Trp53cor1 KO vs WT (Heart)

This file shows the wt-v-ko comparison for Trp53cor1.

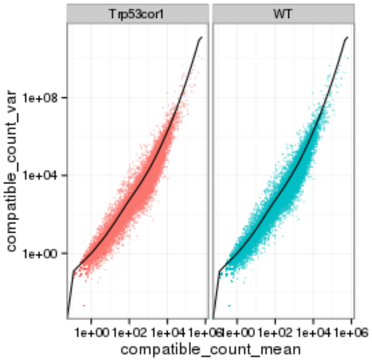
Cuff overview:

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

QC

Dispersion

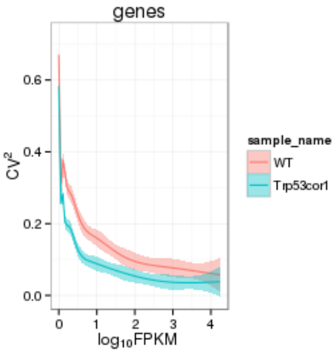
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



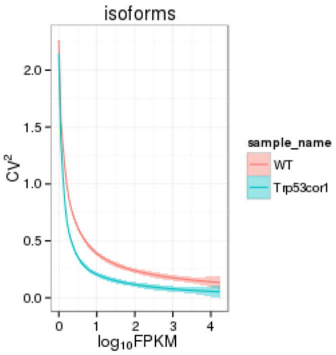
Cross-replicate variability (fpkmSCVplot)

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

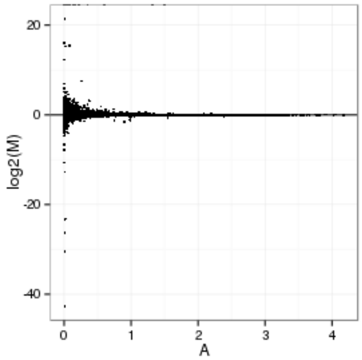
Genes:



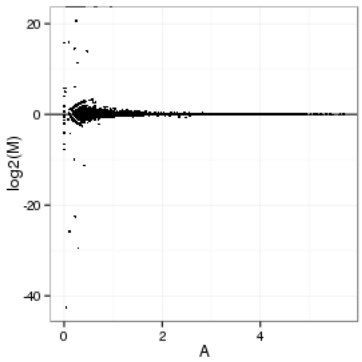
Isoforms:



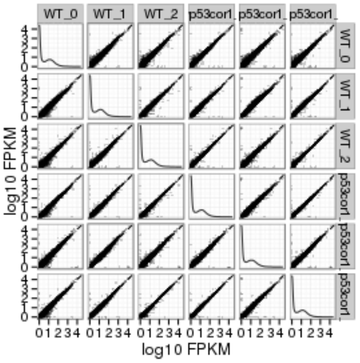
MvA plot



MvA plot counts



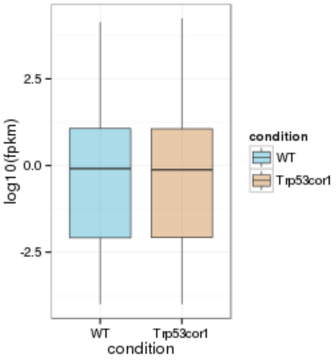
Scatterplot matrix



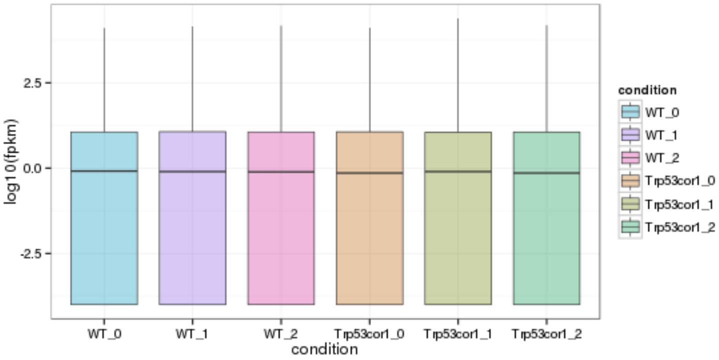
Distributions

Boxplots

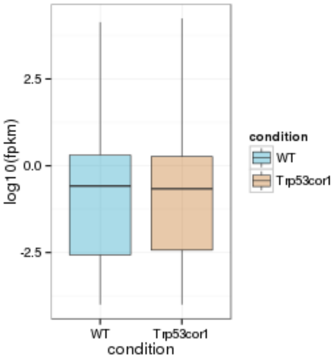
Boxplot (genes)



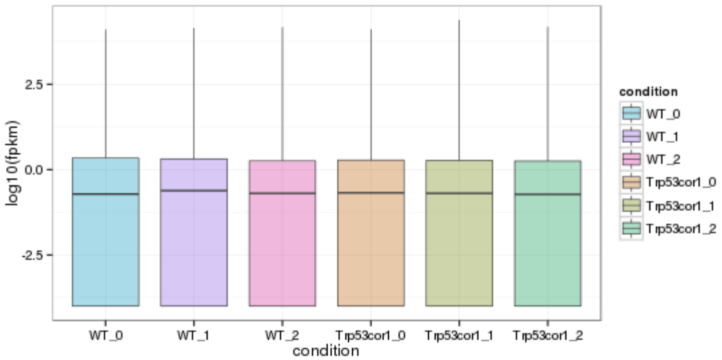
Boxplot (genes, replicates)



Boxplot (isoforms)

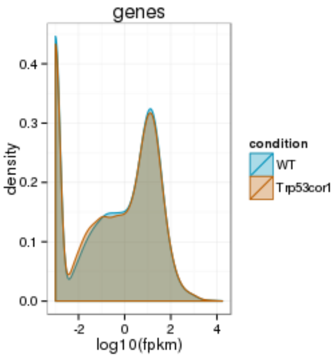


Boxplot (isoforms, replicates)

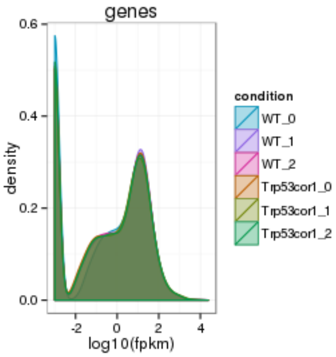


Density

Density (genes)

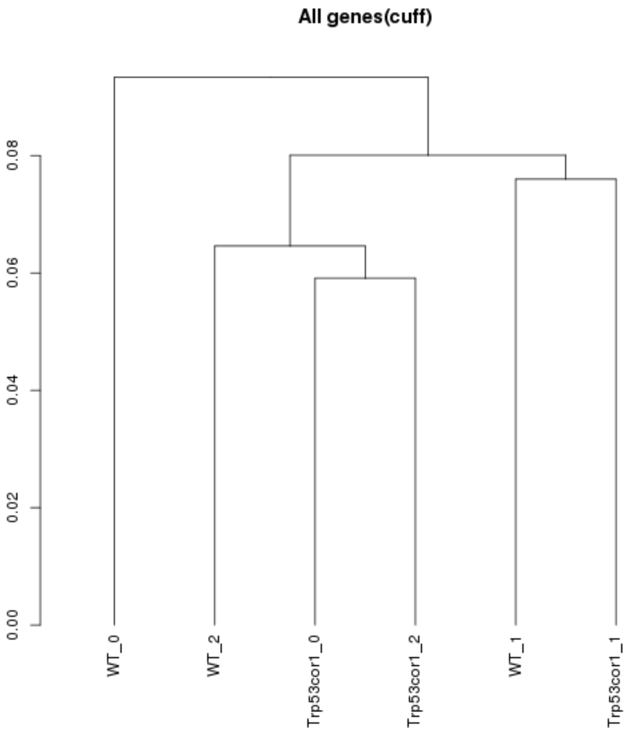


Density (genes, replicates)



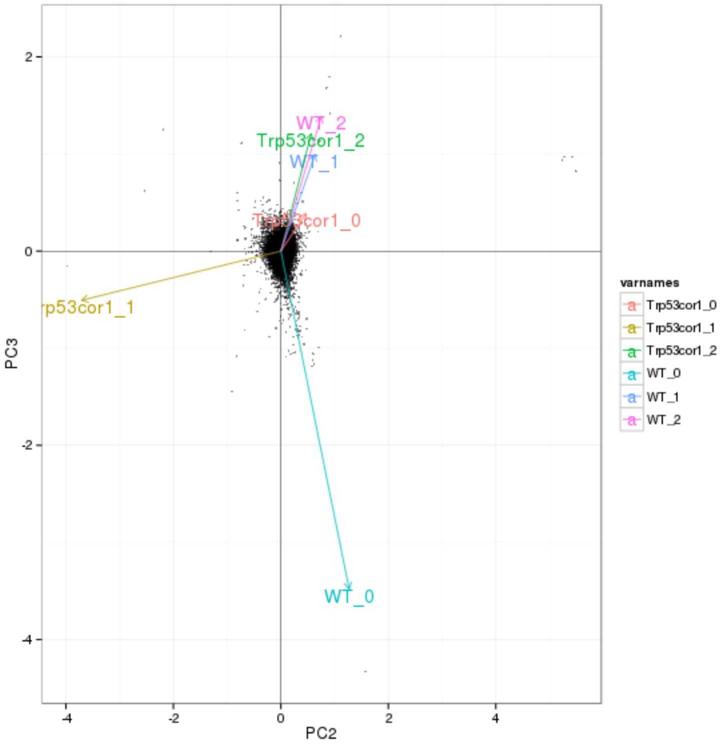
Clustering

Replicate Clusters

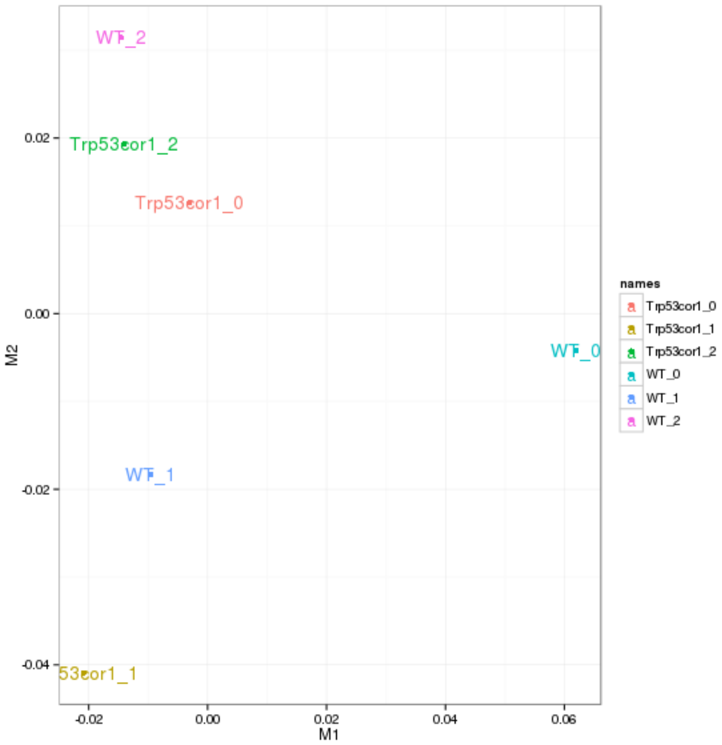


```
## NULL
```

PCA (genes)

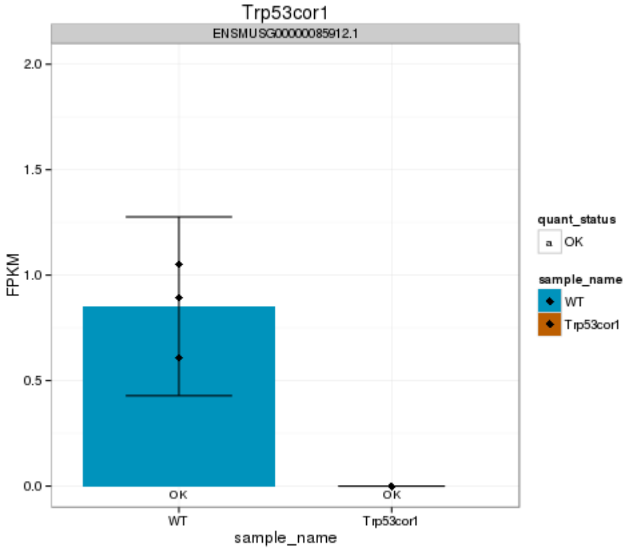


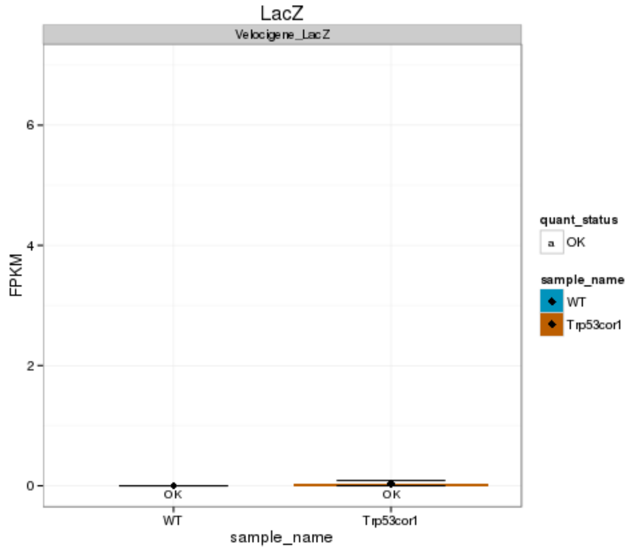
MDS (genes)



KO assessment

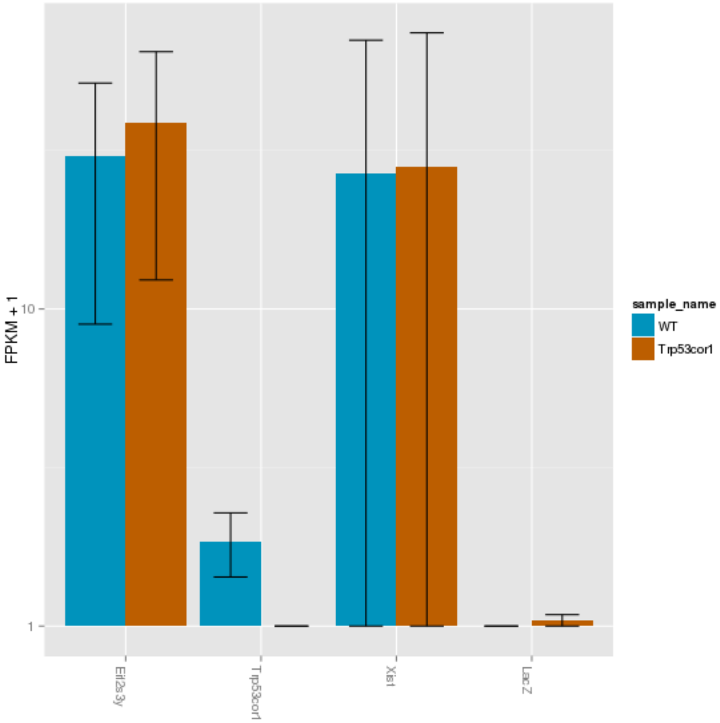
Endogenous lncRNA expression



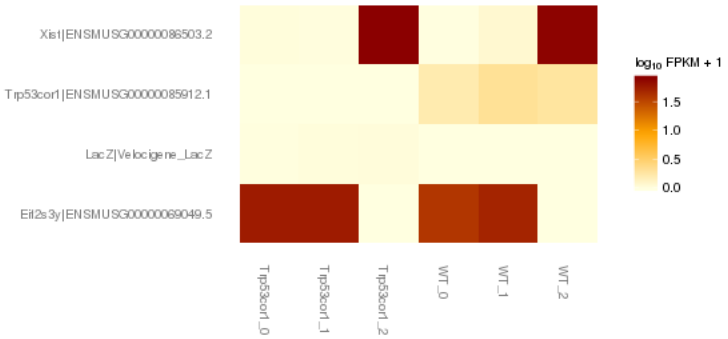


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

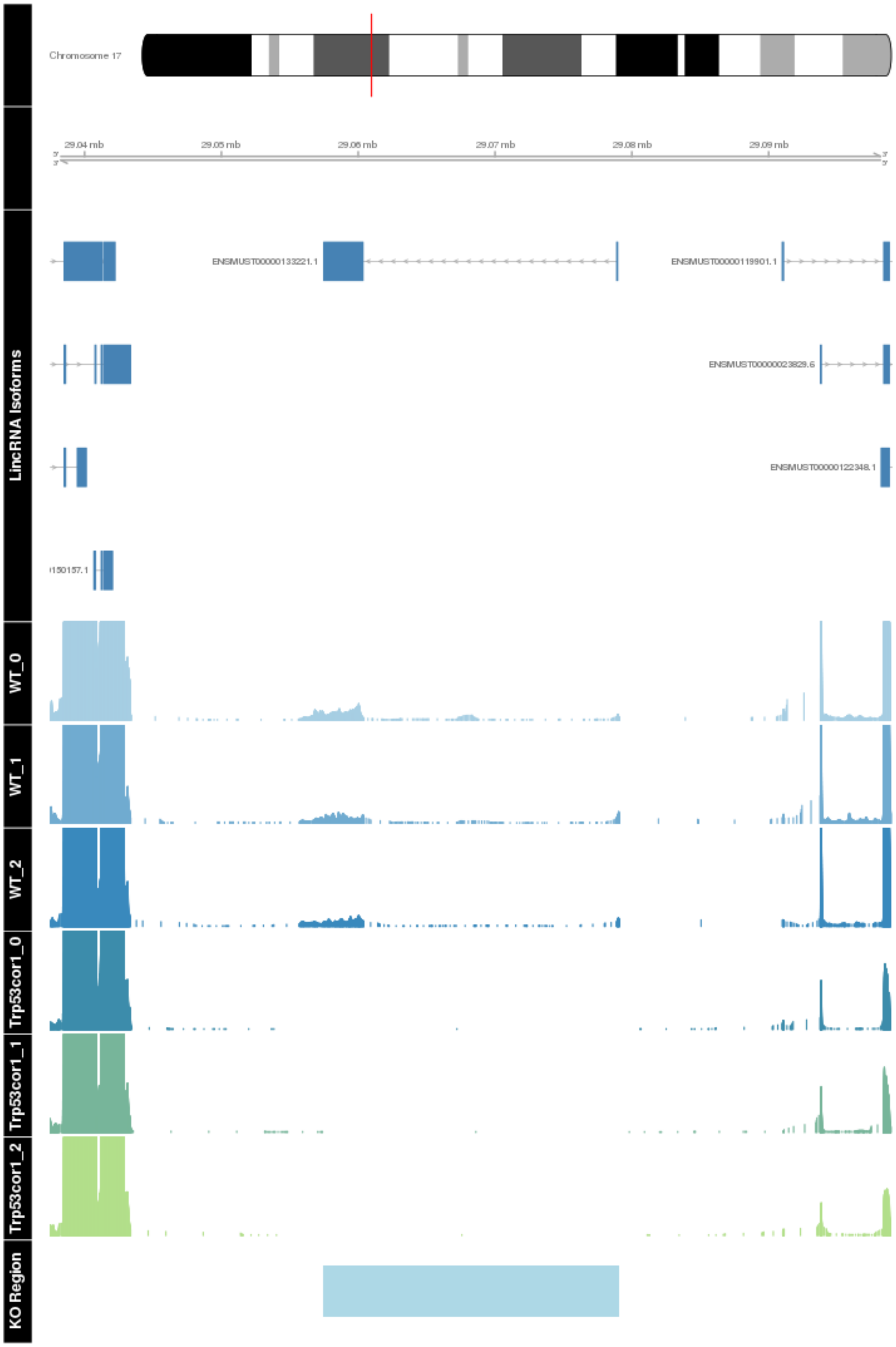
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization



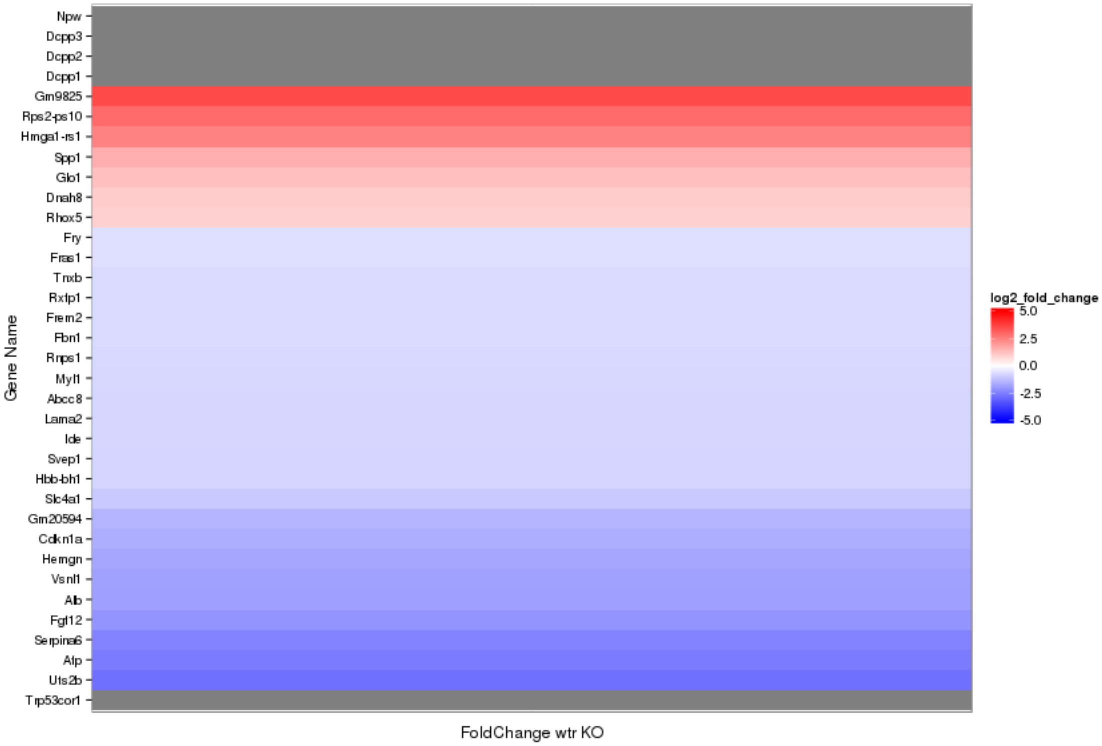
Differential Analysis

Differential Genes

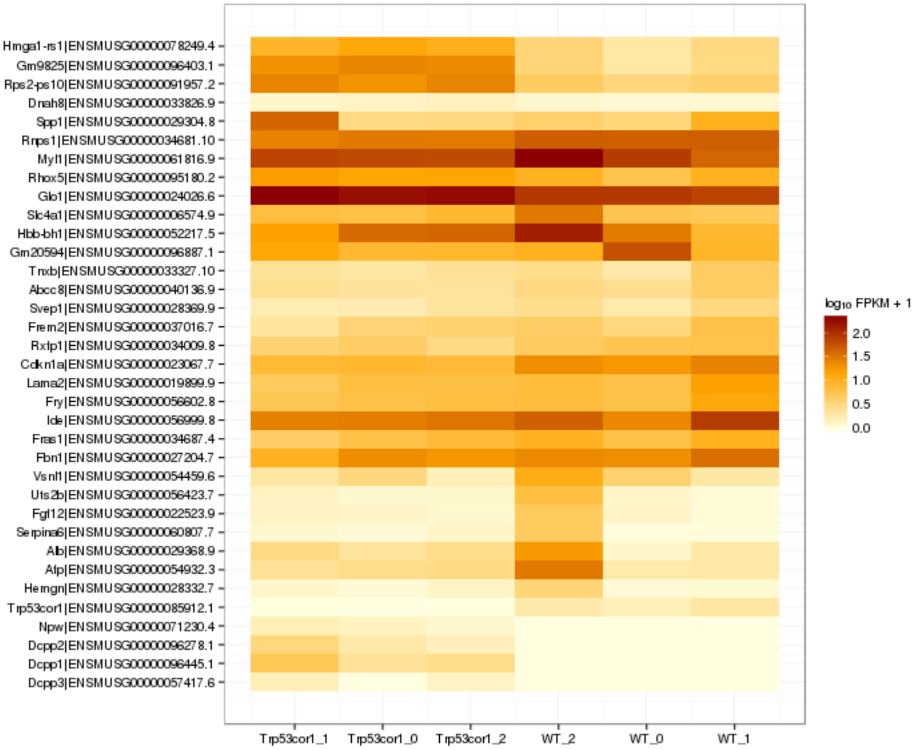
There are 35 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Slc4a1
2	Lama2
3	Fgf12
4	Cdkn1a
5	Glo1
6	Fbn1

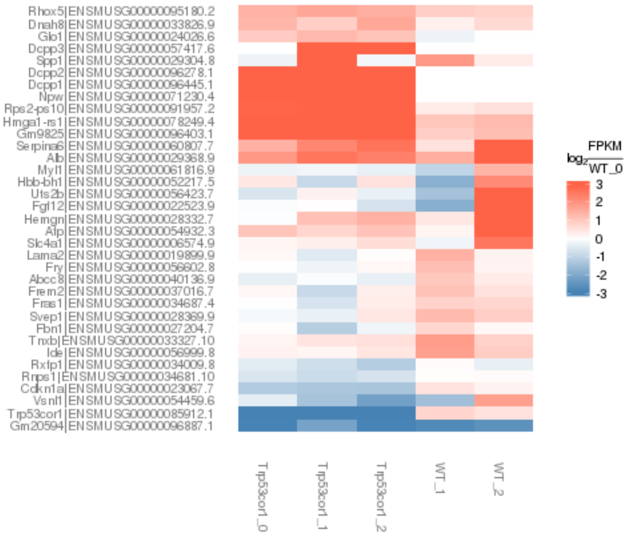
```
 7 Hemgn
 8 Svep1
 9 Spp1
10 Alb
11 Tnxb
12 Dnah8
13 Rxfp1
14 Rnps1
15 Fras1
16 Frem2
17 Abcc8
18 Hbb-bh1
19 Vsnl1
20 Afp
21 Uts2b
22 Fry
23 Ide
24 Dcpp3
25 Serpina6
26 Myl1
27 Npw
28 Hmga1-rs1
29 Trp53cor1
30 Rps2-ps10
31 Rhox5
32 Dcpp2
33 Gm9825
34 Dcpp1
35 Gm20594
```



Expression heatmap of sigGenes



Foldchange heatmap of sigGenes

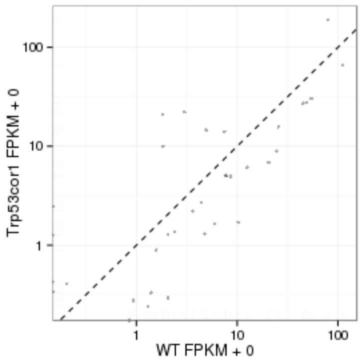


```
## Error in (function (classes, fdef, mtable) : unable to find an inherited method for function 'csFoldChangeHeatma
```

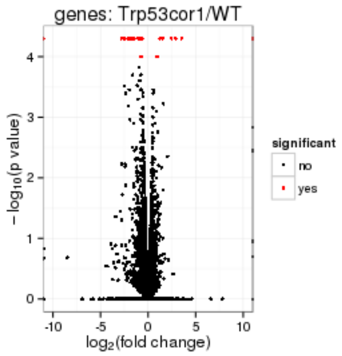
```
## Error in sqliteExecStatement(con, statement, bind.data): RS-DBI driver: (error in statement: near ")": syntax er
```

Expression-level/significance relationship

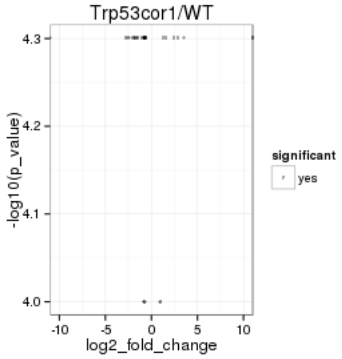
Scatter plot of significant genes only:



Volcano Plot



Volcano plot with significant genes only:



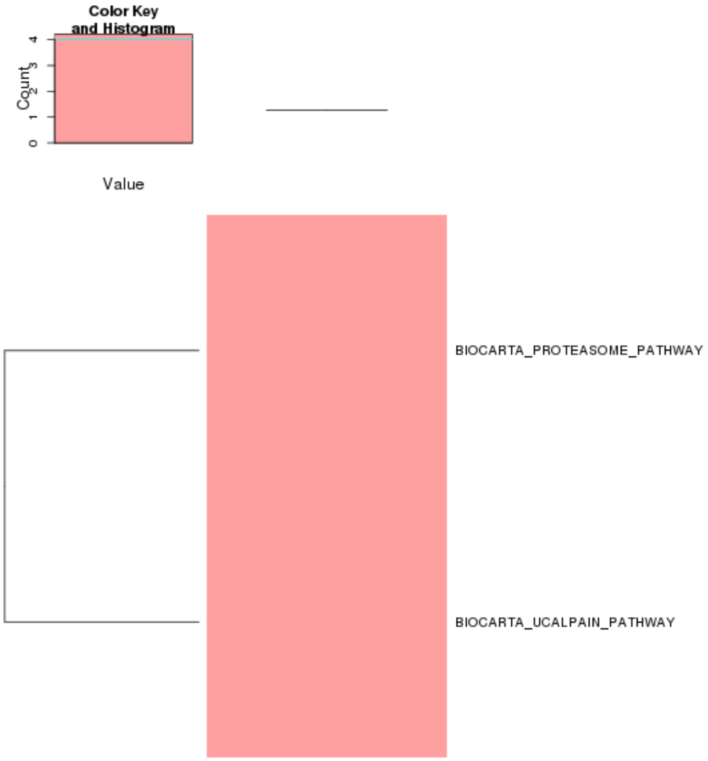
Gene/Pathway Analysis

##

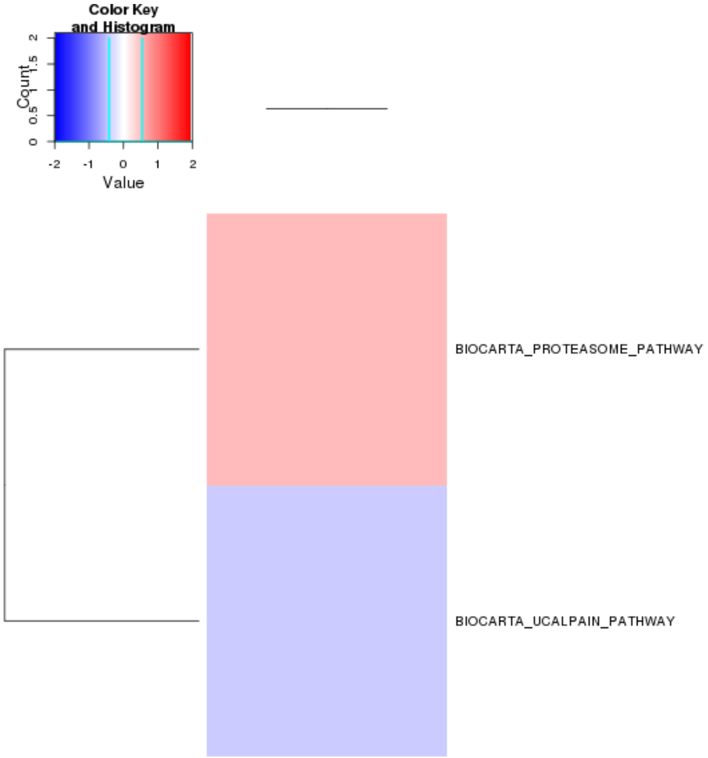
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

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

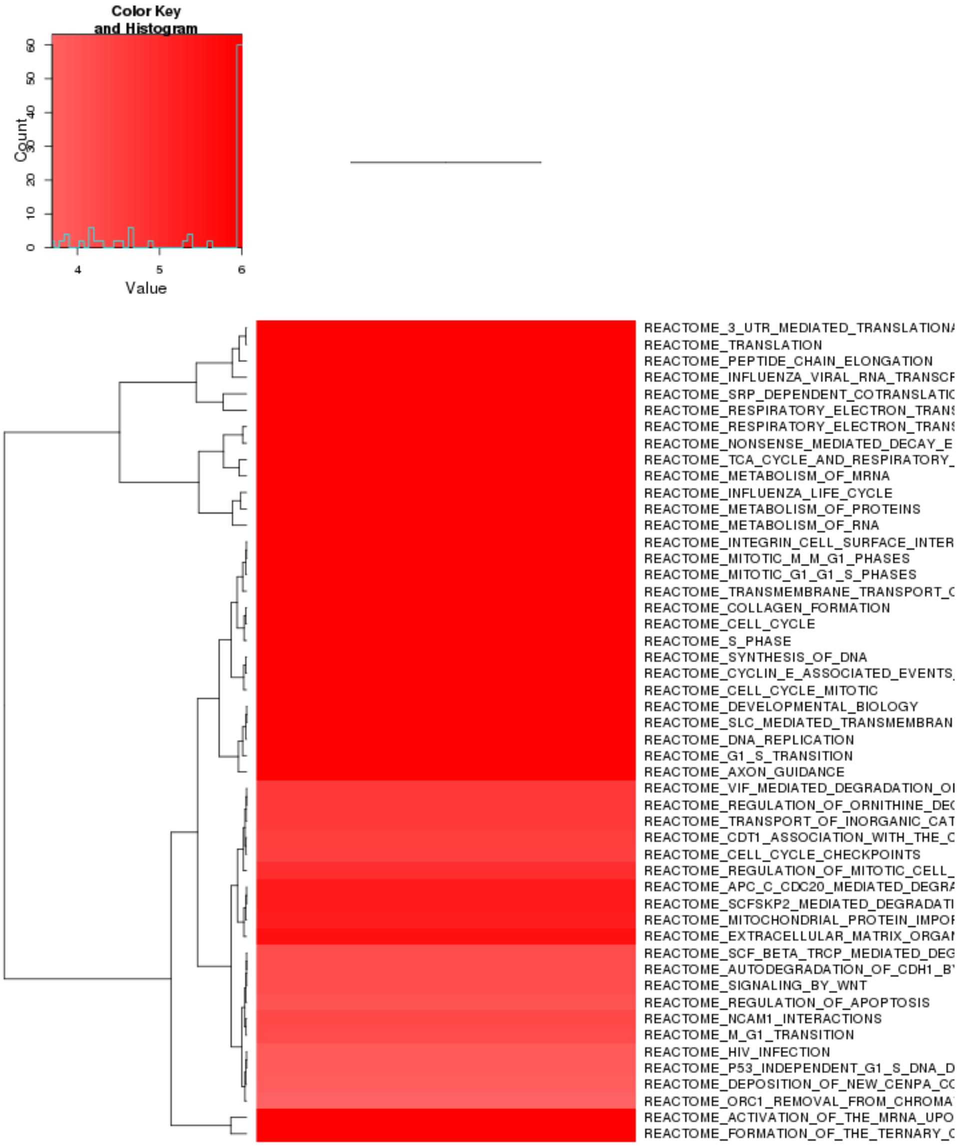
Biocarta enrichment:



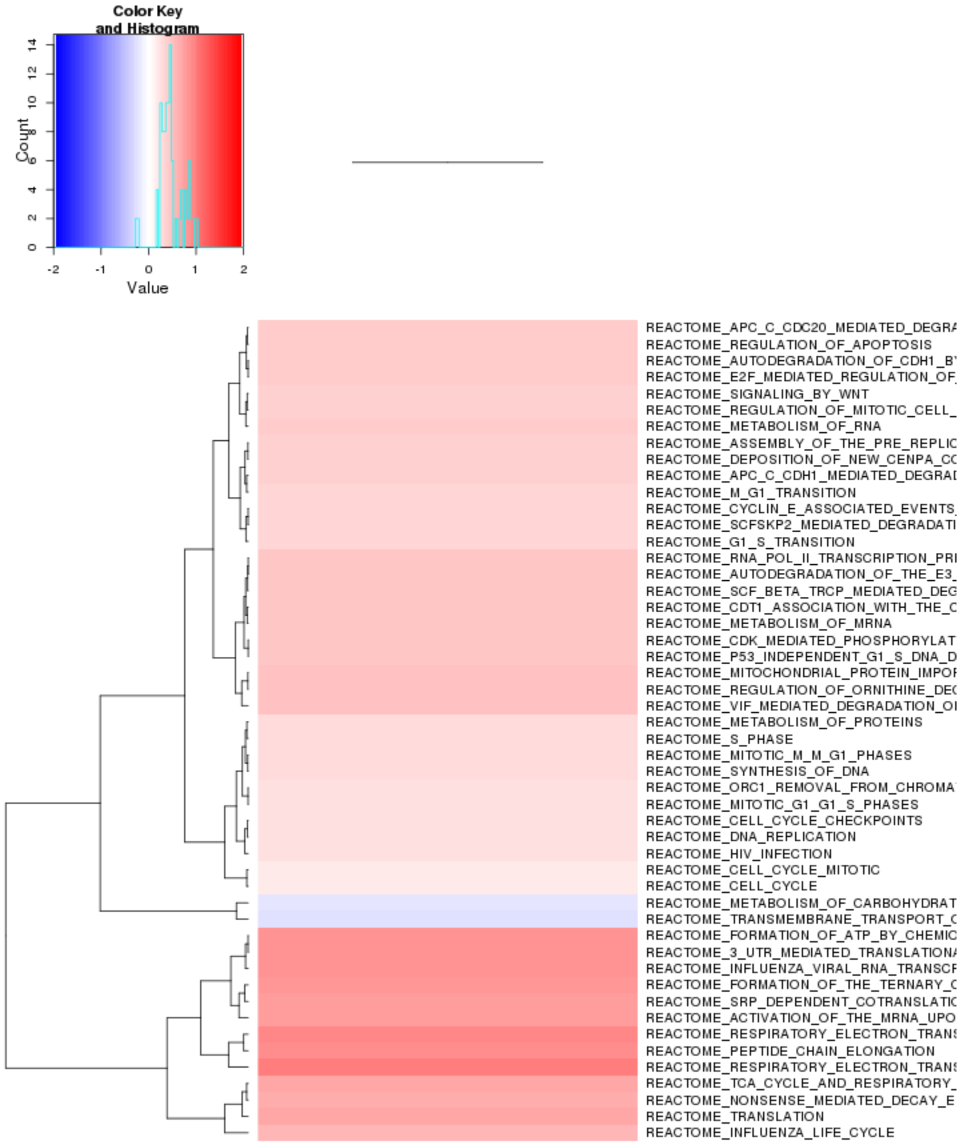
Biocarta zscore:



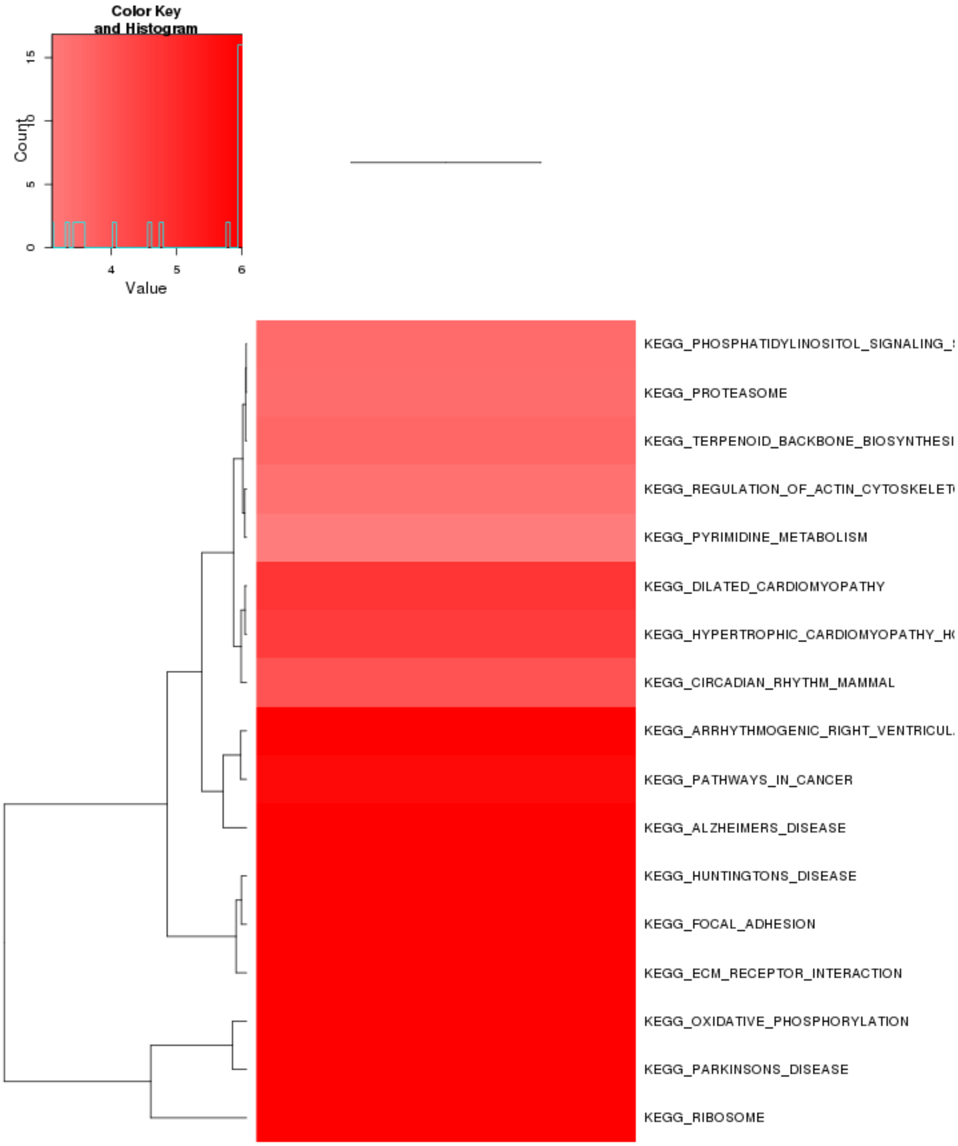
Reactome enrichment:



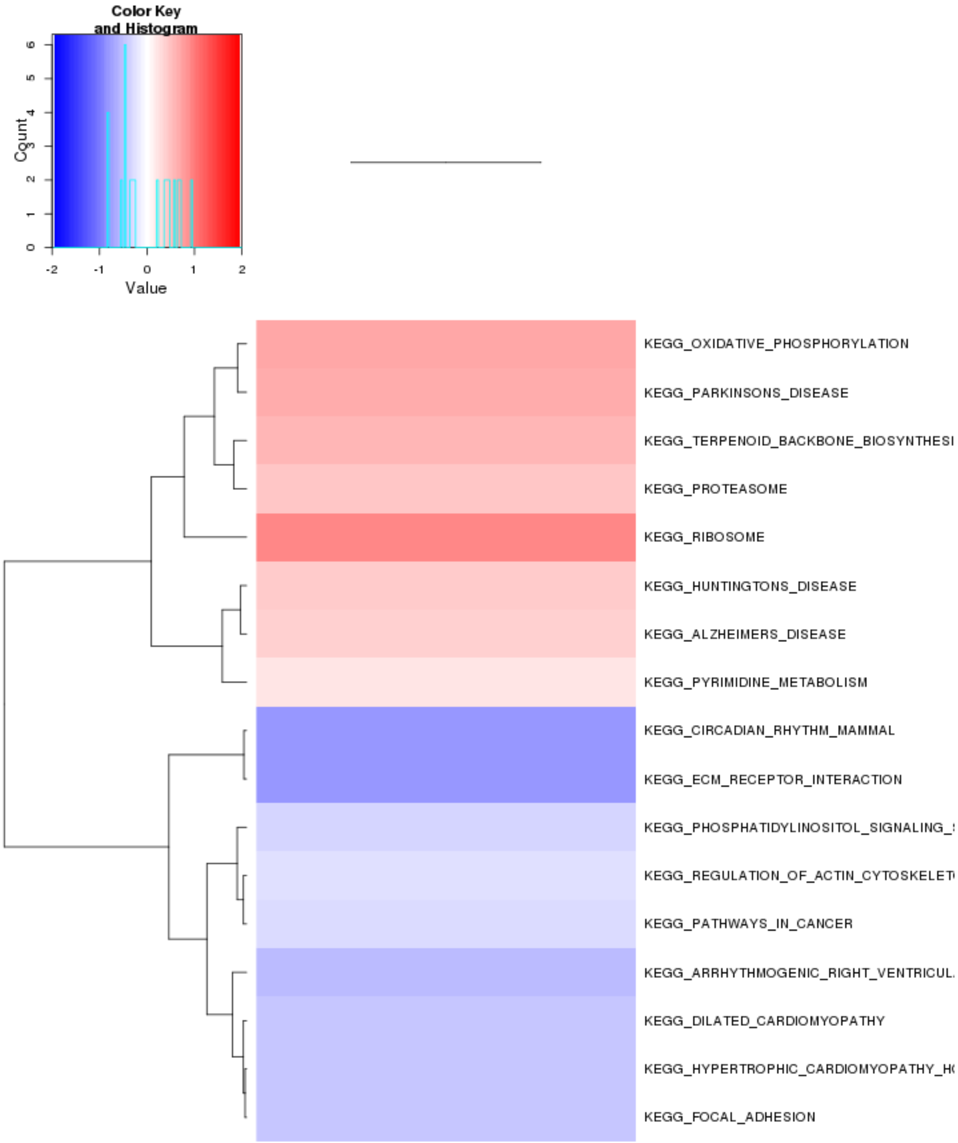
Reactome zscore:



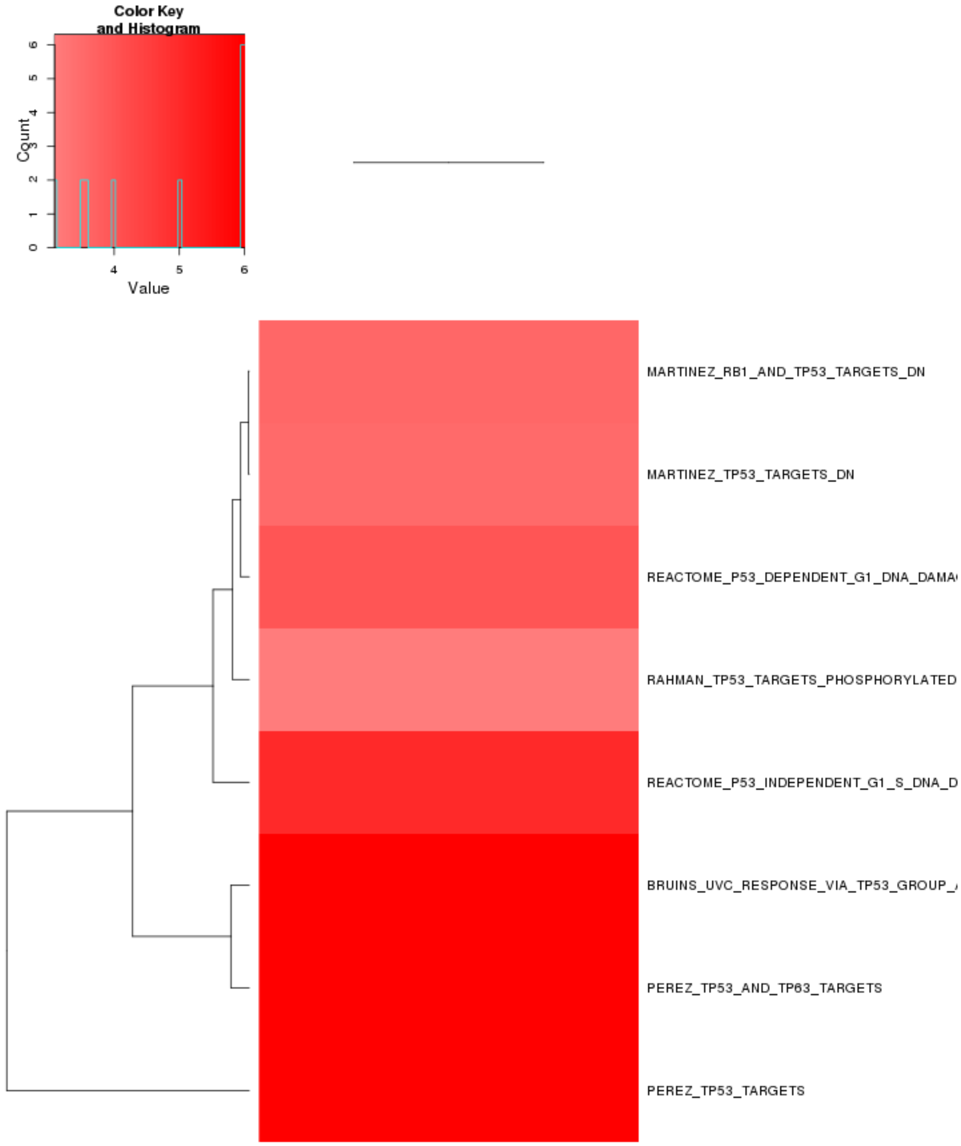
Kegg enrichment:


Color Key
and Histogram
Count
0
5
10
15
4
5
6
Value
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_!
KEGG_PROTEASOME
KEGG_TERPENOID_BACKBONE_BIOSYNTHESI
KEGG_REGULATION_OF_ACTIN_CYTOSKELET(
KEGG_PYRIMIDINE_METABOLISM
KEGG_DILATED_CARDIOMYOPATHY
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_H(
KEGG_CIRCADIAN_RHYTHM_MAMMAL
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICUL
KEGG_PATHWAYS_IN_CANCER
KEGG_ALZHEIMERS_DISEASE
KEGG_HUNTINGTONS_DISEASE
KEGG_FOCAL_ADHESION
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_PARKINSONS_DISEASE
KEGG_RIBOSOME

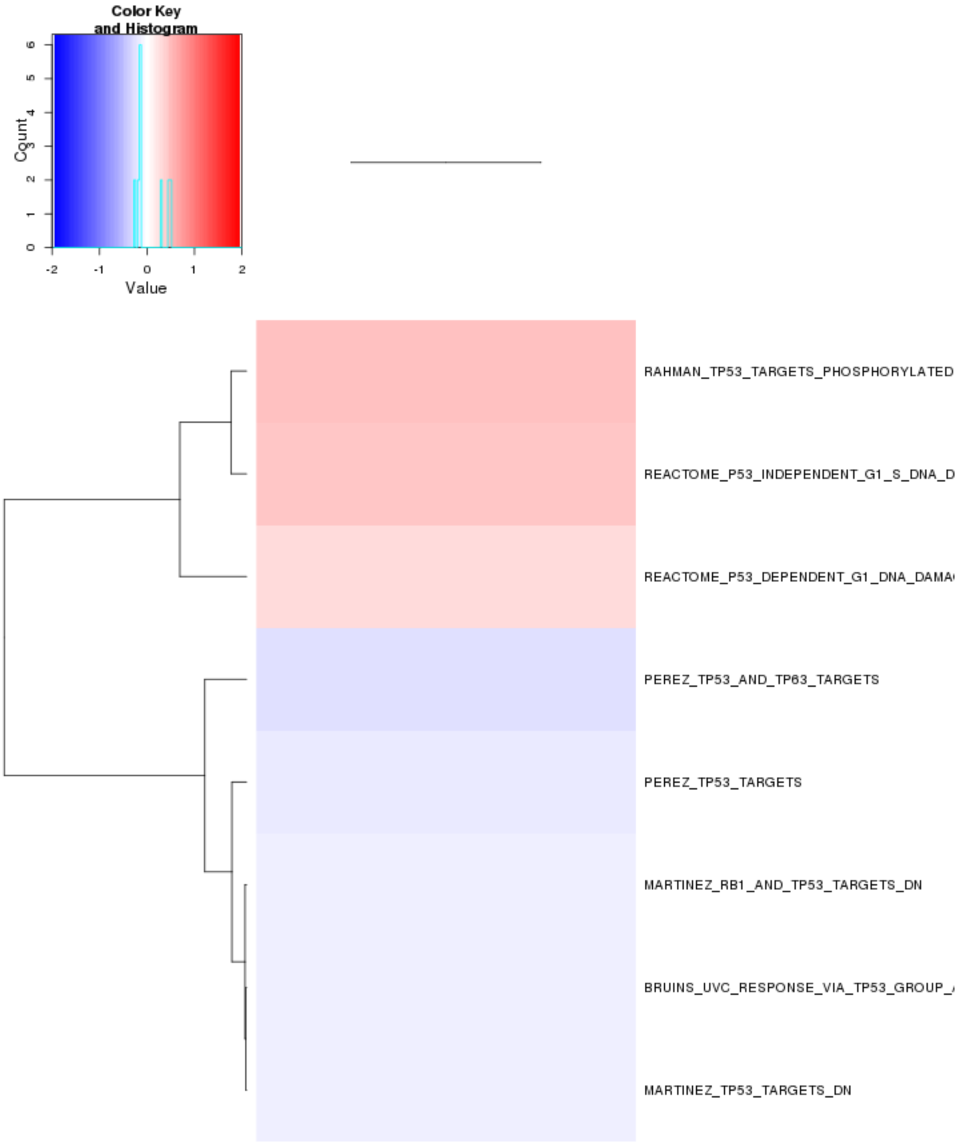
Kegg zscore:



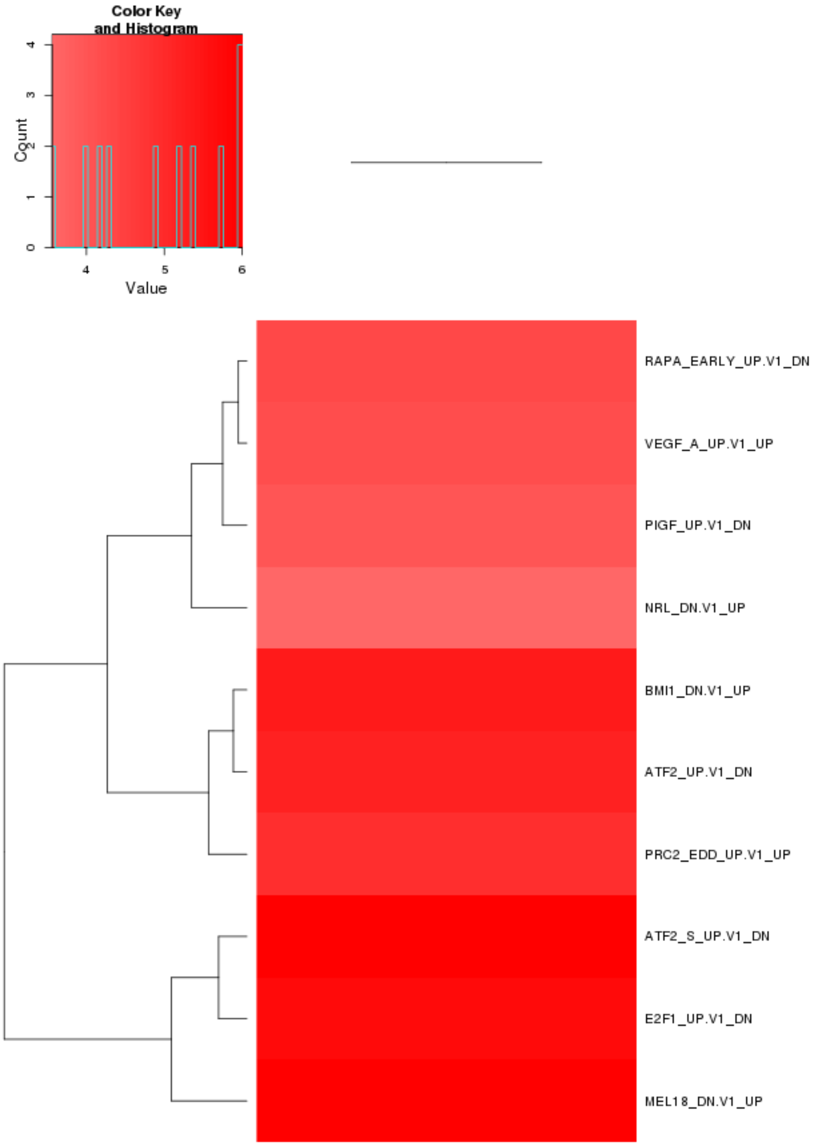
p53 enrichment:


Color Key
and Histogram
Count
0
1
2
3
4
5
6
4
5
6
Value
MARTINEZ_RB1_AND_TP53_TARGETS_DN
MARTINEZ_TP53_TARGETS_DN
REACTOME_P53_DEPENDENT_G1_DNA_DAMA
RAHMAN_TP53_TARGETS_PHOSPHORYLATED
REACTOME_P53_INDEPENDENT_G1_S_DNA_D
BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_
PEREZ_TP53_AND_TP63_TARGETS
PEREZ_TP53_TARGETS

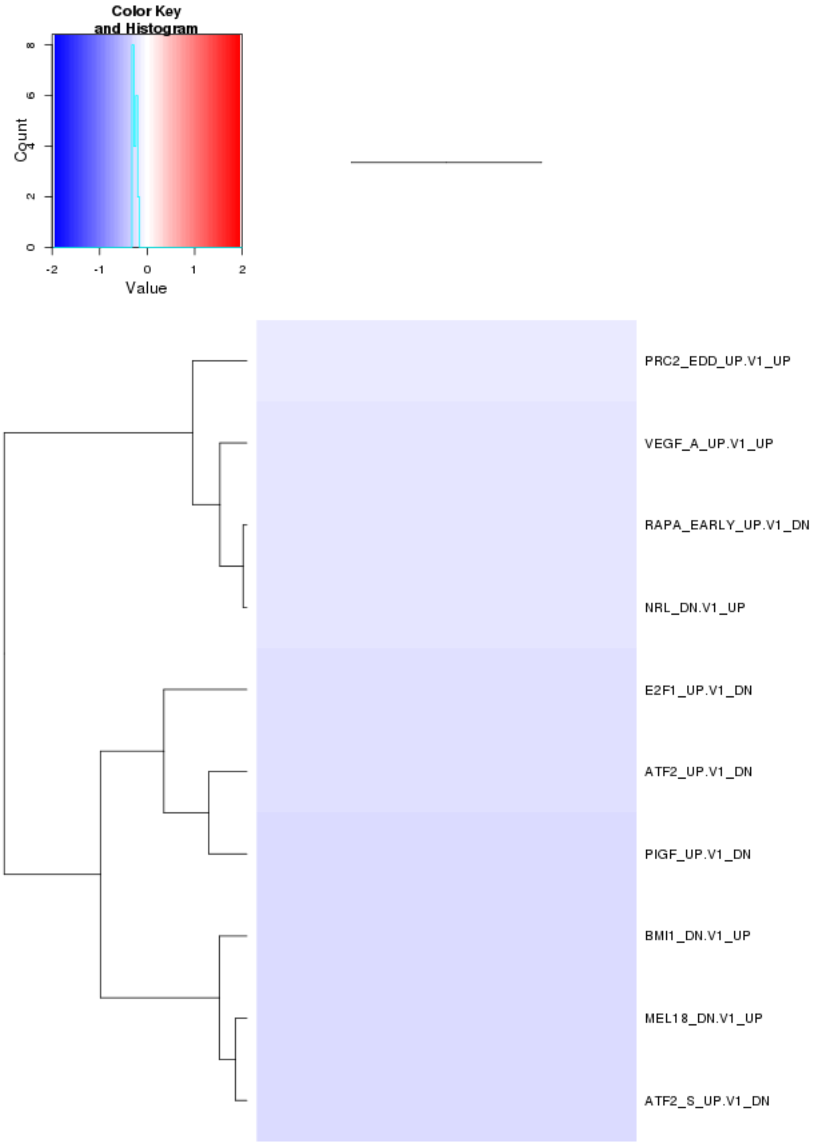
p53 zscore:

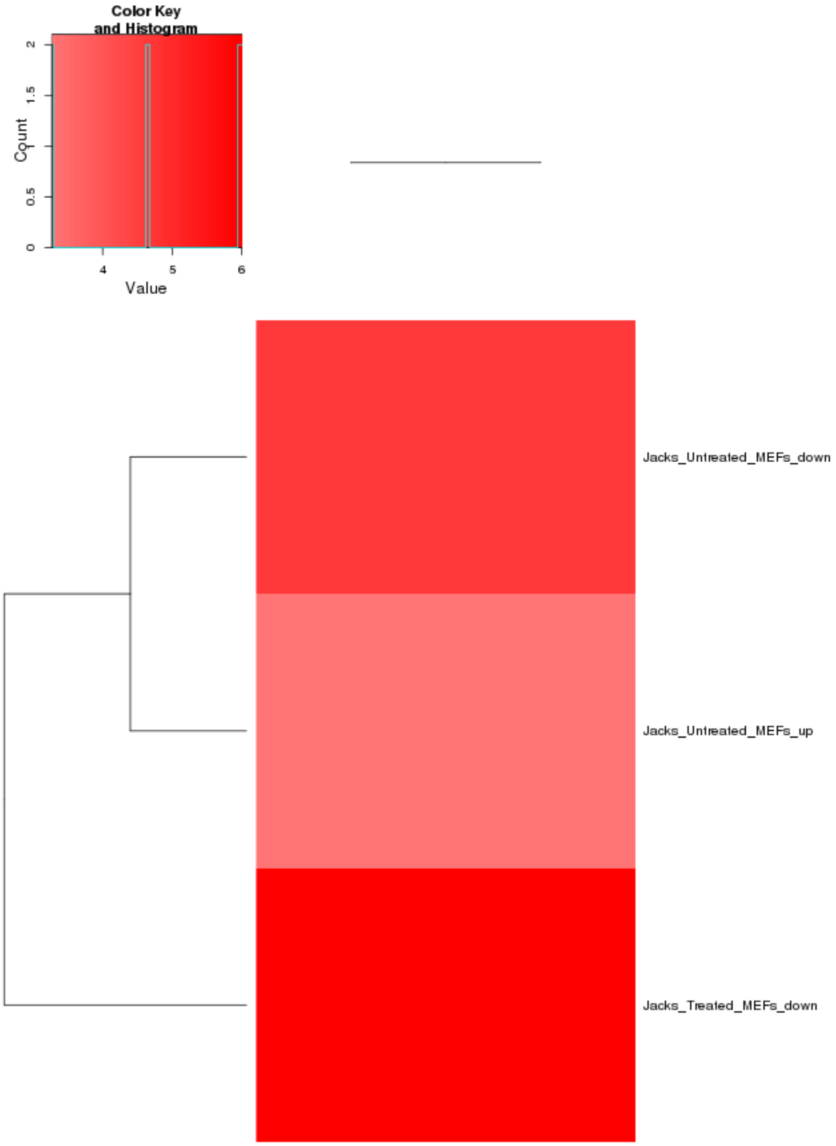


Oncogene enrichment:



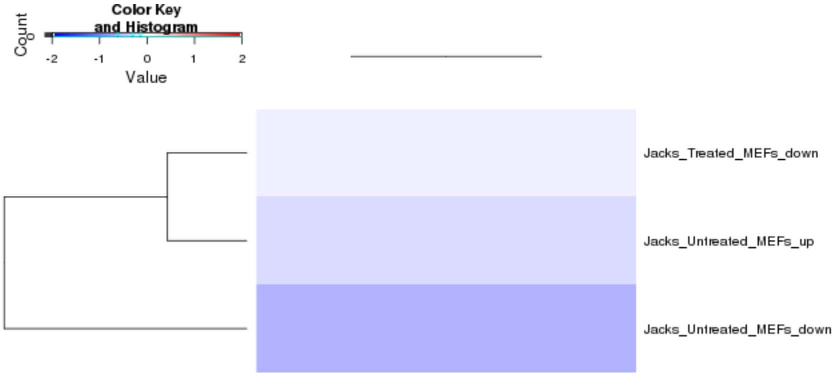
Oncogene zscore:


Color Key
and Histogram
Count
0
2
4
6
8
-2
-1
0
1
2
Value
PRC2_EDD_UP.V1_UP
VEGF_A_UP.V1_UP
RAPA_EARLY_UP.V1_DN
NRL_DN.V1_UP
E2F1_UP.V1_DN
ATF2_UP.V1_DN
PIGF_UP.V1_DN
BMI1_DN.V1_UP
MEL18_DN.V1_UP
ATF2_S_UP.V1_DN



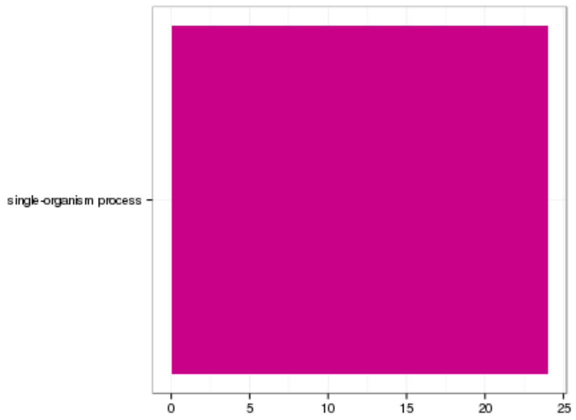
Jacks enrichment

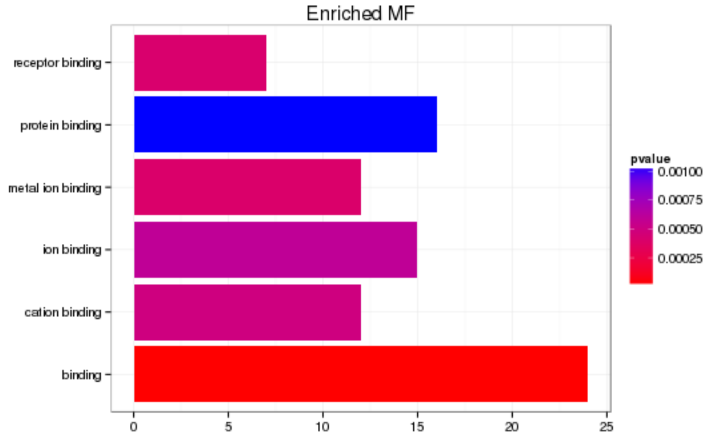
Jacks zscore

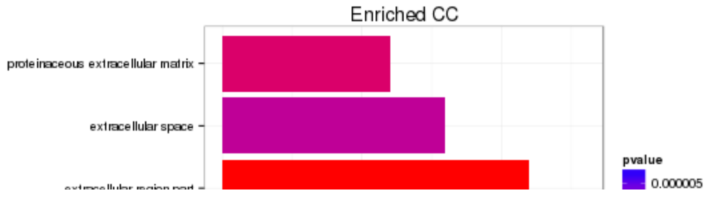


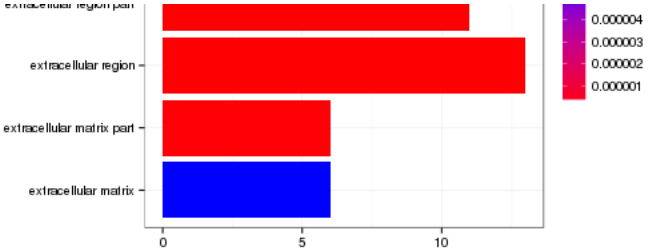
GO enrichment

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


single-organism process
0
5
10
15
20
25


Enriched MF
receptor binding
protein binding
metal ion binding
ion binding
cation binding
binding
0
5
10
15
20
25
pvalue
0.00100
0.00075
0.00050
0.00025


Enriched CC
proteinaceous extracellular matrix
extracellular space
pvalue
0.000005



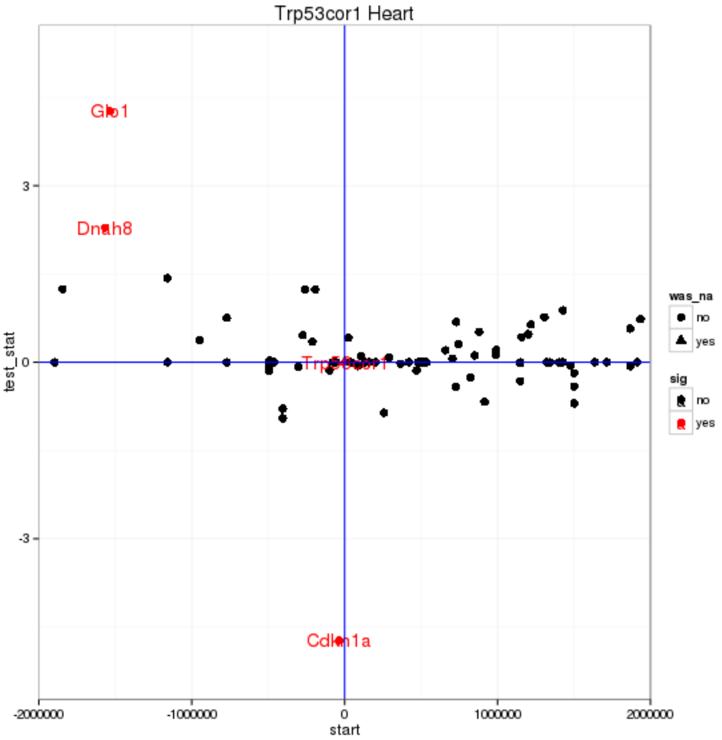
```
## Error in plot.window(...): need finite 'xlim' values
```

```
## Error in plot.window(...): need finite 'xlim' values
```

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 genes significantly regulated in a region this size is: 0.0073



Notes

Samples used are:

	11
1	JR919
2	JR927
3	JR935
4	JR920
5	JR928
6	JR936

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	internal_s
1	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR919/abundances.cxb	WT	0	WT_0	13208700.00	34770500.00	
2	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR927/abundances.cxb	WT	1	WT_1	37517100.00	34770500.00	
3	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR935/abundances.cxb	WT	2	WT_2	42610300.00	34770500.00	
4	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR920/abundances.cxb	Trp53cor1	0	Trp53cor1_0	47074400.00	34770500.00	
5	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR928/abundances.cxb	Trp53cor1	1	Trp53cor1_1	43574500.00	34770500.00	
6	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR936/abundances.cxb	Trp53cor1	2	Trp53cor1_2	40387600.00	34770500.00	

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] GO.db_2.10.1
##  [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_1.8-2
## [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_2.14.2
## [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_0.3.1
## [36] BiocGenerics_0.8.0
## [37] knitr_1.7
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17.1         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_1.0            Formula_1.1-2
## [13] gdata_2.13.3           GenomicFeatures_1.14.5 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_1.1-4
## [28] munsell_0.4.2          org.Hs.eg.db_2.10.1    proto_0.3-10
## [31] qvalue_1.36.0          Rcpp_0.11.3            RCurl_1.95-4.3
## [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,Trp53cor1 -o /n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/diff/Trp53cor1_E14.5_
## 2
## 3
## 4
## 5
```

Trp53cor1 KO vs WT (leg)

This file shows the wt-v-ko comparison for Trp53cor1.

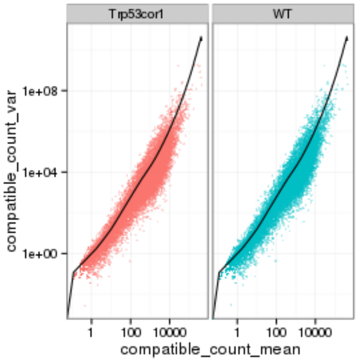
Cuff overview:

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

QC

Dispersion

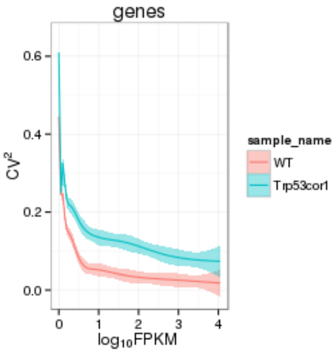
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



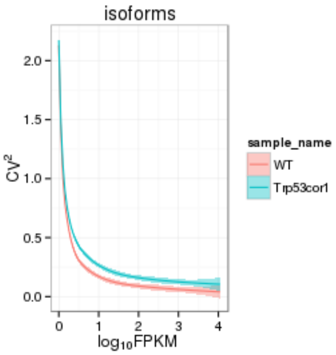
Cross-replicate variability (fpkmSCVplot)

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

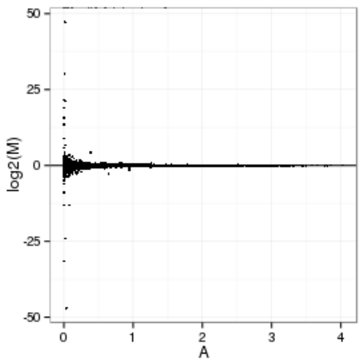
Genes:



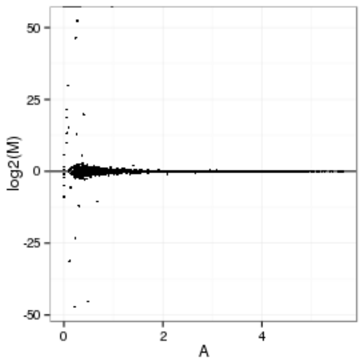
Isoforms:



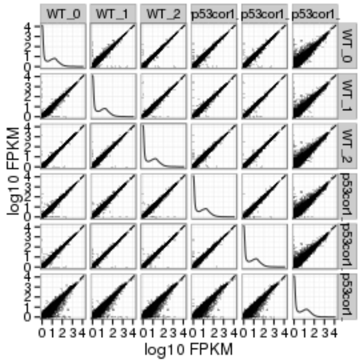
MvA plot



MvA plot counts



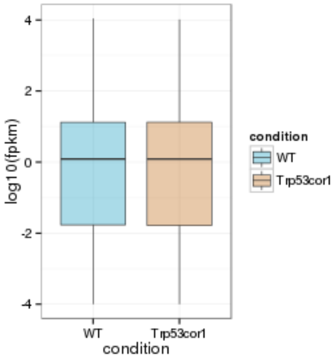
Scatterplot matrix



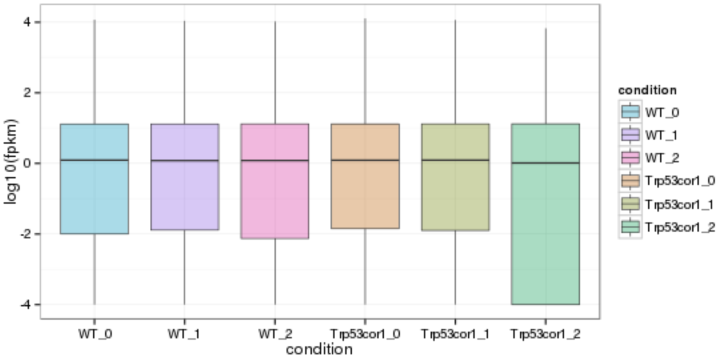
Distributions

Boxplots

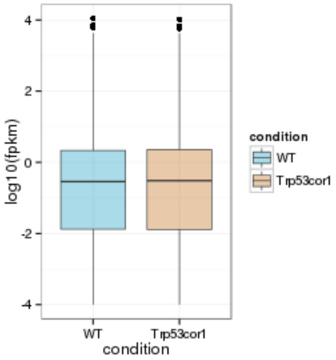
Boxplot (genes)



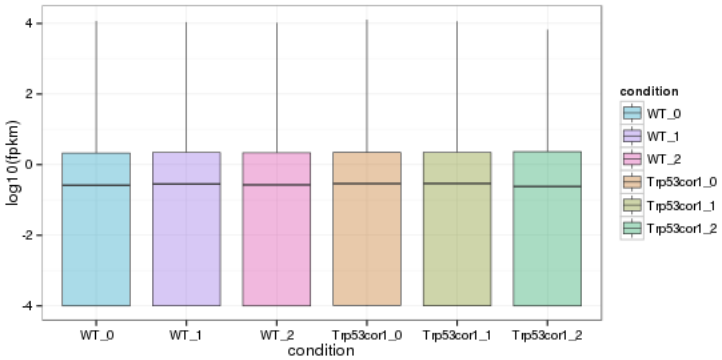
Boxplot (genes, replicates)



Boxplot (isoforms)

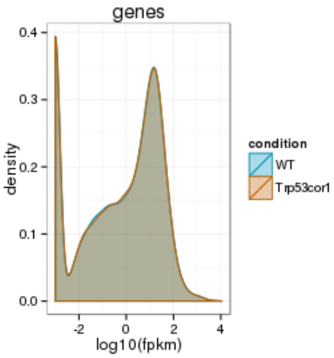


Boxplot (isoforms, replicates)

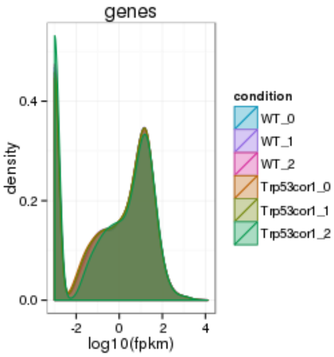


Density

Density (genes)

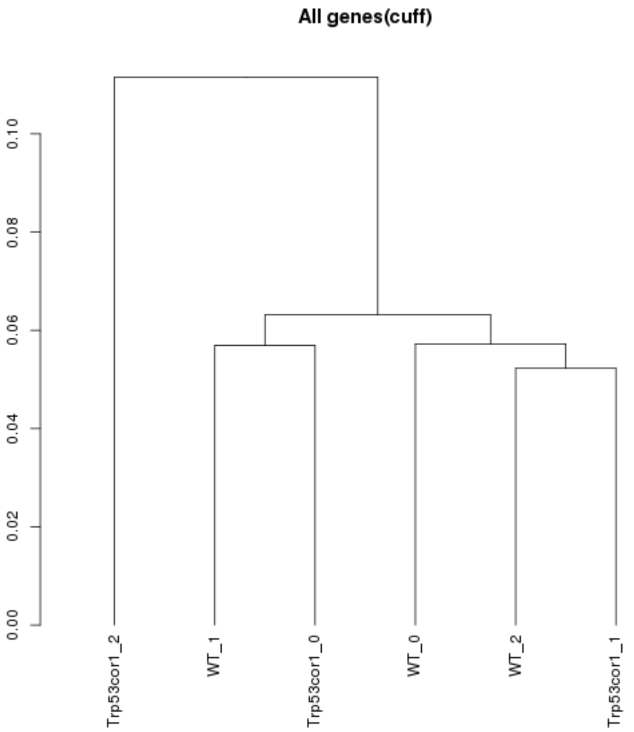


Density (genes, replicates)



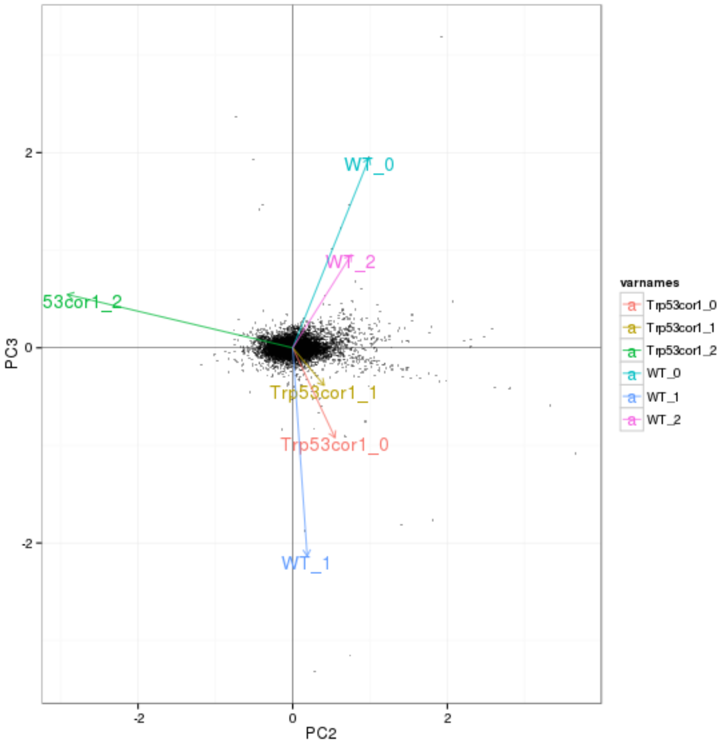
Clustering

Replicate Clusters

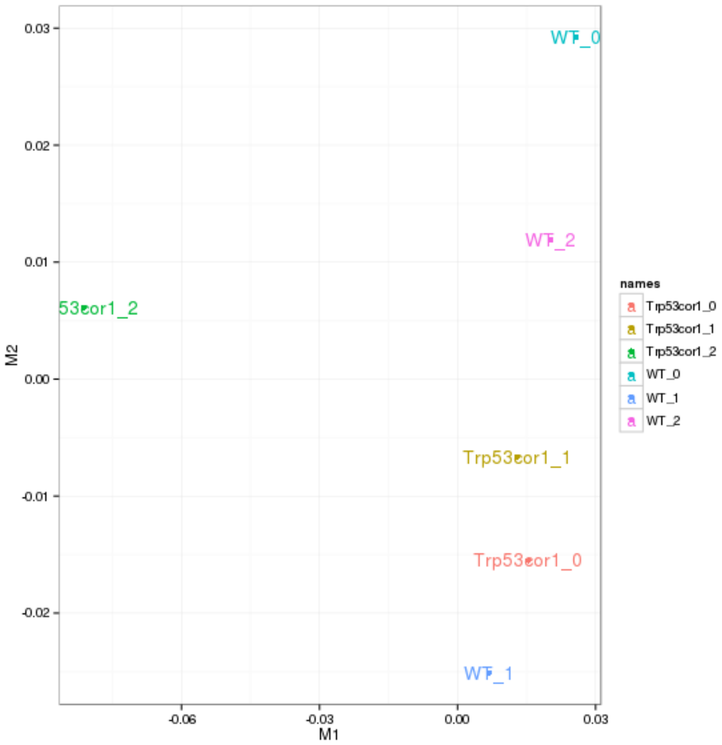


```
## NULL
```

PCA (genes)

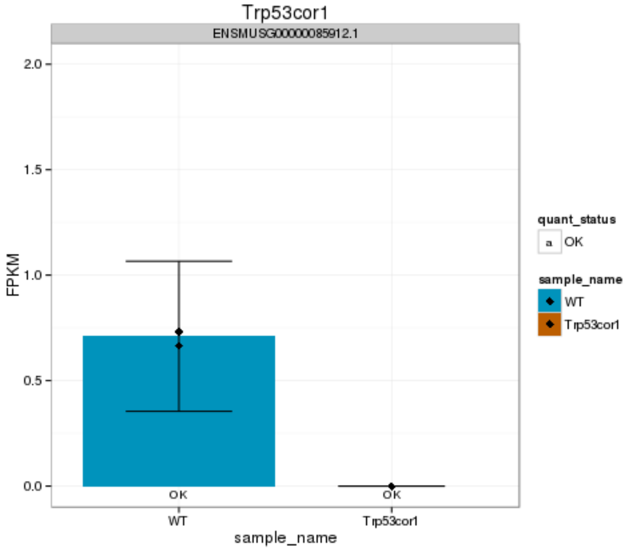


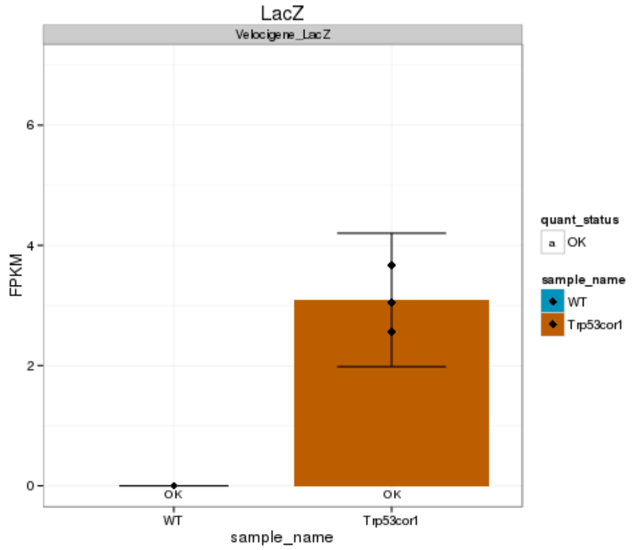
MDS (genes)



KO assessment

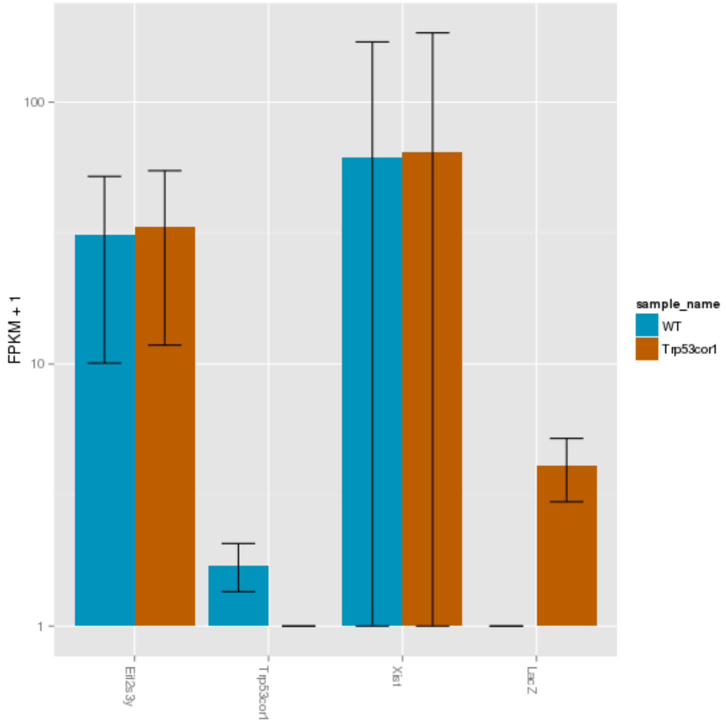
Endogenous lncRNA expression



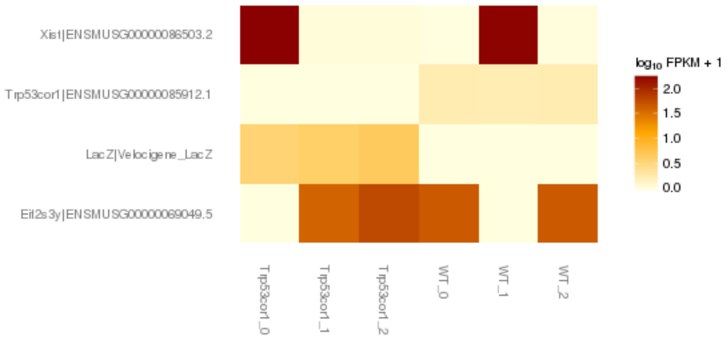


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

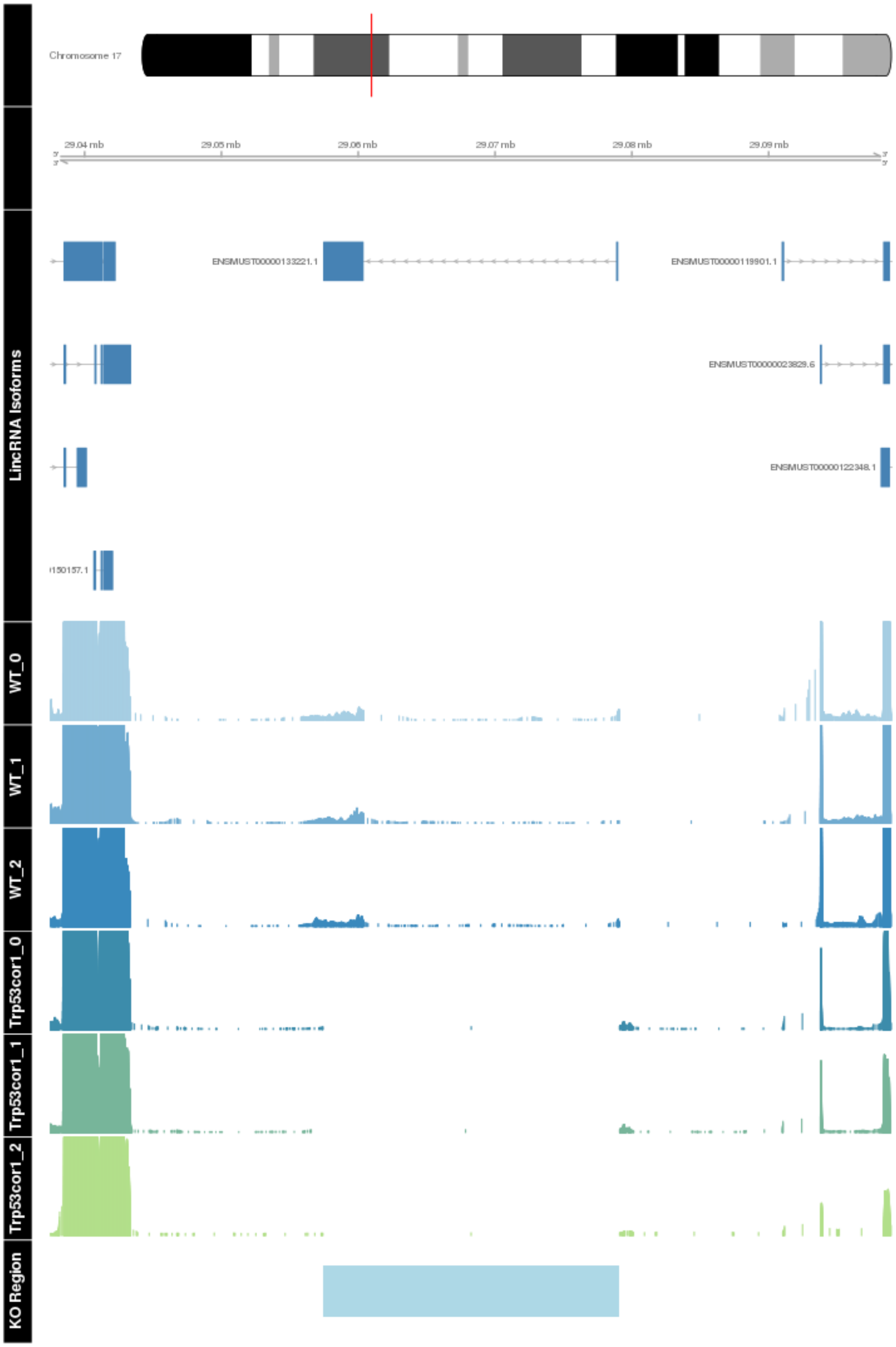
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization



Differential Analysis

Differential Genes

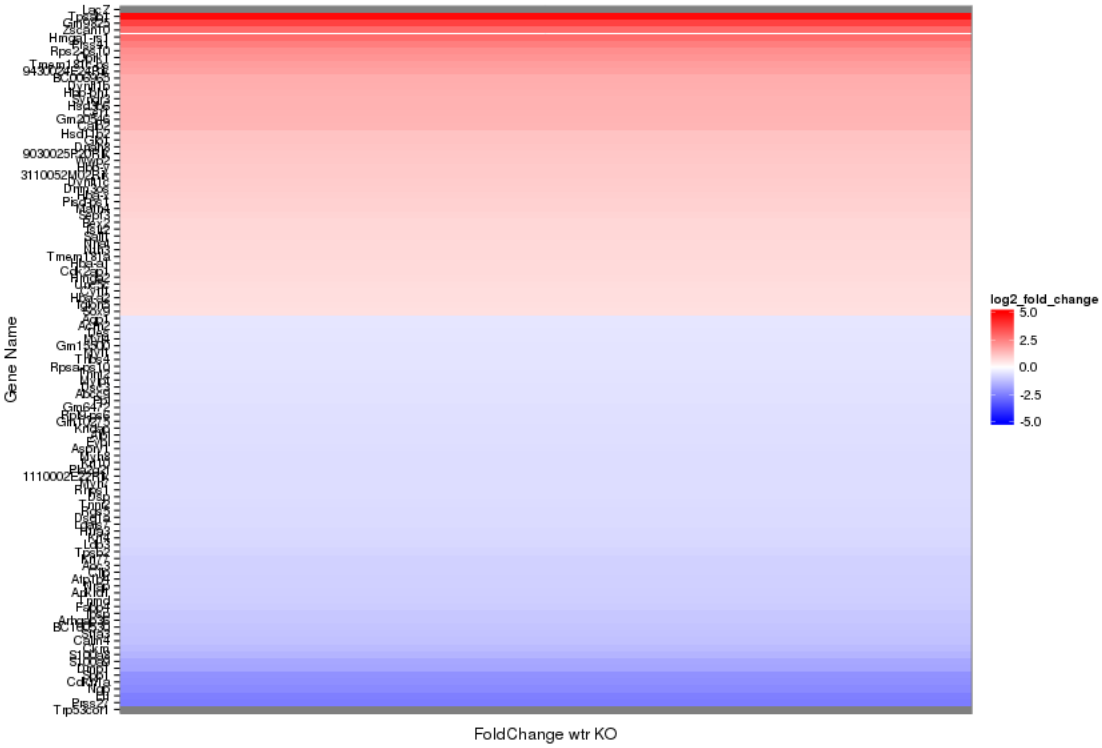
There are 103 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Sox9
2	Dynlt1c
3	Calb2
4	Aqp1
5	Syngr3
6	Iglon5

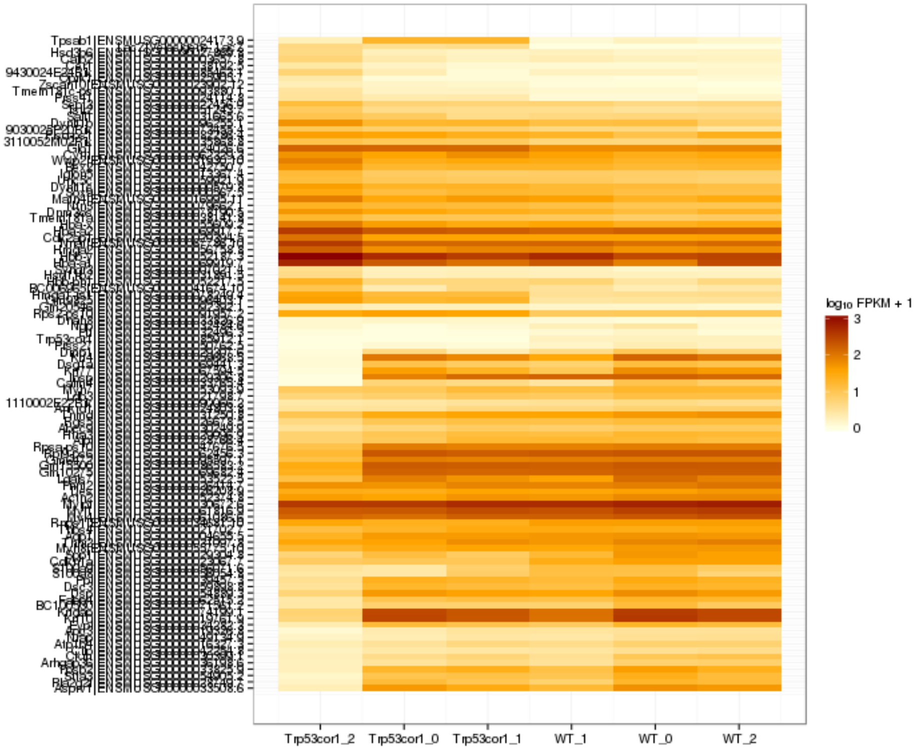
7 Atp1b4
8 Matn4
9 Aoc3
10 Krt10
11 Thbs4
12 Ldb3
13 Sept3
14 Cdkn1a
15 Zscan10
16 Glo1
17 Prss41
18 Tpsab1
19 Ankrd1
20 Oprk1
21 Des
22 Tnnt2
23 Rgs5
24 Hsd3b6
25 Pla2g2f
26 Alpl
27 Htra3
28 Spp1
29 Ibsp
30 Dmp1
31 Cdk2ap1
32 Abcc9
33 Ckm
34 Mylpf
35 Tnni2
36 Tnmd
37 Sall1
38 Hsd11b2
39 Wwp2
40 Ngp
41 Ltf
42 Asprv1
43 Calm4
44 Tpsb2
45 Dnah8
46 Evpl
47 Rnps1
48 3110052M02Rik
49 Arhgap36
50 Tmem181a
51 Cer1
52 Ppl
53 BC006965
54 Cilp
55 Bex2
56 Rpsa-ps10
57 Nrap
58 Prss27
59 Islr2
60 Hbb-y
61 Hbb-bh1
62 Actn2
63 Myh7
64 Lgals7
65 Dsp

66 Stfa3

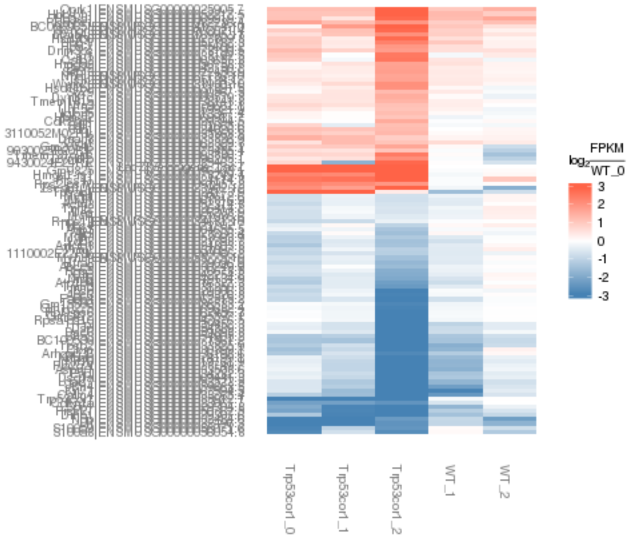
67 Hba-x
68 Myh8
69 S100a8
70 S100a9
71 Hmga2
72 Krt4
73 Dsc3
74 Unc5c
75 Myl4
76 Myl1
77 Cytl1
78 Rpl9-ps6
79 Fabp4
80 Krt77
81 Nnat
82 Dsg1a
83 Gm10275
84 Hba-a2
85 Hba-a1
86 BC100530
87 9030025P20Rik
88 Krtdap
89 Dnm3os
90 Hmga1-rs1
91 Ntn3
92 Pisd-ps1
93 9430024E24Rik
94 Trp53cor1
95 Gm15500
96 1110002E22Rik
97 Rps2-ps10
98 Gm20546
99 Tmem181c-ps
100 Gm6472
101 Dynlt1b
102 Gm9825
103 LacZ



Expression heatmap of sigGenes



Foldchange heatmap of sigGenes

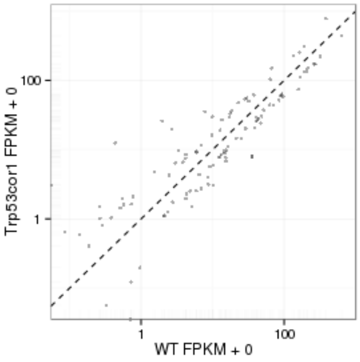


```
## Error in (function (classes, fdef, mtable) : unable to find an inherited method for function 'csFoldChangeHeatma
```

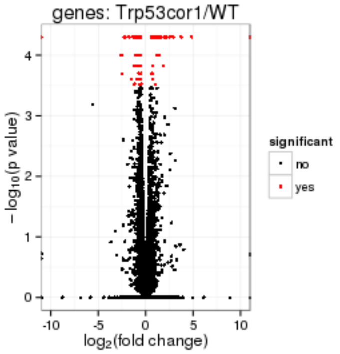
```
## Error in sqliteExecStatement(con, statement, bind.data): RS-DBI driver: (error in statement: near ")": syntax er
```

Expression-level/significance relationship

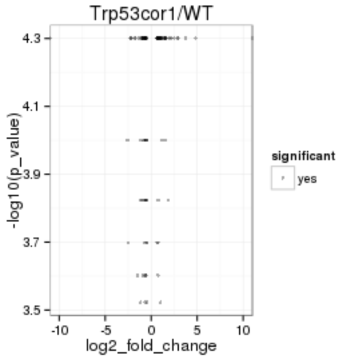
Scatter plot of significant genes only:



Volcano Plot



Volcano plot with significant genes only:



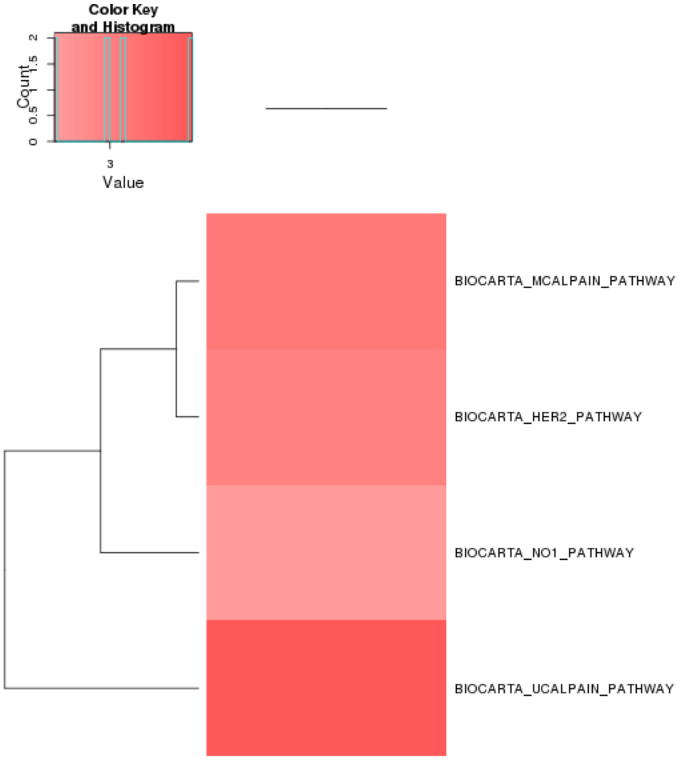
Gene/Pathway Analysis

##

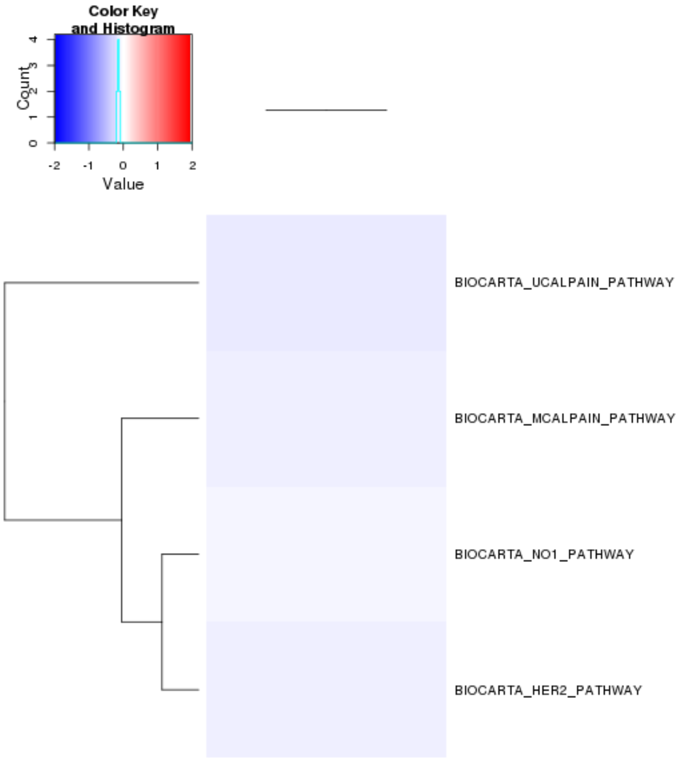
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

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

Biocarta enrichment:

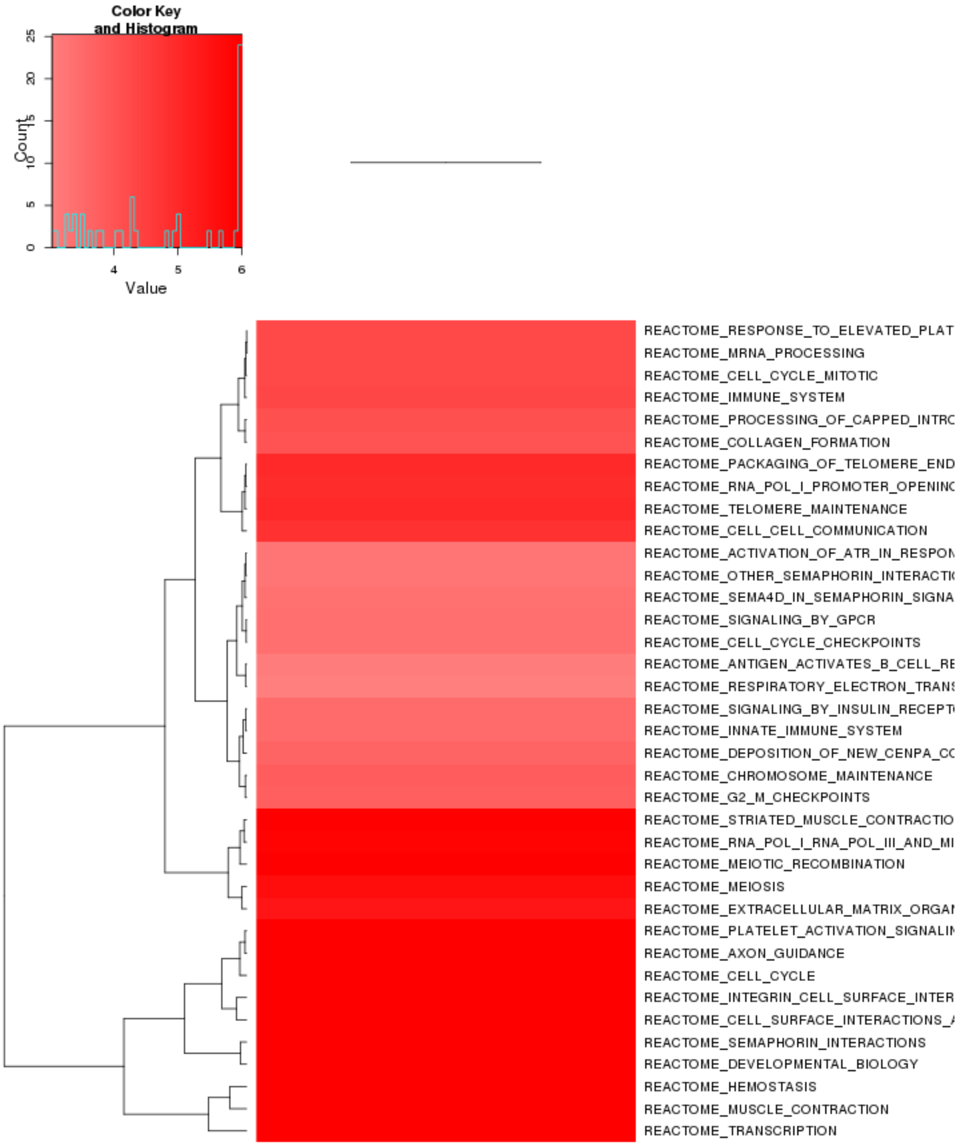


Biocarta zscore:



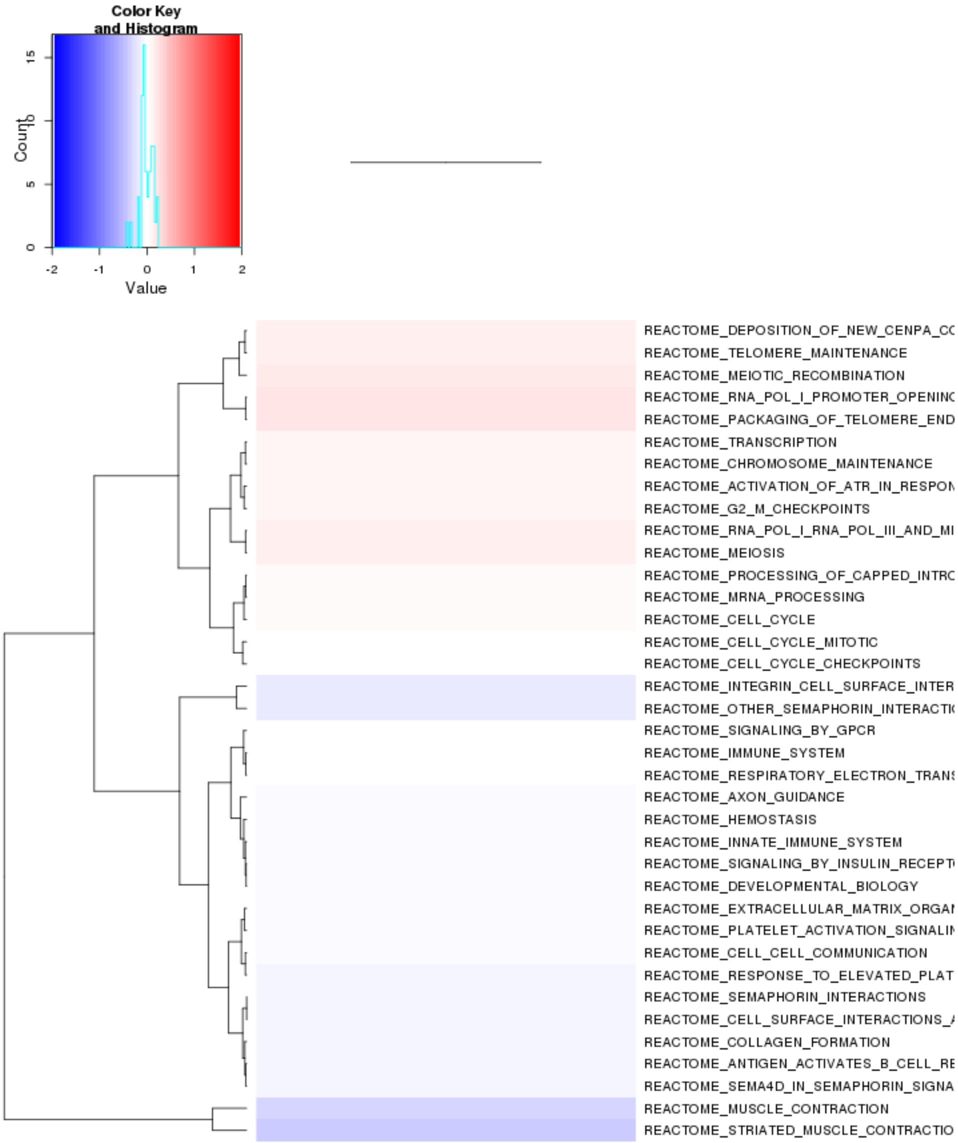
Reactome enrichment:

```
## Error in x_ordered[1:50, ]: subscript out of bounds
```

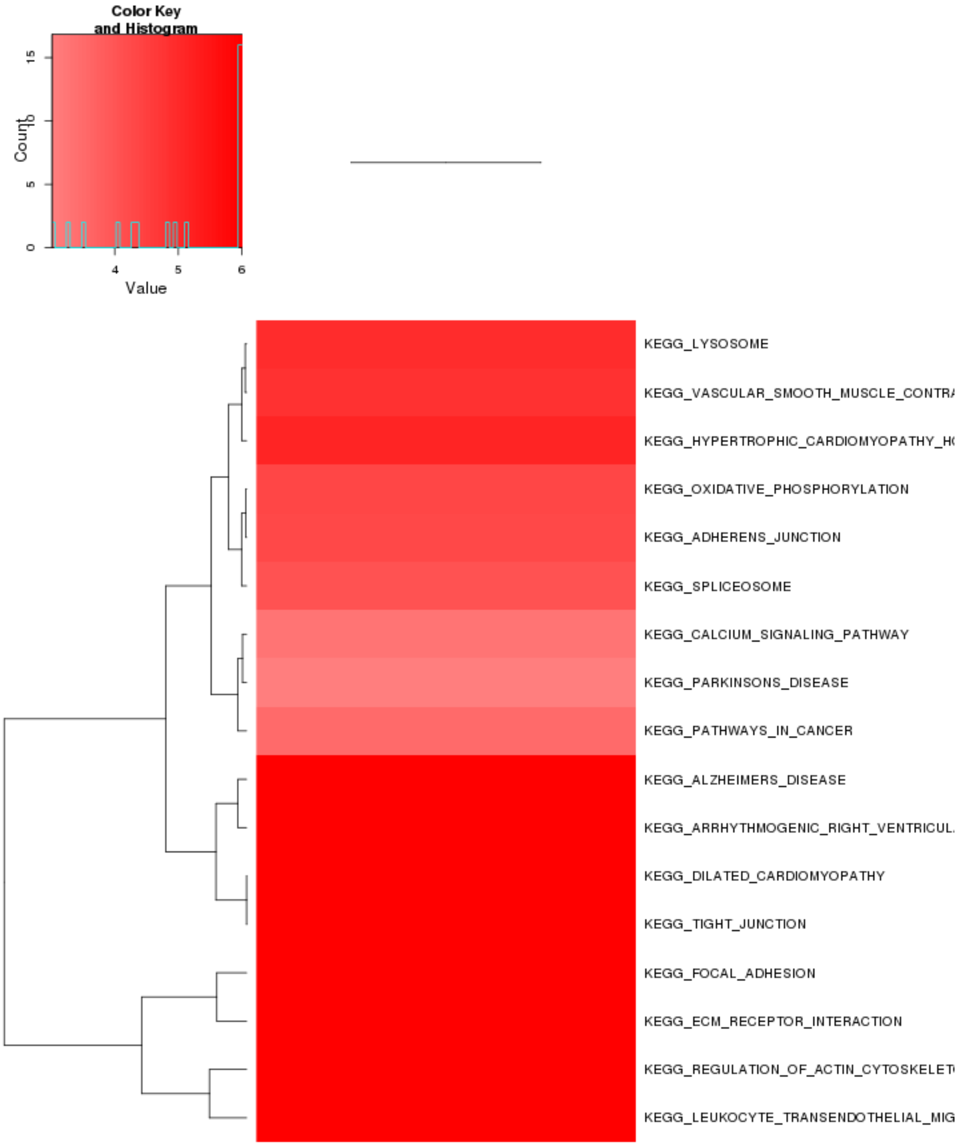


Reactome zscore:

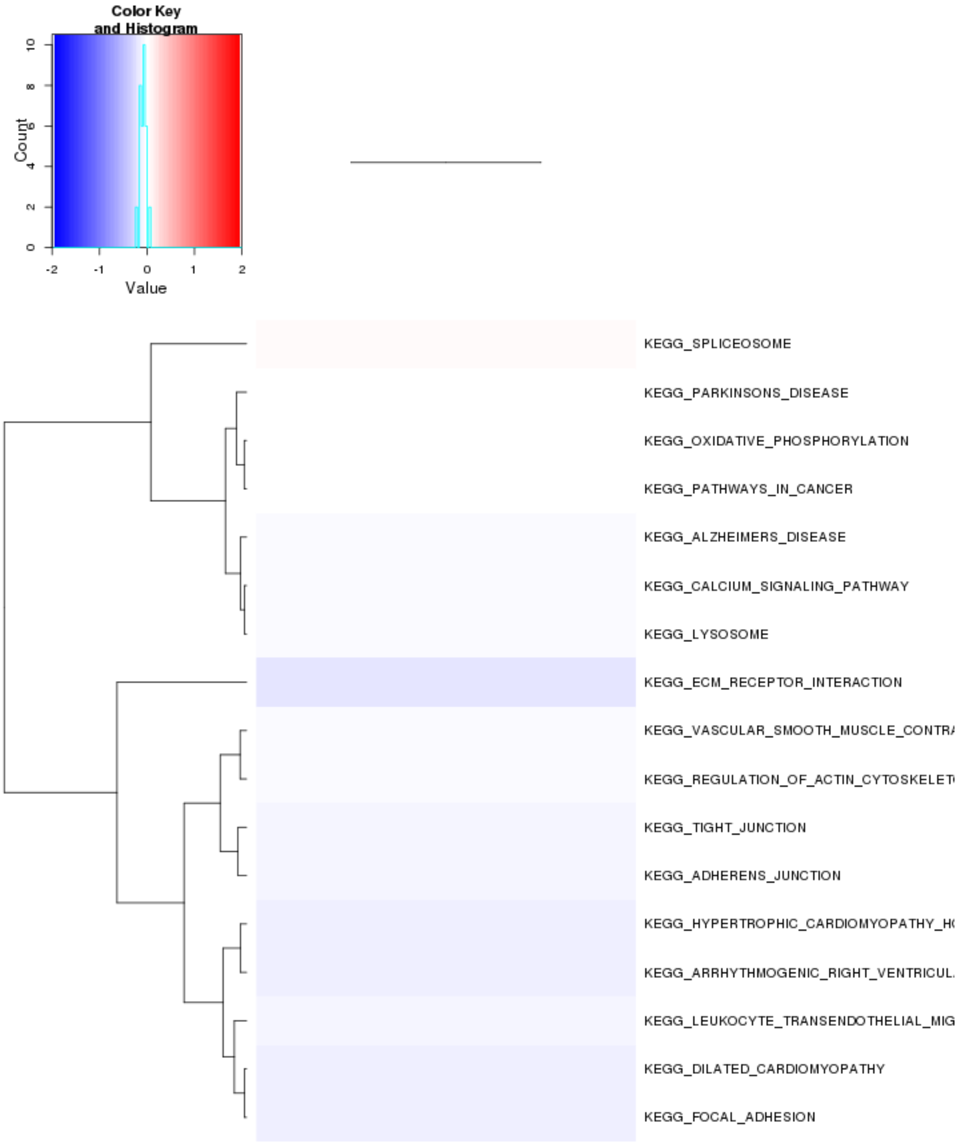
```
## Error in x_ordered[1:50, ]: subscript out of bounds
```



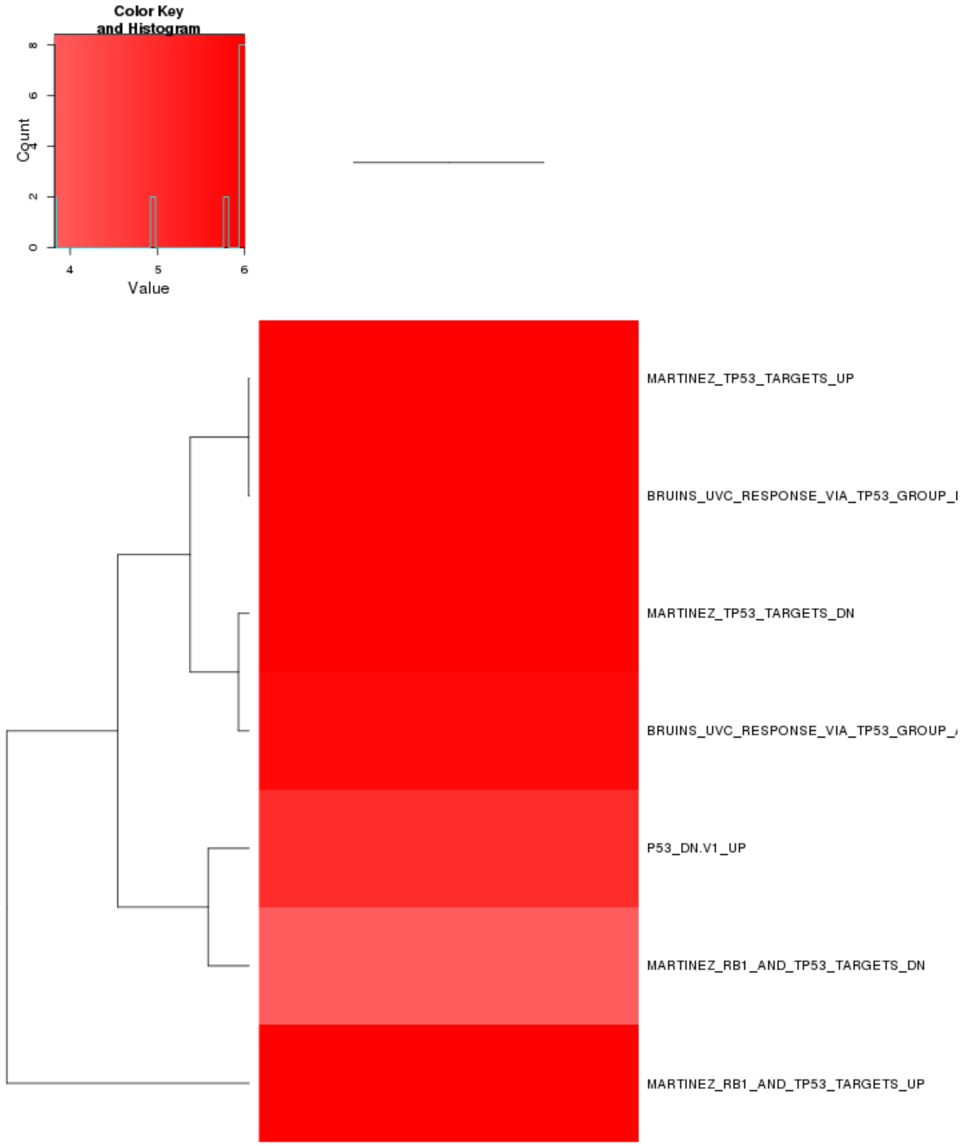
Kegg enrichment:


Color Key
and Histogram
Count
0
5
10
15
4
5
6
Value
KEGG_LYSOSOME
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRA
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_H
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_ADHERENS_JUNCTION
KEGG_SPLICEOSOME
KEGG_CALCIUM_SIGNALING_PATHWAY
KEGG_PARKINSONS_DISEASE
KEGG_PATHWAYS_IN_CANCER
KEGG_ALZHEIMERS_DISEASE
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICUL
KEGG_DILATED_CARDIOMYOPATHY
KEGG_TIGHT_JUNCTION
KEGG_FOCAL_ADHESION
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_REGULATION_OF_ACTIN_CYTOSKELET
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIG

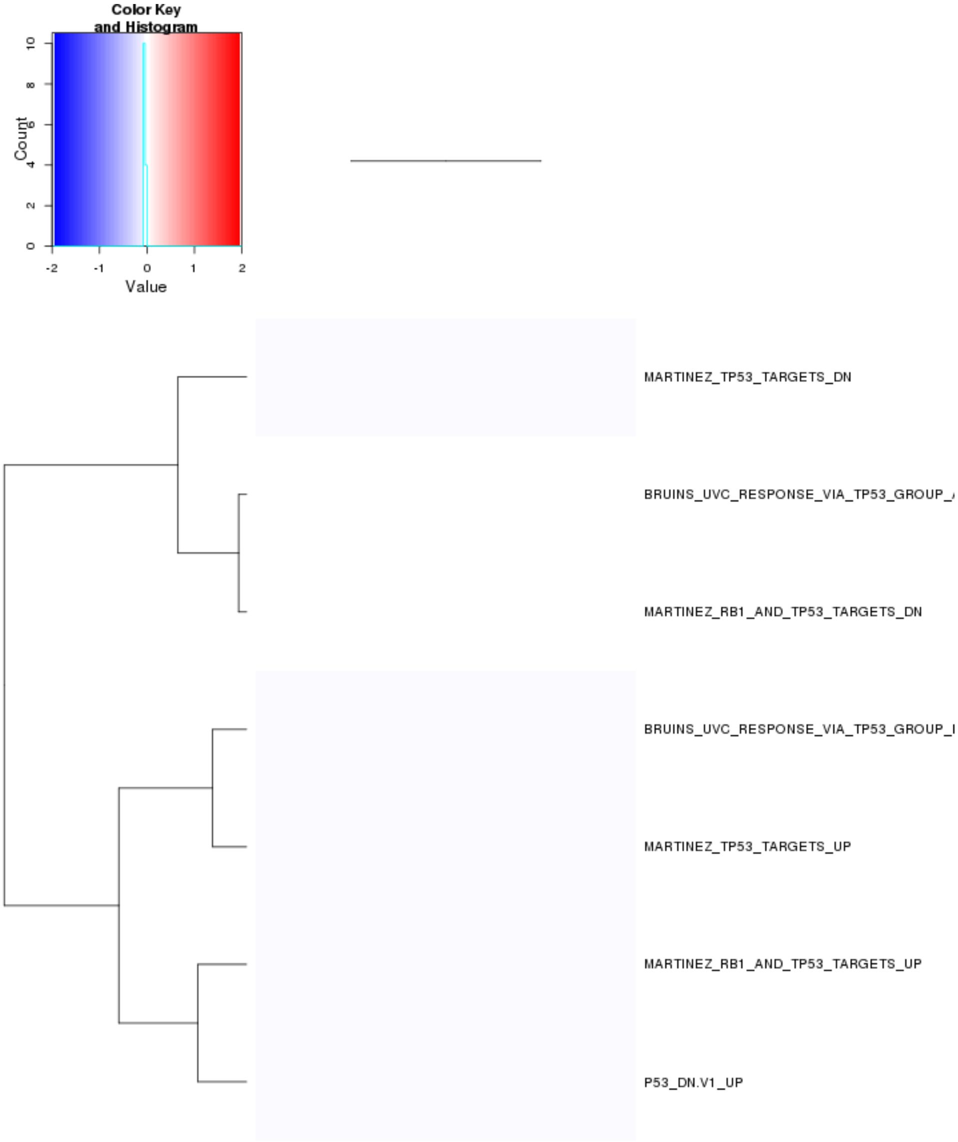
Kegg zscore:



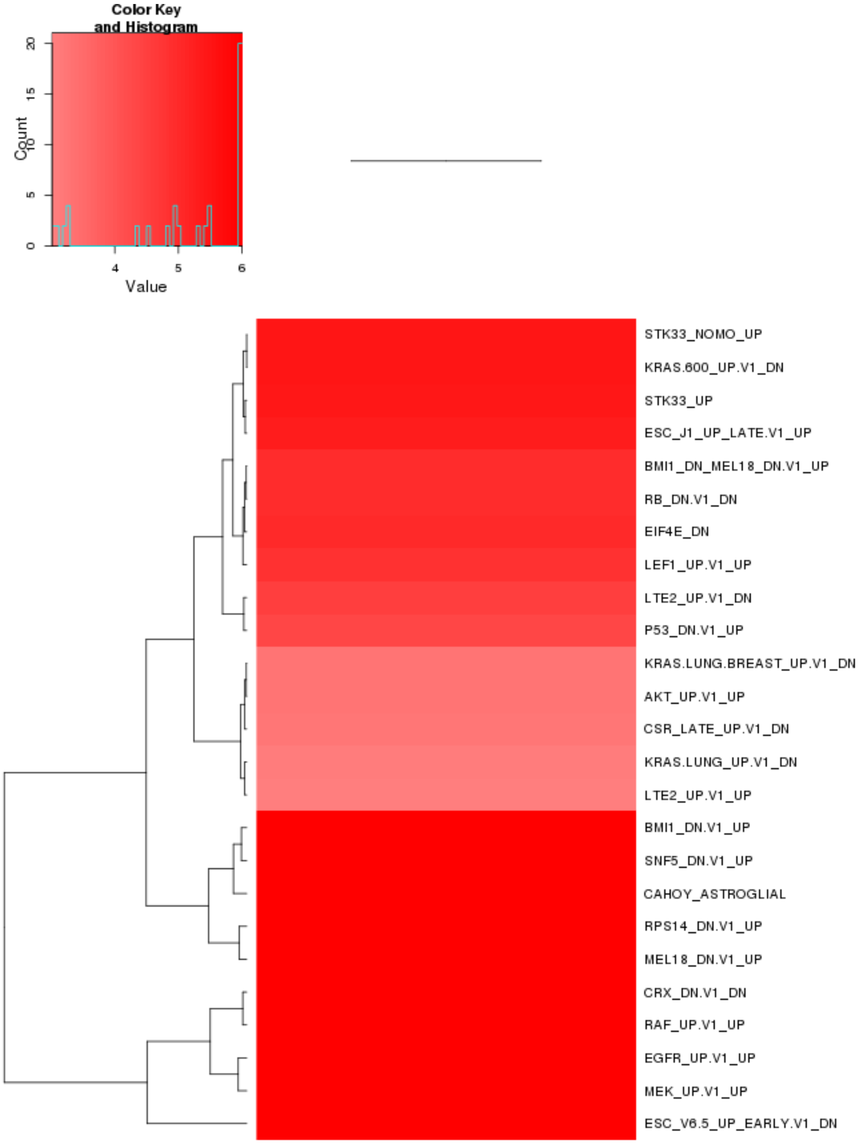
p53 enrichment:


Color Key
and Histogram
Count
0
2
4
6
8
4
5
6
Value
MARTINEZ_TP53_TARGETS_UP
BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_I
MARTINEZ_TP53_TARGETS_DN
BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_
P53_DN.V1_UP
MARTINEZ_RB1_AND_TP53_TARGETS_DN
MARTINEZ_RB1_AND_TP53_TARGETS_UP

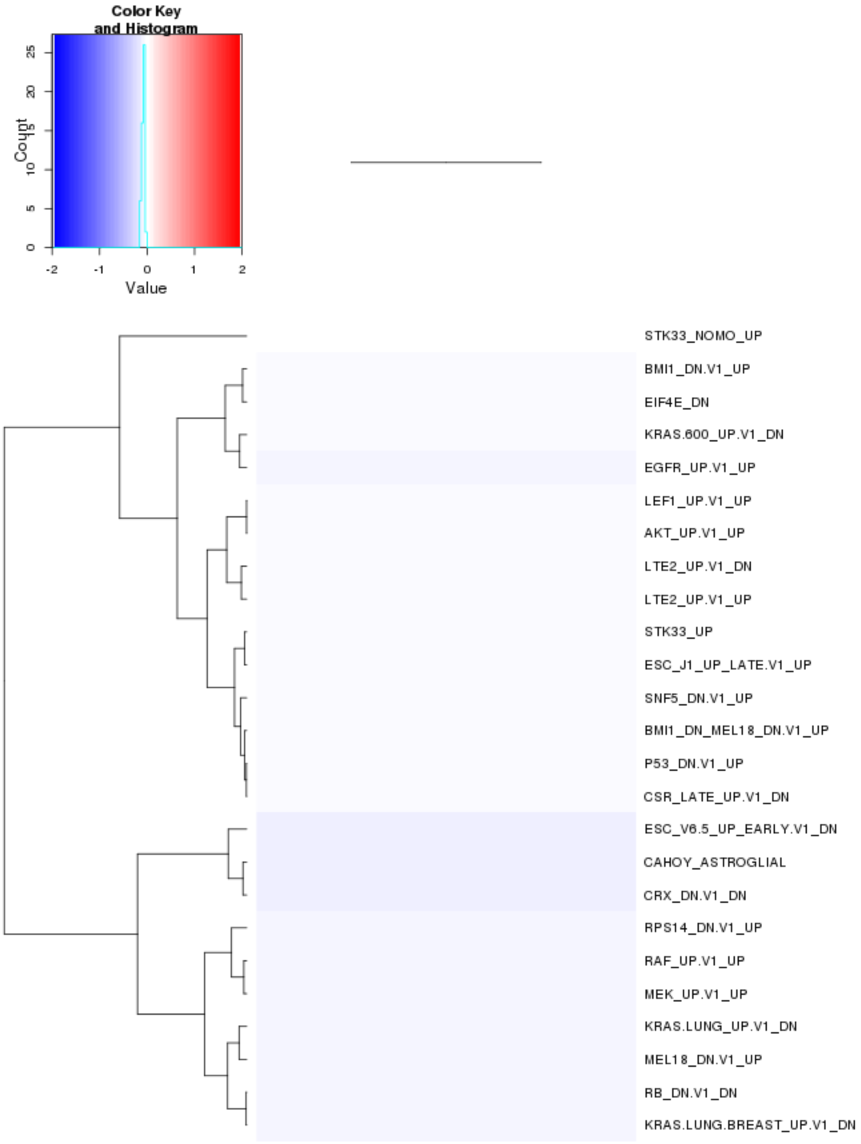
p53 zscore:



Oncogene enrichment:

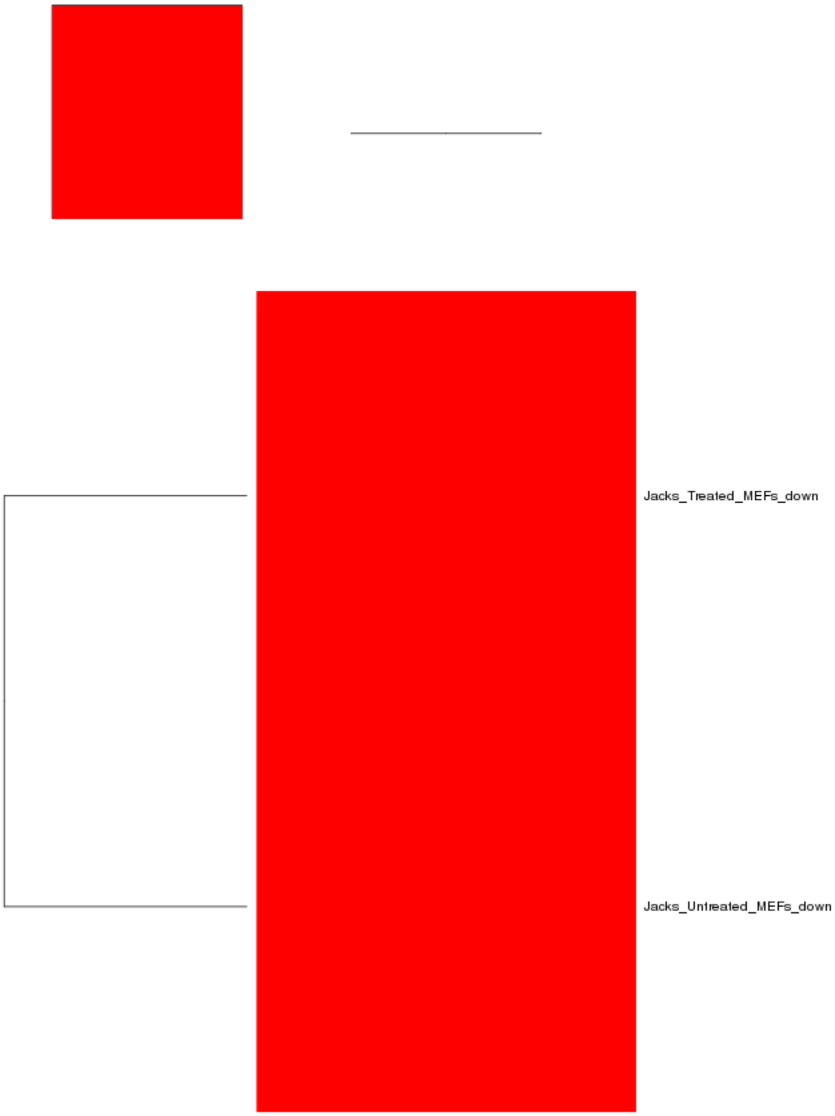


Oncogene zscore:

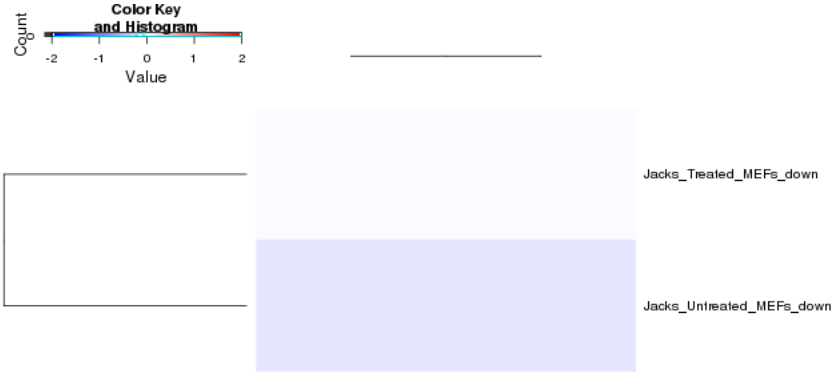


Jacks enrichment

```
## Error in (function (side, at = NULL, labels = TRUE, tick = TRUE, line = NA, : no locations are finite
```

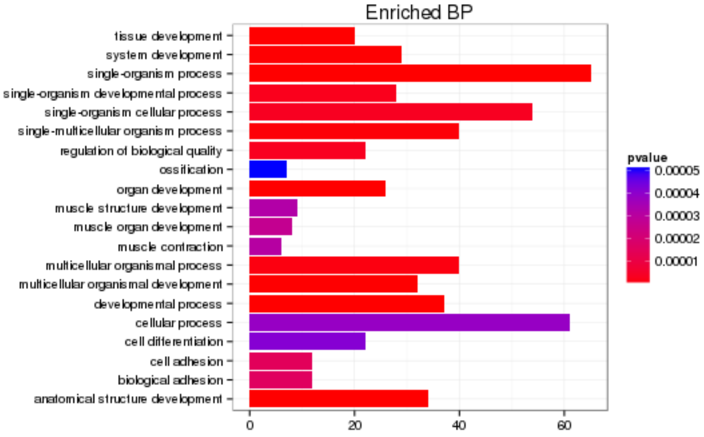


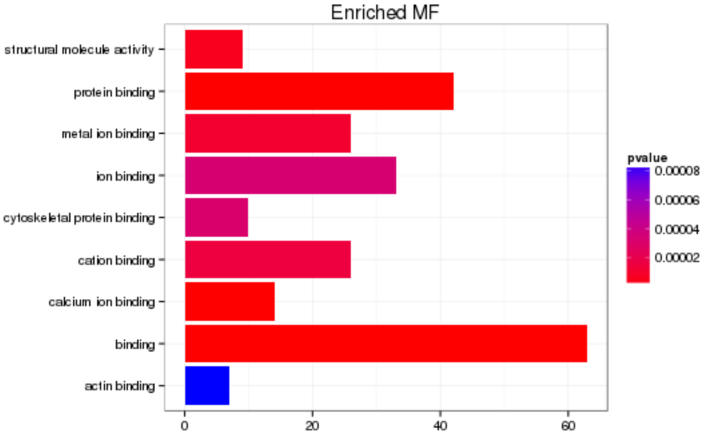
Jacks zscore

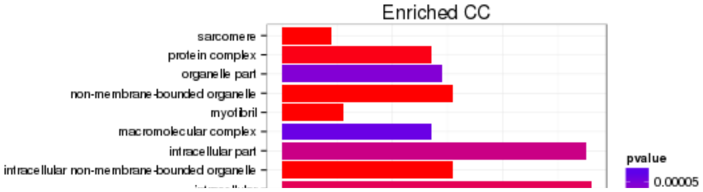


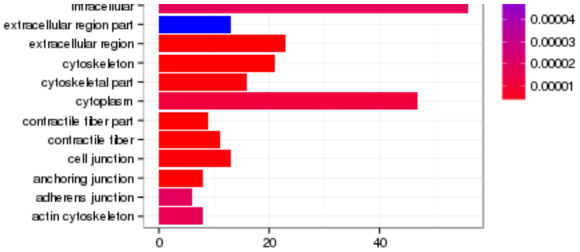
GO enrichment

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

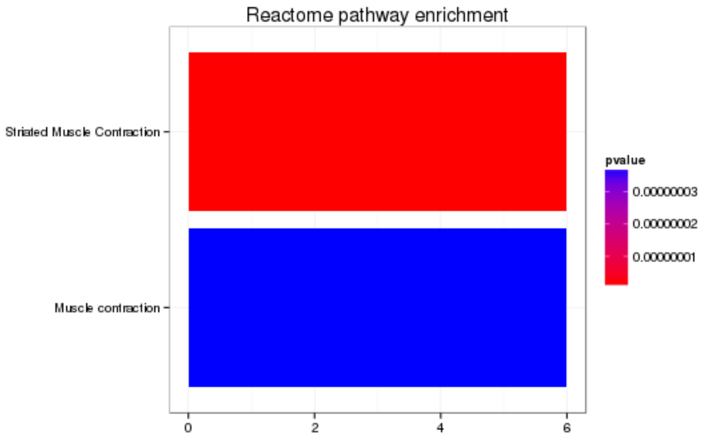

Enriched BP
tissue development
system development
single-organism process
single-organism developmental process
single-organism cellular process
single-multicellular organism process
regulation of biological quality
ossification
organ development
muscle structure development
muscle organ development
muscle contraction
multicellular organismal process
multicellular organismal development
developmental process
cellular process
cell differentiation
cell adhesion
biological adhesion
anatomical structure development
0
20
40
60
pvalue
0.00005
0.00004
0.00003
0.00002
0.00001


Enriched MF
structural molecule activity
protein binding
metal ion binding
ion binding
cytoskeletal protein binding
cation binding
calcium ion binding
binding
actin binding
0
20
40
60
pvalue
0.00008
0.00006
0.00004
0.00002


Enriched CC
sarcomere
protein complex
organelle part
non-membrane-bounded organelle
myofibril
macromolecular complex
intracellular part
intracellular non-membrane-bounded organelle
pvalue
0.00005



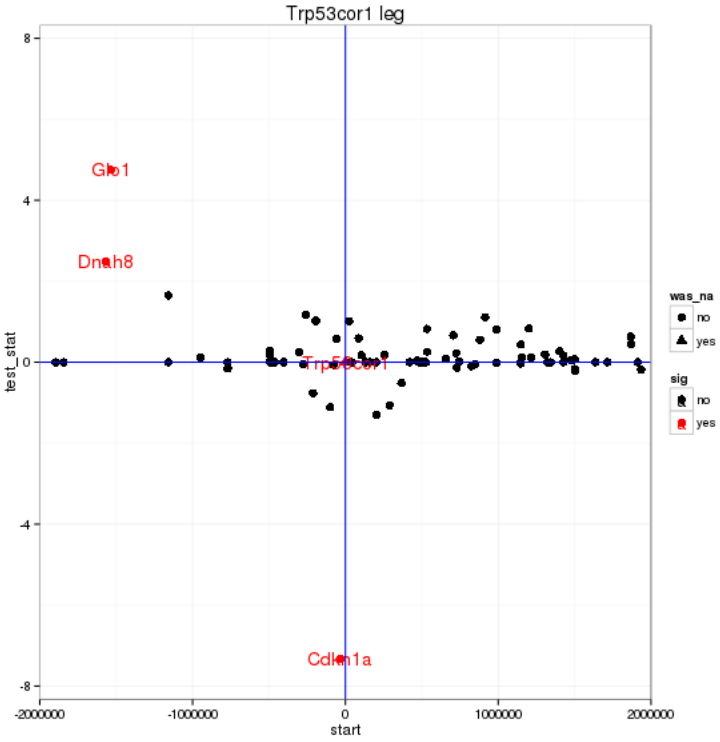
```
## Error in unit(tic_pos.c, "mm"): 'x' and 'units' must have length > 0
```



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 genes significantly regulated in a region this size is: 0.02



Notes

Samples used are:

	11
1	JR878
2	JR880
3	JR881
4	JR882
5	JR883
6	lincp21_Leg_KO4

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	ir
1	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR878/abundances.cxb	WT	0	WT_0	48224900.00	44016600.00	
2	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR880/abundances.cxb	WT	1	WT_1	52725300.00	44016600.00	
3	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR881/abundances.cxb	WT	2	WT_2	43230900.00	44016600.00	
4	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR882/abundances.cxb	Trp53cor1	0	Trp53cor1_0	61630100.00	44016600.00	
5	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR883/abundances.cxb	Trp53cor1	1	Trp53cor1_1	53017900.00	44016600.00	
6	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/lincp21_Leg_KO4/abundances.cxb	Trp53cor1	2	Trp53cor1_2	20607100.00	44016600.00	

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] GO.db_2.10.1                     
##  [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_1.8-2                       
## [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_2.14.2                    
## [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_0.3.1
## [36] BiocGenerics_0.8.0
## [37] knitr_1.7
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17.1         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_1.0            Formula_1.1-2
## [13] gdata_2.13.3           GenomicFeatures_1.14.5 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_1.1-4
## [28] munsell_0.4.2          org.Hs.eg.db_2.10.1    proto_0.3-10
## [31] qvalue_1.36.0          Rcpp_0.11.3            RCurl_1.95-4.3
## [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,Trp53cor1 -o /n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/diff/Trp53cor1_E14.5_
## 2
## 3
## 4
## 5
```

Trp53cor1 KO vs WT (liver)

This file shows the wt-v-ko comparison for Trp53cor1.

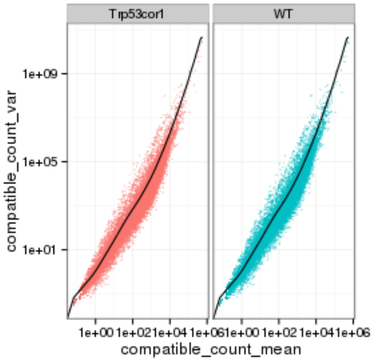
Cuff overview:

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

QC

Dispersion

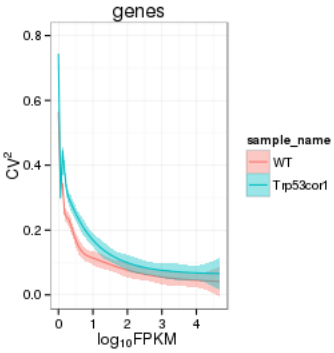
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



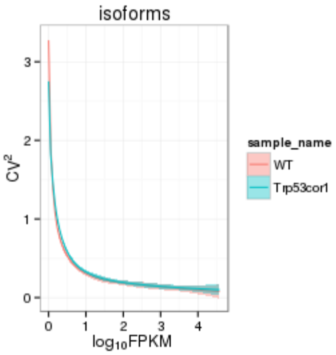
Cross-replicate variability (fpkmSCVplot)

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

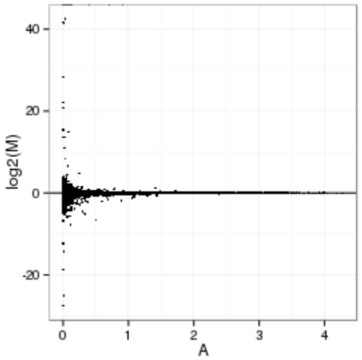
Genes:



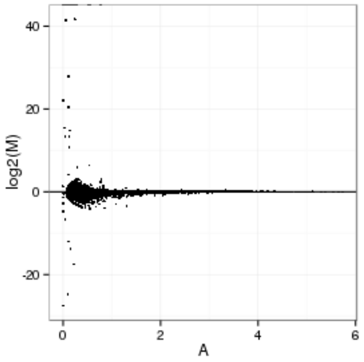
Isoforms:



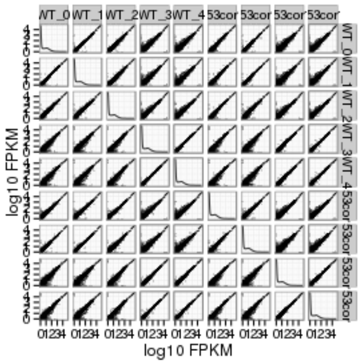
MvA plot



MvA plot counts



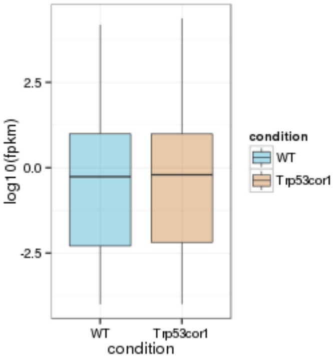
Scatterplot matrix



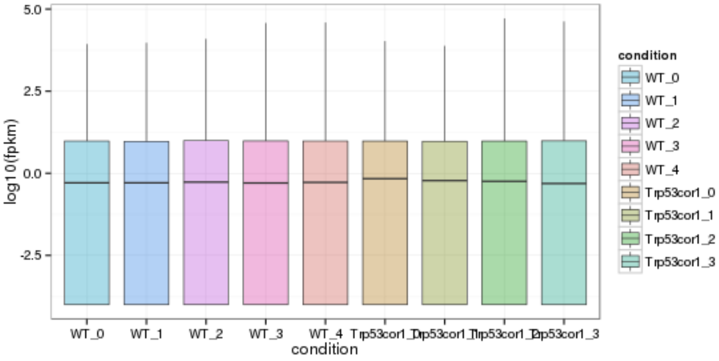
Distributions

Boxplots

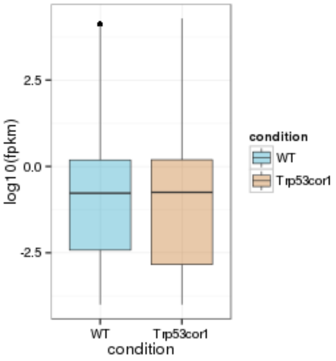
Boxplot (genes)



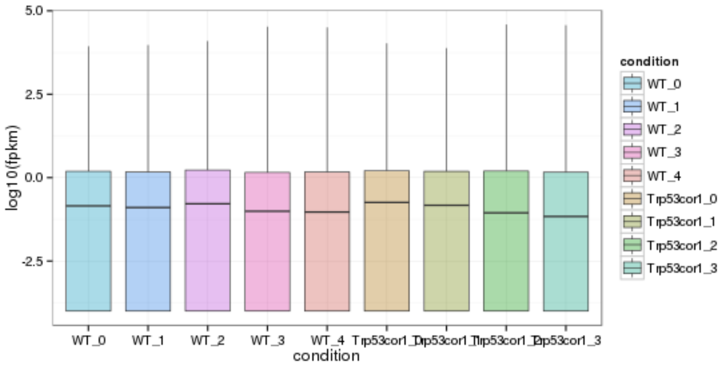
Boxplot (genes, replicates)



Boxplot (isoforms)

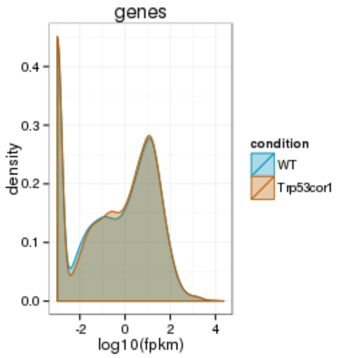


Boxplot (isoforms, replicates)

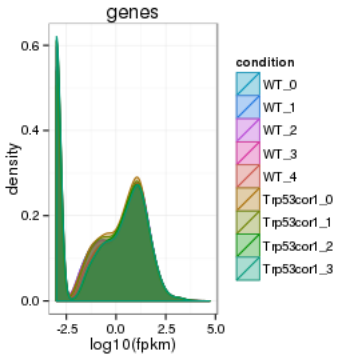


Density

Density (genes)

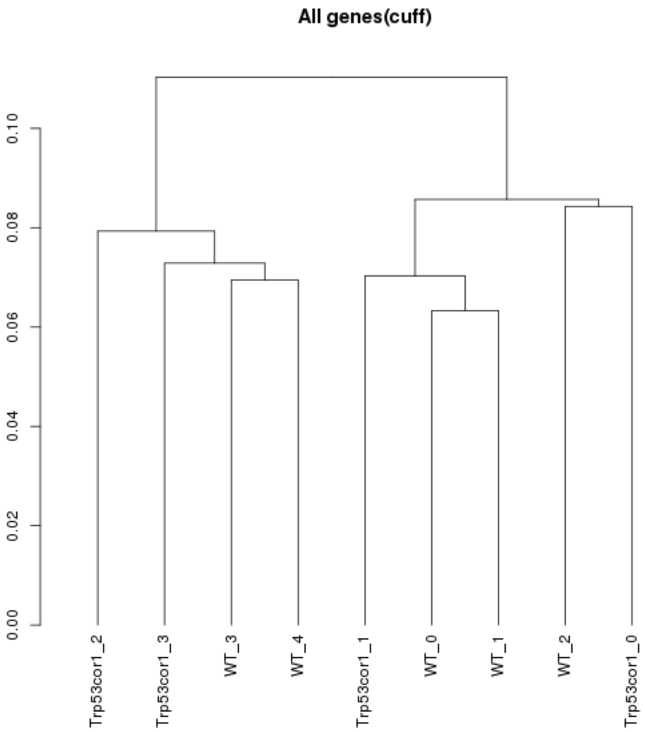


Density (genes, replicates)



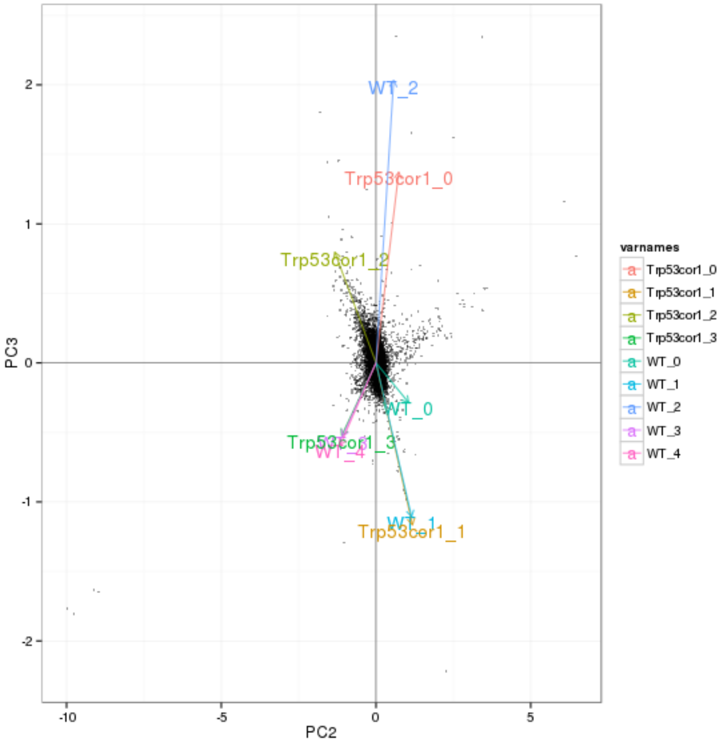
Clustering

Replicate Clusters

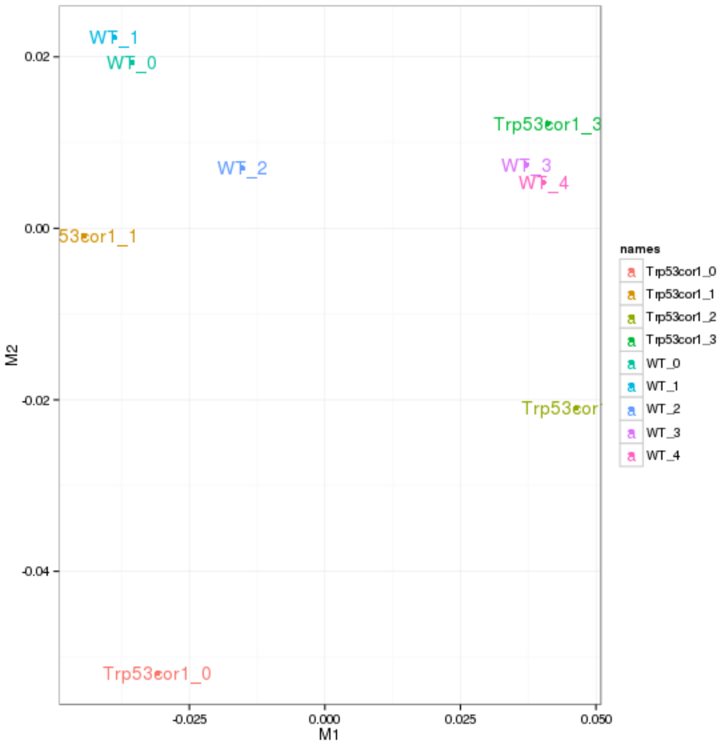


```
## NULL
```

PCA (genes)

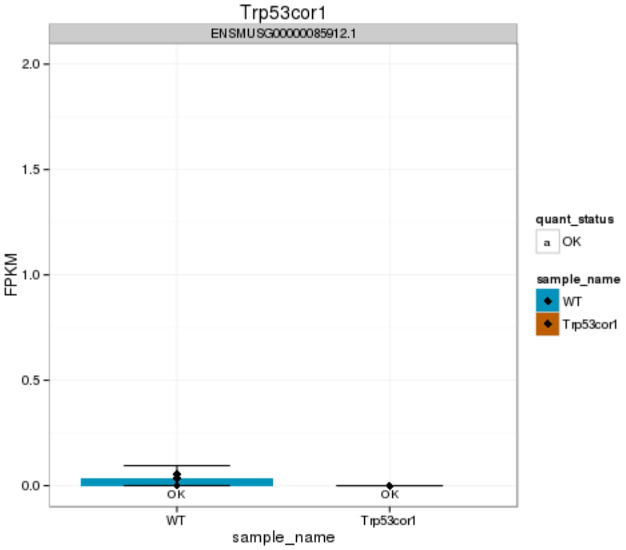


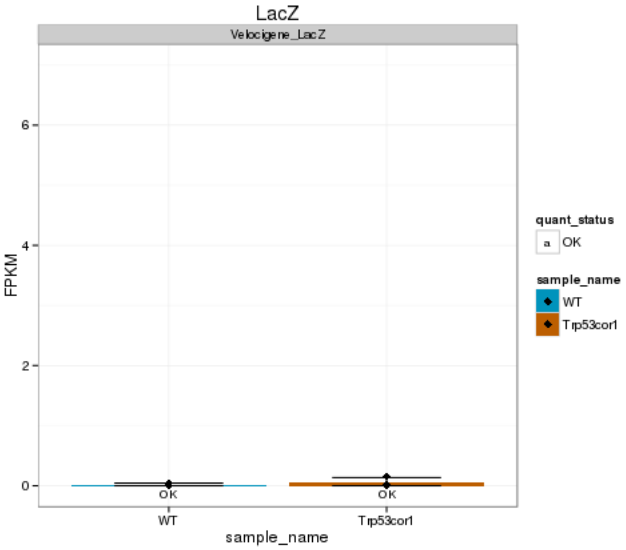
MDS (genes)



KO assessment

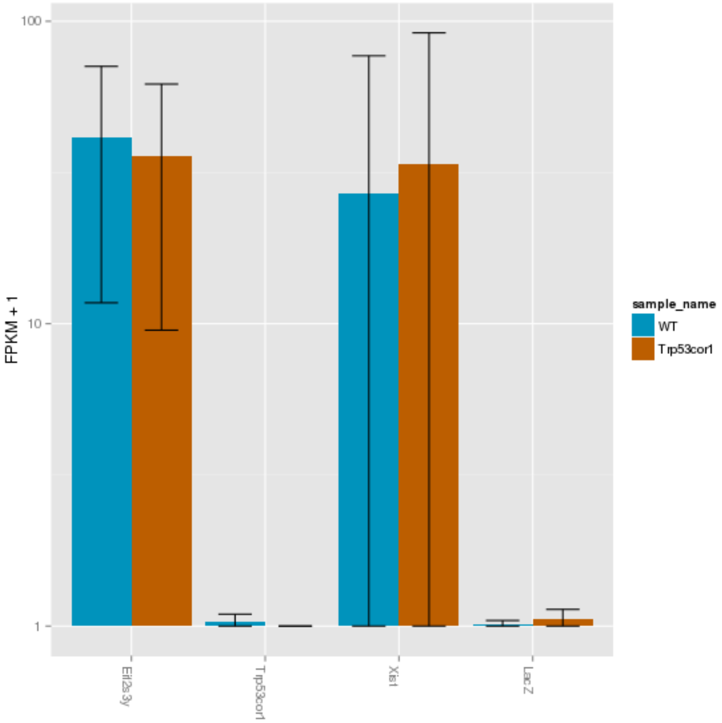
Endogenous lncRNA expression



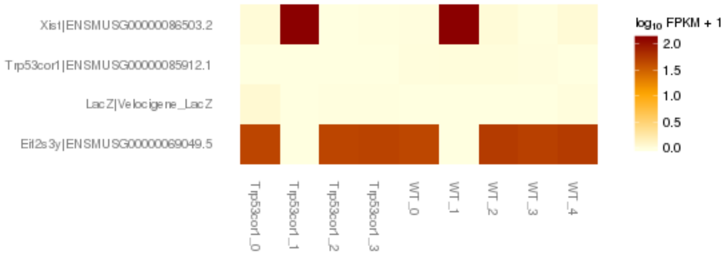


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

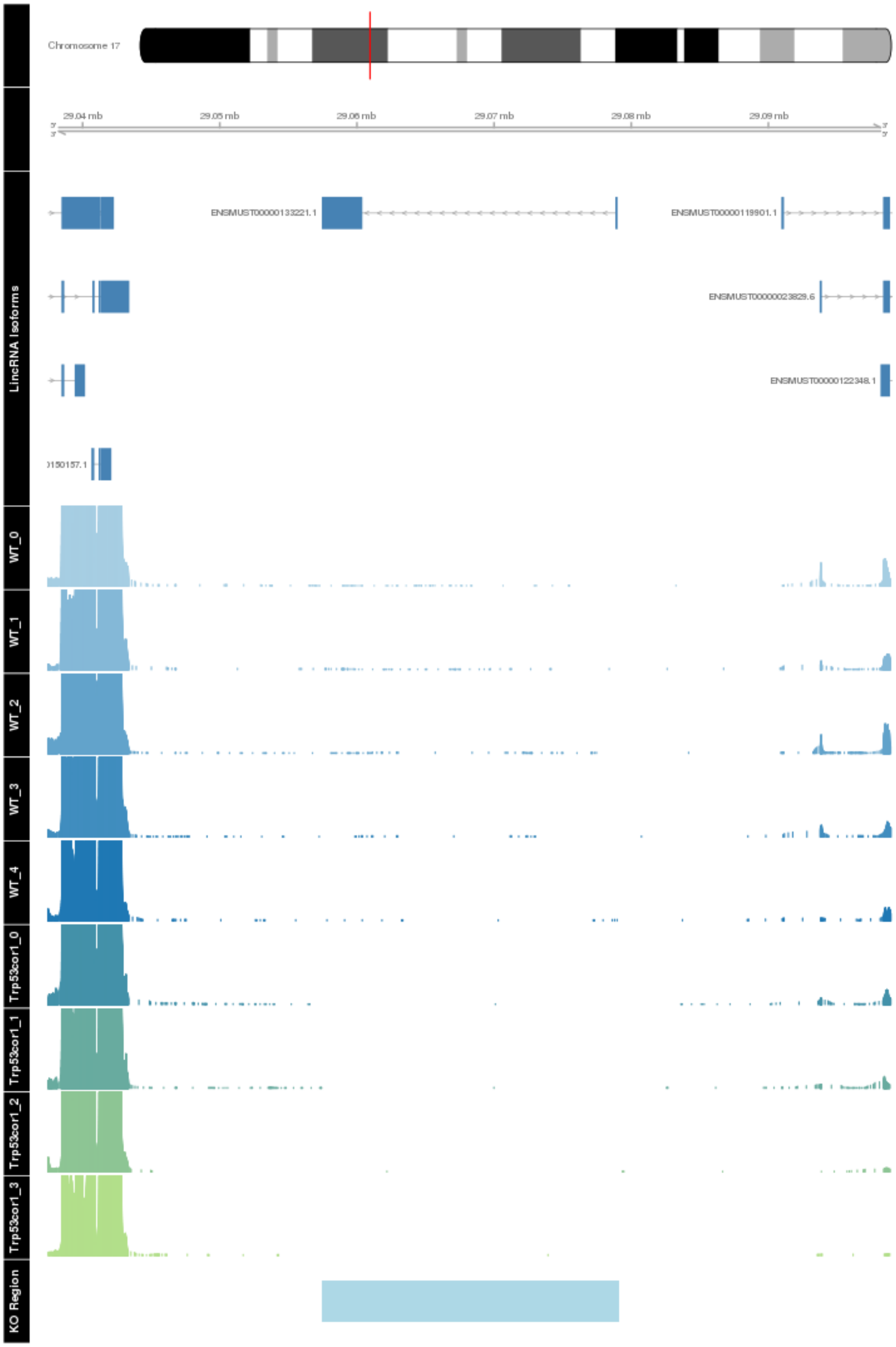
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization



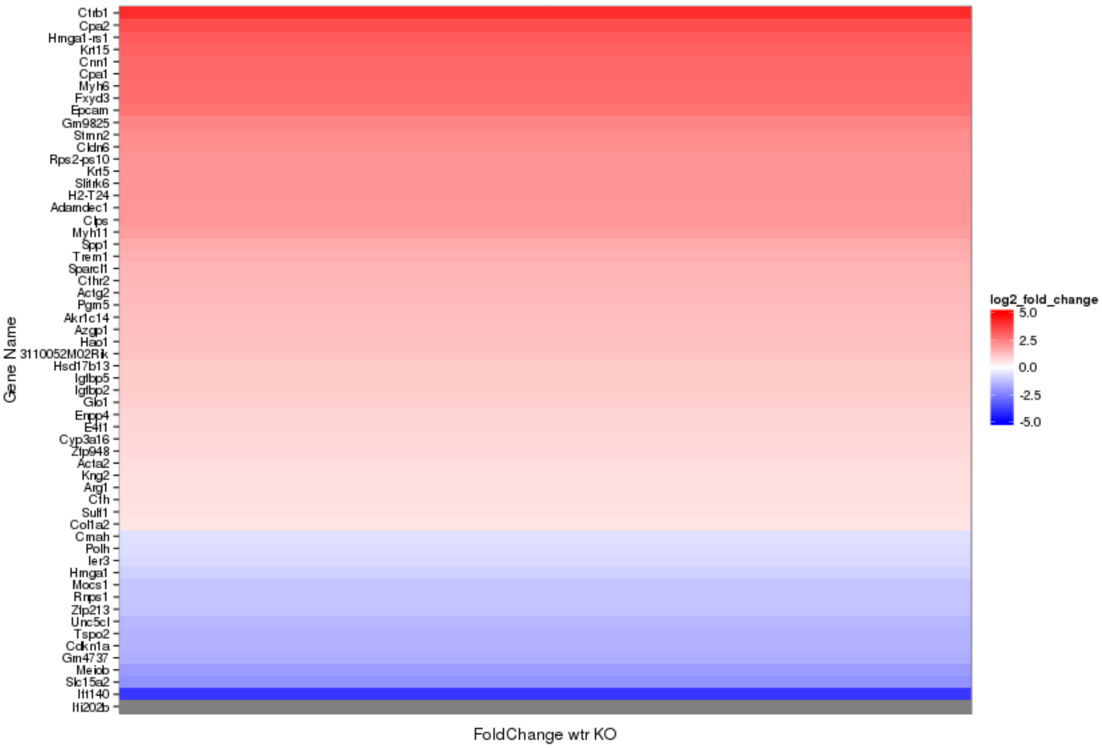
Differential Analysis

Differential Genes

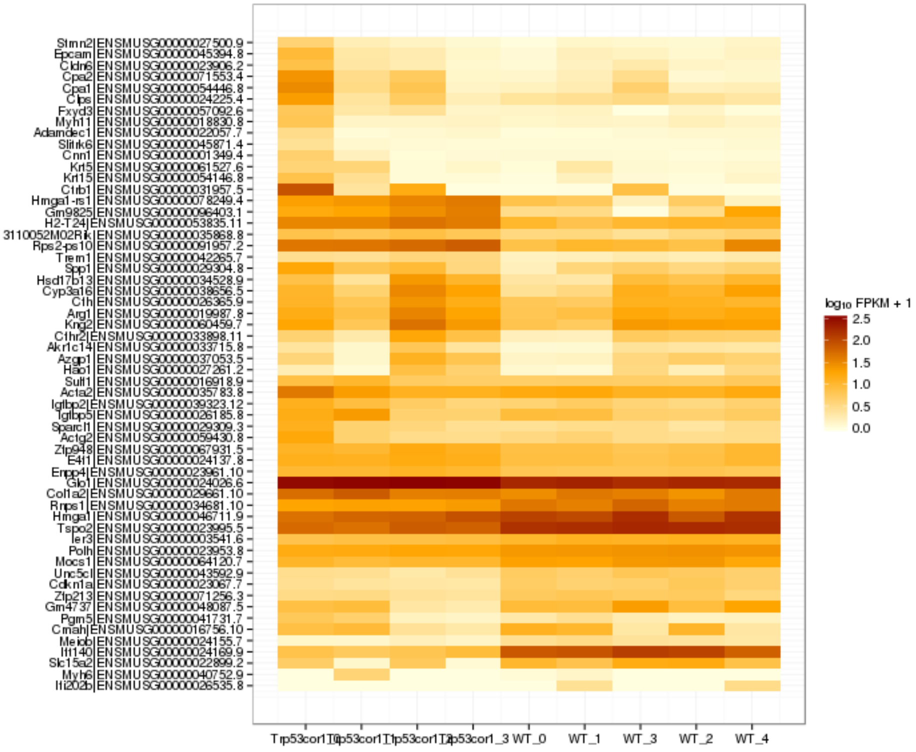
There are 58 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Cnn1
2	Ier3
3	Cmah
4	Sulf1
5	Myh11
6	Arg1

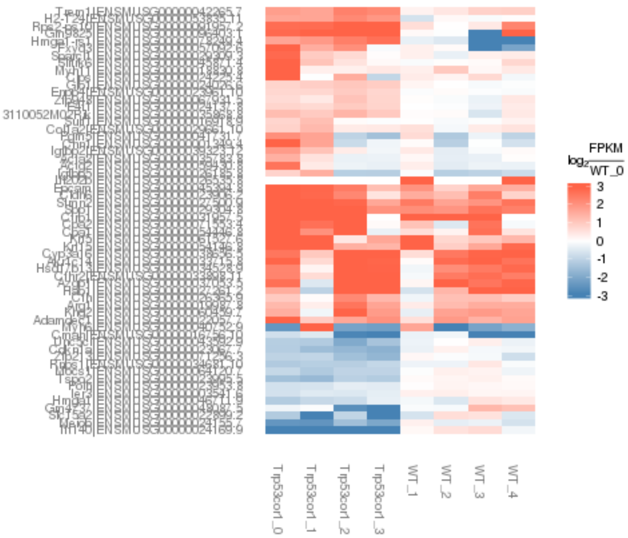
7 Adamdec1
8 Slc15a2
9 Cdkn1a
10 Cldn6
11 Polh
12 Enpp4
13 Tspo2
14 Glo1
15 E4f1
16 Meiob
17 Ift140
18 Clps
19 Igfbp5
20 Cfh
21 Ifi202b
22 Hao1
23 Stmn2
24 Spp1
25 Sparcl1
26 Col1a2
27 Ctrb1
28 Akr1c14
29 Cfhr2
30 Hsd17b13
31 Rnps1
32 Acta2
33 3110052M02Rik
34 Azgp1
35 Cyp3a16
36 Igfbp2
37 Myh6
38 Pgm5
39 Trem1
40 Unc5cl
41 Epcam
42 Slitrk6
43 Hmga1
44 Gm4737
45 H2-T24
46 Krt15
47 Cpa1
48 Fxyd3
49 Actg2
50 Kng2
51 Krt5
52 Mocs1
53 Zfp948
54 Zfp213
55 Cpa2
56 Hmga1-rs1
57 Rps2-ps10
58 Gm9825



Expression heatmap of sigGenes



Foldchange heatmap of sigGenes

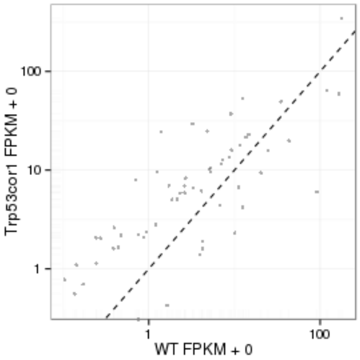


```
## Error in (function (classes, fdef, mtable) : unable to find an inherited method for function 'csFoldChangeHeatma
```

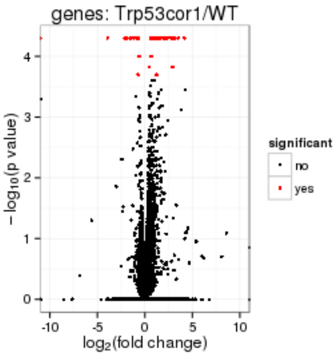
```
## Error in sqliteExecStatement(con, statement, bind.data): RS-DBI driver: (error in statement: near ")": syntax er
```

Expression-level/significance relationship

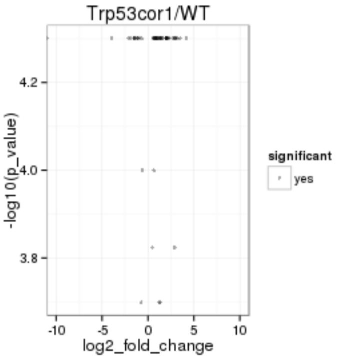
Scatter plot of significant genes only:



Volcano Plot



Volcano plot with significant genes only:



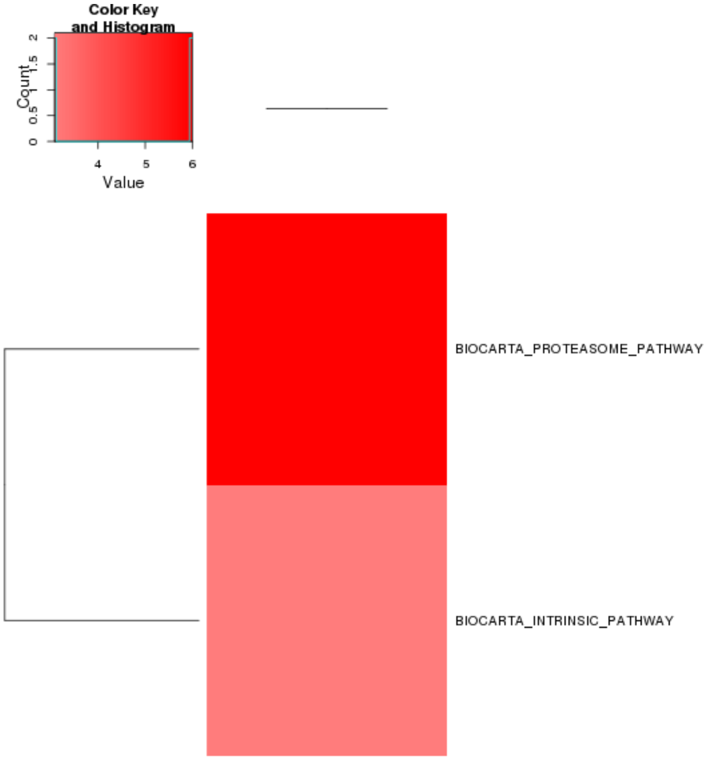
Gene/Pathway Analysis

##

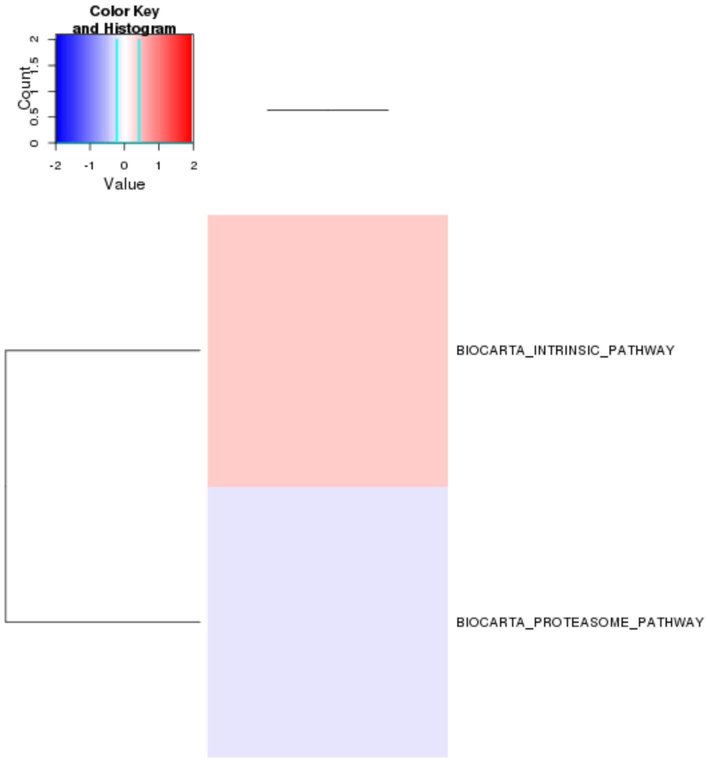
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

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

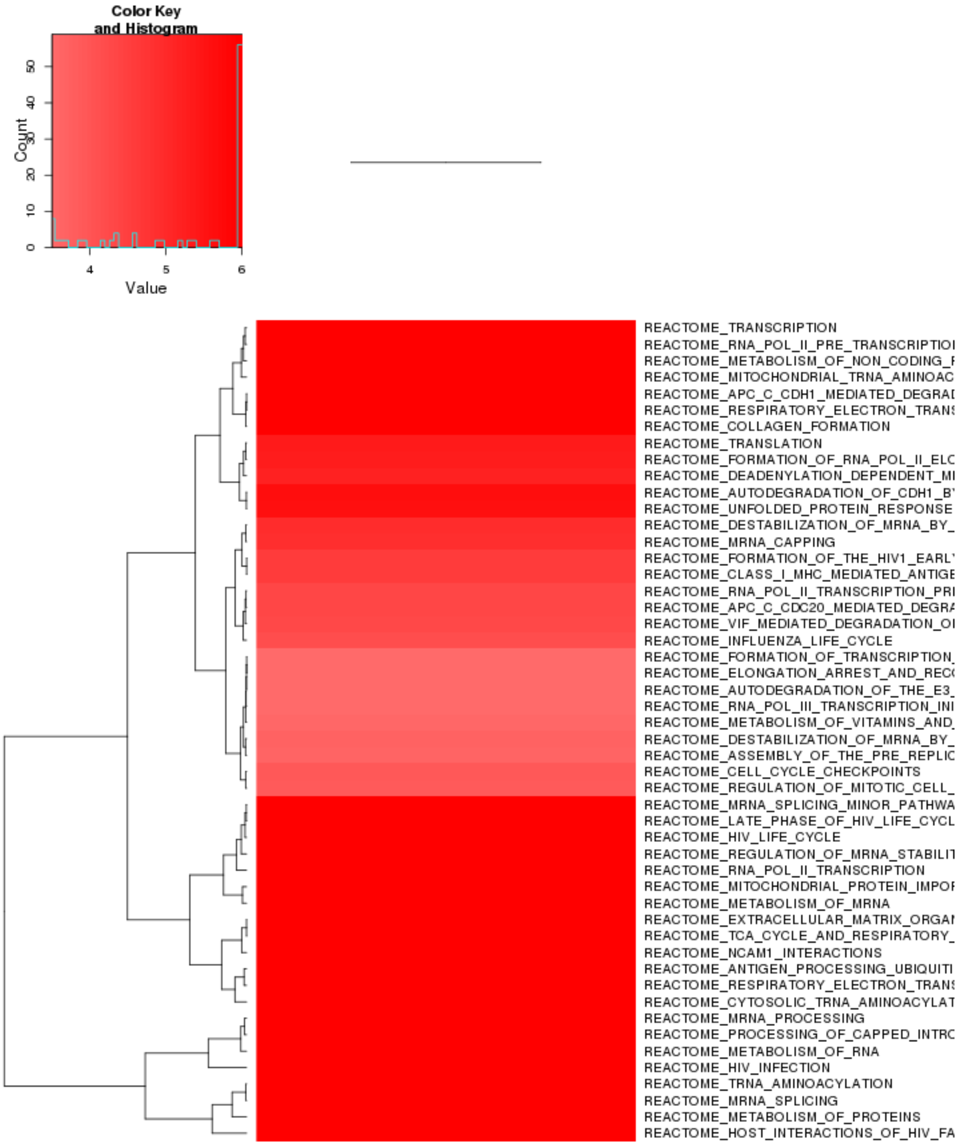
Biocarta enrichment:



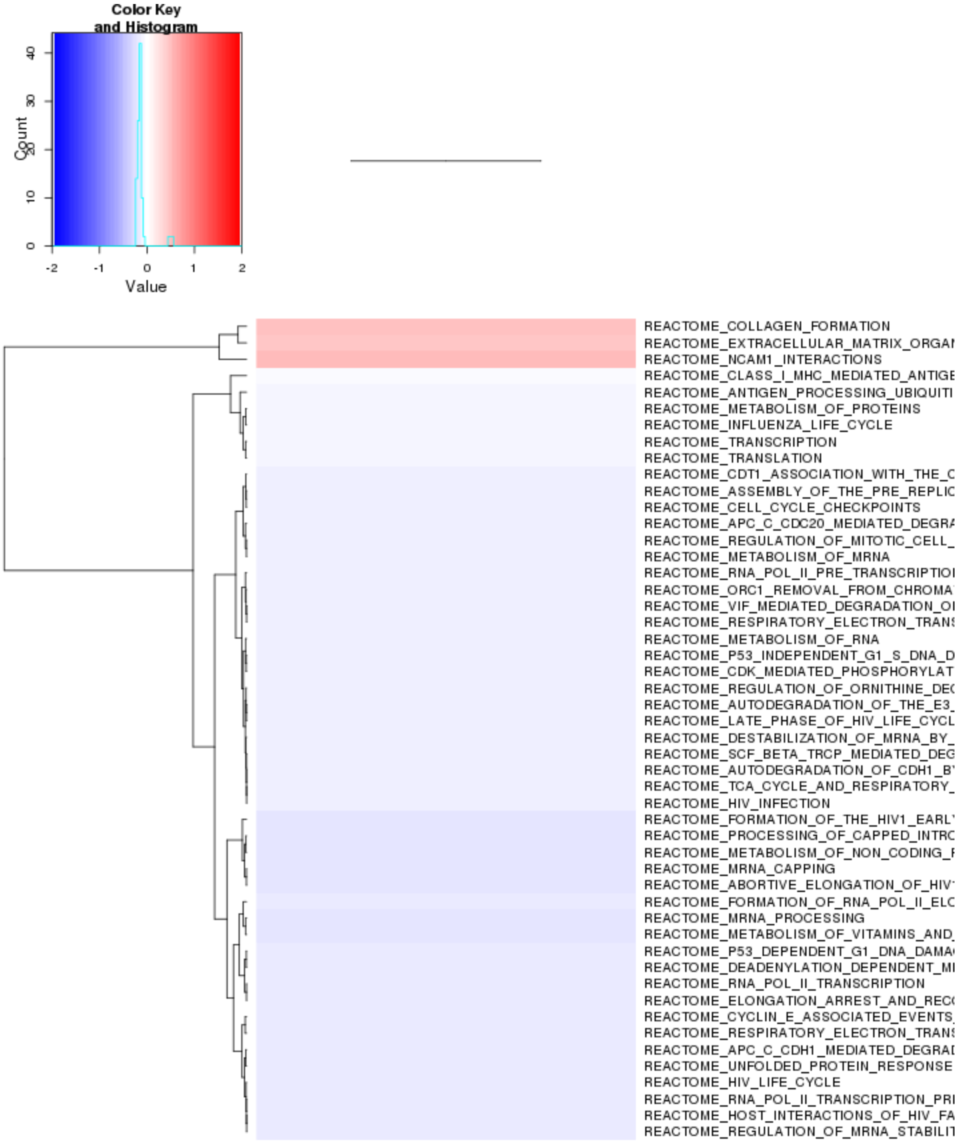
Biocarta zscore:



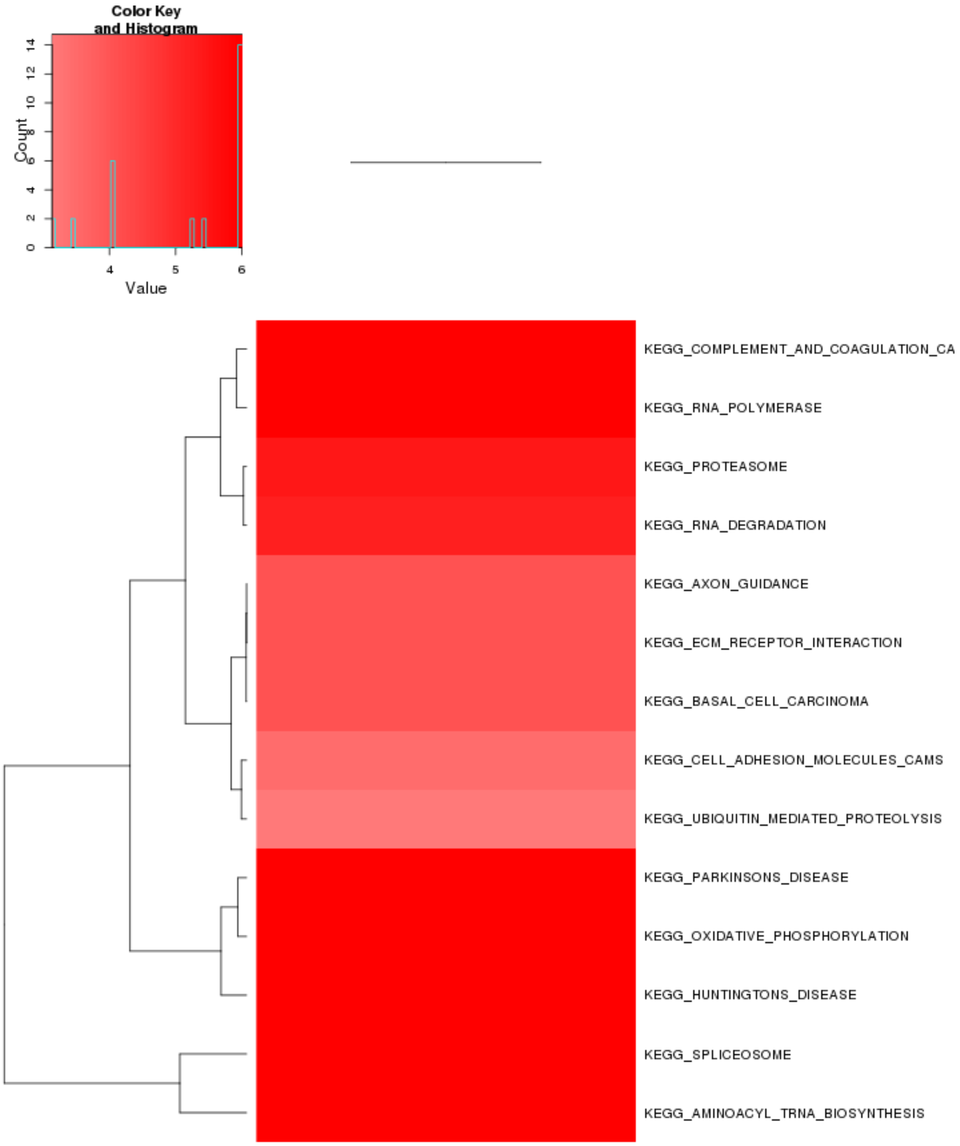
Reactome enrichment:



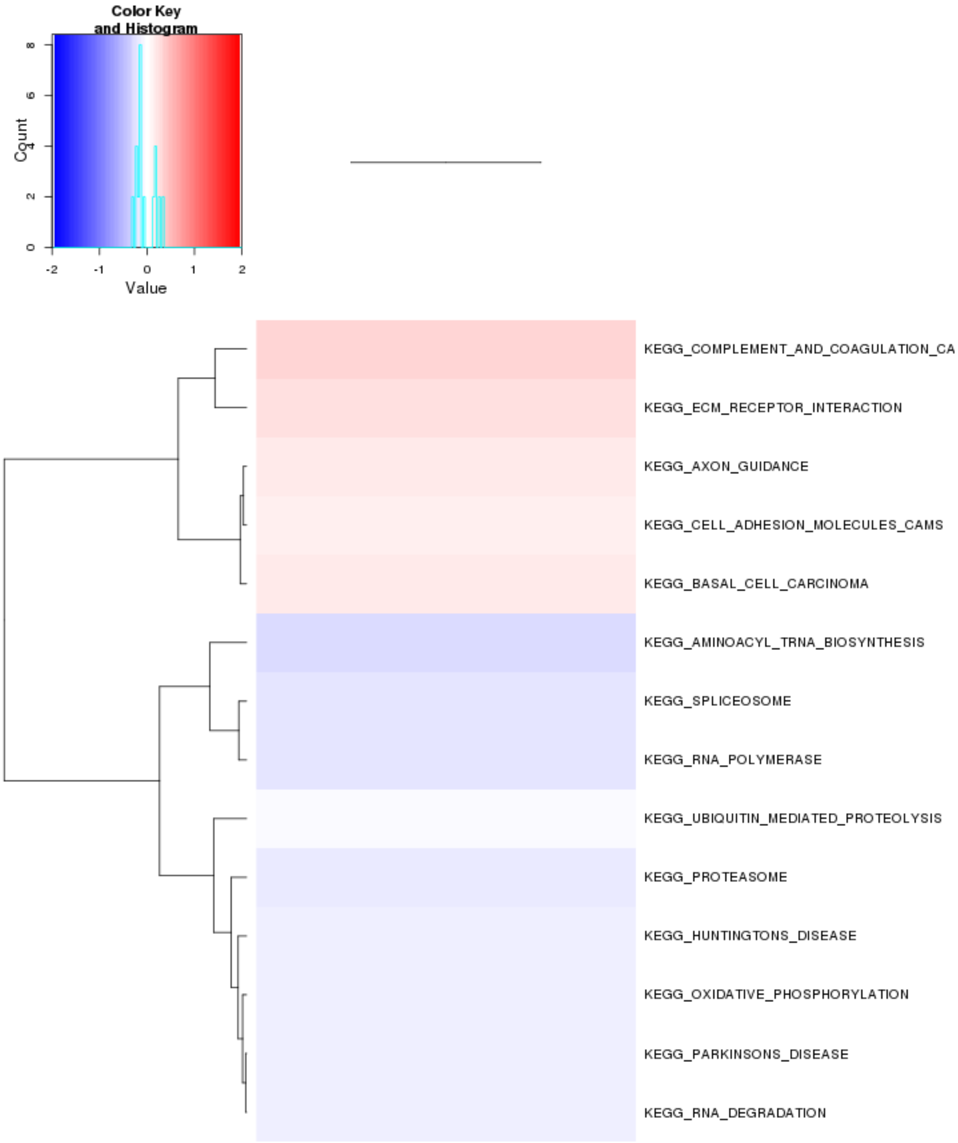
Reactome zscore:



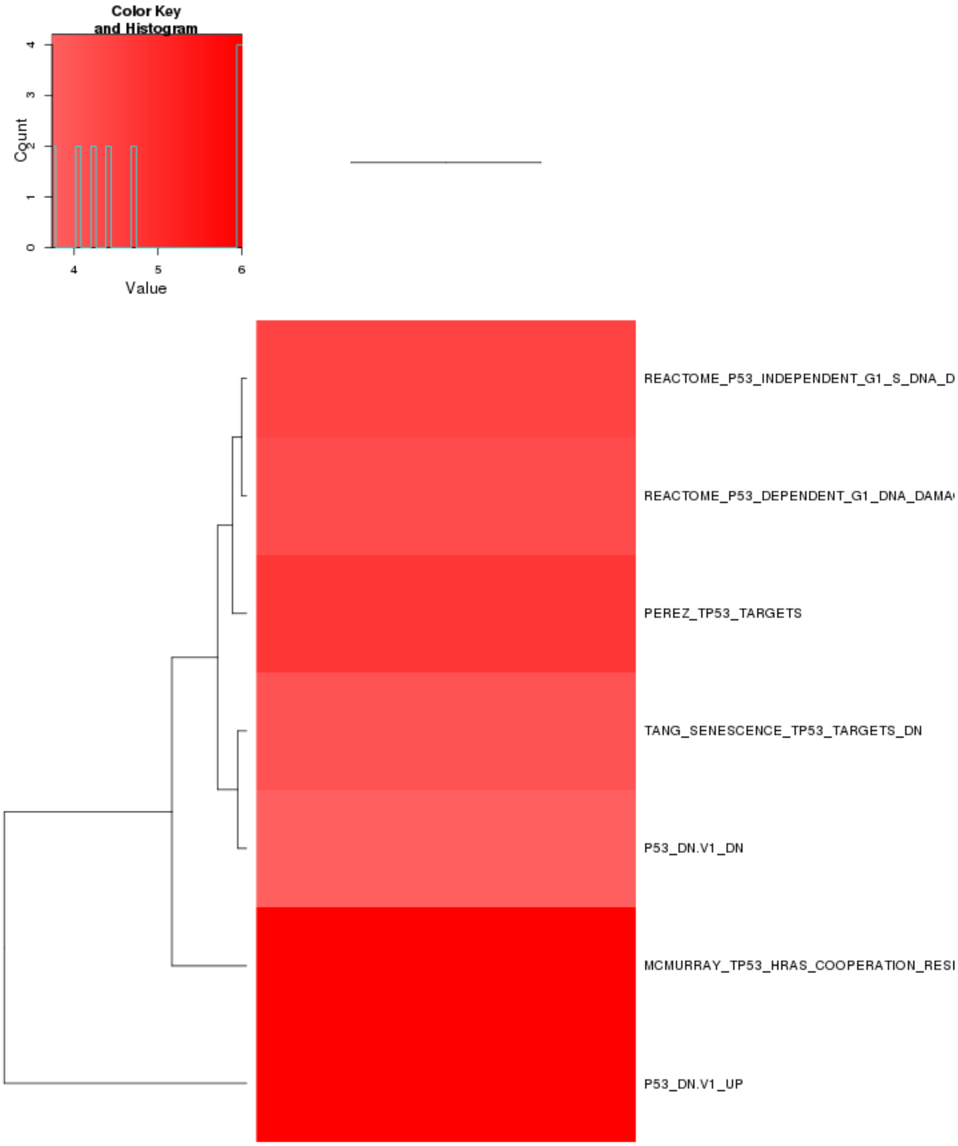
Kegg enrichment:


Color Key
and Histogram
Count
0
2
4
6
8
10
12
14
4
5
6
Value
KEGG_COMPLEMENT_AND_COAGULATION_CA
KEGG_RNA_POLYMERASE
KEGG_PROTEASOME
KEGG_RNA_DEGRADATION
KEGG_AXON_GUIDANCE
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_BASAL_CELL_CARCINOMA
KEGG_CELL_ADHESION_MOLECULES_CAMS
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS
KEGG_PARKINSONS_DISEASE
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_HUNTINGTONS_DISEASE
KEGG_SPLICEOSOME
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS

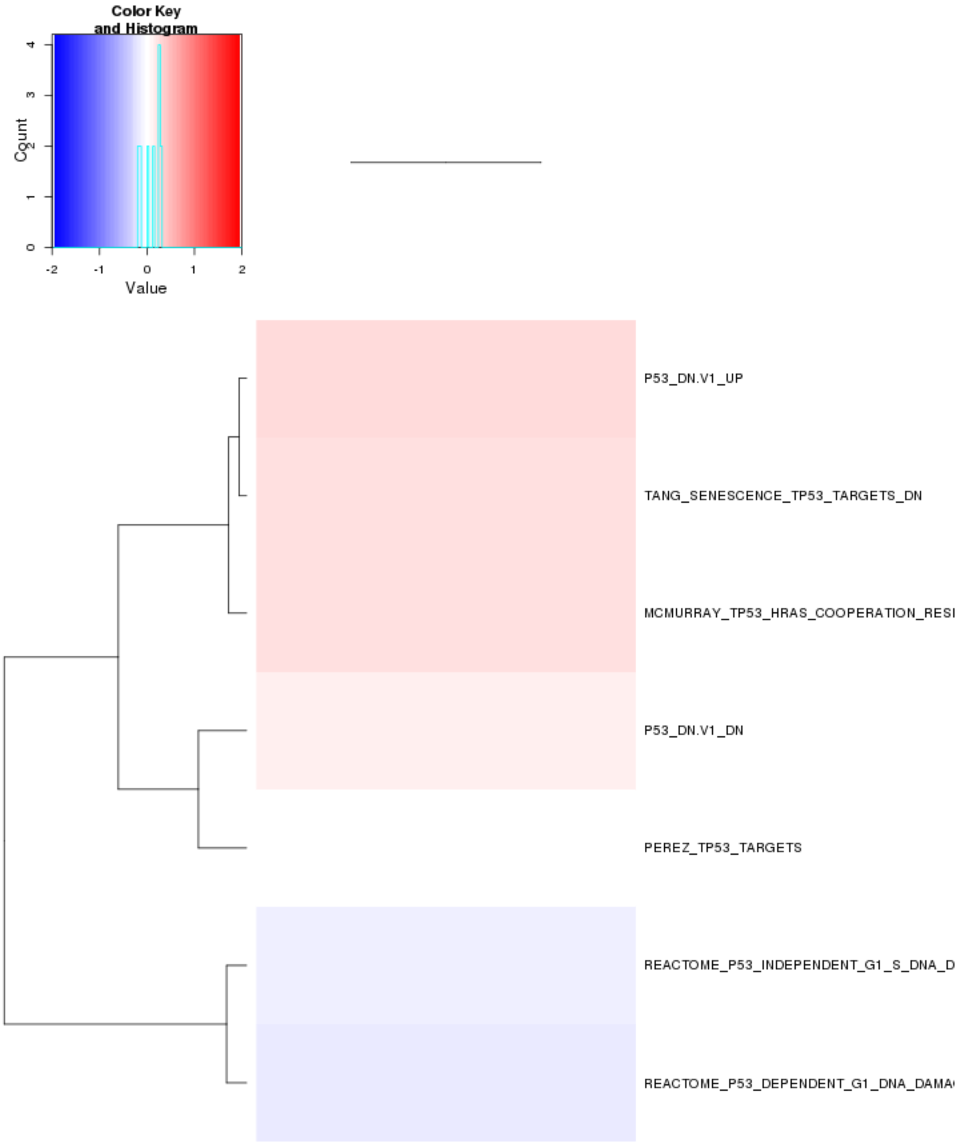
Kegg zscore:



p53 enrichment:

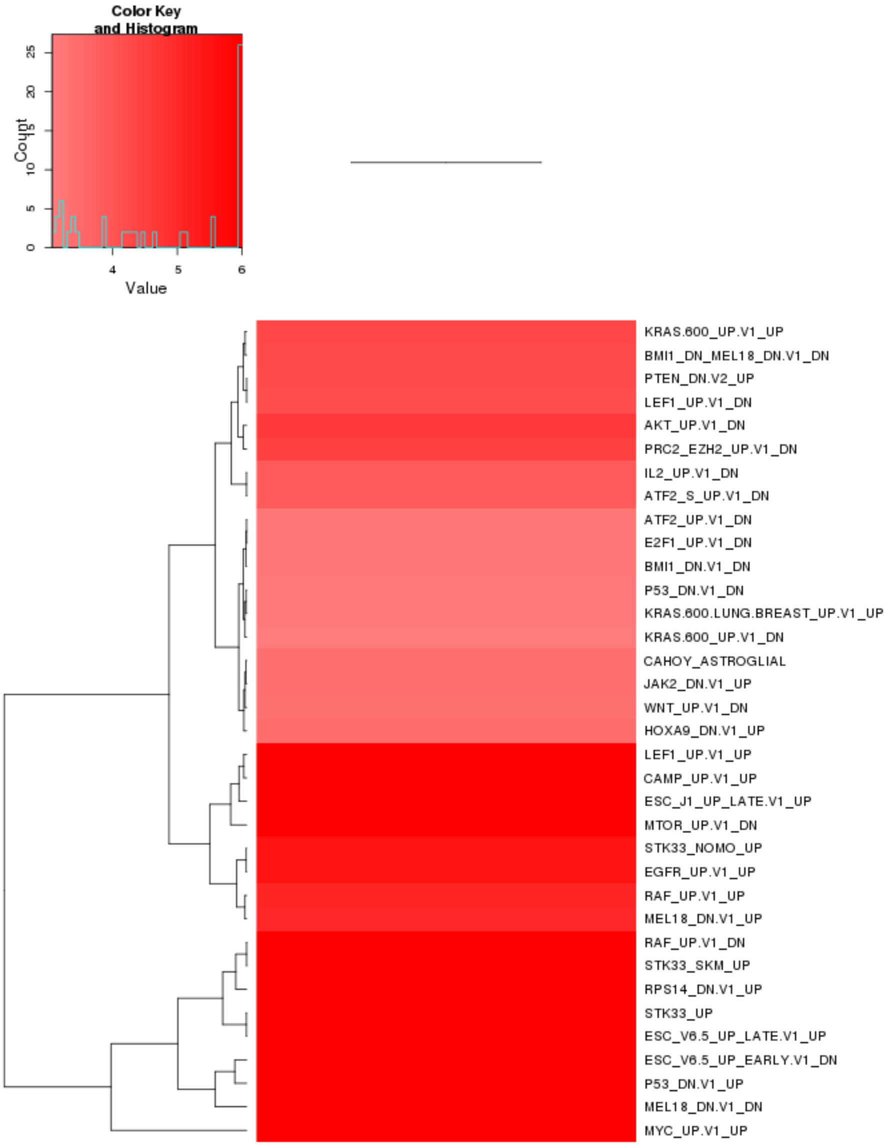

Color Key
and Histogram
Count
0
1
2
3
4
4
5
6
Value
REACTOME_P53_INDEPENDENT_G1_S_DNA_D
REACTOME_P53_DEPENDENT_G1_DNA_DAMA
PEREZ_TP53_TARGETS
TANG_SENESCENCE_TP53_TARGETS_DN
P53_DN.V1_DN
MCMURRAY_TP53_HRAS_COOPERATION_RESI
P53_DN.V1_UP

p53 zscore:



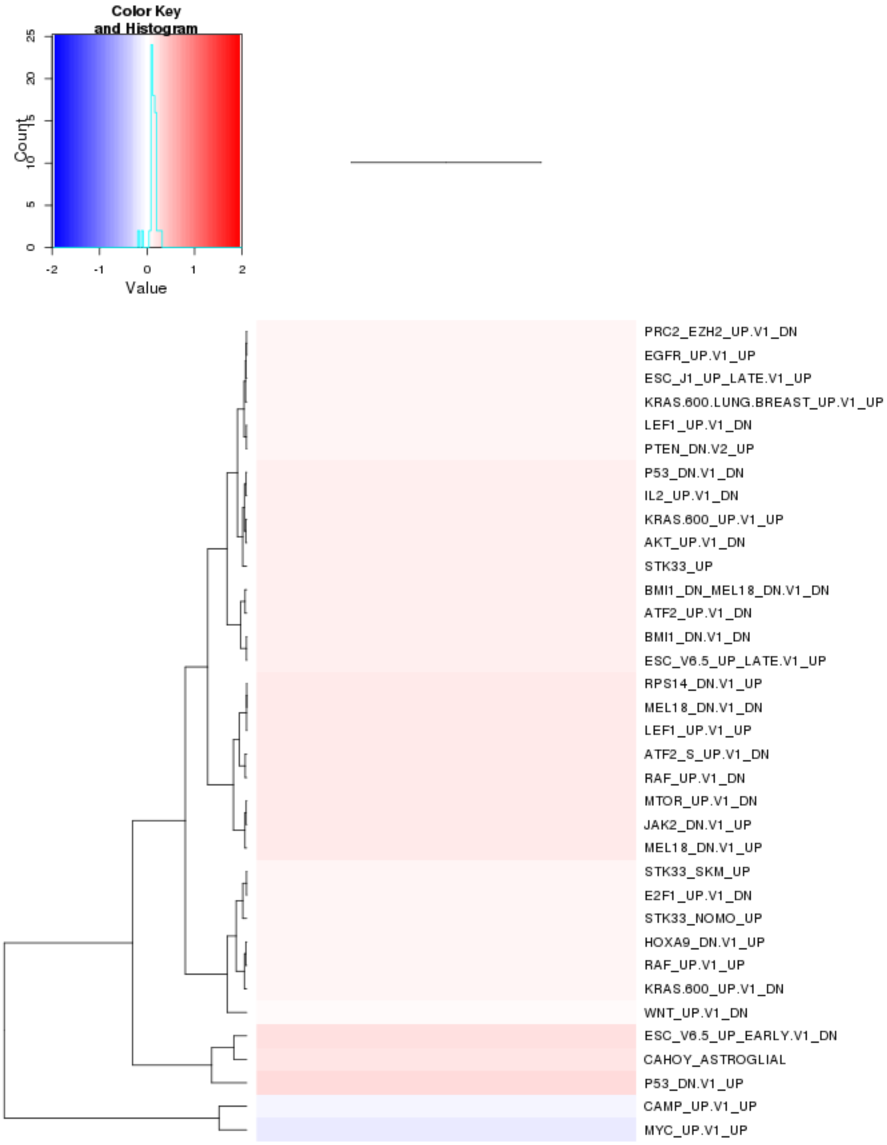
Oncogene enrichment:

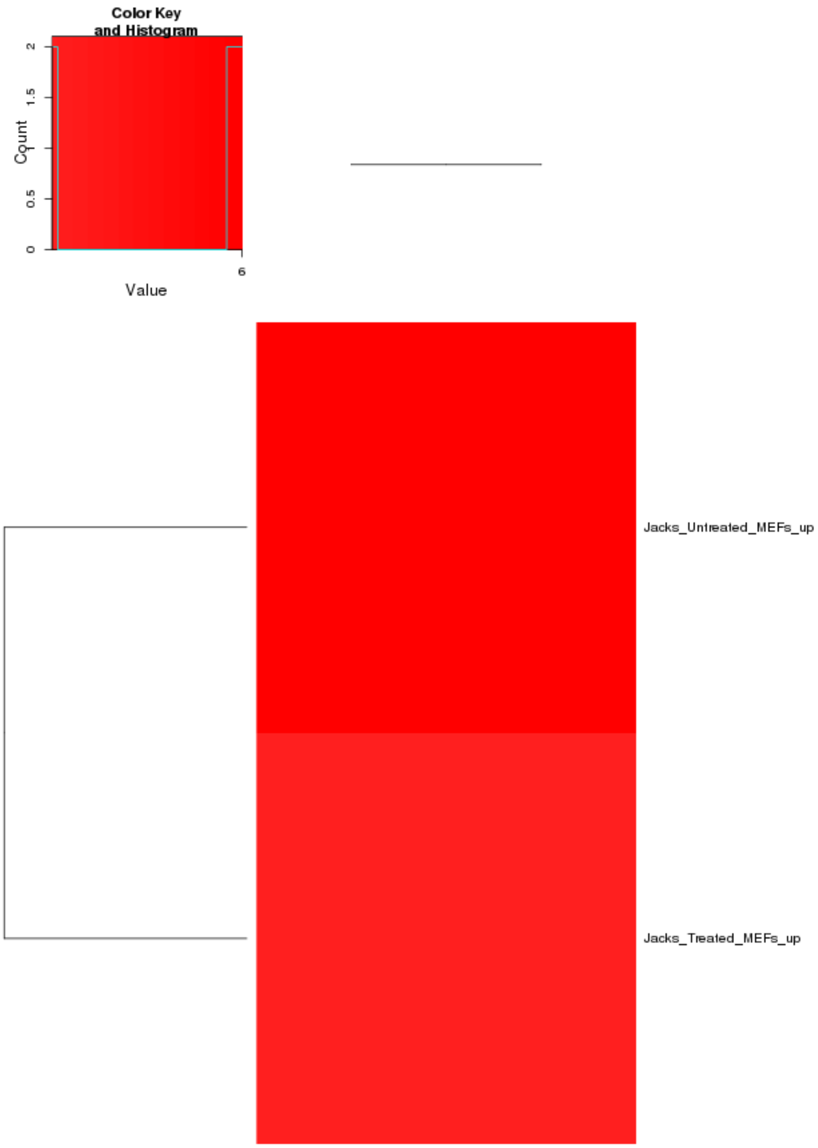
```
## Error in x_ordered[1:50, ]: subscript out of bounds
```



Oncogene zscore:

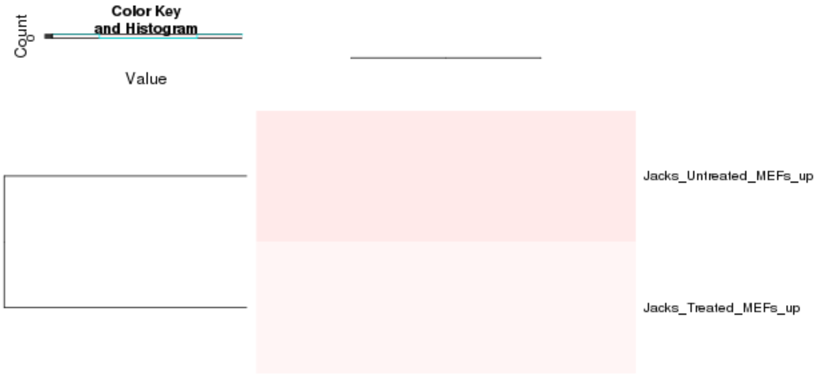
```
## Error in x_ordered[1:50, ]: subscript out of bounds
```


Color Key
and Histogram
Count
0
5
10
15
20
25
-2
-1
0
1
2
Value
PRC2_EZH2_UP.V1_DN
EGFR_UP.V1_UP
ESC_J1_UP_LATE.V1_UP
KRAS.600.LUNG.BREAST_UP.V1_UP
LEF1_UP.V1_DN
PTEN_DN.V2_UP
P53_DN.V1_DN
IL2_UP.V1_DN
KRAS.600_UP.V1_UP
AKT_UP.V1_DN
STK33_UP
BMI1_DN_MEL18_DN.V1_DN
ATF2_UP.V1_DN
BMI1_DN.V1_DN
ESC_V6.5_UP_LATE.V1_UP
RPS14_DN.V1_UP
MEL18_DN.V1_DN
LEF1_UP.V1_UP
ATF2_S_UP.V1_DN
RAF_UP.V1_DN
MTOR_UP.V1_DN
JAK2_DN.V1_UP
MEL18_DN.V1_UP
STK33_SKM_UP
E2F1_UP.V1_DN
STK33_NOMO_UP
HOXA9_DN.V1_UP
RAF_UP.V1_UP
KRAS.600_UP.V1_DN
WNT_UP.V1_DN
ESC_V6.5_UP_EARLY.V1_DN
CAHOY_ASTROGLIAL
P53_DN.V1_UP
CAMP_UP.V1_UP
MYC_UP.V1_UP



Jacks enrichment

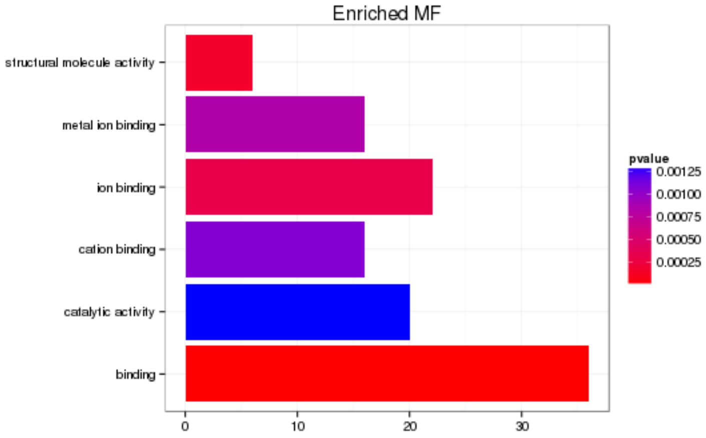
Jacks zscore

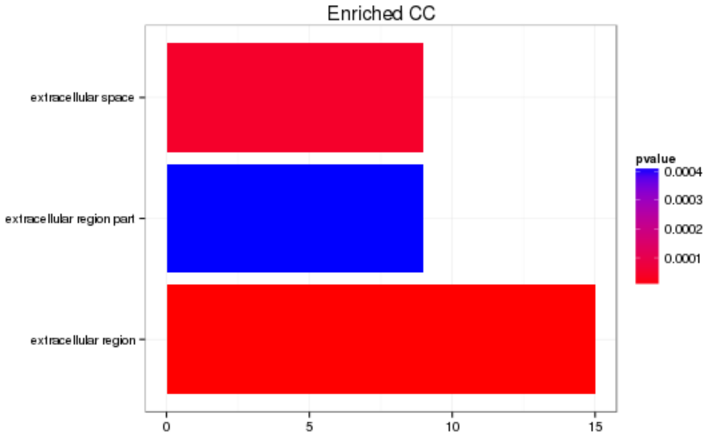


GO enrichment

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

```
## Error in unit(tic_pos.c, "mm"): 'x' and 'units' must have length > 0
```





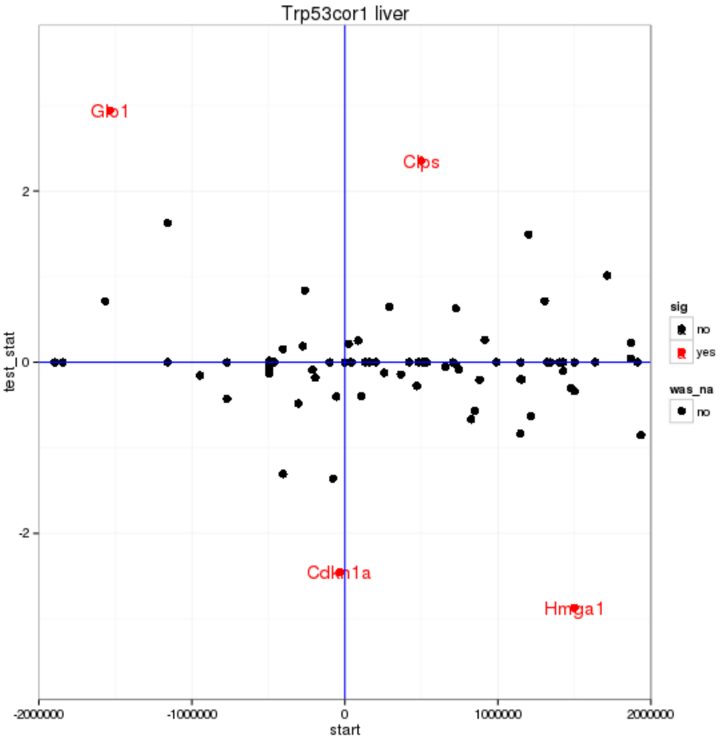
```
## Error in plot.window(...): need finite 'xlim' values
```

```
## Error in unit(tic_pos.c, "mm"): 'x' and 'units' must have length > 0
```

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 genes significantly regulated in a region this size is: 0.0099



Notes

Samples used are:

	11
1	JR917
2	JR933
3	JR925
4	lincp21_Liver_WT1
5	lincp21_Liver_WT2
6	JR926
7	JR934
8	lincp21_Liver_KO1
9	lincp21_Liver_KO2

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	i
1	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR917/abundances.cxb	WT	0	WT_0	37248000.00	26534800.00	
2	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR933/abundances.cxb	WT	1	WT_1	34229100.00	26534800.00	
3	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR925/abundances.cxb	WT	2	WT_2	40066200.00	26534800.00	
4	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/lincp21_Liver_WT1/abundances.cxb	WT	3	WT_3	22564500.00	26534800.00	
5	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/lincp21_Liver_WT2/abundances.cxb	WT	4	WT_4	17810700.00	26534800.00	
6	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR926/abundances.cxb	Trp53cor1	0	Trp53cor1_0	40299500.00	26534800.00	
7	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/JR934/abundances.cxb	Trp53cor1	1	Trp53cor1_1	30681900.00	26534800.00	
8	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/lincp21_Liver_KO1/abundances.cxb	Trp53cor1	2	Trp53cor1_2	15729200.00	26534800.00	
9	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/lincp21_Liver_KO2/abundances.cxb	Trp53cor1	3	Trp53cor1_3	16292900.00	26534800.00	

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] GO.db_2.10.1
##  [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_1.8-2
## [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_2.14.2
## [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_0.3.1
## [36] BiocGenerics_0.8.0
## [37] knitr_1.7
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17.1         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_1.0            Formula_1.1-2
## [13] gdata_2.13.3           GenomicFeatures_1.14.5 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_1.1-4
## [28] munsell_0.4.2          org.Hs.eg.db_2.10.1    proto_0.3-10
## [31] qvalue_1.36.0          Rcpp_0.11.3            RCurl_1.95-4.3
## [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,Trp53cor1 -o /n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/diff/Trp53cor1_E14.5_
## 2
## 3
## 4
## 5
```

Trp53cor1 KO vs WT (lung)

This file shows the wt-v-ko comparison for Trp53cor1.

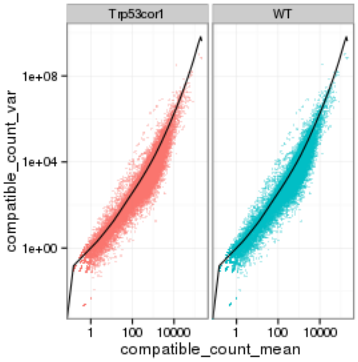
Cuff overview:

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

QC

Dispersion

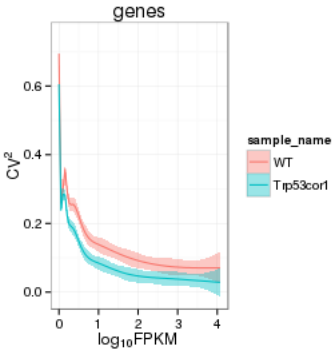
Dispersion plot for genes in cuff: (Overdispersion can lead to innacurate quants)



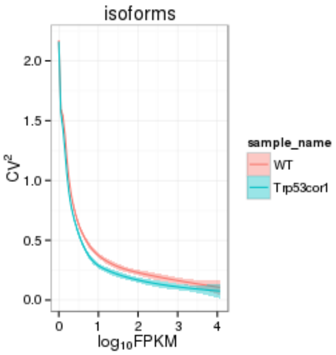
Cross-replicate variability (fpkmSCVplot)

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

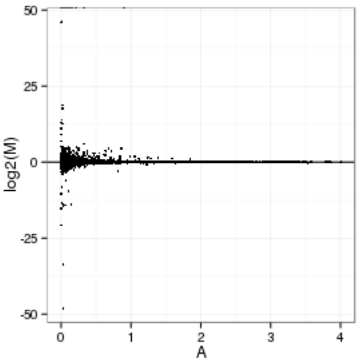
Genes:



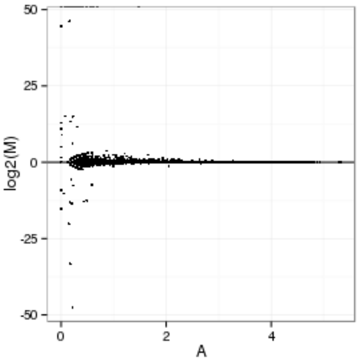
Isoforms:



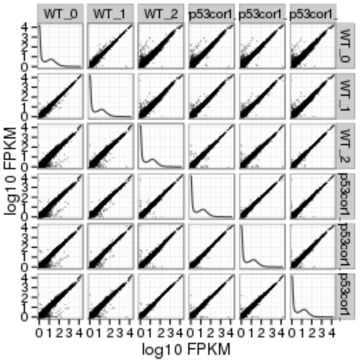
MvA plot



MvA plot counts



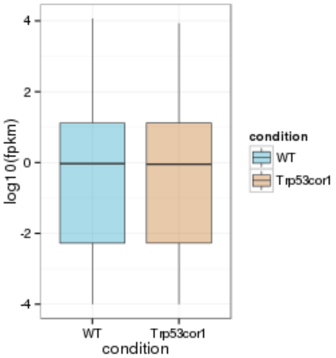
Scatterplot matrix



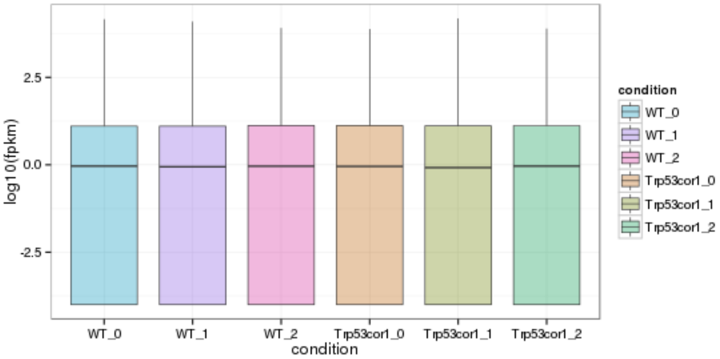
Distributions

Boxplots

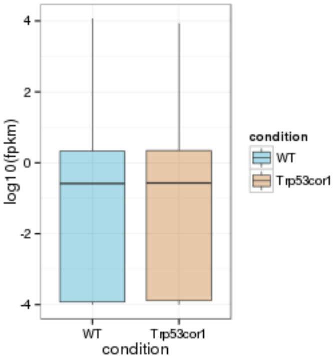
Boxplot (genes)



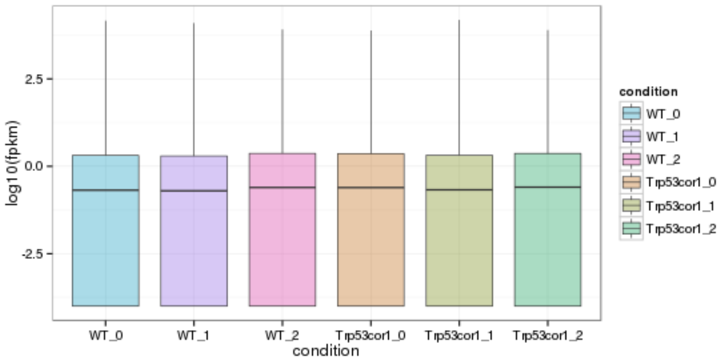
Boxplot (genes, replicates)



Boxplot (isoforms)

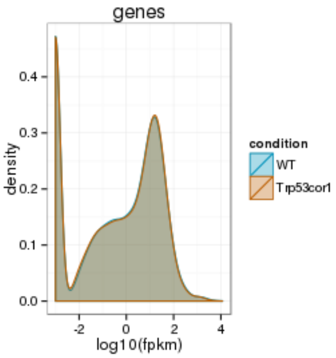


Boxplot (isoforms, replicates)

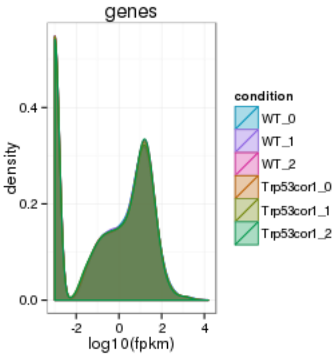


Density

Density (genes)

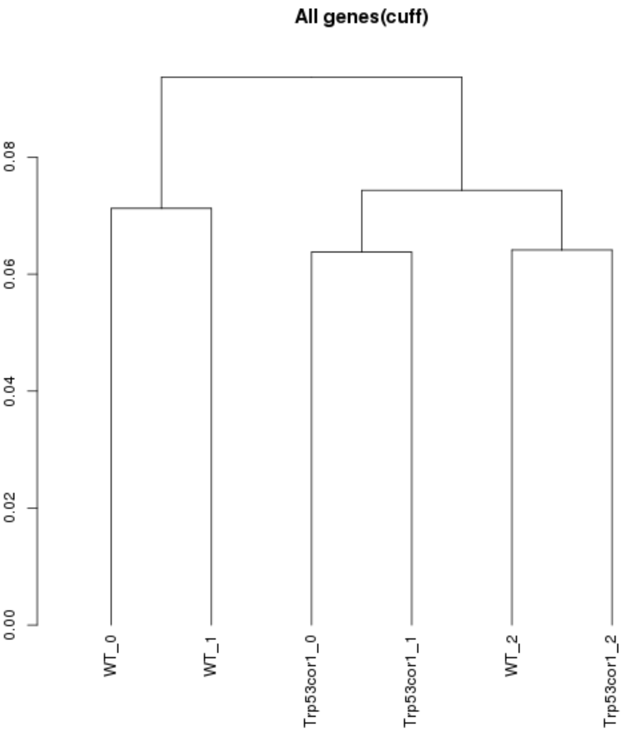


Density (genes, replicates)



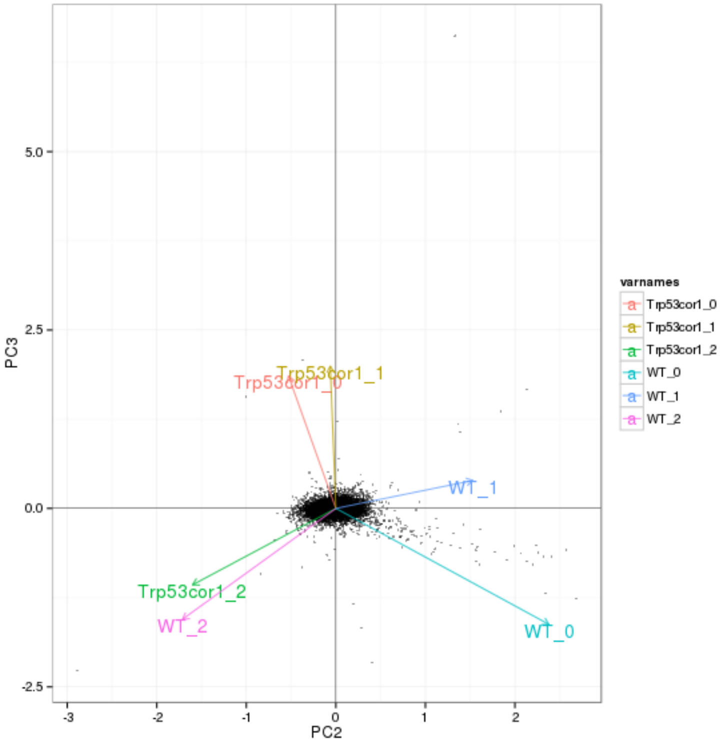
Clustering

Replicate Clusters

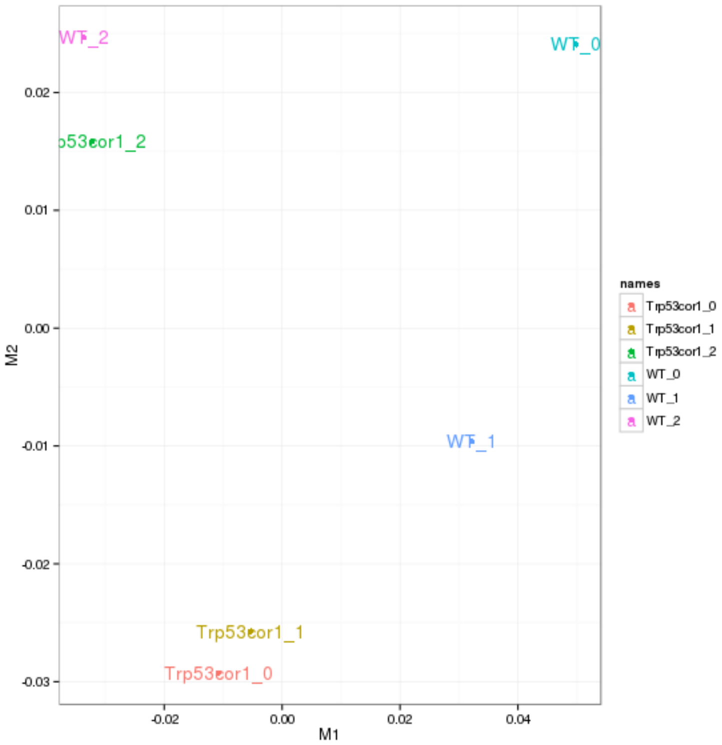


```
## NULL
```

PCA (genes)

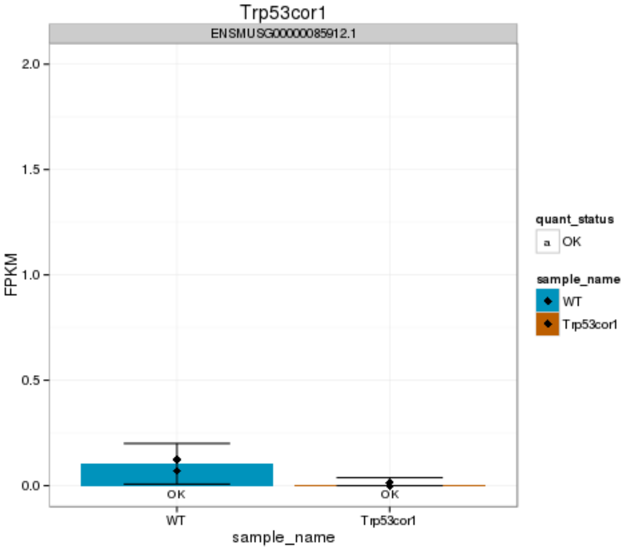


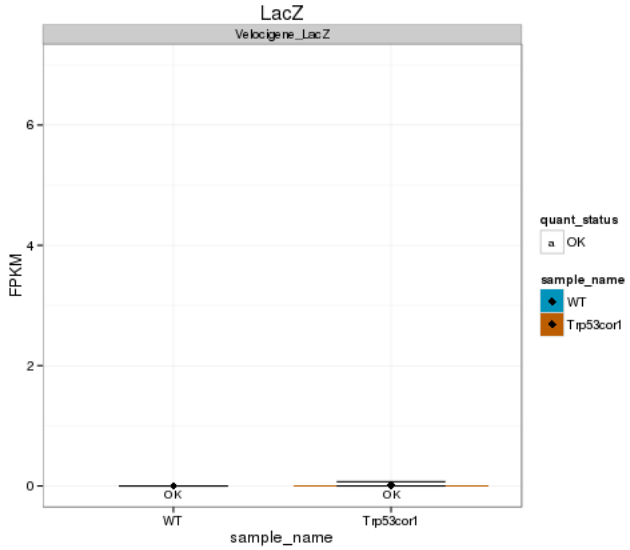
MDS (genes)



KO assessment

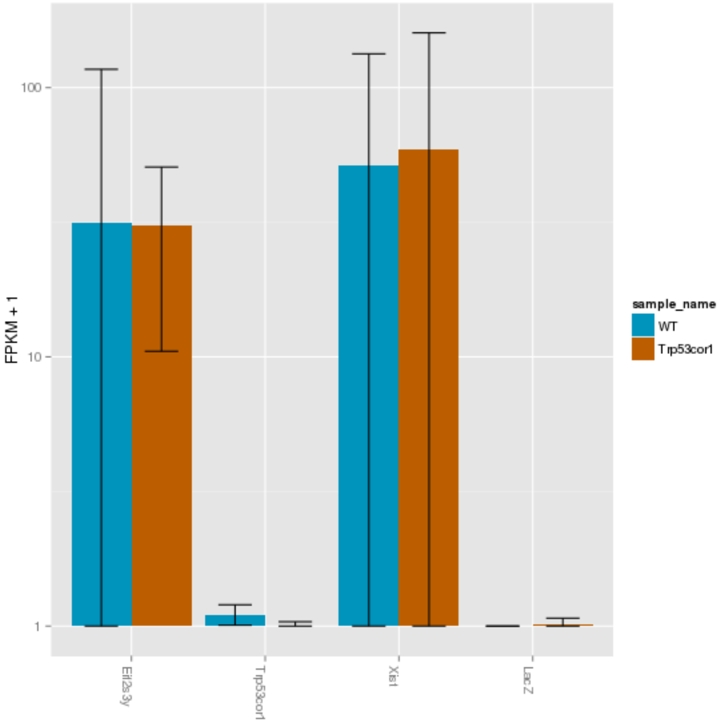
Endogenous lncRNA expression



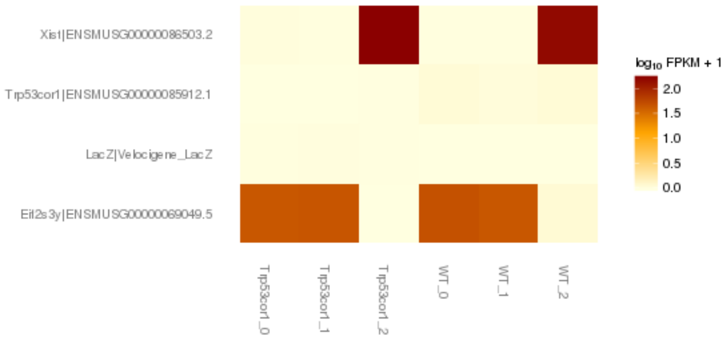


Digital Genotyping (LacZ vs Endogenous lncRNA and Sex)

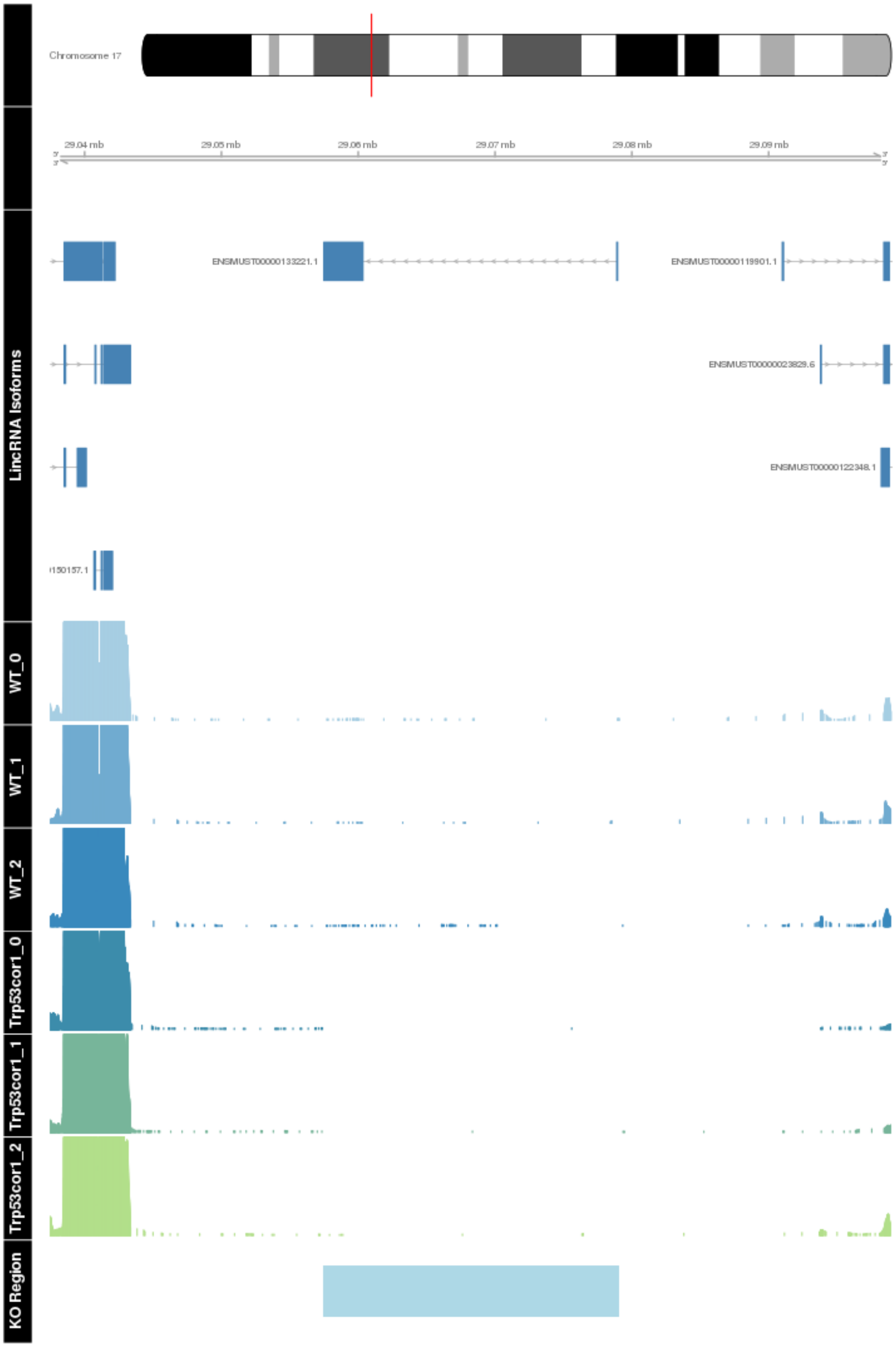
Eif2s3y is a y-expressed gene, Xist is an x-expressed gene Expression plot (endogenous linc, lacZ, Y-expressed gene):



Expression heatmap:



Track visualization



Differential Analysis

Differential Genes

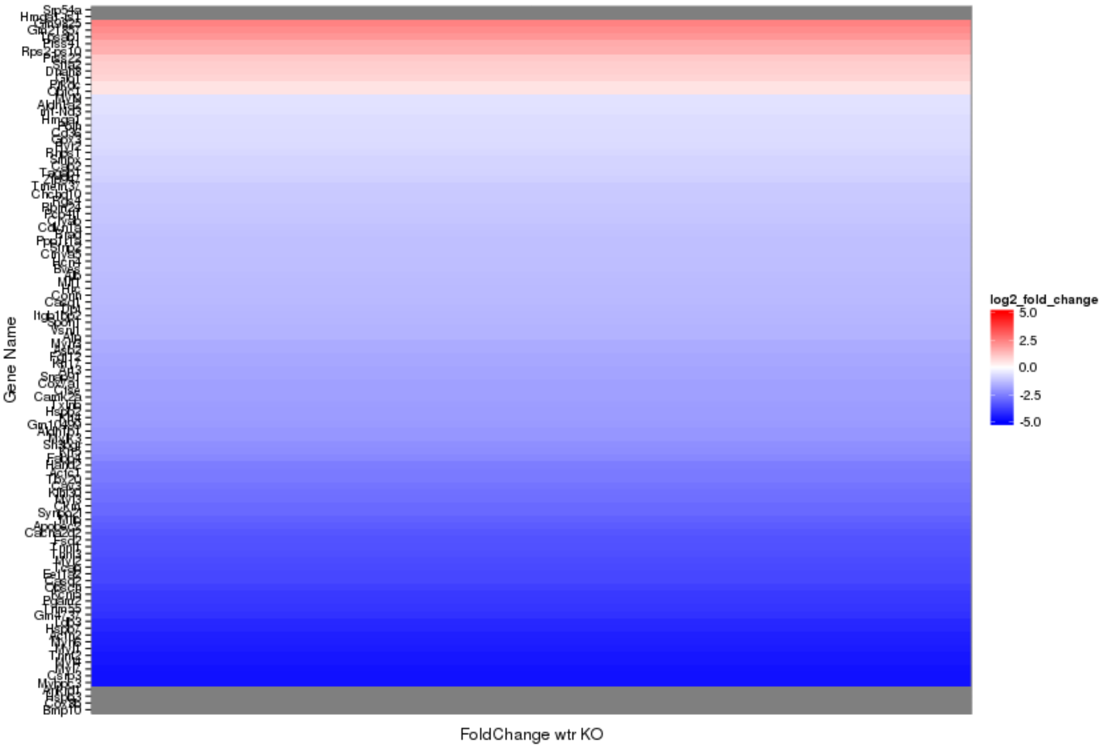
There are 104 significantly differentially expressed genes. They are:

	geneAnnot$gene_short_name
1	Mybpc3
2	Cd36
3	Ctse
4	Corin
5	Hspb7
6	Casq1

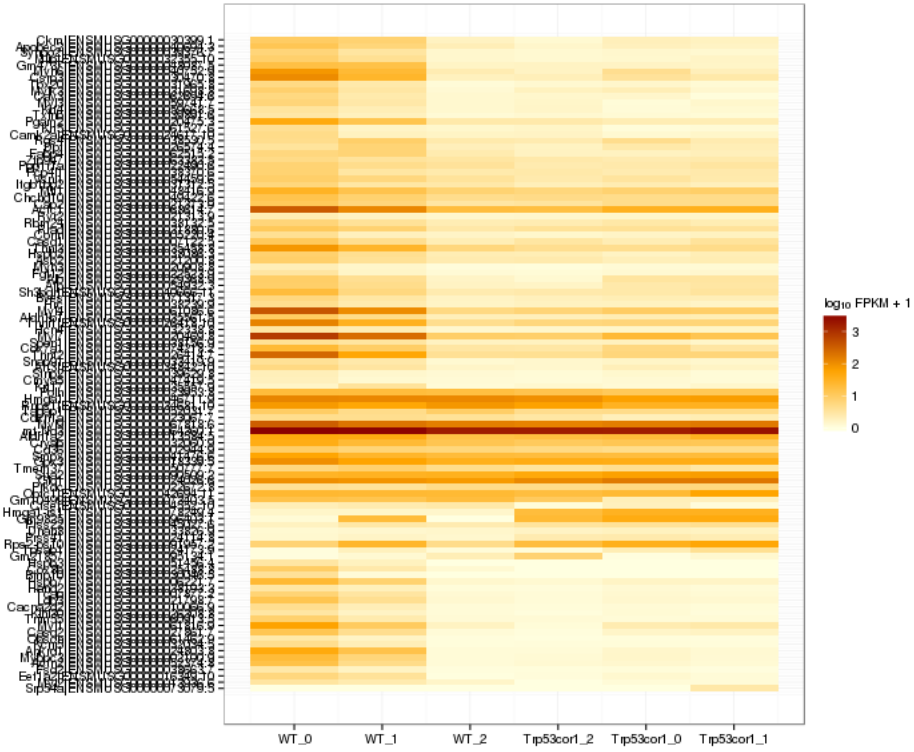
7 Tcap
8 Cacna2d2
9 Aldh1a2
10 Myl2
11 Eef1a2
12 Gpx3
13 Myl7
14 Pgam2
15 Myh3
16 Asb2
17 Ryr2
18 Cap2
19 Ldb3
20 Ppp1r1a
21 Fgf12
22 Prkdc
23 Cdkn1a
24 Polh
25 Glo1
26 Prss41
27 Tpsab1
28 Camk2a
29 Ankrd1
30 Cox8b
31 Klhl30
32 Tnnt2
33 Tnni1
34 Dpt
35 Casq2
36 Alb
37 Bmp10
38 Ckm
39 Csrp3
40 Itgb1bp2
41 Mylk3
42 Rrad
43 Tbx20
44 Kcnj5
45 Cryab
46 Hcn4
47 Mlip
48 Snap91
49 Dnah8
50 Rnps1
51 Art3
52 Tnni3
53 Krt17
54 Aldh1b1
55 Hspb2
56 Rbm24
57 Spon1
58 Hand2
59 Hrc
60 Pcp4l1
61 Rgs4
62 Fsd2
63 Synpo2l
64 Strip2
65 Txlnb

66 Sh3bgr

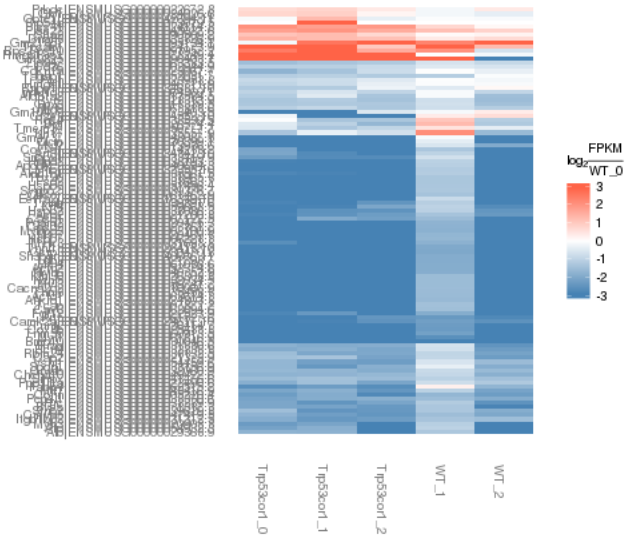
67 Apobec2
68 Myh6
69 Smpx
70 Obfc1
71 Prss22
72 Hmga1
73 Cmya5
74 Gm4737
75 Mlf1
76 Chchd10
77 Tmem37
78 Hspb3
79 Tagap1
80 Actn2
81 Vsnl1
82 Afp
83 Krt4
84 Myl3
85 Trim55
86 Myl4
87 Obscn
88 Krt5
89 Myl1
90 Fabp4
91 Cav3
92 Zfp947
93 mt-Nd3
94 Myl9
95 Actc1
96 Bves
97 Srp54a
98 Gm10499
99 Cox7a1
100 Hmga1-rs1
101 Sfta2
102 Rps2-ps10
103 Gm21857
104 Gm9825



Expression heatmap of sigGenes



Foldchange heatmap of sigGenes

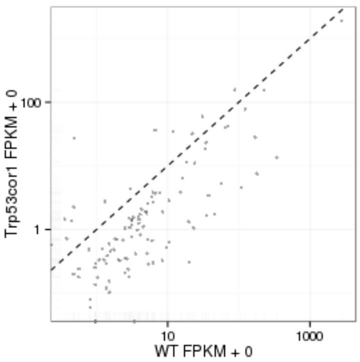


```
## Error in (function (classes, fdef, mtable) : unable to find an inherited method for function 'csFoldChangeHeatma
```

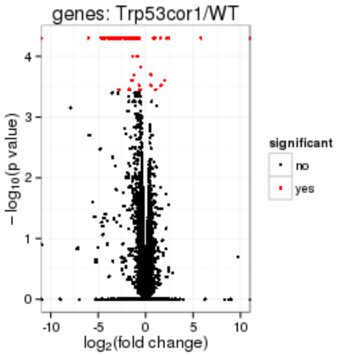
```
## Error in sqliteExecStatement(con, statement, bind.data): RS-DBI driver: (error in statement: near ")": syntax er
```

Expression-level/significance relationship

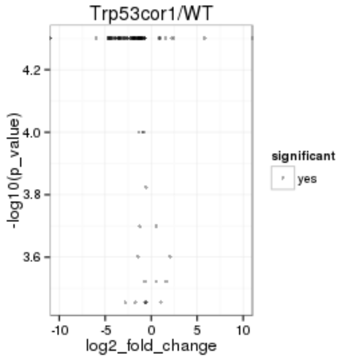
Scatter plot of significant genes only:



Volcano Plot



Volcano plot with significant genes only:



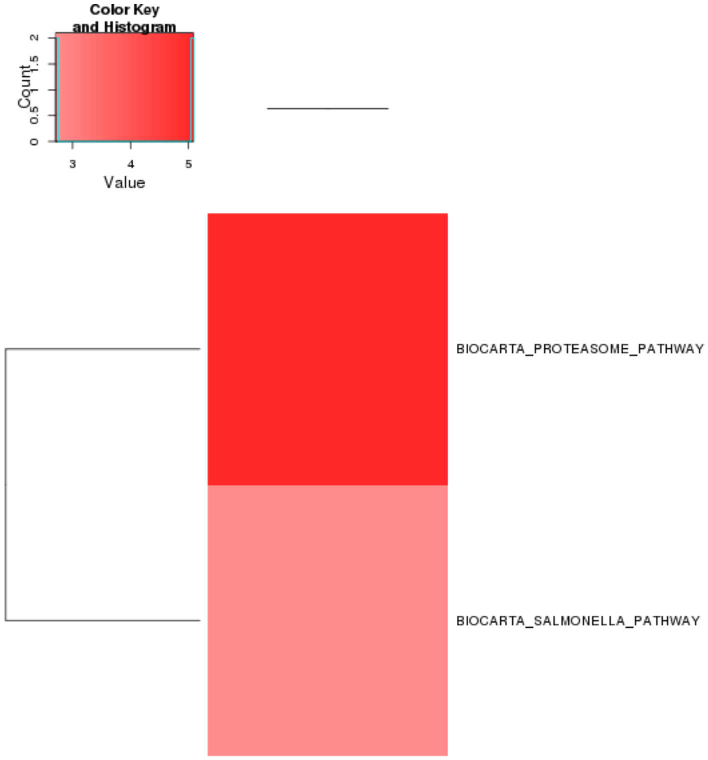
Gene/Pathway Analysis

##

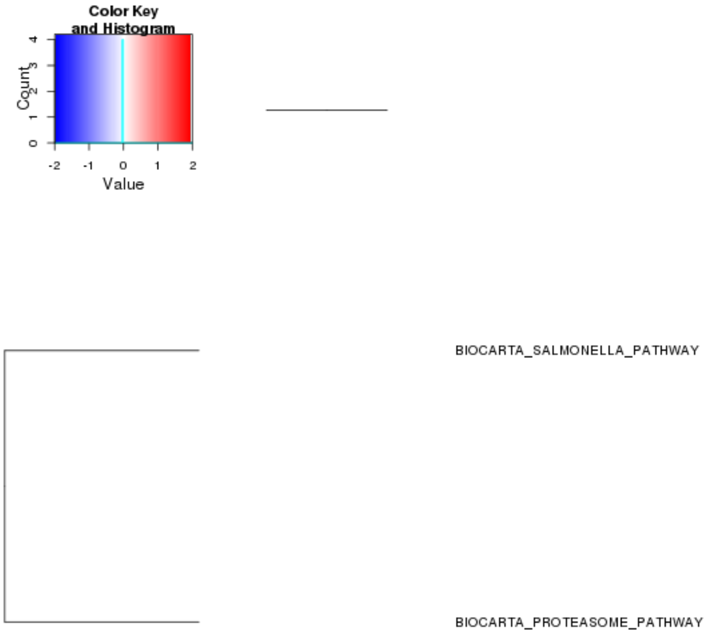
Enrichment and zscores are calculated based on expression in KO vs WT (fpkmKO/fpkmWT), so genes that are down regulated in KO are shown in blue, while upregulation is shown in red.

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

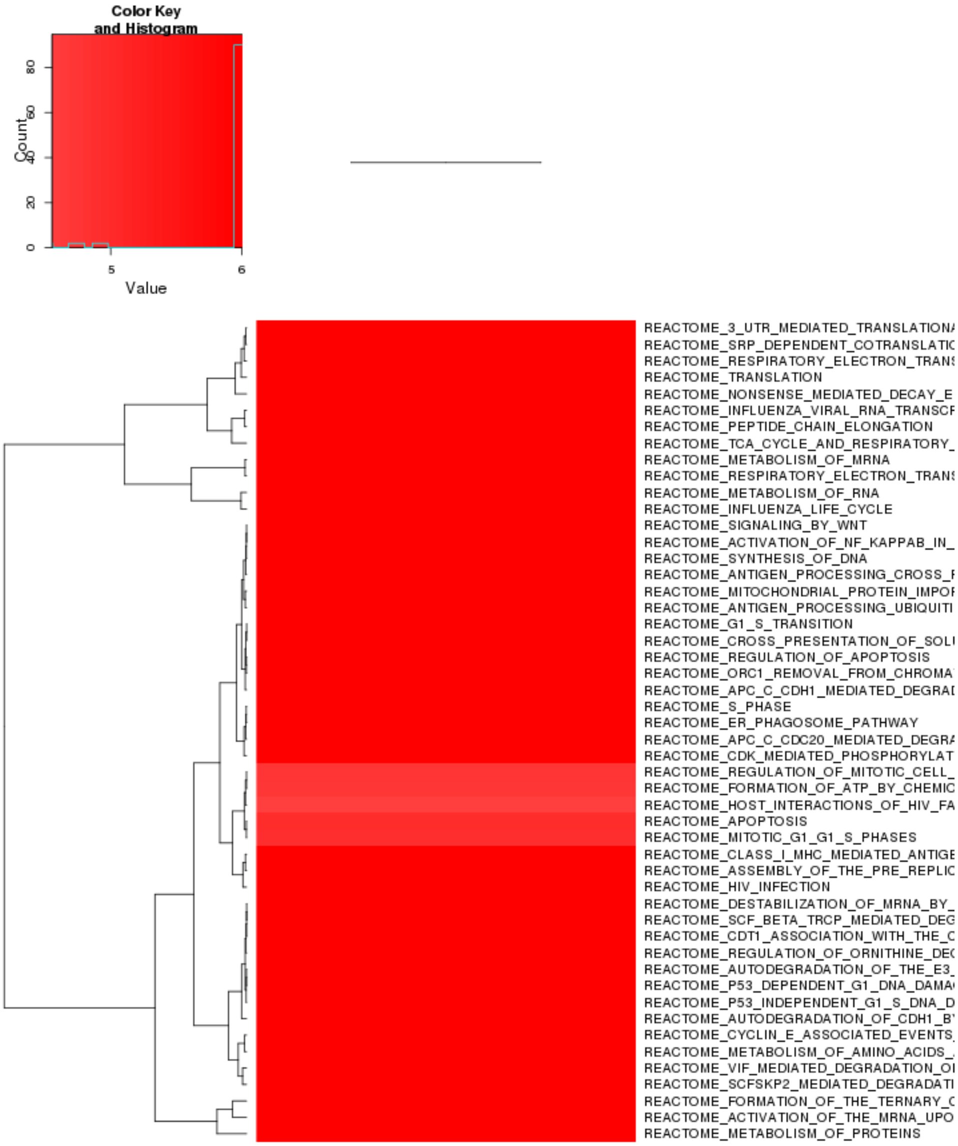
Biocarta enrichment:



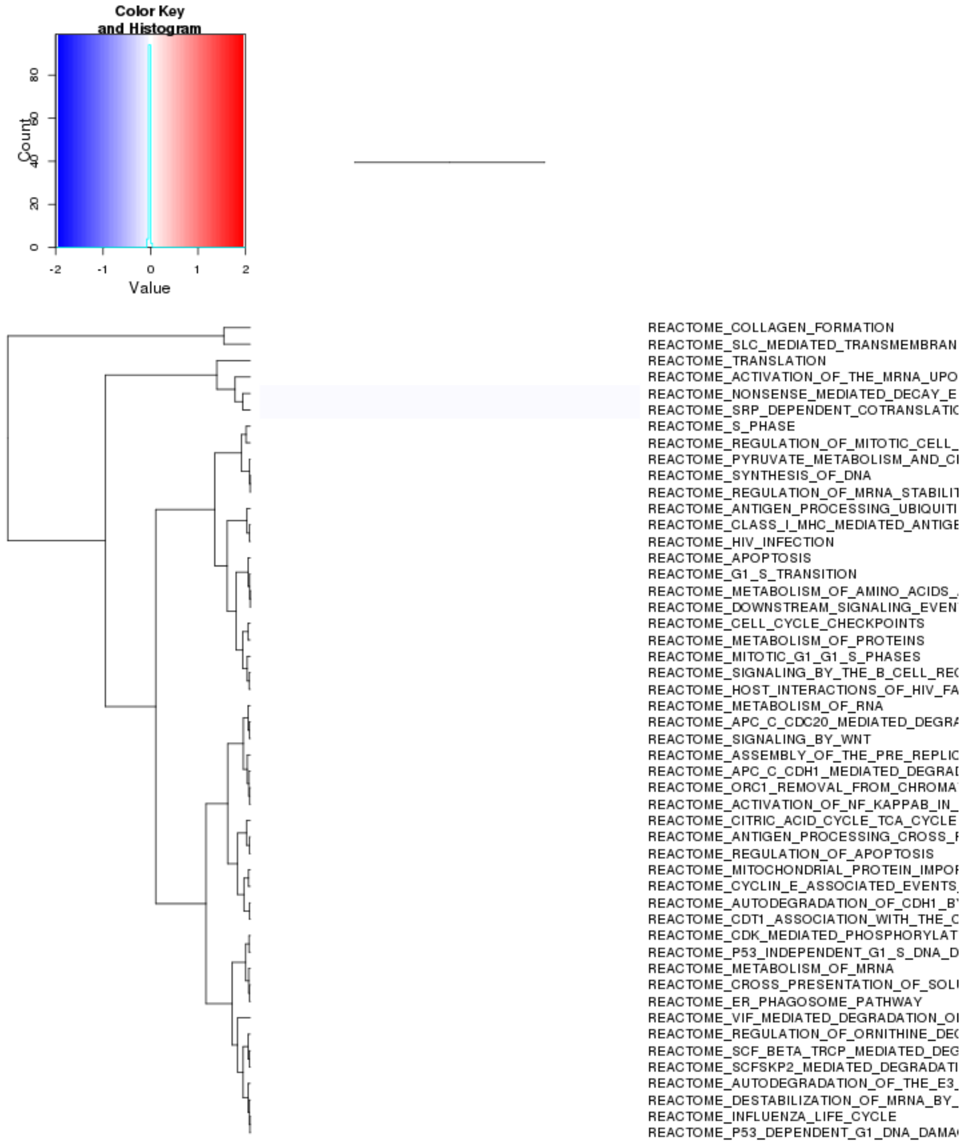
Biocarta zscore:



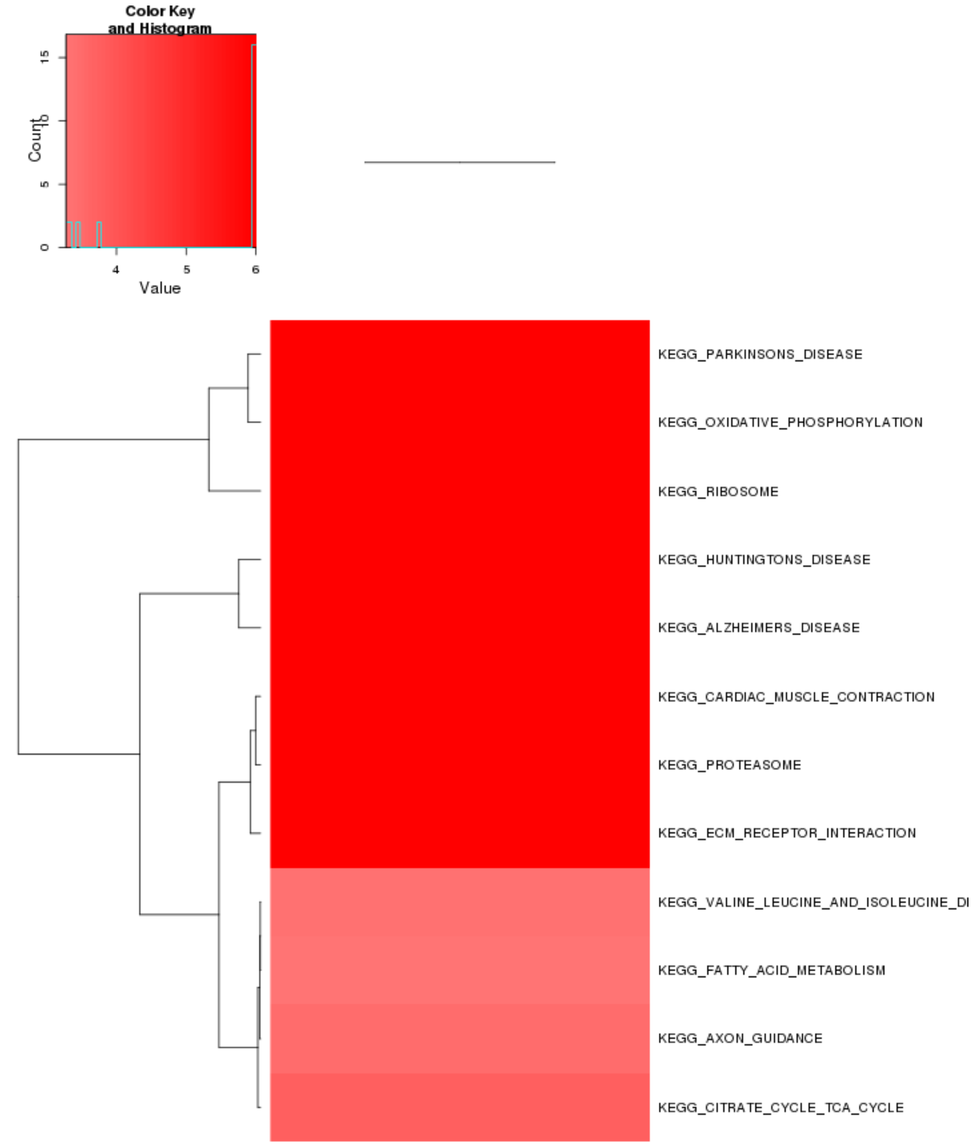
Reactome enrichment:



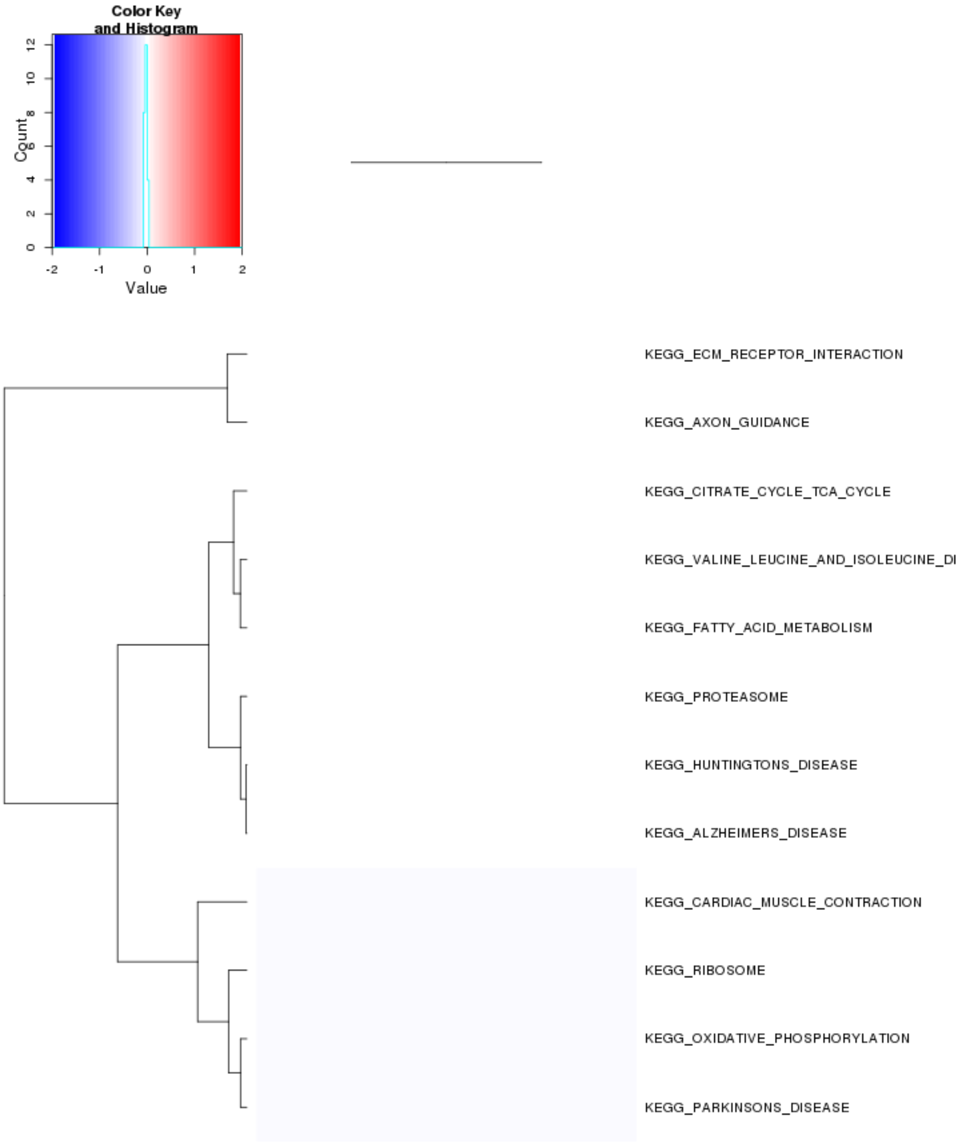
Reactome zscore:



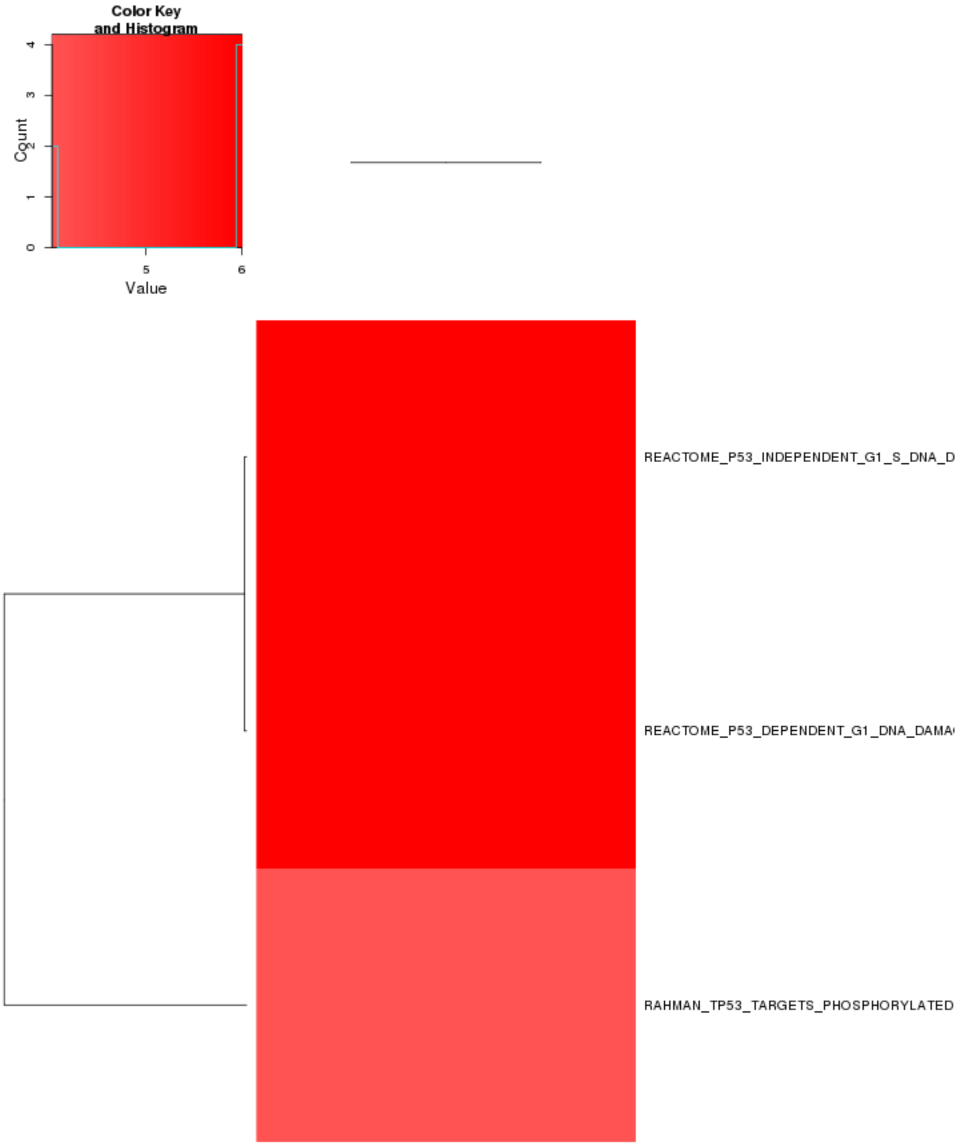
Kegg enrichment:


Color Key
and Histogram
Count
15
10
5
0
4
5
6
Value
KEGG_PARKINSONS_DISEASE
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_RIBOSOME
KEGG_HUNTINGTONS_DISEASE
KEGG_ALZHEIMERS_DISEASE
KEGG_CARDIAC_MUSCLE_CONTRACTION
KEGG_PROTEASOME
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DI
KEGG_FATTY_ACID_METABOLISM
KEGG_AXON_GUIDANCE
KEGG_CITRATE_CYCLE_TCA_CYCLE

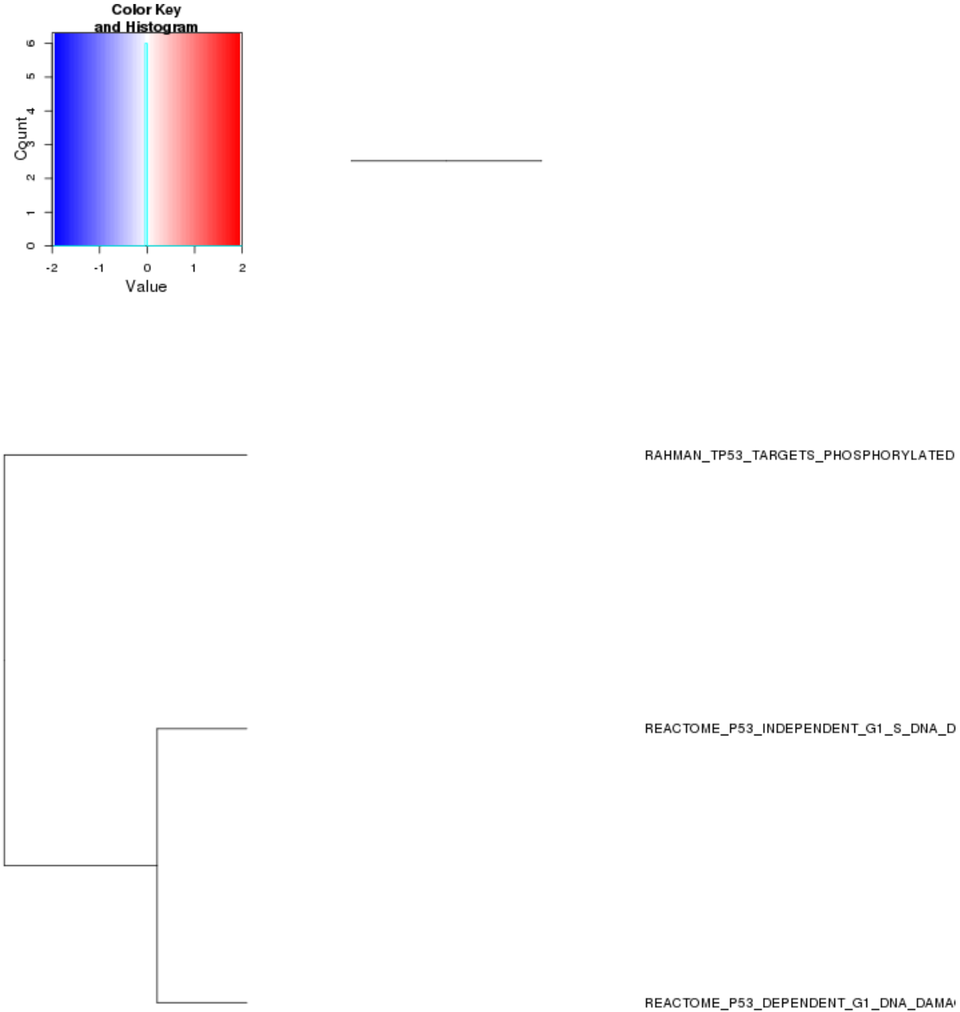
Kegg zscore:



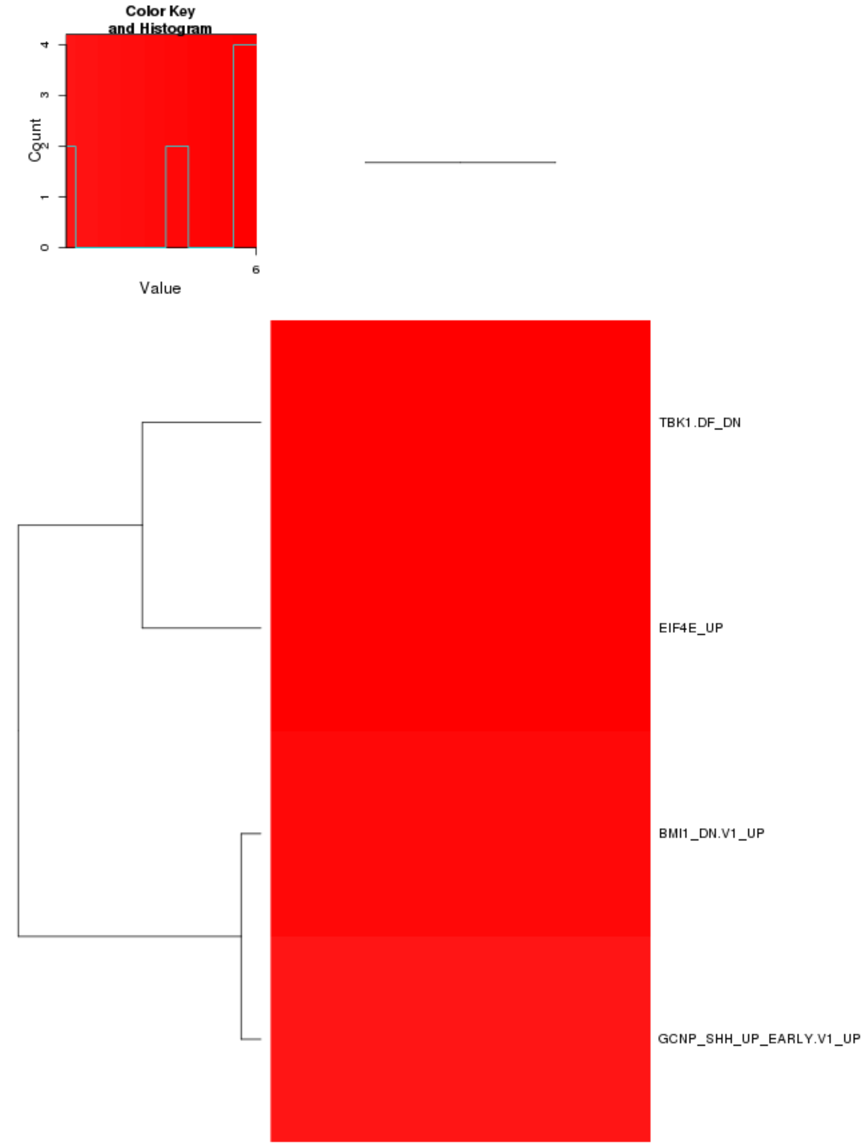
p53 enrichment:


Color Key
and Histogram
Count
0
1
2
3
4
5
6
Value
REACTOME_P53_INDEPENDENT_G1_S_DNA_D
REACTOME_P53_DEPENDENT_G1_DNA_DAMA
RAHMAN_TP53_TARGETS_PHOSPHORYLATED

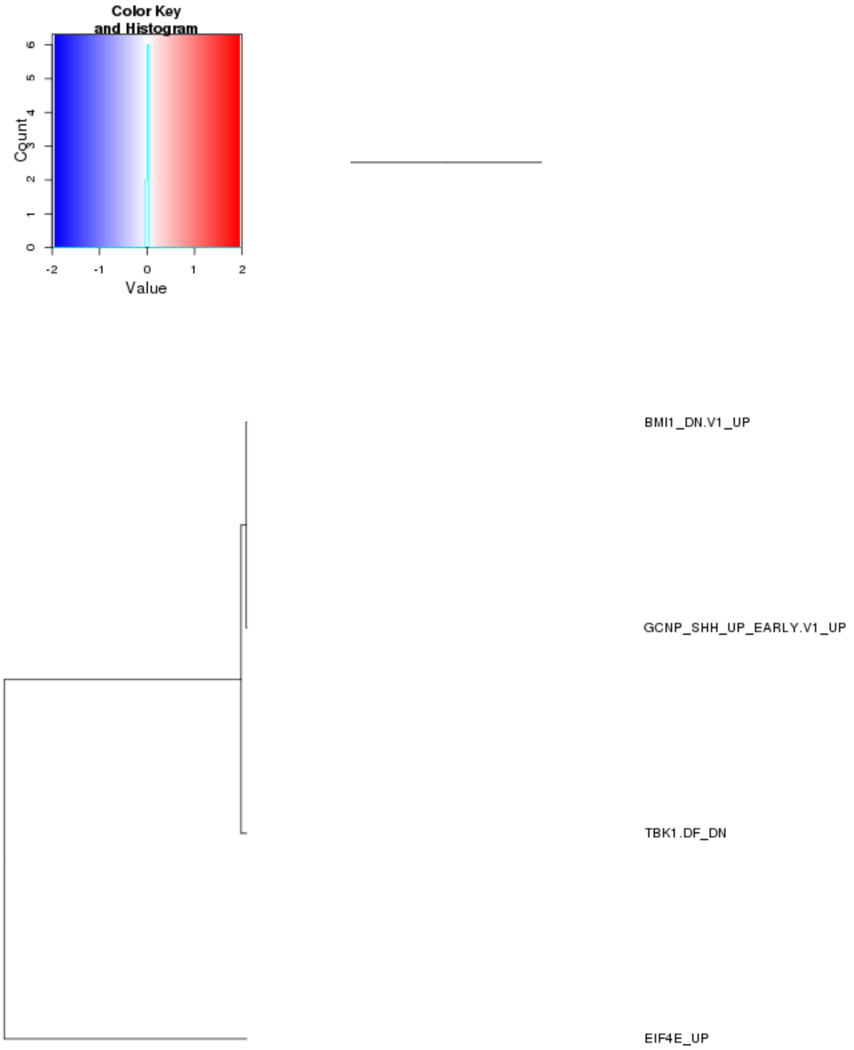
p53 zscore:



Oncogene enrichment:



Oncogene zscore:



Jacks enrichment

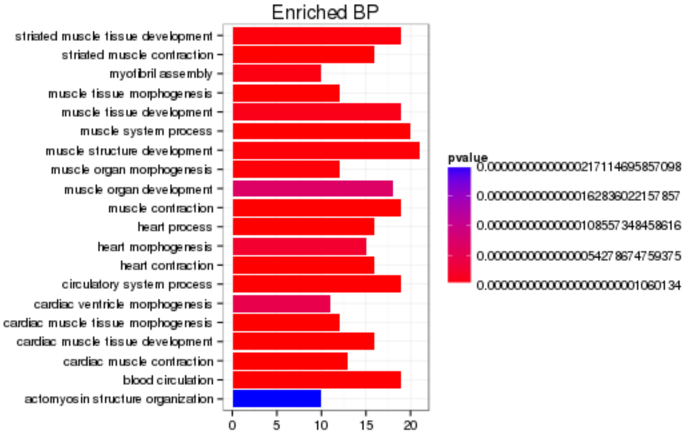
```
## [1] "Not enough significant categories to print a heatmap!"
```

Jacks zscore

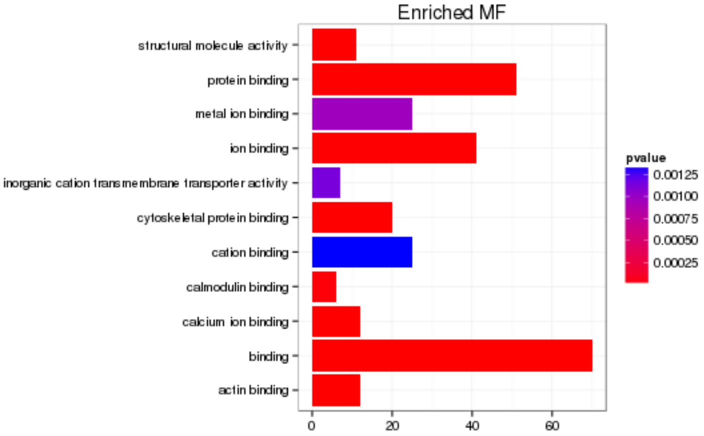
```
## [1] "Not enough significant categories to print a heatmap!"
```

GO enrichment

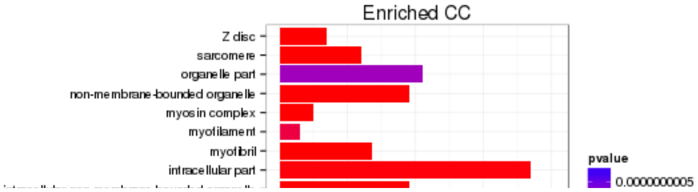
Cluster profiler used to call enrichments of significantly differentially regulated genes that map to Entrez IDs.



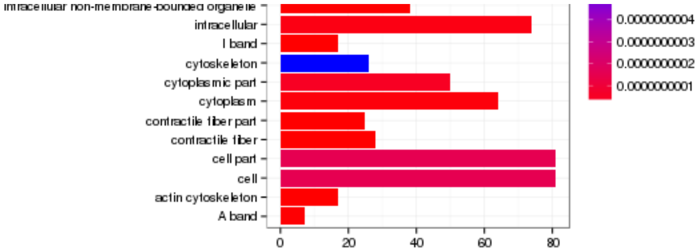
Enriched BP
striated muscle tissue development
striated muscle contraction
myofibril assembly
muscle tissue morphogenesis
muscle tissue development
muscle system process
muscle structure development
muscle organ morphogenesis
muscle organ development
muscle contraction
heart process
heart morphogenesis
heart contraction
circulatory system process
cardiac ventricle morphogenesis
cardiac muscle tissue morphogenesis
cardiac muscle tissue development
cardiac muscle contraction
blood circulation
actomyosin structure organization
0
5
10
15
20
pvalue
0.00000000000000217114695857098
0.00000000000000162836022157857
0.00000000000000108557348458616
0.00000000000000054278674759375
0.0000000000000000000001060134

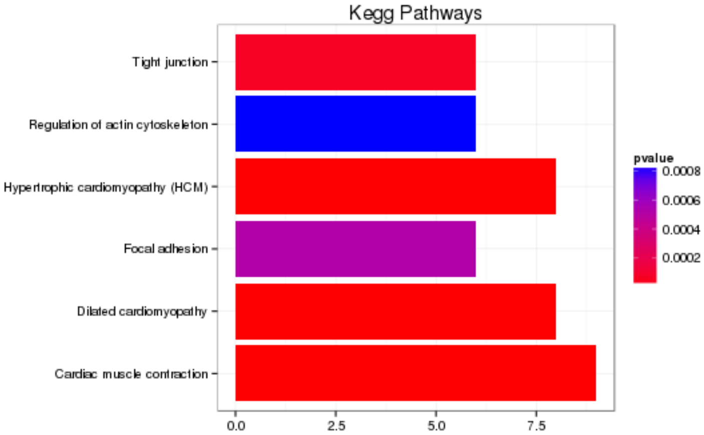


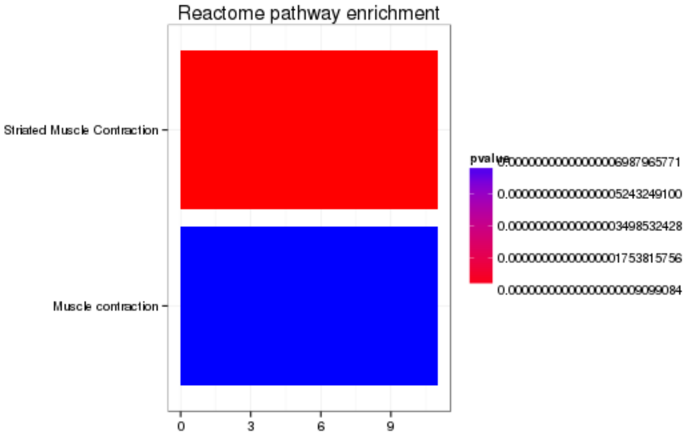
Enriched MF
structural molecule activity
protein binding
metal ion binding
ion binding
inorganic cation transmembrane transporter activity
cytoskeletal protein binding
cation binding
calmodulin binding
calcium ion binding
binding
actin binding
0
20
40
60
pvalue
0.00125
0.00100
0.00075
0.00050
0.00025



Enriched CC
Z disc
sarcomere
organelle part
non-membrane-bounded organelle
myosin complex
myofilament
myofibril
intracellular part
pvalue
0.0000000005



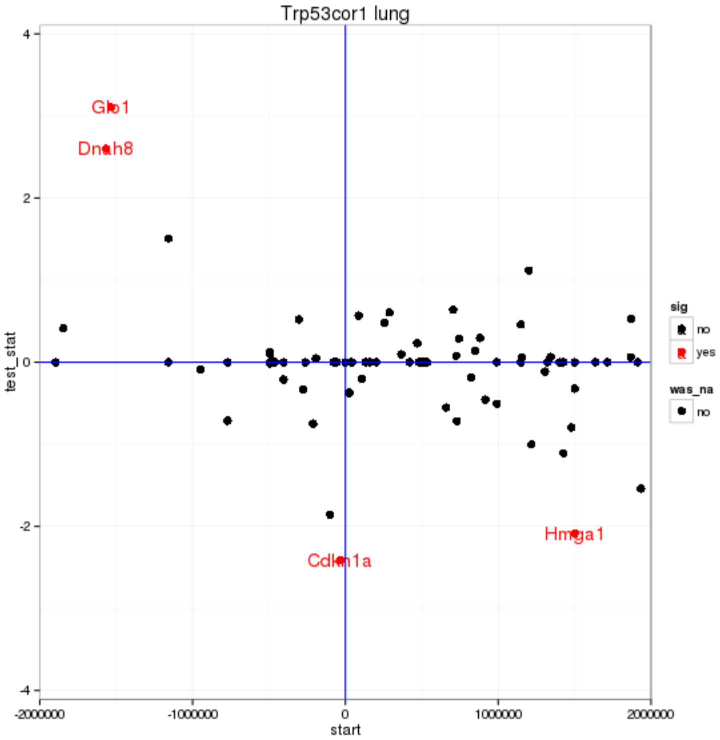




Cis vs Trans (locally)

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 genes significantly regulated in a region this size is: 0.0071



Notes

Samples used are:

	11
1	lincp21_Lung_WT1
2	lincp21_Lung_WT2
3	lincp21_Lung_WT3
4	lincp21_Lung_KO1
5	lincp21_Lung_KO2
6	lincp21_Lung_KO3

Replicates

	file	sample_name	replicate	rep_name	total_mass	norm_mass	i
1	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/lincp21_Lung_WT1/abundances.cxb	WT	0	WT_0	18941100.00	21186400.00	
2	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/lincp21_Lung_WT2/abundances.cxb	WT	1	WT_1	21434800.00	21186400.00	
3	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/lincp21_Lung_WT3/abundances.cxb	WT	2	WT_2	20217700.00	21186400.00	
4	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/lincp21_Lung_KO1/abundances.cxb	Trp53cor1	0	Trp53cor1_0	19968300.00	21186400.00	
5	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/lincp21_Lung_KO2/abundances.cxb	Trp53cor1	1	Trp53cor1_1	23883200.00	21186400.00	
6	/n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/quants/lincp21_Lung_KO3/abundances.cxb	Trp53cor1	2	Trp53cor1_2	23179700.00	21186400.00	

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] GO.db_2.10.1
##  [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_1.8-2
## [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_2.14.2
## [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_0.3.1
## [36] BiocGenerics_0.8.0
## [37] knitr_1.7
##
## loaded via a namespace (and not attached):
##  [1] biomaRt_2.18.0         biovizBase_1.10.8      bitops_1.0-6
##  [4] caTools_1.17.1         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_1.0            Formula_1.1-2
## [13] gdata_2.13.3           GenomicFeatures_1.14.5 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_1.1-4
## [28] munsell_0.4.2          org.Hs.eg.db_2.10.1    proto_0.3-10
## [31] qvalue_1.36.0          Rcpp_0.11.3            RCurl_1.95-4.3
## [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,Trp53cor1 -o /n/rinn_data1/users/agroff/seq/OtherMice/Diana/lincP21/diff/Trp53cor1_E14.5_
## 2
## 3
## 4
## 5
```