Celrr KO vs WT (Adult)

This file shows the wt-v-ko comparison for Celrr.

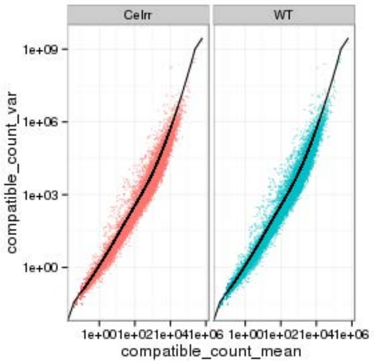
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

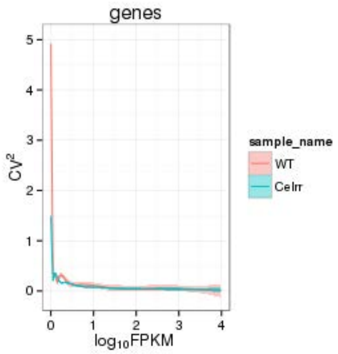
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



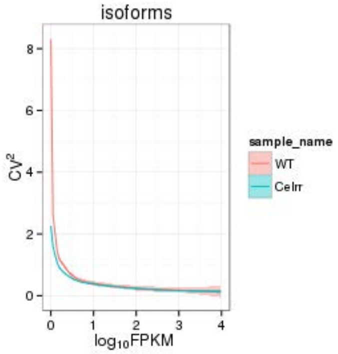
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

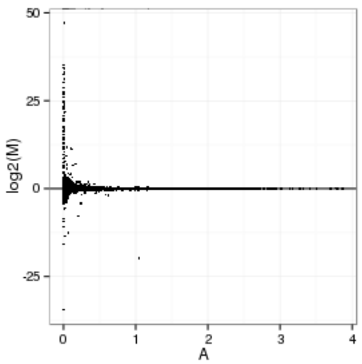
Genes:



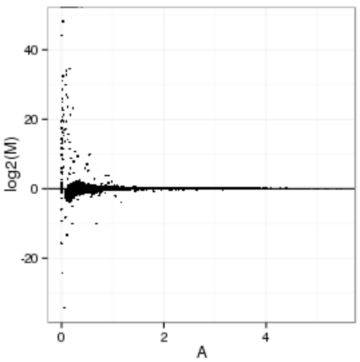
Isoforms:



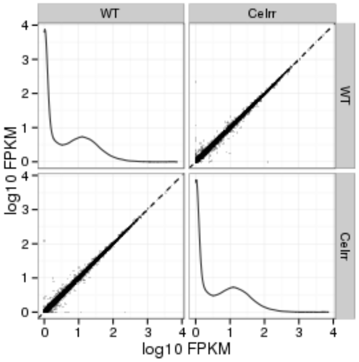
MvA plot



MvA plot counts



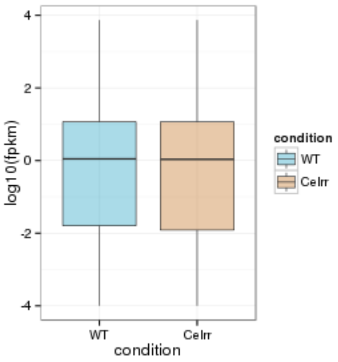
Scatterplot matrix



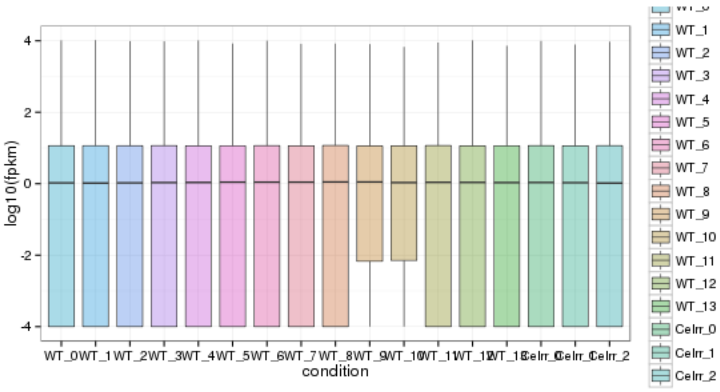
Distributions

Boxplots

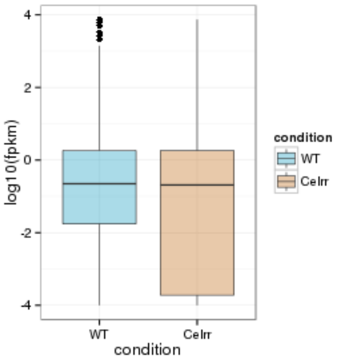
Boxplot (genes)



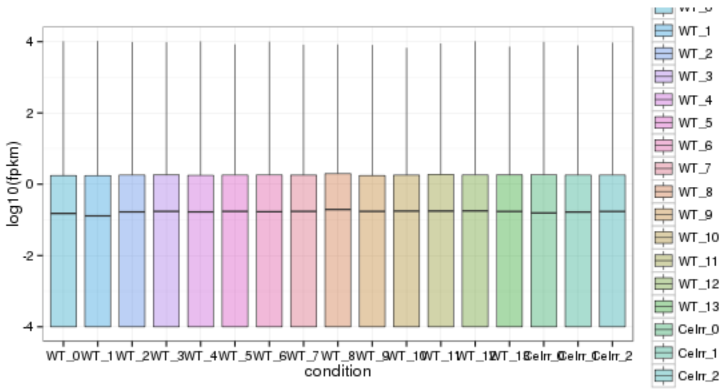
Boxplot (genes, replicates)



Boxplot (isoforms)

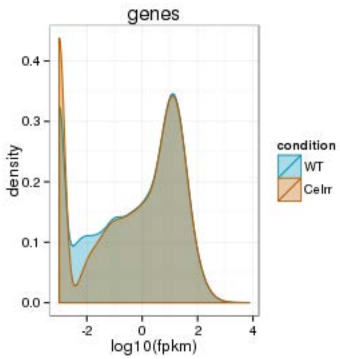


Boxplot (isoforms, replicates)

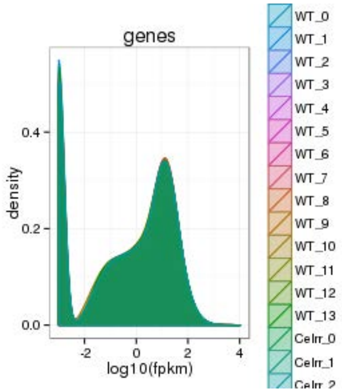


Density

Density (genes)

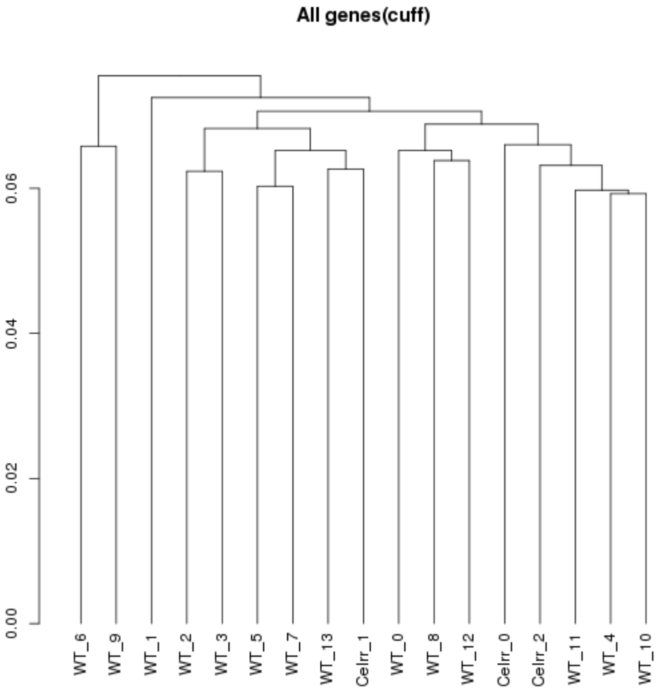


Density (genes, replicates)



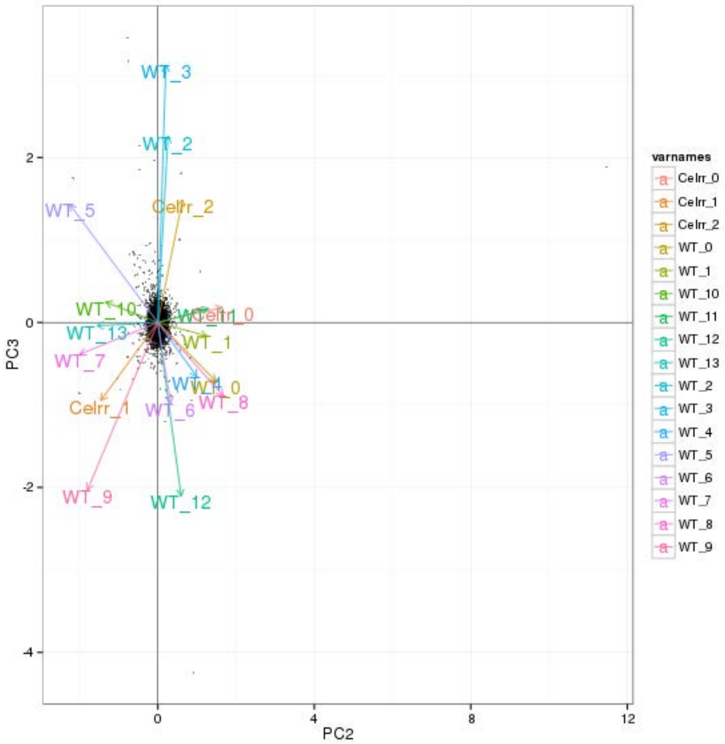
Clustering

Replicate Clusters



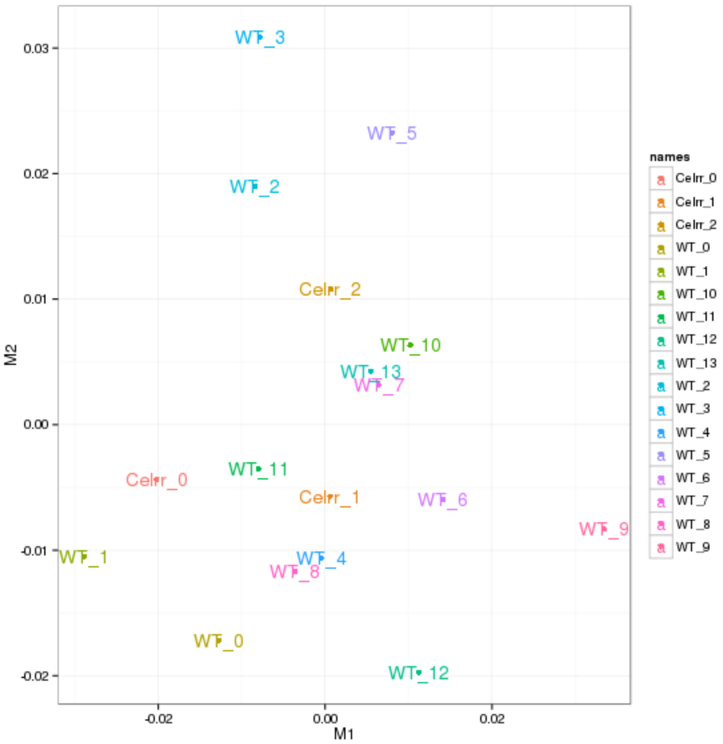
```
## NULL
```

PCA (genes)



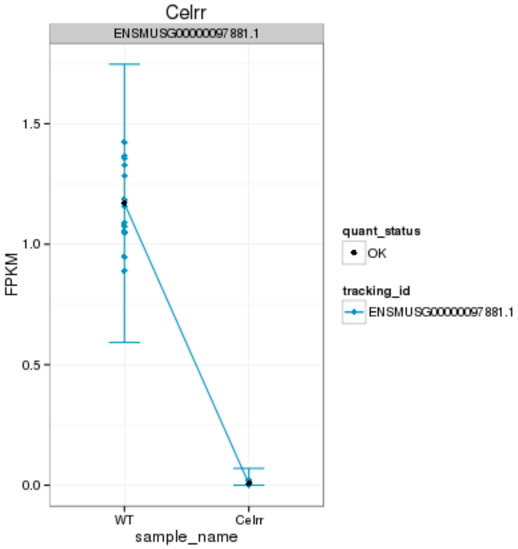
PC3
PC2
2
0
-2
-4
0
4
8
12
WT_3
WT_2
WT_5
Celrr_2
WT_10
WT_13
WT_7
Celrr_1
WT_9
WT_6
WT_12
WT_4
WT_0
WT_8
WT_1
WT_11
Celrr_0
varnames
Celrr_0
Celrr_1
Celrr_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

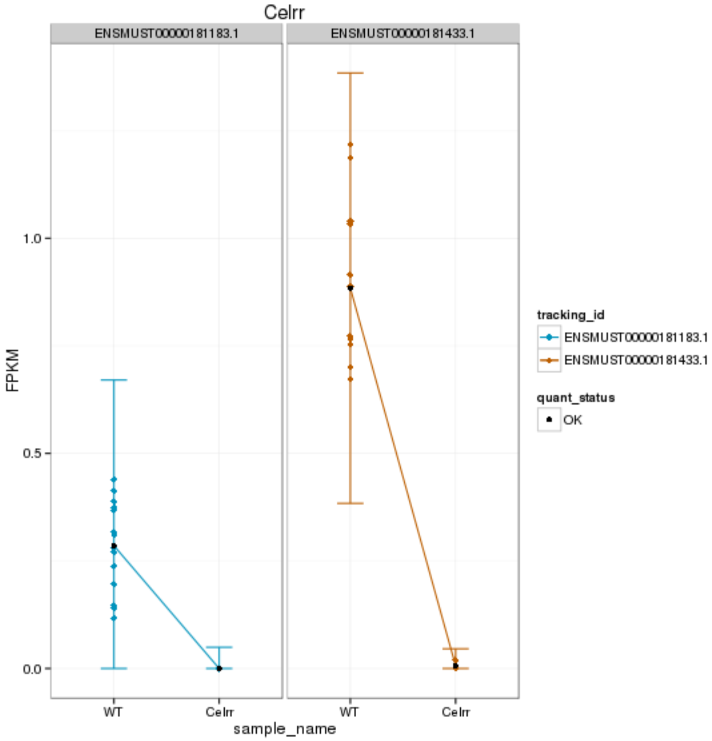


KO assessment

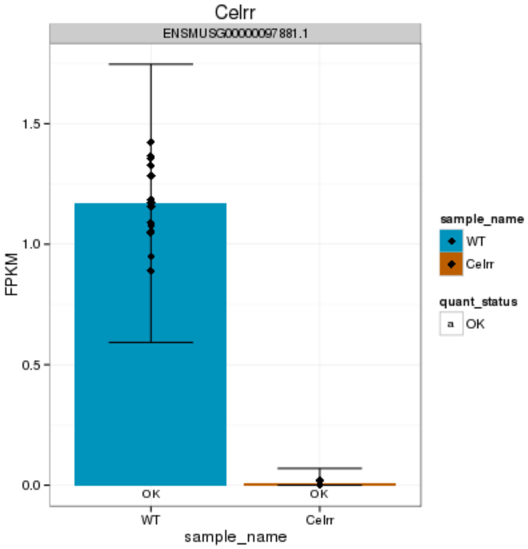
Endogenous lncRNA expression



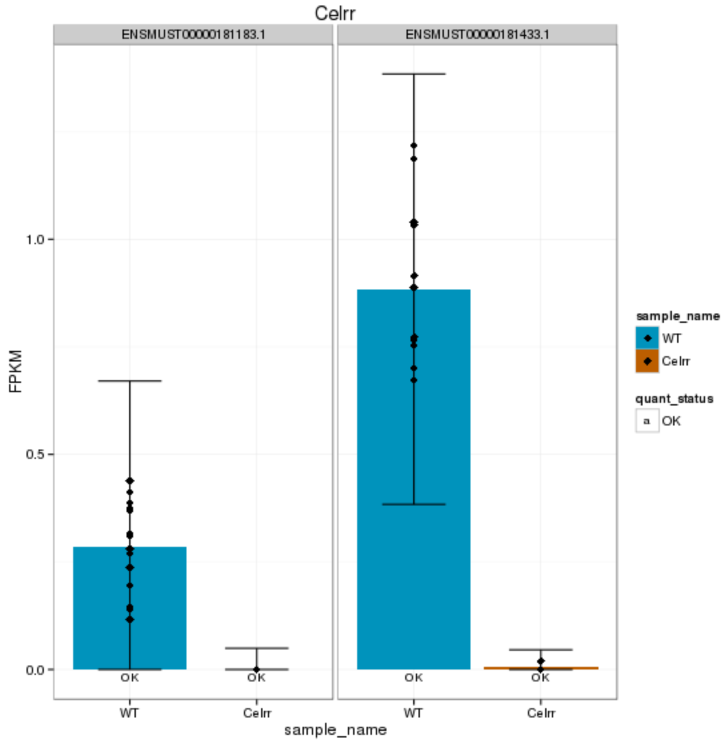
Endogenous expression of Celrr isoforms:



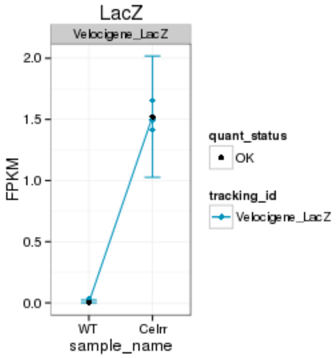
Barplot of gene expression:

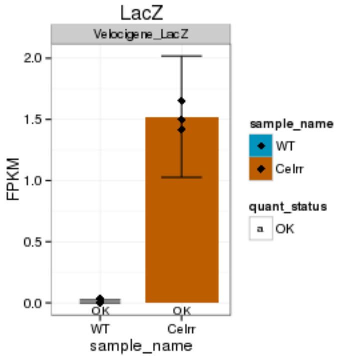


Barplot of isoform expression:



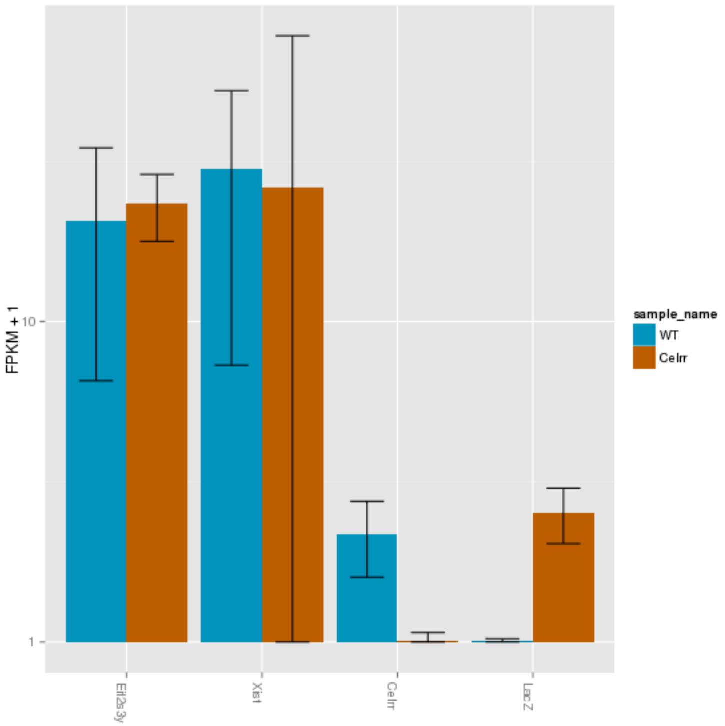
LacZ expression



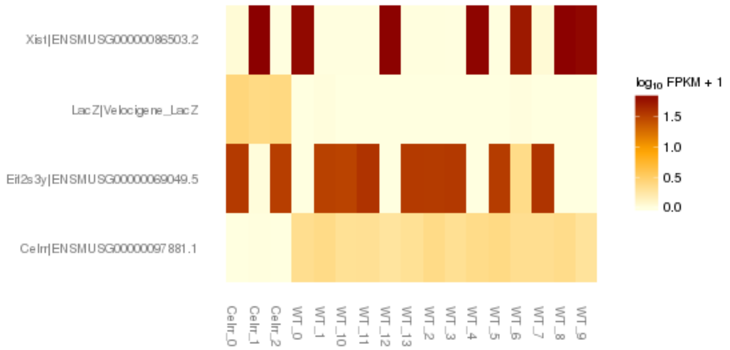


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

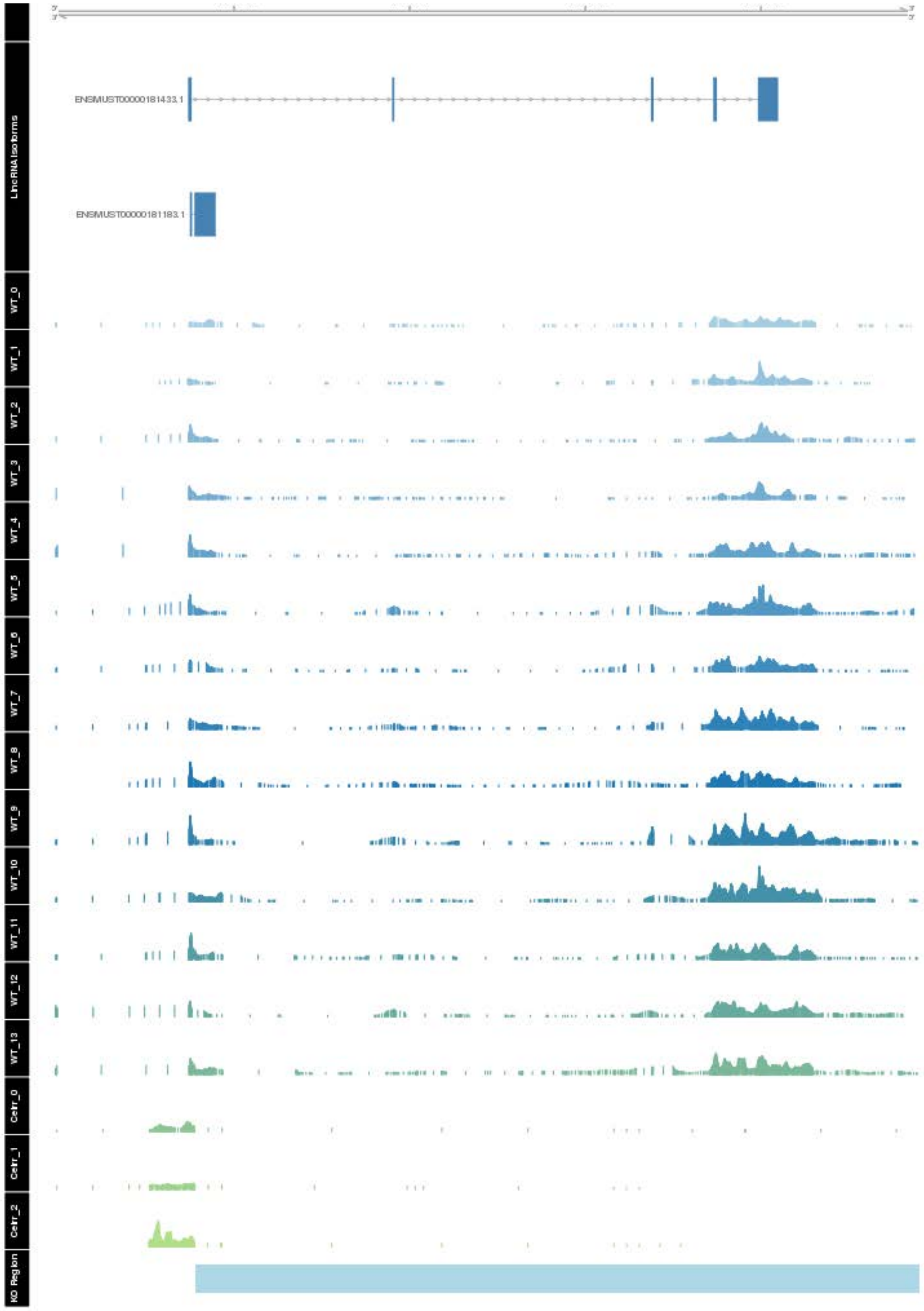
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


5'
3'
5'
3'
LincRNA Isoforms
ENSMUST00000181433.1
ENSMUST00000181183.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Cetr_0
Cetr_1
Cetr_2
KO Region

Differential Analysis

Differential Genes

There are 54 significantly differentially expressed genes. They are:

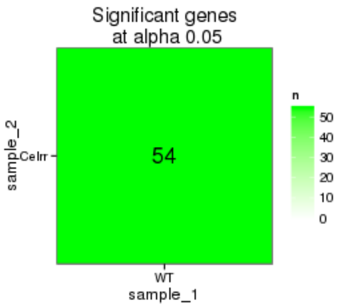
	geneAnnot$gene_short_name
1	Chordc1
2	Nes
3	Dnajb1
4	Dio2
5	Slc38a3
6	P4ha1
7	Btg2
8	Ccdc117
9	Xbp1
10	Pdia6
11	Adi1
12	Serpina3n
13	Fos
14	Arc
15	Sdf2l1
16	Nr4a1
17	Creld2
18	Glo1
19	Dusp1
20	Pdia4
21	Lcn2
22	Hspa5
23	Vcam1
24	Hddc3
25	Tsc22d3
26	Mt2
27	Mt1
28	Pllp
29	Cryab
30	Ptgs2
31	Tlr13
32	Lars2
33	Egr1
34	Fmo2
35	Obfc1
36	Pcsk9
37	Gm9493

38 Acp1
39 Cirbp
40 Npas4
41 Tmem252
42 Opalin
43 Cd14

44 Tpt1
45 Zbtb40
46 Rpl34
47 Ppia
48 Gm7292
49 H2-Bl
50 Wdfy1
51 Hspa1b
52 Hspa1a
53 Neat1
54 AA465934

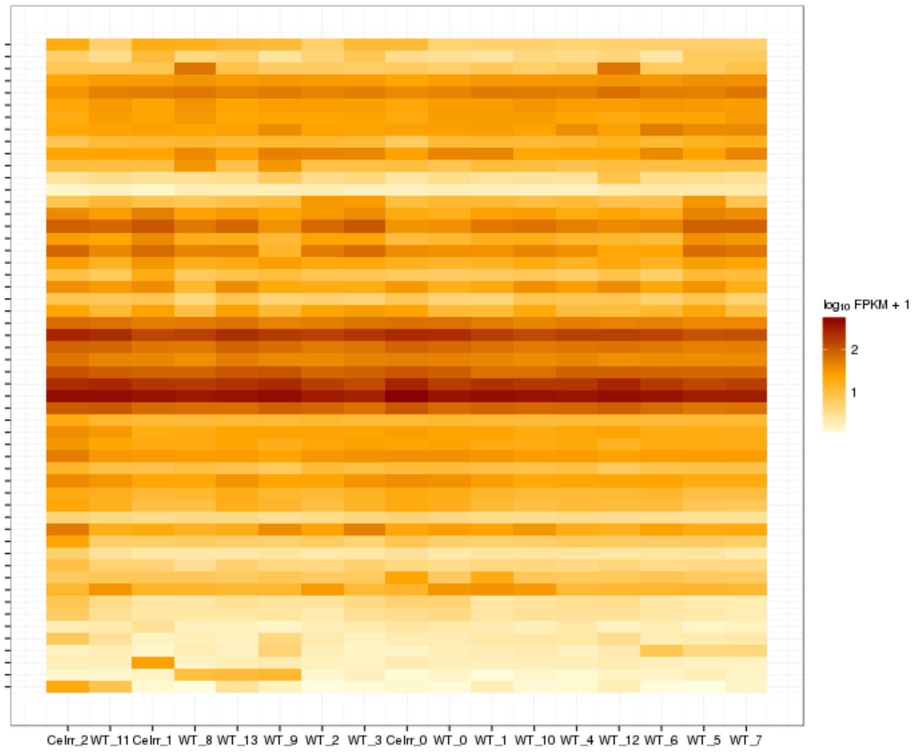
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

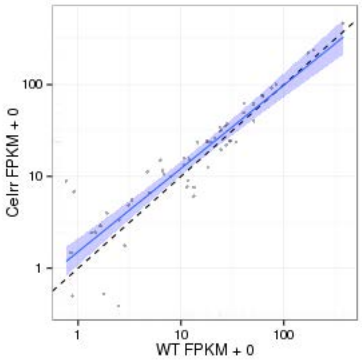


Significant genes with expression >50fpkm (any condition):(turned off)

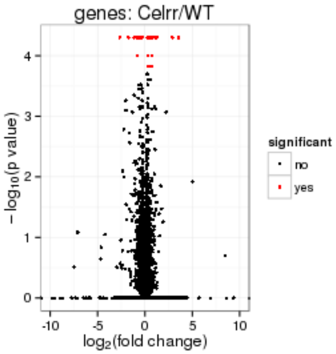
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

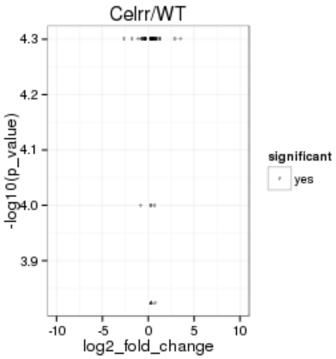
Scatter plot of significant genes only:



Volcano Plot



Volcano plot with significant genes only:

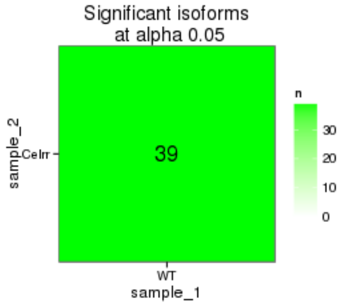


FoldChange Heatmap

Differential Splicing

Differential Isoforms between conditions

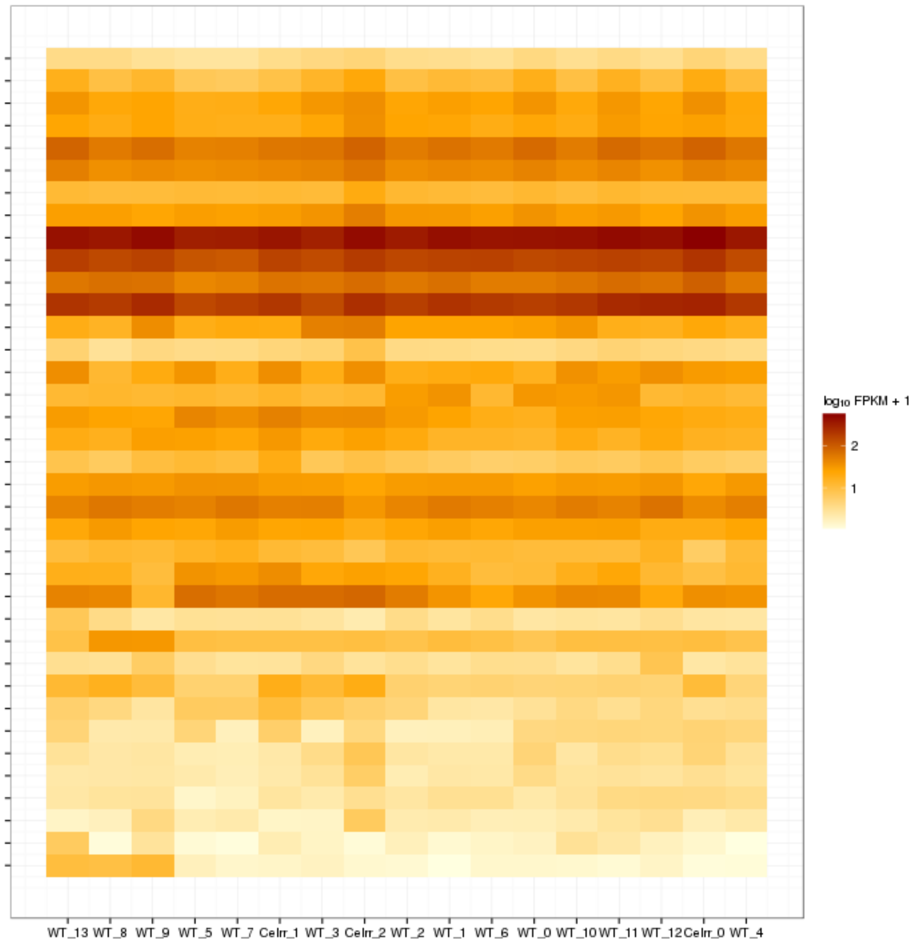
Per isoform difference between conditions:



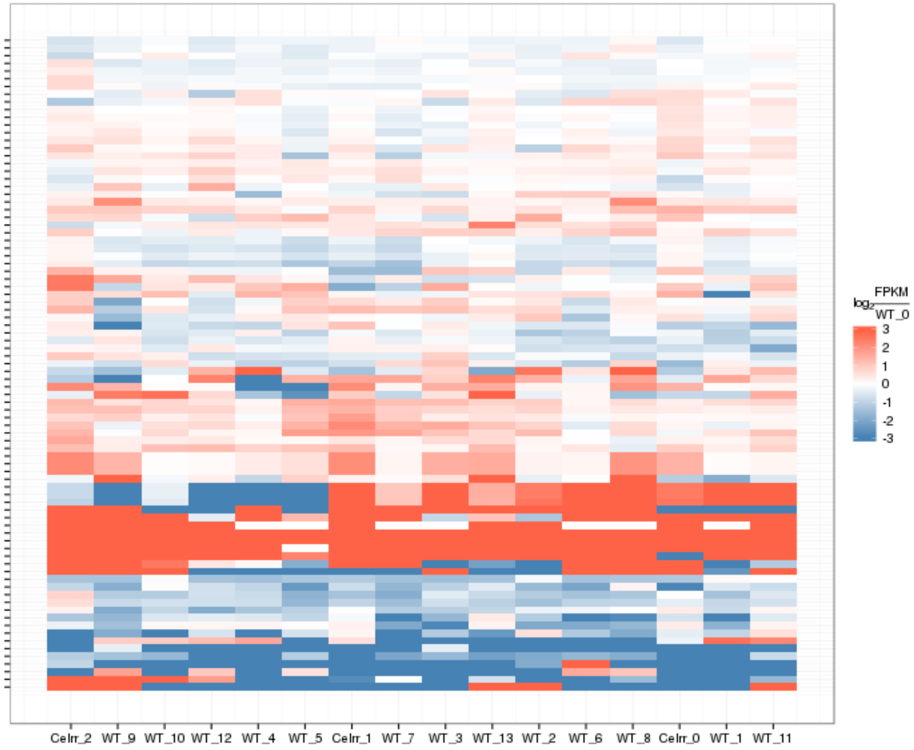
These isoforms are:

	isoAnnot$gene_short_name
1	Chordc1
2	Rec8
3	Hif3a
4	Nes
5	Dnajb1
6	Cyp2a5
7	Dio2
8	Btg2
9	Pdia6
10	Serpina3n
11	Fos
12	Fam107a
13	Arc
14	Sdf2l1
15	Nr4a1
16	Dusp1
17	Pdia4
18	Vcam1
19	Hddc3
20	Mt2
21	Mt1
22	Pllp
23	Ptgs2
24	Lars2
25	Gjb6
26	Gm9493
27	Cirbp
28	Npas4
29	Tmem252
30	Opalin
31	Pla2g4e
32	Zbtb40
33	Gm7292
34	Wdfy1
35	Hspa1b
36	Hspa1a
37	Neat1

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

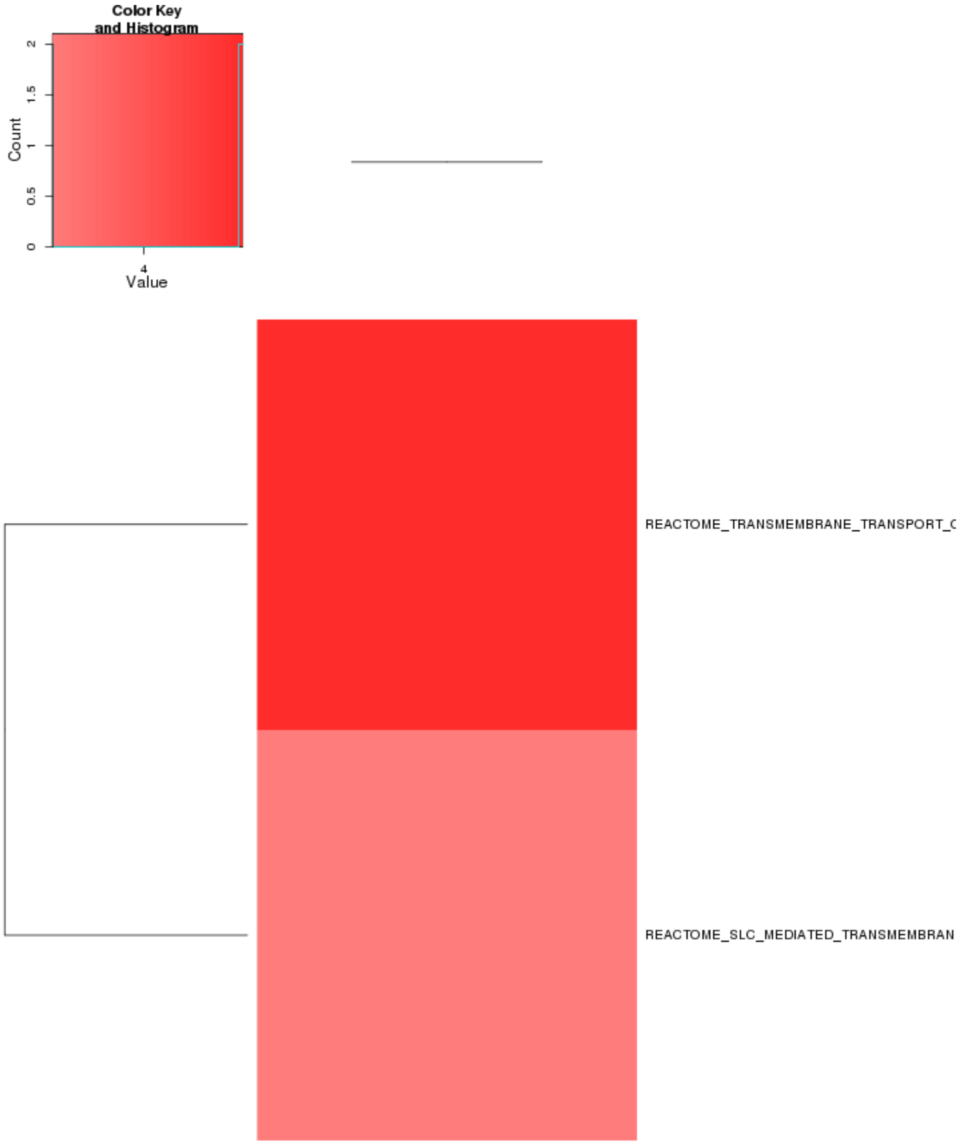
Biocarta enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

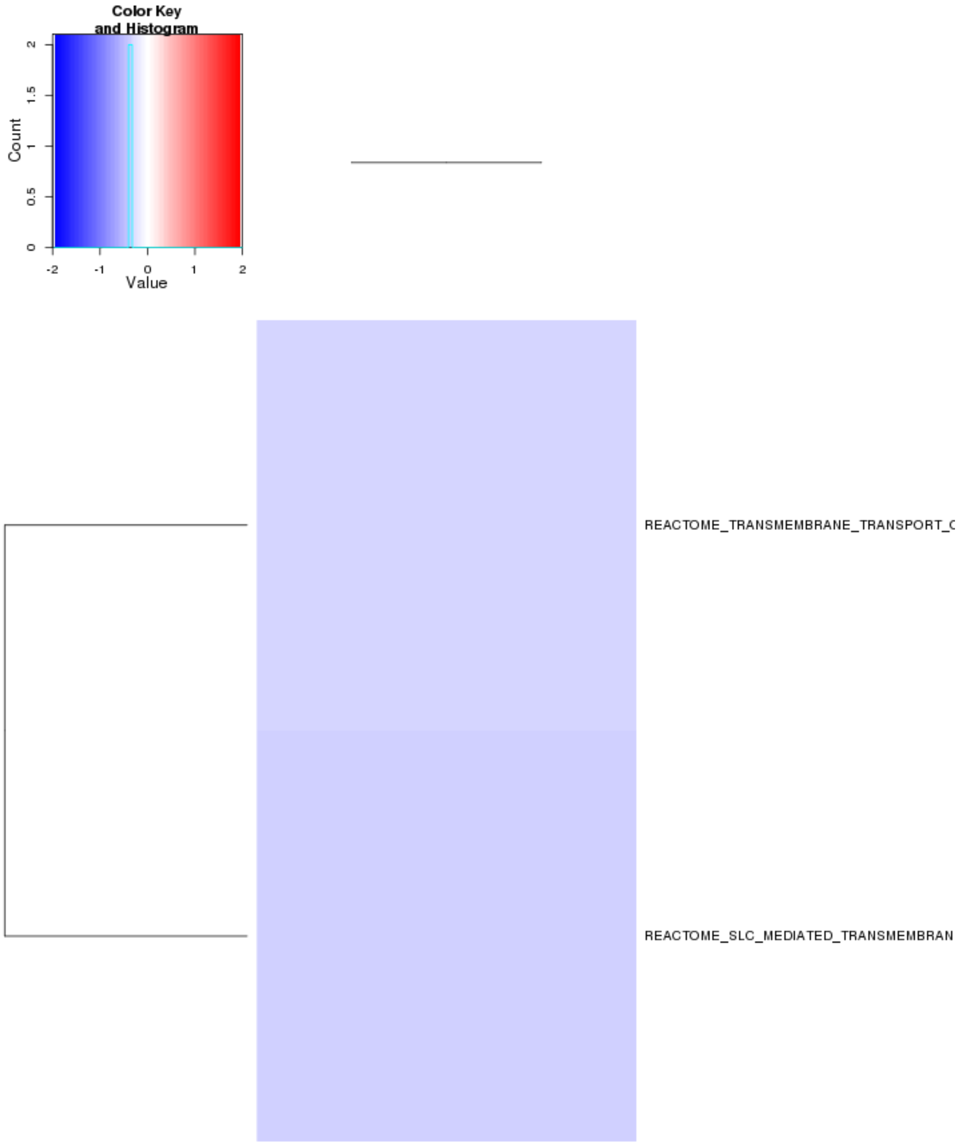
Biocarta zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

Reactome enrichment:



Reactome zscore:



Kegg enrichment:

```
## Error: argument is of length zero
```

Kegg zscore:

```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

Interneuron enrichment:

```
## Error: argument is of length zero
```

Interneuron zscore:

```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

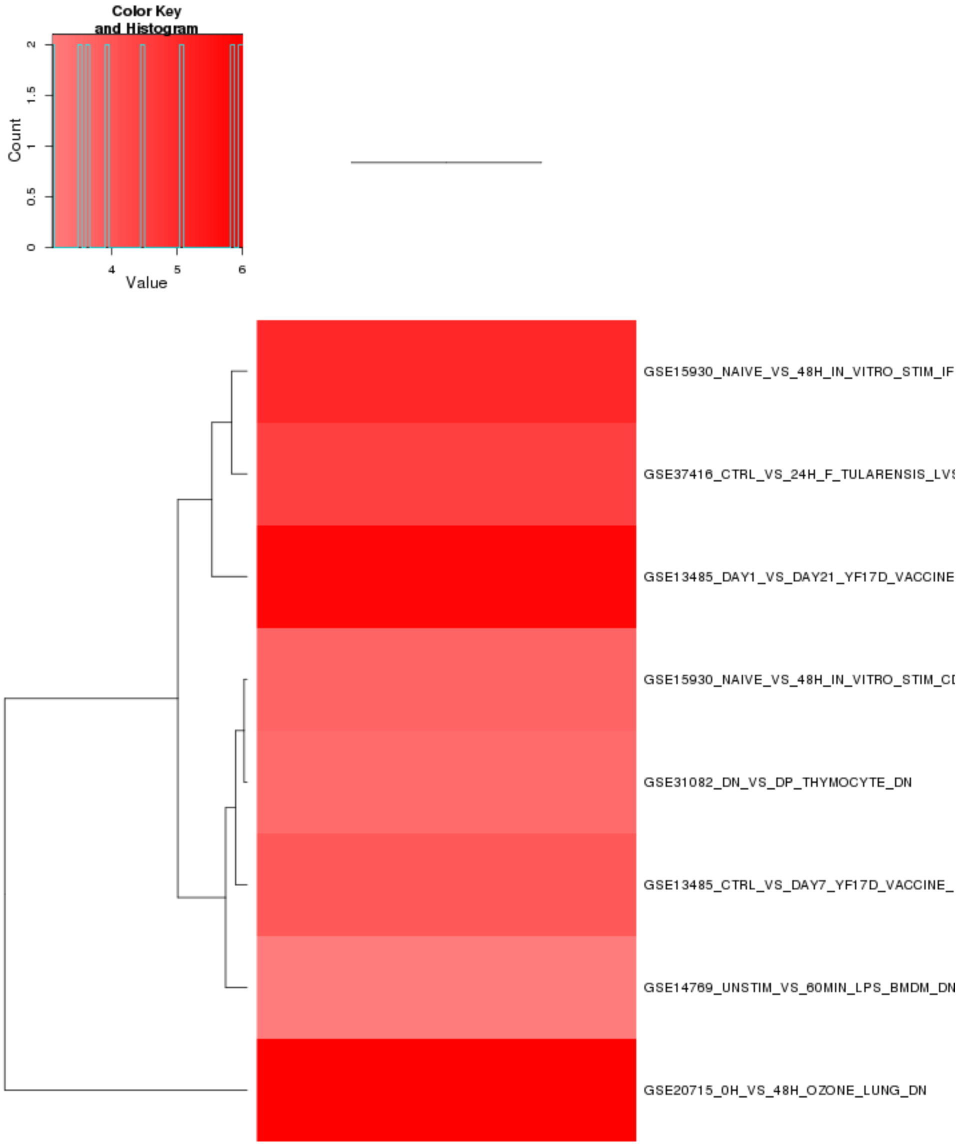
Oncogene enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

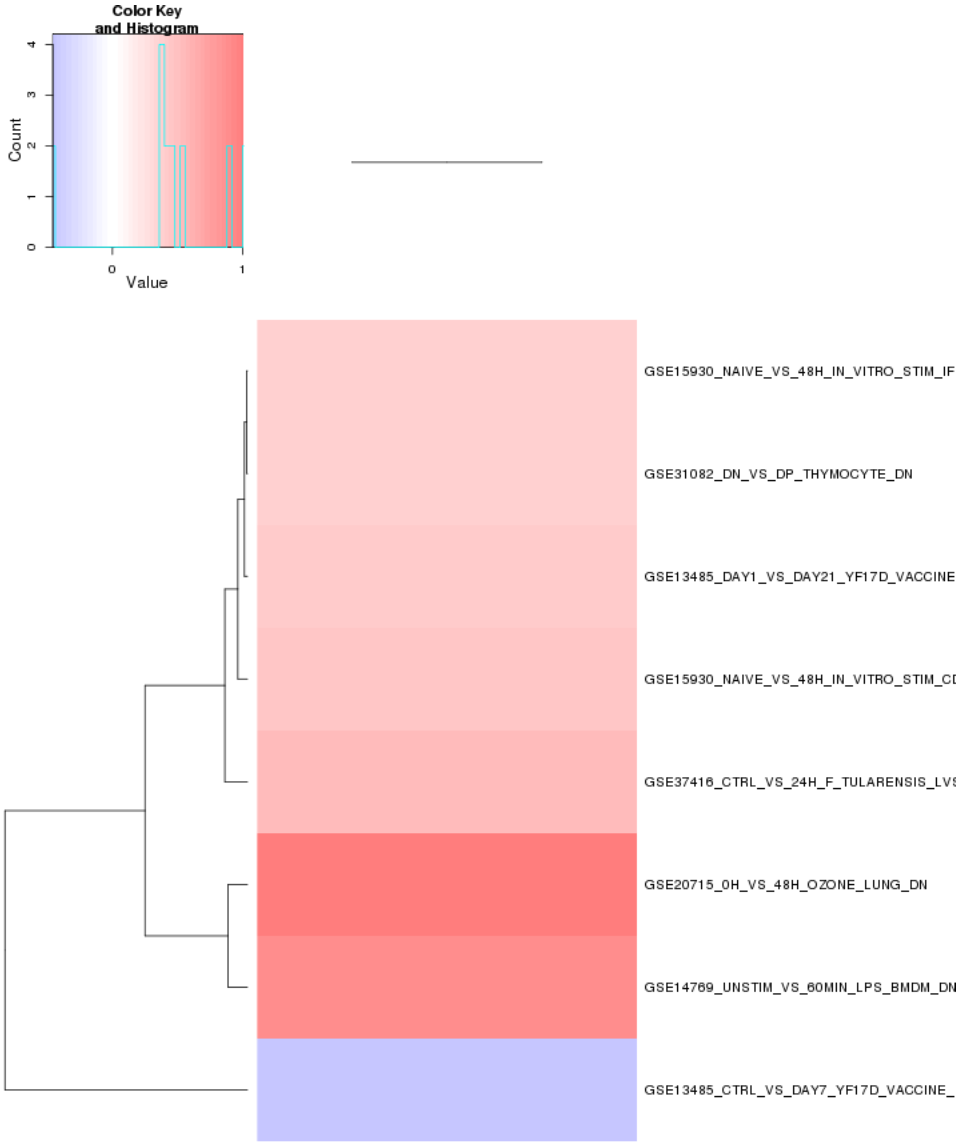
Oncogene zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

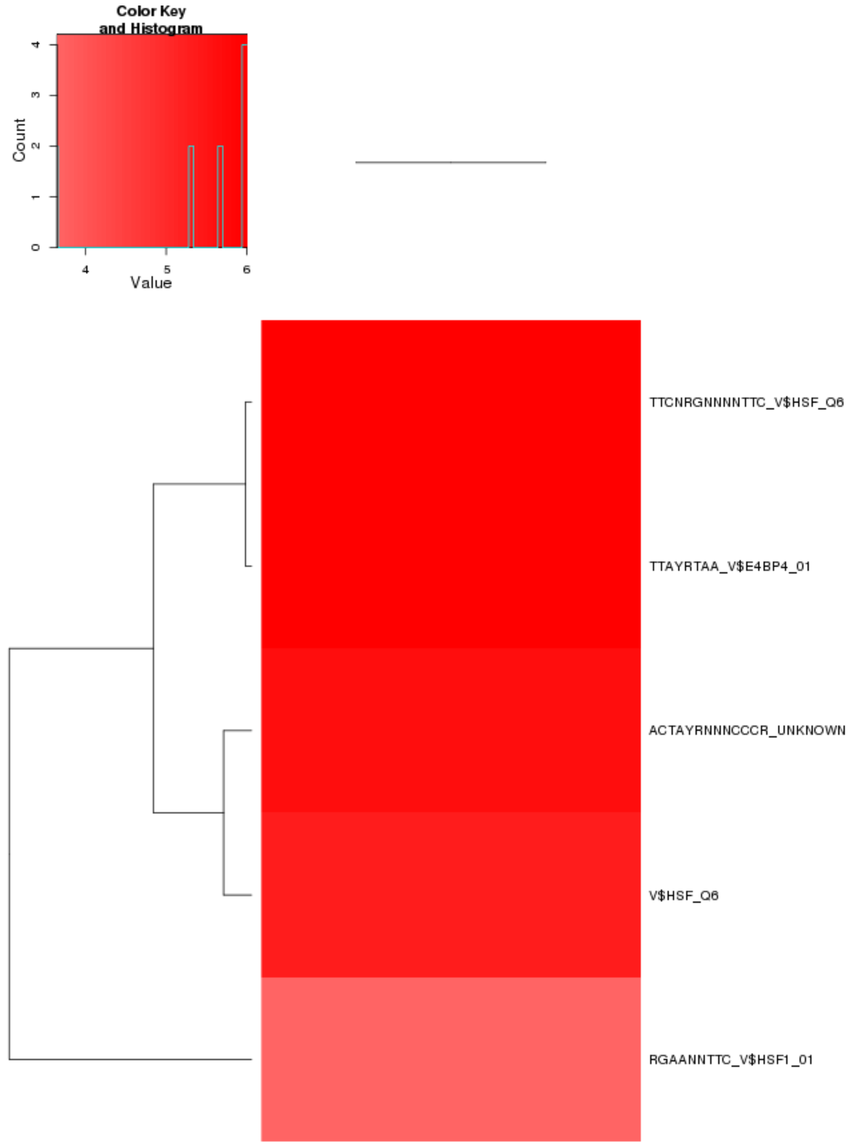
Immuno enrichment:



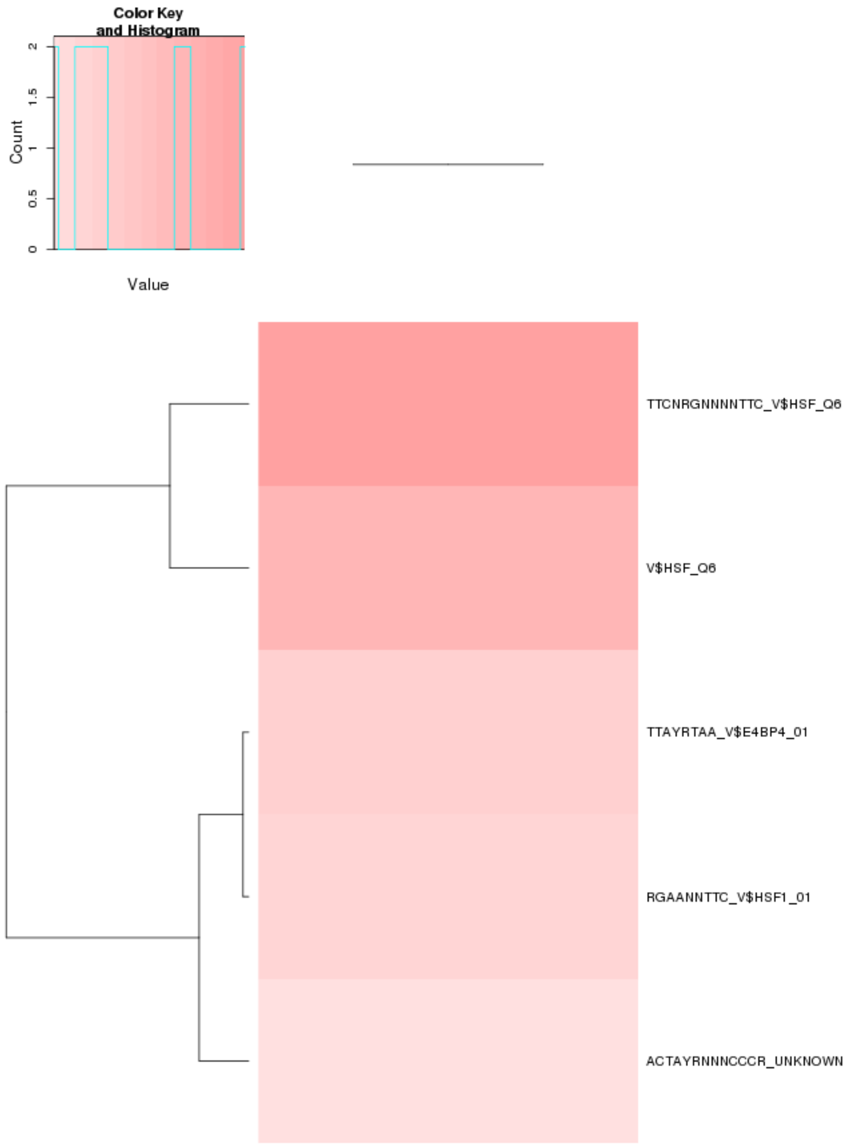
Immuno zscore:



TF enrichment:


Color Key
and Histogram
Count
0
1
2
3
4
4
5
6
Value
TTCNRGNNNNTTC_V$HSF_Q6
TTAYRTAA_V$E4BP4_01
ACTAYRNNNCCCR_UNKNOWN
V$HSF_Q6
RGAANNTTC_V$HSF1_01

TF zscore:

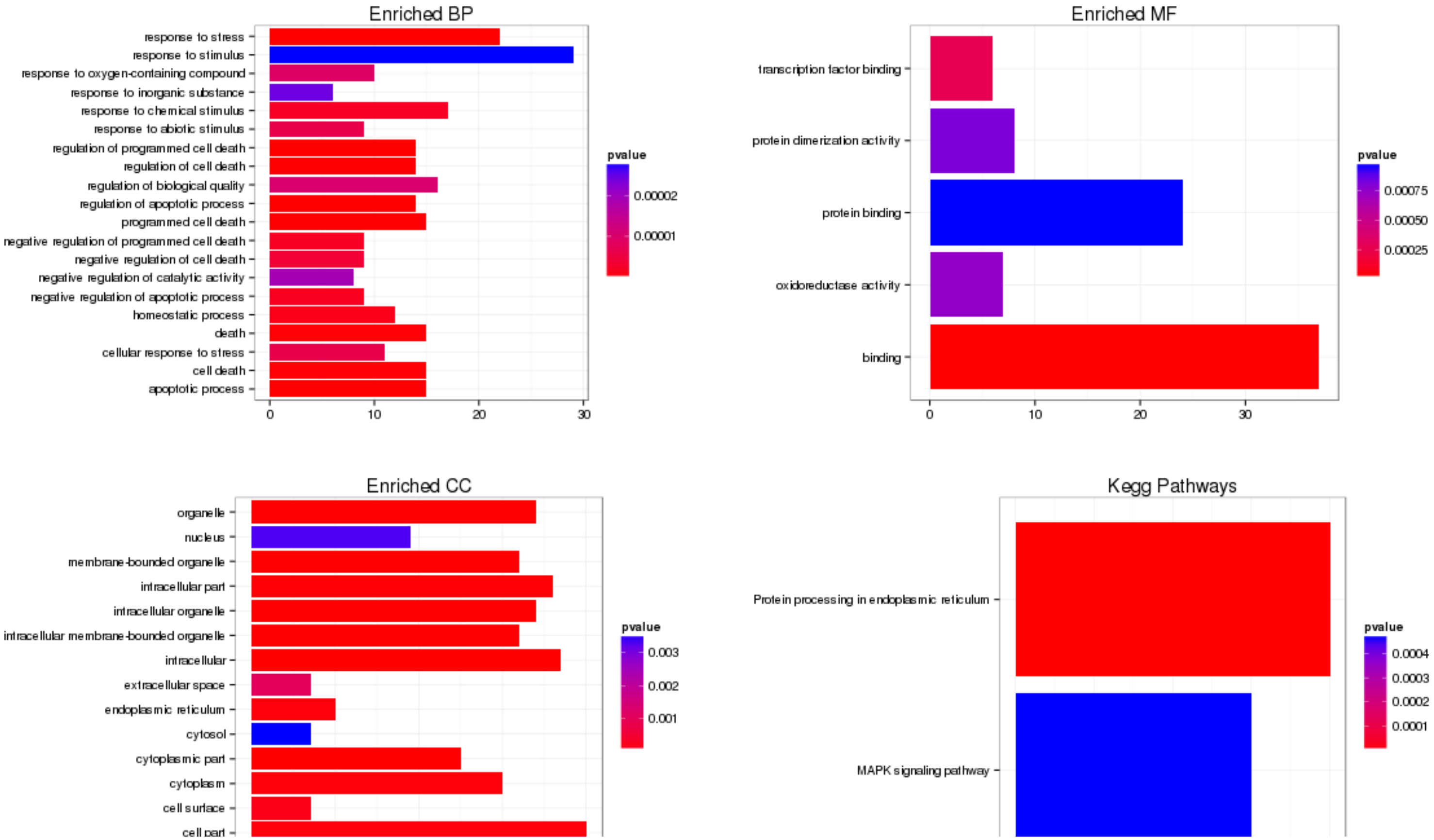


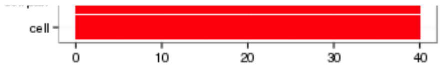
GO enrichment

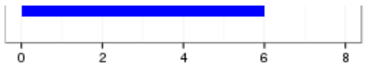
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

```
## [1] "ERROR: The estimated pi0 <= 0. Check that you have valid p-values or use another lambda method."
```

```
## [1] "ERROR: The estimated pi0 <= 0. Check that you have valid p-values or use another lambda method."
```

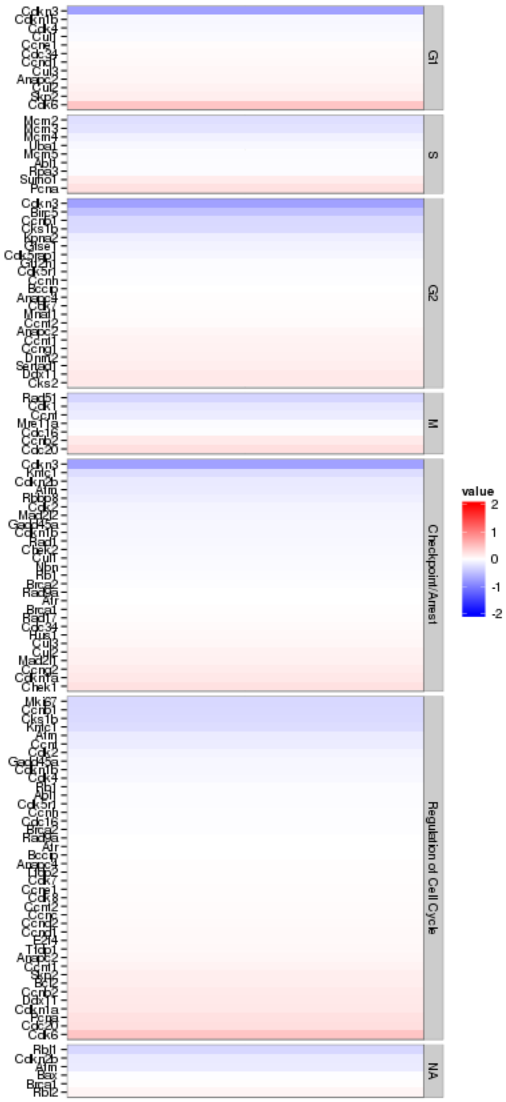




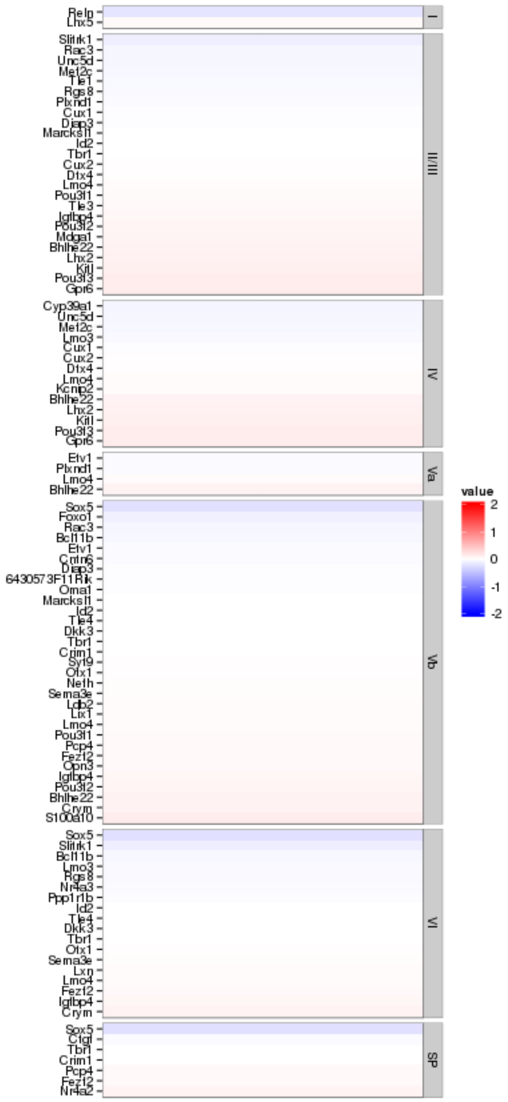


```
## Error: 'x' and 'units' must have length > 0
```

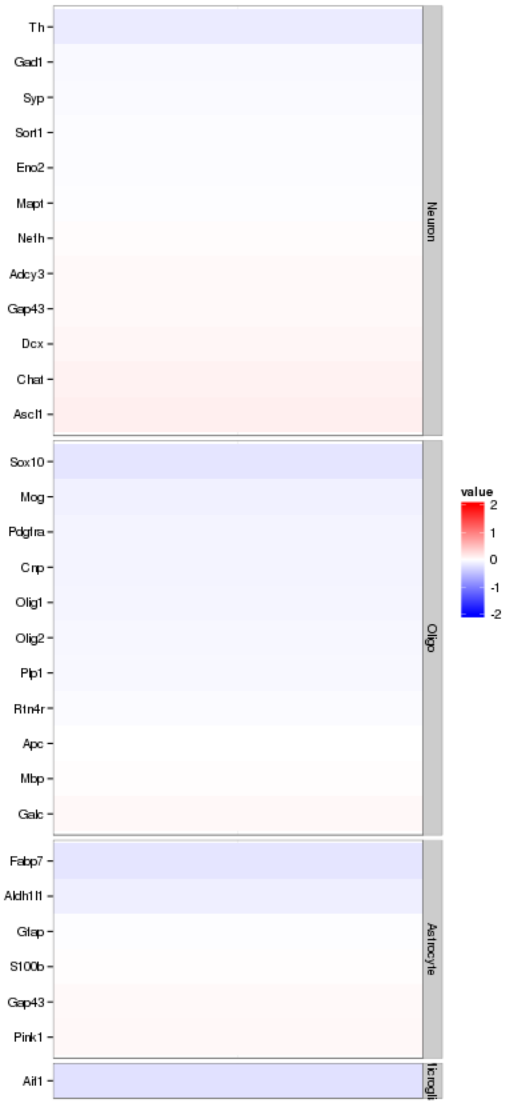
Enrichment or depletion for stage-specific cell cycle markers



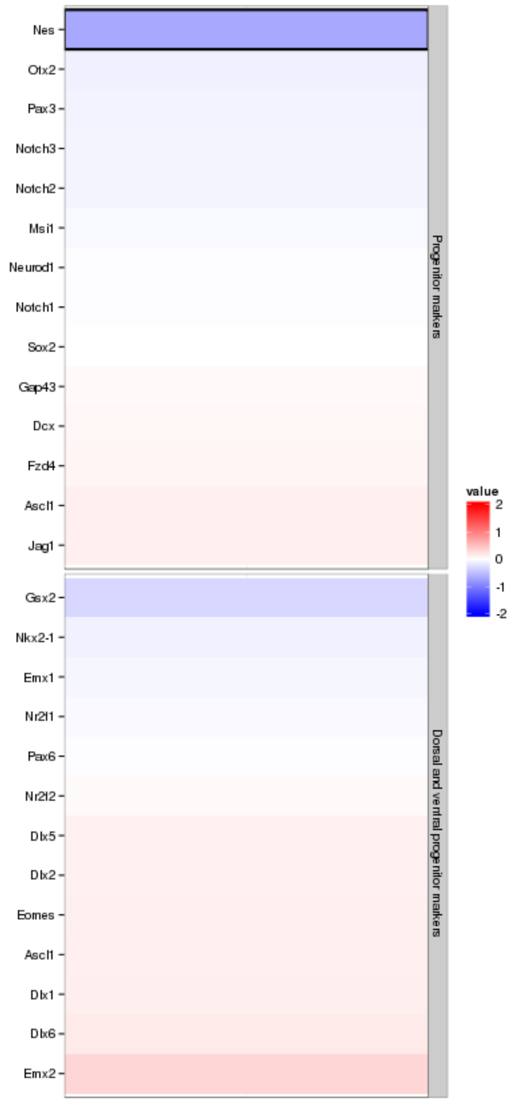
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



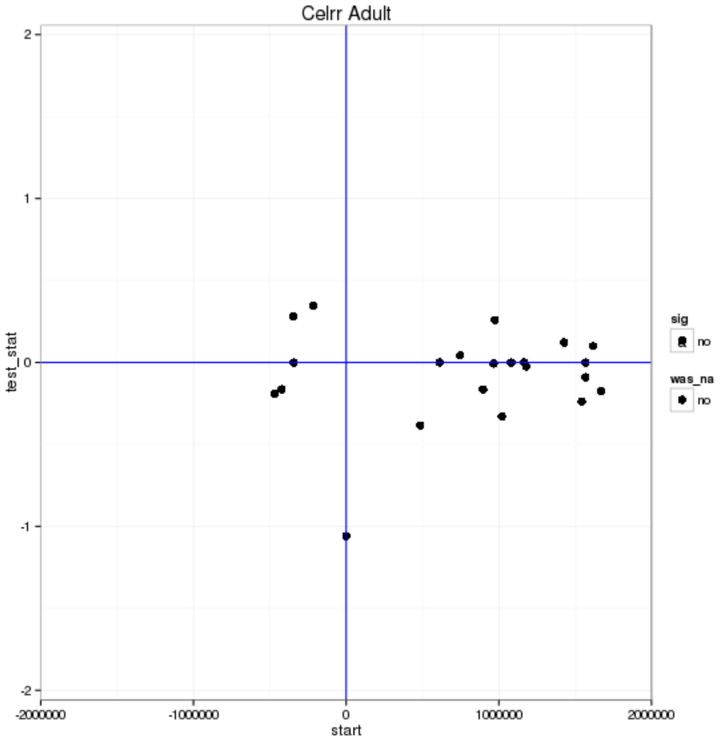
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15	JR739
16	JR783
17	JR804

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	33868500.00	0.78	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	33868500.00	0.60	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	33868500.00	1.00	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	33868500.00	0.82	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	33868500.00	1.06	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	33868500.00	1.10	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	33868500.00	0.82	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	33868500.00	1.18	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	33868500.00	1.03	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	33868500.00	1.33	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	33868500.00	1.54	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	33868500.00	1.04	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	33868500.00	1.00	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	33868500.00	1.23	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR739/abundances.cxb	Celrr	0	Celrr_0	23325900.00	33868500.00	0.69	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR783/abundances.cxb	Celrr	1	Celrr_1	37161800.00	33868500.00	1.10	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR804/abundances.cxb	Celrr	2	Celrr_2	39715300.00	33868500.00	1.16	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils
## [8] datasets  base
##
## other attached packages:
##  [1] plyr_1.8.1
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##            param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,Celrr -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Celrr_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/ar
## 2
## 3
## 4
## 5
```

Celrr KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for Celrr.

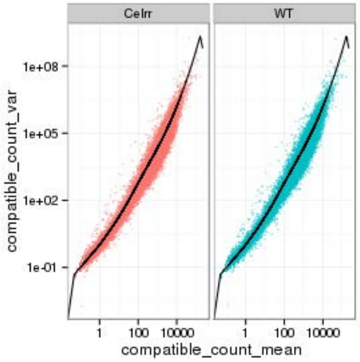
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

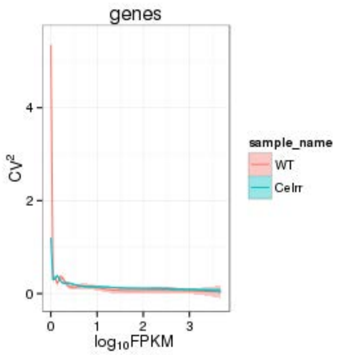
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



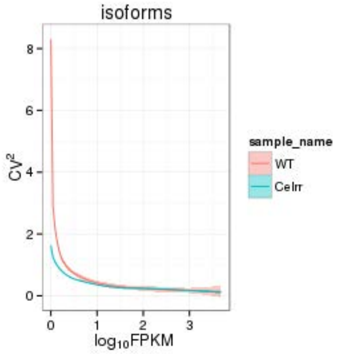
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

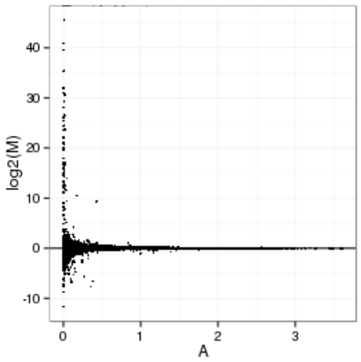
Genes:



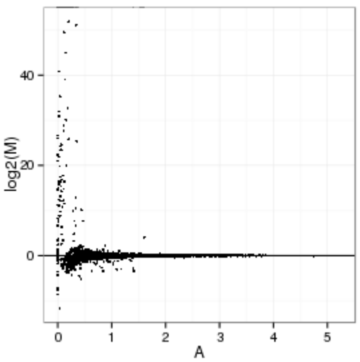
Isoforms:



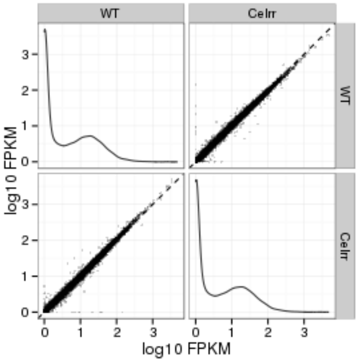
MvA plot



MvA plot counts



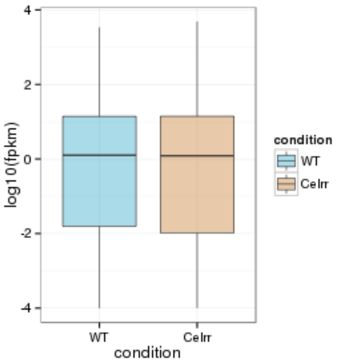
Scatterplot matrix



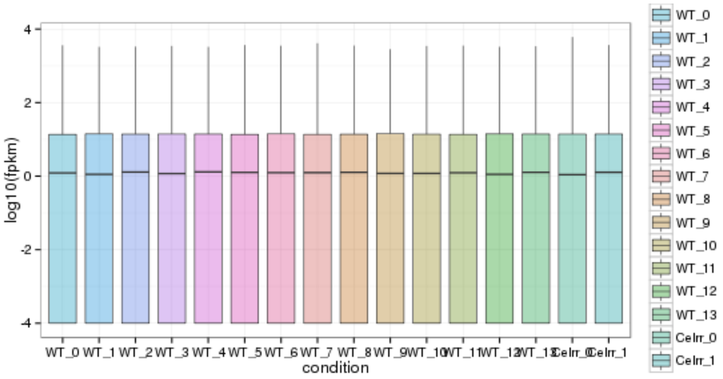
Distributions

Boxplots

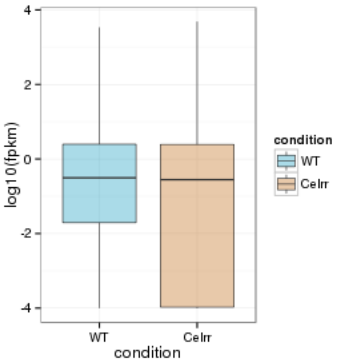
Boxplot (genes)



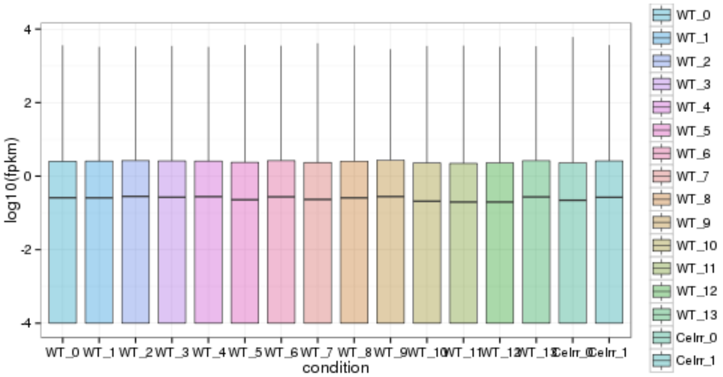
Boxplot (genes, replicates)



Boxplot (isoforms)

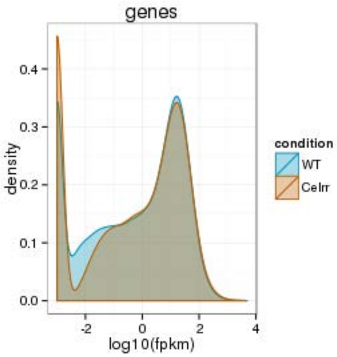


Boxplot (isoforms, replicates)

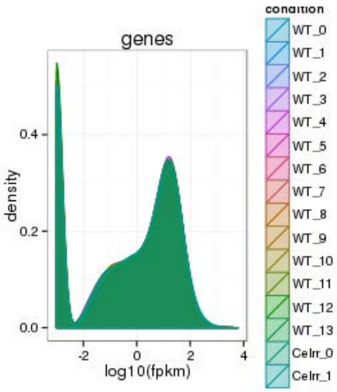


Density

Density (genes)

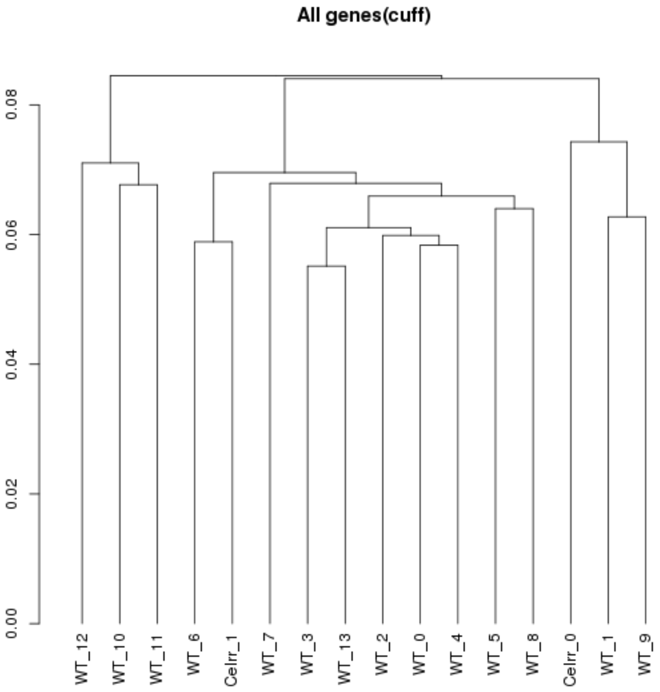


Density (genes, replicates)



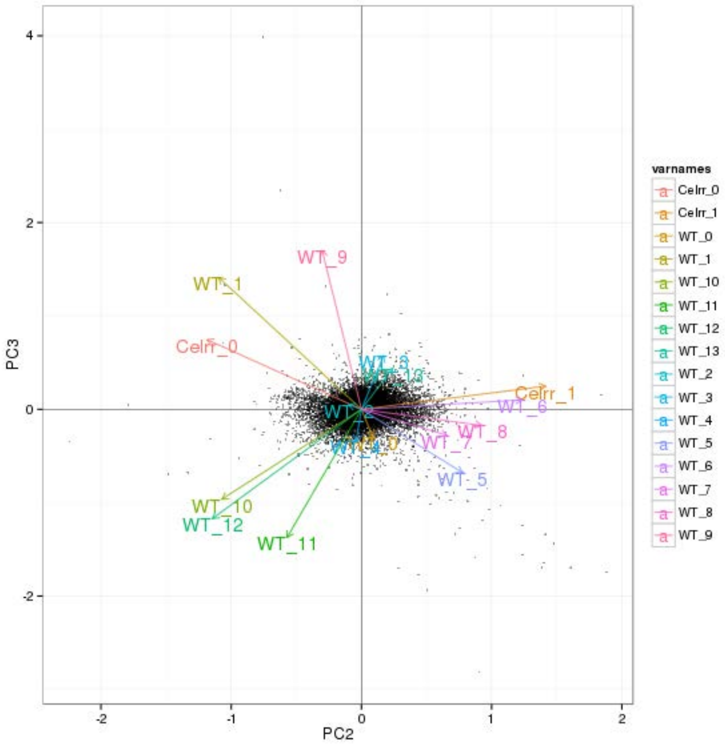
Clustering

Replicate Clusters



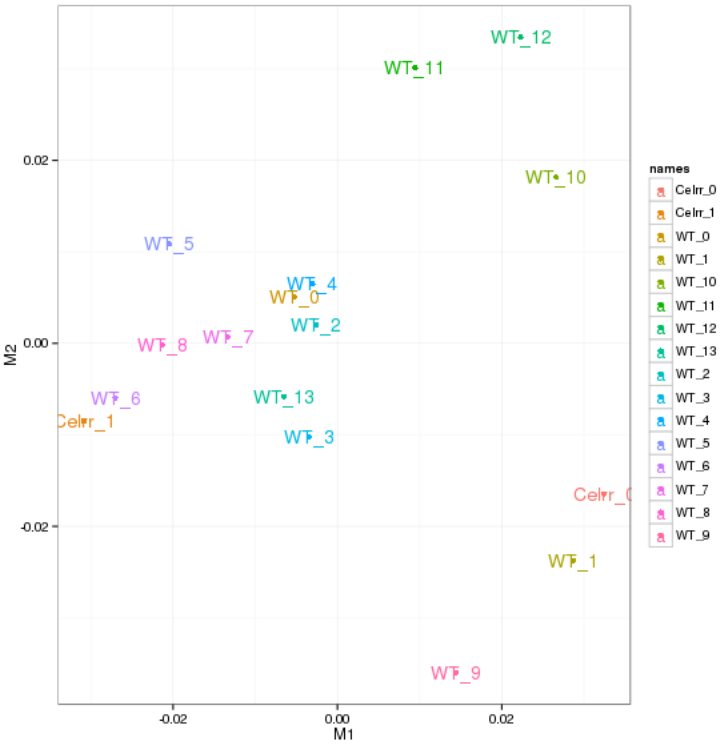
```
## NULL
```

PCA (genes)



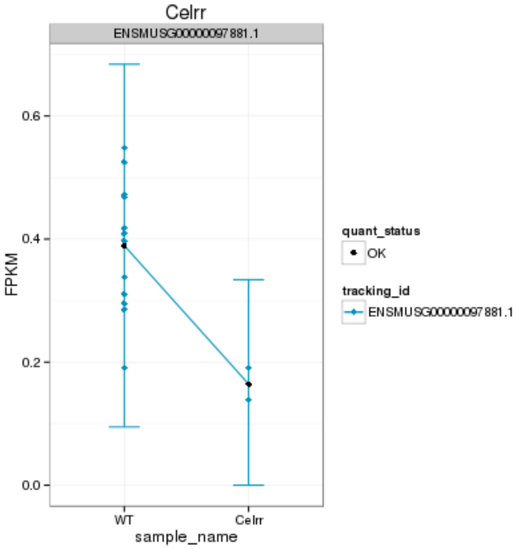
4
2
0
-2
PC3
-2
-1
0
1
2
PC2
WT_9
WT_1
Celrr_0
Celrr_1
WT_6
WT_8
WT_7
WT_5
WT_10
WT_12
WT_11
varnames
Celrr_0
Celrr_1
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

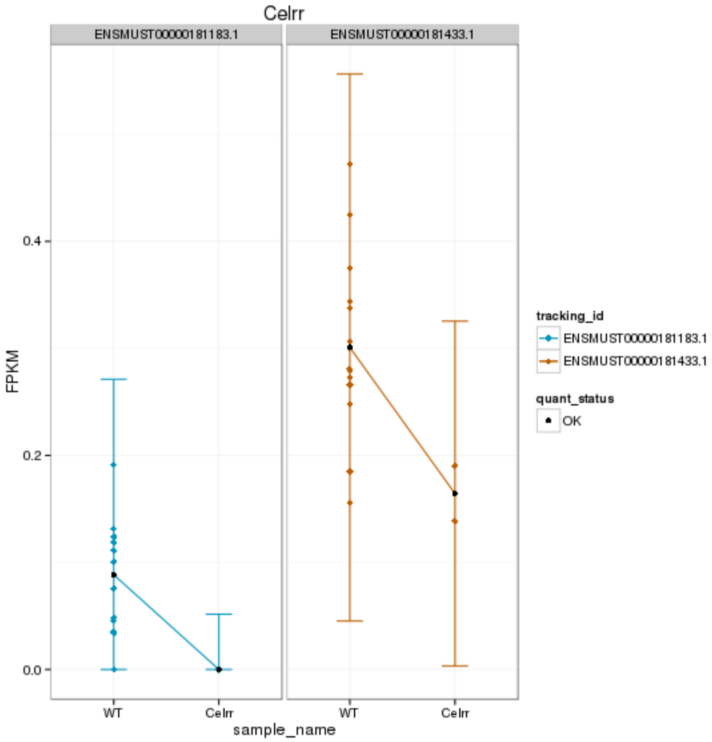


KO assessment

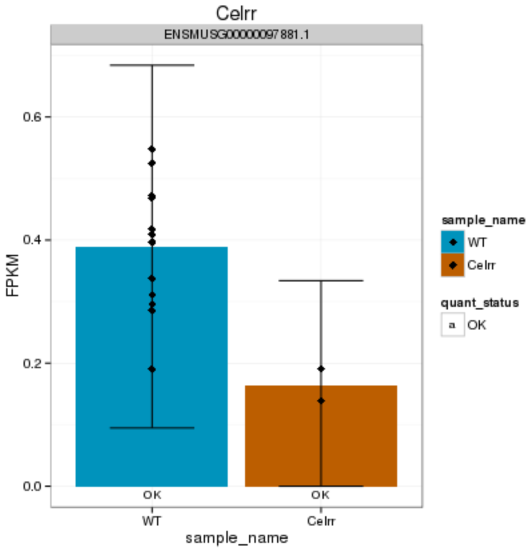
Endogenous lncRNA expression



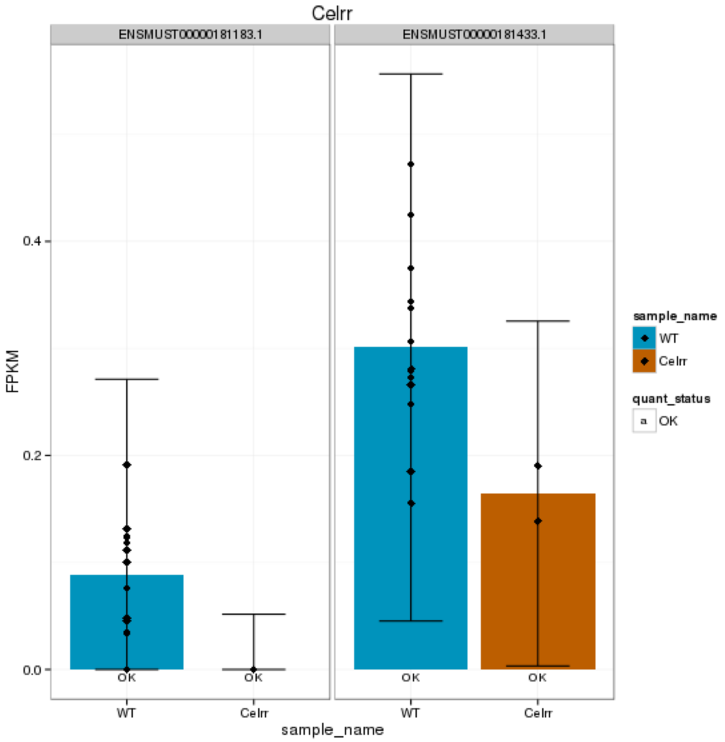
Endogenous expression of Celrr isoforms:



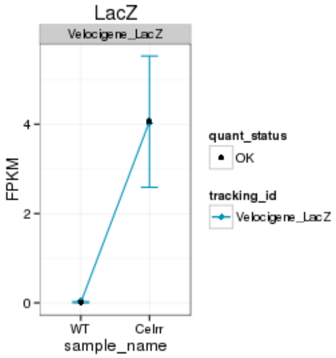
Barplot of gene expression:

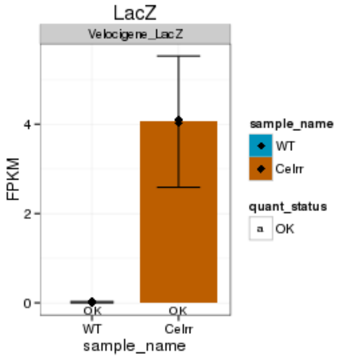


Barplot of isoform expression:



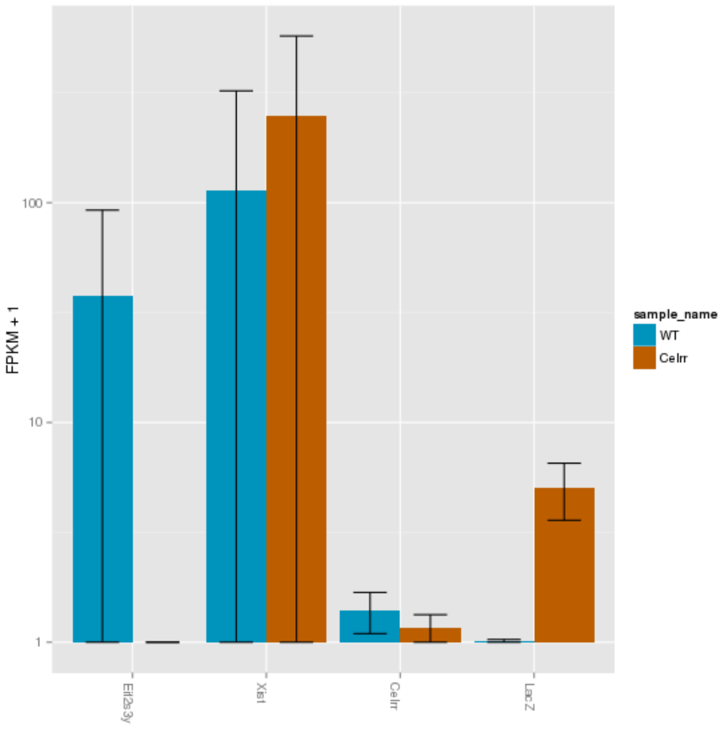
LacZ expression



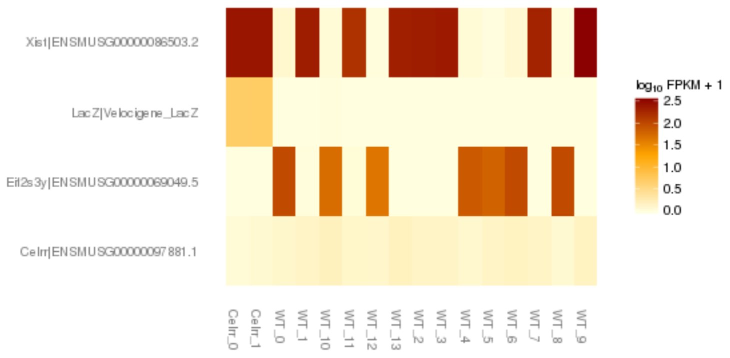


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

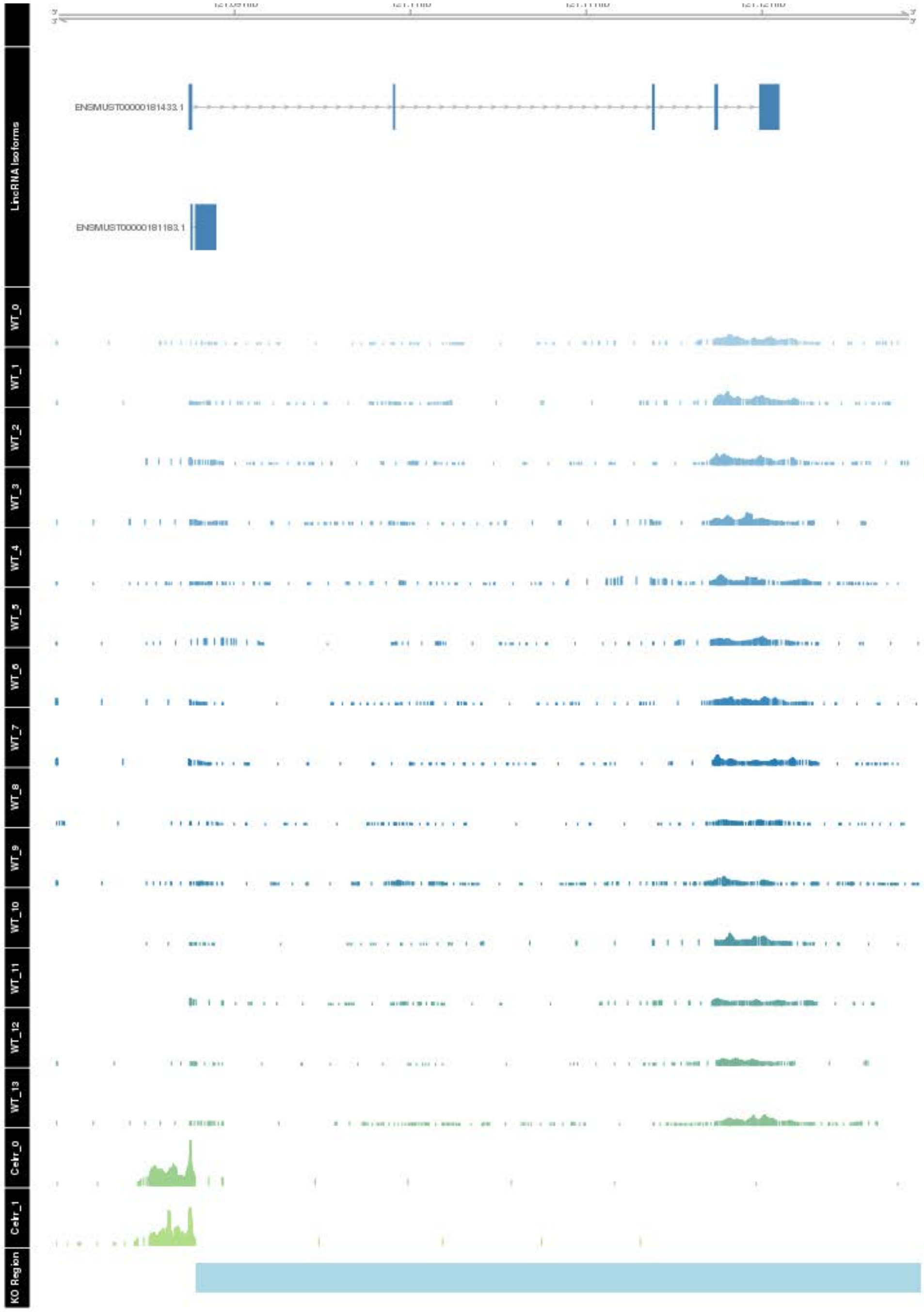
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


5'
3'
3'
5'
LincRNA Isoforms
ENSMUST00000181433.1
ENSMUST00000181183.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Celr_0
Celr_1
KO Region

Differential Analysis

Differential Genes

There are 39 significantly differentially expressed genes. They are:

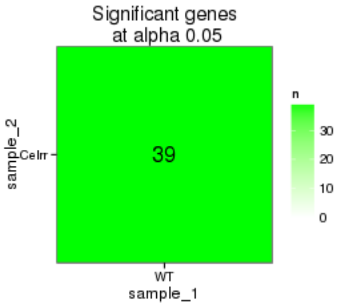
	geneAnnot$gene_short_name
1	Mef2c
2	Phox2b
3	Sulf1
4	Slc16a10
5	Fam49a
6	Ntn1
7	Cxcl14
8	Sla
9	Clic6
10	Rps14
11	Fn1
12	Notch1
13	Notch2
14	Dync1i1
15	Dbx1
16	Slit2
17	Robo3
18	Lama1
19	Kirrel2
20	Neurod6
21	Notch3
22	Spon1
23	Satb2
24	Mpped1
25	Tuba1c
26	Cnpy1
27	Hbb-y
28	Krt15
29	Hba-x
30	Rpl32
31	Rpl26
32	Rps7
33	Rpl35
34	Cyp26b1
35	Ddx3y
36	Fat1
37	Rpl23

38 Rpl39

39 AA465934

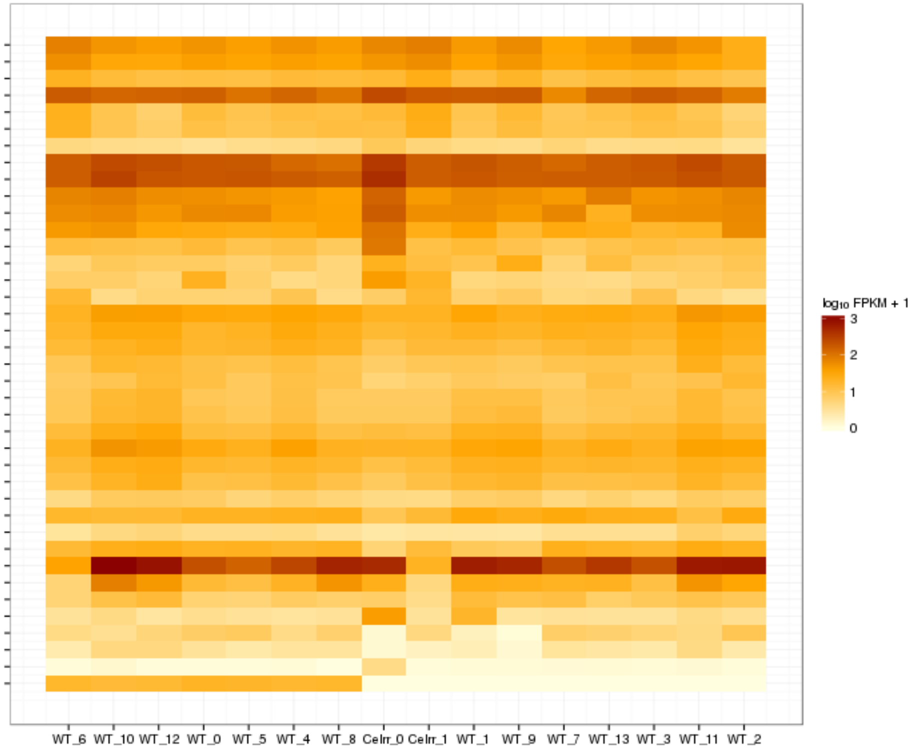
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

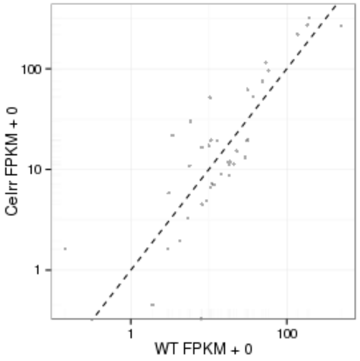


Significant genes with expression >50fpkm (any condition):(turned off)

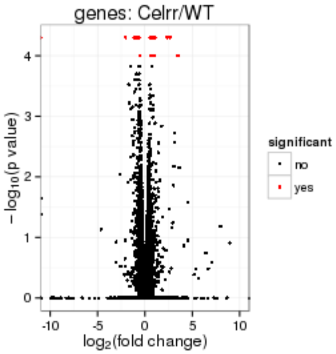
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

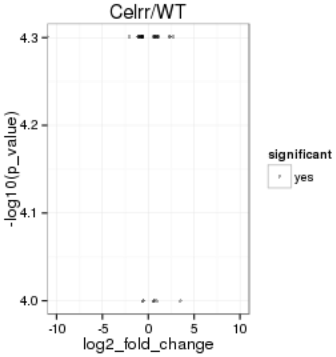
Scatter plot of significant genes only:



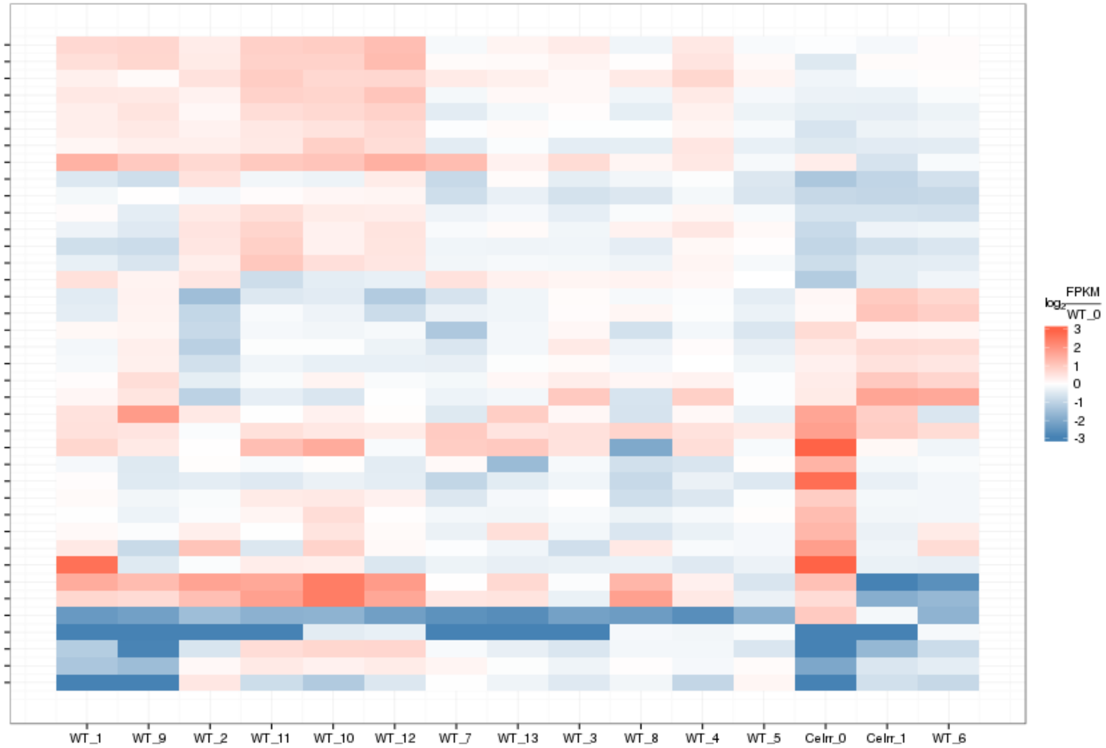
Volcano Plot



Volcano plot with significant genes only:



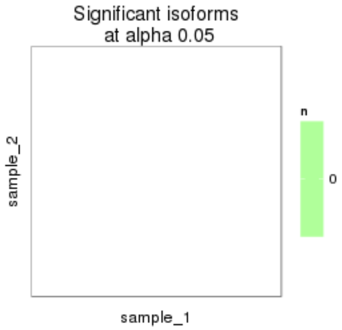
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

[1] “no sig isoforms”

Gene-level DE isoform heatmap

```
## [1] "no sig isoforms"
```

Isoform foldchange heatmap by isoform:

```
## [1] "no sig isoforms"
```

Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

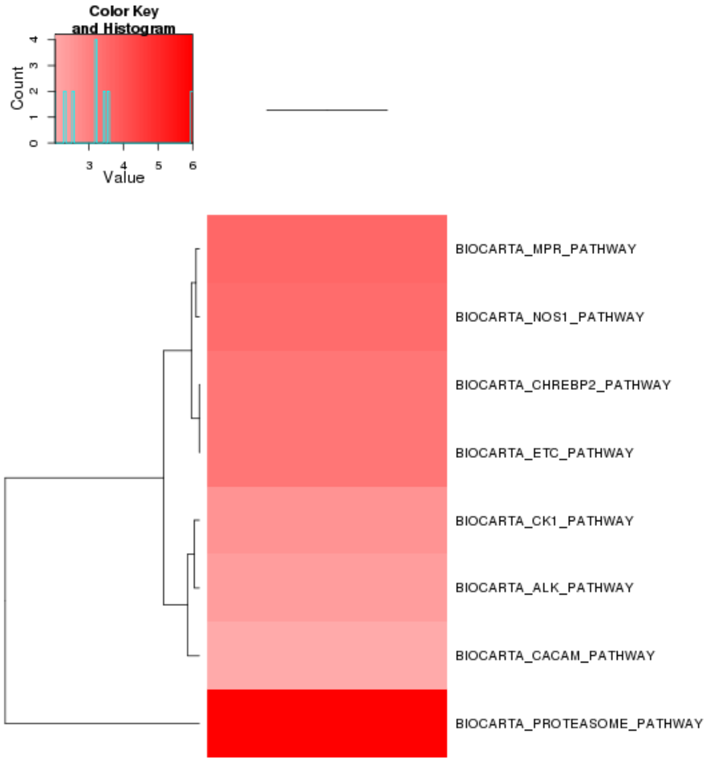
Gene/Pathway Analysis

GSEA

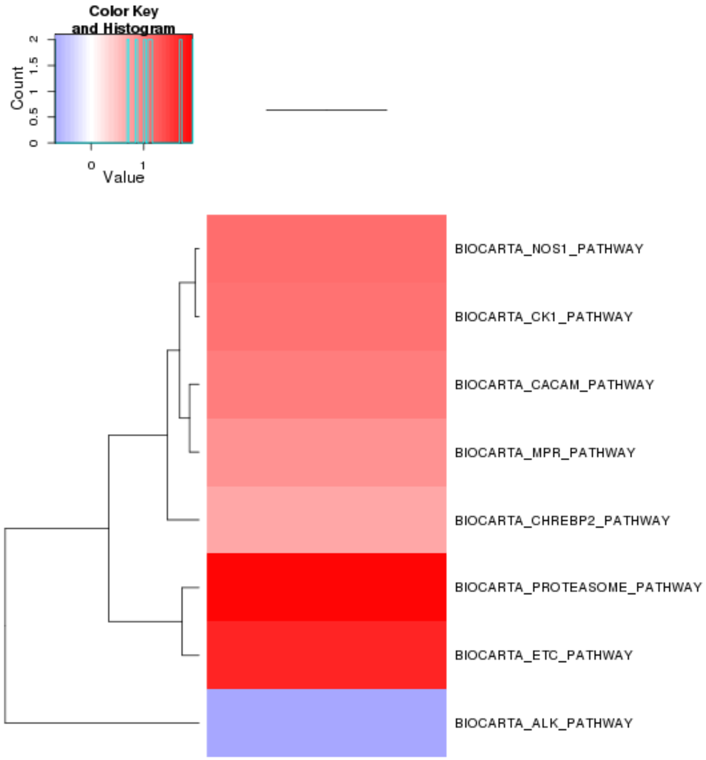
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

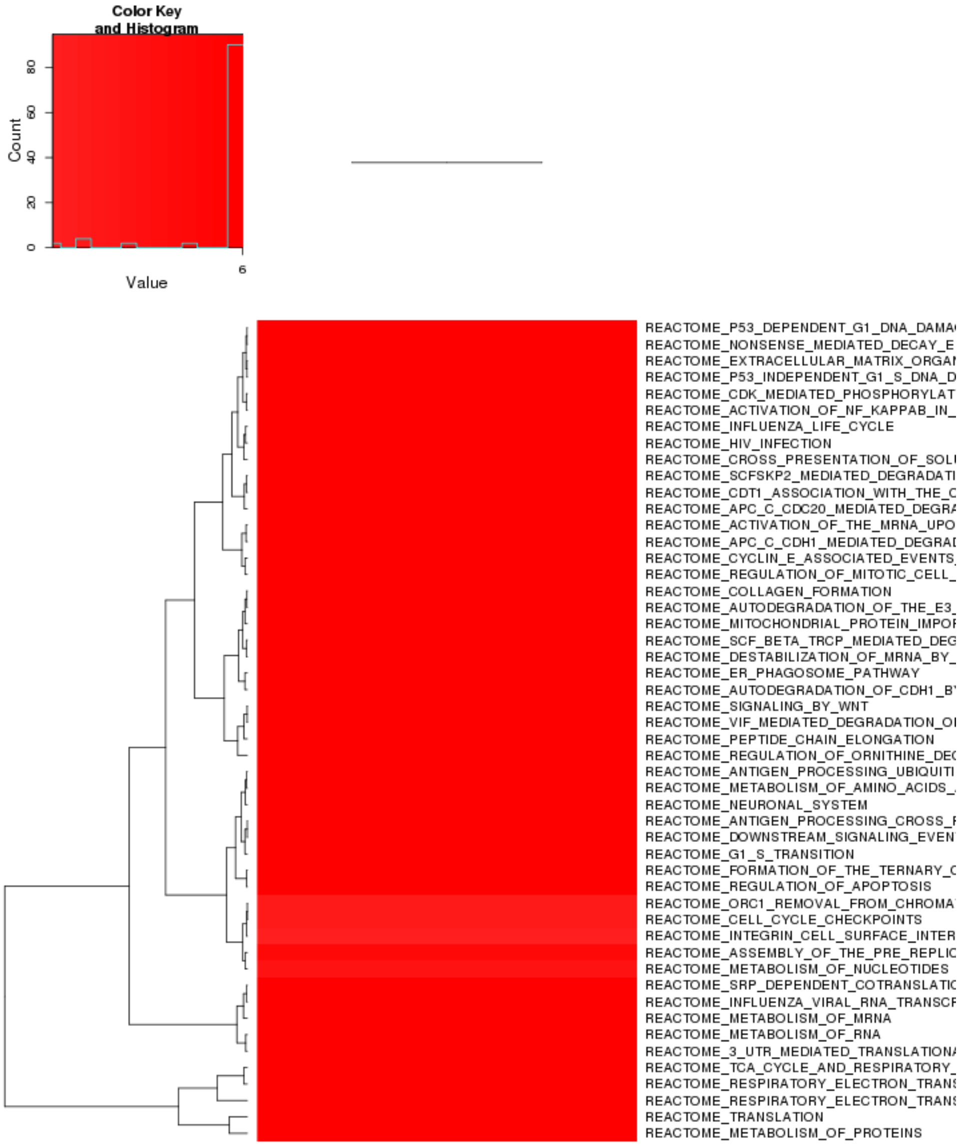
Biocarta enrichment:



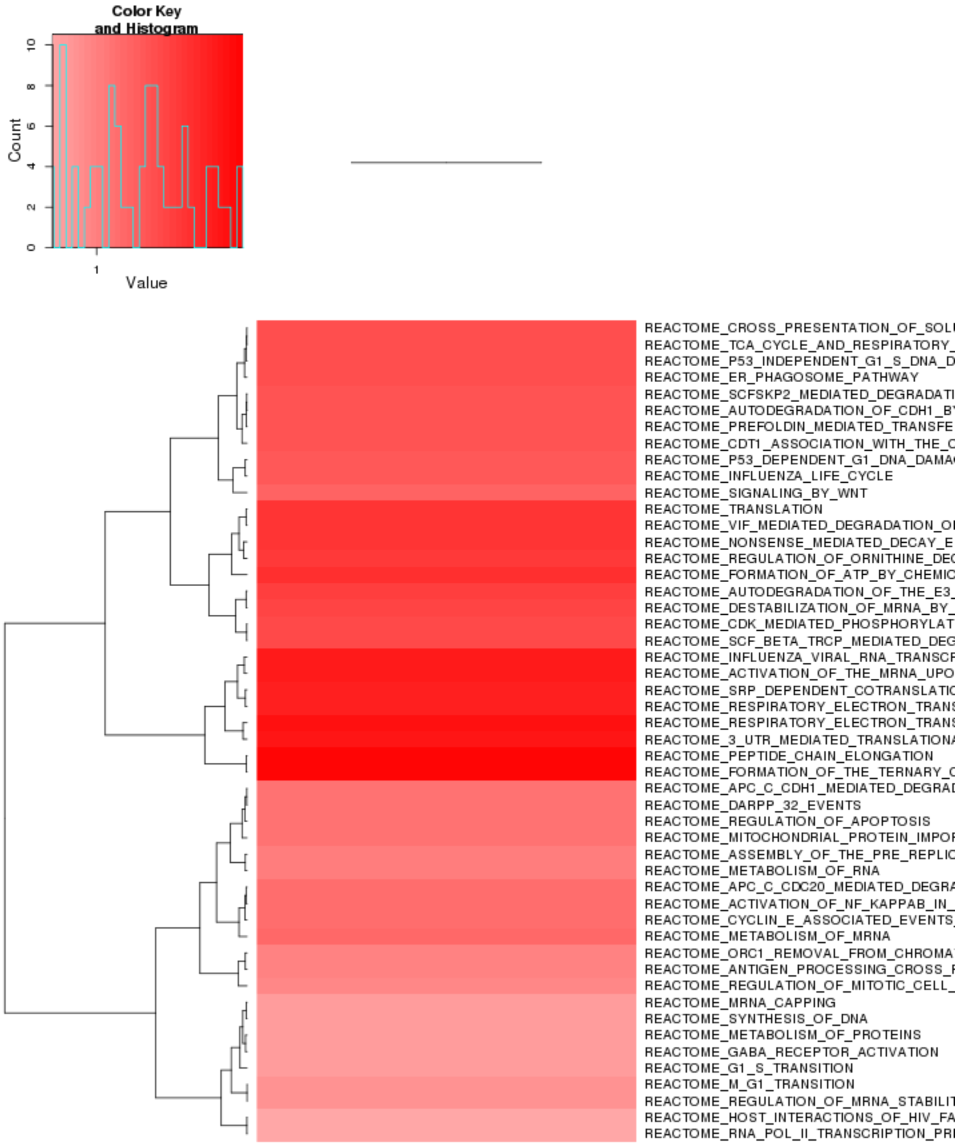
Biocarta zscore:



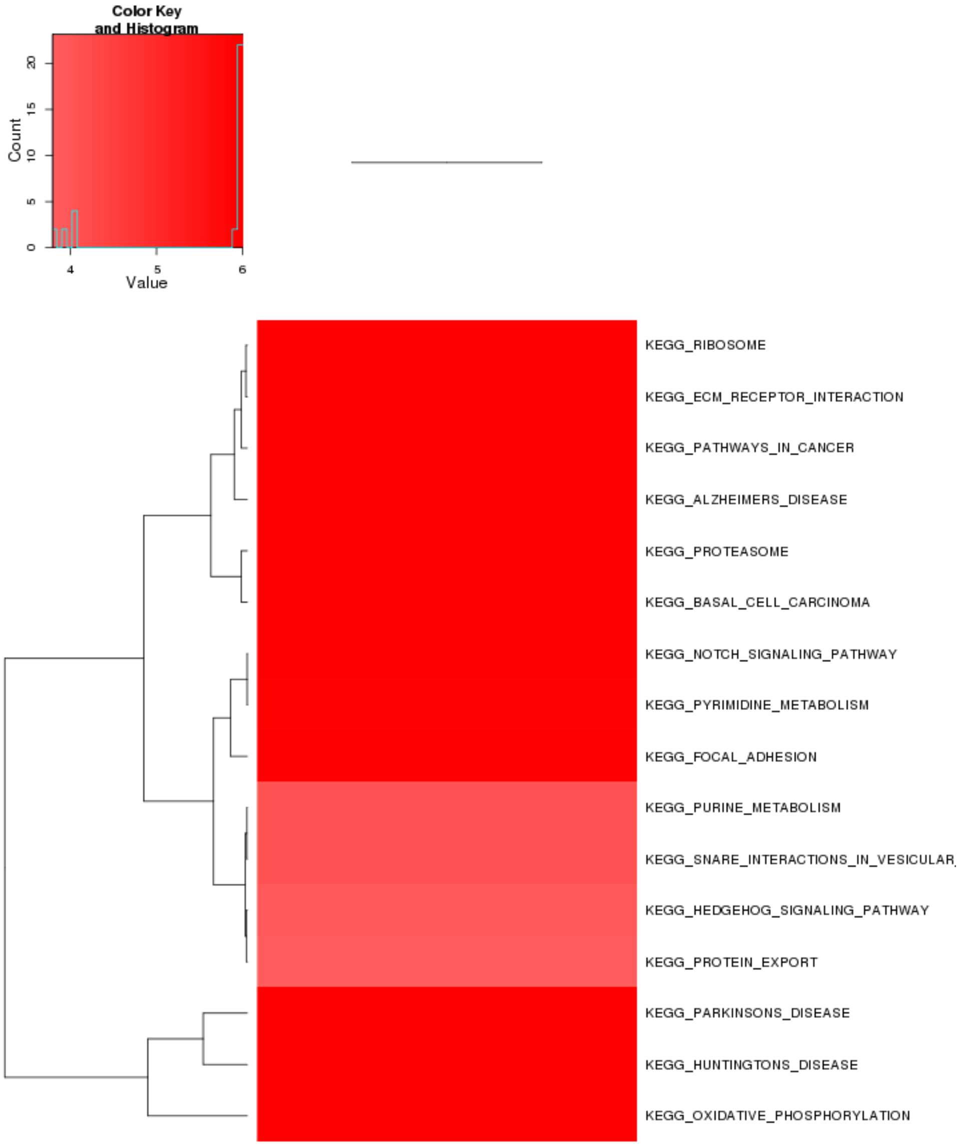
Reactome enrichment:



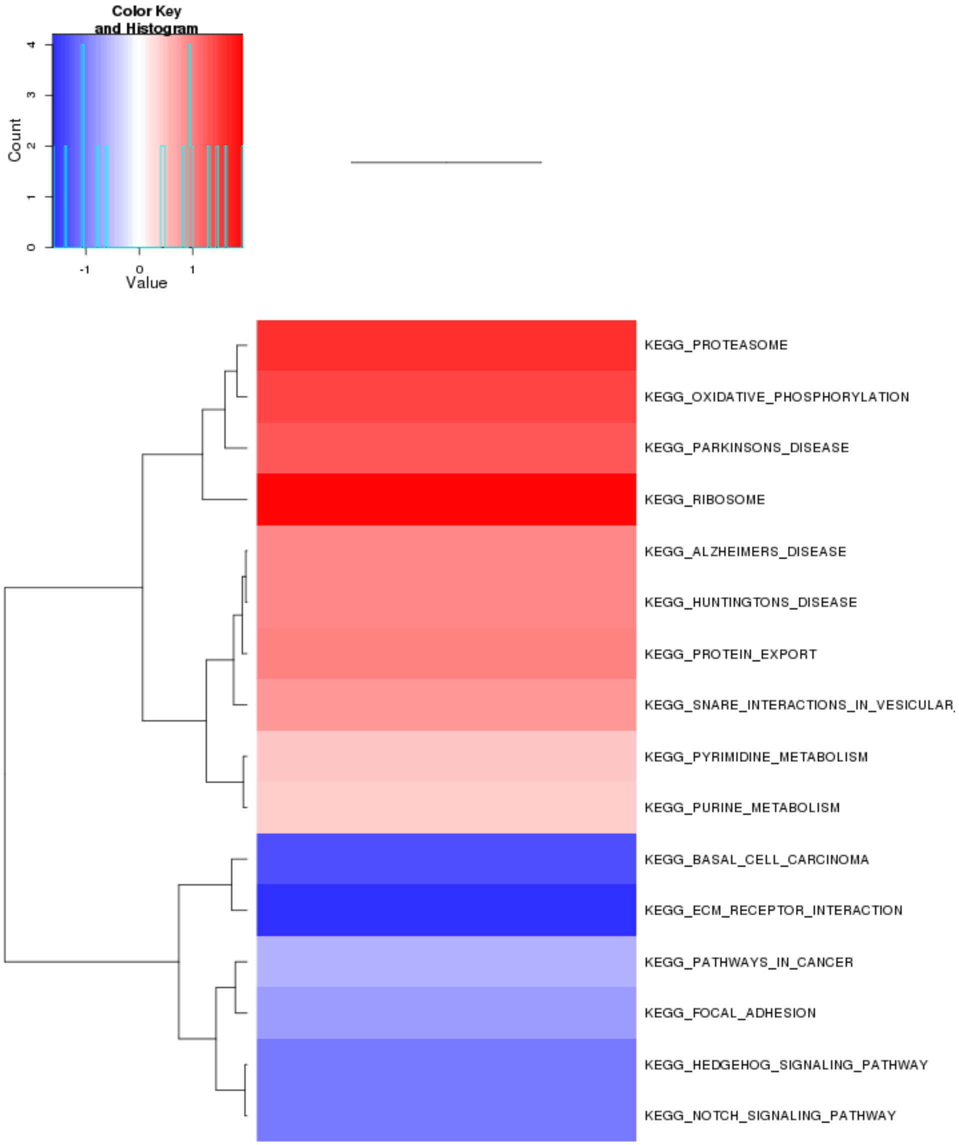
Reactome zscore:



Kegg enrichment:

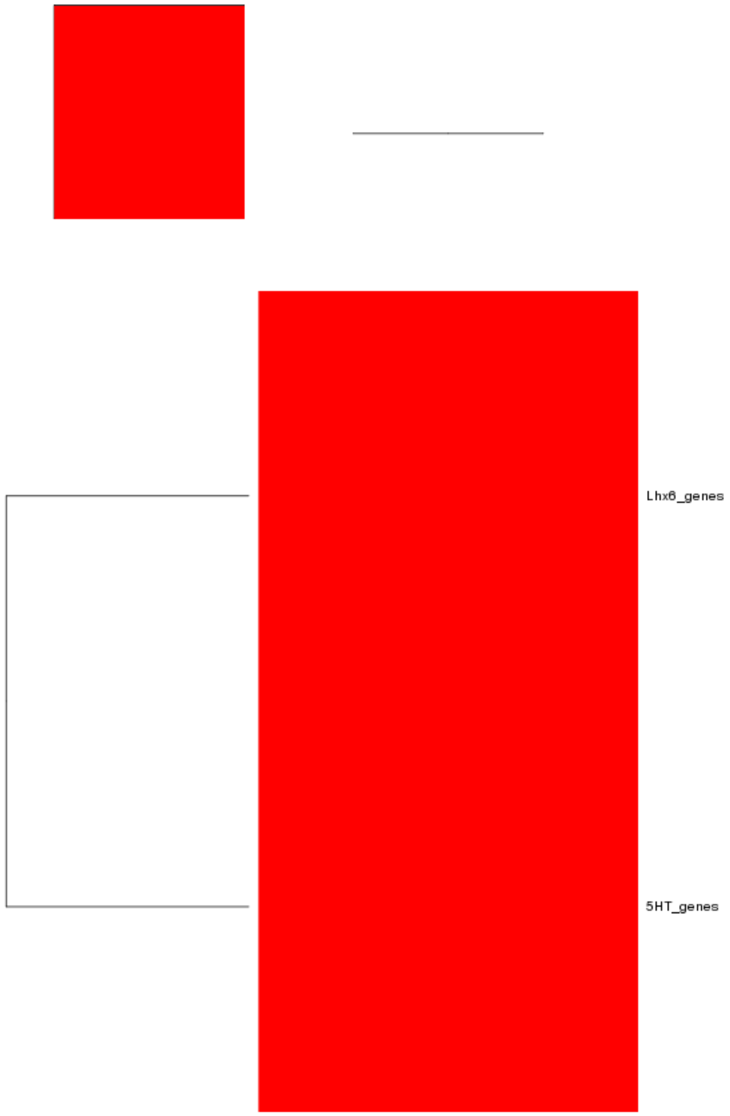

Color Key
and Histogram
Count
0
5
10
15
20
4
5
6
Value
KEGG_RIBOSOME
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_PATHWAYS_IN_CANCER
KEGG_ALZHEIMERS_DISEASE
KEGG_PROTEASOME
KEGG_BASAL_CELL_CARCINOMA
KEGG_NOTCH_SIGNALING_PATHWAY
KEGG_PYRIMIDINE_METABOLISM
KEGG_FOCAL_ADHESION
KEGG_PURINE_METABOLISM
KEGG_SNARE_INTERACTIONS_IN_VESICULAR
KEGG_HEDGEHOG_SIGNALING_PATHWAY
KEGG_PROTEIN_EXPORT
KEGG_PARKINSONS_DISEASE
KEGG_HUNTINGTONS_DISEASE
KEGG_OXIDATIVE_PHOSPHORYLATION

Kegg zscore:

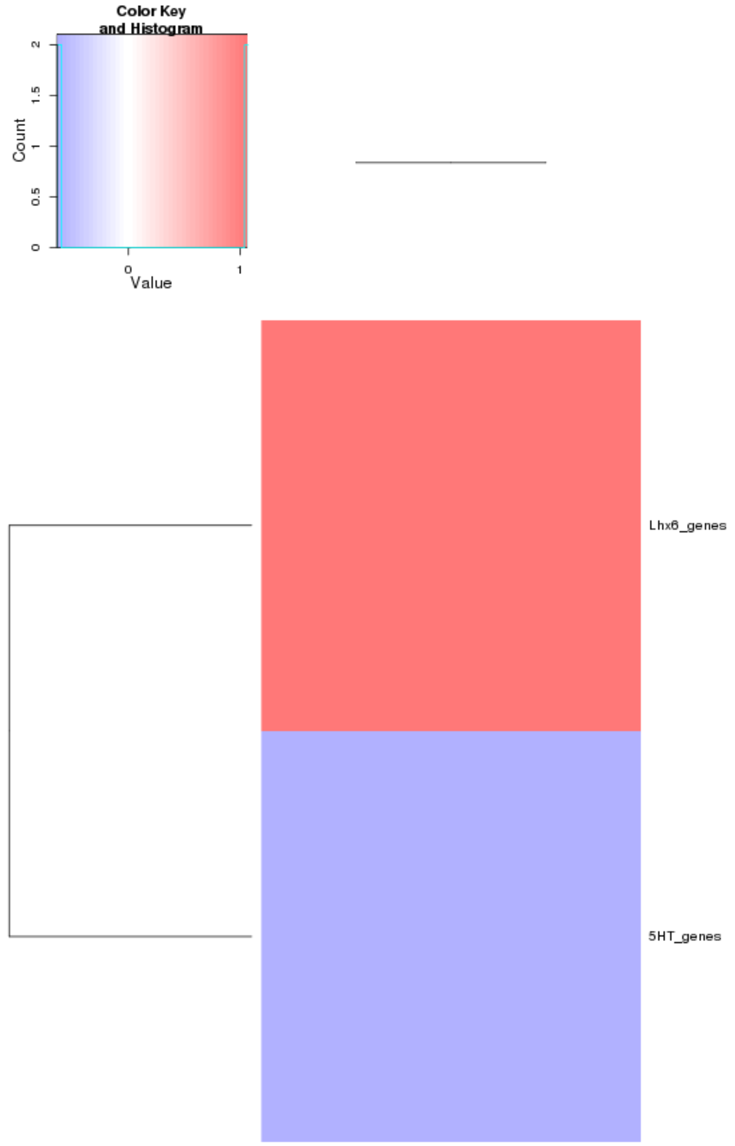


Interneuron enrichment:

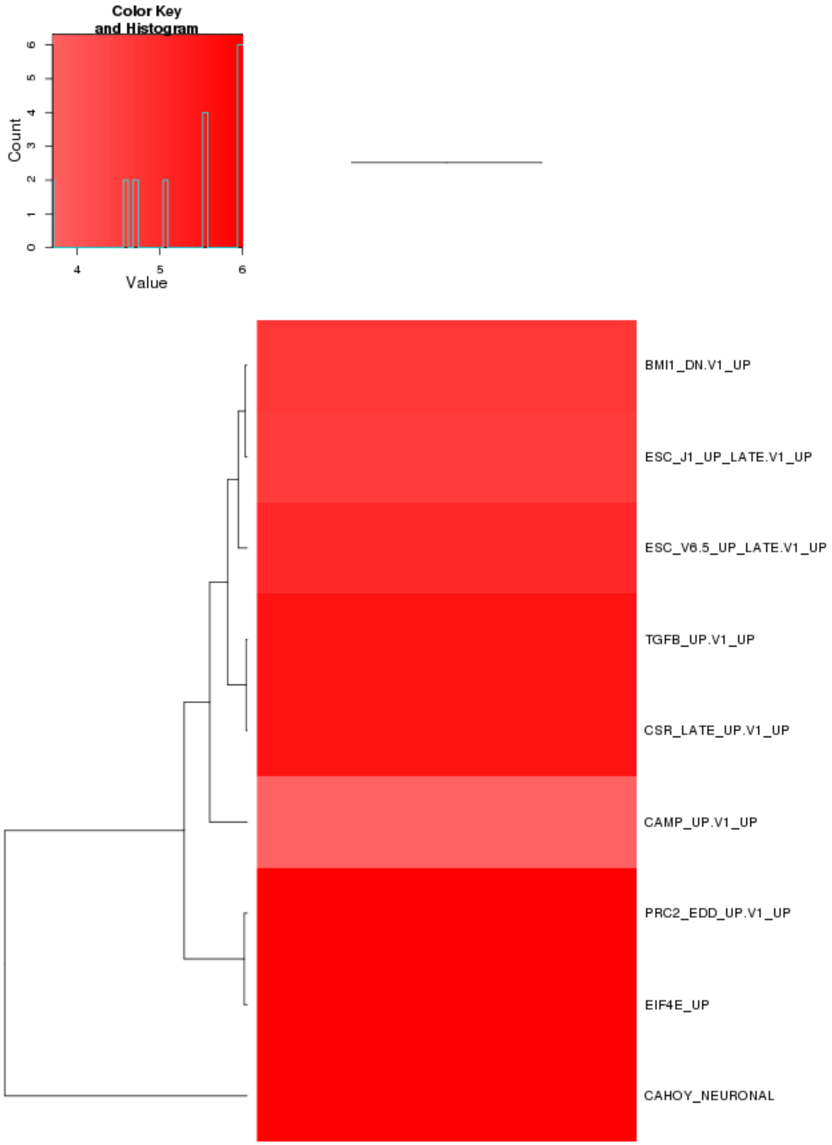
```
## Error: no locations are finite
```



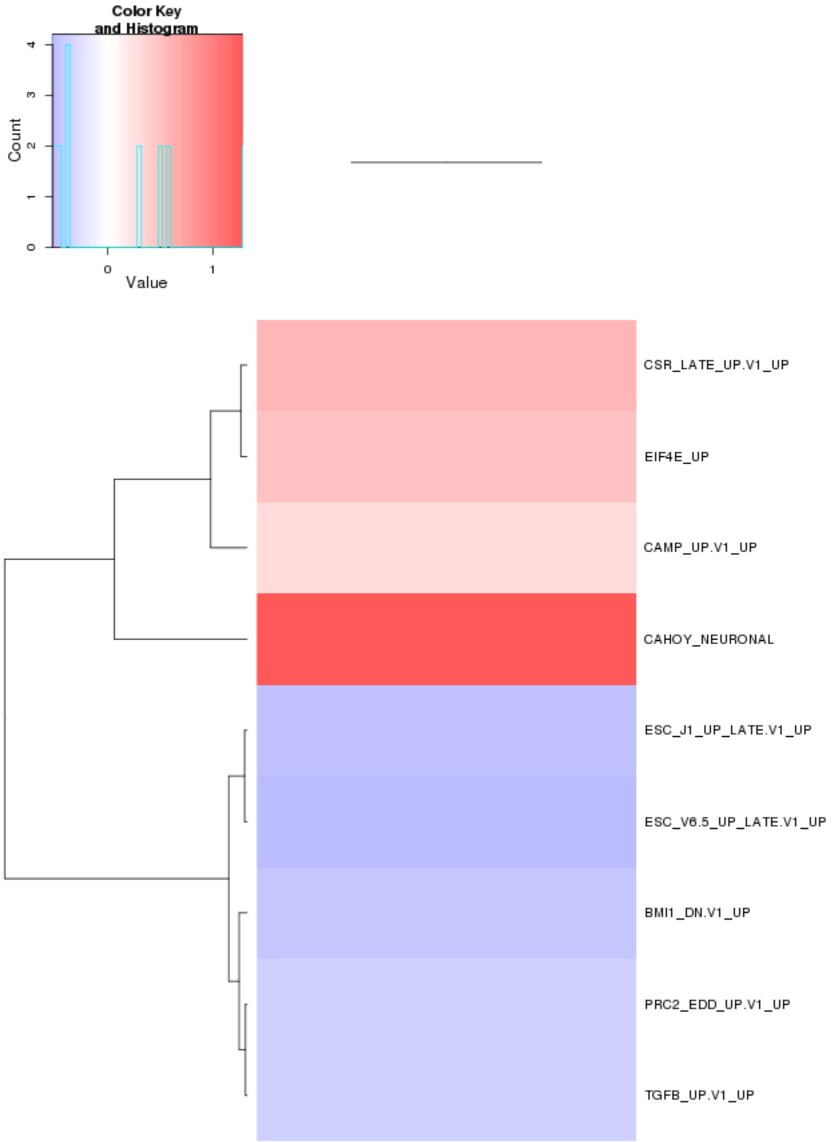
Interneuron zscore:



Oncogene enrichment:



Oncogene zscore:



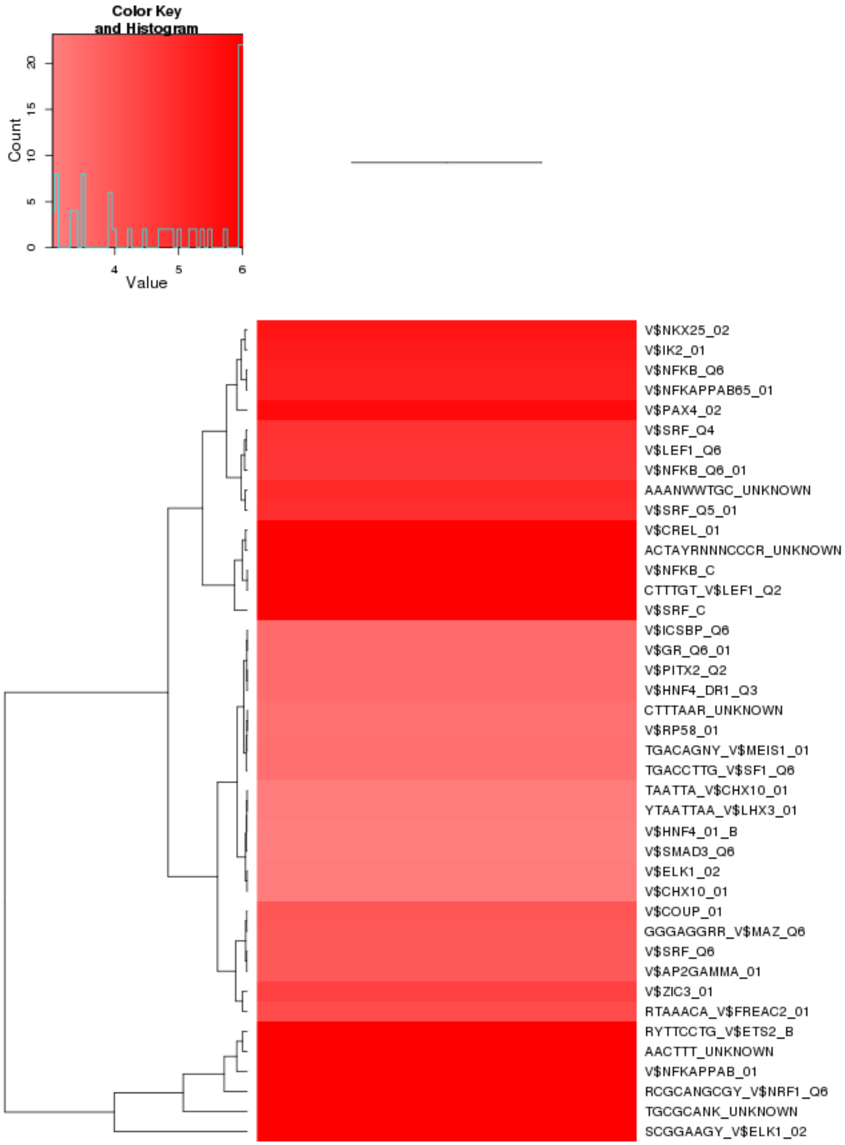
Immuno enrichment:

```
## Error: no locations are finite
```

Immuno zscore:

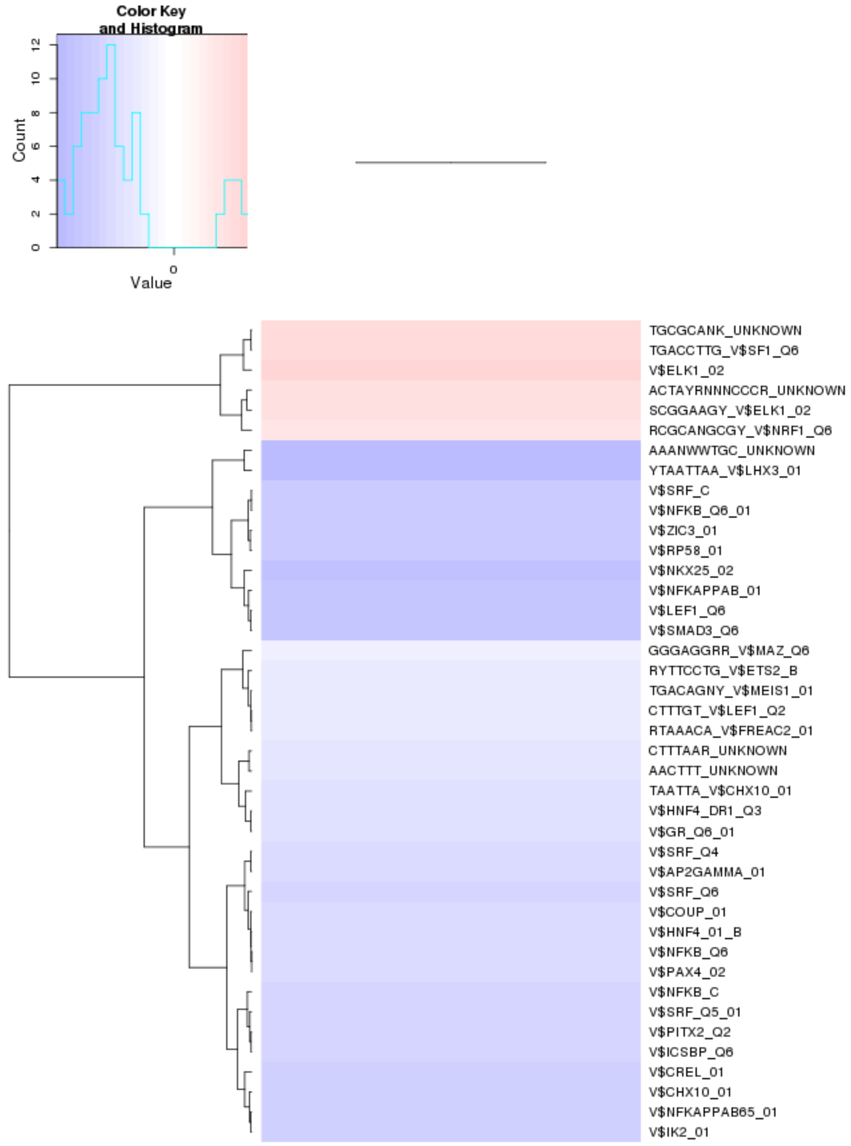
TF enrichment:

```
## Error: subscript out of bounds
```



TF zscore:

```
## Error: subscript out of bounds
```

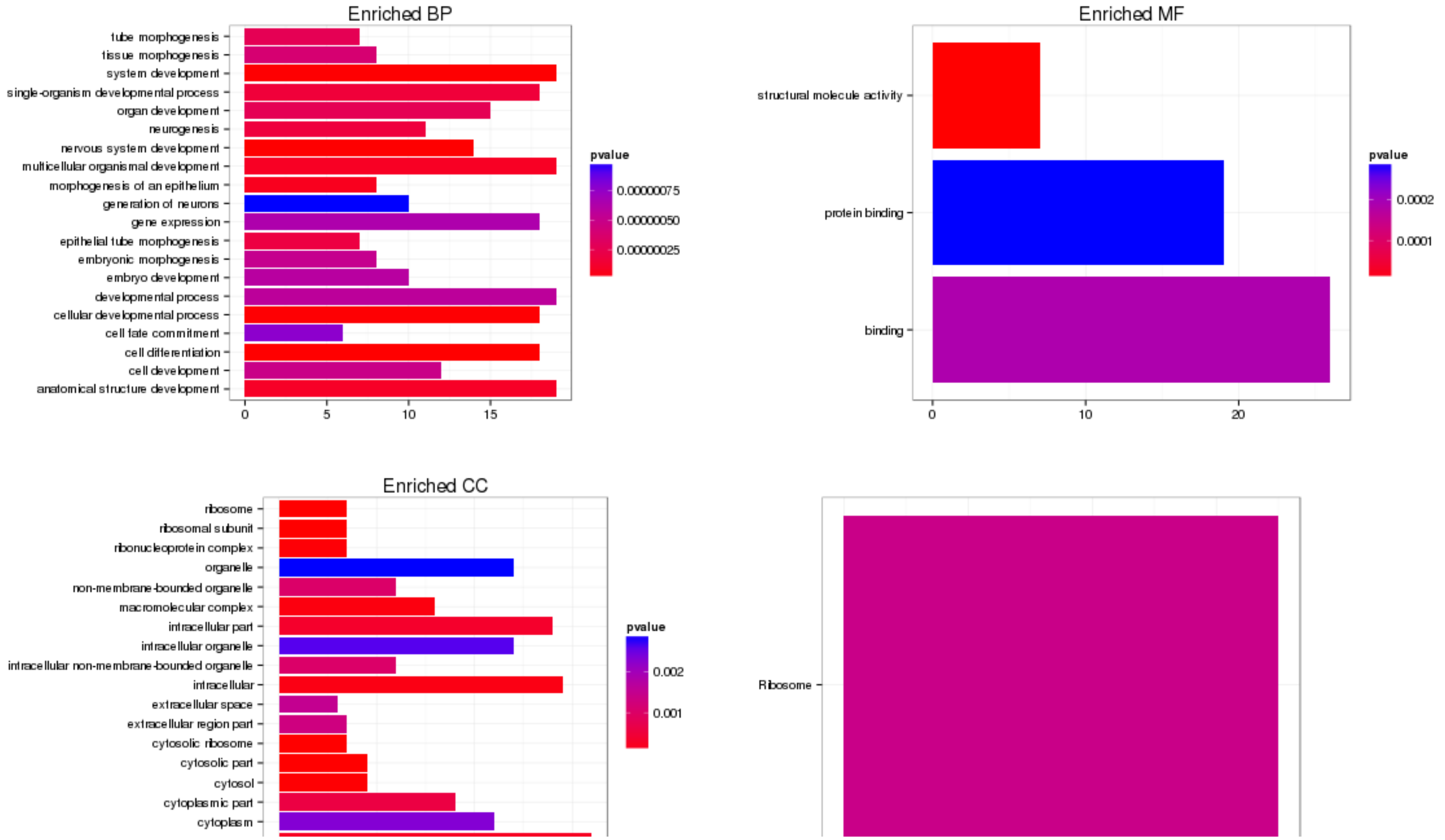


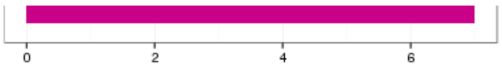
GO enrichment

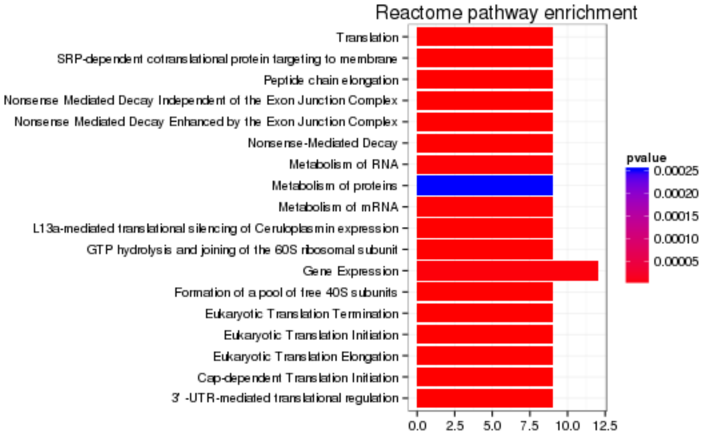
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

```
## [1] "ERROR: The estimated pi0 <= 0. Check that you have valid p-values or use another lambda method."
```

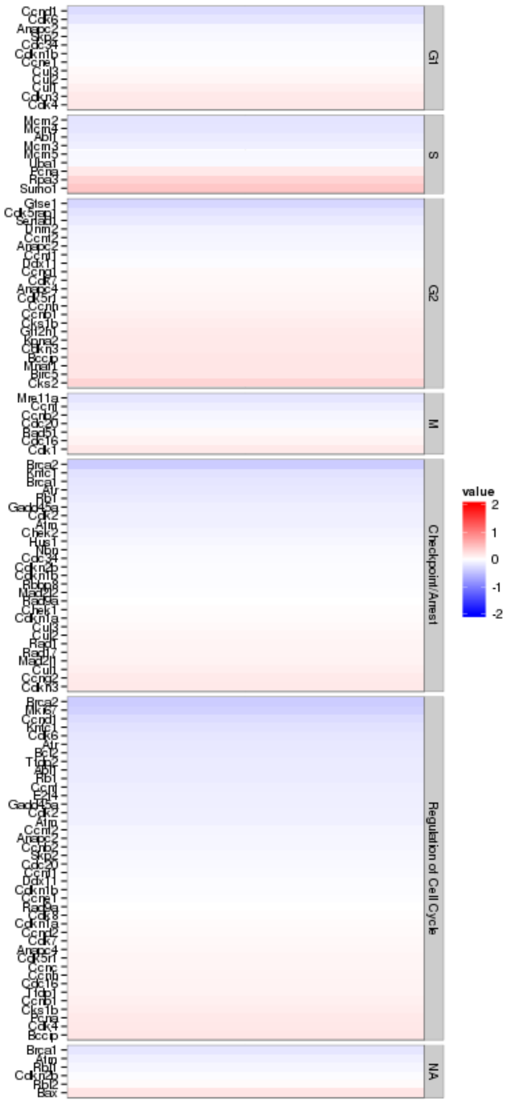
```
## [1] "ERROR: The estimated pi0 <= 0. Check that you have valid p-values or use another lambda method."
```



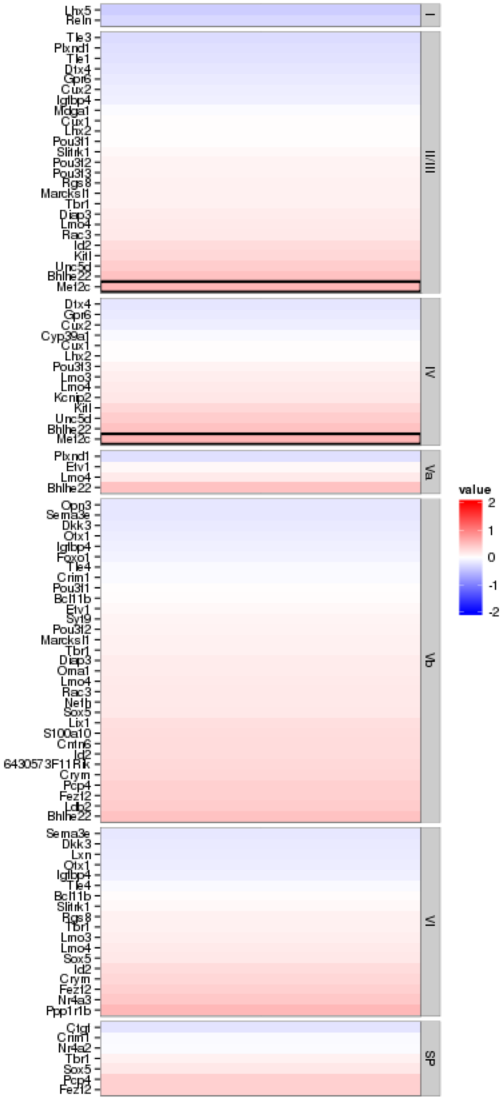




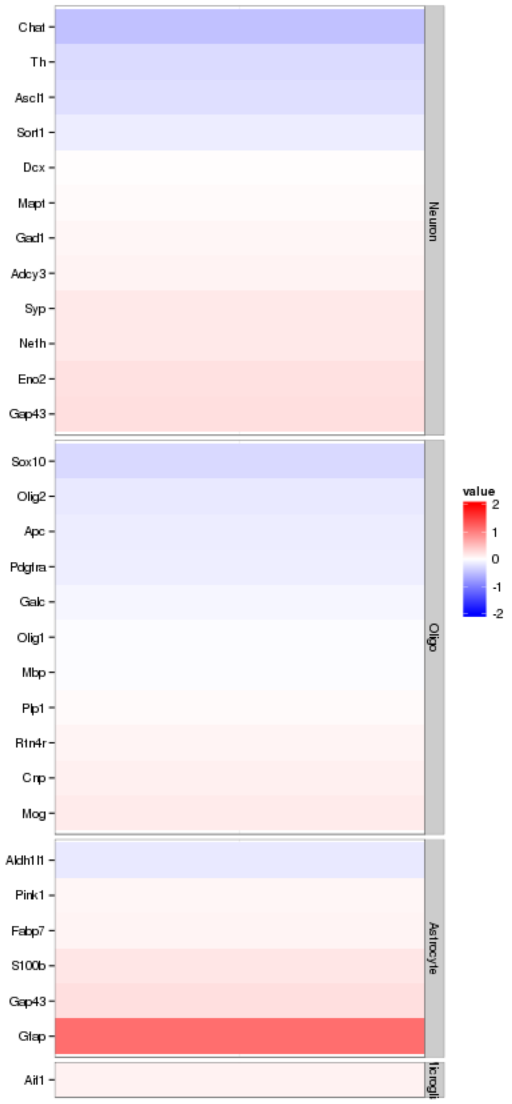
Enrichment or depletion for stage-specific cell cycle markers



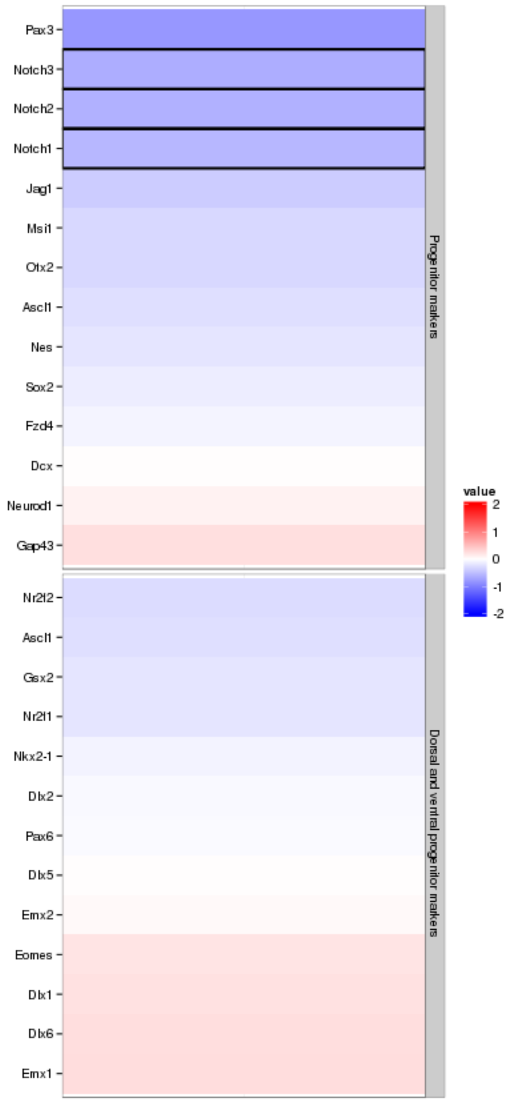
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



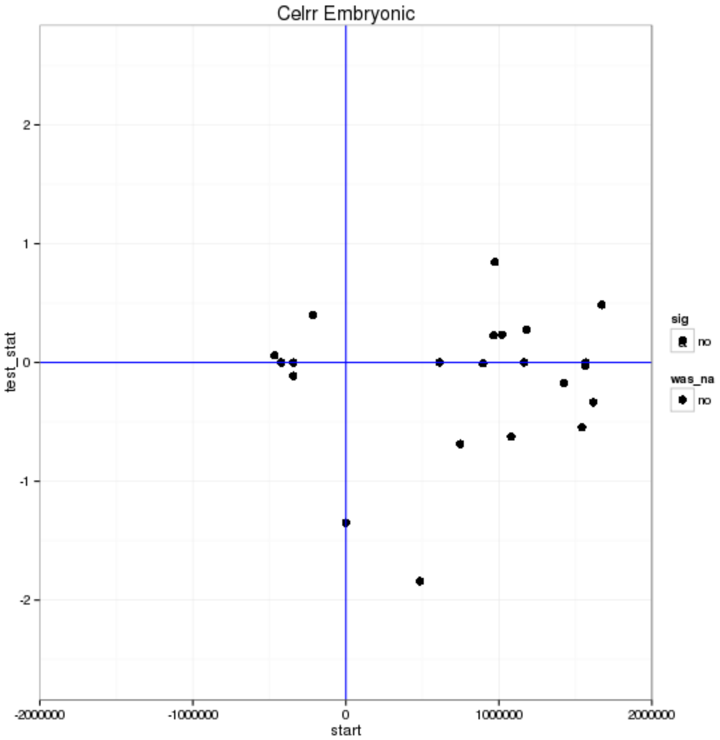
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15	JR773
16	JR760

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	32377800.00	1.26	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	32377800.00	1.10	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	32377800.00	1.23	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	32377800.00	1.29	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	32377800.00	1.20	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	32377800.00	0.89	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	32377800.00	0.97	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	32377800.00	0.92	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	32377800.00	0.86	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	32377800.00	0.96	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	32377800.00	0.81	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	32377800.00	0.80	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	32377800.00	0.68	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	32377800.00	1.21	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR773/abundances.cxb	Celrr	0	Celrr_0	37950800.00	32377800.00	1.13	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR760/abundances.cxb	Celrr	1	Celrr_1	30671700.00	32377800.00	0.94	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils
## [8] datasets  base
##
## other attached packages:
##  [1] plyr_1.8.1
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
```

```
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
## 
## 1 cuffdiff -p 10 -L WT,Celrr -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Celrr_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/BrainMap/dat
## 2
## 3
## 4
## 5
```

Crnde KO vs WT (Adult)

This file shows the wt-v-ko comparison for Crnde.

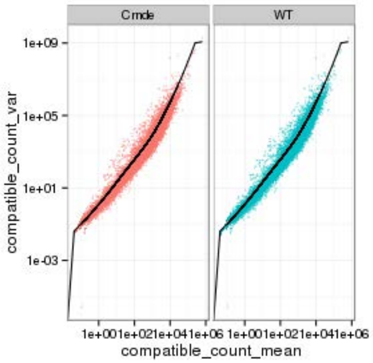
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

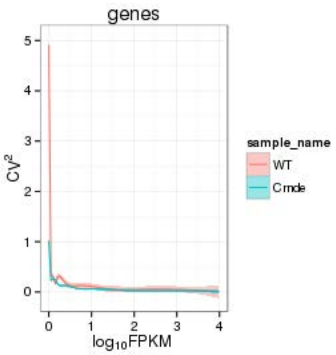
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



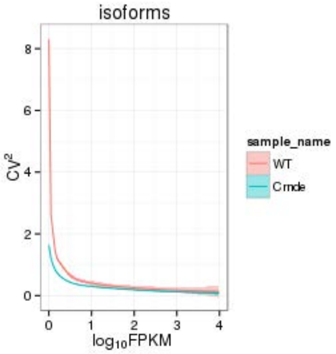
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

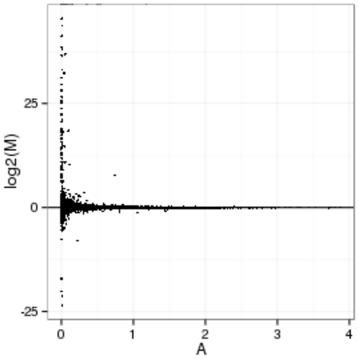
Genes:



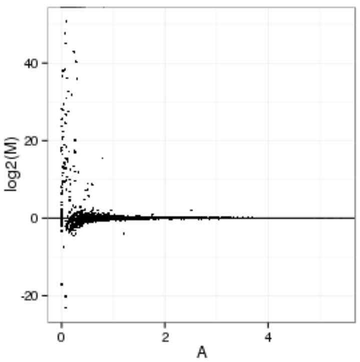
Isoforms:



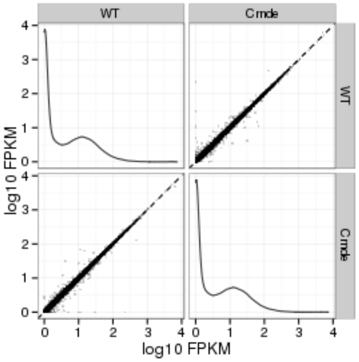
MvA plot



MvA plot counts



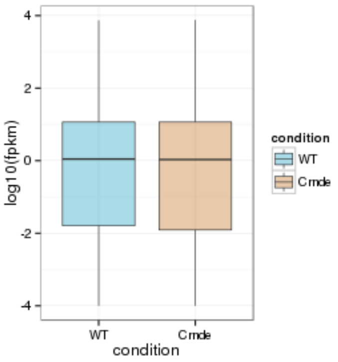
Scatterplot matrix



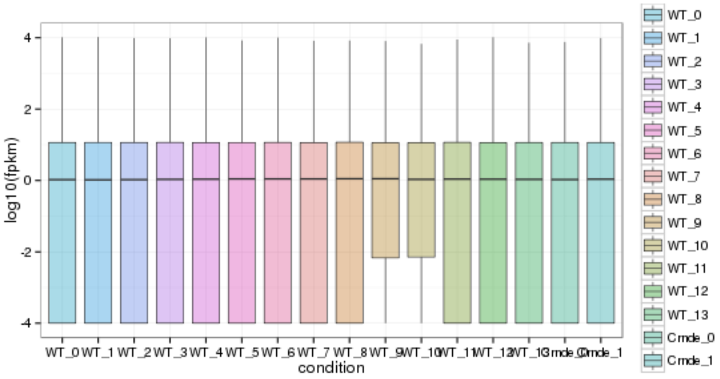
Distributions

Boxplots

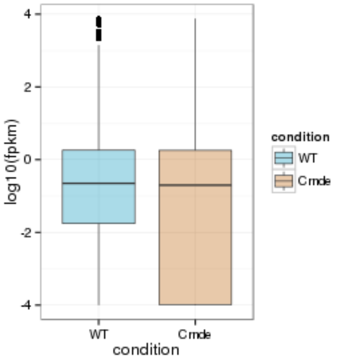
Boxplot (genes)



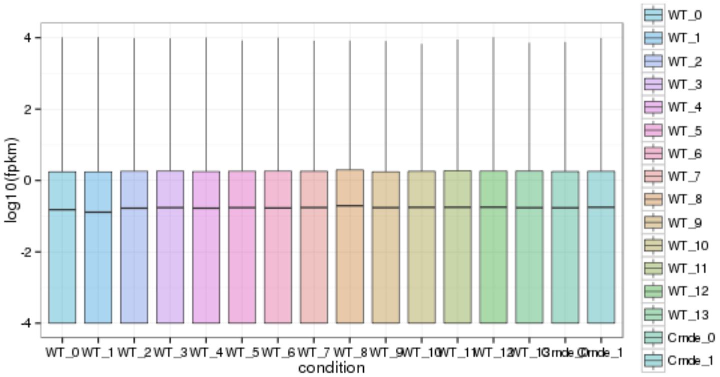
Boxplot (genes, replicates)



Boxplot (isoforms)

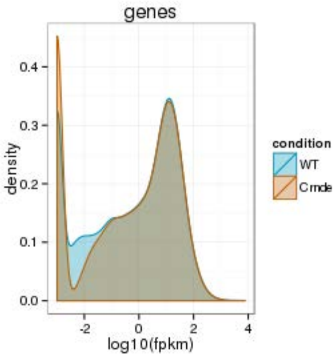


Boxplot (isoforms, replicates)

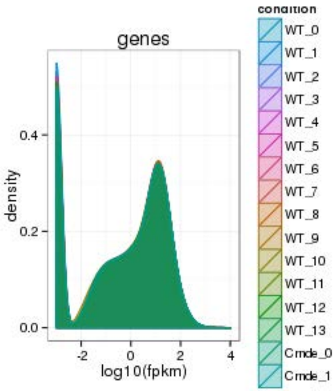


Density

Density (genes)

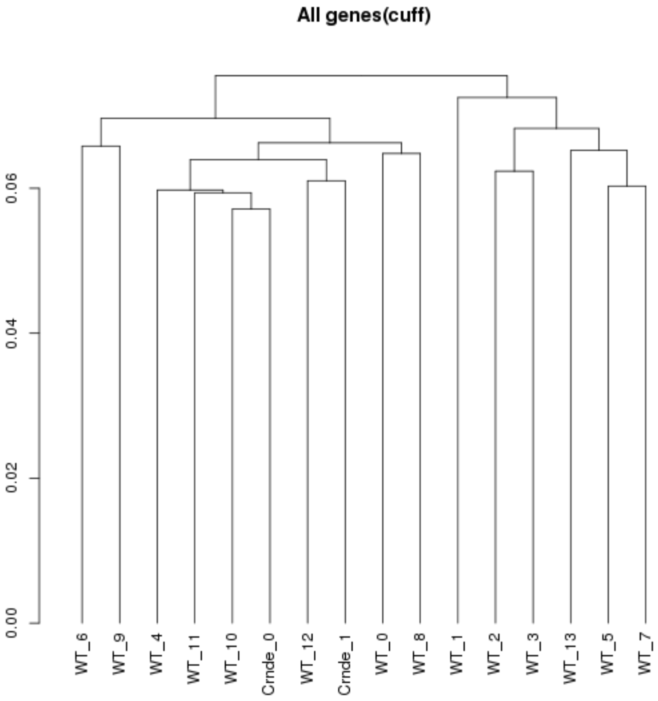


Density (genes, replicates)



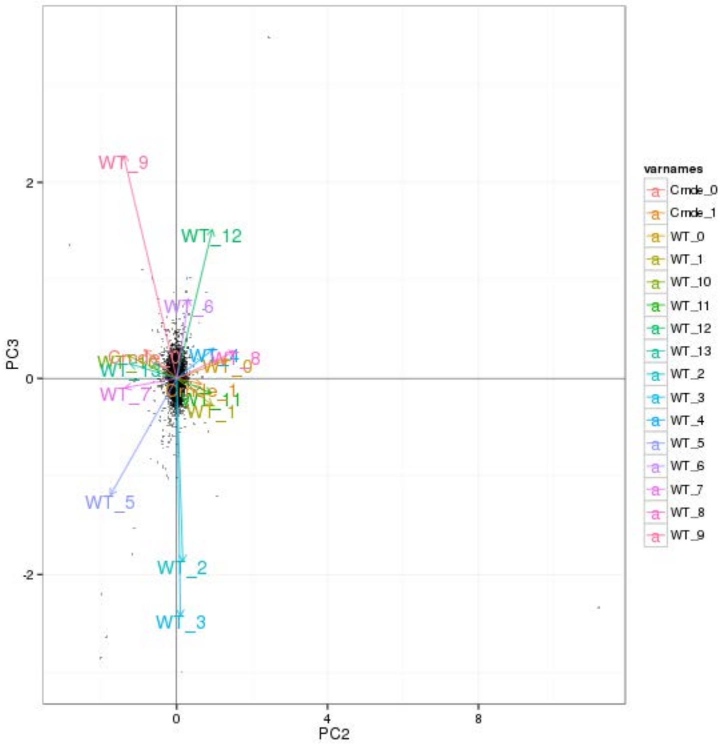
Clustering

Replicate Clusters



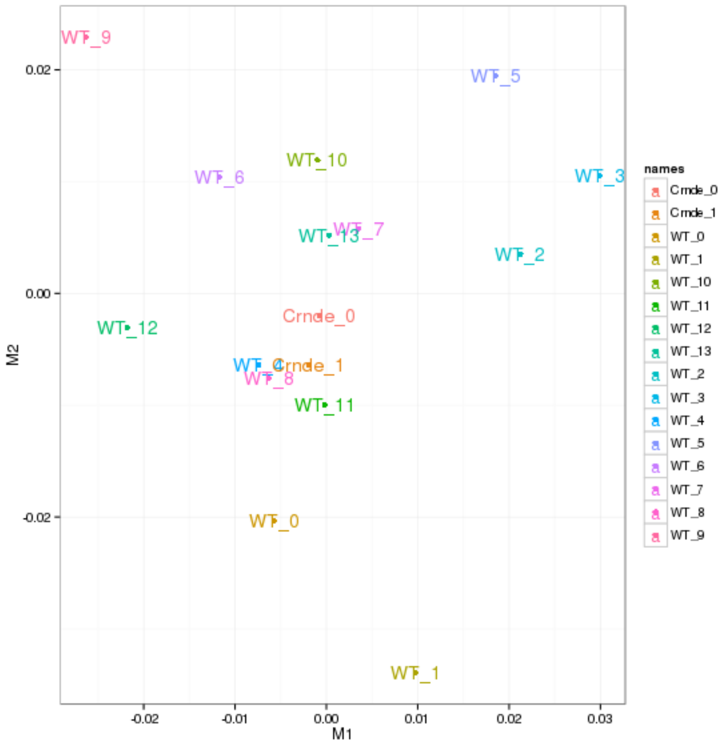
```
## NULL
```

PCA (genes)



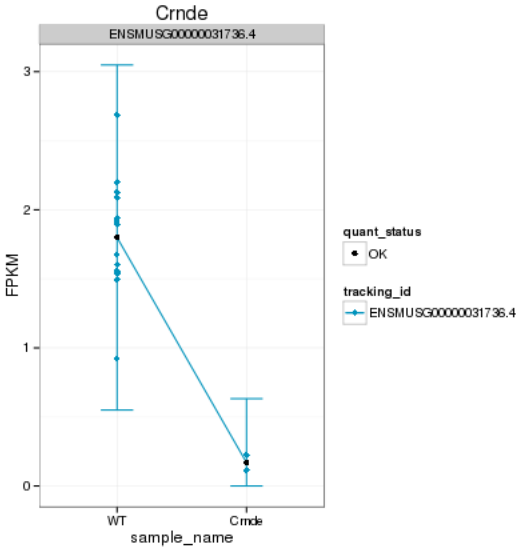
PC3
PC2
2
0
-2
0
4
8
WT_9
WT_12
WT_6
WT_5
WT_2
WT_3
WT_7
WT_13
WT_0
WT_1
WT_11
varnames
Cmde_0
Cmde_1
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

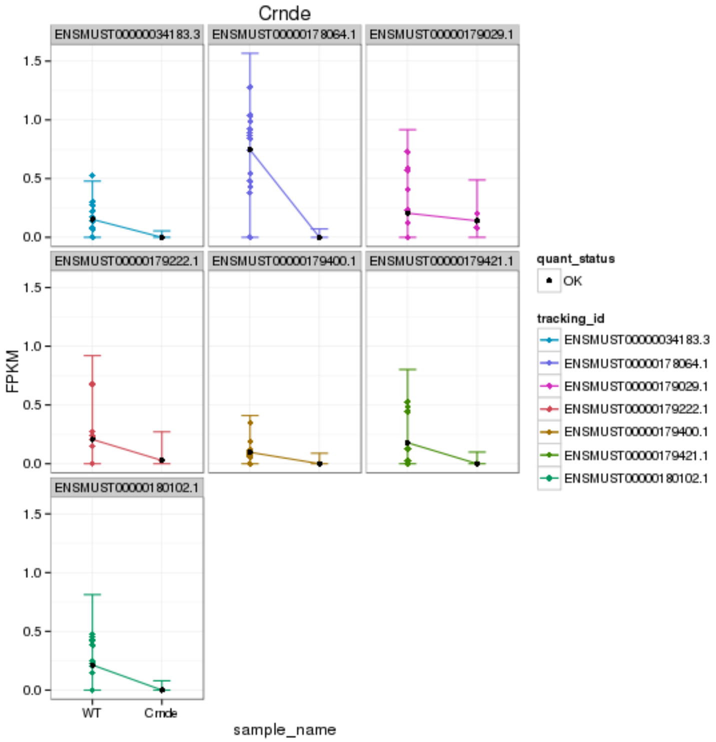


KO assessment

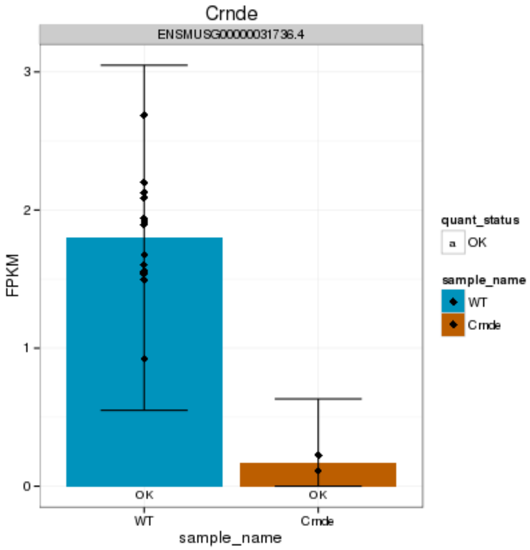
Endogenous lncRNA expression



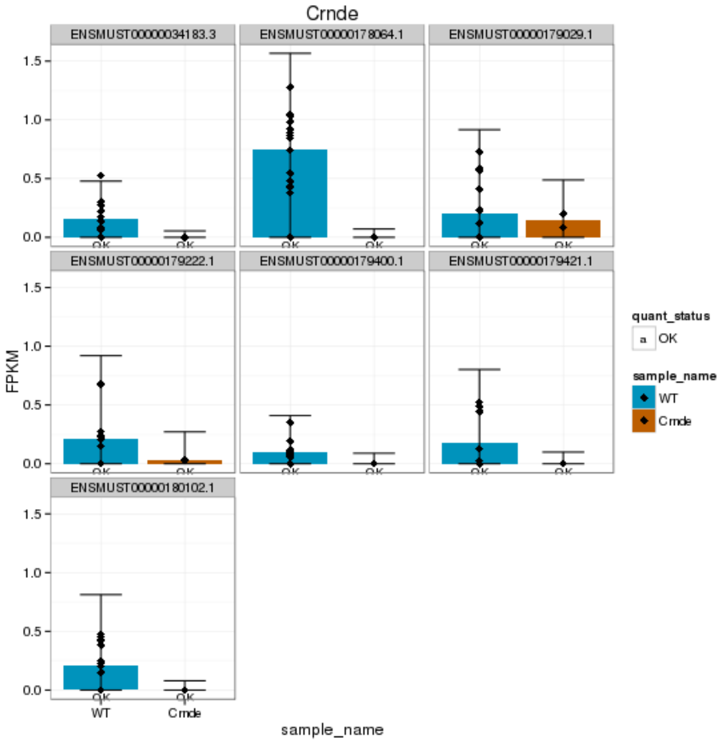
Endogenous expression of Crnde isoforms:



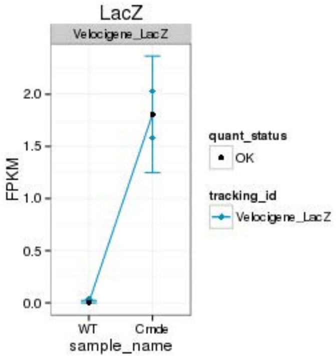
Barplot of gene expression:

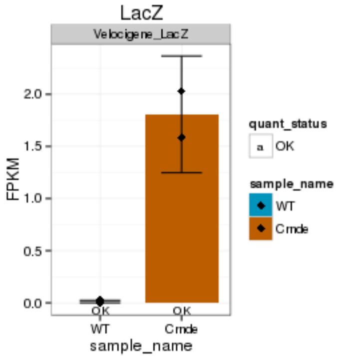


Barplot of isoform expression:



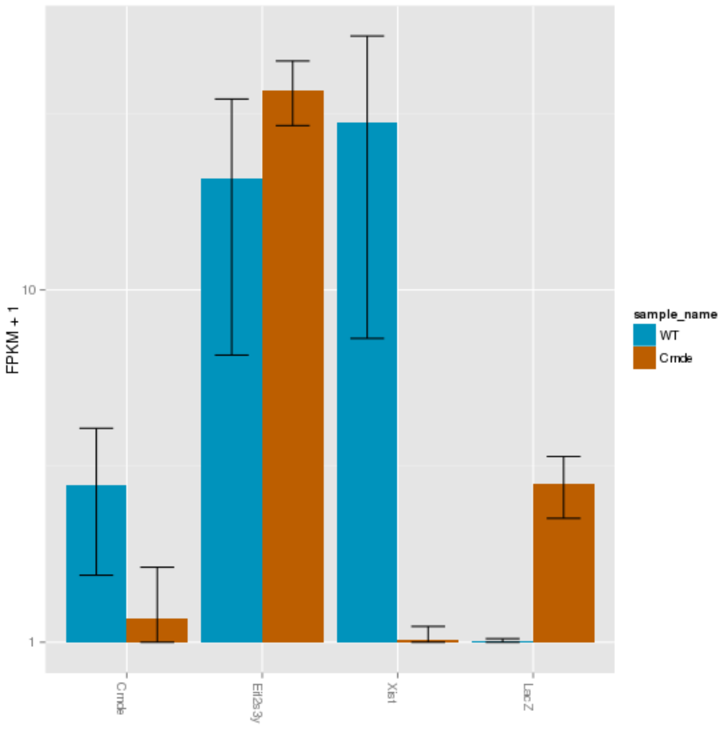
LacZ expression



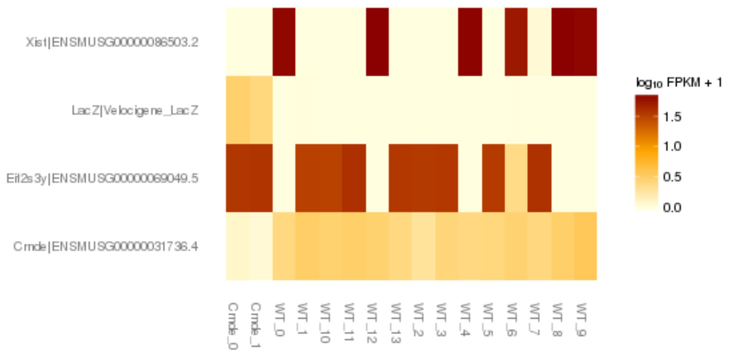


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

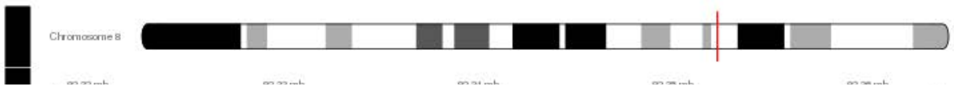
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):

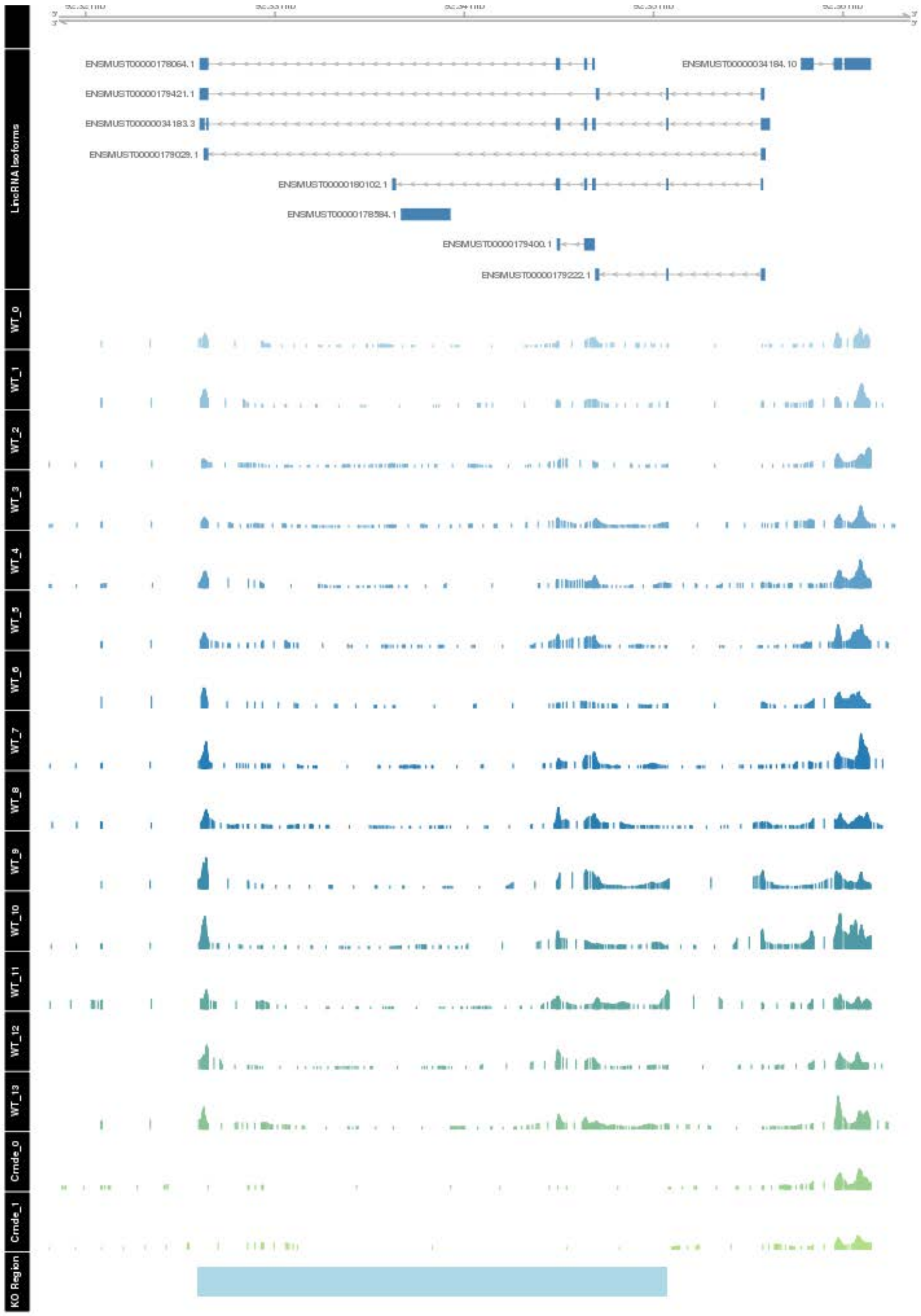


Expression heatmap:



Track visualization




52.32 mb
52.33 mb
52.34 mb
52.35 mb
52.36 mb
5'
3'
3'
5'
LincRNA Isoforms
ENSMUST00000178064.1
ENSMUST00000034184.10
ENSMUST00000179421.1
ENSMUST00000034183.3
ENSMUST00000179029.1
ENSMUST00000180102.1
ENSMUST00000178584.1
ENSMUST00000179400.1
ENSMUST00000179222.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Crnde_0
Crnde_1
KO Region

Differential Analysis

Differential Genes

There are 42 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Fosb
2	Mertk
3	Adi1
4	Fos
5	Arc
6	Nr4a1
7	Cdkn1a
8	Clic5
9	Fkbp5
10	Tma16
11	Unc5a
12	Sgk3
13	Nr4a3
14	Slc2a1
15	Mfsd2a
16	Tinagl1
17	Fosl2
18	Hddc3
19	Mt2
20	Sox10
21	Lpcat2
22	Arhgap27
23	Klf10
24	Egr2
25	Egr1
26	Pcsk1n
27	Cdc42ep4
28	Npas4
29	Cdh19
30	Junb
31	Kdm5d
32	Gm5506
33	Cox5b
34	Scoc
35	Ddx3y
36	Jund
37	Egr4

38 Gm7292

39 A830036E02Rik

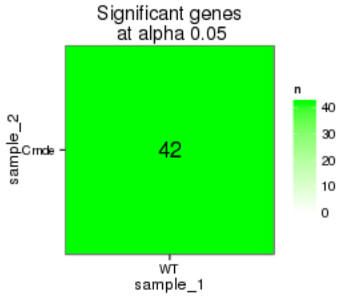
40 Xist

41 AA465934

42 Ccdc85b

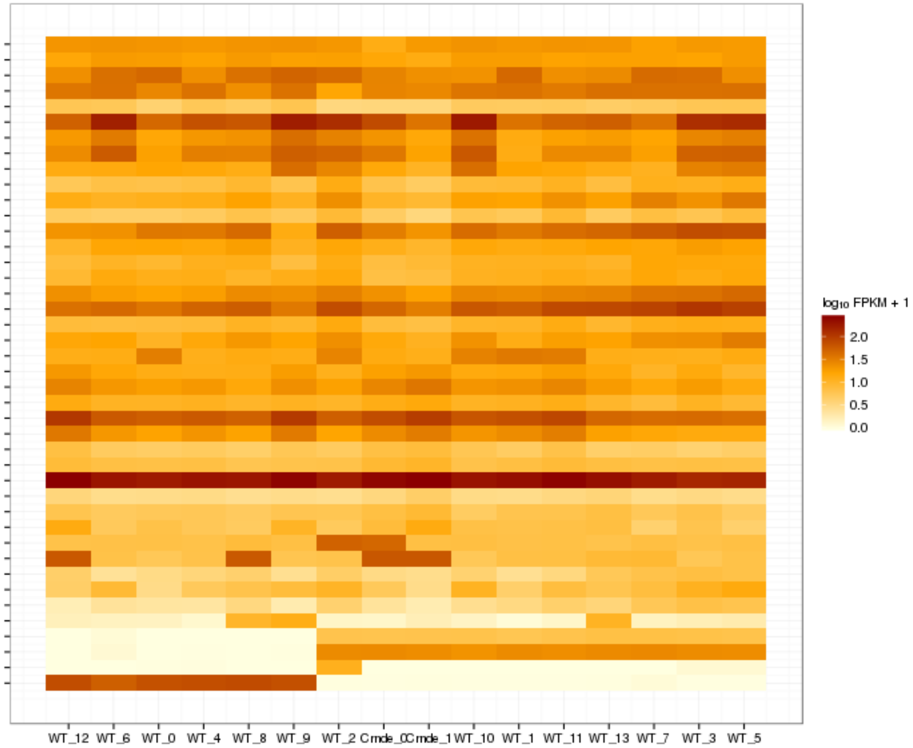
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

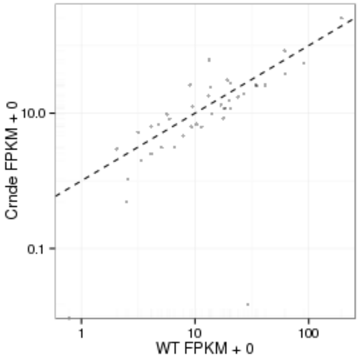


Significant genes with expression >50fpkm (any condition):(turned off)

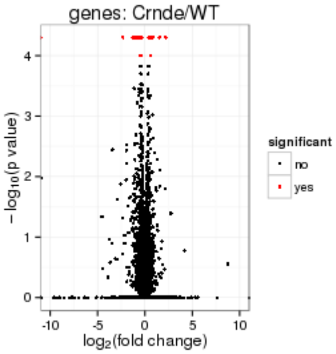
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

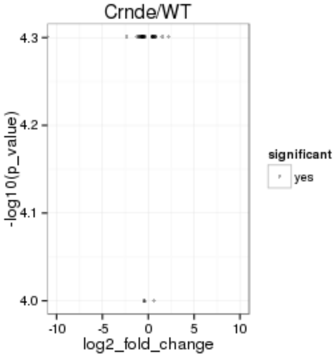
Scatter plot of significant genes only:



Volcano Plot



Volcano plot with significant genes only:

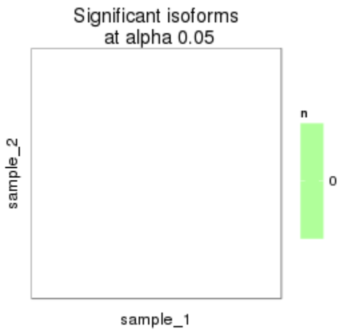


FoldChange Heatmap

Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

[1] “no sig isoforms”

Gene-level DE isoform heatmap

```
## [1] "no sig isoforms"
```

Isoform foldchange heatmap by isoform:

```
## [1] "no sig isoforms"
```

Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

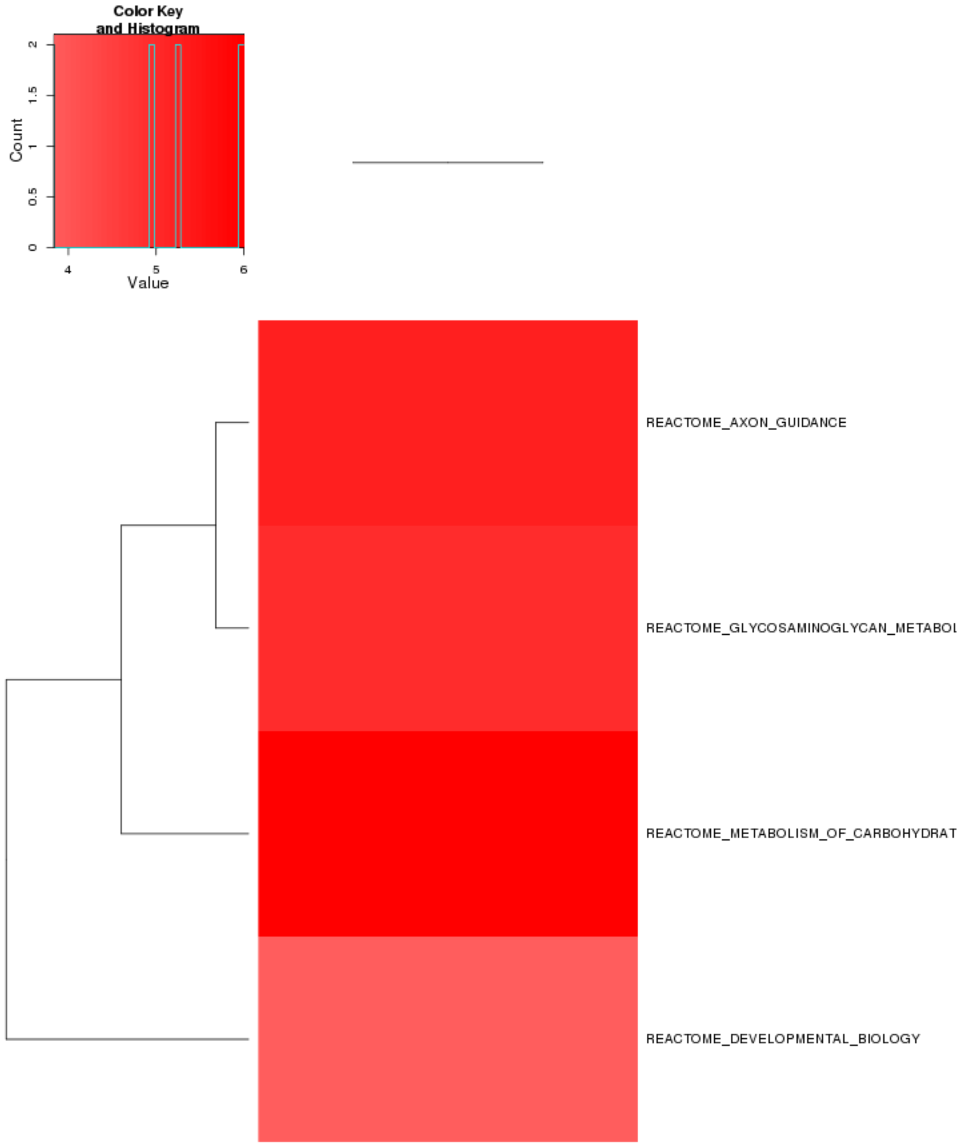
Biocarta enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

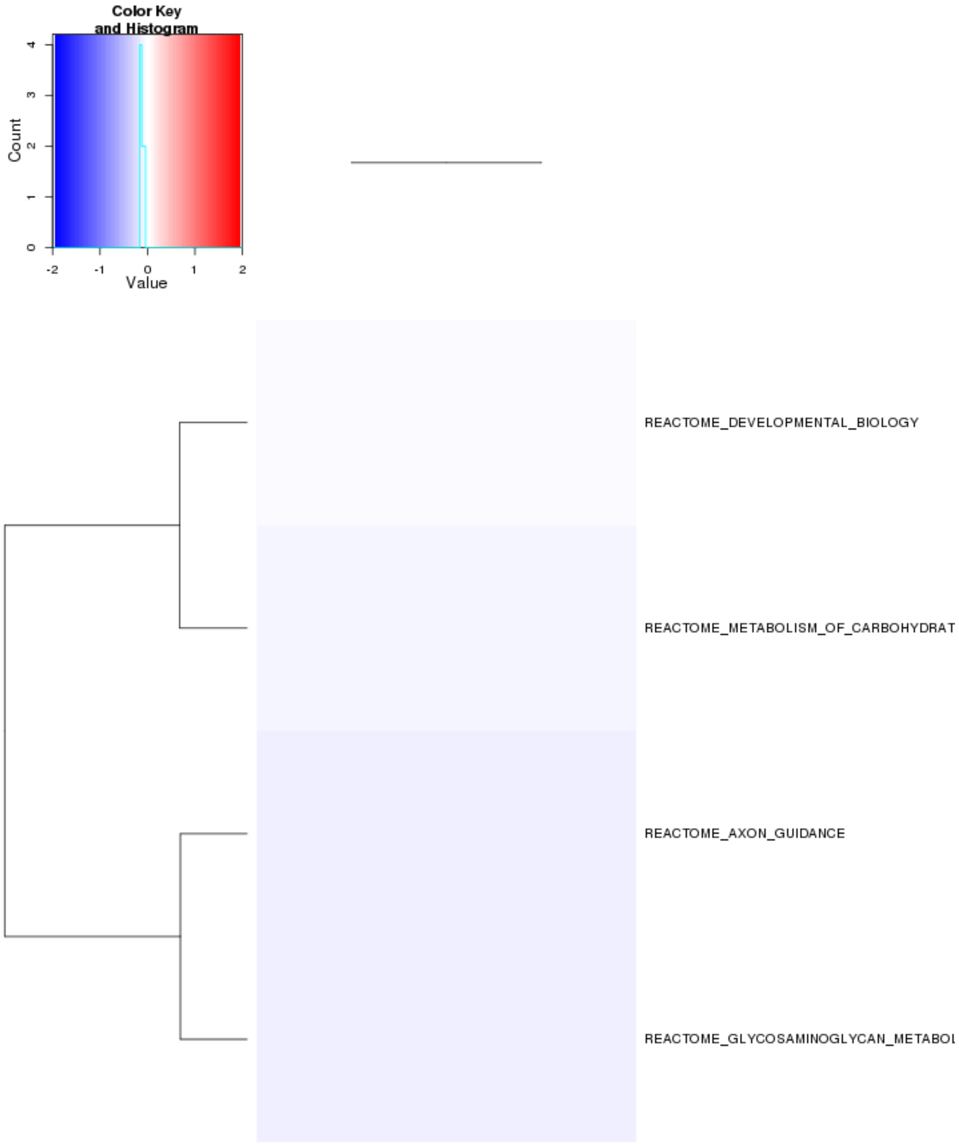
Biocarta zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

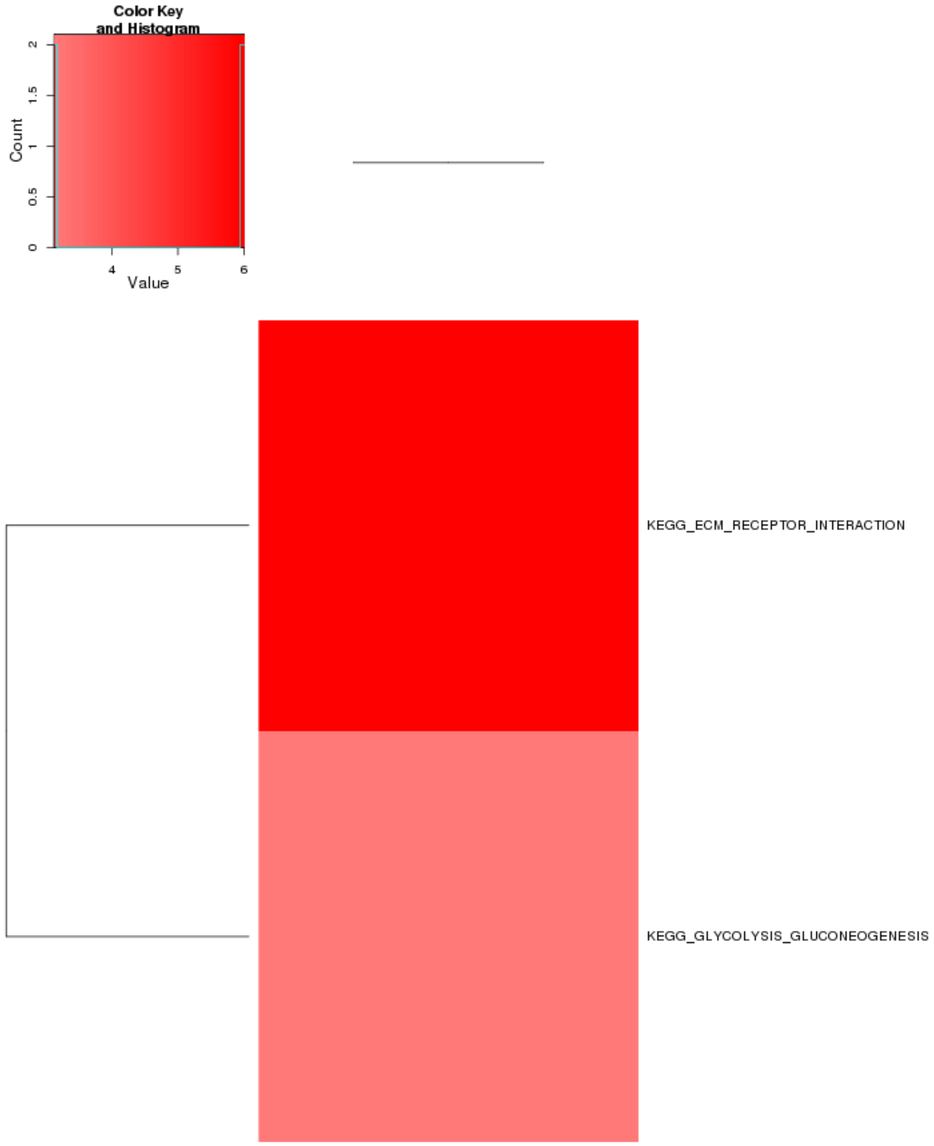
Reactome enrichment:



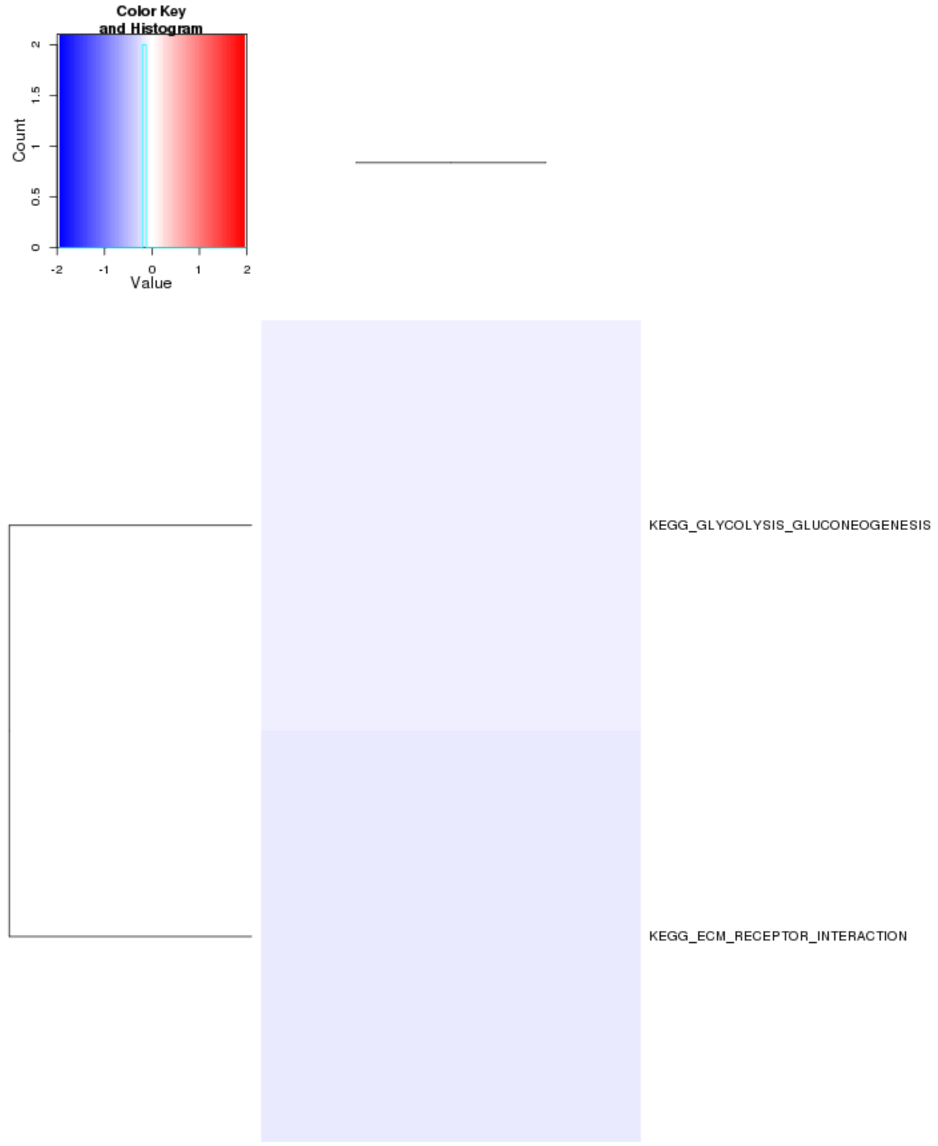
Reactome zscore:



Kegg enrichment:


Color Key
and Histogram
Count
0
0.5
1
1.5
2
4
5
6
Value
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_GLYCOLYSIS_GLUCONEOGENESIS

Kegg zscore:



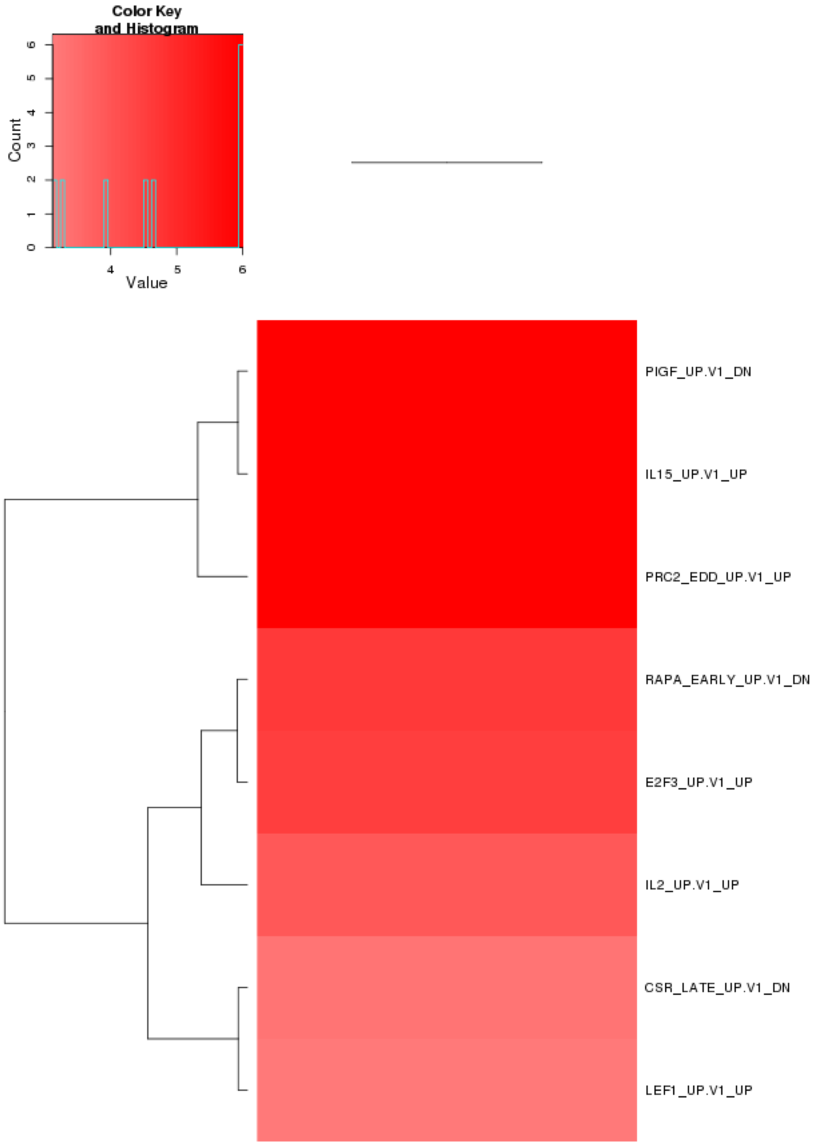
Interneuron enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

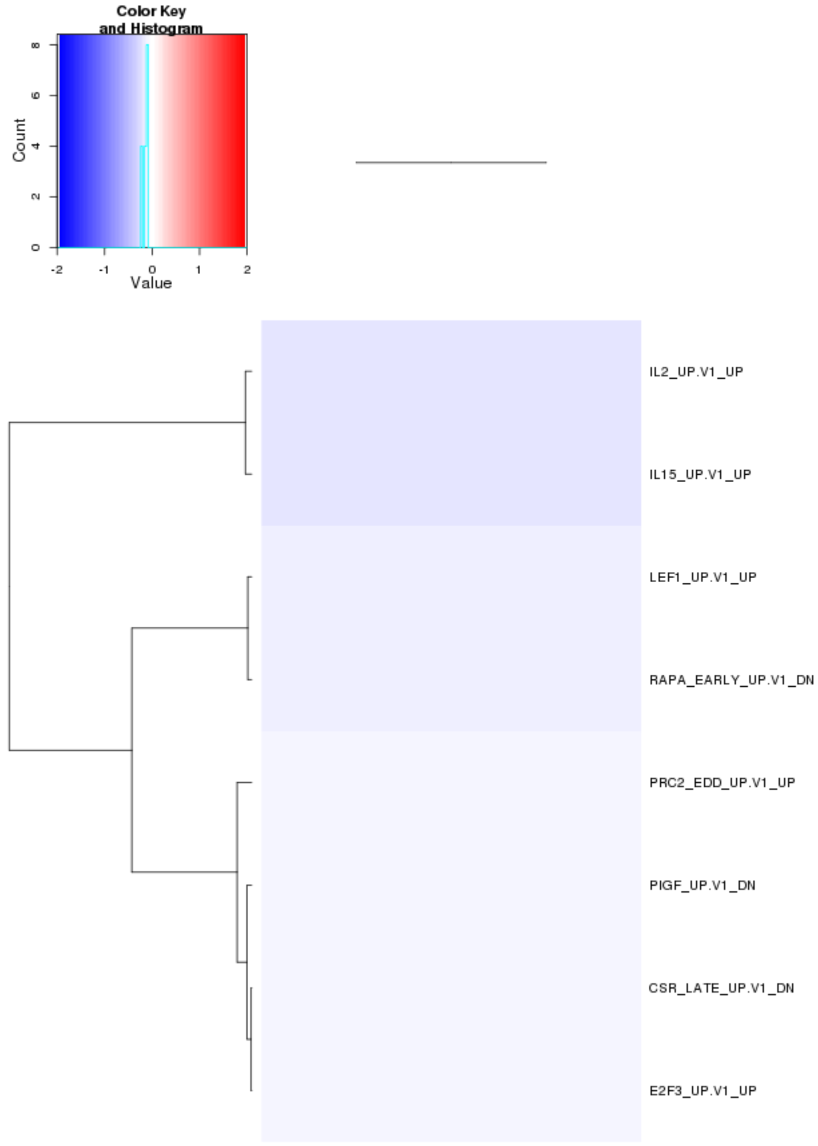
Interneuron zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

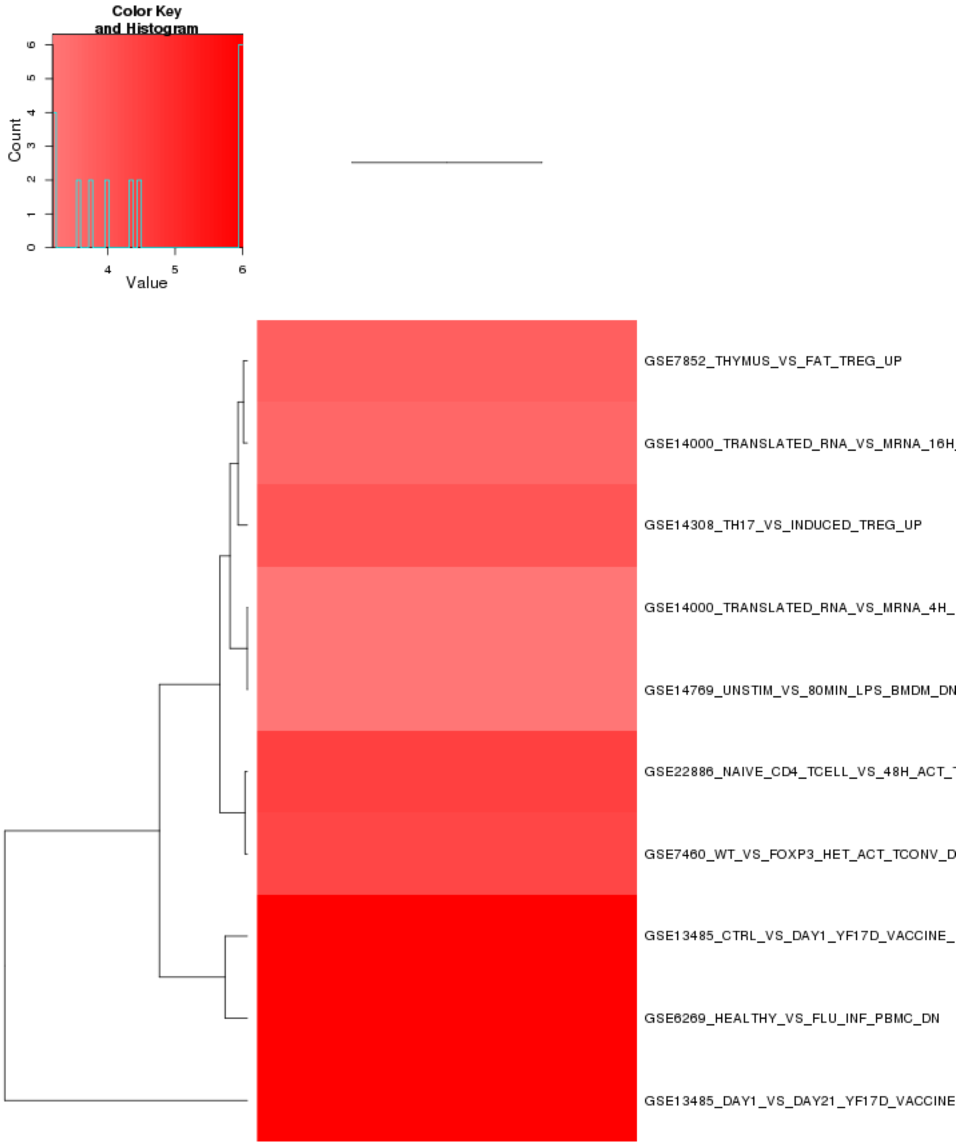
Oncogene enrichment:



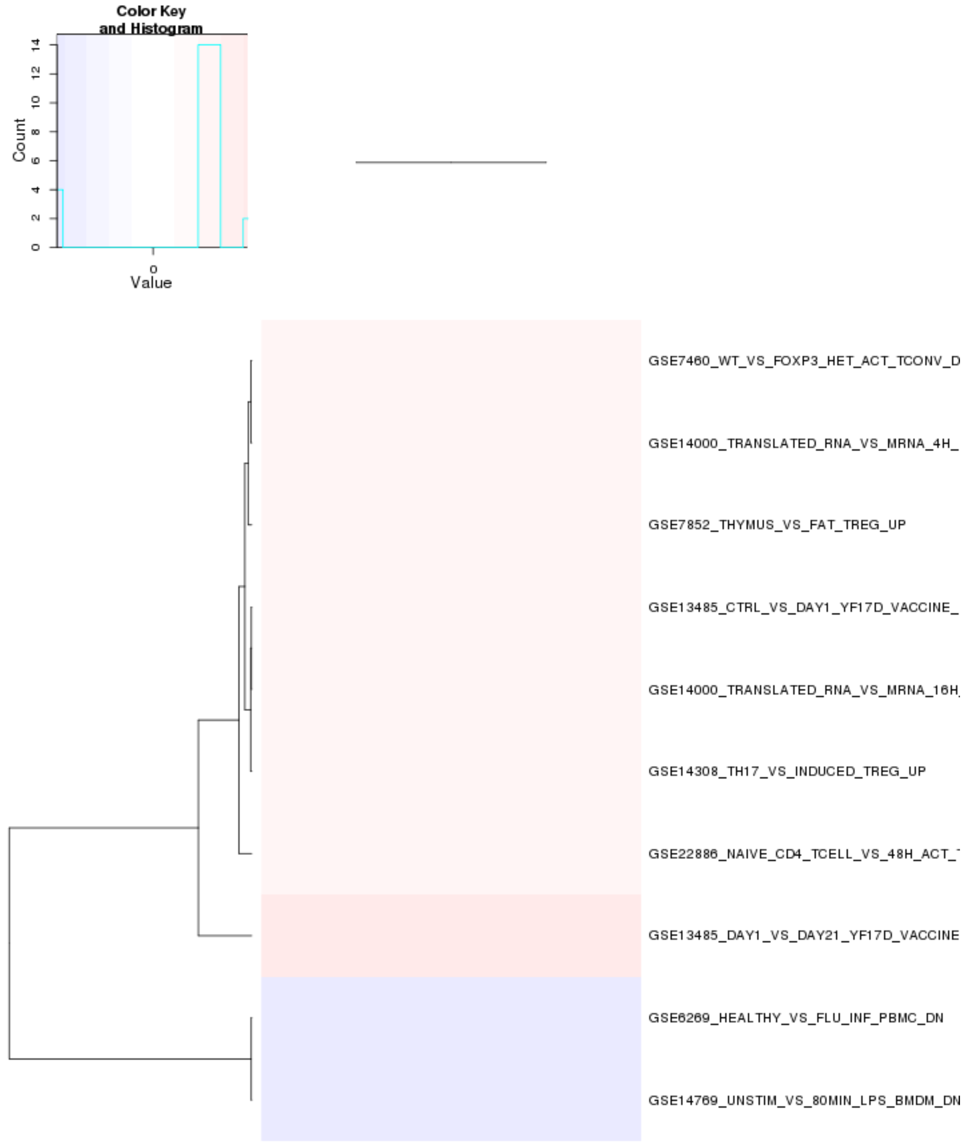
Oncogene zscore:



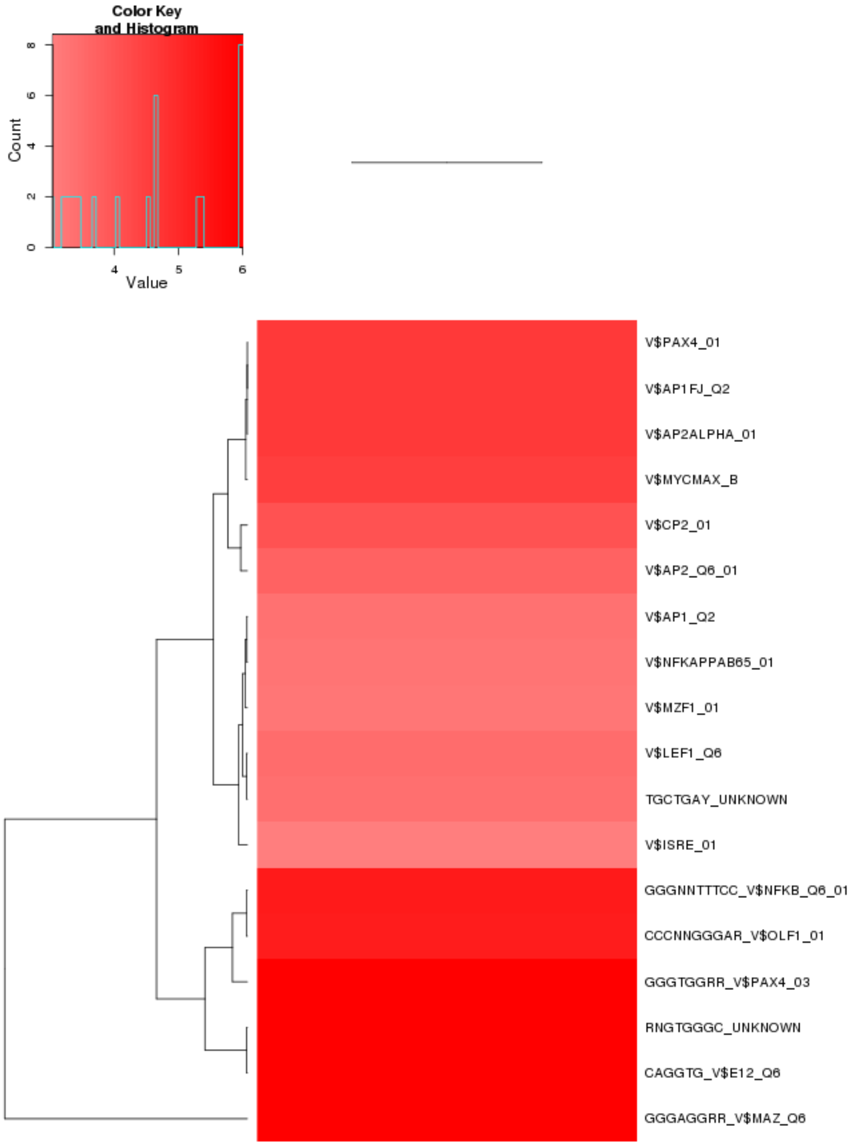
Immuno enrichment:



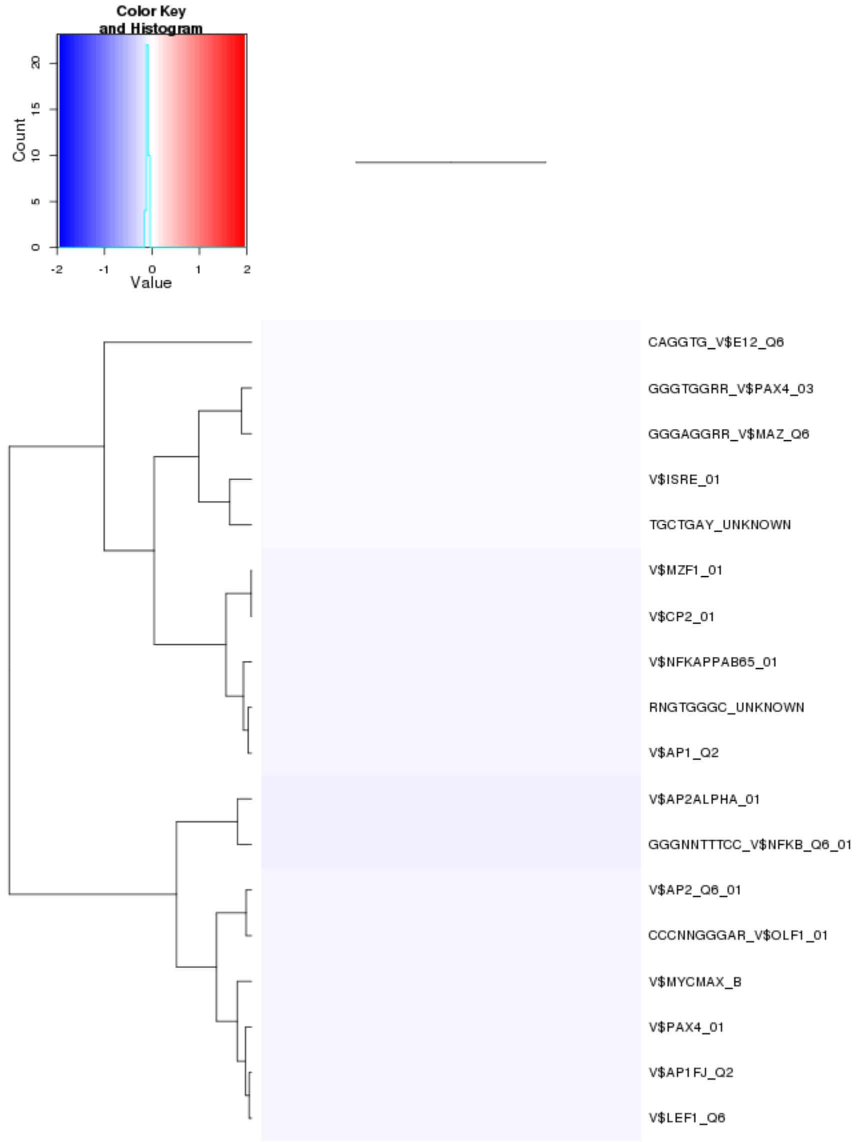
Immuno zscore:



TF enrichment:


Color Key
and Histogram
Count
0
2
4
6
8
4
5
6
Value
V$PAX4_01
V$AP1FJ_Q2
V$AP2ALPHA_01
V$MYCMAX_B
V$CP2_01
V$AP2_Q6_01
V$AP1_Q2
V$NFKAPPAB65_01
V$MZF1_01
V$LEF1_Q6
TGCTGAY_UNKNOWN
V$ISRE_01
GGGNNTTTCC_V$NFKB_Q6_01
CCCNNGGGAR_V$OLF1_01
GGGTGGRR_V$PAX4_03
RNGTGGGC_UNKNOWN
CAGGTG_V$E12_Q6
GGGAGGRR_V$MAZ_Q6

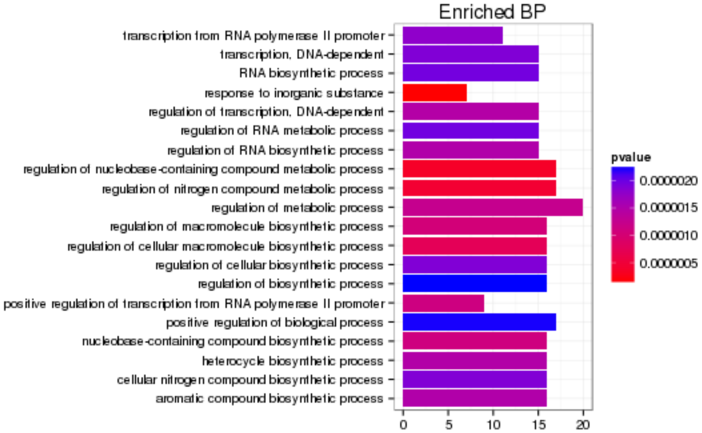
TF zscore:

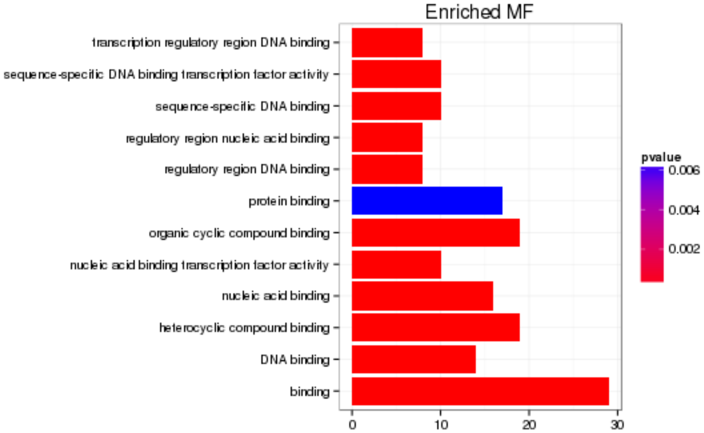


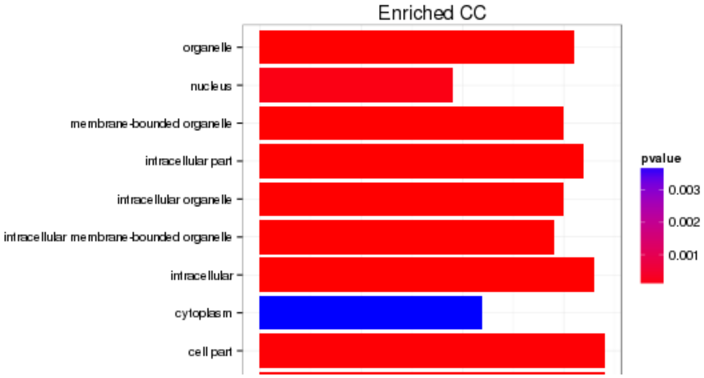
GO enrichment

Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

```
## [1] "ERROR: The estimated pi0 <= 0. Check that you have valid p-values or use another lambda method."
```


Enriched BP
transcription from RNA polymerase II promoter
transcription, DNA-dependent
RNA biosynthetic process
response to inorganic substance
regulation of transcription, DNA-dependent
regulation of RNA metabolic process
regulation of RNA biosynthetic process
regulation of nucleobase-containing compound metabolic process
regulation of nitrogen compound metabolic process
regulation of metabolic process
regulation of macromolecule biosynthetic process
regulation of cellular macromolecule biosynthetic process
regulation of cellular biosynthetic process
regulation of biosynthetic process
positive regulation of transcription from RNA polymerase II promoter
positive regulation of biological process
nucleobase-containing compound biosynthetic process
heterocycle biosynthetic process
cellular nitrogen compound biosynthetic process
aromatic compound biosynthetic process
0
5
10
15
20
pvalue
0.0000020
0.0000015
0.0000010
0.0000005

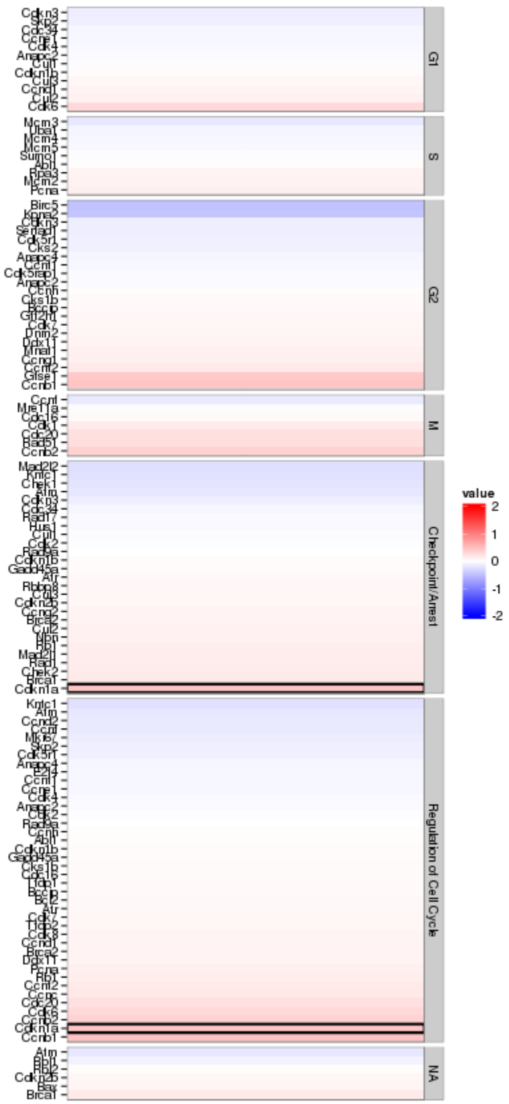

Enriched MF
transcription regulatory region DNA binding
sequence-specific DNA binding transcription factor activity
sequence-specific DNA binding
regulatory region nucleic acid binding
regulatory region DNA binding
protein binding
organic cyclic compound binding
nucleic acid binding transcription factor activity
nucleic acid binding
heterocyclic compound binding
DNA binding
binding
0
10
20
30
pvalue
0.006
0.004
0.002


Enriched CC
organelle
nucleus
membrane-bounded organelle
intracellular part
intracellular organelle
intracellular membrane-bounded organelle
intracellular
cytoplasm
cell part
pvalue
0.003
0.002
0.001

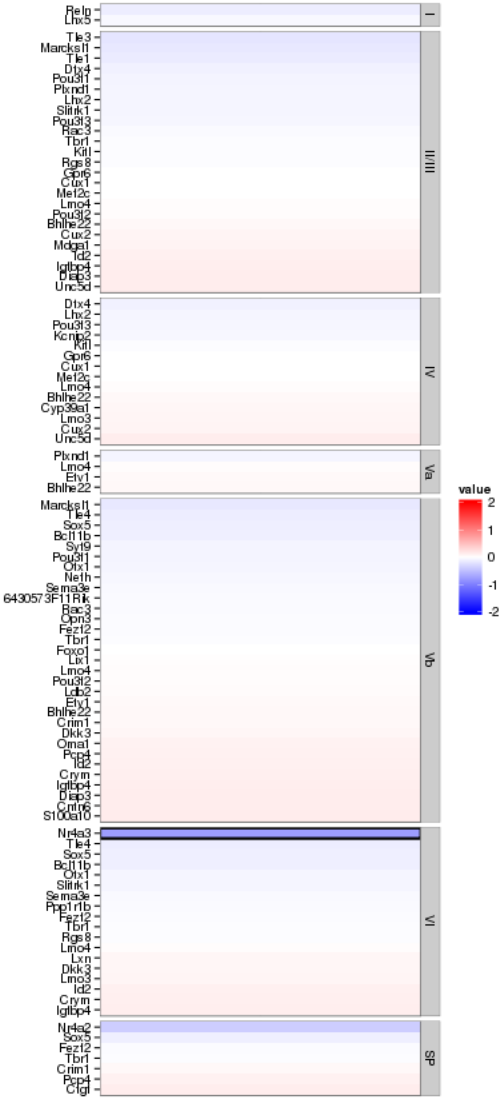
```
## Error: need finite 'xlim' values
```

```
## Error: 'x' and 'units' must have length > 0
```

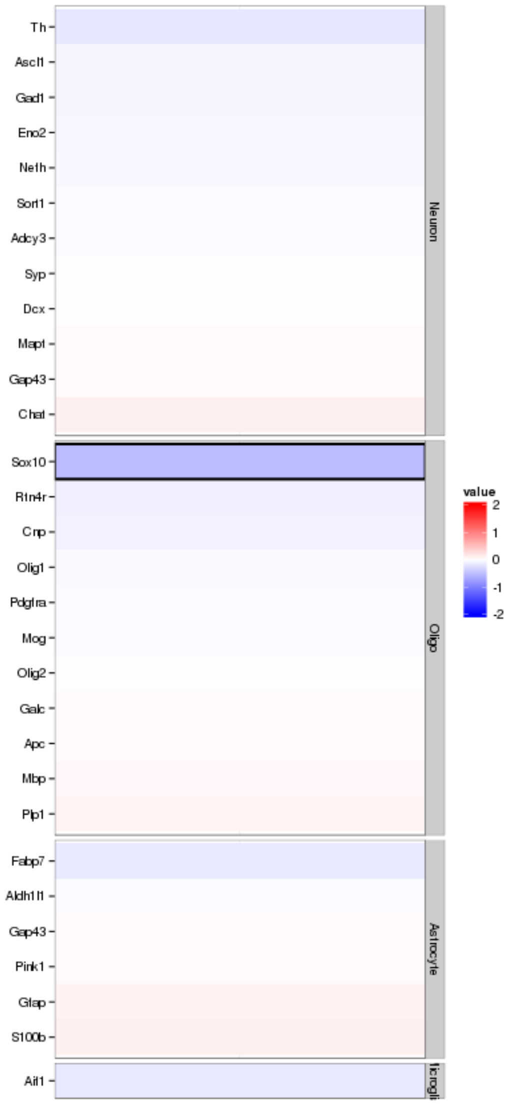
Enrichment or depletion for stage-specific cell cycle markers



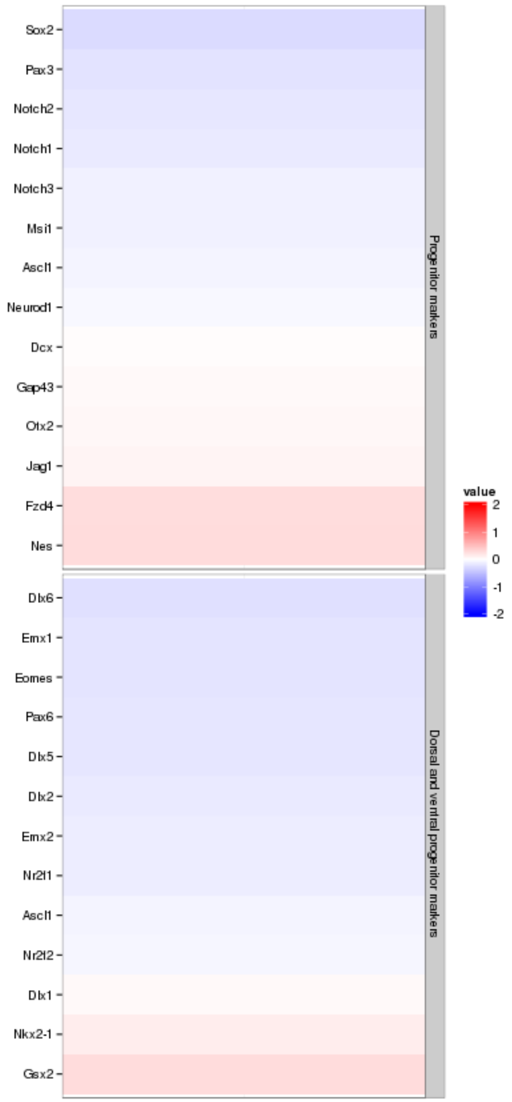
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



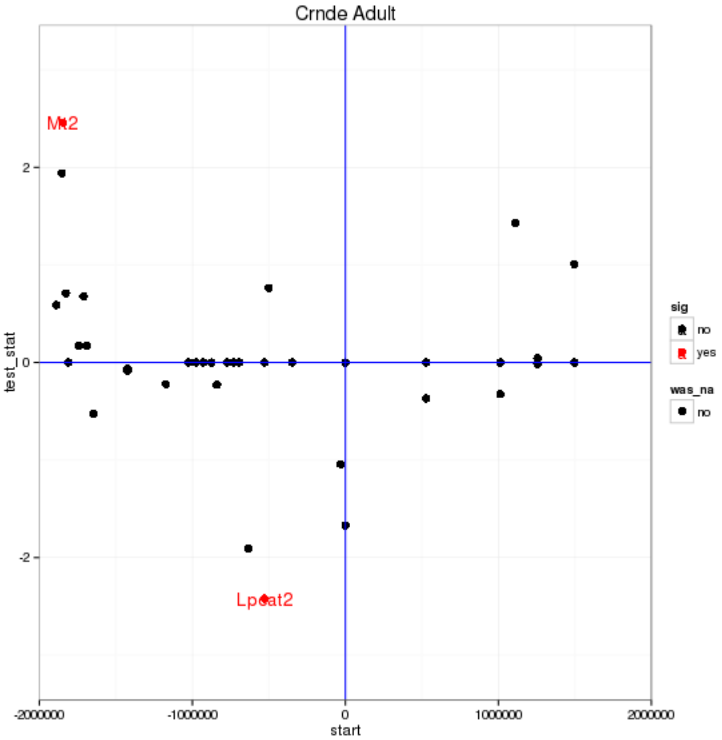
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 2 genes significantly regulated in a region this size is: 0.0189



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15	JR741
16	JR784

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	34590000.00	0.76	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	34590000.00	0.59	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	34590000.00	0.98	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	34590000.00	0.80	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	34590000.00	1.04	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	34590000.00	1.07	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	34590000.00	0.81	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	34590000.00	1.16	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	34590000.00	1.01	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	34590000.00	1.30	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	34590000.00	1.51	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	34590000.00	1.02	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	34590000.00	0.97	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	34590000.00	1.21	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR741/abundances.cxb	Crnde	0	Crnde_0	37686800.00	34590000.00	1.09	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR784/abundances.cxb	Crnde	1	Crnde_1	37652200.00	34590000.00	1.09	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1                        
##  [2] stringr_0.6.2                     
##  [3] seqbias_1.10.0                    
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0                   
##  [6] Biostrings_2.30.1
```

```
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6          
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4      
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7             
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1         
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1          
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4          
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12    
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26   
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2         
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0         
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1    
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2         
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2           
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##            param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,Crnde -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Crnde_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/ar
## 2
## 3
## 4
## 5
```

Crnde KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for Crnde.

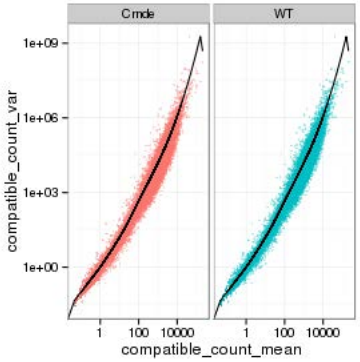
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

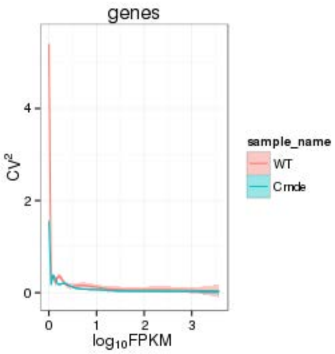
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



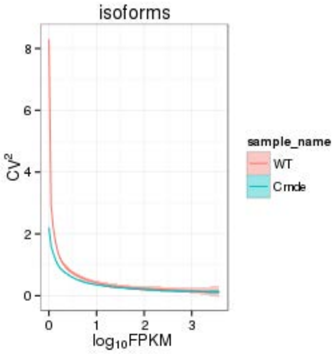
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

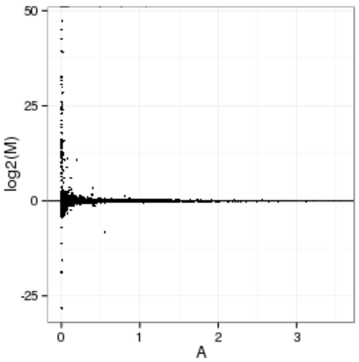
Genes:



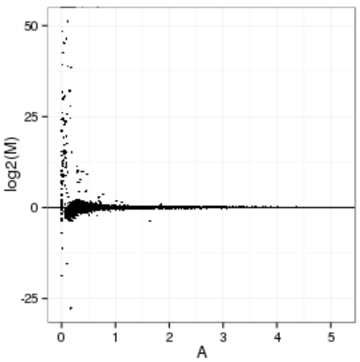
Isoforms:



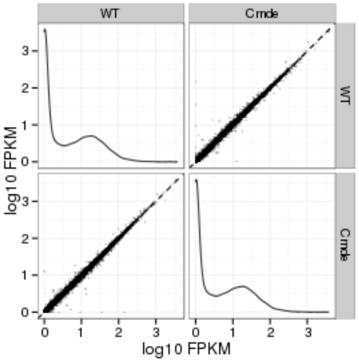
MvA plot



MvA plot counts



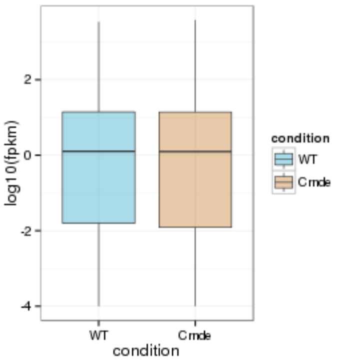
Scatterplot matrix



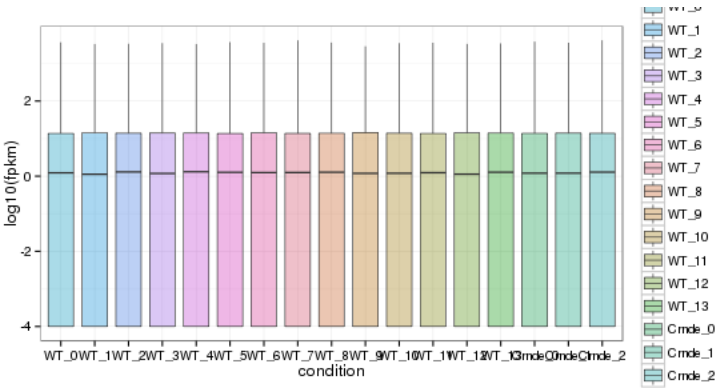
Distributions

Boxplots

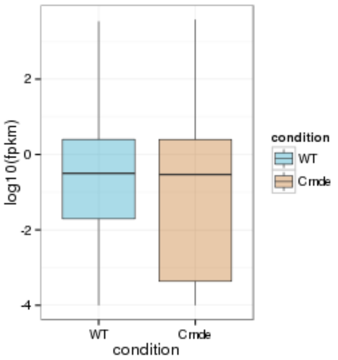
Boxplot (genes)



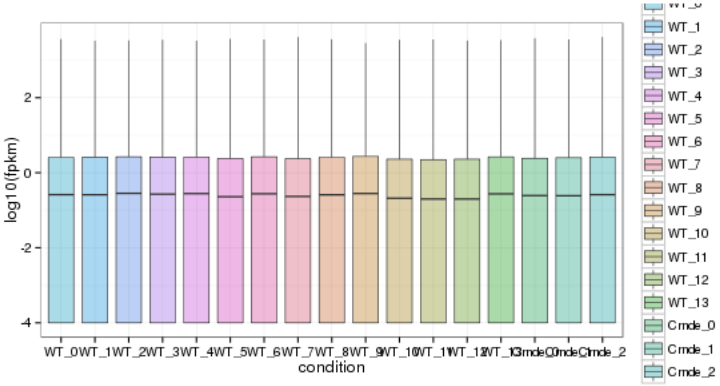
Boxplot (genes, replicates)



Boxplot (isoforms)

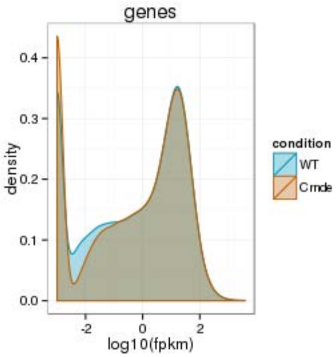


Boxplot (isoforms, replicates)

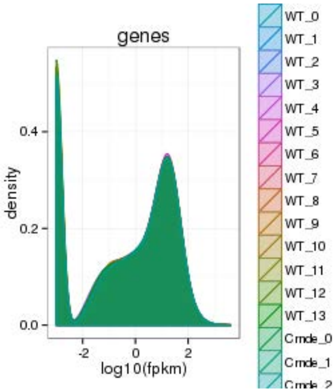


Density

Density (genes)

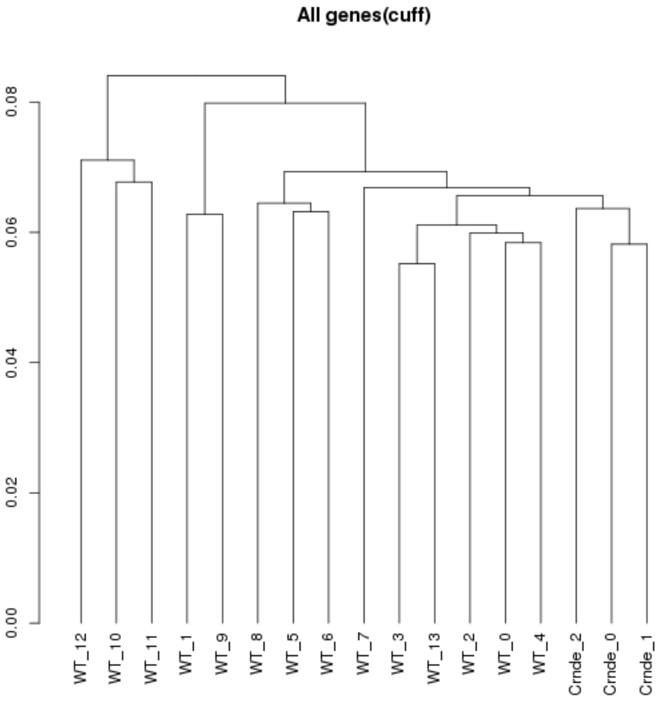


Density (genes, replicates)



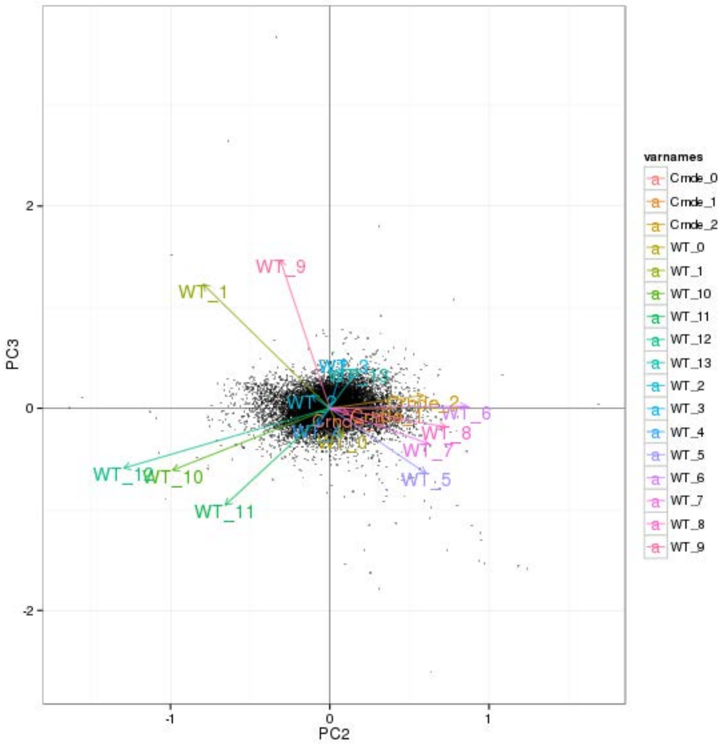
Clustering

Replicate Clusters

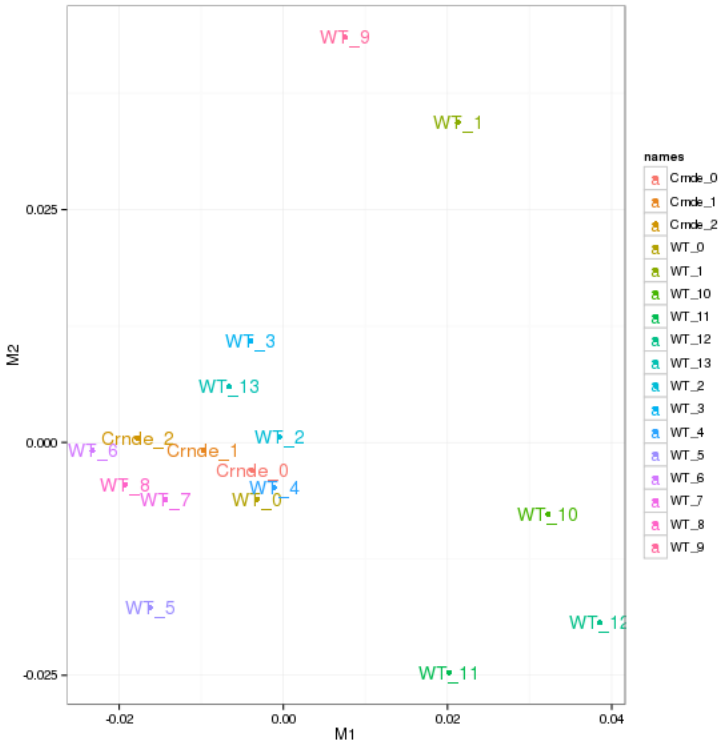


```
## NULL
```

PCA (genes)

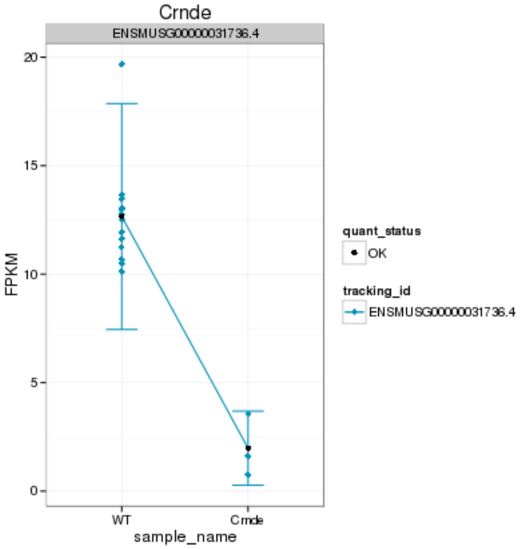

varnames
Cmde_0
Cmde_1
Cmde_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
PC3
PC2
2
0
-2
-1
0
1

MDS (genes)

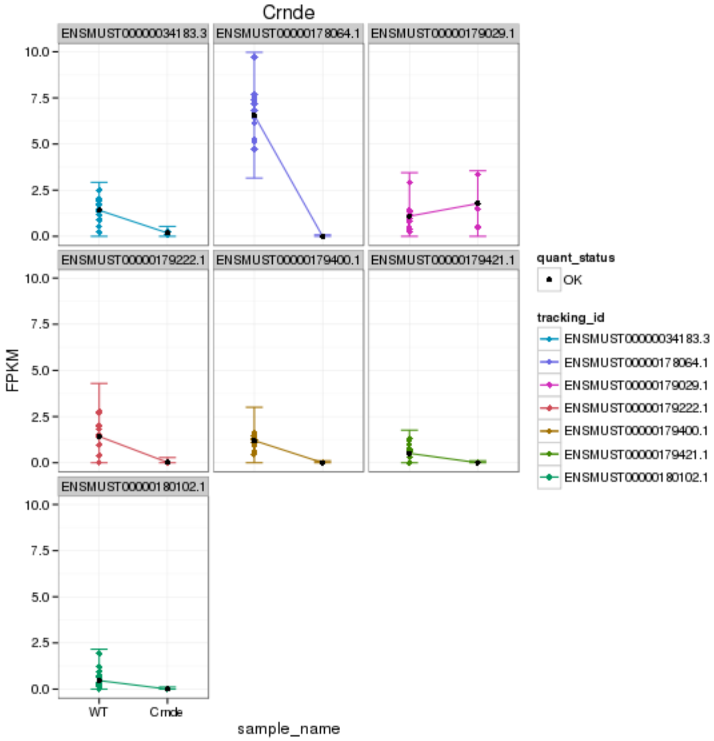


KO assessment

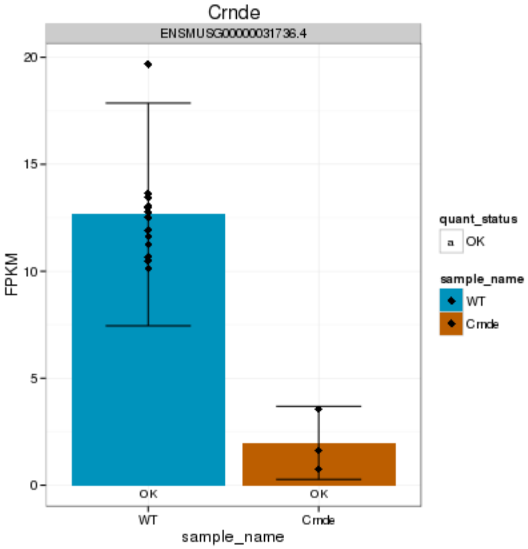
Endogenous lncRNA expression



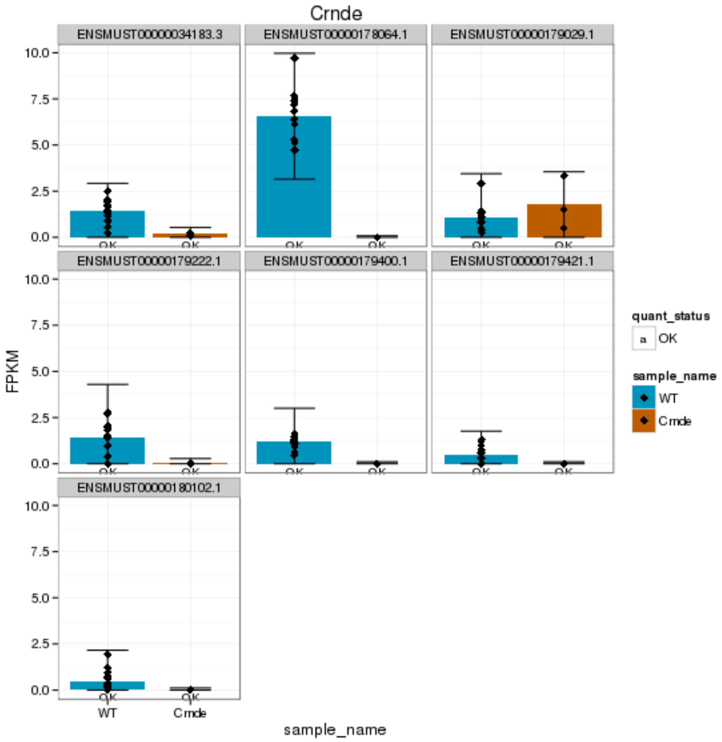
Endogenous expression of Crnde isoforms:



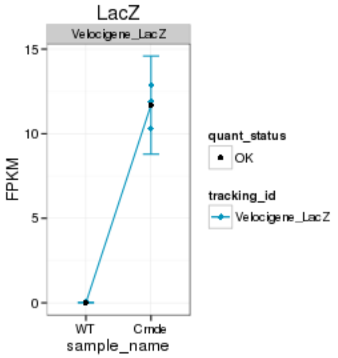
Barplot of gene expression:

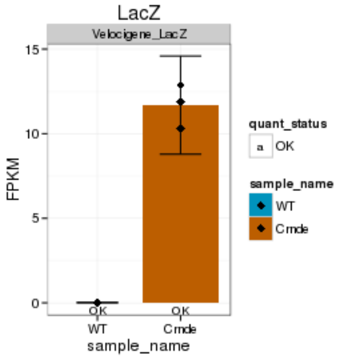


Barplot of isoform expression:



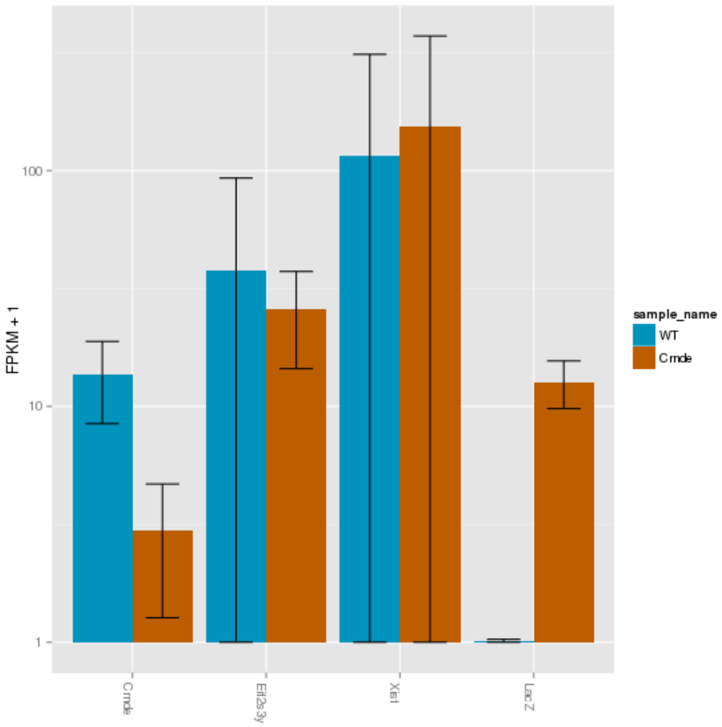
LacZ expression



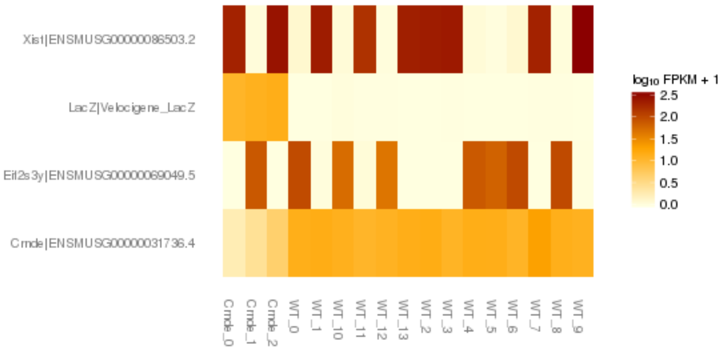


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

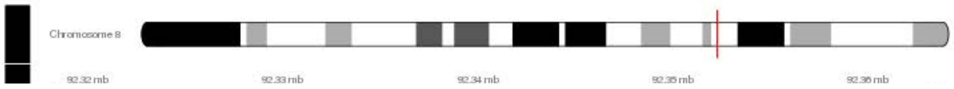
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):

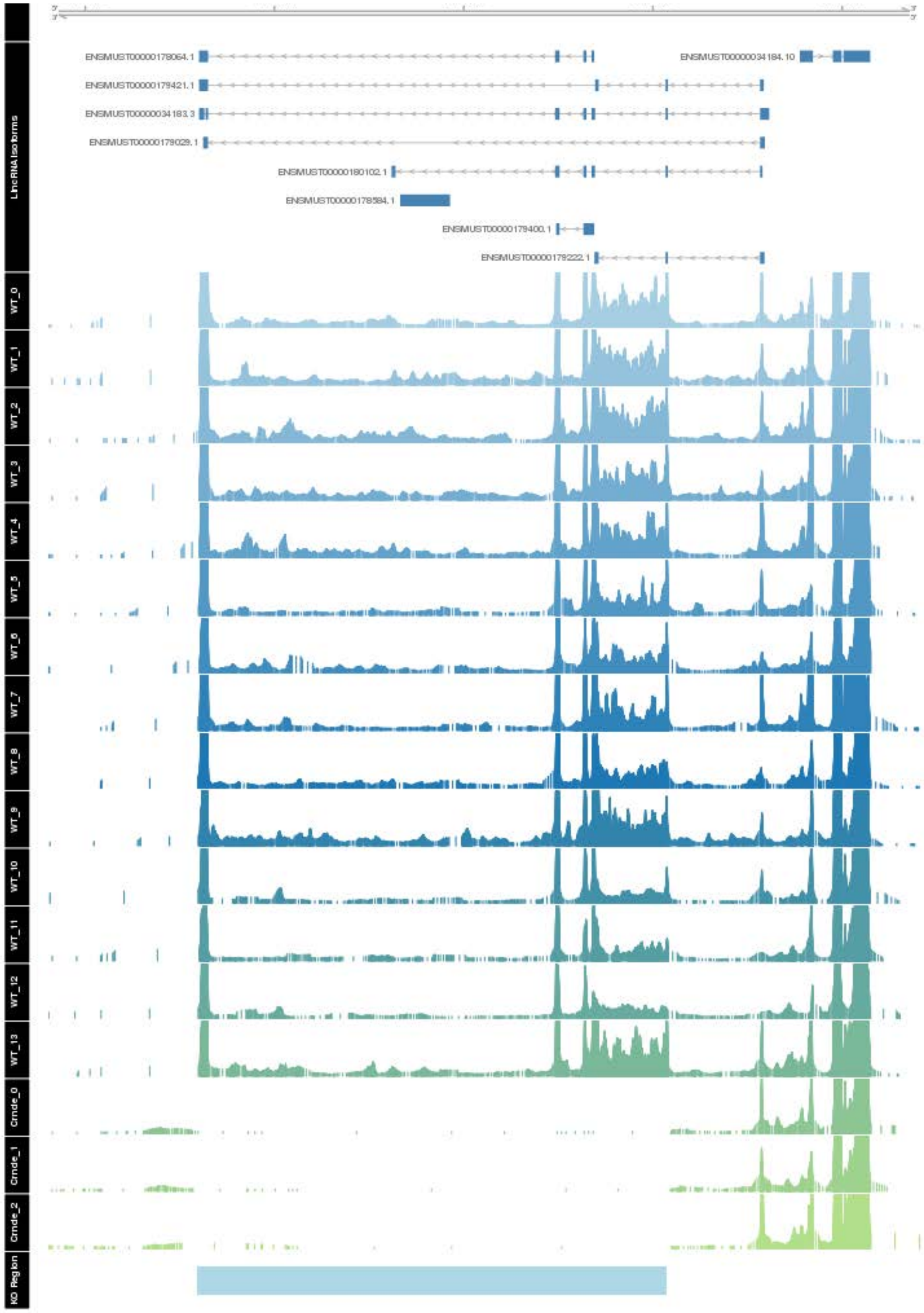


Expression heatmap:



Track visualization




5'
3'
LincRNA Isoforms
ENSMUST00000178064.1
ENSMUST00000034184.10
ENSMUST00000179421.1
ENSMUST00000034183.3
ENSMUST00000179029.1
ENSMUST00000180102.1
ENSMUST00000178584.1
ENSMUST00000179400.1
ENSMUST00000179222.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Crnde_0
Crnde_1
Crnde_2
KO Region

Differential Analysis

Differential Genes

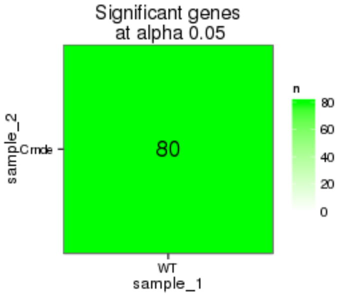
There are 80 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Col6a1
2	Col18a1
3	Col1a1
4	Lamb1
5	Nes
6	Polr2a
7	Nid1
8	Rplp1
9	Hspa8
10	Sulf1
11	Dync1h1
12	Lama2
13	Col6a2
14	Mrc2
15	Prpf8
16	Ntn1
17	Iqgap2
18	Nid2
19	Myh9
20	Igf2r
21	Lox
22	Fbn2
23	Rps14
24	Pdgfrb
25	Rps26
26	Col5a2
27	Col3a1
28	Fn1
29	Lamc1
30	Col5a1
31	Lamc3
32	Notch1
33	Lrp2
34	Fbn1
35	Lrp4
36	Notch2
37	Tnc

38 Svep1
39 Sorcs2
40 Col1a2
41 Aldh1l1
42 Emp1
43 Dera
44 Hddc3
45 Col4a5
46 Col4a1
47 Crnde
48 Itga11
49 Lama1
50 Fras1
51 Lum
52 Wnt8b
53 Frem2
54 Notch3
55 Spon1
56 Neurod2
57 Satb2
58 Atp5l
59 Bend6
60 Gm9493
61 Acp1
62 Mc4r
63 Gm9846
64 Hbb-y
65 Hbb-bh1
66 Lamb2
67 Hba-x
68 Capn11
69 Alox5ap
70 Dcc
71 Rps17
72 Rpl35
73 Scoc
74 Rpl36-ps3
75 3110035E14Rik
76 Flnc
77 Ptprz1
78 Fat1
79 Gm26924
80 Gm19980

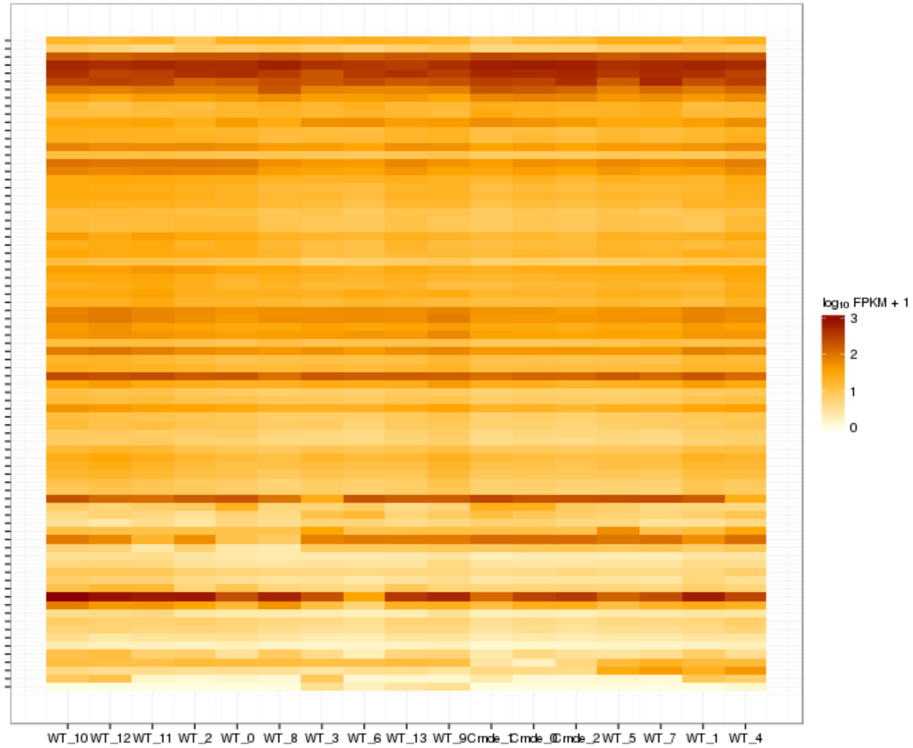
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

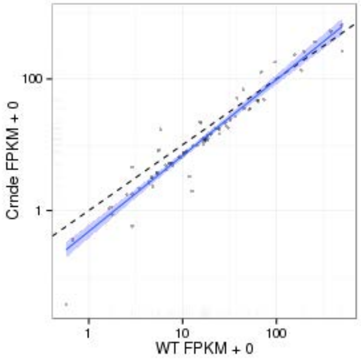


Significant genes with expression >50fpkm (any condition):(turned off)

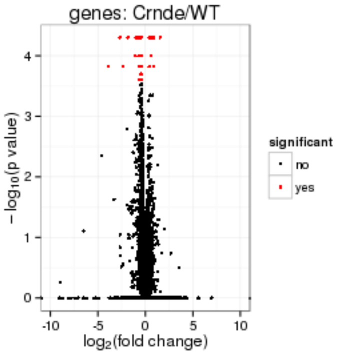
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

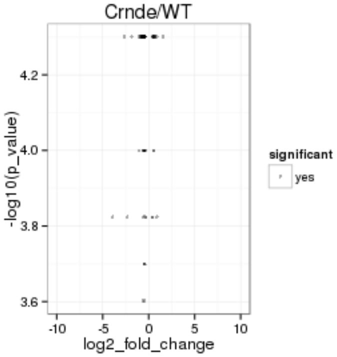
Scatter plot of significant genes only:



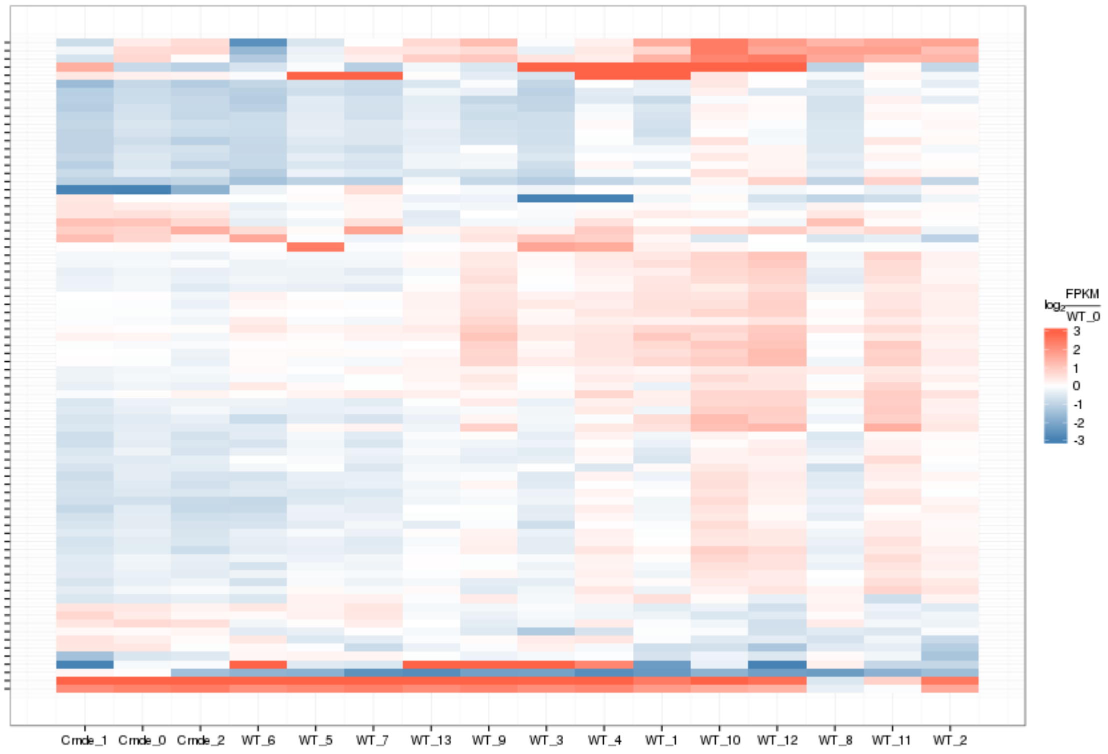
Volcano Plot



Volcano plot with significant genes only:



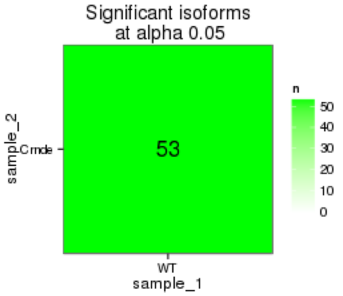
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:

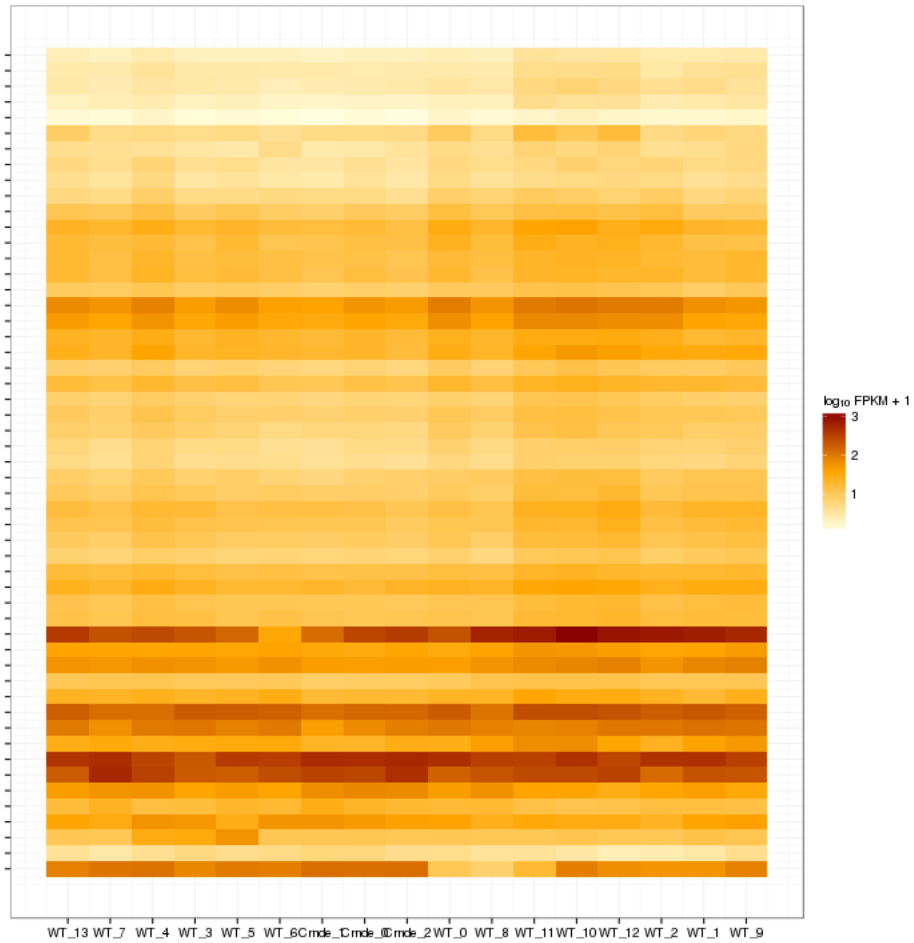


These isoforms are:

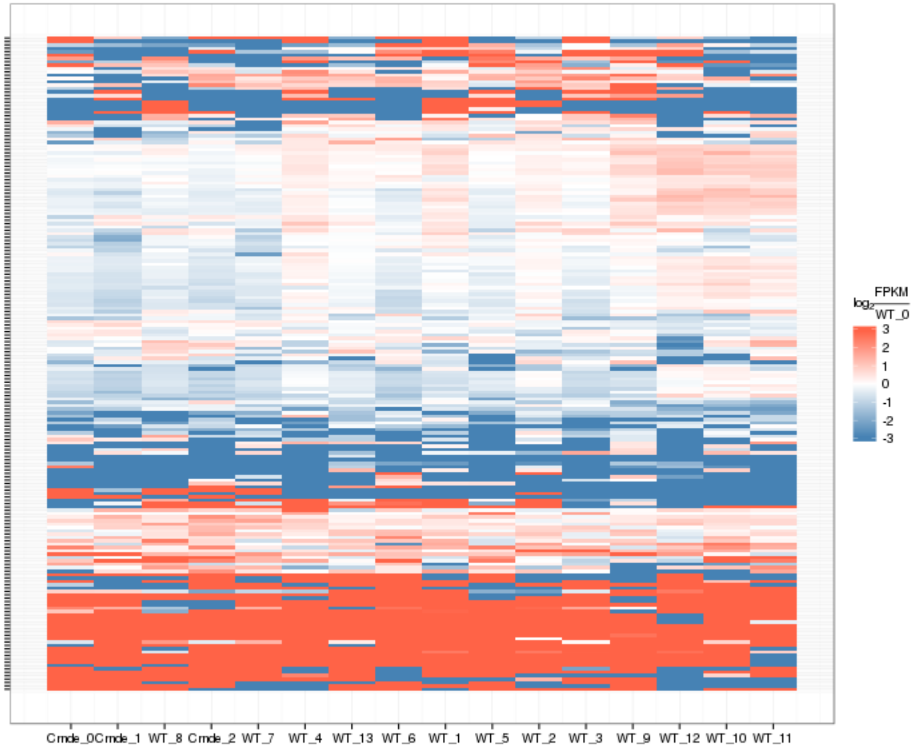
	isoAnnot$gene_short_name
1	Col6a1
2	Col1a1
3	Lamb1
4	Nid1
5	Rplp1
6	Cad
7	Dync1h1
8	Lama2
9	Mrc2
10	Myh9
11	Col2a1
12	Igf2r
13	Fbn2
14	Rps14
15	Pdgfrb
16	Col5a2
17	Col3a1
18	Fn1
19	Lamc1
20	Col5a1
21	Lamc3
22	Notch1
23	Lrp2
24	Fbn1
25	Lrp4
26	Notch2
27	Tnc
28	Svep1
29	Sorcs2
30	Col1a2
31	Emp1
32	Dera
33	Hddc3
34	Lama1
35	Fras1
36	Wnt8b
37	Frem2
38	Notch3
39	Neurod2
40	Lrp1

41 Reln
42 Gm9493
43 Hjurp
44 Mc4r
45 Col6a3
46 Hbb-y
47 Lamb2
48 Rpl36-ps3
49 3110035E14Rik
50 Gpr98
51 Fat1
52 Col22a1
53 Gm26924

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

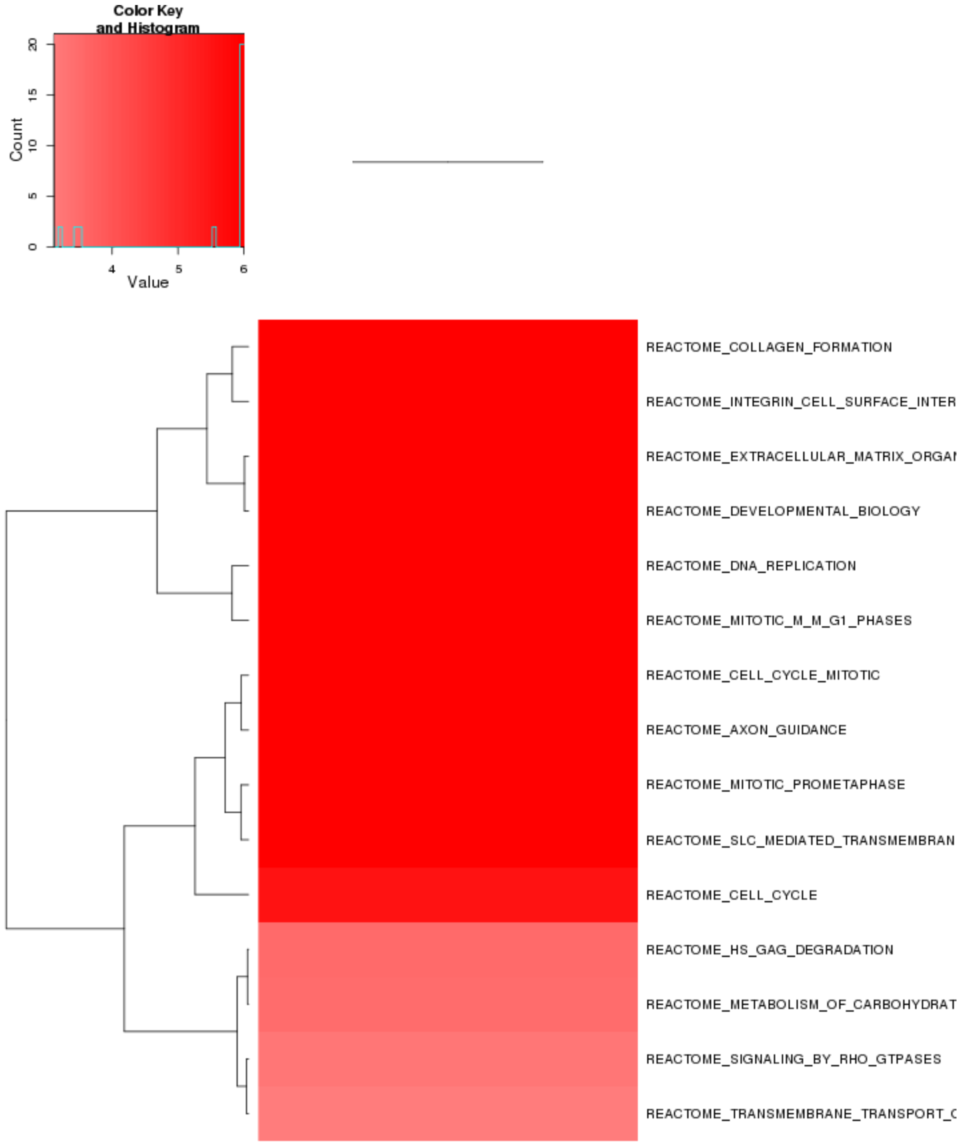
Biocarta enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

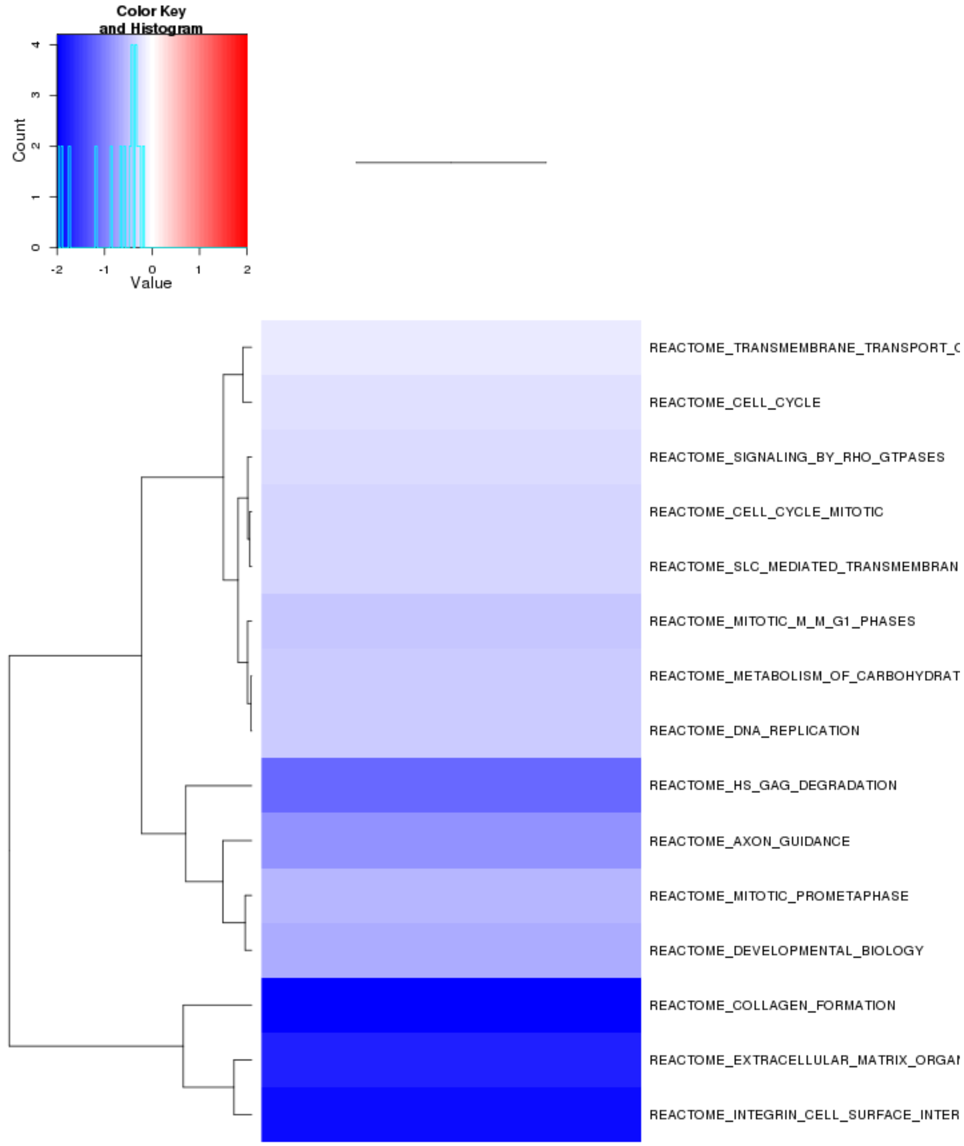
Biocarta zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

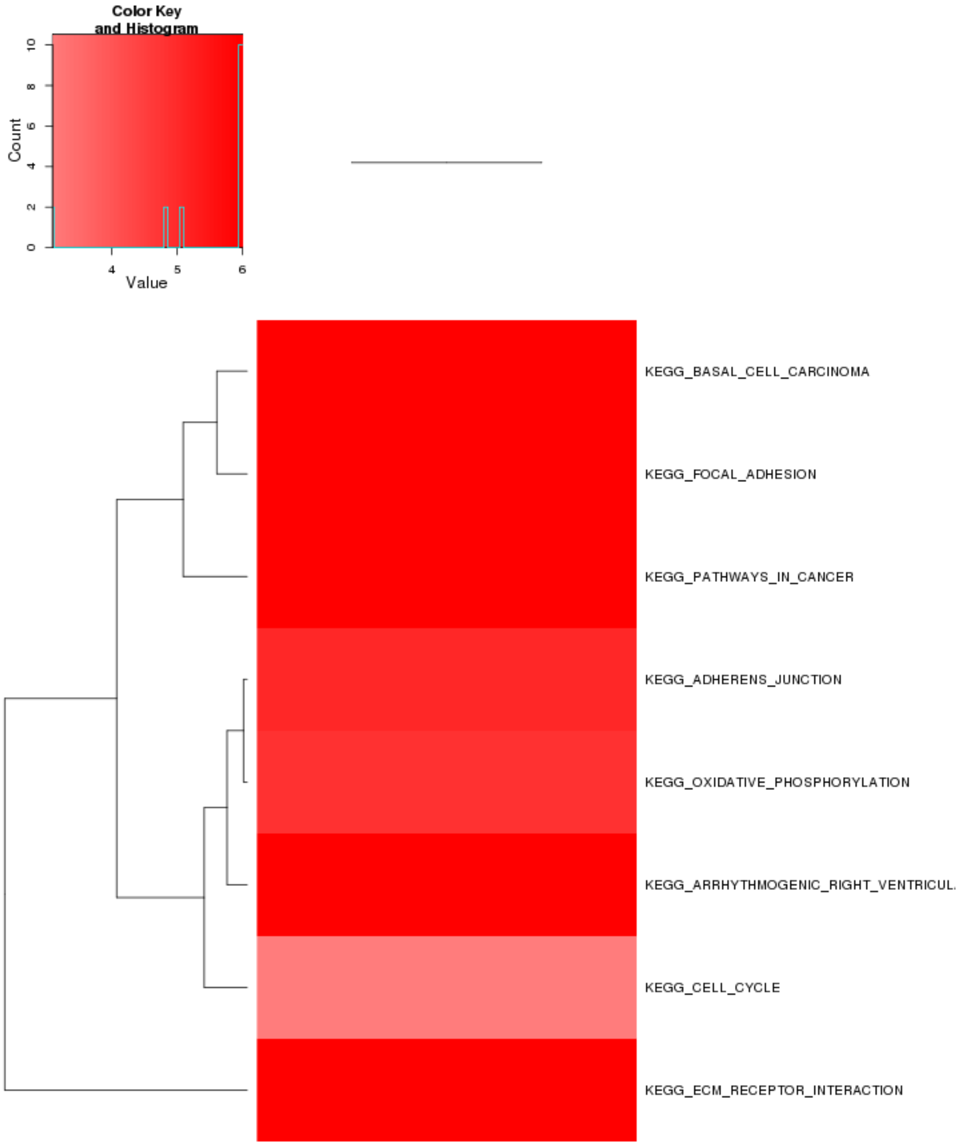
Reactome enrichment:



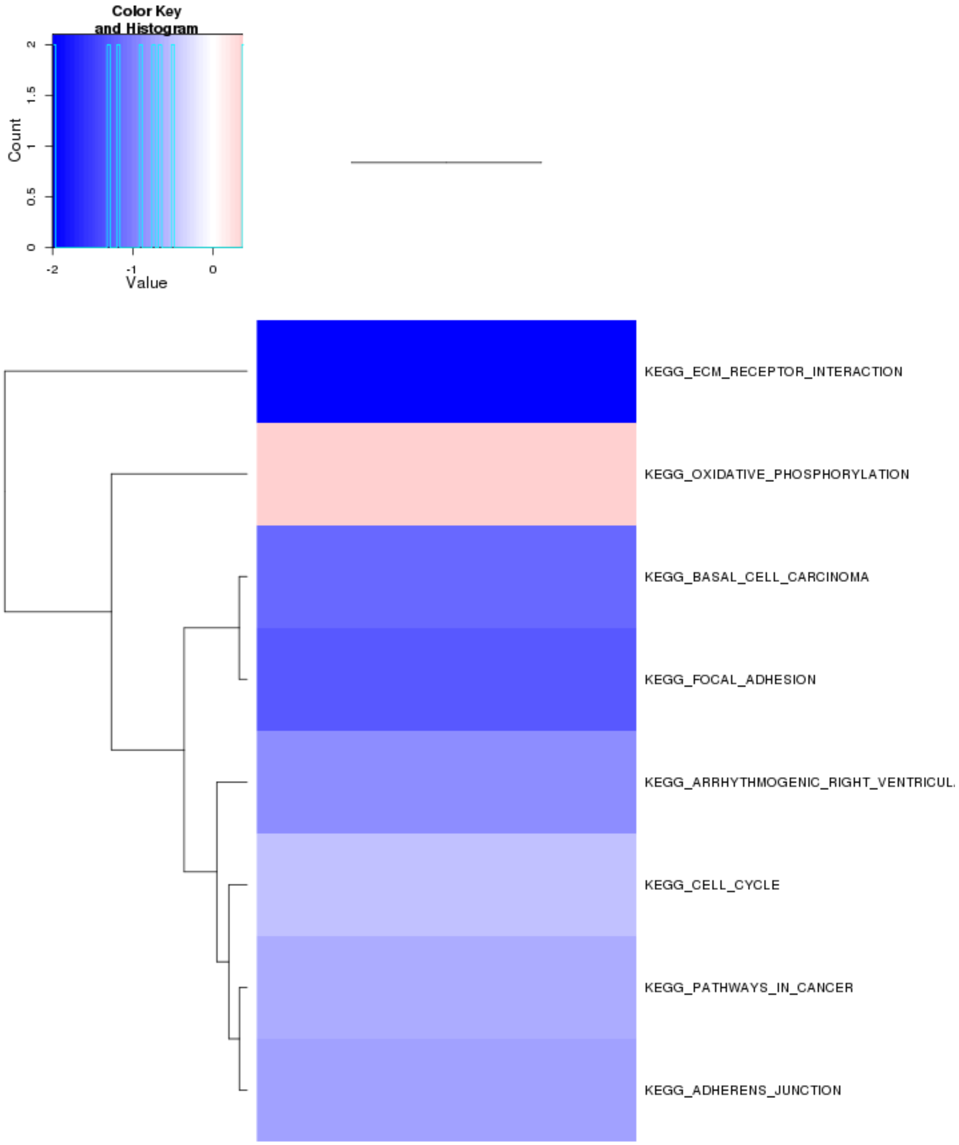
Reactome zscore:



Kegg enrichment:

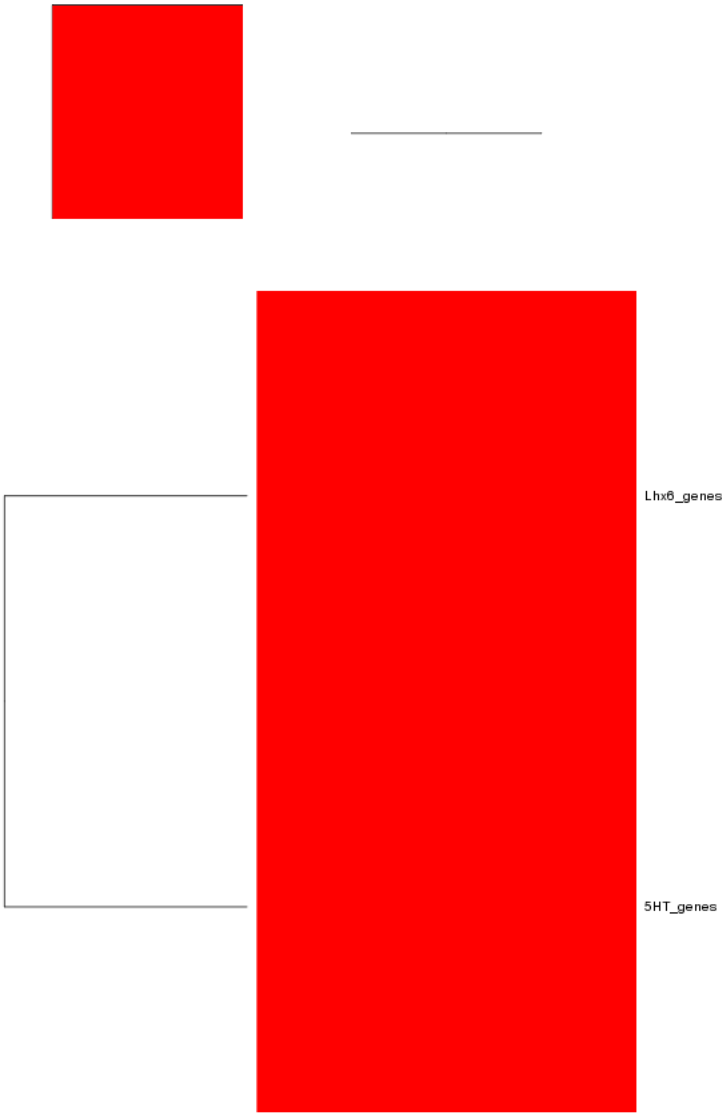

Color Key
and Histogram
Count
0
2
4
6
8
10
4
5
6
Value
KEGG_BASAL_CELL_CARCINOMA
KEGG_FOCAL_ADHESION
KEGG_PATHWAYS_IN_CANCER
KEGG_ADHERENS_JUNCTION
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICUL.
KEGG_CELL_CYCLE
KEGG_ECM_RECEPTOR_INTERACTION

Kegg zscore:

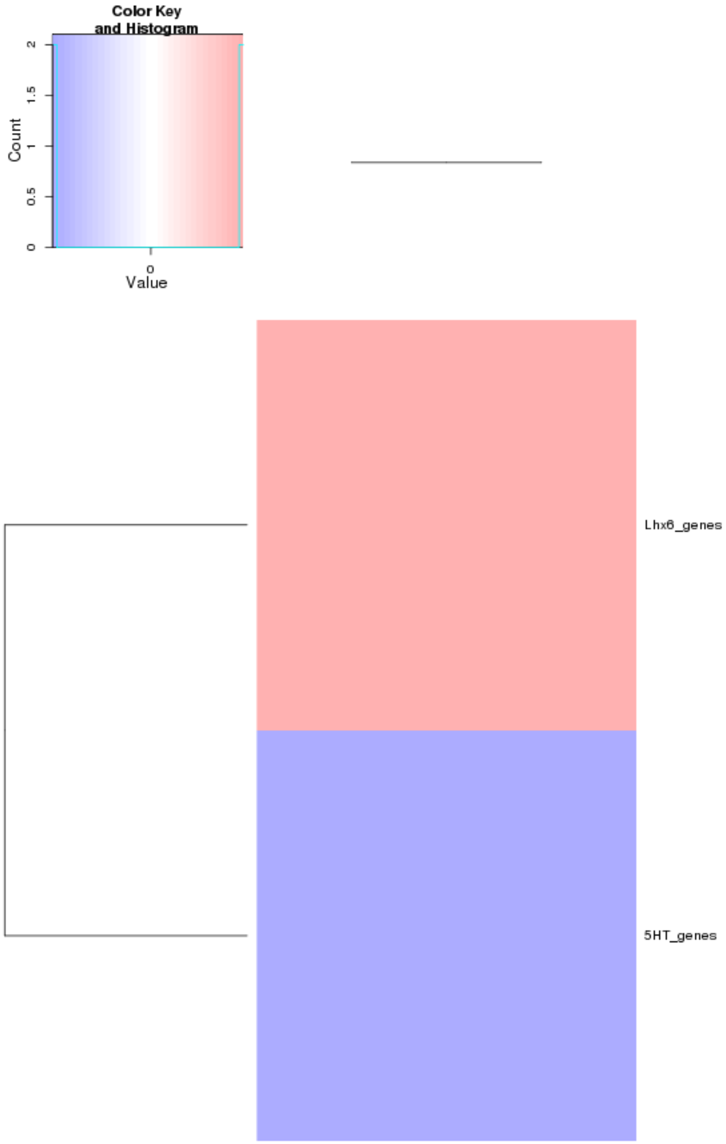


Interneuron enrichment:

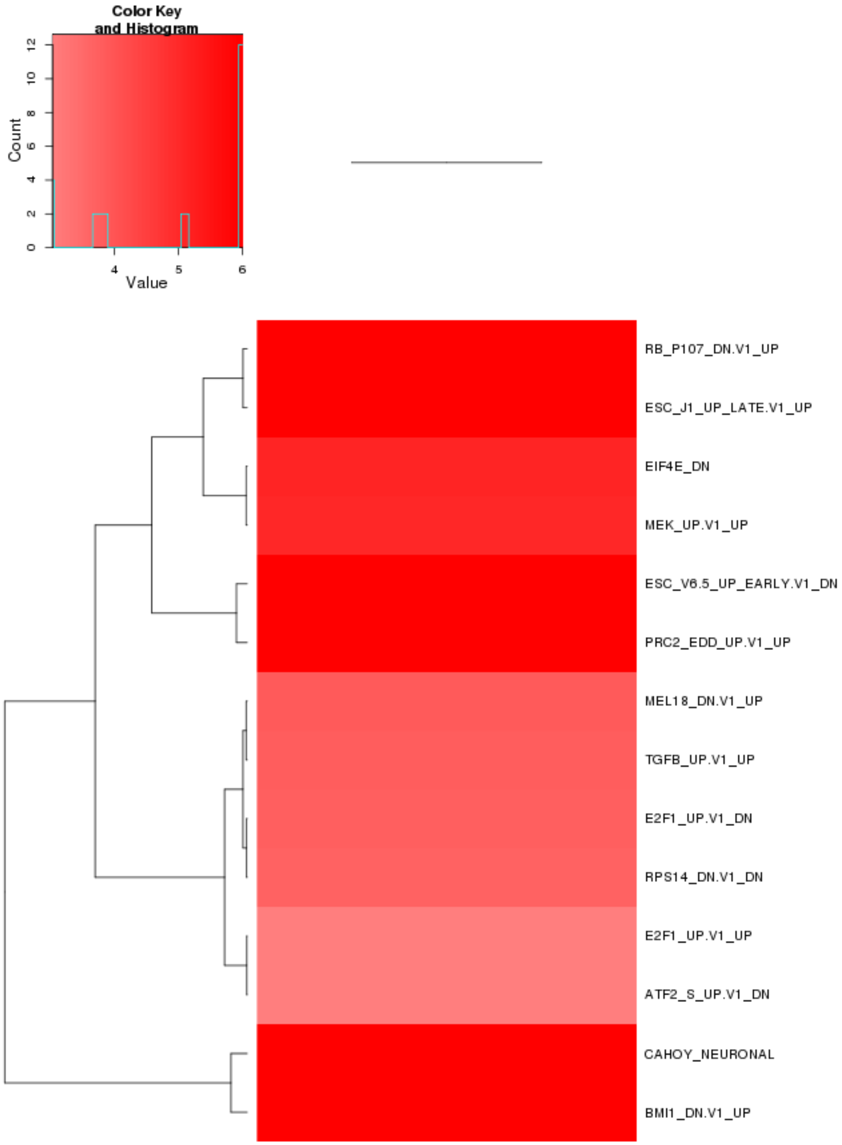
```
## Error: no locations are finite
```



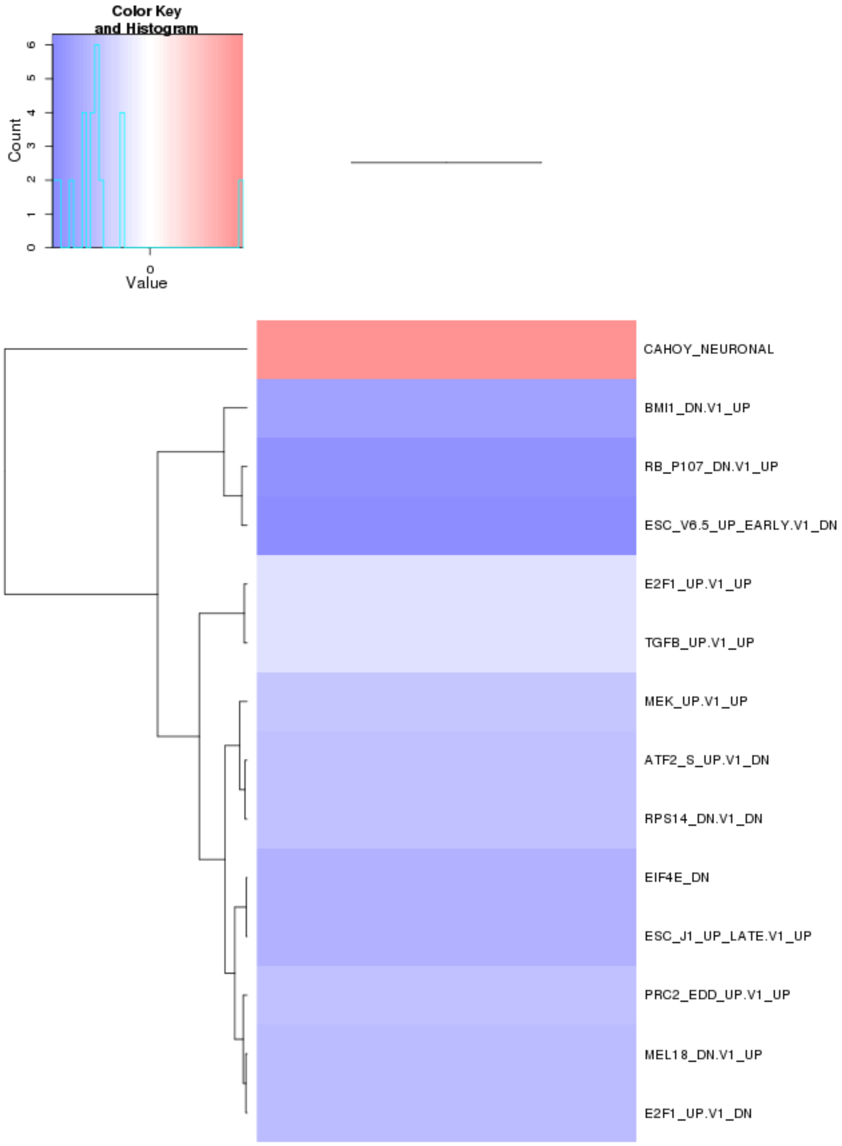
Interneuron zscore:



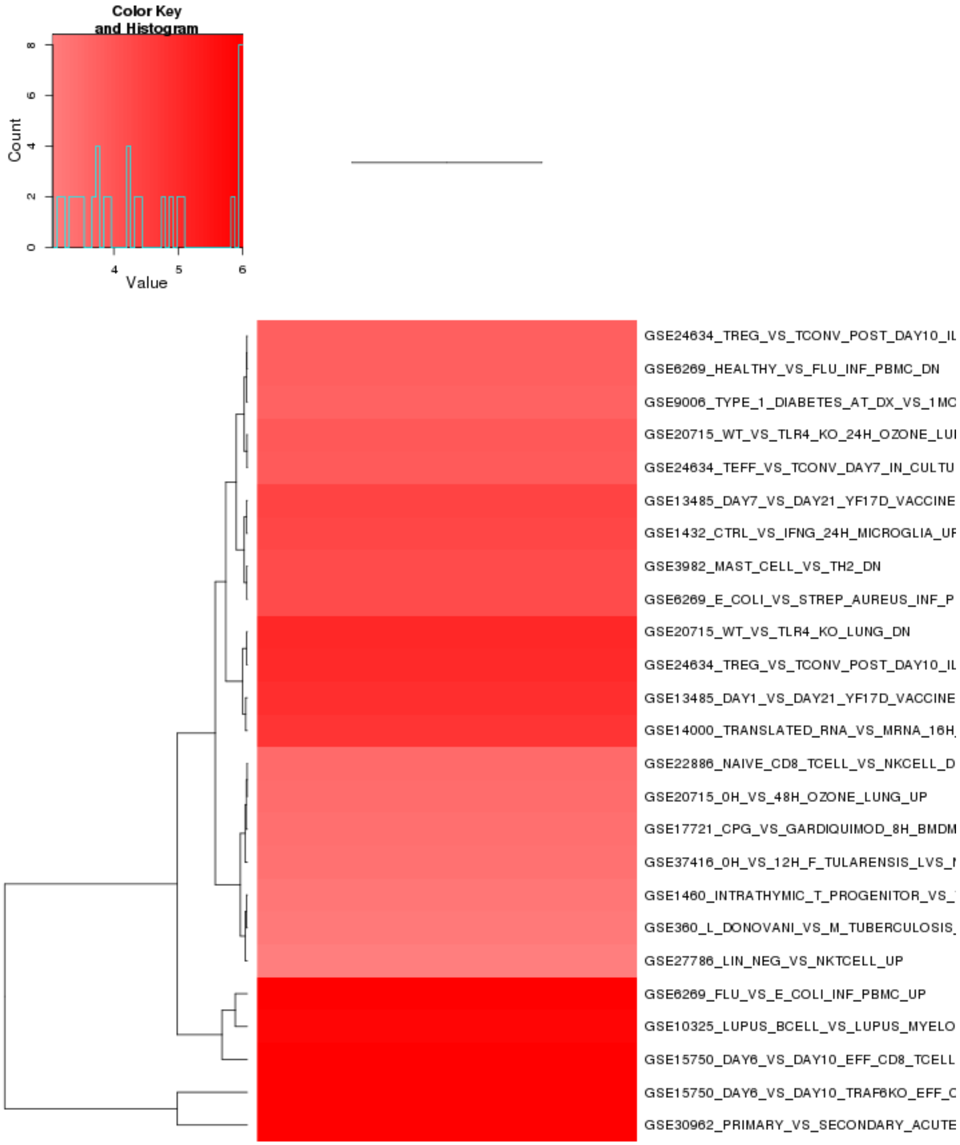
Oncogene enrichment:



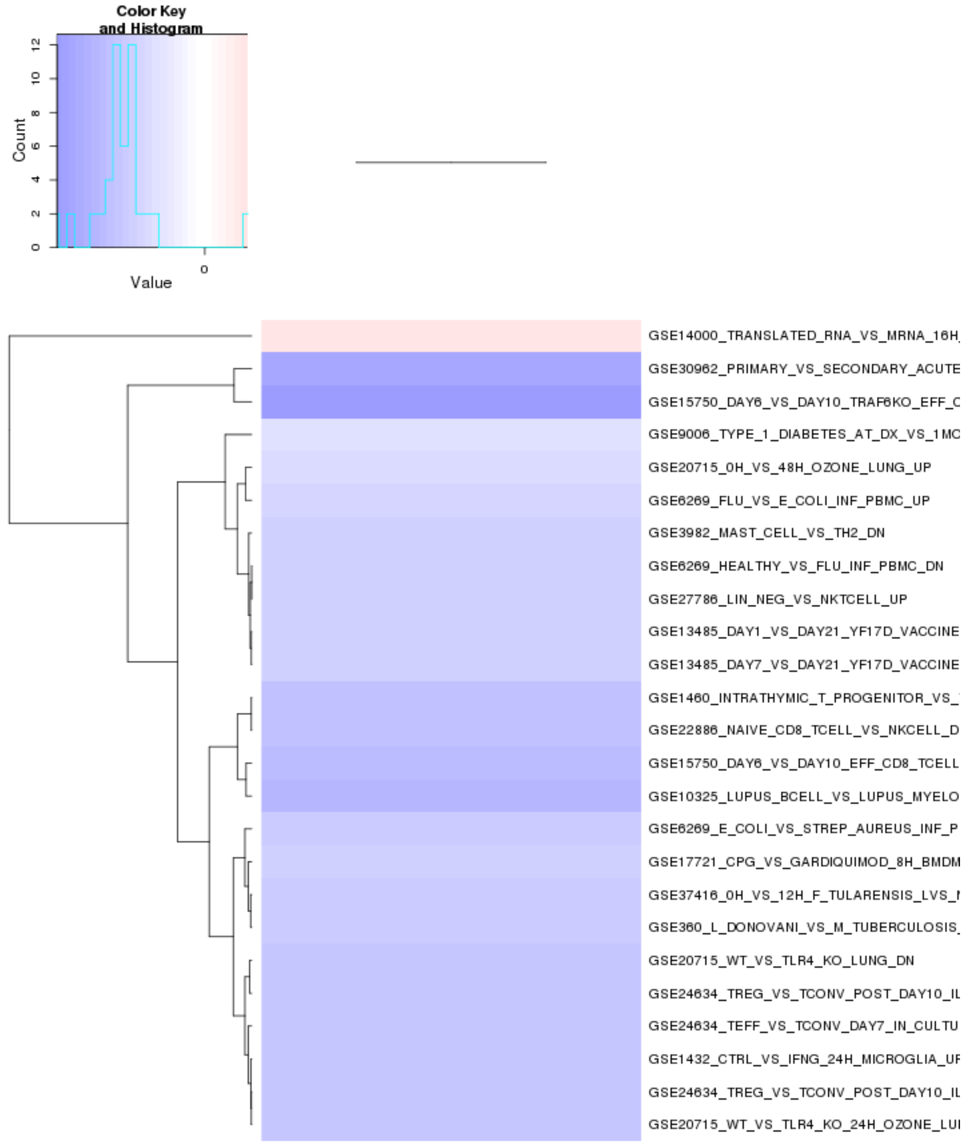
Oncogene zscore:



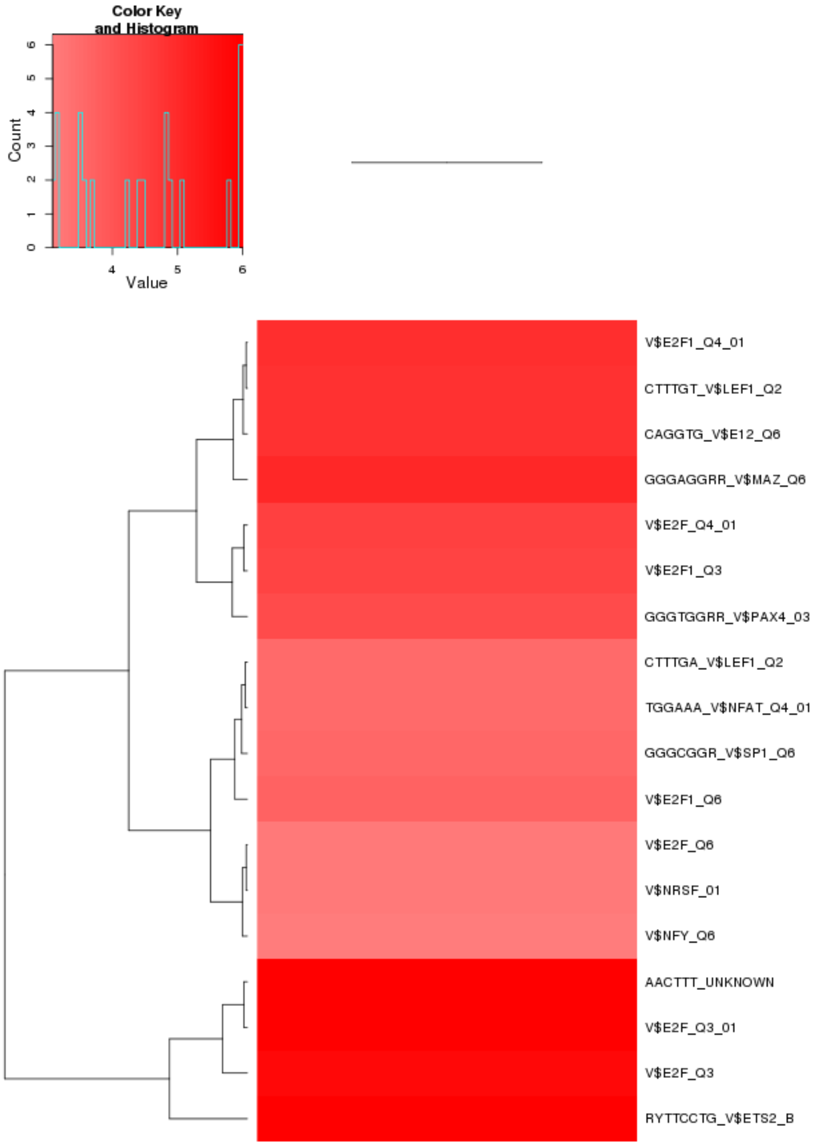
Immuno enrichment:



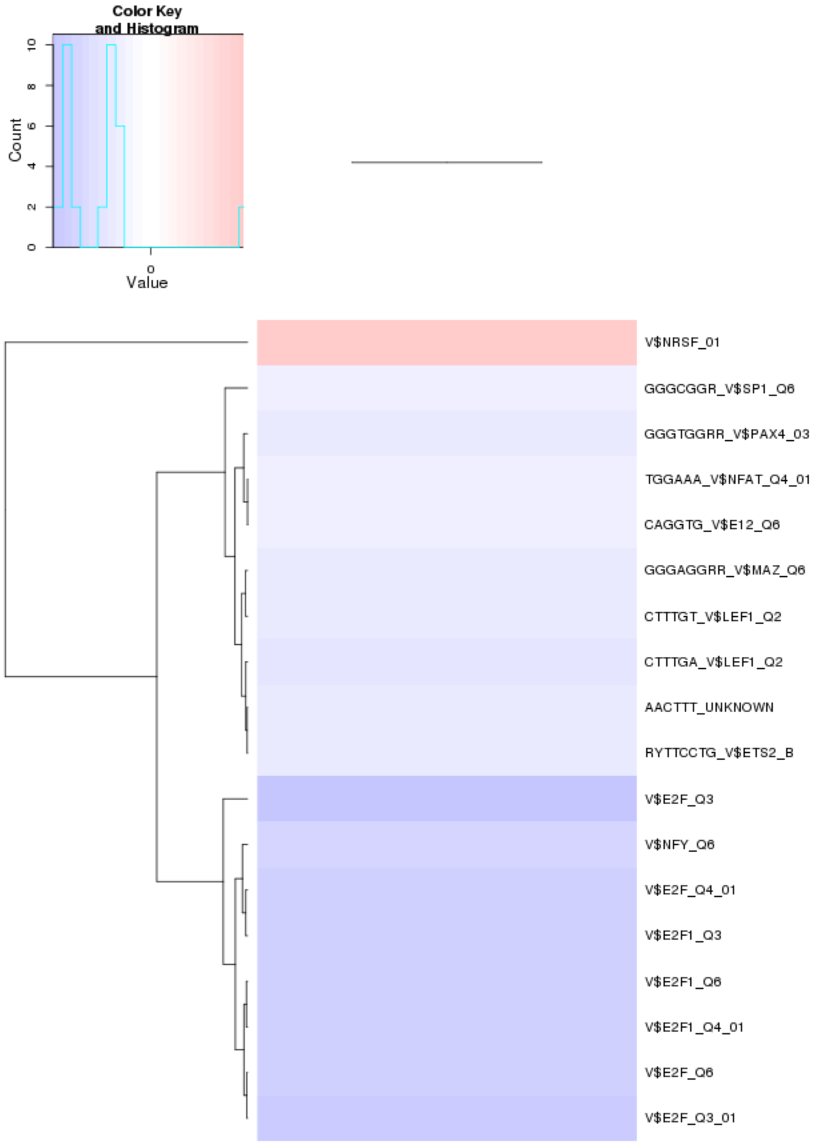
Immuno zscore:



TF enrichment:


Color Key
and Histogram
Count
0
1
2
3
4
5
6
Value
4
5
6
V$E2F1_Q4_01
CTTTGT_V$LEF1_Q2
CAGGTG_V$E12_Q6
GGGAGGRR_V$MAZ_Q6
V$E2F_Q4_01
V$E2F1_Q3
GGGTGGRR_V$PAX4_03
CTTTGA_V$LEF1_Q2
TGGAAA_V$NFAT_Q4_01
GGGCGGR_V$SP1_Q6
V$E2F1_Q6
V$E2F_Q6
V$NRSF_01
V$NFY_Q6
AACTTT_UNKNOWN
V$E2F_Q3_01
V$E2F_Q3
RYTTCCTG_V$ETS2_B

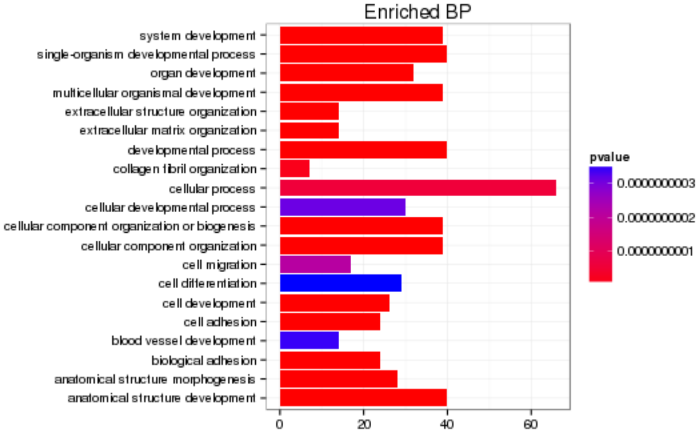
TF zscore:

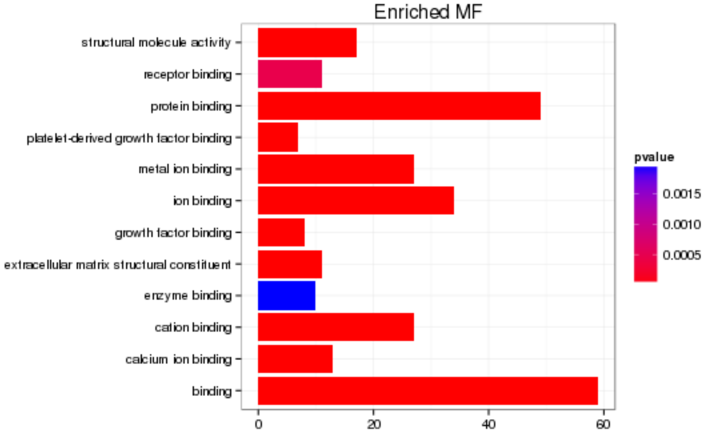


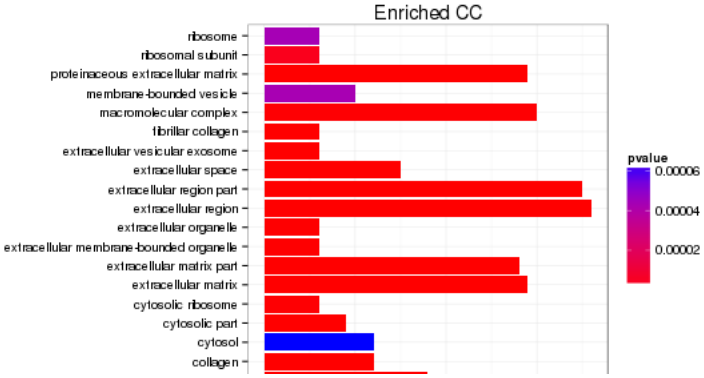
GO enrichment

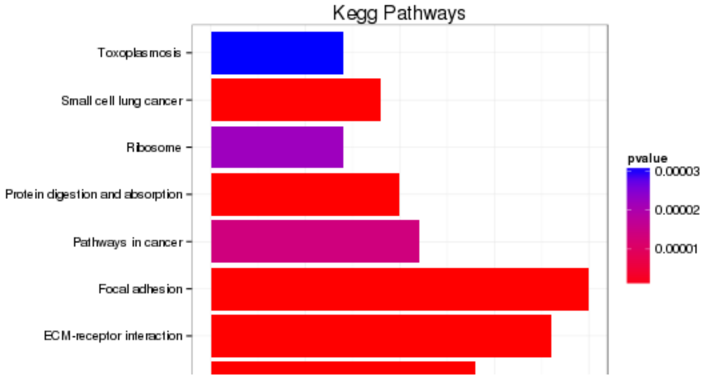
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

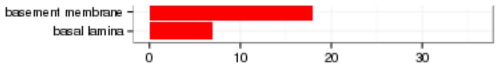
```
## [1] "ERROR: The estimated pi0 <= 0. Check that you have valid p-values or use another lambda method."
```

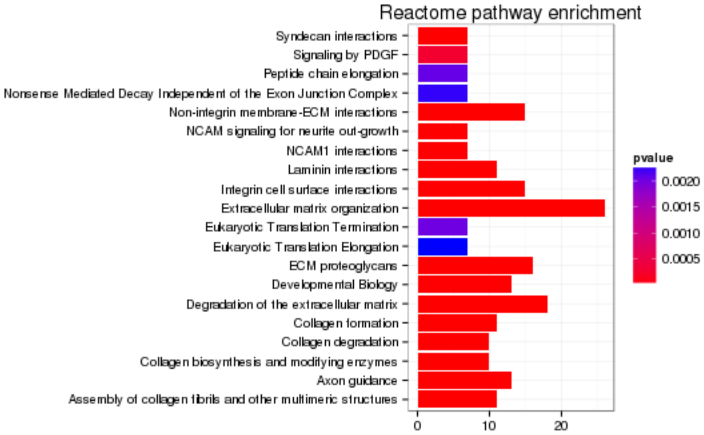

Enriched BP
system development
single-organism developmental process
organ development
multicellular organismal development
extracellular structure organization
extracellular matrix organization
developmental process
collagen fibril organization
cellular process
cellular developmental process
cellular component organization or biogenesis
cellular component organization
cell migration
cell differentiation
cell development
cell adhesion
blood vessel development
biological adhesion
anatomical structure morphogenesis
anatomical structure development
0
20
40
60
pvalue
0.0000000003
0.0000000002
0.0000000001


Enriched MF
structural molecule activity
receptor binding
protein binding
platelet-derived growth factor binding
metal ion binding
ion binding
growth factor binding
extracellular matrix structural constituent
enzyme binding
cation binding
calcium ion binding
binding
0
20
40
60
pvalue
0.0015
0.0010
0.0005

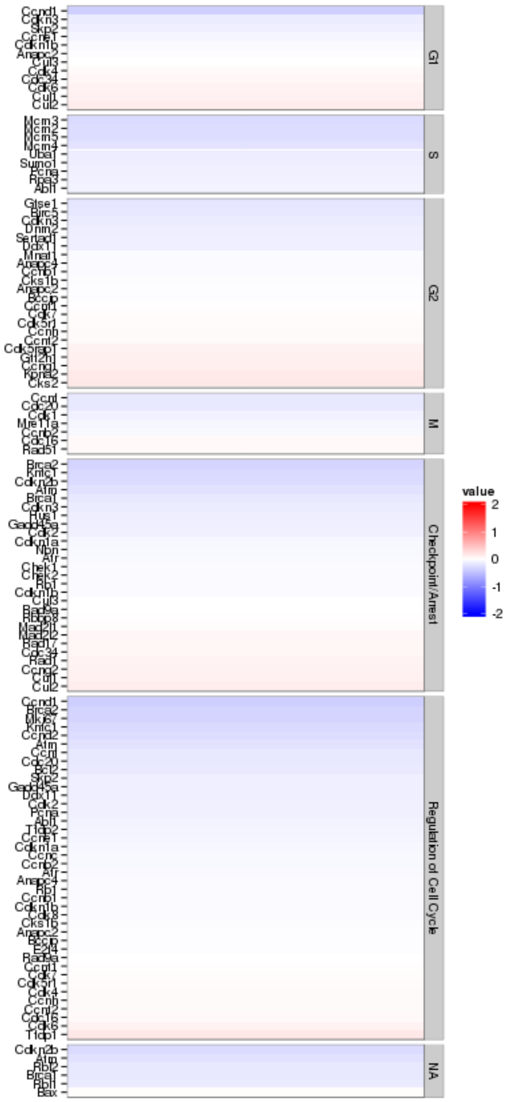

Enriched CC
ribosome
ribosomal subunit
proteinaceous extracellular matrix
membrane-bounded vesicle
macromolecular complex
fibrillar collagen
extracellular vesicular exosome
extracellular space
extracellular region part
extracellular region
extracellular organelle
extracellular membrane-bounded organelle
extracellular matrix part
extracellular matrix
cytosolic ribosome
cytosolic part
cytosol
collagen
pvalue
0.00006
0.00004
0.00002


Kegg Pathways
Toxoplasmosis
Small cell lung cancer
Ribosome
Protein digestion and absorption
Pathways in cancer
Focal adhesion
ECM-receptor interaction
pvalue
0.00003
0.00002
0.00001

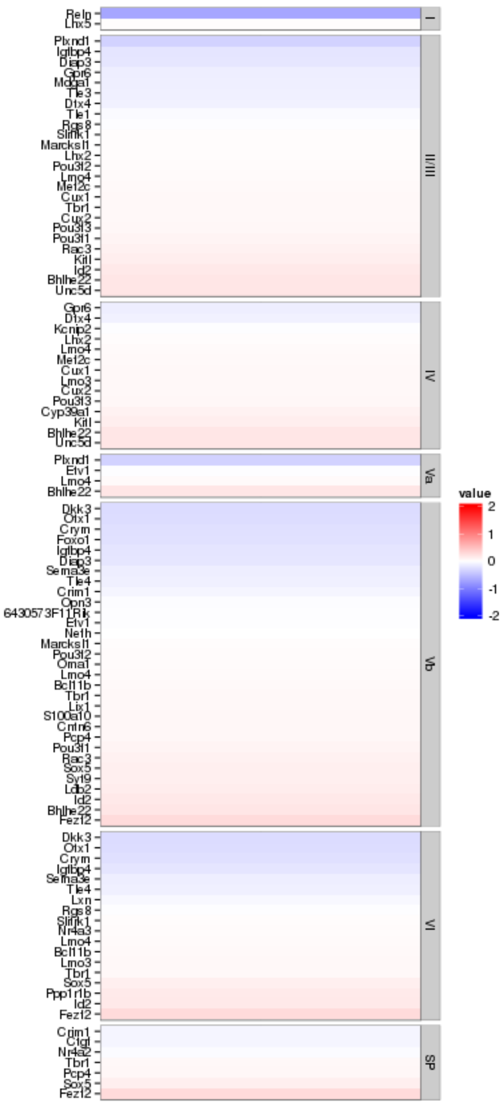




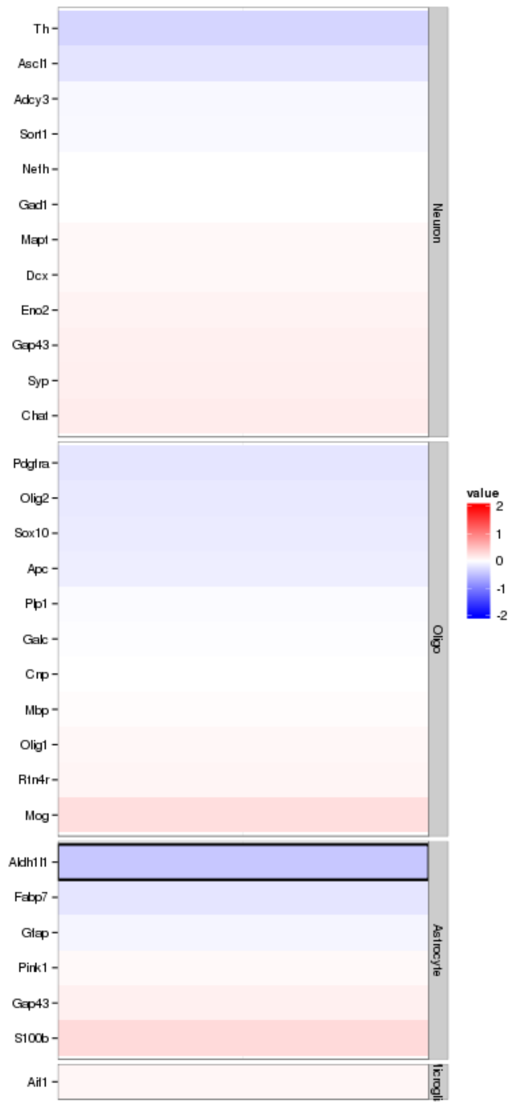
Enrichment or depletion for stage-specific cell cycle markers



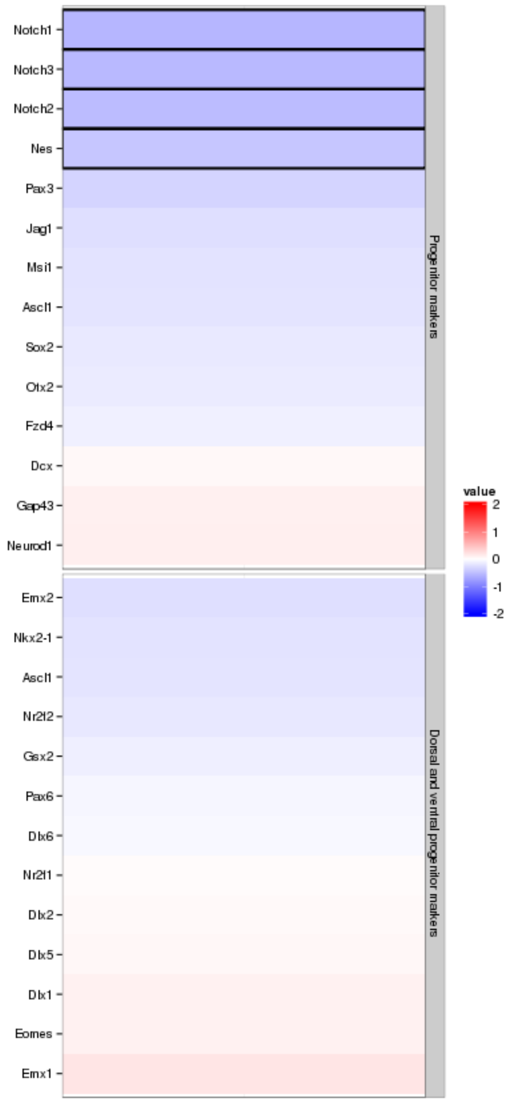
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



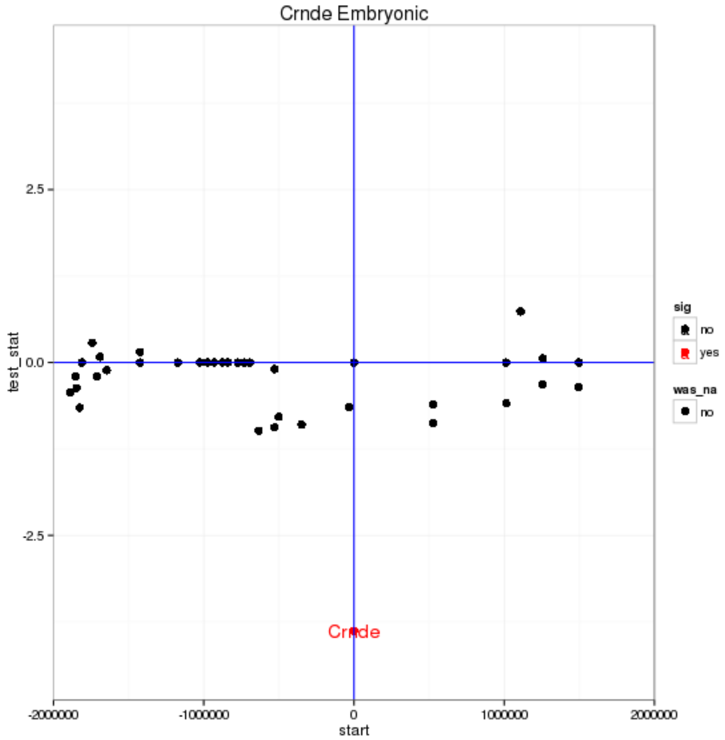
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15	JR793
16	JR790
17	JR830

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	31799500.00	1.28	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	31799500.00	1.11	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	31799500.00	1.24	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	31799500.00	1.30	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	31799500.00	1.22	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	31799500.00	0.90	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	31799500.00	0.99	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	31799500.00	0.93	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	31799500.00	0.87	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	31799500.00	0.97	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	31799500.00	0.82	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	31799500.00	0.81	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	31799500.00	0.69	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	31799500.00	1.23	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR793/abundances.cxb	Crnde	0	Crnde_0	36520100.00	31799500.00	1.16	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR790/abundances.cxb	Crnde	1	Crnde_1	27555700.00	31799500.00	0.87	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR830/abundances.cxb	Crnde	2	Crnde_2	28630200.00	31799500.00	0.91	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1      
##  [2] stringr_0.6.2   
##  [3] seqbias_1.10.0  
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##          param
## 1     cmd_line
## 2      version
## 3  SVN_revision
## 4 boost_version
## 5       genome
##
## 1 cuffdiff -p 10 -L WT,Crnde -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Crnde_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/BrainMap/dat
## 2
## 3
## 4
## 5
```

Eldr KO vs WT (Adult)

This file shows the wt-v-ko comparison for Eldr.

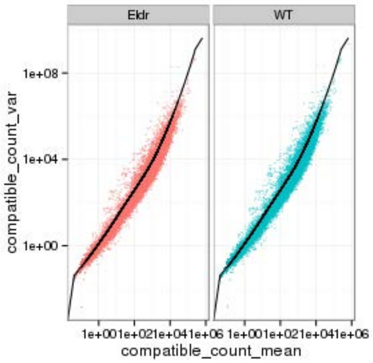
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

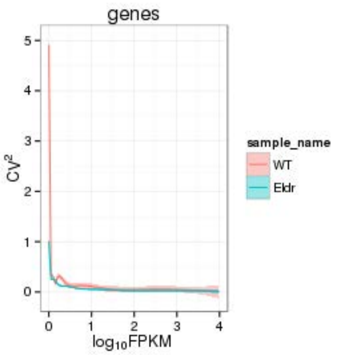
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



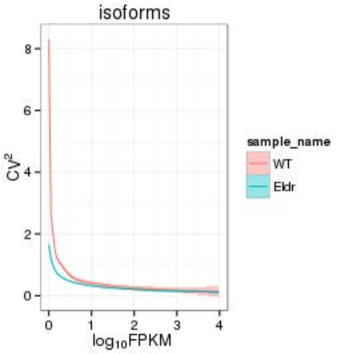
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

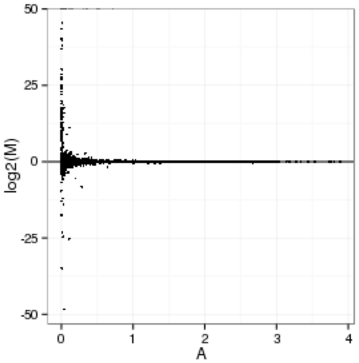
Genes:



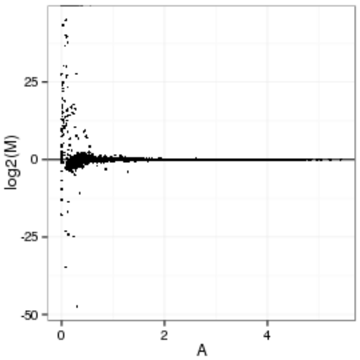
Isoforms:



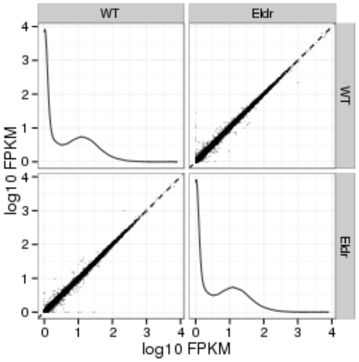
MvA plot



MvA plot counts



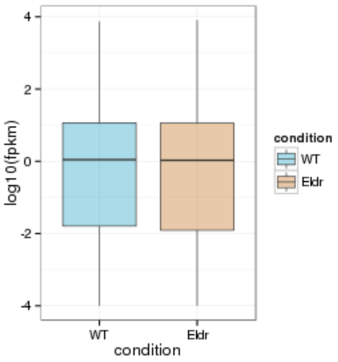
Scatterplot matrix



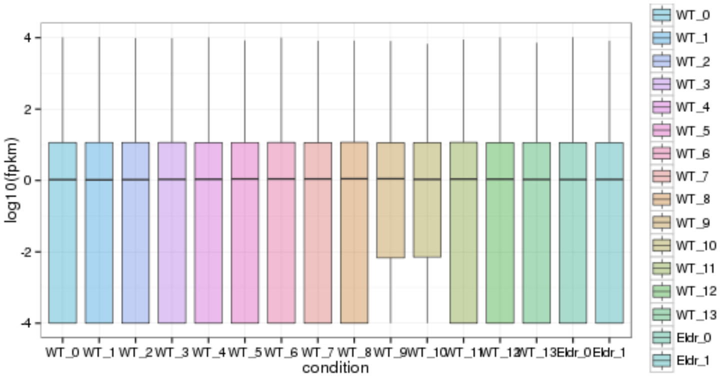
Distributions

Boxplots

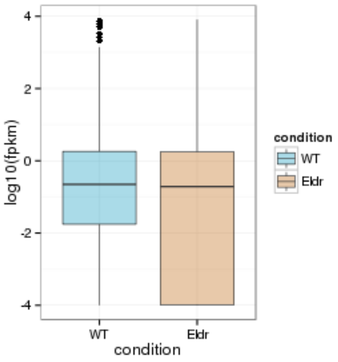
Boxplot (genes)



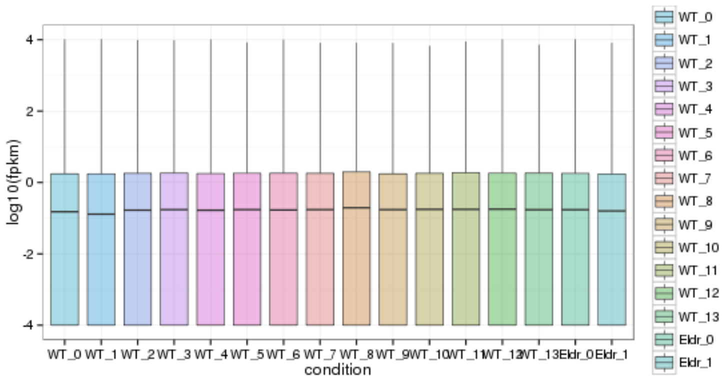
Boxplot (genes, replicates)



Boxplot (isoforms)

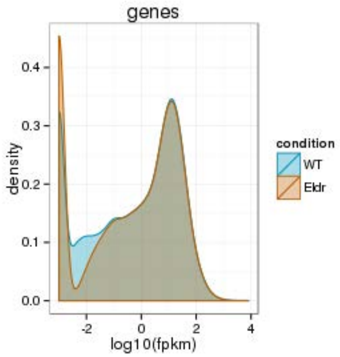


Boxplot (isoforms, replicates)

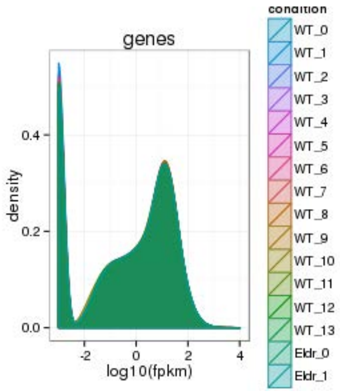


Density

Density (genes)

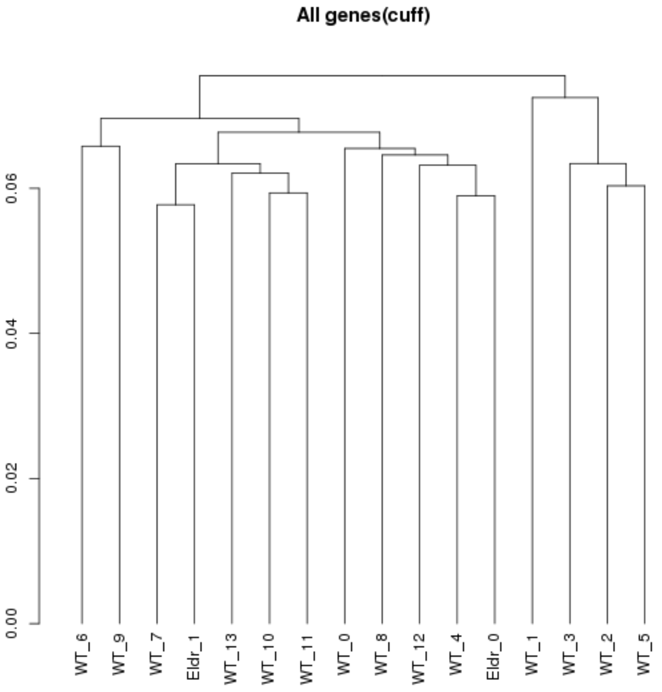


Density (genes, replicates)



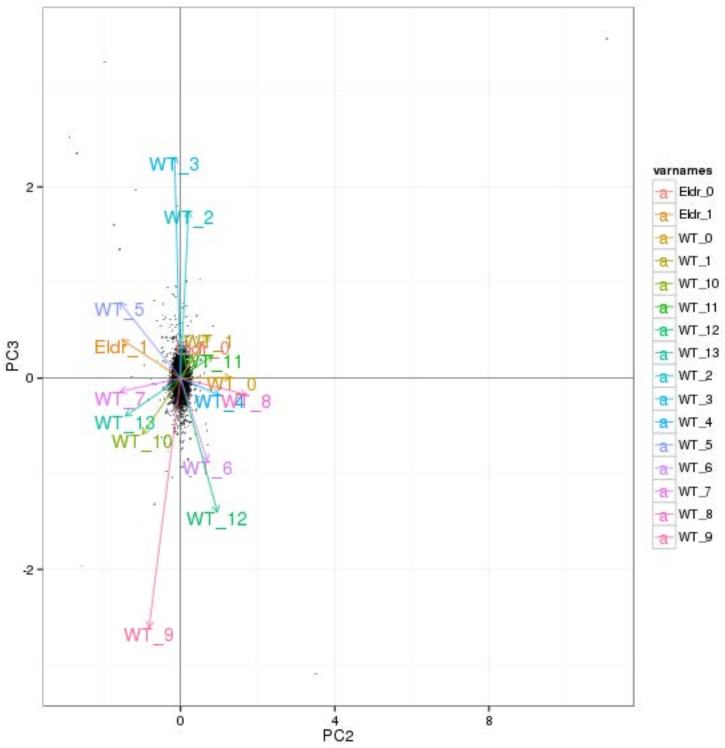
Clustering

Replicate Clusters



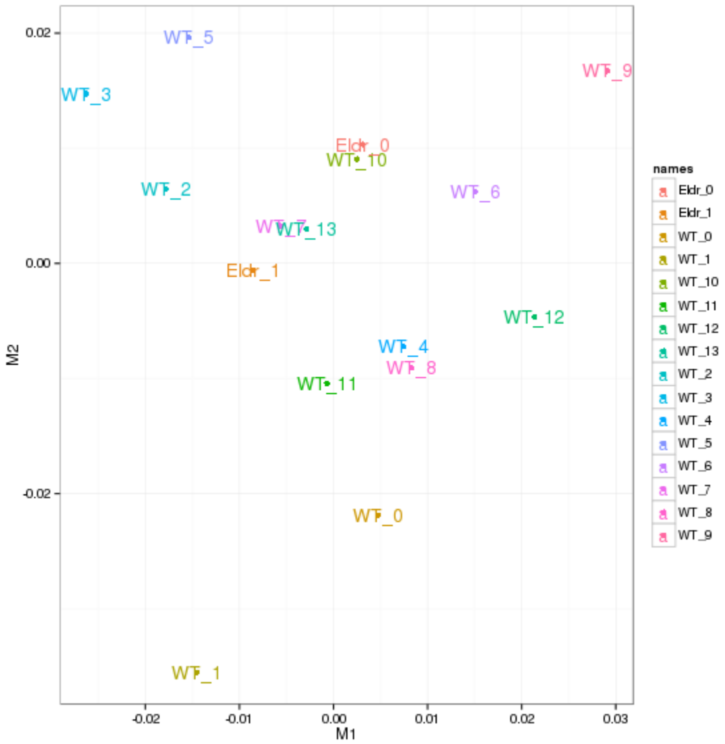
```
## NULL
```

PCA (genes)



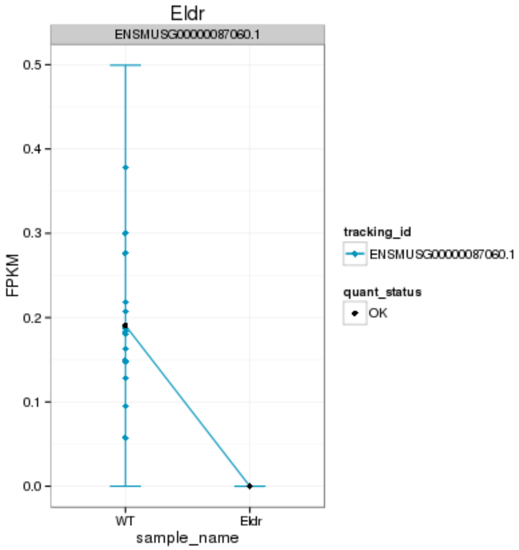
PC3
PC2
2
0
-2
0
4
8
WT_3
WT_2
WT_5
Eldr_1
WT_1
Eldr_0
WT_11
WT_0
WT_4
WT_8
WT_7
WT_13
WT_10
WT_6
WT_12
WT_9
varnames
Eldr_0
Eldr_1
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

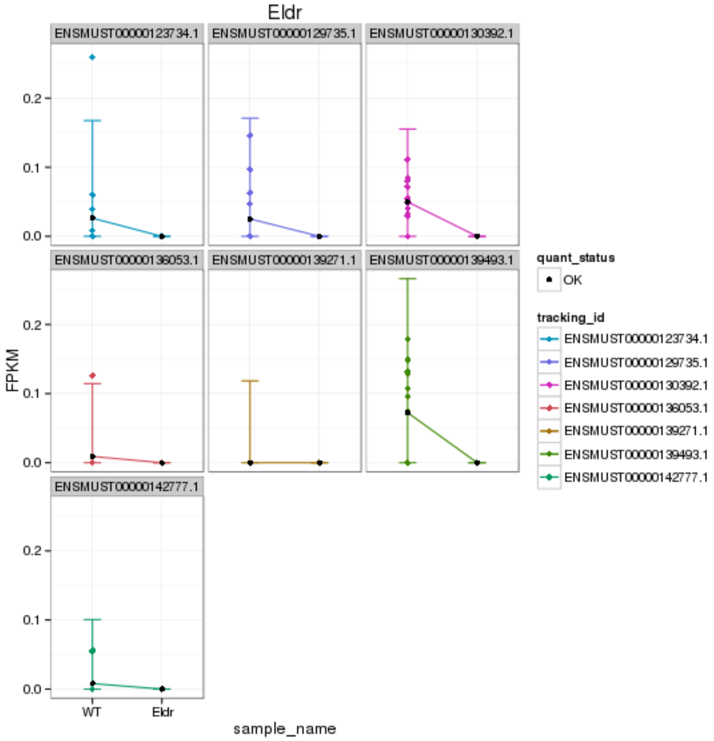


KO assessment

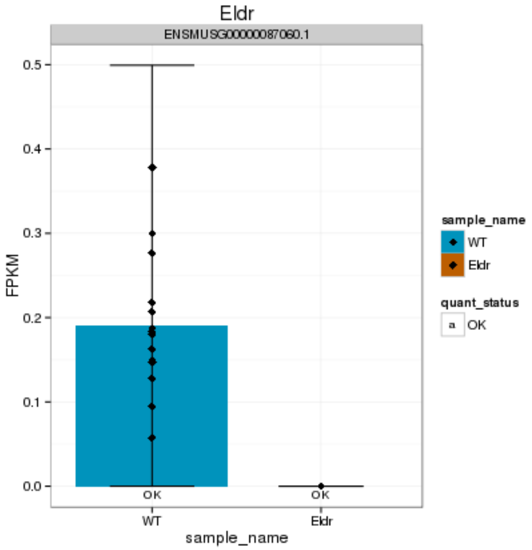
Endogenous lncRNA expression



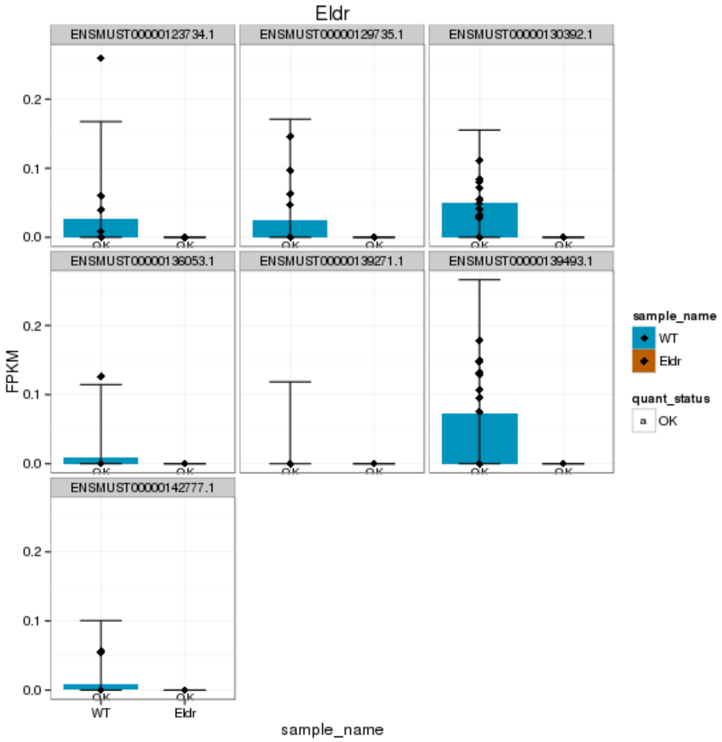
Endogenous expression of Eldr isoforms:



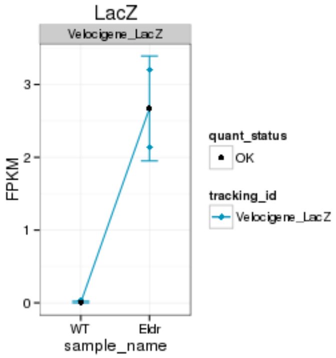
Barplot of gene expression:

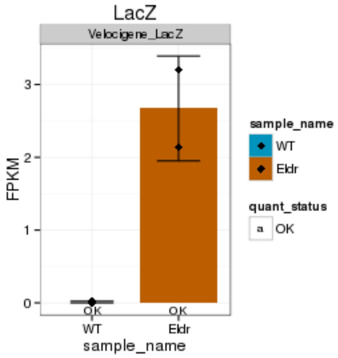


Barplot of isoform expression:



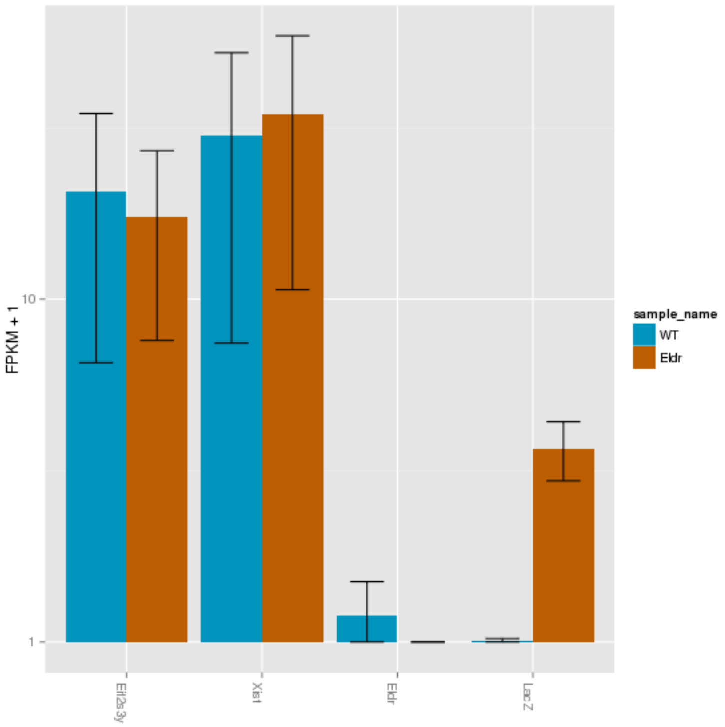
LacZ expression



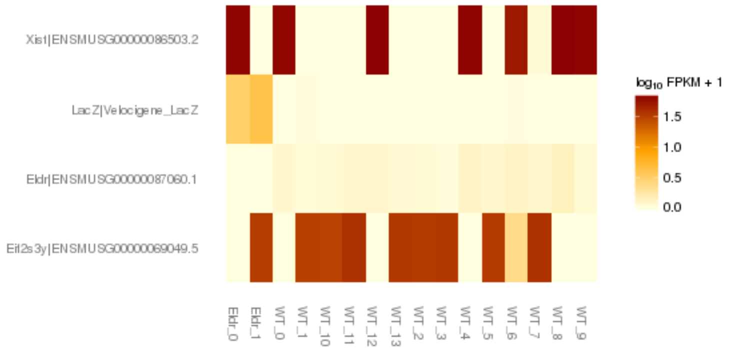


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

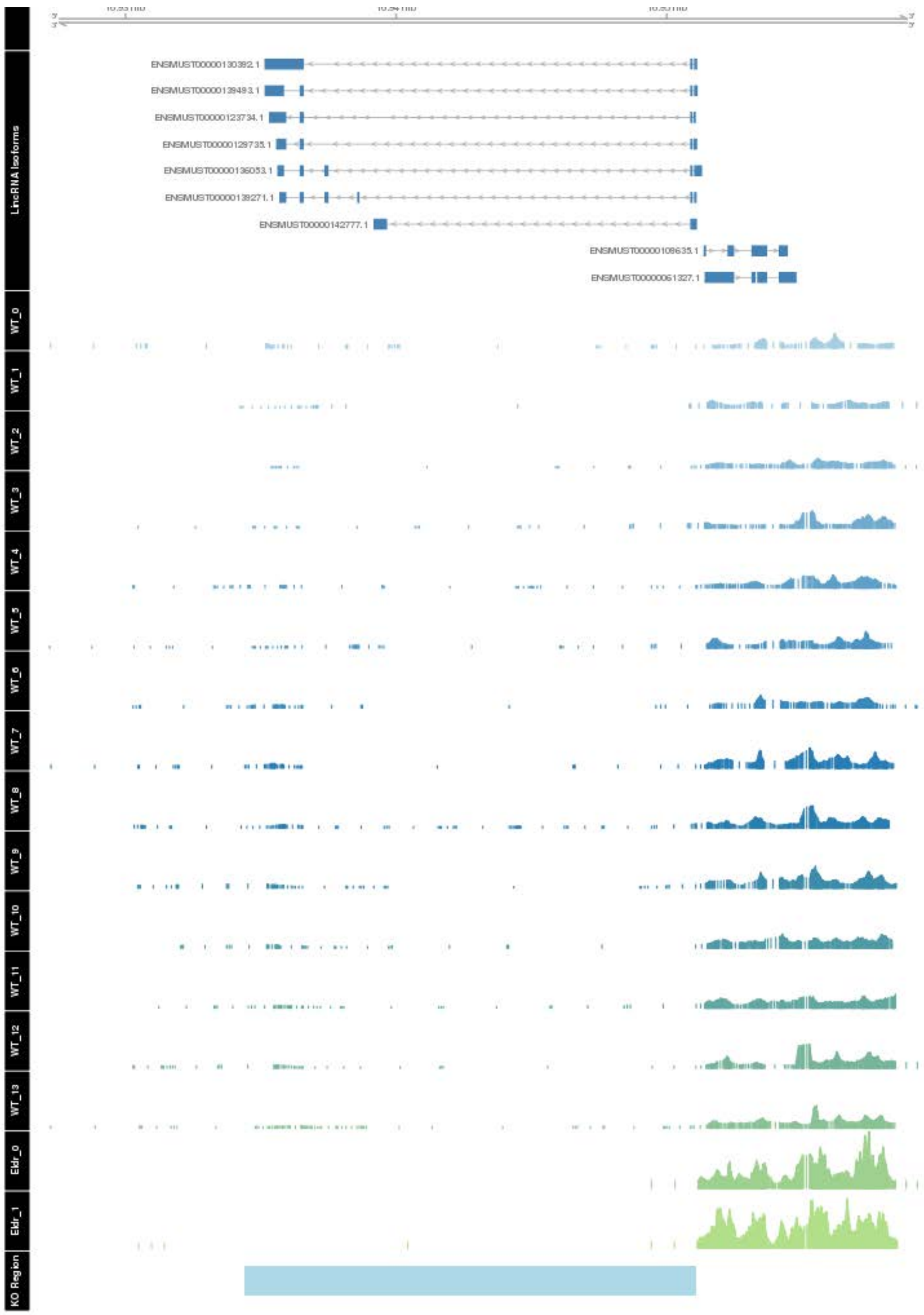
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


10.53 mb
10.54 mb
10.55 mb
5'
3'
LincRNA Isoforms
ENSMUST00000130392.1
ENSMUST00000139493.1
ENSMUST00000123734.1
ENSMUST00000129735.1
ENSMUST00000136053.1
ENSMUST00000139271.1
ENSMUST00000142777.1
ENSMUST00000109635.1
ENSMUST00000061327.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Eklf_0
Eklf_1
KO Region

Differential Analysis

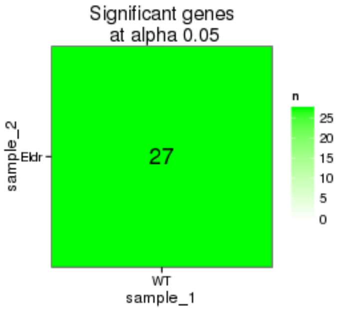
Differential Genes

There are 27 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Nes
2	Ubc
3	Tpgs1
4	Adi1
5	Fos
6	Nr4a1
7	Rps14
8	Rps24
9	Nr4a3
10	Ndufs5
11	Arhgap27
12	Egr2
13	Egr1
14	Pcsk1n
15	Klhl42
16	C1qtnf4
17	Acp1
18	Fbxo48
19	Junb
20	Fat2
21	Capn11
22	Tpt1
23	Egr4
24	Gm9008
25	Wdfy1
26	Apold1
27	AA465934

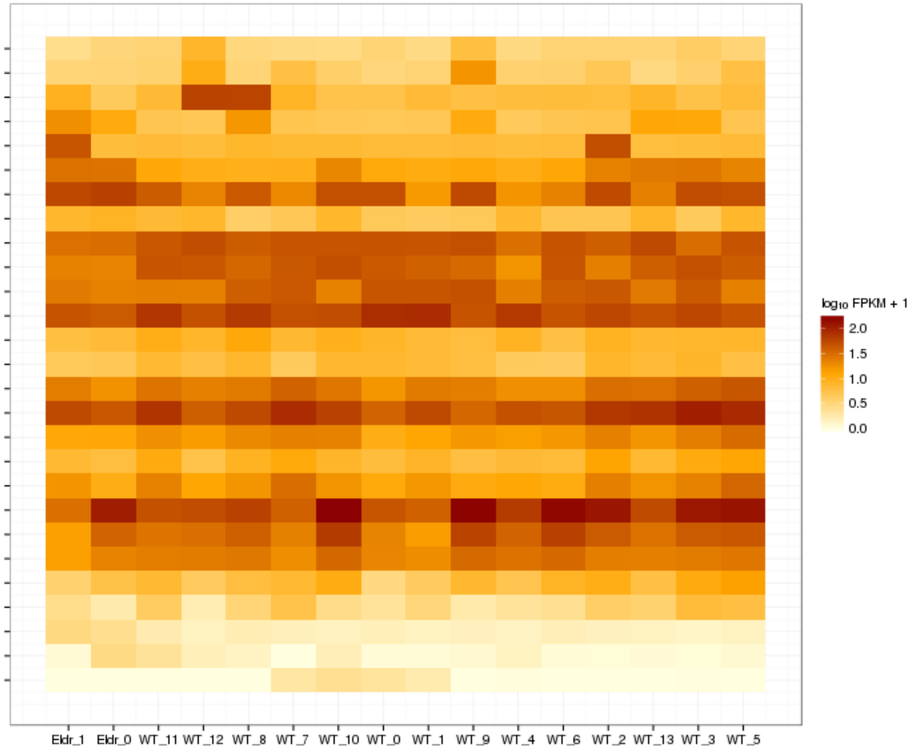
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

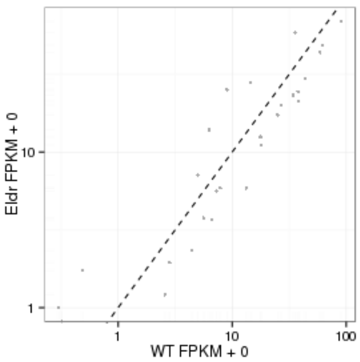


Significant genes with expression >50fpkm (any condition):(turned off)

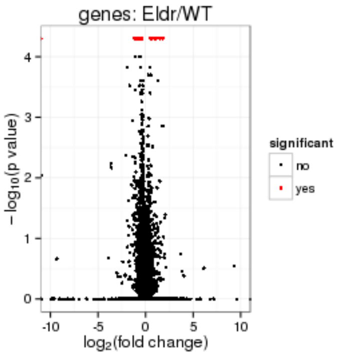
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

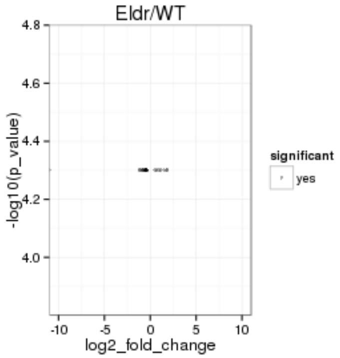
Scatter plot of significant genes only:



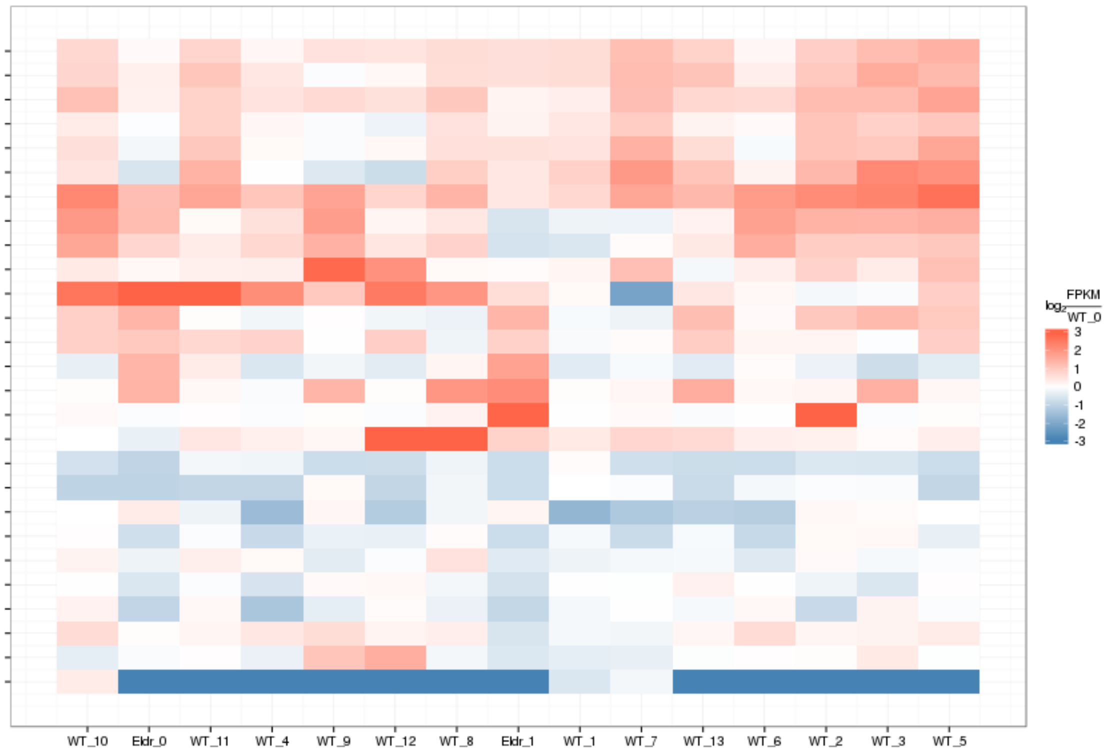
Volcano Plot



Volcano plot with significant genes only:



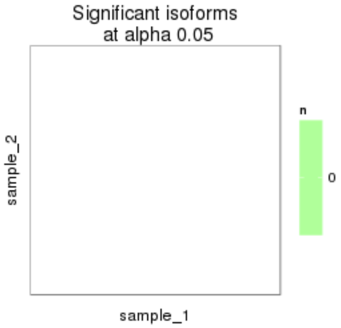
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

[1] “no sig isoforms”

Gene-level DE isoform heatmap

```
## [1] "no sig isoforms"
```

Isoform foldchange heatmap by isoform:

```
## [1] "no sig isoforms"
```

Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

Biocarta zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

Reactome enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

Reactome zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

Kegg enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

Kegg zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

Interneuron enrichment:

```
## Error: argument is of length zero
```

Interneuron zscore:

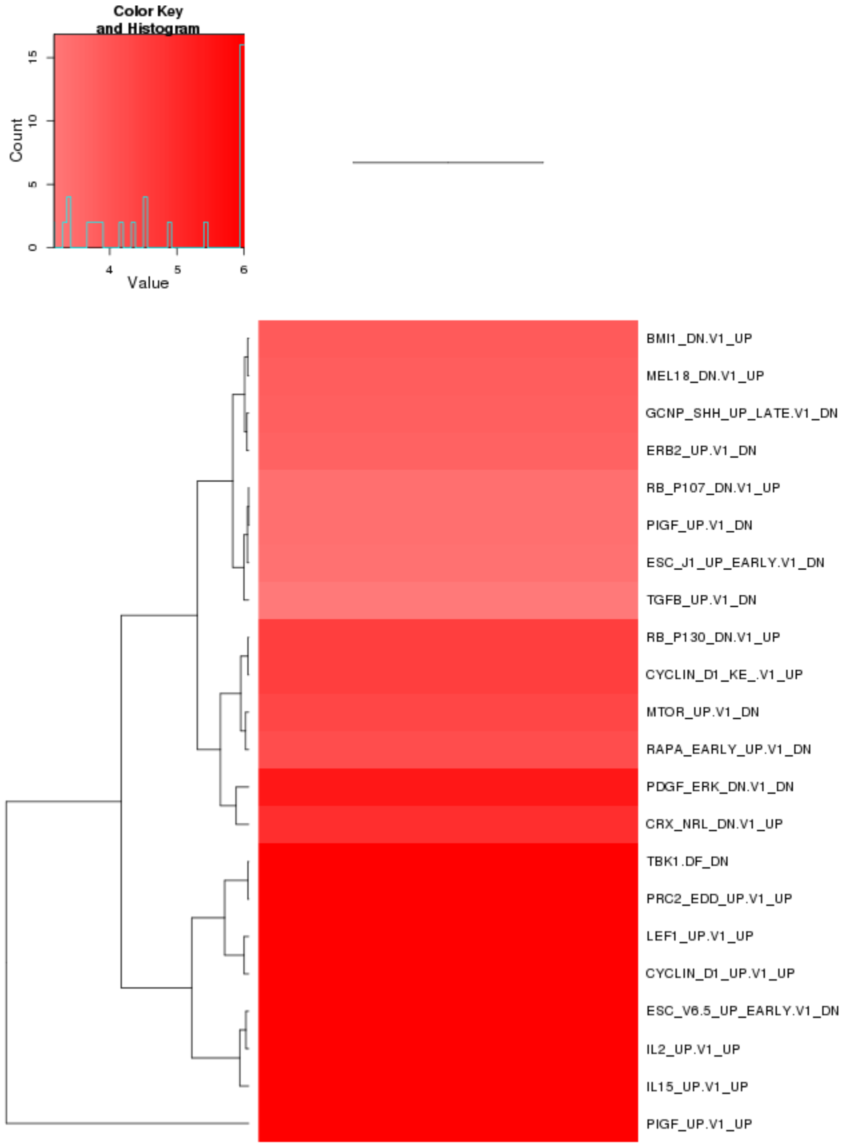
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

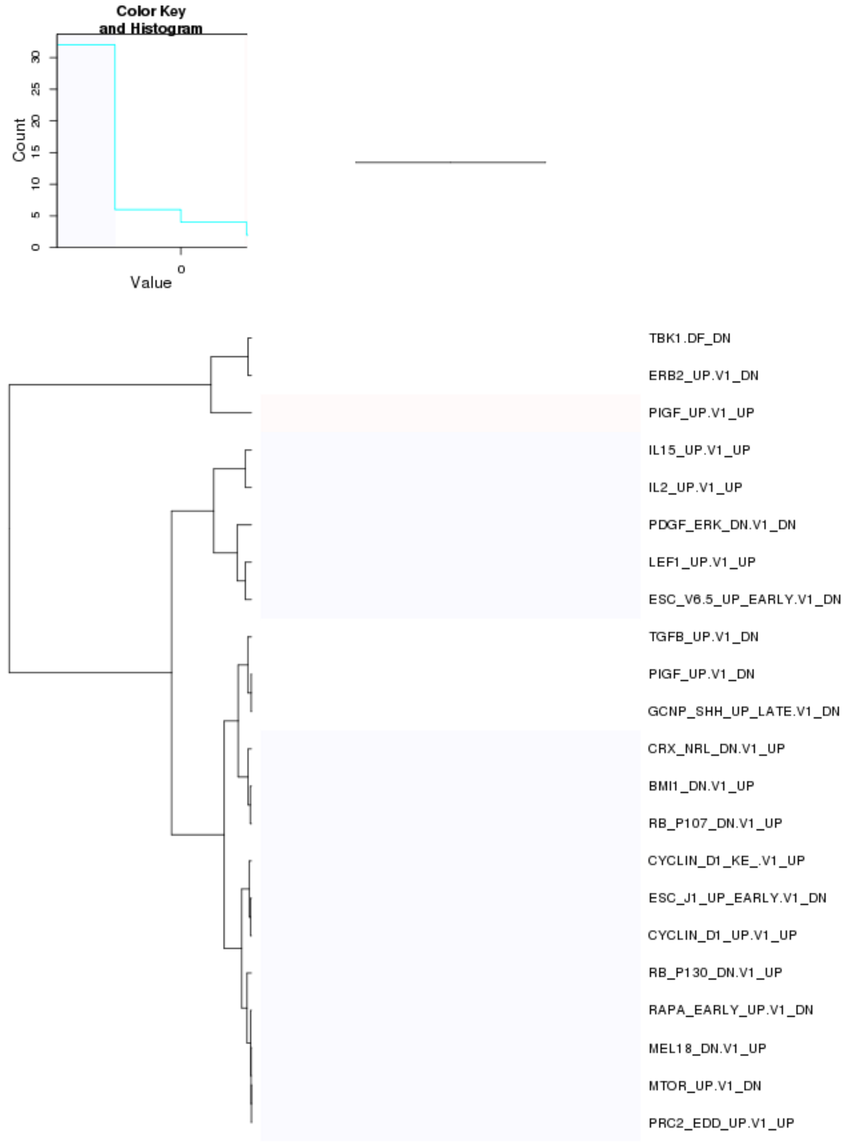
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

Oncogene enrichment:

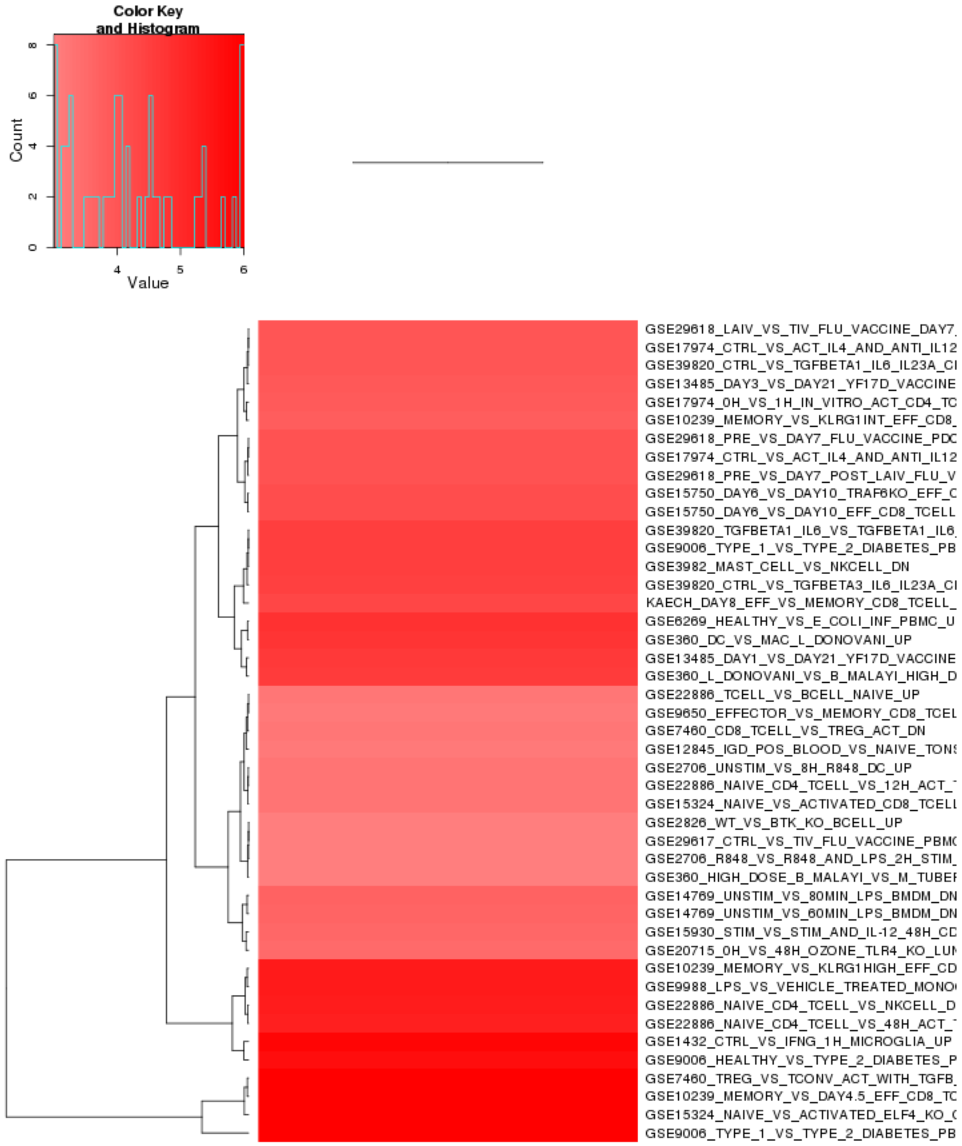


Oncogene zscore:



Immuno enrichment:

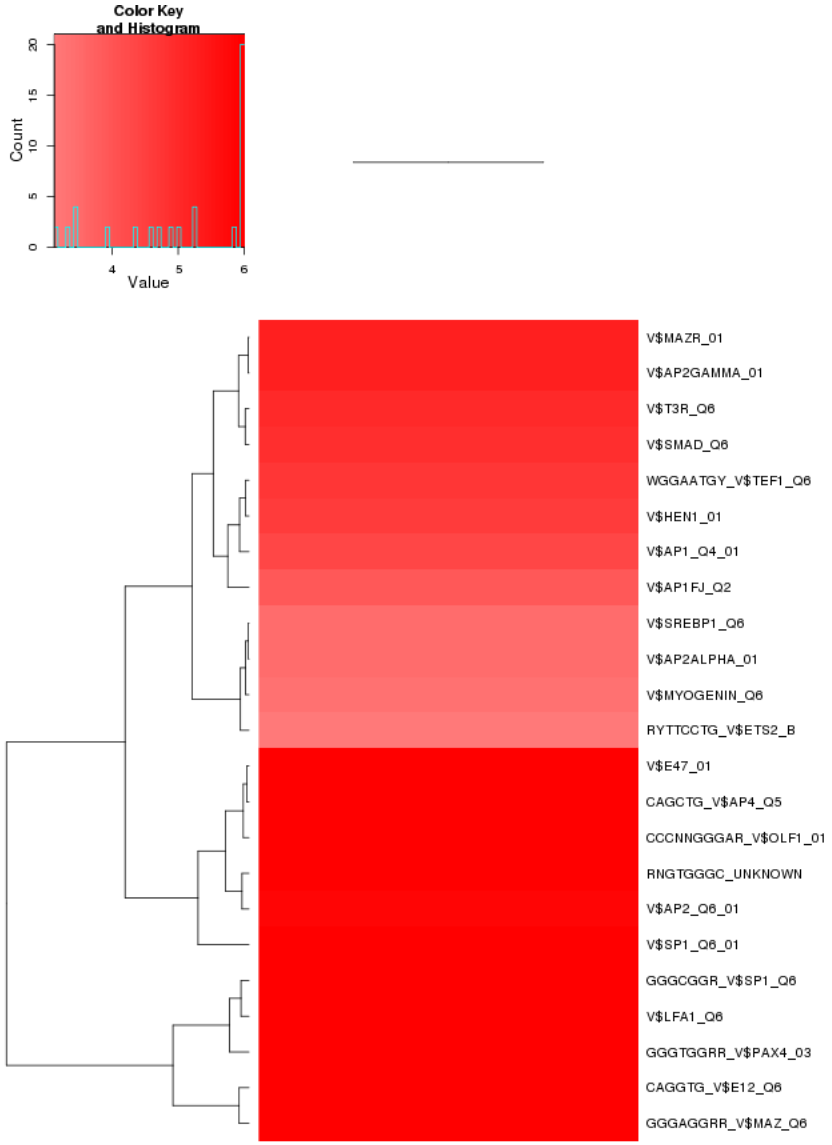
```
## Error: subscript out of bounds
```



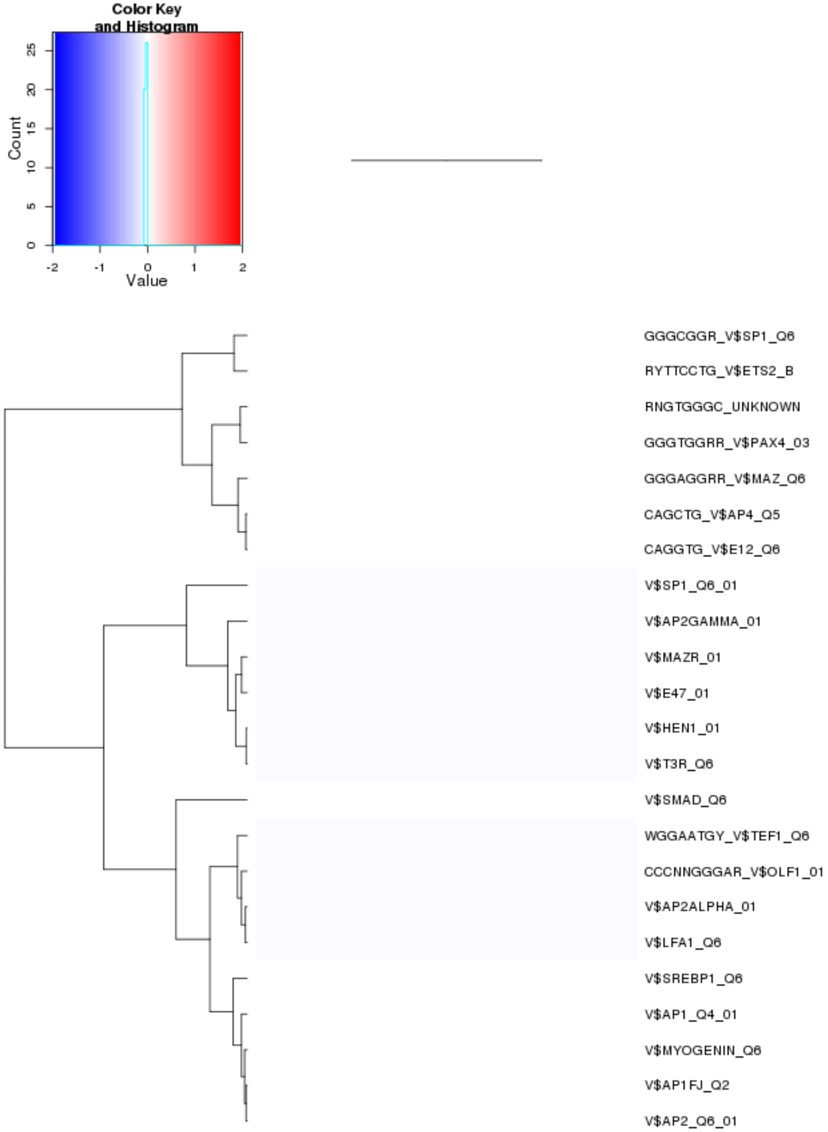
Immuno zscore:

```
## Error: subscript out of bounds
```

TF enrichment:

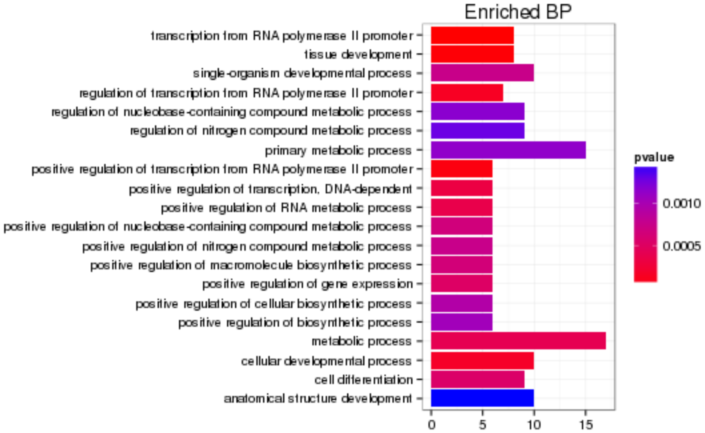

Color Key
and Histogram
Count
0
5
10
15
20
4
5
6
Value
V$MAZR_01
V$AP2GAMMA_01
V$T3R_Q6
V$SMAD_Q6
WGGAATGY_V$TEF1_Q6
V$HEN1_01
V$AP1_Q4_01
V$AP1FJ_Q2
V$SREBP1_Q6
V$AP2ALPHA_01
V$MYOGENIN_Q6
RYTTCCTG_V$ETS2_B
V$E47_01
CAGCTG_V$AP4_Q5
CCCNNGGGAR_V$OLF1_01
RNGTGGGC_UNKNOWN
V$AP2_Q6_01
V$SP1_Q6_01
GGGCGGR_V$SP1_Q6
V$LFA1_Q6
GGGTGGRR_V$PAX4_03
CAGGTG_V$E12_Q6
GGGAGGRR_V$MAZ_Q6

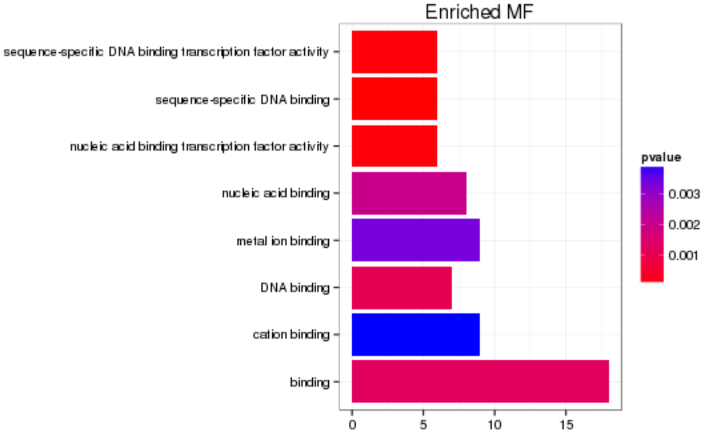
TF zscore:

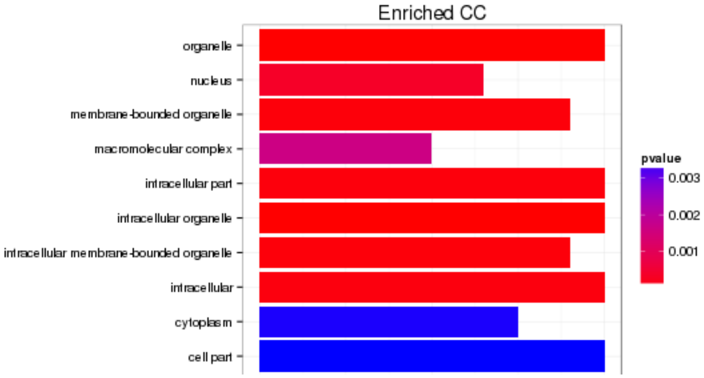


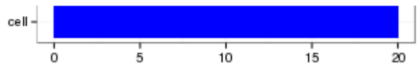
GO enrichment

Cluster profiler used to call enichments of significantly differentially regulated genes that map to Entrez IDs.


Enriched BP


Enriched MF

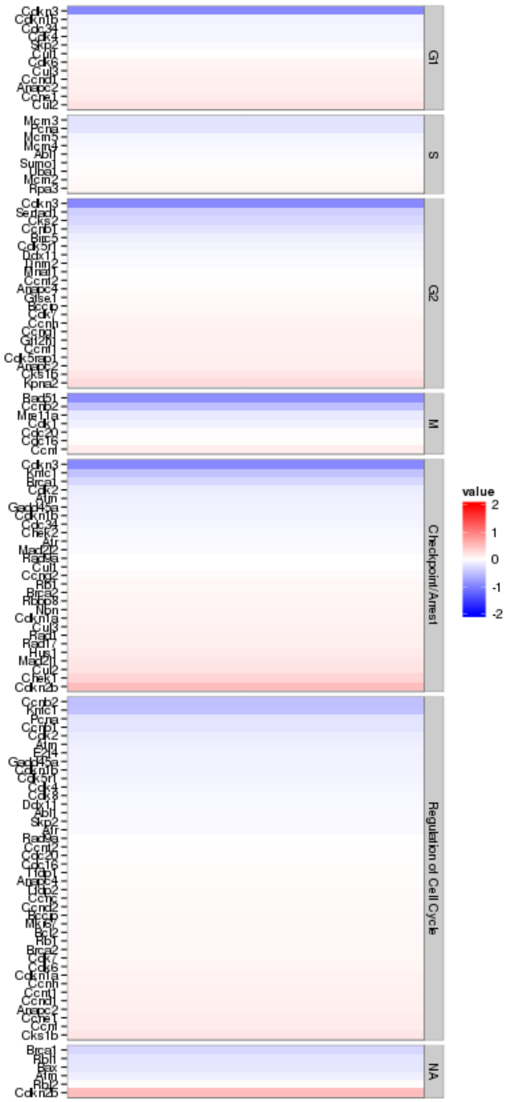

Enriched CC



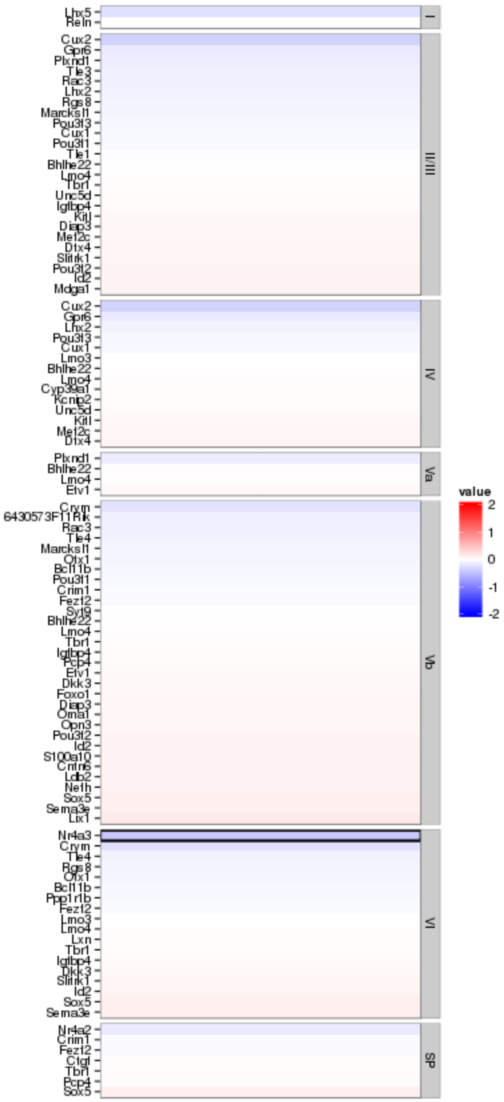
```
## Error: need finite 'xlim' values
```

```
## Error: need finite 'xlim' values
```

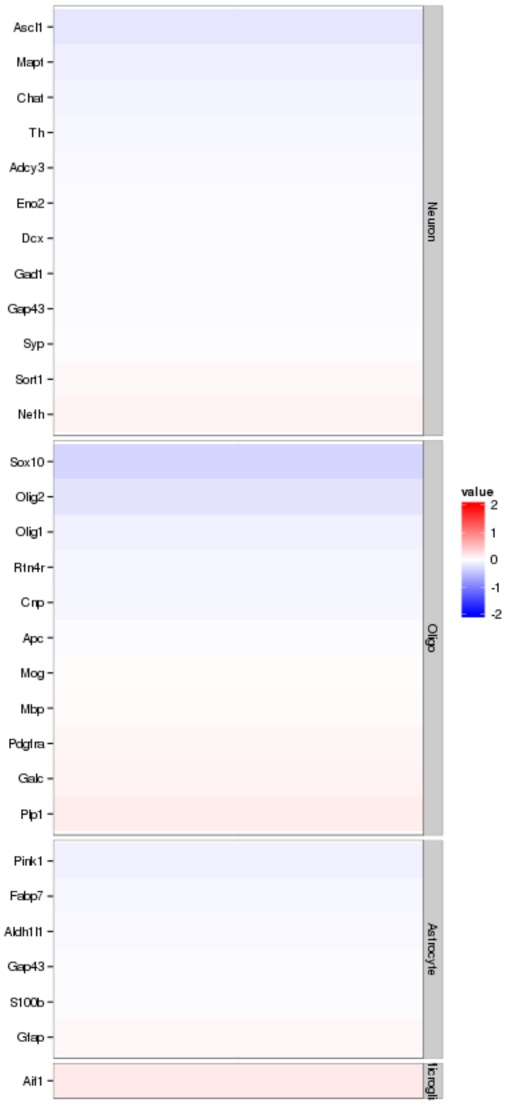
Enrichment or depletion for stage-specific cell cycle markers



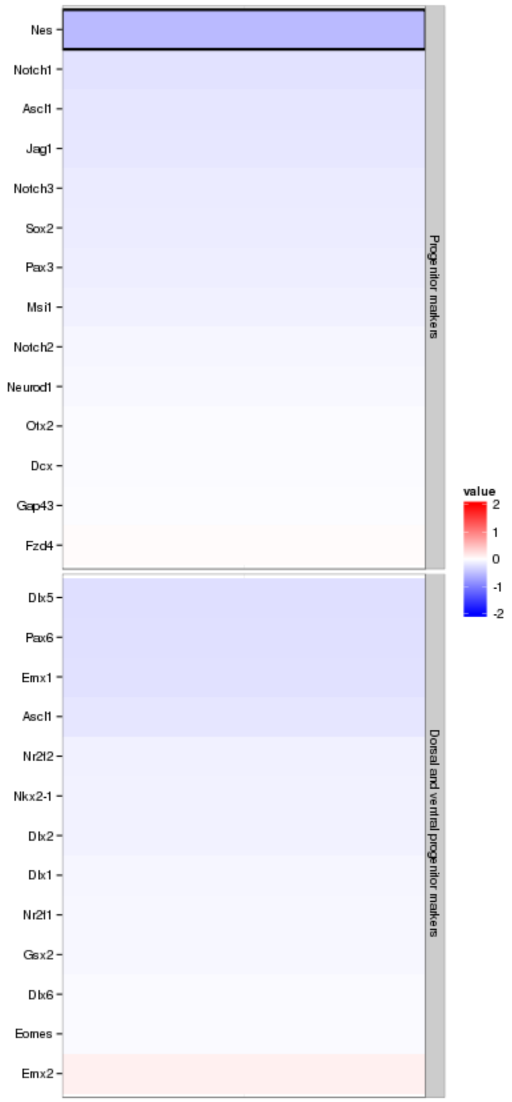
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



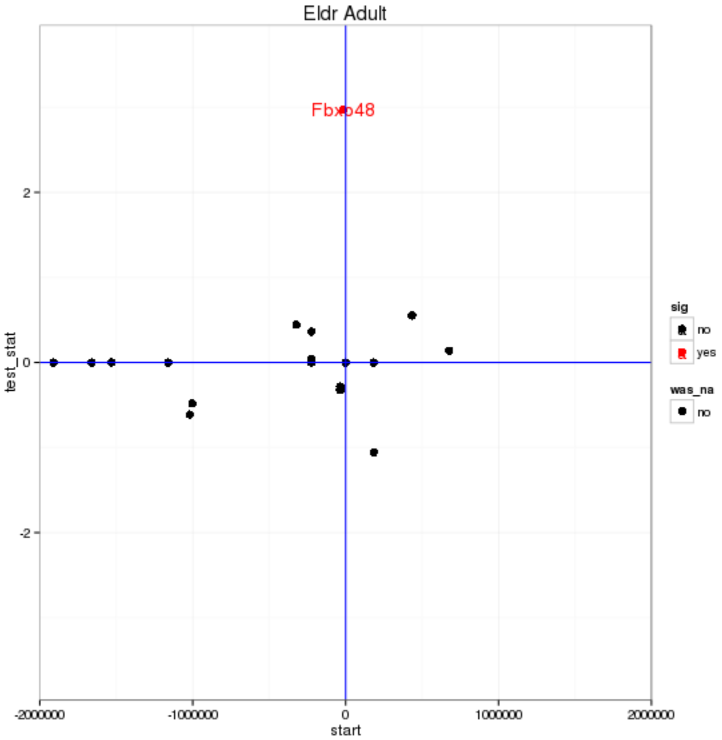
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 1 genes significantly regulated in a region this size is: 0.0788



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15 JR799

16 JR777

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	34779900.00	0.76	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	34779900.00	0.58	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	34779900.00	0.98	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	34779900.00	0.80	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	34779900.00	1.03	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	34779900.00	1.07	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	34779900.00	0.80	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	34779900.00	1.15	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	34779900.00	1.01	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	34779900.00	1.30	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	34779900.00	1.50	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	34779900.00	1.01	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	34779900.00	0.97	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	34779900.00	1.20	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR799/abundances.cxb	Eldr	0	Eldr_0	36453400.00	34779900.00	1.03	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR777/abundances.cxb	Eldr	1	Eldr_1	42739700.00	34779900.00	1.23	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils
## [8] datasets  base
##
## other attached packages:
##  [1] plyr_1.8.1
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
```

```
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,Eldr -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Eldr_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/annc
## 2
## 3
## 4
## 5
```

Eldr KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for Eldr.

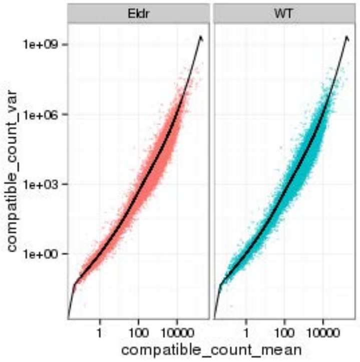
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

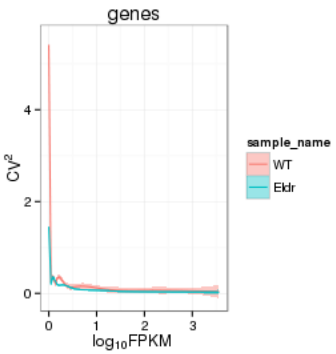
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



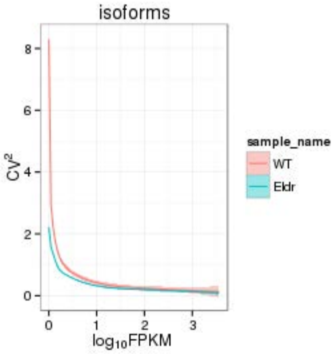
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

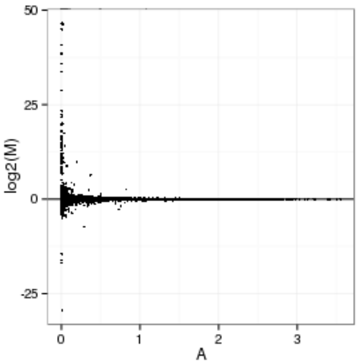
Genes:



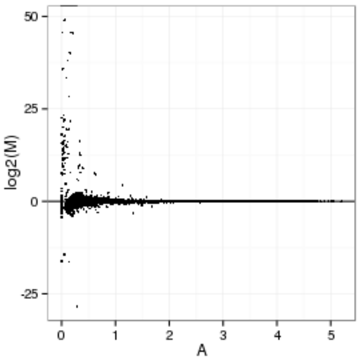
Isoforms:



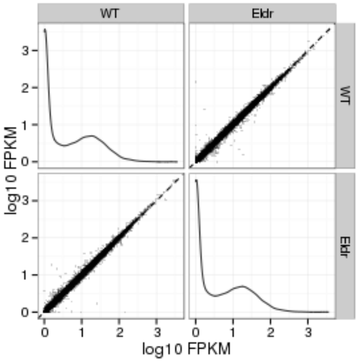
MvA plot



MvA plot counts



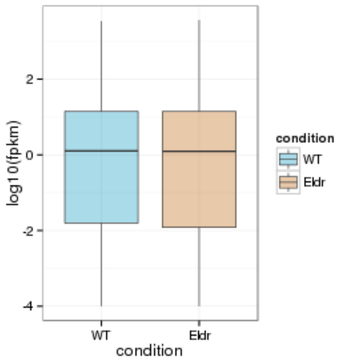
Scatterplot matrix



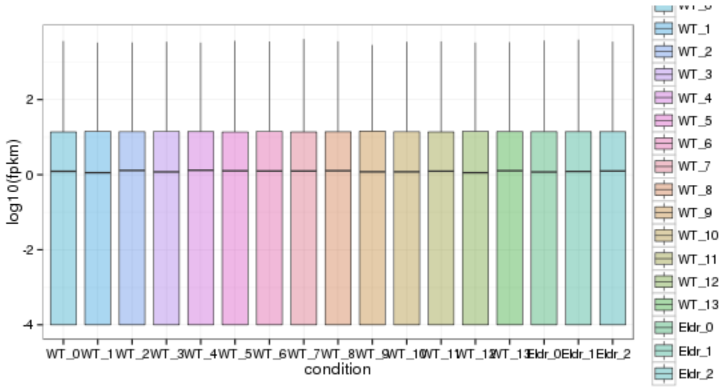
Distributions

Boxplots

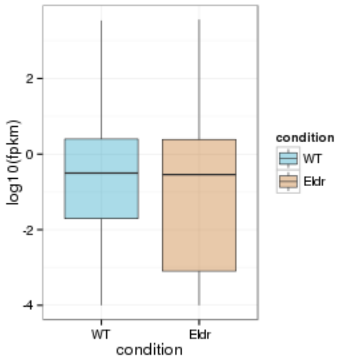
Boxplot (genes)



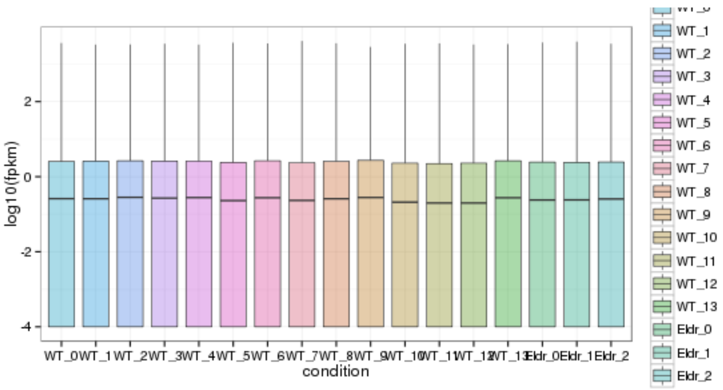
Boxplot (genes, replicates)



Boxplot (isoforms)

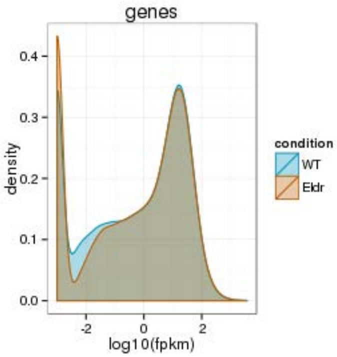


Boxplot (isoforms, replicates)

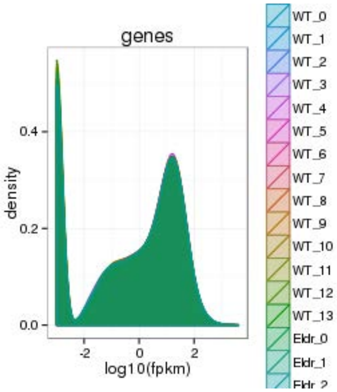


Density

Density (genes)

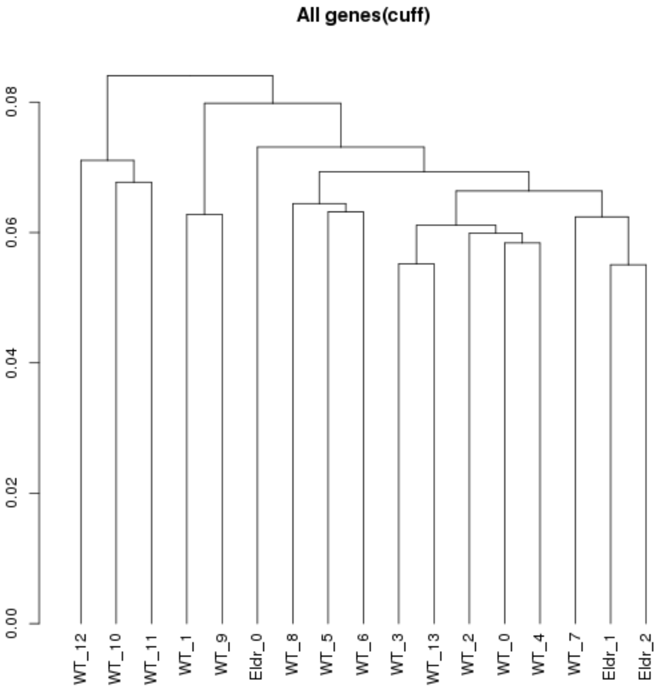


Density (genes, replicates)



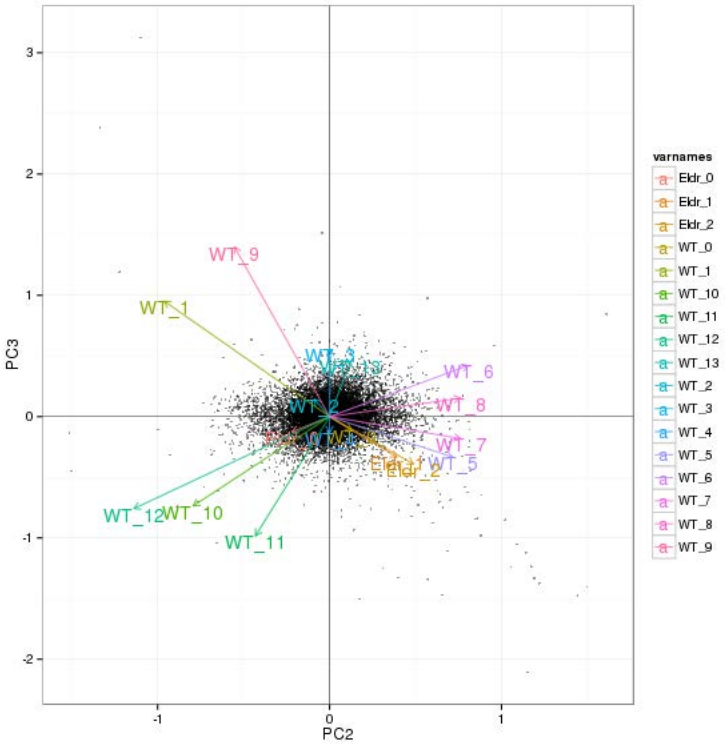
Clustering

Replicate Clusters



```
## NULL
```

PCA (genes)

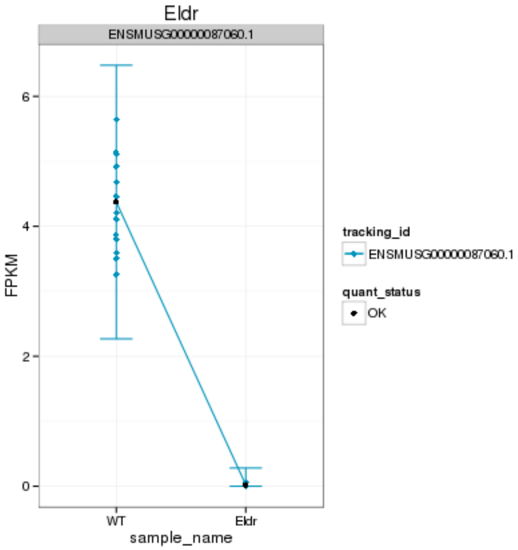


PC3
PC2
3
2
1
0
-1
-2
-1
0
1
WT_9
WT_1
WT_3
WT_13
WT_6
WT_2
WT_8
WT_7
WT_5
Eldr_1
Eldr_2
WT_12
WT_10
WT_11
varnames
Eldr_0
Eldr_1
Eldr_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

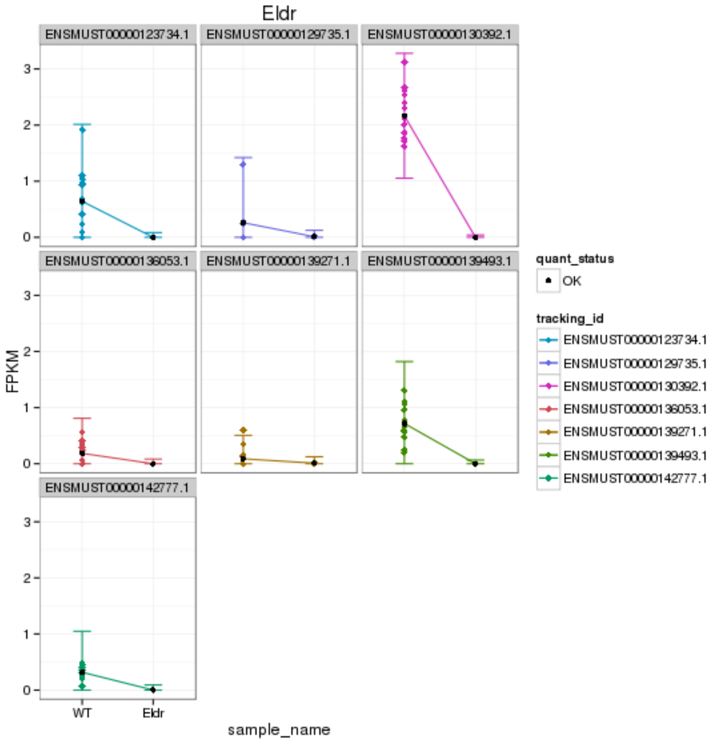
MDS (genes)

KO assessment

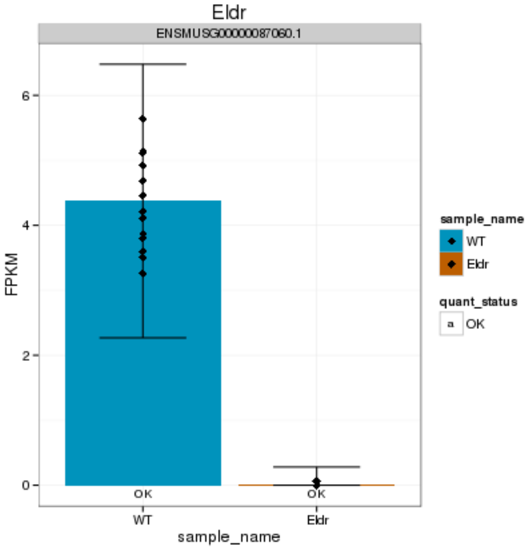
Endogenous lncRNA expression



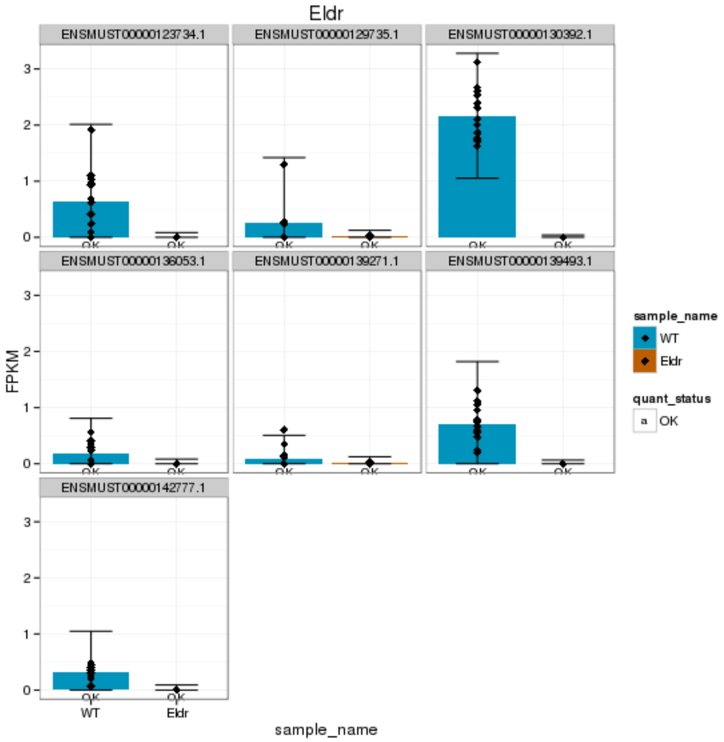
Endogenous expression of Eldr isoforms:



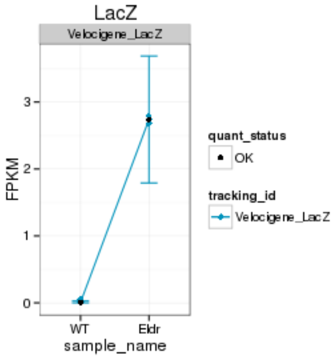
Barplot of gene expression:

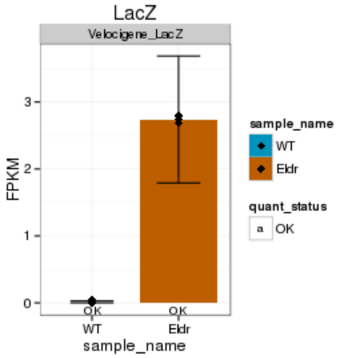


Barplot of isoform expression:



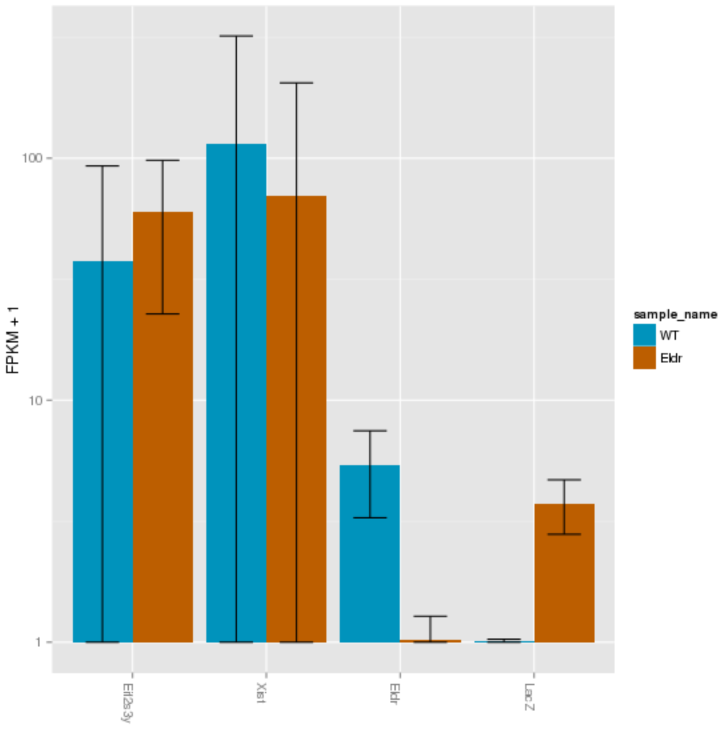
LacZ expression



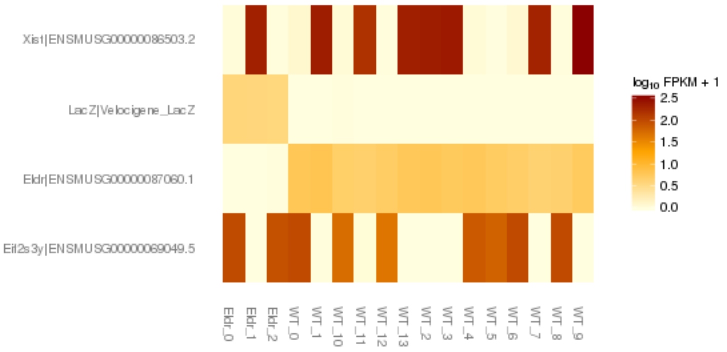


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

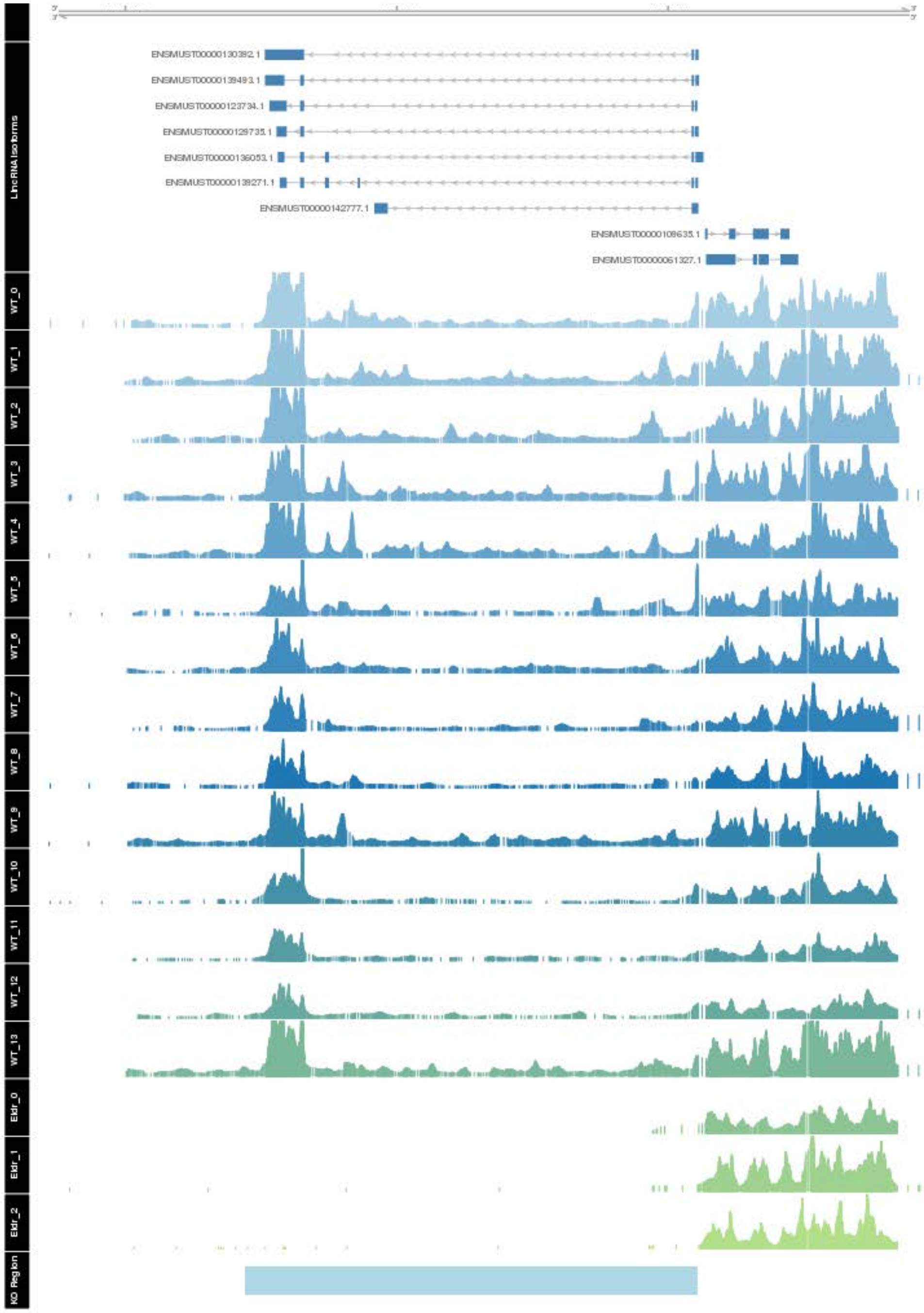
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


LincRNA Isoforms
ENSMUST00000130392.1
ENSMUST00000139493.1
ENSMUST00000123734.1
ENSMUST00000129735.1
ENSMUST00000136053.1
ENSMUST00000139271.1
ENSMUST00000142777.1
ENSMUST00000109635.1
ENSMUST00000061327.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Eldr_0
Eldr_1
Eldr_2
KO Region

Differential Analysis

Differential Genes

There are 151 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Cdh1
2	Col1a1
3	Cacna1e
4	Utp20
5	Polr2a
6	Nid1
7	Vax1
8	Rplp1
9	Ttc9b
10	Ptgds
11	Abca1
12	Dync1h1
13	D10Bwg1379e
14	Lama2
15	Snrpf
16	Egfr
17	Pold2
18	Aebp1
19	Prpf8
20	Hoxb9
21	Pdhb
22	Nid2
23	Sla
24	Myh9
25	Col2a1
26	Dlx2
27	Igf2r
28	Prss41
29	Fbn2
30	Rps14
31	Lbx1
32	Rps26
33	Pgm2
34	Fn1
35	Lamc1
36	Ddr2
37	Lrp2

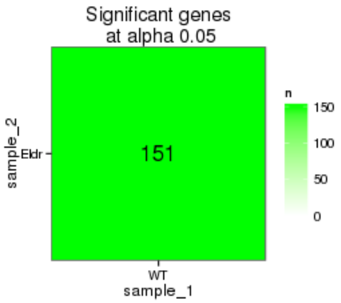
38	Fbn1
39	Notch2
40	Col11a1
41	Tnc
42	Svep1
43	Snapc3
44	Scp2
45	Kcnq4
46	Ndufs5
47	Wdr65
48	Nkx1-1
49	Pdgfra
50	Uncx
51	Lhx5
52	Col1a2
53	Slc13a4
54	Aldh1l1
55	Itpr1
56	Dera
57	Herc2
58	Hddc3
59	Iqgap1
60	Eif3f
61	Lama1
62	3830406C13Rik
63	Adamts15
64	Gbx2
65	Prr7
66	Fras1
67	Vps13c
68	Fignl1
69	Cox8a
70	Frem2
71	Rps16
72	Vstm2l
73	Notch3
74	Ift172
75	Hoxb4
76	Atp5l
77	Srrm2
78	Pcsk1n
79	Klhl42
80	Tlx3

81	C1qtnf4
82	Dnah7b
83	2310036O22Rik
84	Fmod
85	Hebp1
86	Tuba1c
87	Lor
88	Pgp
89	Gm9493
90	Rps2
91	Acp1
92	Sox3
93	Wdr89
94	Scand1
95	Sox18
96	Gm7729
97	Fat4
98	Dync2h1
99	Kmt2d
100	Scrt1
101	Rpl29
102	H2afx
103	Ccdc171
104	Dnah6
105	Lamb2
106	Tusc1
107	Zfp771
108	Mrfap1
109	Gm10020
110	Rpl36
111	Capn11
112	H2afj
113	Tpt1
114	Rps12
115	Rpl35
116	Sox11
117	Zfp428
118	Rpl36-ps3
119	Flnc
120	Ptprz1
121	Ddx3y
122	Nkain2
123	Ahnak

124	Fat1
125	Gm1673
126	Klhl9
127	Jund
128	Gm10340
129	Gm7292
130	Gpr27
131	Srp54a
132	Wdfy1
133	Hbb-bt
134	Fat3
135	Gm3558
136	Gm2974
137	Gm3411
138	Gm2897
139	Gm11273
140	Ccdc85c
141	Ier5l
142	Gm3739
143	Malat1
144	Gm10406
145	Gm3373
146	Gm3526
147	Ccdc85b
148	Gm3500
149	Gm9825
150	Gm5796
151	Gm3591

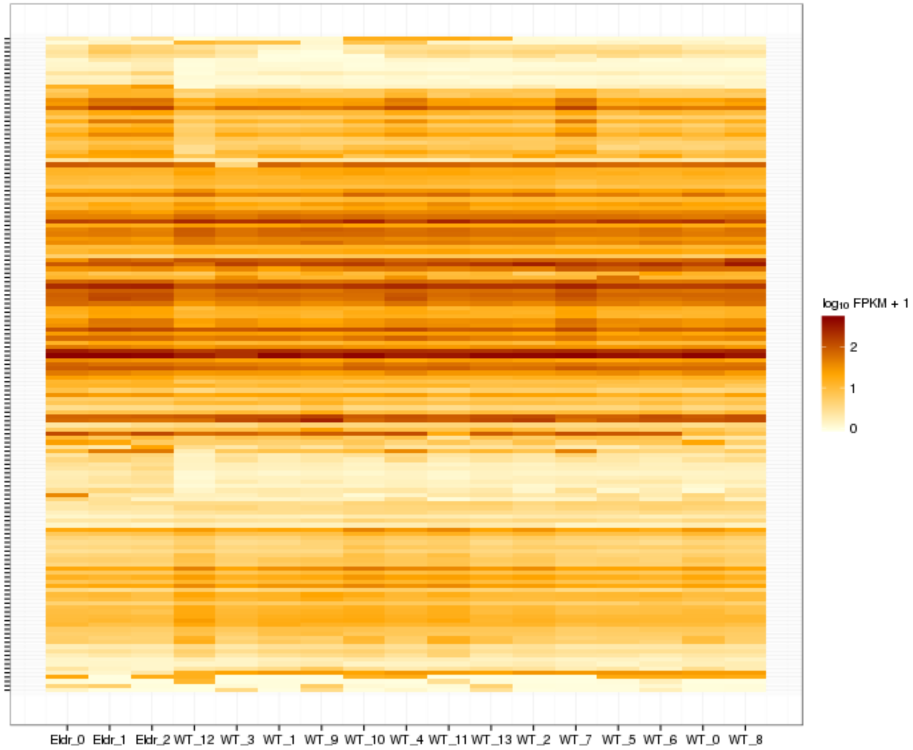
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

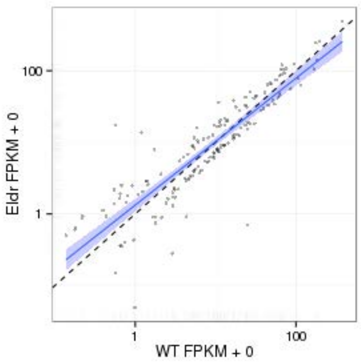


Significant genes with expression >50fpkm (any condition):(turned off)

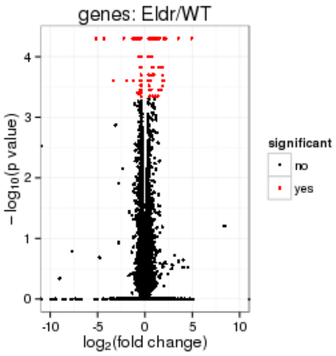
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

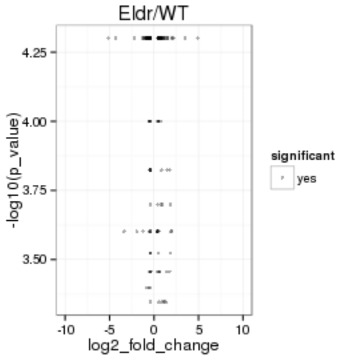
Scatter plot of significant genes only:



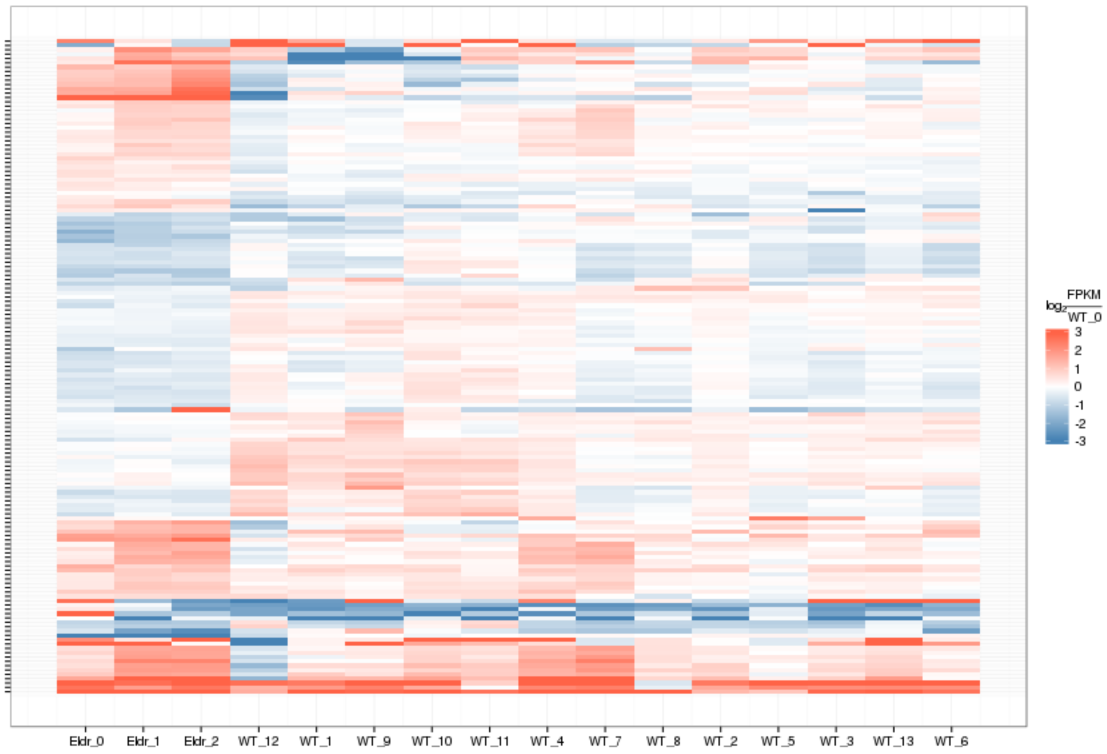
Volcano Plot



Volcano plot with significant genes only:



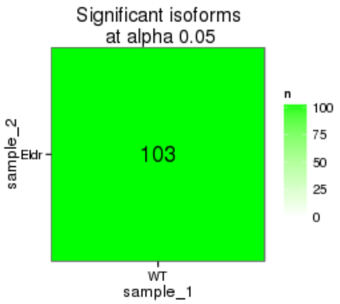
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



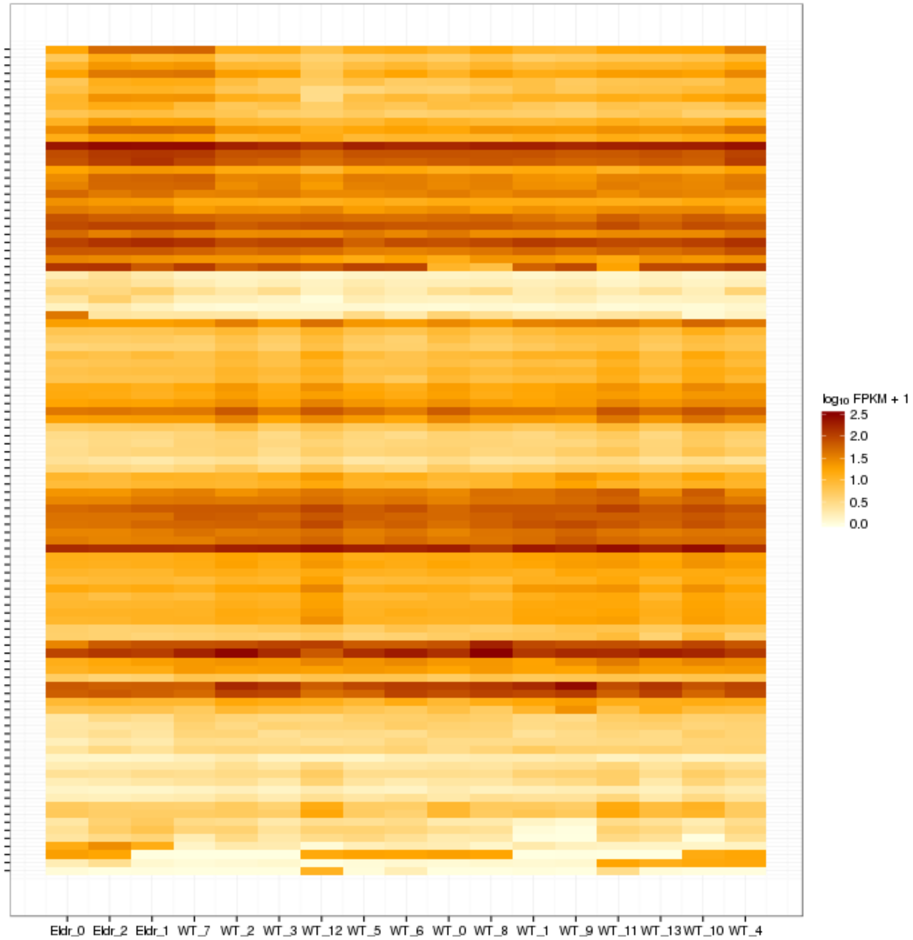
These isoforms are:

	isoAnnot$gene_short_name
1	Cdh1
2	Col1a1
3	Lamb1
4	Nid1
5	Ttc9b
6	Cad
7	Abca1
8	Lama5
9	Dync1h1
10	Lama2
11	Gm872
12	Egfr
13	Pold2
14	Mrc2
15	Hoxb9
16	Nid2
17	Myh9
18	Dlx2
19	Igf2r
20	Fbn2
21	Rps14
22	Fasn
23	Lbx1
24	Pgm2
25	Dst
26	Fn1

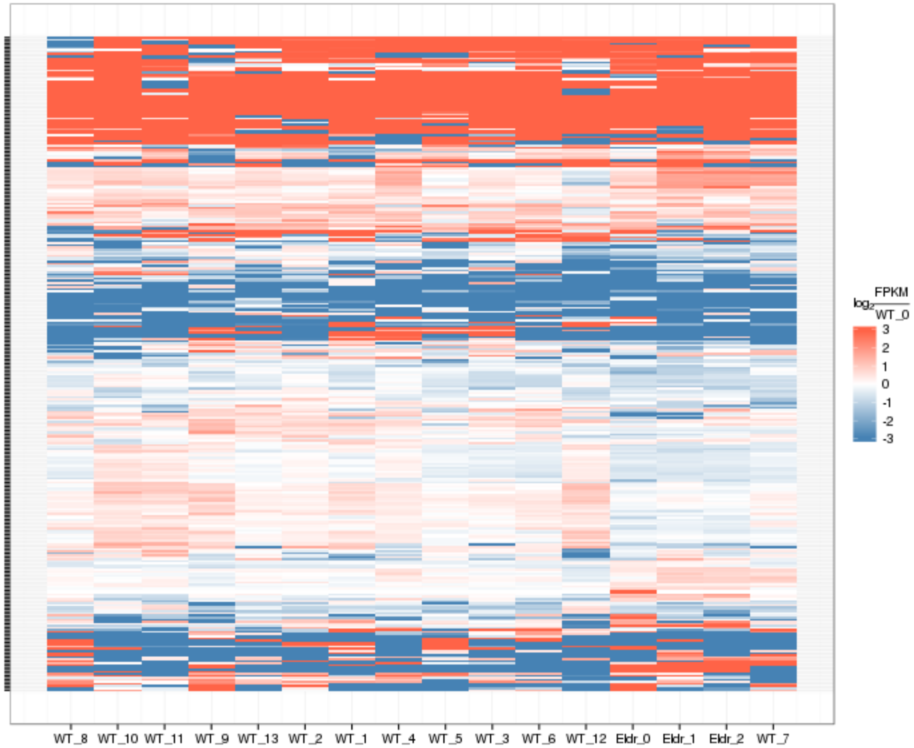
27 Lamc1
28 Col5a1
29 Notch1
30 Lrp2
31 Fbn1
32 Notch2
33 Tnc
34 Svep1
35 Snapc3
36 Scp2
37 Kcnq4
38 Trp73
39 Uncx
40 Col1a2
41 Slc13a4
42 Itpr1
43 Dera
44 Eif3f
45 Col12a1
46 Lama1
47 Szt2
48 Adamts15
49 Gbx2
50 Prr7
51 Fras1
52 Leng8
53 Cox8a
54 Frem2
55 Vstm2l
56 Notch3
57 Hoxb4
58 Pcsk1n
59 Klhl42
60 Lrp1
61 Tlx3
62 C1qtnf4
63 Dnah7b
64 2310036O22Rik
65 Reln
66 Hebp1
67 Tuba1c
68 Gm9493

69 Wdr89
70 Fat4
71 Col6a3
72 H2afx
73 Ccdc171
74 Lamb2
75 Tusc1
76 Zfp771
77 Gm10020
78 Rpl36
79 H2afj
80 Tpt1
81 Rps12
82 Sox11
83 Ptprz1
84 Ddx3y
85 Gpr98
86 Ahnak
87 Fat1
88 Klhl9
89 Jund
90 Gpr27
91 Srp54a
92 Hbb-bt
93 Fat3
94 Gm3558
95 Gm2897
96 Gm11273
97 Ccdc85c
98 Ier5l
99 Malat1
100 Ccdc85b
101 Gm3500
102 Gm9825
103 Gm3591

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:

```
## Error: `x' must have at least 2 rows and 2 columns
```

Biocarta zscore:

```
## Error: incorrect number of dimensions
```

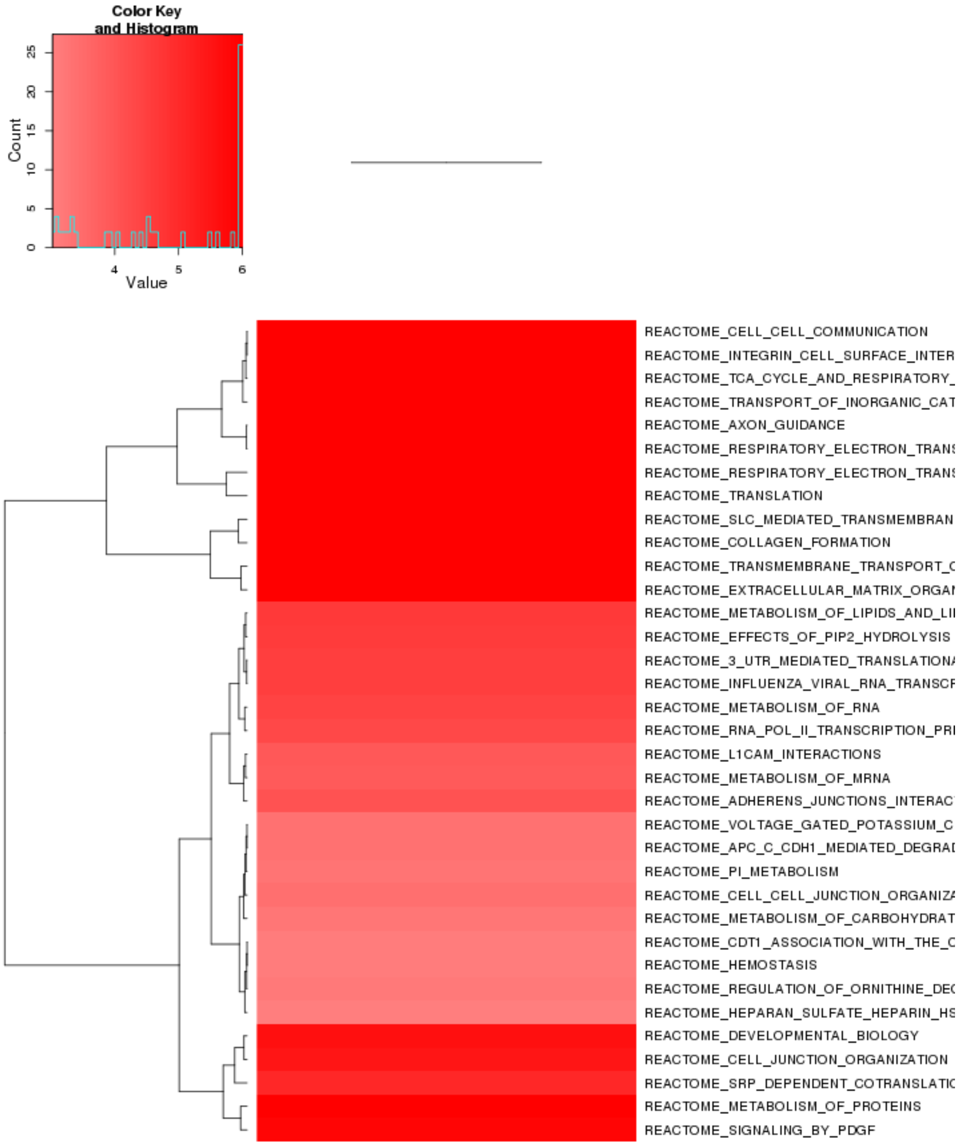
```
## Error: object 'x_ordered' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

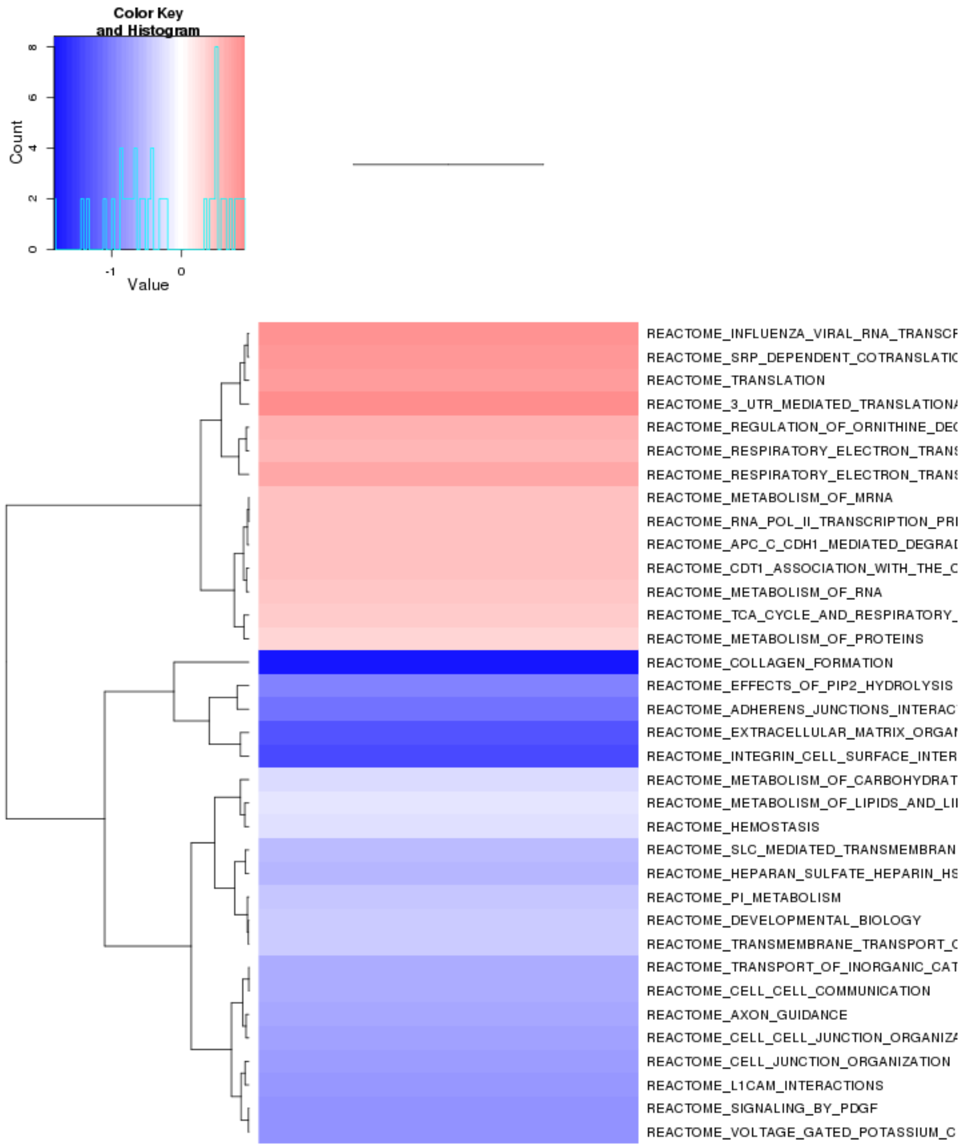
Reactome enrichment:

```
## Error: subscript out of bounds
```

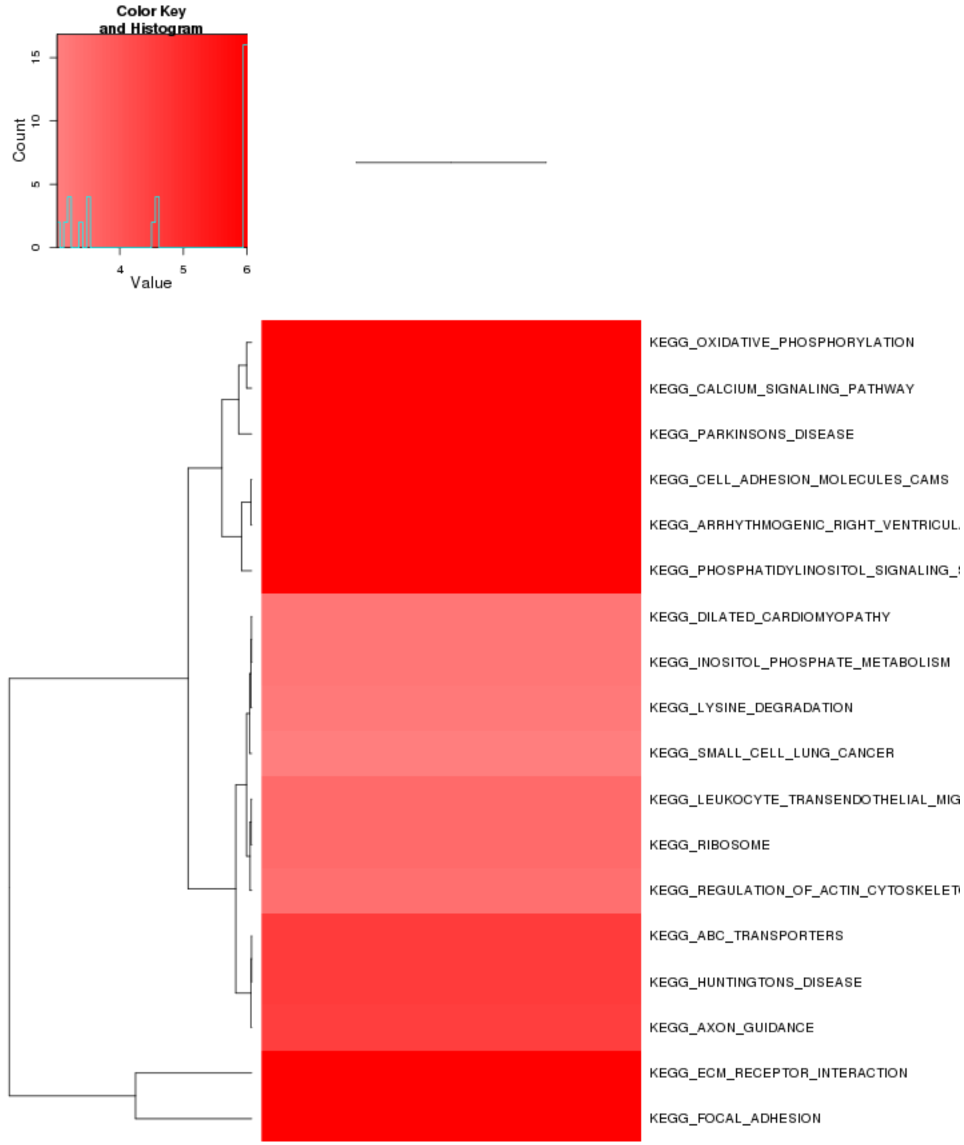


Reactome zscore:

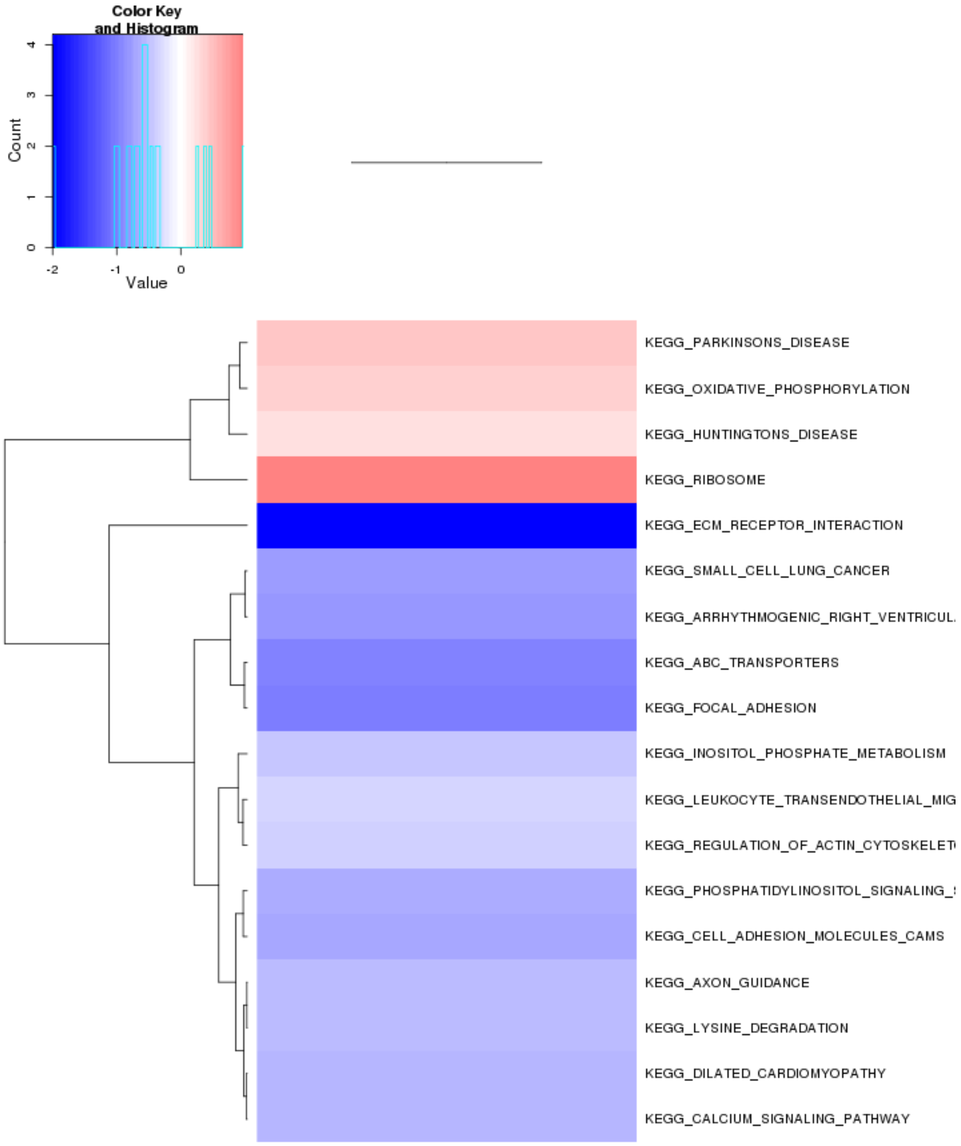
```
## Error: subscript out of bounds
```



Kegg enrichment:

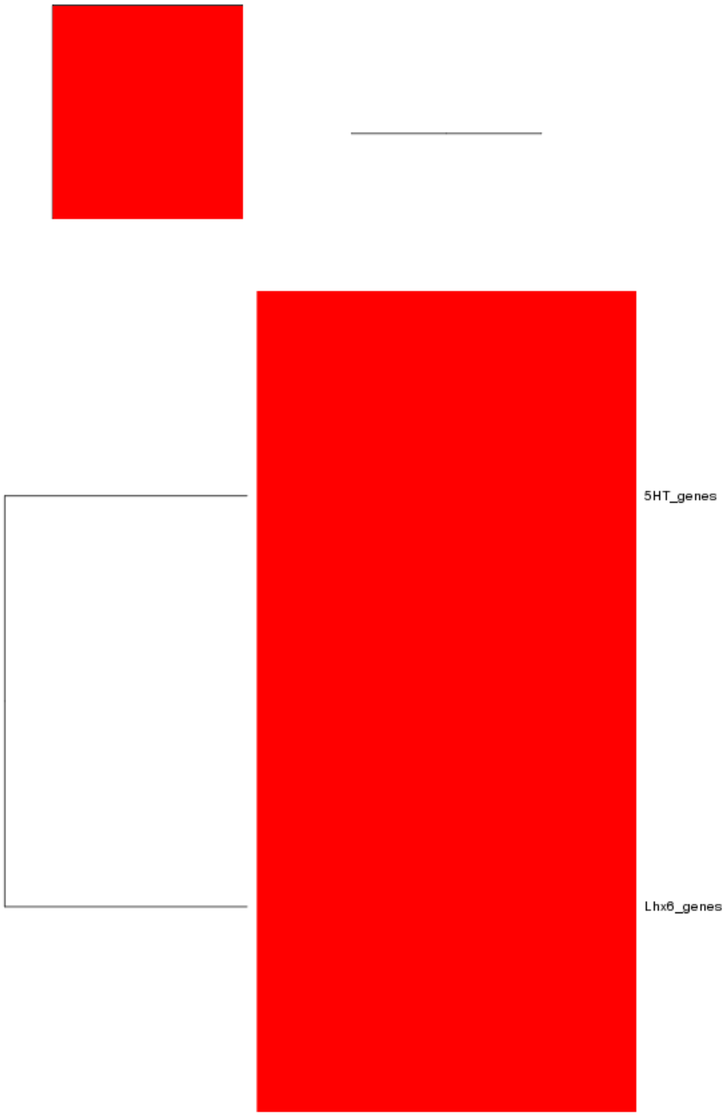

Color Key
and Histogram
Count
0
5
10
15
4
5
6
Value
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_CALCIUM_SIGNALING_PATHWAY
KEGG_PARKINSONS_DISEASE
KEGG_CELL_ADHESION_MOLECULES_CAMS
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICUL
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_
KEGG_DILATED_CARDIOMYOPATHY
KEGG_INOSITOL_PHOSPHATE_METABOLISM
KEGG_LYSINE_DEGRADATION
KEGG_SMALL_CELL_LUNG_CANCER
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIG
KEGG_RIBOSOME
KEGG_REGULATION_OF_ACTIN_CYTOSKELET
KEGG_ABC_TRANSPORTERS
KEGG_HUNTINGTONS_DISEASE
KEGG_AXON_GUIDANCE
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_FOCAL_ADHESION

Kegg zscore:

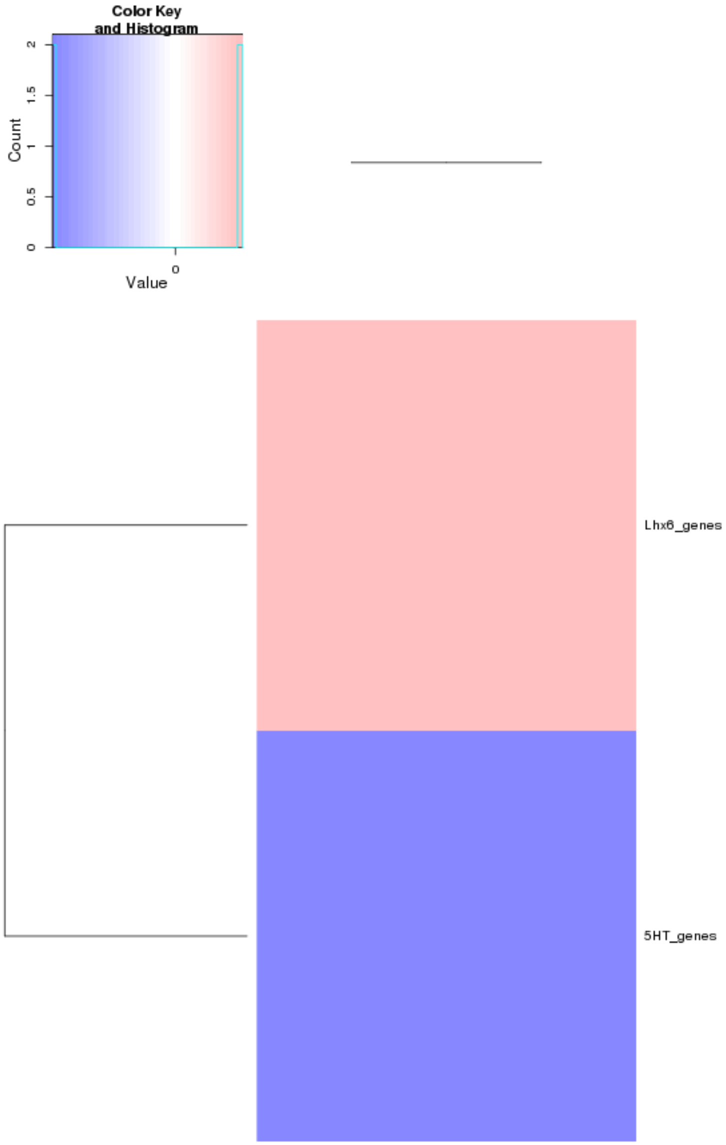


Interneuron enrichment:

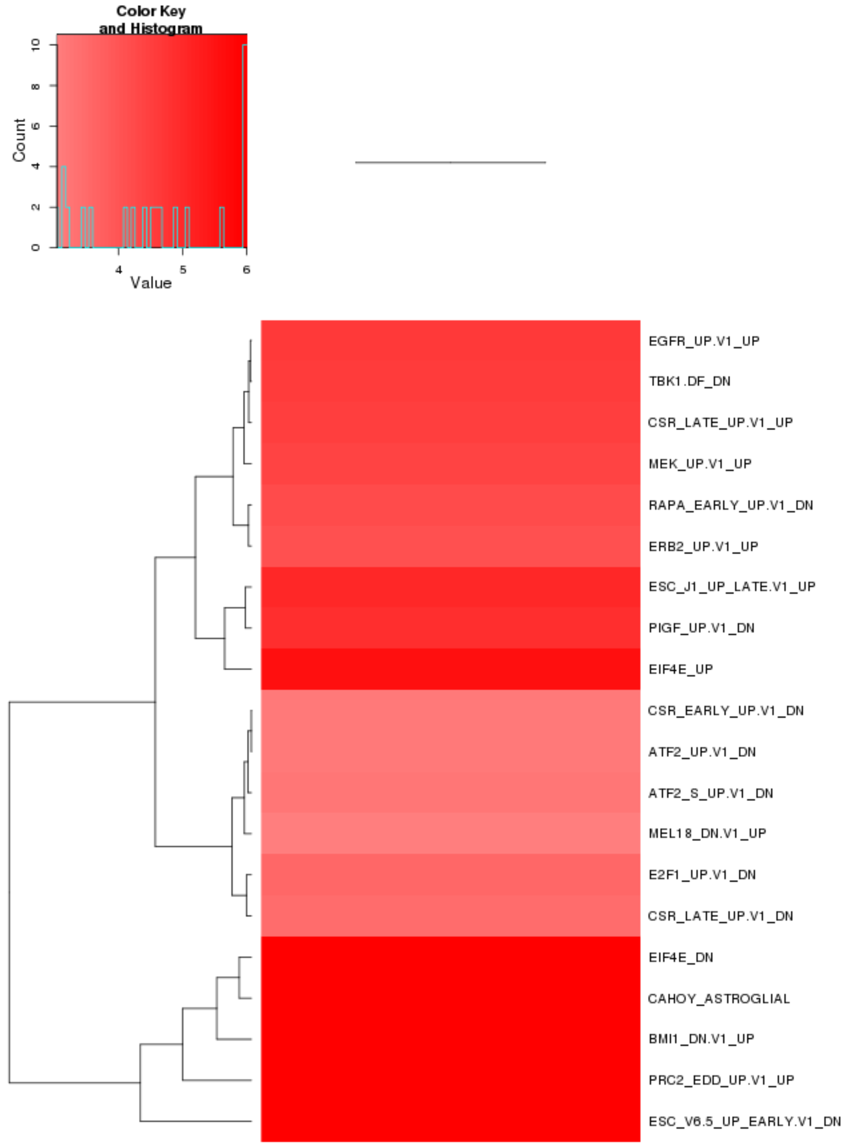
```
## Error: no locations are finite
```



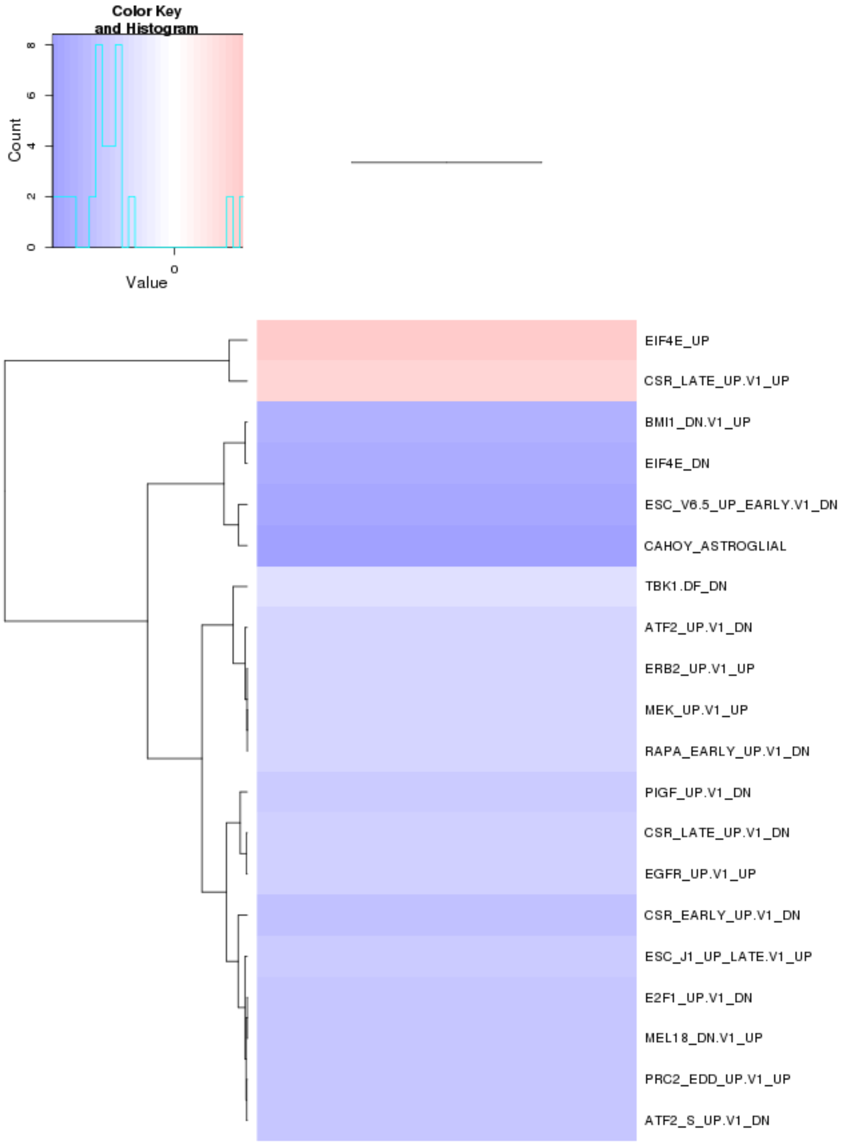
Interneuron zscore:



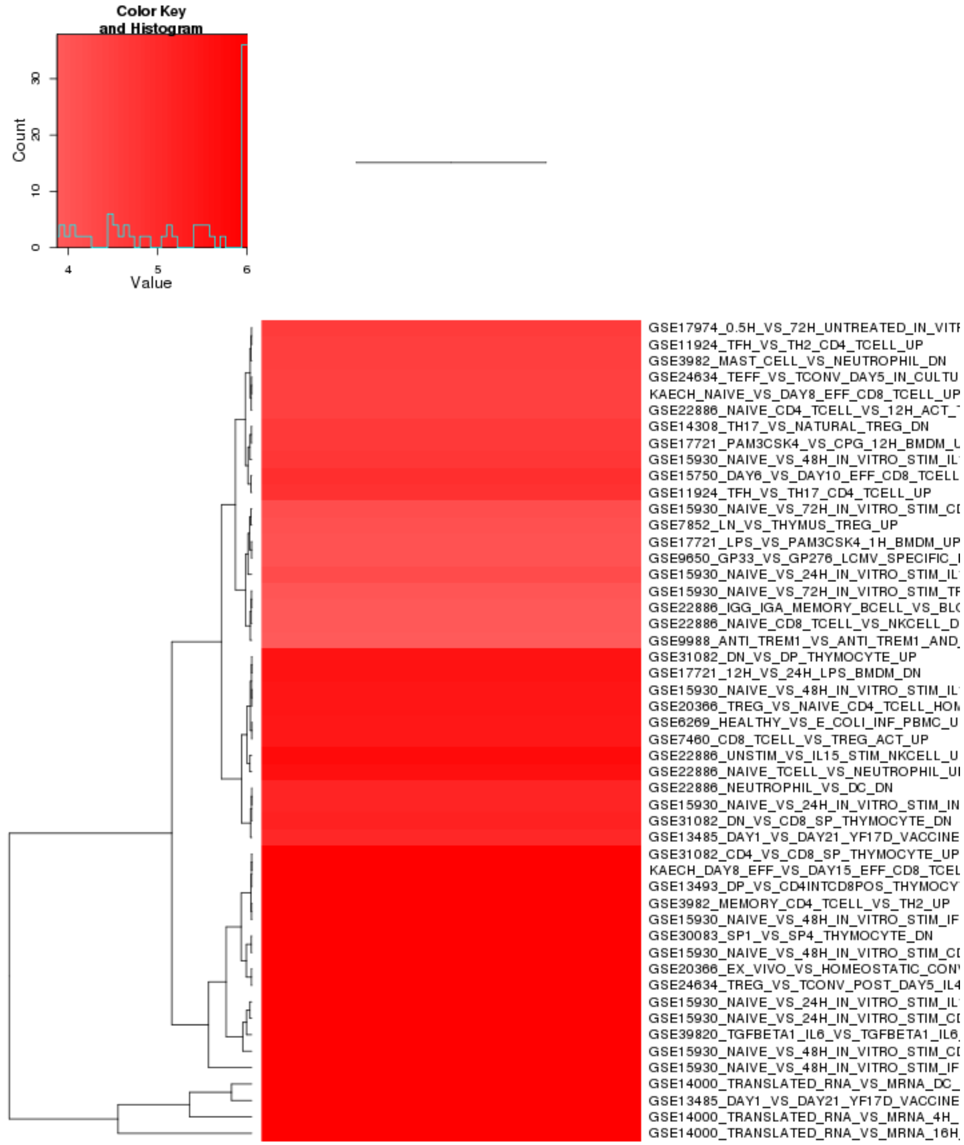
Oncogene enrichment:



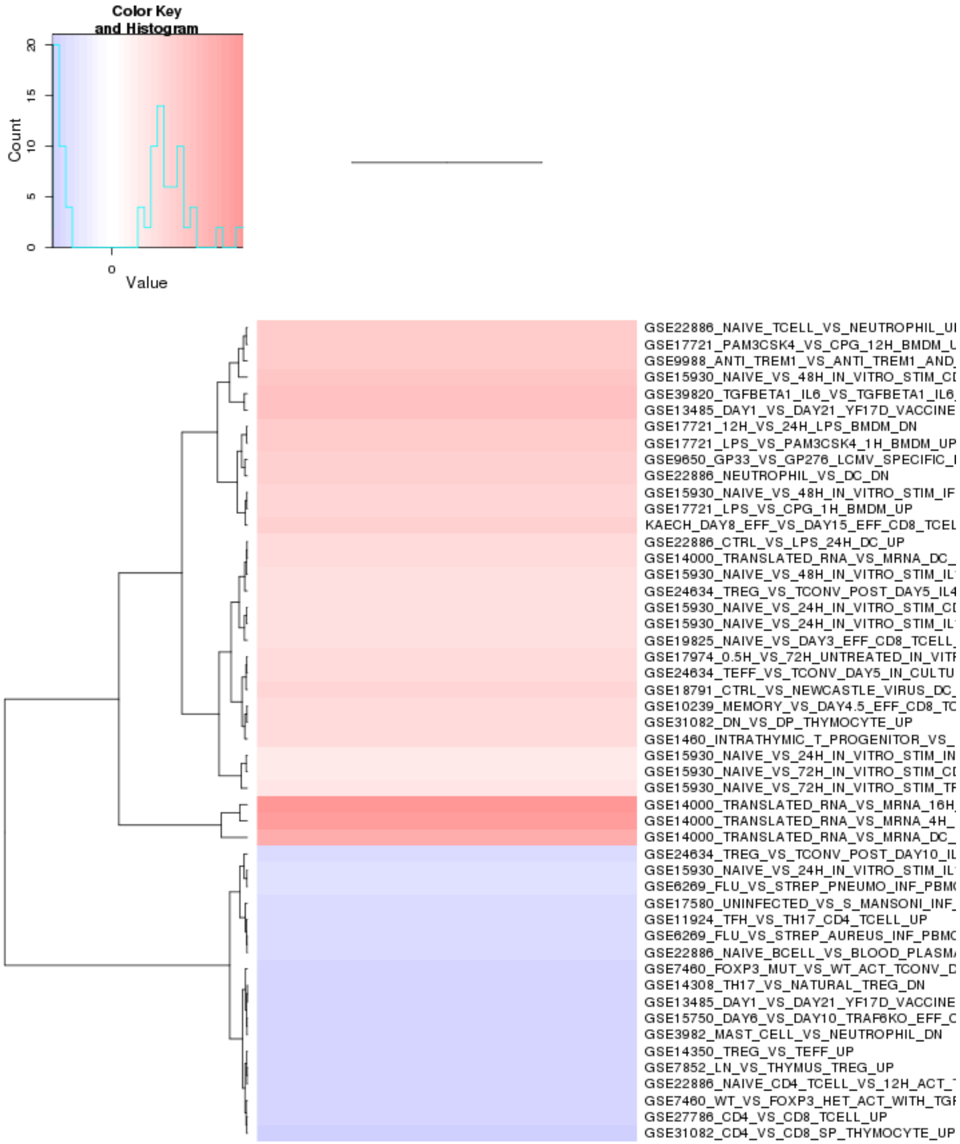
Oncogene zscore:



Immuno enrichment:

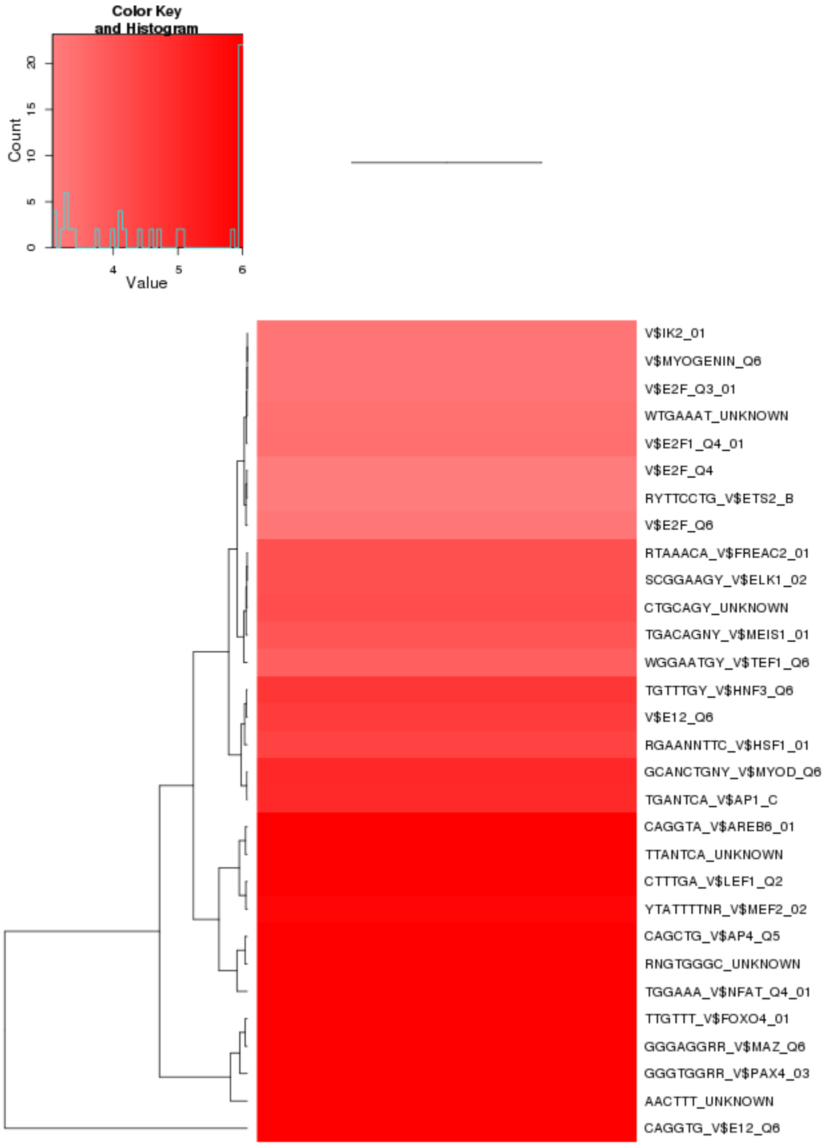


Immuno zscore:



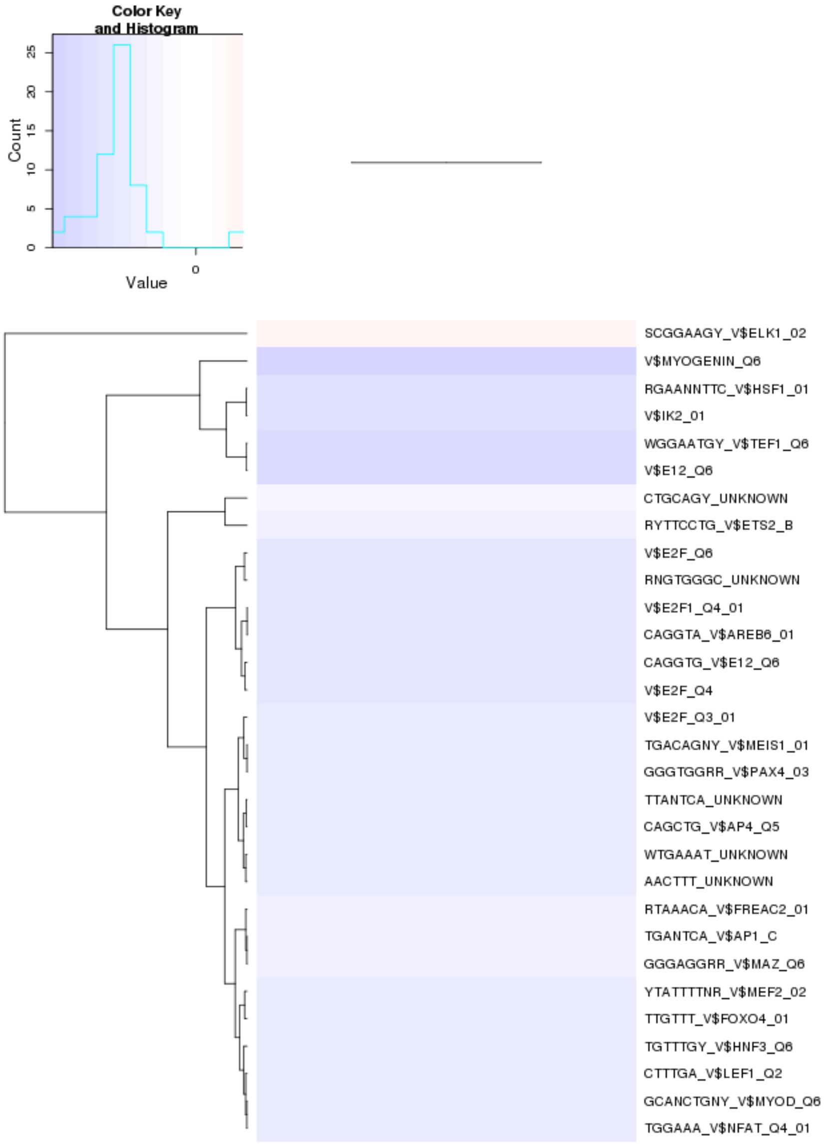
TF enrichment:

```
## Error: subscript out of bounds
```



TF zscore:

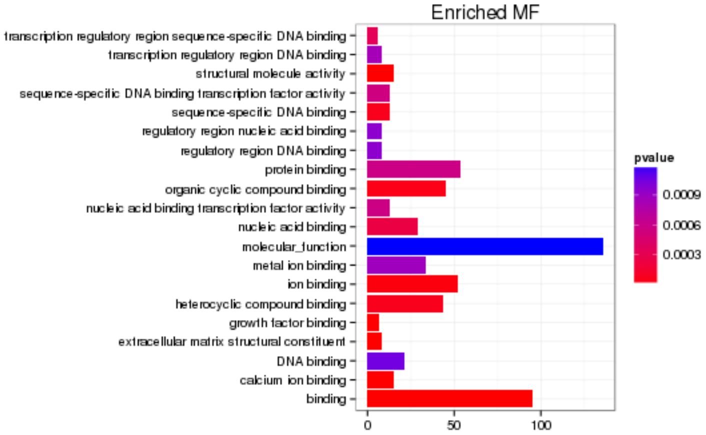
```
## Error: subscript out of bounds
```

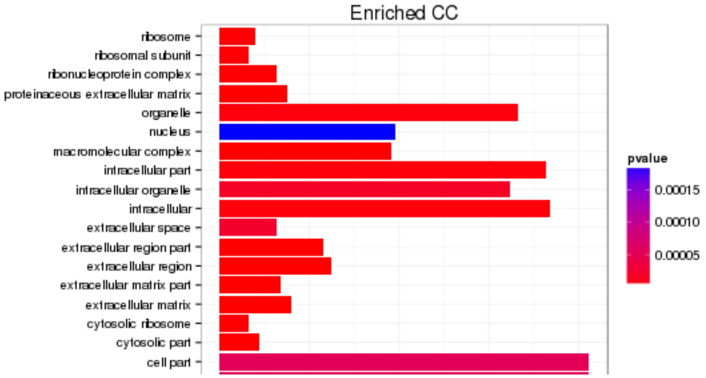


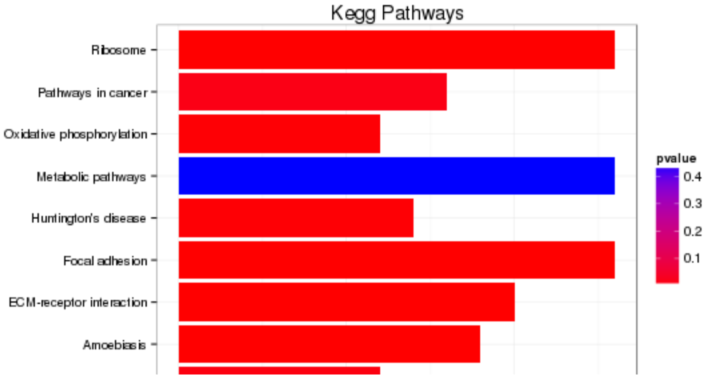
GO enrichment

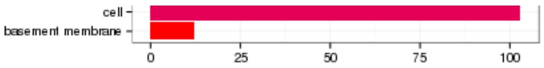
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

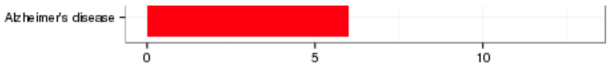

Enriched BP

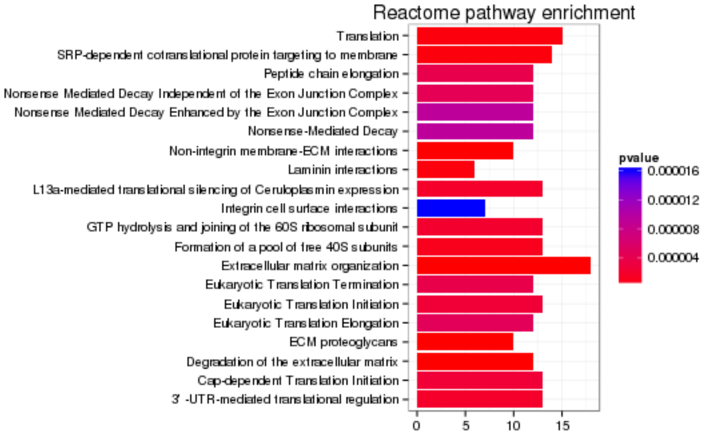

Enriched MF


Enriched CC

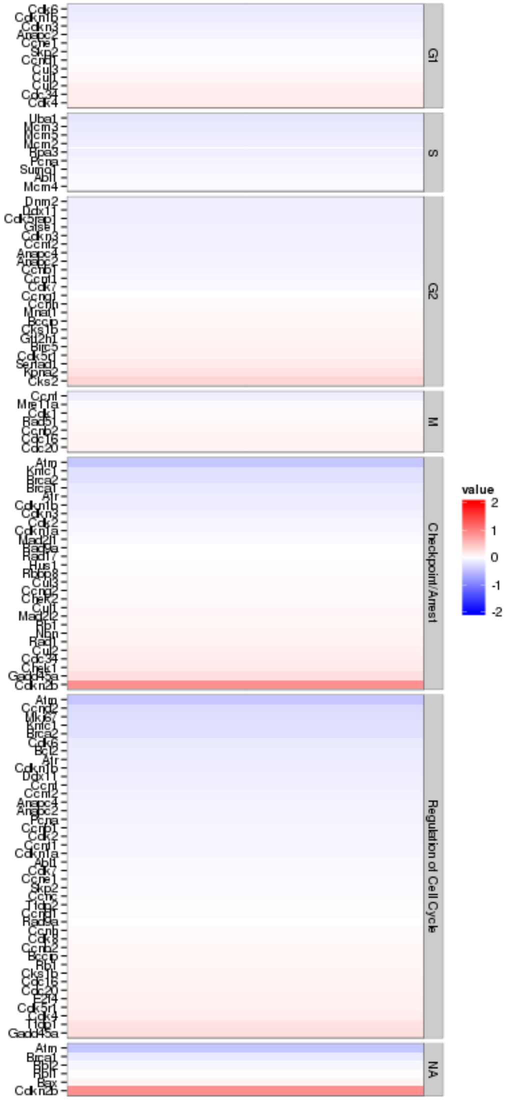

Kegg Pathways



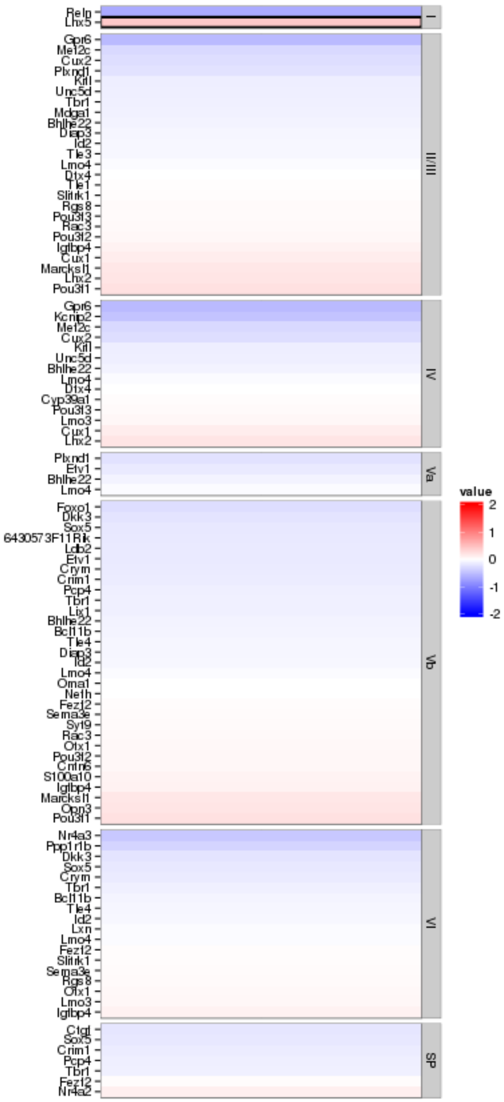




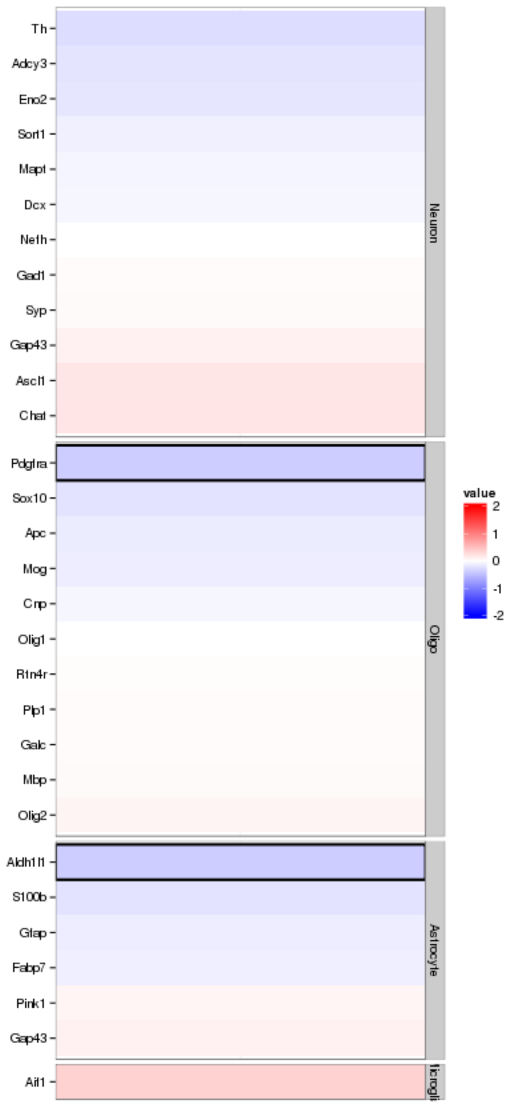
Enrichment or depletion for stage-specific cell cycle markers



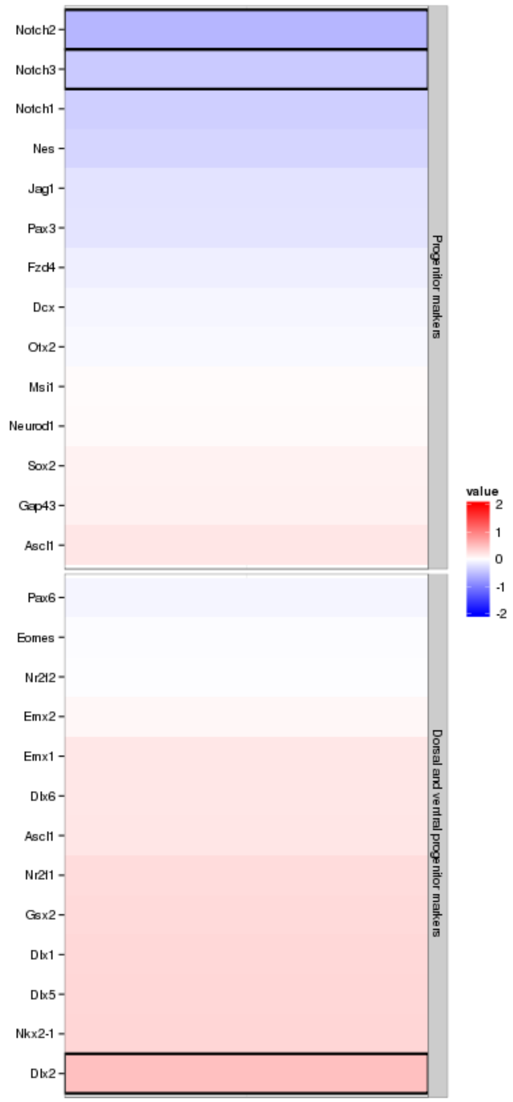
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



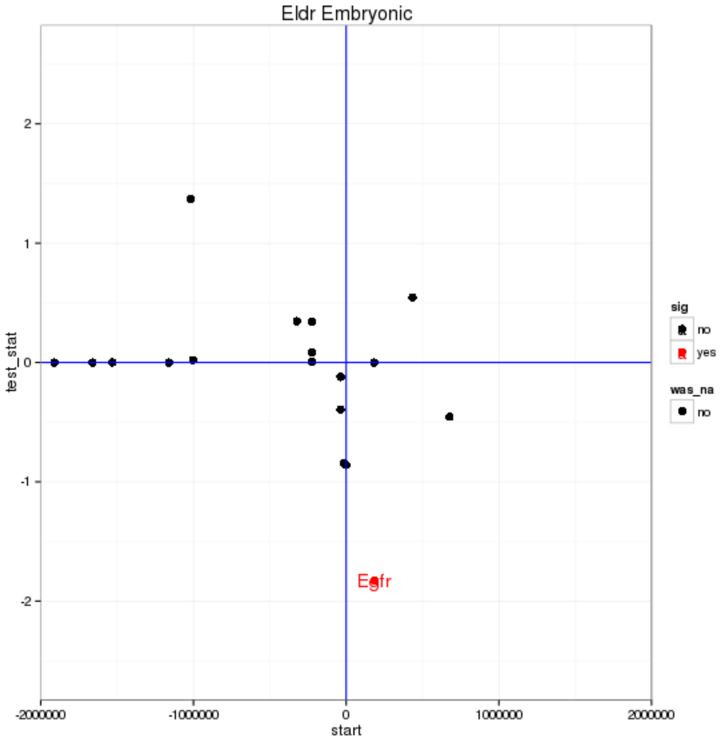
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 1 genes significantly regulated in a region this size is: 0.3083



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15	JR787
16	JR810
17	JR838

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	32543000.00	1.25	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	32543000.00	1.09	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	32543000.00	1.22	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	32543000.00	1.27	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	32543000.00	1.19	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	32543000.00	0.88	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	32543000.00	0.96	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	32543000.00	0.91	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	32543000.00	0.85	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	32543000.00	0.95	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	32543000.00	0.80	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	32543000.00	0.79	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	32543000.00	0.68	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	32543000.00	1.20	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR787/abundances.cxb	Eldr	0	Eldr_0	26894700.00	32543000.00	0.83	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR810/abundances.cxb	Eldr	1	Eldr_1	41828800.00	32543000.00	1.29	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR838/abundances.cxb	Eldr	2	Eldr_2	37002600.00	32543000.00	1.15	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1                        
##  [2] stringr_0.6.2                     
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##            param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,Eldr -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Eldr_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/
## 2
## 3
## 4
## 5
```

Haunt KO vs WT (Adult)

This file shows the wt-v-ko comparison for Haunt.

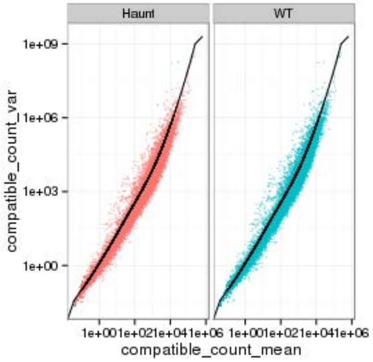
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

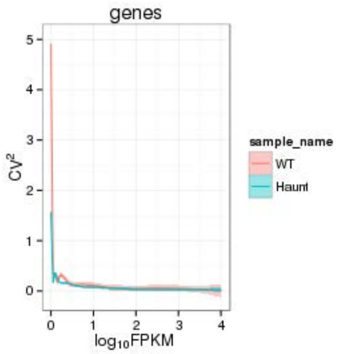
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



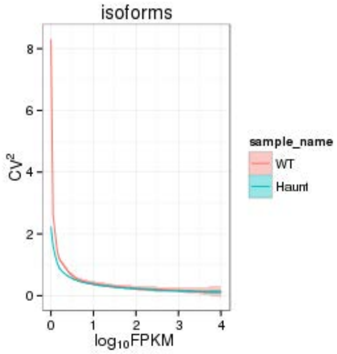
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

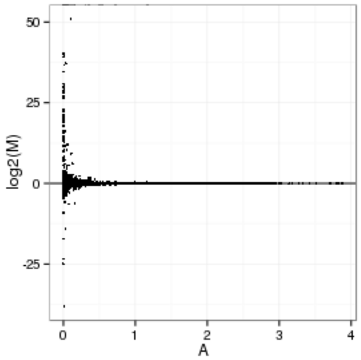
Genes:



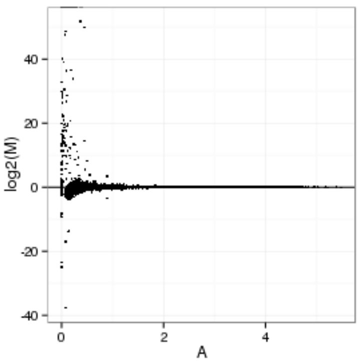
Isoforms:



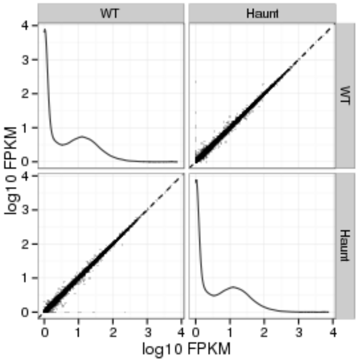
MvA plot



MvA plot counts



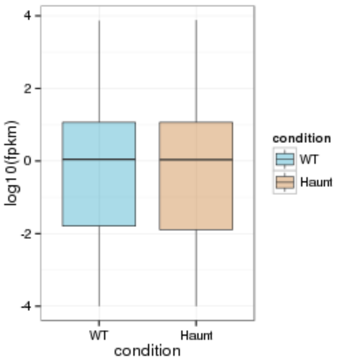
Scatterplot matrix



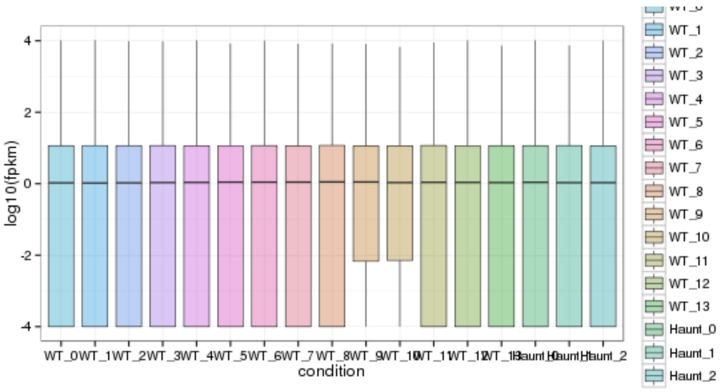
Distributions

Boxplots

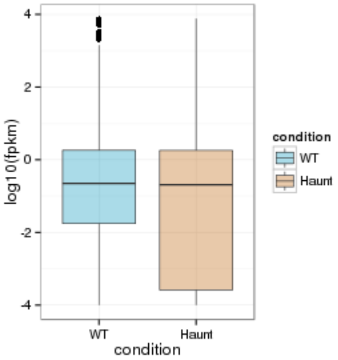
Boxplot (genes)



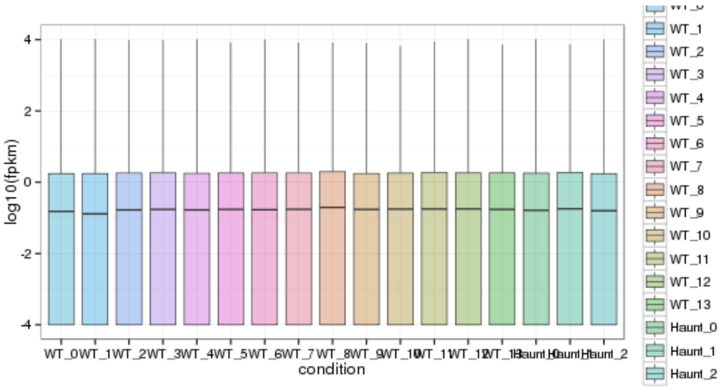
Boxplot (genes, replicates)



Boxplot (isoforms)

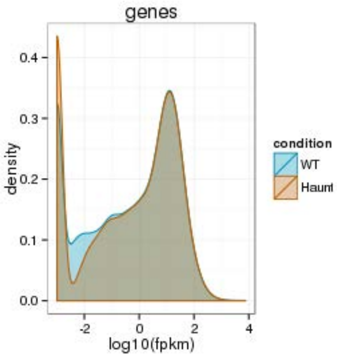


Boxplot (isoforms, replicates)

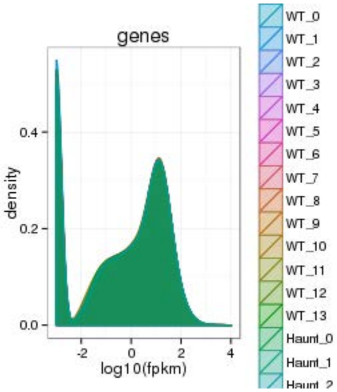


Density

Density (genes)

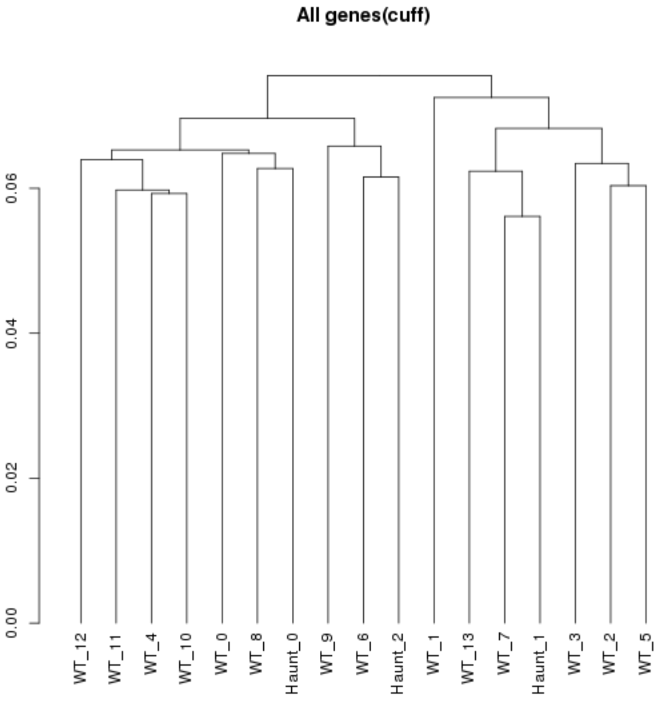


Density (genes, replicates)



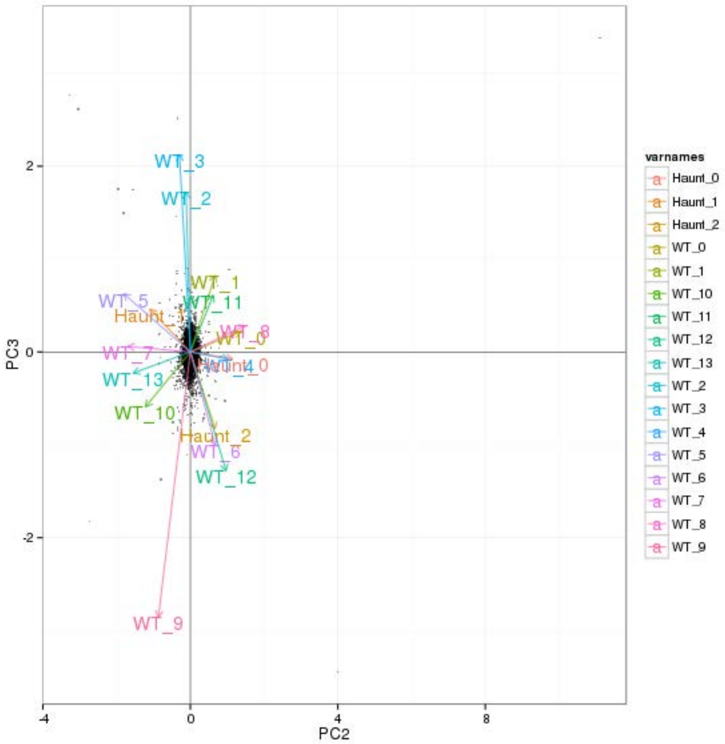
Clustering

Replicate Clusters



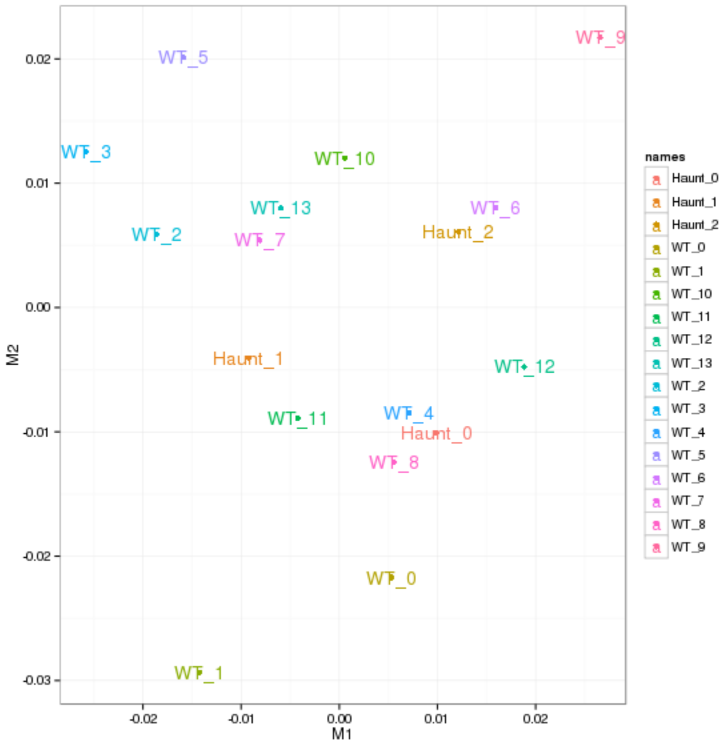
```
## NULL
```

PCA (genes)



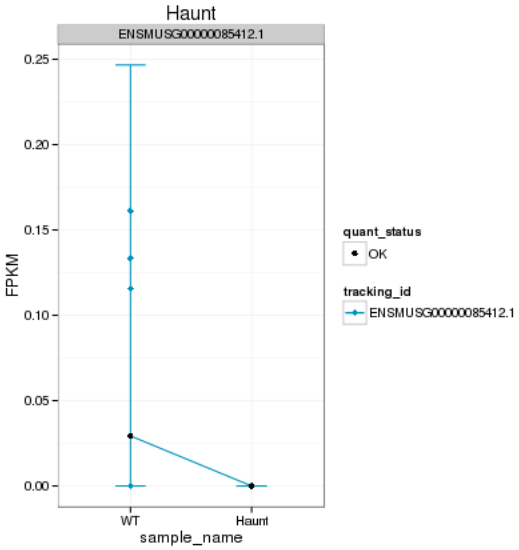
varnames
Haunt_0
Haunt_1
Haunt_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
PC3
PC2
2
0
-2
-4
0
4
8

MDS (genes)

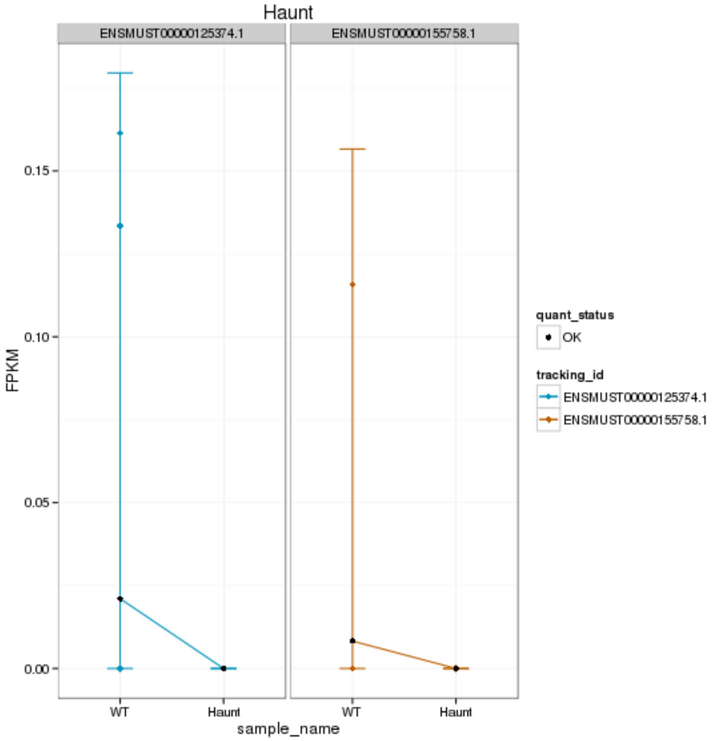


KO assessment

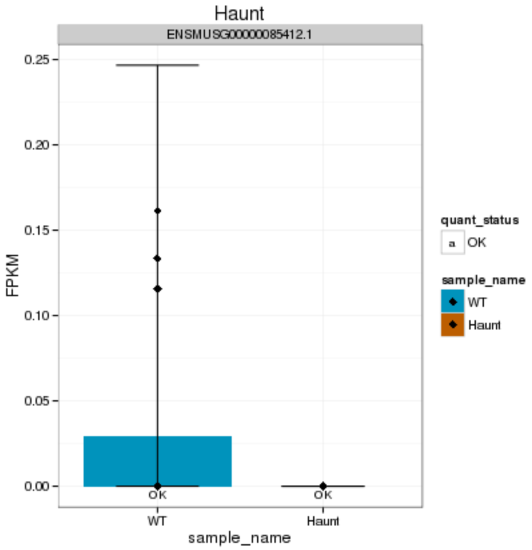
Endogenous lncRNA expression



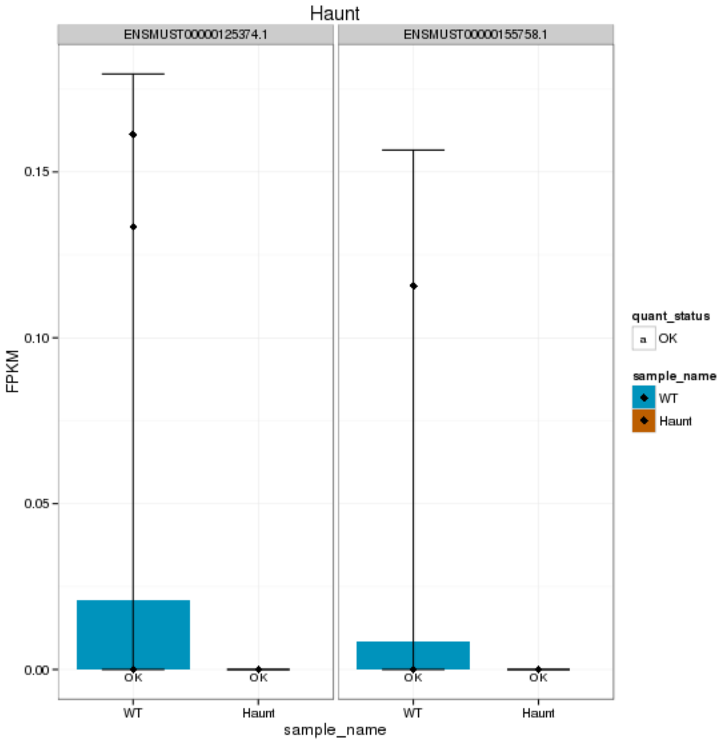
Endogenous expression of Haunt isoforms:



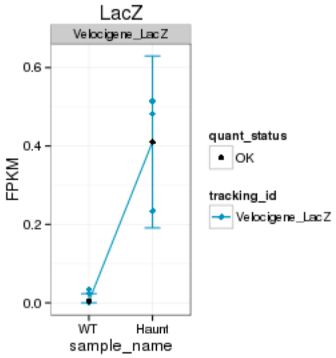
Barplot of gene expression:

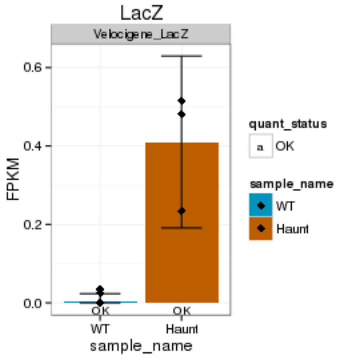


Barplot of isoform expression:



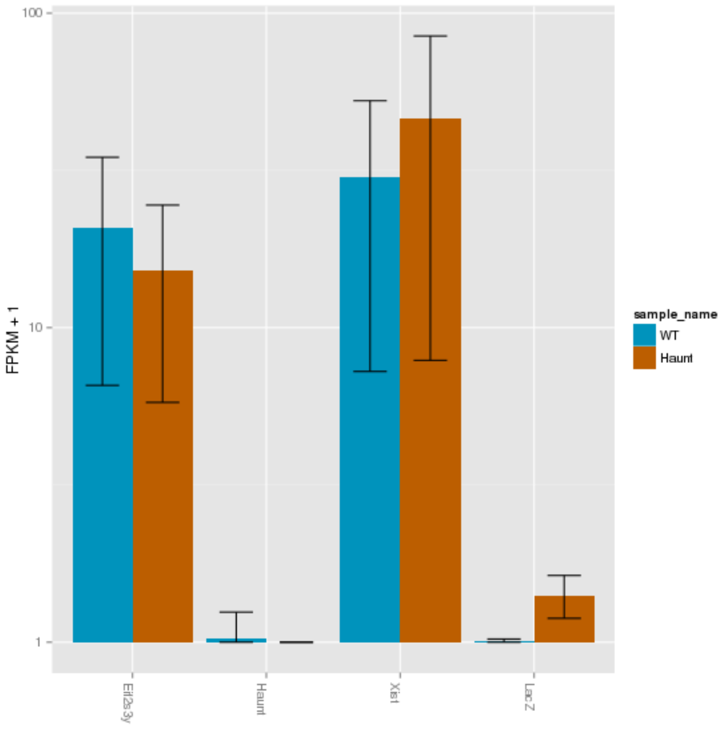
LacZ expression



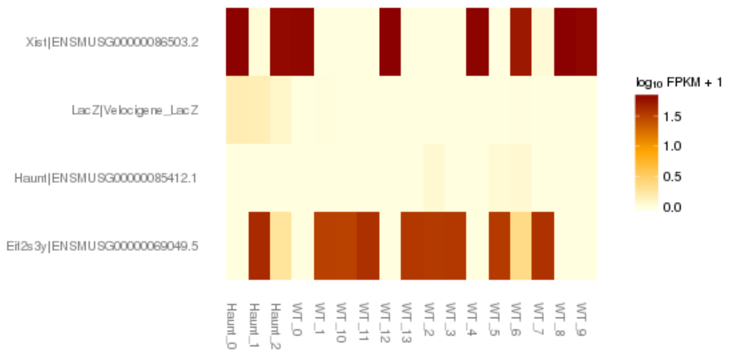


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

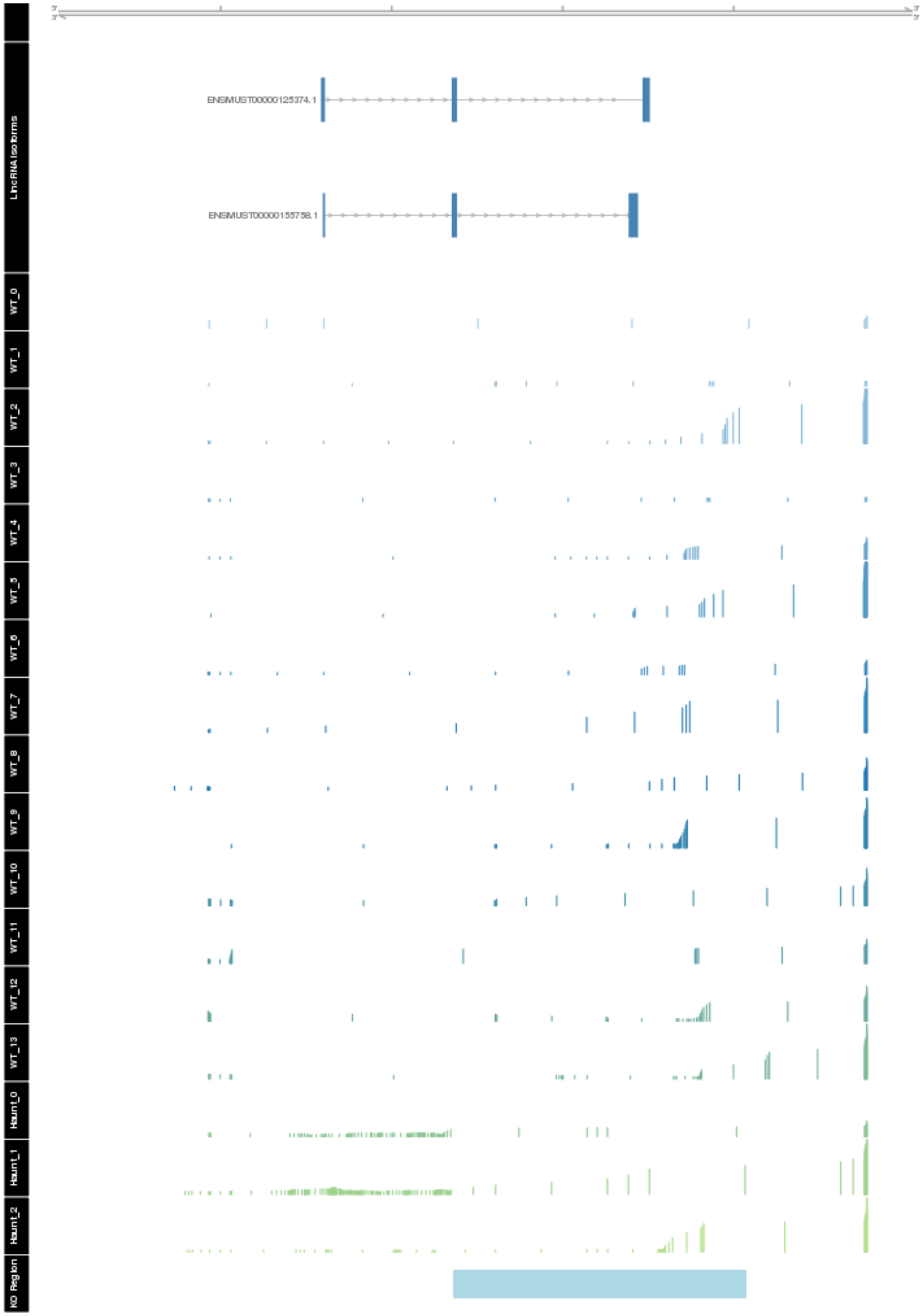
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


LincRNA Isoforms
ENSMUST00000125374.1
ENSMUST00000155758.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Haunt_0
Haunt_1
Haunt_2
KO Region

Differential Analysis

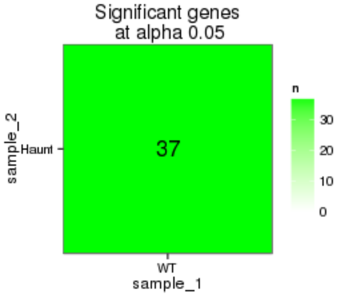
Differential Genes

There are 37 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Hspa8
2	Ubb
3	Dusp6
4	Pttg1
5	Adi1
6	Serpina3n
7	Fos
8	Arc
9	Nr4a1
10	Glo1
11	Xdh
12	Nr4a3
13	Hddc3
14	Cryab
15	Arhgap27
16	Fam214a
17	Filip1
18	Klf10
19	Egr2
20	Txnip
21	Egr1
22	Akap12
23	Atp5l
24	Maff
25	Gm9493
26	Acp1
27	Npas4
28	Hbb-bs
29	Junb
30	Kdm5d
31	Tpm3-rs7
32	Rpl34
33	Ddx3y
34	Egr4
35	Gm7292
36	AA465934
37	Gm26825

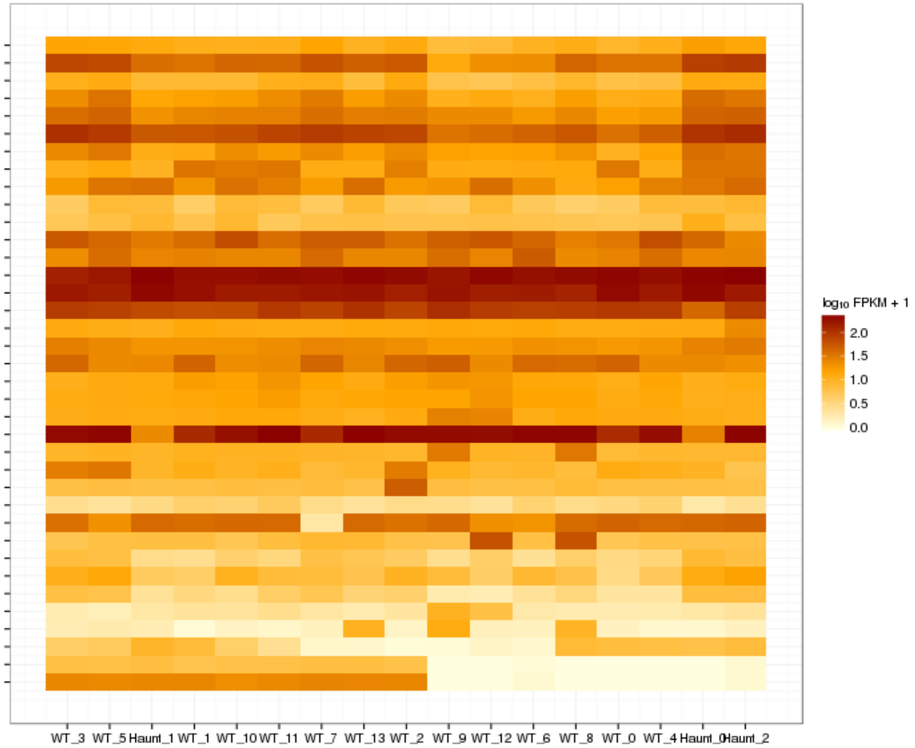
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

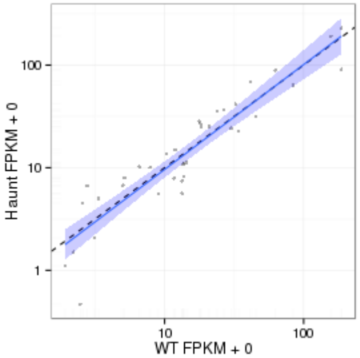


Significant genes with expression >50fpkm (any condition):(turned off)

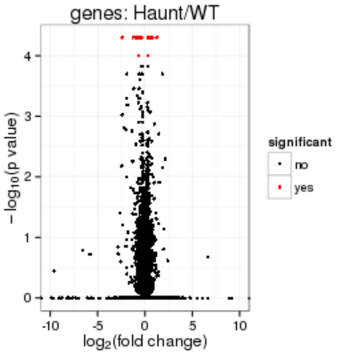
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

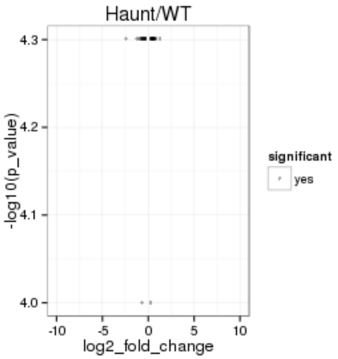
Scatter plot of significant genes only:



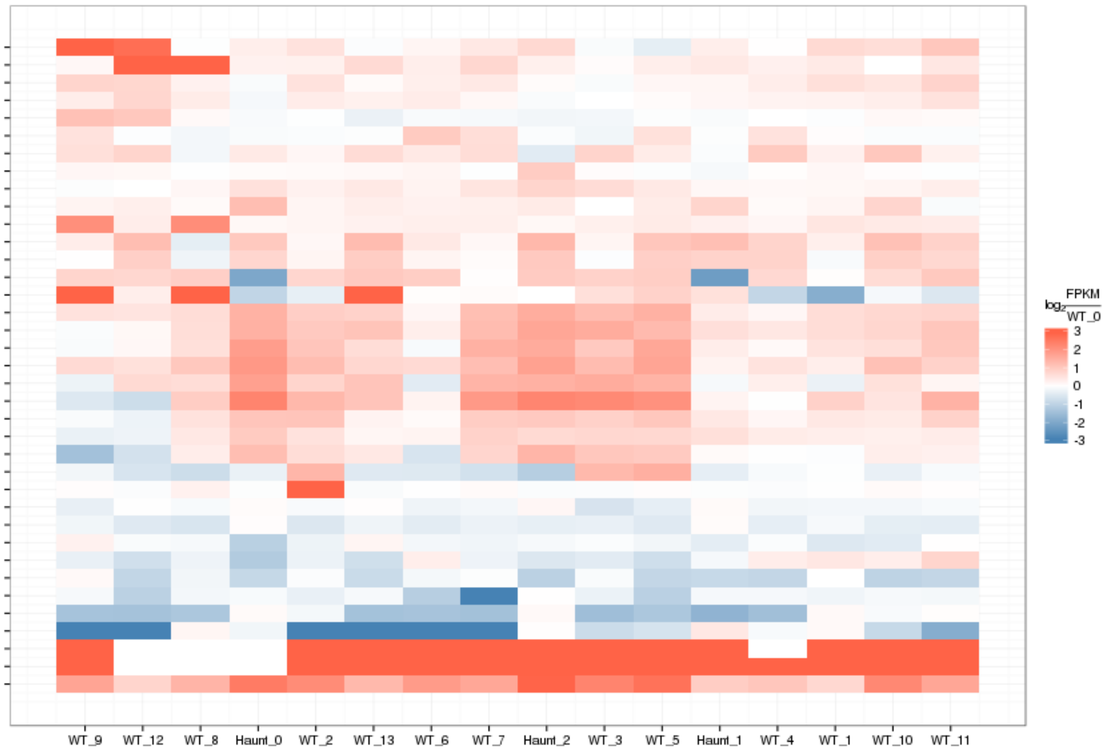
Volcano Plot



Volcano plot with significant genes only:



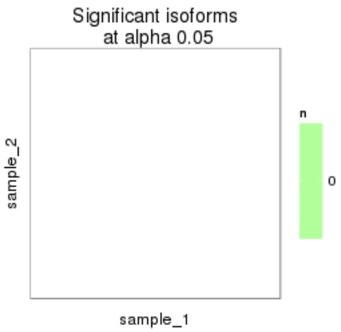
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

[1] “no sig isoforms”

Gene-level DE isoform heatmap

```
## [1] "no sig isoforms"
```

Isoform foldchange heatmap by isoform:

```
## [1] "no sig isoforms"
```

Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:

```
## Error: `x' must have at least 2 rows and 2 columns
```

Biocarta zscore:

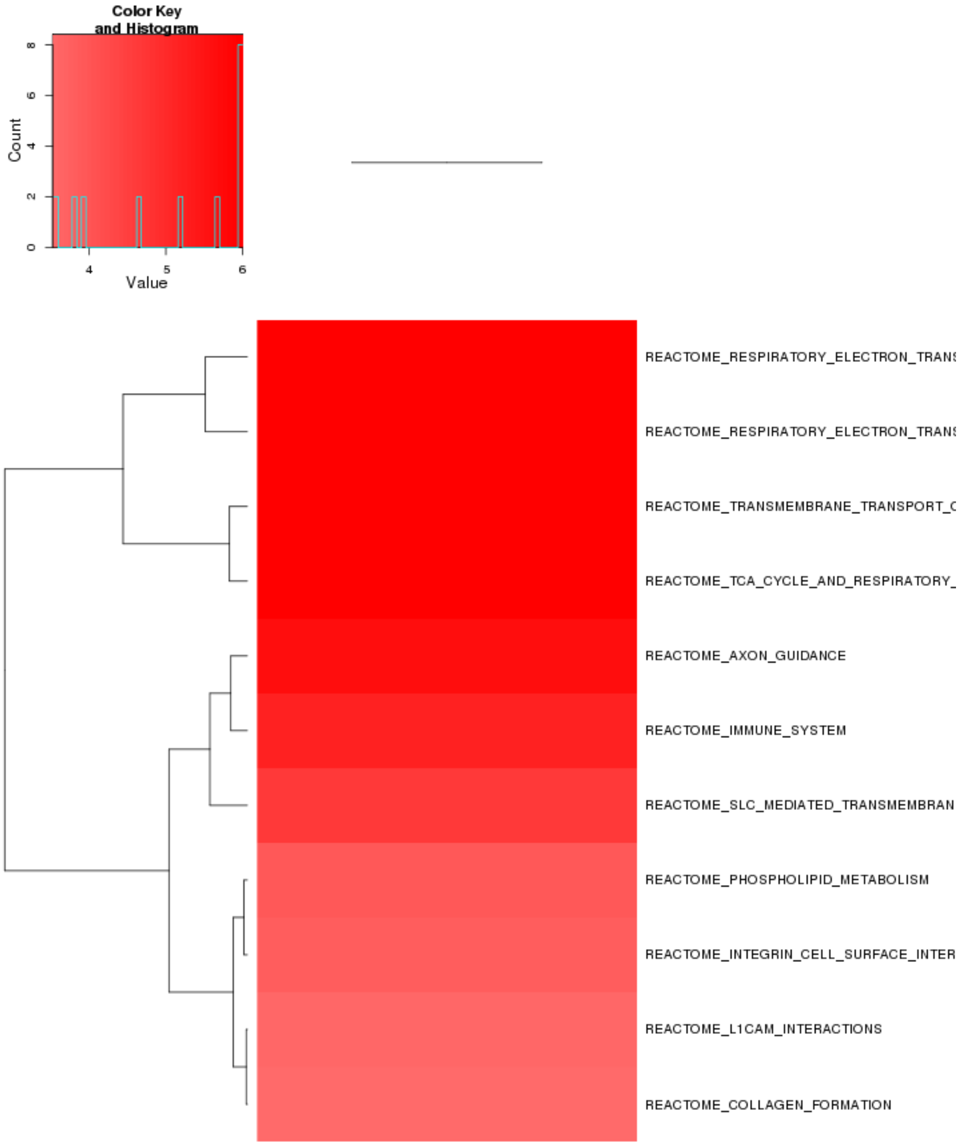
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

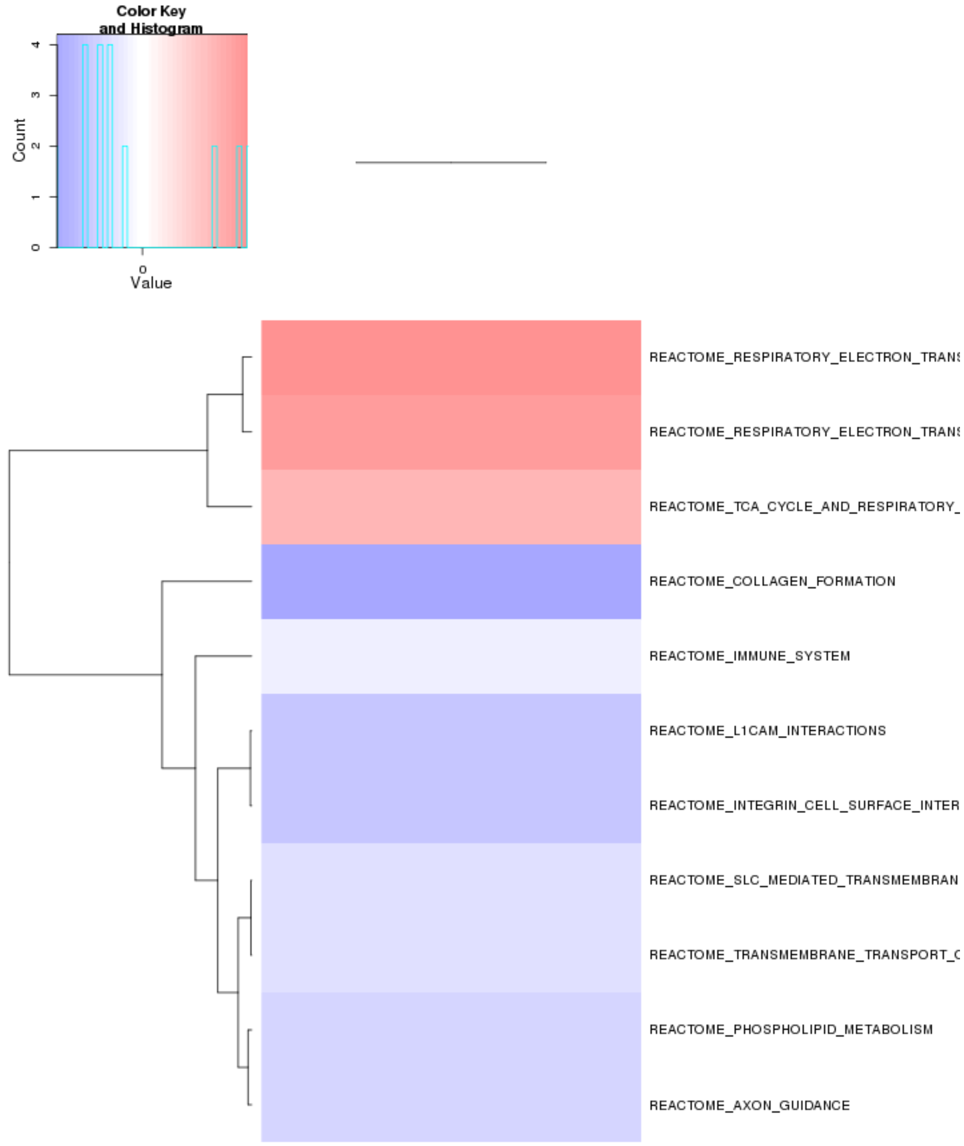
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

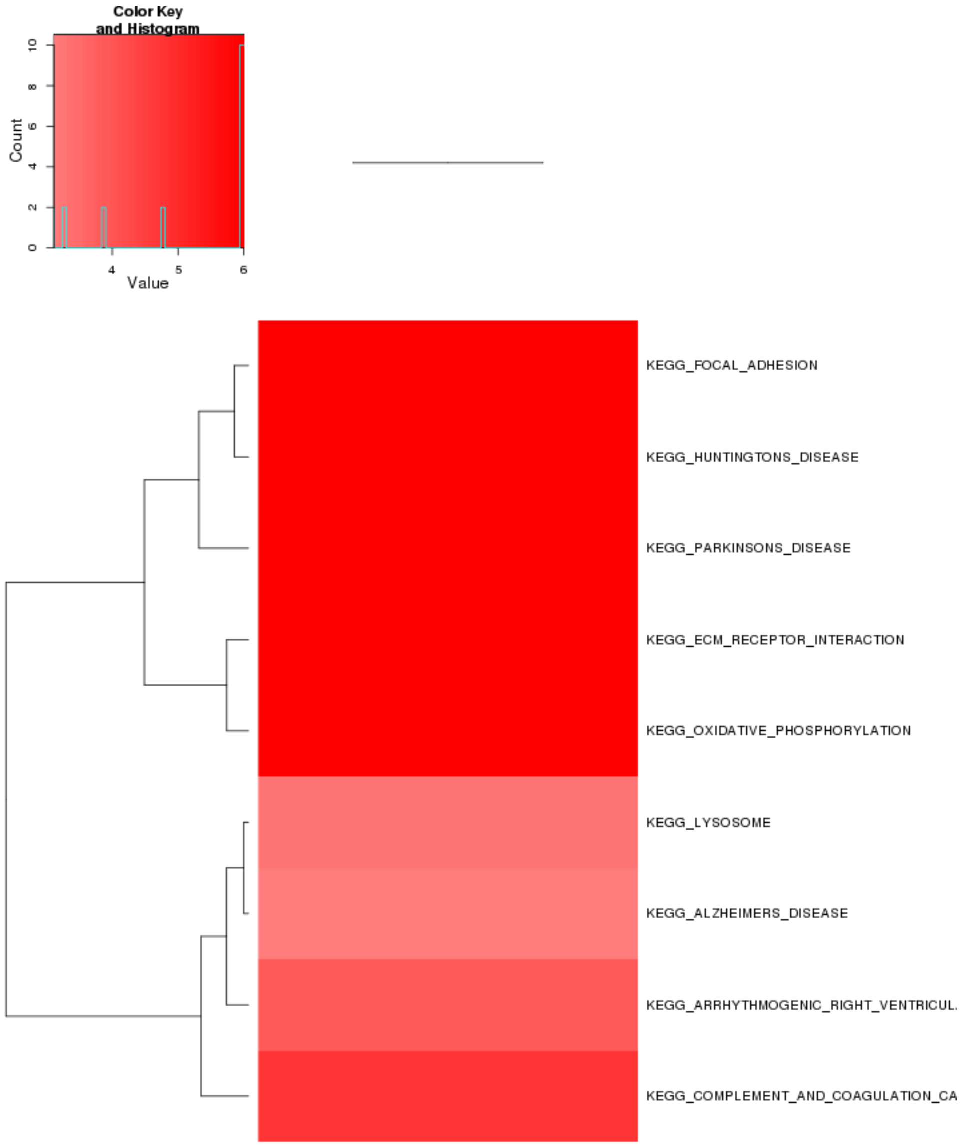
Reactome enrichment:



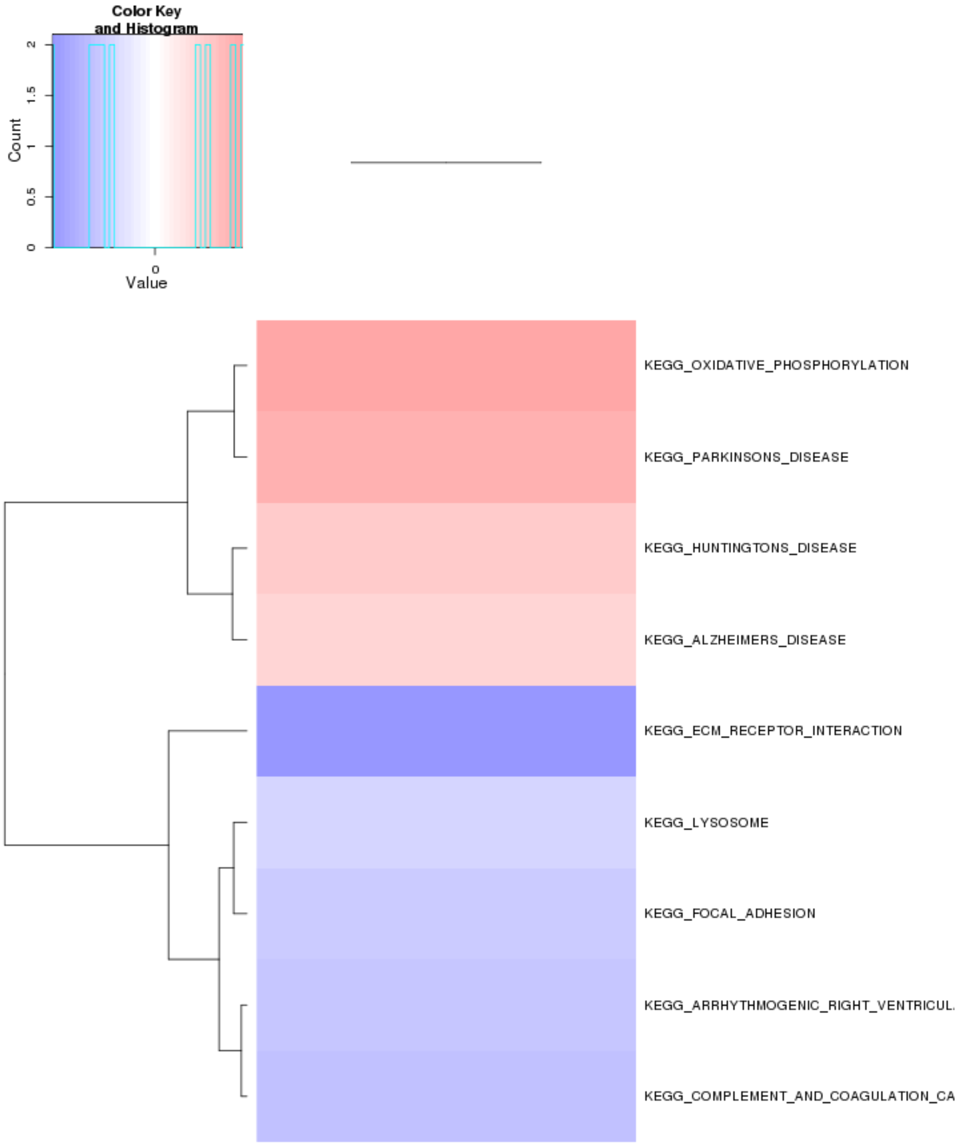
Reactome zscore:



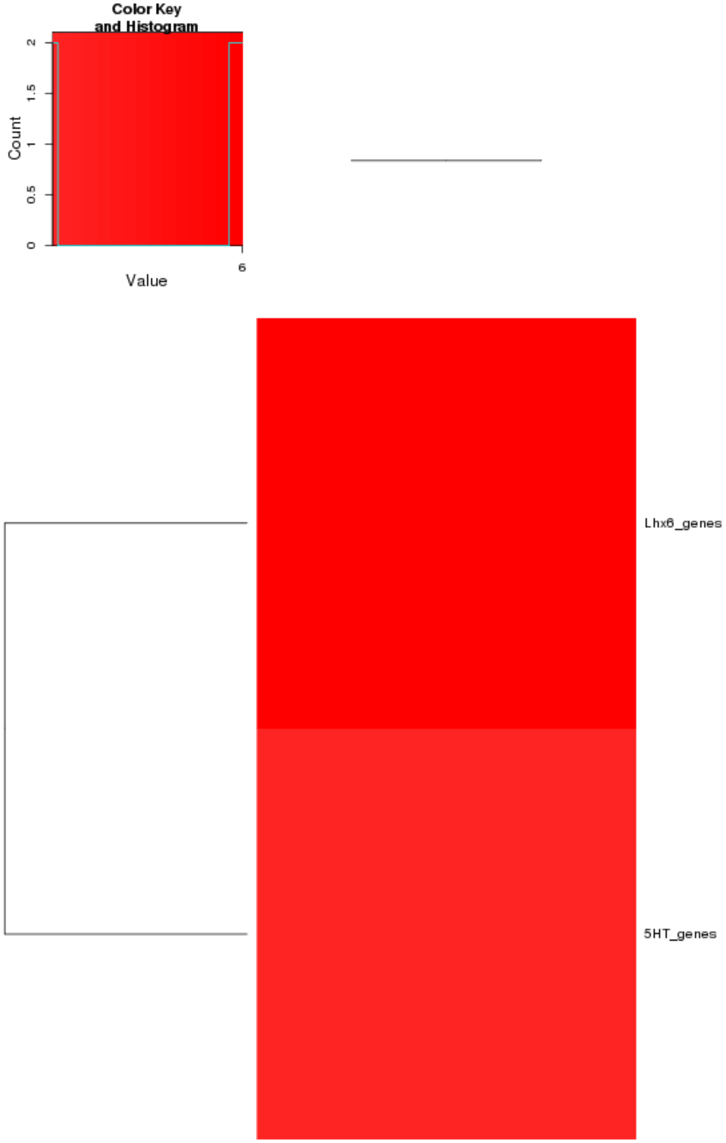
Kegg enrichment:


Color Key
and Histogram
Count
Value
0
2
4
6
8
10
4
5
6
KEGG_FOCAL_ADHESION
KEGG_HUNTINGTONS_DISEASE
KEGG_PARKINSONS_DISEASE
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_LYSOSOME
KEGG_ALZHEIMERS_DISEASE
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICUL.
KEGG_COMPLEMENT_AND_COAGULATION_CA

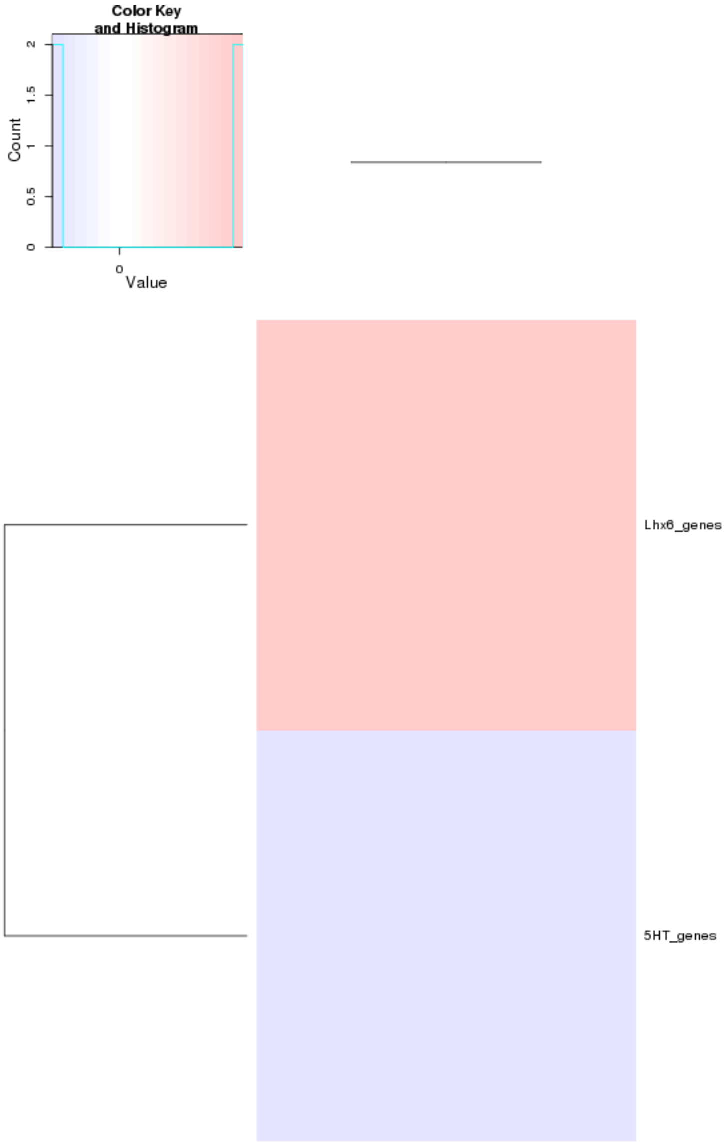
Kegg zscore:



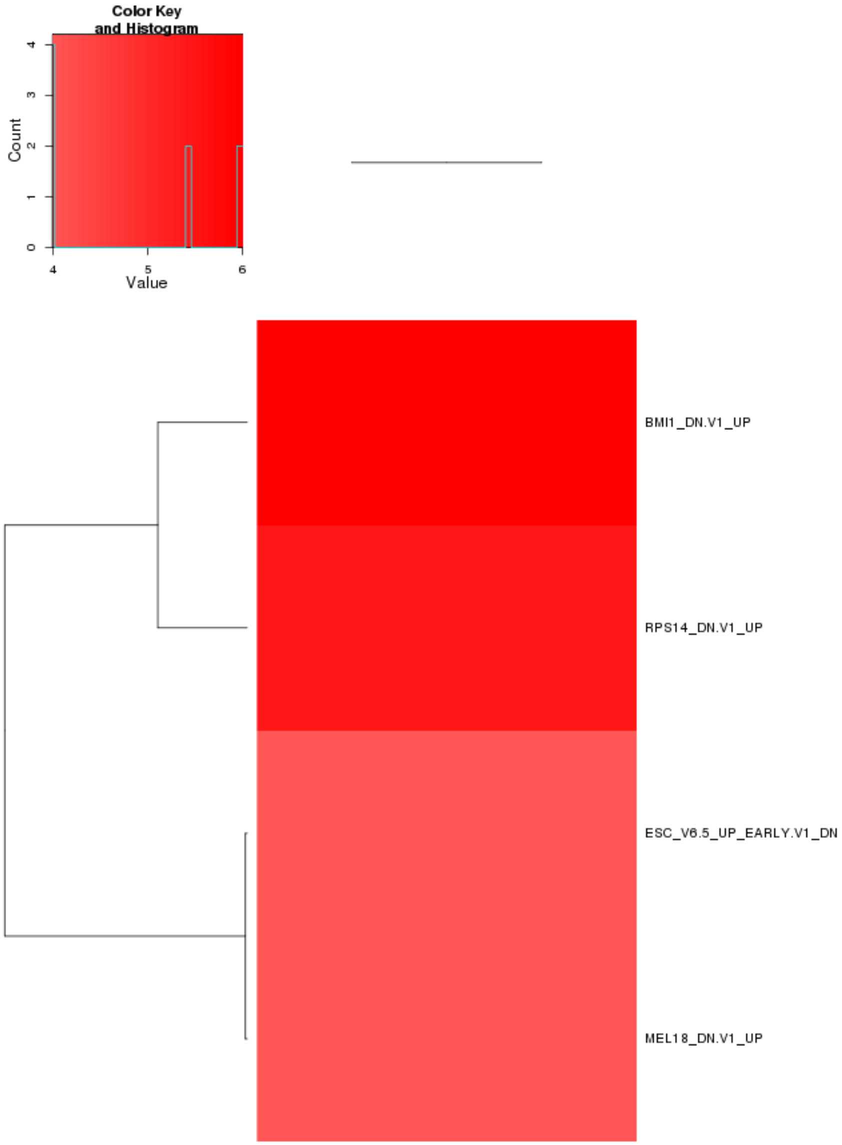
Interneuron enrichment:



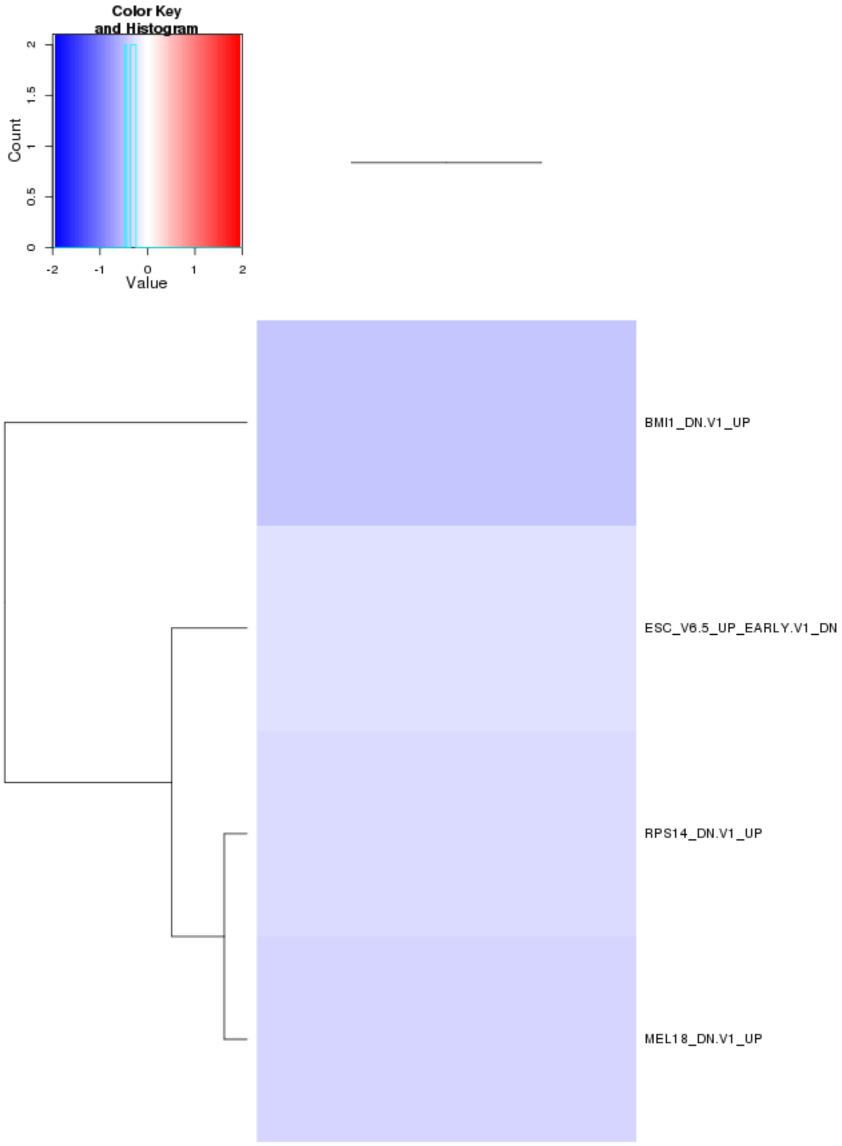
Interneuron zscore:



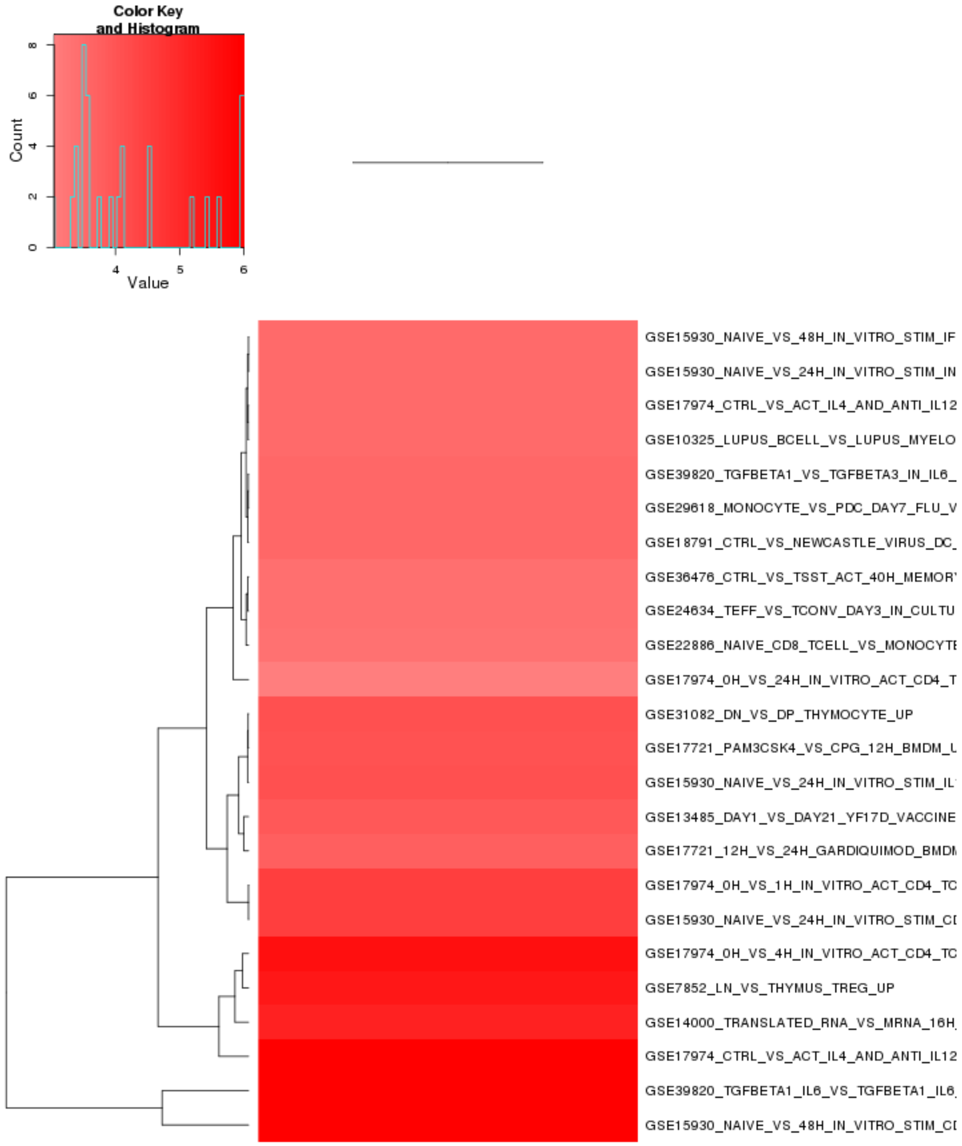
Oncogene enrichment:



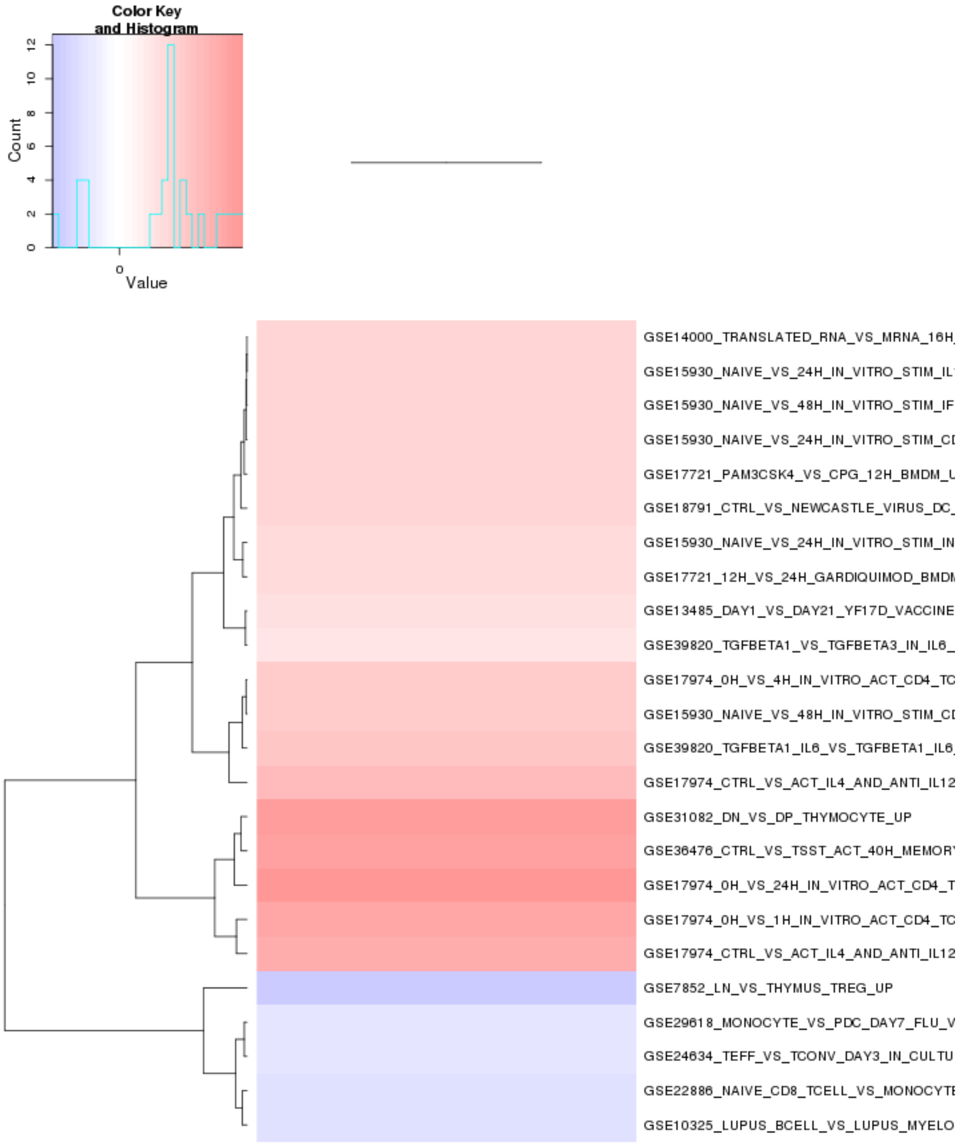
Oncogene zscore:



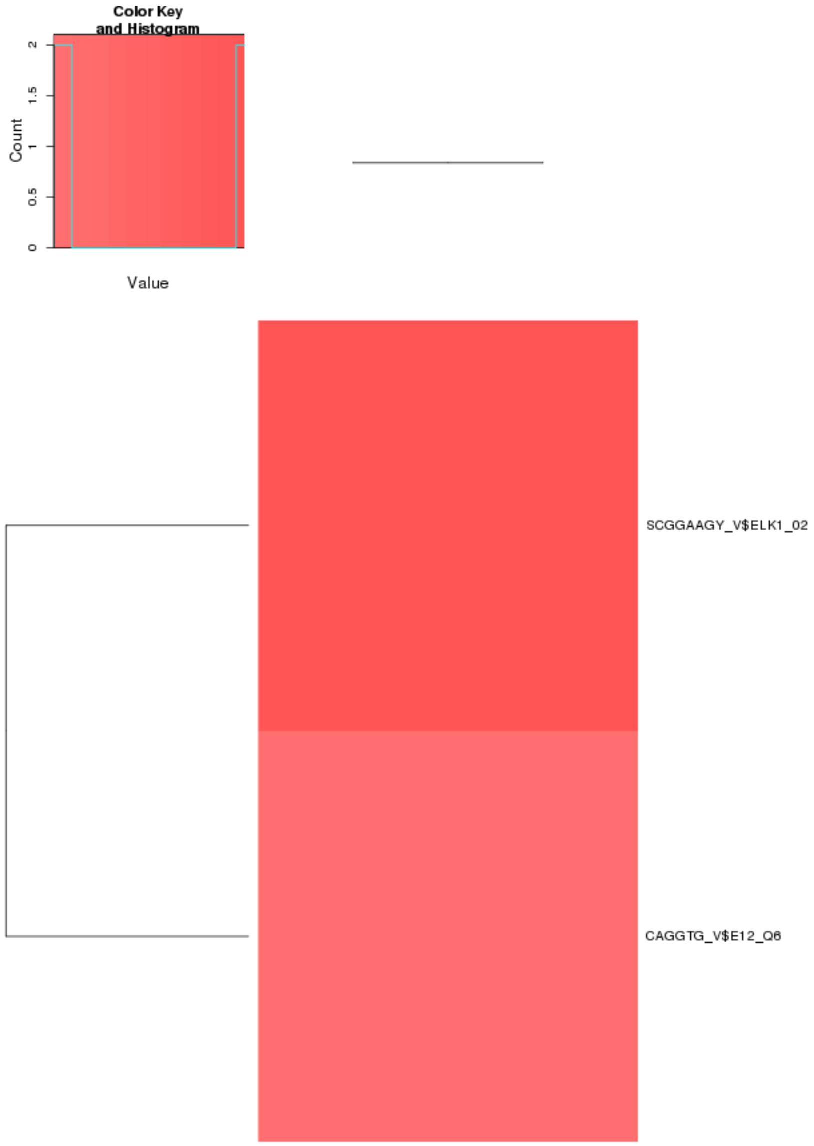
Immuno enrichment:



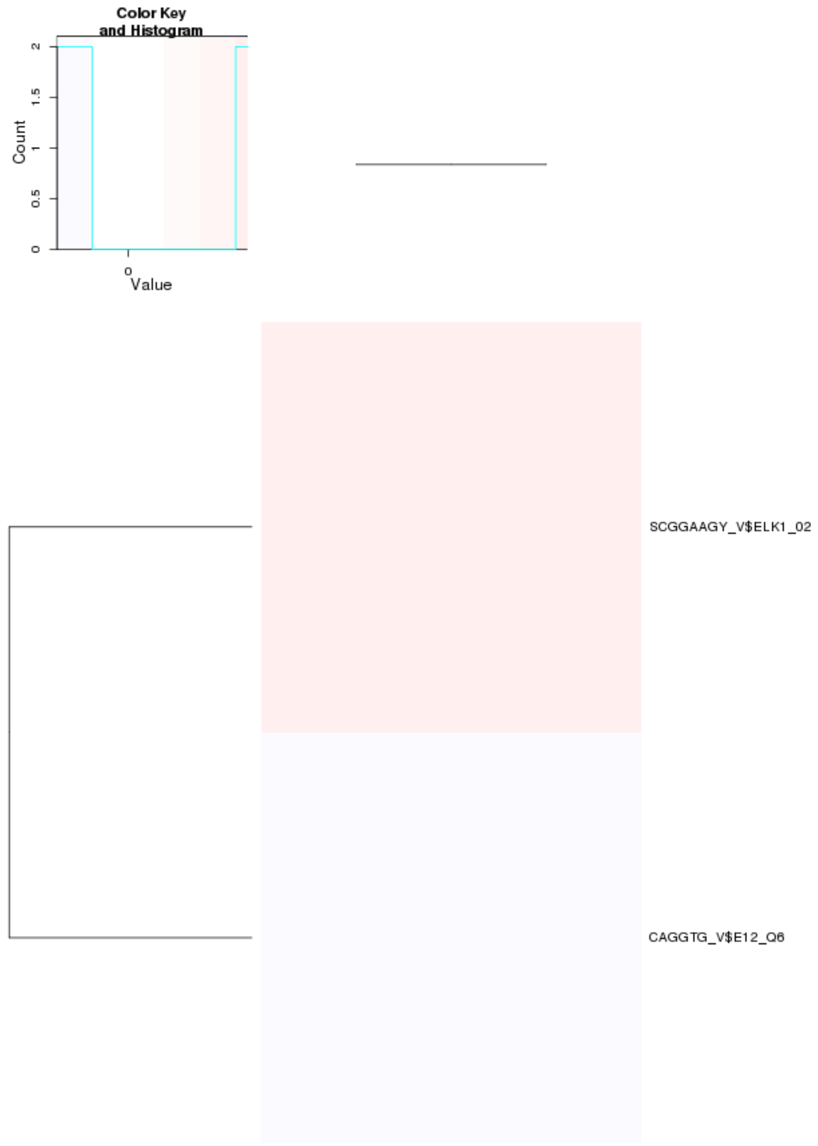
Immuno zscore:



TF enrichment:

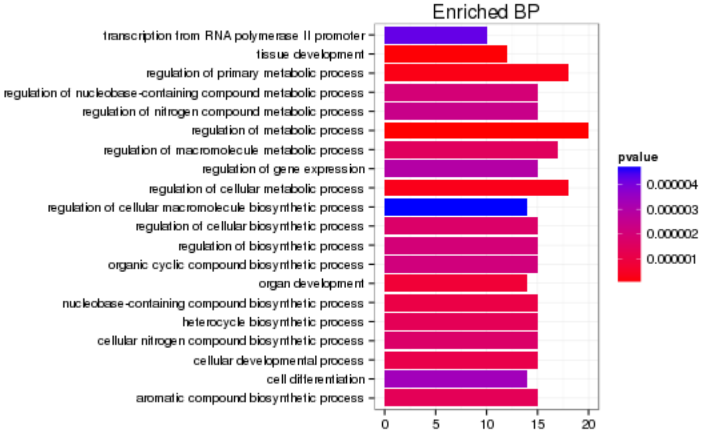

Color Key
and Histogram
Count
0
0.5
1
1.5
2
Value
SCGGAAGY_V$ELK1_02
CAGGTG_V$E12_Q6

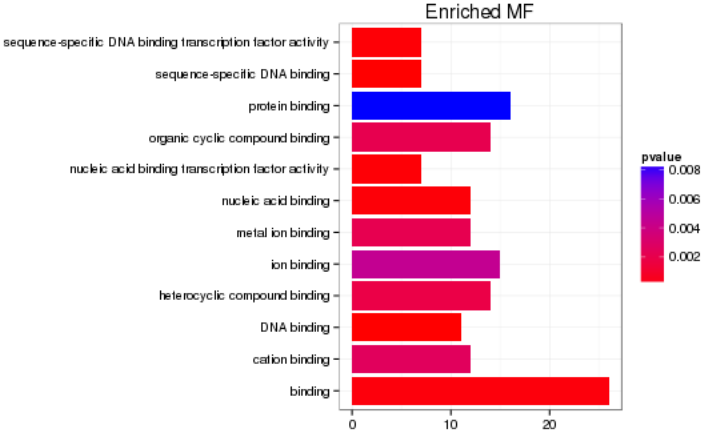
TF zscore:

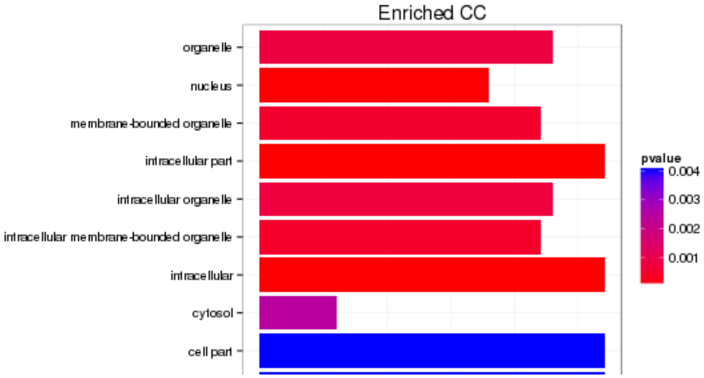


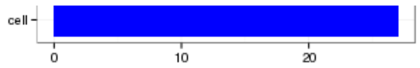
GO enrichment

Cluster profiler used to call enichments of significantly differentially regulated genes that map to Entrez IDs.


Enriched BP


Enriched MF

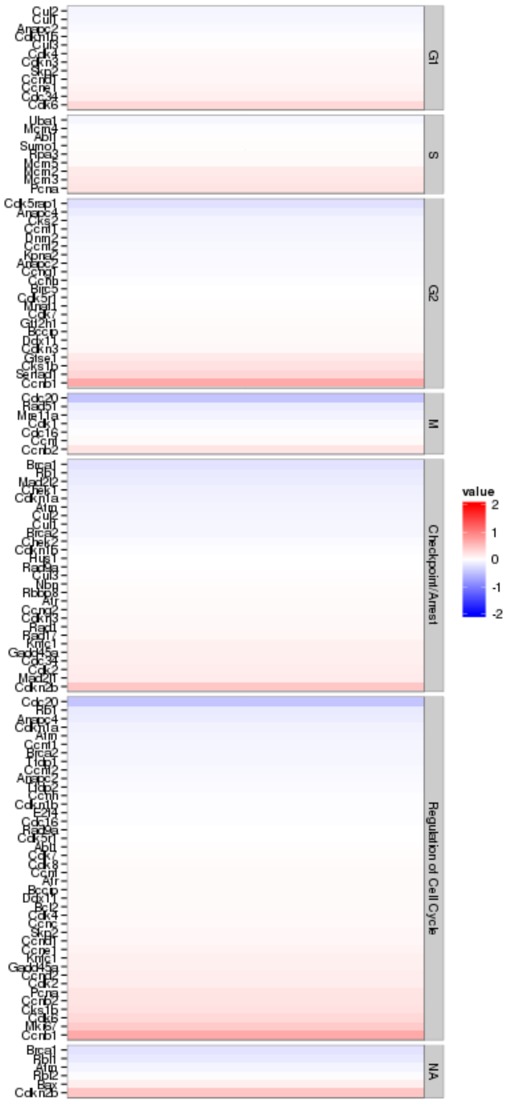

Enriched CC



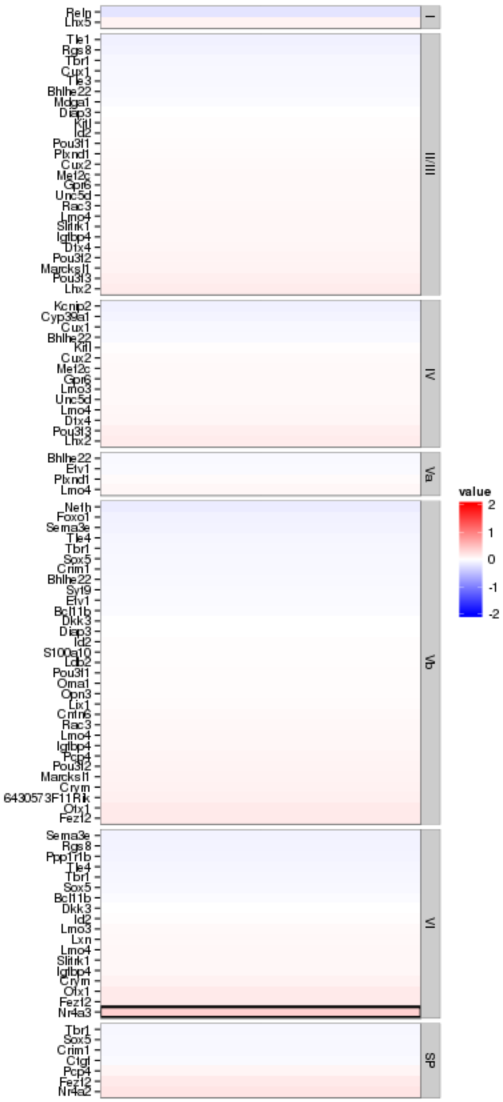
```
## Error: need finite 'xlim' values
```

```
## Error: need finite 'xlim' values
```

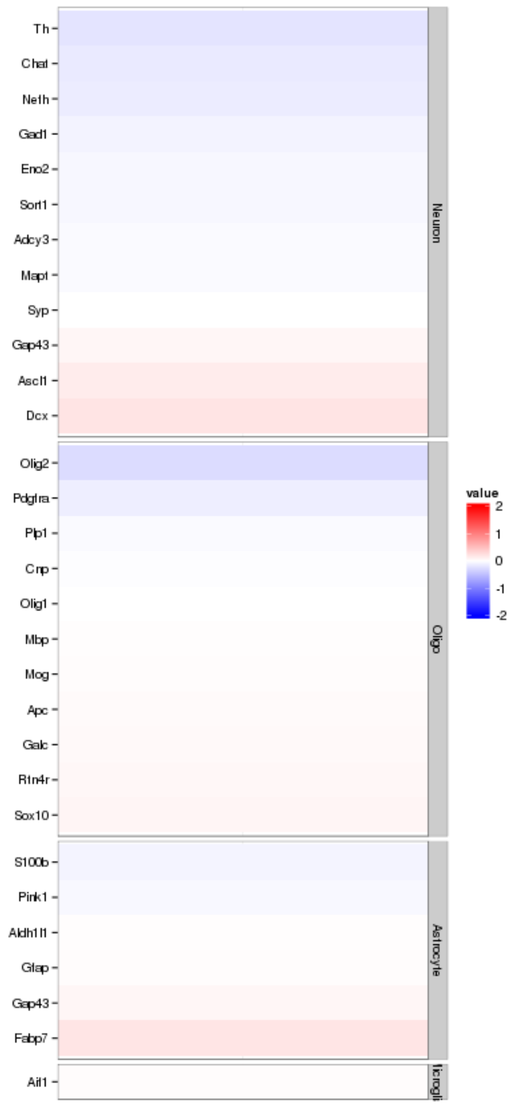
Enrichment or depletion for stage-specific cell cycle markers



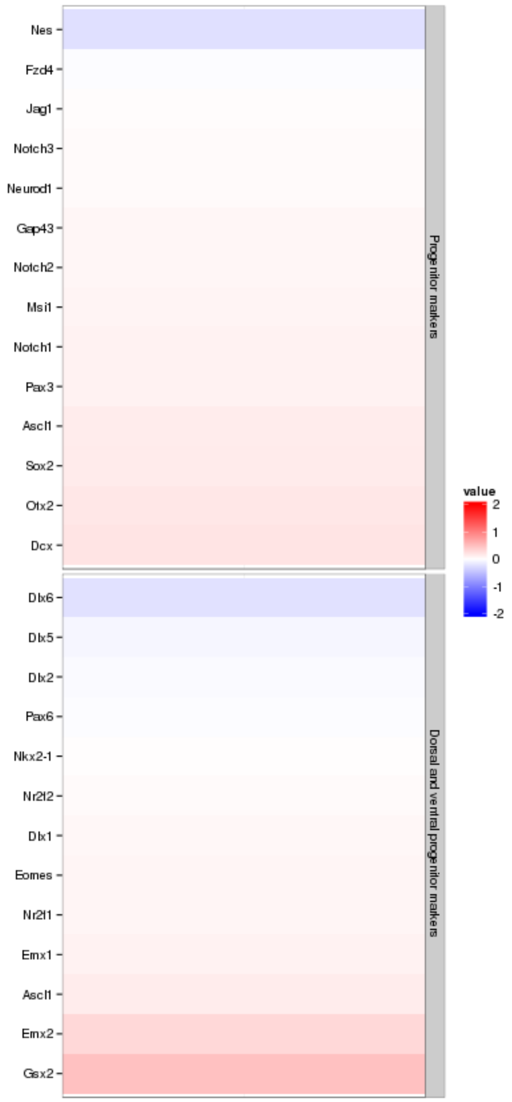
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



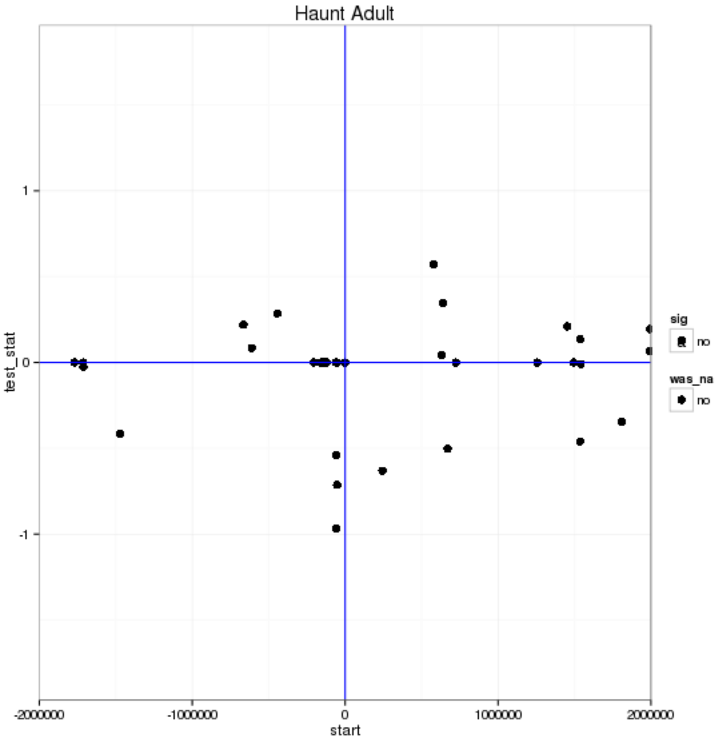
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15 JR738

16 JR782

17 JR826

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	34083500.00	0.77	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	34083500.00	0.59	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	34083500.00	1.00	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	34083500.00	0.81	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	34083500.00	1.05	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	34083500.00	1.09	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	34083500.00	0.82	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	34083500.00	1.17	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	34083500.00	1.03	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	34083500.00	1.32	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	34083500.00	1.53	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	34083500.00	1.03	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	34083500.00	0.99	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	34083500.00	1.22	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR738/abundances.cxb	Haunt	0	Haunt_0	26084100.00	34083500.00	0.77	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR782/abundances.cxb	Haunt	1	Haunt_1	43523200.00	34083500.00	1.28	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR826/abundances.cxb	Haunt	2	Haunt_2	33775800.00	34083500.00	0.99	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1                 
##  [2] stringr_0.6.2              
##  [3] seqbias_1.10.0             
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6          
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4      
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7             
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1         
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1          
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4          
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12    
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26   
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2         
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0         
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1    
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2         
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2           
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,Haunt -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Haunt_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/ar
## 2
## 3
## 4
## 5
```

Haunt KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for Haunt.

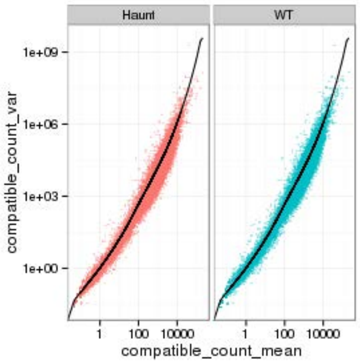
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

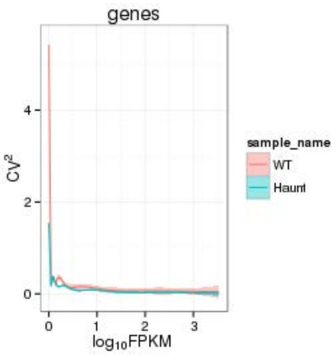
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



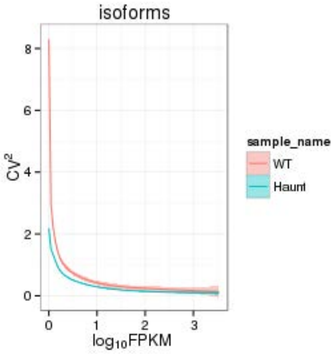
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

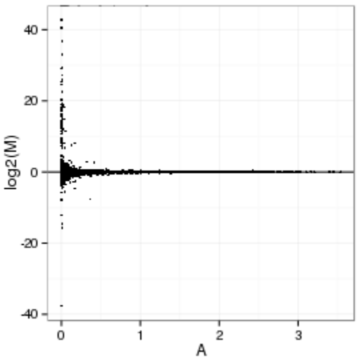
Genes:



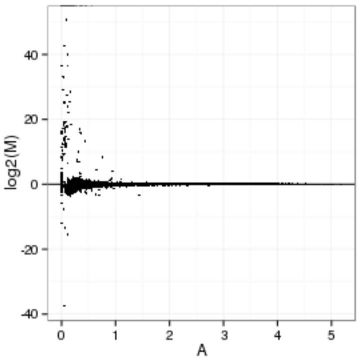
Isoforms:



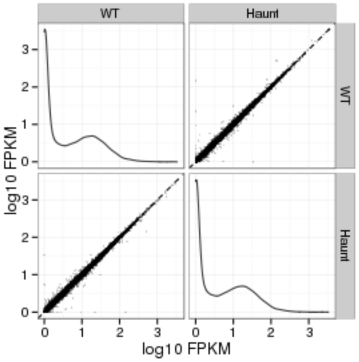
MvA plot



MvA plot counts



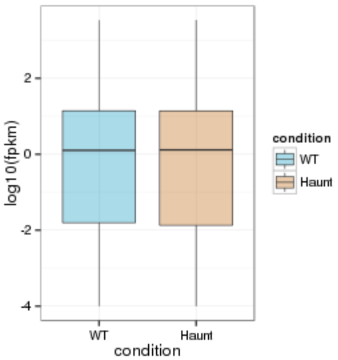
Scatterplot matrix



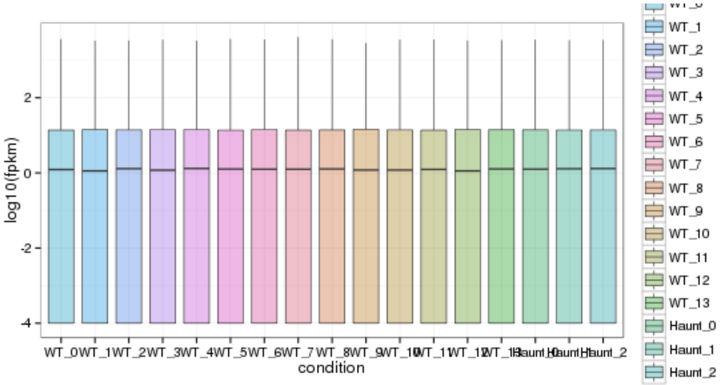
Distributions

Boxplots

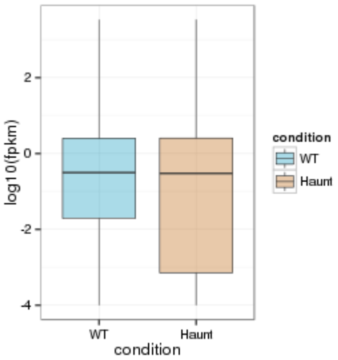
Boxplot (genes)



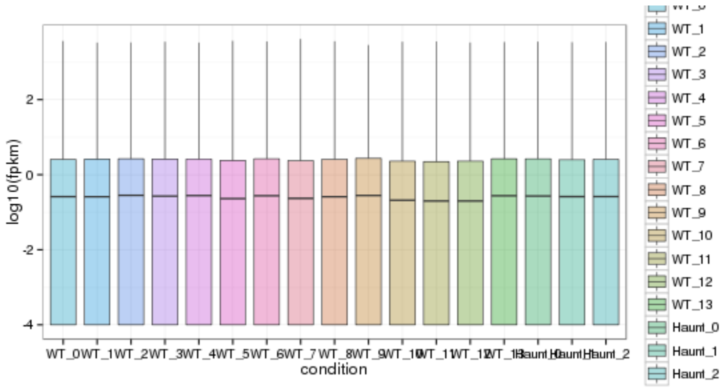
Boxplot (genes, replicates)



Boxplot (isoforms)

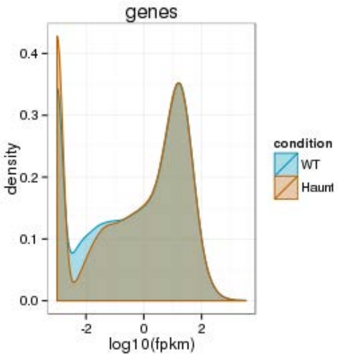


Boxplot (isoforms, replicates)

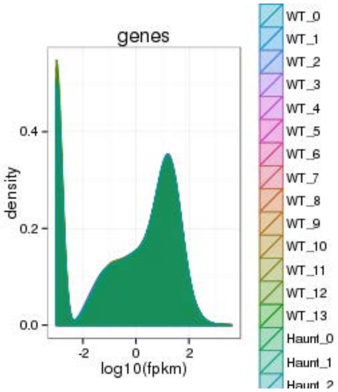


Density

Density (genes)

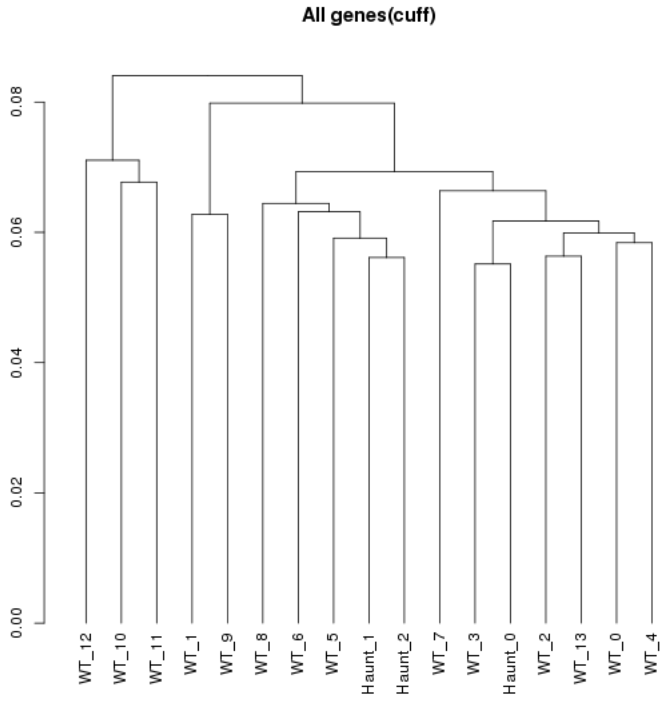


Density (genes, replicates)



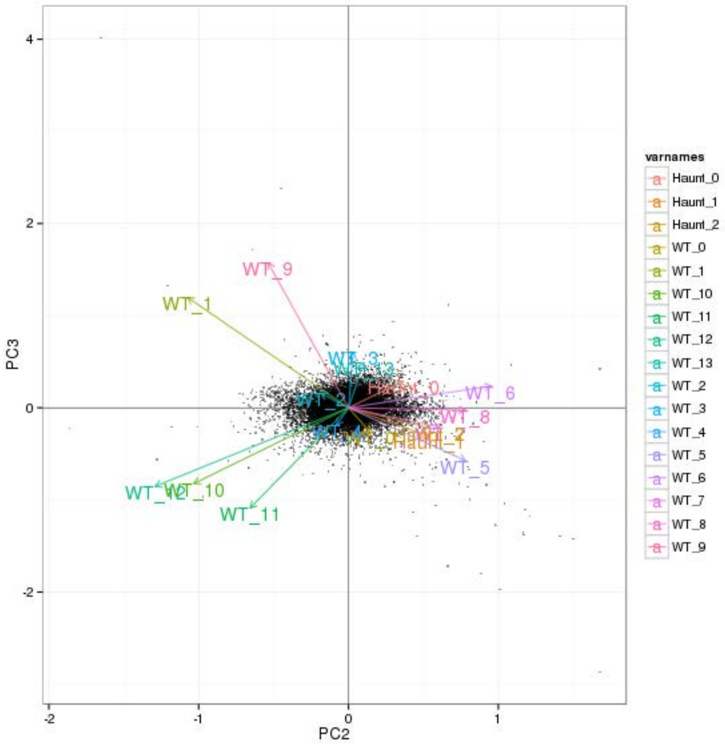
Clustering

Replicate Clusters



```
## NULL
```

PCA (genes)

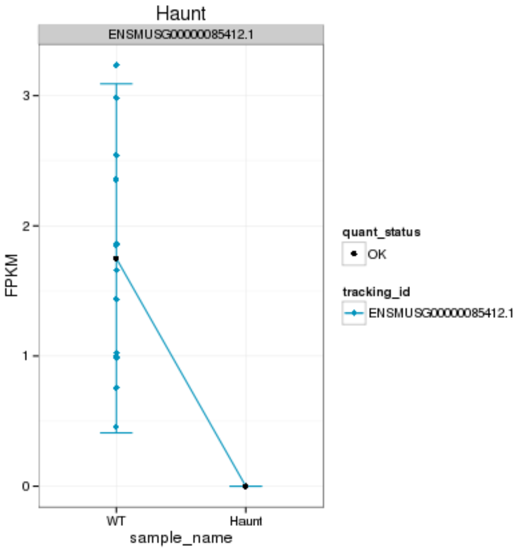


4
2
0
-2
PC3
-2
-1
0
1
PC2
WT_9
WT_1
WT_3
Haunt_0
WT_6
WT_8
Haunt_1
WT_5
WT_12
WT_10
WT_11
varnames
Haunt_0
Haunt_1
Haunt_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

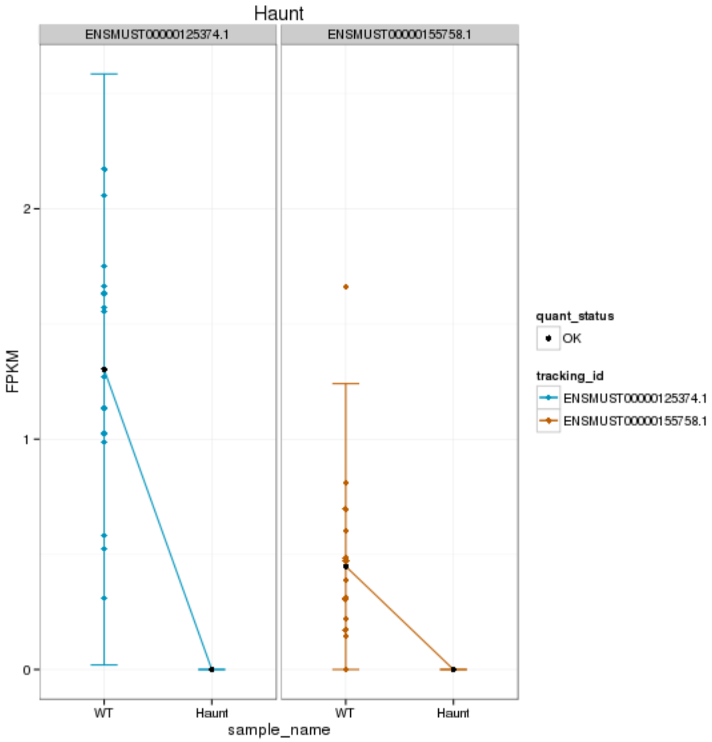
MDS (genes)

KO assessment

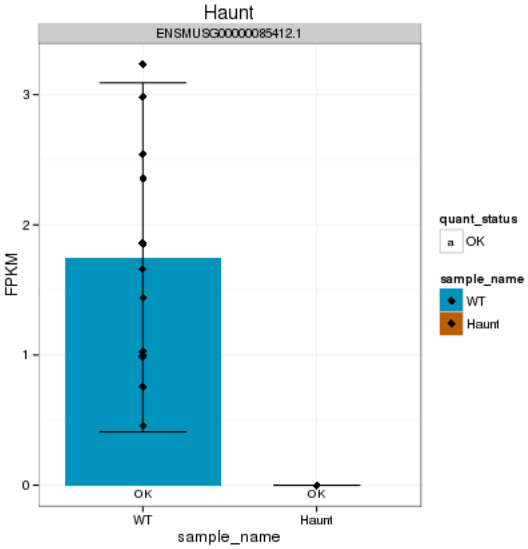
Endogenous lncRNA expression



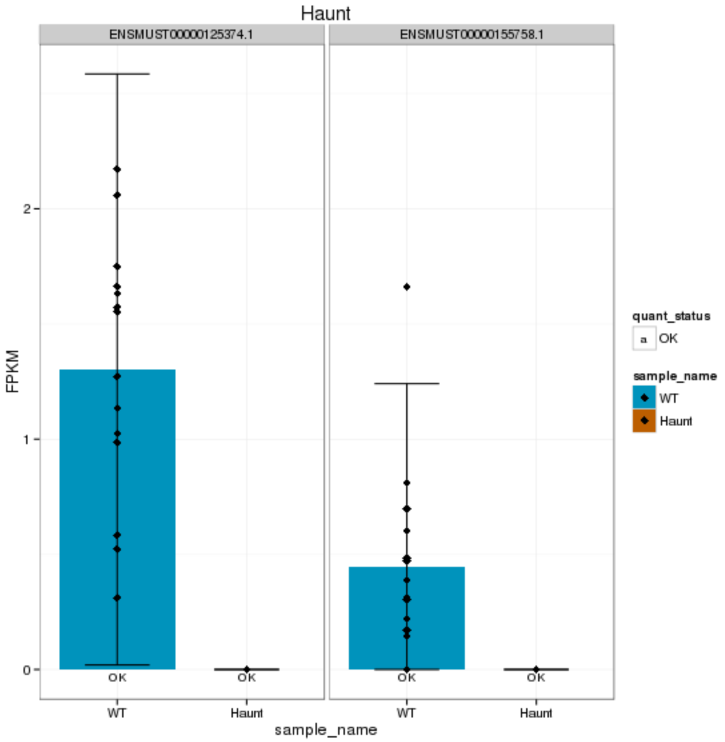
Endogenous expression of Haunt isoforms:



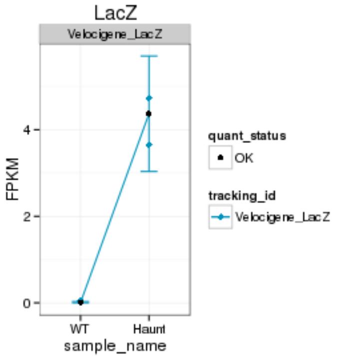
Barplot of gene expression:

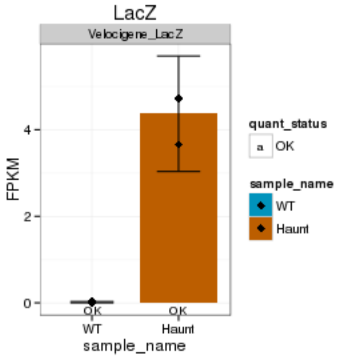


Barplot of isoform expression:



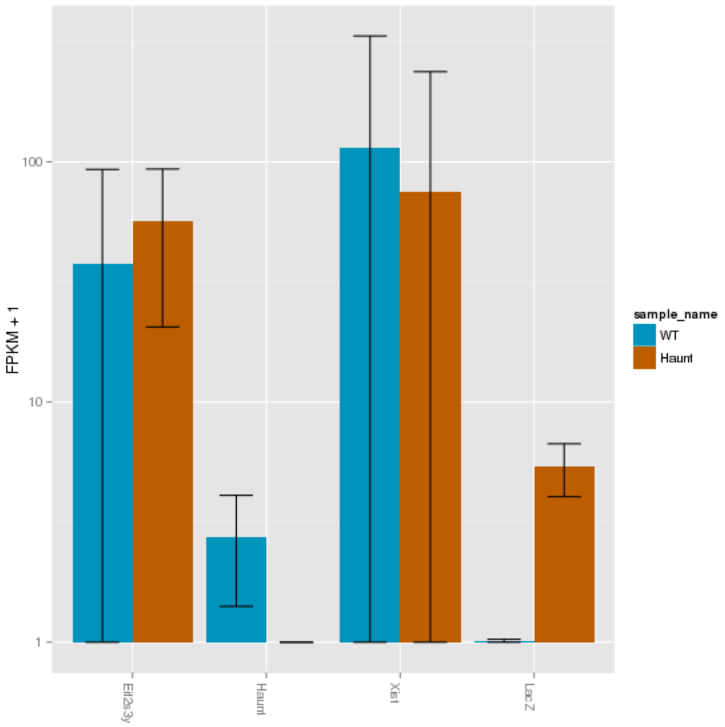
LacZ expression



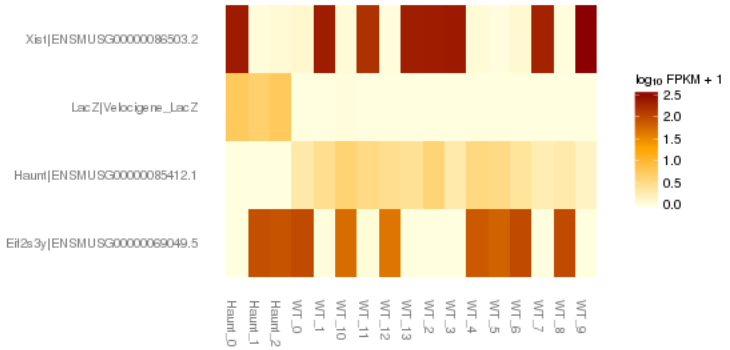


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

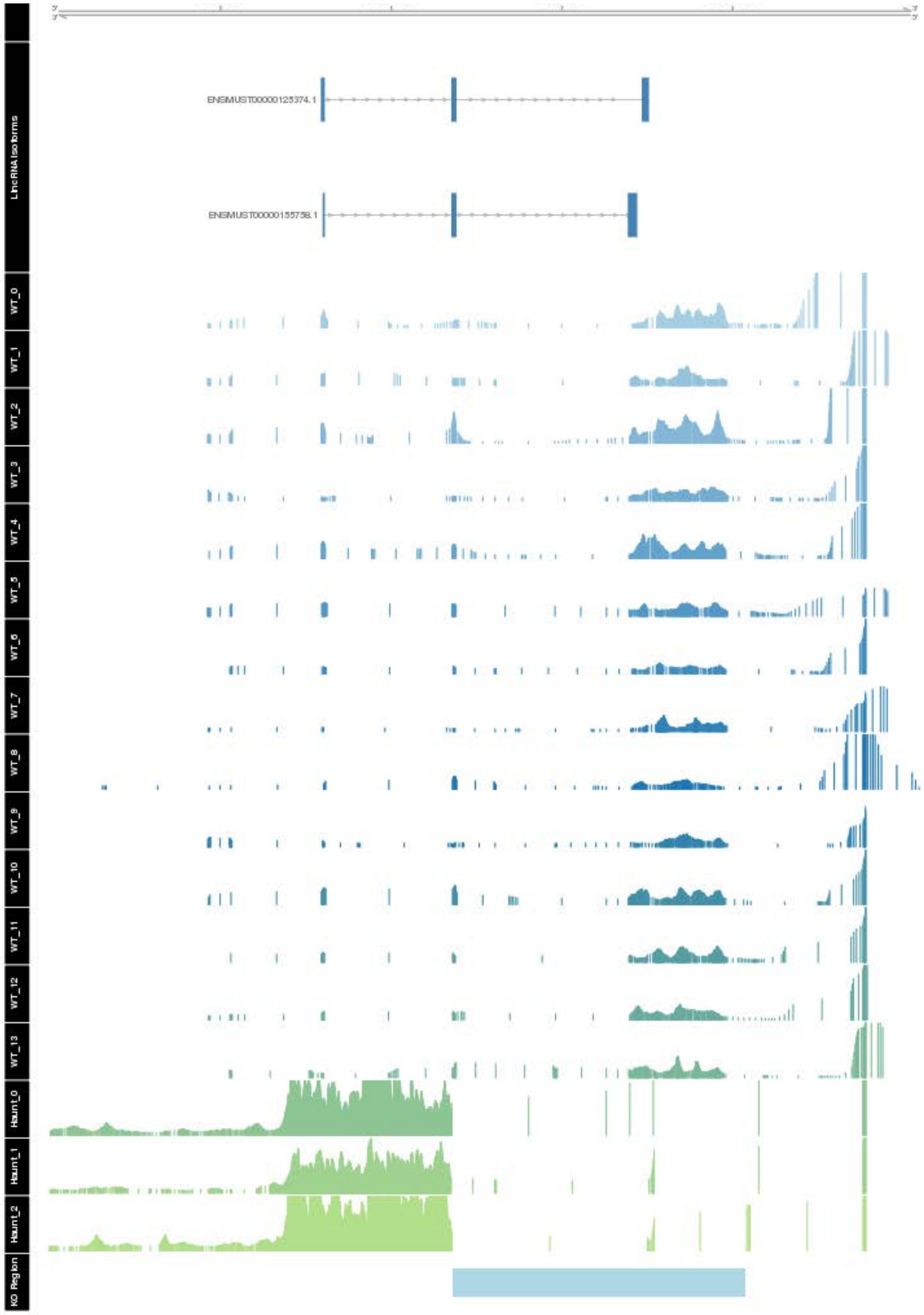
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


5'
3'
LincRNA Isoforms
ENSMUST00000125374.1
ENSMUST00000155758.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Haunt_0
Haunt_1
Haunt_2
KO Region

Differential Analysis

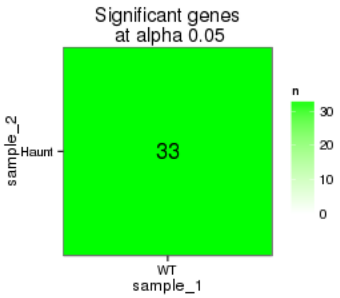
Differential Genes

There are 33 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Nkx2-1
2	Rplp1
3	Hspa8
4	Tshz3
5	Dlx2
6	Clec3b
7	Lhx6
8	Hsd3b6
9	Dlx5
10	Dera
11	Hddc3
12	Mki67
13	Chrna3
14	Cbl
15	Arx
16	Aox4
17	Pcsk1n
18	Dnah7b
19	Tuba1c
20	Rpl29
21	Creg2
22	Hbb-y
23	Hbb-bh1
24	Rnf26
25	Aldh1a1
26	Vsnl1
27	Hba-x
28	Sox11
29	Gm5089
30	Ddx3y
31	Gm9008
32	Haunt
33	Lhx8

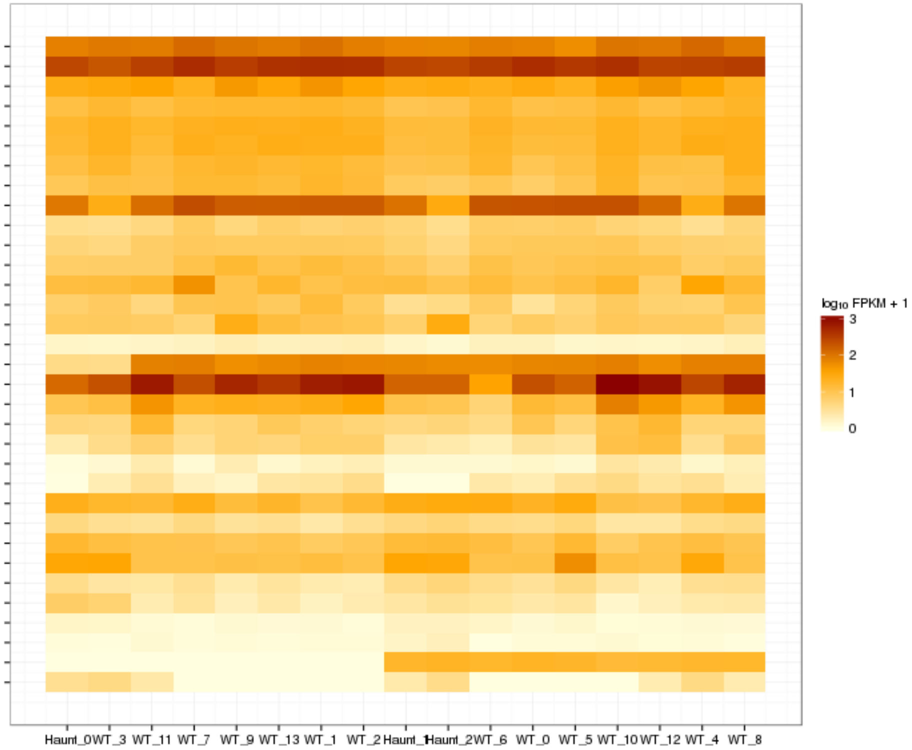
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

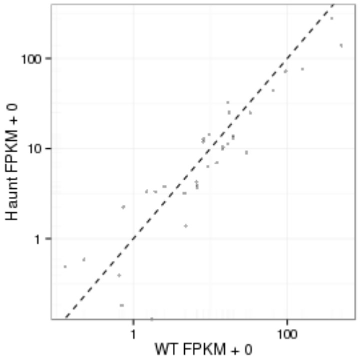


Significant genes with expression >50fpkm (any condition):(turned off)

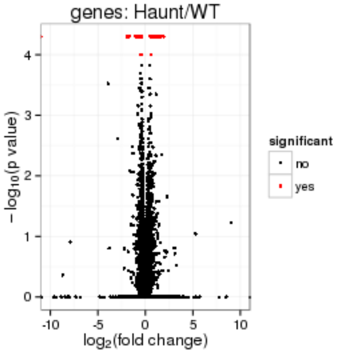
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

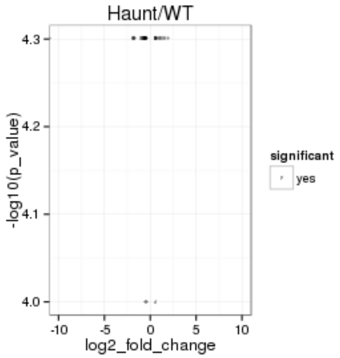
Scatter plot of significant genes only:



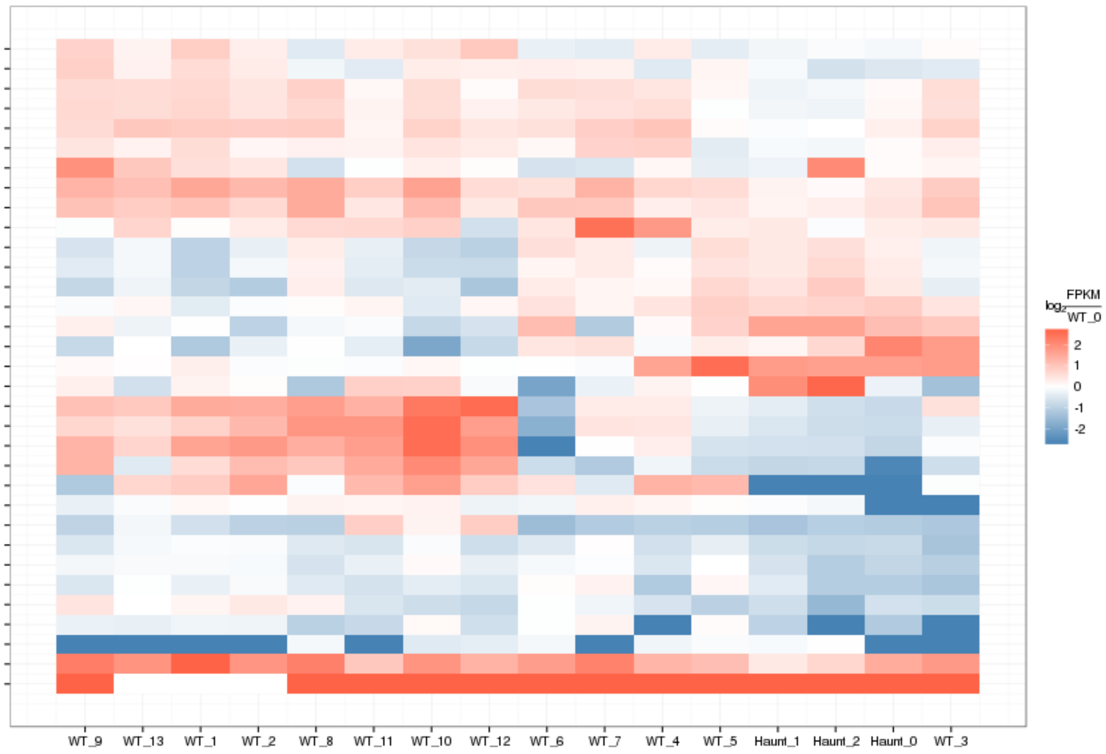
Volcano Plot



Volcano plot with significant genes only:



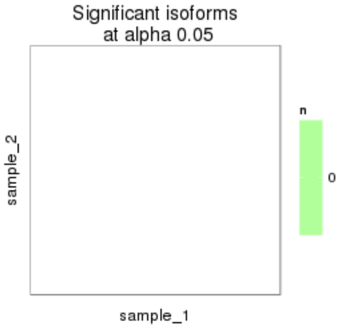
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

[1] “no sig isoforms”

Gene-level DE isoform heatmap

```
## [1] "no sig isoforms"
```

Isoform foldchange heatmap by isoform:

```
## [1] "no sig isoforms"
```

Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

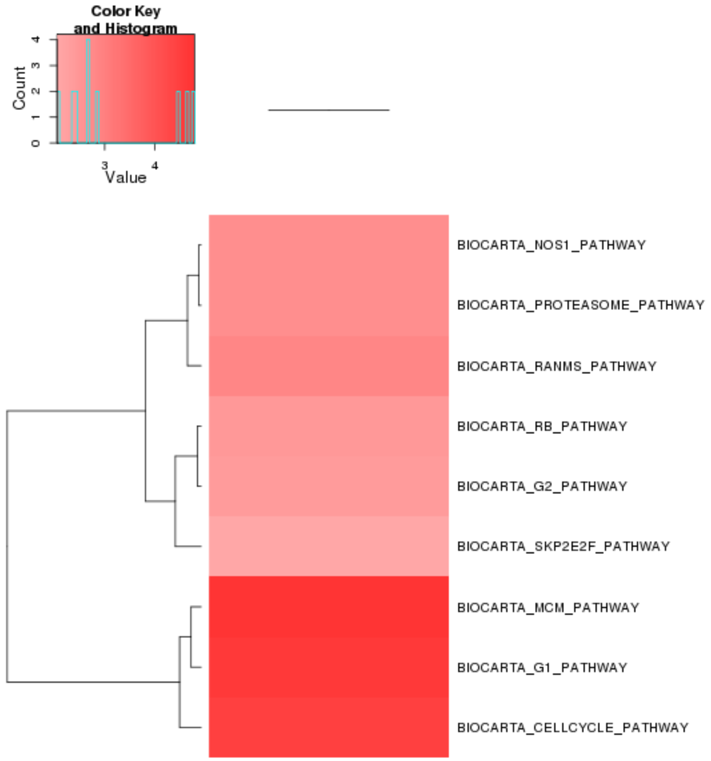
Gene/Pathway Analysis

GSEA

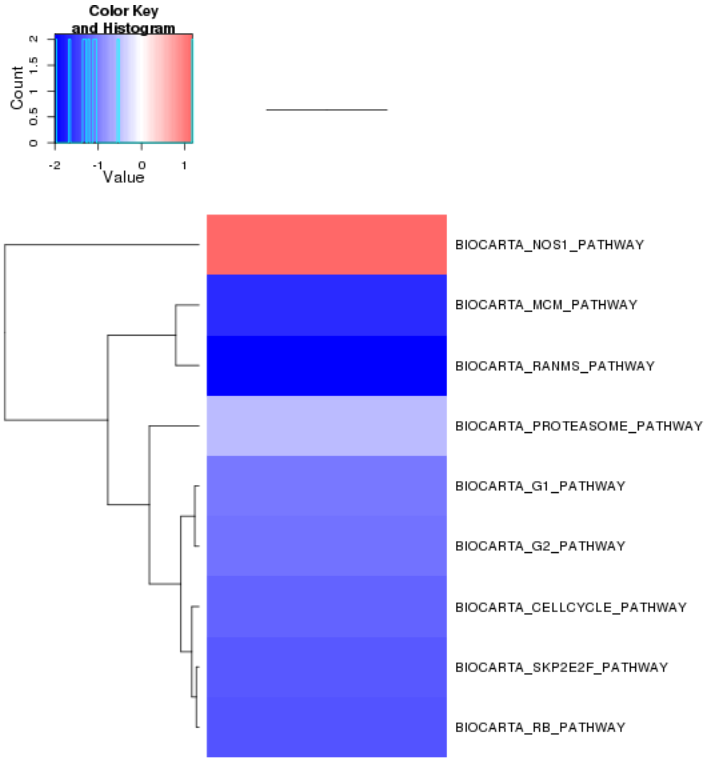
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:

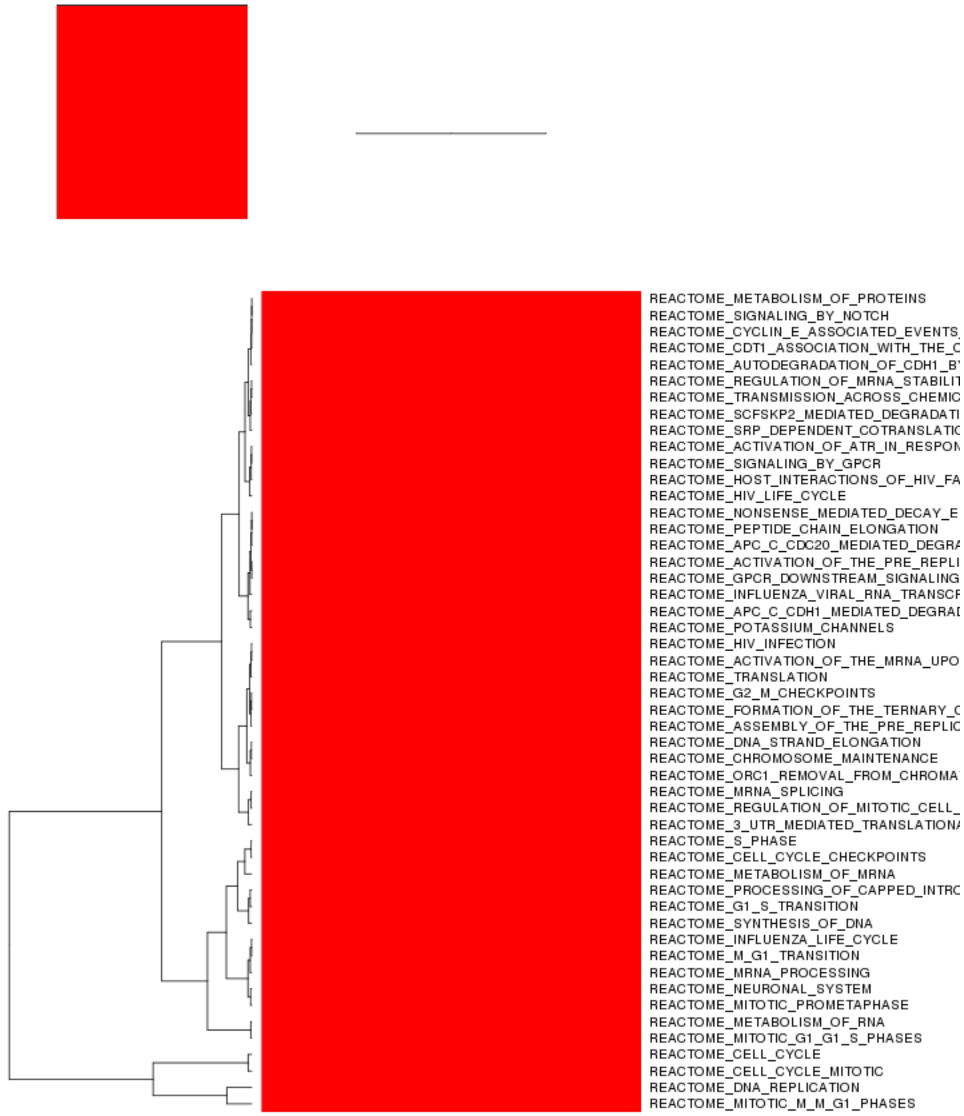


Biocarta zscore:

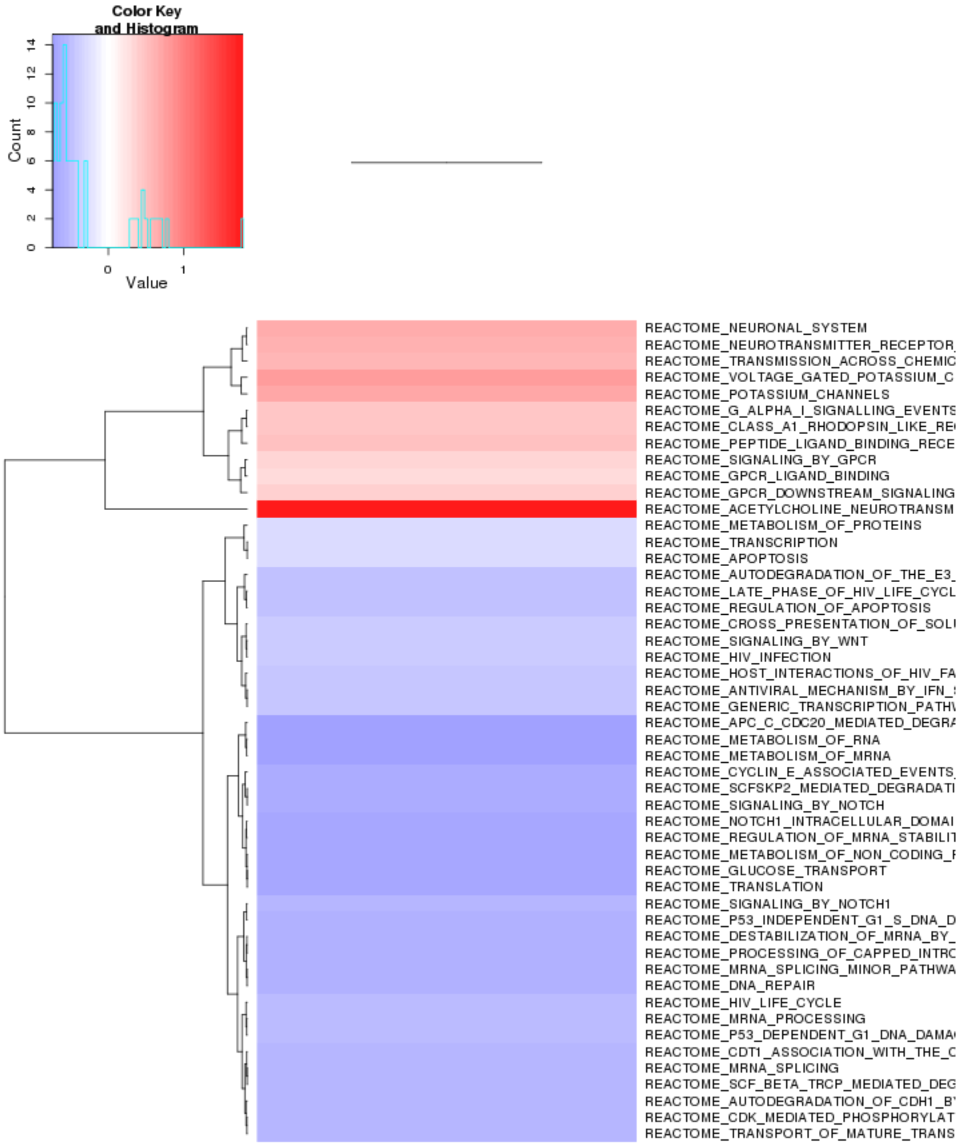


Reactome enrichment:

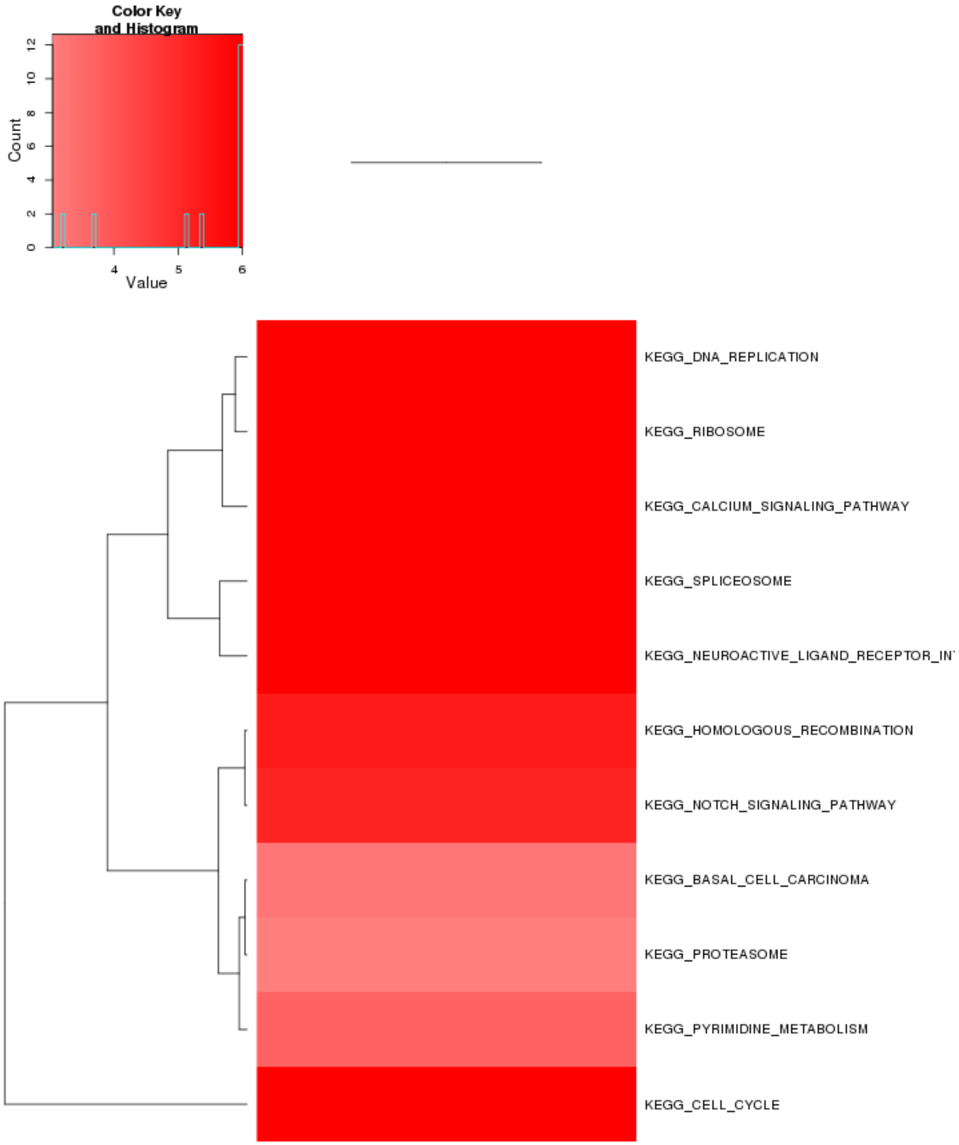
```
## Error: no locations are finite
```



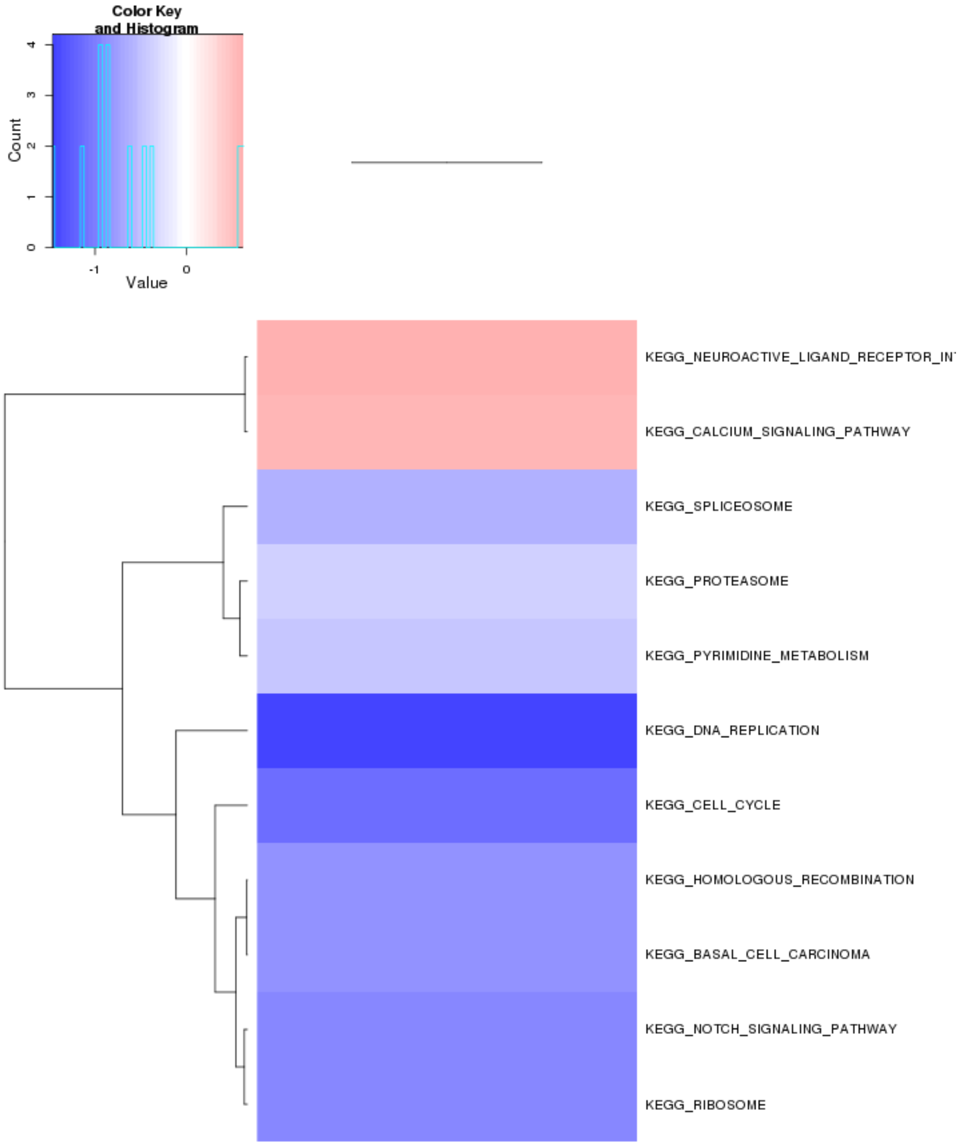
Reactome zscore:



Kegg enrichment:

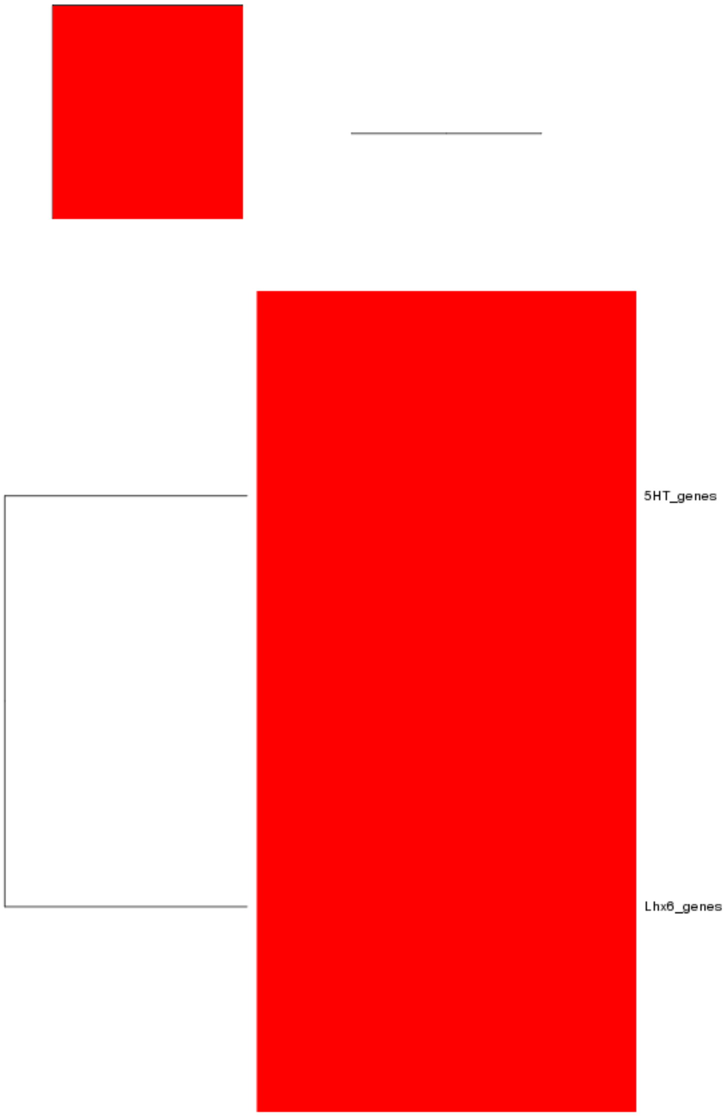

Color Key
and Histogram
Count
0
2
4
6
8
10
12
4
5
6
Value
KEGG_DNA_REPLICATION
KEGG_RIBOSOME
KEGG_CALCIUM_SIGNALING_PATHWAY
KEGG_SPLICEOSOME
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_IN
KEGG_HOMOLOGOUS_RECOMBINATION
KEGG_NOTCH_SIGNALING_PATHWAY
KEGG_BASAL_CELL_CARCINOMA
KEGG_PROTEASOME
KEGG_PYRIMIDINE_METABOLISM
KEGG_CELL_CYCLE

Kegg zscore:

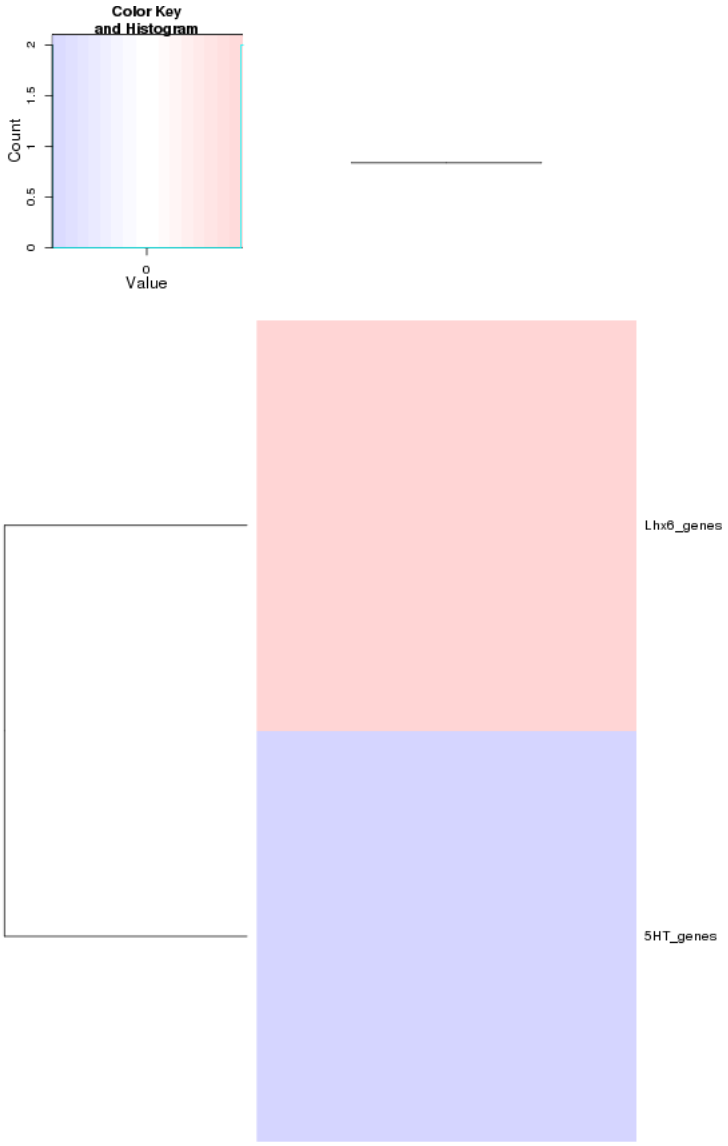


Interneuron enrichment:

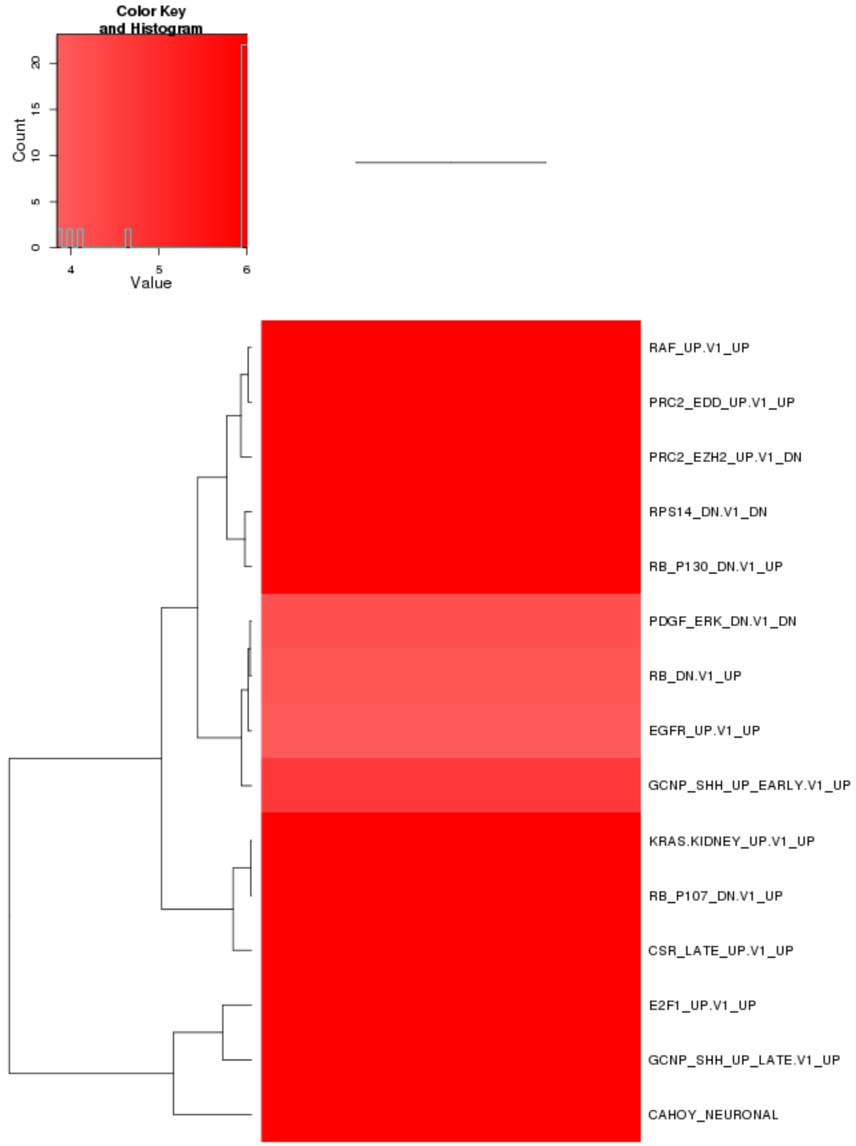
```
## Error: no locations are finite
```



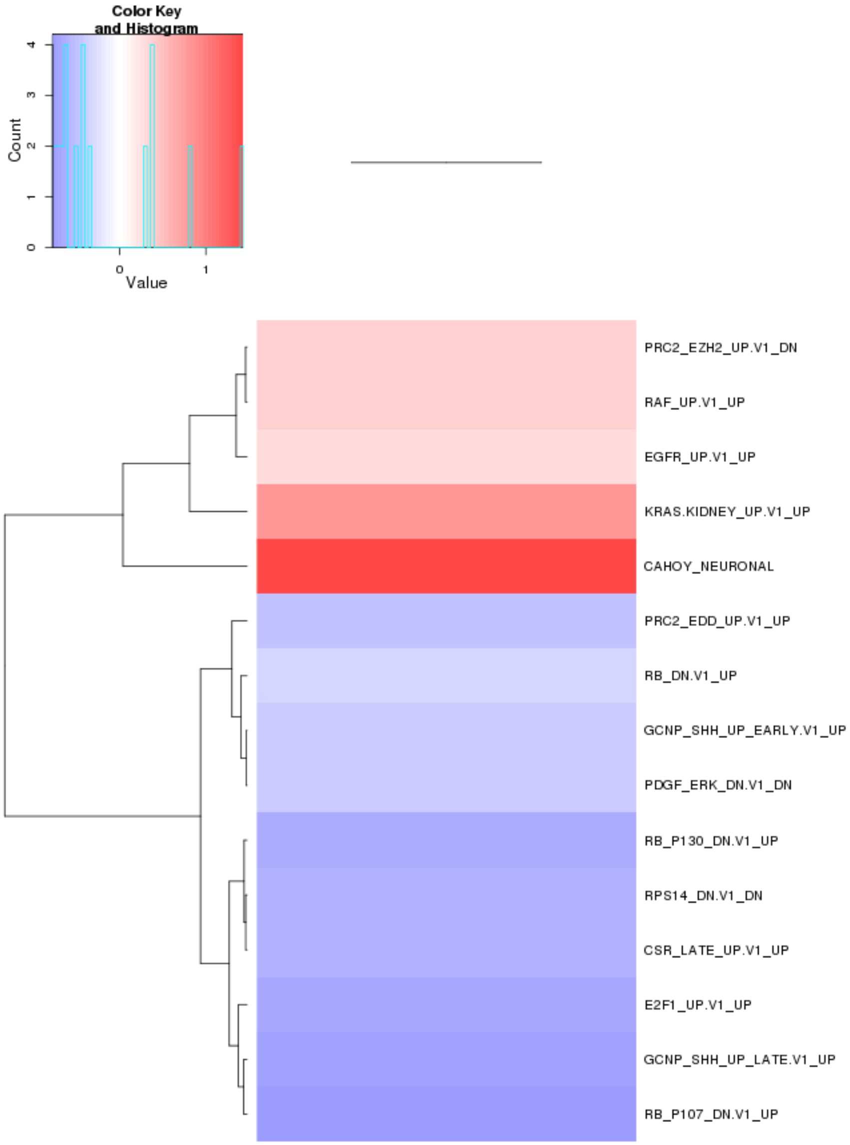
Interneuron zscore:



Oncogene enrichment:



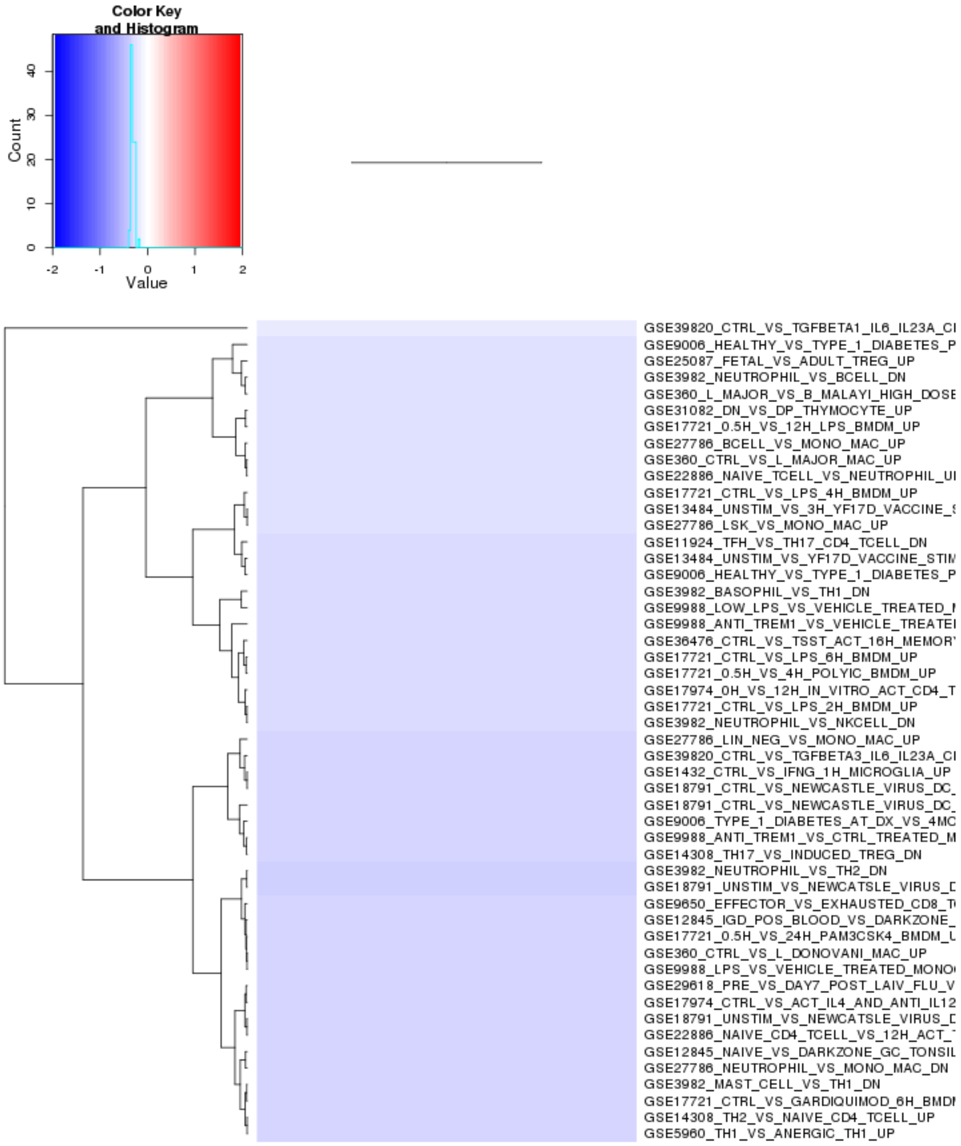
Oncogene zscore:



Immuno enrichment:

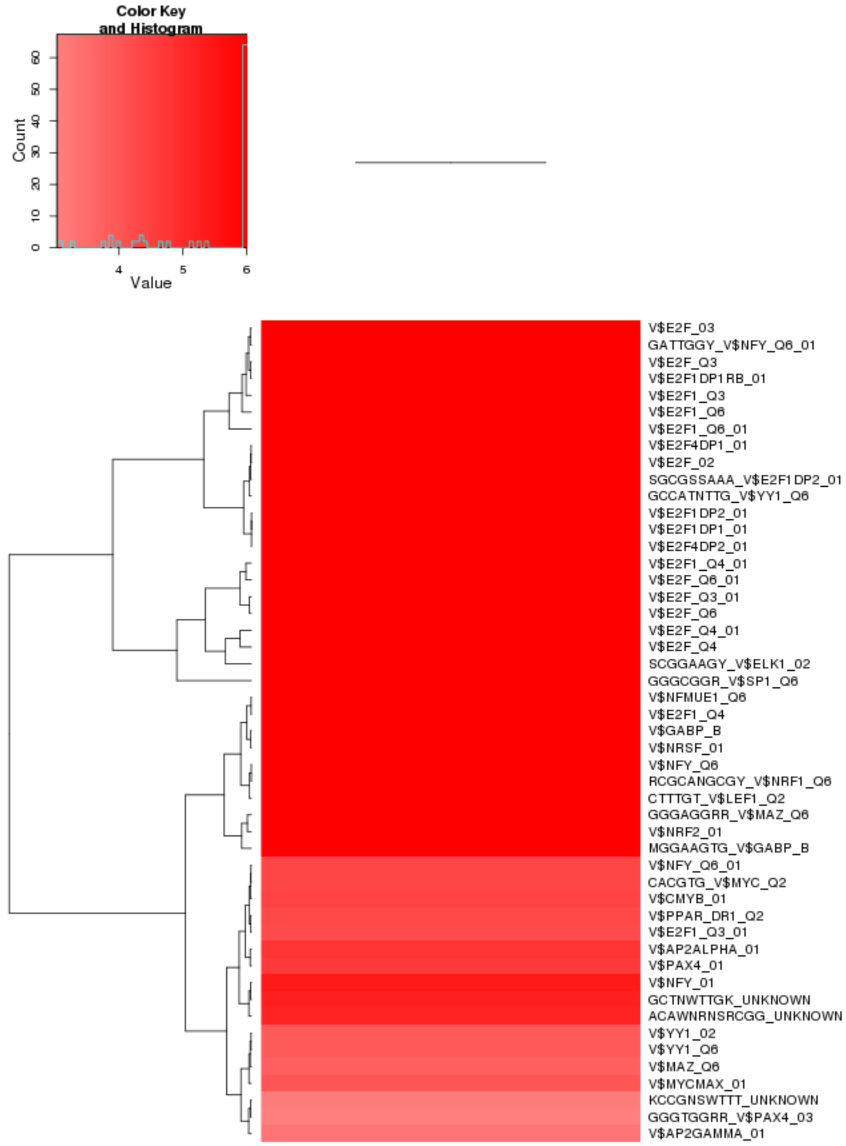
```
## Error: no locations are finite
```

Immuno zscore:



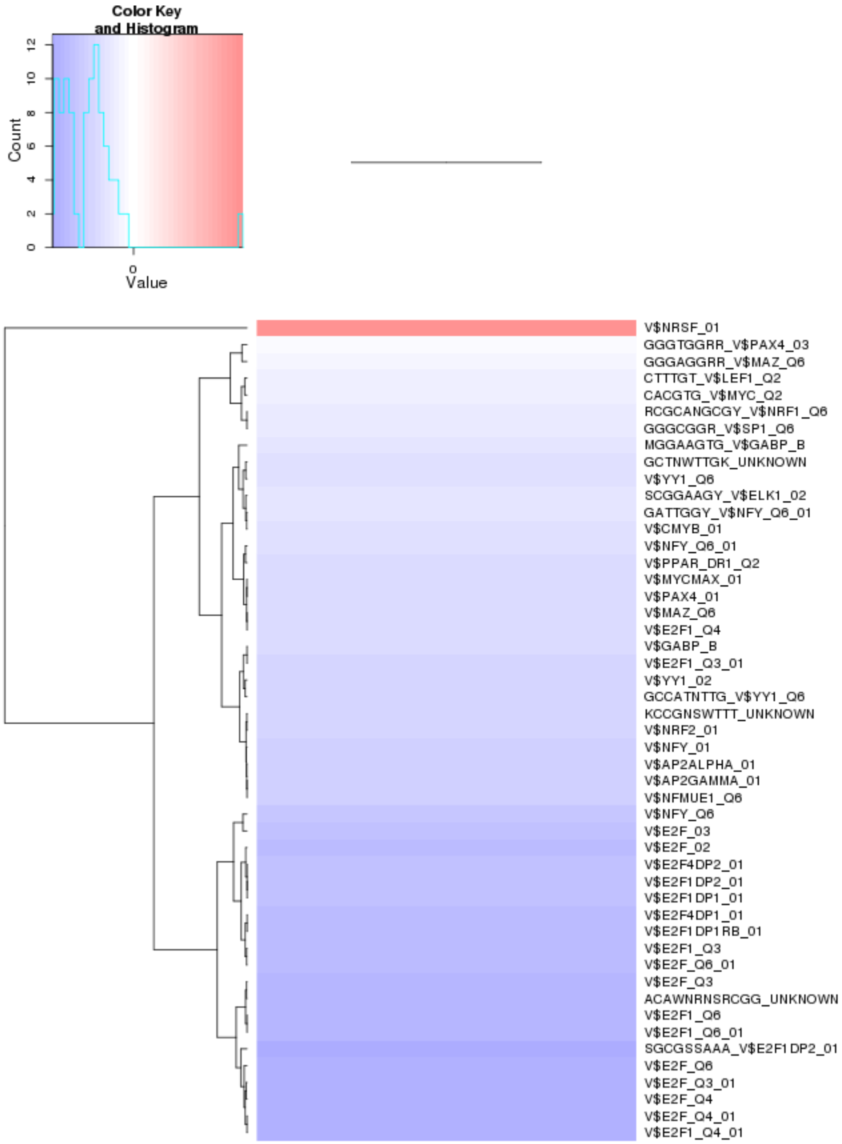
TF enrichment:

```
## Error: subscript out of bounds
```



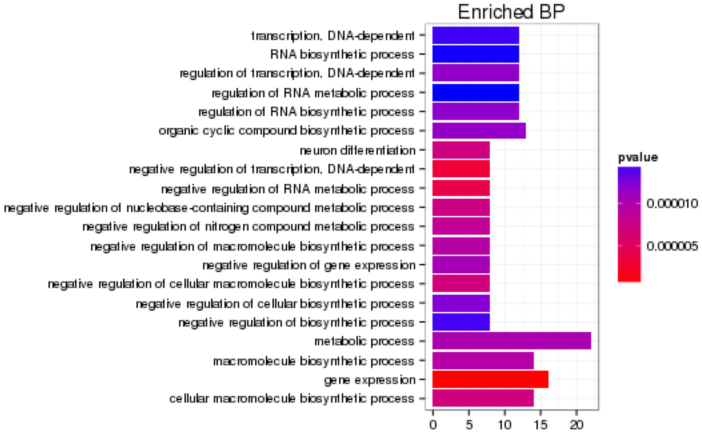
TF zscore:

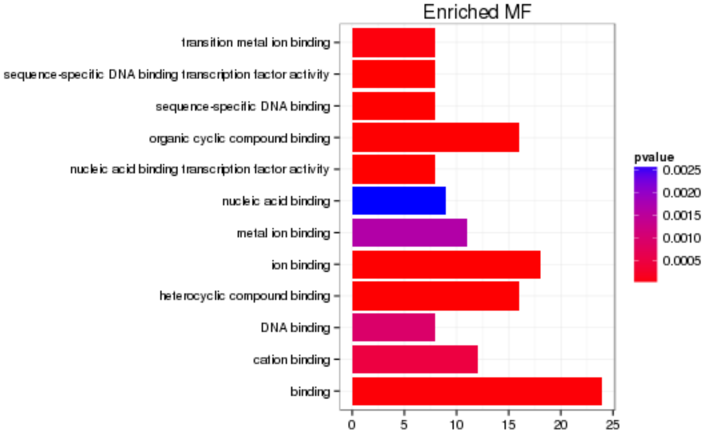
```
## Error: subscript out of bounds
```

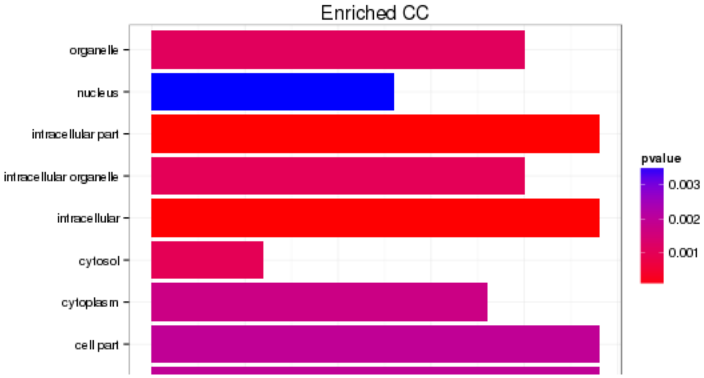


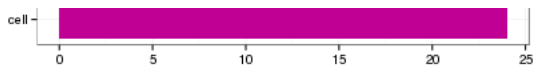
GO enrichment

Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.


Enriched BP


Enriched MF

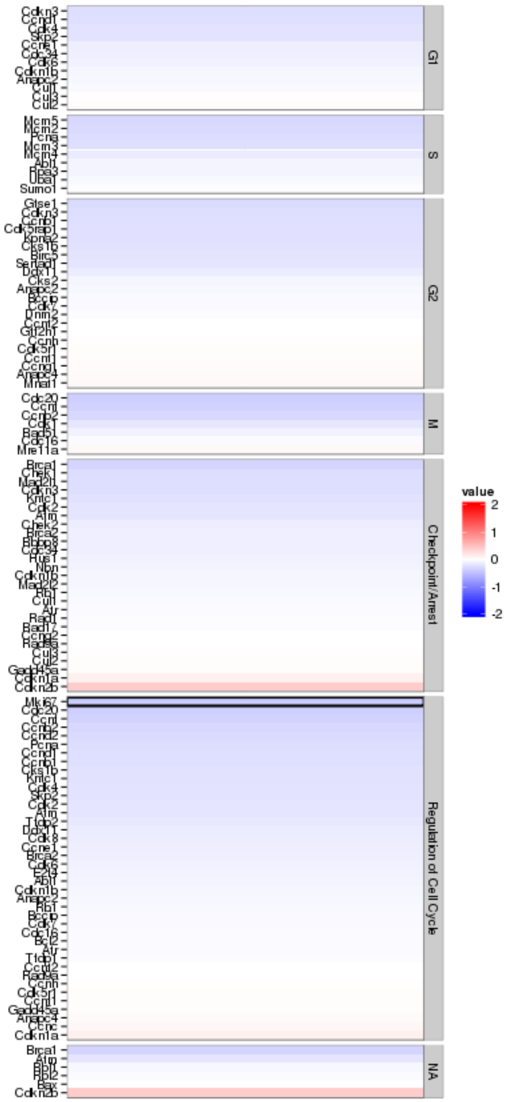

Enriched CC



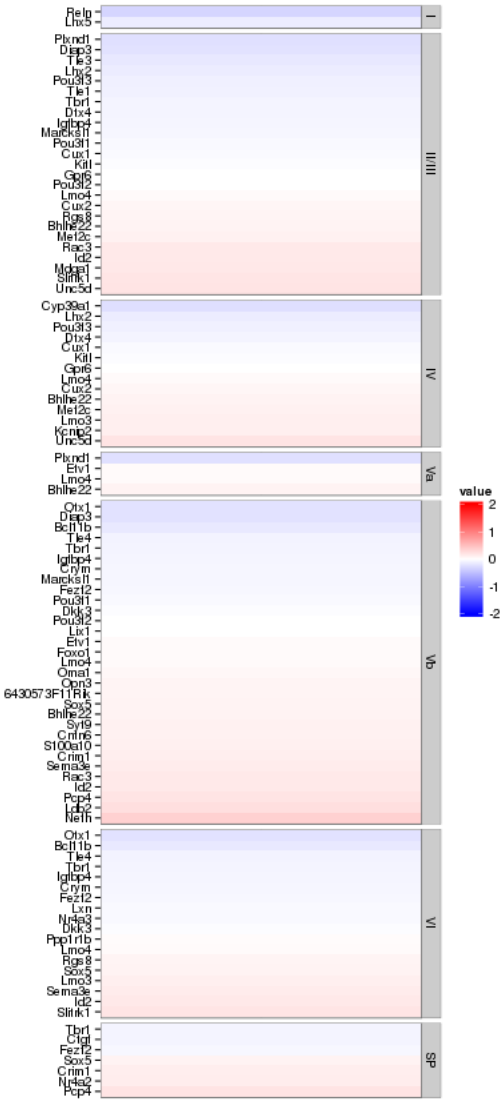
```
## Error: need finite 'xlim' values
```

```
## Error: need finite 'xlim' values
```

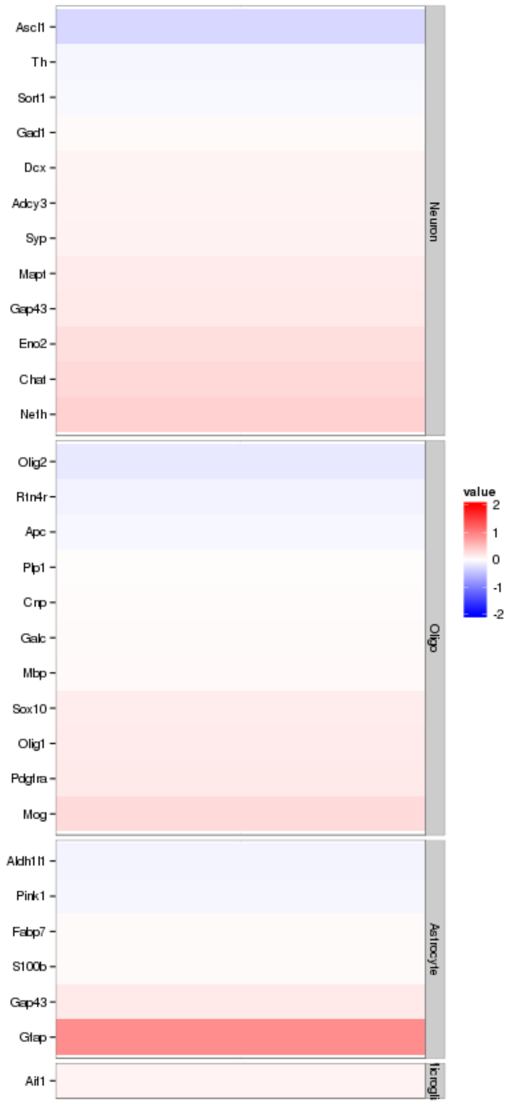
Enrichment or depletion for stage-specific cell cycle markers



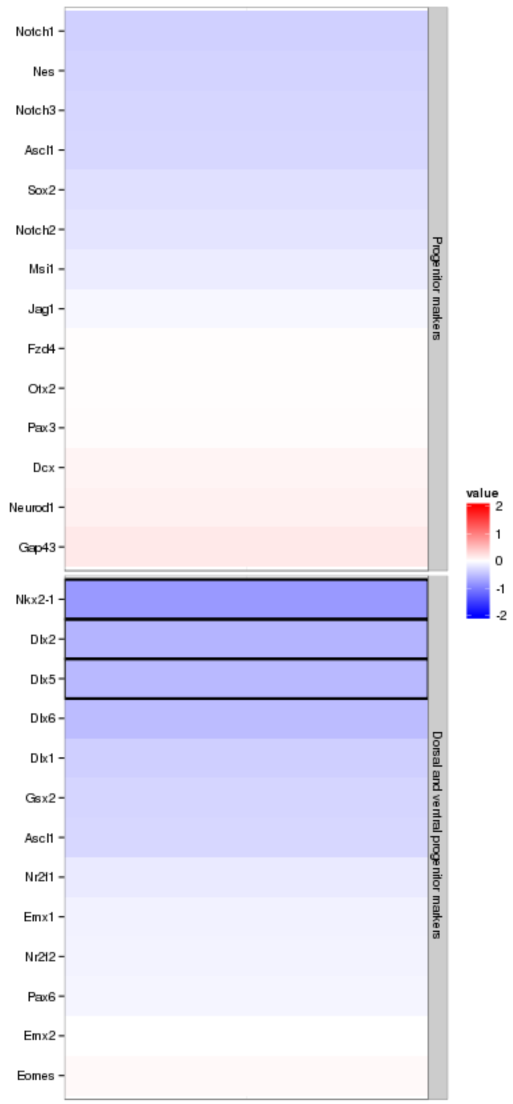
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



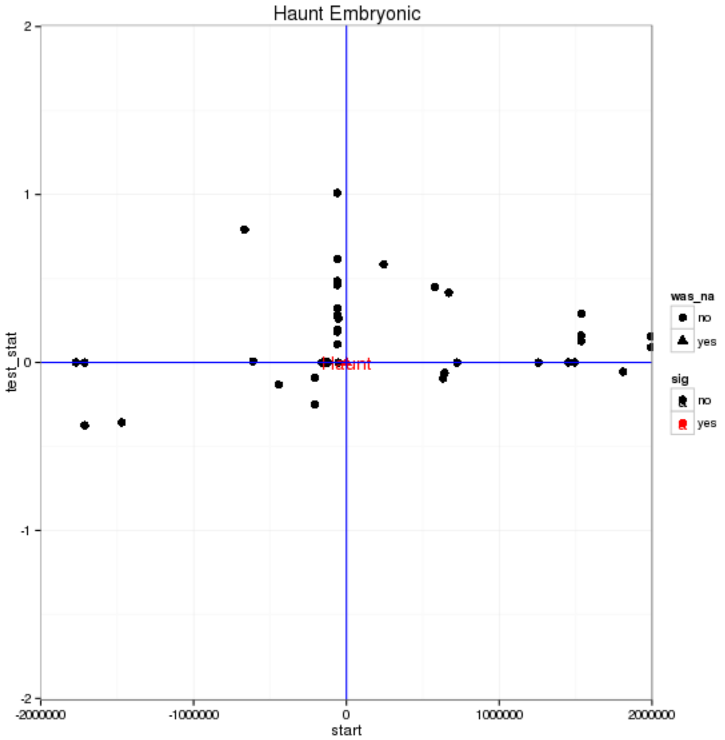
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15	JR754
16	JR767
17	JR759

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	32555300.00	1.25	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	32555300.00	1.09	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	32555300.00	1.22	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	32555300.00	1.27	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	32555300.00	1.19	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	32555300.00	0.88	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	32555300.00	0.96	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	32555300.00	0.91	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	32555300.00	0.85	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	32555300.00	0.95	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	32555300.00	0.80	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	32555300.00	0.79	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	32555300.00	0.68	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	32555300.00	1.20	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR754/abundances.cxb	Haunt	0	Haunt_0	34277200.00	32555300.00	1.05	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR767/abundances.cxb	Haunt	1	Haunt_1	30963400.00	32555300.00	0.96	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR759/abundances.cxb	Haunt	2	Haunt_2	40179300.00	32555300.00	1.25	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils
## [8] datasets  base
##
## other attached packages:
##  [1] plyr_1.8.1
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6          
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4      
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7             
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1         
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1          
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4          
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12    
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26   
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2         
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0         
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1    
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2         
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2           
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##          param
## 1     cmd_line
## 2      version
## 3  SVN_revision
## 4 boost_version
## 5       genome
##
## 1 cuffdiff -p 10 -L WT,Haunt -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Haunt_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/BrainMap/dat
## 2
## 3
## 4
## 5
```

Kantr KO vs WT (Adult)

This file shows the wt-v-ko comparison for Kantr.

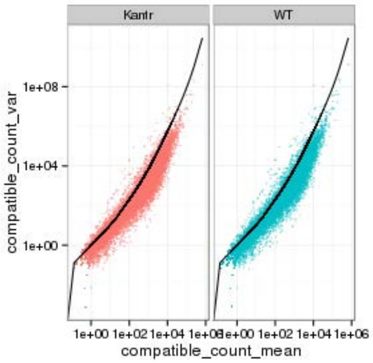
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

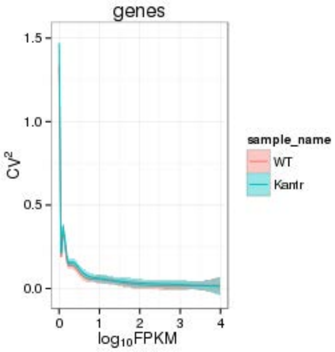
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



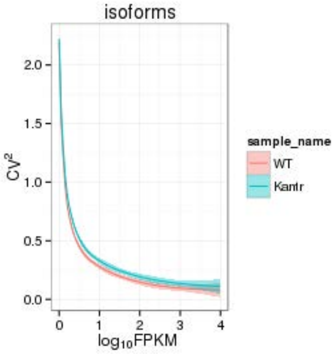
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

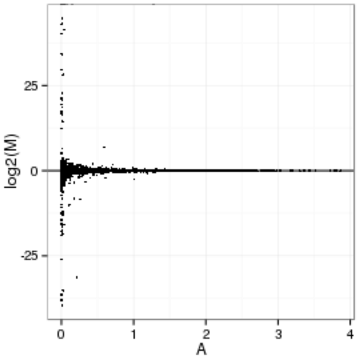
Genes:



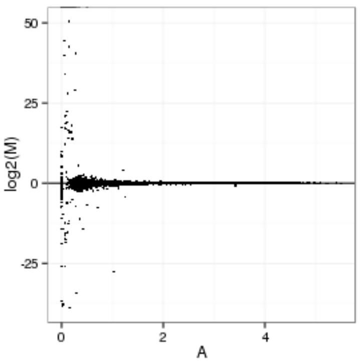
Isoforms:



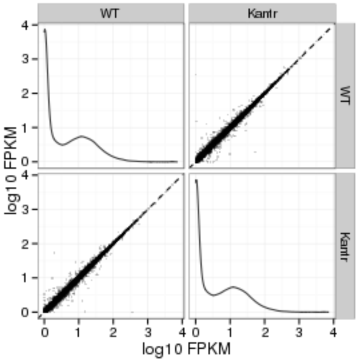
MvA plot



MvA plot counts



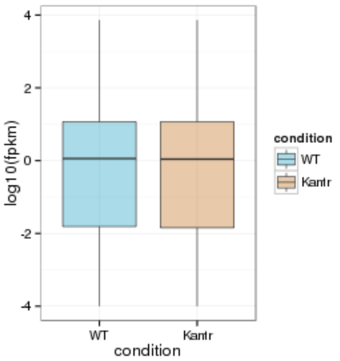
Scatterplot matrix



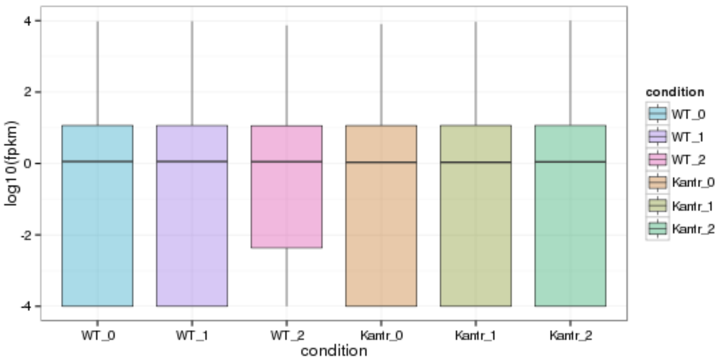
Distributions

Boxplots

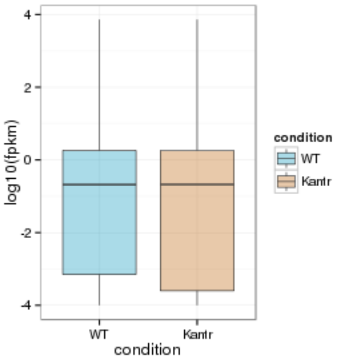
Boxplot (genes)



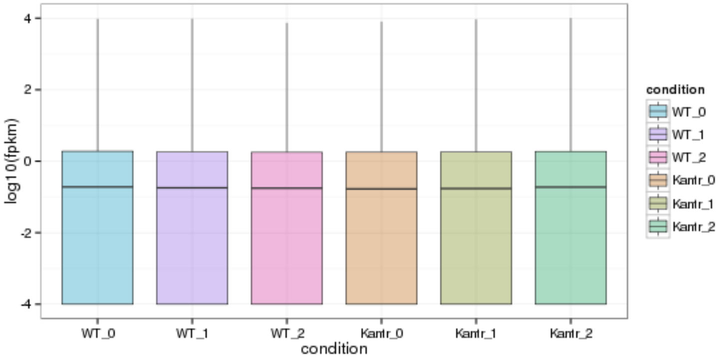
Boxplot (genes, replicates)



Boxplot (isoforms)

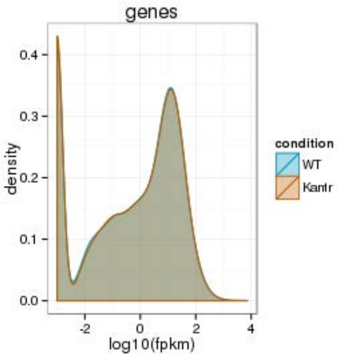


Boxplot (isoforms, replicates)

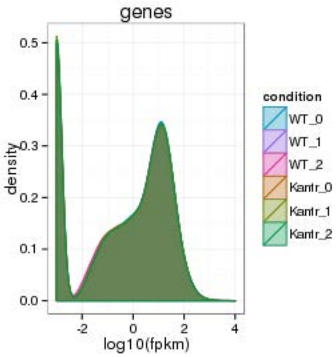


Density

Density (genes)

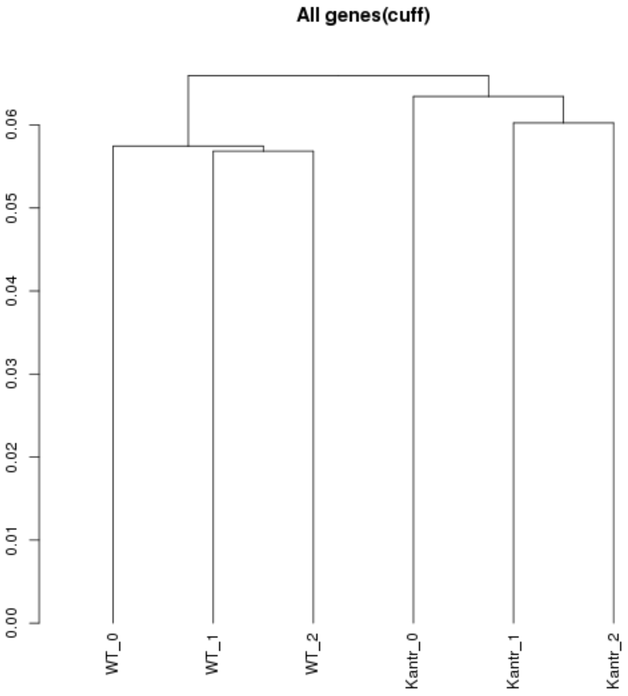


Density (genes, replicates)



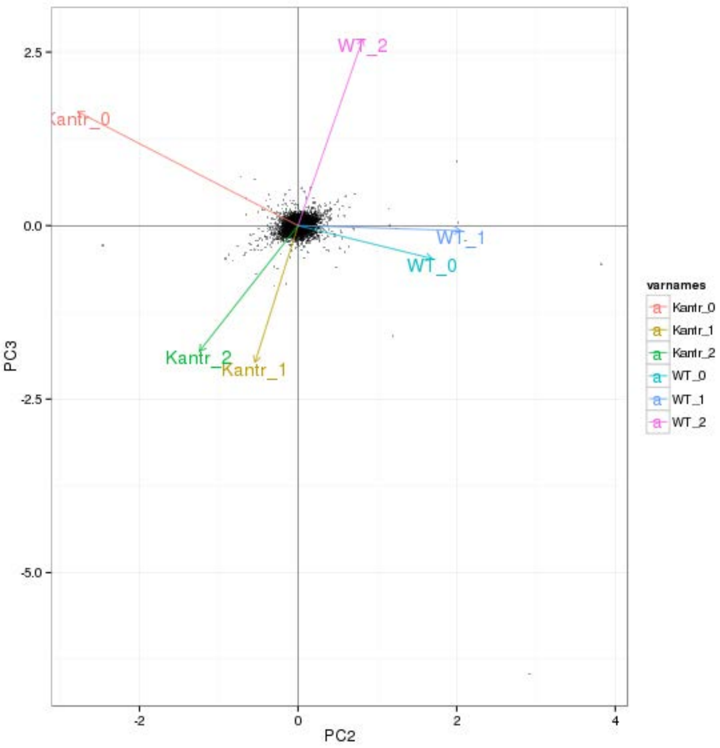
Clustering

Replicate Clusters



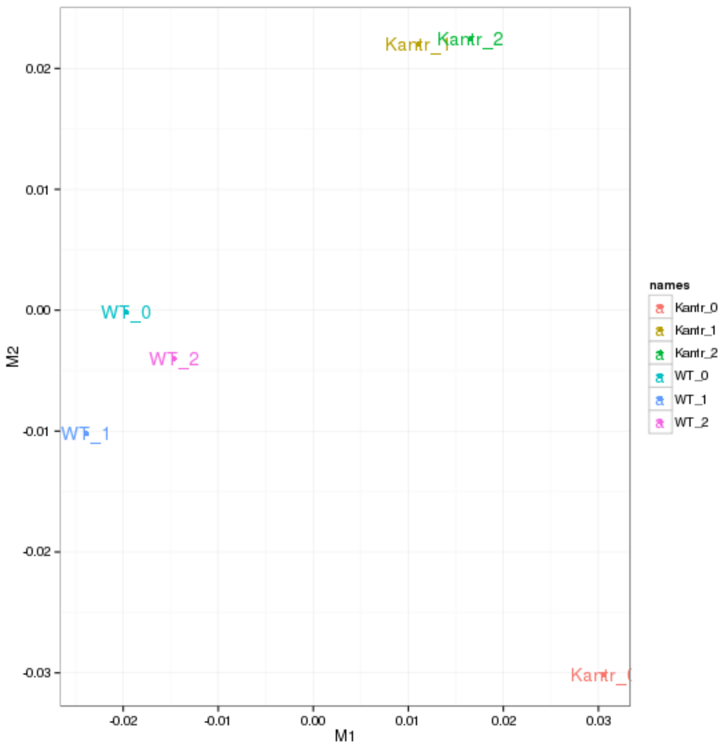
```
## NULL
```

PCA (genes)



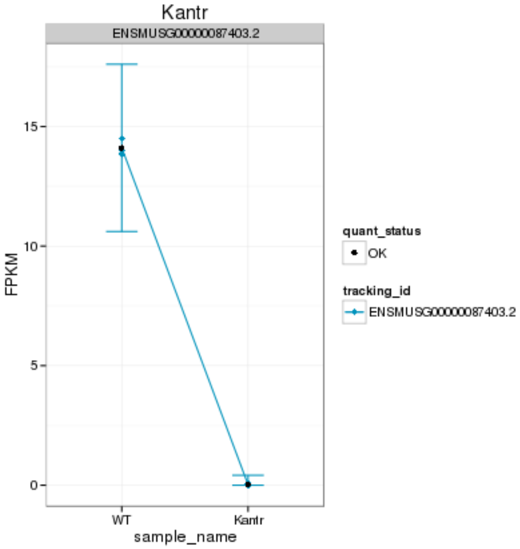
WT_2
Kantr_0
WT_1
WT_0
Kantr_2
Kantr_1
2.5
0.0
-2.5
-5.0
PC3
-2
0
2
4
PC2
varnames
Kantr_0
Kantr_1
Kantr_2
WT_0
WT_1
WT_2

MDS (genes)

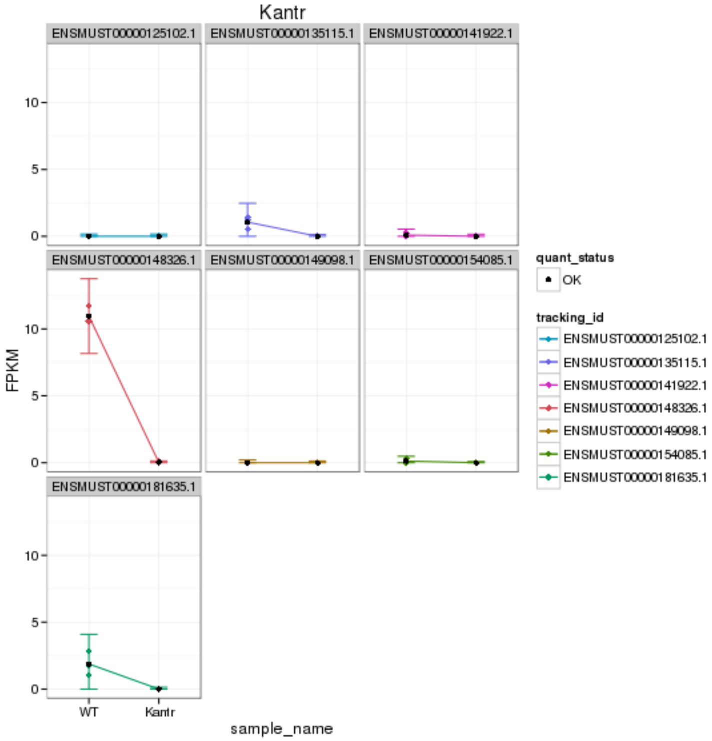


KO assessment

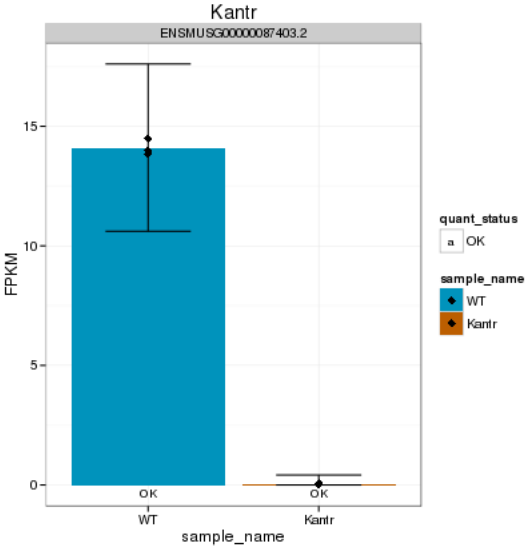
Endogenous lncRNA expression



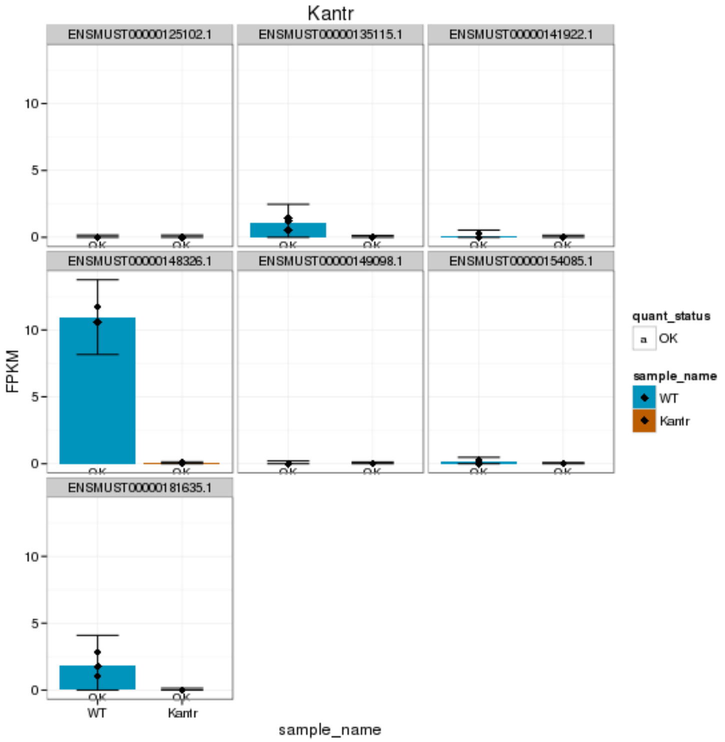
Endogenous expression of Kantr isoforms:



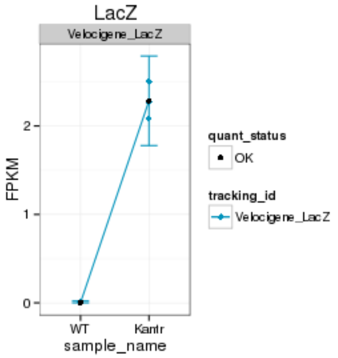
Barplot of gene expression:

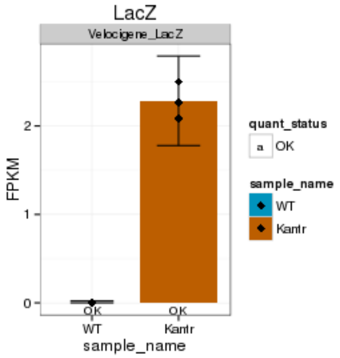


Barplot of isoform expression:



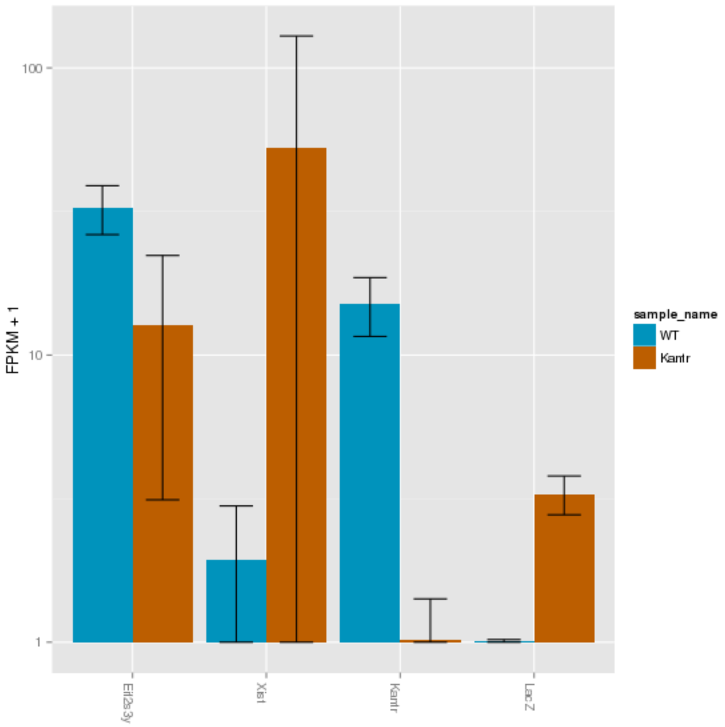
LacZ expression



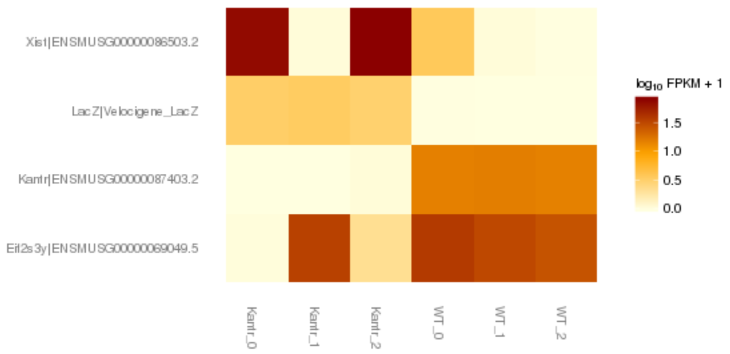


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

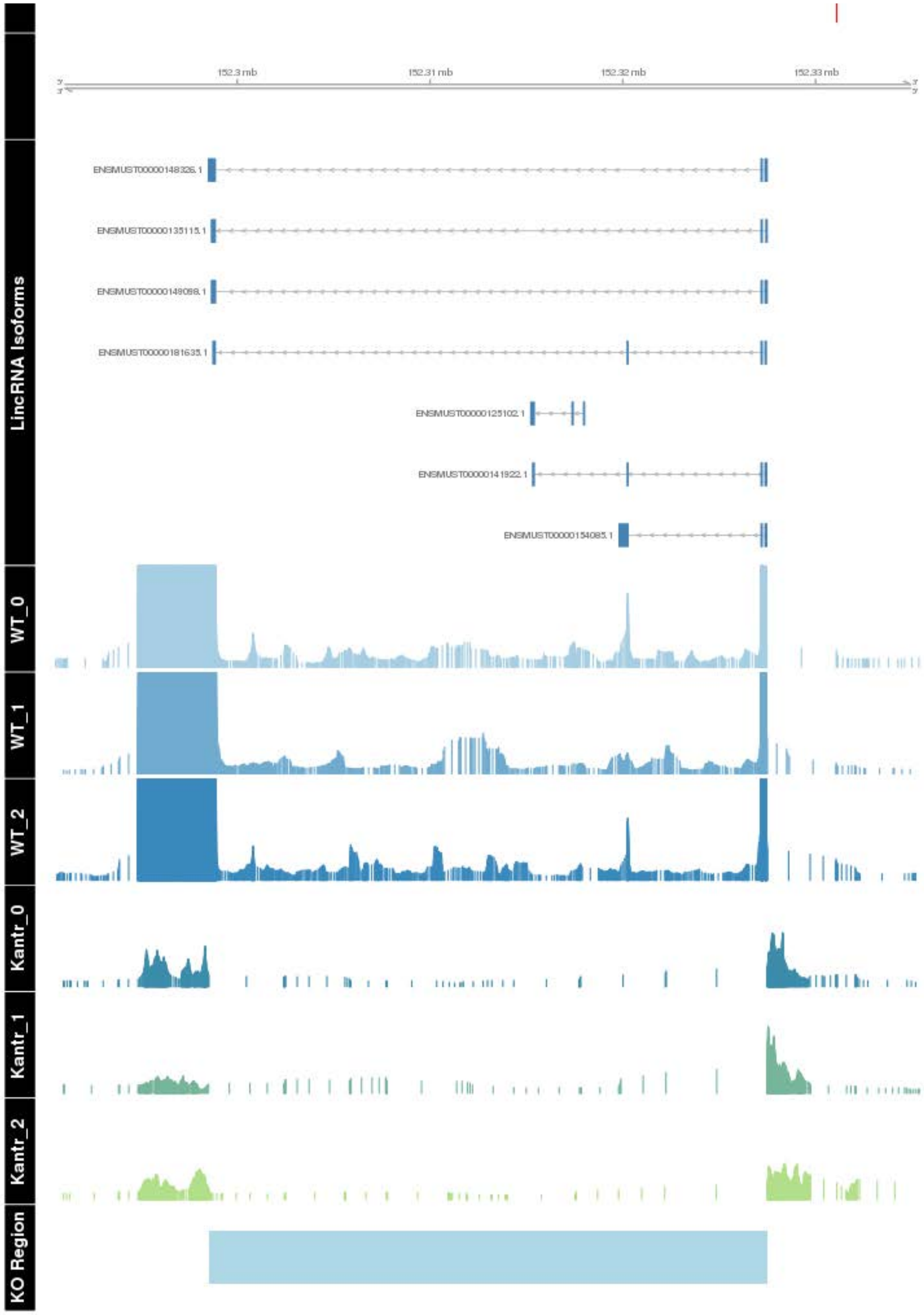
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


152.3 mb
152.31 mb
152.32 mb
152.33 mb
LincRNA Isoforms
ENSMUST00000148326.1
ENSMUST00000135115.1
ENSMUST00000149098.1
ENSMUST00000181635.1
ENSMUST00000125102.1
ENSMUST00000141922.1
ENSMUST00000154085.1
WT_0
WT_1
WT_2
Kantr_0
Kantr_1
Kantr_2
KO Region

Differential Analysis

Differential Genes

There are 315 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Wnt9a
2	Sox9
3	Il12rb1
4	Mmp14
5	S100a5
6	N4bp3
7	Ramp2
8	Meox1
9	Gramd3
10	Plin4
11	Arrdc2
12	Fosb
13	Hif3a
14	9330159F19Rik
15	Cd33
16	Sh2b2
17	Osgep
18	Bcl2l1
19	Dio2
20	Id3
21	Fgfrl1
22	Cd163
23	Derl3
24	Tbx1
25	Gm266
26	Tjap1
27	Trpv4
28	Mertk
29	Gata2
30	Slc25a13
31	Cnksr3
32	Sdc4
33	Rhbdl3
34	Ada
35	Erbb3
36	Ksr1
37	Etnppl

38	Pdk4
39	Lama4
40	Arid5b
41	Sgk1
42	Ddit4
43	Cpm
44	Nipal4
45	Btg2
46	Gatsl3
47	Igfbp3
48	Pomc
49	Gh
50	Nfkbia
51	Zfp36l1
52	Net1
53	Fos
54	Dapk1
55	Elovl7
56	4930452B06Rik
57	Fst
58	Ldb3
59	Galnt15
60	Sema3g
61	Ednrb
62	Psmb5
63	Fzd6
64	Fbxo32
65	Slc38a2
66	Bcl6
67	Crebbp
68	Arc
69	Nde1
70	Adamts1
71	Nr4a1
72	Cdkn1a
73	Tmem52
74	Clic5
75	Trem2
76	Glo1
77	Sik1
78	Xdh
79	Atp6v0c
80	Tekt4

81 Dusp1
82 Fkbp5
83 Nedd4l
84 Cd74
85 Pdgfrb
86 Rab3il1
87 Fas
88 Frmd8
89 Hhex
90 Atp10a
91 Kdm5c
92 Pnpla2
93 D3Ertd751e
94 Sgk3
95 Paqr8
96 Slc40a1
97 Il1r1
98 2810459M11Rik
99 Myoc
100 Lcn2
101 Col5a1
102 Depdc7
103 Dll4
104 Bpifa1
105 Fam83d
106 Anxa5
107 Exosc9
108 Dclre1b
109 Tmem144
110 Cyr61
111 Trp53inp1
112 Gbp3
113 Gbp2
114 Nr4a3
115 Slc44a5
116 Rps6
117 Slc2a1
118 Mfsd2a
119 Alpl
120 Tinagl1
121 Map3k6
122 Errfi1
123 Ugt2a1

124 Gbp9
125 Aff1
126 Rasgef1b
127 Bmp3
128 Rilpl1
129 Uncx
130 Lfng
131 Nfe2l3
132 Gkn3
133 Klf15
134 Lag3
135 Clec2d
136 Adipor2
137 Dusp16
138 Rhpn2
139 Sult1a1
140 Lyve1
141 Cckbr
142 Slc38a5
143 Tsc22d3
144 Plat
145 Sall1
146 Gpt2
147 Gab1
148 Mt2
149 Mt1
150 Cmtm3
151 Ets1
152 Mcam
153 Ldlr
154 Paqr5
155 Igdcc3
156 Heyl
157 Gng11
158 Alox12b
159 Slc16a1
160 Sox10
161 Tbc1d4
162 Tlr13
163 Ston1
164 Klf9
165 Trim36
166 Neu4

167 Igsf9b
168 Trim59
169 Cbl
170 Pla2g3
171 Nostrin
172 Fam214a
173 Eva1a
174 Lars2
175 Tmem98
176 Prr5
177 Tmem260
178 Micall2
179 Kirrel2
180 Tenc1
181 Ppp1r14a
182 Mxd4
183 Galnt6
184 Uvssa
185 Avp
186 Dzip1l
187 Egr2
188 Smim3
189 Foxf2
190 Egr1
191 Olfml2b
192 Atp5l
193 Mboat1
194 Pcsk1n
195 Tnfsf10
196 Hlx
197 Atp8b1
198 Zfp189
199 Gpr37
200 Spsb1
201 Gbp5
202 Rps19
203 Cables1
204 Nkx6-2
205 Cldn5
206 Syt15
207 Cdc42ep4
208 Pkp2
209 Klhl6

210 Gjc2
211 Dmrta1
212 Zfp488
213 Tlr7
214 Serpinb1a
215 Lsm11
216 Rassf9
217 S1pr5
218 Cirbp
219 Insig1
220 Zfp36l2
221 Npas4
222 Clec14a
223 Gjb2
224 Hmga1
225 Kcne4
226 Gjb1
227 Kmt2d
228 Ccdc6
229 Dact2
230 Acap2
231 Cdc42ep1
232 Cyp2g1
233 Rasd1
234 Opalin
235 Fzd2
236 Ppp1r3g
237 Plekho2
238 Hs3st1
239 Olfml1
240 Lingo3
241 Islr2
242 Gfod1
243 BC068281
244 Klf13
245 Hbb-y
246 Gpr17
247 Hbb-bs
248 Nrros
249 Jun
250 Junb
251 Creb5
252 Ier2

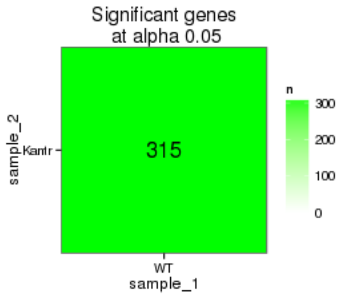
253 Iigp1
254 Lifr
255 Lrrc8c
256 Zcchc24
257 Per2
258 S100a9
259 1810011O10Rik
260 Kdm5d
261 Chsy3
262 Sclt1
263 Fhit

264 Zbtb40
265 Rpl26
266 Cox5b
267 Ksr2
268 Kdr
269 D630045J12Rik
270 Srrm4
271 Phactr4
272 Zbtb16
273 Ppp1r3c
274 Uty
275 Il3ra
276 Ddx3y
277 Eif2s3y
278 Ahnak
279 Hba-a1
280 1700084C01Rik
281 Rasgrp3
282 Jund
283 Egr4
284 Ccnb1ip1
285 Ppp1r3e
286 Gm7292
287 H2-Bl
288 H2-Ab1
289 Tmem88b
290 Hbb-bt
291 Plekhf1
292 Adh1
293 Sox2
294 Bpifb4
295 B3galt5

296 Nrarp
297 Gm17414
298 Gbp4
299 Ms4a6c
300 Gm15631
301 Xist
302 BC064078
303 Slc5a3
304 Apold1
305 Sox2ot
306 Myl6
307 A930018M24Rik
308 Neat1
309 Gm10406
310 Gm7094
311 Fam181a
312 4732491K20Rik
313 Gm26782
314 Bin2
315 Gm26924

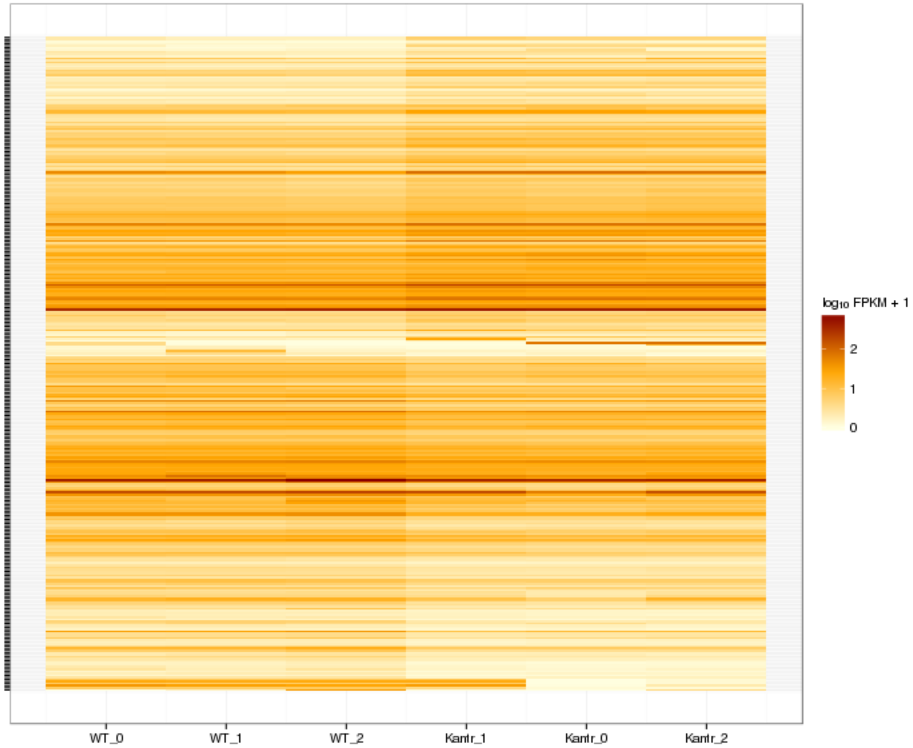
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

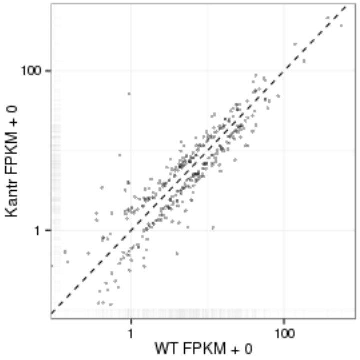


Significant genes with expression >50fpkm (any condition):(turned off)

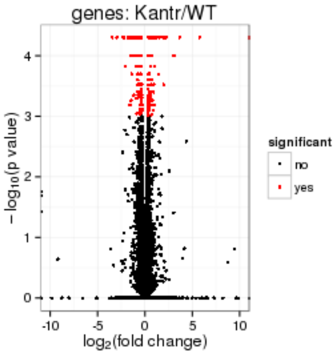
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

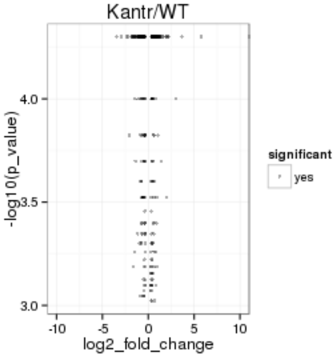
Scatter plot of significant genes only:



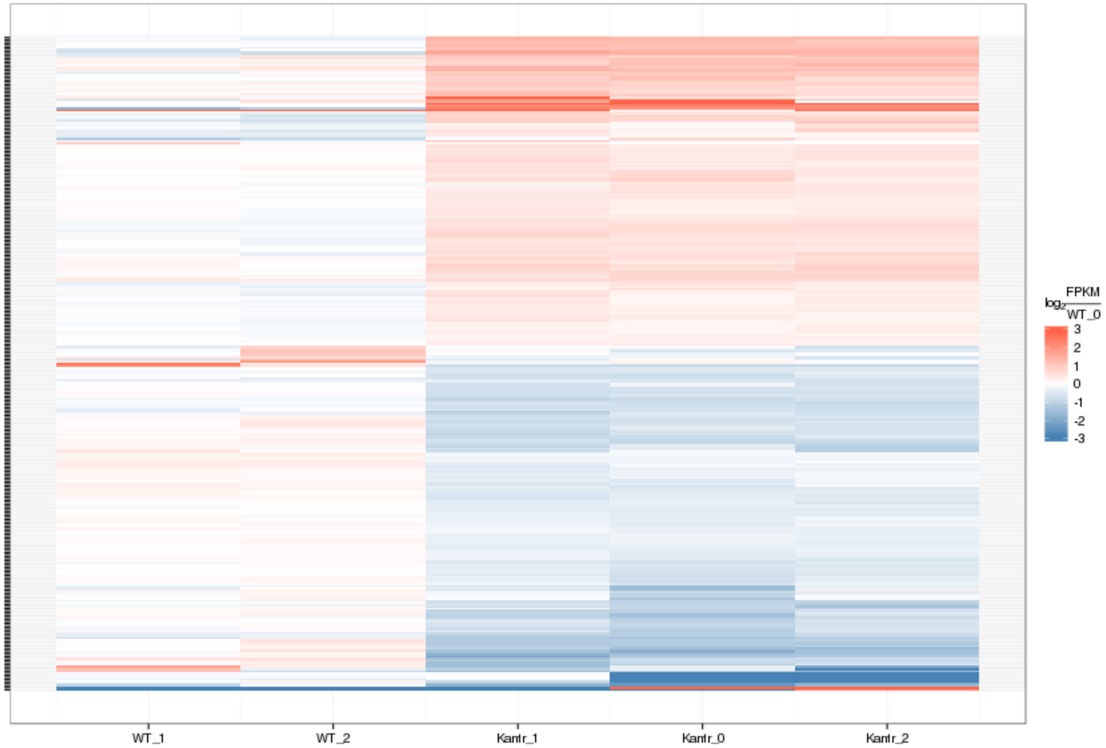
Volcano Plot



Volcano plot with significant genes only:



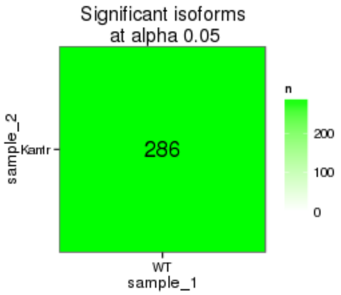
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

	isoAnnot$gene_short_name
1	Sox9
2	Mmp14
3	N4bp3
4	Gramd3
5	Angptl4
6	Slc9a3r2
7	Golga2
8	Plin4
9	Arrdc2
10	Fosb
11	Hif3a
12	9330159F19Rik
13	Sh2b2
14	Prlr
15	Cyp2a5
16	Lrrc8a
17	Bcl2l1
18	Dio2
19	Id3
20	Derl3
21	Gm266
22	Med15
23	Tjap1
24	Mertk
25	Slc25a13
26	Cnksr3
27	Notch4
28	Camk1g
29	Sdc4
30	Ada
31	Erbb3
32	Ksr1
33	Pdk4
34	Sema6a
35	Lama4
36	Arid5b
37	Sgk1
38	Ddit4
39	Vps54
40	Ddc

41 Cpm
42 Nipal4
43 Tns3
44 Btg2
45 Gatsl3
46 Pomc
47 Pxdn
48 Gh
49 Helz
50 Nfkbia
51 Zfp36l1
52 Otub2
53 Net1
54 Fos
55 Zkscan3
56 Elovl7
57 4930452B06Rik
58 Fst
59 Galnt15
60 Sema3g
61 Psmb5
62 Myo10
63 Slc38a2
64 Litaf
65 Bcl6
66 Arc
67 Adamts1
68 Slc15a2
69 Nr4a1
70 Cdkn1a
71 Vegfa
72 Clic5
73 Glo1
74 Sik1
75 Xdh
76 Atp6v0c
77 Tekt4
78 Dusp1
79 Fkbp5
80 Sncaip
81 Pdgfrb
82 Fas
83 Frmd8

84	Uhrf2
85	Hhex
86	Alas2
87	Atp10a
88	Tma16
89	D3Ertd751e
90	Sgk3
91	Paqr8
92	Slc40a1
93	Lamc1
94	Myoc
95	Lypd6b
96	Lcn2
97	Depdc7
98	Jag1
99	Dll4
100	Nkx2-2
101	Bpifa1
102	Fam83d
103	Anxa5
104	Exosc9
105	Dclre1b
106	Fam198b
107	Alpk1
108	Cyr61
109	Gbp2
110	Nr4a3
111	Slc2a1
112	Mfsd2a
113	Hspg2
114	Tinagl1
115	Map3k6
116	Arhgef19
117	Errfi1
118	Ugt2a1
119	Aff1
120	Rasgef1b
121	Lfng
122	Nfe2l3
123	Gkn3
124	Klf15
125	Lag3
126	Clec2d

127 Adipor2
128 Dusp16
129 Slco1a4
130 Rhpn2
131 Sult1a1
132 Disp1
133 Lyve1
134 Cckbr
135 Slc38a5
136 Col4a5
137 Mtm1
138 Tsc22d3
139 Plat
140 Sall1
141 Gpt2
142 Gab1
143 Mt2
144 Mt1
145 Cmtm3
146 Ets1
147 Ldlr
148 Heyl
149 Gng11
150 Alox12b
151 Rnft2
152 Slc16a1
153 Sox10
154 Tbc1d4
155 Ucp2
156 Klf9
157 Trim36
158 Igsf9b
159 Trim59
160 Nostrin
161 Eva1a
162 Lars2
163 Tmem98
164 Prr5
165 Tmem260
166 Micall2
167 Kirrel2
168 Ppp1r14a
169 Mxd4
170 4932438A13Rik

171 Ovol2
172 Avp
173 Egr2
174 Sh3rf3
175 Smim3
176 Galnt11
177 Foxf2
178 Egr1
179 Olfml2b
180 Atp5l
181 Mboat1
182 Pcsk1n
183 Tnfsf10
184 Atp8b1
185 Zfp189
186 Cercam
187 Gpr37
188 Spsb1
189 Gjb6
190 Gbp5
191 Erf
192 Cables1
193 Nkx6-2
194 Cldn5
195 Syt15
196 Sdk2
197 Cdc42ep4
198 Pkp2
199 Greb1l
200 Aplnr
201 Zfp488
202 Tlr7
203 Serpinb1a
204 Rassf9
205 Cirbp
206 Insig1
207 Zfp36l2
208 Npas4
209 Clec14a
210 Gjb2
211 Kcne4
212 Gjb1
213 Kmt2d

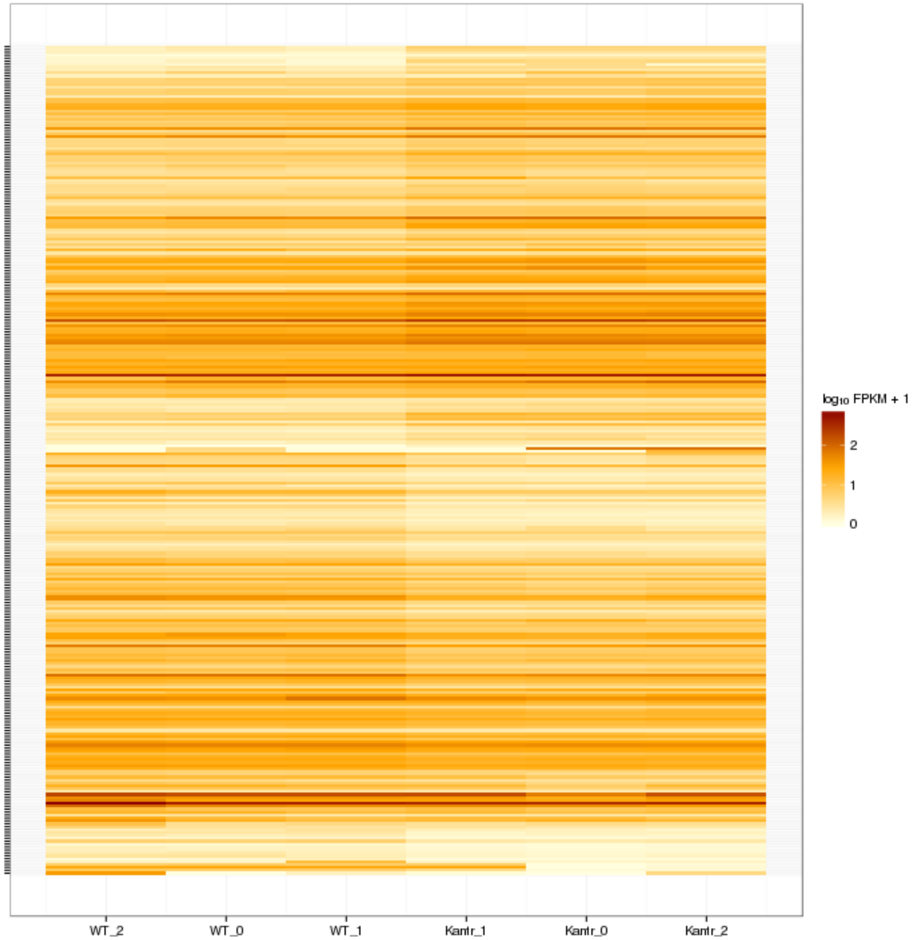
214 Ranbp3l
215 Ccdc6
216 Dact2
217 Acap2
218 Cdc42ep1
219 Rasd1
220 Opalin
221 Fzd2
222 Ppp1r3g
223 Plekho2
224 Olfml1
225 Klf13
226 Hbb-y
227 Gpr17
228 Hbb-bs
229 Junb

230 Creb5
231 Ier2
232 Lifr
233 Lrrc8c
234 Wdr86
235 Per2
236 Pla2g4a
237 Ncoa4
238 1810011O10Rik
239 Kdm5d
240 Chsy3
241 Calcrl
242 Zbtb40
243 Rpl26
244 Cxcl12
245 Cox5b
246 Kdr
247 Hspb11
248 Slc22a8
249 Srrm4
250 Zfp428
251 Cntn4
252 Zbtb16
253 Ppp1r3c
254 Ddx3y
255 Ahnak
256 1700084C01Rik

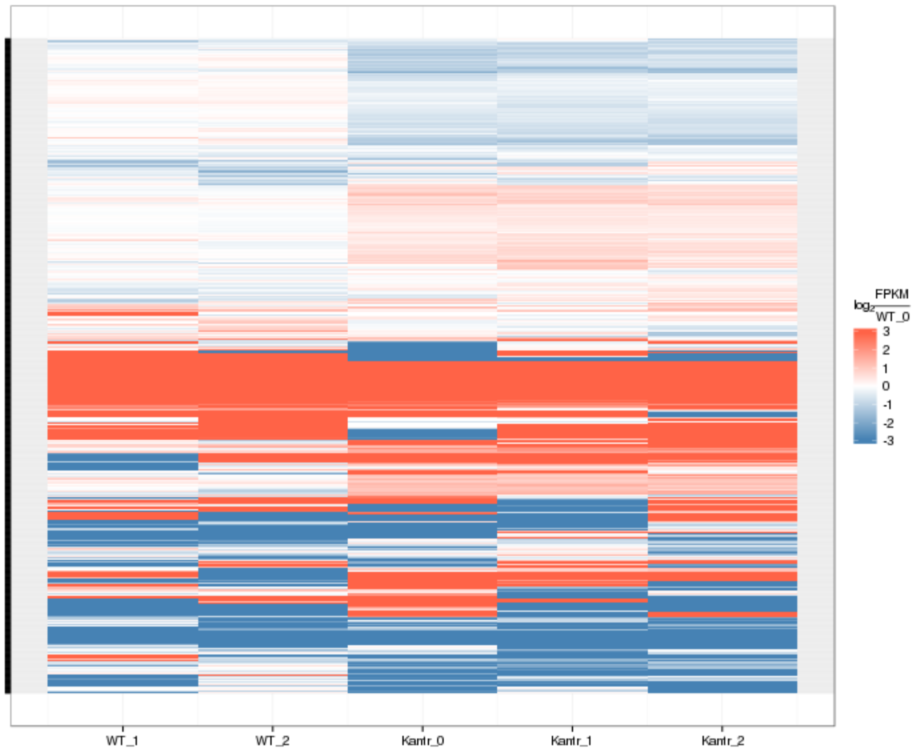
257 Jund
258 Egr4
259 Ccnb1ip1
260 Ppp1r3e
261 Gm7292
262 H2-Bl
263 Tmem88b
264 Hbb-bt
265 Plekhf1
266 Adh1
267 B3galt5
268 Nrarp
269 Aoc2
270 Gm3411
271 Nhsl2
272 Gm15631
273 Xist
274 BC064078
275 Apold1
276 Sox2ot
277 Myl6
278 Neat1
279 Malat1
280 Gm21092
281 Gm7094
282 Fam181a
283 Gm26782
284 Bin2

285 Gm26924

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:

```
## Error: `x' must have at least 2 rows and 2 columns
```

Biocarta zscore:

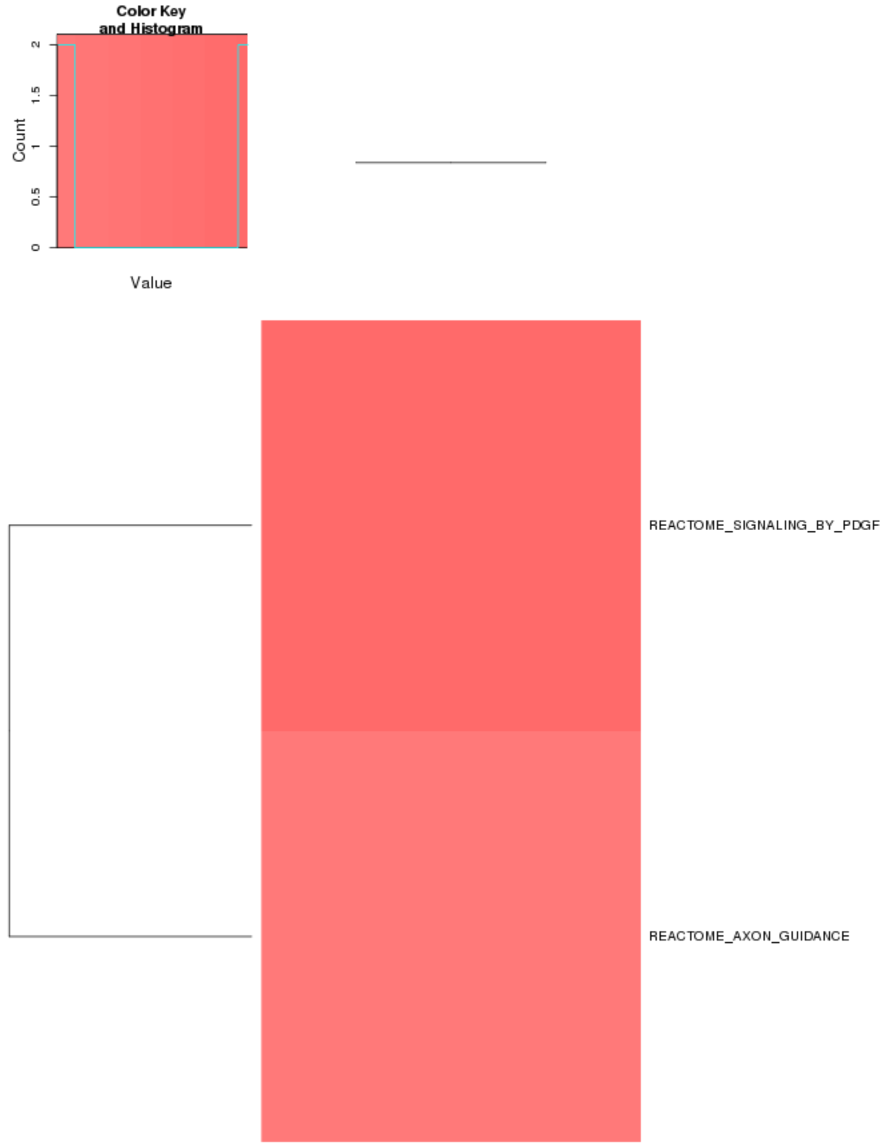
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

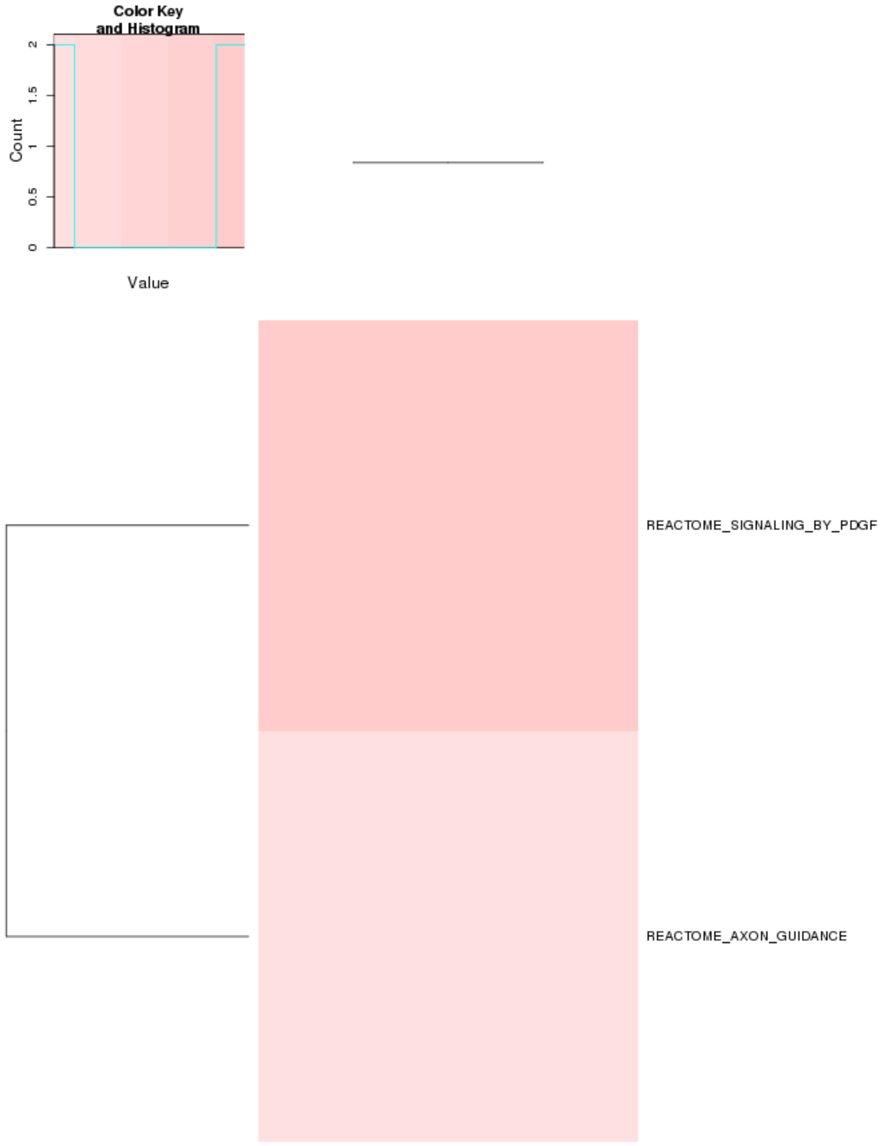
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

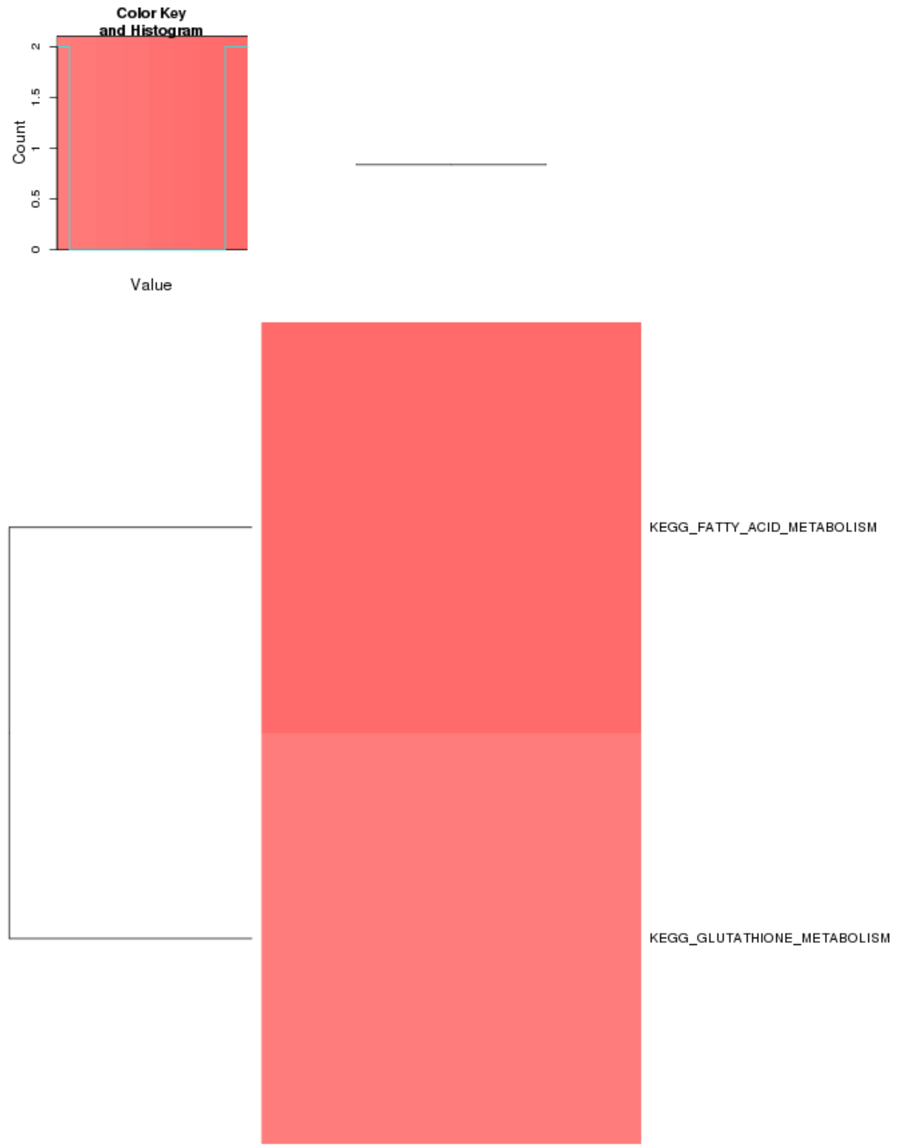
Reactome enrichment:



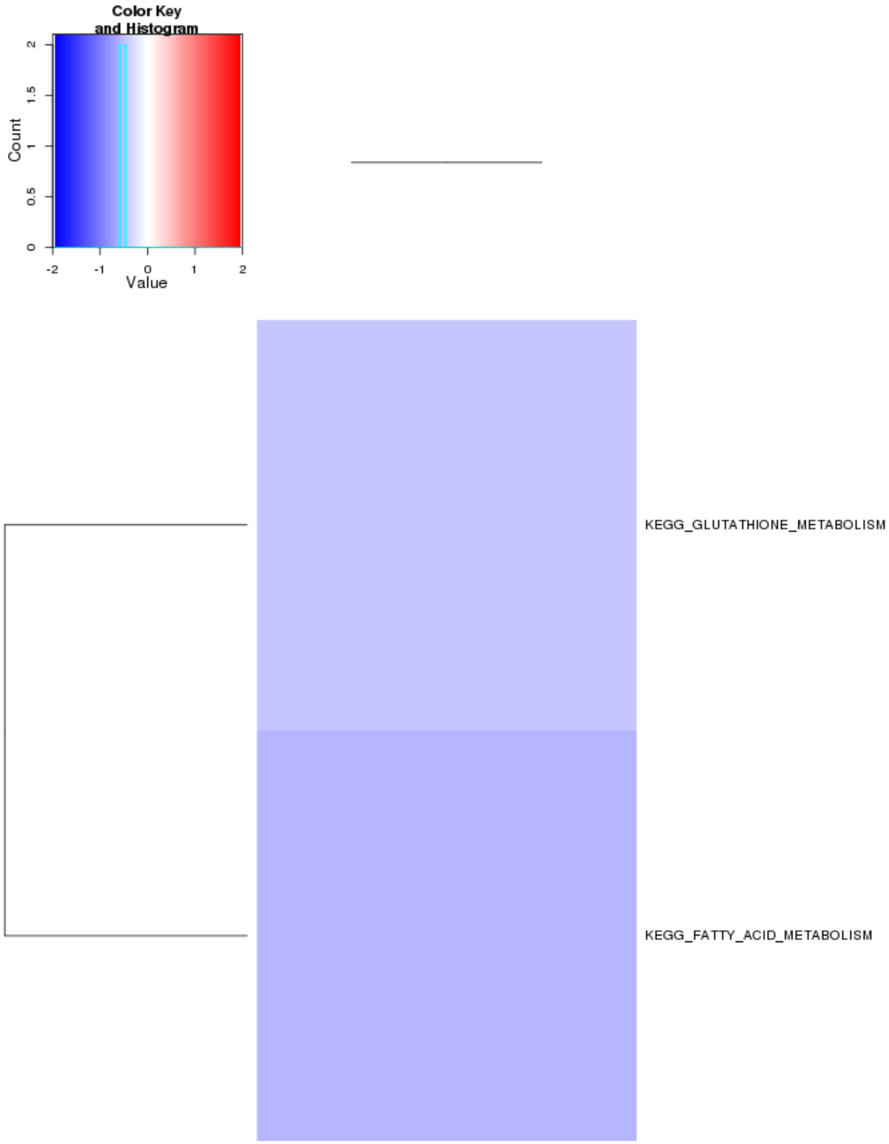
Reactome zscore:



Kegg enrichment:

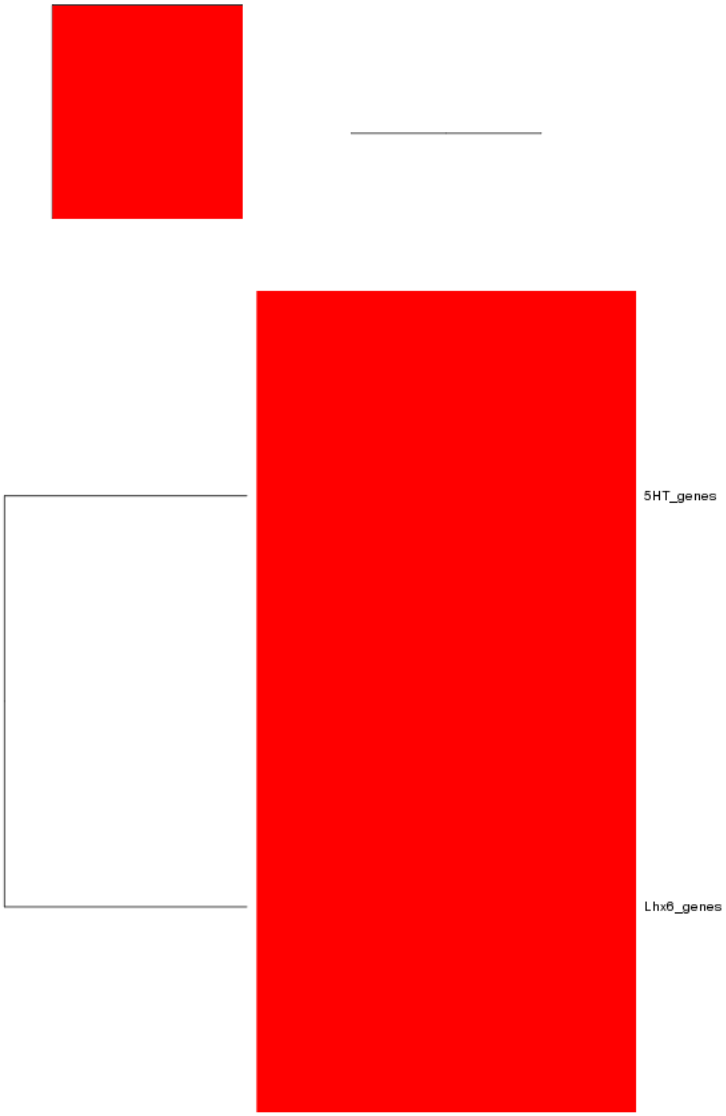

Color Key
and Histogram
Count
2
1.5
1
0.5
0
Value
KEGG_FATTY_ACID_METABOLISM
KEGG_GLUTATHIONE_METABOLISM

Kegg zscore:

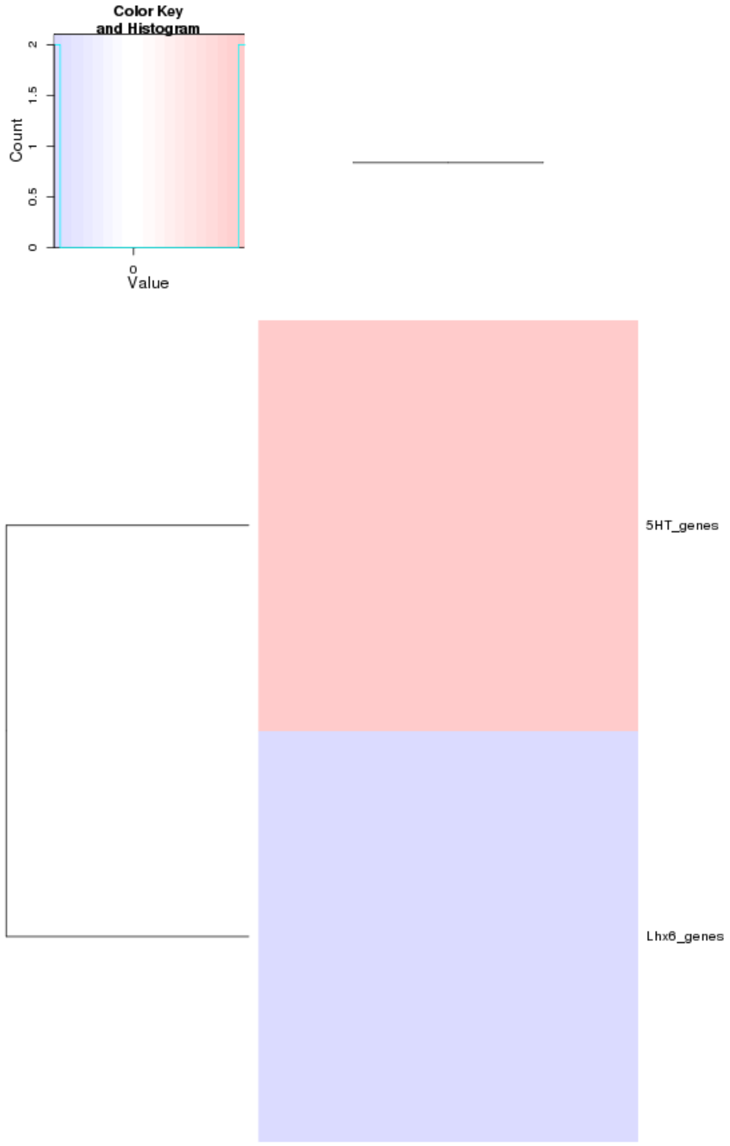


Interneuron enrichment:

```
## Error: no locations are finite
```



Interneuron zscore:



Oncogene enrichment:

```
## Error: argument is of length zero
```

Oncogene zscore:

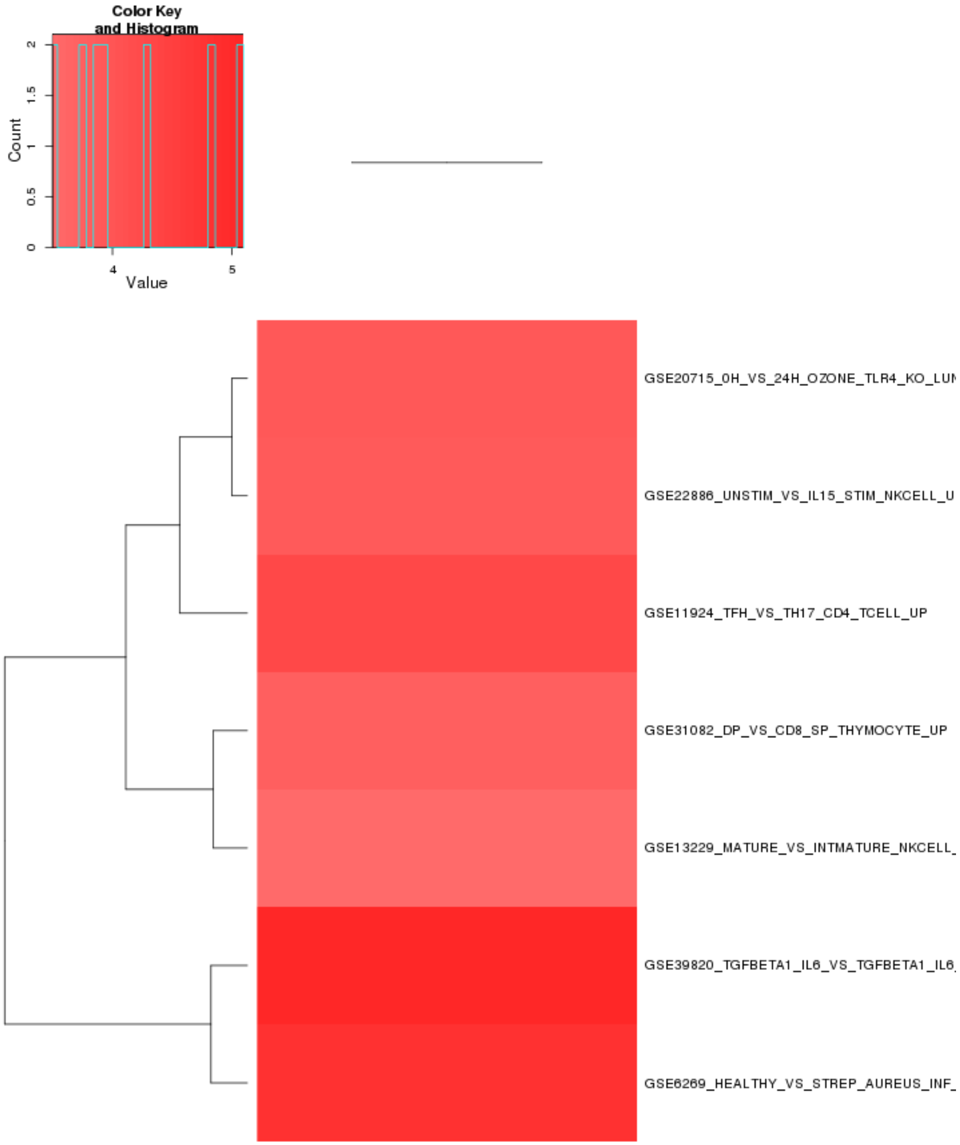
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

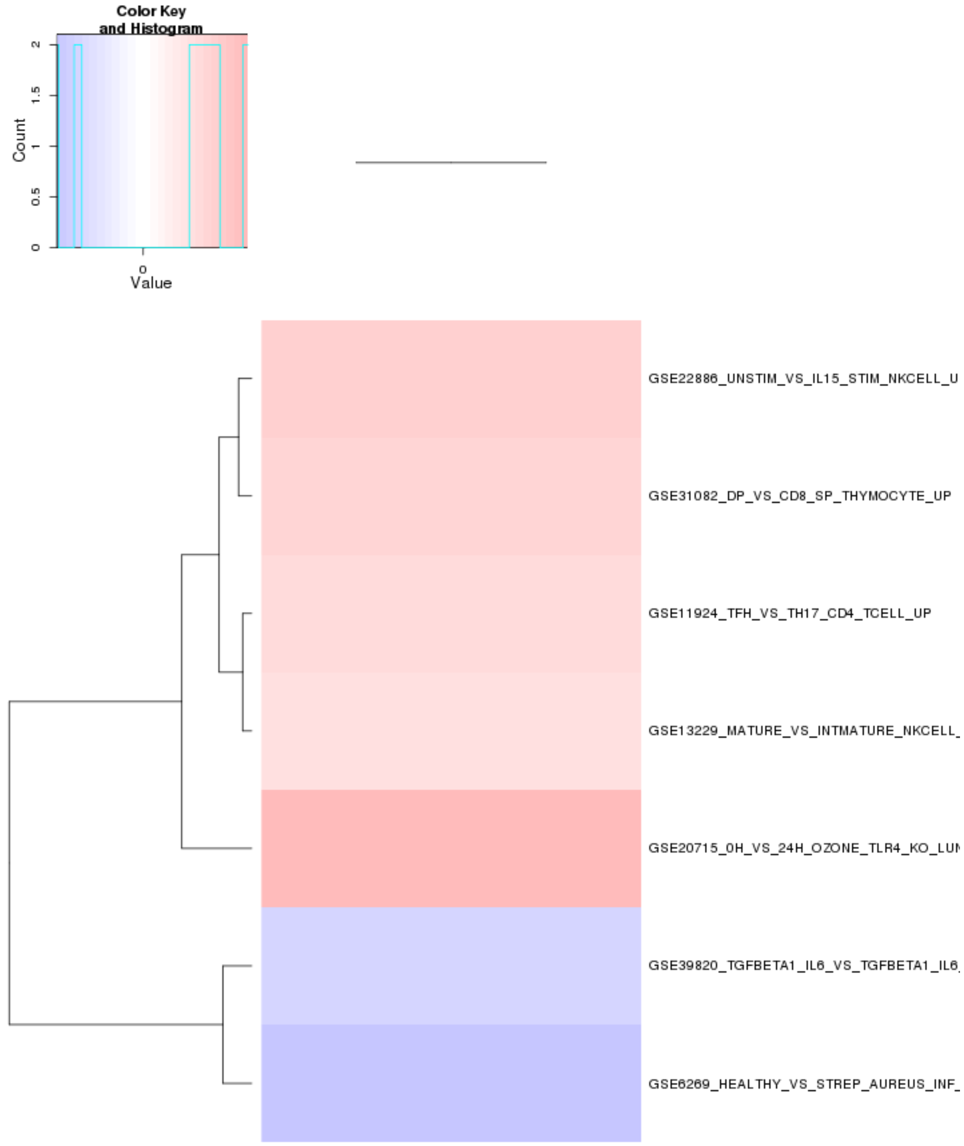
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

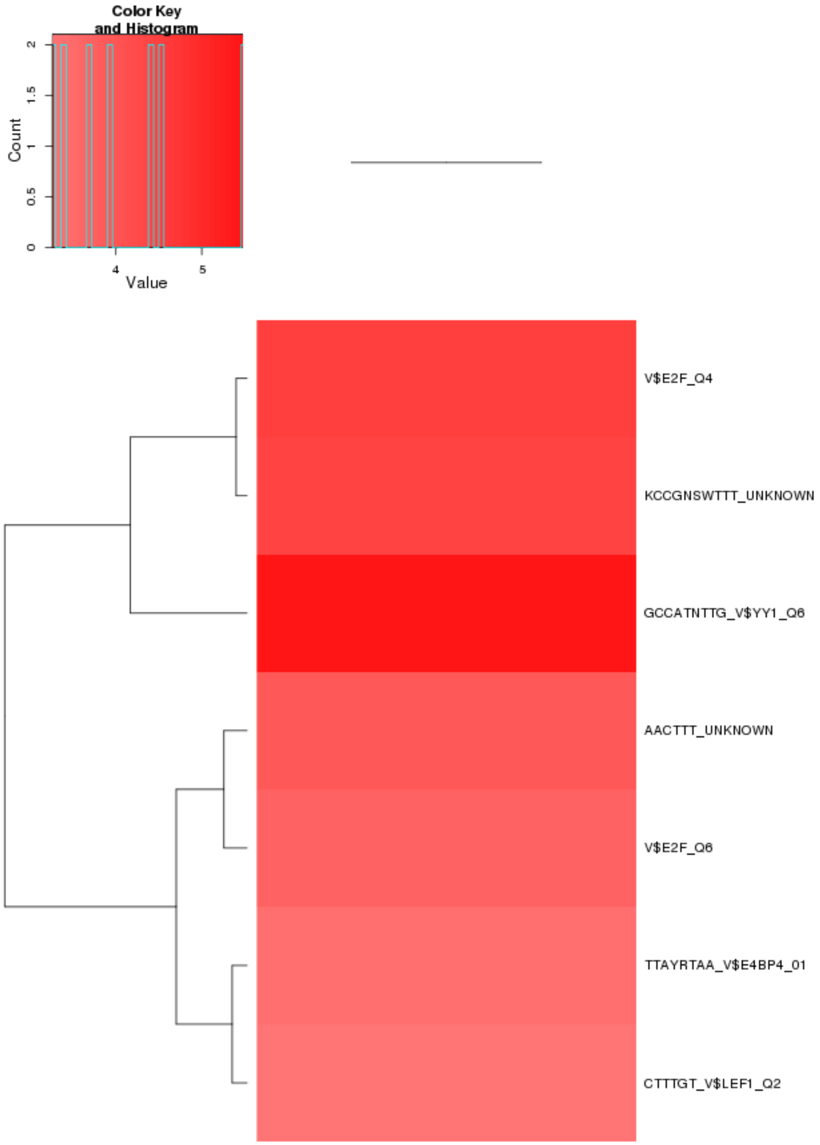
Immuno enrichment:



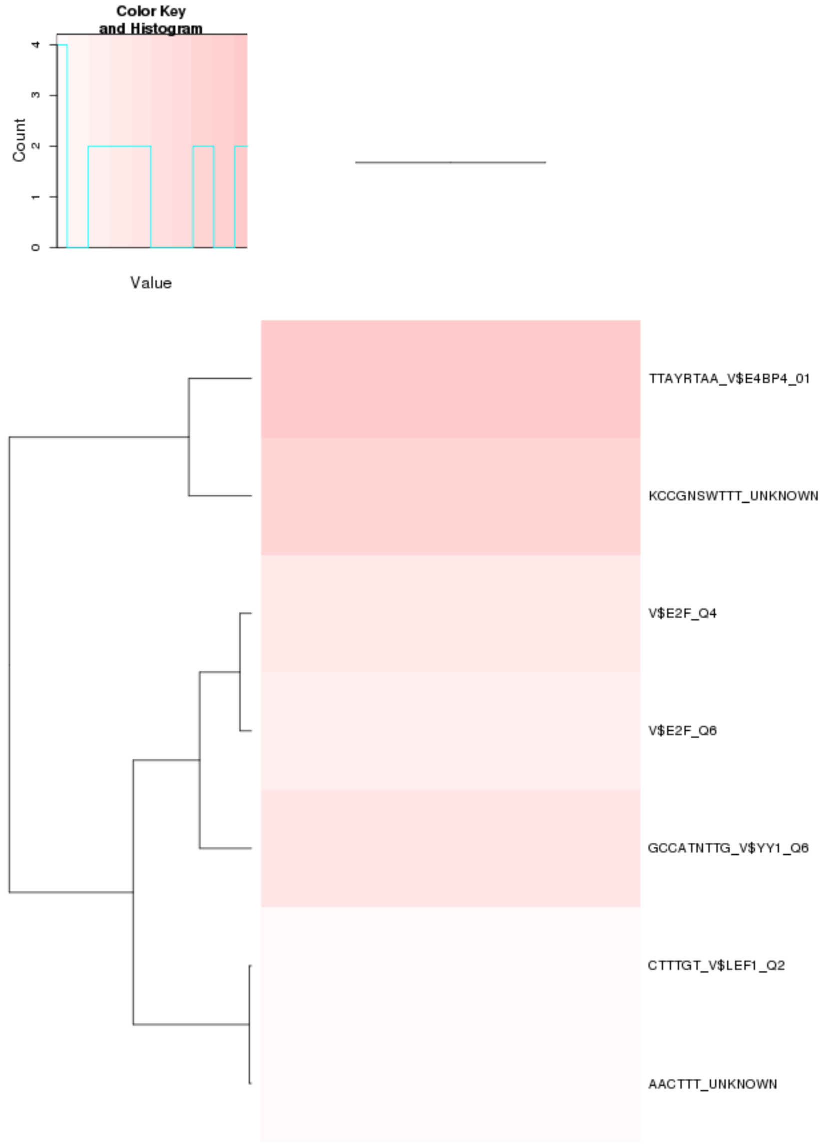
Immuno zscore:



TF enrichment:

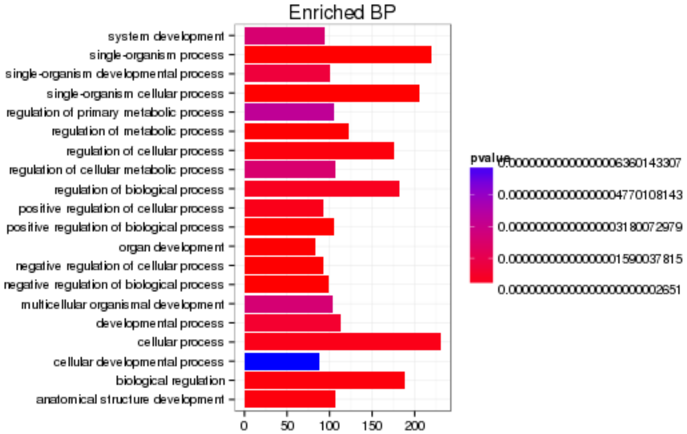

Color Key
and Histogram
Count
0
0.5
1
1.5
2
4
5
Value
V$E2F_Q4
KCCGNSWTTT_UNKNOWN
GCCATNTTG_V$YY1_Q6
AACTTT_UNKNOWN
V$E2F_Q6
TTAYRTAA_V$E4BP4_01
CTTTGT_V$LEF1_Q2

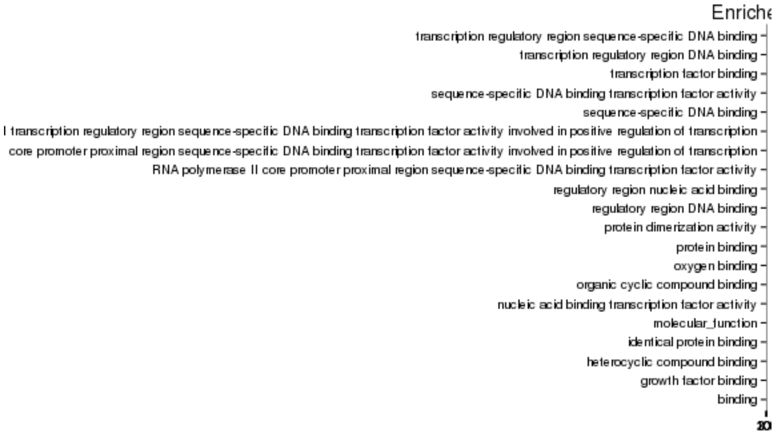
TF zscore:

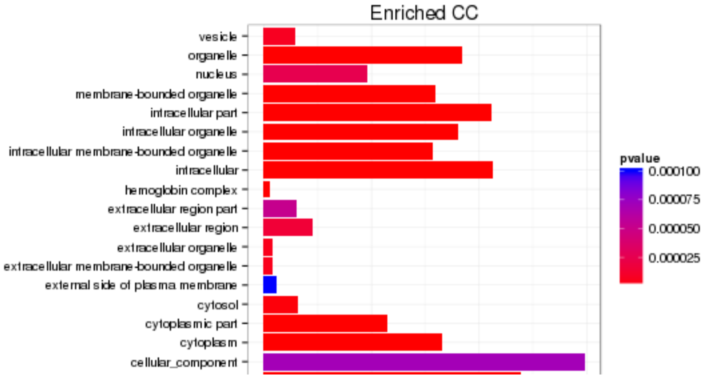


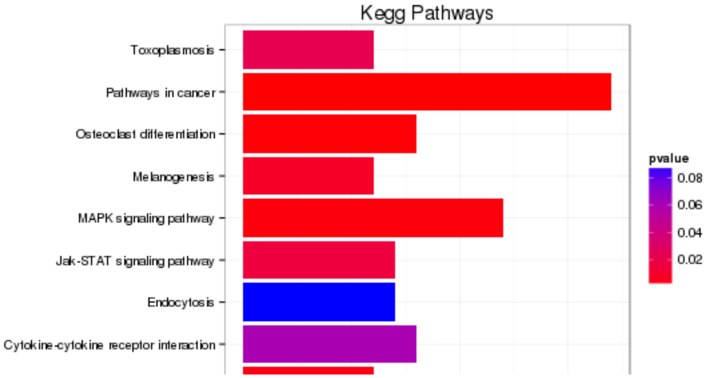
GO enrichment

Cluster profiler used to call enichments of significantly differentially regulated genes that map to Entrez IDs.


Enriched BP
system development
single-organism process
single-organism developmental process
single-organism cellular process
regulation of primary metabolic process
regulation of metabolic process
regulation of cellular process
regulation of cellular metabolic process
regulation of biological process
positive regulation of cellular process
positive regulation of biological process
organ development
negative regulation of cellular process
negative regulation of biological process
multicellular organismal development
developmental process
cellular process
cellular developmental process
biological regulation
anatomical structure development
0
50
100
150
200
pvalue
0.0000000000000000006360143307
0.0000000000000000004770108143
0.0000000000000000003180072979
0.0000000000000000001590037815
0.000000000000000000000002651

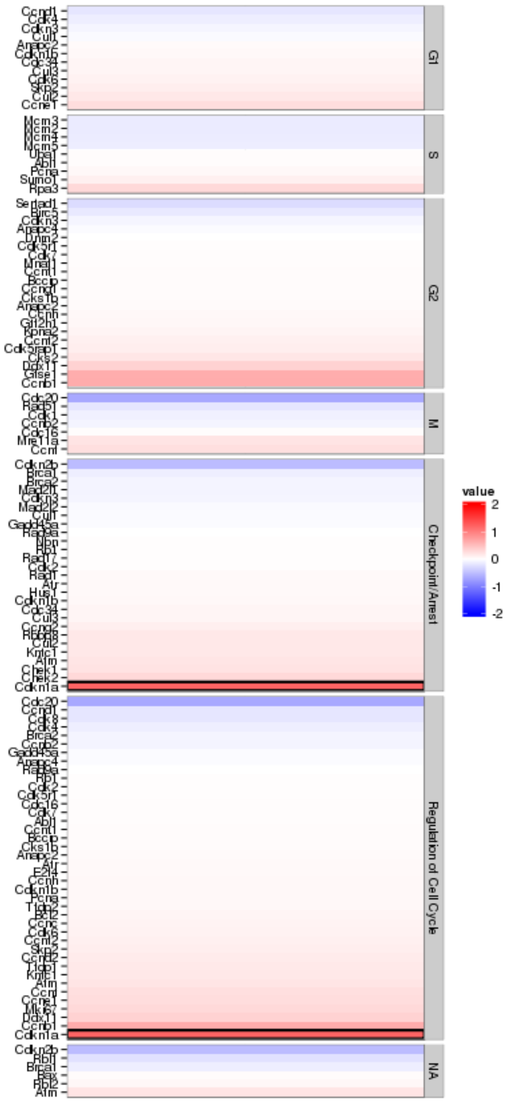

Enriche
transcription regulatory region sequence-specific DNA binding
transcription regulatory region DNA binding
transcription factor binding
sequence-specific DNA binding transcription factor activity
sequence-specific DNA binding
l transcription regulatory region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription
core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription
RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity
regulatory region nucleic acid binding
regulatory region DNA binding
protein dimerization activity
protein binding
oxygen binding
organic cyclic compound binding
nucleic acid binding transcription factor activity
molecular_function
identical protein binding
heterocyclic compound binding
growth factor binding
binding
20


Enriched CC
vesicle
organelle
nucleus
membrane-bounded organelle
intracellular part
intracellular organelle
intracellular membrane-bounded organelle
intracellular
hemoglobin complex
extracellular region part
extracellular region
extracellular organelle
extracellular membrane-bounded organelle
external side of plasma membrane
cytosol
cytoplasmic part
cytoplasm
cellular_component
pvalue
0.000100
0.000075
0.000050
0.000025

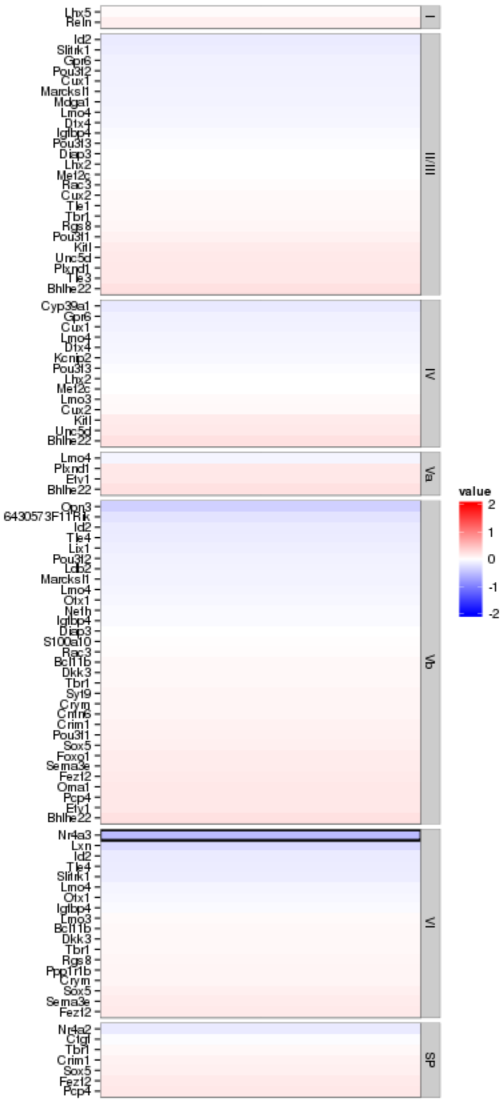

Kegg Pathways
Toxoplasmosis
Pathways in cancer
Osteoclast differentiation
Melanogenesis
MAPK signaling pathway
Jak-STAT signaling pathway
Endocytosis
Cytokine-cytokine receptor interaction
pvalue
0.08
0.06
0.04
0.02

```
## Error: 'x' and 'units' must have length > 0
```

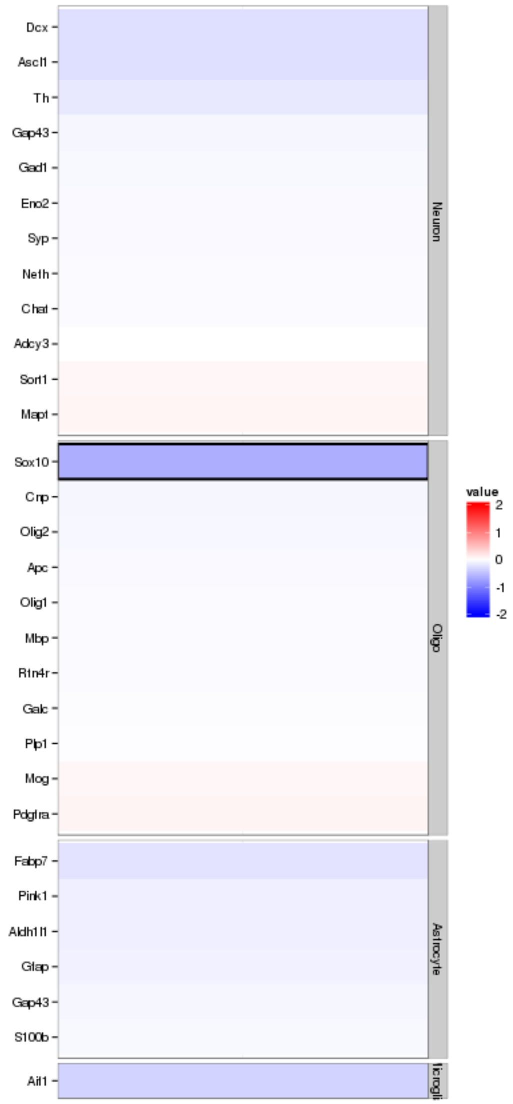
Enrichment or depletion for stage-specific cell cycle markers



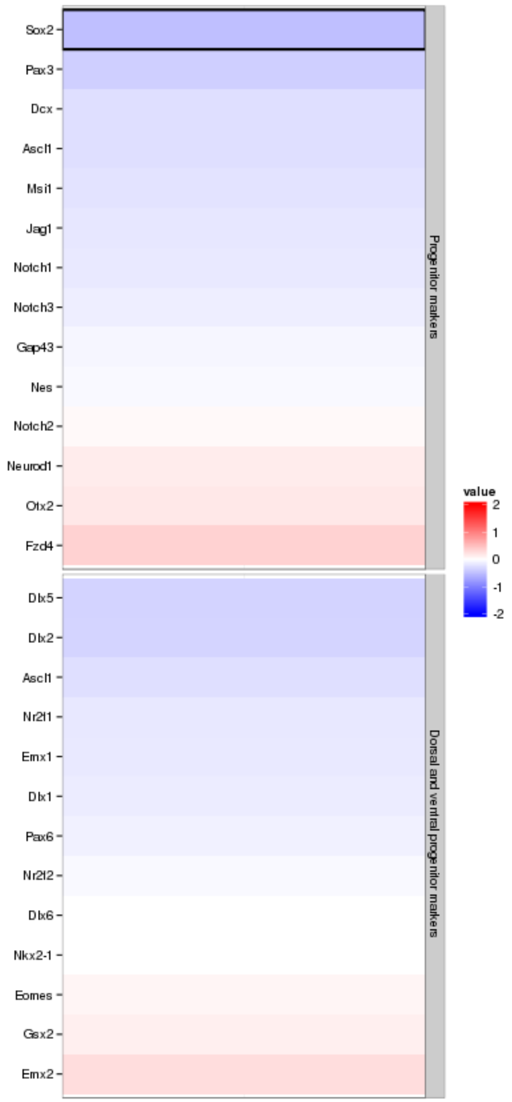
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



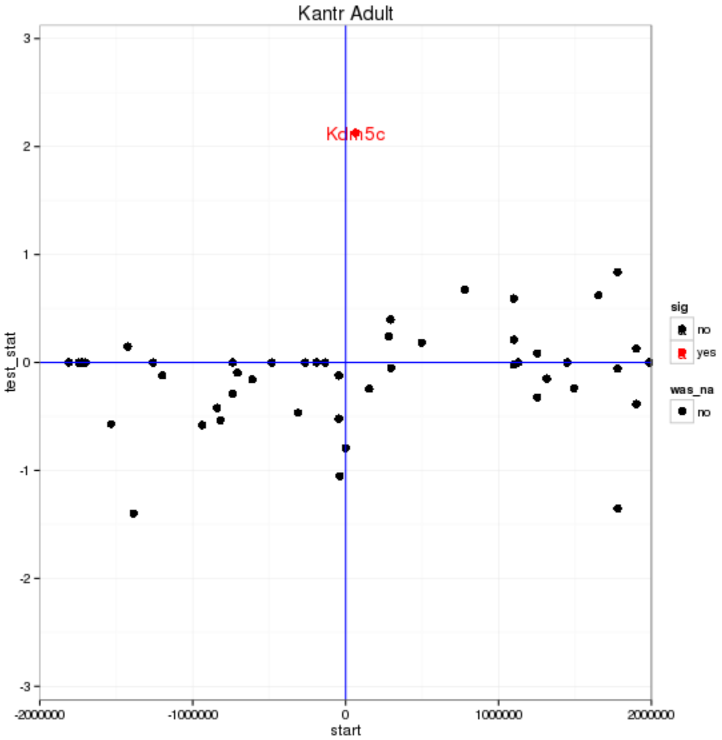
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 1 genes significantly regulated in a region this size is: 0.4783



Notes

Samples used are:

	10
1	JR824
2	JR820
3	JR821
4	JR742
5	JR819
6	JR823

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR824/abundances.cxb	WT	0	WT_0	34306900.00	36012300.00	0.96	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR820/abundances.cxb	WT	1	WT_1	36256500.00	36012300.00	1.01	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR821/abundances.cxb	WT	2	WT_2	45848800.00	36012300.00	1.29	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR742/abundances.cxb	Kantr	0	Kantr_0	35615300.00	36012300.00	0.98	1.00

5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR819/abundances.cxb	Kantr	1	Kantr_1	32408700.00	36012300.00	0.89	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR823/abundances.cxb	Kantr	2	Kantr_2	33428000.00	36012300.00	0.92	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1                       
##  [2] stringr_0.6.2                    
##  [3] seqbias_1.10.0                   
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0                  
##  [6] Biostrings_2.30.1                
##  [7] gdata_2.13.3                     
##  [8] GO.db_2.10.1                     
##  [9] org.Mm.eg.db_2.10.1              
## [10] clusterProfiler_1.13.1           
## [11] DOSE_2.0.0                       
## [12] ReactomePA_1.6.1                 
## [13] AnnotationDbi_1.24.0             
## [14] Biobase_2.22.0                   
## [15] mgcv_1.7-29                      
## [16] nlme_3.1-117                     
## [17] RMySQL_0.9-3                     
## [18] RColorBrewer_1.0-5               
## [19] gridExtra_0.9.1                  
## [20] gtable_0.1.2                     
## [21] marray_1.40.0                    
## [22] gplots_2.13.0                    
## [23] GSA_1.03                         
## [24] limma_3.18.13                    
## [25] xtable_1.7-3                     
## [26] cummeRbund_2.7.2                 
## [27] Gviz_1.6.0                       
## [28] rtracklayer_1.22.7               
## [29] GenomicRanges_1.14.4             
## [30] XVector_0.2.0                    
```

```
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##             param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,Kantr -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Kantr_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/ar
## 2
## 3
## 4
## 5
```

Kantr KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for Kantr.

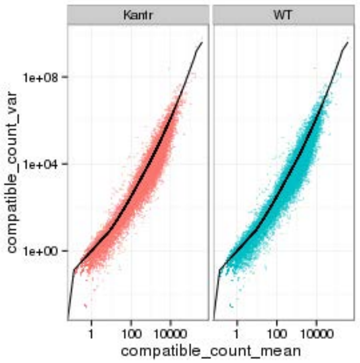
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

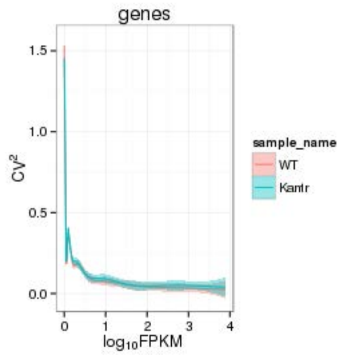
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



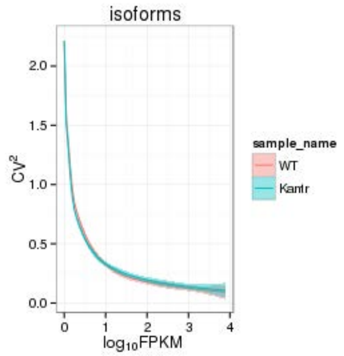
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

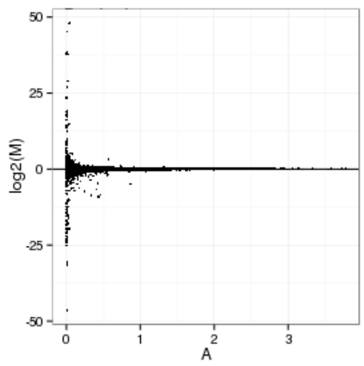
Genes:



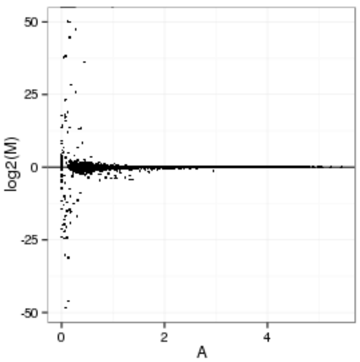
Isoforms:



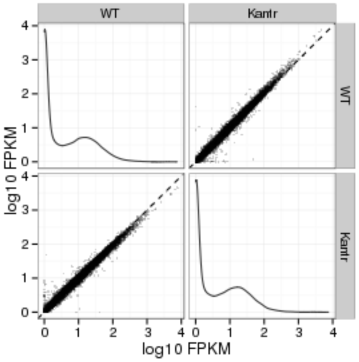
MvA plot



MvA plot counts



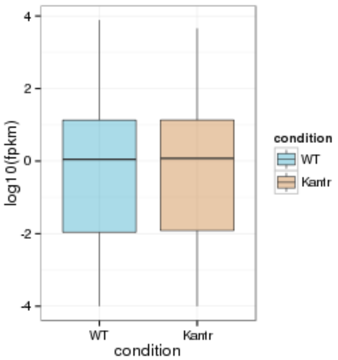
Scatterplot matrix



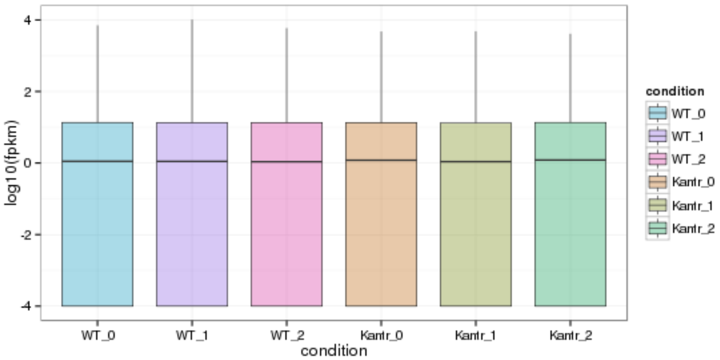
Distributions

Boxplots

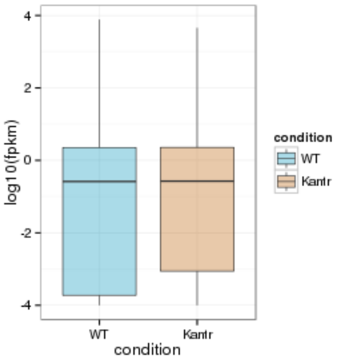
Boxplot (genes)



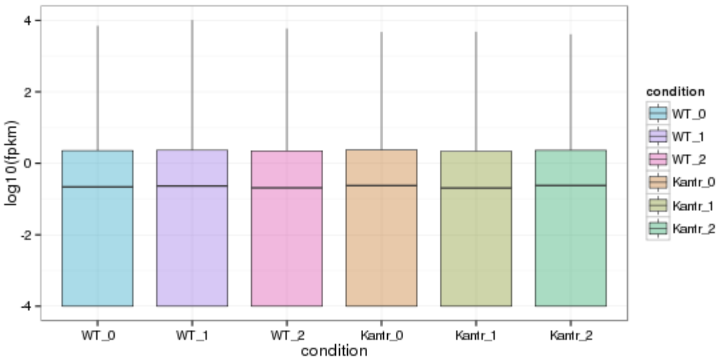
Boxplot (genes, replicates)



Boxplot (isoforms)

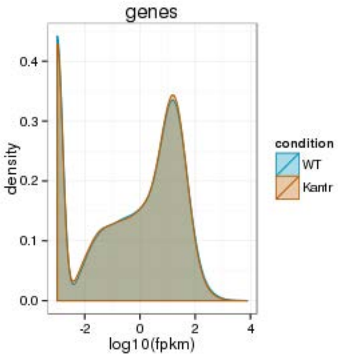


Boxplot (isoforms, replicates)

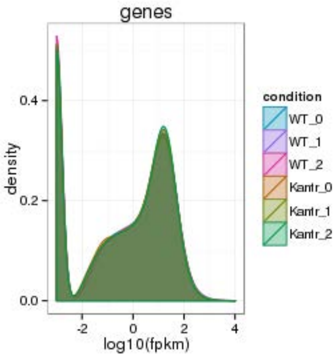


Density

Density (genes)

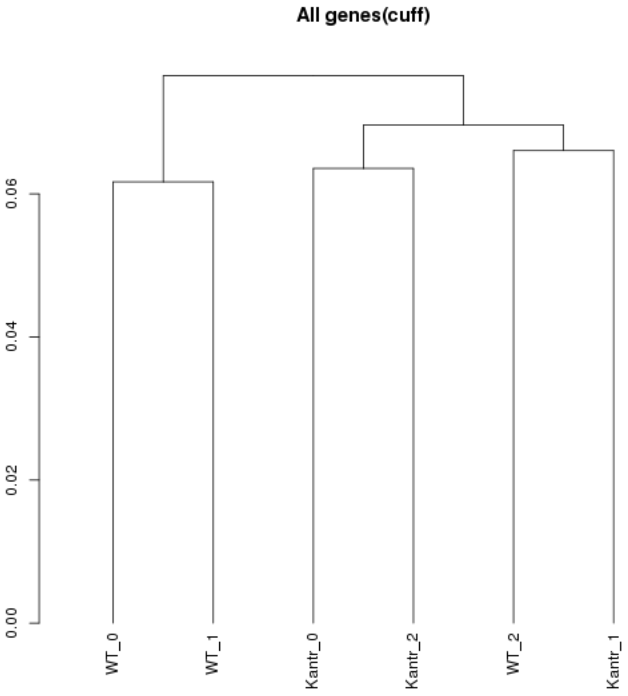


Density (genes, replicates)



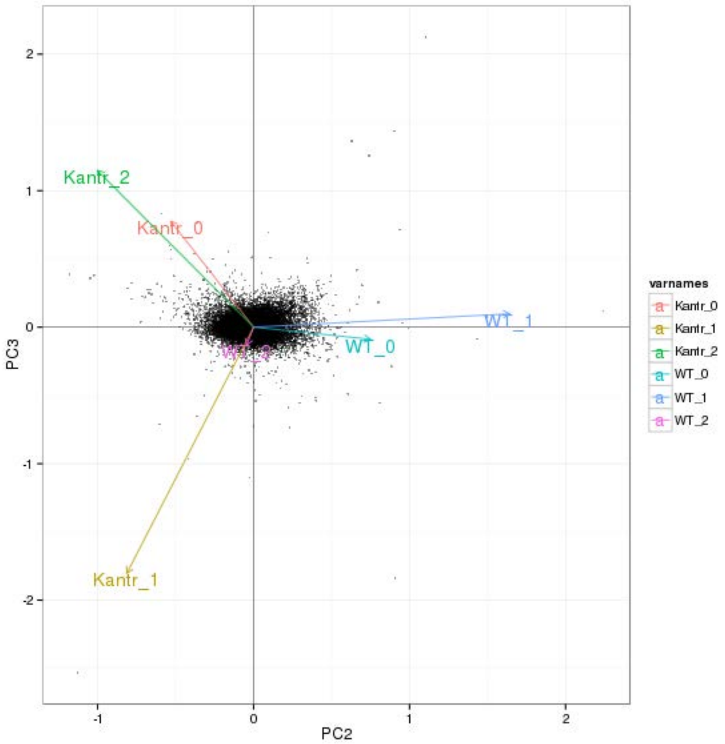
Clustering

Replicate Clusters



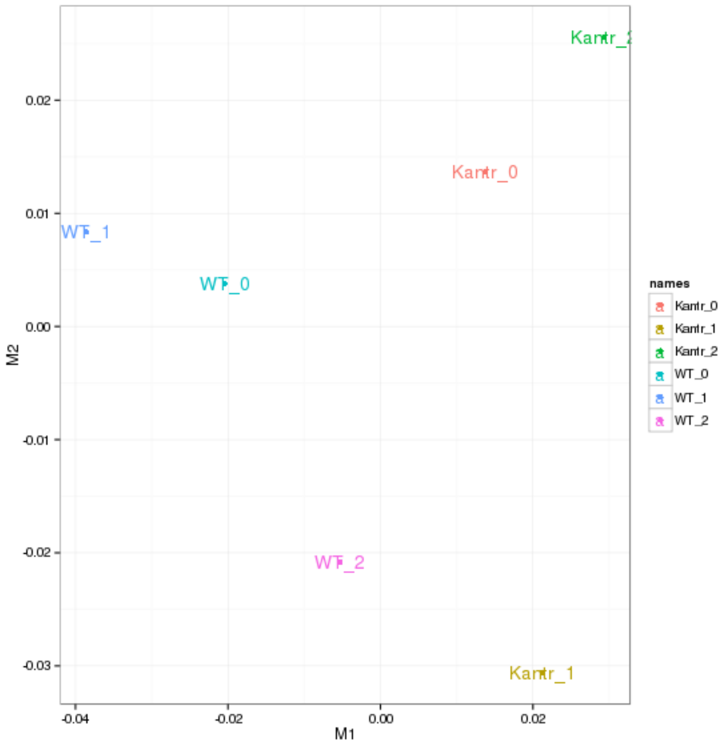
```
## NULL
```

PCA (genes)



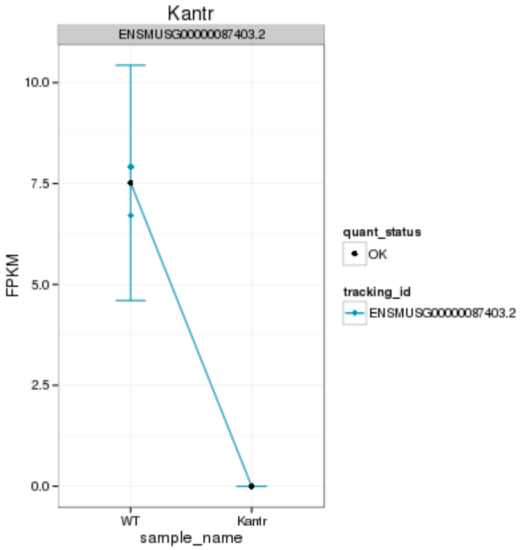
Kantr_2
Kantr_0
WT_1
WT_0
WT_2
Kantr_1
PC3
PC2
2
1
0
-1
-2
-1
0
1
2
varnames
Kantr_0
Kantr_1
Kantr_2
WT_0
WT_1
WT_2

MDS (genes)

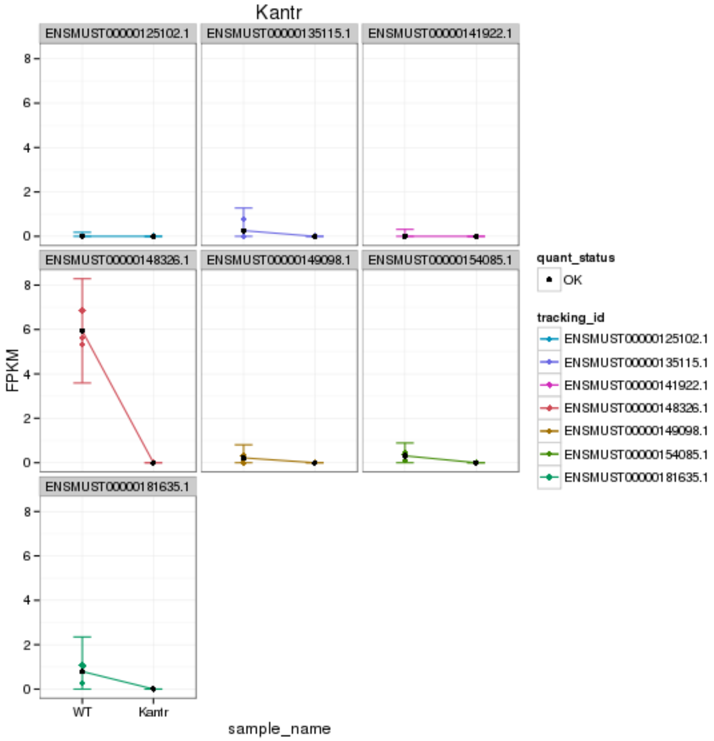


KO assessment

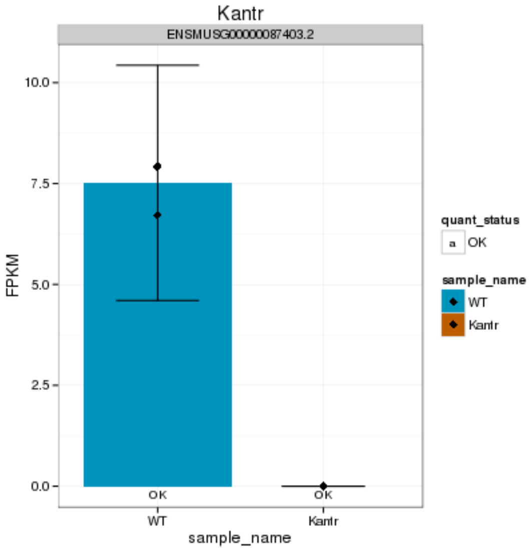
Endogenous lncRNA expression



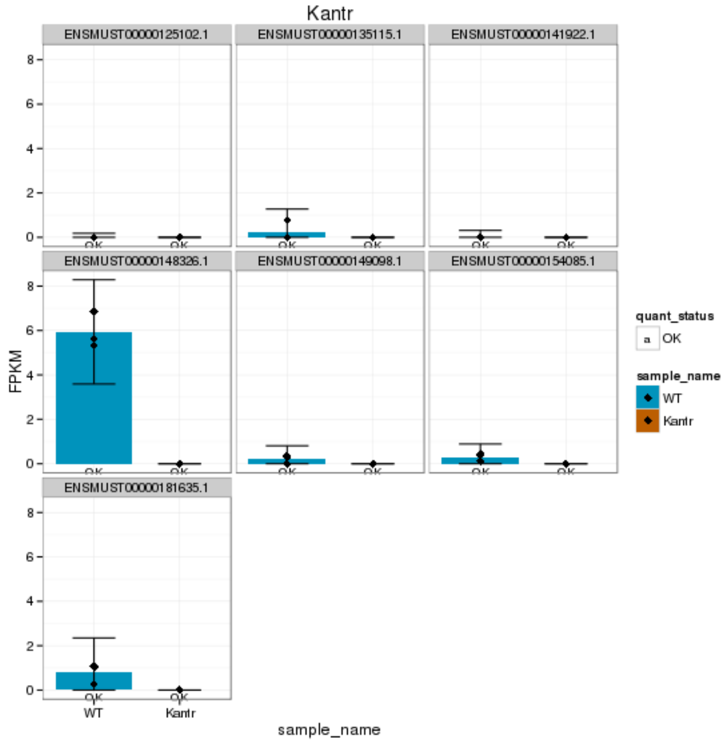
Endogenous expression of Kantr isoforms:



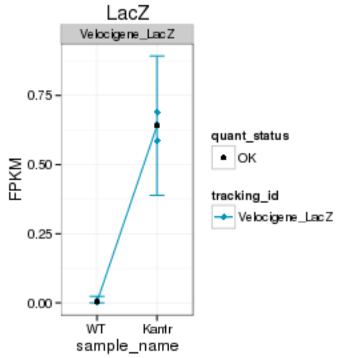
Barplot of gene expression:

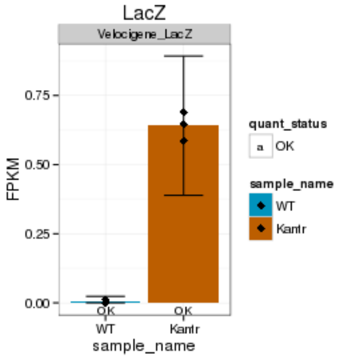


Barplot of isoform expression:



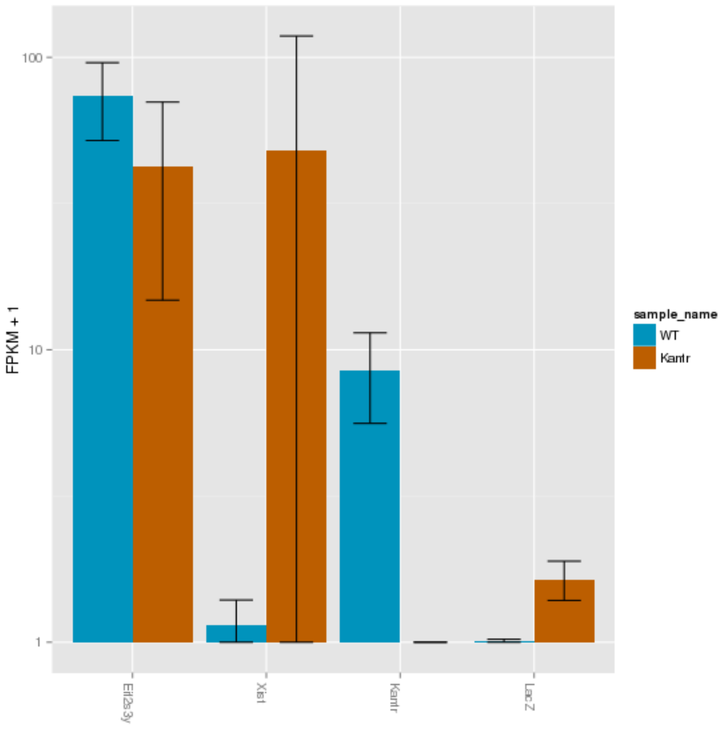
LacZ expression



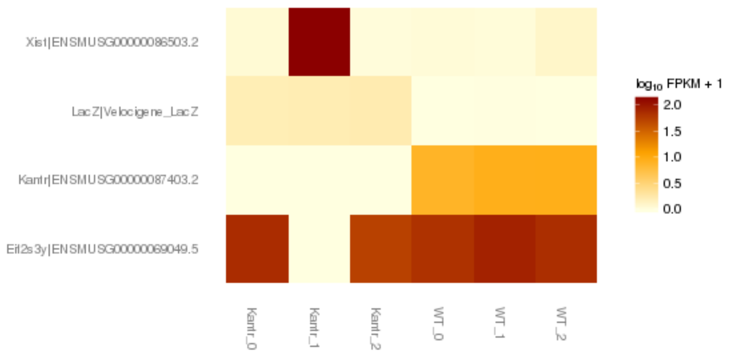


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

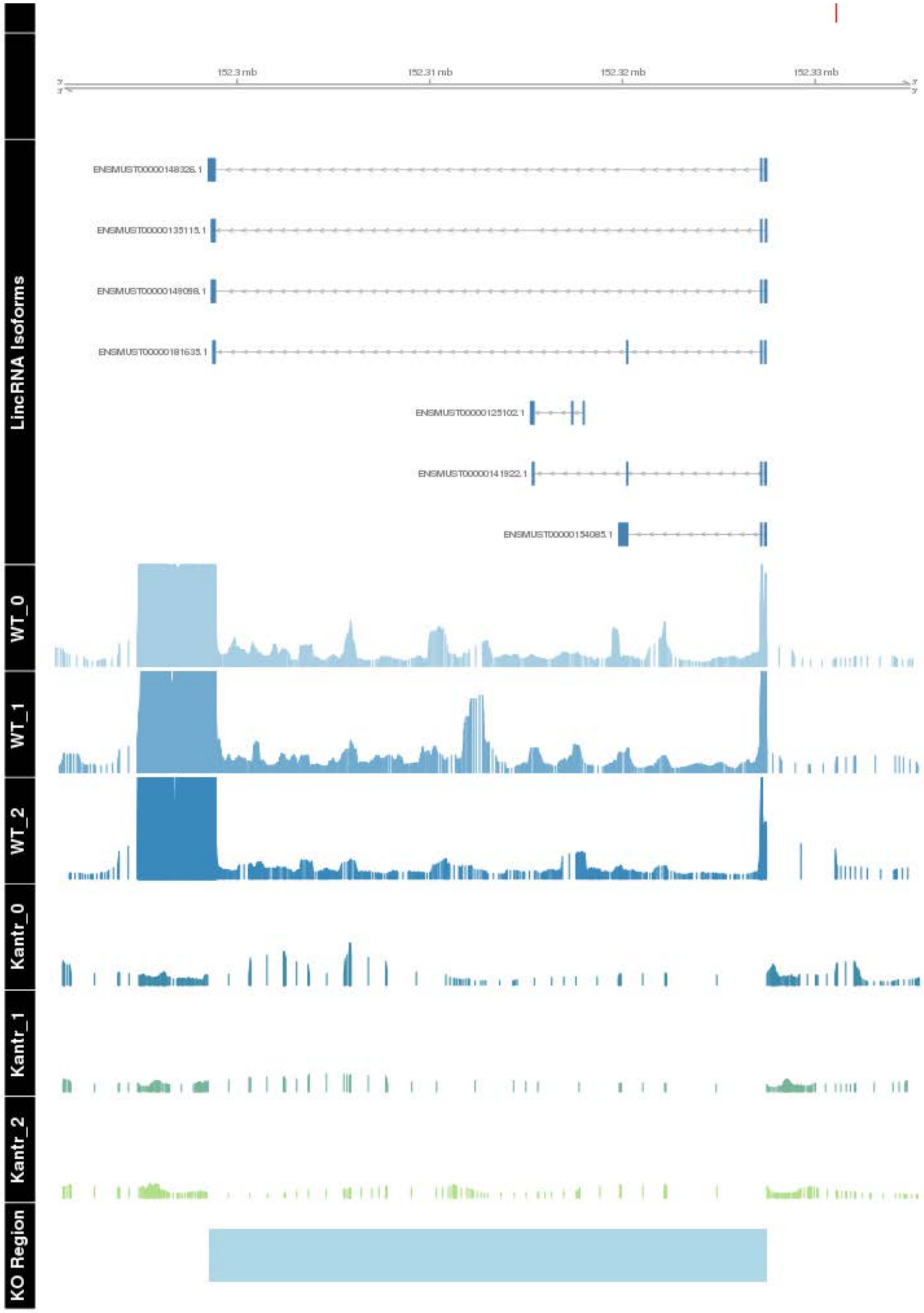
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


LincRNA Isoforms
WT_0
WT_1
WT_2
Kantr_0
Kantr_1
Kantr_2
KO Region
152.3 mb
152.31 mb
152.32 mb
152.33 mb
5'
3'
3'
5'
ENSMUST00000148326.1
ENSMUST00000135115.1
ENSMUST00000149098.1
ENSMUST00000181635.1
ENSMUST00000125102.1
ENSMUST00000141922.1
ENSMUST00000154085.1

Differential Analysis

Differential Genes

There are 766 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	H19
2	Tbx2
3	Ngfr
4	Glra1
5	Hddc2
6	Cdh1
7	Mcts1
8	Itga5
9	Gabra2
10	Col6a1
11	Snrnp27
12	Gabrg1
13	Col18a1
14	Col1a1
15	Eef1e1
16	Sept7
17	Use1
18	Hltf
19	Zfp40
20	Shh
21	Lamb1
22	Fcgrt
23	Bicd1
24	Calb2
25	Zfp81
26	Ptrf
27	Pax2
28	Sst
29	Col26a1
30	Aqp1
31	Tmem242
32	Wisp1
33	Polr2a
34	Corin
35	Nid1
36	Evx1
37	Tep1

38 Fbln1
39 Nphs1
40 Acot13
41 Gabrb2
42 Khsrp
43 Dio2

44 0610009B22Rik
45 Zmiz1
46 Arid1a
47 Rplp1
48 Snrpb2
49 Bmp7
50 Sdhb
51 Slc38a3
52 Mrpl52
53 Ebf3
54 Gabra1
55 Scarf2
56 Rpa3
57 Phox2b
58 Rps5
59 Slc41a1
60 Aldh1a2
61 Tctex1d2
62 Cacybp
63 Ndufa2
64 Cox6c
65 Srp19
66 Hoxa2
67 Gata2
68 Ptgds
69 Psma2
70 Mrpl32
71 Capza2
72 Lcorl
73 Lbp
74 Atp5e
75 Ndufa1
76 Plgrkt
77 Mrps18c
78 Sulf1
79 Etaa1
80 Vtn

81	Erbb3
82	Trove2
83	Anxa6
84	Glra2
85	Slc35g3
86	Slc16a10
87	Lama4
88	Fabp7
89	Nts
90	Lama2
91	Actr6
92	Kitl
93	Enpp3
94	Meis1
95	Grb10
96	Snrpd3
97	Phlda1
98	Col6a2
99	Hint1
100	Hmmr
101	Flt4
102	Sar1b
103	Nefh
104	Gabrg2
105	Rps27a
106	Ccdc104
107	Aebp1
108	Smc6
109	Bcap29
110	Txndc17
111	Ntn1
112	Klhl28
113	Fkbp3
114	Scfd1
115	Nemf
116	Psma6
117	Mpp5
118	Eif2s1
119	Smoc1
120	2010107E04Rik
121	Tfap2a
122	Dek
123	Nol8

124 Ror2
125 A530054K11Rik
126 Cetn3
127 Irx4
128 Slc6a3
129 Serf1
130 Otp
131 Trim23
132 Cenpk
133 Ndufs4
134 Fam213a
135 Cdhr1
136 Psmc6
137 Chat
138 Zdhhc20
139 Dnajc15
140 Sugt1
141 Bnip3l
142 Nefm
143 Uchl3
144 Dab2
145 Sub1
146 Npr3
147 Skor1
148 Oxr1
149 Angpt1
150 Eif3h
151 Matn2
152 Eif3e
153 Emc2
154 Kcnv1
155 Ndufb9
156 Sla
157 Lrrc6
158 Enpp2
159 Myh9
160 Ndufa6
161 Plec
162 Ube2v2
163 B3gnt5
164 Sidt1
165 Ncam2
166 Arhgap31

167	Sncg
168	Ndufa5
169	Scg5
170	Prph
171	Igf2r
172	Thbs2
173	Zfp51
174	Pla2g7
175	Slc5a7
176	Arhgap28
177	Cyp1b1
178	Ndufv2
179	Epas1
180	Cript
181	Uqcc2
182	Cox7a2l
183	Slc25a46
184	Rock1
185	Esco1
186	Rnf138
187	Pggt1b
188	Yipf5
189	Sec11c
190	C330018D20Rik
191	Fbn2
192	Rps14
193	Tmx3
194	Pdgfrb
195	Slc22a6
196	Aldh1a7
197	Kif20b
198	Capn1
199	Slit1
200	Kazald1
201	Tlx1
202	Lbx1
203	Alas2
204	Rps24
205	Itgb8
206	Rps26
207	Esyt1
208	Zfp711
209	Gaa

210	Tmem47
211	Gdap1
212	Itih5
213	Rpl14
214	Xiap
215	Kbtbd3
216	Cwf19l2
217	Mybl1
218	Mob4
219	Nop58
220	Sumo1
221	Ndufb3
222	Sgol2
223	Col5a2
224	Col3a1
225	Tex30
226	Pdcl3
227	Mrpl30
228	Ormdl1
229	1110058L19Rik
230	Fn1
231	Nppc
232	Cfh
233	Tfcp2l1
234	Dbi
235	Syt2
236	Lamc1
237	Kif26b
238	Dusp27
239	Ptpn14
240	Vamp4
241	Mrc1
242	Rabgap1l
243	Yme1l1
244	Acbd5
245	Ermn
246	Lamc3
247	Gsn
248	Pax8
249	Kif18a
250	Lin7c
251	B230118H07Rik
252	Eif3m

253 Fbn1
254 Cops2
255 Creb3l1
256 Map1a
257 Lamp5
258 Nusap1
259 Casc5
260 Otor
261 Pkia
262 Snx16
263 Lrrcc1
264 Psma7
265 Sec62
266 Dcun1d1
267 Hmgcs2
268 Olfm3
269 Sfrp2
270 Enpep
271 Aimp1
272 Rps3a1
273 Depdc1a
274 Rps20
275 Casp8ap2
276 Smc2
277 Svep1
278 Zfp37
279 Bspry
280 Nudt2
281 Rps6
282 Ift74
283 Magoh
284 Ccdc23
285 Cmpk1
286 Rpl22
287 Tomm7
288 Orc5
289 Slc30a3
290 Emilin1
291 Gabra4
292 Pdgfra
293 Epha5
294 Tgfbr3
295 Sparcl1

296 Alb
297 Ndufa4
298 Col1a2
299 Nt5c3
300 Slc13a4
301 Zyx
302 Mrps33
303 Zfml
304 Kbtbd8
305 Plxna1
306 Slc6a13
307 Ret
308 A2m
309 Dera
310 Slc6a11
311 Zfp606
312 Gipr
313 Zfp273
314 Dbx1
315 Mphosph10
316 Ccdc90b
317 Tmem126a
318 Zfand6

319 Ndufc2
320 Pik3c2a
321 Rps3
322 Bag3
323 Ndufb11
324 Mrgprf
325 Vbp1
326 Rab39b
327 Cox7b
328 Hmgn5
329 Sh3bgrl
330 Col4a6
331 Col4a5
332 Cetn2
333 Ap1s2
334 Bgn
335 Gpr124
336 Col4a1
337 Col4a2
338 Polb

339 Slit2
340 Pcm1
341 Scrg1
342 Irx3
343 Irx5
344 Mmp2
345 Mt3
346 Cdh5
347 Hsd11b2
348 Ankrd49
349 Cfdp1
350 Tbx20
351 Pts
352 Mpzl2
353 Robo4
354 Robo3
355 Kank2
356 Dock6
357 Itga11
358 Phip
359 Crabp1
360 Isl2
361 Stra6
362 Tmem30a
363 Cox7a2
364 Snapc5
365 Tgfbr2
366 Rpsa
367 Mst1r
368 Gpbp1
369 Lama1
370 Sox10
371 Mzt1
372 Wnt6
373 Antxr1

374 Lgi3
375 Adra2a
376 Tlr13
377 9430020K01Rik
378 Zbtb41
379 Zfp944
380 Gria2
381 Lsm3

382 Smc4
383 Gbx2
384 Hdx
385 Ankrd12
386 Lrrn1
387 Ppp1r1c
388 Pcdh11x
389 Plvap
390 Parm1
391 Arhgap5
392 Nkx6-1
393 Lars2
394 Trim13
395 Ssc5d
396 Lysmd3
397 Fnip1
398 Colec12
399 Pnpla8
400 Rpl39-ps
401 Lum
402 March1
403 Rps27l
404 Neto2
405 Bcorl1
406 Anapc10
407 Tenc1
408 Sep15
409 Islr
410 Matr3
411 0610009D07Rik
412 Thoc2
413 Cldn11
414 Cdkn3
415 Avp
416 Neurod6
417 2700029M09Rik
418 Cntln
419 Notch3
420 Spon1
421 Fam126b
422 Fau
423 Foxf2
424 Akap12

425 Gng10
426 Med30
427 Creb3l2
428 Atp5j2

429 Lmx1b
430 Rps21
431 Timm8b
432 Anpep
433 Zfp503
434 Rpl22l1
435 Pcsk1n
436 Ralyl
437 Slc6a5
438 Gjb6
439 Nxph4
440 Zfp770
441 Cdh12
442 Tlx3
443 St8sia4
444 Snrnp25
445 Slc22a2
446 Npnt
447 Trim62
448 Ostc
449 Nbl1
450 Arhgap11a
451 Car8
452 Tmem29
453 Piezo2
454 Fmod
455 Gucy1a2
456 Fcho2
457 Prrxl1
458 Slc24a4
459 Abca9
460 Tbca
461 Zfp386
462 Bend6
463 Nxt2
464 Rbm7
465 Dctpp1
466 Klhl14
467 Shfm1

468 Sh2b3
469 Tfap2d
470 Itpr3
471 Immp1l
472 Selk
473 Wbp5
474 B630005N14Rik
475 Hebp1
476 Tuba1c
477 Hic1
478 Aqp6
479 Smco3
480 Rab9b
481 Tril
482 Rpl7
483 Pura

484 Sptssa
485 Gm9493
486 Rin3
487 Zfp758
488 Trmt10c
489 Rpl18a
490 Dpy19l4
491 Cenpe
492 Defb11
493 Gprin3
494 Onecut3
495 Penk
496 Olig3
497 Esf1
498 Zfp36l2
499 Polr2k
500 Zfp62
501 Gjb2
502 C77370
503 Olfml2a
504 Ppp1r3b
505 Ccdc108
506 Zfp654
507 Dynlrb1
508 Adamts12
509 Mafa
510 Rps8

511 Rpsa-ps10
512 Zcchc5
513 Tmem196
514 Pirt
515 Crebrf
516 Sacs
517 Zfp738
518 Osr1
519 Ranbp3l
520 Igf2
521 Myof
522 C1galt1c1
523 Mterfd3
524 Gm8186
525 Plcxd3
526 Zfp518a
527 Tceal1
528 Adamts16
529 2410015M20Rik
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531 Shisa3
532 Foxc1
533 Gm9843
534 Foxl2
535 Gm9846
536 Atp5k
537 Zfp366
538 Gja1

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544 Gm6563
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546 Coa6
547 Gypa
548 Xkr4
549 Pfdn4
550 Rps10
551 Gpr17
552 Hbb-bs
553 Lamb2

554 C130021I20Rik
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556 Sec61b
557 Zfp943
558 Thoc7
559 Atf7ip
560 Spock3
561 Atpif1
562 Adam12
563 Mmrn1
564 Hmgb2
565 Zfp182
566 Fsd1l
567 Zfp935
568 Zfp101
569 Tns1
570 Fut9
571 Maf
572 Zfp458
573 Gpc3
574 Zfp277
575 Triqk
576 AI504432
577 Col8a2
578 Uts2b
579 Cd248
580 Foxk1
581 Mpz
582 Kdm5d
583 Foxb2
584 Gadl1
585 Gm7536
586 Npm1
587 Zfp759
588 Mab21l2
589 Zfp119a
590 Rpl32
591 AA987161
592 Gm5148
593 Zfp68
594 Zfp85-rs1
595 Gpc6
596 Zfp958

597 Col13a1
598 Zfp708
599 Gm10053
600 Zfp945
601 Rpl11
602 Zfp933
603 Zfp930
604 Unc5c
605 Gm10073
606 Rp2h
607 Tpt1
608 Gm10076
609 BC002059
610 Scrt2
611 2610008E11Rik
612 linc-Brn1a
613 Rps10-ps1
614 Tsga10
615 Rpl26
616 Zfp873
617 Rps7
618 Zic2
619 Zfp229
620 Tac1
621 Rps12
622 Rpl34
623 Rpl9-ps6
624 Rps3a2
625 Zfp677
626 Zfp938
627 Gm10123
628 Kdr
629 Mrpl42
630 Sox7
631 3300002I08Rik
632 Zfp947
633 Cyp26b1
634 Rps15
635 Col23a1
636 Chchd1
637 Uqcrh
638 Fbln2
639 Gm10146

640 mt-Nd1
641 mt-Nd2
642 mt-Co1
643 mt-Co2
644 mt-Co3
645 mt-Nd4
646 Rpl36-ps3
647 Cntnap5b
648 Foxd3

649 Tspan6
650 Zfp763
651 Gm10221
652 Zfp760
653 Zfp948
654 Zfp160
655 Zfp442
656 Zfp120
657 Ndufaf2
658 Col8a1
659 Gm11808
660 Slc4a5
661 Efcab1
662 Flnc
663 Gm10250
664 Rap1a
665 Ssb
666 Ddx3y
667 Gm10260
668 Nxph2
669 Zfp72
670 Gm10275
671 Gm5595
672 Zfp820
673 Hba-a2
674 Hba-a1
675 Gm10288
676 Tmem256
677 Smim15
678 Zfp946
679 Zfp942
680 Zfp71-rs1
681 Rpl23
682 Phf20l1

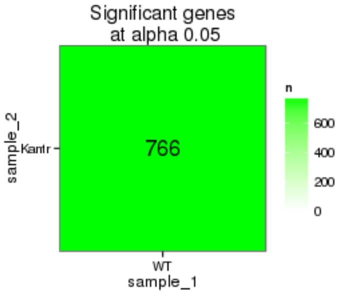
683 Gm13826
684 4930522L14Rik
685 Vma21
686 Trim10
687 Dok6
688 Myeov2
689 Nbeal1
690 Hbb-bt
691 9830147E19Rik
692 Zfp788
693 Mafb
694 Gm10742
695 Thbd
696 Gm561
697 Zfp808
698 Ctxn2
699 Accsl
700 Hoxc4
701 Nynrin
702 Selt
703 Rpl23a-ps3

704 Gm2000
705 Gm3940
706 Foxd1
707 Sarnp
708 AU041133
709 Abracl
710 2210404O09Rik
711 Zfp931
712 Gm14326
713 Gm14322
714 Gm14418
715 Gm14305
716 Gm14391
717 D130040H23Rik
718 Jrkl
719 Ccdc82
720 Haus3
721 Hoxa3
722 Rpl39
723 Tceb1
724 Zfp703
725 Gm12688

726 Xist
727 Gm15500
728 Kantr
729 Gm15501
730 Tmsb15b2
731 Dlx6os1
732 Gm10177
733 Pcp4
734 2810055G20Rik
735 Snrpe
736 Gm5611
737 Zfp712
738 Myl6
739 Lrrc32
740 Gm5141
741 Gm10269
742 Skor2
743 Tma7
744 Lsm5
745 Cox16
746 Gm4540
747 Zfp804b
748 Zfp141
749 Rpl41
750 Zfp955a
751 Gm14403
752 Rps2-ps6
753 Fignl2
754 Gm6472
755 Gm7094
756 Gm4944
757 Zfp955b
758 Foxl2os
759 A330076H08Rik
760 Gm26917
761 Gm17750
762 Gm26924
763 A430106G13Rik
764 Gm27031
765 Snhg6
766 RP23-442I7.1

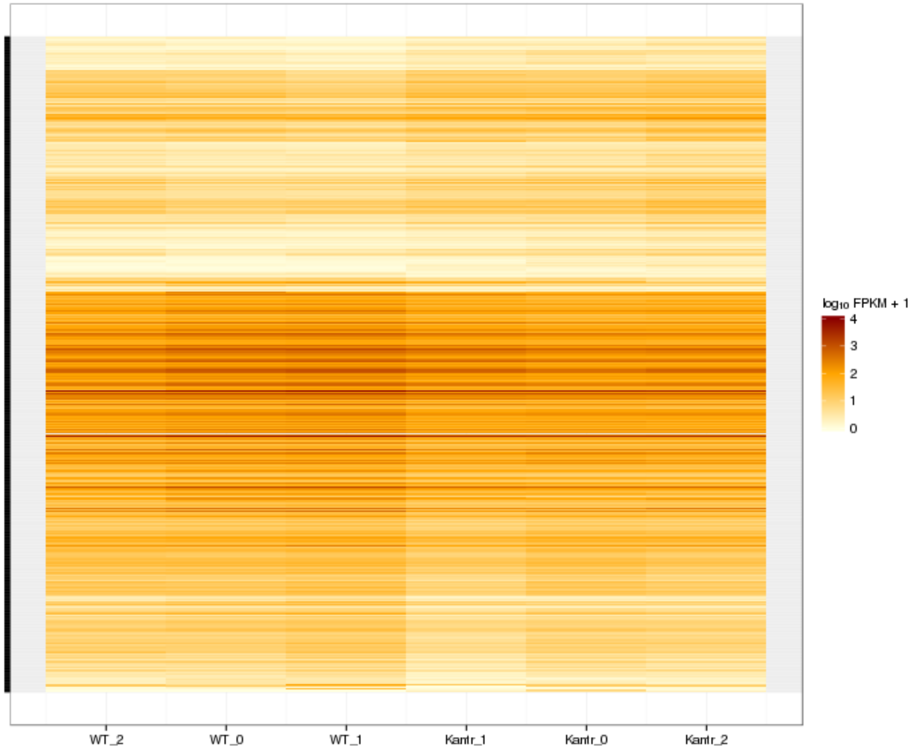
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

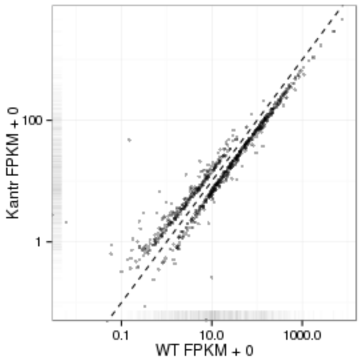


Significant genes with expression >50fpkm (any condition):(turned off)

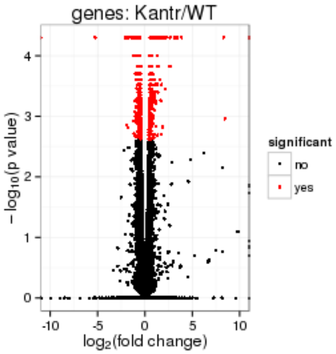
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

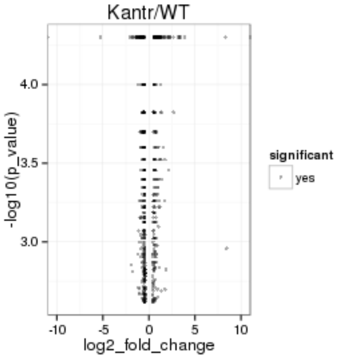
Scatter plot of significant genes only:



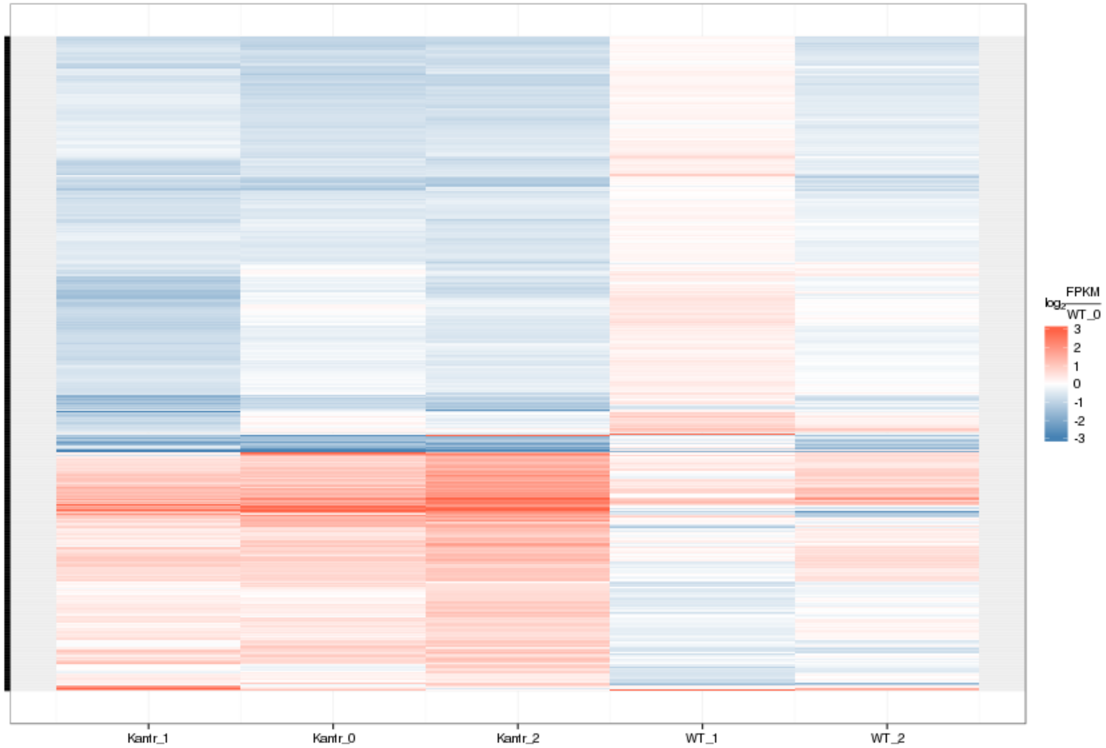
Volcano Plot



Volcano plot with significant genes only:



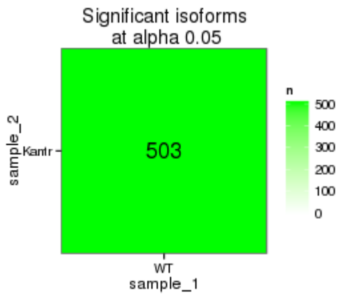
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

	isoAnnot$gene_short_name
1	H19
2	Tbx2
3	Ngfr
4	Hddc2
5	Cdh1
6	Mcts1
7	Gabra2
8	C1d
9	Serpinf1
10	Col6a1
11	Gabrg1
12	Col18a1
13	Col1a1
14	Eef1e1
15	Use1
16	Zfp40
17	Lamb1
18	Dvl3
19	Fcgrt
20	Bicd1
21	Zfp81
22	Ptrf
23	Pax2
24	Hif3a
25	Sst
26	Aqp1

27 Tmem242
28 Wisp1
29 Corin
30 Nid1
31 Kif5b
32 Gabrb2
33 Dio2
34 0610009B22Rik
35 Rplp1
36 Snrpb2
37 Bmp7
38 Gabra1
39 Scarf2
40 Phox2b
41 Rps5
42 Cacybp
43 Cox6c
44 Hoxa2
45 Gata2
46 Ptgds
47 Psma2
48 Mrpl32
49 Capza2
50 Atp5e
51 Ndufa1
52 Mrps18c
53 Vtn
54 Erbb3
55 Trove2
56 Glra2
57 Slc35g3
58 Slc16a10
59 Lama4
60 Fabp7
61 Nts
62 Lama2
63 Actr6
64 Kitl
65 Moxd1
66 Meis1
67 Col6a2
68 Hmmr

69 Flt4
70 Sar1b
71 Nefh
72 Rps27a
73 Ccdc104
74 Aebp1
75 Smc6
76 Fam20a
77 Bcap29
78 Mrc2
79 Ntn1
80 Fkbp3
81 Scfd1
82 Mpp5
83 Eif2s1
84 Hsp90aa1
85 2010107E04Rik
86 Dek
87 Nol8
88 A530054K11Rik
89 Cetn3
90 Ankrd32
91 Irx4
92 Otp
93 Trim23
94 Ndufs4
95 Cdhr1
96 Psmc6
97 Chat
98 Zdhhc20
99 Dnajc15
100 Sugt1
101 Nefm
102 Uchl3
103 Dab2
104 Npr3
105 Oxr1
106 Angpt1
107 Eif3h
108 Eif3e
109 Emc2
110 Kcnv1
111 Col14a1
112 Enpp2

113 Myh9
114 Ndufa6
115 Ube2v2
116 B3gnt5
117 Zbtb20
118 Fgd4
119 Arhgap31
120 Sncg
121 Prph
122 Thbs2
123 Zfp51
124 Pla2g7
125 Slc5a7
126 Arhgap28
127 Cyp1b1
128 Ndufv2
129 Epas1
130 Uqcc2
131 Esco1
132 Fbn2
133 Rps14
134 Tmx3
135 Pdgfrb
136 Slc22a6
137 Kif20b
138 Lbx1
139 Rps24
140 Rps26
141 Esyt1
142 Zfp711
143 Tmem47
144 Itih5
145 Stag2
146 Cwf19l2
147 Lypla1
148 Rb1cc1
149 Mob4
150 Nop58
151 Sumo1
152 Ndufb3
153 Col5a2
154 Col3a1
155 Mrpl30

156 1110058L19Rik
157 Fn1
158 Nppc
159 Dbi
160 Syt2
161 Lamc1
162 Cenpf
163 Mrc1
164 Itga8
165 Col5a1
166 Lamc3
167 Pax8
168 Kif18a
169 Eif3m
170 Fbn1
171 Cops2
172 Lamp5
173 Otor
174 Pkia

175 Dcun1d1
176 Pdcd10
177 Sfrp2
178 Enpep
179 Aimp1
180 Rps3a1
181 Abca4
182 Tmem68
183 Casp8ap2
184 Svep1
185 Zfp37
186 Bspry
187 Rps6
188 Ift74
189 Magoh
190 Col9a2
191 Tomm7
192 Orc5
193 Mxra8
194 Slc30a3
195 Tgfbr3
196 Ndufa4
197 Col1a2
198 Slc13a4

199 Zyx
200 Slc6a13
201 Ret
202 A2m
203 Dera
204 Dbx1
205 Mphosph10
206 Ccdc90b
207 Zfand6
208 Ndufc2
209 Ndufb11
210 Zfp300
211 Vbp1
212 Atrx
213 Cox7b
214 Hmgn5
215 Sh3bgrl
216 Col4a6
217 Bgn
218 Col4a1
219 Pcm1
220 Mmp2
221 Cdh5
222 Tbx20
223 Mpzl2
224 Robo3
225 Kank2
226 Dock6
227 Rora
228 Itga11
229 Phip
230 Crabp1
231 Tmem30a
232 Cox7a2
233 Tgfbr2
234 Rpsa
235 Ccdc88a
236 Lama1
237 Sox10
238 Wnt6
239 Lgi3
240 Zfp944
241 Gria2

242 Lsm3
243 Smc4
244 Gbx2
245 Pcdh11x
246 Parm1
247 Wnk4
248 Arhgap5
249 1110059E24Rik
250 Nkx6-1
251 Lars2
252 Trim13
253 Scai
254 G2e3
255 Lysmd3
256 Rpl39-ps
257 Rps27l
258 Neto2
259 Anapc10
260 Islr
261 Matr3
262 Itih2
263 0610009D07Rik
264 Thoc2
265 Cldn11
266 Neurod6
267 Spon1
268 Fam126b
269 Foxf2
270 Akap12
271 Atp5j2
272 Lmx1b
273 Rps21
274 Timm8b
275 Zfp503
276 Rpl22l1
277 Slc6a5
278 Gjb6
279 Nxph4
280 Cdh12
281 Tlx3
282 St8sia4
283 Slc22a2
284 Phf8

285 Car8
286 Fmod
287 Gucy1a2
288 Prrxl1
289 Abca9
290 Tbca
291 Zfp386
292 Bend6
293 Ehbp1
294 Dctpp1
295 Shfm1
296 Itpr3
297 Immp1l
298 Selk
299 Wbp5
300 B630005N14Rik
301 Hebp1
302 Egflam
303 Tuba1c
304 Hic1
305 Aqp6
306 Tril
307 Rpl7
308 Sptssa
309 Gm9493
310 Trmt10c
311 Cenpe
312 Onecut3
313 Penk
314 Olig3
315 Esf1
316 Zfp322a
317 Gjb2
318 Olfml2a
319 Tefm
320 Zfp654
321 Dynlrb1
322 Adamts12
323 Mafa
324 Rps8
325 Rpsa-ps10
326 Zcchc5
327 Sned1
328 Tmem196

329 Pirt
330 Col6a3
331 Zfp738
332 Osr1
333 Ranbp3l
334 Igf2
335 Plcxd3
336 Zfp518a
337 Tmsb4x
338 Shisa3
339 Foxc1
340 Gm9843
341 Gm9846
342 Vstm4
343 Atp5k
344 Gja1
345 Sv2c
346 Commd3
347 Nhlh1
348 Gm6563
349 Six1
350 Tceal8
351 Coa6
352 Gypa
353 Pfdn4
354 Il1rapl1
355 C130021I20Rik
356 Aldh1a1
357 Sec61b
358 Zfp943
359 Thoc7
360 Atf7ip
361 Atpif1
362 Adam12
363 Mmrn1
364 Klhl18
365 Tns1
366 Fut9
367 Gpc3
368 Triqk
369 AI504432
370 Col8a2
371 Uts2b

372 Slit3
373 Cd248
374 Mpz
375 Kdm5d
376 Foxb2
377 Gadl1
378 Gm7536
379 Zfp759
380 Mab21l2
381 Rpl32
382 AA987161
383 Gda
384 Zfp958
385 Zfp708
386 Gm10053
387 Zfp933
388 Zfp930
389 Gm10073
390 Rp2h
391 Scrt2
392 2610008E11Rik
393 Zfp868
394 Rps10-ps1

395 Rpl26
396 Zfp873
397 Rps7
398 Zic2
399 Rps12
400 Rpl34
401 Rpl9-ps6
402 Rps3a2
403 Zfp938
404 Kdr
405 Mrpl42
406 Cyp26b1
407 Rps15
408 Col23a1
409 Chchd1
410 Uqcrh
411 Fbln2
412 Gm10146
413 mt-Nd1
414 mt-Nd2

415 mt-Nd4
416 Foxd3
417 Zfp763
418 Gm10221
419 Zfp760
420 Zfp948
421 Zfp160
422 Ndufaf2
423 Col8a1
424 Gm11808
425 Slc4a5
426 Efcab1
427 Rap1a
428 Ssb
429 Ddx3y
430 Gm10260
431 Nxph2
432 Zfp72
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434 Gm10288
435 Smim15
436 Zfp946
437 Zfp942
438 Zfp71-rs1
439 Rpl23
440 Gm13826
441 Dok6
442 Myeov2
443 Nbeal1
444 Hbb-bt
445 Rpl13a
446 9830147E19Rik
447 Ehd2
448 Mafb
449 Gm10742

450 Thbd
451 Gm561
452 Zfp808
453 Scn2a1
454 Hoxc4
455 Rpl23a-ps3
456 Gm2000
457 Gm3940

458 Foxd1
459 AU041133
460 Abracl
461 2210404O09Rik
462 Zfp931
463 Gm14326
464 Gm14418
465 Jrkl
466 Haus3
467 Rpl39
468 Tceb1
469 Zfp703
470 Gm12688
471 Xist
472 Gm15500
473 Kantr
474 Tmsb15b2
475 3110047P20Rik
476 Gm10177
477 Pcp4
478 2810055G20Rik
479 Snrpe
480 Zfp712
481 Myl6
482 Lrrc32
483 Gm5141
484 Gm10269
485 Tma7
486 Gm4540
487 Zfp804b
488 Zfp141
489 Rpl41
490 Zfp955a
491 Gm14325
492 Zfp748
493 Gm6472
494 Gm4944
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497 Gm26924
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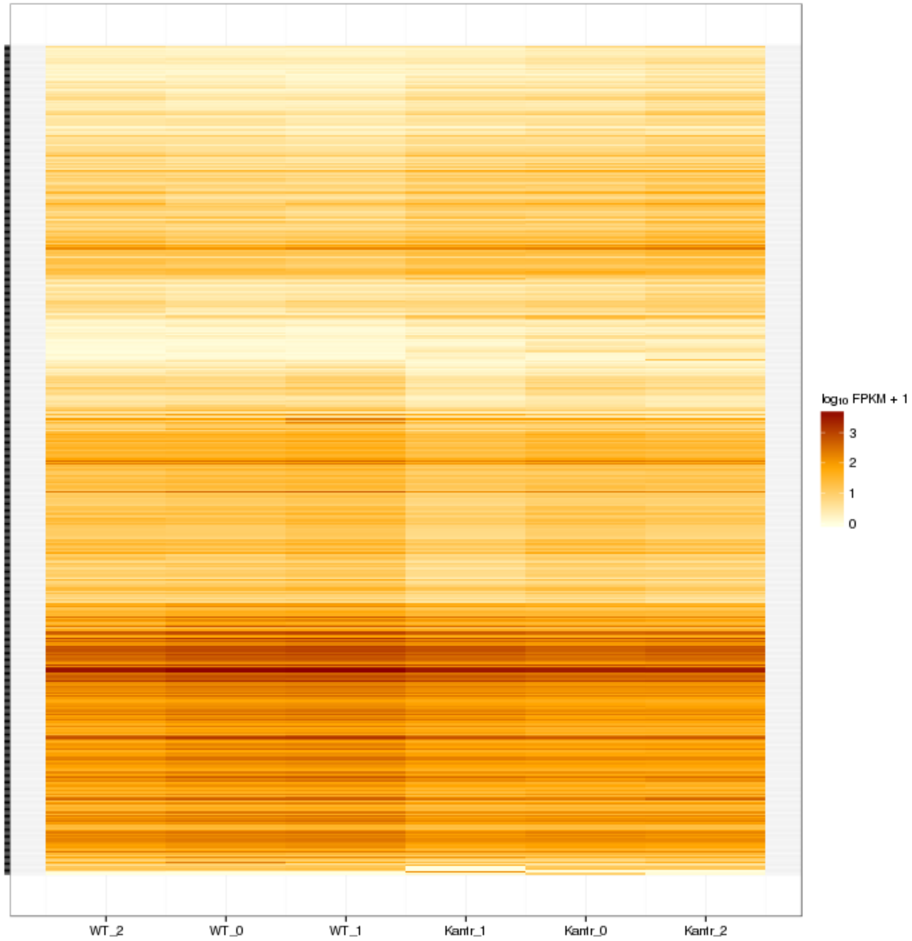
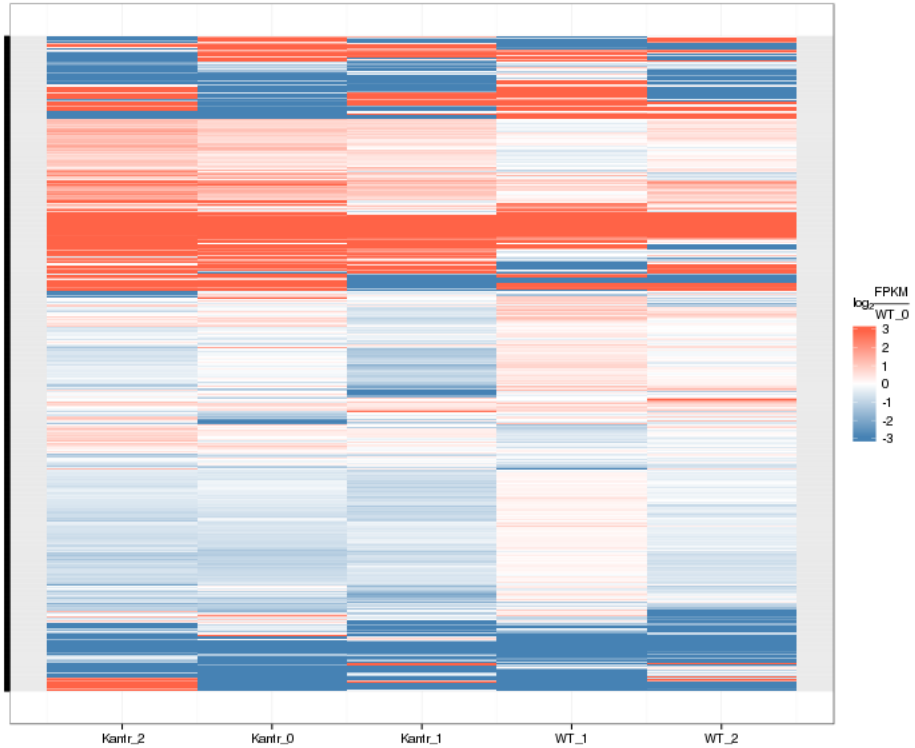
500 Snhg6

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

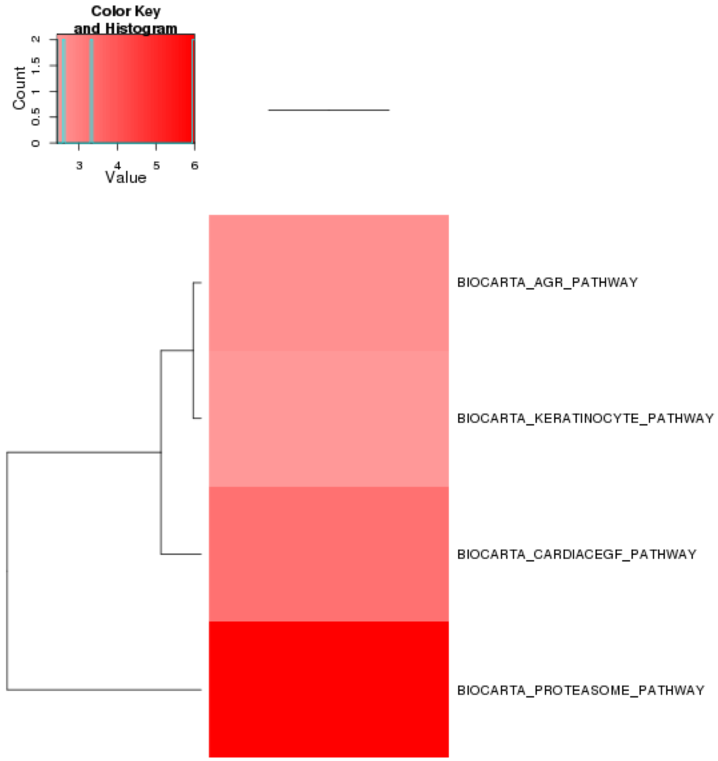
Gene/Pathway Analysis

GSEA

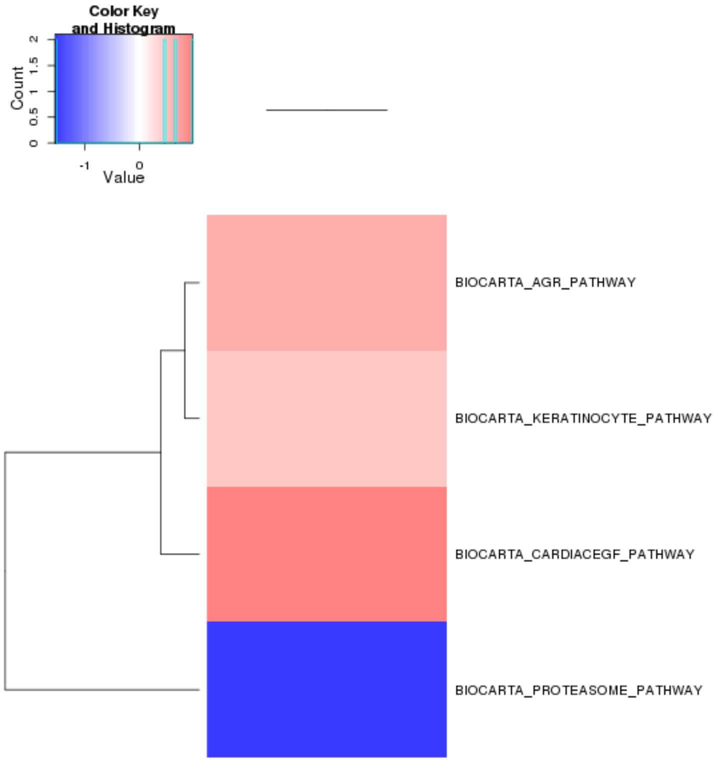
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

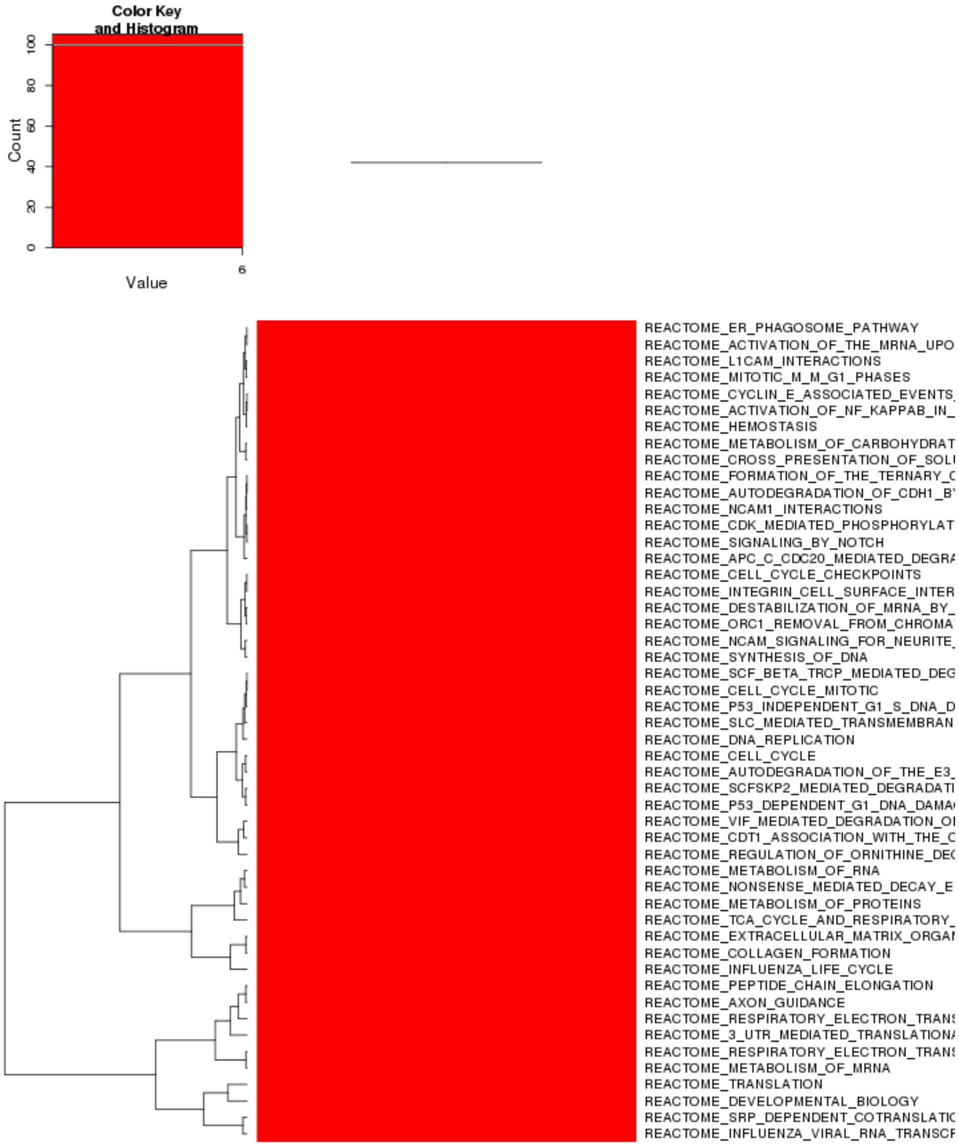
Biocarta enrichment:



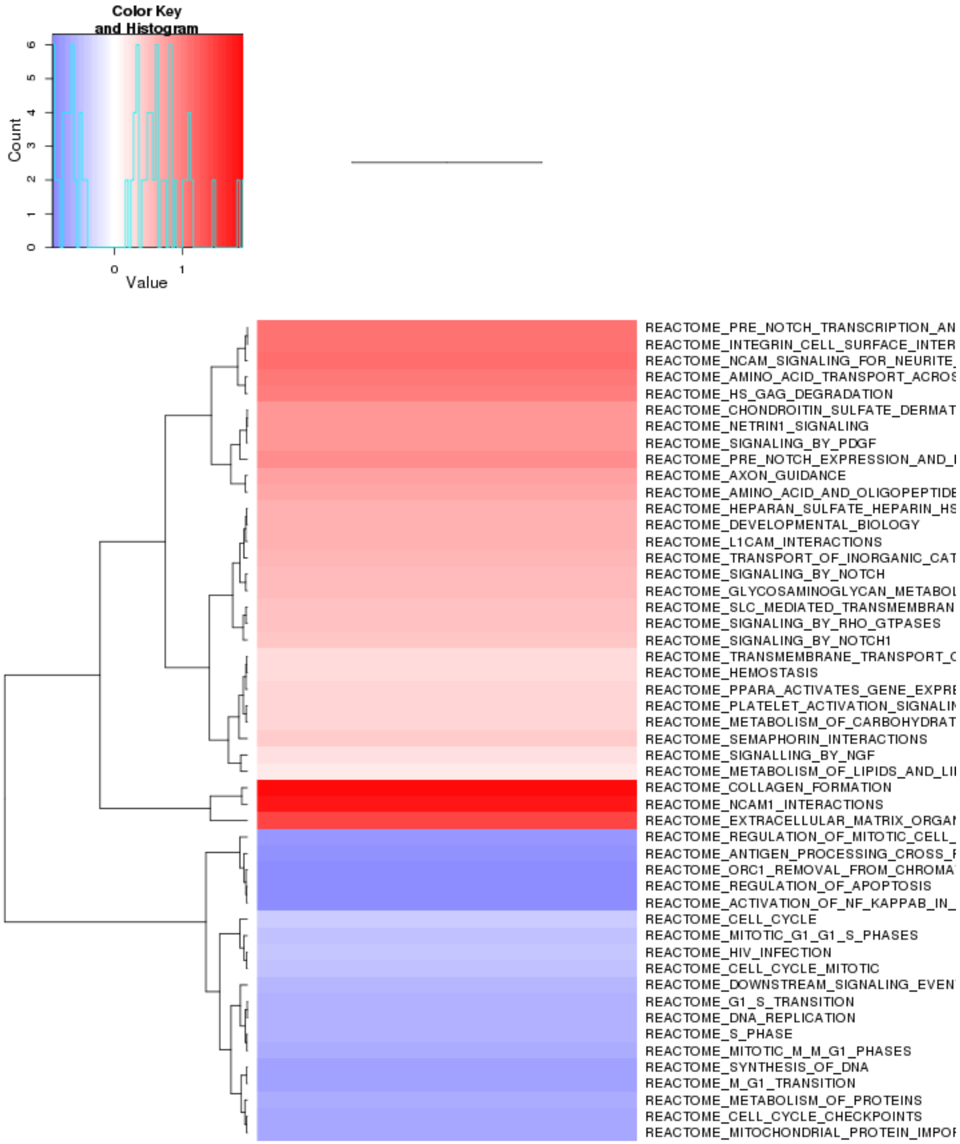
Biocarta zscore:



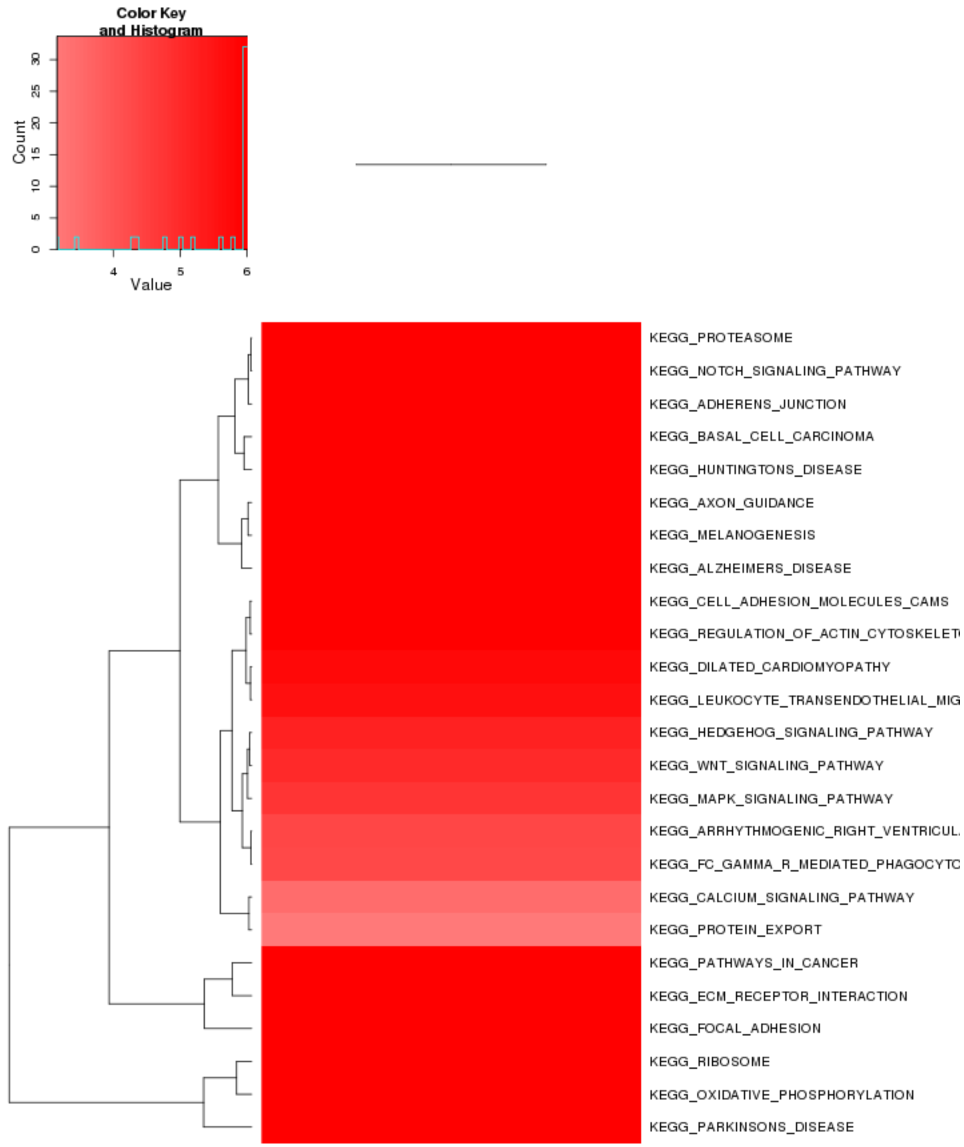
Reactome enrichment:



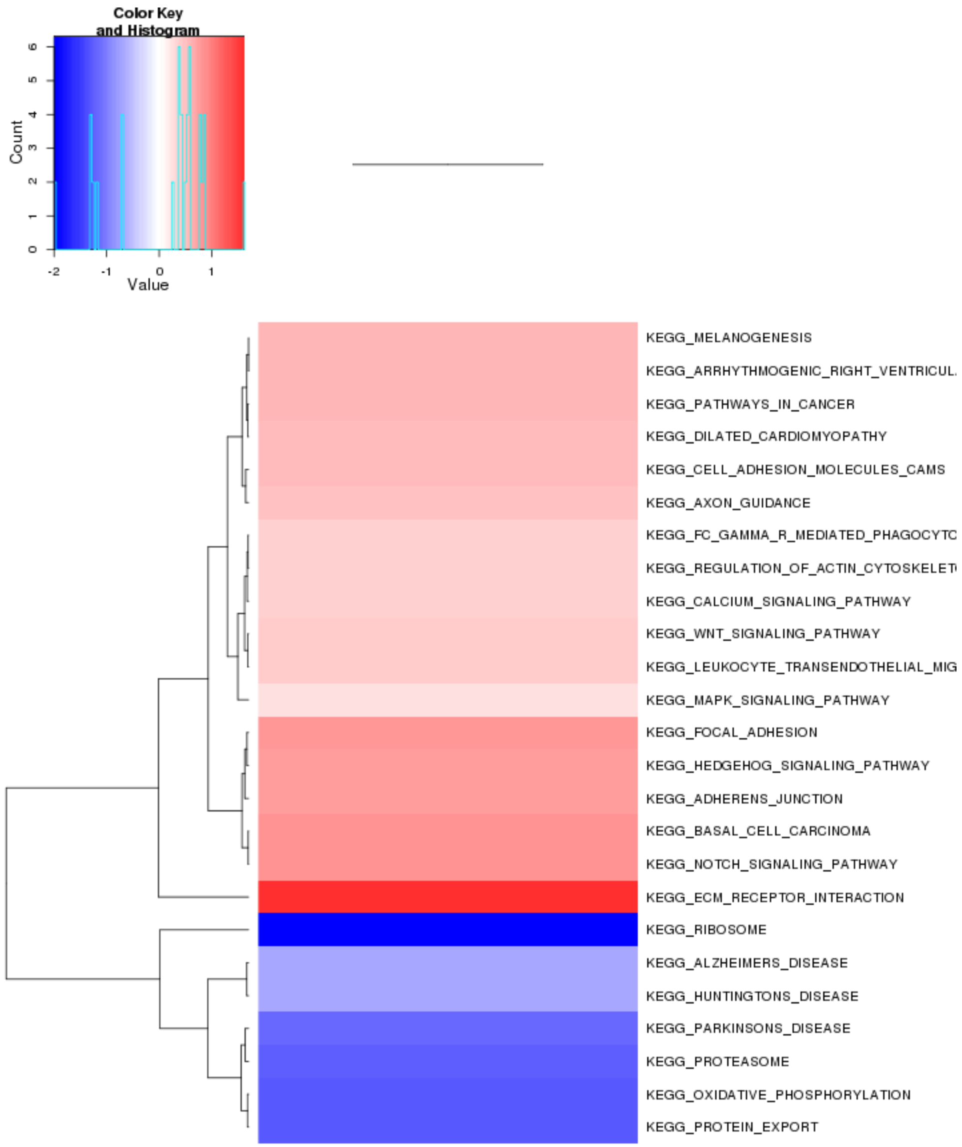
Reactome zscore:



Kegg enrichment:


Color Key
and Histogram
Count
0
5
10
15
20
25
30
4
5
6
Value
KEGG_PROTEASOME
KEGG_NOTCH_SIGNALING_PATHWAY
KEGG_ADHERENS_JUNCTION
KEGG_BASAL_CELL_CARCINOMA
KEGG_HUNTINGTONS_DISEASE
KEGG_AXON_GUIDANCE
KEGG_MELANOGENESIS
KEGG_ALZHEIMERS_DISEASE
KEGG_CELL_ADHESION_MOLECULES_CAMS
KEGG_REGULATION_OF_ACTIN_CYTOSKELET
KEGG_DILATED_CARDIOMYOPATHY
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIG
KEGG_HEDGEHOG_SIGNALING_PATHWAY
KEGG_WNT_SIGNALING_PATHWAY
KEGG_MAPK_SIGNALING_PATHWAY
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICUL
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYT
KEGG_CALCIUM_SIGNALING_PATHWAY
KEGG_PROTEIN_EXPORT
KEGG_PATHWAYS_IN_CANCER
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_FOCAL_ADHESION
KEGG_RIBOSOME
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_PARKINSONS_DISEASE

Kegg zscore:



Interneuron enrichment:

```
## Error: argument is of length zero
```

Interneuron zscore:

```
## Error: incorrect number of dimensions
```

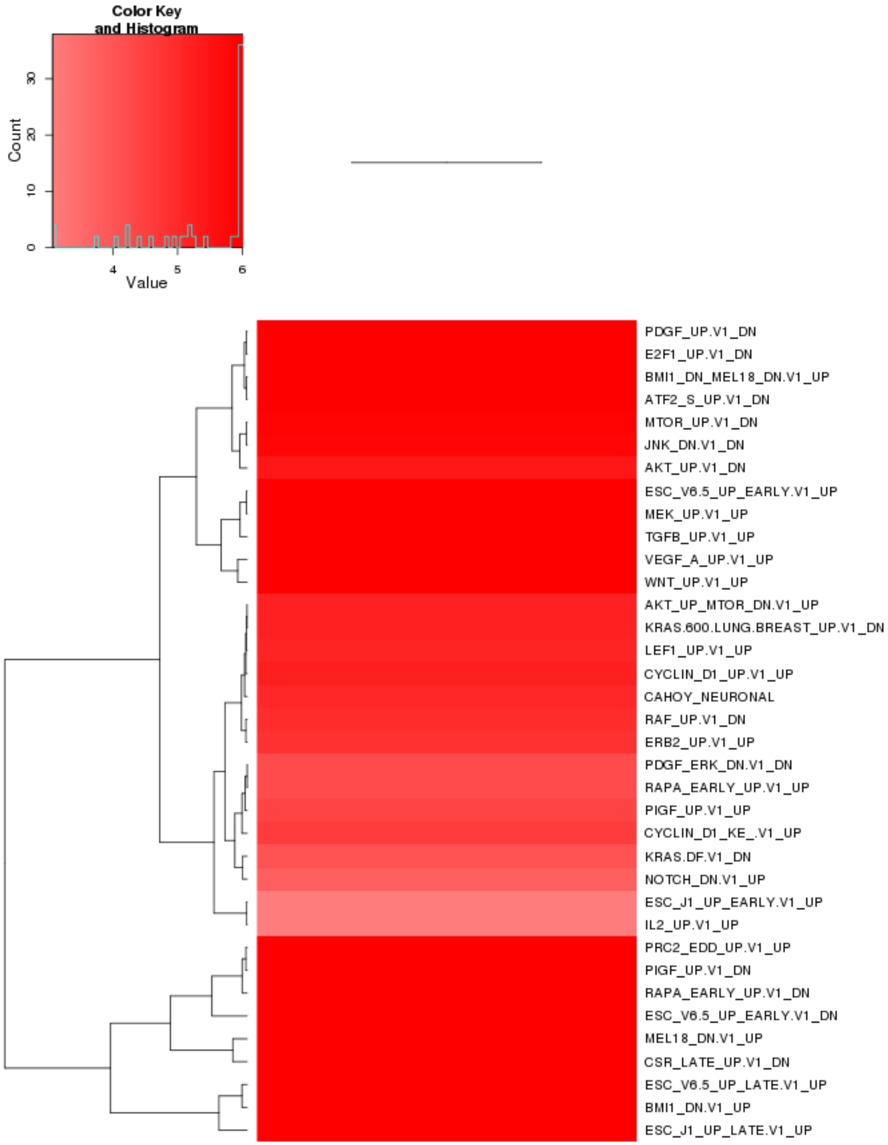
```
## Error: object 'x_ordered' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

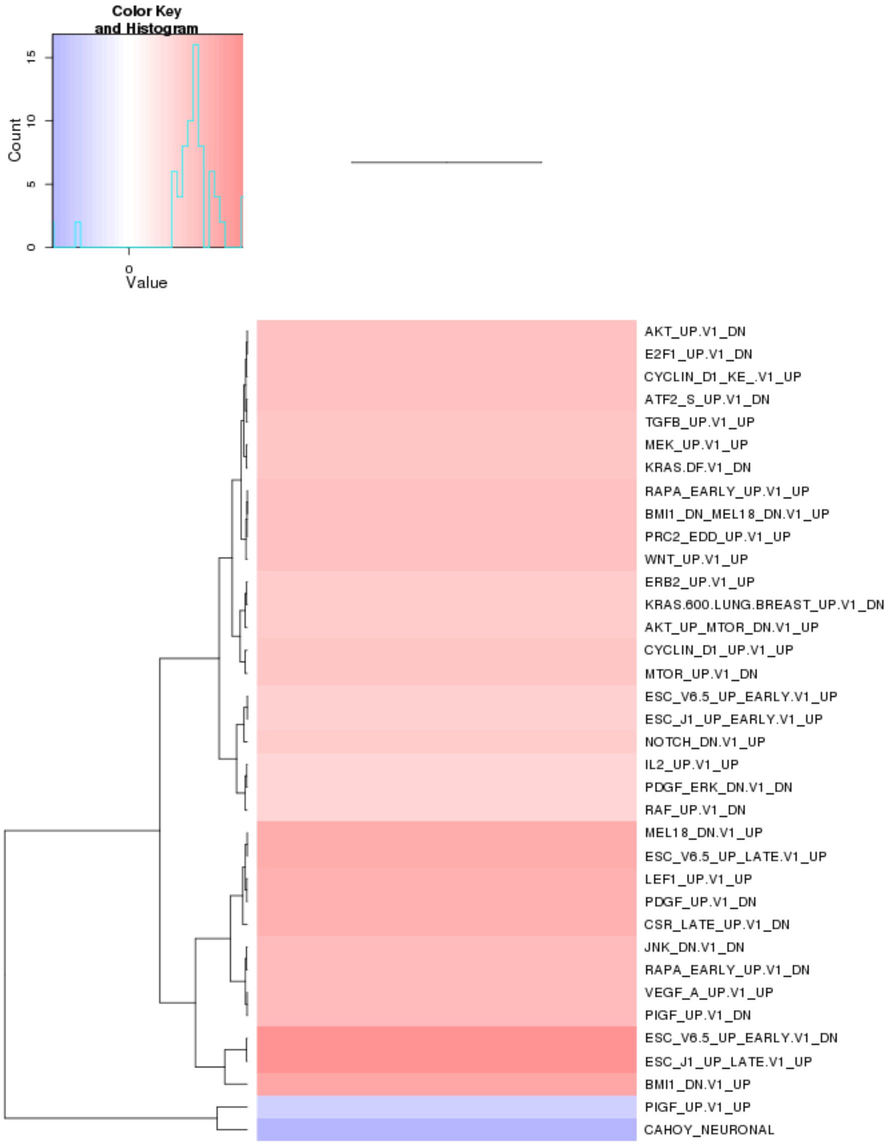
Oncogene enrichment:

```
## Error: subscript out of bounds
```



Oncogene zscore:

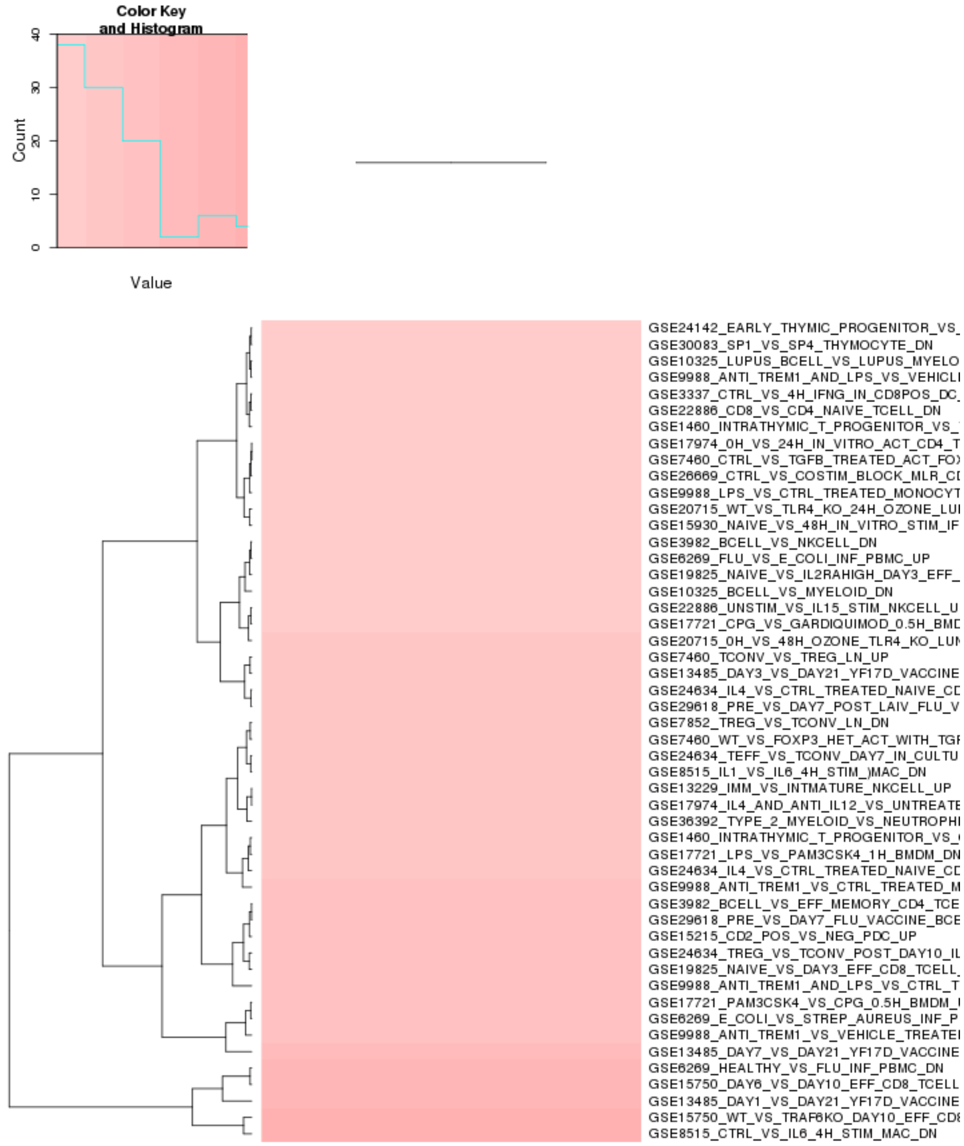
```
## Error: subscript out of bounds
```



Immuno enrichment:

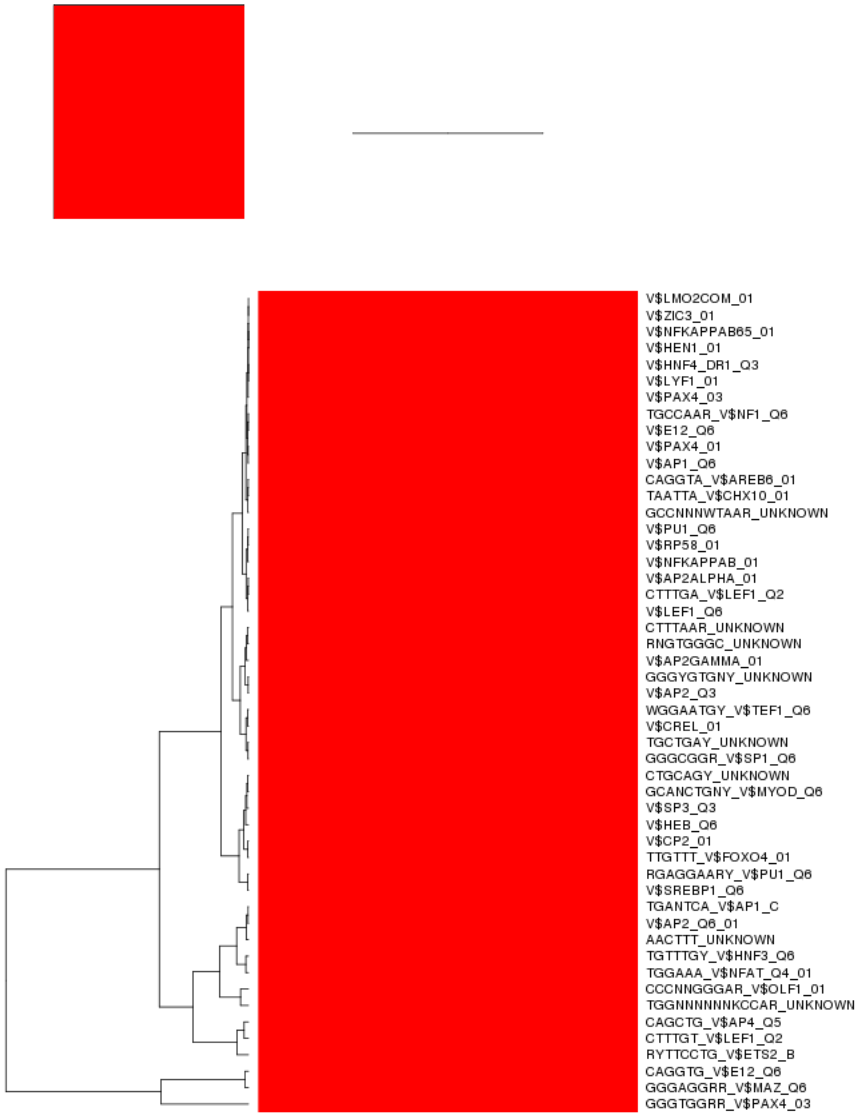
```
## Error: no locations are finite
```

Immuno zscore:

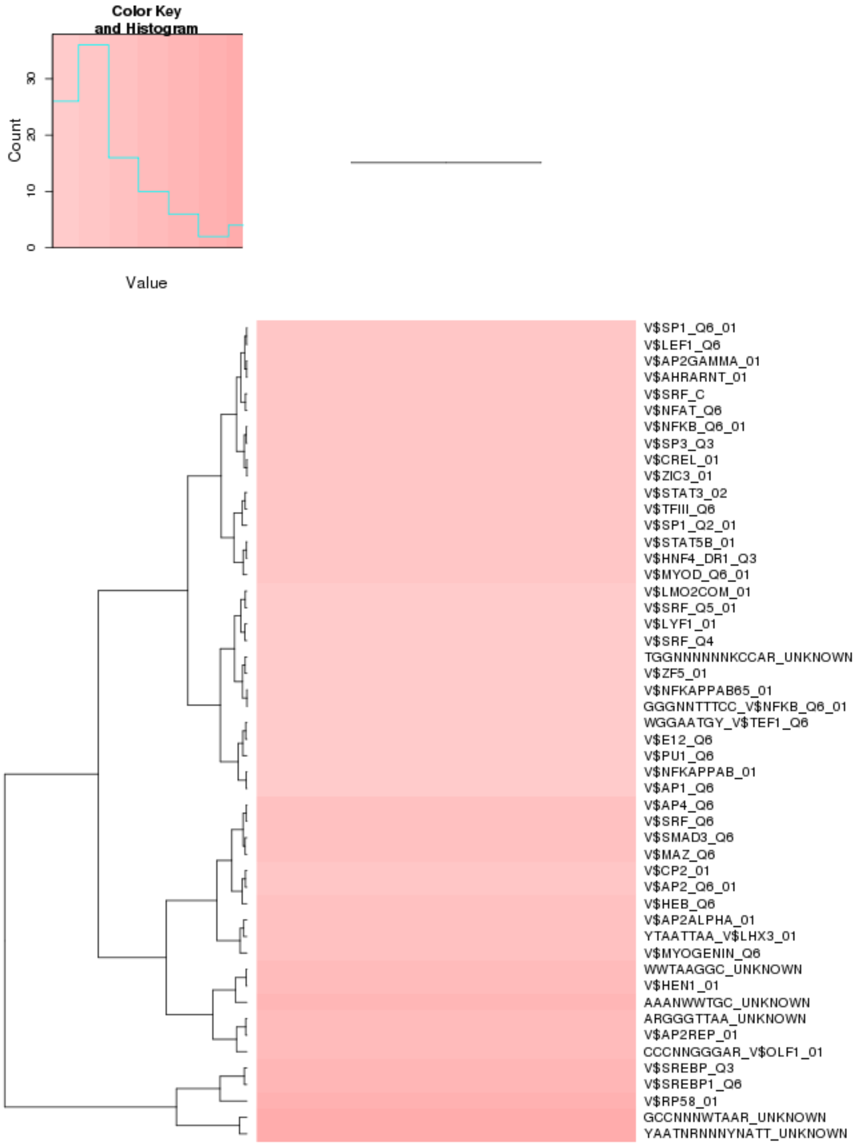


TF enrichment:

```
## Error: no locations are finite
```

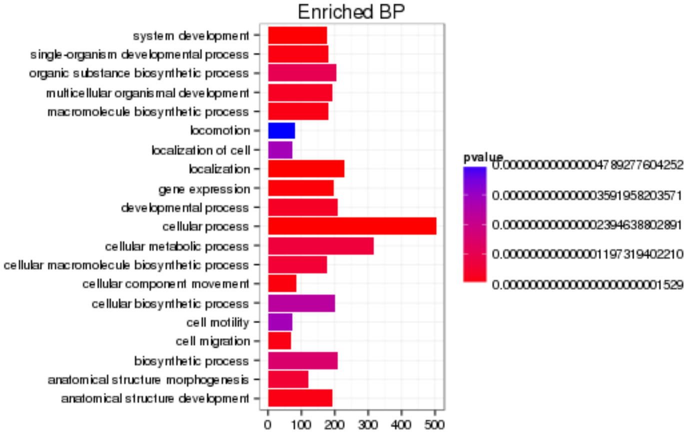

V$LMO2COM_01
V$ZIC3_01
V$NFKAPPAB65_01
V$HEN1_01
V$HNF4_DR1_Q3
V$LYF1_01
V$PAX4_03
TGCCAAR_V$NF1_Q6
V$E12_Q6
V$PAX4_01
V$AP1_Q6
CAGGTA_V$AREB6_01
TAATTA_V$CHX10_01
GCCNNNWTAAR_UNKNOWN
V$PU1_Q6
V$RP58_01
V$NFKAPPAB_01
V$AP2ALPHA_01
CTTTGA_V$LEF1_Q2
V$LEF1_Q6
CTTTAAR_UNKNOWN
RNGTGGGC_UNKNOWN
V$AP2GAMMA_01
GGGYGTGNY_UNKNOWN
V$AP2_Q3
WGGAATGY_V$TEF1_Q6
V$CREL_01
TGCTGAY_UNKNOWN
GGGCGGR_V$SP1_Q6
CTGCAGY_UNKNOWN
GCANCTGNY_V$MYOD_Q6
V$SP3_Q3
V$HEB_Q6
V$CP2_01
TTGTTT_V$FOXO4_01
RGAGGAARY_V$PU1_Q6
V$SREBP1_Q6
TGANTCA_V$AP1_C
V$AP2_Q6_01
AACTTT_UNKNOWN
TGTTTGY_V$HNF3_Q6
TGGAAA_V$NFAT_Q4_01
CCCNNGGGAR_V$OLF1_01
TGGNNNNNNKCCAR_UNKNOWN
CAGCTG_V$AP4_Q5
CTTTGT_V$LEF1_Q2
RYTTCCTG_V$ETS2_B
CAGGTG_V$E12_Q6
GGGAGGRR_V$MAZ_Q6
GGGTGGRR_V$PAX4_03

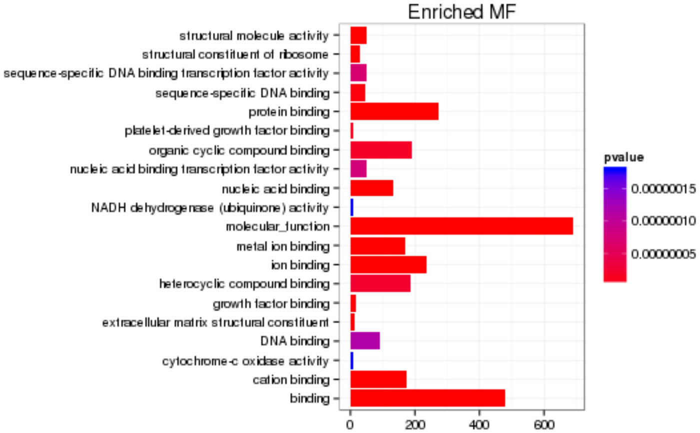
TF zscore:

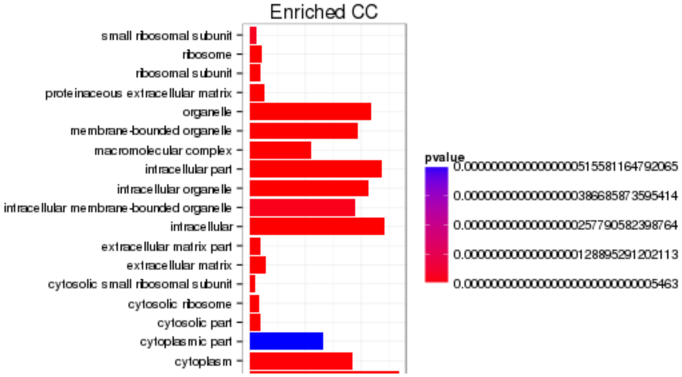


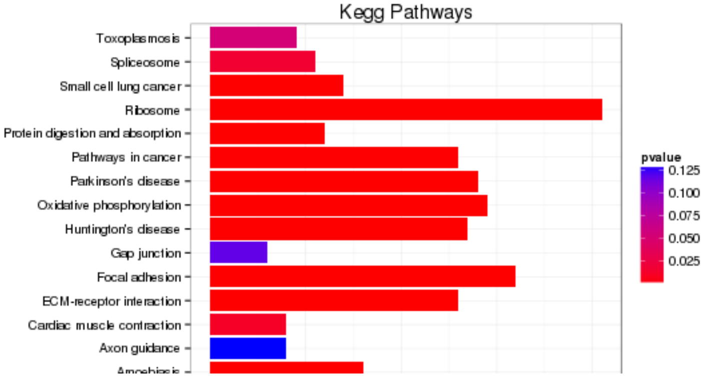
GO enrichment

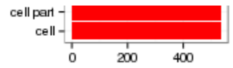
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

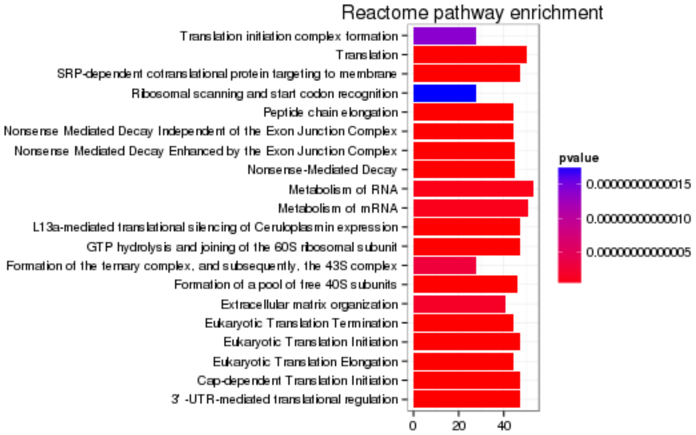

Enriched BP
system development
single-organism developmental process
organic substance biosynthetic process
multicellular organismal development
macromolecule biosynthetic process
locomotion
localization of cell
localization
gene expression
developmental process
cellular process
cellular metabolic process
cellular macromolecule biosynthetic process
cellular component movement
cellular biosynthetic process
cell motility
cell migration
biosynthetic process
anatomical structure morphogenesis
anatomical structure development
0
100
200
300
400
500
pvalue
0.0000000000000004789277604252
0.0000000000000003591958203571
0.0000000000000002394638802891
0.0000000000000001197319402210
0.000000000000000000000000001529


Enriched MF
structural molecule activity
structural constituent of ribosome
sequence-specific DNA binding transcription factor activity
sequence-specific DNA binding
protein binding
platelet-derived growth factor binding
organic cyclic compound binding
nucleic acid binding transcription factor activity
nucleic acid binding
NADH dehydrogenase (ubiquinone) activity
molecular_function
metal ion binding
ion binding
heterocyclic compound binding
growth factor binding
extracellular matrix structural constituent
DNA binding
cytochrome-c oxidase activity
cation binding
binding
0
200
400
600
pvalue
0.00000015
0.00000010
0.00000005

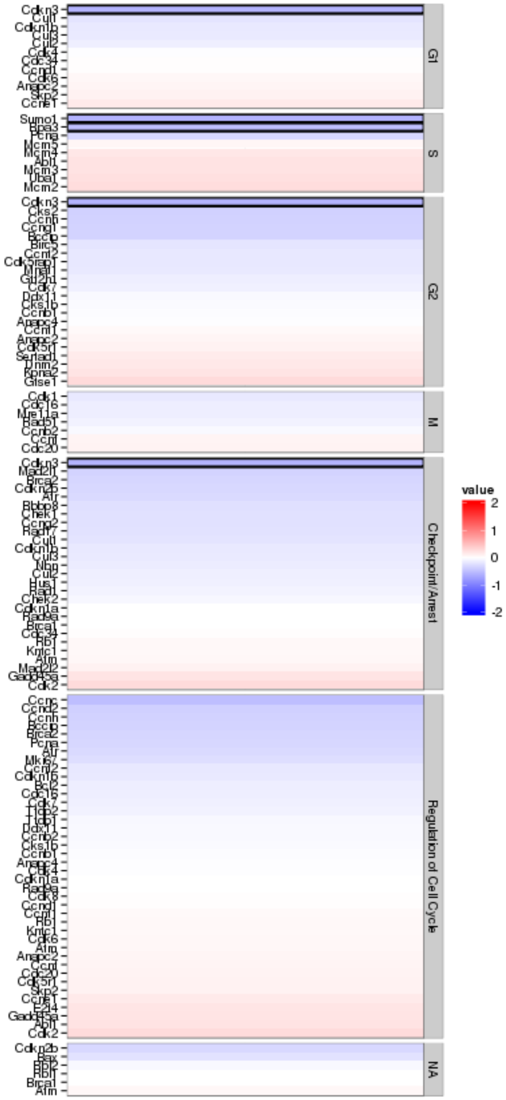

Enriched CC
small ribosomal subunit
ribosome
ribosomal subunit
proteinaceous extracellular matrix
organelle
membrane-bounded organelle
macromolecular complex
intracellular part
intracellular organelle
intracellular membrane-bounded organelle
intracellular
extracellular matrix part
extracellular matrix
cytosolic small ribosomal subunit
cytosolic ribosome
cytosolic part
cytoplasmic part
cytoplasm
pvalue
0.000000000000000000515581164792065
0.000000000000000000386685873595414
0.000000000000000000257790582398764
0.000000000000000000128895291202113
0.000000000000000000000000000005463


Kegg Pathways
Toxoplasmosis
Spliceosome
Small cell lung cancer
Ribosome
Protein digestion and absorption
Pathways in cancer
Parkinson's disease
Oxidative phosphorylation
Huntington's disease
Gap junction
Focal adhesion
ECM-receptor interaction
Cardiac muscle contraction
Axon guidance
Amoebiasis
pvalue
0.125
0.100
0.075
0.050
0.025

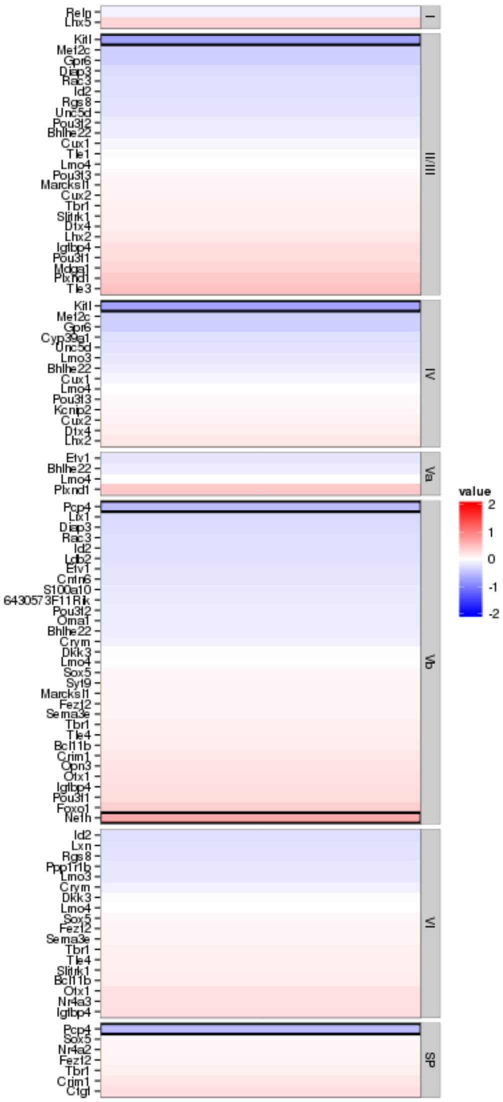




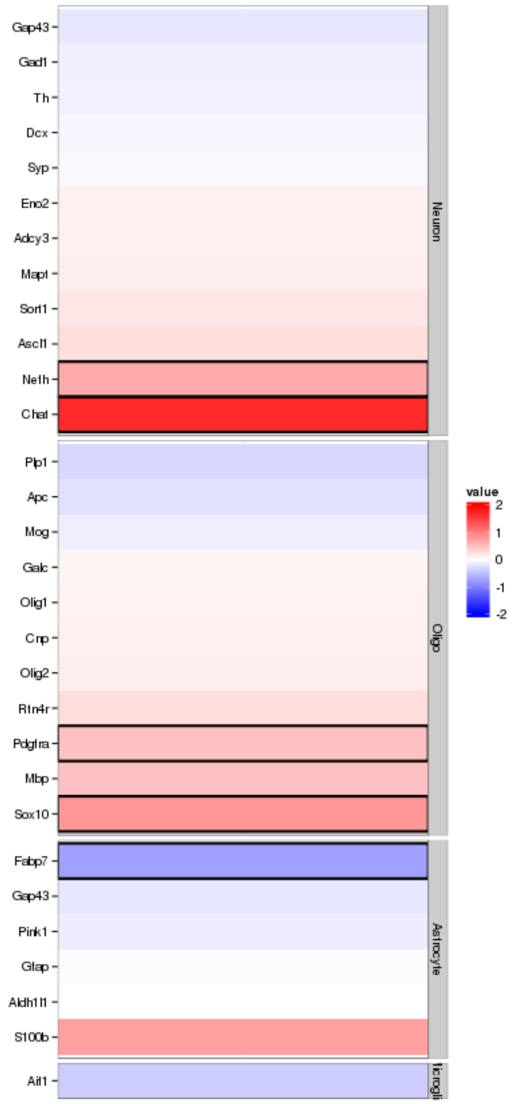
Enrichment or depletion for stage-specific cell cycle markers



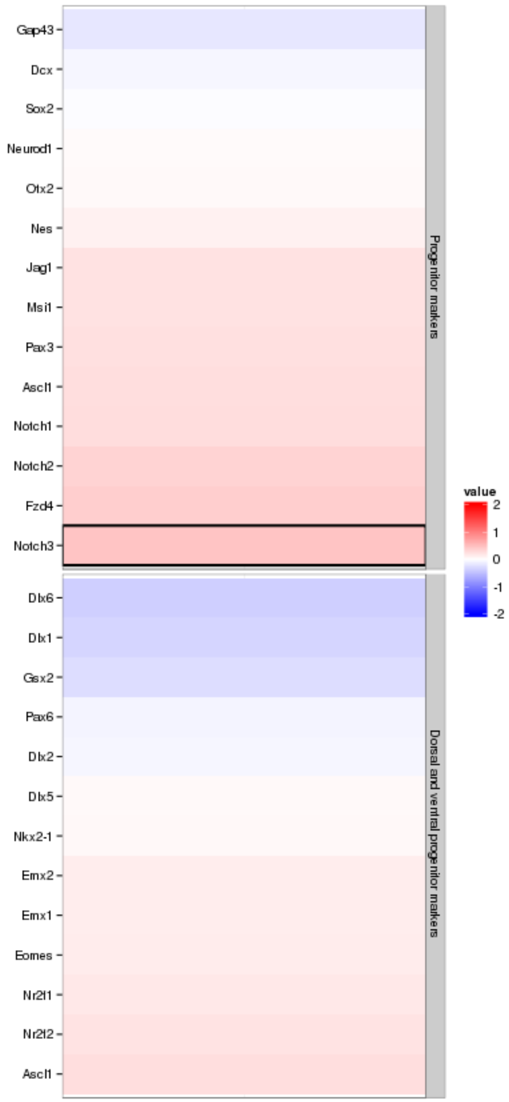
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



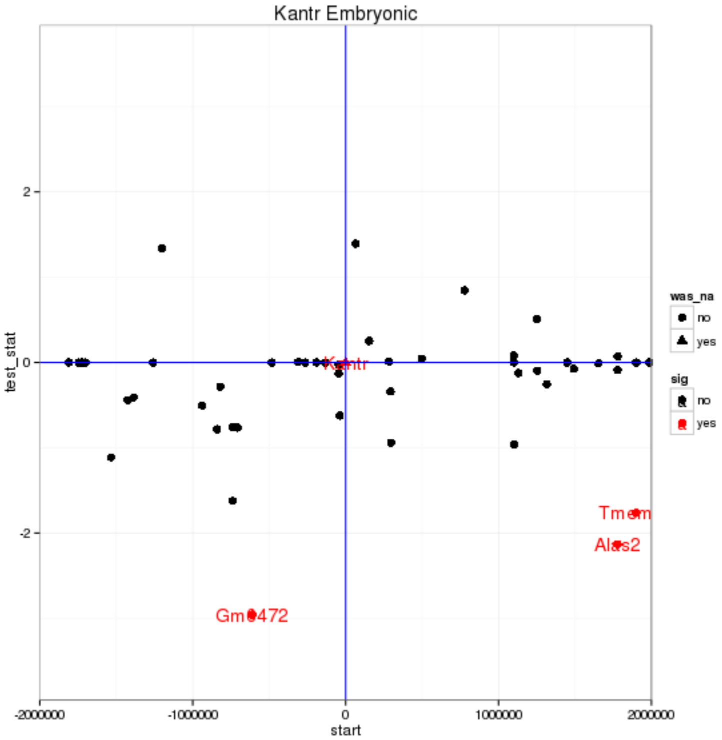
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 3 genes significantly regulated in a region this size is: 0.3615



Notes

Samples used are:

	10
1	JR762
2	JR774
3	JR746
4	JR775
5	JR747
6	JR812

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR762/abundances.cxb	WT	0	WT_0	32218100.00	33340200.00	0.95	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR774/abundances.cxb	WT	1	WT_1	32505000.00	33340200.00	0.95	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR746/abundances.cxb	WT	2	WT_2	27986400.00	33340200.00	0.83	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR775/abundances.cxb	Kantr	0	Kantr_0	41486000.00	33340200.00	1.27	1.00

5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR747/abundances.cxb	Kantr	1	Kantr_1	33582200.00	33340200.00	1.03	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR812/abundances.cxb	Kantr	2	Kantr_2	34934000.00	33340200.00	1.08	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1                        
##  [2] stringr_0.6.2                     
##  [3] seqbias_1.10.0                    
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0                   
##  [6] Biostrings_2.30.1                 
##  [7] gdata_2.13.3                      
##  [8] GO.db_2.10.1                      
##  [9] org.Mm.eg.db_2.10.1               
## [10] clusterProfiler_1.13.1            
## [11] DOSE_2.0.0                        
## [12] ReactomePA_1.6.1                  
## [13] AnnotationDbi_1.24.0              
## [14] Biobase_2.22.0                    
## [15] mgcv_1.7-29                       
## [16] nlme_3.1-117                      
## [17] RMySQL_0.9-3                      
## [18] RColorBrewer_1.0-5                
## [19] gridExtra_0.9.1                   
## [20] gtable_0.1.2                      
## [21] marray_1.40.0                     
## [22] gplots_2.13.0                     
## [23] GSA_1.03                          
## [24] limma_3.18.13                     
## [25] xtable_1.7-3                      
## [26] cummeRbund_2.7.2                  
## [27] Gviz_1.6.0                        
## [28] rtracklayer_1.22.7                
## [29] GenomicRanges_1.14.4              
## [30] XVector_0.2.0                     
```

```
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0        biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17          cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0       digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5        formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3       graph_1.40.1
## [16] graphite_1.8.1        gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1          KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2          lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33           Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1   proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2           RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3      scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2          survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2           XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##          param
## 1     cmd_line
## 2      version
## 3  SVN_revision
## 4 boost_version
## 5       genome
##
## 1 cuffdiff -p 10 -L WT,Kantr -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Kantr_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/BrainMap/dat
## 2
## 3
## 4
## 5
```

linc-Brn1a KO vs WT (Adult)

This file shows the wt-v-ko comparison for linc-Brn1a.

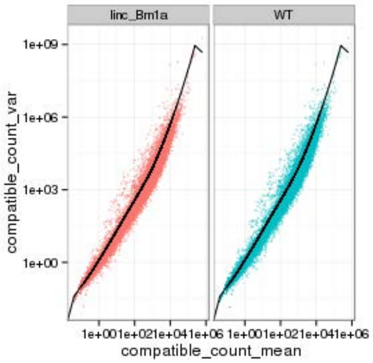
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

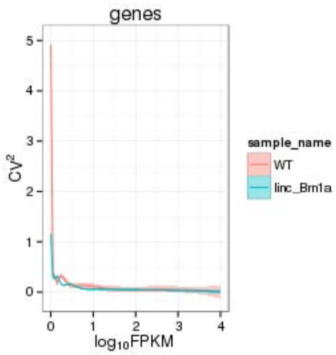
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



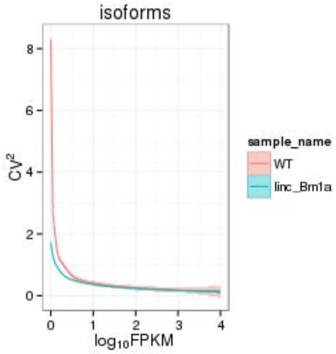
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

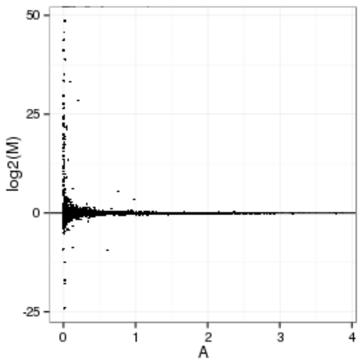
Genes:



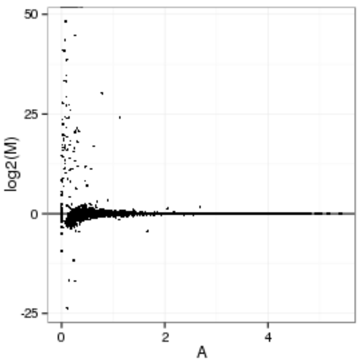
Isoforms:



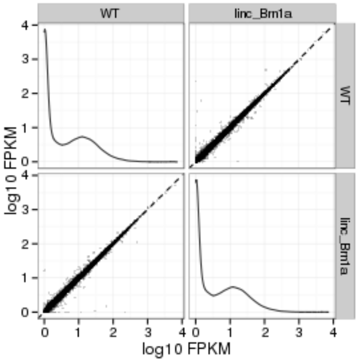
MvA plot



MvA plot counts



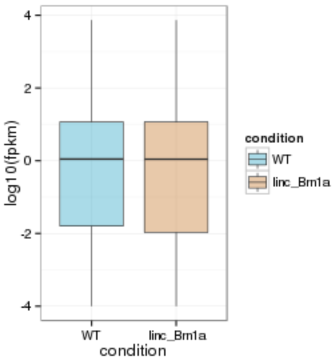
Scatterplot matrix



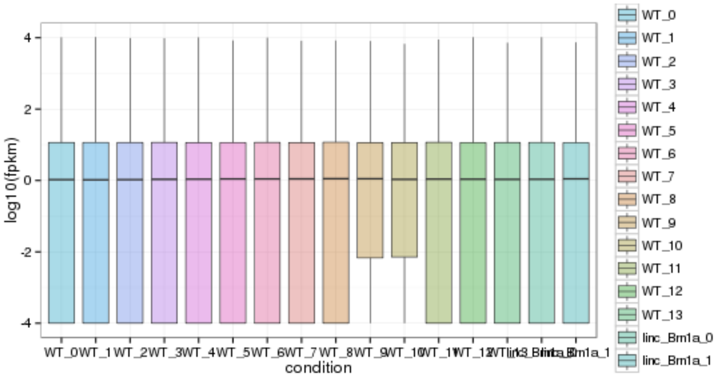
Distributions

Boxplots

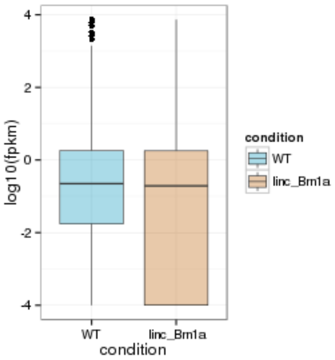
Boxplot (genes)



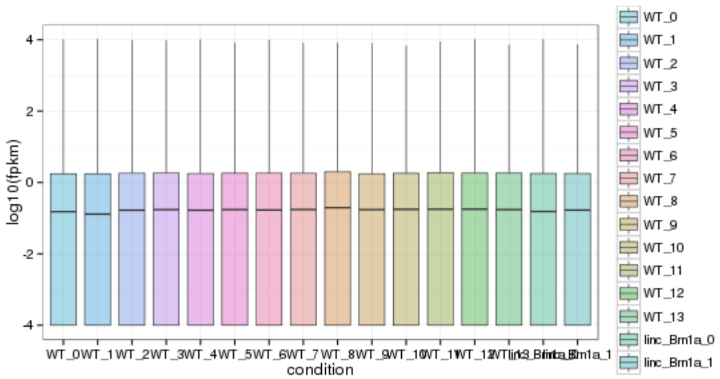
Boxplot (genes, replicates)



Boxplot (isoforms)

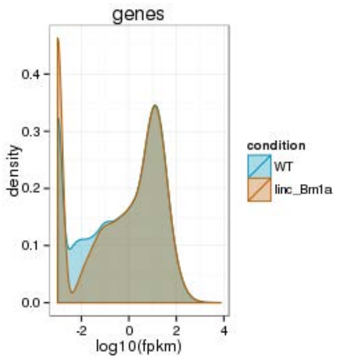


Boxplot (isoforms, replicates)

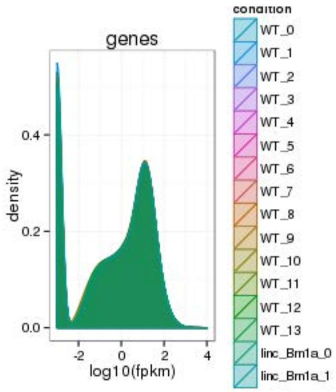


Density

Density (genes)

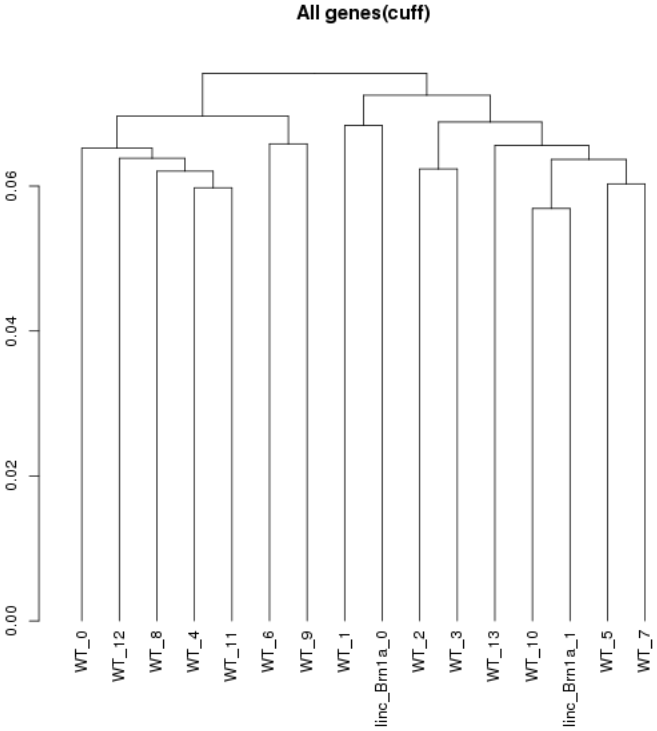


Density (genes, replicates)



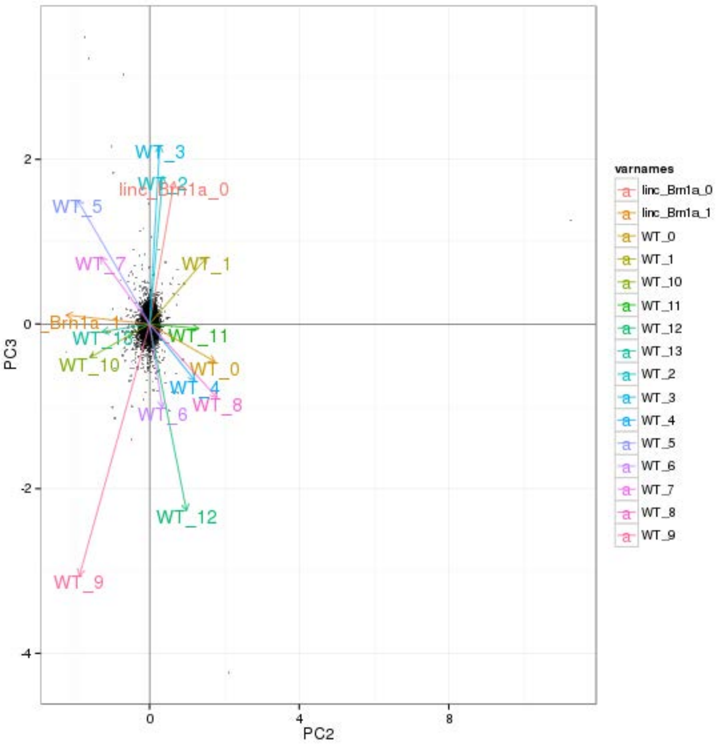
Clustering

Replicate Clusters



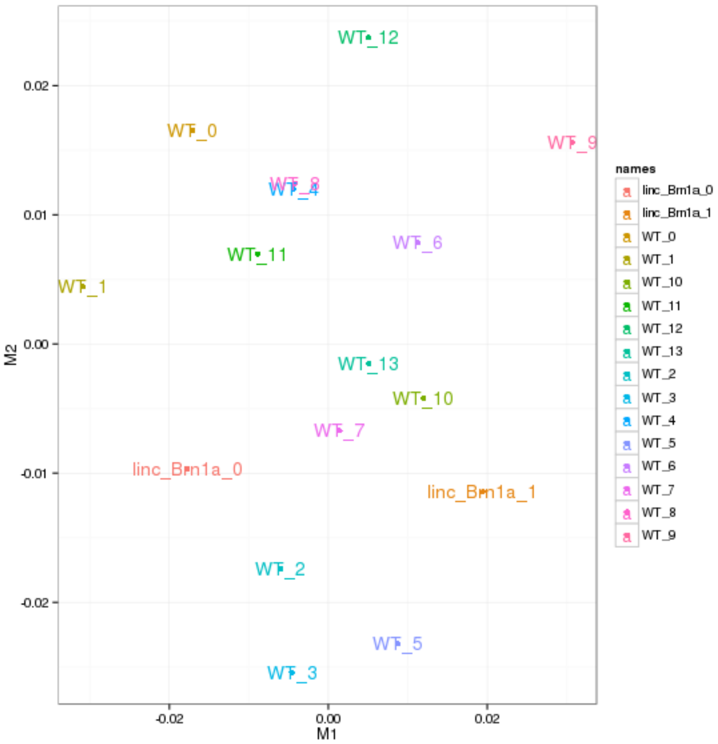
```
## NULL
```

PCA (genes)



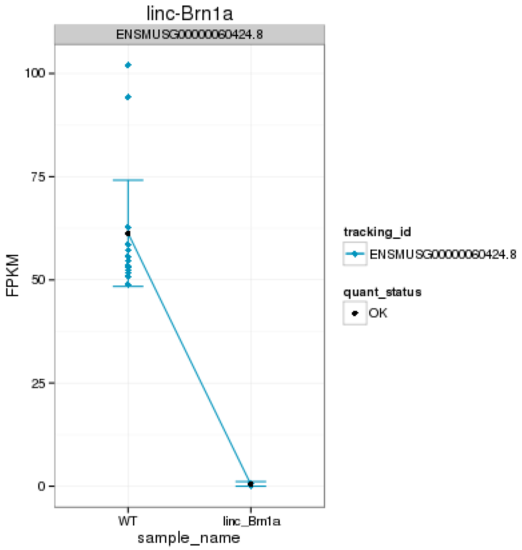
PC3
PC2
2
0
-2
-4
0
4
8
WT_3
WT_2
linc_Brn1a_0
WT_5
WT_7
WT_1
Brn1a_1
WT_11
WT_13
WT_10
WT_0
WT_4
WT_8
WT_6
WT_12
WT_9
varnames
linc_Brn1a_0
linc_Brn1a_1
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

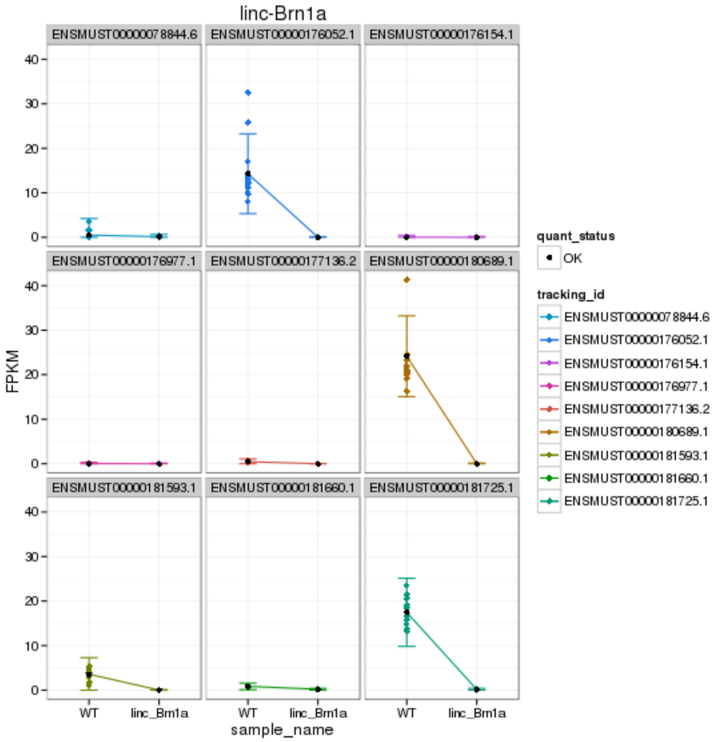


KO assessment

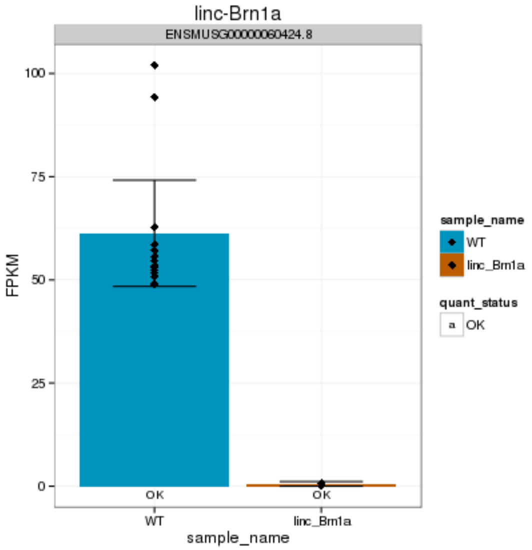
Endogenous lncRNA expression



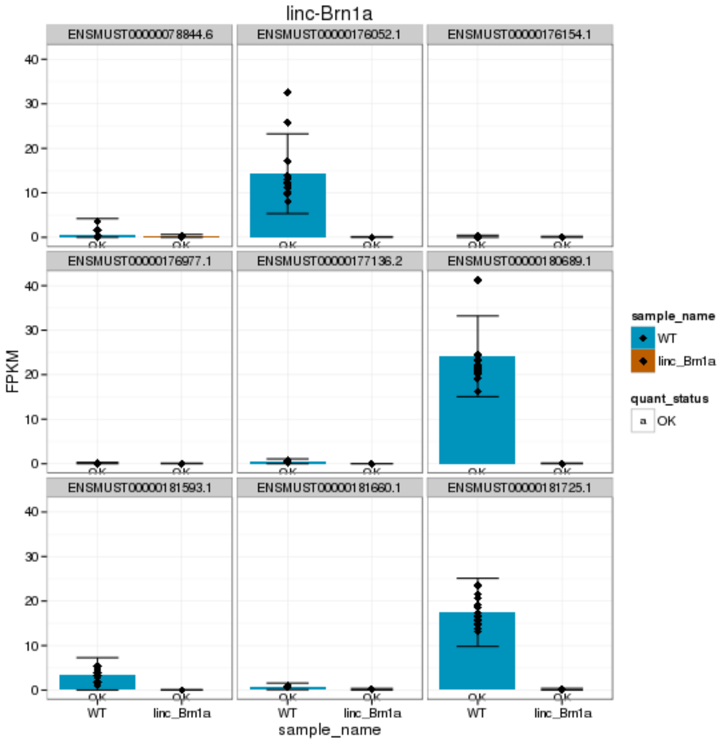
Endogenous expression of linc-Brn1a isoforms:



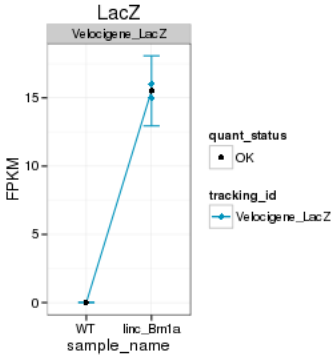
Barplot of gene expression:

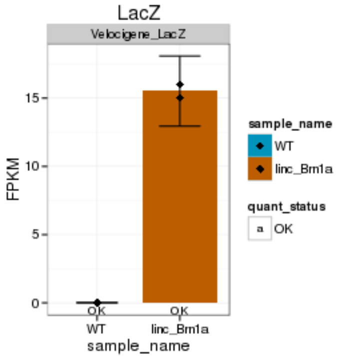


Barplot of isoform expression:



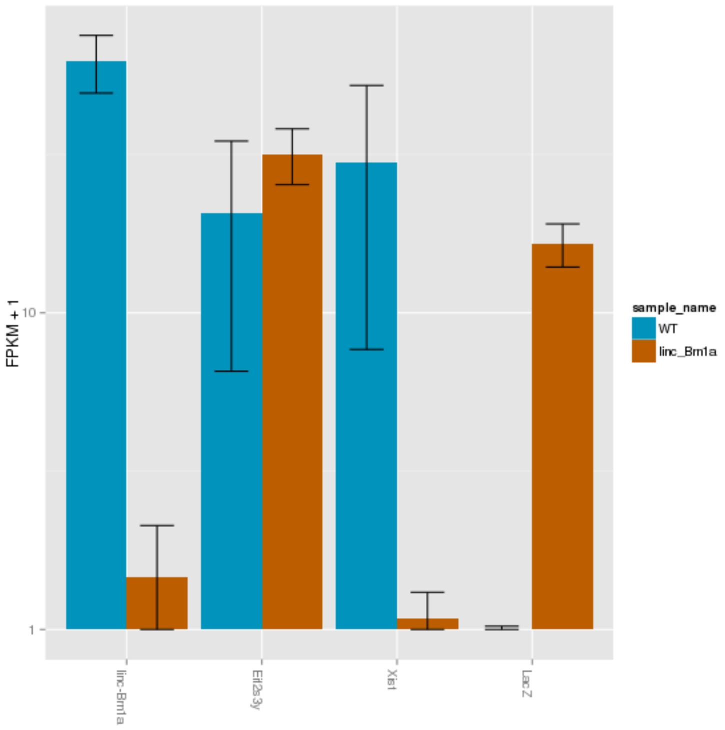
LacZ expression



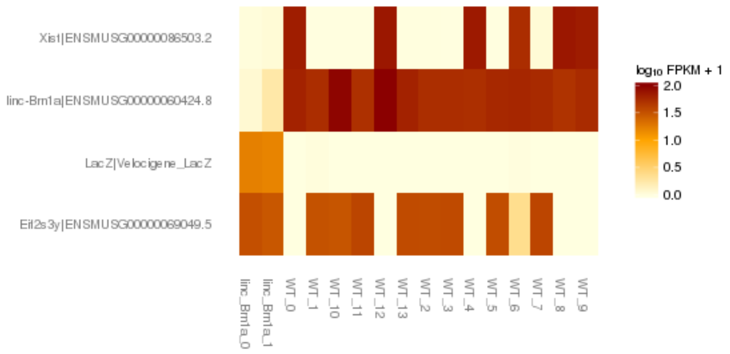


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

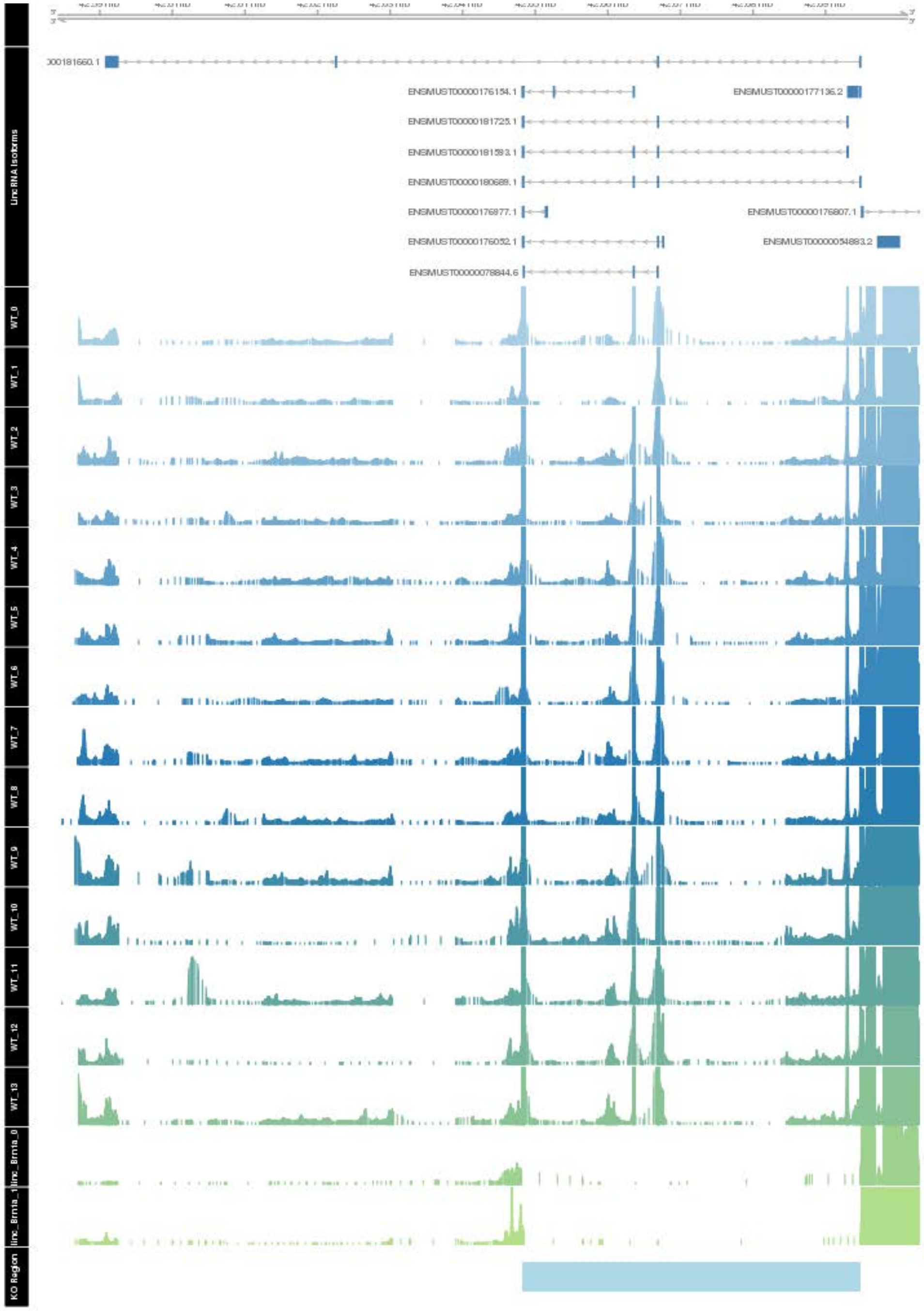
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization



Linc RNA Isoforms
)00181660.1
ENSMUST00000176154.1
ENSMUST00000177136.2
ENSMUST00000181725.1
ENSMUST00000181593.1
ENSMUST00000180688.1
ENSMUST00000176977.1
ENSMUST00000176807.1
ENSMUST00000176052.1
ENSMUST00000054883.2
ENSMUST00000078844.6
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
linc_Brn1a_0
linc_Brn1a_1
KO Region

Differential Analysis

Differential Genes

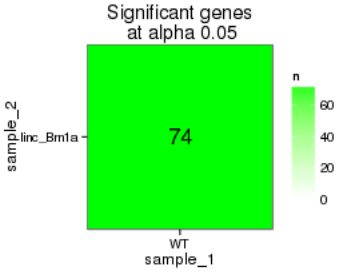
There are 74 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Rec8
2	Arrdc2
3	Fosb
4	Dio2
5	Mertk
6	Hspa8
7	Vip
8	Fabp7
9	Sgk1
10	Mybpc1
11	Btg2
12	Xbp1
13	Fos
14	Rgcc
15	Dnajc3
16	Arc
17	Sdf2l1
18	Nr4a1
19	Cdkn1a
20	Sik1
21	Xdh
22	Dusp1
23	Fkbp5
24	Il33
25	Pdia4
26	Paqr8
27	Mcm6
28	Tfcp2l1
29	Hspa5
30	Cyr61
31	Nr4a3
32	Alad
33	Slc2a1
34	Mfsd2a
35	Adipor2
36	Abcc9
37	Pglyrp1

38 Hddc3
39 Tsc22d3
40 Cryab
41 Ldlr
42 Ndn
43 Igsf9b
44 Cbl
45 Nostrin
46 Lars2
47 Anln
48 Tob1
49 Egr2
50 Smim3
51 Egr1
52 Hdhd3
53 Daam2
54 Tlr7
55 Npas4
56 Nrros
57 Ccdc171
58 Jun
59 Junb
60 Ier2
61 Per2
62 Kdm5d
63 linc-Brn1a
64 Usp31
65 Zbtb16
66 Ddx3y
67 Klhl9
68 Egr4
69 Gm7292
70 Xist
71 Cdr1
72 AA465934
73 Gm6472
74 Gm26924

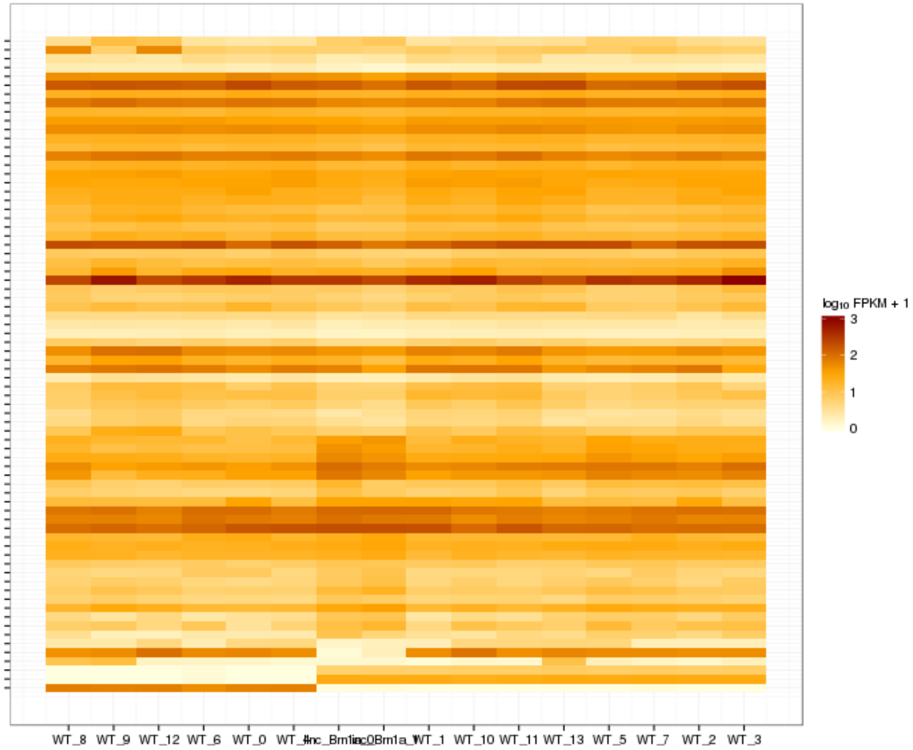
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

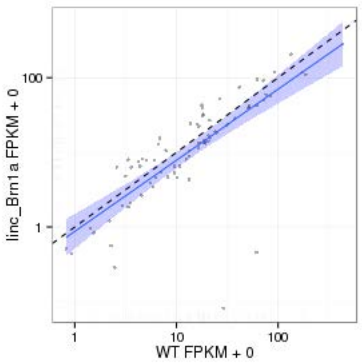


Significant genes with expression >50fpkm (any condition):(turned off)

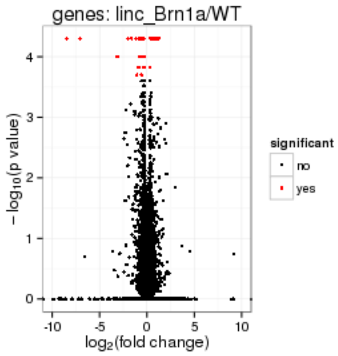
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

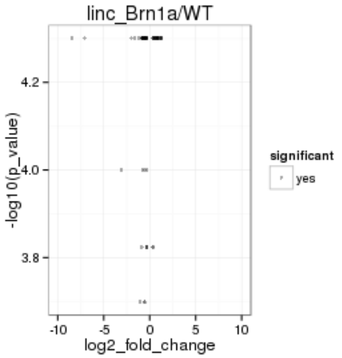
Scatter plot of significant genes only:



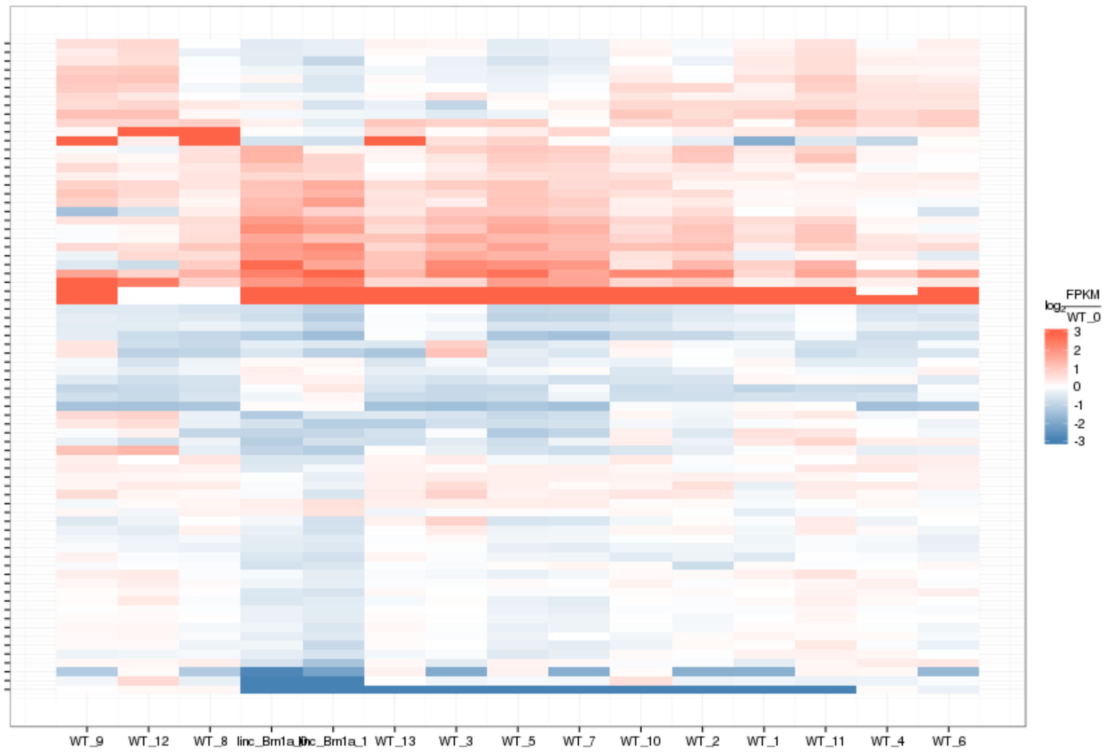
Volcano Plot



Volcano plot with significant genes only:



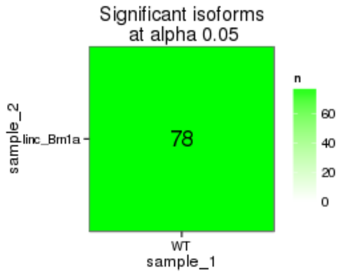
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

	isoAnnot$gene_short_name
1	Rec8
2	Arrdc2
3	Fosb
4	Hif3a
5	Dio2
6	Mertk
7	Hspa8
8	Vip
9	Fabp7
10	Cpm
11	Tns3
12	Btg2
13	Xbp1
14	Atp2a3
15	Fos
16	Arc
17	Zbtb20
18	Sdf2l1
19	Nr4a1
20	Cdkn1a
21	Sik1
22	Xdh
23	Atp6v0c
24	Dusp1
25	Fkbp5
26	Il33

27 Pdia4
28 Paqr8
29 Tfcp2l1
30 Hspa5
31 Cyr61
32 Alad
33 Slc2a1
34 Mfsd2a
35 Ago3
36 Map3k6
37 Ccnl2
38 Adipor2
39 Pglyrp1
40 Hddc3
41 Tsc22d3
42 Cryab
43 Kdm4a
44 Ndn
45 Vps8
46 Igsf9b
47 Cbl
48 Anln
49 Kirrel2
50 Egr2
51 Smim3
52 Egr1
53 Hdhd3
54 Eltd1
55 Daam2
56 Dmtf1
57 Npas4
58 Ezr
59 Jun
60 Junb
61 Ier2
62 Per2
63 Kdm5d
64 Usp31
65 Sepp1
66 Zbtb16
67 Ddx3y
68 Ahnak

69 Klhl9

70 Egr4

71 Gm7292

72 Xist

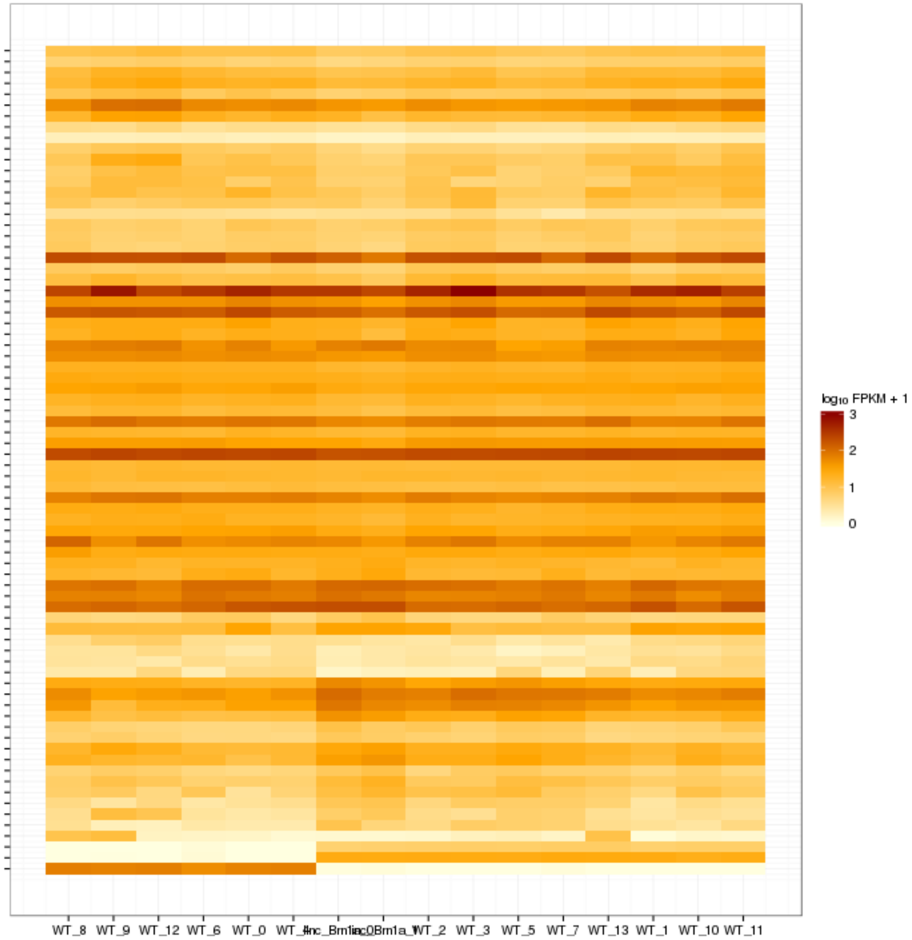
73 Cdr1

74 Malat1

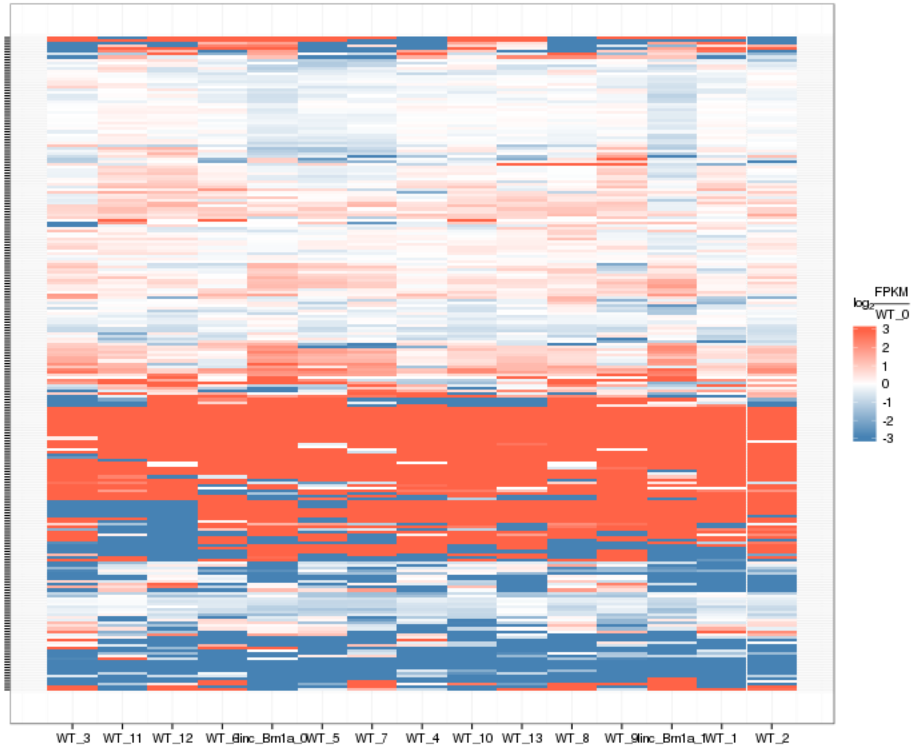
75 Gm6472

76 Gm26924

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

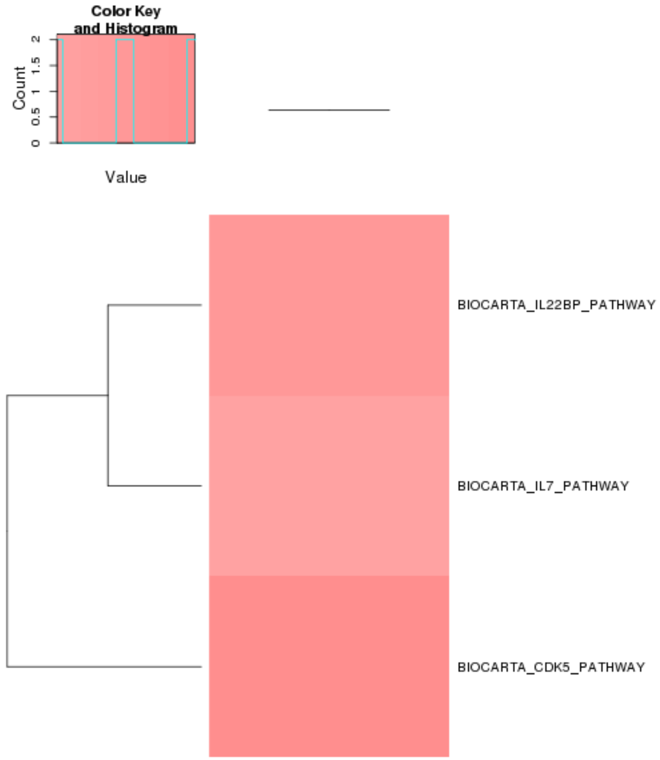
Gene/Pathway Analysis

GSEA

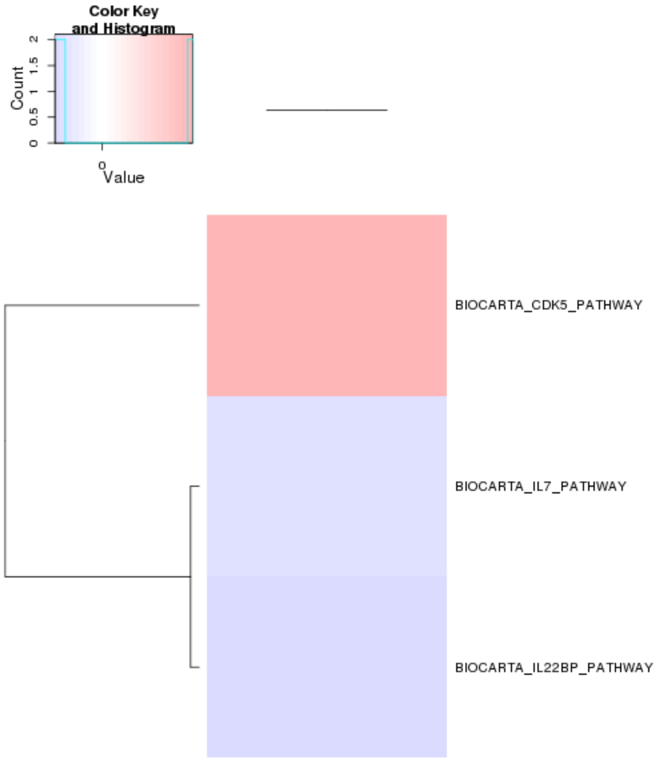
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:

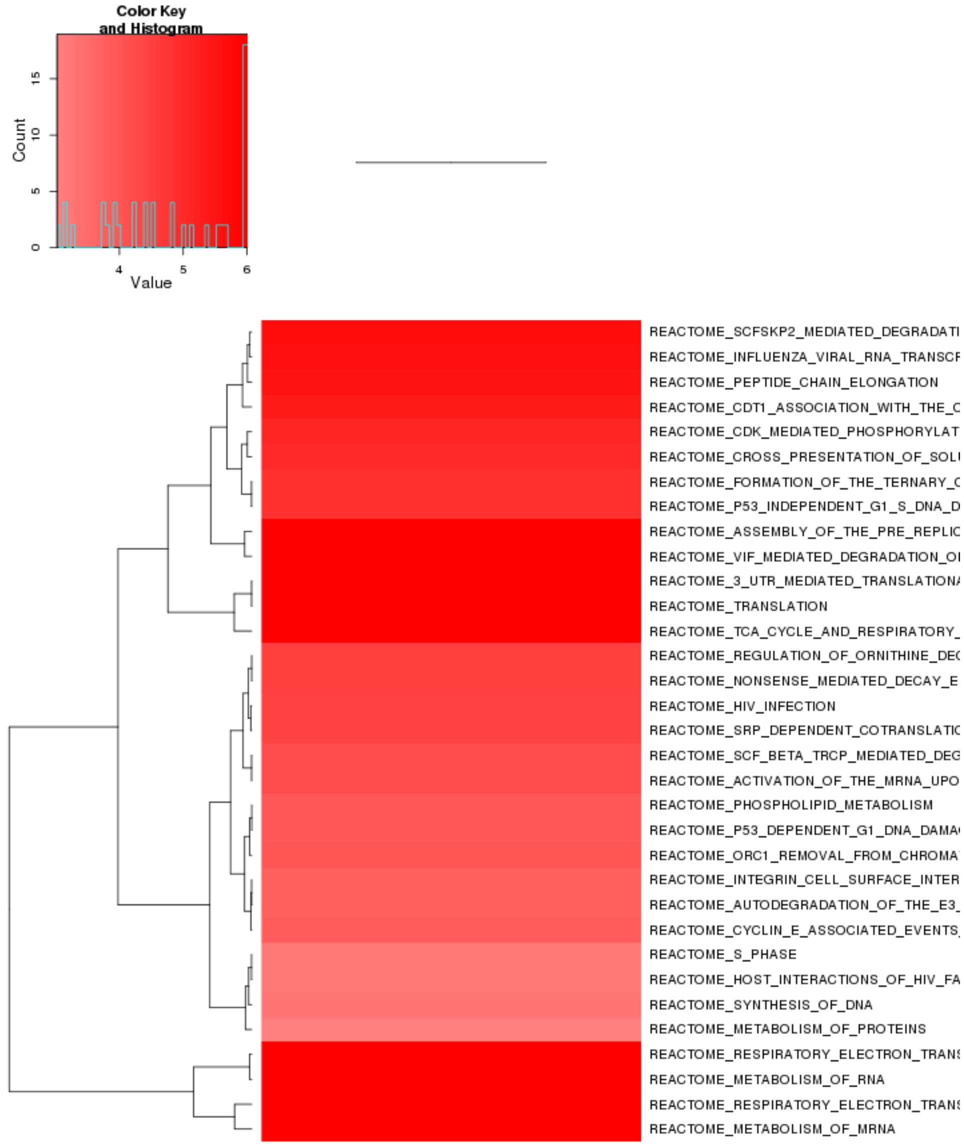


Biocarta zscore:



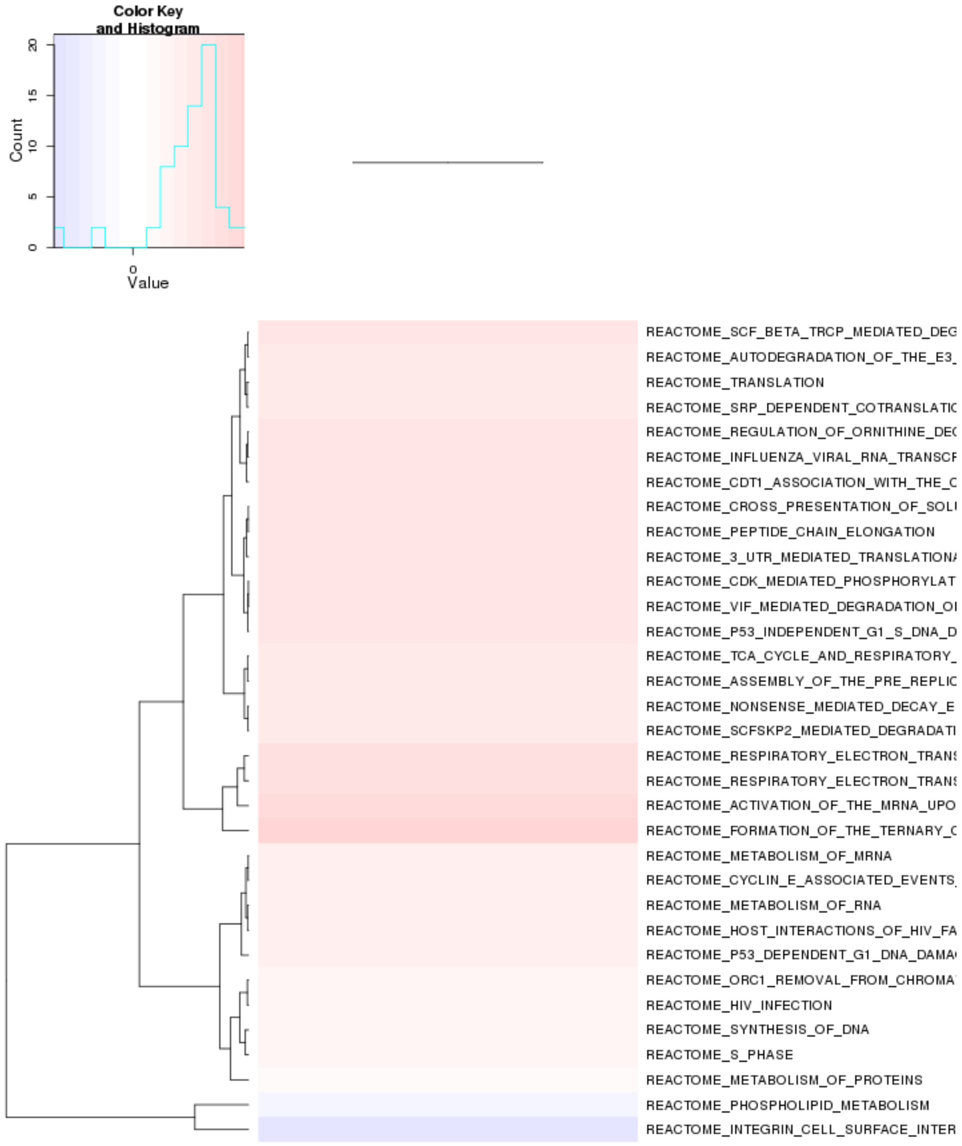
Reactome enrichment:

```
## Error: subscript out of bounds
```

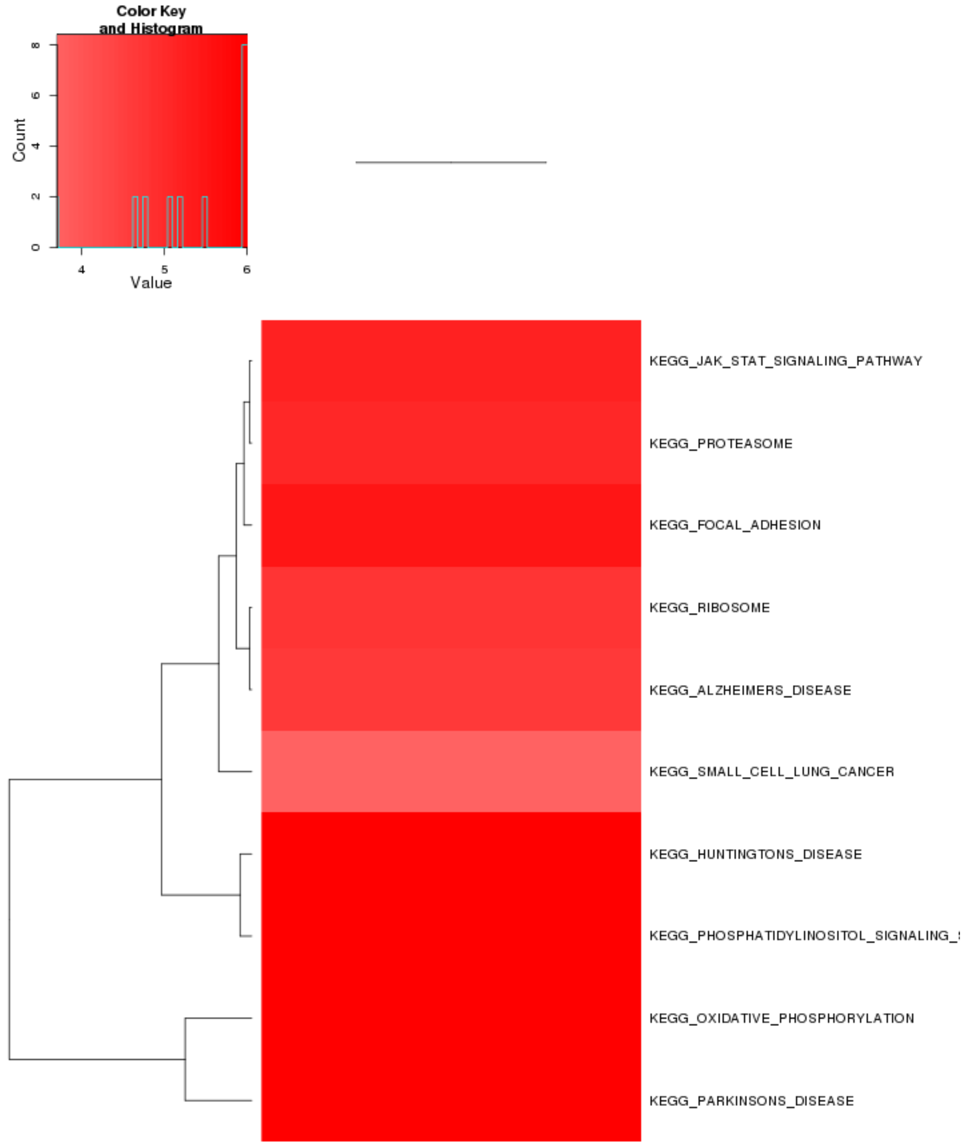


Reactome zscore:

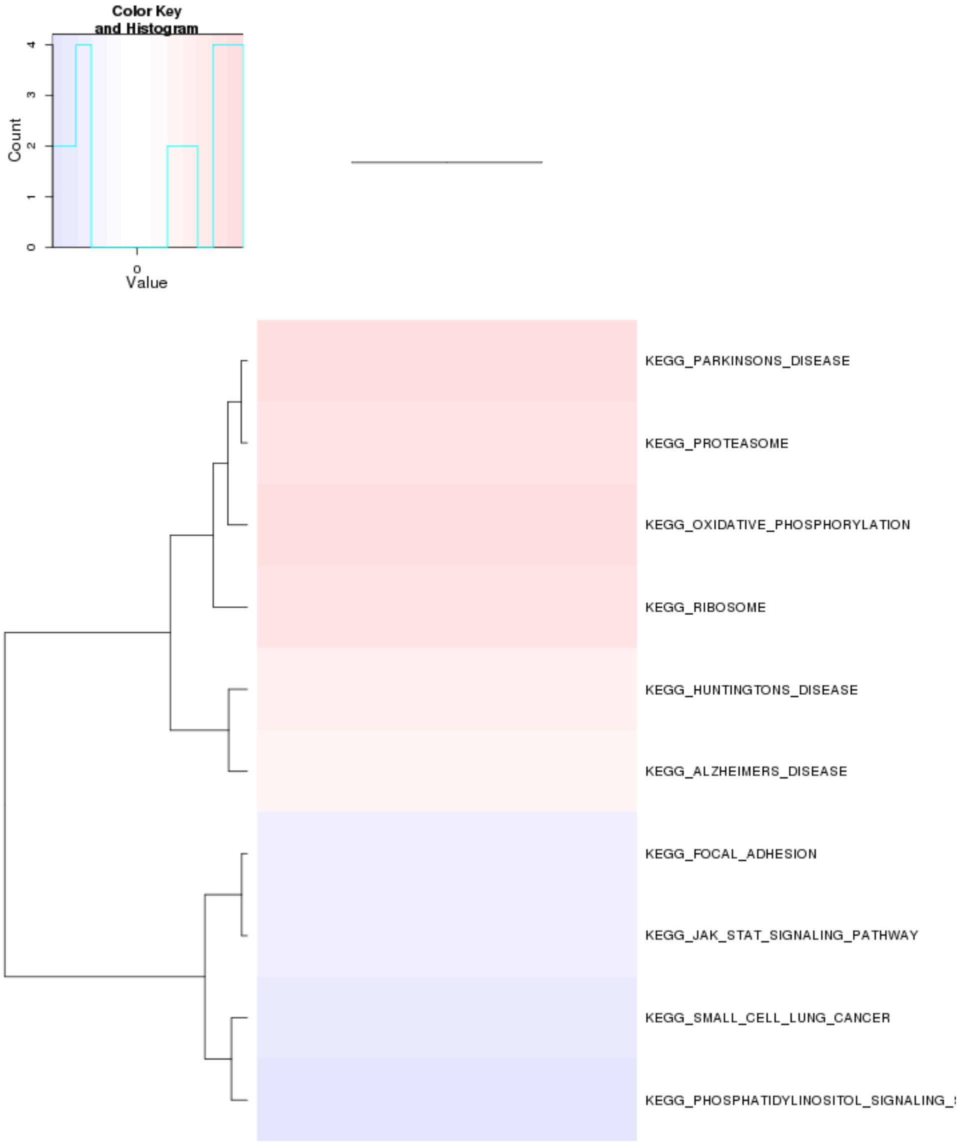
```
## Error: subscript out of bounds
```



Kegg enrichment:

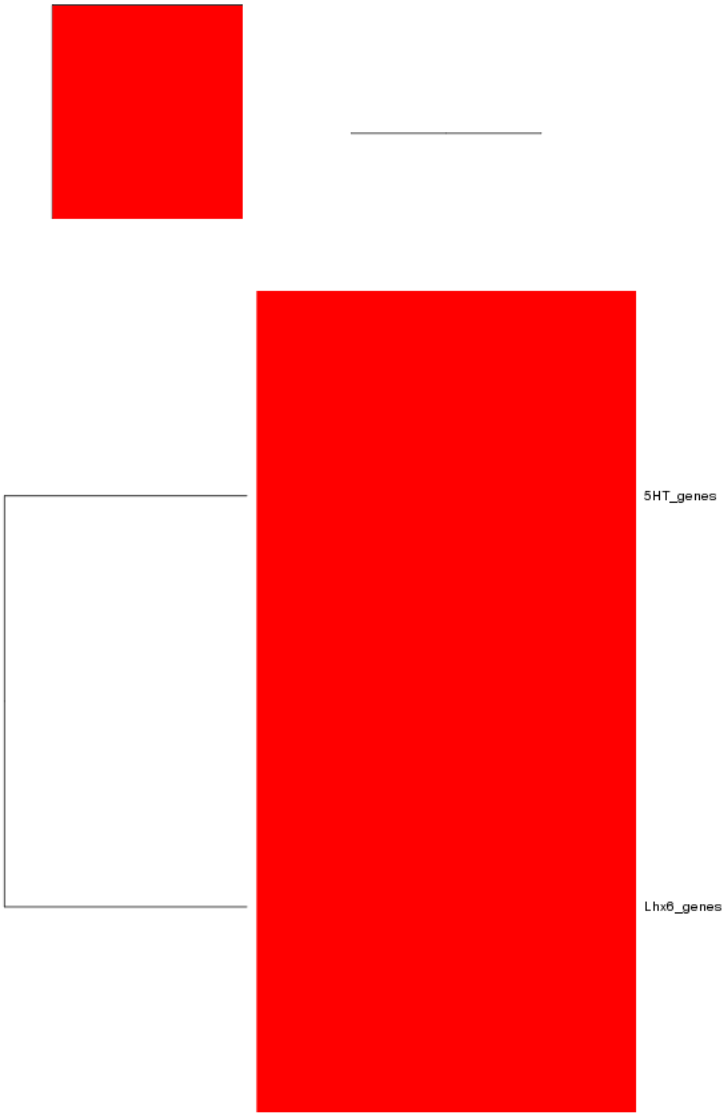

Color Key
and Histogram
Count
0
2
4
6
8
4
5
6
Value
KEGG_JAK_STAT_SIGNALING_PATHWAY
KEGG_PROTEASOME
KEGG_FOCAL_ADHESION
KEGG_RIBOSOME
KEGG_ALZHEIMERS_DISEASE
KEGG_SMALL_CELL_LUNG_CANCER
KEGG_HUNTINGTONS_DISEASE
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_PARKINSONS_DISEASE

Kegg zscore:

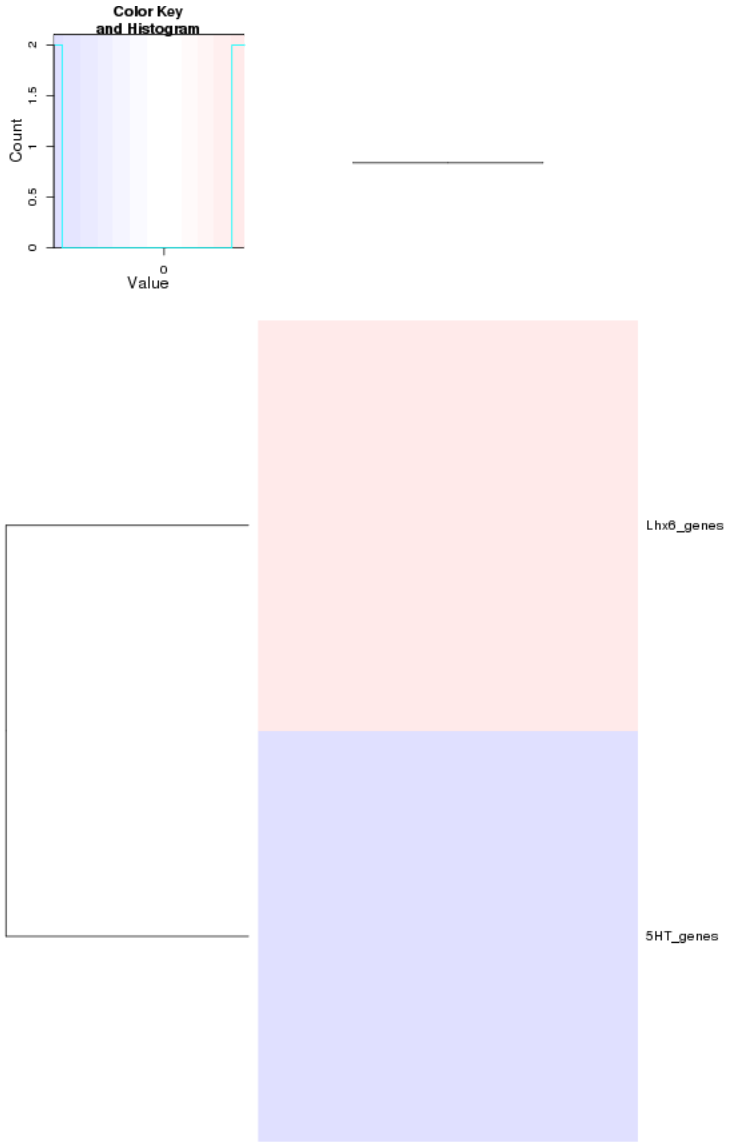


Interneuron enrichment:

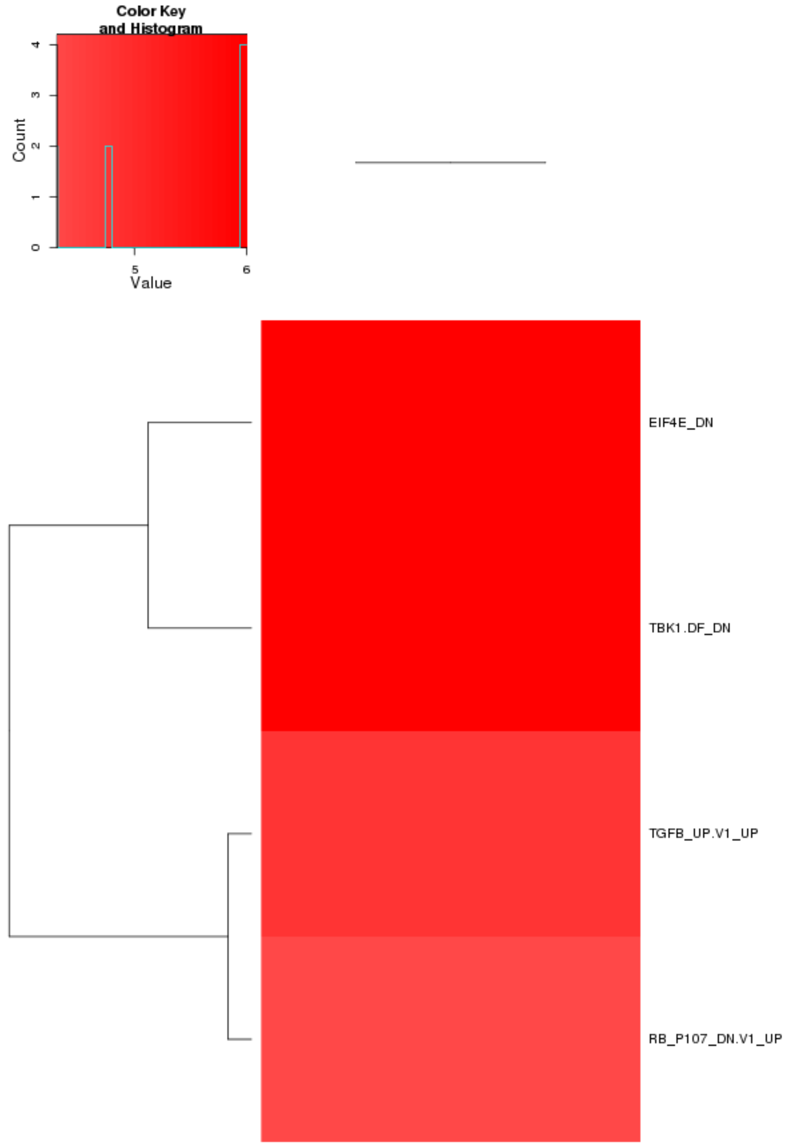
```
## Error: no locations are finite
```



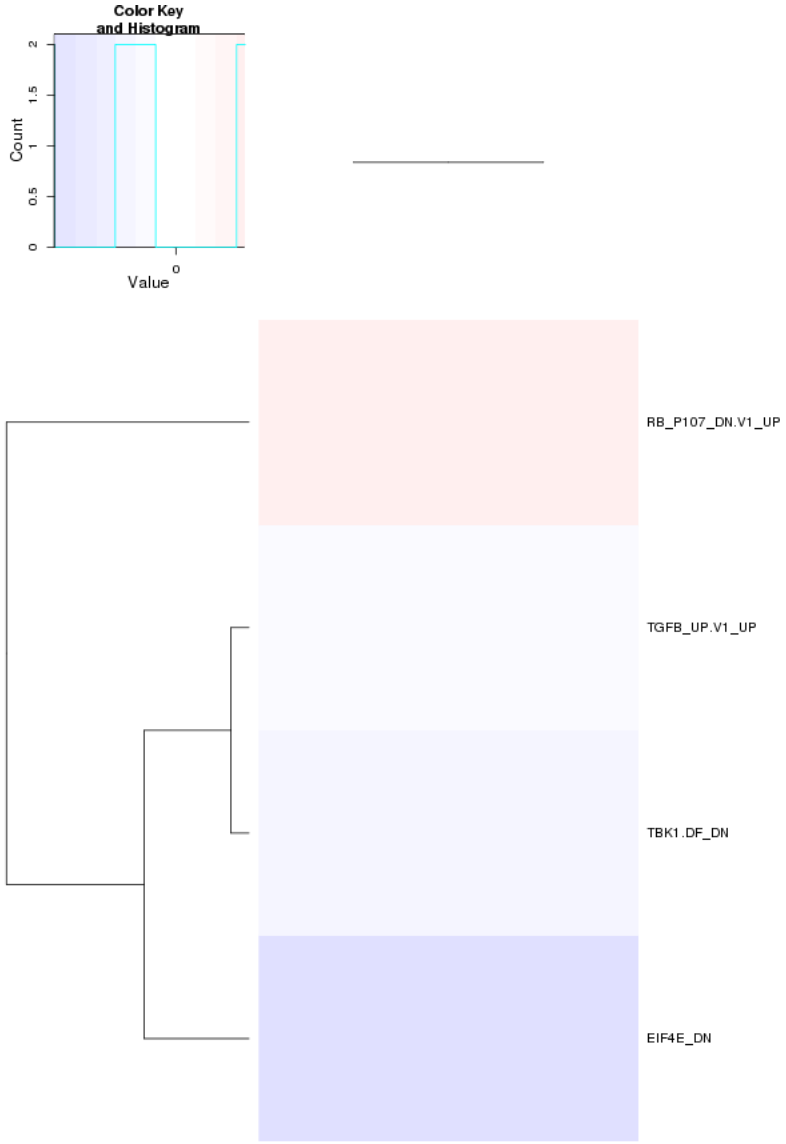
Interneuron zscore:



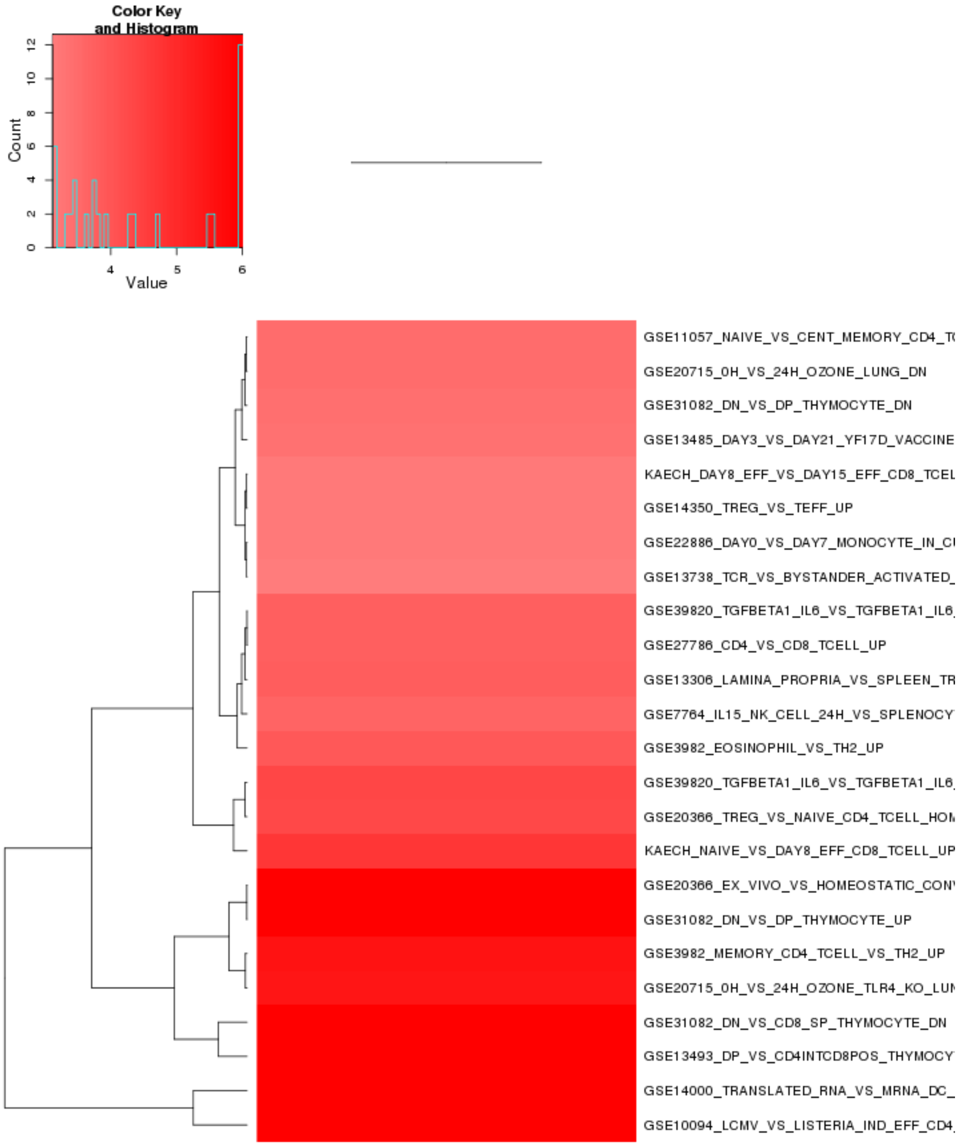
Oncogene enrichment:



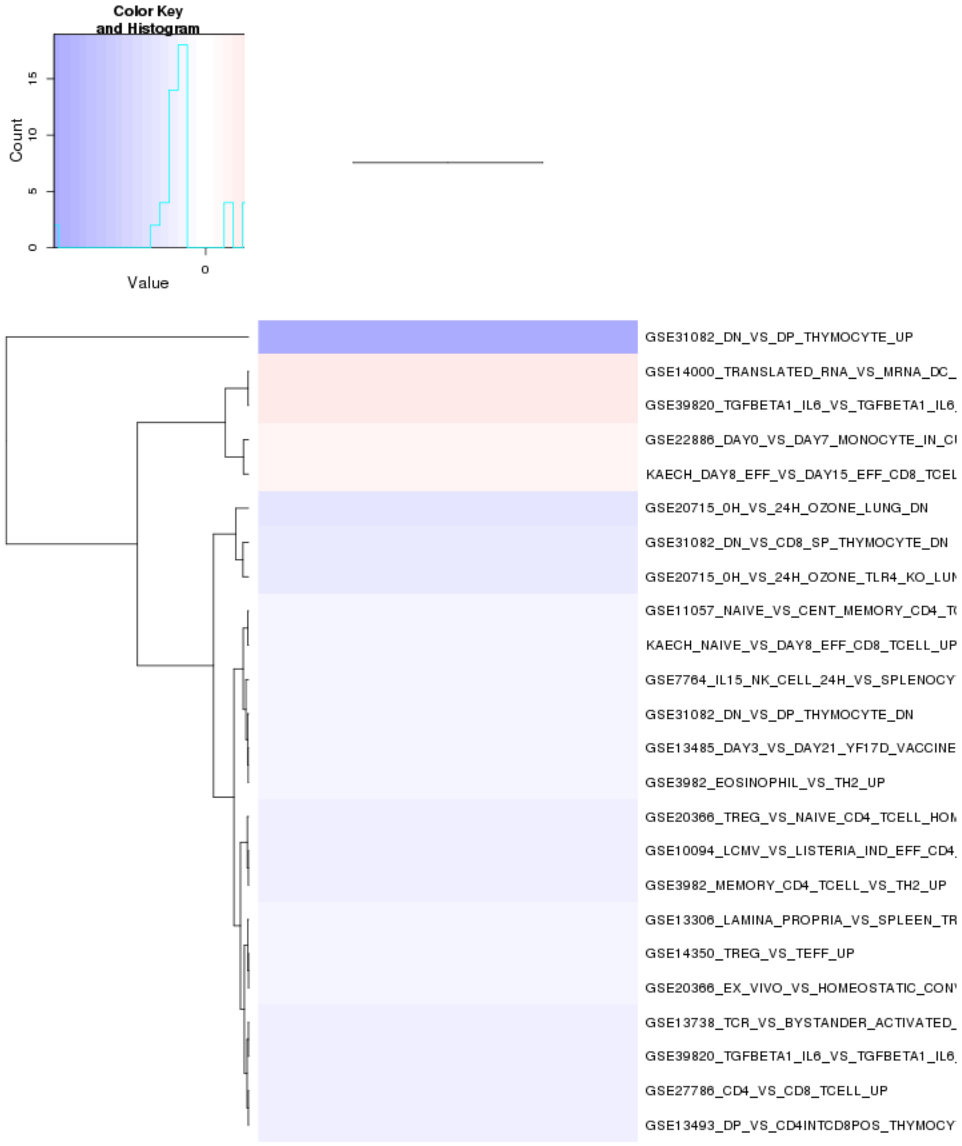
Oncogene zscore:



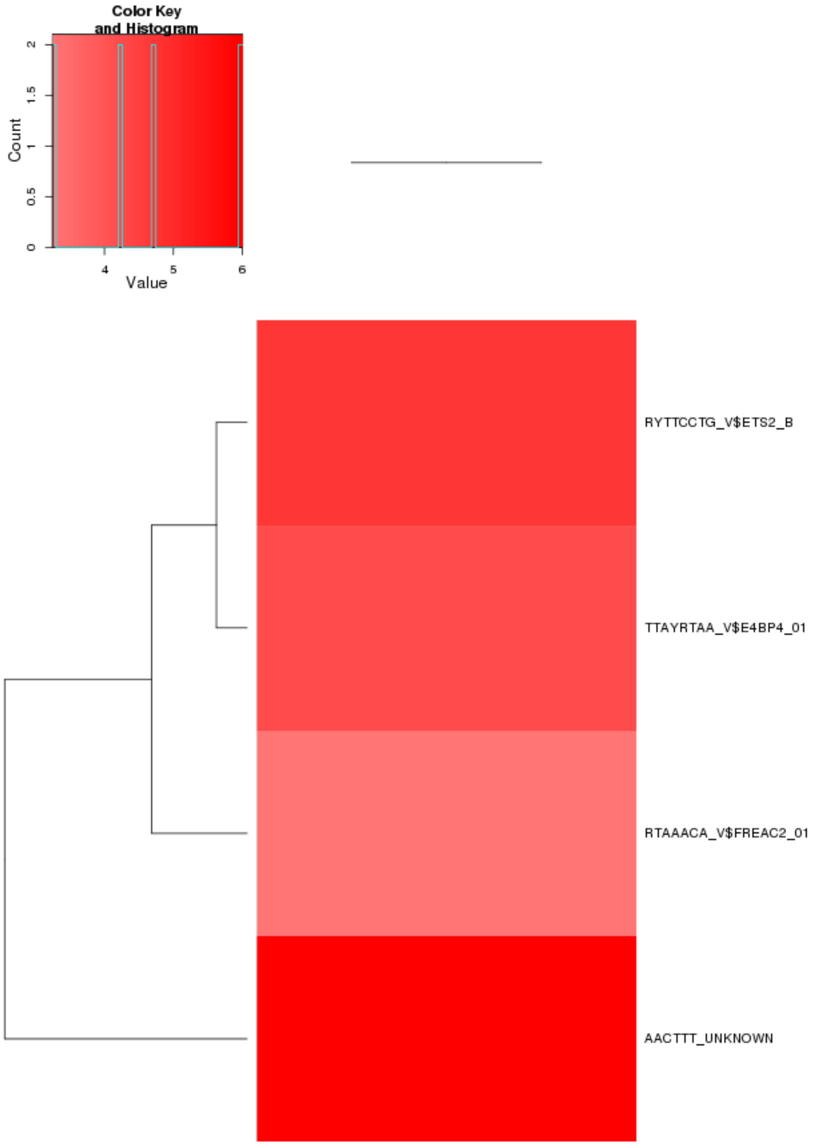
Immuno enrichment:



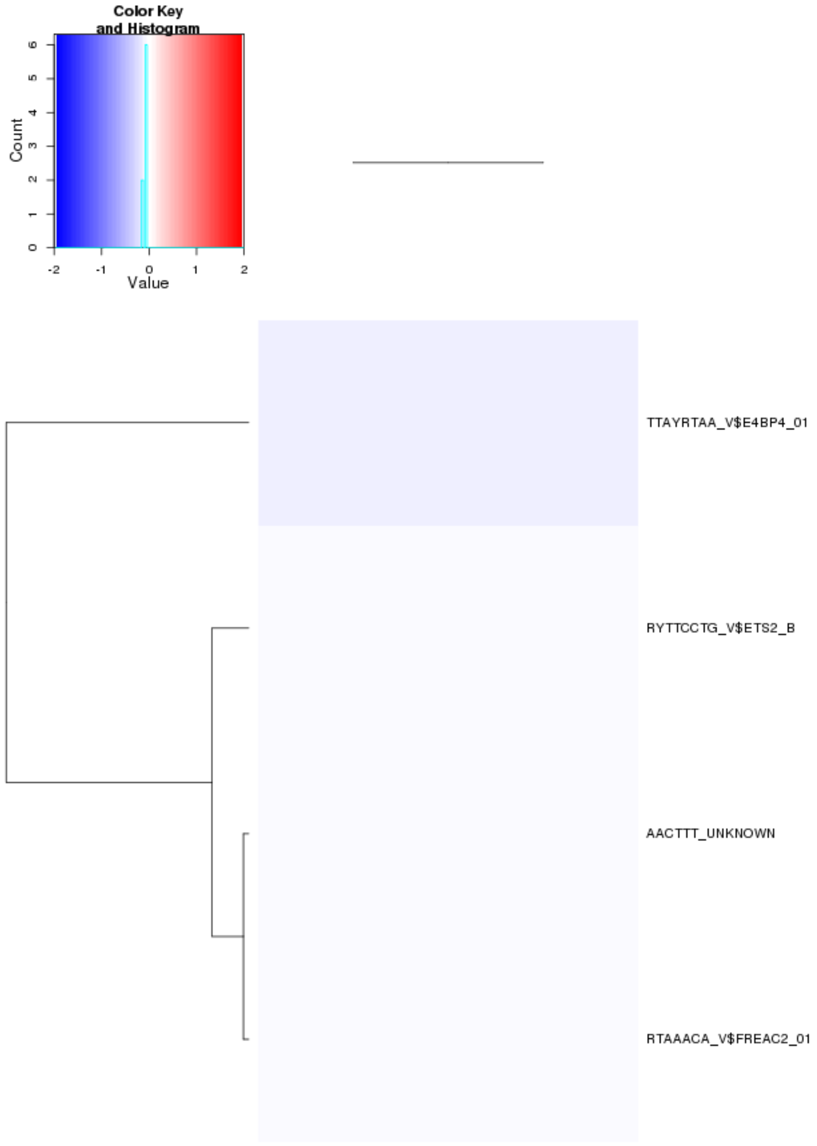
Immuno zscore:



TF enrichment:


Color Key
and Histogram
Count
0
0.5
1
1.5
2
4
5
6
Value
RYTTCCTG_V$ETS2_B
TTAYRTAA_V$E4BP4_01
RTAAACA_V$FREAC2_01
AACTTT_UNKNOWN

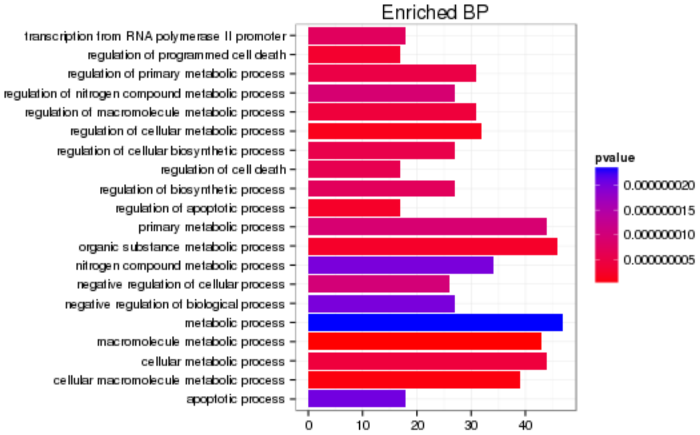
TF zscore:

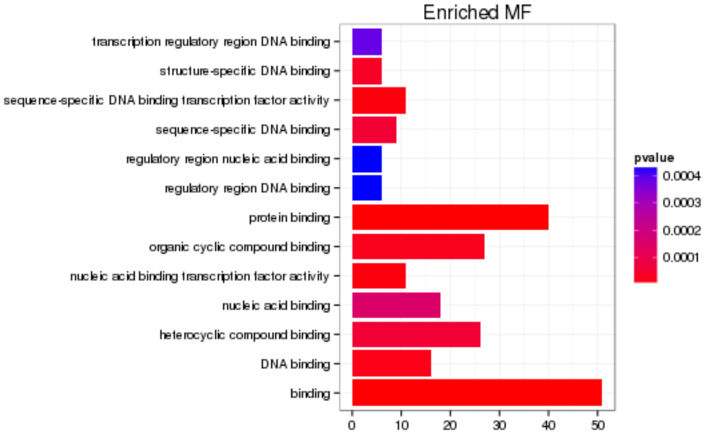


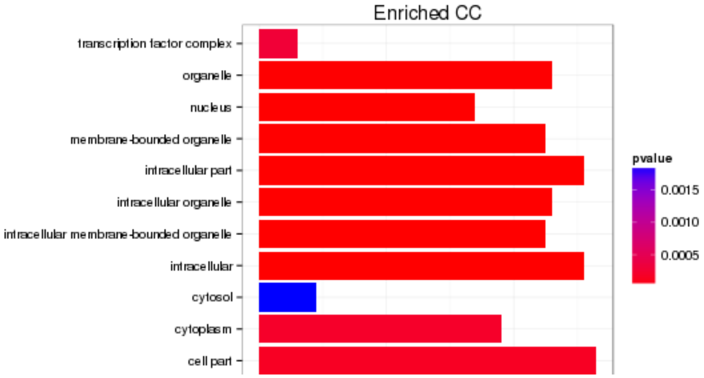
GO enrichment

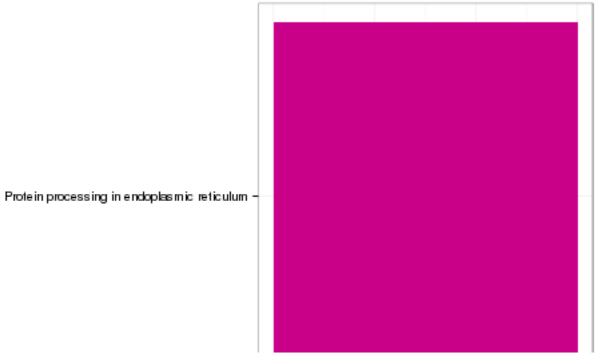
Cluster profiler used to call enichments of significantly differentially regulated genes that map to Entrez IDs.

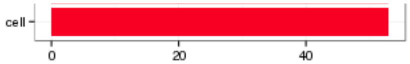
```
## [1] "ERROR: The estimated pi0 <= 0. Check that you have valid p-values or use another lambda method."
```

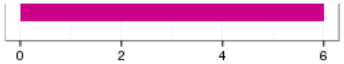

Enriched BP
transcription from RNA polymerase II promoter
regulation of programmed cell death
regulation of primary metabolic process
regulation of nitrogen compound metabolic process
regulation of macromolecule metabolic process
regulation of cellular metabolic process
regulation of cellular biosynthetic process
regulation of cell death
regulation of biosynthetic process
regulation of apoptotic process
primary metabolic process
organic substance metabolic process
nitrogen compound metabolic process
negative regulation of cellular process
negative regulation of biological process
metabolic process
macromolecule metabolic process
cellular metabolic process
cellular macromolecule metabolic process
apoptotic process
0
10
20
30
40
pvalue
0.000000020
0.000000015
0.000000010
0.000000005


Enriched MF
transcription regulatory region DNA binding
structure-specific DNA binding
sequence-specific DNA binding transcription factor activity
sequence-specific DNA binding
regulatory region nucleic acid binding
regulatory region DNA binding
protein binding
organic cyclic compound binding
nucleic acid binding transcription factor activity
nucleic acid binding
heterocyclic compound binding
DNA binding
binding
0
10
20
30
40
50
pvalue
0.0004
0.0003
0.0002
0.0001


Enriched CC
transcription factor complex
organelle
nucleus
membrane-bounded organelle
intracellular part
intracellular organelle
intracellular membrane-bounded organelle
intracellular
cytosol
cytoplasm
cell part
pvalue
0.0015
0.0010
0.0005

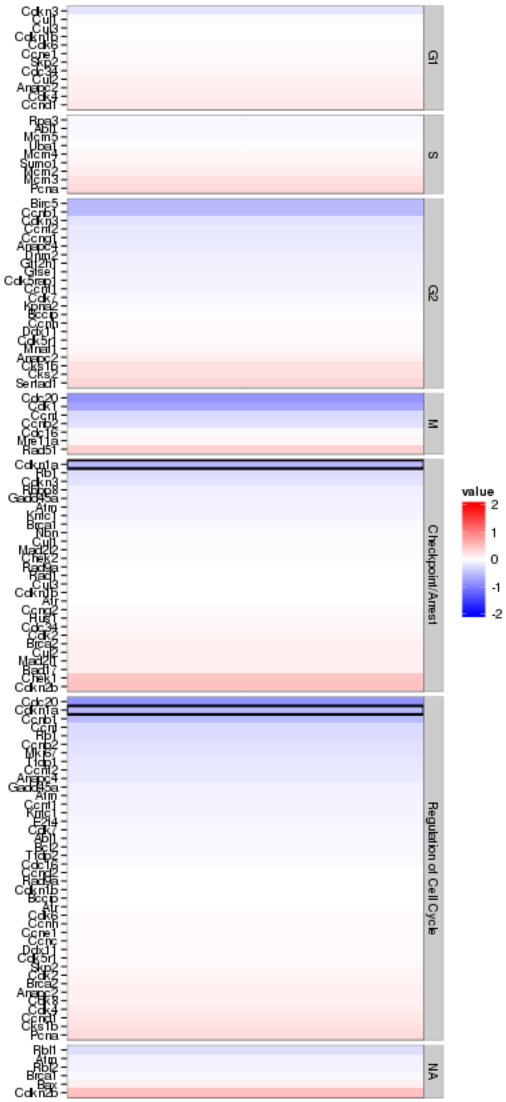

Protein processing in endoplasmic reticulum



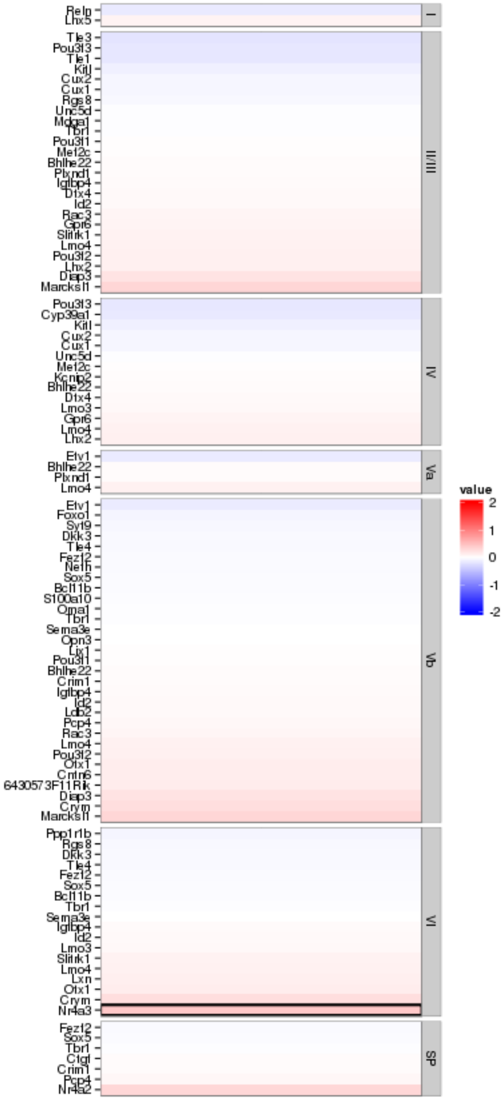


```
## Error: 'x' and 'units' must have length > 0
```

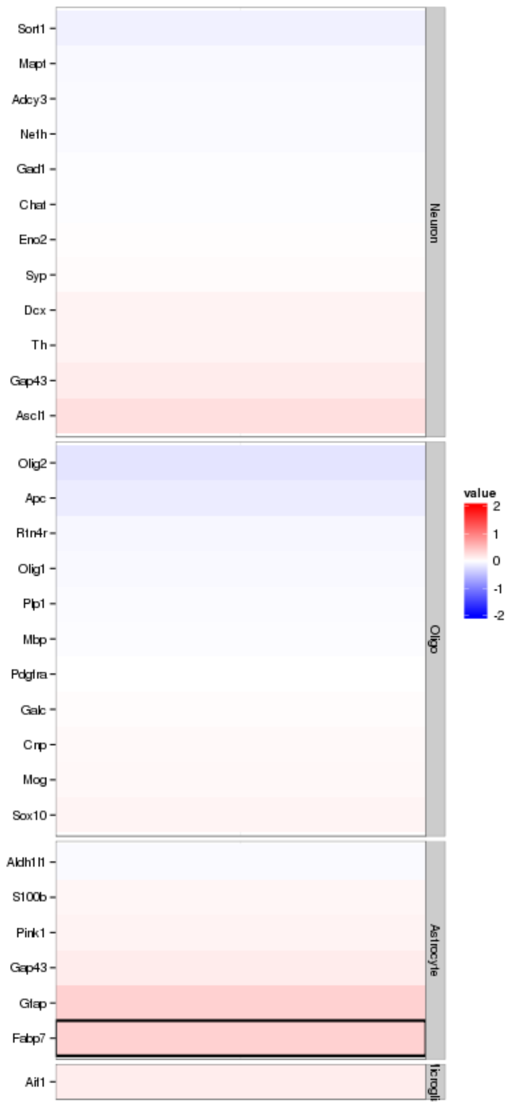
Enrichment or depletion for stage-specific cell cycle markers



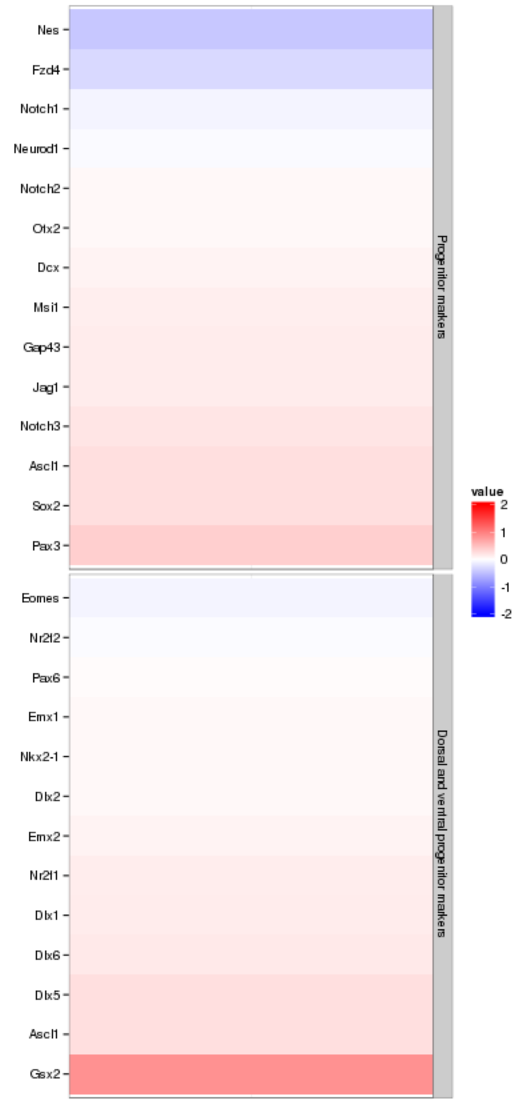
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



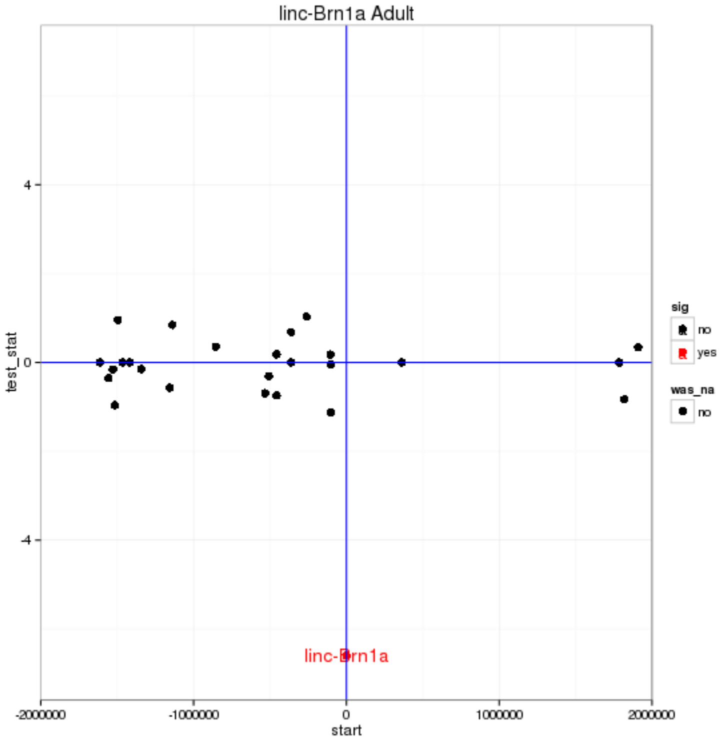
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15 JR730

16 JR837

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	33756400.00	0.78	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	33756400.00	0.60	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	33756400.00	1.00	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	33756400.00	0.82	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	33756400.00	1.06	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	33756400.00	1.10	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	33756400.00	0.83	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	33756400.00	1.18	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	33756400.00	1.04	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	33756400.00	1.33	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	33756400.00	1.54	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	33756400.00	1.04	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	33756400.00	1.00	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	33756400.00	1.24	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR730/abundances.cxb	linc_Brn1a	0	linc_Brn1a_0	24947000.00	33756400.00	0.74	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR837/abundances.cxb	linc_Brn1a	1	linc_Brn1a_1	38529800.00	33756400.00	1.16	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1                     
##  [2] stringr_0.6.2                  
##  [3] seqbias_1.10.0                 
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0                
##  [6] Biostrings_2.30.1
```

```
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6          
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4      
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7             
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1         
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1          
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4          
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12    
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26   
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2         
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0         
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1    
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2         
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2           
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,linc-Brn1a -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/linc-Brn1a_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainM
## 2
## 3
## 4
## 5
```

linc-Brn1a KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for linc-Brn1a.

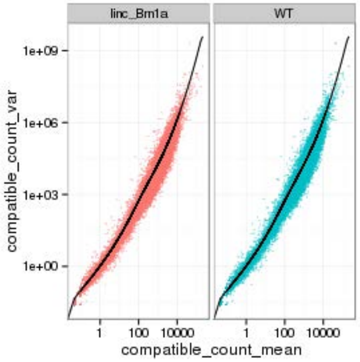
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

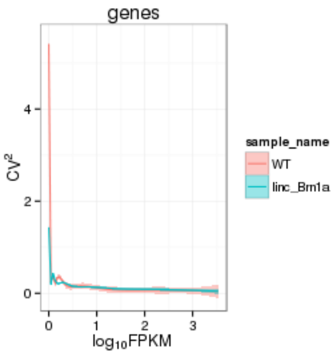
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



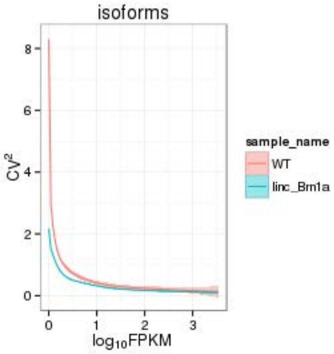
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

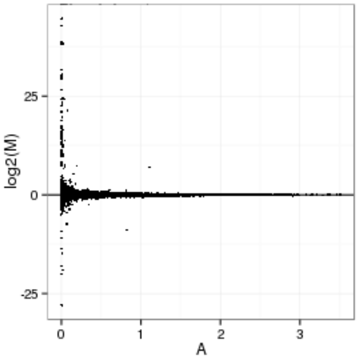
Genes:



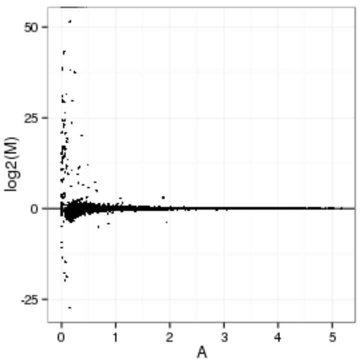
Isoforms:



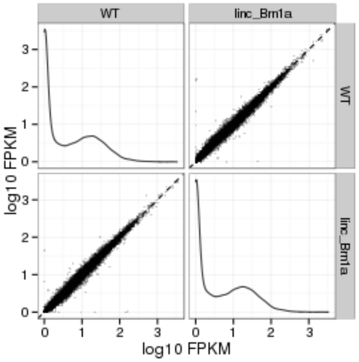
MvA plot



MvA plot counts



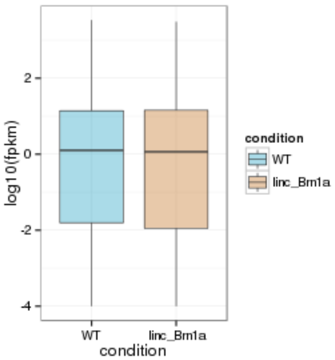
Scatterplot matrix



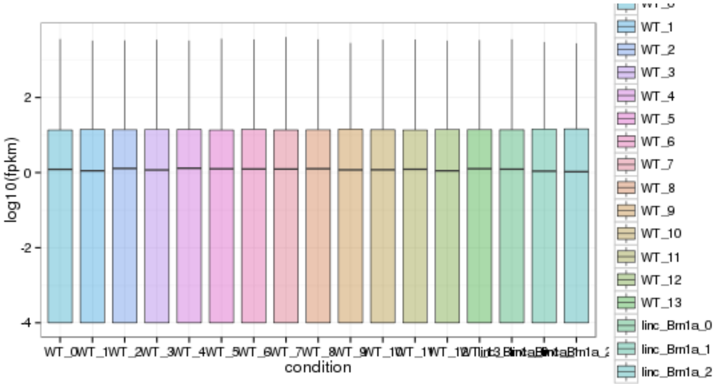
Distributions

Boxplots

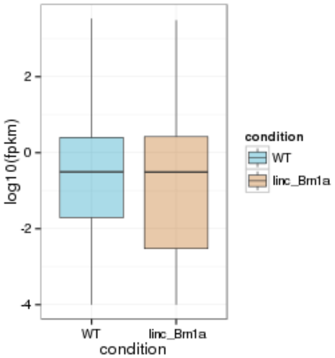
Boxplot (genes)



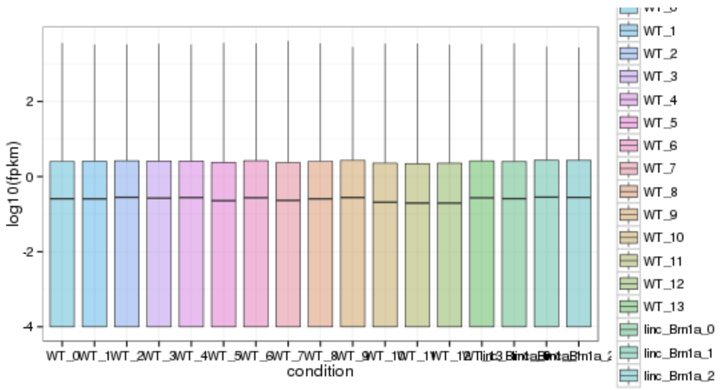
Boxplot (genes, replicates)



Boxplot (isoforms)

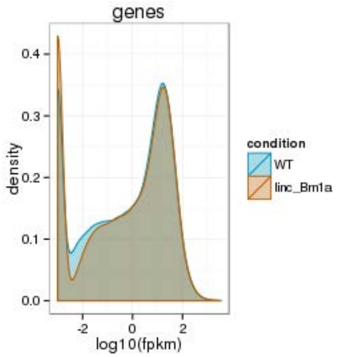


Boxplot (isoforms, replicates)

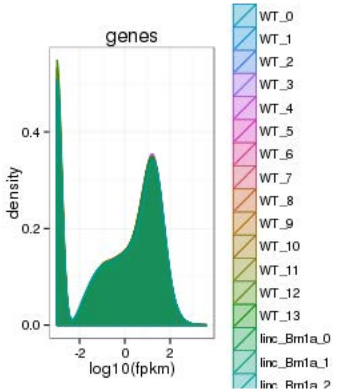


Density

Density (genes)

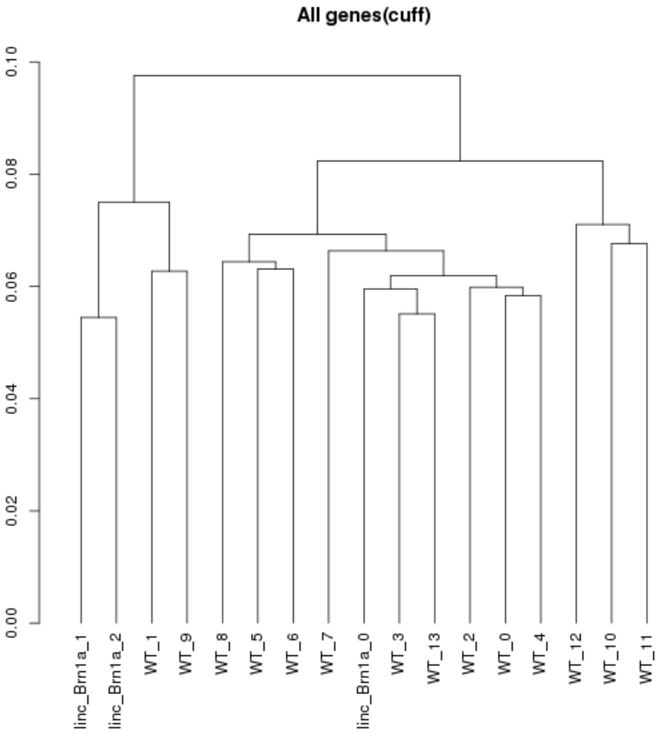


Density (genes, replicates)



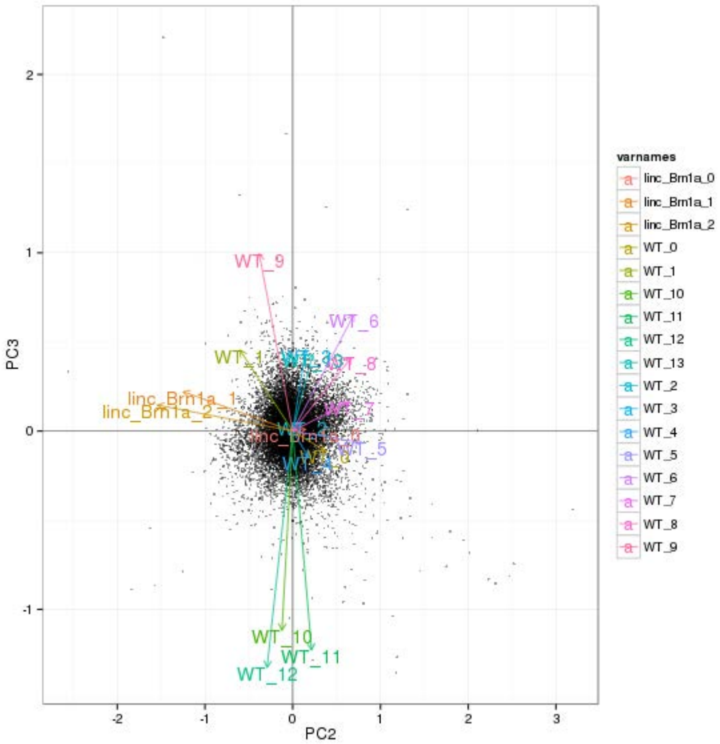
Clustering

Replicate Clusters



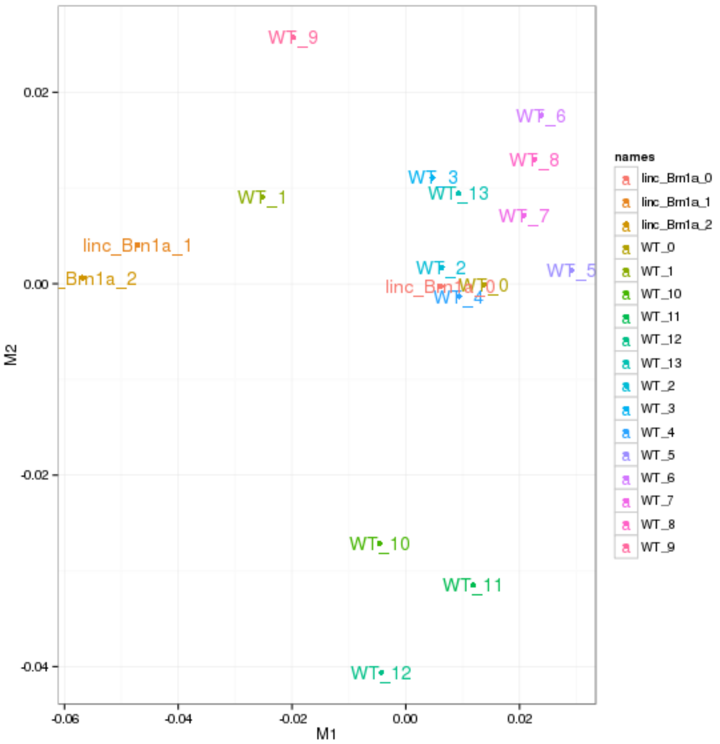
```
## NULL
```

PCA (genes)



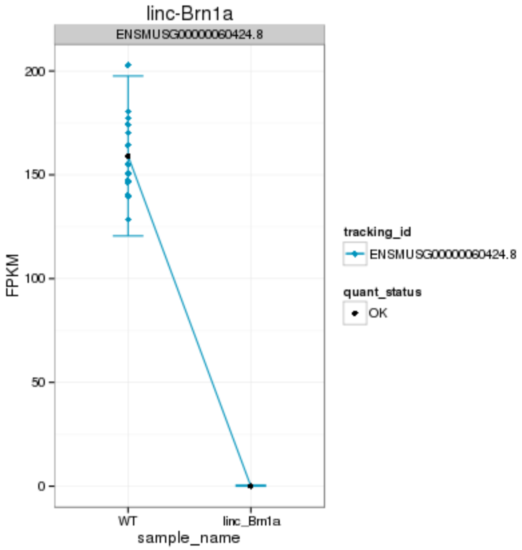
PC3
PC2
2
1
0
-1
-2
-1
0
1
2
3
WT_9
WT_6
WT_1
WT_13
WT_8
linc_Bm1a_1
linc_Bm1a_2
linc_Bm1a_0
WT_5
WT_10
WT_11
WT_12
varnames
linc_Bm1a_0
linc_Bm1a_1
linc_Bm1a_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

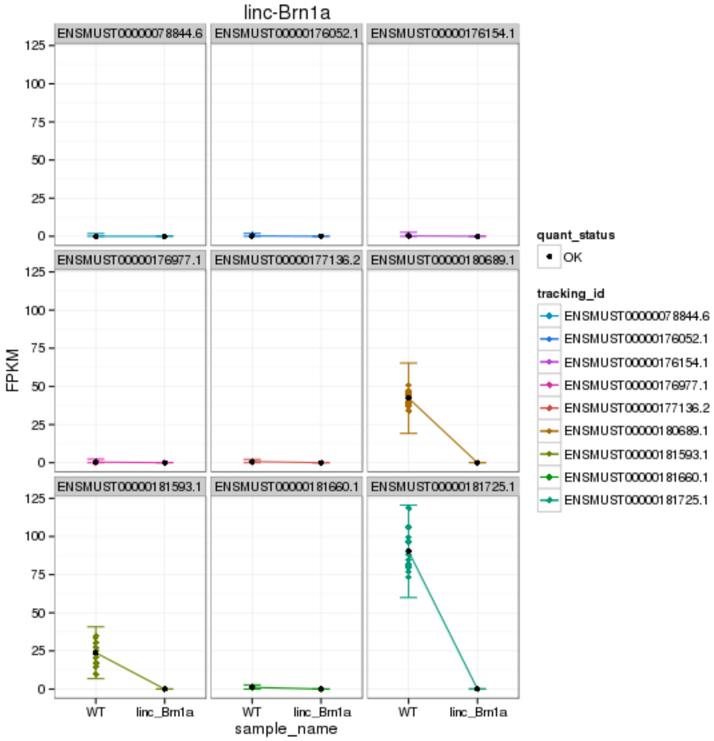


KO assessment

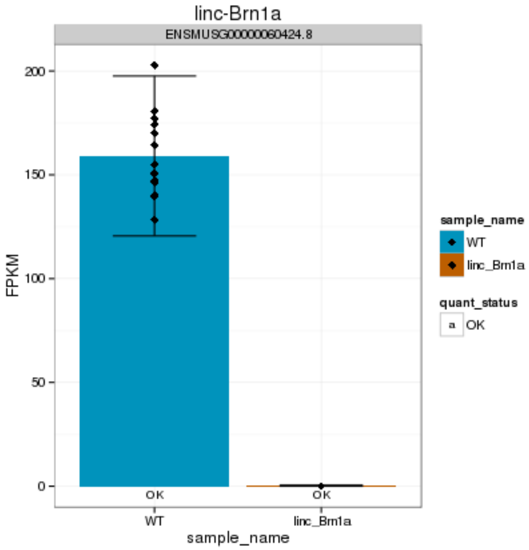
Endogenous lncRNA expression



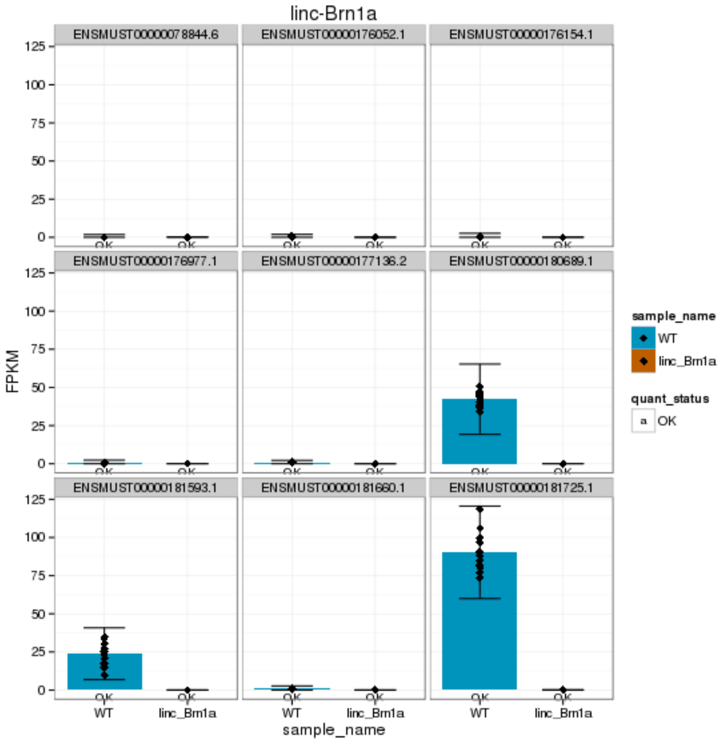
Endogenous expression of linc-Brn1a isoforms:



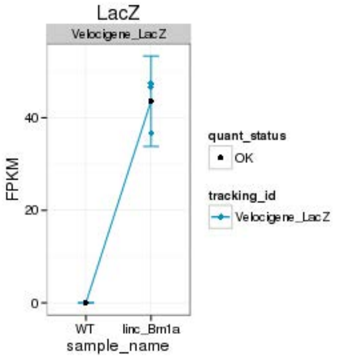
Barplot of gene expression:

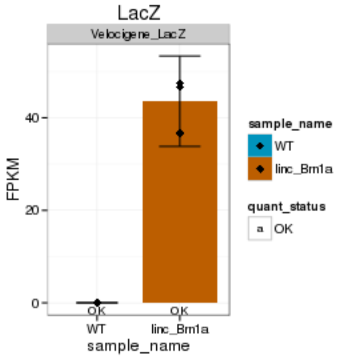


Barplot of isoform expression:



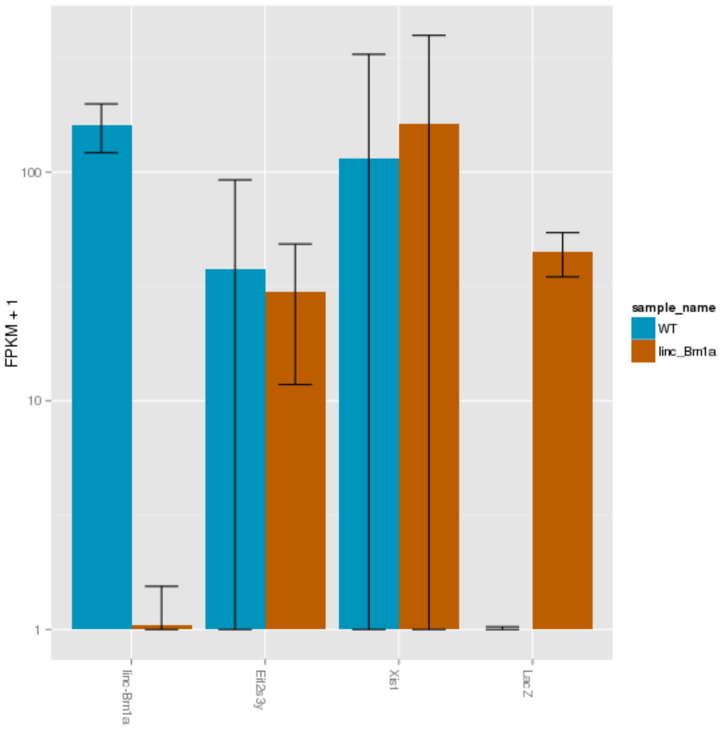
LacZ expression



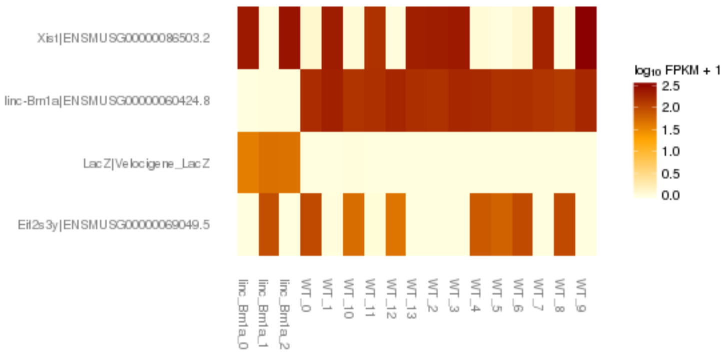


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

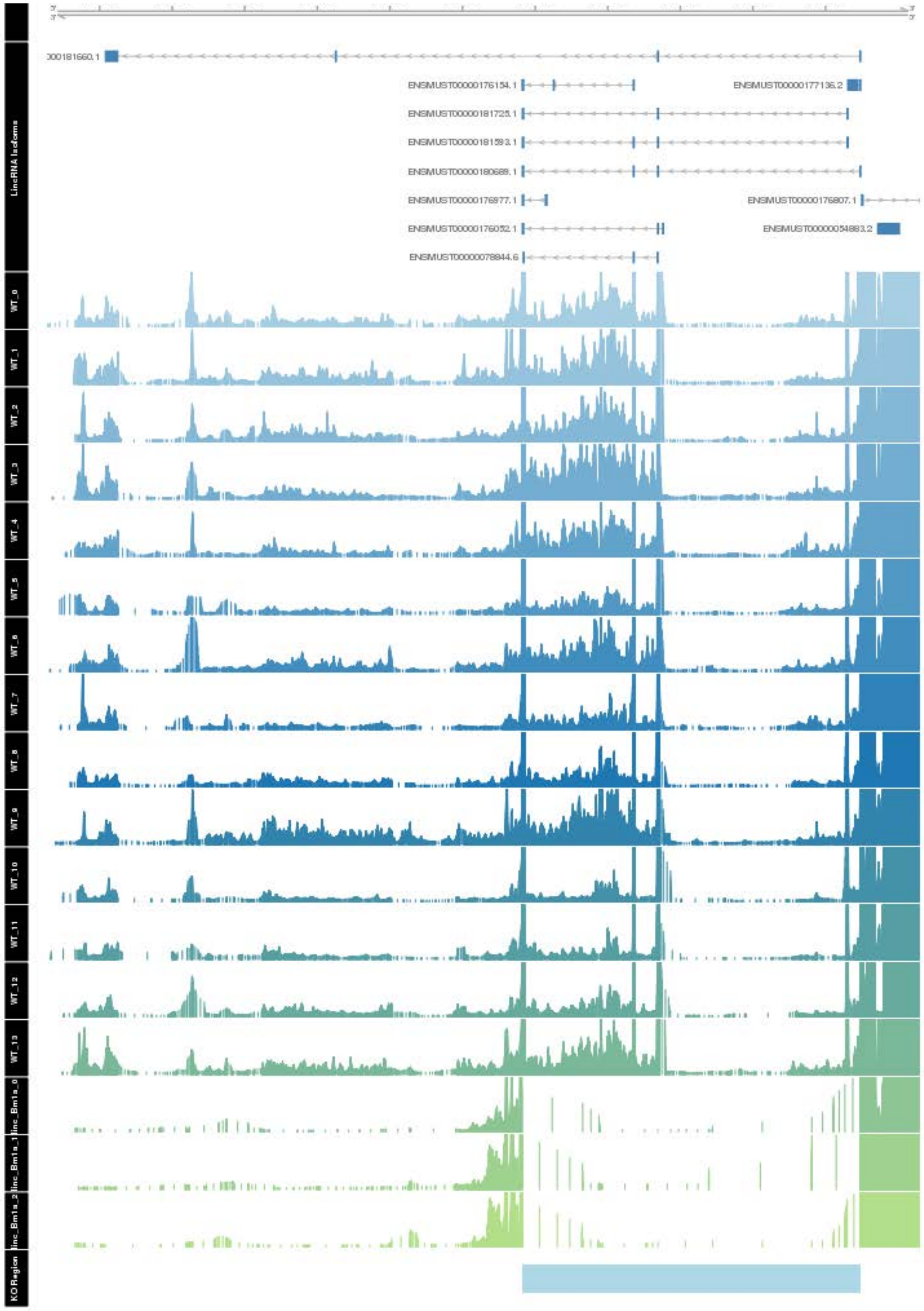
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


LincRNA Isoforms
000181660.1
ENSMUST00000176154.1
ENSMUST00000177136.2
ENSMUST00000181725.1
ENSMUST00000181593.1
ENSMUST00000180689.1
ENSMUST00000176977.1
ENSMUST00000176807.1
ENSMUST00000176052.1
ENSMUST00000054883.2
ENSMUST00000078844.6
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
linc_Bm1a_0
linc_Bm1a_1
linc_Bm1a_2
KO Region

Differential Analysis

Differential Genes

There are 1536 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	H19
2	Nalcn
3	Lhx2
4	Cdh1
5	Ckmt1
6	Sox9
7	Sema4f
8	Hk2
9	Rpa1
10	S100a6
11	Col6a1
12	Pcnt
13	Uhrf1
14	Gabrg1
15	Ckb
16	Sp1
17	Fndc5
18	Ube2c
19	Nkx2-1
20	Col1a1
21	Foxm1
22	Smo
23	Fbxo7
24	Folr1
25	Slc1a5
26	Pnck
27	Spag5
28	Tead3
29	Dbf4
30	Rec8
31	Baz1b
32	Chaf1a
33	Mcm2
34	Kcnn1
35	Ppp1r17
36	Cd36
37	Apoe

38 Prkar2b
39 Hmgn2
40 Cdk12
41 Slc2a3
42 Dlgap1
43 Plag1

44 Fcgrt
45 Dll3
46 Phyhip
47 Ddr1
48 Calb2
49 Snrnp200
50 Man1a
51 Hlf
52 Grm3
53 Brinp2
54 Ptrf
55 Dnmt1
56 Cacna1e
57 Kifc2
58 Pax2
59 Eno2
60 Utp20
61 9330159F19Rik
62 Sst
63 Ndrg2
64 Aqp1
65 Arid3b
66 Emr1
67 Chmp2b
68 Pax3
69 Lbr
70 Crabp2

71 Nes
72 Bcan
73 Slc25a18
74 Matk
75 Syt5
76 Prkacb
77 Chd5
78 Wisp1
79 Ndrg1
80 Polr2a

81	Spc25
82	Slc1a6
83	Slc1a3
84	Nid1
85	Mcm5
86	Asf1b
87	Mef2c
88	Pan2
89	Ampd3
90	Pvalb
91	Slc30a4
92	Reep5
93	Otx1
94	Fam131c
95	Vax1
96	Cdc20
97	Neurl1a
98	Epha2
99	Slc4a1
100	Nphs1
101	Pola1
102	Gmnn
103	Cdk4
104	B4galnt1
105	Tph2
106	Klk4
107	Syngr3
108	Pole
109	Pcdha2
110	Tinf2
111	Tgfbr1
112	Khsrp
113	Rplp1
114	Fhl2
115	Rbfox1
116	Ewsr1
117	Bcl2l13
118	Fam163b
119	Slc16a12
120	Syn2
121	Nuak2
122	Slc38a3
123	Pifo

124 Raver1
125 Eya4
126 Myt1
127 Lmbr1
128 Odc1
129 Sptbn4
130 Gltp
131 Kif11
132 Phox2b
133 Enkd1
134 Igf2bp1
135 Aldh1a2
136 Cad
137 Dll1
138 Ptgds
139 Slc25a13
140 Ube2i
141 Nolc1
142 Abca1
143 Cd83
144 Hivep2
145 Anp32e
146 Eps8
147 Tnr
148 Rxrg
149 Ncapg
150 Stk32c
151 Celsr1
152 Slc25a5
153 Eef1a2

154 Mapkapk2
155 Phf21b
156 Matn4
157 Il13ra1
158 Rnd3
159 Brca1
160 Vtn
161 Traf4
162 Aldoc
163 Timp2
164 Rarb
165 Cdc6
166 Atad5

167 Zfp334
168 Rhbdl3
169 Birc5
170 Wfdc2
171 Mmp9
172 Slc12a7
173 Mybl2
174 Rac3
175 Erbb3
176 Mfng
177 Pmp22
178 Anxa6
179 Kpna2
180 Mapt
181 Glra2
182 Sparc
183 Crhr1
184 Ikzf1
185 Cbx1
186 Lhx1
187 Sfrp5
188 Sult4a1
189 E2f2
190 Cacng2
191 Scn1b
192 Lhx9
193 Syne1
194 Fbxo5
195 Nr2e1
196 Plagl1
197 Grm1
198 Perp
199 Smpdl3a
200 Fabp7
201 Nts
202 Slc6a15
203 Sim1
204 Dcn
205 Cdk1
206 Actr6
207 Tmpo
208 Kitl

209 Ahi1

210	Nedd1
211	Mtfr2
212	Stx7
213	Moxd1
214	Usp44
215	Ascl1
216	Ptprr
217	Mum1
218	Meis1
219	Tcf3
220	Cobl
221	Grb10
222	E2f7
223	Mdm1
224	Col6a2
225	Glyctk
226	Hmmr
227	Hcn2
228	Slc22a4
229	Rasgef1c
230	Sar1b
231	Nefh
232	Btg2
233	Igfbp3
234	Adcy1
235	Aebp1
236	Prr11
237	Gria1
238	Shmt1
239	Llgl1
240	Pctp
241	Fam49a
242	Fam84a
243	Id2
244	Rrm2
245	Ace
246	Rasl10b
247	Asic2
248	Slc9a3r1
249	Fam64a
250	Cygb
251	Pld2
252	Slc6a4

253 Doc2b
254 Prpf8
255 Aurkb
256 Pfas
257 Top2a
258 Higd1b
259 Pole2
260 Ptpn21
261 Ngb
262 Sptb
263 Zfp36l1

264 Efcab11
265 Ccdc88c
266 Fbln5
267 Lgmn
268 Tshz3
269 Rgs6
270 Ppp1r13b
271 Kif26a
272 Gng4
273 Ryr2
274 Amph
275 Gli3
276 Dek
277 Ogn
278 Gadd45g
279 Ror2
280 Habp4
281 Drd1a
282 Adcy2
283 Golm1
284 Trip13
285 Cep72
286 Slc6a3
287 Ocln
288 Arhgef28
289 Iqgap2
290 Elovl7
291 Depdc1b
292 Rasgrf2
293 Nln
294 Rgs7bp
295 Htr1a

296 Hcn1
297 Cdhr1
298 Dnajc9
299 Otx2
300 Slc35f4
301 Rnase4
302 Sh3bp5
303 Arhgef3
304 Gdf10
305 Xpo4
306 Ska3
307 Ints9
308 Cacna2d3
309 Wnt5a
310 Diap3
311 Pbk
312 Esco2
313 Clu
314 Ephx2
315 Stmn4
316 Ebf2
317 Bora
318 Klhl1

319 Fgf17
320 Osmr
321 Haus4
322 Ajuba
323 Psmb5
324 Efs
325 Cpne6
326 Sema5a
327 Cmbl
328 Rai14
329 Baalc
330 Csmd3
331 Cdh10
332 Shcbp1
333 Matn2
334 Kcnv1
335 Atad2
336 Sla
337 Adcy8
338 Gtse1

339 Syngr1
340 Dscc1
341 Enpp2
342 Col2a1
343 Shisa9
344 Emp2
345 Cldn1
346 Fgf12
347 Hrasls
348 Apod
349 Ly6h
350 Lynx1
351 Mapk12
352 Cd200
353 Prkdc
354 Mcm4
355 Nde1
356 Mpv17l
357 Boc
358 Sidt1
359 Slc7a4
360 Ncam2
361 Itgb5
362 Ccdc14
363 Adcy5
364 Grik1
365 Chaf1b
366 Clic6
367 Gart
368 Tmem50b
369 Ifngr2
370 Faim2
371 Racgap1
372 Krt18
373 Sncg

374 Rttn
375 Serinc2
376 Kcnk5
377 Dlx2
378 Prph
379 Cdca3
380 Tiam2
381 Thbs2

382 Smoc2
383 Pla2g7
384 Slc5a7
385 Enpp5
386 Pim1
387 Ndc80
388 Crim1
389 Cyp1b1
390 Lhcgr
391 Hn1l
392 Syt4
393 Kifc5b
394 Aqp4
395 Lama3
396 Ndfip1
397 Mal2
398 Hbegf
399 Ppp2r2b
400 Rab27b
401 Gnal
402 Lox
403 Cep192
404 Slc14a2
405 Lmnb1
406 Megf10
407 Slc22a6
408 Anxa1
409 Incenp
410 Fads3
411 Fen1
412 Tmem2
413 Stambpl1
414 Cdca5
415 Kif20b
416 Htr7
417 Gldc
418 Pola2
419 Eif1ad
420 Apba1
421 Slc1a1
422 Rcor2
423 Cep55
424 Rbp4

425 Hells
426 Aldh18a1
427 Lcor
428 Maoa

429 Pdcd11
430 Nhlrc2
431 Afap1l2
432 Ablim1
433 Hspa12a
434 Bhlhe22
435 Arhgap19
436 Lbx1
437 Kcnip2
438 Limd1
439 Itga7
440 Cdk2
441 Cdh9
442 Aatk
443 Agap2
444 Caly
445 Ifitm3
446 Lrdd
447 Dock9
448 Tk1
449 Cbx2
450 Klhl4
451 Sdc3
452 Tyms
453 Plk4
454 Gdap1
455 Itih5
456 Clec3b
457 Ccr1
458 Nrp1
459 Prkar1b
460 Snca
461 Gria4
462 Paqr8
463 Slco5a1
464 Slc40a1
465 Ica1l
466 Sgol2
467 Col3a1

468 1500015O10Rik
469 2010300C02Rik
470 Tmeff2
471 Sphkap
472 Bard1
473 2810459M11Rik
474 Nppc
475 Serpine2
476 Lypd1
477 Mcm6
478 Cfh
479 Epb4.1l5
480 Dbi
481 Cd55
482 Tnni1
483 Slc45a3
484 Pik3c2b
485 Ppfia4
486 Lamc2
487 Parp1
488 Cnih3
489 Rgs7
490 Uck2
491 Atp1b1
492 Kifap3
493 Cenpf
494 Nek2
495 Mcm10
496 Optn
497 Ddr2
498 Hsd17b7
499 Rgs5
500 Nuf2
501 Prdx6
502 Mrc1
503 Rabgap1l
504 Nr5a1
505 Prkcq
506 Mastl
507 Stxbp1
508 Traf1
509 Grb14
510 Slc4a10

511	Notch1
512	Sapcd2
513	Grin1
514	Hnmt
515	Cybrd1
516	Lrp2
517	Slc43a1
518	Kif18a
519	Pax6
520	Dut
521	Mdk
522	Wdr76
523	Lrp4
524	Lamp5
525	Snap25
526	Nusap1
527	Gfra4
528	Rad51
529	Casc5
530	Knstrn
531	Pcna
532	Bub1
533	Pdyn
534	Nkx2-2
535	Acss1
536	Gins1
537	Tpx2
538	E2f1
539	Aurka
540	Pkia
541	Rbm38
542	Snx16
543	Atp9a
544	Sall4
545	Col9a3
546	Map1lc3a
547	Mmp24
548	Dsn1
549	Rbl1
550	Tti1
551	Fam83d
552	Gnb4
553	Ect2

554 Anxa5
555 Ccna2
556 Slc7a11
557 Postn
558 Tm4sf1
559 Shox2
560 Hsd3b6
561 Hmgcs2
562 Sypl2
563 Slc6a17
564 Kcnc4
565 Neurog2
566 Gucy1b3
567 Glrb
568 Enpep
569 Cks1b
570 Pmf1
571 Iqgap3
572 Chd1l
573 Them4
574 Cdh17
575 Smc2
576 Anp32b
577 Nr4a3
578 Brinp1
579 Tnc
580 Pappa
581 Bspry
582 Mpdz
583 Tal2
584 Kif24
585 Cntfr
586 Sh3gl2
587 Prkaa2
588 Pde4b
589 Dnajc6
590 Jak1
591 Usp1
592 Dmrtb1
593 Col9a2

594 Tfap2c
595 Slc2a1
596 Ephb2

597 Kif2c
598 Plk3
599 Nasp
600 Rad54l
601 Stil
602 Pax7
603 Hpca
604 Rspo1
605 Cdca8
606 Rpa2
607 Rcc1
608 Epb4.1
609 Abcf2
610 Prom1
611 Kcnip4
612 Gpr125
613 Ablim2
614 Ppp2r2c
615 Stk32b
616 Nsg1
617 Rnf32
618 Fosl2
619 Cgref1
620 Cenpa
621 Rfc1
622 Pds5a
623 Gabra4
624 Gabrb1
625 Tec
626 Pdgfra
627 Tgfbr3
628 Spp1
629 Sparcl1
630 Hsd17b11
631 Nos1
632 Dck
633 Pf4
634 Shroom3
635 Cdkl2
636 Abcb9
637 Kntc1
638 Rimbp2
639 Uncx

640 Ung
641 Lhx5
642 Rph3a
643 Col1a2
644 Fam3c
645 Eln
646 Ezh2
647 Fezf1
648 Asns

649 Dync1i1
650 Akr1b8
651 Igf2bp3
652 Npy
653 Ptn
654 Slc13a4
655 Kel
656 Dbpht2
657 Mad2l1
658 Tgfa
659 Fbxl14
660 Cntn3
661 Chl1
662 Aldh1l1
663 Cntn6
664 Grip2
665 Slc6a13
666 Slc6a12
667 Ret
668 A2m
669 Rasgef1a
670 Dusp16
671 Emp1
672 Plbd1
673 Mgp
674 Slco1c1
675 Rad18
676 Tmtc1
677 Slc6a11
678 Cand2
679 Mbd4
680 Pianp
681 Cd9
682 Rad51ap1

683 Tspan11
684 U2af2
685 Dbx1
686 Blm
687 Hddc3
688 Idh2
689 Mfge8
690 Ndufc2
691 Ipo5
692 Kif22
693 Nupr1
694 Syt3
695 Dkk3
696 Lyve1
697 Tead2
698 Plk1
699 Rrm1
700 Mki67
701 Wee1
702 Mrgprf
703 Fgf15
704 Ano1
705 Fgf13
706 Syp
707 Slc38a5
708 Msn
709 Efnb1
710 Magee1
711 Itm2a
712 2610002M06Rik
713 Phka2
714 Gabra3
715 Ap1s2
716 Zfp92
717 Atp2b3
718 Tceal6
719 Rnf128
720 Gas6
721 Chrna6
722 Gpm6a
723 Tmem66
724 Plat
725 Sfrp1

726 Scrg1
727 Sall1
728 Itfg1
729 Irx3
730 Irx5
731 Il34
732 Cenpn
733 Mt3
734 Cntnap4
735 Gpr56
736 Rab3a
737 Cdh13
738 BC021891
739 Bean1
740 Hsd11b2
741 Jam3
742 Pdgfd
743 Thy1
744 Kirrel3
745 Cryab
746 Mpzl2
747 Robo3
748 Olfm2
749 Ldlr
750 Ccnb2
751 Anxa2
752 Kif23
753 Pkm
754 1700017B05Rik
755 Nptn
756 Mlip
757 Car12
758 Igdcc3
759 Tipin
760 Zwilch
761 Tfdp2
762 Clstn2
763 Cdc25a
764 Cspg5
765 Dclk3
766 Scn5a
767 Slco2a1
768 Topbp1

769 Thsd7a
770 Colgalt2
771 Ablim3
772 Inppl1
773 Chrm1
774 Troap
775 Pdxk
776 Ccdc85a
777 Rims3
778 Itgbl1
779 Camkv
780 Nup93
781 Rasgrp2
782 Sox10
783 Cdo1
784 C330027C09Rik
785 Cntnap3
786 Gas7
787 Mgll
788 S100b
789 Ttf2
790 Wnt6
791 Ttll4
792 Galnt9
793 4833424O15Rik
794 Snap91
795 Adamts15
796 Prss35
797 Cdc14a
798 Bai3
799 Ndn
800 Rfwd3
801 Cplx1
802 Gabrb3
803 Adra2a
804 Emx1
805 Fndc3c1
806 Recql4
807 D930015E06Rik
808 Map9
809 Gucy1a3
810 Zswim5
811 Aspm

812	9430020K01Rik
813	Gria2
814	Kcnk1
815	Fancd2
816	Rpap1
817	Fstl5
818	Polq
819	Rhov
820	Slc25a37
821	Tmem132d
822	Kif4
823	Cbl
824	Smc4
825	Ramp1
826	Barhl2
827	Gbx2
828	Slc41a2
829	Pbx2
830	Tdg
831	Fras1
832	Mfrp
833	Pcdh11x
834	BC030867
835	Nrip3
836	Larp6
837	Plvap
838	Sncb
839	Ncaph
840	Htr2a
841	Dpp4
842	Ncapd3
843	Brinp3
844	Lars2
845	Rims4
846	Arx
847	Mid1
848	Lzts2
849	Tmem98
850	Fignl1
851	Pcdh17
852	Lrfn5
853	Zswim4
854	Melk

855 Mlc1
856 Ddx11
857 Ids
858 Syt1
859 Tmem59l
860 Colec12
861 Prickle1
862 Sostdc1
863 Ska1
864 Lrrn3
865 Cep135
866 Npy1r
867 March1
868 Greb1
869 Fxyd1
870 Fxyd7
871 Aaas
872 Zcchc12
873 Tubb4b
874 Dner
875 Kif15
876 Anln
877 Dpp10
878 Plch1
879 Wnt4
880 Dna2
881 C1qa
882 C1qc
883 Neto2
884 Fzd8
885 Slc39a12
886 Wnt8b
887 Spryd3
888 Hk1
889 Sstr4
890 1110059M19Rik
891 Mgarp
892 Ppp1r14a
893 Pacrg
894 Islr
895 Clic4
896 Itih2
897 Tacc3

898 Slc9a7
899 Paqr7
900 Nov
901 Endod1
902 Vgf
903 4930427A07Rik
904 Dtl
905 Dlgap5
906 Wdhd1
907 Cldn11
908 Ckap2
909 Phyhipl
910 Ppp1r16b
911 Slc16a9
912 Ctnna1
913 Neurod6
914 Rmi2
915 Dhx38
916 Igsf9
917 Cramp1l
918 Haus6
919 2410066E13Rik
920 Kcna6
921 AW551984
922 Cdon
923 Camk4

924 Notch3
925 Cep250
926 Ncapd2
927 Glra3
928 Fau
929 Satb2
930 Ttk
931 Sv2a
932 Rgs4
933 Akap12
934 Pold1
935 Hoxb4
936 Trhr
937 Ephx1
938 Prc1
939 Tspyl5
940 Bmp6

941 Cpq
942 Myo16
943 Anpep
944 En2
945 Htr5a
946 F13a1
947 Gpr126
948 Prune2
949 Camk1d
950 Akna
951 Tekt5
952 Rbpj
953 Suv39h1
954 AF529169
955 Rnf122
956 March4
957 Neil3
958 Tspyl4
959 Cntn5
960 Mmd2
961 Grin3a
962 Tmem246
963 Strip2
964 Kcne2
965 Ncoa7
966 Ldb2
967 Ralyl
968 Slc6a5
969 Exo1
970 Cpeb2
971 Gabbr2
972 Xkr5
973 Arhgap29
974 Fam60a
975 Timeless
976 Baz2a
977 Bub1b
978 Gpr176

979 Abcc8
980 Kcns1
981 2810417H13Rik
982 Sema3d
983 Dnm3

984 Hey1
985 Cacng5
986 Cdh18
987 Cdh12
988 Prdm13
989 Necab1
990 Pitpnm3
991 C3ar1
992 Abcb1a
993 Ildr2
994 Erc2
995 Ppp1r14c
996 Rad54l2
997 St8sia4
998 Il17rd
999 Hnrnpul1
1000 Six5
1001 Reps2
1002 Atp1a3
1003 Tet2
1004 Rcc2
1005 Slc22a2
1006 Npnt
1007 Nrg3
1008 Fam117b
1009 Pif1
1010 Grid1
1011 Nbl1
1012 H2afv
1013 Dnah7b
1014 Brca2
1015 Arhgap11a
1016 Chd7
1017 Rbbp8
1018 Car8
1019 Nkx6-2
1020 Inhba
1021 Atp1b2
1022 Wrap53
1023 Rap1gap
1024 4930506M07Rik
1025 Cldn5
1026 Dicer1

1027 Pik3r1
1028 Ccnb1
1029 Gpr12
1030 Kif14
1031 Ago1
1032 Fmod
1033 Nlrp5-ps

1034 Cdc42ep4
1035 Rims1
1036 Kcnj2
1037 Mpped1
1038 Trpc5
1039 Kirrel
1040 Plekha6
1041 Myrip
1042 Abca9
1043 Ptpre
1044 Mcm3
1045 Ipo9
1046 S100a10
1047 Spidr
1048 Elmod1
1049 Foxn4
1050 Ncapg2
1051 Tbca
1052 Bend6
1053 Slc35f2
1054 Specc1
1055 Grap2
1056 Dmrt3
1057 Adora1
1058 Clspn
1059 Kcnj12
1060 Golga7b
1061 Jhdm1d
1062 Mrap2
1063 Hebp1
1064 Smg7
1065 Muc1
1066 Egflam
1067 Onecut1
1068 Smco3
1069 B3galnt1

1070 Kcnj6
1071 Tmem130
1072 E130012A19Rik
1073 Elfn2
1074 Acpl2
1075 Adamts3
1076 Diras1
1077 Dmrta1
1078 1700048O20Rik
1079 Clrn1
1080 Fam19a2
1081 Cdc25c
1082 Snhg11
1083 Shisa2
1084 Fam46c
1085 Rps2
1086 Cnrip1
1087 D3Bwg0562e
1088 Fzd1

1089 Cnpy1
1090 Ccnjl
1091 Kcnj10
1092 Fads6
1093 Syt16
1094 Napepld
1095 Ankrd34b
1096 Prkce
1097 Pcdhb7
1098 Lingo2
1099 Sox3
1100 Shroom2
1101 Lrrc3b
1102 Cenph
1103 Lhfpl2
1104 Cenpe
1105 Gprin3
1106 Bhlhe23
1107 Penk
1108 Frrs1l
1109 Olig3
1110 Dbx2
1111 Chrm2
1112 Zfp629

1113 Vwc2l
1114 Plekha7
1115 Cdc42ep2
1116 Mms22l
1117 C2cd4c
1118 Sdpr
1119 Onecut2
1120 Hpcal4
1121 Chrm3
1122 Olig1
1123 Nxph1
1124 E2f8
1125 Gsg1l
1126 Iqub
1127 Hepacam
1128 Ankle1
1129 Hs3st2
1130 Gjb2
1131 Camk2n1
1132 C77370
1133 Ticrr
1134 Hrk
1135 Olfml2a
1136 Hmga1
1137 Nxph3
1138 Ppp1r3b
1139 Fam211b
1140 Vat1l
1141 Fbl
1142 Spsb4
1143 Zfp41
1144 Fbxo41
1145 Dmrta2
1146 Helt
1147 C2cd3
1148 Mc4r
1149 Gap43
1150 Mettl21c
1151 Fam180a
1152 Rnf152
1153 Mis18bp1
1154 Cltb
1155 Fgfbp3

1156 Lix1
1157 Cdca4
1158 Diras2
1159 Tshz2
1160 Hes5
1161 Ldlrad3
1162 Pirt
1163 Tmem72
1164 Rbm15
1165 Col6a3
1166 Dmrt2
1167 Nwd1
1168 Gpr85
1169 Slitrk3
1170 Ckap2l
1171 Pou4f1
1172 Arxes1
1173 Fgfbp1
1174 Gli2
1175 Nhlh2
1176 Sp8
1177 Igf2
1178 Myof
1179 Rhno1
1180 Rpl29
1181 Lonrf2
1182 Vstm2a
1183 Neurog1
1184 Cdca2
1185 Atp13a5
1186 Nrsn1
1187 Rapgef4
1188 Oxtr
1189 Frmd3
1190 Frmpd4
1191 Lrp1b
1192 Kcnk3
1193 Scn3b
1194 Zfp219
1195 Rps23
1196 Lingo1
1197 Grm5
1198 Crh

1199 Armcx4
1200 Fam26e
1201 2610318N02Rik
1202 H2afx
1203 Ankrd55
1204 Hic2
1205 Fzd2
1206 Neto1
1207 Lgals3
1208 Tcf19
1209 Pcdh20
1210 Adra1b
1211 Trhde
1212 Vstm4
1213 Emilin3
1214 Scg2
1215 Sgms2
1216 Gja1
1217 Kcns2
1218 Lin28a
1219 Olfml1
1220 P4ha3
1221 Lingo3
1222 Mblac2
1223 Sv2c
1224 Ercc6l
1225 Gen1
1226 Msrb3
1227 Nhlh1
1228 4930422G04Rik
1229 Gfod1
1230 Ncald
1231 Plagl2
1232 Kcnj16
1233 Arhgef39
1234 Map3k19
1235 Mest
1236 Sox6
1237 Xkr4
1238 Slc6a7
1239 Zfp217
1240 Sema5b
1241 Hbb-y

1242	Hbb-bh1
1243	Gpr17
1244	Hbb-bs
1245	Dlg2
1246	Lrrtm4
1247	Jun
1248	Reep1
1249	Dnah6
1250	Prkcb
1251	Gas1
1252	Ube2ql1
1253	Sv2b
1254	Yap1
1255	E330013P04Rik
1256	Rnf26
1257	Gsx1
1258	Mapk11
1259	Ptprt
1260	Arhgap20
1261	Aldh1a1
1262	AI854703
1263	Phgdh
1264	Kdm3a
1265	Kcnip1
1266	Plxnb1
1267	Exoc6
1268	Ppfia2
1269	Cnn3
1270	6330403A02Rik
1271	Tmem179
1272	Nt5dc3
1273	Skp2
1274	Spock3
1275	4922502B01Rik
1276	Fgfr3
1277	Msi1
1278	Cadps
1279	Sytl5
1280	Vsnl1
1281	Slc8a1
1282	Hmgb2
1283	6330419J24Rik
1284	Tmem158

1285 Nyap2
1286 Lrtm2
1287 Cntn1
1288 Gabra5
1289 Ntrk2
1290 Nell1
1291 Maf
1292 Alk
1293 Epha6
1294 Hba-x
1295 Cdca7
1296 Gpc3
1297 Nap1l3
1298 Abcd2
1299 Car10
1300 Col8a2
1301 Synpr
1302 Lig1
1303 Adap1
1304 Pign
1305 Mpz
1306 Trnp1
1307 Fry
1308 Grm7

1309 Hmga2
1310 Pou3f4
1311 Jakmip3
1312 Hist3h2ba
1313 Magel2
1314 Slc35f3
1315 Cep110
1316 4922502B01Rik
1317 Rit2
1318 Gnai1
1319 Ldoc1
1320 A830018L16Rik
1321 Lepr
1322 Camk2b
1323 Palld
1324 Gm10036
1325 Gstm1
1326 Tspan7
1327 Espl1

1328 Spock2
1329 Nrf1
1330 Znrf2
1331 Gpc6
1332 Anks1b
1333 Gda
1334 Capn11
1335 Samd12
1336 Tubb2a
1337 Zfp516
1338 Pde1a
1339 Skap2
1340 Fam19a1
1341 Il1rapl2
1342 Hopx
1343 Fcgr3
1344 Trp53
1345 Rcan3
1346 Zfp422
1347 Ntm
1348 Alox5ap
1349 Cend1
1350 Scrt2
1351 Caln1
1352 Rnf14
1353 Dcc
1354 Hist1h4i
1355 Kcnd2
1356 Acyp2
1357 Csmd1
1358 Slc4a4
1359 Cdh3
1360 Gm10093
1361 Maml3
1362 Fiz1
1363 Acvr2b
1364 Hipk2
1365 Snrpa
1366 Sox21
1367 Pclo
1368 Mdc1
1369 Tmem91
1370 Ppp1r1b

1371 Tac1
1372 Ttr
1373 Suclg2
1374 Galntl6
1375 Myt1l
1376 Unc13c
1377 Tgif2
1378 Cks2
1379 Opcml
1380 Trank1
1381 Otof
1382 Dgkk
1383 Nsl1
1384 Sim2
1385 Mtap
1386 Kcnma1
1387 Tmem117
1388 Luzp2
1389 Cyp26b1
1390 Sema3e
1391 Jazf1
1392 Unc5d
1393 Sox11
1394 Jakmip1
1395 Crb1
1396 Slc22a8
1397 Alms1
1398 Slc24a3
1399 Gm7964
1400 Fbln2
1401 Ifi27
1402 Cntn4
1403 Clasp1
1404 Scn1a
1405 Sepp1
1406 Dhrs3
1407 Phactr4
1408 Kndc1
1409 Numa1
1410 Lefty2
1411 Psg16
1412 Gm10184
1413 Cntnap5b

1414 Hes6
1415 Xpo5
1416 Lgi1
1417 Foxd3
1418 Ppp1r3c

1419 Cbln4
1420 Pcna-ps2
1421 Cenpm
1422 Ninl
1423 Col8a1
1424 Gm608
1425 Slc4a5
1426 Cep152
1427 Gpr88
1428 Trp53i11
1429 Celsr2
1430 Psrc1
1431 Col28a1
1432 Ddx3y
1433 Slc7a14
1434 Nxph2
1435 Prdm6
1436 Lyz2
1437 Nkain2
1438 Slfn9
1439 Hba-a2
1440 Ccnd1
1441 Fam217b
1442 Tmem132b
1443 Peg12
1444 Cntnap5a
1445 Gm10282
1446 Zfp804a
1447 Jund
1448 Syndig1l
1449 2410004P03Rik
1450 Rpl23
1451 Grid2
1452 Ccnf
1453 Fam84b
1454 Gm7292
1455 Sod3
1456 Drc1

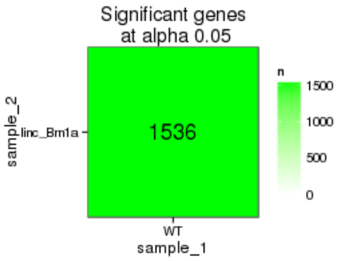
1457 Arhgdig
1458 Cep76
1459 Wdfy1
1460 5730409E04Rik
1461 4632427E13Rik
1462 Snrnp40
1463 Spc24
1464 Mafb
1465 Zcchc3
1466 Thbd
1467 Gas2l3
1468 Ctxn2
1469 Pak6
1470 Ptar1
1471 Fibin
1472 Heg1
1473 Pde11a

1474 Scn2a1
1475 Selm
1476 2700094K13Rik
1477 Gm16485
1478 Gm12184
1479 Nrarp
1480 Fam43b
1481 AI593442
1482 Aunip
1483 Hs3st4
1484 Rad54b
1485 Slc8a3
1486 Gm14446
1487 Kifc1
1488 Clec2l
1489 Prrt4
1490 Fzd10
1491 Nap1l2
1492 Ccdc85c
1493 Gm12371
1494 Gm14342
1495 D030055H07Rik
1496 9130020K20Rik
1497 Mia
1498 Ier5l
1499 Gm16586

1500 3110047P20Rik
1501 Pcp4
1502 Mndal
1503 Cdr1
1504 Gm340
1505 Hspa1b
1506 Tcerg1l
1507 Smim13
1508 D17H6S56E-5
1509 Gm19345
1510 Six3os1
1511 Gm9866
1512 Pou3f2
1513 Fignl2
1514 Sox1
1515 Kcnj11
1516 H1f0
1517 Fam181a
1518 Galntl6
1519 Gm26872
1520 AI854517
1521 Gm3764
1522 1700037F24Rik
1523 A930011O12Rik
1524 Gm17388
1525 Miat
1526 Gm5101
1527 Gm26809
1528 2810011L19Rik
1529 Gm26981
1530 Gm27032
1531 Gm17750
1532 Gm27031
1533 Pclo
1534 RP23-45G16.5
1535 KCTD12
1536 RP24-312B12.1

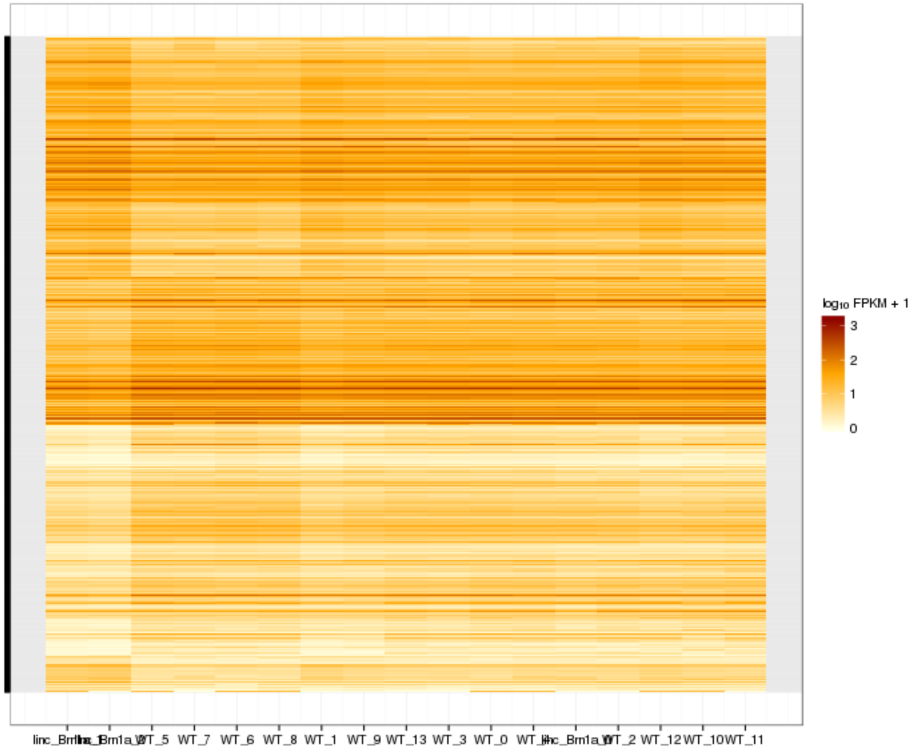
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

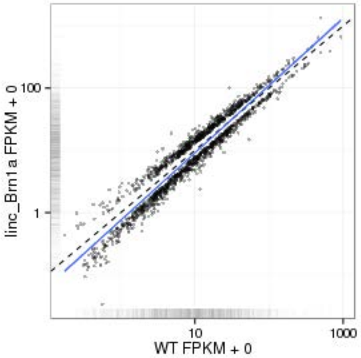


Significant genes with expression >50fpkm (any condition):(turned off)

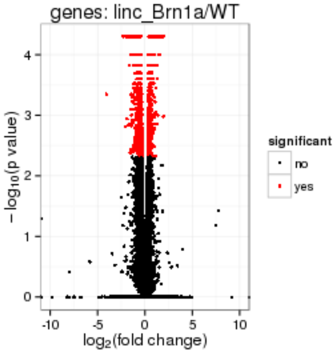
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

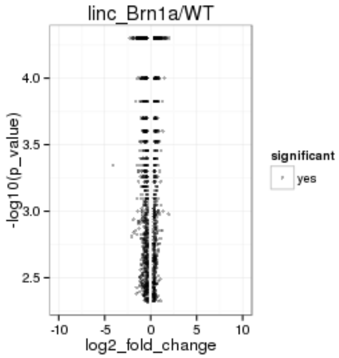
Scatter plot of significant genes only:



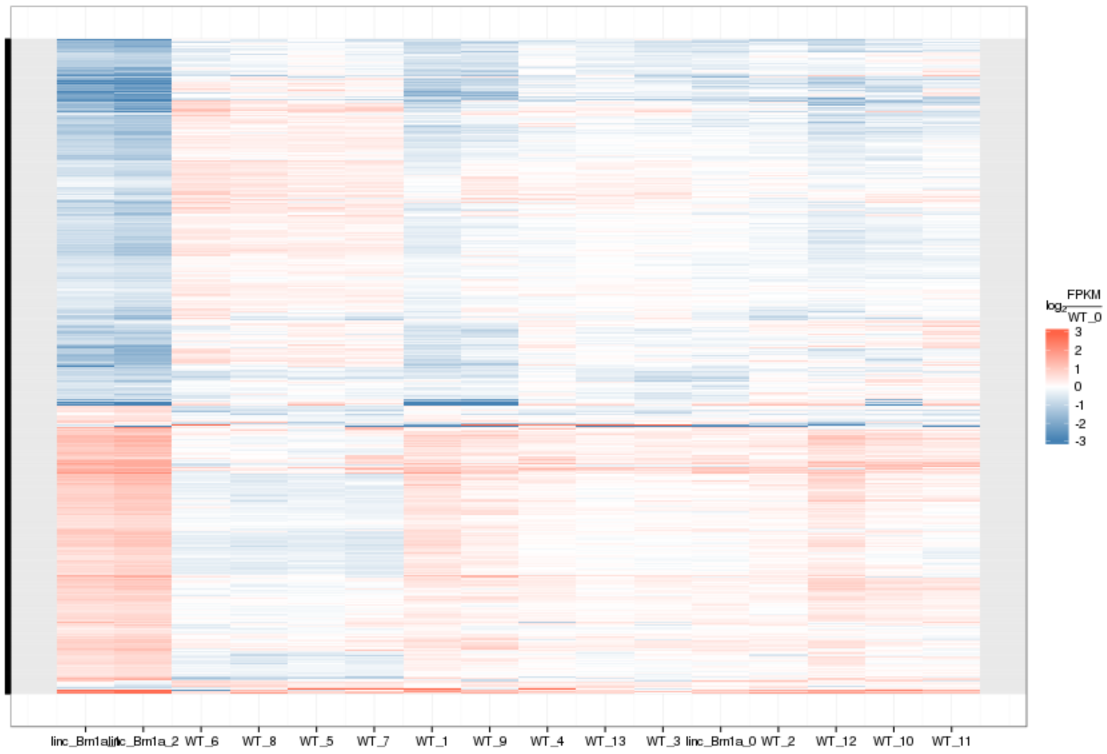
Volcano Plot



Volcano plot with significant genes only:



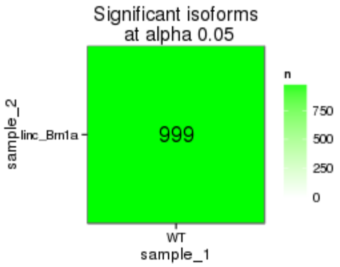
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

	isoAnnot$gene_short_name
1	H19
2	Nalcn
3	Lhx2
4	Cdh1
5	Ckmt1
6	C1d
7	Hk2
8	Rpa1
9	Snrpn
10	S100a6
11	Col6a1
12	Pcnt
13	Uhrf1
14	Gabrg1
15	Ckb
16	Ube2c
17	Col1a1
18	Foxm1
19	Smo
20	Nfix
21	Gria3
22	Spag5
23	Ccne1
24	Rec8
25	Grin2d
26	Mcm2

27 Kcnn1
28 Apoe
29 Hmgn2
30 Slc2a3
31 Dlgap1
32 Fcgrt
33 Dll3
34 Calb2
35 Snrnp200
36 Man1a
37 Hlf
38 Grm3
39 Ptrf
40 Cacna1e
41 Kifc2
42 Eno2
43 9330159F19Rik
44 Sst
45 Ndrg2
46 Aqp1
47 Chmp2b
48 Lbr
49 Crabp2
50 Nes
51 Bcan
52 Slc25a18
53 Syt5
54 Ndrg1
55 Polr2a
56 Spc25
57 Slc1a6
58 Slc1a3
59 Nid1
60 Mcm5
61 Asf1b
62 Mef2c
63 Ampd3
64 Reep5
65 Otx1
66 Fam131c
67 Cdc20
68 Slc4a1

69 Nphs1
70 Pola1
71 Gmnn
72 Tph2
73 Syngr3
74 Pole
75 Stx1a
76 Tinf2
77 Khsrp
78 Fhl2
79 Rbfox1
80 Fam163b
81 Slc16a12
82 Syn2
83 Myt1
84 Gabra1
85 Odc1
86 Kif11
87 Phox2b
88 Igf2bp1
89 Aldh1a2
90 Cad
91 Dll1
92 Slc25a13
93 Abca1
94 Cd83
95 Hivep2
96 Rxrg
97 Celsr1
98 Eef1a2
99 E2f3
100 Mapkapk2
101 Brca1
102 Vtn
103 Timp2
104 Rarb
105 Cdc6
106 Zfp334
107 Rhbdl3
108 Birc5
109 Wfdc2
110 Mmp9
111 Slc12a5
112 Slc12a7

113 Mybl2
114 Rac3
115 Erbb3
116 Mfng
117 Pmp22
118 Kpna2
119 Mapt
120 G3bp1
121 Glra2
122 Crhr1
123 Lhx1
124 Abca5
125 Sfrp5
126 Sult4a1
127 E2f2
128 Scn1b
129 Chtf18
130 Syne1
131 Fbxo5
132 Rgs17
133 Nr2e1
134 Plagl1
135 Grm1
136 Perp
137 Fabp7
138 Nts
139 Slc6a15
140 Sim1
141 Dcn
142 Cdk1
143 Tmpo
144 Kitl
145 Nedd1
146 Stx7
147 Moxd1
148 Usp44
149 Ascl1
150 Igf1
151 Egfr
152 Grb10
153 E2f7
154 Col6a2
155 Hmmr

156 Rasgef1c
157 Nefh
158 Btg2
159 Igfbp3
160 Adcy1
161 Aebp1
162 Prr11
163 Gria1
164 Fam49a
165 Fam84a
166 Id2
167 Rrm2
168 Ace
169 Fam64a
170 Pld2
171 Doc2b
172 Aurkb
173 Pfas
174 Top2a

175 Sptb
176 Cdca7l
177 Efcab11
178 Fbln5
179 Tshz3
180 Ppp1r13b
181 Kif26a
182 Gng4
183 Amph
184 Gli3
185 Gadd45g
186 Drd1a
187 Adcy2
188 Golm1
189 Slc6a3
190 Iqgap2
191 Depdc1b
192 Rasgrf2
193 Nln
194 Rgs7bp
195 Htr1a
196 Cdhr1
197 Sh3bp5
198 Arhgef3

199 Gdf10
200 Ska3
201 Cacna2d3
202 Pbk
203 Esco2
204 Clu
205 Bora
206 Fgf17
207 Haus4
208 Ajuba
209 Efs
210 Sema5a
211 Cmbl
212 Rai14
213 Cdh10
214 Shcbp1
215 Kcnv1
216 Atad2
217 Adcy8
218 Gtse1
219 Syngr1
220 Enpp2
221 Shisa9
222 Emp2
223 Cldn1
224 Fgf12
225 Apod
226 Scrib
227 Lynx1
228 Mapk12
229 Alcam
230 Pvrl3
231 Cd200
232 Slc35a5
233 Mcm4
234 Nde1
235 Boc
236 Sidt1
237 Ncam2
238 Itgb5
239 Adcy5
240 Chaf1b
241 Clic6

242 Tmem50b
243 Faim2
244 Racgap1
245 Krt18
246 Rttn
247 Serinc2
248 Kcnk5
249 Dlx2
250 Prph
251 Cdca3
252 Tiam2
253 Thbs2
254 Smoc2
255 Pla2g7
256 Sgol1
257 Slc5a7
258 Enpp5
259 Pim1
260 Ndc80
261 Cyp1b1
262 Lhcgr
263 Nrxn1
264 Hn1l
265 Syt4
266 Kifc5b
267 Ndfip1
268 Mal2
269 Ppp2r2b
270 Gnal
271 Lox
272 Cep192
273 Lmnb1
274 Slc22a6
275 Anxa1
276 Incenp
277 Fads3
278 Tmem2
279 Cdca5
280 Kif20b
281 Gldc
282 Pola2
283 Apba1
284 Slc1a1

285 Cep55
286 Hells
287 Lcor
288 Afap1l2
289 Ablim1
290 Hspa12a
291 Bhlhe22
292 Arhgap19
293 Lbx1
294 Cdk2
295 Cdh9
296 Cbx2
297 Gdap1
298 Clec3b
299 Ccr1
300 Prkar1b
301 Snca
302 Paqr8
303 Slc40a1
304 Lancl1
305 Ica1l
306 Sgol2
307 1500015O10Rik
308 Sphkap
309 Bard1
310 2810459M11Rik
311 Serpine2
312 Ngef
313 Asb1
314 Lypd1
315 Mcm6
316 Cfh
317 Dbi
318 Slc45a3
319 Pik3c2b
320 Ppfia4
321 Lamc2
322 Parp1
323 Vangl2
324 Atp1b1
325 Cenpf
326 Nek2
327 Mcm10
328 Ddr2

329 Rgs5
330 Mrc1
331 Rabgap1l
332 Prkcq
333 Mastl
334 Grb14
335 Notch1
336 Nacc2
337 Grin1
338 Rbms1
339 Cybrd1

340 Lrp2
341 Traf6
342 Cd82
343 Mdk
344 Wdr76
345 Lrp4
346 Lamp5
347 Snap25
348 Nusap1
349 Casc5
350 Pcna
351 Bub1
352 Pdyn
353 Acss1
354 Pkia
355 Snx16
356 Sall4
357 Col9a3
358 Mmp24
359 Dsn1
360 Rbl1
361 Fam83d
362 Ccna2
363 Slc7a11
364 Serpini1
365 Hmgcs2
366 Gpsm2
367 Slc6a17
368 Kcnc4
369 Neurog2
370 Gucy1b3
371 Glrb

372	Enpep
373	Cks1b
374	Pmf1
375	Iqgap3
376	Sh3d19
377	Them4
378	Cdh17
379	Anp32b
380	Brinp1
381	Zfp618
382	Tnc
383	Pappa
384	Mpdz
385	Tal2
386	Kif24
387	Sh3gl2
388	Pde4b
389	Orc1
390	Col9a2
391	Hivep3
392	Kif2c
393	Nasp
394	Stil
395	Pax7
396	Sema3c
397	Hpca
398	Cdca8
399	Sema3a
400	Rpa2
401	Mthfr
402	Prom1
403	Ppp2r2c
404	Stk32b
405	Fosl2
406	Cgref1
407	Ppargc1a
408	Cenpa
409	Gabra4
410	Gabrb1
411	Pdgfra
412	Sparcl1
413	Hsd17b11
414	Cds1

415 Nos1
416 Kntc1
417 Uncx
418 Tmem106b
419 Lhx5
420 Rph3a
421 Col1a2
422 Fam3c
423 Eln
424 Fezf1
425 Asns
426 Dync1i1
427 Akr1b8
428 Igf2bp3
429 Npy
430 Slc13a4
431 Kel
432 C130060K24Rik
433 Tgfa
434 Cntn3
435 Chl1
436 Aldh1l1
437 Grip2
438 Slc6a13
439 Ret
440 A2m
441 Rasgef1a
442 Emp1
443 Grin2b
444 Slco1c1
445 Slco1a4
446 Slc6a11
447 Cand2
448 Cd9
449 Tspan11

450 Oca2
451 Dbx1
452 Blm
453 Hddc3
454 Mfge8
455 Ndufc2
456 Kif22
457 Nupr1

458 Tead2
459 Plk1
460 Rrm1
461 Mki67
462 Wee1
463 Mrgprf
464 Fgf15
465 Syp
466 Slc38a5
467 Msn
468 Efnb1
469 Itm2a
470 Gabra3
471 Gas6
472 Plat
473 Sfrp1
474 Plekha2
475 Scrg1
476 Sall1
477 Irx3
478 Irx5
479 Cenpn
480 Mt3
481 Cntnap4
482 Gpr56
483 Cdh13
484 Hsd11b2
485 Jam3
486 Thy1
487 Acat1
488 Cryab
489 Mpzl2
490 Robo3
491 Olfm2
492 Ccnb2
493 Anxa2
494 Kif23
495 Pkm
496 Stra6
497 Nptn
498 Rasgrf1
499 Igdcc3
500 Tipin

501 Zwilch
502 Clstn2
503 Cdc25a
504 Cspg5

505 Dclk3
506 Topbp1
507 Cpne4
508 Ablim3
509 Inppl1
510 Cntrob
511 Troap
512 Pdxk
513 Ccdc85a
514 Camkv
515 Sox10
516 C330027C09Rik
517 Gas7
518 Ttf2
519 Wnt6
520 Szt2
521 Ttll4
522 Galnt9
523 4833424O15Rik
524 Snap91
525 Adamts15
526 Cdc14a
527 Rfwd3
528 Cplx1
529 Emx1
530 Fndc3c1
531 Recql4
532 Map9
533 Gucy1a3
534 Zswim5
535 Aspm
536 Kcnk1
537 Fancd2
538 Wbscr17
539 Fstl5
540 Tmem132d
541 Kif4
542 Brip1
543 Cbl

544 Ramp1
545 Barhl2
546 Six4
547 Gbx2
548 Slc41a2
549 Fras1
550 Pcdh11x
551 BC030867
552 Larp6
553 Sncb
554 Ncaph
555 Htr2a
556 Dpp4
557 Baz1a
558 Rims4
559 Klhl35
560 Pcdh17
561 Lrfn5
562 Zswim4
563 Melk
564 Ddx11
565 Syt1
566 Tmem59l
567 Zranb3
568 Sostdc1
569 Csgalnact1
570 Gng12
571 Npy1r
572 Ndrg4
573 Fxyd7
574 Aaas
575 Zcchc12
576 Dner
577 Kif15
578 Anln
579 Dpp10
580 Wnt4
581 Dna2
582 Fzd8
583 Slc39a12
584 Wnt8b
585 Spryd3
586 1110059M19Rik

587 Ppp1r14a
588 Islr
589 Clic4
590 Itih2
591 Tacc3
592 Nov
593 Endod1
594 4930427A07Rik
595 Dtl
596 Zmat4
597 Dlgap5
598 Wdhd1
599 Cldn11
600 Ckap2
601 Slc16a9
602 Neurod6
603 Rmi2
604 Igsf9
605 Cramp1l
606 Haus6
607 AW551984
608 Camk4
609 Notch3
610 Ncapd2
611 Ttk
612 Rgs4
613 Pold1
614 Hoxb4

615 Trhr
616 Bmp6
617 Cpq
618 En2
619 Htr5a
620 F13a1
621 Gpr126
622 Akna
623 Cdk5rap2
624 AF529169
625 March4
626 Neil3
627 Tspyl4
628 Cntn5
629 Mmd2

630 Grin3a
631 Rbms3
632 Strip2
633 Kcne2
634 Ldb2
635 Ralyl
636 Slc6a5
637 Bahcc1
638 Exo1
639 Cpeb2
640 Gabbr2
641 Negr1
642 Gjb6
643 Bub1b
644 Gramd1b
645 Abcc8
646 Kcns1
647 2810417H13Rik
648 Sema3d
649 Dnm3
650 Pacsin1
651 Hey1
652 Cdh18
653 Cdh12
654 Necab1
655 Erc2
656 Ppp1r14c
657 Hnrnpul1
658 Six5
659 Erf
660 Atp1a3
661 Rcc2
662 Slc22a2
663 Npnt
664 Nrg3
665 Map7d2
666 Nbl1
667 H2afv
668 Dnah7b
669 Brca2
670 Chd7
671 Rbbp8
672 Car8

673 Nkx6-2
674 Atp1b2
675 Cldn5
676 Gpr12
677 Kif14
678 Ago1
679 Fmod
680 Nlrp5-ps
681 Cdc42ep4
682 Mpped1
683 Trpc5
684 Myrip
685 Abca9
686 Mcm3
687 S100a10
688 Foxn4
689 Ncapg2
690 Bend6
691 Grap2
692 Dmrt3
693 Adora1
694 Clspn
695 Kcnj12
696 Jhdm1d
697 Hebp1
698 Muc1
699 Lrrtm3
700 Onecut1
701 Tmem130
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703 Elfn2
704 Acpl2
705 Dmrta1
706 Emx2
707 Fam19a2
708 Rnf182
709 Cdc25c
710 Snhg11
711 Shisa2
712 Fam46c
713 Cnrip1
714 D3Bwg0562e
715 Fzd1

716 Cnpy1
717 Ccnjl
718 Kcnj10
719 Syt16
720 Ankrd34b
721 Prkce
722 Lingo2
723 Sox3
724 Shroom2

725 Cenph
726 Cenpe
727 Bhlhe23
728 Penk
729 Frrs1l
730 Olig3
731 Dbx2
732 Chrm2
733 Mms22l
734 Sdpr
735 Hpcal4
736 Chrm3
737 Olig1
738 Iqub
739 Hepacam
740 Hs3st2
741 Gjb2
742 C77370
743 Ticrr
744 Hrk
745 Olfml2a
746 Nxph3
747 Ppp1r3b
748 Vat1l
749 Spsb4
750 Zfp41
751 Dmrta2
752 Cyp4x1
753 Helt
754 C2cd3
755 Mc4r
756 Gap43
757 Mettl21c
758 Rnf152

759 Lix1
760 Cdca4
761 Diras2
762 Hes5
763 Tmem72
764 Rbm15
765 Col6a3

766 Nwd1
767 Ckap2l
768 Pou4f1
769 Fgfbp1
770 Gli2
771 Nhlh2
772 Sp8
773 Igf2
774 Lonrf2
775 Vstm2a
776 Neurog1
777 Cdca2
778 Atp13a5
779 Rapgef4

780 Pcdh10
781 Frmd3
782 Zfp219
783 Htr1b
784 Rps23
785 Grm5
786 2610318N02Rik
787 H2afx
788 Fzd2
789 Neto1
790 Trhde
791 Scg2
792 Gja1
793 Kcns2
794 Prkca
795 Lin28a
796 Lingo3
797 Mblac2
798 Sv2c
799 Plcb1
800 Ercc6l
801 Gen1

802 Msrb3
803 Nhlh1
804 4930422G04Rik
805 Ncald
806 Plagl2
807 Mest
808 Klhdc1
809 Slc6a7
810 Hbb-y
811 Hbb-bh1
812 Gpr17
813 Nup188
814 Gas1
815 Jam2
816 E330013P04Rik
817 Gsx1
818 Mapk11
819 Arhgap20
820 Aldh1a1
821 Kdm3a
822 Plxnb1
823 Ppfia2
824 6330403A02Rik
825 Tmem179
826 Nt5dc3
827 Skp2
828 4922502B01Rik
829 Msi1
830 Vsnl1
831 Adam12
832 Srsf12
833 Tmem158
834 Nyap2

835 Lrtm2
836 Gabrg3
837 Gabra5
838 Ntrk2
839 Nell1
840 Maf
841 Alk
842 Hba-x
843 Cdca7
844 Gpc3

845 Nap1l3
846 Abcd2
847 9330182L06Rik
848 Car10
849 Col8a2
850 Synpr
851 Adap1
852 Pign
853 Mpz
854 Trnp1
855 Fry
856 Grm7
857 Hmga2
858 Pou3f4
859 Jakmip3
860 Magel2
861 Rit2
862 Gnai1
863 Ldoc1
864 Lepr
865 Camk2b
866 Gm10036
867 Tspan7
868 Espl1
869 Spock2
870 Znrf2
871 Gda
872 Capn11
873 Tubb2a
874 Fam19a1
875 Hopx
876 Ntm
877 Scrt2
878 Dcc
879 Hist1h4i
880 Slc9a6
881 Kcnd2
882 Csmd1
883 Slc4a4
884 Cdh3
885 Gm10093
886 Lsamp
887 Naca

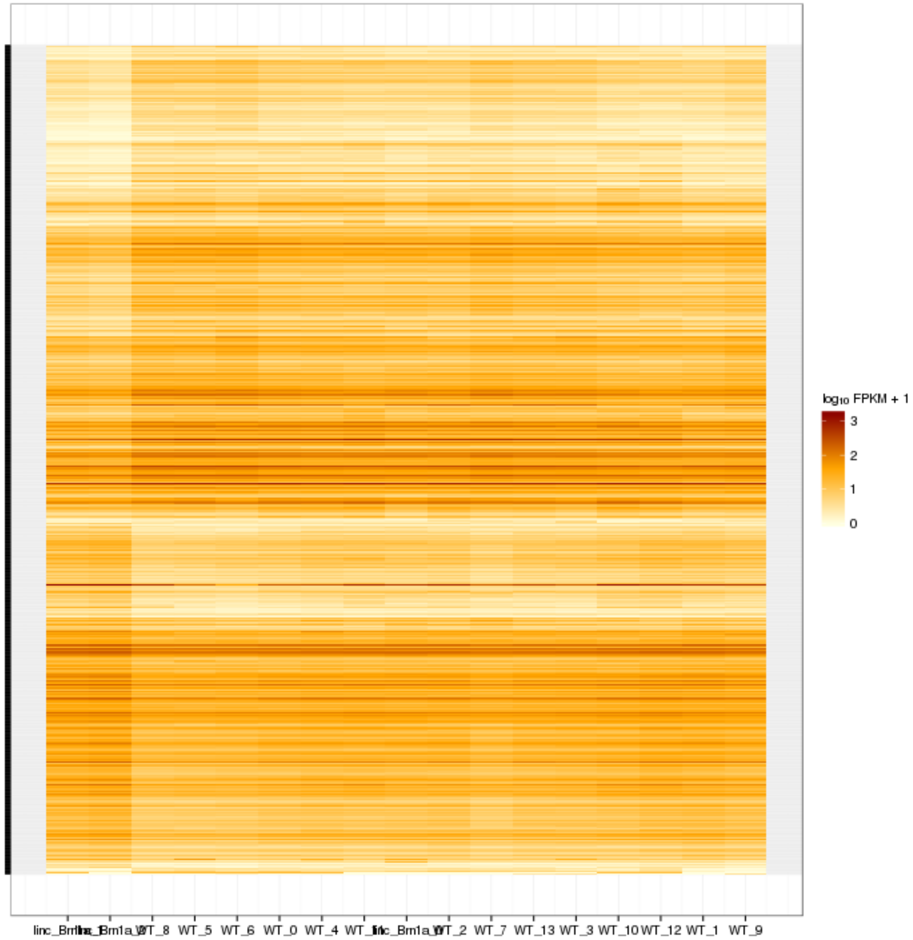
888 Tmem151a
889 Sox21
890 Mdc1
891 Ttr
892 Unc13c
893 Cks2
894 Opcml
895 Trank1
896 Nsl1
897 Sim2
898 Tmem117
899 Luzp2
900 Cyp26b1
901 Jazf1
902 Sox11
903 Jakmip1
904 Alms1
905 Slc24a3
906 Nlgn1
907 Cadm2
908 Sepp1
909 Kndc1
910 Gm10184
911 Cntnap5b
912 Hes6
913 Xpo5
914 Lgi1
915 Ppp1r3c
916 Cbln4
917 Pcna-ps2
918 Zic3
919 Ninl
920 Col8a1
921 Slc4a5
922 Cep152
923 Gpr88
924 Celsr2
925 Psrc1
926 Col28a1
927 Ddx3y
928 Slc7a14
929 Nxph2
930 Gpr98

931 Lyz2
932 Nkain2
933 Hba-a2
934 Ccnd1
935 Fam217b
936 Tmem132b
937 Peg12
938 Cntnap5a
939 Gm10282
940 Zfp804a
941 Jund
942 Syndig1l
943 Grid2
944 Ccnf

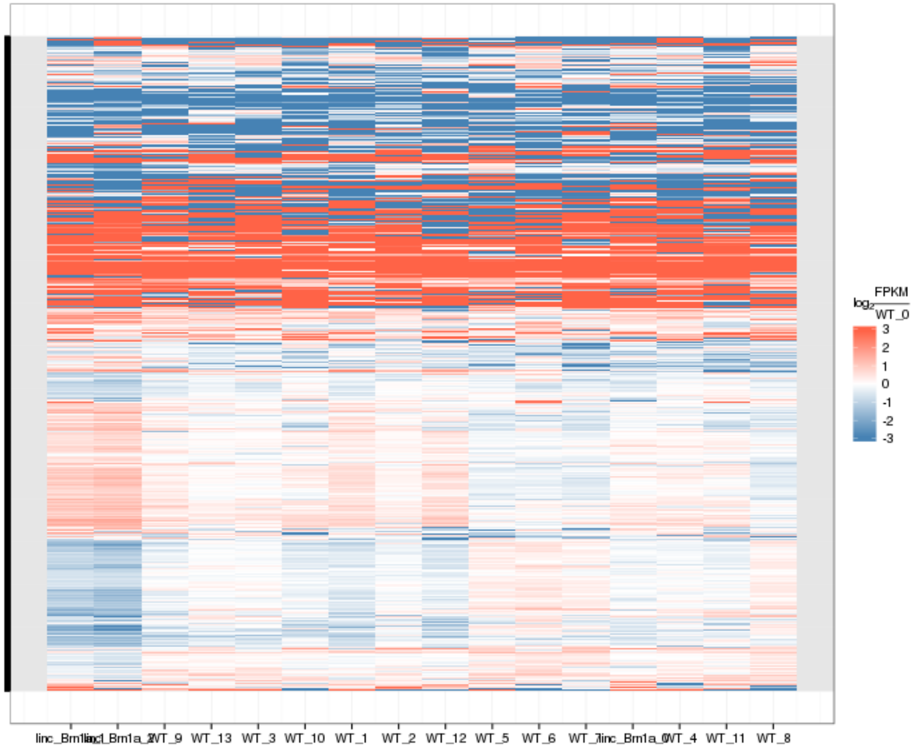
945 Sod3
946 Arhgdig
947 Mob3b
948 4632427E13Rik
949 Spc24
950 Mafb
951 Zcchc3
952 Thbd
953 Ctxn2
954 Pak6
955 Fibin
956 Gm12184
957 Nrarp
958 Fam43b
959 AI593442
960 Aunip
961 Hs3st4
962 Kifc1
963 Clec2l
964 Fzd10
965 Gm12371
966 Gm14342
967 D030055H07Rik
968 9130020K20Rik
969 Ier5l
970 Gm16586
971 3110047P20Rik
972 Pcp4
973 Mndal

974 Cdr1
975 Tcerg1l
976 D17H6S56E-5
977 Smim17
978 Pou3f2
979 H1f0
980 Fam181a
981 Galntl6
982 Gm26872
983 Miat
984 Gm5101
985 Gm26981
986 Gm17750
987 Gm27031
988 Pclo
989 KCTD12
990 RP24-312B12.1

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

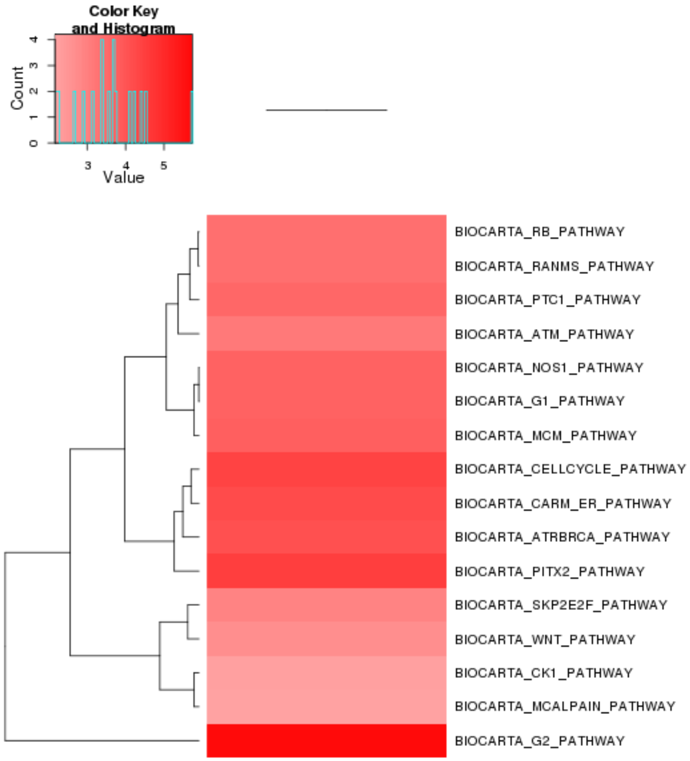
Gene/Pathway Analysis

GSEA

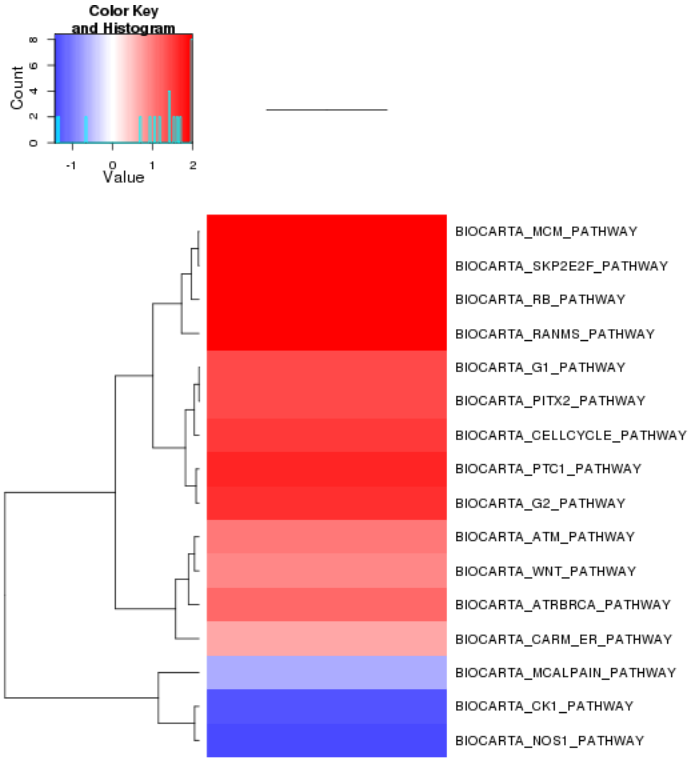
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:

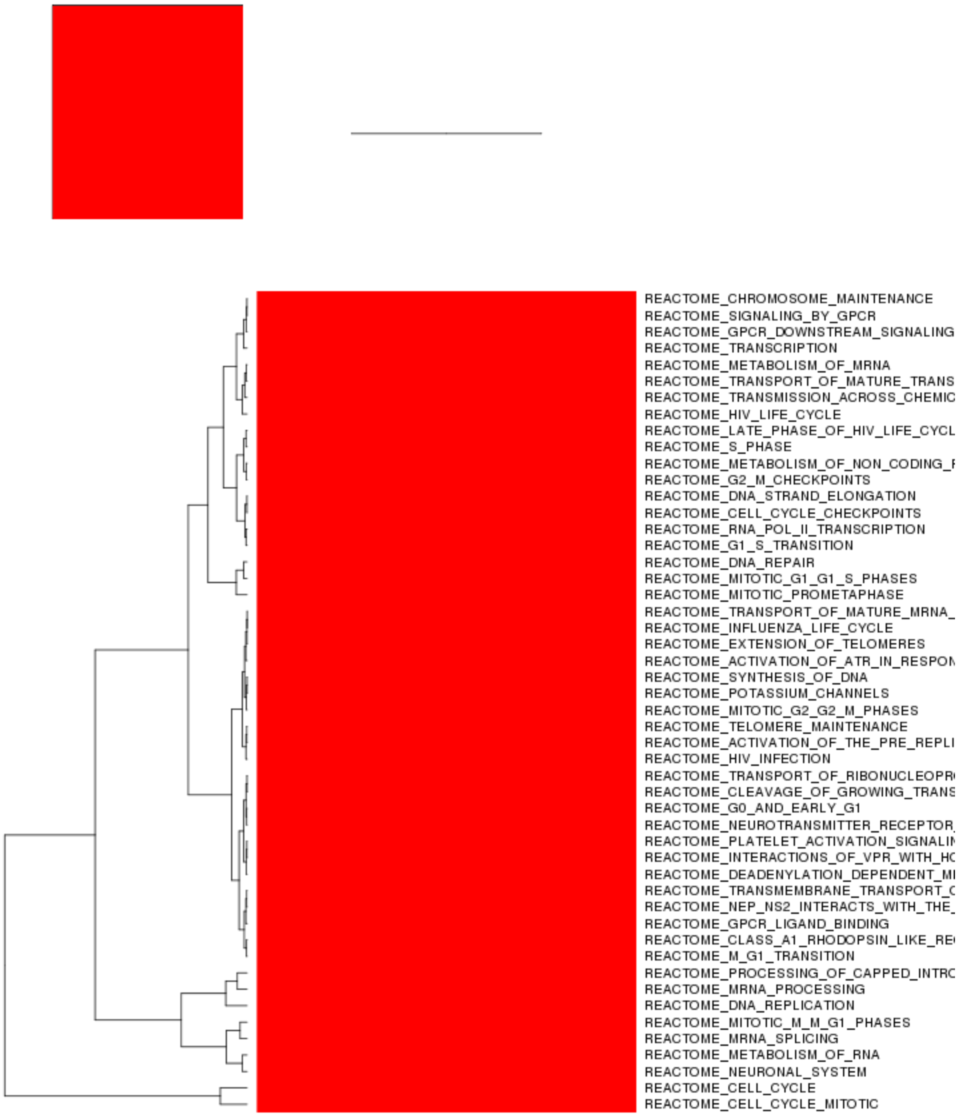


Biocarta zscore:

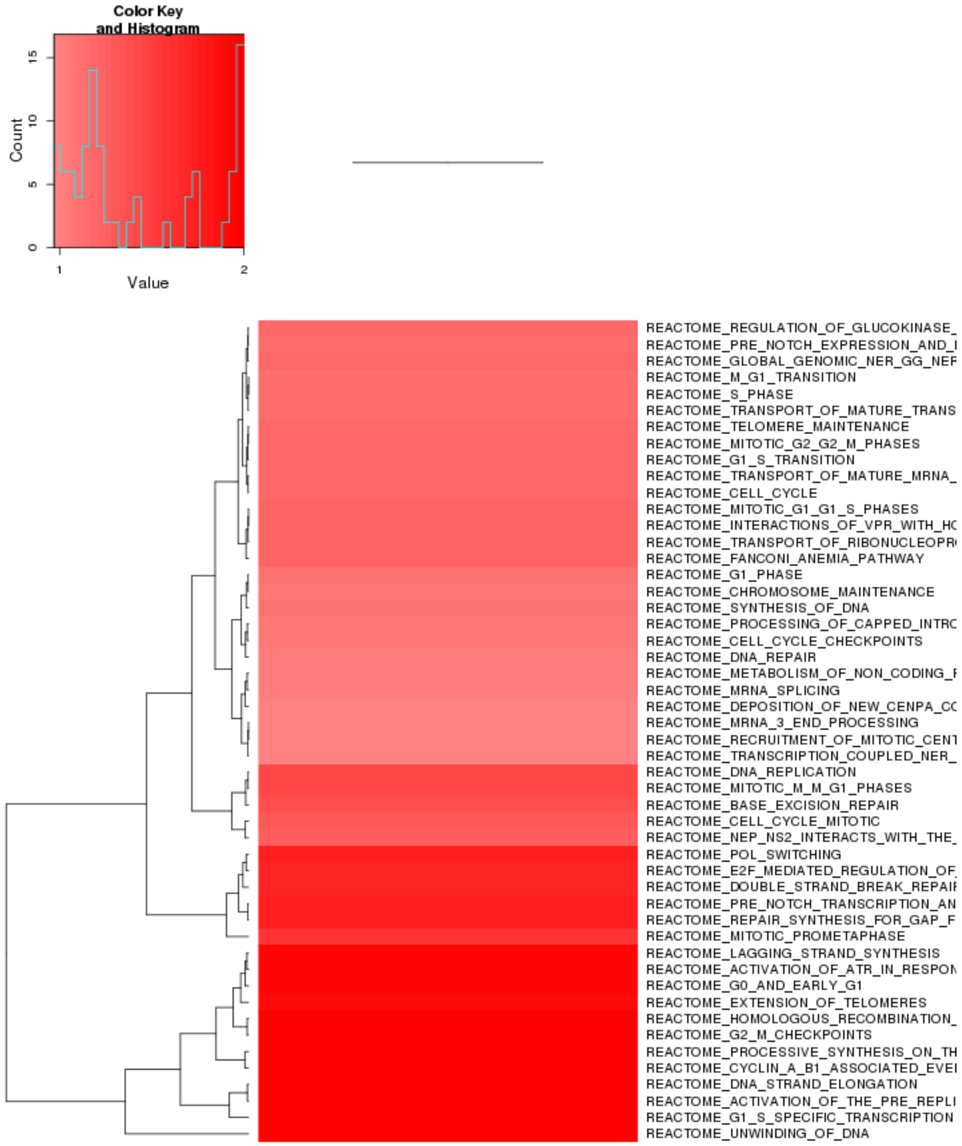


Reactome enrichment:

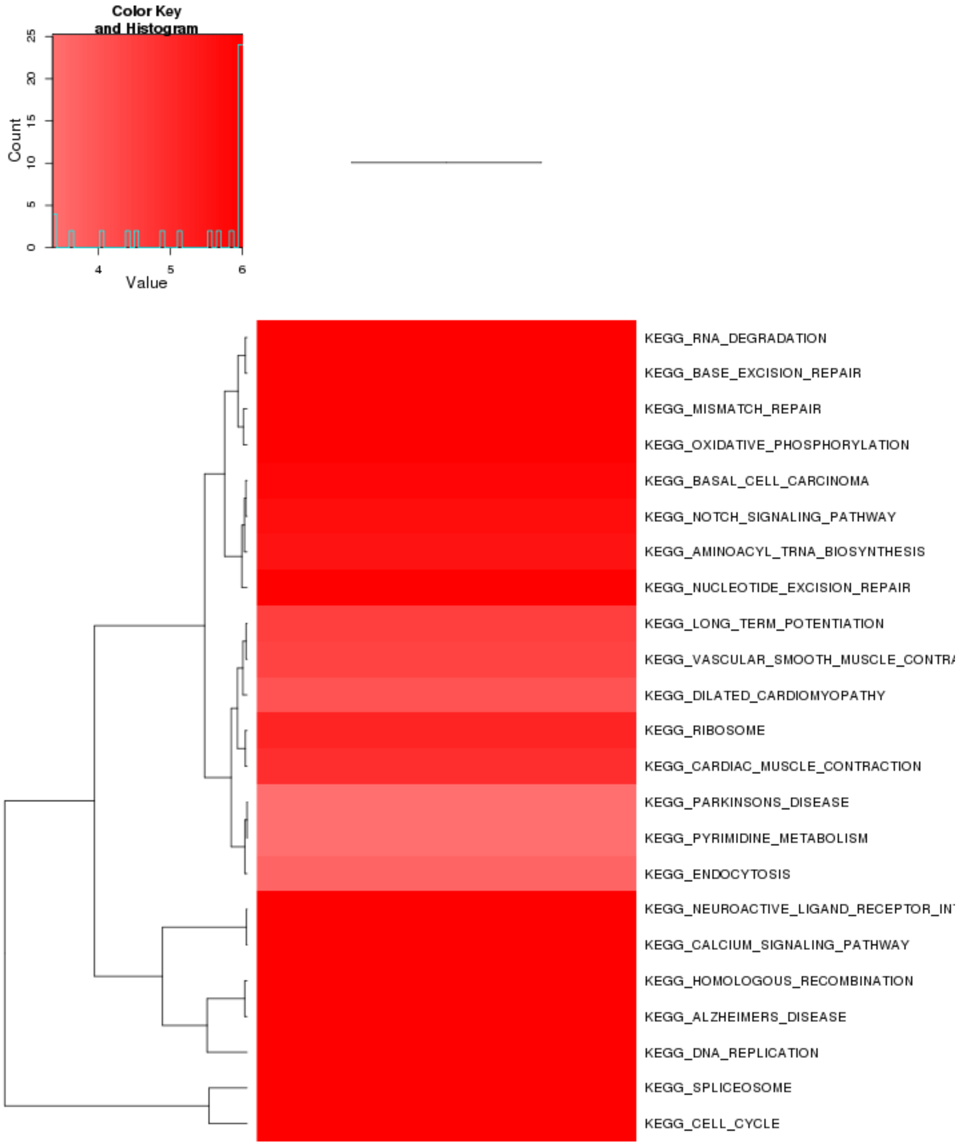
```
## Error: no locations are finite
```



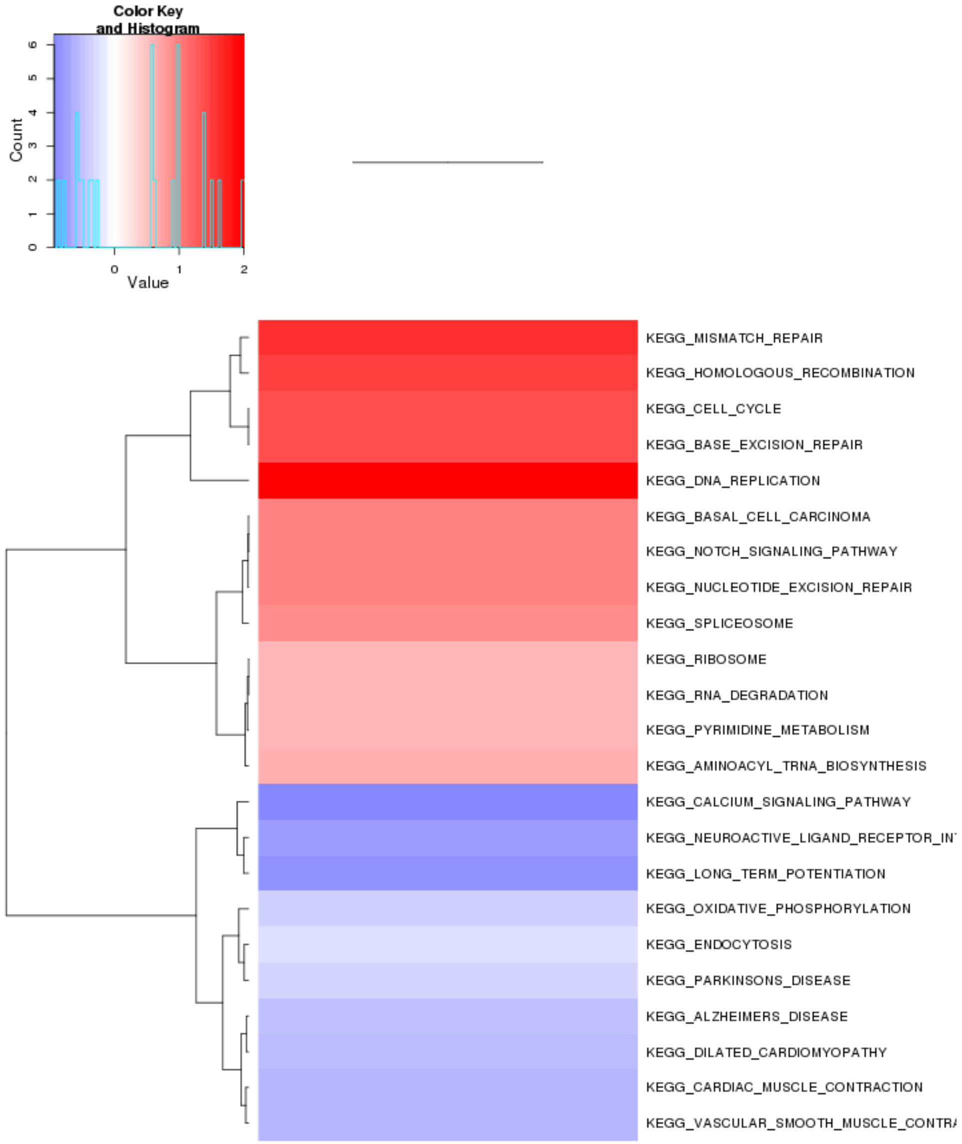
Reactome zscore:



Kegg enrichment:

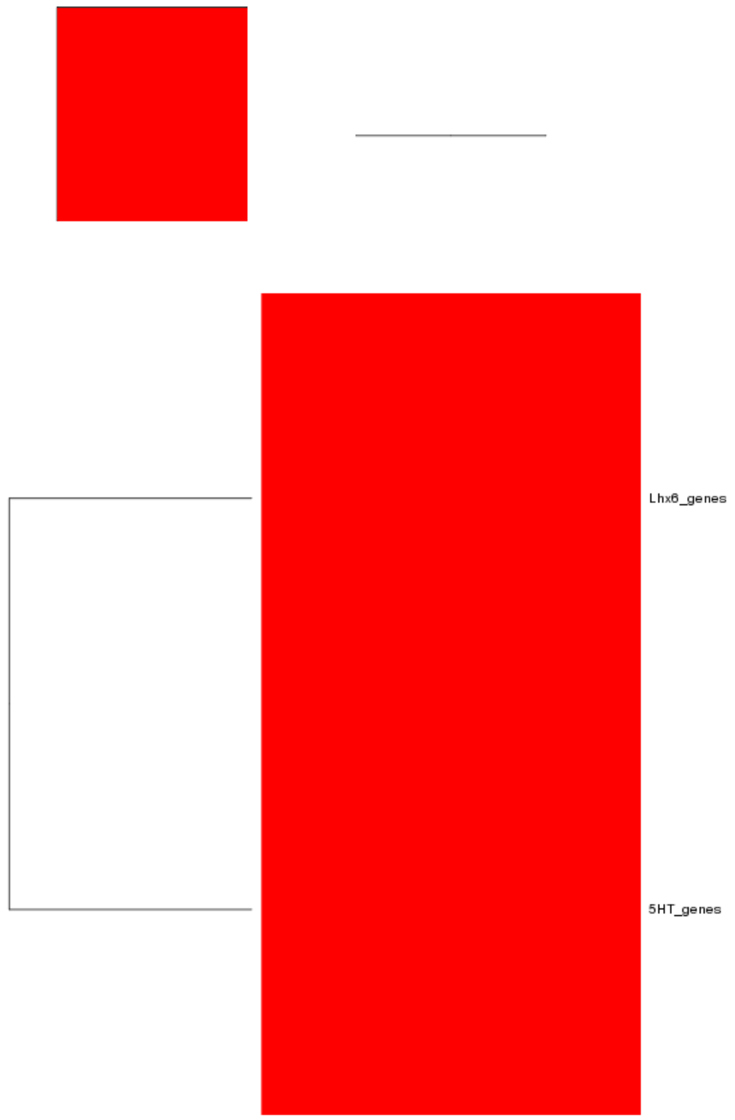

Color Key
and Histogram
Count
0
5
10
15
20
25
4
5
6
Value
KEGG_RNA_DEGRADATION
KEGG_BASE_EXCISION_REPAIR
KEGG_MISMATCH_REPAIR
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_BASAL_CELL_CARCINOMA
KEGG_NOTCH_SIGNALING_PATHWAY
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS
KEGG_NUCLEOTIDE_EXCISION_REPAIR
KEGG_LONG_TERM_POTENTIATION
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTR
KEGG_DILATED_CARDIOMYOPATHY
KEGG_RIBOSOME
KEGG_CARDIAC_MUSCLE_CONTRACTION
KEGG_PARKINSONS_DISEASE
KEGG_PYRIMIDINE_METABOLISM
KEGG_ENDOCYTOSIS
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_IN
KEGG_CALCIUM_SIGNALING_PATHWAY
KEGG_HOMOLOGOUS_RECOMBINATION
KEGG_ALZHEIMERS_DISEASE
KEGG_DNA_REPLICATION
KEGG_SPLICEOSOME
KEGG_CELL_CYCLE

Kegg zscore:

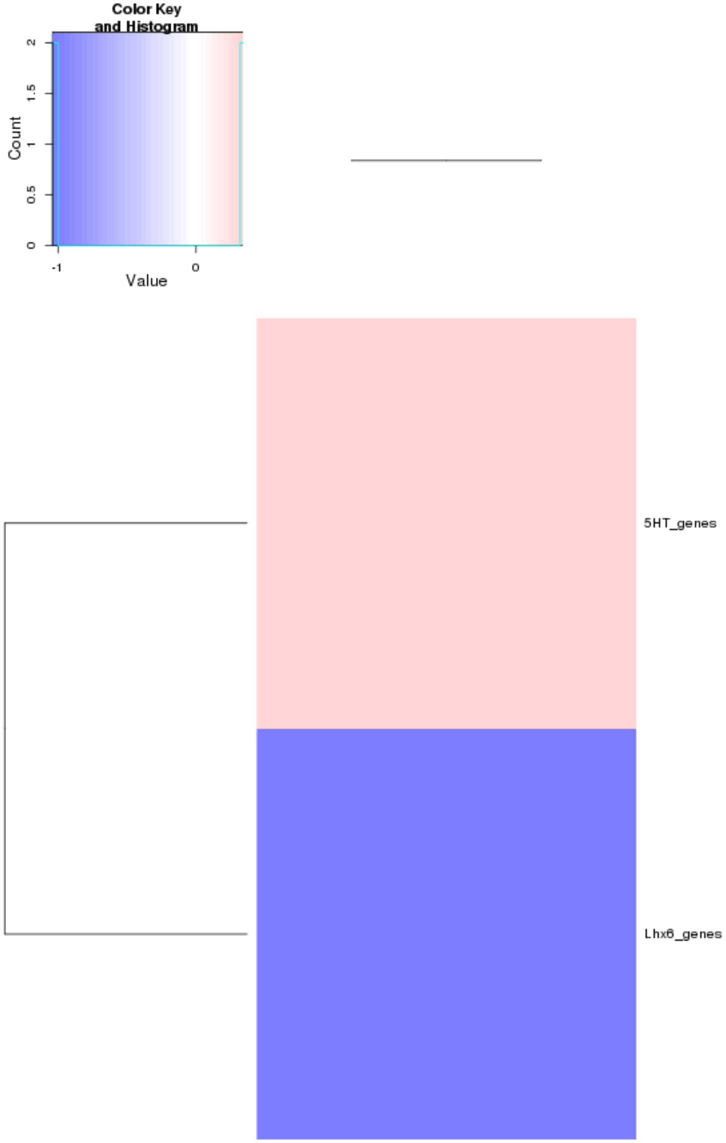


Interneuron enrichment:

```
## Error: no locations are finite
```

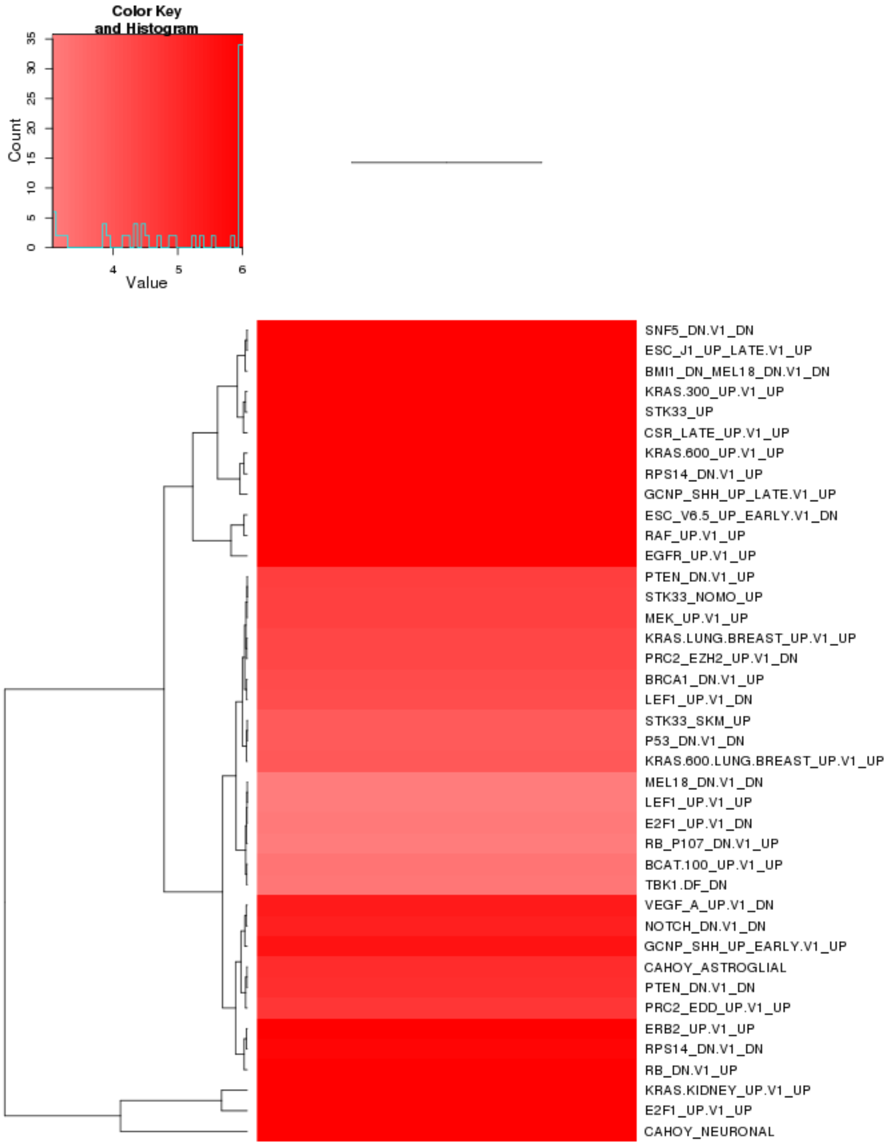


Interneuron zscore:



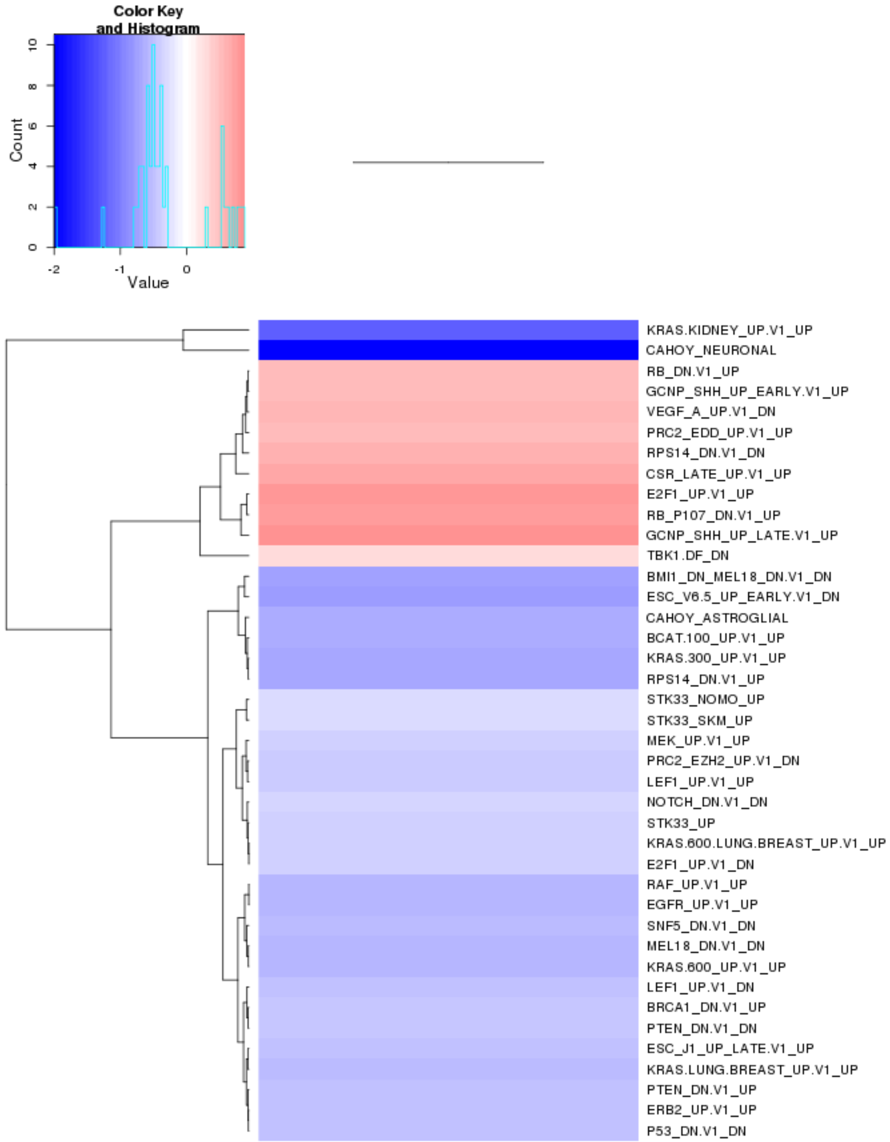
Oncogene enrichment:

```
## Error: subscript out of bounds
```



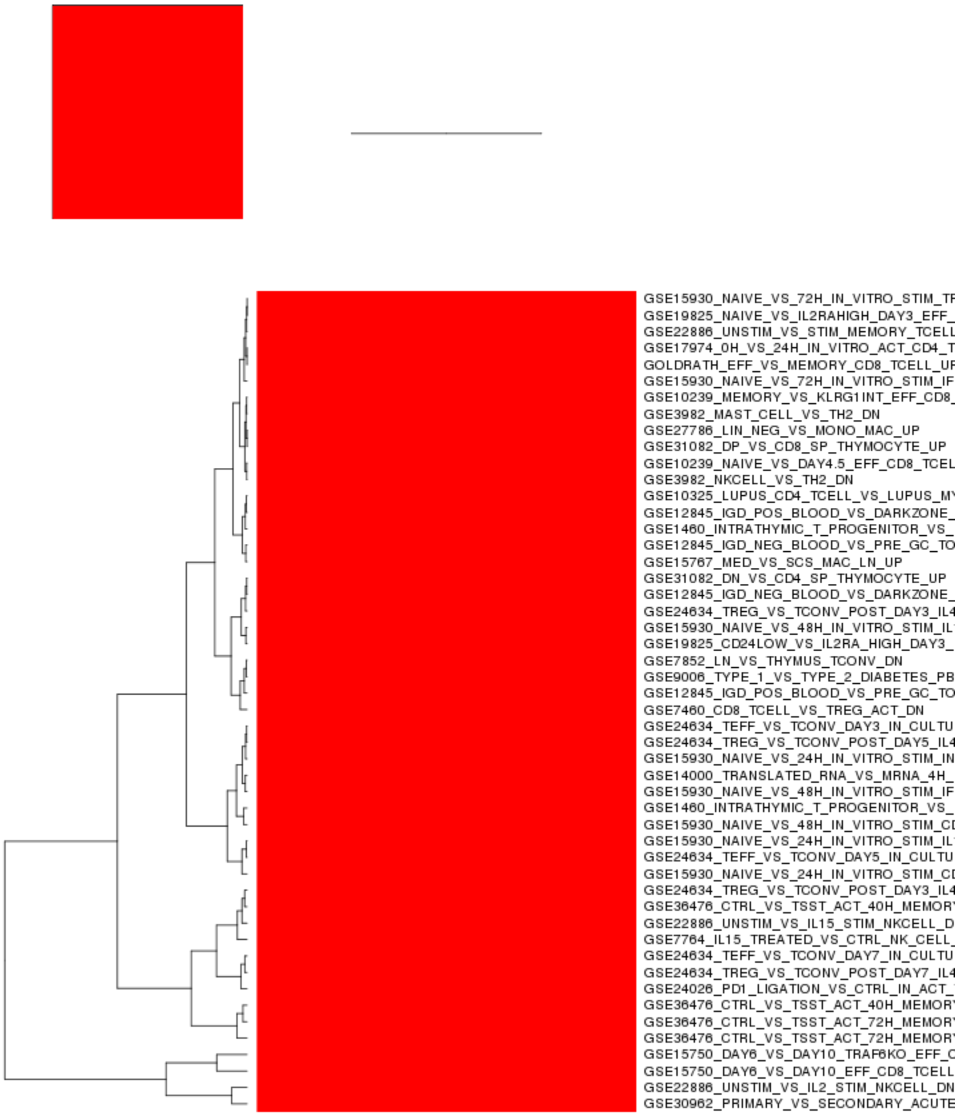
Oncogene zscore:

```
## Error: subscript out of bounds
```

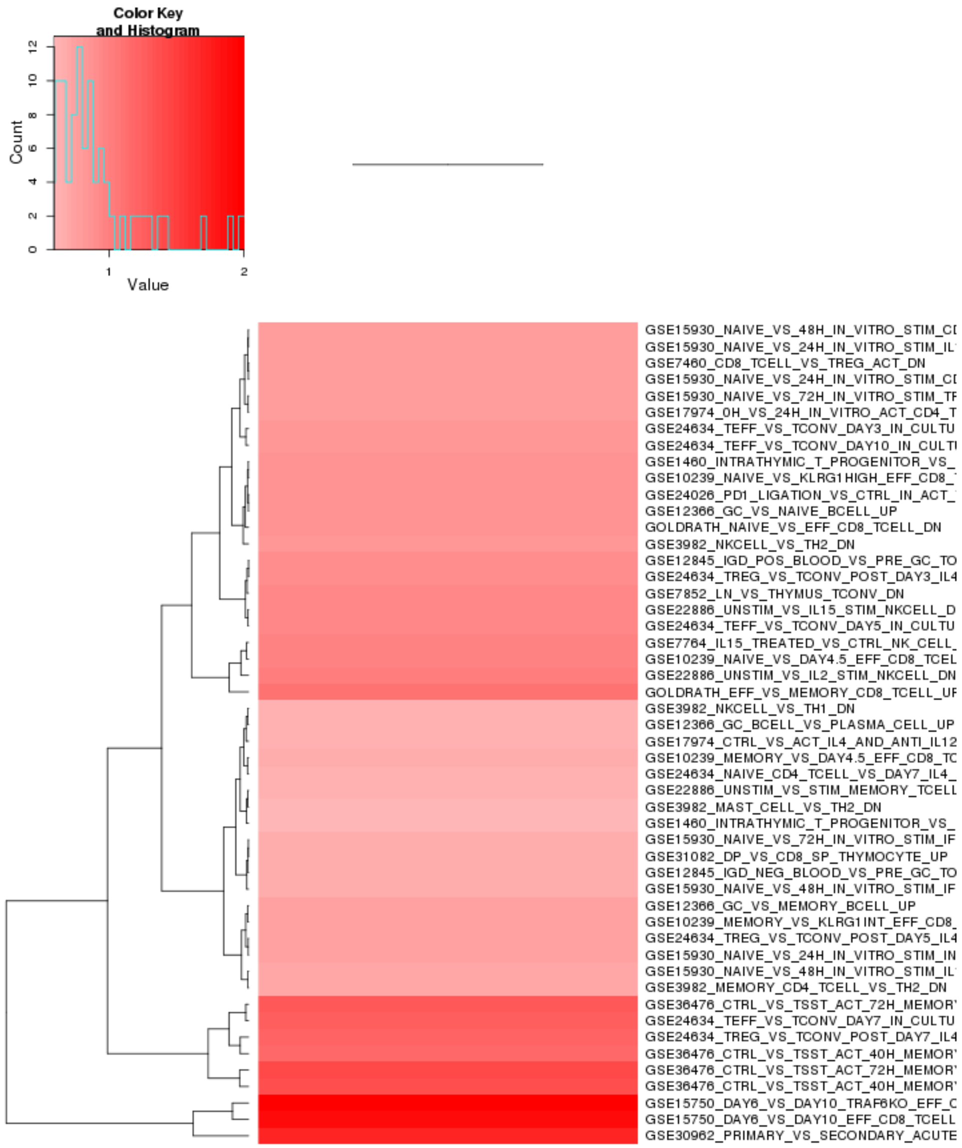


Immuno enrichment:

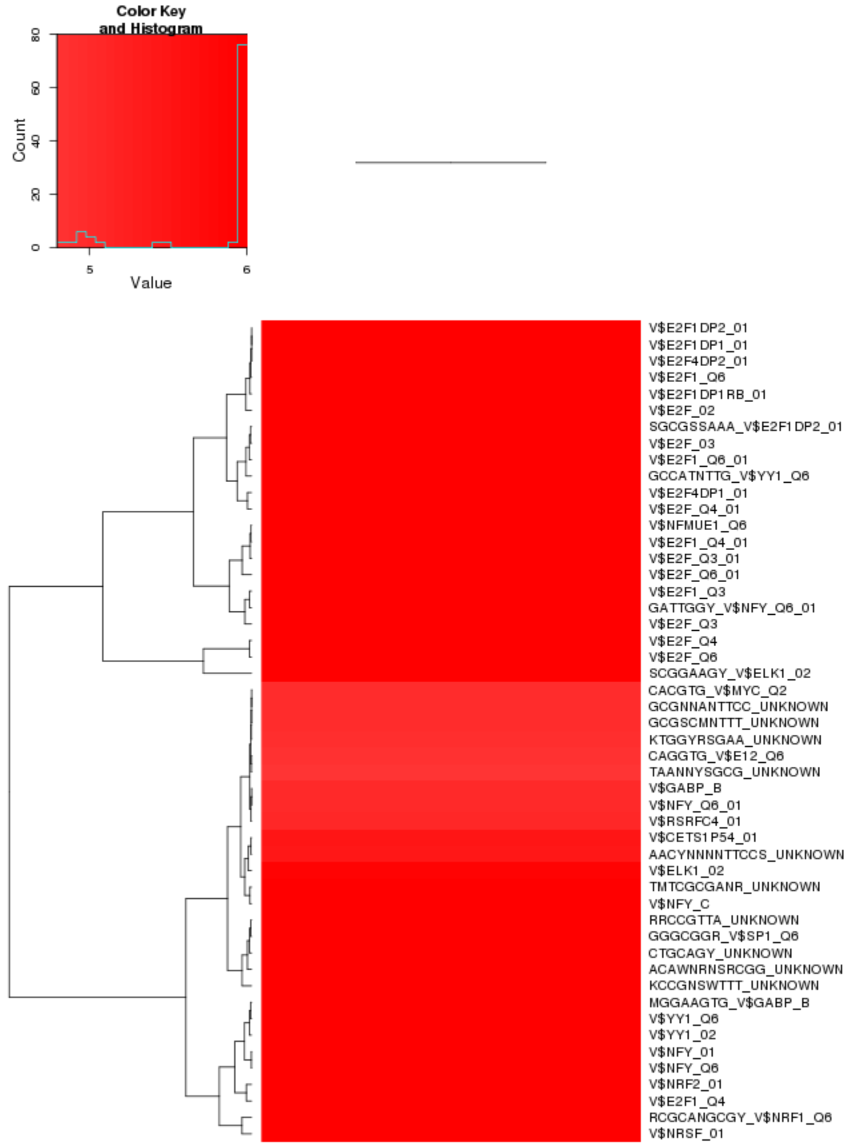
```
## Error: no locations are finite
```



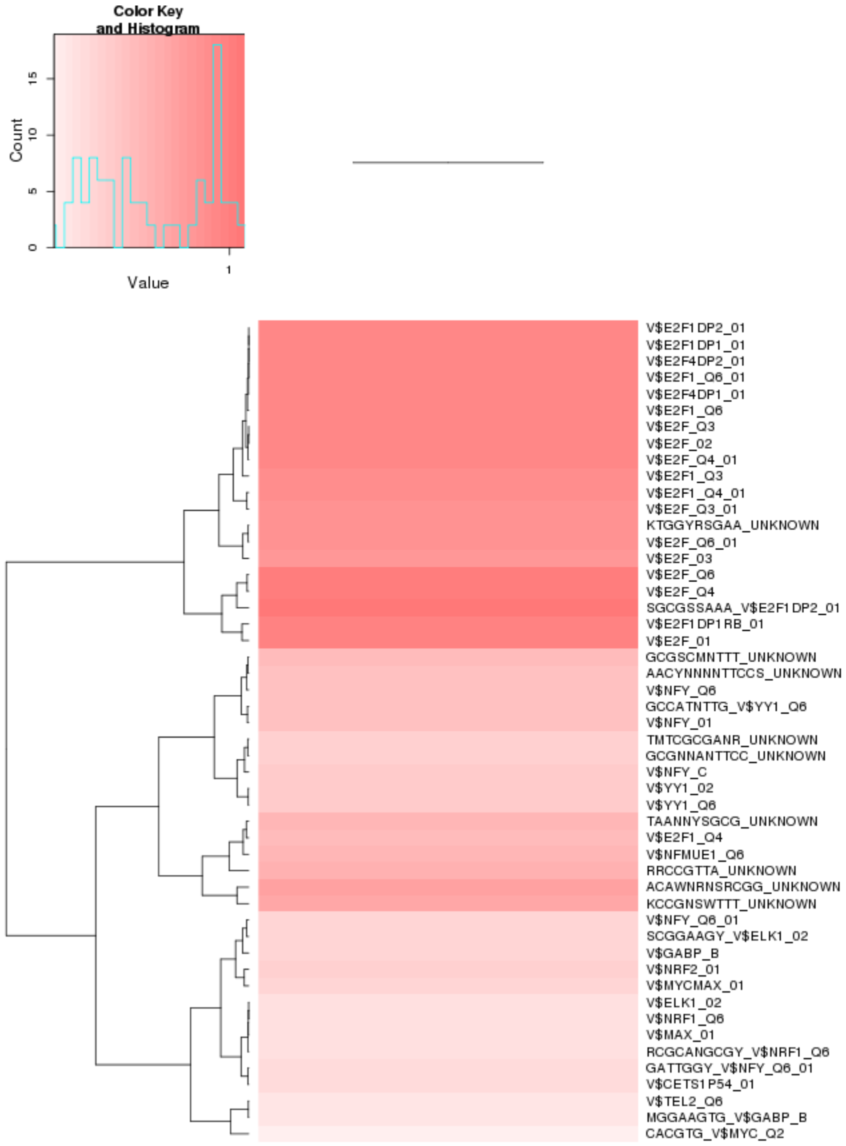
Immuno zscore:



TF enrichment:

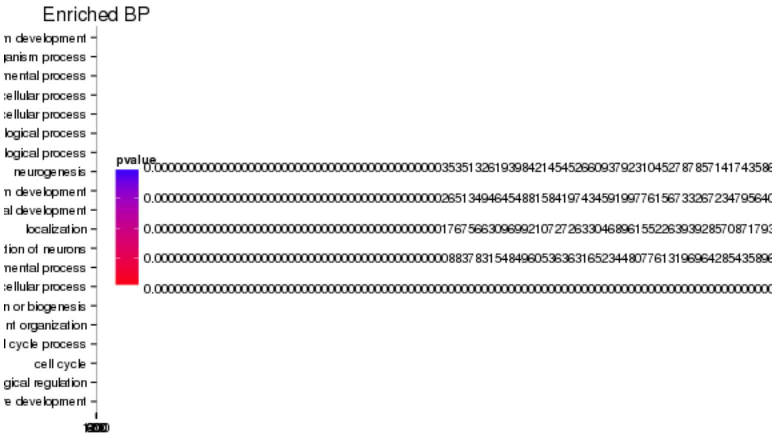

Color Key
and Histogram
Count
0
20
40
60
80
5
6
Value
V$E2F1DP2_01
V$E2F1DP1_01
V$E2F4DP2_01
V$E2F1_Q6
V$E2F1DP1RB_01
V$E2F_02
SGCGSSAAA_V$E2F1DP2_01
V$E2F_03
V$E2F1_Q6_01
GCCATNTTG_V$YY1_Q6
V$E2F4DP1_01
V$E2F_Q4_01
V$NFMUE1_Q6
V$E2F1_Q4_01
V$E2F_Q3_01
V$E2F_Q6_01
V$E2F1_Q3
GATTGGY_V$NFY_Q6_01
V$E2F_Q3
V$E2F_Q4
V$E2F_Q6
SCGGAAGY_V$ELK1_02
CACGTG_V$MYC_Q2
GCGNNANTTCC_UNKNOWN
GCGSCMNTTT_UNKNOWN
KTGGYRSGAA_UNKNOWN
CAGGTG_V$E12_Q6
TAANNYSGCG_UNKNOWN
V$GABP_B
V$NFY_Q6_01
V$RSRFC4_01
V$CETS1P54_01
AACYNNNNTTCCS_UNKNOWN
V$ELK1_02
TMTCGCGANR_UNKNOWN
V$NFY_C
RRCCGTTA_UNKNOWN
GGGCGGR_V$SP1_Q6
CTGCAGY_UNKNOWN
ACAWNRNSRCGG_UNKNOWN
KCCGNSWTTT_UNKNOWN
MGGAAGTG_V$GABP_B
V$YY1_Q6
V$YY1_02
V$NFY_01
V$NFY_Q6
V$NRF2_01
V$E2F1_Q4
RCGCANGCGY_V$NRF1_Q6
V$NRSF_01

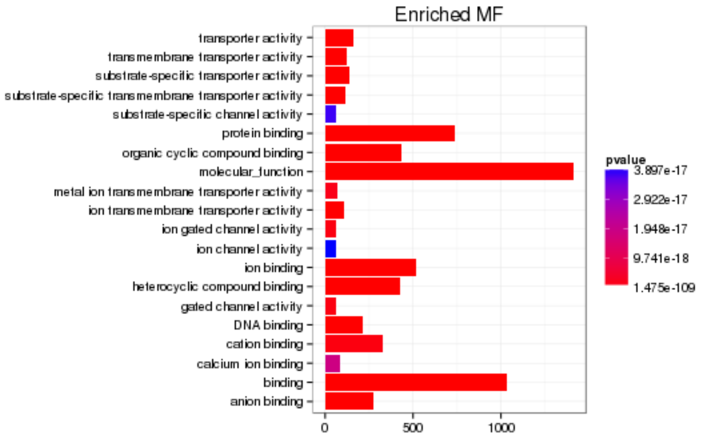
TF zscore:

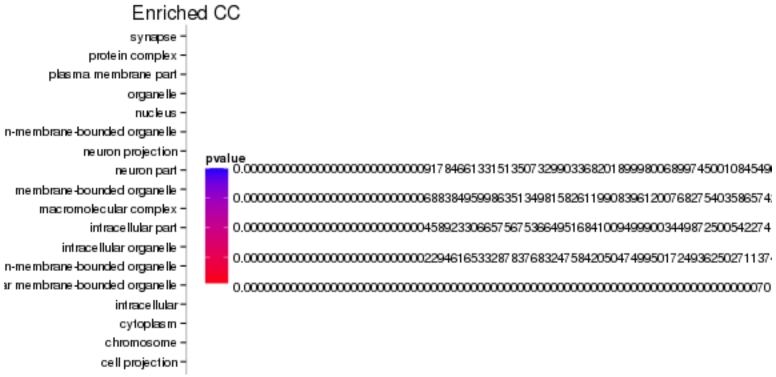


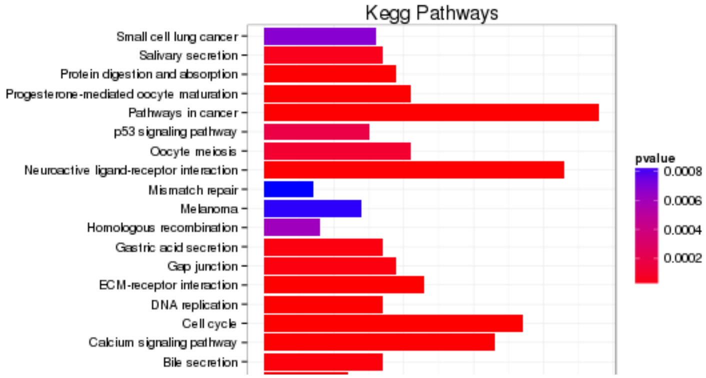
GO enrichment

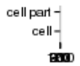
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

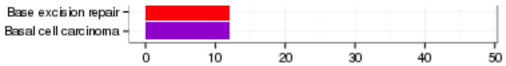

Enriched BP

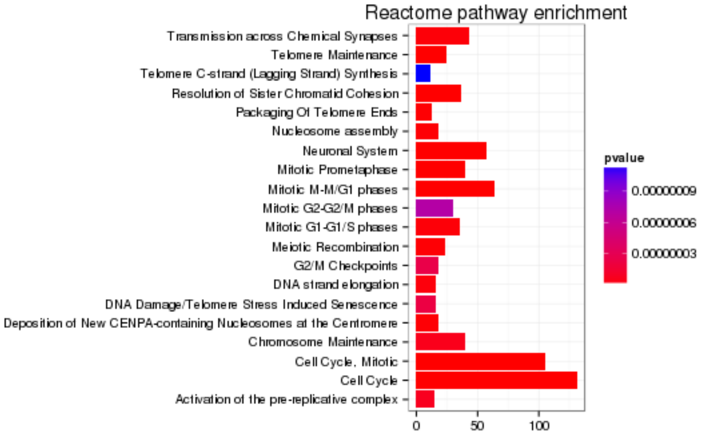

Enriched MF


Enriched CC

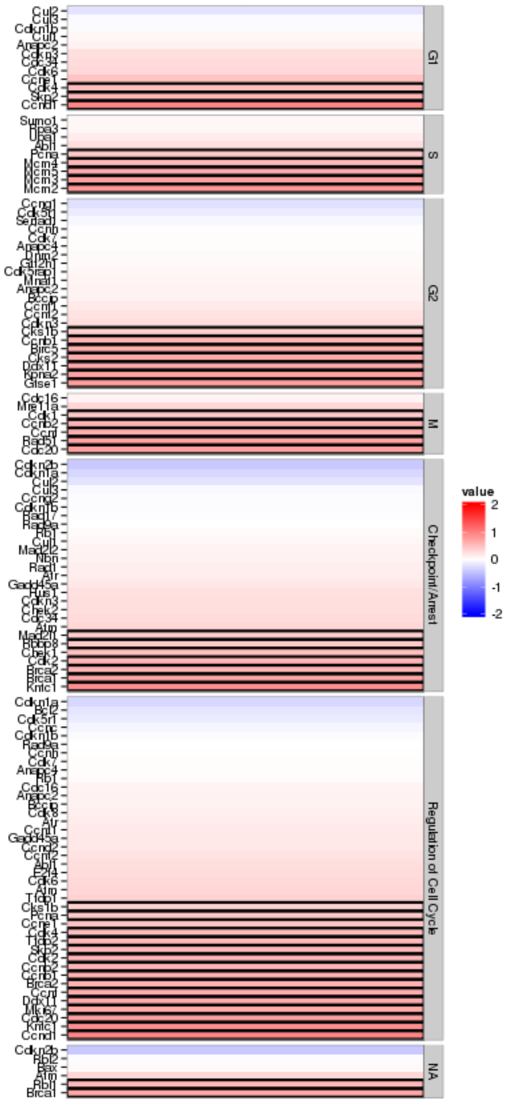

Kegg Pathways



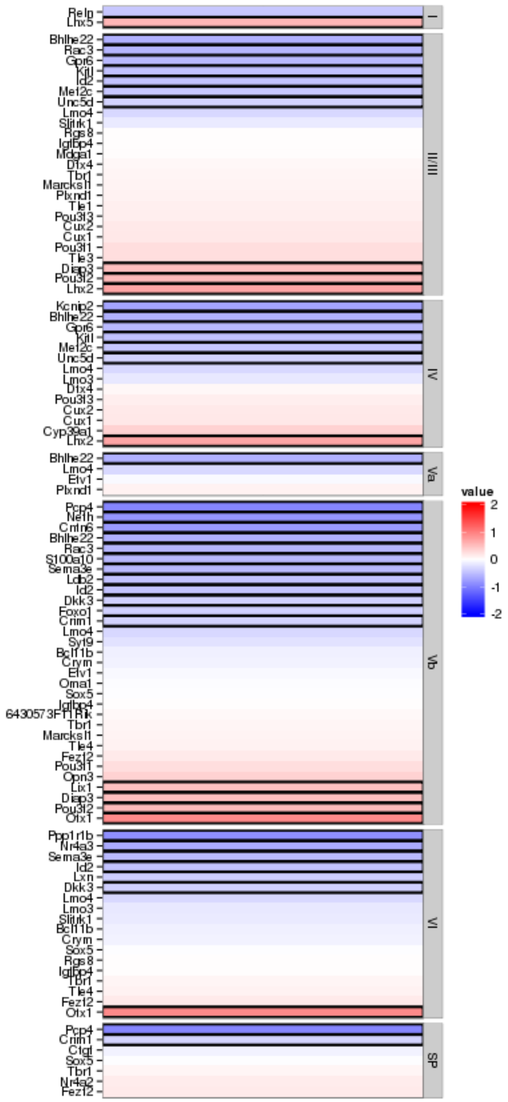




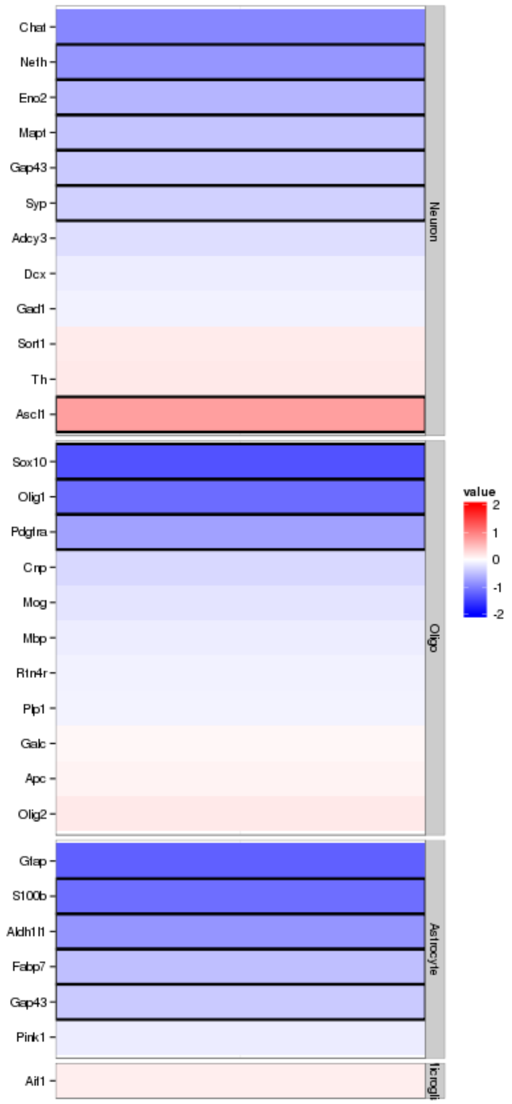
Enrichment or depletion for stage-specific cell cycle markers



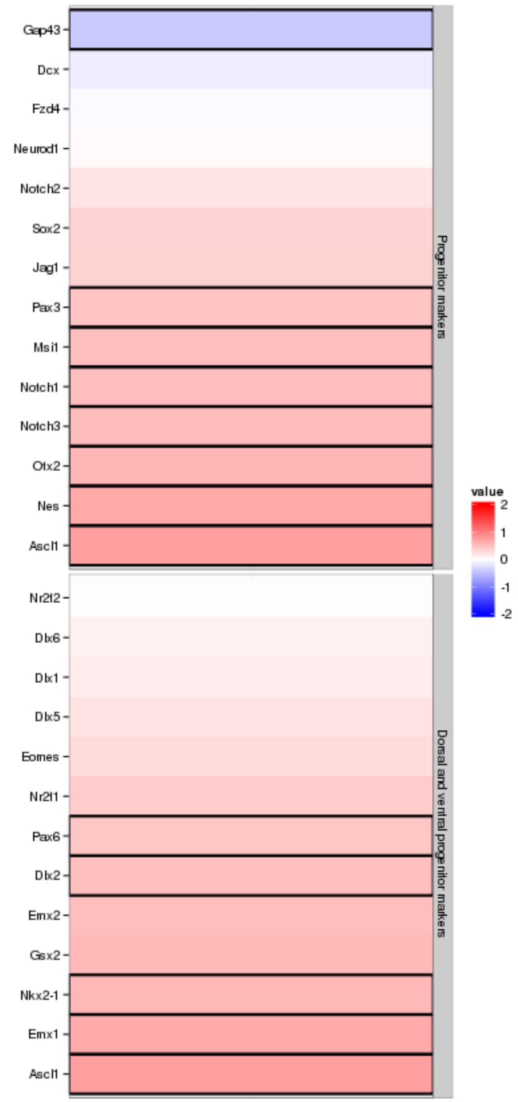
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



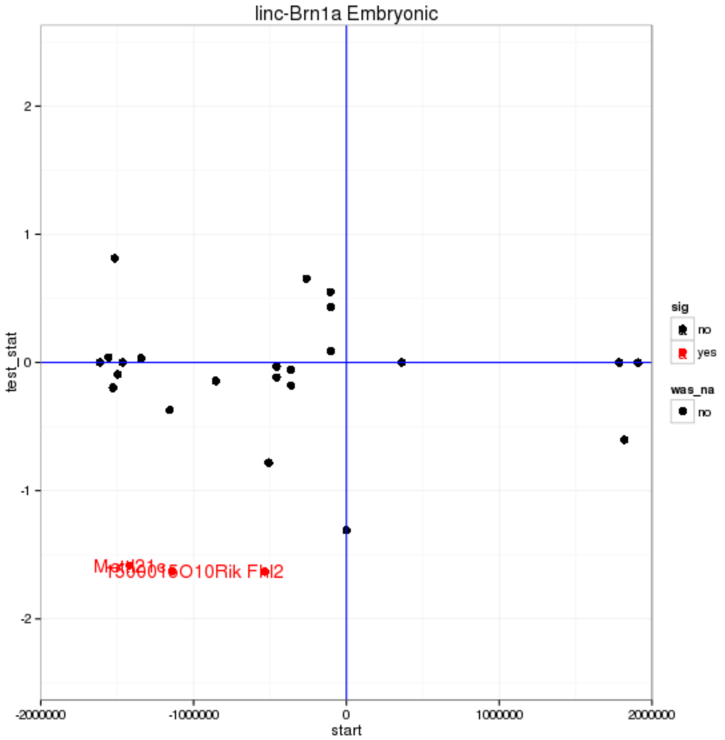
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 3 genes significantly regulated in a region this size is: 0.6938



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15	JR858
16	JR859
17	JR860

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	33371600.00	1.23	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	33371600.00	1.07	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	33371600.00	1.19	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	33371600.00	1.25	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	33371600.00	1.16	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	33371600.00	0.87	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	33371600.00	0.94	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	33371600.00	0.90	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	33371600.00	0.84	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	33371600.00	0.93	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	33371600.00	0.78	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	33371600.00	0.78	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	33371600.00	0.67	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	33371600.00	1.18	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR858/abundances.cxb	linc_Brn1a	0	linc_Brn1a_0	34867700.00	33371600.00	1.08	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR859/abundances.cxb	linc_Brn1a	1	linc_Brn1a_1	45282400.00	33371600.00	1.30	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR860/abundances.cxb	linc_Brn1a	2	linc_Brn1a_2	41604700.00	33371600.00	1.20	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils
## [8] datasets  base
##
## other attached packages:
##  [1] plyr_1.8.1
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6          
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4      
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7             
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1         
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1          
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4          
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12    
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26   
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2         
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0         
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1    
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2         
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2           
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,linc-Brn1a -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/linc-Brn1a_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/Br
## 2
## 3
## 4
## 5
```

linc-Brn1b KO vs WT (Adult)

This file shows the wt-v-ko comparison for linc-Brn1b.

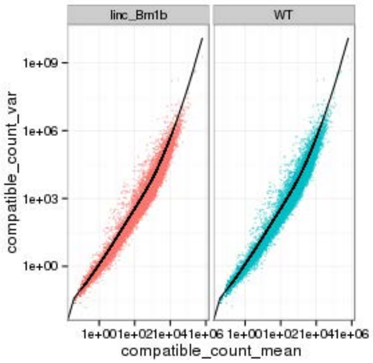
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

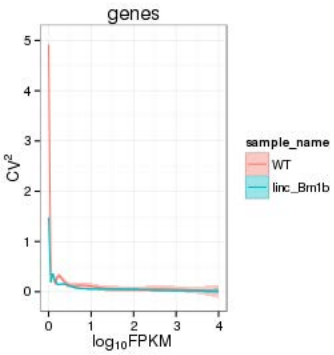
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



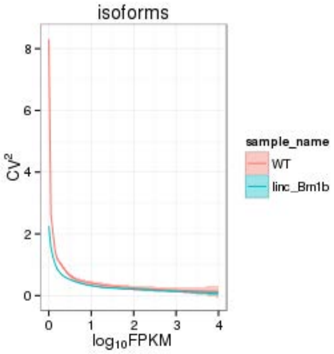
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

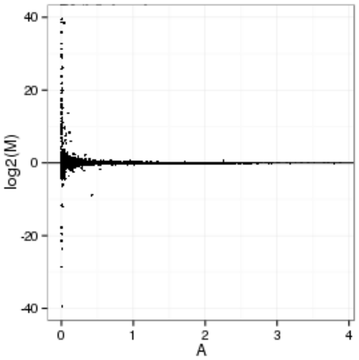
Genes:



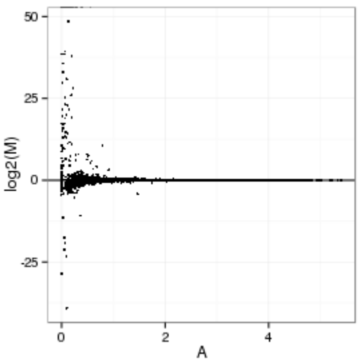
Isoforms:



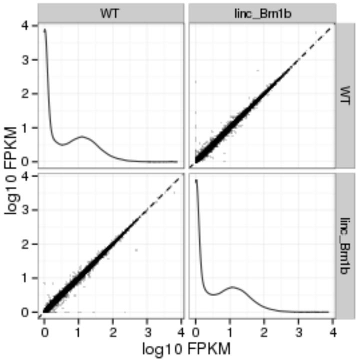
MvA plot



MvA plot counts



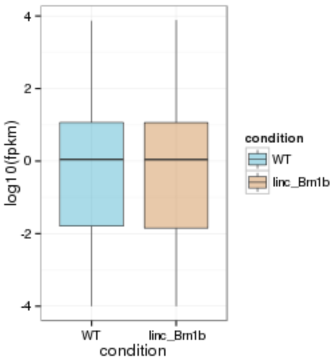
Scatterplot matrix



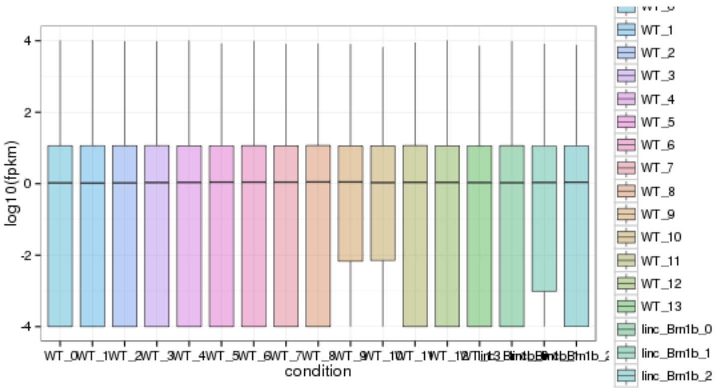
Distributions

Boxplots

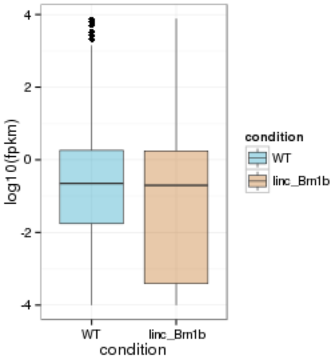
Boxplot (genes)



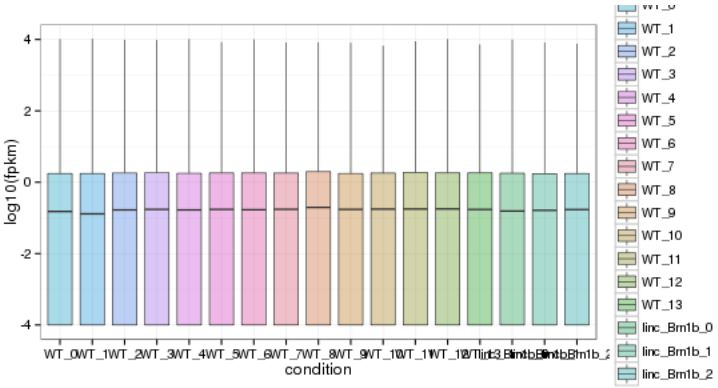
Boxplot (genes, replicates)



Boxplot (isoforms)

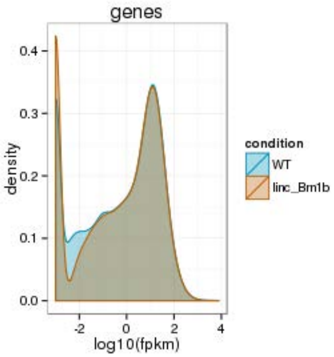


Boxplot (isoforms, replicates)

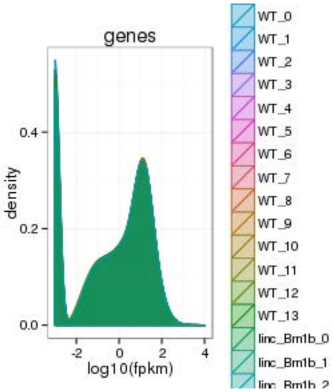


Density

Density (genes)

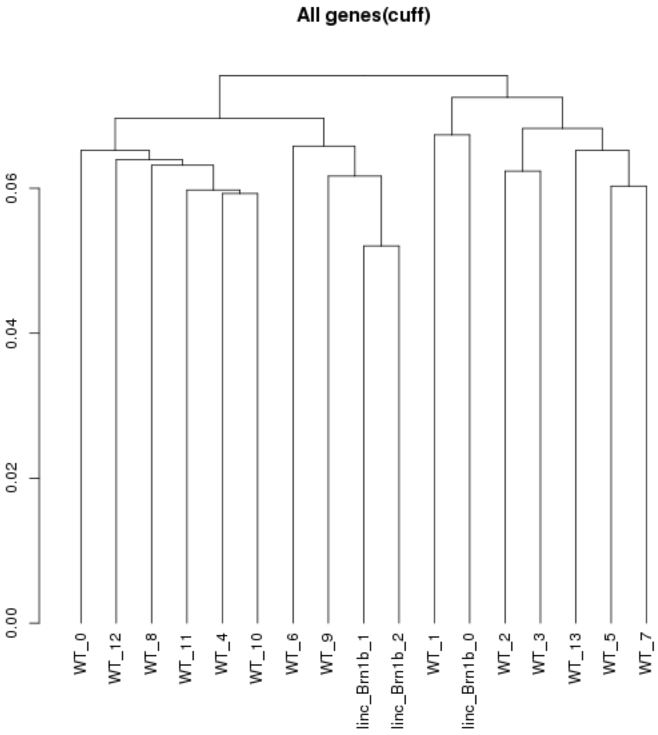


Density (genes, replicates)



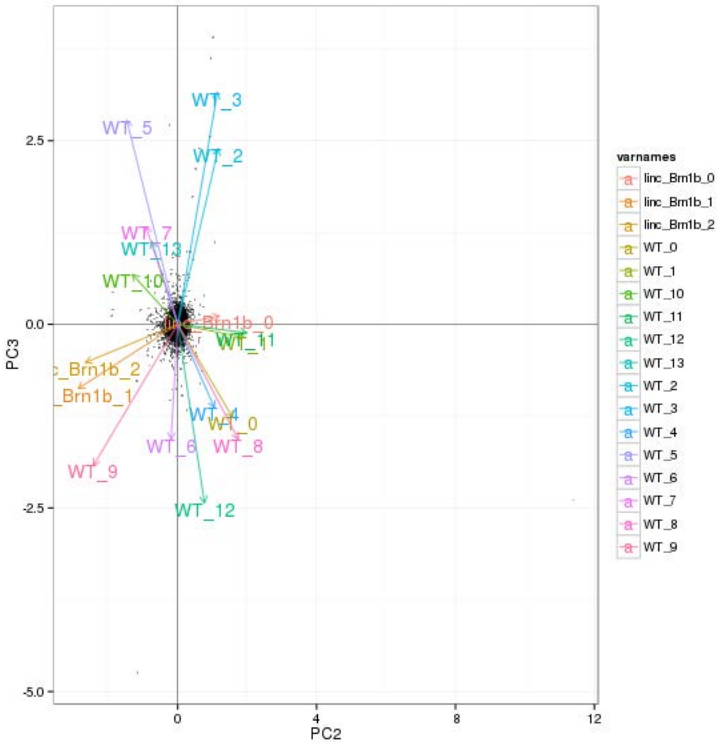
Clustering

Replicate Clusters



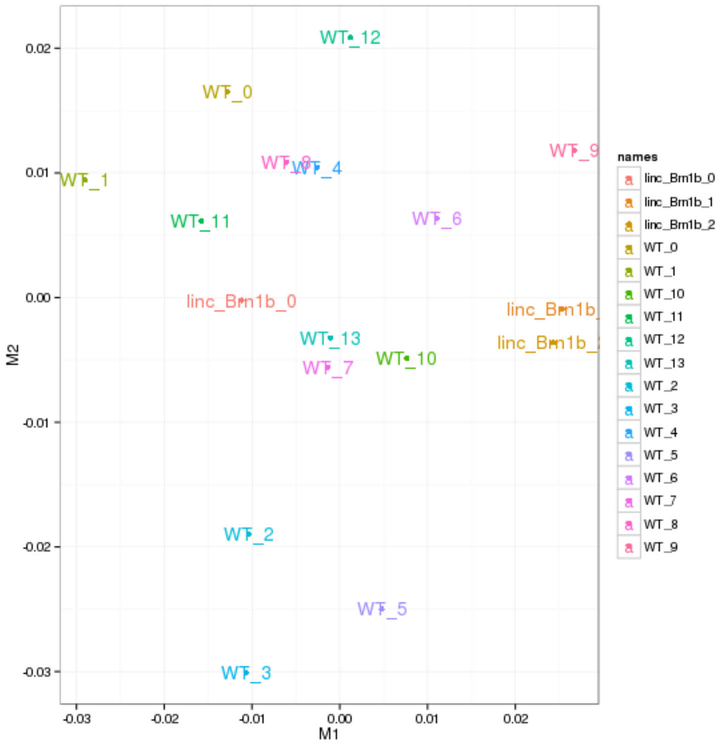
```
## NULL
```

PCA (genes)



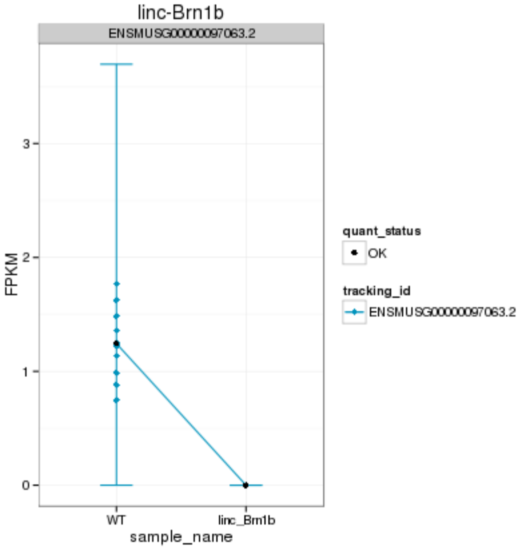
PC3
PC2
2.5
0.0
-2.5
-5.0
0
4
8
12
WT_3
WT_5
WT_2
WT_7
WT_13
WT_10
Brn1b_0
WT_11
c_Brn1b_2
_Brn1b_1
WT_4
WT_0
WT_6
WT_8
WT_9
WT_12
varnames
linc_Brn1b_0
linc_Brn1b_1
linc_Brn1b_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

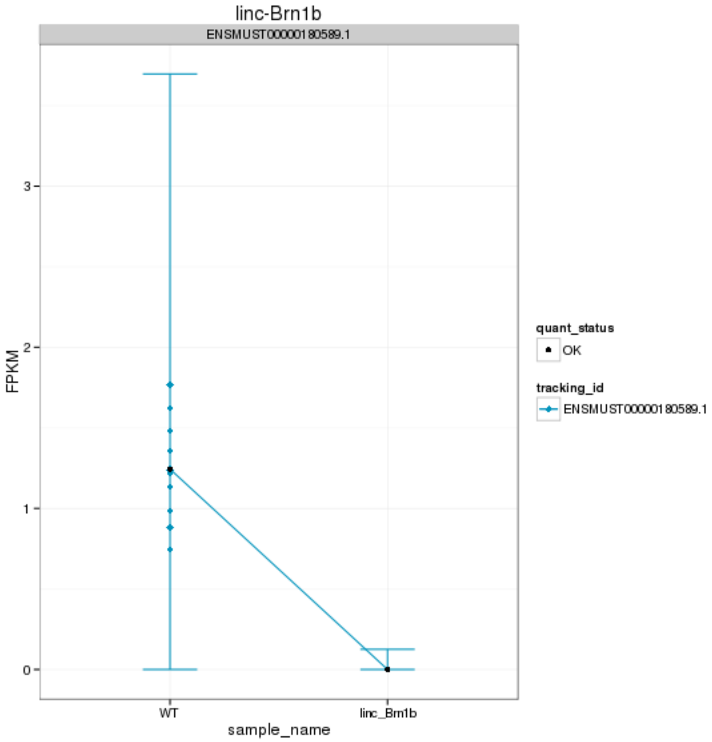


KO assessment

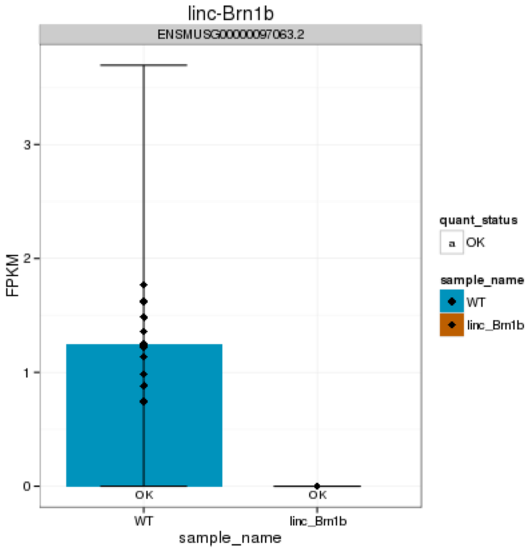
Endogenous lncRNA expression



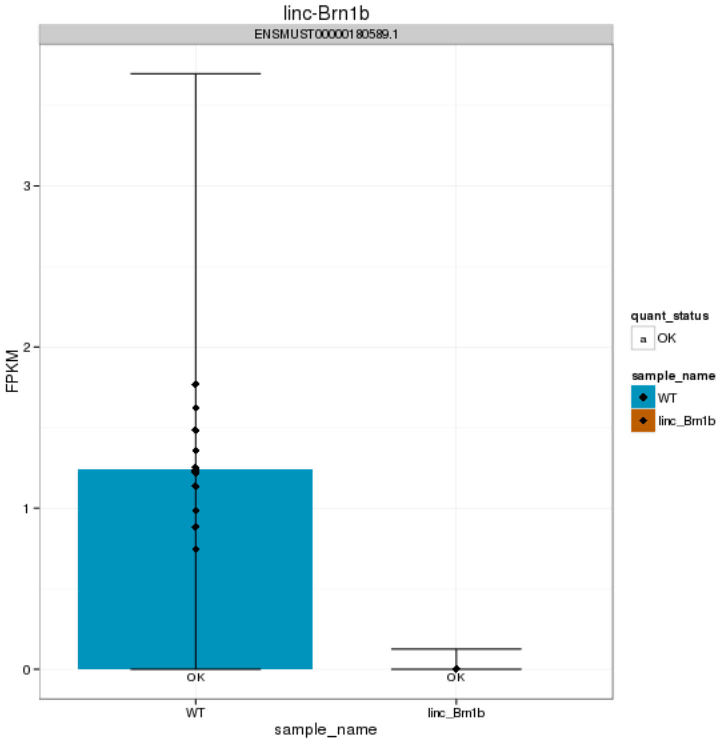
Endogenous expression of linc-Brn1b isoforms:



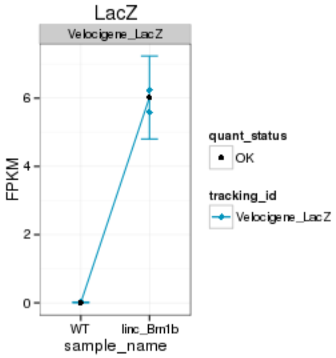
Barplot of gene expression:

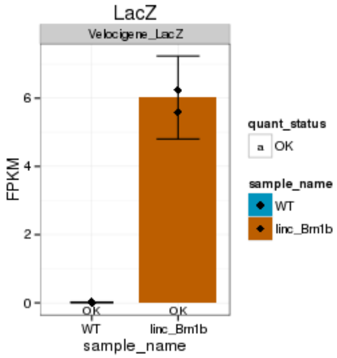


Barplot of isoform expression:



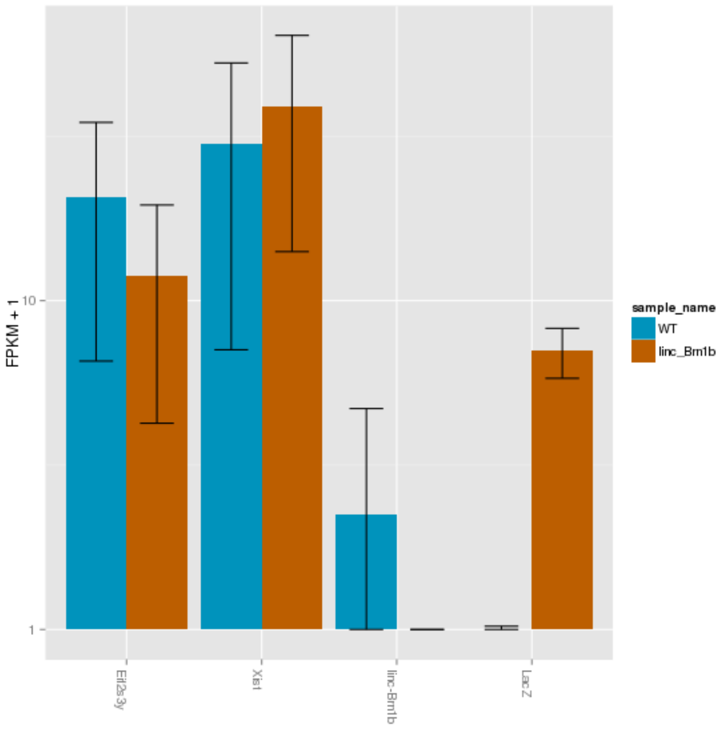
LacZ expression



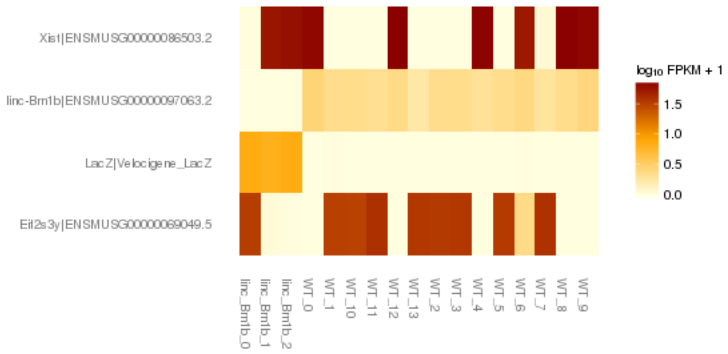


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

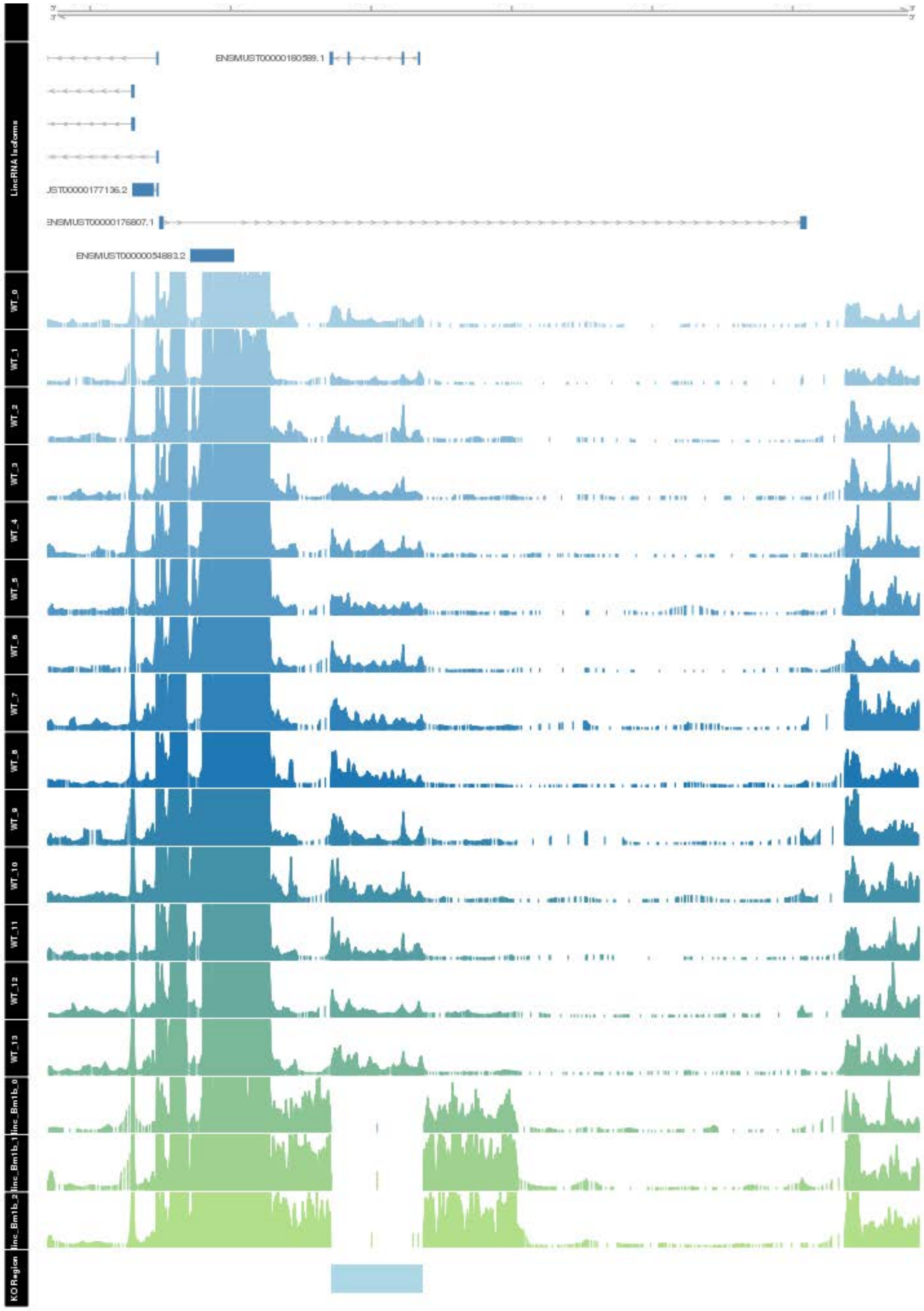
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


LincRNA Isoforms
ENSMUST00000180588.1
JST00000177136.2
ENSMUST00000176807.1
ENSMUST00000054883.2
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
linc_Bm1b_0
linc_Bm1b_1
linc_Bm1b_2
KO Region

Differential Analysis

Differential Genes

There are 193 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Gabra2
2	Sox9
3	Folh1
4	Kmt2a
5	Rec8
6	Arrdc2
7	Calr
8	Gpx6
9	Pde1c
10	Nes
11	Epha2
12	Homer1
13	Dio2
14	Hnrnpa0
15	Ttc9b
16	Carhsp1
17	Tppp3
18	Etnppl
19	Pdk4
20	P4ha1
21	Arid5b
22	Sgk1
23	Timp3
24	Ddit4
25	Btg2
26	Xbp1
27	Pdia6
28	Pxdn
29	Nfkbia
30	Serpina3n
31	Fos
32	Gpr137b
33	Zkscan3
34	Esd
35	Dnajc3
36	Slc38a2
37	Bcl6

38 Sdf2l1
39 Cdkn1a
40 Creld2
41 Glo1
42 Xdh
43 Atp6v0c
44 Dusp1
45 Fkbp5
46 Syt4
47 Rps24
48 Pdia4
49 Slc40a1
50 Clk1
51 2810459M11Rik
52 Bok
53 Mlph
54 Serpinb8
55 Dbi
56 Atf3
57 Lcn2
58 Hspa5
59 Itpka
60 Spred1
61 F3
62 Trp53inp1
63 Nr4a3
64 Slc2a1
65 Tinagl1
66 Errfi1
67 Ccnl2
68 Fosl2
69 Uncx
70 Klf15
71 Adipor2
72 Pglyrp1
73 Tmem238
74 Hddc3
75 Polr3e
76 Tsc22d3
77 Plat
78 Mt2
79 Tdgf1
80 Mlh1

81 Cck
82 Trf
83 Ugt8a
84 Tbc1d4
85 Egr3
86 Tlr13
87 Slc25a37
88 Arhgap27
89 Pla2g3
90 Tiparp
91 Prr7
92 Nostrin
93 Filip1
94 Arl4d
95 Cox8a
96 H2-Q4
97 Anln
98 Tob1
99 Avp
100 Vstm2l
101 Smim3
102 Camk4
103 Txnip
104 Foxq1
105 Akap12
106 Irs2
107 Pcsk1n
108 Tnfsf10
109 Zfp189
110 Slc6a5
111 C1qtnf4
112 Nkx6-2
113 Cldn5
114 Kcnj2
115 Maff
116 Tuba1c
117 Lor
118 Nxpe4
119 Ctla2a
120 Snhg11
121 Rps2
122 Hjurp
123 Pcdhb7

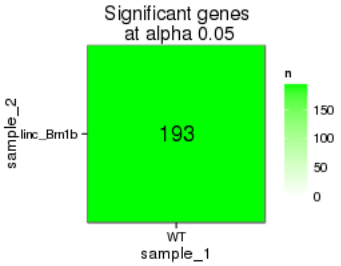
124 Cirbp
125 Nudt18
126 Pcdhb3
127 Zfp36l2
128 Npas4
129 Clec14a
130 Plaur
131 Mpeg1
132 Cdh19
133 Gimap6
134 Hes5
135 Tmem252
136 Ctxn1
137 Ccdc6
138 Dact2
139 Chchd10
140 Rasd1
141 Rasl11b
142 Klk6
143 Kcnk12
144 Plekho2
145 Pcdhb6
146 Hbb-bs
147 Junb
148 Ier2
149 Mat2a
150 Iigp1
151 Tmem158
152 5033411D12Rik
153 Zcchc24

154 Pign
155 Kdm5d
156 Ero1lb
157 Mex3b
158 C030014I23Rik
159 Cox5b
160 Rpl34
161 Scoc
162 BC048507
163 Zbtb16
164 Bpifb9b
165 Bpifb3
166 Ddx3y

167 Irgm2
168 Gm1673
169 Jund
170 Egr4
171 Gm7292
172 Gpr27
173 H2-Bl
174 Wdfy1
175 Plekhf1
176 Arrdc3
177 Fjx1
178 Rprm
179 Nrarp
180 Gbp4
181 Gm11273
182 Slc5a3
183 Cdr1
184 Apold1
185 Hspa1b
186 Malat1
187 AA465934
188 Gm21967
189 Ccdc85b
190 Gm6472
191 AI848285
192 4930480K23Rik
193 Gpr137b-ps

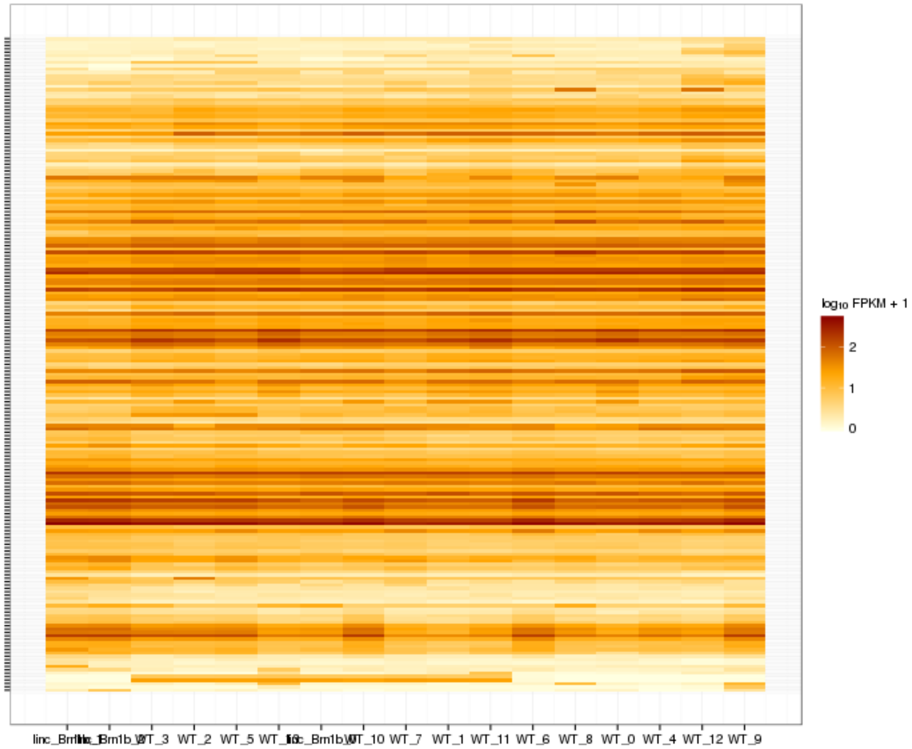
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

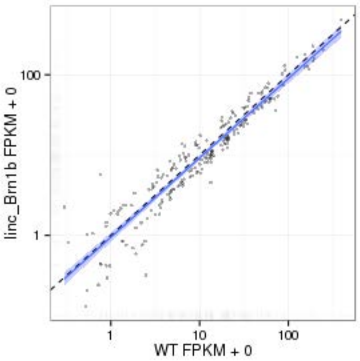


Significant genes with expression >50fpkm (any condition):(turned off)

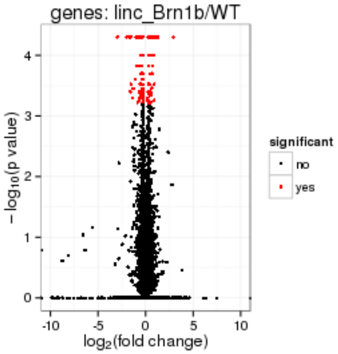
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

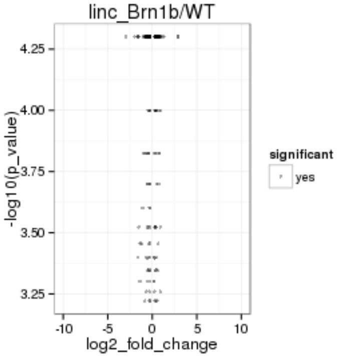
Scatter plot of significant genes only:



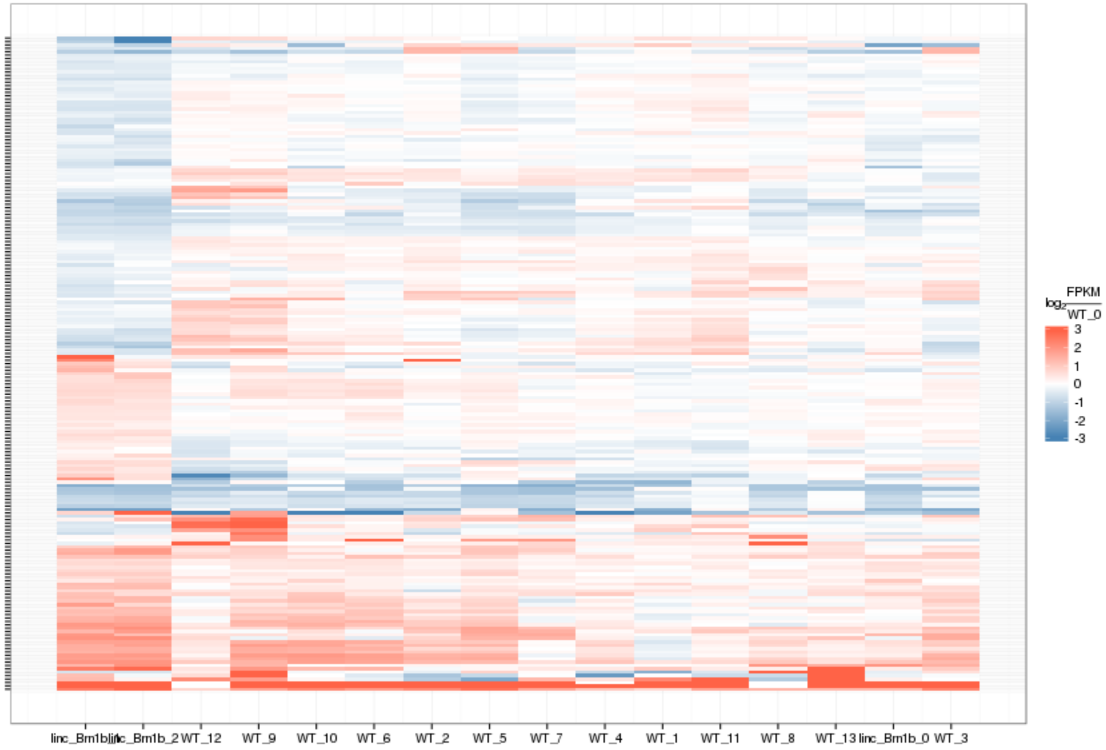
Volcano Plot



Volcano plot with significant genes only:



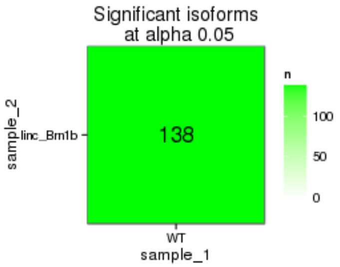
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

	isoAnnot$gene_short_name
1	Gabra2
2	Sox9
3	Rec8
4	Arrdc2
5	Calr
6	Hif3a
7	Nes
8	Ndrg1
9	Dio2
10	Ttc9b
11	Pdk4
12	Sgk1
13	Tmcc3
14	Timp3
15	Ddit4
16	Cpm
17	Tns3
18	Btg2
19	Xbp1
20	Pxdn
21	Nfkbia
22	Serpina3n
23	Fos
24	Gpr137b
25	Thbs4
26	Kat6b
27	Dnajc3
28	Slc38a2
29	Bcl6
30	Sdf2l1
31	Tfrc
32	Cdkn1a
33	Glo1
34	Xdh
35	Atp6v0c
36	Dusp1
37	Fkbp5
38	Rps24
39	Pdia4
40	Bok

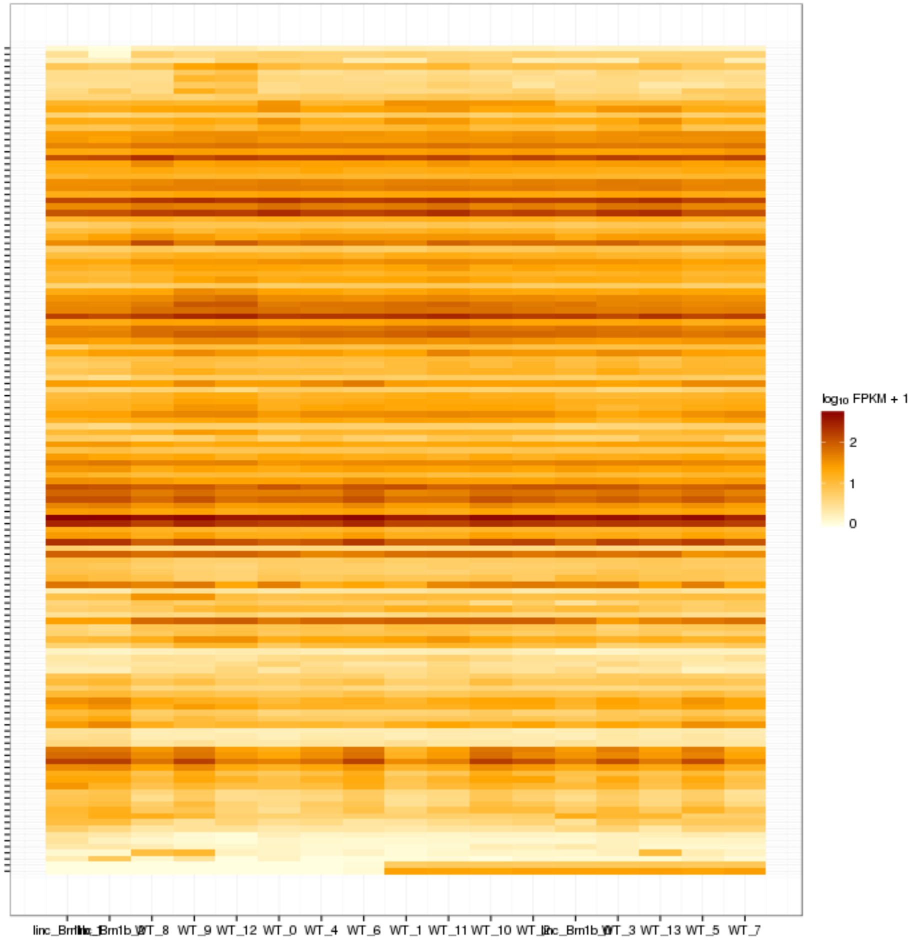
41 Mlph
42 Hspa5
43 Spred1
44 F3
45 Slc2a1
46 Ago3
47 Map3k6
48 Errfi1
49 Ccnl2
50 Fosl2
51 Adipor2
52 Pglyrp1
53 Hddc3
54 Tsc22d3
55 Mt2
56 Mlh1
57 Cck
58 Ugt8a
59 Fndc3a
60 Akr1c14
61 Egr3
62 Slc25a37
63 Tiparp
64 Prr7
65 Arl4d
66 Cox8a
67 Anln
68 Tob1
69 Avp
70 Vstm2l
71 Acer2
72 Smim3
73 Camk4
74 Slc43a2
75 Aox4
76 Txnip
77 Foxq1
78 Akap12
79 Pcsk1n
80 Tnfsf10
81 Slc6a5
82 Gjb6
83 C1qtnf4

84 Nkx6-2
85 Cldn5
86 Kcnj2
87 Ctla2a
88 Snhg11
89 Acp1
90 Hjurp
91 Pcdhb7
92 Nudt18
93 Zfp36l2
94 Npas4
95 Cdh19
96 Hes5
97 Dact2
98 Chchd10
99 Kcnk12
100 Pcdhb6
101 Adarb2
102 Junb
103 Ier2
104 Mat2a
105 Zfp771
106 Tmem158
107 5033411D12Rik
108 Pign
109 Kdm5d
110 Ero1lb
111 Mex3b
112 Zbtb16
113 Bpifb9b
114 Ddx3y
115 Ahnak
116 Jund
117 Egr4
118 Gm7292
119 Gpr27

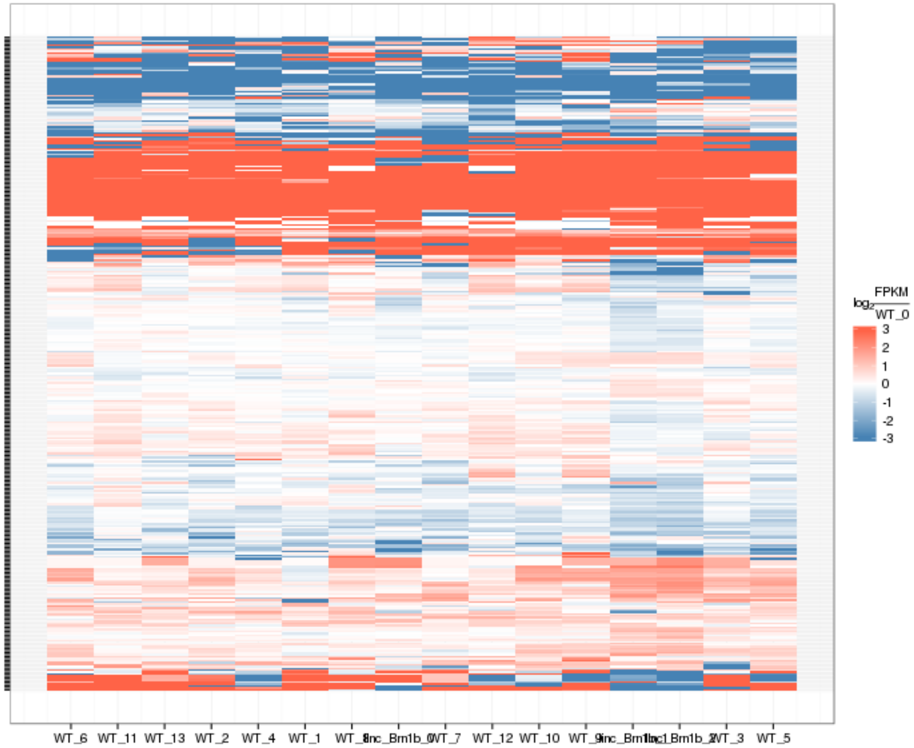
120 Wdfy1
121 Plekhf1
122 Arrdc3
123 Fjx1
124 Rprm
125 Nrarp
126 Gbp4

127 Gm11273
128 Cdr1
129 Apold1
130 Hspa1b
131 Malat1
132 Ccdc85b
133 Gm6472
134 AI848285
135 4930480K23Rik
136 Gpr137b-ps

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

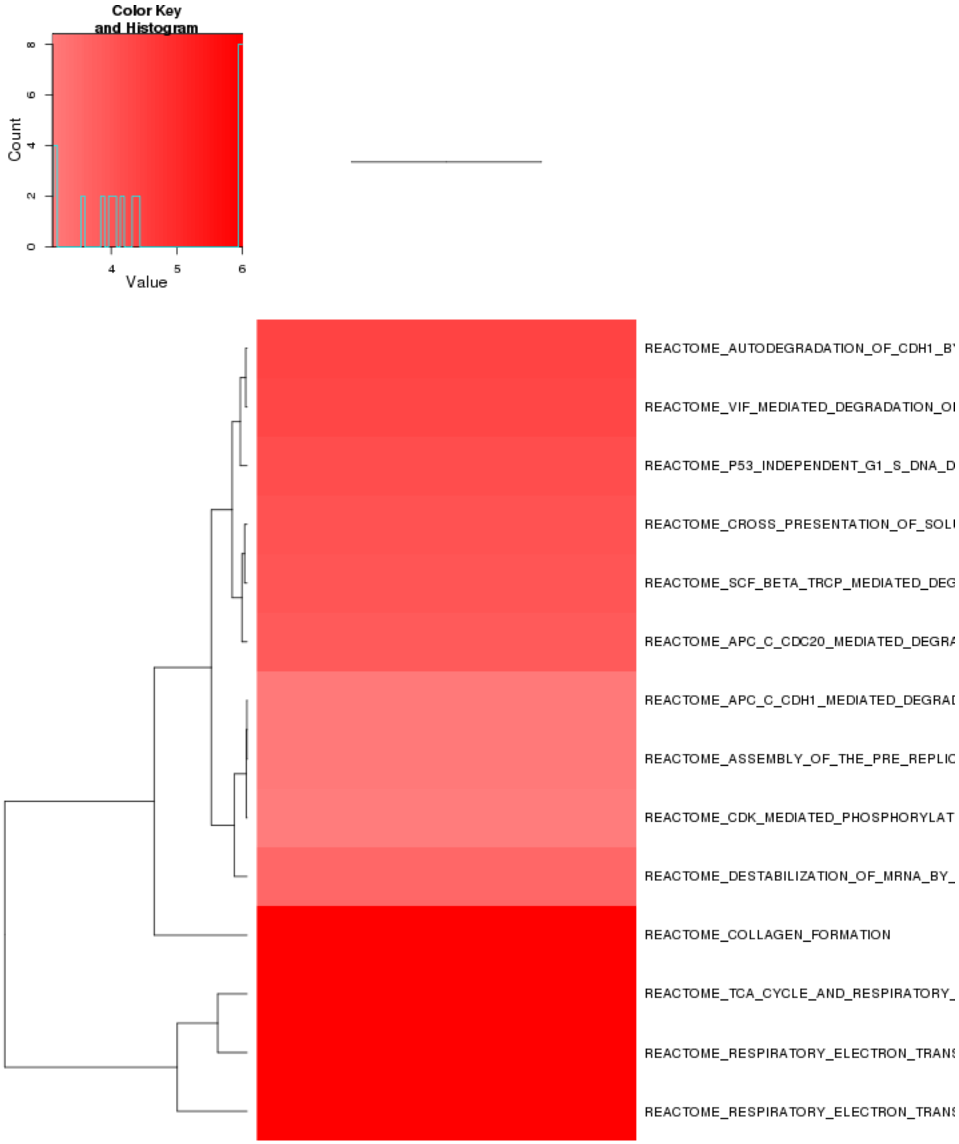
Biocarta enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

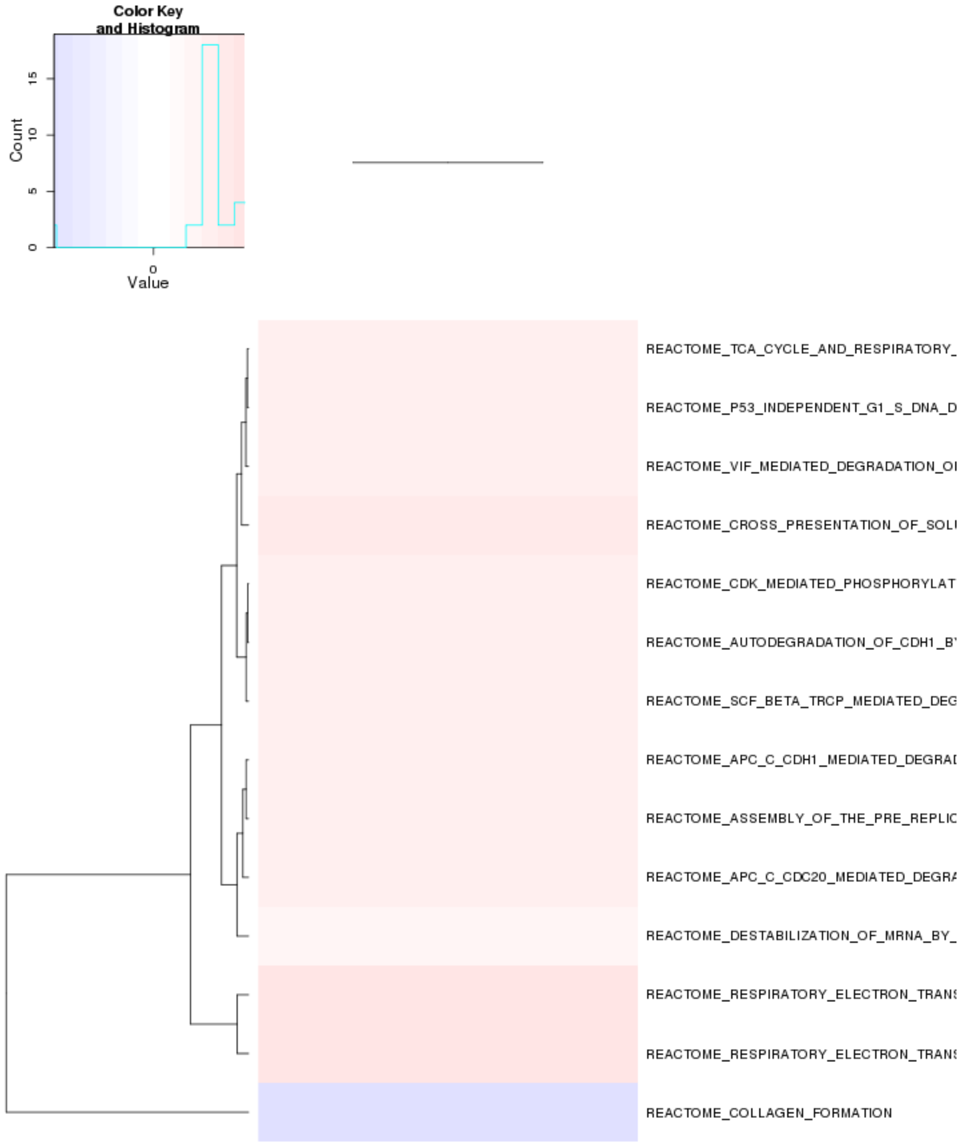
Biocarta zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

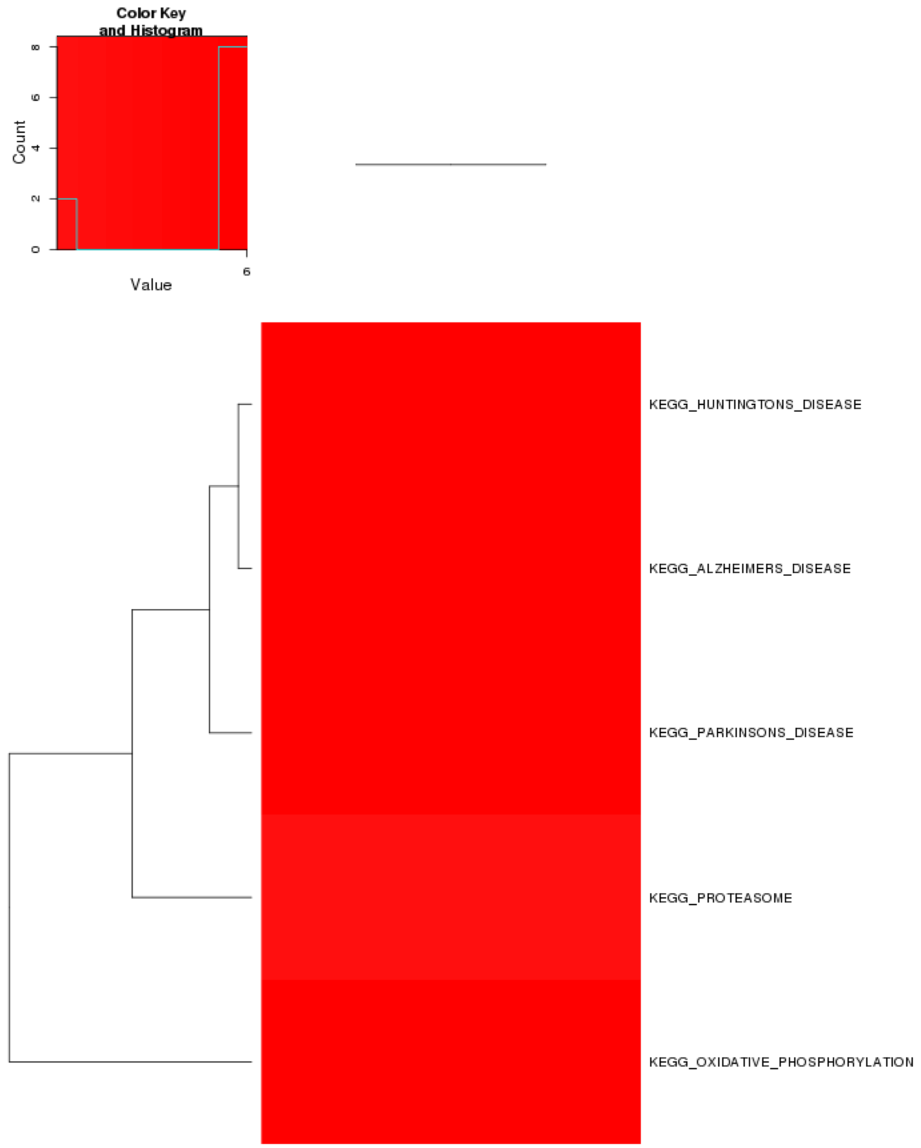
Reactome enrichment:



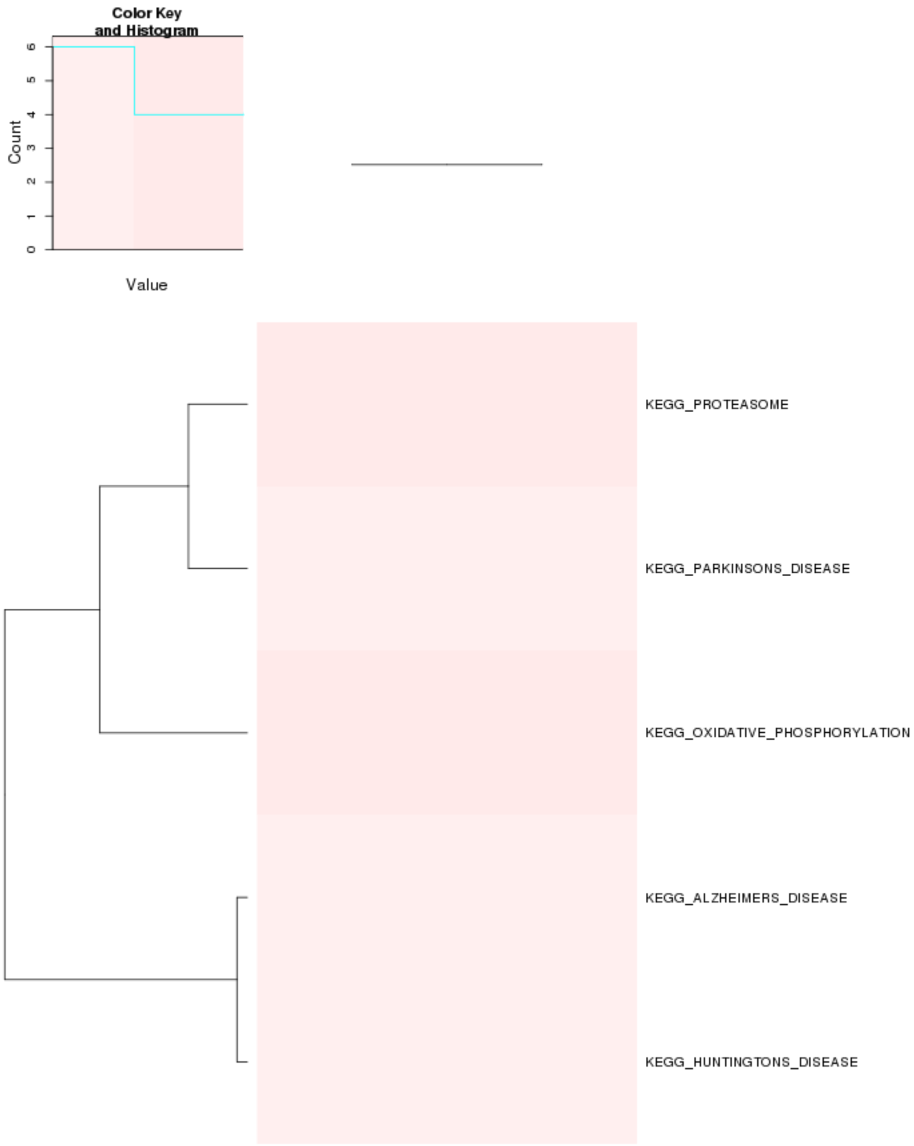
Reactome zscore:



Kegg enrichment:

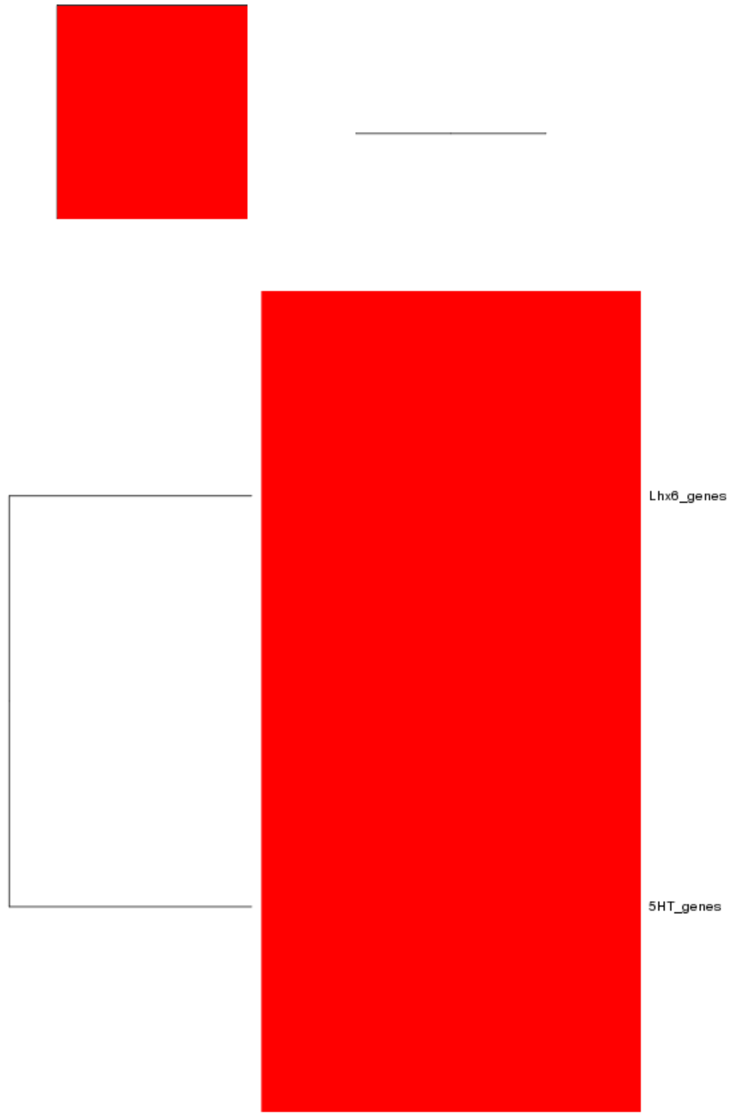

Color Key
and Histogram
Count
0
2
4
6
8
Value
6
KEGG_HUNTINGTONS_DISEASE
KEGG_ALZHEIMERS_DISEASE
KEGG_PARKINSONS_DISEASE
KEGG_PROTEASOME
KEGG_OXIDATIVE_PHOSPHORYLATION

Kegg zscore:

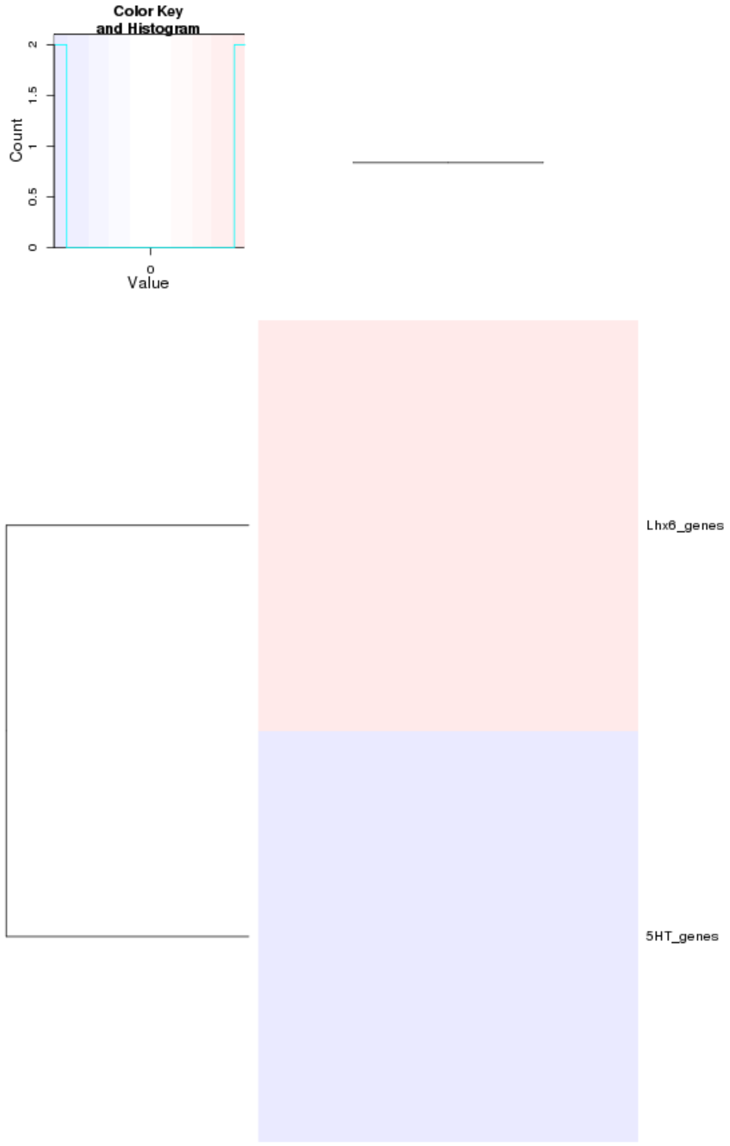


Interneuron enrichment:

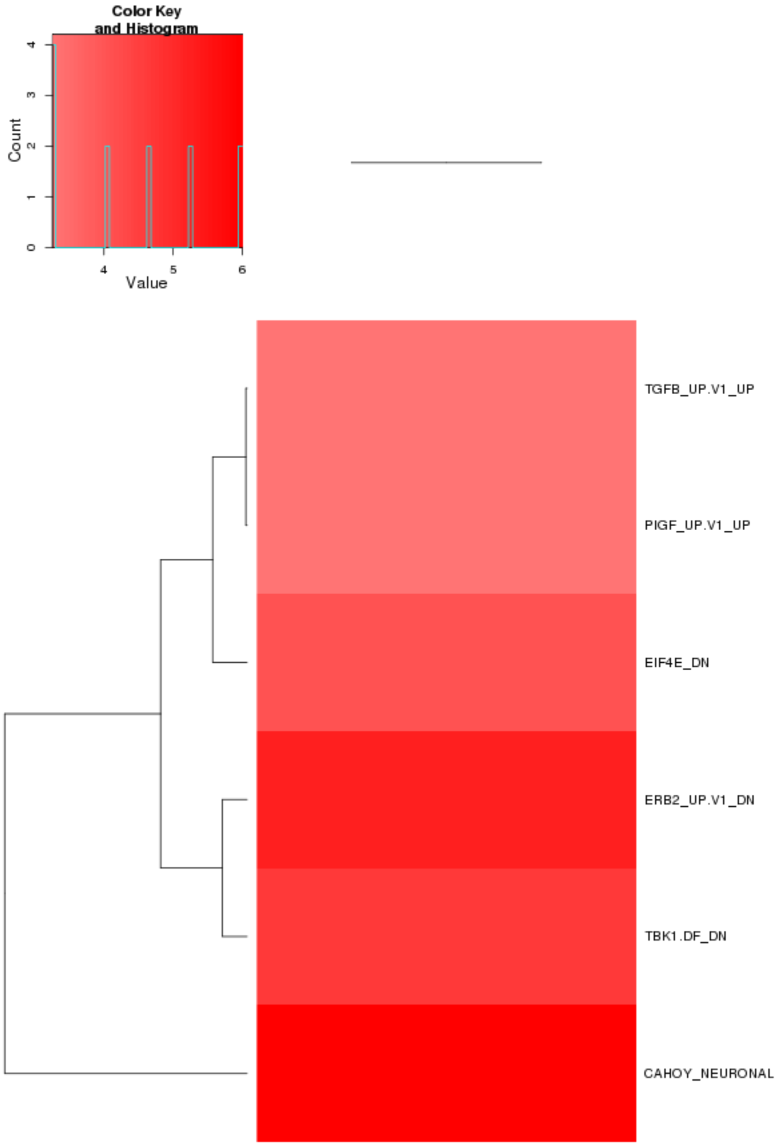
```
## Error: no locations are finite
```



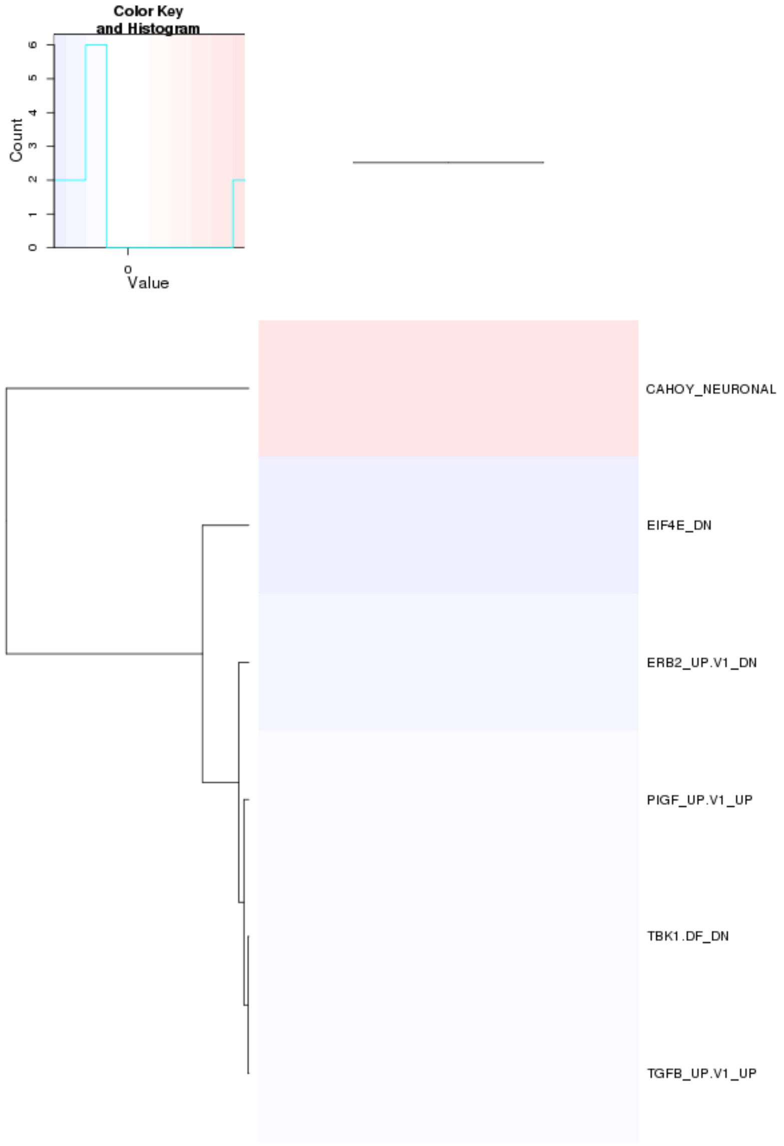
Interneuron zscore:



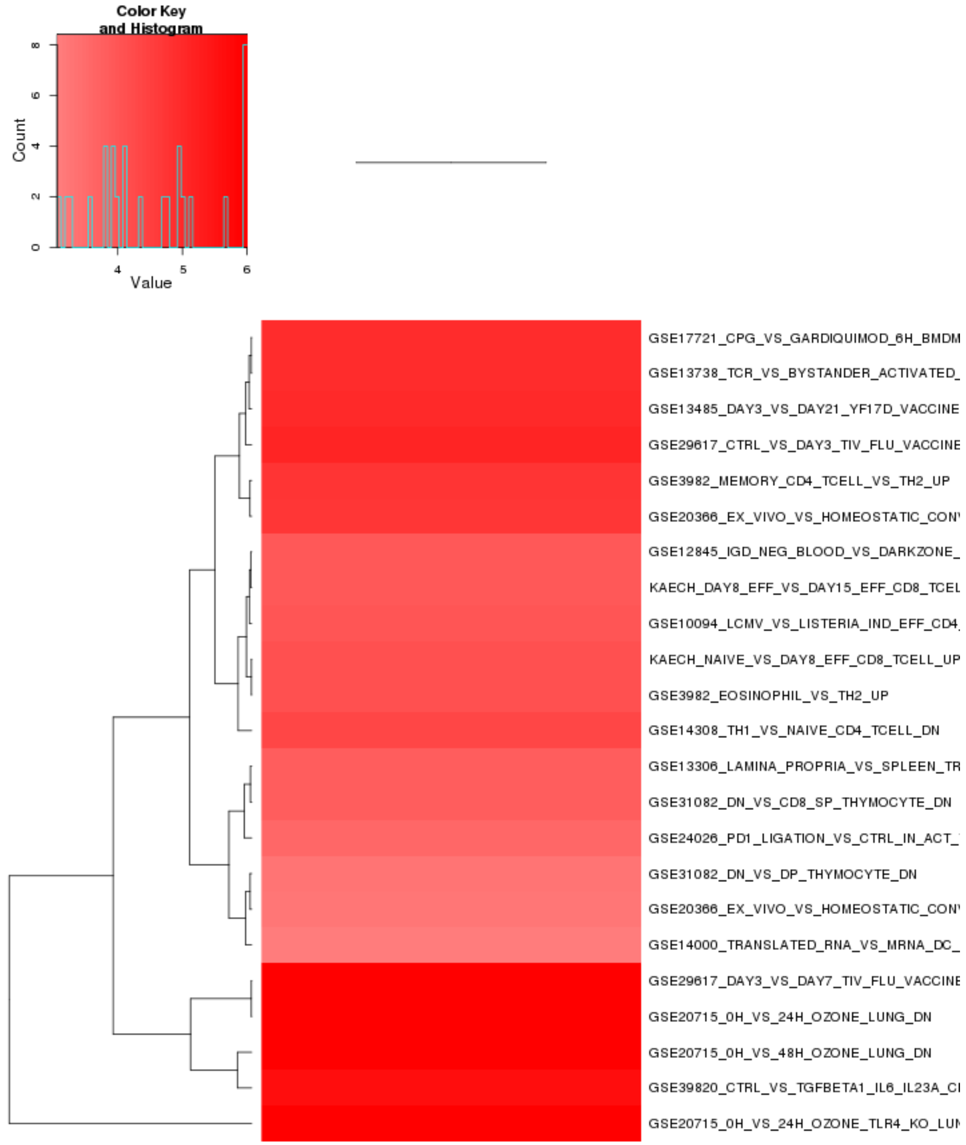
Oncogene enrichment:



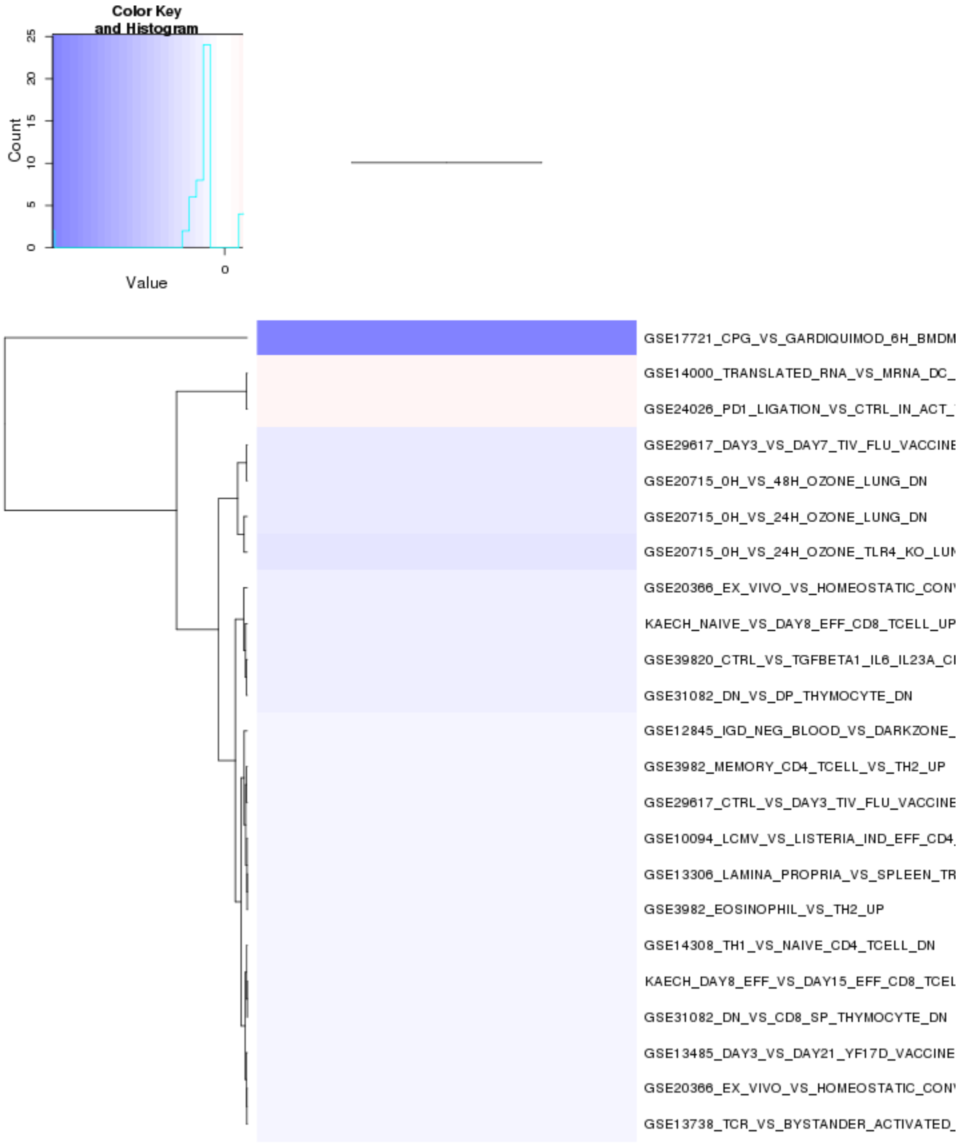
Oncogene zscore:



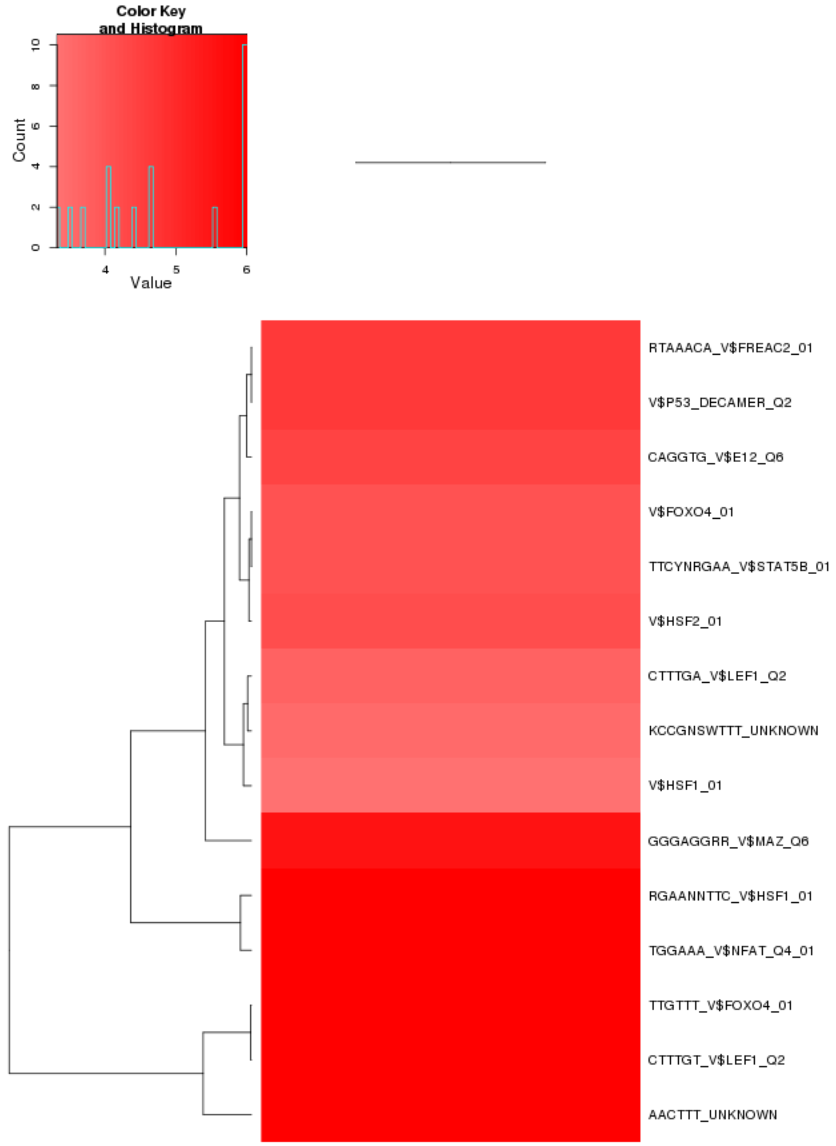
Immuno enrichment:



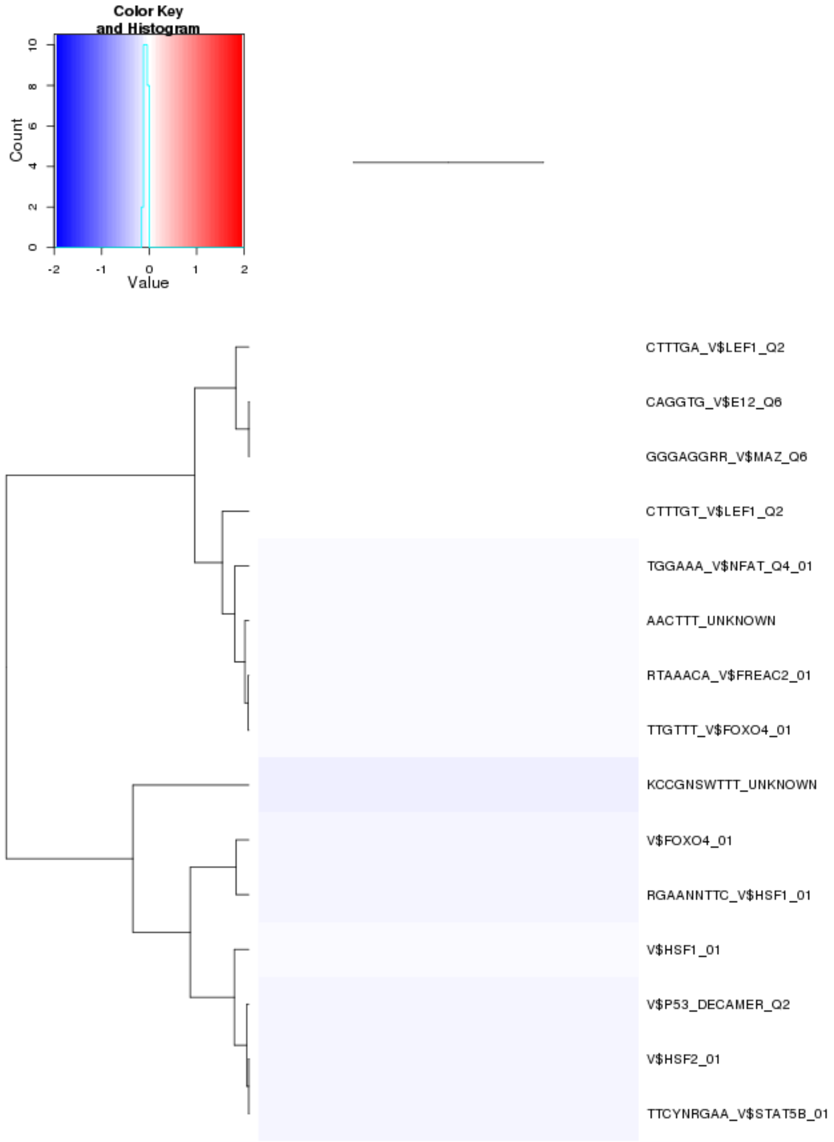
Immuno zscore:



TF enrichment:

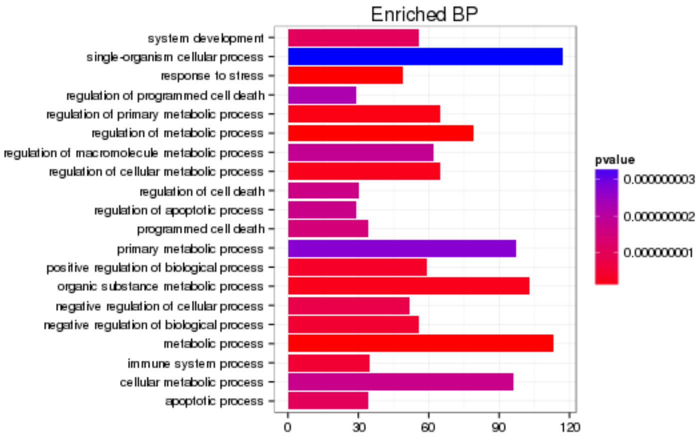

Color Key
and Histogram
Count
0
2
4
6
8
10
4
5
6
Value
RTAAACA_V$FREAC2_01
V$P53_DECAMER_Q2
CAGGTG_V$E12_Q6
V$FOXO4_01
TTCYNRGAA_V$STAT5B_01
V$HSF2_01
CTTTGA_V$LEF1_Q2
KCCGNSWTTT_UNKNOWN
V$HSF1_01
GGGAGGRR_V$MAZ_Q6
RGAANNTTC_V$HSF1_01
TGGAAA_V$NFAT_Q4_01
TTGTTT_V$FOXO4_01
CTTTGT_V$LEF1_Q2
AACTTT_UNKNOWN

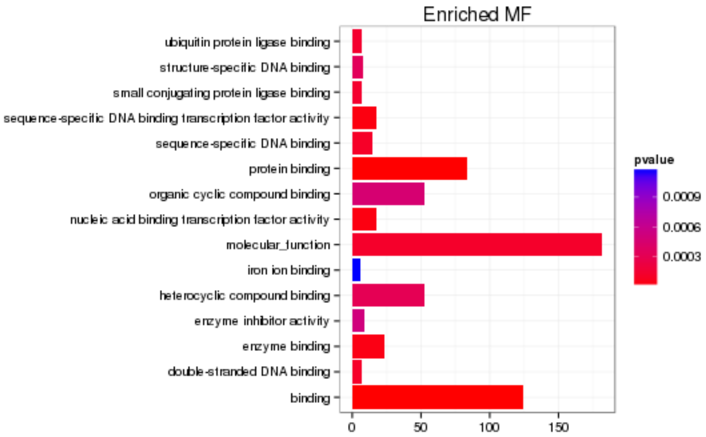
TF zscore:

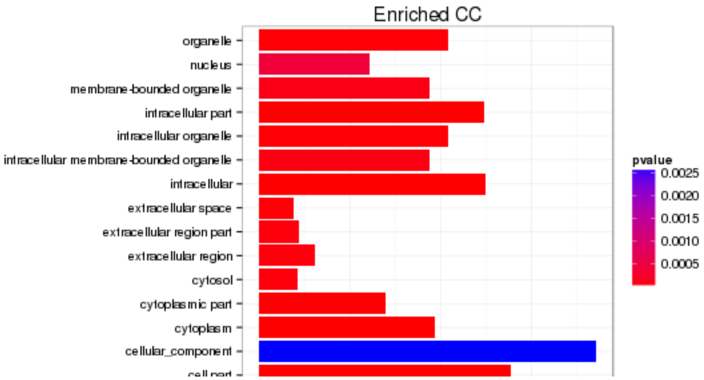


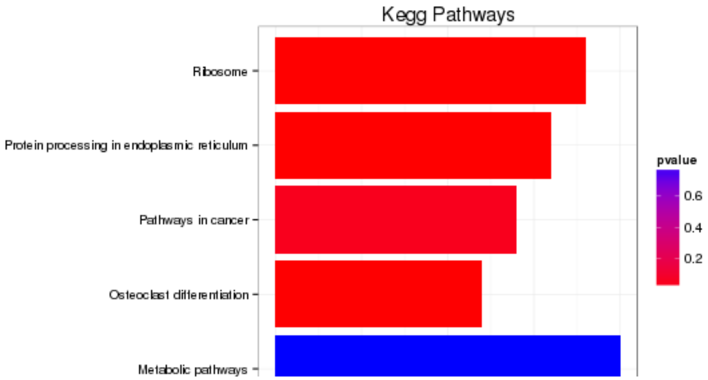
GO enrichment

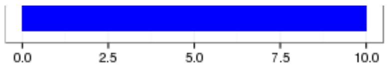
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

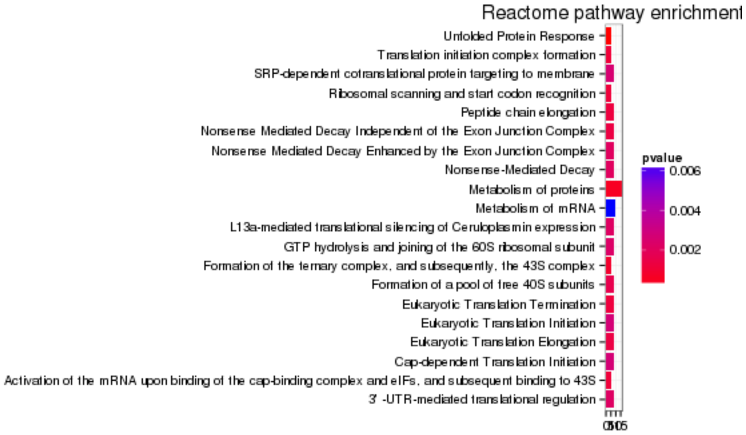

Enriched BP


Enriched MF

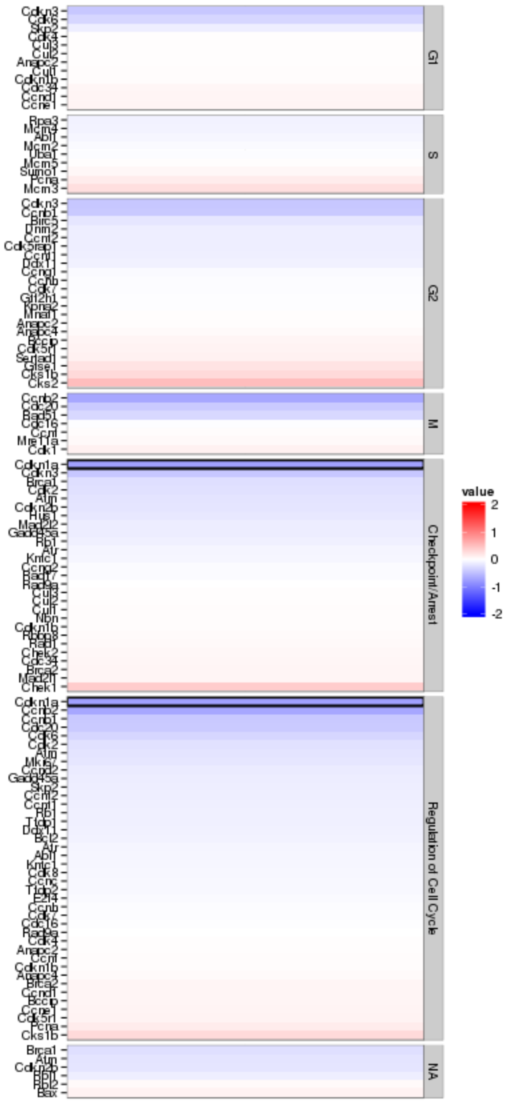

Enriched CC


Kegg Pathways

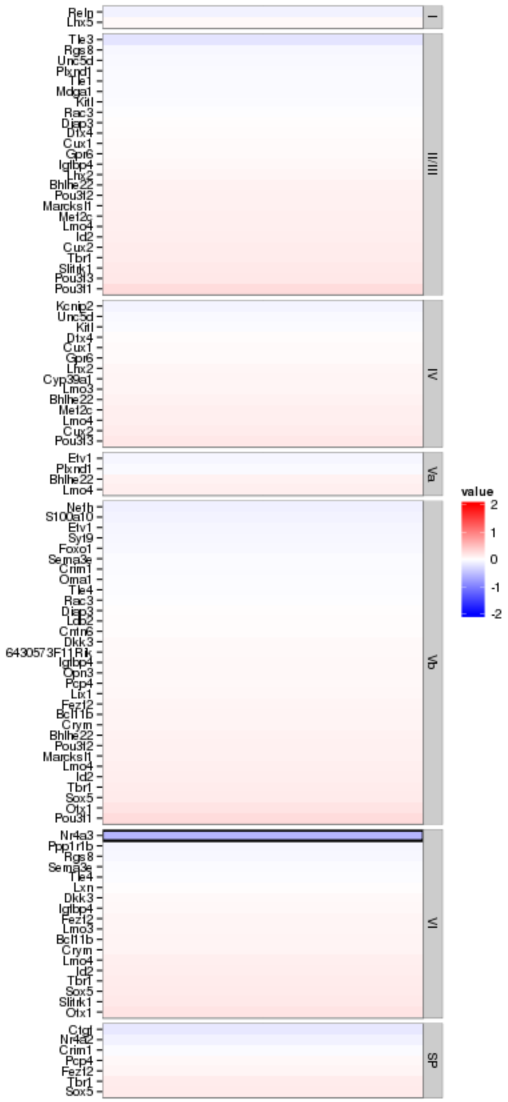



Reactome pathway enrichment

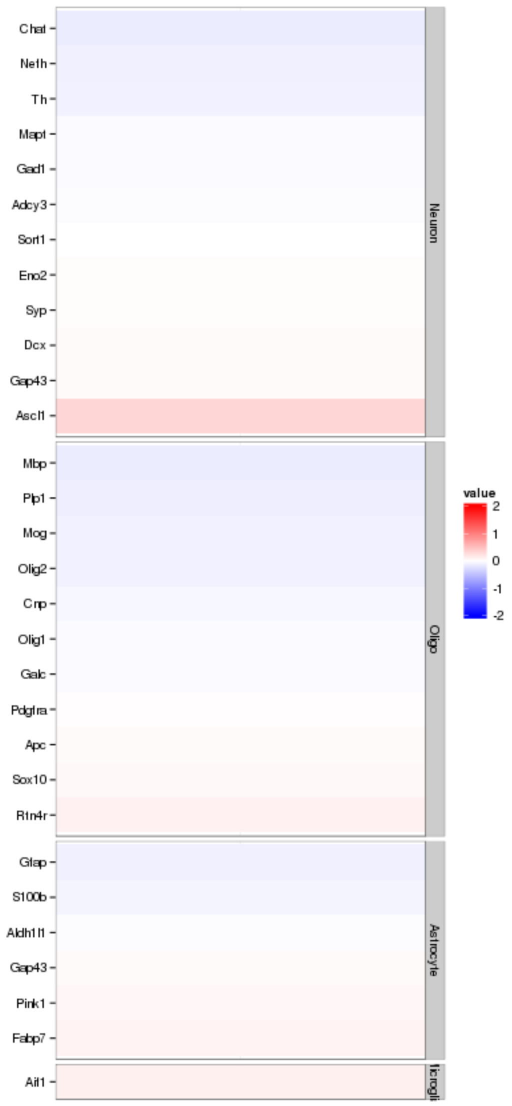
Enrichment or depletion for stage-specific cell cycle markers



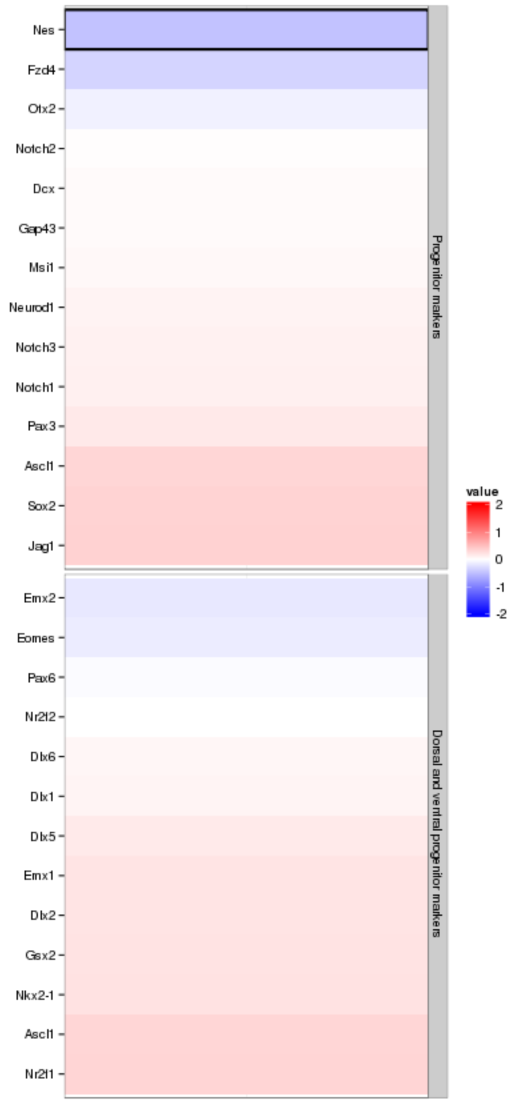
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



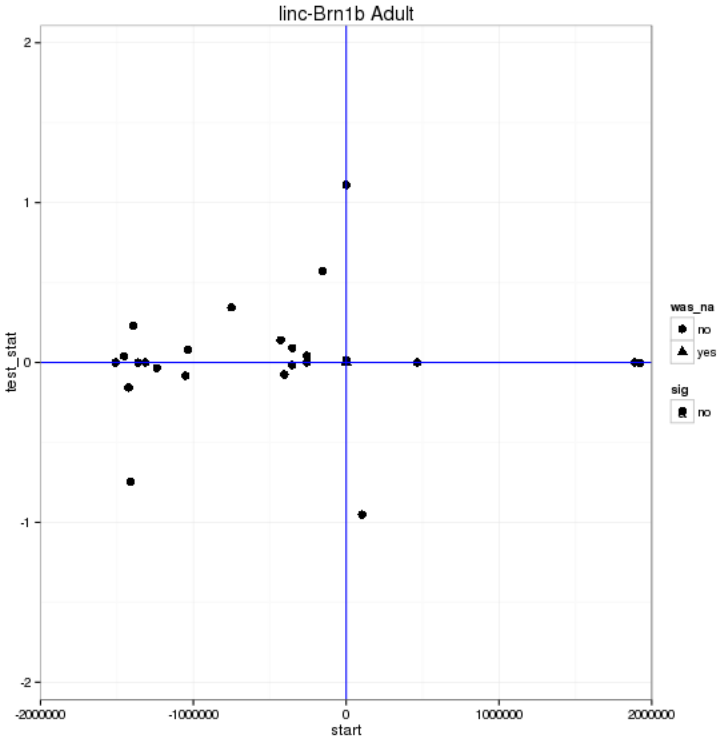
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15	JR731
16	JR835
17	JR836

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	34504400.00	0.76	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	34504400.00	0.59	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	34504400.00	0.98	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	34504400.00	0.80	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	34504400.00	1.04	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	34504400.00	1.07	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	34504400.00	0.81	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	34504400.00	1.16	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	34504400.00	1.01	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	34504400.00	1.30	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	34504400.00	1.51	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	34504400.00	1.02	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	34504400.00	0.98	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	34504400.00	1.21	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR731/abundances.cxb	linc_Brn1b	0	linc_Brn1b_0	24288100.00	34504400.00	0.70	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR835/abundances.cxb	linc_Brn1b	1	linc_Brn1b_1	44561200.00	34504400.00	1.30	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR836/abundances.cxb	linc_Brn1b	2	linc_Brn1b_2	43675800.00	34504400.00	1.27	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1        
##  [2] stringr_0.6.2     
##  [3] seqbias_1.10.0    
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6          
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4      
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7             
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1         
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1          
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4          
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12    
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26   
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2         
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0         
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1    
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2         
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2           
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##            param
## 1       cmd_line
## 2        version
## 3   SVN_revision
## 4 boost_version
## 5         genome
##  
## 1 cuffdiff -p 10 -L WT,linc-Brn1b -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/linc-Brn1b_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainM
## 2 
## 3 
## 4 
## 5 
```

linc-Brn1b KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for linc-Brn1b.

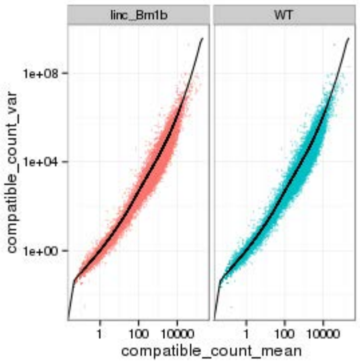
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

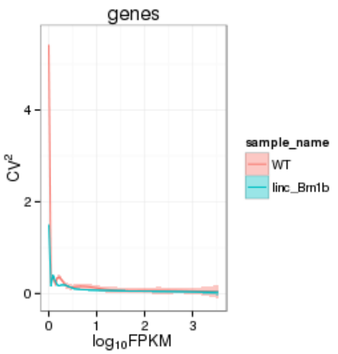
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



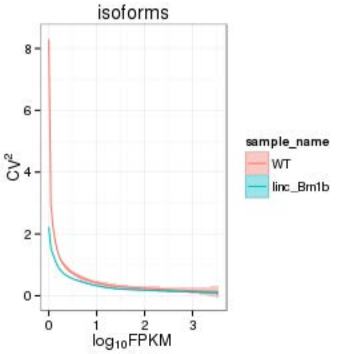
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

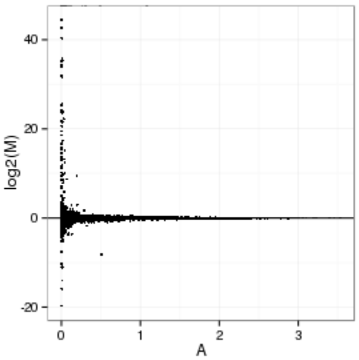
Genes:



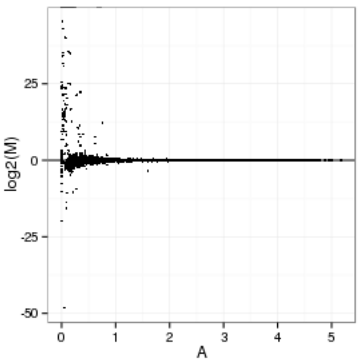
Isoforms:



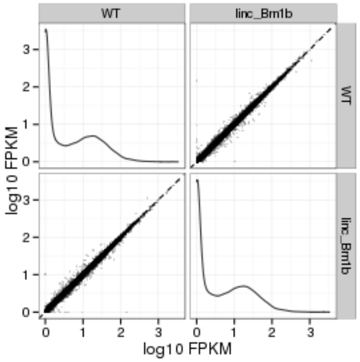
MvA plot



MvA plot counts



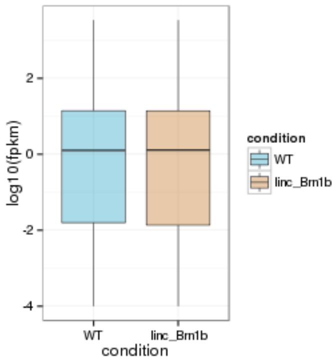
Scatterplot matrix



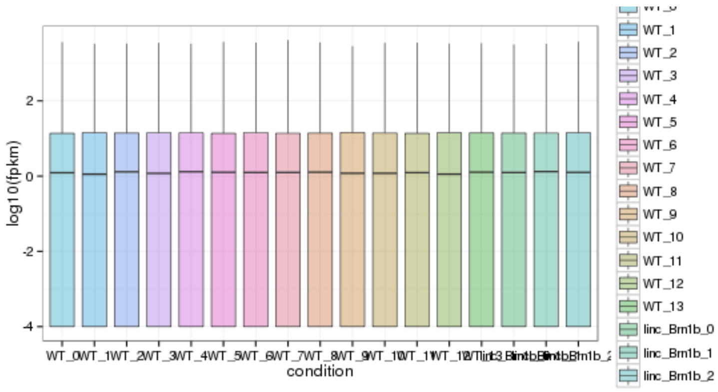
Distributions

Boxplots

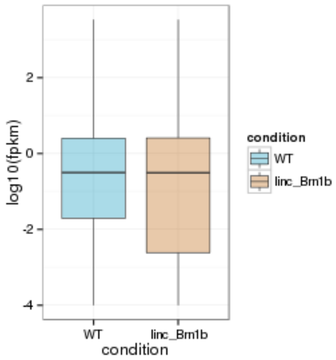
Boxplot (genes)



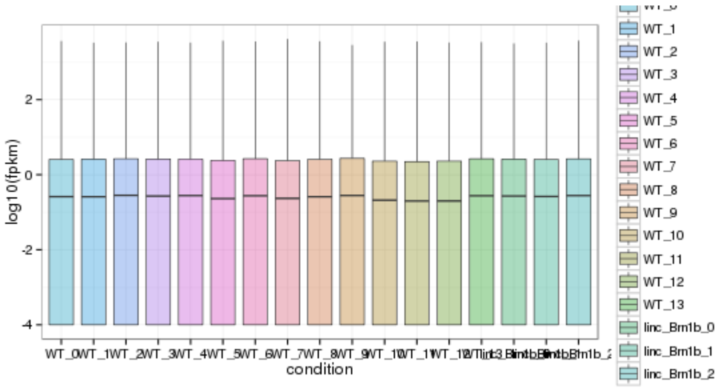
Boxplot (genes, replicates)



Boxplot (isoforms)

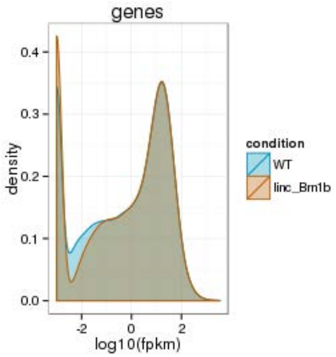


Boxplot (isoforms, replicates)

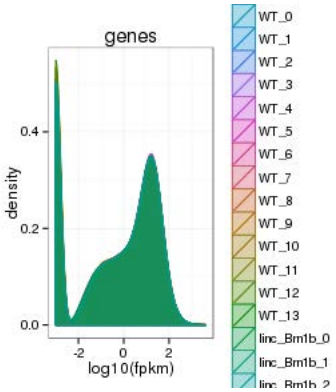


Density

Density (genes)

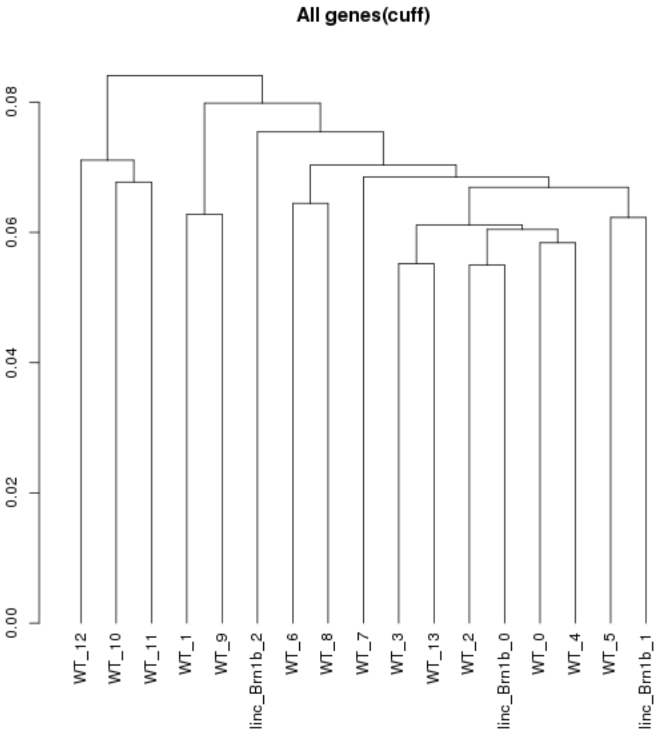


Density (genes, replicates)



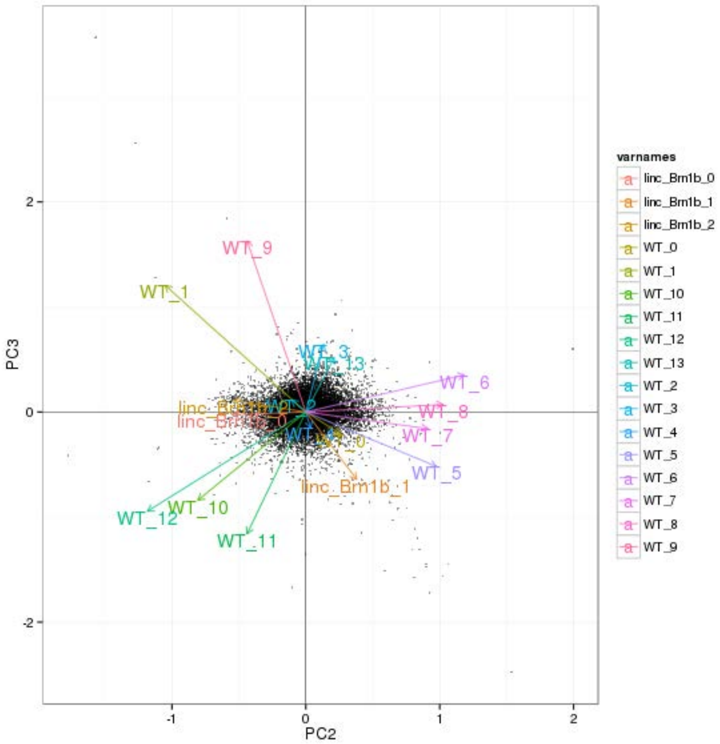
Clustering

Replicate Clusters

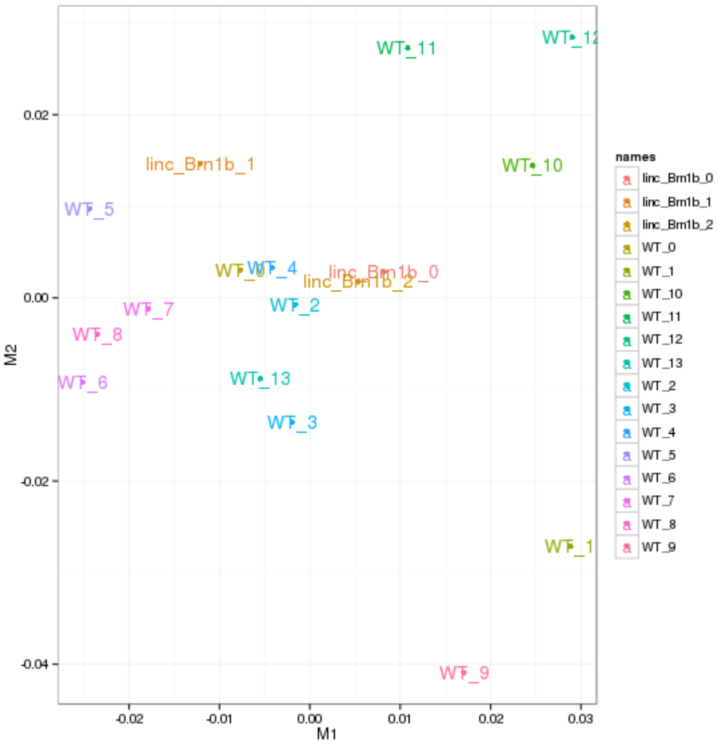


```
## NULL
```

PCA (genes)

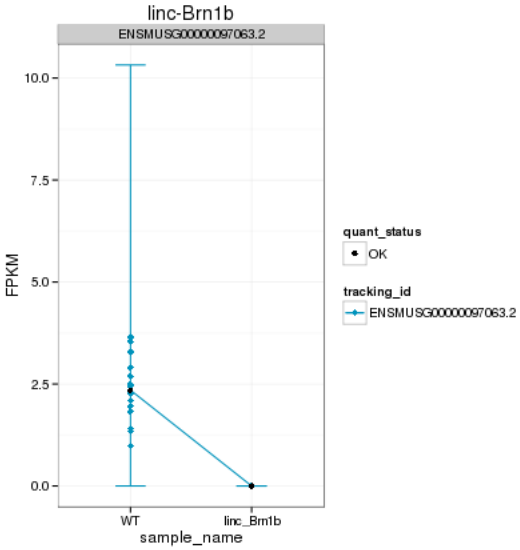

PC3
PC2
2
0
-2
-1
0
1
2
WT_9
WT_1
WT_3
WT_13
WT_6
WT_8
WT_7
WT_5
linc_Bm1b_1
WT_12
WT_10
WT_11
varnames
linc_Bm1b_0
linc_Bm1b_1
linc_Bm1b_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

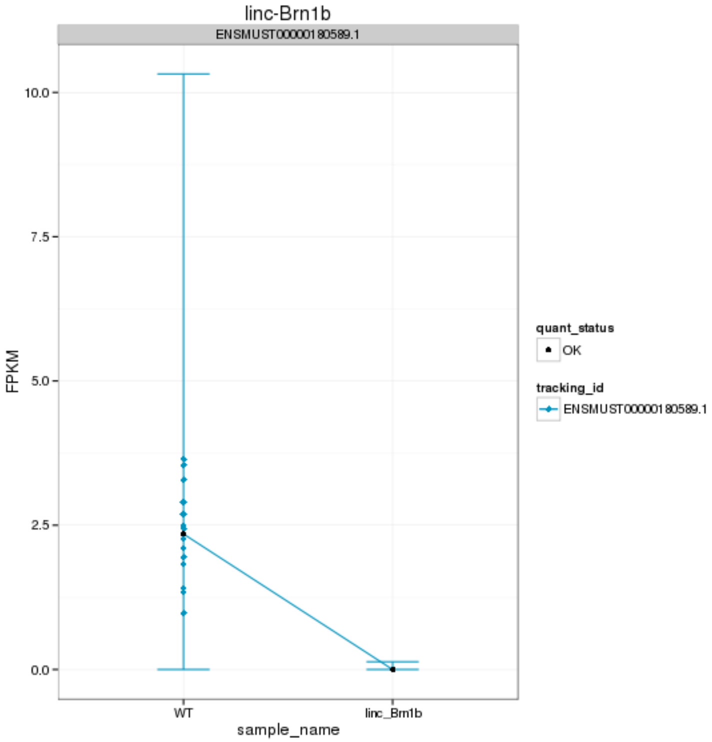


KO assessment

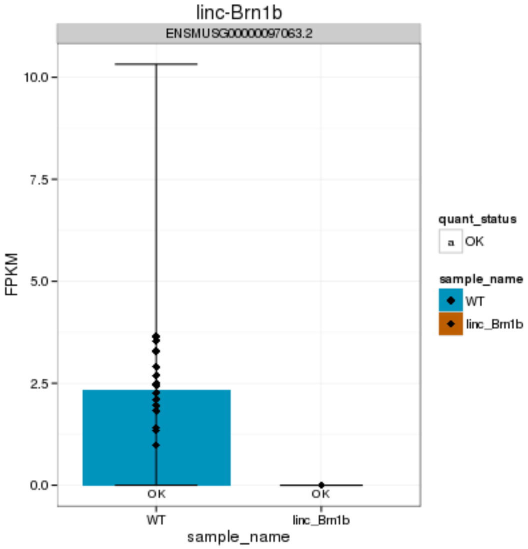
Endogenous lncRNA expression



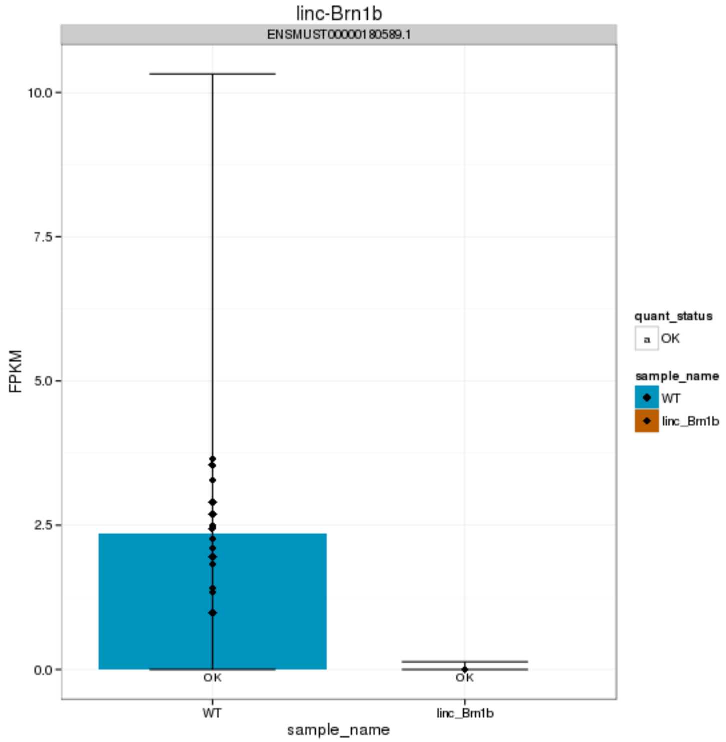
Endogenous expression of linc-Brn1b isoforms:



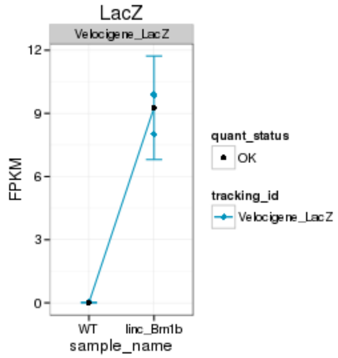
Barplot of gene expression:

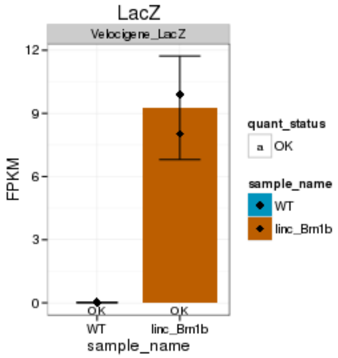


Barplot of isoform expression:



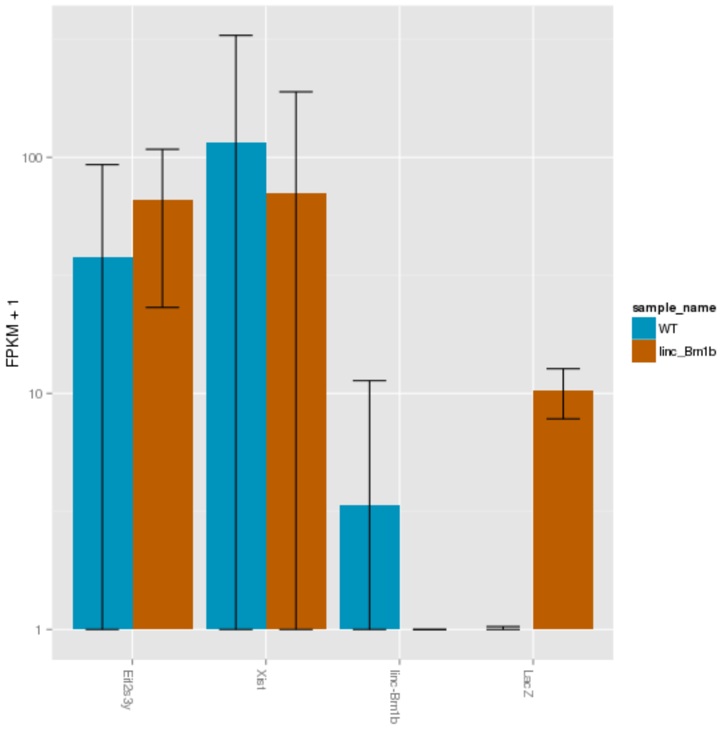
LacZ expression



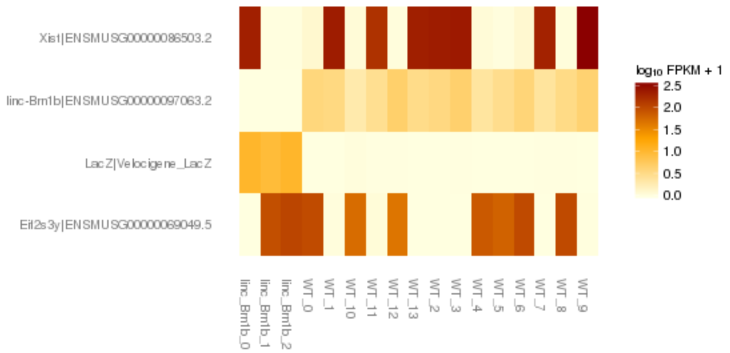


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

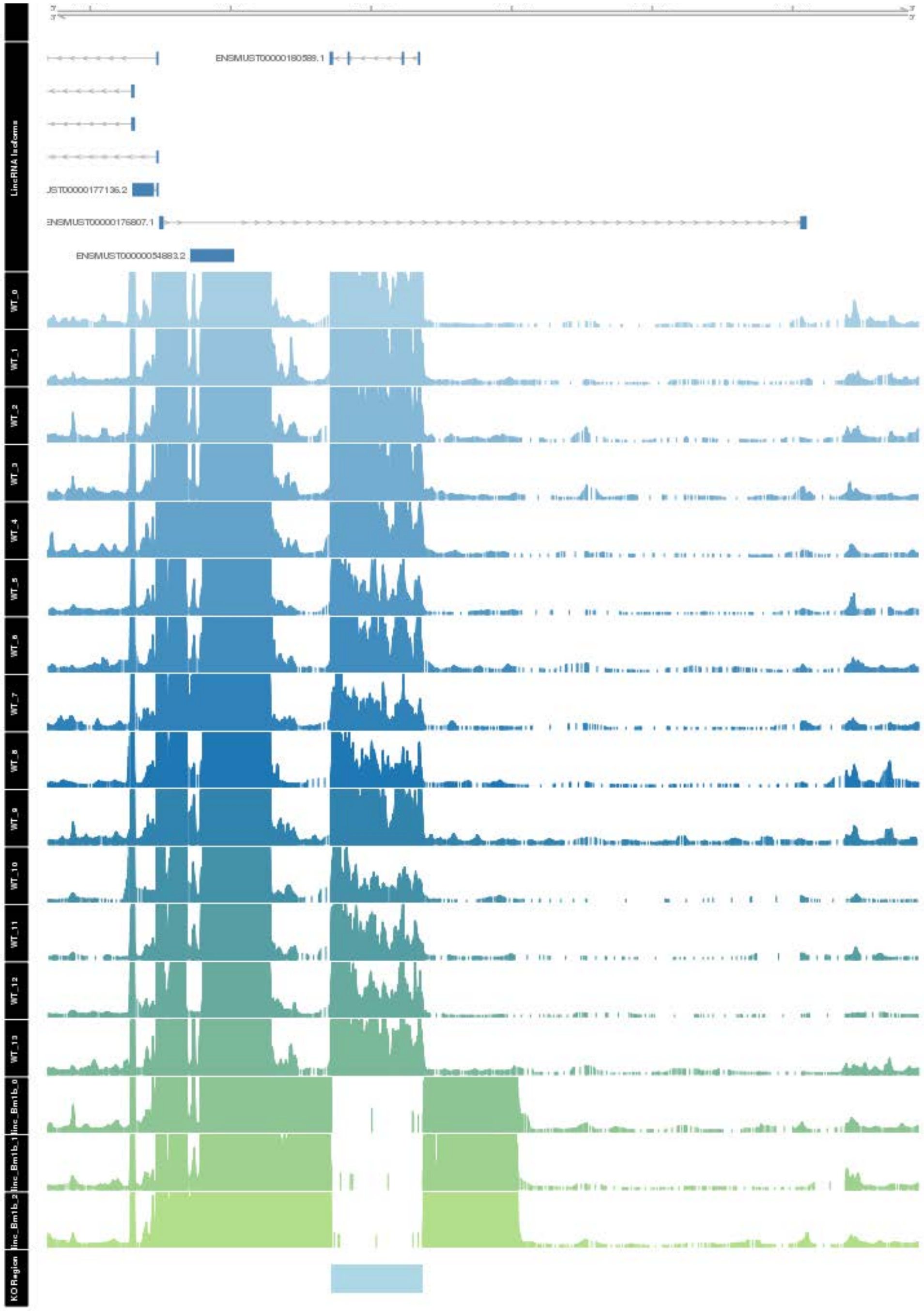
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


LincRNA Isoforms
ENSMUST00000180588.1
JST00000177136.2
ENSMUST00000176807.1
ENSMUST00000054883.2
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
linc_Bm1b_0
linc_Bm1b_1
linc_Bm1b_2
KO Region

Differential Analysis

Differential Genes

There are 130 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Glra1
2	Sez6
3	Nfix
4	Grik3
5	Dlgap1
6	Cacna1e
7	Pax2
8	Sst
9	Crabp2
10	Ndrg1
11	Mef2c
12	Syngr3
13	Syn2
14	Prox1
15	Ebf3
16	Phox2b
17	Ptgds
18	Hivep2
19	Rxrg
20	Celsr1
21	Lhx1
22	Kitl
23	Gria1
24	Fam49a
25	Foxg1
26	Tfap2a
27	Fezf2
28	Skor1
29	Sla
30	Sncg
31	Dlx2
32	Prph
33	Tiam2
34	Lbx1
35	Nnt
36	Msx3
37	Asb1

38 Plxna2
39 Lhx6
40 Syt13
41 Chst1
42 Lamp5
43 Ntsr1

44 Hsd3b6
45 Nr4a3
46 Tal2
47 Ppp2r2c
48 Fosl2
49 Nos1
50 Mmp17
51 Uncx
52 Rph3a
53 Dlx5
54 Dync1i1
55 Rasgef1a
56 Hddc3
57 Mfge8
58 Tbx20
59 Thy1
60 Kirrel3
61 Dscaml1
62 Robo3
63 Camkv
64 Cntnap3
65 Gas7
66 Tbc1d4
67 Ttc28
68 4833424O15Rik
69 Gucy1a3
70 Sncb

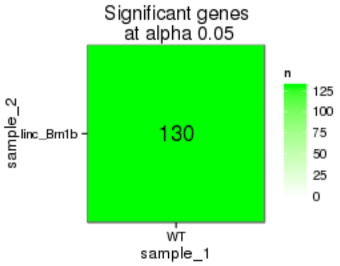
71 Arl4d
72 Tbr1
73 Lars2
74 Arx
75 Vgf
76 Kcnh3
77 Neurod6
78 Neurod2
79 Satb2
80 Ttk

81	Hoxb4
82	Slc6a5
83	Abcc8
84	Zfp704
85	Tlx3
86	Mpped1
87	Dlx1
88	Adamts3
89	Gm9493
90	D3Bwg0562e
91	Cnpy1
92	Prkce
93	Hpcal4
94	Olig1
95	Nxph3
96	Fat4
97	Mc4r
98	Pirt
99	Bcl11b
100	Pou4f1
101	Rpl29
102	Pla2g4e
103	Slc6a7
104	Hbb-y
105	Hbb-bh1
106	Adamts18
107	Hba-x
108	Pign
109	Kdm5d
110	Sez6l
111	Gda
112	Ppp1r1b
113	Trank1
114	Zbtb18
115	D430041D05Rik
116	Gpr88
117	Ptprz1
118	Ddx3y
119	Slc17a7
120	Gm9008
121	Wdfy1
122	Gm10709
123	Kcng1

124 Hs3st4
125 Dlx6os1
126 Myl6
127 Skor2
128 Lhx8
129 Gm26924
130 RP24-312G4.2

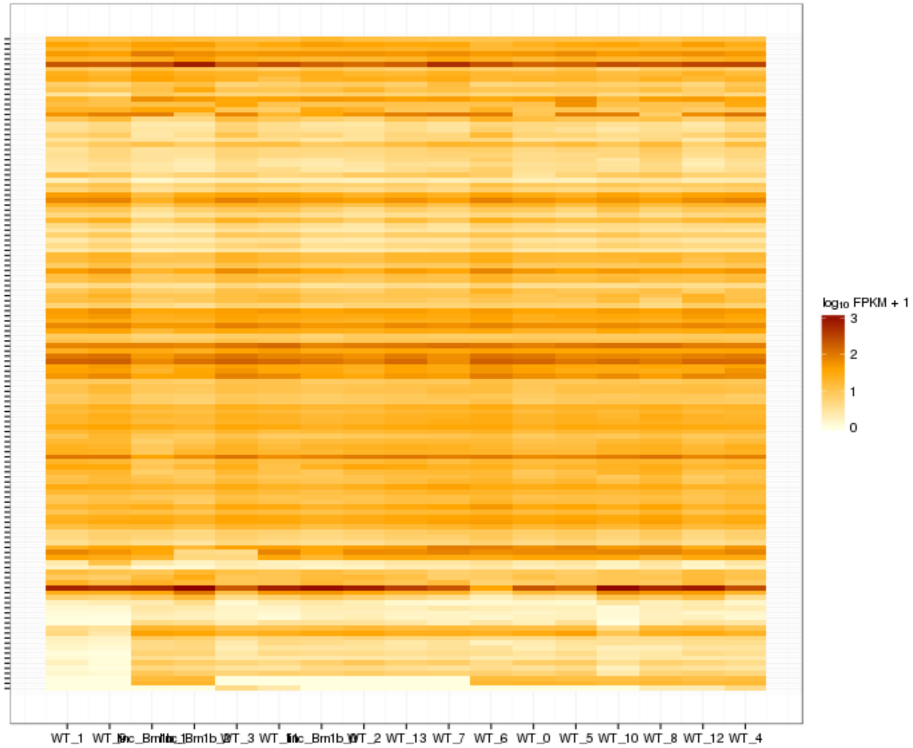
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

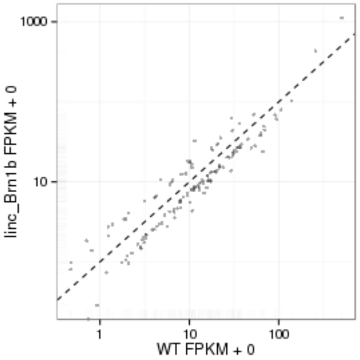


Significant genes with expression >50fpkm (any condition):(turned off)

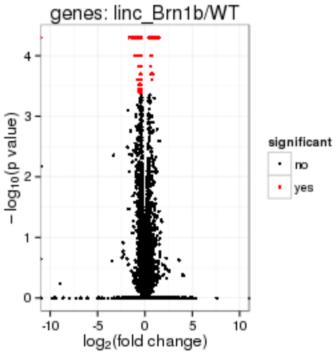
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

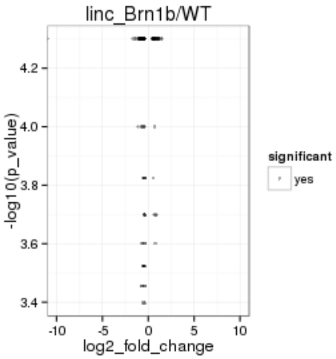
Scatter plot of significant genes only:



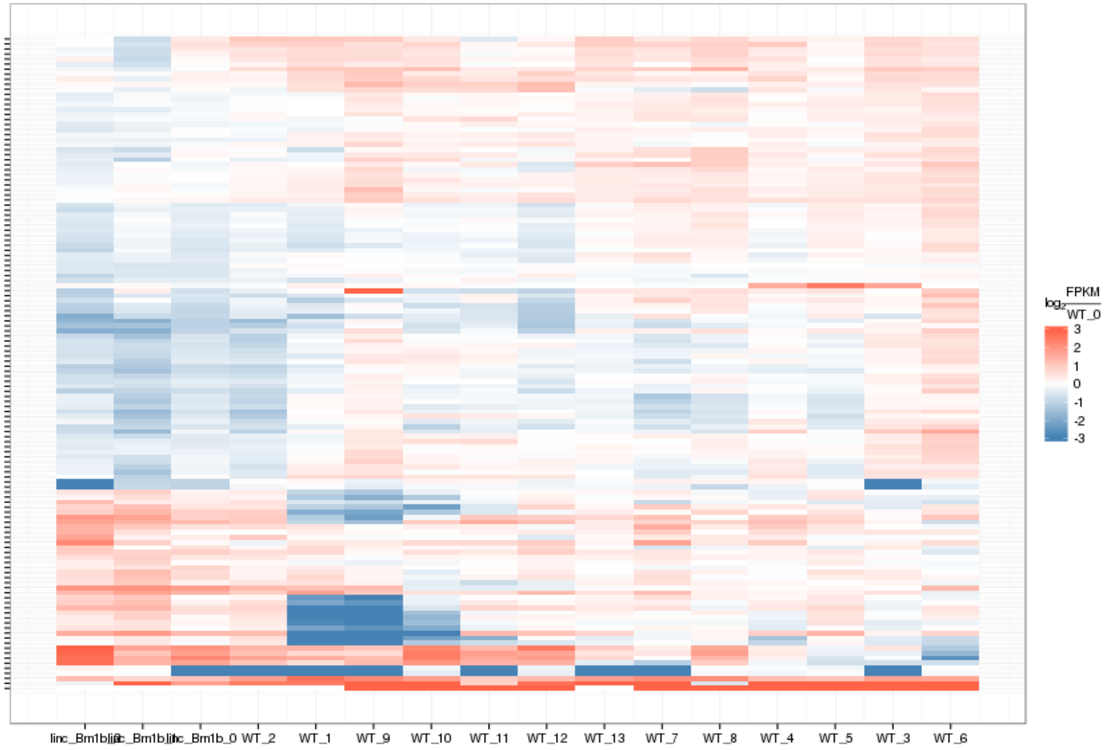
Volcano Plot



Volcano plot with significant genes only:



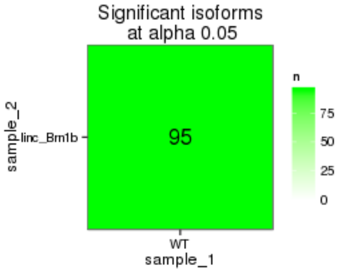
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



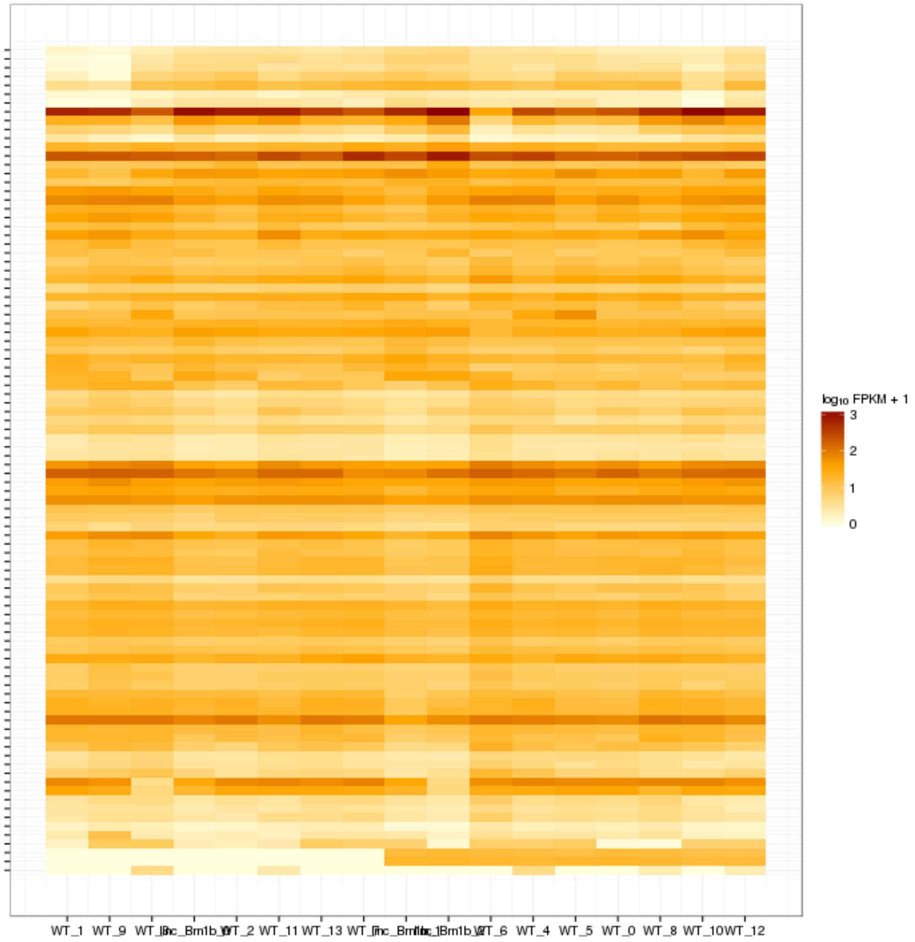
These isoforms are:

	isoAnnot$gene_short_name
1	Nfix
2	Grik3
3	Rec8
4	Crabp2
5	Ndrg1
6	Mef2c
7	Phox2b
8	Hivep2
9	Celsr1
10	Lhx1
11	Kitl
12	Foxg1
13	Fezf2
14	Sla
15	Sncg
16	Dlx2
17	Prph
18	Tiam2
19	Lbx1
20	Nnt
21	Lancl1
22	Ngef
23	Asb1
24	Lypd1
25	Lhx6
26	Syt13
27	Ntsr1
28	Tal2
29	Fosl2
30	Nos1
31	Dlx5
32	Dync1i1
33	Rasgef1a
34	Hddc3
35	Thy1
36	Kirrel3
37	Dscaml1
38	Camkv
39	Gas7
40	Fndc3c1

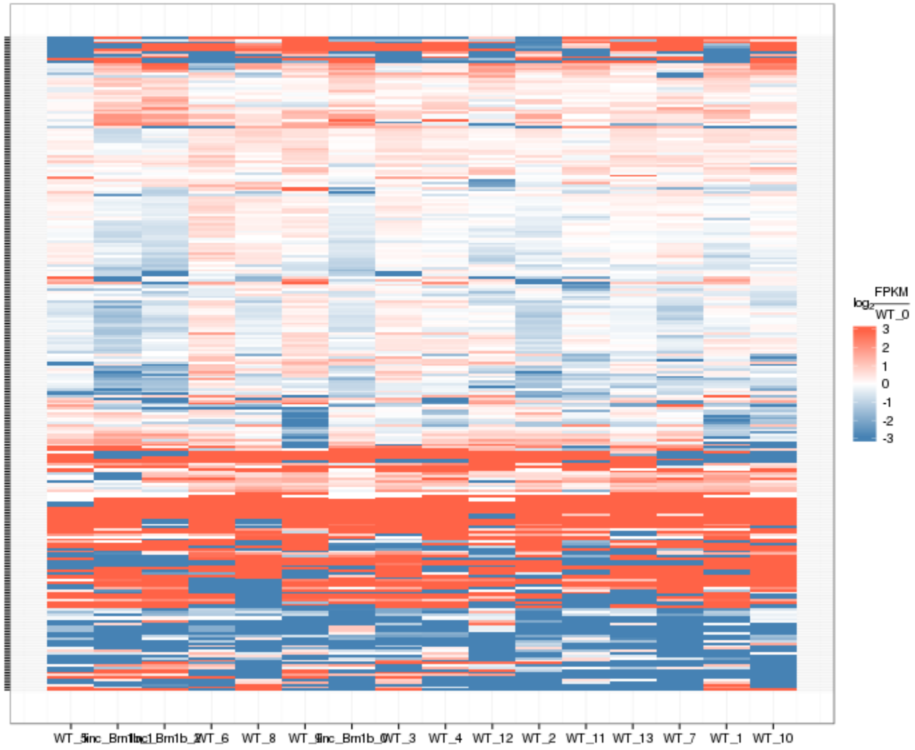
41 Gucy1a3
42 Sncb
43 Arl4d
44 Tbr1
45 Lars2
46 Arx
47 Kcnh3
48 Neurod6
49 Sh3rf3
50 Satb2
51 Ttk
52 Hoxb4
53 Slc6a5
54 Abcc8
55 Tlx3
56 Sox5
57 Mpped1
58 Dlx1
59 Reln
60 Adamts3
61 Prkce
62 Olig1
63 Nxph3
64 Fat4
65 Mc4r
66 Pirt
67 Bcl11b
68 Pou4f1
69 Rpl29
70 Pla2g4e
71 Slc6a7
72 Hbb-y
73 Hbb-bh1
74 C130021I20Rik
75 Adamts18
76 Hba-x
77 Kcnq3
78 Pign
79 Kdm5d
80 Gda
81 Opcml
82 Ptprz1
83 Ddx3y

84 Tmem132b
85 Slc17a7
86 Gm9008
87 D2hgdh
88 Wdfy1
89 Gm10709
90 Kcng1
91 Hs3st4
92 Myl6
93 Gm26924
94 RP24-312G4.2

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

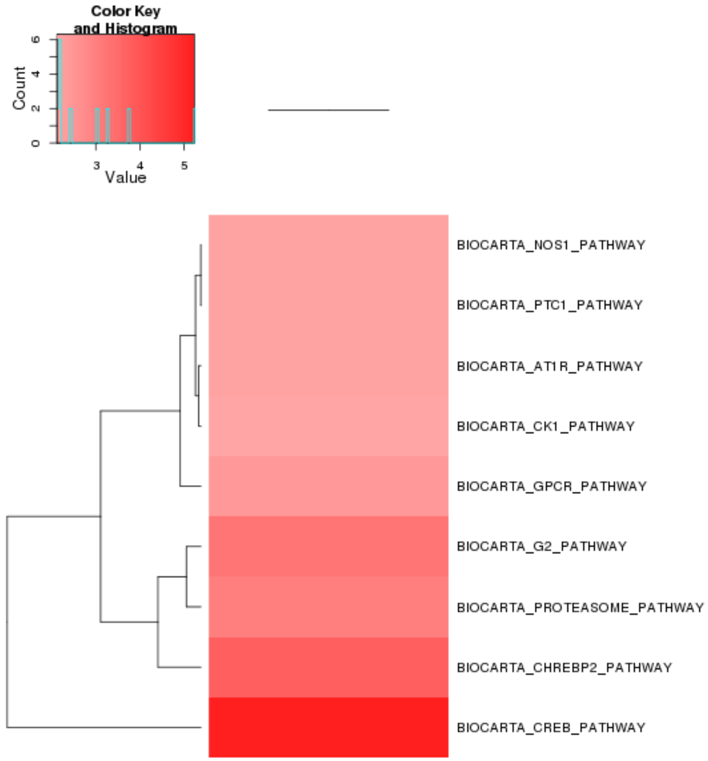
Gene/Pathway Analysis

GSEA

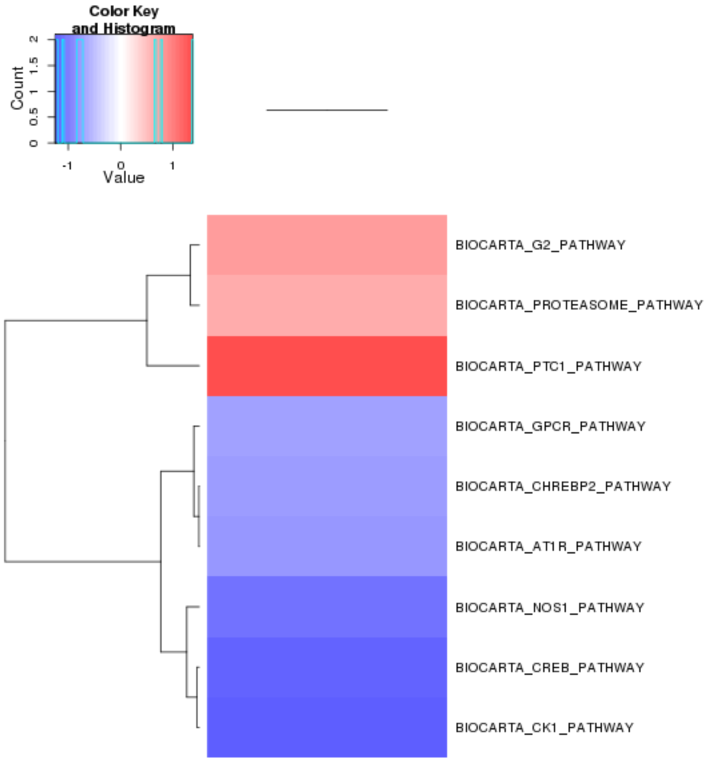
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

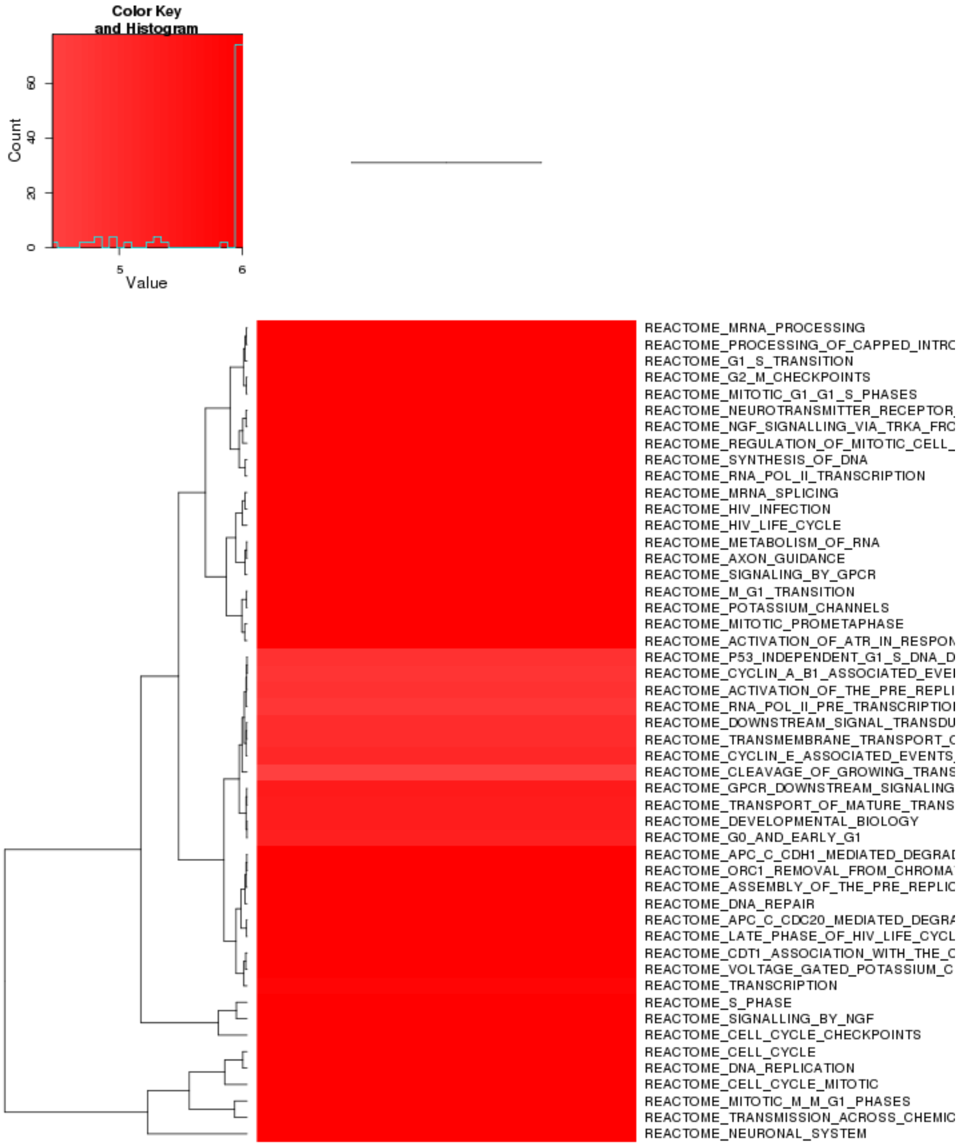
Biocarta enrichment:



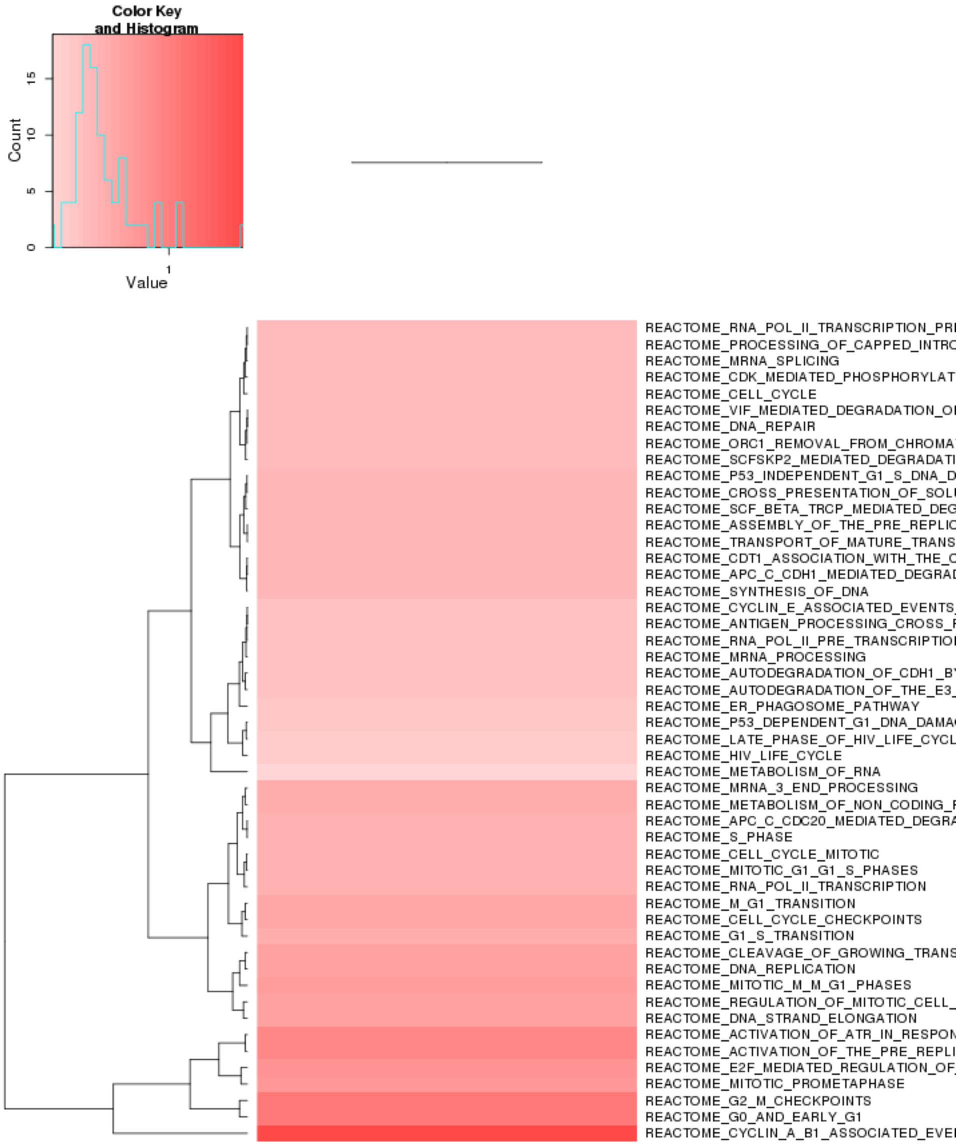
Biocarta zscore:



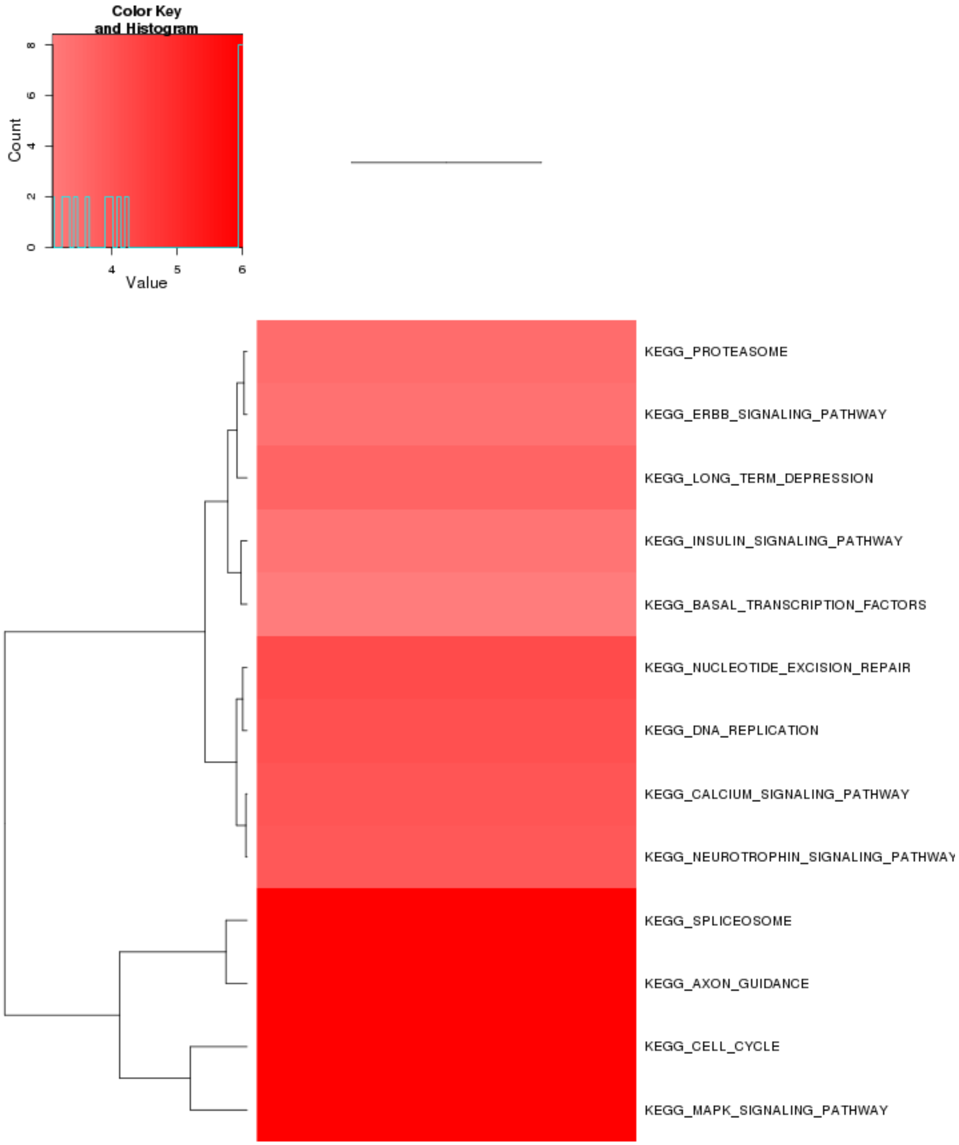
Reactome enrichment:



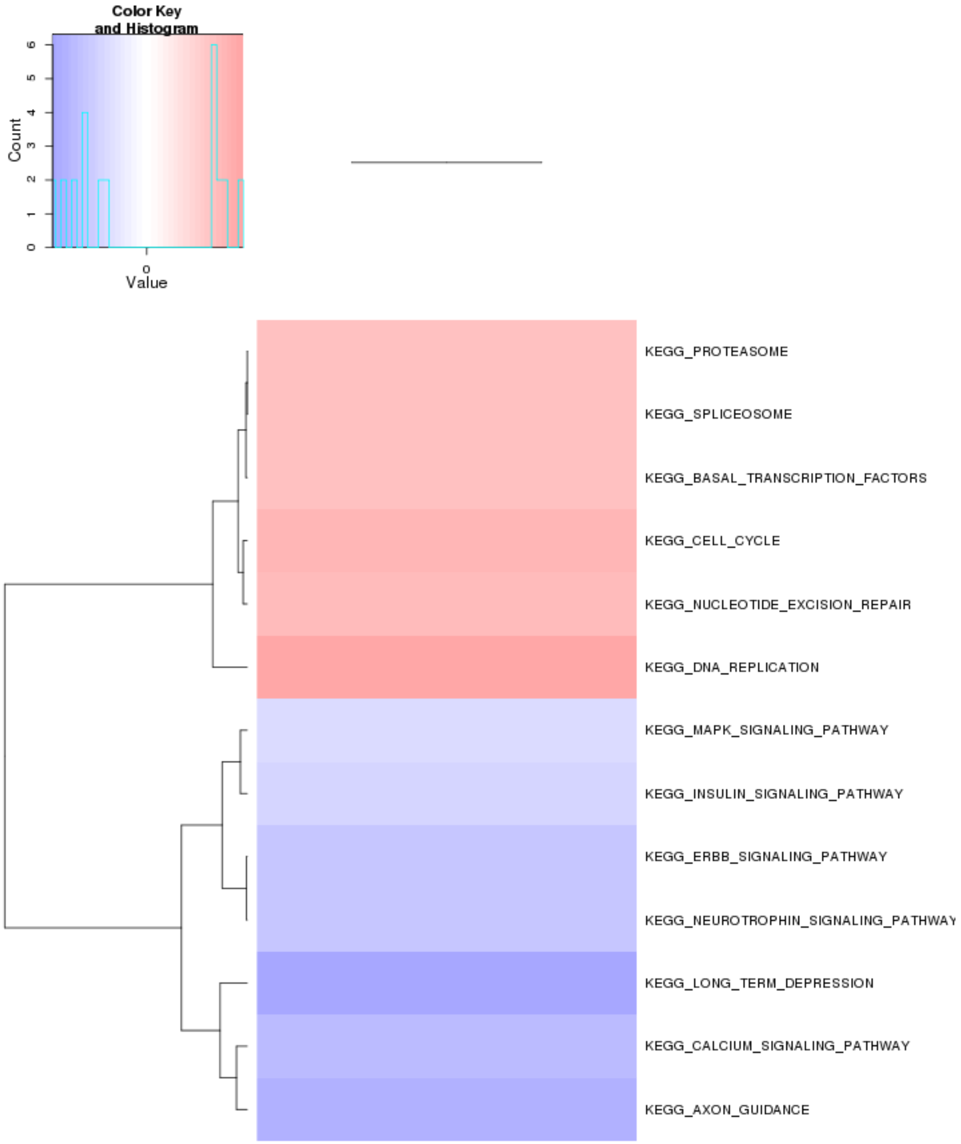
Reactome zscore:



Kegg enrichment:


Color Key
and Histogram
Count
0
2
4
6
8
4
5
6
Value
KEGG_PROTEASOME
KEGG_ERBB_SIGNALING_PATHWAY
KEGG_LONG_TERM_DEPRESSION
KEGG_INSULIN_SIGNALING_PATHWAY
KEGG_BASAL_TRANSCRIPTION_FACTORS
KEGG_NUCLEOTIDE_EXCISION_REPAIR
KEGG_DNA_REPLICATION
KEGG_CALCIUM_SIGNALING_PATHWAY
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY
KEGG_SPLICEOSOME
KEGG_AXON_GUIDANCE
KEGG_CELL_CYCLE
KEGG_MAPK_SIGNALING_PATHWAY

Kegg zscore:



Interneuron enrichment:

```
## Error: argument is of length zero
```

Interneuron zscore:

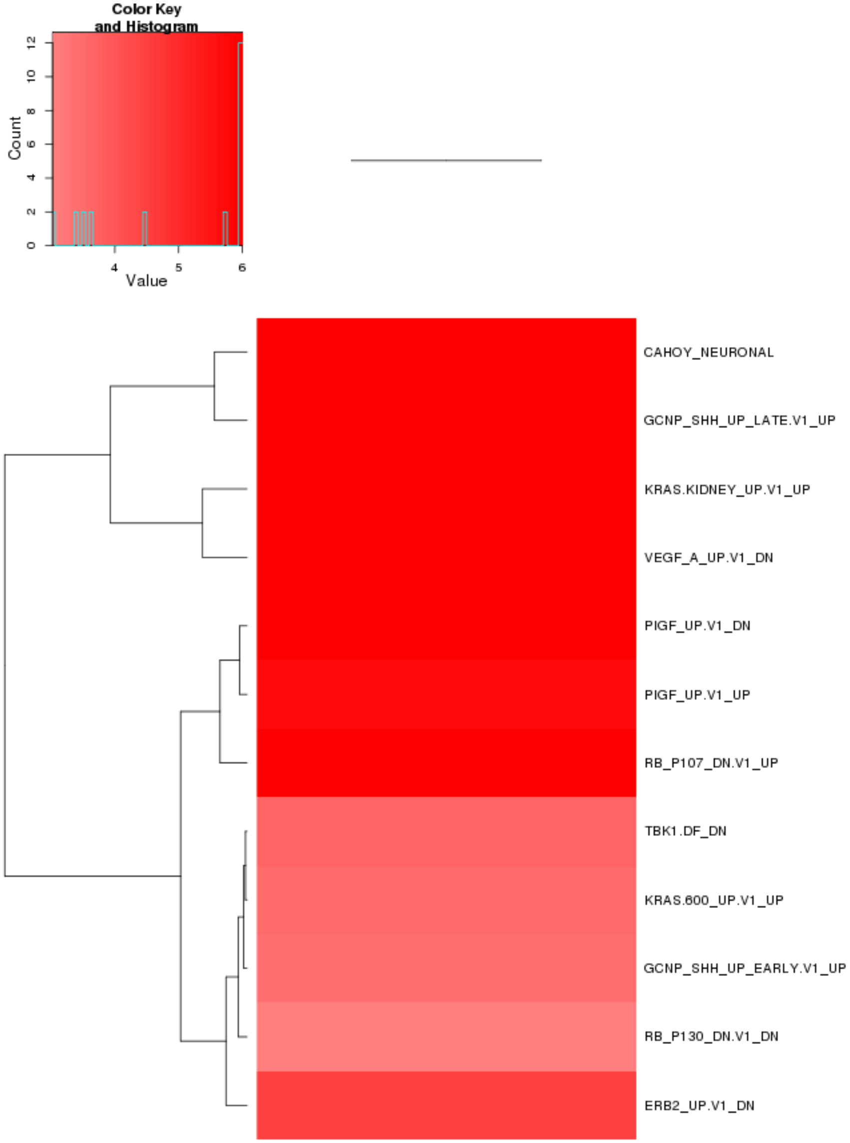
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

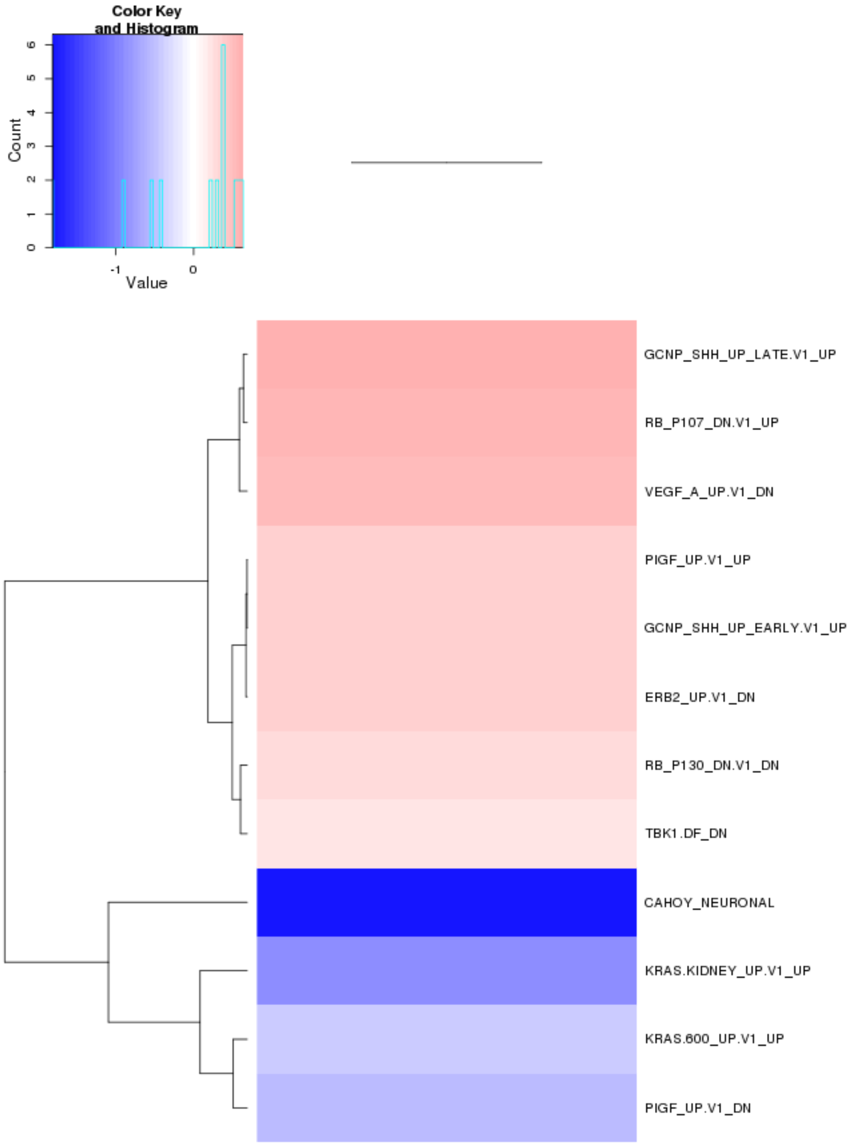
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

Oncogene enrichment:

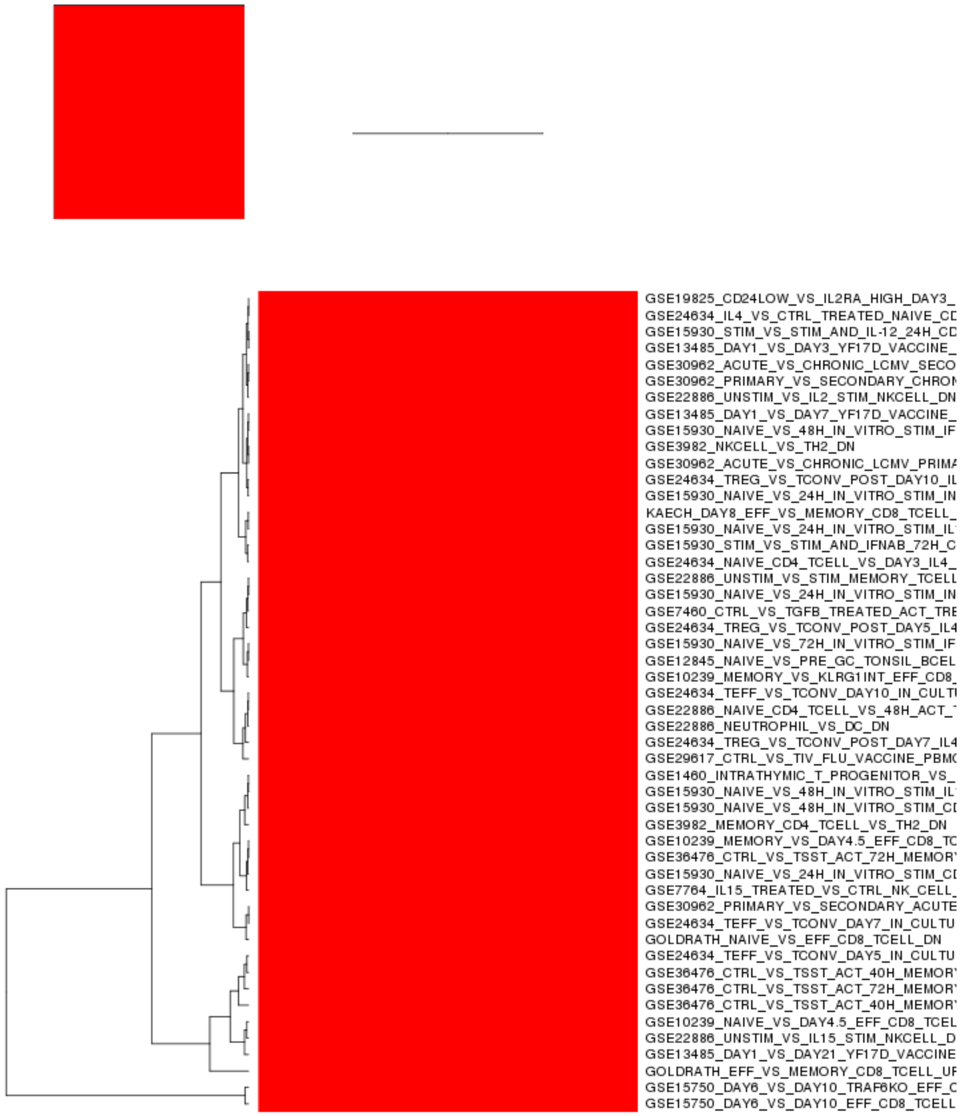


Oncogene zscore:



Immuno enrichment:

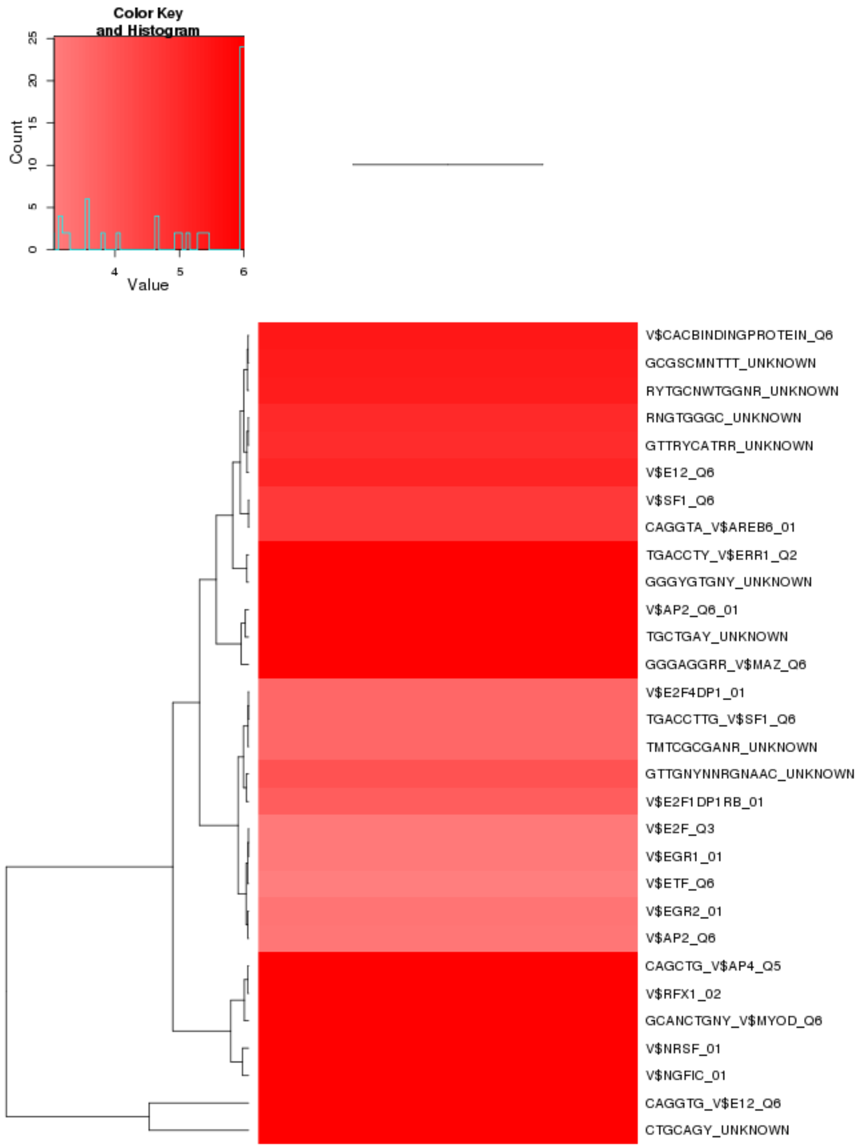
```
## Error: no locations are finite
```



Immuno zscore:

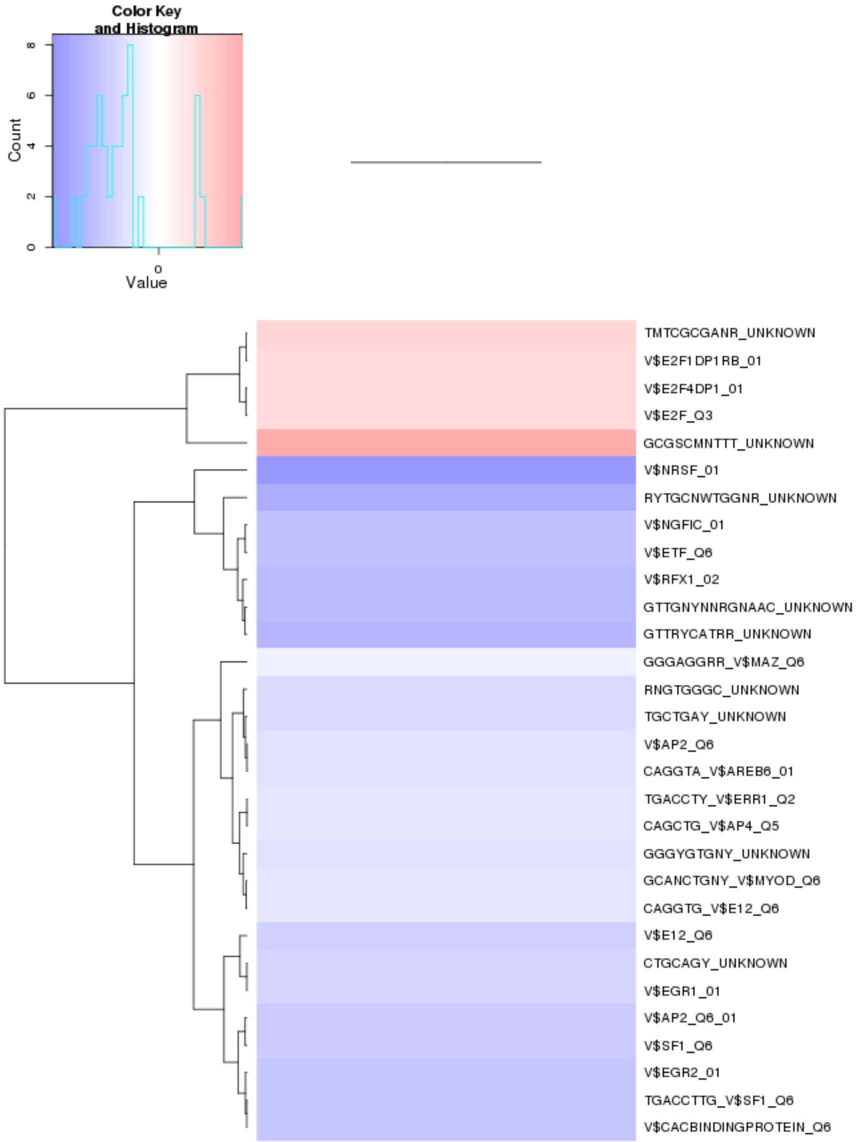
TF enrichment:

```
## Error: subscript out of bounds
```



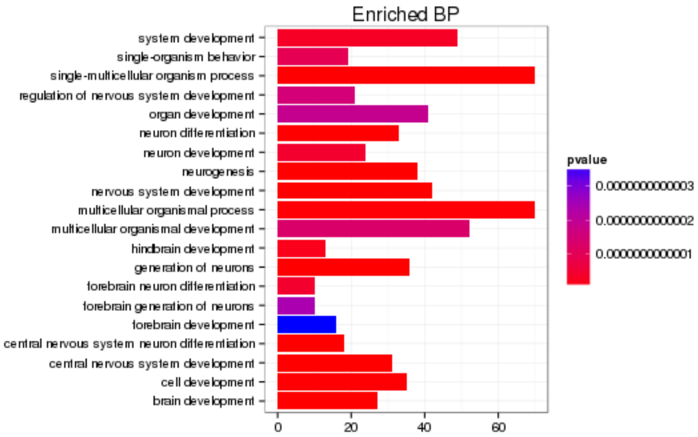
TF zscore:

```
## Error: subscript out of bounds
```

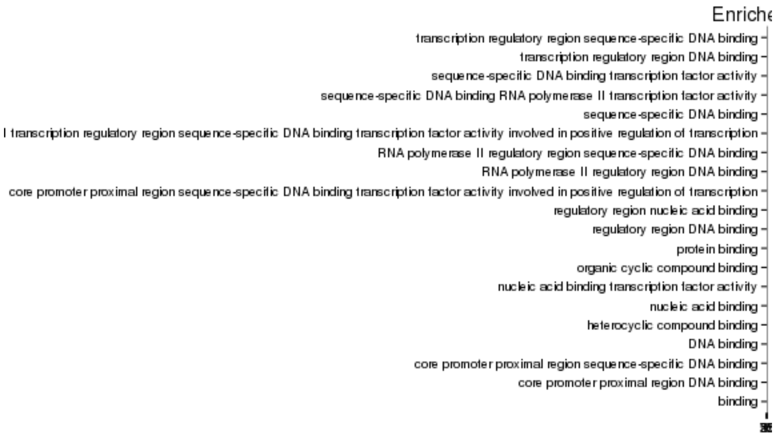


GO enrichment

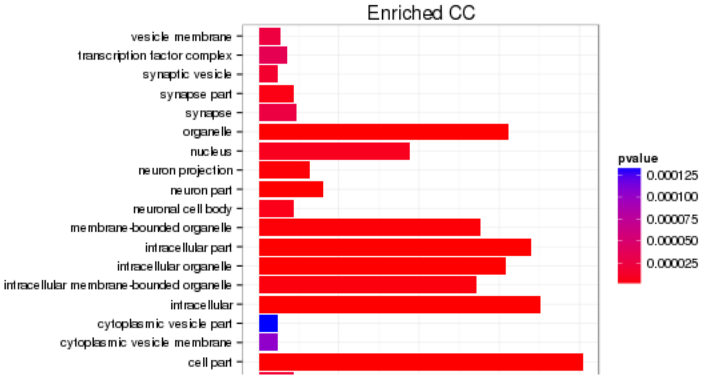
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.



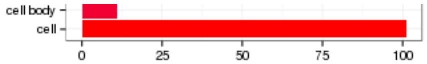
Enriched BP



Enriche

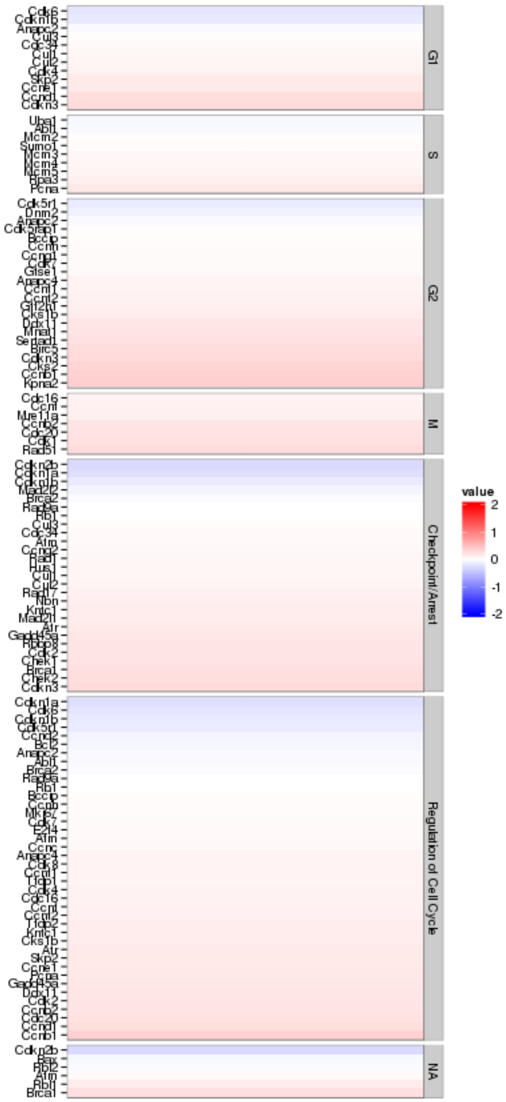


Enriched CC

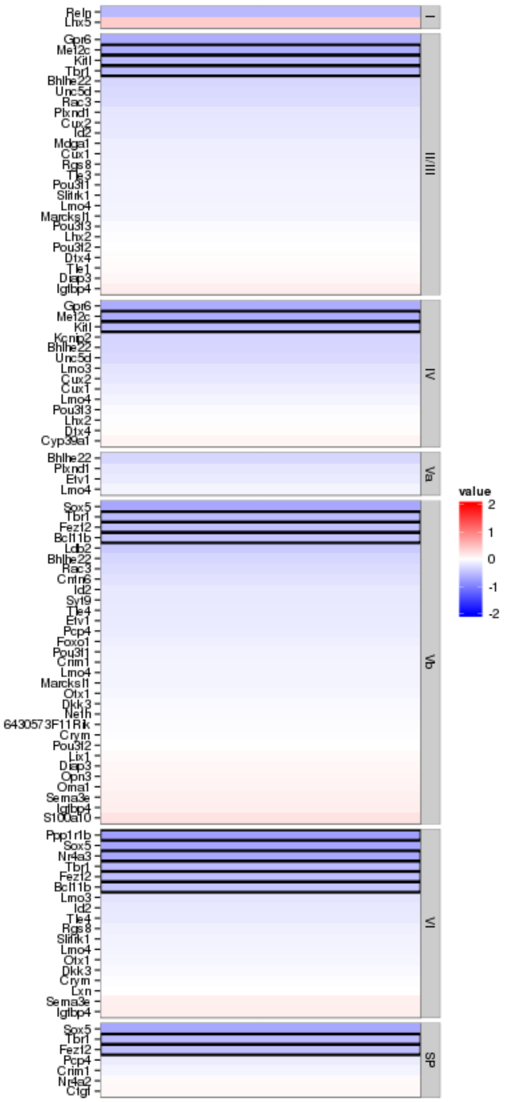


```
## Error: 'x' and 'units' must have length > 0
```

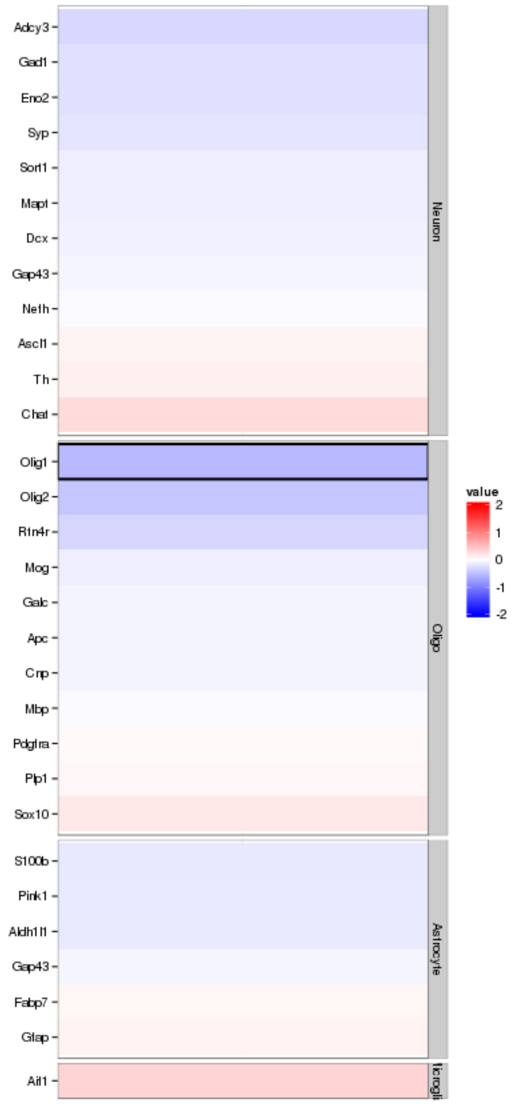
Enrichment or depletion for stage-specific cell cycle markers



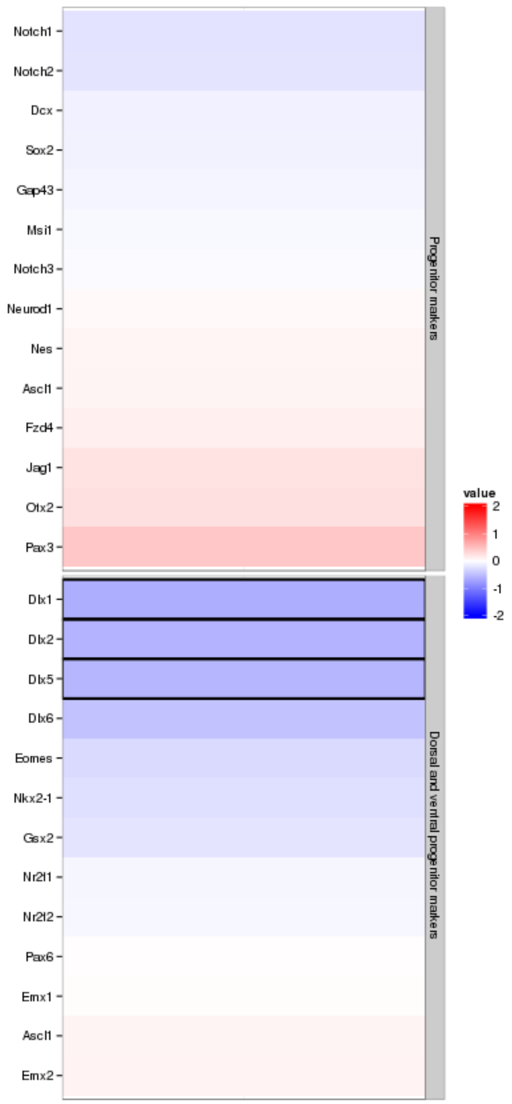
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



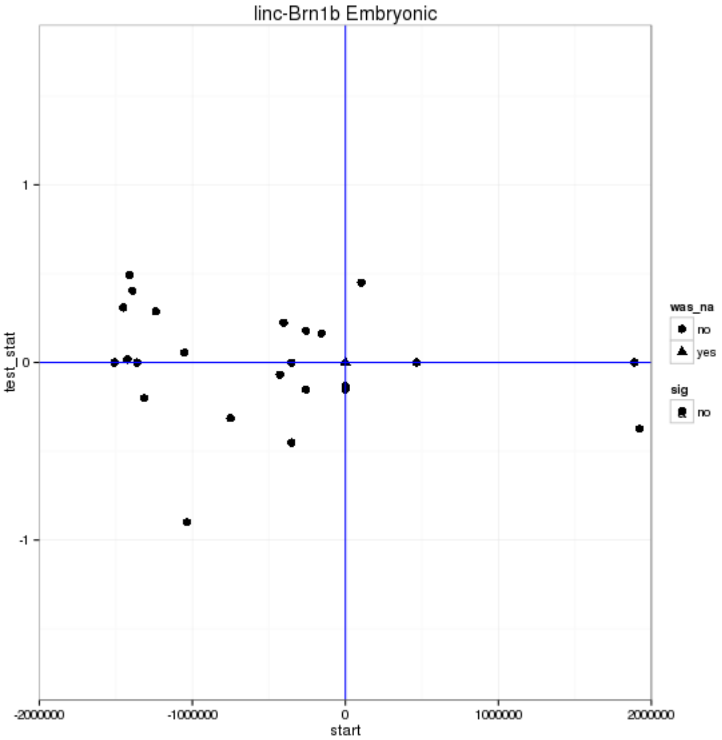
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15	JR758
16	JR764
17	JR808

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	32398700.00	1.25	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	32398700.00	1.09	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	32398700.00	1.22	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	32398700.00	1.28	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	32398700.00	1.19	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	32398700.00	0.89	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	32398700.00	0.97	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	32398700.00	0.91	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	32398700.00	0.85	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	32398700.00	0.95	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	32398700.00	0.80	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	32398700.00	0.79	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	32398700.00	0.68	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	32398700.00	1.20	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR758/abundances.cxb	linc_Brn1b	0	linc_Brn1b_0	41595700.00	32398700.00	1.31	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR764/abundances.cxb	linc_Brn1b	1	linc_Brn1b_1	30294500.00	32398700.00	0.95	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR808/abundances.cxb	linc_Brn1b	2	linc_Brn1b_2	31223700.00	32398700.00	0.97	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1                             
##  [2] stringr_0.6.2                          
##  [3] seqbias_1.10.0                         
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6          
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4      
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7             
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1         
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1          
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4          
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12    
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26   
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2         
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0         
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1    
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2         
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2           
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,linc-Brn1b -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/linc-Brn1b_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/Br
## 2
## 3
## 4
## 5
```

linc-Cox2 KO vs WT (Adult)

This file shows the wt-v-ko comparison for linc-Cox2.

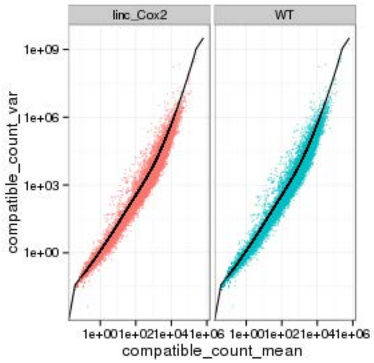
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

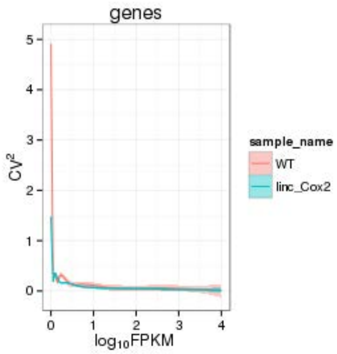
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



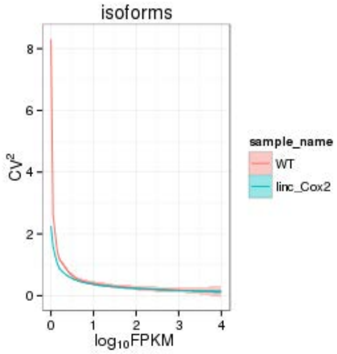
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

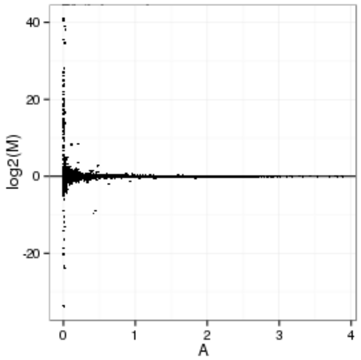
Genes:



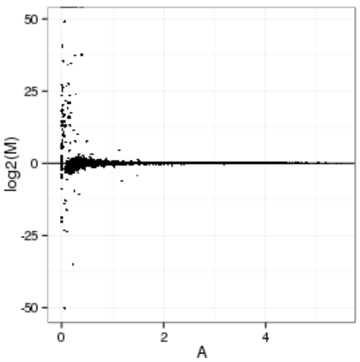
Isoforms:



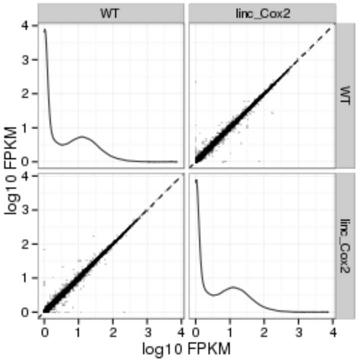
MvA plot



MvA plot counts



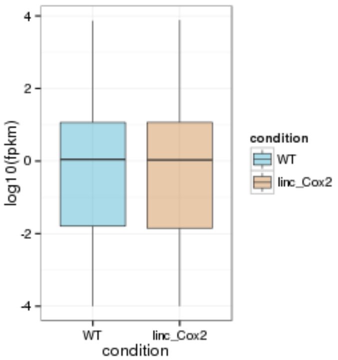
Scatterplot matrix



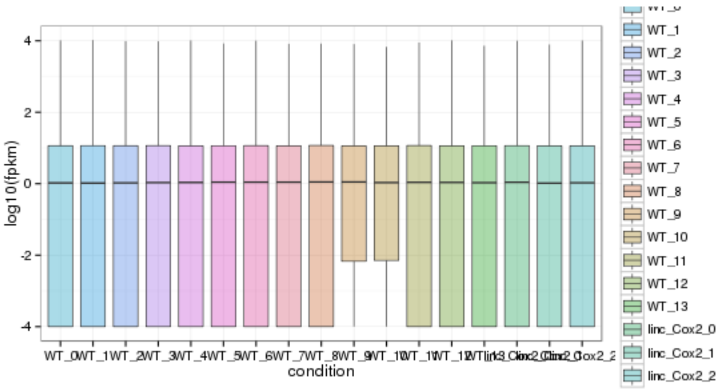
Distributions

Boxplots

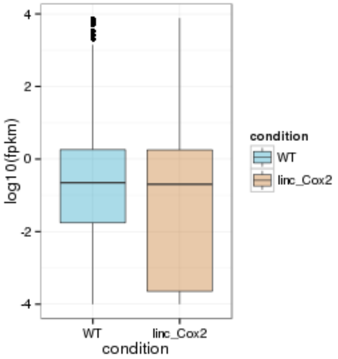
Boxplot (genes)



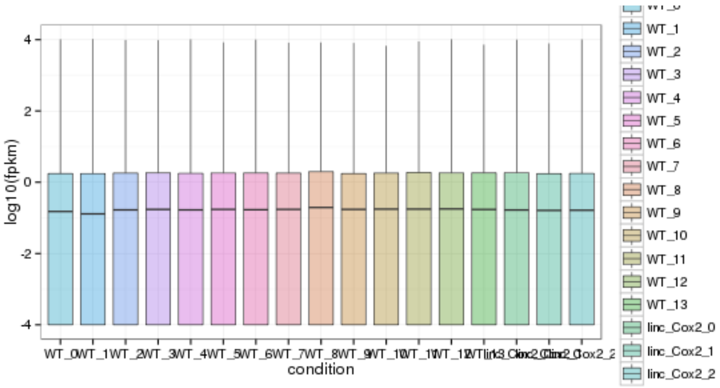
Boxplot (genes, replicates)



Boxplot (isoforms)

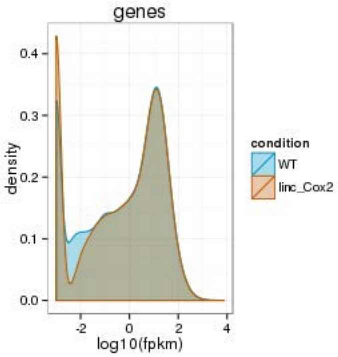


Boxplot (isoforms, replicates)

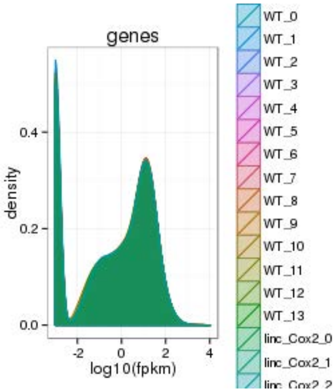


Density

Density (genes)

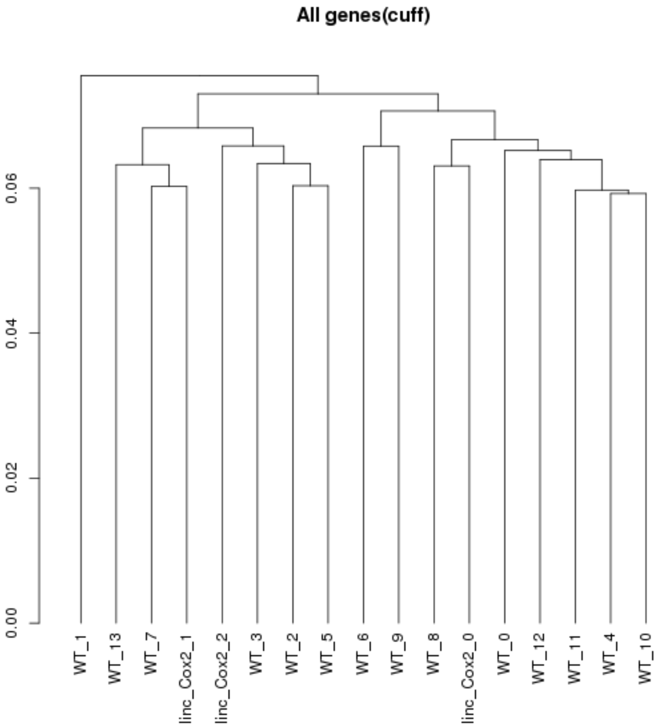


Density (genes, replicates)



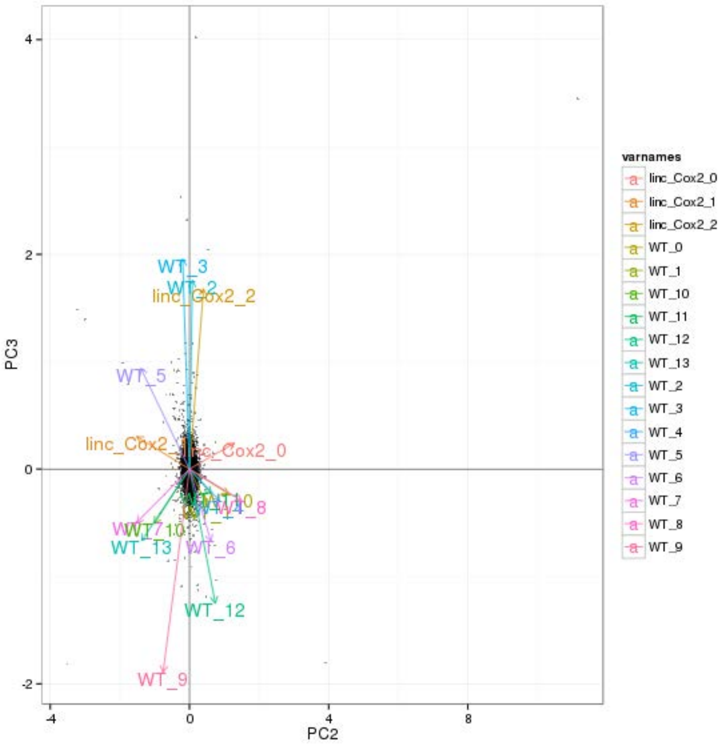
Clustering

Replicate Clusters



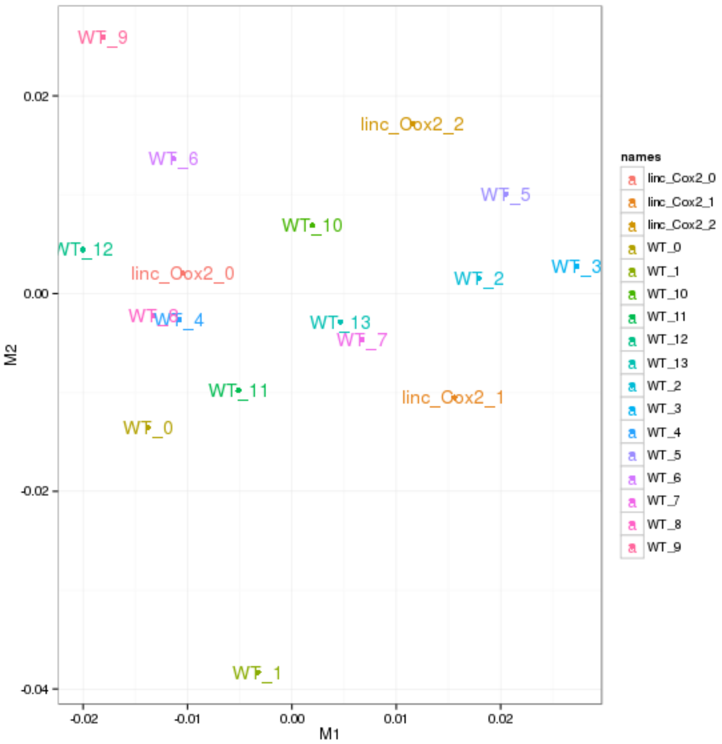
```
## NULL
```

PCA (genes)



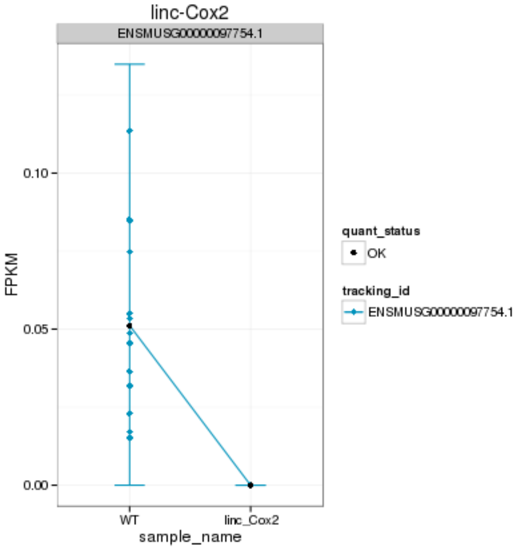
PC3
PC2
4
2
0
-2
-4
0
4
8
WT_3
WT_2
linc_Cox2_2
WT_5
linc_Cox2_1
linc_Cox2_0
WT_10
WT_4
WT_8
WT_7
WT_1
WT_0
WT_13
WT_6
WT_12
WT_9
varnames
linc_Cox2_0
linc_Cox2_1
linc_Cox2_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

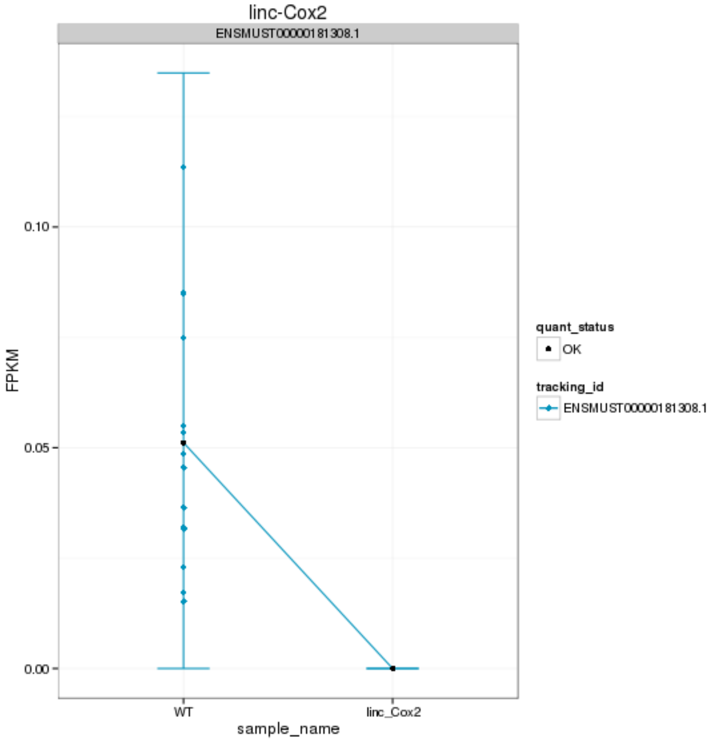


KO assessment

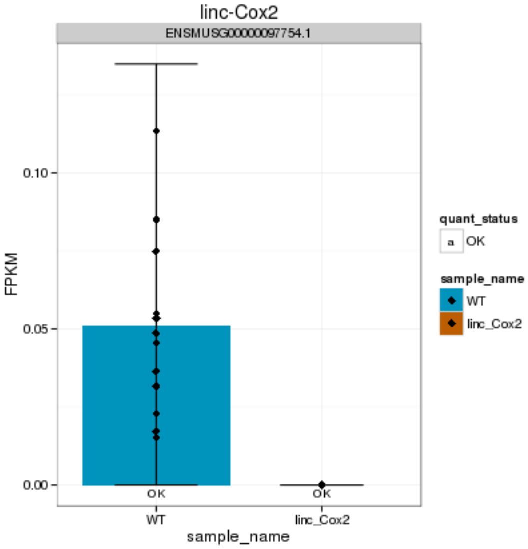
Endogenous lncRNA expression



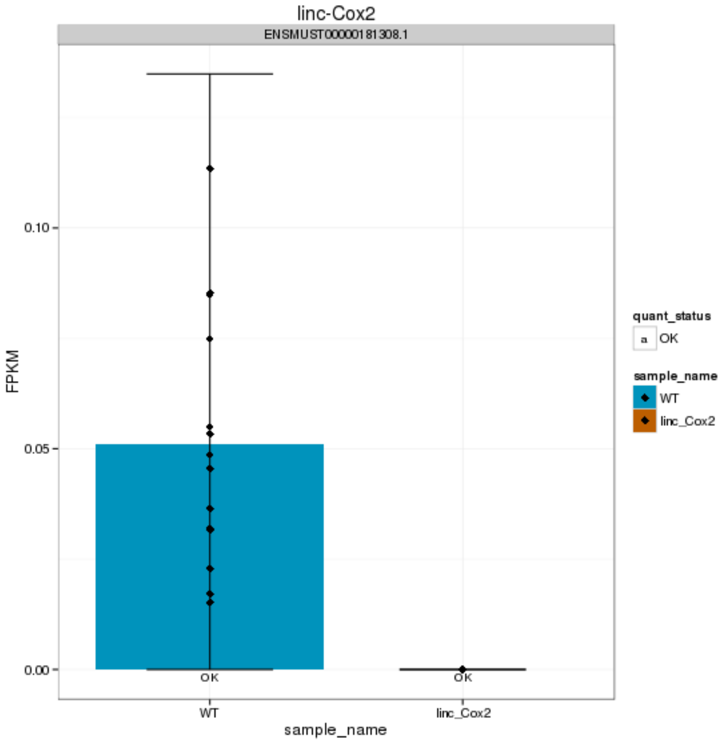
Endogenous expression of linc-Cox2 isoforms:



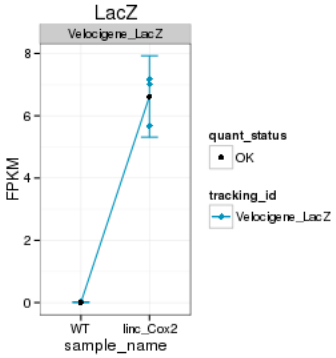
Barplot of gene expression:

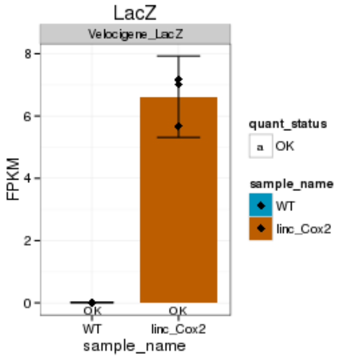


Barplot of isoform expression:



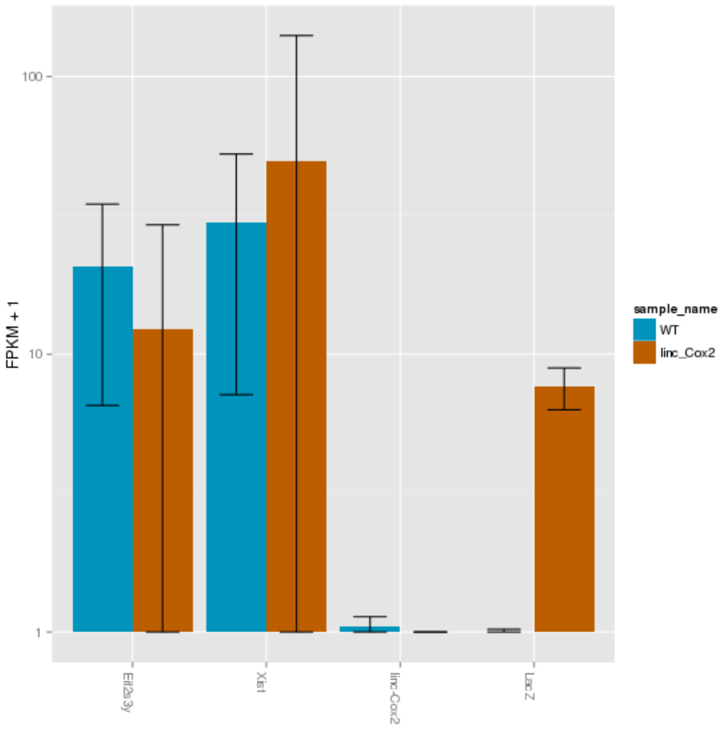
LacZ expression



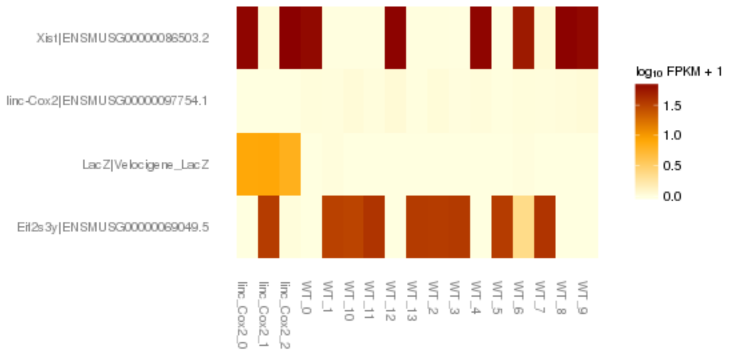


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

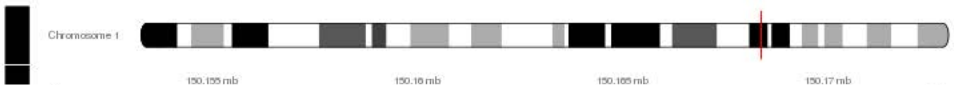
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):

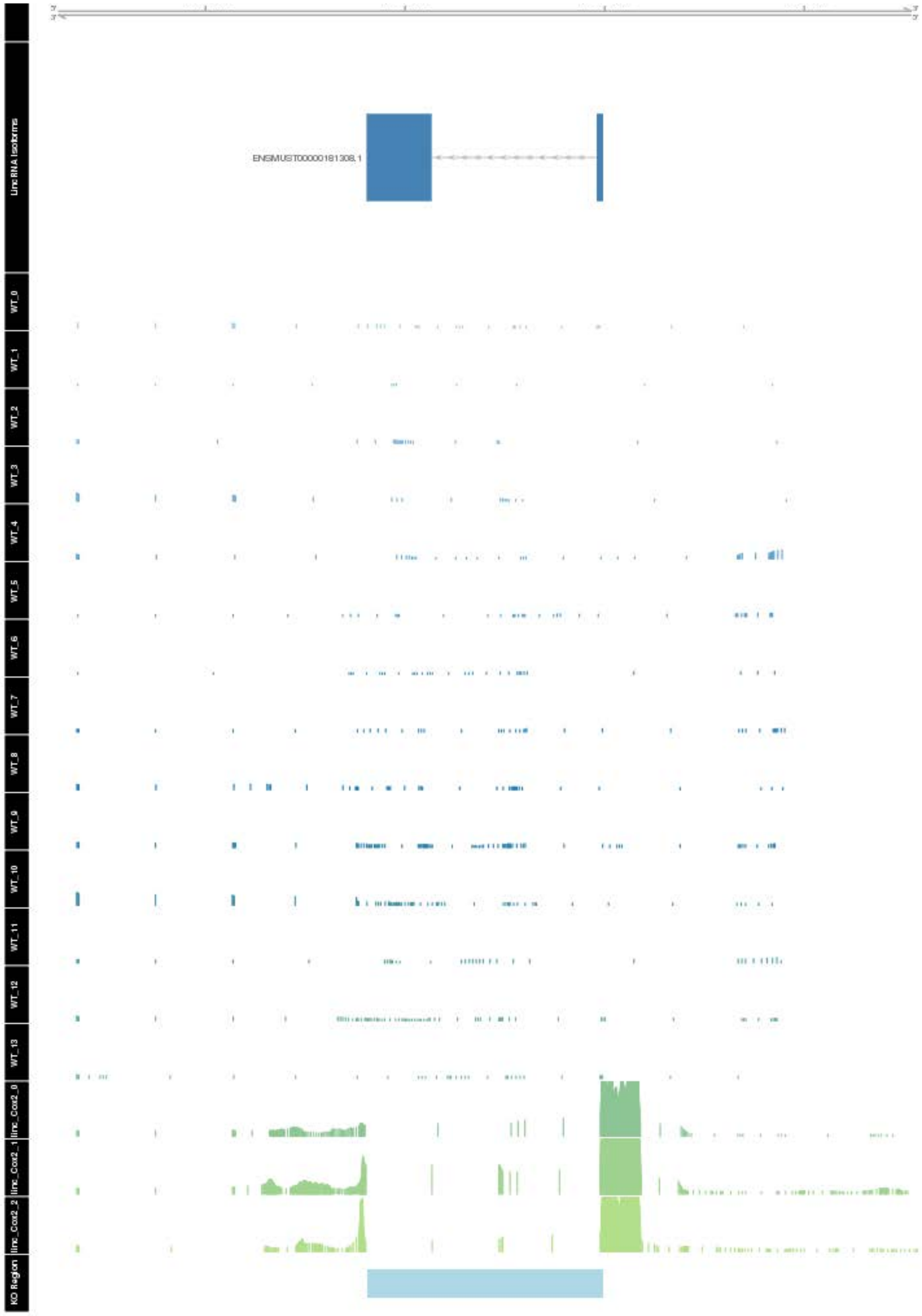


Expression heatmap:



Track visualization




Linc RNA Isoforms
ENSMUST00000181308.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
linc_Cox2_0
linc_Cox2_1
linc_Cox2_2
KO Region

Differential Analysis

Differential Genes

There are 94 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Tubb6
2	Folh1
3	Nes
4	Epha2
5	Nav1
6	Vtn
7	Fabp7
8	Adi1
9	Serpina3n
10	Fos
11	Emp2
12	Arc
13	Sdf2l1
14	Nr4a1
15	Cdkn1a
16	Park2
17	Glo1
18	Prss41
19	Atp6v0c
20	Eci1
21	Lars
22	Camk2a
23	Cnksr2
24	Mcm6
25	Dbi
26	Tnni1
27	Lamc2
28	Rgs5
29	Myoc
30	Lypd6b
31	Lcn2
32	Hspa5
33	Olfml3
34	Rps3a1
35	Nr4a3
36	Tinagl1
37	Padi2

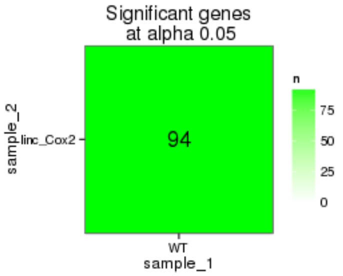
38 Hes3
39 Fbxo44
40 Fosl2
41 Gkn3
42 Hddc3
43 Col4a1

44 Ptgs2
45 Ndn
46 Arhgap27
47 Rnps1
48 Prr7
49 Zranb3
50 Arl5a
51 Mgat5
52 Decr2
53 Psenen
54 Egr1
55 Akap12
56 Pcsk1n
57 Trub2
58 Fmo2
59 Slc25a34
60 Cldn5
61 Gucy1a2
62 Kif21b
63 Shisa4
64 Maff
65 Id1
66 Acp1
67 4930503L19Rik
68 Pcdhb3
69 Olfml2a
70 Tnrc6b
71 Lmod1
72 Tagap1
73 Aldh7a1
74 Per2
75 S100a9
76 Kcnq3
77 Pign
78 Kdm5d
79 Tpm3-rs7
80 Capn11

81 Gm5506
82 Pyroxd2
83 Eno1
84 Chi3l1
85 Clasp1
86 Ddx3y
87 Gm7292
88 Wdfy1
89 Apold1
90 Hspa1b
91 Scnm1
92 AA465934
93 Gm10524
94 RP24-390G17.1

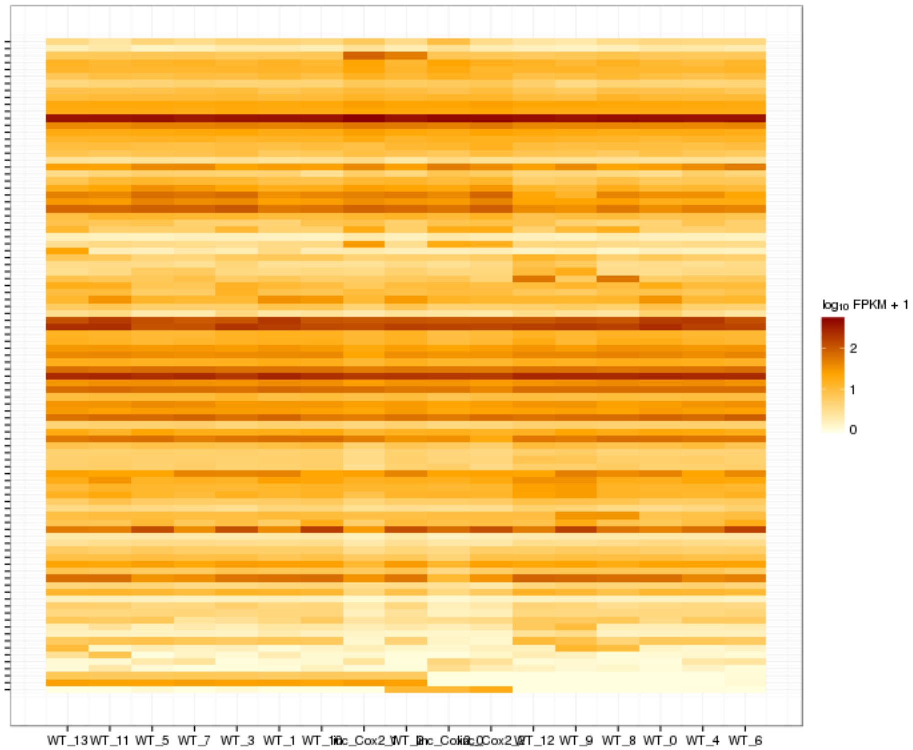
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

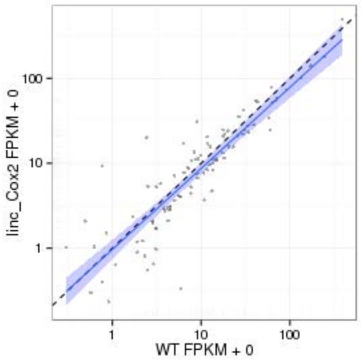


Significant genes with expression >50fpkm (any condition):(turned off)

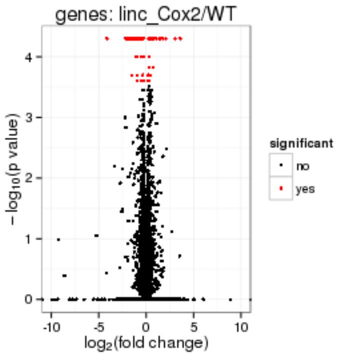
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

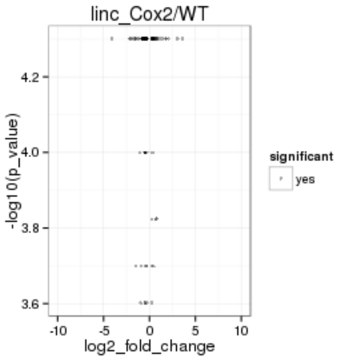
Scatter plot of significant genes only:



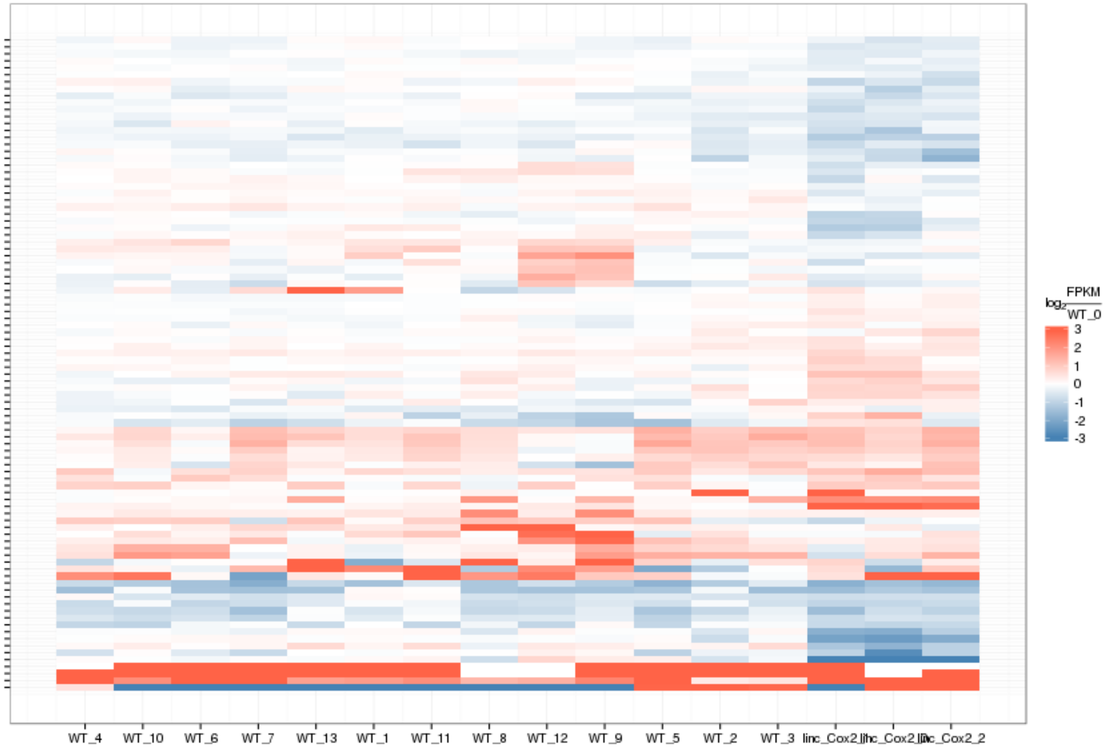
Volcano Plot



Volcano plot with significant genes only:



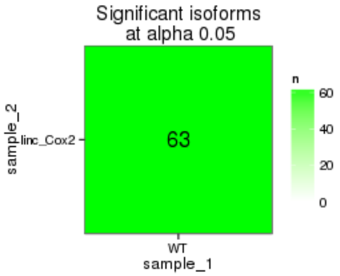
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:

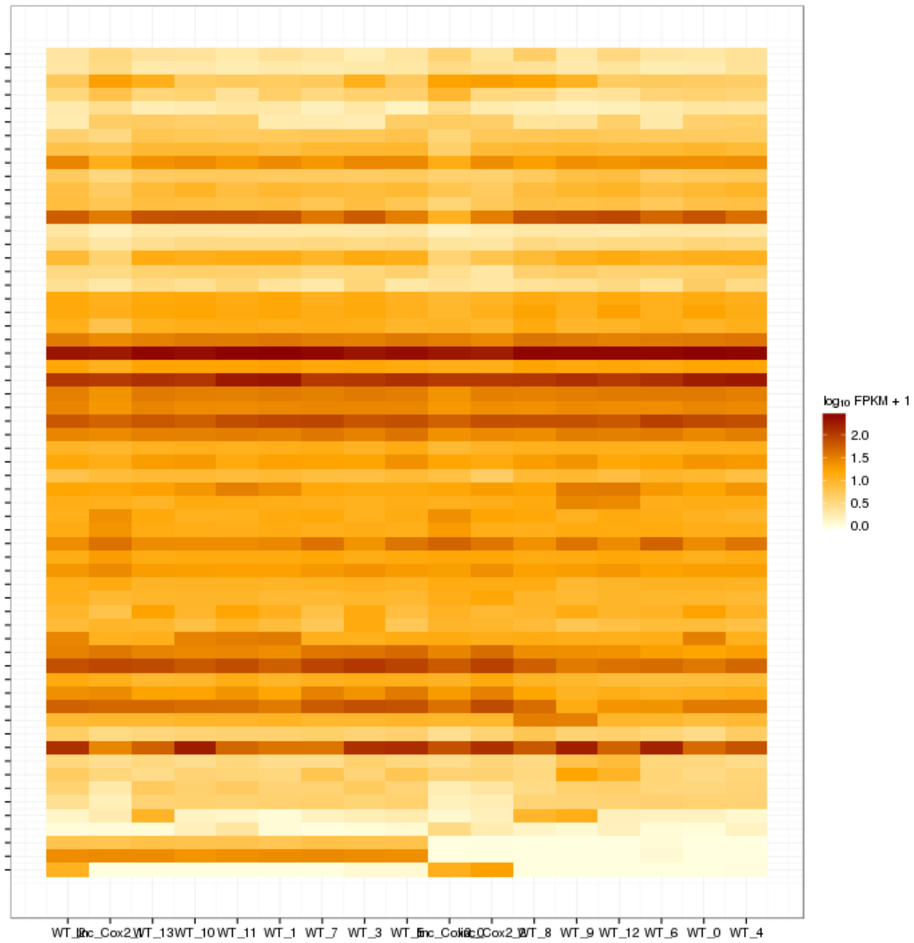


These isoforms are:

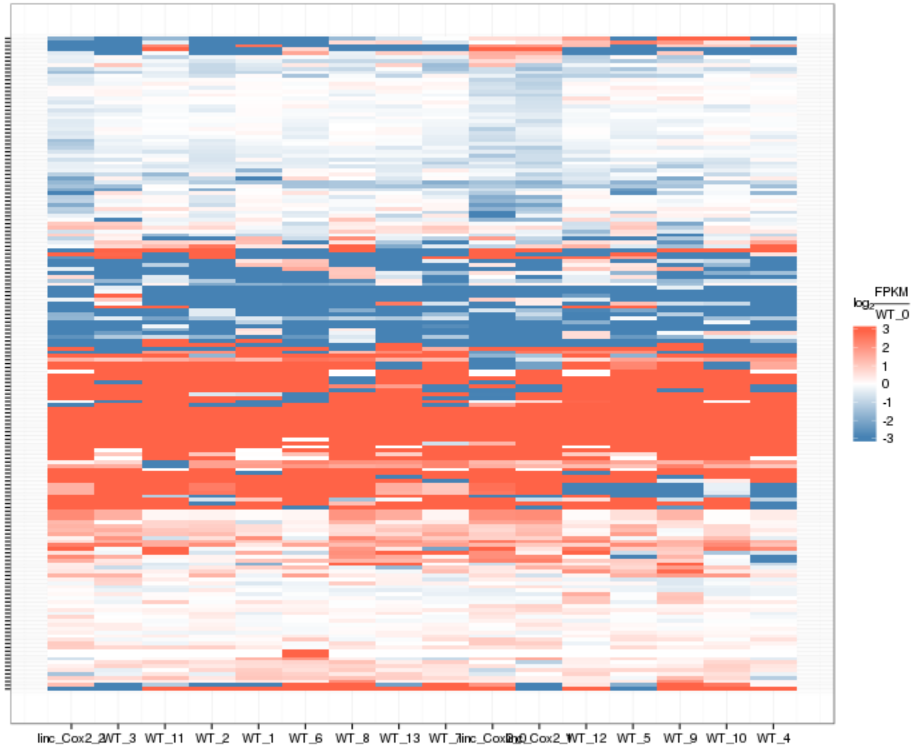
	isoAnnot$gene_short_name
1	Tubb6
2	Rec8
3	Nes
4	Vtn
5	Fabp7
6	Serpina3n
7	Fos
8	Emp2
9	Arc
10	Sdf2l1
11	Nr4a1
12	Cdkn1a
13	Glo1
14	Atp6v0c
15	Eci1
16	Lars
17	Cdh7
18	Mcm6
19	Dbi
20	Lamc2
21	Rgs5
22	Myoc
23	Lypd6b
24	Olfml3
25	Tpm3
26	Rps3a1
27	Arhgef19
28	Padi2
29	Hes3
30	Fosl2
31	Gkn3
32	Hddc3
33	Ptgs2
34	Ndn
35	Rnps1
36	Arl5a
37	Decr2
38	Egr1
39	Akap12
40	Pcsk1n

41 Cercam
42 Trub2
43 Fmo2
44 Zfp236
45 Cldn5
46 Kif21b
47 Pm20d1
48 Olfml2a
49 Tagap1
50 Per2
51 Kcnq3
52 Kdm5d
53 Tpm3-rs7
54 Capn11
55 Gm5506
56 Ddx3y
57 Gm7292
58 Wdfy1
59 Apold1
60 Hspa1b
61 Ptprv

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

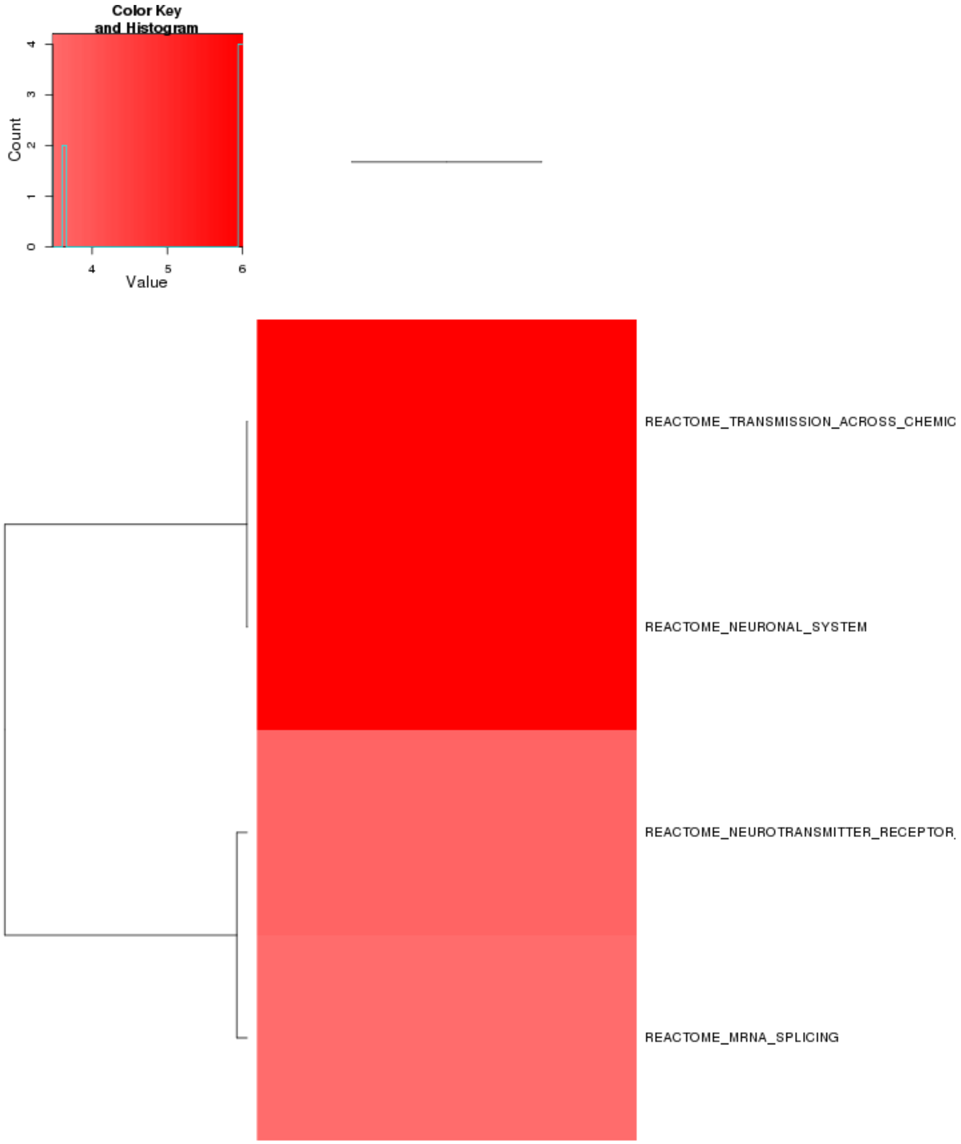
Biocarta enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

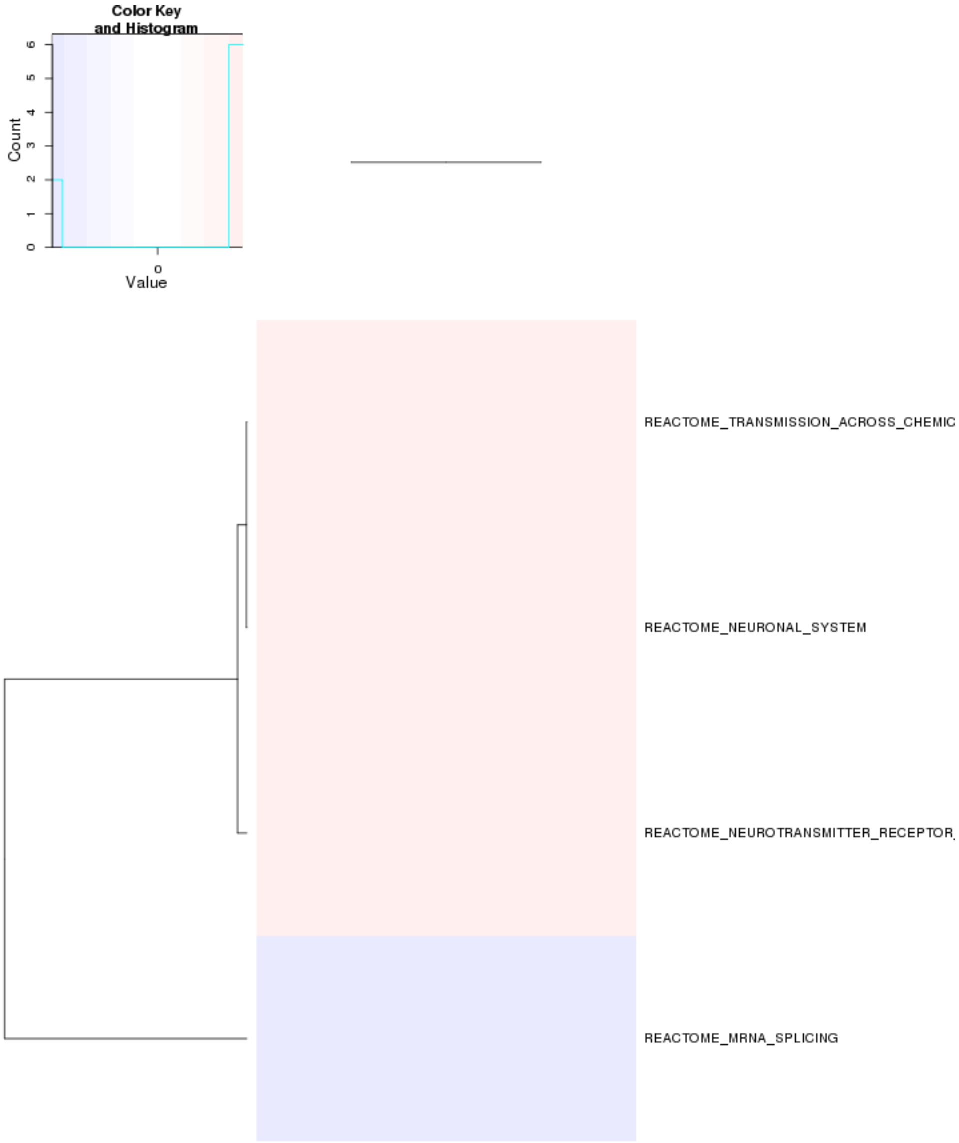
Biocarta zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

Reactome enrichment:



Reactome zscore:



Kegg enrichment:

```
## Error: argument is of length zero
```

Kegg zscore:

```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

Interneuron enrichment:

```
## Error: argument is of length zero
```

Interneuron zscore:

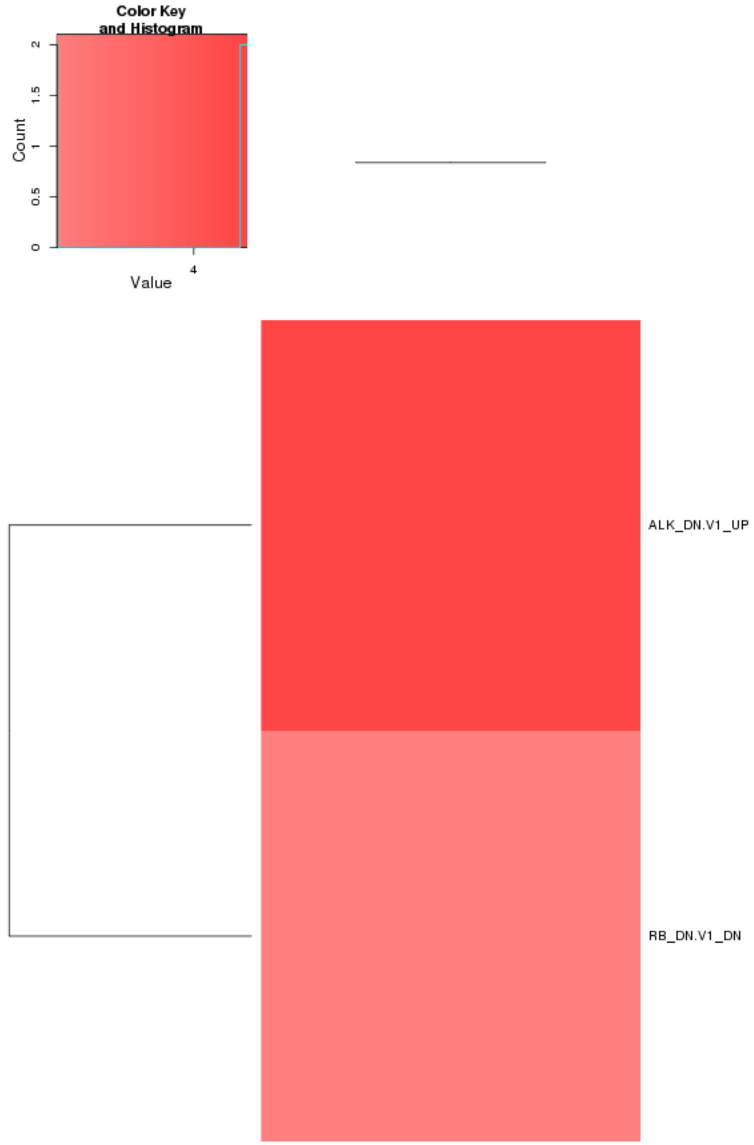
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

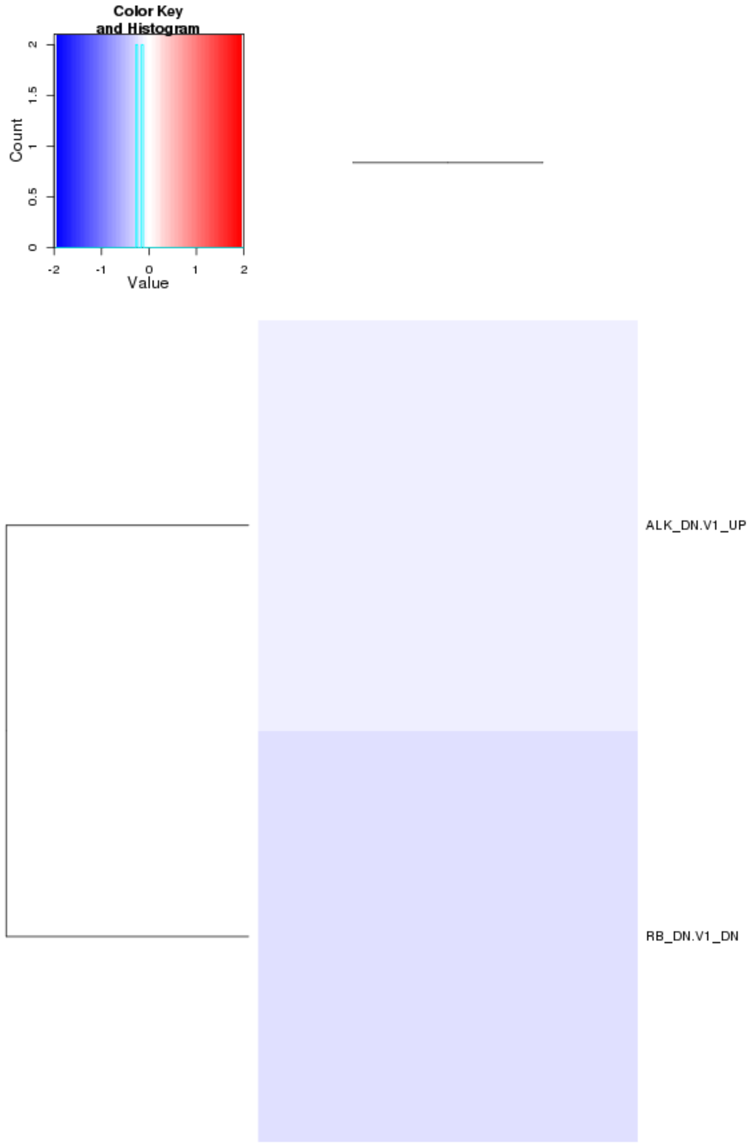
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

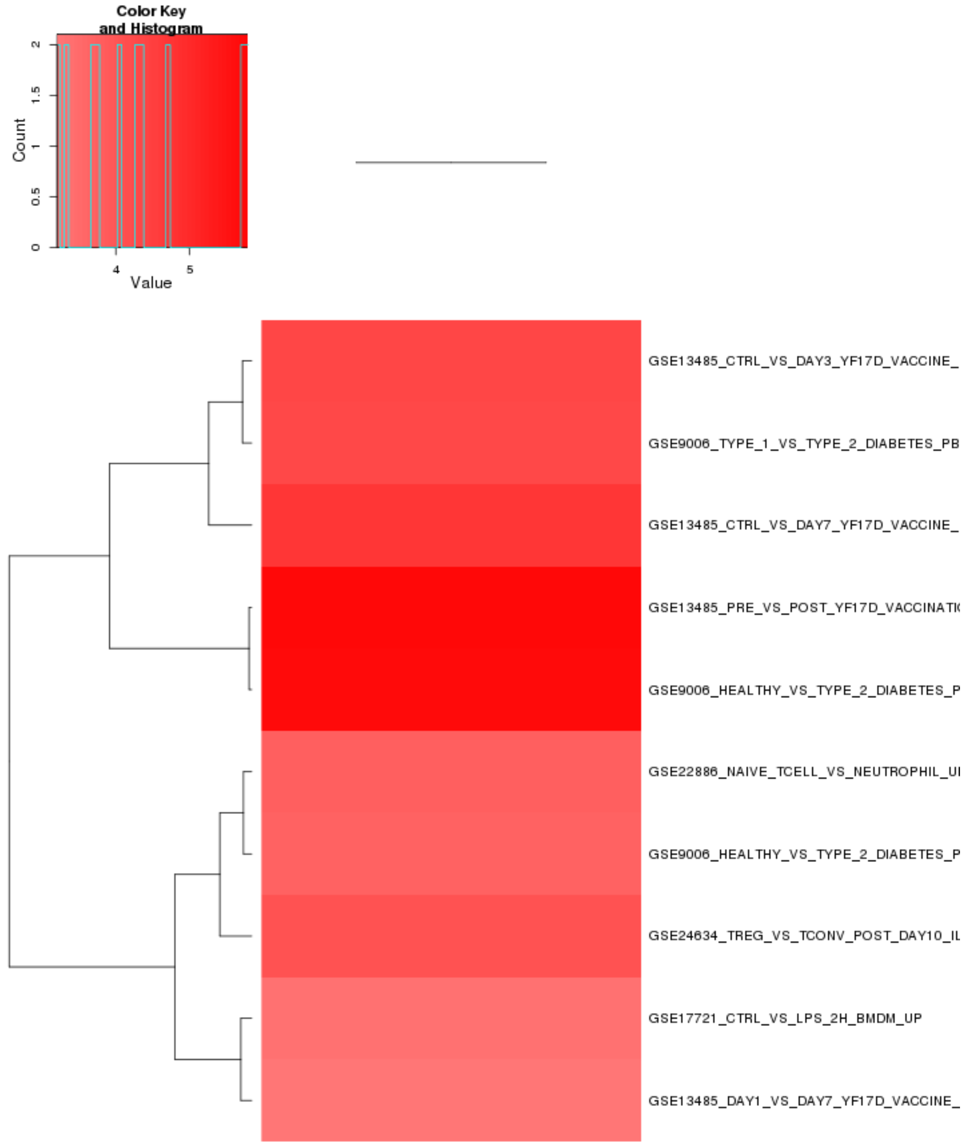
Oncogene enrichment:



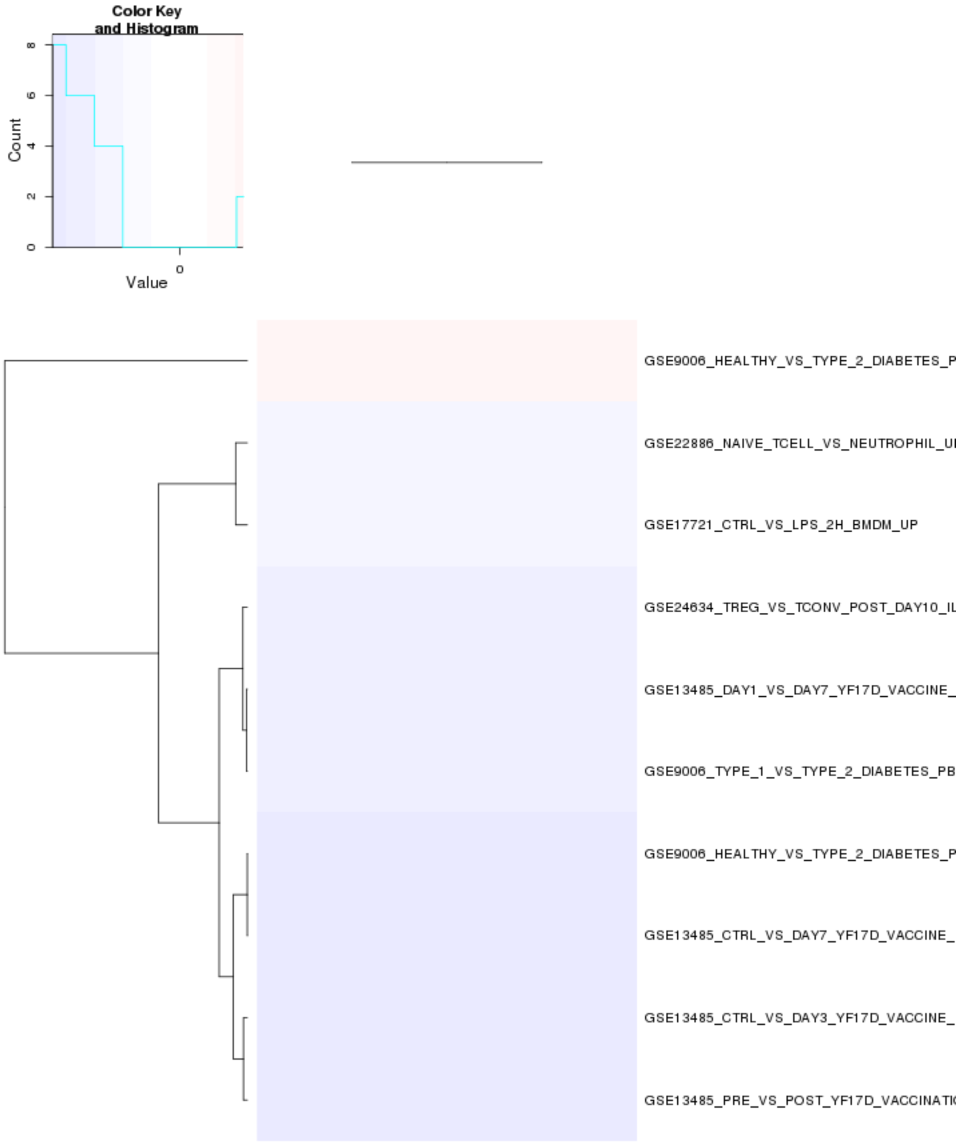
Oncogene zscore:



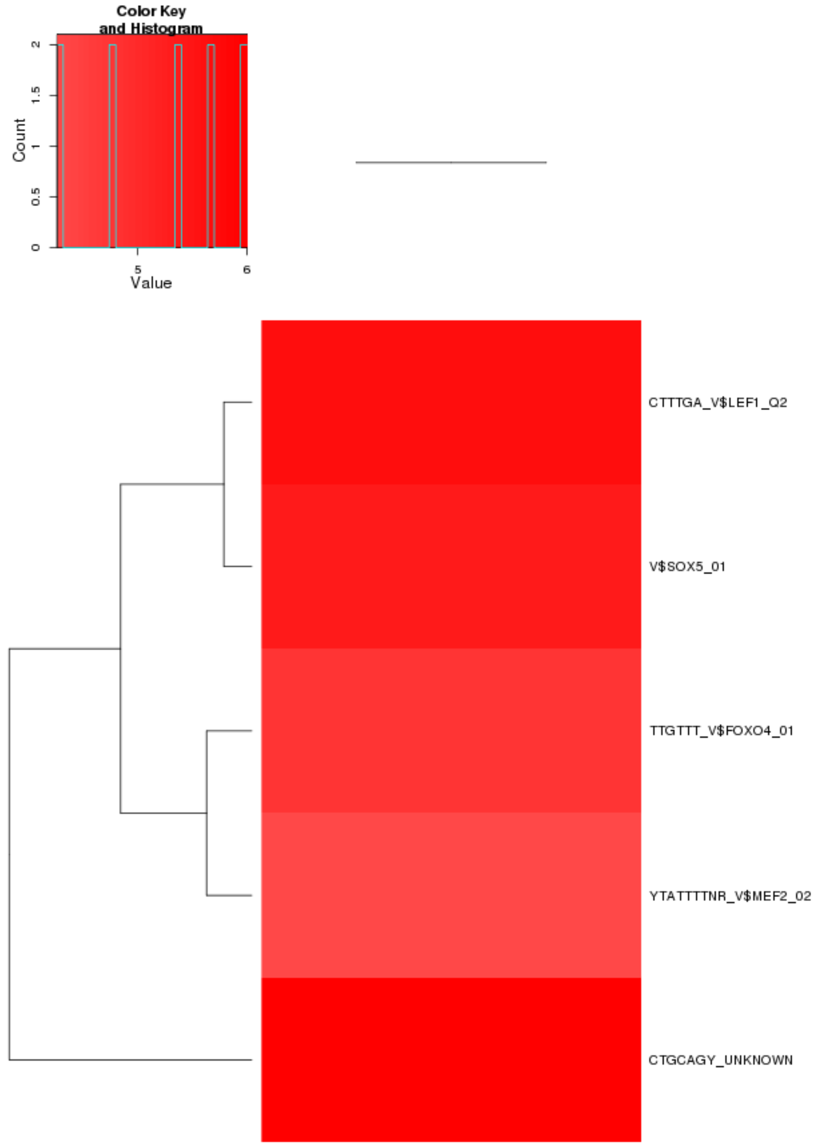
Immuno enrichment:



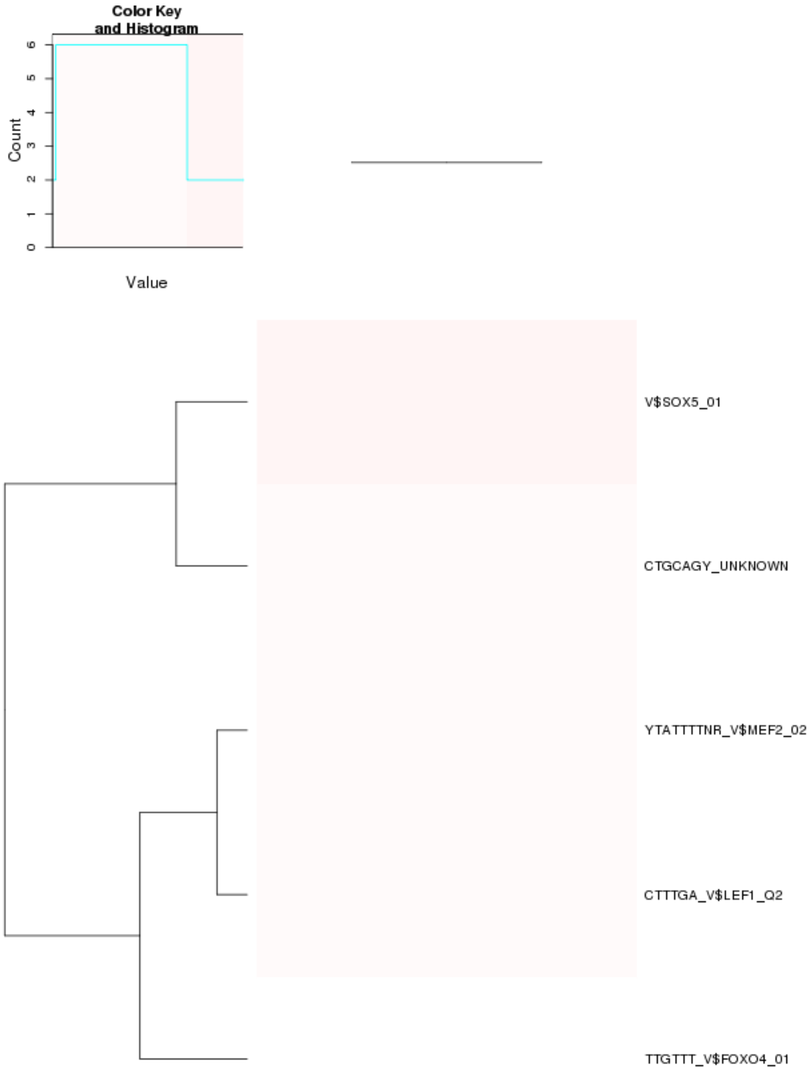
Immuno zscore:



TF enrichment:

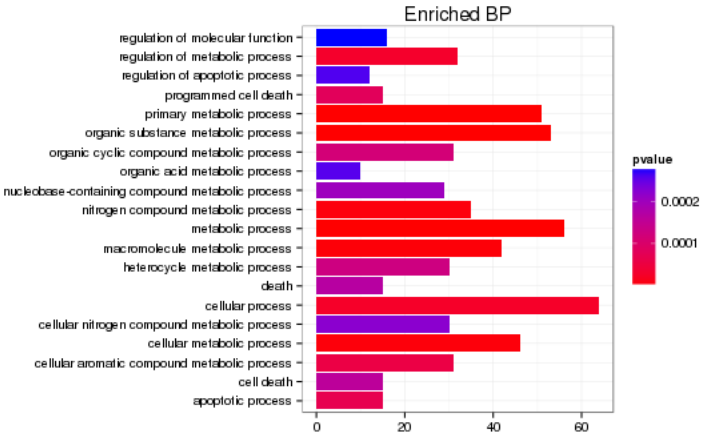

Color Key
and Histogram
Count
0
0.5
1
1.5
2
5
6
Value
CTTTGA_V$LEF1_Q2
V$SOX5_01
TTGTTT_V$FOXO4_01
YTATTTTNR_V$MEF2_02
CTGCAGY_UNKNOWN

TF zscore:

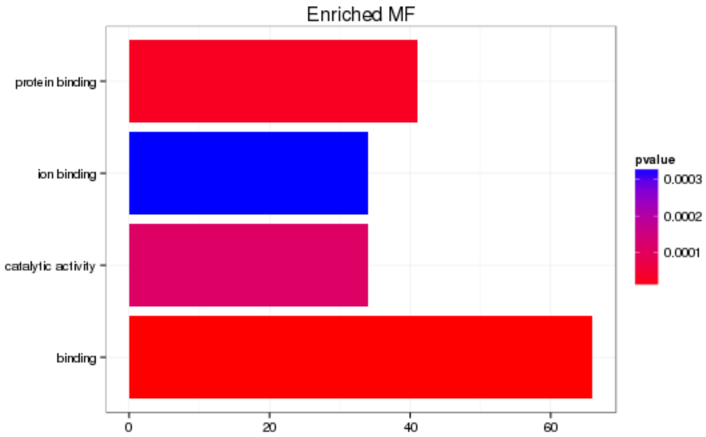


GO enrichment

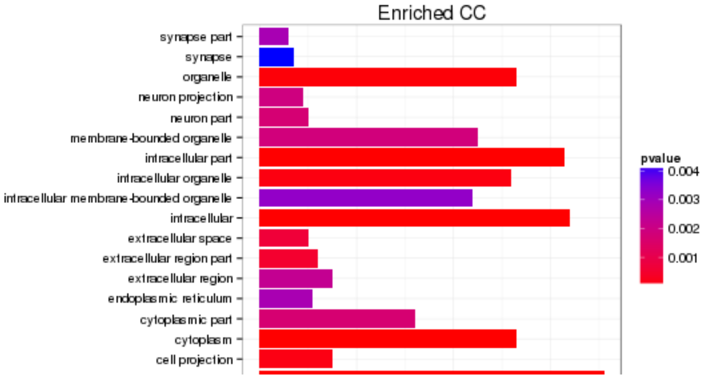
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.



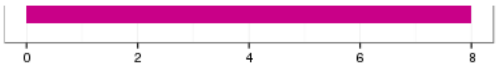
Enriched BP



Enriched MF

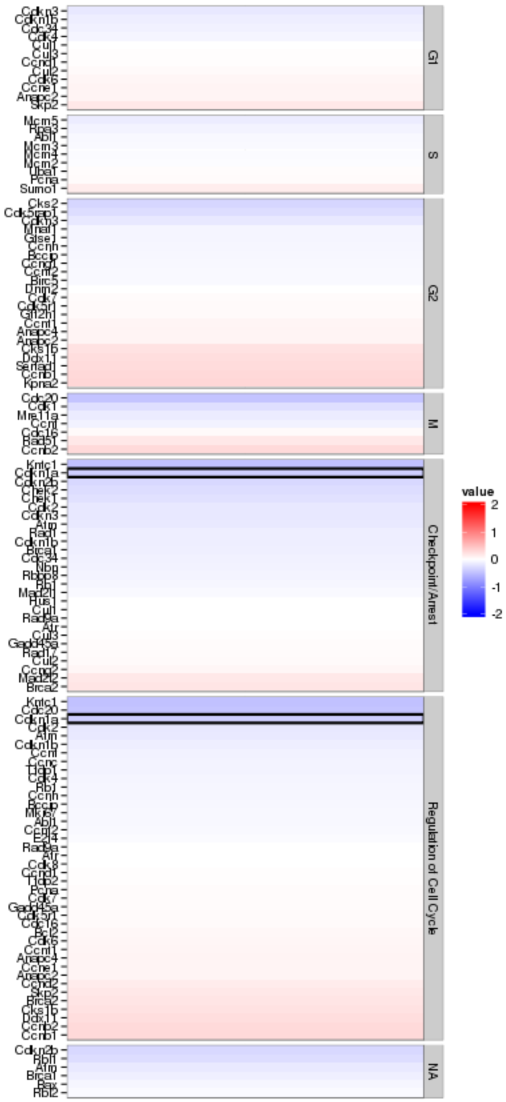


Enriched CC

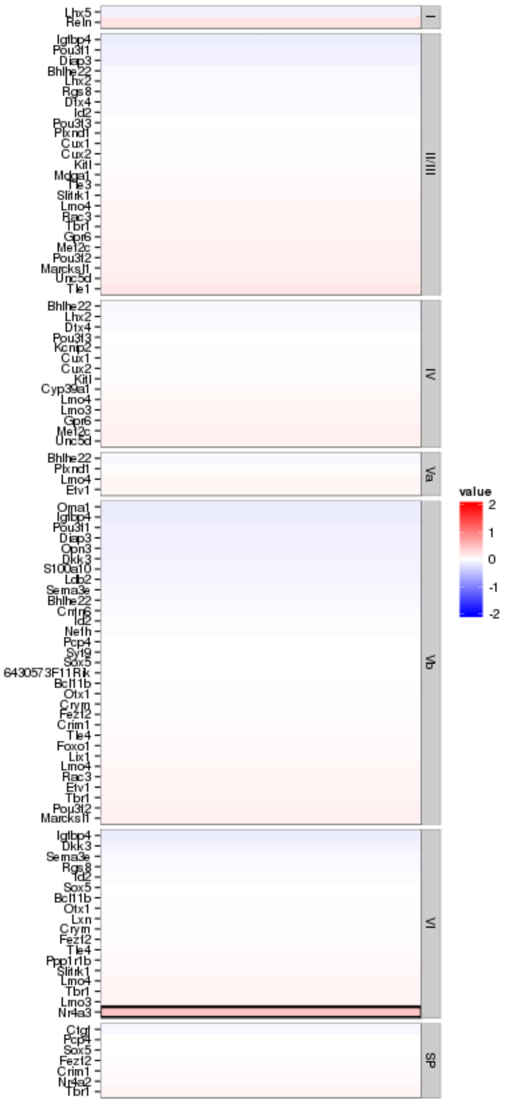


```
## Error: 'x' and 'units' must have length > 0
```

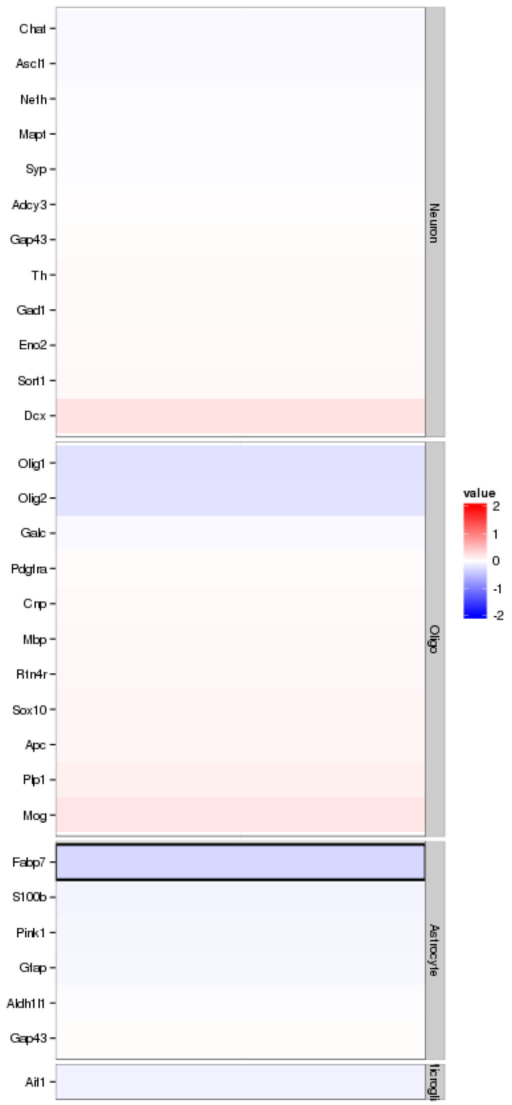
Enrichment or depletion for stage-specific cell cycle markers



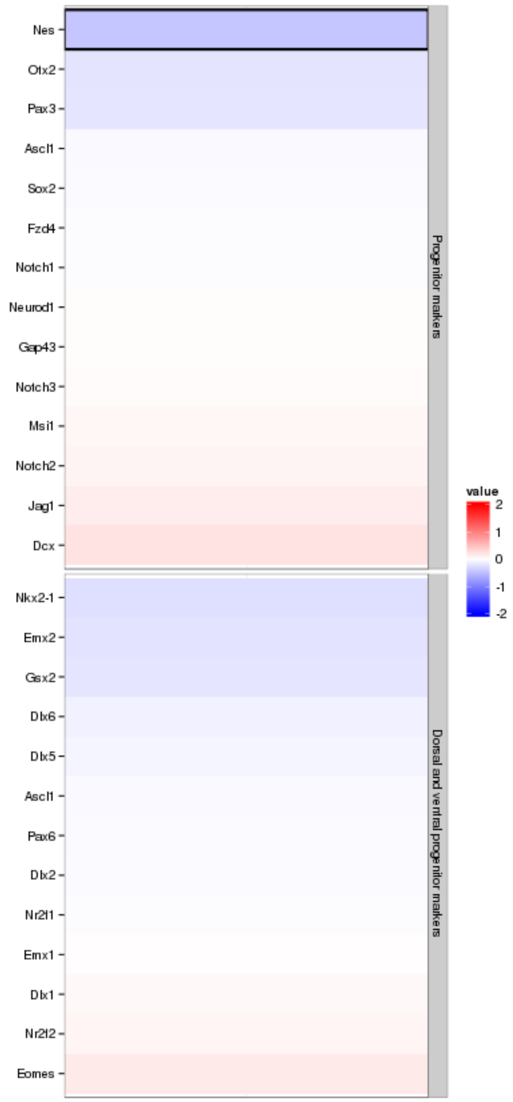
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



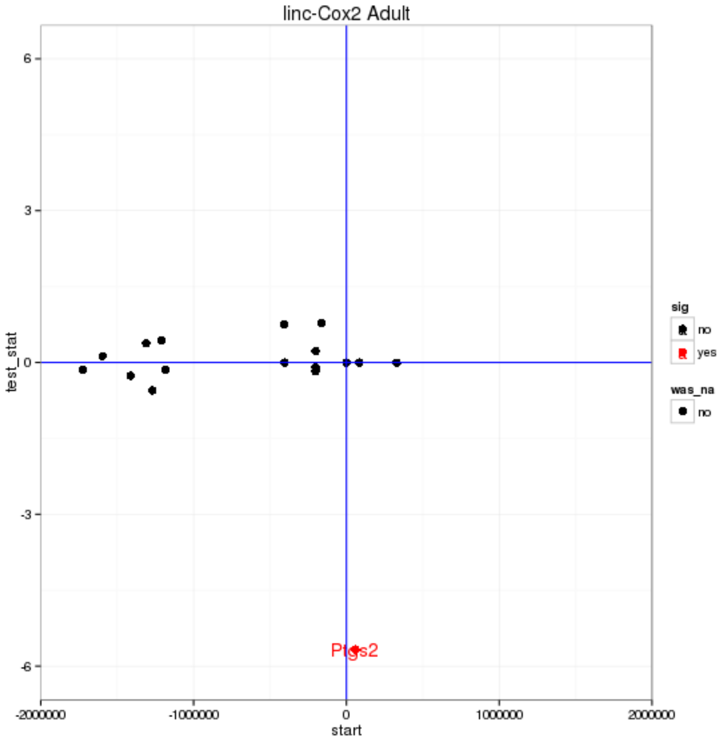
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 1 genes significantly regulated in a region this size is: 0.1821



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15	JR732
16	JR776
17	JR798

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	34095400.00	0.77	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	34095400.00	0.59	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	34095400.00	1.00	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	34095400.00	0.82	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	34095400.00	1.05	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	34095400.00	1.09	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	34095400.00	0.82	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	34095400.00	1.18	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	34095400.00	1.03	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	34095400.00	1.32	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	34095400.00	1.53	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	34095400.00	1.03	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	34095400.00	0.99	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	34095400.00	1.23	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR732/abundances.cxb	linc_Cox2	0	linc_Cox2_0	27439100.00	34095400.00	0.81	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR776/abundances.cxb	linc_Cox2	1	linc_Cox2_1	39517800.00	34095400.00	1.14	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR798/abundances.cxb	linc_Cox2	2	linc_Cox2_2	35636800.00	34095400.00	1.03	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils
## [8] datasets  base
##
## other attached packages:
##  [1] plyr_1.8.1
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,linc-Cox2 -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/linc-Cox2_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainMap
## 2
## 3
## 4
## 5
```

linc-Cox2 KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for linc-Cox2.

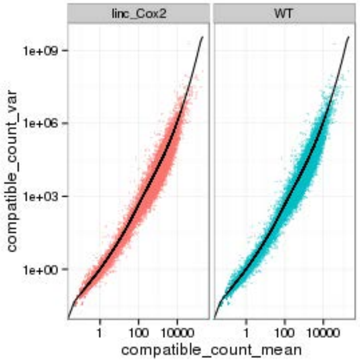
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

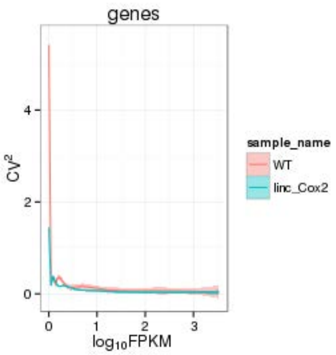
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



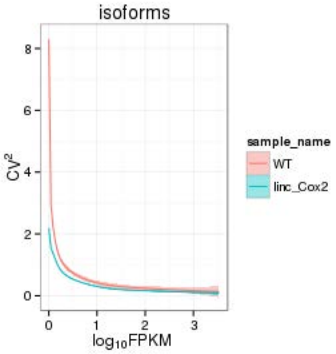
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

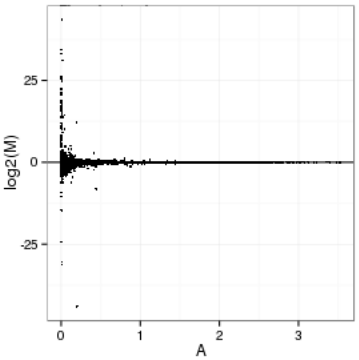
Genes:



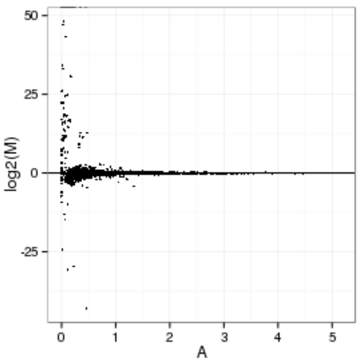
Isoforms:



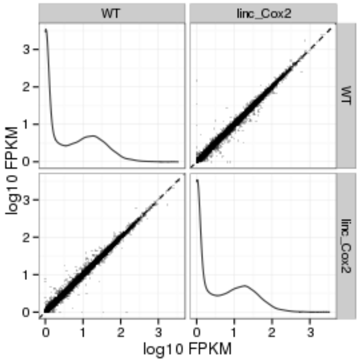
MvA plot



MvA plot counts



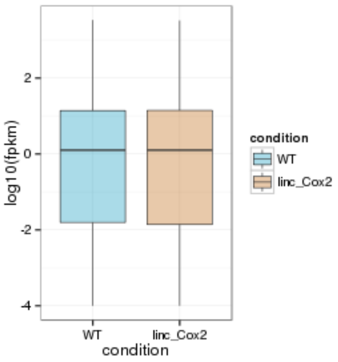
Scatterplot matrix



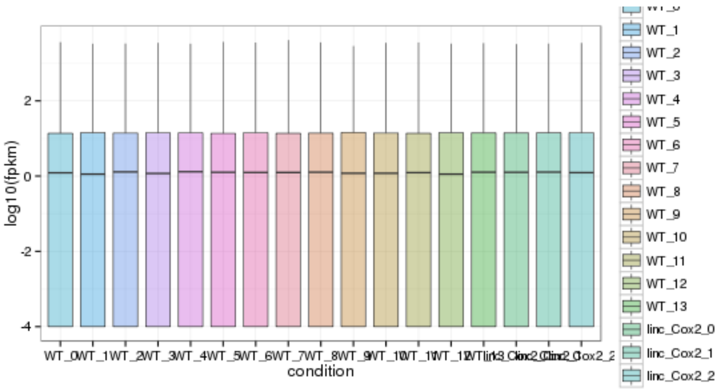
Distributions

Boxplots

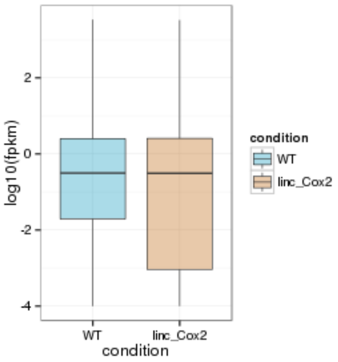
Boxplot (genes)



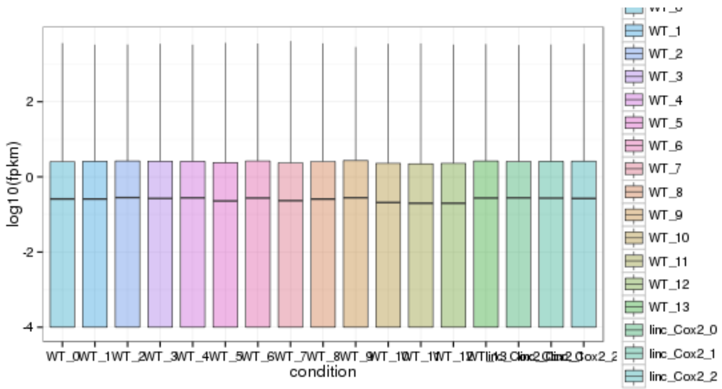
Boxplot (genes, replicates)



Boxplot (isoforms)

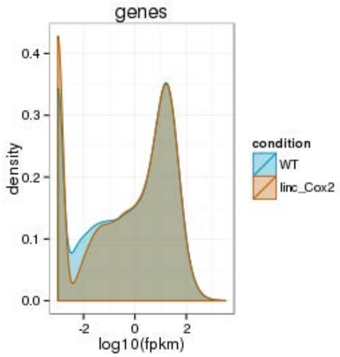


Boxplot (isoforms, replicates)

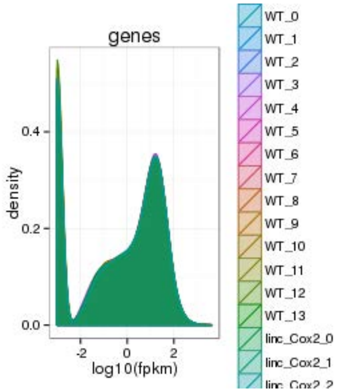


Density

Density (genes)

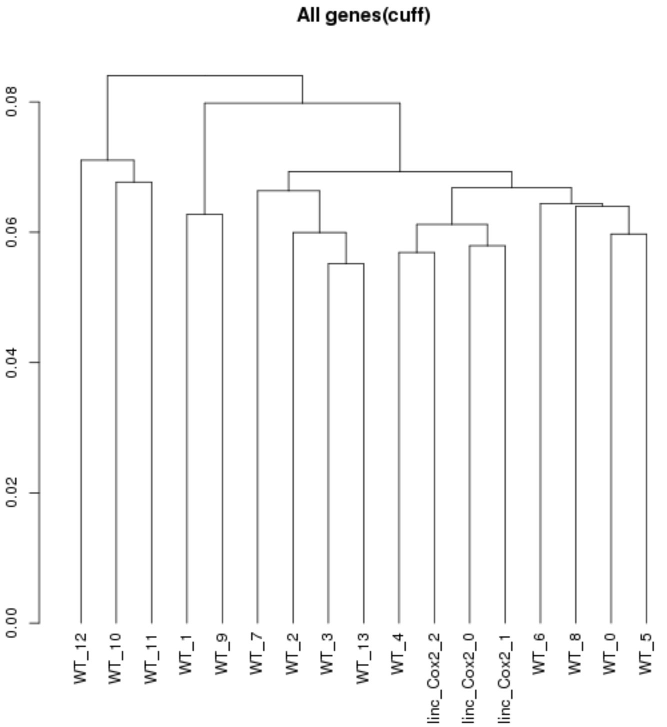


Density (genes, replicates)



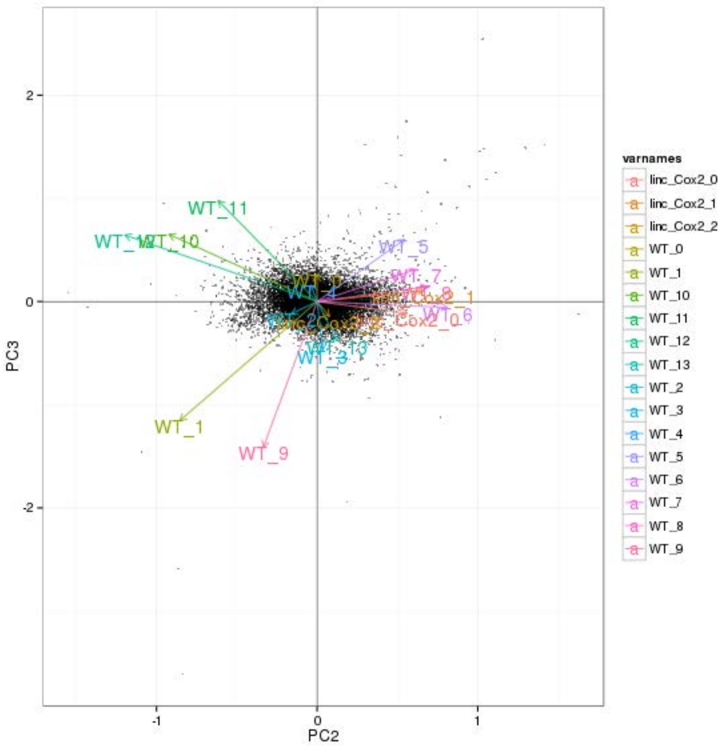
Clustering

Replicate Clusters



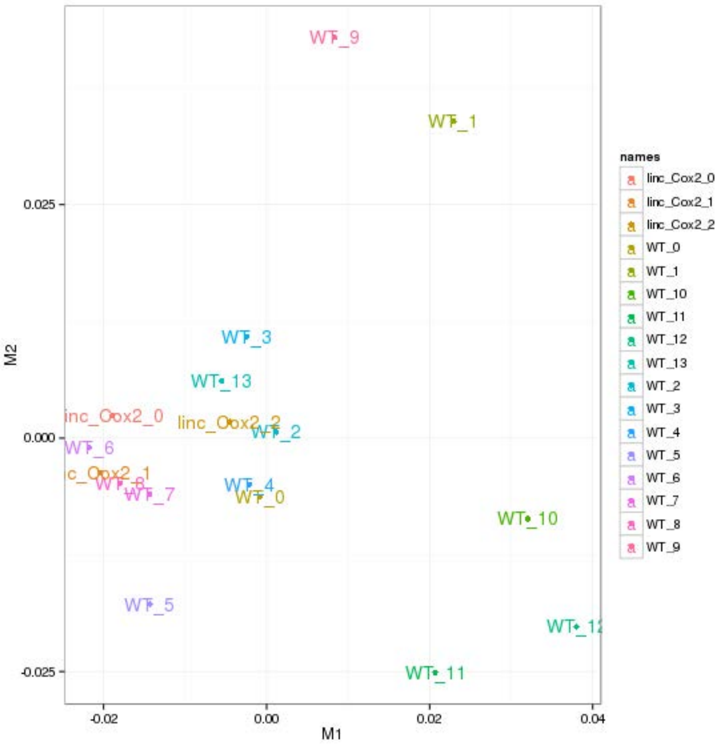
```
## NULL
```

PCA (genes)



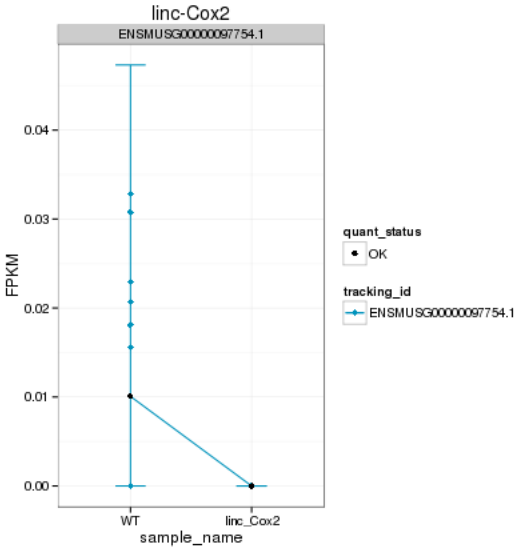
PC3
PC2
2
0
-2
-1
0
1
WT_11
WT_12
WT_10
WT_5
WT_7
linc_Cox2_1
linc_Cox2_0
WT_6
WT_13
WT_3
WT_1
WT_9
varnames
linc_Cox2_0
linc_Cox2_1
linc_Cox2_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

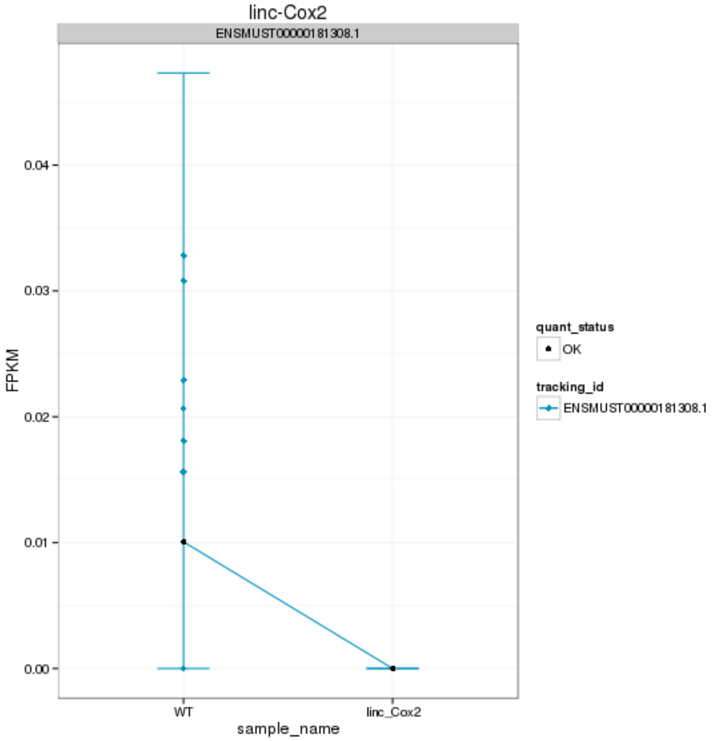


KO assessment

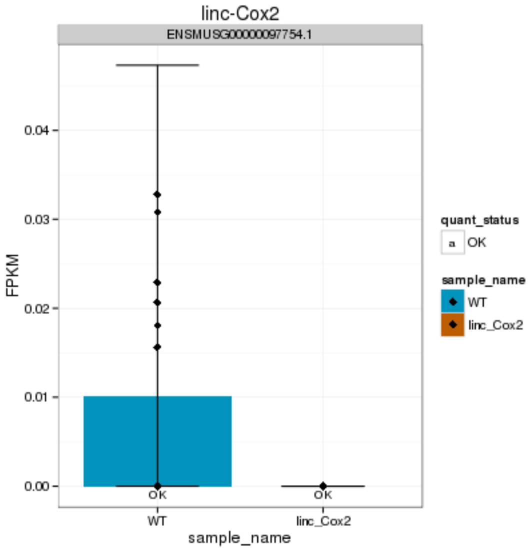
Endogenous lncRNA expression



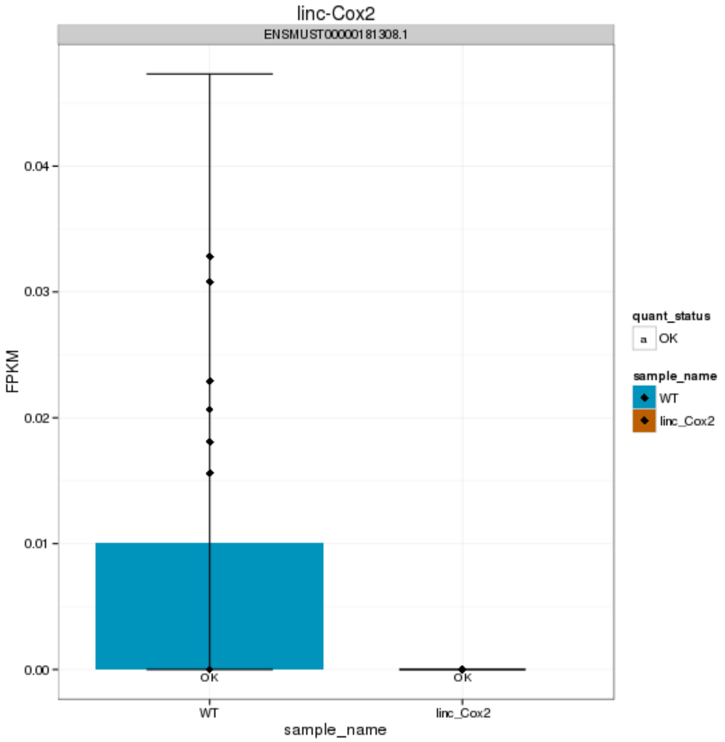
Endogenous expression of linc-Cox2 isoforms:



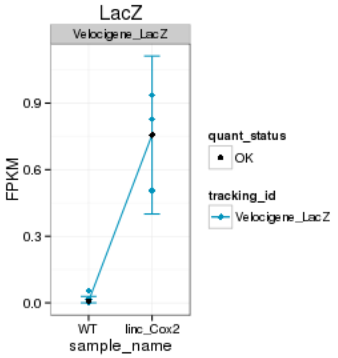
Barplot of gene expression:

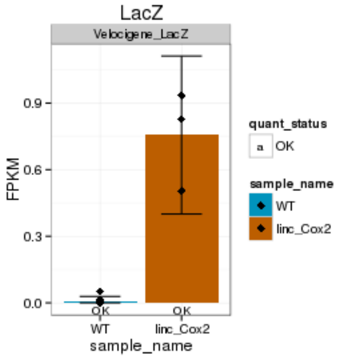


Barplot of isoform expression:



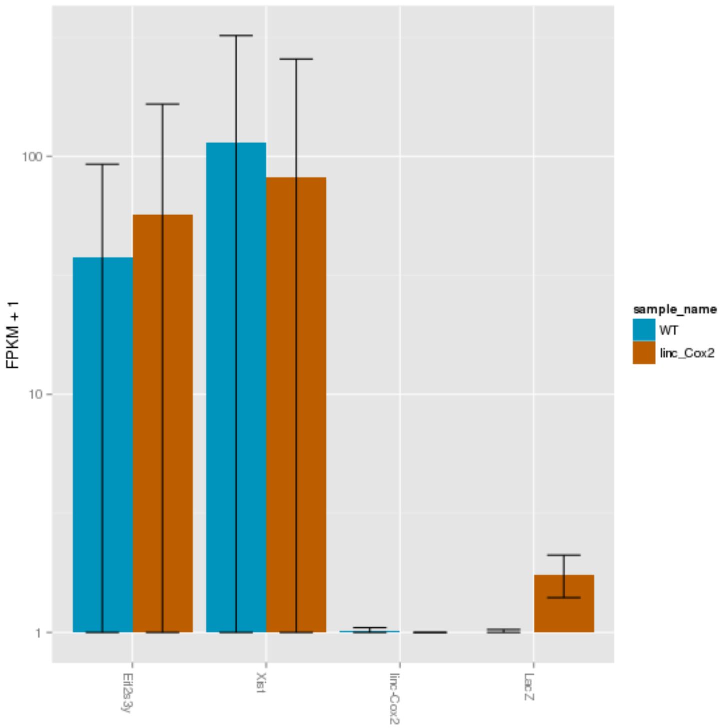
LacZ expression



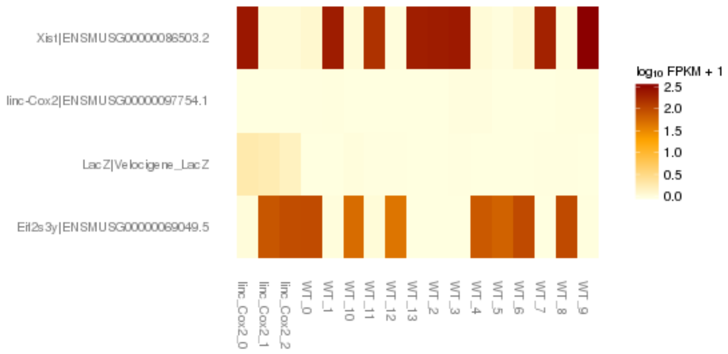


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

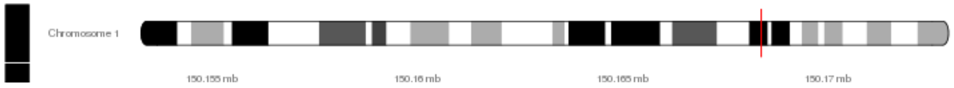
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):

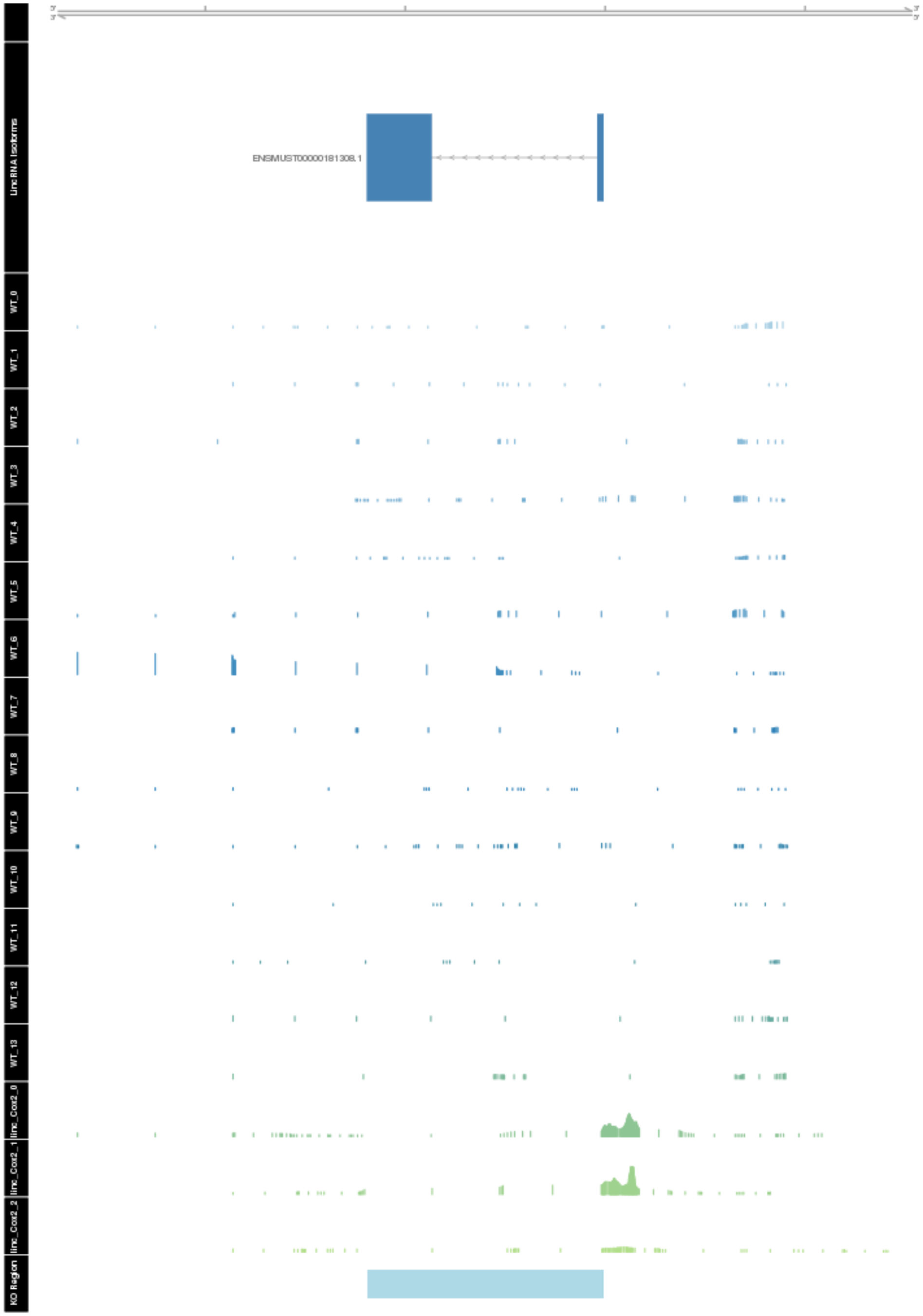


Expression heatmap:



Track visualization




5'
3'
3'
5'
Linc RNA Isoforms
ENSMUST00000181308.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
linc_Cox2_0
linc_Cox2_1
linc_Cox2_2
KO Region

Differential Analysis

Differential Genes

There are 97 significantly differentially expressed genes. They are:

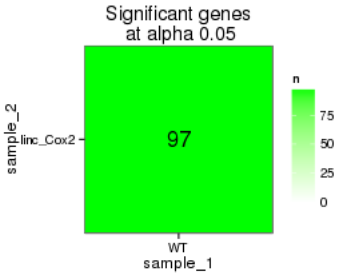
	geneAnnot$gene_short_name
1	Col1a1
2	Rec8
3	Zfp40
4	Fam131c
5	Vax1
6	Ttc9b
7	Lama2
8	Snrpf
9	Skor1
10	Dlx2
11	Park2
12	Glo1
13	Prss41
14	Atp6v0c
15	Hn1l
16	Lox
17	Fbn2
18	Rps14
19	Lbx1
20	Col3a1
21	Fn1
22	Bok
23	Mcm6
24	Dbi
25	Fbn1
26	Syt13
27	Rps3a1
28	Svep1
29	Uncx
30	Emp1
31	Dera
32	Hddc3
33	Pgls
34	Col12a1
35	Dnah8
36	Irf2bpl
37	Arhgap27

38	Gbx2
39	Rnps1
40	Prr7
41	Lars2
42	Arx
43	3110052M02Rik
44	Mgat5
45	Lum
46	Decr2
47	Cldn11
48	Vstm2l
49	Hoxb4
50	Shank1
51	Pcsk1n
52	Tlx3
53	C1qtnf4
54	2310036O22Rik
55	Fmod
56	Shisa4
57	Hebp1
58	Pgp
59	Gm9493
60	Rps2
61	Acp1
62	Olfml2a
63	Hmga1
64	Lrrc4b
65	Dmrta2
66	Mafa
67	Tagap1
68	Hbb-y
69	Zfp771
70	Pign
71	Kdm5d
72	Capn11
73	H2afj
74	Alox5ap
75	Rpl26
76	Sox11
77	Zfp428
78	Sp9
79	Nkain2
80	Ssbp4

81 Gm1673
82 Jund
83 Gpr27
84 9030025P20Rik
85 Wdfy1
86 Hbb-bt
87 Rpl39
88 Gm11273
89 Ccdc85c
90 Ier5l
91 Myl6
92 Rnaset2b
93 Ccdc85b
94 Gm6472
95 Gm9825
96 Gm26917
97 Gm26924

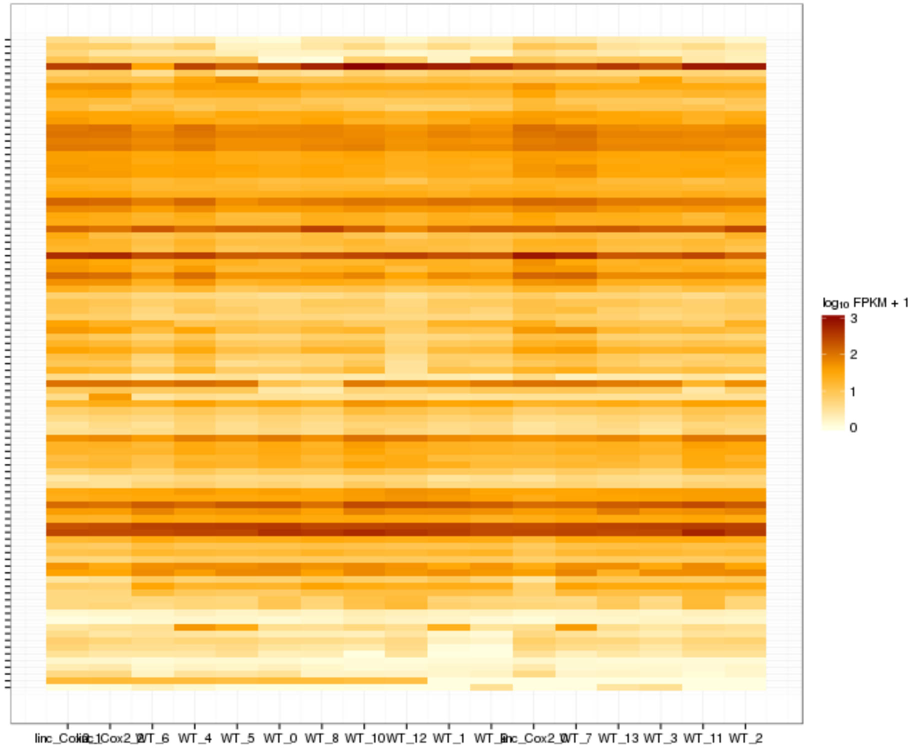
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

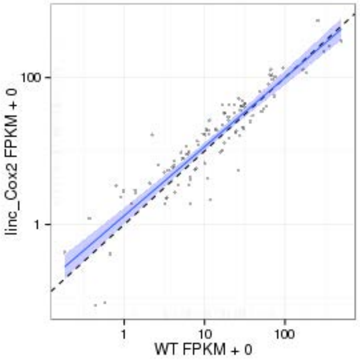


Significant genes with expression >50fpkm (any condition):(turned off)

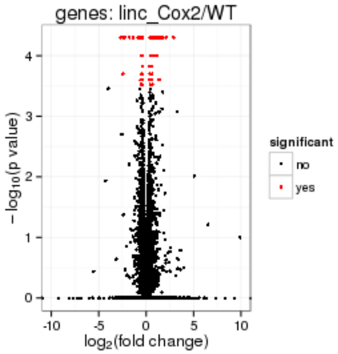
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

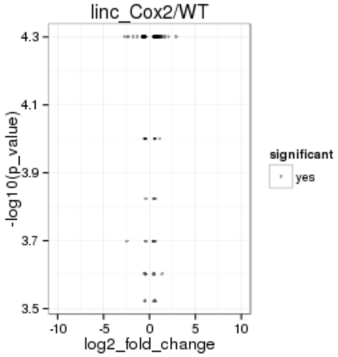
Scatter plot of significant genes only:



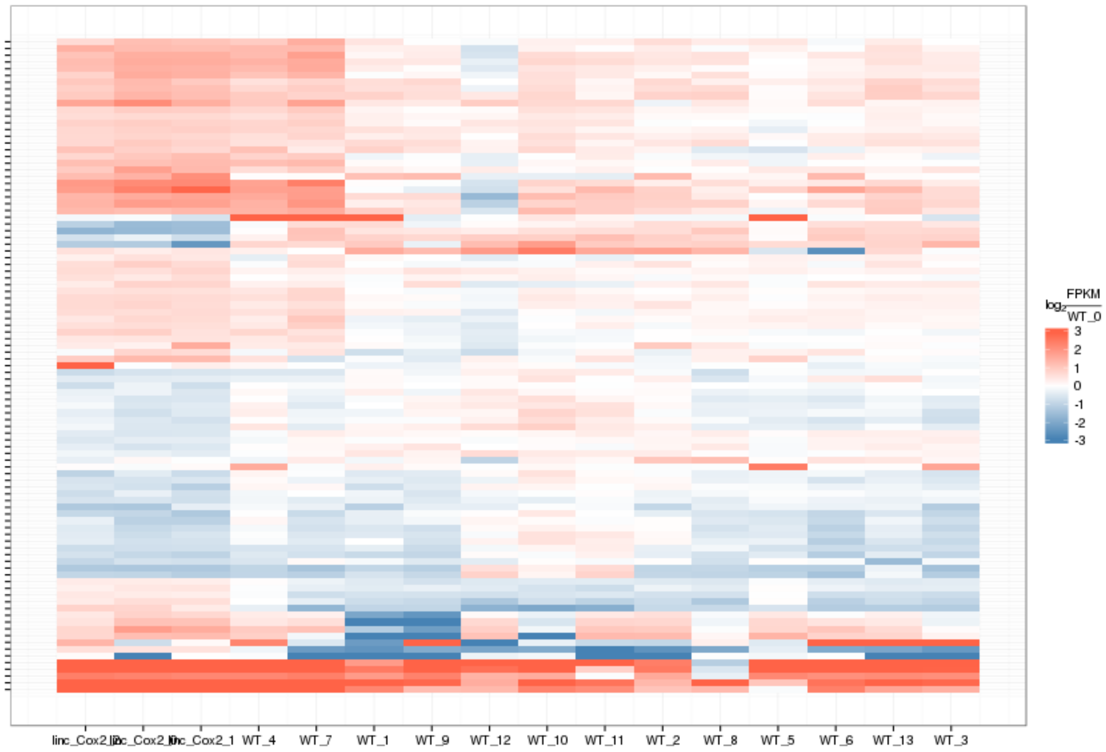
Volcano Plot



Volcano plot with significant genes only:



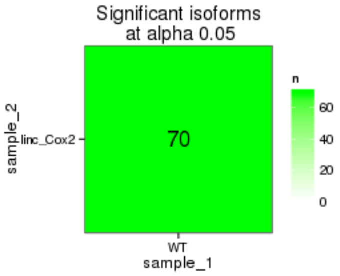
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:

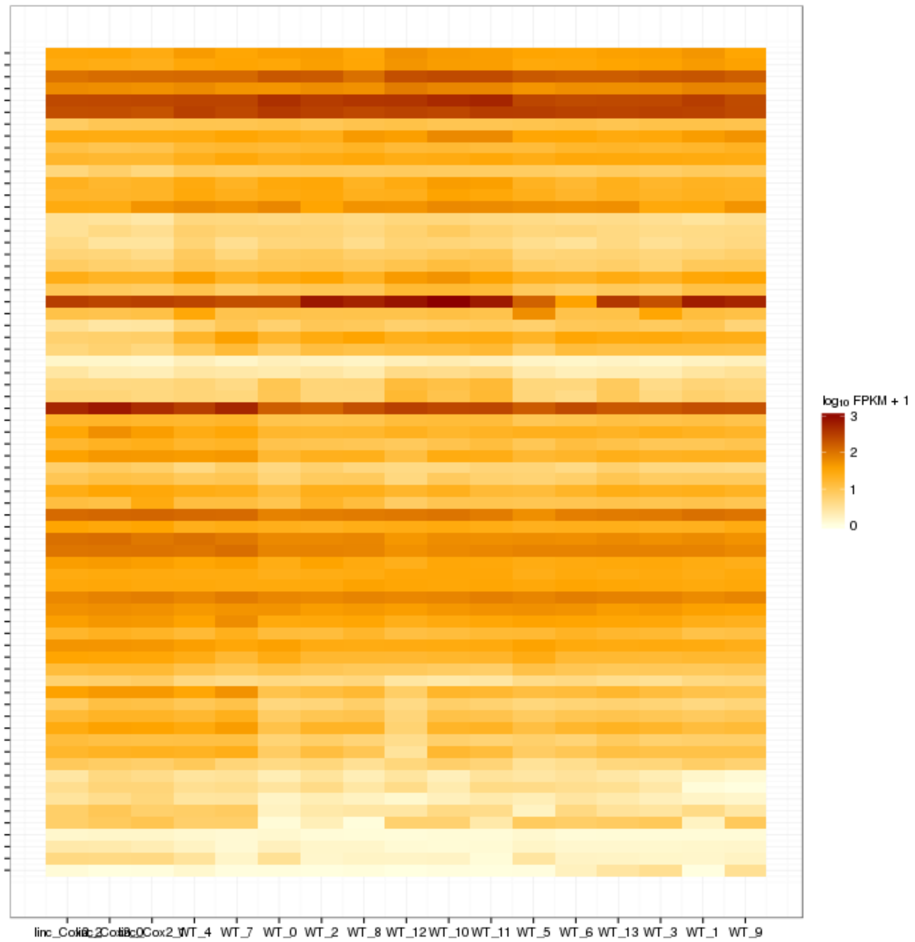


These isoforms are:

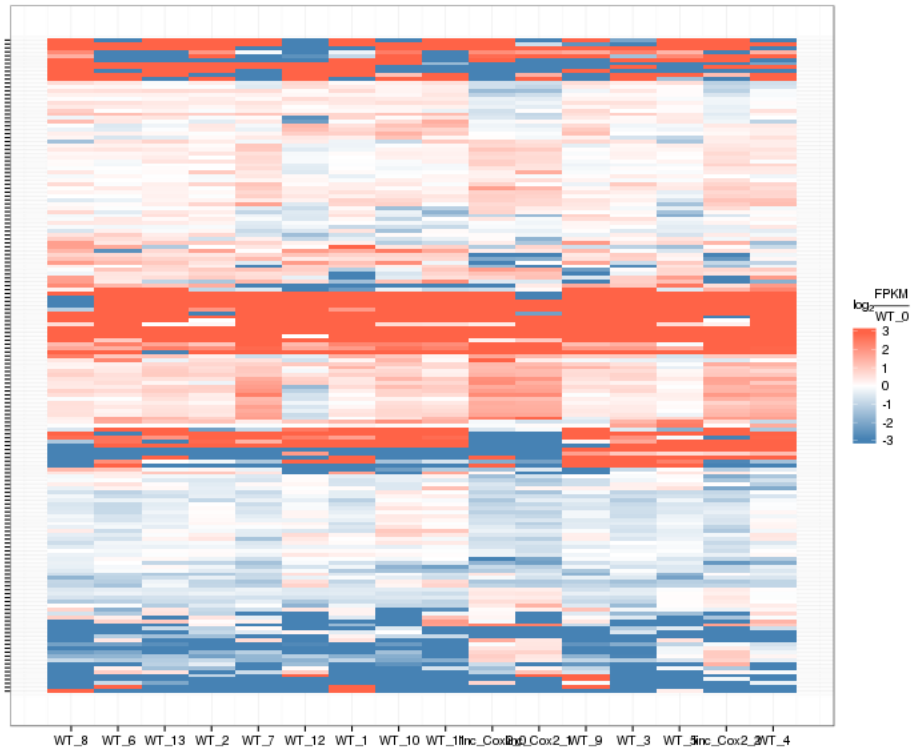
	isoAnnot$gene_short_name
1	Dynlt1c
2	Col1a1
3	Rec8
4	Zfp40
5	Lama2
6	Snrpf
7	Prpf8
8	Dlx2
9	Hcfc1r1
10	Glo1
11	Prss41
12	Atp6v0c
13	Hn1l
14	Lox
15	Rps14
16	Lbx1
17	Fn1
18	Bok
19	Asb1
20	Mcm6
21	Dbi
22	Lrp2
23	Rps3a1
24	Svep1
25	Ski
26	Dera
27	Hddc3
28	Dnah8
29	Gbx2
30	Rnps1
31	Fam171a2
32	Prr7
33	Lars2
34	3110052M02Rik
35	Cldn11
36	Vstm2l
37	Pcsk1n
38	Dgkz
39	Tlx3
40	C1qtnf4

41 2310036O22Rik
42 Fmod
43 Dlgap3
44 Reln
45 Hebp1
46 Olfml2a
47 Hmga1
48 Dmrta2
49 Mafa
50 Col6a3
51 Tagap1
52 Hbb-y
53 Zfp771
54 Pign
55 Capn11
56 Sox11
57 Sp9
58 Gpr98
59 Ssbp4
60 Jund
61 Gpr27
62 9030025P20Rik
63 Gm11273
64 Ccdc85c
65 Myl6
66 Ccdc85b
67 Gm6472
68 Gm9825
69 Gm26917
70 Gm26924

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

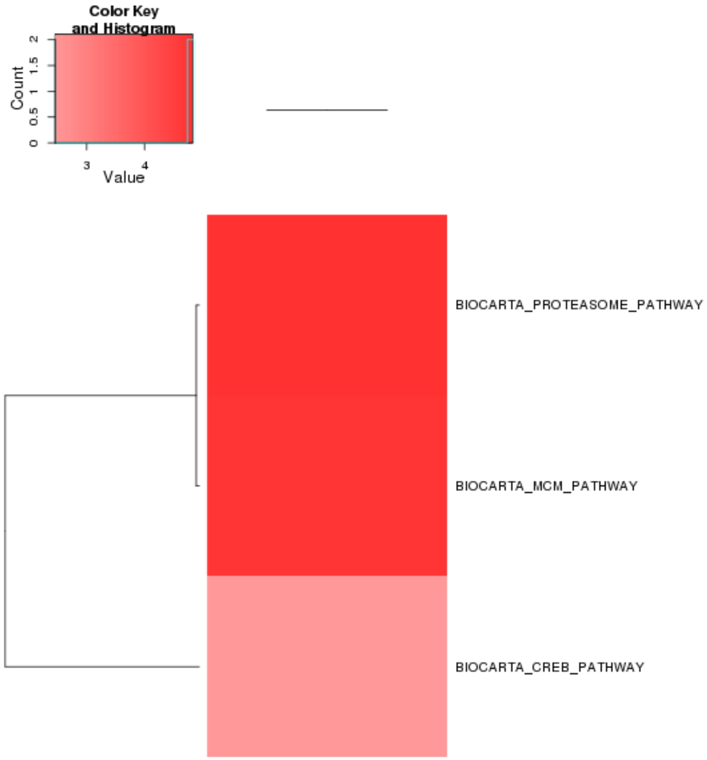
Gene/Pathway Analysis

GSEA

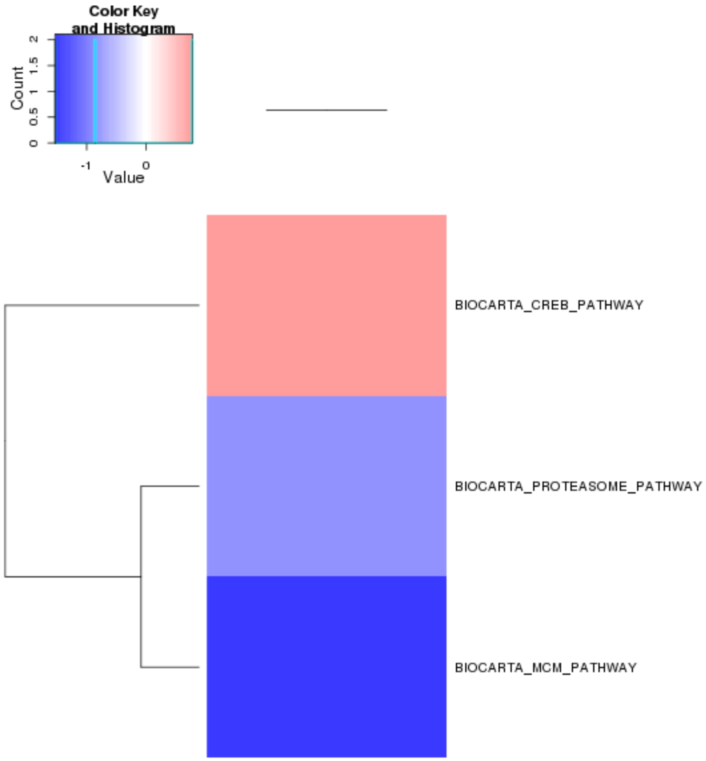
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:



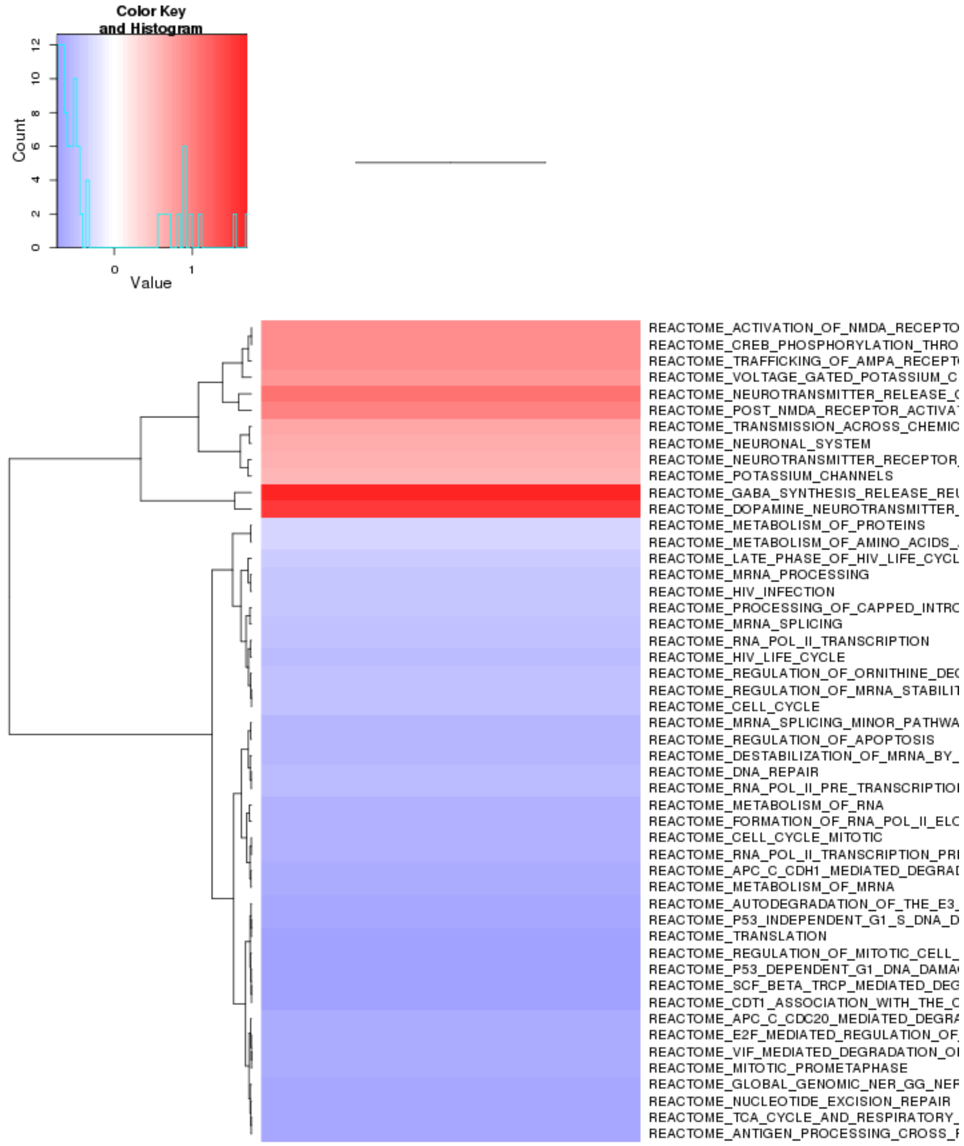
Biocarta zscore:



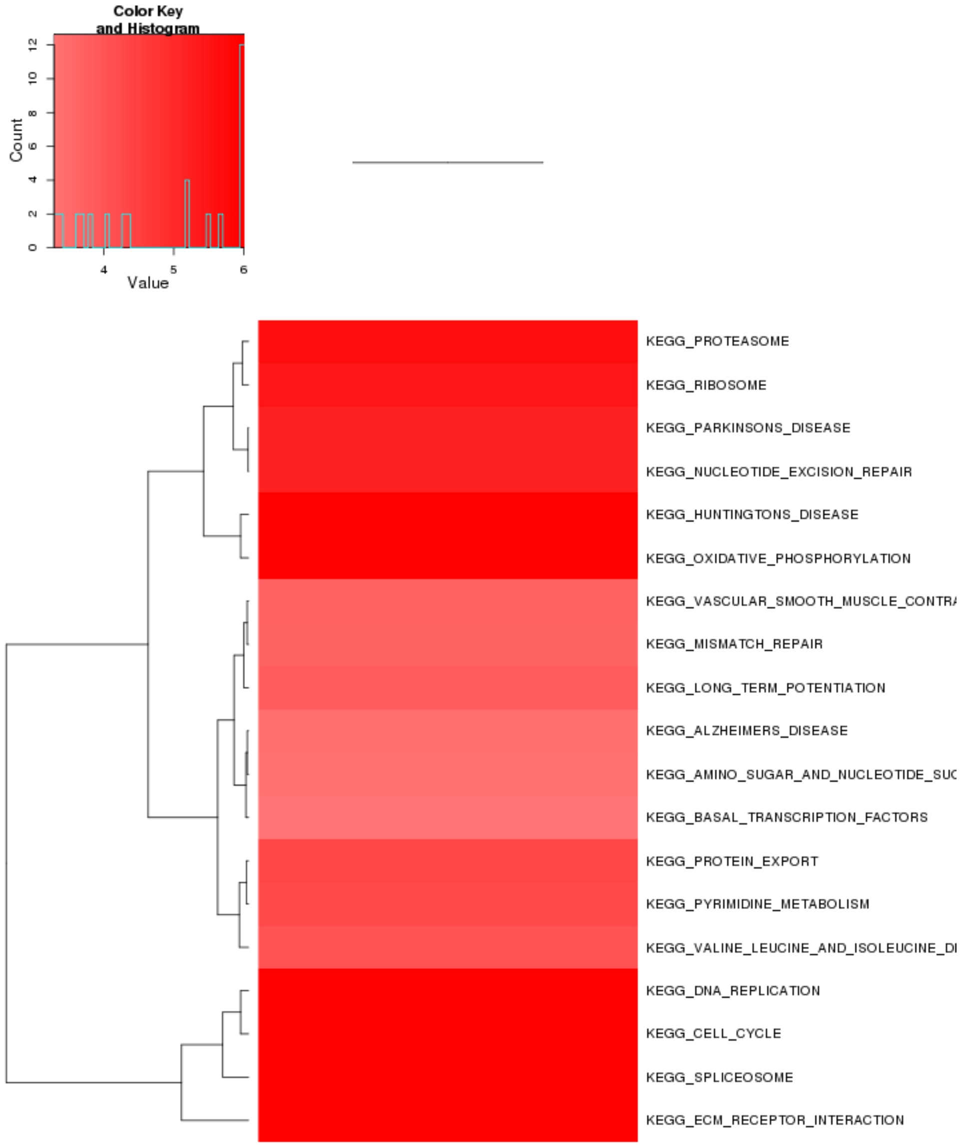
Reactome enrichment:

```
## Error: no locations are finite
```

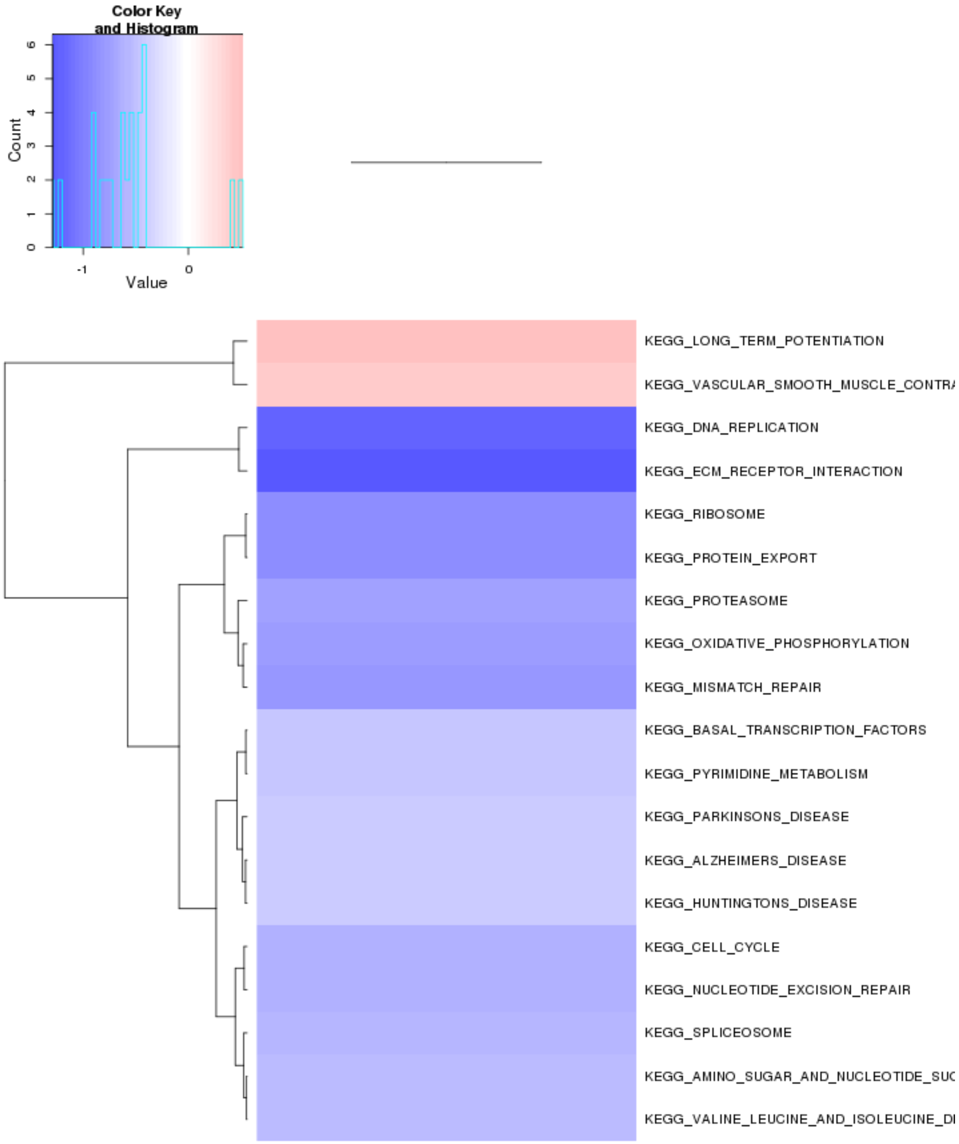
Reactome zscore:



Kegg enrichment:


Color Key
and Histogram
Count
0
2
4
6
8
10
12
4
5
6
Value
KEGG_PROTEASOME
KEGG_RIBOSOME
KEGG_PARKINSONS_DISEASE
KEGG_NUCLEOTIDE_EXCISION_REPAIR
KEGG_HUNTINGTONS_DISEASE
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRA
KEGG_MISMATCH_REPAIR
KEGG_LONG_TERM_POTENTIATION
KEGG_ALZHEIMERS_DISEASE
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SU
KEGG_BASAL_TRANSCRIPTION_FACTORS
KEGG_PROTEIN_EXPORT
KEGG_PYRIMIDINE_METABOLISM
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_D
KEGG_DNA_REPLICATION
KEGG_CELL_CYCLE
KEGG_SPLICEOSOME
KEGG_ECM_RECEPTOR_INTERACTION

Kegg zscore:



Interneuron enrichment:

```
## Error: argument is of length zero
```

Interneuron zscore:

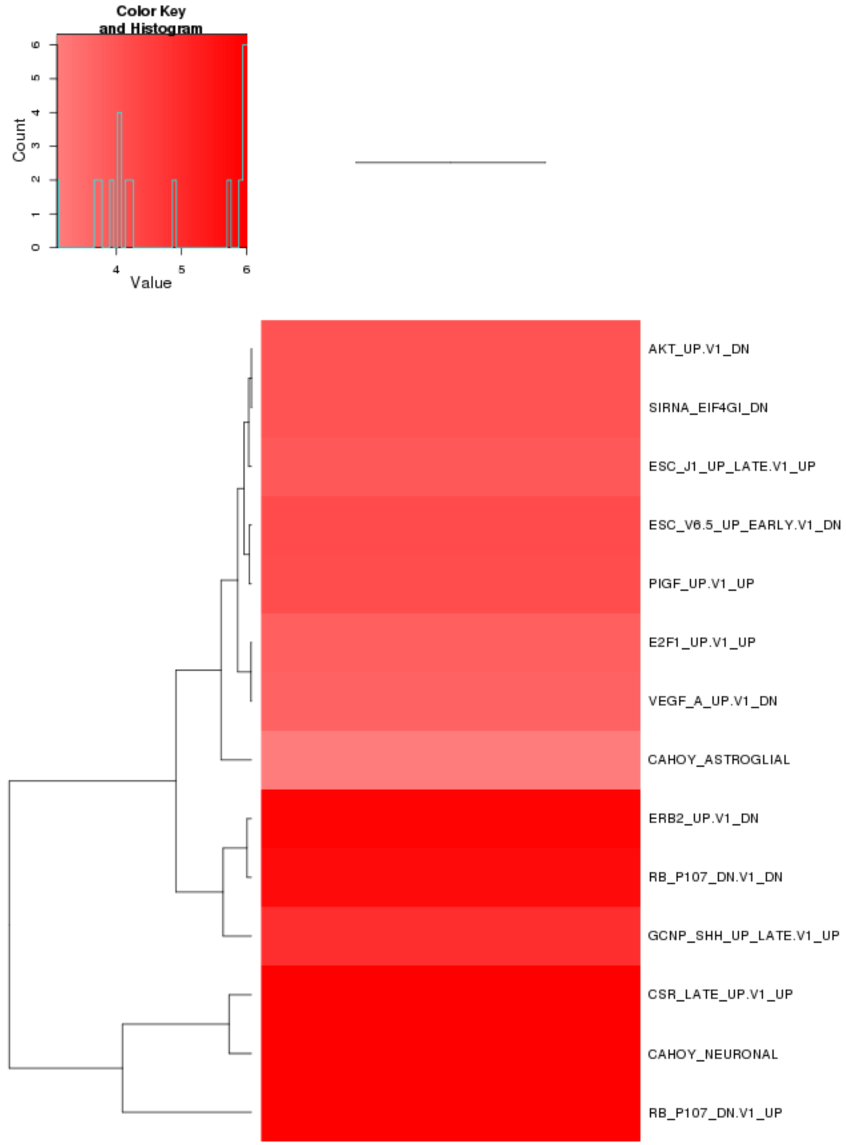
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

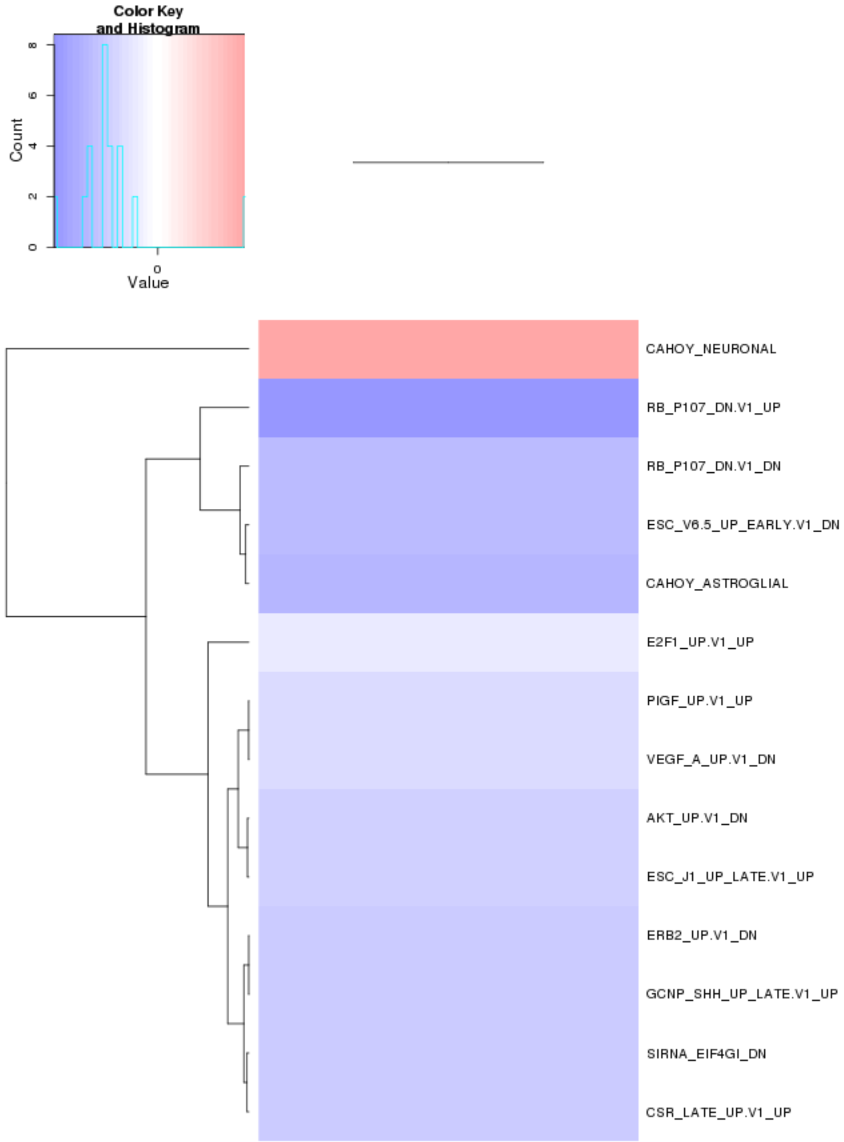
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

Oncogene enrichment:

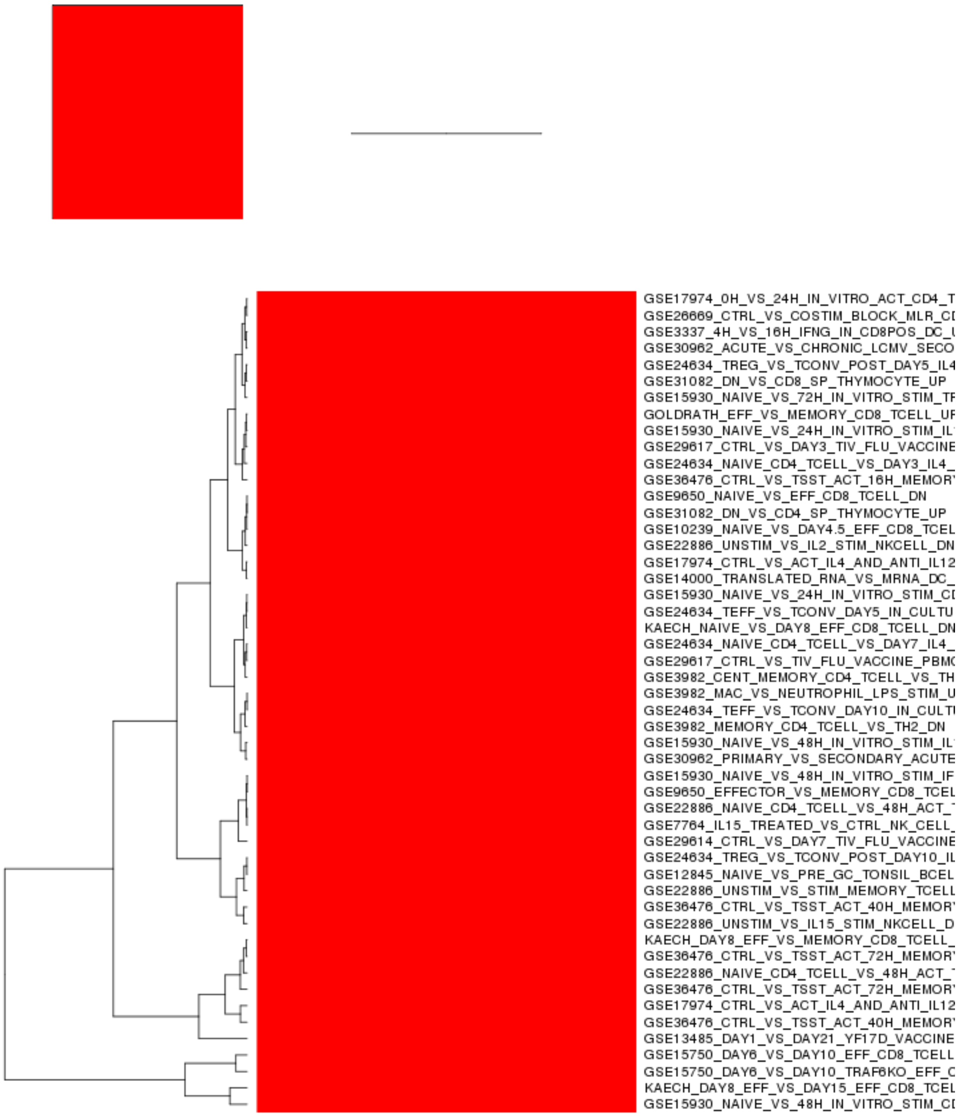


Oncogene zscore:

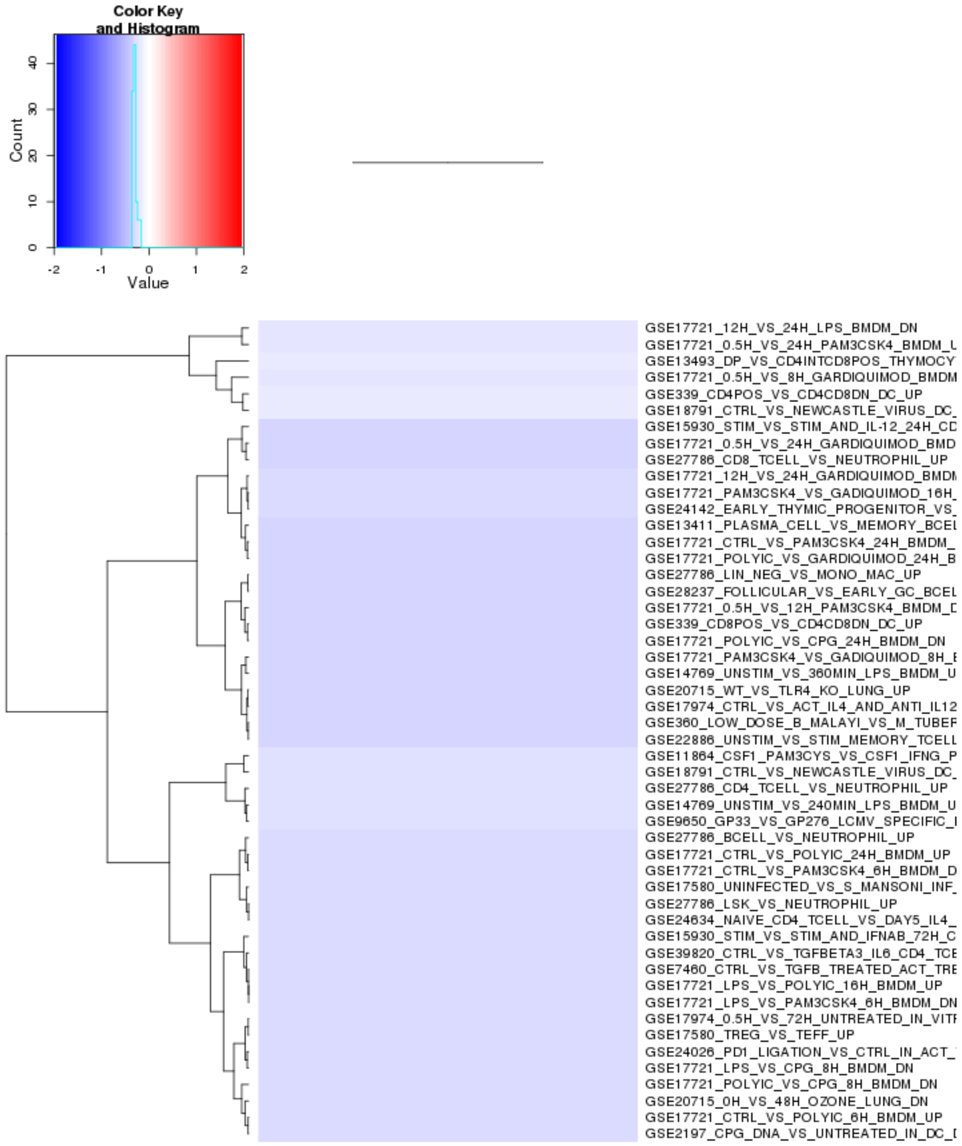


Immuno enrichment:

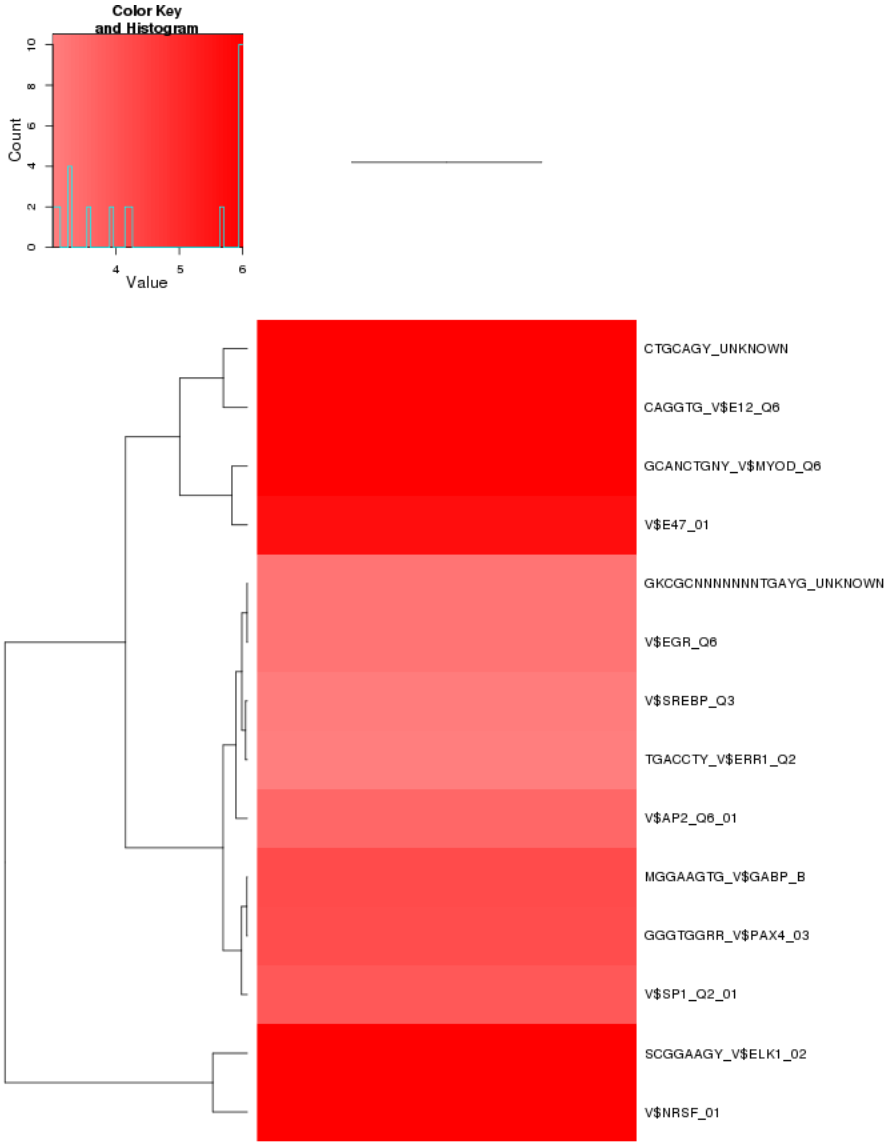
```
## Error: no locations are finite
```



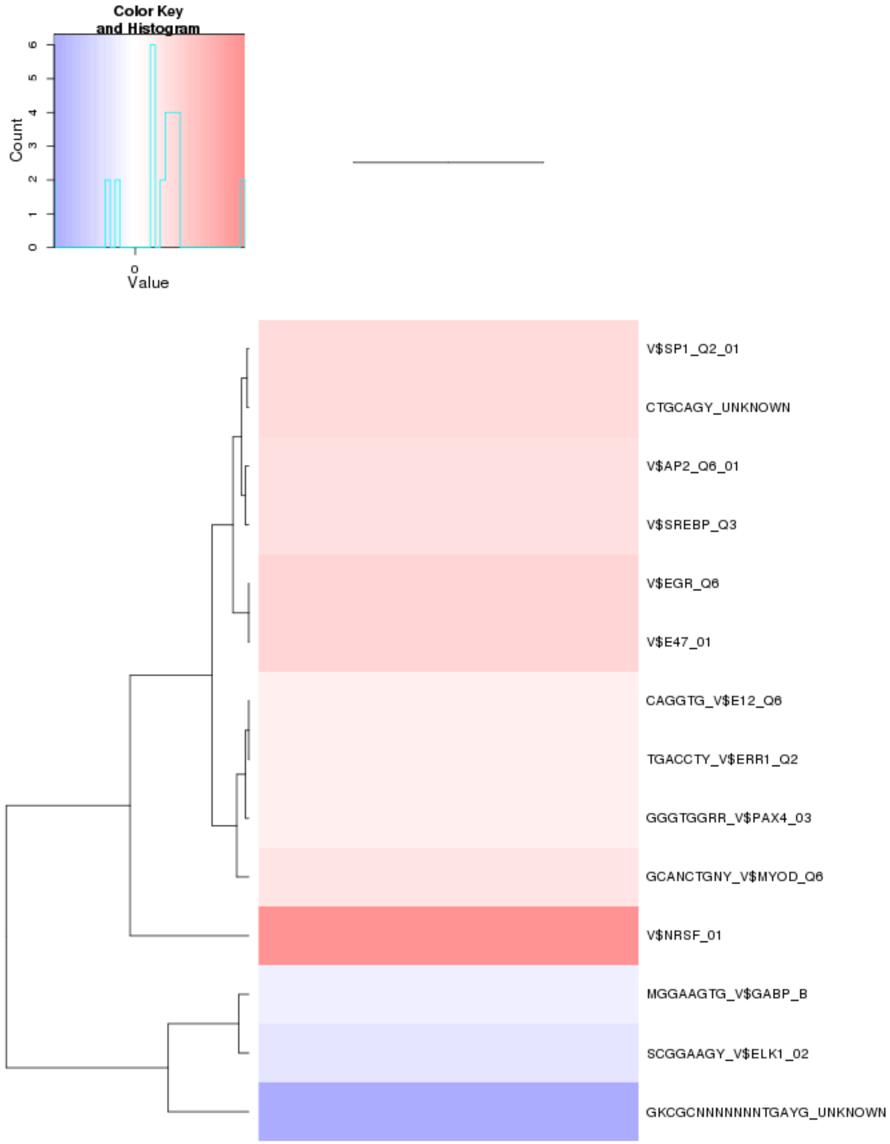
Immuno zscore:



TF enrichment:

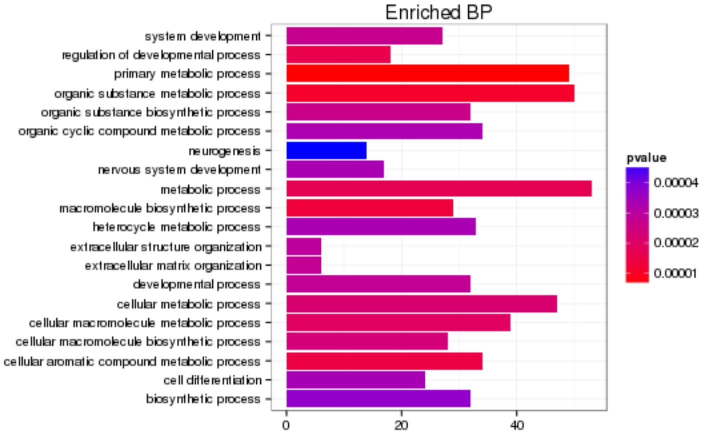

Color Key
and Histogram
Count
0
2
4
6
8
10
Value
4
5
6
CTGCAGY_UNKNOWN
CAGGTG_V$E12_Q6
GCANCTGNY_V$MYOD_Q6
V$E47_01
GKCGCNNNNNNNTGAYG_UNKNOWN
V$EGR_Q6
V$SREBP_Q3
TGACCTY_V$ERR1_Q2
V$AP2_Q6_01
MGGAAGTG_V$GABP_B
GGGTGGRR_V$PAX4_03
V$SP1_Q2_01
SCGGAAGY_V$ELK1_02
V$NRSF_01

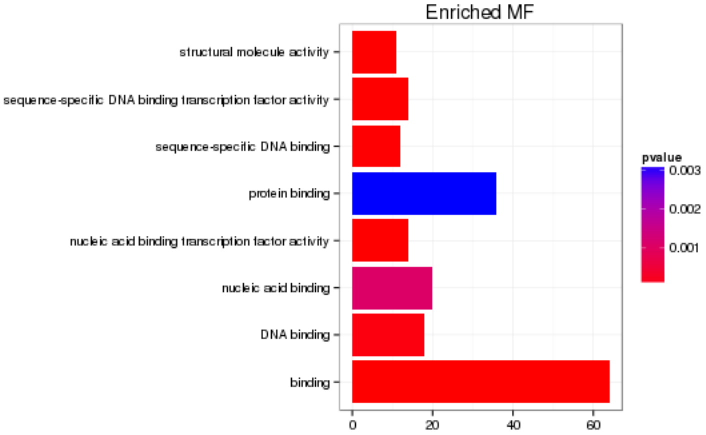
TF zscore:

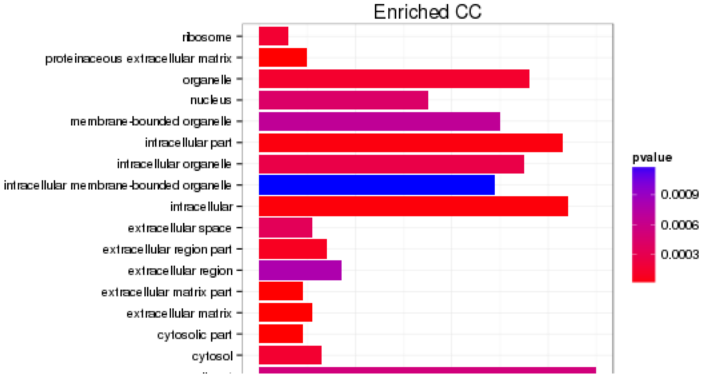


GO enrichment

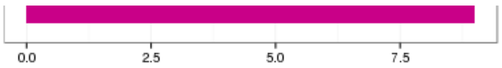
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

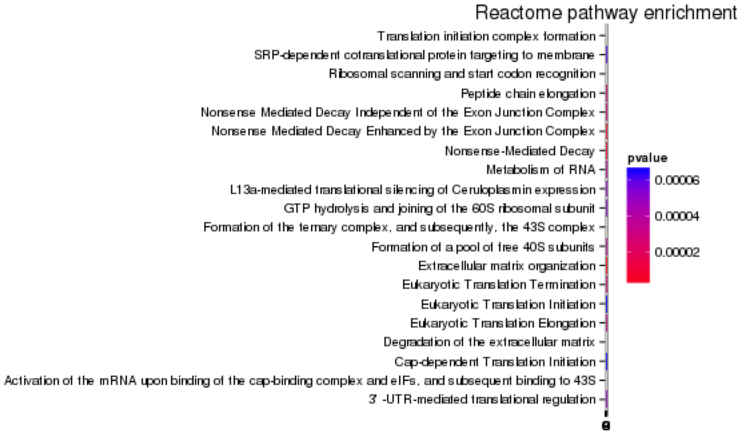

Enriched BP
system development
regulation of developmental process
primary metabolic process
organic substance metabolic process
organic substance biosynthetic process
organic cyclic compound metabolic process
neurogenesis
nervous system development
metabolic process
macromolecule biosynthetic process
heterocycle metabolic process
extracellular structure organization
extracellular matrix organization
developmental process
cellular metabolic process
cellular macromolecule metabolic process
cellular macromolecule biosynthetic process
cellular aromatic compound metabolic process
cell differentiation
biosynthetic process
0
20
40
pvalue
0.00004
0.00003
0.00002
0.00001


Enriched MF
structural molecule activity
sequence-specific DNA binding transcription factor activity
sequence-specific DNA binding
protein binding
nucleic acid binding transcription factor activity
nucleic acid binding
DNA binding
binding
0
20
40
60
pvalue
0.003
0.002
0.001

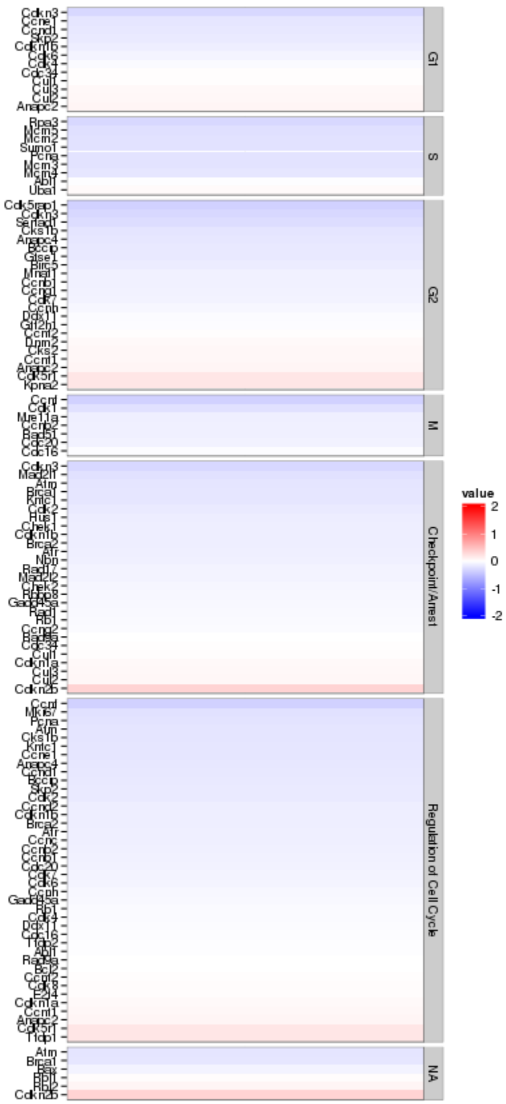

Enriched CC
ribosome
proteinaceous extracellular matrix
organelle
nucleus
membrane-bounded organelle
intracellular part
intracellular organelle
intracellular membrane-bounded organelle
intracellular
extracellular space
extracellular region part
extracellular region
extracellular matrix part
extracellular matrix
cytosolic part
cytosol
pvalue
0.0009
0.0006
0.0003


Ribosome

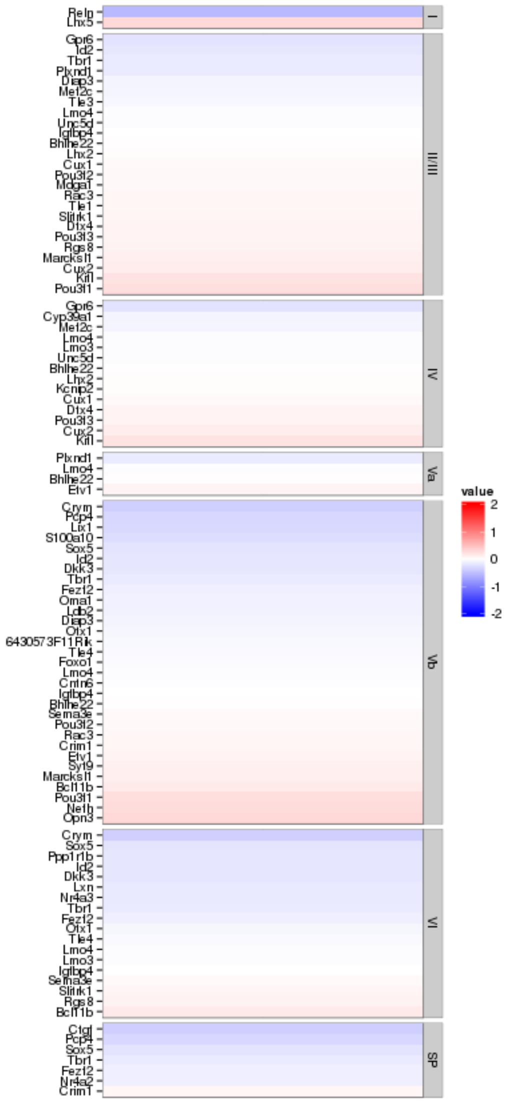




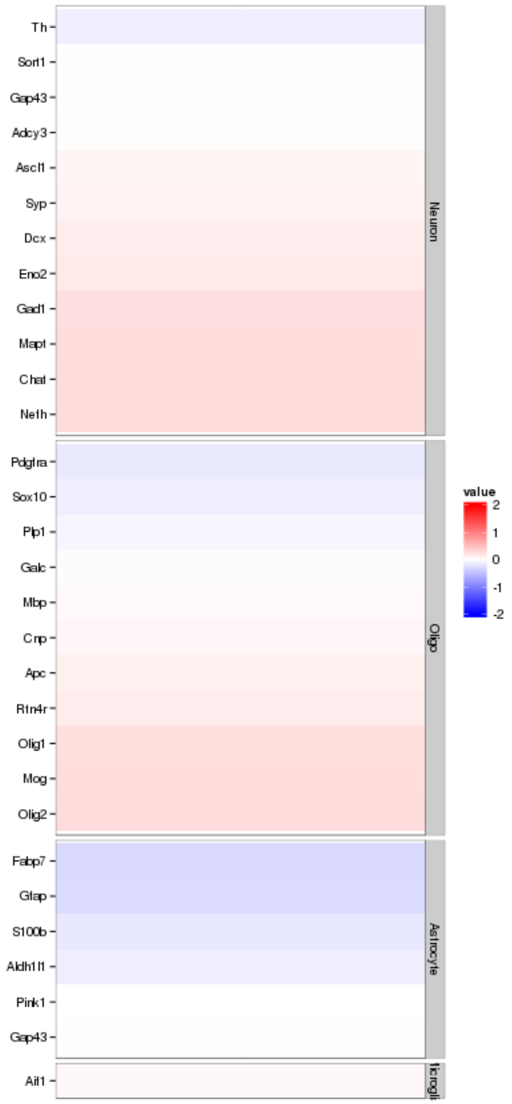
Enrichment or depletion for stage-specific cell cycle markers



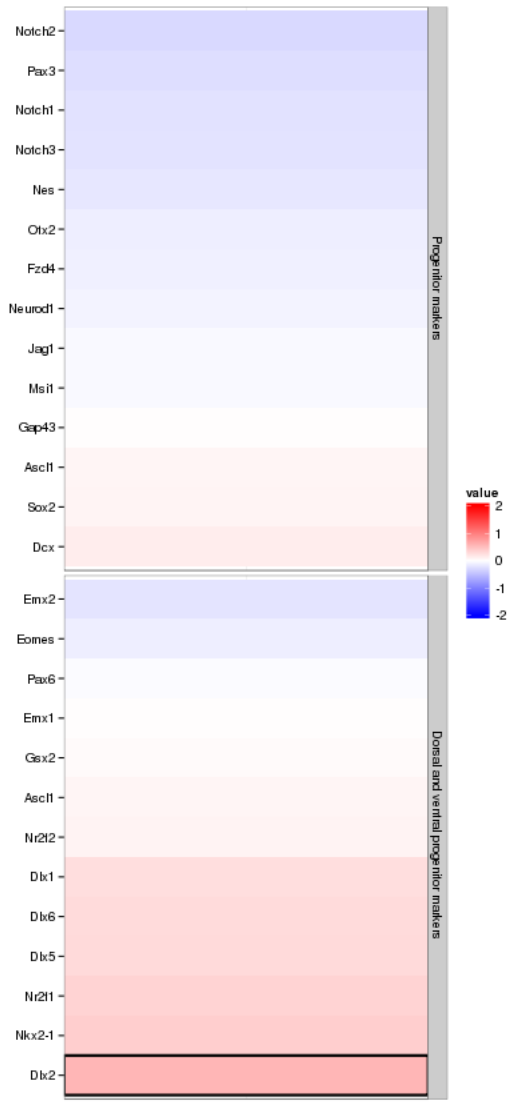
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



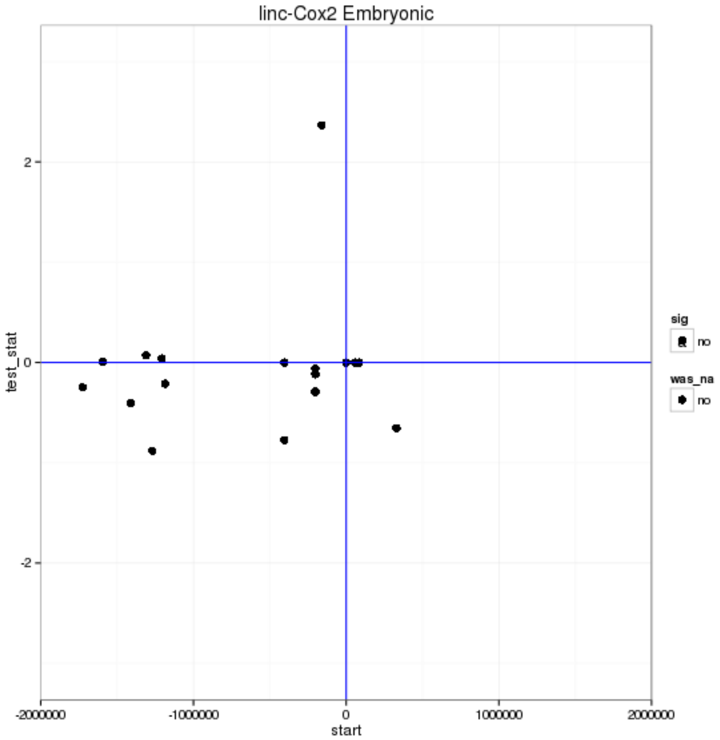
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15	JR809
16	JR816
17	JR829

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	32194900.00	1.27	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	32194900.00	1.10	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	32194900.00	1.23	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	32194900.00	1.29	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	32194900.00	1.21	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	32194900.00	0.90	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	32194900.00	0.98	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	32194900.00	0.93	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	32194900.00	0.86	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	32194900.00	0.96	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	32194900.00	0.81	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	32194900.00	0.80	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	32194900.00	0.69	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	32194900.00	1.22	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR809/abundances.cxb	linc_Cox2	0	linc_Cox2_0	36051200.00	32194900.00	1.11	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR816/abundances.cxb	linc_Cox2	1	linc_Cox2_1	31829200.00	32194900.00	0.98	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR829/abundances.cxb	linc_Cox2	2	linc_Cox2_2	30833100.00	32194900.00	0.95	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6          
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4      
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7             
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1         
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1          
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4          
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12    
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26   
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2         
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0         
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1    
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2         
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2           
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##              param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,linc-Cox2 -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/linc-Cox2_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/Brai
## 2
## 3
## 4
## 5
```

linc-Enc1 KO vs WT (Adult)

This file shows the wt-v-ko comparison for linc-Enc1.

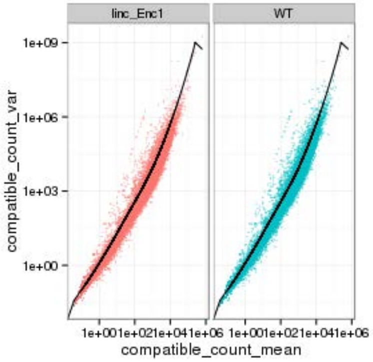
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

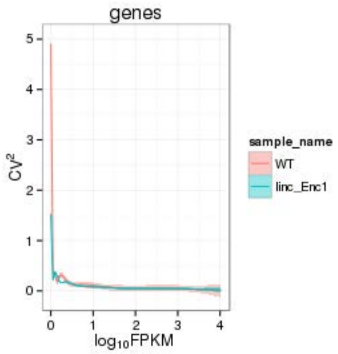
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



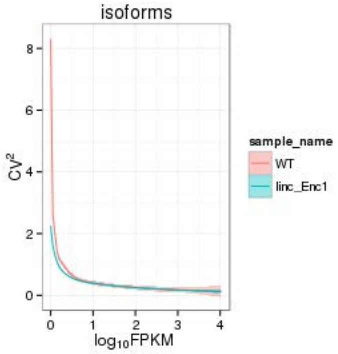
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

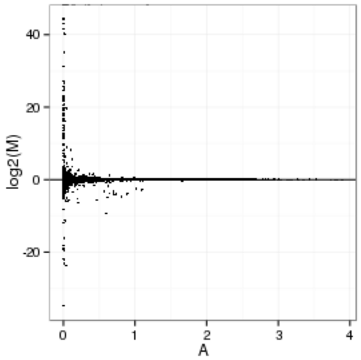
Genes:



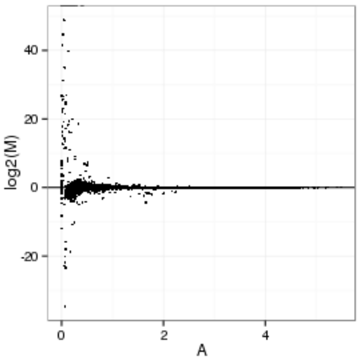
Isoforms:



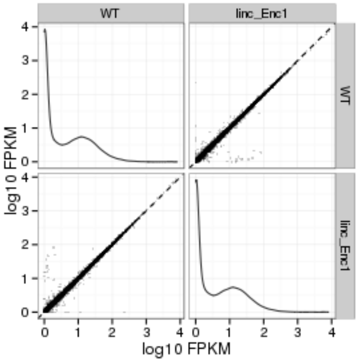
MvA plot



MvA plot counts



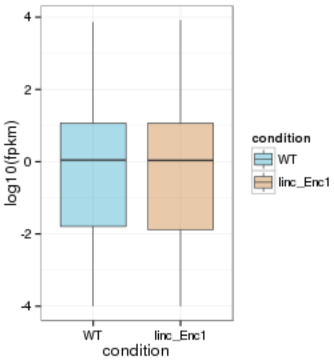
Scatterplot matrix



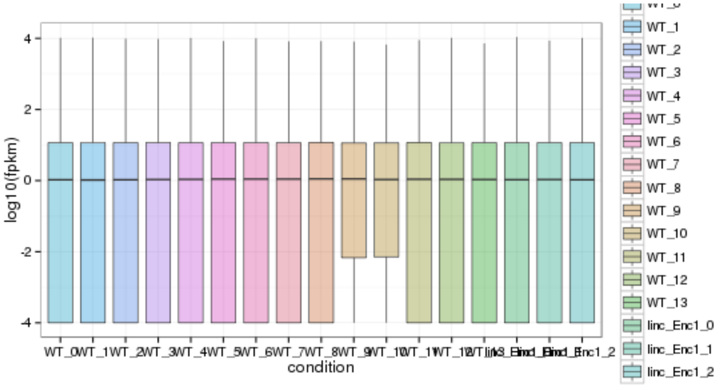
Distributions

Boxplots

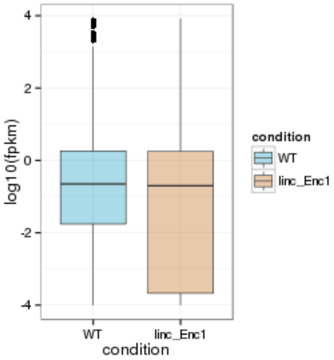
Boxplot (genes)



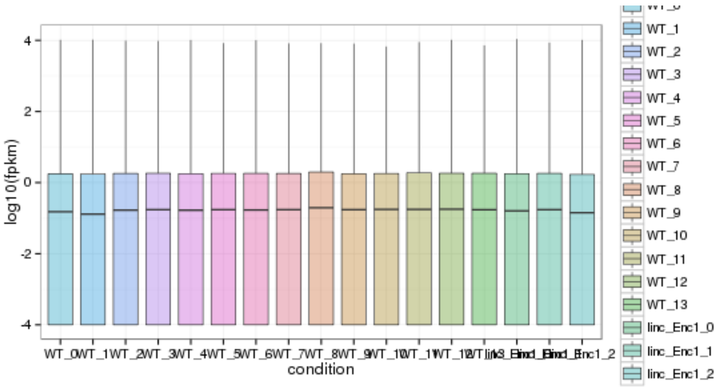
Boxplot (genes, replicates)



Boxplot (isoforms)

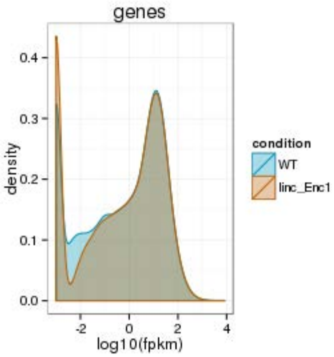


Boxplot (isoforms, replicates)

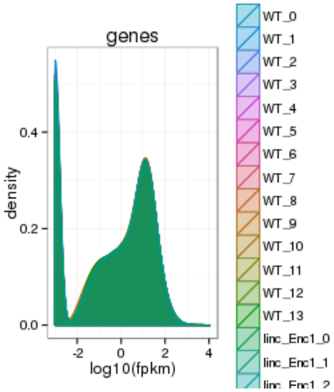


Density

Density (genes)

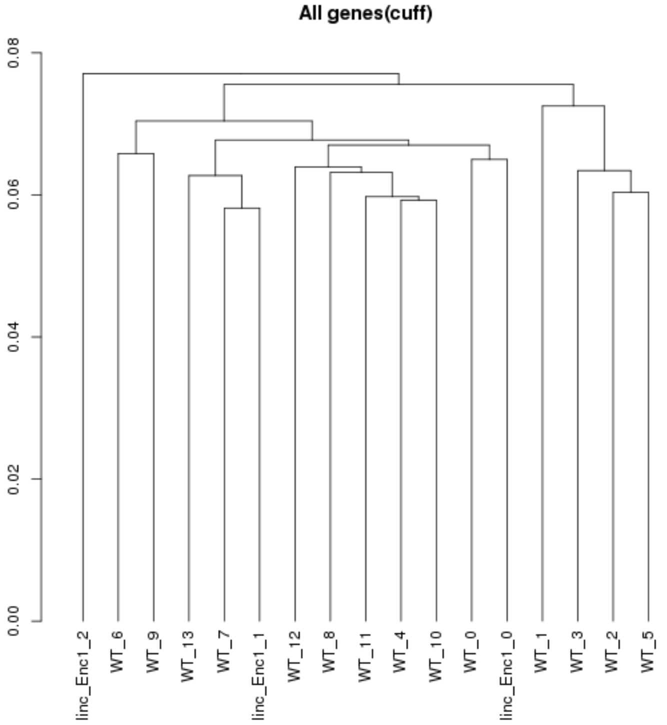


Density (genes, replicates)



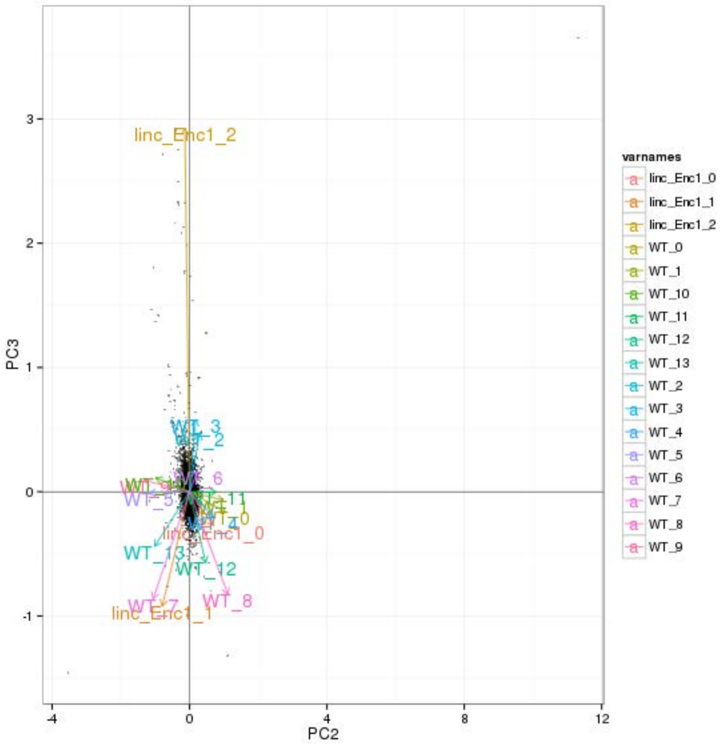
Clustering

Replicate Clusters

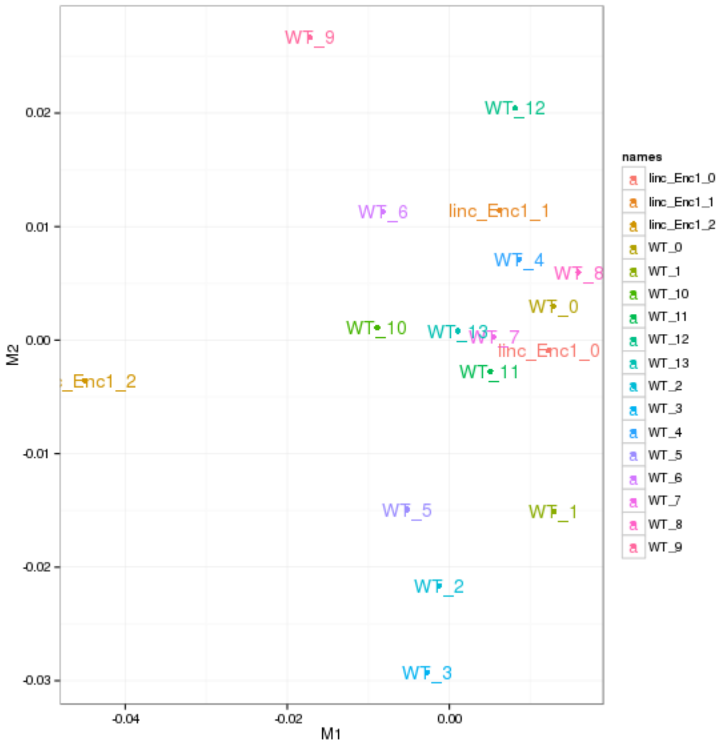


```
## NULL
```

PCA (genes)

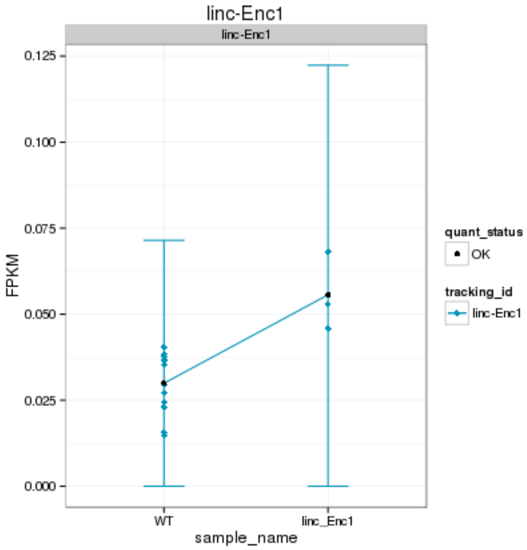

PC3
PC2
3
2
1
0
-1
-4
0
4
8
12
linc_Enc1_2
linc_Enc1_0
linc_Enc1_1
WT_3
WT_2
WT_5
WT_6
WT_11
WT_10
WT_13
WT_12
WT_7
WT_8
varnames
a linc_Enc1_0
a linc_Enc1_1
a linc_Enc1_2
a WT_0
a WT_1
a WT_10
a WT_11
a WT_12
a WT_13
a WT_2
a WT_3
a WT_4
a WT_5
a WT_6
a WT_7
a WT_8
a WT_9

MDS (genes)

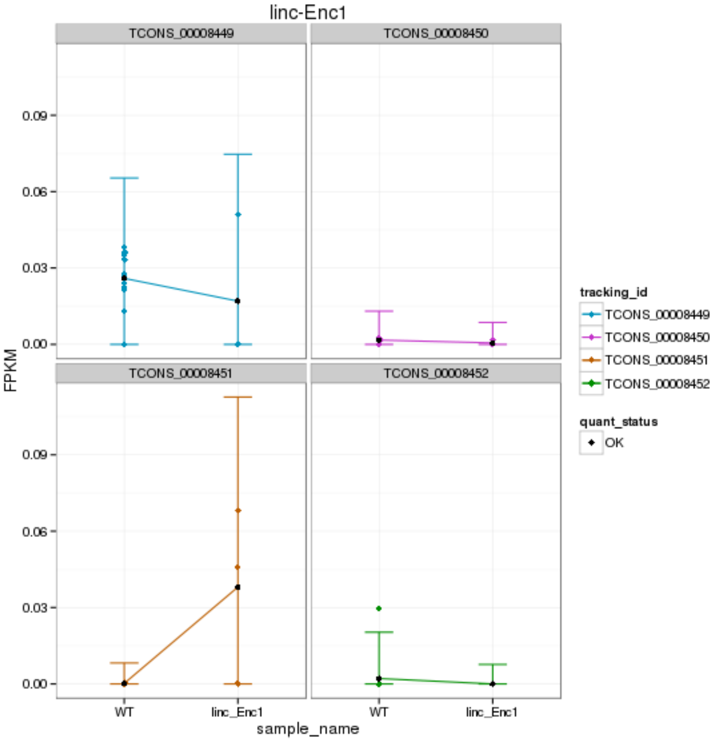


KO assessment

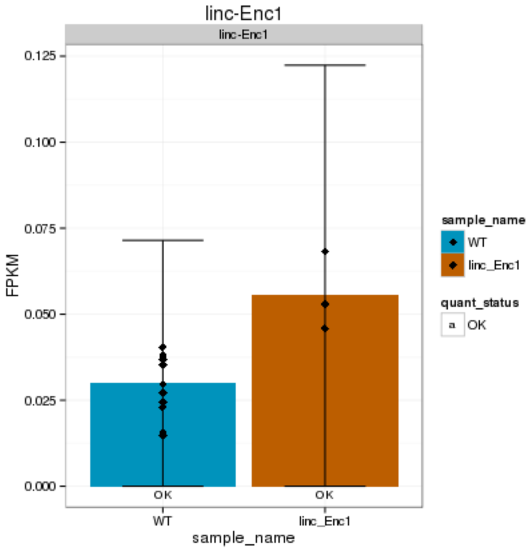
Endogenous lncRNA expression



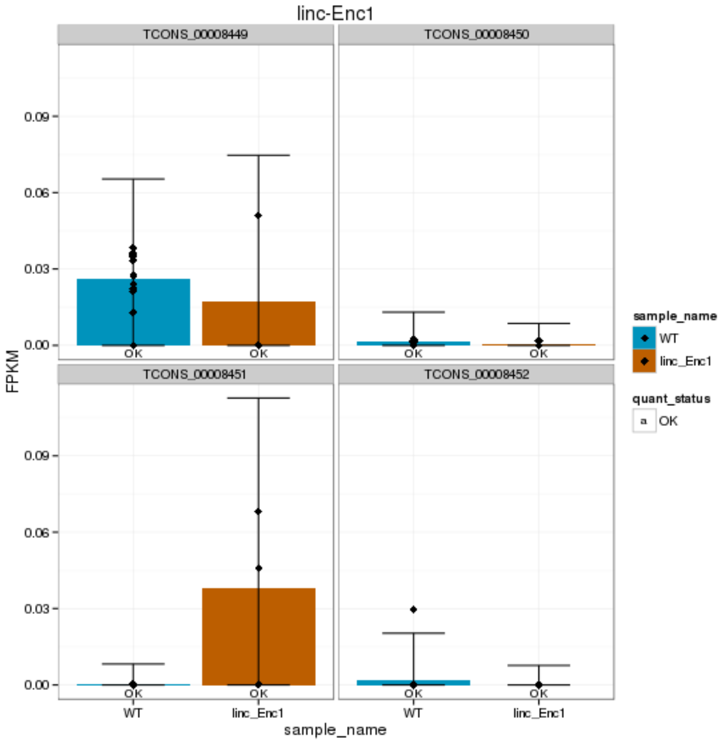
Endogenous expression of linc-Enc1 isoforms:



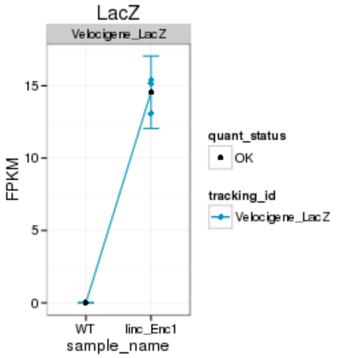
Barplot of gene expression:

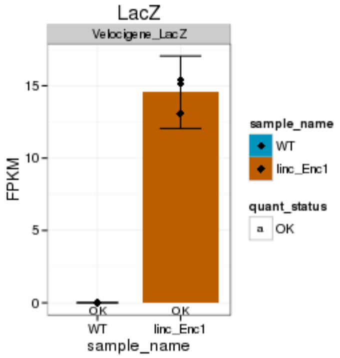


Barplot of isoform expression:



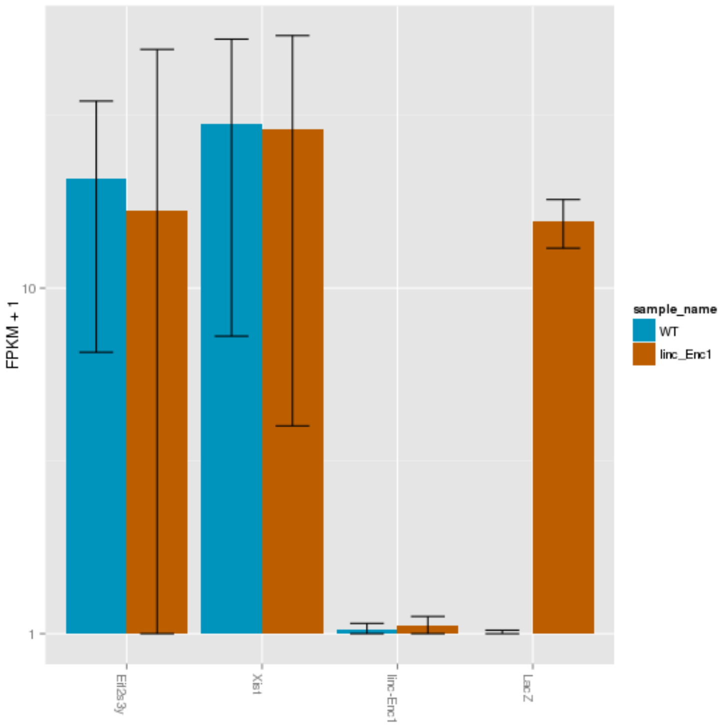
LacZ expression



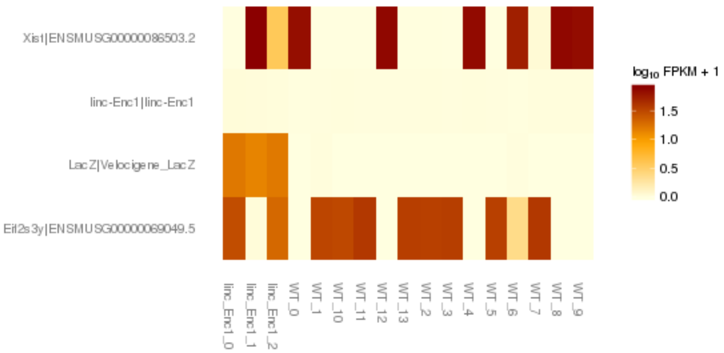


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

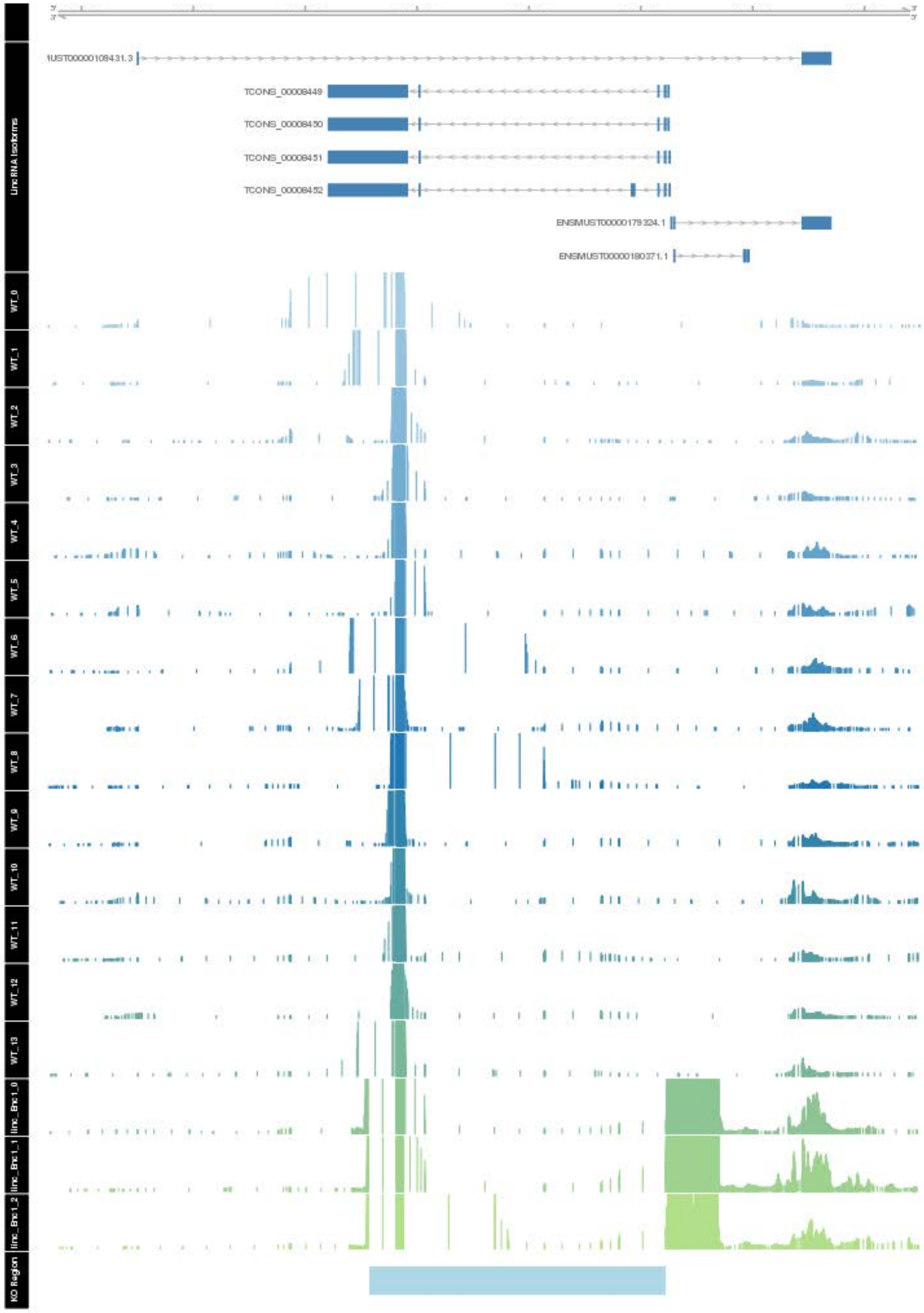
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


LincRNA Isoforms
1UST00000108431.3
TCONS_00008449
TCONS_00008450
TCONS_00008451
TCONS_00008452
ENSMUST00000179324.1
ENSMUST00000180371.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
linc_Bnc1_0
linc_Bnc1_1
linc_Bnc1_2
KO Region

Differential Analysis

Differential Genes

There are 52 significantly differentially expressed genes. They are:

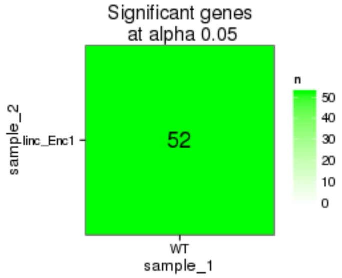
	geneAnnot$gene_short_name
1	Nes
2	Dnajb1
3	Pttg1
4	Adi1
5	Psmb5
6	Arc
7	Mut
8	Glo1
9	Flnb
10	Nnt
11	Lcn2
12	Cyr61
13	Alad
14	Ugt2a1
15	Hddc3
16	Arhgap27
17	Tmem260
18	Hdhd3
19	Car8
20	Mup4
21	Enc1
22	Tuba1c
23	5430402E10Rik
24	Gm9493
25	Zfp488
26	Acp1
27	Cd24a
28	BC048546
29	Myh7
30	BC051076
31	Mup5
32	Cox5b
33	Rpl34
34	Obp2a
35	Obp1b
36	Obp1a
37	Bpifb9b

38 Bpifb3
39 Ppp1r3e
40 Gm7292
41 H2-Bl
42 Ccl28
43 Gm2373

44 Gm14744
45 Obp2b
46 4930412C18Rik
47 Hspa1b
48 Hspa1a
49 AA465934
50 4930480K23Rik
51 Gm26825
52 Gm26924

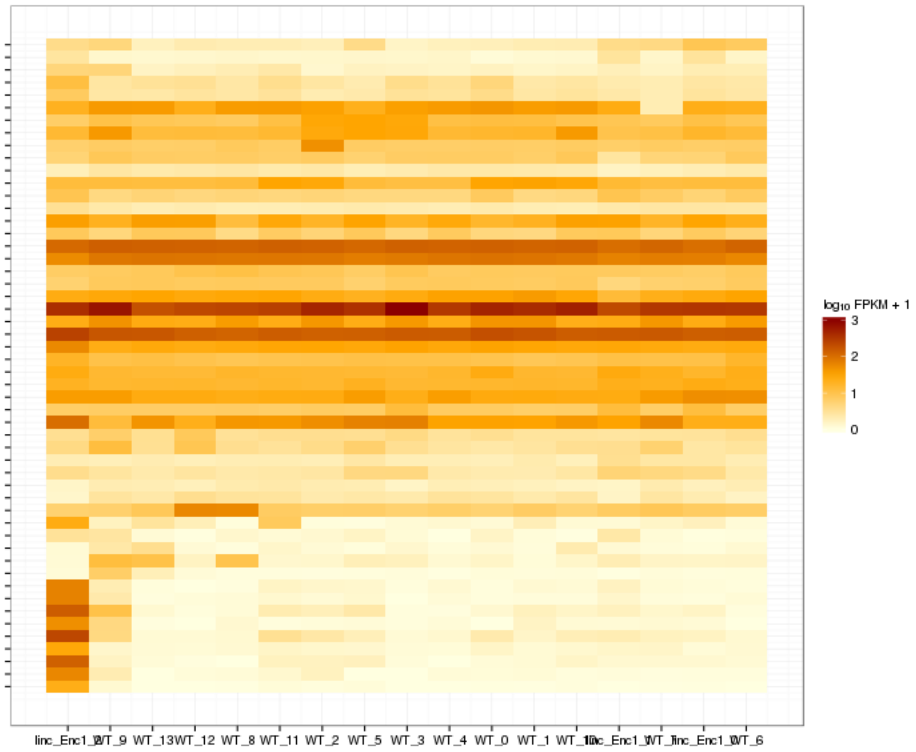
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

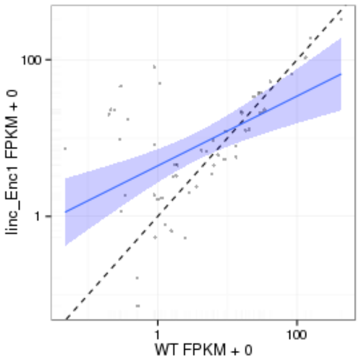


Significant genes with expression >50fpkm (any condition):(turned off)

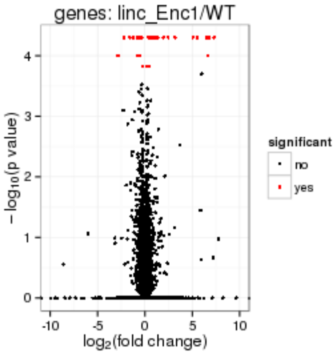
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

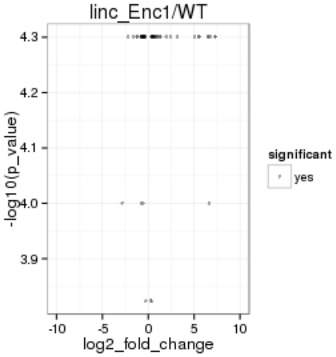
Scatter plot of significant genes only:



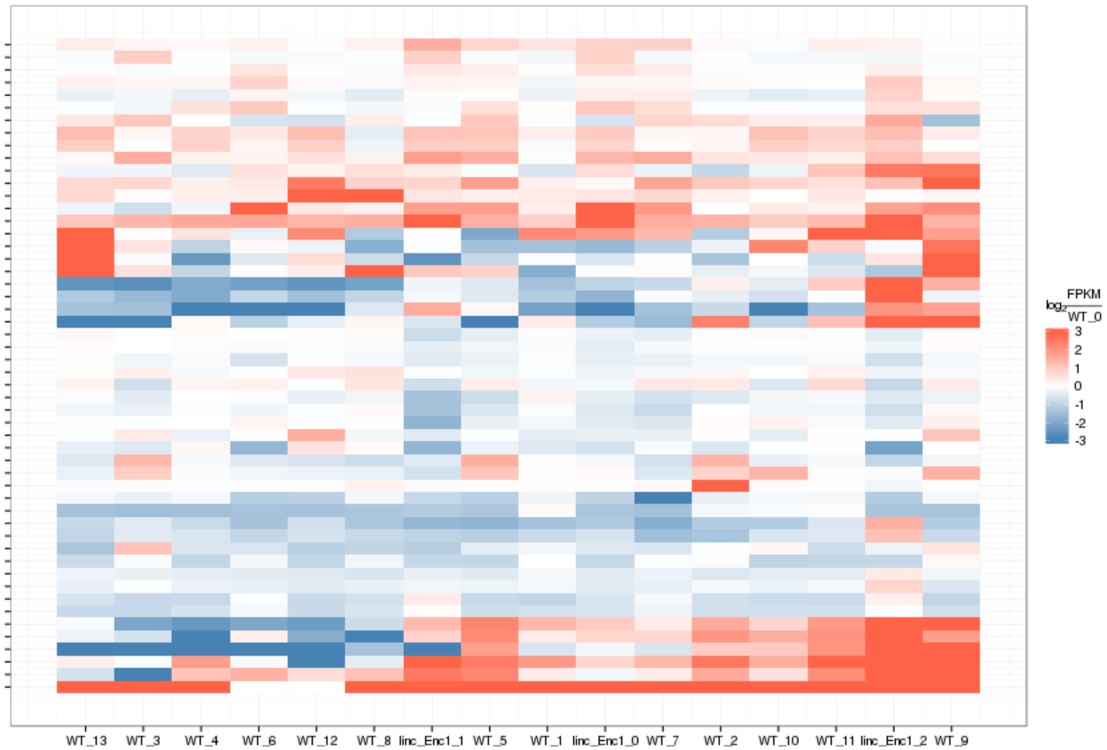
Volcano Plot



Volcano plot with significant genes only:



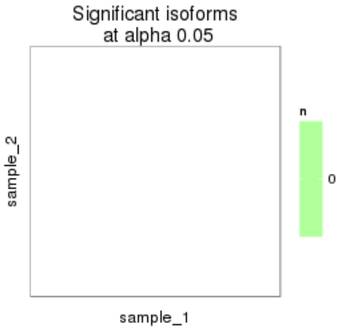
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

[1] “no sig isoforms”

Gene-level DE isoform heatmap

```
## [1] "no sig isoforms"
```

Isoform foldchange heatmap by isoform:

```
## [1] "no sig isoforms"
```

Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:

```
## Error: `x' must have at least 2 rows and 2 columns
```

Biocarta zscore:

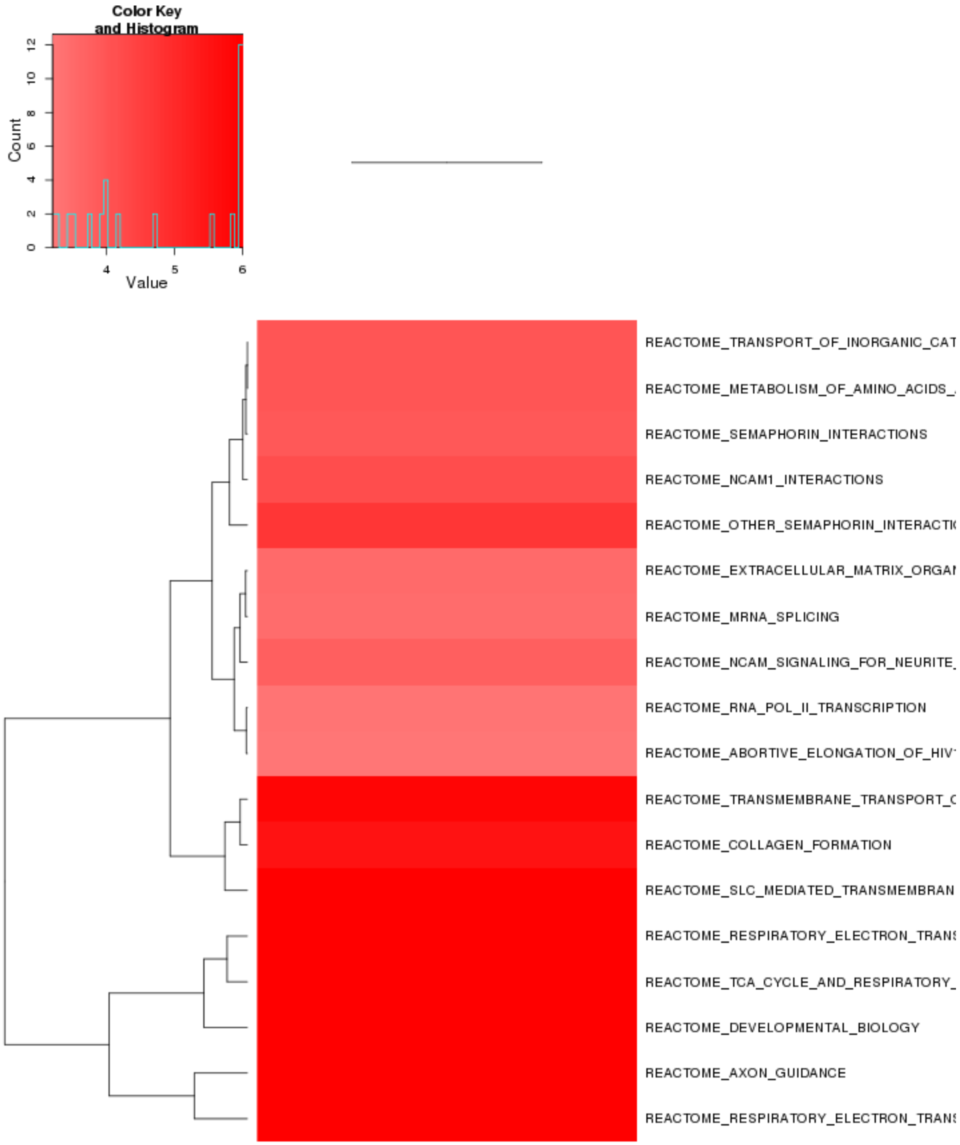
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

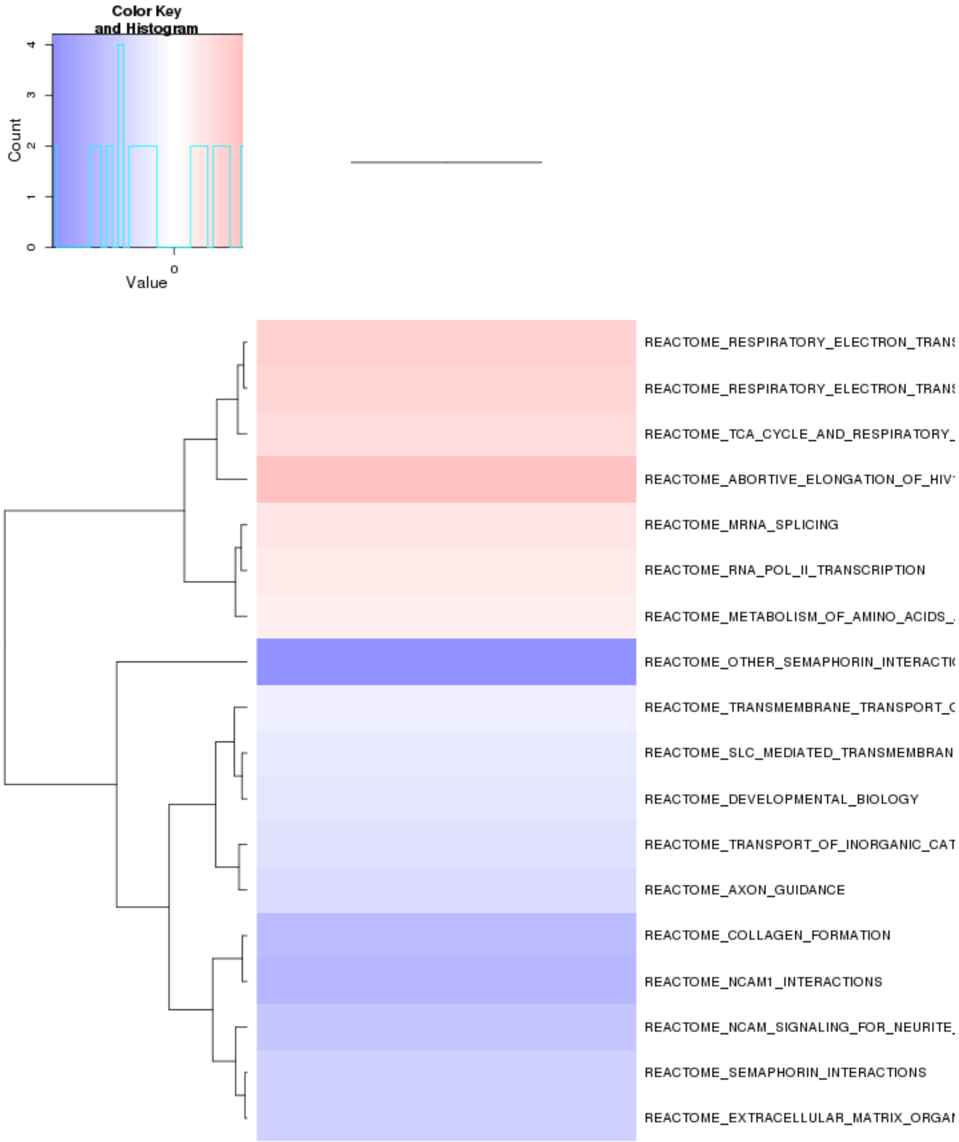
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

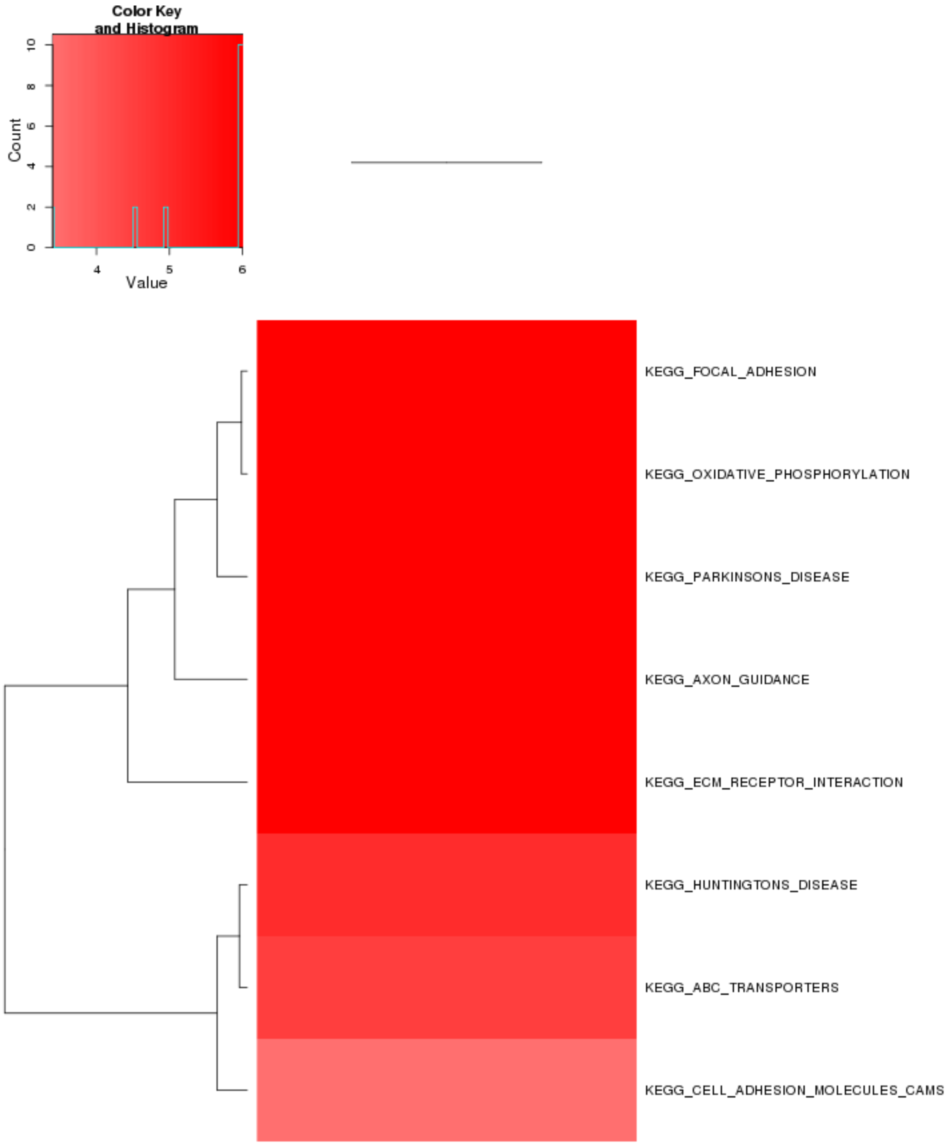
Reactome enrichment:



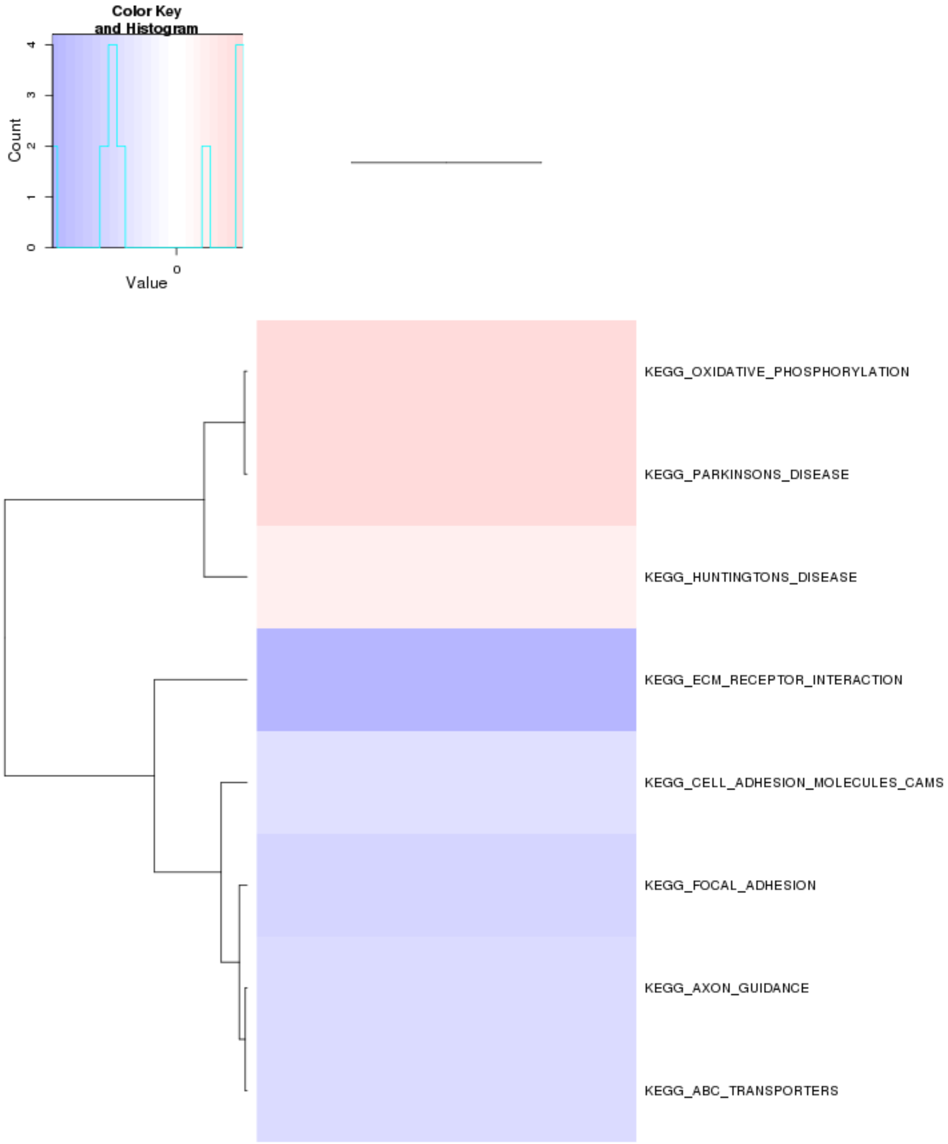
Reactome zscore:



Kegg enrichment:

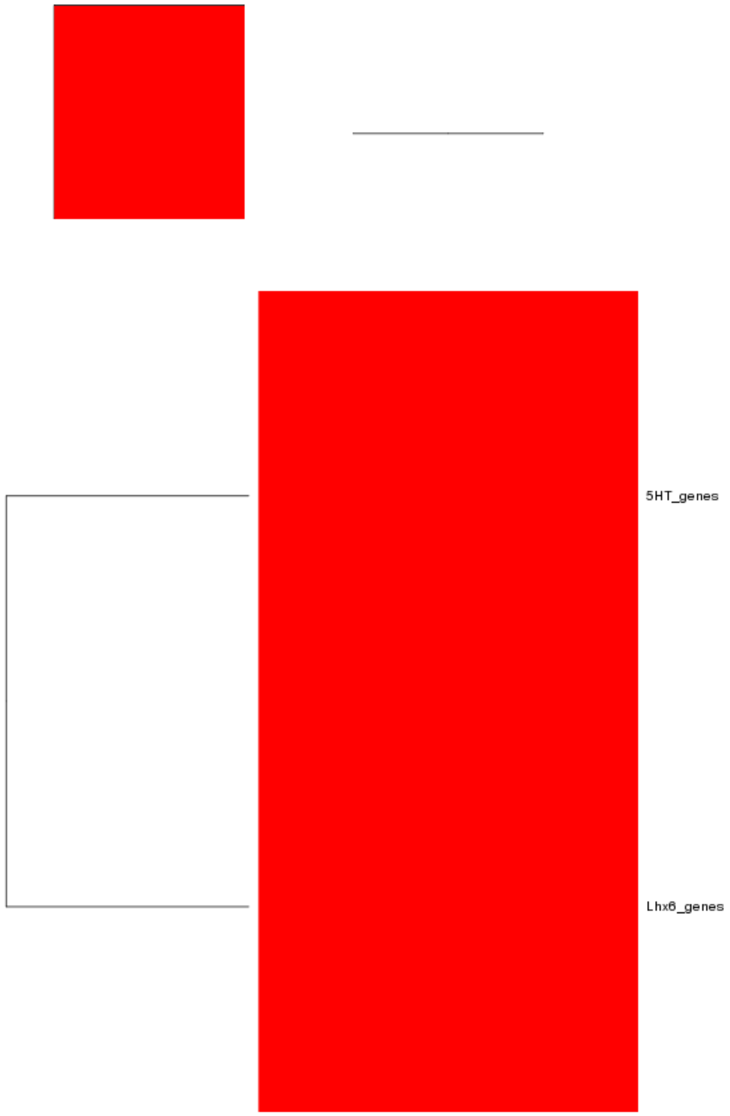

Color Key
and Histogram
Count
0
2
4
6
8
10
4
5
6
Value
KEGG_FOCAL_ADHESION
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_PARKINSONS_DISEASE
KEGG_AXON_GUIDANCE
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_HUNTINGTONS_DISEASE
KEGG_ABC_TRANSPORTERS
KEGG_CELL_ADHESION_MOLECULES_CAMS

Kegg zscore:

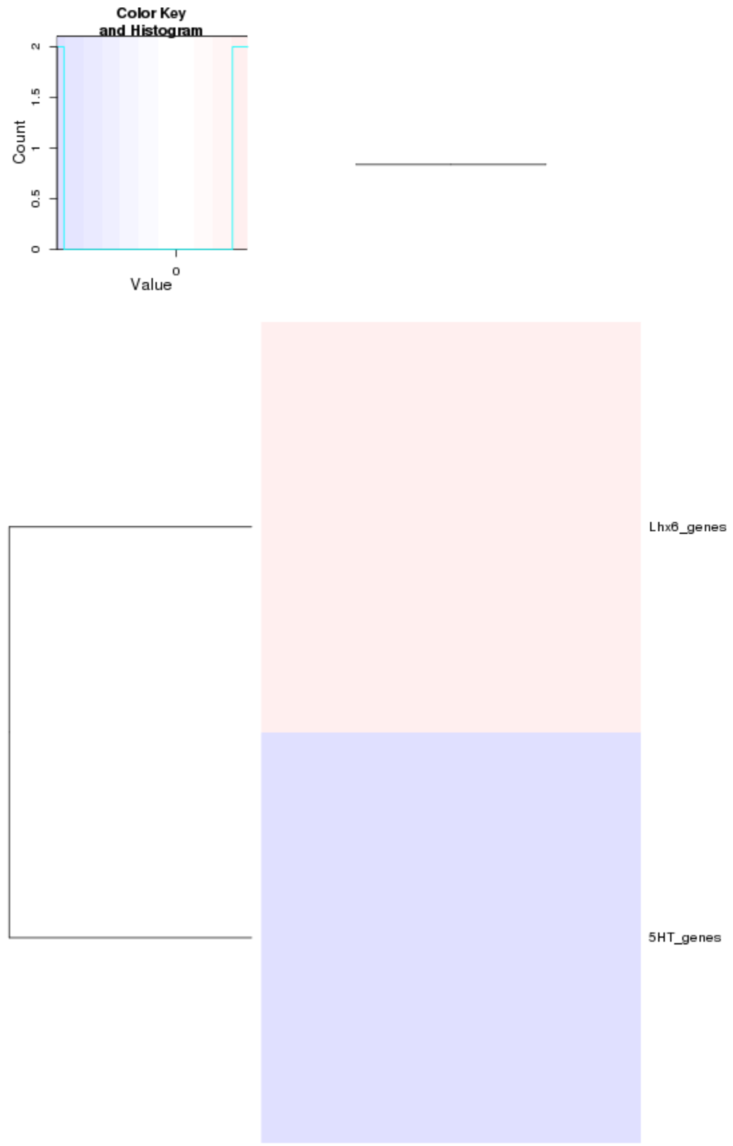


Interneuron enrichment:

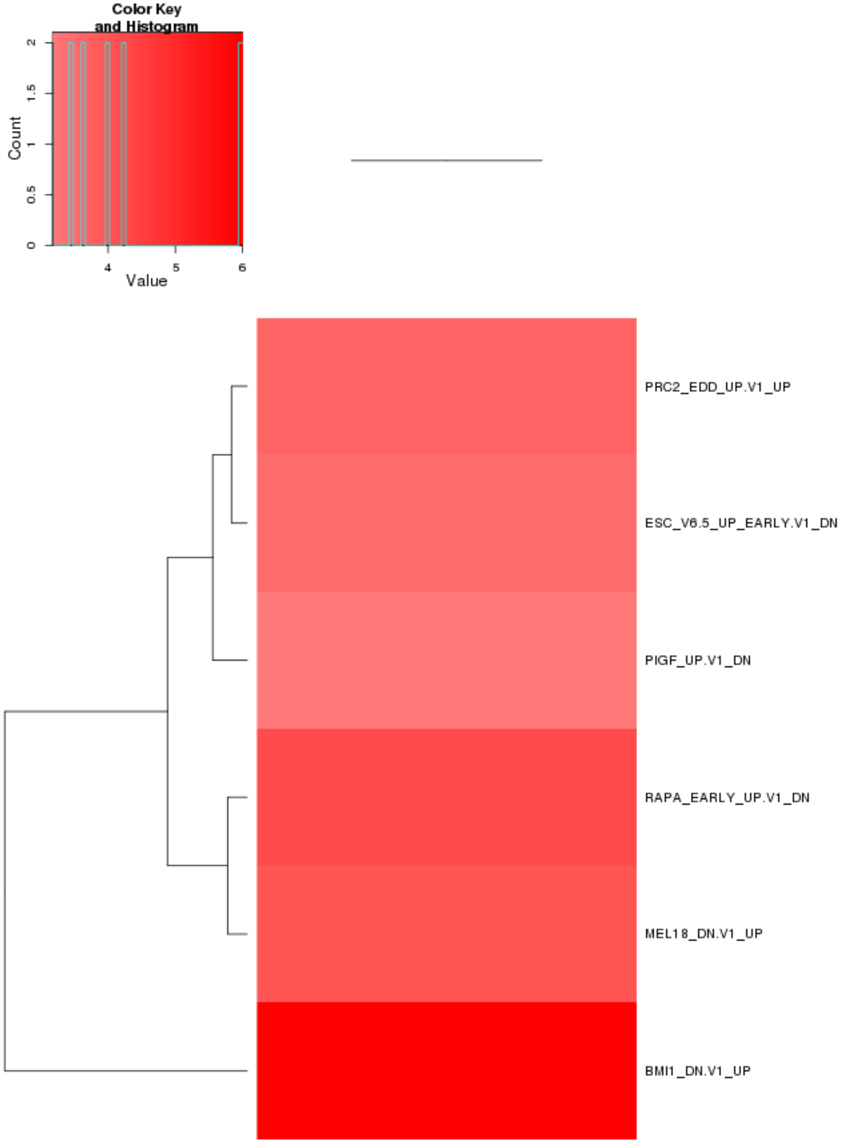
```
## Error: no locations are finite
```



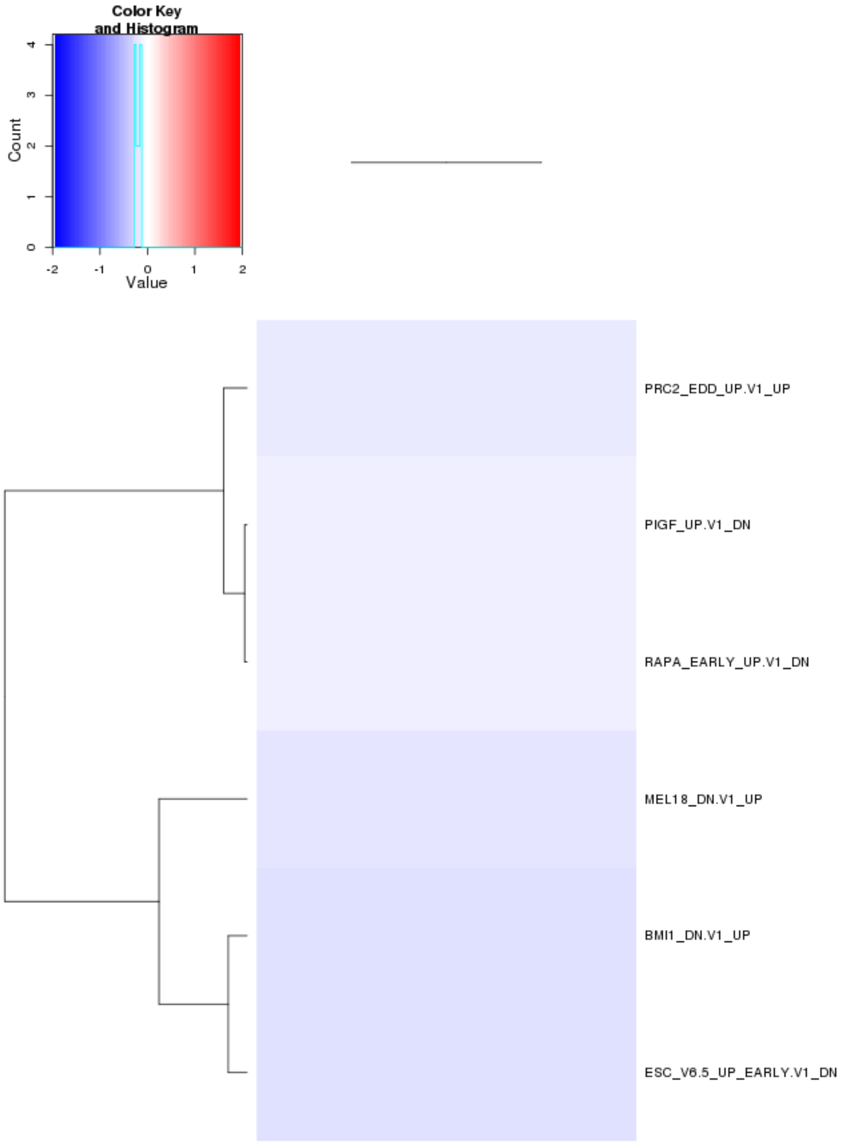
Interneuron zscore:



Oncogene enrichment:

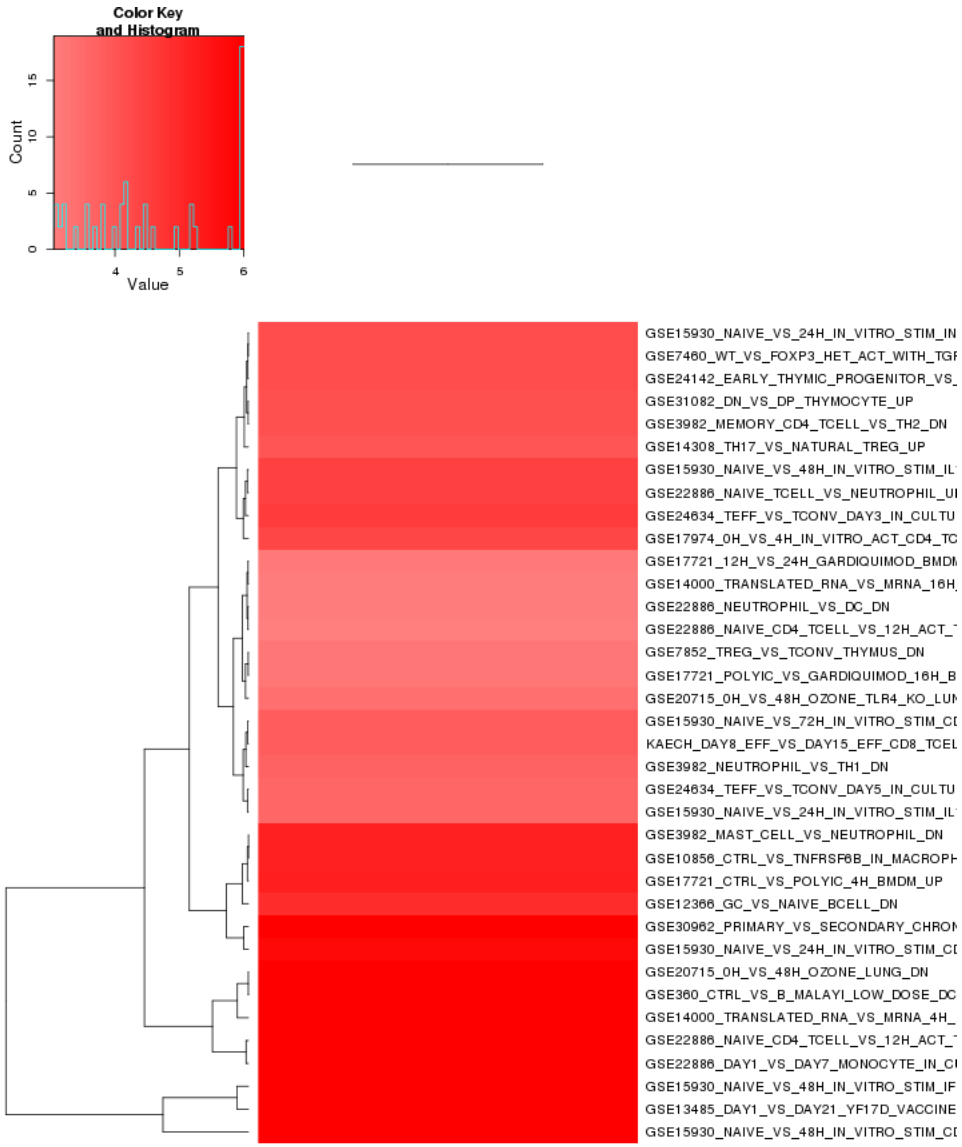


Oncogene zscore:



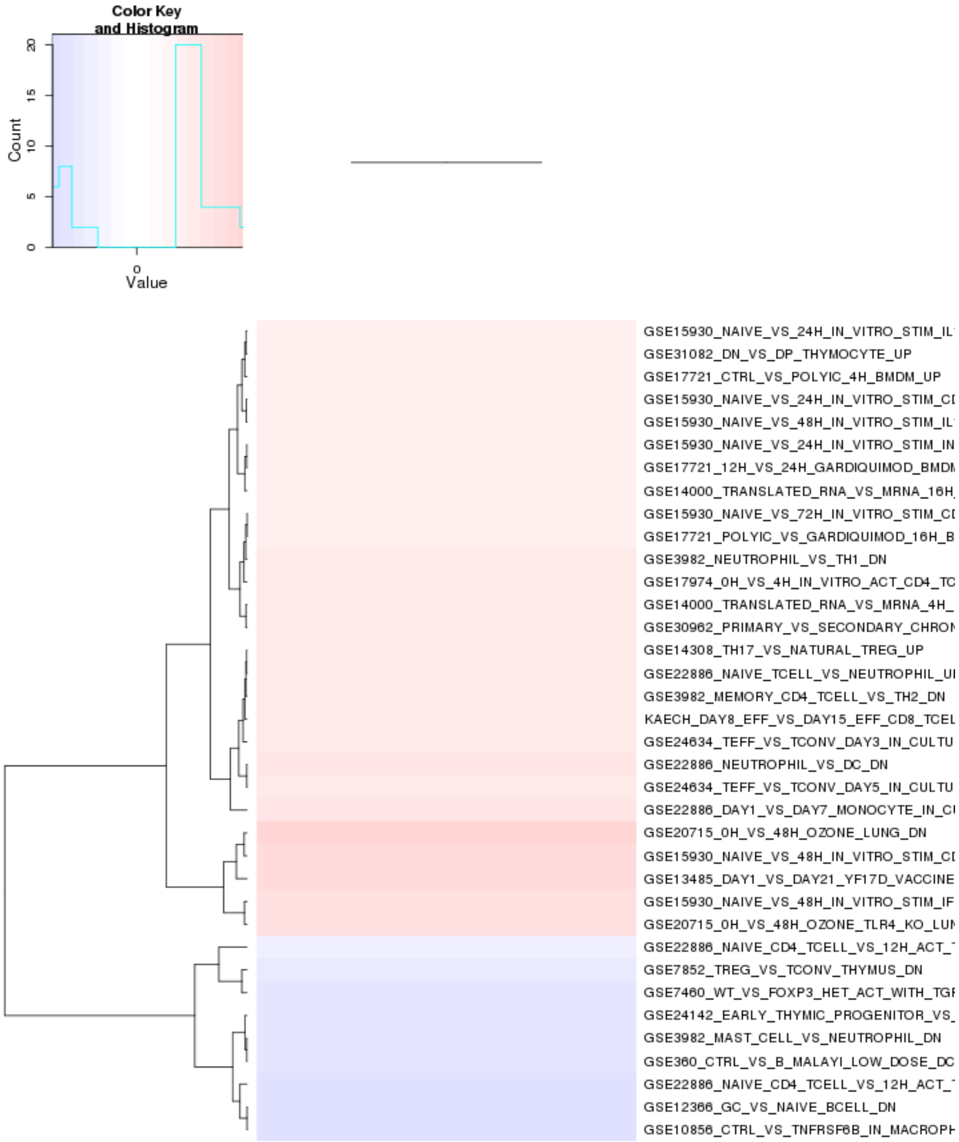
Immuno enrichment:

```
## Error: subscript out of bounds
```

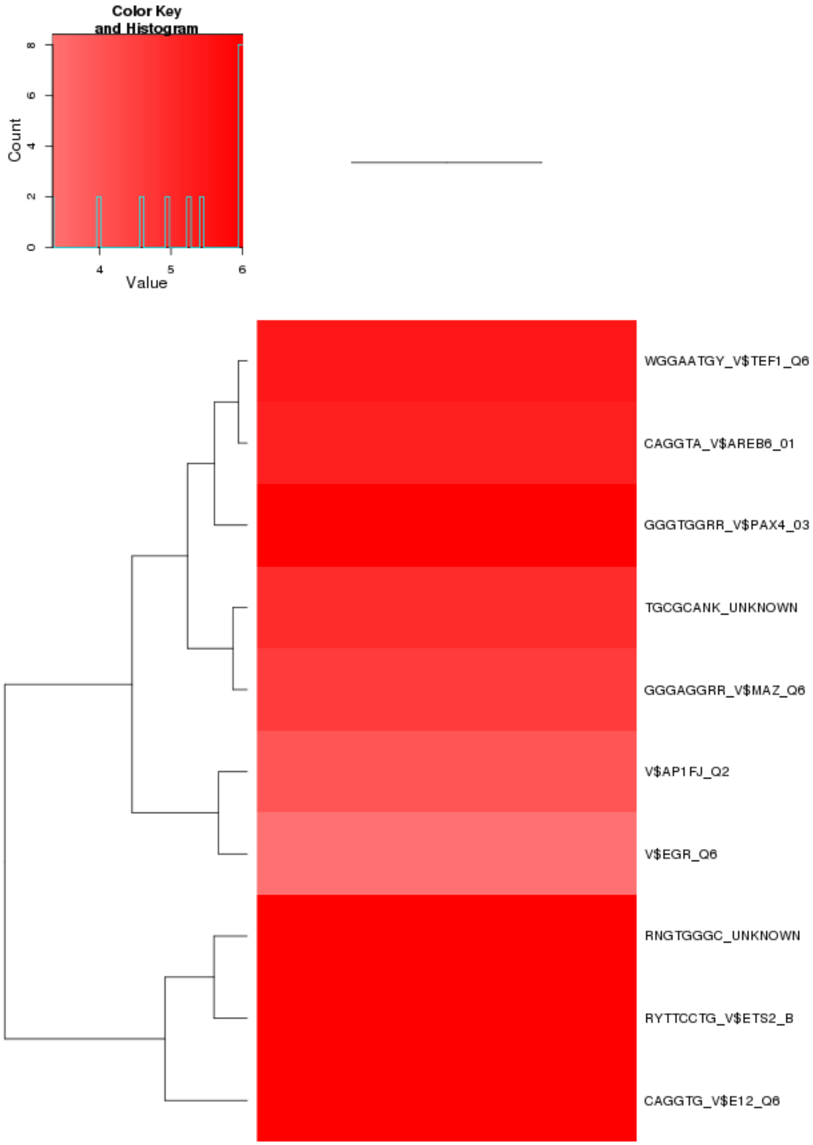


Immuno zscore:

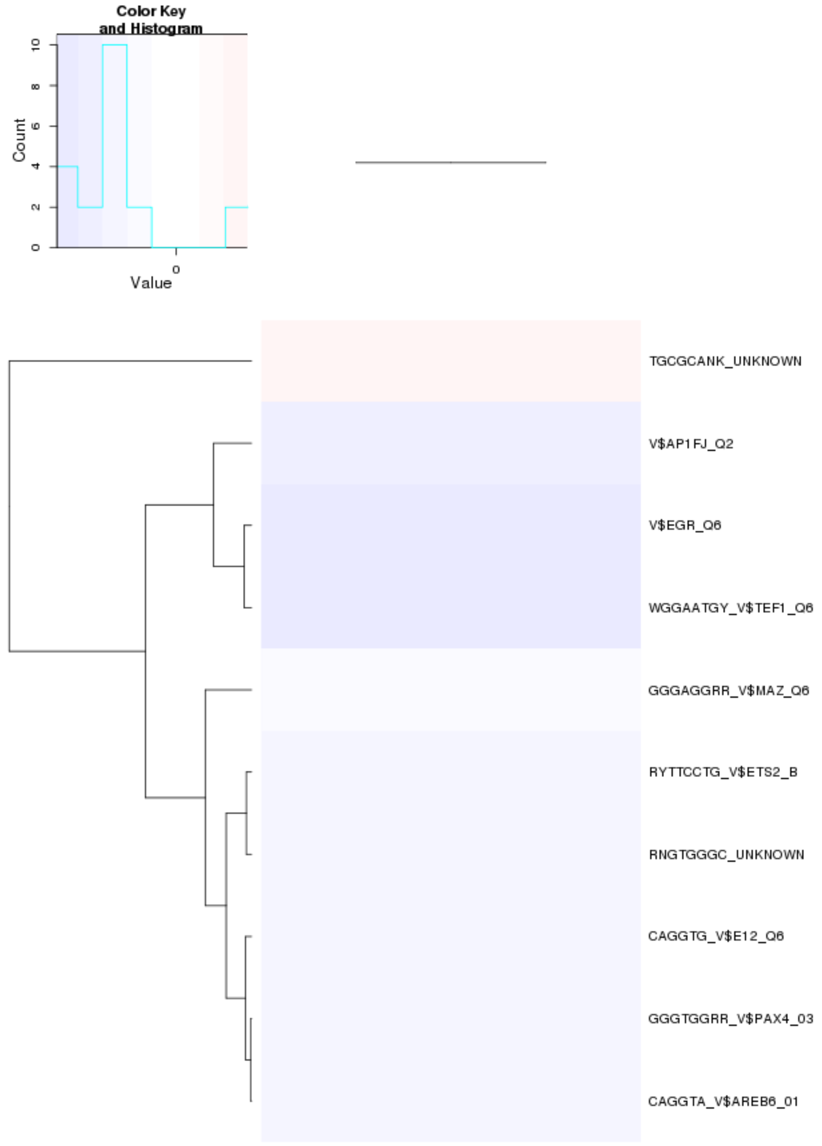
```
## Error: subscript out of bounds
```



TF enrichment:


Color Key
and Histogram
Count
0
2
4
6
8
4
5
6
Value
WGGAATGY_V$TEF1_Q6
CAGGTA_V$AREB6_01
GGGTGGRR_V$PAX4_03
TGCGCANK_UNKNOWN
GGGAGGRR_V$MAZ_Q6
V$AP1FJ_Q2
V$EGR_Q6
RNGTGGGC_UNKNOWN
RYTTCCTG_V$ETS2_B
CAGGTG_V$E12_Q6

TF zscore:



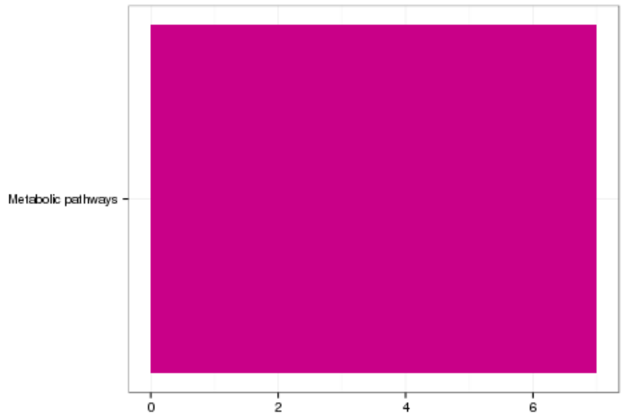
GO enrichment

Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

```
## Error: 'x' and 'units' must have length > 0
```

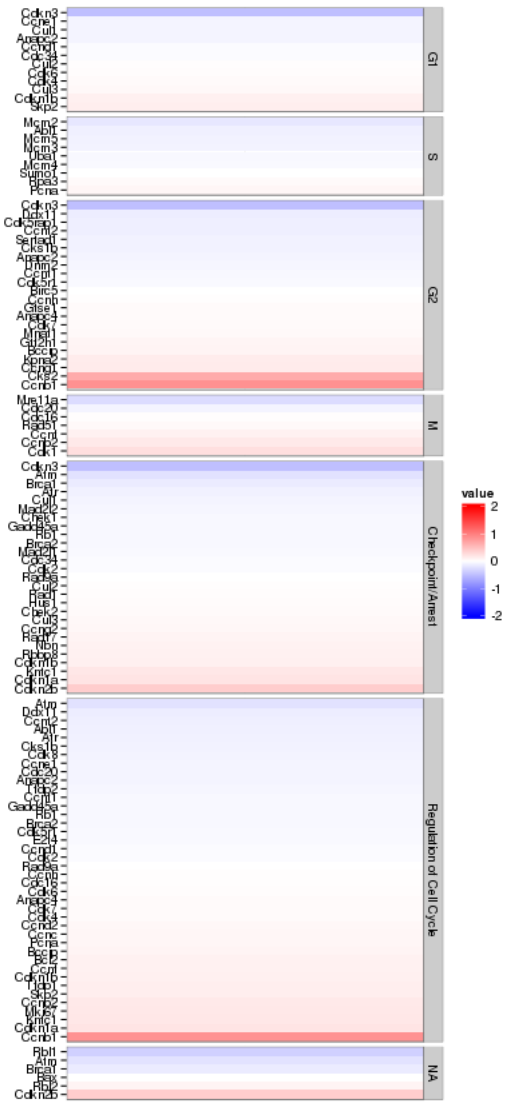
```
## Error: 'x' and 'units' must have length > 0
```

```
## Error: 'x' and 'units' must have length > 0
```

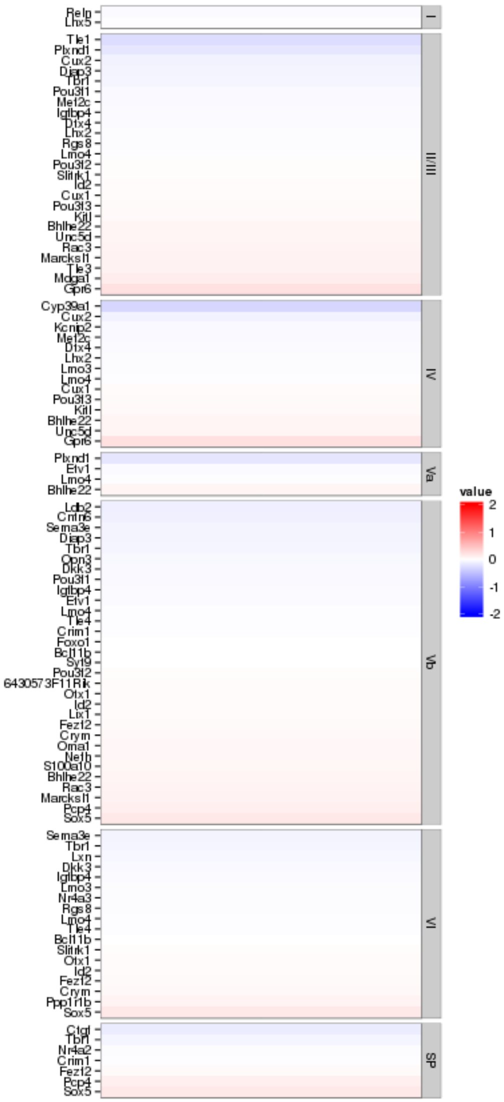


```
## Error: 'x' and 'units' must have length > 0
```

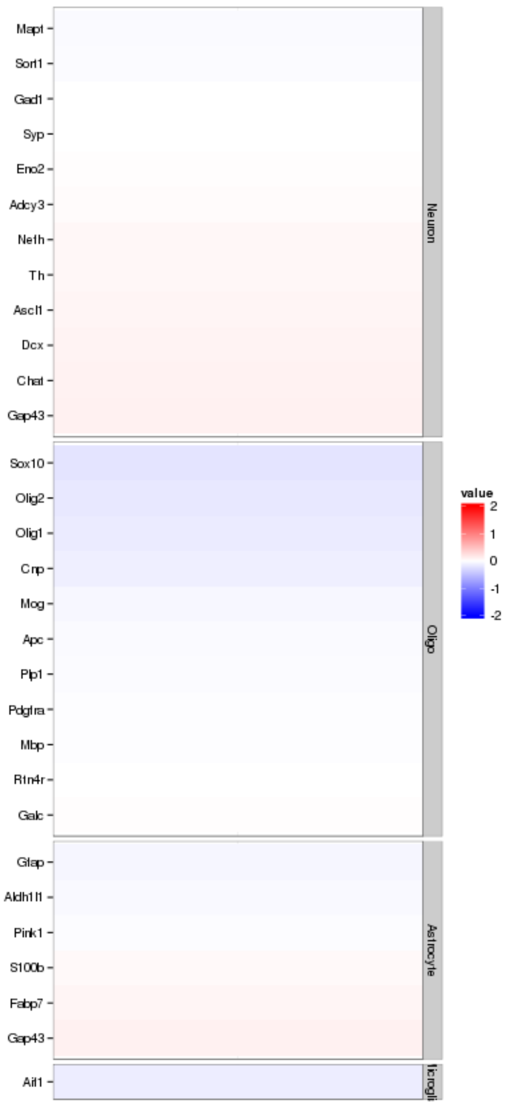
Enrichment or depletion for stage-specific cell cycle markers



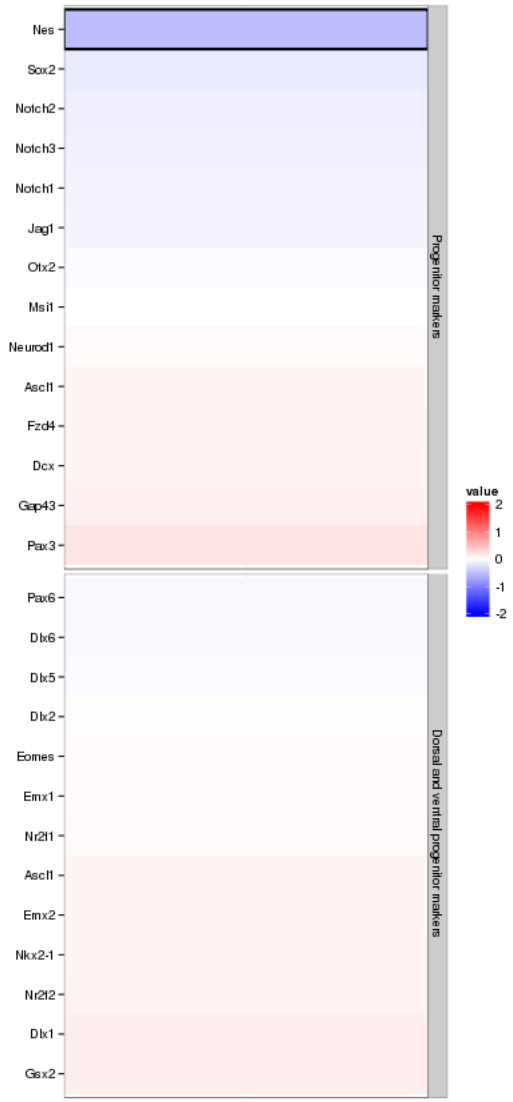
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



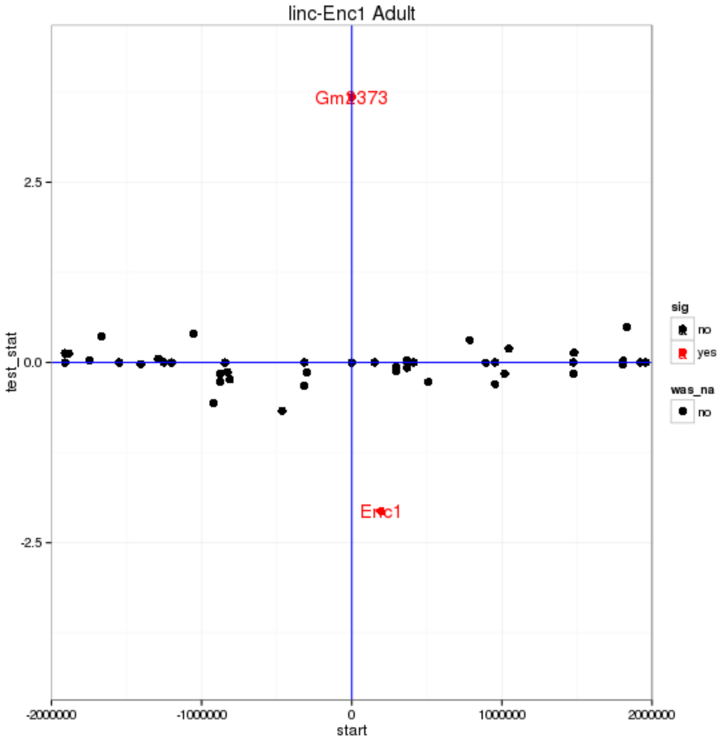
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 1 genes significantly regulated in a region this size is: 0.0947



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15	JR736
16	JR779
17	JR825

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	34110000.00	0.77	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	34110000.00	0.59	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	34110000.00	1.00	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	34110000.00	0.82	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	34110000.00	1.05	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	34110000.00	1.09	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	34110000.00	0.82	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	34110000.00	1.17	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	34110000.00	1.03	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	34110000.00	1.32	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	34110000.00	1.53	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	34110000.00	1.03	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	34110000.00	0.99	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	34110000.00	1.23	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR736/abundances.cxb	linc_Enc1	0	linc_Enc1_0	30101500.00	34110000.00	0.88	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR779/abundances.cxb	linc_Enc1	1	linc_Enc1_1	38936900.00	34110000.00	1.14	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR825/abundances.cxb	linc_Enc1	2	linc_Enc1_2	33174000.00	34110000.00	0.96	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils
## [8] datasets  base
##
## other attached packages:
##  [1] plyr_1.8.1
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0        biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17          cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0       digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5        formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3       graph_1.40.1
## [16] graphite_1.8.1        gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1          KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2          lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33           Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1   proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2           RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3      scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2          survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2           XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,linc-Enc1 -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/linc-Enc1_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainMap
## 2
## 3
## 4
## 5
```

linc-Enc1 KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for linc-Enc1.

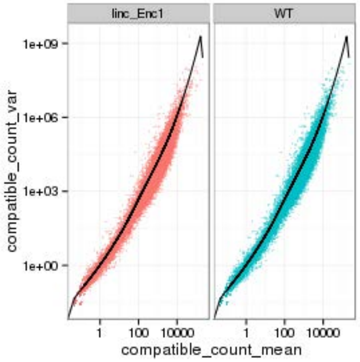
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

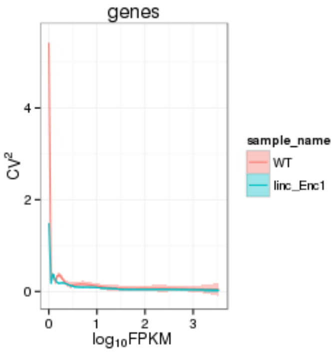
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



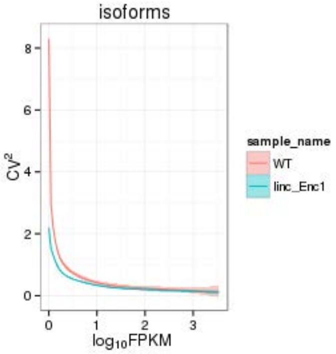
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

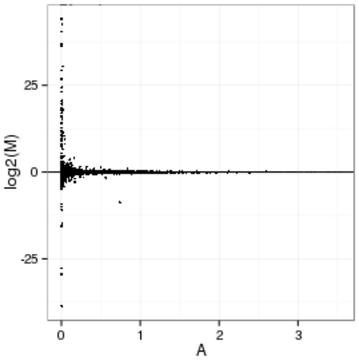
Genes:



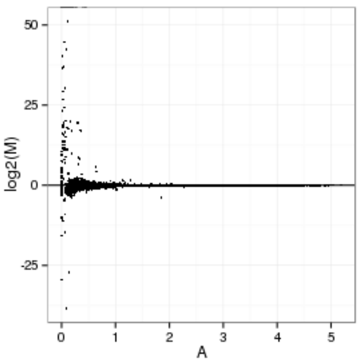
Isoforms:



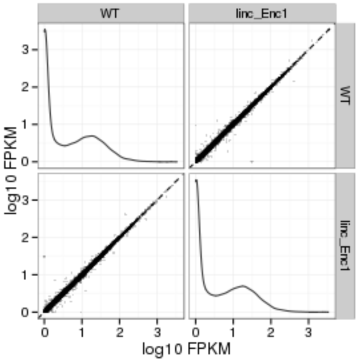
MvA plot



MvA plot counts



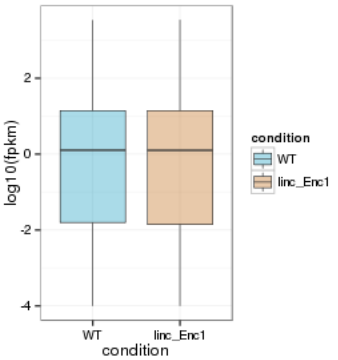
Scatterplot matrix



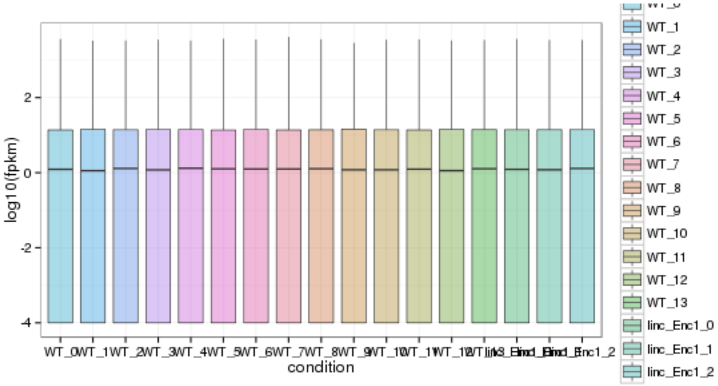
Distributions

Boxplots

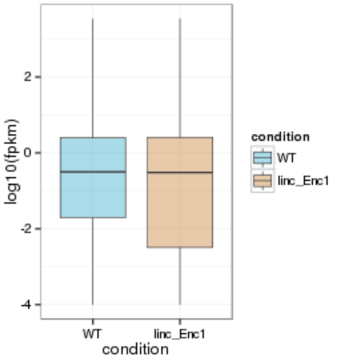
Boxplot (genes)



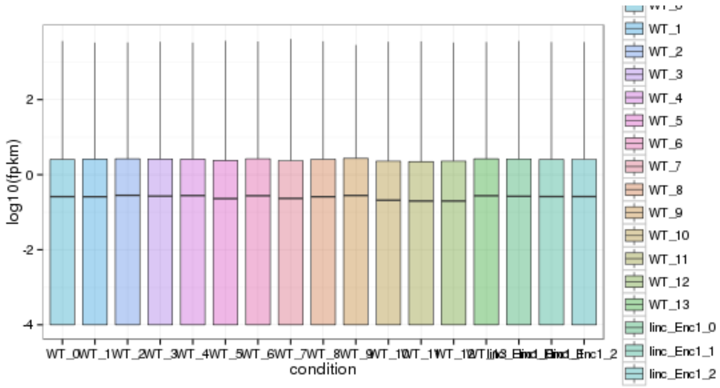
Boxplot (genes, replicates)



Boxplot (isoforms)

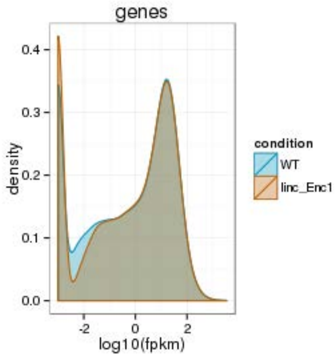


Boxplot (isoforms, replicates)

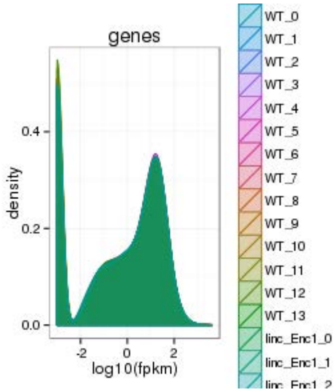


Density

Density (genes)

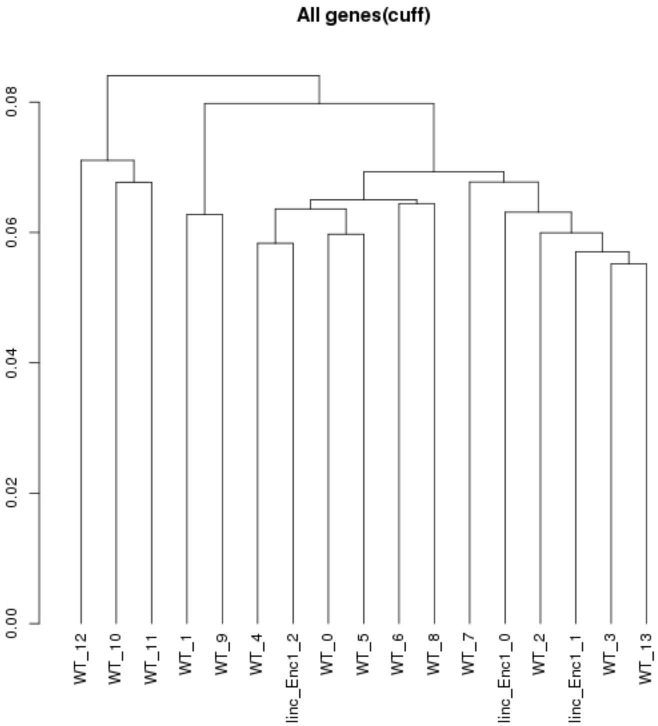


Density (genes, replicates)



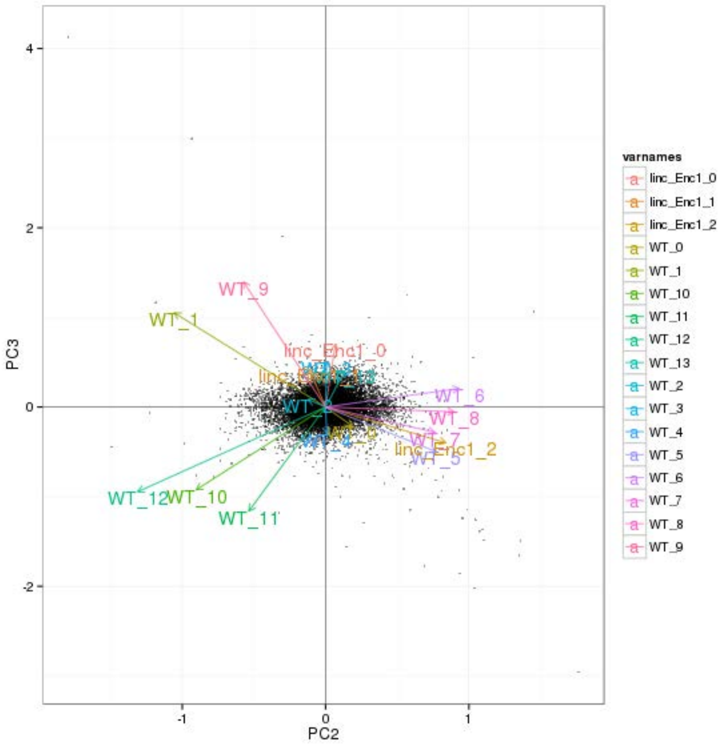
Clustering

Replicate Clusters

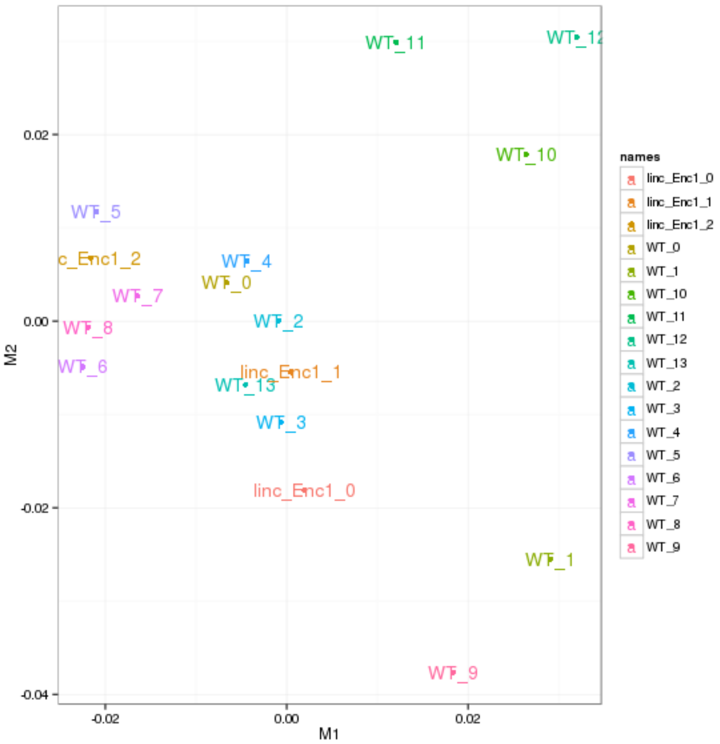


```
## NULL
```

PCA (genes)

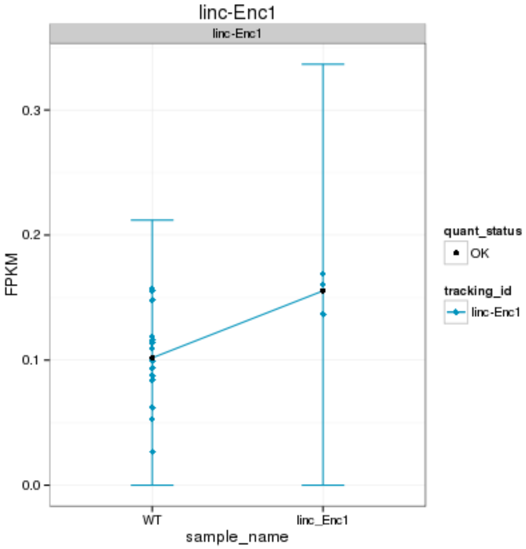

4
2
0
-2
-1
0
1
PC3
PC2
WT_9
WT_1
linc_Enc1_0
WT_6
WT_8
WT_7
linc_Enc1_2
WT_5
WT_12
WT_10
WT_11
varnames
linc_Enc1_0
linc_Enc1_1
linc_Enc1_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

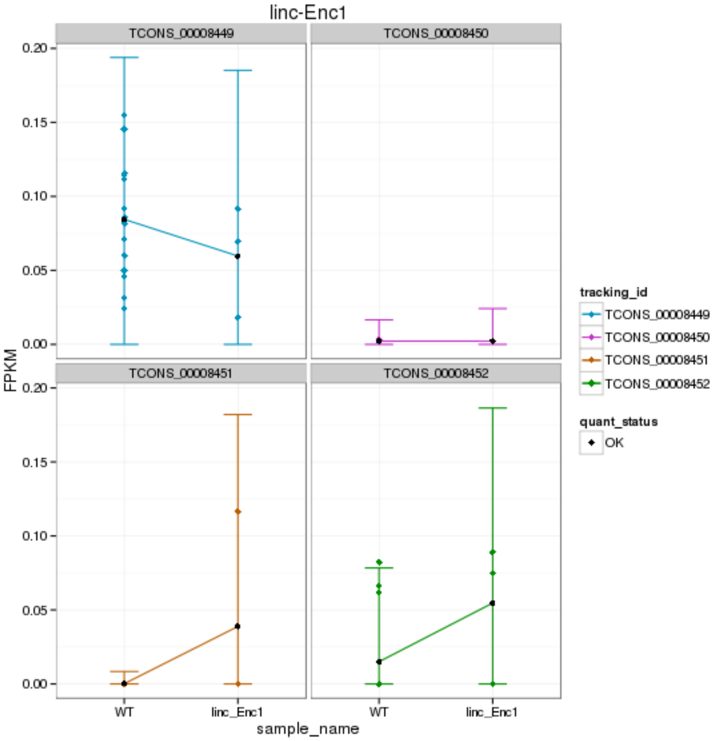


KO assessment

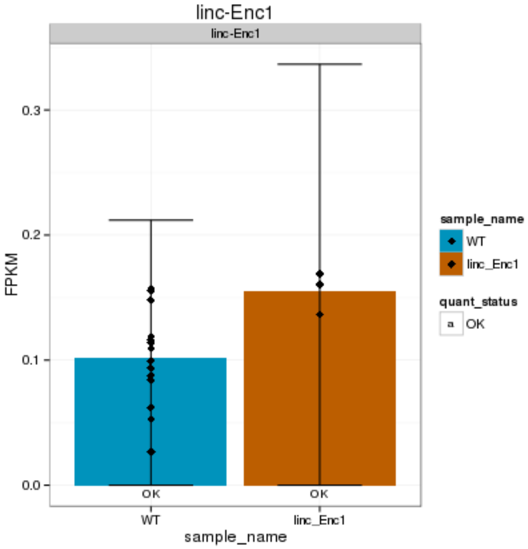
Endogenous lncRNA expression



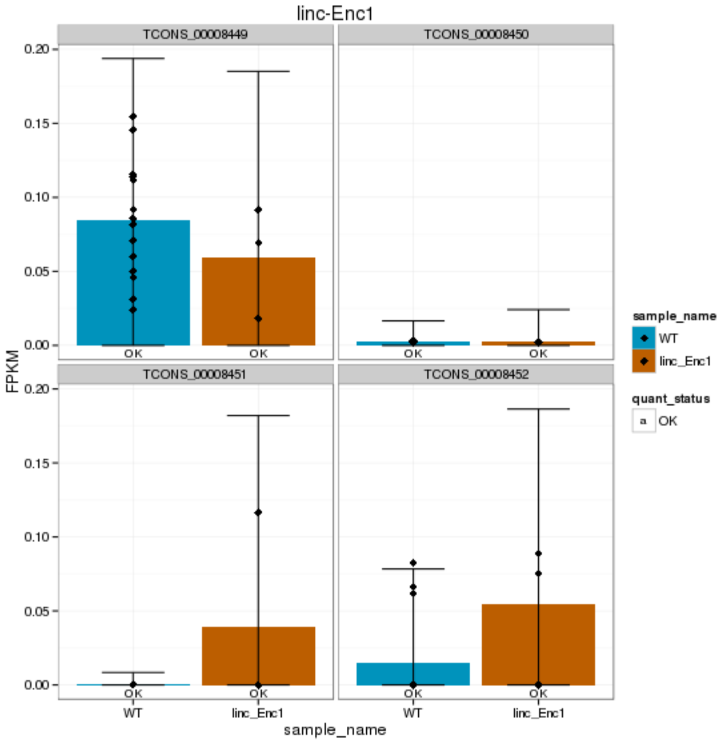
Endogenous expression of linc-Enc1 isoforms:



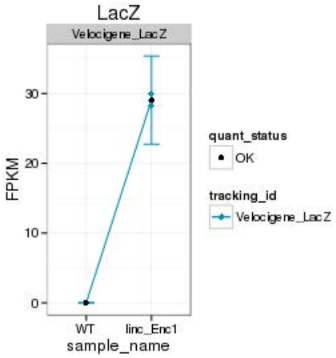
Barplot of gene expression:

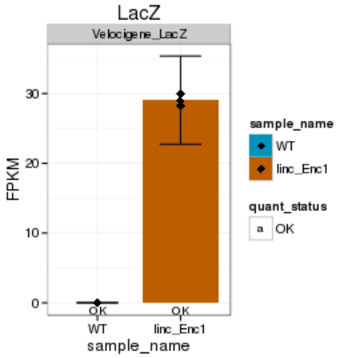


Barplot of isoform expression:



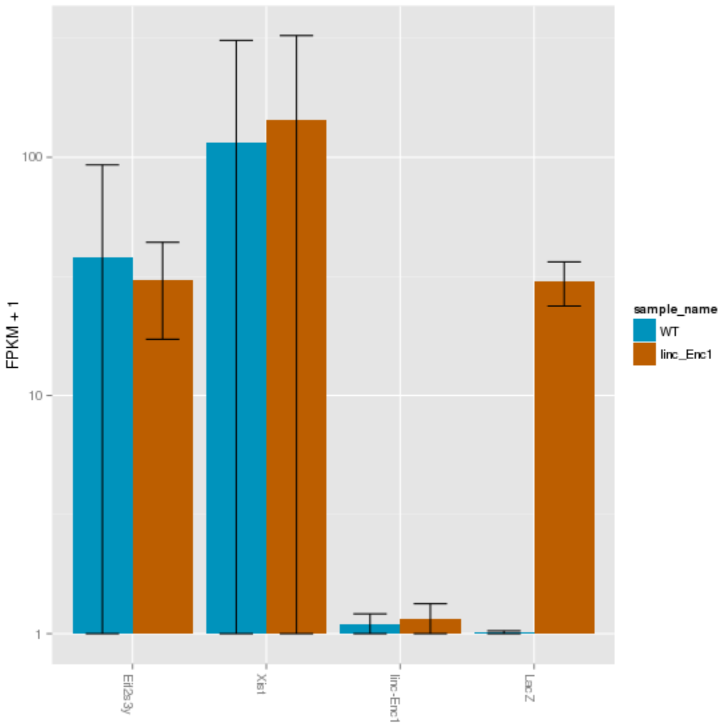
LacZ expression



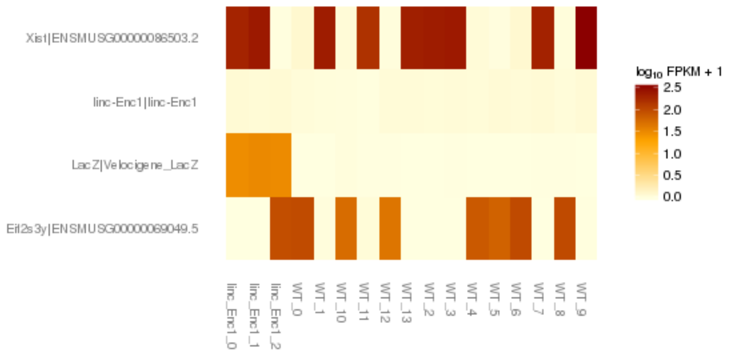


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

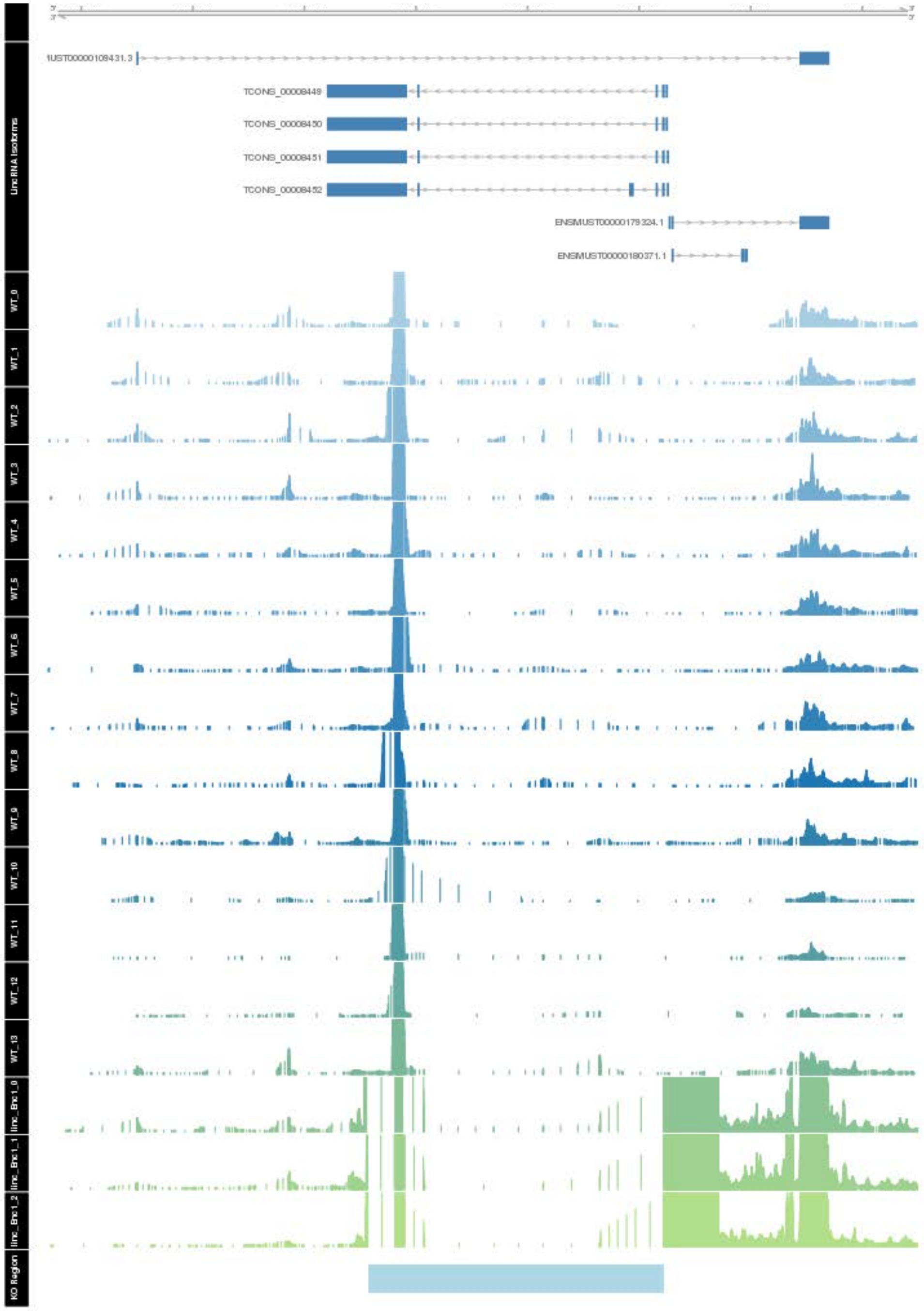
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization



Linc RNA Isoforms
1UST00000108431.3
TCONS_00008449
TCONS_00008450
TCONS_00008451
TCONS_00008452
ENSMUST00000179324.1
ENSMUST00000180371.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
linc_Bnc1_0
linc_Bnc1_1
linc_Bnc1_2
KO Region

Differential Analysis

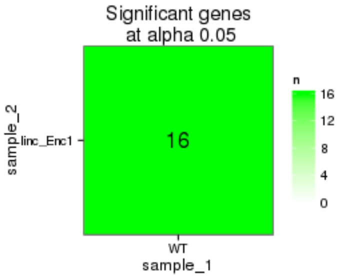
Differential Genes

There are 16 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Rec8
2	Nnt
3	Fn1
4	Bspry
5	Hddc3
6	Foxj1
7	Enc1
8	Gm9493
9	Fat4
10	Hbb-y
11	Hbb-bh1
12	Hba-x
13	Alox5ap
14	Gstm6
15	Fat1
16	Gm2373

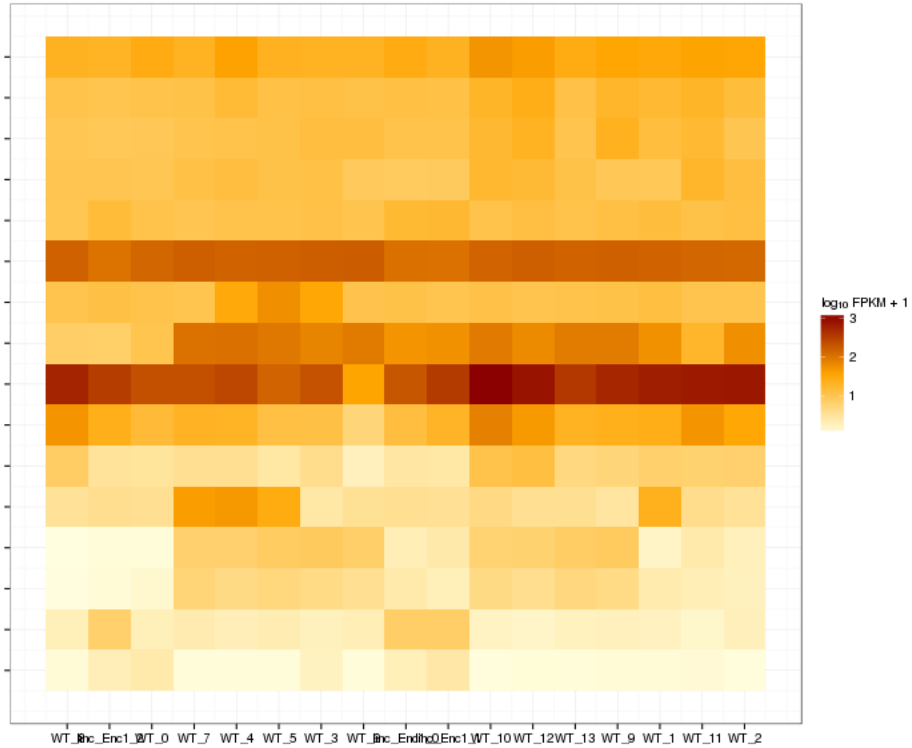
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

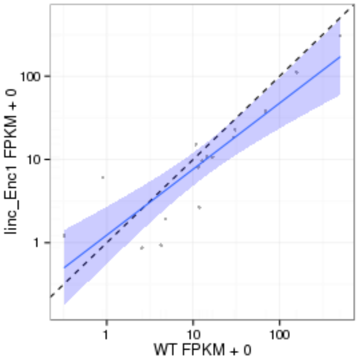


Significant genes with expression >50fpkm (any condition):(turned off)

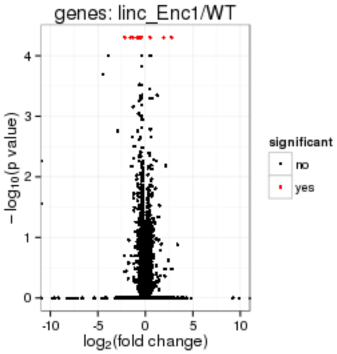
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

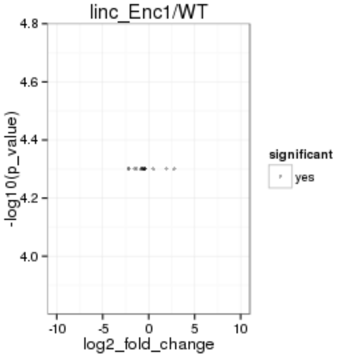
Scatter plot of significant genes only:



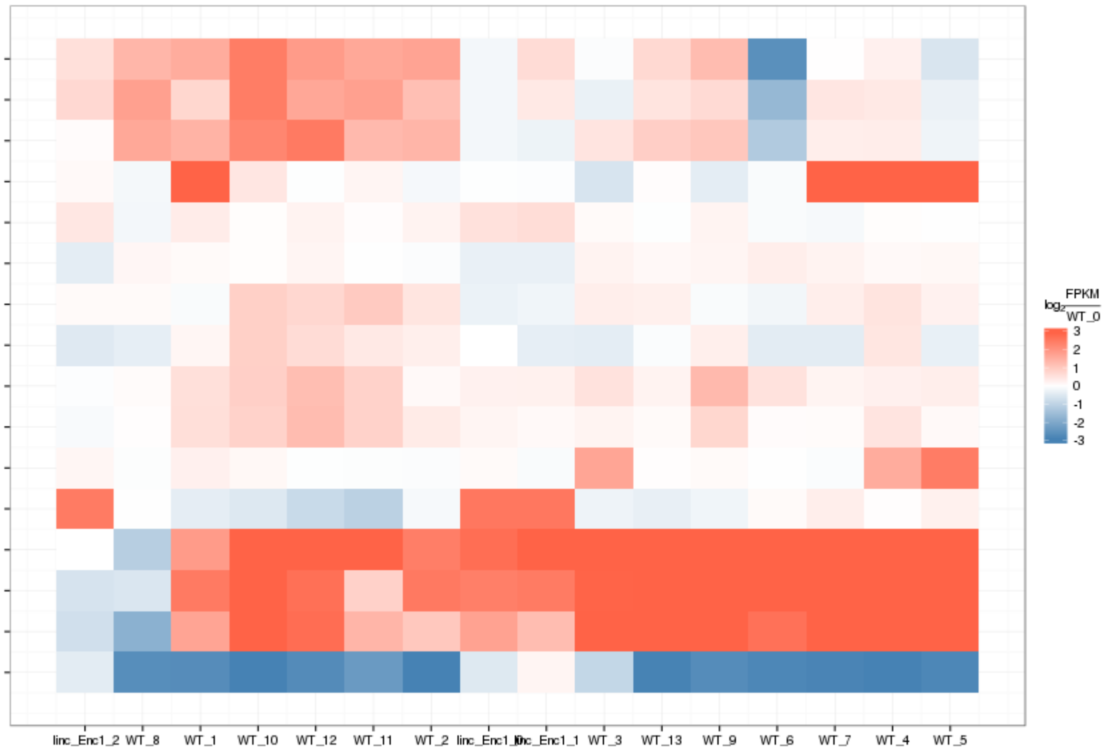
Volcano Plot



Volcano plot with significant genes only:



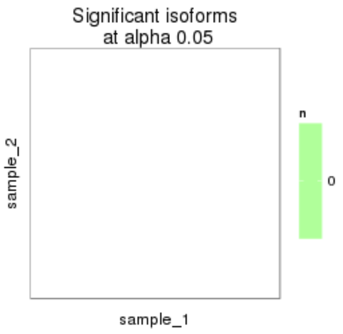
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

[1] “no sig isoforms”

Gene-level DE isoform heatmap

```
## [1] "no sig isoforms"
```

Isoform foldchange heatmap by isoform:

```
## [1] "no sig isoforms"
```

Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

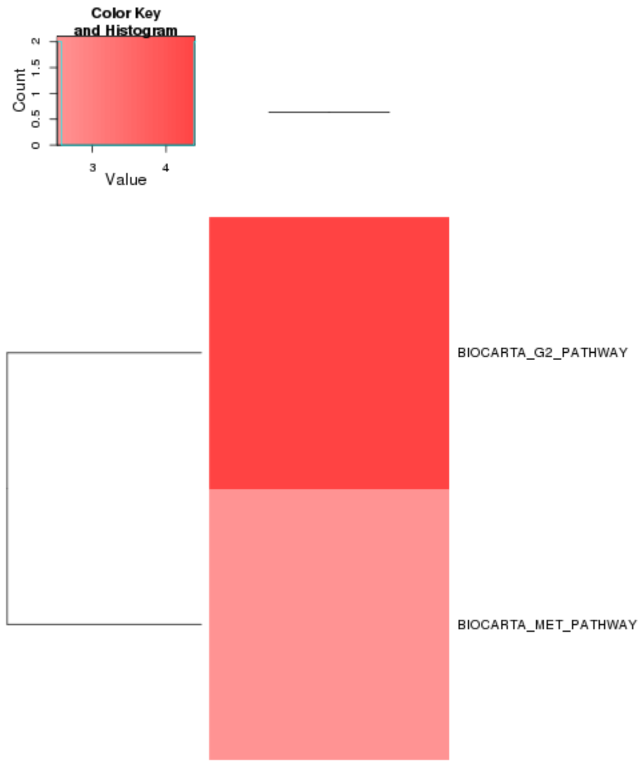
Gene/Pathway Analysis

GSEA

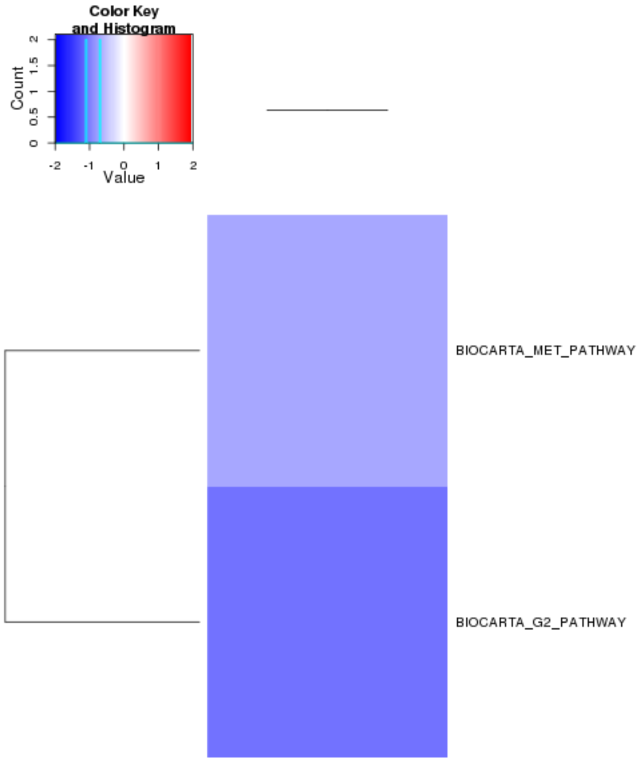
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

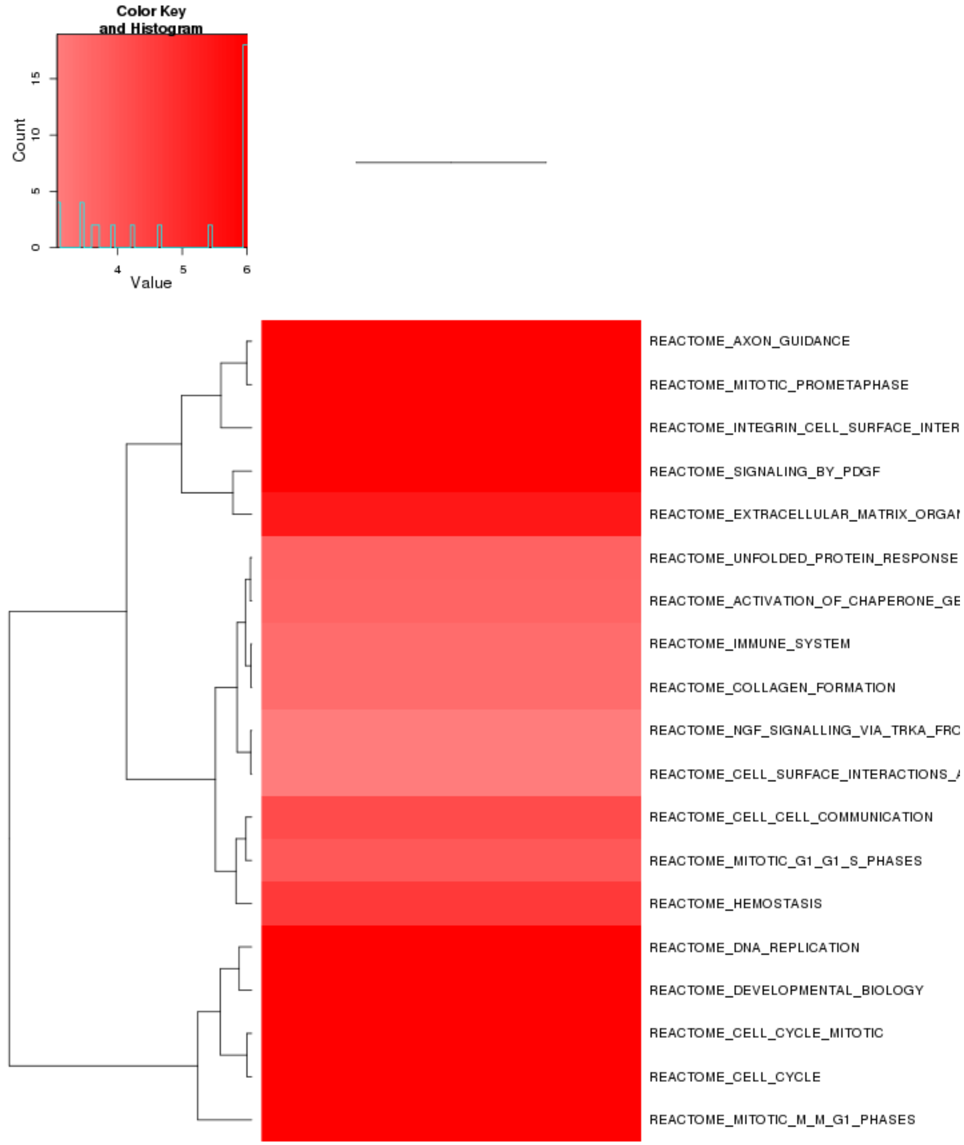
Biocarta enrichment:



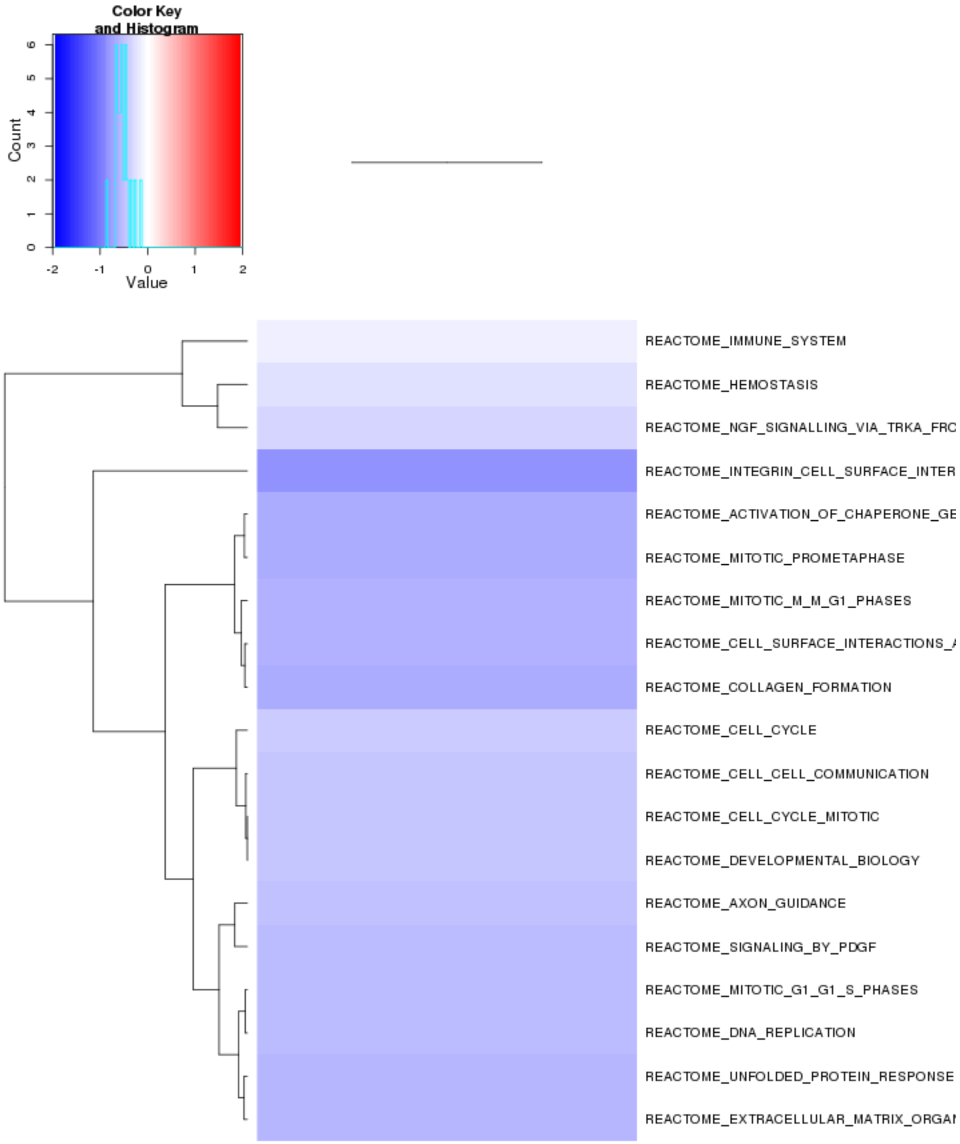
Biocarta zscore:



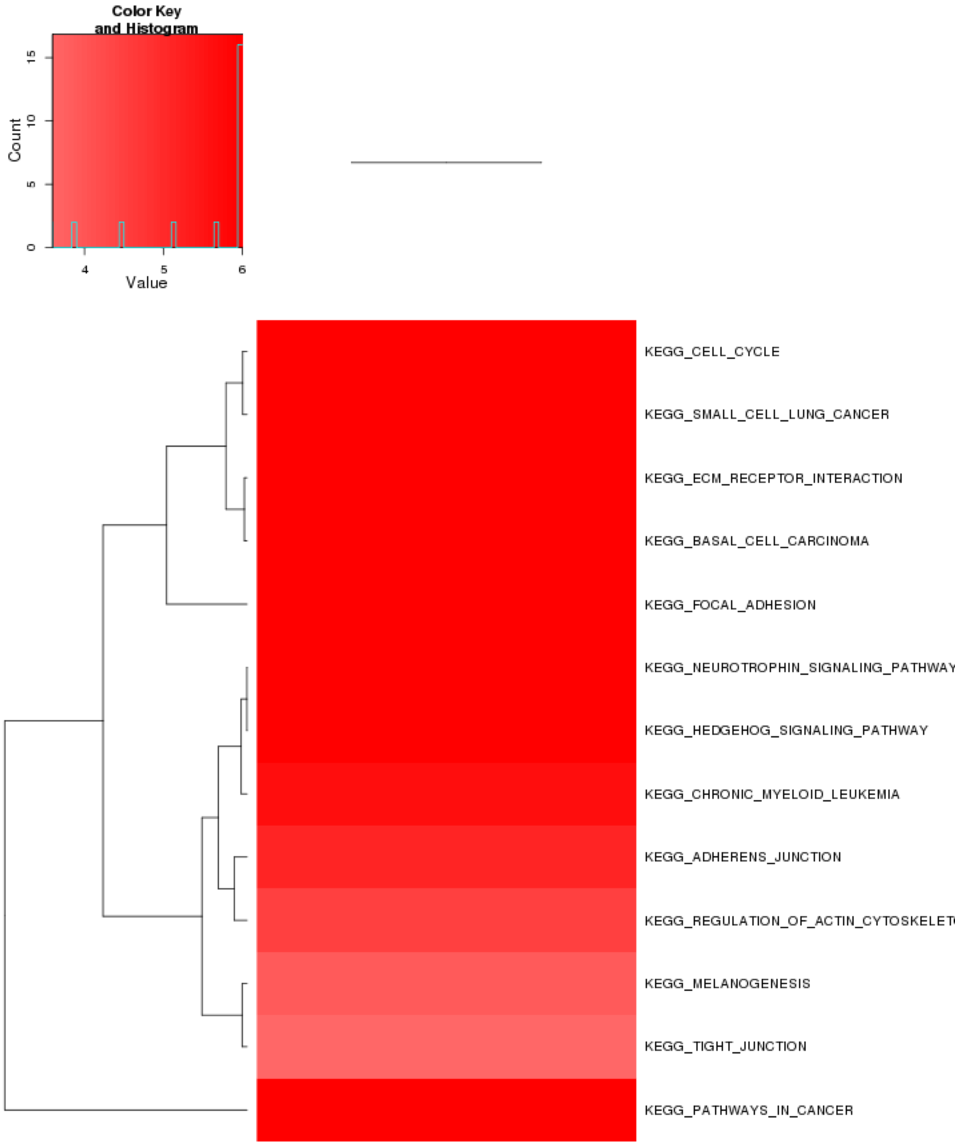
Reactome enrichment:



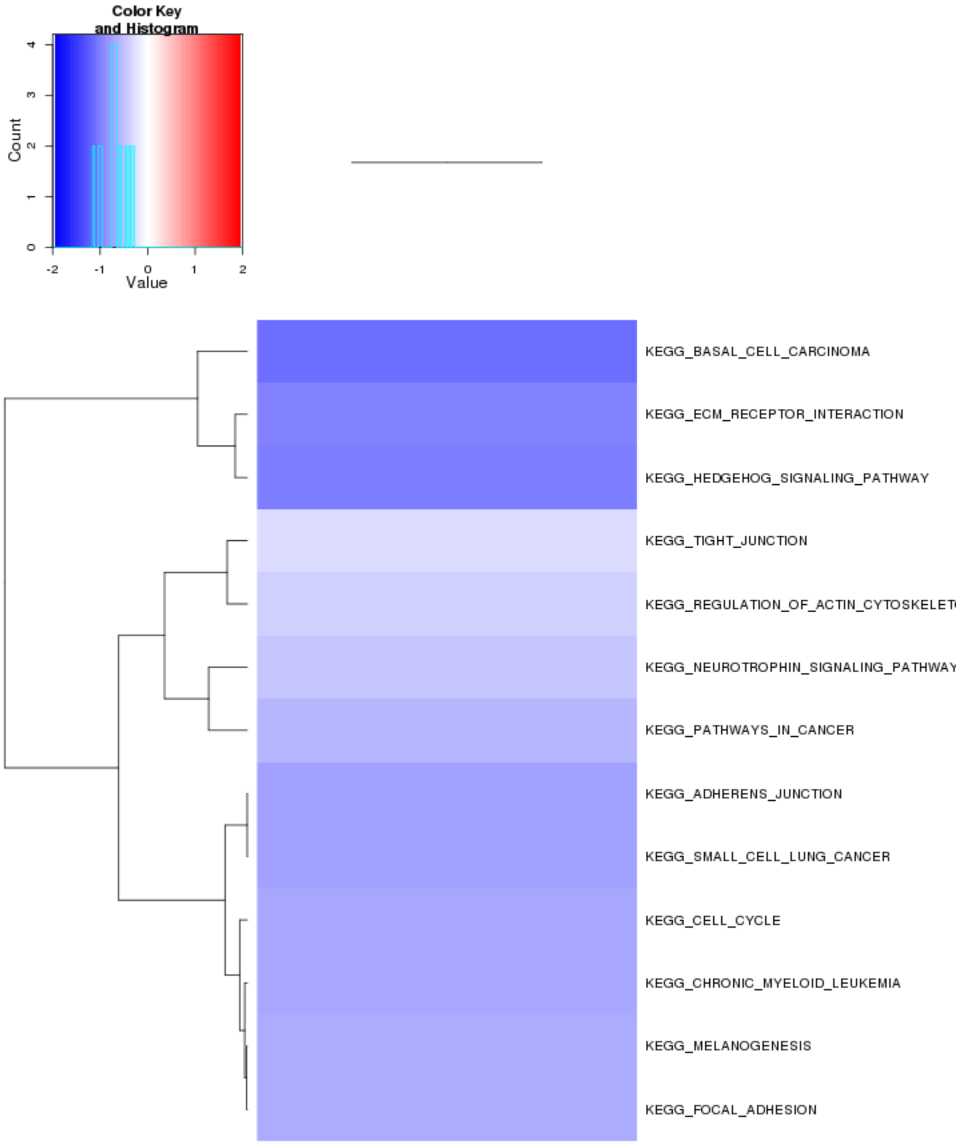
Reactome zscore:



Kegg enrichment:


Color Key
and Histogram
Count
0
5
10
15
4
5
6
Value
KEGG_CELL_CYCLE
KEGG_SMALL_CELL_LUNG_CANCER
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_BASAL_CELL_CARCINOMA
KEGG_FOCAL_ADHESION
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY
KEGG_HEDGEHOG_SIGNALING_PATHWAY
KEGG_CHRONIC_MYELOID_LEUKEMIA
KEGG_ADHERENS_JUNCTION
KEGG_REGULATION_OF_ACTIN_CYTOSKELET
KEGG_MELANOGENESIS
KEGG_TIGHT_JUNCTION
KEGG_PATHWAYS_IN_CANCER

Kegg zscore:



Interneuron enrichment:

```
## Error: argument is of length zero
```

Interneuron zscore:

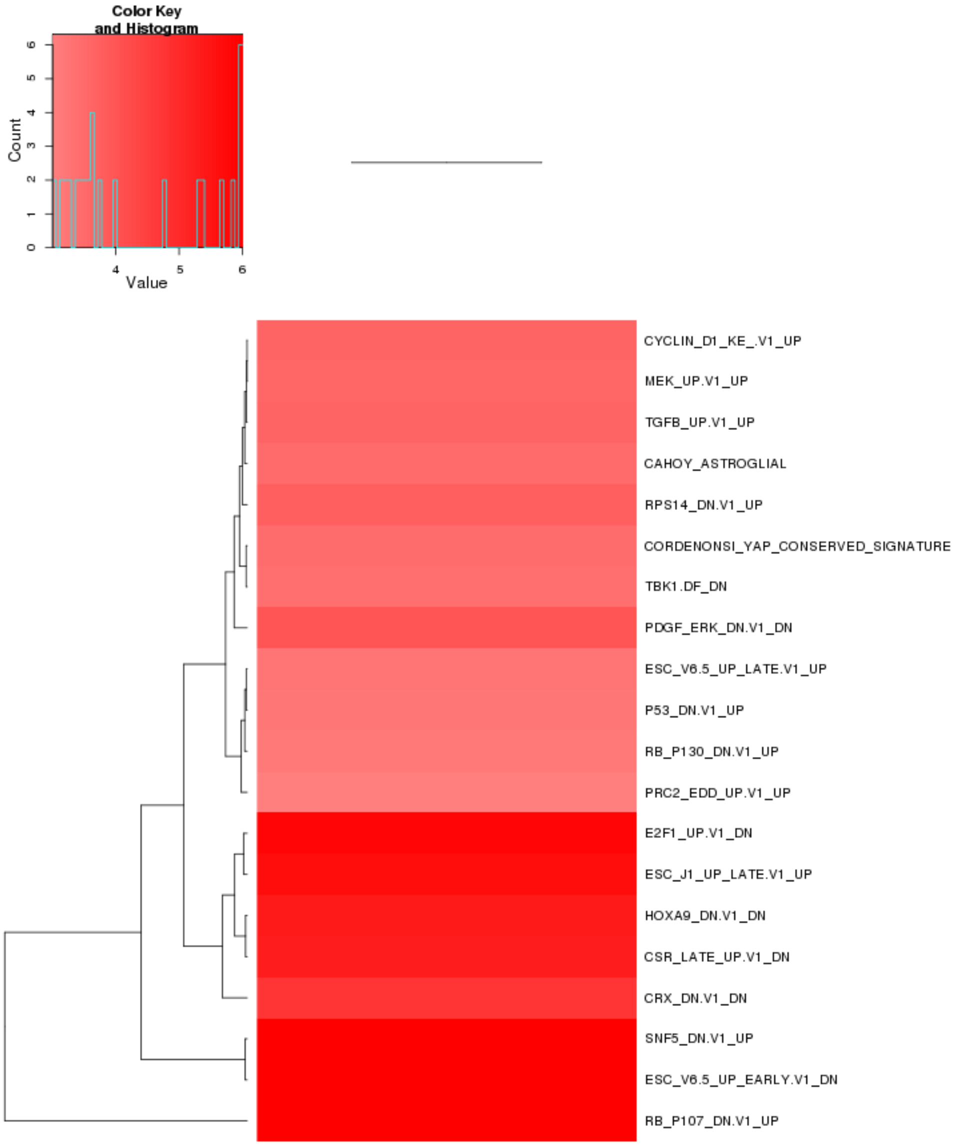
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

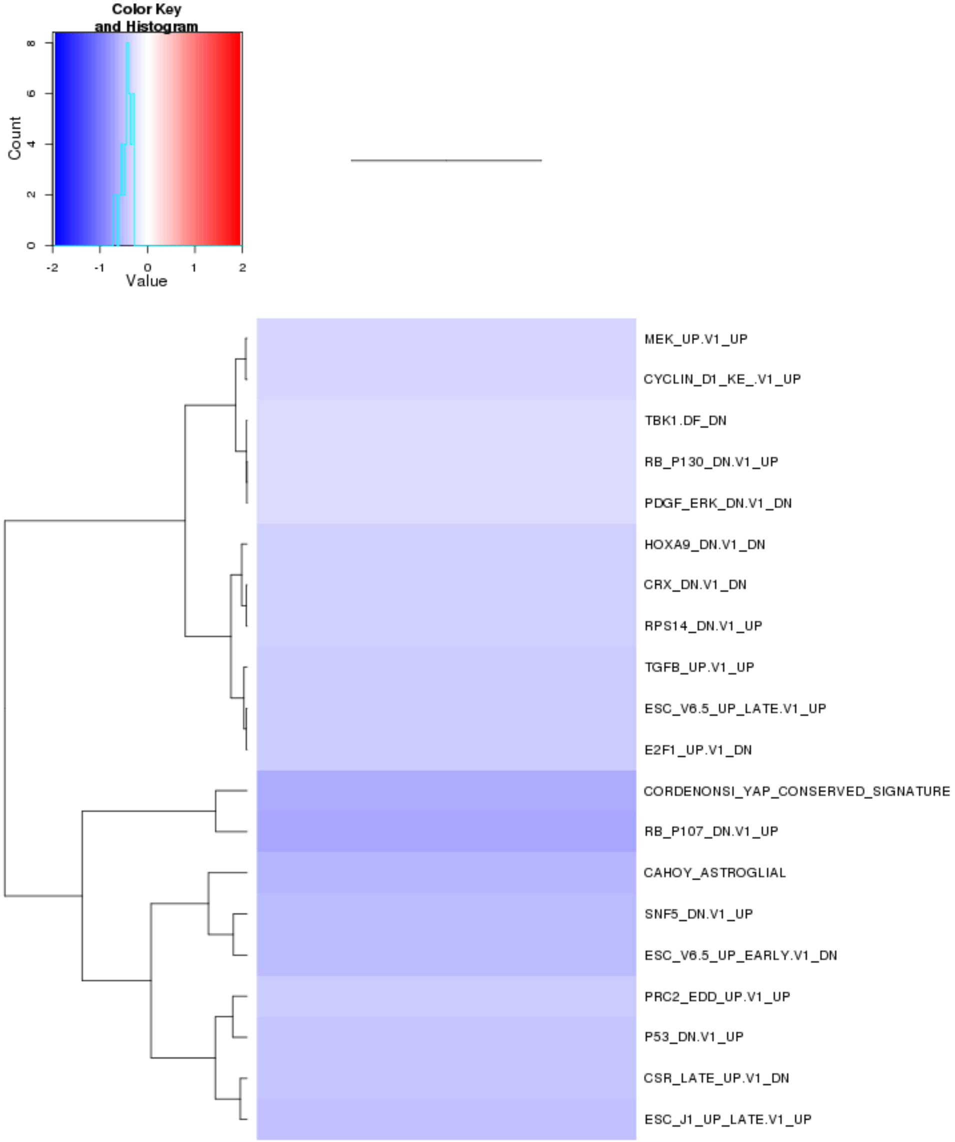
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

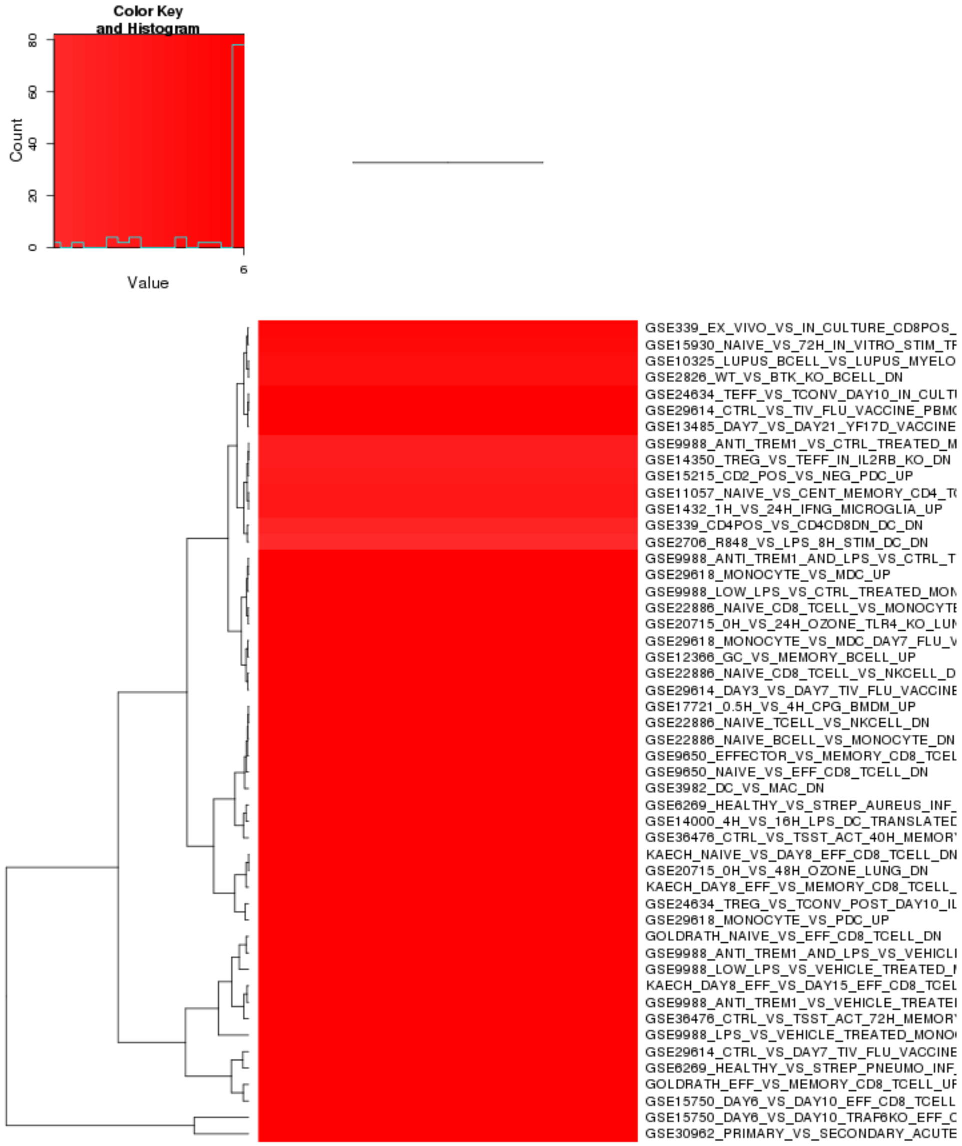
Oncogene enrichment:



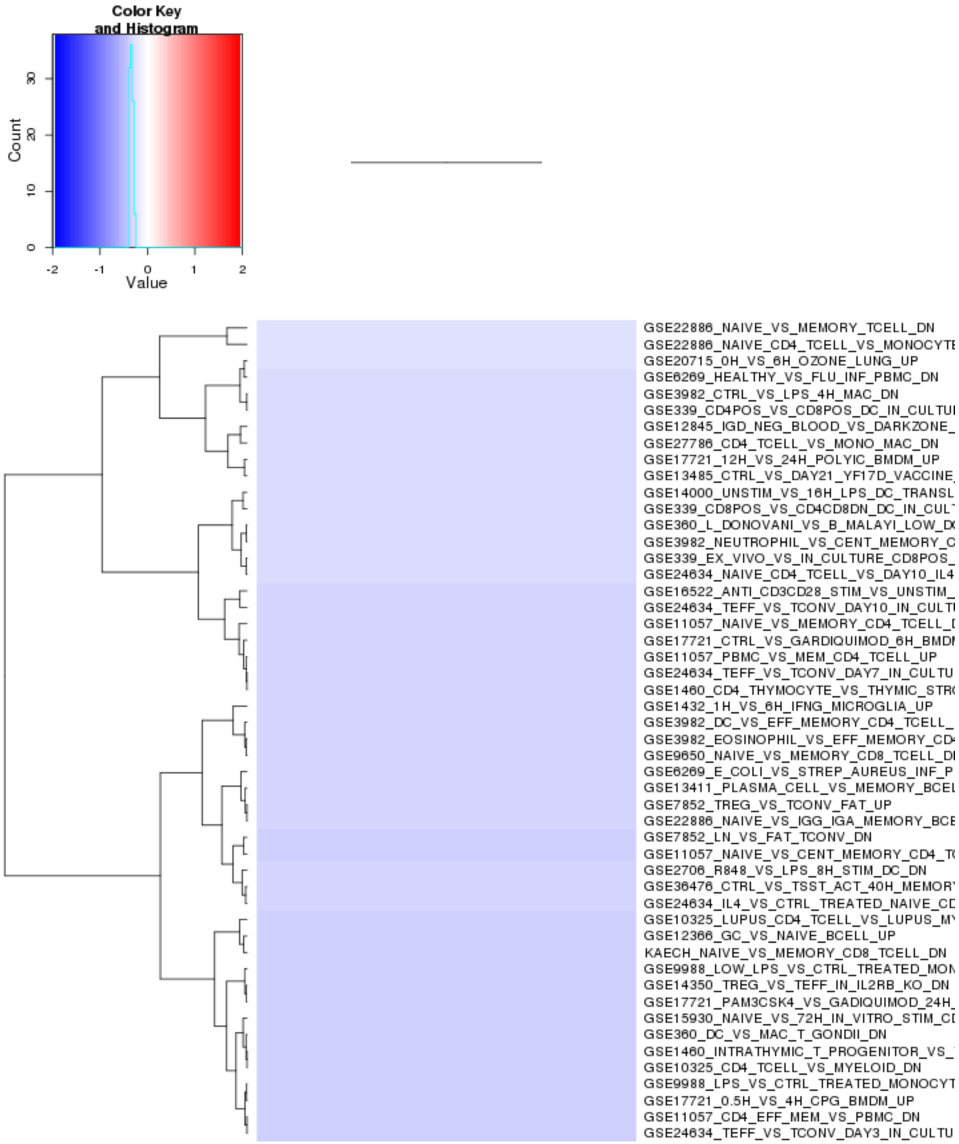
Oncogene zscore:



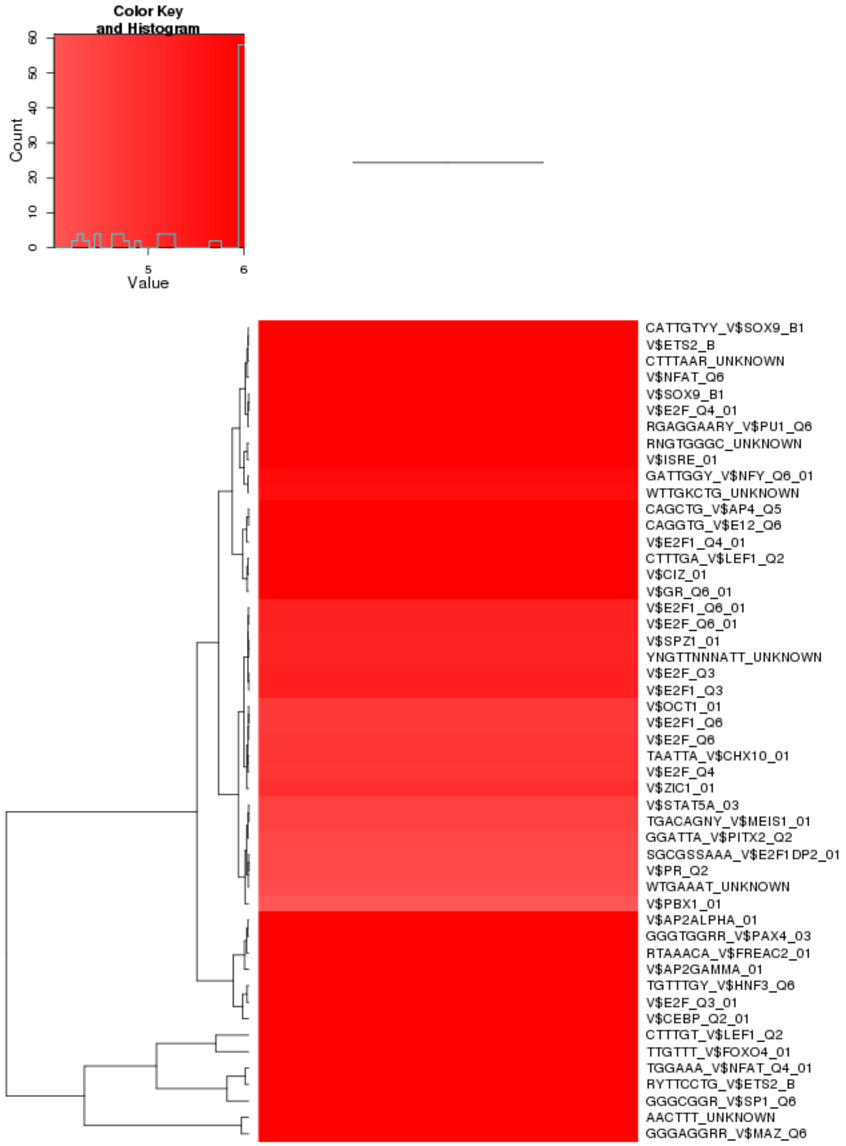
Immuno enrichment:



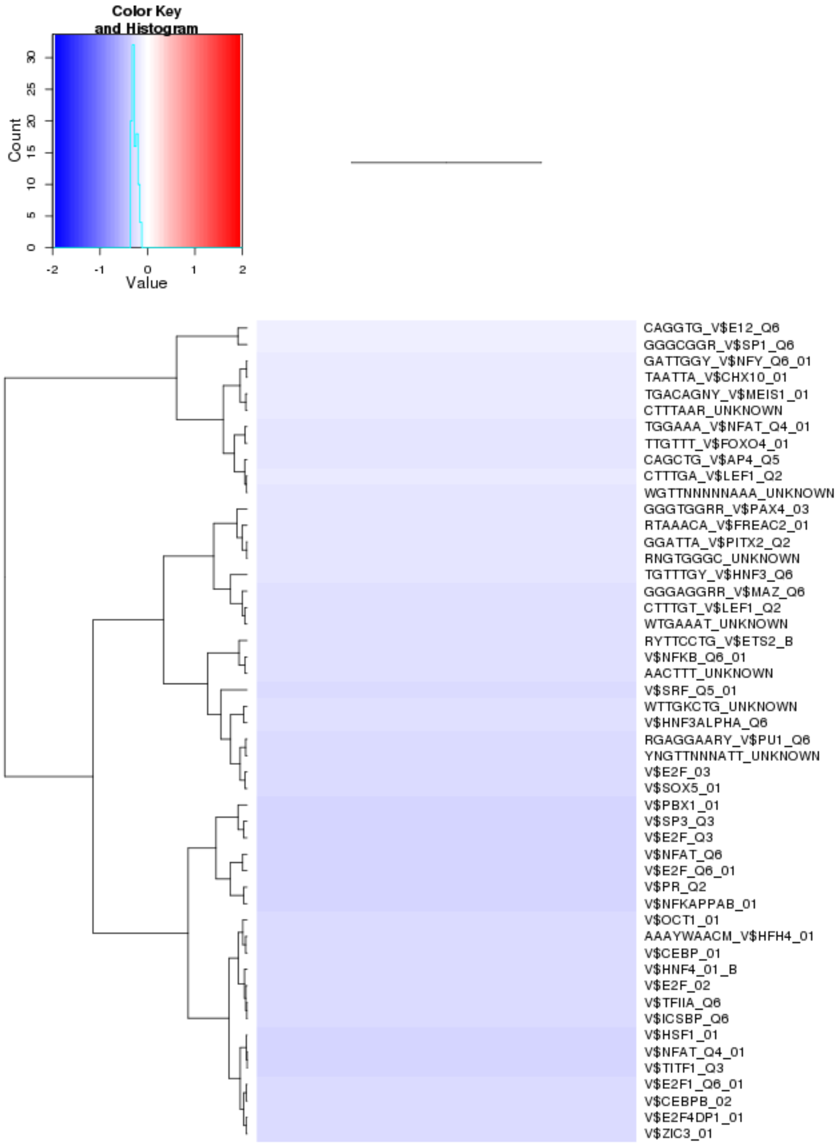
Immuno zscore:



TF enrichment:


Color Key
and Histogram
Count
0
10
20
30
40
50
60
5
6
Value
CATTGTYY_V$SOX9_B1
V$ETS2_B
CTTTAAR_UNKNOWN
V$NFAT_Q6
V$SOX9_B1
V$E2F_Q4_01
RGAGGAARY_V$PU1_Q6
RNGTGGGC_UNKNOWN
V$ISRE_01
GATTGGY_V$NFY_Q6_01
WTTGKCTG_UNKNOWN
CAGCTG_V$AP4_Q5
CAGGTG_V$E12_Q6
V$E2F1_Q4_01
CTTTGA_V$LEF1_Q2
V$CIZ_01
V$GR_Q6_01
V$E2F1_Q6_01
V$E2F_Q6_01
V$SPZ1_01
YNGTTNNNATT_UNKNOWN
V$E2F_Q3
V$E2F1_Q3
V$OCT1_01
V$E2F1_Q6
V$E2F_Q6
TAATTA_V$CHX10_01
V$E2F_Q4
V$ZIC1_01
V$STAT5A_03
TGACAGNY_V$MEIS1_01
GGATTA_V$PITX2_Q2
SGCGSSAAA_V$E2F1DP2_01
V$PR_Q2
WTGAAAT_UNKNOWN
V$PBX1_01
V$AP2ALPHA_01
GGGTGGRR_V$PAX4_03
RTAAACA_V$FREAC2_01
V$AP2GAMMA_01
TGTTTGY_V$HNF3_Q6
V$E2F_Q3_01
V$CEBP_Q2_01
CTTTGT_V$LEF1_Q2
TTGTTT_V$FOXO4_01
TGGAAA_V$NFAT_Q4_01
RYTTCCTG_V$ETS2_B
GGGCGGR_V$SP1_Q6
AACTTT_UNKNOWN
GGGAGGRR_V$MAZ_Q6

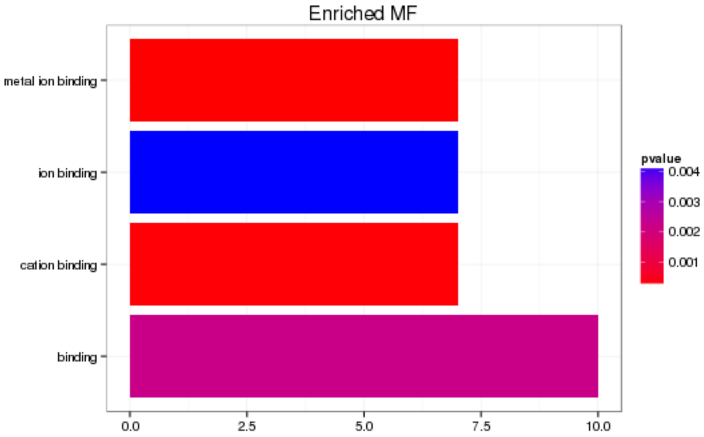
TF zscore:



GO enrichment

Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

```
## Error: 'x' and 'units' must have length > 0
```

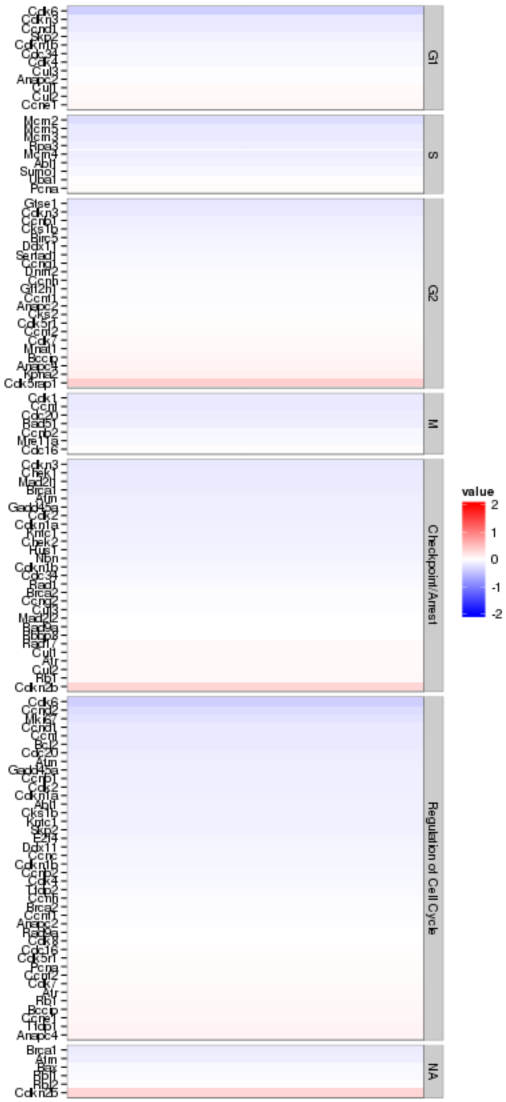


```
## Error: 'x' and 'units' must have length > 0
```

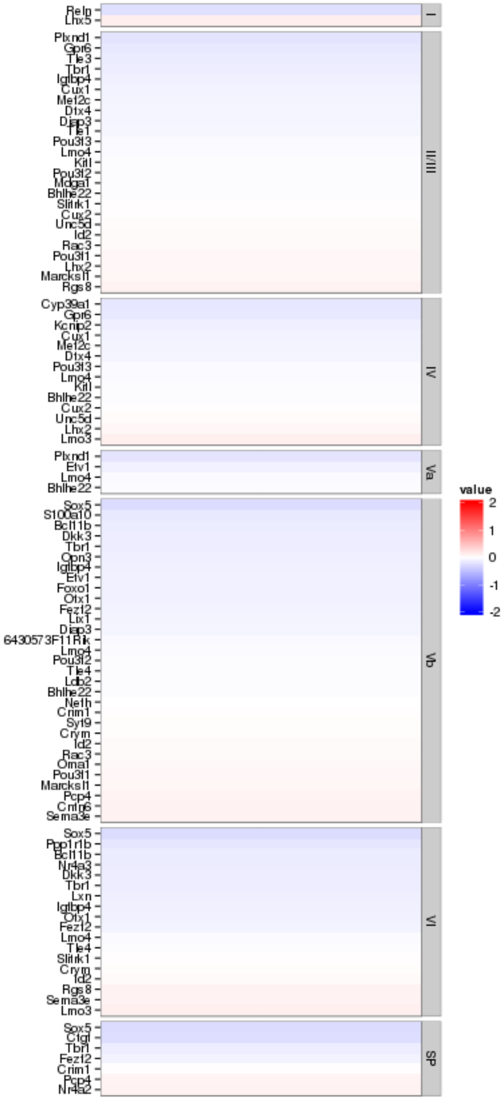
```
## Error: need finite 'xlim' values
```

```
## Error: need finite 'xlim' values
```

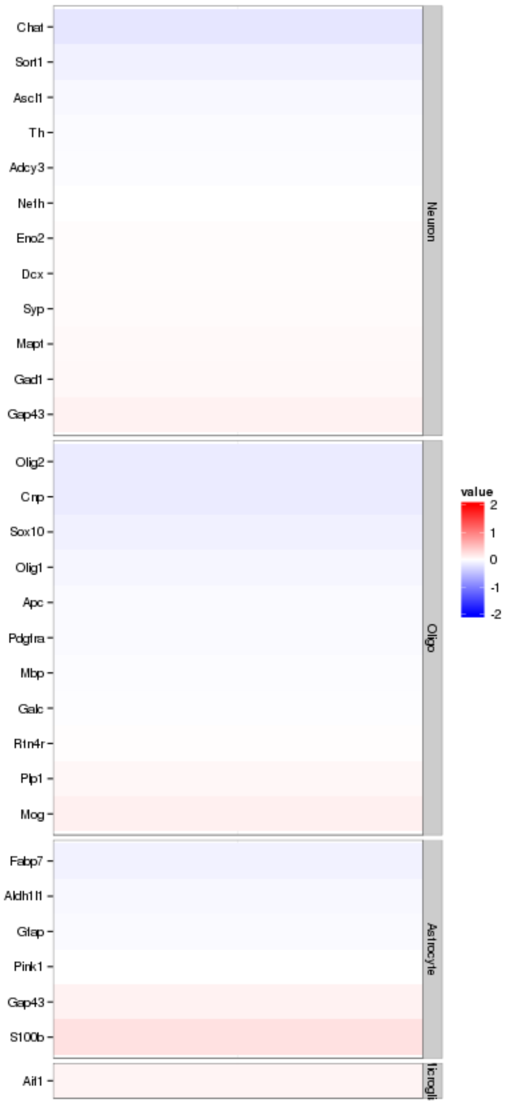
Enrichment or depletion for stage-specific cell cycle markers



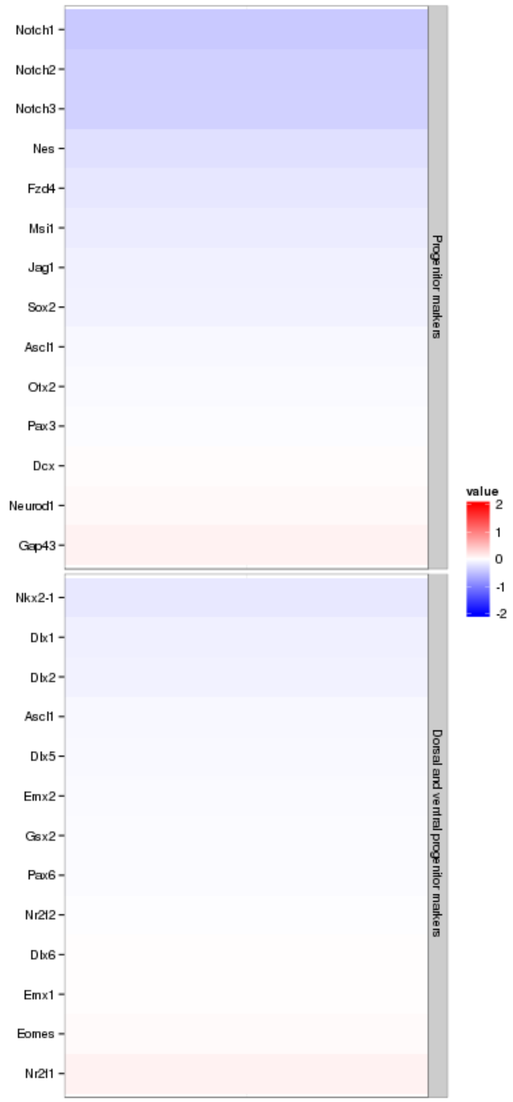
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



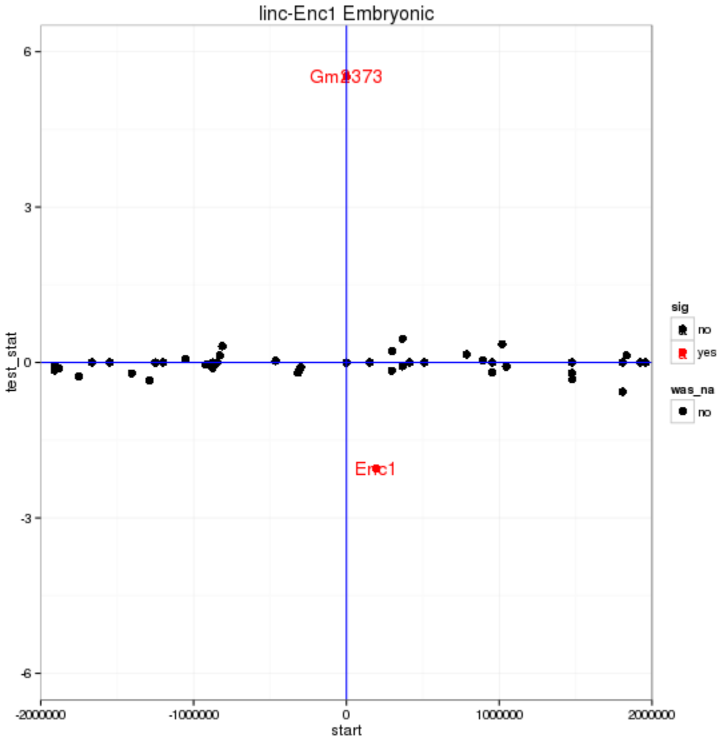
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 1 genes significantly regulated in a region this size is: 0.0409



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15	JR752
16	JR770
17	JR839

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	33003900.00	1.23	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	33003900.00	1.07	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	33003900.00	1.20	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	33003900.00	1.26	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	33003900.00	1.17	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	33003900.00	0.87	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	33003900.00	0.95	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	33003900.00	0.90	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	33003900.00	0.84	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	33003900.00	0.94	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	33003900.00	0.79	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	33003900.00	0.78	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	33003900.00	0.67	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	33003900.00	1.18	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR752/abundances.cxb	linc_Enc1	0	linc_Enc1_0	37182200.00	33003900.00	1.13	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR770/abundances.cxb	linc_Enc1	1	linc_Enc1_1	42845600.00	33003900.00	1.30	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR839/abundances.cxb	linc_Enc1	2	linc_Enc1_2	33810100.00	33003900.00	1.03	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils
## [8] datasets  base
##
## other attached packages:
##  [1] plyr_1.8.1
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##             param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              
## 1 cuffdiff -p 10 -L WT,linc-Enc1 -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/linc-Enc1_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/Brai
## 2
## 3
## 4
## 5
```

Manr KO vs WT (Adult)

This file shows the wt-v-ko comparison for Manr.

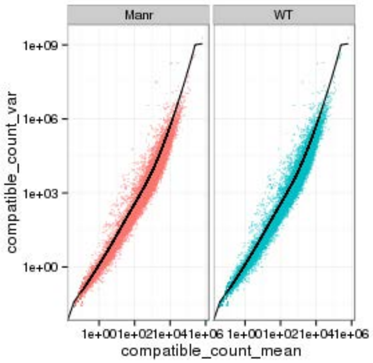
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

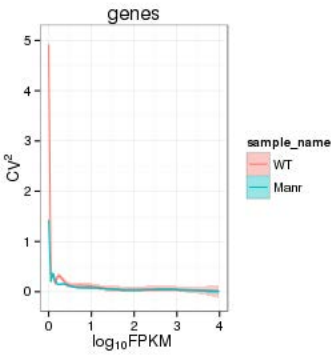
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



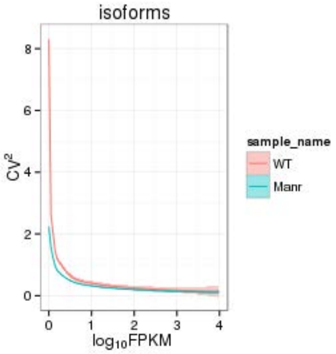
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

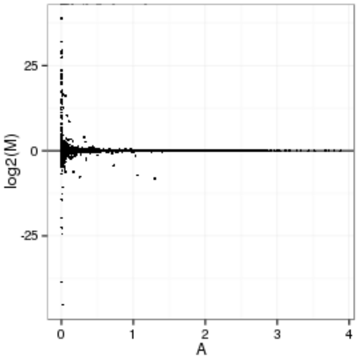
Genes:



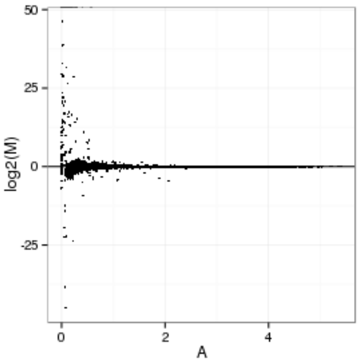
Isoforms:



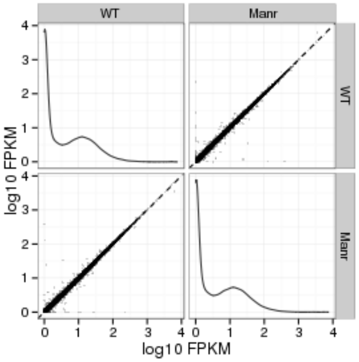
MvA plot



MvA plot counts



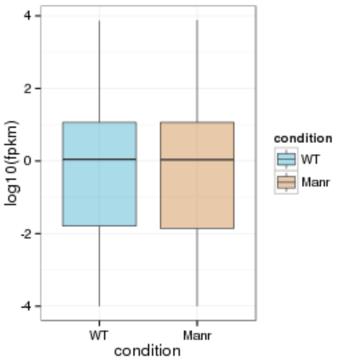
Scatterplot matrix



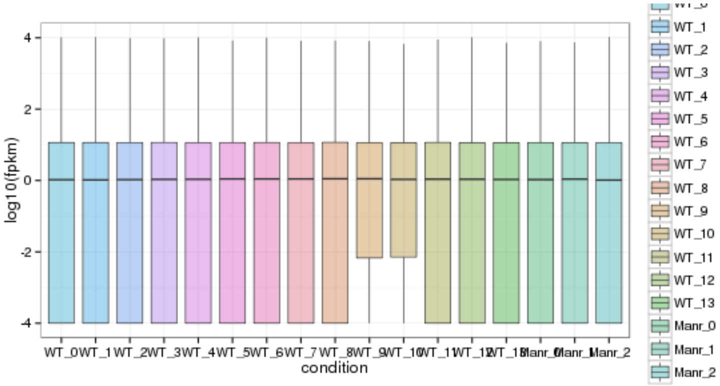
Distributions

Boxplots

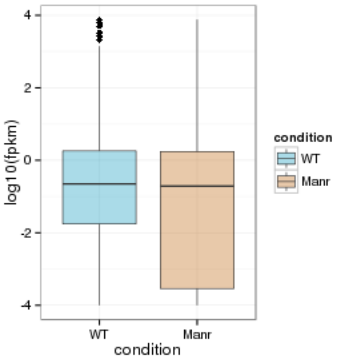
Boxplot (genes)



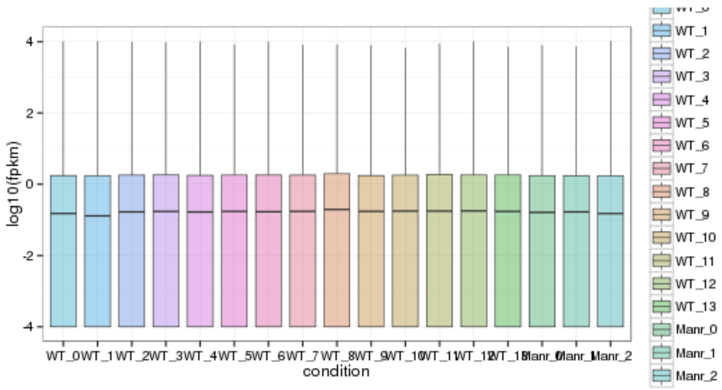
Boxplot (genes, replicates)



Boxplot (isoforms)

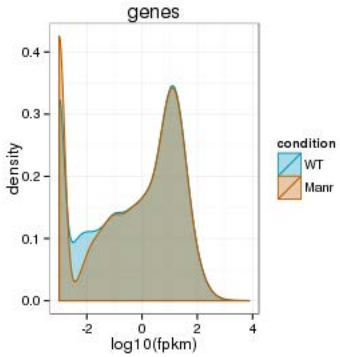


Boxplot (isoforms, replicates)

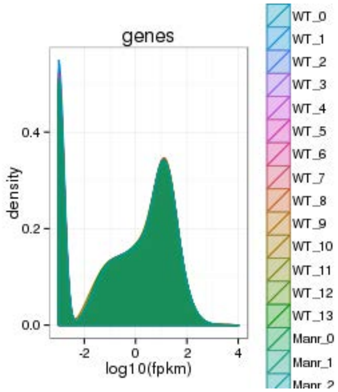


Density

Density (genes)

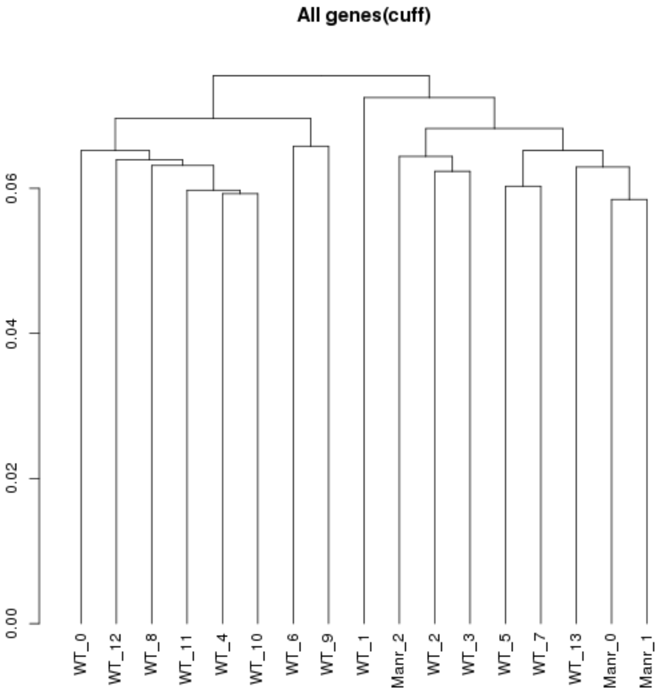


Density (genes, replicates)



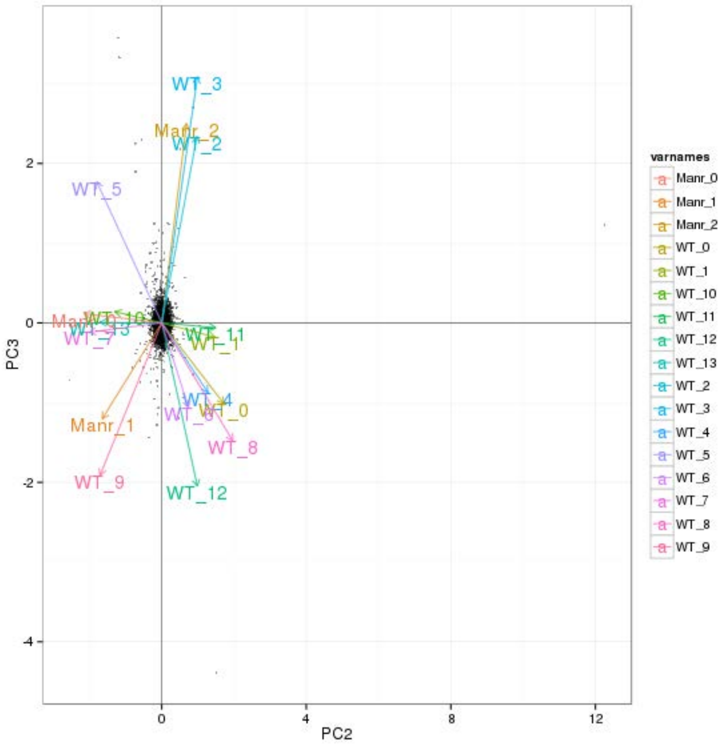
Clustering

Replicate Clusters

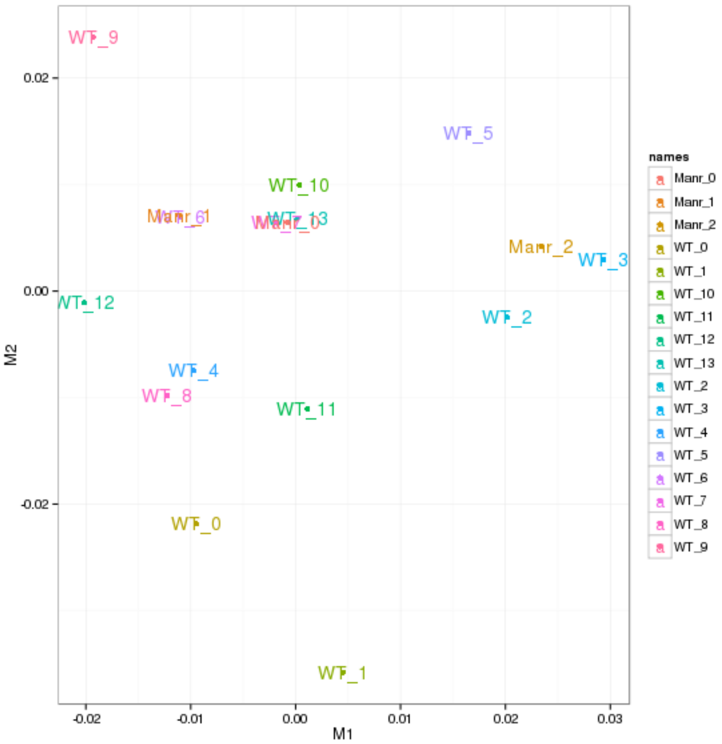


```
## NULL
```

PCA (genes)

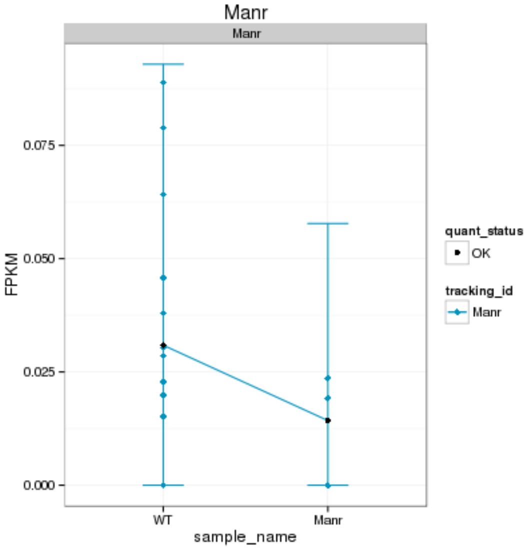

WT_3
Manr_2
WT_2
WT_5
Manr_0
WT_10
WT_13
WT_7
WT_11
WT_1
WT_4
WT_0
WT_6
WT_8
Manr_1
WT_9
WT_12
PC3
PC2
2
0
-2
-4
0
4
8
12
varnames
Manr_0
Manr_1
Manr_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

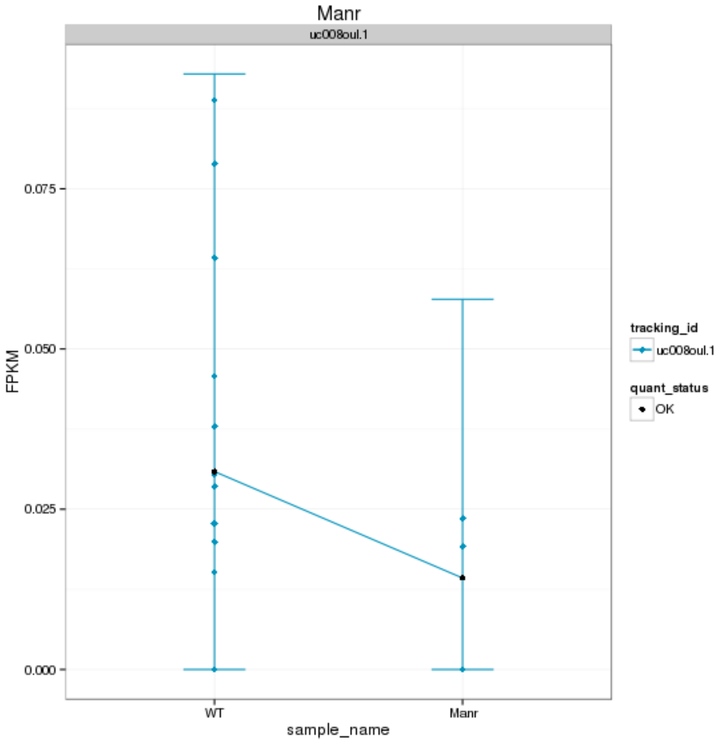


KO assessment

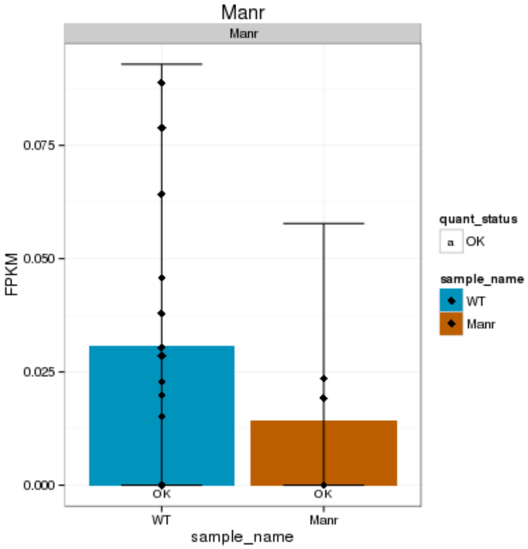
Endogenous lncRNA expression



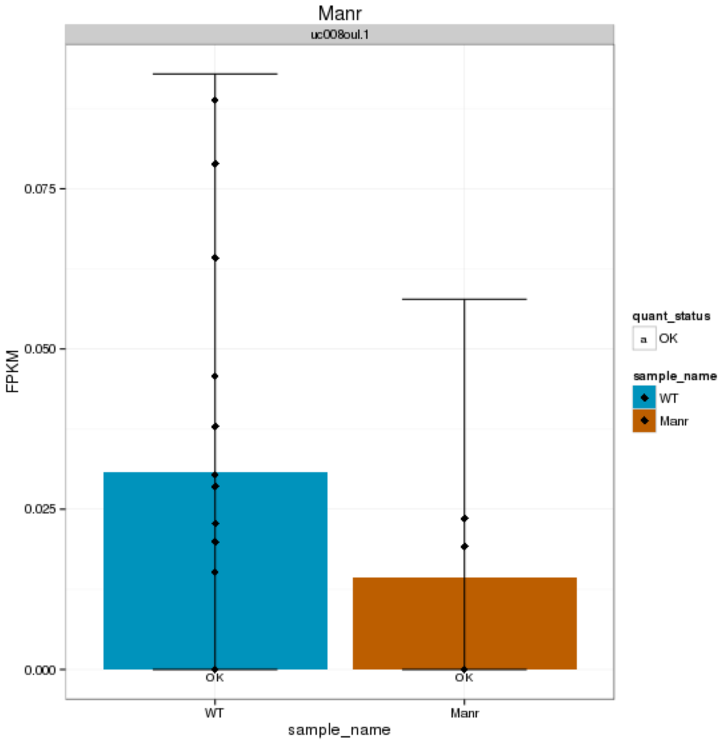
Endogenous expression of Manr isoforms:



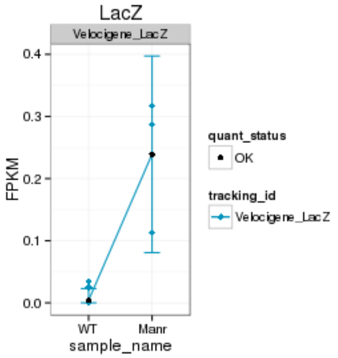
Barplot of gene expression:

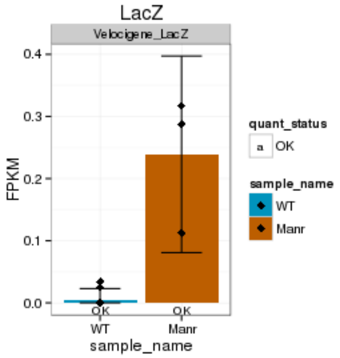


Barplot of isoform expression:



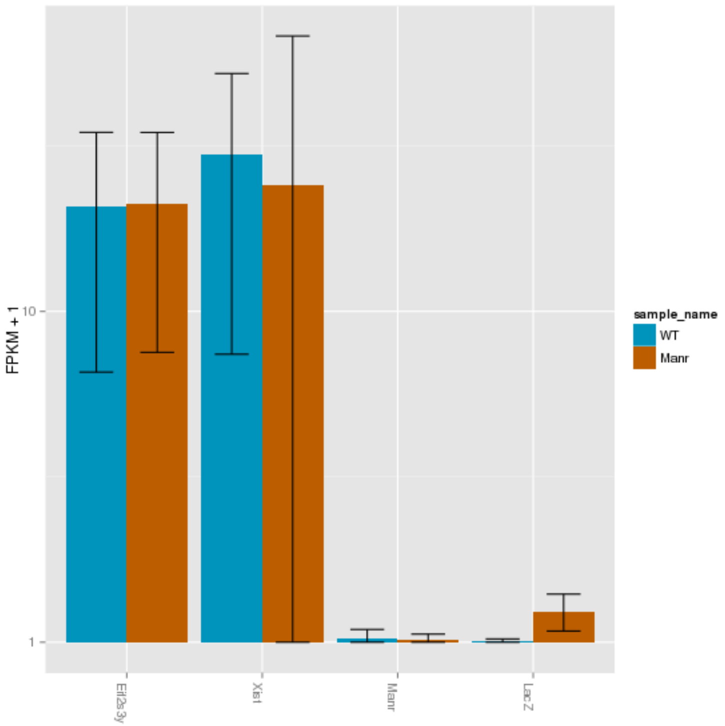
LacZ expression



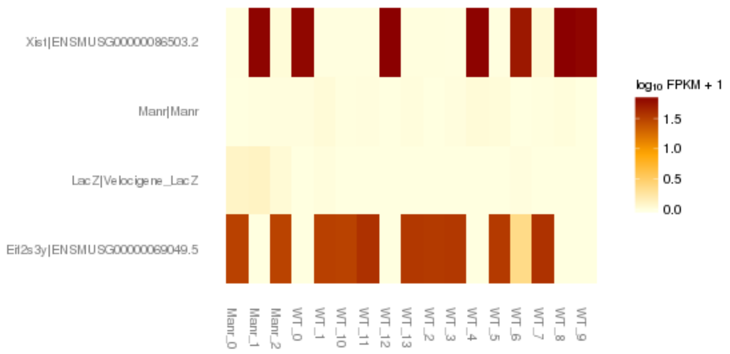


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization

5'
3'
3'
5'
LincRNA Isoforms
uc008oul.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Manr_0
Manr_1
Manr_2
KO Region

Differential Analysis

Differential Genes

There are 49 significantly differentially expressed genes. They are:

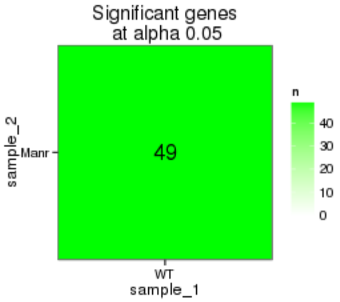
	geneAnnot$gene_short_name
1	Slc5a5
2	Col6a1
3	Arrdc2
4	Nes
5	Lpl
6	Pdk4
7	Pttg1
8	Adi1
9	Pomc
10	Serpina3n
11	Fos
12	Arc
13	Nr4a1
14	Podxl
15	Lcn2
16	Fabp5
17	Anxa5
18	Tshb
19	Tmem144
20	Rps3a1
21	Nr4a3
22	Tinagl1
23	Hddc3
24	Dis3l
25	Arhgap27
26	Pla2g3
27	Plvap
28	Lars2
29	Tmem59l
30	Egr2
31	Egr1
32	Sgsm1
33	Tuba1c
34	Snhg11
35	Acp1
36	Epcam
37	Junb

38 Tpm3-rs7
39 Trank1
40 Grm4
41 Rps15
42 Bpifb3
43 Gm9008

44 Gm7292
45 Srp54a
46 Wdfy1
47 Scnm1
48 AA465934
49 Gm26924

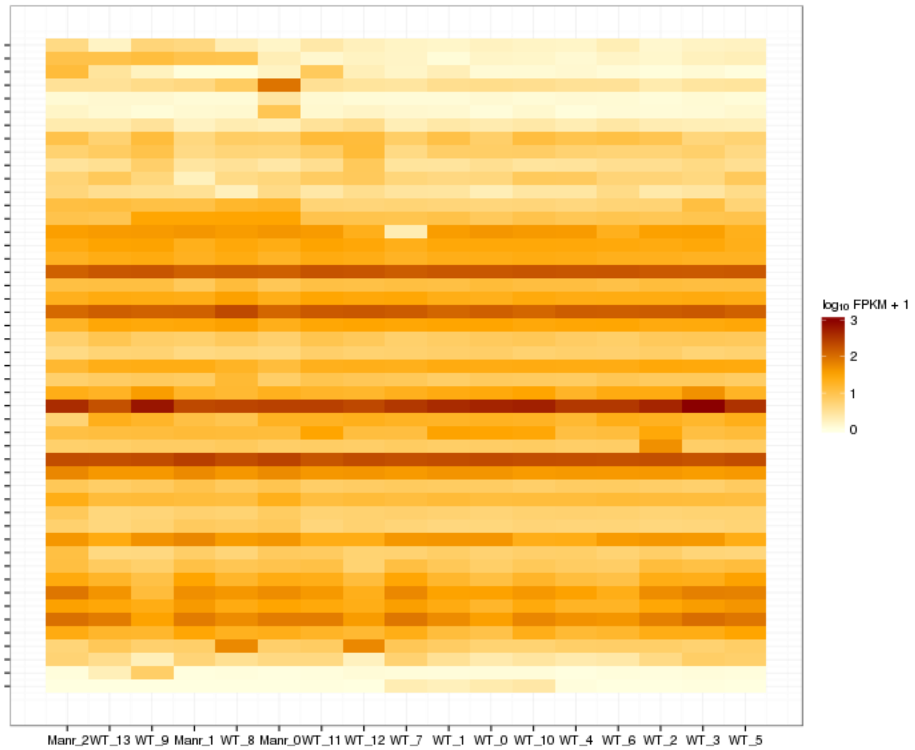
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

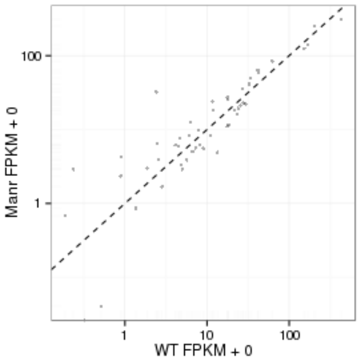


Significant genes with expression >50fpkm (any condition):(turned off)

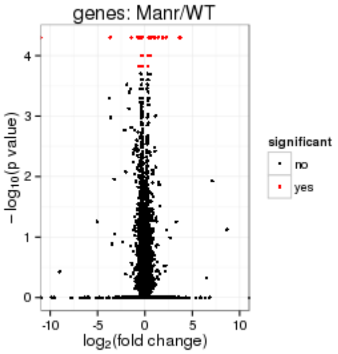
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

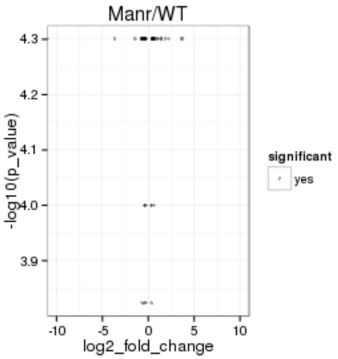
Scatter plot of significant genes only:



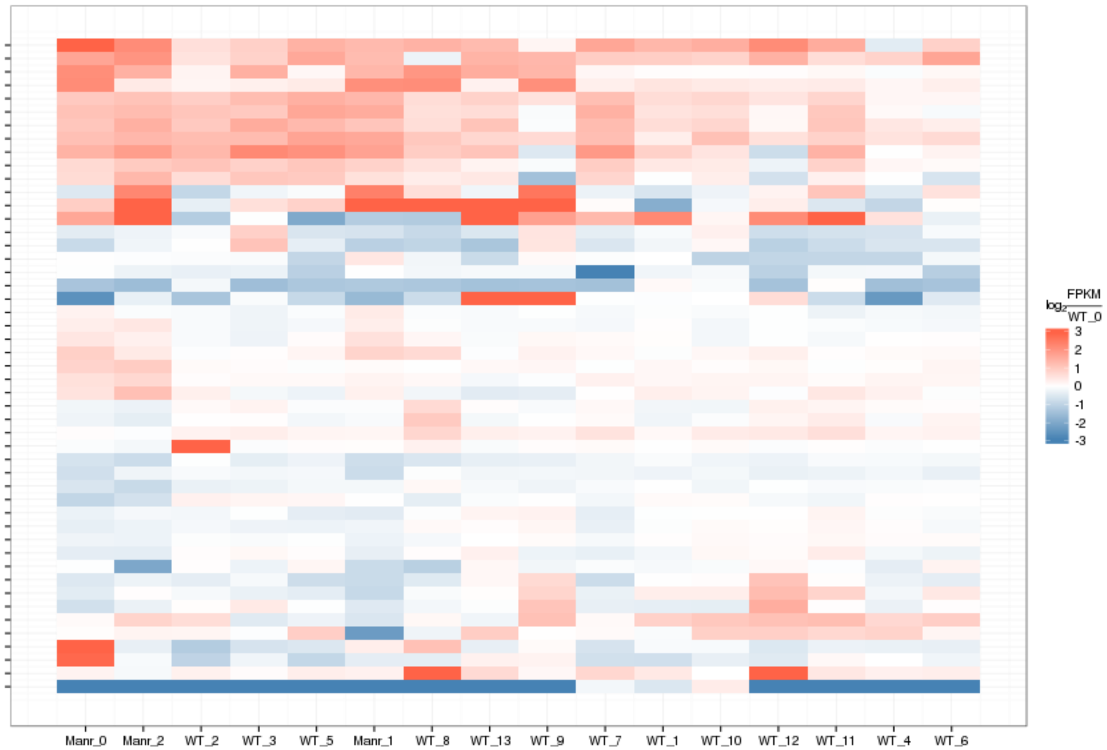
Volcano Plot



Volcano plot with significant genes only:



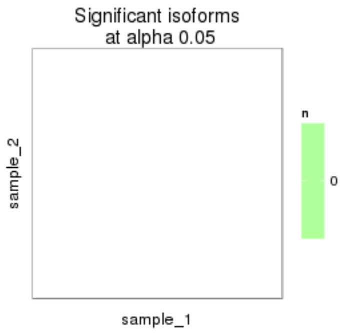
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

[1] “no sig isoforms”

Gene-level DE isoform heatmap

```
## [1] "no sig isoforms"
```

Isoform foldchange heatmap by isoform:

```
## [1] "no sig isoforms"
```

Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

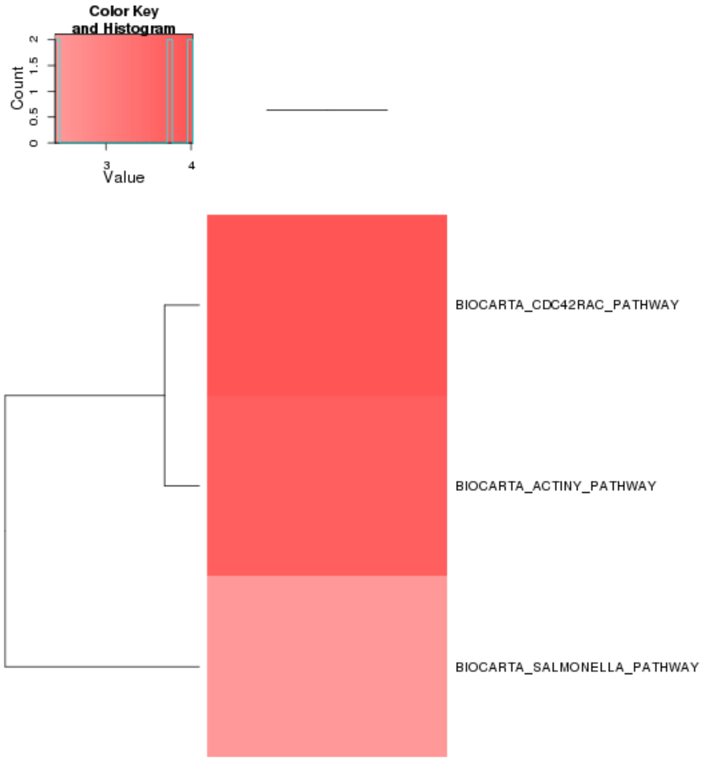
Gene/Pathway Analysis

GSEA

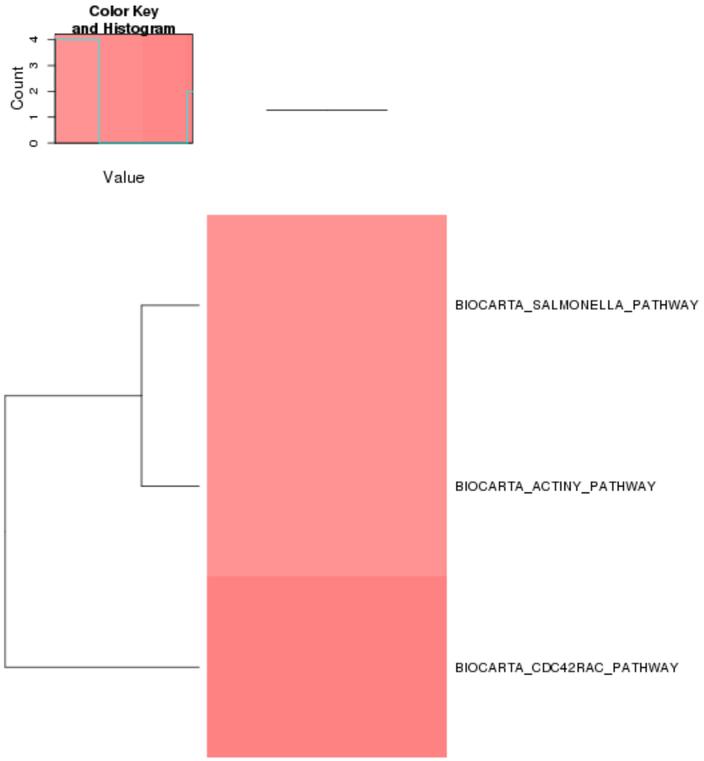
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

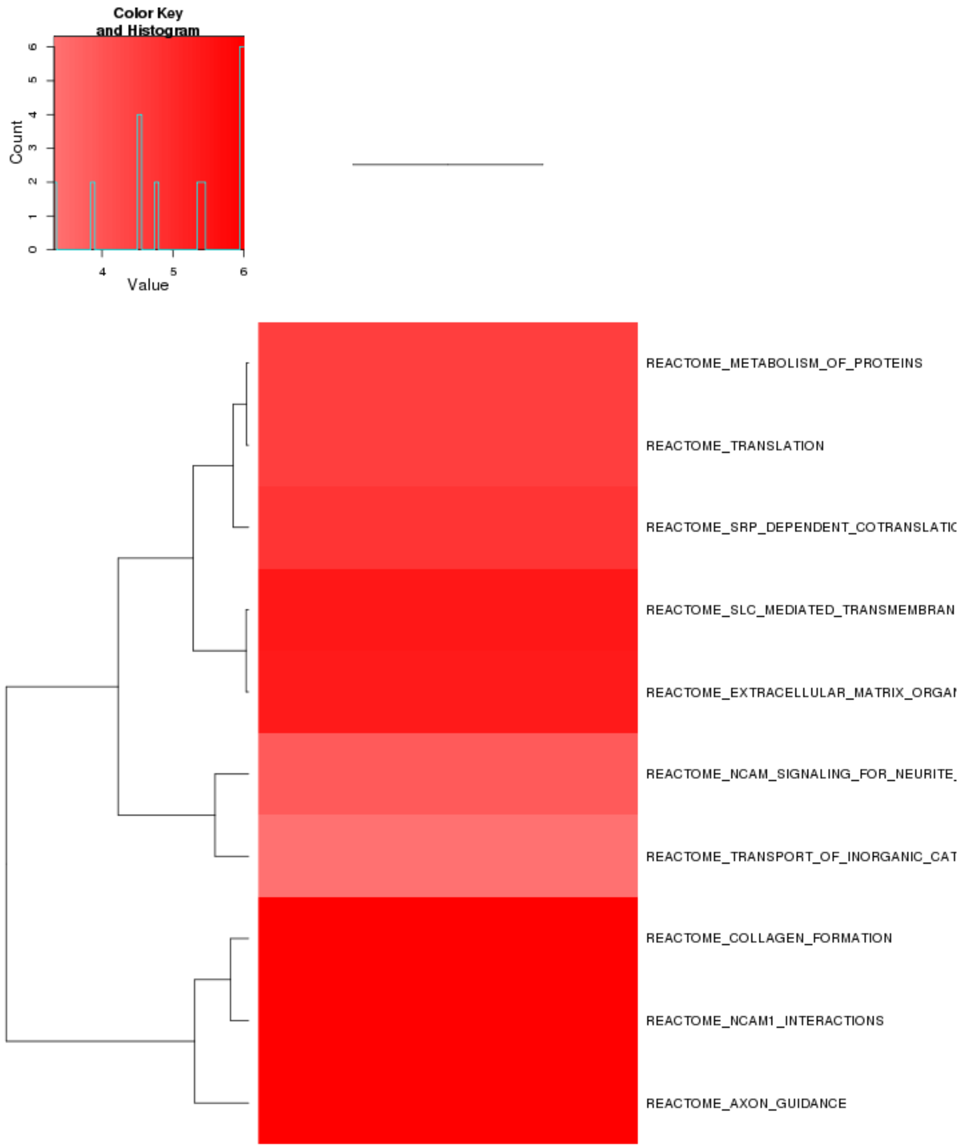
Biocarta enrichment:



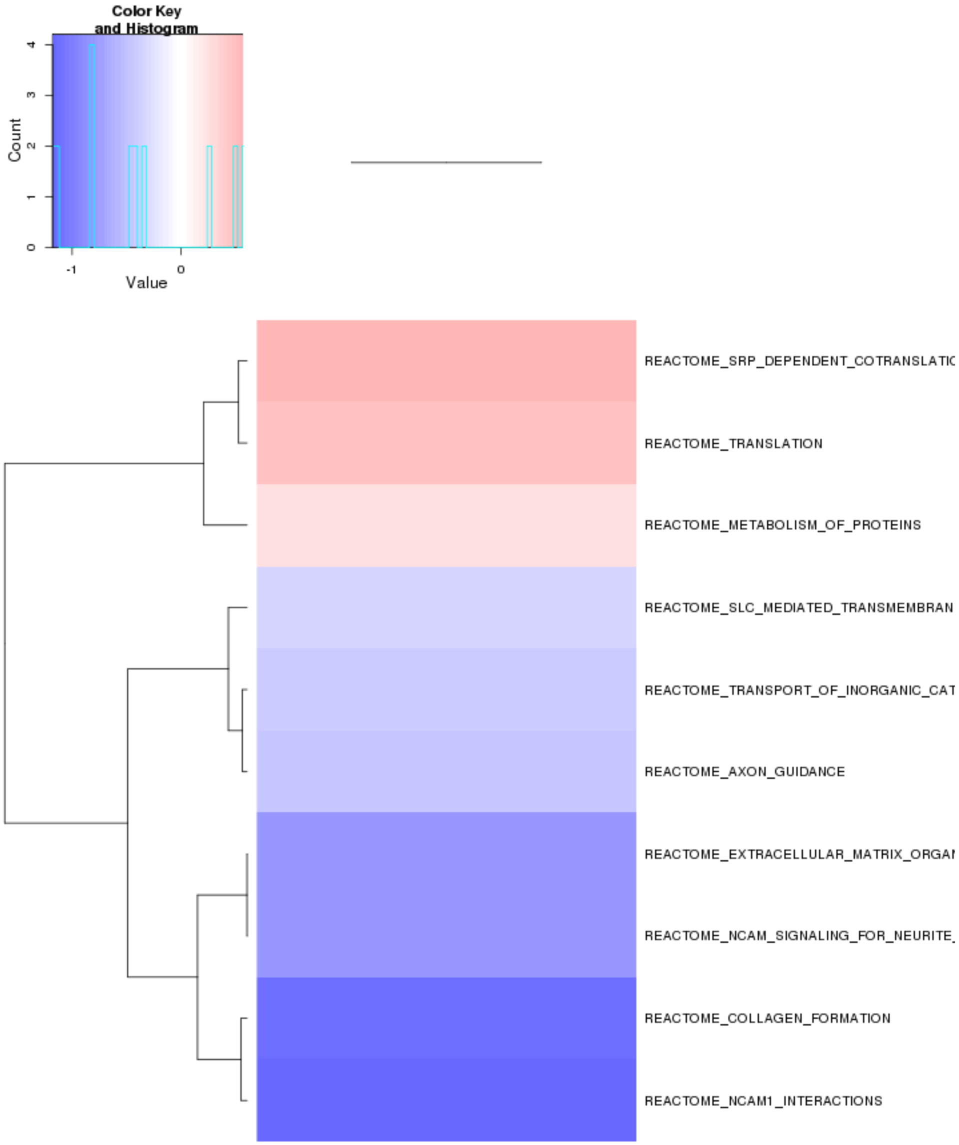
Biocarta zscore:



Reactome enrichment:



Reactome zscore:



Kegg enrichment:

```
## Error: argument is of length zero
```

Kegg zscore:

```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

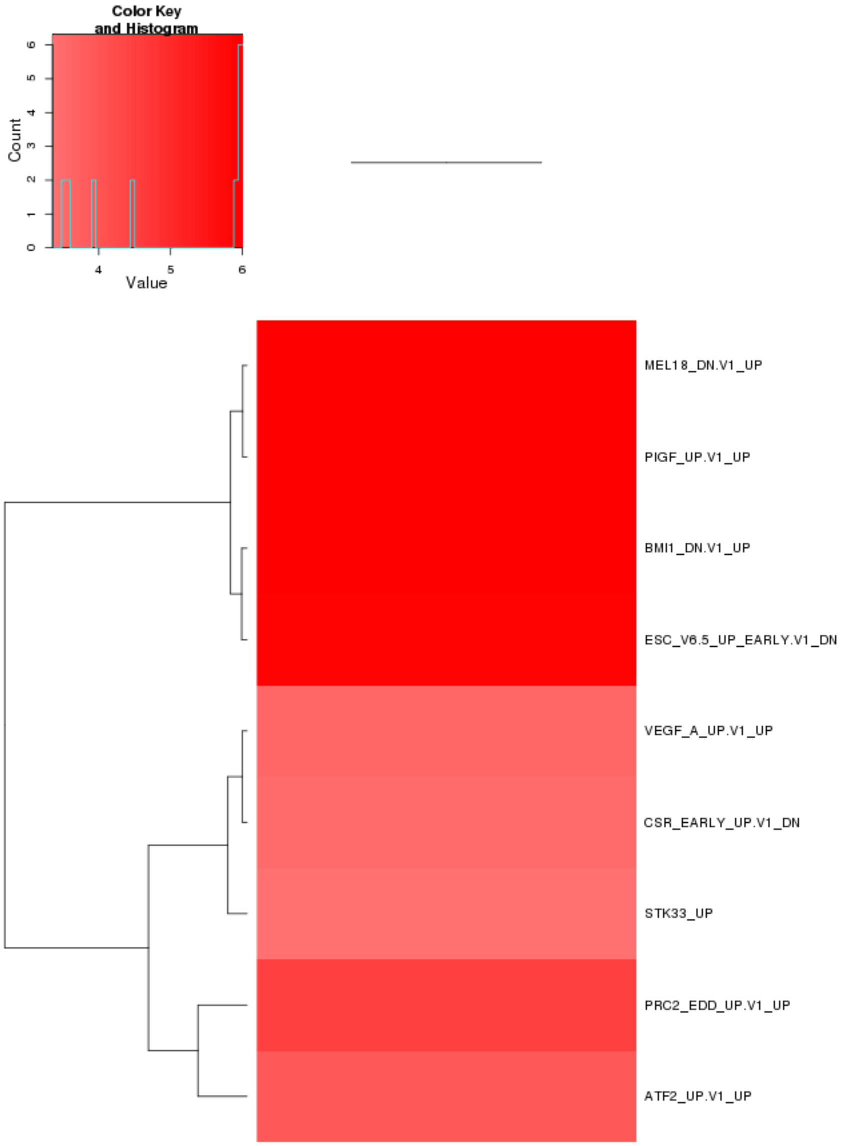
Interneuron enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

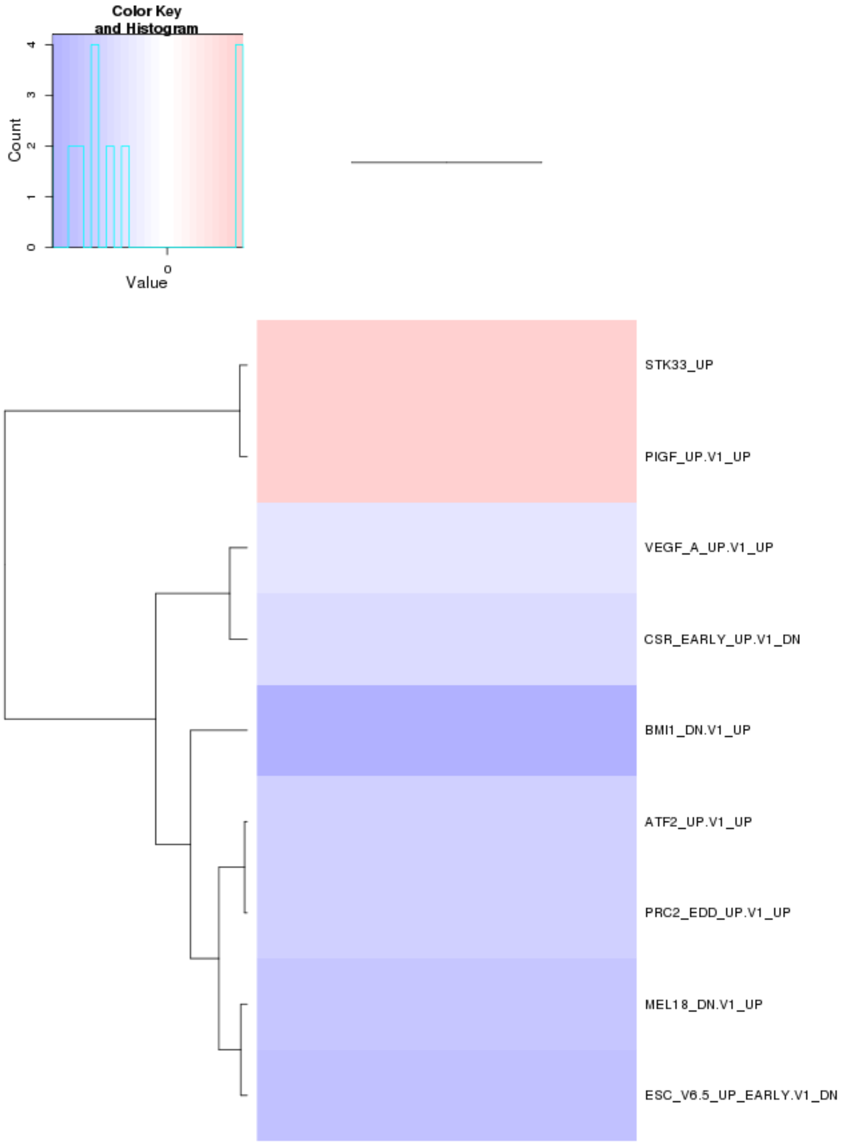
Interneuron zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

Oncogene enrichment:

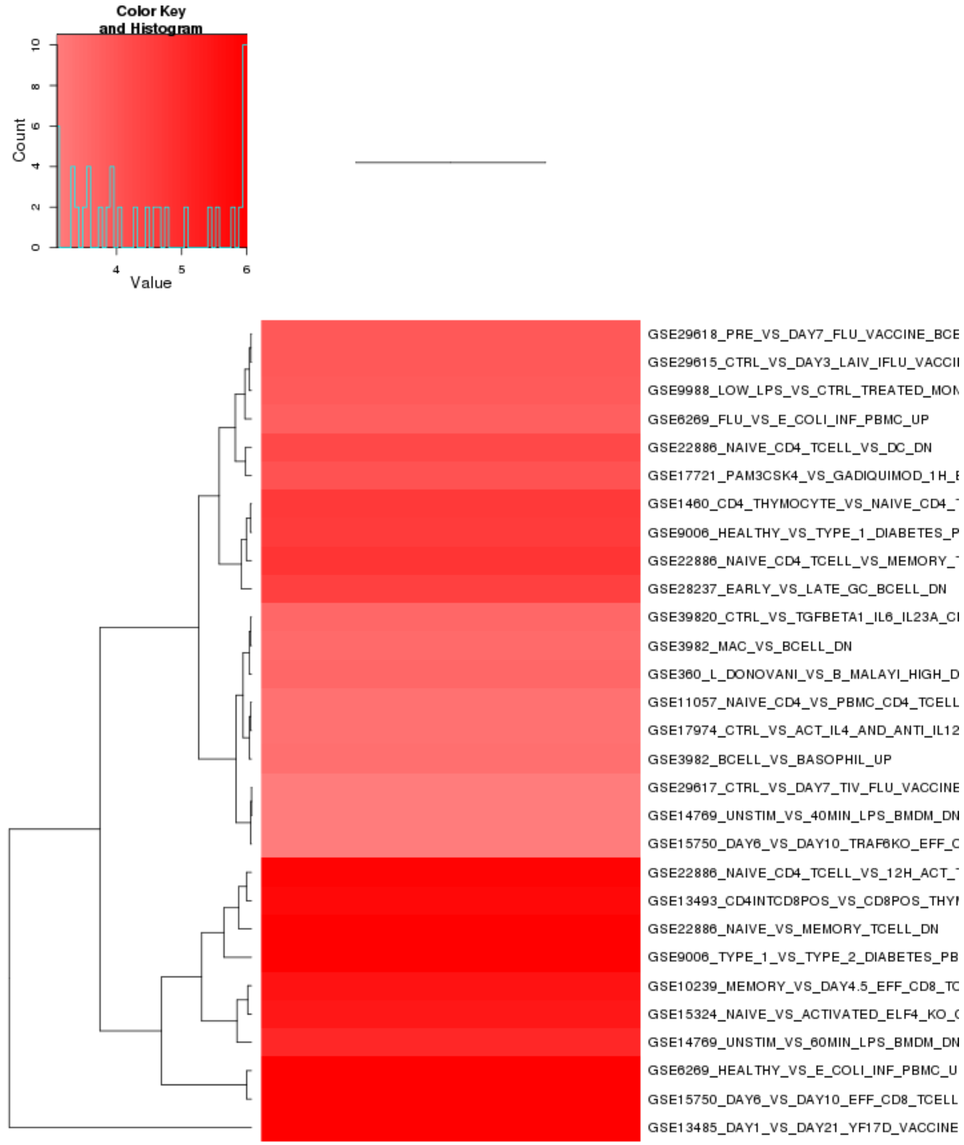


Oncogene zscore:



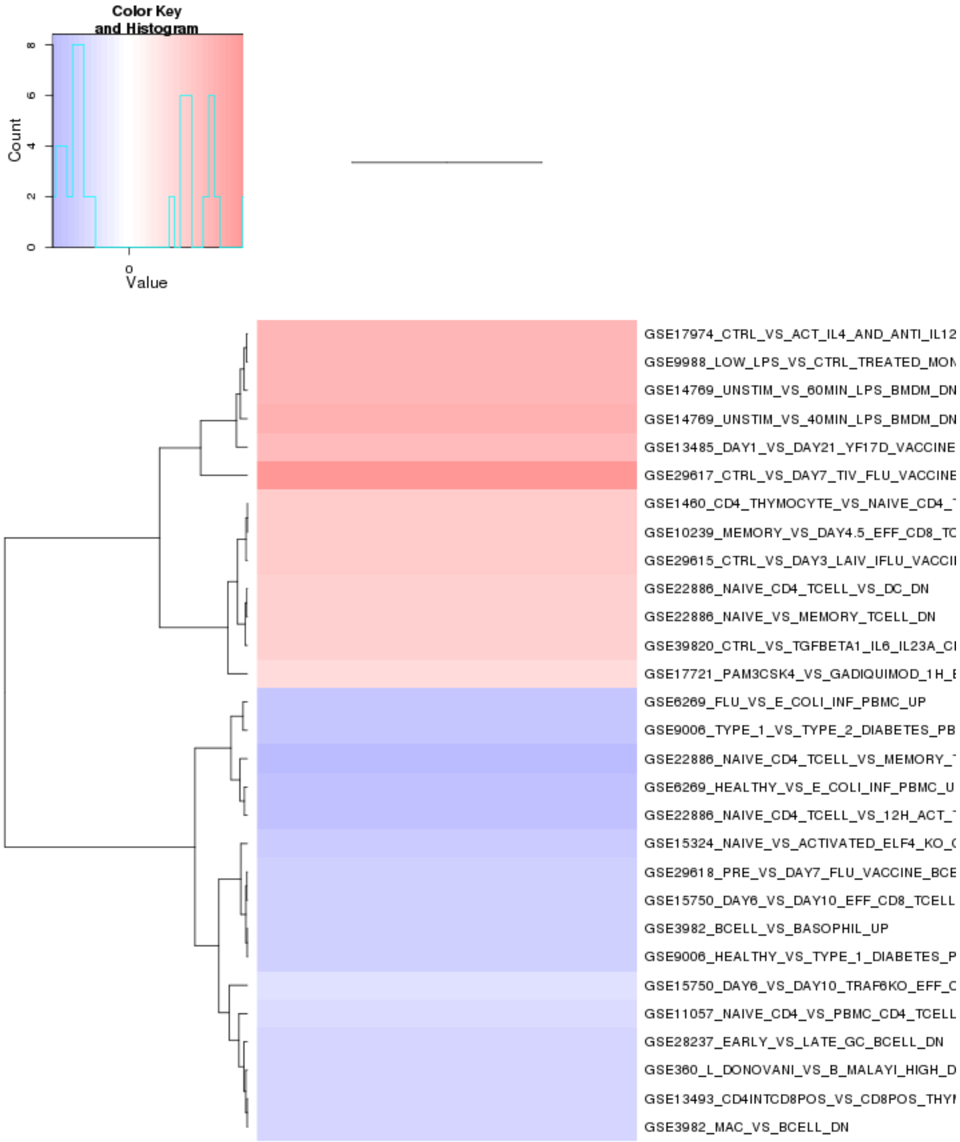
Immuno enrichment:

```
## Error: subscript out of bounds
```

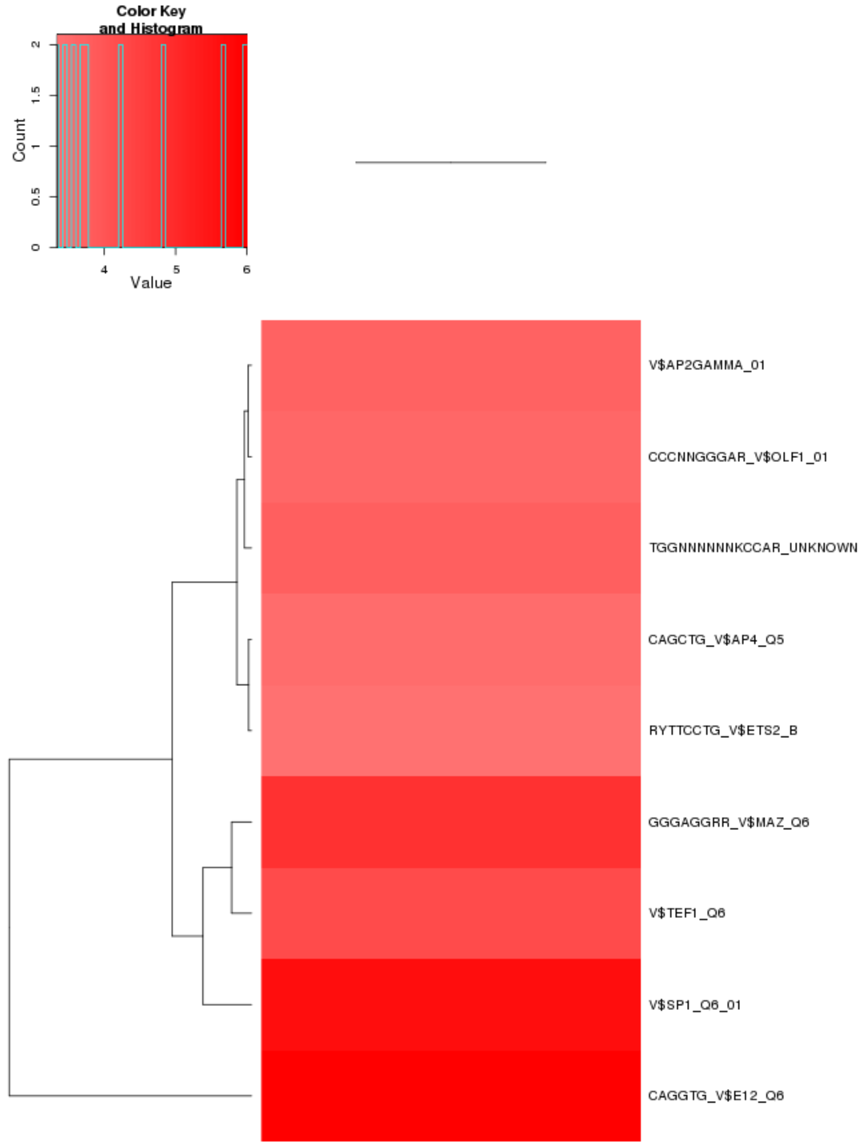


Immuno zscore:

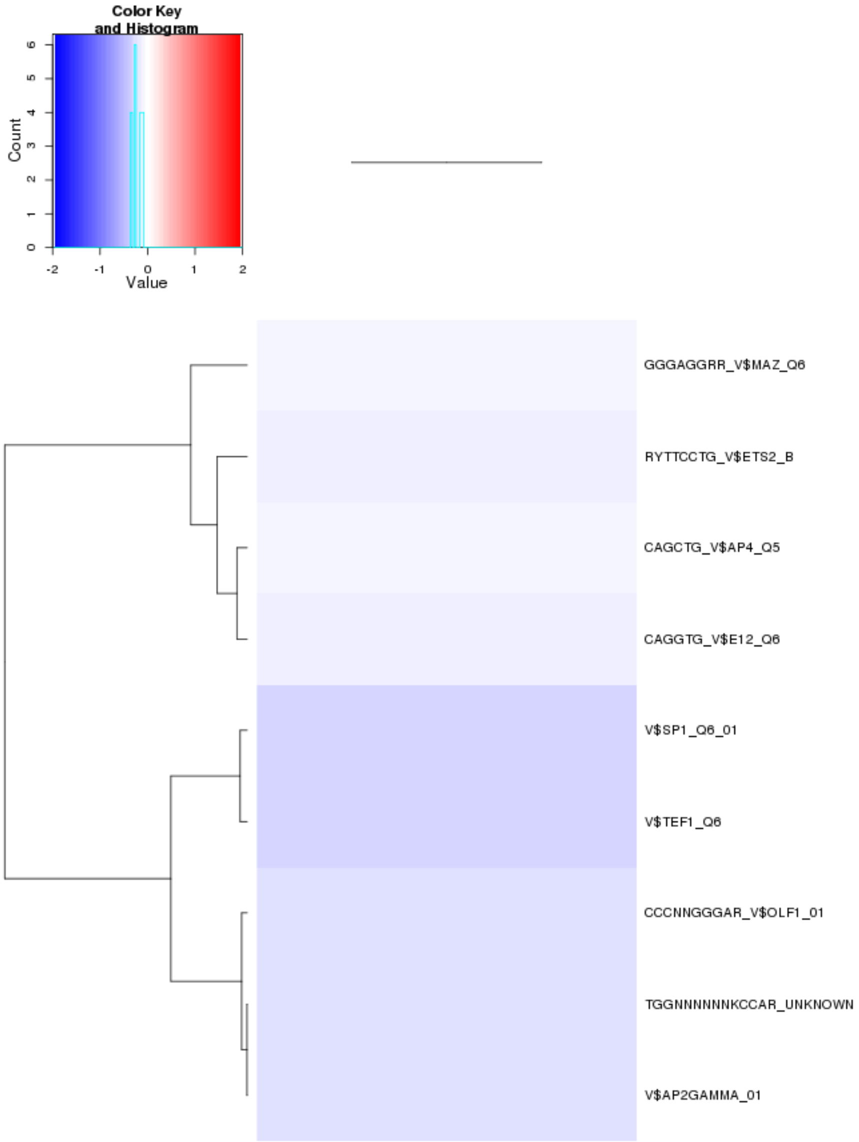
```
## Error: subscript out of bounds
```



TF enrichment:


Color Key
and Histogram
Count
0
0.5
1
1.5
2
4
5
6
Value
V$AP2GAMMA_01
CCCNNGGGAR_V$OLF1_01
TGGNNNNNNKCCAR_UNKNOWN
CAGCTG_V$AP4_Q5
RYTTCCTG_V$ETS2_B
GGGAGGRR_V$MAZ_Q6
V$TEF1_Q6
V$SP1_Q6_01
CAGGTG_V$E12_Q6

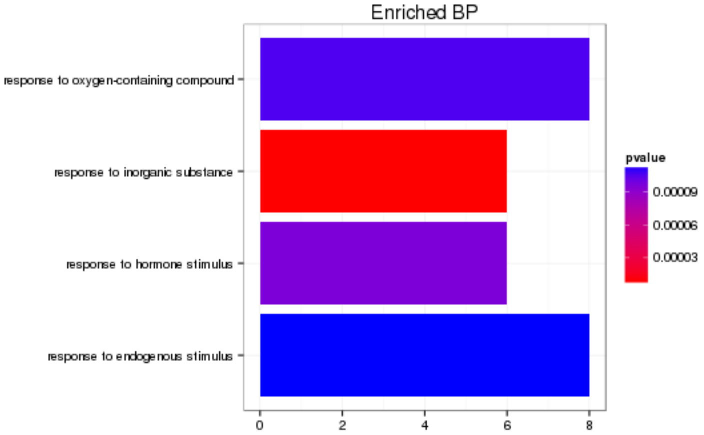
TF zscore:

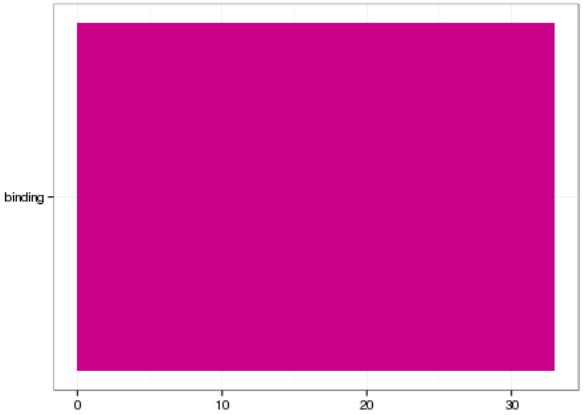


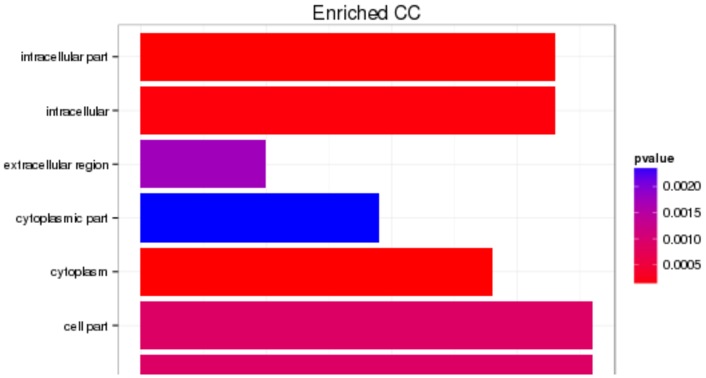
GO enrichment

Cluster profiler used to call enichments of significantly differentially regulated genes that map to Entrez IDs.

```
## [1] "ERROR: The estimated pi0 <= 0. Check that you have valid p-values or use another lambda method."
```

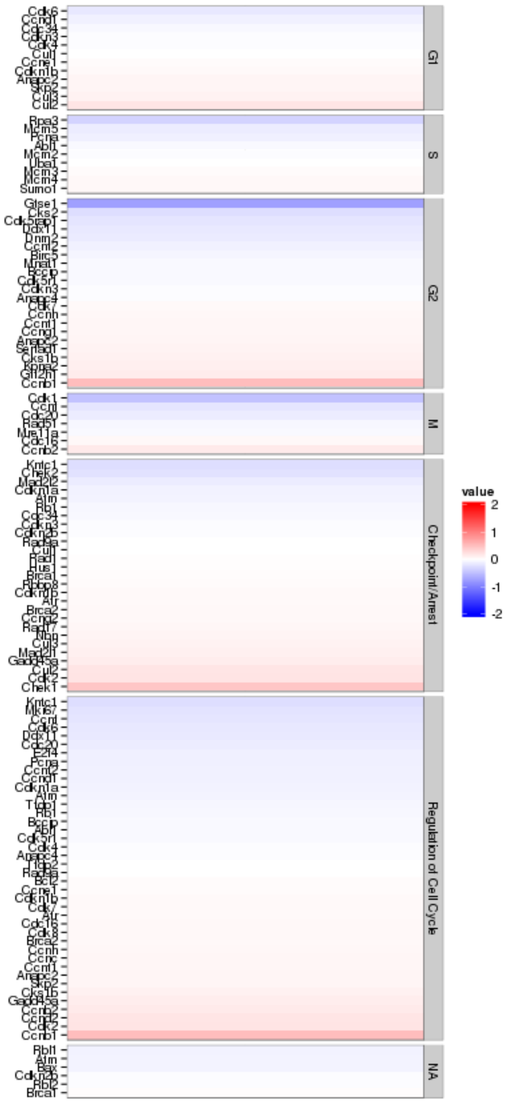

Enriched BP



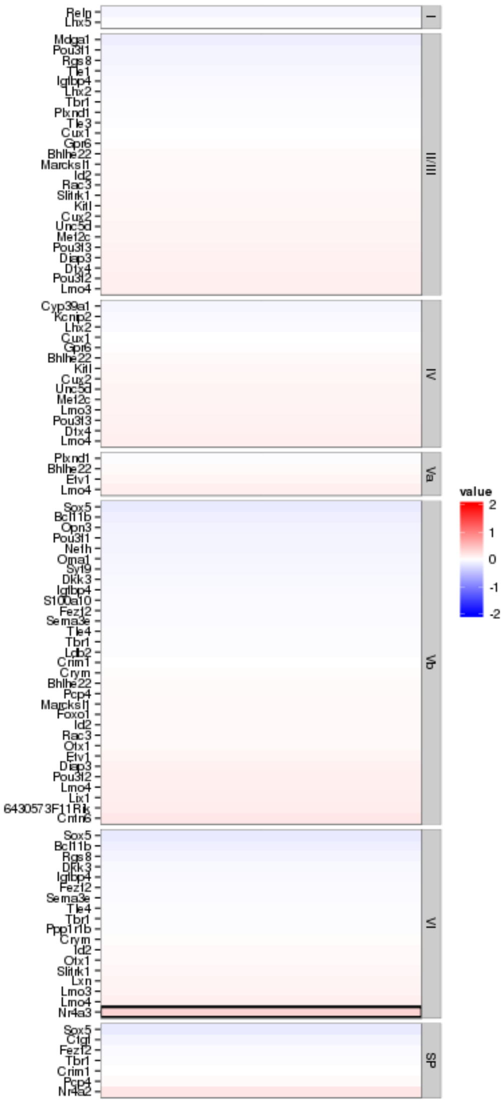

Enriched CC

```
## Error: need finite 'xlim' values
```

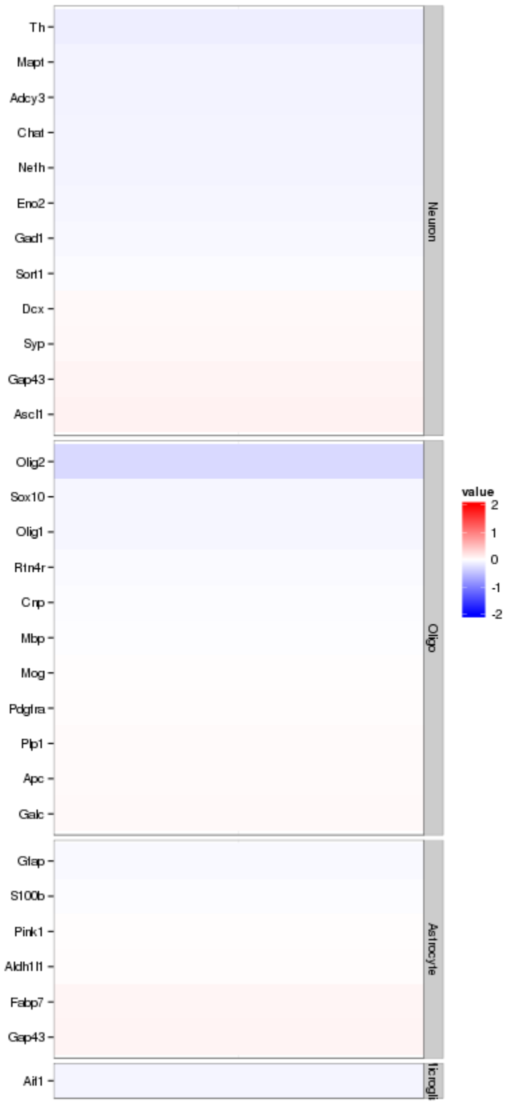
Enrichment or depletion for stage-specific cell cycle markers



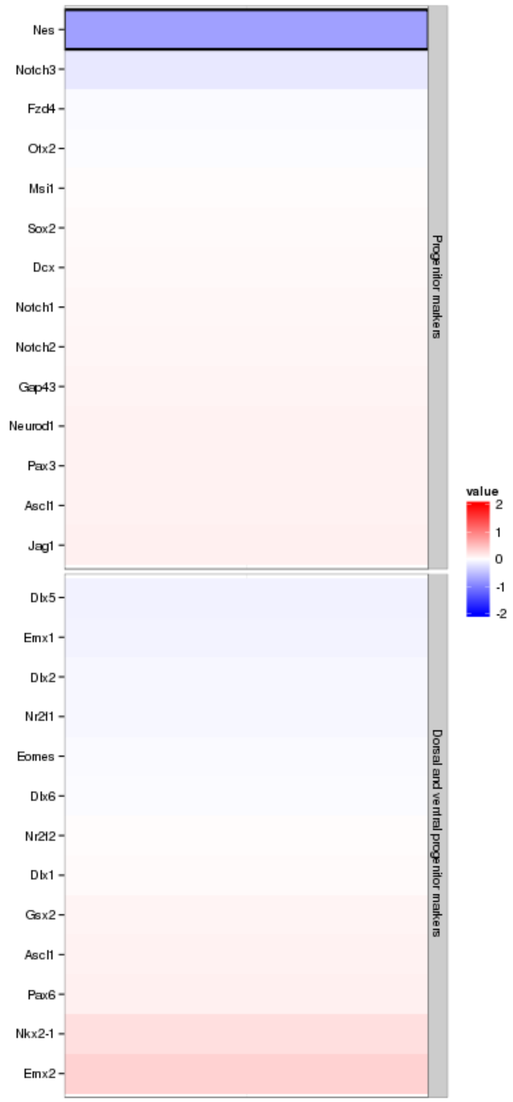
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



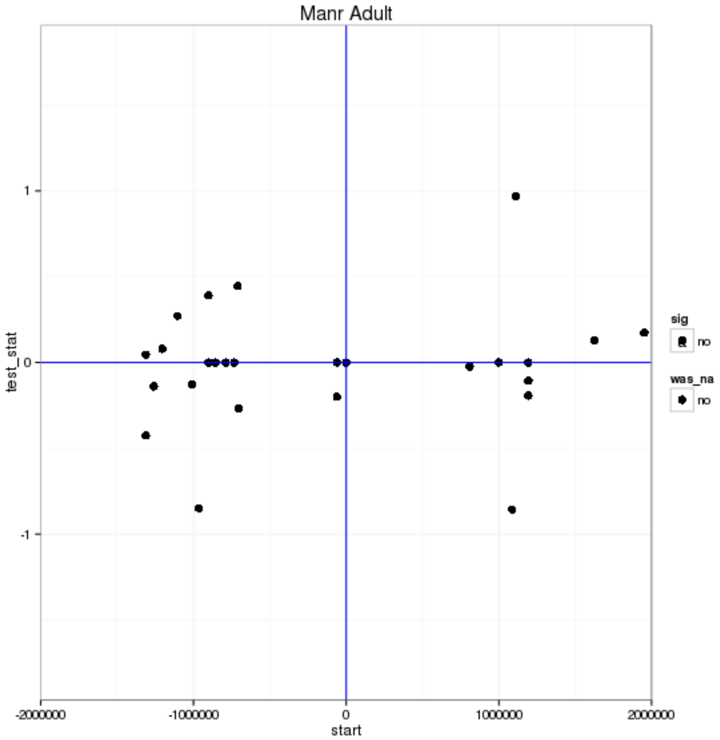
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15	JR780
16	JR737
17	JR801

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	34899700.00	0.75	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	34899700.00	0.58	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	34899700.00	0.97	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	34899700.00	0.80	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	34899700.00	1.03	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	34899700.00	1.06	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	34899700.00	0.80	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	34899700.00	1.15	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	34899700.00	1.00	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	34899700.00	1.29	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	34899700.00	1.49	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	34899700.00	1.01	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	34899700.00	0.97	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	34899700.00	1.20	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR780/abundances.cxb	Manr	0	Manr_0	40782700.00	34899700.00	1.17	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR737/abundances.cxb	Manr	1	Manr_1	40835900.00	34899700.00	1.19	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR801/abundances.cxb	Manr	2	Manr_2	34495500.00	34899700.00	0.96	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1                
##  [2] stringr_0.6.2             
##  [3] seqbias_1.10.0            
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,Manr -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Manr_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/annc
## 2
## 3
## 4
## 5
```

Manr KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for Manr.

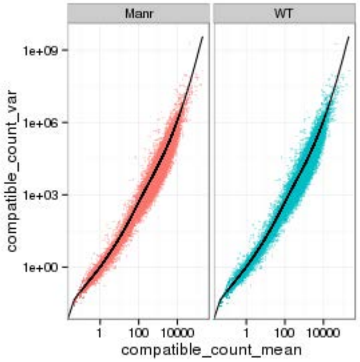
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

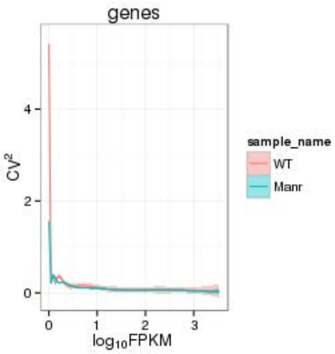
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



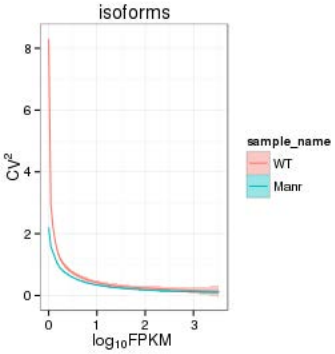
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

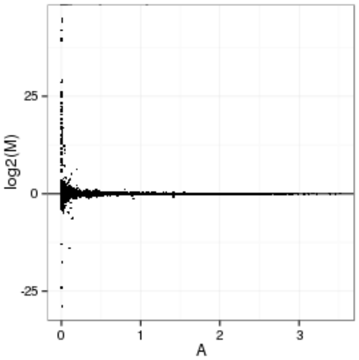
Genes:



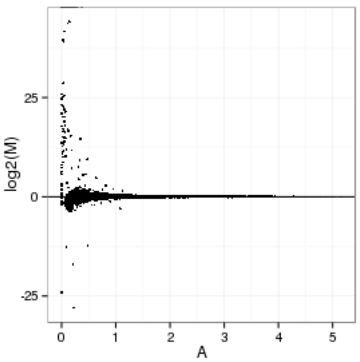
Isoforms:



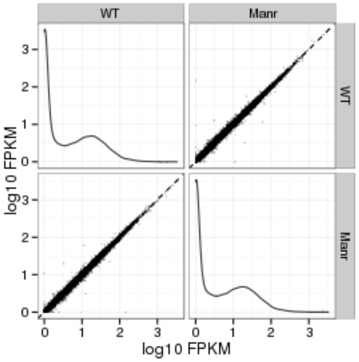
MvA plot



MvA plot counts



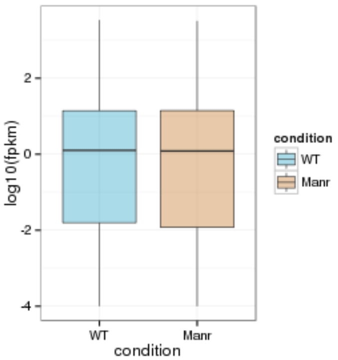
Scatterplot matrix



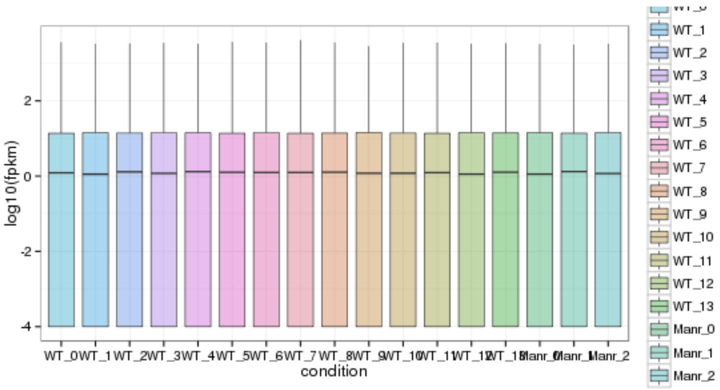
Distributions

Boxplots

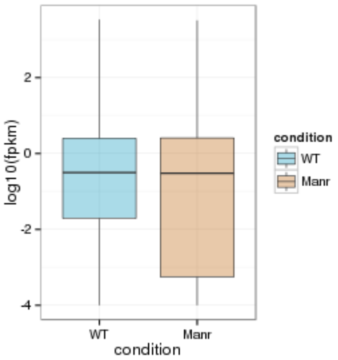
Boxplot (genes)



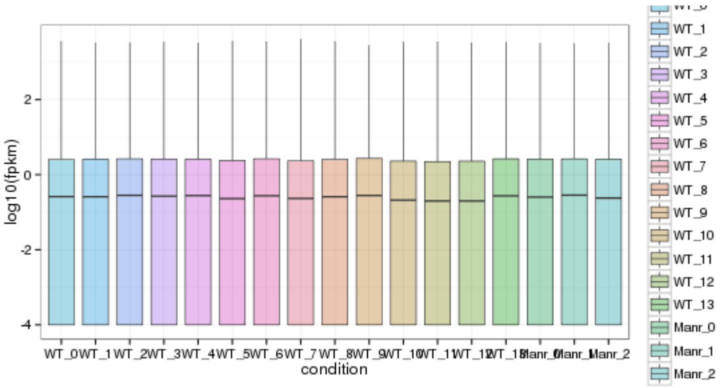
Boxplot (genes, replicates)



Boxplot (isoforms)

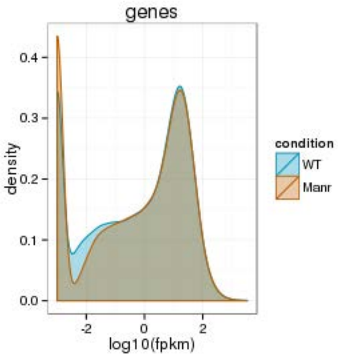


Boxplot (isoforms, replicates)

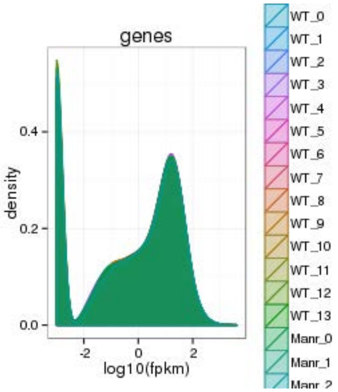


Density

Density (genes)

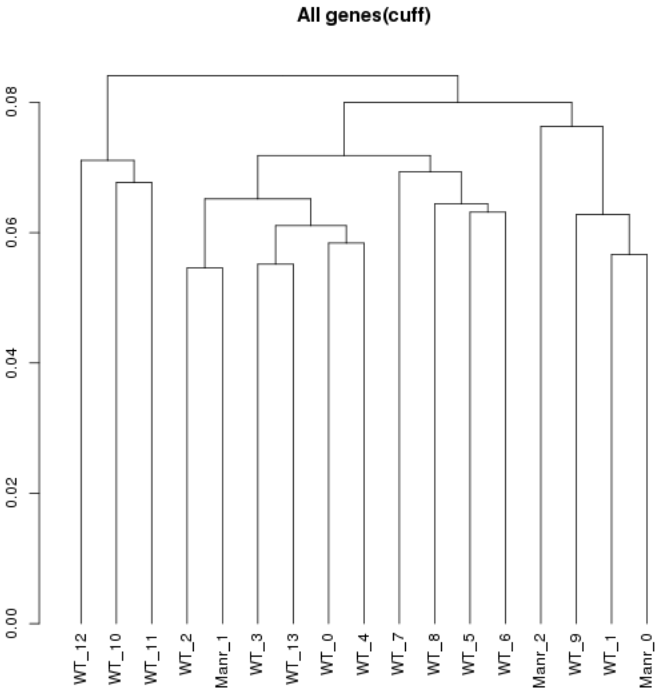


Density (genes, replicates)



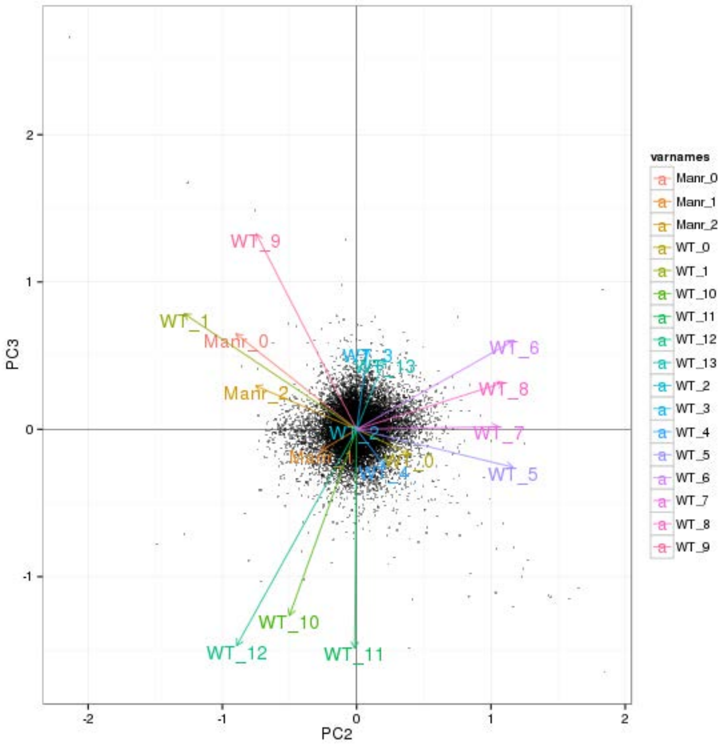
Clustering

Replicate Clusters



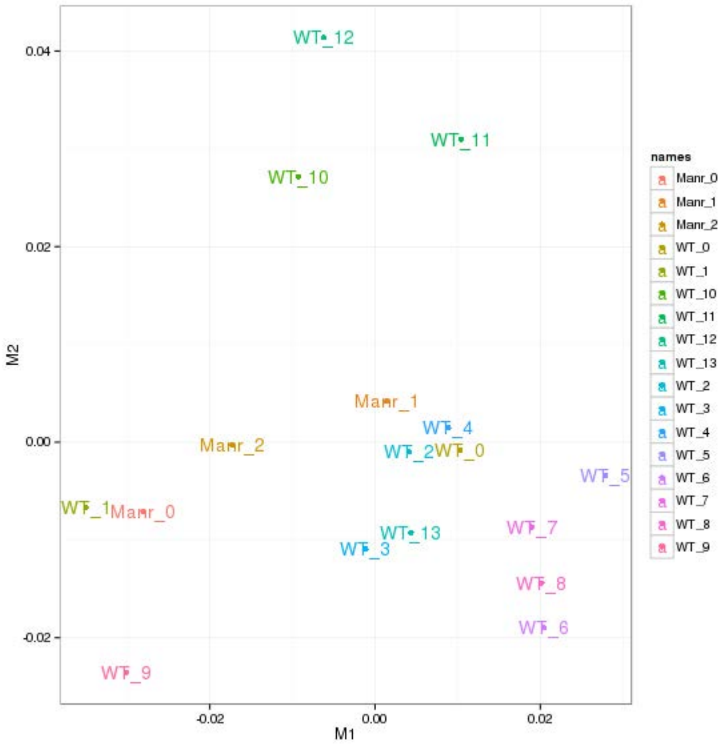
```
## NULL
```

PCA (genes)



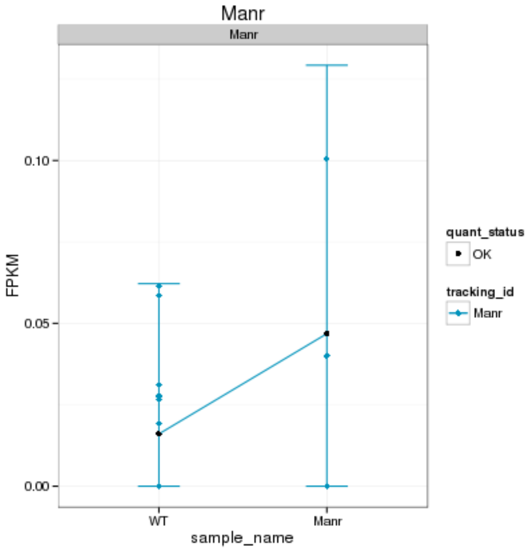
PC3
PC2
2
1
0
-1
-2
-1
0
1
2
WT_9
WT_1
Manr_0
Manr_2
WT_3
WT_13
WT_6
WT_8
WT_7
WT_2
Manr_1
WT_0
WT_4
WT_5
WT_10
WT_12
WT_11
varnames
Manr_0
Manr_1
Manr_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

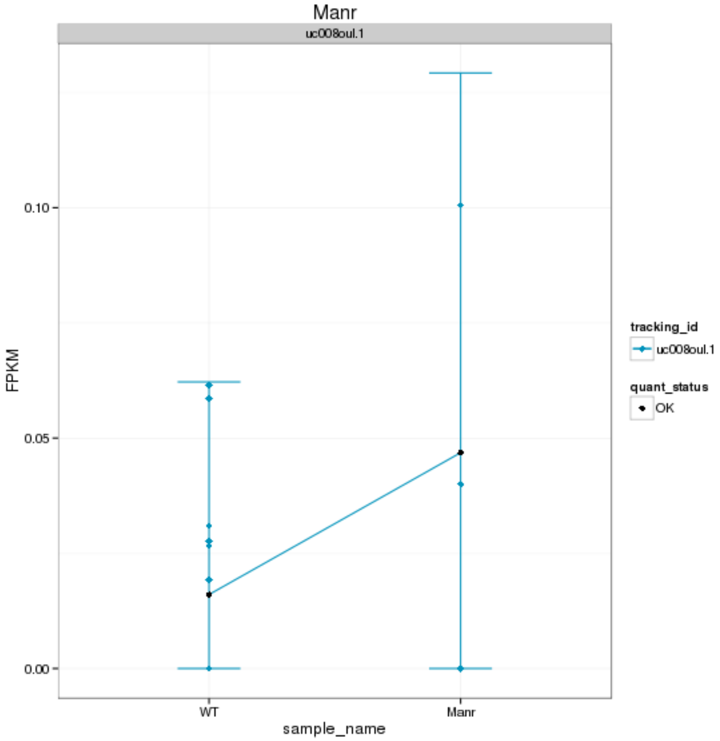


KO assessment

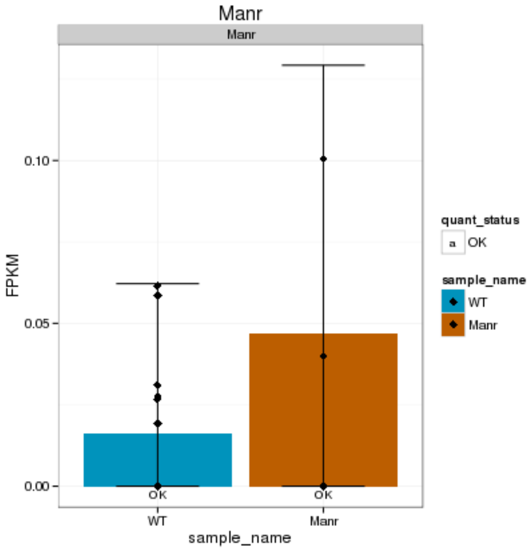
Endogenous lncRNA expression



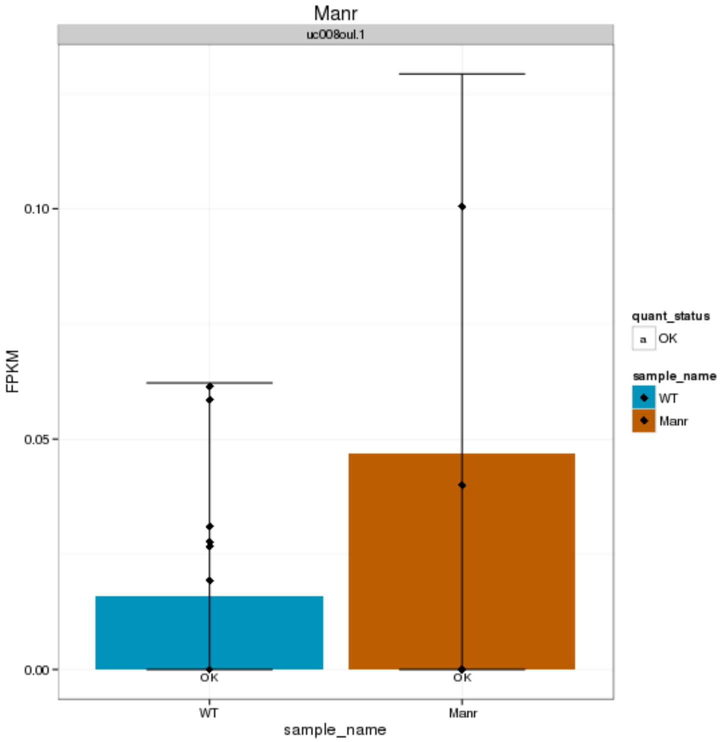
Endogenous expression of Manr isoforms:



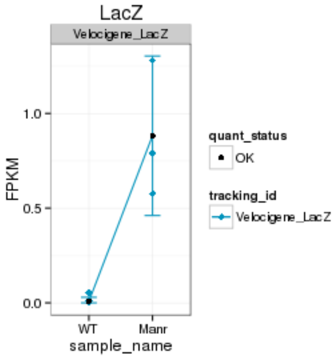
Barplot of gene expression:

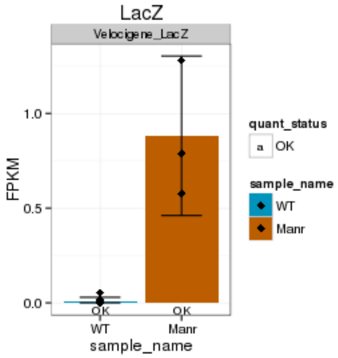


Barplot of isoform expression:



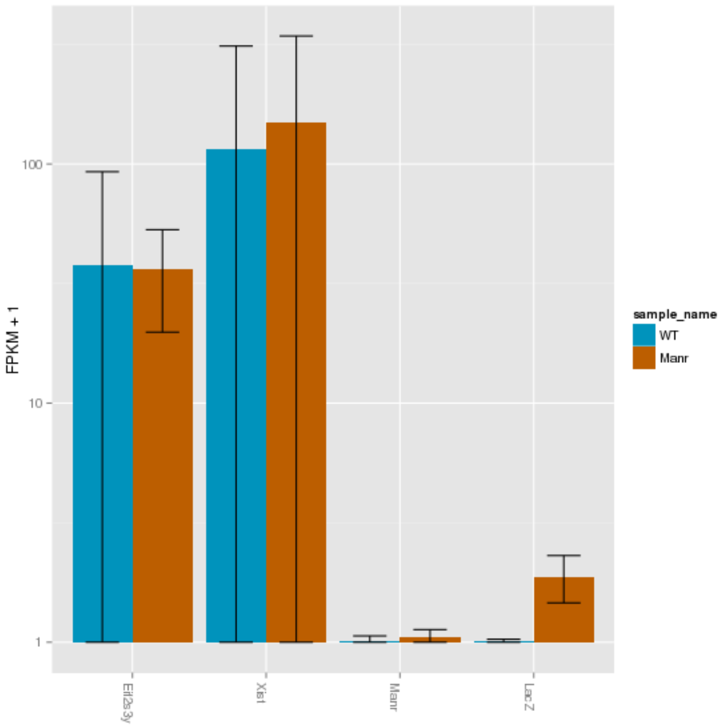
LacZ expression



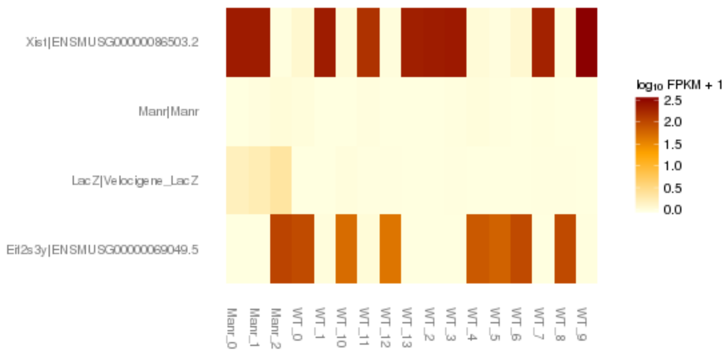


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

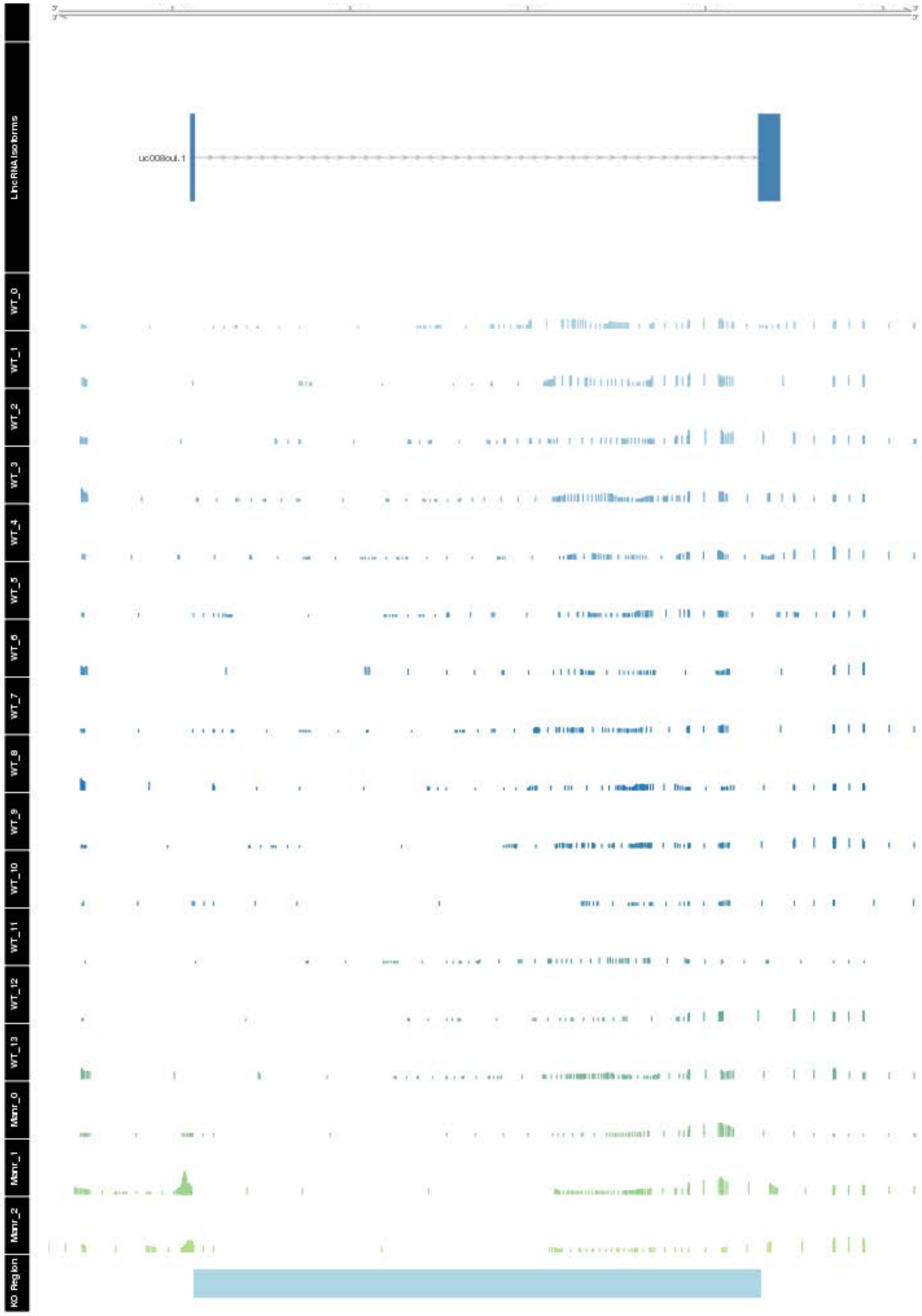
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


5'
3'
3'
5'
LincRNA Isoforms
uc008oul.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Mamr_0
Mamr_1
Mamr_2
KO Region

Differential Analysis

Differential Genes

There are 86 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Gabra2
2	Col1a1
3	Nfix
4	Phyhip
5	Cacna1e
6	Mef2c
7	Fam131c
8	Ptgds
9	Hivep2
10	Eef1a2
11	Ascl1
12	Adcy1
13	Doc2b
14	Clu
15	Sla
16	Shisa9
17	Lynx1
18	Mal2
19	Gnal
20	Snca
21	Sphkap
22	Cybrd1
23	Fabp5
24	Slc7a11
25	Hmgcs2
26	Rps3a1
27	Nr4a3
28	Tnc
29	Tal2
30	Hpca
31	Ppp2r2c
32	Fosl2
33	Rph3a
34	Eln
35	Dync1i1
36	Slc6a11
37	Dbx1

38 Hddc3
39 Mfge8
40 Thy1
41 Robo3
42 Cspg5
43 Ablim3
44 Rims3
45 Camkv
46 Mgll
47 Arhgap27
48 Sncb
49 Mid1
50 Nov
51 Vgf
52 Camk4
53 Pcsk1n
54 Grin3a
55 Gabbr2
56 Necab1
57 Abcb1a
58 Mpped1
59 Bend6
60 Hebp1
61 Tuba1c
62 Cnpy1
63 Prkce
64 Olig1
65 Nxph3
66 Mc4r
67 Tmem72
68 Grm5
69 Slc6a7
70 Gpr17
71 Hbb-bs
72 Aldh1a1
73 AI854703
74 6330403A02Rik
75 Vsnl1
76 Gabra5
77 Adap1
78 Hmga2
79 Rps12
80 Pcna-ps2

81 Rpl23

82 Wdfy1

83 Hbb-bt

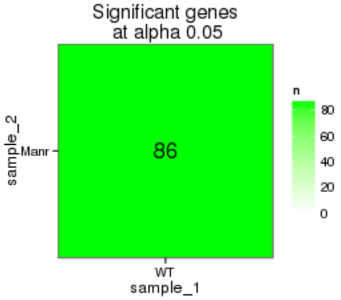
84 AI593442

85 Hs3st4

86 AA465934

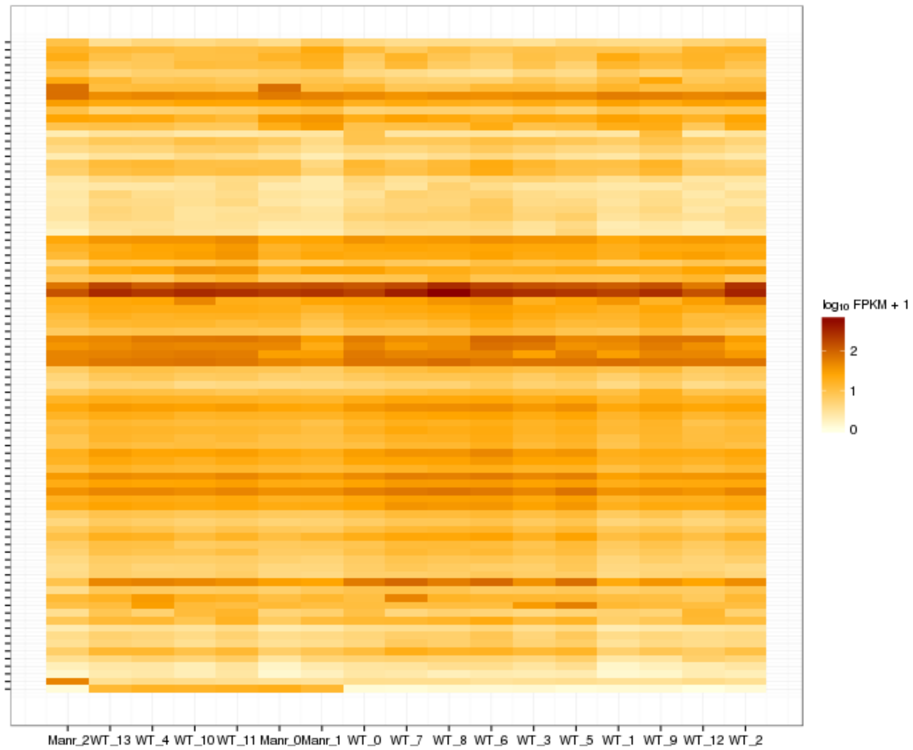
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

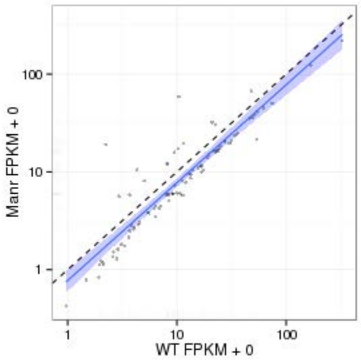


Significant genes with expression >50fpkm (any condition):(turned off)

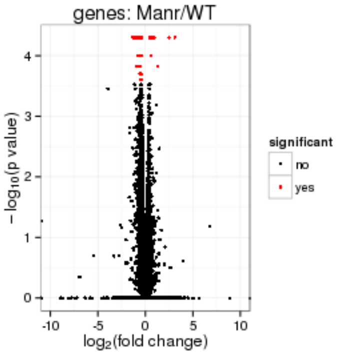
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

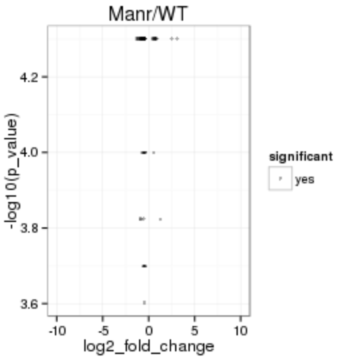
Scatter plot of significant genes only:



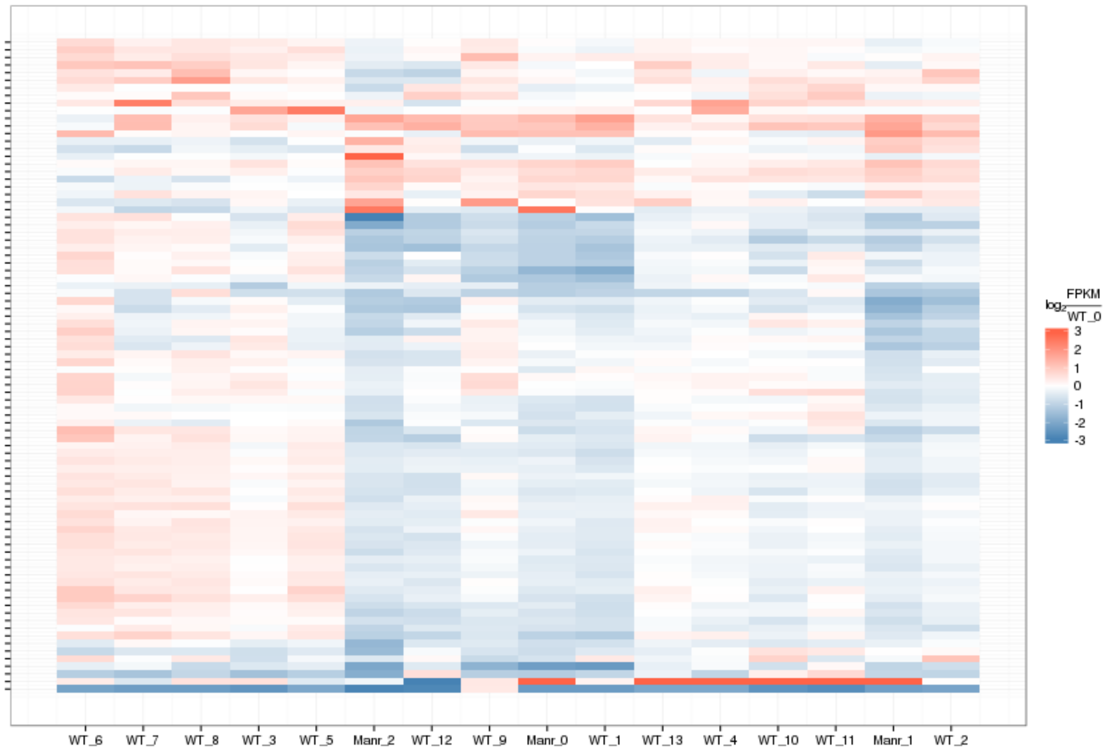
Volcano Plot



Volcano plot with significant genes only:



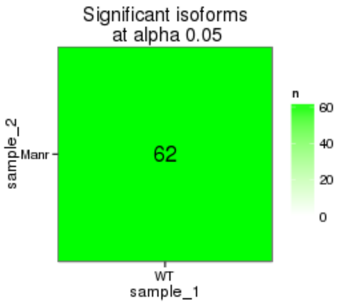
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:

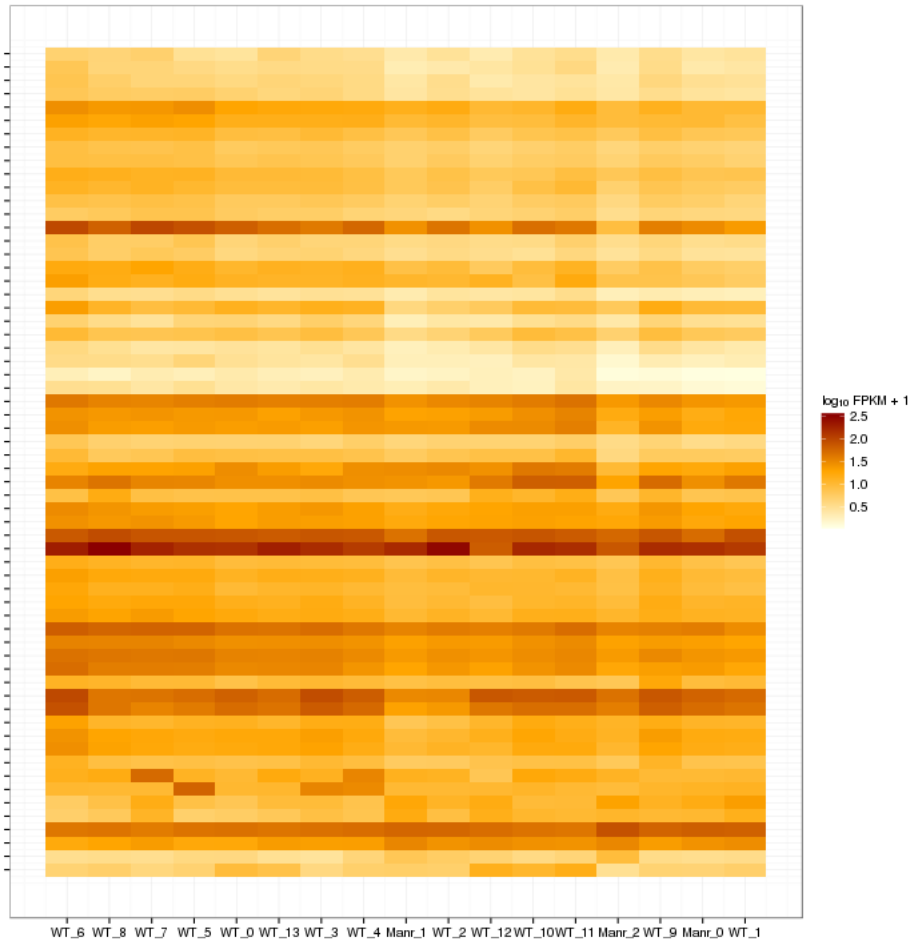


These isoforms are:

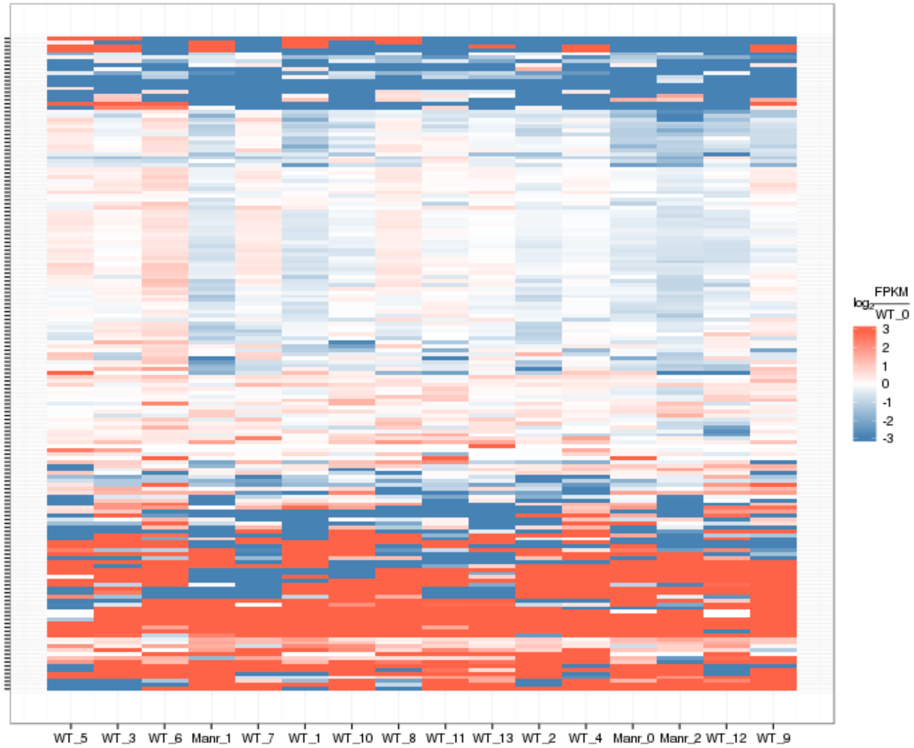
	isoAnnot$gene_short_name
1	Gabra2
2	Col1a1
3	Nfix
4	Cacna1e
5	Ndrg1
6	Fam131c
7	Ptgds
8	Hivep2
9	Eef1a2
10	Kitl
11	Ascl1
12	Adcy1
13	Doc2b
14	Gng4
15	Clu
16	Sla
17	Lynx1
18	Mal2
19	Fabp5
20	Slc7a11
21	Tnc
22	Tal2
23	Ppp2r2c
24	Fosl2
25	Eln
26	Slc6a11
27	Dbx1
28	Hddc3
29	Mfge8
30	Thy1
31	Cspg5
32	Camkv
33	Gas7
34	Sncb
35	Vgf
36	Pcsk1n
37	Gabbr2
38	Necab1
39	Mpped1
40	Bend6

41 Reln
42 Hebp1
43 Prkce
44 Hpcal4
45 Olig1
46 Nxph3
47 Mc4r
48 Tmem72
49 Grm5
50 Slc6a7
51 Gpr17
52 Aldh1a1
53 AI854703
54 6330403A02Rik
55 Vsnl1
56 Gabra5
57 Slc4a4
58 Opcml
59 Pcna-ps2
60 Hbb-bt
61 AI593442
62 Hs3st4

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

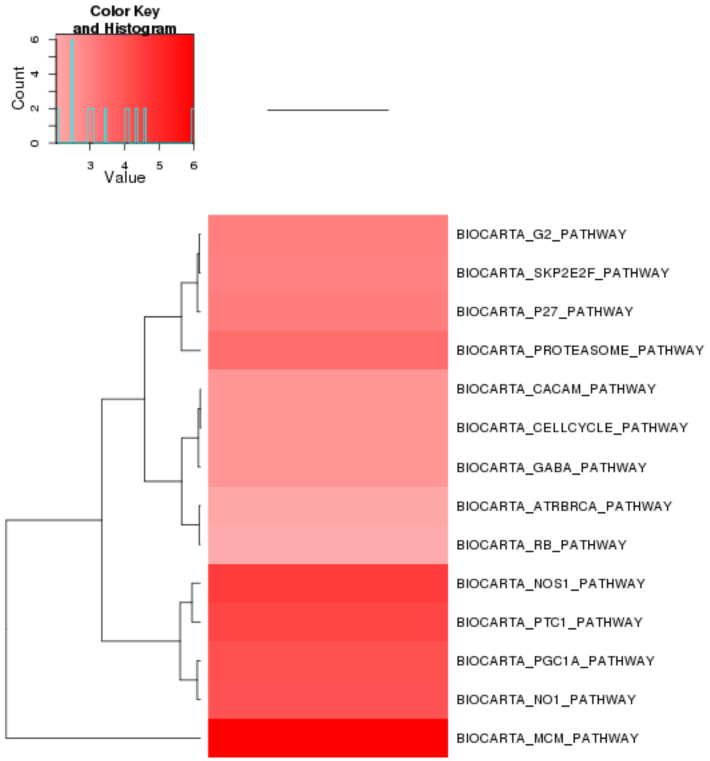
Gene/Pathway Analysis

GSEA

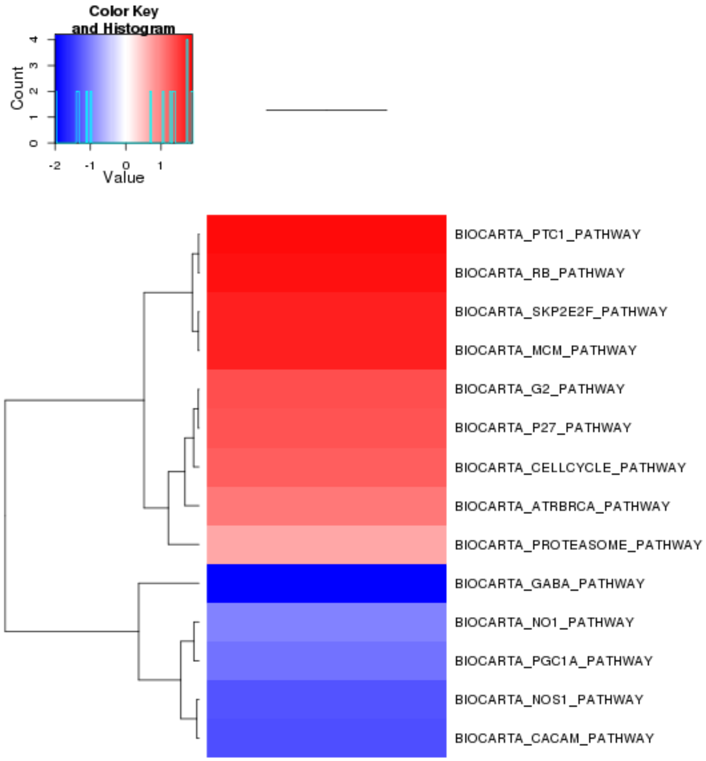
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:



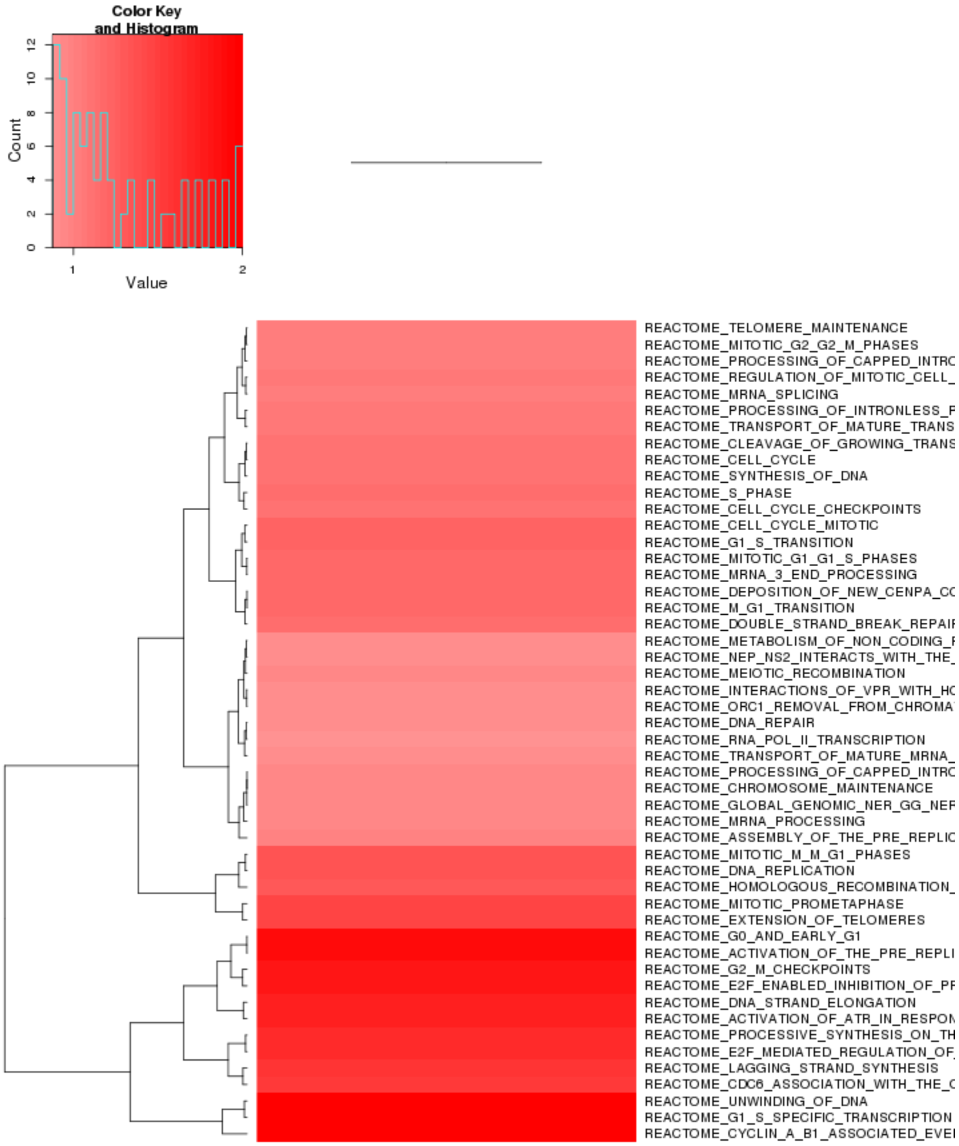
Biocarta zscore:



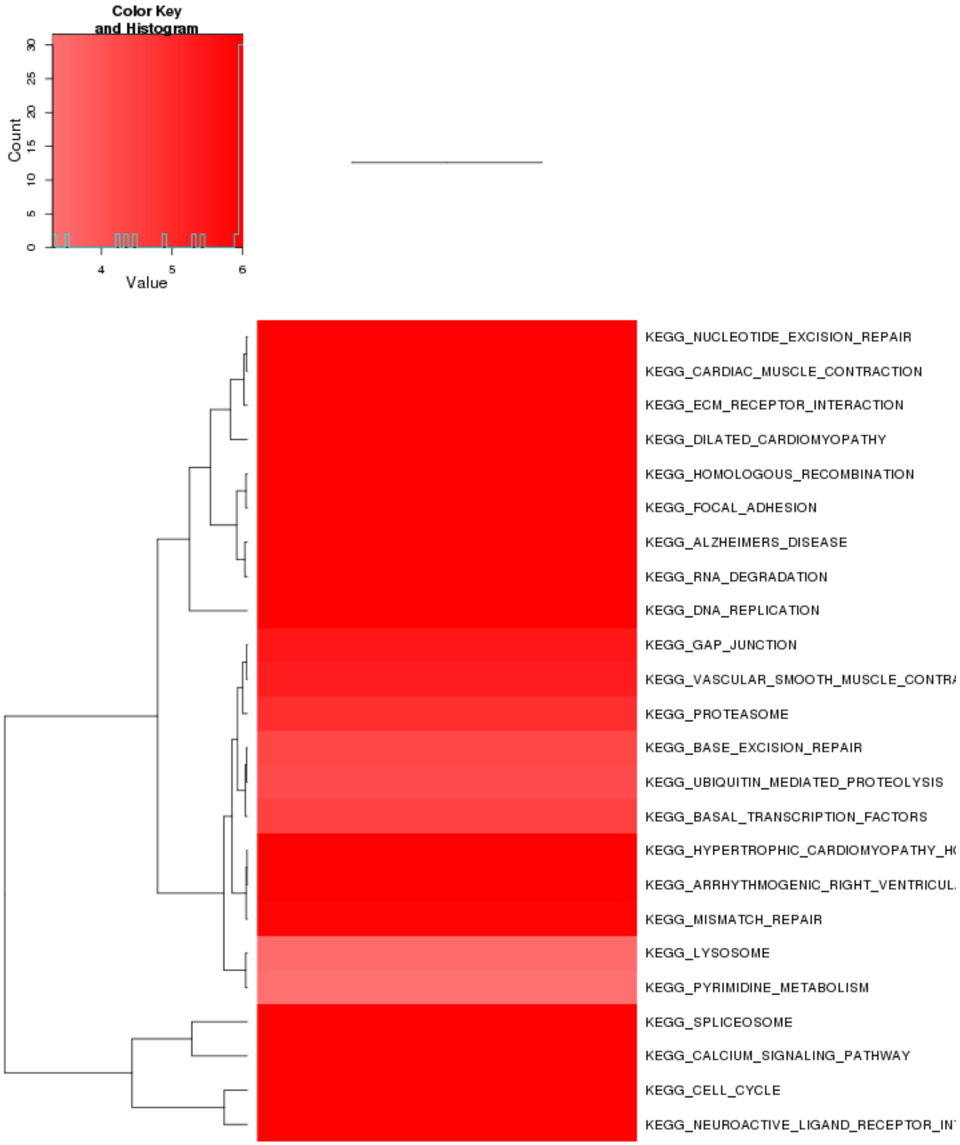
Reactome enrichment:

```
## Error: no locations are finite
```

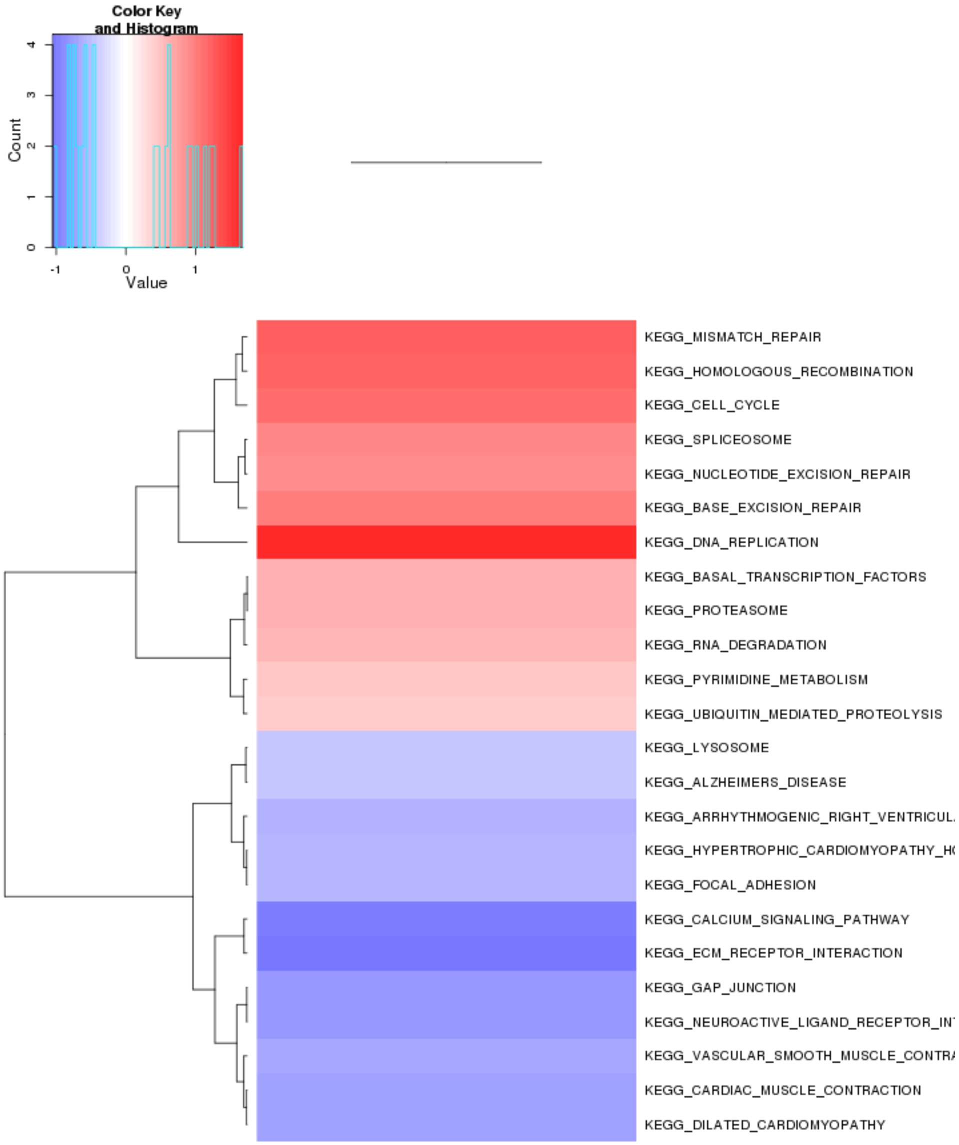
Reactome zscore:



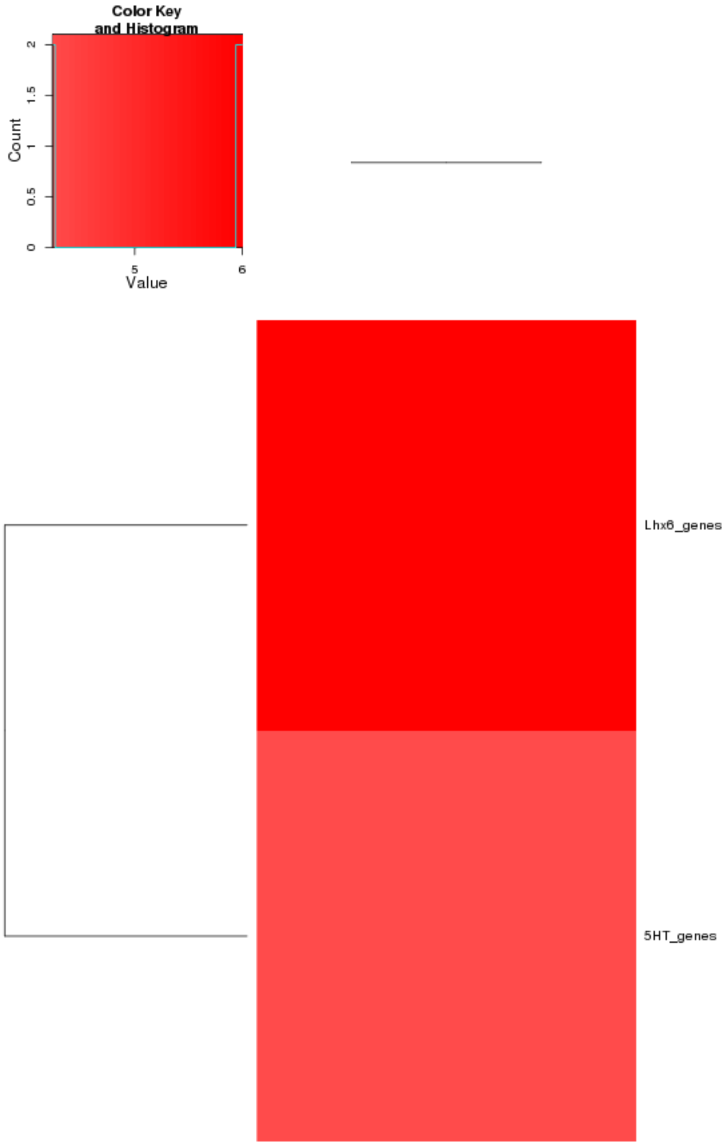
Kegg enrichment:


Color Key
and Histogram
Count
0
5
10
15
20
25
30
4
5
6
Value
KEGG_NUCLEOTIDE_EXCISION_REPAIR
KEGG_CARDIAC_MUSCLE_CONTRACTION
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_DILATED_CARDIOMYOPATHY
KEGG_HOMOLOGOUS_RECOMBINATION
KEGG_FOCAL_ADHESION
KEGG_ALZHEIMERS_DISEASE
KEGG_RNA_DEGRADATION
KEGG_DNA_REPLICATION
KEGG_GAP_JUNCTION
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTR
KEGG_PROTEASOME
KEGG_BASE_EXCISION_REPAIR
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS
KEGG_BASAL_TRANSCRIPTION_FACTORS
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_H
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICUL
KEGG_MISMATCH_REPAIR
KEGG_LYSOSOME
KEGG_PYRIMIDINE_METABOLISM
KEGG_SPLICEOSOME
KEGG_CALCIUM_SIGNALING_PATHWAY
KEGG_CELL_CYCLE
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_IN

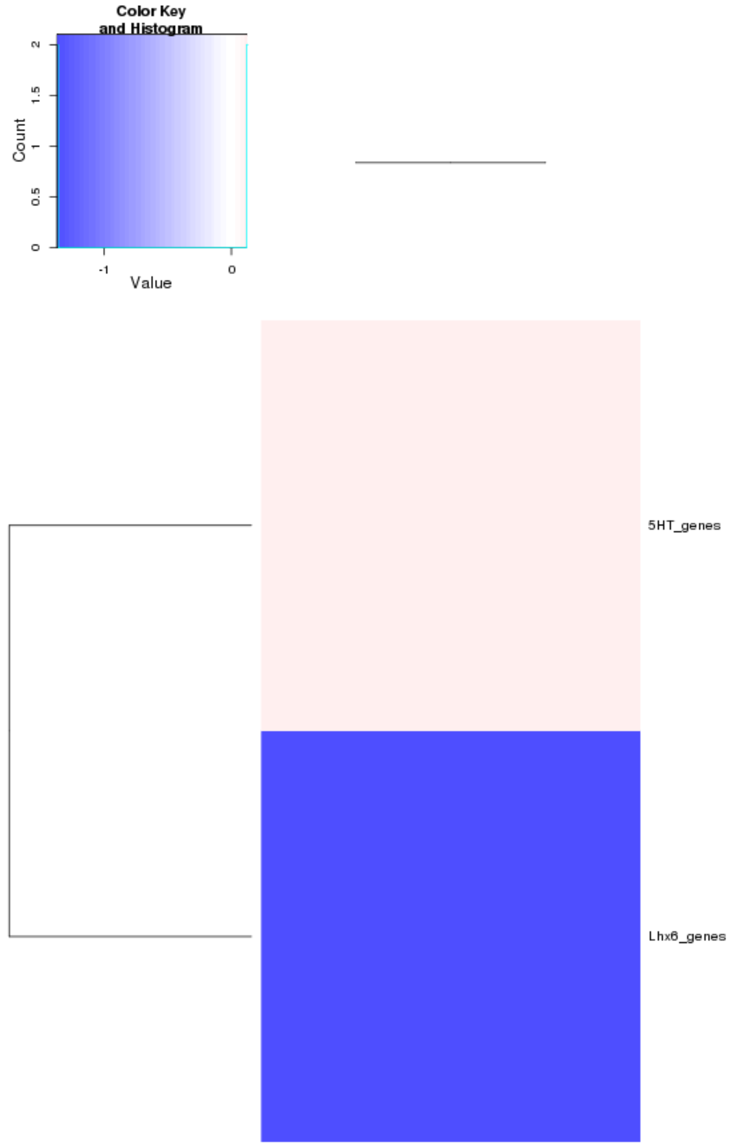
Kegg zscore:



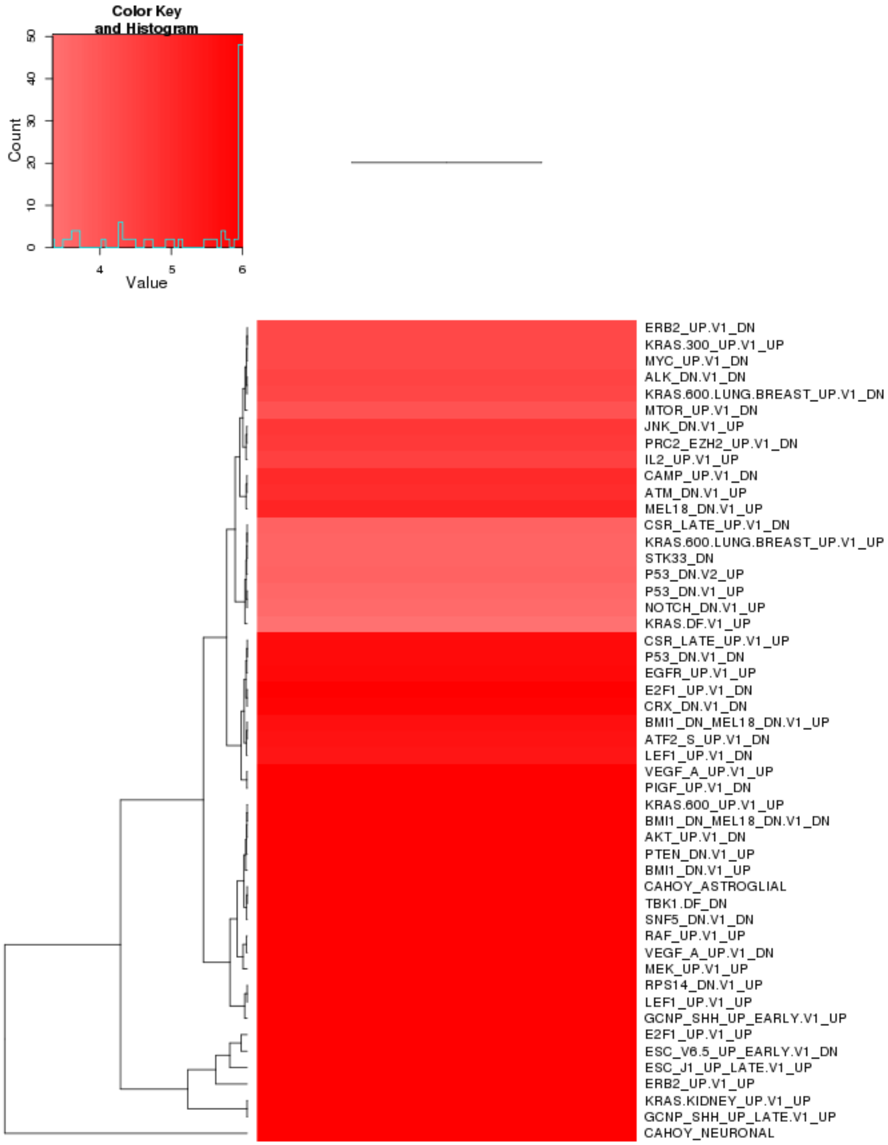
Interneuron enrichment:



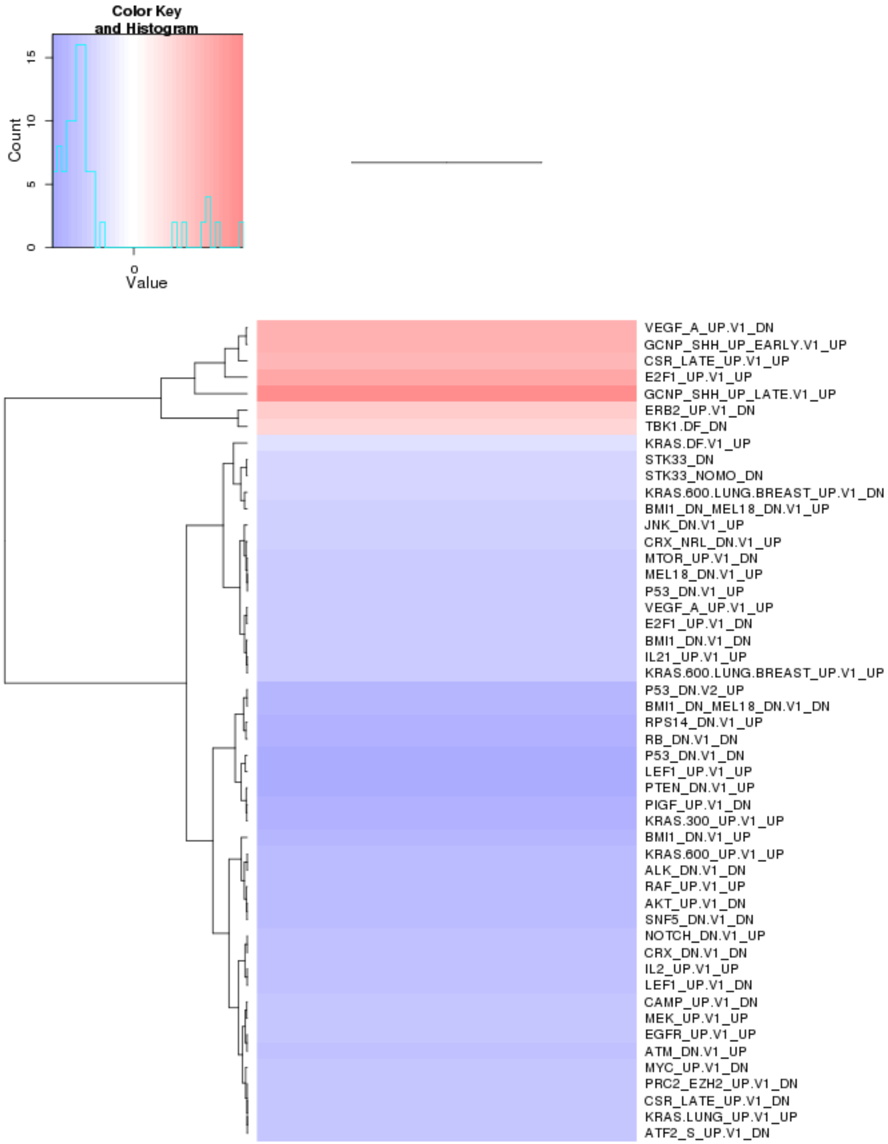
Interneuron zscore:



Oncogene enrichment:



Oncogene zscore:

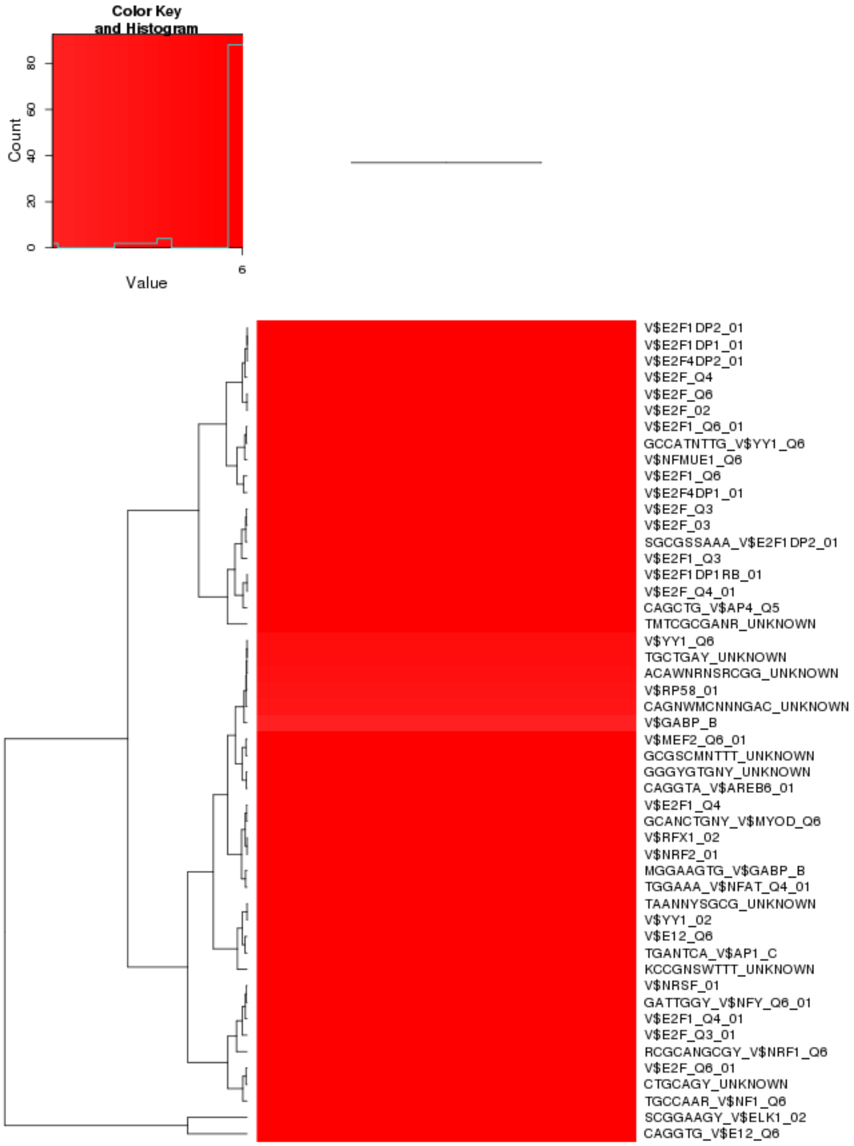


Immuno enrichment:

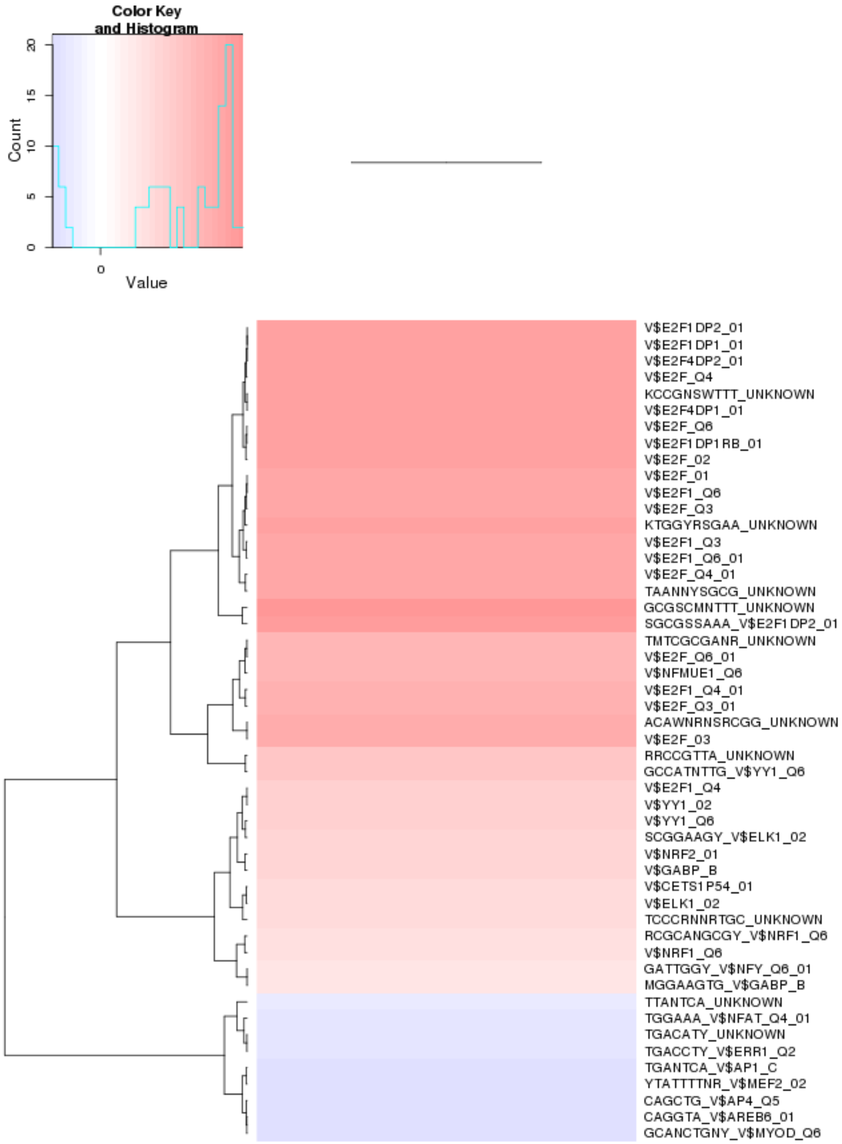
```
## Error: no locations are finite
```

Immuno zscore:

TF enrichment:


Color Key
and Histogram
Count
0
20
40
60
80
6
Value
V$E2F1DP2_01
V$E2F1DP1_01
V$E2F4DP2_01
V$E2F_Q4
V$E2F_Q6
V$E2F_02
V$E2F1_Q6_01
GCCATNTTG_V$YY1_Q6
V$NFMUE1_Q6
V$E2F1_Q6
V$E2F4DP1_01
V$E2F_Q3
V$E2F_03
SGCGSSAAA_V$E2F1DP2_01
V$E2F1_Q3
V$E2F1DP1RB_01
V$E2F_Q4_01
CAGCTG_V$AP4_Q5
TMTCGCGANR_UNKNOWN
V$YY1_Q6
TGCTGAY_UNKNOWN
ACAWNRNSRCGG_UNKNOWN
V$RP58_01
CAGNWMCNNNGAC_UNKNOWN
V$GABP_B
V$MEF2_Q6_01
GCGSCMNTTT_UNKNOWN
GGGYGTGNY_UNKNOWN
CAGGTA_V$AREB6_01
V$E2F1_Q4
GCANCTGNY_V$MYOD_Q6
V$RFX1_02
V$NRF2_01
MGGAAGTG_V$GABP_B
TGGAAA_V$NFAT_Q4_01
TAANNYSGCG_UNKNOWN
V$YY1_02
V$E12_Q6
TGANTCA_V$AP1_C
KCCGNSWTTT_UNKNOWN
V$NRSF_01
GATTGGY_V$NFY_Q6_01
V$E2F1_Q4_01
V$E2F_Q3_01
RCGCANGCGY_V$NRF1_Q6
V$E2F_Q6_01
CTGCAGY_UNKNOWN
TGCCAAR_V$NF1_Q6
SCGGAAGY_V$ELK1_02
CAGGTG_V$E12_Q6

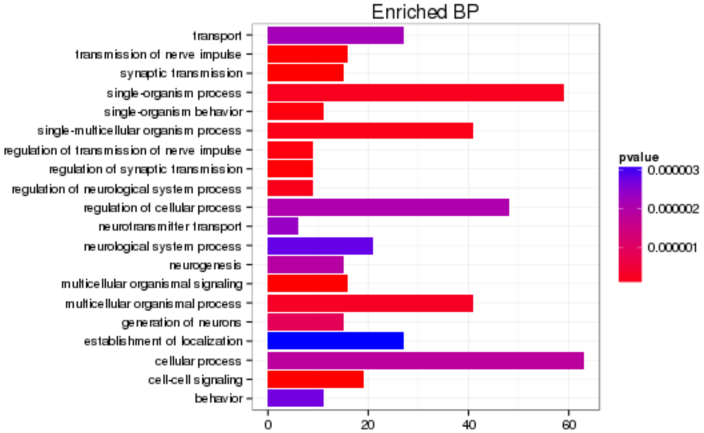
TF zscore:

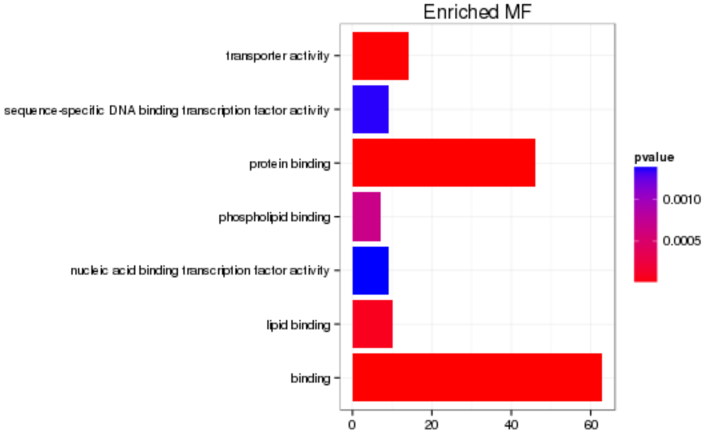


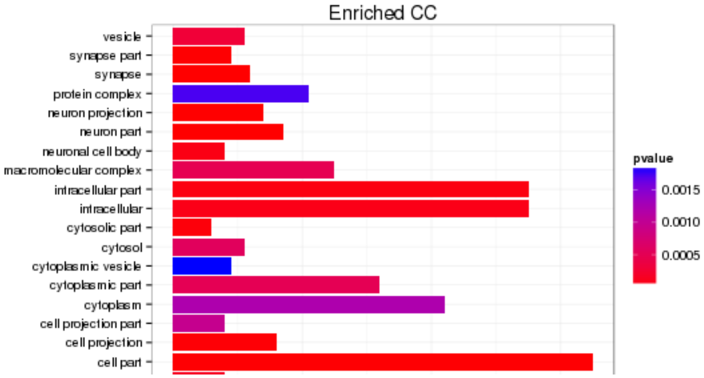
GO enrichment

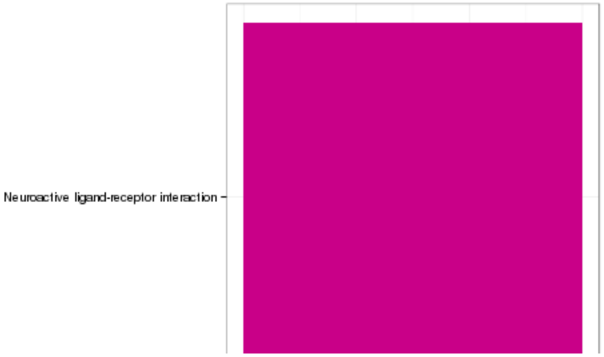
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

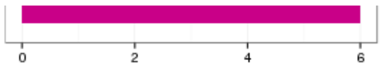
```
## [1] "ERROR: The estimated pi0 <= 0. Check that you have valid p-values or use another lambda method."
```

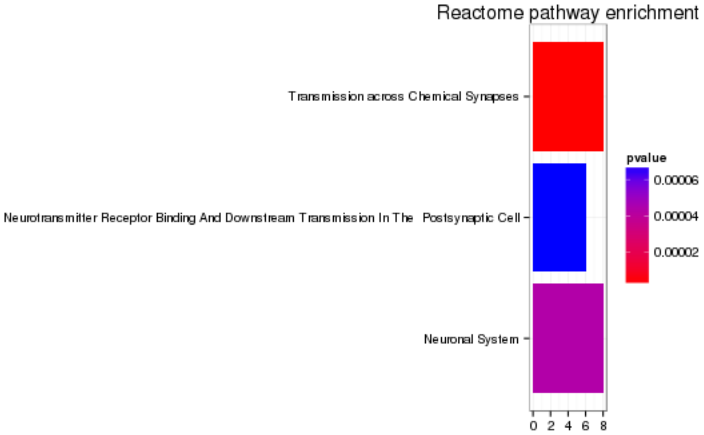

Enriched BP
transport
transmission of nerve impulse
synaptic transmission
single-organism process
single-organism behavior
single-multicellular organism process
regulation of transmission of nerve impulse
regulation of synaptic transmission
regulation of neurological system process
regulation of cellular process
neurotransmitter transport
neurological system process
neurogenesis
multicellular organismal signaling
multicellular organismal process
generation of neurons
establishment of localization
cellular process
cell-cell signaling
behavior
0
20
40
60
pvalue
0.000003
0.000002
0.000001


Enriched MF
transporter activity
sequence-specific DNA binding transcription factor activity
protein binding
phospholipid binding
nucleic acid binding transcription factor activity
lipid binding
binding
0
20
40
60
pvalue
0.0010
0.0005

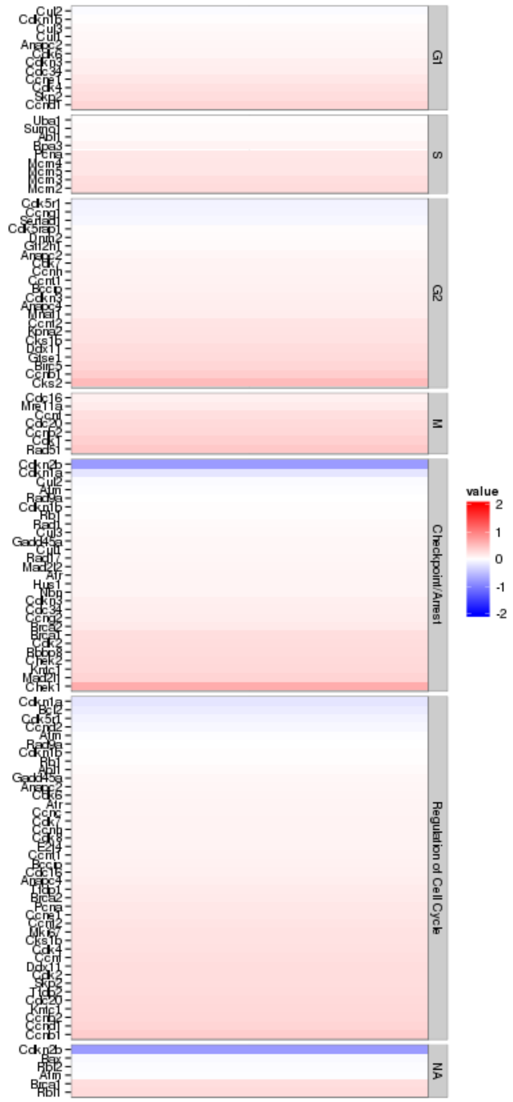

Enriched CC
vesicle
synapse part
synapse
protein complex
neuron projection
neuron part
neuronal cell body
macromolecular complex
intracellular part
intracellular
cytosolic part
cytosol
cytoplasmic vesicle
cytoplasmic part
cytoplasm
cell projection part
cell projection
cell part
pvalue
0.0015
0.0010
0.0005


Neuroactive ligand-receptor interaction

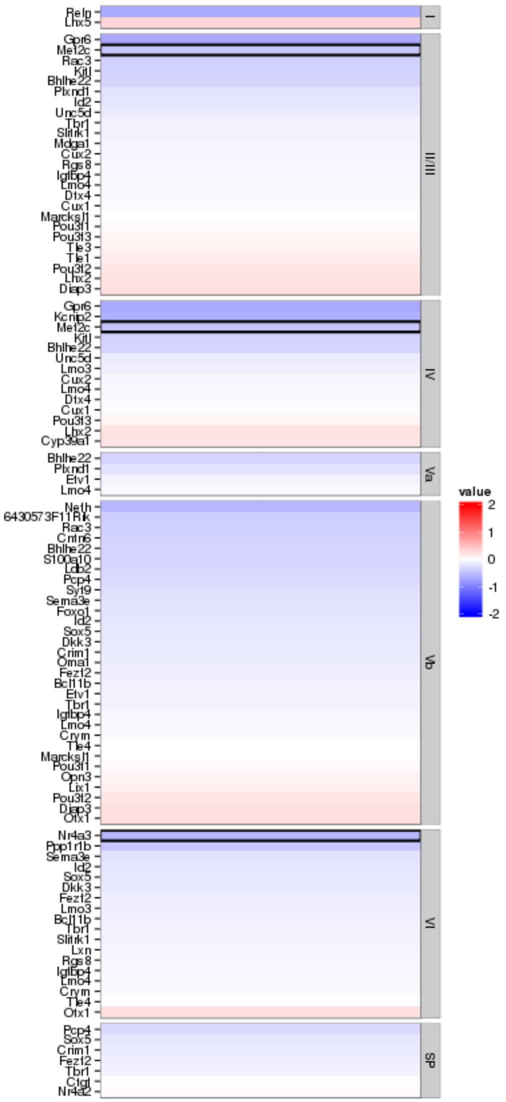



Reactome pathway enrichment

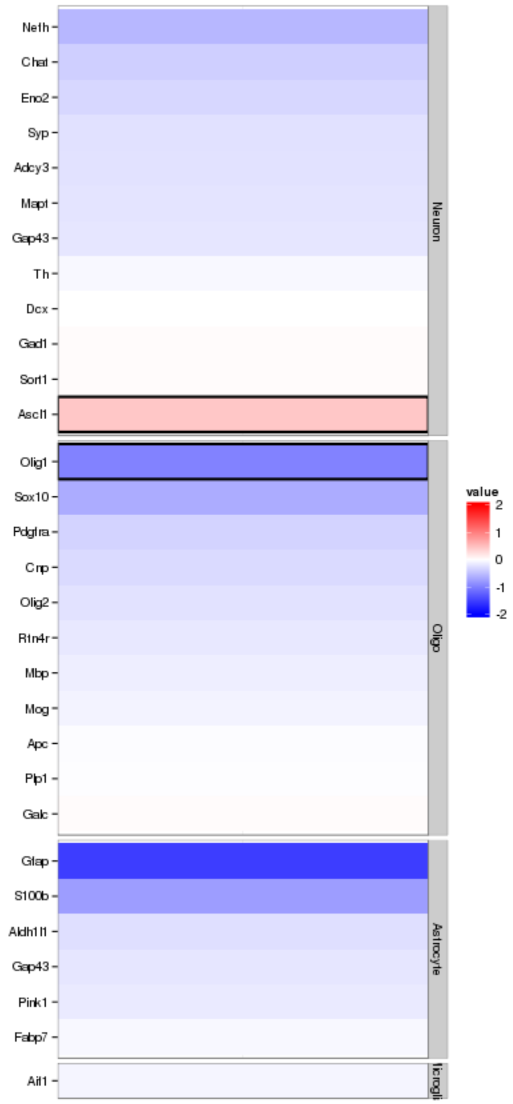
Enrichment or depletion for stage-specific cell cycle markers



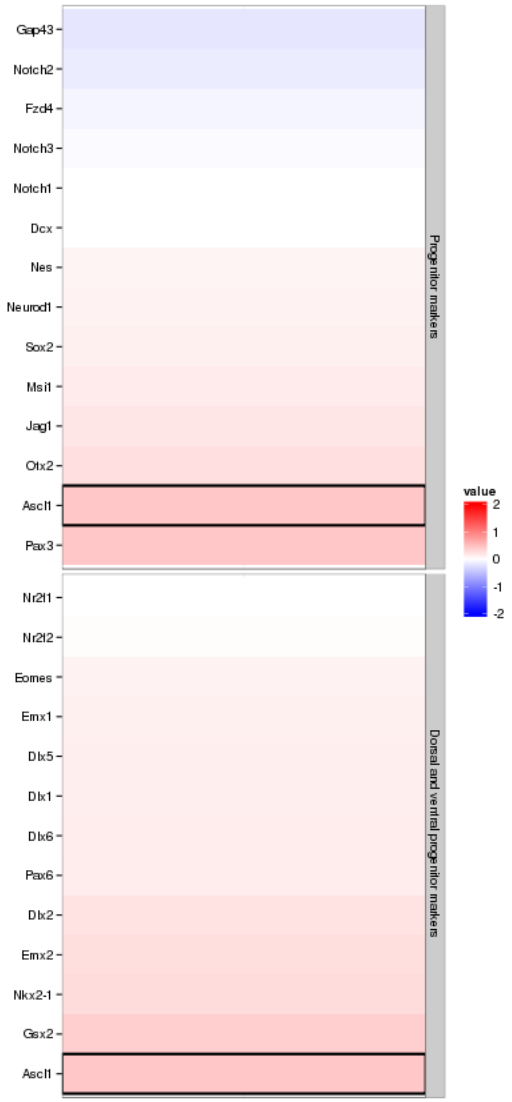
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



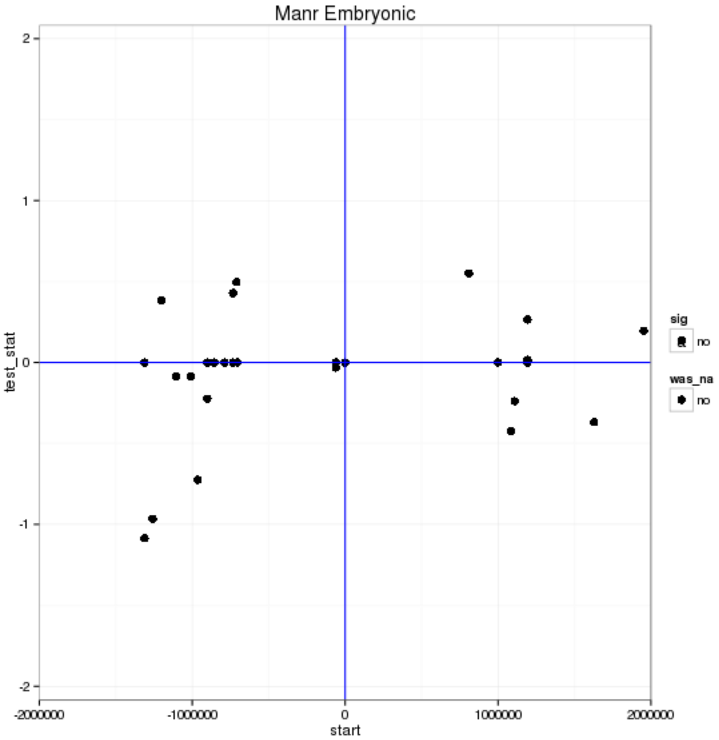
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15	JR751
16	JR772
17	JR788

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	31913100.00	1.28	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	31913100.00	1.11	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	31913100.00	1.24	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	31913100.00	1.30	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	31913100.00	1.21	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	31913100.00	0.90	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	31913100.00	0.98	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	31913100.00	0.93	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	31913100.00	0.87	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	31913100.00	0.97	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	31913100.00	0.82	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	31913100.00	0.81	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	31913100.00	0.69	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	31913100.00	1.23	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR751/abundances.cxb	Manr	0	Manr_0	33259800.00	31913100.00	1.03	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR772/abundances.cxb	Manr	1	Manr_1	39063700.00	31913100.00	1.25	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR788/abundances.cxb	Manr	2	Manr_2	23795600.00	31913100.00	0.74	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1   
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##                                                                                                                                                                
## 1 cuffdiff -p 10 -L WT,Manr -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Manr_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/
## 2
## 3
## 4
## 5
```

Peril KO vs WT (Adult)

This file shows the wt-v-ko comparison for Peril.

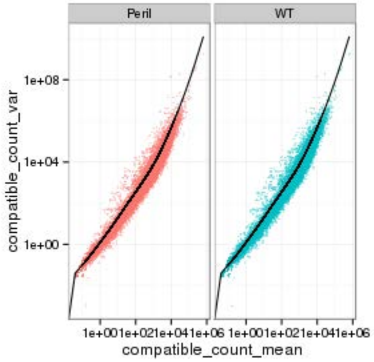
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

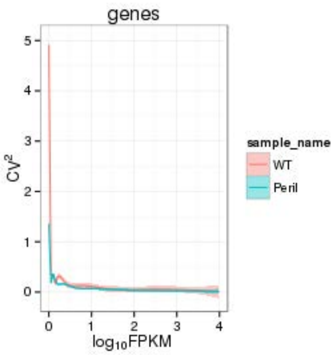
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



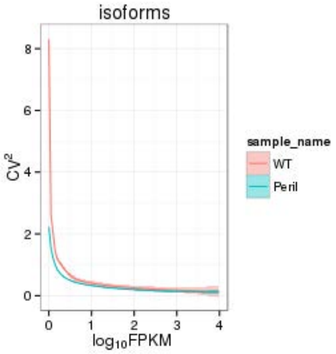
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

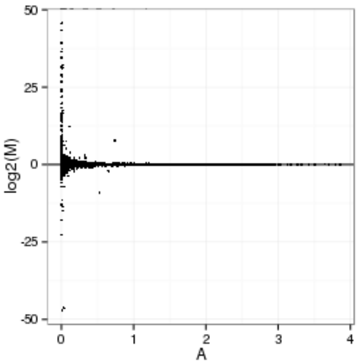
Genes:



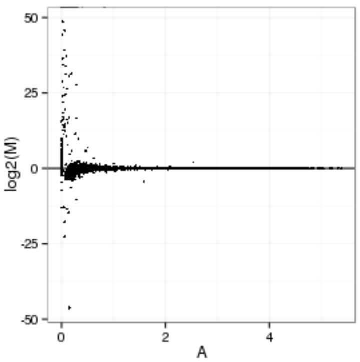
Isoforms:



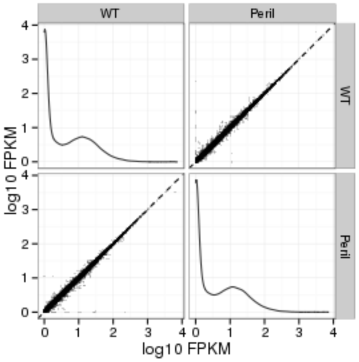
MvA plot



MvA plot counts



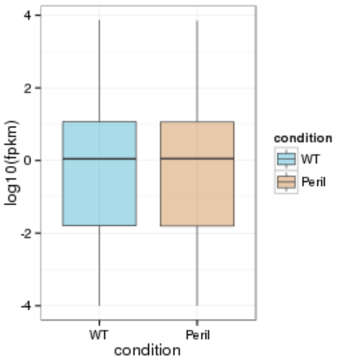
Scatterplot matrix



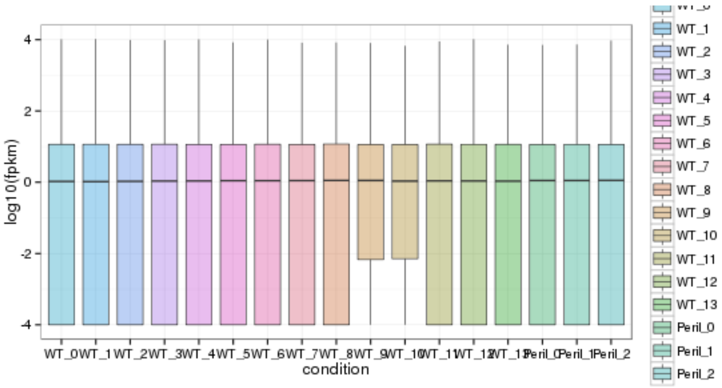
Distributions

Boxplots

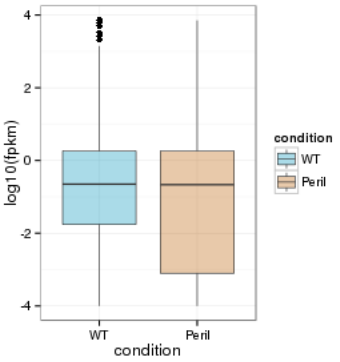
Boxplot (genes)



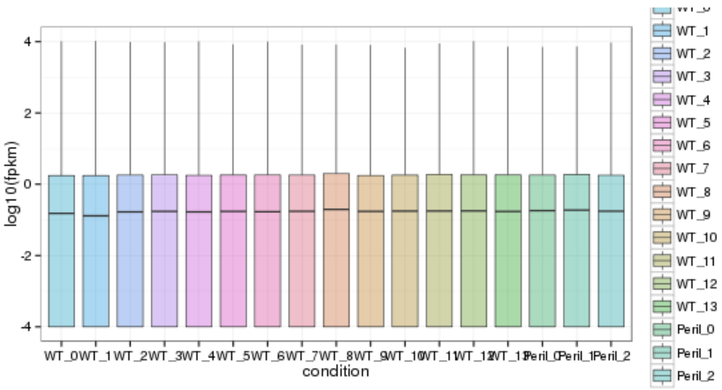
Boxplot (genes, replicates)



Boxplot (isoforms)

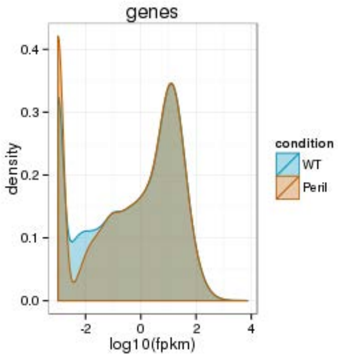


Boxplot (isoforms, replicates)

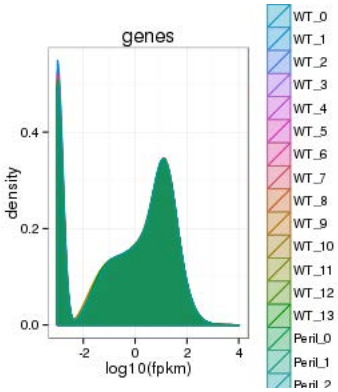


Density

Density (genes)

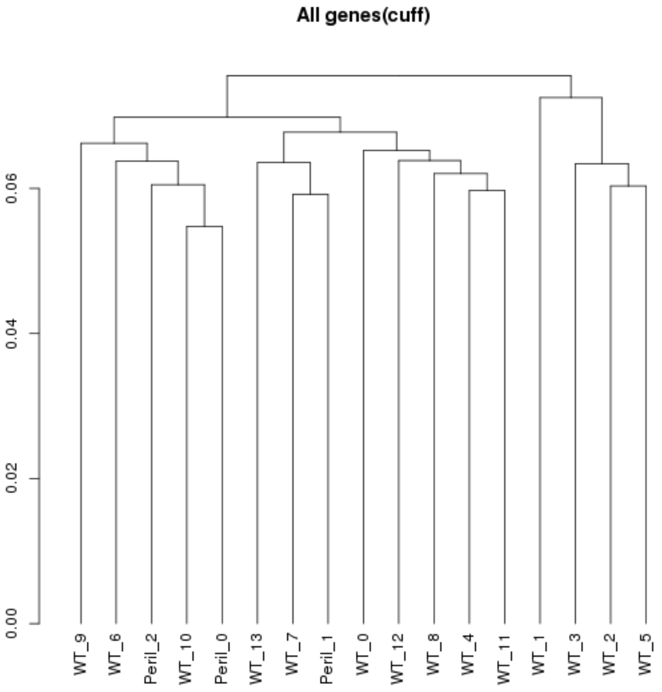


Density (genes, replicates)



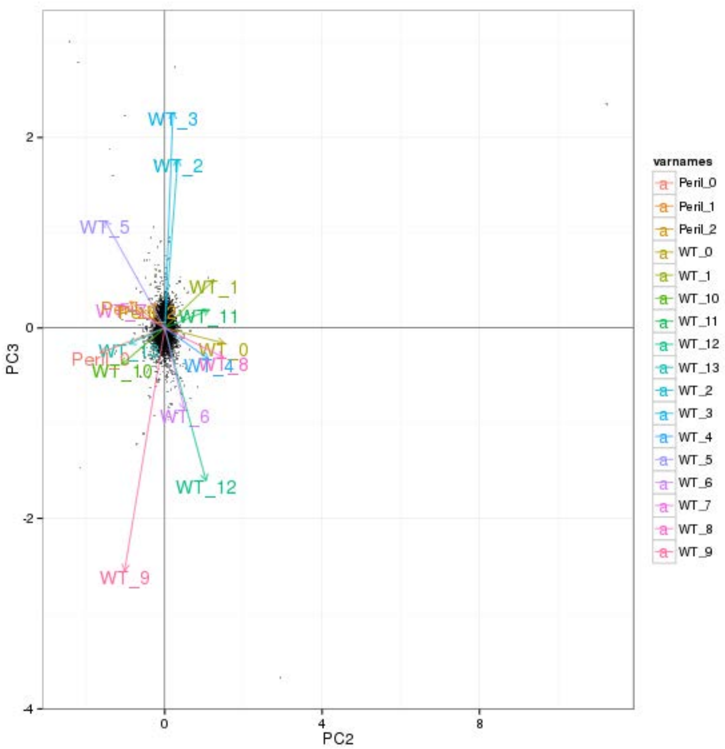
Clustering

Replicate Clusters

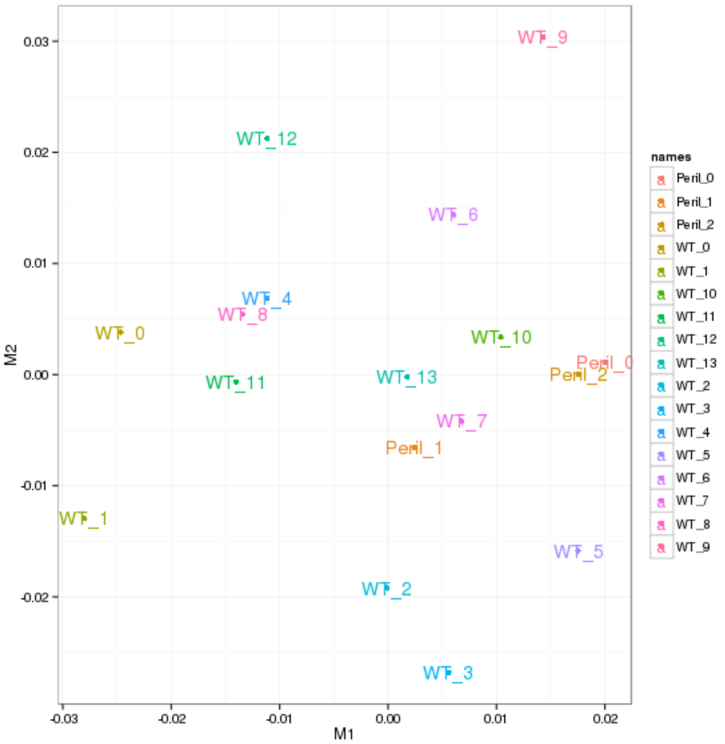


```
## NULL
```

PCA (genes)

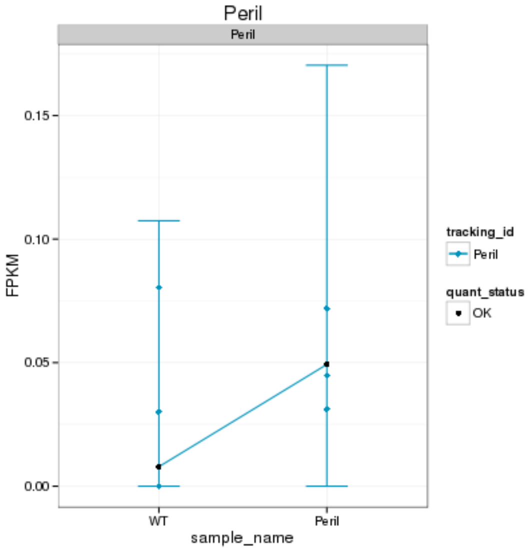

WT_3
WT_2
WT_5
WT_1
WT_11
WT_0
WT_4
WT_8
Peril_0
WT_10
WT_6
WT_12
WT_9
2
0
-2
-4
0
4
8
PC2
PC3
varnames
Peril_0
Peril_1
Peril_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

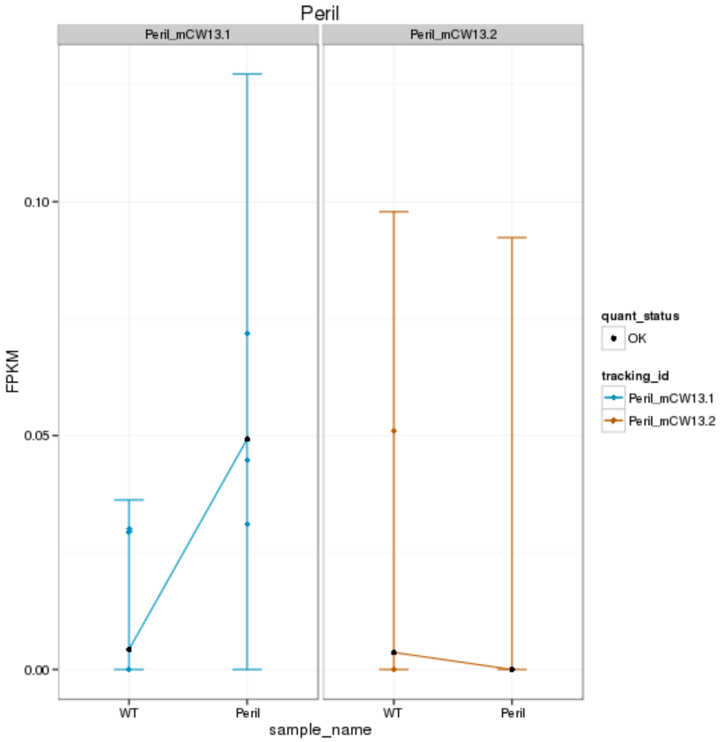


KO assessment

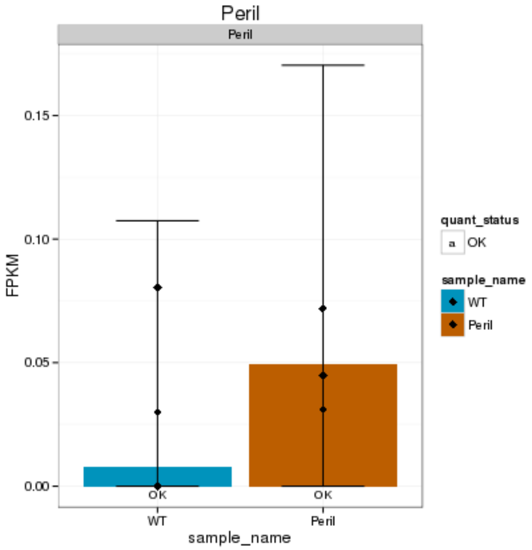
Endogenous lncRNA expression



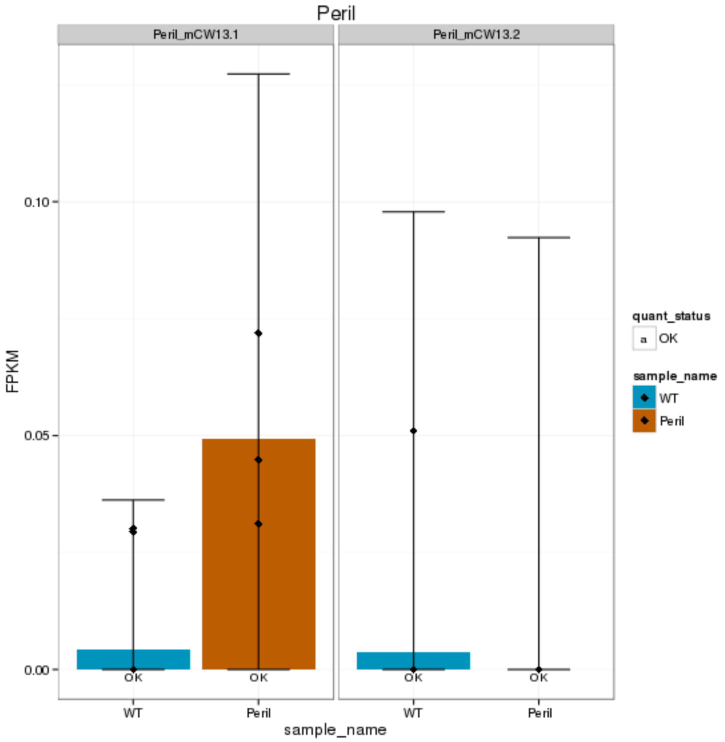
Endogenous expression of Peril isoforms:



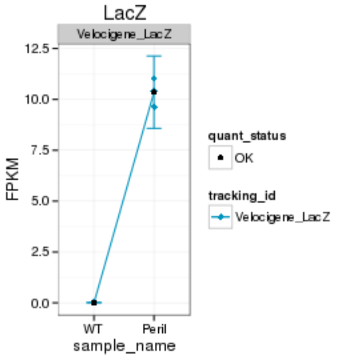
Barplot of gene expression:

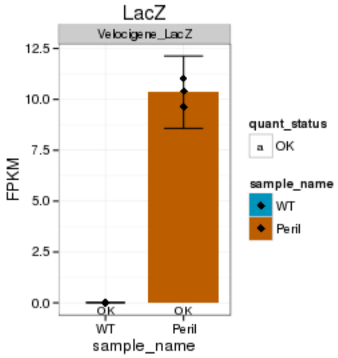


Barplot of isoform expression:



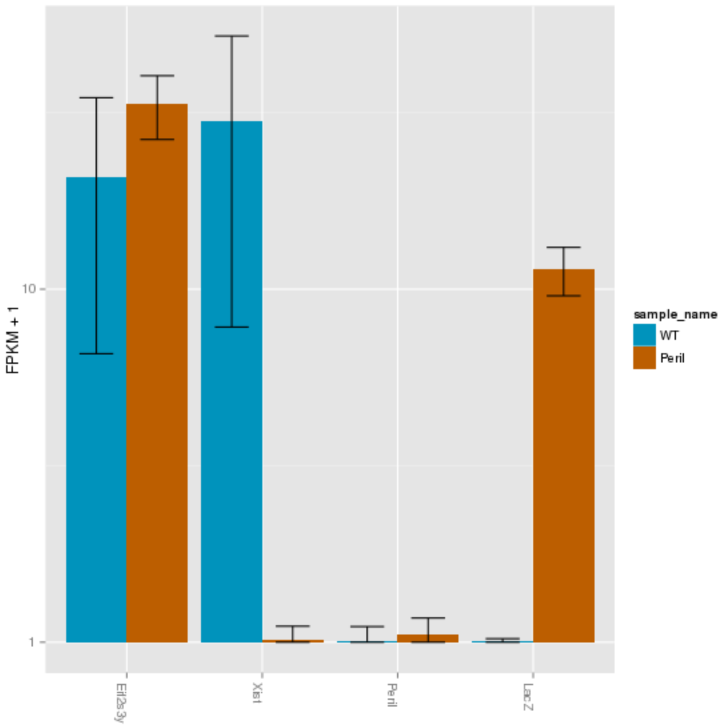
LacZ expression



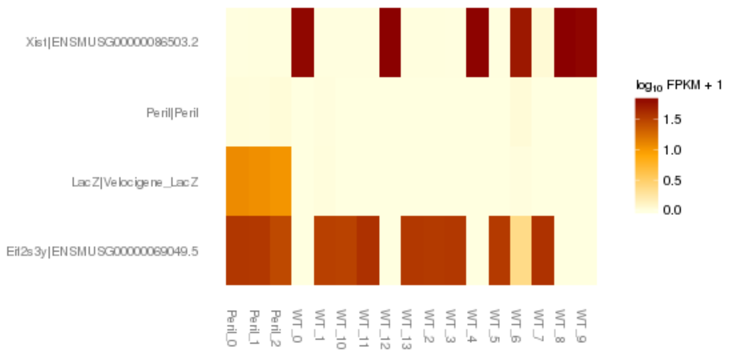


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

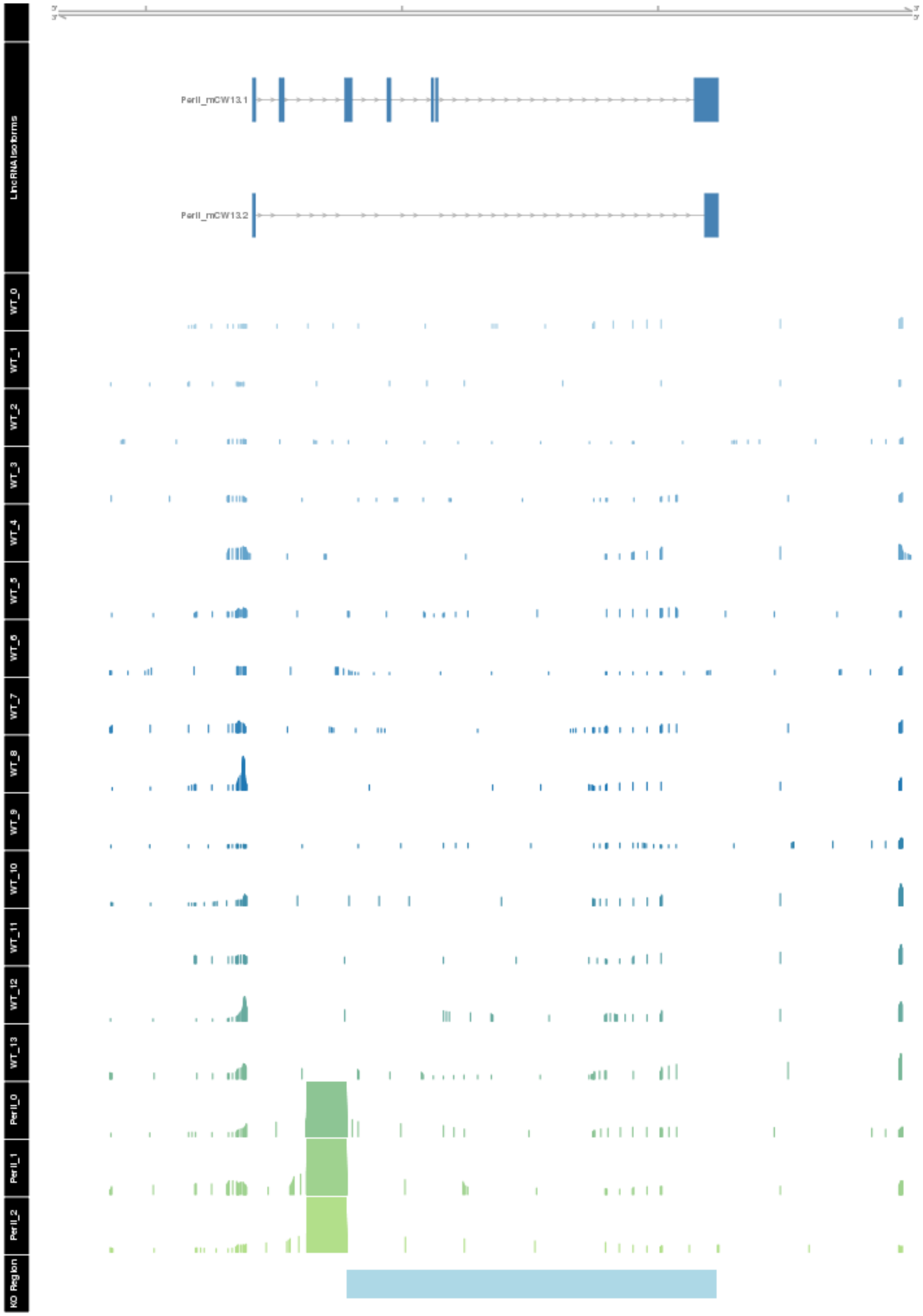
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization



5'
3'
3'
5'
LincRNA Isoforms
Peril_mCW13.1
Peril_mCW13.2
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Peril_0
Peril_1
Peril_2
KO Region

Differential Analysis

Differential Genes

There are 215 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Wnt9a
2	Gabra2
3	Sox9
4	Mmp14
5	Chordc1
6	Plin4
7	Arrdc2
8	Klf4
9	Calr
10	Hif3a
11	9330159F19Rik
12	Nes
13	Epha2
14	Lrrc8a
15	Homer1
16	Bcl2l1
17	Dio2
18	Mertk
19	Camk1g
20	Sdc4
21	Ada
22	Etnppl
23	P4ha1
24	Arid5b
25	Sgk1
26	Gm872
27	Ndufa12
28	Timp3
29	Pttg1
30	Btg2
31	Gatsl3
32	Xbp1
33	Pdia6
34	Fam20a
35	Adi1
36	Camkk1
37	Per1

38 Nfkbia
39 Serpina3n
40 Zfp36l1
41 Fos
42 Pcsk1
43 Fam107a
44 Dnajc3
45 Fzd6
46 Myh9
47 Slc38a2
48 Bcl6
49 Arc
50 Sdf2l1
51 Arhgap31
52 Ifnar1
53 Cdkn1a
54 Creld2
55 Tnfrsf12a
56 Xdh
57 Tekt4
58 Dusp1
59 Fkbp5
60 Spry4
61 Pdgfrb
62 Atp10a
63 Kdm5c
64 D3Ertd751e
65 Pdia4
66 Paqr8
67 Slc40a1
68 Pfkfb3
69 Lcn2
70 Hspa5
71 Spred1
72 Fam83d
73 Anxa5
74 Exosc9
75 Schip1
76 F3
77 Trp53inp1
78 Nr4a3
79 Slc2a1
80 Mfsd2a

81 Tinagl1
82 Errfi1
83 Fosl2
84 Aff1
85 Rasgef1b
86 Lfng
87 Hsph1
88 Klf15
89 Slc6a6
90 Bhlhe40
91 Adipor2
92 Emp1
93 Pglyrp1
94 Rhpn2
95 Hddc3
96 Sult1a1
97 Lyve1
98 Polr3e
99 Tsc22d3
100 Dusp4
101 Plat
102 Galnt7
103 Gpt2
104 Mt2
105 Herpud1
106 Ldlr
107 Eomes
108 Slc16a1
109 Tbc1d4
110 Galnt9
111 Egr3
112 Tlr13
113 Klf9
114 Trim36
115 Trim59
116 Pla2g3
117 Prr7
118 Nostrin
119 Dusp5
120 Arl4d
121 Lars2
122 Adrb1
123 Dnajb5

124 Micall2
125 Anln
126 Psenen
127 Mxd4
128 Tob1
129 Avp
130 Smim3
131 Bend3
132 Txnip
133 Irs2
134 Eltd1
135 Pcsk1n
136 Tnfsf10
137 C1qtnf4
138 Rps19
139 Cables1
140 Nkx6-2
141 Mup4
142 Cldn5
143 Pkp2
144 Sgsm1
145 Jhdm1d
146 Maff
147 Id1
148 Tuba1c
149 Gjc2
150 1700048O20Rik
151 Nxpe4
152 Ctla2a
153 Cirbp

154 Zfp36l2
155 Npas4
156 Plaur
157 Fat4
158 Marcksl1
159 Stbd1
160 Hes5
161 Bdnf
162 Mex3d
163 Dact2
164 Pdp1
165 Cdc42ep1
166 Rasd1

167 Opalin
168 Ppp1r3g
169 Plekho2
170 Islr2
171 Klf13
172 Jun
173 Junb
174 Tnfaip6
175 Ier2
176 Mat2a
177 1810037I17Rik
178 A930005H10Rik
179 Mettl7a1
180 Per2
181 1810011O10Rik
182 Kdm5d
183 Mex3b
184 Tpm3-rs7
185 Rpl30
186 Gm5506
187 Sclt1
188 Alox5ap
189 Zbtb40
190 Rps7
191 Cox5b
192 Rpl34
193 Kdr
194 Aldoart2
195 mt-Co1
196 Zbtb16
197 Zfp810
198 Ddx3y
199 Jund
200 Egr4
201 Gm7292
202 Plekhf1
203 B3galt5
204 Fjx1
205 Rprm
206 Ly6a
207 Ly6c1
208 Gm11273

209 Xist

210 Slc5a3

211 A930033H14Rik

212 Apold1

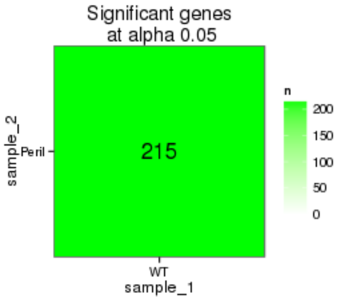
213 Hspa1b

214 AA465934

215 Gm7094

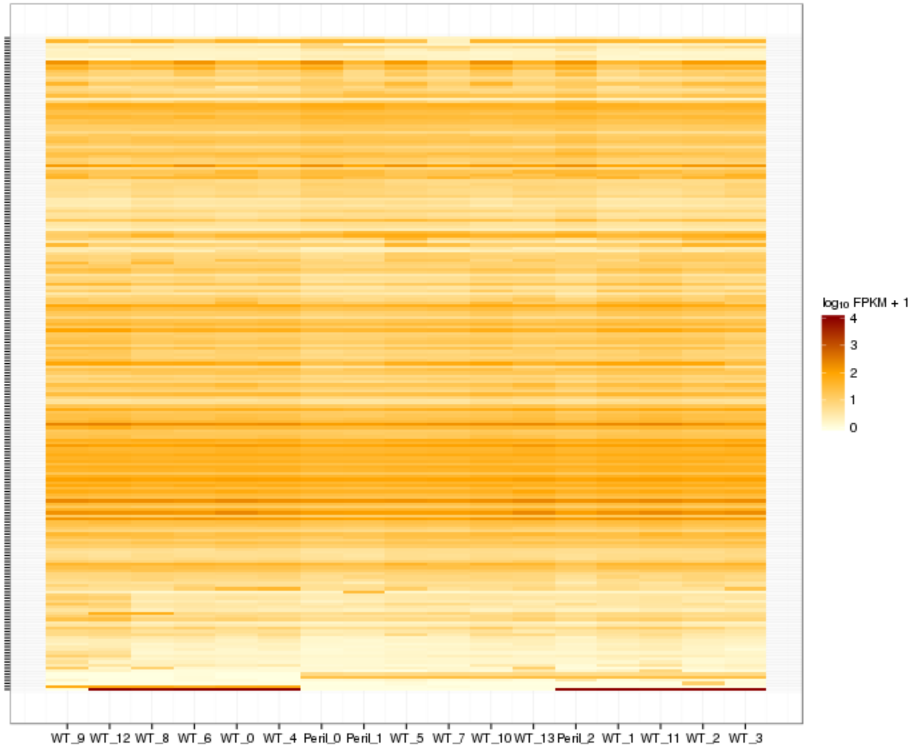
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

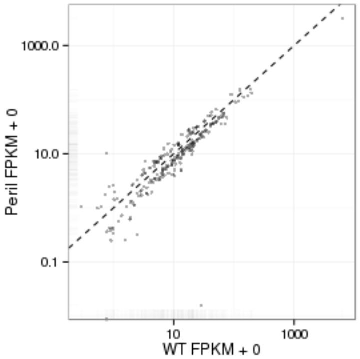


Significant genes with expression >50fpkm (any condition):(turned off)

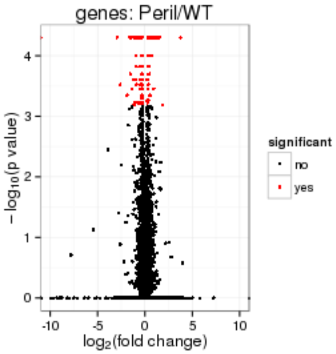
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

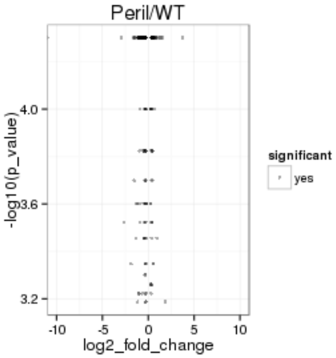
Scatter plot of significant genes only:



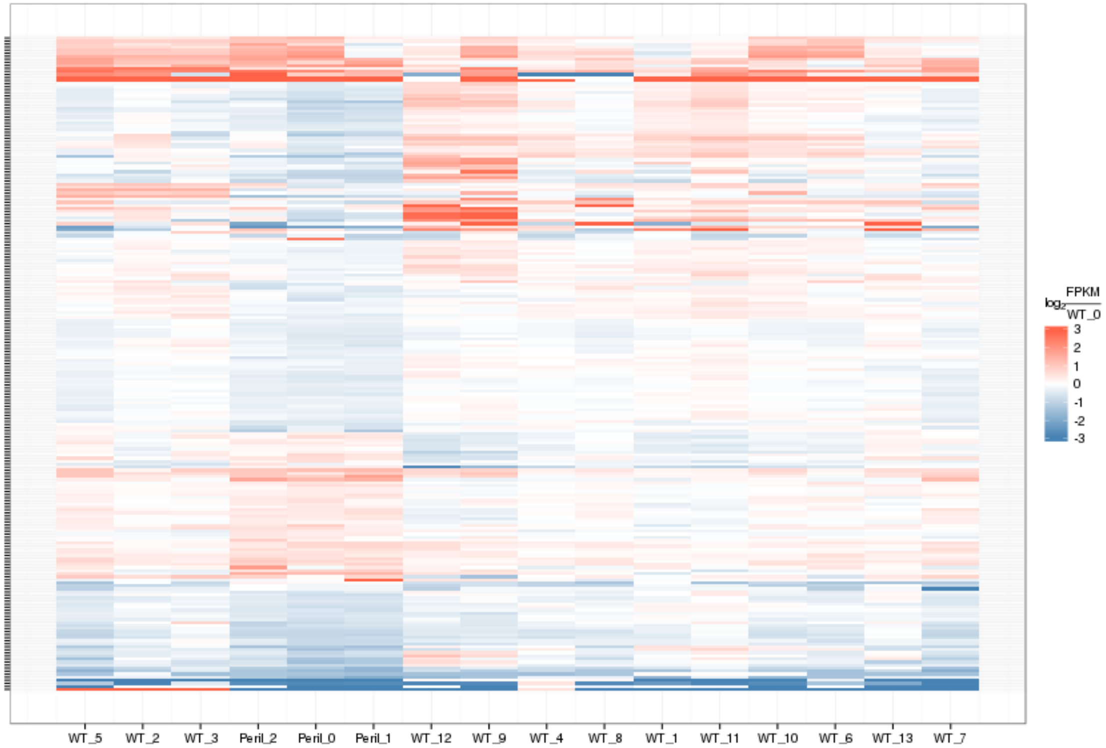
Volcano Plot



Volcano plot with significant genes only:



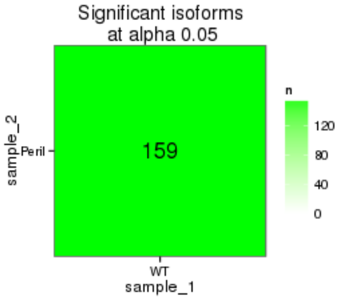
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

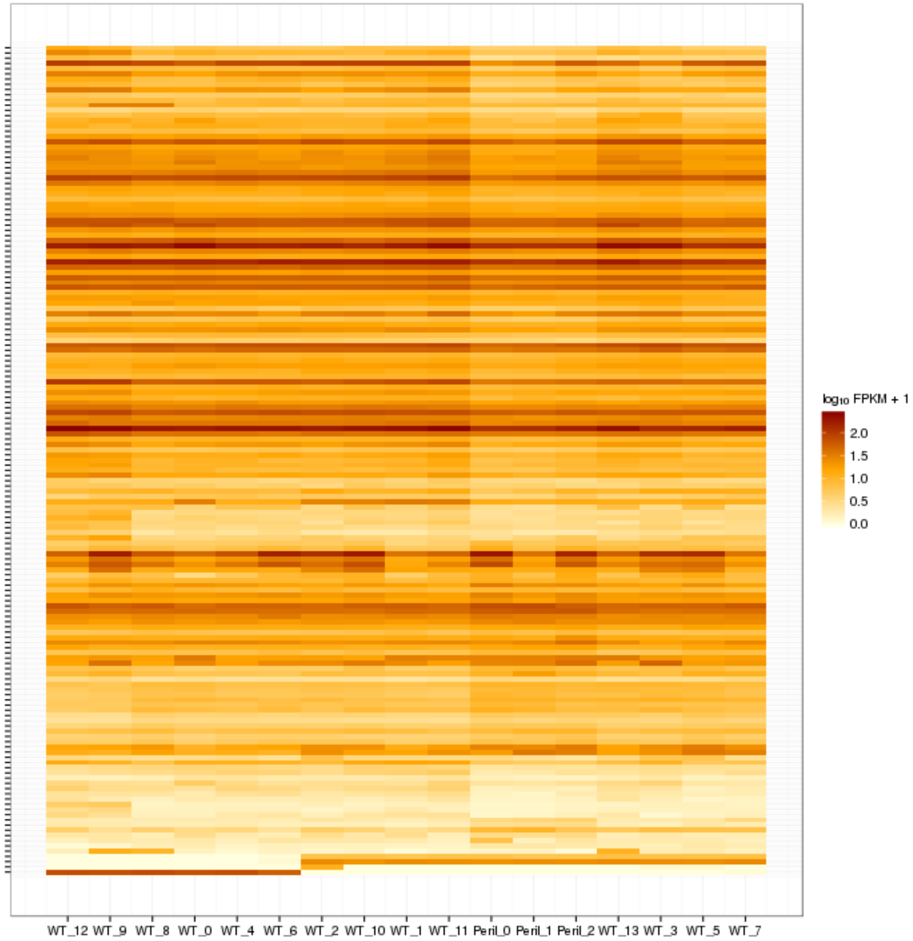
	isoAnnot$gene_short_name
1	Gabra2
2	Sox9
3	Mmp14
4	Arrdc2
5	Klf4
6	Hif3a
7	9330159F19Rik
8	Nes
9	Prlr
10	Epha2
11	Lrrc8a
12	Homer1
13	Dio2
14	Mertk
15	Camk1g
16	Sdc4
17	Ada
18	Arid5b
19	Sgk1
20	Gm872
21	Ntn4
22	Fgd6
23	Timp3
24	Cpm
25	Tns3
26	Btg2
27	Xbp1
28	Pdia6
29	Fam20a
30	Nfkbia
31	Serpina3n
32	Zfp36l1
33	Otub2
34	Fos
35	Pcsk1
36	Fam107a
37	Dnajc3
38	Myh9
39	Slc38a2
40	Bcl6

41 Sdf2l1
42 Arhgap31
43 Ap2m1
44 Cdkn1a
45 Tnfrsf12a
46 Xdh
47 Fkbp5
48 Pdgfrb
49 Kdm5c
50 D3Ertd751e
51 Pdia4
52 Paqr8
53 Slc40a1
54 Hspa5
55 Fam83d
56 Mccc1
57 Anxa5
58 Exosc9
59 Trpc3
60 F3
61 Slc2a1
62 Mfsd2a
63 Tinagl1
64 Map3k6
65 Errfi1
66 Fosl2
67 Lfng
68 Bhlhe40
69 Adipor2
70 Emp1
71 Pglyrp1
72 Hddc3
73 Sult1a1
74 Lyve1
75 Tsc22d3
76 Dusp4
77 Plat
78 Gpt2
79 Mt2
80 Ldlr
81 Paqr5
82 Smad3
83 Heyl

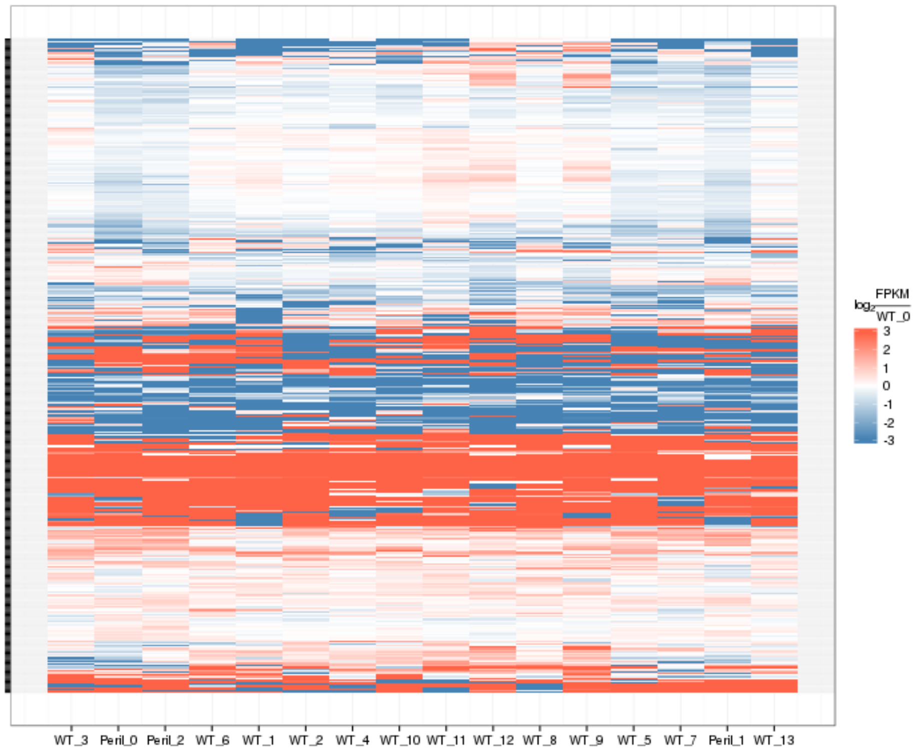
84 Slc16a1
85 Egr3
86 Klf9
87 Trim59
88 Nostrin
89 Dusp5
90 Lars2
91 Uba6
92 Dnajb5
93 Anln
94 Psenen
95 Mxd4
96 Tob1
97 Acer2
98 Smim3
99 Irs2
100 Eltd1
101 Pcsk1n
102 Tnfsf10
103 Spsb1
104 Gjb6
105 Fmo2
106 C1qtnf4
107 Nkx6-2
108 Cldn5
109 Sgsm1
110 Hps4
111 Jhdm1d
112 Id1
113 Gjc2
114 Nxpe4
115 Ctla2a
116 Cirbp
117 Zfp36l2
118 Npas4
119 Plaur
120 Stbd1
121 Hes5
122 Mex3d
123 Rasd1
124 Opalin
125 Ppp1r3g
126 Plekho2

127 Klf13
128 Junb
129 Tnfaip6
130 Ier2
131 Mat2a
132 1810037I17Rik
133 Mettl7a1
134 Per2
135 Kdm5d
136 Mex3b
137 Tpm3-rs7
138 Gm5506
139 Zbtb40
140 Rps7
141 Cox5b
142 Kdr
143 Aldoart2
144 Zbtb16
145 Ddx3y
146 Ahnak
147 Jund
148 Egr4
149 Gm7292
150 Plekhf1
151 B3galt5
152 Fjx1
153 Rprm
154 Ly6a
155 Xist
156 Slc5a3
157 A930033H14Rik
158 Apold1
159 Hspa1b

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

Biocarta zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

Reactome enrichment:

```
## Error: argument is of length zero
```

Reactome zscore:

```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

Kegg enrichment:

```
## Error: argument is of length zero
```

Kegg zscore:

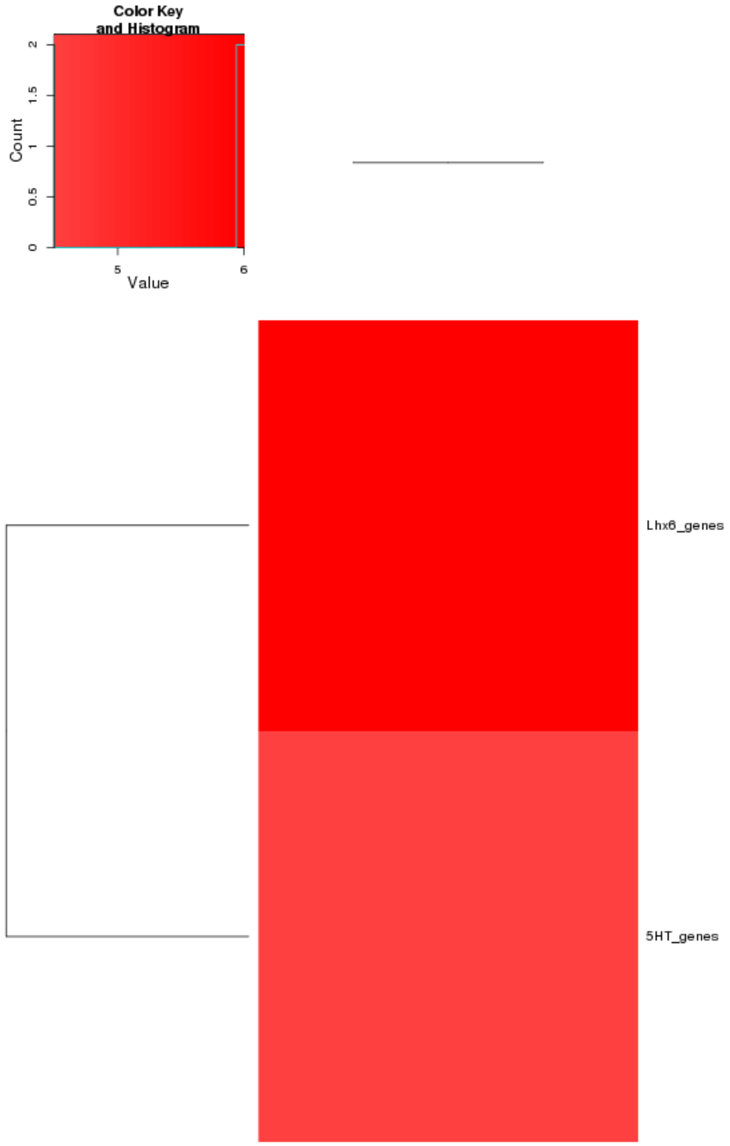
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

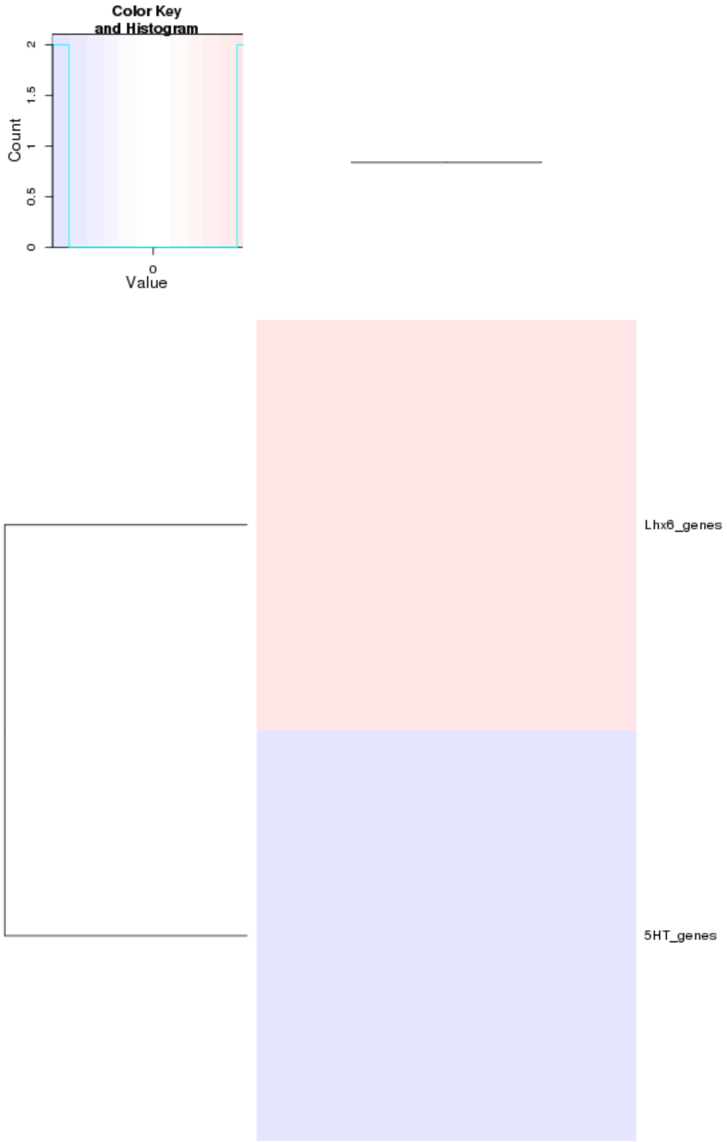
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

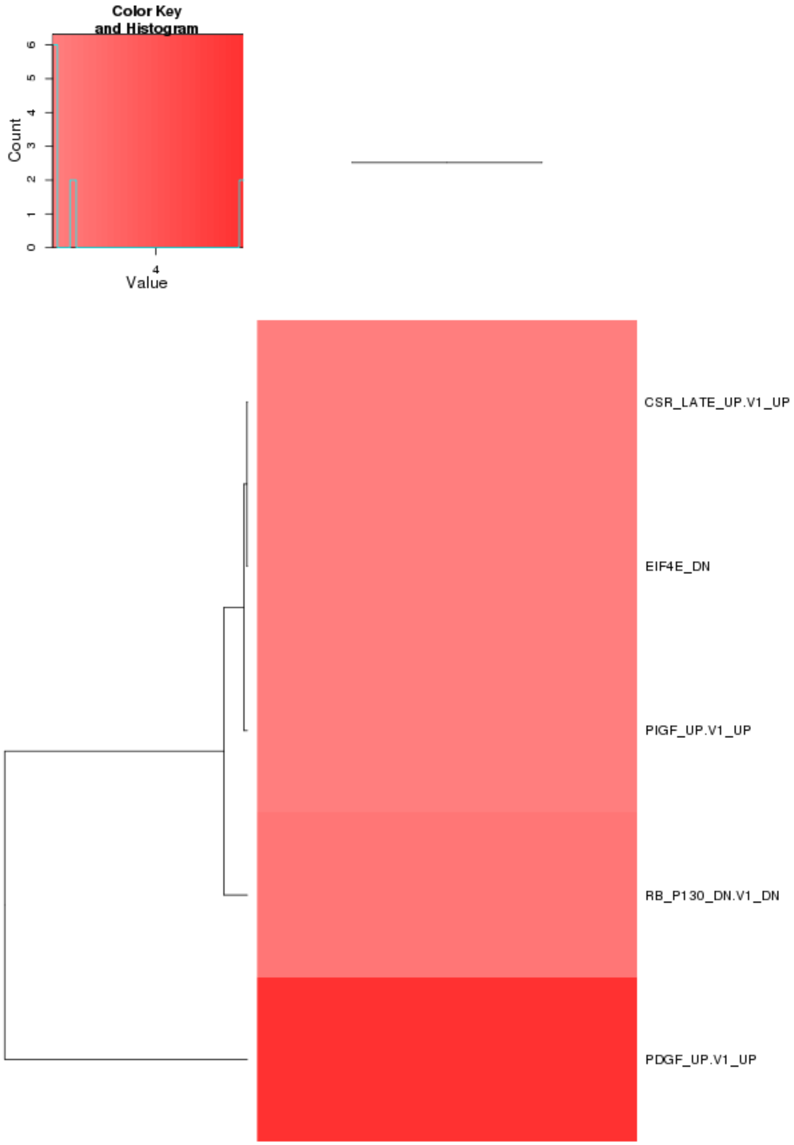
Interneuron enrichment:



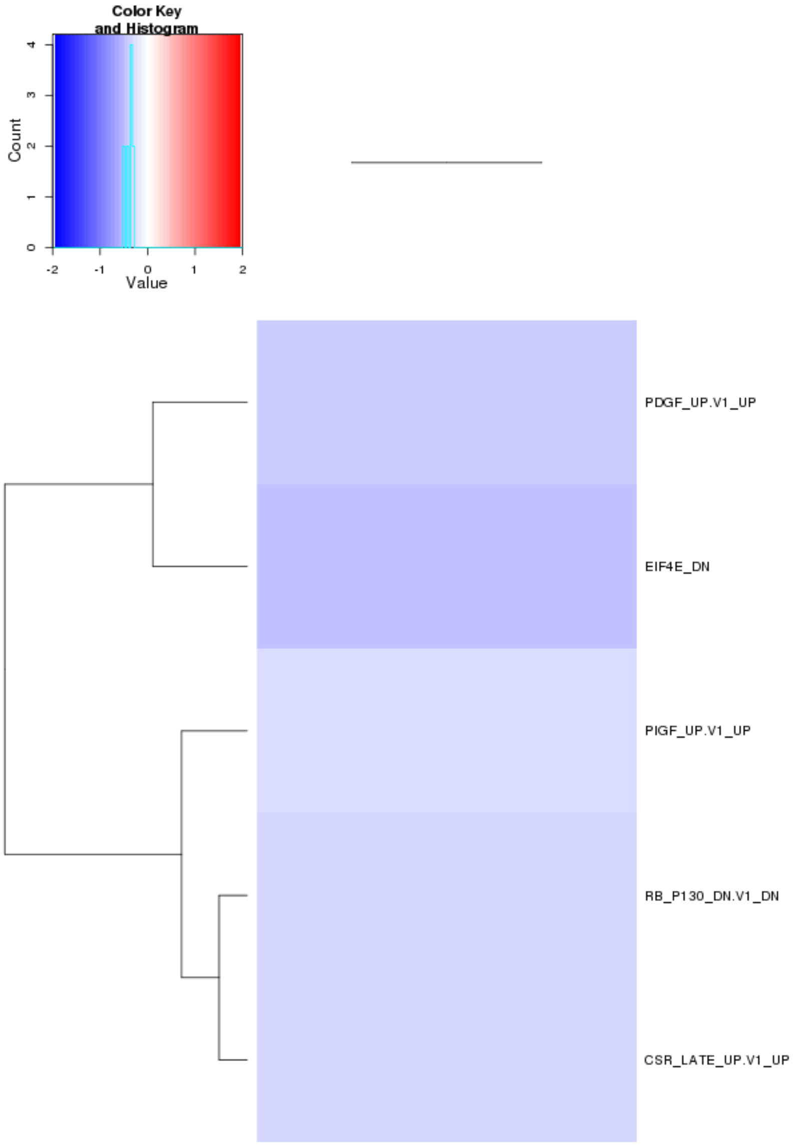
Interneuron zscore:



Oncogene enrichment:

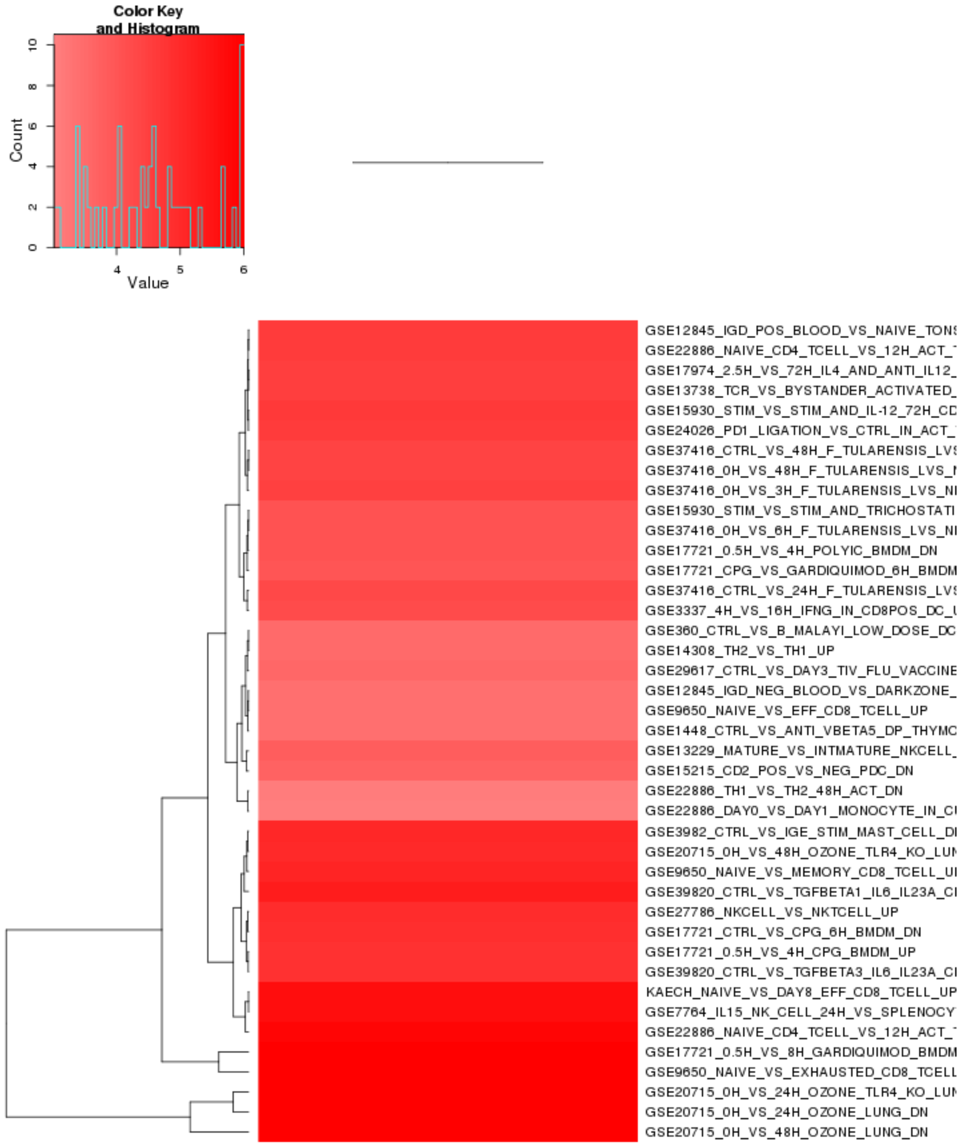


Oncogene zscore:



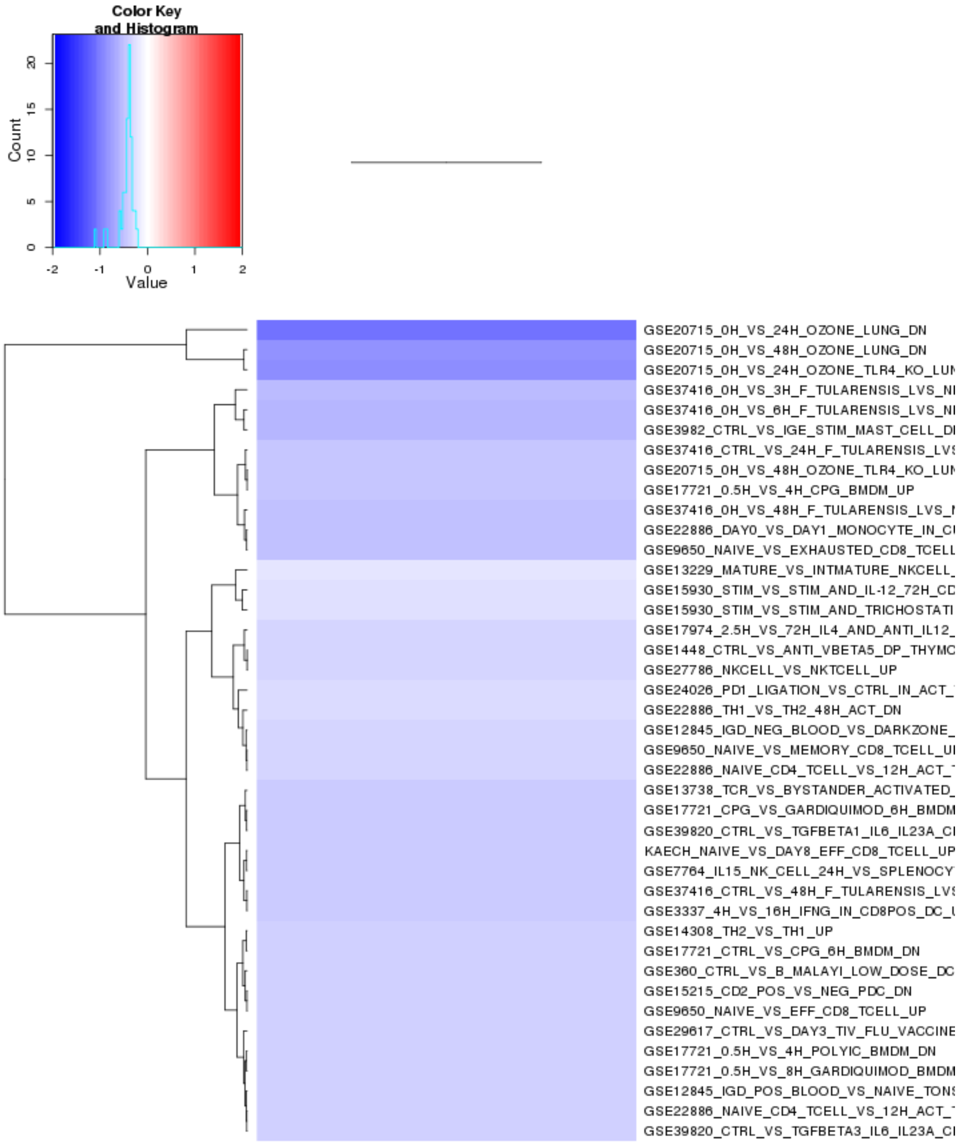
Immuno enrichment:

```
## Error: subscript out of bounds
```

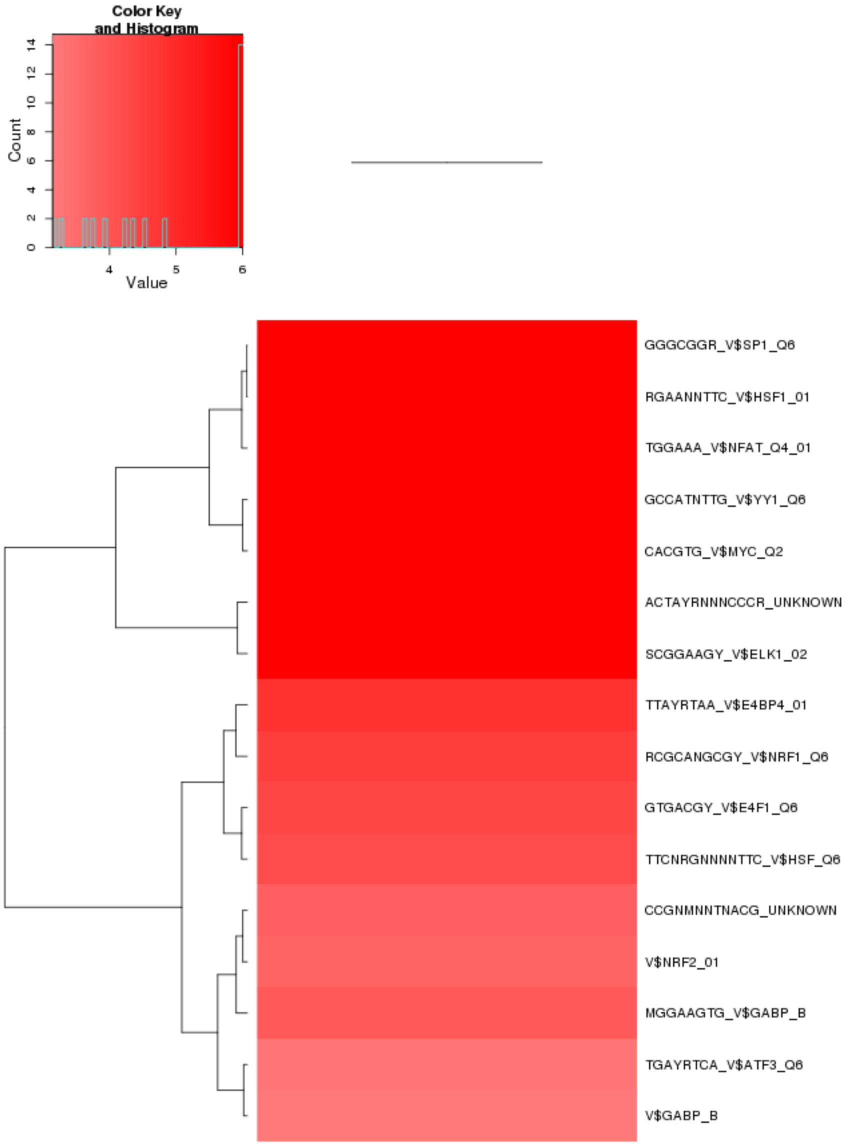


Immuno zscore:

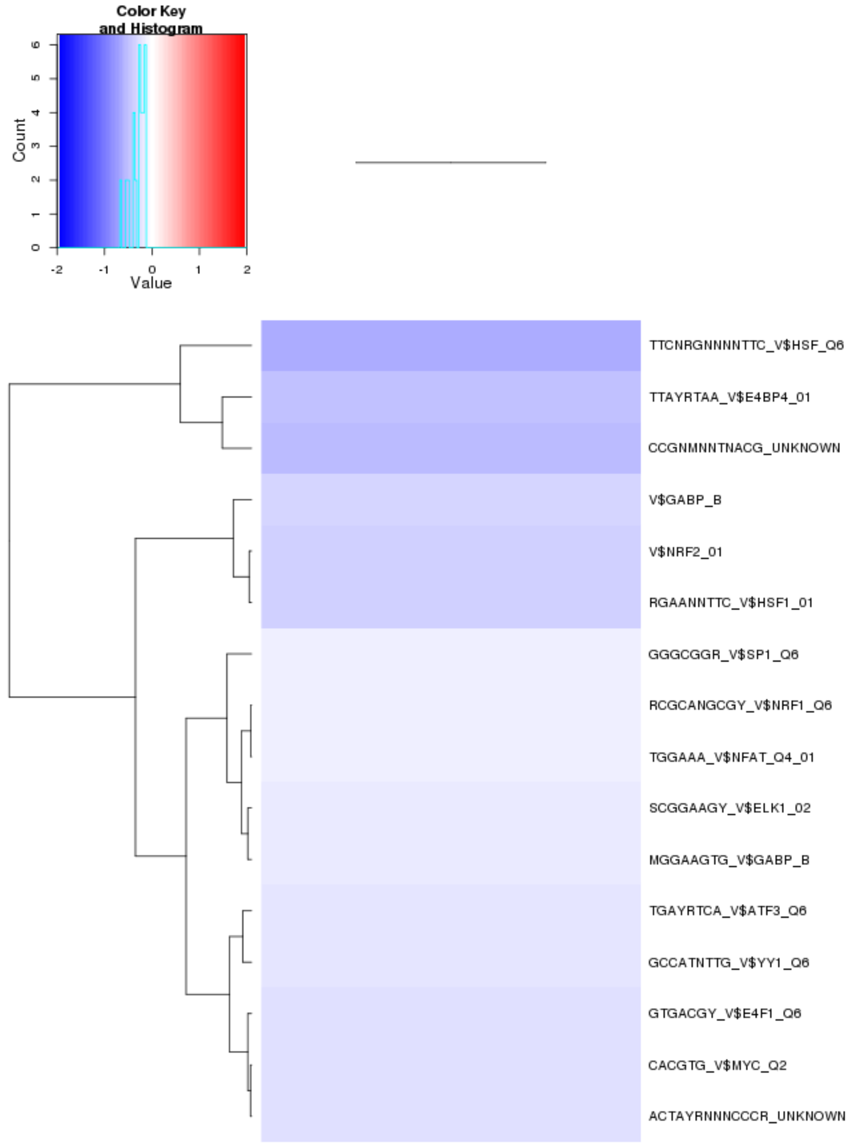
```
## Error: subscript out of bounds
```



TF enrichment:

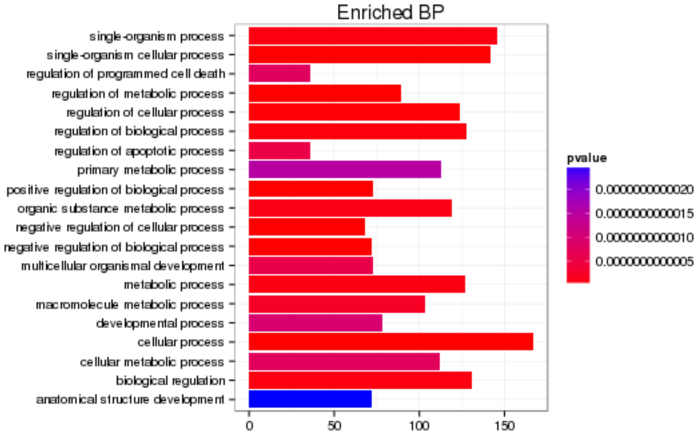

Color Key
and Histogram
Count
0
2
4
6
8
10
12
14
4
5
6
Value
GGGCGGR_V$SP1_Q6
RGAANNTTC_V$HSF1_01
TGGAAA_V$NFAT_Q4_01
GCCATNTTG_V$YY1_Q6
CACGTG_V$MYC_Q2
ACTAYRNNNCCCR_UNKNOWN
SCGGAAGY_V$ELK1_02
TTAYRTAA_V$E4BP4_01
RCGCANGCGY_V$NRF1_Q6
GTGACGY_V$E4F1_Q6
TTCNRGNNNNTTC_V$HSF_Q6
CCGNMNNTNACG_UNKNOWN
V$NRF2_01
MGGAAGTG_V$GABP_B
TGAYRTCA_V$ATF3_Q6
V$GABP_B

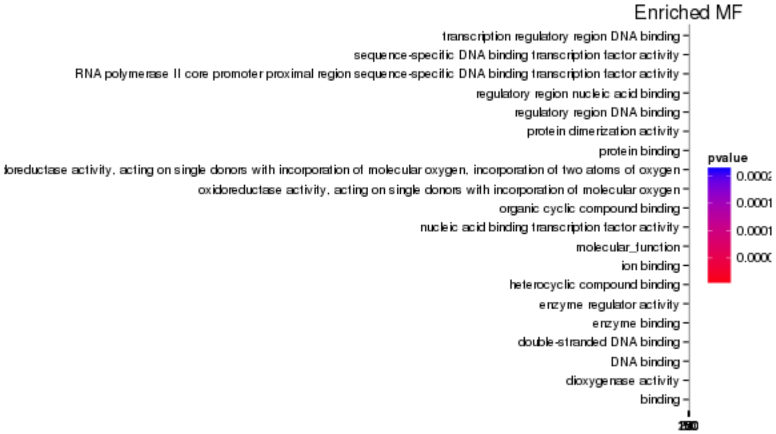
TF zscore:

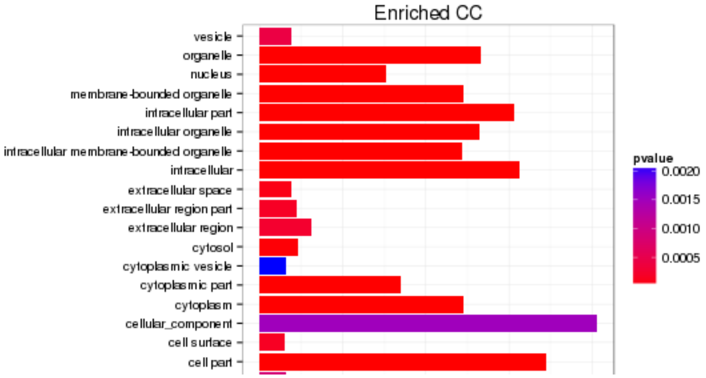


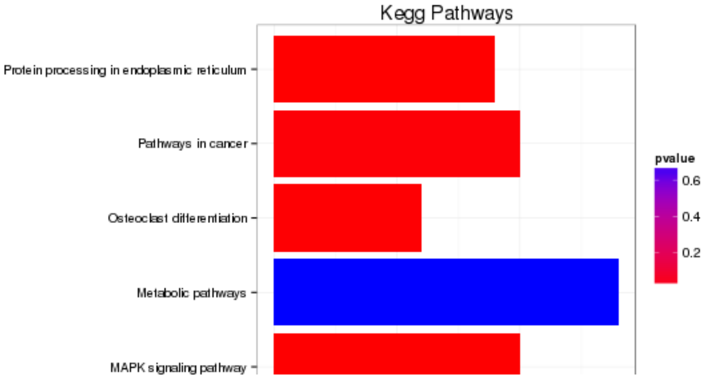
GO enrichment

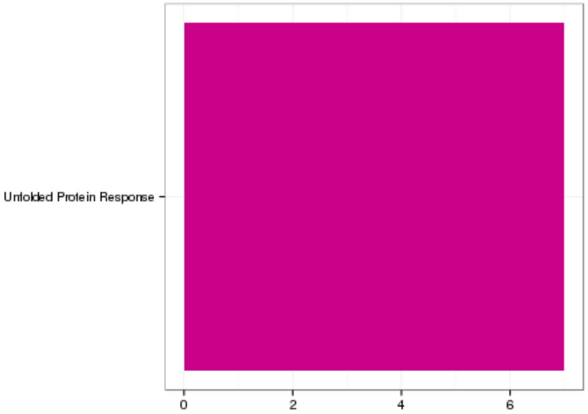
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.


Enriched BP

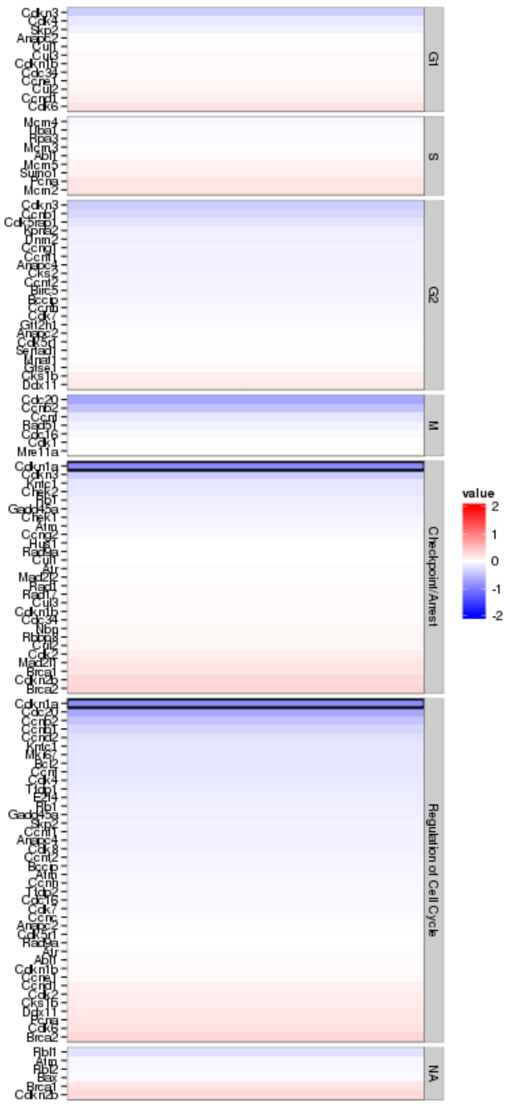

Enriched MF


Enriched CC

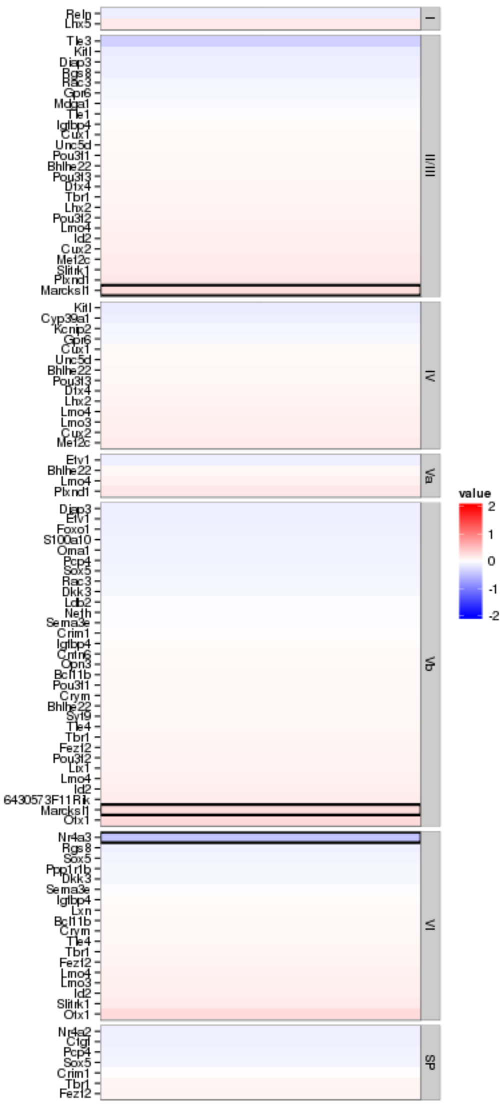

Kegg Pathways



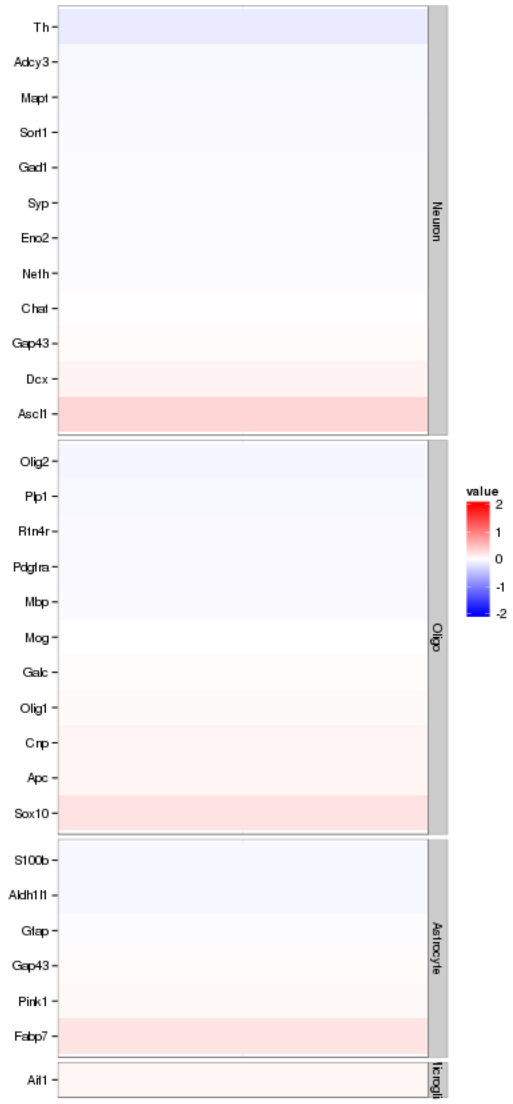
Enrichment or depletion for stage-specific cell cycle markers



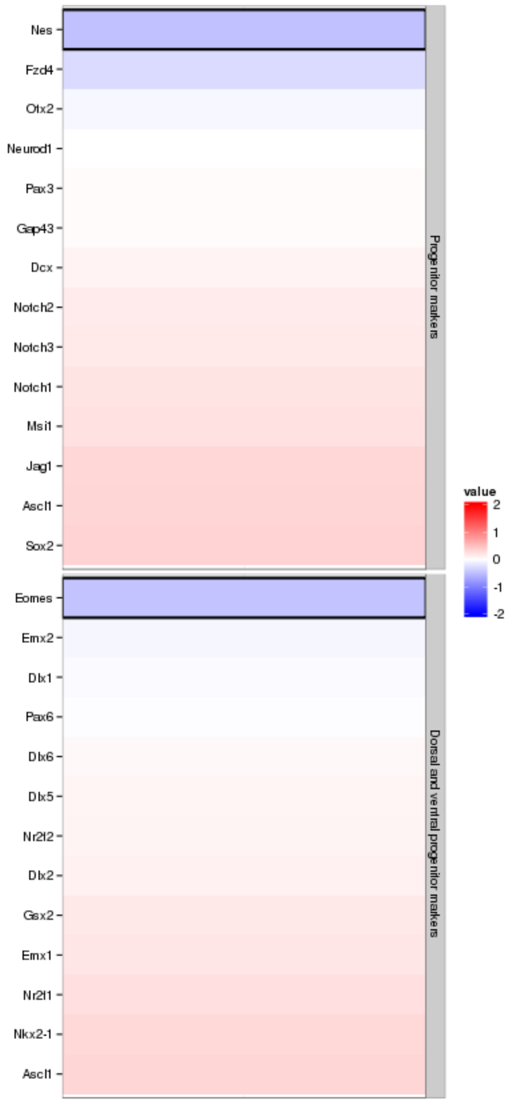
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



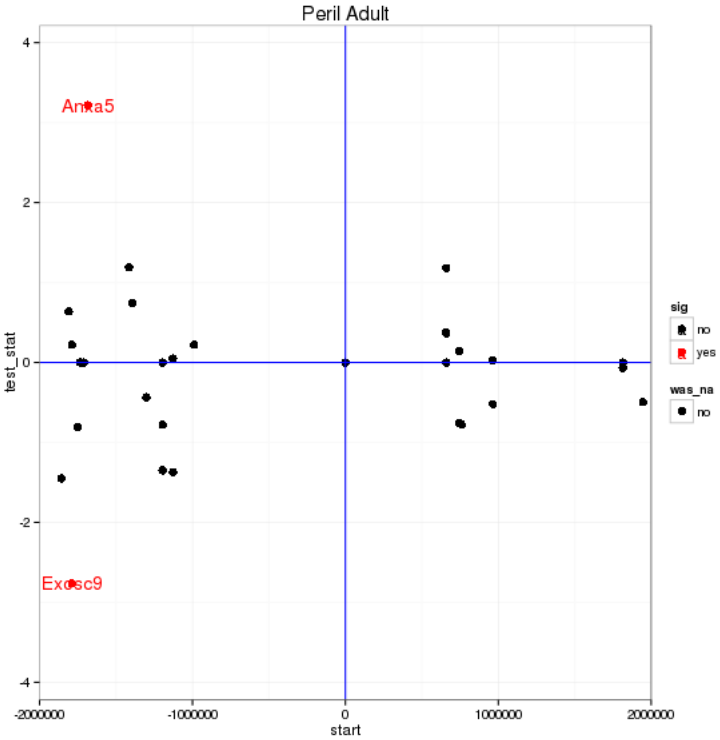
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 2 genes significantly regulated in a region this size is: 0.1516



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15	JR806
16	JR744
17	JR822

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	34714900.00	0.76	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	34714900.00	0.58	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	34714900.00	0.98	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	34714900.00	0.80	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	34714900.00	1.03	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	34714900.00	1.07	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	34714900.00	0.80	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	34714900.00	1.15	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	34714900.00	1.01	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	34714900.00	1.30	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	34714900.00	1.50	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	34714900.00	1.01	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	34714900.00	0.97	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	34714900.00	1.20	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR806/abundances.cxb	Peril	0	Peril_0	40528700.00	34714900.00	1.17	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR744/abundances.cxb	Peril	1	Peril_1	38767500.00	34714900.00	1.13	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR822/abundances.cxb	Peril	2	Peril_2	33329500.00	34714900.00	0.97	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1           
##  [2] stringr_0.6.2        
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,Peril -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Peril_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/ar
## 2
## 3
## 4
## 5
```

Peril KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for Peril.

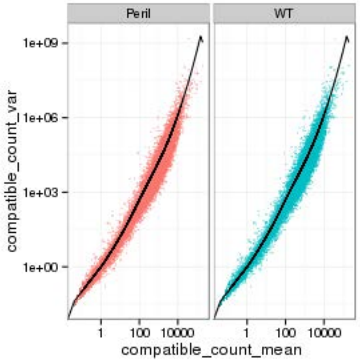
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

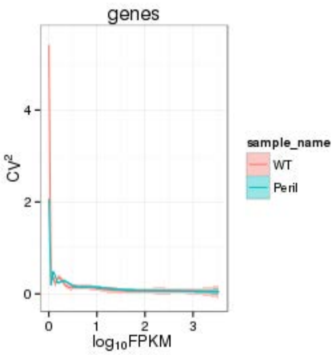
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



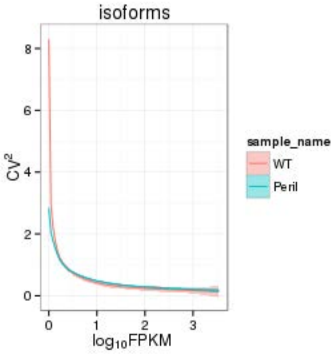
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

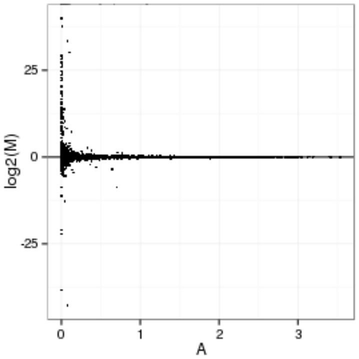
Genes:



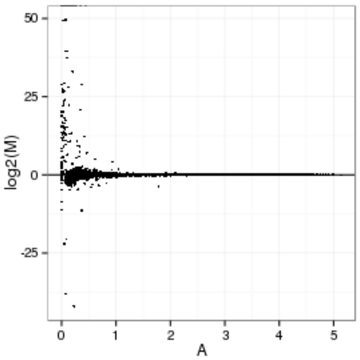
Isoforms:



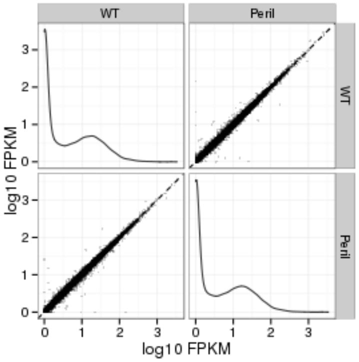
MvA plot



MvA plot counts



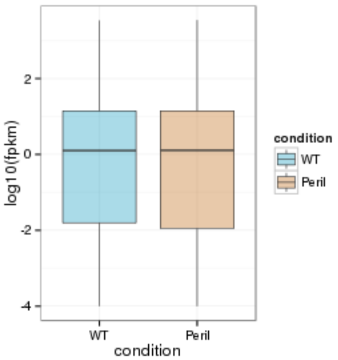
Scatterplot matrix



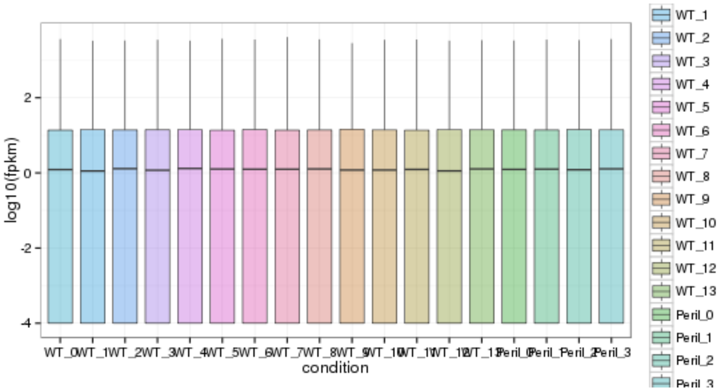
Distributions

Boxplots

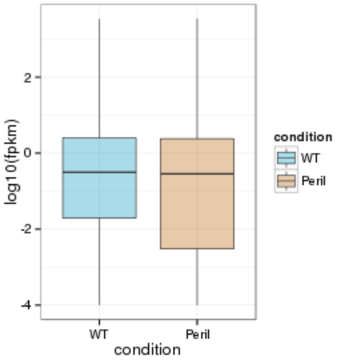
Boxplot (genes)



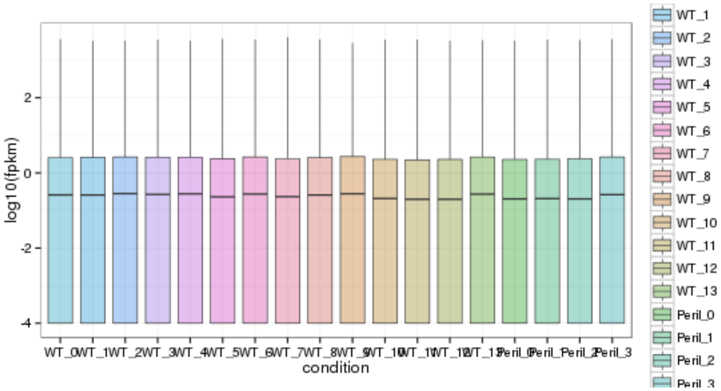
Boxplot (genes, replicates)



Boxplot (isoforms)

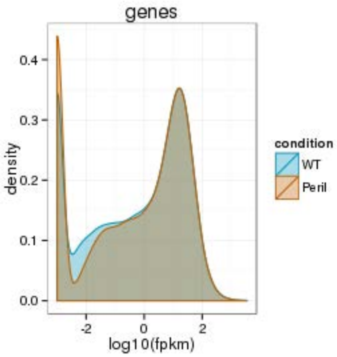


Boxplot (isoforms, replicates)

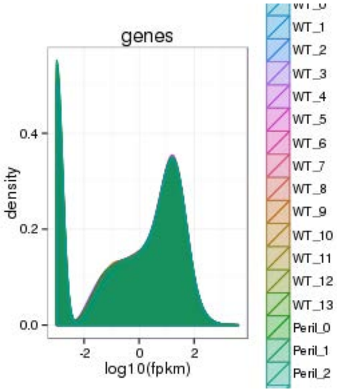


Density

Density (genes)

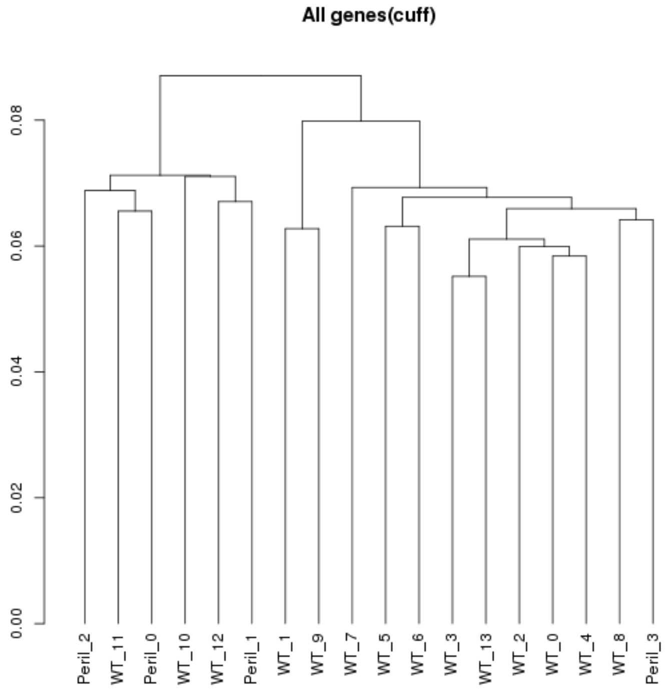


Density (genes, replicates)



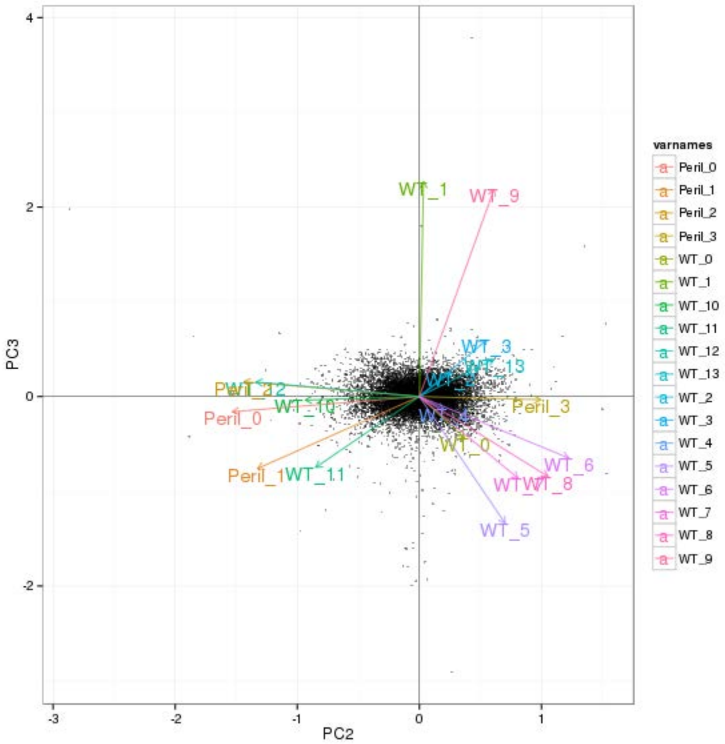
Clustering

Replicate Clusters

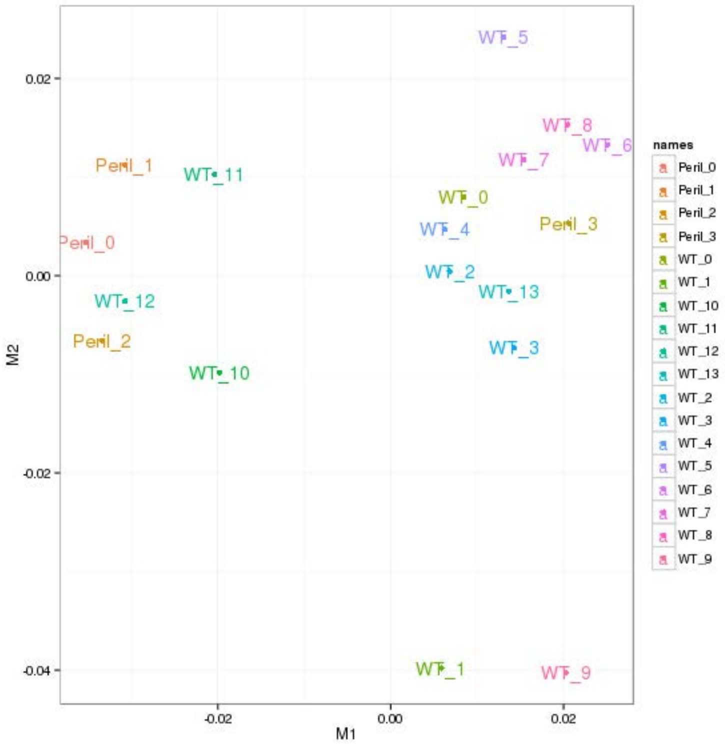


```
## NULL
```

PCA (genes)

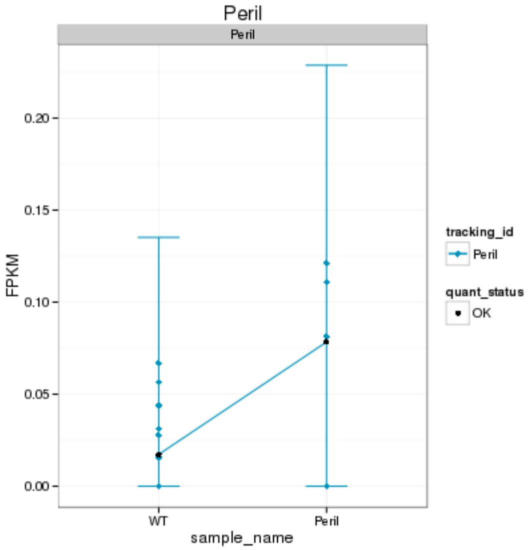

PC3
PC2
4
2
0
-2
-3
-2
-1
0
1
WT_1
WT_9
WT_3
WT_13
PWT_12
WT_10
Peril_0
Peril_3
WT_0
WT_6
Peril_1
WT_11
WT_7
WT_8
WT_5
varnames
Peril_0
Peril_1
Peril_2
Peril_3
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

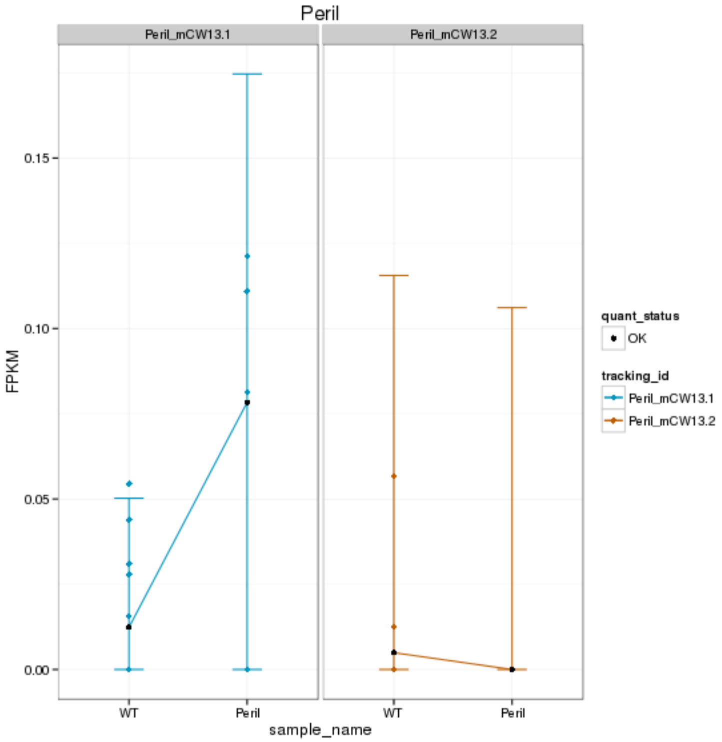


KO assessment

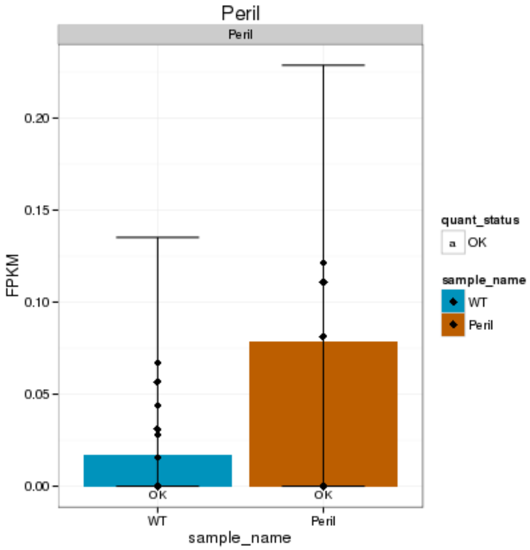
Endogenous lncRNA expression



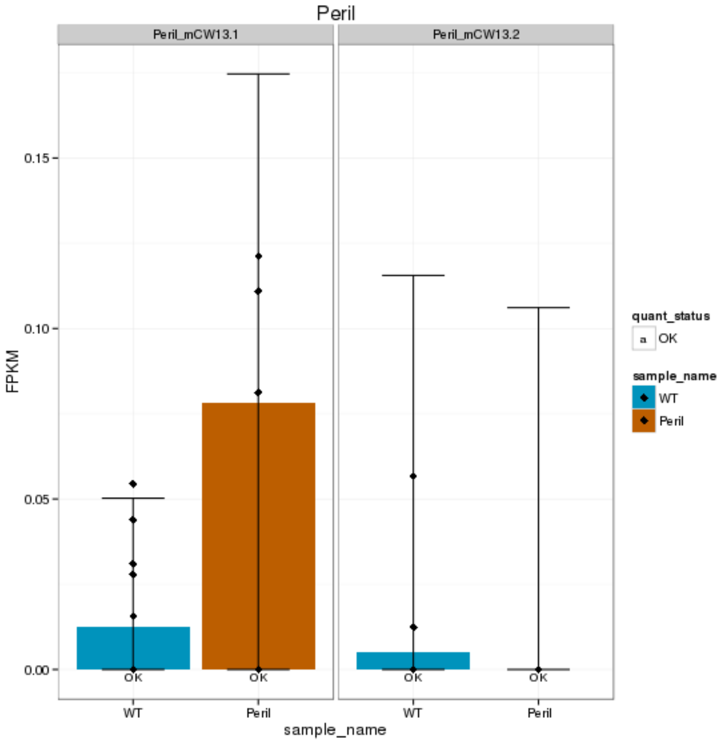
Endogenous expression of Peril isoforms:



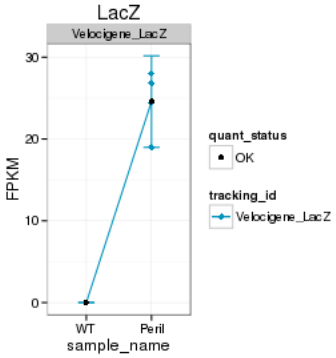
Barplot of gene expression:

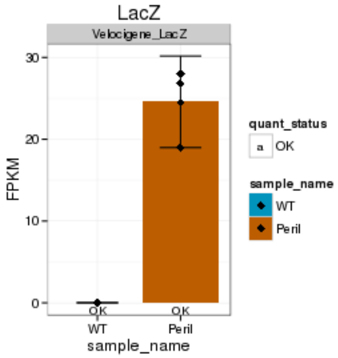


Barplot of isoform expression:



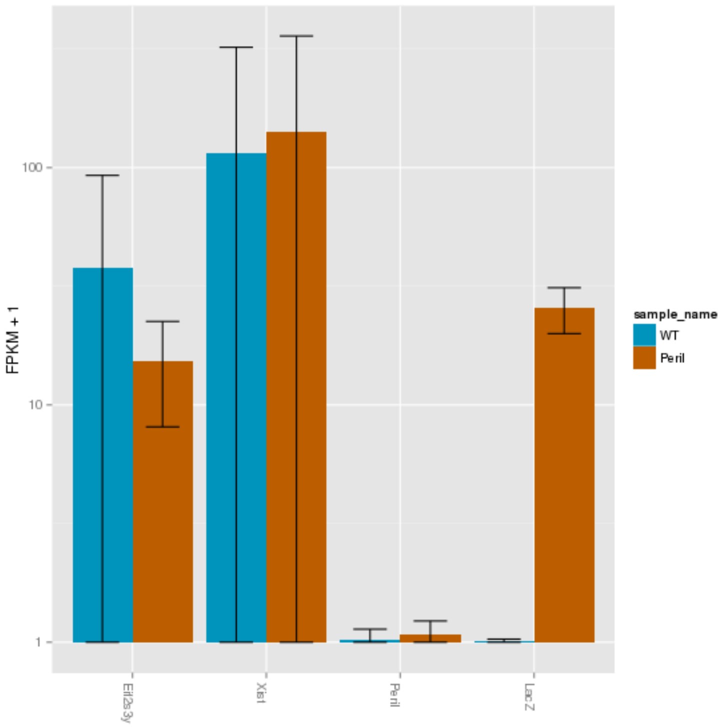
LacZ expression



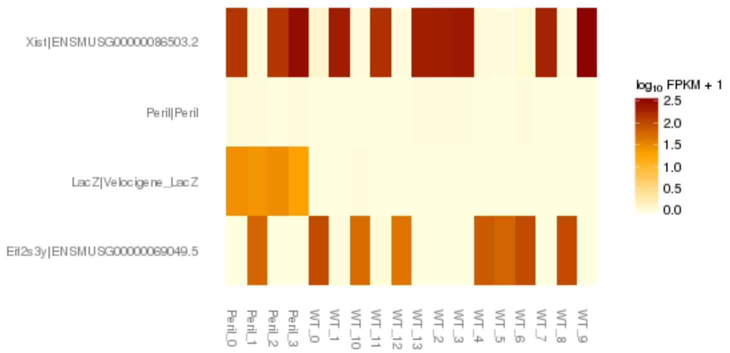


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

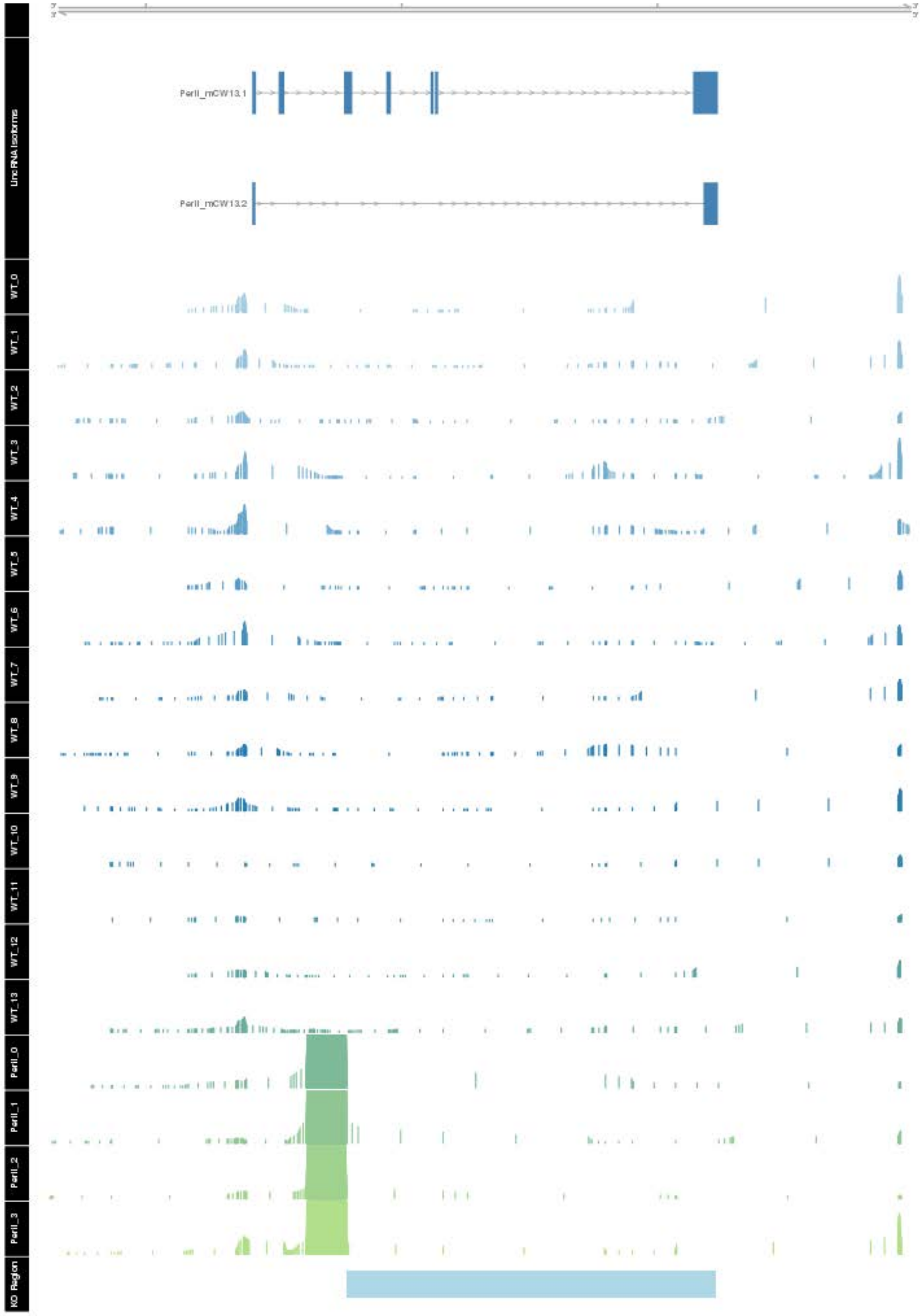
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


LincRNA Isoforms
PerII_mCW13.1
PerII_mCW13.2
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
PerII_0
PerII_1
PerII_2
PerII_3
KO Region

Differential Analysis

Differential Genes

There are 254 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Ccnd2
2	Itga5
3	Gabra2
4	Col18a1
5	Col1a1
6	Phyhip
7	Ddr1
8	Aqp1
9	Pax3
10	Nes
11	Nid1
12	Hmox1
13	Osgep
14	Rplp1
15	Wnt3a
16	Odc1
17	Aldh1a2
18	Dennd6b
19	Celsr1
20	Sulf1
21	Anxa6
22	Slc16a10
23	Lrriq1
24	Lama2
25	Ndufa12
26	Rfx4
27	Col6a2
28	Aebp1
29	Pomc
30	Galk1
31	Nxn
32	Ntn1
33	Amn
34	Nid2
35	Gdf10
36	Esd
37	Tnfrsf10b

38 Psmb5
39 Npr3
40 Col14a1
41 Wnt7b
42 Myh9
43 Plec

44 Arhgap31
45 Clic6
46 Wnt1
47 Krt18
48 Dlx2
49 Igf2r
50 Gfra3
51 H2-M5
52 Pou4f3
53 Lox
54 Megf10
55 Fbn2
56 Pdgfrb
57 Gldc
58 Cpt1a
59 Slc18a2
60 Rps24
61 Podxl
62 Col5a2
63 Col3a1
64 Igfbp5
65 Fn1
66 Ptma
67 Lamc1
68 Ptpn14
69 Ddr2
70 Lmx1a

71 Gad2
72 Col5a1
73 Lamc3
74 Hspa5
75 Lhx6
76 Notch1
77 Lrp2
78 Fbn1
79 Cd82
80 Tspan18

81 Syt13
82 Mccc1
83 Slc7a11
84 Hsd3b6
85 Notch2
86 Vcam1
87 Hadh
88 Wls
89 Tnc
90 Svep1
91 Stmn1
92 Trp73
93 Pdgfra
94 Gm996
95 Col1a2
96 Ephb4
97 Dlx5
98 Lrig1
99 Aldh1l1
100 Plxnd1
101 Emp1
102 Dbx1
103 Trpm1
104 Hddc3
105 Zkscan2
106 Lyve1
107 Heph
108 Col4a5
109 Plat
110 Slit2
111 Hsd11b2
112 Itga11
113 Gsta4
114 Car12
115 Smad3
116 Lama1
117 Tlr13
118 Gria2
119 Foxj1
120 Tmem132c
121 Scn10a
122 Ptpn13
123 Tdg

124 Prr7
125 Fras1
126 Arl4d
127 Arx
128 Ror1
129 Ccl2
130 Ccdc11
131 Tgfbi
132 Cox8a
133 Colec12
134 Lum
135 C1ql2
136 Wnt8b
137 Frem2
138 Atp11b
139 Vstm2l
140 Notch3
141 Spon1
142 Satb2
143 Akap12
144 Atp5l
145 Itpkb
146 Anpep
147 Rbpj
148 Pcsk1n
149 Igfbp2
150 Kcne2
151 Bmf
152 Thbs1
153 Abcb1a

154 Ildr2
155 C1qtnf4
156 Abhd4
157 Npnt
158 Fzd7
159 Ccdc8
160 Arhgap11a
161 Htr2c
162 Prelp
163 Nlrp5-ps
164 Dlx1
165 Rassf4
166 Dmrt3

167	Lor
168	A030009H04Rik
169	Tmem145
170	Wfikkn2
171	Snhg11
172	Gm9493
173	Acp1
174	Cnpy1
175	Basp1
176	Olig1
177	Scand1
178	Fat4
179	Tmem164
180	Adamts12
181	Rps8
182	Pirt
183	Shisa3
184	Pla2g4e
185	Gja1
186	Rspo2
187	Pfdn4
188	Hbb-y
189	Hbb-bh1
190	Dnah6
191	Lamb2
192	Yap1
193	Sh3pxd2a
194	Hba-x
195	Dach1
196	Myh8
197	Col8a2
198	Pgpep1
199	Slit3
200	Cd248
201	Kdm5d
202	Gulp1
203	Hist3h2ba
204	Gm5148
205	Capn11
206	Sclt1
207	Hydin
208	Dcc
209	Cdh3

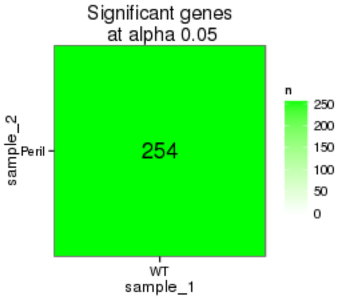
210 Trank1
211 Otof
212 Ldha
213 Cyp26b1
214 Col23a1
215 Scn1a
216 Cldn9
217 Lgals1
218 Slc4a5
219 Flnc
220 Sp9
221 Ddx3y
222 Ahnak
223 Hba-a2
224 Fat1
225 Ccnd1
226 Serpinh1
227 Gm10282
228 Gm1673
229 Gad1
230 Jund
231 Ppia
232 Fam84b
233 Gm7292
234 Drc1
235 2410018L13Rik
236 Wdfy1
237 Hbb-bt
238 Nynrin
239 Ywhaq
240 Fzd10
241 Pisd-ps1
242 Gm14204
243 Ier5l
244 Dlx6os1
245 Pou3f1
246 Ccdc85b
247 Gm21781
248 Gm6472
249 Dynlt1f
250 Lhx8
251 A330076H08Rik
252 4930480K23Rik

253 A930011O12Rik

254 Gm27000

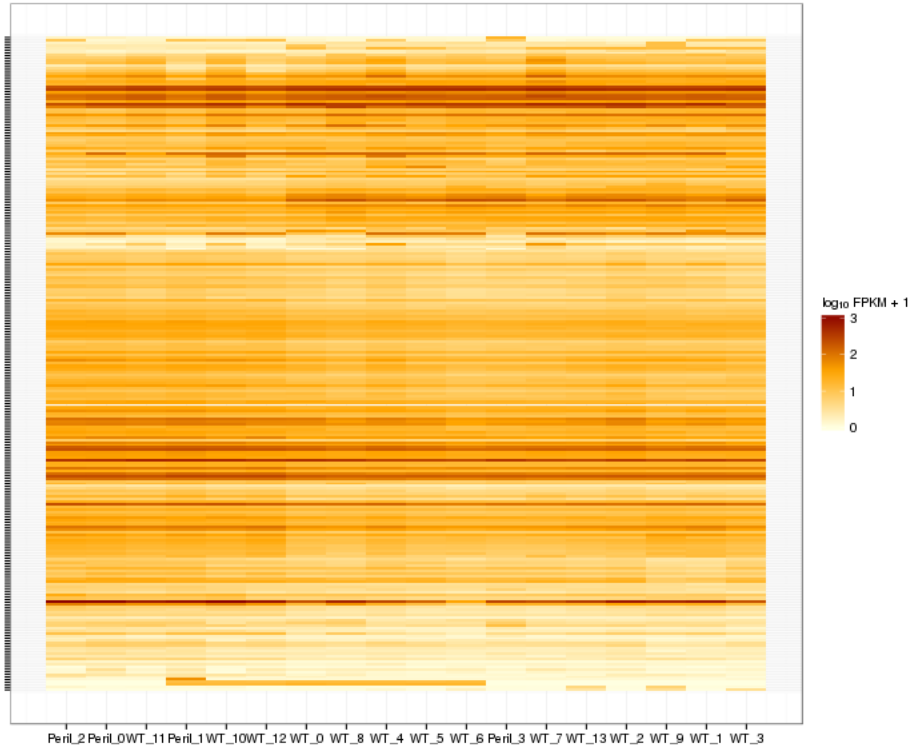
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

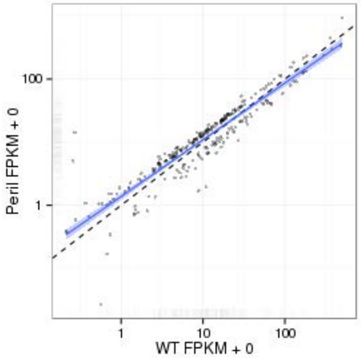


Significant genes with expression >50fpkm (any condition):(turned off)

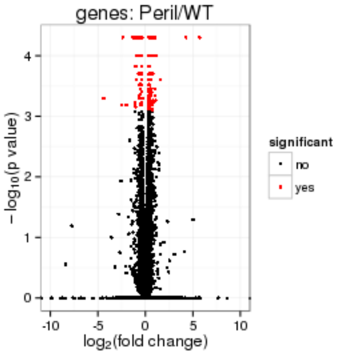
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

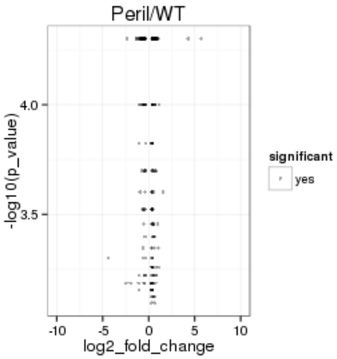
Scatter plot of significant genes only:



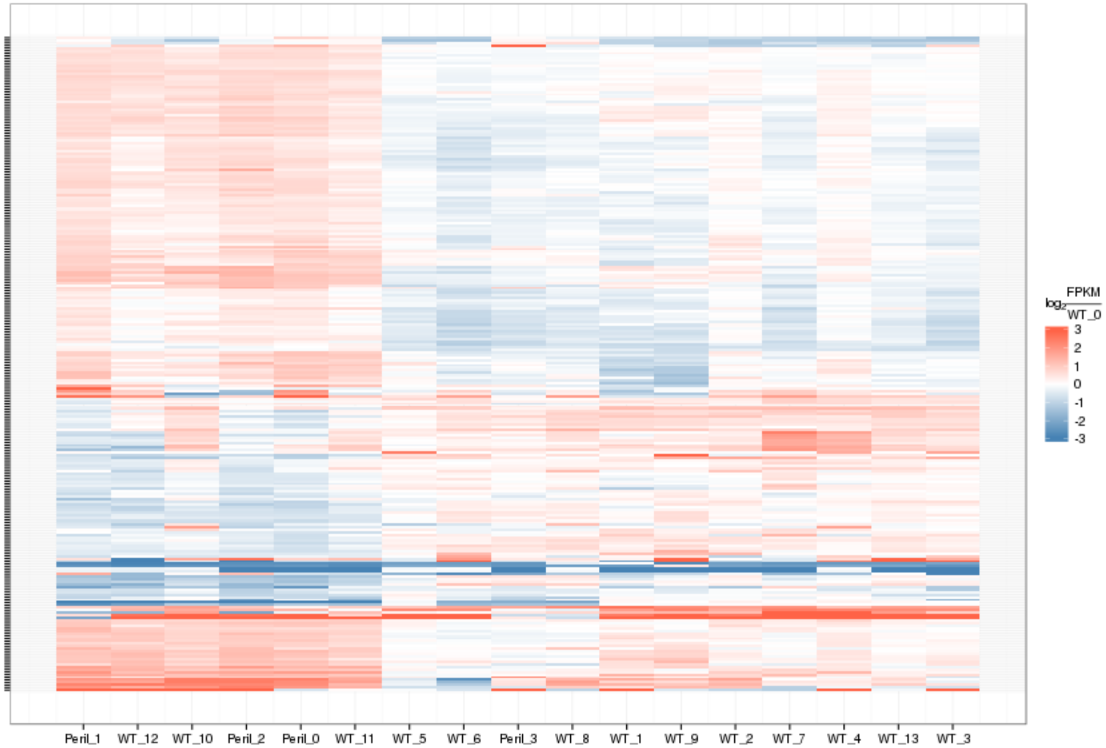
Volcano Plot



Volcano plot with significant genes only:



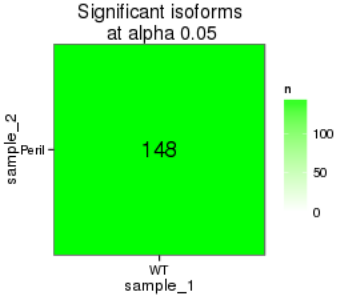
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

	isoAnnot$gene_short_name
1	Ccnd2
2	Gabra2
3	Col18a1
4	Col1a1
5	Aqp1
6	Nes
7	Nid1
8	Hmox1
9	Rplp1
10	Odc1
11	Cad
12	Lama5
13	Sulf1
14	Slc16a10
15	Lrriq1
16	Lama2
17	Gm872
18	Ndufa12
19	Pomc
20	Mrc2
21	Galk1
22	Nxn
23	Ntn1
24	Tnfrsf10b
25	Psmb5
26	Npr3
27	Col14a1
28	Zbtb20
29	Arhgap31
30	Adamts1
31	Clic6
32	Dlx2
33	Igf2r
34	Svil
35	H2-M5
36	Pou4f3
37	Fbn2
38	Pdgfrb
39	Gldc
40	Slc18a2

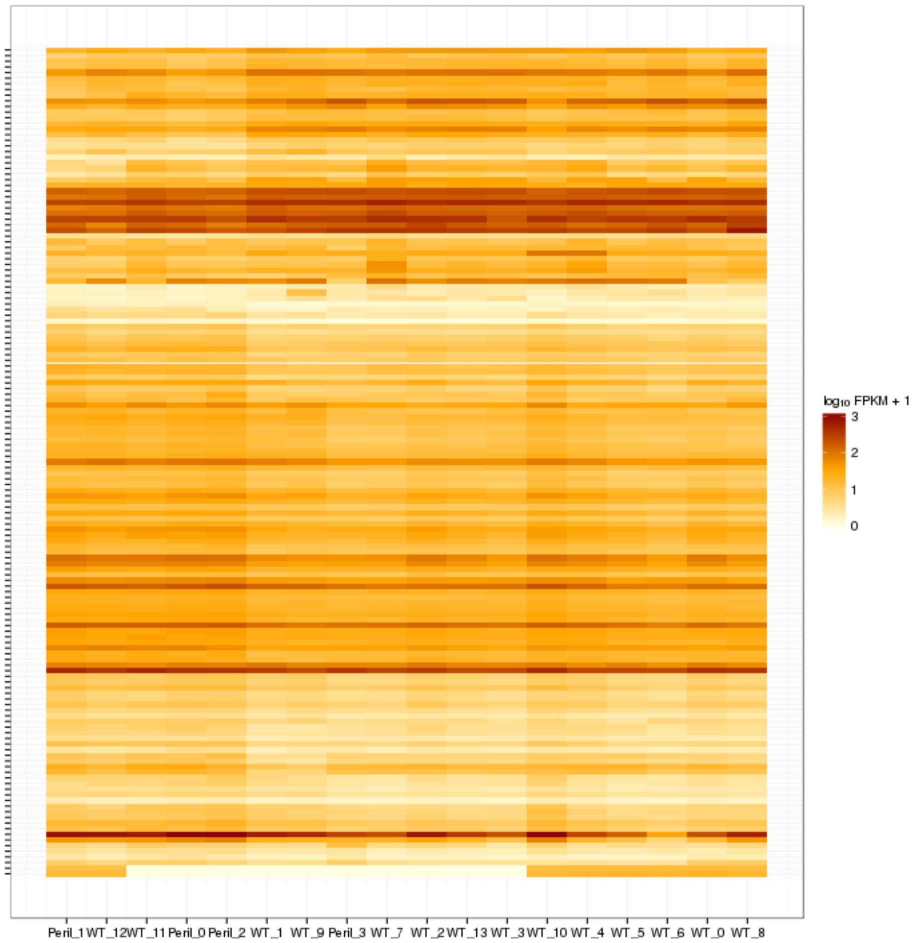
41 Podxl
42 Col5a2
43 Col3a1
44 Igfbp5
45 Fn1
46 Ptma
47 Lamc1
48 Lmx1a
49 Gad2
50 Col5a1
51 Notch1
52 Lrp2
53 Fbn1
54 Tspan18
55 Syt13
56 Rrbp1
57 Mccc1
58 Notch2
59 Vcam1
60 Svep1
61 Hspg2
62 Rspo1
63 Trp73
64 Col1a2
65 Dlx5
66 Aldh1l1
67 Smad3
68 Lama1
69 Foxj1
70 Tmem132c
71 Ptpn13
72 Prr7
73 Fras1
74 Arl4d
75 Arx
76 Cox8a
77 Colec12
78 Lum
79 Wnt8b
80 Frem2
81 D4Wsu53e
82 Notch3
83 Spon1

84 Akap12
85 Pcsk1n
86 Kcne2
87 Thbs1
88 C1qtnf4
89 Ccdc8
90 Arhgap11a
91 Prelp
92 Nlrp5-ps
93 Dlx1
94 Rassf4
95 Dmrt3
96 Reln
97 Lor
98 Wfikkn2
99 Snhg11
100 Gm9493
101 Basp1
102 Olig1
103 Fat4
104 Adamts12
105 Rps8
106 Col6a3
107 Pla2g4e
108 Rspo2
109 Hbb-y
110 Hbb-bs
111 Ezr
112 Lamb2
113 Glis3
114 Yap1
115 Zfp771
116 Hba-x
117 Myh8
118 Col8a2
119 Pgpep1

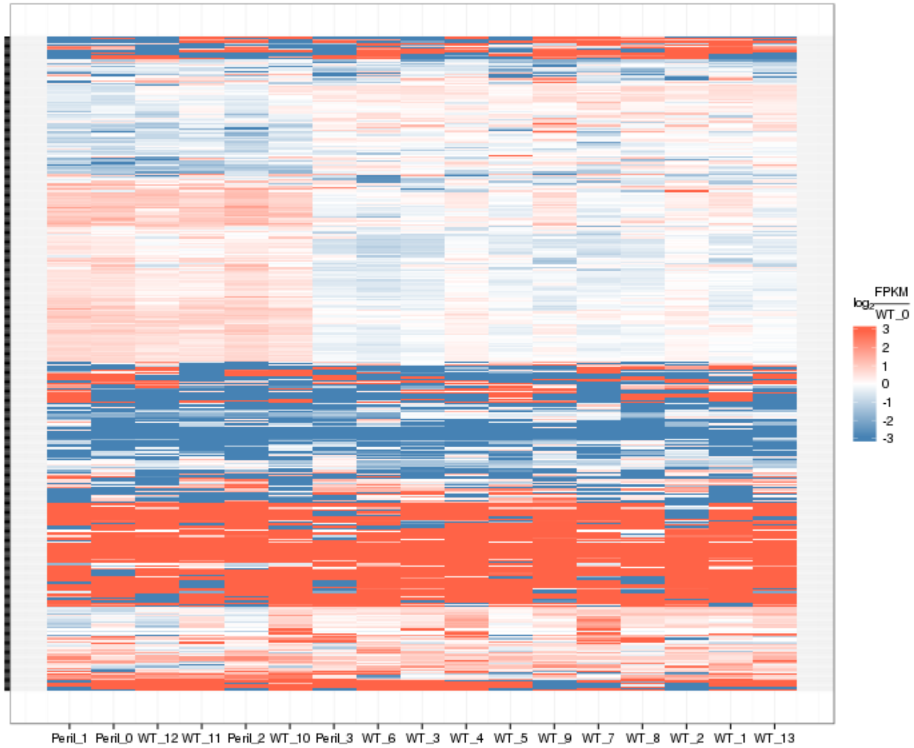
120 Ncoa4
121 Kdm5d
122 Hist3h2ba
123 Hydin
124 Trank1
125 Flnc
126 Sp9

127 Ddx3y
128 Gpr98
129 Ahnak
130 Fat1
131 Serpinh1
132 Gm10282
133 Jund
134 Fam84b
135 Drc1
136 Hbb-bt
137 Col22a1
138 Fzd10
139 Ier5l
140 Dlx6os1
141 Pou3f1
142 Ccdc85b
143 Gm6472
144 4930480K23Rik
145 Rmst
146 A930011O12Rik
147 Gm27000

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

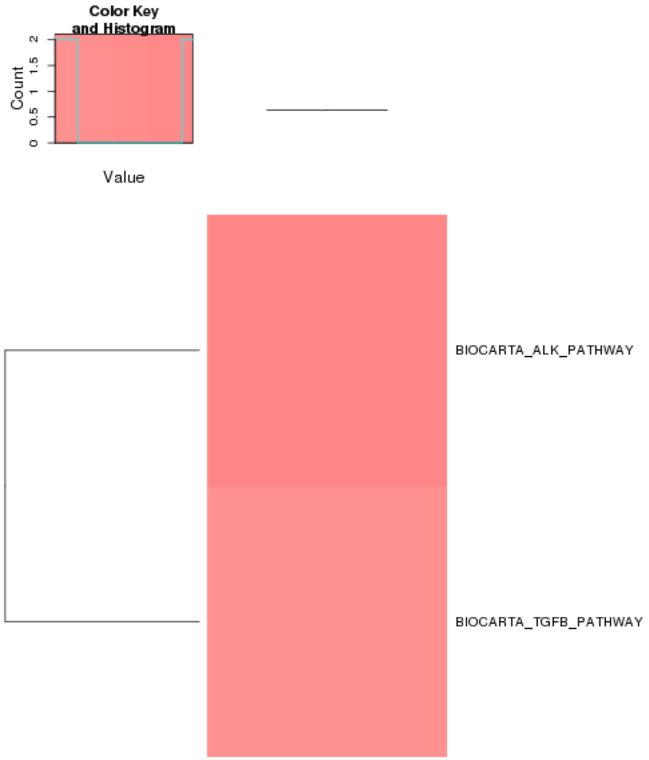
Gene/Pathway Analysis

GSEA

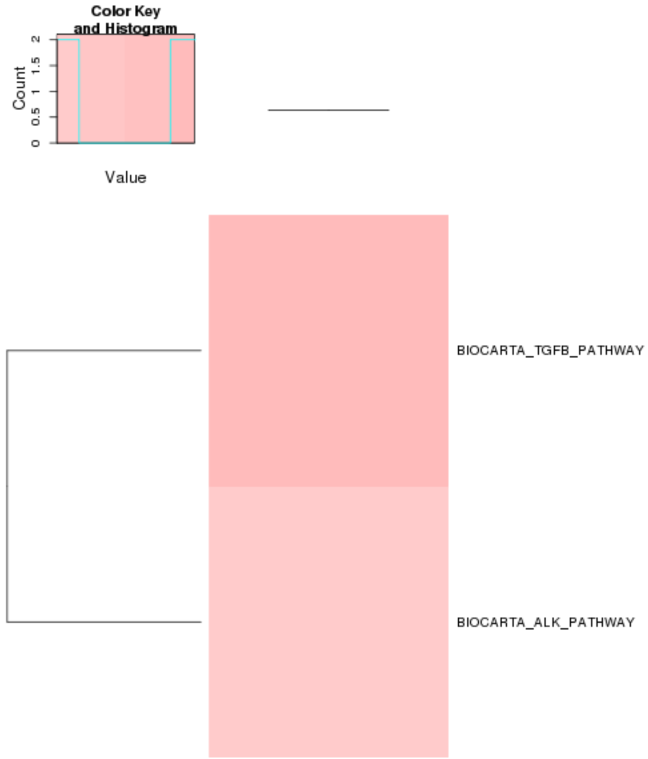
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

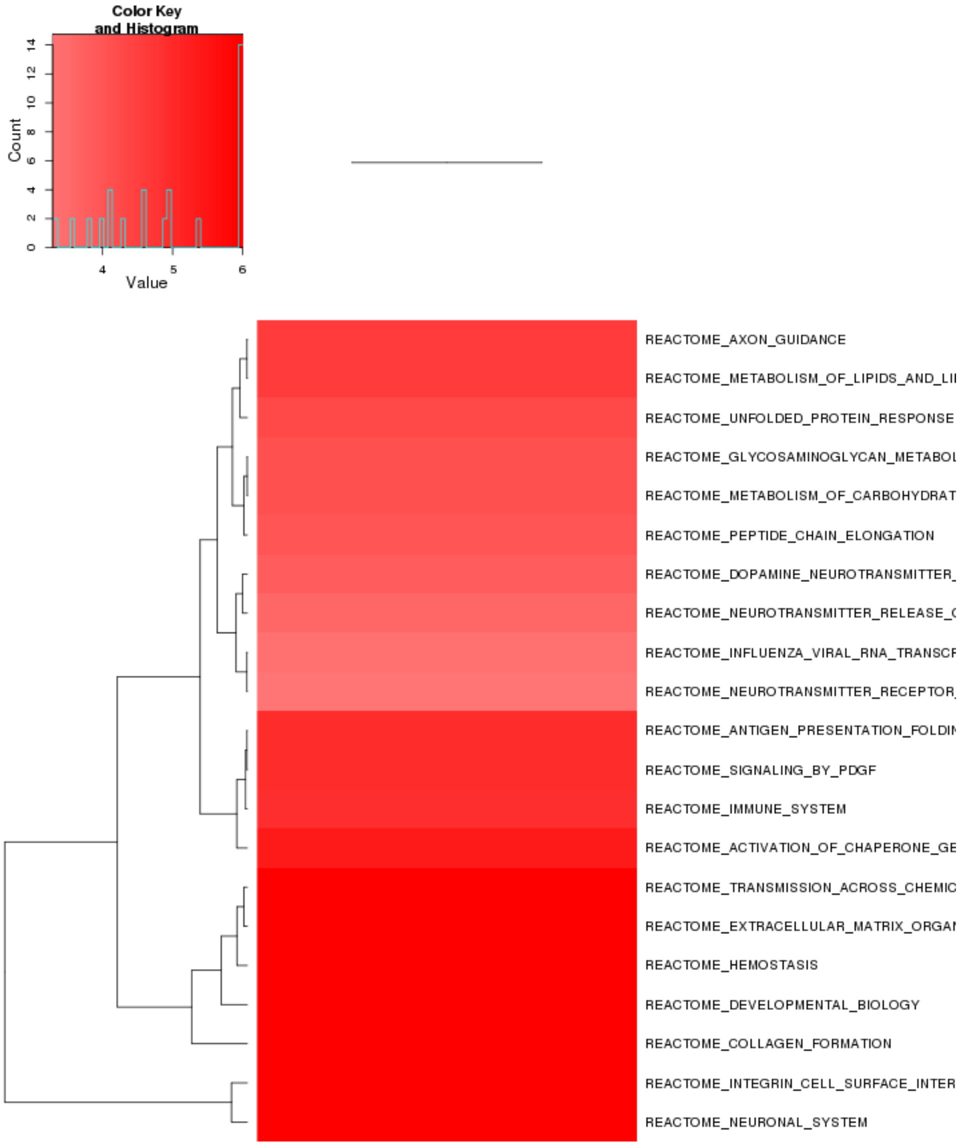
Biocarta enrichment:



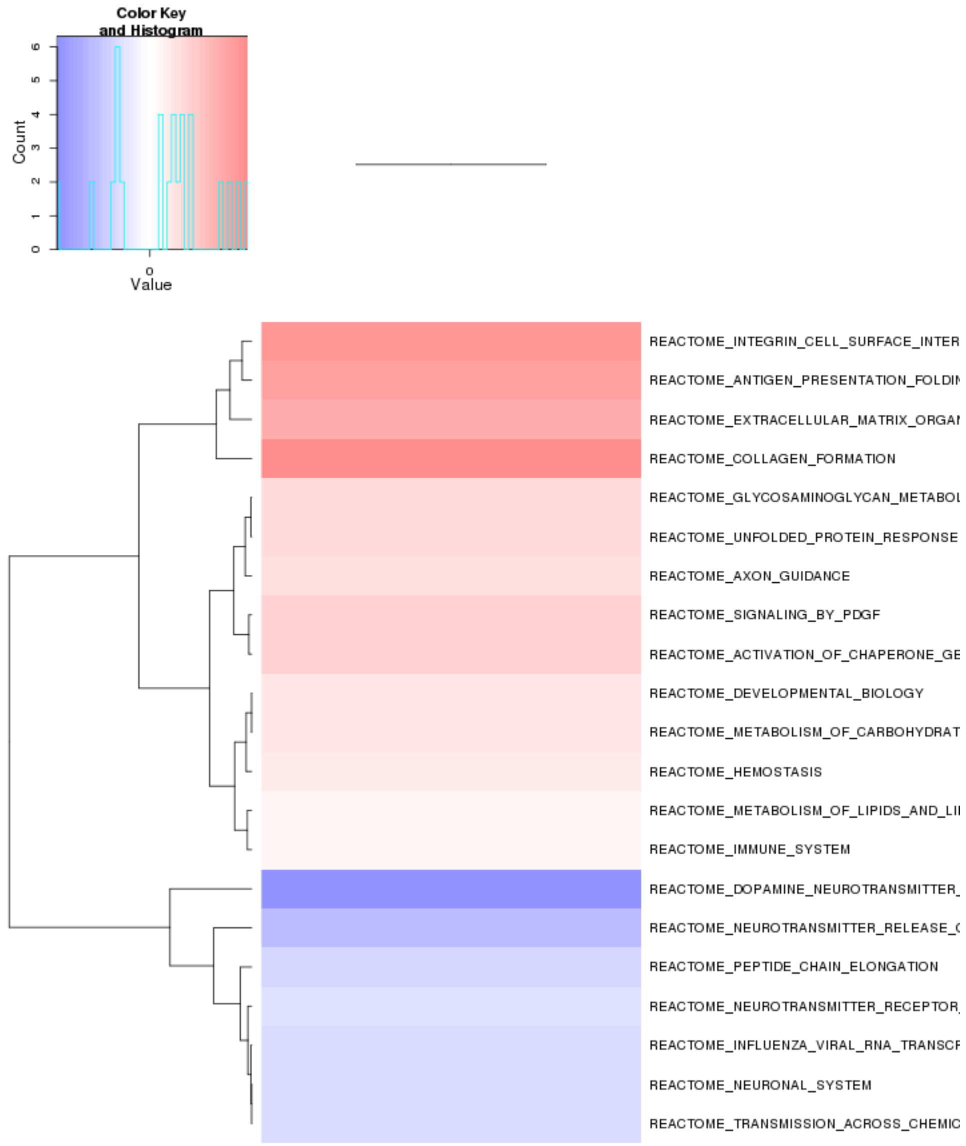
Biocarta zscore:



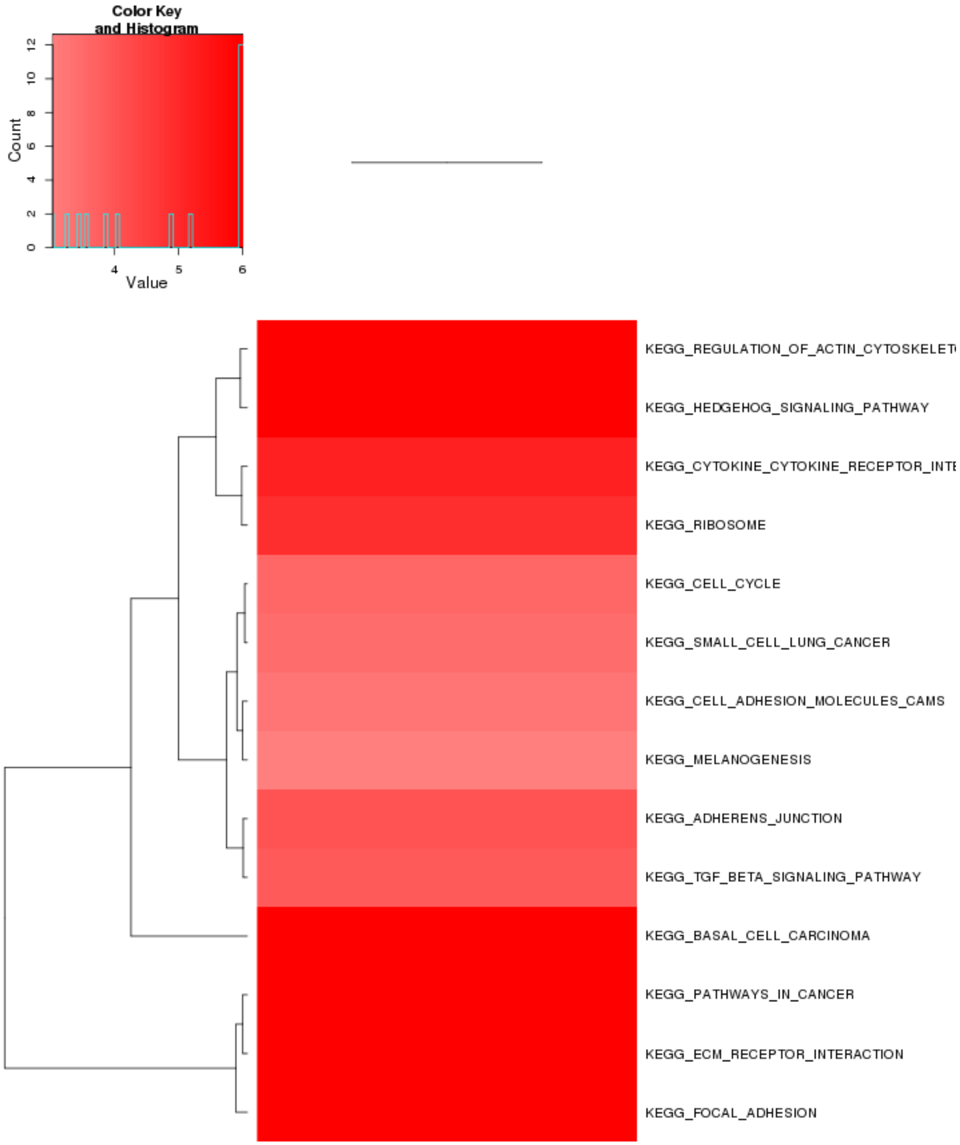
Reactome enrichment:



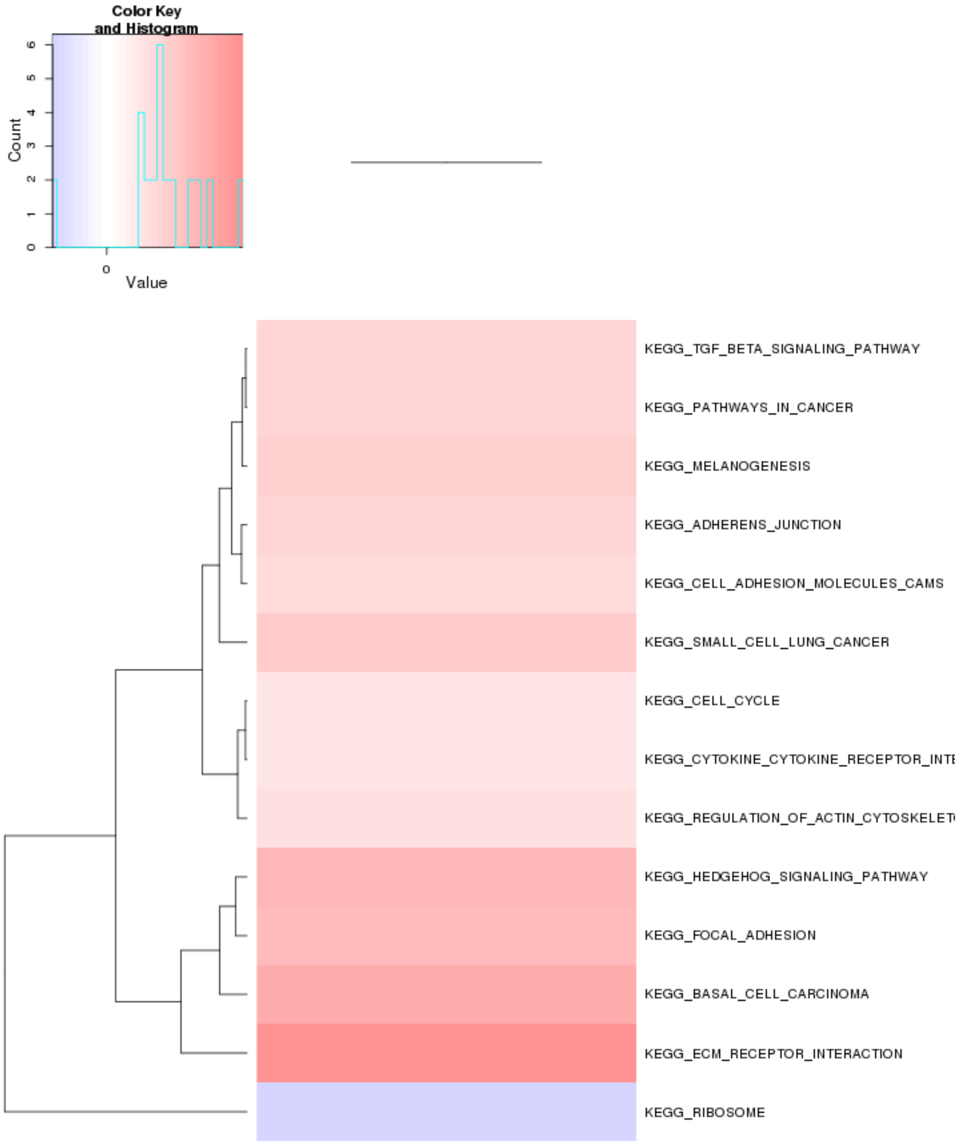
Reactome zscore:



Kegg enrichment:


Color Key
and Histogram
Count
0
2
4
6
8
10
12
4
5
6
Value
KEGG_REGULATION_OF_ACTIN_CYTOSKELET
KEGG_HEDGEHOG_SIGNALING_PATHWAY
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTE
KEGG_RIBOSOME
KEGG_CELL_CYCLE
KEGG_SMALL_CELL_LUNG_CANCER
KEGG_CELL_ADHESION_MOLECULES_CAMS
KEGG_MELANOGENESIS
KEGG_ADHERENS_JUNCTION
KEGG_TGF_BETA_SIGNALING_PATHWAY
KEGG_BASAL_CELL_CARCINOMA
KEGG_PATHWAYS_IN_CANCER
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_FOCAL_ADHESION

Kegg zscore:



Interneuron enrichment:

```
## Error: argument is of length zero
```

Interneuron zscore:

```
## Error: incorrect number of dimensions
```

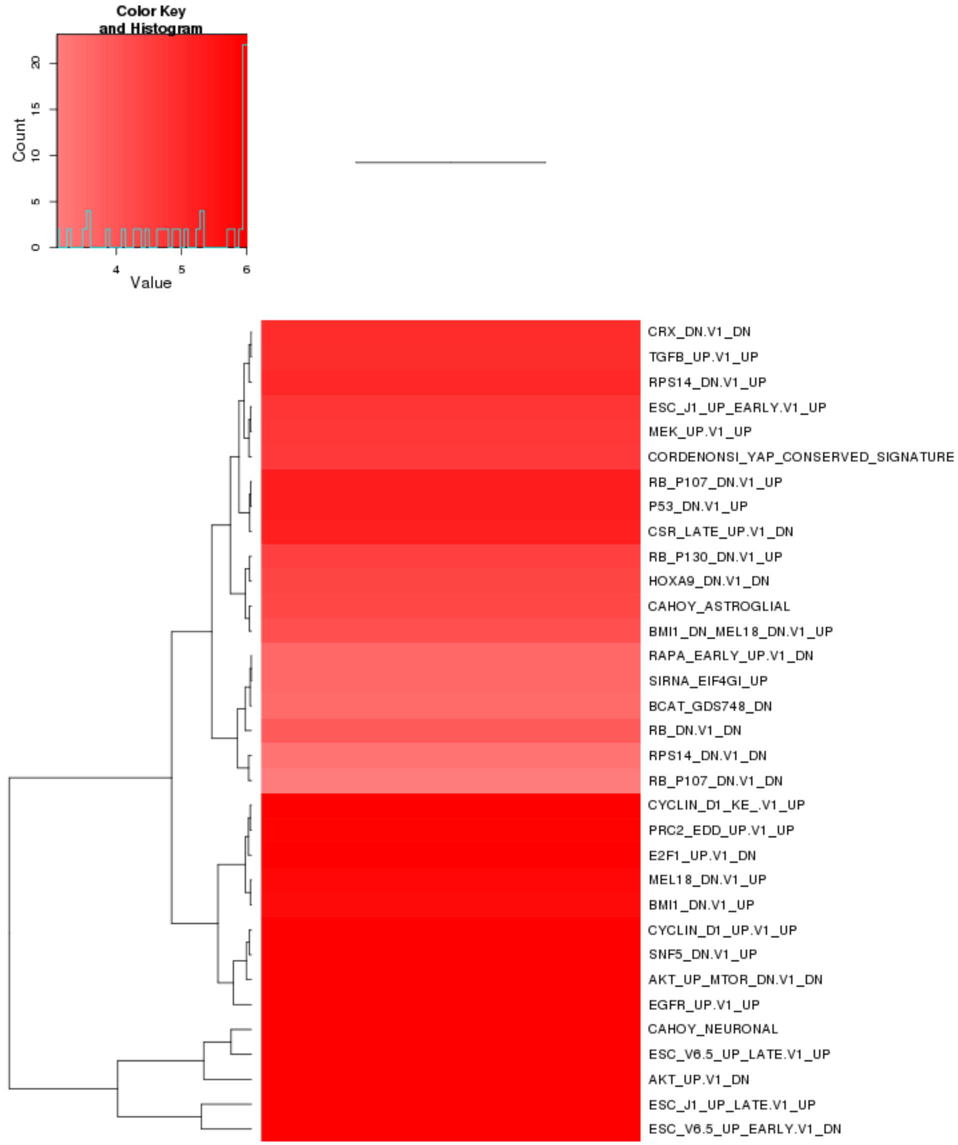
```
## Error: object 'x_ordered' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

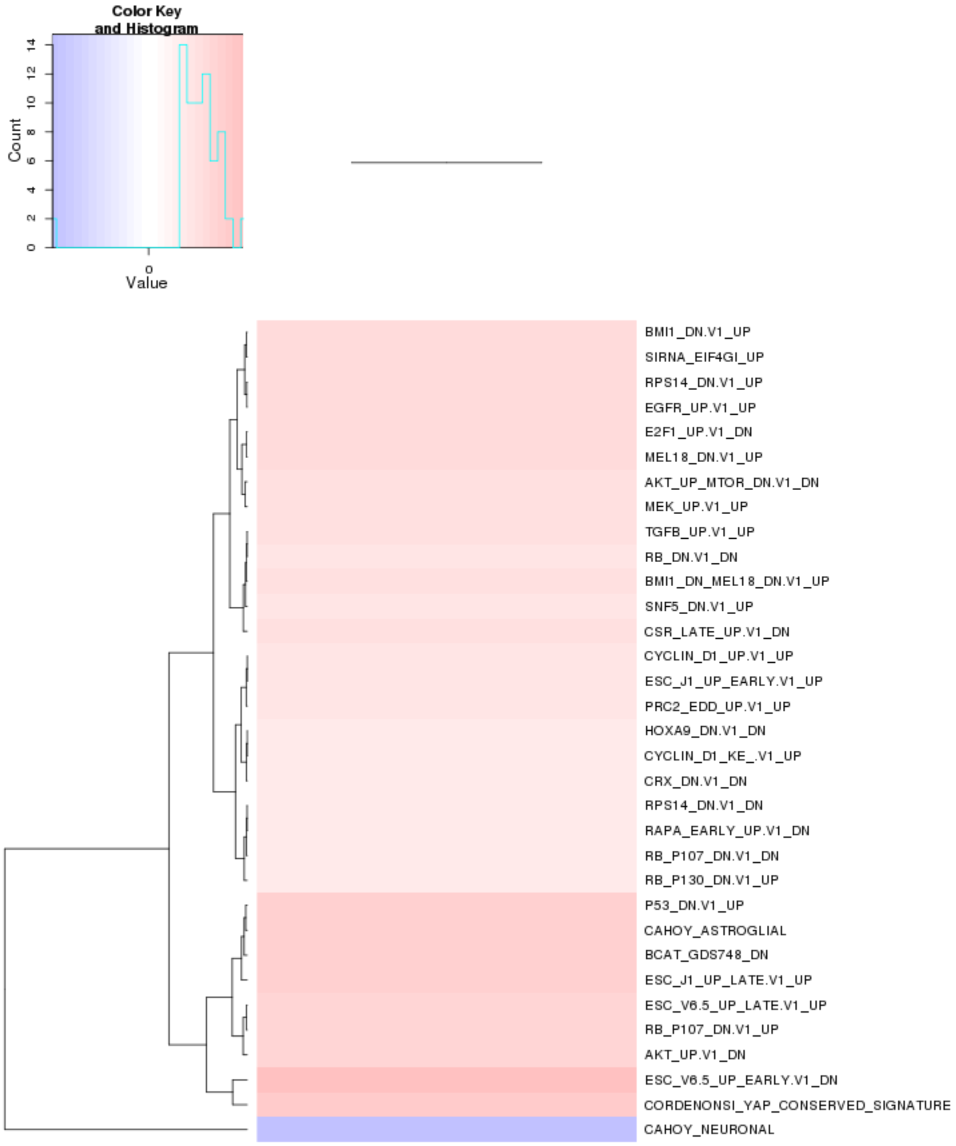
Oncogene enrichment:

```
## Error: subscript out of bounds
```

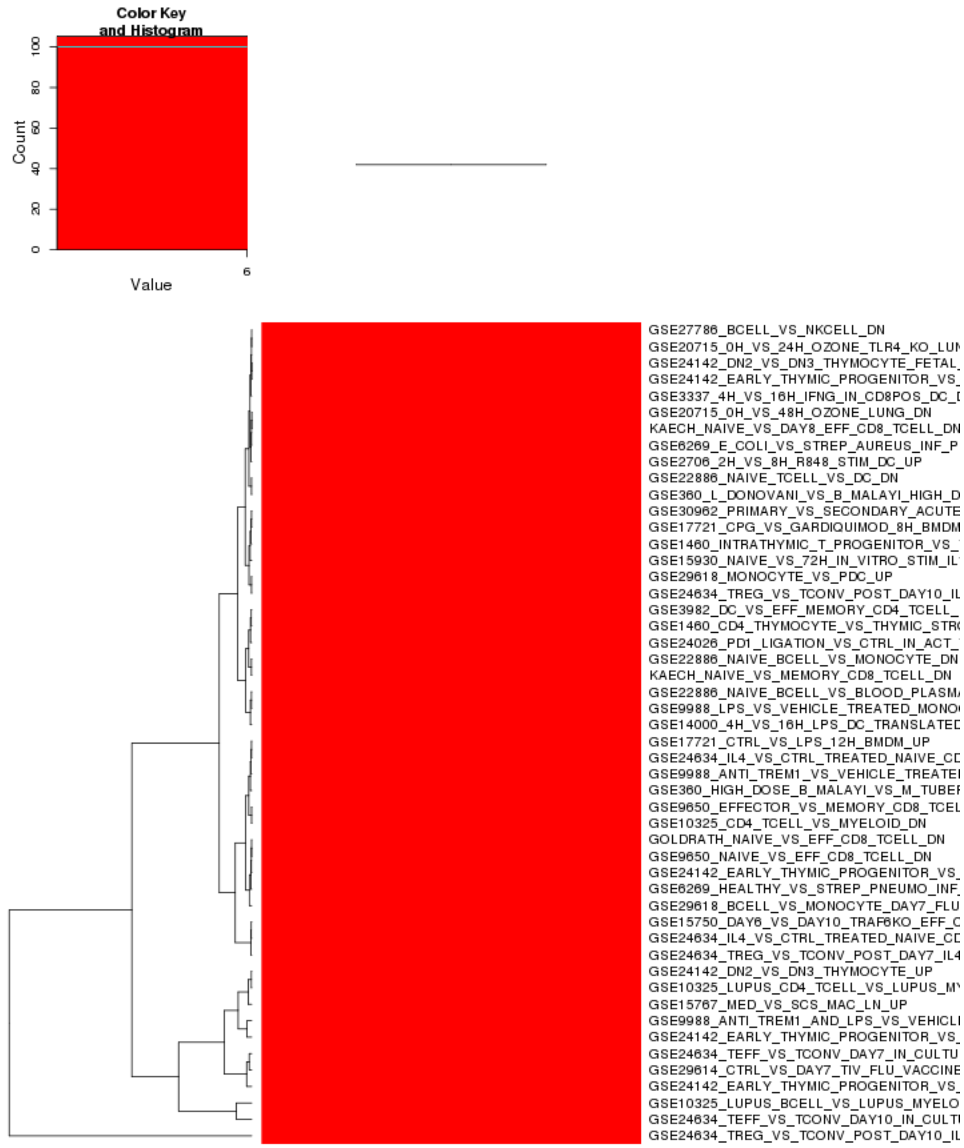


Oncogene zscore:

```
## Error: subscript out of bounds
```

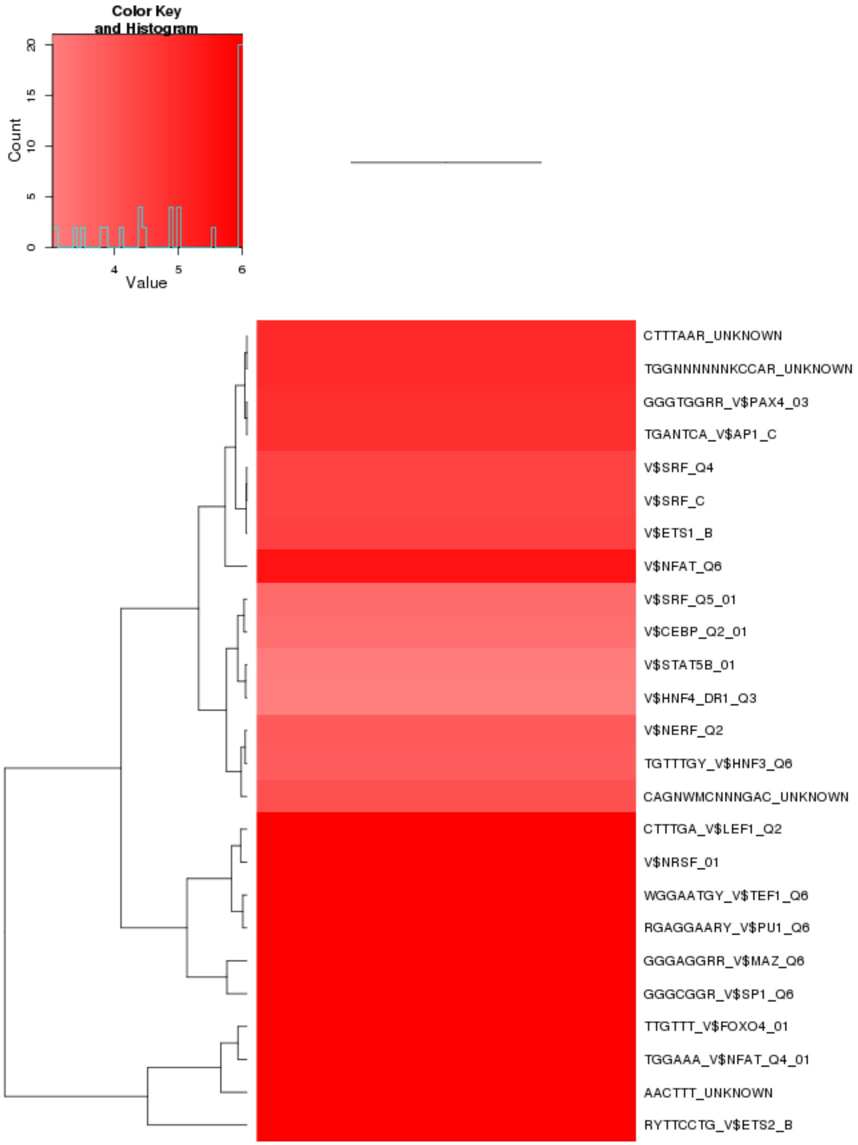


Immuno enrichment:

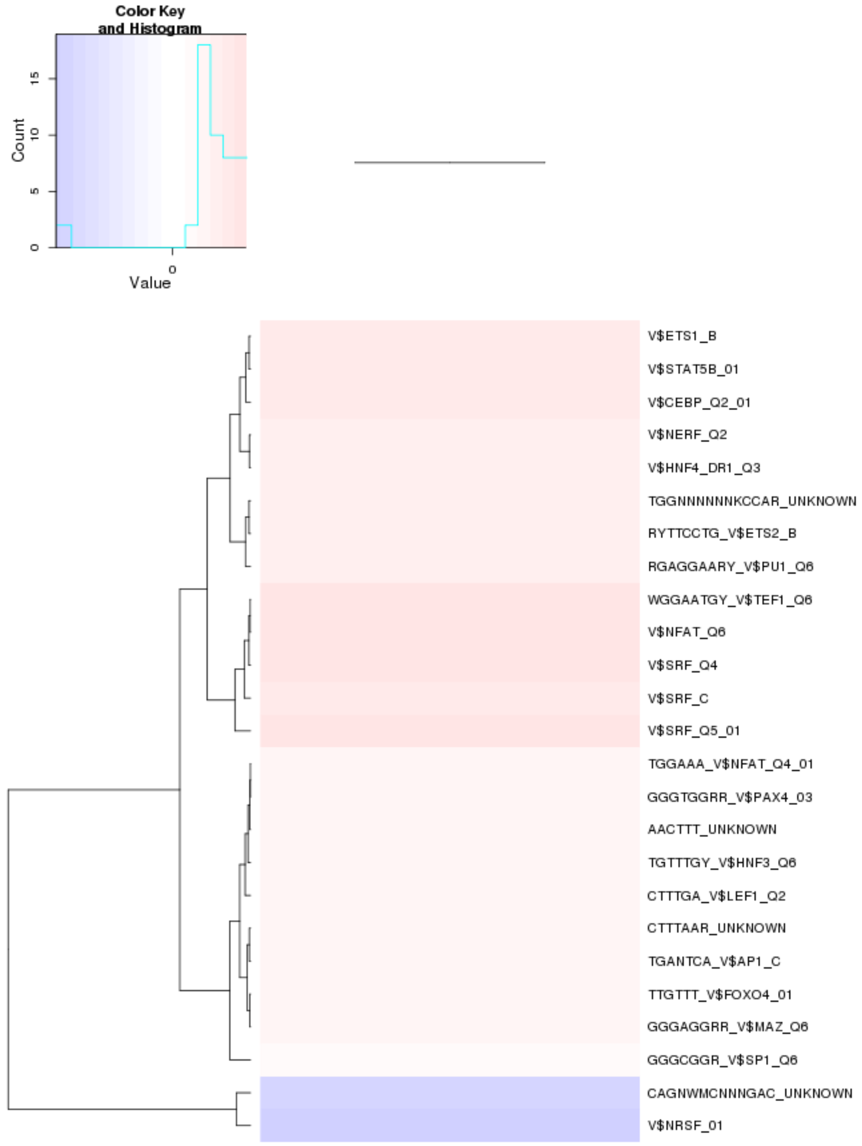


Immuno zscore:

TF enrichment:

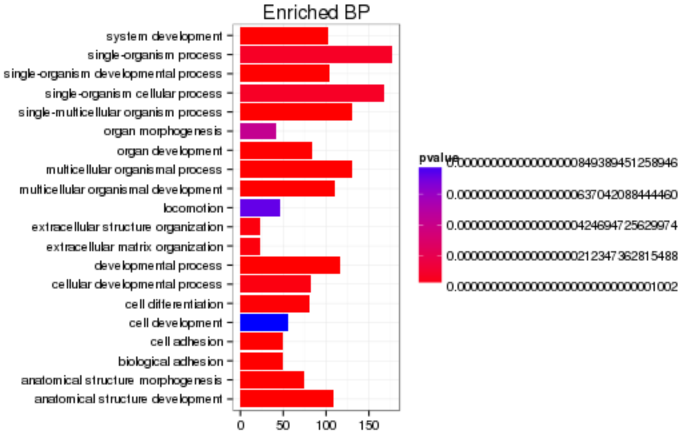

Color Key
and Histogram
Count
0
5
10
15
20
4
5
6
Value
CTTTAAR_UNKNOWN
TGGNNNNNNKCCAR_UNKNOWN
GGGTGGRR_V$PAX4_03
TGANTCA_V$AP1_C
V$SRF_Q4
V$SRF_C
V$ETS1_B
V$NFAT_Q6
V$SRF_Q5_01
V$CEBP_Q2_01
V$STAT5B_01
V$HNF4_DR1_Q3
V$NERF_Q2
TGTTTGY_V$HNF3_Q6
CAGNWMCNNNGAC_UNKNOWN
CTTTGA_V$LEF1_Q2
V$NRSF_01
WGGAATGY_V$TEF1_Q6
RGAGGAARY_V$PU1_Q6
GGGAGGRR_V$MAZ_Q6
GGGCGGR_V$SP1_Q6
TTGTTT_V$FOXO4_01
TGGAAA_V$NFAT_Q4_01
AACTTT_UNKNOWN
RYTTCCTG_V$ETS2_B

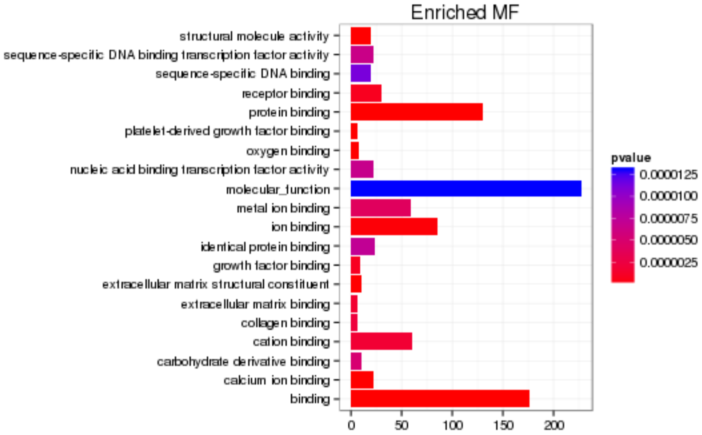
TF zscore:

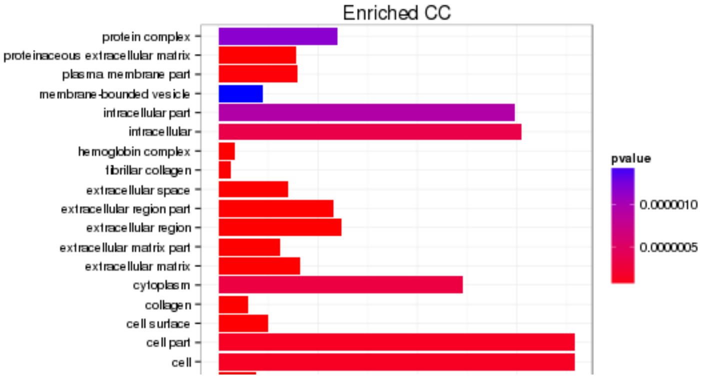


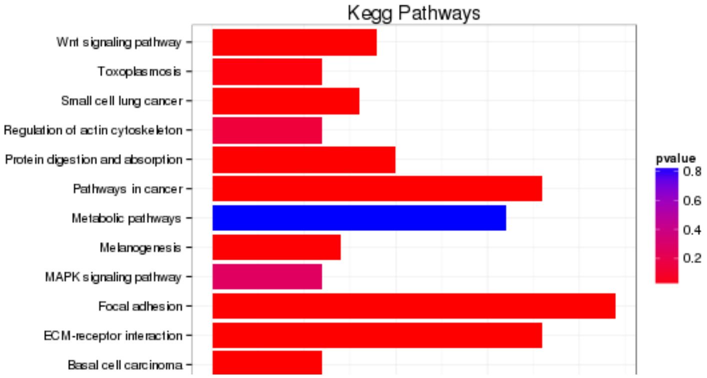
GO enrichment

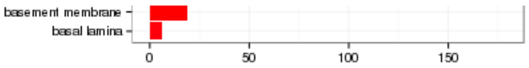
Cluster profiler used to call enichments of significantly differentially regulated genes that map to Entrez IDs.

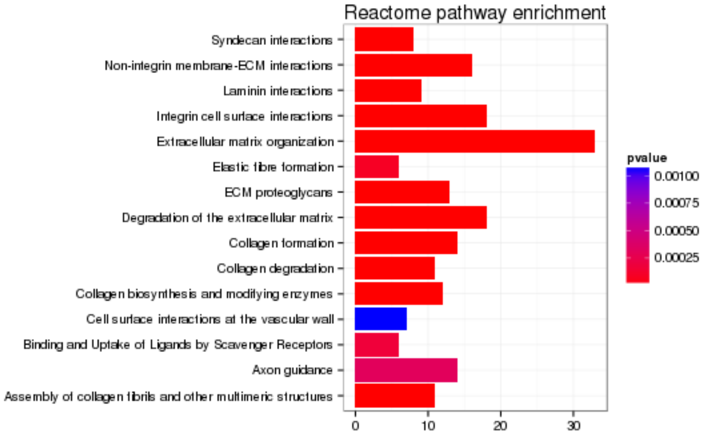

Enriched BP
system development
single-organism process
single-organism developmental process
single-organism cellular process
single-multicellular organism process
organ morphogenesis
organ development
multicellular organismal process
multicellular organismal development
locomotion
extracellular structure organization
extracellular matrix organization
developmental process
cellular developmental process
cell differentiation
cell development
cell adhesion
biological adhesion
anatomical structure morphogenesis
anatomical structure development
0
50
100
150
pvalue
0.00000000000000000000849389451258946
0.00000000000000000000637042088444460
0.00000000000000000000424694725629974
0.00000000000000000000212347362815488
0.00000000000000000000000000000001002


Enriched MF
structural molecule activity
sequence-specific DNA binding transcription factor activity
sequence-specific DNA binding
receptor binding
protein binding
platelet-derived growth factor binding
oxygen binding
nucleic acid binding transcription factor activity
molecular_function
metal ion binding
ion binding
identical protein binding
growth factor binding
extracellular matrix structural constituent
extracellular matrix binding
collagen binding
cation binding
carbohydrate derivative binding
calcium ion binding
binding
0
50
100
150
200
pvalue
0.0000125
0.0000100
0.0000075
0.0000050
0.0000025

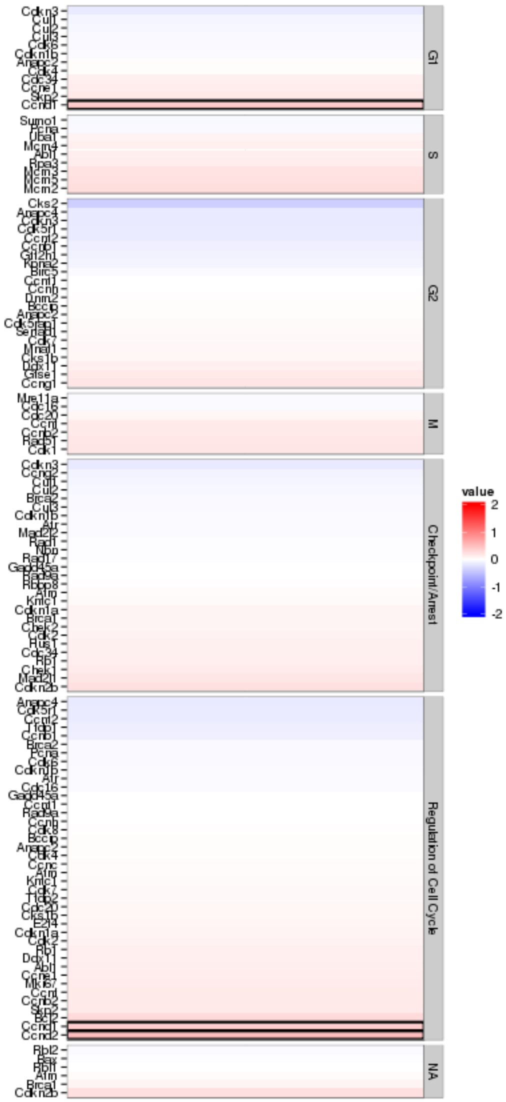

Enriched CC
protein complex
proteinaceous extracellular matrix
plasma membrane part
membrane-bounded vesicle
intracellular part
intracellular
hemoglobin complex
fibrillar collagen
extracellular space
extracellular region part
extracellular region
extracellular matrix part
extracellular matrix
cytoplasm
collagen
cell surface
cell part
cell
pvalue
0.0000010
0.0000005


Kegg Pathways
Wnt signaling pathway
Toxoplasmosis
Small cell lung cancer
Regulation of actin cytoskeleton
Protein digestion and absorption
Pathways in cancer
Metabolic pathways
Melanogenesis
MAPK signaling pathway
Focal adhesion
ECM-receptor interaction
Basal cell carcinoma
pvalue
0.8
0.6
0.4
0.2

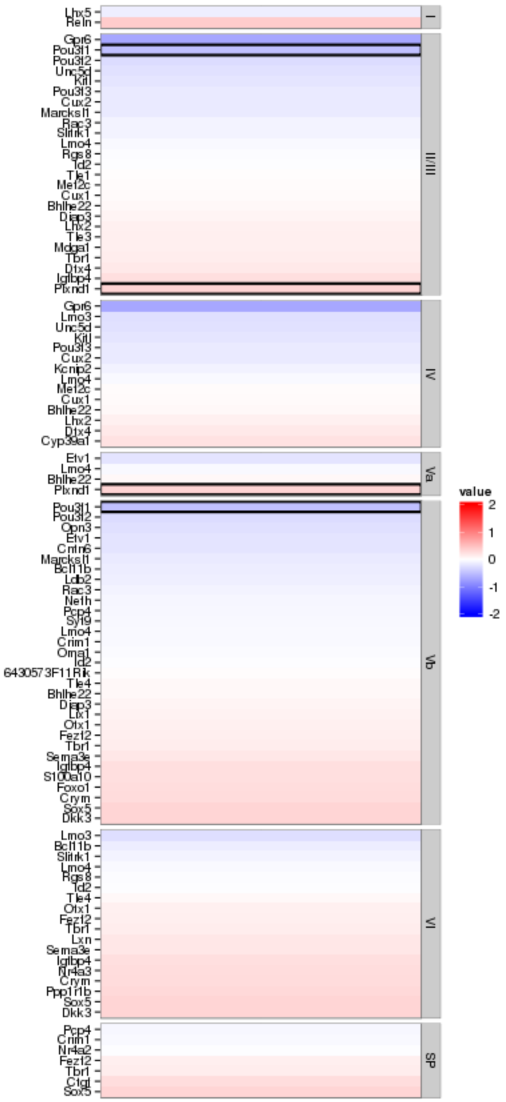




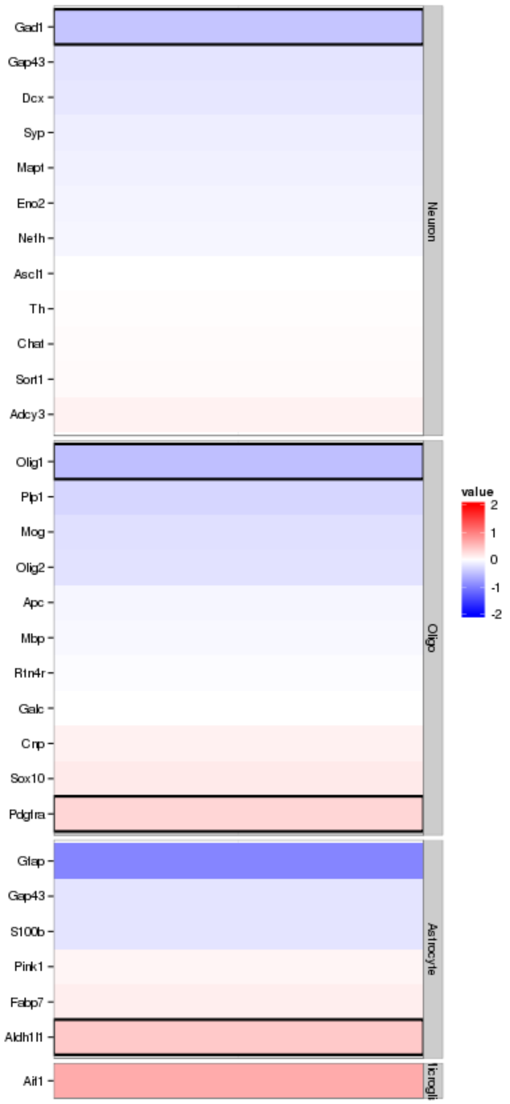
Enrichment or depletion for stage-specific cell cycle markers



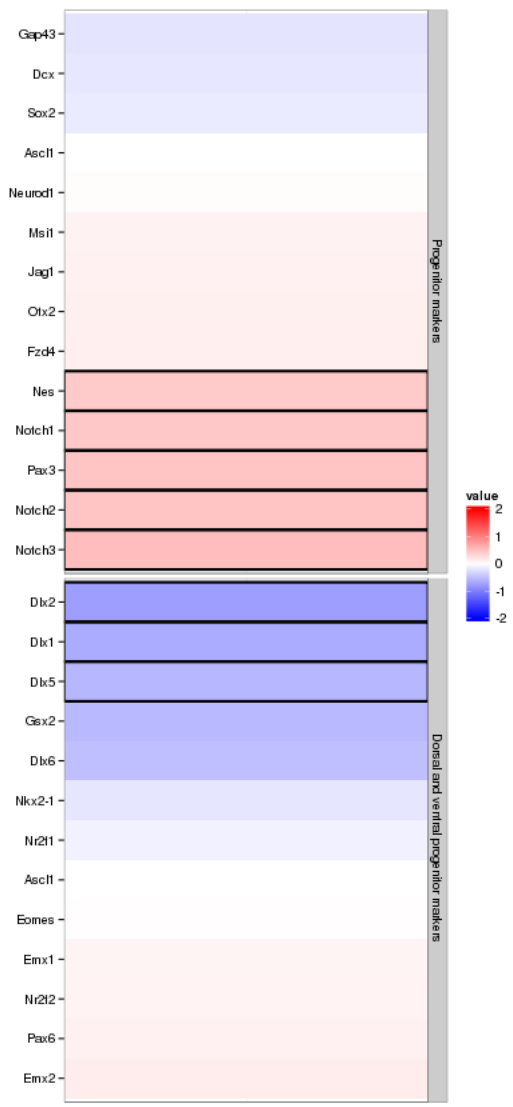
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



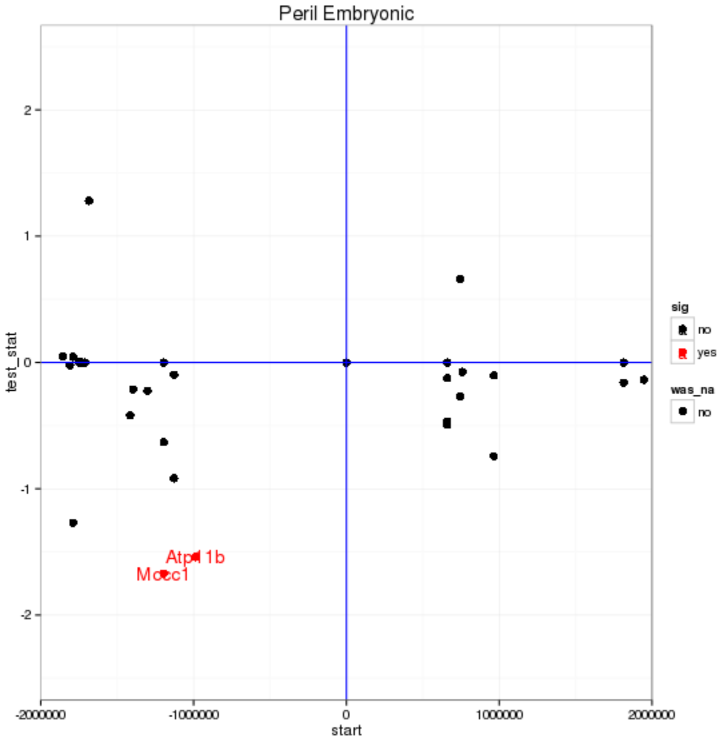
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 2 genes significantly regulated in a region this size is: 0.1906



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15 JR721
16 JR718
17 JR720
18 JR792

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	30202700.00	1.35	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	30202700.00	1.18	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	30202700.00	1.31	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	30202700.00	1.38	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	30202700.00	1.28	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	30202700.00	0.95	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	30202700.00	1.04	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	30202700.00	0.98	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	30202700.00	0.92	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	30202700.00	1.03	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	30202700.00	0.87	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	30202700.00	0.85	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	30202700.00	0.73	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	30202700.00	1.30	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR721/abundances.cxb	Peril	0	Peril_0	22593200.00	30202700.00	0.75	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR718/abundances.cxb	Peril	1	Peril_1	27635500.00	30202700.00	0.92	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR720/abundances.cxb	Peril	2	Peril_2	19589600.00	30202700.00	0.64	1.00
18	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR792/abundances.cxb	Peril	3	Peril_3	29654500.00	30202700.00	0.99	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils
## [8] datasets  base
##
## other attached packages:
##  [1] plyr_1.8.1
```

```
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
```

```
## [40] tools_3.0.2           XML_3.98-1.1          zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,Peril -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Peril_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/BrainMap/dat
## 2
## 3
## 4
## 5
```

Trp53cor1 KO vs WT (Adult)

This file shows the wt-v-ko comparison for Trp53cor1.

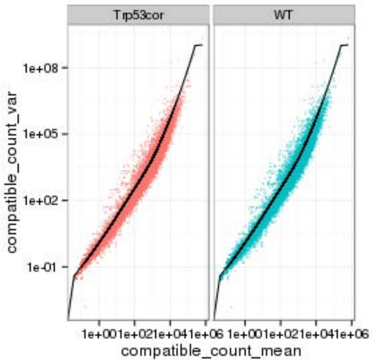
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

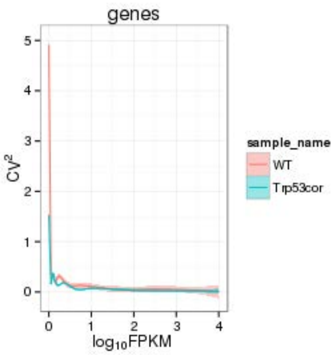
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



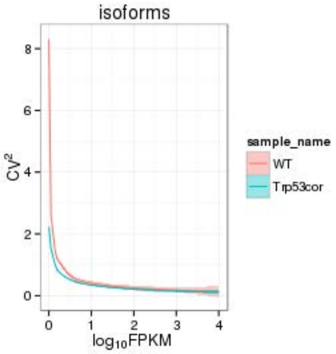
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

Genes:



Isoforms:



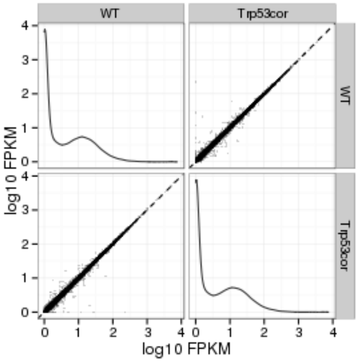
MvA plot

```
## Error: non-numeric argument to binary operator
```

MvA plot counts

```
## Error: non-numeric argument to binary operator
```

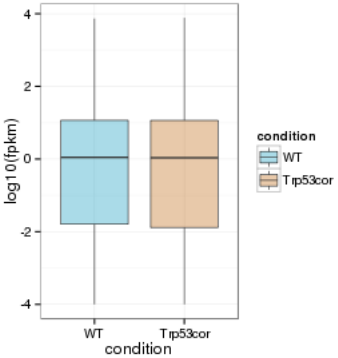
Scatterplot matrix



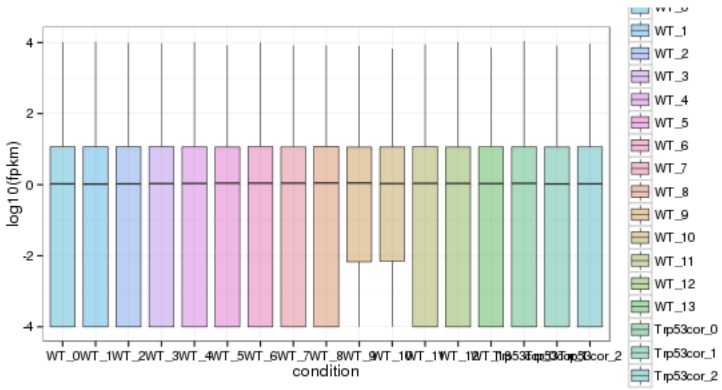
Distributions

Boxplots

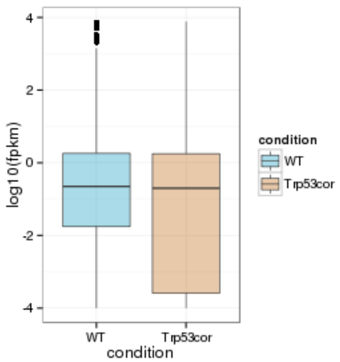
Boxplot (genes)



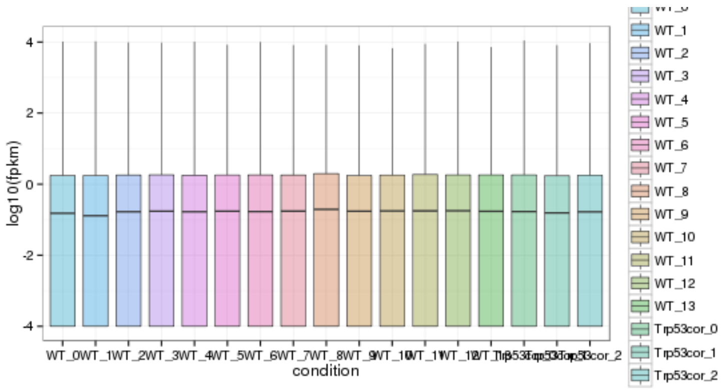
Boxplot (genes, replicates)



Boxplot (isoforms)

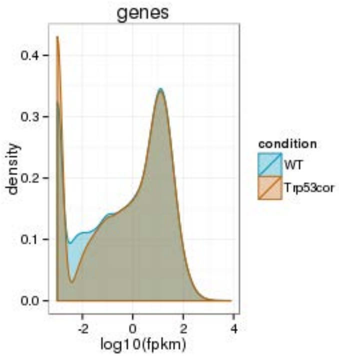


Boxplot (isoforms, replicates)

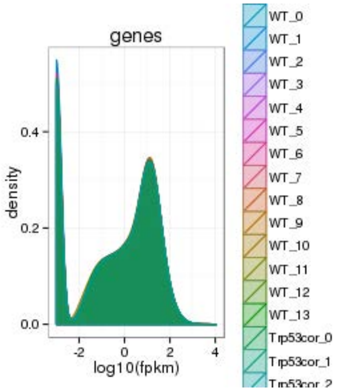


Density

Density (genes)

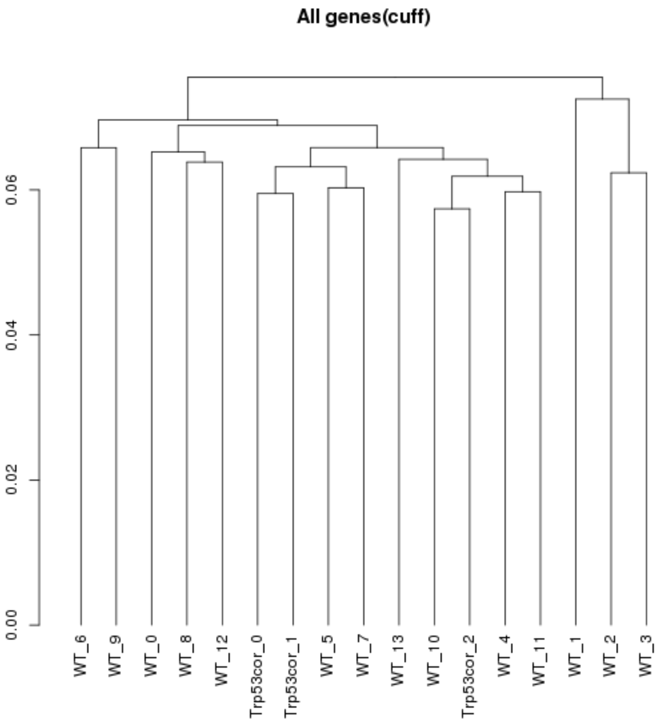


Density (genes, replicates)



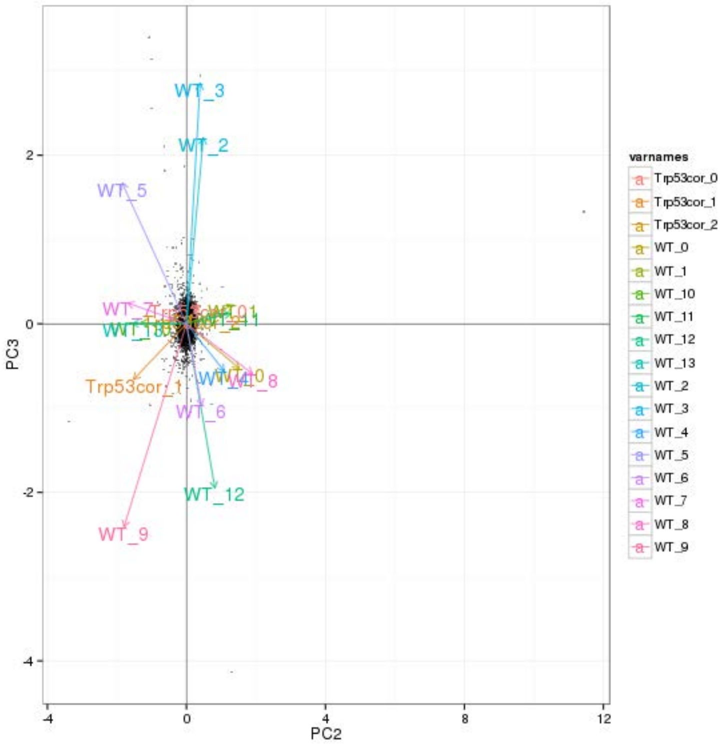
Clustering

Replicate Clusters

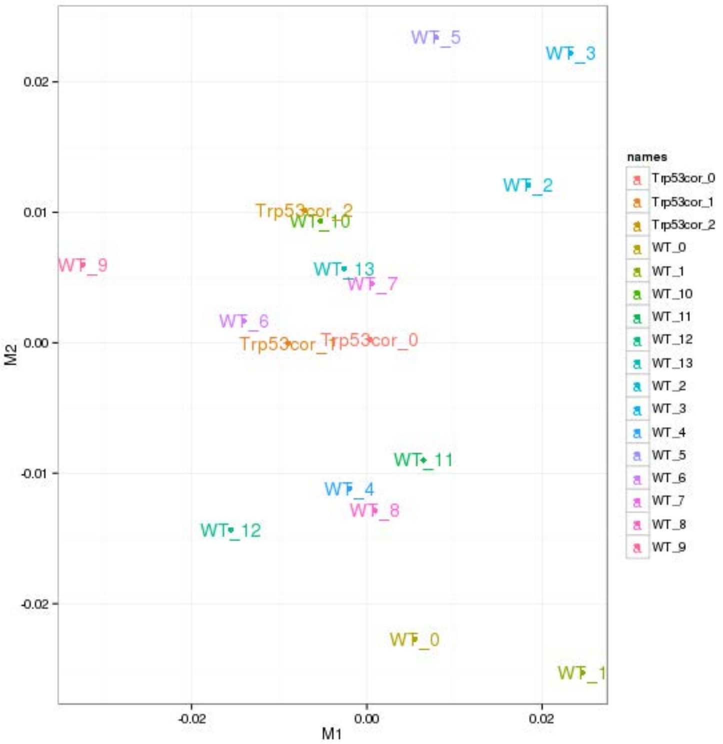


```
## NULL
```

PCA (genes)

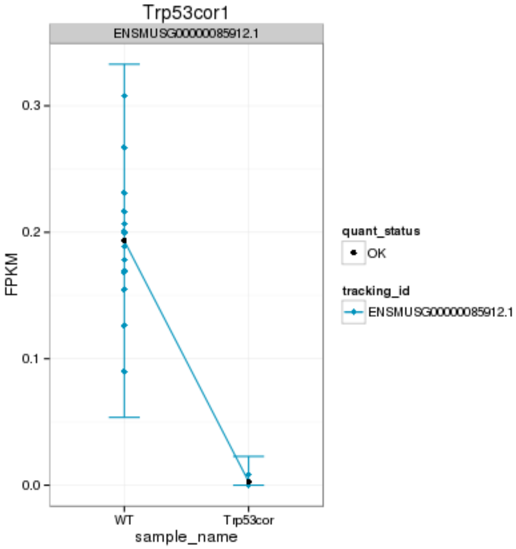

WT_3
WT_2
WT_5
WT_7
Trp53cor_1
WT_6
WT_8
WT_12
WT_9
2
0
-2
-4
PC3
-4
0
4
8
12
PC2
varnames
Trp53cor_0
Trp53cor_1
Trp53cor_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

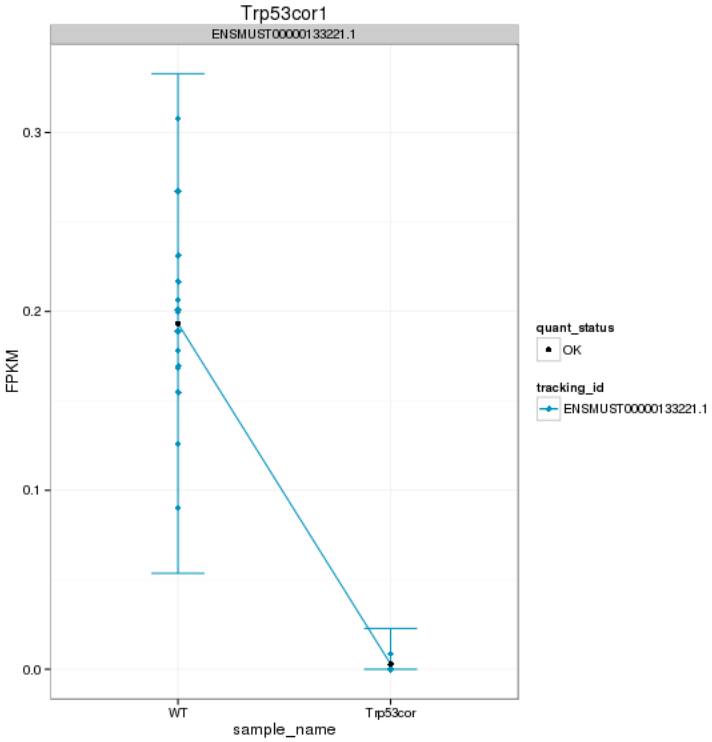


KO assessment

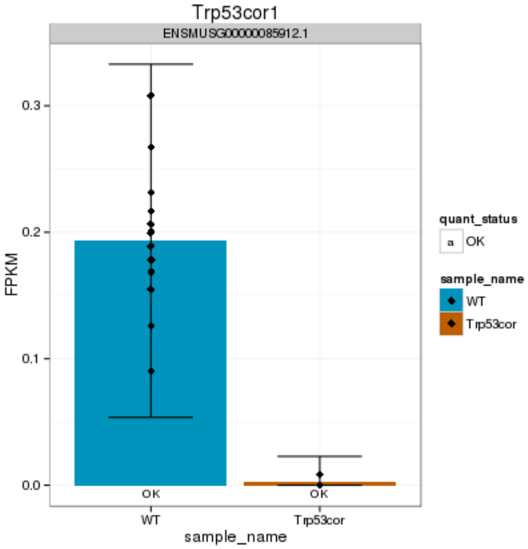
Endogenous lncRNA expression



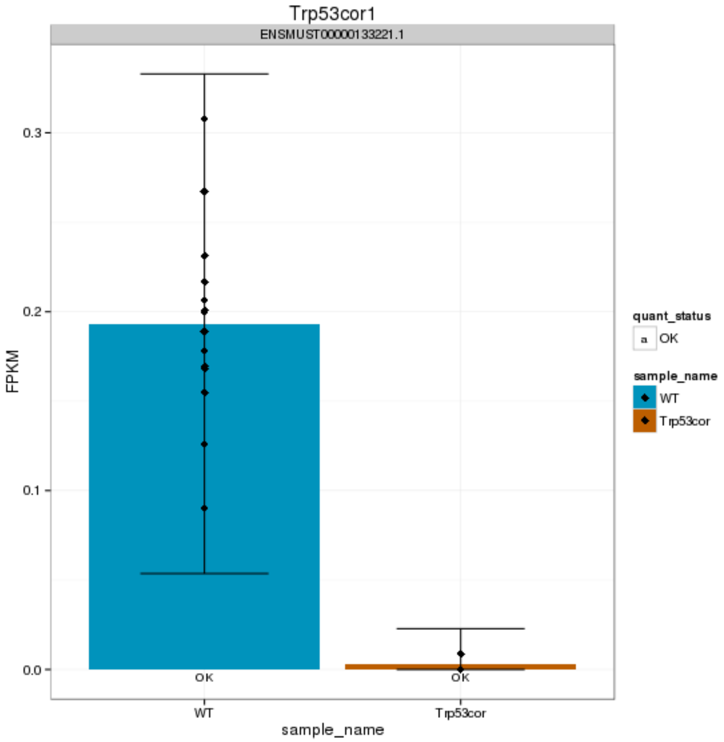
Endogenous expression of Trp53cor1 isoforms:



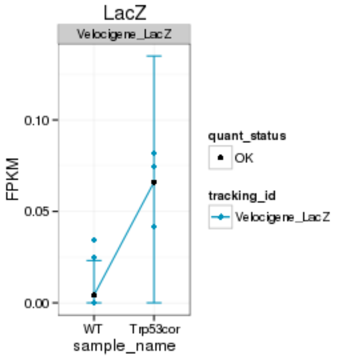
Barplot of gene expression:

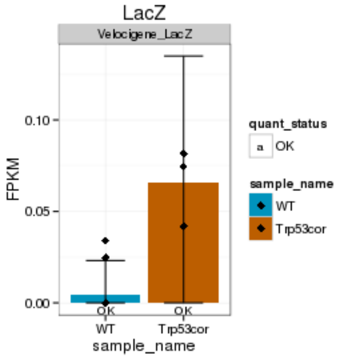


Barplot of isoform expression:



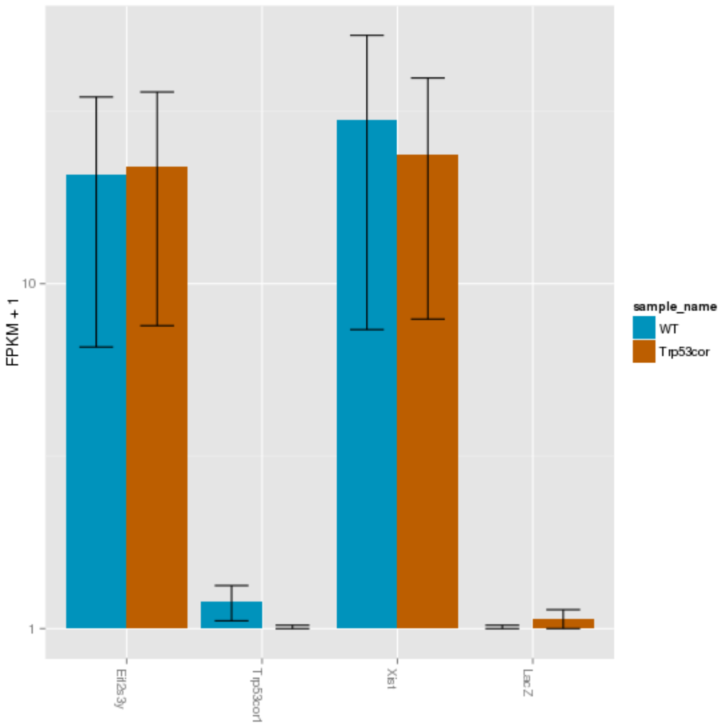
LacZ expression



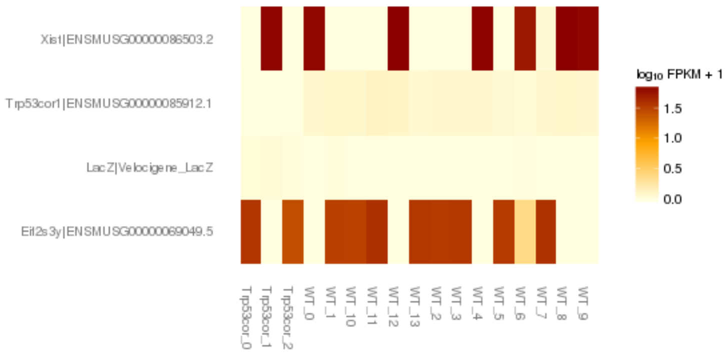


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

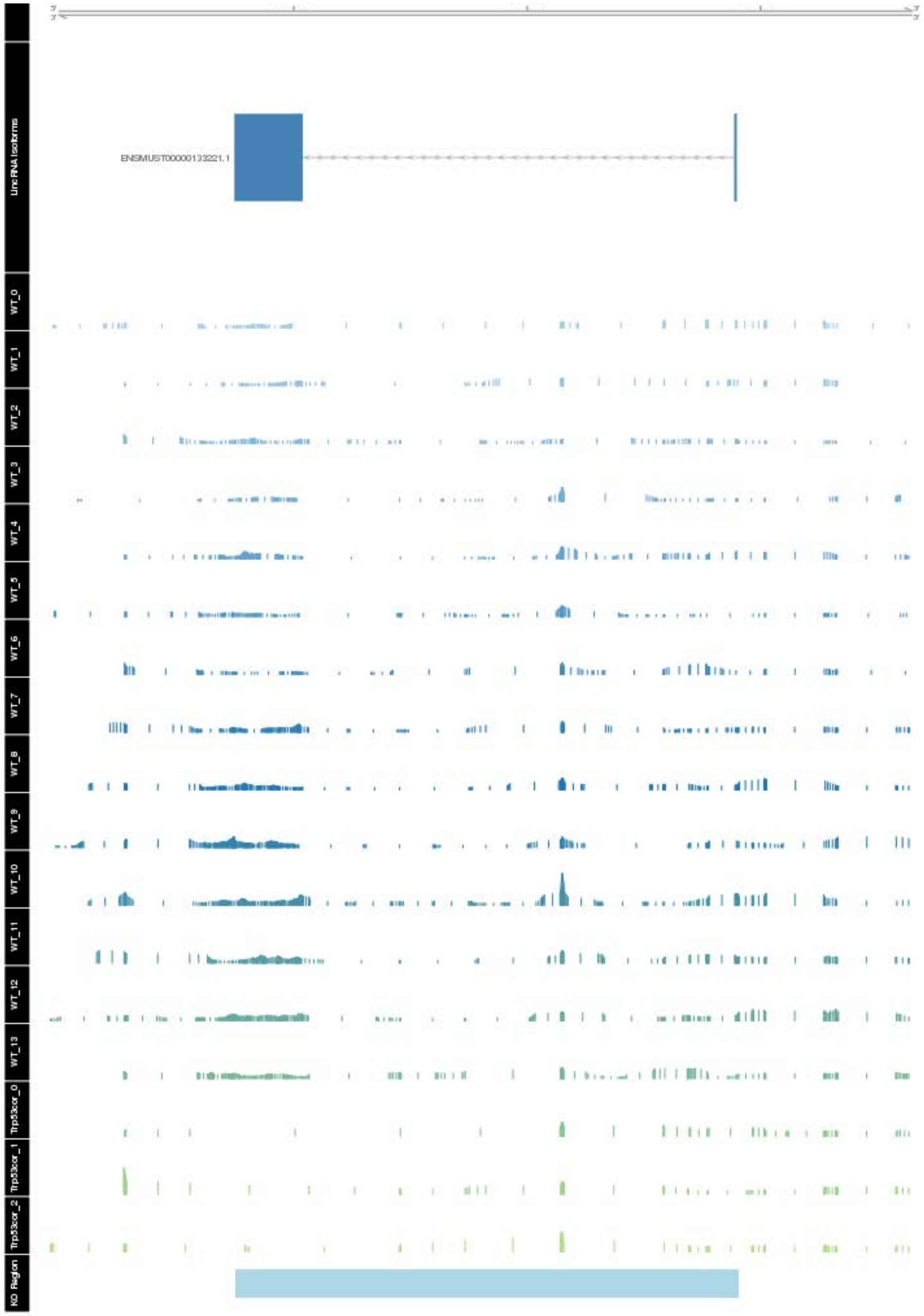
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


LincRNA Isoforms
ENSMUST00000133221.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Trp53cor_0
Trp53cor_1
Trp53cor_2
KO Region

Differential Analysis

Differential Genes

There are 69 significantly differentially expressed genes. They are:

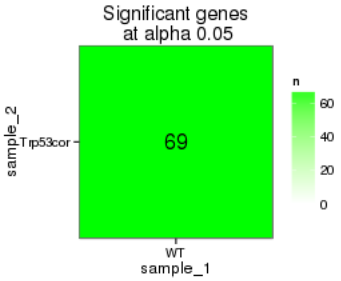
	geneAnnot$gene_short_name
1	Gabra2
2	Arrdc2
3	Nes
4	Epha2
5	Khsrp
6	Odc1
7	Tjap1
8	Etnppl
9	Fabp7
10	Sgk1
11	Adi1
12	Serpina3n
13	Kcnv1
14	Cdkn1a
15	Park2
16	Mpc1
17	Flywch2
18	Mut
19	Enpp4
20	Ppil1
21	Cpne5
22	Pi16
23	Glo1
24	Prss41
25	Atp6v0c
26	Spsb3
27	Adamts10
28	Rps24
29	Rps6
30	Adamts9
31	Gkn3
32	A2m
33	Hddc3
34	Tlr13
35	Arhgap27
36	Rnps1
37	Lars2

38 3110052M02Rik
39 Decr2
40 Cramp1l
41 Gm129
42 Akap12
43 Itpkb

44 Lyplal1
45 Fmo2
46 Rps19
47 Maff
48 Gm9493
49 Zfp758
50 Acp1
51 Hmga1
52 Tmem252
53 Pla2g4e
54 Tagap1
55 Arntl
56 Per2
57 H2-T22
58 Ide
59 Cox5b
60 H2-T23
61 Zfp760
62 H2-Bl
63 9030025P20Rik
64 Hmga1-rs1
65 Apold1
66 AA465934
67 Rpl41
68 Gm9825
69 Tmem181b-ps

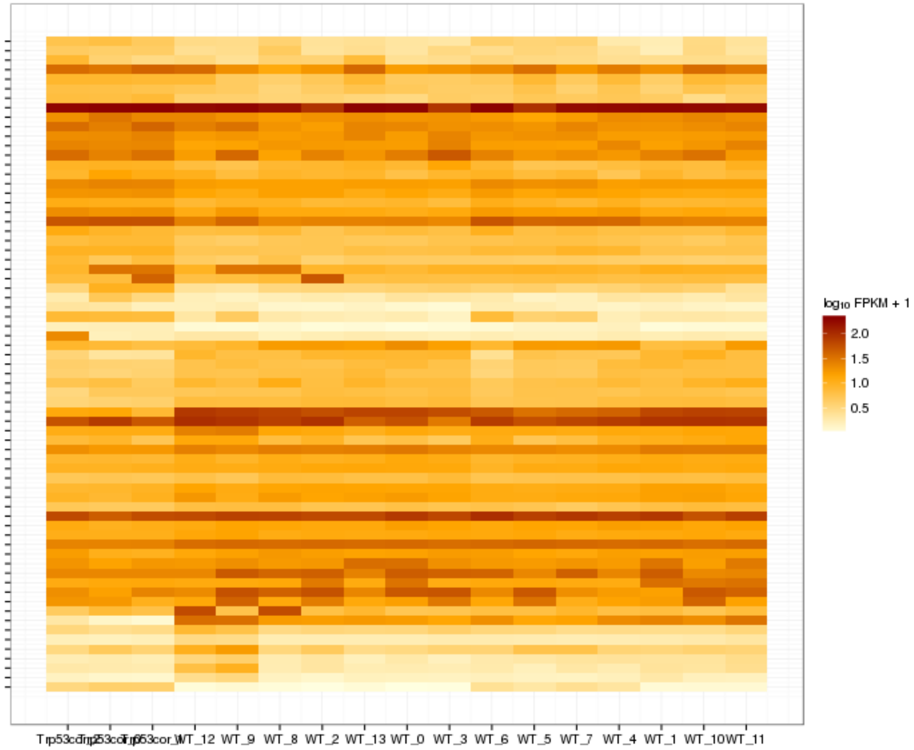
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)



Significant genes with expression >50fpkm (any condition):(turned off)

An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

Scatter plot of significant genes only:

```
## Error: One or more values of 'x' or 'y' are not valid sample names!
```

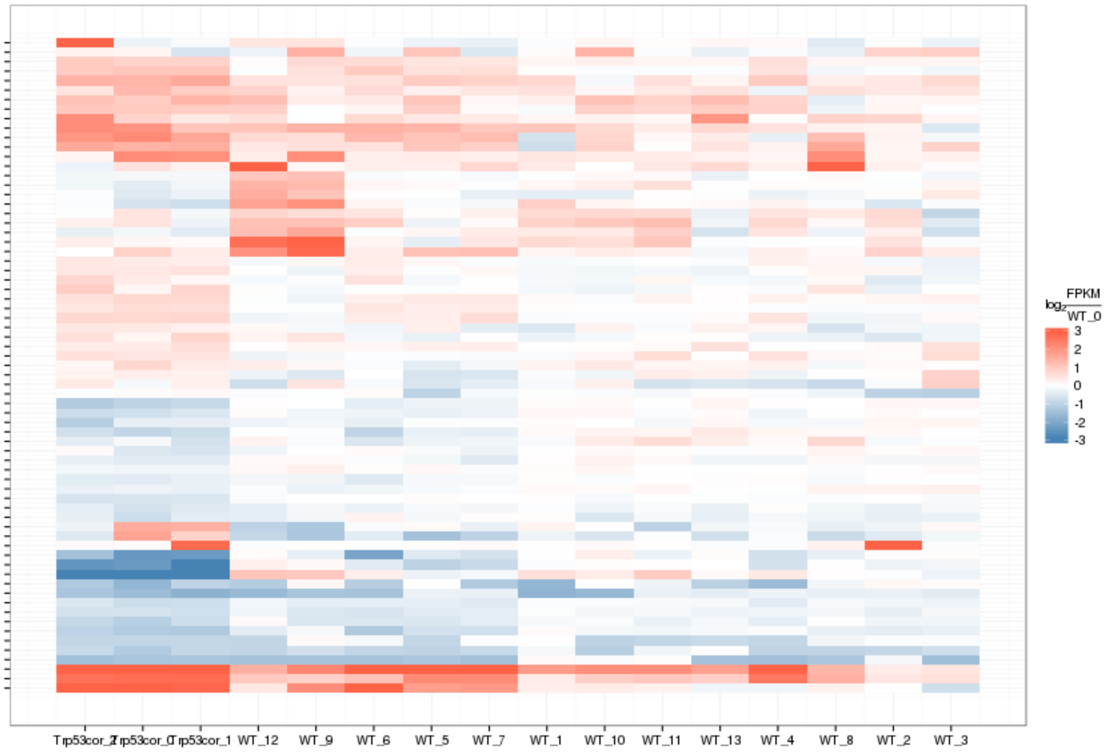
Volcano Plot

```
## Error: One or more values of 'x' or 'y' are not valid sample names!
```

Volcano plot with significant genes only:

```
## Error: One or more values of 'x' or 'y' are not valid sample names!
```

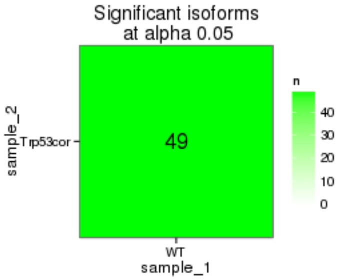
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:

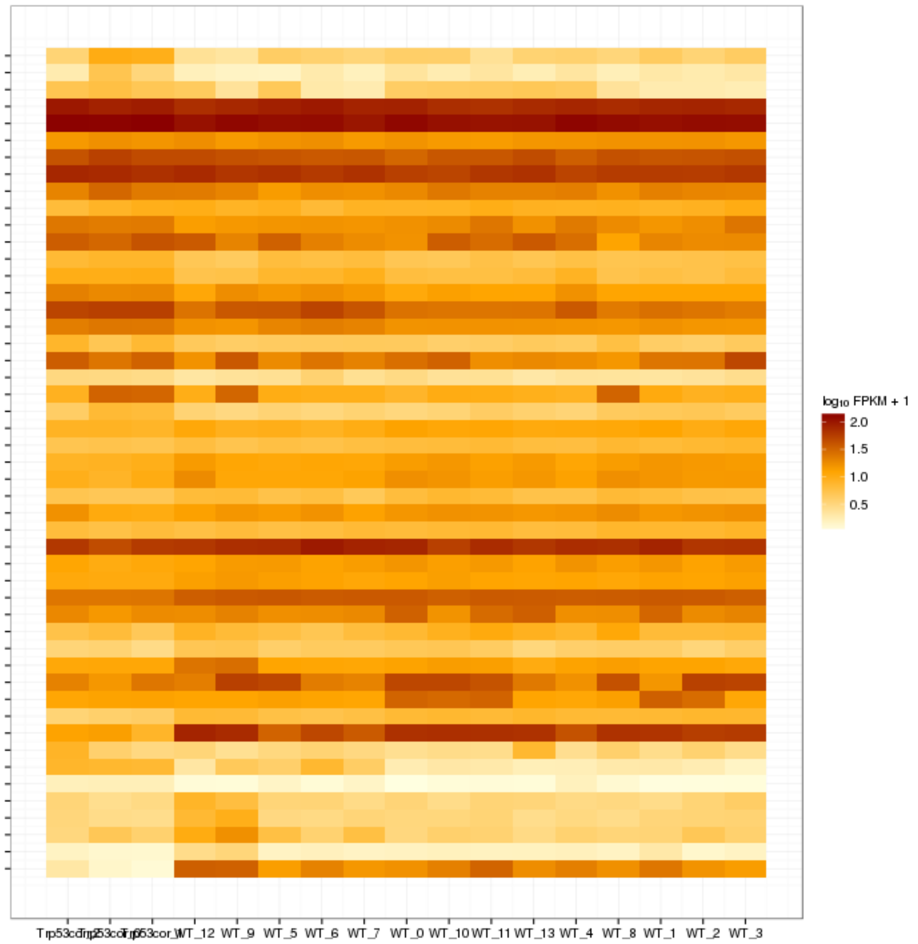


These isoforms are:

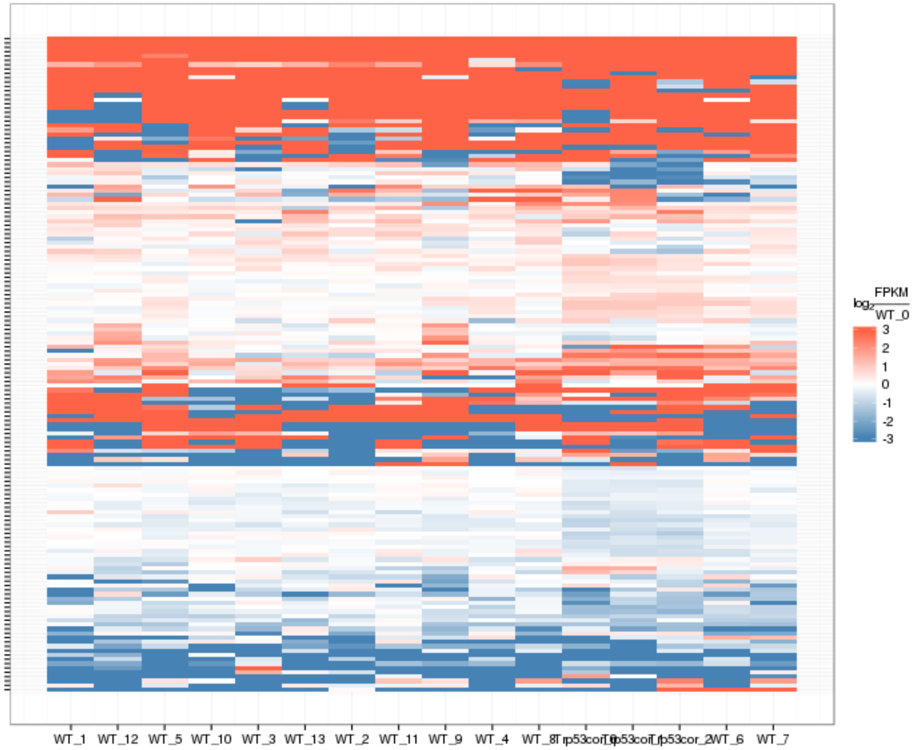
	isoAnnot$gene_short_name
1	Gabra2
2	Rec8
3	Klf4
4	Nes
5	Prlr
6	Epha2
7	Khsrp
8	Etnppl
9	Fabp7
10	Serpina3n
11	Tfrc
12	Cdkn1a
13	Hcfc1r1
14	Mut
15	Ppil1
16	Cpne5
17	Glo1
18	Atp6v0c
19	Adamts10
20	Rps24
21	Gng13
22	Gkn3
23	A2m
24	Hddc3
25	Vps8
26	Rnps1

27 Lars2
28 3110052M02Rik
29 Decr2
30 Cramp1l
31 Ano2
32 Akap12
33 Itpkb
34 Lyplal1
35 Fmo2
36 Bcor
37 Gm9493
38 Pla2g4e
39 Tagap1
40 Arntl
41 Ide
42 Zfp945
43 Zfp760
44 Fndc1
45 H2-Bl
46 9030025P20Rik
47 Mog
48 Apold1
49 Gm9825

Gene-level DE isoform heatmap



Isoform foldchange heatmap by isoform:



Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

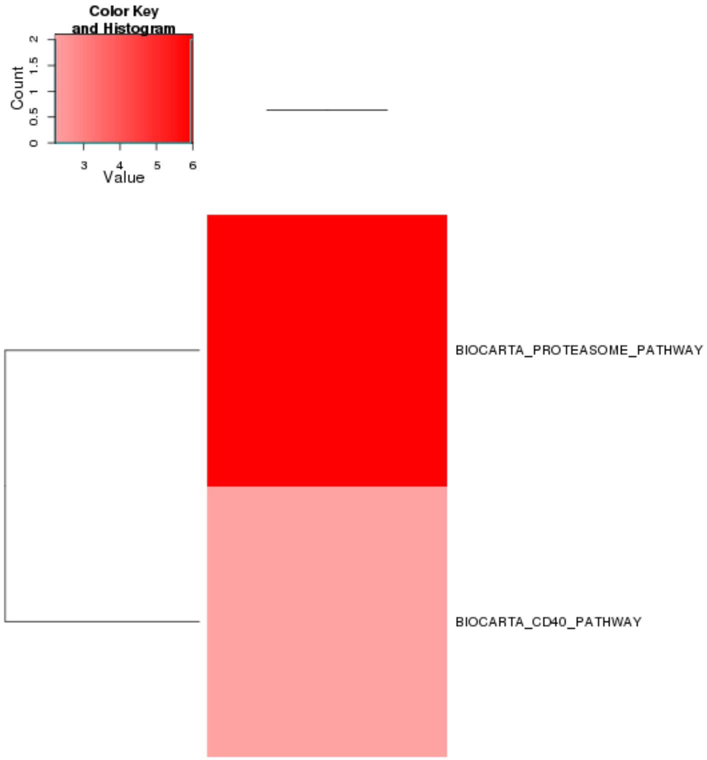
Gene/Pathway Analysis

GSEA

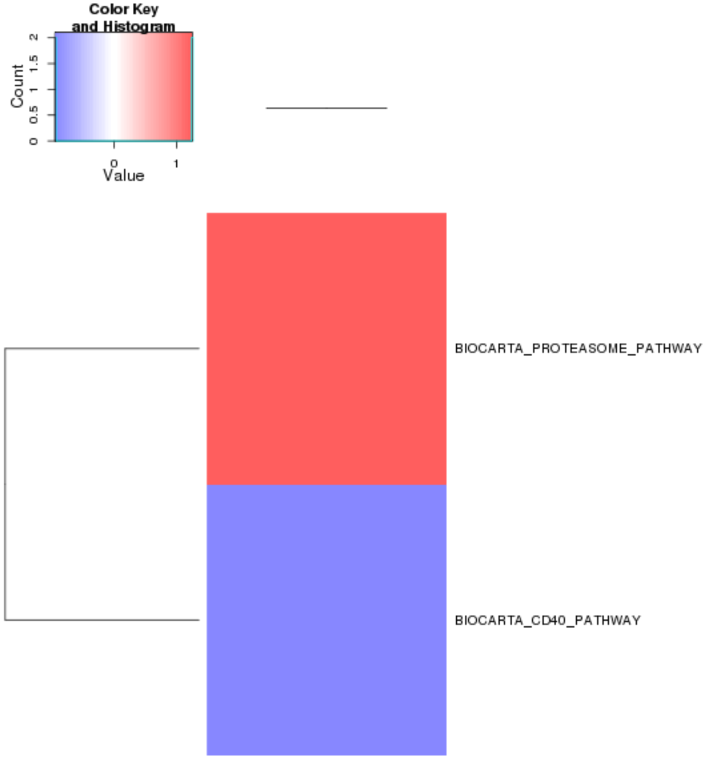
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

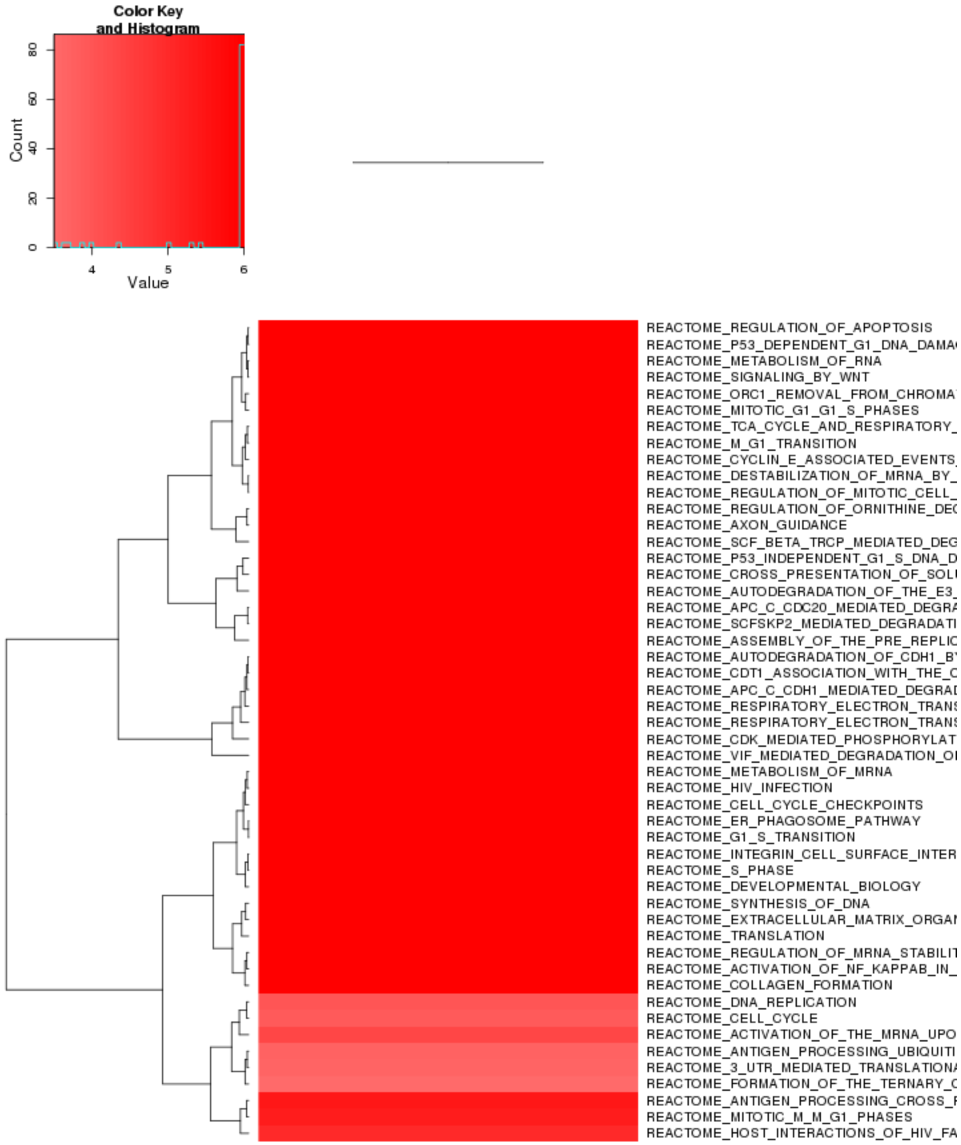
Biocarta enrichment:



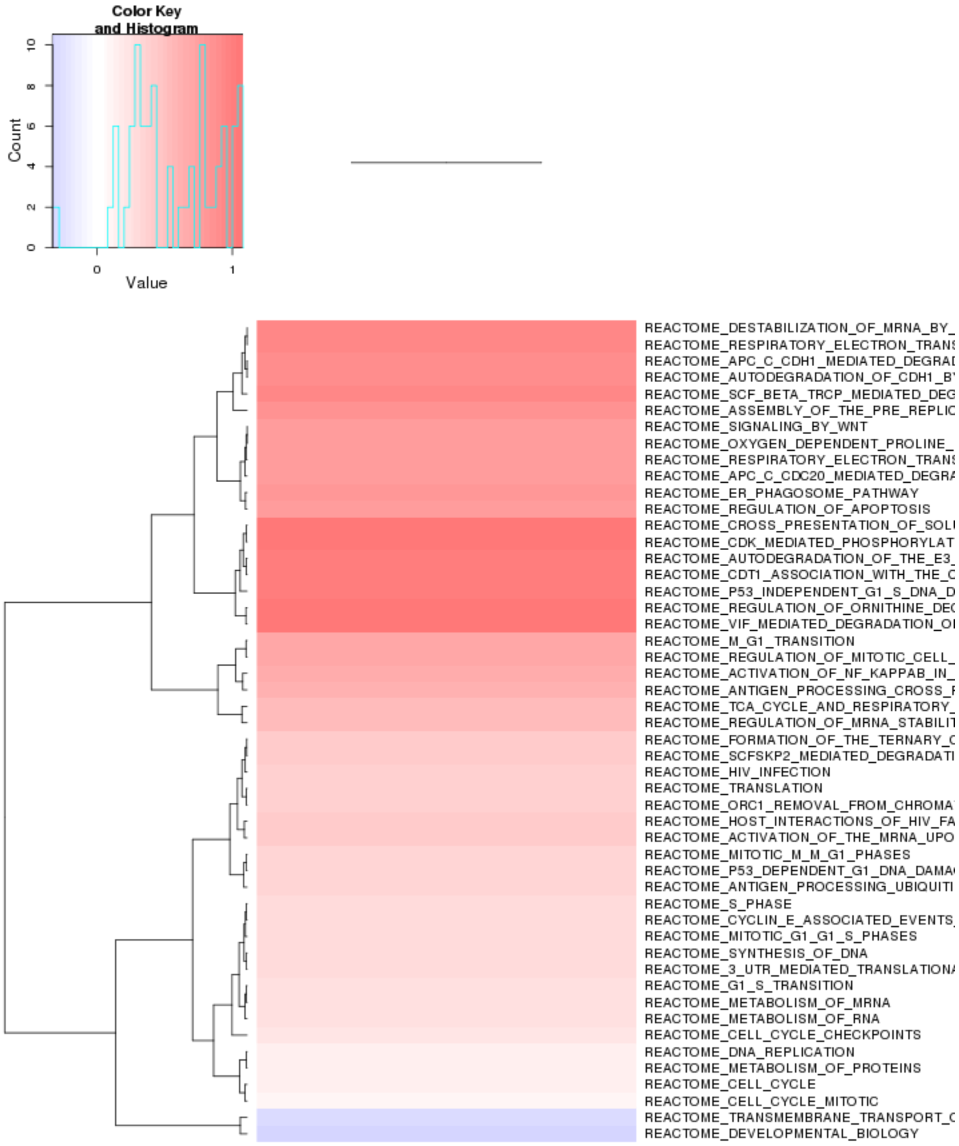
Biocarta zscore:



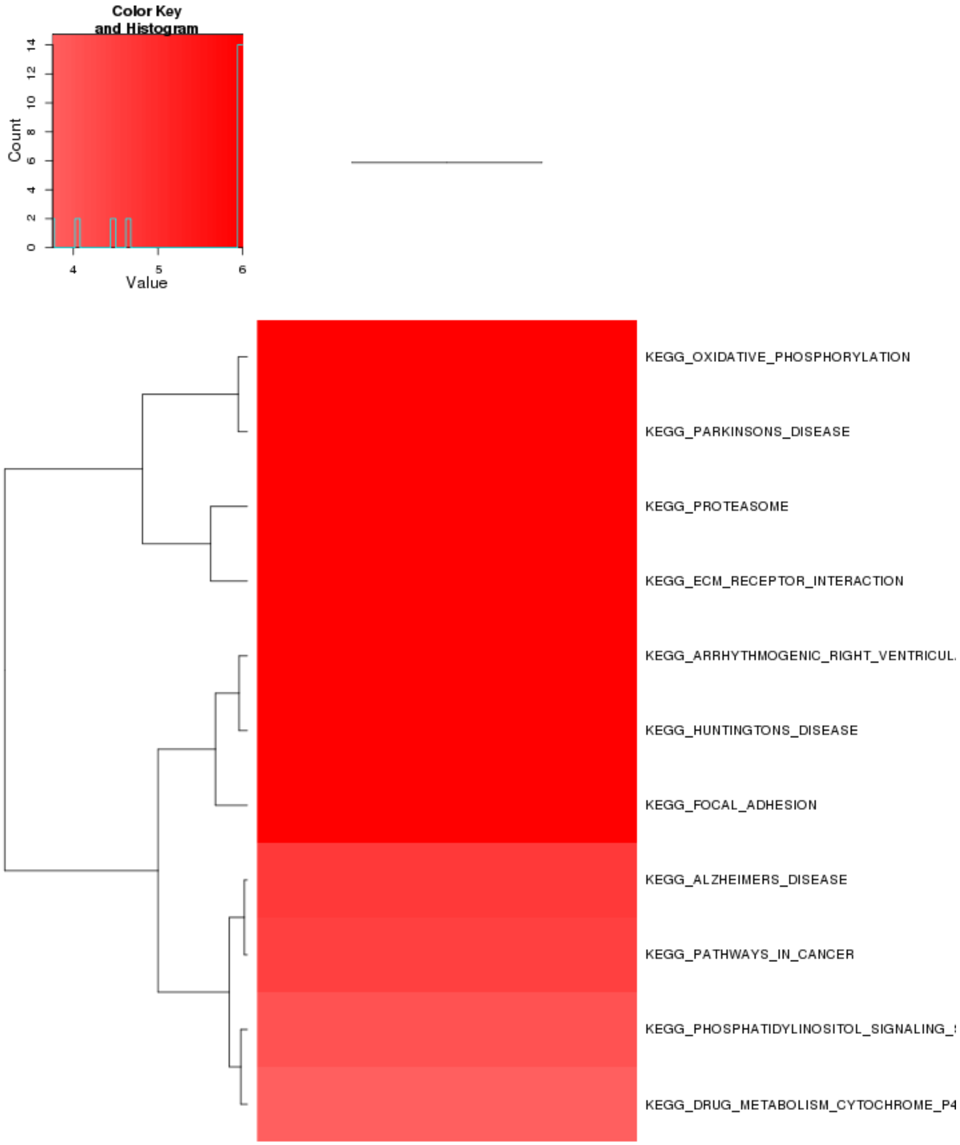
Reactome enrichment:



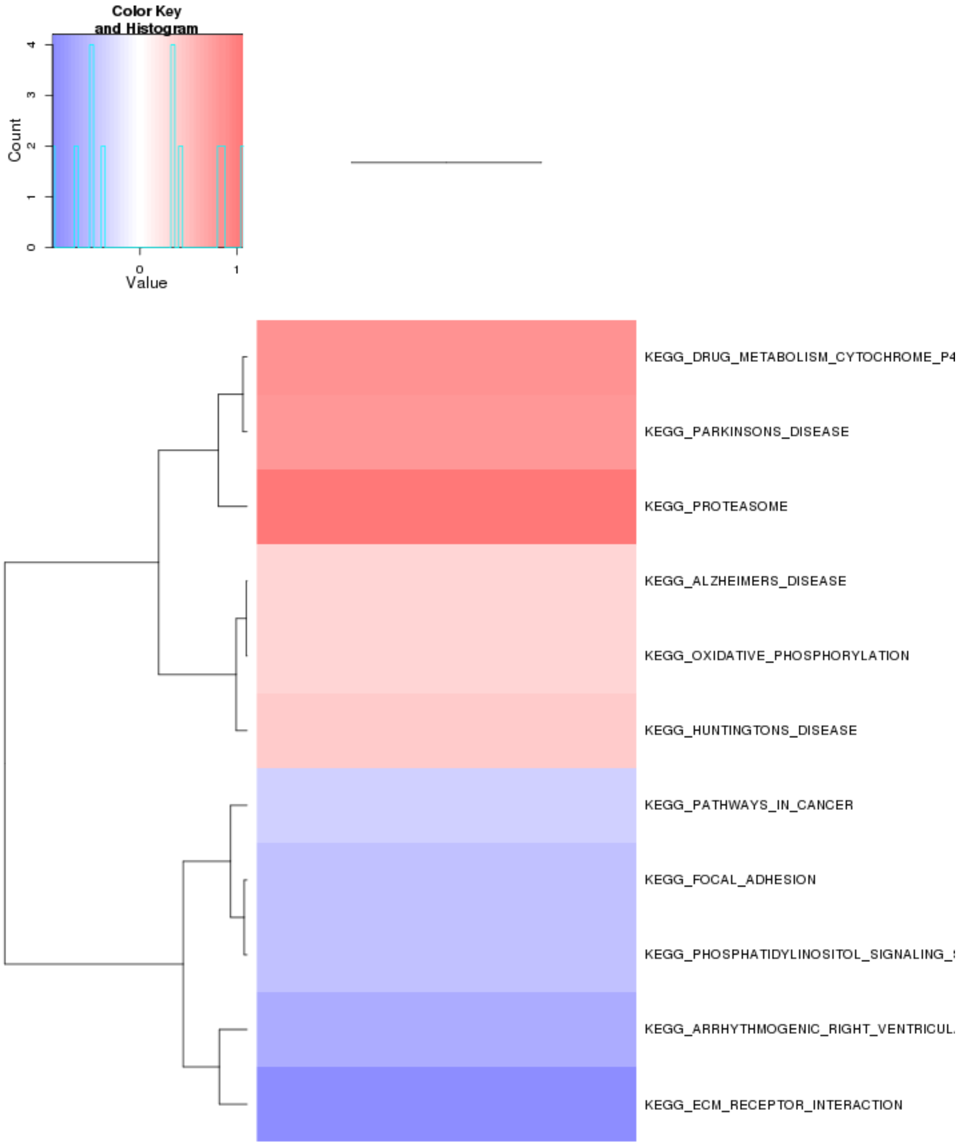
Reactome zscore:



Kegg enrichment:

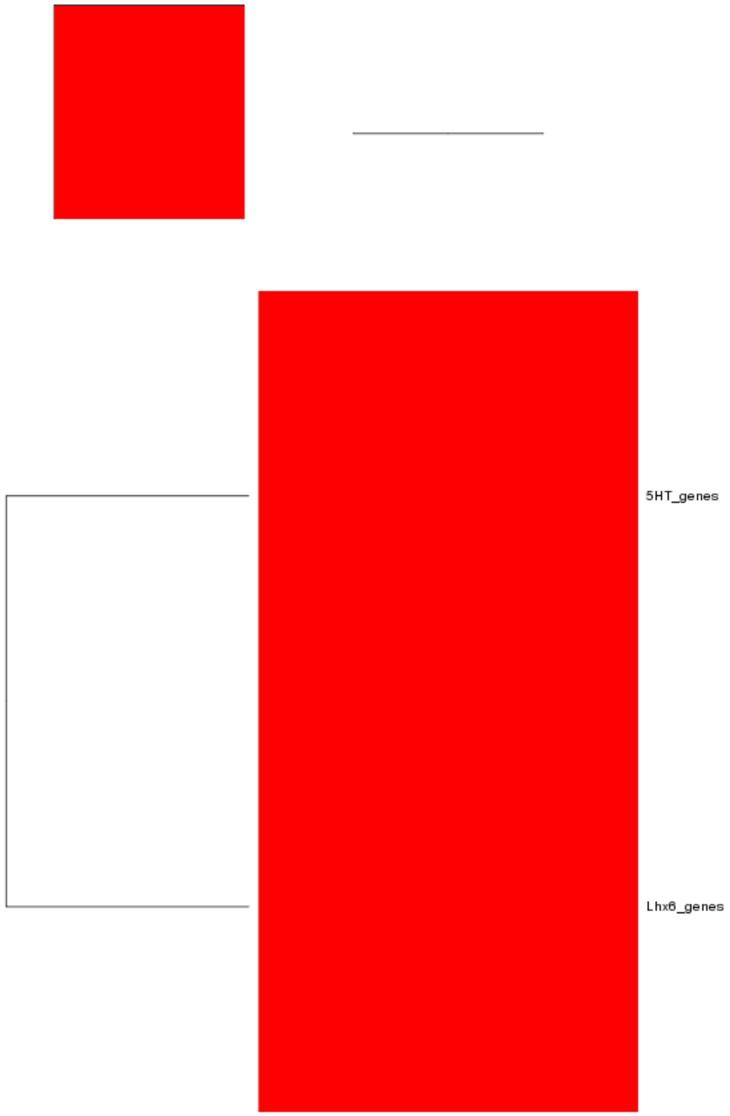

Color Key
and Histogram
Count
0
2
4
6
8
10
12
14
4
5
6
Value
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_PARKINSONS_DISEASE
KEGG_PROTEASOME
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICUL
KEGG_HUNTINGTONS_DISEASE
KEGG_FOCAL_ADHESION
KEGG_ALZHEIMERS_DISEASE
KEGG_PATHWAYS_IN_CANCER
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_
KEGG_DRUG_METABOLISM_CYTOCHROME_P4

Kegg zscore:

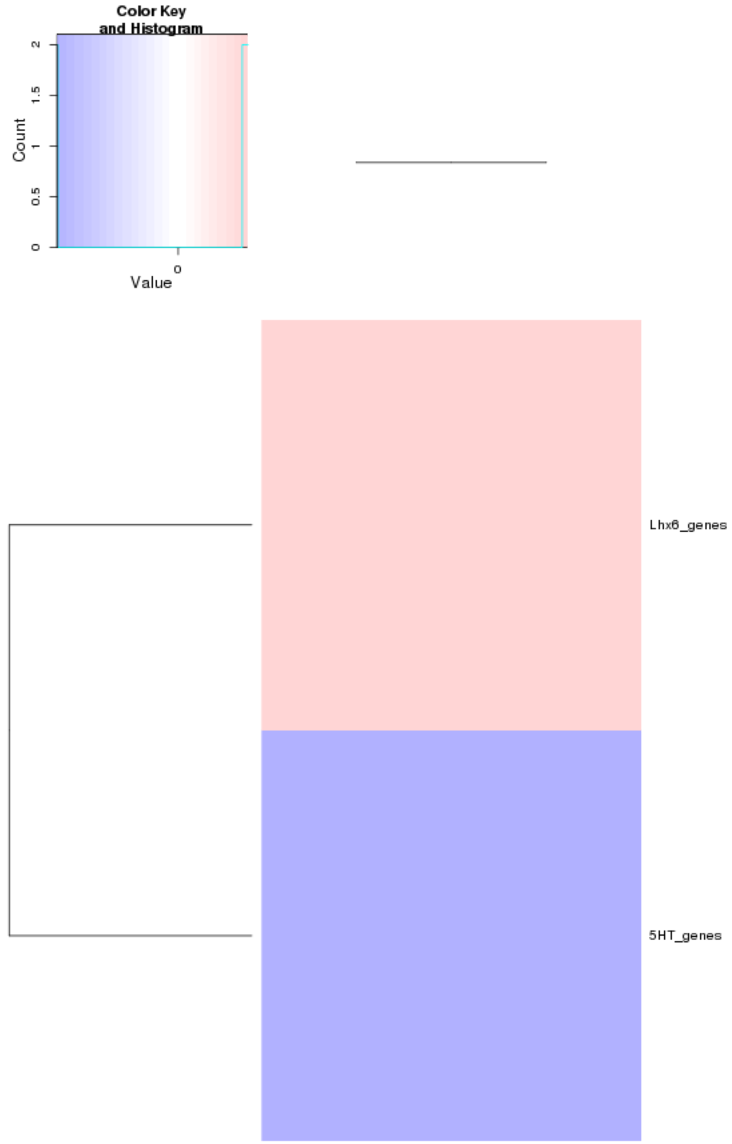


Interneuron enrichment:

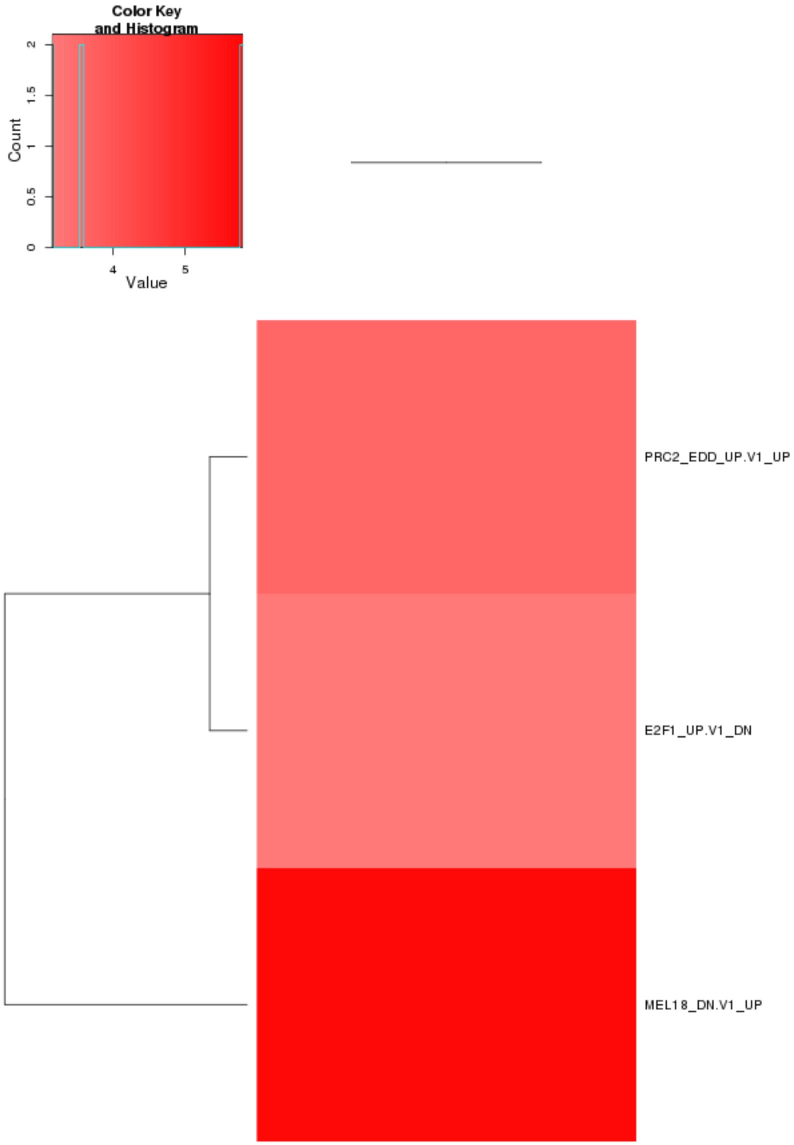
```
## Error: no locations are finite
```



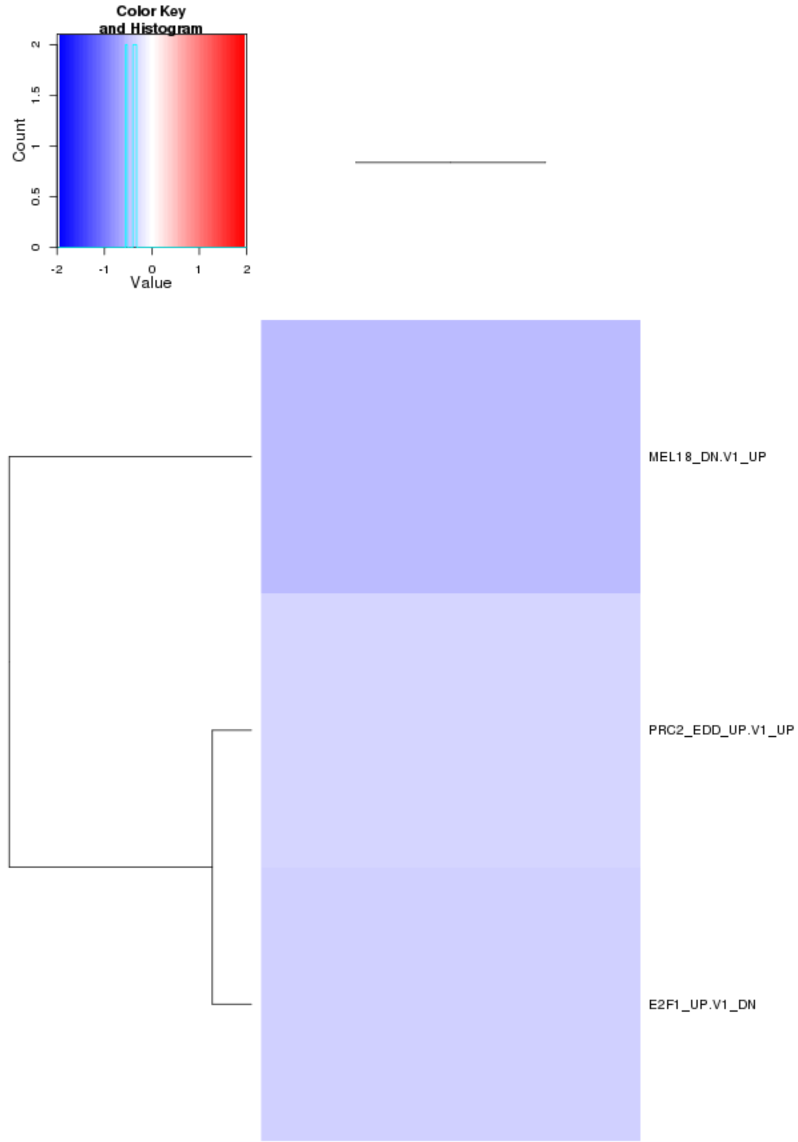
Interneuron zscore:



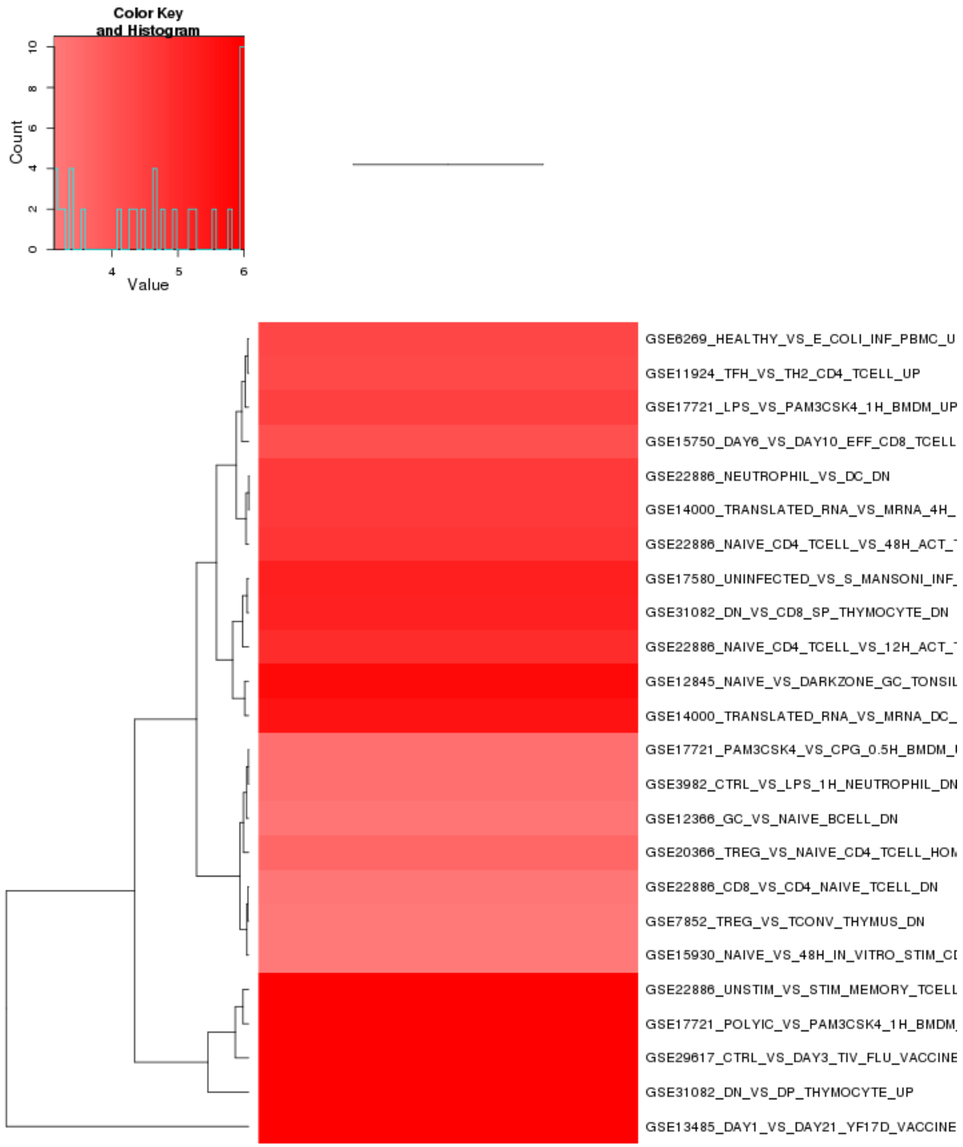
Oncogene enrichment:



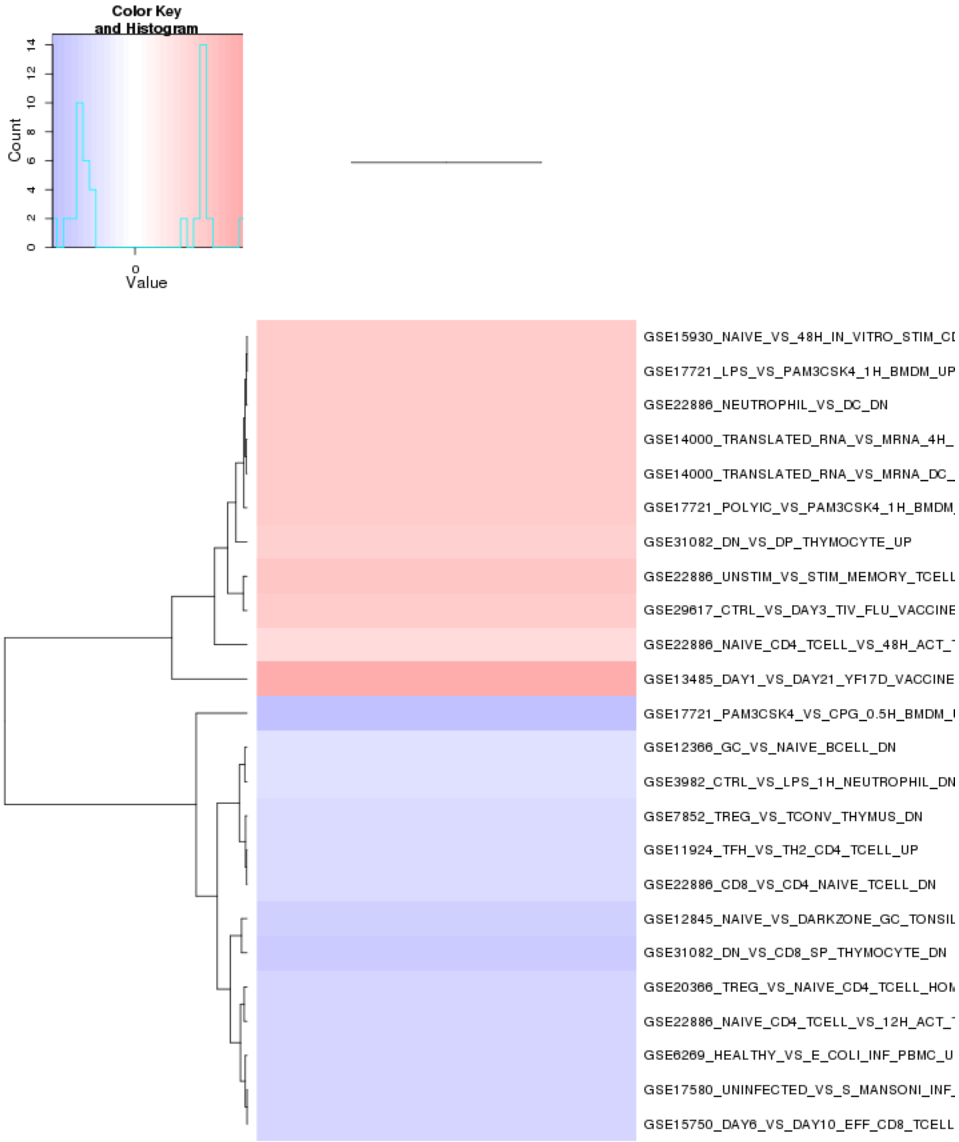
Oncogene zscore:



Immuno enrichment:

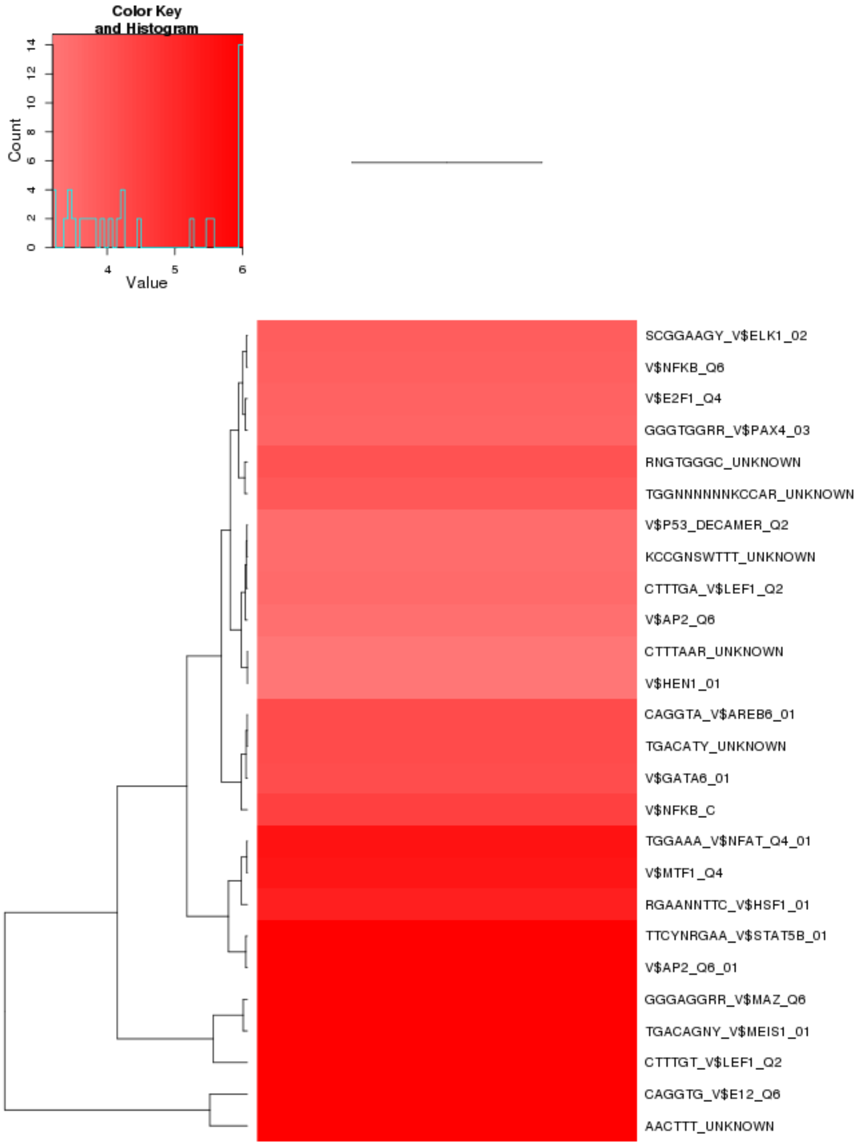


Immuno zscore:



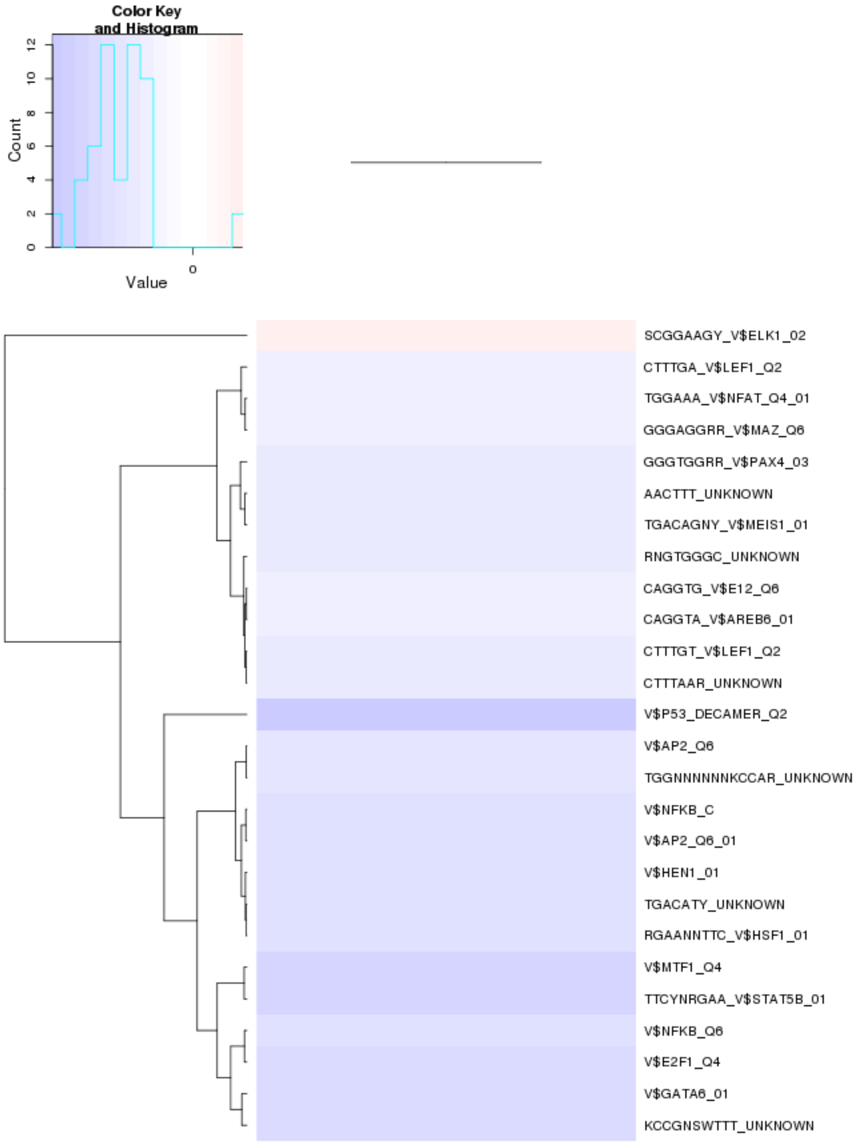
TF enrichment:

```
## Error: subscript out of bounds
```



TF zscore:

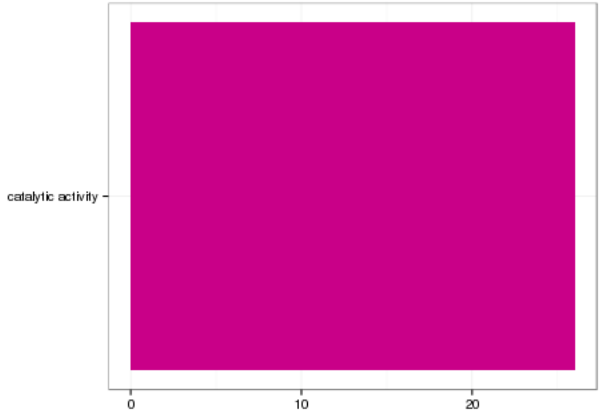
```
## Error: subscript out of bounds
```



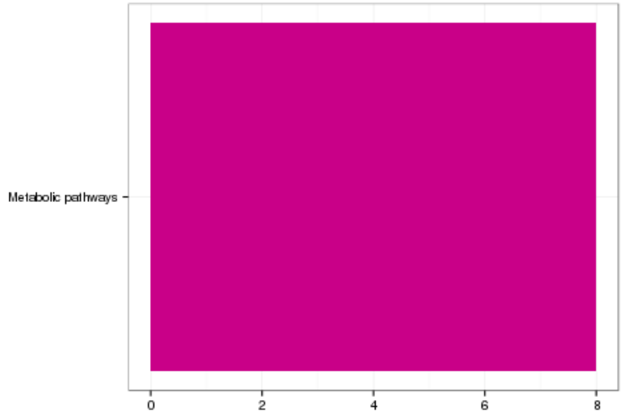
GO enrichment

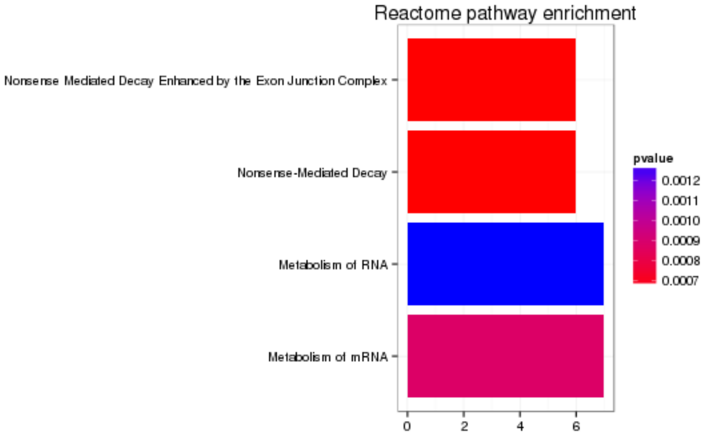
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

```
## Error: 'x' and 'units' must have length > 0
```

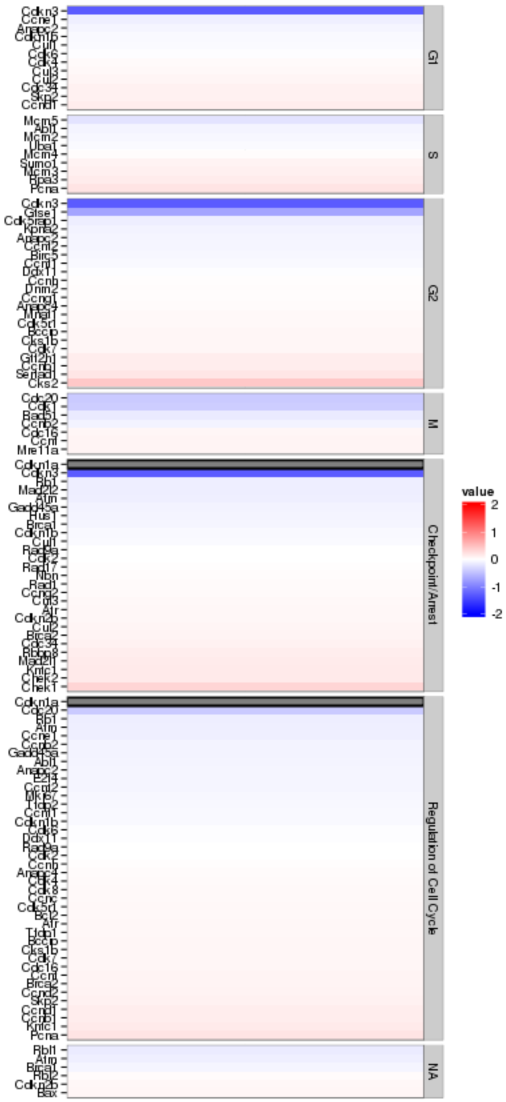


```
## Error: 'x' and 'units' must have length > 0
```

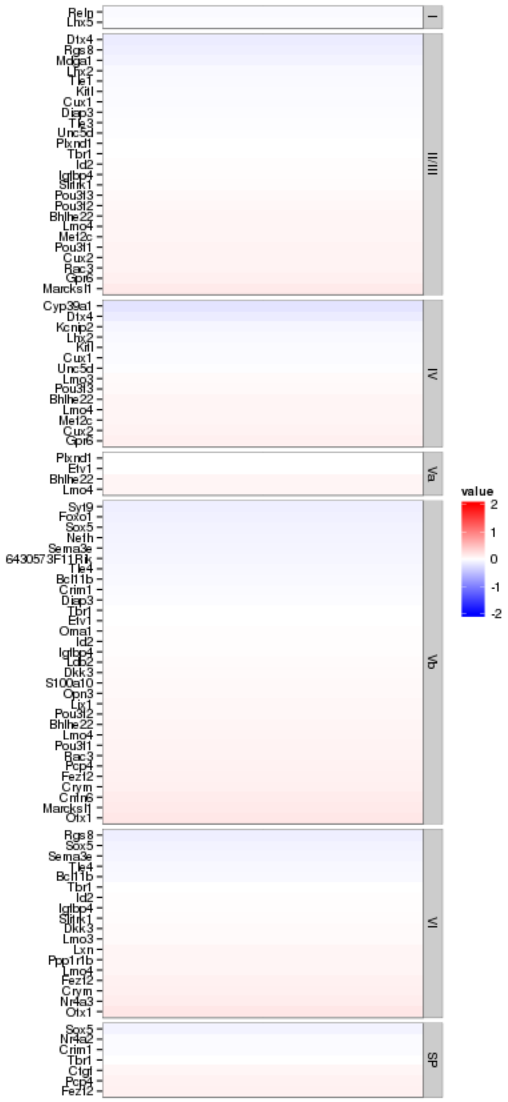




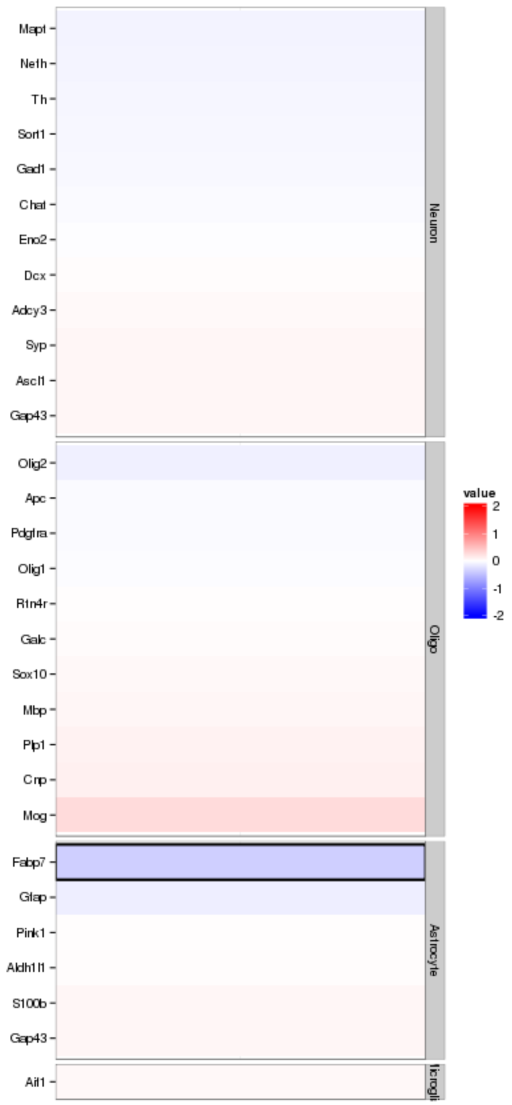
Enrichment or depletion for stage-specific cell cycle markers



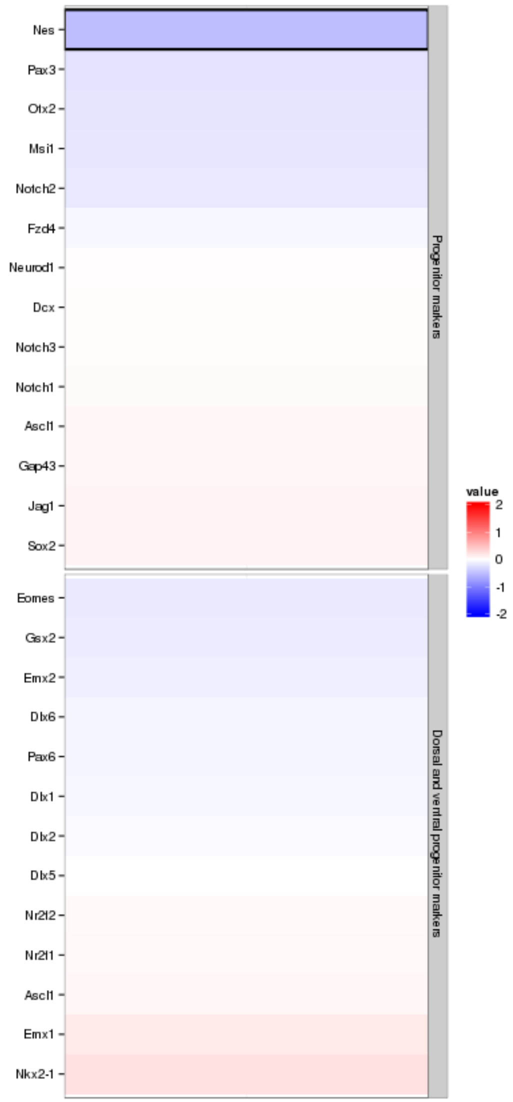
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



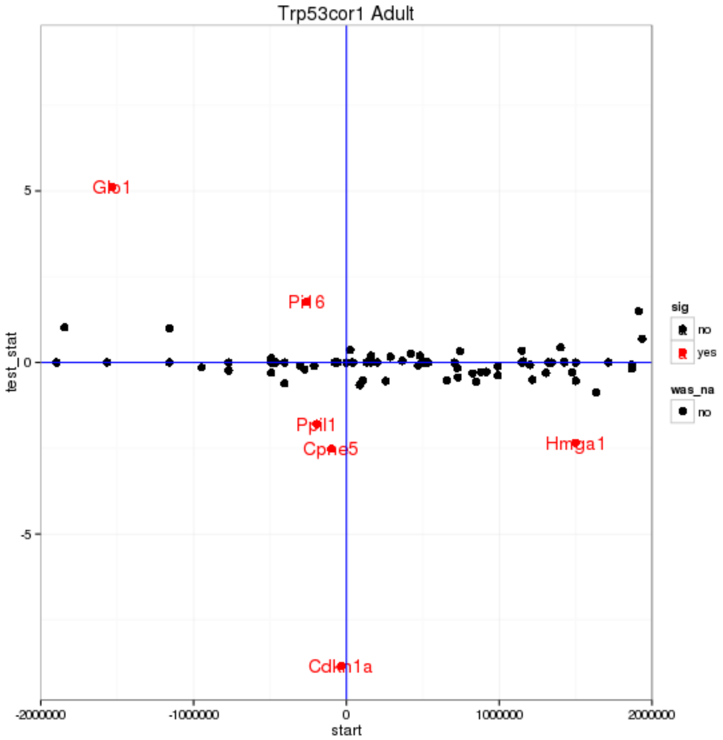
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 6 genes significantly regulated in a region this size is: 0.0038



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15	JR743
16	JR786
17	JR805

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	34671700.00	0.76	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	34671700.00	0.58	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	34671700.00	0.98	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	34671700.00	0.80	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	34671700.00	1.03	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	34671700.00	1.07	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	34671700.00	0.81	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	34671700.00	1.15	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	34671700.00	1.01	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	34671700.00	1.30	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	34671700.00	1.50	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	34671700.00	1.02	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	34671700.00	0.97	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	34671700.00	1.21	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR743/abundances.cxb	Trp53cor	0	Trp53cor_0	32358500.00	34671700.00	0.94	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR786/abundances.cxb	Trp53cor	1	Trp53cor_1	38185400.00	34671700.00	1.10	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR805/abundances.cxb	Trp53cor	2	Trp53cor_2	41355100.00	34671700.00	1.19	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils
## [8] datasets  base
##
## other attached packages:
##  [1] plyr_1.8.1
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##            param
## 1       cmd_line
## 2        version
## 3   SVN_revision
## 4 boost_version
## 5         genome
##
## 1 cuffdiff -p 10 -L WT,Trp53cor -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Trp53cor_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainMap/c
## 2
## 3
## 4
## 5
```

Trp53cor1 KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for Trp53cor1.

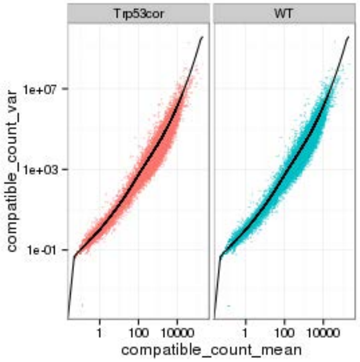
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

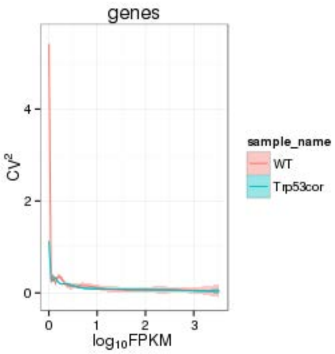
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



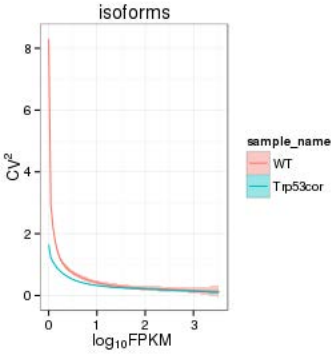
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

Genes:



Isoforms:



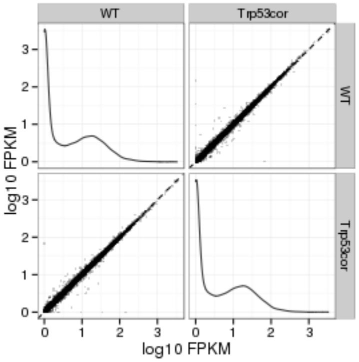
MvA plot

```
## Error: non-numeric argument to binary operator
```

MvA plot counts

```
## Error: non-numeric argument to binary operator
```

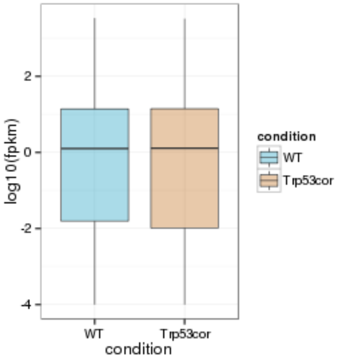
Scatterplot matrix



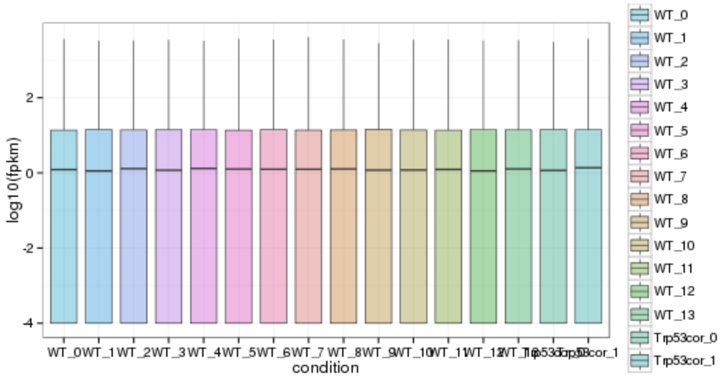
Distributions

Boxplots

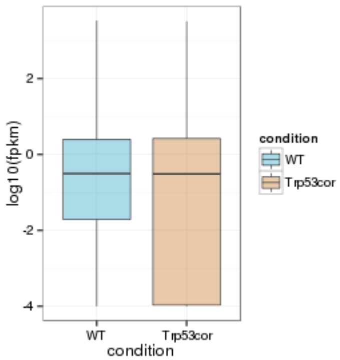
Boxplot (genes)



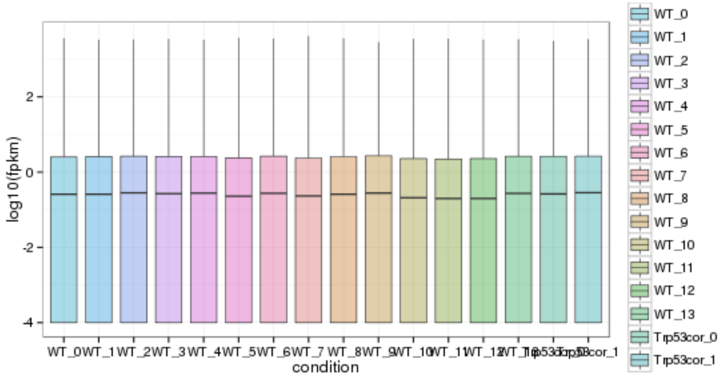
Boxplot (genes, replicates)



Boxplot (isoforms)

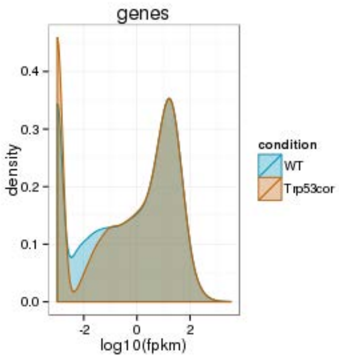


Boxplot (isoforms, replicates)

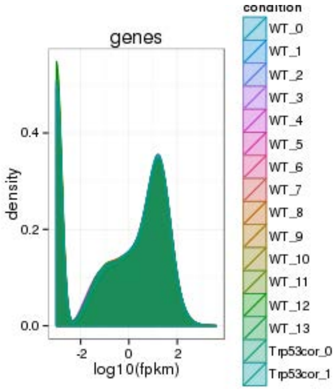


Density

Density (genes)

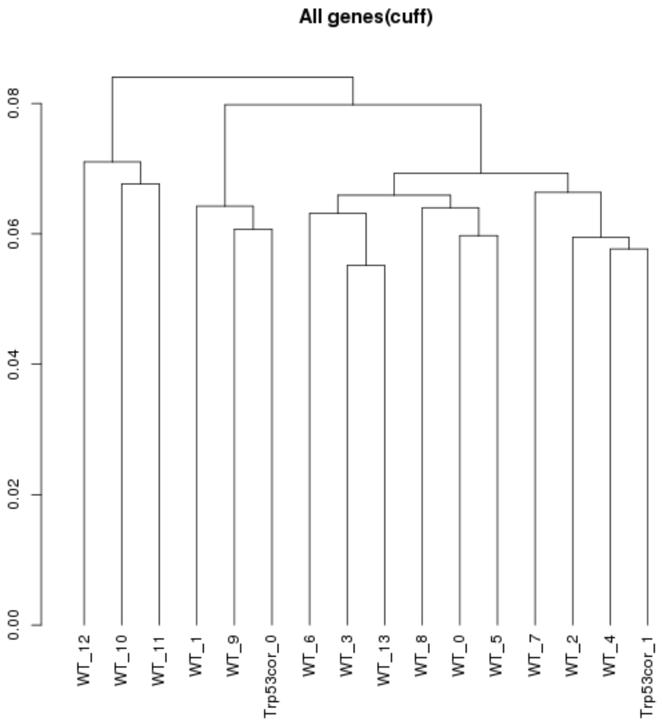


Density (genes, replicates)



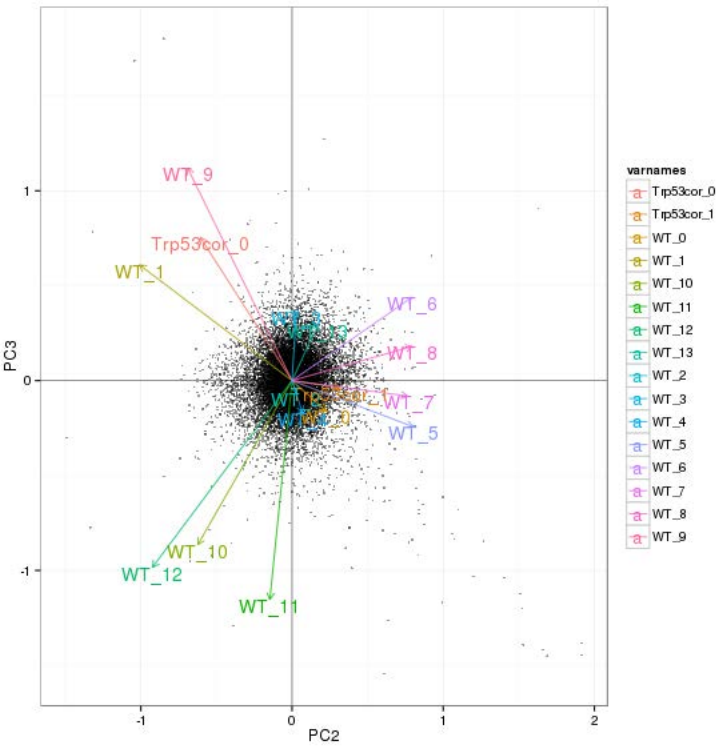
Clustering

Replicate Clusters



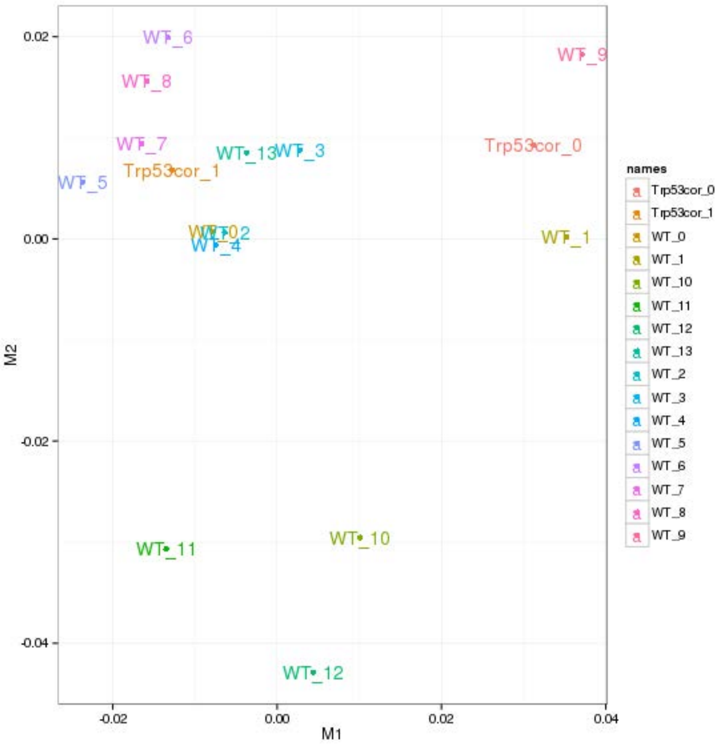
```
## NULL
```

PCA (genes)



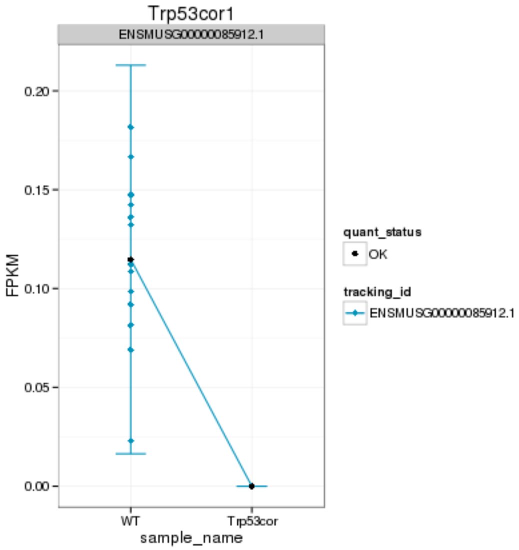
WT_9
Trp53cor_0
WT_1
WT_6
WT_8
WT_7
WT_5
WT_10
WT_12
WT_11
PC3
PC2
1
0
-1
-1
0
1
2
varnames
Trp53cor_0
Trp53cor_1
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

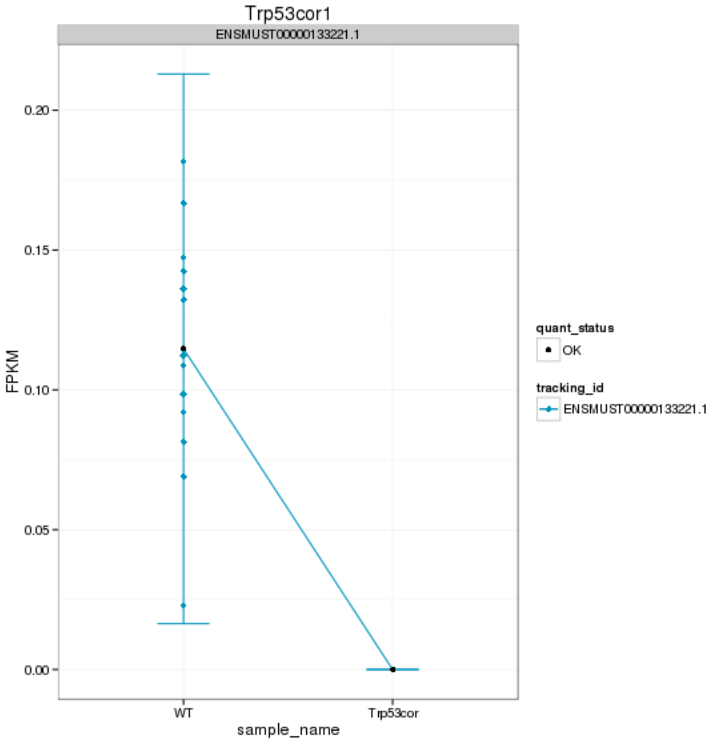


KO assessment

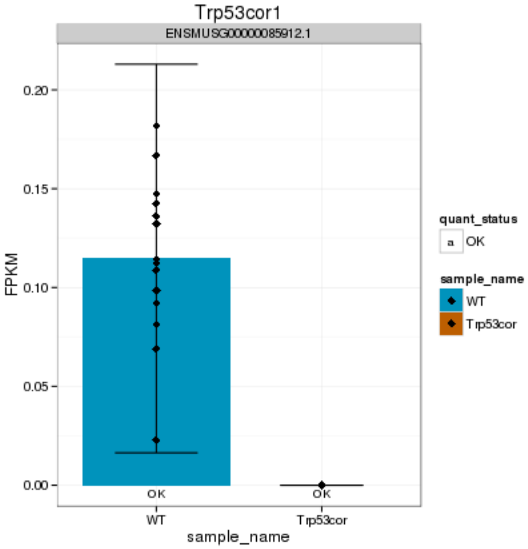
Endogenous lncRNA expression



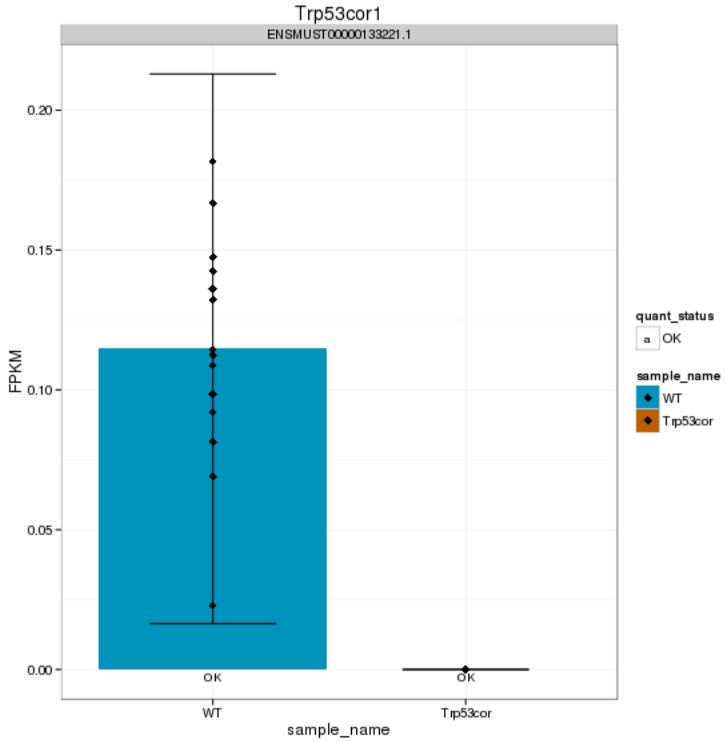
Endogenous expression of Trp53cor1 isoforms:



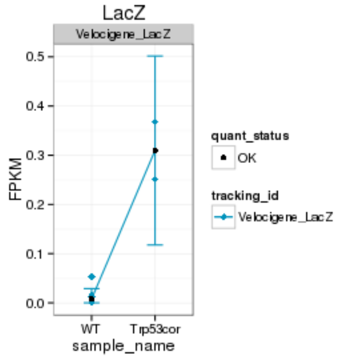
Barplot of gene expression:

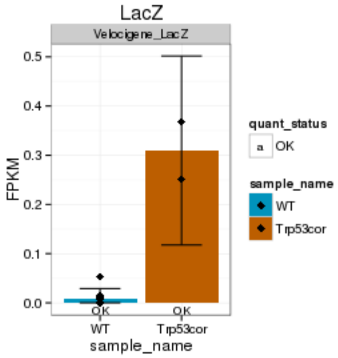


Barplot of isoform expression:



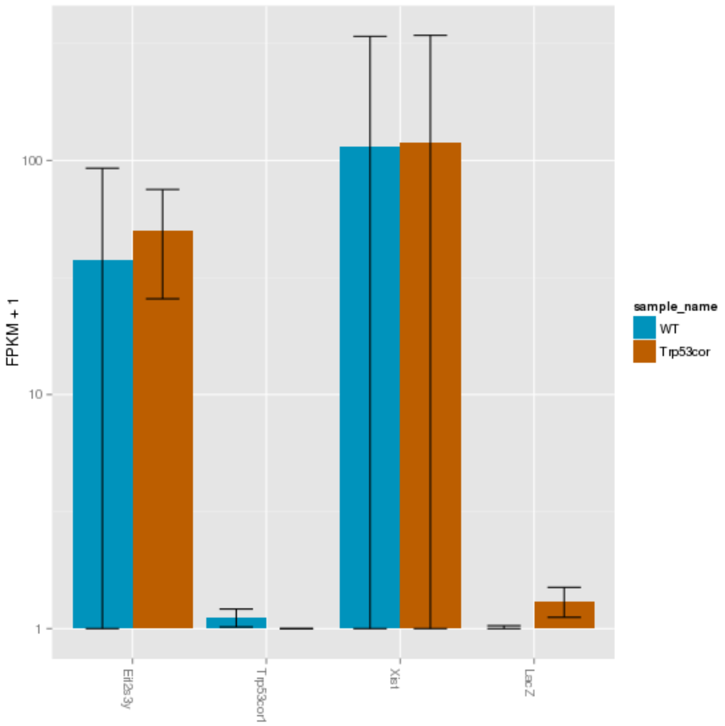
LacZ expression



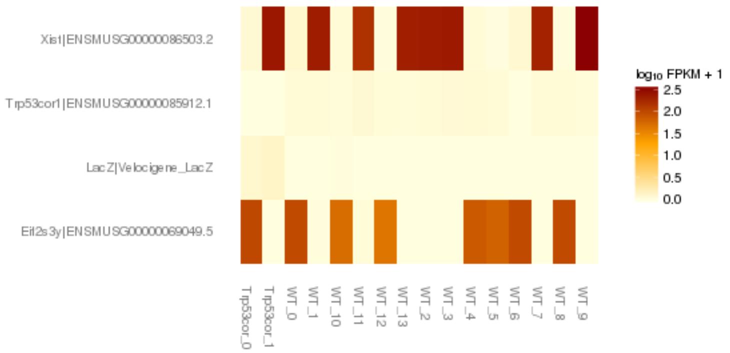


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

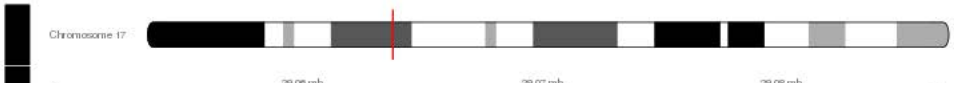
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):

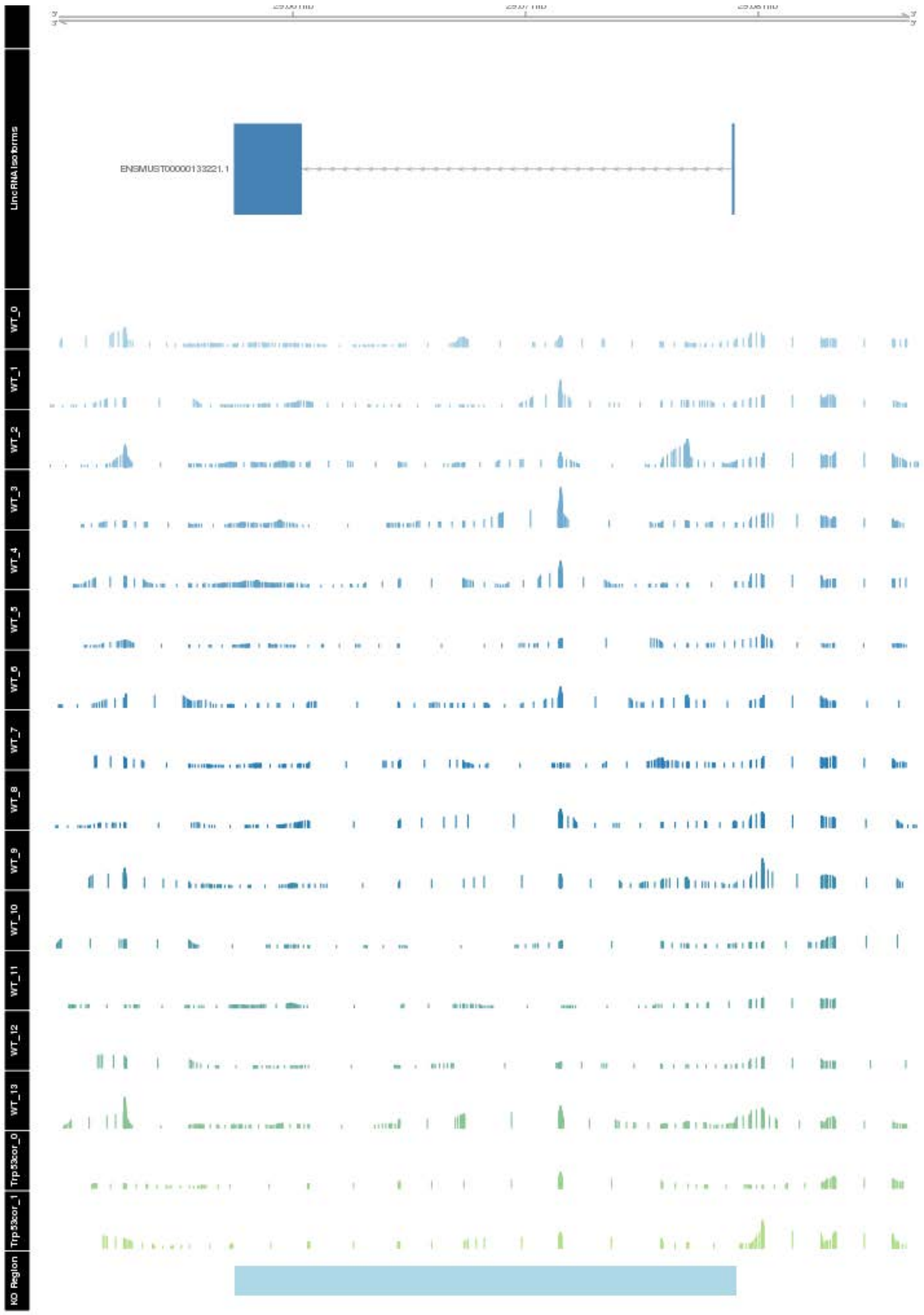


Expression heatmap:



Track visualization




5'
3'
29.06 mb
29.07 mb
29.08 mb
3'
5'
LincRNA Isoforms
ENSMUST00000133221.1
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Trp53cor_0
Trp53cor_1
KO Region

Differential Analysis

Differential Genes

```
## Error: RS-DBI driver: (error in statement: near ")": syntax error)
```

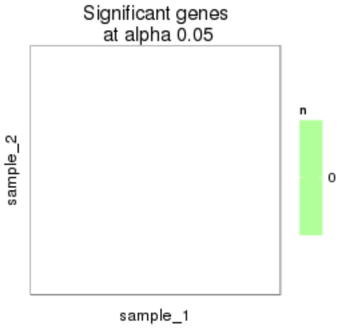
```
## Error: error in evaluating the argument 'object' in selecting a method for function 'annotation': Error: object 'sigGenes' not found
```

There are 0 significantly differentially expressed genes. They are:

[1] “No sig genes!”

Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

```
## Error: error in evaluating the argument 'object' in selecting a method for function 'csHeatmap': Error: object 'sigGenes' not found
```

Significant genes with expression >50fpkm (any condition):(turned off)

An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

Scatter plot of significant genes only:

```
## Error: error in evaluating the argument 'object' in selecting a method for function 'csScatter': Error: object 'sigGenes' not found
```

Volcano Plot

```
## Error: One or more values of 'x' or 'y' are not valid sample names!
```

Volcano plot with significant genes only:

```
## Error: error in evaluating the argument 'object' in selecting a method for function 'csVolcano': Error: object 'sigGenes' not found
```

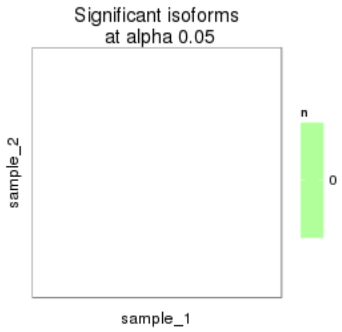
FoldChange Heatmap

```
## Error: error in evaluating the argument 'object' in selecting a method for function 'csFoldChangeHeatmap': Error: object 'sigGenes' not found
```

Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

[1] “no sig isoforms”

Gene-level DE isoform heatmap

```
## [1] "no sig isoforms"
```

Isoform foldchange heatmap by isoform:

```
## [1] "no sig isoforms"
```

Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

Biocarta enrichment:

```
## Error: `x' must have at least 2 rows and 2 columns
```

Biocarta zscore:

```
## Error: incorrect number of dimensions
```

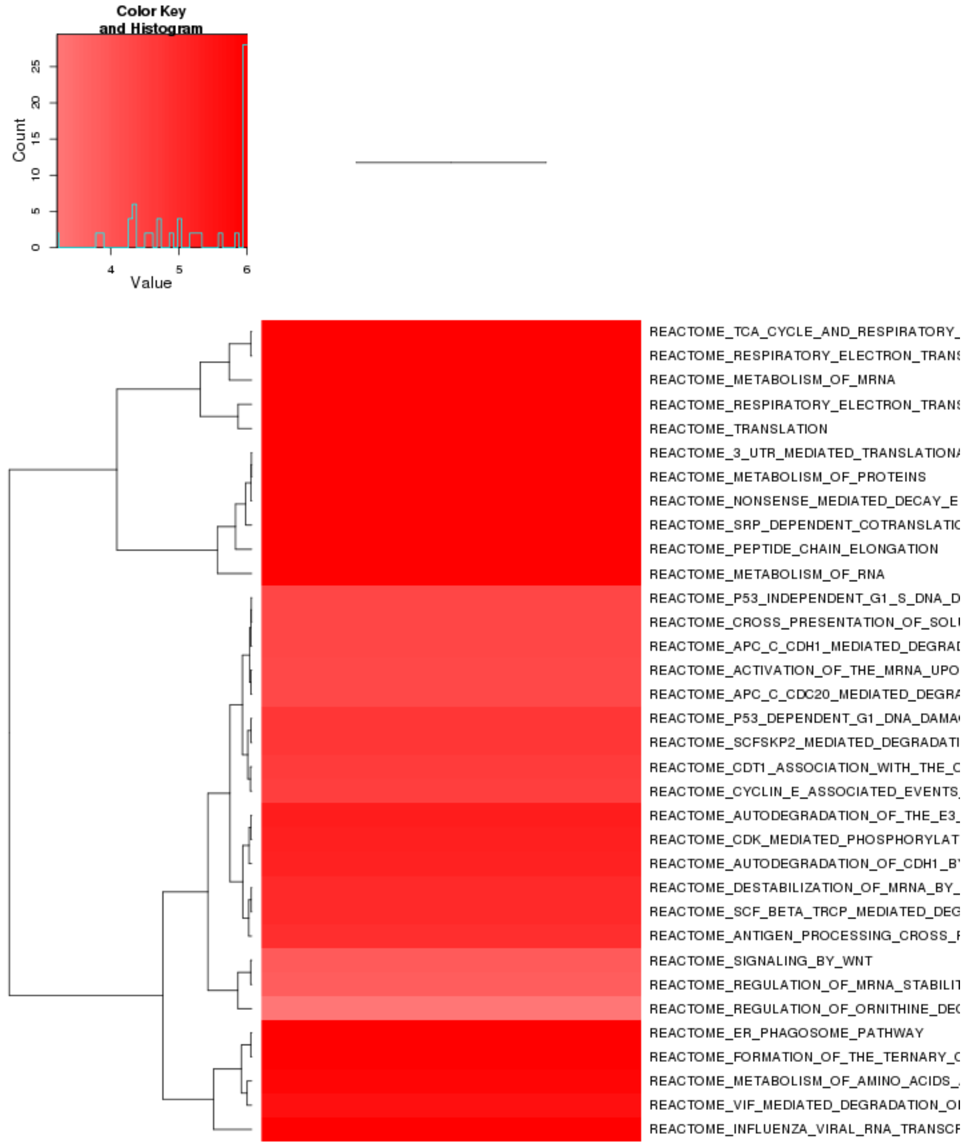
```
## Error: object 'x_ordered' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

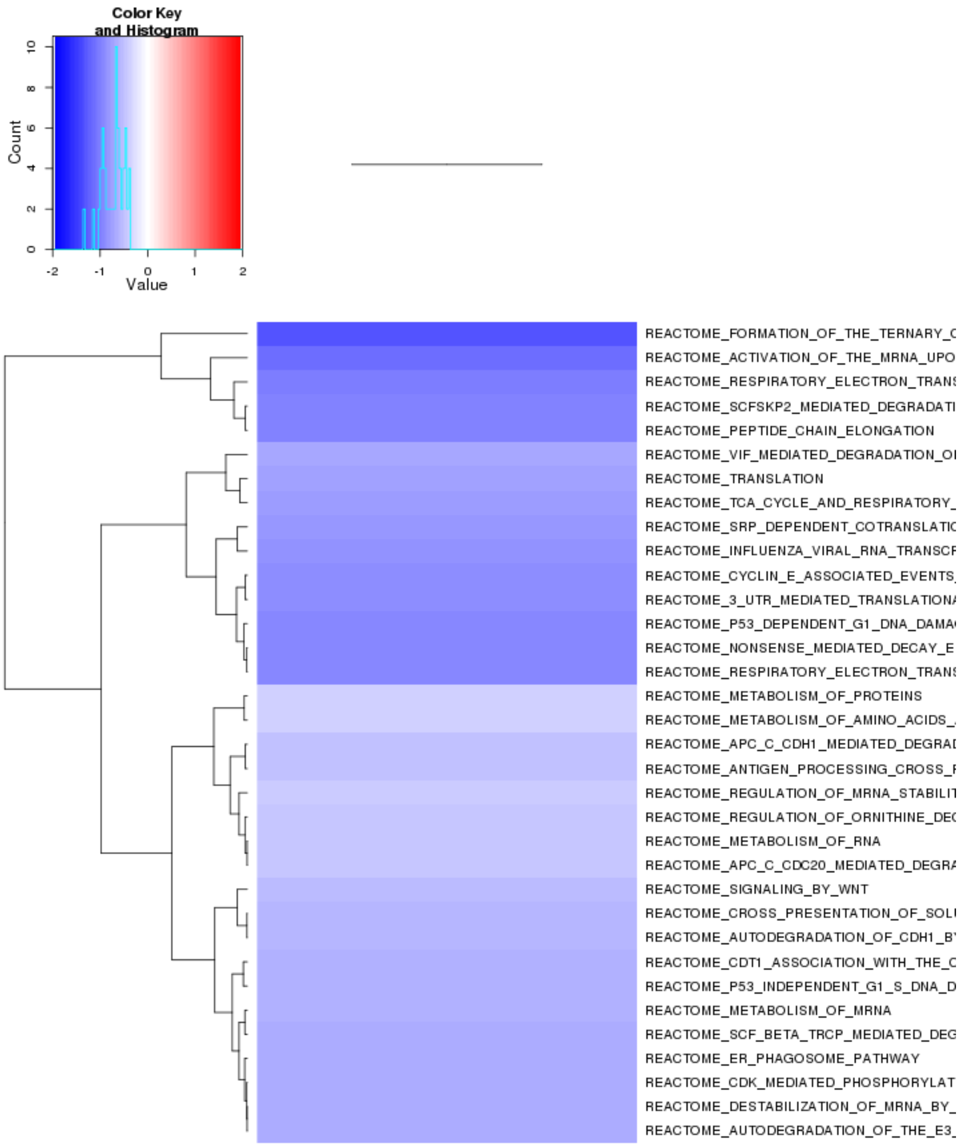
Reactome enrichment:

```
## Error: subscript out of bounds
```

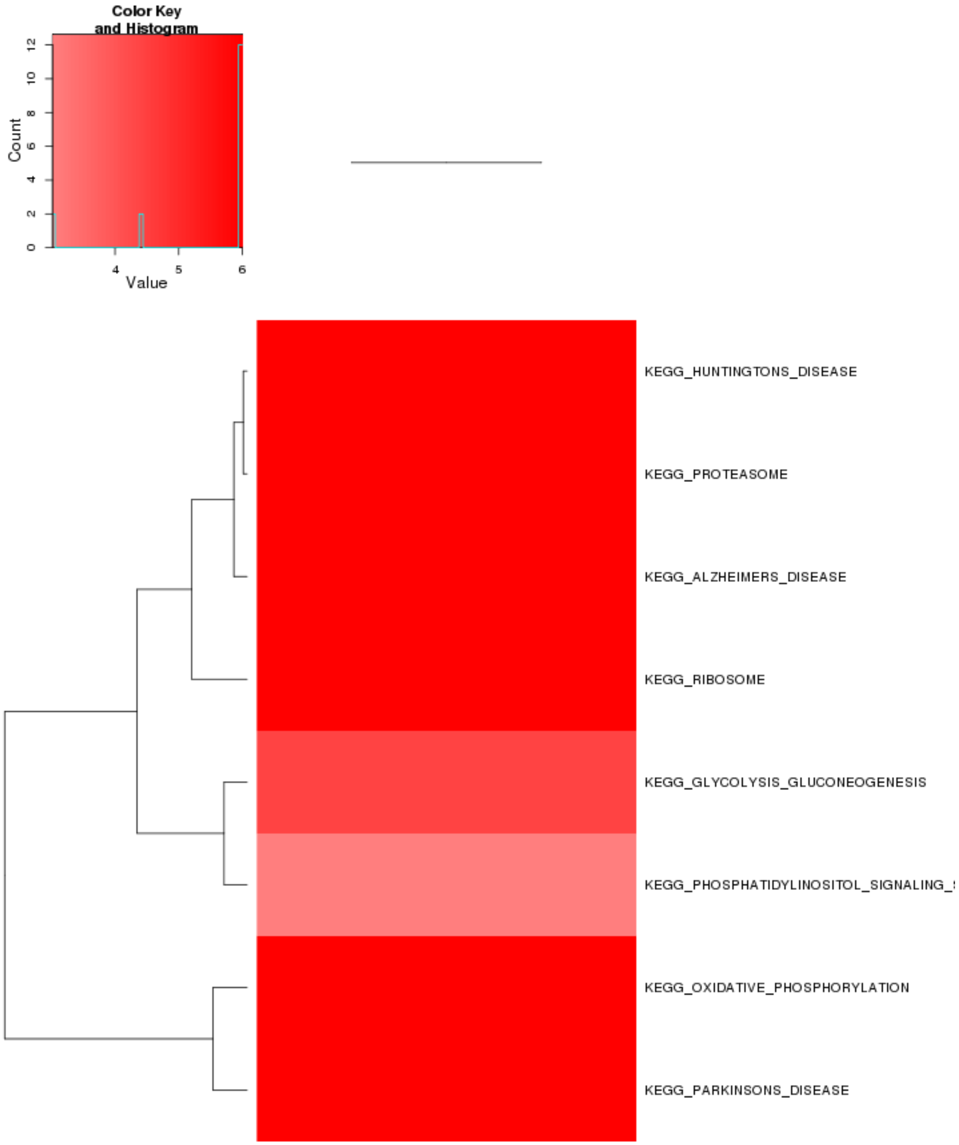


Reactome zscore:

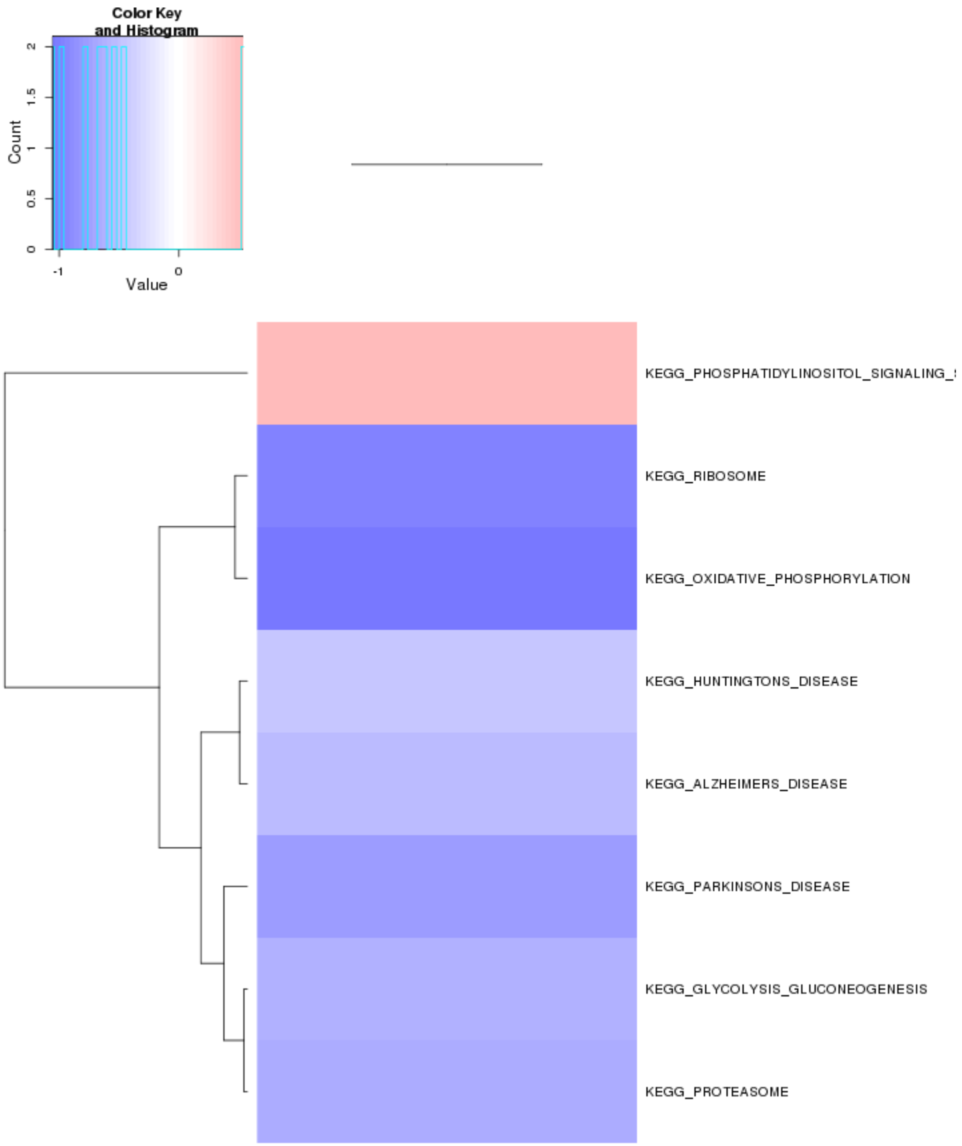
```
## Error: subscript out of bounds
```



Kegg enrichment:

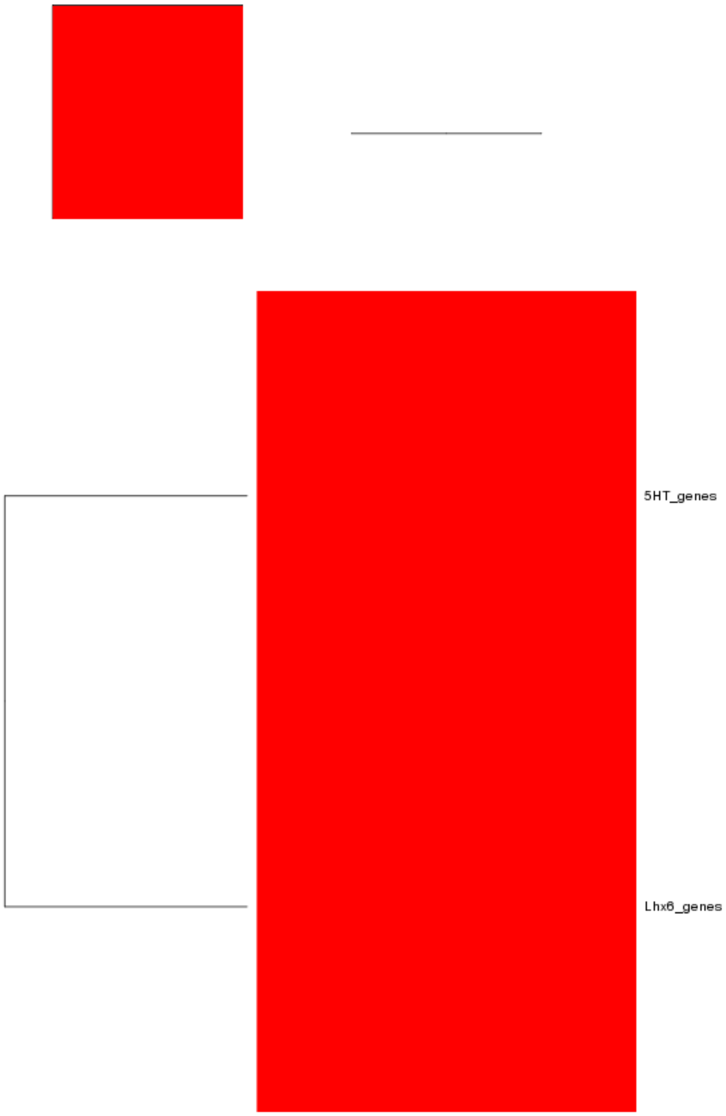

Color Key
and Histogram
Count
0
2
4
6
8
10
12
4
5
6
Value
KEGG_HUNTINGTONS_DISEASE
KEGG_PROTEASOME
KEGG_ALZHEIMERS_DISEASE
KEGG_RIBOSOME
KEGG_GLYCOLYSIS_GLUCONEOGENESIS
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_PARKINSONS_DISEASE

Kegg zscore:

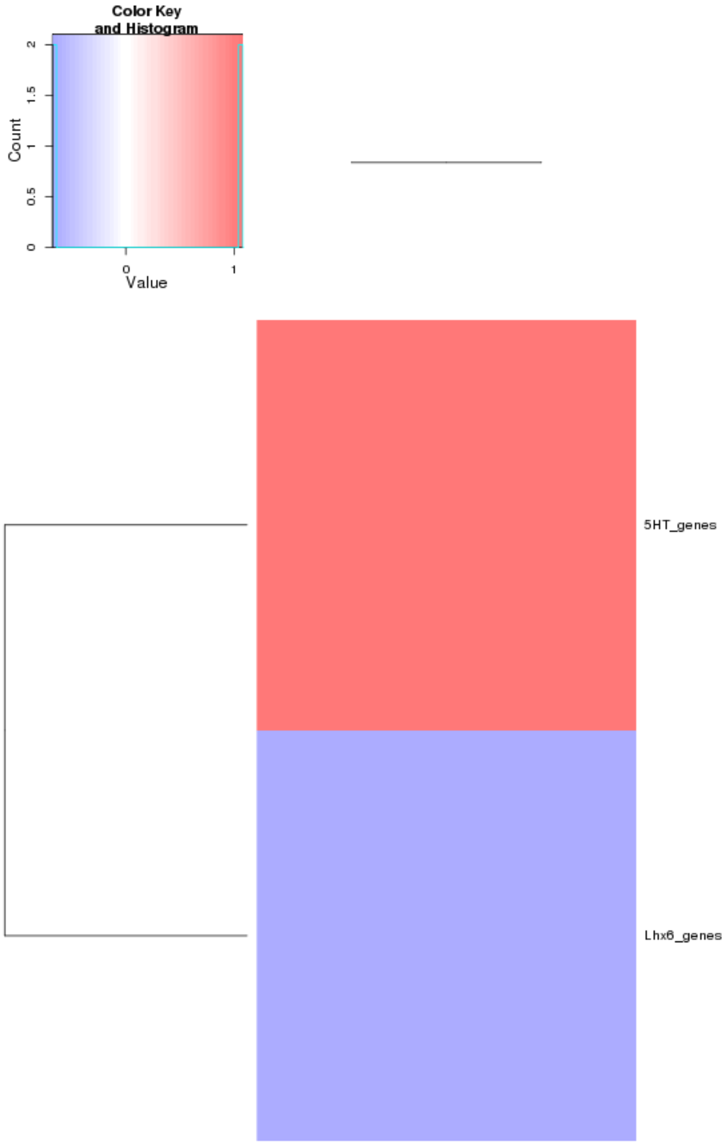


Interneuron enrichment:

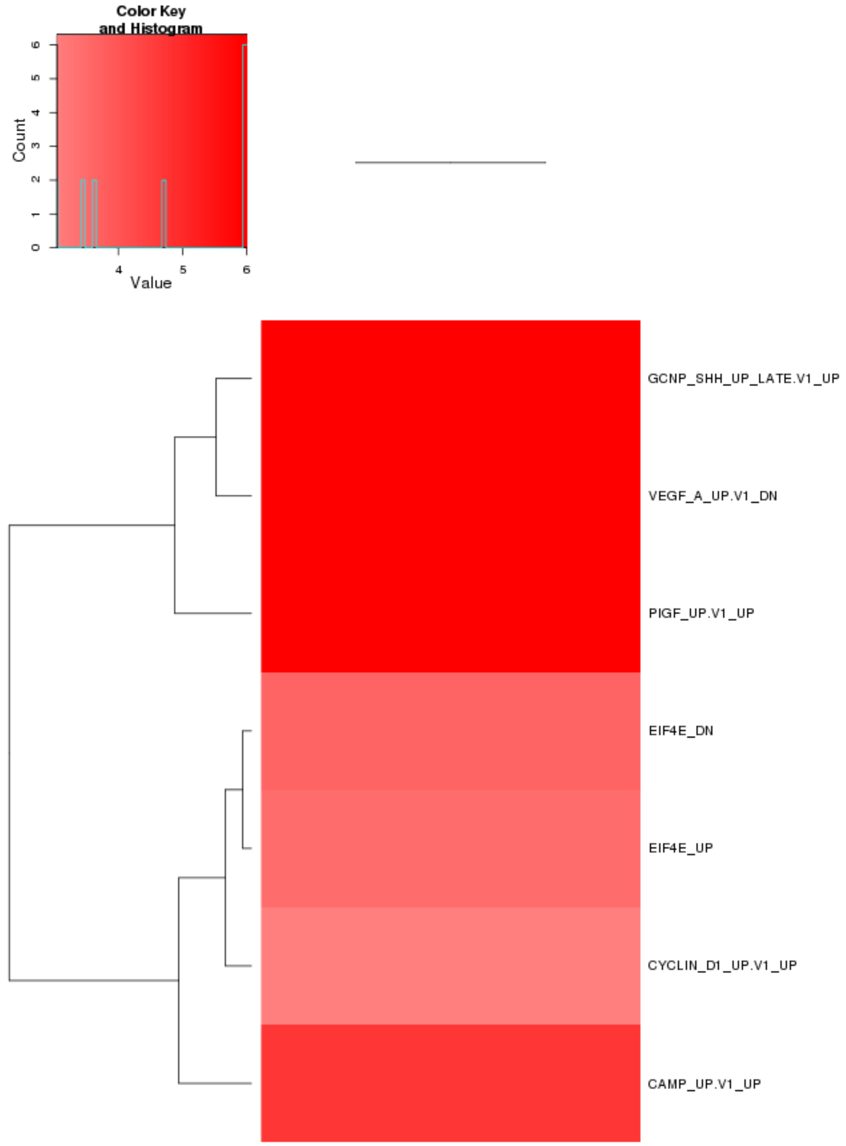
```
## Error: no locations are finite
```



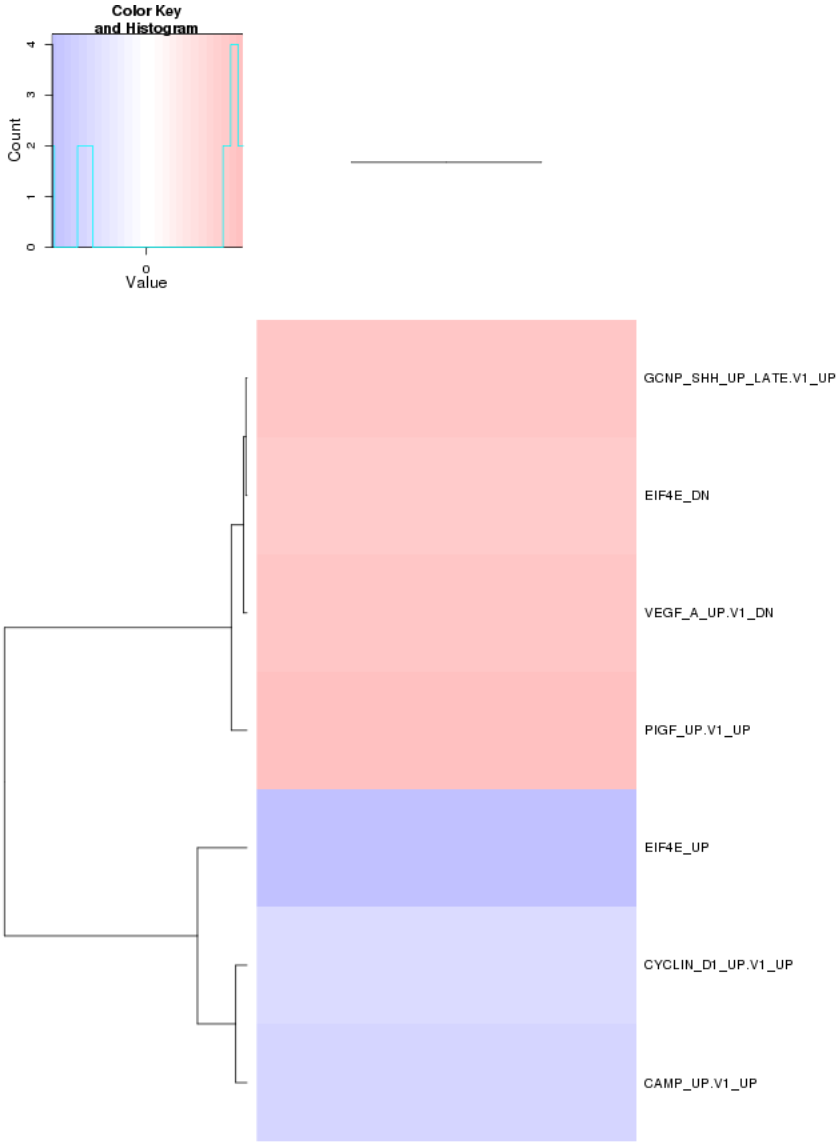
Interneuron zscore:



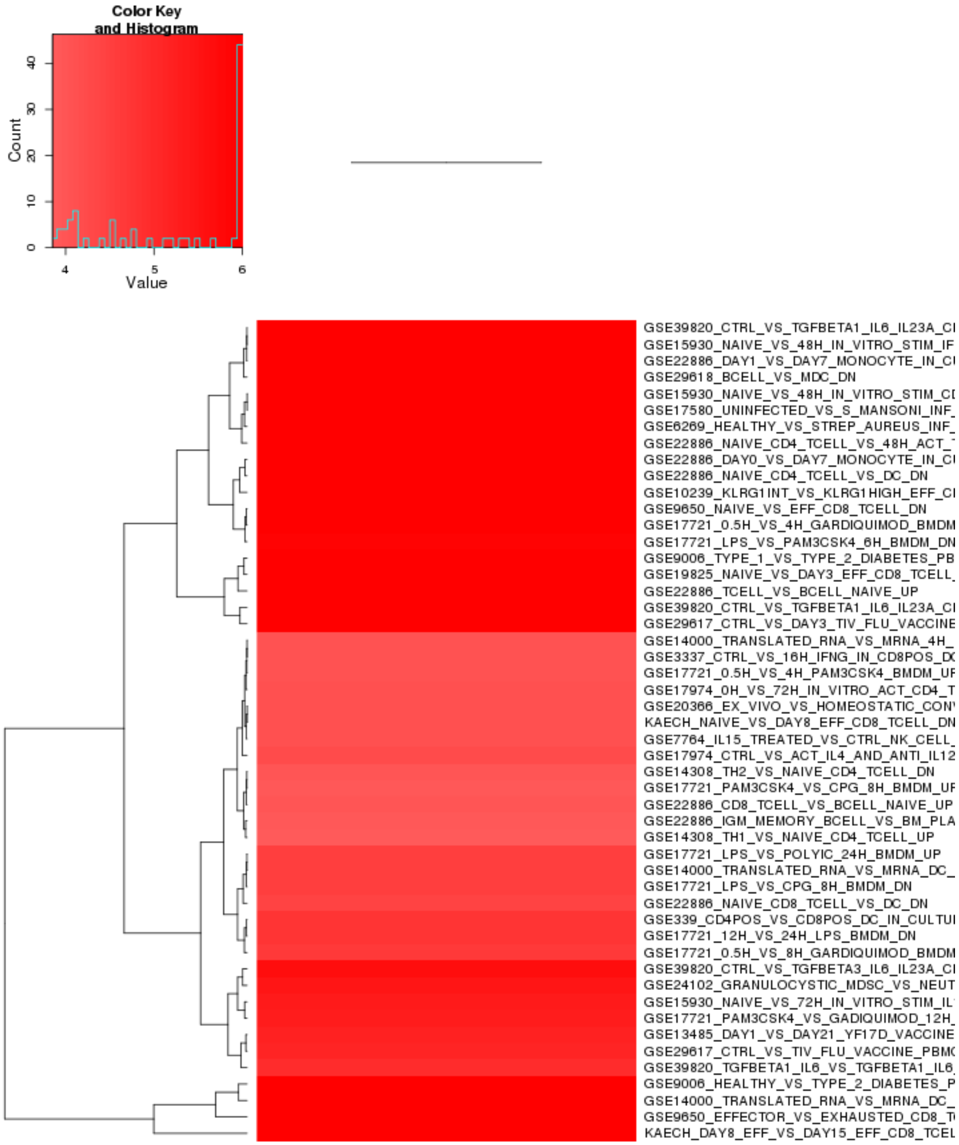
Oncogene enrichment:



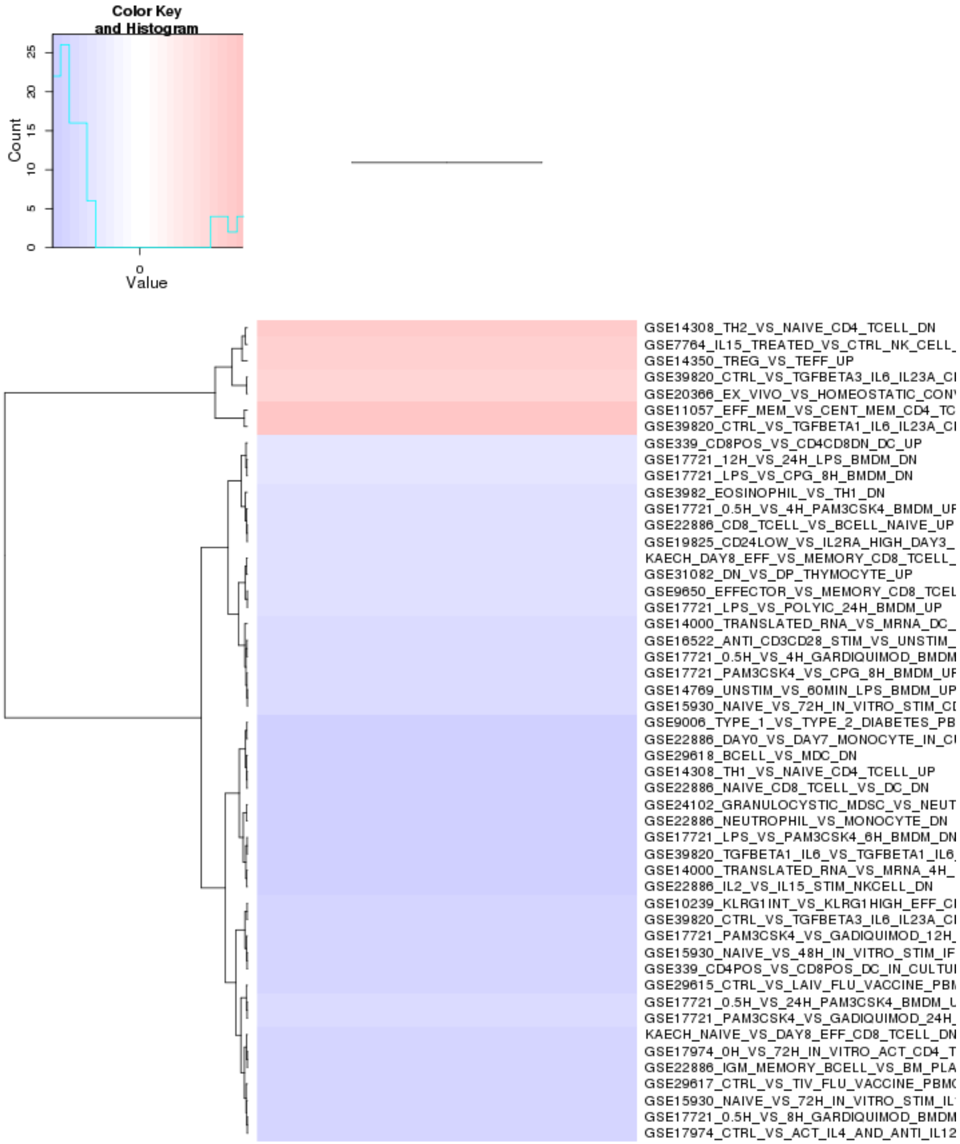
Oncogene zscore:



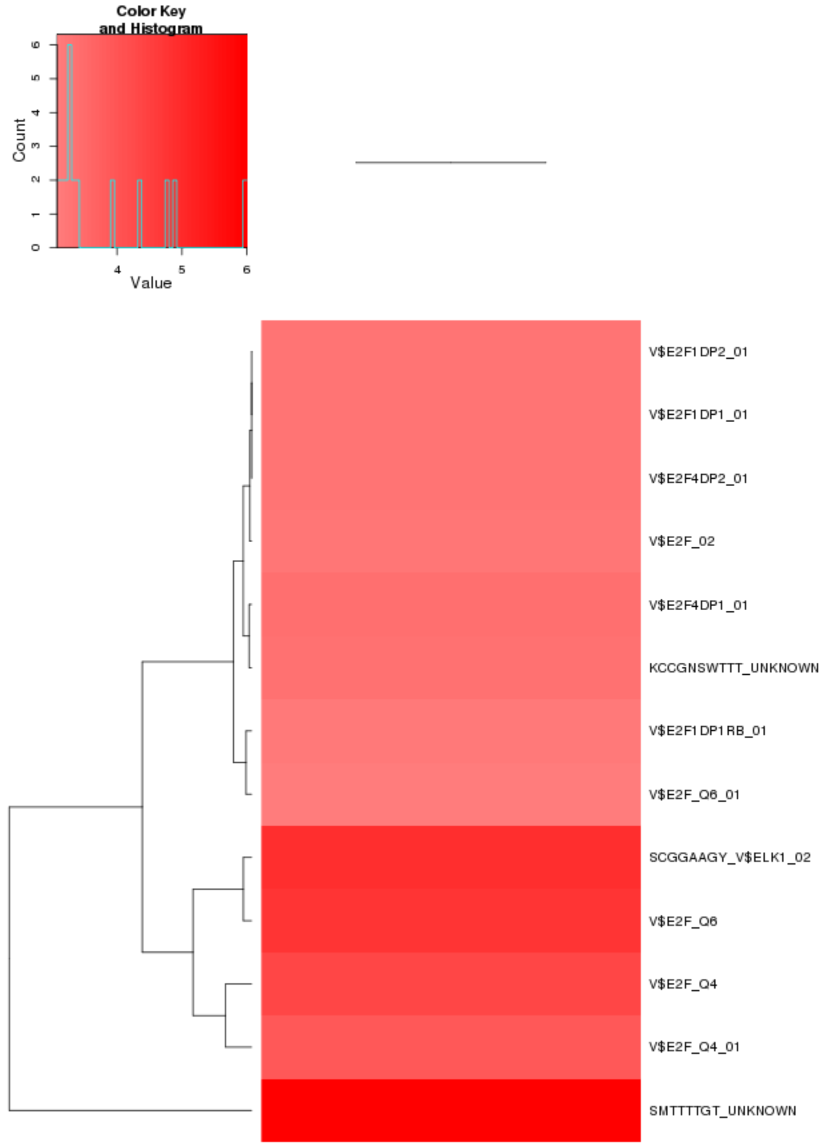
Immuno enrichment:



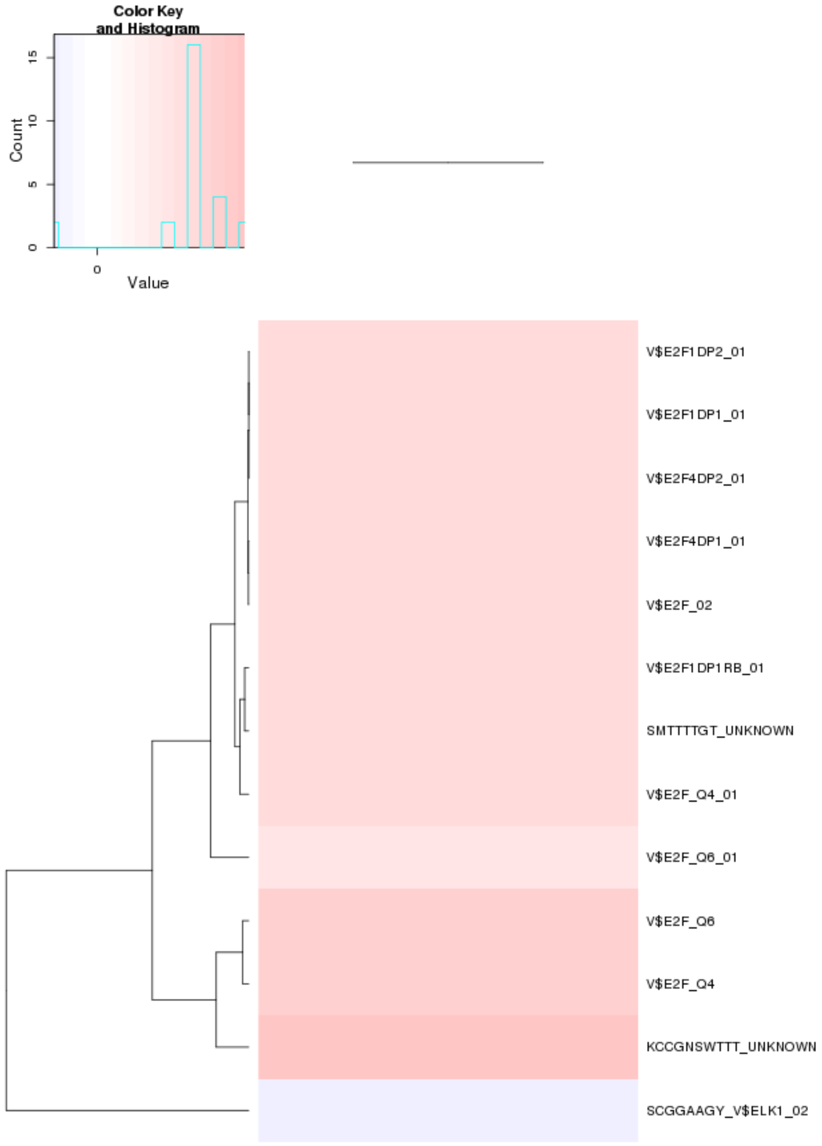
Immuno zscore:



TF enrichment:


Color Key
and Histogram
Count
0
1
2
3
4
5
6
4
5
6
Value
V$E2F1DP2_01
V$E2F1DP1_01
V$E2F4DP2_01
V$E2F_02
V$E2F4DP1_01
KCCGNSWTTT_UNKNOWN
V$E2F1DP1RB_01
V$E2F_Q6_01
SCGGAAGY_V$ELK1_02
V$E2F_Q6
V$E2F_Q4
V$E2F_Q4_01
SMTTTTGT_UNKNOWN

TF zscore:



GO enrichment

Cluster profiler used to call enichments of significantly differentially regulated genes that map to Entrez IDs.

```
## Error: RS-DBI driver: (error in statement: near ")": syntax error)
```

```
## Error: error in evaluating the argument 'object' in selecting a method for function 'annotation': Error: object 'sigGenes' not found
```

```
## Error: object 'geneAnnot' not found
```

```
## Error: error in evaluating the argument 'object' in selecting a method for function 'diffData': Error: object 'sigGenes' not found
```

```
## Error: object 'sigDiff' not found
```

```
## Error: object 'geneNames' not found
```

```
## Error: object 'sigEntrez' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'unlist': Error: object 'sigEZ' not found
```

```
## Error: object 'sigEZ' not found
```

```
## Error: object 'sigEZ' not found
```

```
## Error: object 'sigEZ' not found
```

```
## Error: object 'sigEZ' not found
```

```
## Error: object 'sigEZ' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'plot': Error: object 'goBP' not found
```

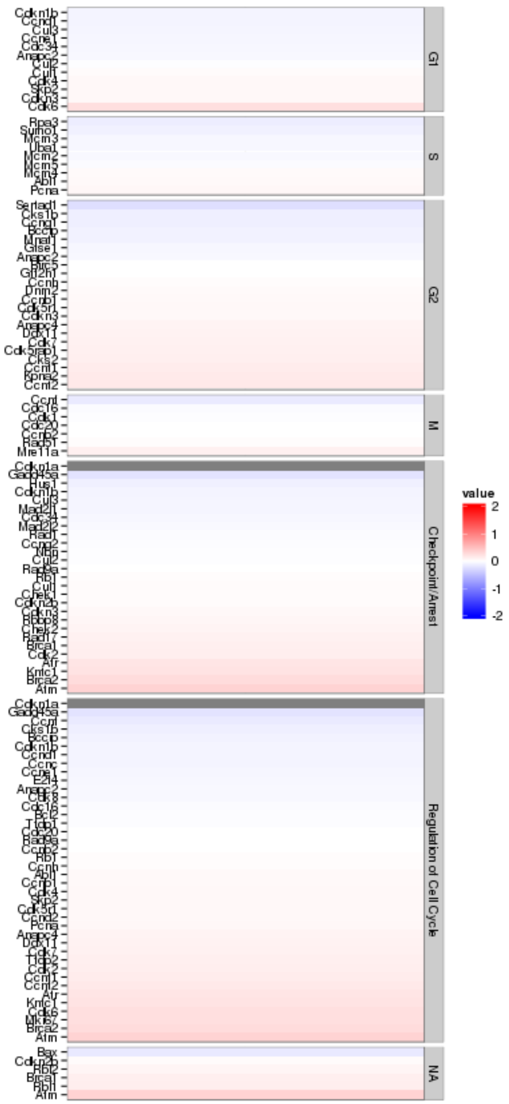
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'plot': Error: object 'goMF' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'plot': Error: object 'goCC' not found
```

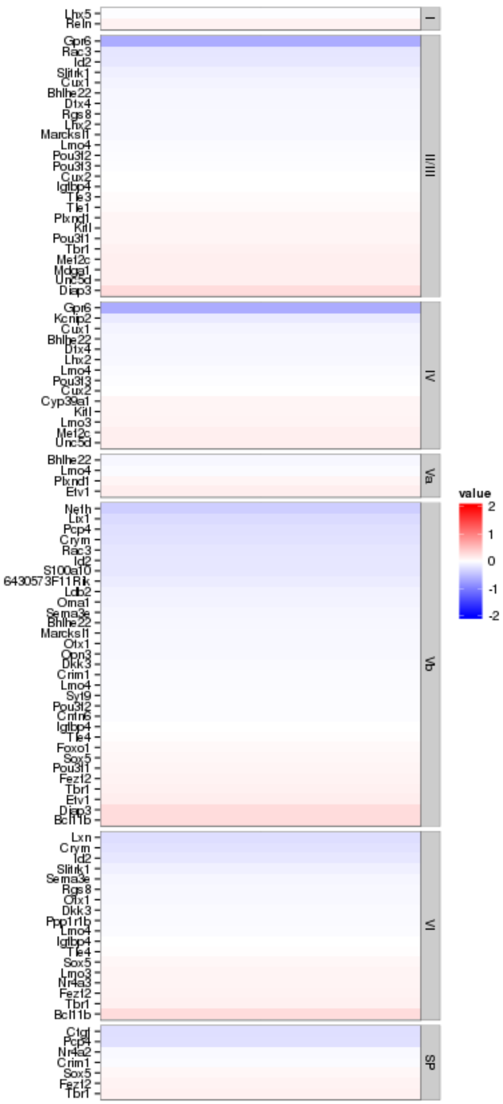
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'plot': Error: object 'kegg' not found
```

```
## Error: error in evaluating the argument 'x' in selecting a method for function 'plot': Error: object 'pathway' not found
```

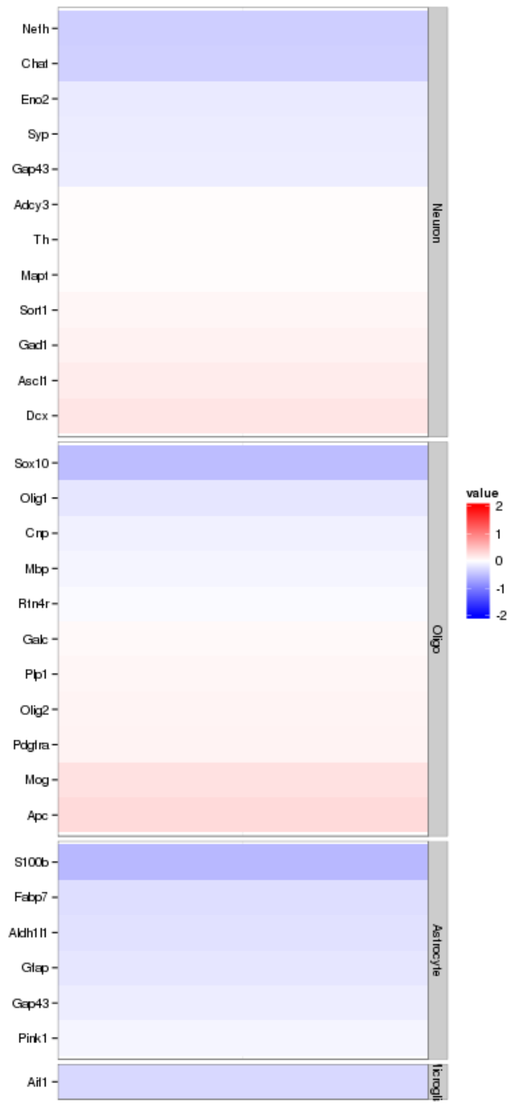
Enrichment or depletion for stage-specific cell cycle markers



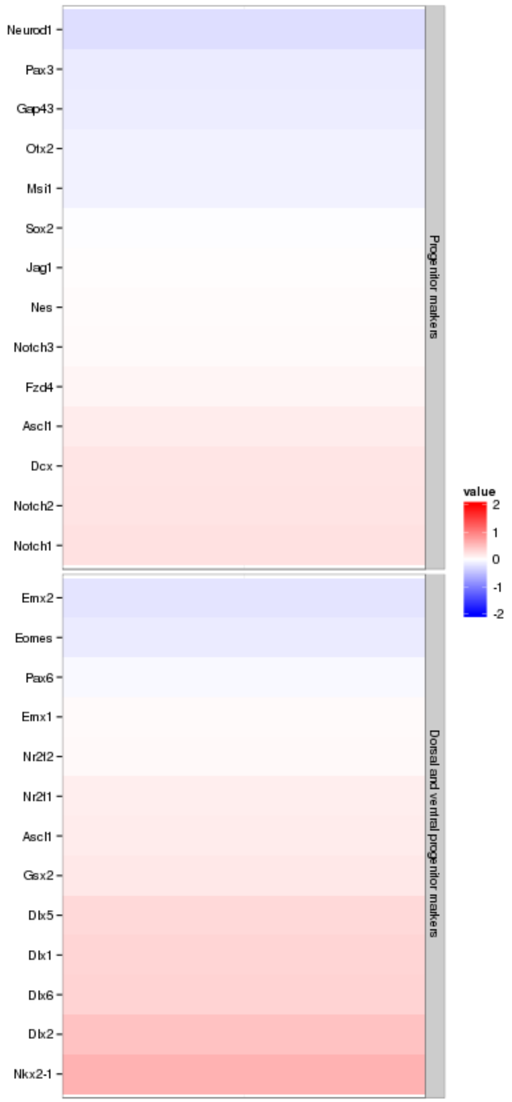
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



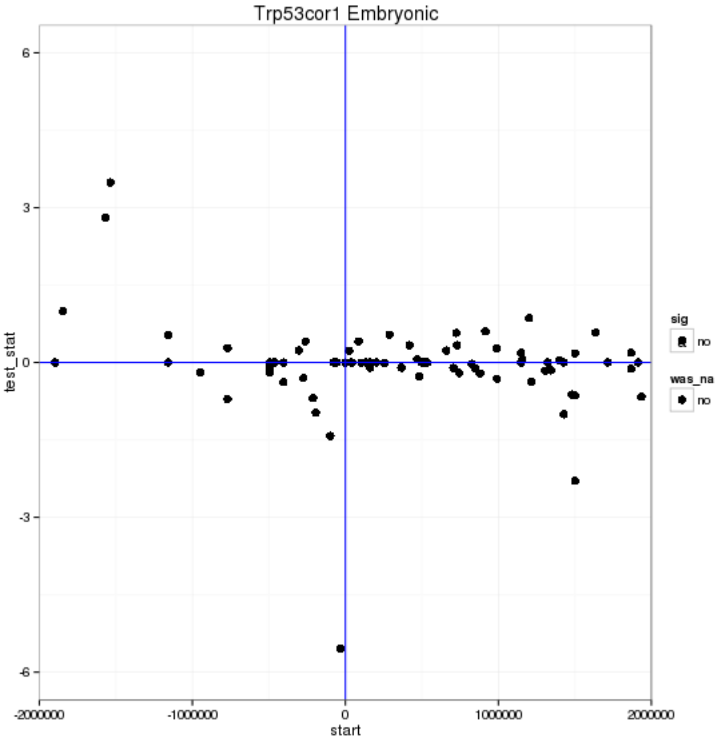
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 0 genes significantly regulated in a region this size is: 1



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15 JR749

16 JR814

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	31980100.00	1.28	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	31980100.00	1.11	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	31980100.00	1.24	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	31980100.00	1.30	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	31980100.00	1.21	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	31980100.00	0.90	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	31980100.00	0.98	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	31980100.00	0.93	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	31980100.00	0.87	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	31980100.00	0.97	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	31980100.00	0.82	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	31980100.00	0.81	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	31980100.00	0.69	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	31980100.00	1.23	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR749/abundances.cxb	Trp53cor	0	Trp53cor_0	31241000.00	31980100.00	0.95	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR814/abundances.cxb	Trp53cor	1	Trp53cor_1	31403400.00	31980100.00	1.00	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1                     
##  [2] stringr_0.6.2                  
##  [3] seqbias_1.10.0                 
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0                
##  [6] Biostrings_2.30.1
```

```
##  [7] gdata_2.13.3
##  [8] org.Mm.eg.db_2.10.1
##  [9] clusterProfiler_1.13.1
## [10] DOSE_2.0.0
## [11] ReactomePA_1.6.1
## [12] AnnotationDbi_1.24.0
## [13] Biobase_2.22.0
## [14] mgcv_1.7-29
## [15] nlme_3.1-117
## [16] RMySQL_0.9-3
## [17] RColorBrewer_1.0-5
## [18] gridExtra_0.9.1
## [19] gtable_0.1.2
## [20] marray_1.40.0
## [21] gplots_2.13.0
## [22] GSA_1.03
## [23] limma_3.18.13
## [24] xtable_1.7-3
## [25] cummeRbund_2.7.2
## [26] Gviz_1.6.0
## [27] rtracklayer_1.22.7
## [28] GenomicRanges_1.14.4
## [29] XVector_0.2.0
## [30] IRanges_1.20.7
## [31] fastcluster_1.1.13
## [32] reshape2_1.4
## [33] ggplot2_1.0.0
## [34] RSQLite_0.11.4
## [35] DBI_0.2-7
## [36] BiocGenerics_0.8.0
## [37] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GO.db_2.10.1           GOSemSim_1.20.3
## [16] graph_1.40.1           graphite_1.8.1         gtools_3.4.1
## [19] Hmisc_3.14-4           igraph_0.7.1           KEGG.db_2.10.1
## [22] KernSmooth_2.23-12     labeling_0.2           lattice_0.20-29
## [25] latticeExtra_0.6-26    MASS_7.3-33            Matrix_1.1-3
## [28] munsell_0.4.2          org.Hs.eg.db_2.10.1    proto_0.3-10
## [31] qvalue_1.36.0          Rcpp_0.11.2            RCurl_1.95-4.1
## [34] reactome.db_1.46.1     Rsamtools_1.14.3       scales_0.2.4
## [37] splines_3.0.2          stats4_3.0.2           survival_2.37-7
## [40] tcltk_3.0.2            tools_3.0.2            XML_3.98-1.1
## [43] zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,Trp53cor -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Trp53cor_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/Brain
## 2
## 3
## 4
## 5
```

Tug1 KO vs WT (Adult)

This file shows the wt-v-ko comparison for Tug1.

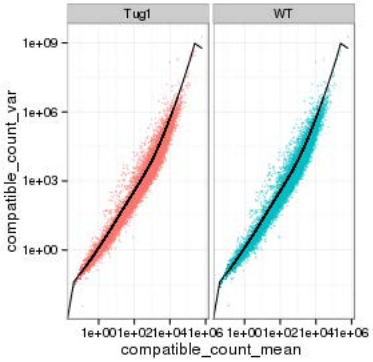
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

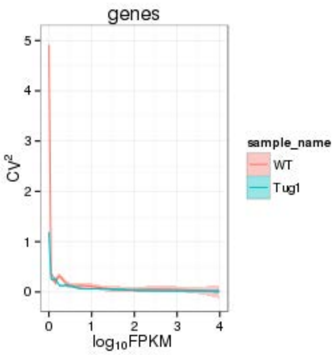
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



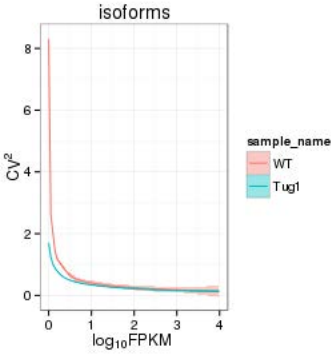
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

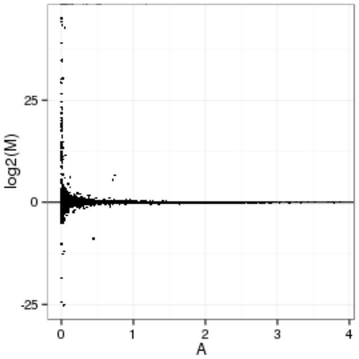
Genes:



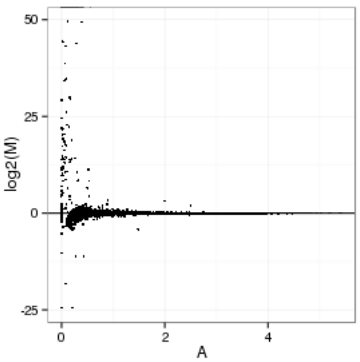
Isoforms:



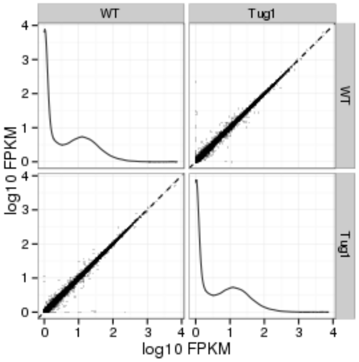
MvA plot



MvA plot counts



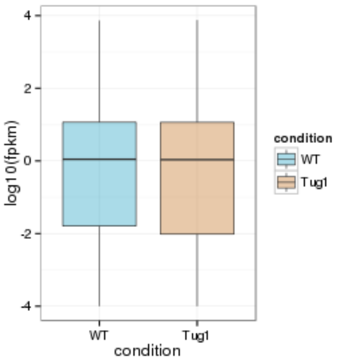
Scatterplot matrix



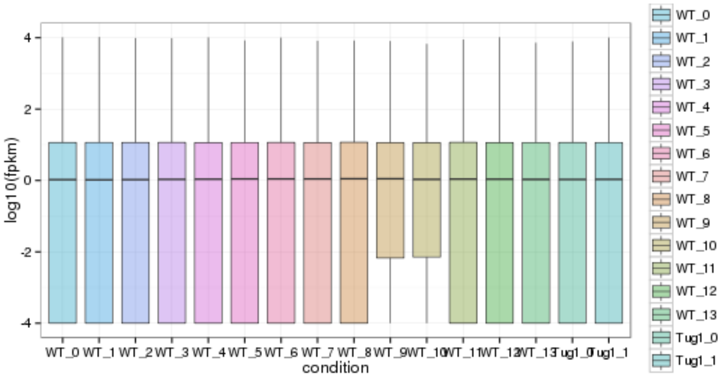
Distributions

Boxplots

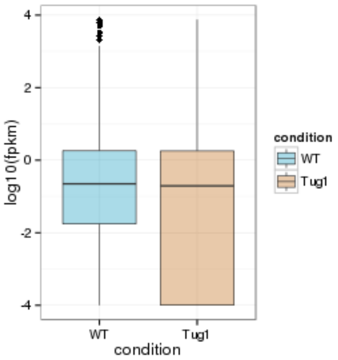
Boxplot (genes)



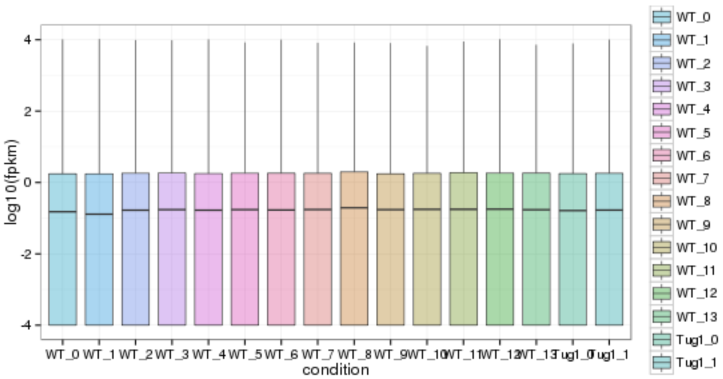
Boxplot (genes, replicates)



Boxplot (isoforms)

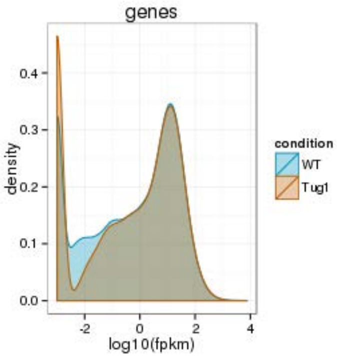


Boxplot (isoforms, replicates)

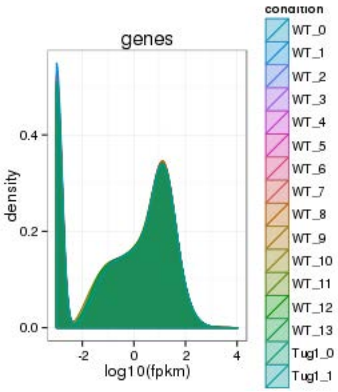


Density

Density (genes)

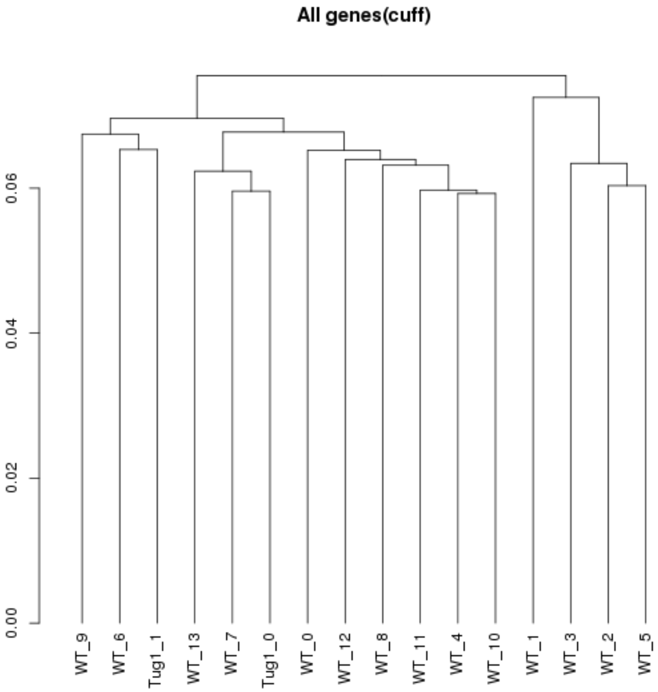


Density (genes, replicates)



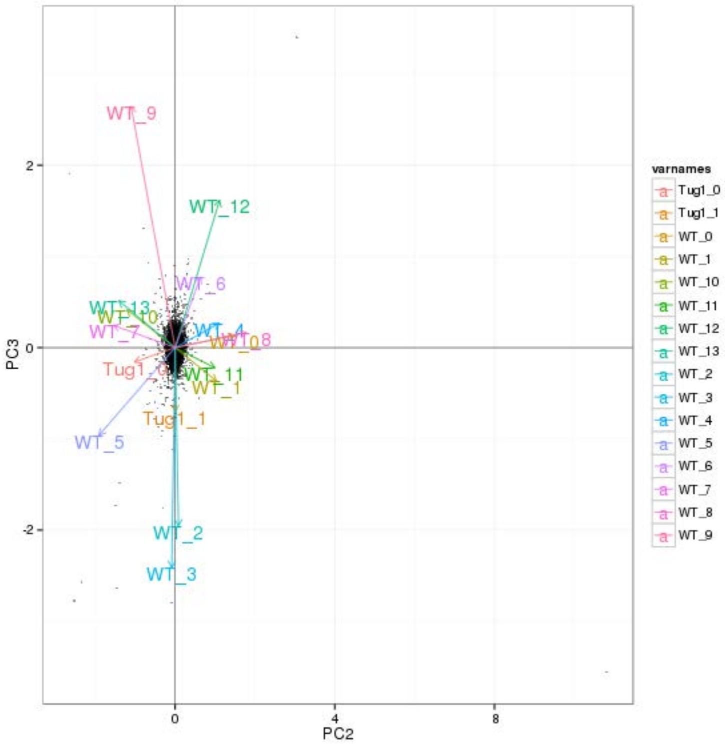
Clustering

Replicate Clusters

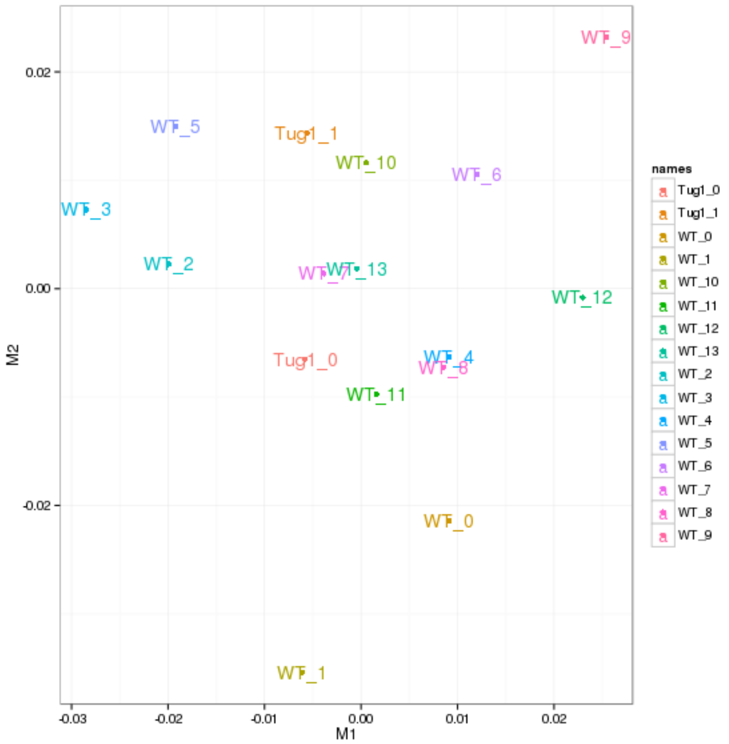


```
## NULL
```

PCA (genes)

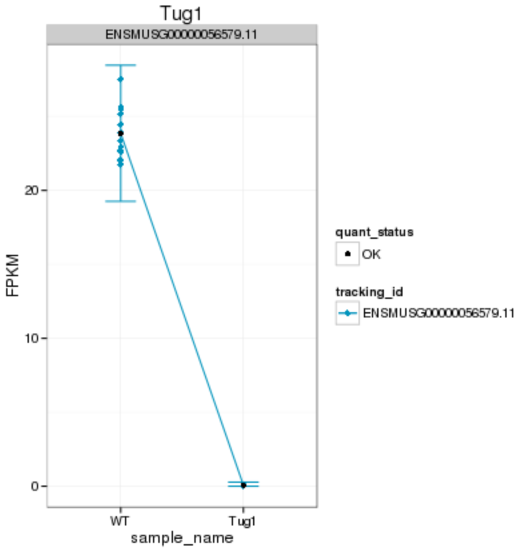

WT_9
WT_12
WT_6
WT_13
WT_10
WT_7
WT_4
WT_0
WT_8
Tug1_0
WT_11
WT_1
Tug1_1
WT_5
WT_2
WT_3
2
0
-2
0
4
8
PC3
PC2
varnames
Tug1_0
Tug1_1
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

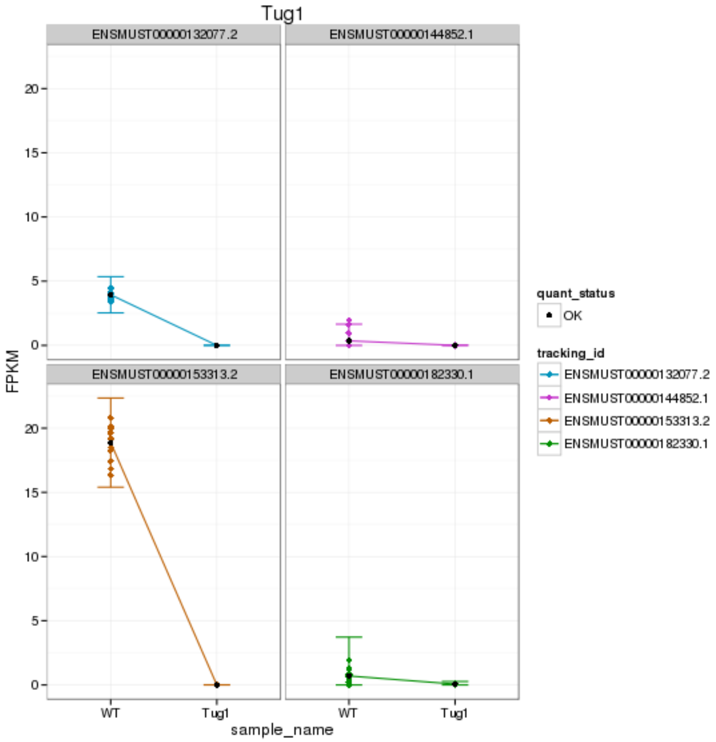


KO assessment

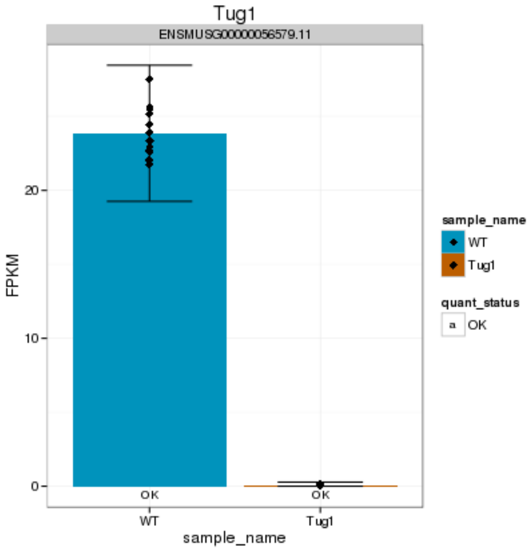
Endogenous lncRNA expression



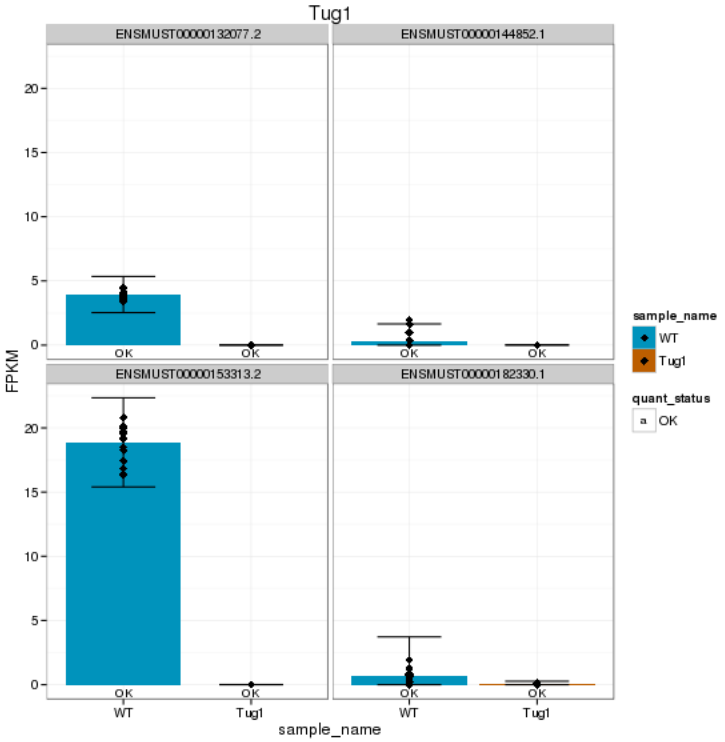
Endogenous expression of Tug1 isoforms:



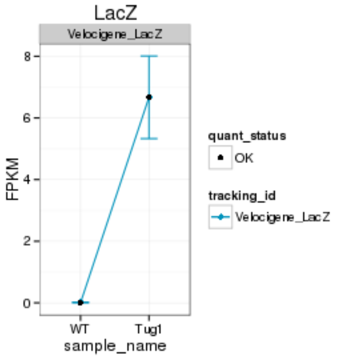
Barplot of gene expression:

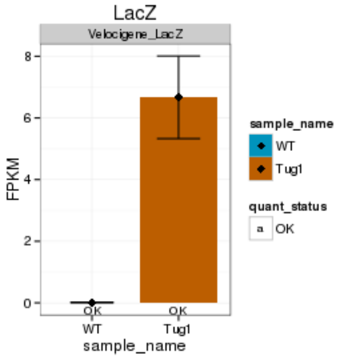


Barplot of isoform expression:



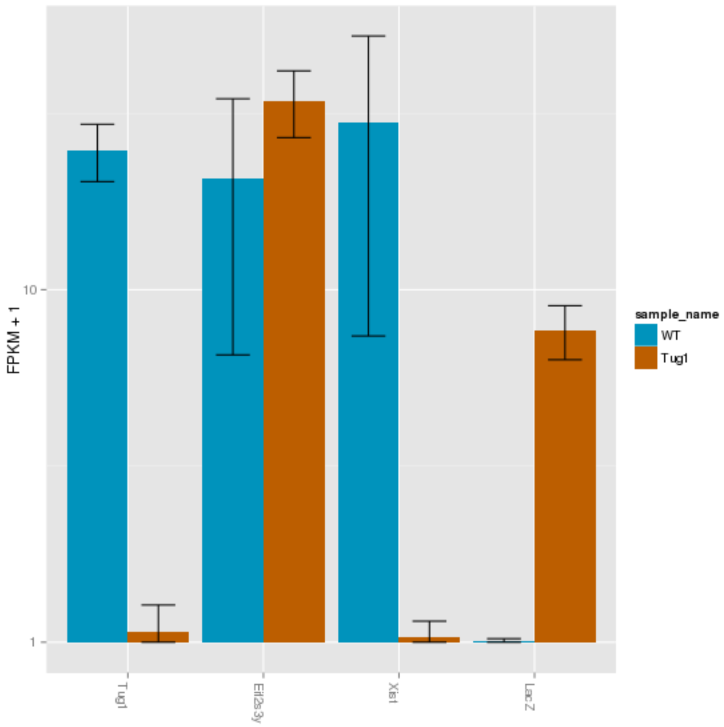
LacZ expression



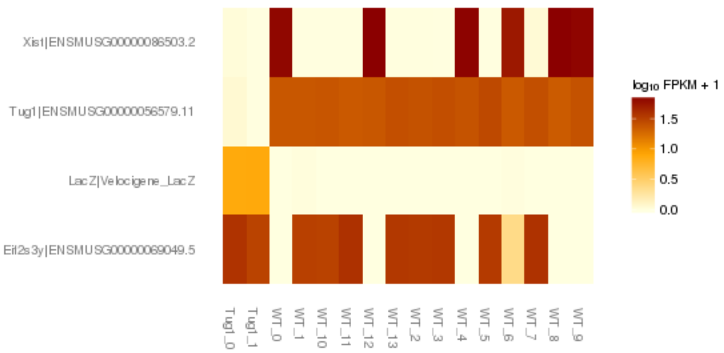


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

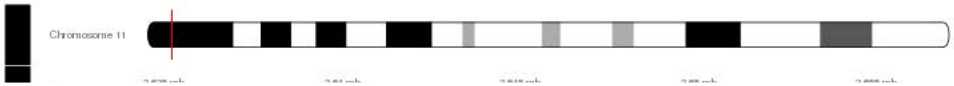
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):

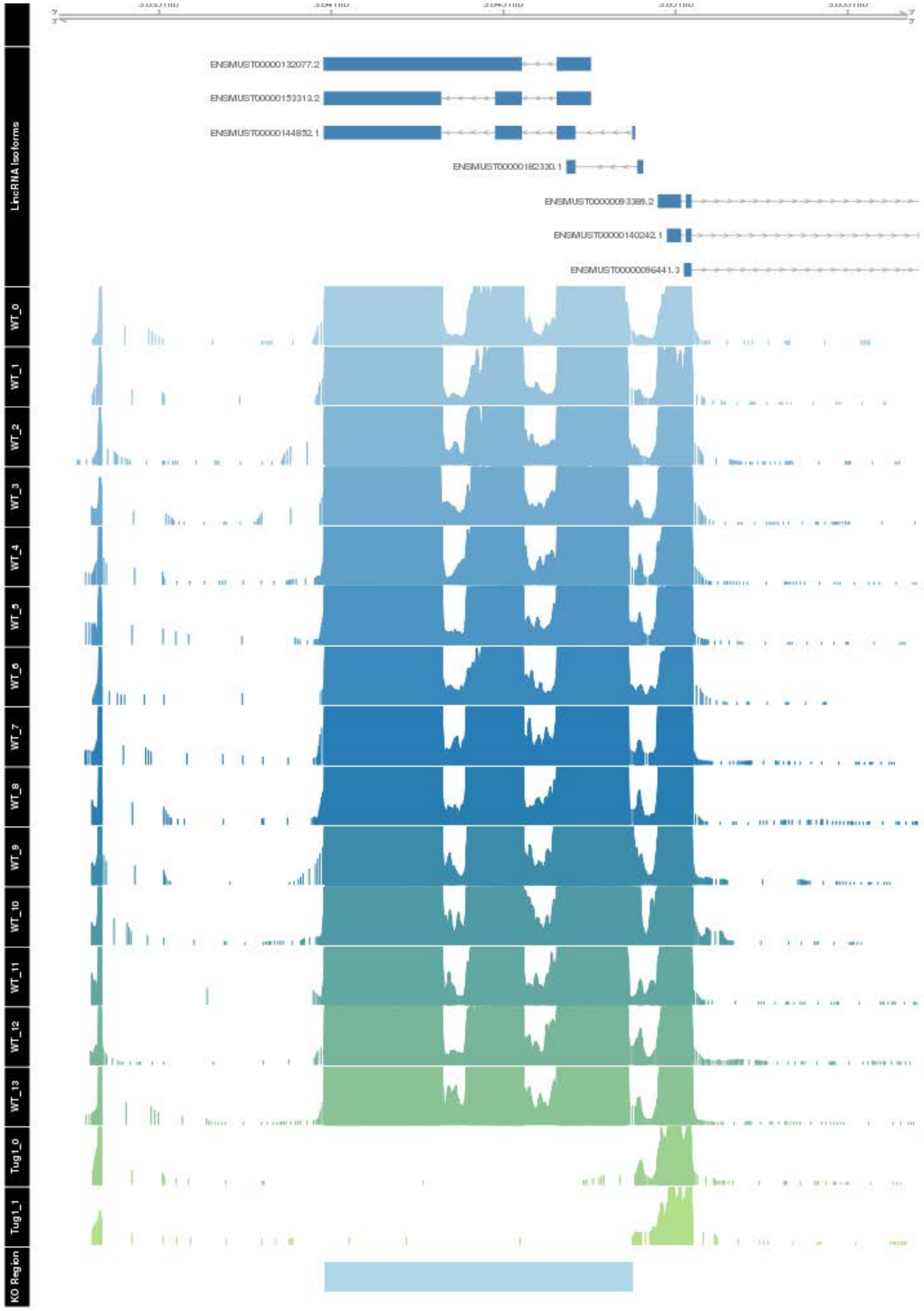


Expression heatmap:



Track visualization




LincRNA Isoforms
ENSMUST00000132077.2
ENSMUST00000153313.2
ENSMUST00000144852.1
ENSMUST00000182330.1
ENSMUST00000093388.2
ENSMUST00000140242.1
ENSMUST00000096441.3
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Tug1_0
Tug1_1
KO Region

Differential Analysis

Differential Genes

There are 39 significantly differentially expressed genes. They are:

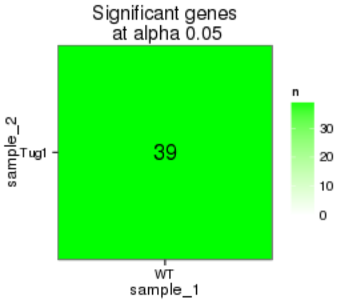
	geneAnnot$gene_short_name
1	Gabra2
2	Pde1c
3	Nes
4	Plxdc1
5	Ubb
6	Pdk4
7	Mybpc1
8	Rnf185
9	Adi1
10	Serpina3n
11	Esco1
12	Rps24
13	Myoc
14	Herc6
15	Hddc3
16	Dis3l
17	Ndn
18	Arhgap27
19	Morc2a
20	Inpp5j
21	8430429K09Rik
22	Anln
23	Akap12
24	Pyurf
25	Nhlrc1
26	Fat2
27	Kdm5d
28	Cox5b
29	Zbtb16
30	Ddx3y
31	Egr4
32	Gm9008
33	3222401L13Rik
34	Selm
35	Gm14418
36	Xist
37	AA465934

38 Gm14403

39 Gm26924

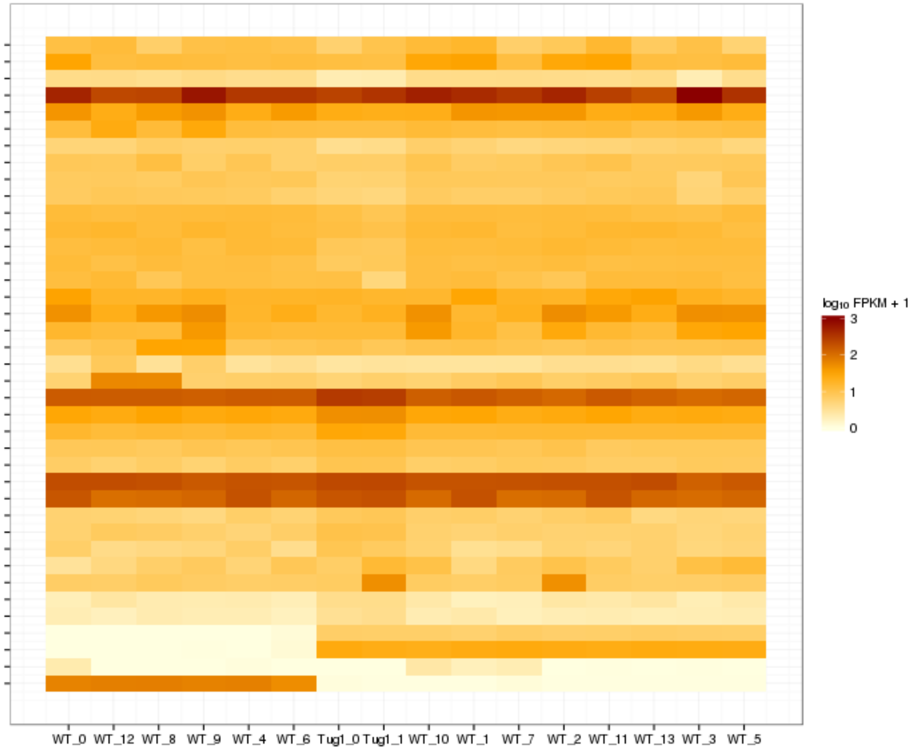
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

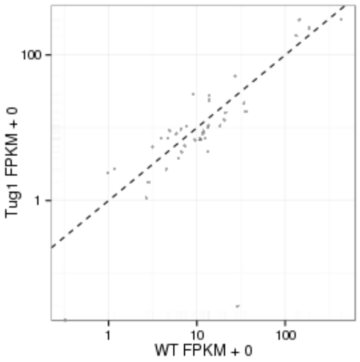


Significant genes with expression >50fpkm (any condition):(turned off)

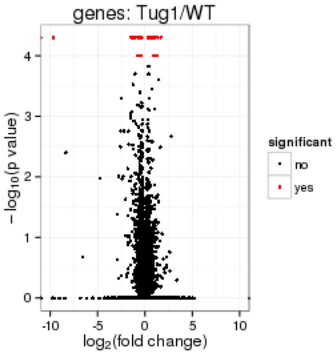
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

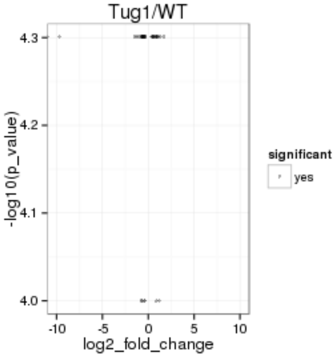
Scatter plot of significant genes only:



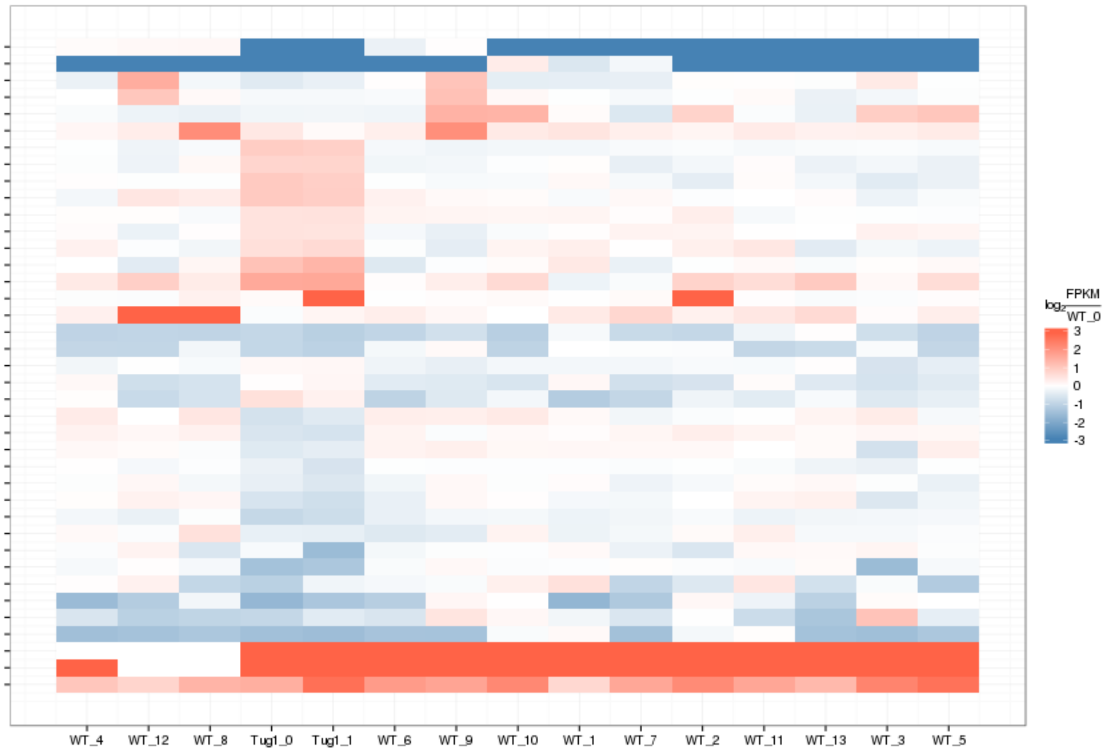
Volcano Plot



Volcano plot with significant genes only:



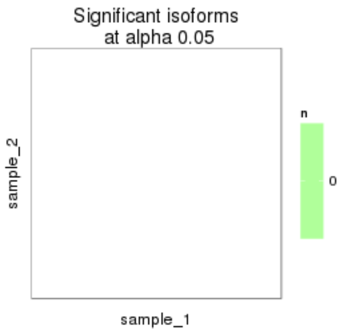
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

[1] “no sig isoforms”

Gene-level DE isoform heatmap

```
## [1] "no sig isoforms"
```

Isoform foldchange heatmap by isoform:

```
## [1] "no sig isoforms"
```

Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

Gene/Pathway Analysis

GSEA

Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

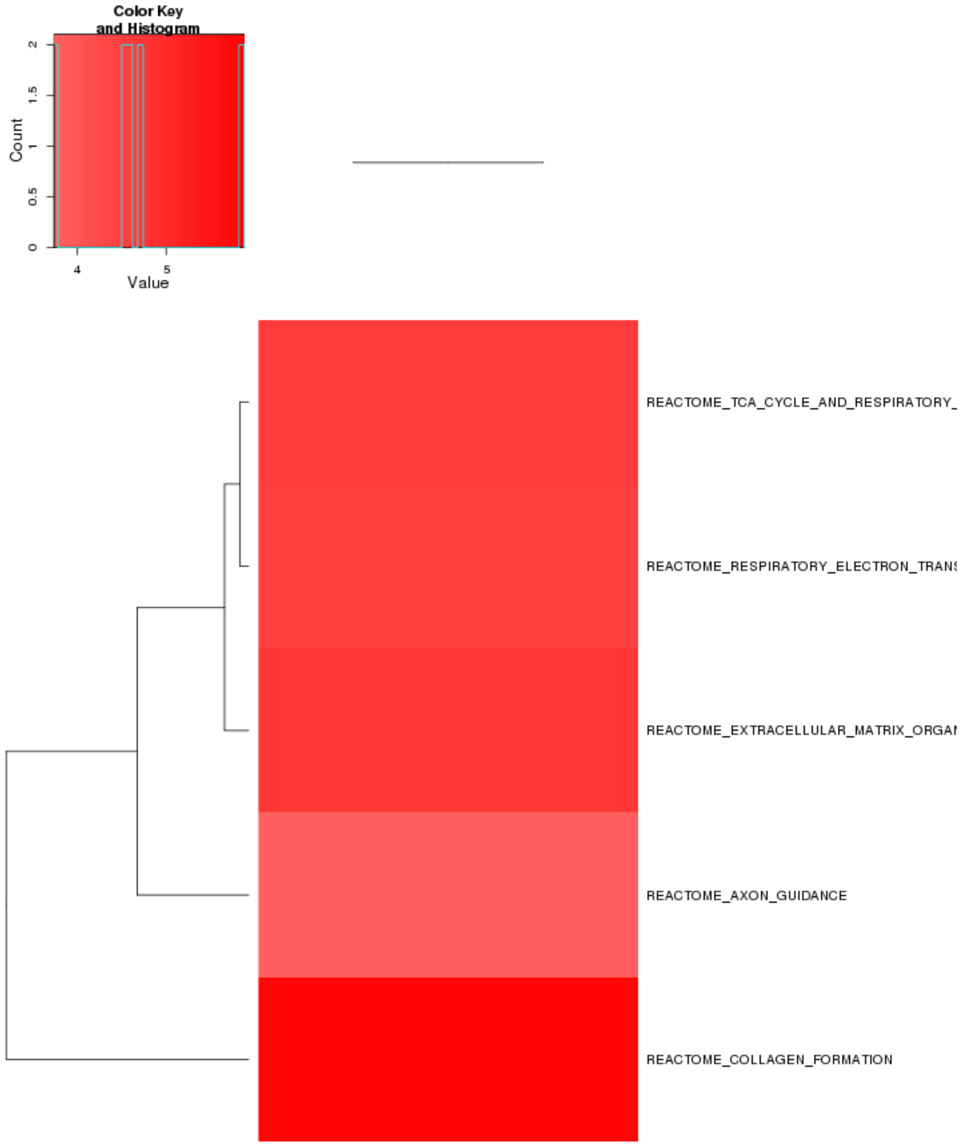
Biocarta enrichment:

```
## [1] "Not enough significant categories to print a heatmap!"
```

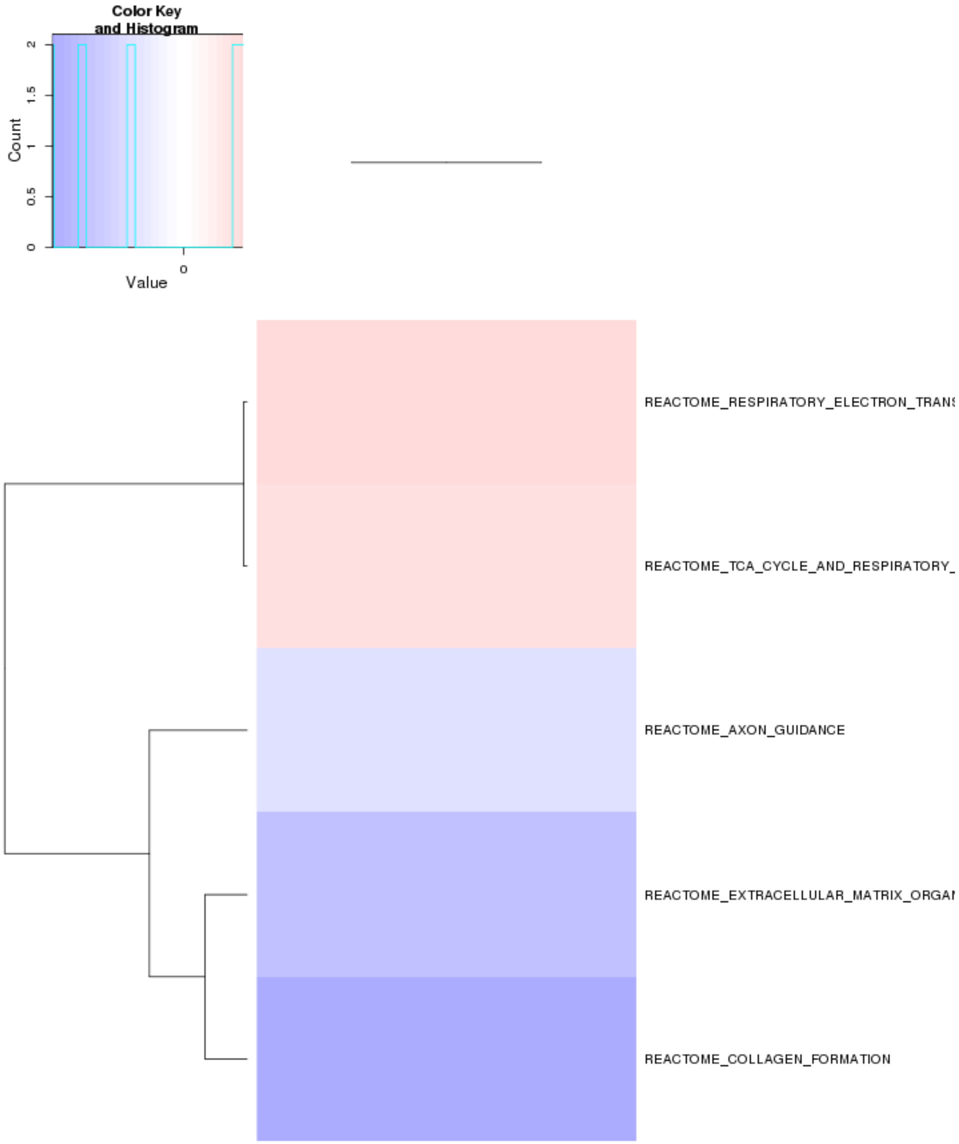
Biocarta zscore:

```
## [1] "Not enough significant categories to print a heatmap!"
```

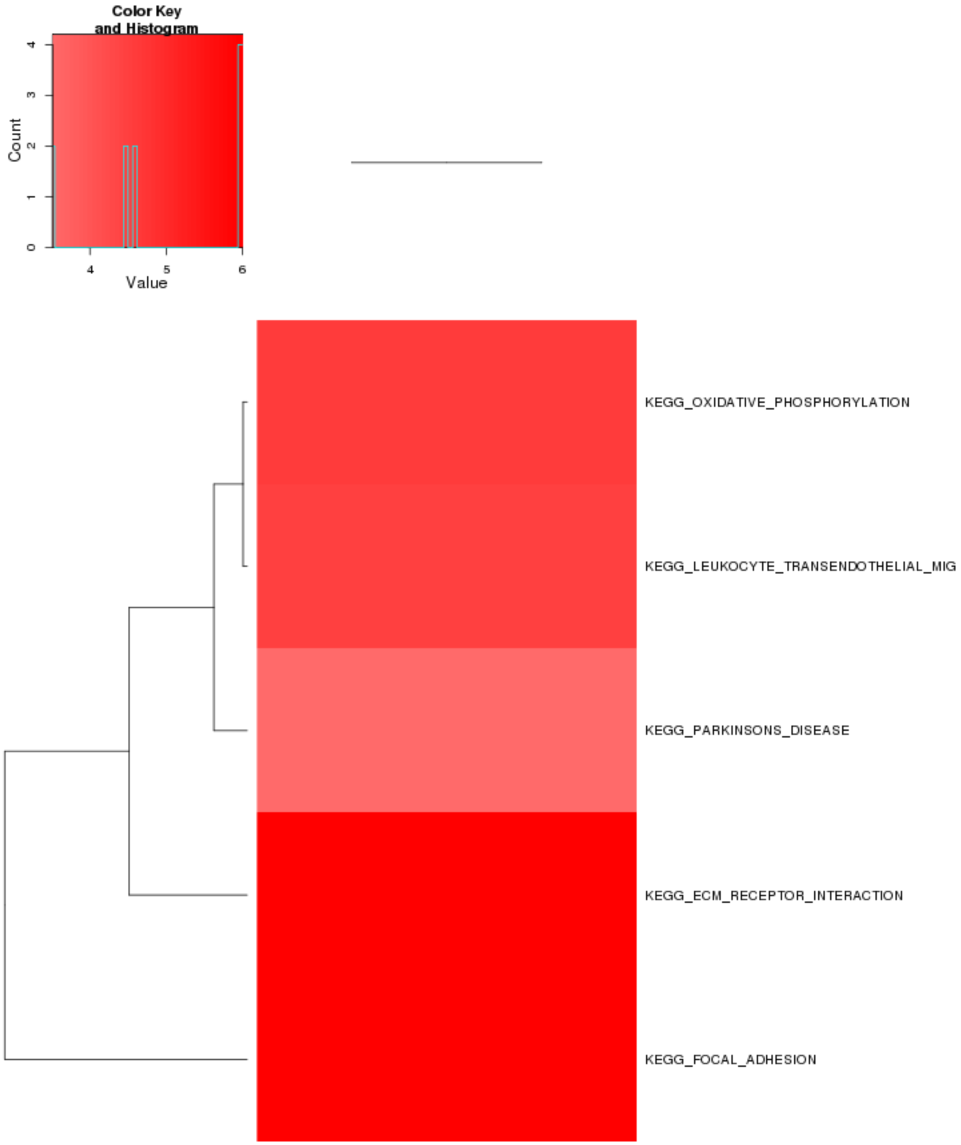
Reactome enrichment:



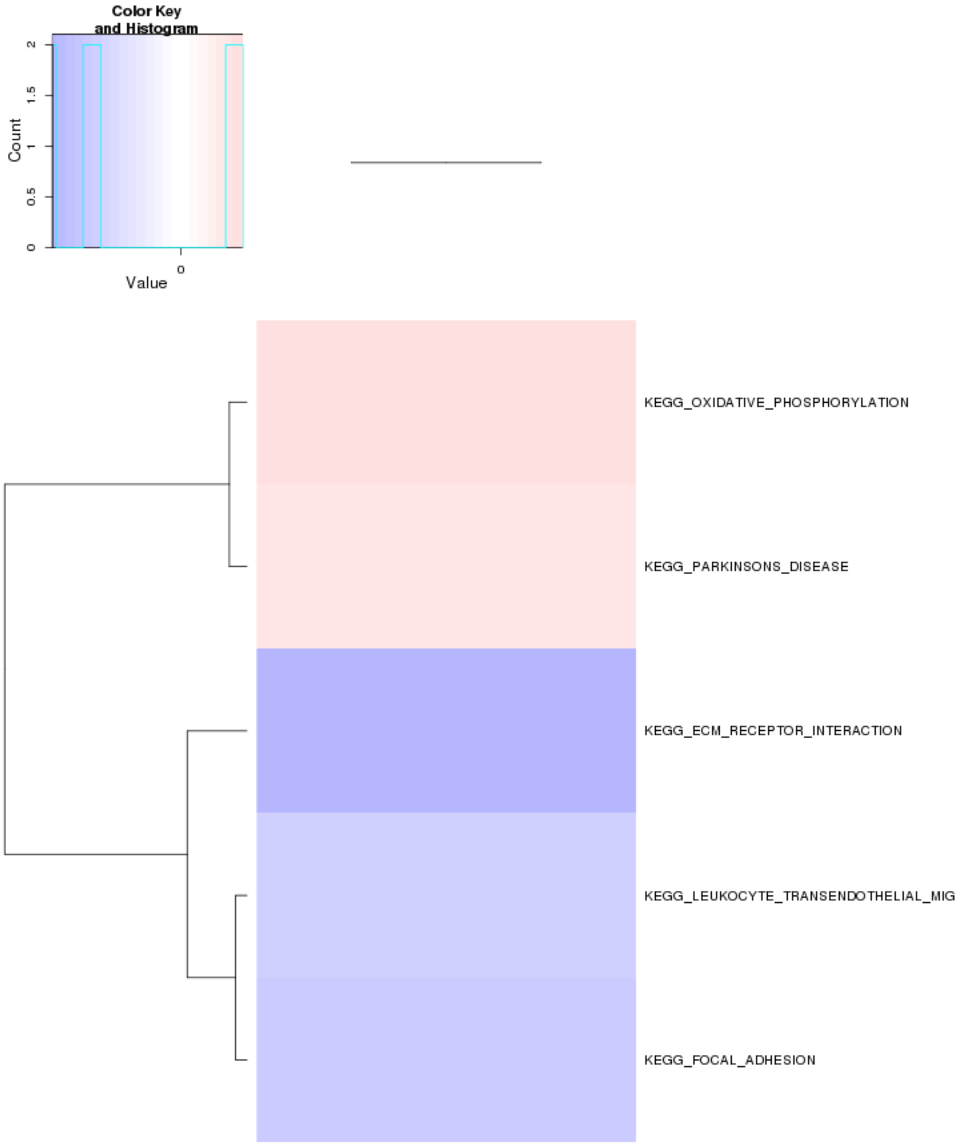
Reactome zscore:



Kegg enrichment:

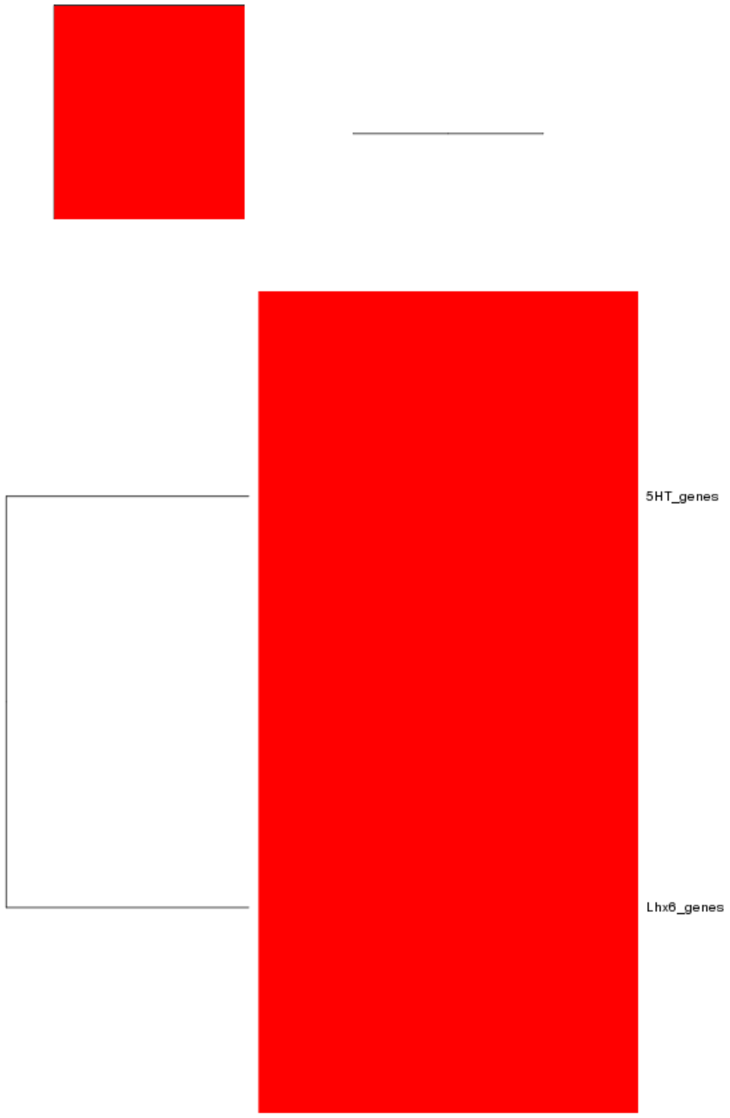

Color Key
and Histogram
Count
0
1
2
3
4
Value
4
5
6
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIG
KEGG_PARKINSONS_DISEASE
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_FOCAL_ADHESION

Kegg zscore:

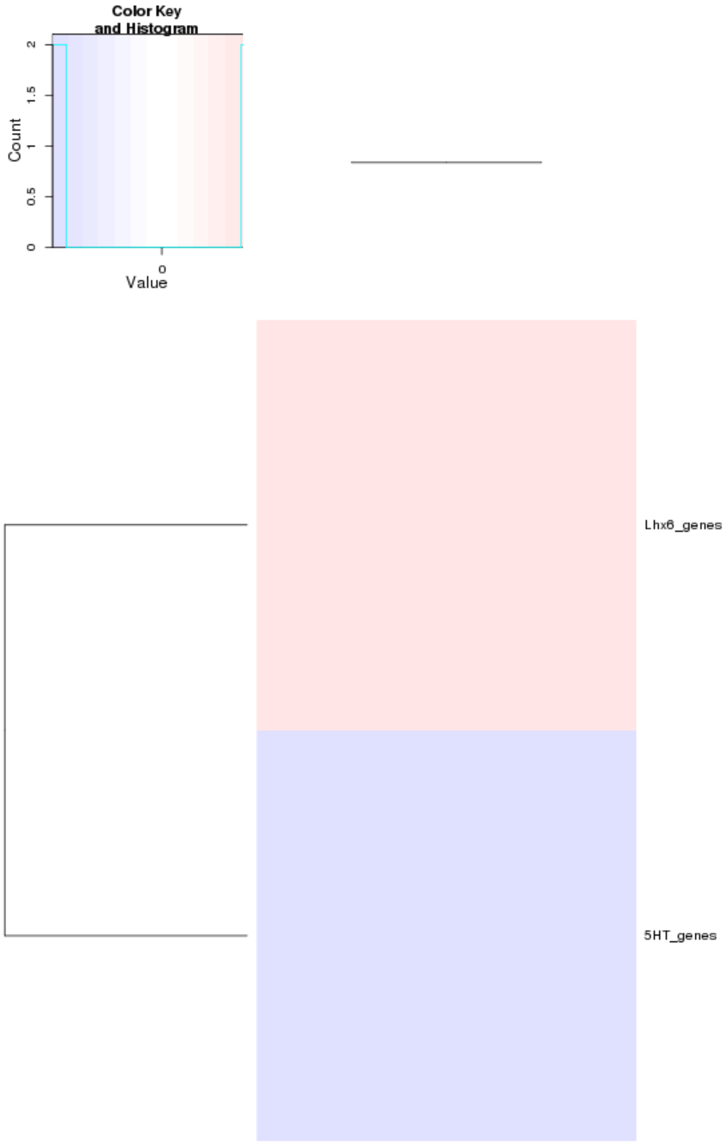


Interneuron enrichment:

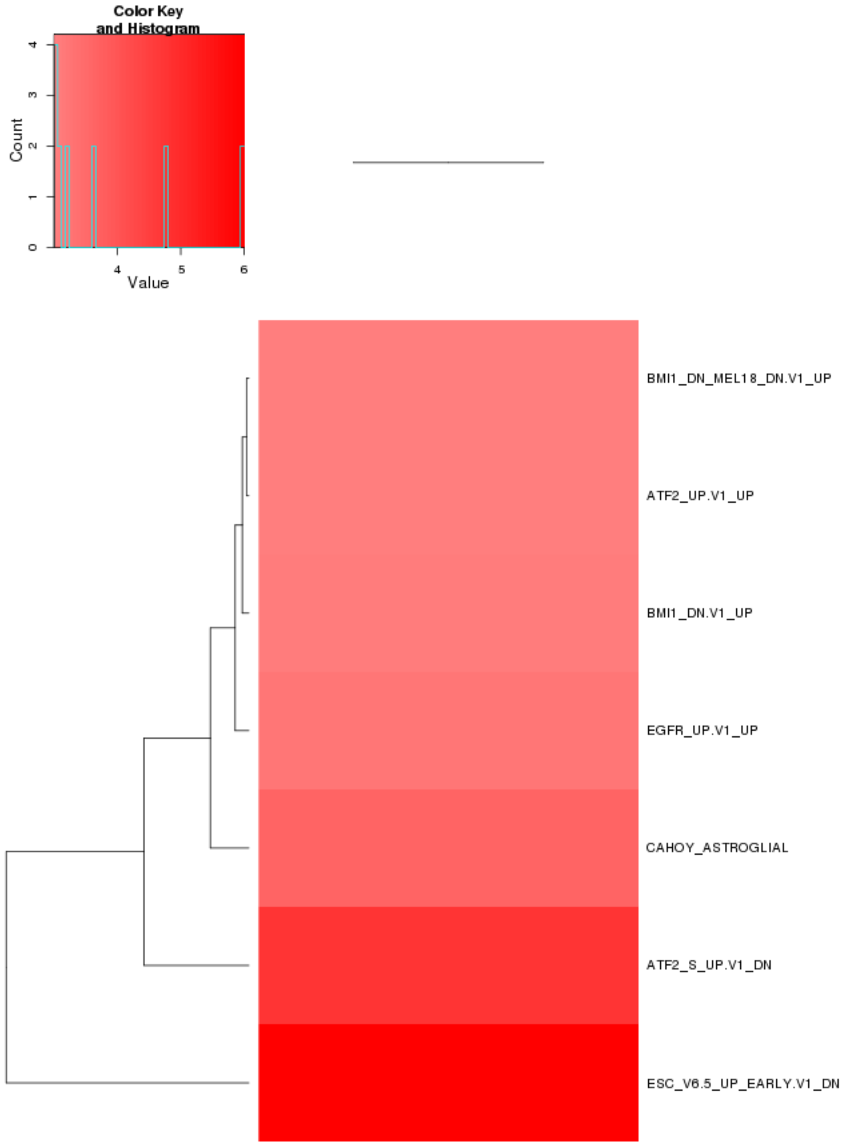
```
## Error: no locations are finite
```



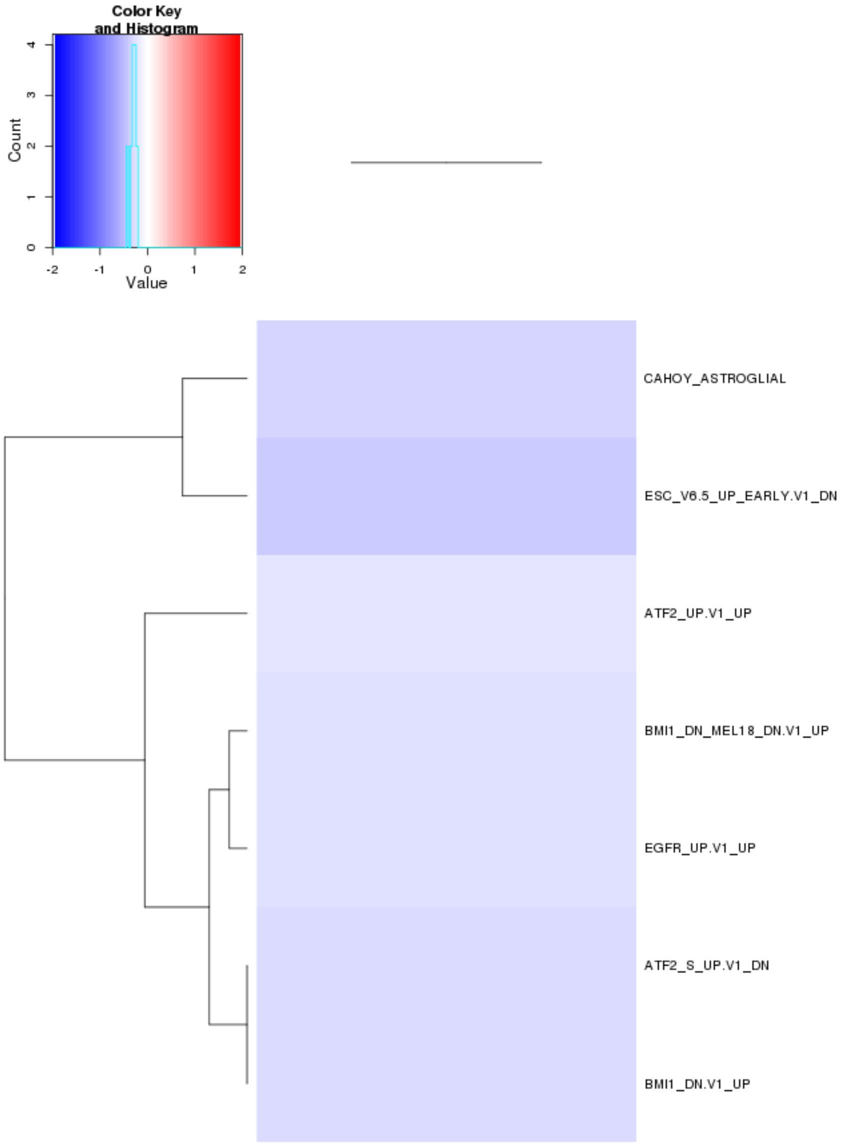
Interneuron zscore:



Oncogene enrichment:



Oncogene zscore:



Immuno enrichment:

```
## Error: argument is of length zero
```

Immuno zscore:

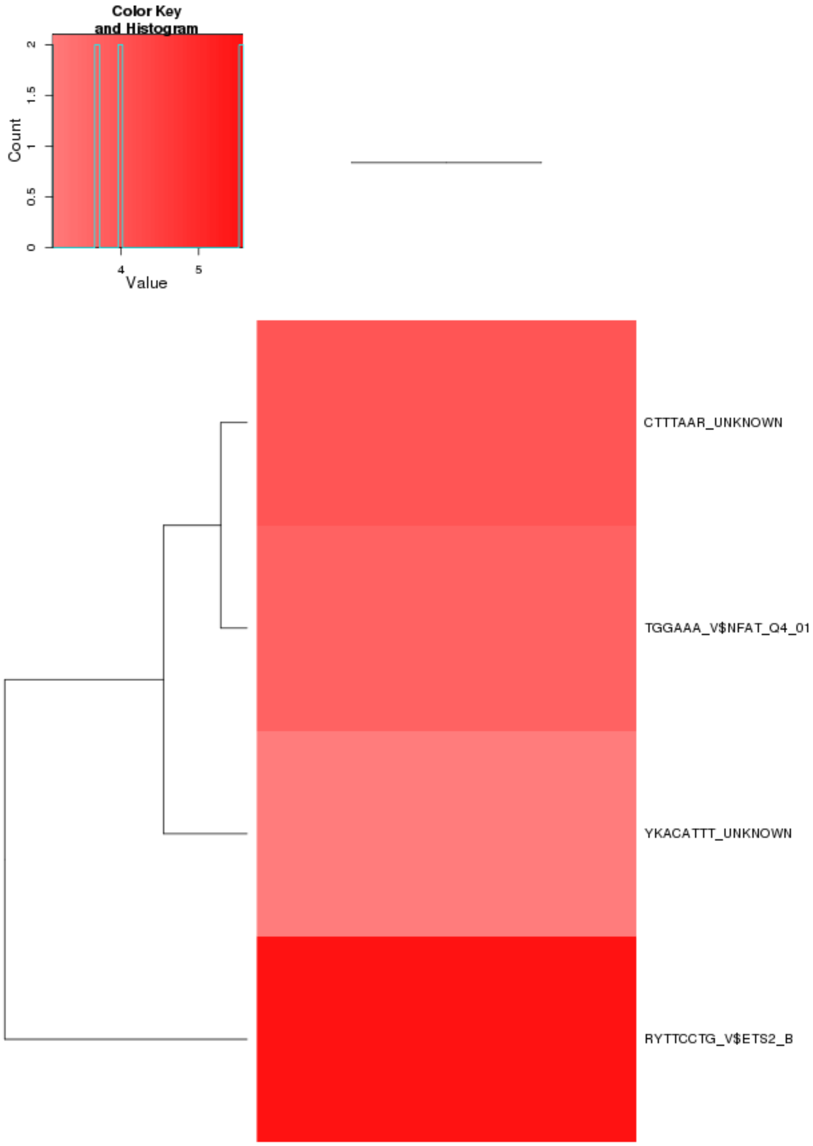
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

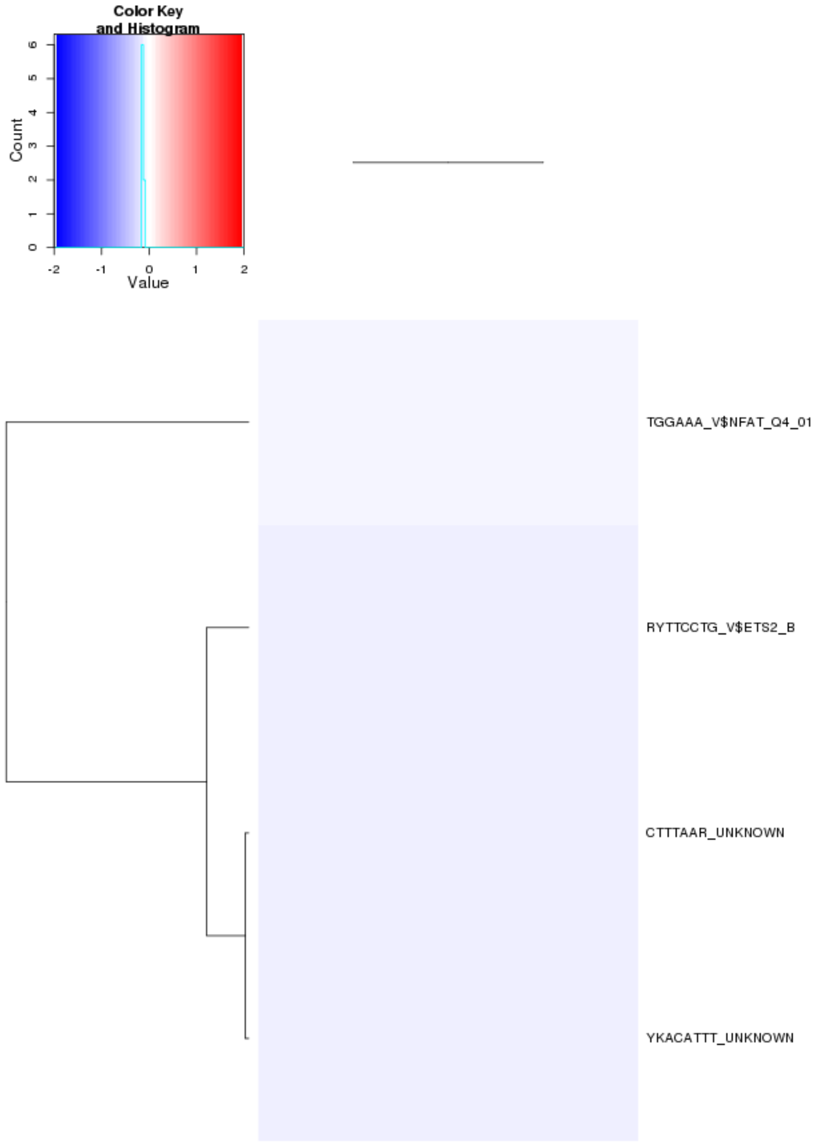
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

TF enrichment:


Color Key
and Histogram
Count
0
0.5
1
1.5
2
4
5
Value
CTTTAAR_UNKNOWN
TGGAAA_V$NFAT_Q4_01
YKACATTT_UNKNOWN
RYTTCCTG_V$ETS2_B

TF zscore:

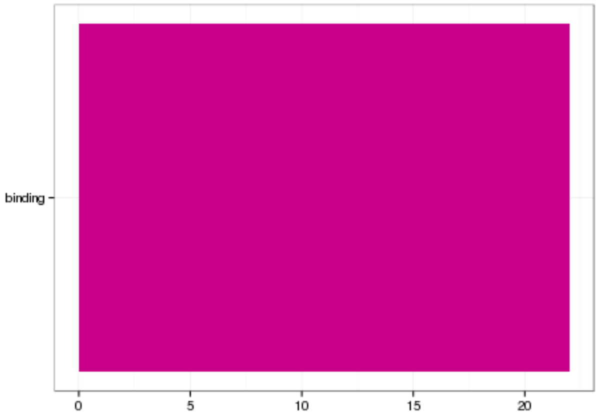


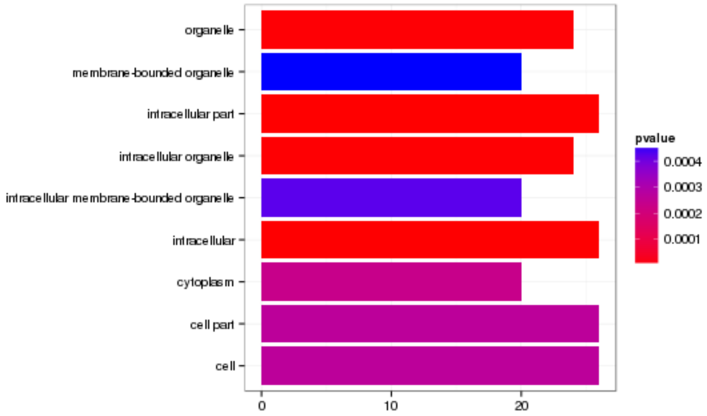
GO enrichment

Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

```
## Error: 'x' and 'units' must have length > 0
```

Enriched CC

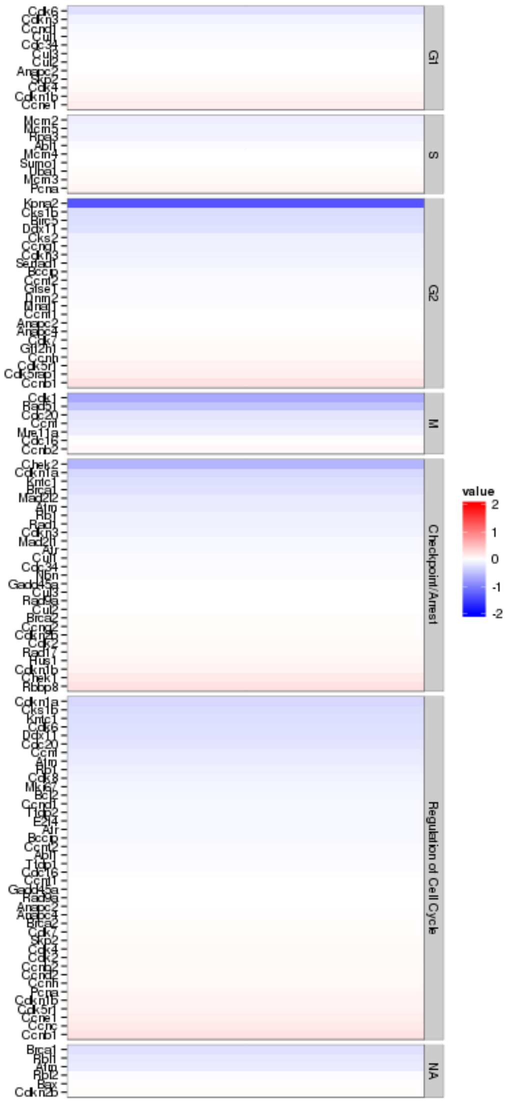




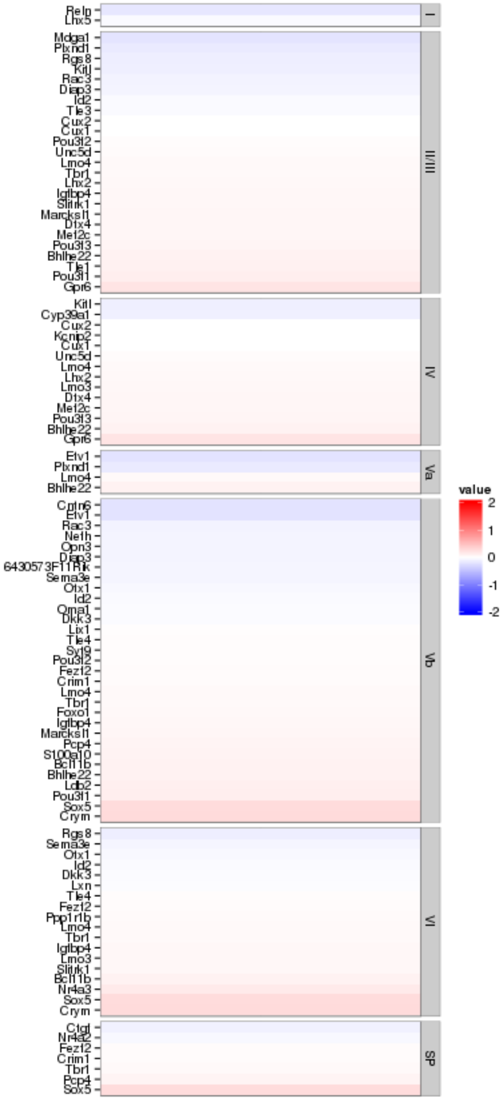
```
## Error: need finite 'xlim' values
```

```
## Error: need finite 'xlim' values
```

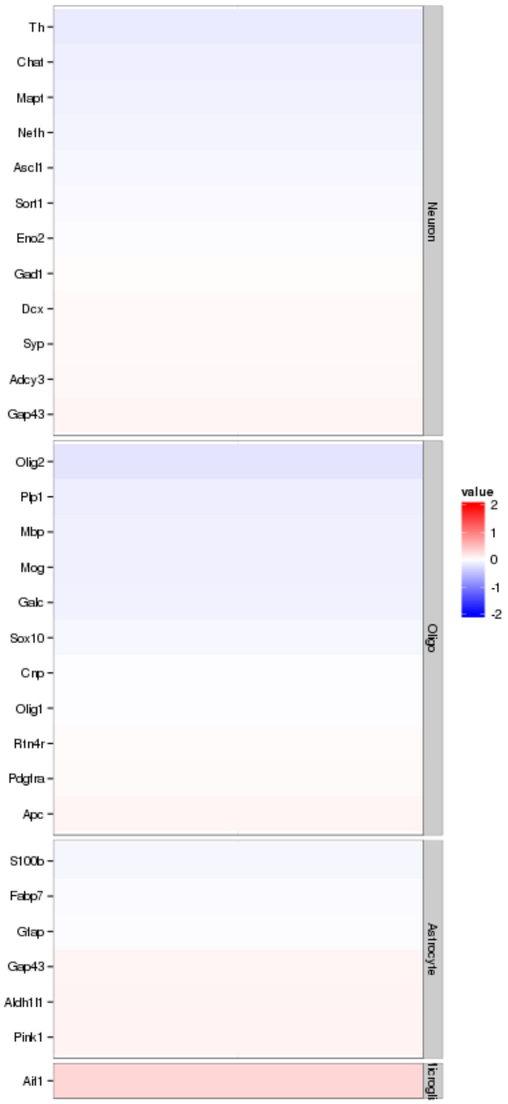
Enrichment or depletion for stage-specific cell cycle markers



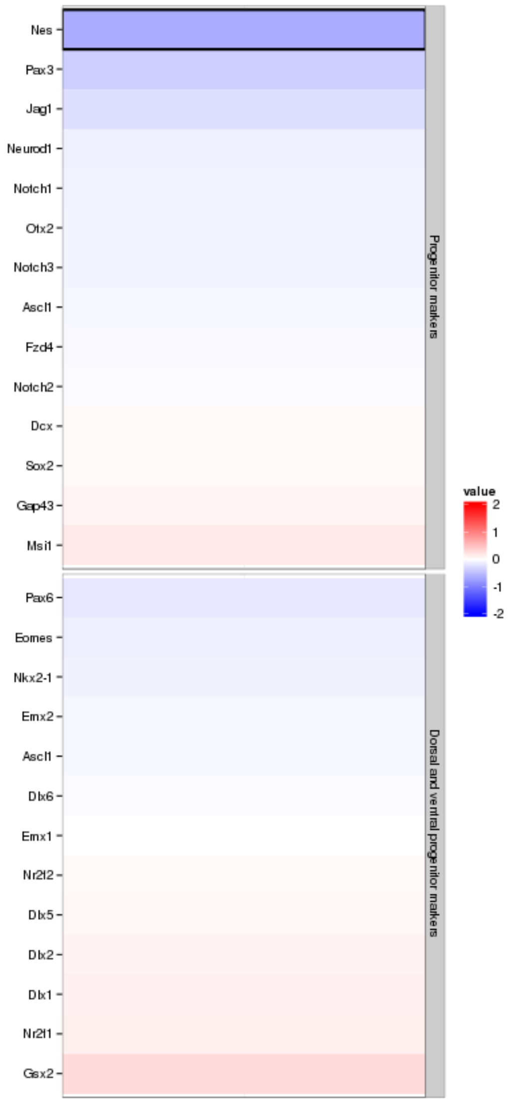
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



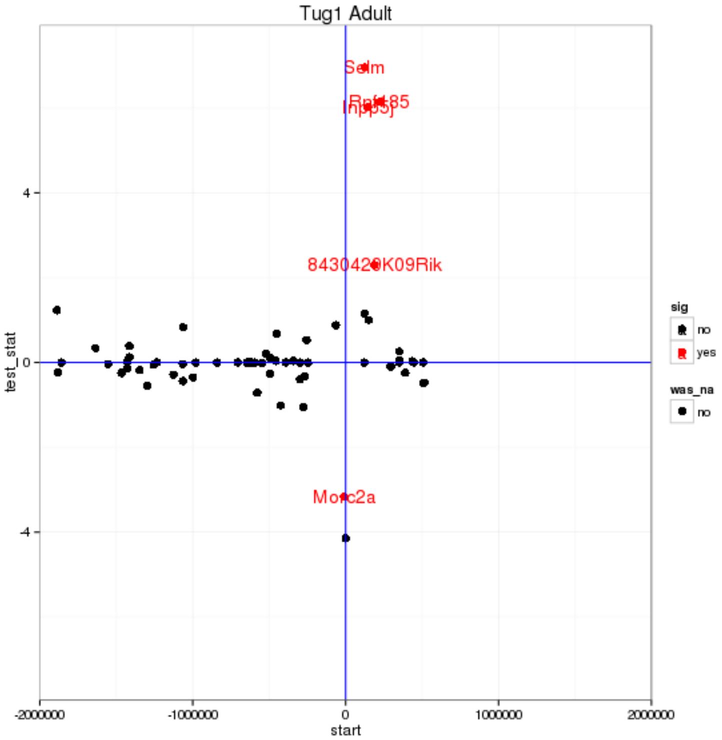
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 5 genes significantly regulated in a region this size is: 0.0023



Notes

Samples used are:

	10
1	JR729
2	JR728
3	JR796
4	JR797
5	JR740
6	JR800
7	JR827
8	JR778
9	JR734
10	JR802
11	JR803
12	JR735
13	JR785
14	JR781

15 JR745

16 JR807

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR729/abundances.cxb	WT	0	WT_0	26334400.00	34125900.00	0.77	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR728/abundances.cxb	WT	1	WT_1	20329200.00	34125900.00	0.59	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR796/abundances.cxb	WT	2	WT_2	34089000.00	34125900.00	1.00	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR797/abundances.cxb	WT	3	WT_3	28103300.00	34125900.00	0.81	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR740/abundances.cxb	WT	4	WT_4	35808200.00	34125900.00	1.05	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR800/abundances.cxb	WT	5	WT_5	37012200.00	34125900.00	1.09	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR827/abundances.cxb	WT	6	WT_6	27786600.00	34125900.00	0.82	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR778/abundances.cxb	WT	7	WT_7	39541900.00	34125900.00	1.17	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR734/abundances.cxb	WT	8	WT_8	34480600.00	34125900.00	1.03	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR802/abundances.cxb	WT	9	WT_9	45467400.00	34125900.00	1.32	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR803/abundances.cxb	WT	10	WT_10	52130400.00	34125900.00	1.53	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR735/abundances.cxb	WT	11	WT_11	34994400.00	34125900.00	1.03	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR785/abundances.cxb	WT	12	WT_12	34173600.00	34125900.00	0.99	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR781/abundances.cxb	WT	13	WT_13	41538900.00	34125900.00	1.23	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR745/abundances.cxb	Tug1	0	Tug1_0	38091200.00	34125900.00	1.12	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR807/abundances.cxb	Tug1	1	Tug1_1	29979900.00	34125900.00	0.87	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## 
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8    
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8   
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                 
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C            
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C       
## 
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils    
## [8] datasets  base     
## 
## other attached packages:
##  [1] plyr_1.8.1                       
##  [2] stringr_0.6.2                    
##  [3] seqbias_1.10.0                   
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0                  
##  [6] Biostrings_2.30.1                
```

```
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
## 
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6          
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4      
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7             
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1         
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1          
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4          
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12    
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26   
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2         
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0         
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1    
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2         
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2           
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##             param
## 1        cmd_line
## 2         version
## 3    SVN_revision
## 4  boost_version
## 5          genome
##
## 1 cuffdiff -p 10 -L WT,Tug1 -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Tug1_vs_WT_Adult /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/annc
## 2
## 3
## 4
## 5
```

Tug1 KO vs WT (Embryonic)

This file shows the wt-v-ko comparison for Tug1.

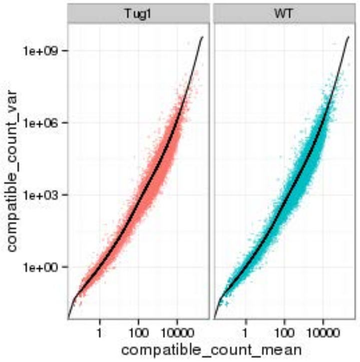
Cuff overview:

```
## CuffSet instance with:
##   2 samples
##   26754 genes
##   77524 isoforms
##   0 TSS
##   23066 CDS
##   0 promoters
##   0 splicing
##   19954 relCDS
```

QC

Dispersion

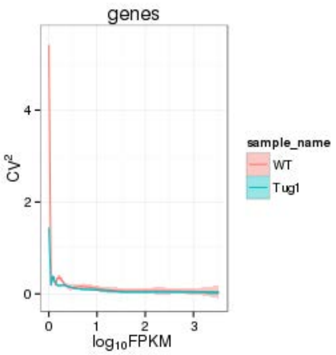
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



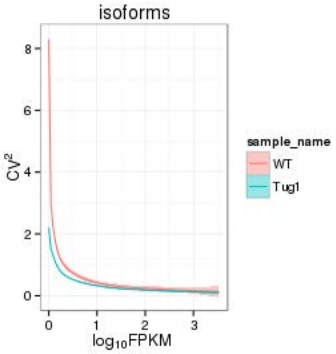
Cross-replicate variability (fpkmSCVplot)

Differences in CV 2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

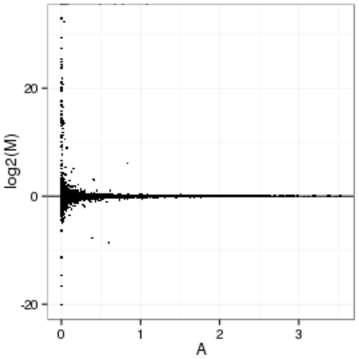
Genes:



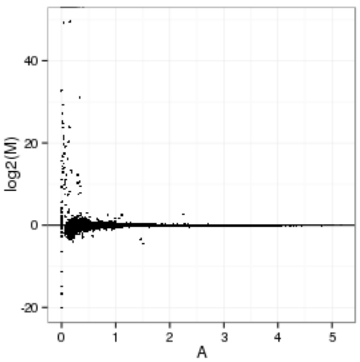
Isoforms:



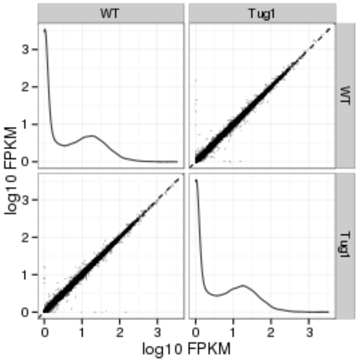
MvA plot



MvA plot counts



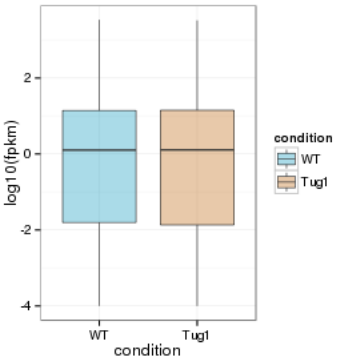
Scatterplot matrix



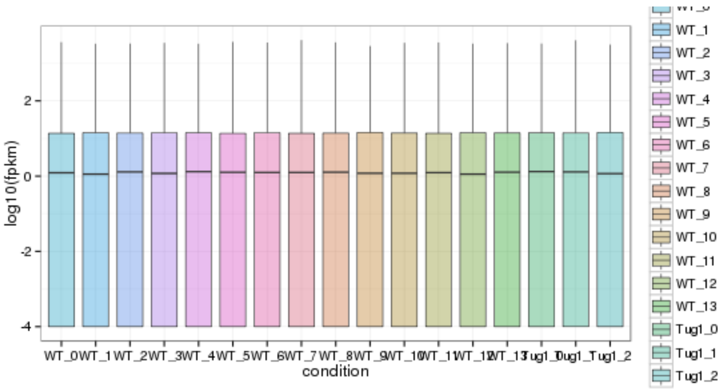
Distributions

Boxplots

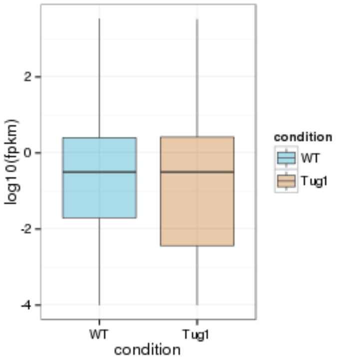
Boxplot (genes)



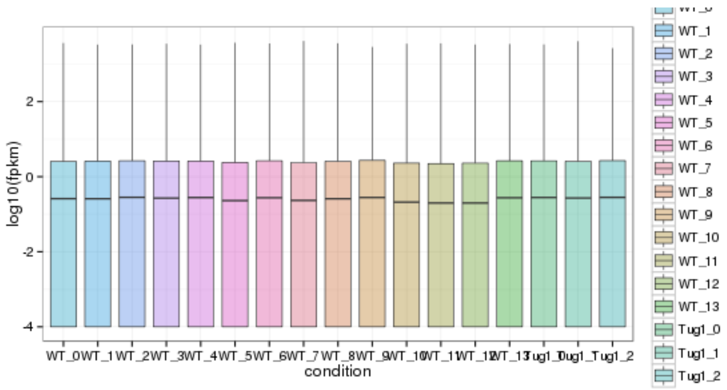
Boxplot (genes, replicates)



Boxplot (isoforms)

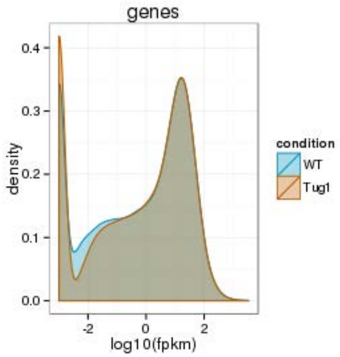


Boxplot (isoforms, replicates)

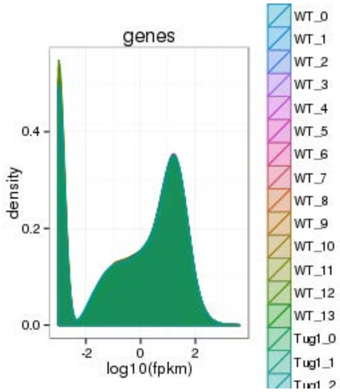


Density

Density (genes)

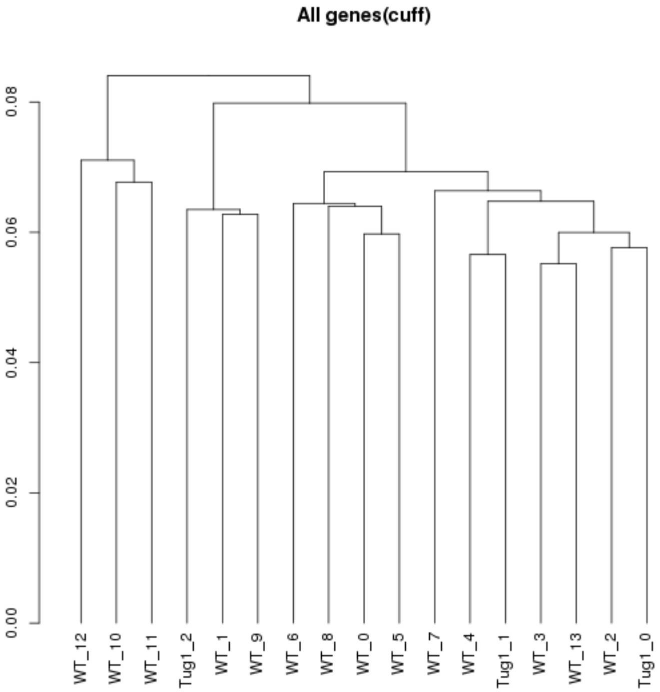


Density (genes, replicates)



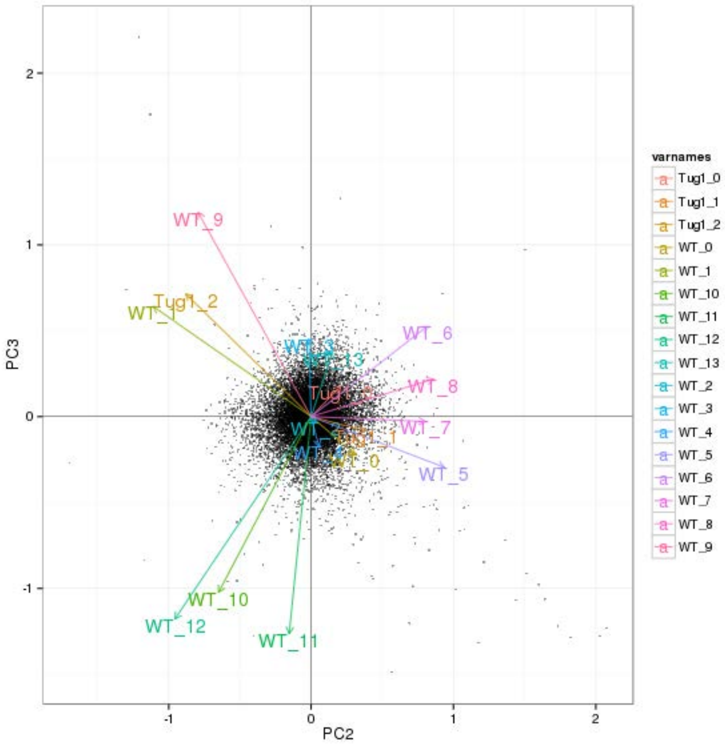
Clustering

Replicate Clusters

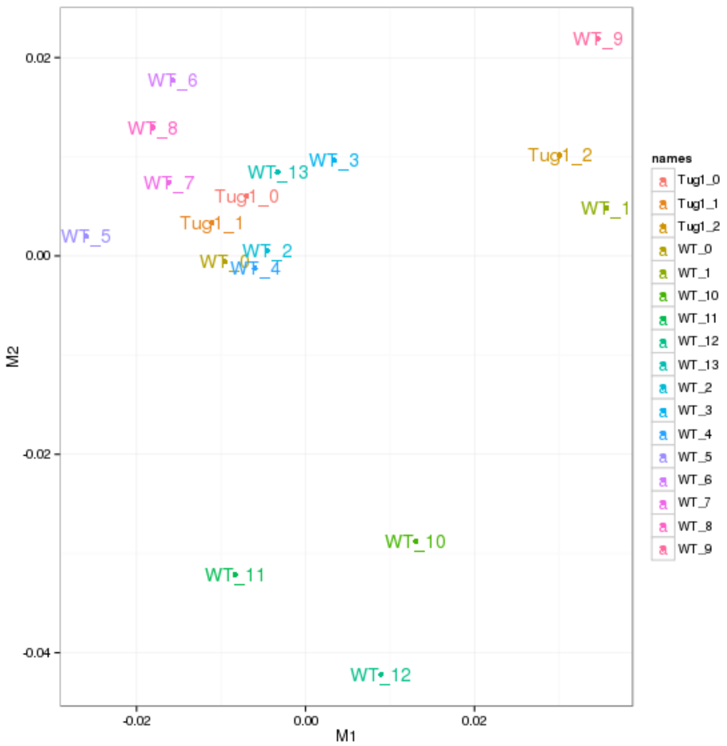


```
## NULL
```

PCA (genes)

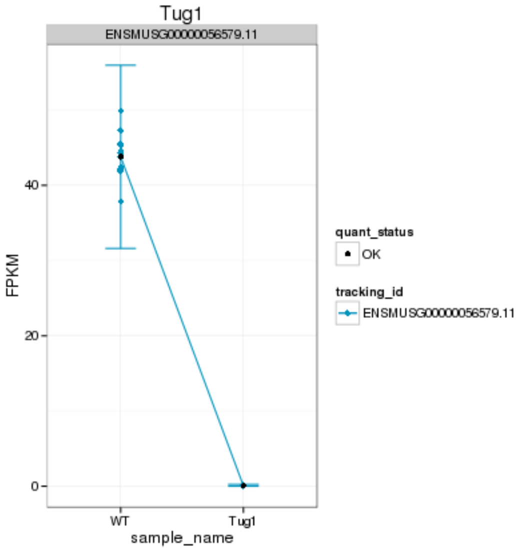

PC3
PC2
2
1
0
-1
-1
0
1
2
WT_9
Tug1_2
WT_1
WT_6
WT_3
WT_13
WT_8
Tug1_0
WT_2
Tug1_1
WT_7
WT_4
WT_0
WT_5
WT_10
WT_12
WT_11
varnames
Tug1_0
Tug1_1
Tug1_2
WT_0
WT_1
WT_10
WT_11
WT_12
WT_13
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9

MDS (genes)

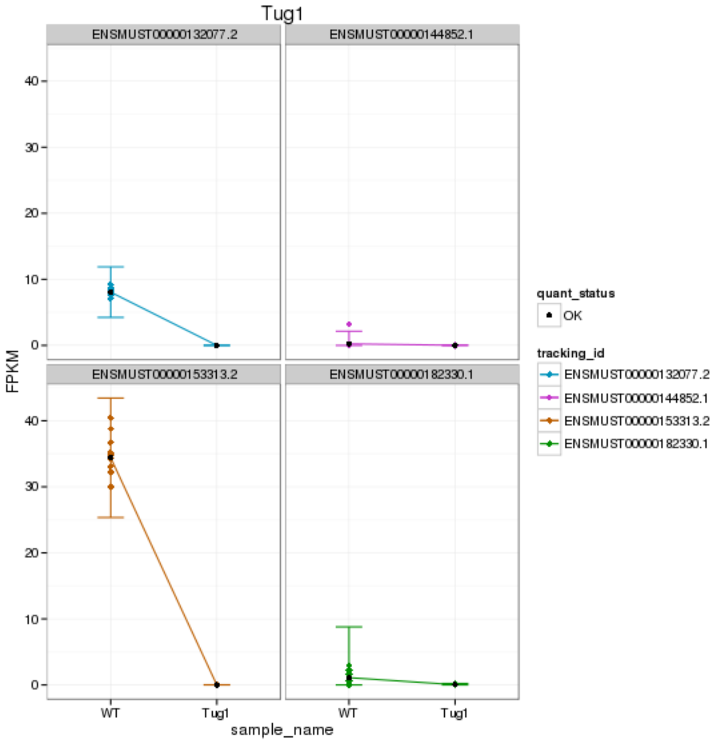


KO assessment

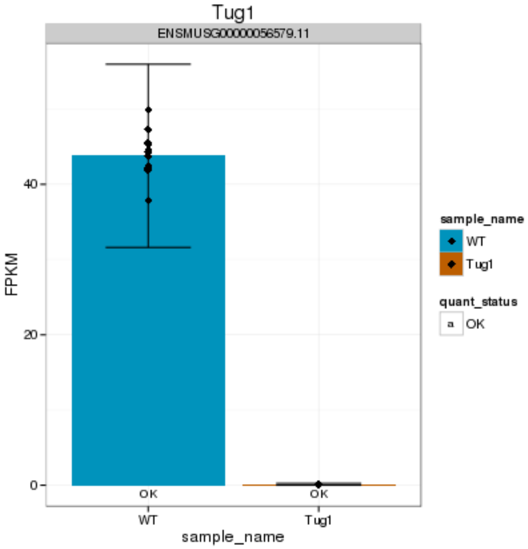
Endogenous lncRNA expression



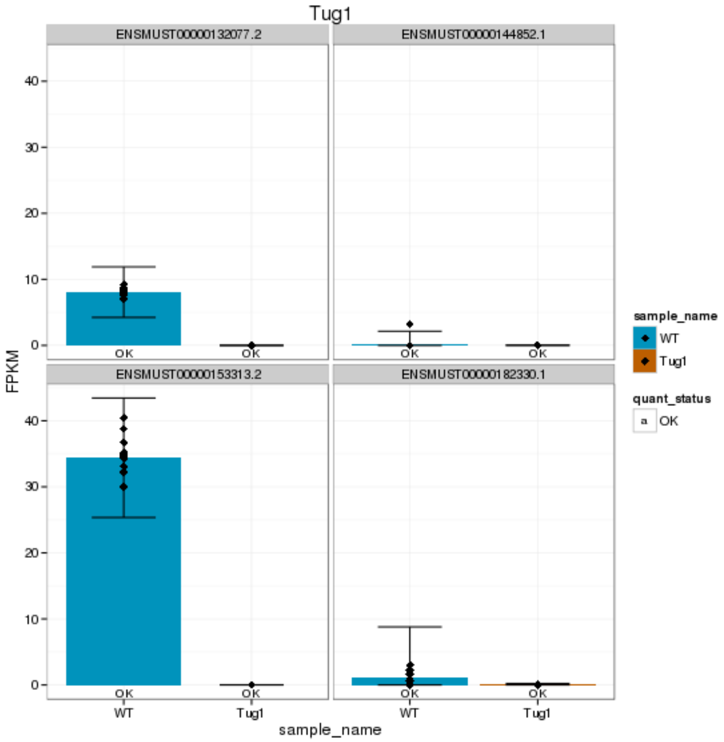
Endogenous expression of Tug1 isoforms:



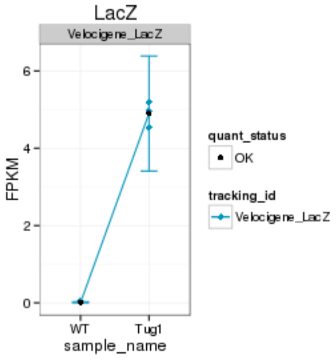
Barplot of gene expression:

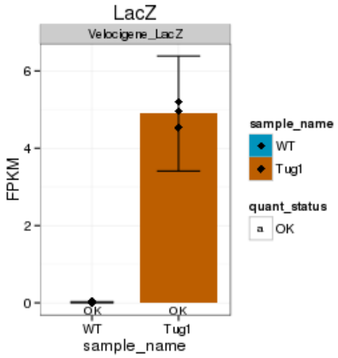


Barplot of isoform expression:



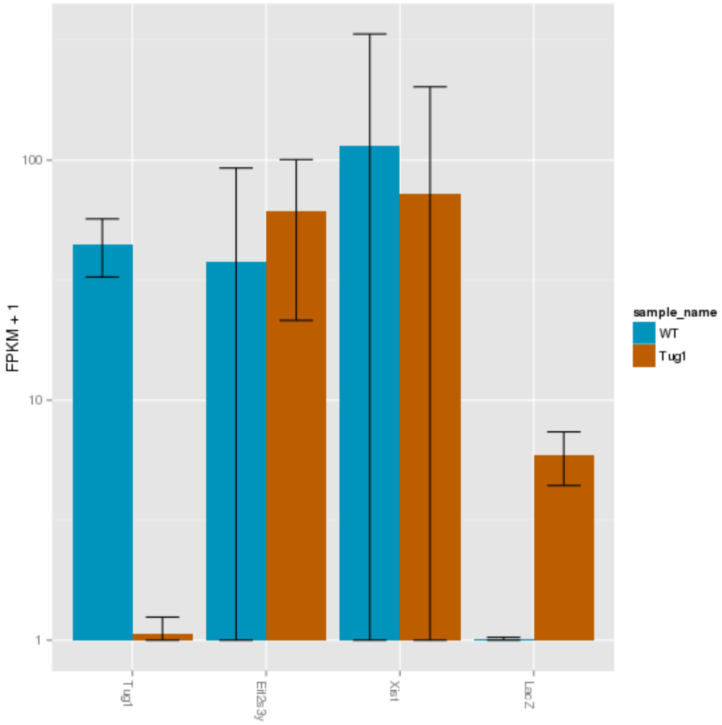
LacZ expression



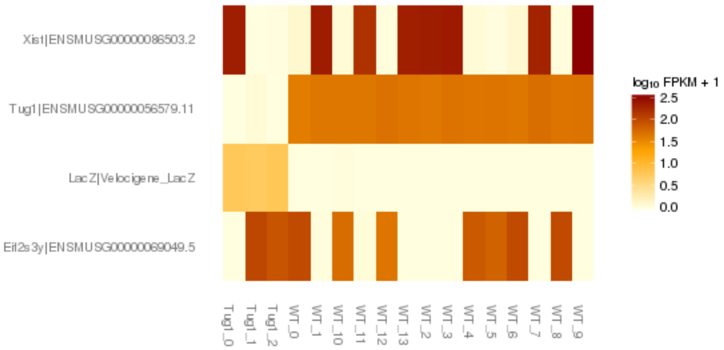


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

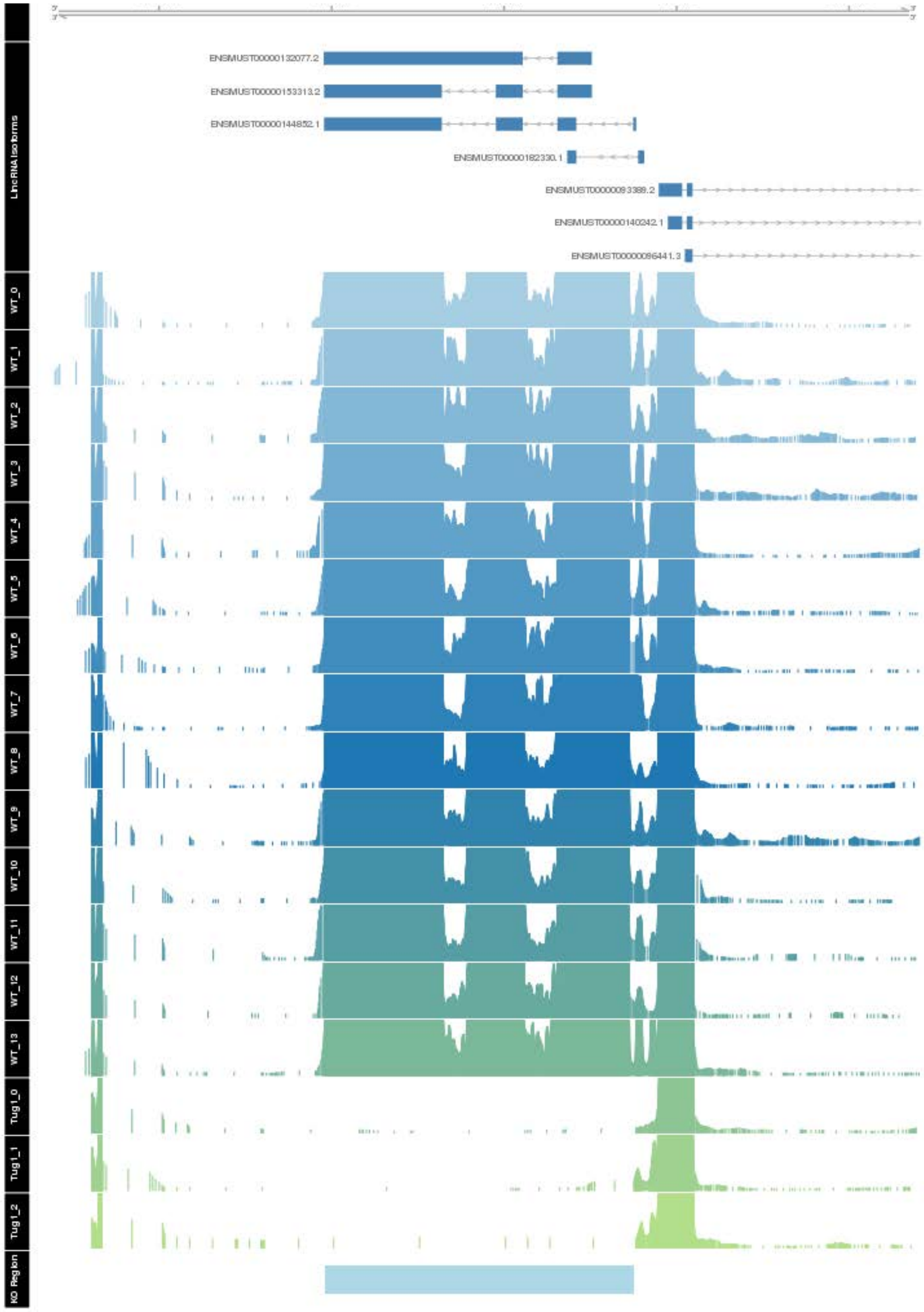
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization


LincRNA Isoforms
ENSMUST00000132077.2
ENSMUST00000153313.2
ENSMUST00000144852.1
ENSMUST00000182330.1
ENSMUST00000093388.2
ENSMUST00000140242.1
ENSMUST00000096441.3
WT_0
WT_1
WT_2
WT_3
WT_4
WT_5
WT_6
WT_7
WT_8
WT_9
WT_10
WT_11
WT_12
WT_13
Tug1_0
Tug1_1
Tug1_2
KO Region

Differential Analysis

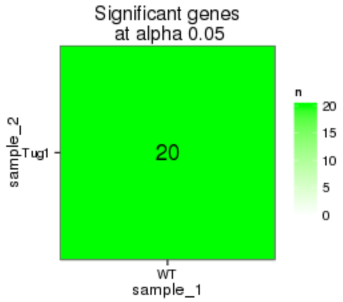
Differential Genes

There are 20 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Rec8
2	Rnf185
3	Rps14
4	Morc2a
5	Inpp5j
6	8430429K09Rik
7	Fmod
8	Map10
9	Hbb-bs
10	Tug1
11	Kdm5d
12	Cox5b
13	Rps4y2
14	Eno1
15	Lyz2
16	Slfn9
17	3222401L13Rik
18	Hbb-bt
19	Selm
20	Gm26809

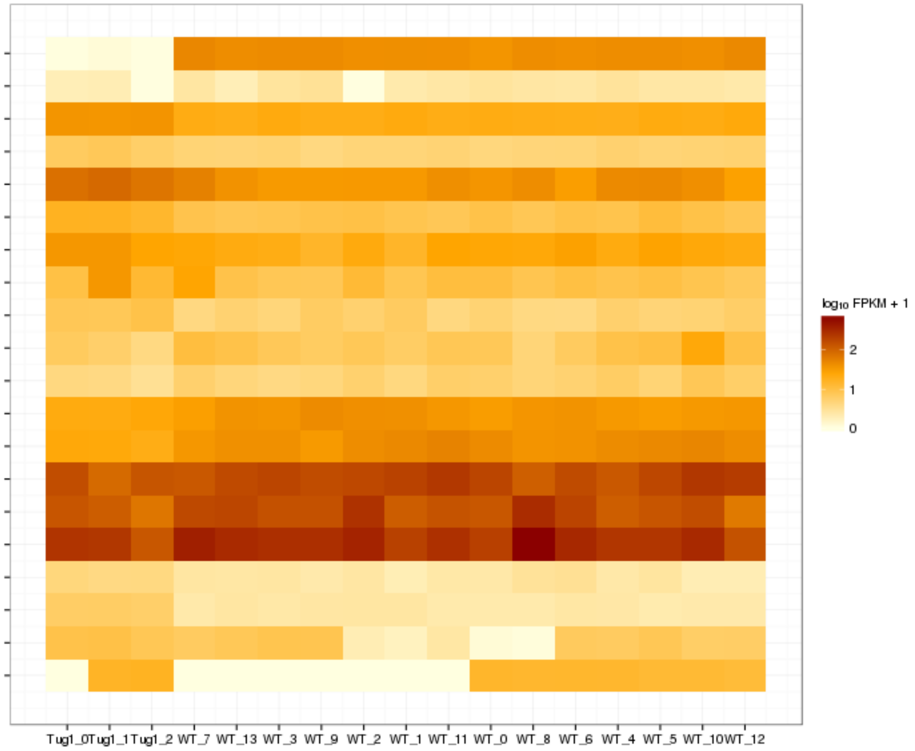
Matrix of gene significant differences between conditions

(skip for Brainmap wt-v-ko comparisons)



Significant gene expression differences between conditions

Expression plot (genes):(turned off)

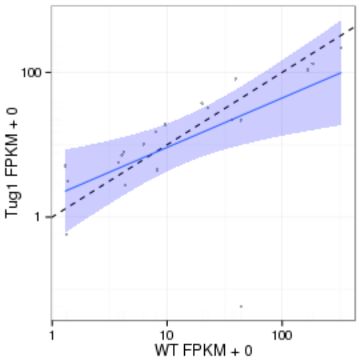


Significant genes with expression >50fpkm (any condition):(turned off)

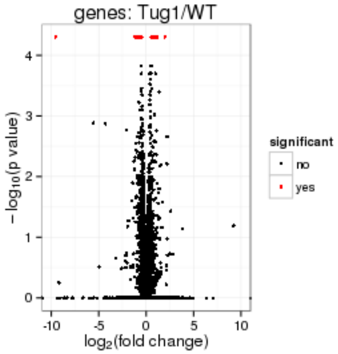
An individual look at each of the highly expressed significantly differentially regulated genes: (eval=false for first pass)

Expression-level/significance relationship

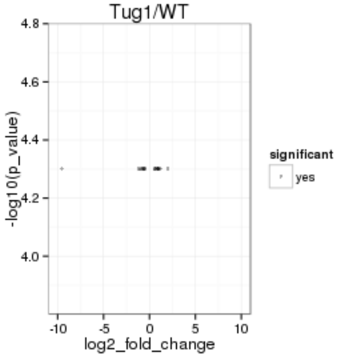
Scatter plot of significant genes only:



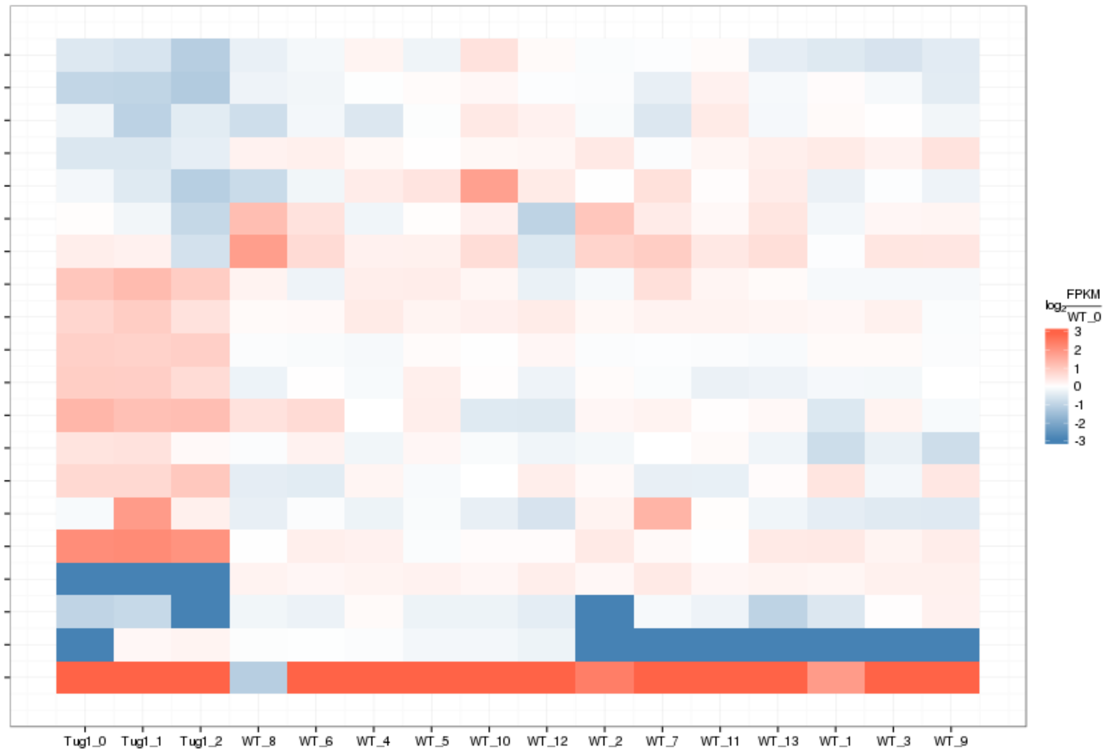
Volcano Plot



Volcano plot with significant genes only:



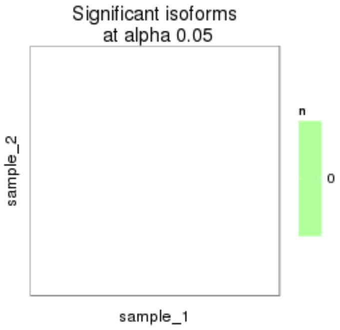
FoldChange Heatmap



Differential Splicing

Differential Isoforms between conditions

Per isoform difference between conditions:



These isoforms are:

[1] “no sig isoforms”

Gene-level DE isoform heatmap

```
## [1] "no sig isoforms"
```

Isoform foldchange heatmap by isoform:

```
## [1] "no sig isoforms"
```

Differential Splicing between conditions

(eval false for first pass)

Per condition differences in isoforms (Does gene have diff piechart between conditions?)

These genes are:

Splicing heatmap by isoform:

Splicing heatmap by gene

The following are significantly differentially spliced genes (relative portion of isoform per condition):

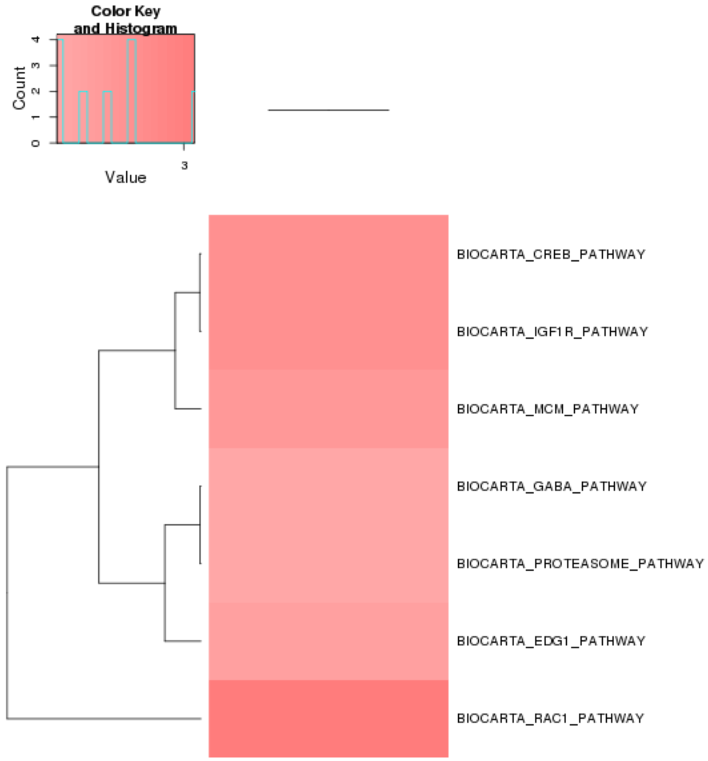
Gene/Pathway Analysis

GSEA

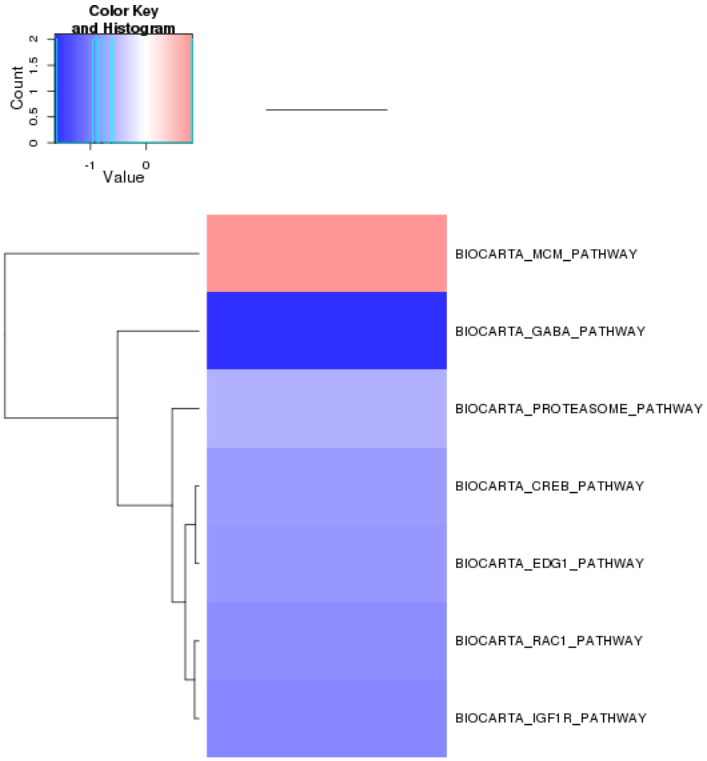
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

KO/WT Blue = down in KO Red = Up in KO

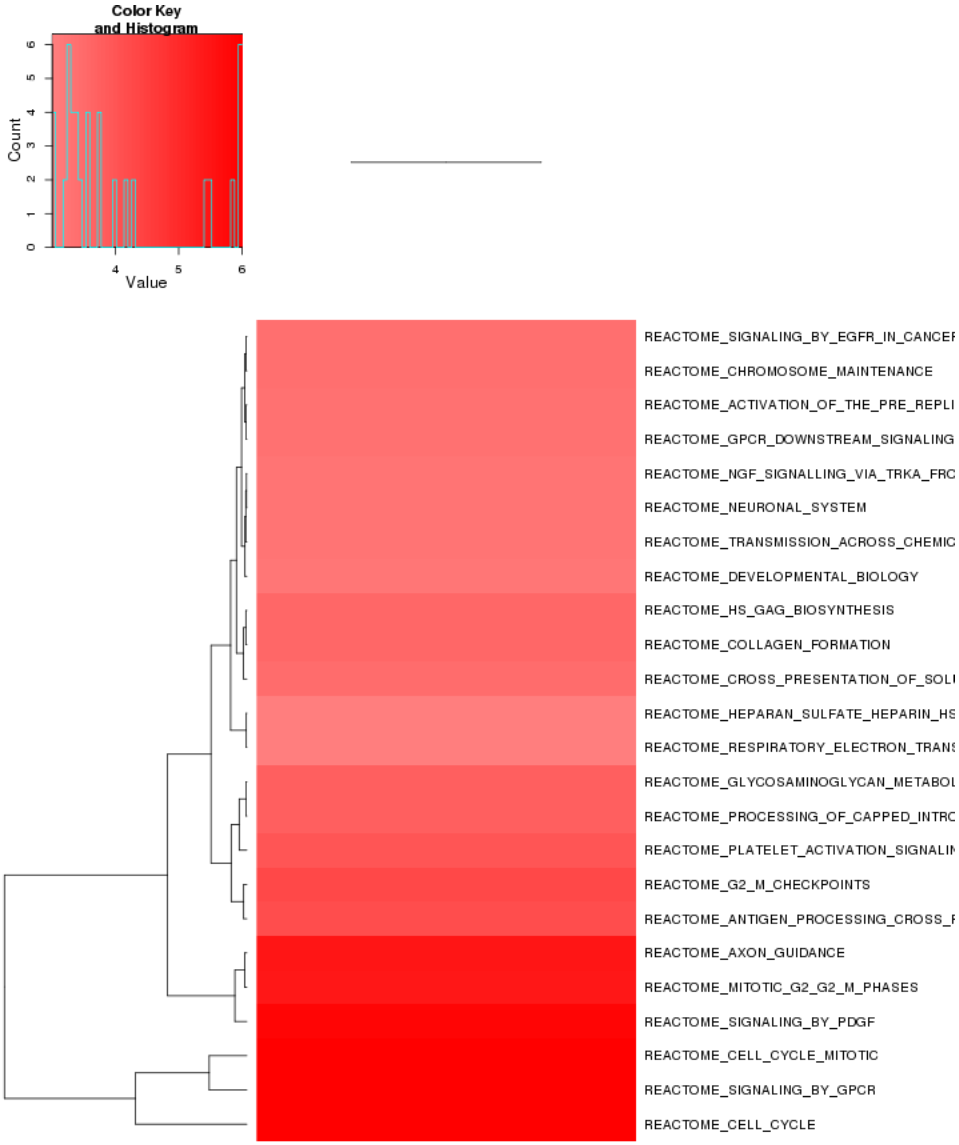
Biocarta enrichment:



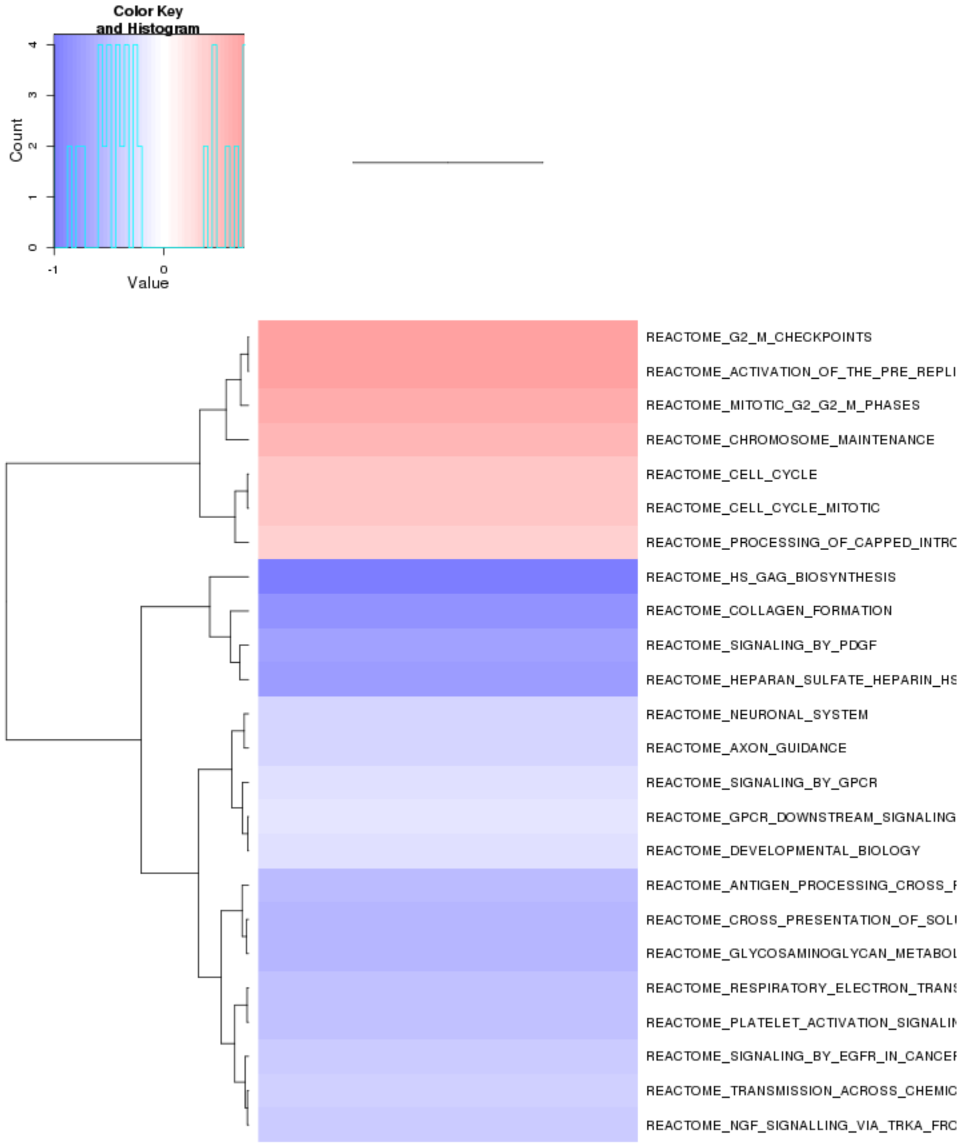
Biocarta zscore:



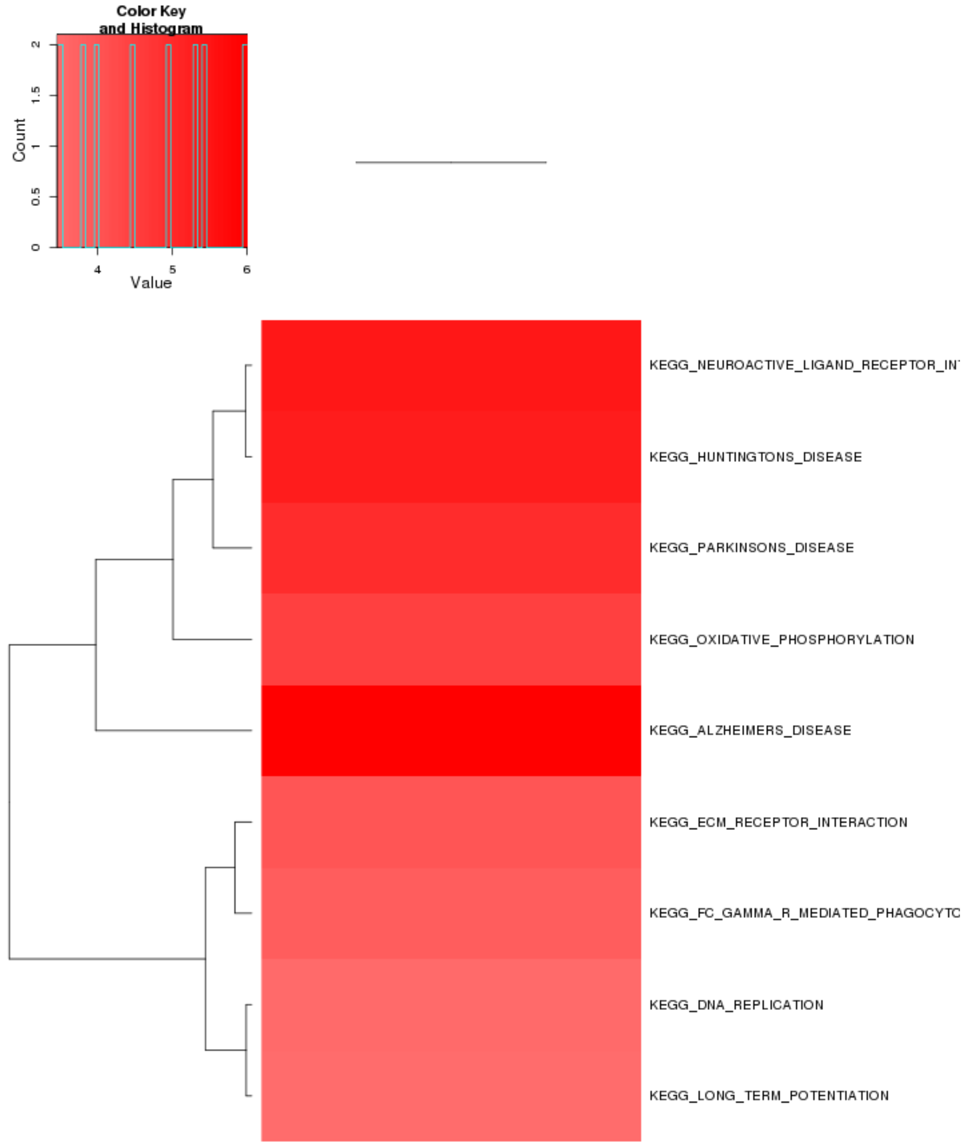
Reactome enrichment:



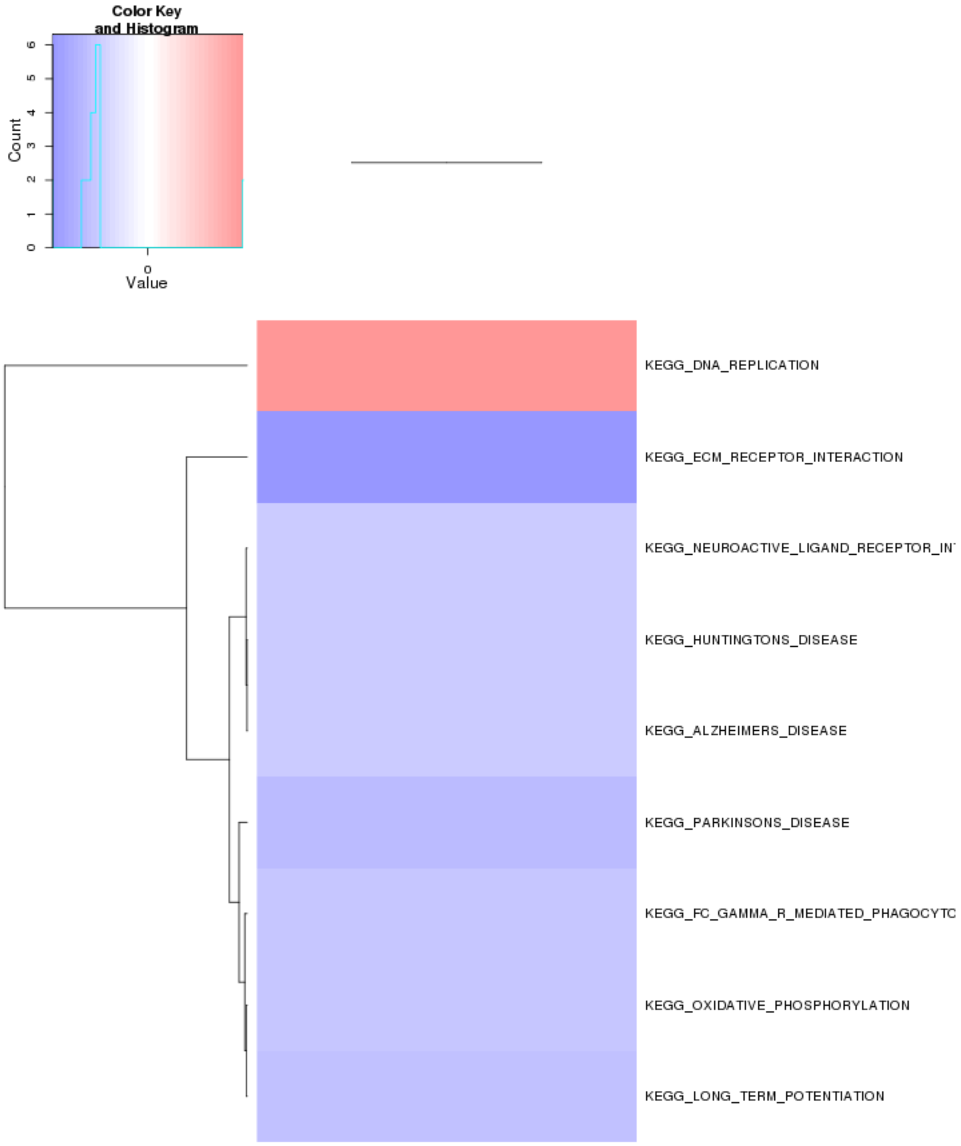
Reactome zscore:



Kegg enrichment:


Color Key
and Histogram
Count
0
0.5
1
1.5
2
4
5
6
Value
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_IN
KEGG_HUNTINGTONS_DISEASE
KEGG_PARKINSONS_DISEASE
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_ALZHEIMERS_DISEASE
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTO
KEGG_DNA_REPLICATION
KEGG_LONG_TERM_POTENTIATION

Kegg zscore:



Interneuron enrichment:

```
## Error: argument is of length zero
```

Interneuron zscore:

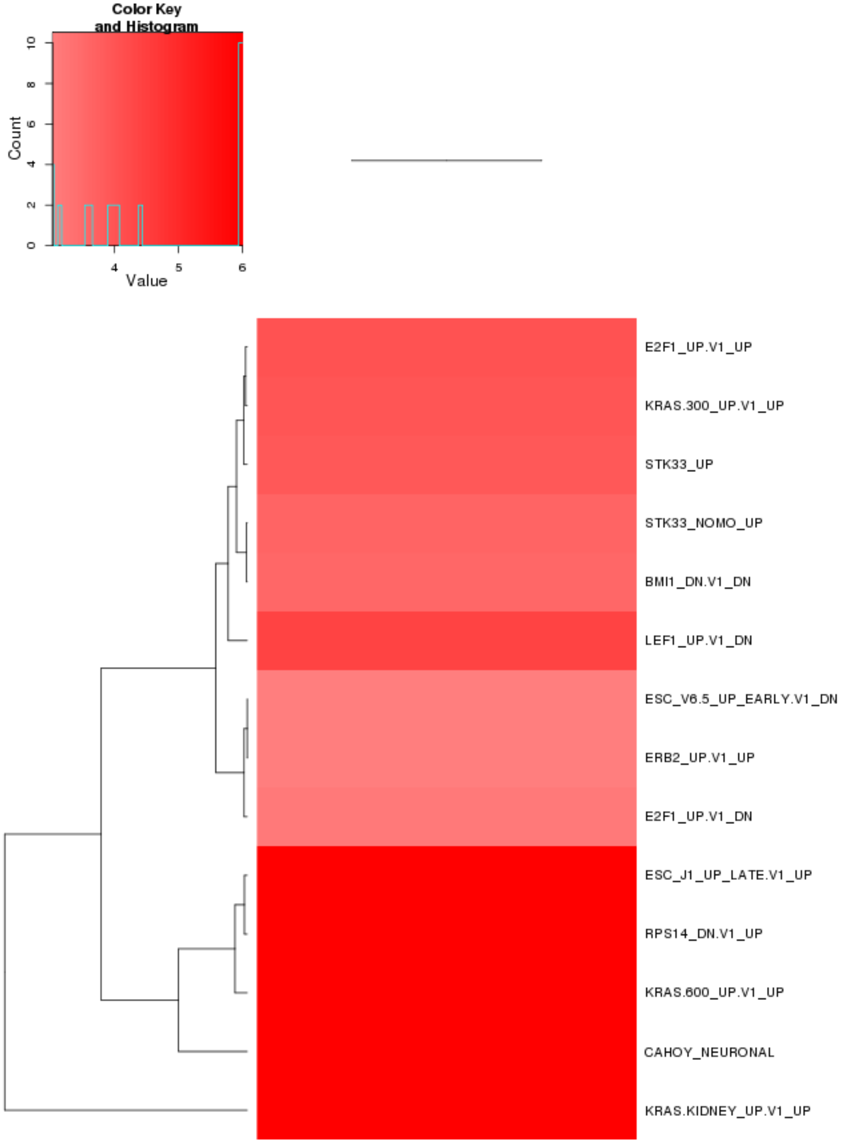
```
## Error: incorrect number of dimensions
```

```
## Error: object 'x_ordered' not found
```

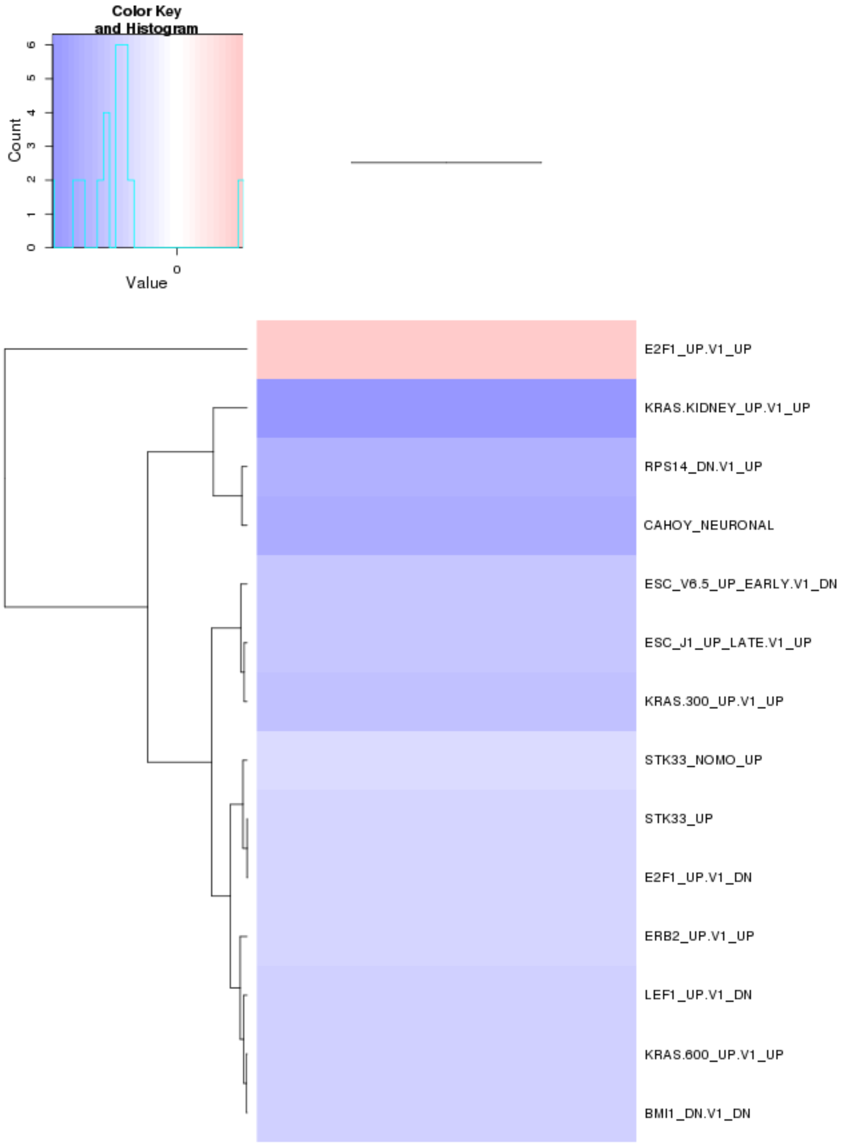
```
## Error: error in evaluating the argument 'x' in selecting a method for function 'as.matrix': Error: object 'x_ordered' not found
```

```
## Error: object 'x_ordered' not found
```

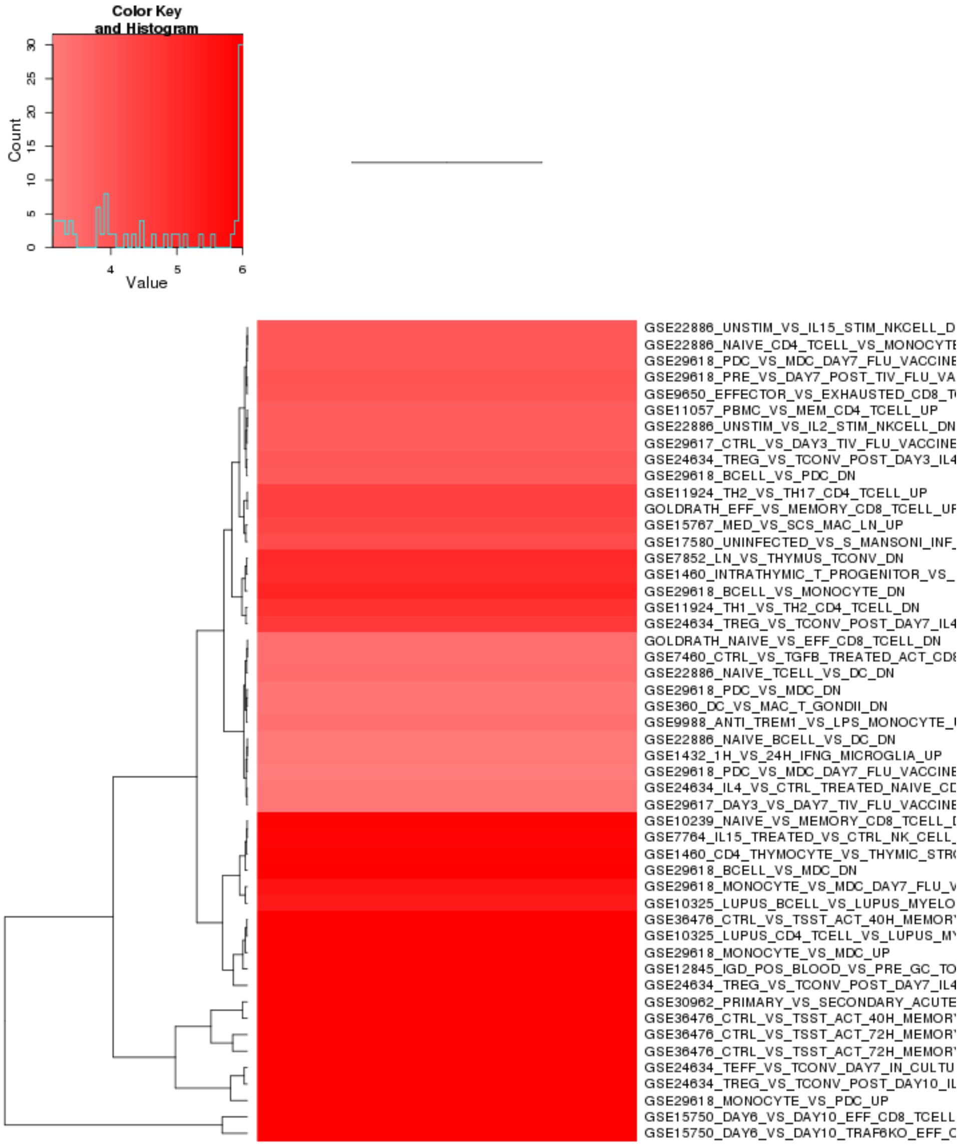
Oncogene enrichment:



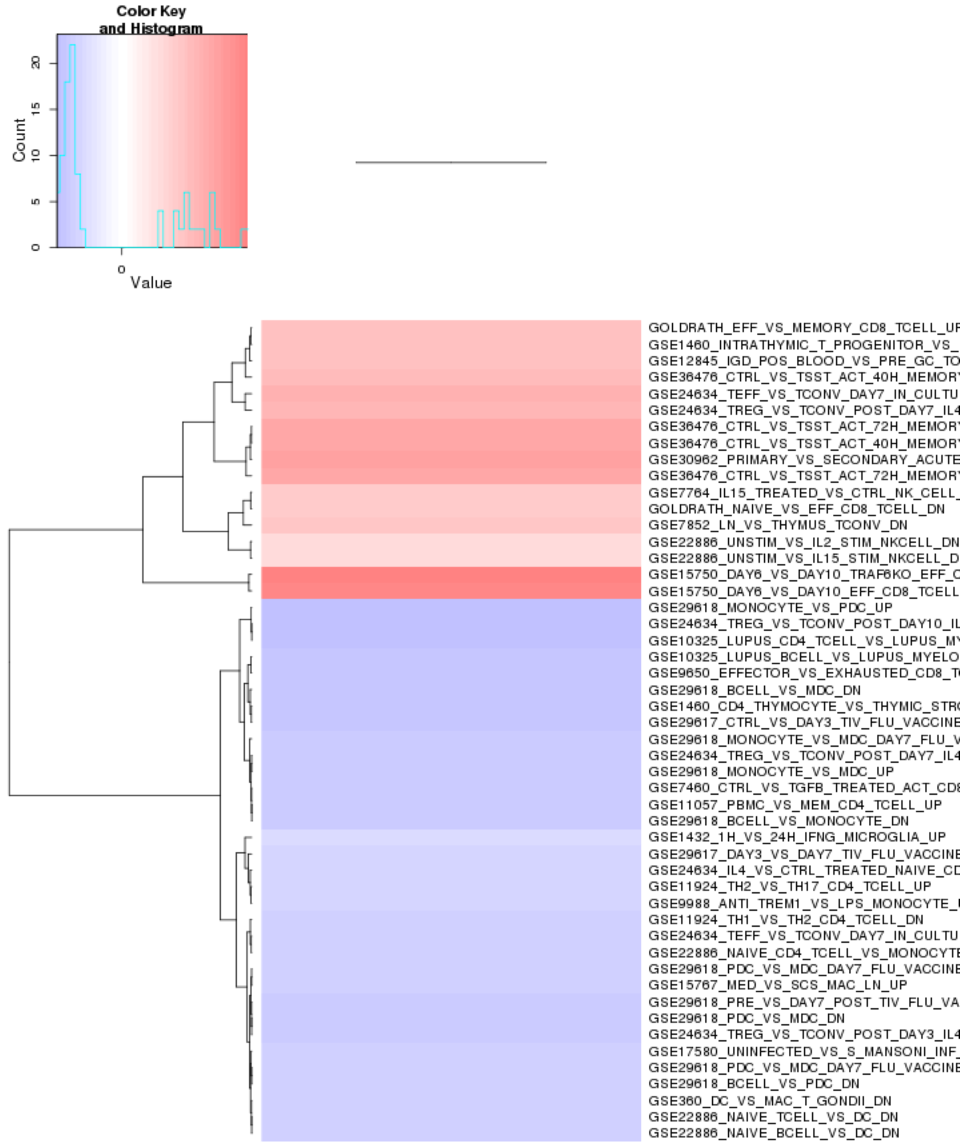
Oncogene zscore:



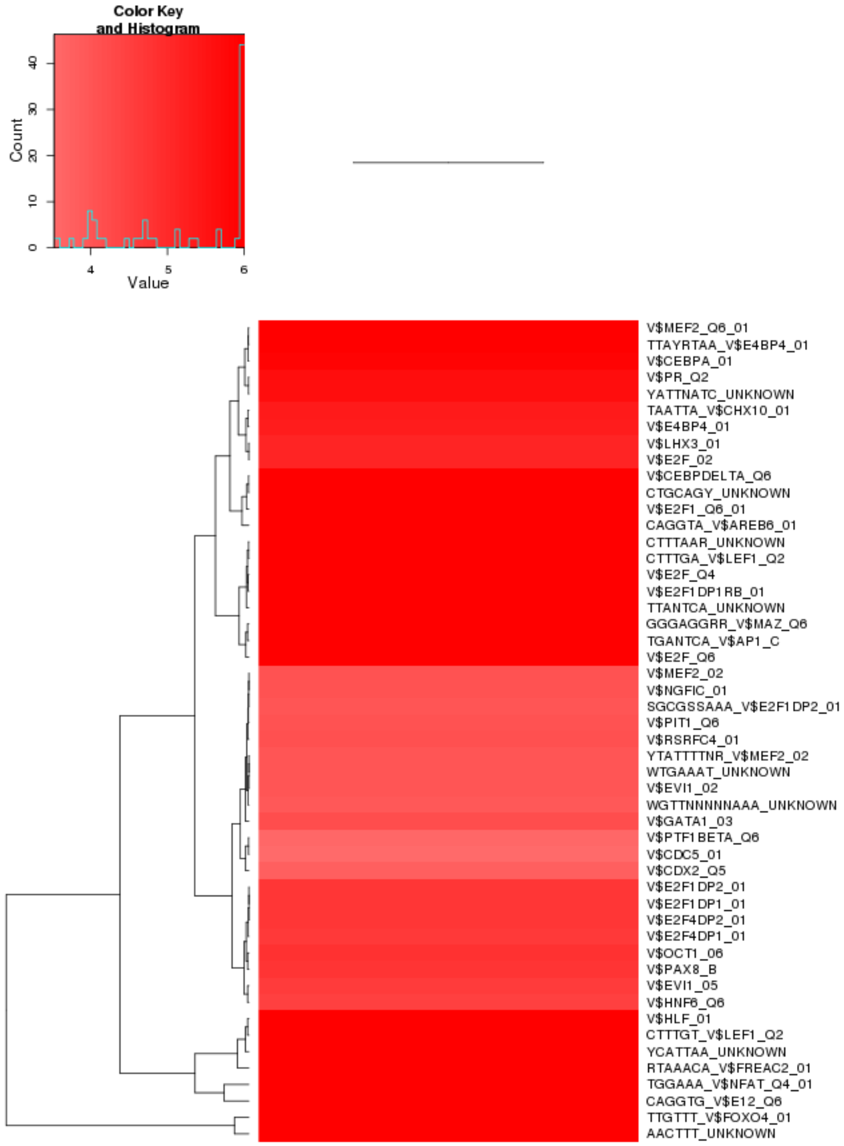
Immuno enrichment:



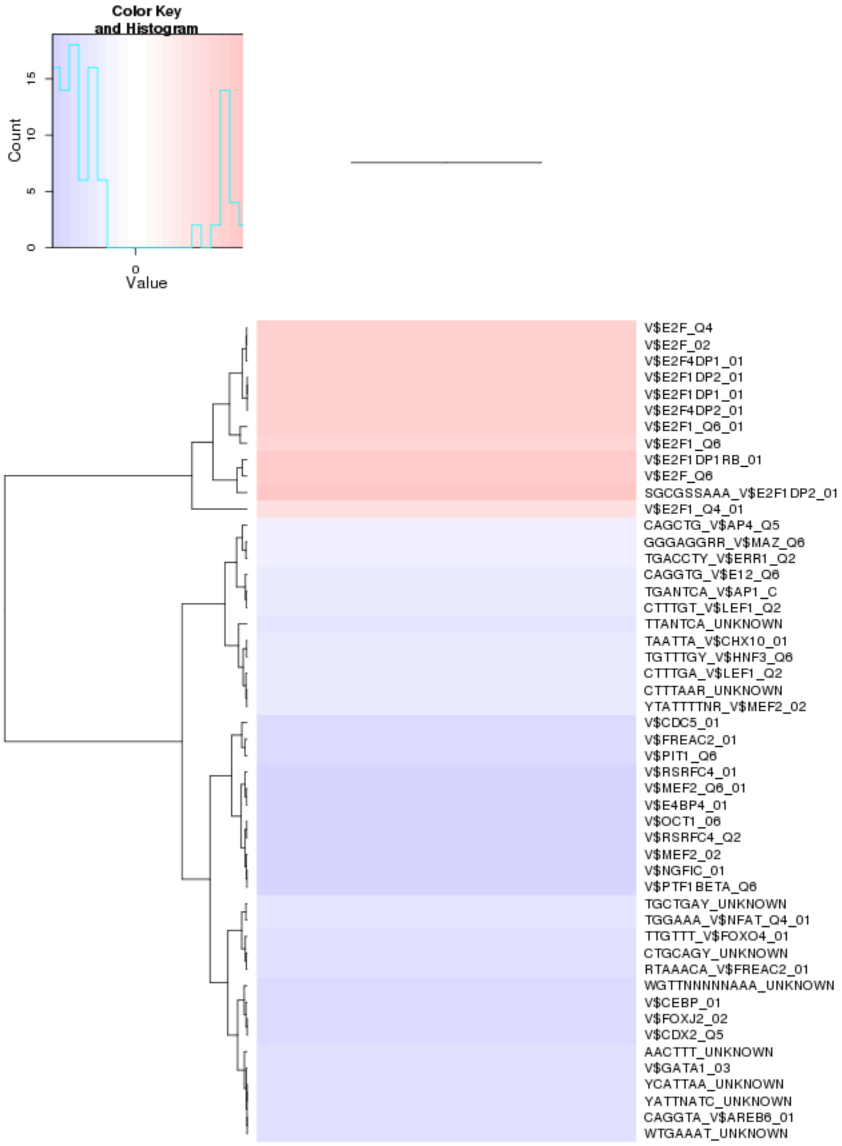
Immuno zscore:



TF enrichment:


Color Key
and Histogram
Count
0
10
20
30
40
4
5
6
Value
V$MEF2_Q6_01
TTAYRTAA_V$E4BP4_01
V$CEBPA_01
V$PR_Q2
YATTNATC_UNKNOWN
TAATTA_V$CHX10_01
V$E4BP4_01
V$LHX3_01
V$E2F_02
V$CEBPDELTA_Q6
CTGCAGY_UNKNOWN
V$E2F1_Q6_01
CAGGTA_V$AREB6_01
CTTTAAR_UNKNOWN
CTTTGA_V$LEF1_Q2
V$E2F_Q4
V$E2F1DP1RB_01
TTANTCA_UNKNOWN
GGGAGGRR_V$MAZ_Q6
TGANTCA_V$AP1_C
V$E2F_Q6
V$MEF2_02
V$NGFIC_01
SGCGSSAAA_V$E2F1DP2_01
V$PIT1_Q6
V$RSRFC4_01
YTATTTTNR_V$MEF2_02
WTGAAAT_UNKNOWN
V$EVI1_02
WGTTNNNNNAAA_UNKNOWN
V$GATA1_03
V$PTF1BETA_Q6
V$CDC5_01
V$CDX2_Q5
V$E2F1DP2_01
V$E2F1DP1_01
V$E2F4DP2_01
V$E2F4DP1_01
V$OCT1_06
V$PAX8_B
V$EVI1_05
V$HNF6_Q6
V$HLF_01
CTTTGT_V$LEF1_Q2
YCATTAA_UNKNOWN
RTAAACA_V$FREAC2_01
TGGAAA_V$NFAT_Q4_01
CAGGTG_V$E12_Q6
TTGTTT_V$FOXO4_01
AACTTT_UNKNOWN

TF zscore:



GO enrichment

Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.

```
## Error: 'x' and 'units' must have length > 0
```

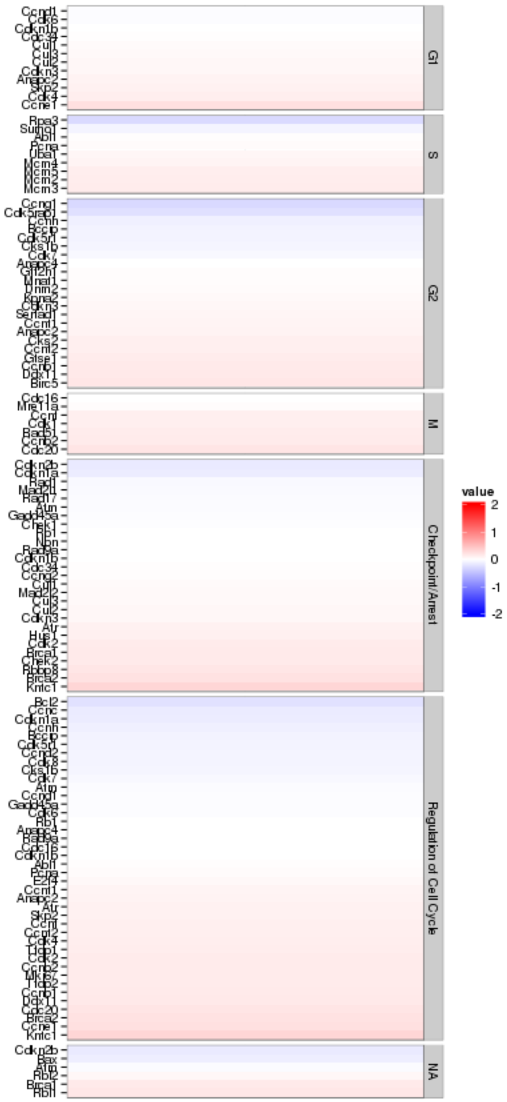
```
## Error: 'x' and 'units' must have length > 0
```

```
## Error: 'x' and 'units' must have length > 0
```

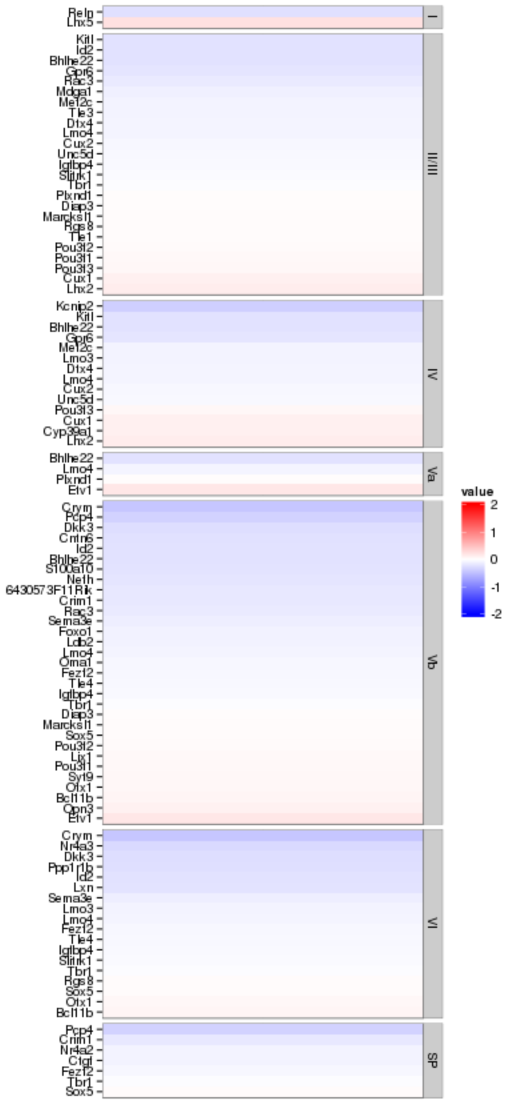
```
## Error: need finite 'xlim' values
```

```
## Error: need finite 'xlim' values
```

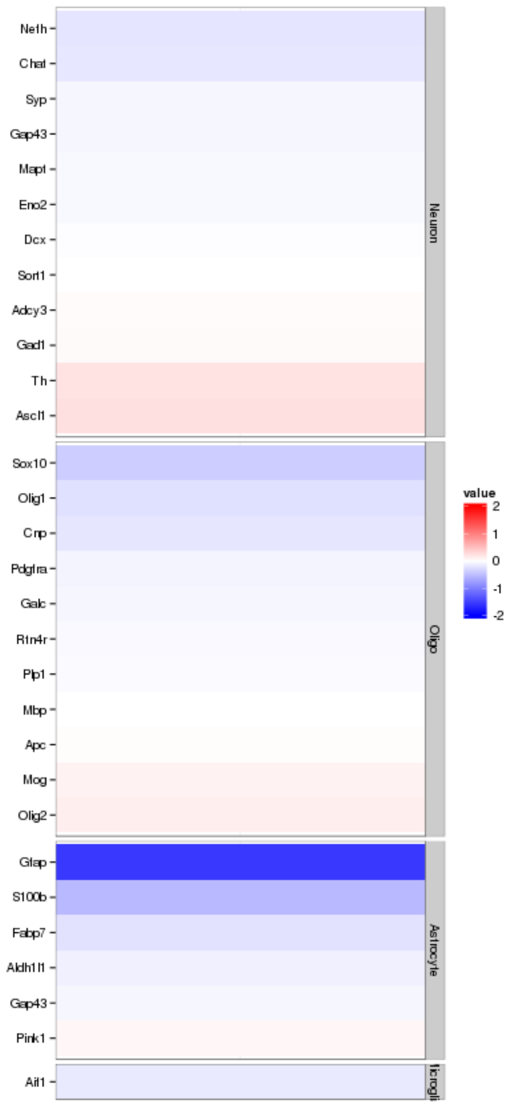
Enrichment or depletion for stage-specific cell cycle markers



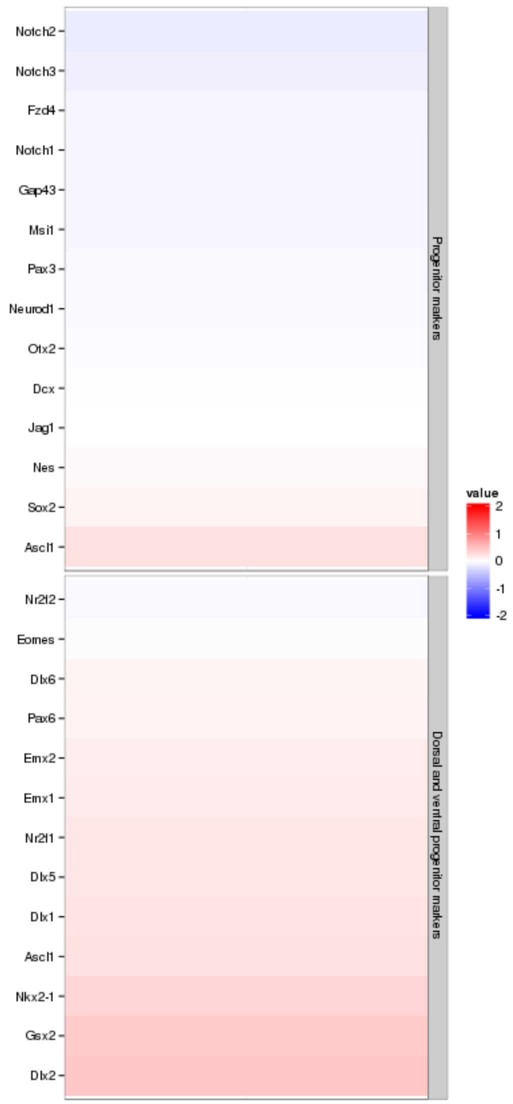
Enrichment or depletion for markers of specific cortical layers



Enrichment or depletion for specific neural cell types



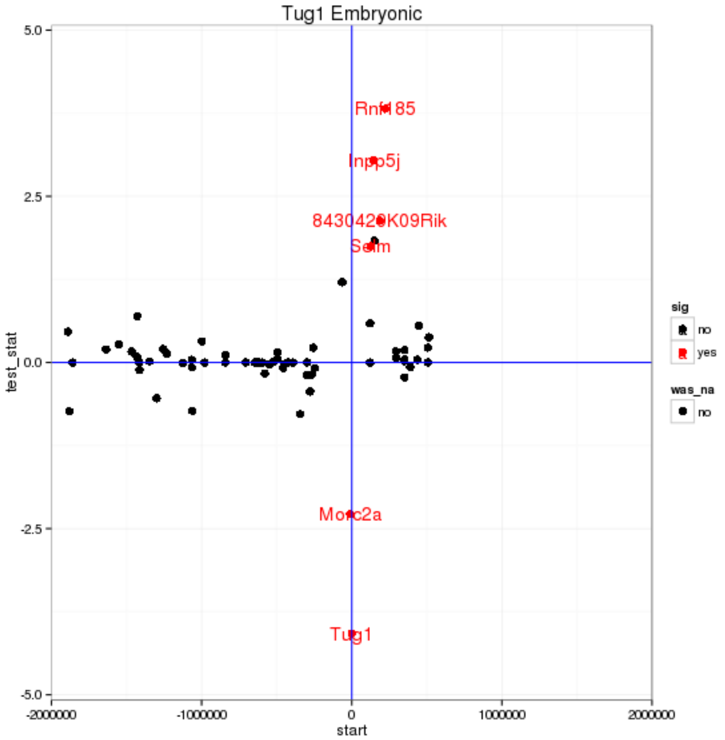
Enrichment or Depletion of neural differentiation markers



Cis vs Trans (locally)

log2 Foldchange and test statistic are calculated with the ratio of fpkm(KO)/fpkm(WT), thus the test_stat is positive if a gene is higher in the KO and negative if a gene has lower expression in the KO

The pvalue for 5 genes significantly regulated in a region this size is: 0.0023



Notes

Samples used are:

	10
1	JR753
2	JR750
3	JR771
4	JR755
5	JR811
6	JR768
7	JR761
8	JR815
9	JR789
10	JR748
11	JR716
12	JR717
13	JR719
14	JR756

15 JR757

16 JR857

17 JR861

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_scale	external_scale
1	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR753/abundances.cxb	WT	0	WT_0	39331900.00	33091500.00	1.23	1.00
2	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR750/abundances.cxb	WT	1	WT_1	36031100.00	33091500.00	1.07	1.00
3	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR771/abundances.cxb	WT	2	WT_2	38857100.00	33091500.00	1.20	1.00
4	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR755/abundances.cxb	WT	3	WT_3	41811300.00	33091500.00	1.25	1.00
5	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR811/abundances.cxb	WT	4	WT_4	38172800.00	33091500.00	1.17	1.00
6	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR768/abundances.cxb	WT	5	WT_5	28375200.00	33091500.00	0.87	1.00
7	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR761/abundances.cxb	WT	6	WT_6	31706200.00	33091500.00	0.95	1.00
8	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR815/abundances.cxb	WT	7	WT_7	29733100.00	33091500.00	0.90	1.00
9	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR789/abundances.cxb	WT	8	WT_8	27681500.00	33091500.00	0.84	1.00
10	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR748/abundances.cxb	WT	9	WT_9	32367000.00	33091500.00	0.94	1.00
11	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR716/abundances.cxb	WT	10	WT_10	26144700.00	33091500.00	0.79	1.00
12	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR717/abundances.cxb	WT	11	WT_11	25565400.00	33091500.00	0.78	1.00
13	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR719/abundances.cxb	WT	12	WT_12	22697800.00	33091500.00	0.67	1.00
14	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR756/abundances.cxb	WT	13	WT_13	38948900.00	33091500.00	1.18	1.00
15	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR757/abundances.cxb	Tug1	0	Tug1_0	33398300.00	33091500.00	1.02	1.00
16	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR857/abundances.cxb	Tug1	1	Tug1_1	39157600.00	33091500.00	1.22	1.00
17	/n/rinn_data1/seq/lgoff/Projects/BrainMap/data/quants/JR861/abundances.cxb	Tug1	2	Tug1_2	43124000.00	33091500.00	1.27	1.00

Session Info

```
## R version 3.0.2 (2013-09-25)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  methods   stats     graphics  grDevices utils
## [8] datasets  base
##
## other attached packages:
##  [1] plyr_1.8.1
##  [2] stringr_0.6.2
##  [3] seqbias_1.10.0
```

```
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.3.19
##  [5] BSgenome_1.30.0
##  [6] Biostrings_2.30.1
##  [7] gdata_2.13.3
##  [8] GO.db_2.10.1
##  [9] org.Mm.eg.db_2.10.1
## [10] clusterProfiler_1.13.1
## [11] DOSE_2.0.0
## [12] ReactomePA_1.6.1
## [13] AnnotationDbi_1.24.0
## [14] Biobase_2.22.0
## [15] mgcv_1.7-29
## [16] nlme_3.1-117
## [17] RMySQL_0.9-3
## [18] RColorBrewer_1.0-5
## [19] gridExtra_0.9.1
## [20] gtable_0.1.2
## [21] marray_1.40.0
## [22] gplots_2.13.0
## [23] GSA_1.03
## [24] limma_3.18.13
## [25] xtable_1.7-3
## [26] cummeRbund_2.7.2
## [27] Gviz_1.6.0
## [28] rtracklayer_1.22.7
## [29] GenomicRanges_1.14.4
## [30] XVector_0.2.0
## [31] IRanges_1.20.7
## [32] fastcluster_1.1.13
## [33] reshape2_1.4
## [34] ggplot2_1.0.0
## [35] RSQLite_0.11.4
## [36] DBI_0.2-7
## [37] BiocGenerics_0.8.0
## [38] knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17           cluster_1.15.2         colorspace_1.2-4
##  [7] dichromat_2.0-0        digest_0.6.4           DO.db_2.7
## [10] evaluate_0.5.5         formatR_0.10           Formula_1.1-1
## [13] GenomicFeatures_1.14.5 GOSemSim_1.20.3        graph_1.40.1
## [16] graphite_1.8.1         gtools_3.4.1           Hmisc_3.14-4
## [19] igraph_0.7.1           KEGG.db_2.10.1         KernSmooth_2.23-12
## [22] labeling_0.2           lattice_0.20-29        latticeExtra_0.6-26
## [25] MASS_7.3-33            Matrix_1.1-3           munsell_0.4.2
## [28] org.Hs.eg.db_2.10.1    proto_0.3-10           qvalue_1.36.0
## [31] Rcpp_0.11.2            RCurl_1.95-4.1         reactome.db_1.46.1
## [34] Rsamtools_1.14.3       scales_0.2.4           splines_3.0.2
## [37] stats4_3.0.2           survival_2.37-7        tcltk_3.0.2
## [40] tools_3.0.2            XML_3.98-1.1           zlibbioc_1.8.0
```

Run Info

```
##           param
## 1      cmd_line
## 2       version
## 3  SVN_revision
## 4 boost_version
## 5        genome
##
## 1 cuffdiff -p 10 -L WT,Tug1 -o /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/diffs/Tug1_vs_WT_Embryonic /n/rinn_data1/seq/lgoff/Projects/BrainMap/data/
## 2
## 3
## 4
## 5
```