Title:	Project X: Data Analysis
Project:	Project
CICPT:	007
Date:	21 May, 2020
Investigators:	,
Organization:	Analysis Group

Contents

1 Overview

The goal of this analysis is to examine the correlation of individual probesets to the RSI score, across several large datasets. We will use three different datasets: TCC (HuRSTA array), EXPO (U133 arrays) and CCLE (U133 arrays).

```
suppressPackageStartupMessages({
  library(readxl)
  library(knitr)
  library(kableExtra)
  library(ggplot2)
  library(dplyr)
  library(Biobase)
})
```

2 Load Data

Load the three different datasets.

```
ccle<-readRDS(file="../data.raw/ccle_cel.rds")
expo<-readRDS(file="../data.raw/expo_rma_exprs.rds")
tcc<-readRDS(file="../data.raw/tcc.primary.rds")

translation<-read_excel("../data.raw/Translation.xlsx")
```

```
## New names:
## * `` -> ...11
```

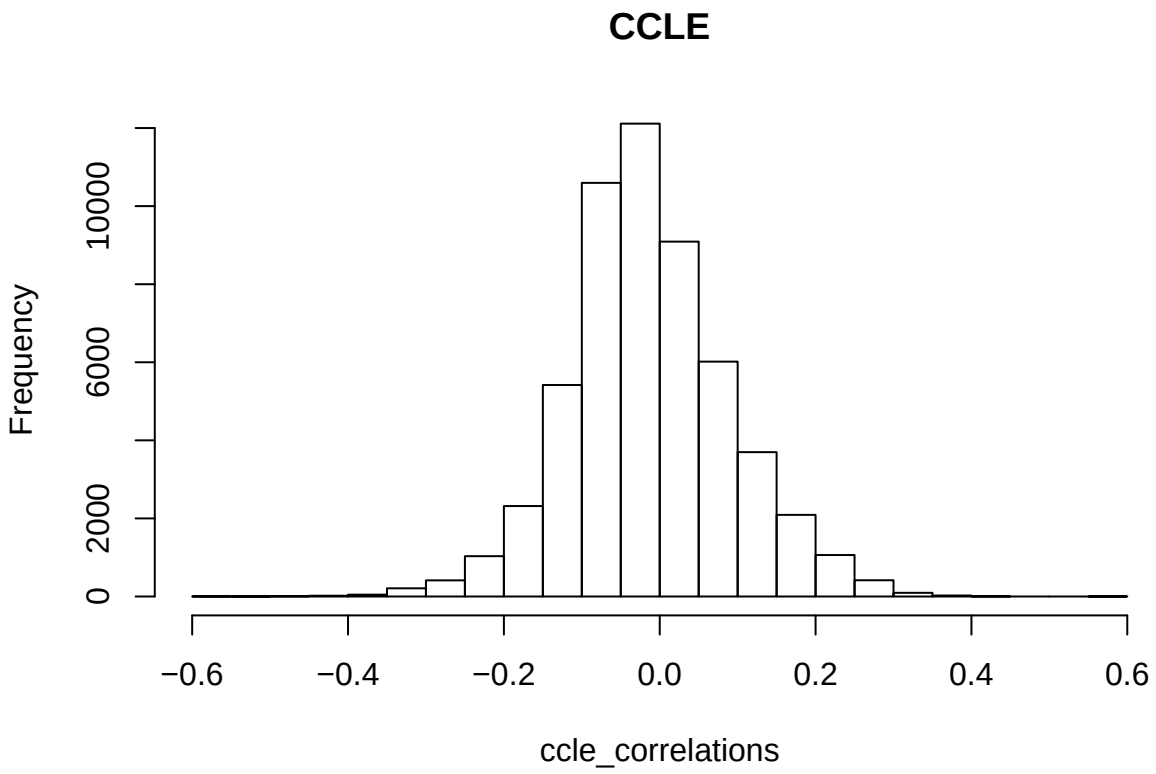
3 Run correlations

```
ccle_correlations<-apply(exprs(ccle), 1, function(y){cor(y, ccle$RSI)})
expo_correlations<-apply(exprs(expo), 1, function(y){cor(y, expo$rsi)})
tcc_correlations<-apply(exprs(tcc), 1, function(y){cor(y, tcc$RSI)})
```

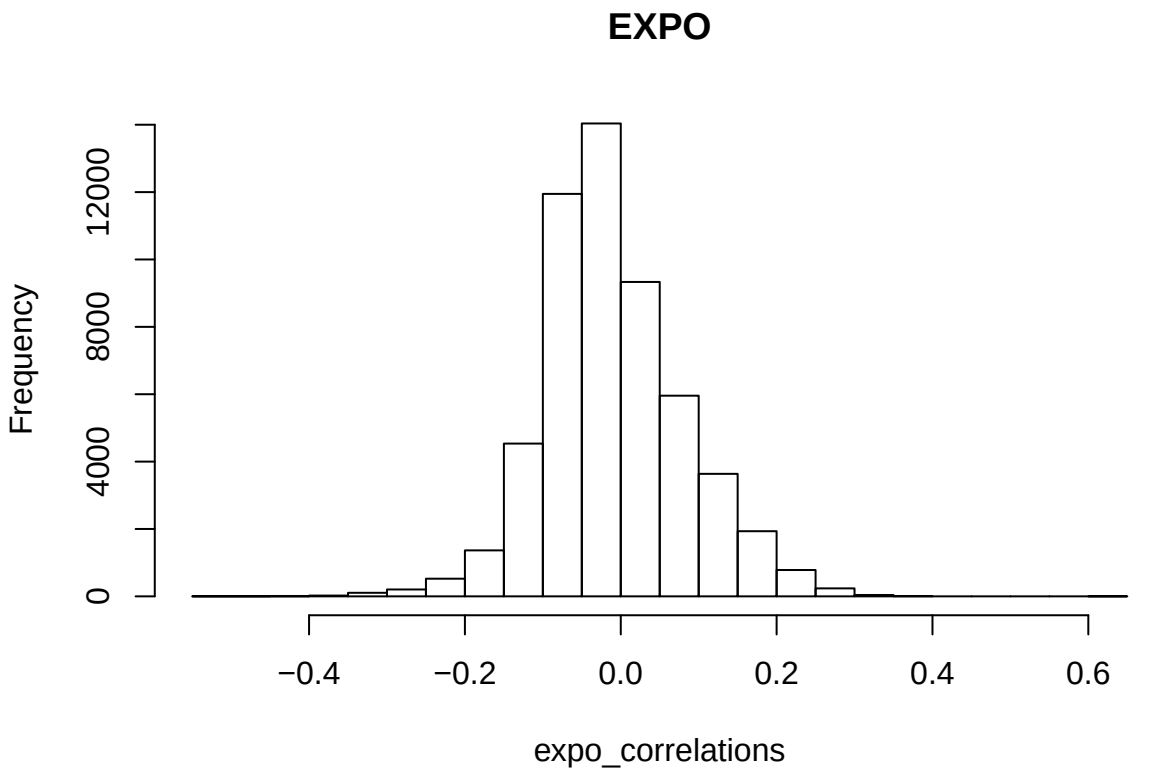
4 Analysis of correlations

This shows that most genes are not correlated to RSI.

```
hist(ccle_correlations, main="CCLE")
```




```
hist(expo_correlations, main="EXPO")
```



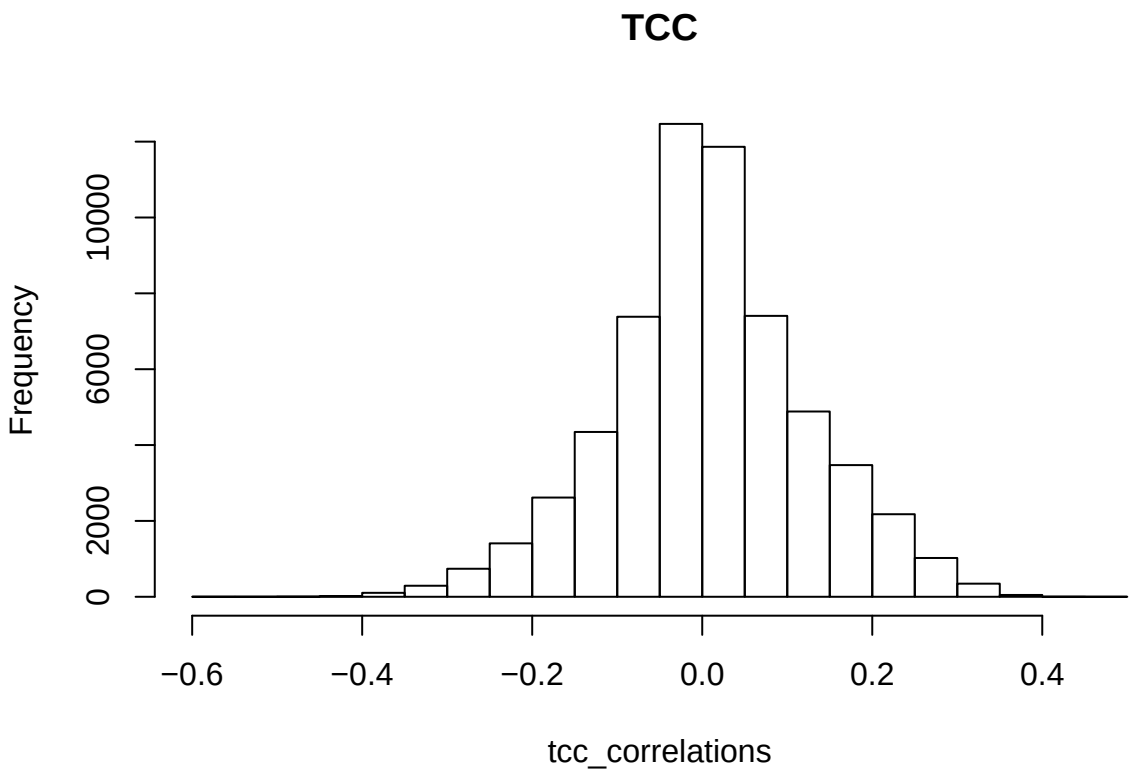

```
hist(tcc_correlations, main="TCC")
```

Table 1: TCC Correlated probesets

	R
merck-NM_176783_at	-0.5017434
merck-NM_002198_at	-0.5834575
merck2-AW137708_at	-0.5581379
merck2-DQ891838_at	-0.5115138

Table 2: EXPO correlated probesets

	R
202123_s_at	0.6209414
202531_at	-0.5324200



What probesets are correlated at a modest R=0.5?

```
kable(tcc_correlations[which(abs(tcc_correlations)>0.5)], col.names=c("R"), caption="TCC Correl
```

```
kable(expo_correlations[which(abs(expo_correlations)>0.5)], col.names=c("R"), caption="EXPO co
```

```
kable(ccle_correlations[which(abs(ccle_correlations)>0.5)], col.names=c("R"), caption="CCLE co
```

```
    u133_coeffs<-c("AFFX-HUMISGF3A/M97935_MA_at"=0.0254552046046931,
           "201209_at" = -0.020446868981449,
```

Table 3: CCLE correlated probesets

	R
202123_s_at	0.5855299
202531_at	-0.5848877
230405_at	-0.5149779
238725_at	-0.5830651

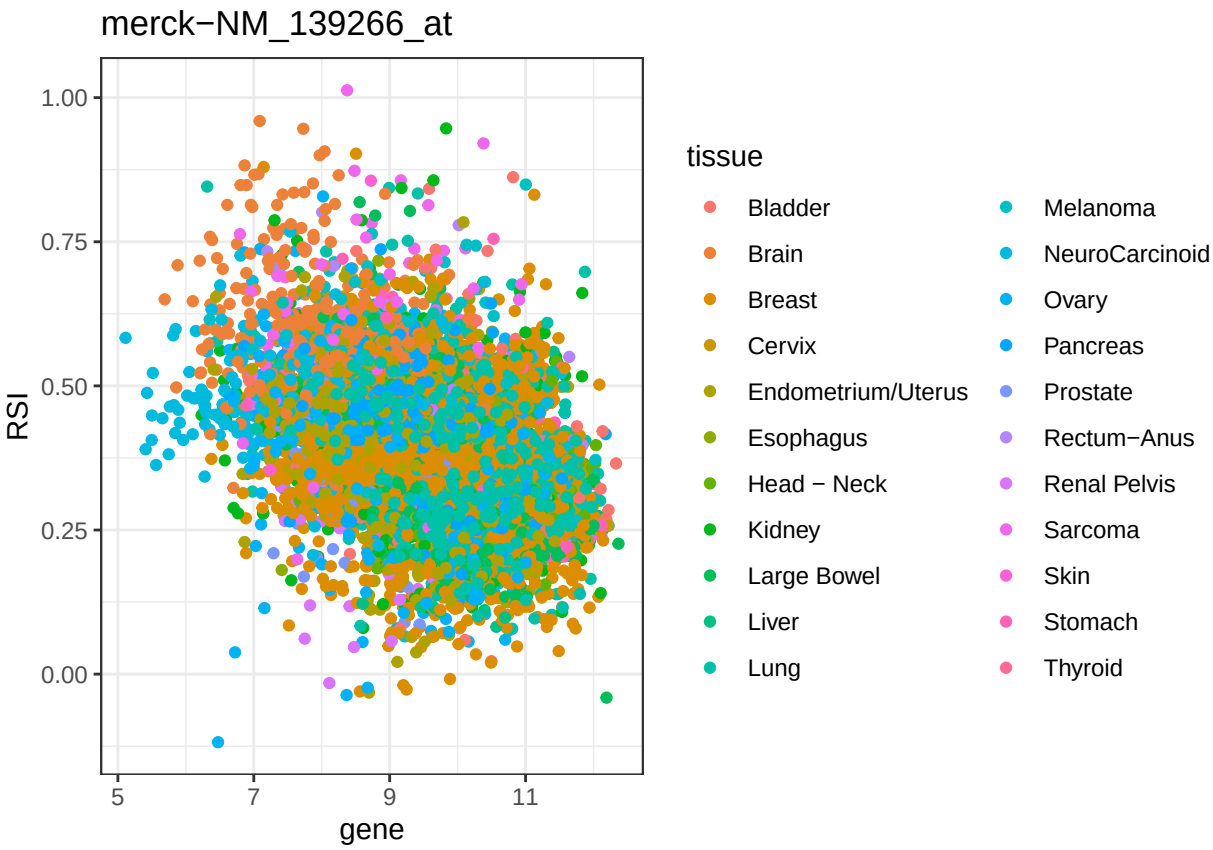
```
            "201466_s_at" = 0.0128282697929755,
            "201783_s_at" = -0.00381713588908642,
            "202123_s_at" = 0.107021274358643,
            "202531_at" = -0.0441682719957224,
            "205962_at" = -0.00924314364533049,
            "207957_s_at" = -0.00175888592095915,
            "208762_at" = -0.00025093287356907,
            "211110_s_at" = -0.00980092741843779)

  hursta_coeffs<-c("merck-NM_139266_at"=0.0254552046046931,
            "merck-NM_004964_at" = -0.020446868981449,
            "merck-NM_002228_at" = 0.0128282697929755,
            "merck2-BC069248_at" = -0.00381713588908642,
            "merck-NM_007313_s_at" = 0.107021274358643,
            "merck-NM_002198_at" = -0.0441682719957224,
            "merck-BQ646444_a_at" = -0.00924314364533049,
            "merck2-X06318_at" = -0.00175888592095915,
            "merck-NM_001005782_s_at" = -0.00025093287356907,
            "merck-NM_000044_a_at" = -0.00980092741843779)
```

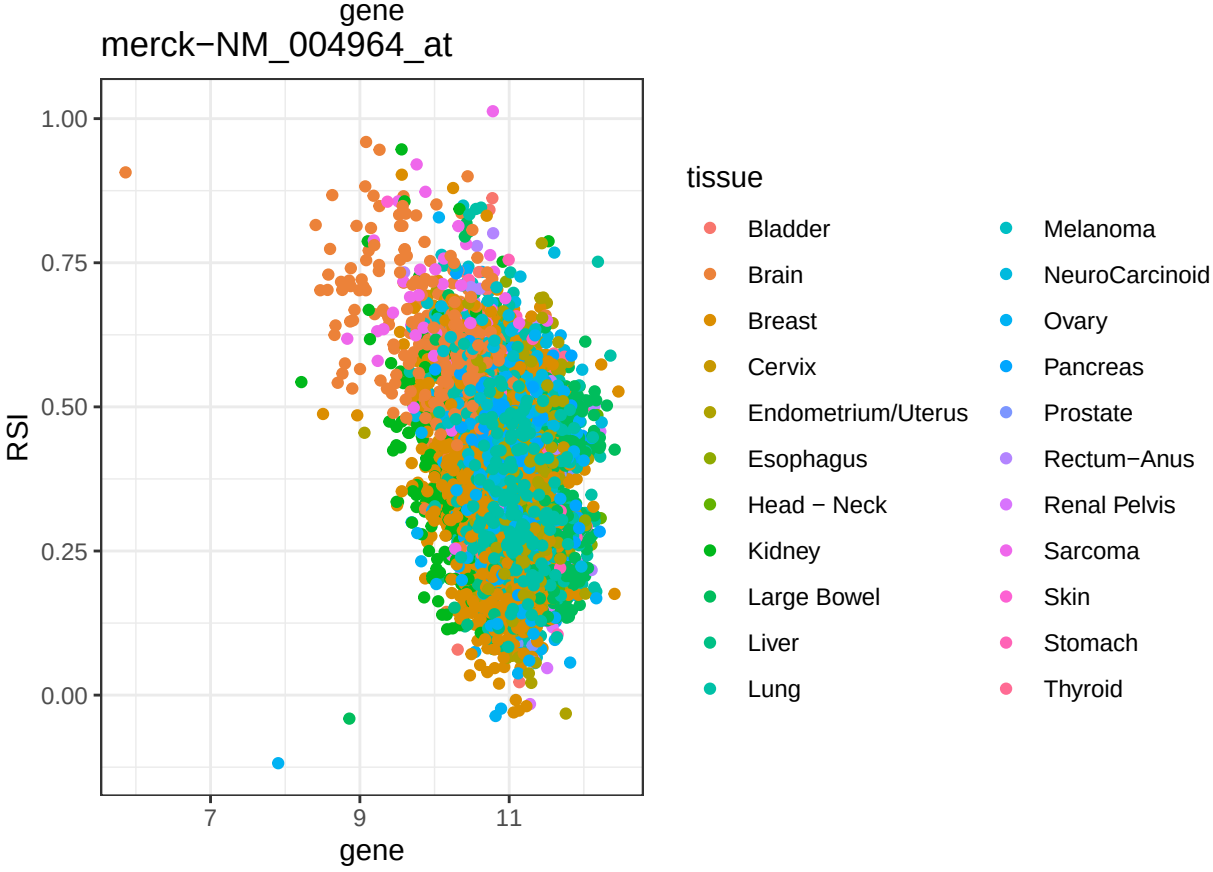
5 Gene Correlations

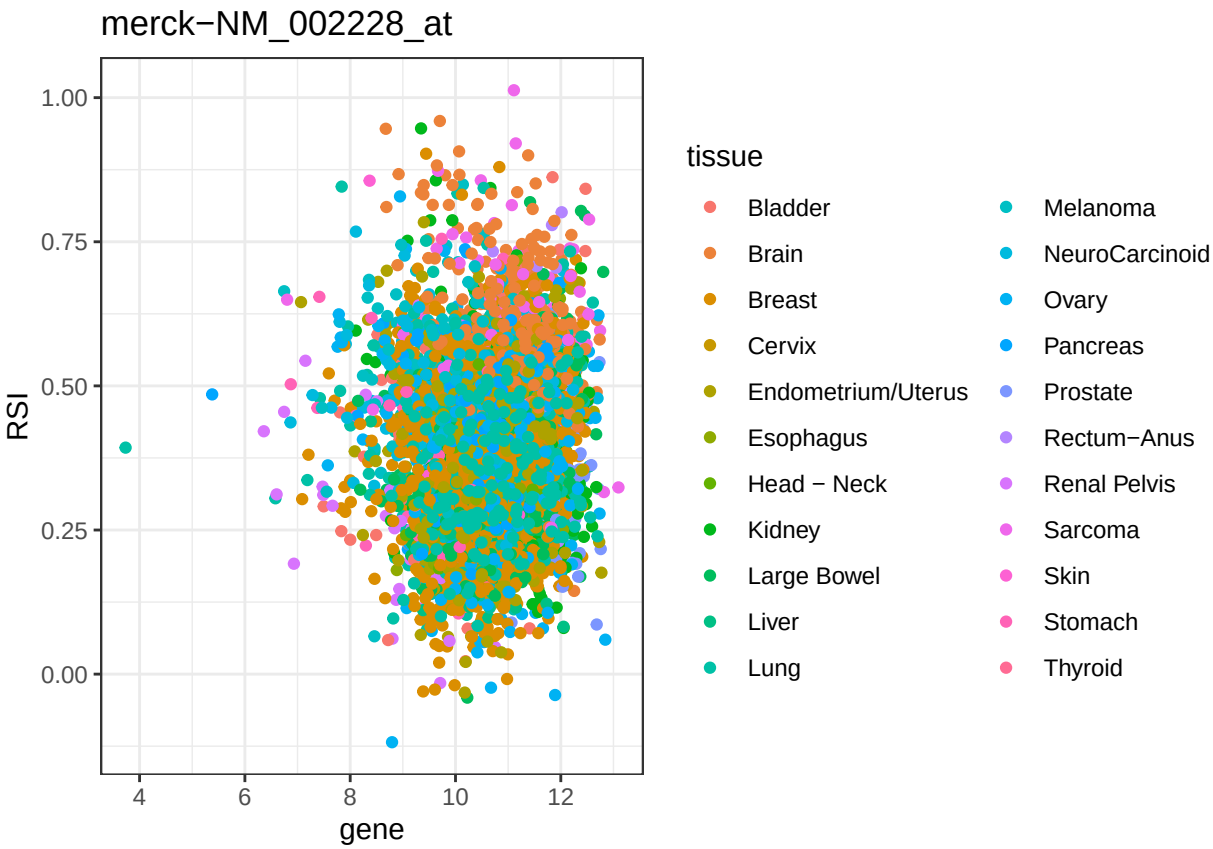
Show the correlations of the ten genes.

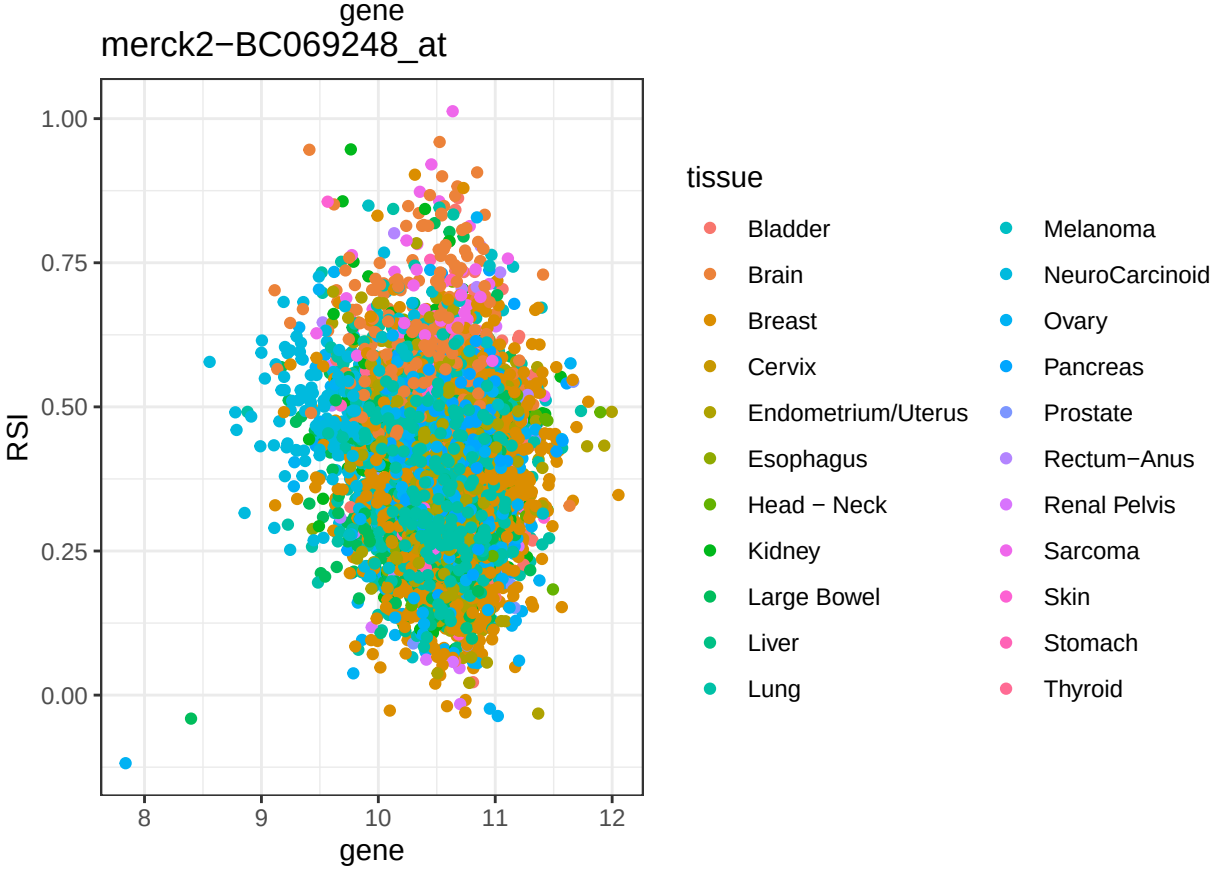
5.1 TCC

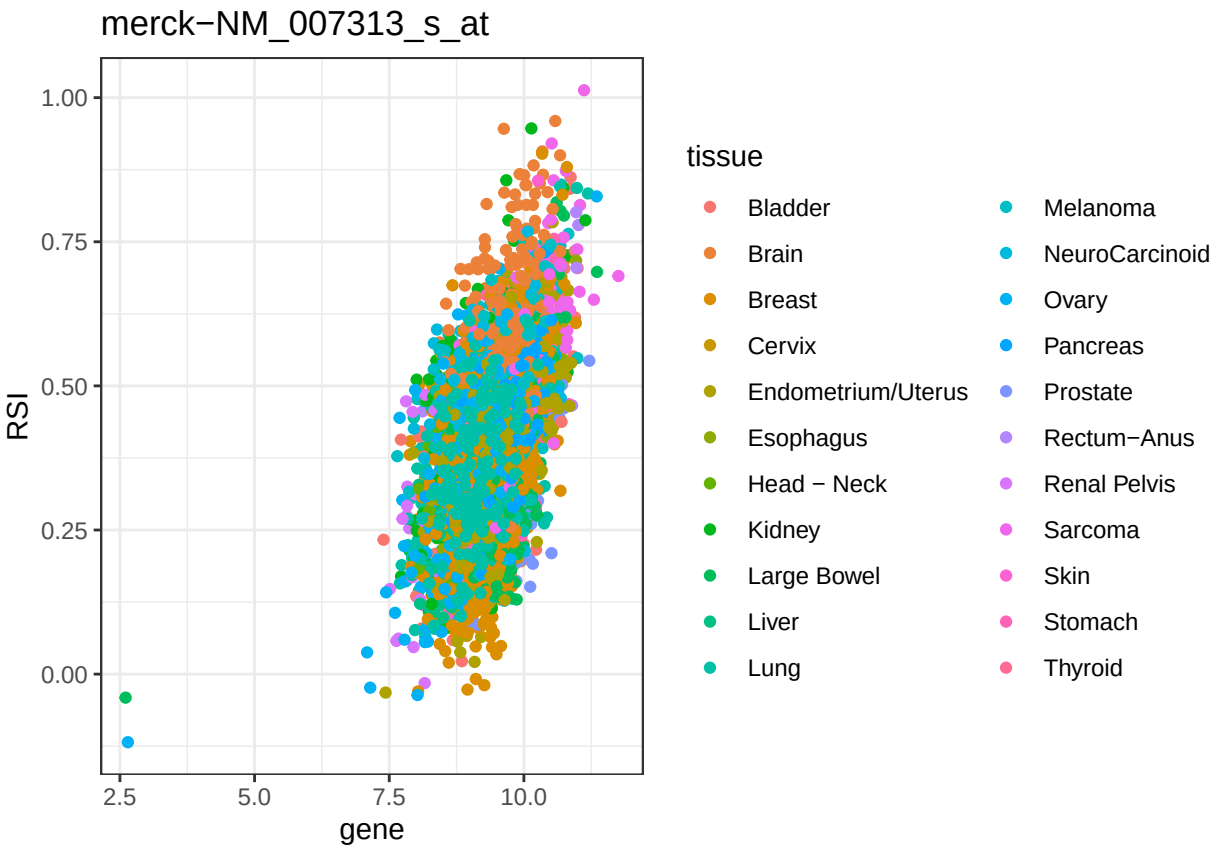
```
for (g in names(hursta_coeffs)) {
  myplot<-ggplot(data.frame(gene=exprs(tcc)[g,], RSI=tcc$RSI, tissue=tcc$SOO_Conformed), aes(x=
    geom_point() +
    theme_bw() +
    ggtitle(g)

  print(myplot)
}
```


merck−NM_139266_at
RSI
1.00
0.75
0.50
0.25
0.00
5
7
9
11
gene
tissue
Bladder
Brain
Breast
Cervix
Endometrium/Uterus
Esophagus
Head − Neck
Kidney
Large Bowel
Liver
Lung
Melanoma
NeuroCarcinoid
Ovary
Pancreas
Prostate
Rectum−Anus
Renal Pelvis
Sarcoma
Skin
Stomach
Thyroid


merck−NM_004964_at
RSI
1.00
0.75
0.50
0.25
0.00
7
9
11
gene
tissue
Bladder
Brain
Breast
Cervix
Endometrium/Uterus
Esophagus
Head − Neck
Kidney
Large Bowel
Liver
Lung
Melanoma
NeuroCarcinoid
Ovary
Pancreas
Prostate
Rectum−Anus
Renal Pelvis
Sarcoma
Skin
Stomach
Thyroid


merck−NM_002228_at
RSI
1.00
0.75
0.50
0.25
0.00
4
6
8
10
12
gene
tissue
Bladder
Brain
Breast
Cervix
Endometrium/Uterus
Esophagus
Head − Neck
Kidney
Large Bowel
Liver
Lung
Melanoma
NeuroCarcinoid
Ovary
Pancreas
Prostate
Rectum−Anus
Renal Pelvis
Sarcoma
Skin
Stomach
Thyroid


merck2−BC069248_at
RSI
1.00
0.75
0.50
0.25
0.00
8
9
10
11
12
gene
tissue
Bladder
Brain
Breast
Cervix
Endometrium/Uterus
Esophagus
Head − Neck
Kidney
Large Bowel
Liver
Lung
Melanoma
NeuroCarcinoid
Ovary
Pancreas
Prostate
Rectum−Anus
Renal Pelvis
Sarcoma
Skin
Stomach
Thyroid


merck−NM_007313_s_at
RSI
1.00
0.75
0.50
0.25
0.00
2.5
5.0
7.5
10.0
gene
tissue
Bladder
Brain
Breast
Cervix
Endometrium/Uterus
Esophagus
Head − Neck
Kidney
Large Bowel
Liver
Lung
Melanoma
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Ovary
Pancreas
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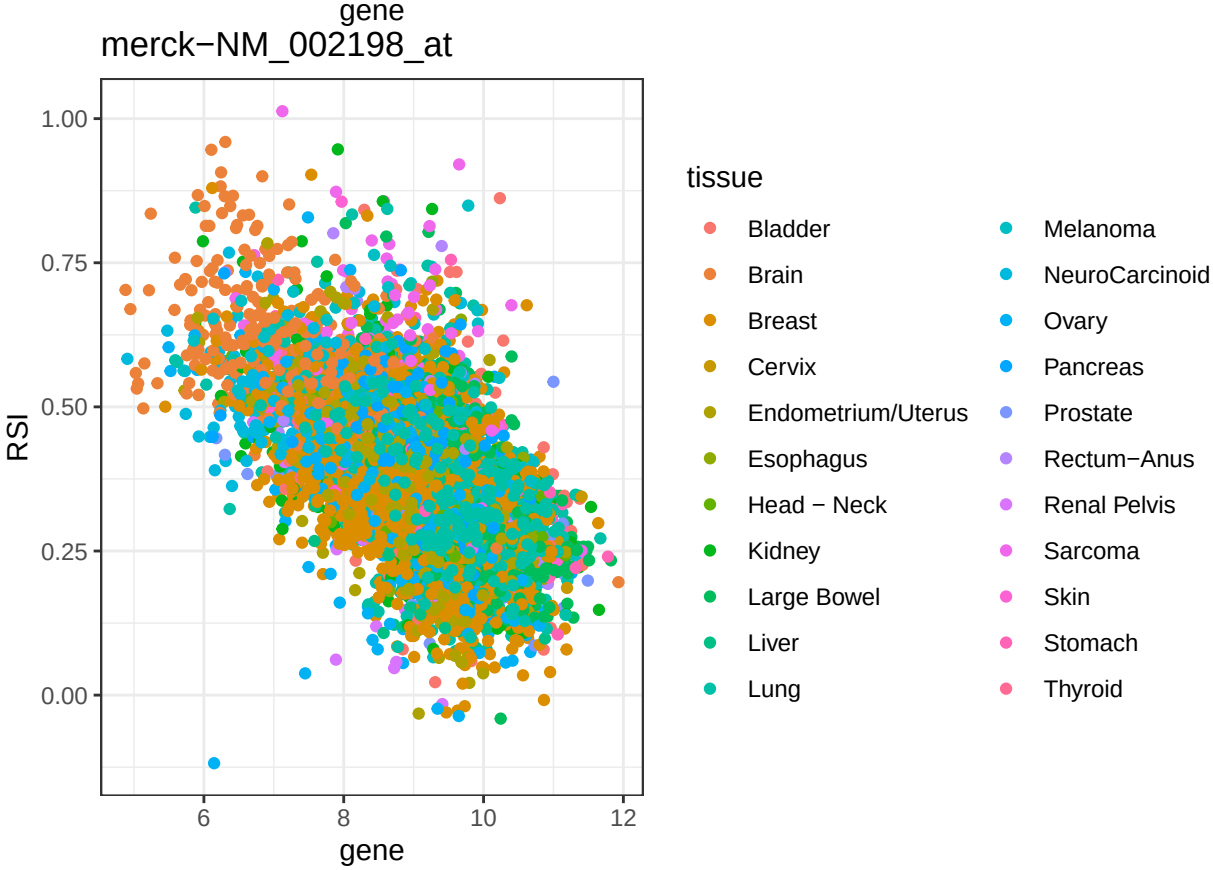
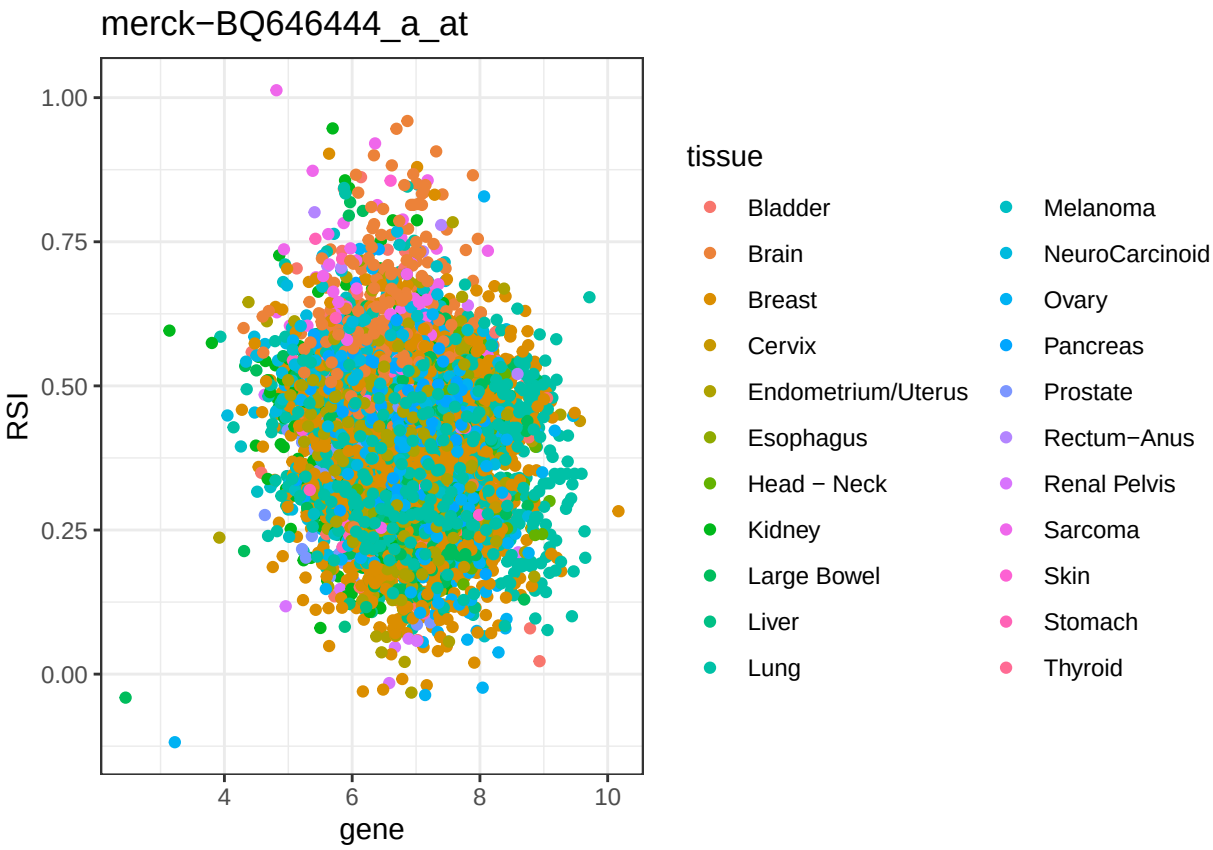
Rectum−Anus
Renal Pelvis
Sarcoma
Skin
Stomach
Thyroid


merck−NM_002198_at
RSI
1.00
0.75
0.50
0.25
0.00
6
8
10
12
gene
tissue
Bladder
Brain
Breast
Cervix
Endometrium/Uterus
Esophagus
Head − Neck
Kidney
Large Bowel
Liver
Lung
Melanoma
NeuroCarcinoid
Ovary
Pancreas
Prostate
Rectum−Anus
Renal Pelvis
Sarcoma
Skin
Stomach
Thyroid


merck−BQ646444_a_at
RSI
1.00
0.75
0.50
0.25
0.00
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gene
tissue
Bladder
Brain
Breast
Cervix
Endometrium/Uterus
Esophagus
Head − Neck
Kidney
Large Bowel
Liver
Lung
Melanoma
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Ovary
Pancreas
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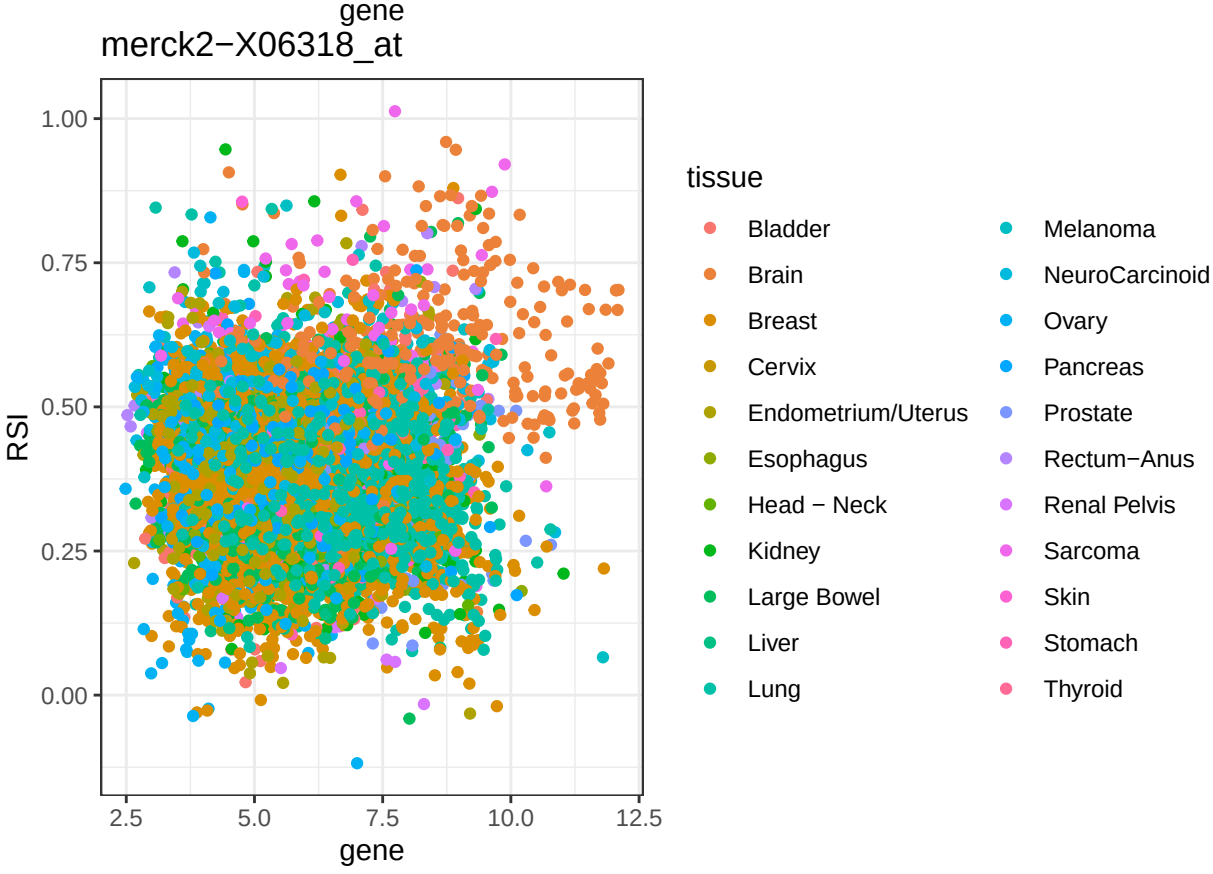
Rectum−Anus
Renal Pelvis
Sarcoma
Skin
Stomach
Thyroid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RSI
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0.75
0.50
0.25
0.00
2.5
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7.5
10.0
12.5
gene
tissue
Bladder
Brain
Breast
Cervix
Endometrium/Uterus
Esophagus
Head − Neck
Kidney
Large Bowel
Liver
Lung
Melanoma
NeuroCarcinoid
Ovary
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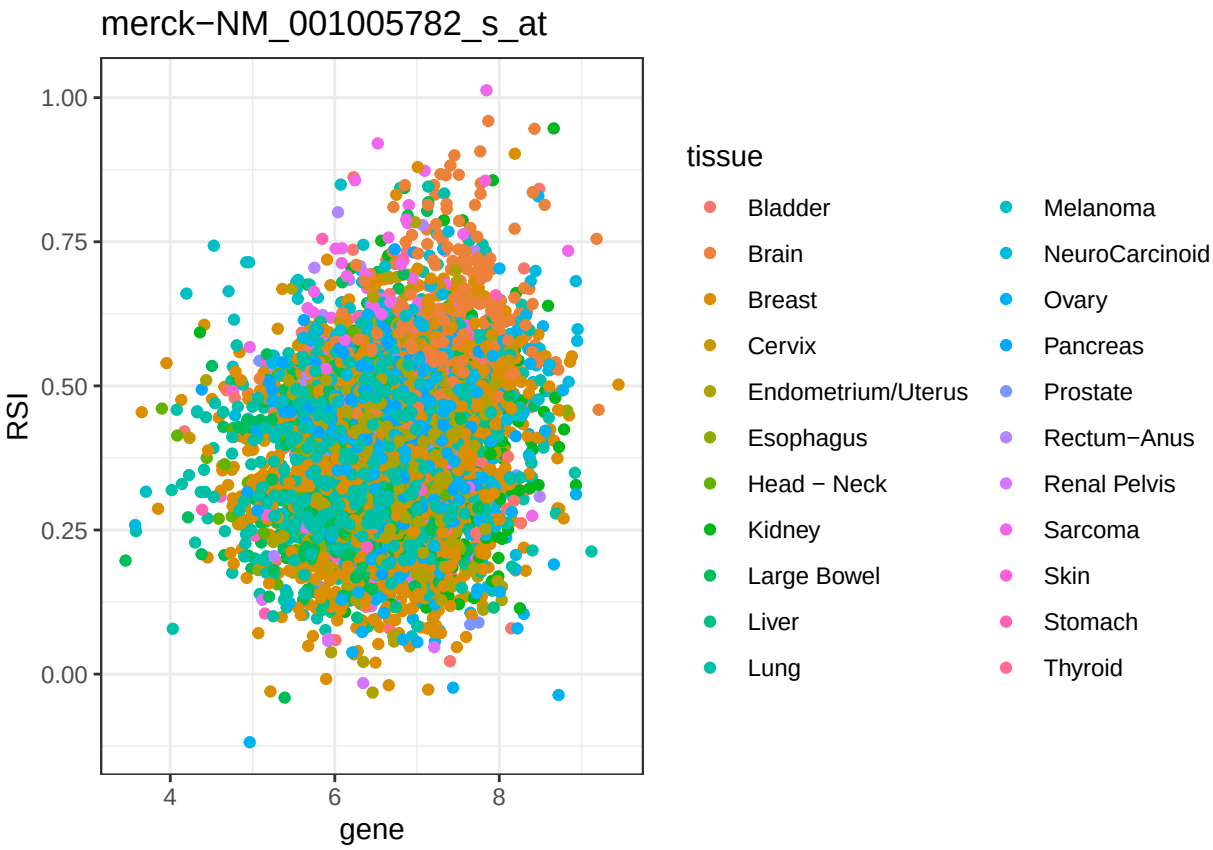
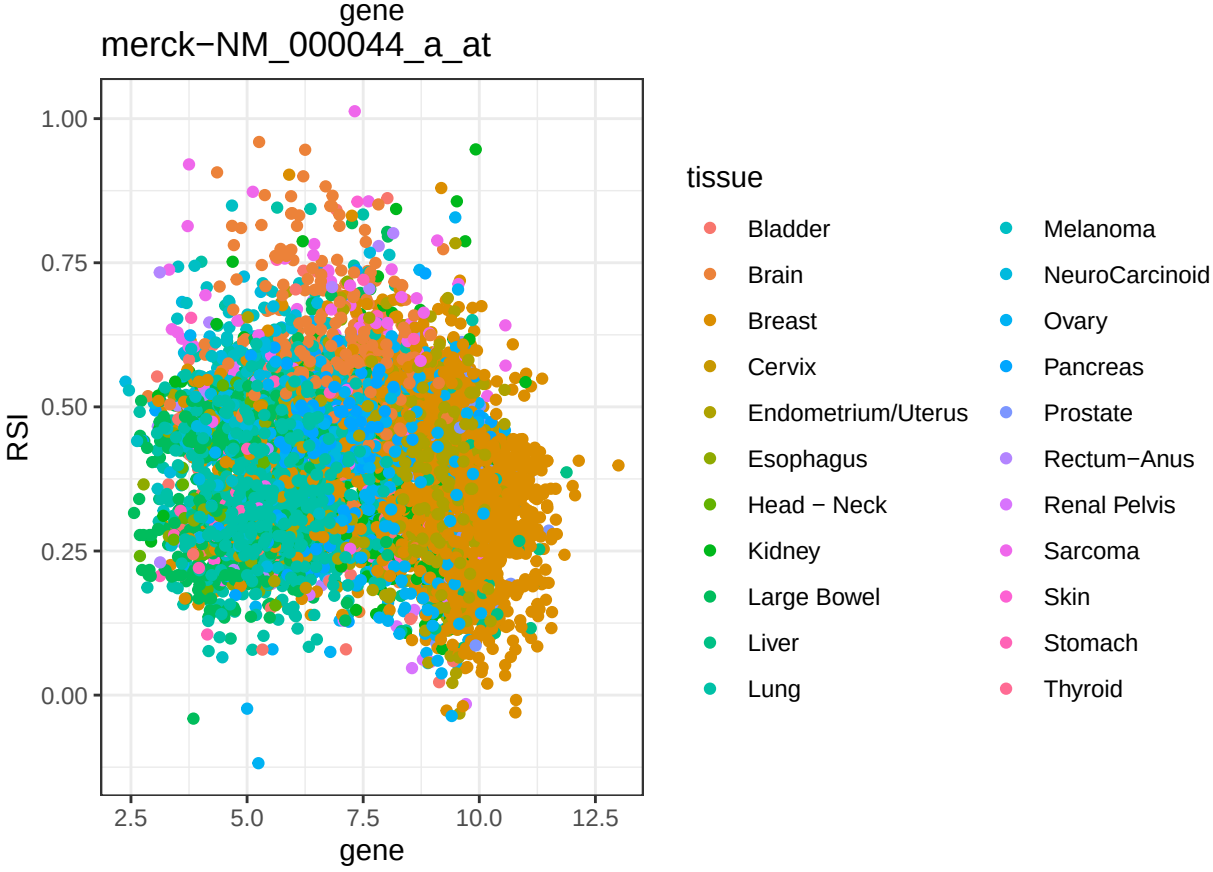
Prostate
Rectum−Anus
Renal Pelvis
Sarcoma
Skin
Stomach
Thyroid

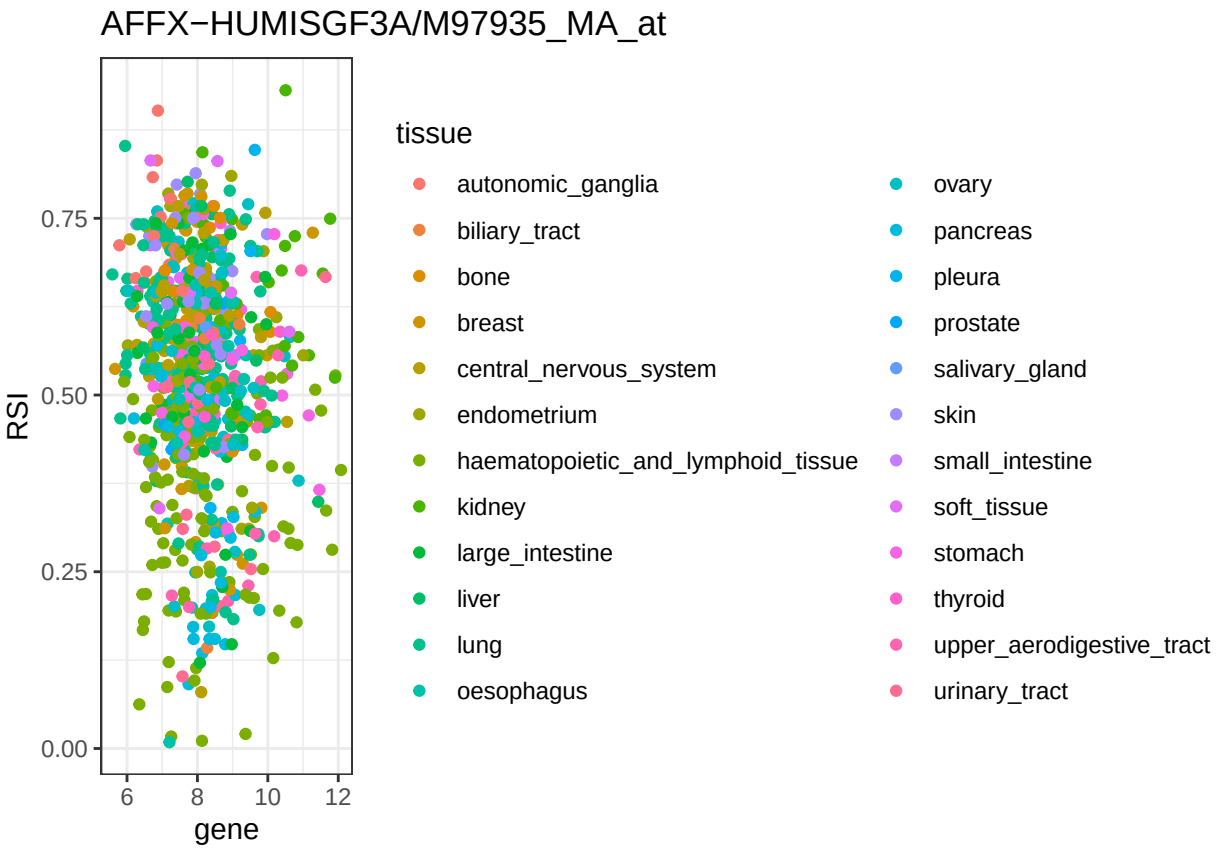

merck−NM_001005782_s_at
RSI
1.00
0.75
0.50
0.25
0.00
4
6
8
gene
tissue
Bladder
Brain
Breast
Cervix
Endometrium/Uterus
Esophagus
Head − Neck
Kidney
Large Bowel
Liver
Lung
Melanoma
NeuroCarcinoid
Ovary
Pancreas
Prostate
Rectum−Anus
Renal Pelvis
Sarcoma
Skin
Stomach
Thyroid

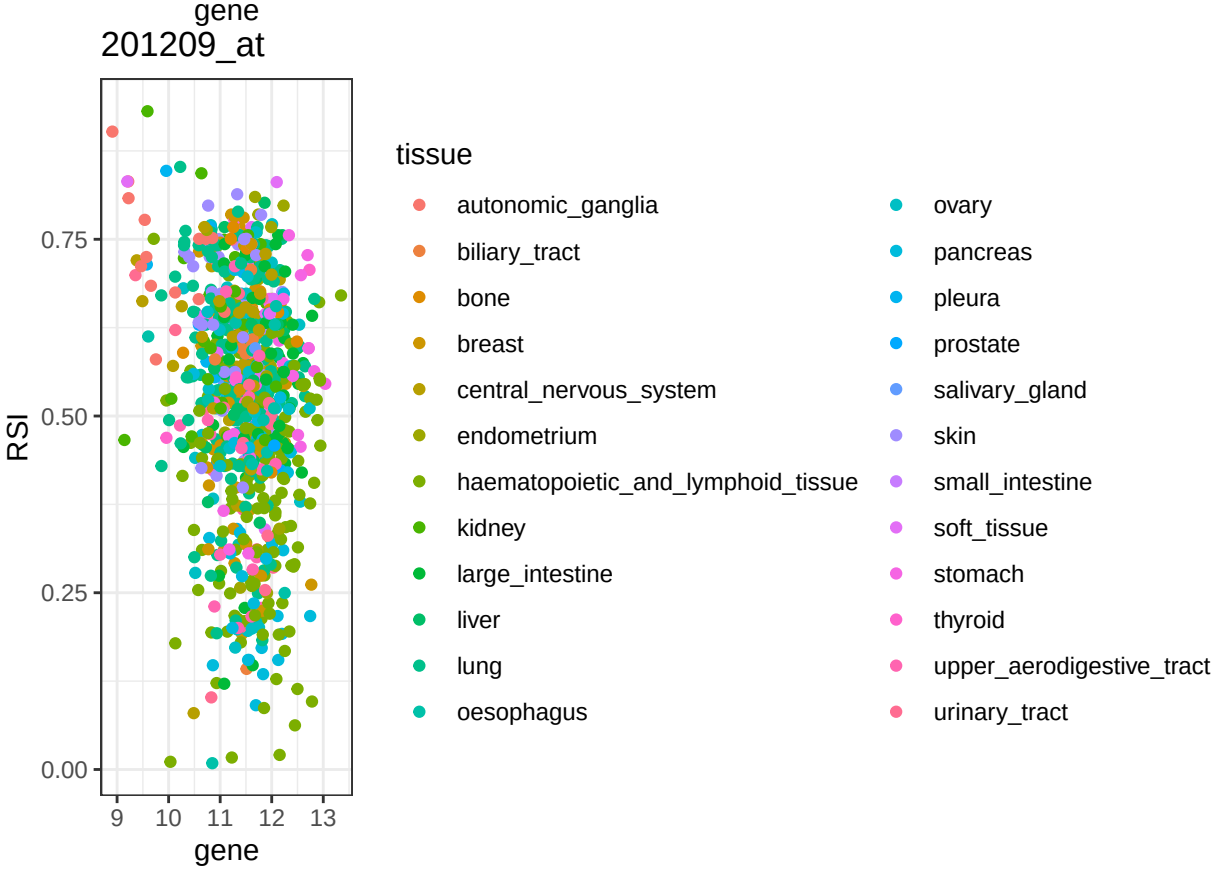

merck−NM_000044_a_at
RSI
1.00
0.75
0.50
0.25
0.00
2.5
5.0
7.5
10.0
12.5
gene
tissue
Bladder
Brain
Breast
Cervix
Endometrium/Uterus
Esophagus
Head − Neck
Kidney
Large Bowel
Liver
Lung
Melanoma
NeuroCarcinoid
Ovary
Pancreas
Prostate
Rectum−Anus
Renal Pelvis
Sarcoma
Skin
Stomach
Thyroid

5.2 CCLE

```
for (g in names(u133_coeffs)) {
  myplot<-ggplot(data.frame(gene=exprs(ccle)[g,], RSI=ccle$RSI, tissue=ccle$`Site Primary`), ae
    geom_point() +
    theme_bw() +
    ggtitle(g)

  print(myplot)
}
```


AFFX−HUMISGF3A/M97935_MA_at
RSI
0.00
0.25
0.50
0.75
6
8
10
12
gene
tissue
autonomic_ganglia
biliary_tract
bone
breast
central_nervous_system
endometrium
haematopoietic_and_lymphoid_tissue
kidney
large_intestine
liver
lung
oesophagus
ovary
pancreas
pleura
prostate
salivary_gland
skin
small_intestine
soft_tissue
stomach
thyroid
upper_aerodigestive_tract
urinary_tract


201209_at
RSI
0.00
0.25
0.50
0.75
9
10
11
12
13
gene
tissue
autonomic_ganglia
biliary_tract
bone
breast
central_nervous_system
endometrium
haematopoietic_and_lymphoid_tissue
kidney
large_intestine
liver
lung
oesophagus
ovary
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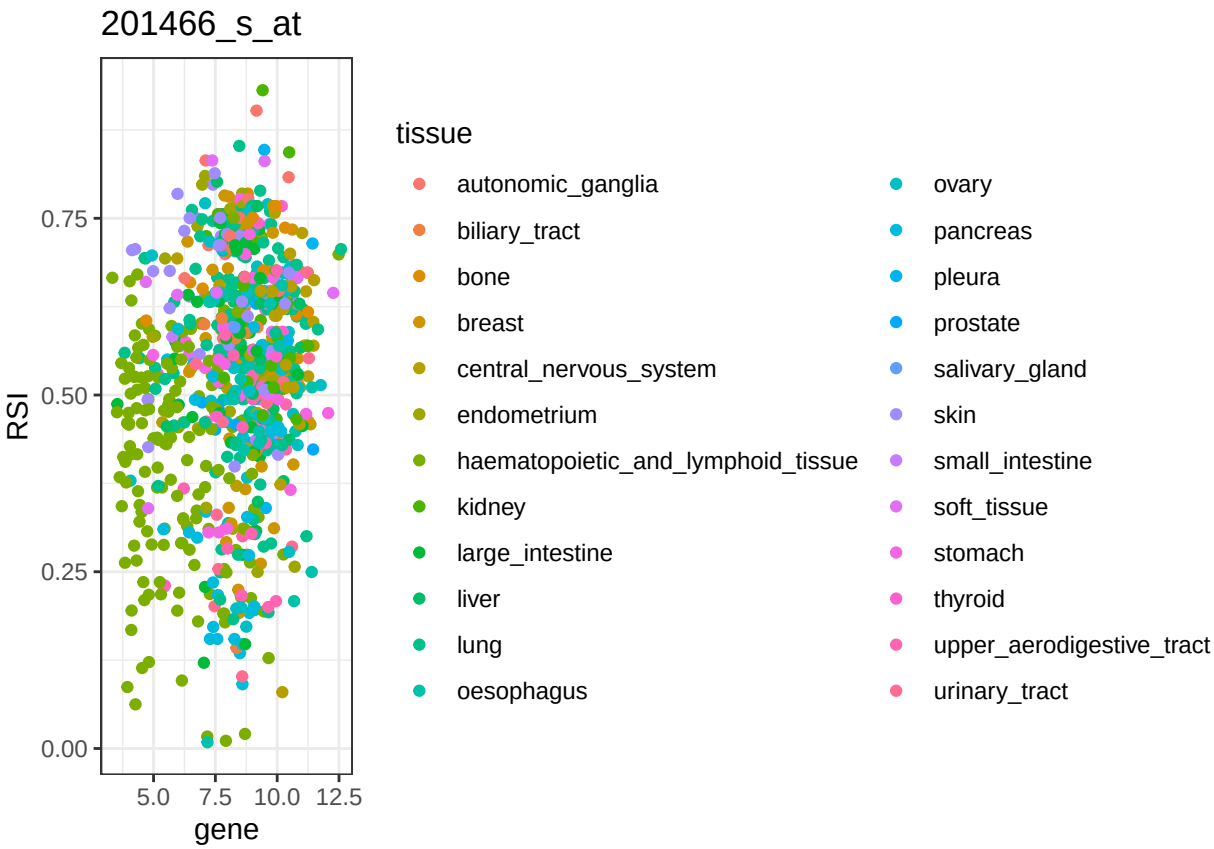
thyroid
upper_aerodigestive_tract
urinary_tract


201466_s_at
RSI
0.00
0.25
0.50
0.75
5.0
7.5
10.0
12.5
gene
tissue
autonomic_ganglia
biliary_tract
bone
breast
central_nervous_system
endometrium
haematopoietic_and_lymphoid_tissue
kidney
large_intestine
liver
lung
oesophagus
ovary
pancreas
pleura
prostate
salivary_gland
skin
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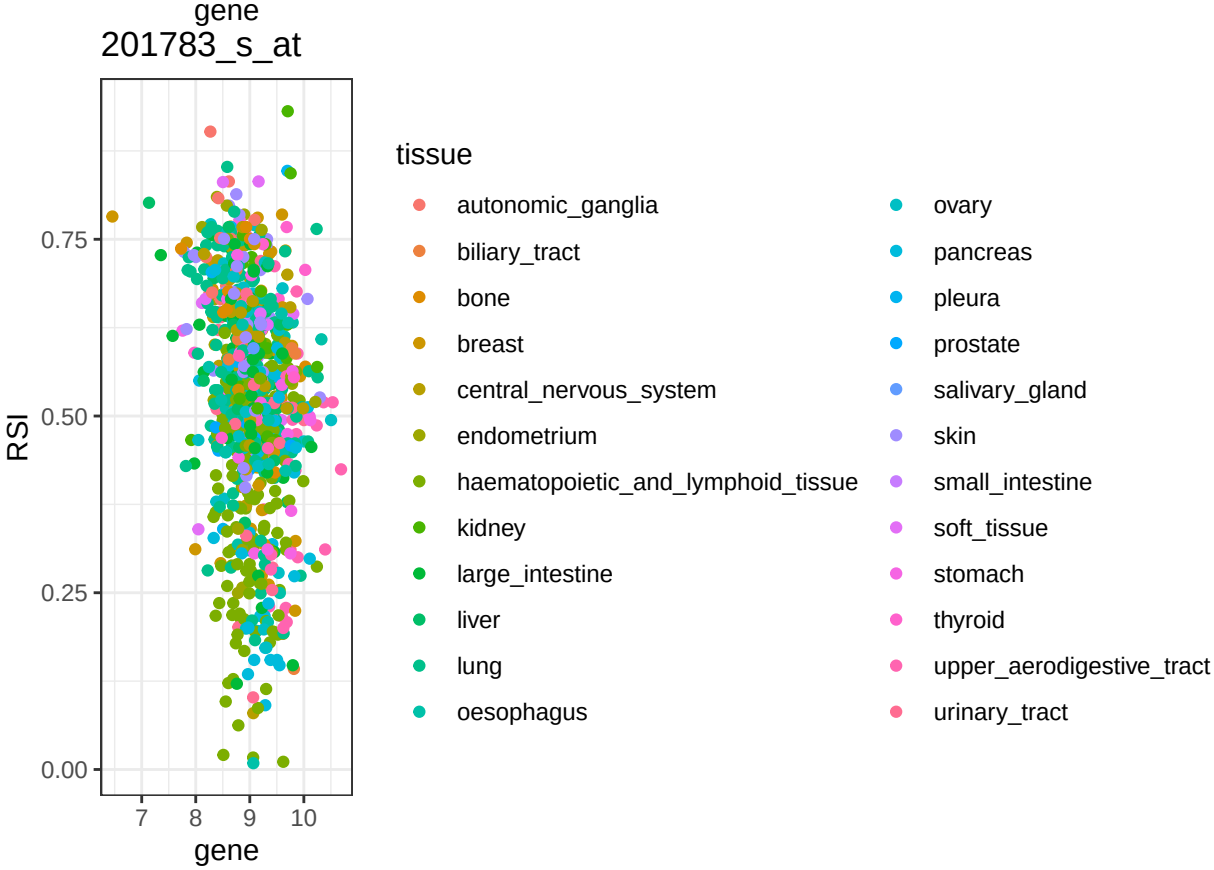
stomach
thyroid
upper_aerodigestive_tract
urinary_tract


201783_s_at
RSI
0.00
0.25
0.50
0.75
7
8
9
10
gene
tissue
autonomic_ganglia
biliary_tract
bone
breast
central_nervous_system
endometrium
haematopoietic_and_lymphoid_tissue
kidney
large_intestine
liver
lung
oesophagus
ovary
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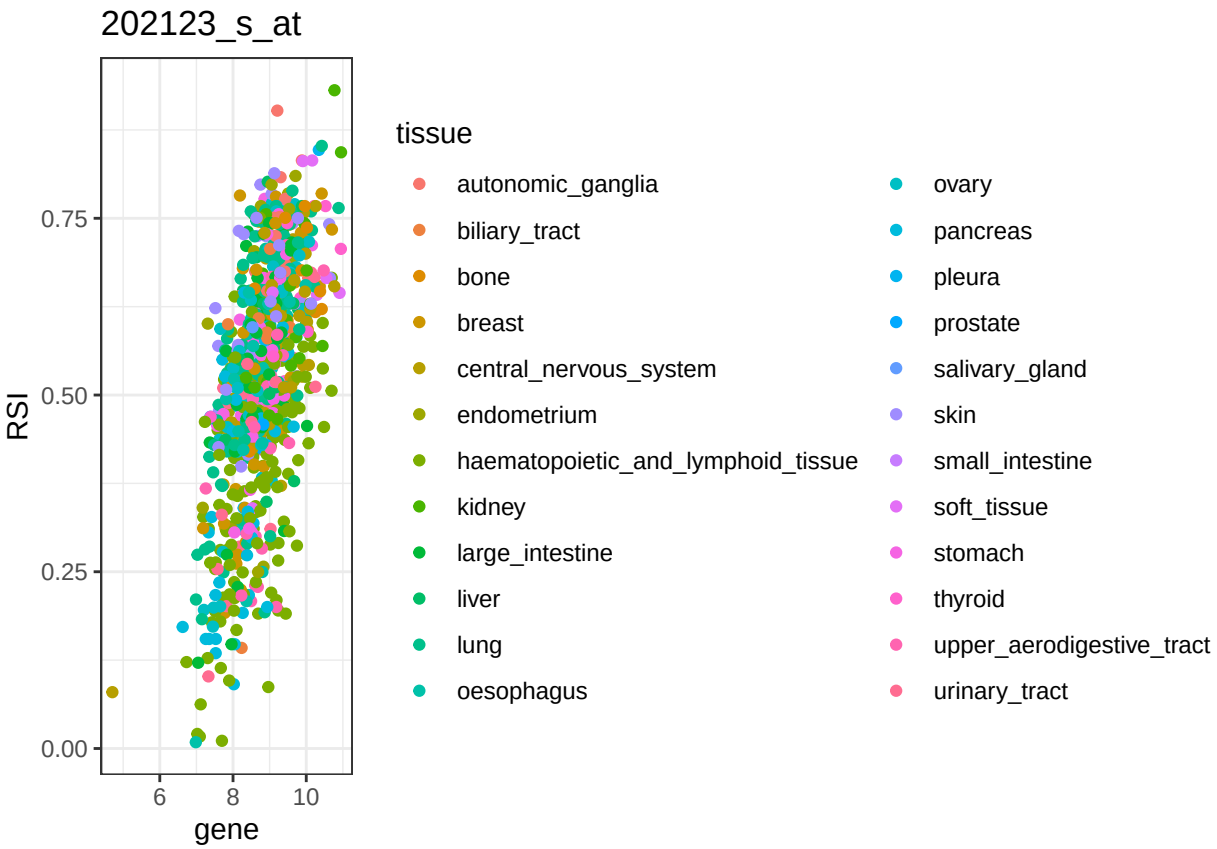
stomach
thyroid
upper_aerodigestive_tract
urinary_tract


202123_s_at
RSI
0.00
0.25
0.50
0.75
6
8
10
gene
tissue
autonomic_ganglia
biliary_tract
bone
breast
central_nervous_system
endometrium
haematopoietic_and_lymphoid_tissue
kidney
large_intestine
liver
lung
oesophagus
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pancreas
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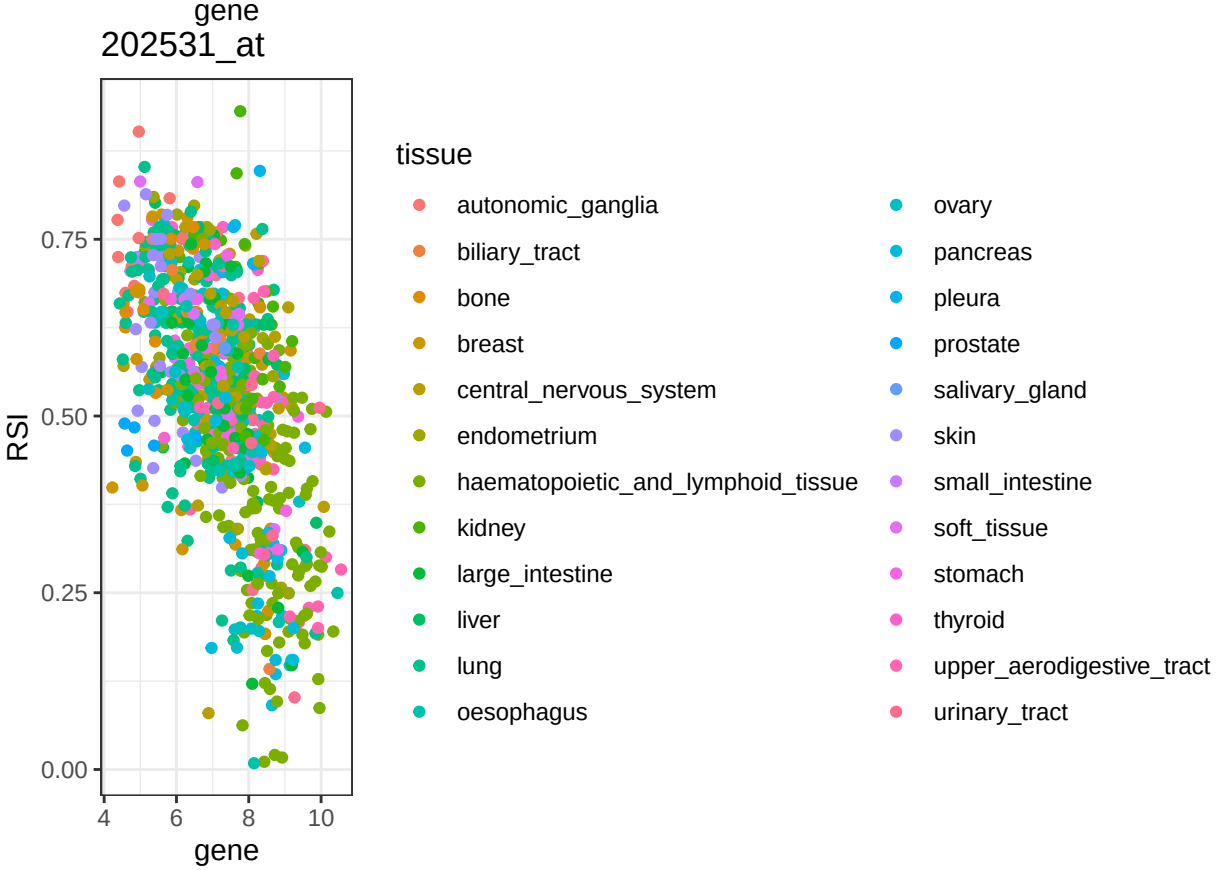
stomach
thyroid
upper_aerodigestive_tract
urinary_tract


202531_at
RSI
0.00
0.25
0.50
0.75
4
6
8
10
gene
tissue
autonomic_ganglia
biliary_tract
bone
breast
central_nervous_system
endometrium
haematopoietic_and_lymphoid_tissue
kidney
large_intestine
liver
lung
oesophagus
ovary
pancreas
pleura
prostate
salivary_gland
skin
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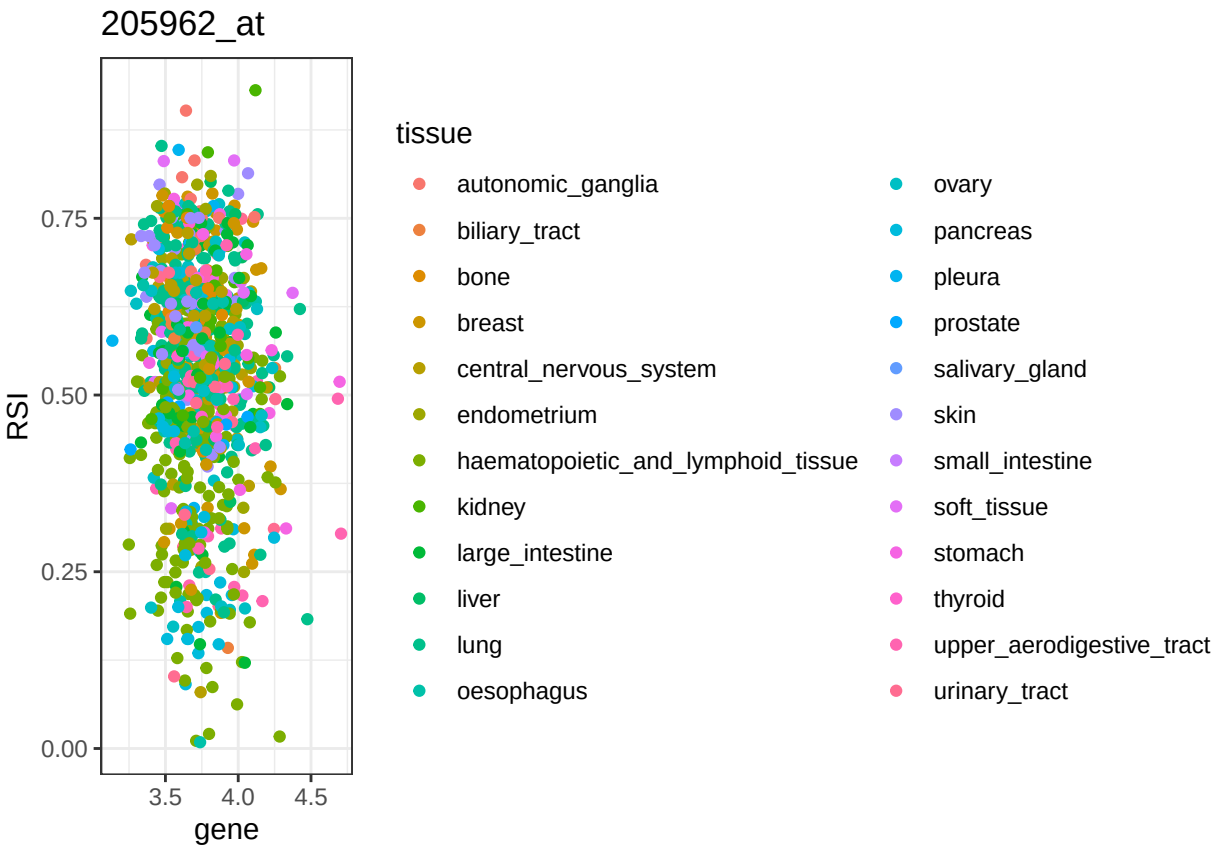
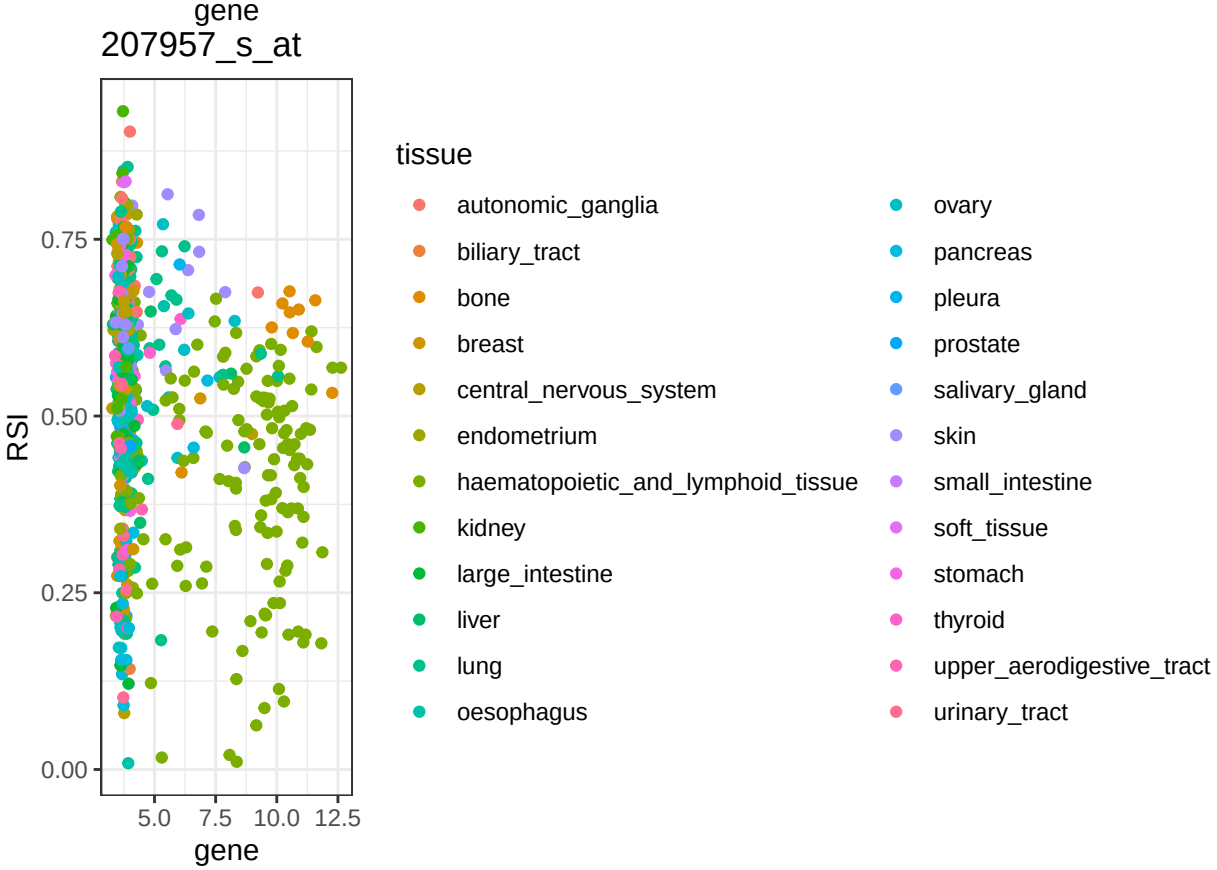
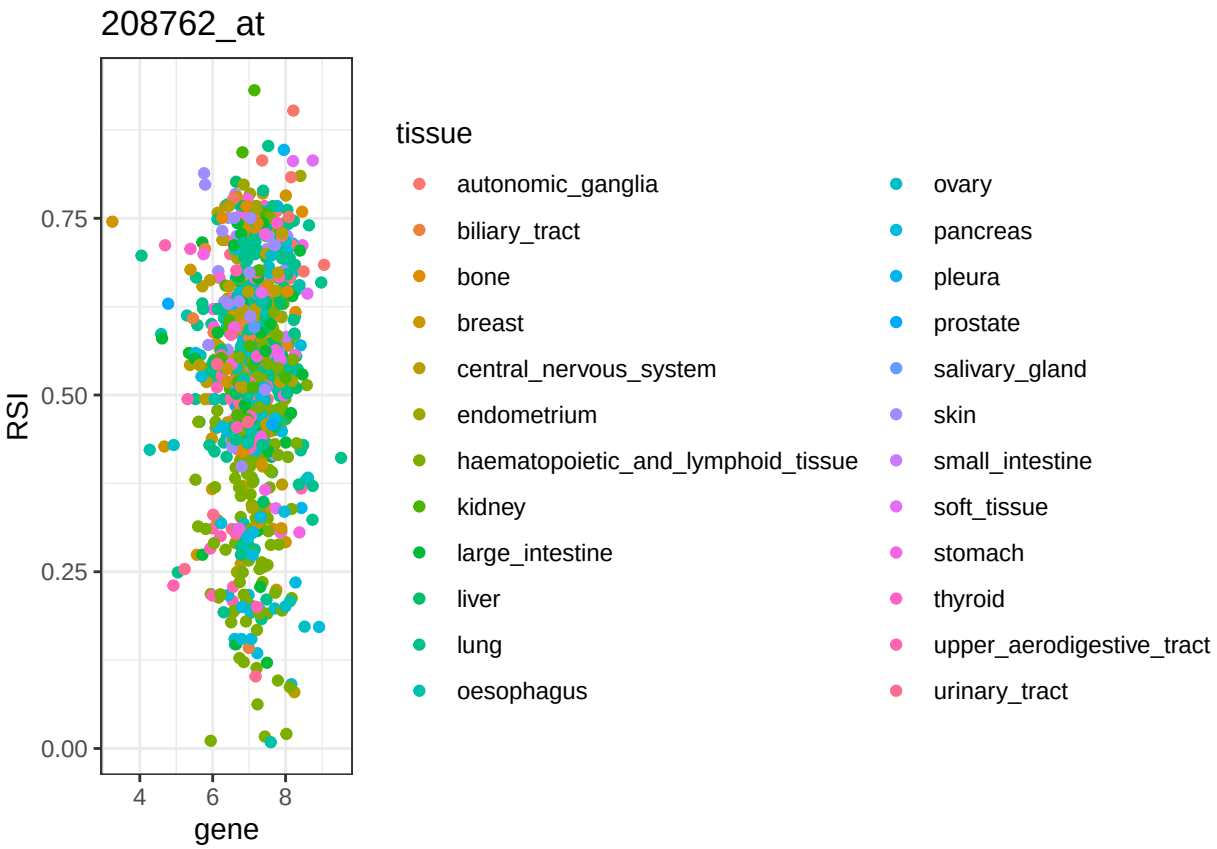
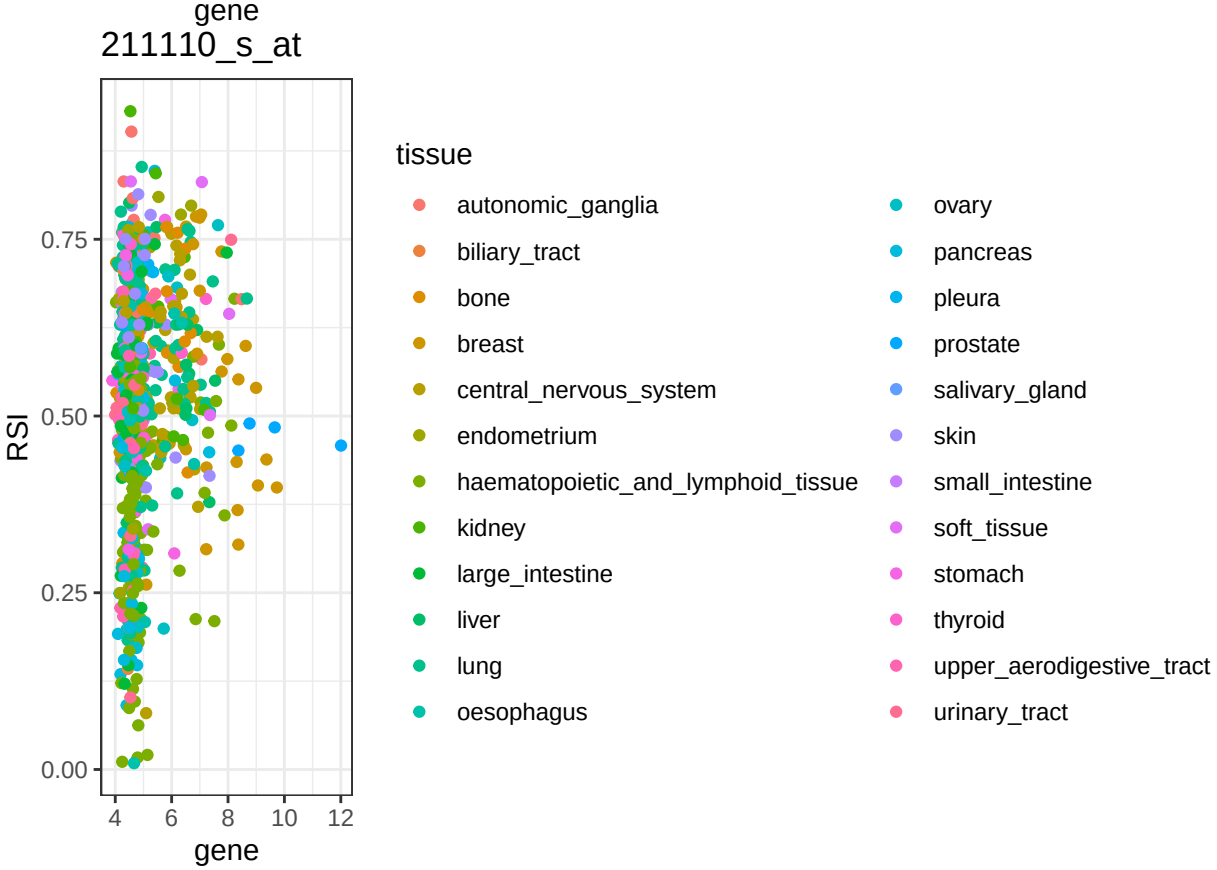
stomach
thyroid
upper_aerodigestive_tract
urinary_tract


205962_at
RSI
0.00
0.25
0.50
0.75
3.5
4.0
4.5
gene
tissue
autonomic_ganglia
biliary_tract
bone
breast
central_nervous_system
endometrium
haematopoietic_and_lymphoid_tissue
kidney
large_intestine
liver
lung
oesophagus
ovary
pancreas
pleura
prostate
salivary_gland
skin
small_intestine
soft_tissue
stomach
thyroid
upper_aerodigestive_tract
urinary_tract

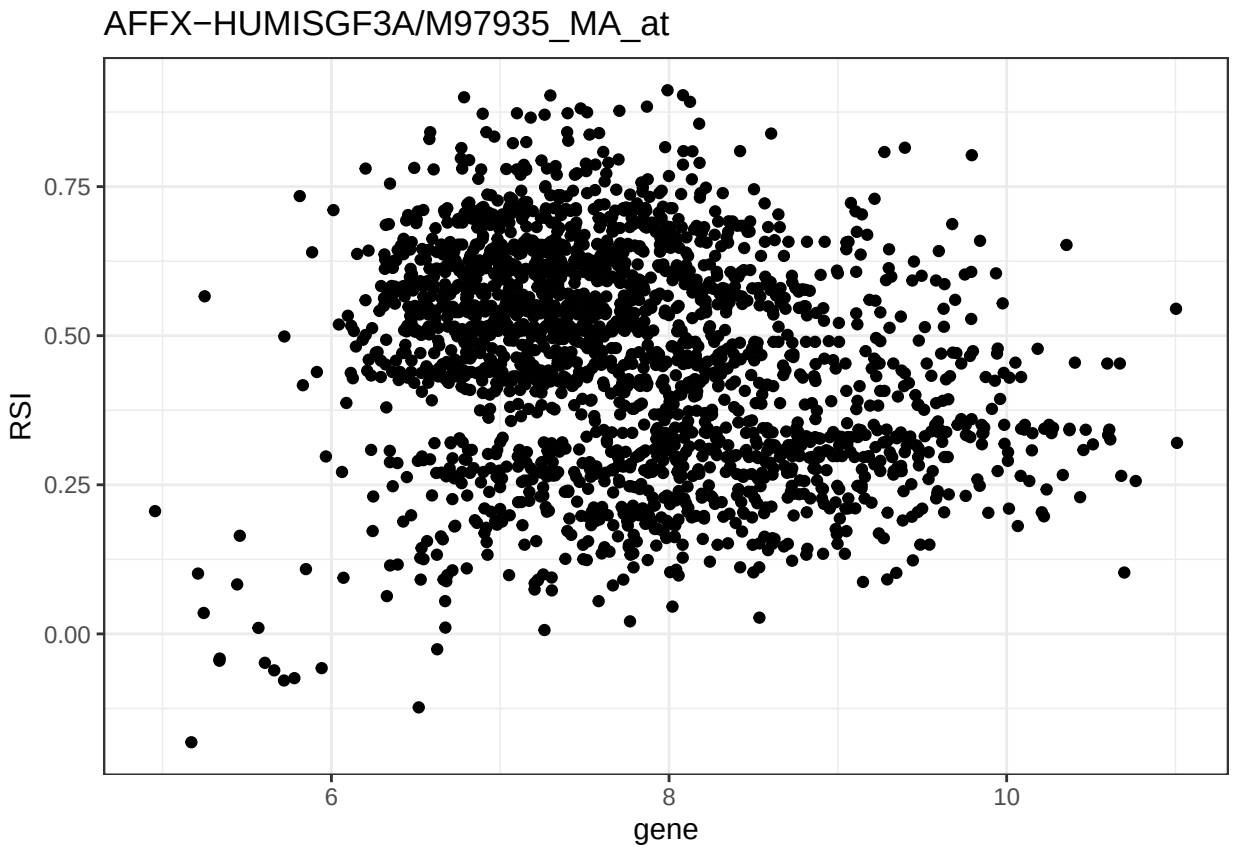

207957_s_at
RSI
0.00
0.25
0.50
0.75
5.0
7.5
10.0
12.5
gene
tissue
autonomic_ganglia
biliary_tract
bone
breast
central_nervous_system
endometrium
haematopoietic_and_lymphoid_tissue
kidney
large_intestine
liver
lung
oesophagus
ovary
pancreas
pleura
prostate
salivary_gland
skin
small_intestine
soft_tissue
stomach
thyroid
upper_aerodigestive_tract
urinary_tract

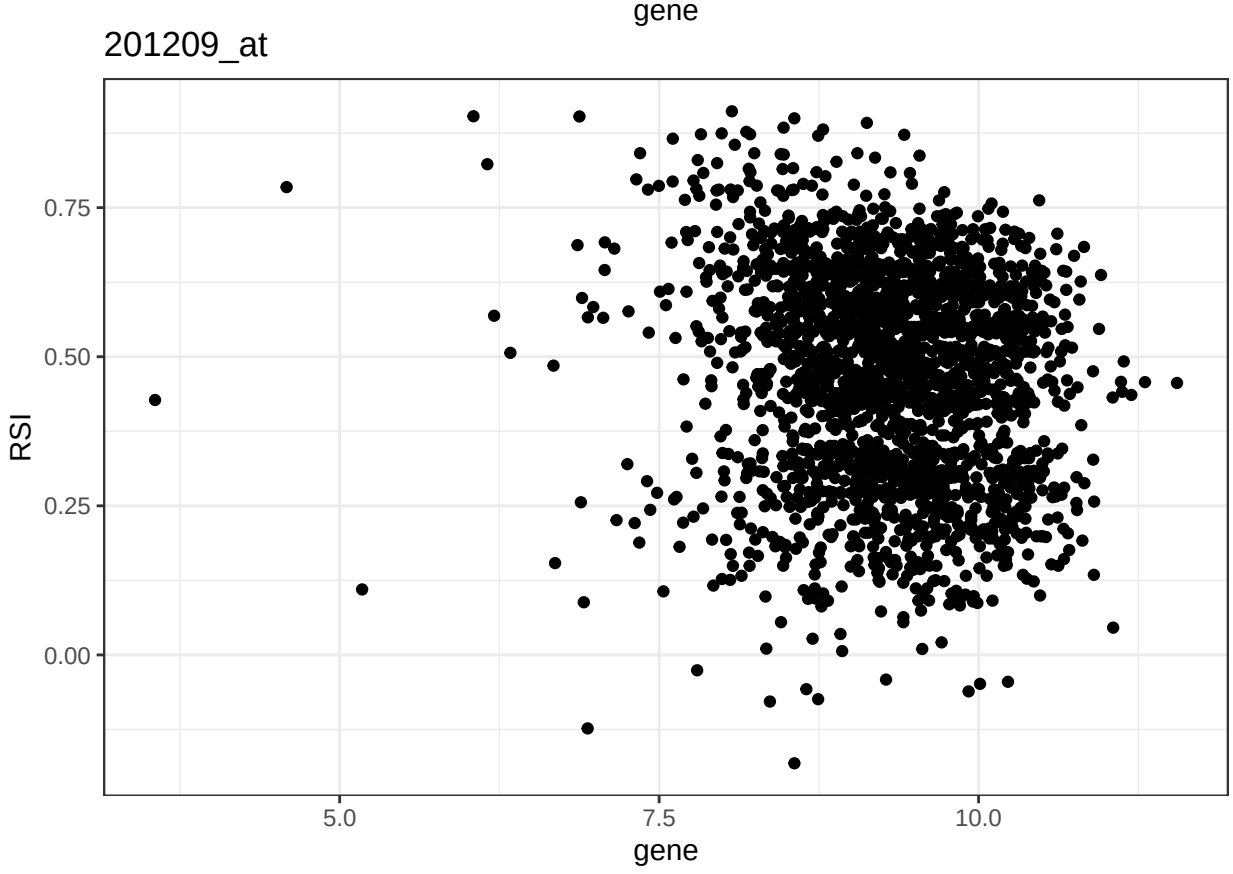

208762_at
RSI
0.00
0.25
0.50
0.75
4
6
8
gene
tissue
autonomic_ganglia
biliary_tract
bone
breast
central_nervous_system
endometrium
haematopoietic_and_lymphoid_tissue
kidney
large_intestine
liver
lung
oesophagus
ovary
pancreas
pleura
prostate
salivary_gland
skin
small_intestine
soft_tissue
stomach
thyroid
upper_aerodigestive_tract
urinary_tract

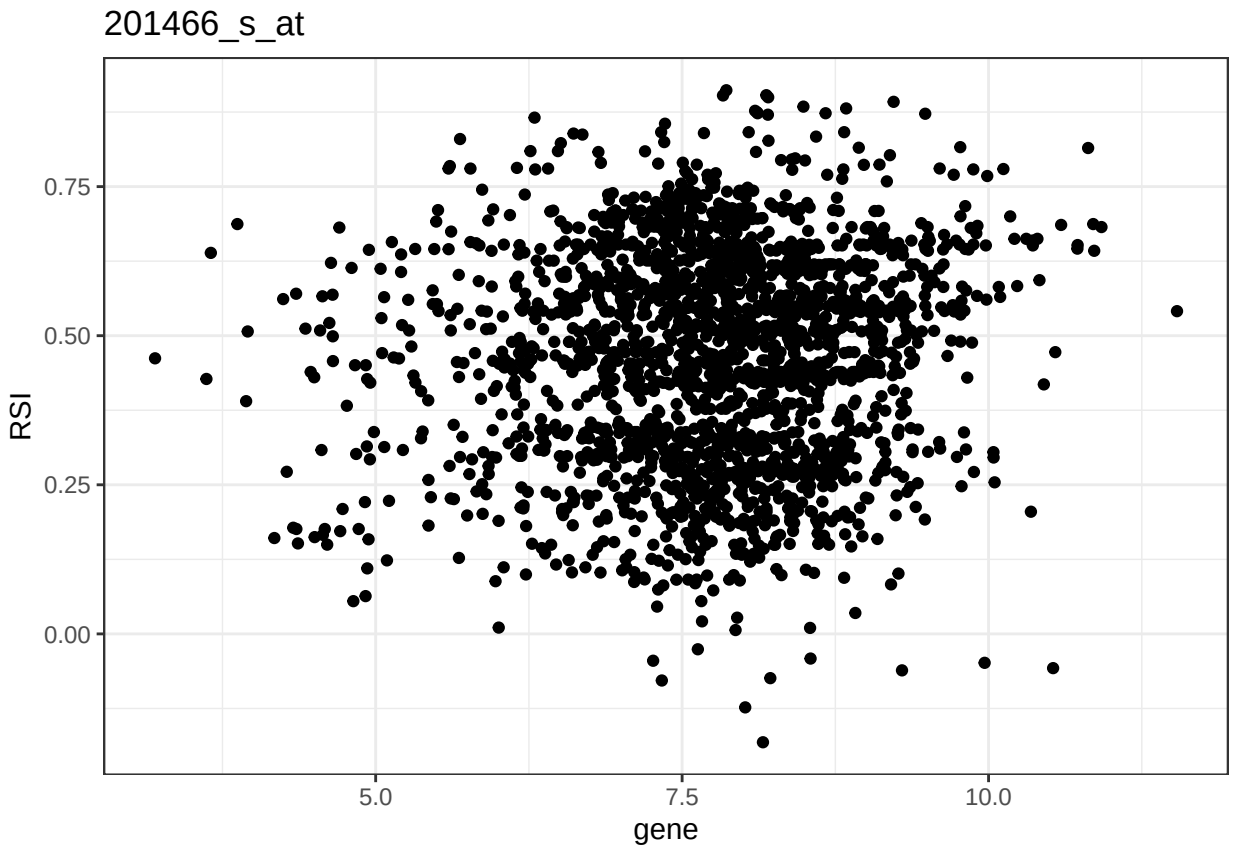

211110_s_at
RSI
0.00
0.25
0.50
0.75
4
6
8
10
12
gene
tissue
autonomic_ganglia
biliary_tract
bone
breast
central_nervous_system
endometrium
haematopoietic_and_lymphoid_tissue
kidney
large_intestine
liver
lung
oesophagus
ovary
pancreas
pleura
prostate
salivary_gland
skin
small_intestine
soft_tissue
stomach
thyroid
upper_aerodigestive_tract
urinary_tract

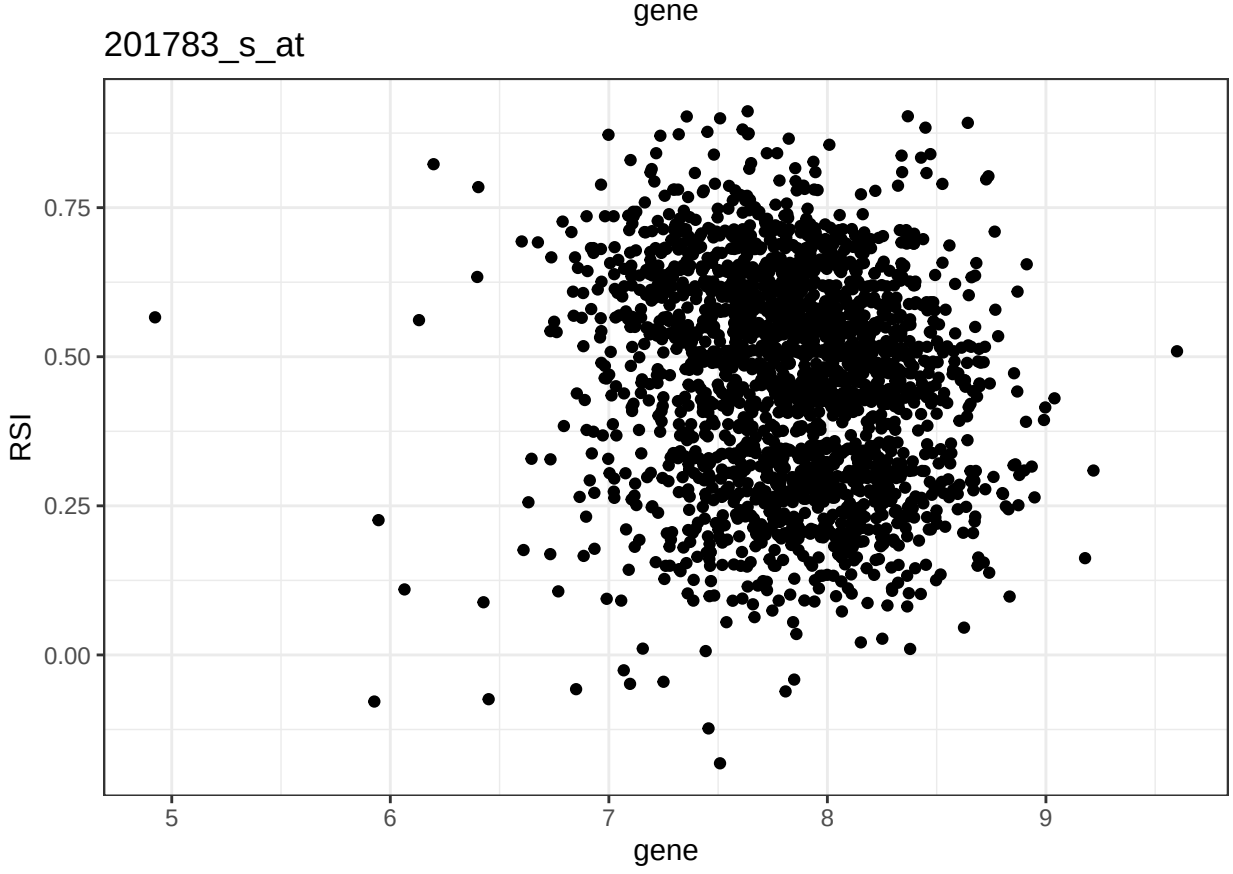
5.3 EXPO

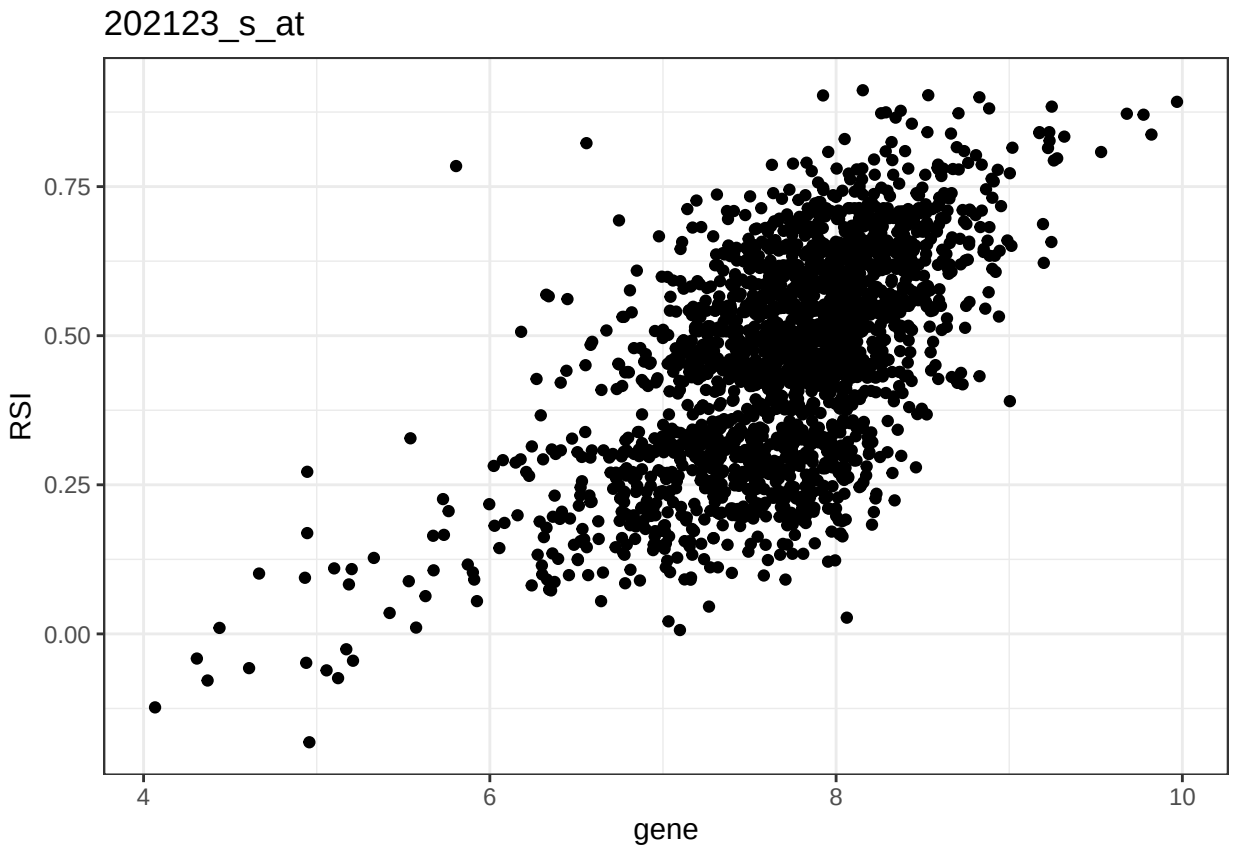
```
for (g in names(u133_coeffs)) {
  myplot<-ggplot(data.frame(gene=exprs(expo)[g,], RSI=expo$rsi, tissue=expo$source_name_ch1), a
    geom_point() +
    theme_bw() +
    ggtitle(g)

  print(myplot)
}
```

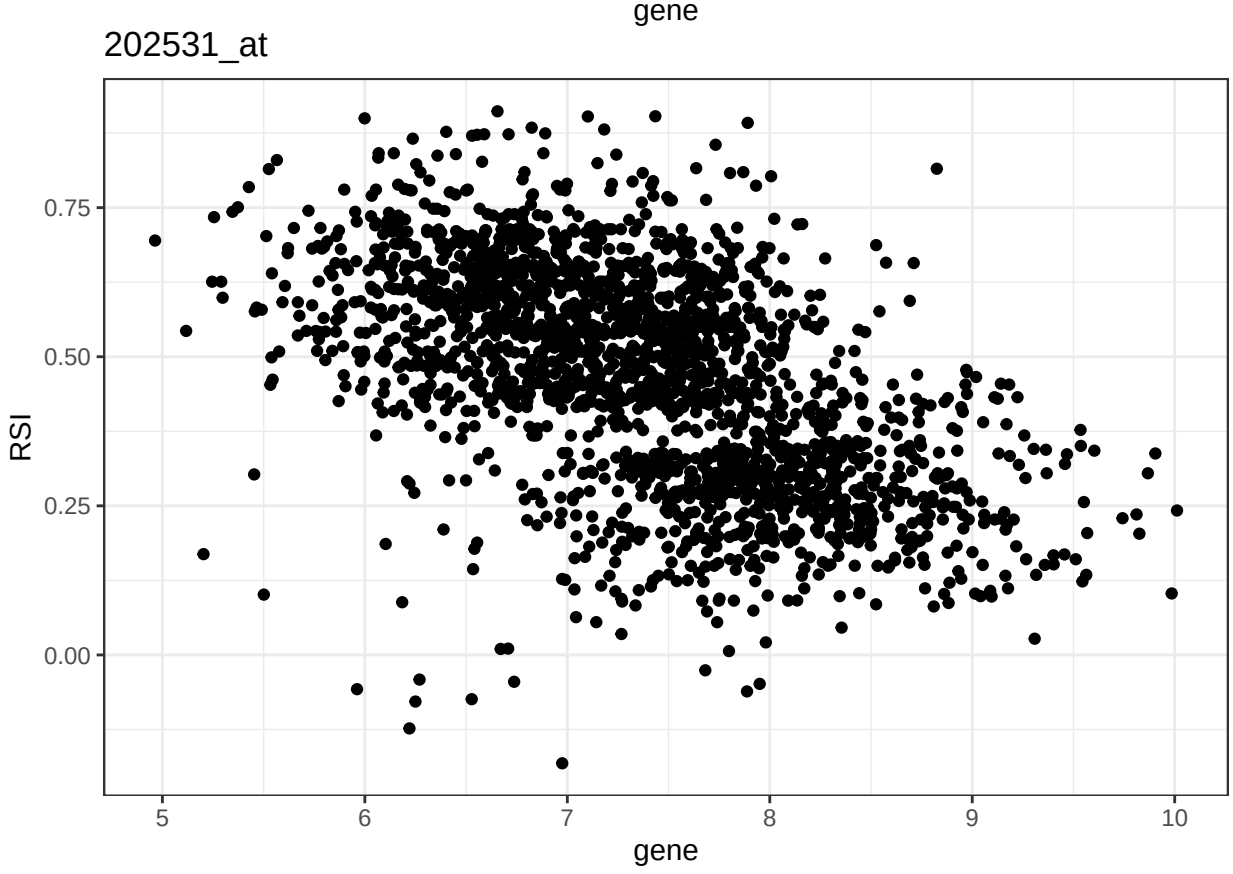

AFFX−HUMISGF3A/M97935_MA_at
RSI
0.75
0.50
0.25
0.00
6
8
10
gene

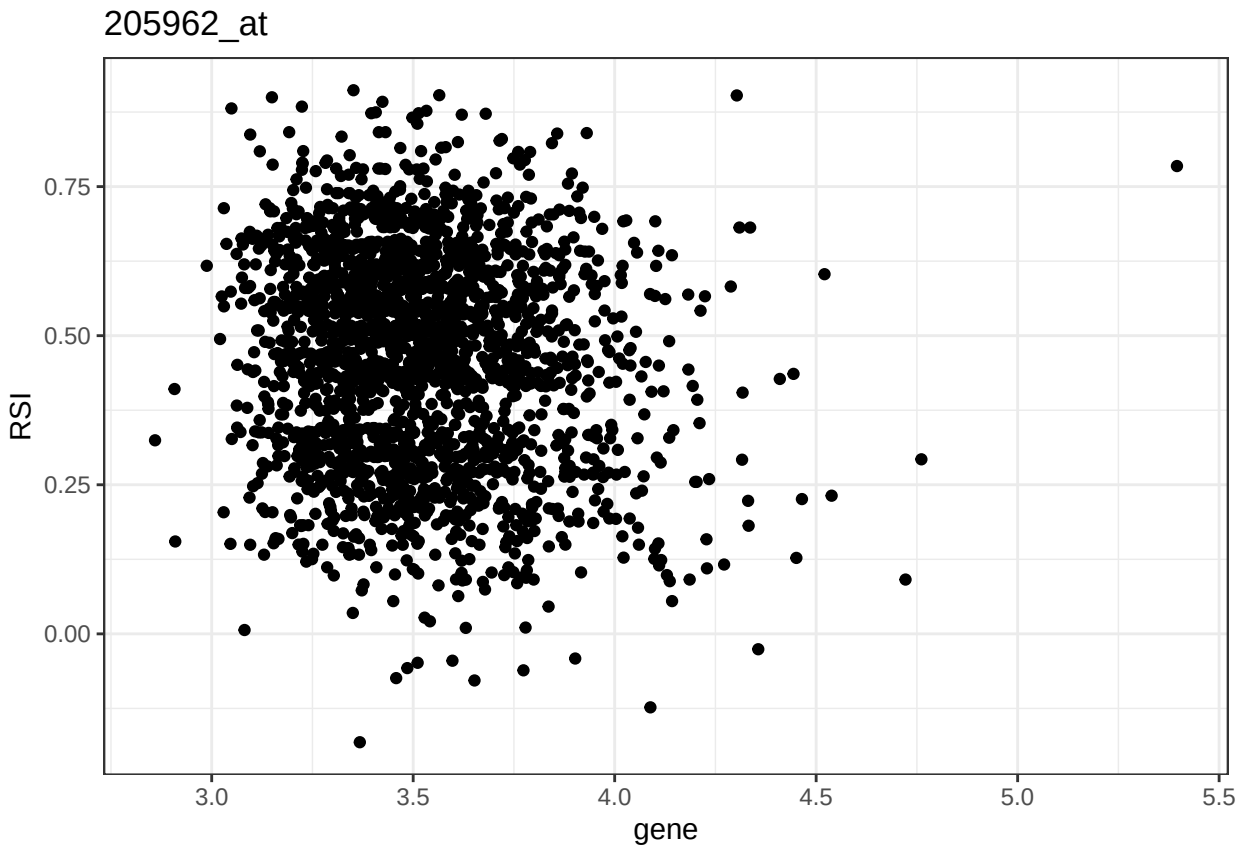

201209_at
RSI
0.75
0.50
0.25
0.00
5.0
7.5
10.0
gene

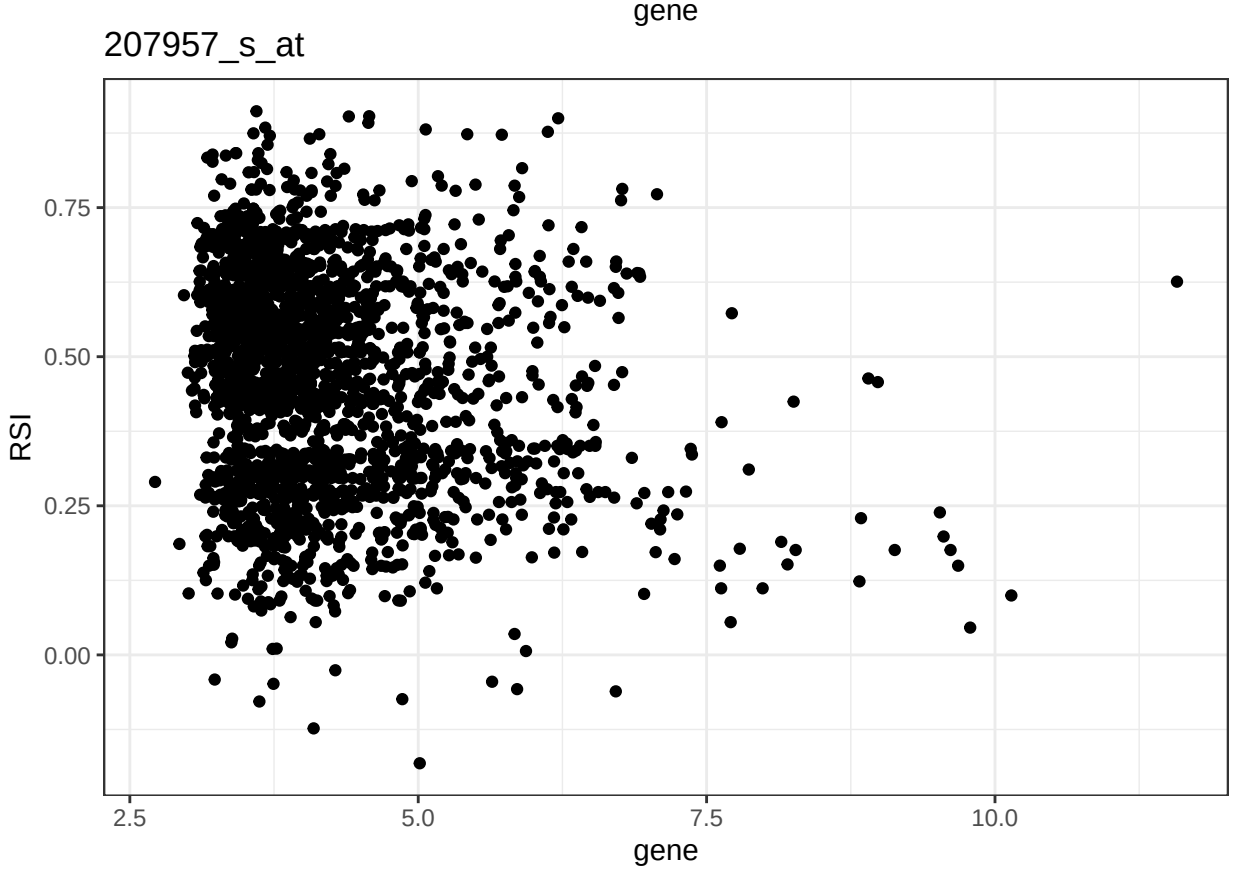

201466_s_at
RSI
0.75
0.50
0.25
0.00
5.0
7.5
10.0
gene


201783_s_at
RSI
0.75
0.50
0.25
0.00
5
6
7
8
9
gene

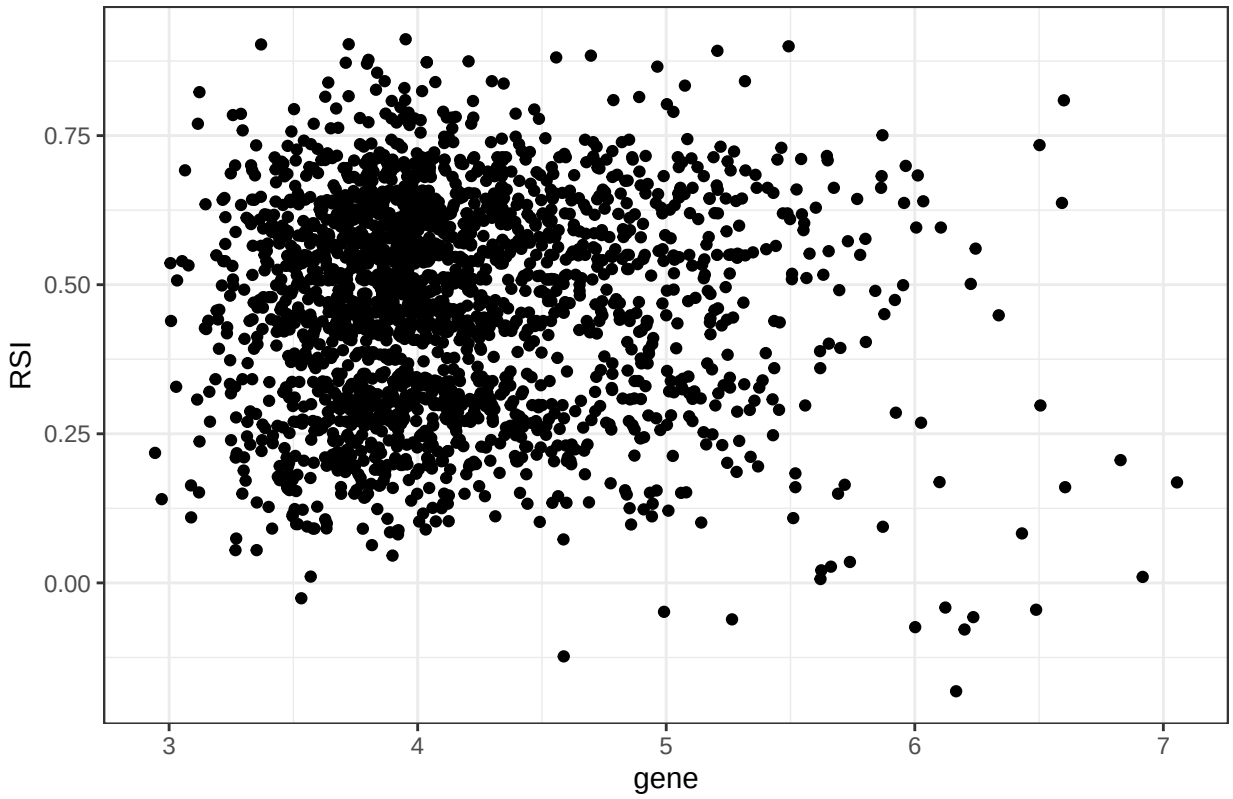

202123_s_at
RSI
0.75
0.50
0.25
0.00
4
6
8
10
gene


202531_at
RSI
0.75
0.50
0.25
0.00
5
6
7
8
9
10
gene

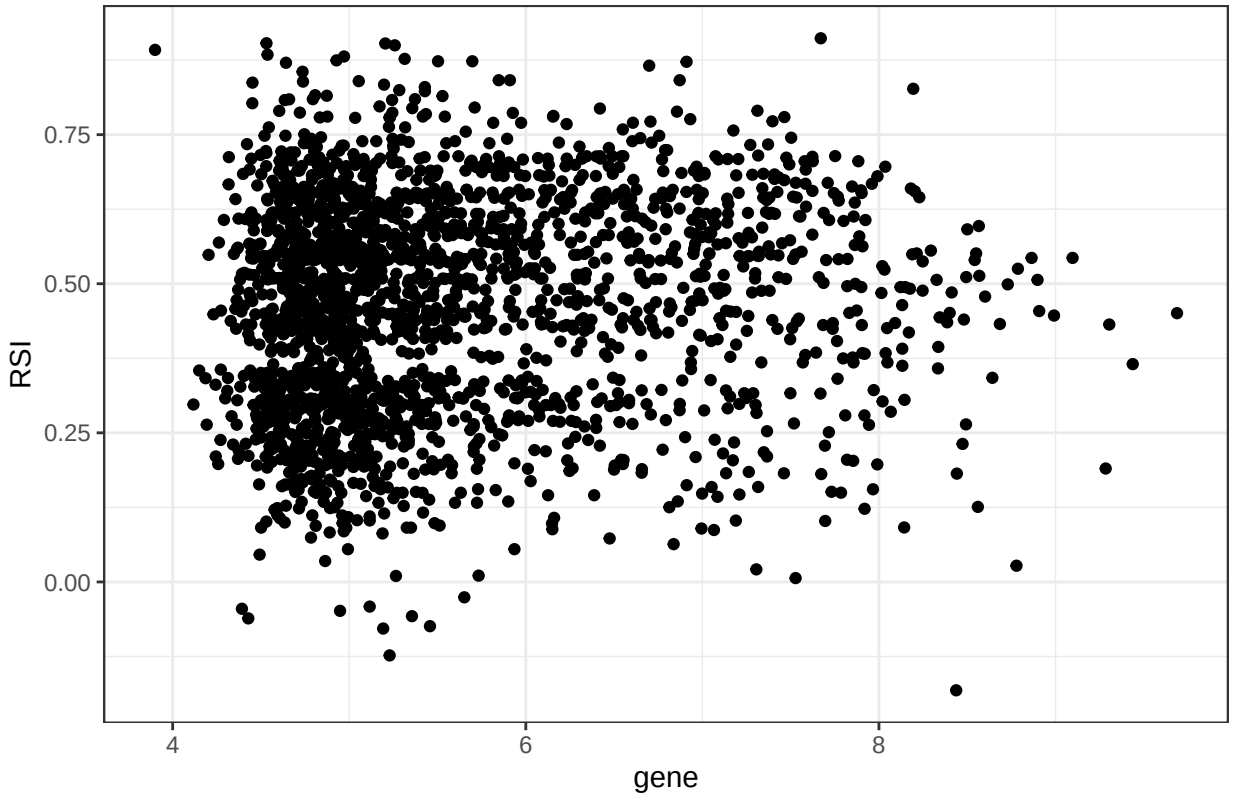

205962_at
RSI
0.75
0.50
0.25
0.00
3.0
3.5
4.0
4.5
5.0
5.5
gene


207957_s_at
RSI
0.75
0.50
0.25
0.00
2.5
5.0
7.5
10.0
gene

208762_at



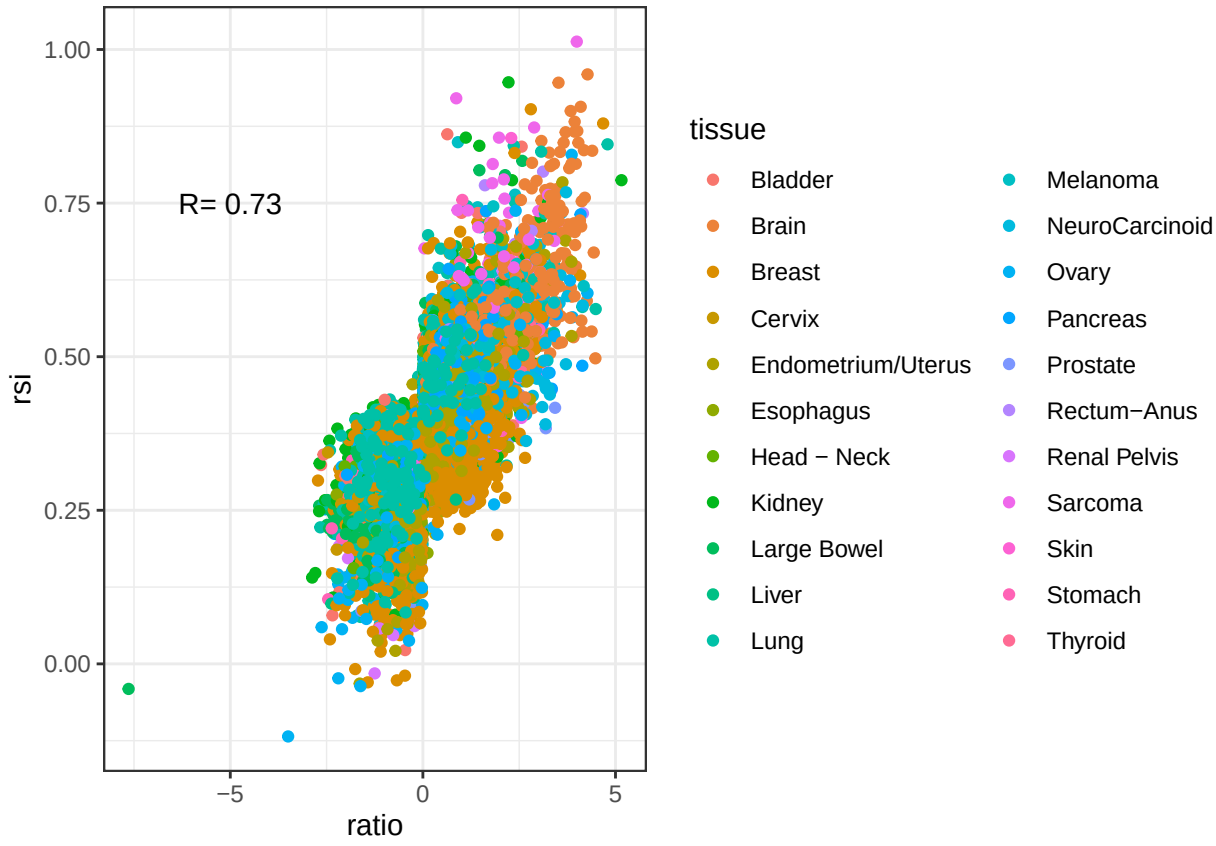
211110_s_at



6 ABL-IRF1

7 TCC

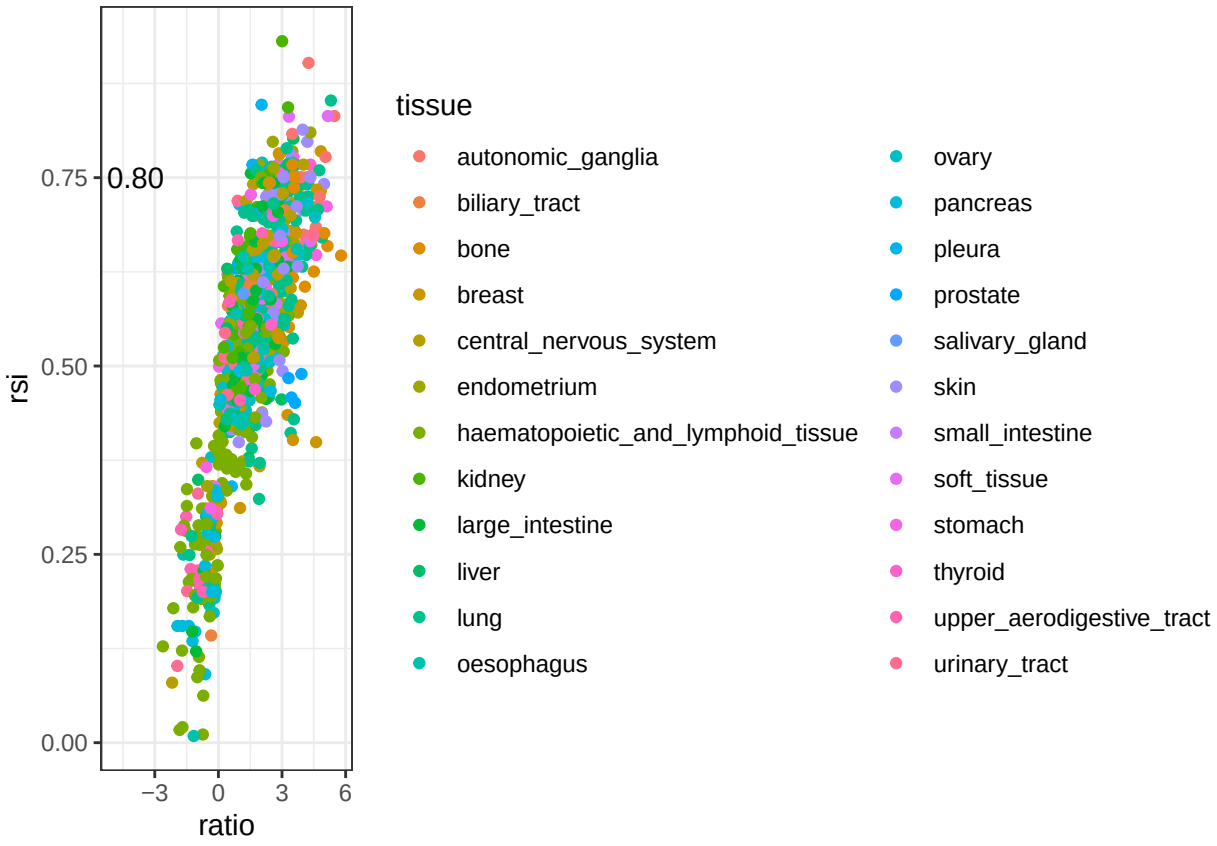
```
ABL1<-translation %>% filter(`Gene Symbol`=="ABL1") %>% pull("HuRSTA Array")
IRF1<-translation %>% filter(`Gene Symbol`=="IRF1") %>% pull("HuRSTA Array")

ratio<-exprs(tcc)[ABL1,]-exprs(tcc)[IRF1,]

ggplot(data.frame(ratio=ratio, rsi=tcc$RSI, tissue=tcc$SOO_Conformed), aes(x=ratio, y=rsi, col=
  geom_point() +
  theme_bw() +
  annotate(geom="text",x=-5,y=0.75, label=sprintf("R=%5.2f",cor(ratio, tcc$RSI)))
```



8 CCLE

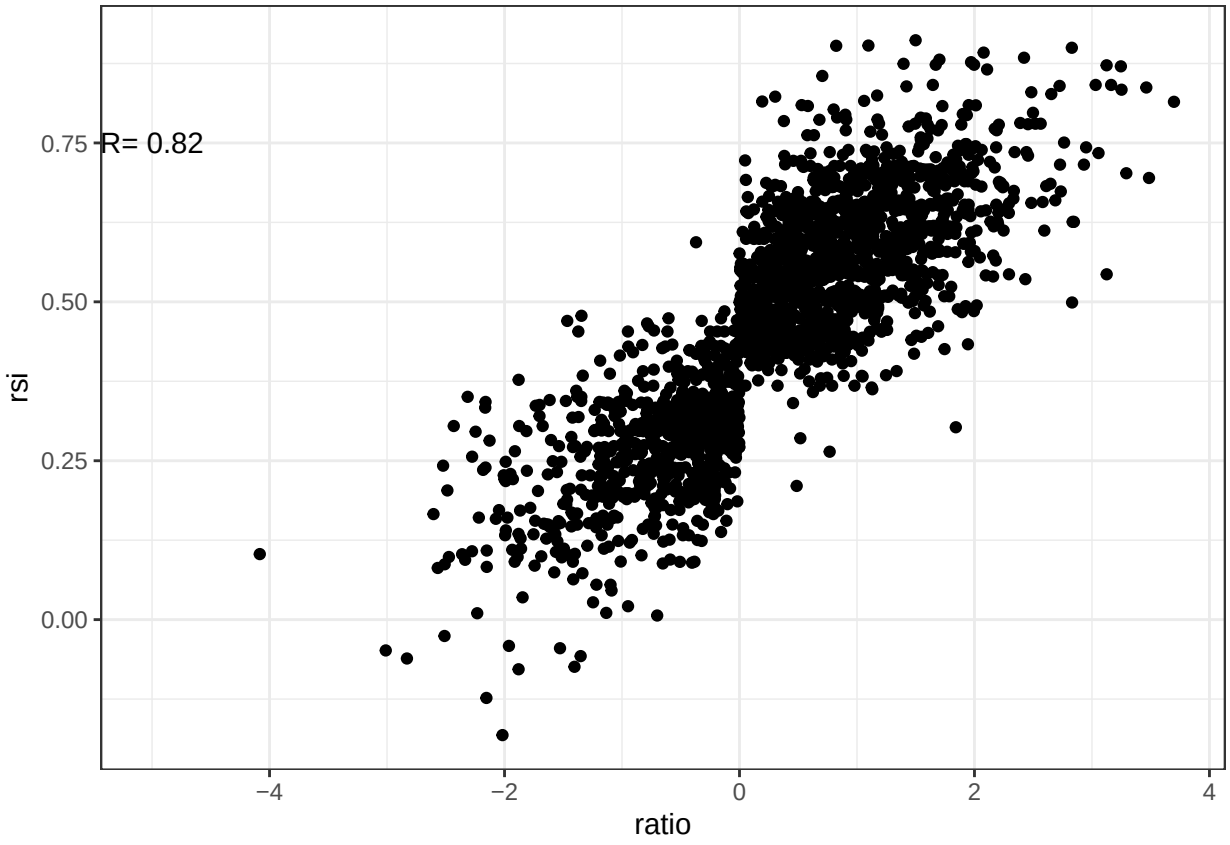
```
ABL1<-translation %>% filter(`Gene Symbol`=="ABL1") %>% pull("HG-U133 Plus 2.0 Probeset")
IRF1<-translation %>% filter(`Gene Symbol`=="IRF1") %>% pull("HG-U133 Plus 2.0 Probeset")

ratio<-exprs(ccle)[ABL1,]-exprs(ccle)[IRF1,]
```

```
ggplot(data.frame(ratio=ratio, rsi=ccle$RSI, tissue=ccle$`Site Primary`), aes(x=ratio, y=rsi, c
  geom_point() +
  theme_bw() +
  annotate(geom="text",x=-5,y=0.75, label=sprintf("R=%5.2f",cor(ratio, ccle$RSI)))
```



9 expo

```
ABL1<-translation %>% filter(`Gene Symbol`=="ABL1") %>% pull("HG-U133 Plus 2.0 Probeset")
IRF1<-translation %>% filter(`Gene Symbol`=="IRF1") %>% pull("HG-U133 Plus 2.0 Probeset")

ratio<-exprs(expo)[ABL1,]-exprs(expo)[IRF1,]

ggplot(data.frame(ratio=ratio, rsi=expo$rsi, tissue=expo$source_name_ch1), aes(x=ratio, y=rsi)
  geom_point() +
  theme_bw() +
  annotate(geom="text",x=-5,y=0.75, label=sprintf("R=%5.2f",cor(ratio, expo$rsi)))
```


R= 0.82
0.75
0.50
0.25
0.00
rsi
−4
−2
0
2
4
ratio

Session Information This information is included in the report to facilitate reproducible research. The specific environment under which the code was run is detailed. Also included are the packages that are loaded during the run.

```
## Warning in system("timedatectl", intern = TRUE): running command 'timedatectl'
## had status 1
```

Table 4: Supplemental Table: Reproducibility Software Session Information

	Setting
version	R version 3.6.3 (2020-02-29)
os	Ubuntu 16.04.6 LTS
system	x86_64, linux-gnu
ui	X11
language	(EN)
collate	en_US.UTF-8
ctype	en_US.UTF-8
tz	Etc/UTC
date	2020-05-21

Table 5: Supplemental Table: Reproducibility Software Package Version Information

	loadedversion	date	source	library
assertthat	0.2.1	2019-03-21	CRAN (R 3.6.3)	[1]
backports	1.1.7	2020-05-13	CRAN (R 3.6.3)	[1]
Biobase	2.46.0	2019-10-29	Bioconductor	[1]
BiocGenerics	0.32.0	2019-10-29	Bioconductor	[1]
callr	3.4.3	2020-03-28	CRAN (R 3.6.3)	[1]
cellranger	1.1.0	2016-07-27	CRAN (R 3.6.3)	[1]
cli	2.0.2	2020-02-28	CRAN (R 3.6.3)	[1]
colorspace	1.4-1	2019-03-18	CRAN (R 3.6.3)	[1]
CosmosReportTemplates	0.0.4	2020-05-18	local	[1]
crayon	1.3.4	2017-09-16	CRAN (R 3.6.3)	[1]
desc	1.2.0	2018-05-01	CRAN (R 3.6.3)	[1]
devtools	2.3.0	2020-04-10	CRAN (R 3.6.3)	[1]
digest	0.6.25	2020-02-23	CRAN (R 3.6.3)	[1]
dplyr	0.8.5	2020-03-07	CRAN (R 3.6.3)	[1]
ellipsis	0.3.1	2020-05-15	CRAN (R 3.6.3)	[1]
evaluate	0.14	2019-05-28	CRAN (R 3.6.3)	[1]
fansi	0.4.1	2020-01-08	CRAN (R 3.6.3)	[1]
farver	2.0.3	2020-01-16	CRAN (R 3.6.3)	[1]
fs	1.4.1	2020-04-04	CRAN (R 3.6.3)	[1]
ggplot2	3.3.0	2020-03-05	CRAN (R 3.6.3)	[1]

Table 5: Supplemental Table: Reproducibility Software Package Version Information *(continued)*

	loadedversion	date	source	library
glue	1.4.1	2020-05-13	CRAN (R 3.6.3)	[1]
gtable	0.3.0	2019-03-25	CRAN (R 3.6.3)	[1]
hms	0.5.3	2020-01-08	CRAN (R 3.6.3)	[1]
htmltools	0.4.0	2019-10-04	CRAN (R 3.6.3)	[1]
httr	1.4.1	2019-08-05	CRAN (R 3.6.3)	[1]
kableExtra	1.1.0	2019-03-16	CRAN (R 3.6.3)	[1]
knitr	1.28	2020-02-06	CRAN (R 3.6.3)	[1]
labeling	0.3	2014-08-23	CRAN (R 3.6.3)	[1]
lifecycle	0.2.0	2020-03-06	CRAN (R 3.6.3)	[1]
magrittr	1.5	2014-11-22	CRAN (R 3.6.3)	[1]
memoise	1.1.0	2017-04-21	CRAN (R 3.6.3)	[1]
munsell	0.5.0	2018-06-12	CRAN (R 3.6.3)	[1]
pillar	1.4.4	2020-05-05	CRAN (R 3.6.3)	[1]
pkgbuild	1.0.8	2020-05-07	CRAN (R 3.6.3)	[1]
pkgconfig	2.0.3	2019-09-22	CRAN (R 3.6.3)	[1]
pkgload	1.0.2	2018-10-29	CRAN (R 3.6.3)	[1]
prettyunits	1.1.1	2020-01-24	CRAN (R 3.6.3)	[1]
processx	3.4.2	2020-02-09	CRAN (R 3.6.3)	[1]
ps	1.3.3	2020-05-08	CRAN (R 3.6.3)	[1]
purrr	0.3.4	2020-04-17	CRAN (R 3.6.3)	[1]
R6	2.4.1	2019-11-12	CRAN (R 3.6.3)	[1]
Rcpp	1.0.4.6	2020-04-09	CRAN (R 3.6.3)	[1]
readr	1.3.1	2018-12-21	CRAN (R 3.6.3)	[1]
readxl	1.3.1	2019-03-13	CRAN (R 3.6.3)	[1]
remotes	2.1.1	2020-02-15	CRAN (R 3.6.3)	[1]
rlang	0.4.6	2020-05-02	CRAN (R 3.6.3)	[1]
rmarkdown	2.1	2020-01-20	CRAN (R 3.6.3)	[1]
rprojroot	1.3-2	2018-01-03	CRAN (R 3.6.3)	[1]
rstudioapi	0.11	2020-02-07	CRAN (R 3.6.3)	[1]
rvest	0.3.5	2019-11-08	CRAN (R 3.6.3)	[1]
scales	1.1.1	2020-05-11	CRAN (R 3.6.3)	[1]
sessioninfo	1.1.1	2018-11-05	CRAN (R 3.6.3)	[1]
stringi	1.4.6	2020-02-17	CRAN (R 3.6.3)	[1]
stringr	1.4.0	2019-02-10	CRAN (R 3.6.3)	[1]
testthat	2.3.2	2020-03-02	CRAN (R 3.6.3)	[1]
tibble	3.0.1	2020-04-20	CRAN (R 3.6.3)	[1]
tidyselect	1.1.0	2020-05-11	CRAN (R 3.6.3)	[1]
usethis	1.6.1	2020-04-29	CRAN (R 3.6.3)	[1]
vctrs	0.3.0	2020-05-11	CRAN (R 3.6.3)	[1]

Table 5: Supplemental Table: Reproducibility Software Package Version Information *(continued)*

	loadedversion	date	source	library
viridisLite	0.3.0	2018-02-01	CRAN (R 3.6.3)	[1]
webshot	0.5.2	2019-11-22	CRAN (R 3.6.3)	[1]
withr	2.2.0	2020-04-20	CRAN (R 3.6.3)	[1]
xfun	0.14	2020-05-20	CRAN (R 3.6.3)	[1]
xml2	1.3.2	2020-04-23	CRAN (R 3.6.3)	[1]
yaml	2.2.1	2020-02-01	CRAN (R 3.6.3)	[1]

[1] /share/data2/eschrich/R/x86_64-pc-linux-gnu-library/3.6
[2] /usr/local/lib/R/site-library
[3] /usr/lib/R/site-library
[4] /usr/lib/R/library

Table 6: Supplemental Table: Reproducibility Software Environment Information

name	value
username	eschris
file name	rsi_correlations.Rmd
git	Not in git
local dir	/share/data2/RSI/Projects/RSI_RNASeq_Translation/rsi_correlations
hostname	compute-0-31.local