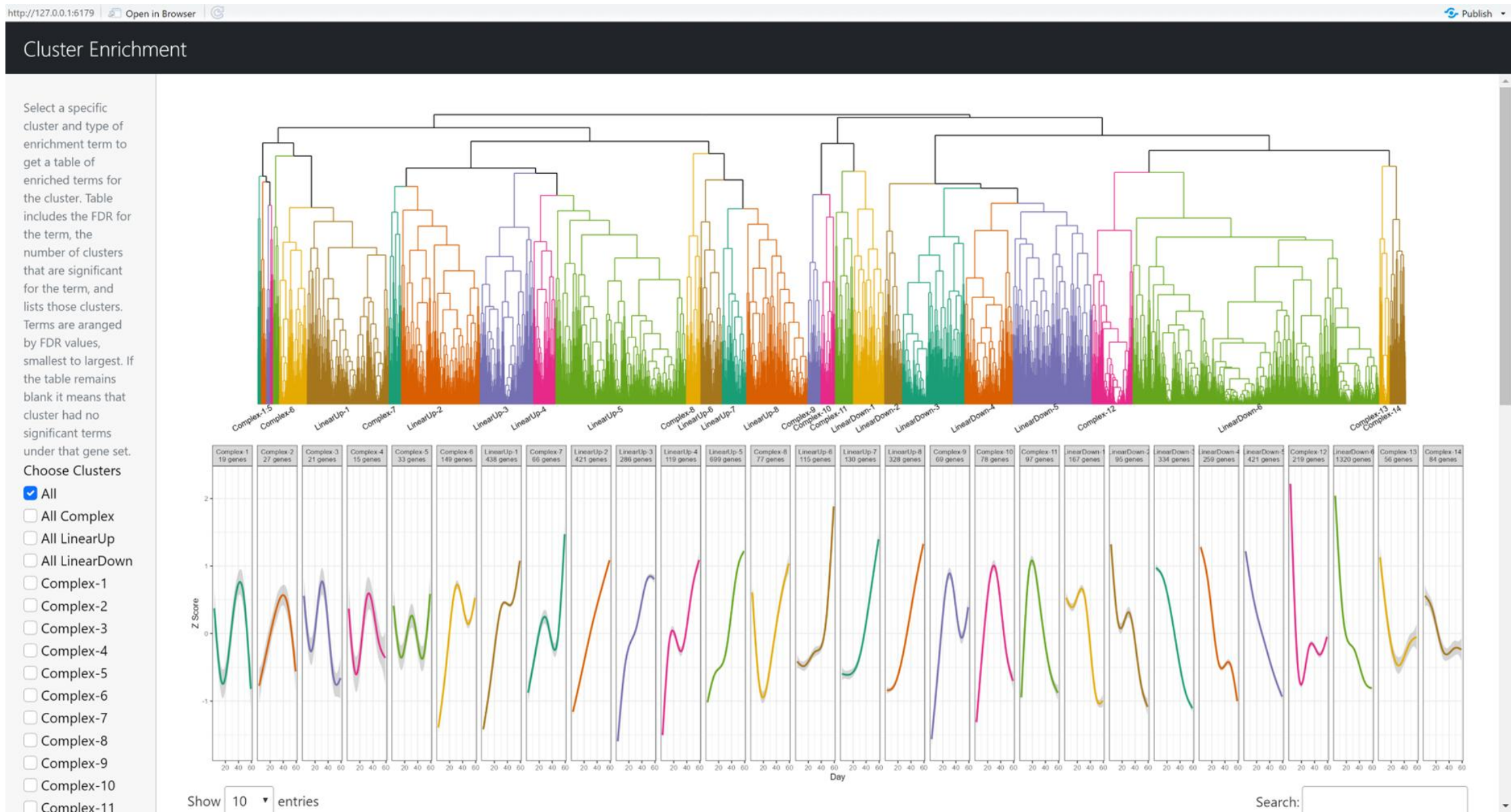
Cluster Comparison

☒ Show All Terms

☐ Show Shared Terms between Clusters

☐ Show Unique Terms between Clusters

Dendrogram in the top panel, and representative cluster expression curves in the second panel. The dendrogram will highlight clusters that are selected, and only the representative curves of selected clusters will be plotted.



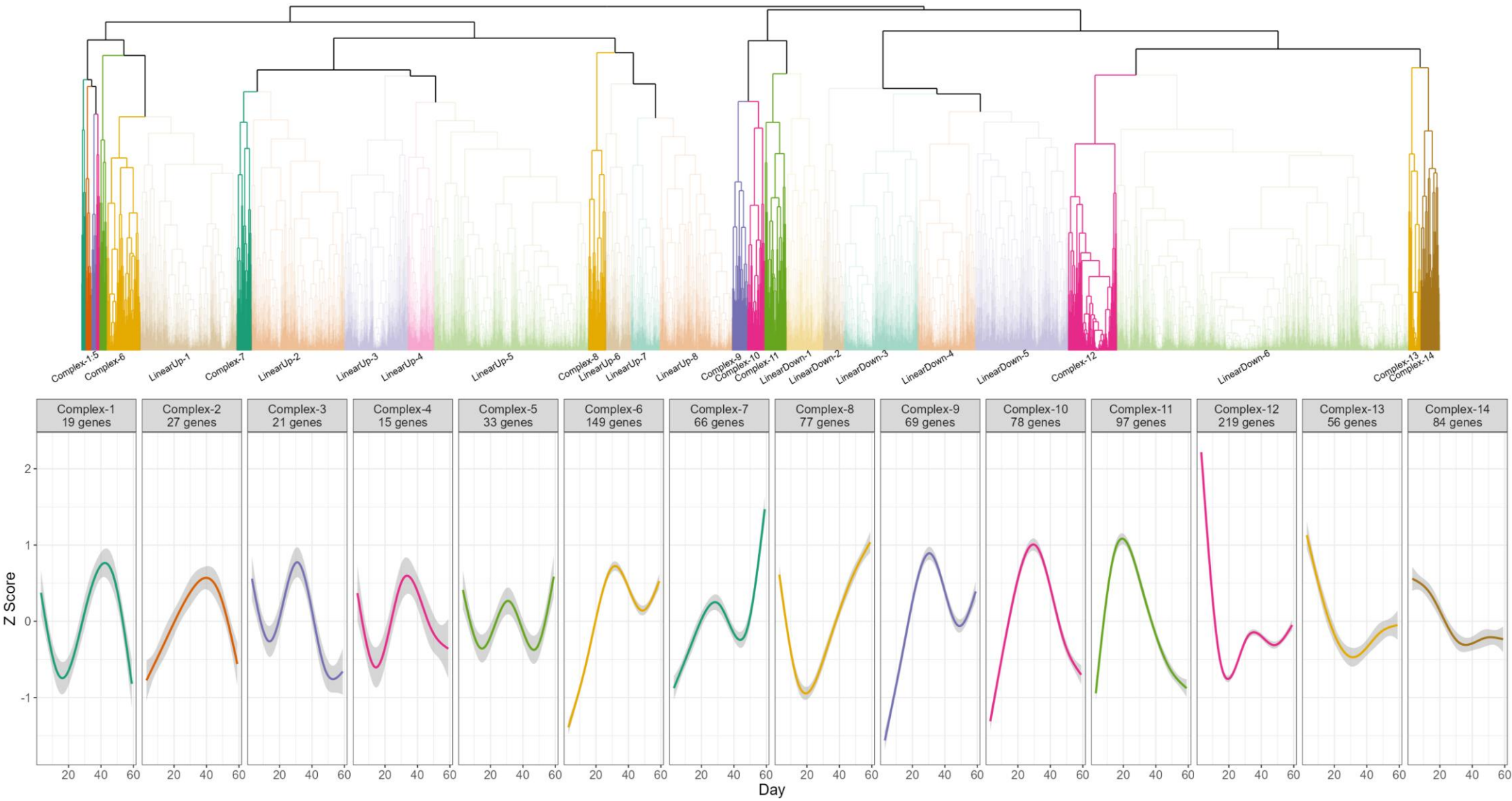
Only Complex clusters are selected in this example.

Cluster Enrichment

Select a specific cluster and type of enrichment term to get a table of enriched terms for the cluster. Table includes the FDR for the term, the number of clusters that are significant for the term, and lists those clusters. Terms are arranged by FDR values, smallest to largest. If the table remains blank it means that cluster had no significant terms under that gene set.

Choose Clusters

- ☐ All
- ☒ All Complex
- ☐ All LinearUp
- ☐ All LinearDown
- ☐ Complex-1
- ☐ Complex-2
- ☐ Complex-3
- ☐ Complex-4
- ☐ Complex-5
- ☐ Complex-6
- ☐ Complex-7
- ☐ Complex-8
- ☐ Complex-9
- ☐ Complex-10
- ☐ Complex-11



Show 10 entries

Search:

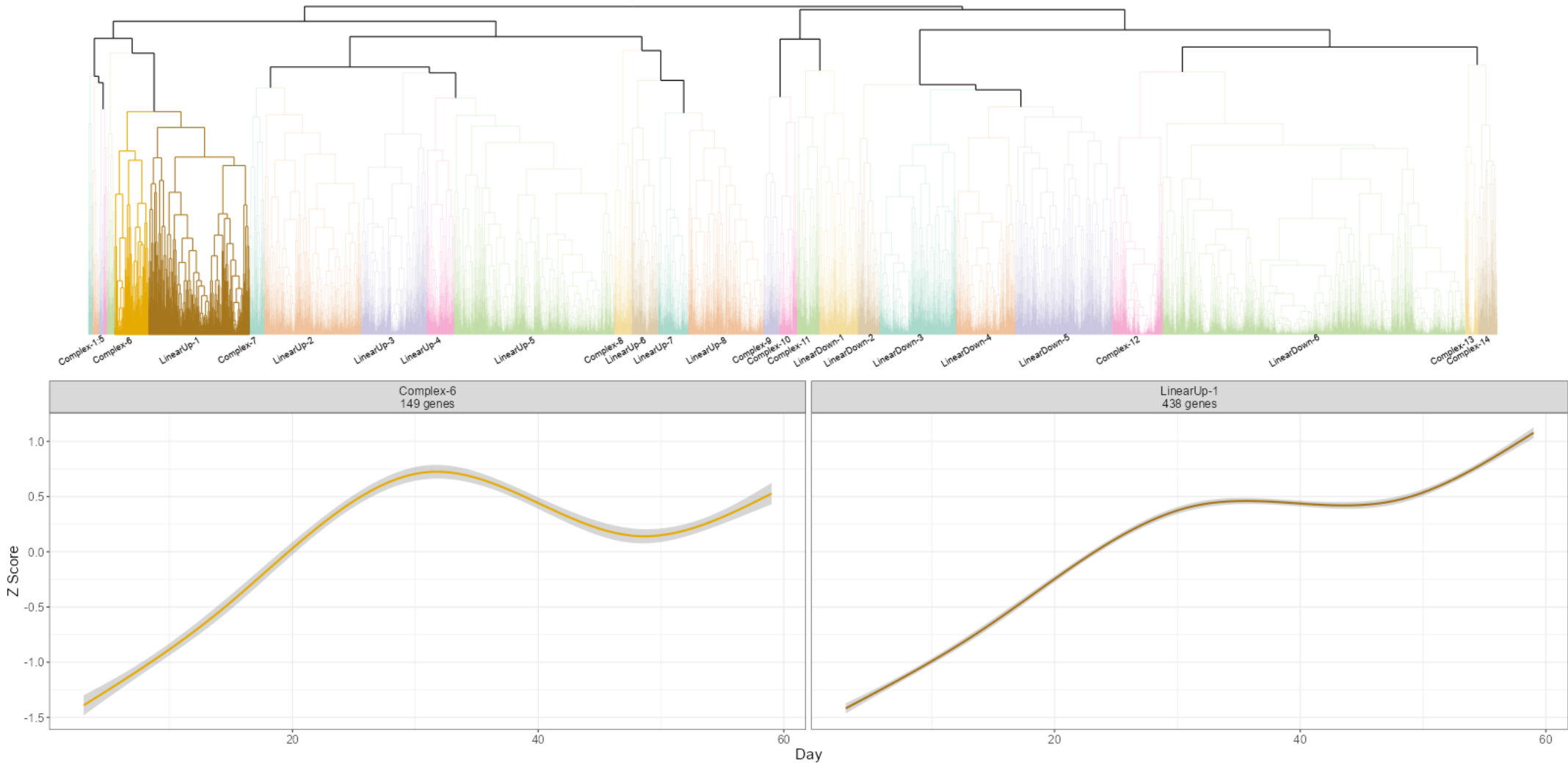
Only Complex-6 and LinearUp-1 are selected here.

Cluster Enrichment

Select a specific cluster and type of enrichment term to get a table of enriched terms for the cluster. Table includes the FDR for the term, the number of clusters that are significant for the term, and lists those clusters. Terms are arranged by FDR values, smallest to largest. If the table remains blank it means that cluster had no significant terms under that gene set.

Choose Clusters

- ☒ All
- ☐ All Complex
- ☐ All LinearUp
- ☐ All LinearDown
- ☐ Complex-1
- ☐ Complex-2
- ☐ Complex-3
- ☐ Complex-4
- ☐ Complex-5
- ☒ Complex-6
- ☐ Complex-7
- ☐ Complex-8
- ☐ Complex-9
- ☐ Complex-10
- ☐ Complex-11
- ☐ Complex-12
- ☐ Complex-13
- ☐ Complex-14
- ☒ LinearUp-1
- ☐ LinearUp-2



Show 10 entries

Search:

The last panel is a table of the selected cluster's enriched terms. Here we are listing all the enriched SLIM2 GO BP terms in all the clusters based on selections in our sidebar.

Cluster Enrichment

☐ Complex-13

☐ Complex-14

☐ LinearUp-1

☐ LinearUp-2

☐ LinearUp-3

☐ LinearUp-4

☐ LinearUp-5

☐ LinearUp-6

☐ LinearUp-7

☐ LinearUp-8

☐ LinearDown-1

☐ LinearDown-2

☐ LinearDown-3

☐ LinearDown-4

☐ LinearDown-5

☐ LinearDown-6

Select All Enrichment Term Types

☒ SLIM2 GO BP

☐ SLIM2 GO CC

☐ SLIM2 GO MF

☐ DRSC GLAD Gene Group

☐ FlyBase Gene Group

☐ REACTOME pathway

Cluster Comparison

☒ Show All Terms

☐ Show Shared Terms between Clusters

☐ Show Unique Terms between Clusters

Show

10

 entries

Search:

	Gene.Set	Gene.Set.ID	Gene.Set.Name	Cluster	FDR	Num.Cluster.Genes	Gene.Set.Size	Total.Num.Cluster.Genes	Num.Sig.Clusters	All.Sig.Clusters
1	SLIM2 GO BP	GO:0042254	ribosome biogenesis	LinearUp-4	5.5e-24	34	206	119	4	LinearUp-1, LinearUp-2, LinearUp-4, LinearUp-6
2	SLIM2 GO BP	GO:0002181	cytoplasmic translation	LinearUp-1	8e-24	42	128	438	3	Complex-6, LinearUp-1, LinearUp-2
3	SLIM2 GO BP	GO:0006811	ion transport	LinearDown-6	8.1e-24	136	514	1320	2	Complex-12, LinearDown-6
4	SLIM2 GO BP	GO:0002181	cytoplasmic translation	Complex-6	3.07e-21	24	128	149	3	Complex-6, LinearUp-1, LinearUp-2
5	SLIM2 GO BP	GO:0016072	rRNA metabolic process	LinearUp-4	6.13e-19	21	138	119	3	LinearUp-1, LinearUp-4, LinearUp-6
6	SLIM2 GO BP	GO:0050808	synapse organization	LinearDown-6	1.02e-11	72	295	1320	3	LinearDown-3, LinearDown-4, LinearDown-6
7	SLIM2 GO BP	GO:0006091	generation of precursor metabolites and energy	LinearDown-6	1.11e-10	57	218	1320	3	Complex-12, Complex-3, LinearDown-6
8	SLIM2 GO BP	GO:0016192	vesicle-mediated transport	LinearUp-7	1.32e-09	25	510	130	5	LinearDown-4, LinearDown-6, LinearUp-5, LinearUp-7, LinearUp-8
9	SLIM2 GO BP	GO:0007399	nervous system development	LinearDown-4	1.6e-09	56	1112	259	5	LinearDown-3, LinearDown-4, LinearDown-6, LinearUp-2, LinearUp-5
10	SLIM2 GO BP	GO:0006281	DNA repair	LinearUp-3	2.82e-09	22	179	286	2	LinearUp-2, LinearUp-3

Showing 1 to 10 of 141 entries

Previous

1

2

3

4

5

...

15

Next

Breakdown of enriched terms table:

Term identification information			Enriched cluster		Benjamini Hochberg false discovery rate	Number of genes in cluster associated with term	Total number of genes associated with term	Total number of genes in the cluster	Total number of enriched clusters	List of all enriched clusters
Gene.Set	Gene.Set.ID	Gene.Set.Name	Cluster	FDR	Num.Cluster.Genes	Gene.Set.Size	Total.Num.Cluster.Genes	Num.Sig.Clusters	All.Sig.Clusters	
1	SLIM2 GO BP	GO:0042254	ribosome biogenesis	LinearUp-4	5.5e-24	34	206	119	4	LinearUp-1, LinearUp-2, LinearUp-4, LinearUp-6
2	SLIM2 GO BP	GO:0002181	cytoplasmic translation	LinearUp-1	8e-24	42	128	438	3	Complex-6, LinearUp-1, LinearUp-2
3	SLIM2 GO BP	GO:0006811	ion transport	LinearDown-6	8.1e-24	136	514	1320	2	Complex-12, LinearDown-6
4	SLIM2 GO BP	GO:0002181	cytoplasmic translation	Complex-6	3.07e-21	24	128	149	3	Complex-6, LinearUp-1, LinearUp-2

Can use search bar to lookup terms containing certain words.

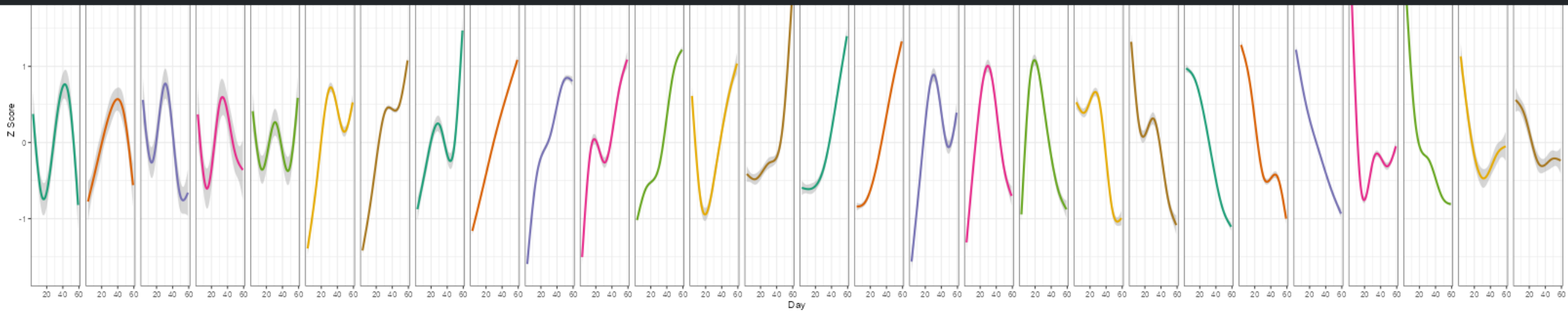
Here we have pulled out enriched terms across all clusters that are part of SLIM2 GO BP and MF sets that have “ribosome” within their name.

Cluster Enrichment

- ☐ Complex-13
- ☐ Complex-14
- ☐ LinearUp-1
- ☐ LinearUp-2
- ☐ LinearUp-3
- ☐ LinearUp-4
- ☐ LinearUp-5
- ☐ LinearUp-6
- ☐ LinearUp-7
- ☐ LinearUp-8
- ☐ LinearDown-1
- ☐ LinearDown-2
- ☐ LinearDown-3
- ☐ LinearDown-4
- ☐ LinearDown-5
- ☐ LinearDown-6

- Select All Enrichment Term Types
- ☒ SLIM2 GO BP
 - ☐ SLIM2 GO CC
 - ☒ SLIM2 GO MF
 - ☐ DRSC GLAD Gene Group
 - ☐ FlyBase Gene Group
 - ☐ REACTOME pathway

- Cluster Comparison
- ☒ Show All Terms
 - ☐ Show Shared Terms between Clusters
 - ☐ Show Unique Terms between Clusters



Show entries Search:

	Gene.Set	Gene.Set.ID	Gene.Set.Name	Cluster	FDR	Num.Cluster.Genes	Gene.Set.Size	Total.Num.Cluster.Genes	Num.Sig.Clusters	All.Sig.Clusters
1	SLIM2 GO BP	GO:0042254	ribosome biogenesis	LinearUp-4	5.5e-24	34	206	119	4	LinearUp-1, LinearUp-2, LinearUp-4, LinearUp-6
4	SLIM2 GO MF	GO:0003735	structural constituent of ribosome	LinearUp-1	1.34e-21	40	171	438	2	Complex-6, LinearUp-1
8	SLIM2 GO MF	GO:0003735	structural constituent of ribosome	Complex-6	4.01e-17	23	171	149	2	Complex-6, LinearUp-1
26	SLIM2 GO BP	GO:0042254	ribosome biogenesis	LinearUp-1	7.12e-07	25	206	438	4	LinearUp-1, LinearUp-2, LinearUp-4, LinearUp-6
81	SLIM2 GO BP	GO:0042254	ribosome biogenesis	LinearUp-6	0.00201	9	206	115	4	LinearUp-1, LinearUp-2, LinearUp-4, LinearUp-6
115	SLIM2 GO BP	GO:0042254	ribosome biogenesis	LinearUp-2	0.0105	15	206	421	4	LinearUp-1, LinearUp-2, LinearUp-4, LinearUp-6

We can also compare clusters based on the selected cluster comparison option on the sidebar. Here we are showing terms that are shared by LinearUp-2, LinearUp-5, and LinearUp-8 across all term sets.

Cluster Enrichment

☐ Complex-13

☐ Complex-14

☐ LinearUp-1

☒ LinearUp-2

☐ LinearUp-3

☐ LinearUp-4

☒ LinearUp-5

☐ LinearUp-6

☐ LinearUp-7

☒ LinearUp-8

☐ LinearDown-1

☐ LinearDown-2

☐ LinearDown-3

☐ LinearDown-4

☐ LinearDown-5

☐ LinearDown-6

Select All Enrichment Term Types

☒ SLIM2 GO BP

☒ SLIM2 GO CC

☒ SLIM2 GO MF

☒ DRSC GLAD Gene Group

☒ FlyBase Gene Group

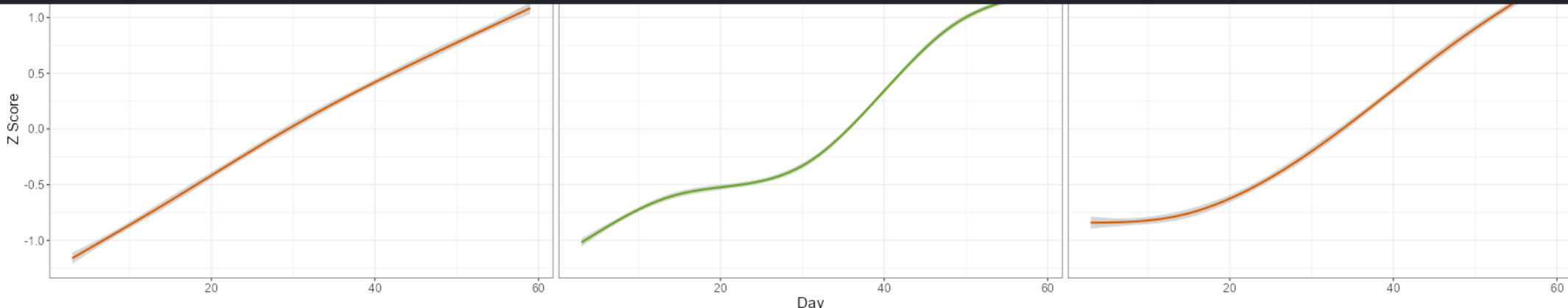
☒ REACTOME pathway

Cluster Comparison

☐ Show All Terms

☒ Show Shared Terms between Clusters

☐ Show Unique Terms between Clusters



Show

10

 entries

Search:

	Gene.Set	Gene.Set.ID	Gene.Set.Name	Cluster	FDR	Num.Cluster.Genes	Gene.Set.Size	Total.Num.Cluster.Genes	Num.Sig.Clusters	All.Sig.Clusters
1	SLIM2 GO BP	GO:0006950	response to stress	LinearUp-2	5.37e-09	80	1197	421	5	LinearUp-2, LinearUp-3, LinearUp-5, LinearUp-7, LinearUp-8
2	SLIM2 GO BP	GO:0006950	response to stress	LinearUp-5	3.05e-09	115	1197	699	5	LinearUp-2, LinearUp-3, LinearUp-5, LinearUp-7, LinearUp-8
3	SLIM2 GO BP	GO:0006950	response to stress	LinearUp-8	0.000351	54	1197	328	5	LinearUp-2, LinearUp-3, LinearUp-5, LinearUp-7, LinearUp-8
4	SLIM2 GO BP	GO:0006955	immune response	LinearUp-2	0.00105	22	287	421	3	LinearUp-2, LinearUp-5, LinearUp-8
5	SLIM2 GO BP	GO:0006955	immune response	LinearUp-5	1.85e-06	38	287	699	3	LinearUp-2, LinearUp-5, LinearUp-8
6	SLIM2 GO BP	GO:0006955	immune response	LinearUp-8	2e-04	22	287	328	3	LinearUp-2, LinearUp-5, LinearUp-8

Now showing enriched terms in LinearUp-2, 5 and 8 that are not shared with each other. The term doesn't have to be unique to that cluster, it just can't be found in the other two, as seen in rows 4-7 of the table.

Cluster Enrichment

☐ Complex-13

☐ Complex-14

☐ LinearUp-1

☒ LinearUp-2

☐ LinearUp-3

☐ LinearUp-4

☒ LinearUp-5

☐ LinearUp-6

☐ LinearUp-7

☒ LinearUp-8

☐ LinearDown-1

☐ LinearDown-2

☐ LinearDown-3

☐ LinearDown-4

☐ LinearDown-5

☐ LinearDown-6

Select All Enrichment Term Types

☒ SLIM2 GO BP

☒ SLIM2 GO CC

☒ SLIM2 GO MF

☒ DRSC GLAD Gene Group

☒ FlyBase Gene Group

☒ REACTOME pathway

Cluster Comparison

☐ Show All Terms

☐ Show Shared Terms between Clusters

☒ Show Unique Terms between Clusters

204060204060204060204060

Day

Show 10 entries

Search:

	Gene.Set	Gene.Set.ID	Gene.Set.Name	Cluster	FDR	Num.Cluster.Genes	Gene.Set.Size	Total.Num.Cluster.Genes	Num.Sig.Clusters	All.Sig.Clusters
1	FlyBase Gene Group	FBgg0000721	BOMANINS	LinearUp-5	1.58e-07	9	12	699	1	LinearUp-5
2	DRSC GLAD Gene Group	GLAD:24590	Major signaling pathways	LinearUp-5	1.72e-05	40	330	699	1	LinearUp-5
3	SLIM2 GO BP	GO:0060541	respiratory system development	LinearUp-5	3.89e-05	32	252	699	1	LinearUp-5
4	FlyBase Gene Group	FBgg0000215	ENDOSOMAL SORTING COMPLEXES REQUIRED FOR TRANSPORT	LinearUp-5	5.5e-05	9	20	699	2	LinearUp-1, LinearUp-5
5	SLIM2 GO BP	GO:0051301	cell division	LinearUp-2	0.000127	24	269	421	3	LinearUp-2, LinearUp-3, LinearUp-7
6	SLIM2 GO BP	GO:0051321	meiotic cell cycle	LinearUp-2	0.000129	21	221	421	2	LinearUp-2, LinearUp-3
7	SLIM2 GO BP	GO:0000278	mitotic cell cycle	LinearUp-2	0.000173	34	487	421	2	LinearUp-2, LinearUp-3
8	SLIM2 GO BP	GO:0006260	DNA replication	LinearUp-2	0.000241	13	103	421	1	LinearUp-2
9	FlyBase Gene Group	FBgg0000390	CYTOPLASMIC AMINOACYL-TRNA SYNTHETASES	LinearUp-5	0.000925	7	16	699	1	LinearUp-5
10	FlyBase Gene Group	FBgg0001102	UNCLASSIFIED ANTIMICROBIAL PEPTIDES	LinearUp-5	0.000925	5	7	699	1	LinearUp-5

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