# masters eo project

2025-01-22

## R Markdown

installing packages

```r
#install.packages("factoextra")
#install.packages("tidyr")
#install.packages("readr")
#install.packages("ggplot2")
#install.packages("DescTools")
#install.packages('ggrepel')
#install.packages("minpack.lm")
#install.packages("drc")
#install.packages("purrr")
library(tidyr)
library(readr)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(ggplot2)
library(DescTools)
library(ggrepel)
library(minpack.lm)
library(drc)
```

```
## Loading required package: MASS

##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##     select

##
## 'drc' has been loaded.

## Please cite R and 'drc' if used for a publication,

## for references type 'citation()' and 'citation('drc')'.
```

```
##
## Attaching package: 'drc'

## The following objects are masked from 'package:stats':
##
##     gaussian, getInitial
```

```
library(factoextra)
```

```
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

```
library(purrr)
```

we now load in the data file downloaded from the drive

```
setwd('~/Documents/Masters_project/')
HIV1_vector_data=read_csv('inputs/HIV1_vectors_collated_n0_uncleaned(Sheet1).csv')
```

```
## Rows: 1019175 Columns: 15
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr  (4): assay, cell_line, titre, condition
## dbl (11): index, batch, plate_column, replicate, screen, screen_nb, infectio...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

need to clean data, cleaning up NAs and empty rows in the original dataset, only keeping useful column we also get rid of NA

```
HIV1_vector_data=HIV1_vector_data[,c(2,5,6,7:13,15)]
HIV1_vector_data=na.omit(HIV1_vector_data)
```

here we get rid of reduced values, this normally represents dying cells which is irrelevant to our analysis. in this code if a data point with a higher volume within a replicate is less than 80% of the max for that replicate it is replaced with the maximum. This practically means that as the graph increases it plateaus at the max instead of decreasing

```
library(dplyr)
HIV1_vector_data=HIV1_vector_data%>%group_by(cell_line,screen_nb,replicate)%>%
  mutate(max_gfp=max(assay_output),max_gfp_titre=which.max(assay_output)) %>%
mutate(assay_output=if_else((infection_volume_ul>infection_volume_ul[max_gfp_titre] & assay_output  <= 0
```

subsetting data for each cell line, creates a list of dataframes for each cell line (makes it easier to manipulate) per cell line

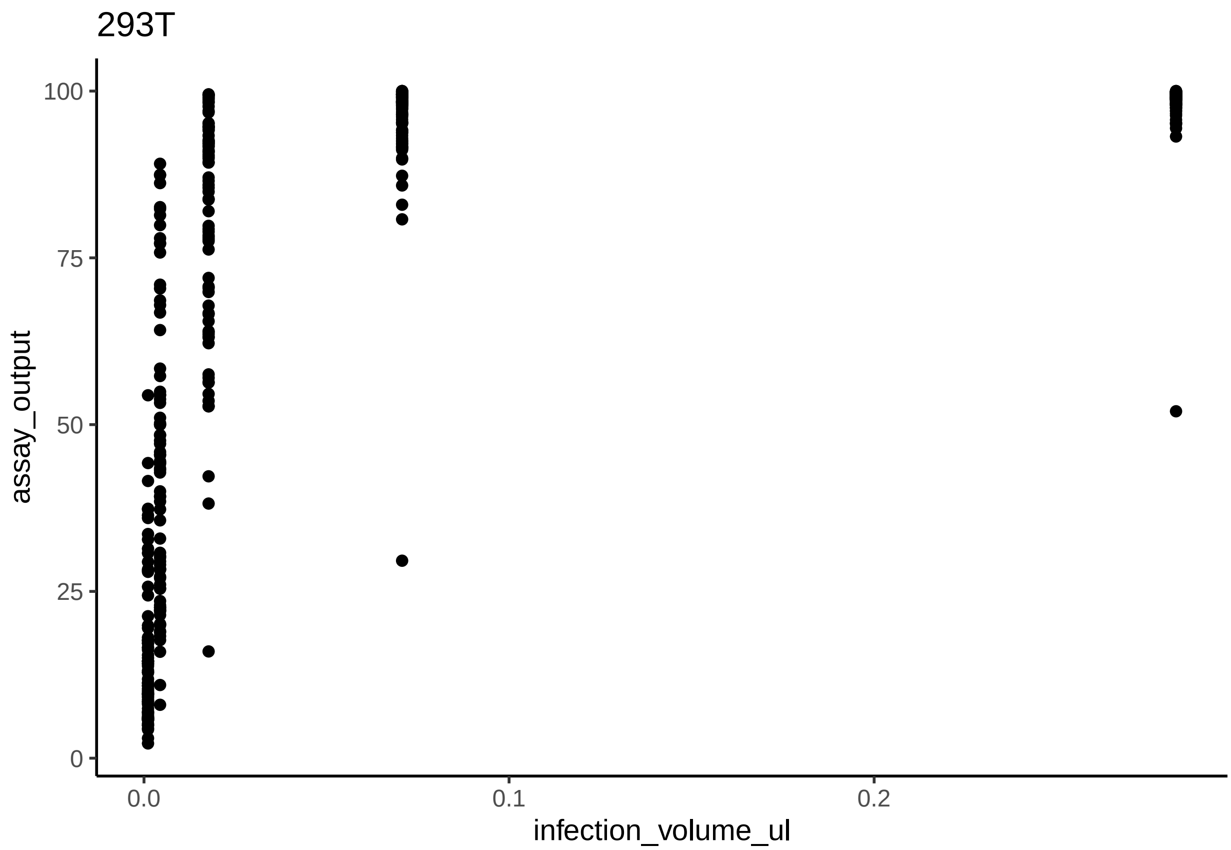
```
vector_data_per_cell_line=HIV1_vector_data%>%nest_by(cell_line,.keep = T)
```

this points all plots by titre amount and separated by screen, allows you to see general shape of data, separated by

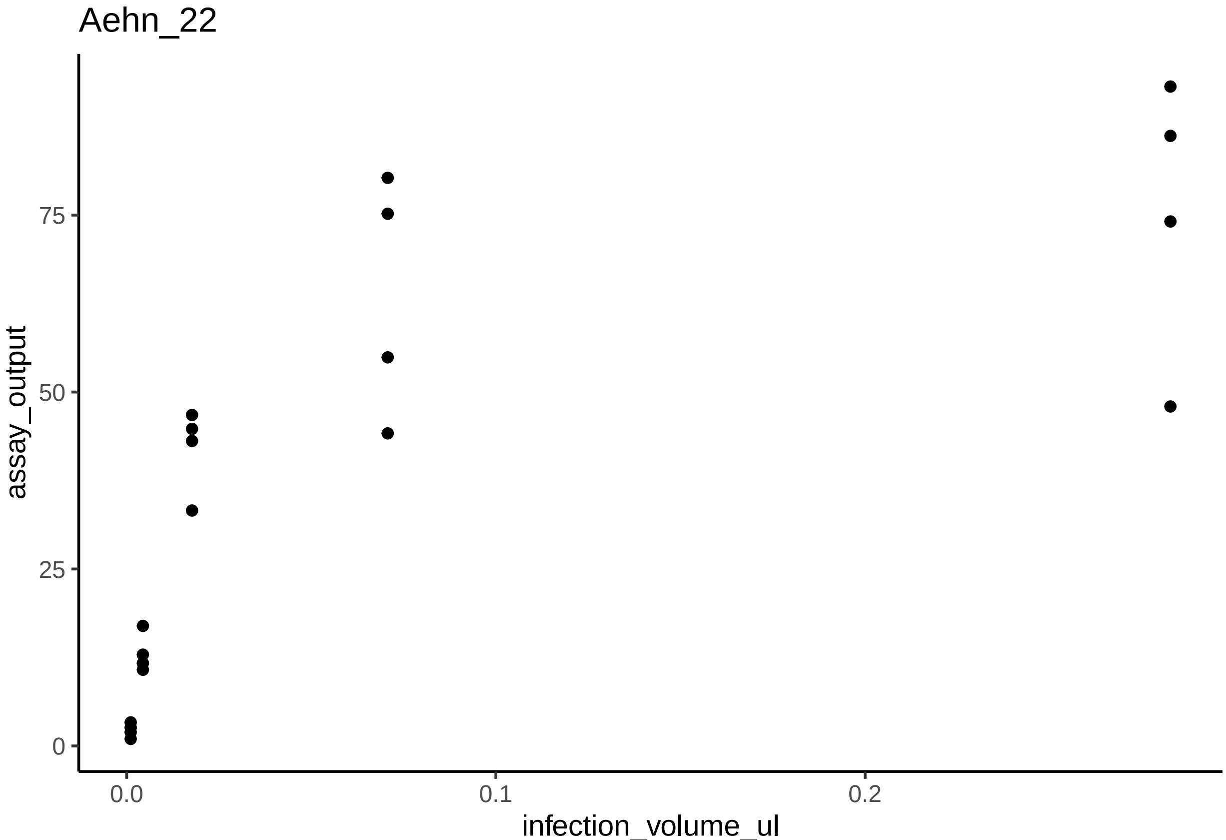
```
apply_plot=function(i){ggplot(data = i,aes(x=infection_volume_ul,y=assay_output,group = interaction(scre
  geom_point()+
  ggtitle(i$cell_line[1])+
  theme_classic()
}
```

```
purrr::map(vector_data_per_cell_line$data,apply_plot)
```

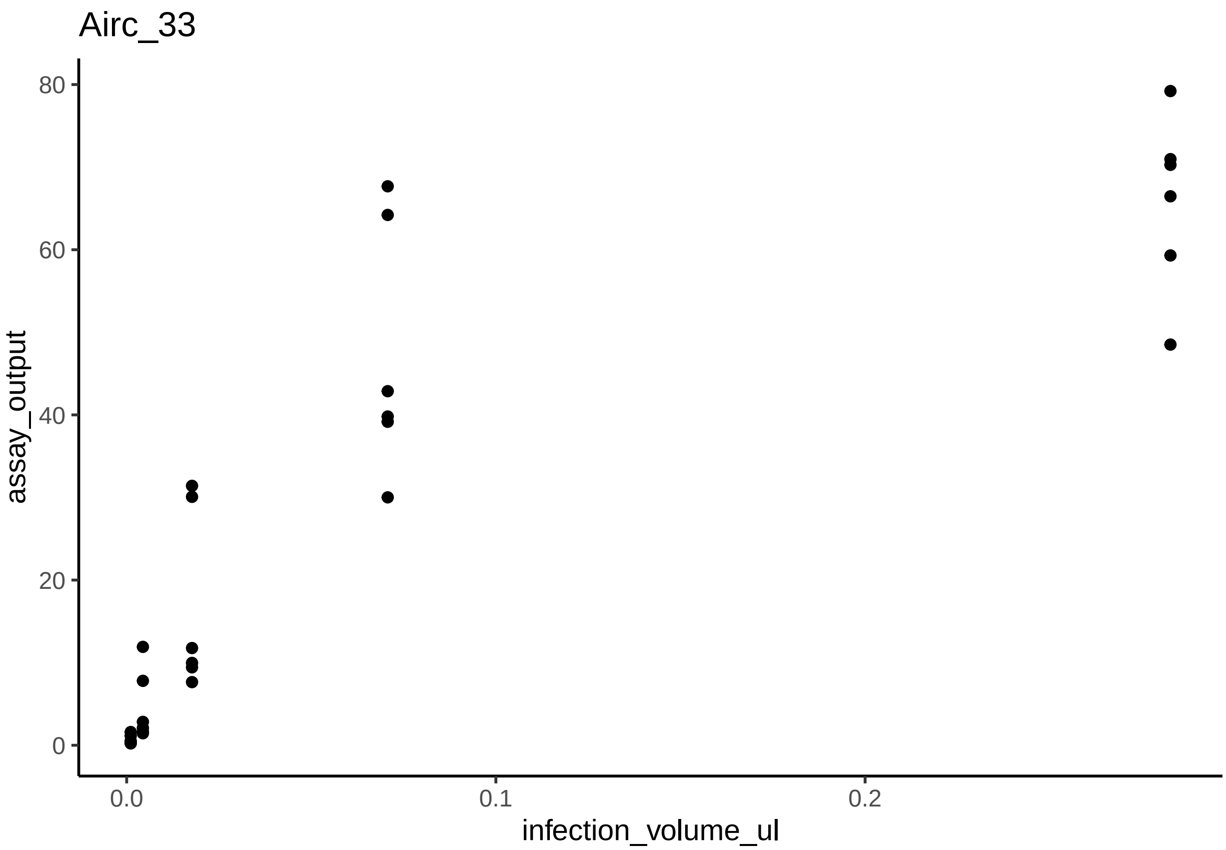
```
## [[1]]
```



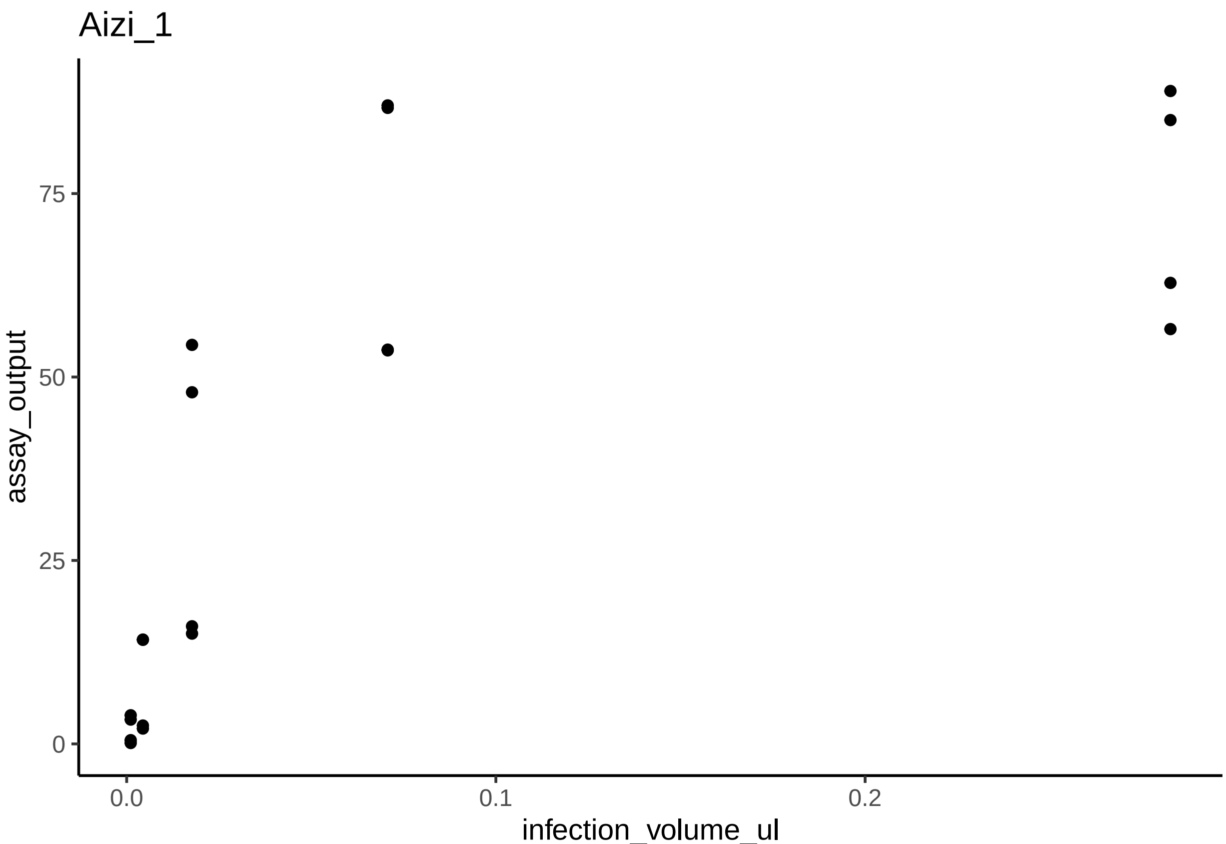

```
##
## [[2]]
```



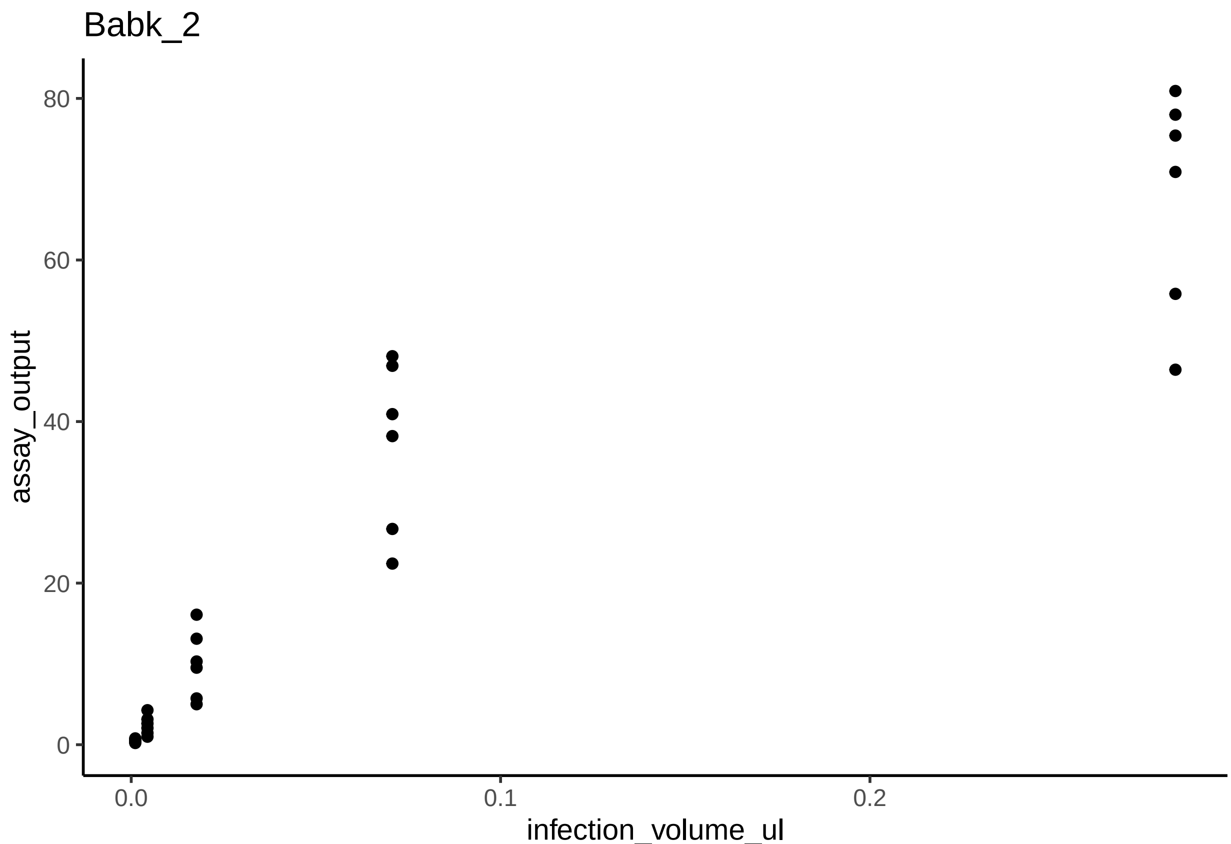

```
##
## [[3]]
```



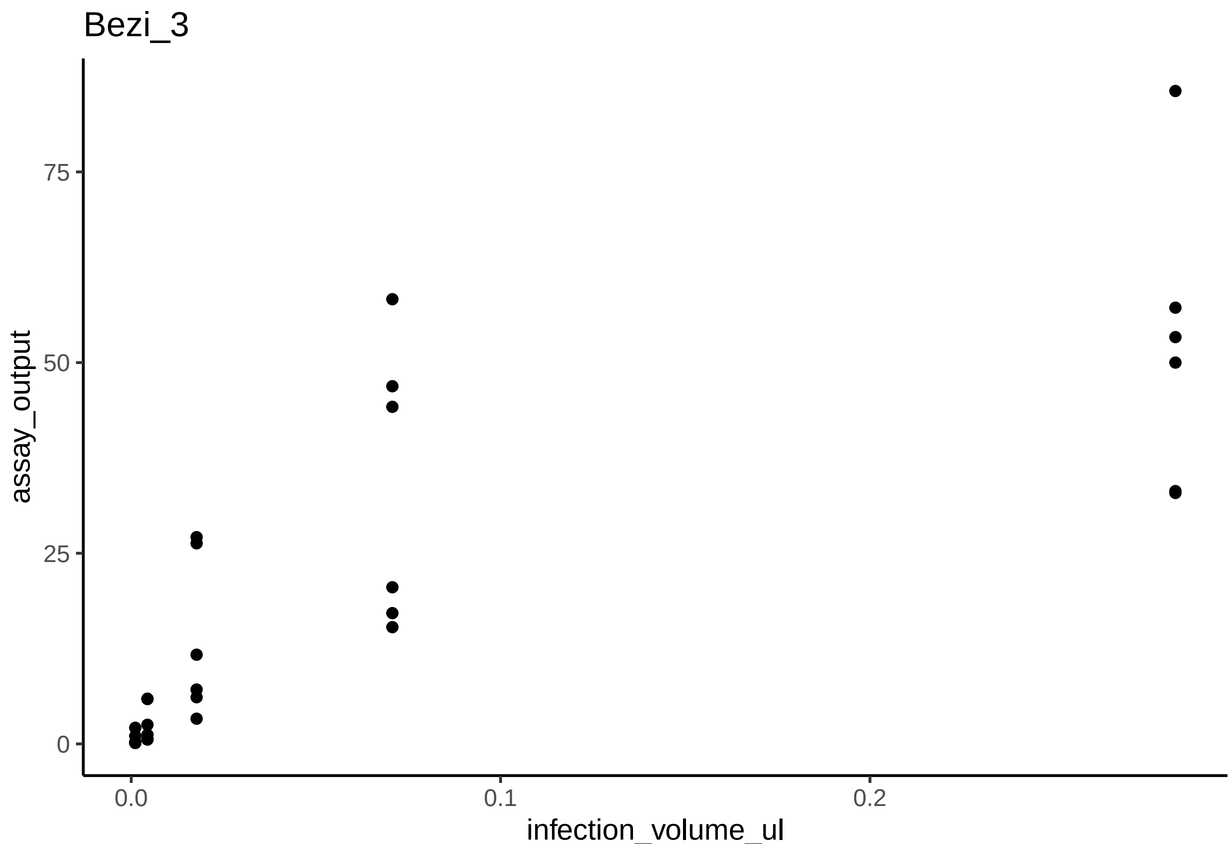

```
##
## [[4]]
```



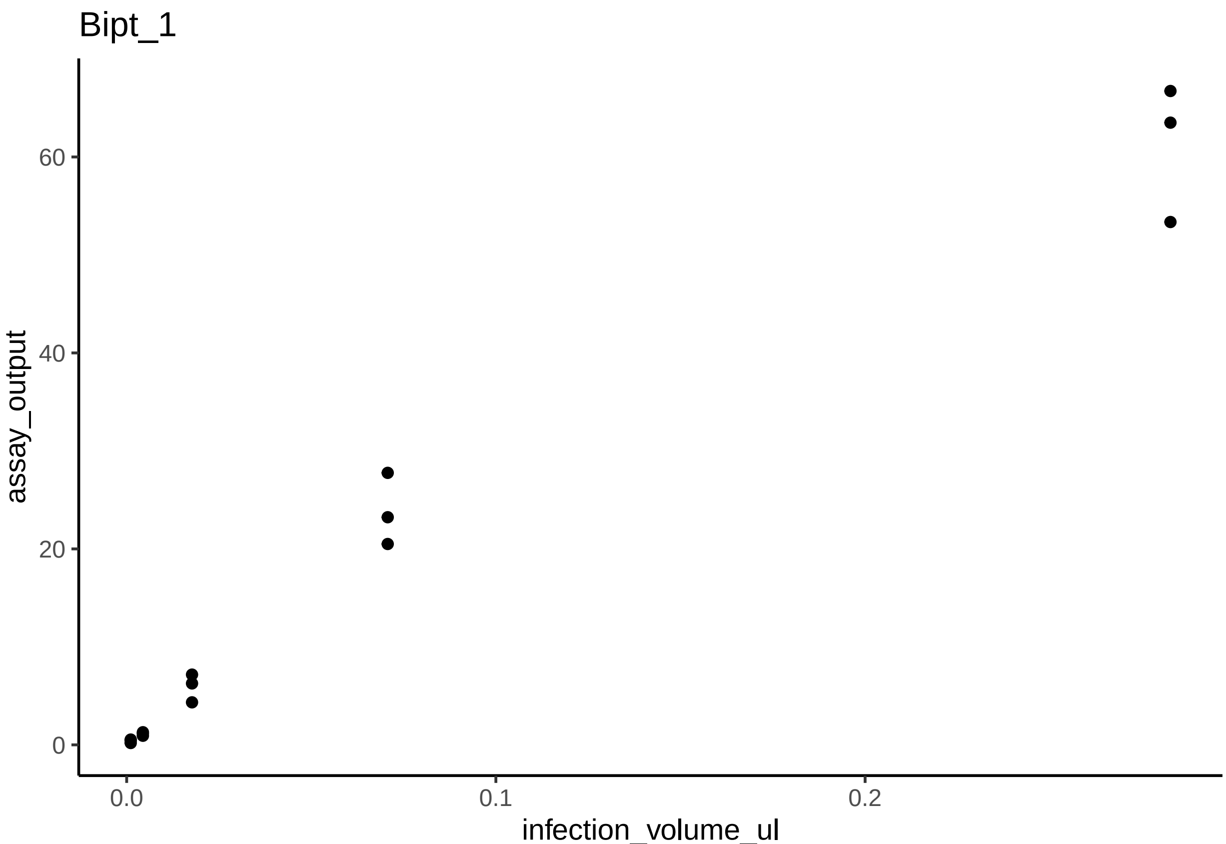

```
##
## [[5]]
```



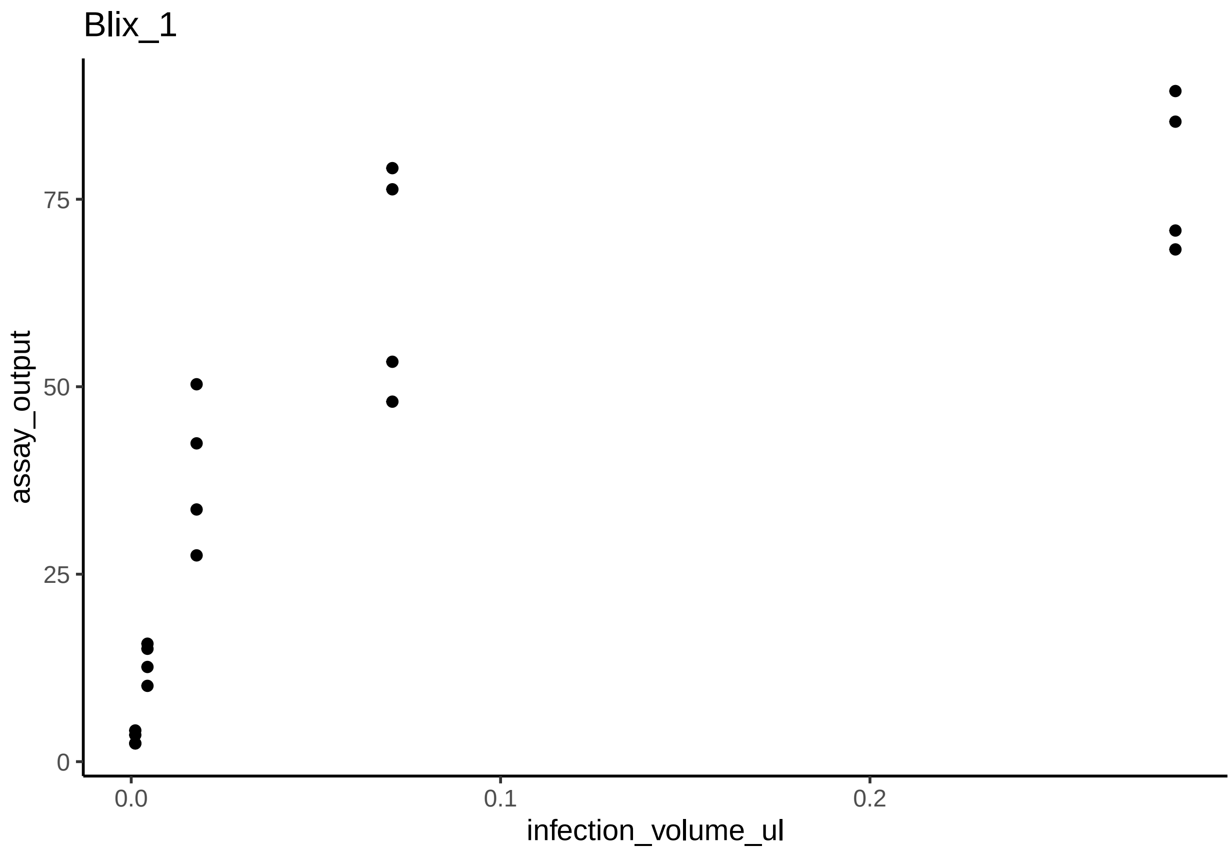

```
##
## [[6]]
```



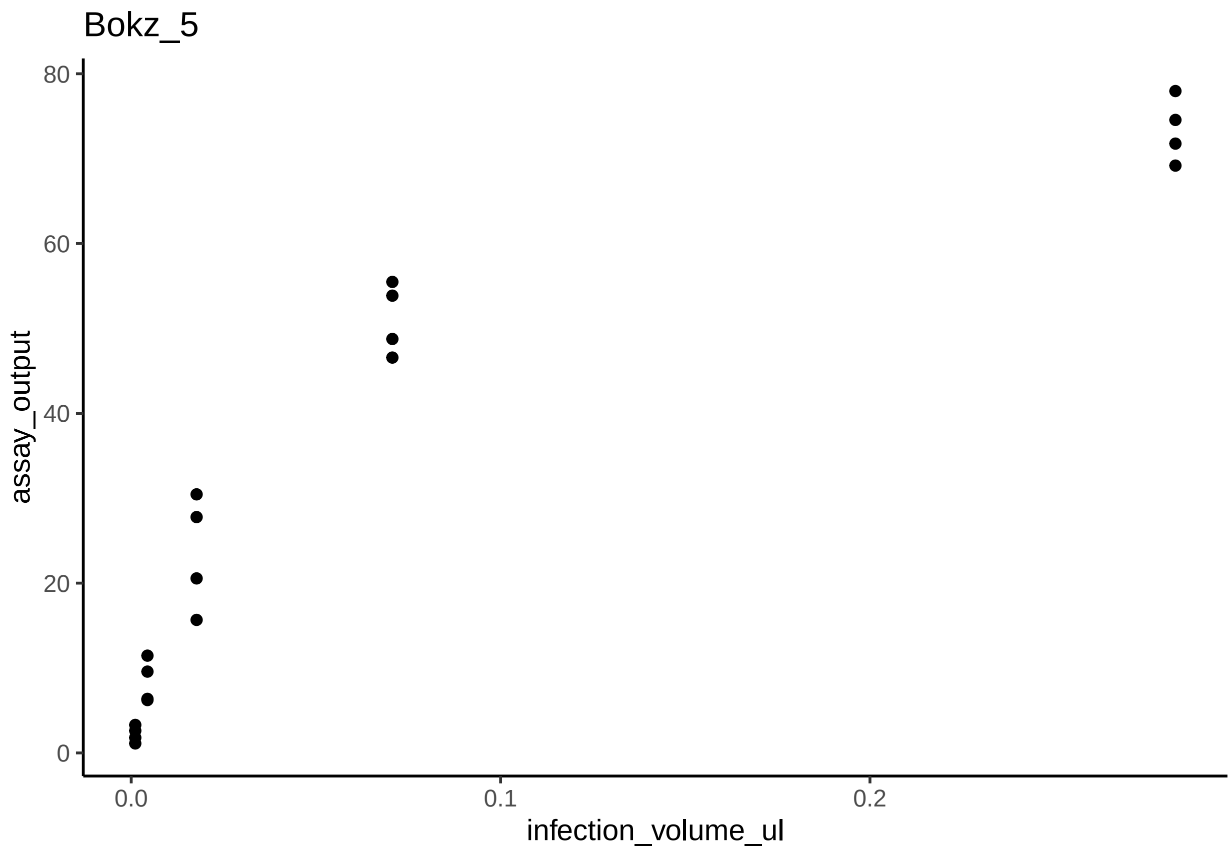

```
##
## [[7]]
```



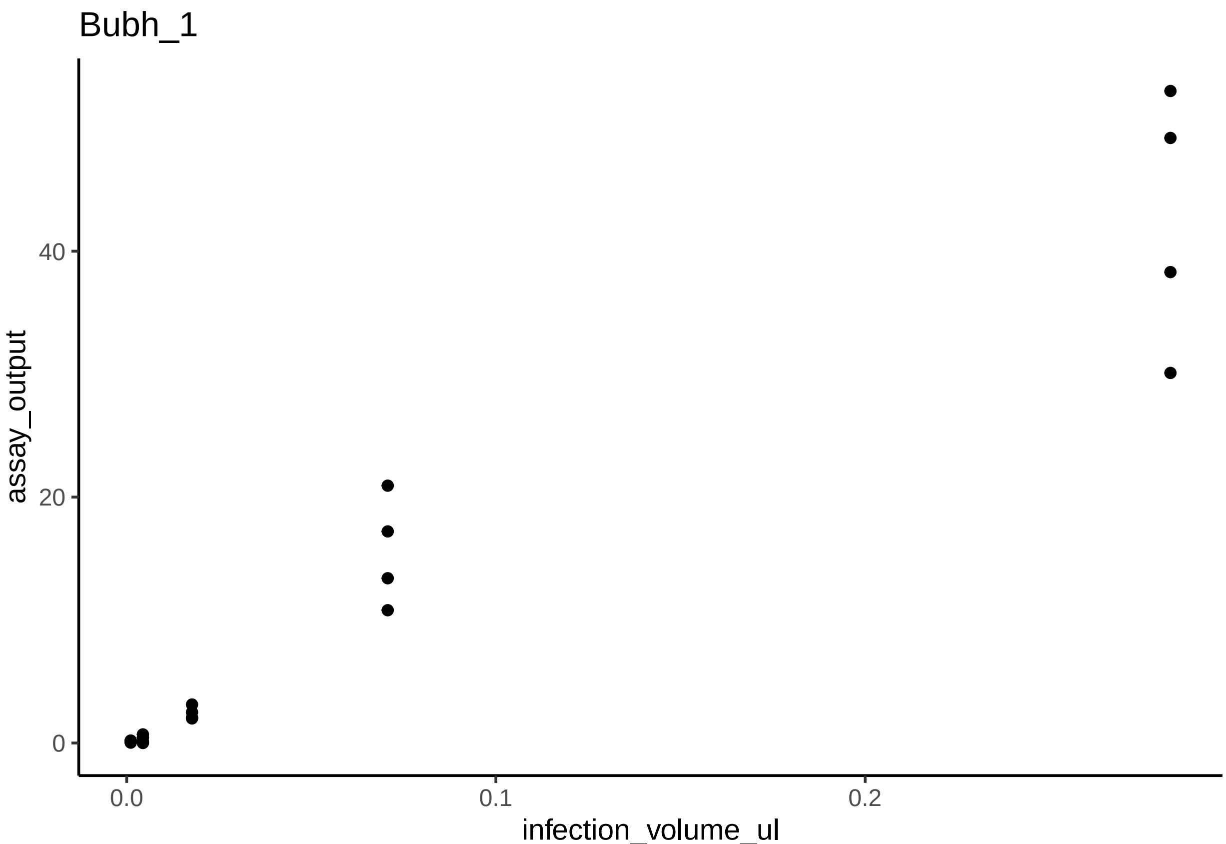

```
##
## [[8]]
```



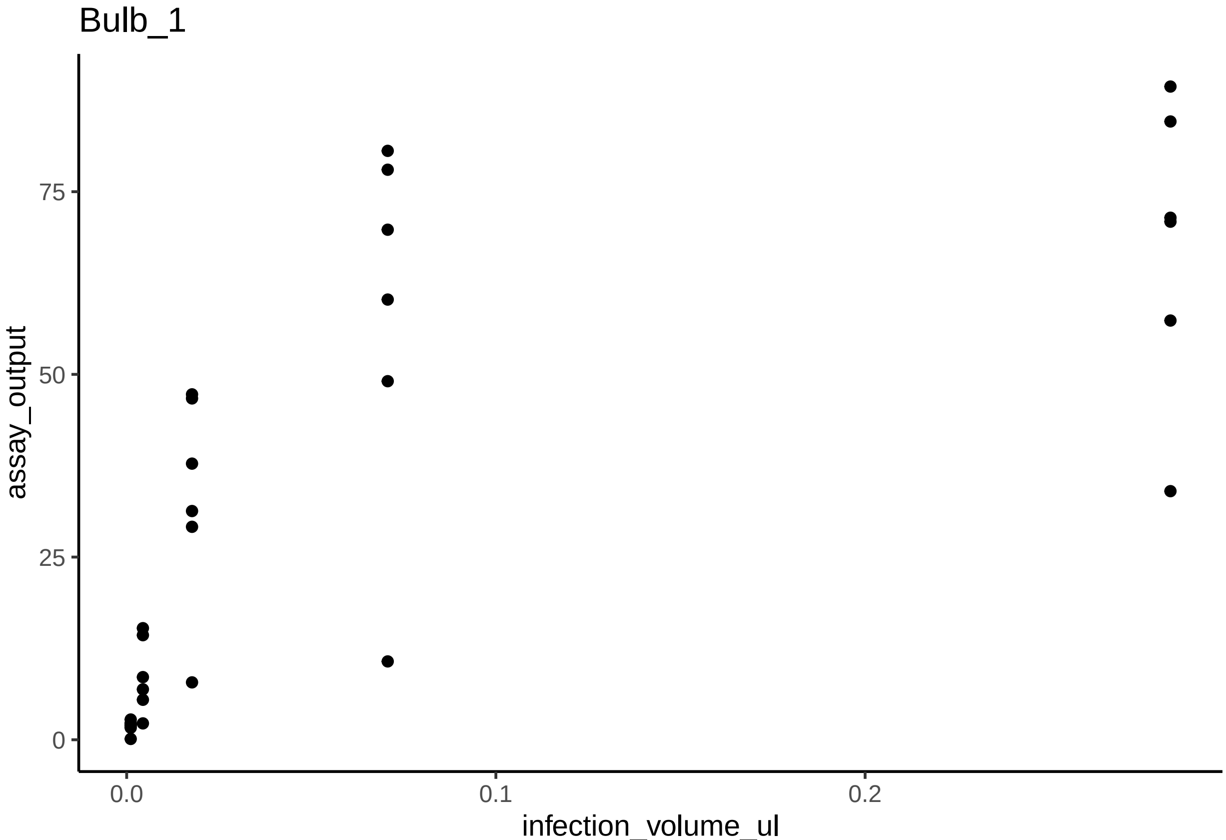

```
##
## [[9]]
```



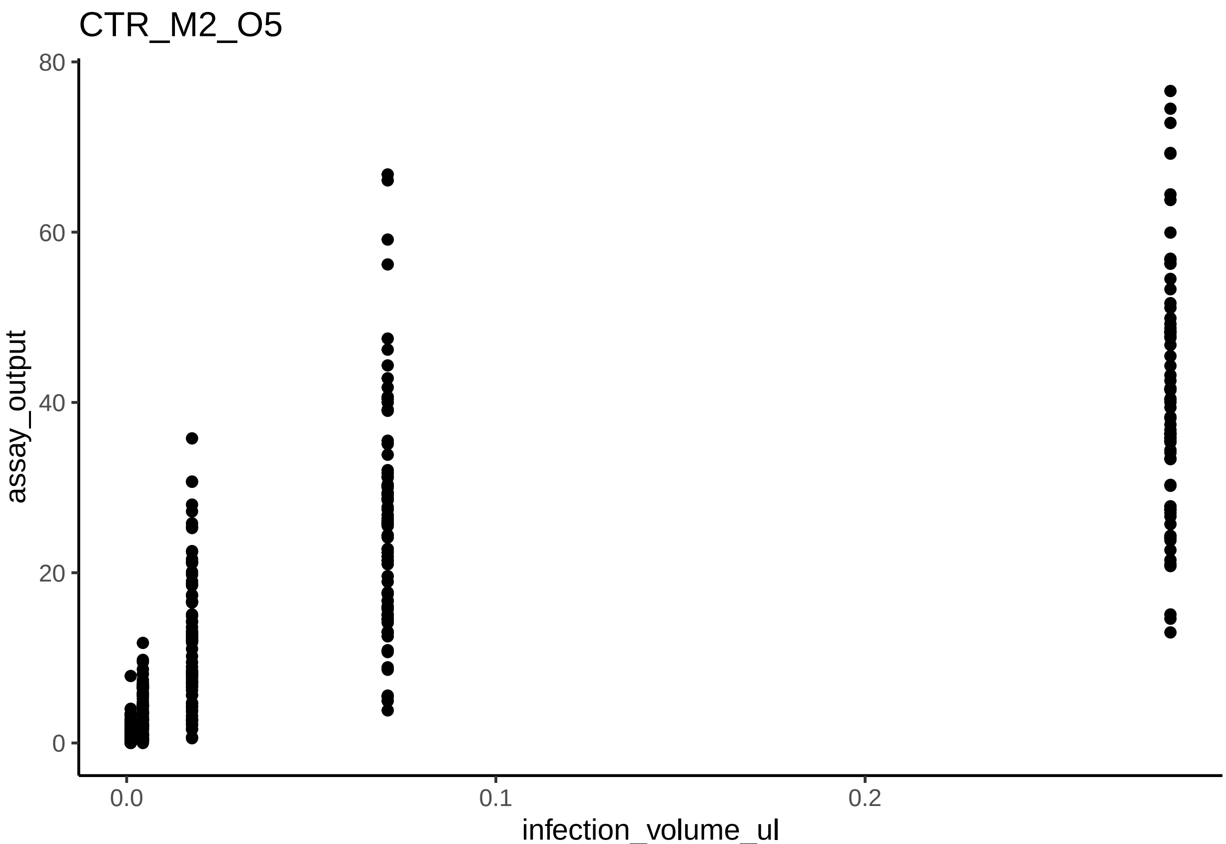

```
##
## [[10]]
```



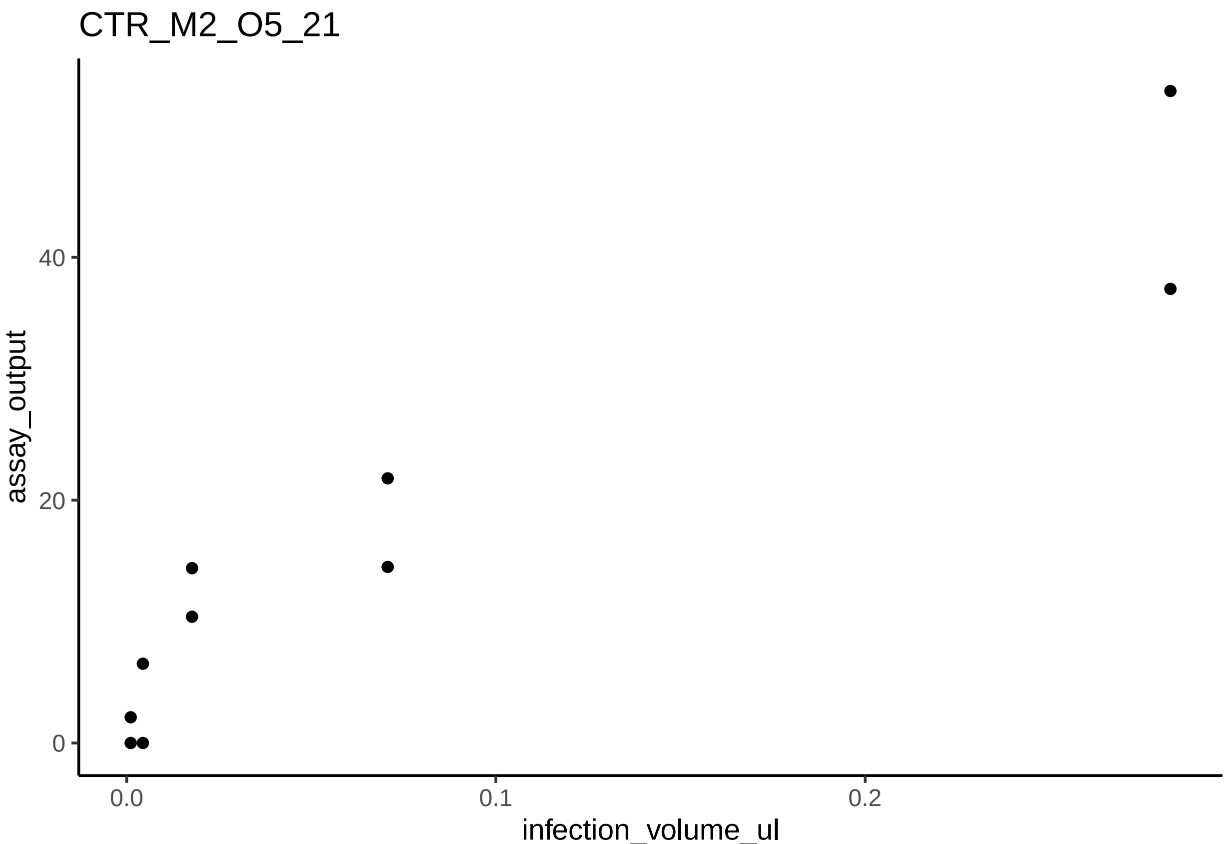

```
##
## [[11]]
```



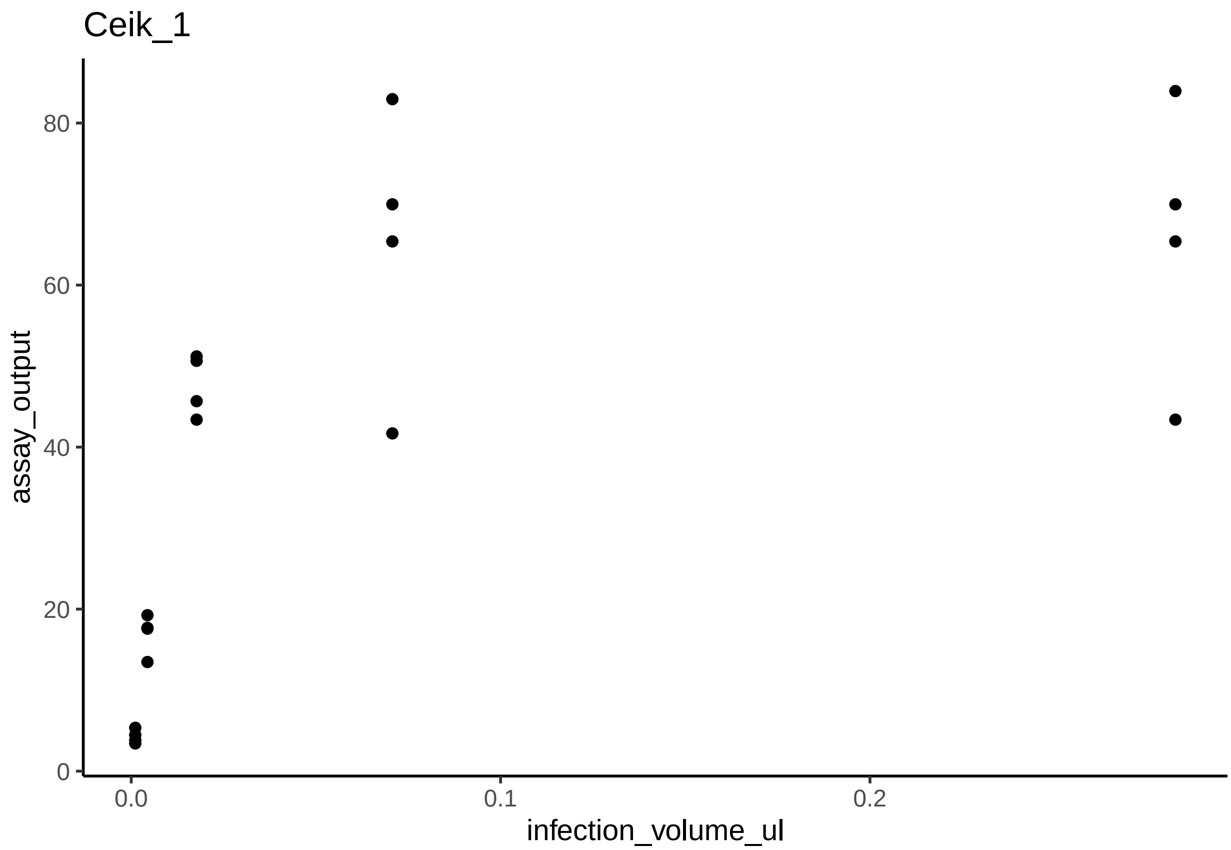

```
##
## [[12]]
```


CTR_M2_O5
80
60
40
20
0
assay_output
0.0
0.1
0.2
infection_volume_ul

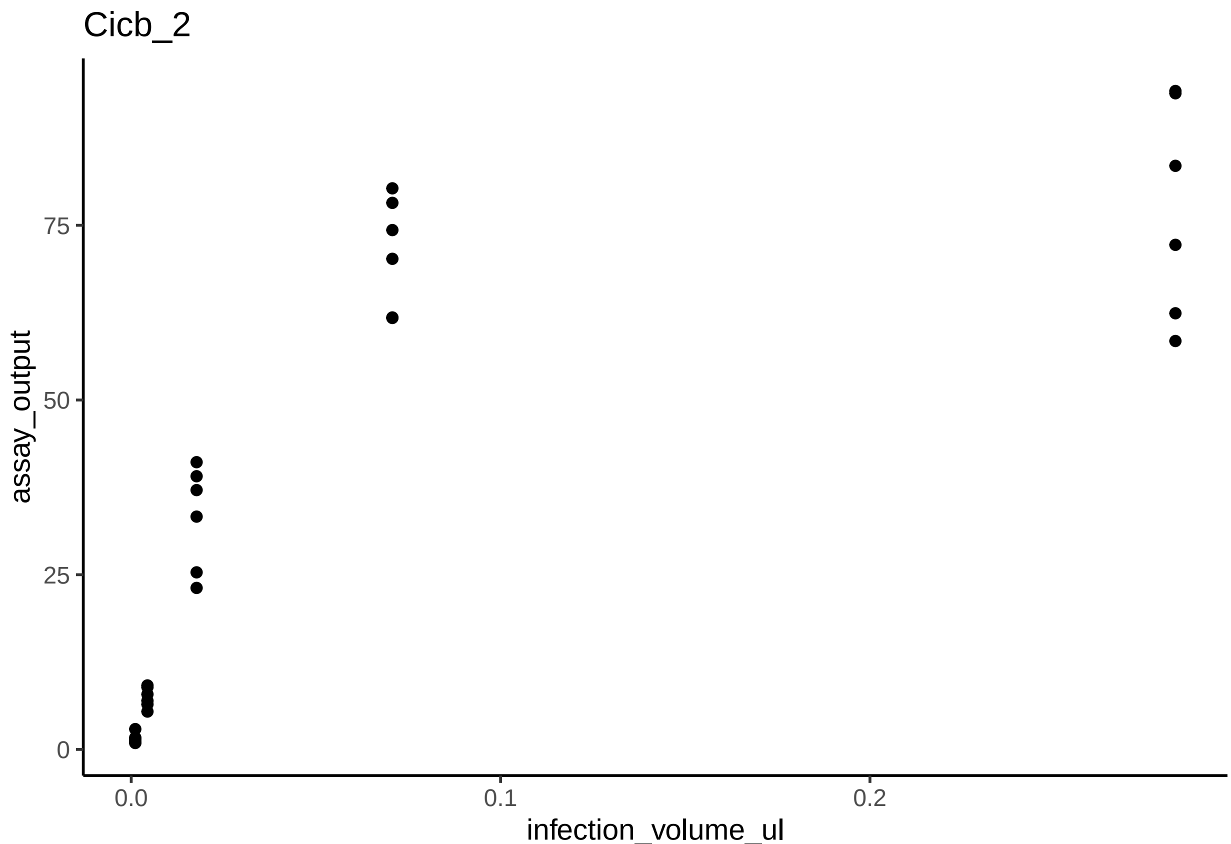
```
##
## [[13]]
```



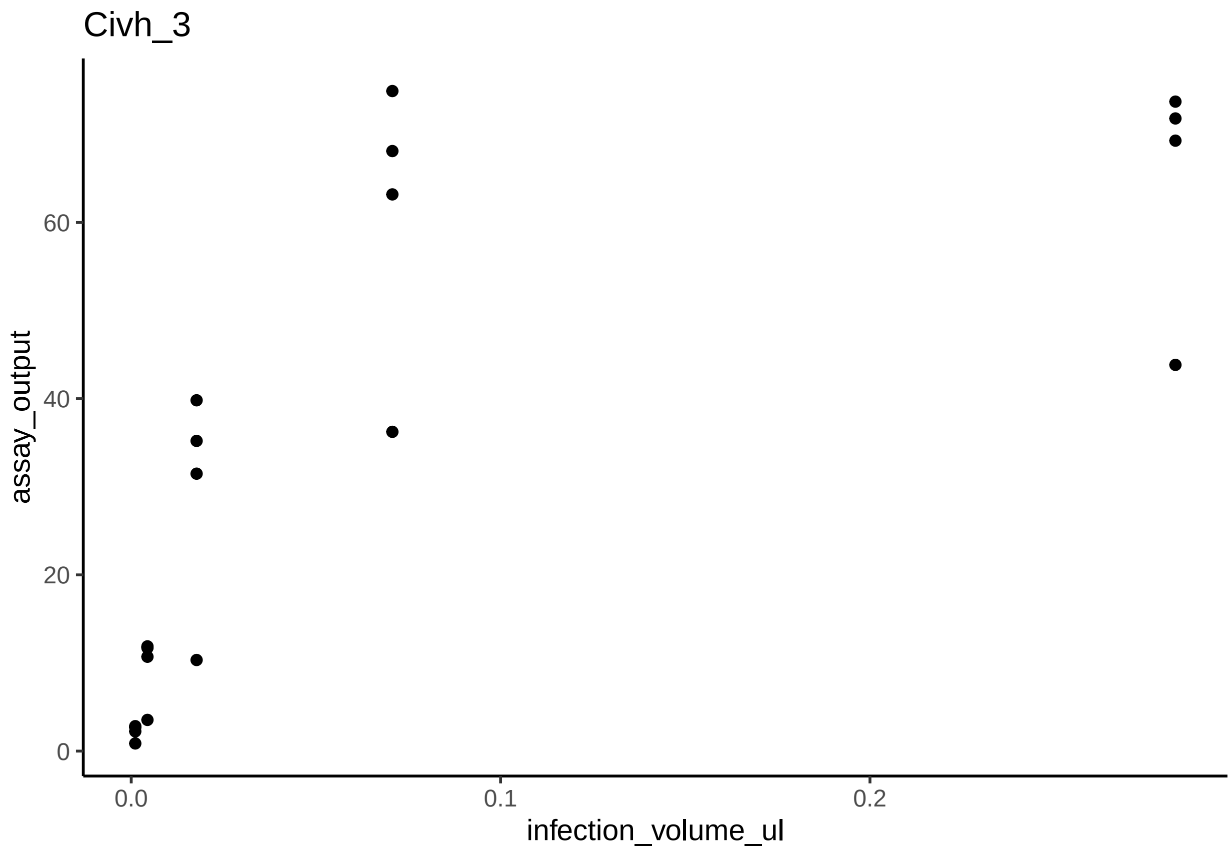

```
##
## [[14]]
```



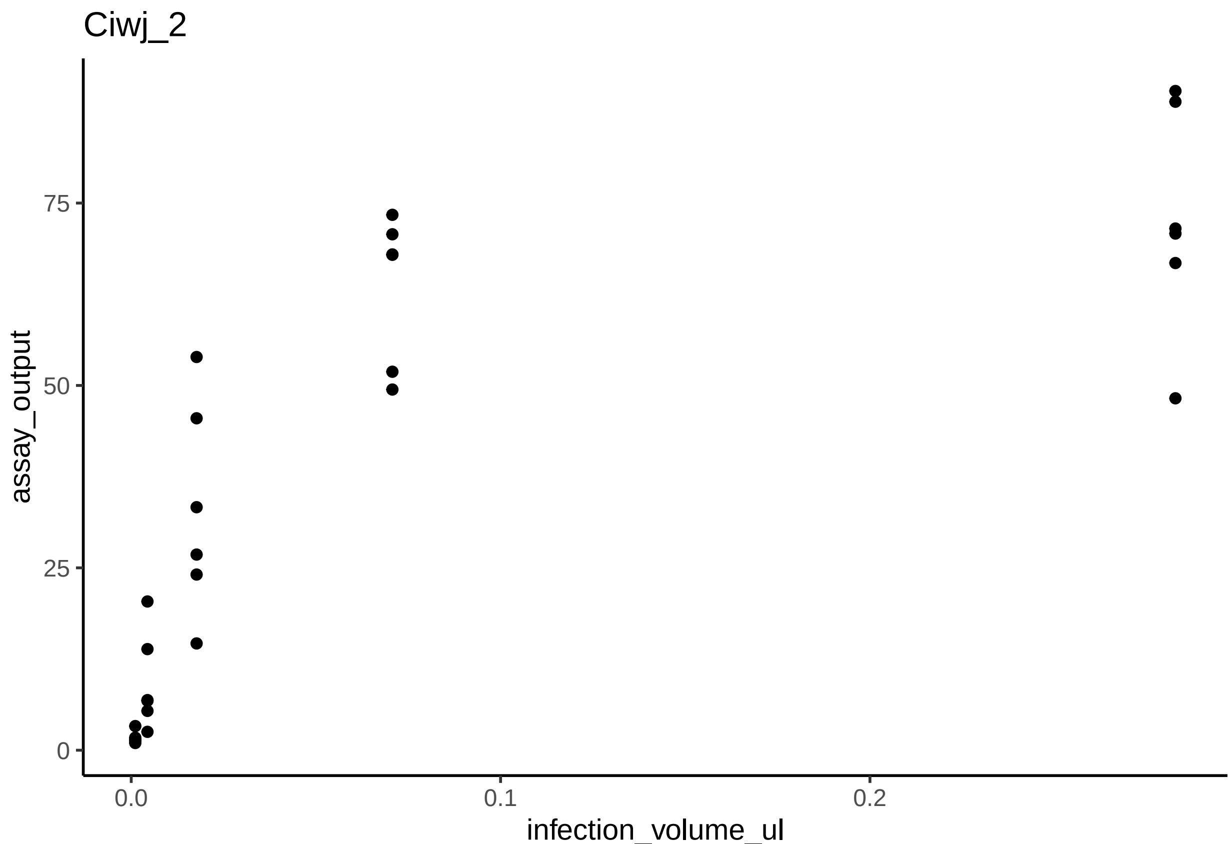

```
##
## [[15]]
```



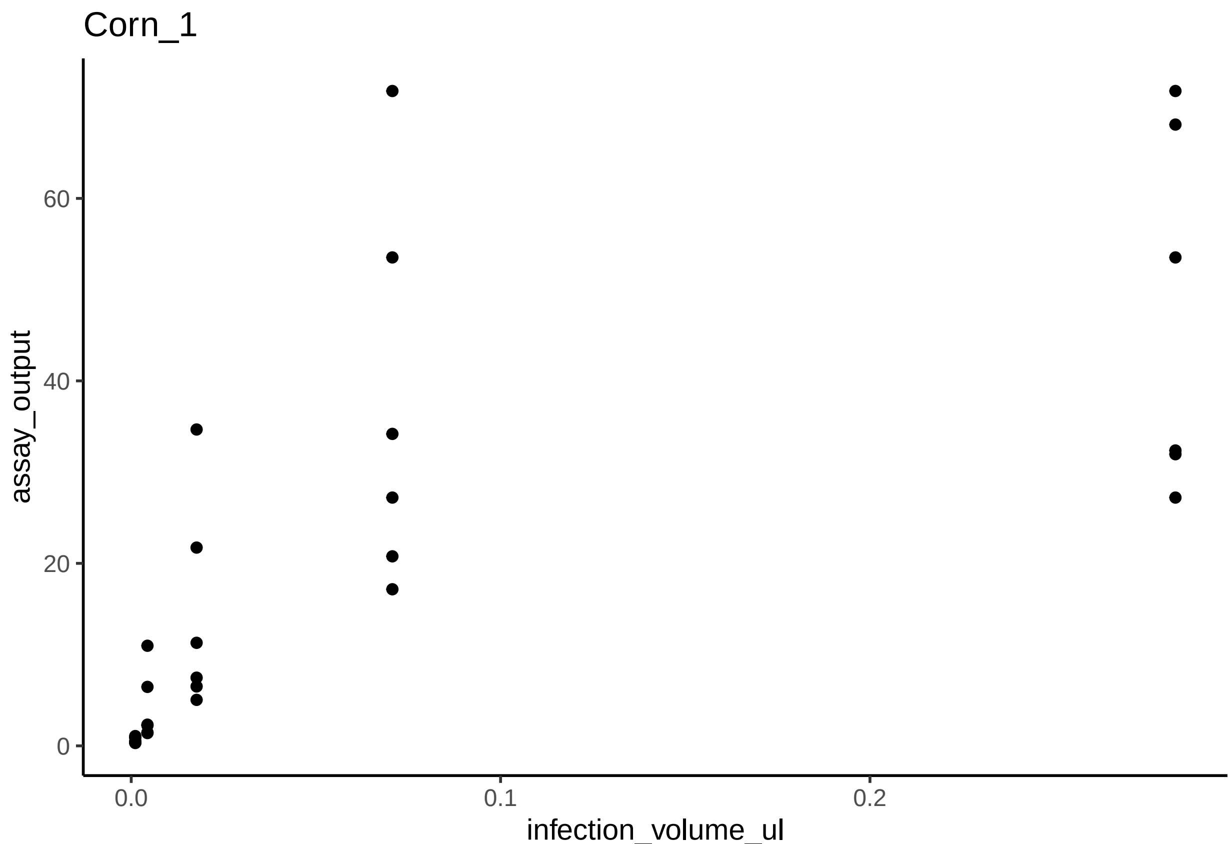

```
##
## [[16]]
```



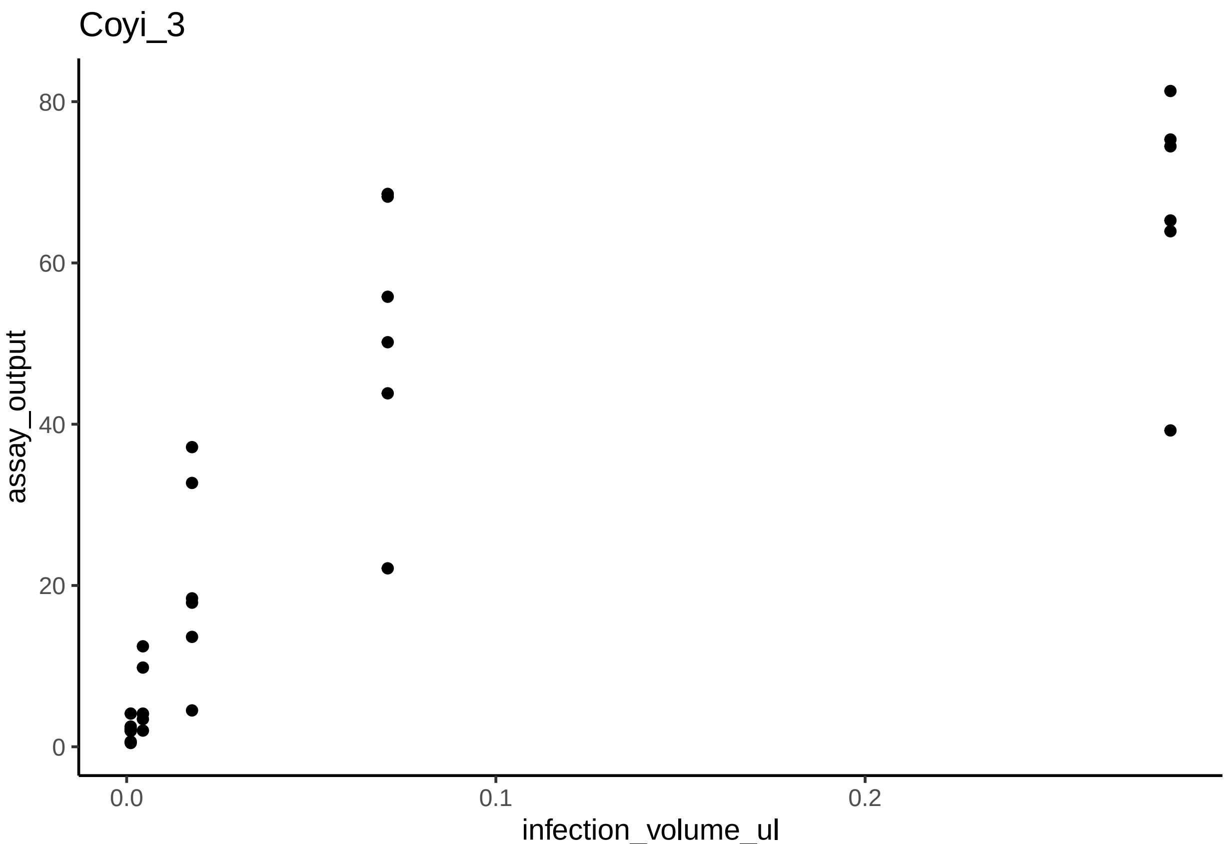

```
##
## [[17]]
```



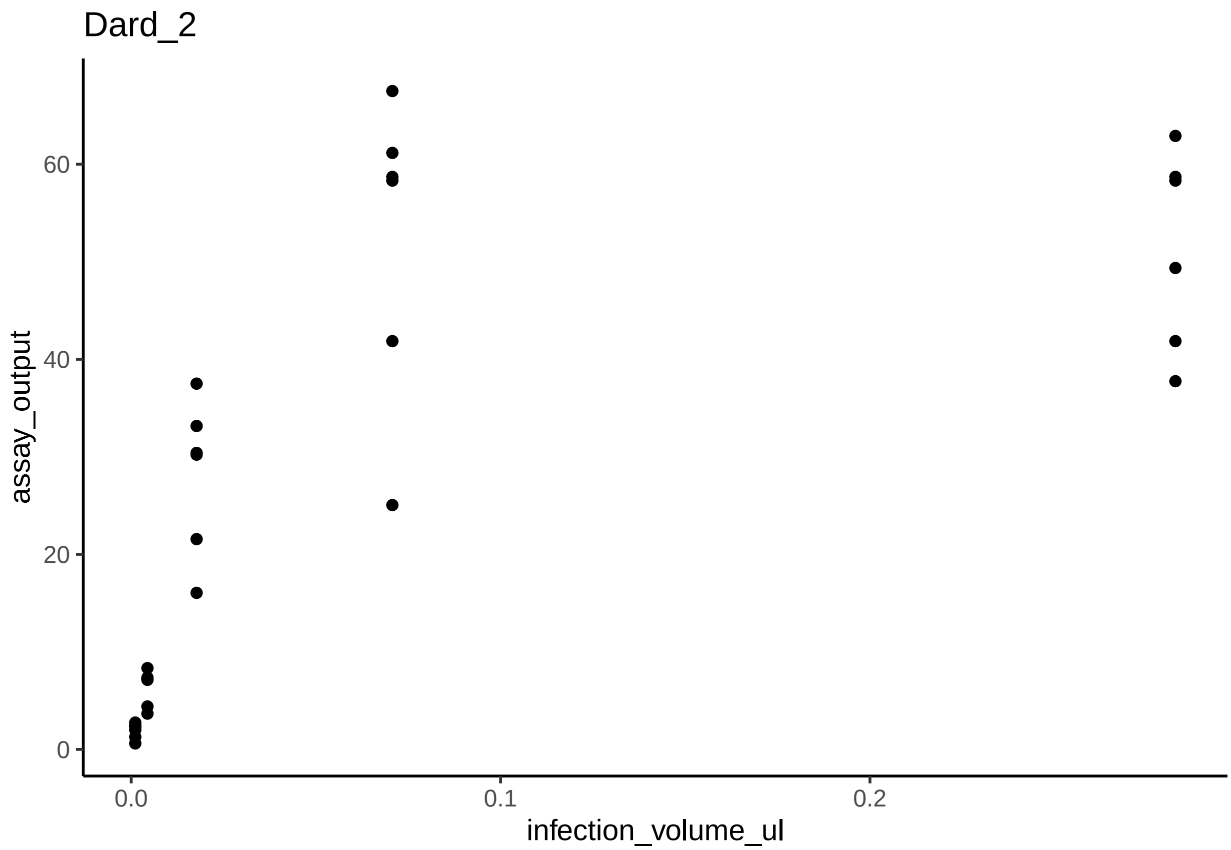

```
##
## [[18]]
```



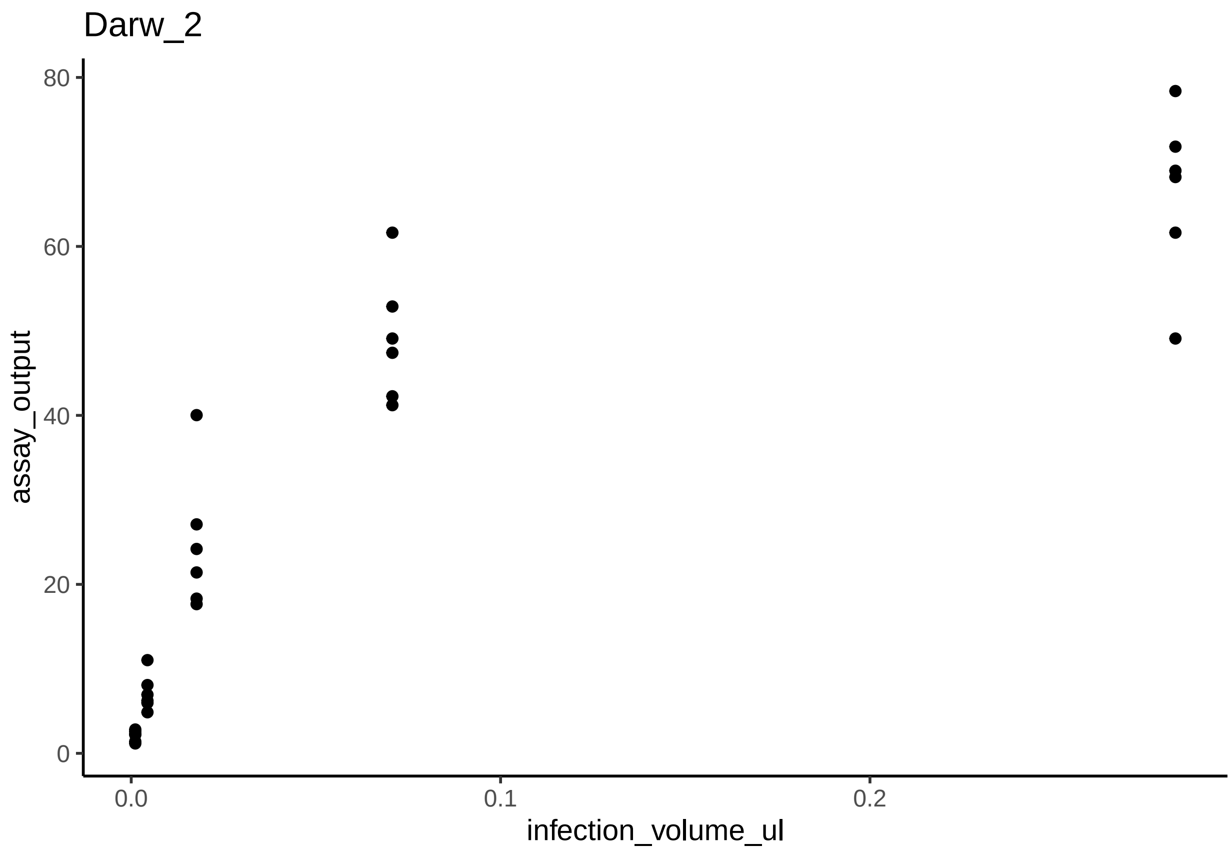

```
##
## [[19]]
```



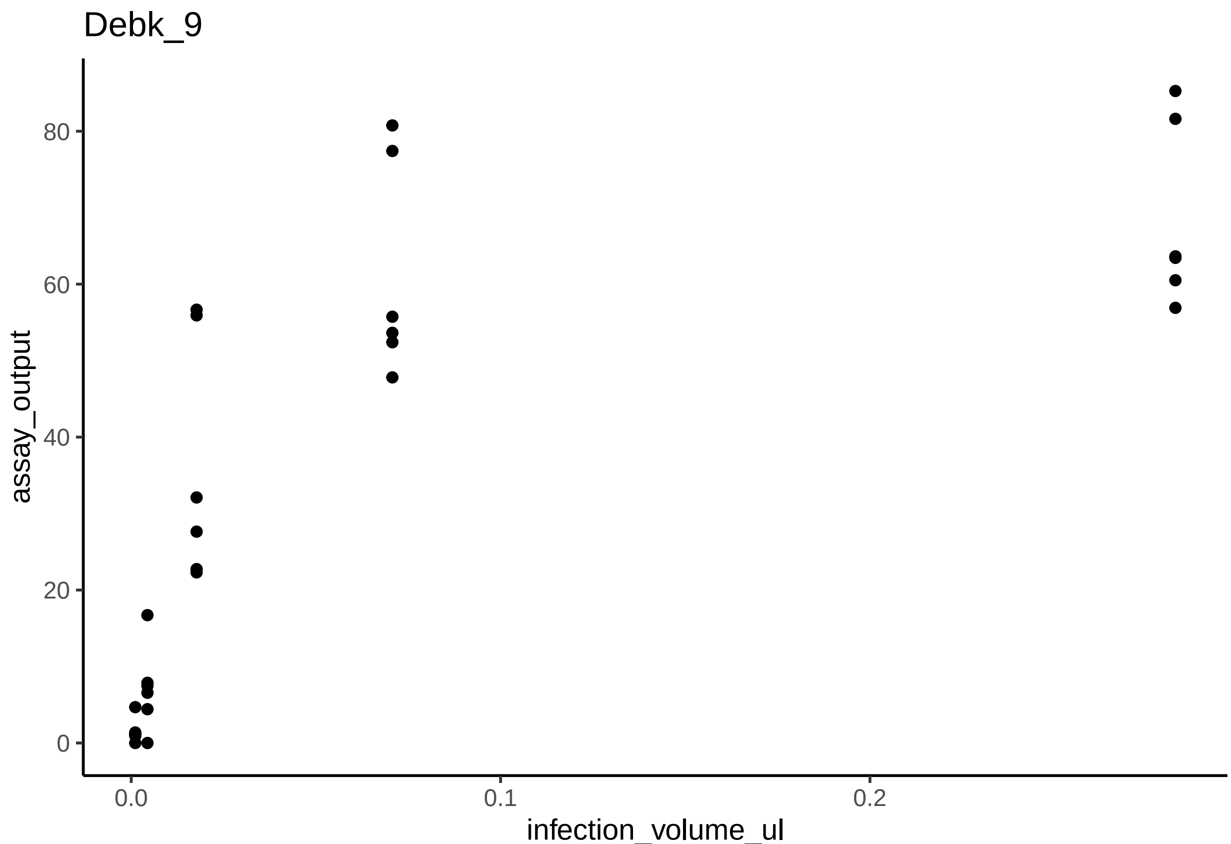

```
##
## [[20]]
```



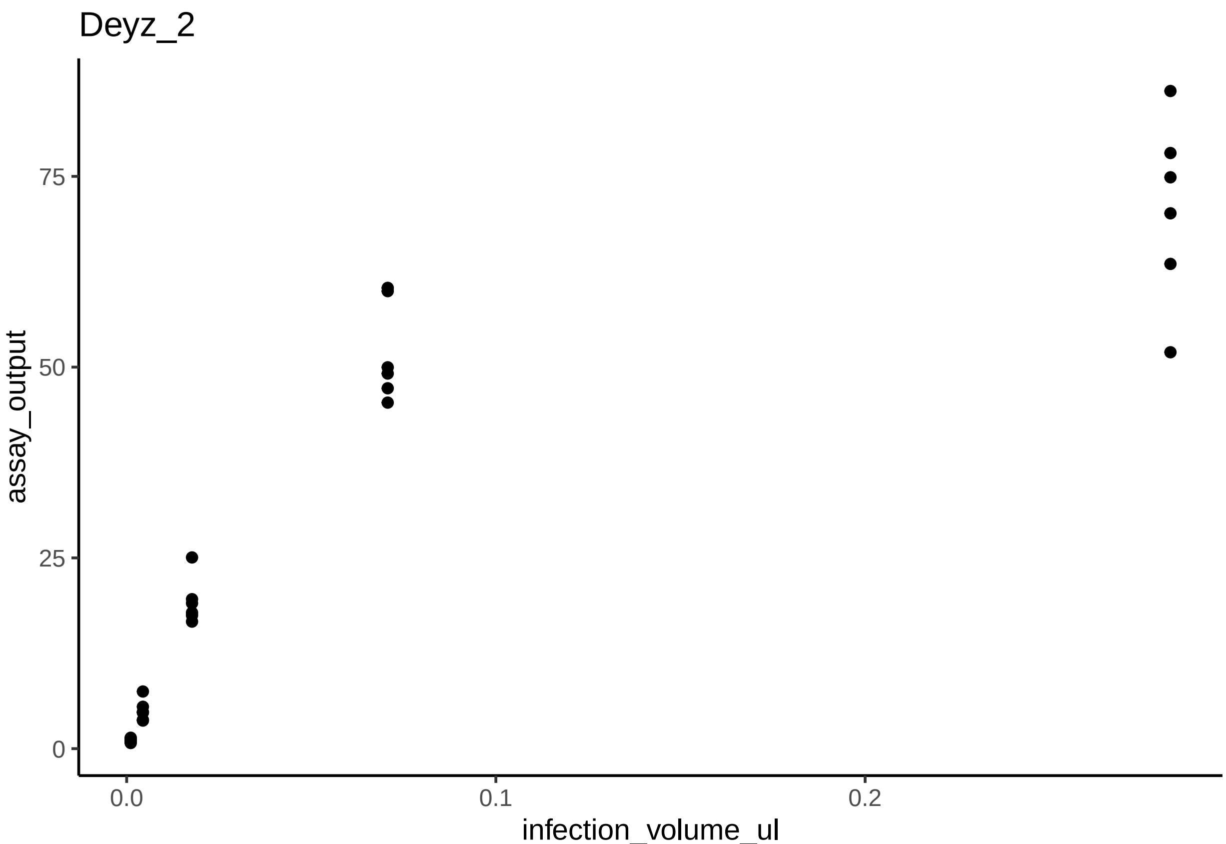

```
##
## [[21]]
```



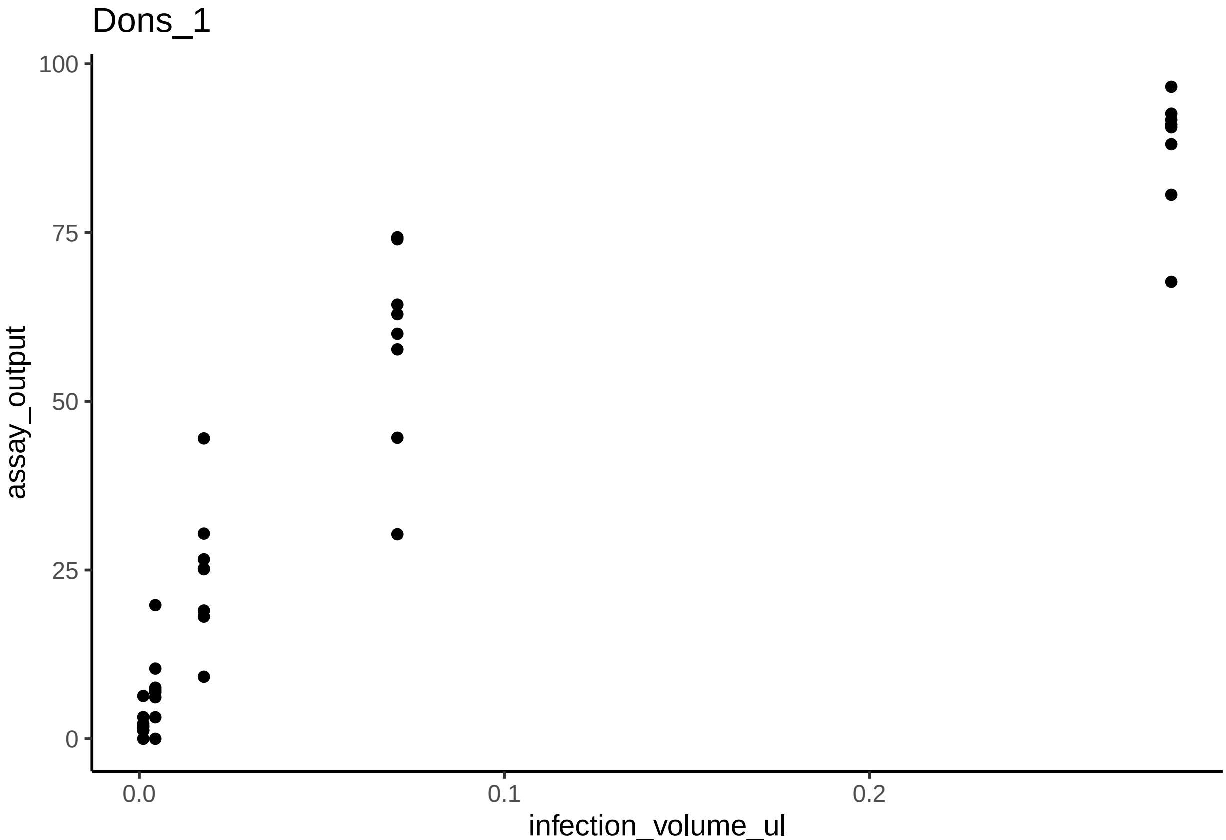

```
##
## [[22]]
```



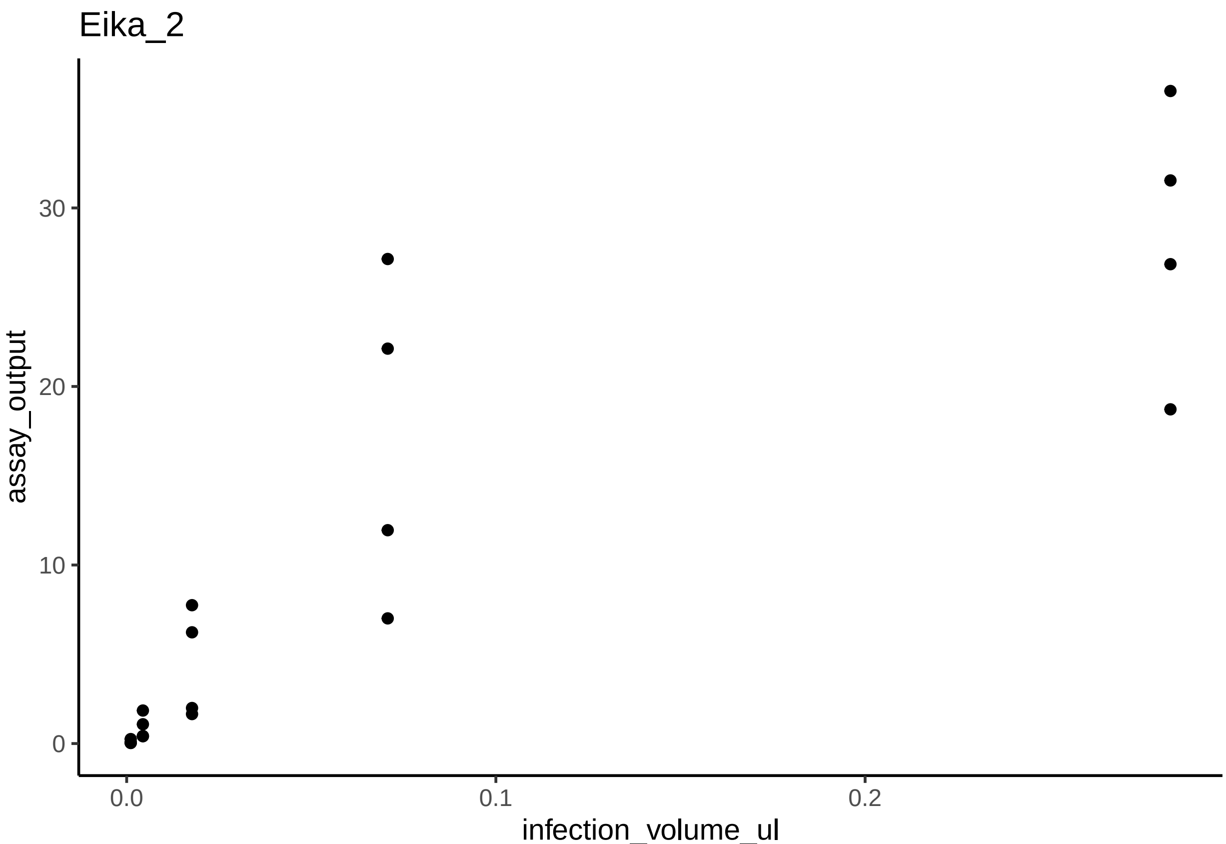

```
##
## [[23]]
```



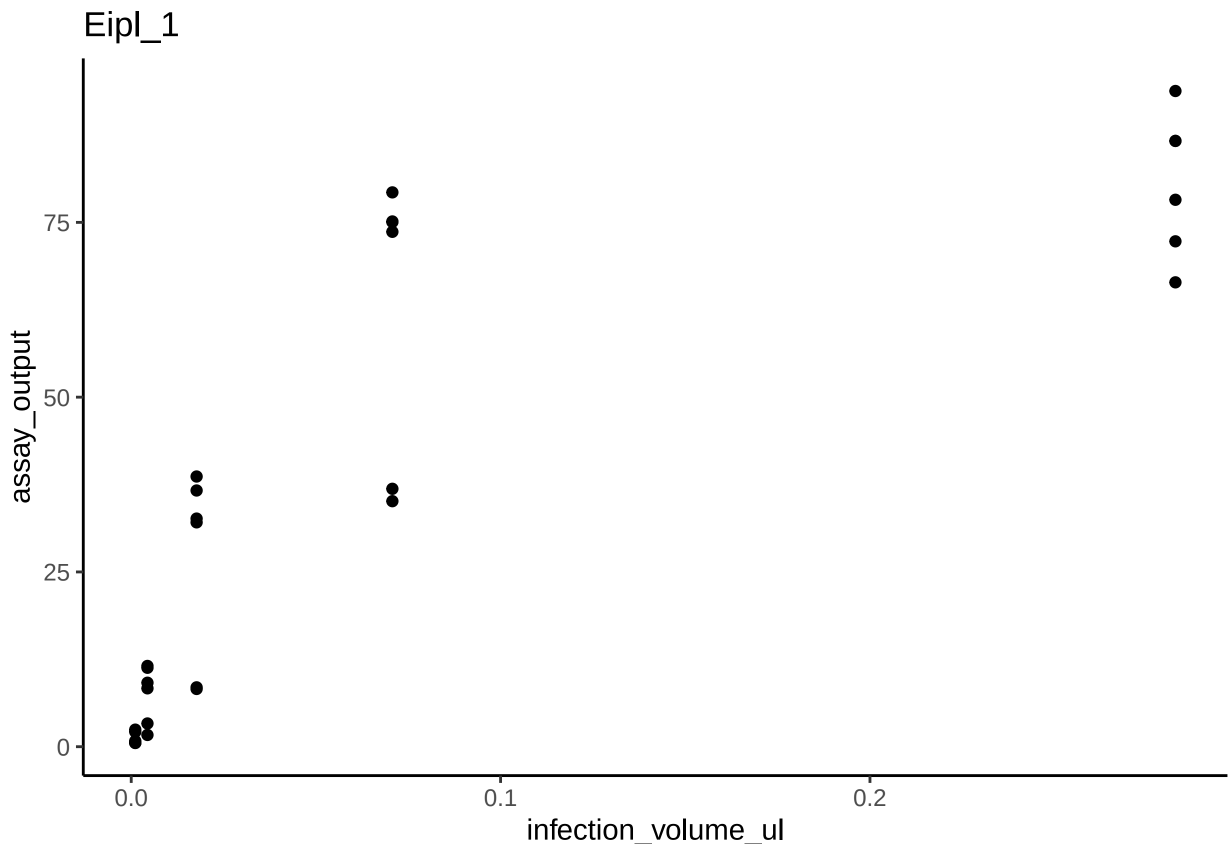

```
##
## [[24]]
```



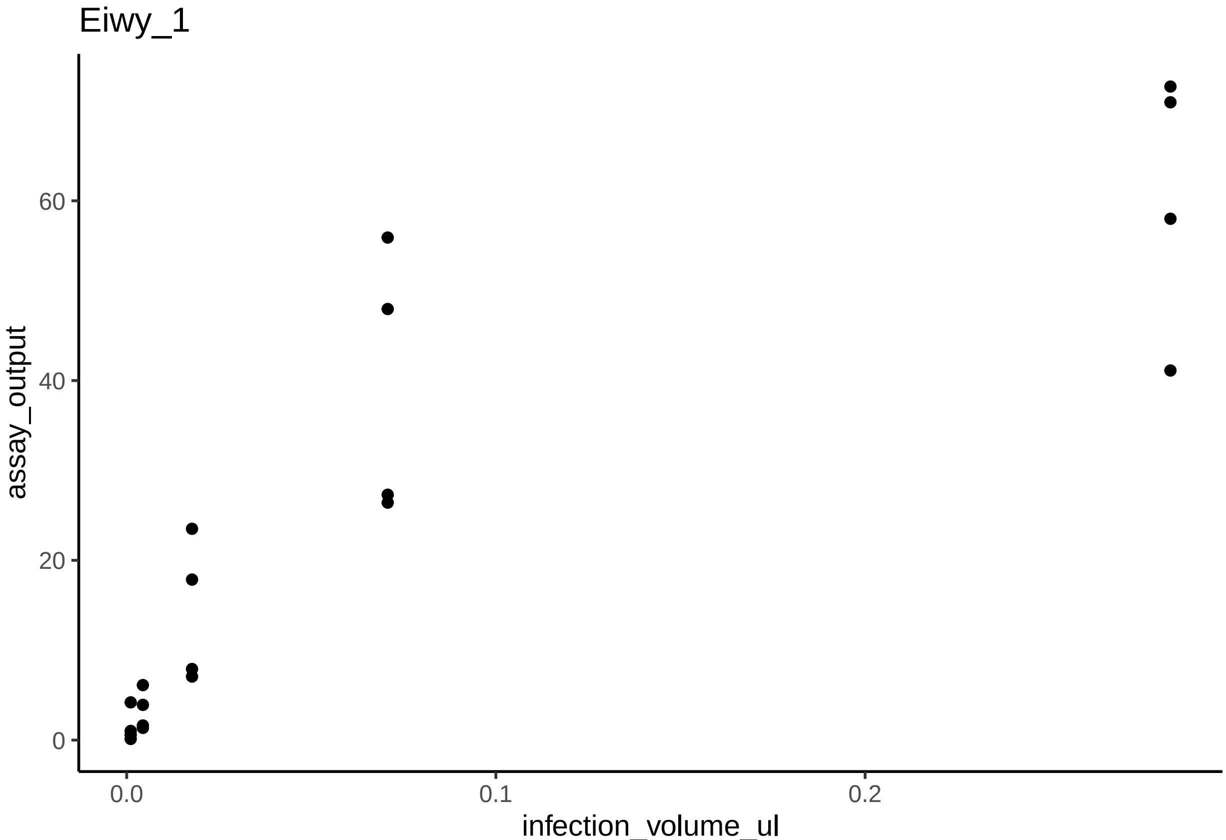

```
##
## [[25]]
```



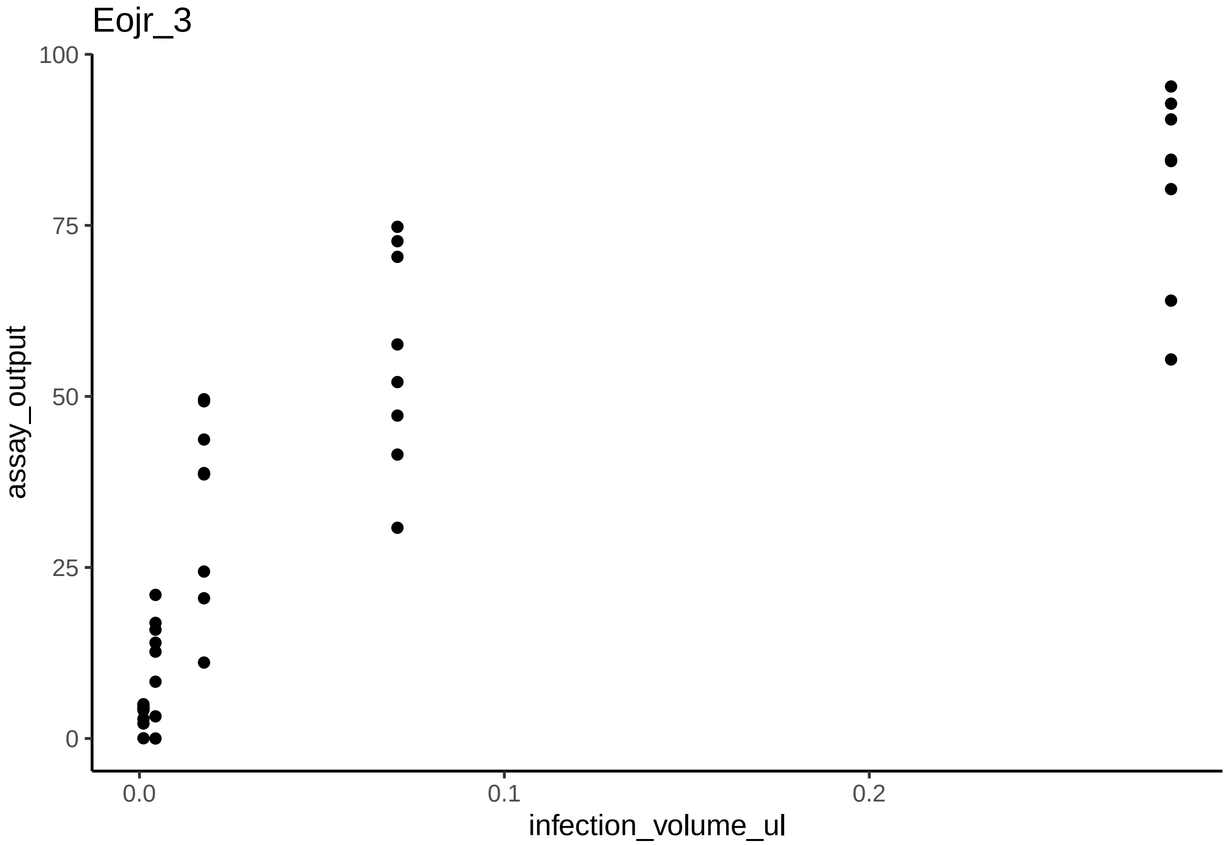

```
##
## [[26]]
```



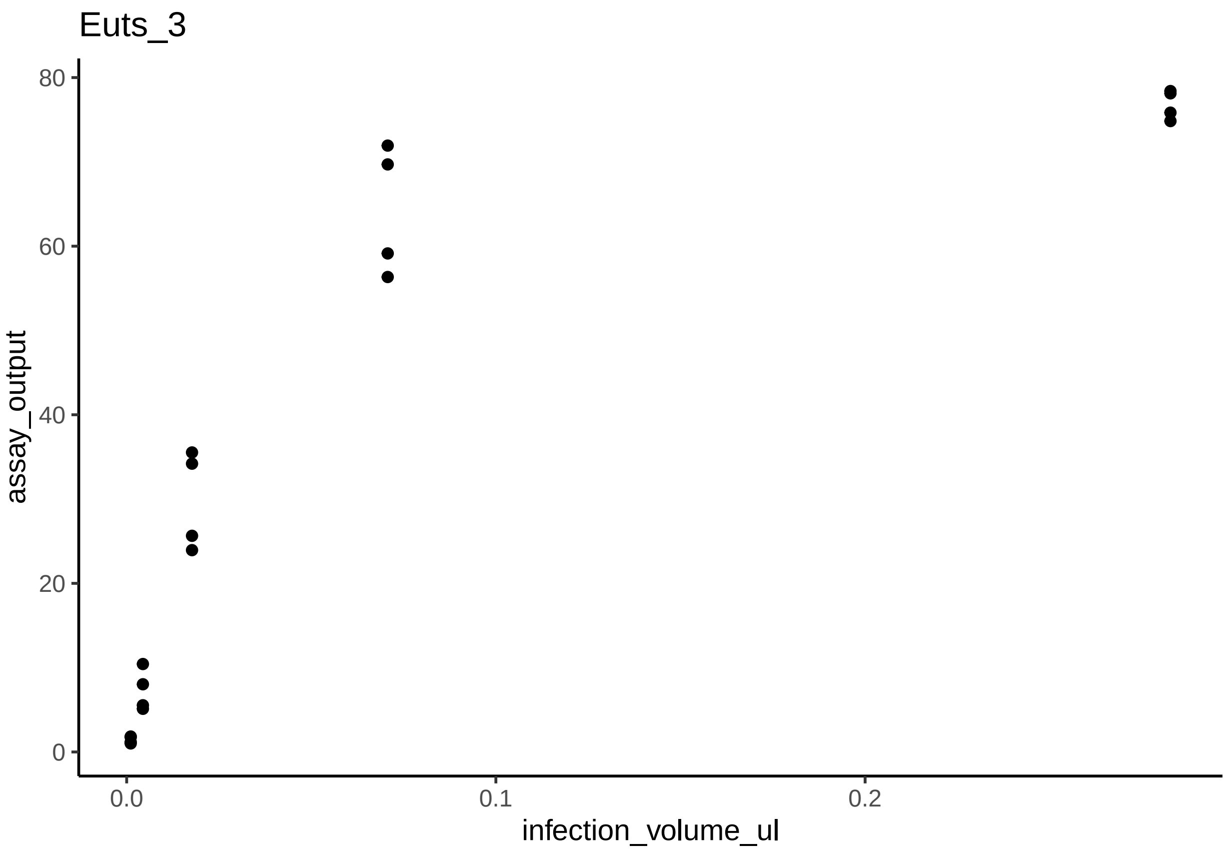

```
##
## [[27]]
```



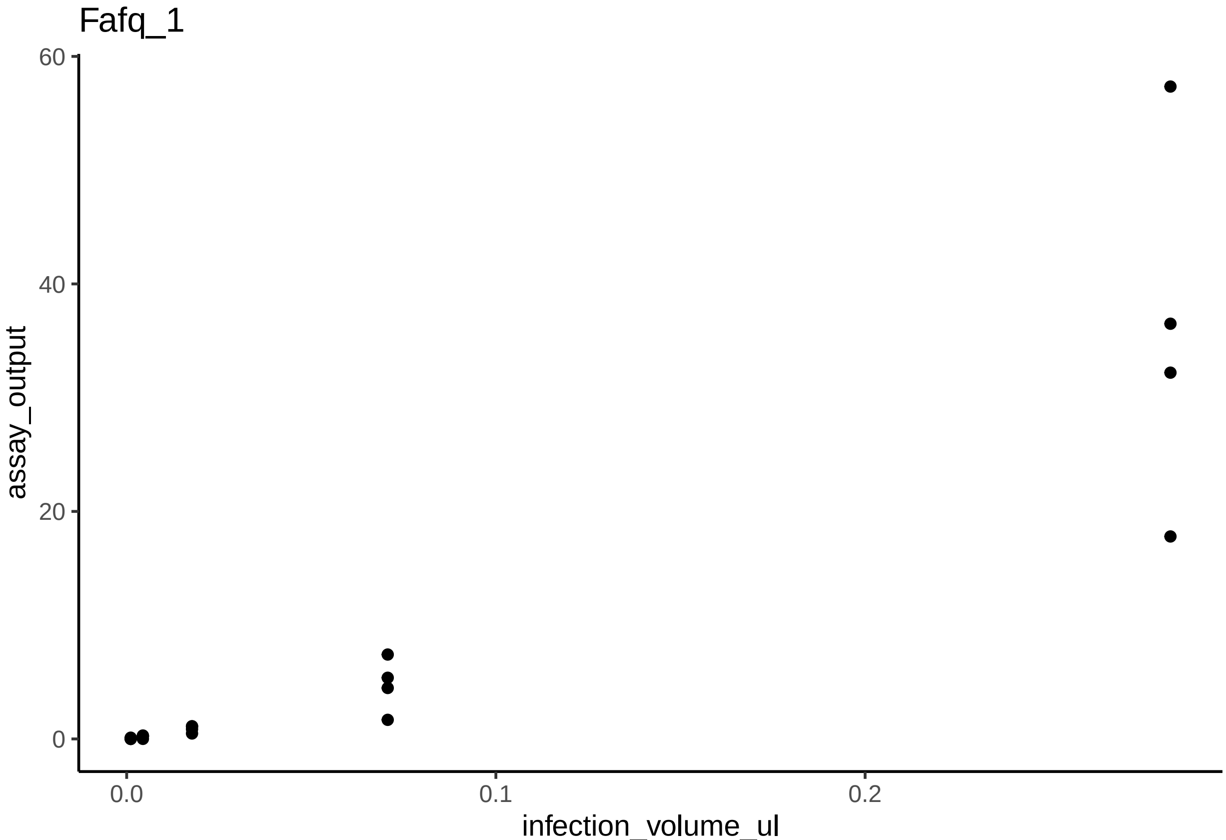

```
##
## [[28]]
```



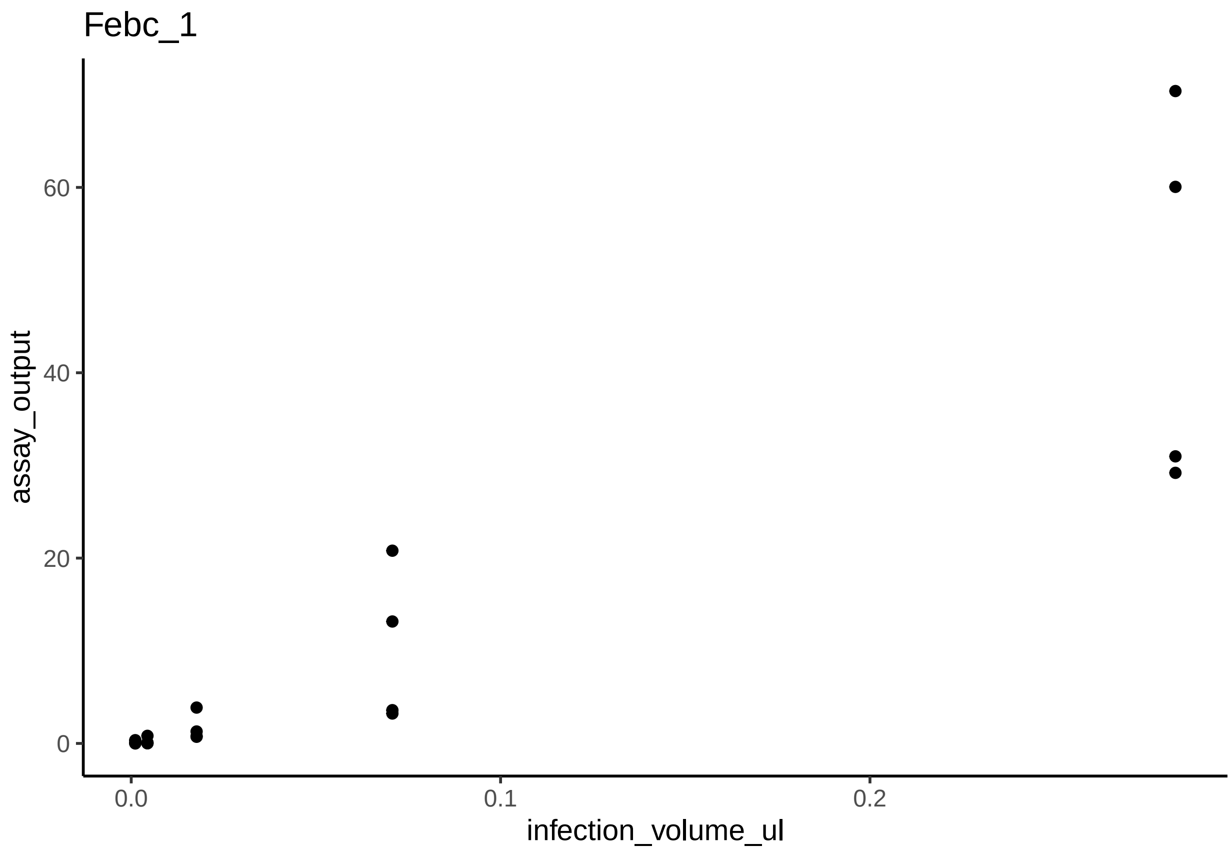

```
##
## [[29]]
```



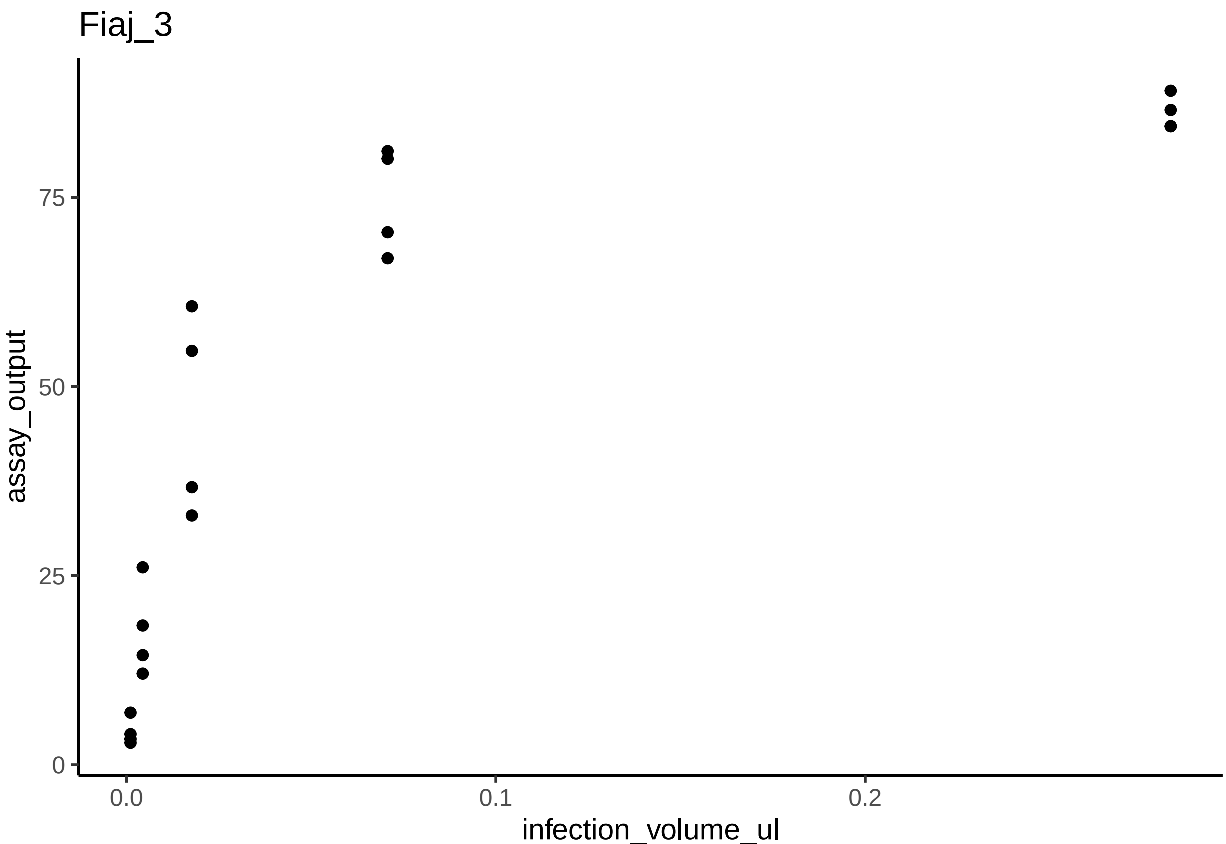

```
##
## [[30]]
```



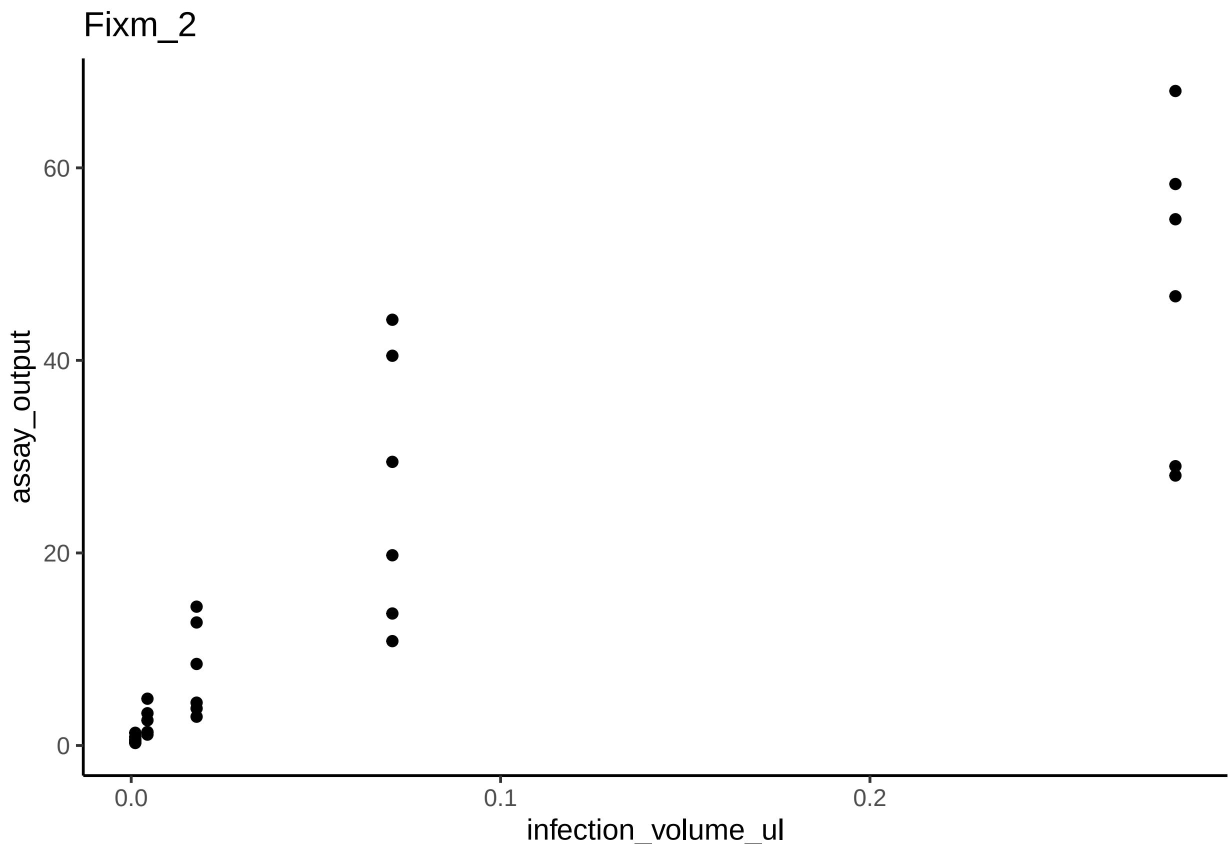

```
##
## [[31]]
```



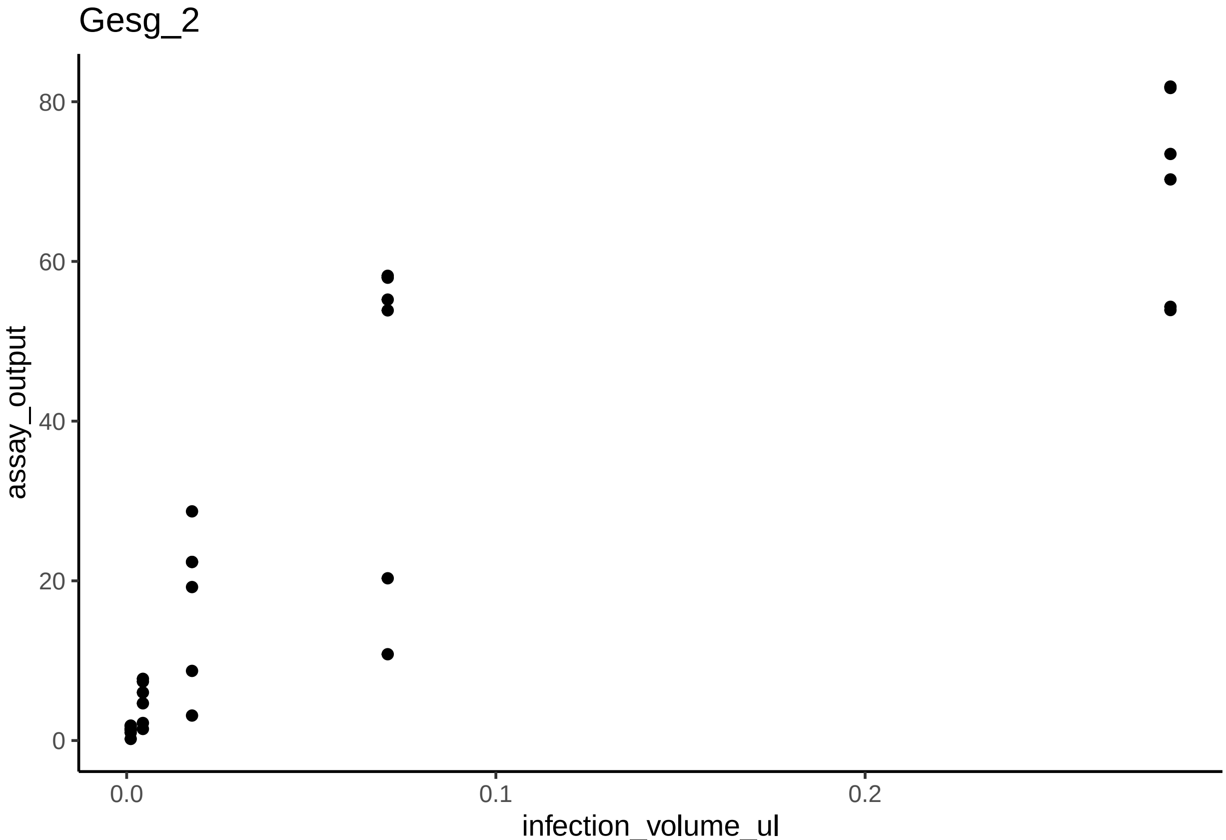

```
##
## [[32]]
```



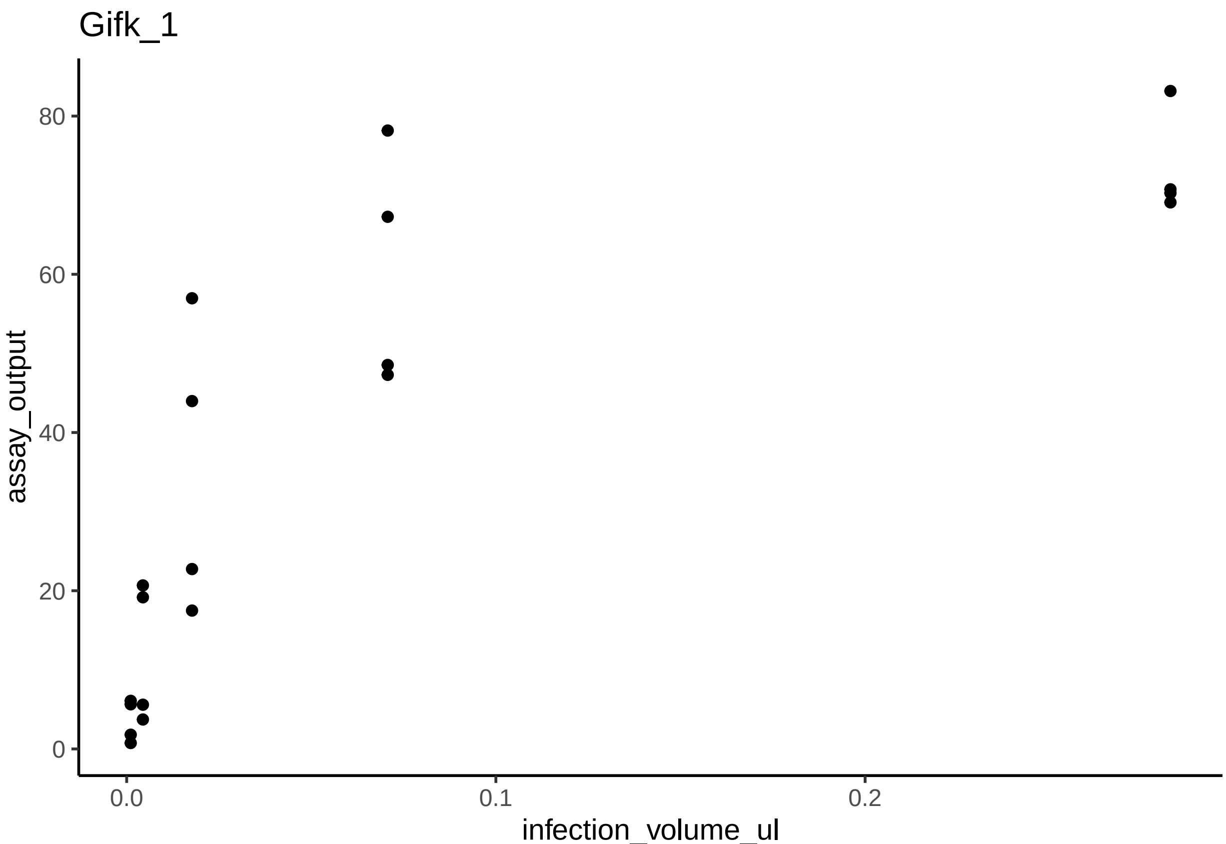

```
##
## [[33]]
```



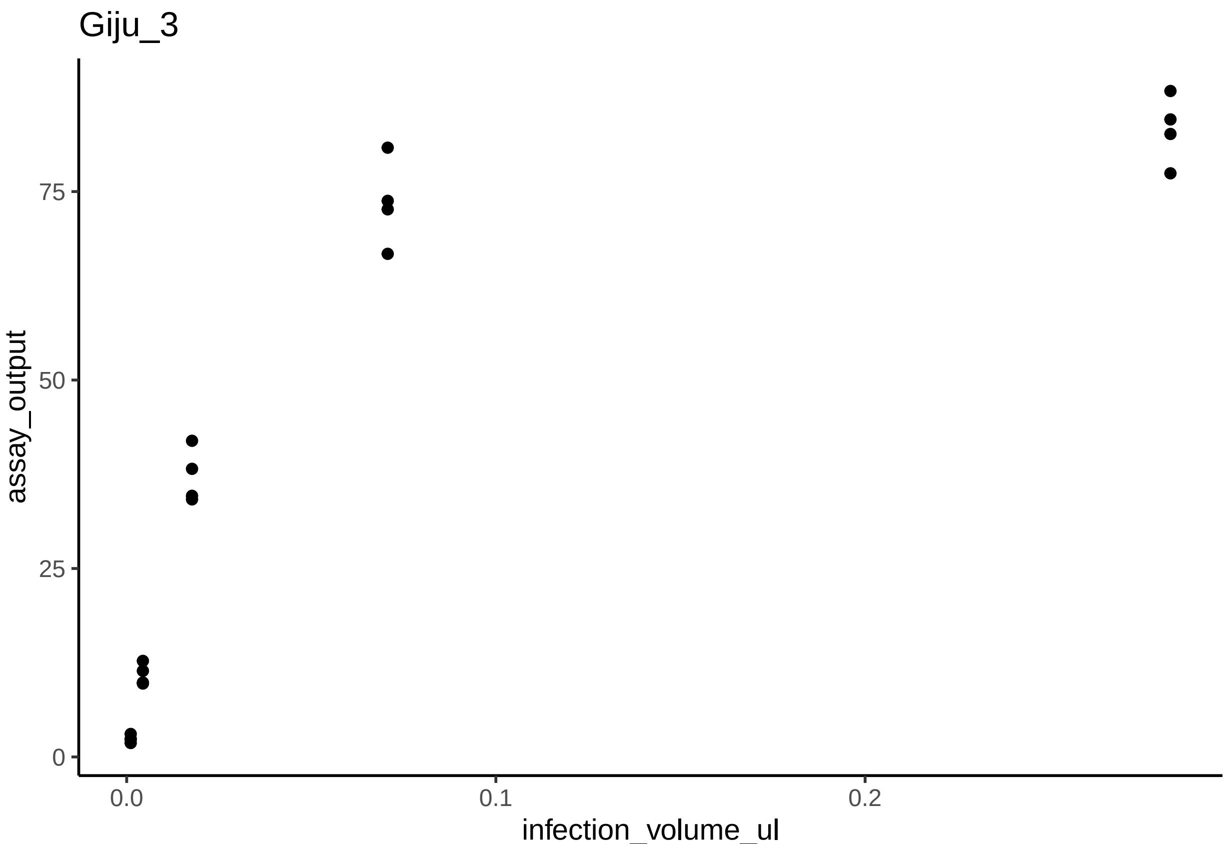

```
##
## [[34]]
```



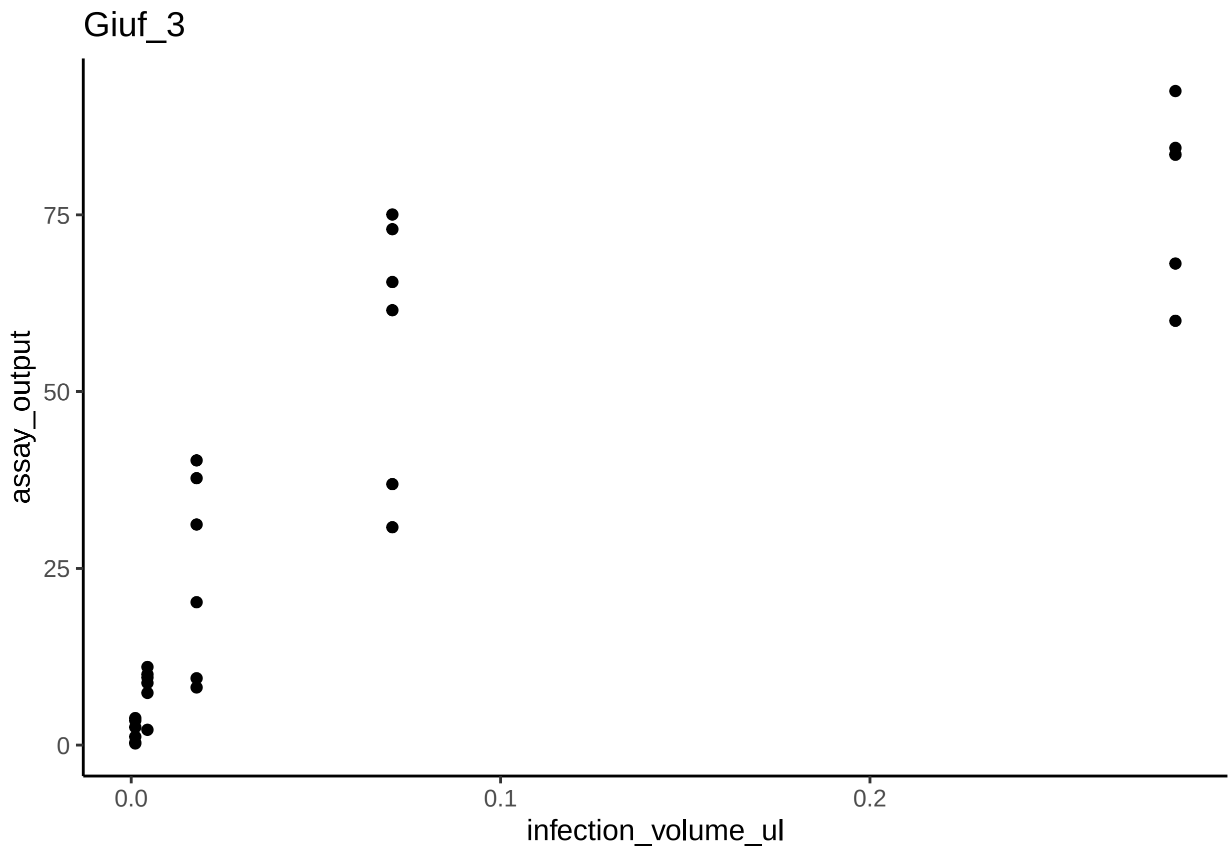

```
##
## [[35]]
```



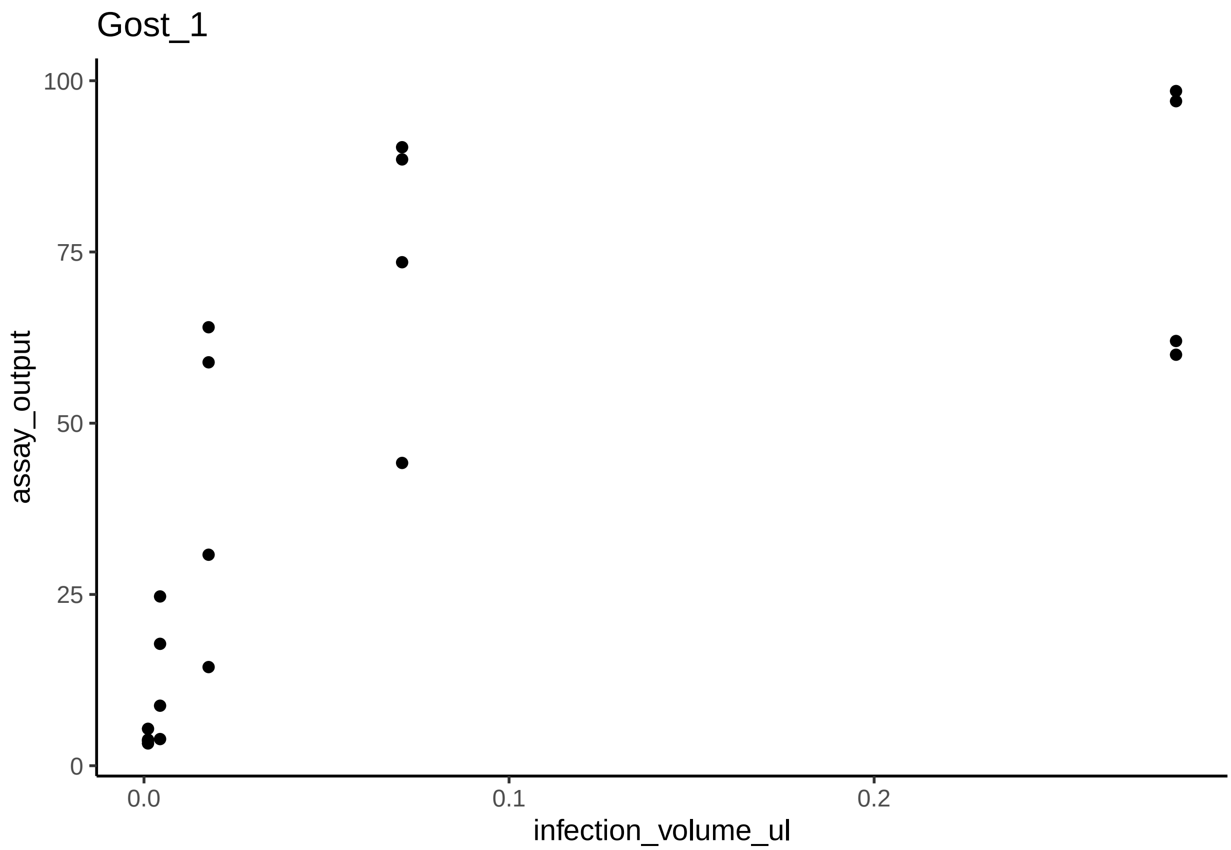

```
##
## [[36]]
```



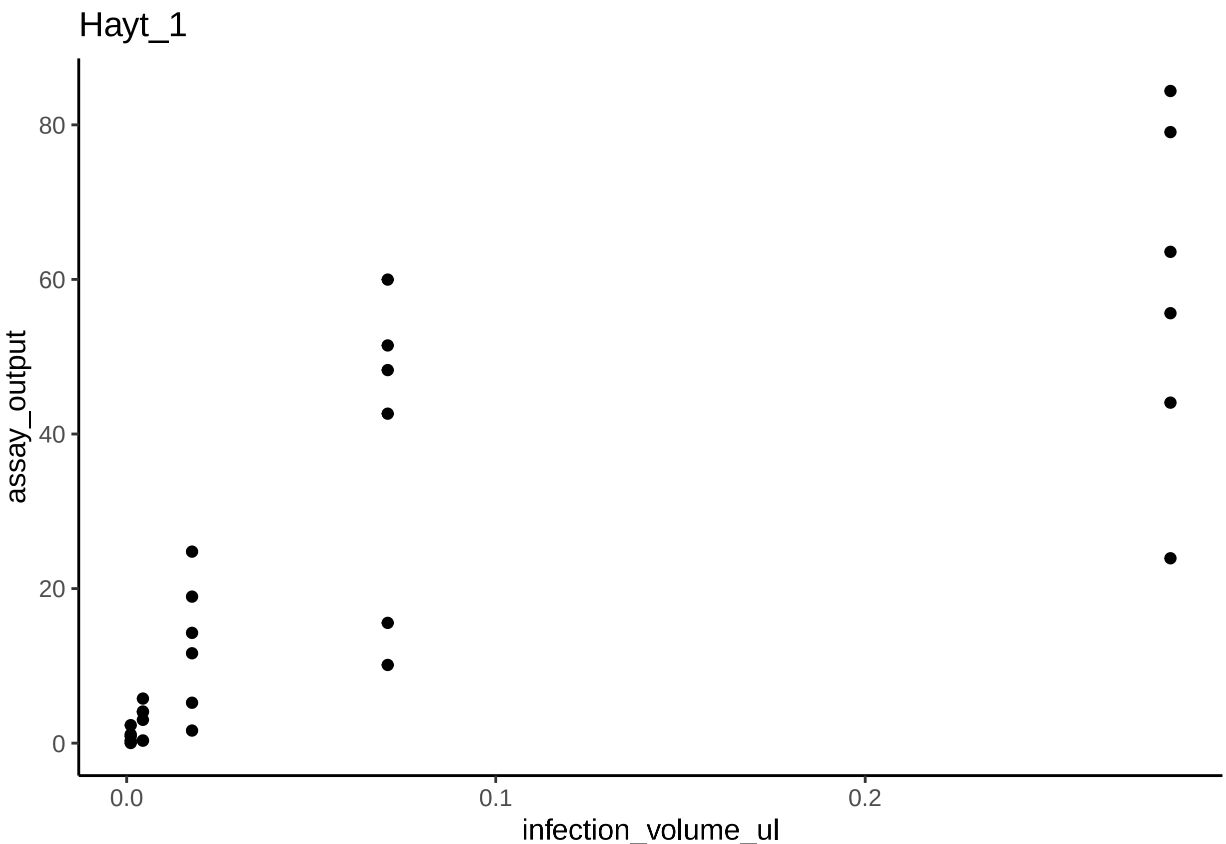

```
##
## [[37]]
```



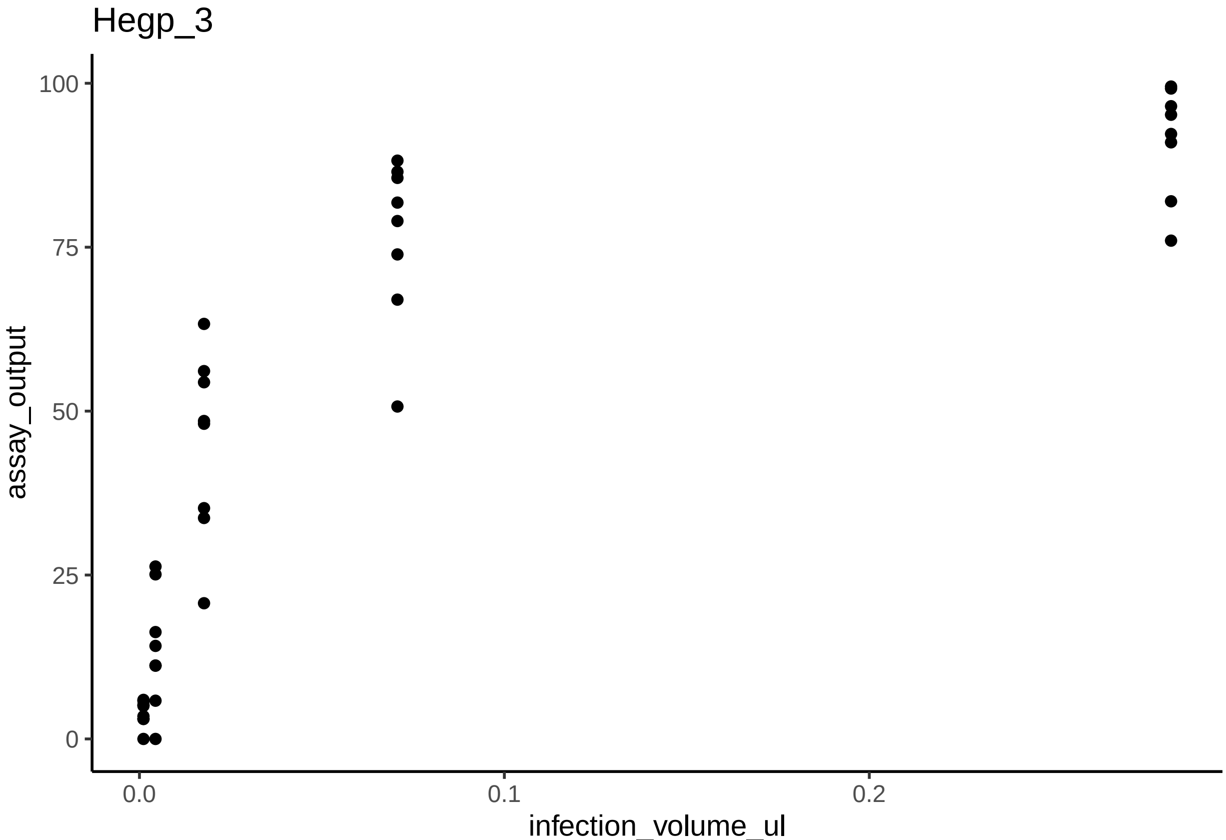

```
##
## [[38]]
```



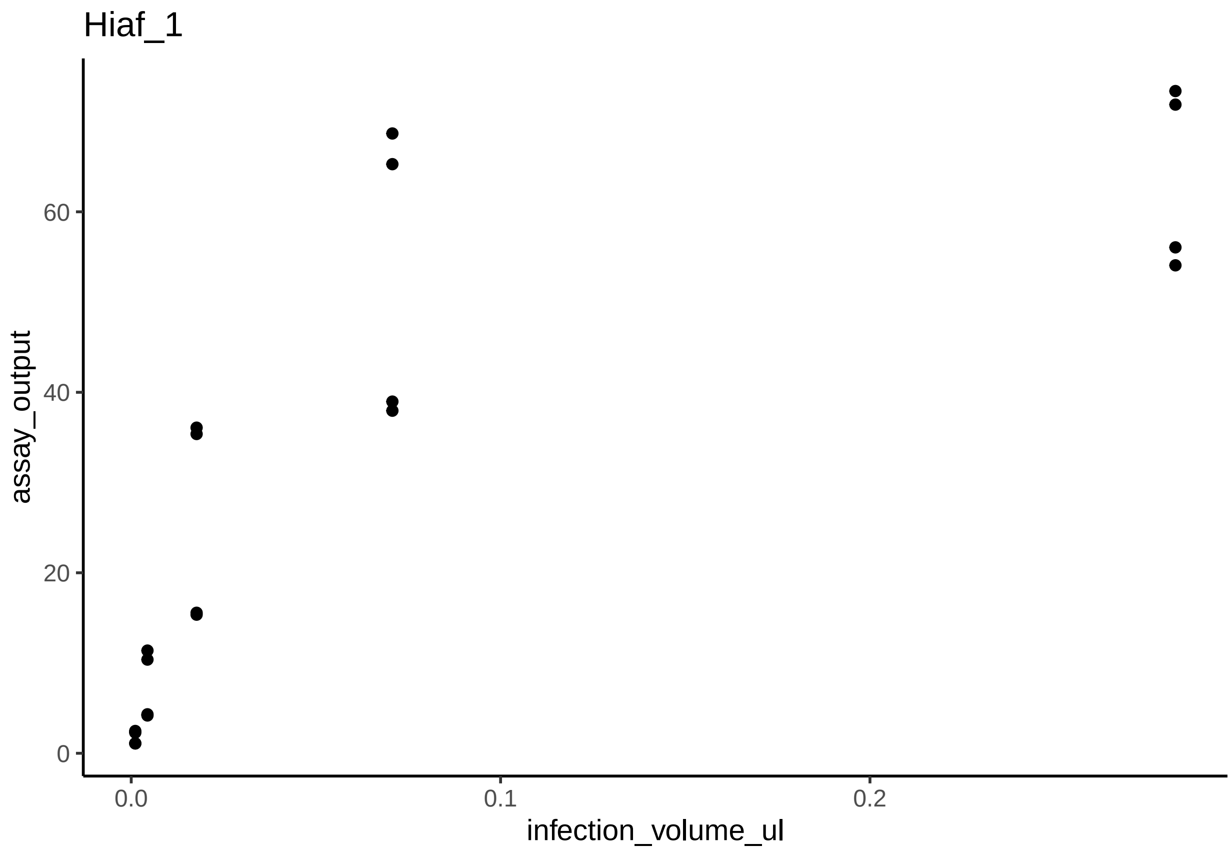

```
##
## [[39]]
```



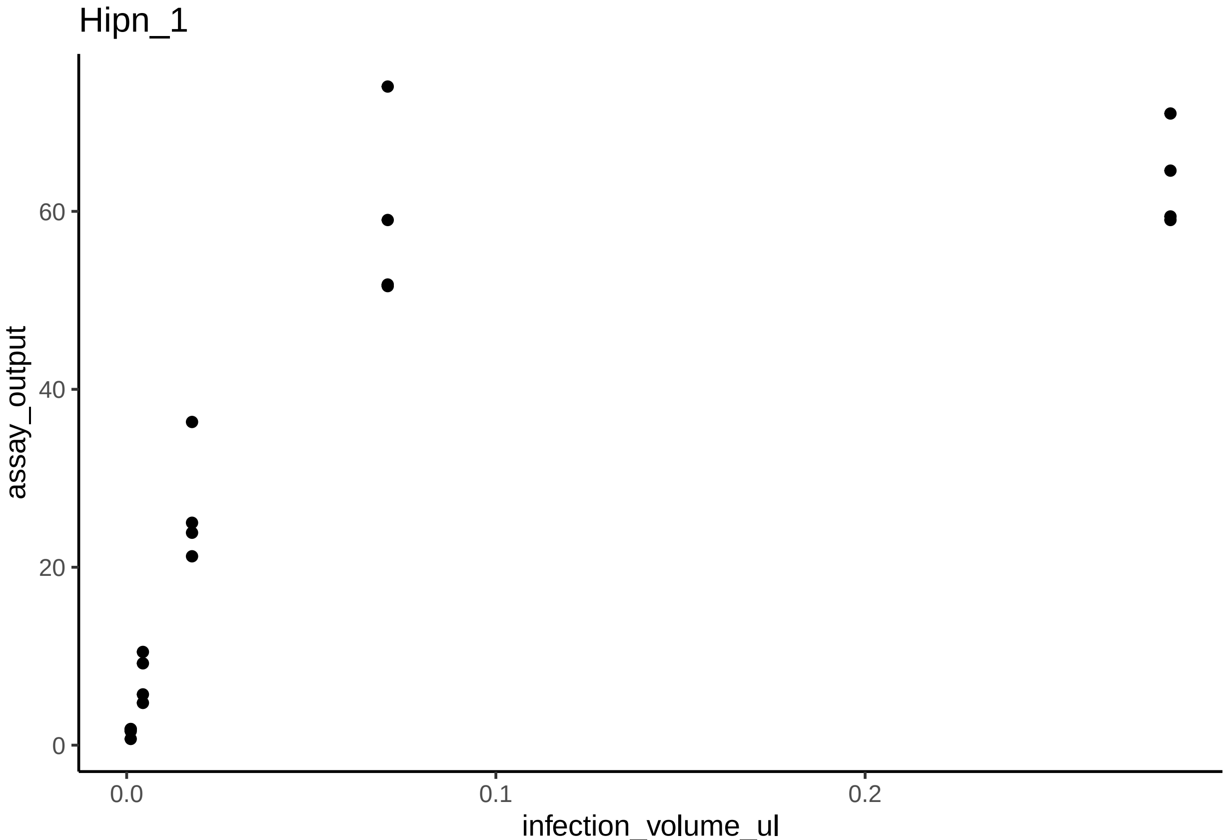

```
##
## [[40]]
```



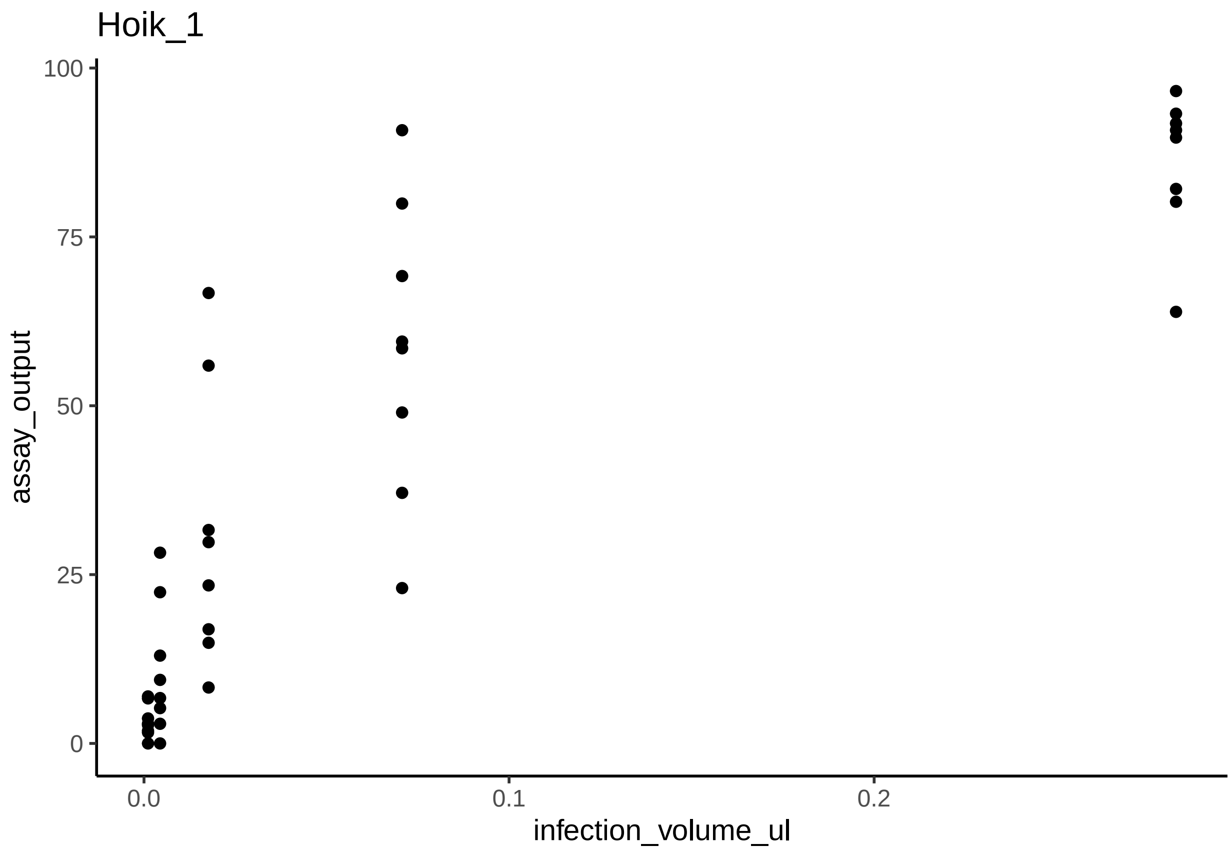

```
##
## [[41]]
```



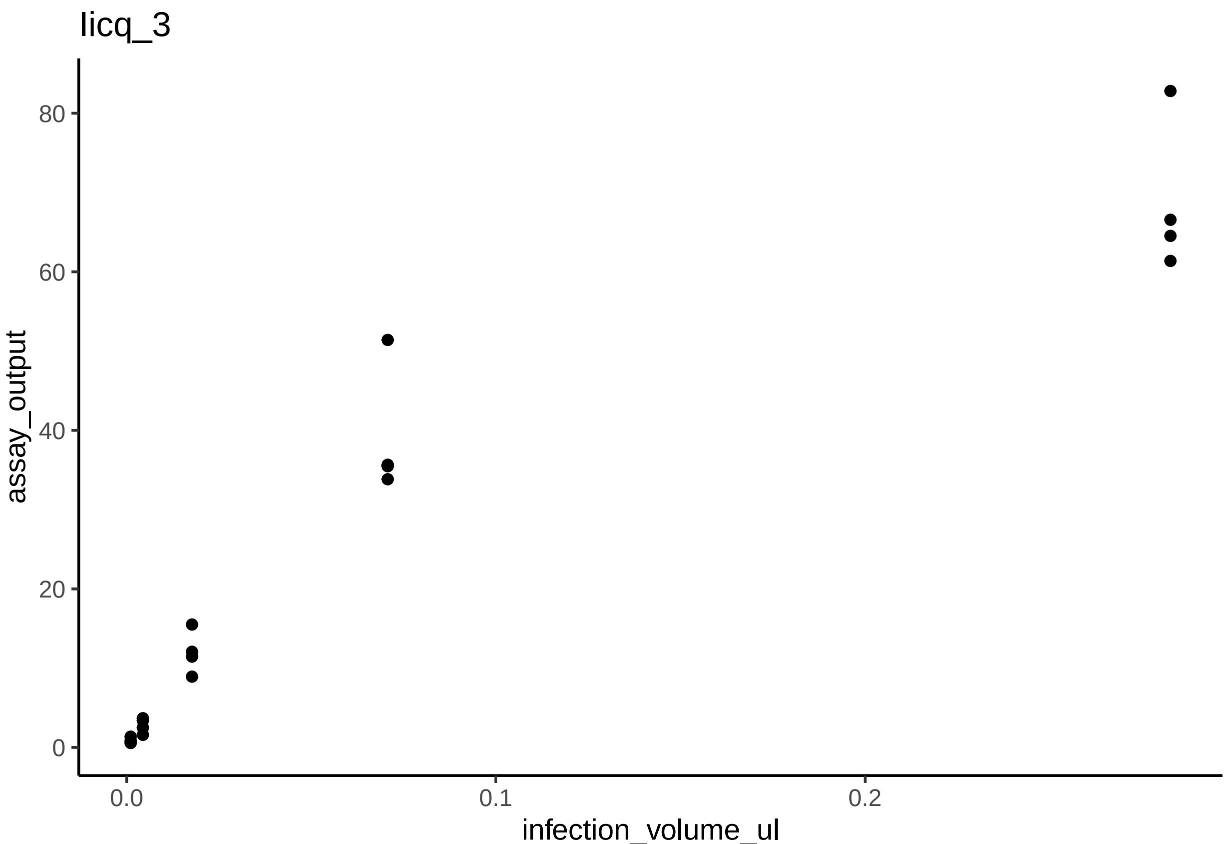

```
##
## [[42]]
```



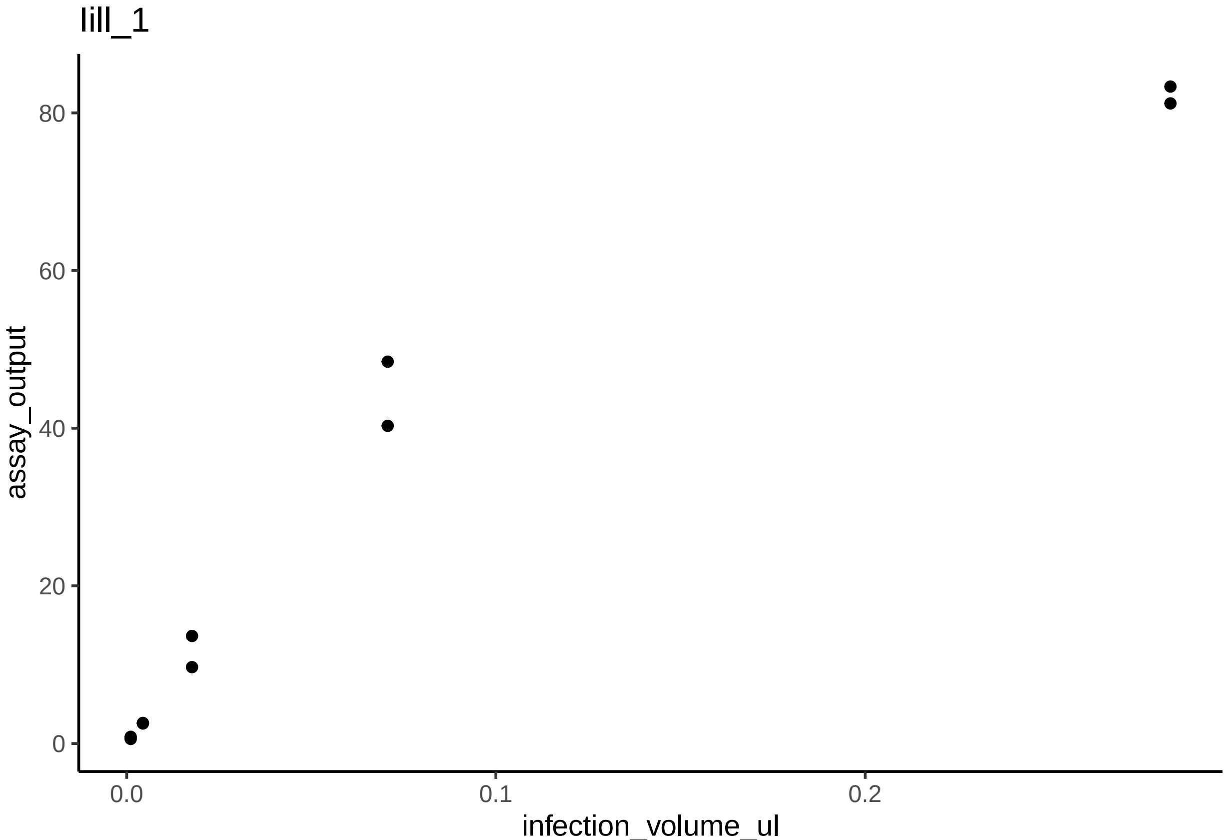

```
##
## [[43]]
```



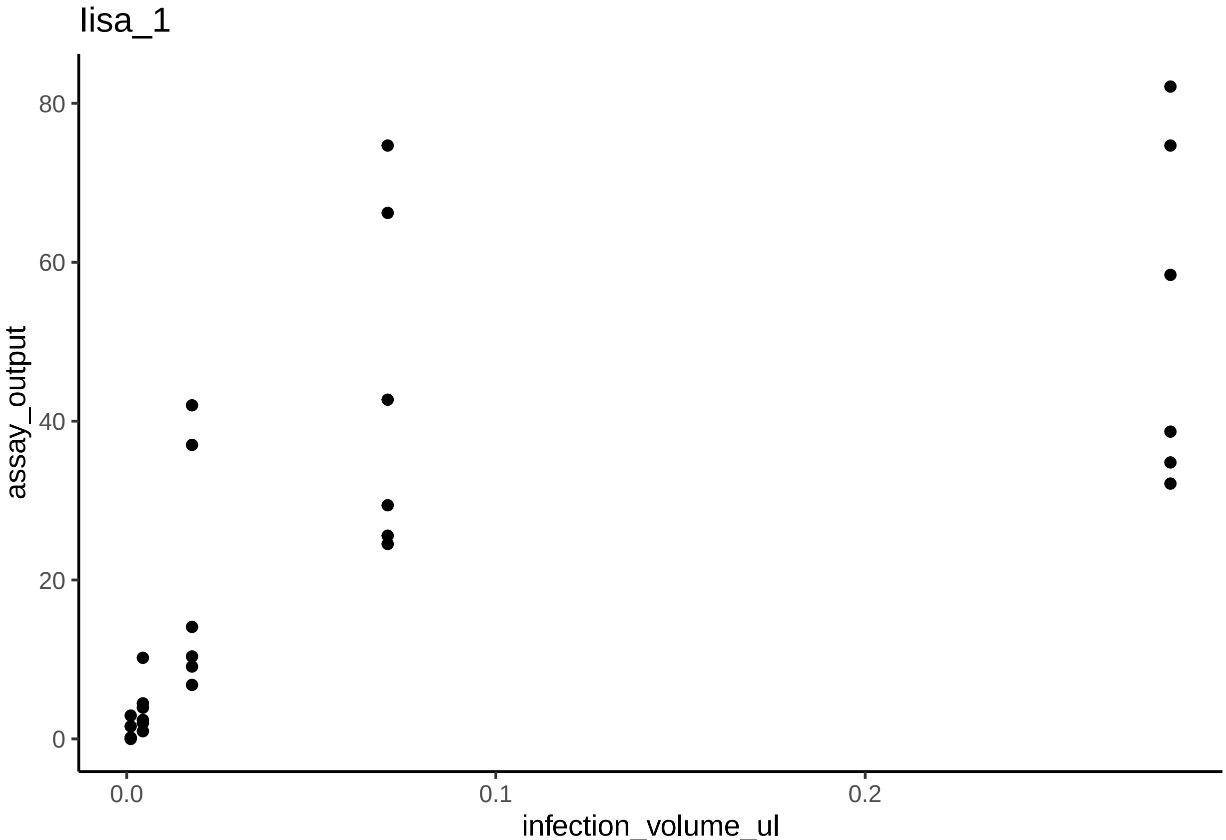

```
##
## [[44]]
```



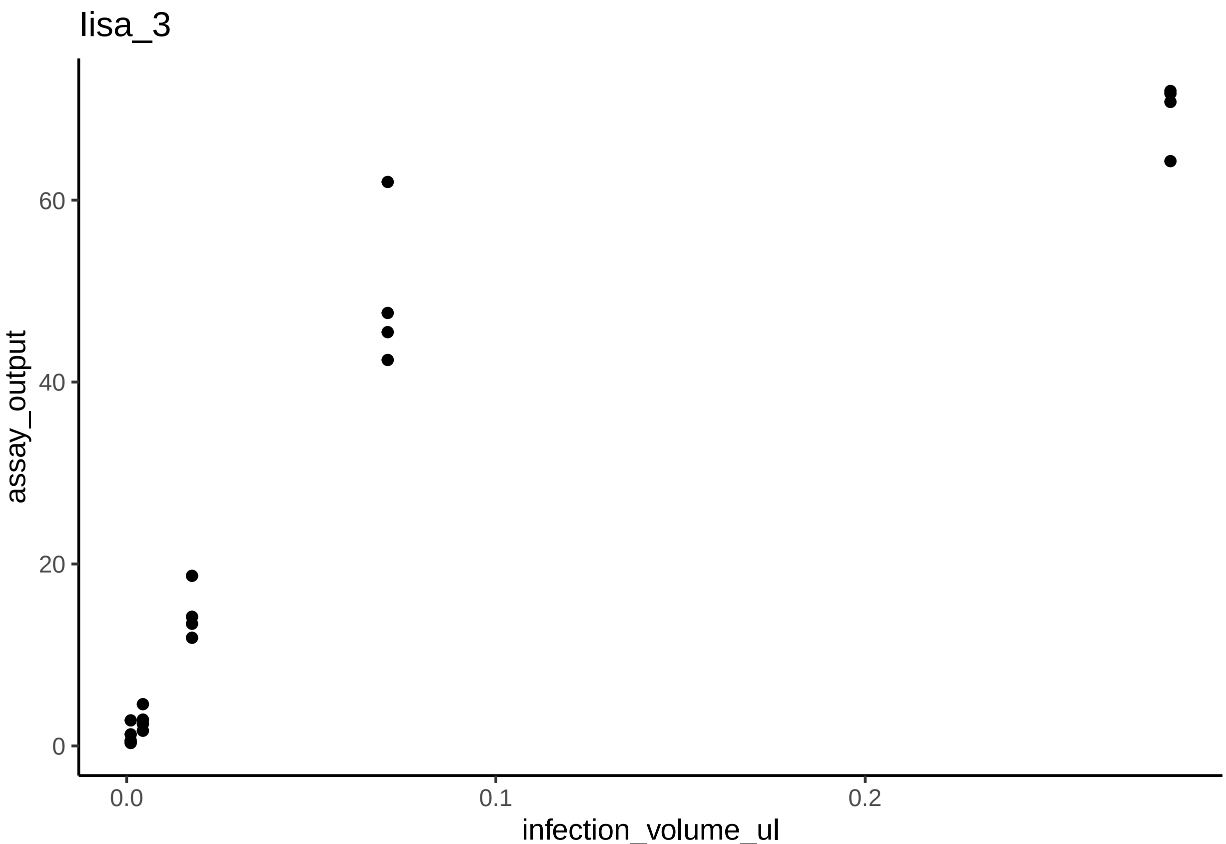

```
##
## [[45]]
```



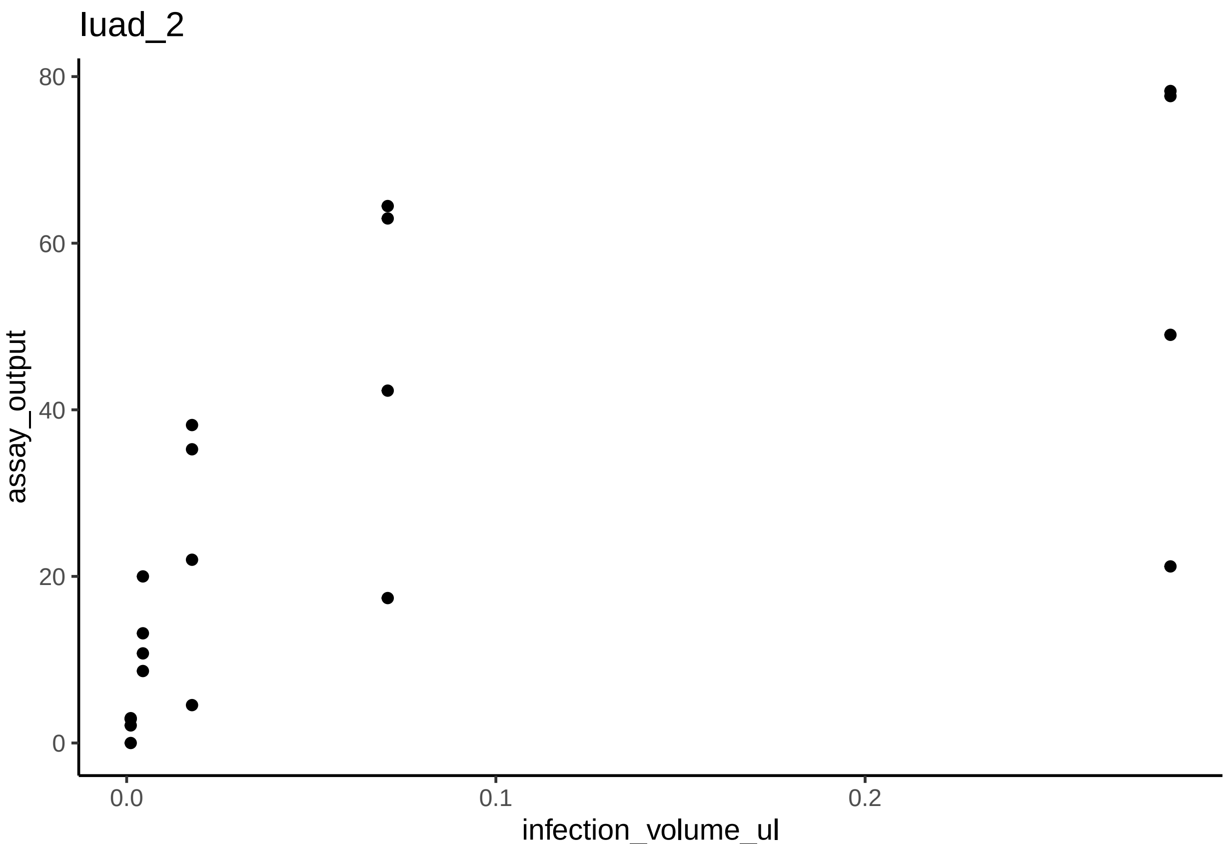

```
##
## [[46]]
```



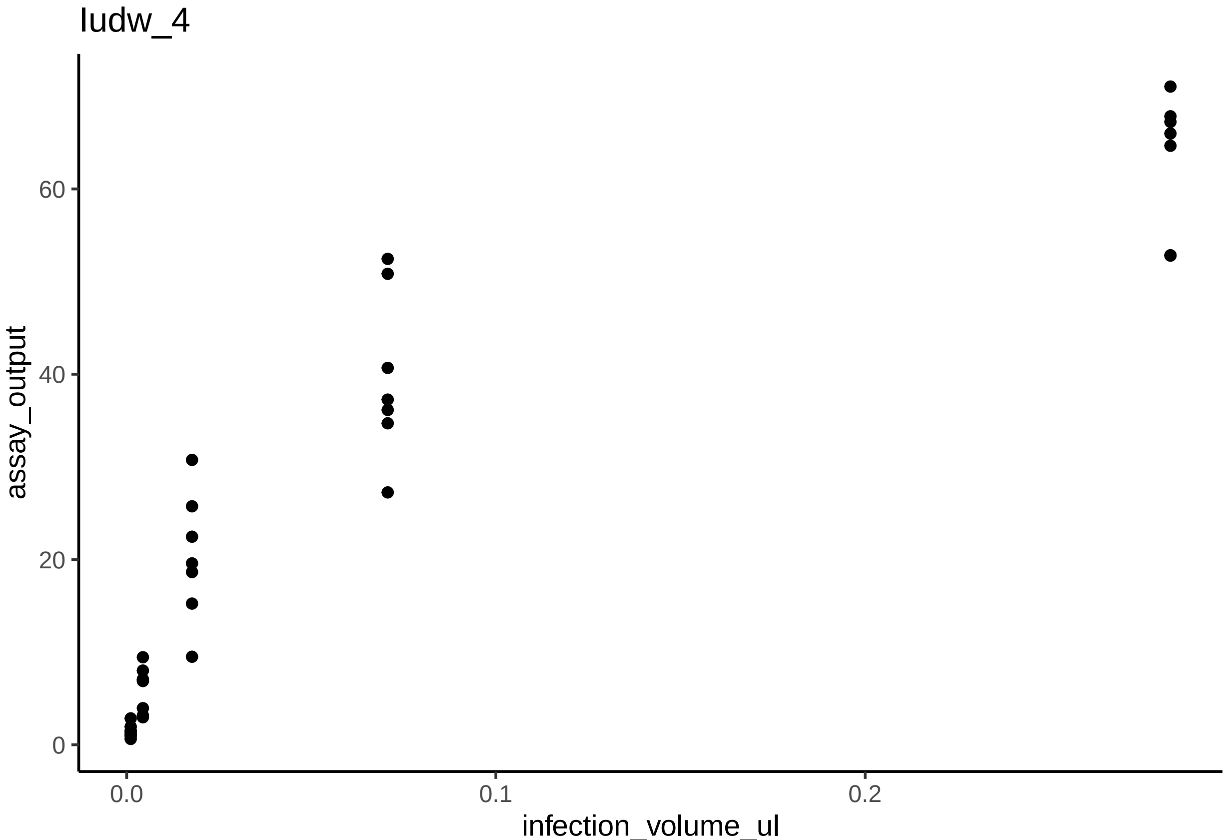

```
##
## [[47]]
```



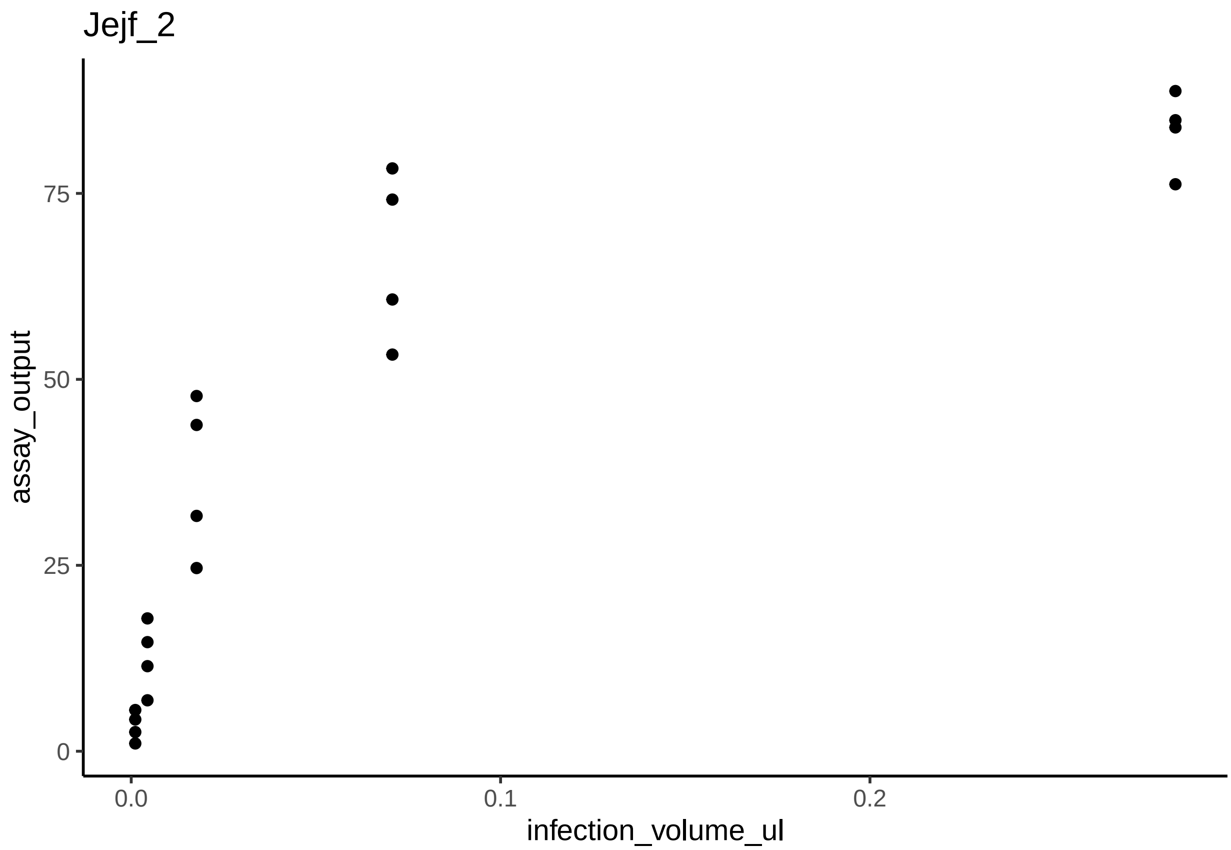

```
##
## [[48]]
```



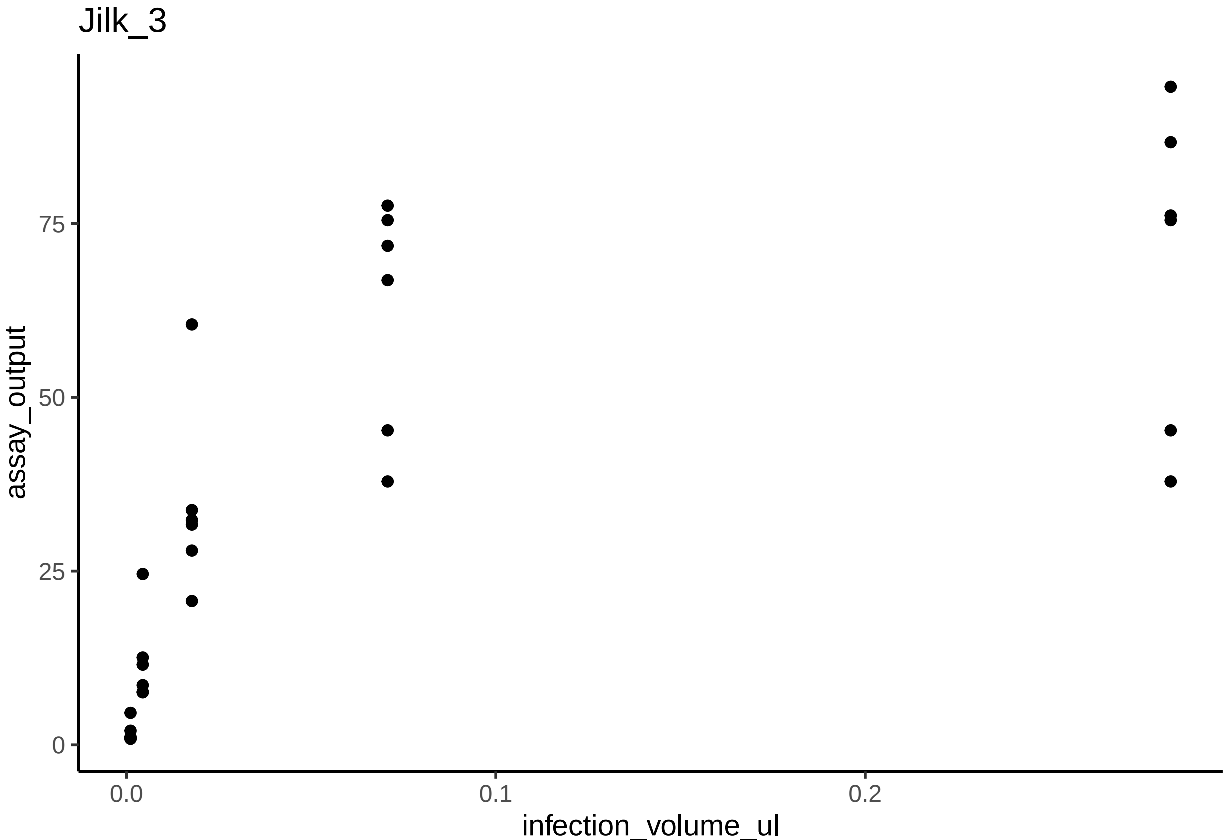

```
##
## [[49]]
```



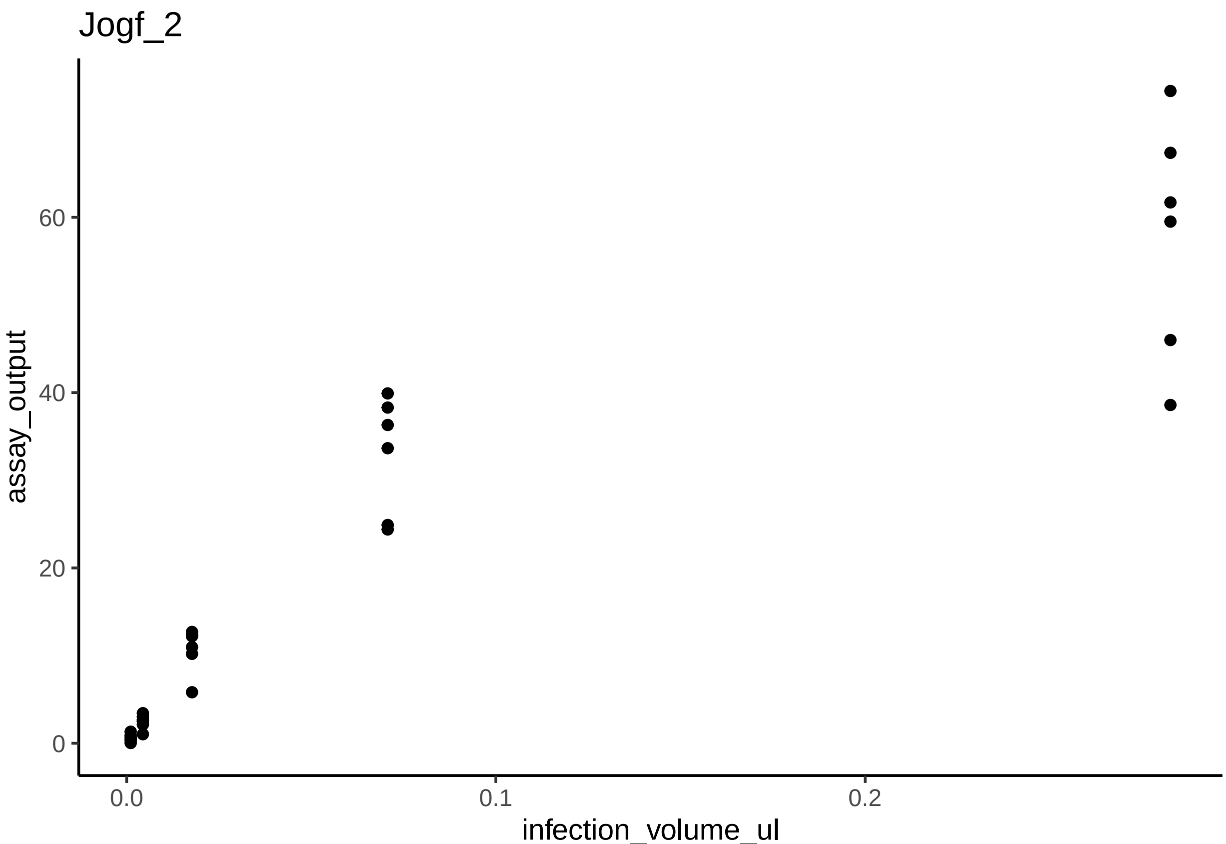

```
##
## [[50]]
```



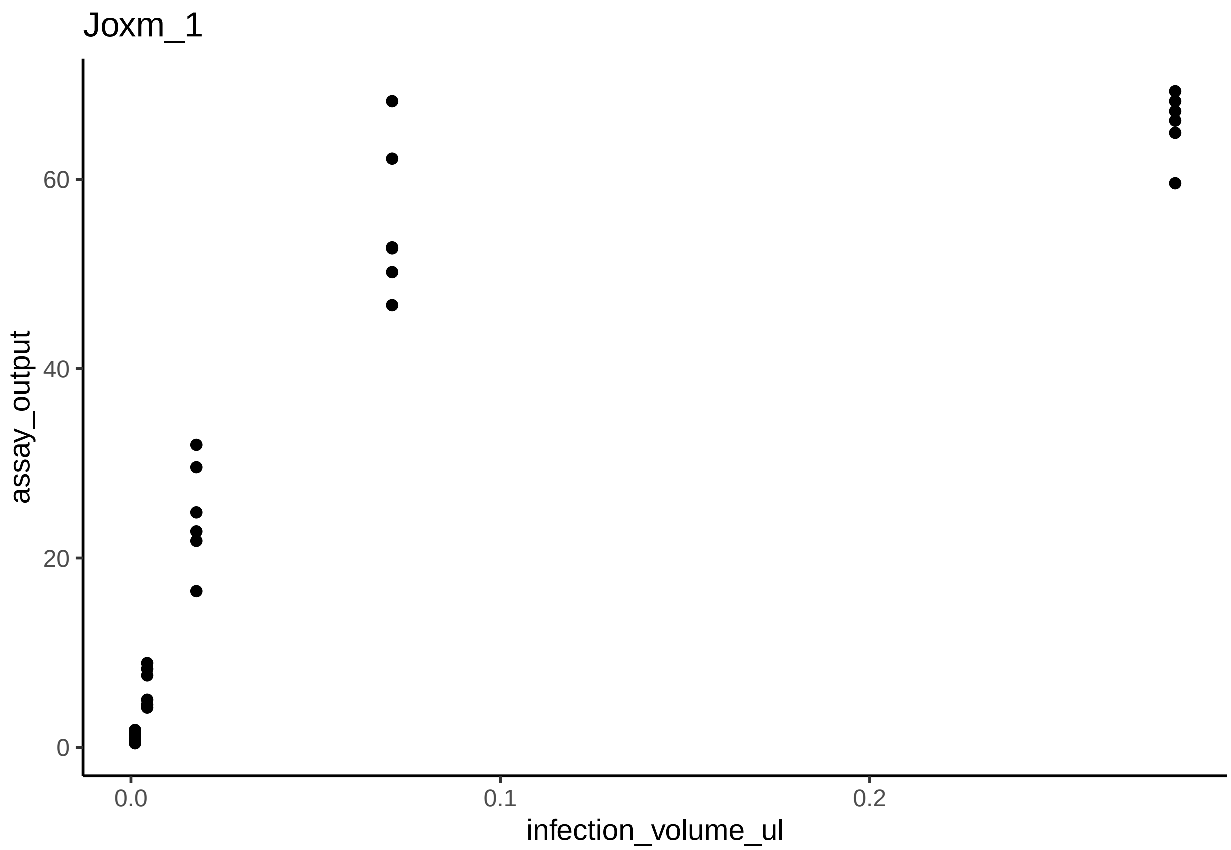

```
##
## [[51]]
```



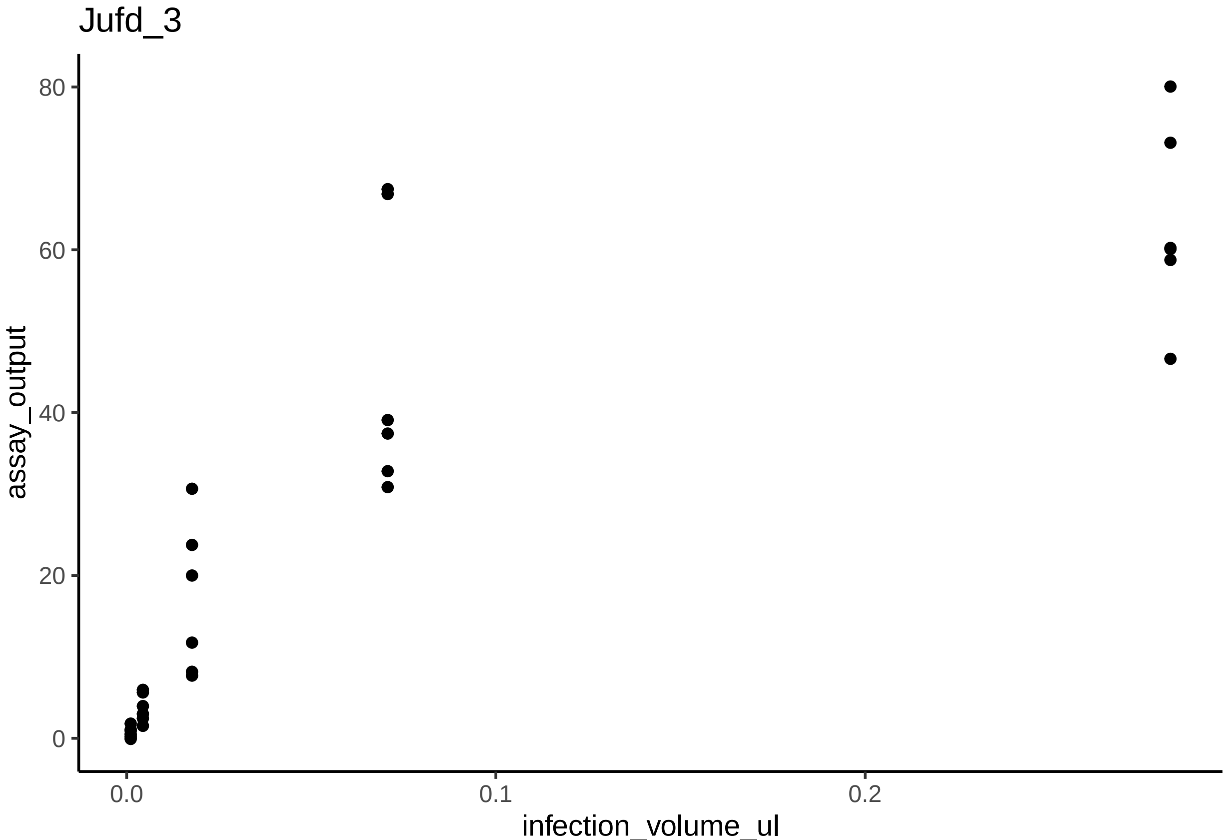

```
##
## [[52]]
```



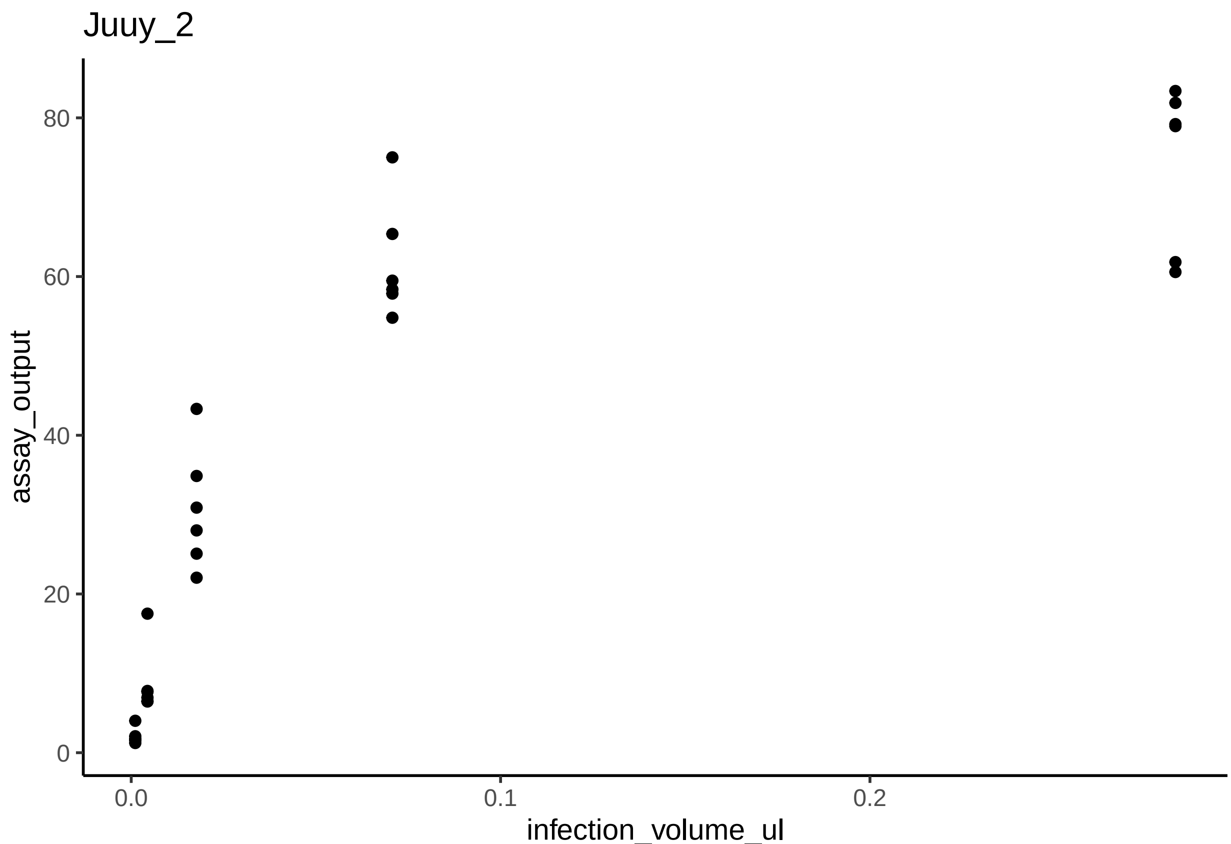

```
##
## [[53]]
```



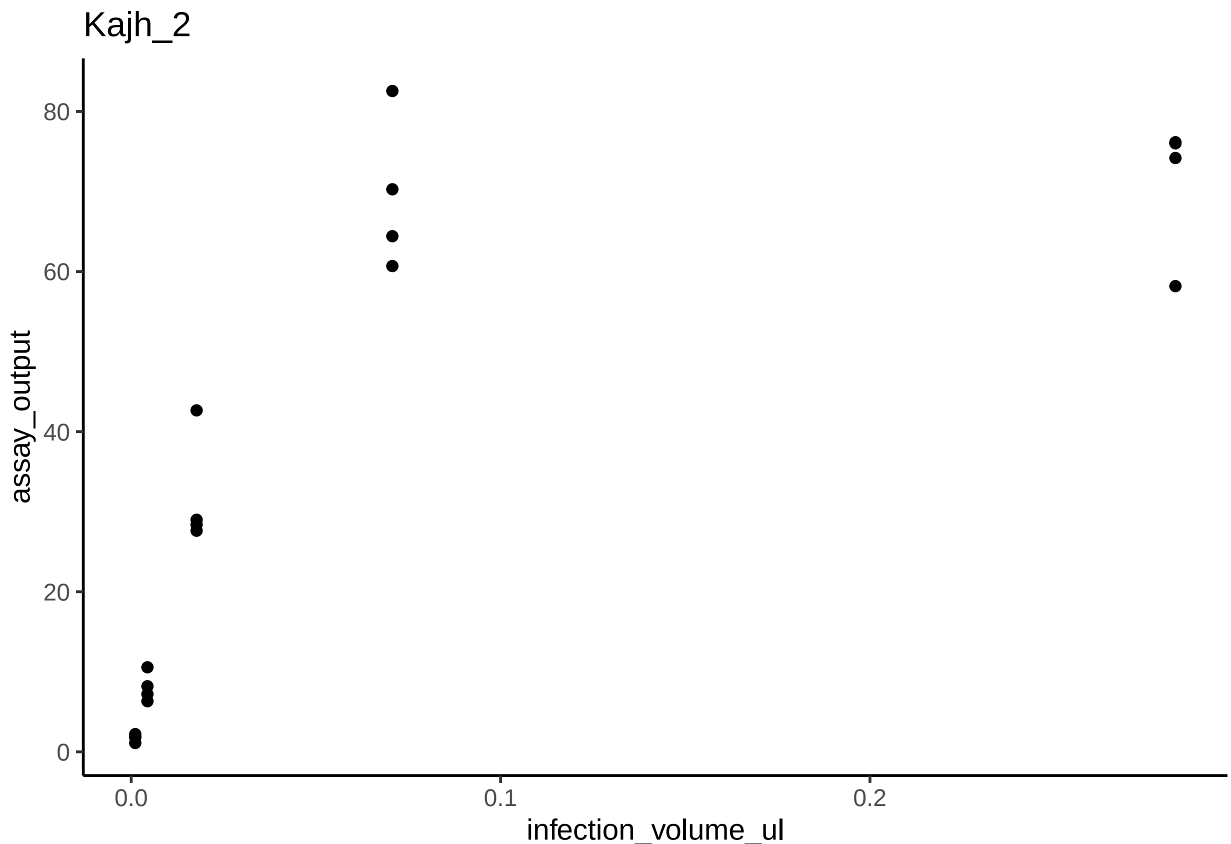

```
##
## [[54]]
```



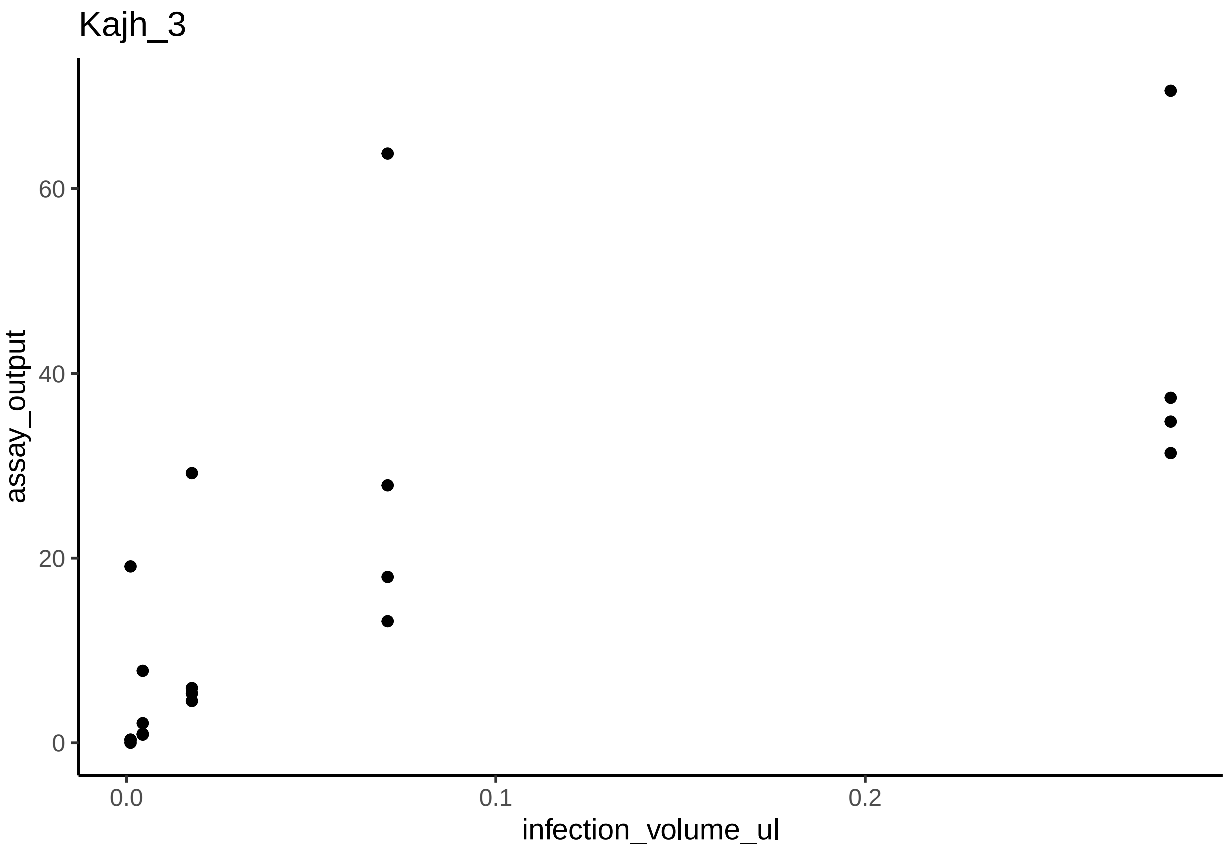

```
##
## [[55]]
```



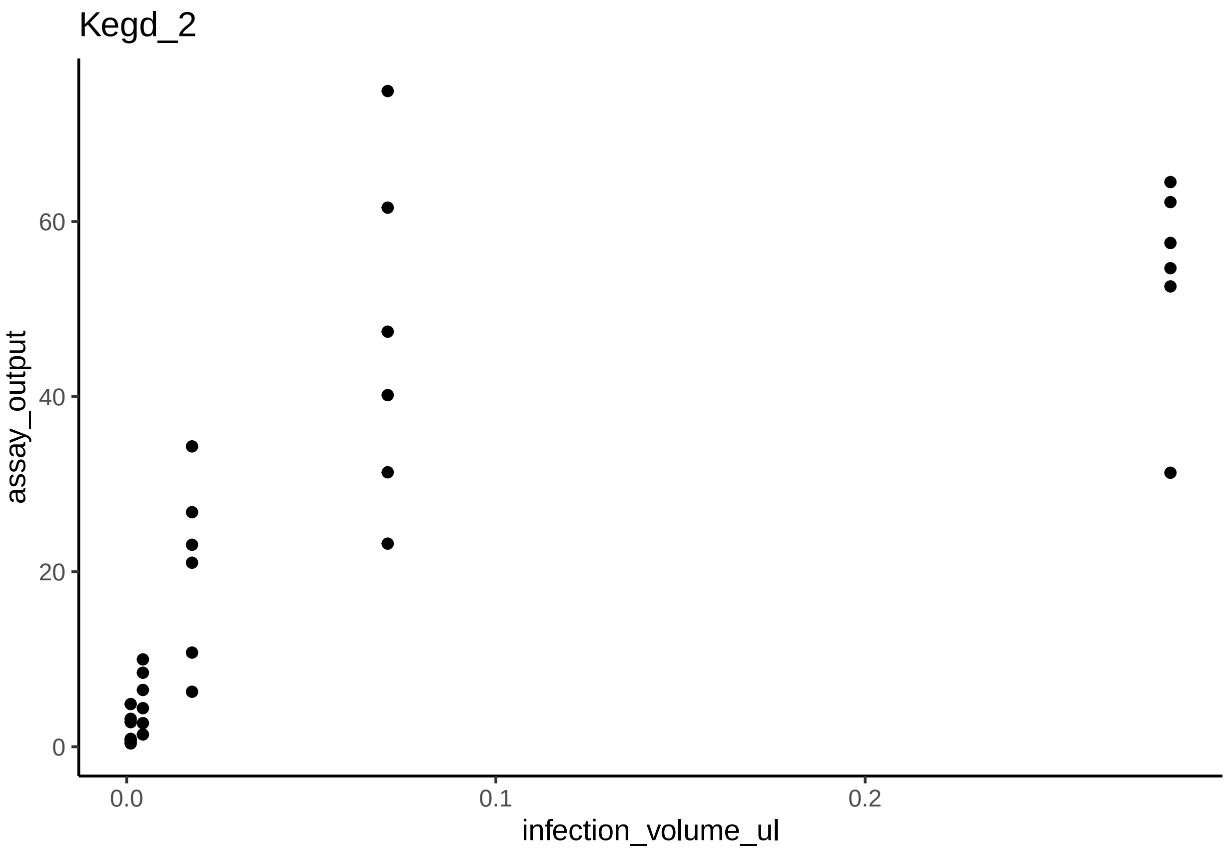

```
##
## [[56]]
```



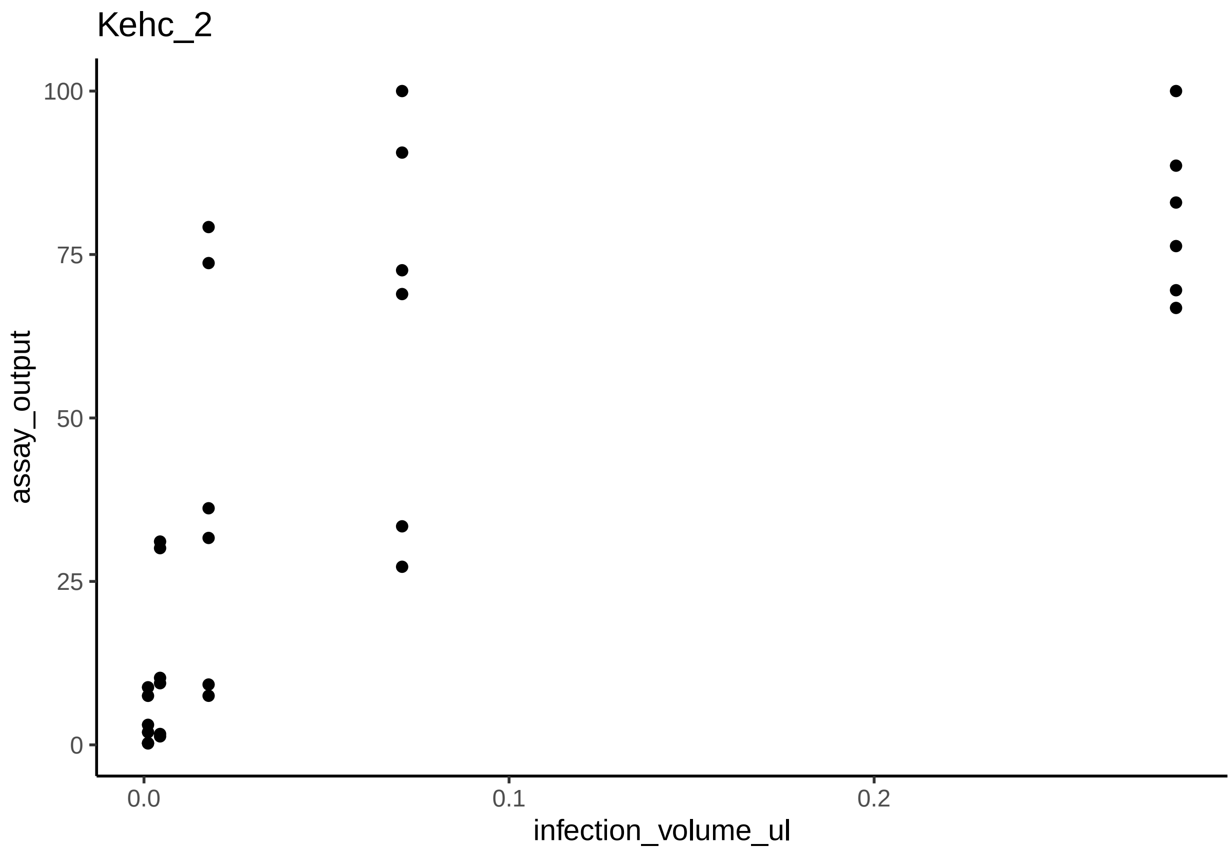

```
##
## [[57]]
```



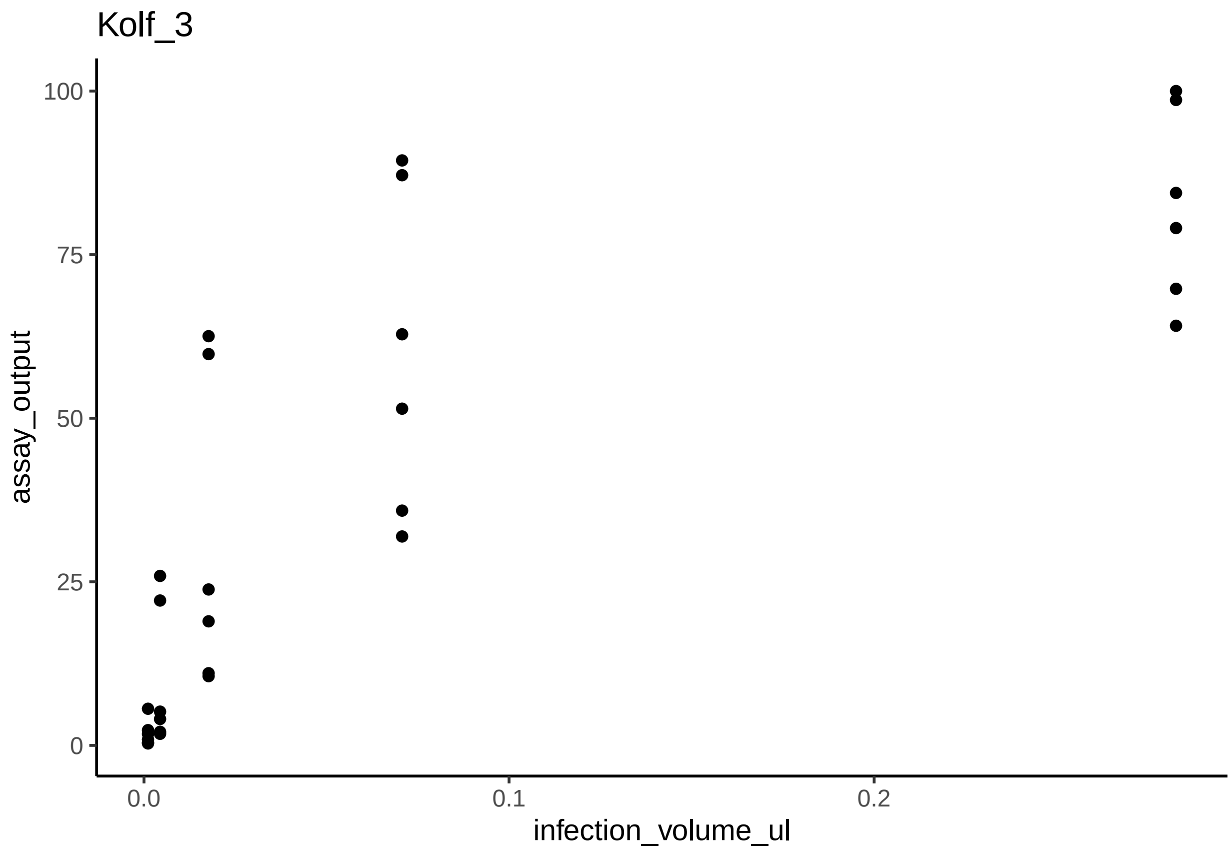

```
##
## [[58]]
```



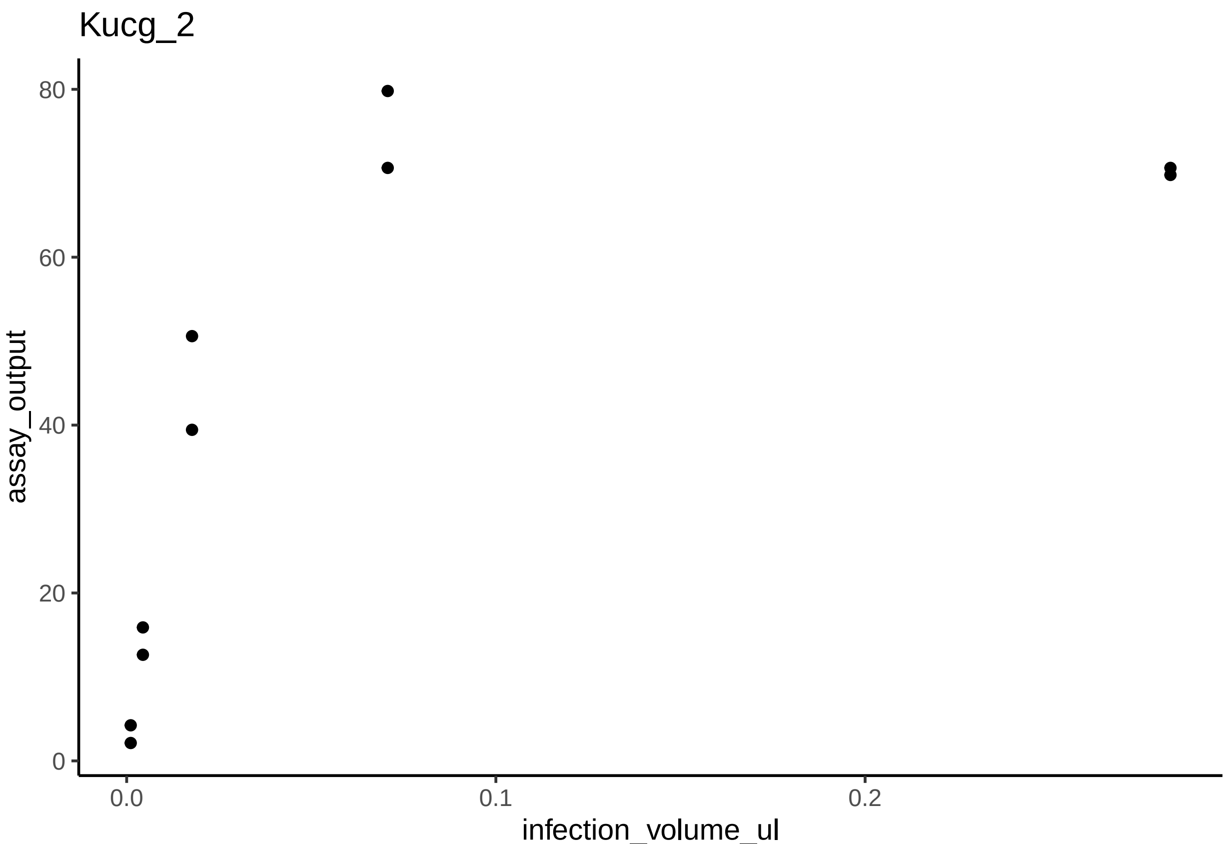

```
##
## [[59]]
```



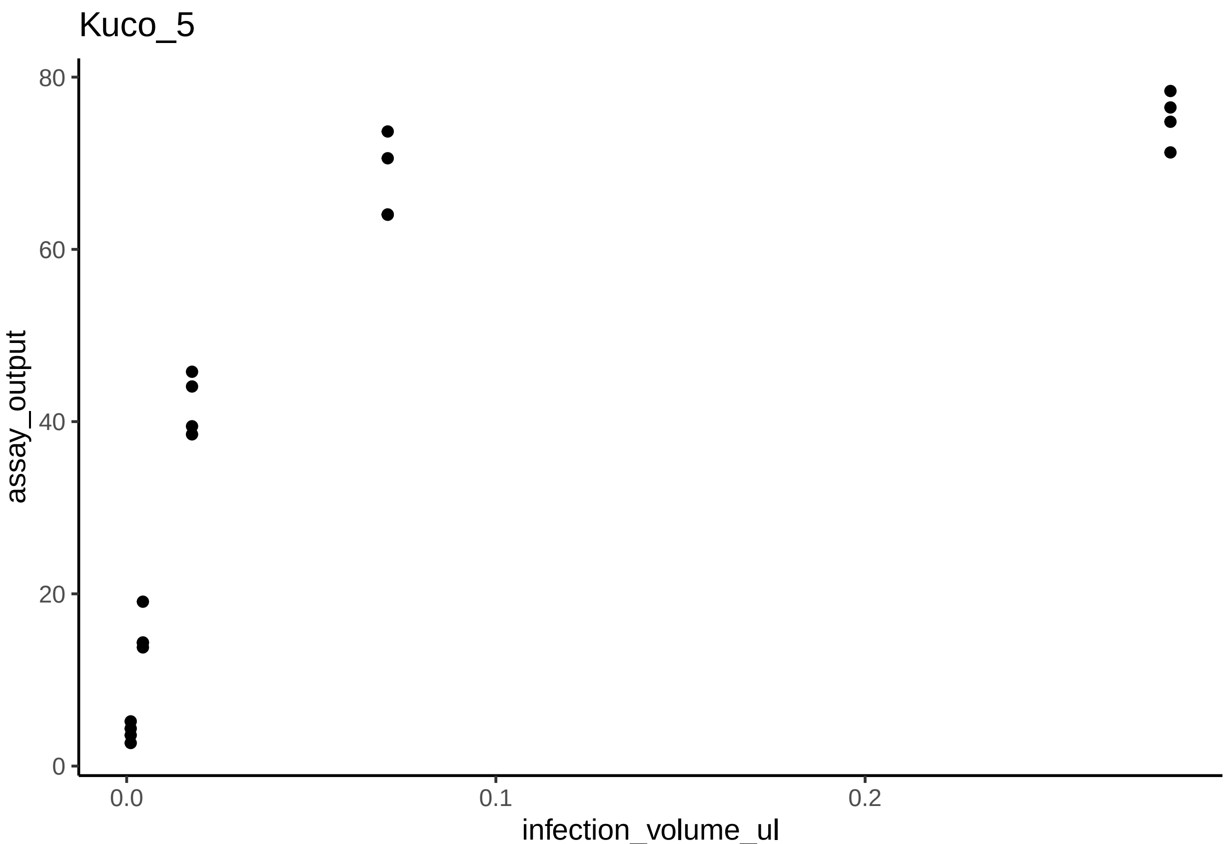

```
##
## [[60]]
```



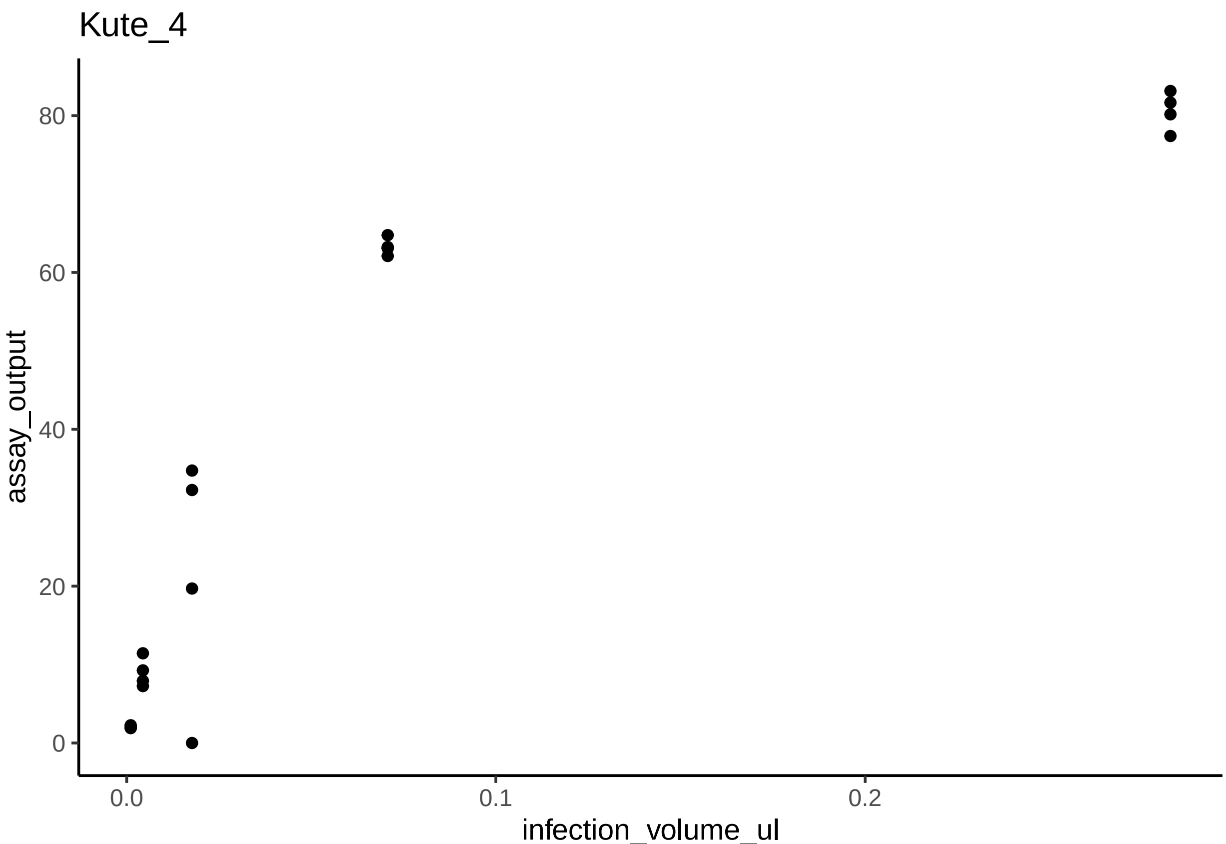

```
##
## [[61]]
```



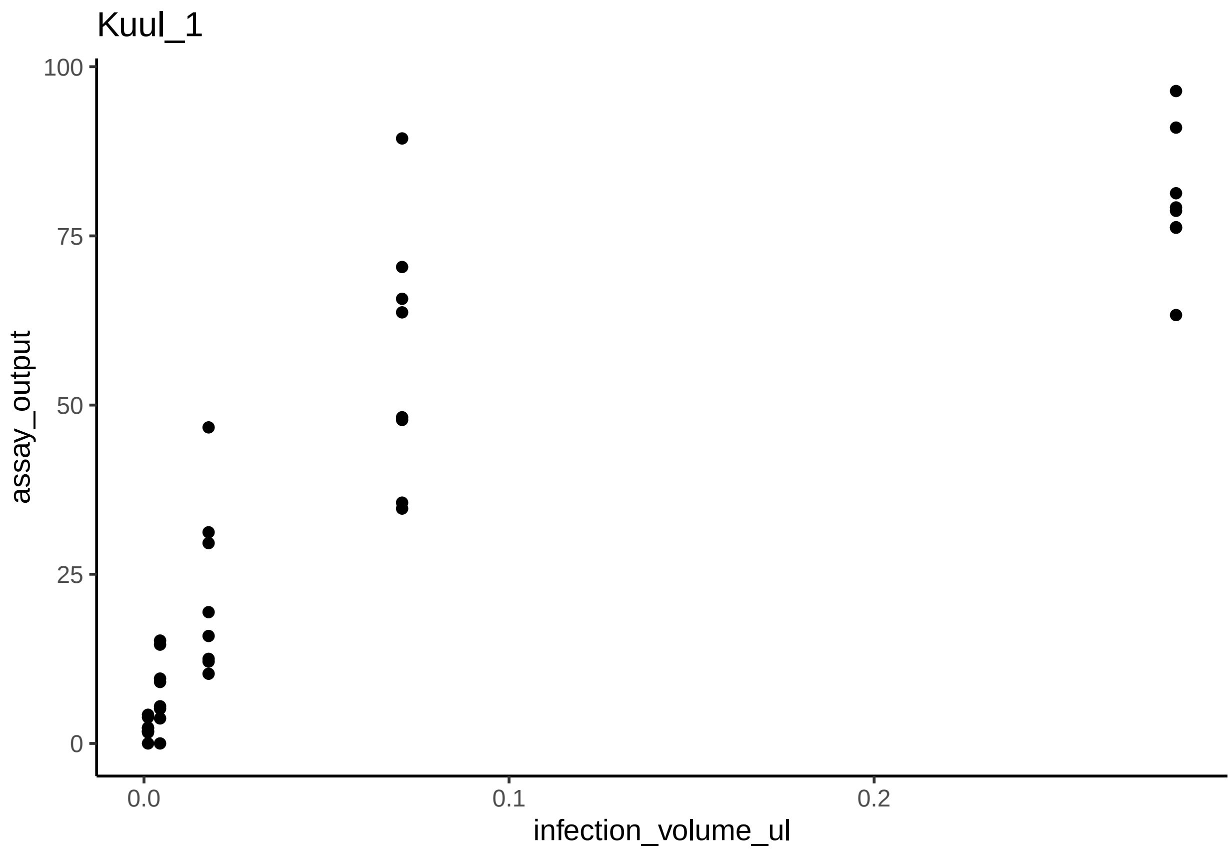

```
##
## [[62]]
```



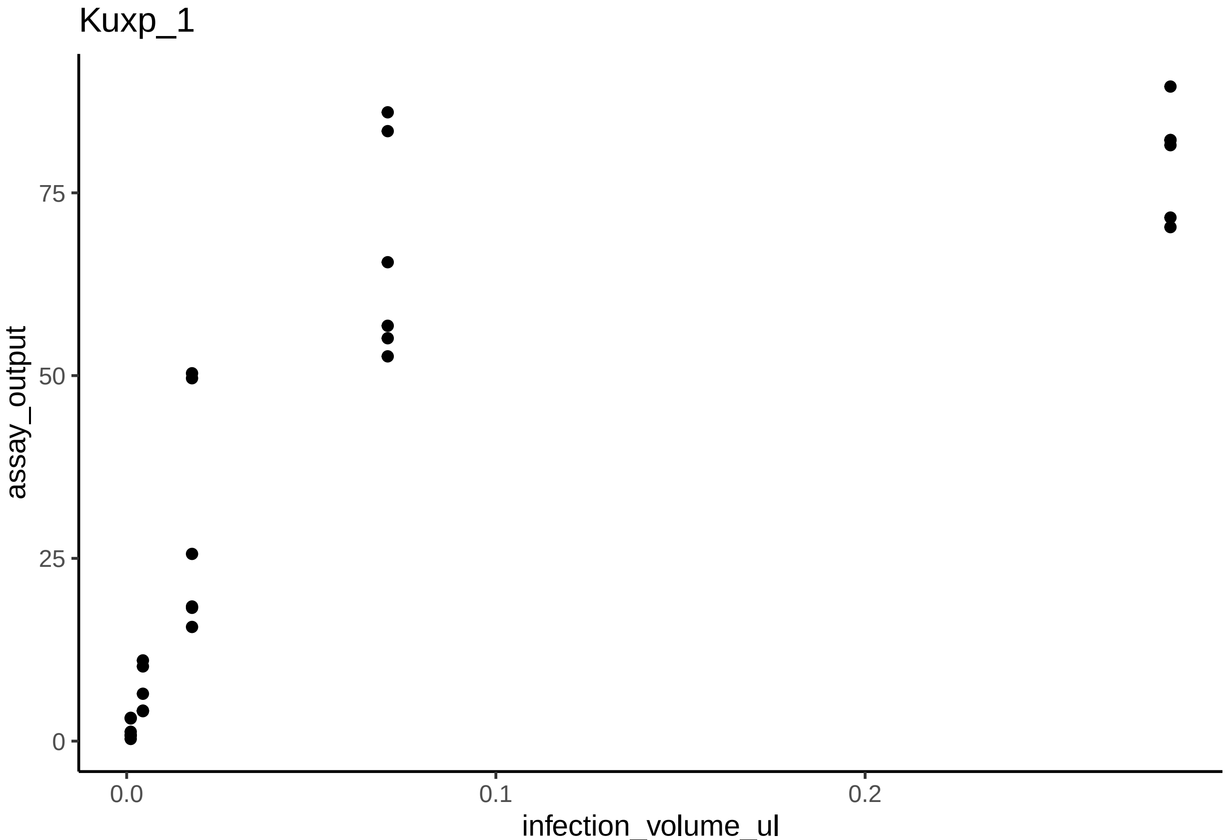

```
##
## [[63]]
```



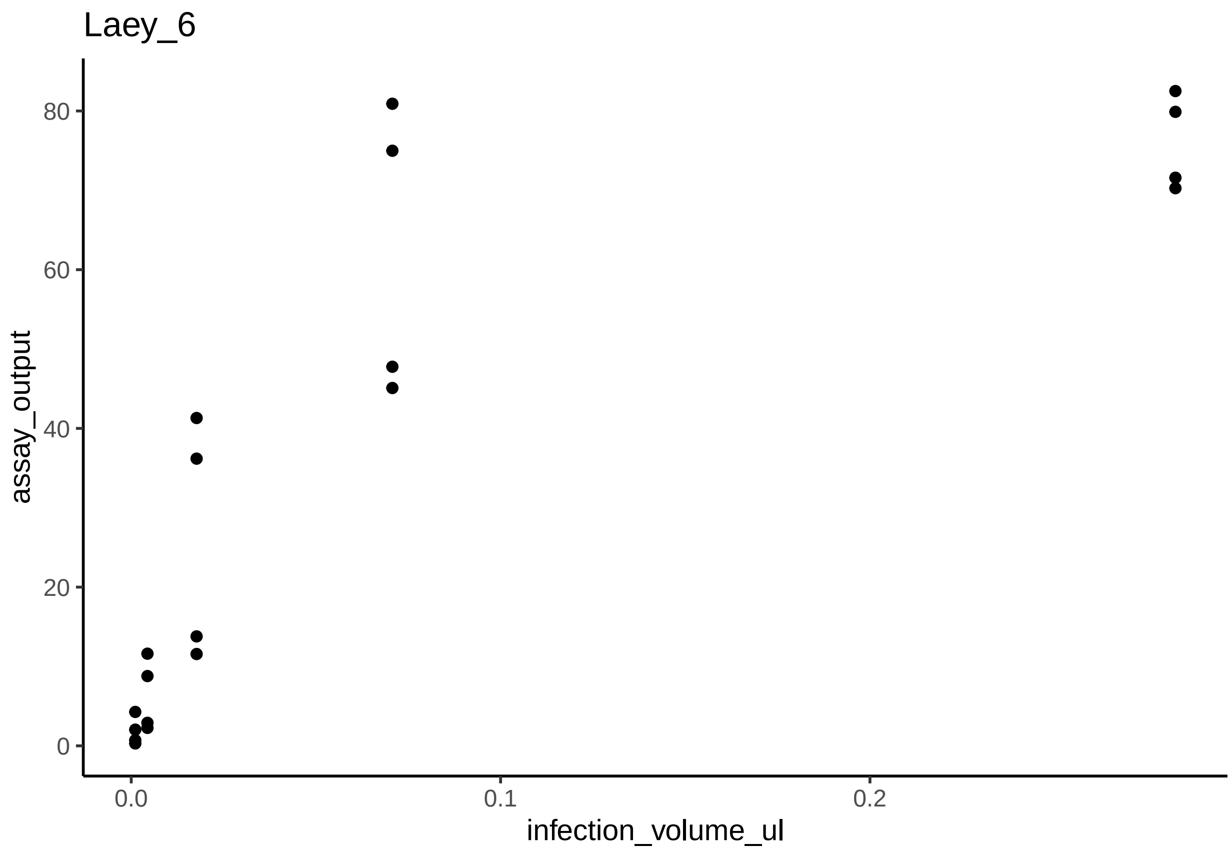

```
##
## [[64]]
```



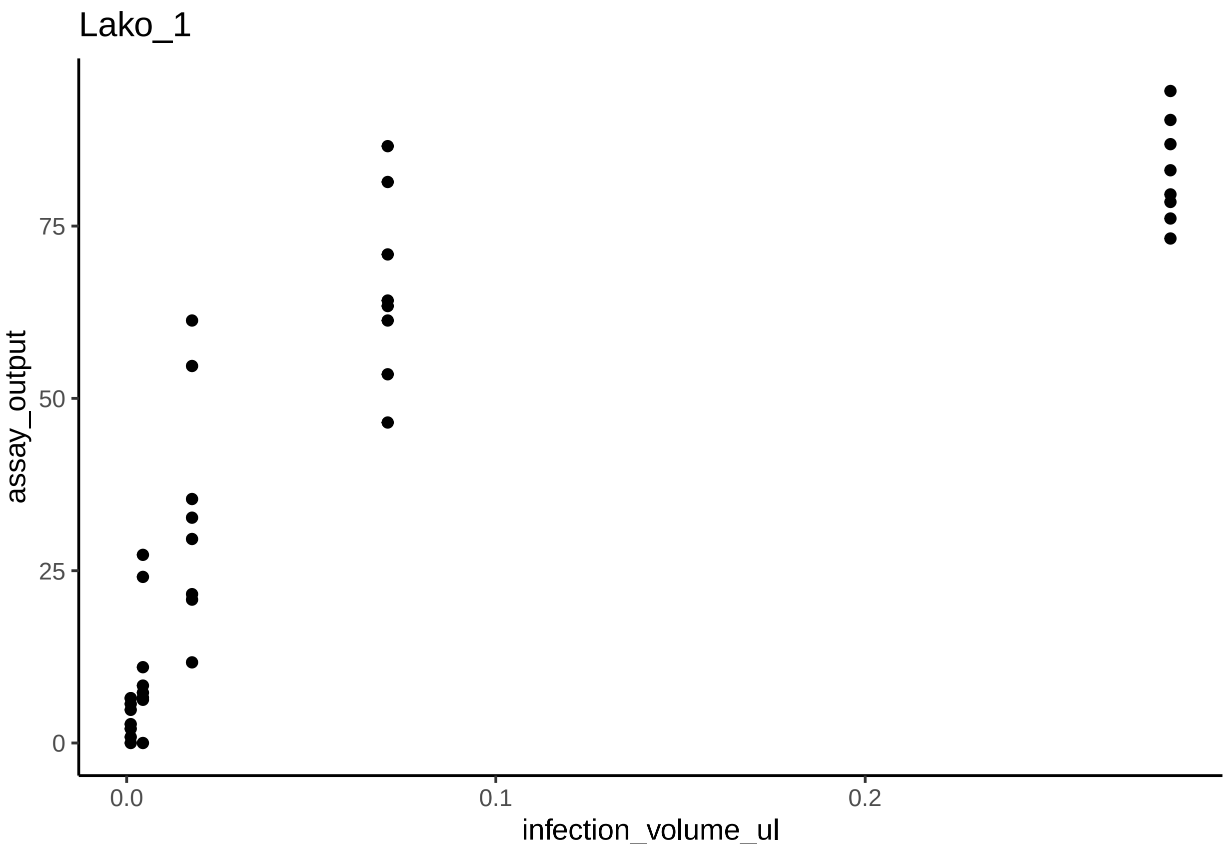

```
##
## [[65]]
```



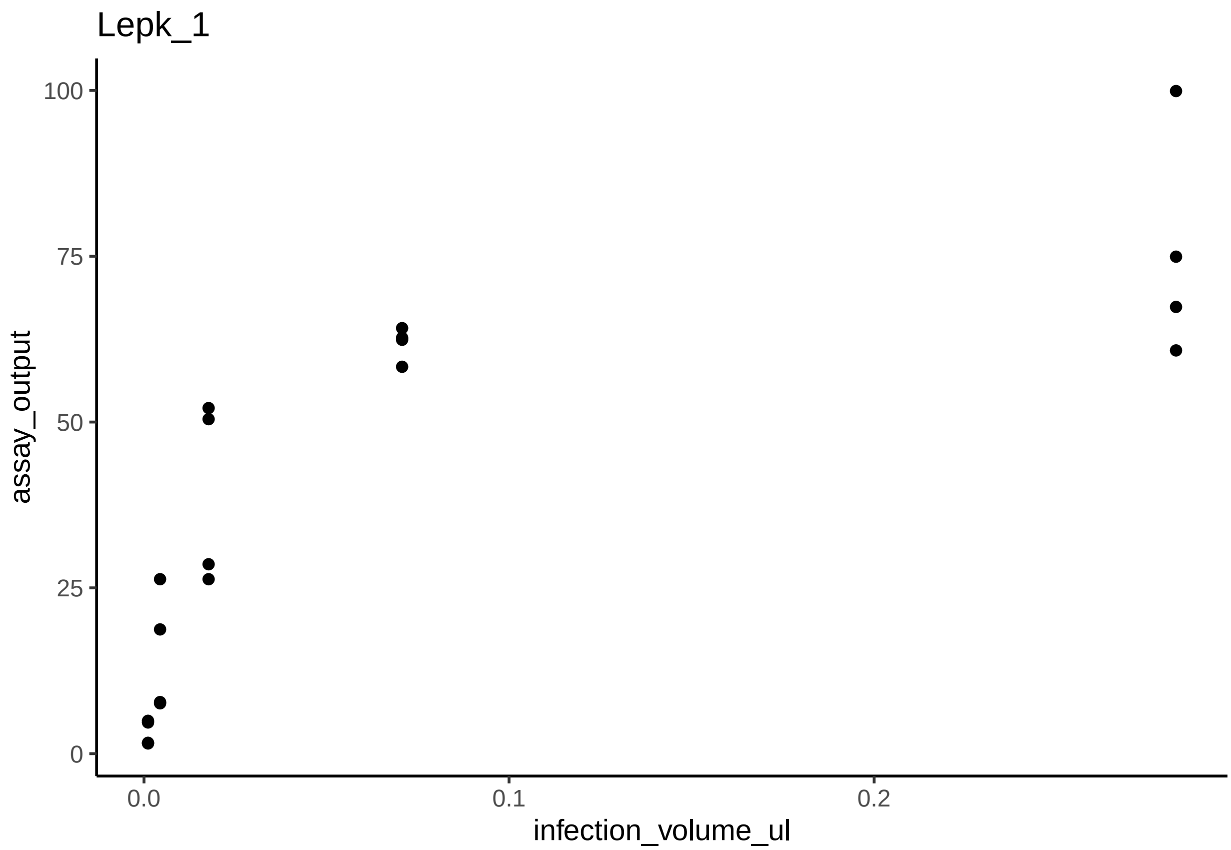

```
##
## [[66]]
```



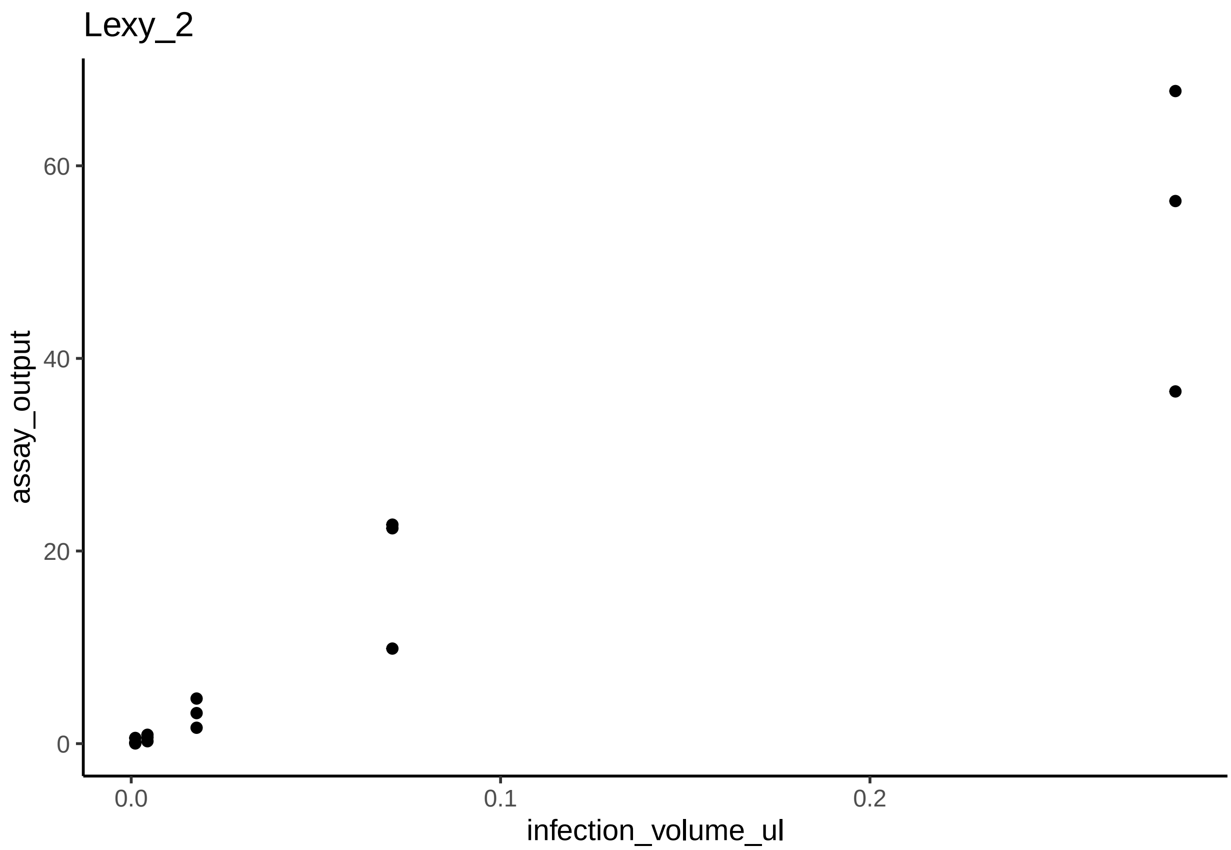

```
##
## [[67]]
```



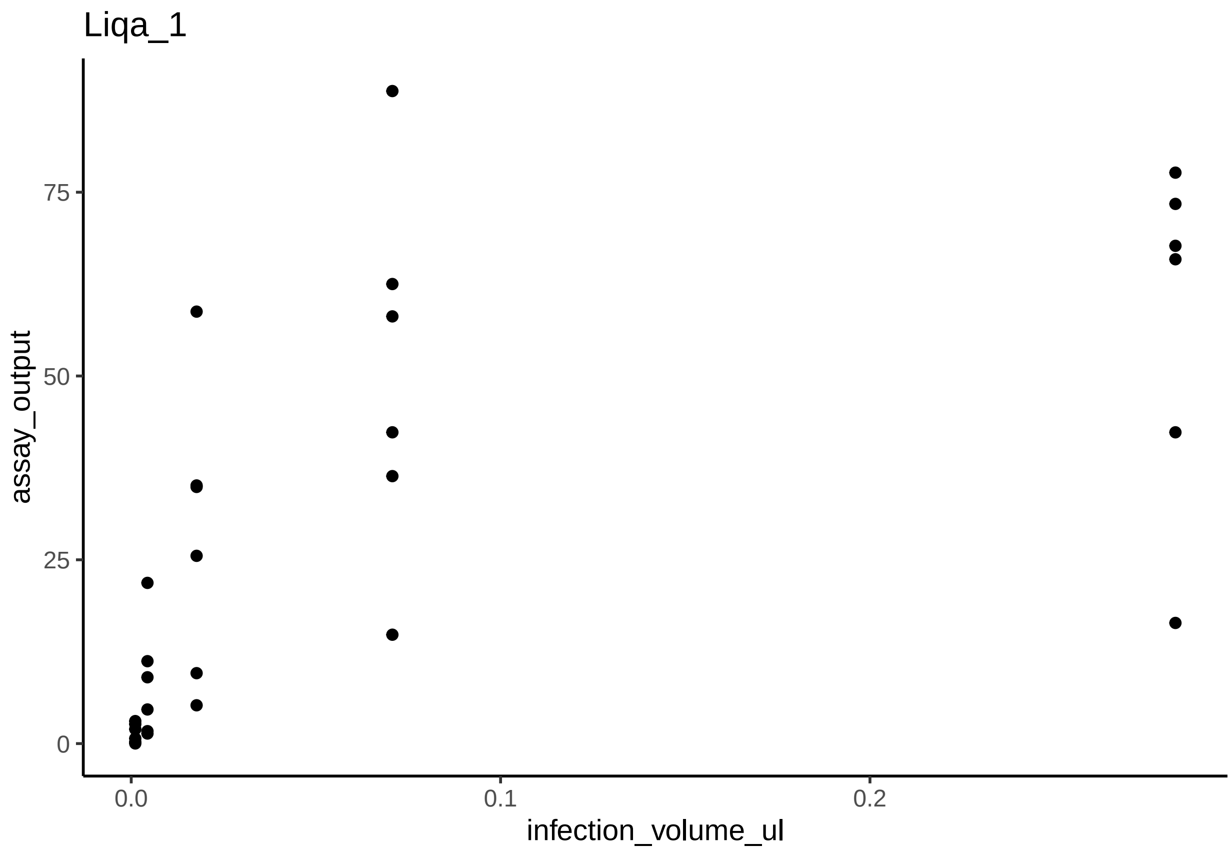

```
##
## [[68]]
```



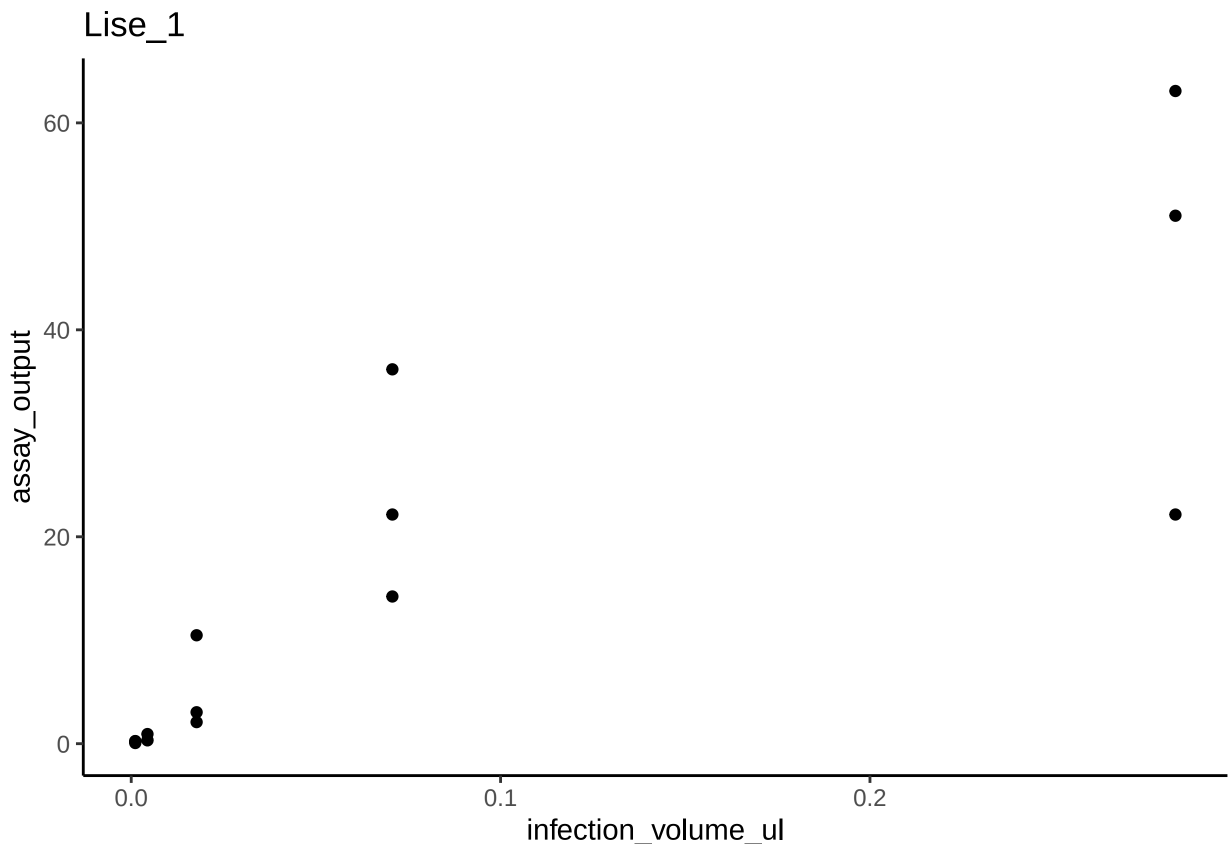

```
##
## [[69]]
```



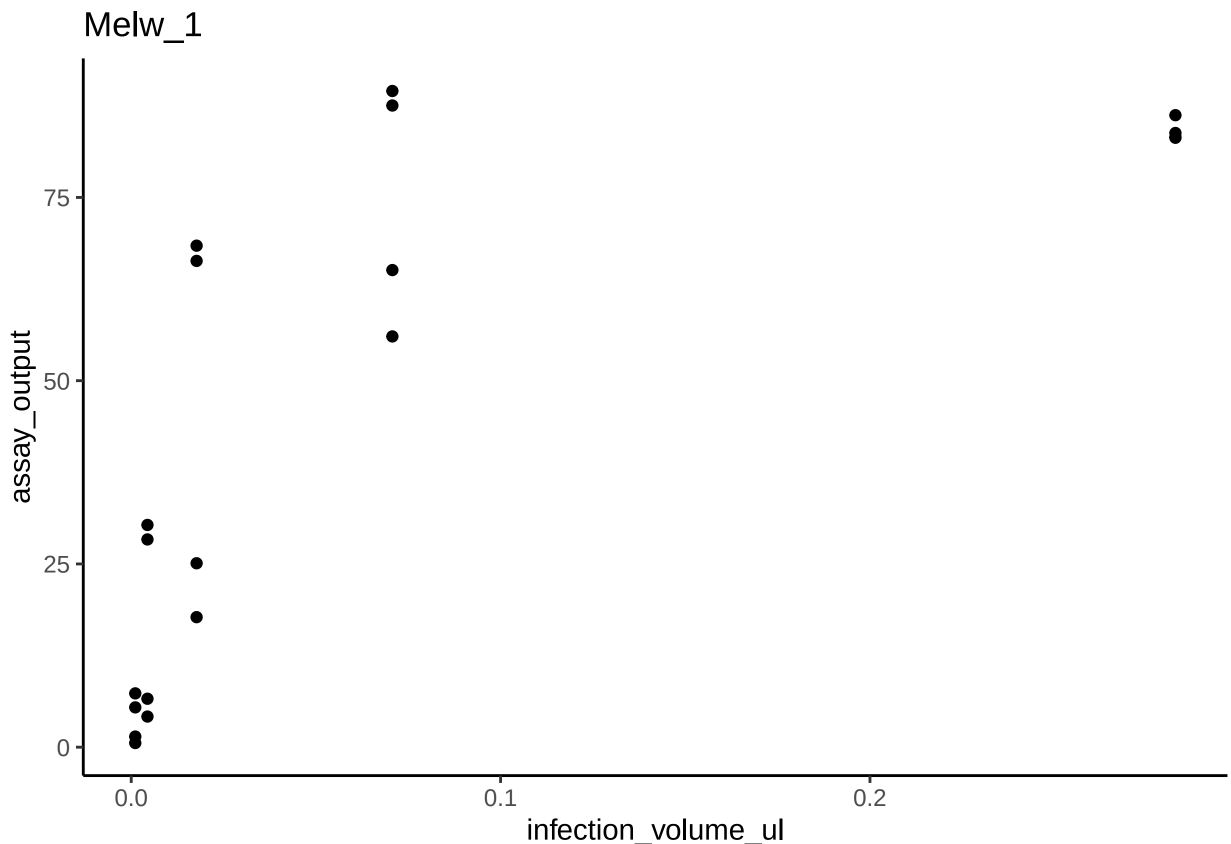

```
##
## [[70]]
```



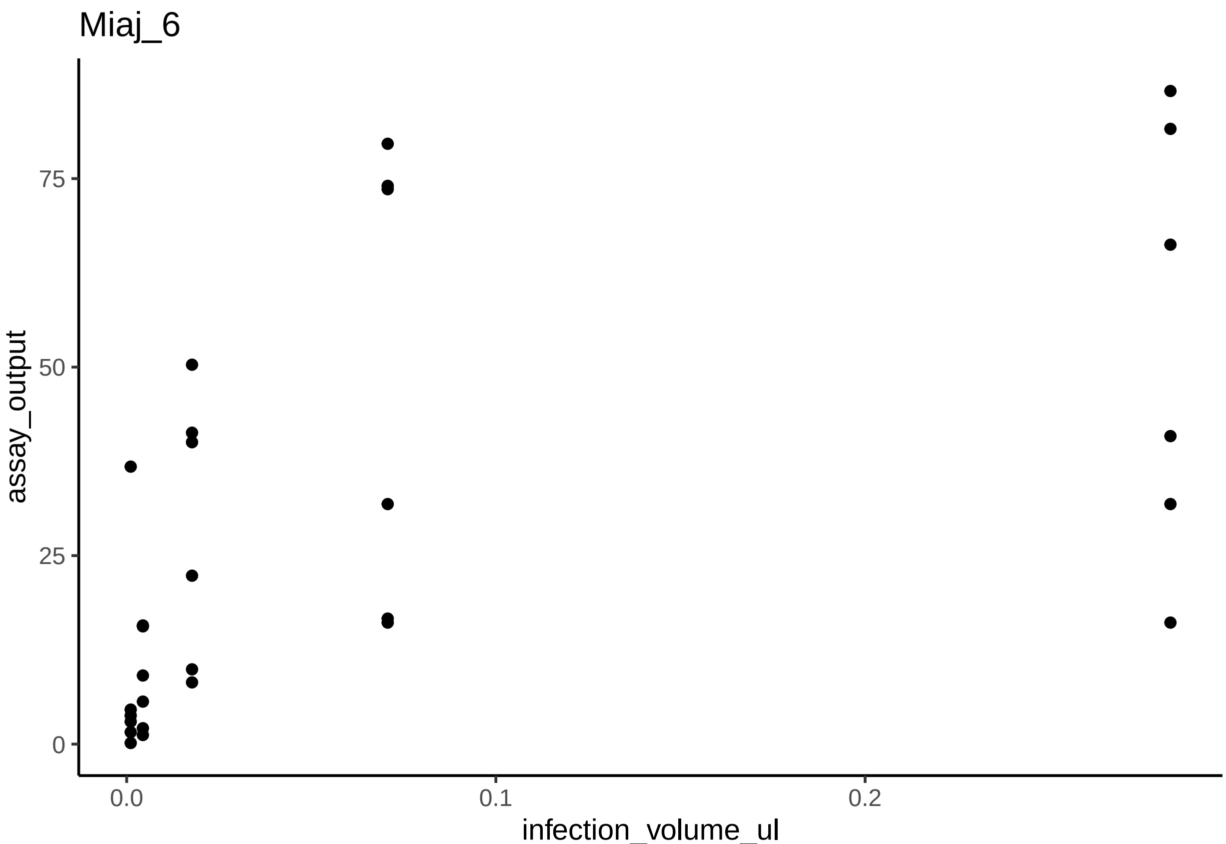

```
##
## [[71]]
```



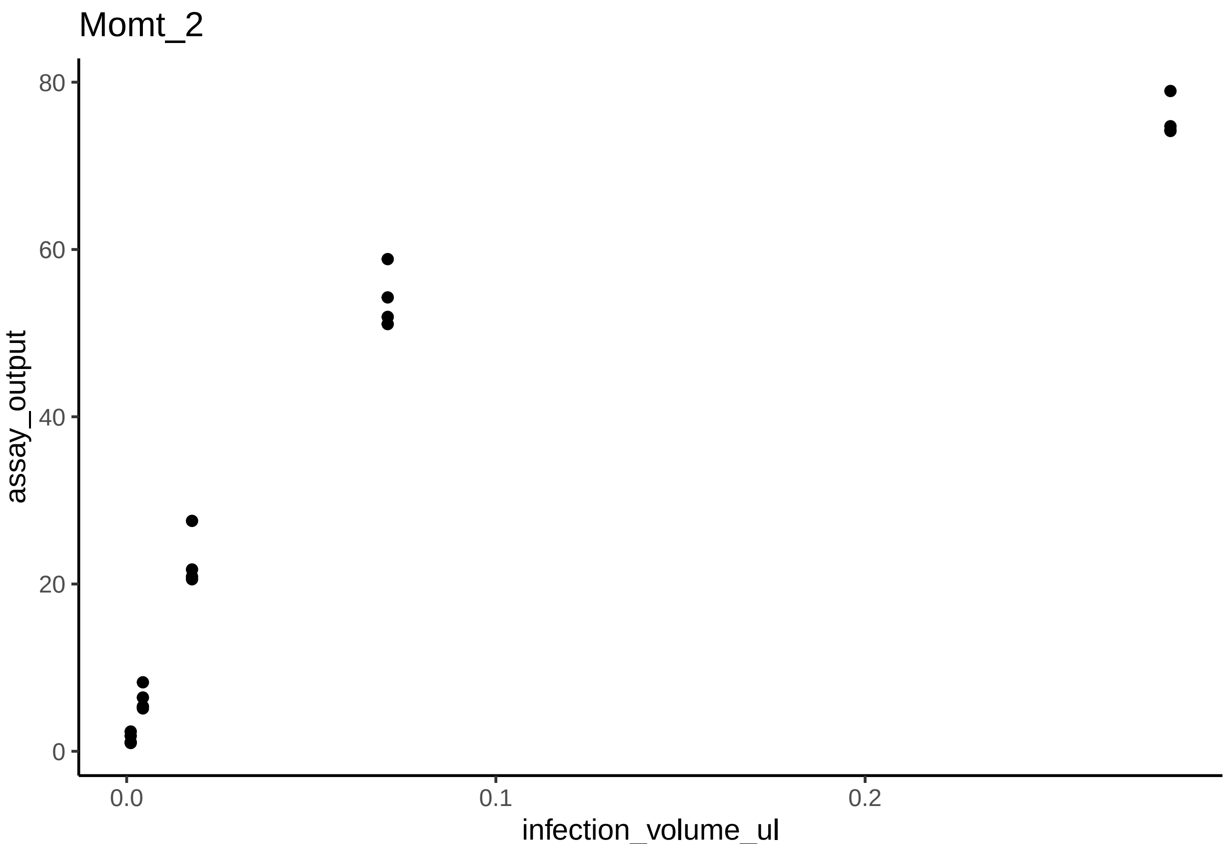

```
##
## [[72]]
```



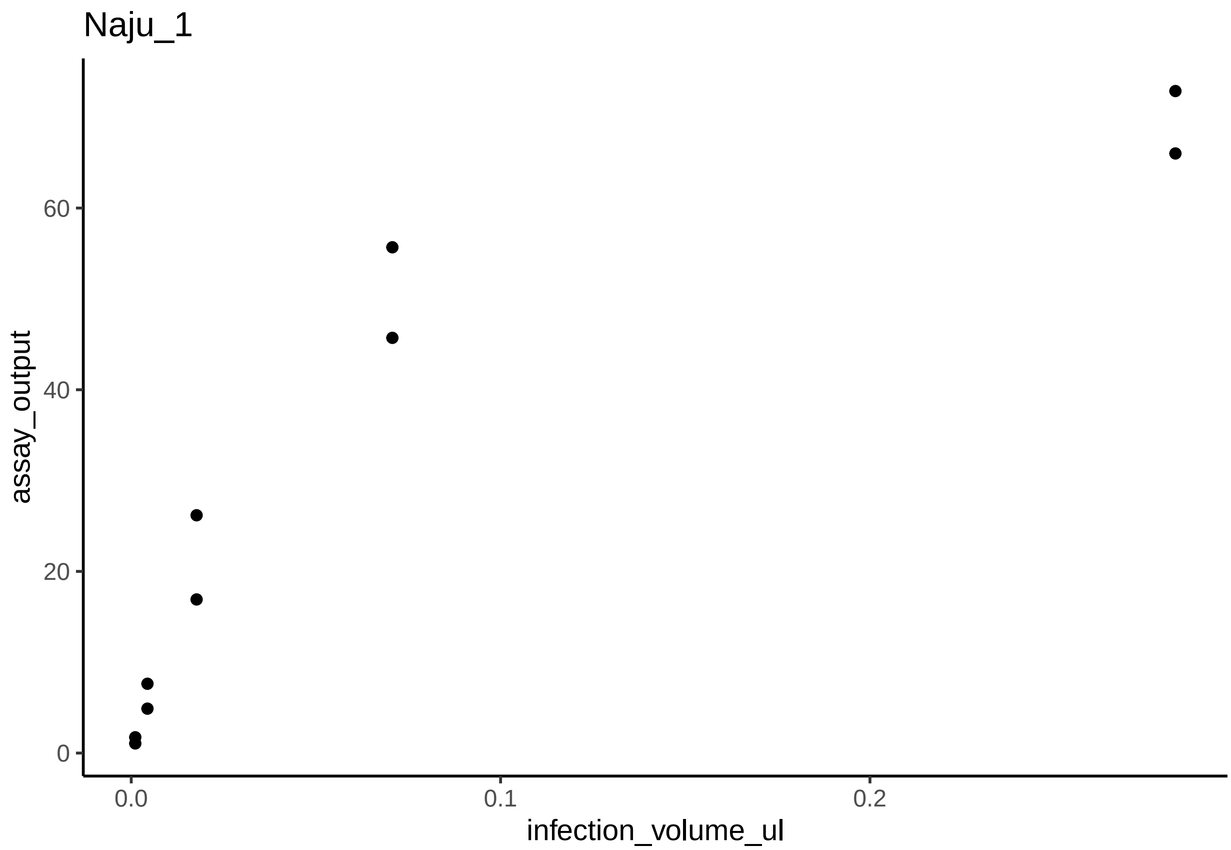

```
##
## [[73]]
```



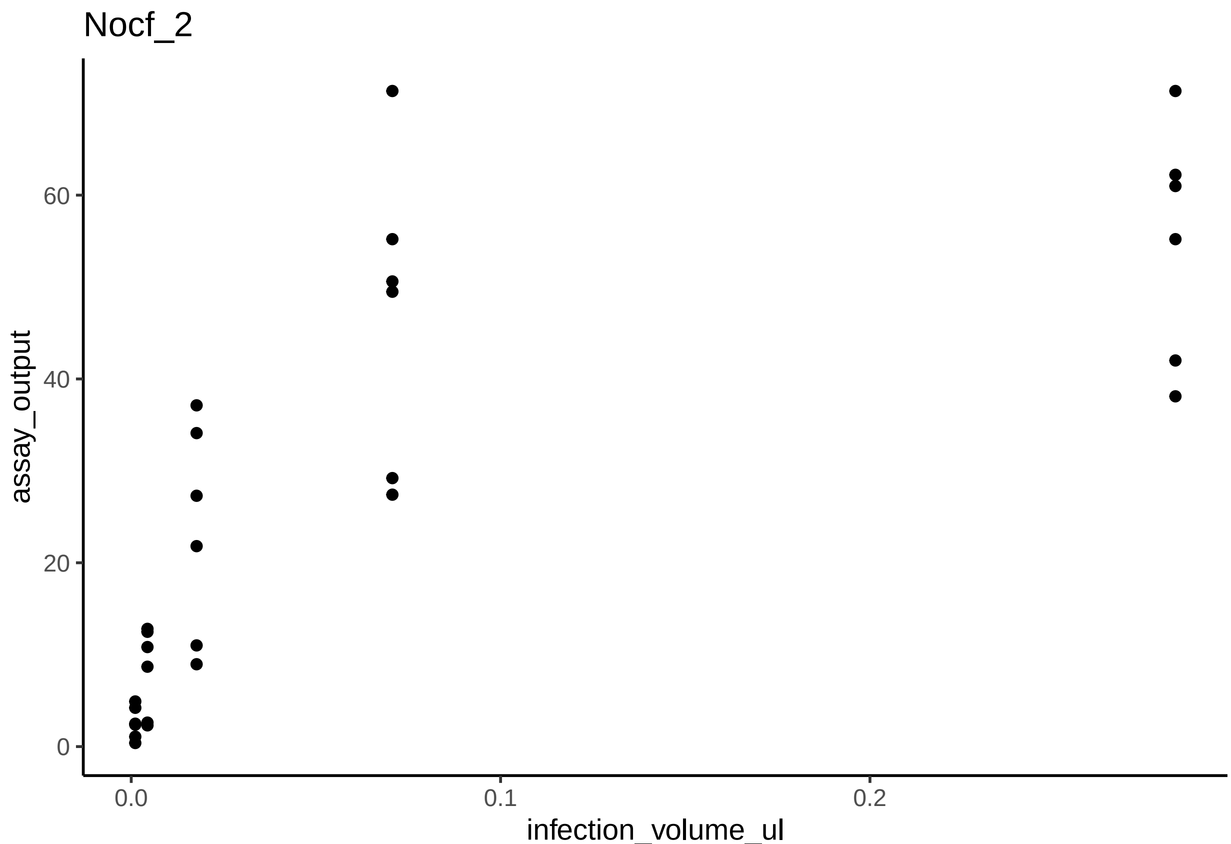

```
##
## [[74]]
```



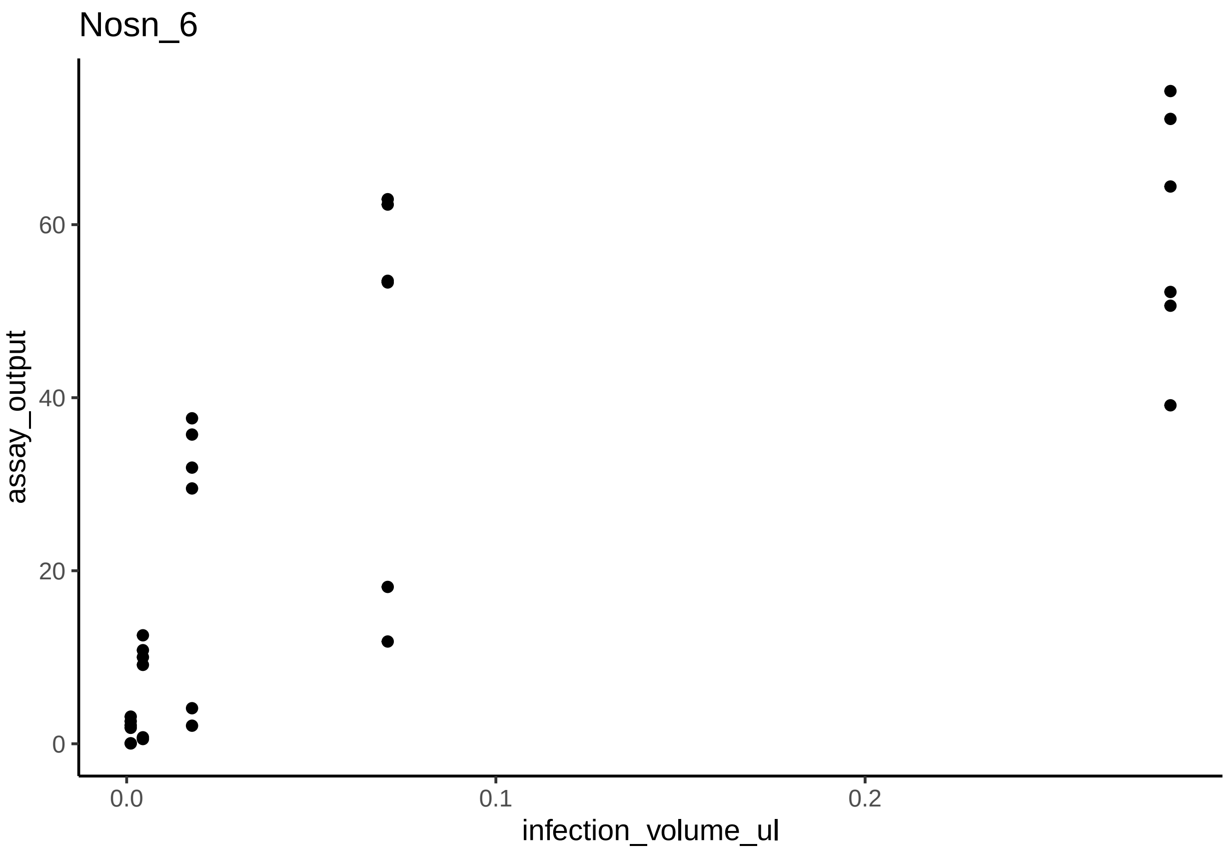

```
##
## [[75]]
```



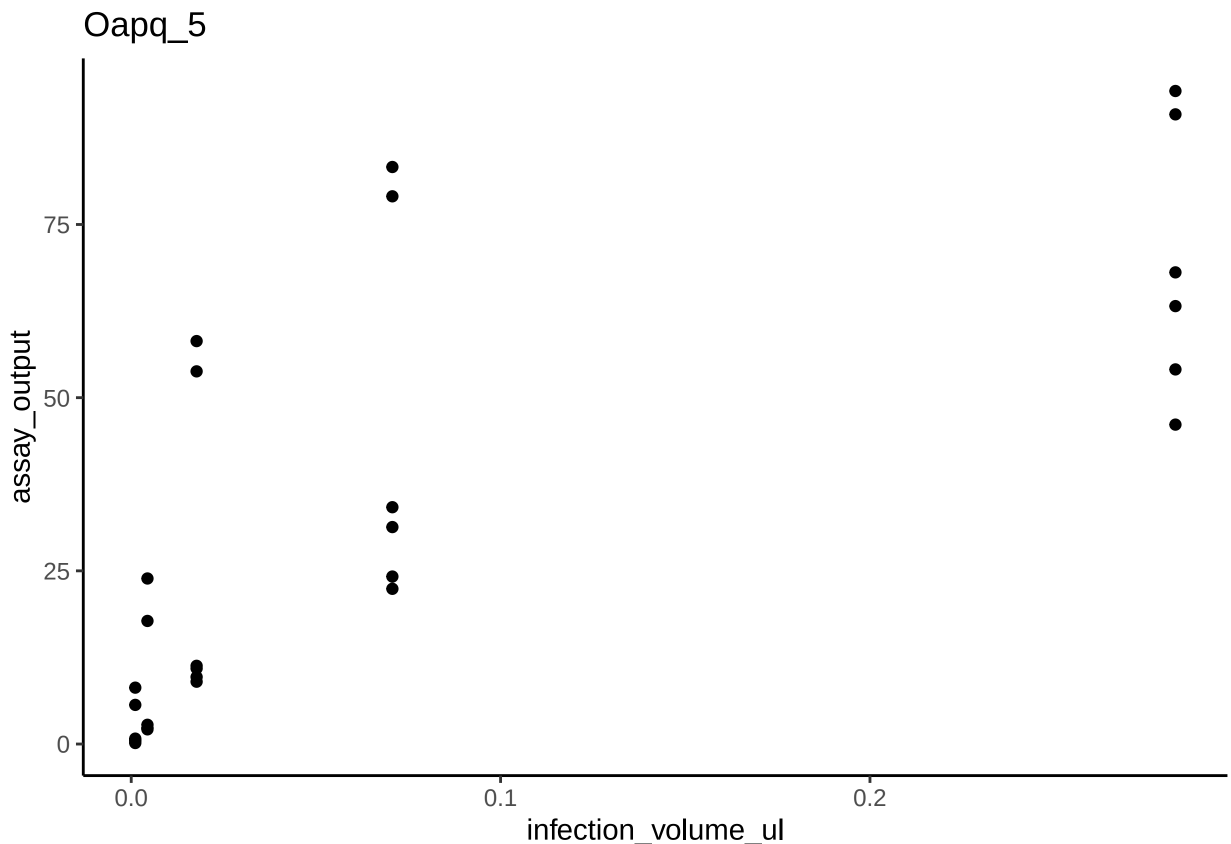

```
##
## [[76]]
```



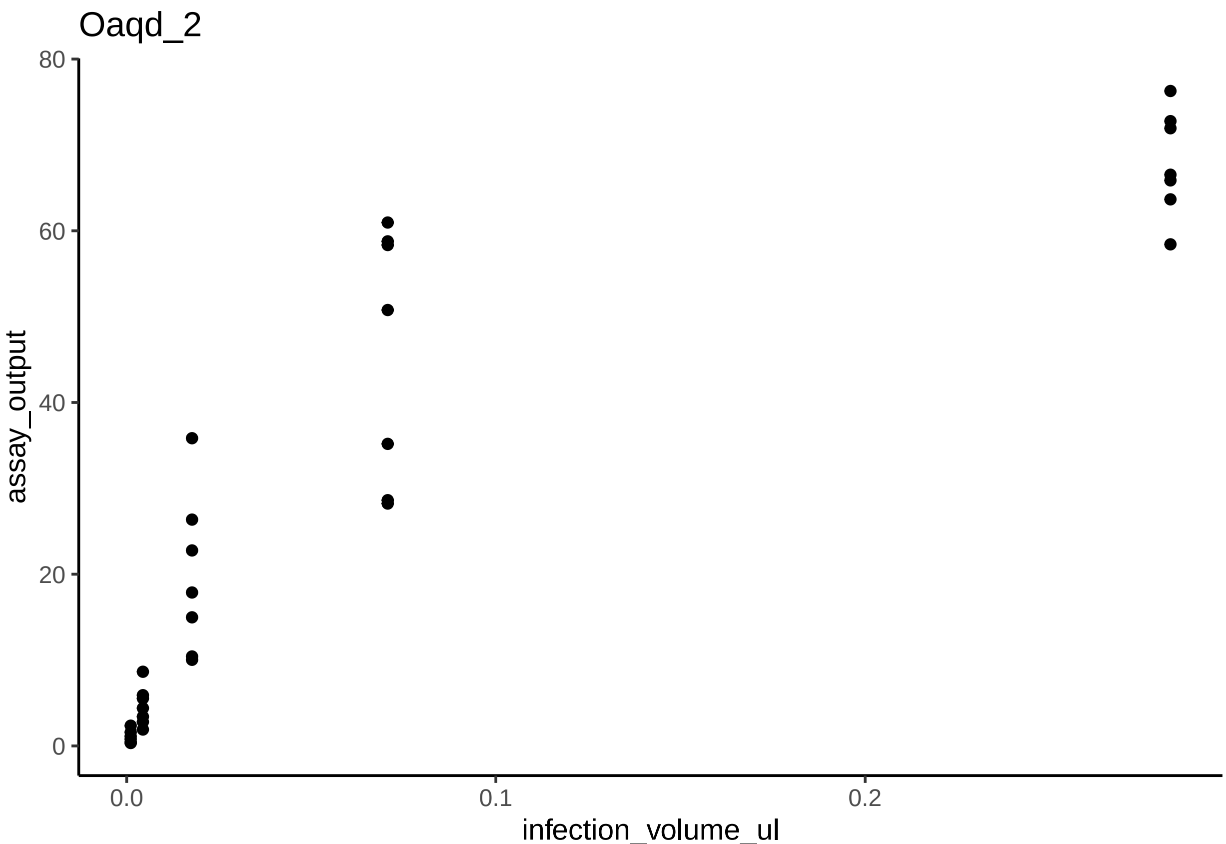

```
##
## [[77]]
```



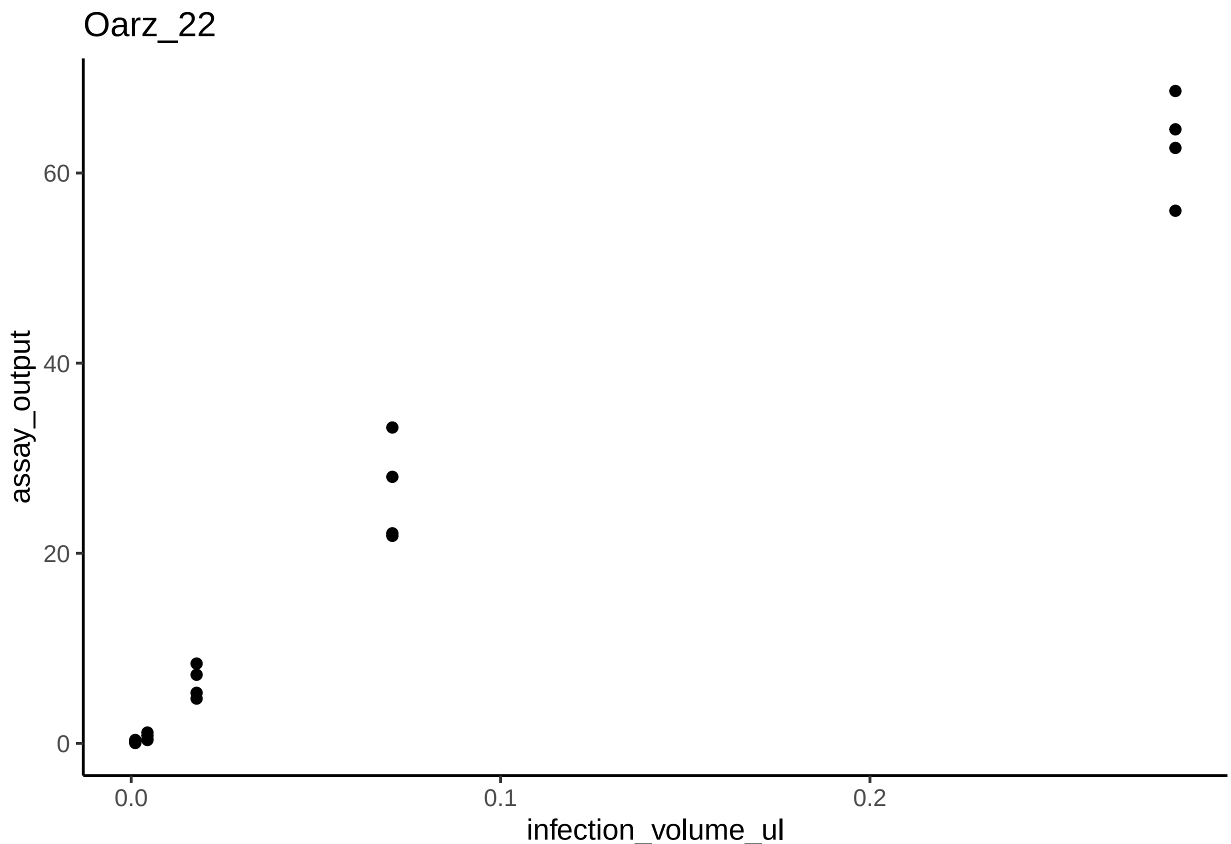

```
##
## [[78]]
```



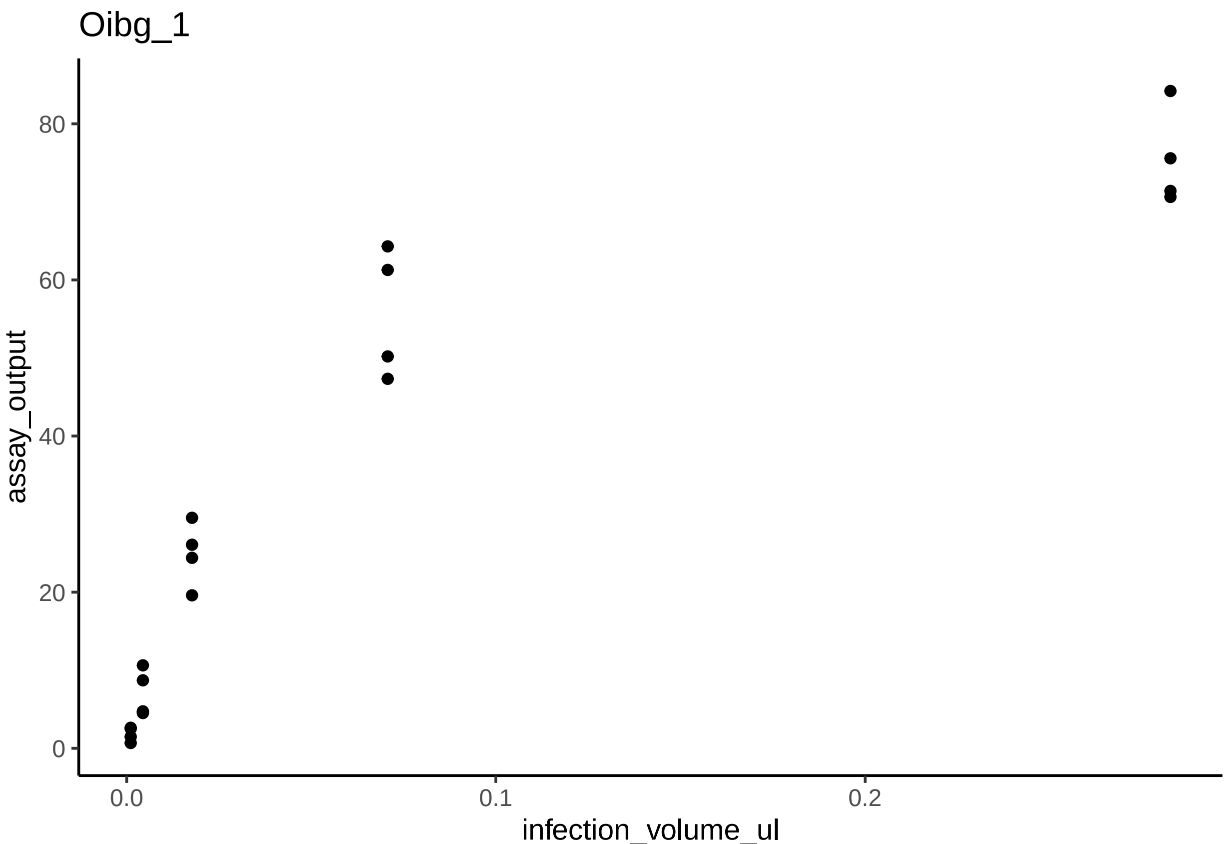

```
##
## [[79]]
```



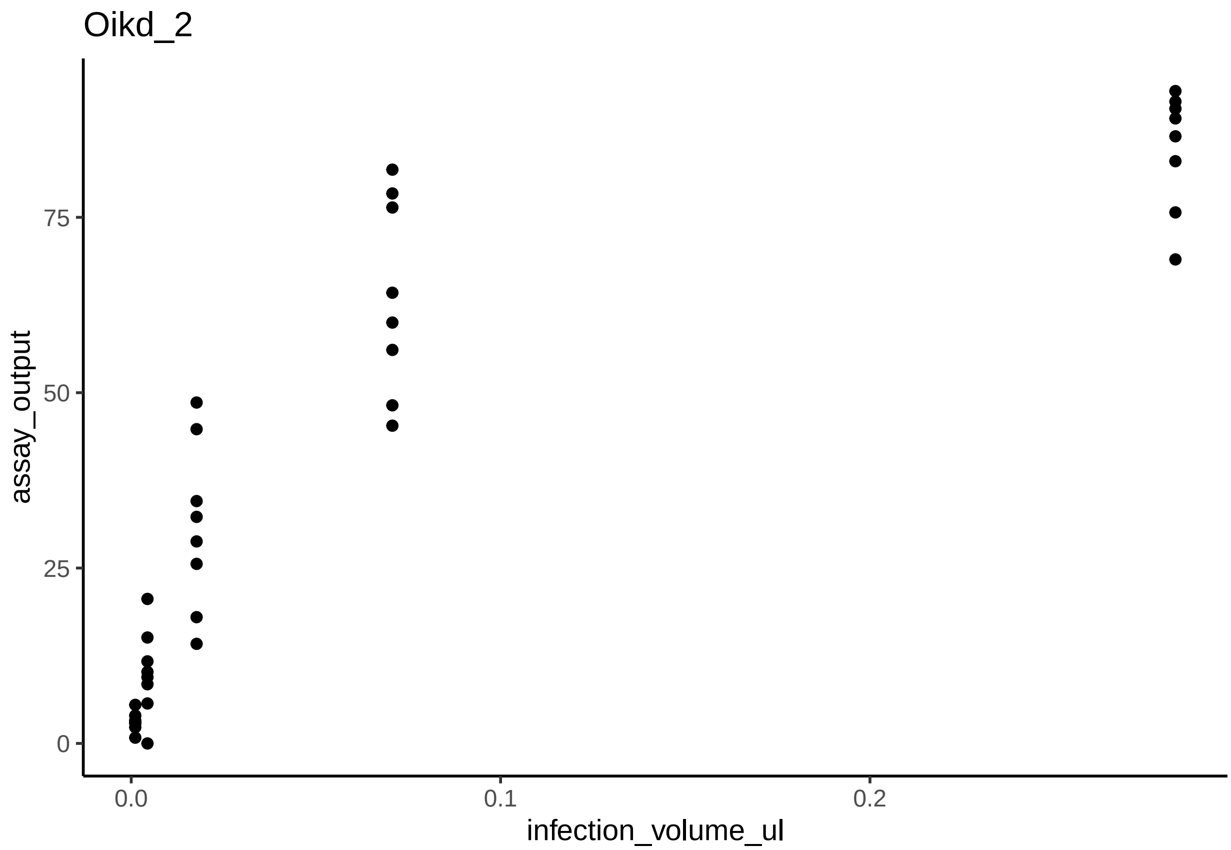

```
##
## [[80]]
```



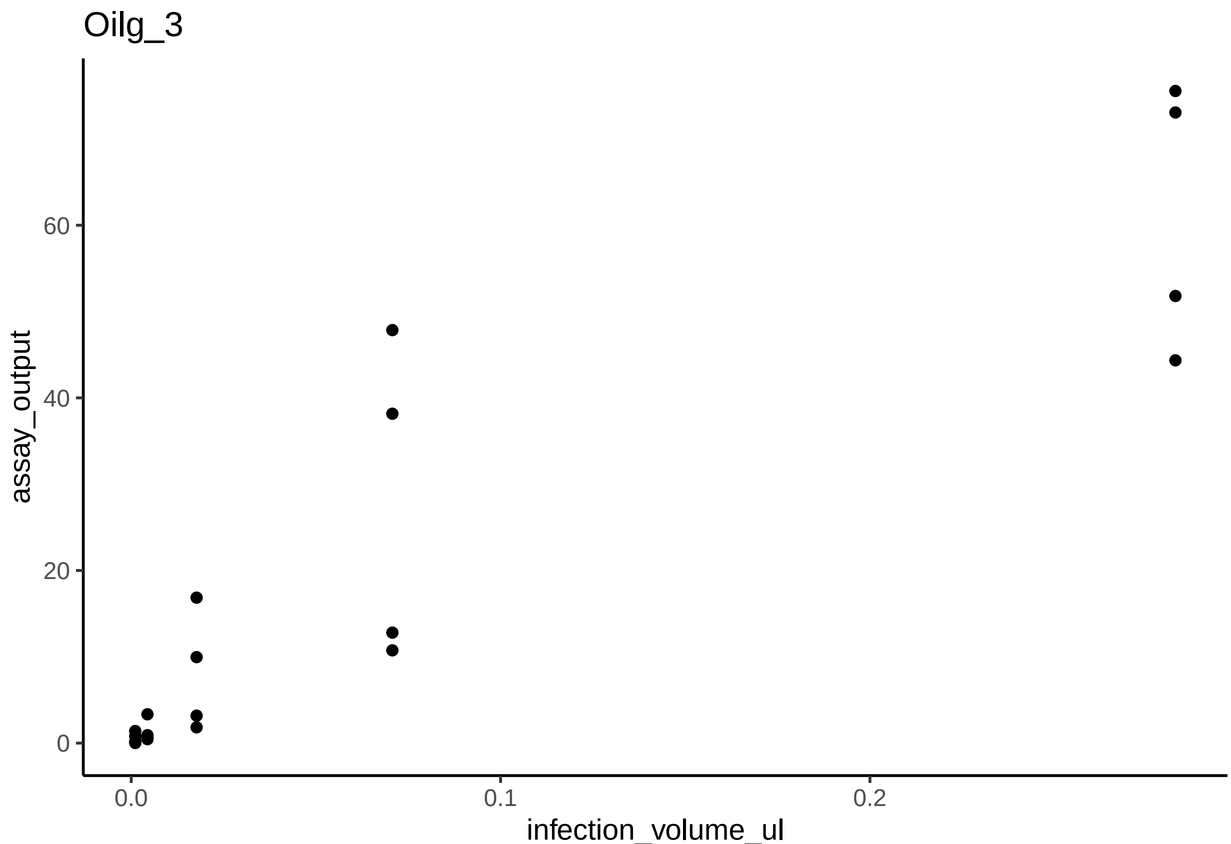

```
##
## [[81]]
```



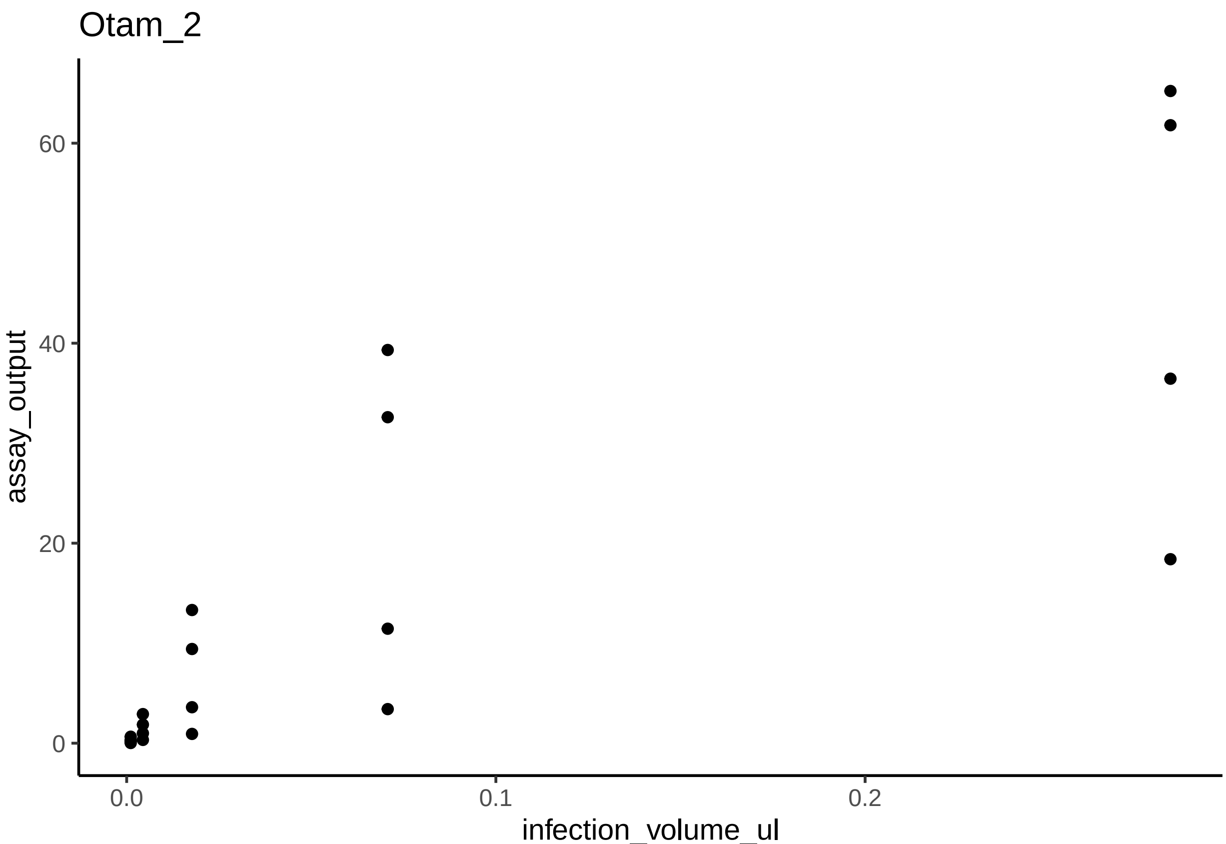

```
##
## [[82]]
```



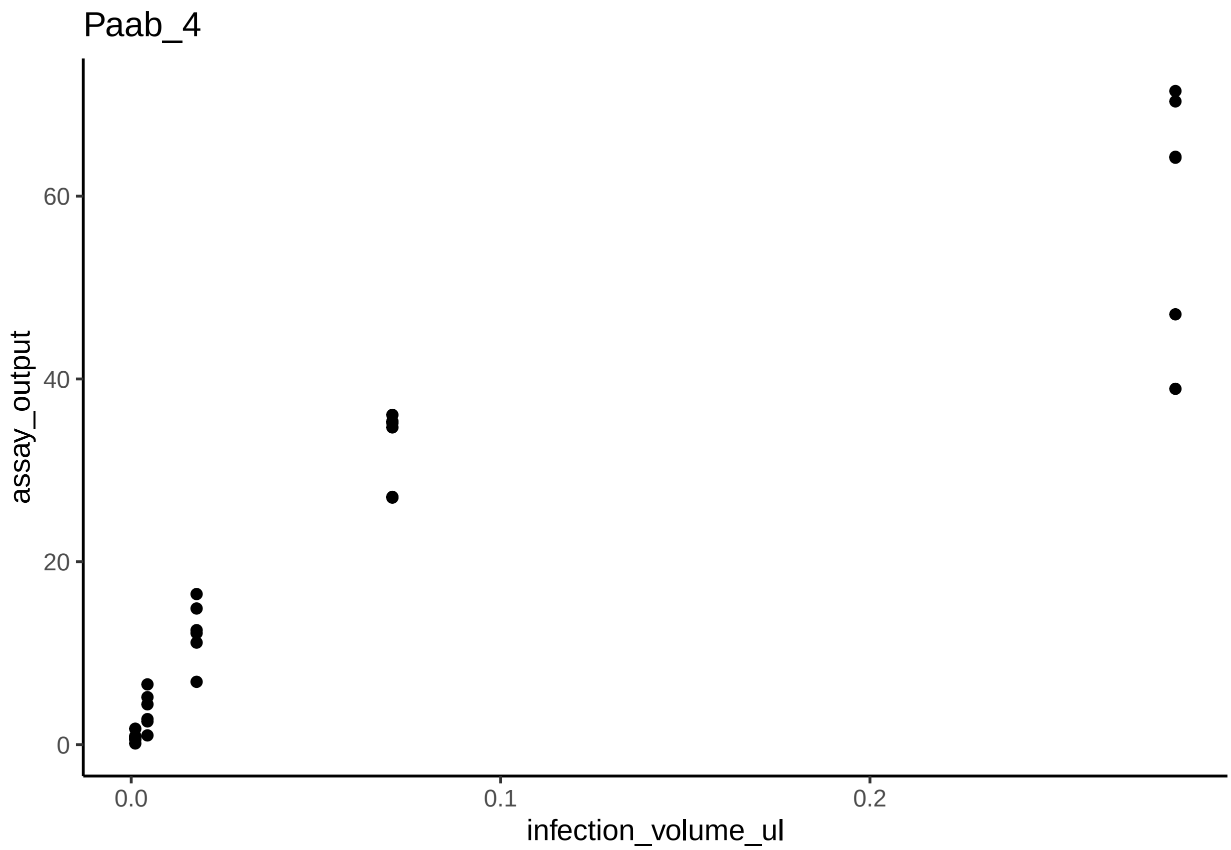

```
##
## [[83]]
```




```
##
## [[84]]
```

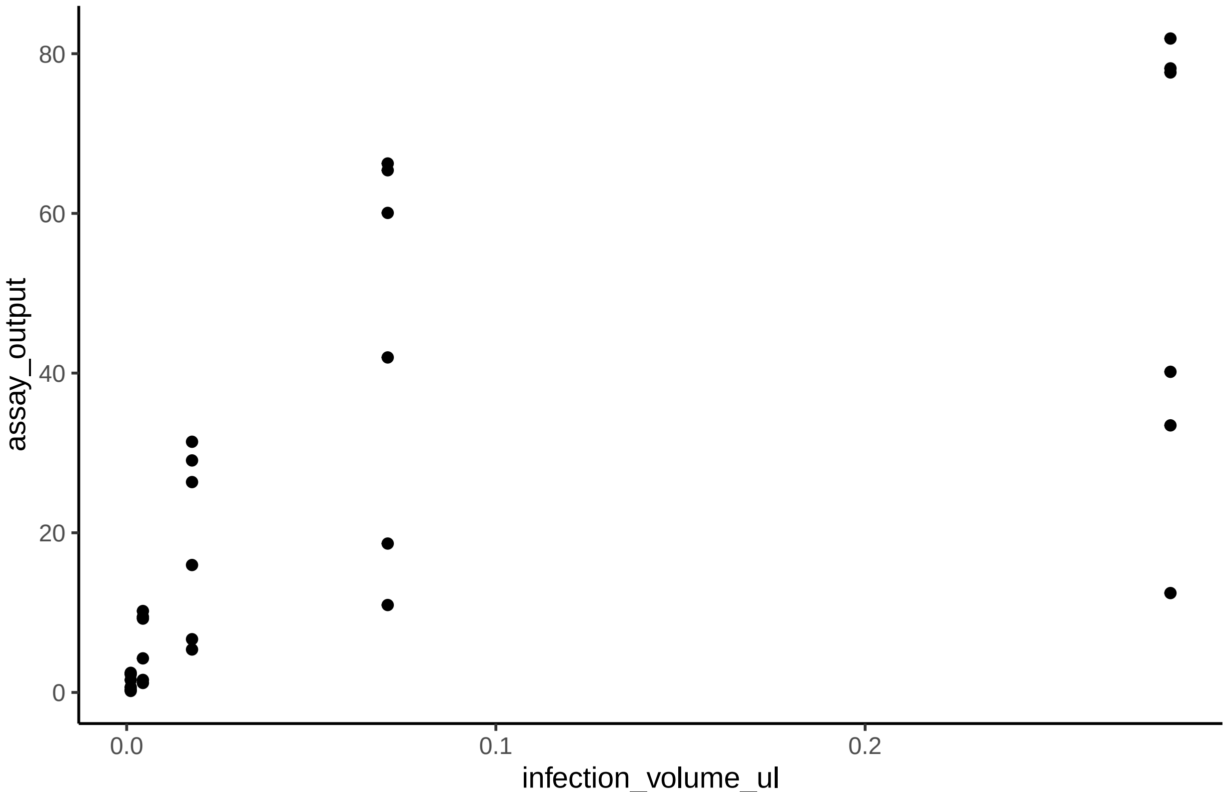



```
##
## [[85]]
```

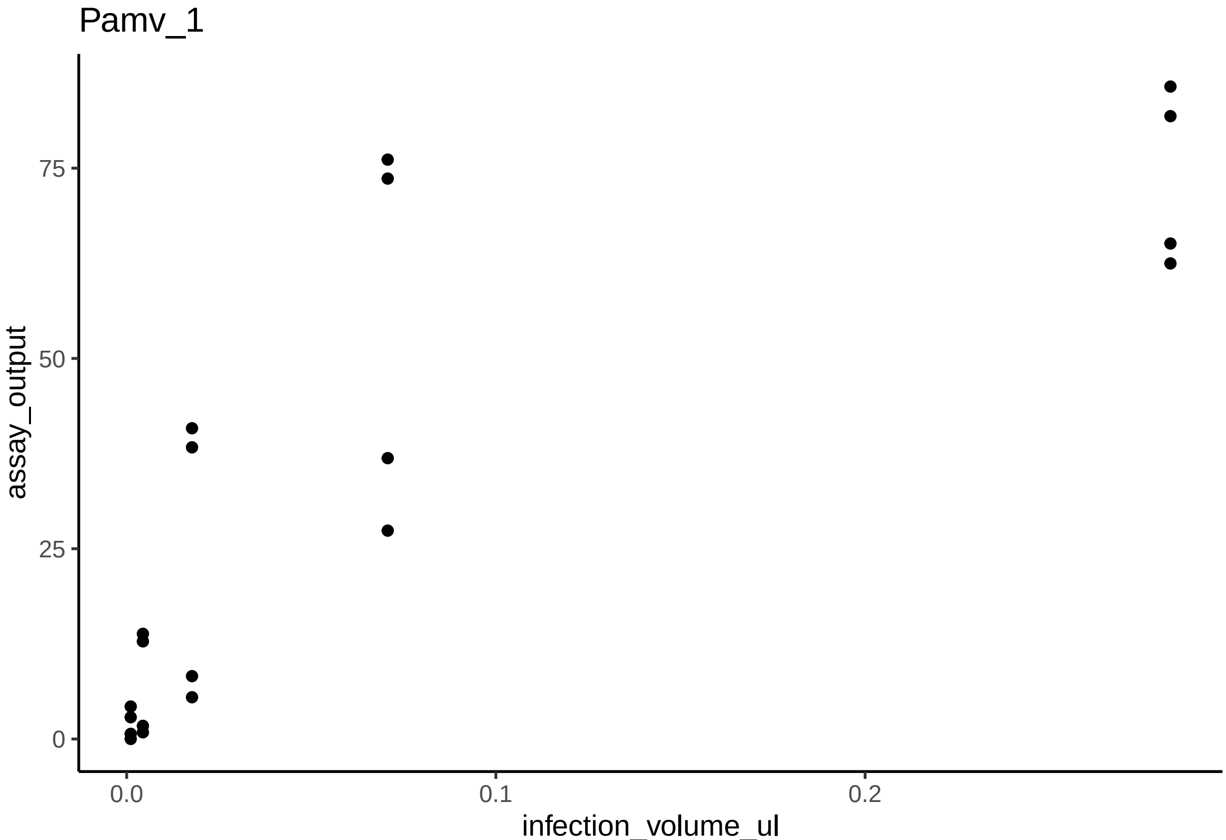



```
##
## [[86]]
```

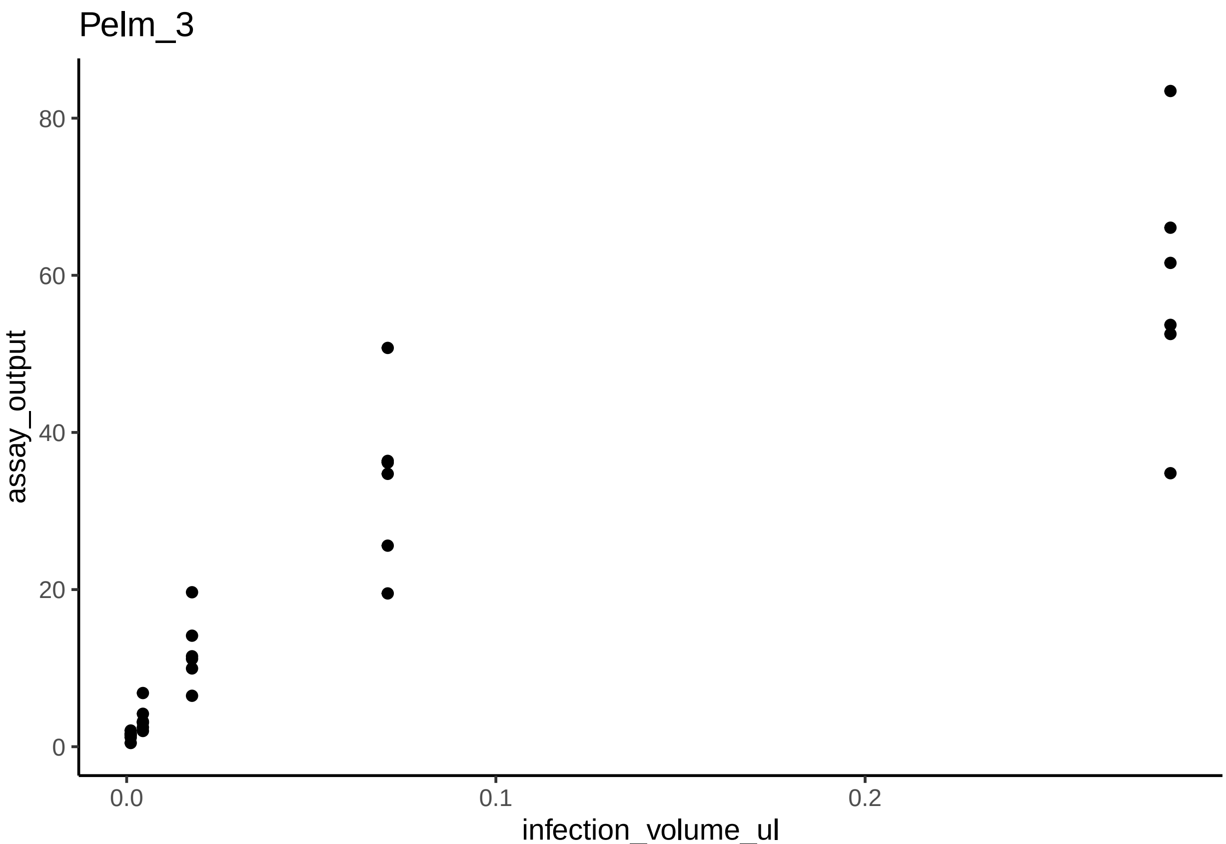
Pahc_5



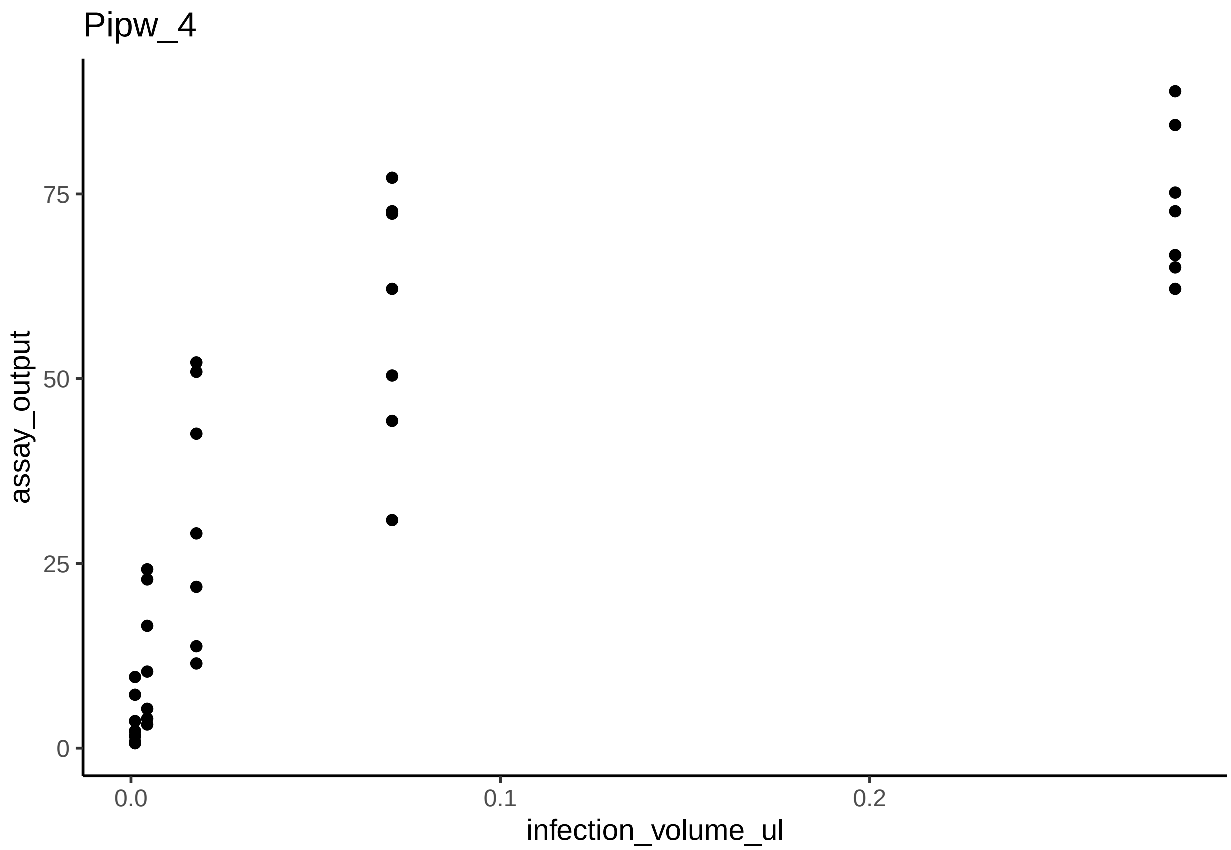

```
##
## [[87]]
```



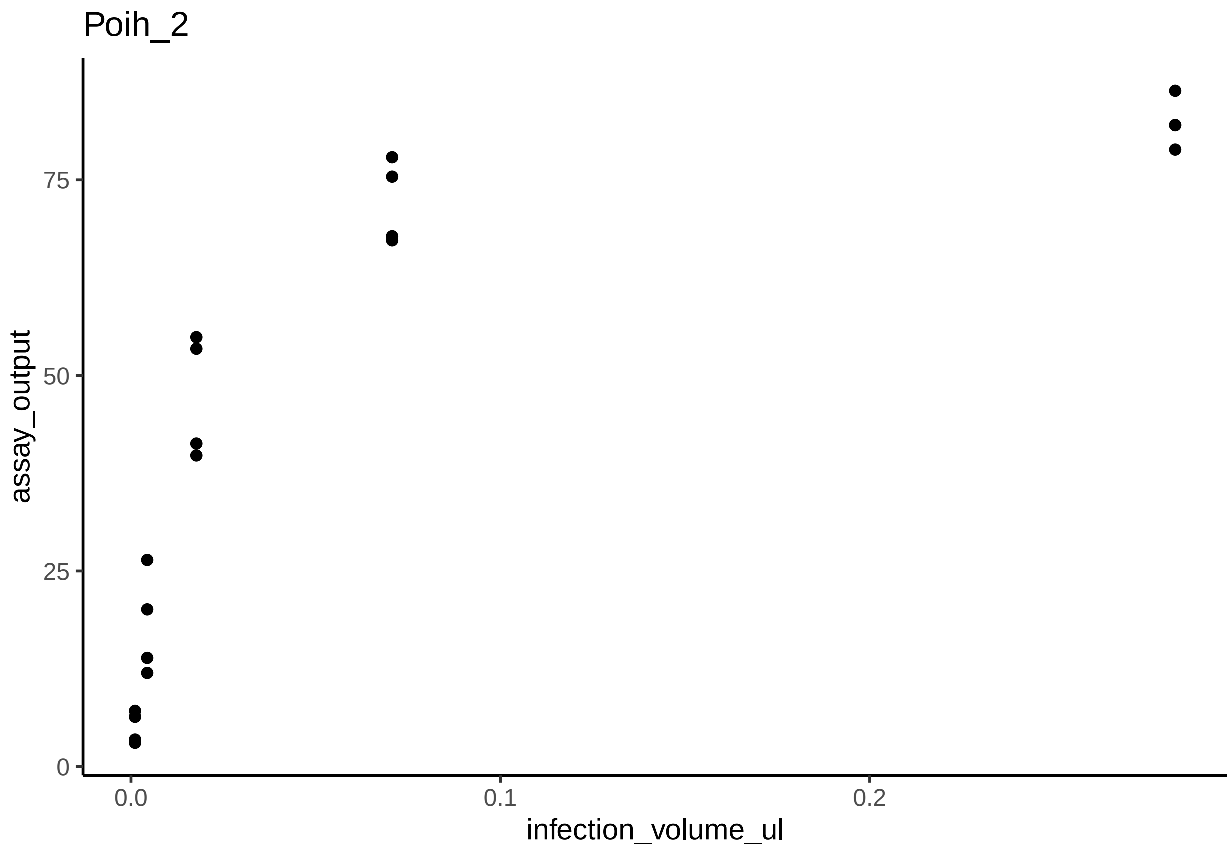

```
##
## [[88]]
```



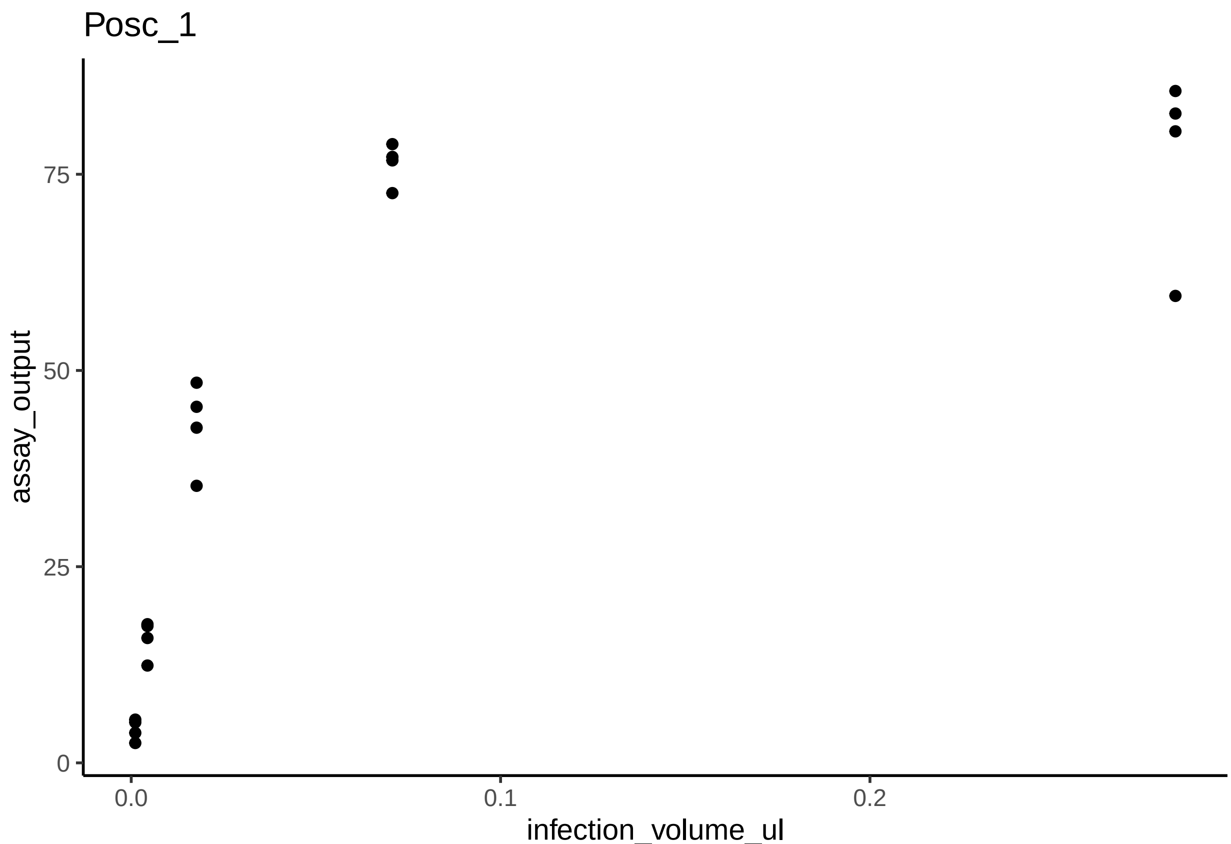

```
##
## [[89]]
```



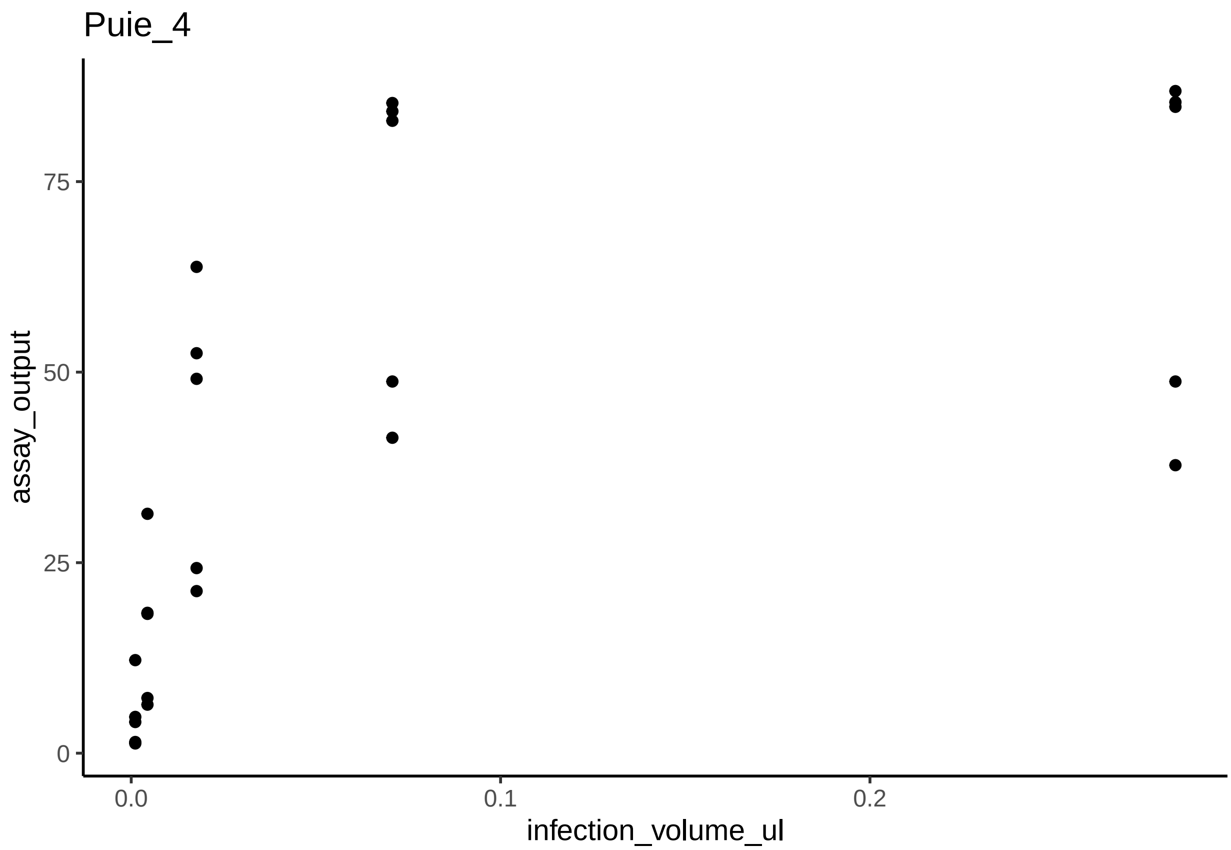

```
##
## [[90]]
```



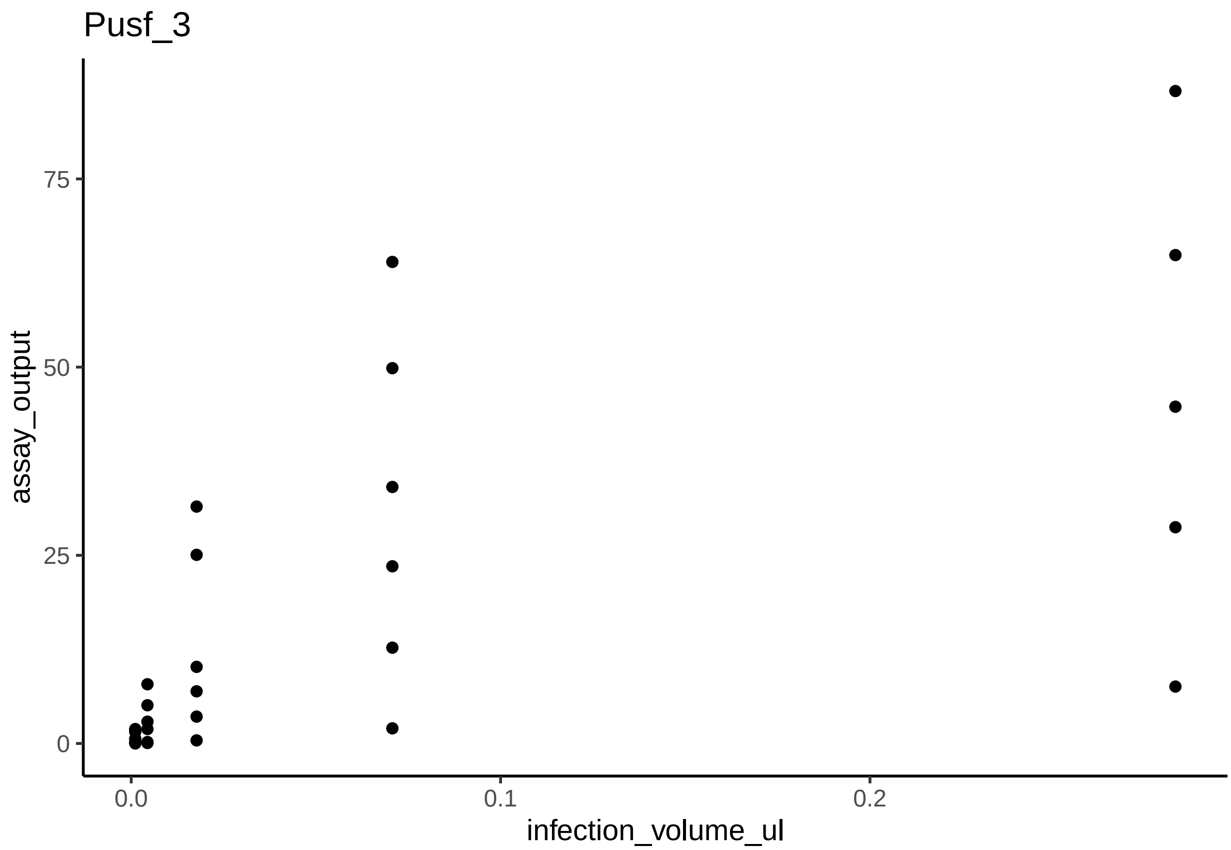

```
##
## [[91]]
```



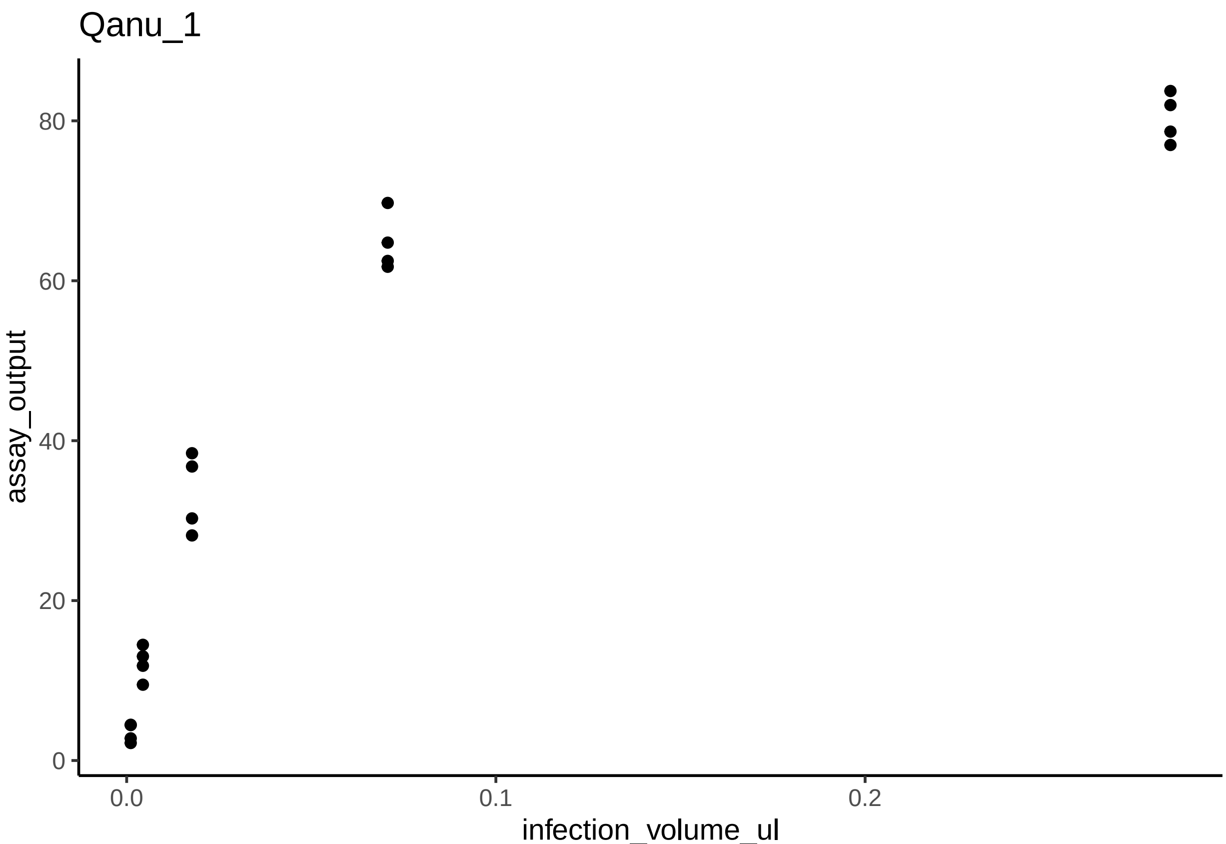

```
##
## [[92]]
```



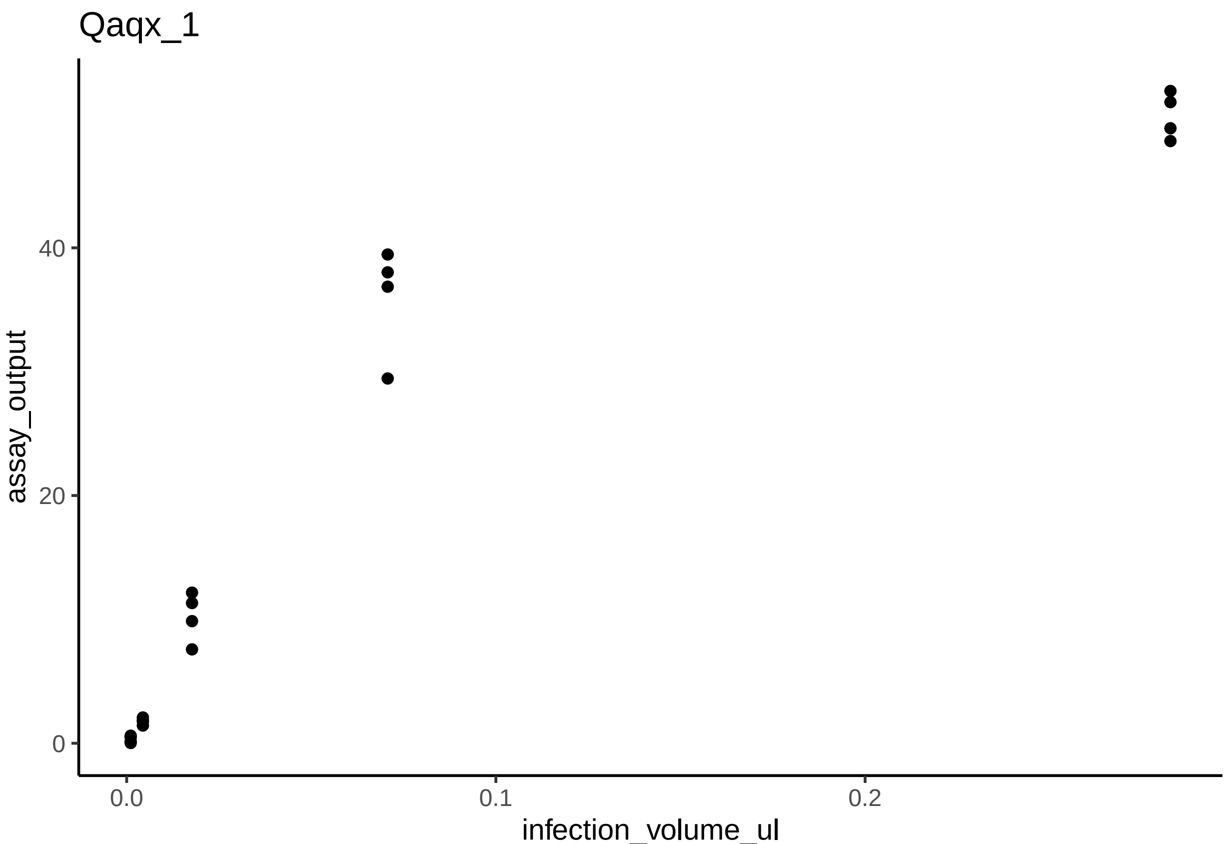

```
##
## [[93]]
```



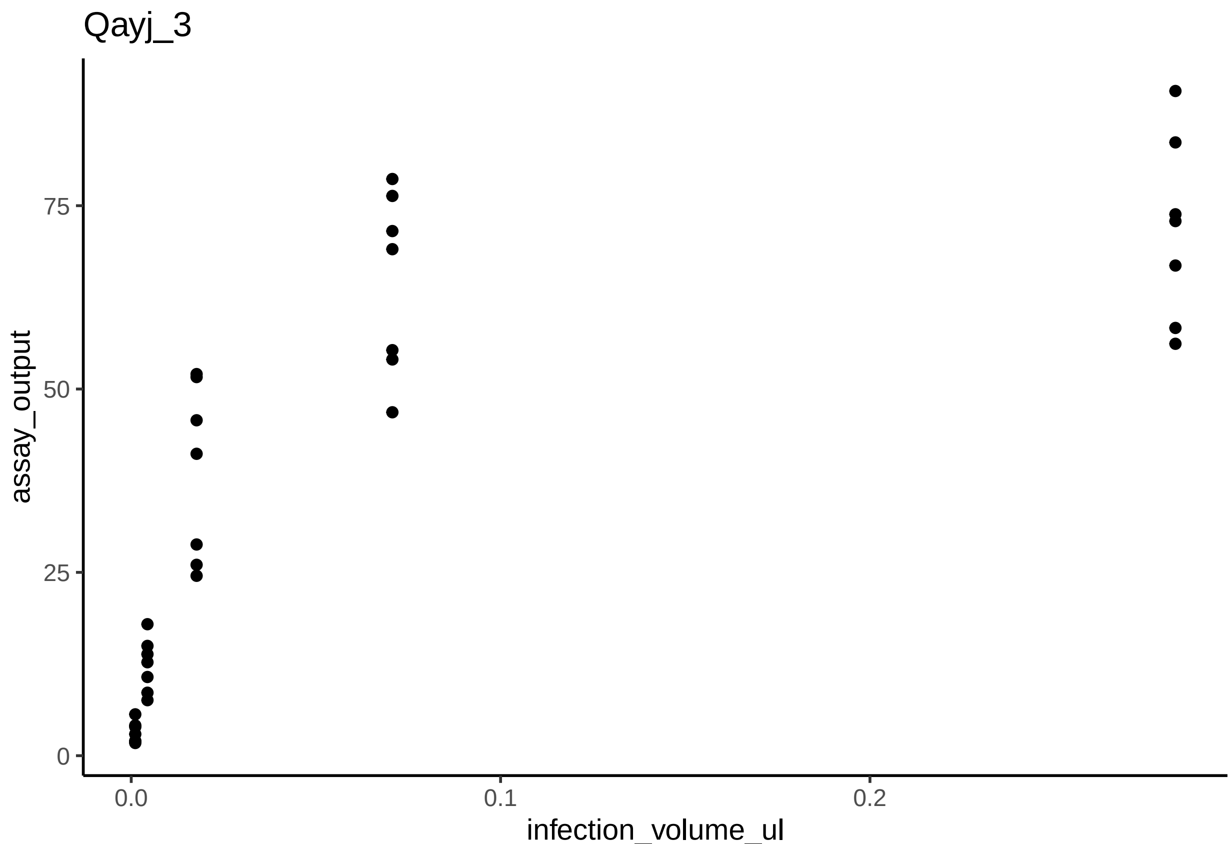

```
##
## [[94]]
```



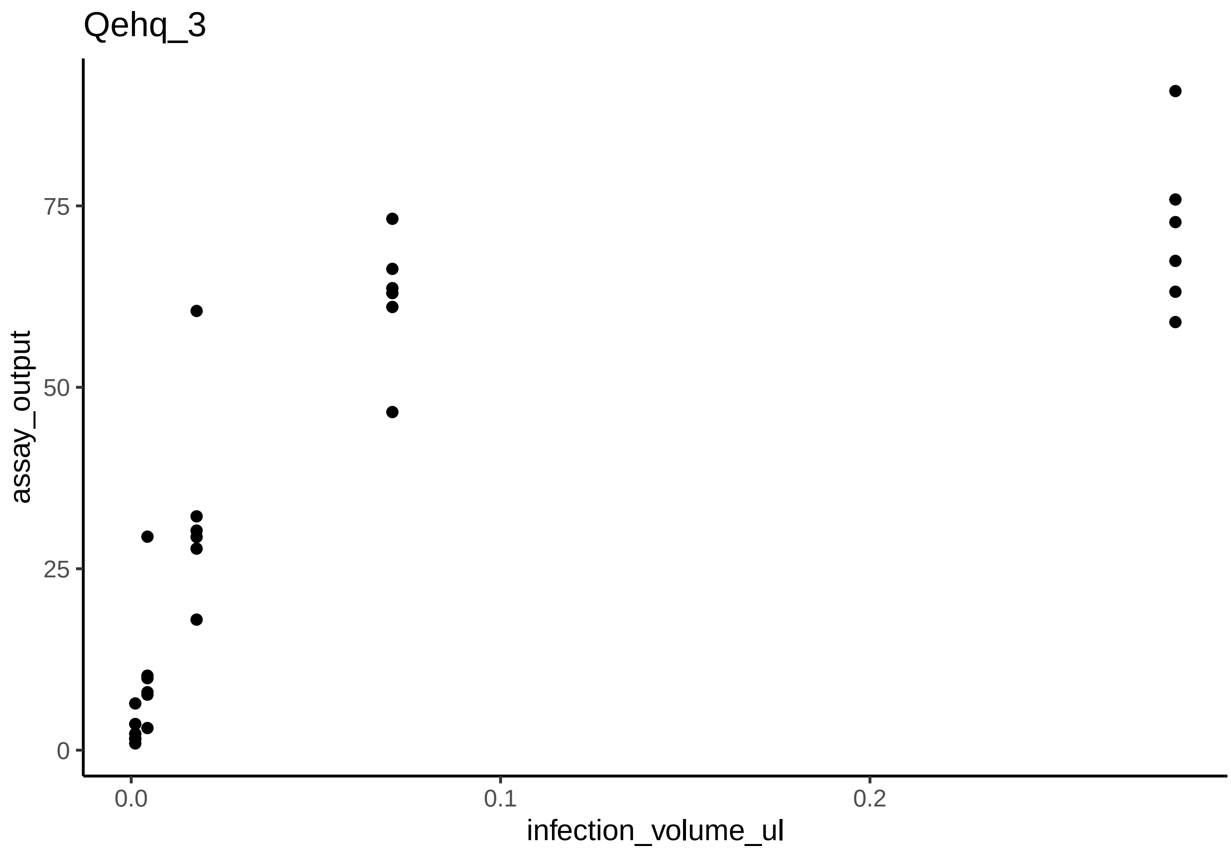

```
##
## [[95]]
```



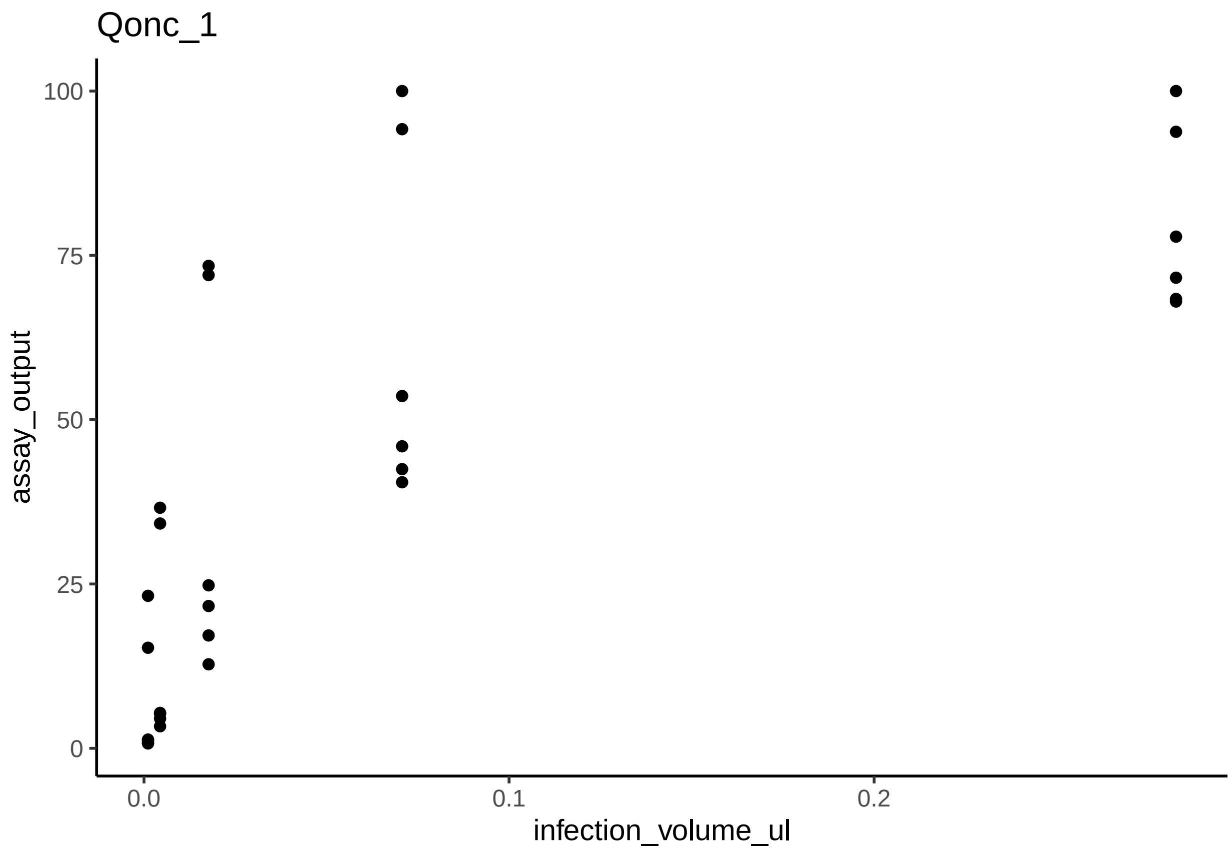

```
##
## [[96]]
```



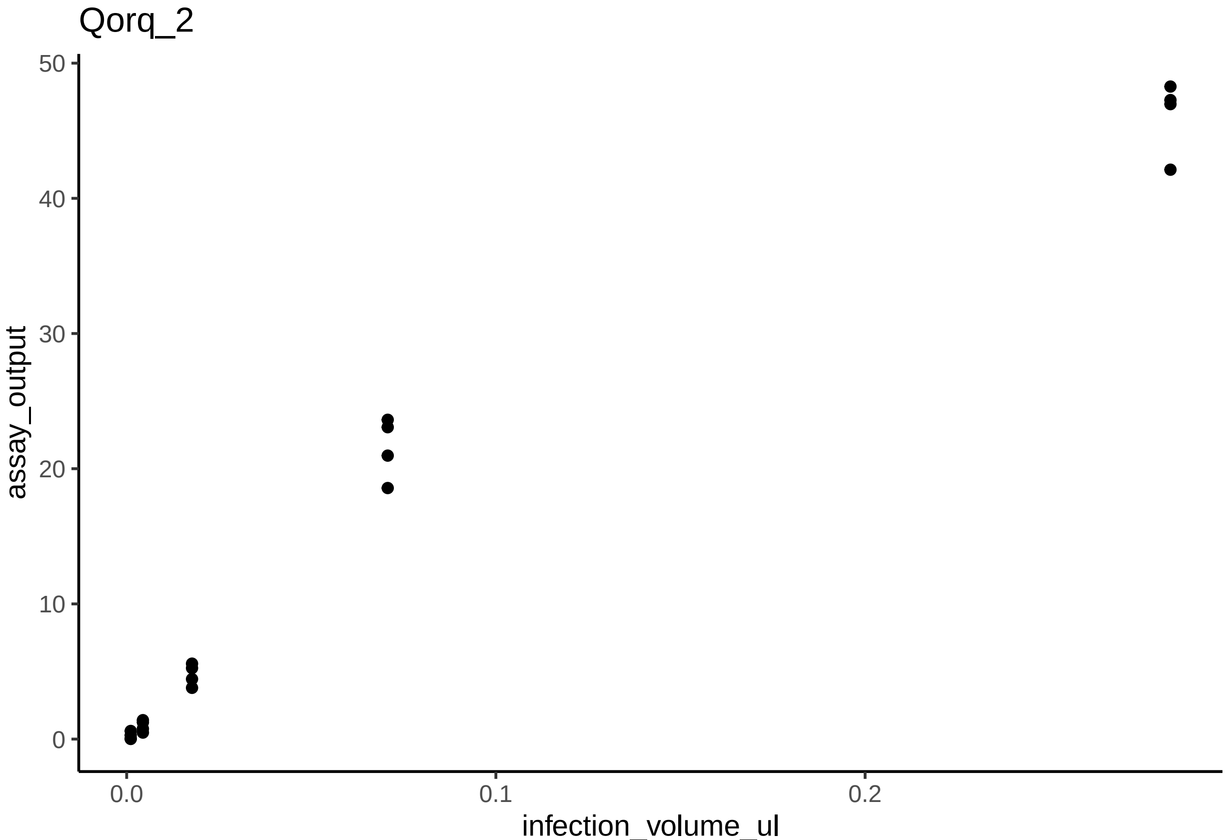

```
##
## [[97]]
```



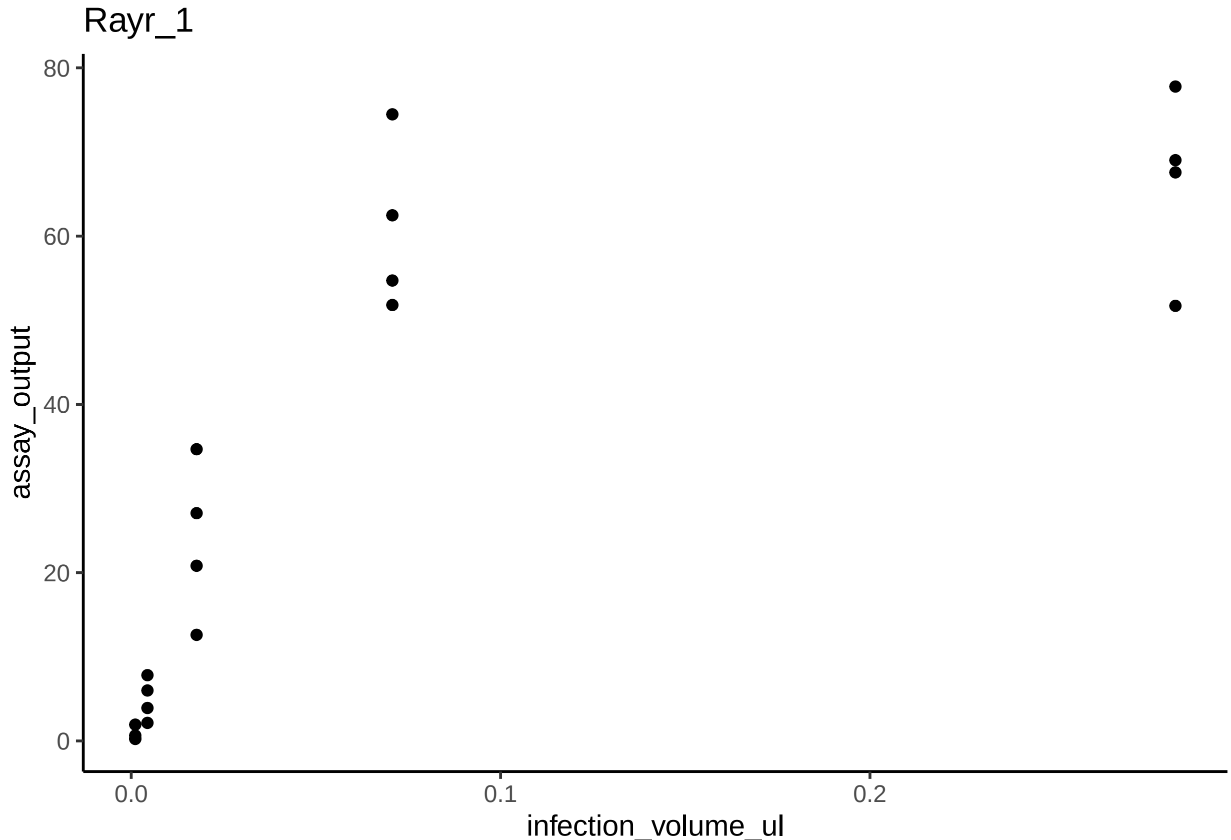

```
##
## [[98]]
```



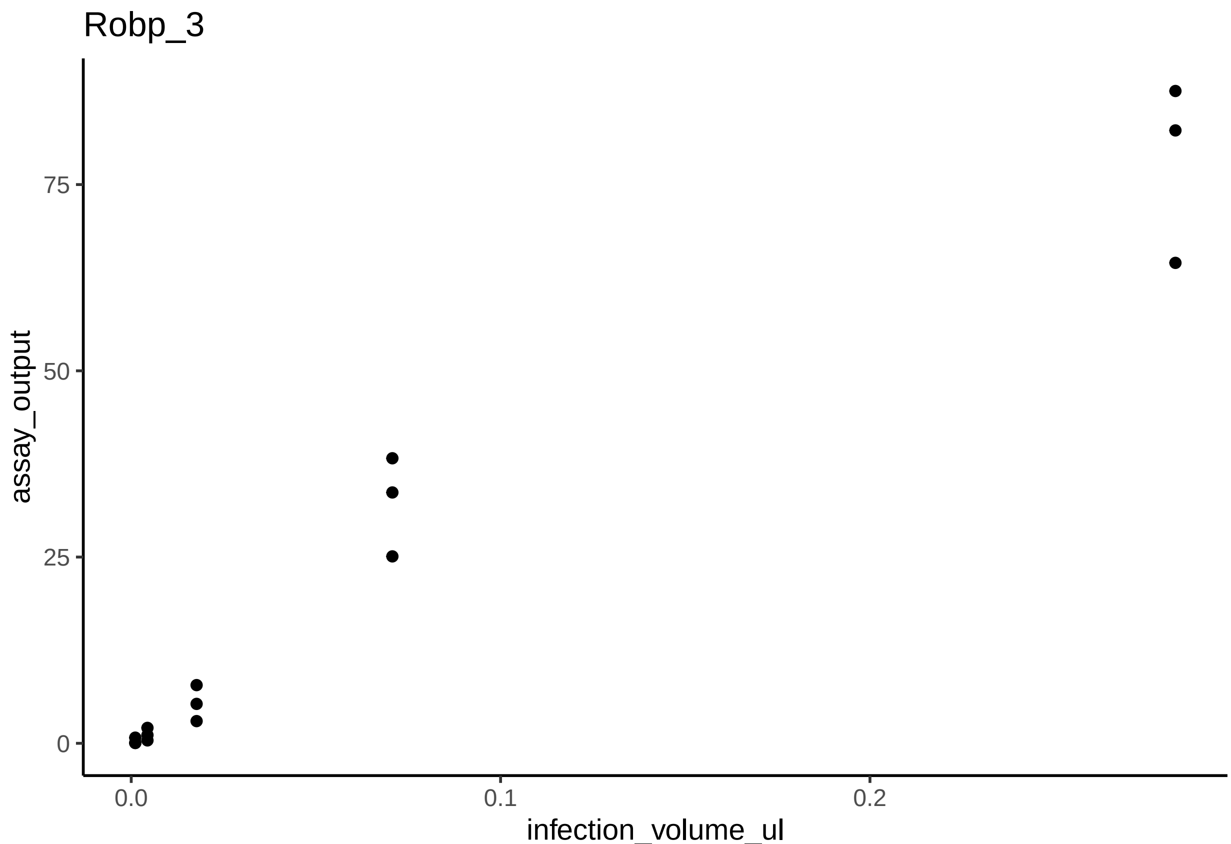

```
##
## [[99]]
```


Qorq_2
assay_output
infection_volume_ul
50
40
30
20
10
0
0.0
0.1
0.2

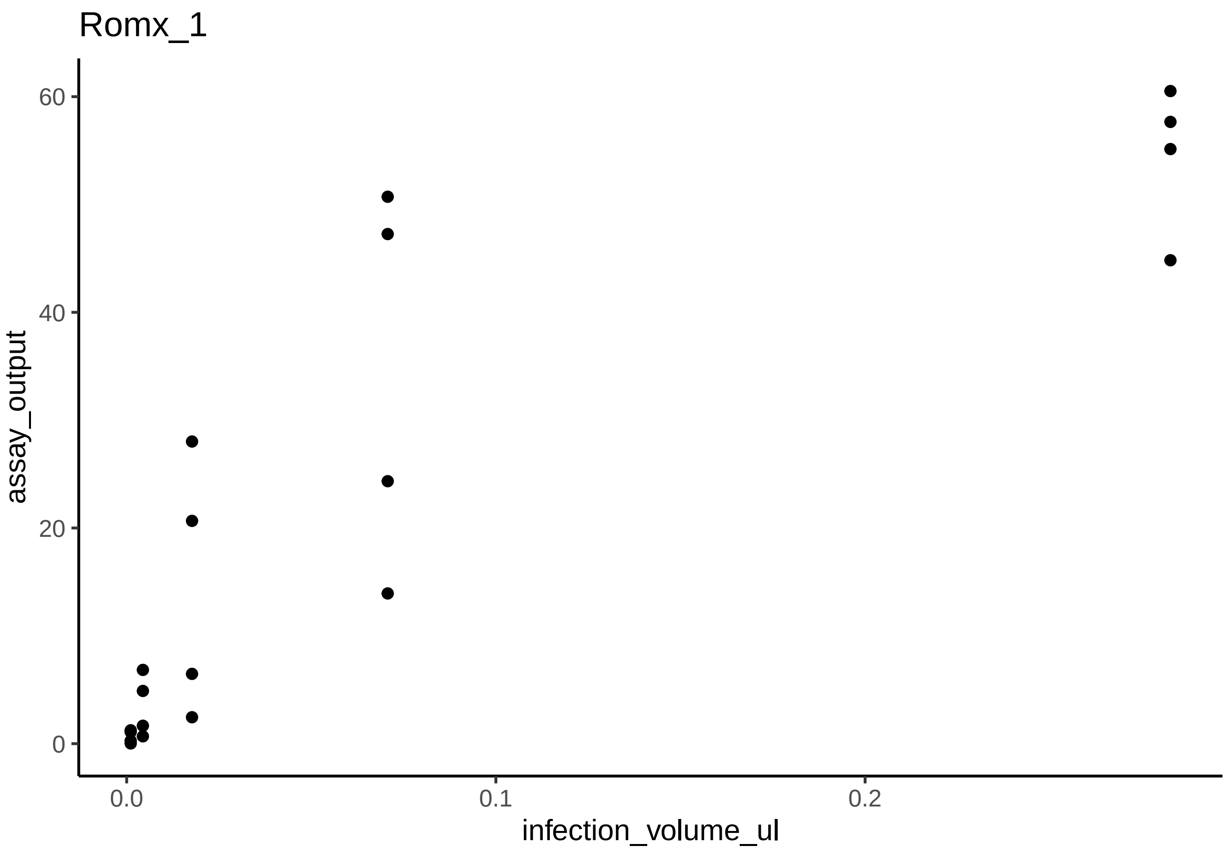
```
##
## [[100]]
```



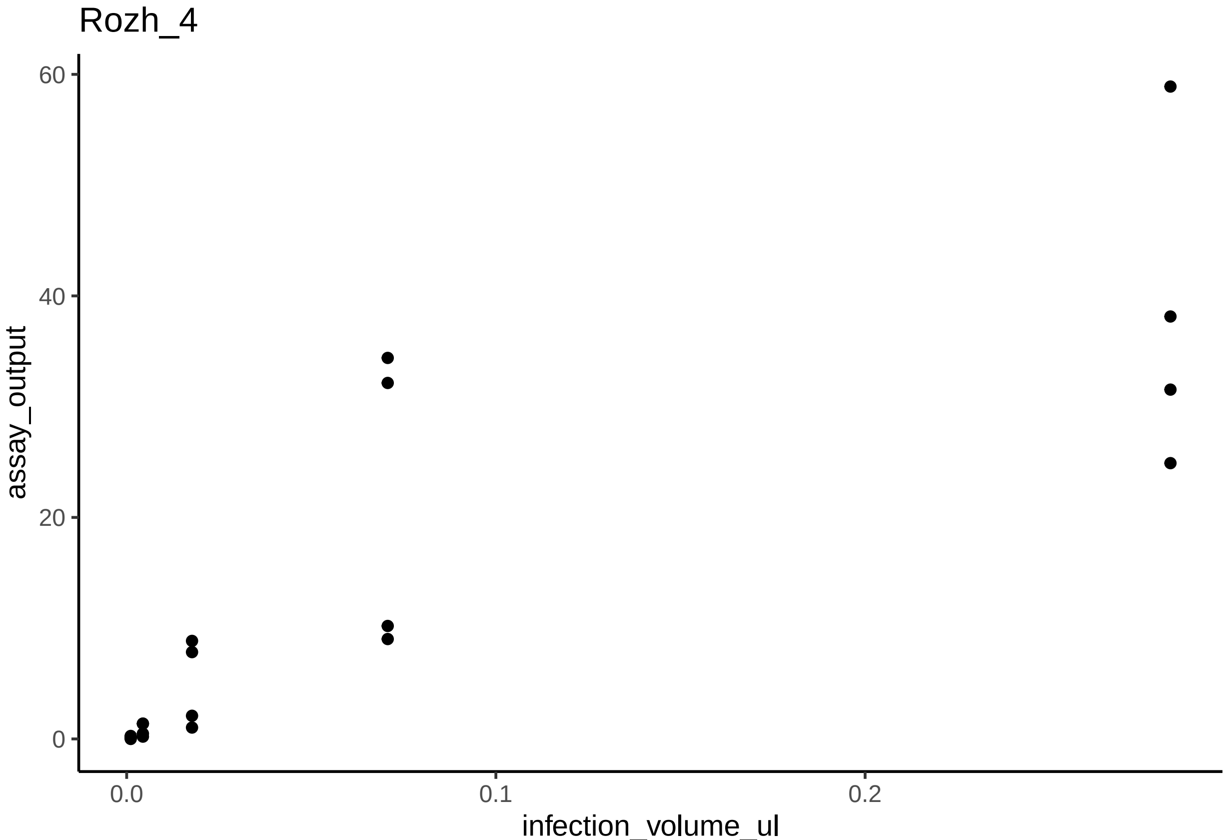

```
##
## [[101]]
```



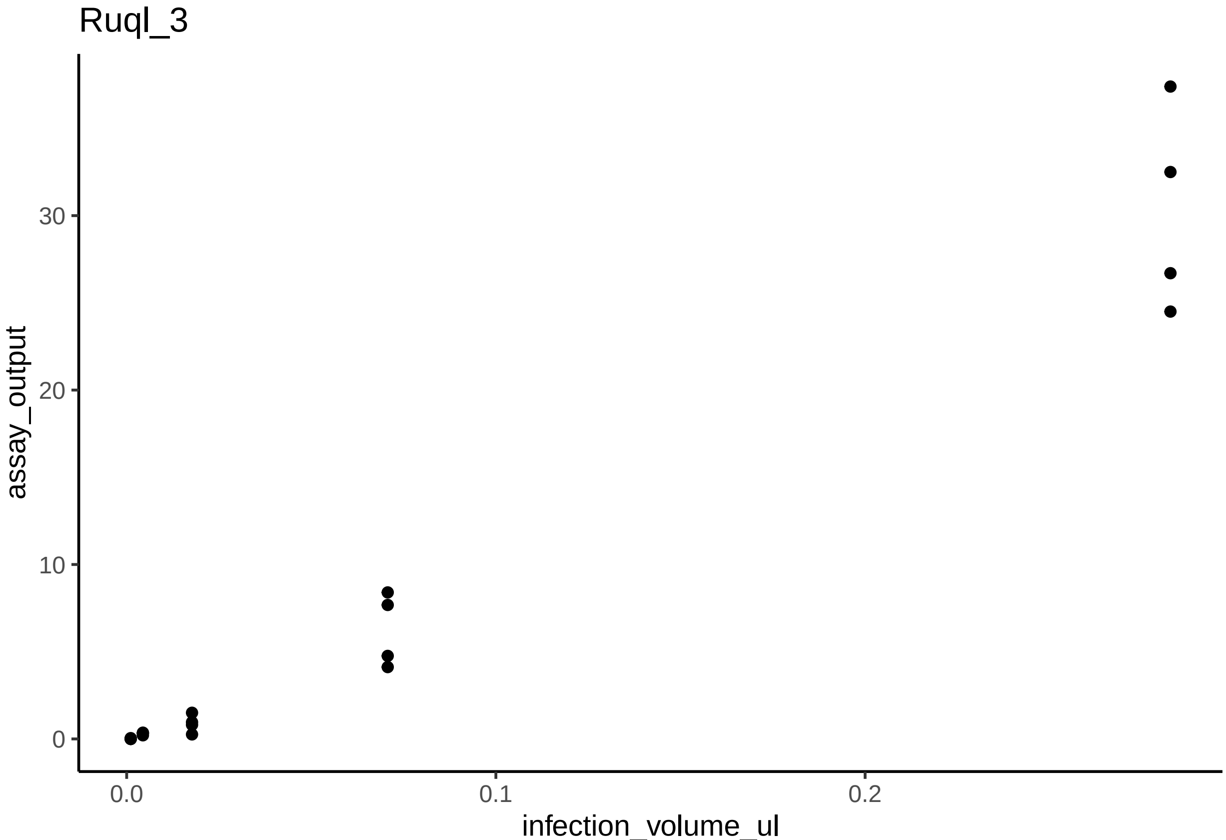

```
##
## [[102]]
```



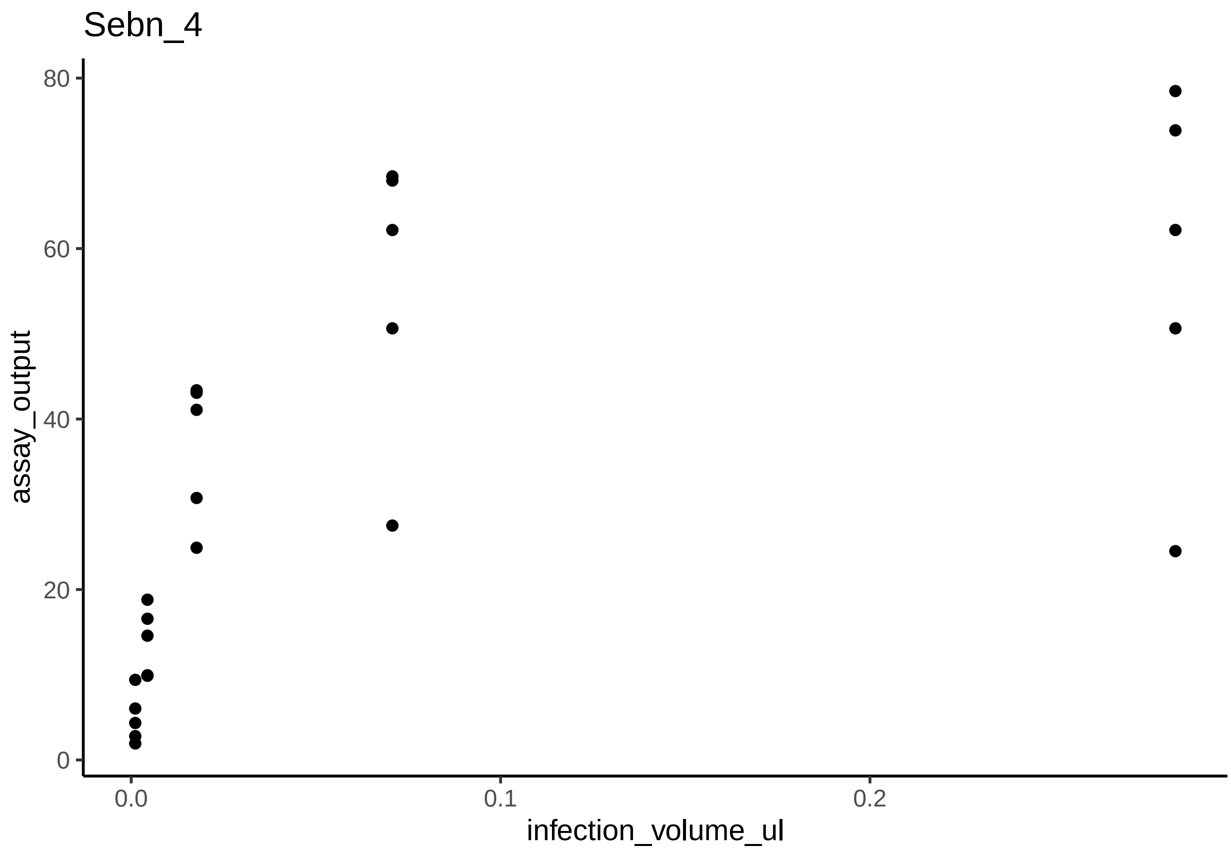

```
##
## [[103]]
```



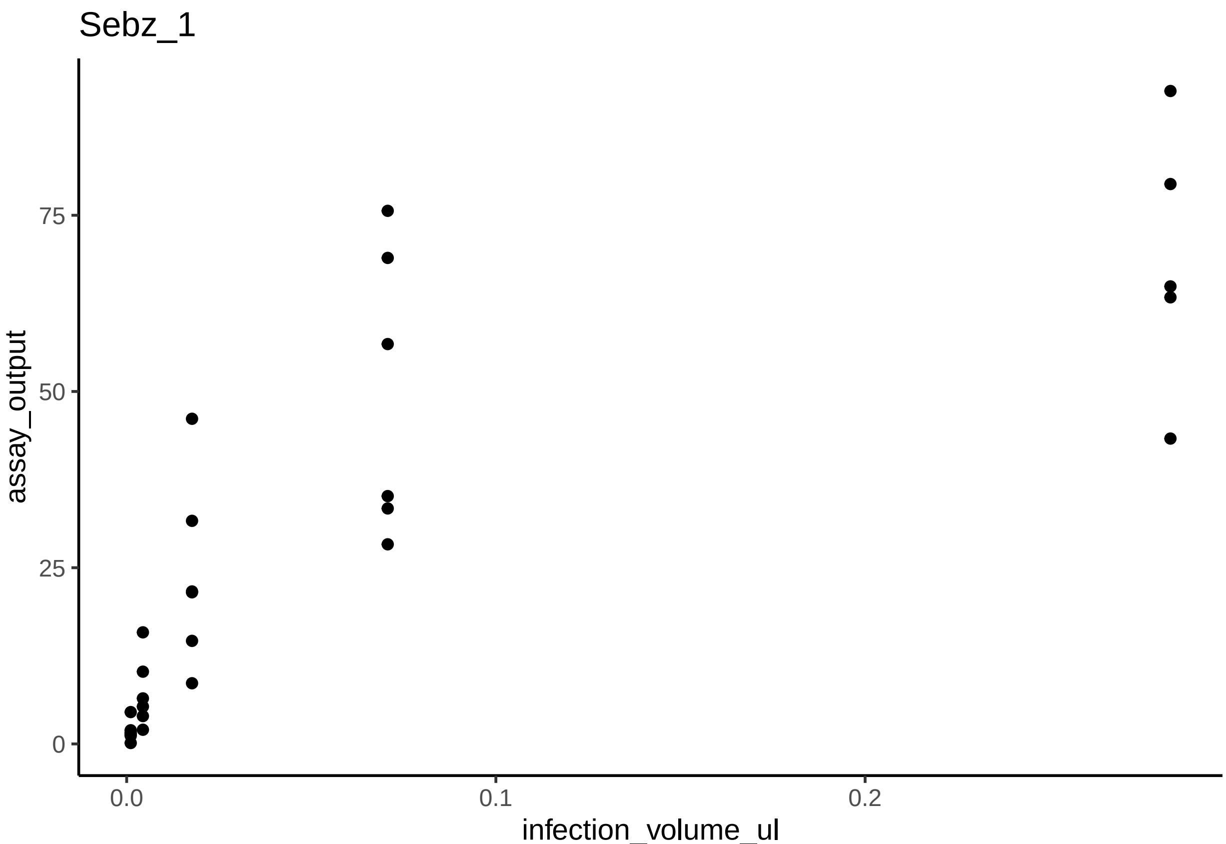

```
##
## [[104]]
```



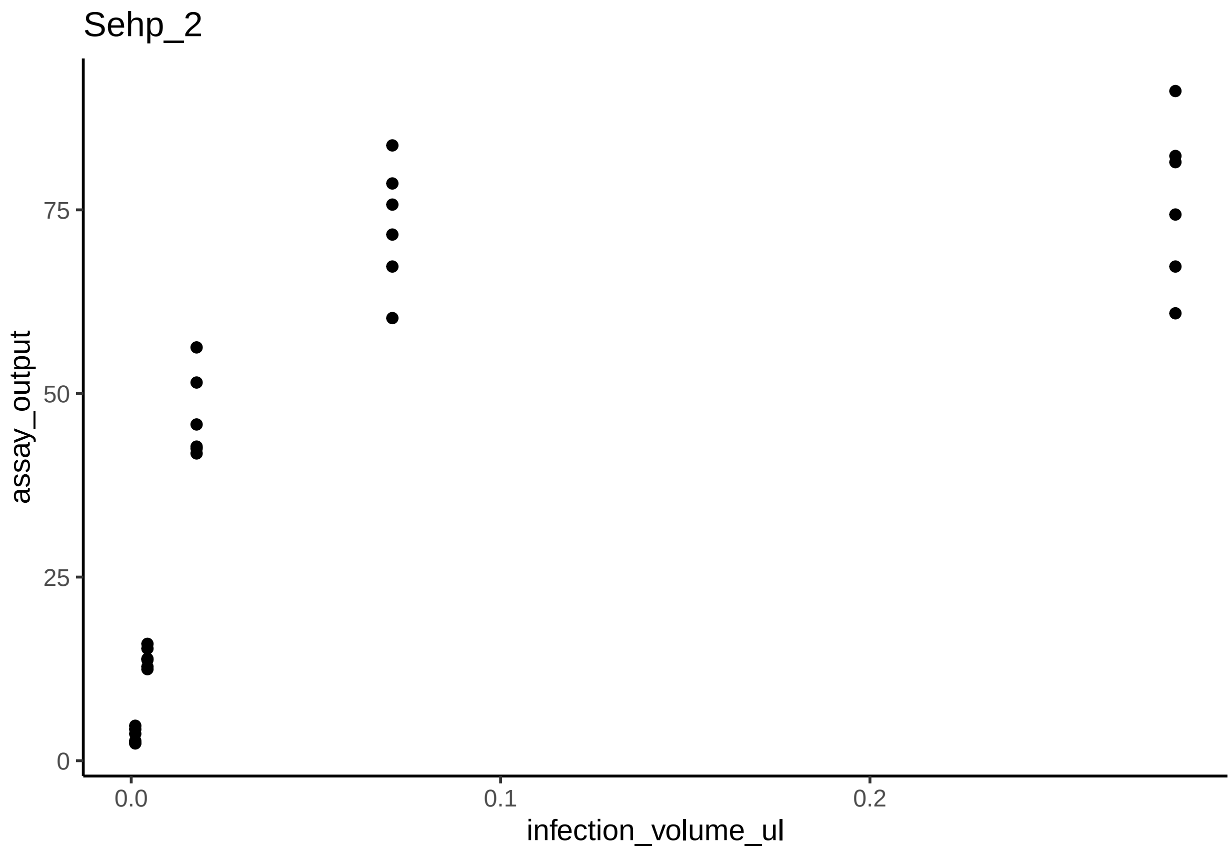

```
##
## [[105]]
```



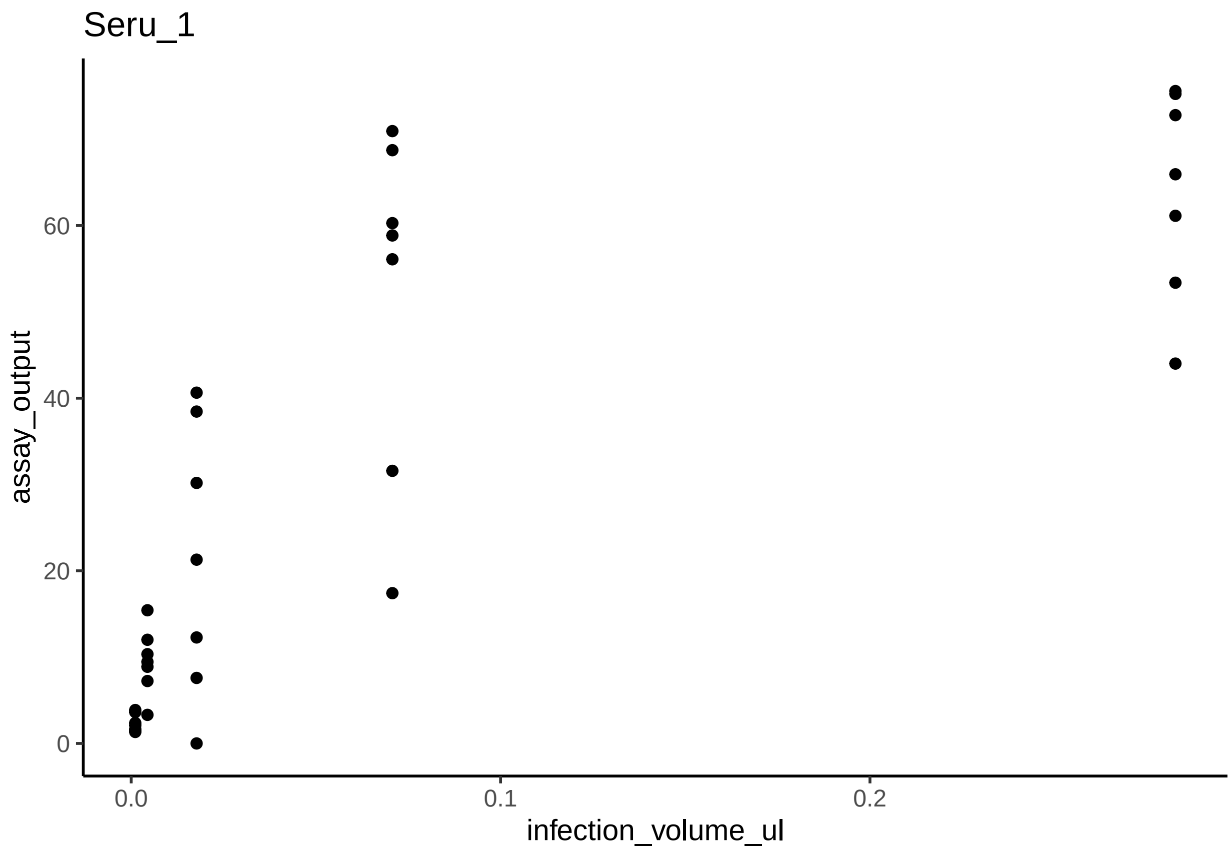

```
##
## [[106]]
```



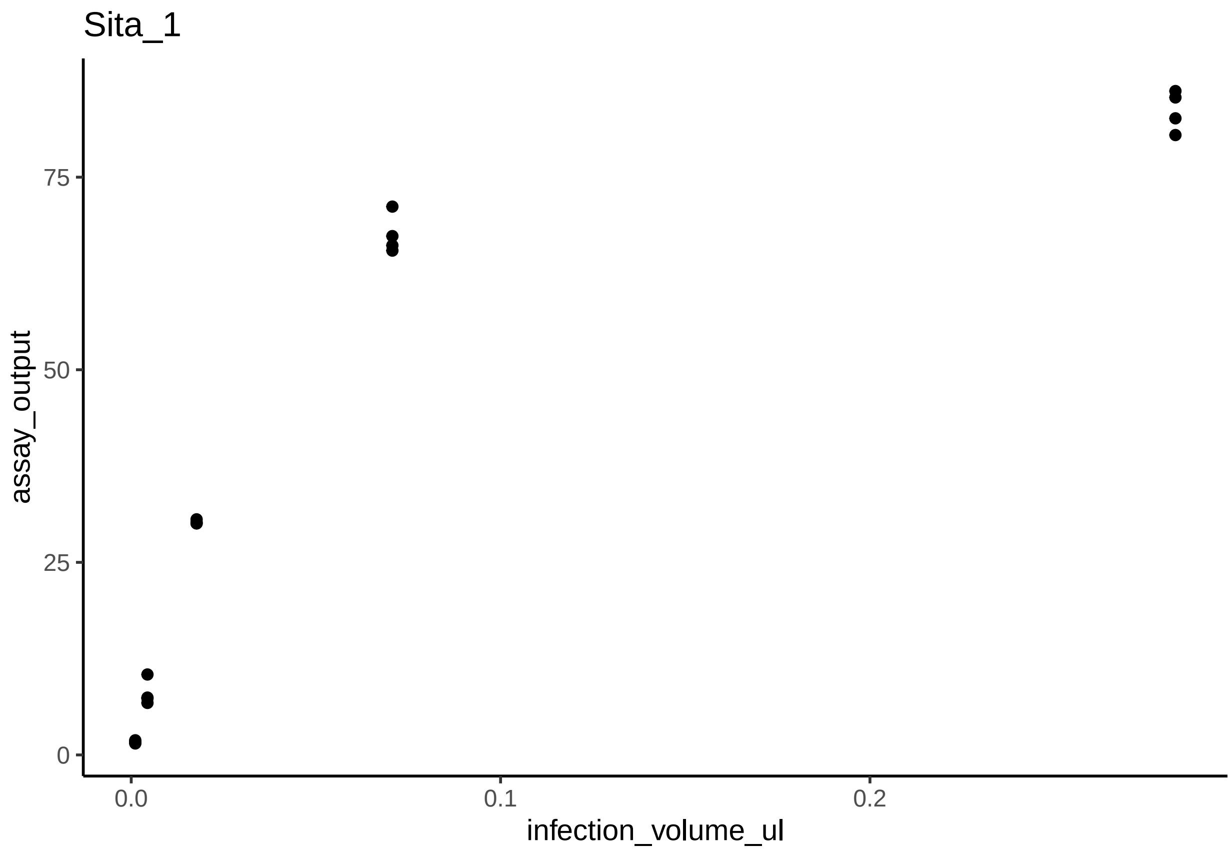

```
##
## [[107]]
```



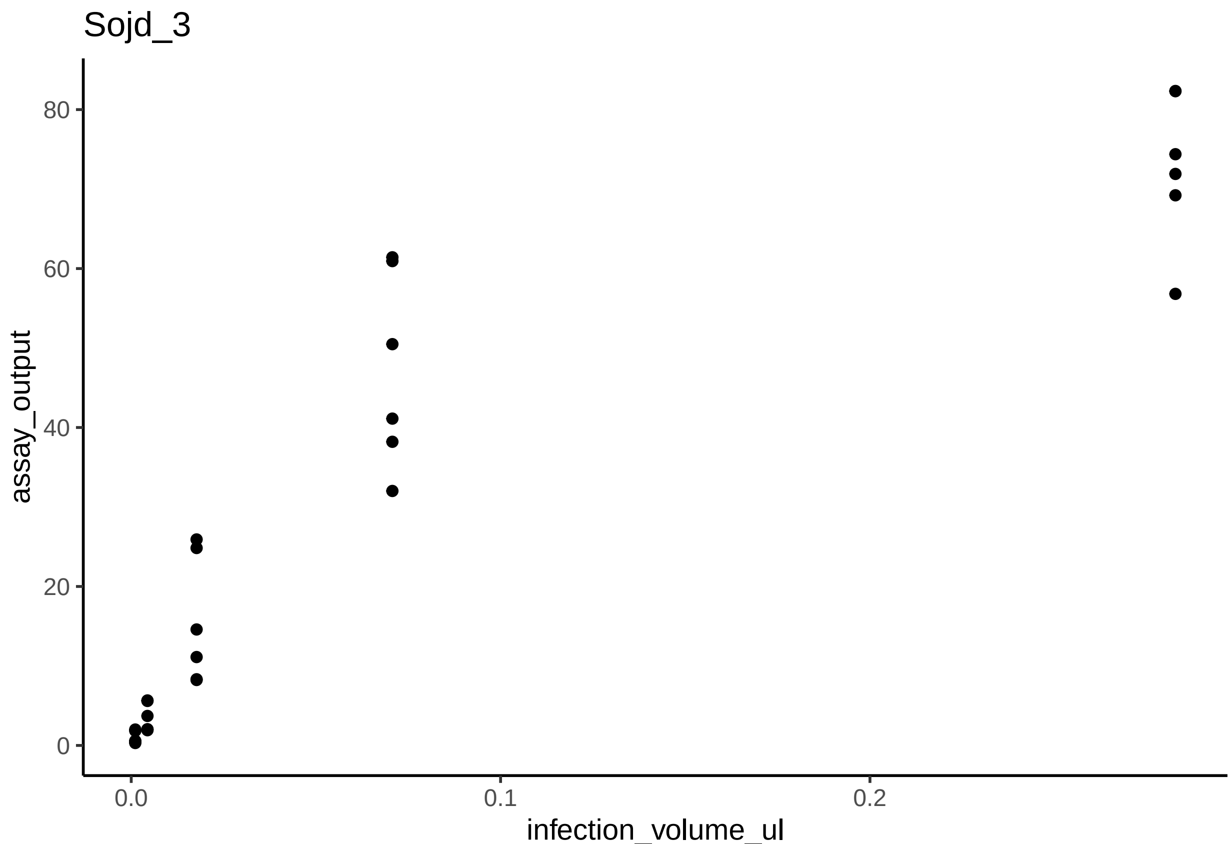

```
##
## [[108]]
```



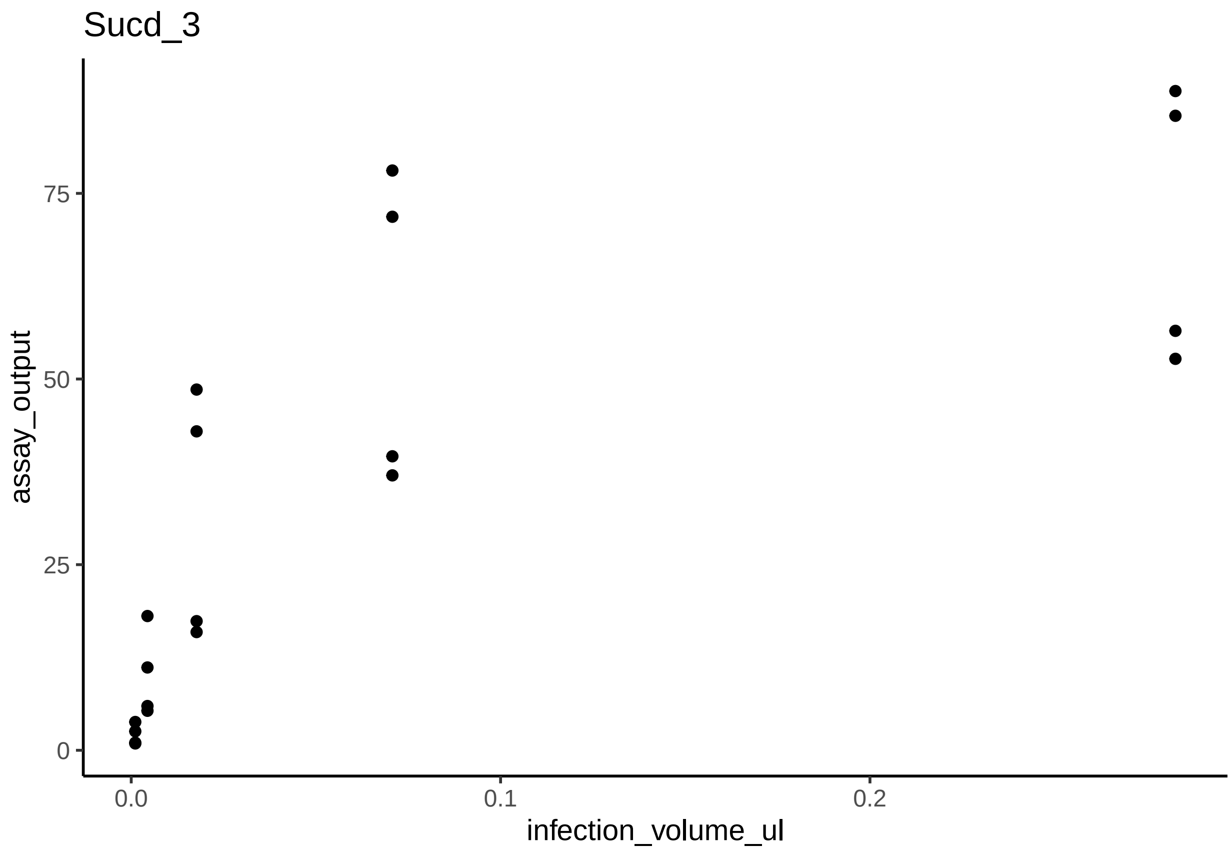

```
##
## [[109]]
```



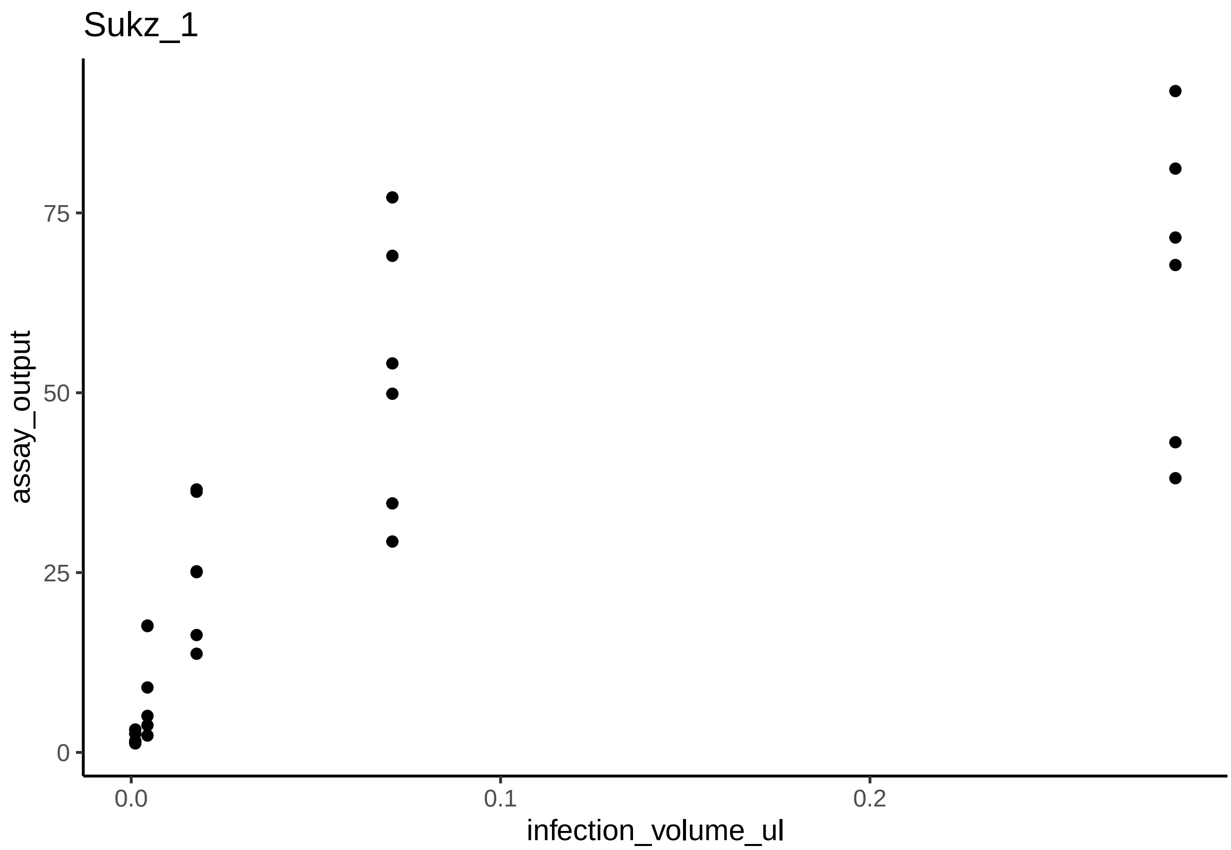

```
##
## [[110]]
```



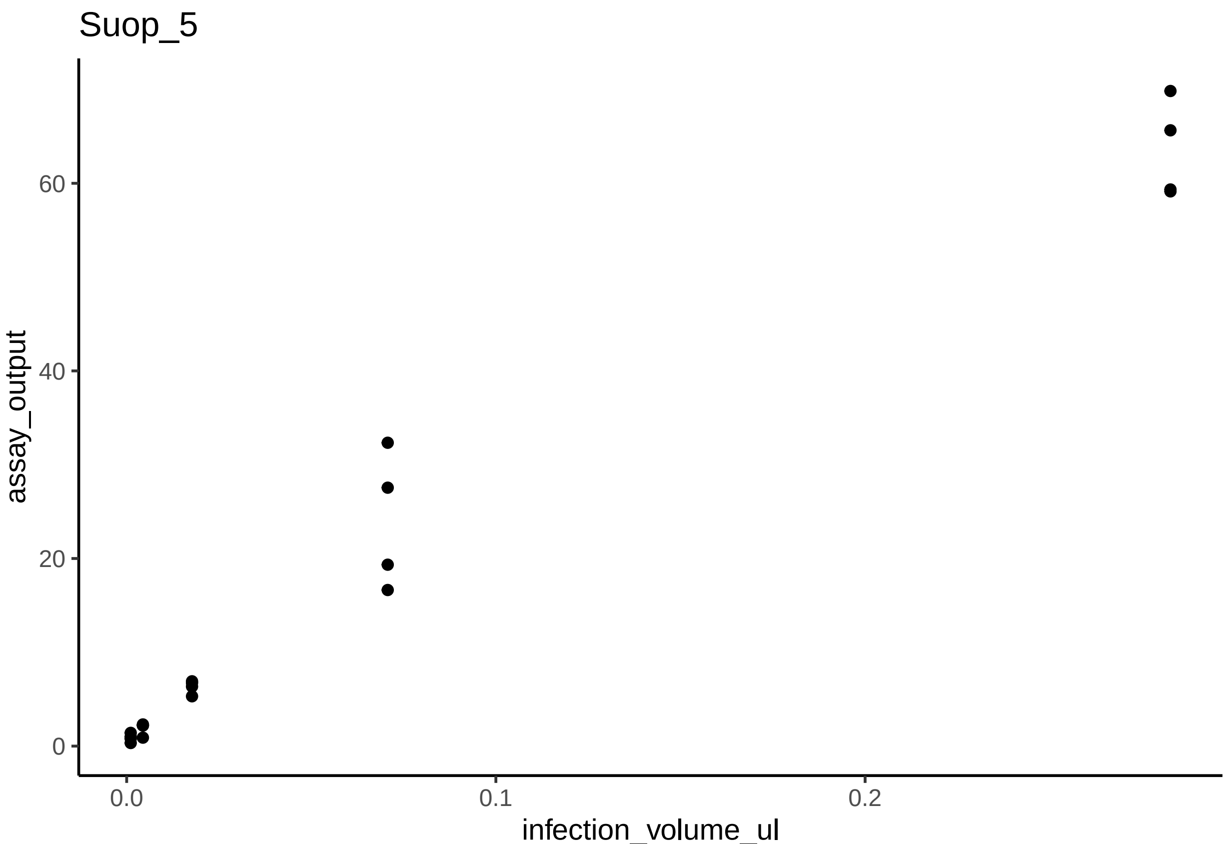

```
##
## [[111]]
```



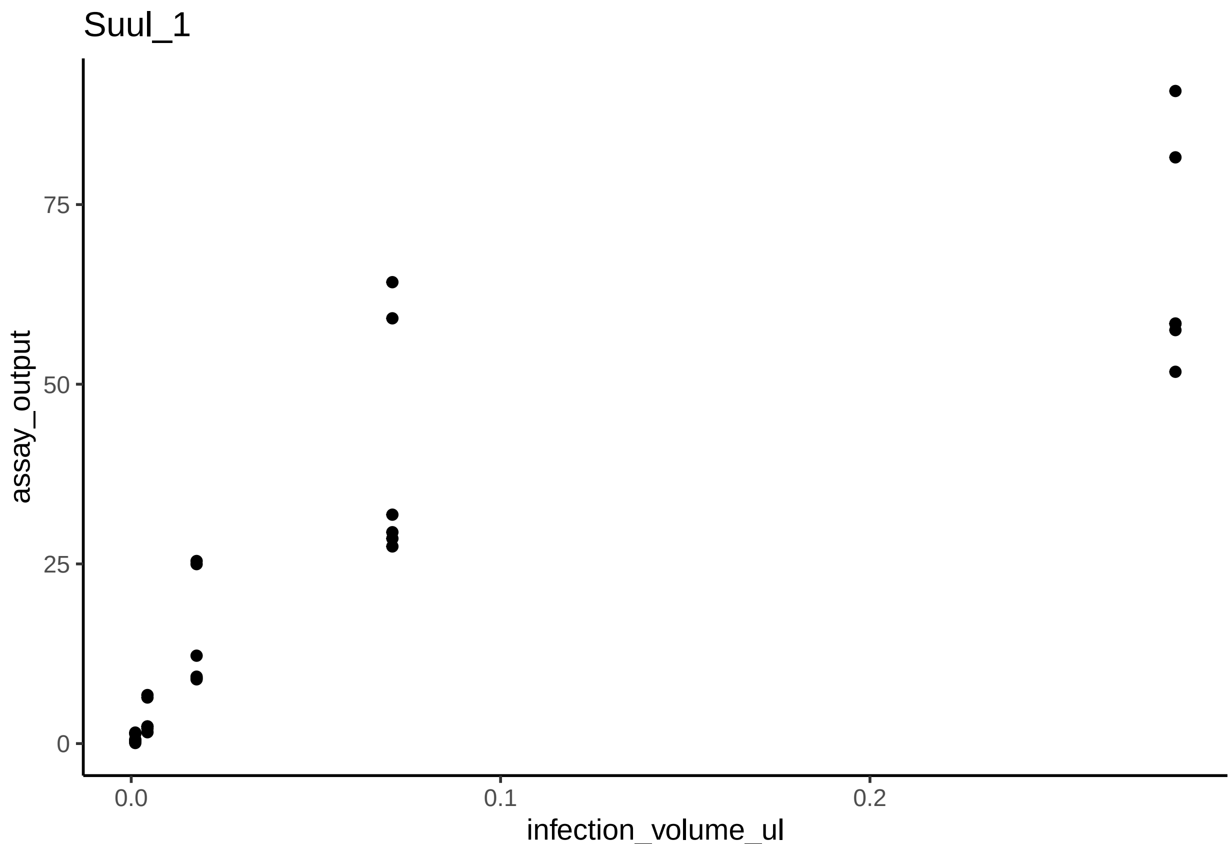

```
##
## [[112]]
```



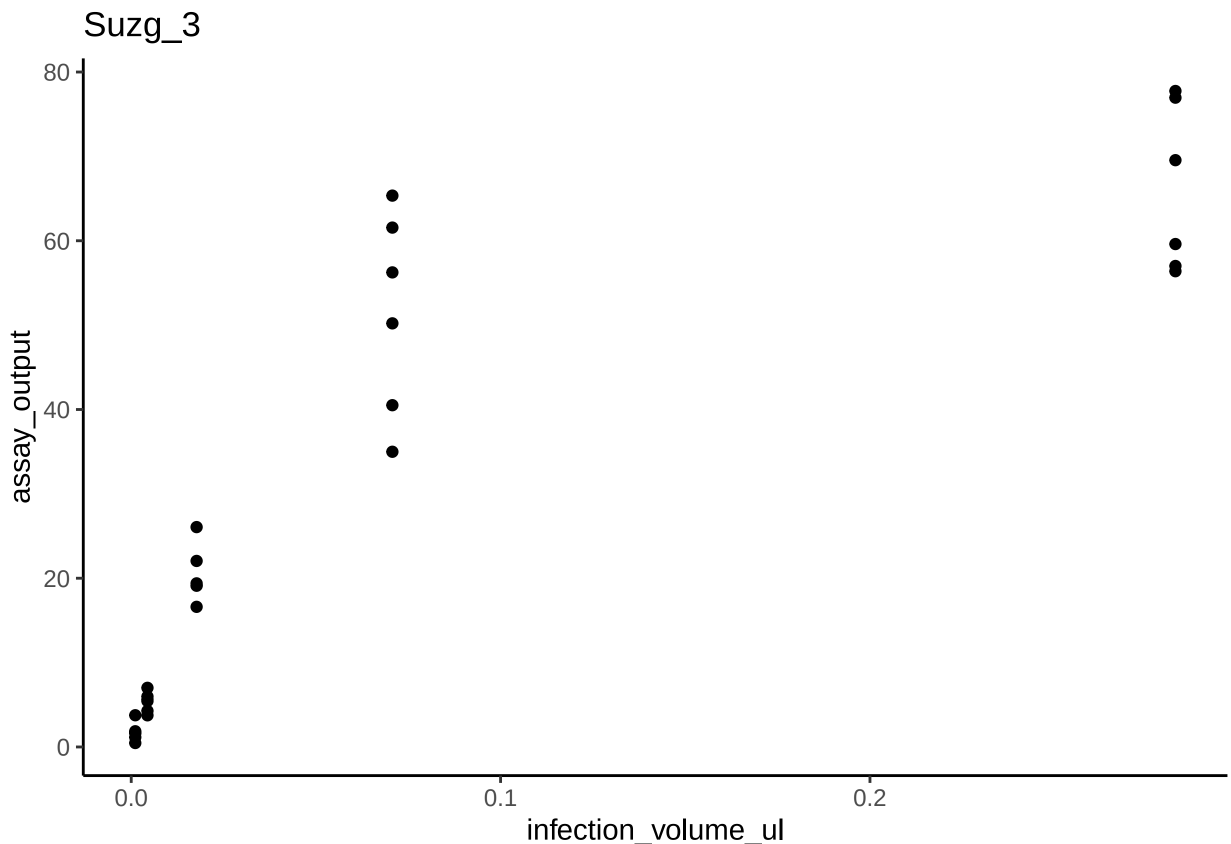

```
##
## [[113]]
```



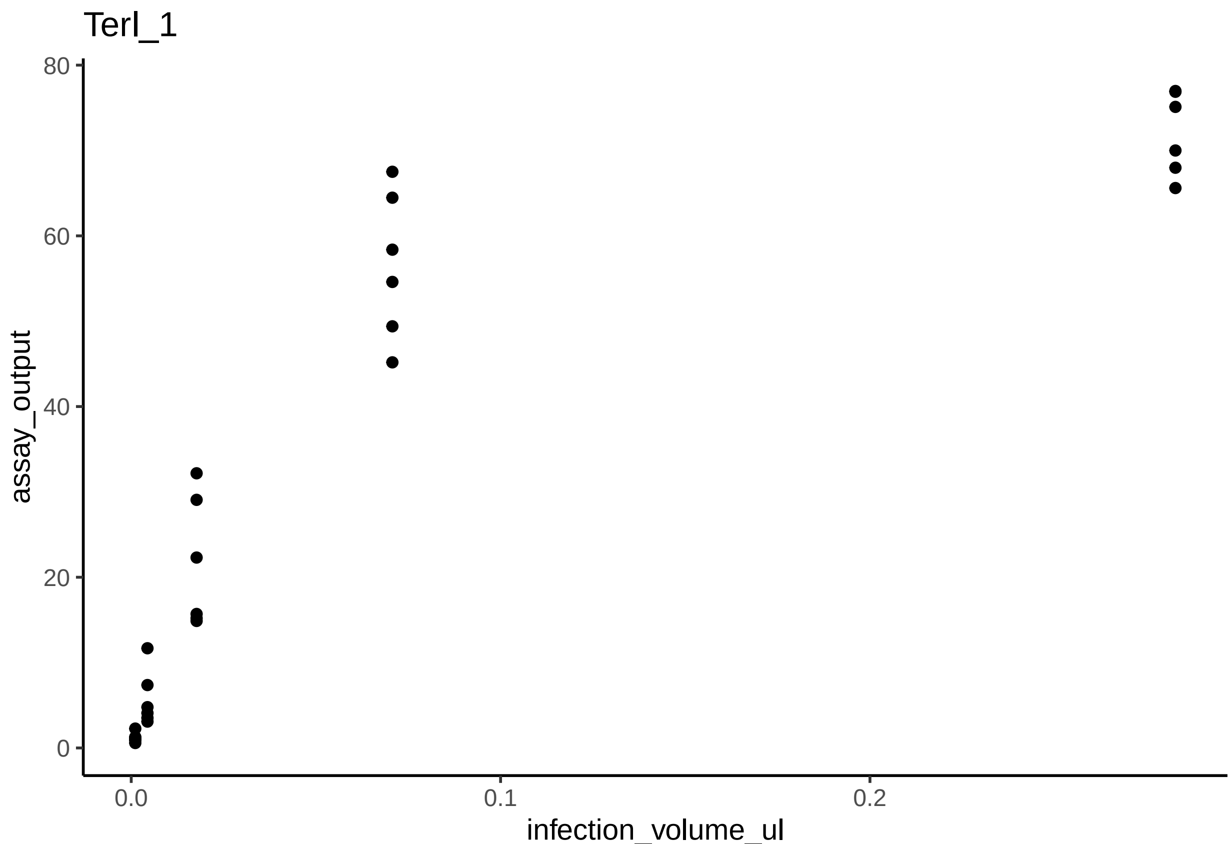

```
##
## [[114]]
```



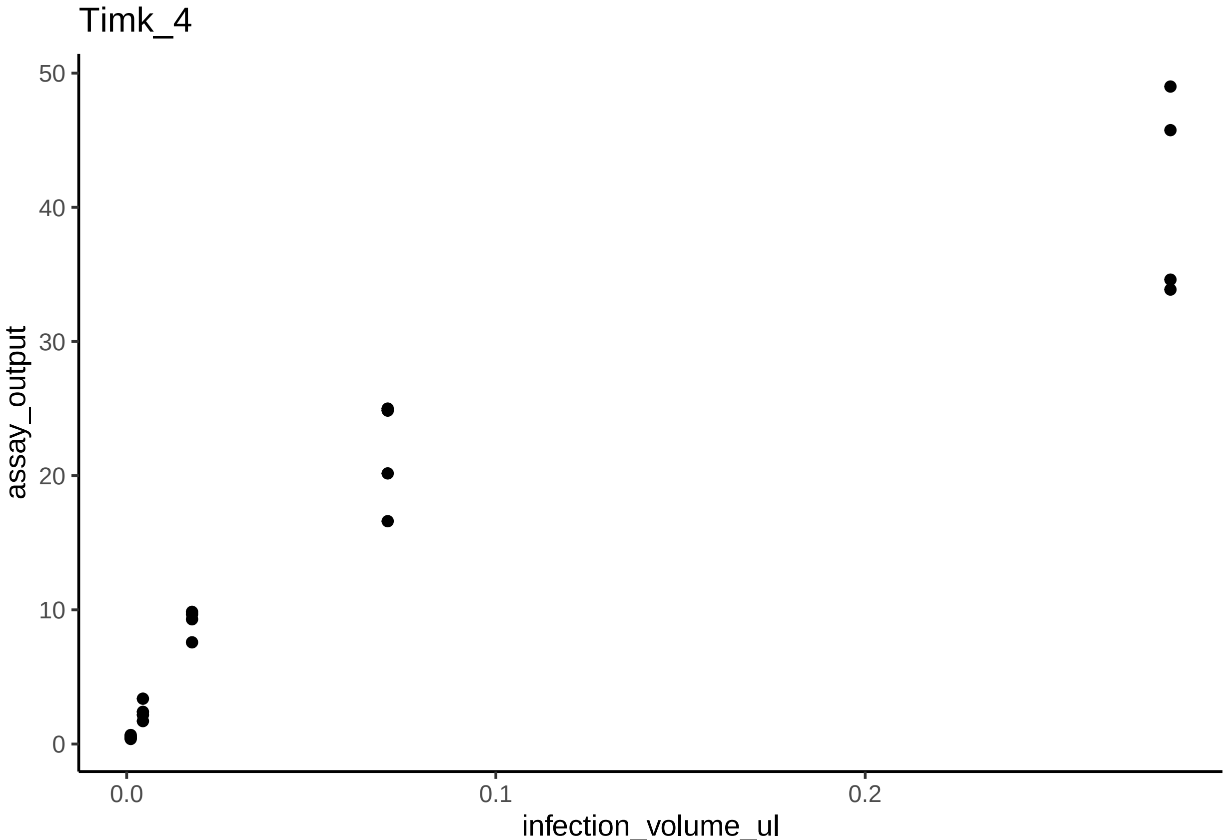

```
##
## [[115]]
```




```
##
## [[116]]
```

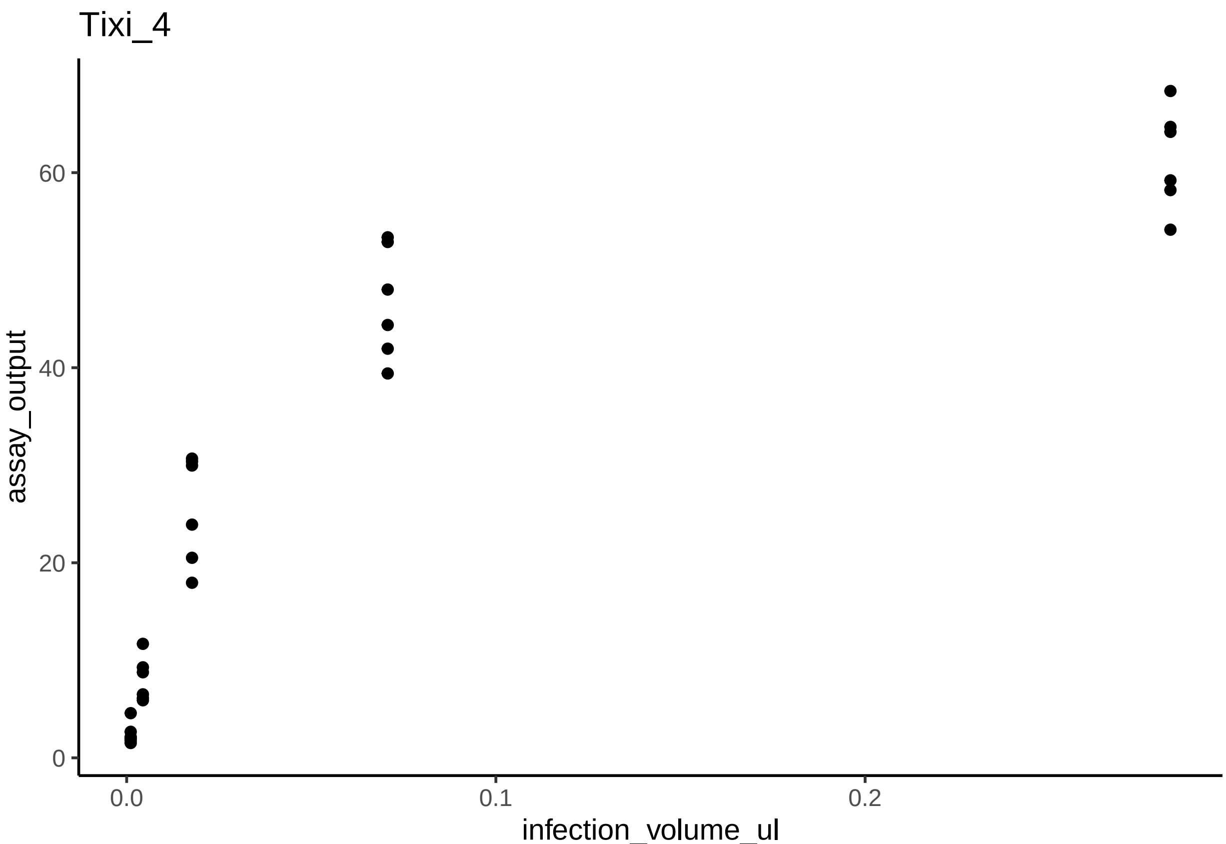



```
##
## [[117]]
```

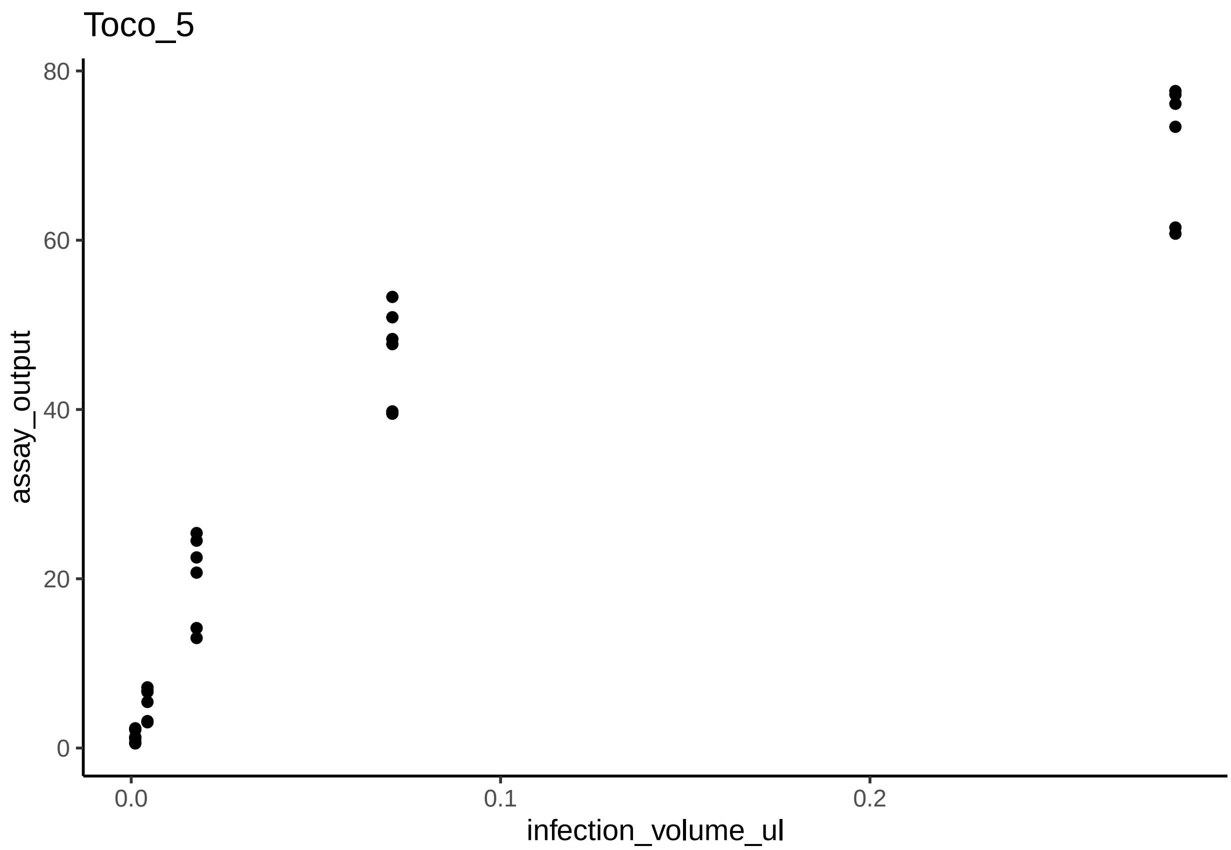


Timk_4
50
40
30
20
10
0
assay_output
0.0
0.1
0.2
infection_volume_ul

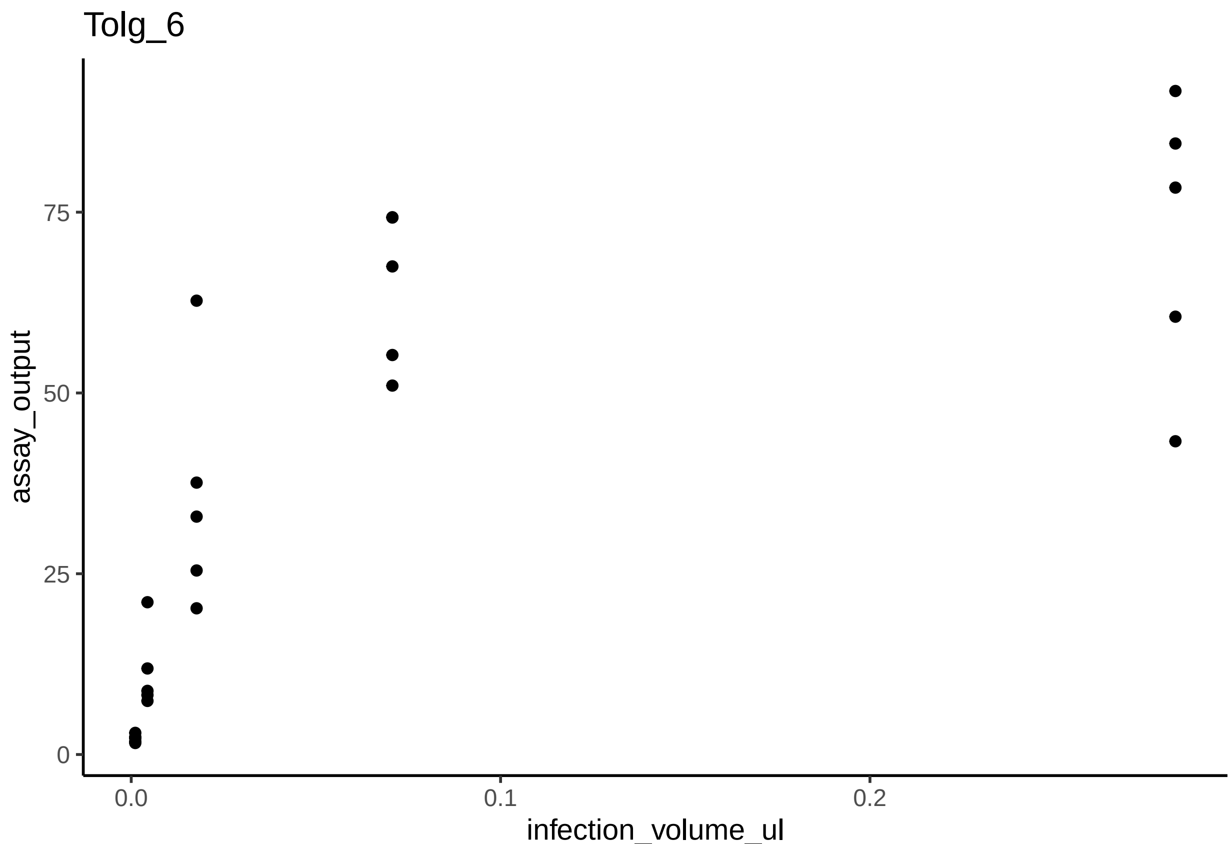

```
##
## [[118]]
```



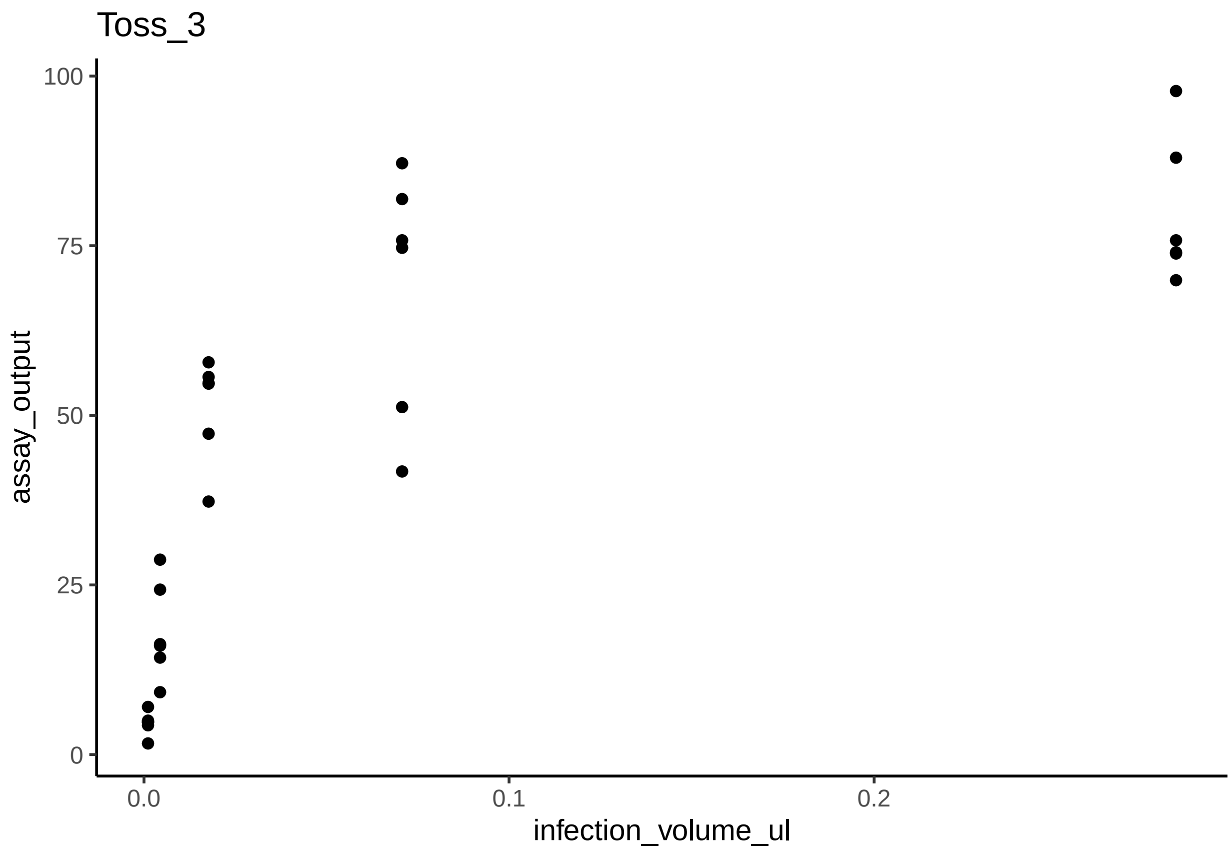

```
##
## [[119]]
```



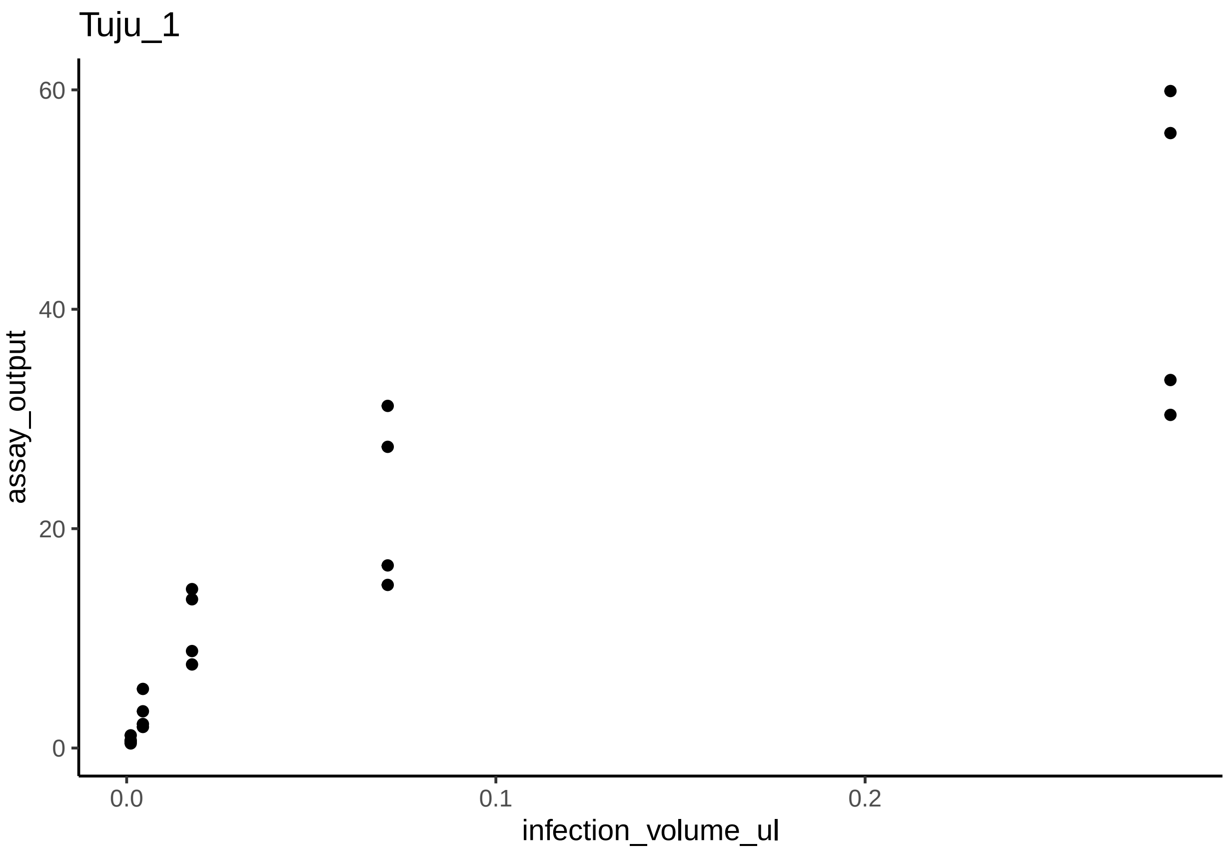

```
##
## [[120]]
```



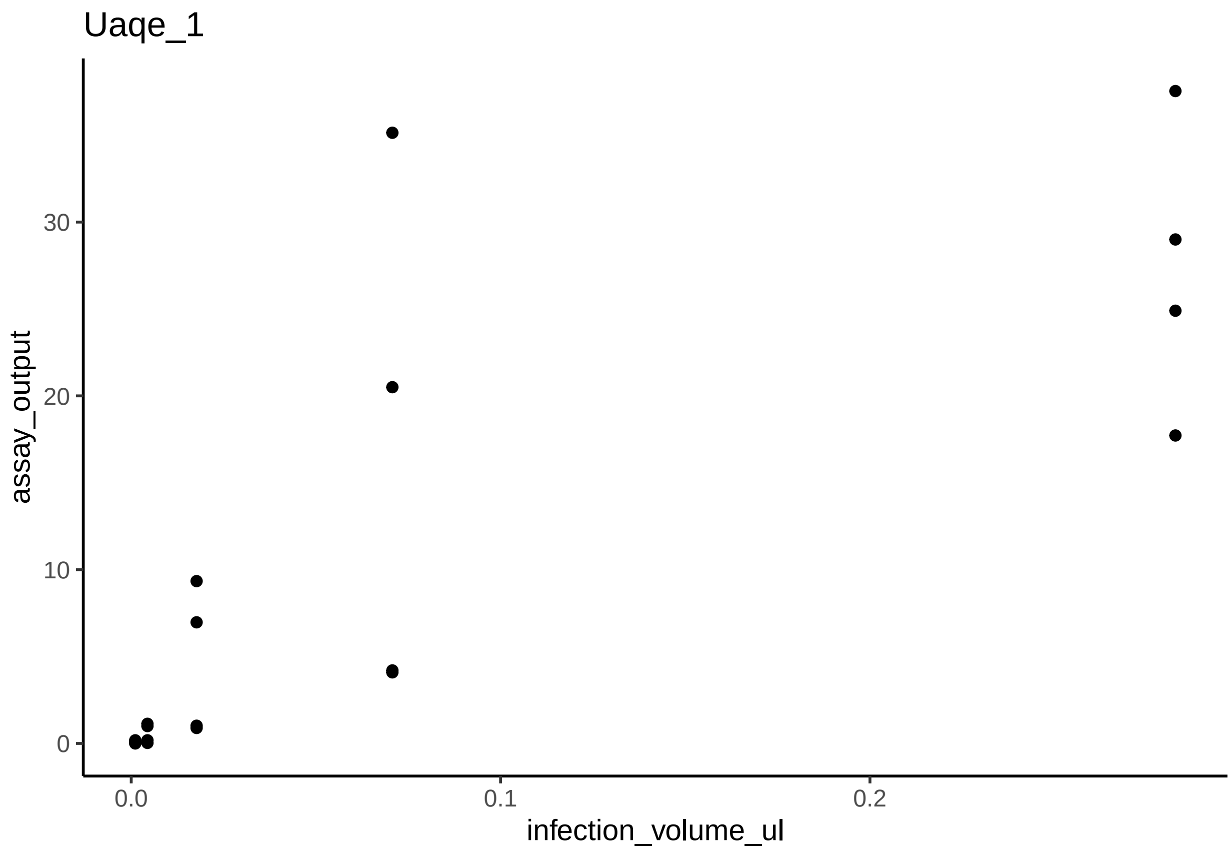

```
##
## [[121]]
```



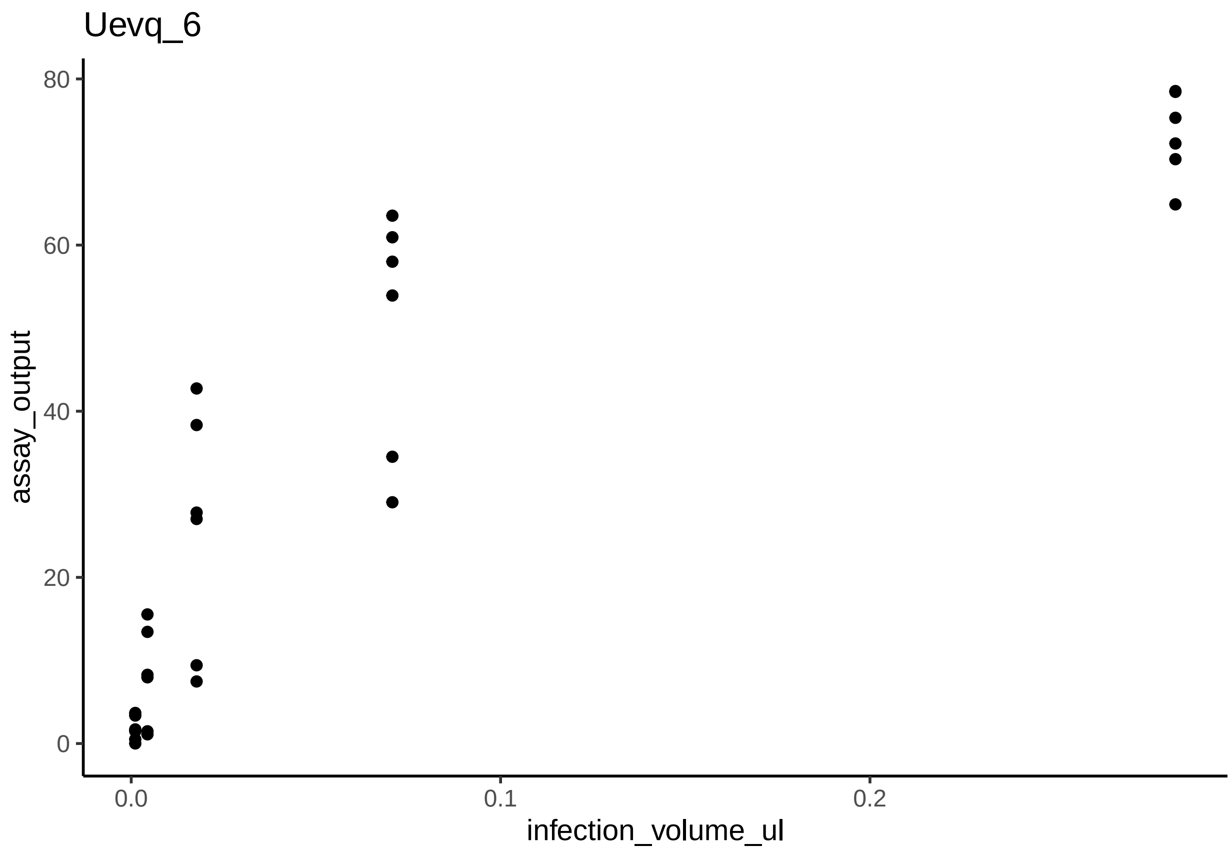

```
##
## [[122]]
```



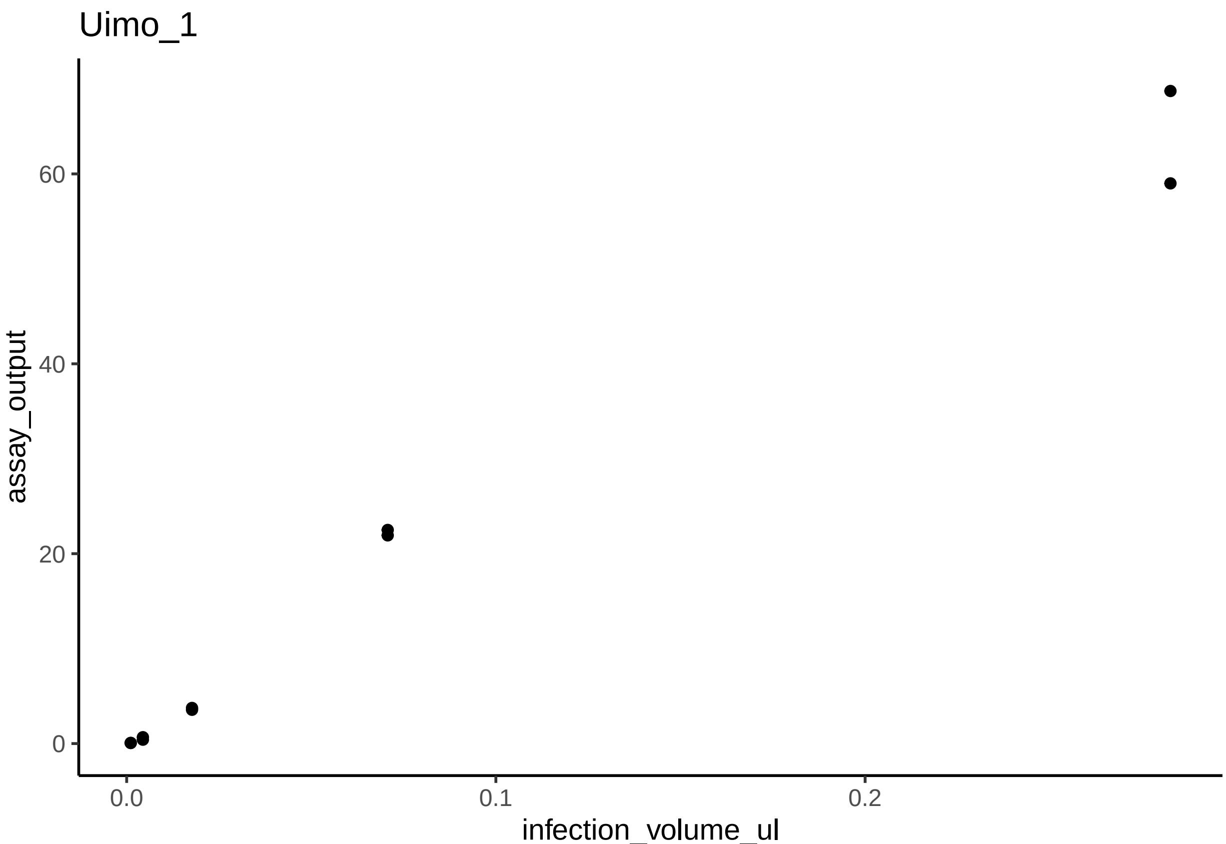

```
##
## [[123]]
```



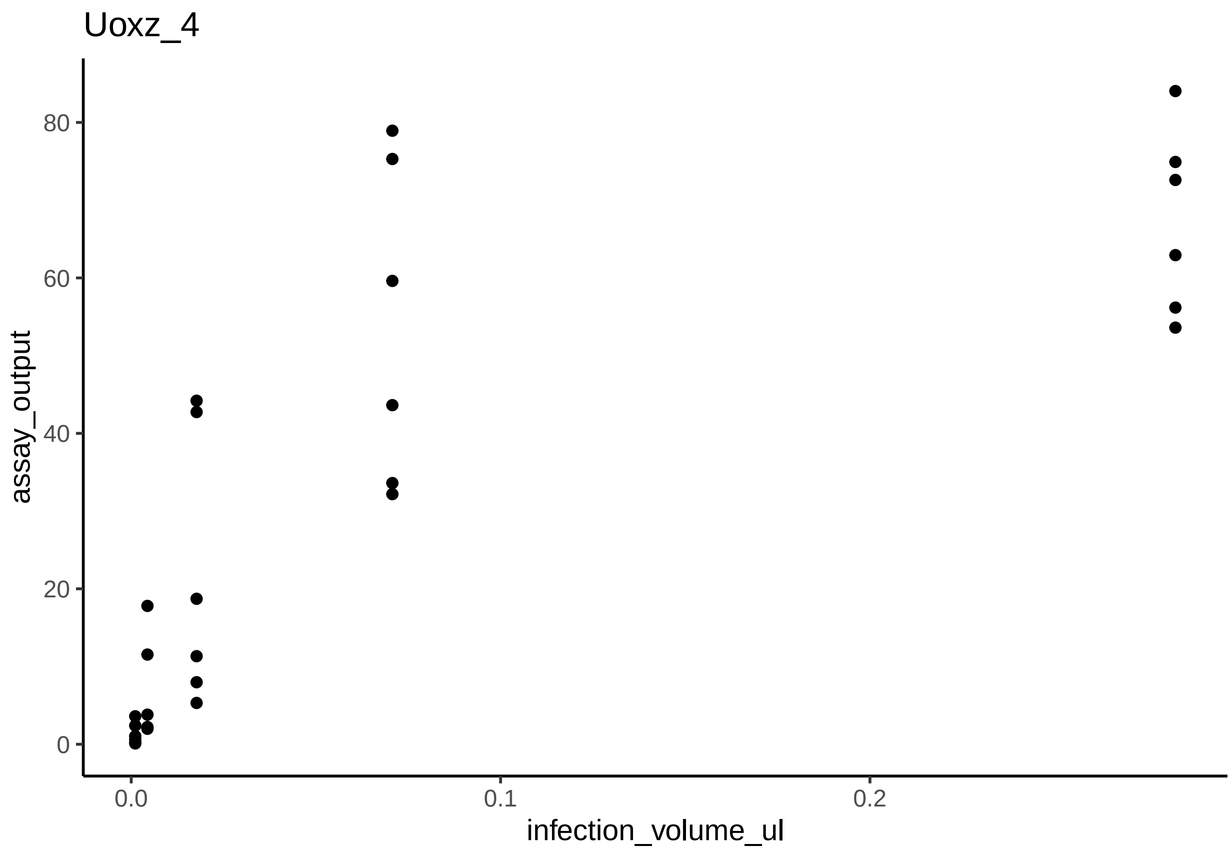

```
##
## [[124]]
```



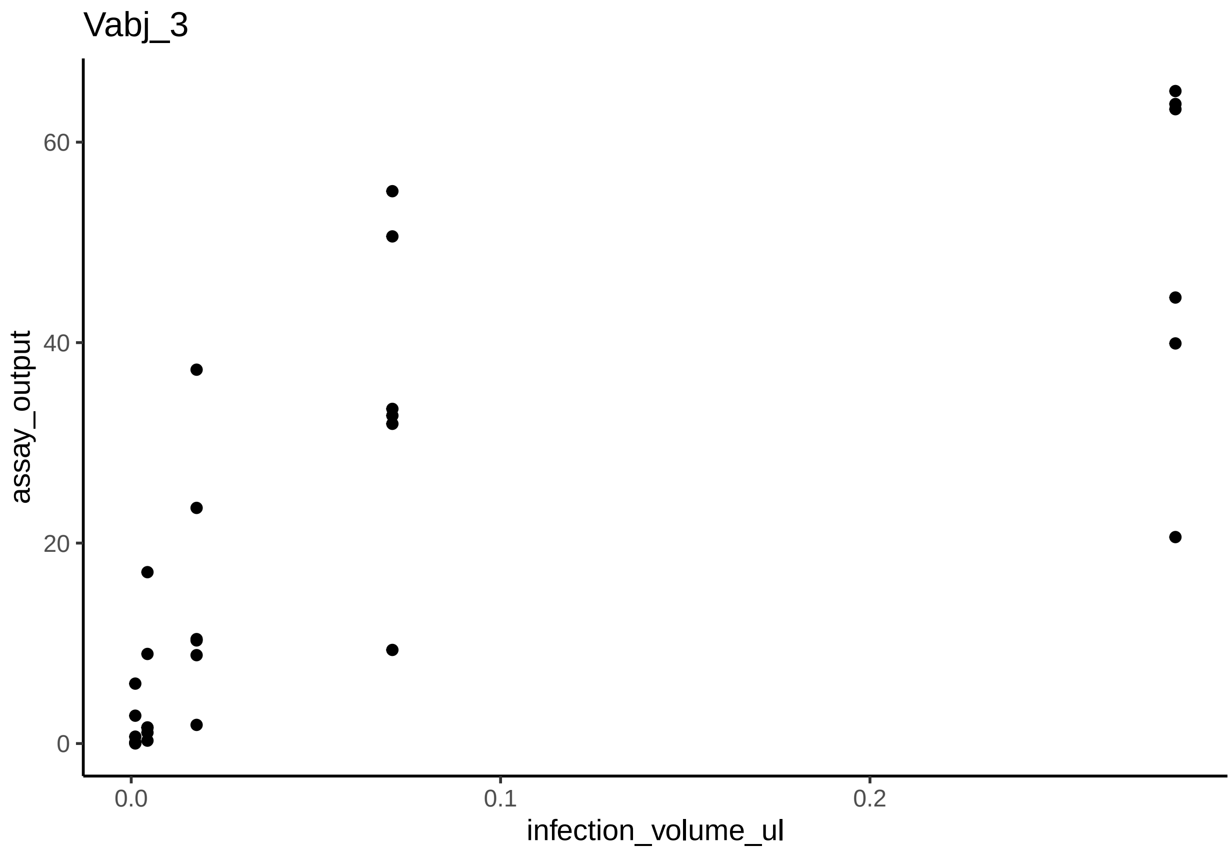

```
##
## [[125]]
```



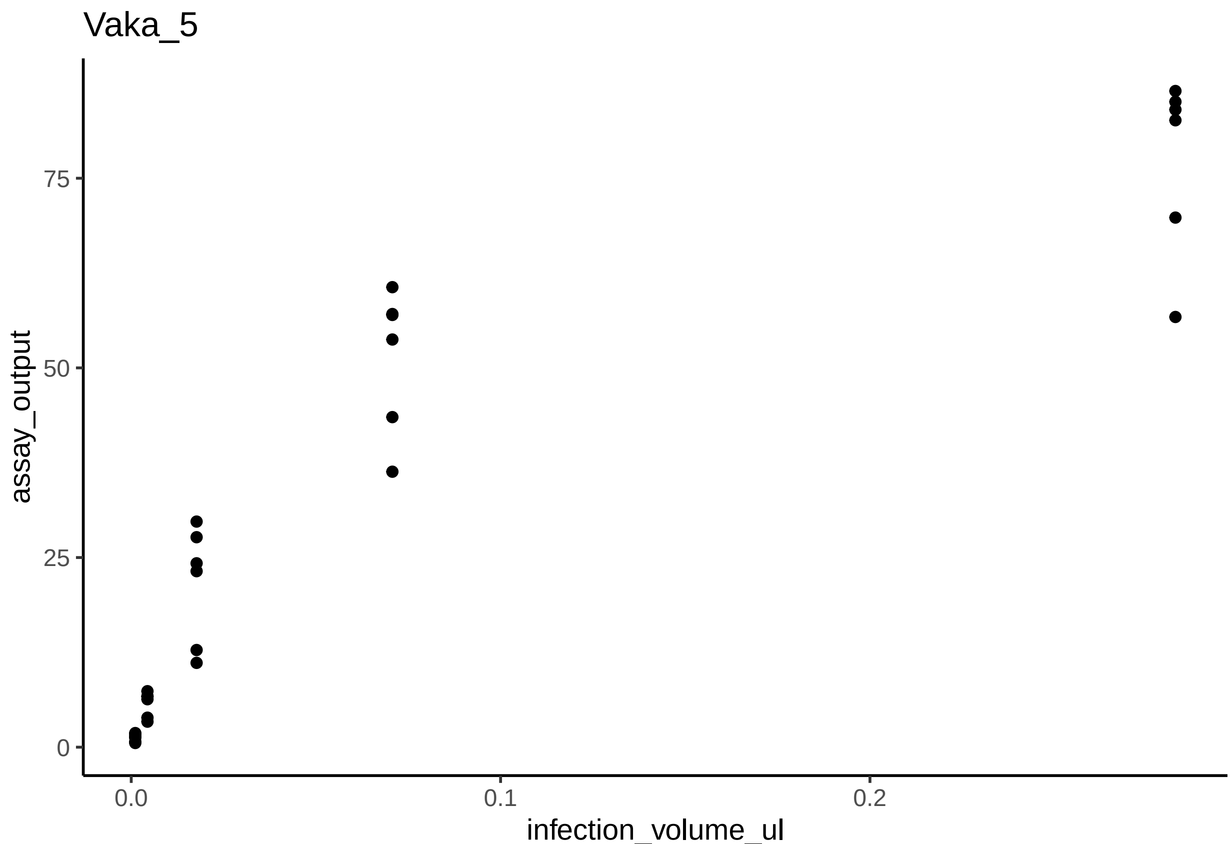

```
##
## [[126]]
```



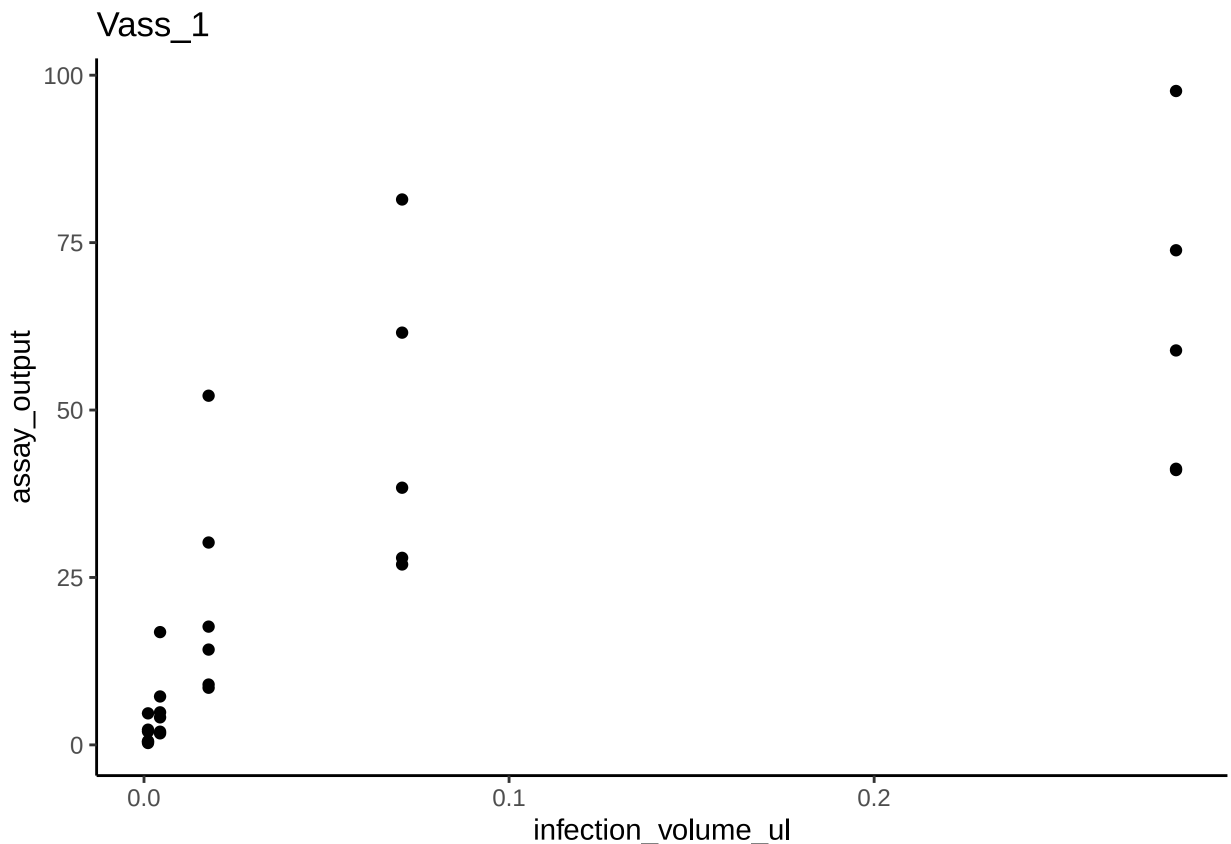

```
##
## [[127]]
```



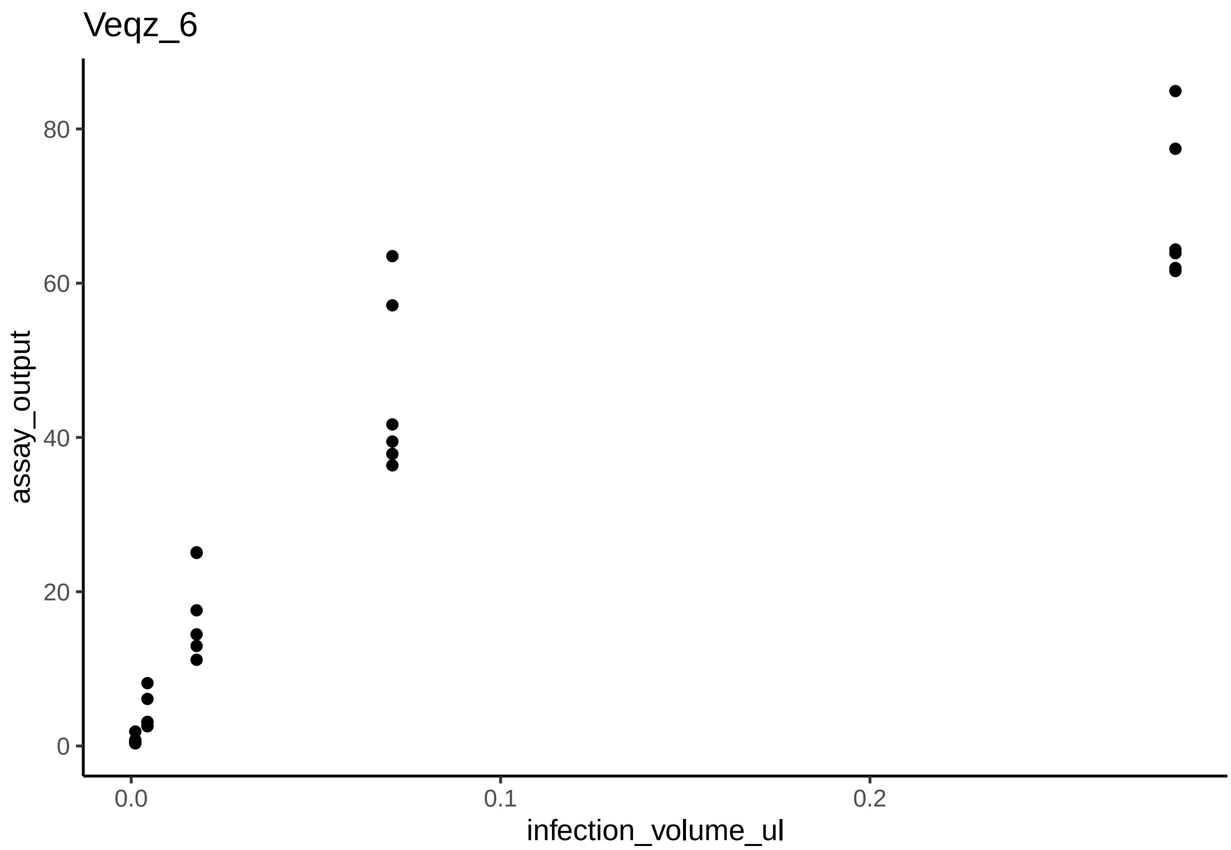

```
##
## [[128]]
```



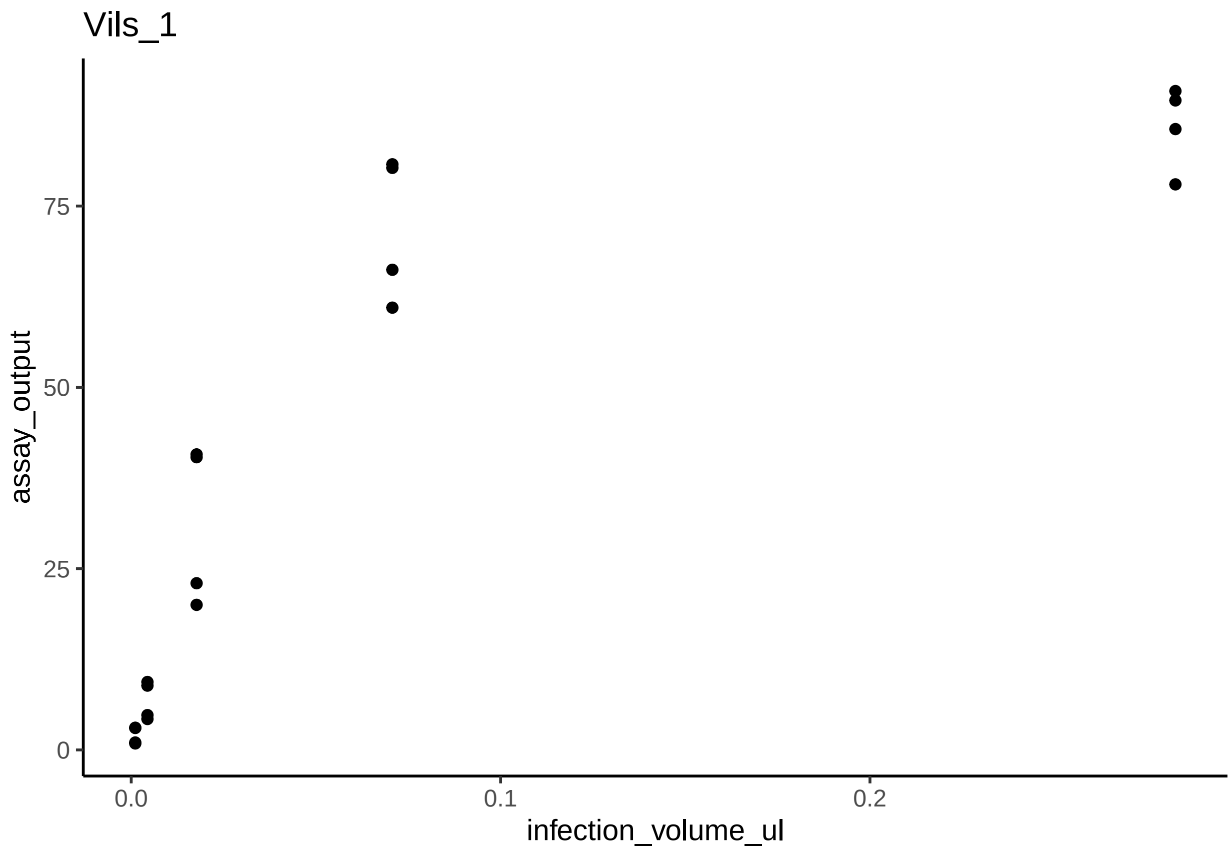

```
##
## [[129]]
```



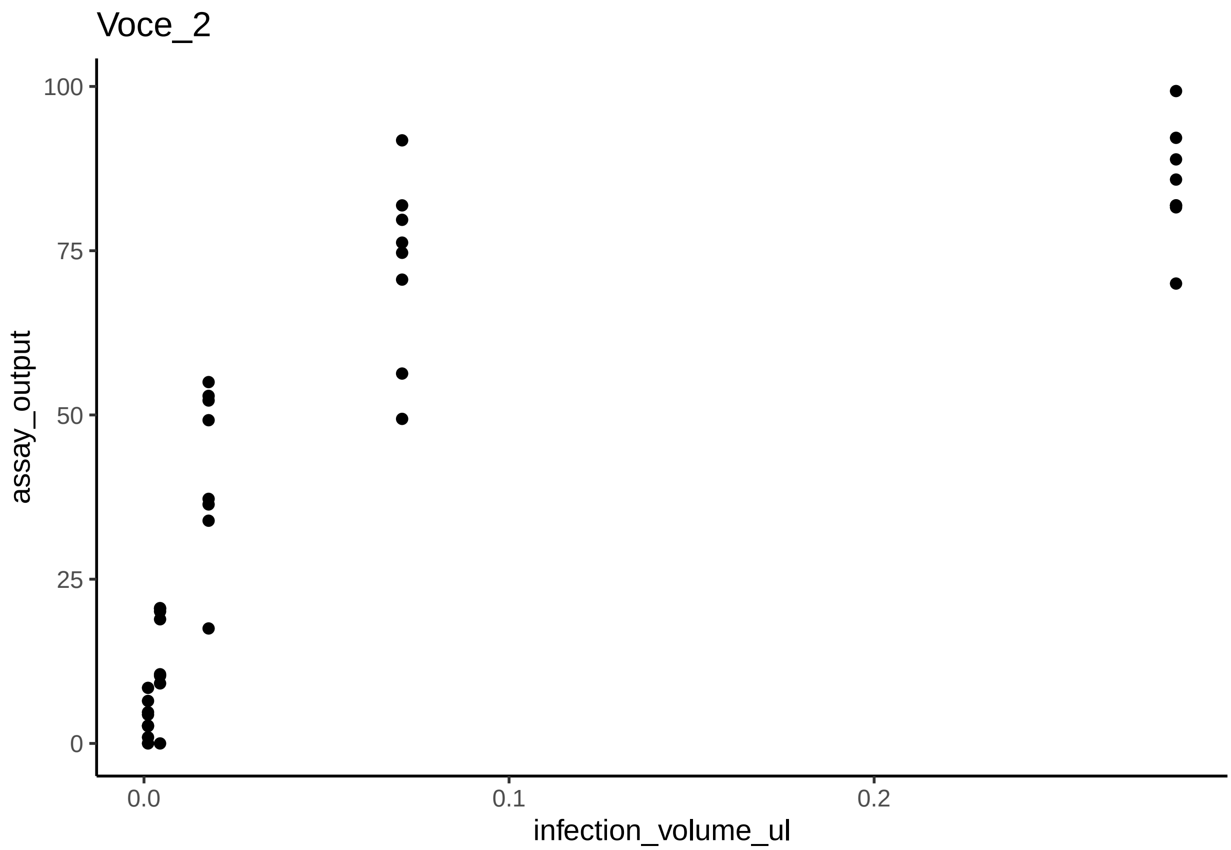

```
##
## [[130]]
```



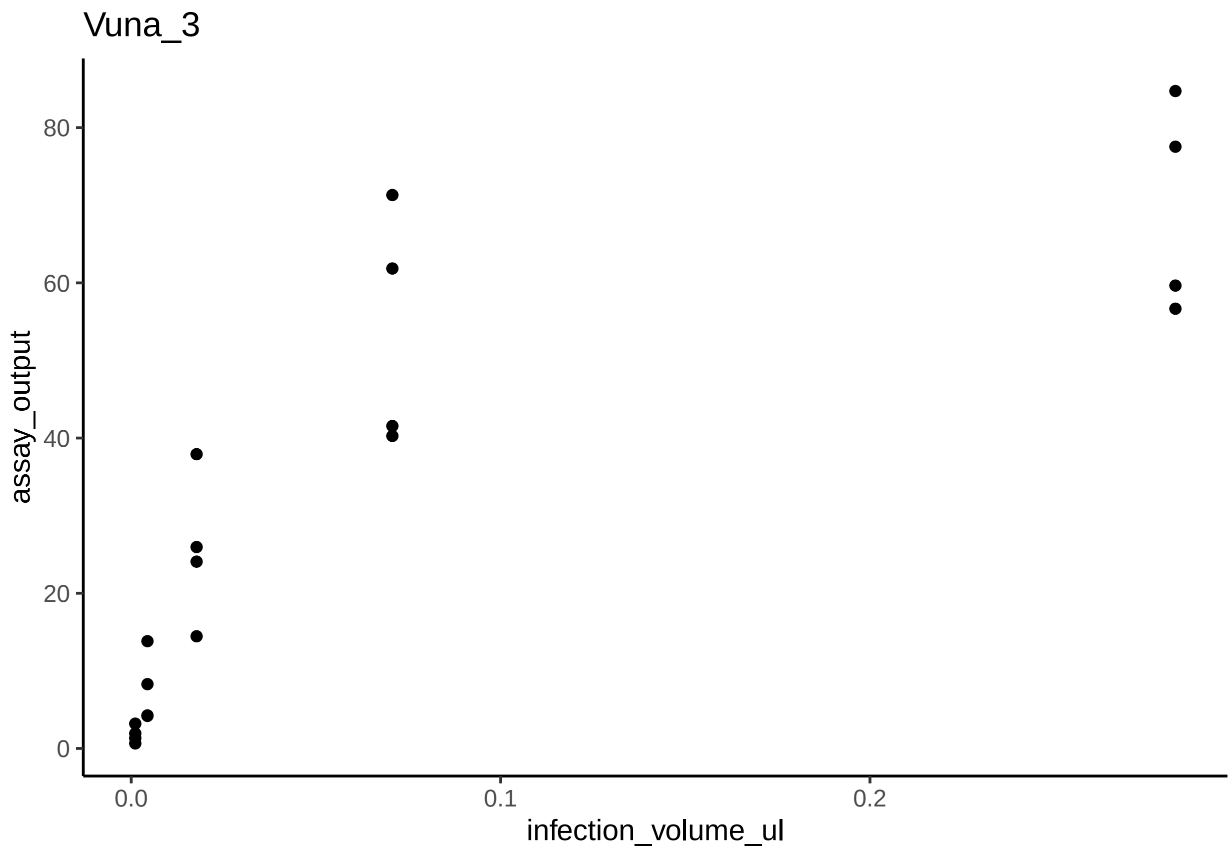

```
##
## [[131]]
```



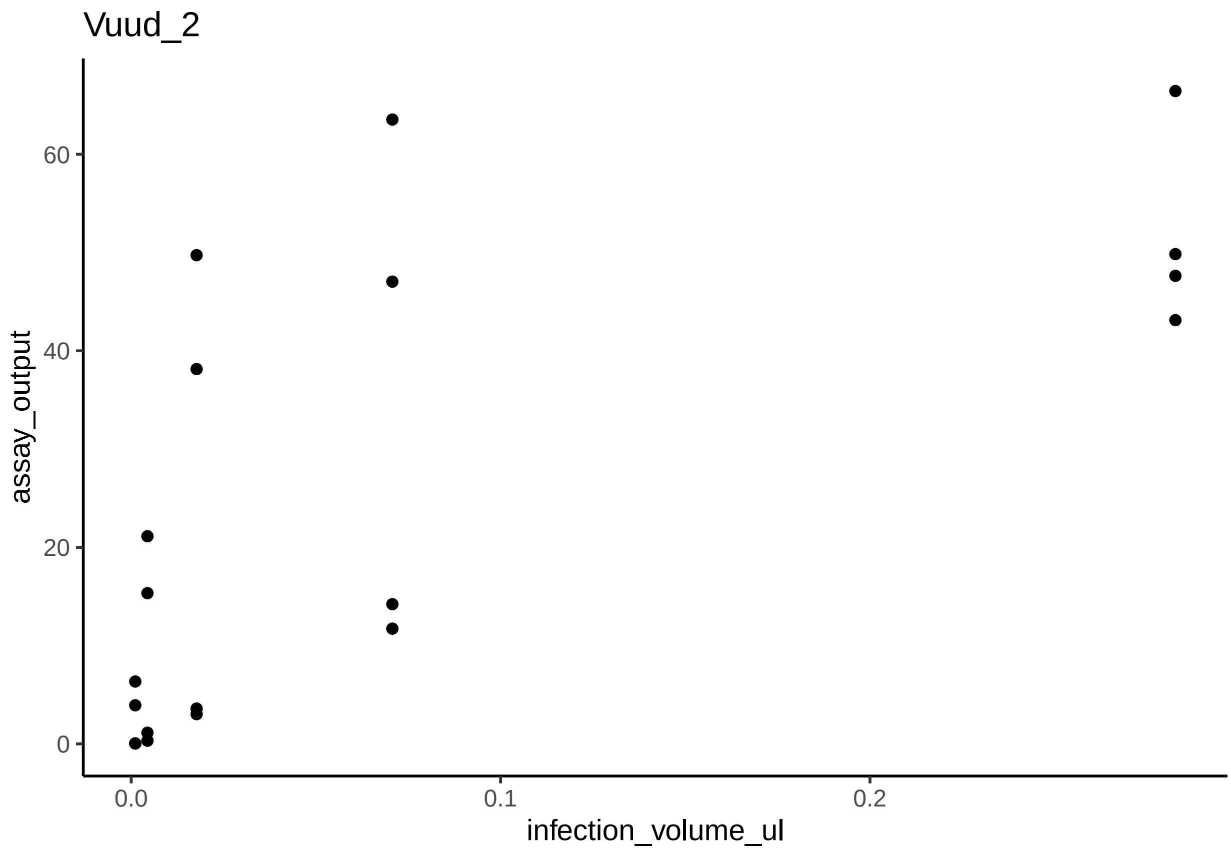

```
##
## [[132]]
```



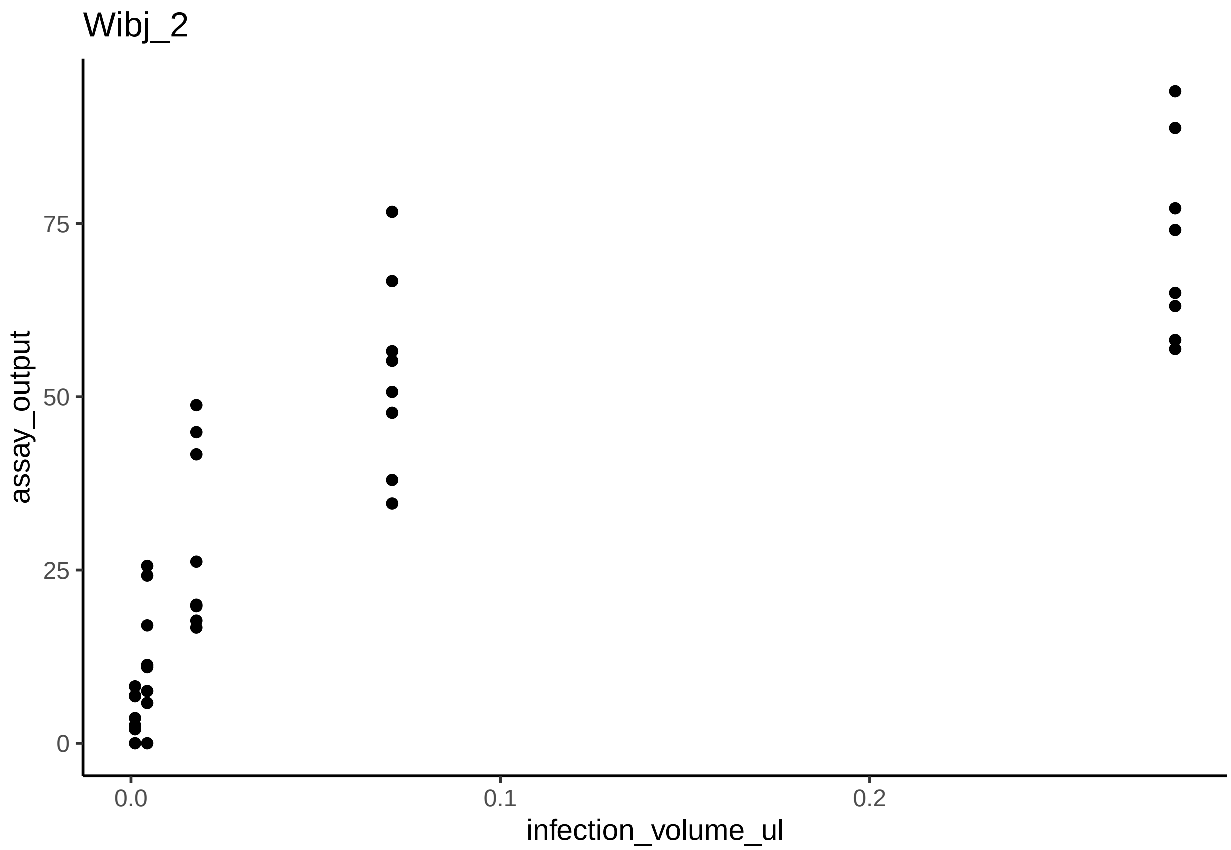

```
##
## [[133]]
```



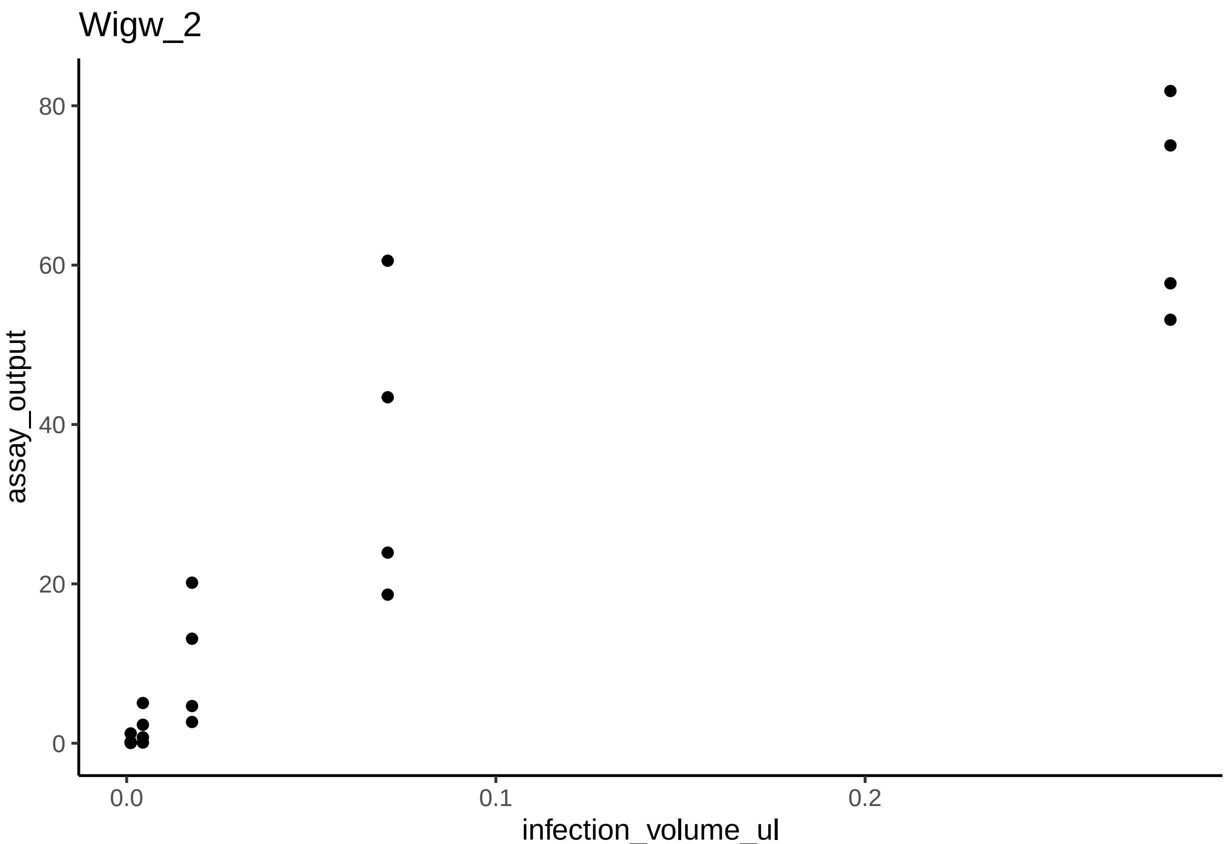

```
##
## [[134]]
```



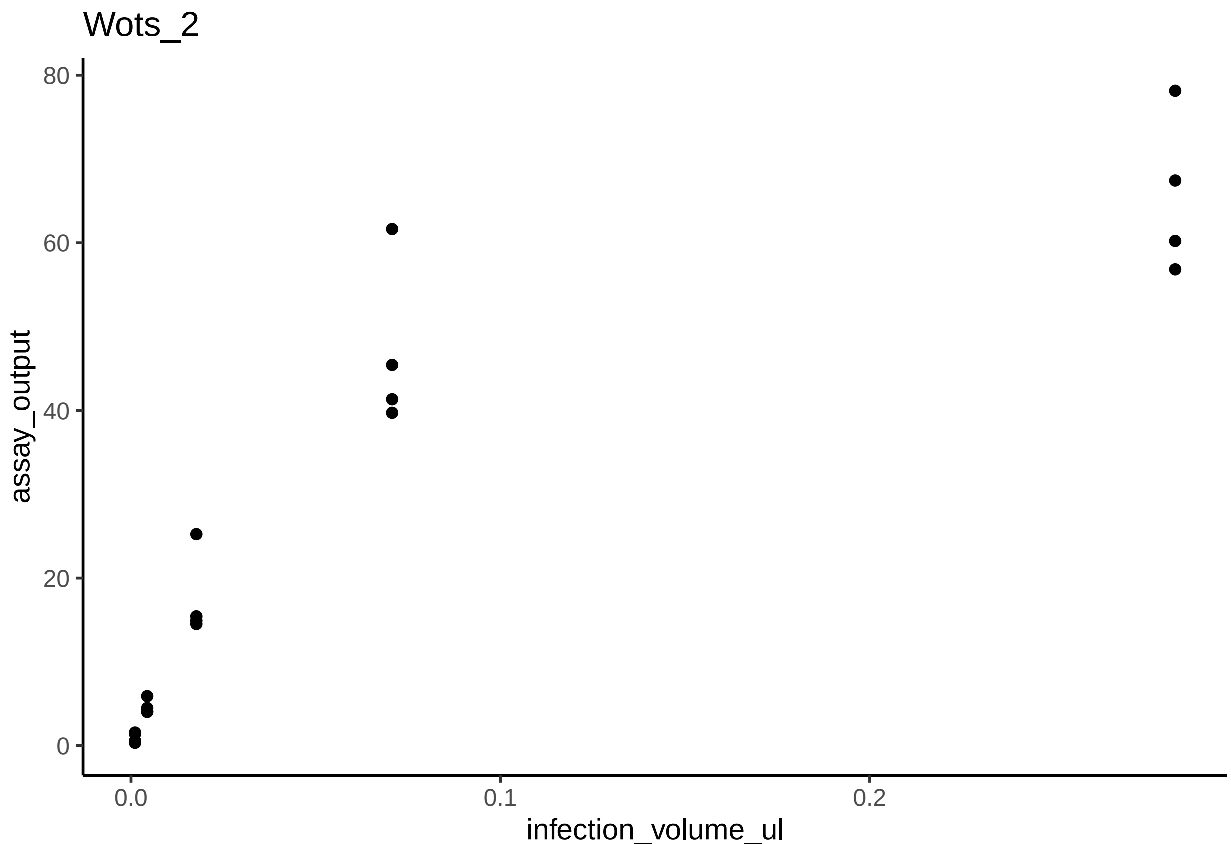

```
##
## [[135]]
```



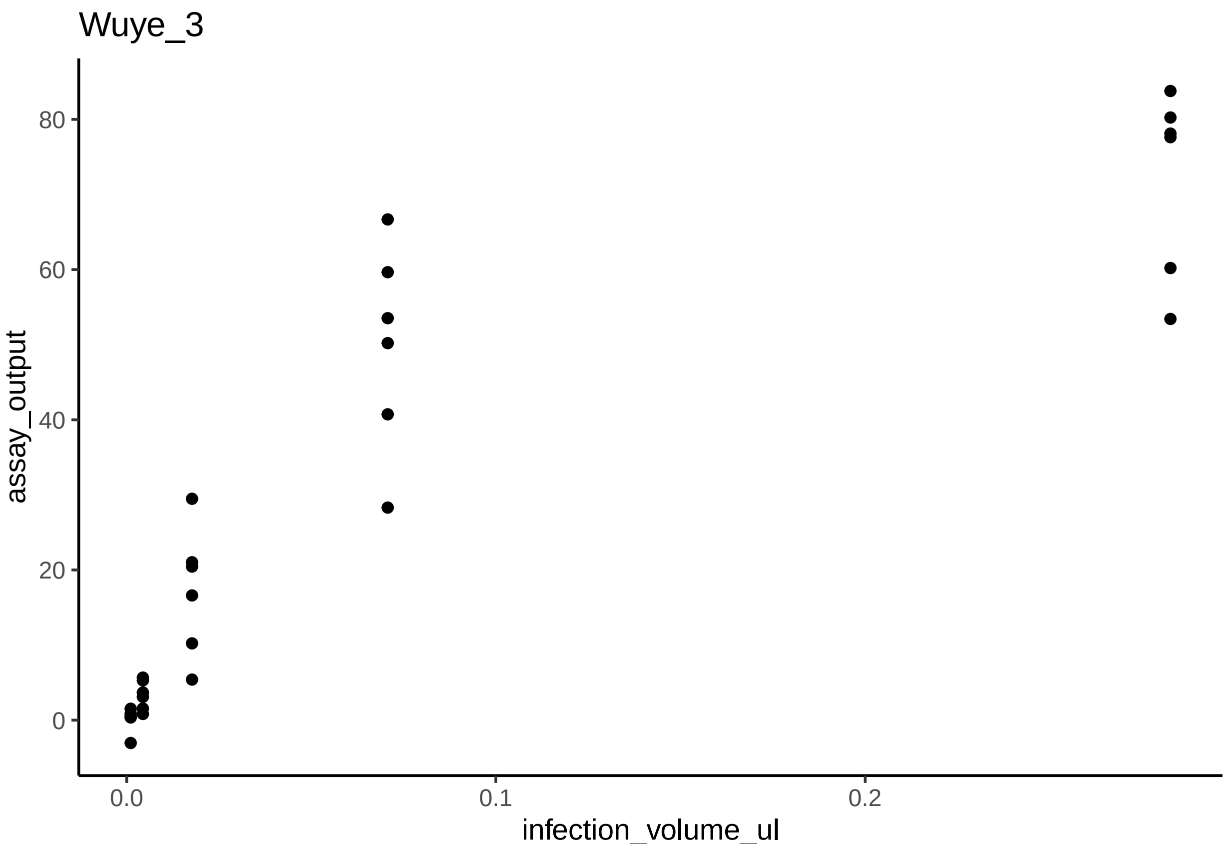

```
##
## [[136]]
```



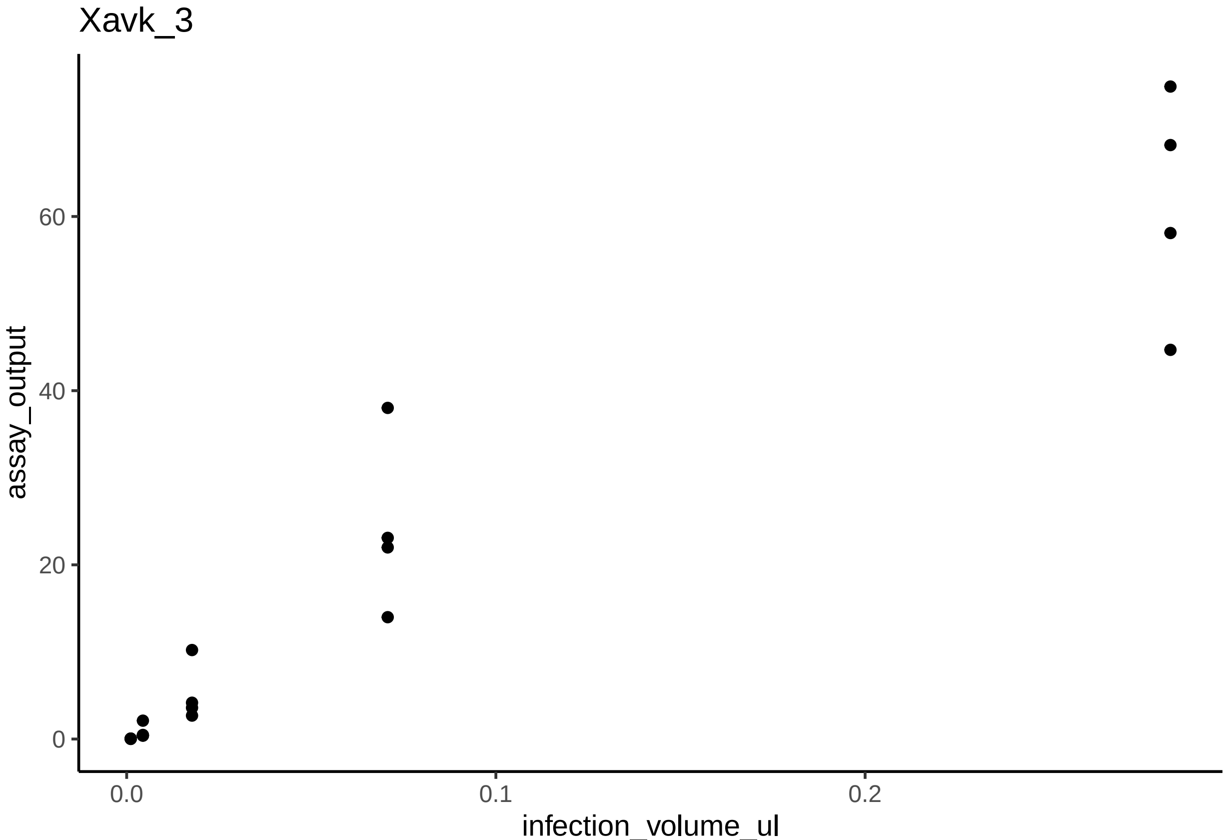

```
##
## [[137]]
```



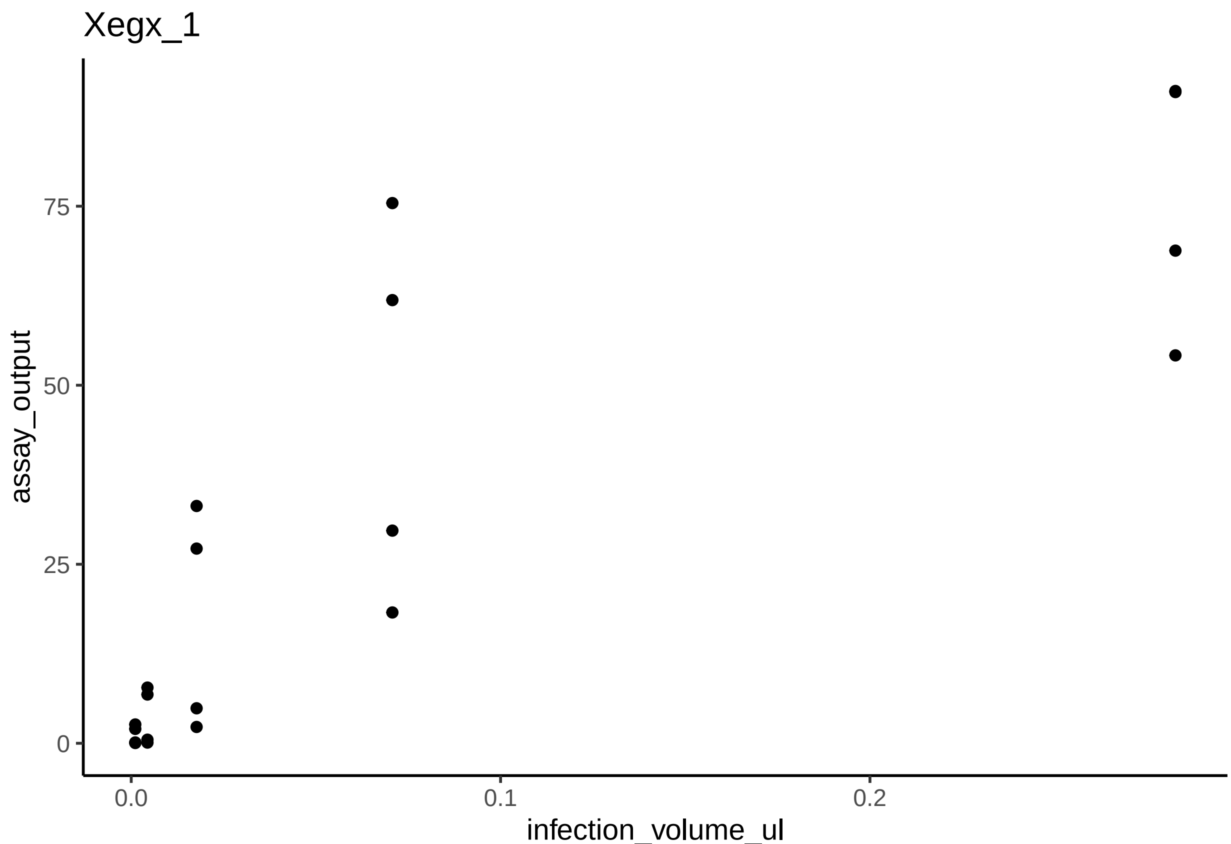

```
##
## [[138]]
```



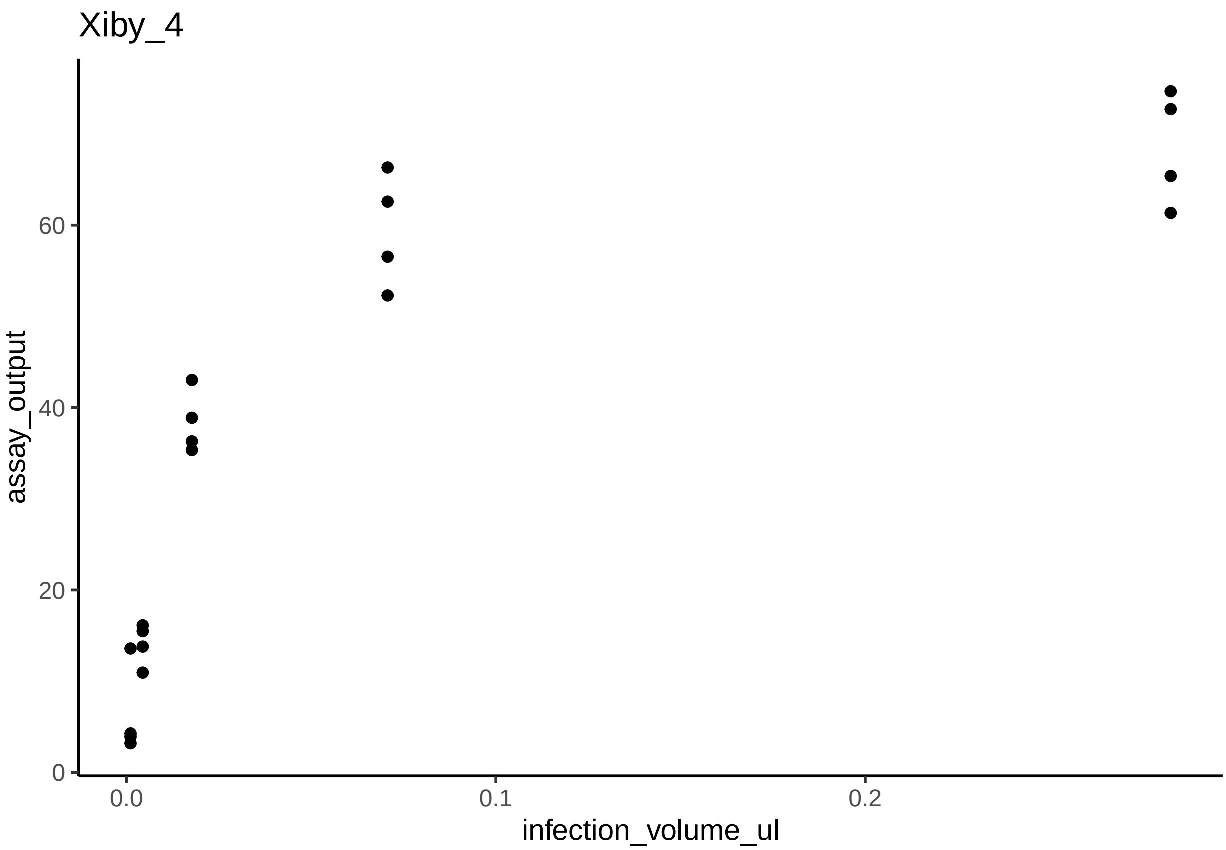

```
##
## [[139]]
```



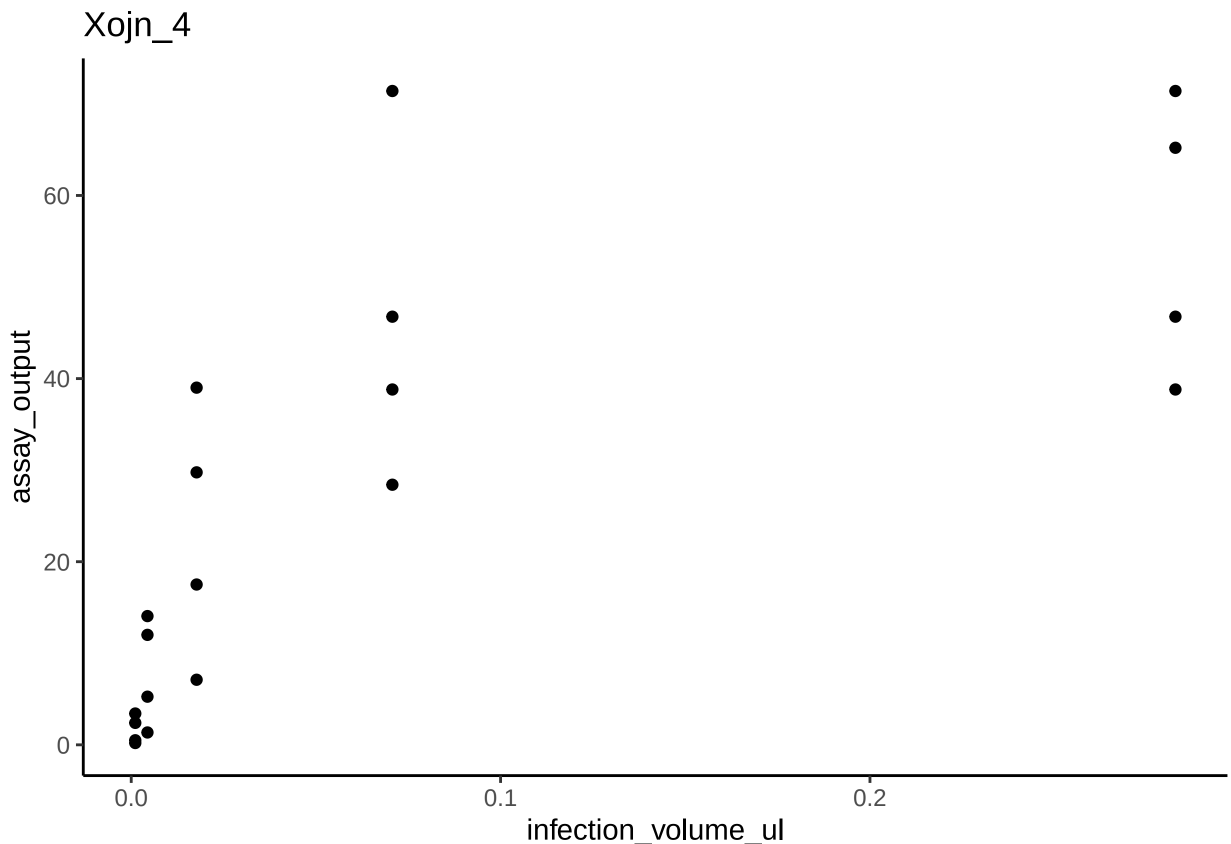

```
##
## [[140]]
```



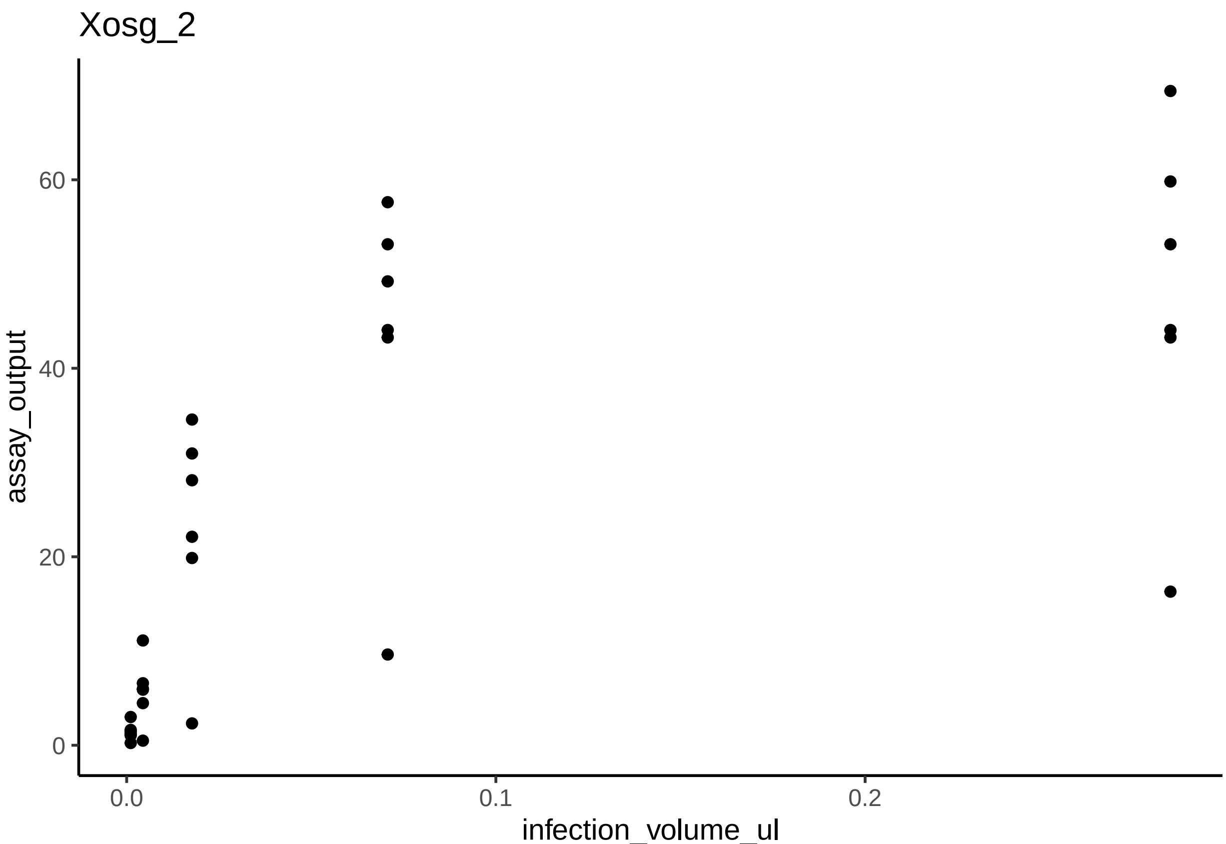

```
##
## [[141]]
```



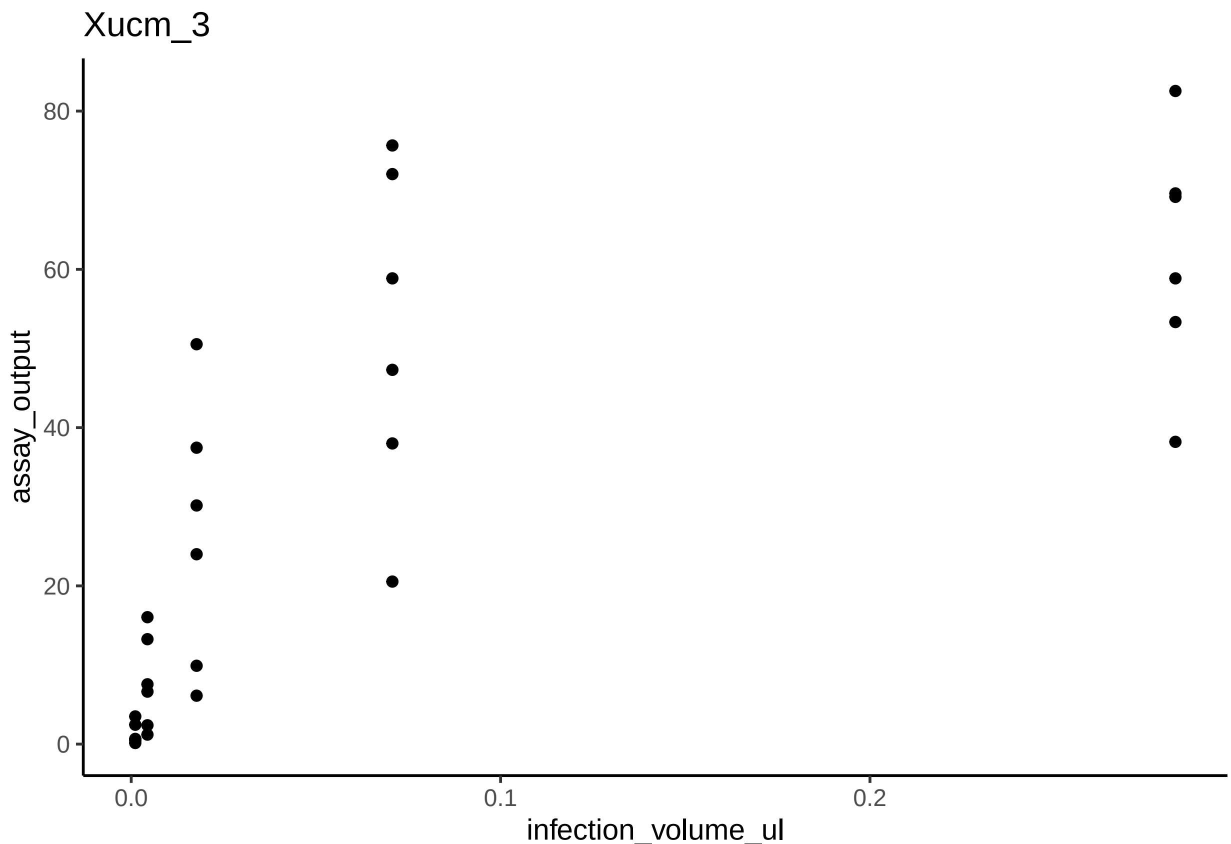

```
##
## [[142]]
```



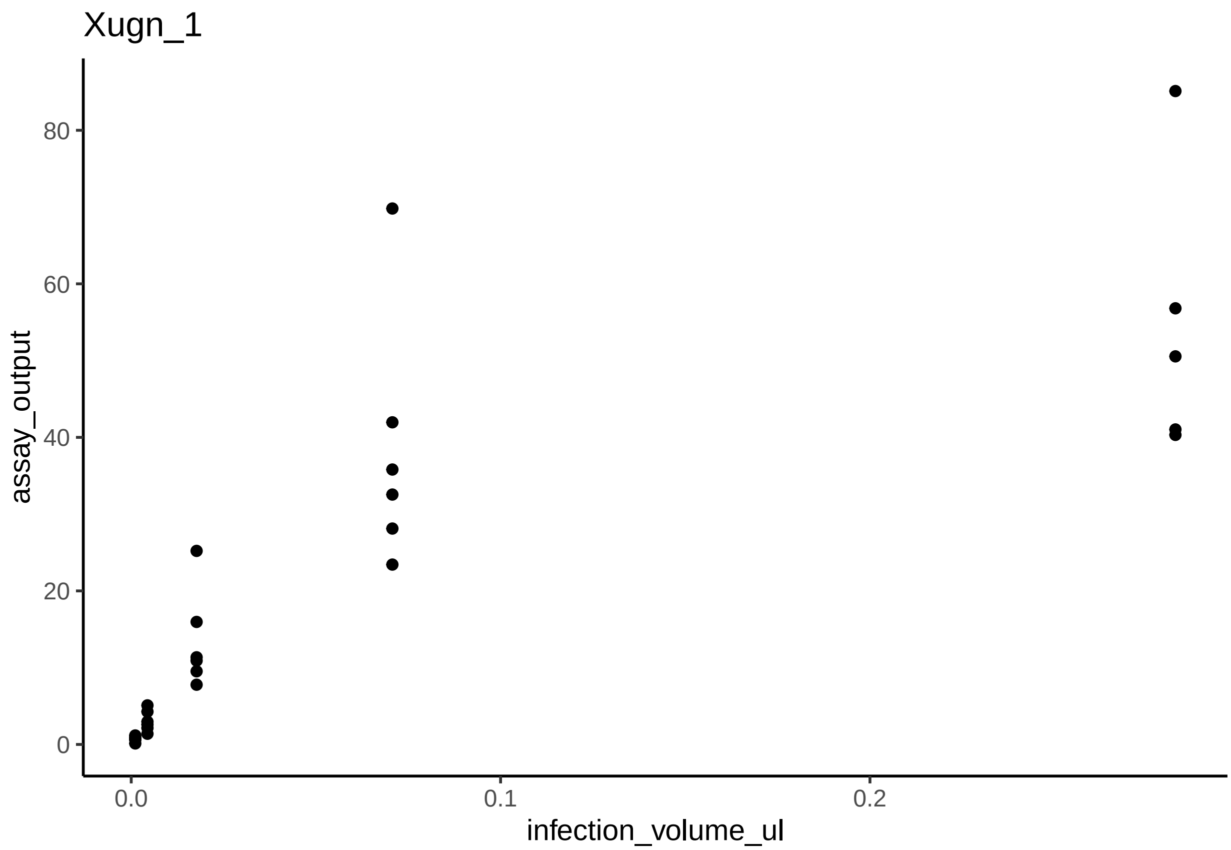

```
##
## [[143]]
```



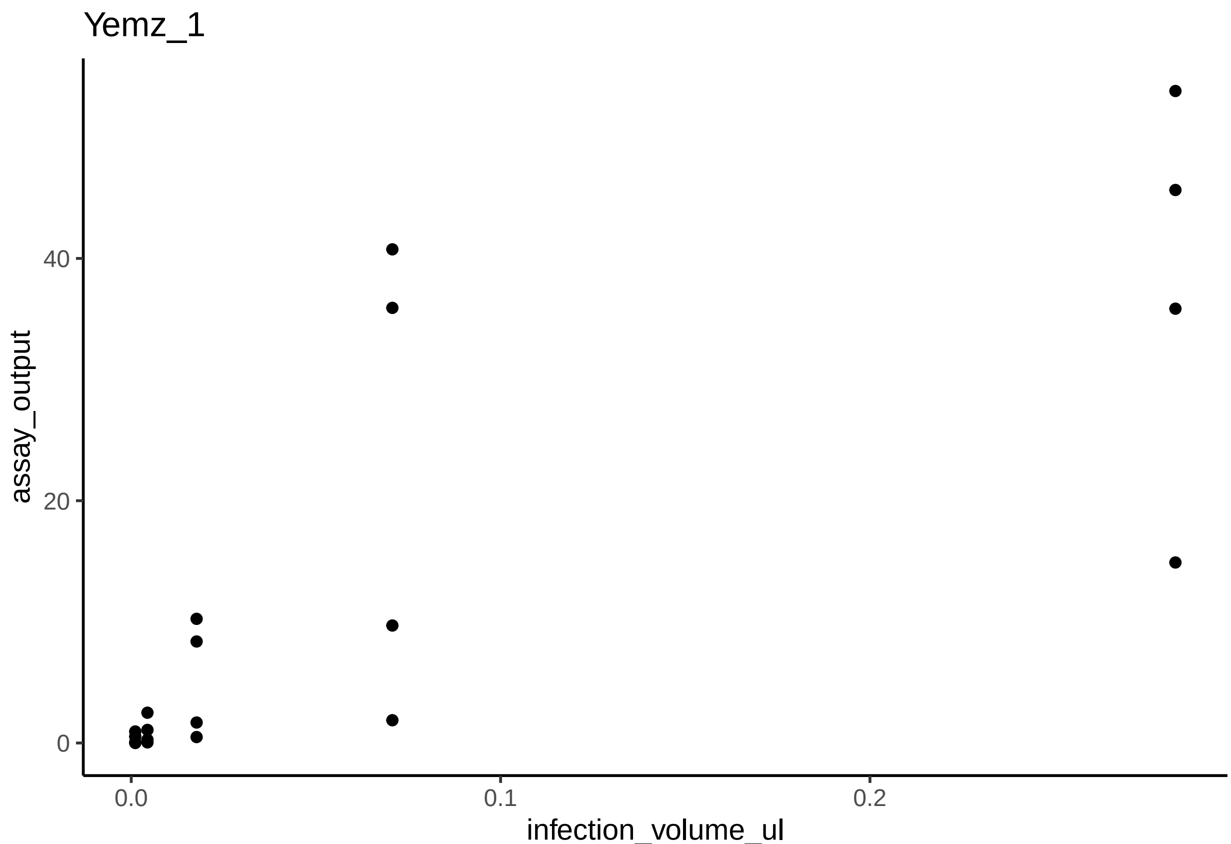

```
##
## [[144]]
```



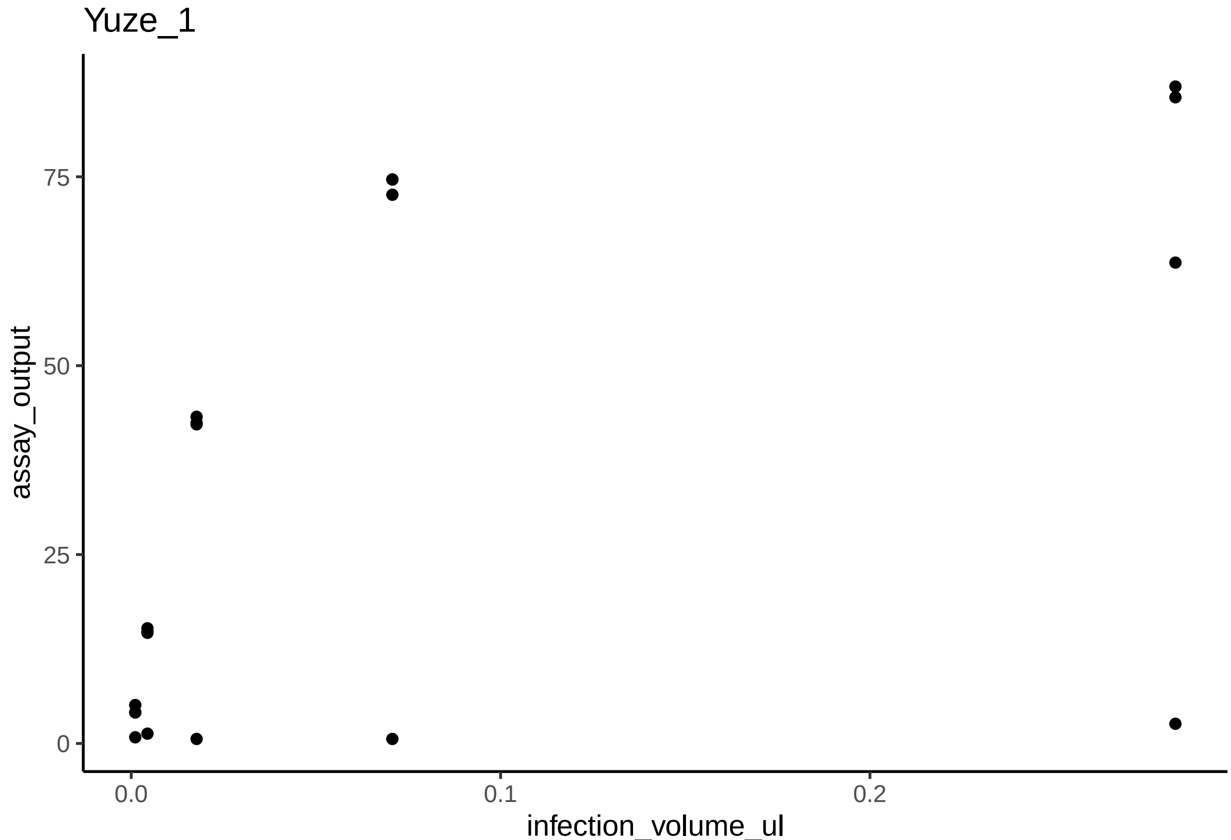

```
##
## [[145]]
```



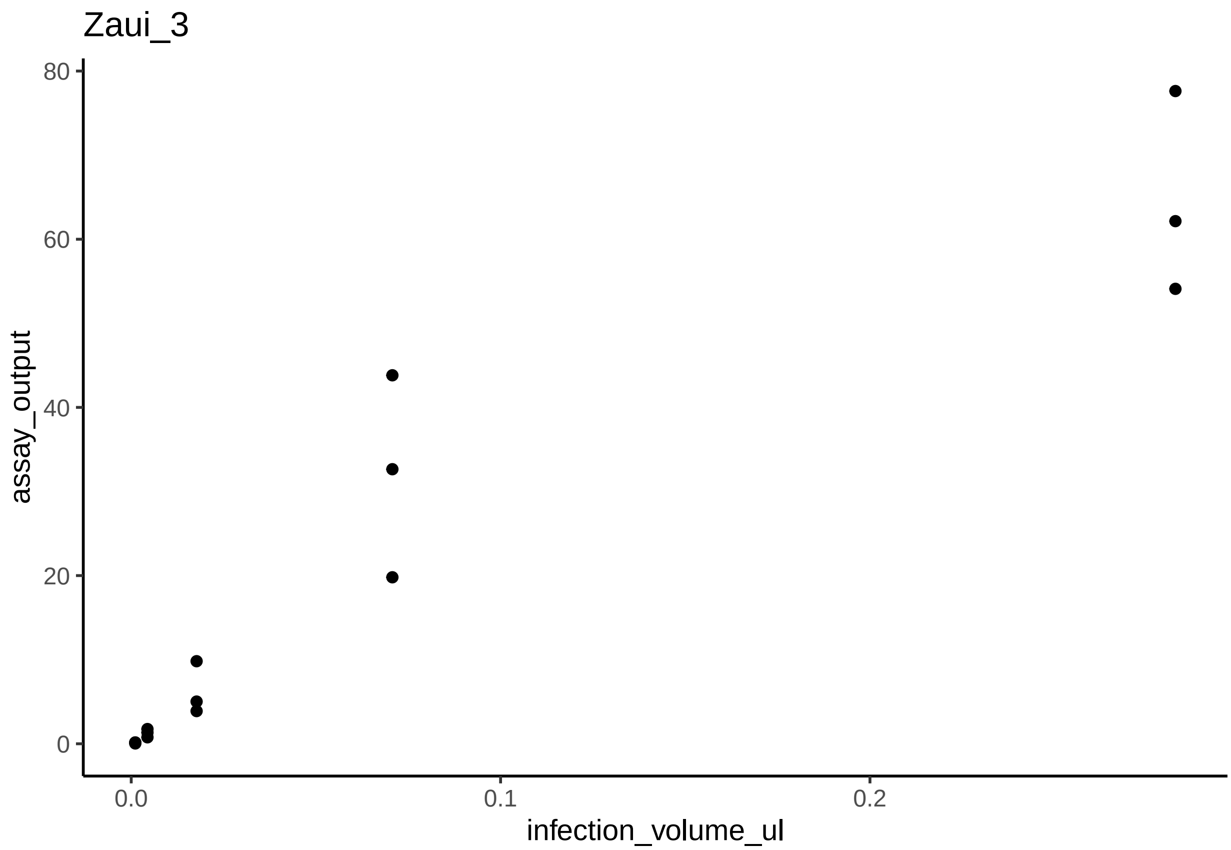

```
##
## [[146]]
```



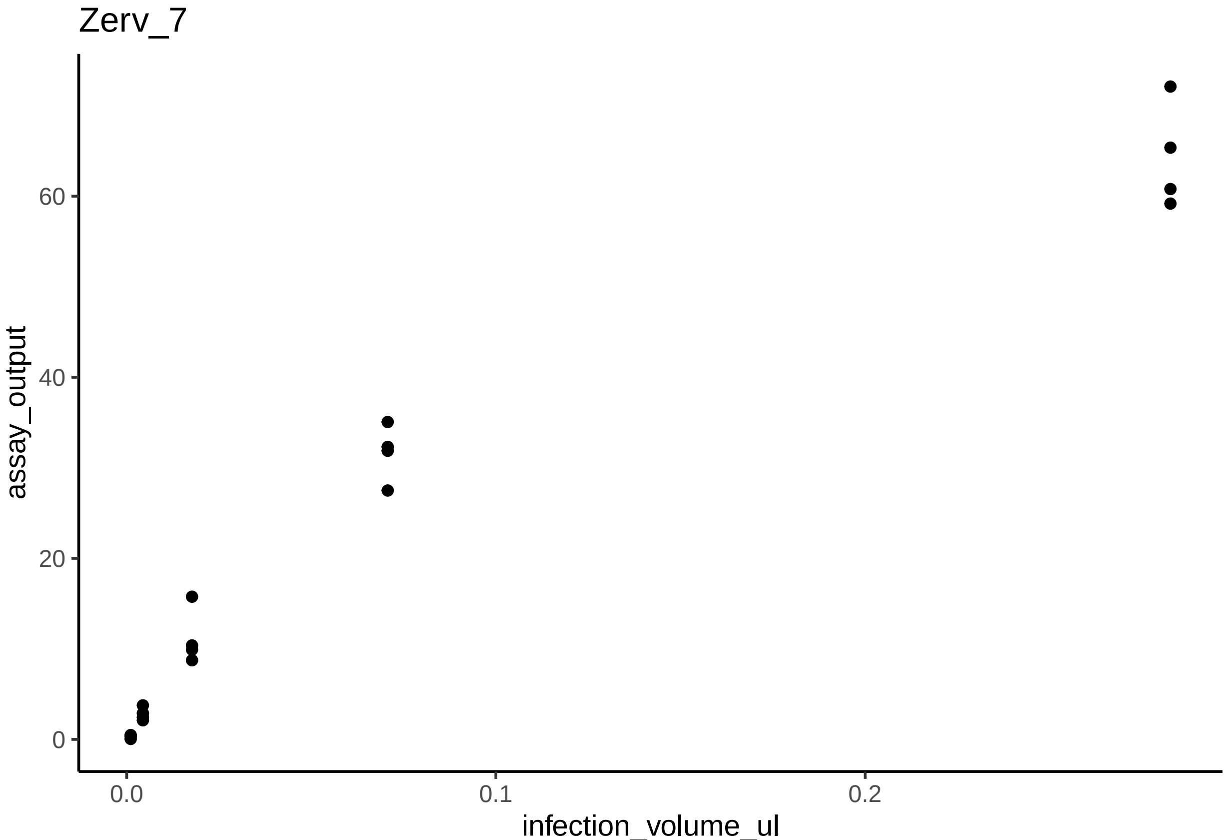

```
##
## [[147]]
```



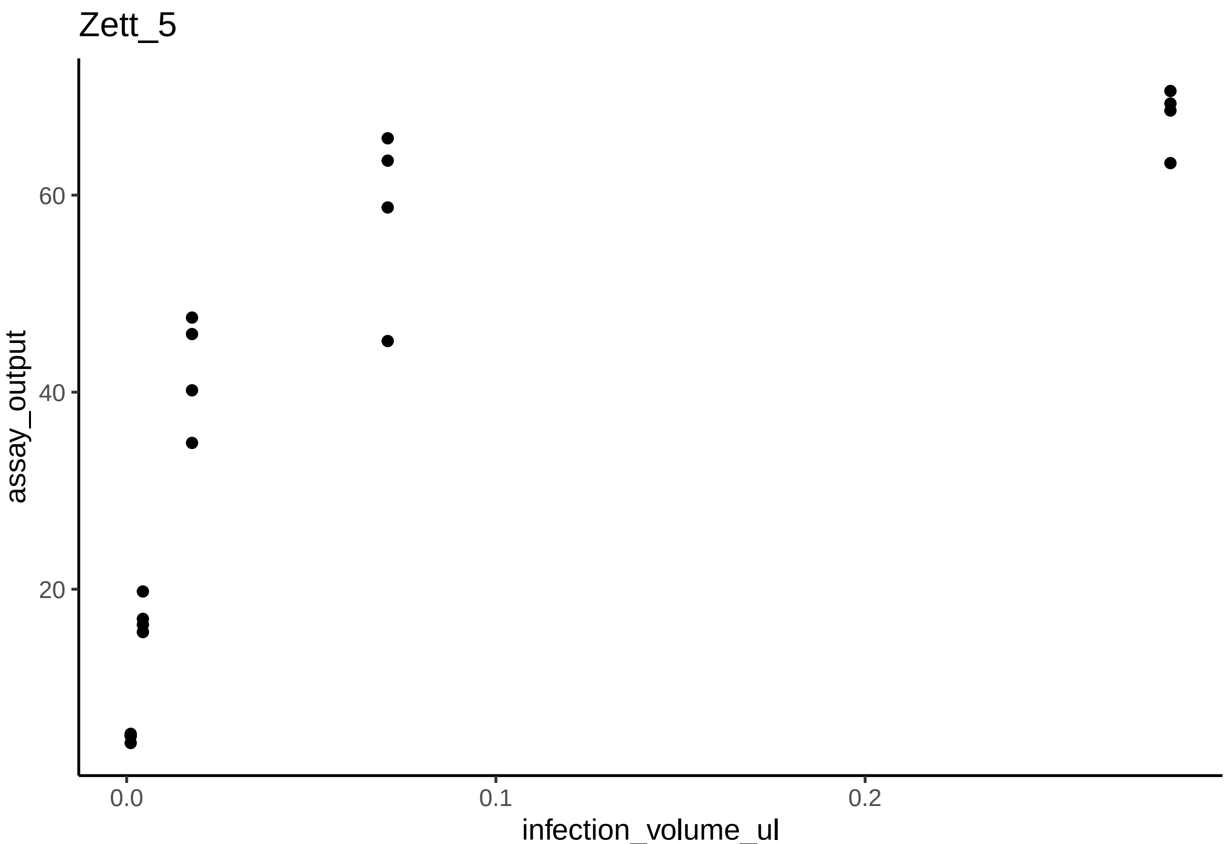

```
##
## [[148]]
```



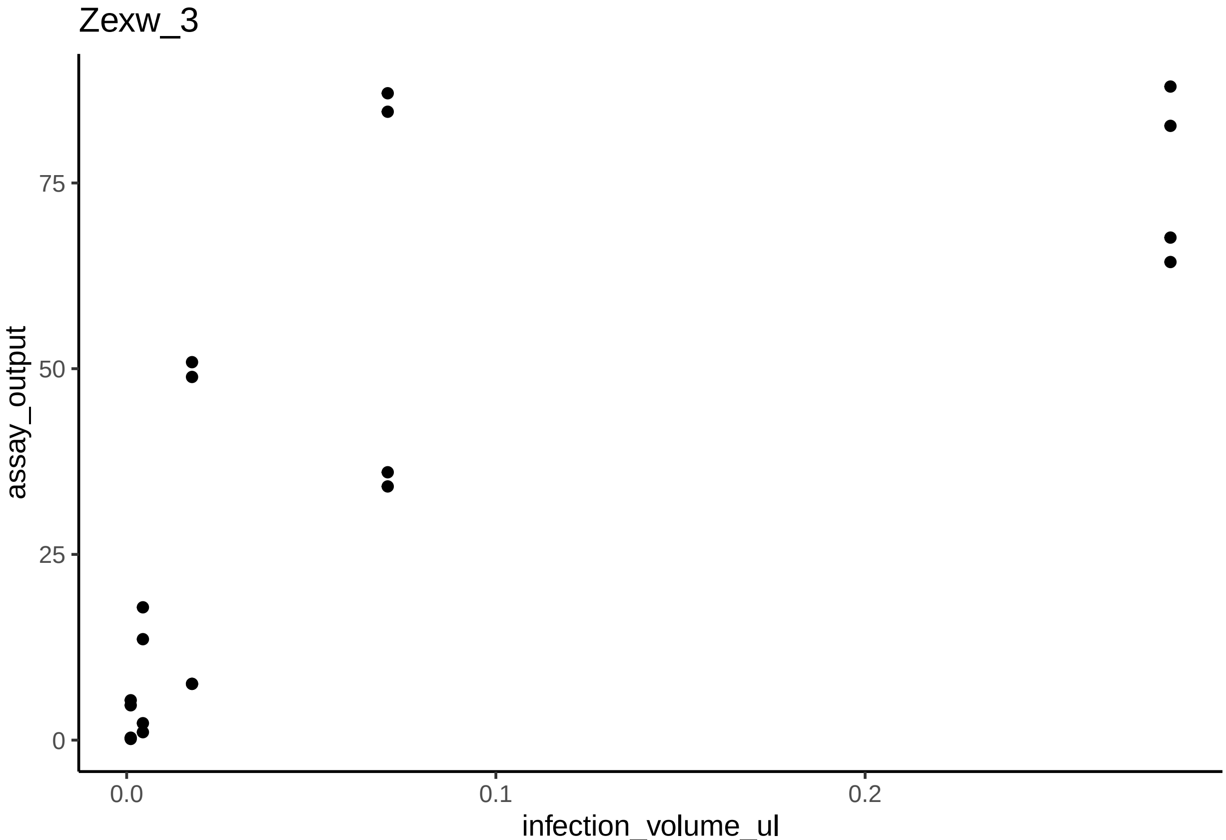

```
##
## [[149]]
```



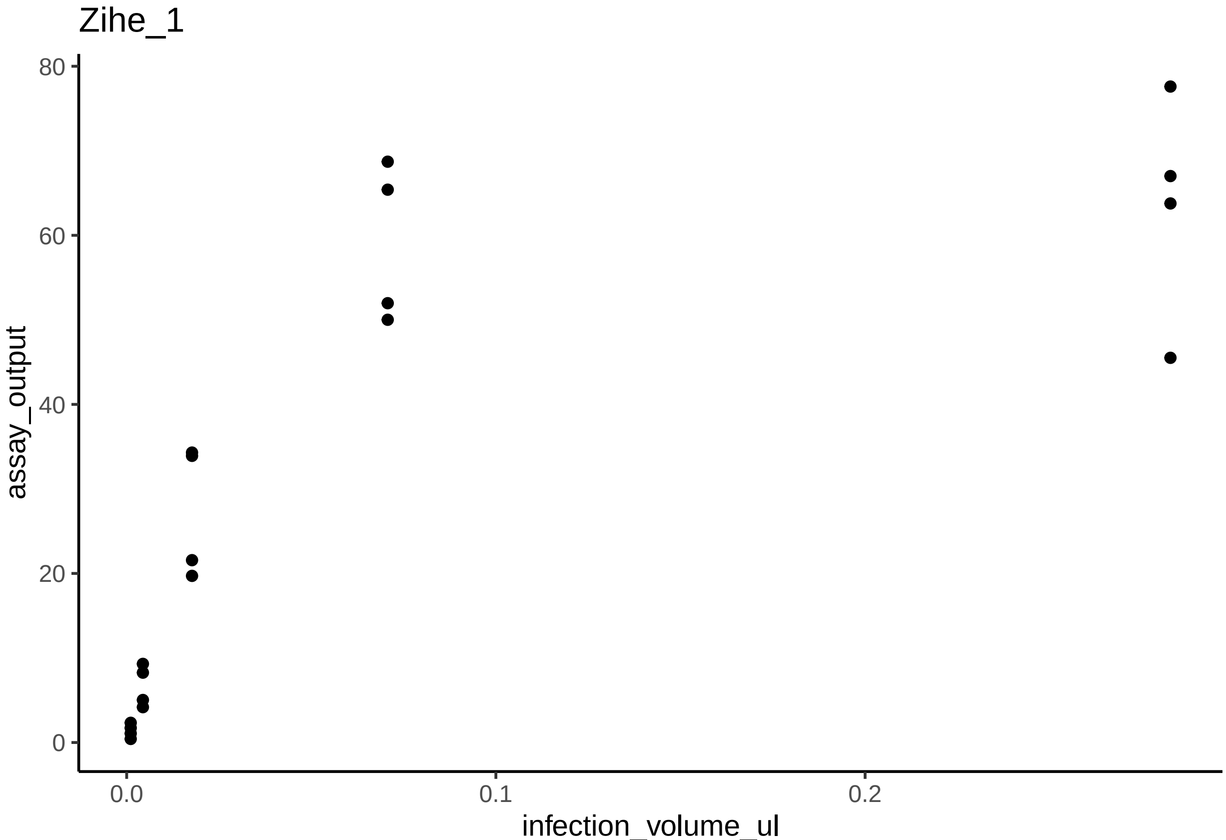

```
##
## [[150]]
```



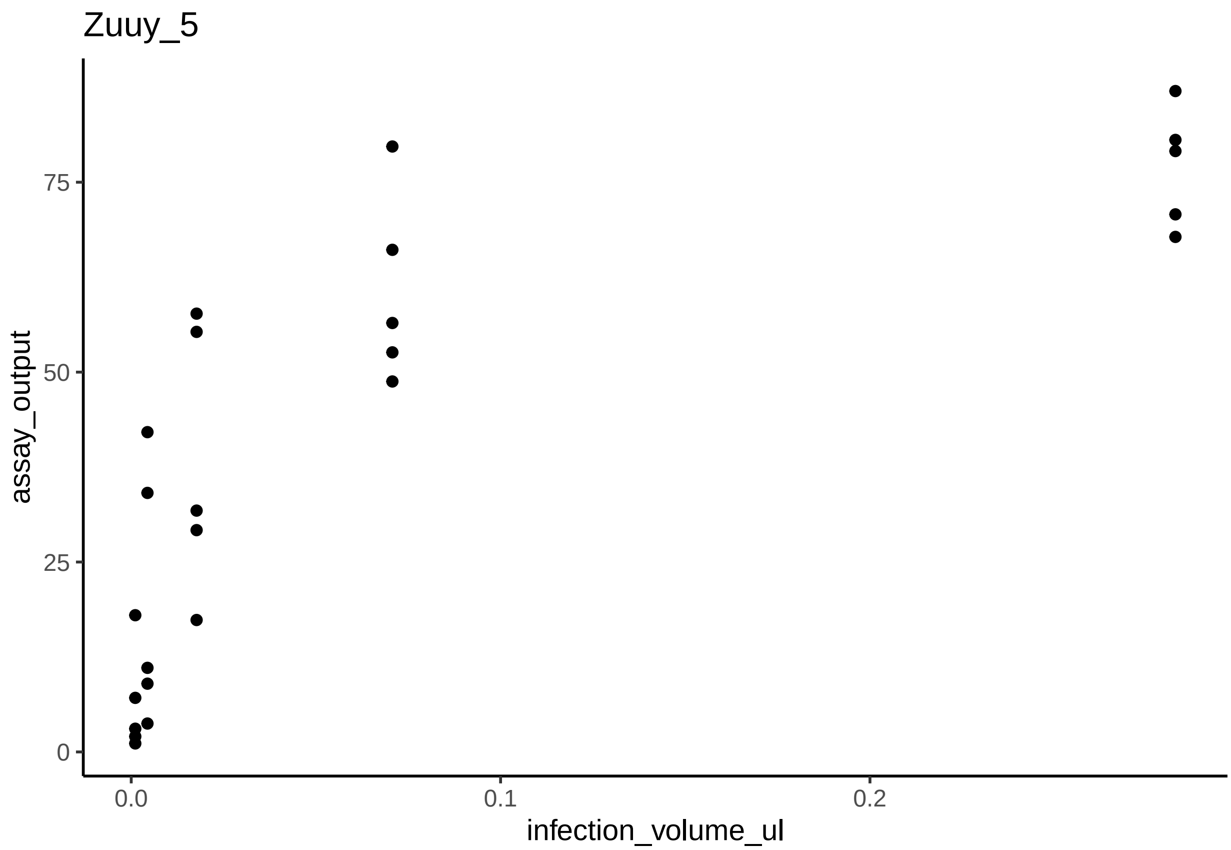

```
##
## [[151]]
```




```
##
## [[152]]
```




```
##
## [[153]]
```




```
#names(scatter_plot_vector)=vector_data_per_cell_line$cell_line
```

making a boxplot of the assay output per cell and per titre, can use this to see distribution between screens and replicates and see the initial outliers, stat summary lets you see the upper quartile, median, lower quartile and max and min values

```
apply_plot_boxplot=function(i){ggplot(data = i,aes(y=assay_output,x=titre,))+
  geom_boxplot()+
  ggtitle(i$cell_line[1])+
  stat_summary(geom="text", fun.y=quantile,
               aes(label=sprintf("%1.1f", ..y..), color=factor(titre)),
               position=position_nudge(x=0.6), size=3.5) +
  theme_classic()
}
```

code to apply function

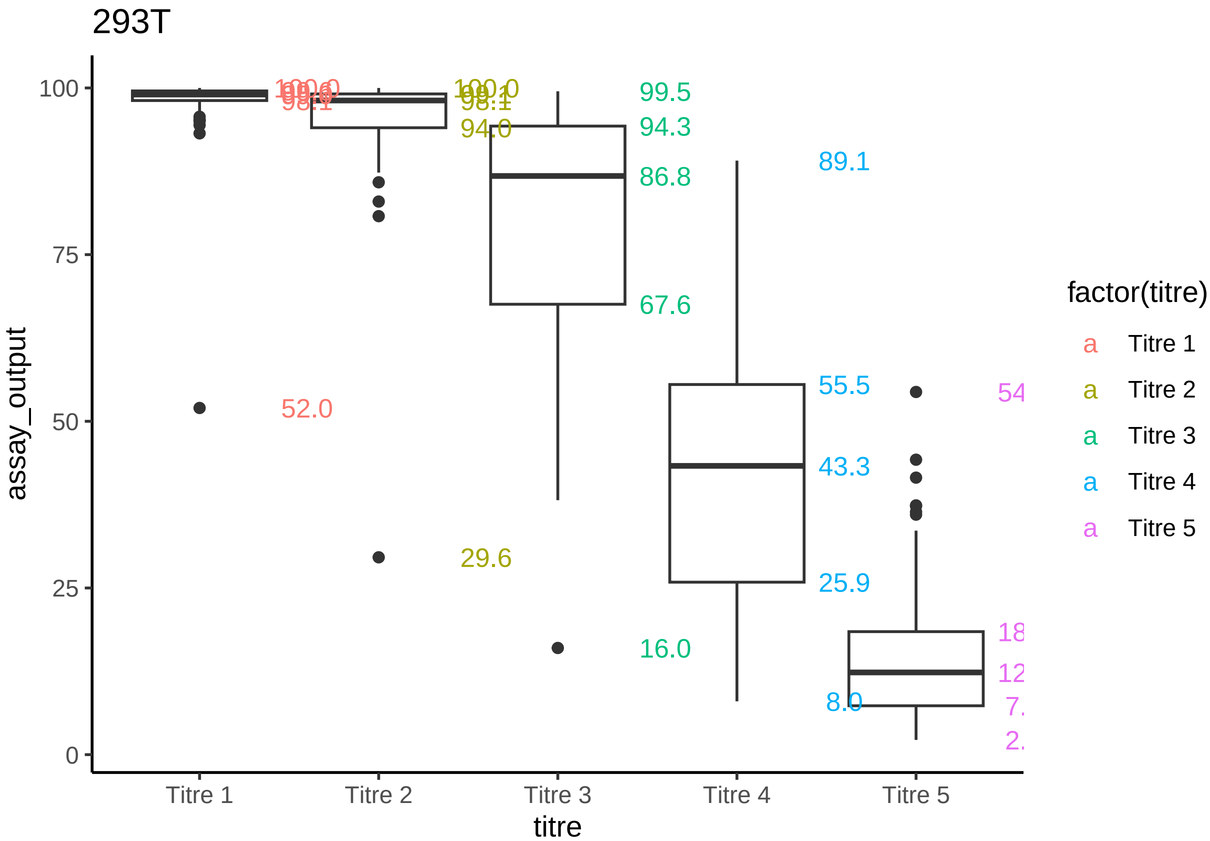
```
purrr::map(vector_data_per_cell_line$data,apply_plot_boxplot)
```

```
## Warning: The `fun.y` argument of `stat_summary()` is deprecated as of ggplot2 3.3.0.
## i Please use the `fun` argument instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

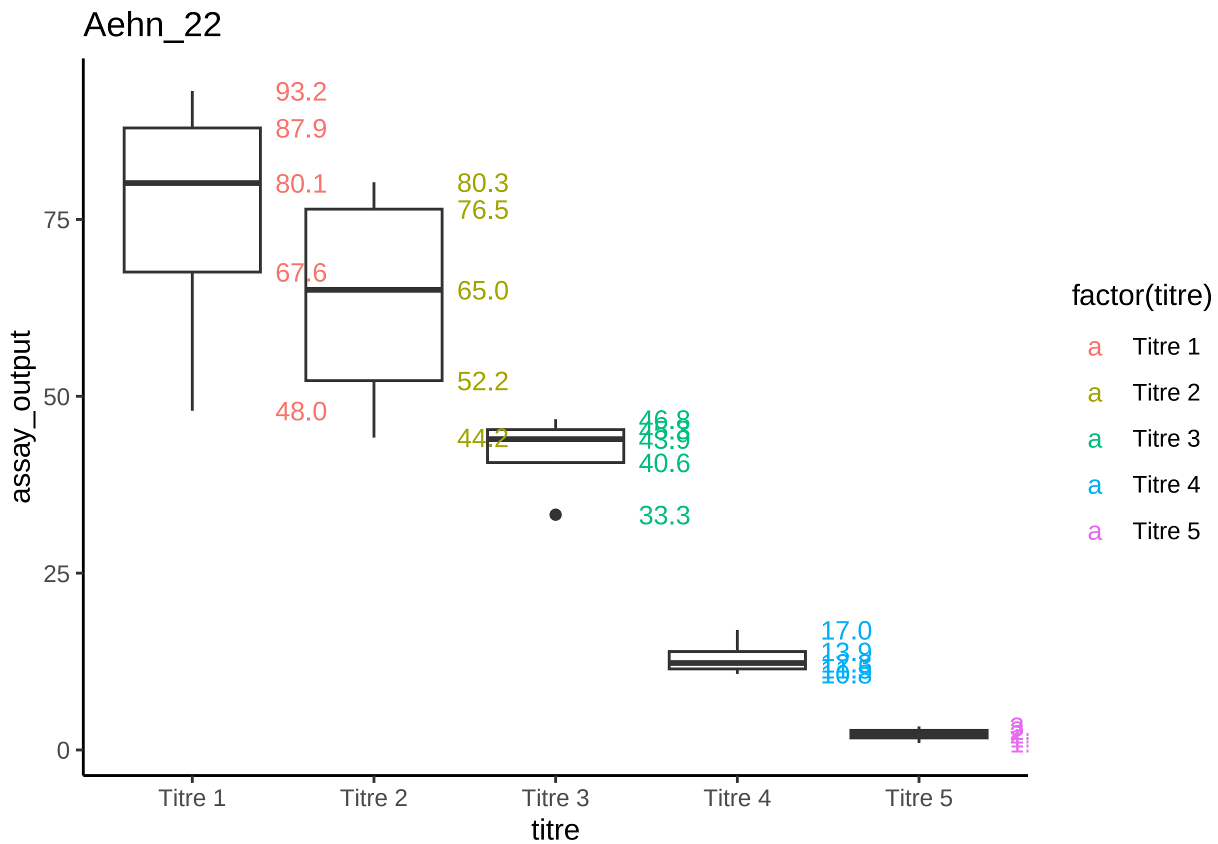
```
## [[1]]
```

```
## Warning: The dot-dot notation (`..y..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(y)` instead.
## This warning is displayed once every 8 hours.
```

```
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

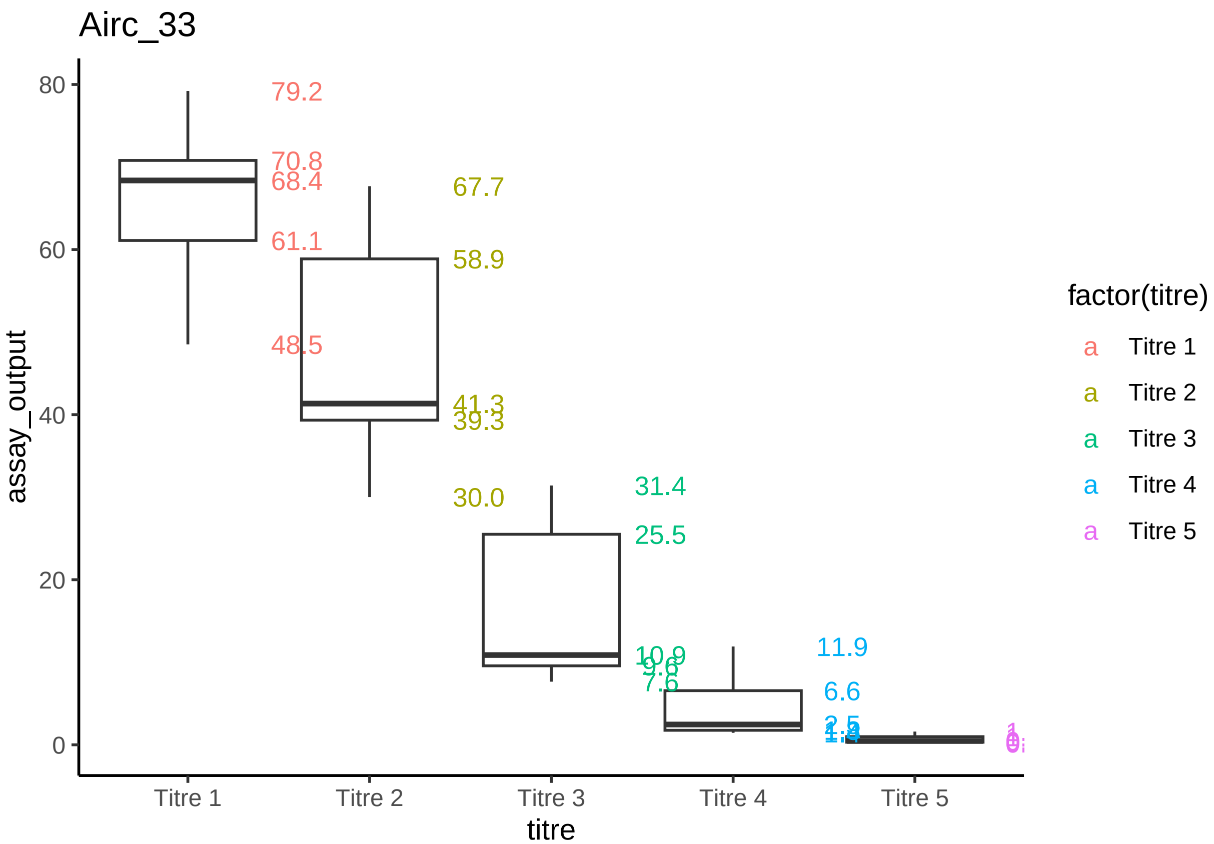



```
##
## [[2]]
```

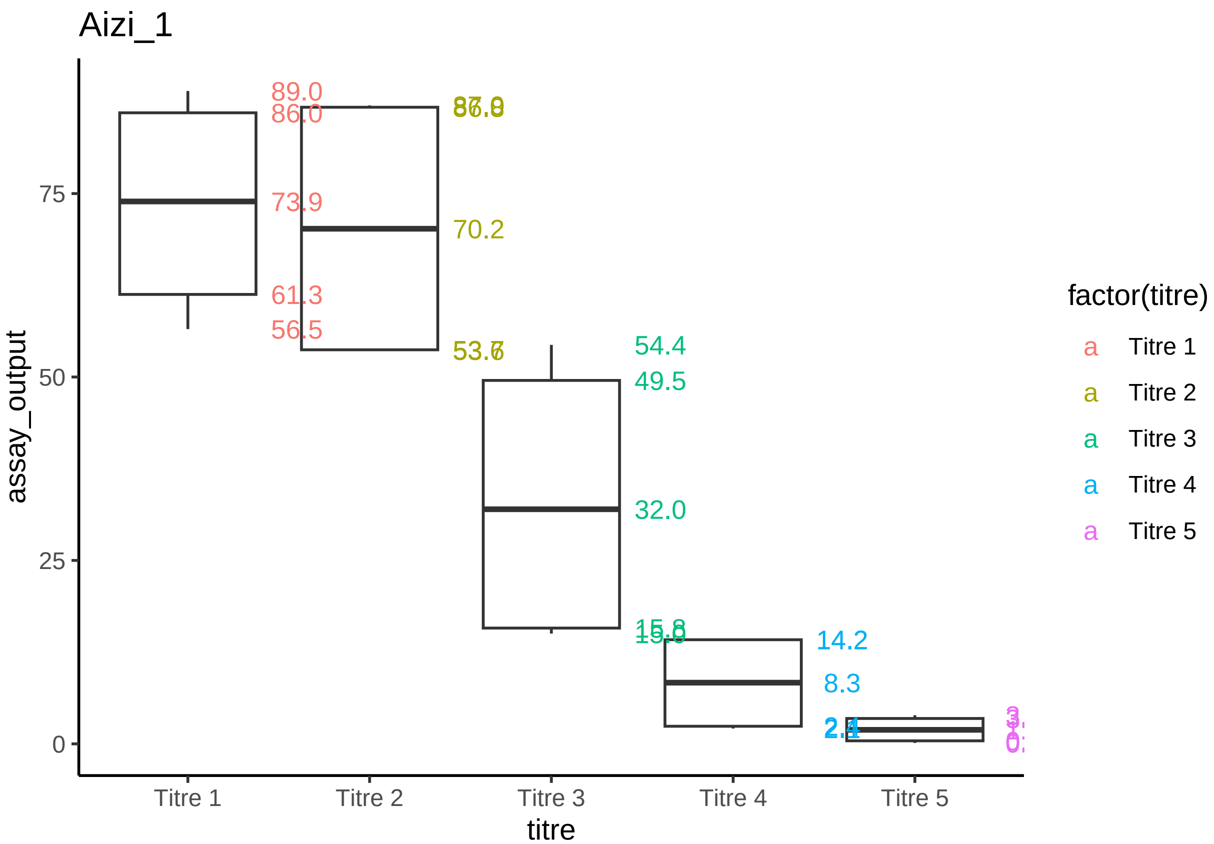


Aehn_22
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
25
50
75
93.2
87.9
80.1
67.6
48.0
80.3
76.5
65.0
52.2
44.2
46.8
40.6
33.3
17.0
13.9
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[3]]
```

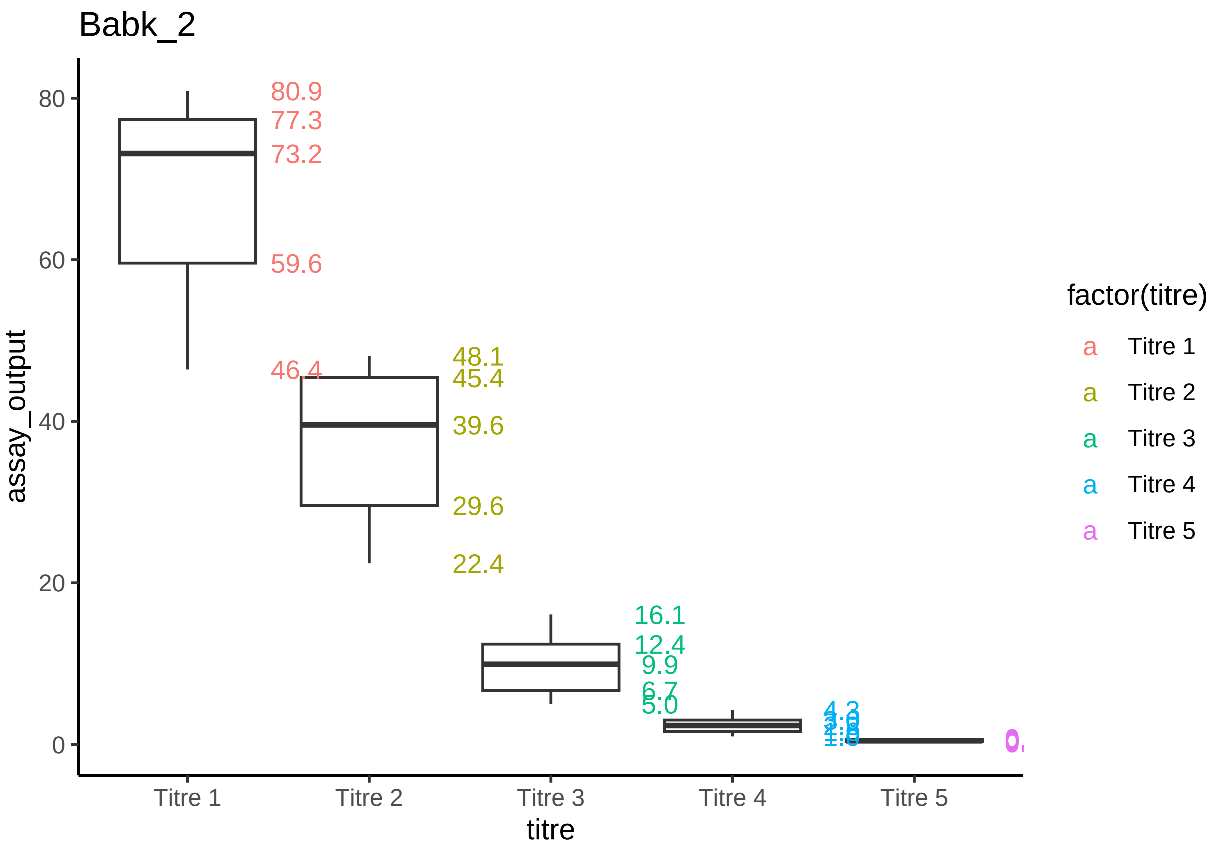

Airc_33
assay_output
80
60
40
20
0
79.2
70.8
68.4
61.1
48.5
67.7
58.9
41.3
39.3
30.0
31.4
25.5
10.9
9.6
7.6
11.9
6.6
2.5
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[4]]
```



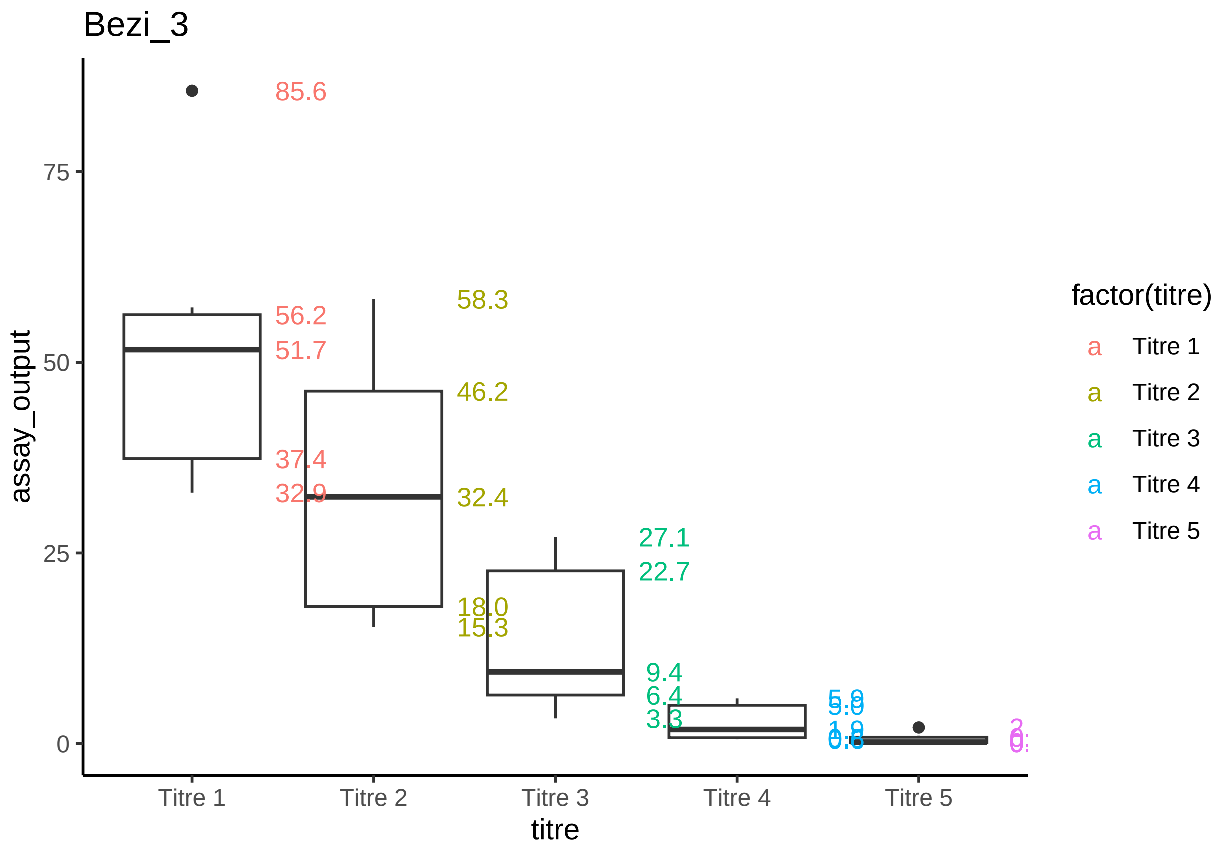
Aizi_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
25
50
75
89.0
86.0
73.9
61.3
56.5
70.2
53.7
54.4
49.5
32.0
14.2
8.3
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[5]]
```



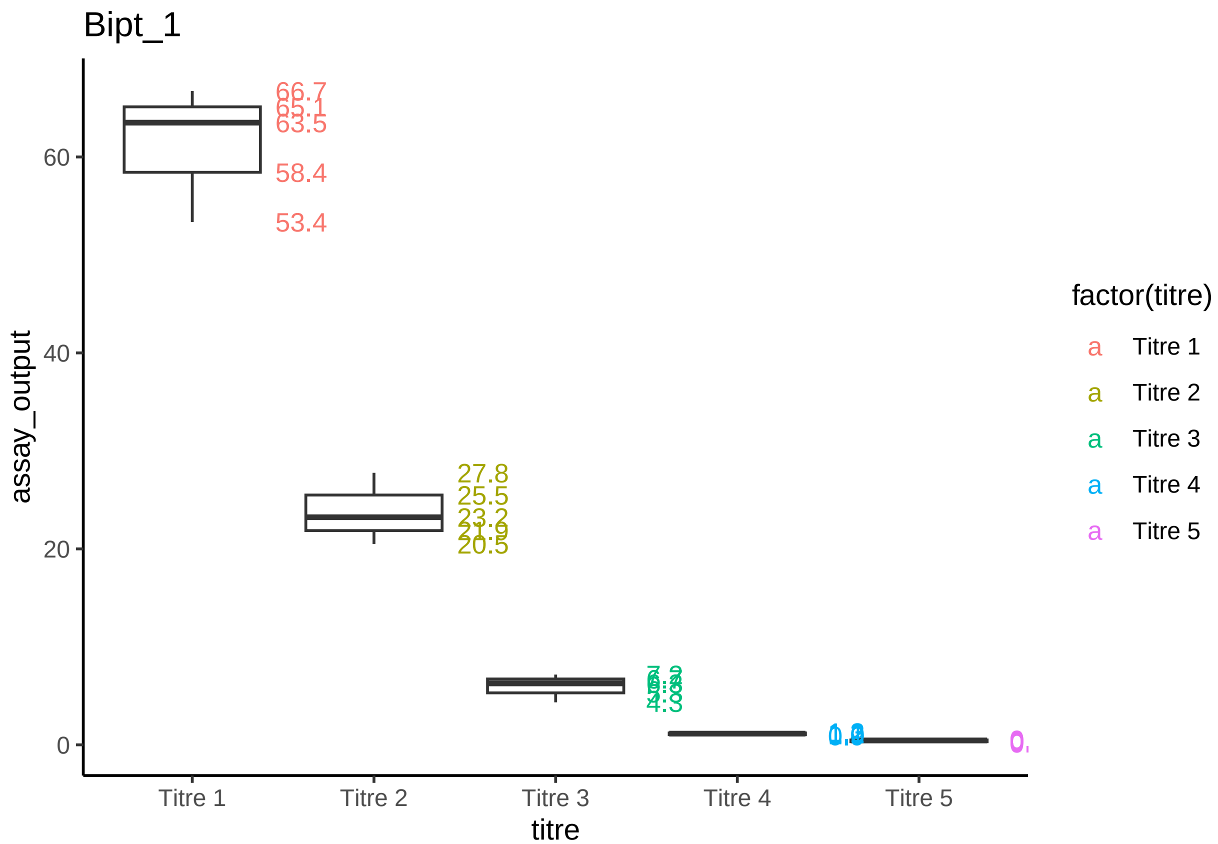
Babk_2
80.9
77.3
73.2
59.6
46.4
48.1
45.4
39.6
29.6
22.4
16.1
12.4
9.9
6.7
5.0
4.3
assay_output
80
60
40
20
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[6]]
```



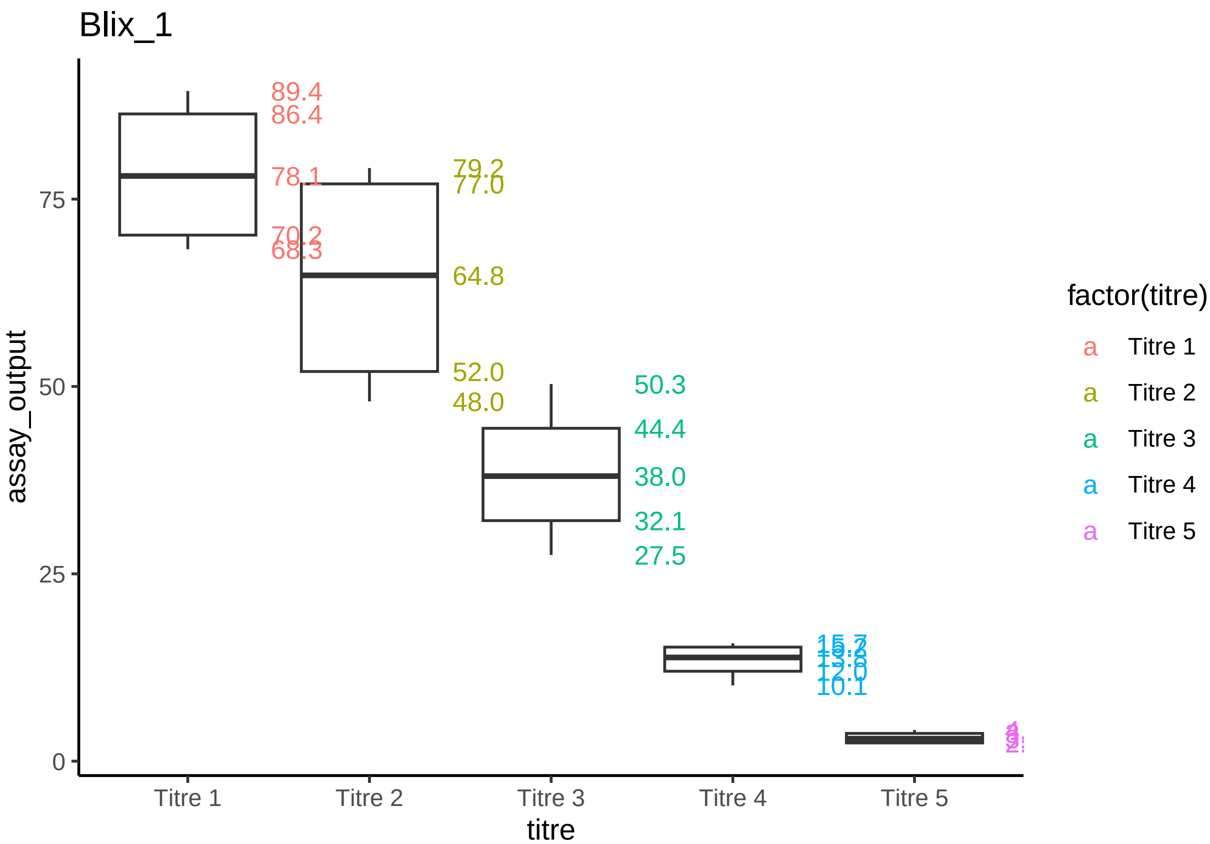
Bezi_3
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
85.6
56.2
51.7
37.4
32.9
58.3
46.2
32.4
18.0
15.3
27.1
22.7
9.4
6.4
3.3


```
##
## [[7]]
```

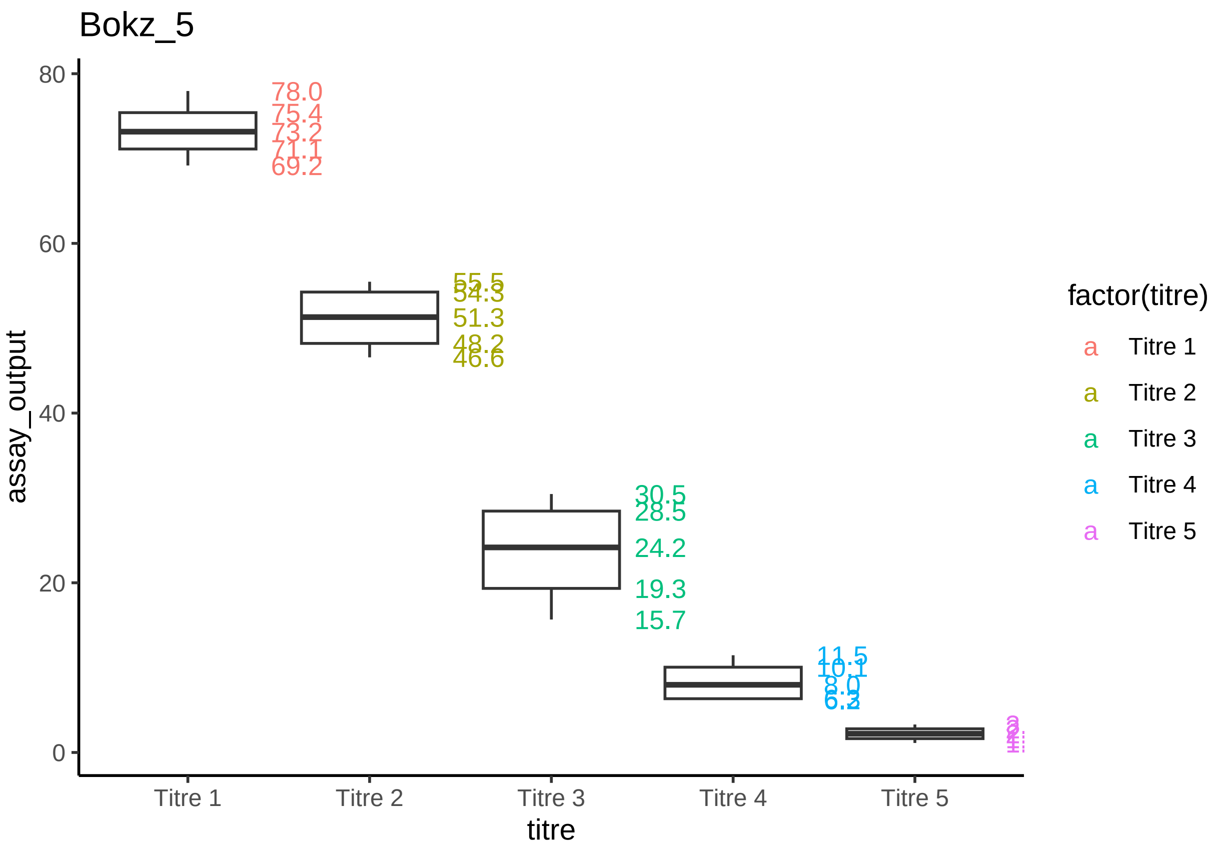


Bipt_1
66.7
65.1
63.5
58.4
53.4
27.8
25.5
23.2
21.9
20.5
4.3
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[8]]
```

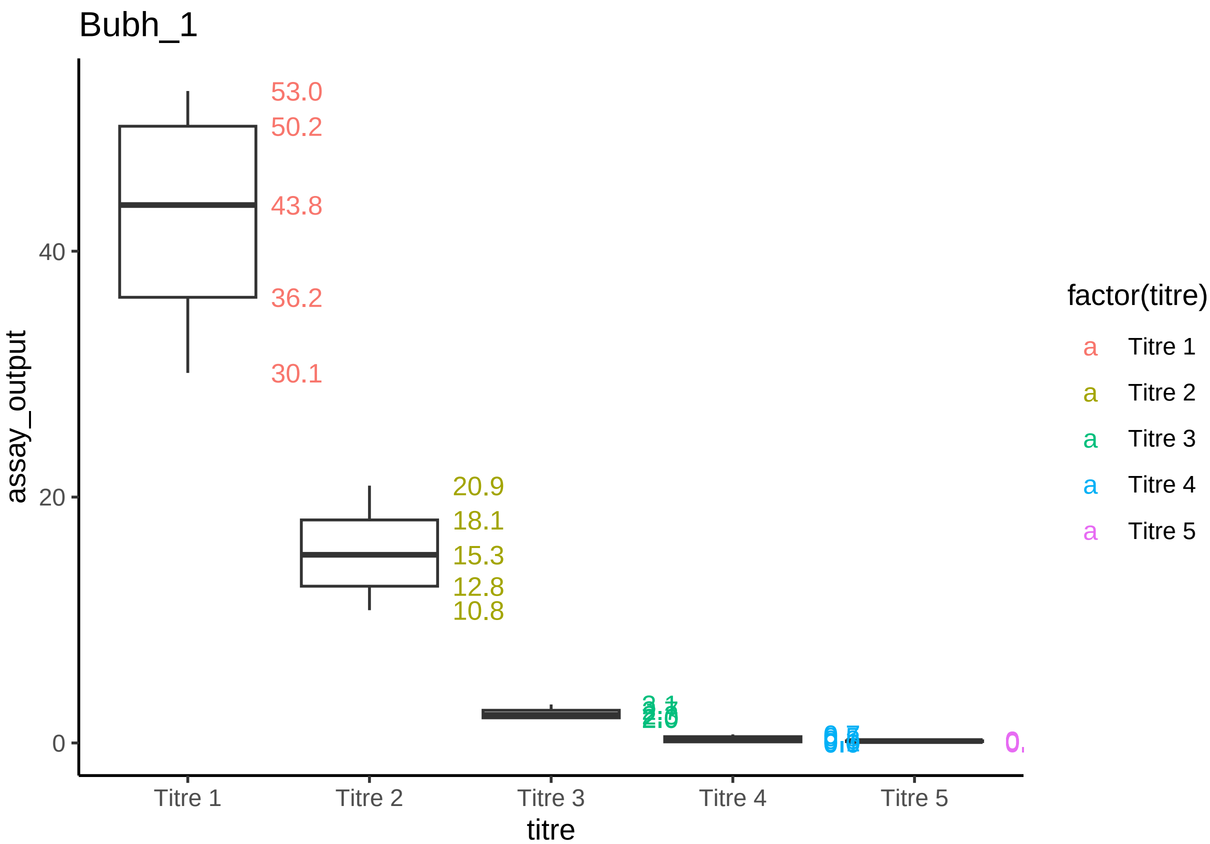

Blix_1
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
89.4
86.4
78.1
70.2
68.3
79.2
77.0
64.8
52.0
48.0
50.3
44.4
38.0
32.1
27.5
10.1
0
25
50
75

```
##
## [[9]]
```

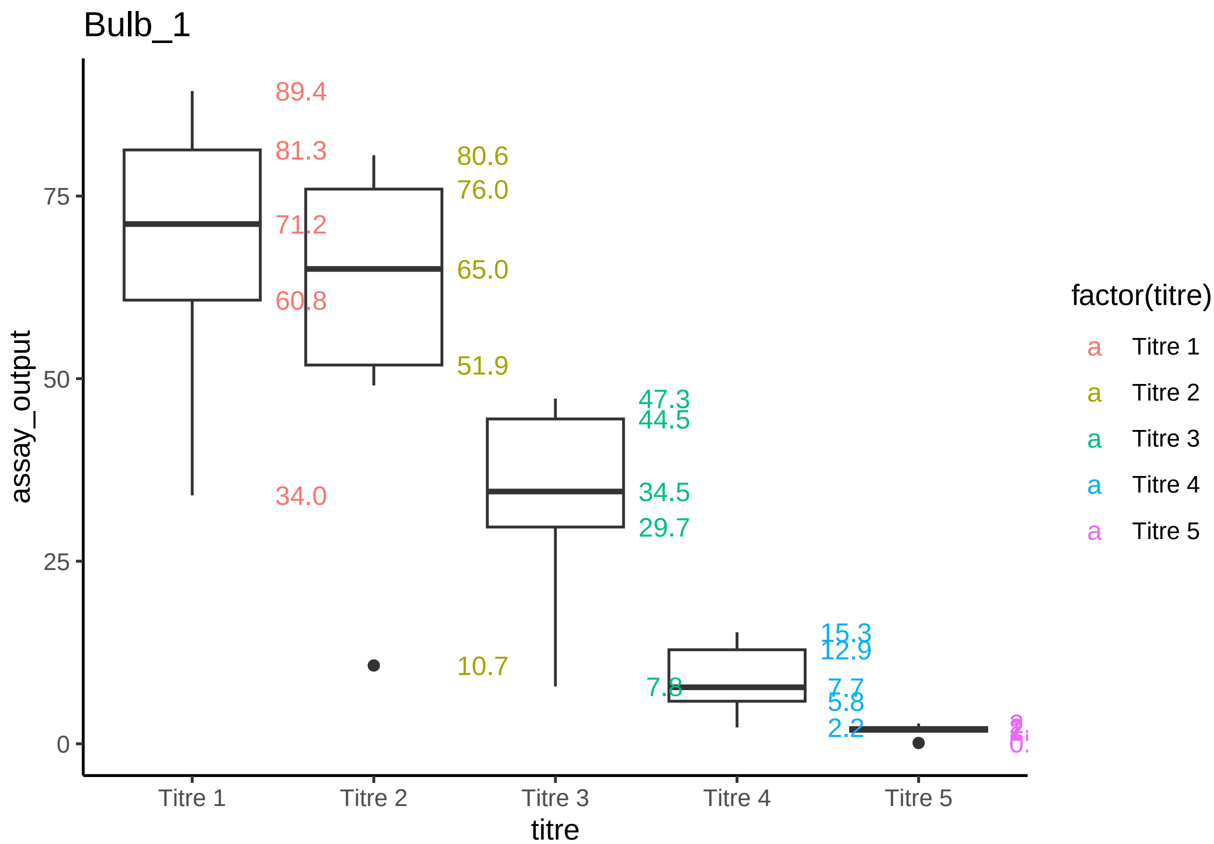


Bokz_5
80
60
40
20
0
assay_output
78.0
75.4
73.2
71.1
69.2
55.5
54.3
51.3
48.2
46.6
30.5
28.5
24.2
19.3
15.7
11.5
10.1
8.0
6.3
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[10]]
```

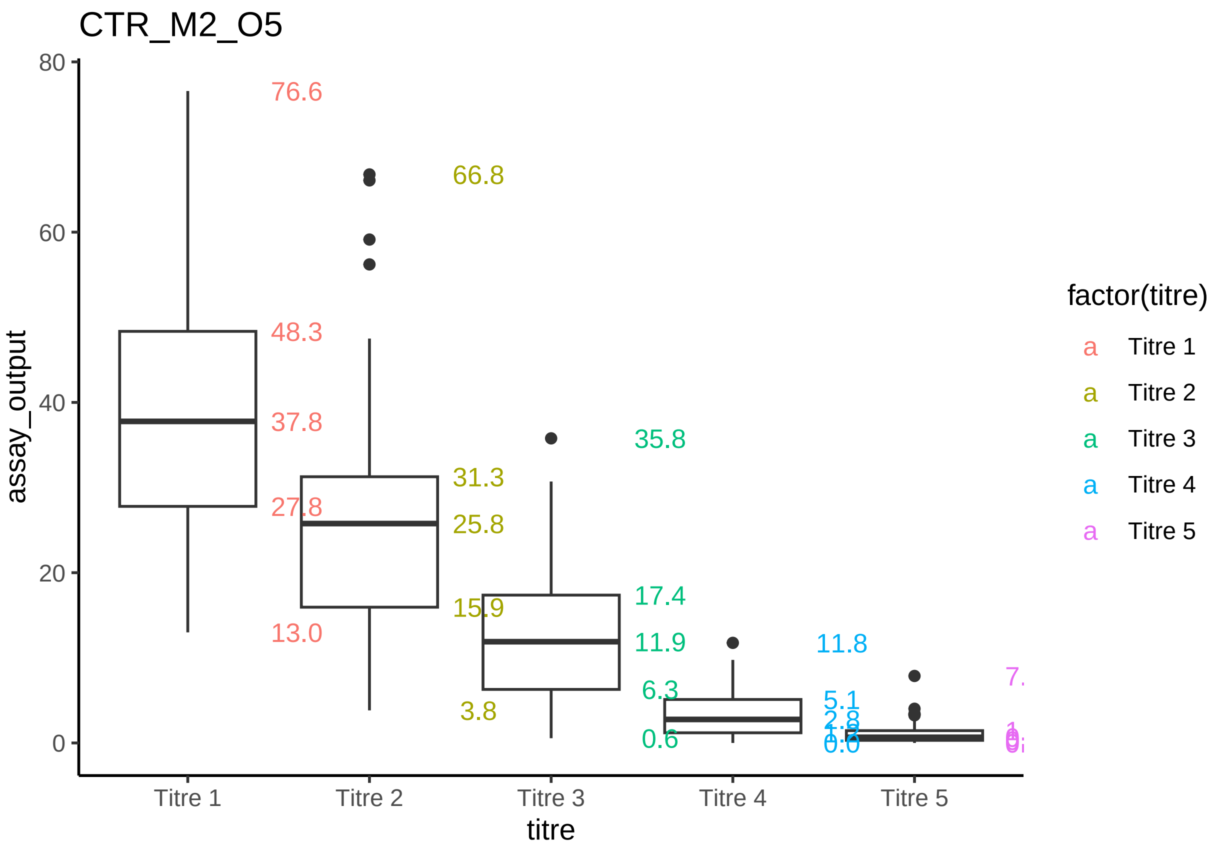

Bubh_1
53.0
50.2
43.8
36.2
30.1
20.9
18.1
15.3
12.8
10.8
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[11]]
```

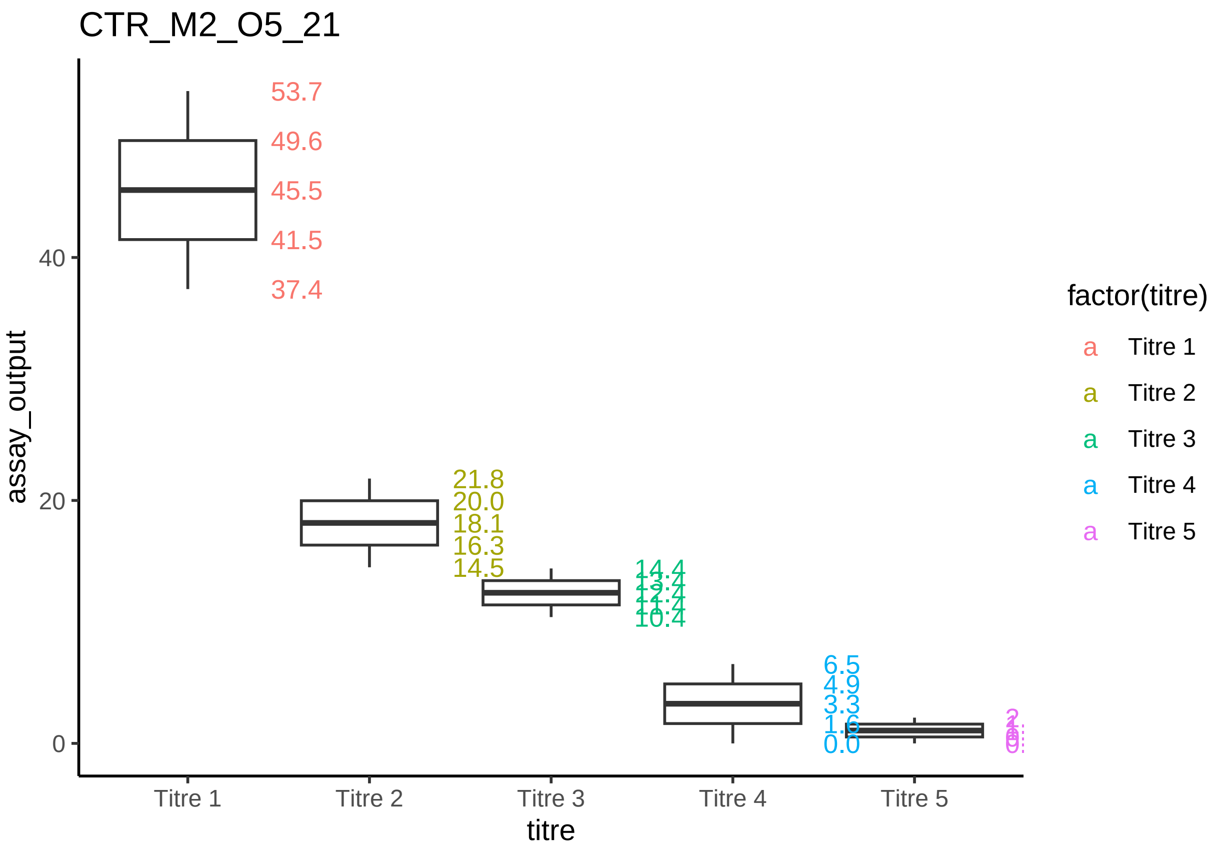


Bulb_1
89.4
81.3
71.2
60.8
34.0
80.6
76.0
65.0
51.9
10.7
47.3
44.5
34.5
29.7
7.8
15.3
12.9
7.7
5.8
2.2
75
50
25
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

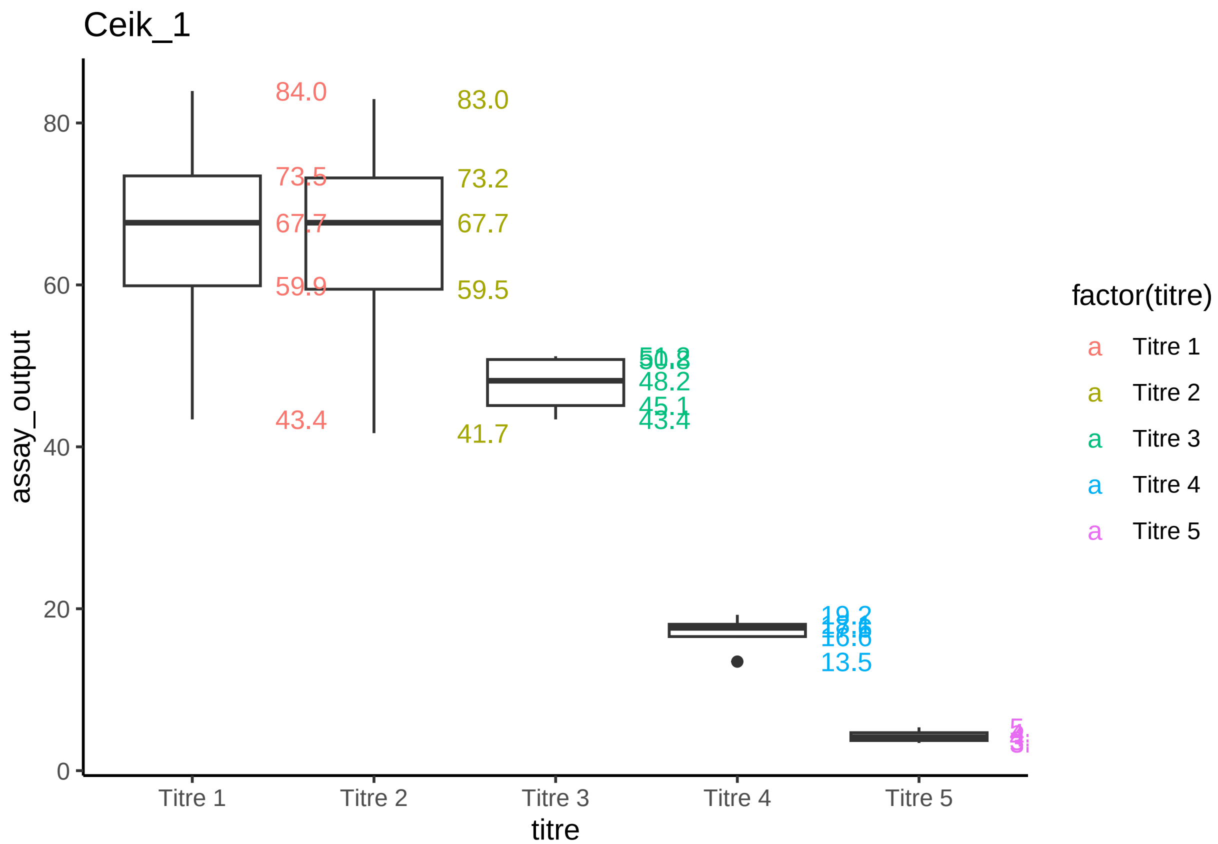

```
##
## [[12]]
```


CTR_M2_O5
assay_output
titre
80
60
40
20
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
76.6
48.3
37.8
27.8
13.0
66.8
31.3
25.8
15.9
3.8
35.8
17.4
11.9
6.3
0.6
11.8
5.1
2.8
0.0
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[13]]
```

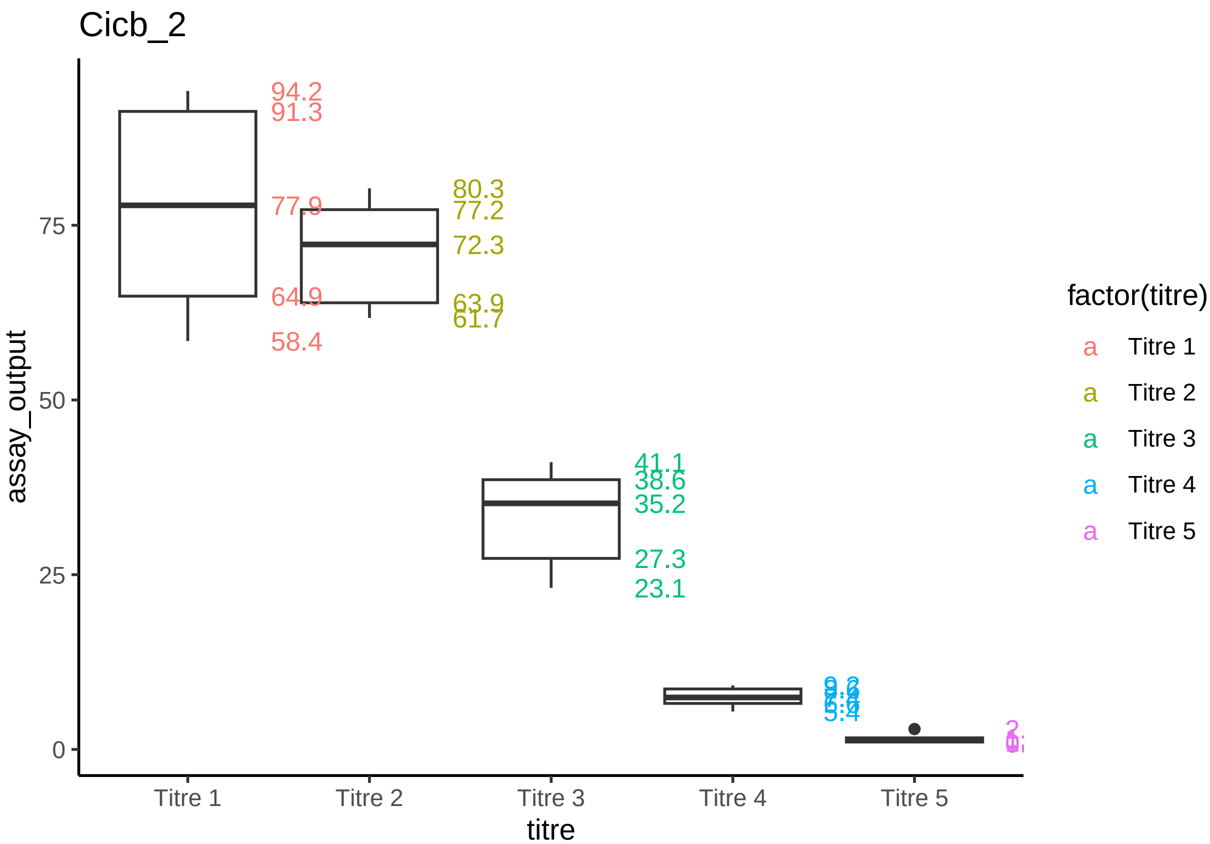

CTR_M2_O5_21
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
20
40
53.7
49.6
45.5
41.5
37.4
21.8
20.0
18.1
16.3
14.5
6.5
4.9
3.3
0.0
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[14]]
```

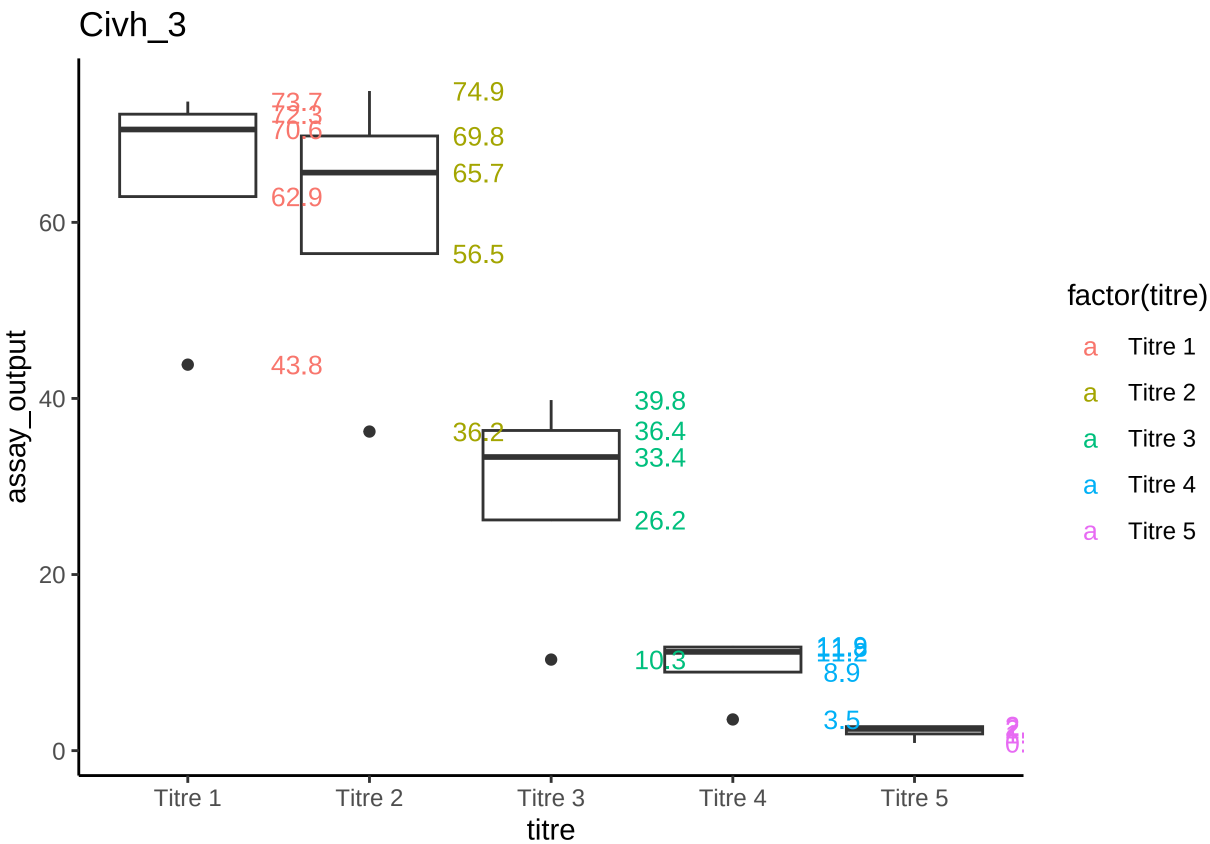


Ceik_1
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
84.0
73.5
67.7
59.9
43.4
83.0
73.2
67.7
59.5
41.7
48.2
45.1
43.4
19.2
13.5

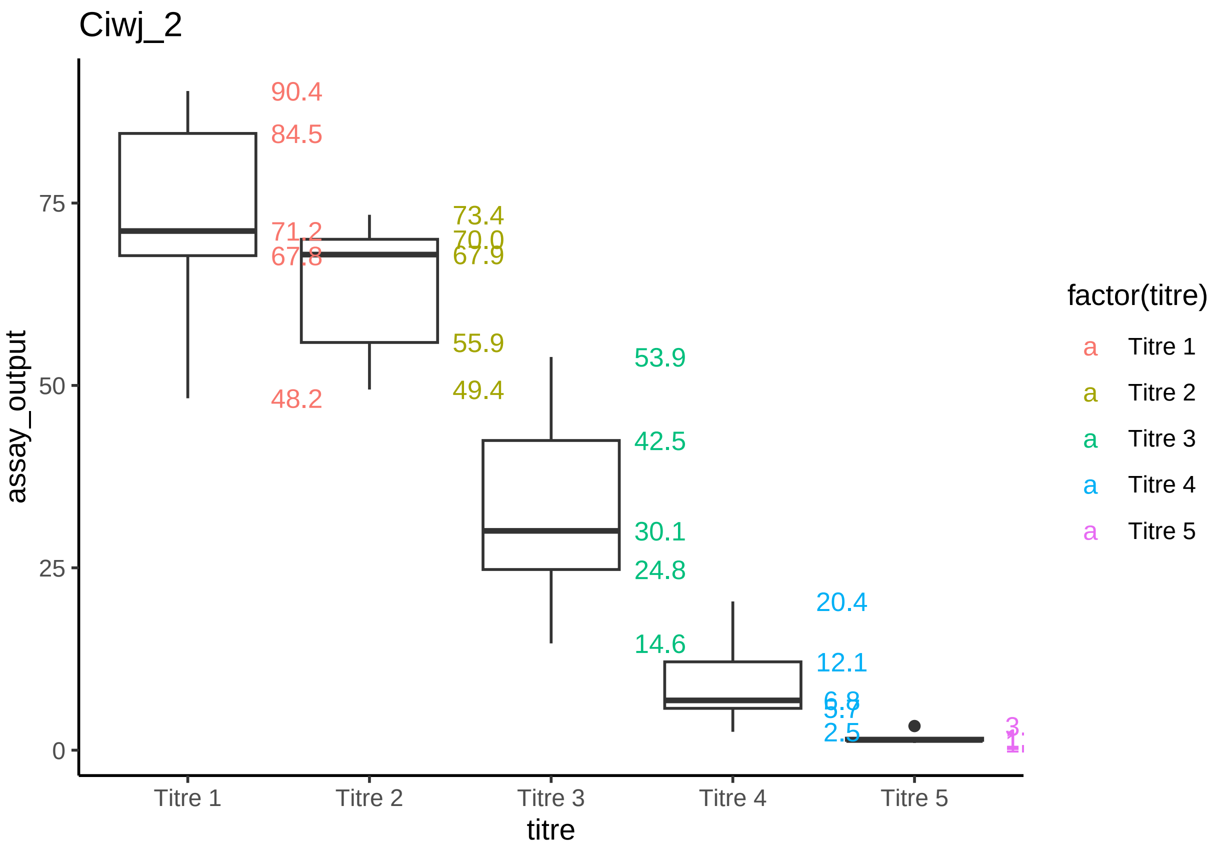

```
##
## [[15]]
```


Cicb_2
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
94.2
91.3
77.9
64.9
58.4
80.3
77.2
72.3
63.9
61.7
41.1
38.6
35.2
27.3
23.1
5.4

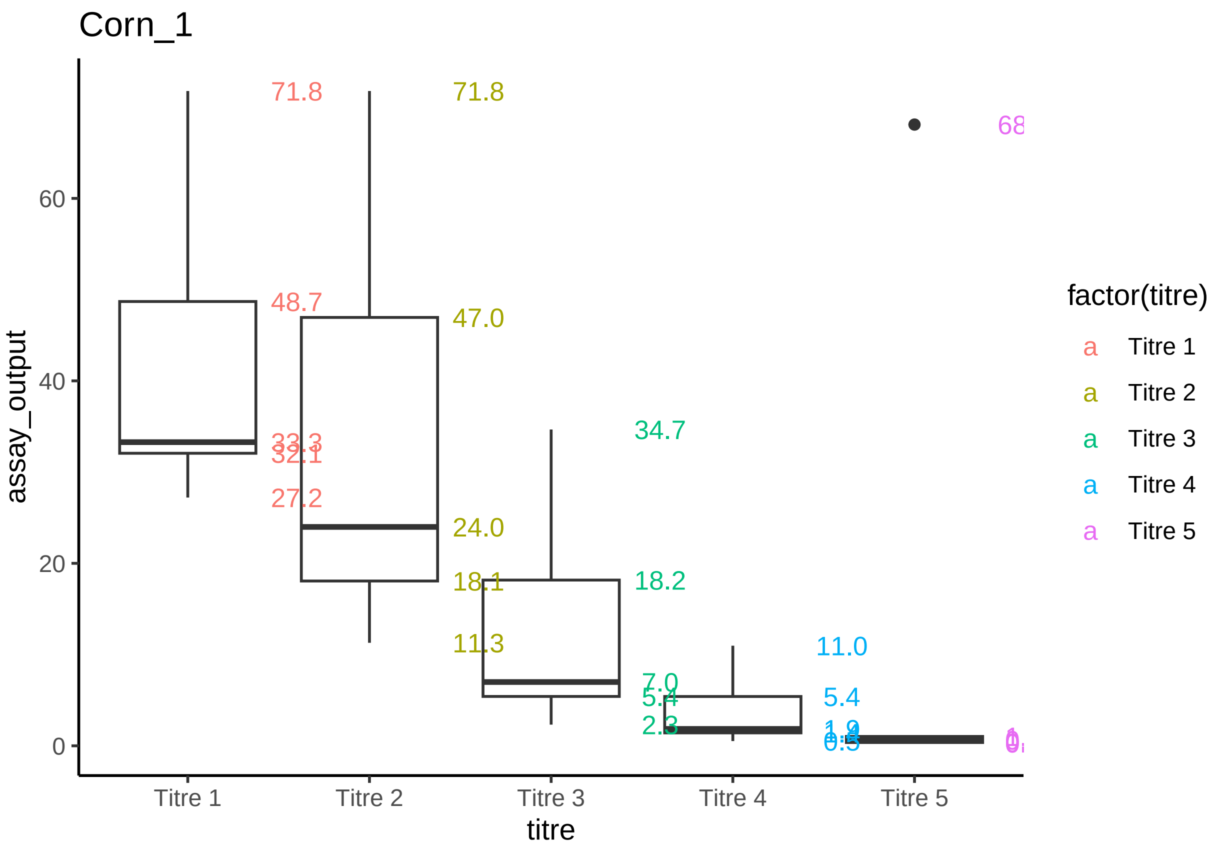
```
##
## [[16]]
```


Civh_3
assay_output
titre
60
40
20
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
73.7
72.3
70.6
62.9
43.8
74.9
69.8
65.7
56.5
36.2
39.8
36.4
33.4
26.2
10.3
11.9
11.2
8.9
3.5
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[17]]
```

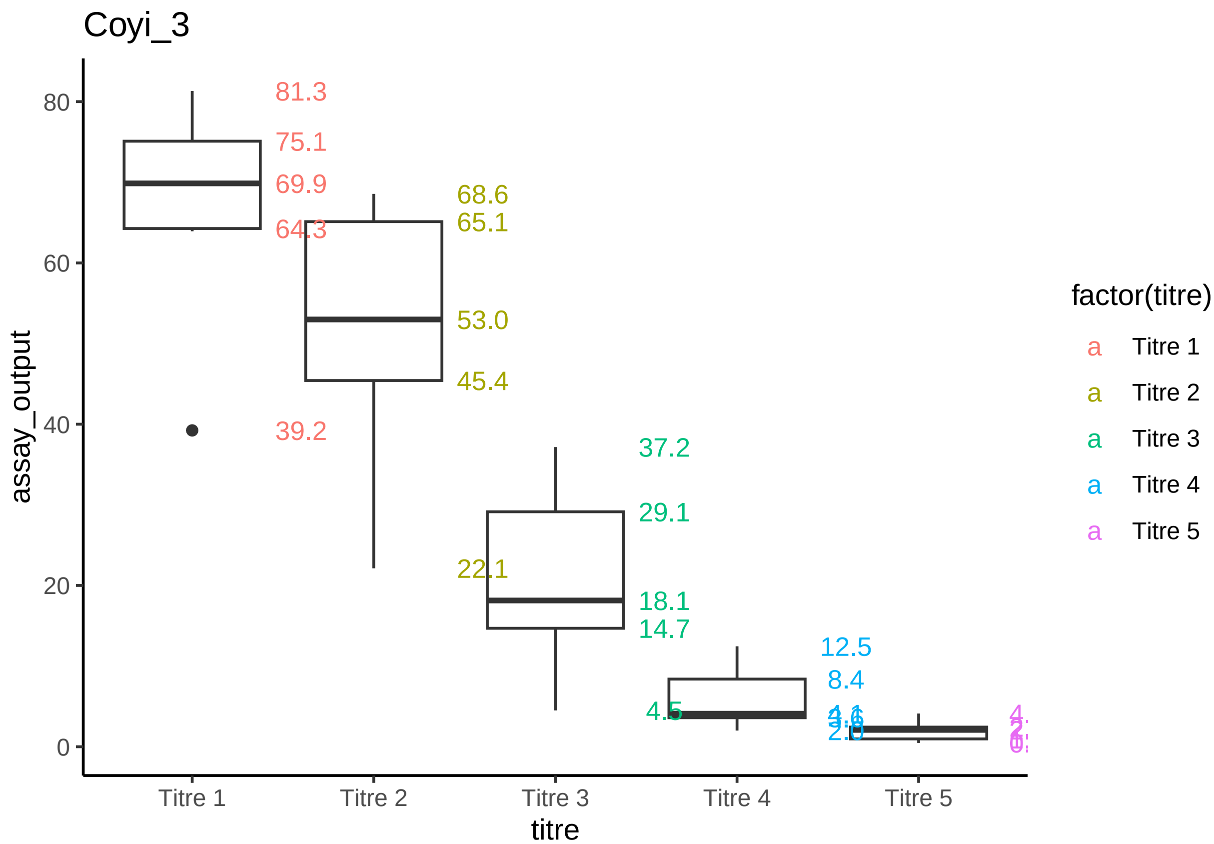

Ciwj_2
assay_output
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
25
50
75
90.4
84.5
71.2
67.8
48.2
73.4
70.0
67.9
55.9
49.4
53.9
42.5
30.1
24.8
14.6
20.4
12.1
6.8
5.7
2.5

```
##
## [[18]]
```

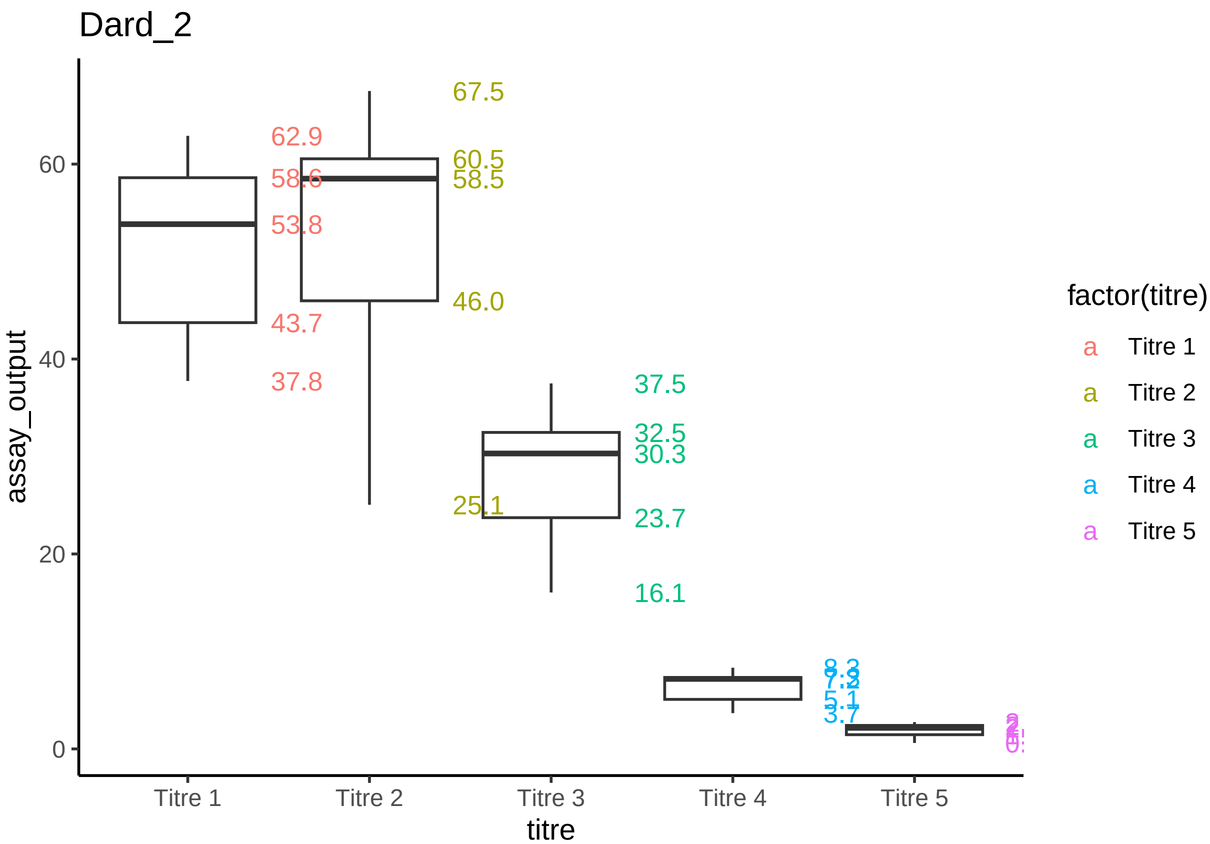


Corn_1
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
71.8
71.8
48.7
47.0
33.3
32.1
27.2
24.0
34.7
18.1
18.2
11.3
11.0
7.0
5.4
5.4
2.3
1.9
0.5
0
20
40
60


```
##
## [[19]]
```

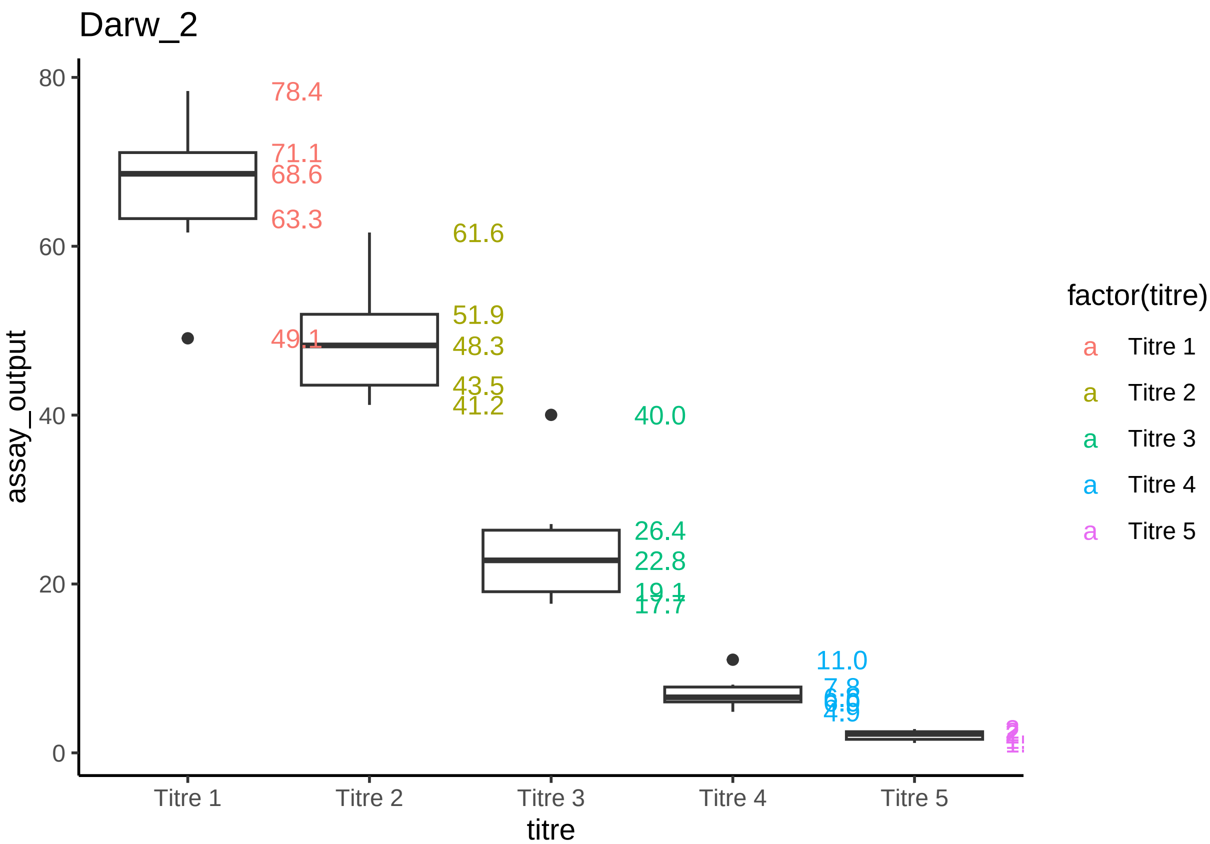

Coyi_3
assay_output
titre
80
60
40
20
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
81.3
75.1
69.9
64.3
39.2
68.6
65.1
53.0
45.4
22.1
37.2
29.1
18.1
14.7
4.5
12.5
8.4
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[20]]
```

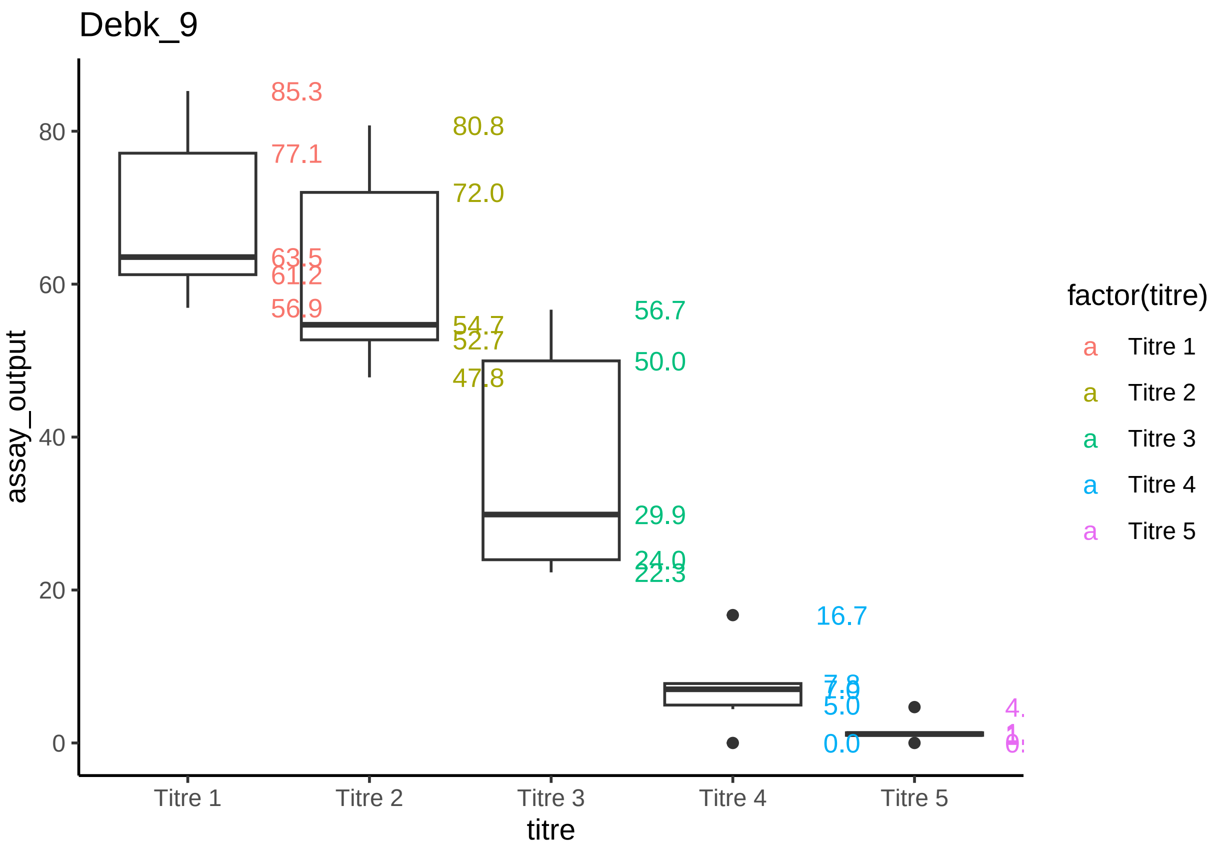


Dard_2
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
62.9
58.6
53.8
43.7
37.8
67.5
60.5
58.5
46.0
25.1
37.5
32.5
30.3
23.7
16.1
3.7
5.1


```
##
## [[21]]
```

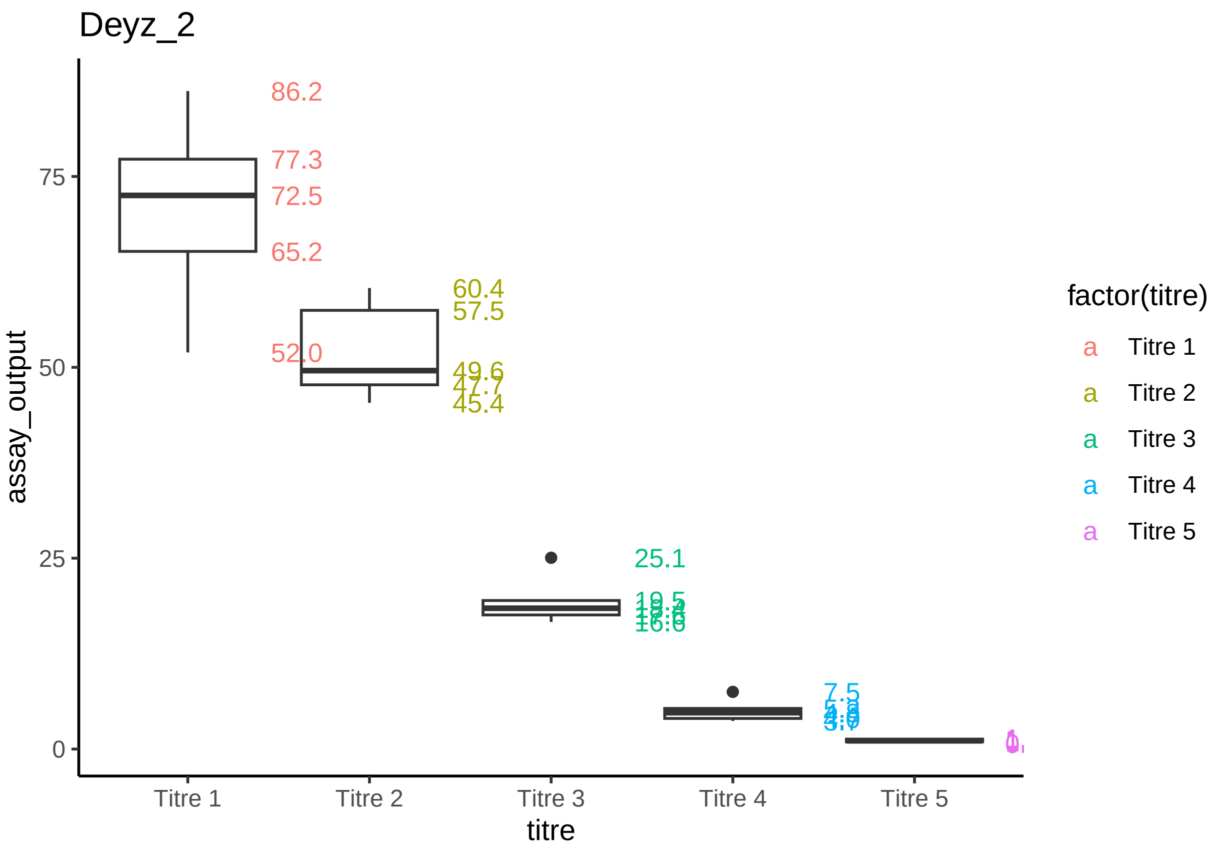

Darw_2
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
78.4
71.1
68.6
63.3
49.1
61.6
51.9
48.3
43.5
41.2
40.0
26.4
22.8
19.1
17.7
11.0
factor(titre)

```
##
## [[22]]
```

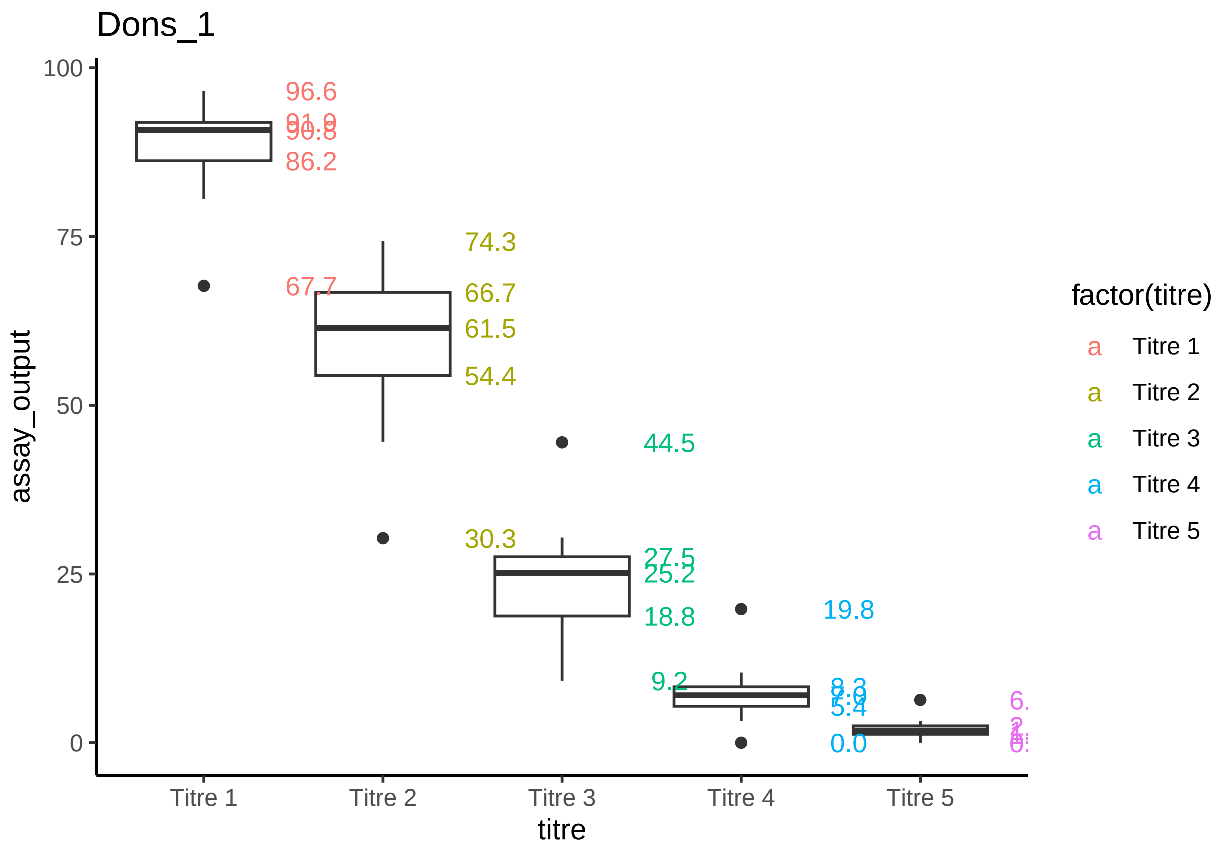


Debk_9
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
85.3
77.1
63.5
61.2
56.9
80.8
72.0
54.7
52.7
47.8
56.7
50.0
29.9
24.0
22.3
16.7
7.8
7.0
5.0
0.0

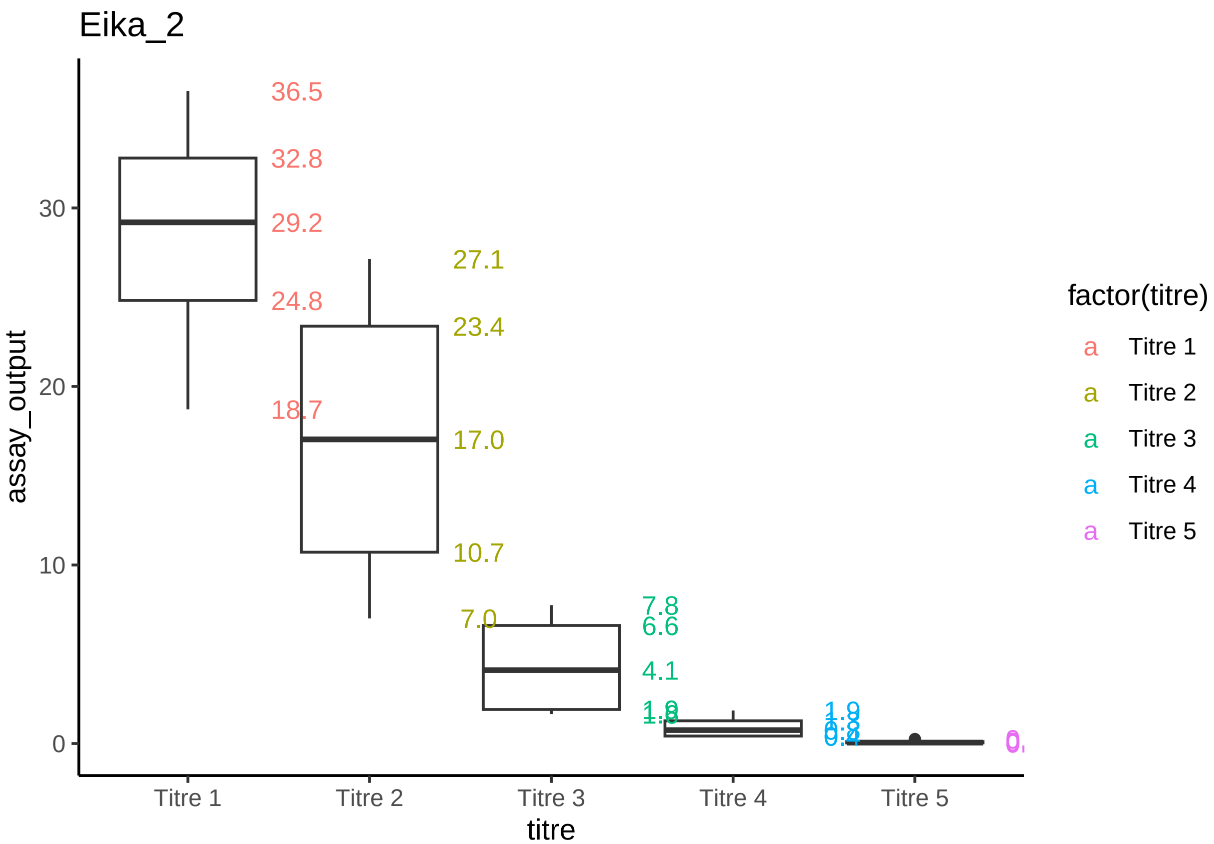

```
##
## [[23]]
```


Deyz_2
86.2
77.3
72.5
65.2
52.0
60.4
57.5
49.6
47.7
45.4
25.1
19.5
7.5
assay_output
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

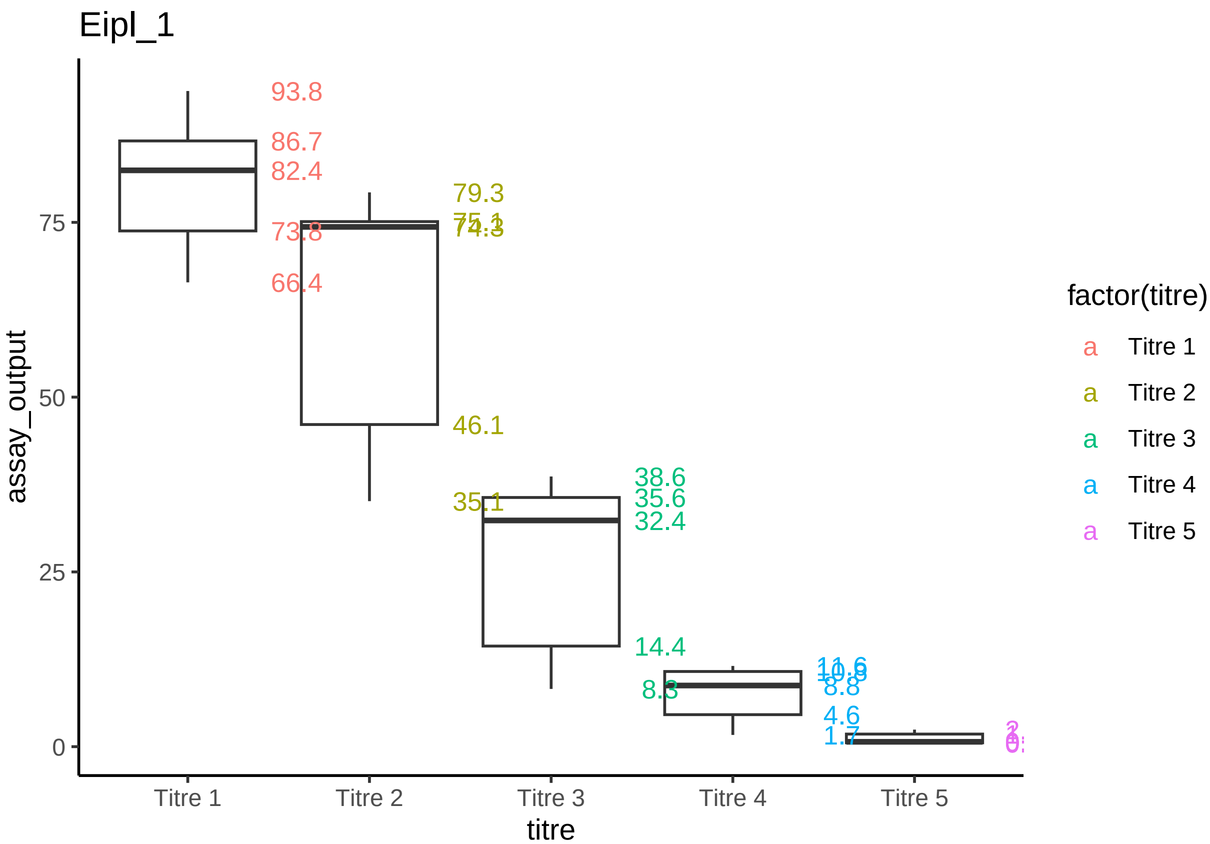
```
##
## [[24]]
```


Dons_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
100
75
50
25
0
96.6
91.9
90.8
86.2
67.7
74.3
66.7
61.5
54.4
30.3
44.5
27.5
25.2
18.8
9.2
19.8
8.3
5.4
0.0
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

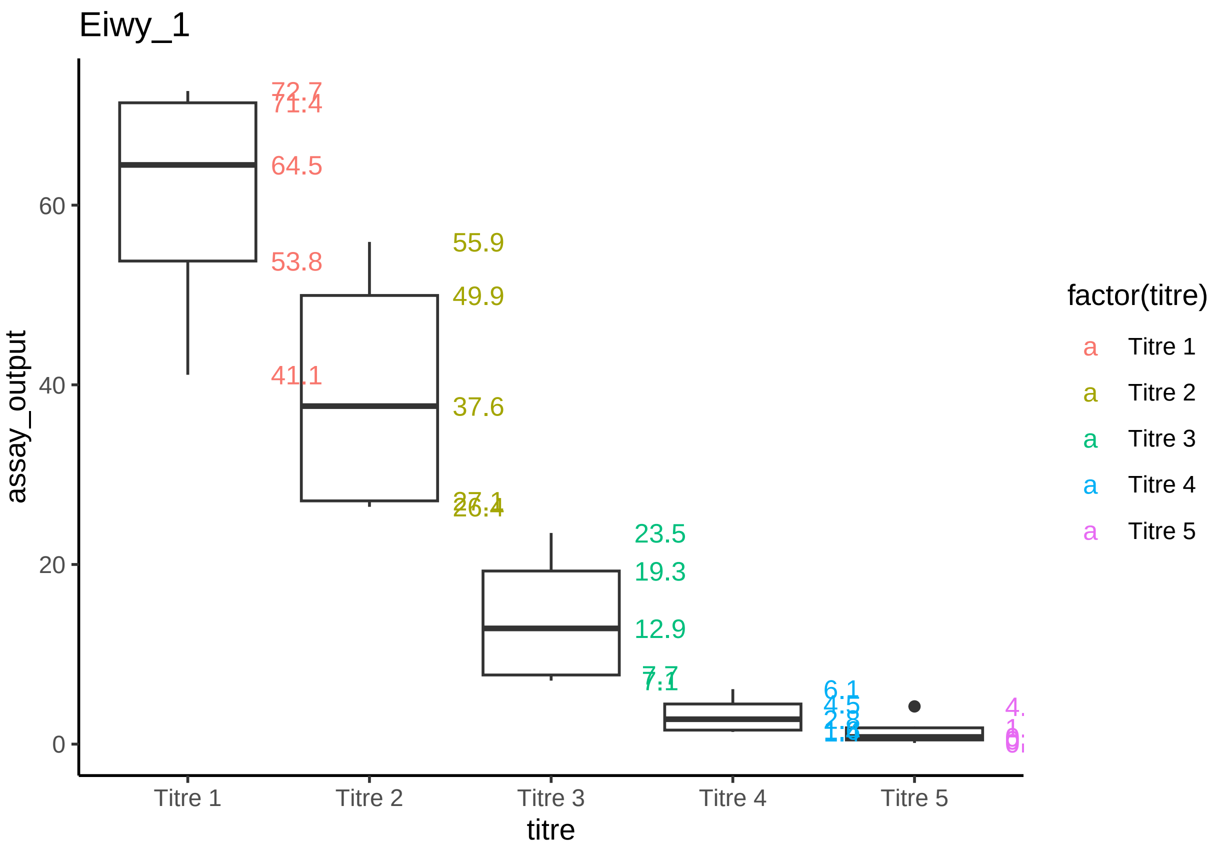
```
##
## [[25]]
```


Eika_2
36.5
32.8
29.2
24.8
18.7
27.1
23.4
17.0
10.7
7.0
7.8
6.6
4.1
assay_output
30
20
10
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

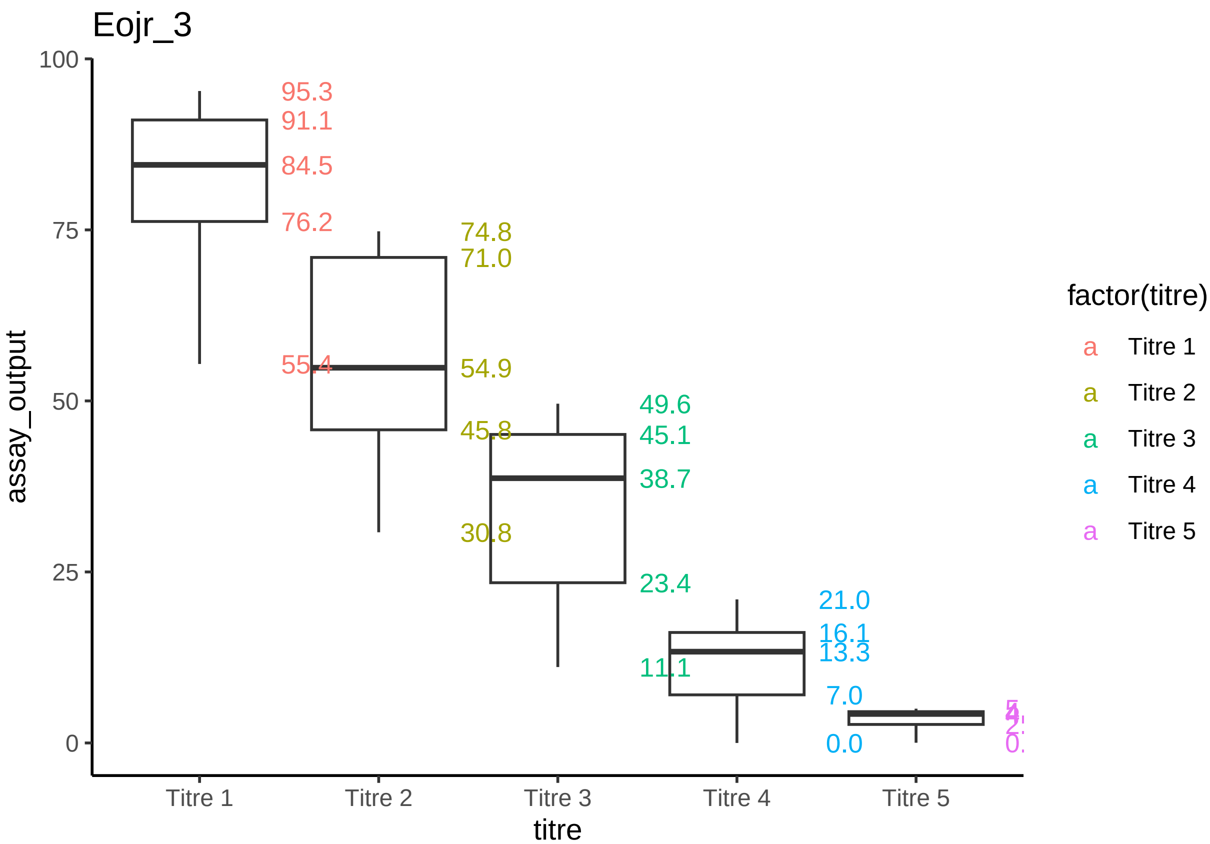
```
##
## [[26]]
```


Eipl_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
25
50
75
93.8
86.7
82.4
66.4
79.3
46.1
35.1
38.6
35.6
32.4
14.4
4.6
1.7
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[27]]
```

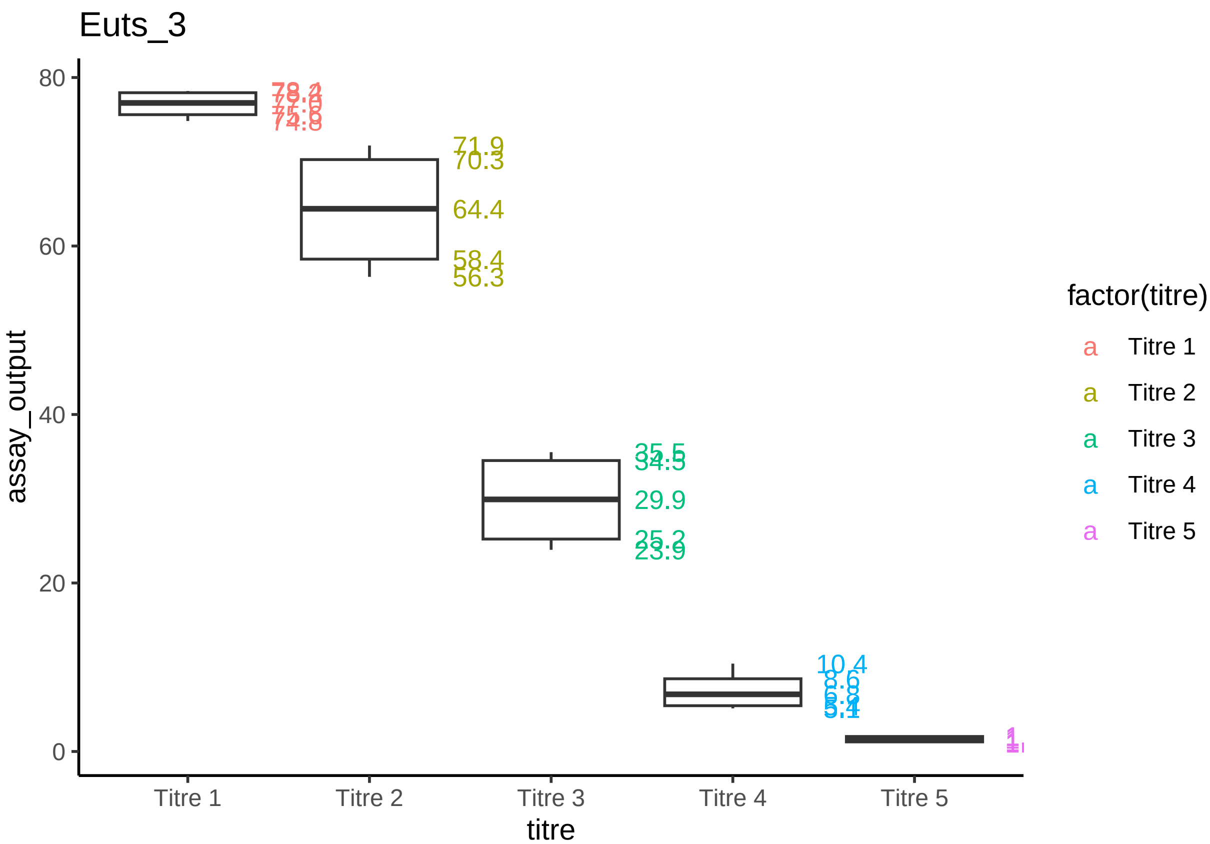

Eiwy_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
72.7
71.4
64.5
53.8
41.1
55.9
49.9
37.6
27.1
26.4
23.5
19.3
12.9
7.7
7.1
6.1
4.5
60
40
20
0

```
##
## [[28]]
```

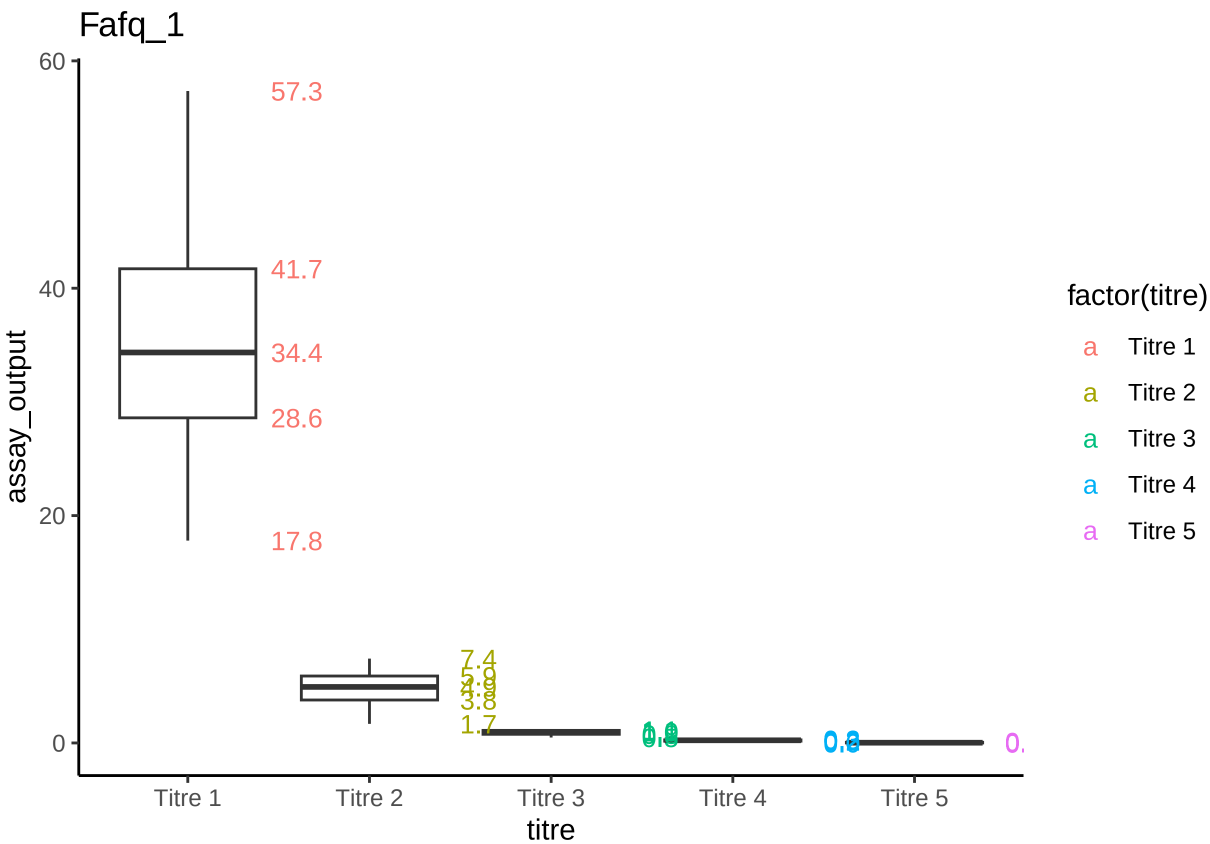


Eojr_3
100
75
50
25
0
assay_output
95.3
91.1
84.5
76.2
55.4
74.8
71.0
54.9
45.8
30.8
49.6
45.1
38.7
23.4
11.1
21.0
16.1
13.3
7.0
0.0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

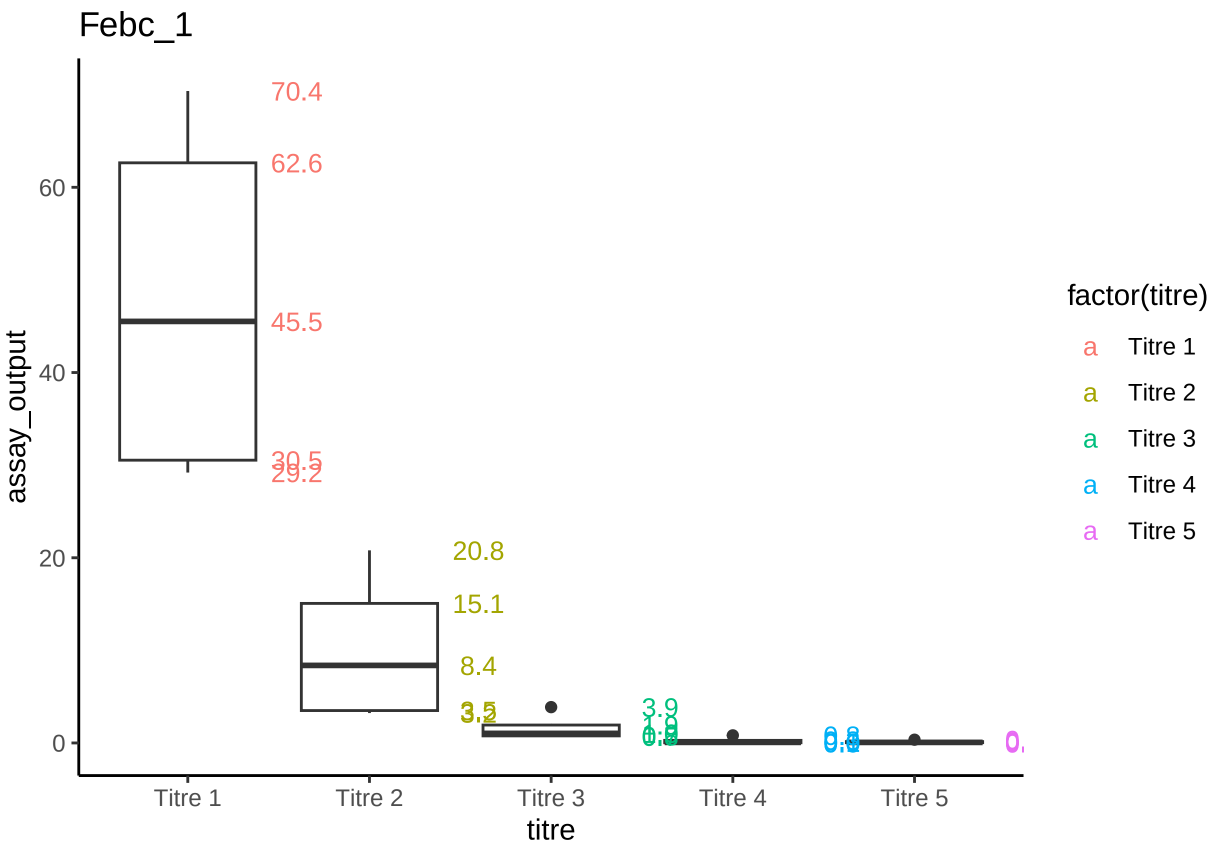

```
##
## [[29]]
```


Euts_3
assay_output
80
60
40
20
0
78.2
77.4
75.6
74.8
71.9
70.3
64.4
58.4
56.3
35.5
34.5
29.9
25.2
23.9
10.4
8.6
6.8
5.4
5.1
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

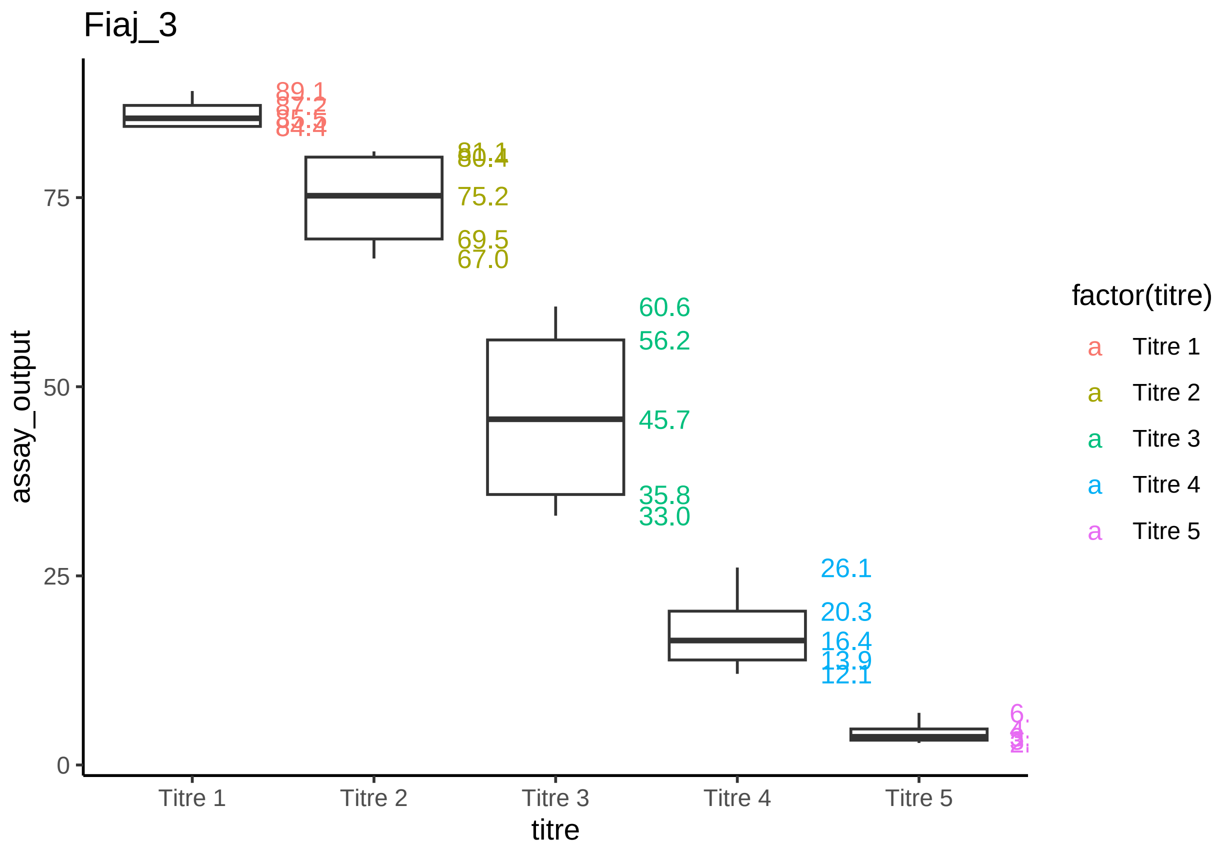
```
##
## [[30]]
```


Fafq_1
60
40
20
0
assay_output
57.3
41.7
34.4
28.6
17.8
7.4
3.8
1.7
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

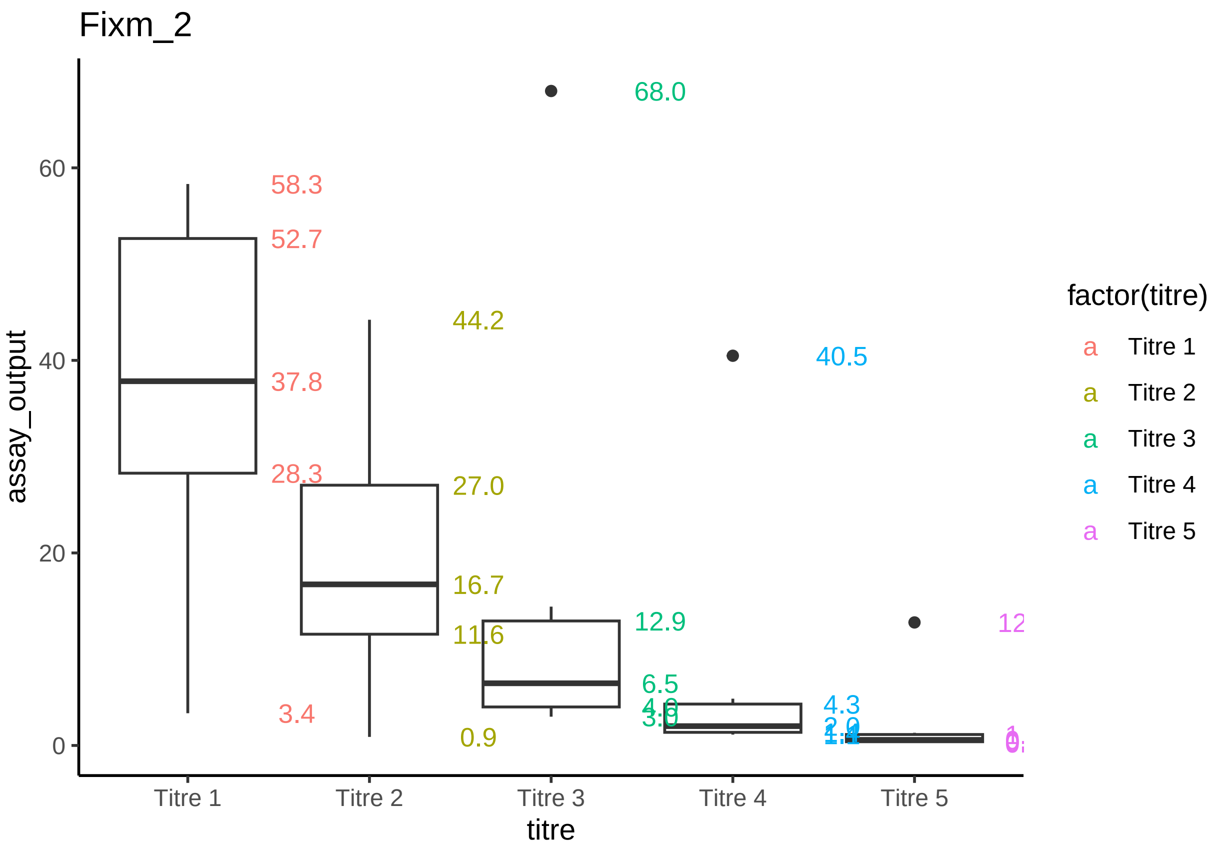
```
##
## [[31]]
```


Febc_1
70.4
62.6
45.5
30.5
29.2
20.8
15.1
8.4
3.5
3.2
3.9
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

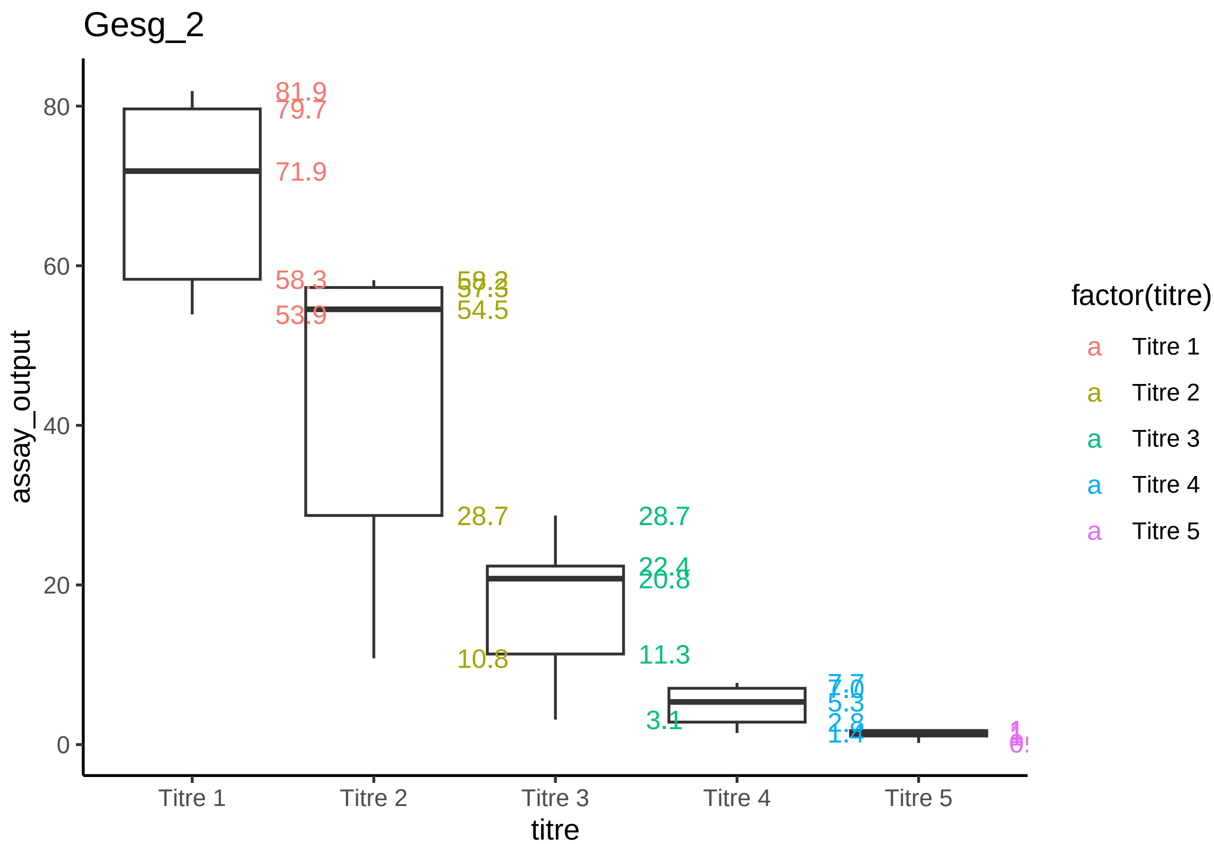
```
##
## [[32]]
```


Fiaj_3
89.1
75.2
69.5
67.0
60.6
56.2
45.7
35.8
33.0
26.1
20.3
16.4
13.9
12.1
assay_output
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[33]]
```

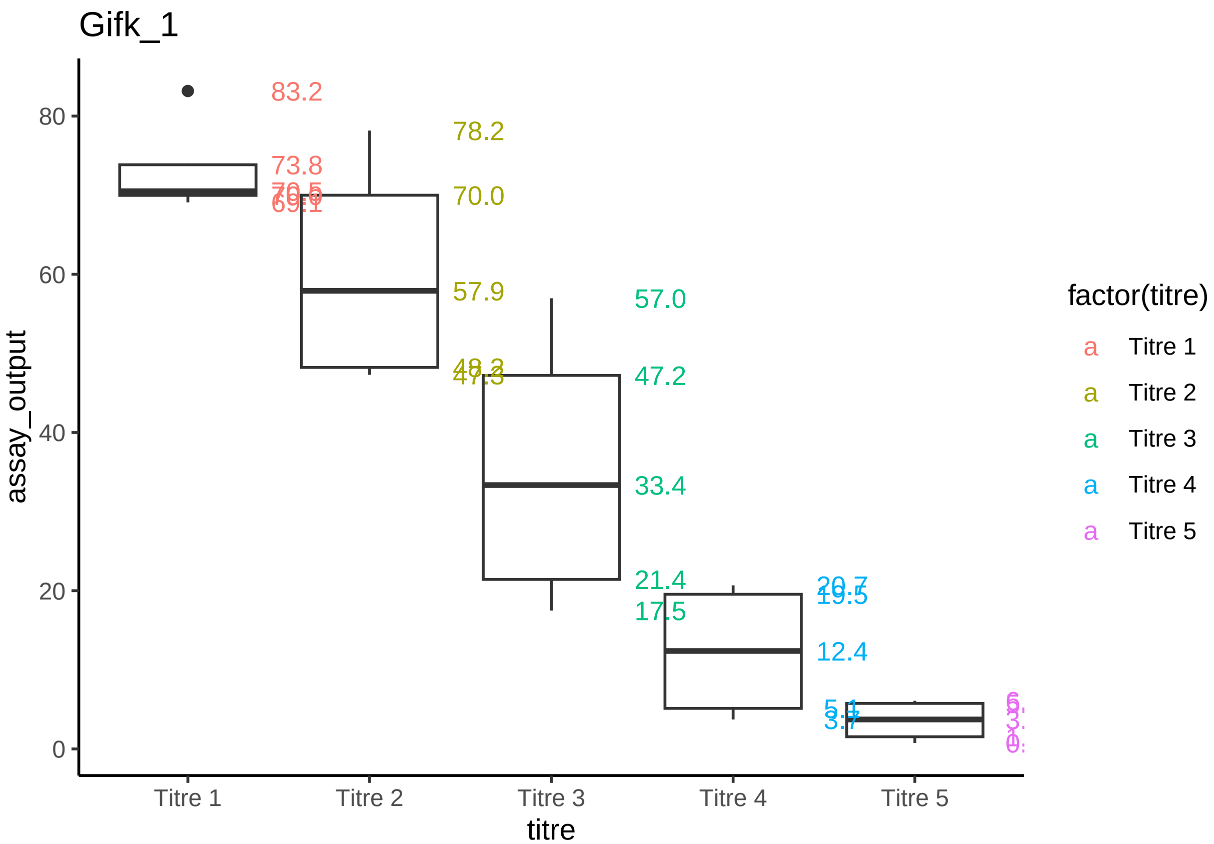

Fixm_2
68.0
58.3
52.7
44.2
40.5
37.8
28.3
27.0
16.7
12.9
11.6
6.5
3.4
4.3
0.9
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[34]]
```

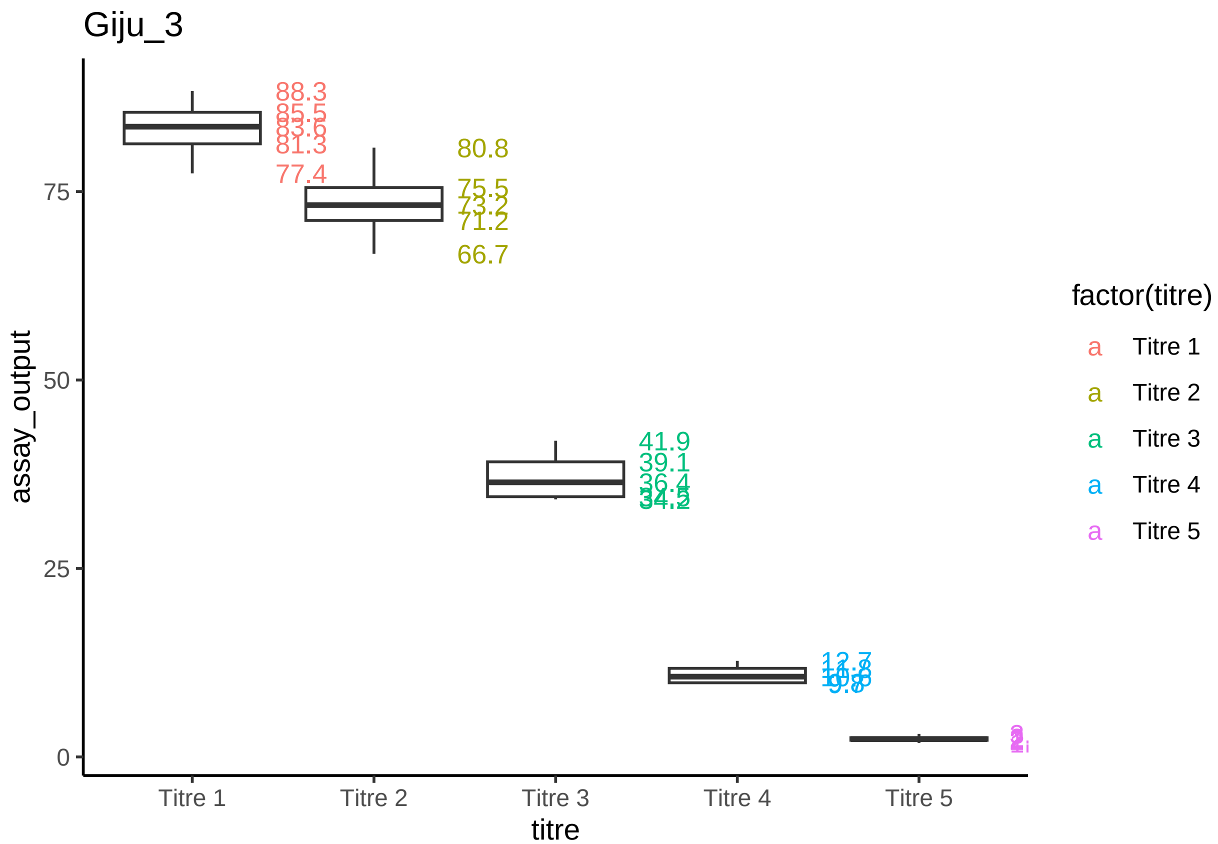


Gesg_2
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
81.9
79.7
71.9
58.3
53.9
58.2
57.3
54.5
28.7
10.8
28.7
22.4
20.8
11.3
3.1
7.7
7.0
5.3
2.8
1.4

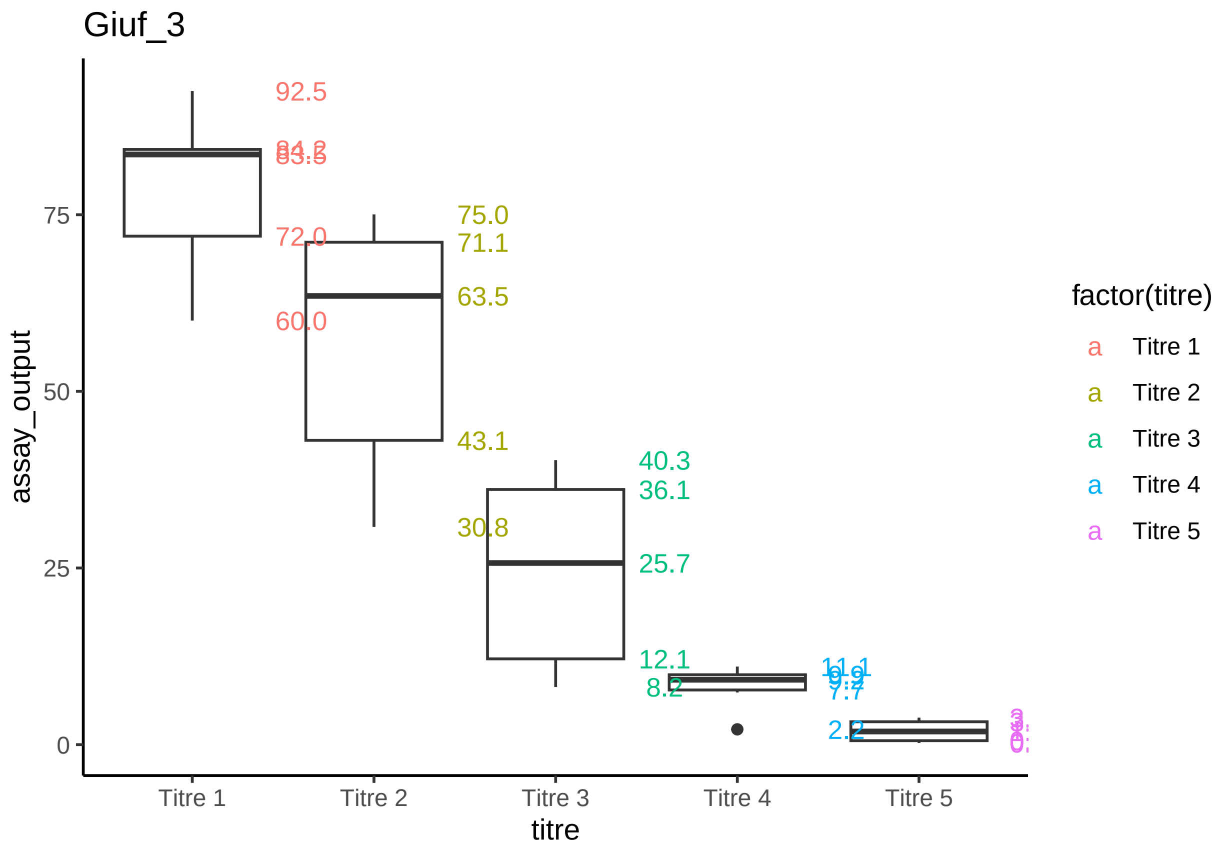

```
##
## [[35]]
```


Gifk_1
83.2
78.2
73.8
70.5
69.1
70.0
57.9
48.3
47.3
57.0
47.2
33.4
21.4
17.5
20.7
19.5
12.4
5.1
3.7
80
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

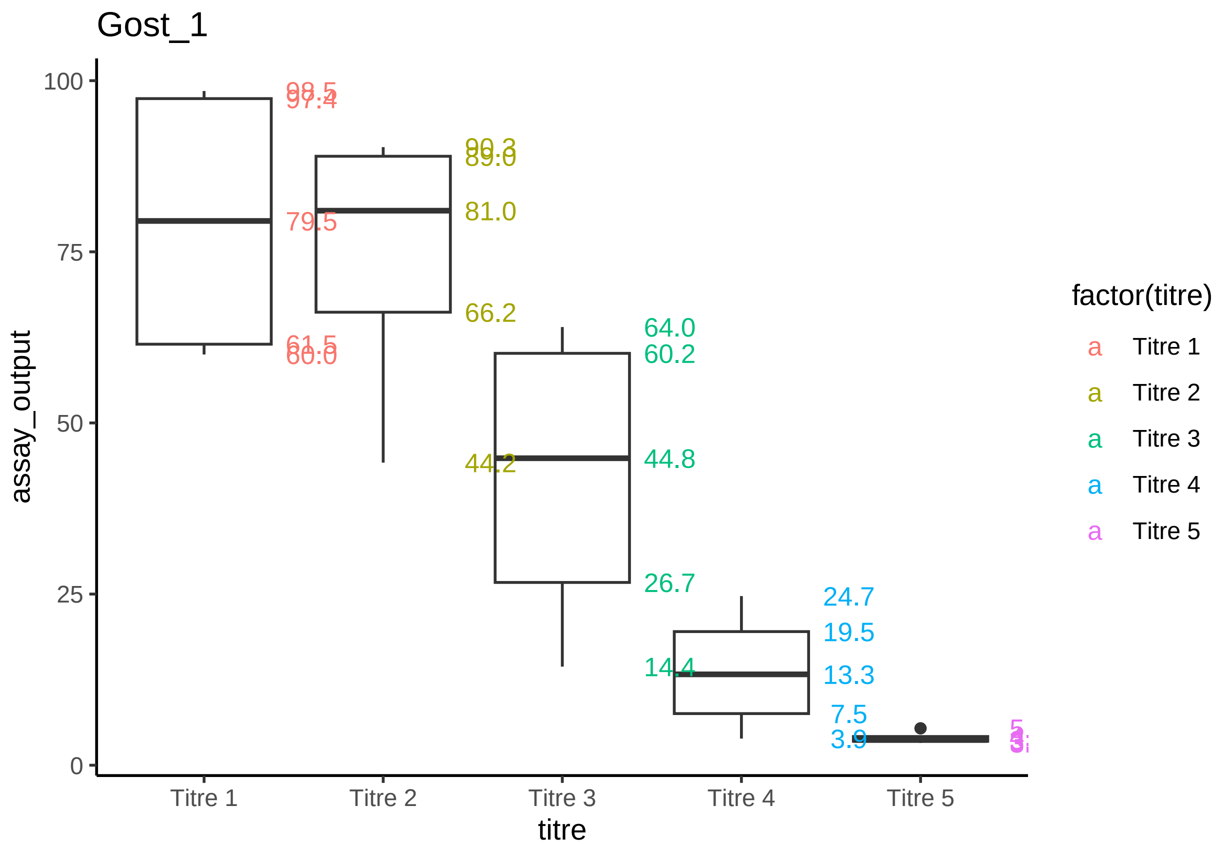
```
##
## [[36]]
```


Giju_3
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
88.3
77.4
80.8
66.7
41.9
39.1

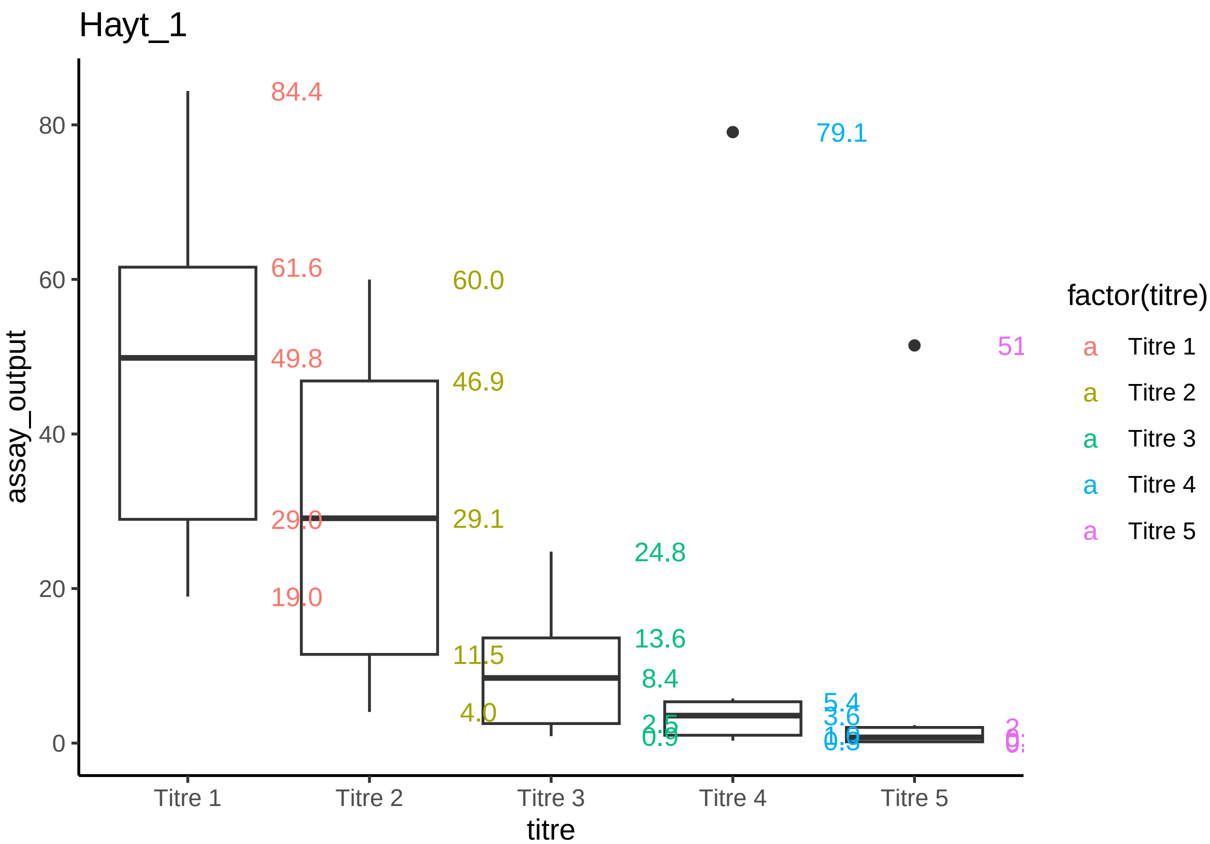

```
##
## [[37]]
```


Giuf_3
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
25
50
75
92.5
84.2
83.5
72.0
60.0
75.0
71.1
63.5
43.1
30.8
40.3
36.1
25.7
12.1
8.2
11.1
9.9
7.7
2.2
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

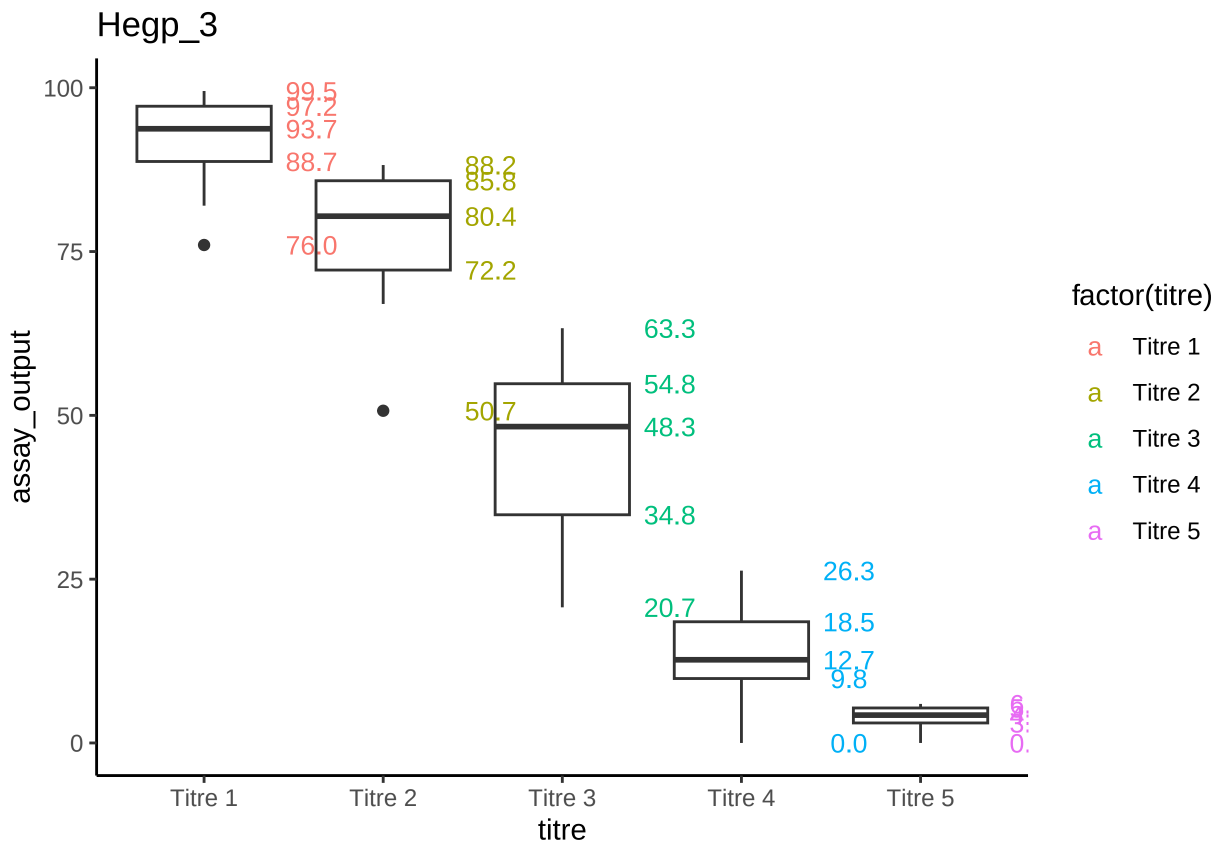
```
##
## [[38]]
```


Gost_1
100
75
50
25
0
assay_output
98.5
97.4
79.5
61.5
60.0
90.3
89.0
81.0
66.2
44.2
64.0
60.2
44.8
26.7
14.4
24.7
19.5
13.3
7.5
3.9
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

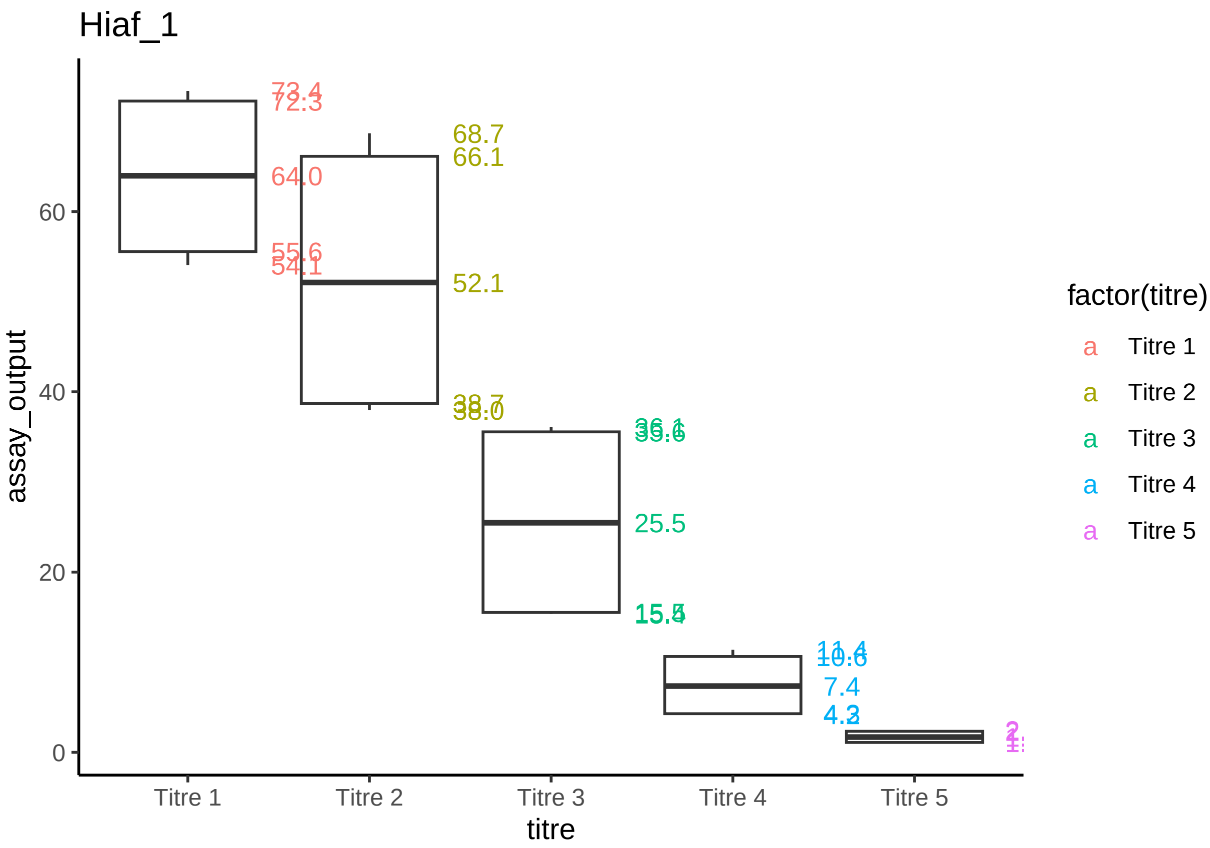
```
##
## [[39]]
```


Hayt_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
84.4
61.6
49.8
29.0
19.0
60.0
46.9
29.1
11.5
4.0
24.8
13.6
8.4
2.5
0.9
79.1
5.4
3.6
1.9
0.9
51

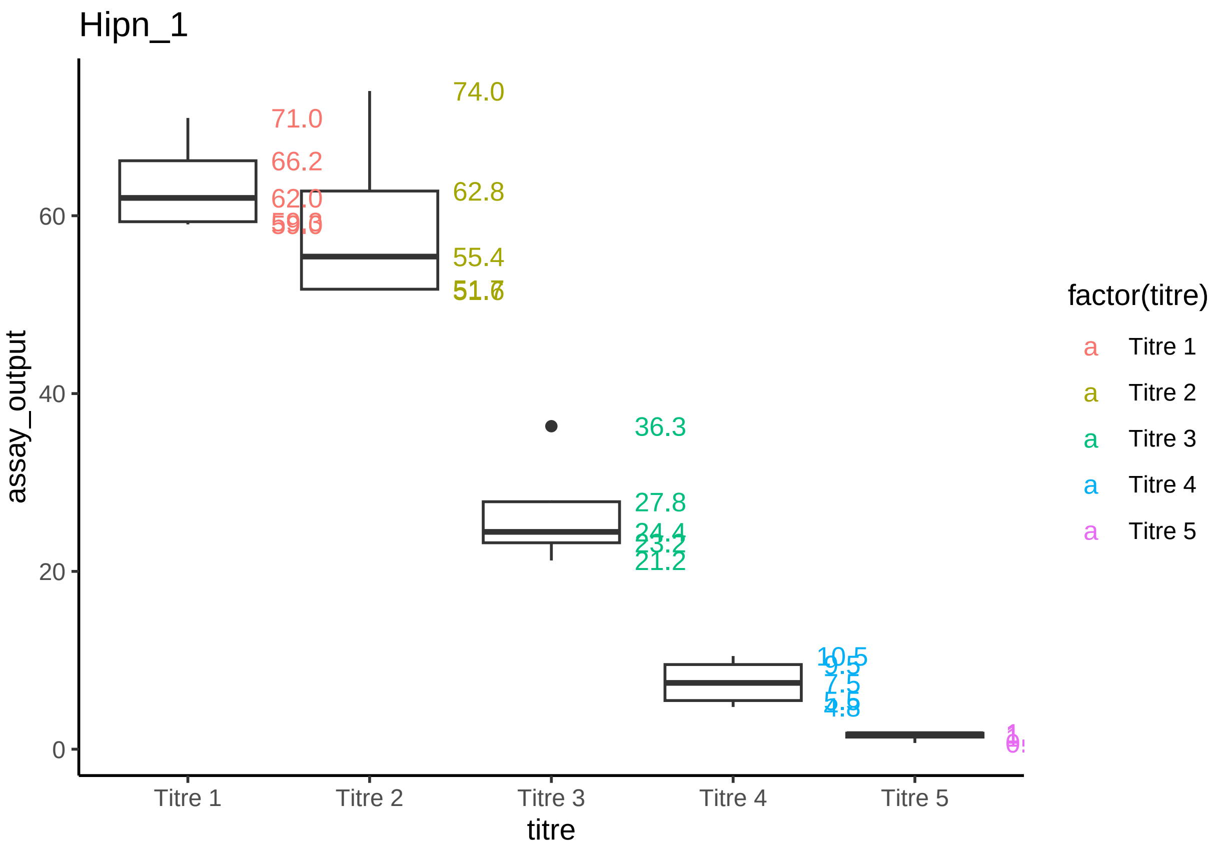
```
##
## [[40]]
```


Hegp_3
assay_output
100
75
50
25
0
99.5
97.2
93.7
88.7
76.0
88.2
85.8
80.4
72.2
50.7
63.3
54.8
48.3
34.8
20.7
26.3
18.5
12.7
9.8
0.0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[41]]
```

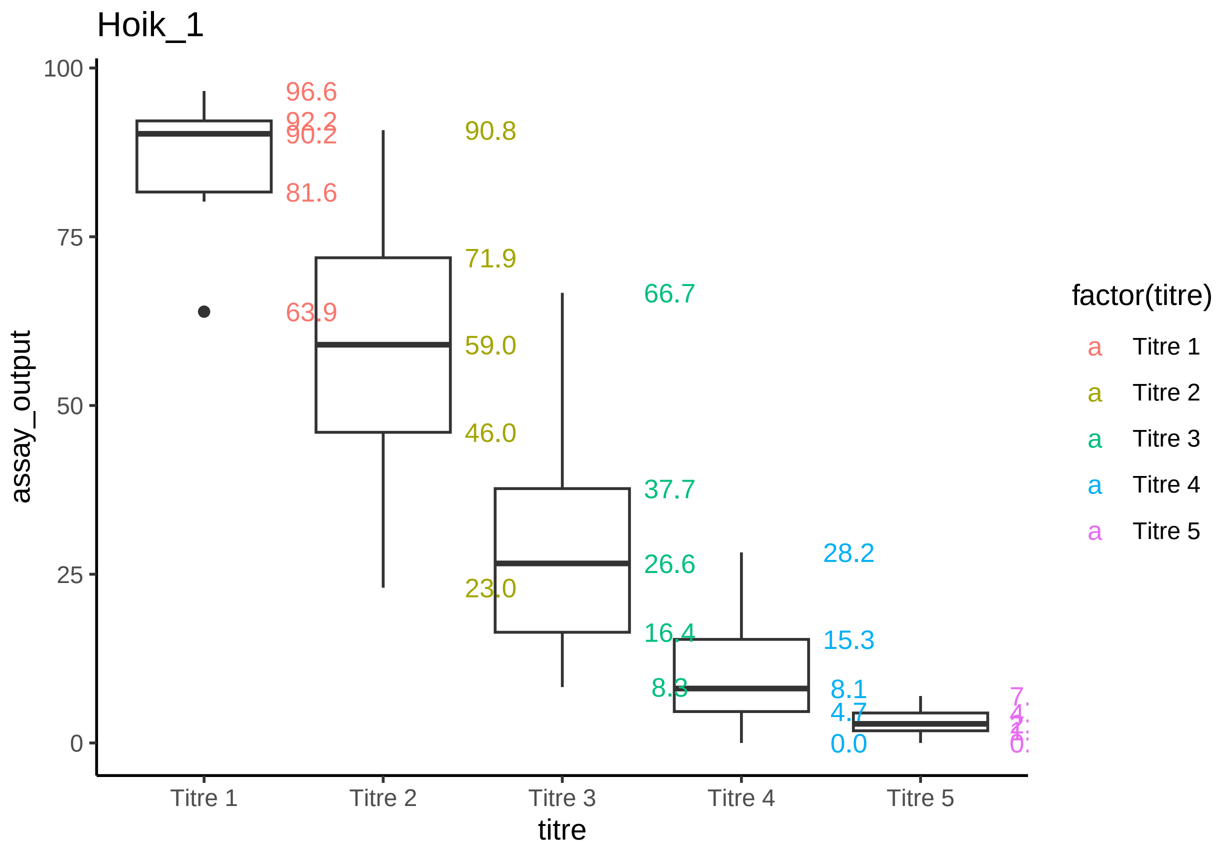

Hiaf_1
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5


```
##
## [[42]]
```

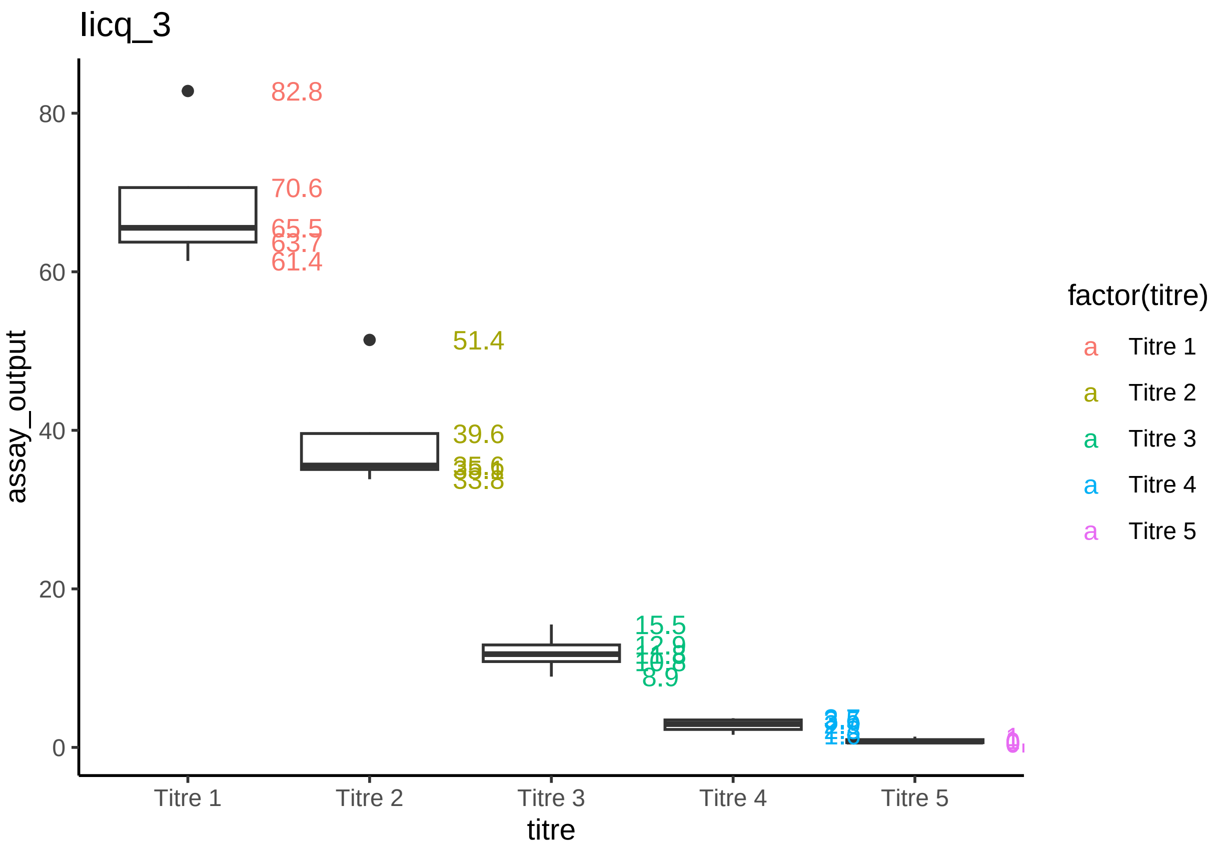


Hipn_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
20
40
60
71.0
66.2
62.0
74.0
62.8
55.4
36.3
27.8
21.2
10.5
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

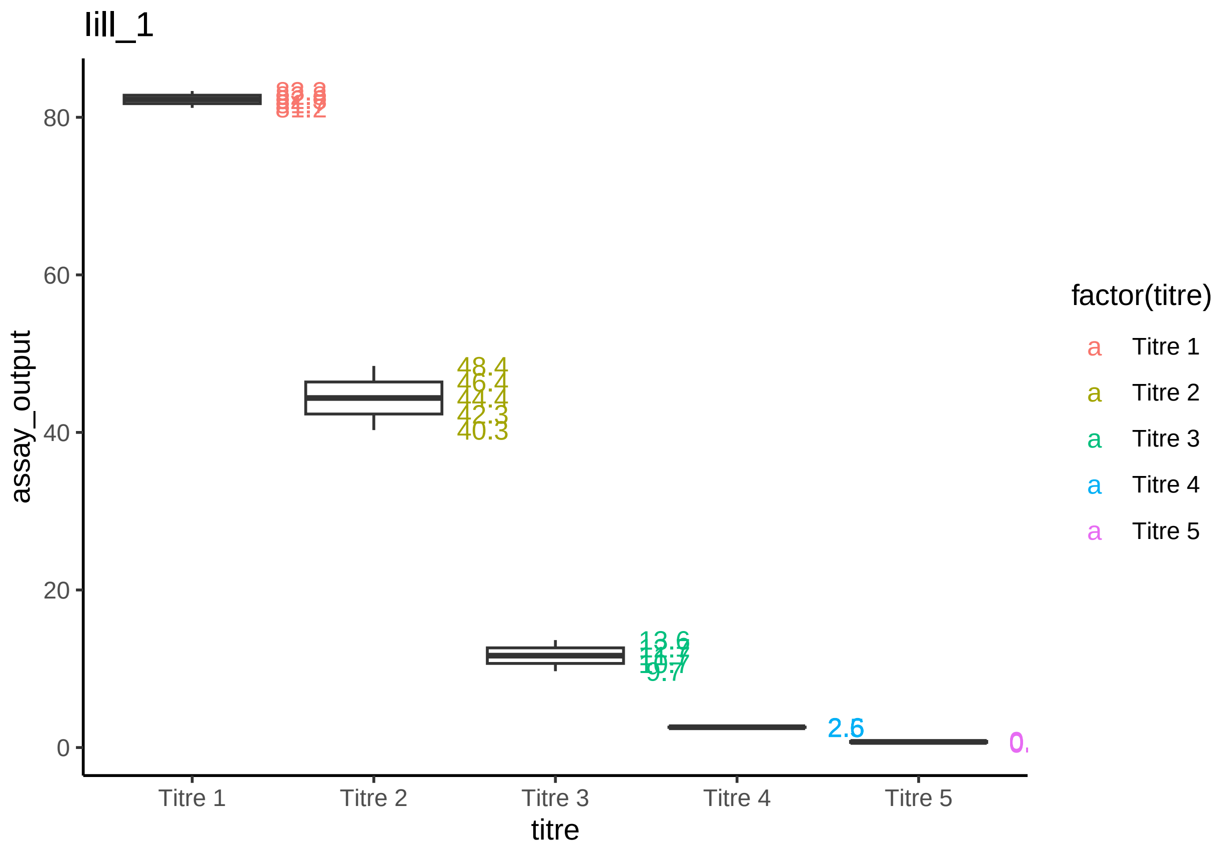

```
##
## [[43]]
```


Hoik_1
100
75
50
25
0
assay_output
96.6
92.2
90.2
81.6
63.9
90.8
71.9
59.0
46.0
23.0
66.7
37.7
26.6
16.4
8.3
28.2
15.3
8.1
4.7
0.0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

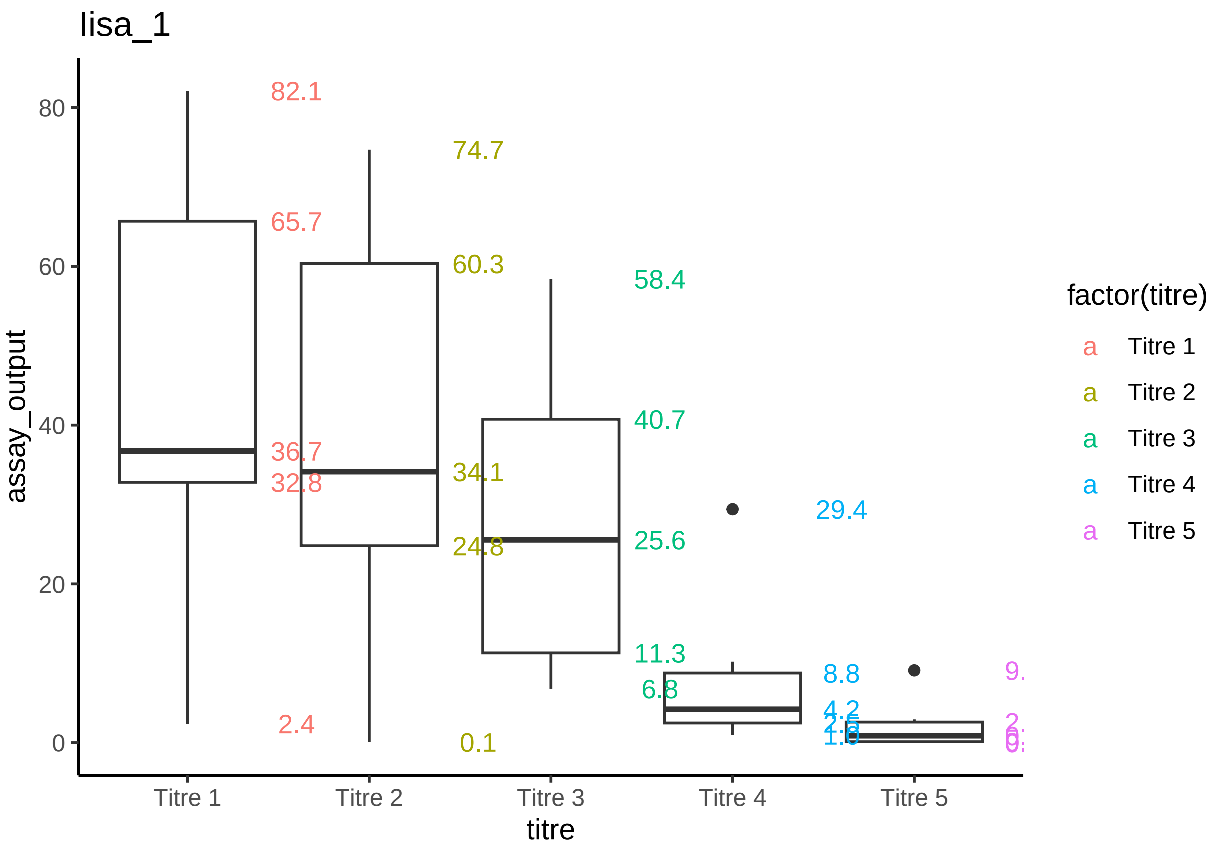
```
##
## [[44]]
```


licq_3
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
82.8
70.6
61.4
51.4
39.6
15.5
8.9


```
##
## [[45]]
```

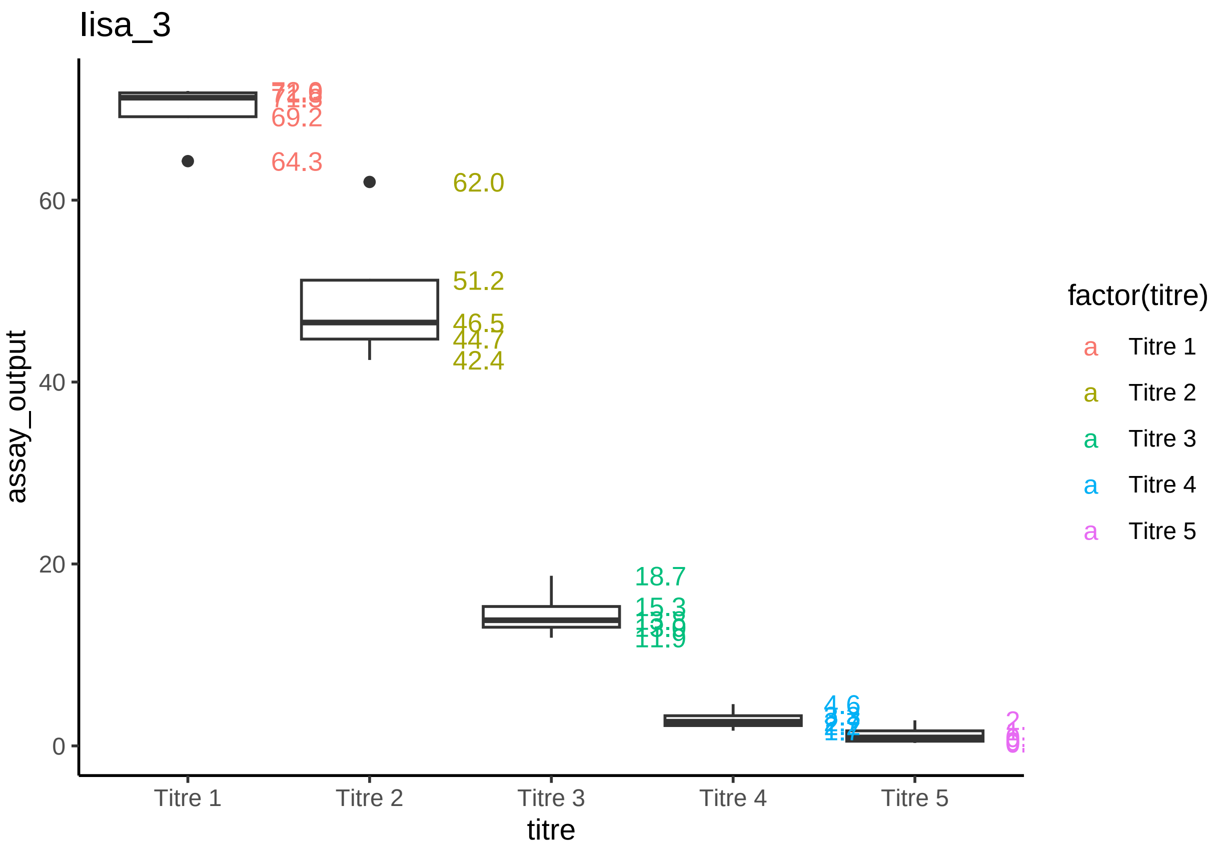

Iill_1
assay_output
80
60
40
20
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
48.4
46.4
44.4
42.3
40.3
13.6
9.7
2.6
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[46]]
```

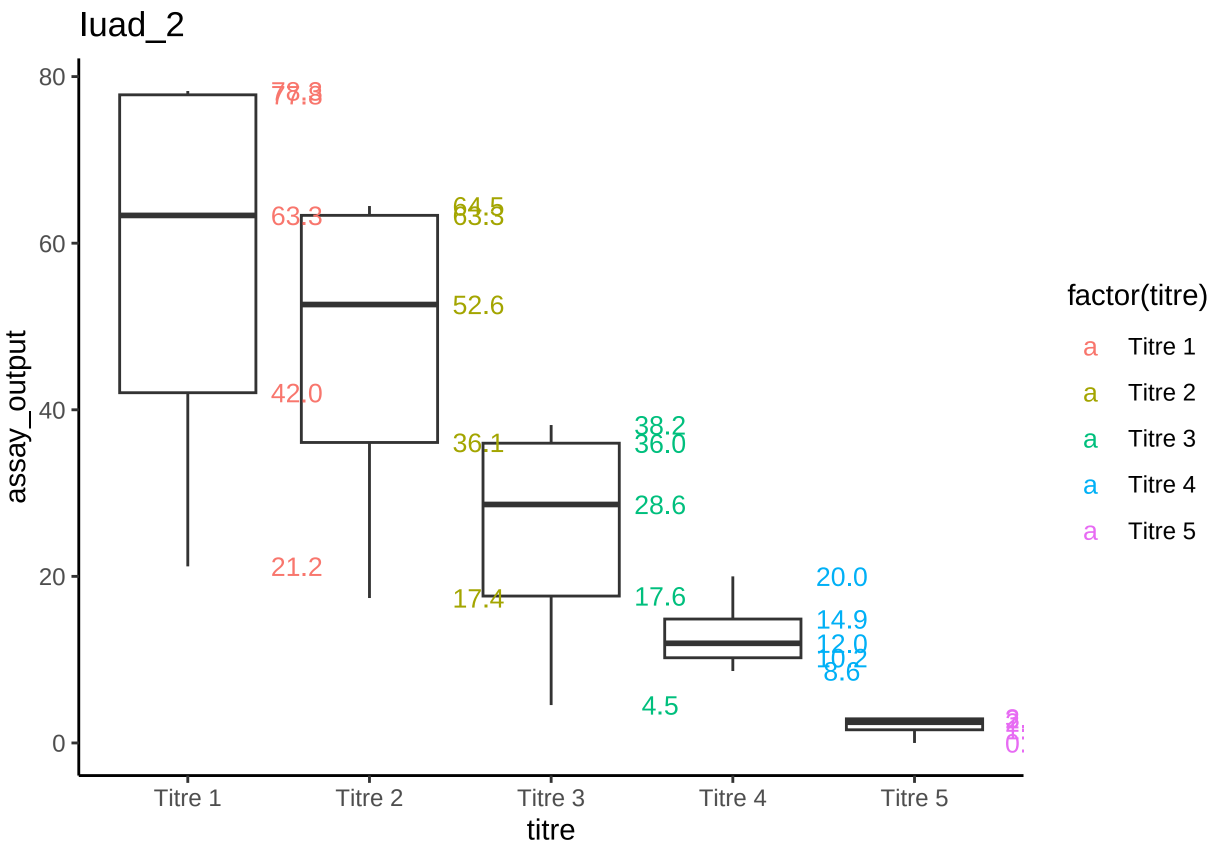


lisa_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5
82.1
65.7
36.7
32.8
2.4
74.7
60.3
34.1
24.8
0.1
58.4
40.7
25.6
11.3
6.8
29.4
8.8
4.2

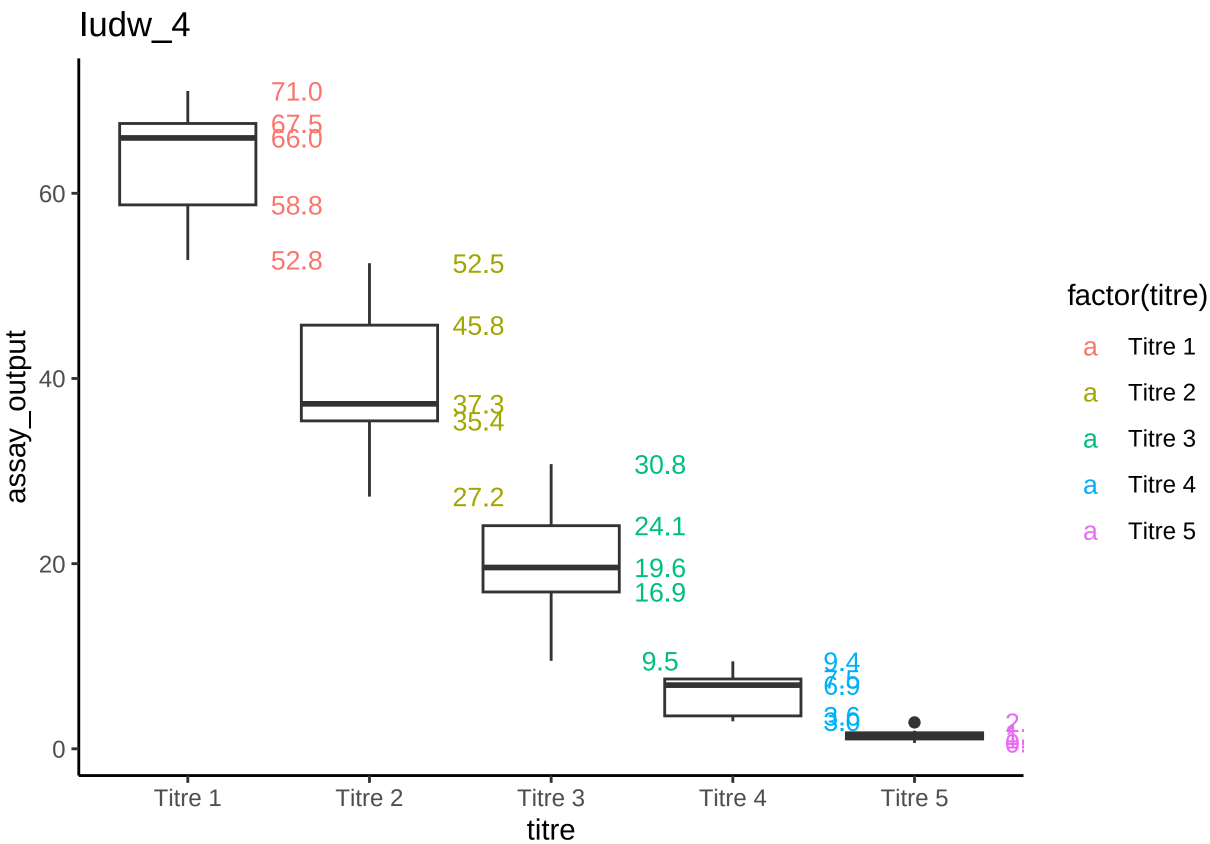

```
##
## [[47]]
```


lisa_3
assay_output
60
40
20
0
64.3
69.2
62.0
51.2
46.5
44.7
42.4
18.7
15.3
11.9
4.6
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[48]]
```

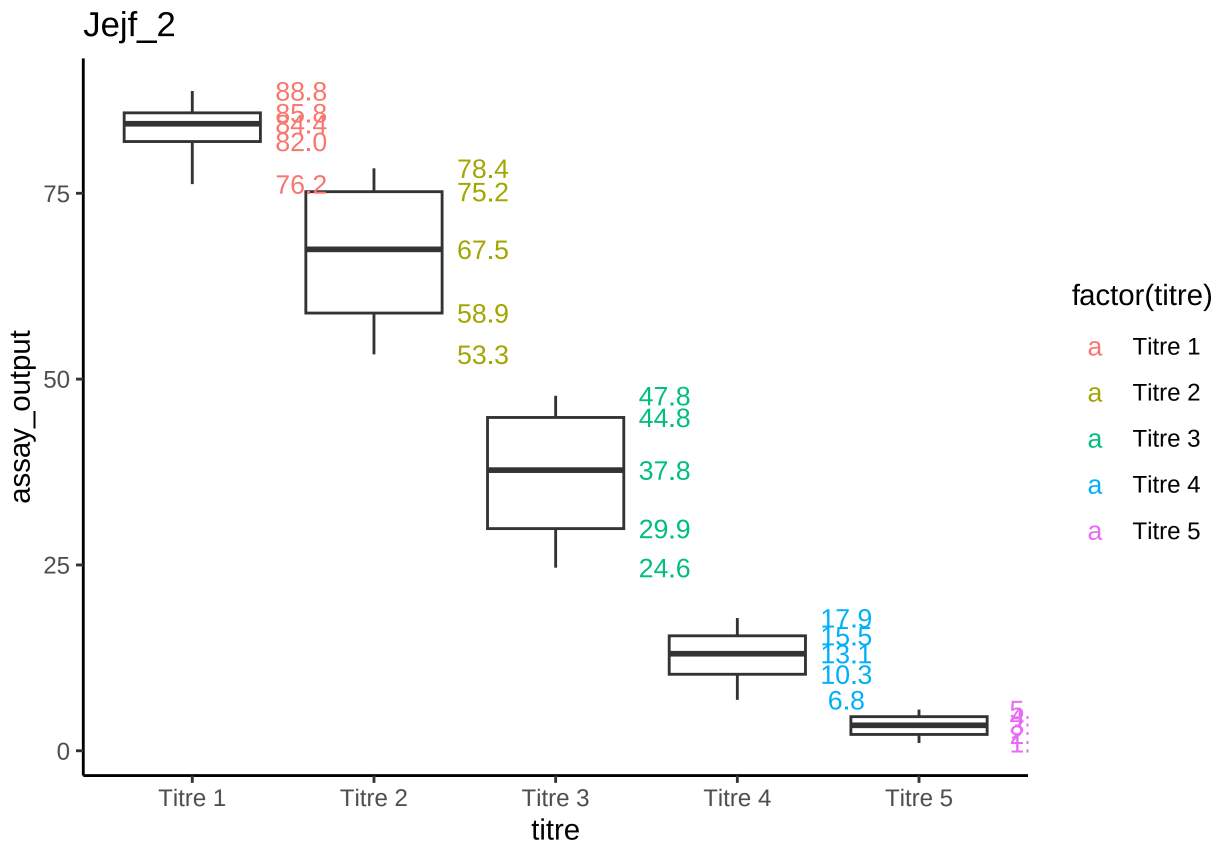

luad_2
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
78.8
77.8
63.3
42.0
21.2
64.5
63.3
52.6
36.1
17.4
38.2
36.0
28.6
17.6
4.5
20.0
14.9
12.0
10.2
8.6
0
20
40
60
80

```
##
## [[49]]
```

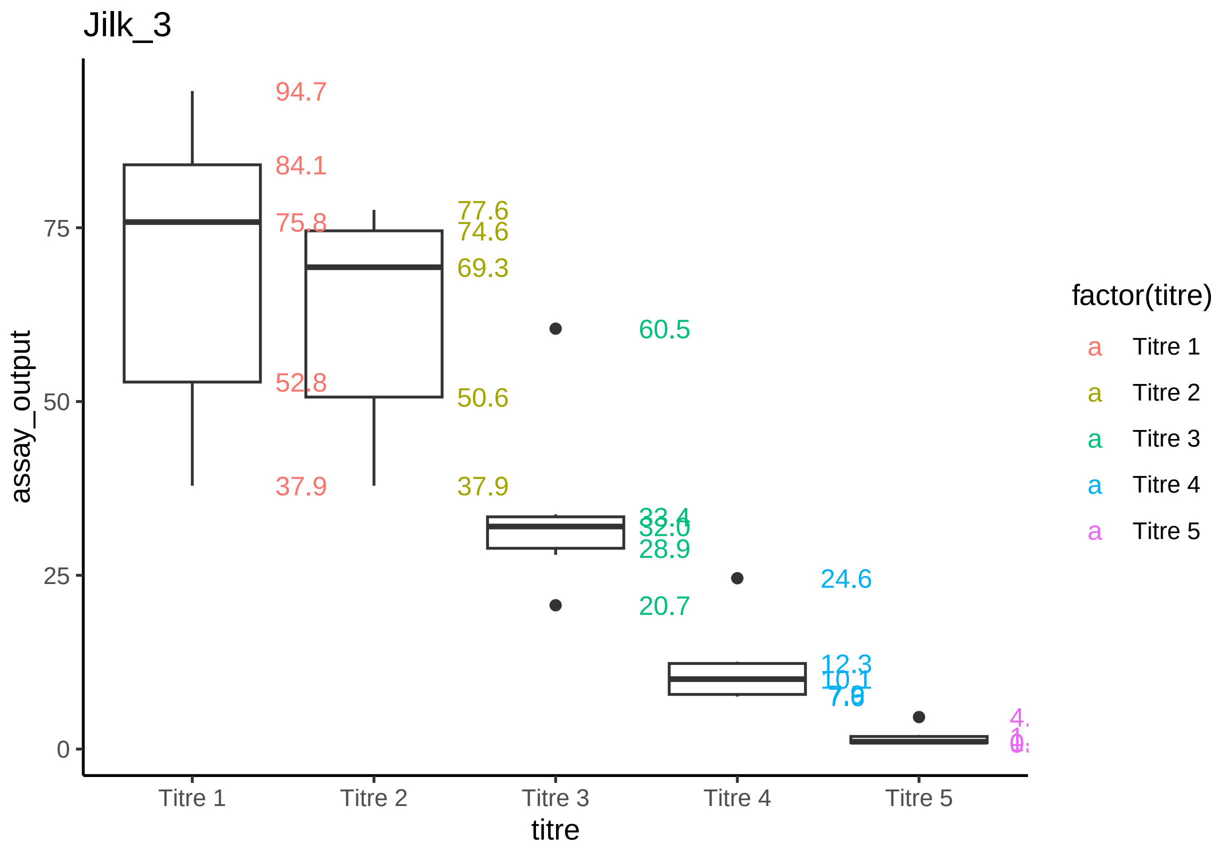


ludw_4
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
71.0
67.5
66.0
58.8
52.8
52.5
45.8
37.3
35.4
27.2
30.8
24.1
19.6
16.9
9.5
9.4
7.5
6.9
3.6
3.0


```
##
## [[50]]
```

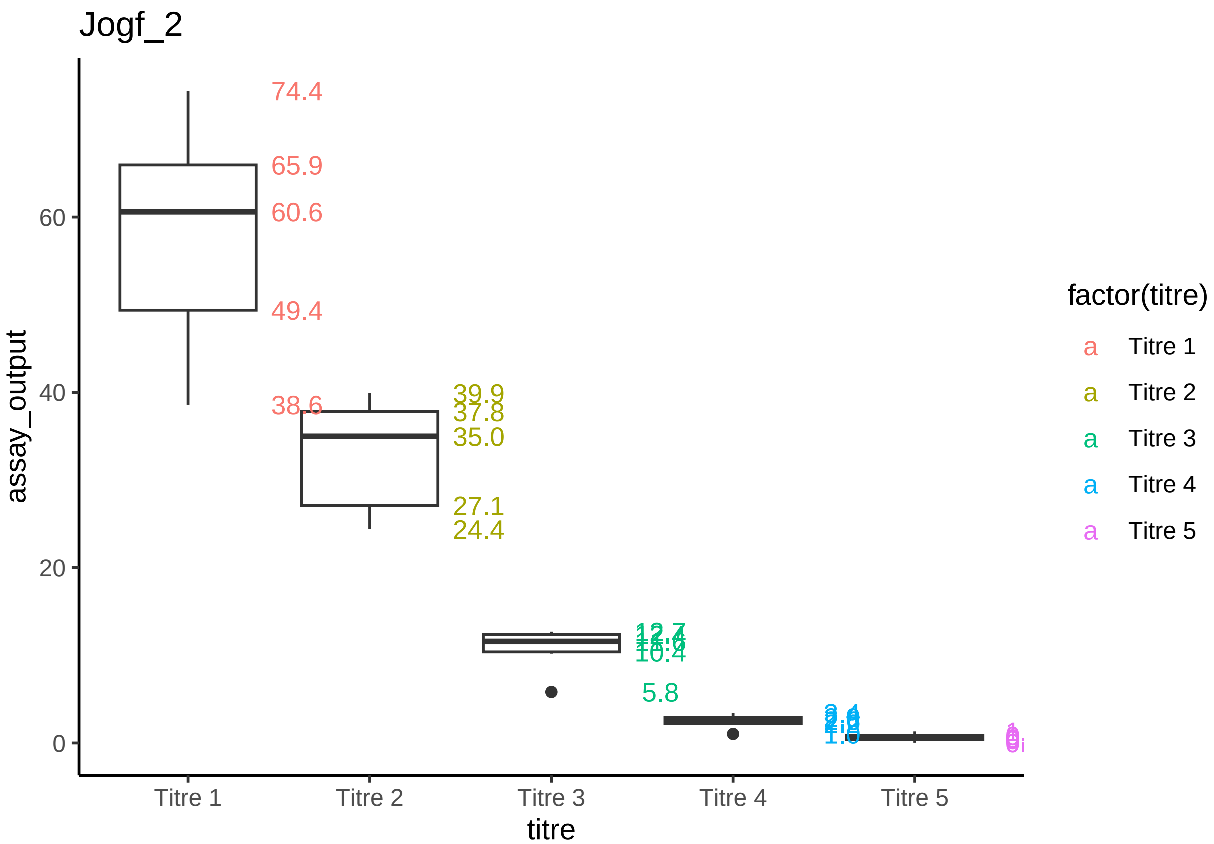

Jejf_2
88.8
85.8
84.4
82.0
76.2
78.4
75.2
67.5
58.9
53.3
47.8
44.8
37.8
29.9
24.6
17.9
15.5
13.1
10.3
6.8
75
50
25
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[51]]
```

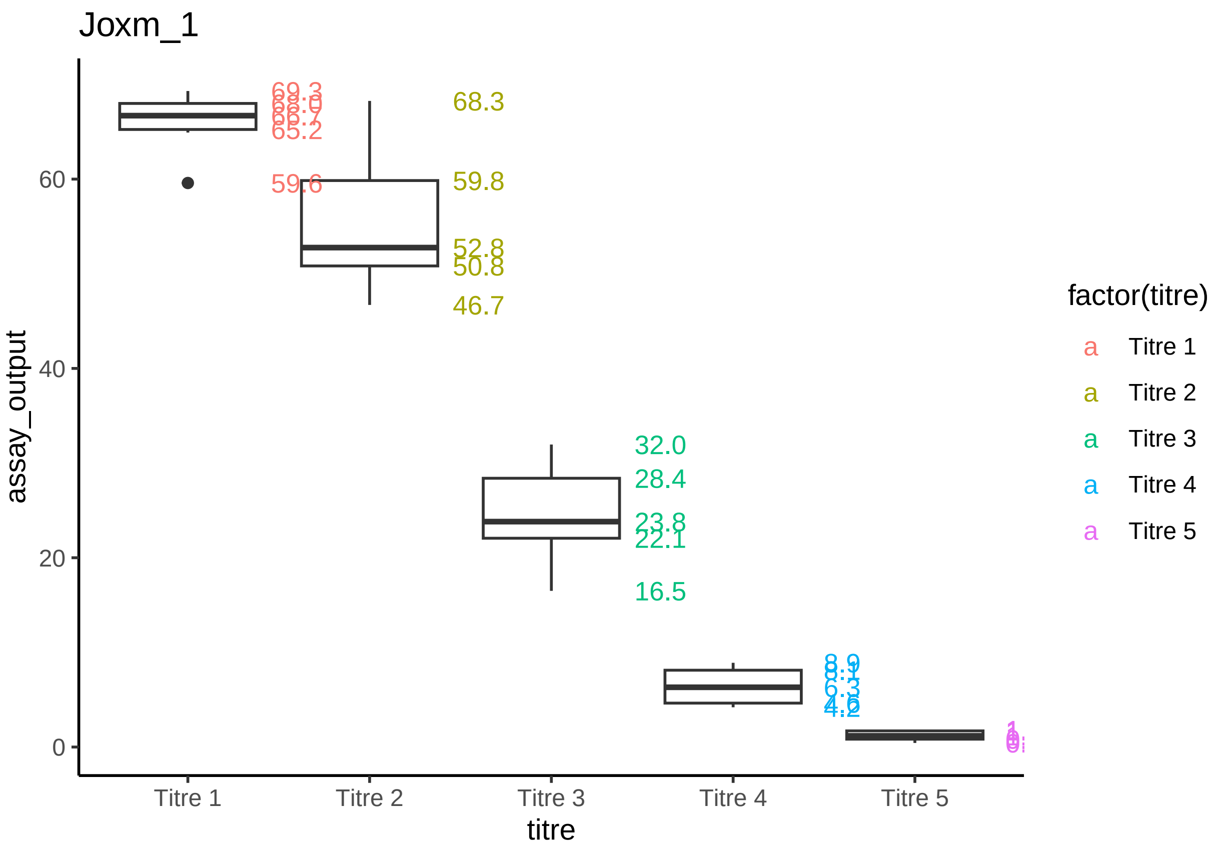


Jilk_3
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
25
50
75
94.7
84.1
75.8
52.8
37.9
77.6
74.6
69.3
50.6
37.9
60.5
33.4
32.0
28.9
20.7
24.6
12.3
10.1
7.0
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[52]]
```

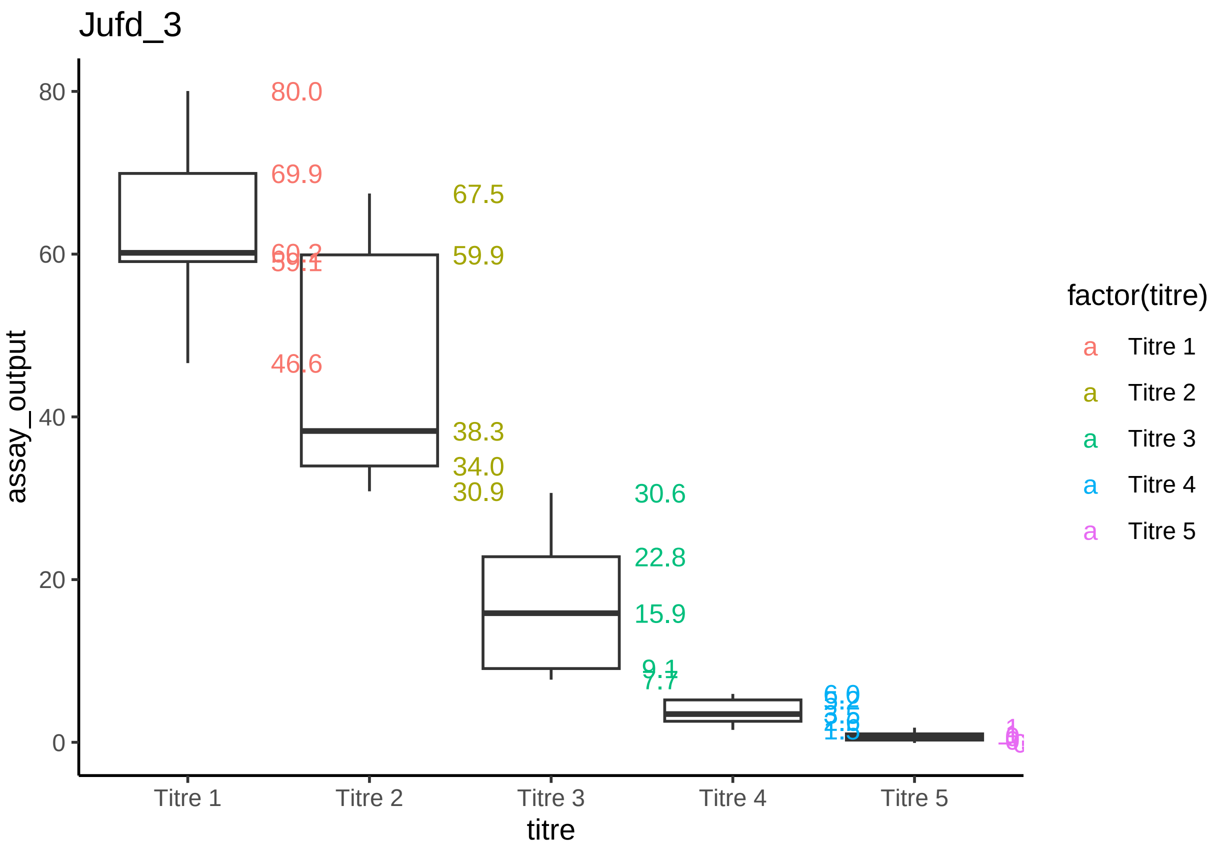

Jogf_2
assay_output
titre
0
20
40
60
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
74.4
65.9
60.6
49.4
38.6
39.9
37.8
35.0
27.1
24.4
5.8
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[53]]
```



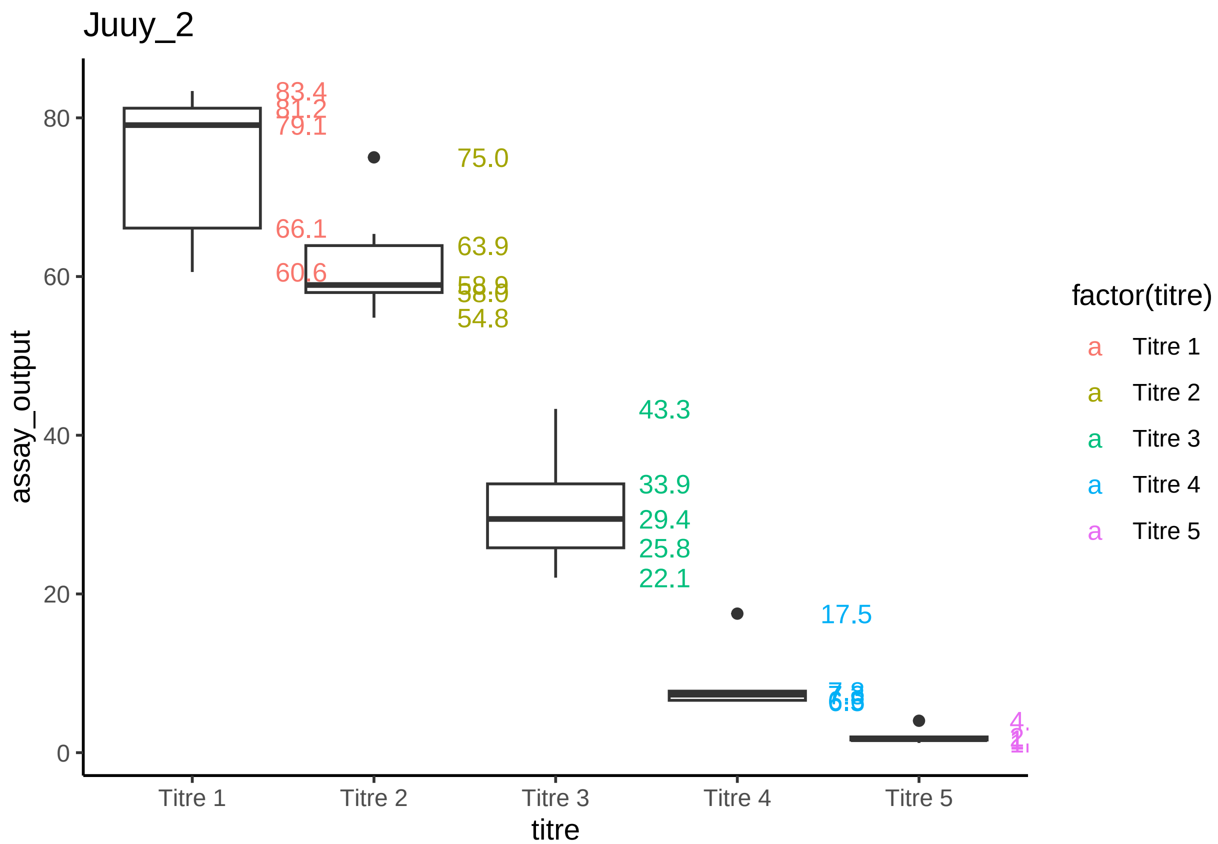
Joxm_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
68.3
59.8
46.7
32.0
28.4
16.5


```
##
## [[54]]
```

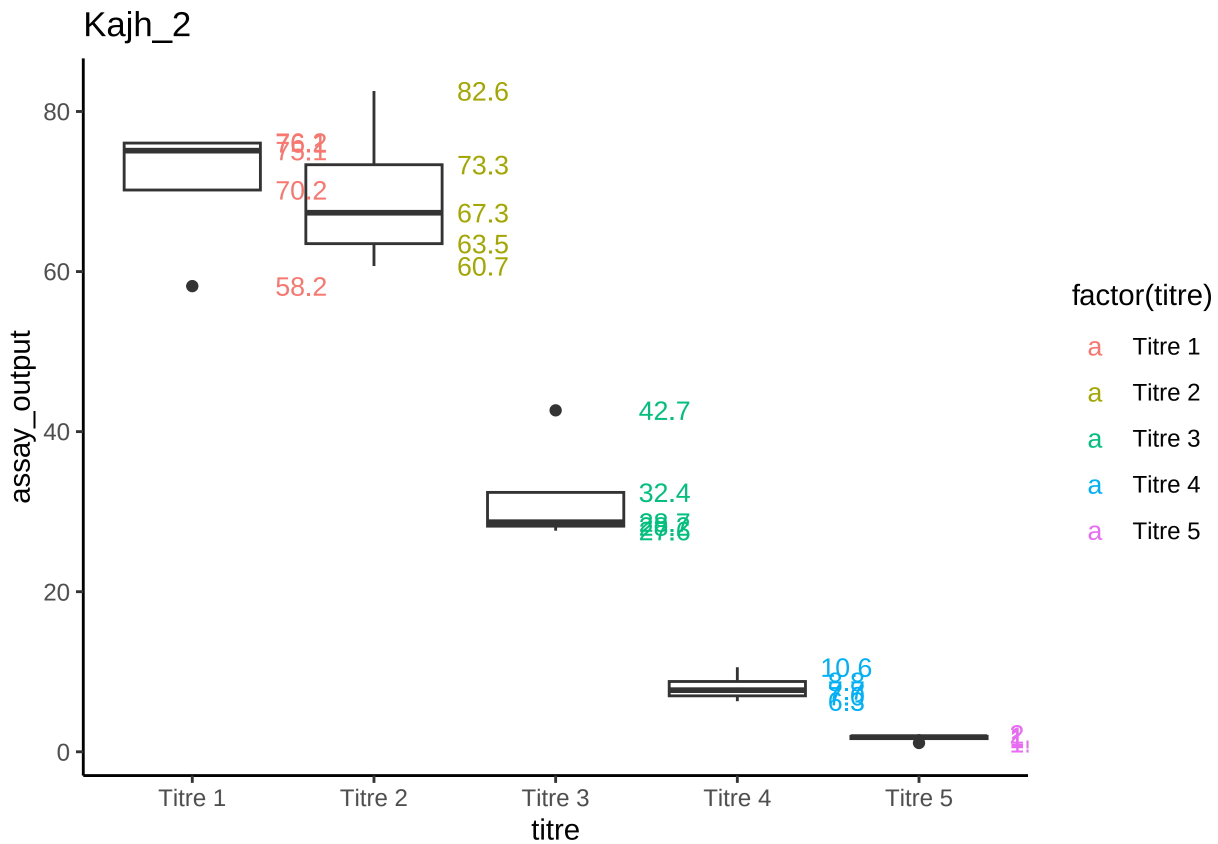


Jufd_3
80.0
69.9
60.2
59.1
46.6
67.5
59.9
38.3
34.0
30.9
30.6
22.8
15.9
9.1
7.7
6.0
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)

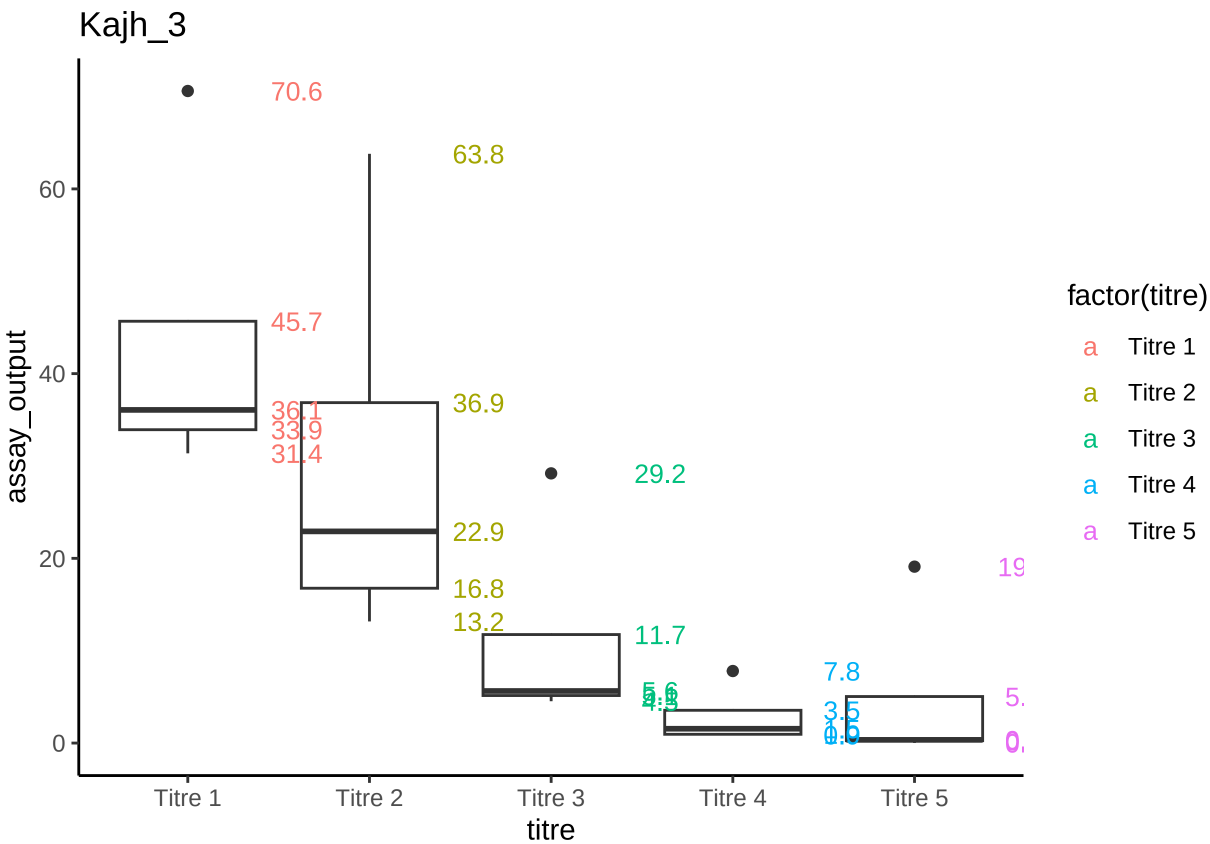

```
##
## [[55]]
```


Juuy_2
assay_output
80
60
40
20
0
83.4
81.2
79.1
66.1
60.6
75.0
63.9
54.8
43.3
33.9
29.4
25.8
22.1
17.5
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

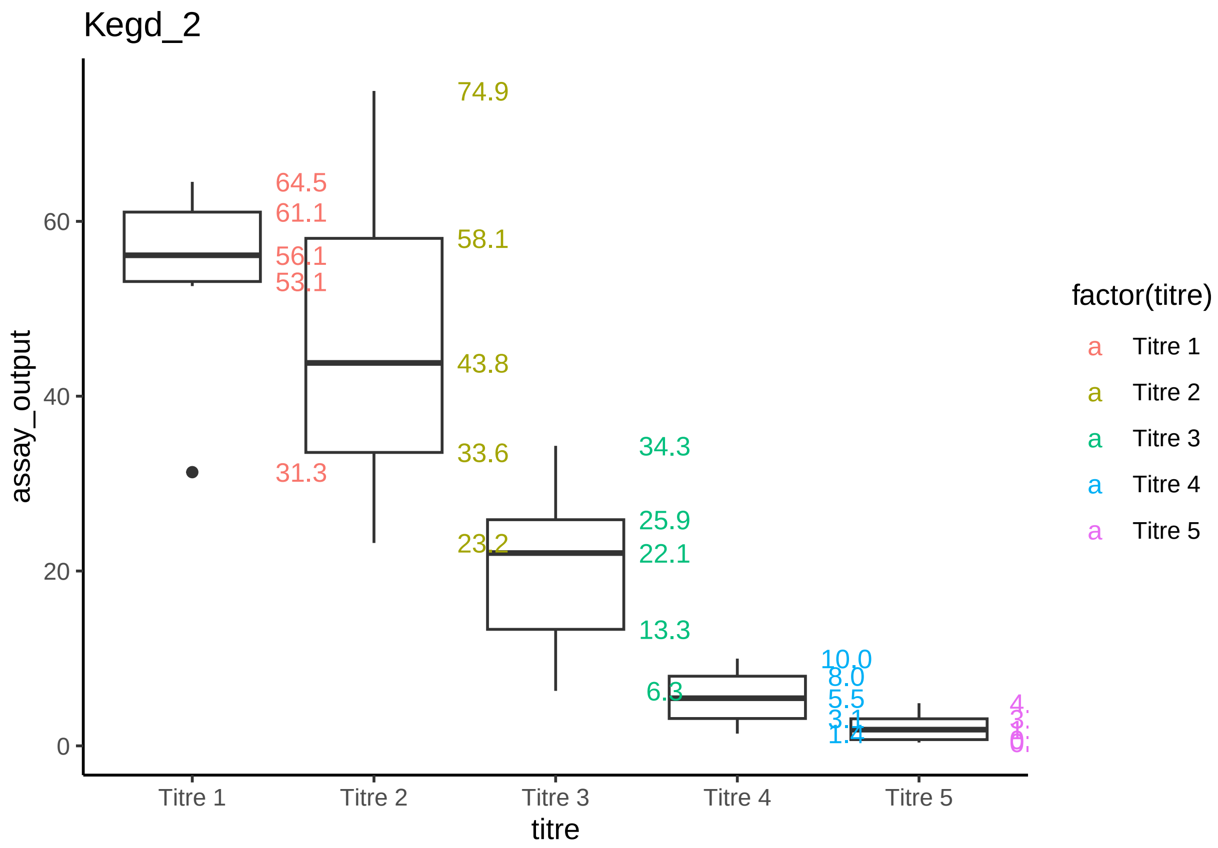
```
##
## [[56]]
```


Kajh_2
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
82.6
73.3
67.3
63.5
60.7
70.2
58.2
42.7
32.4
10.6

```
##
## [[57]]
```

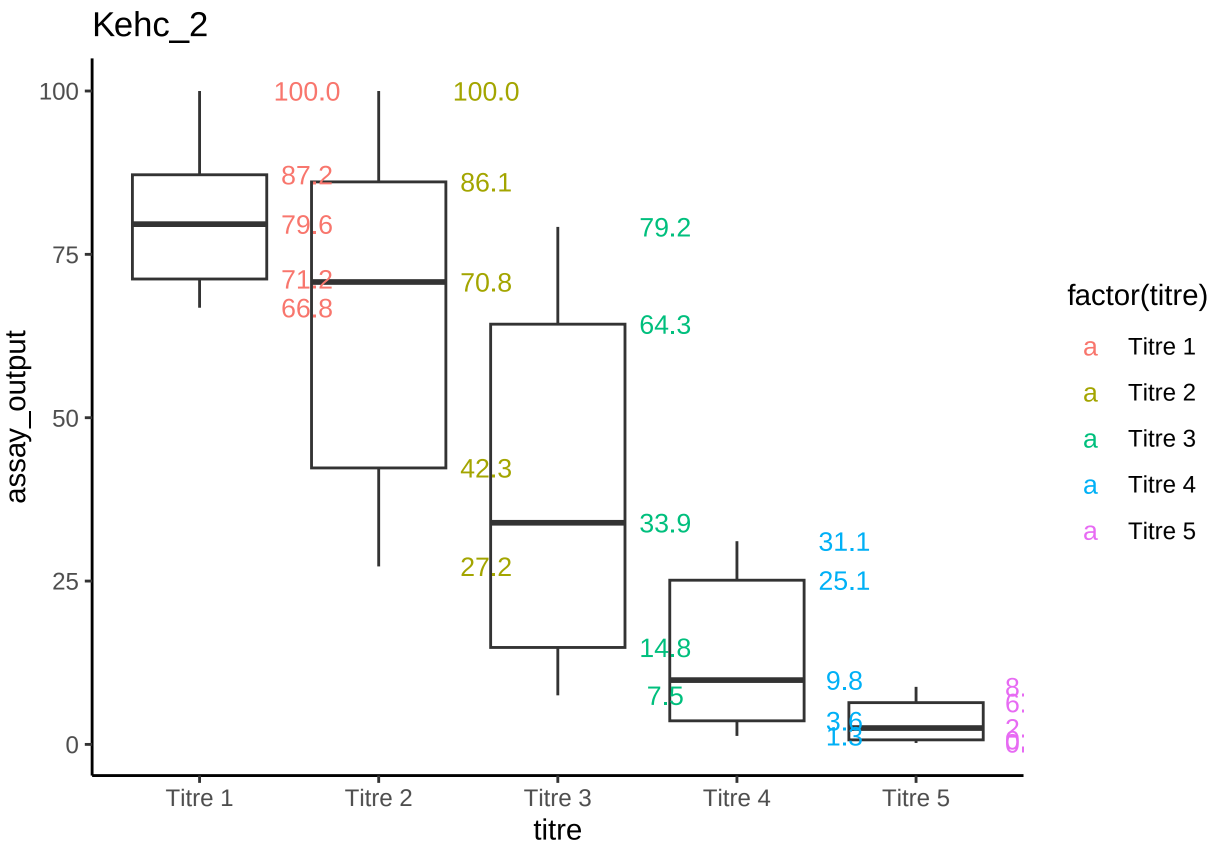

Kajh_3
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
70.6
63.8
45.7
36.9
29.2
22.9
16.8
13.2
11.7
7.8

```
##
## [[58]]
```

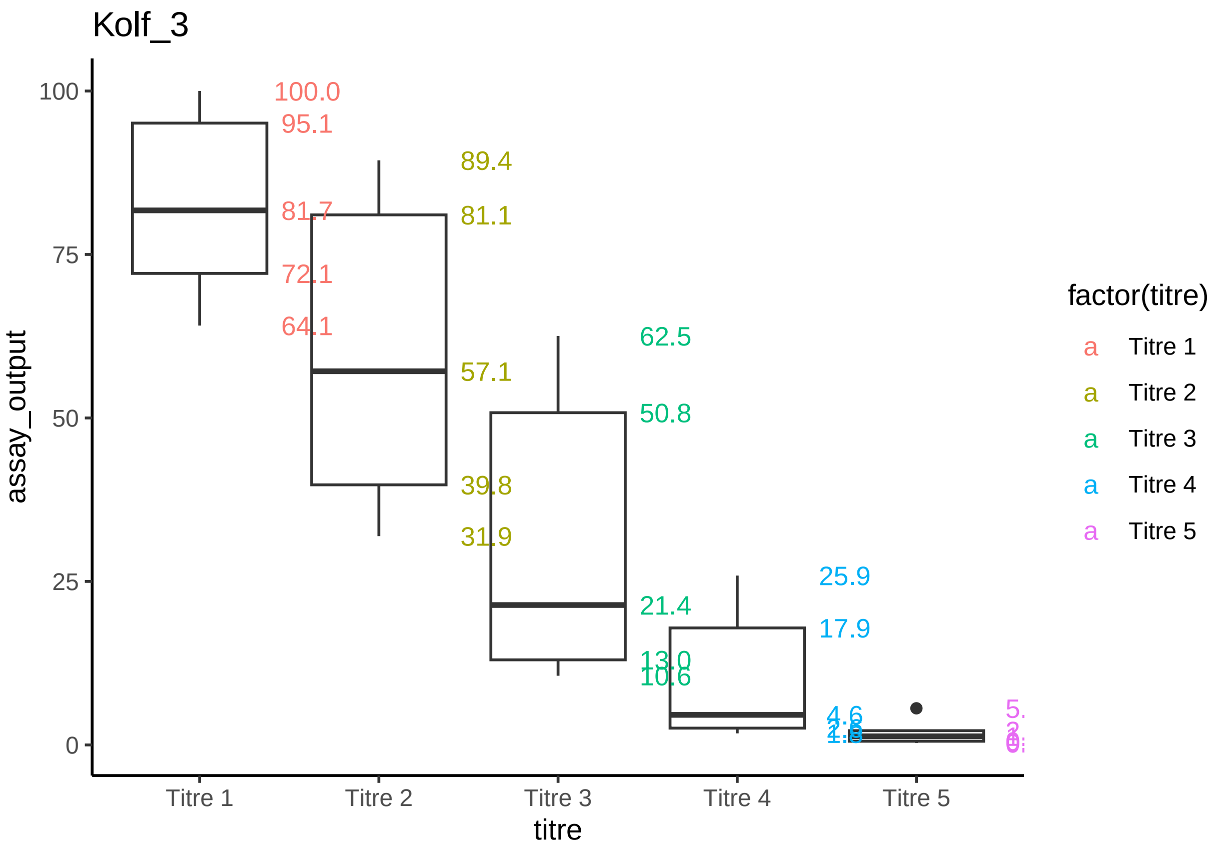


Kegd_2
74.9
64.5
61.1
58.1
56.1
53.1
43.8
33.6
34.3
31.3
25.9
23.2
22.1
13.3
10.0
8.0
6.3
5.5
3.1
1.4
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

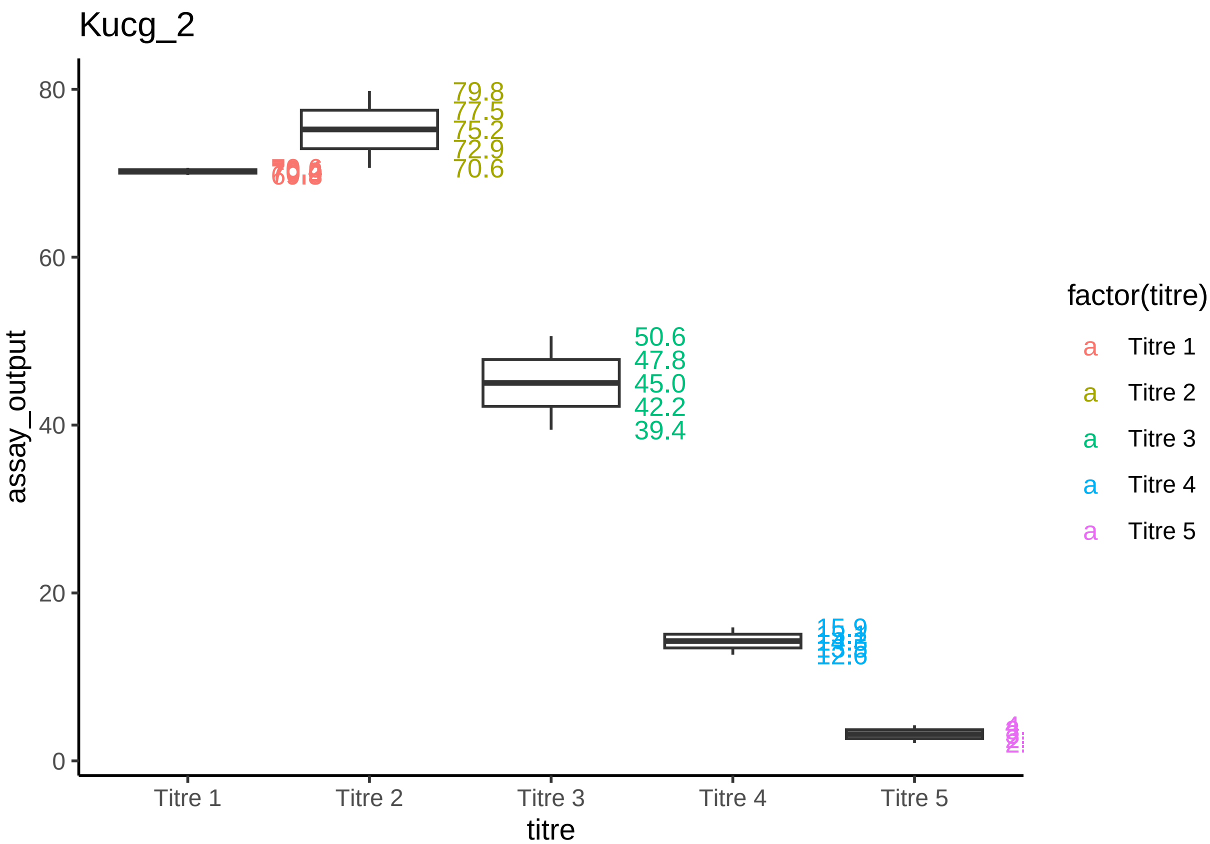

```
##
## [[59]]
```


Kehc_2
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
100.0
87.2
79.6
71.2
66.8
100.0
86.1
70.8
42.3
27.2
79.2
64.3
33.9
14.8
7.5
31.1
25.1
9.8
3.6
1.3

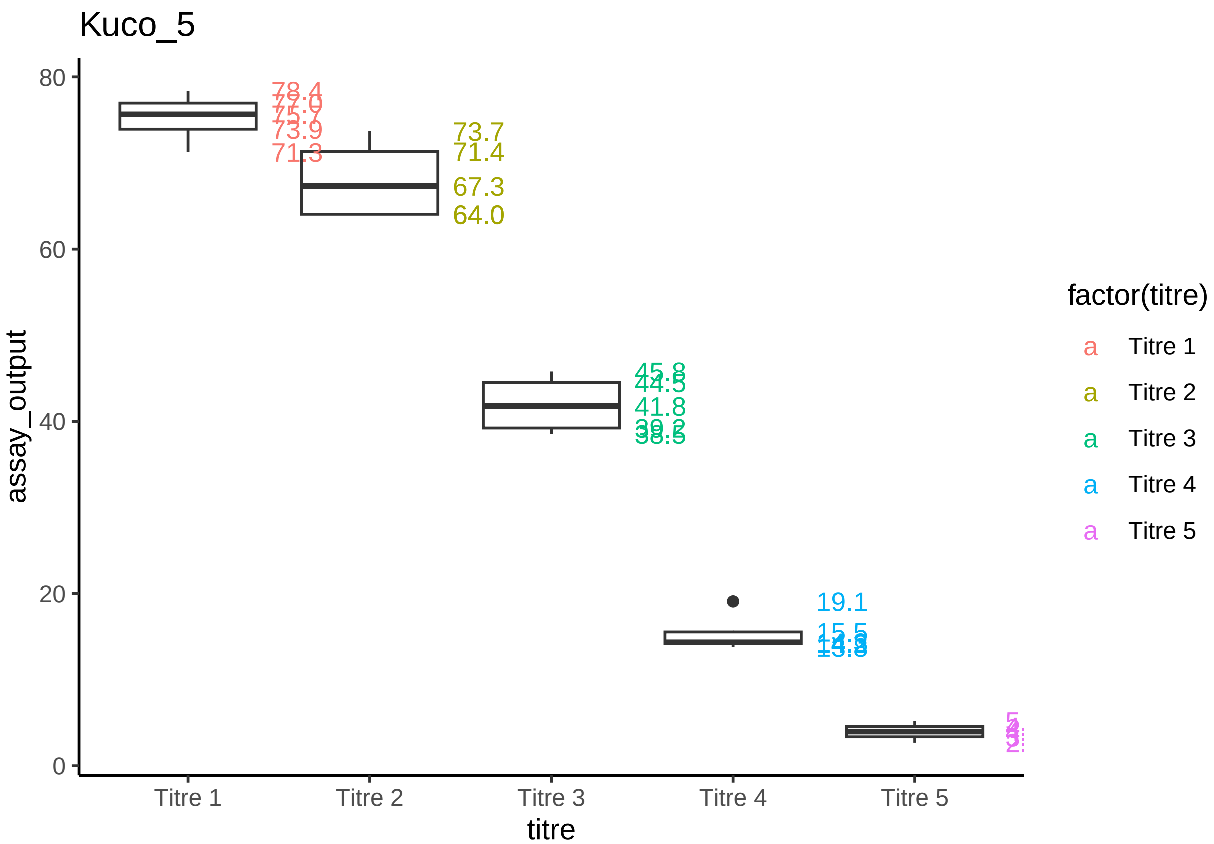
```
##
## [[60]]
```


Kolf_3
assay_output
100
75
50
25
0
100.0
95.1
81.7
72.1
64.1
89.4
81.1
57.1
39.8
31.9
62.5
50.8
21.4
13.0
10.6
25.9
17.9
4.6
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[61]]
```

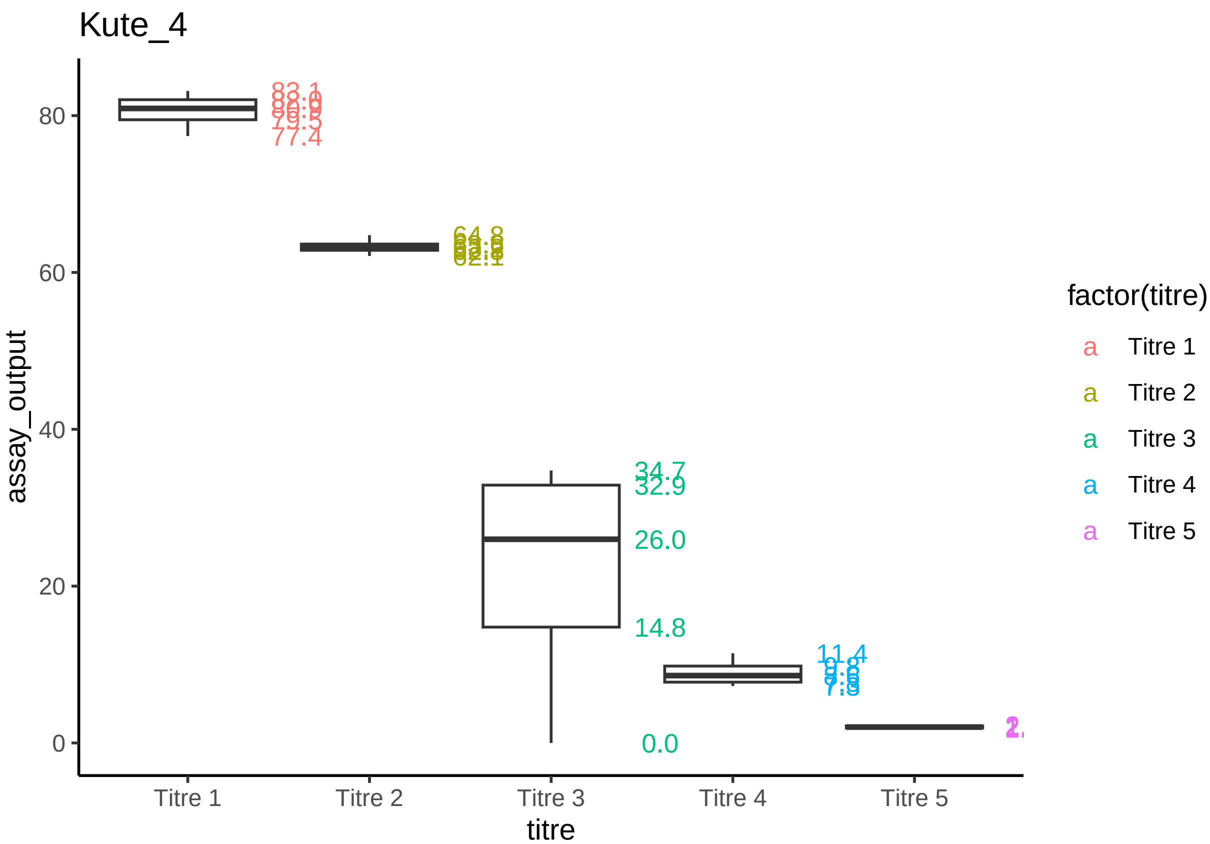

Kucg_2
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
assay_output
titre
79.8
77.5
75.2
72.9
70.6
50.6
47.8
45.0
42.2
39.4

```
##
## [[62]]
```

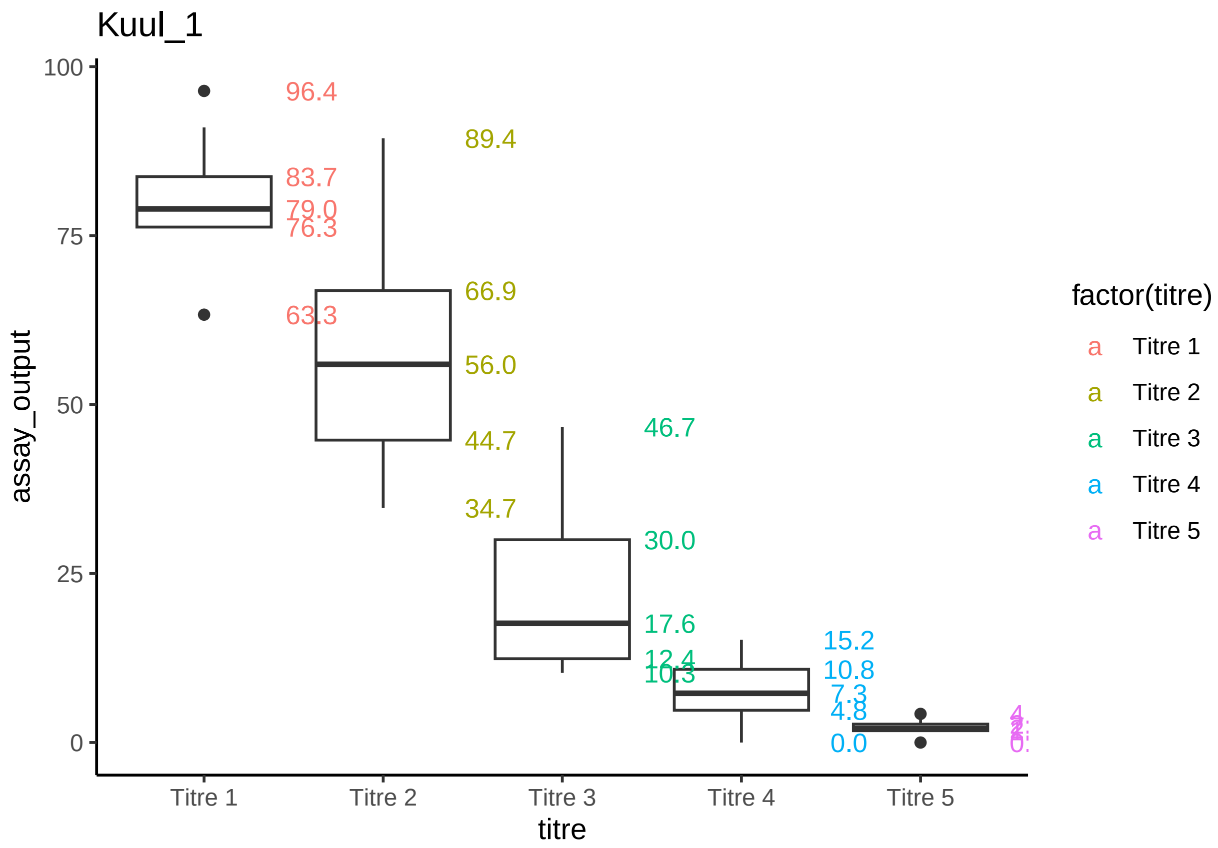


Kuco_5
80
60
40
20
0
assay_output
78.4
73.9
71.3
73.7
71.4
67.3
64.0
45.8
44.5
41.8
38.5
19.1
15.5
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[63]]
```

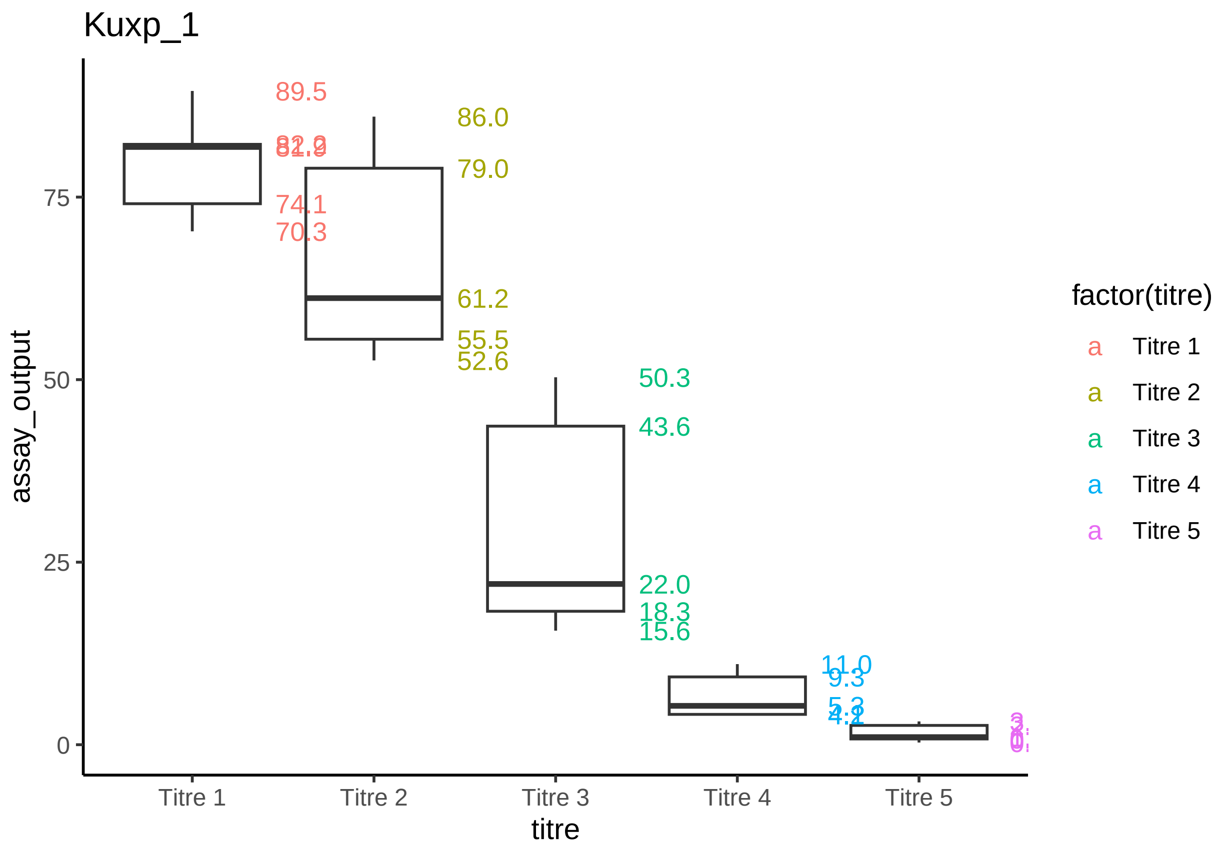

Kute_4
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
34.7
32.9
26.0
14.8
0.0
11.4
77.4
64.8

```
##
## [[64]]
```

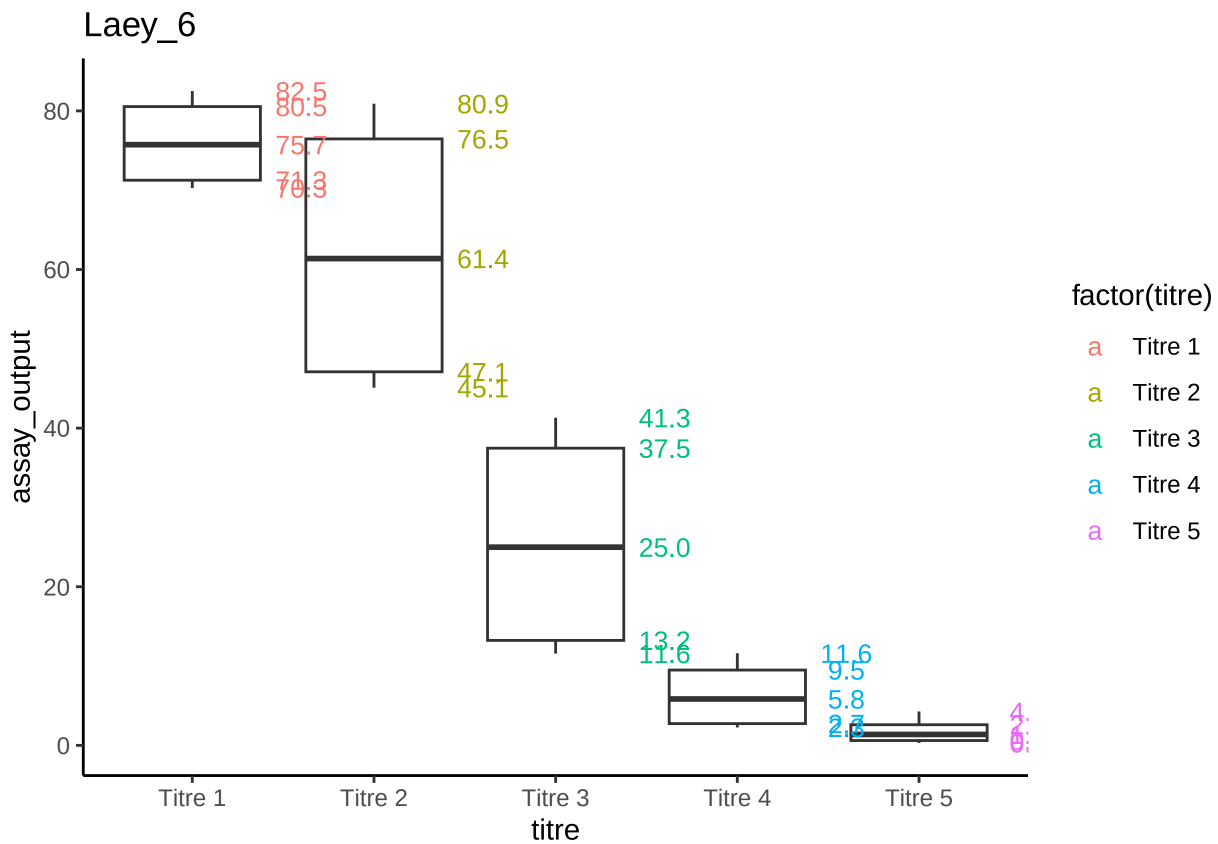


Kuul_1
100
75
50
25
0
assay_output
96.4
83.7
79.0
76.3
63.3
89.4
66.9
56.0
44.7
34.7
46.7
30.0
17.6
12.4
10.3
15.2
10.8
7.3
4.8
0.0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[65]]
```

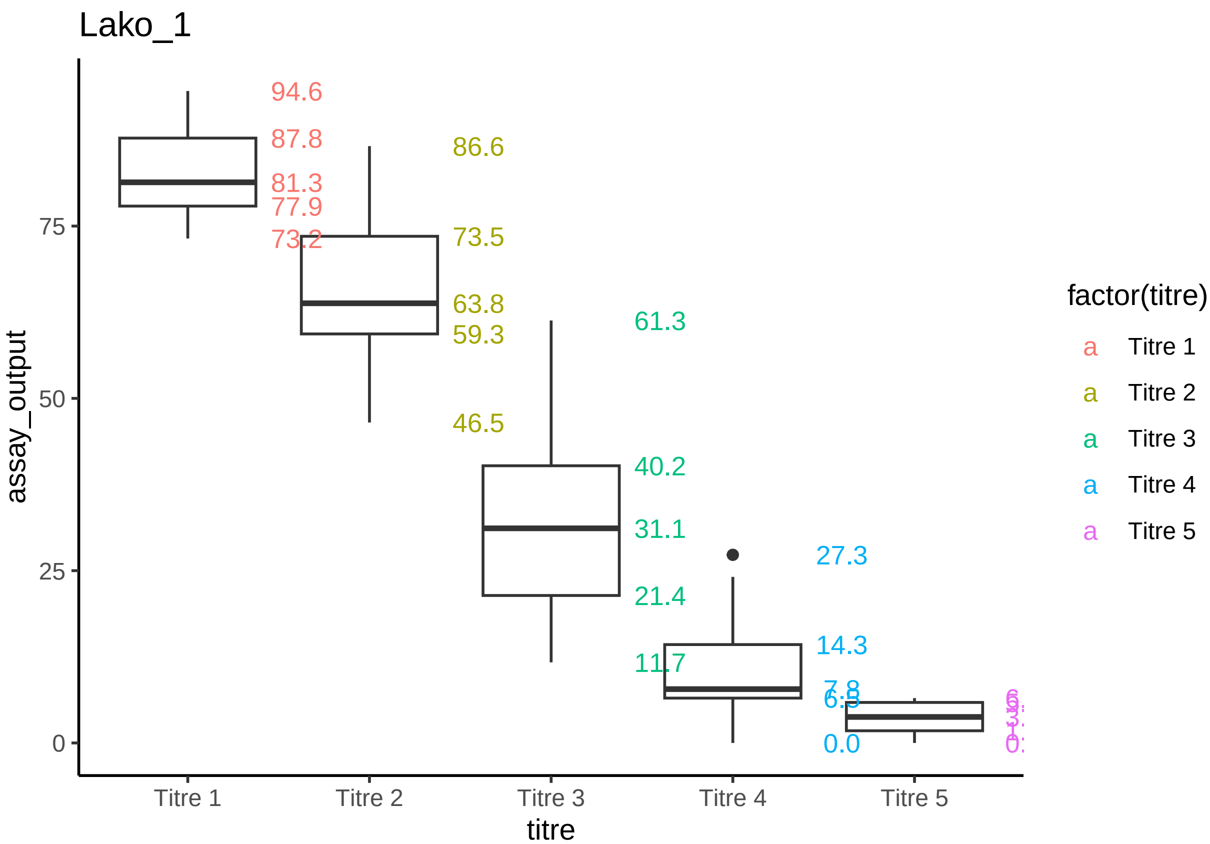

Kuxp_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
25
50
75
89.5
74.1
70.3
86.0
79.0
61.2
55.5
52.6
50.3
43.6
22.0
18.3
15.6
11.0
9.3
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[66]]
```

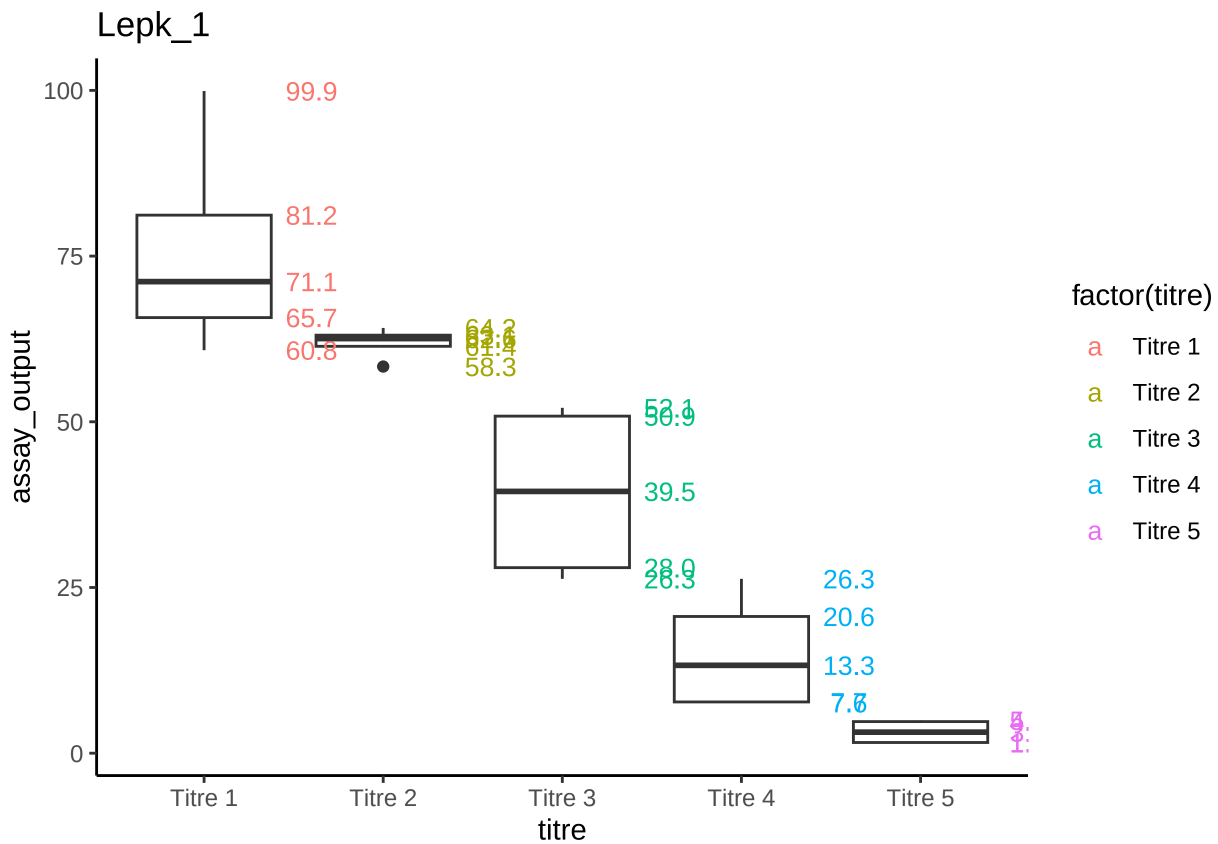


Laey_6
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5

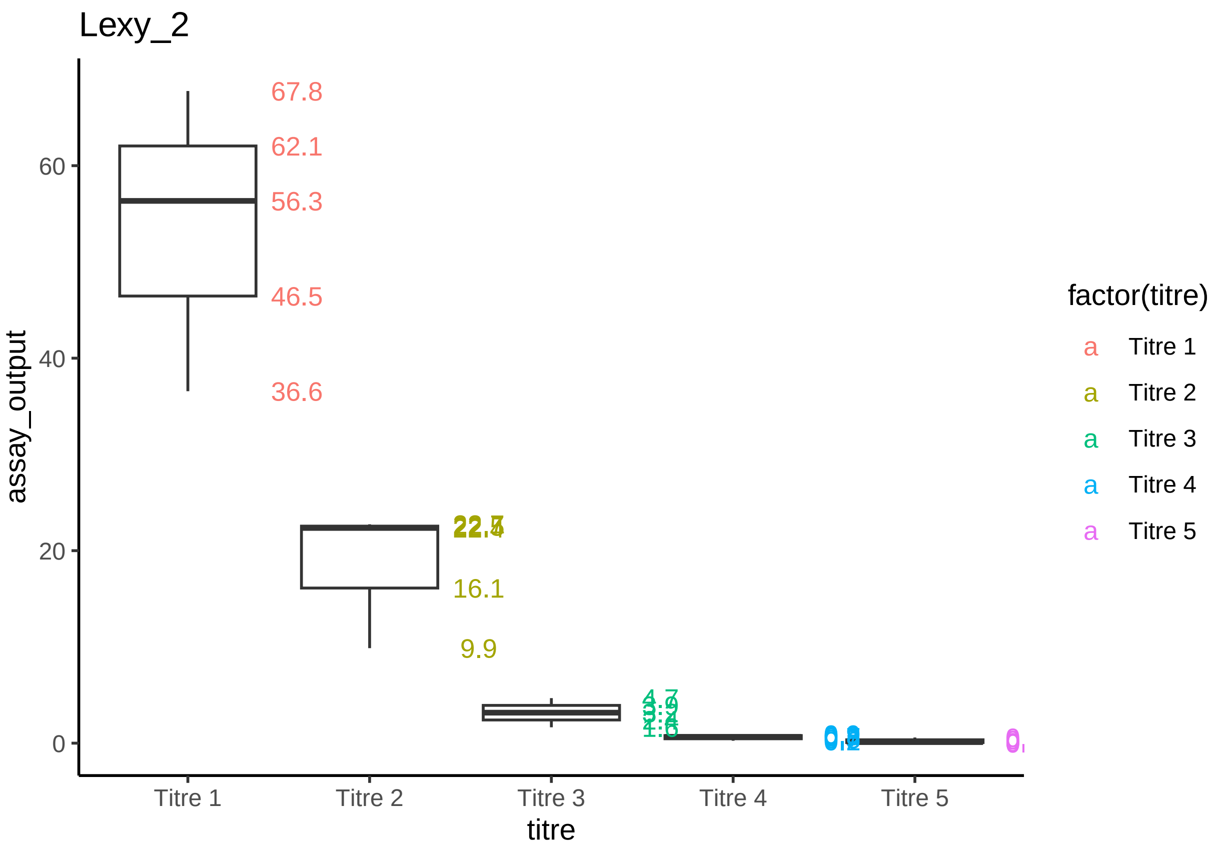

```
##
## [[67]]
```


Lako_1
assay_output
75
50
25
0
94.6
87.8
81.3
77.9
73.2
86.6
73.5
63.8
59.3
46.5
61.3
40.2
31.1
21.4
11.7
27.3
14.3
7.8
6.5
0.0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[68]]
```

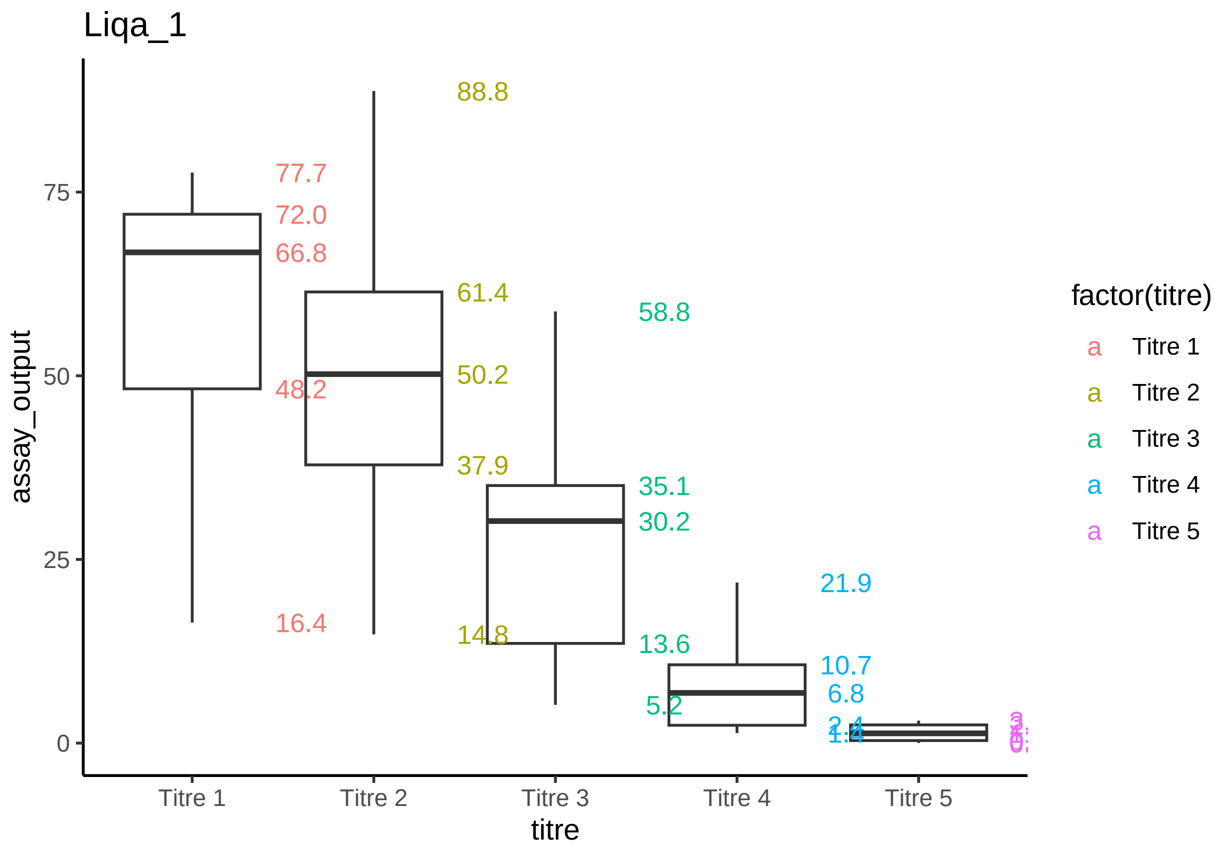

Lepk_1
100
75
50
25
0
assay_output
99.9
81.2
71.1
65.7
60.8
58.3
39.5
26.3
20.6
13.3
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[69]]
```

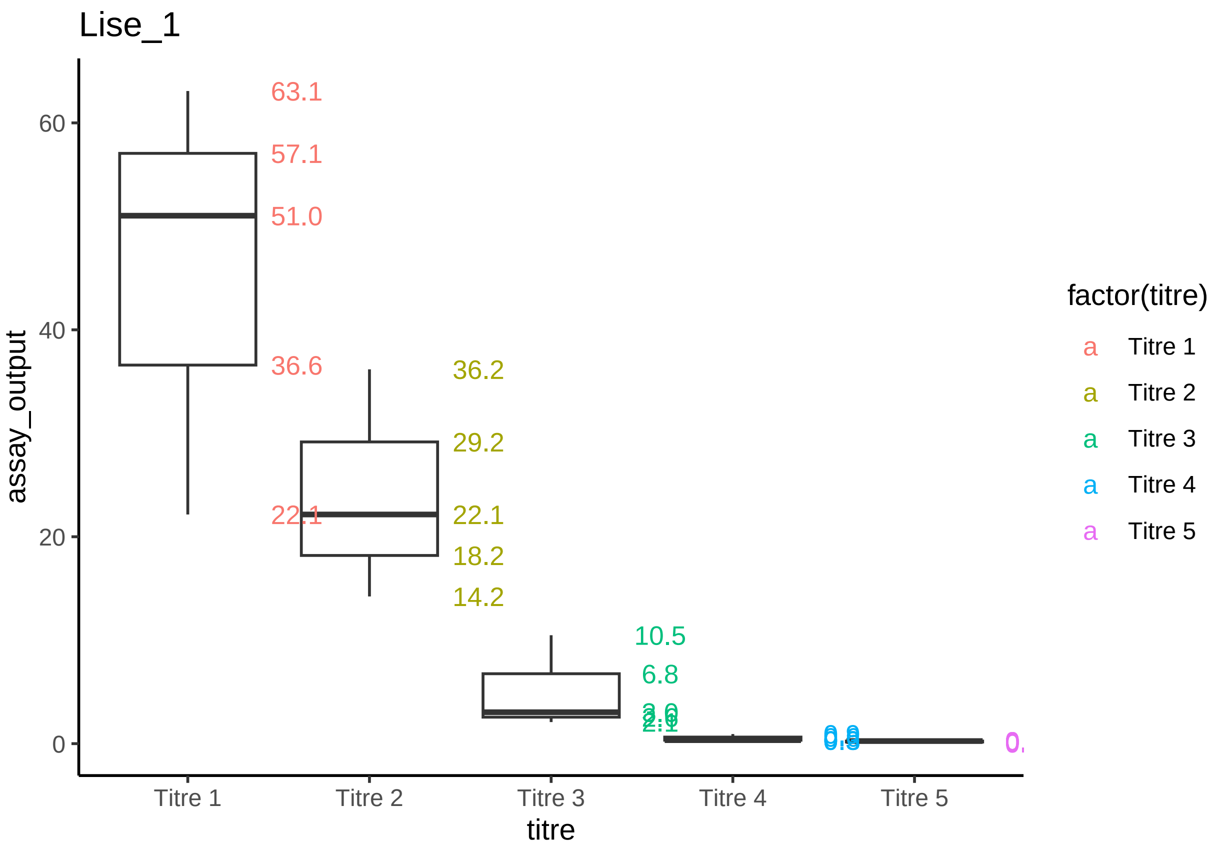


Lexy_2
assay_output
titre
60
40
20
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
67.8
62.1
56.3
46.5
36.6
16.1
9.9
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

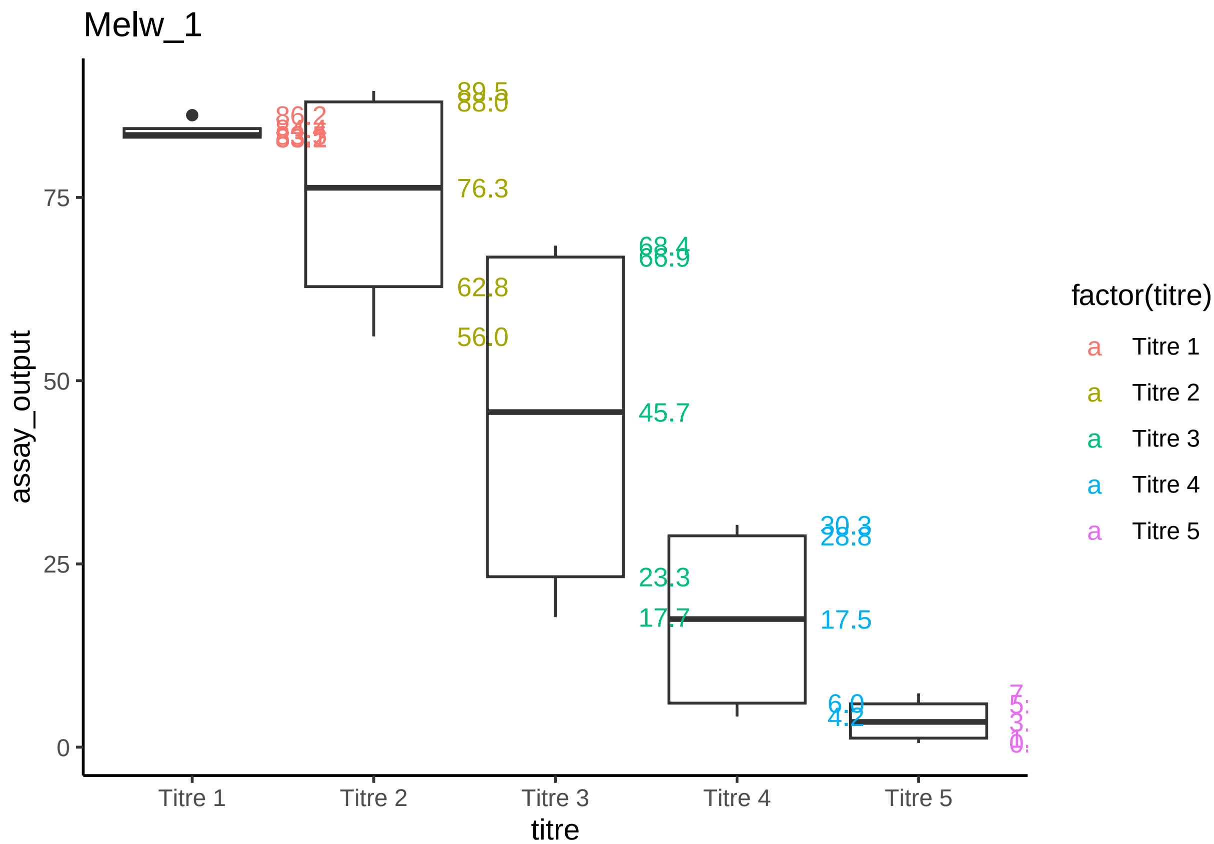

```
##
## [[70]]
```


Liqa_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
77.7
72.0
66.8
48.2
16.4
88.8
61.4
50.2
37.9
14.8
58.8
35.1
30.2
13.6
5.2
21.9
10.7
6.8


```
##
## [[71]]
```

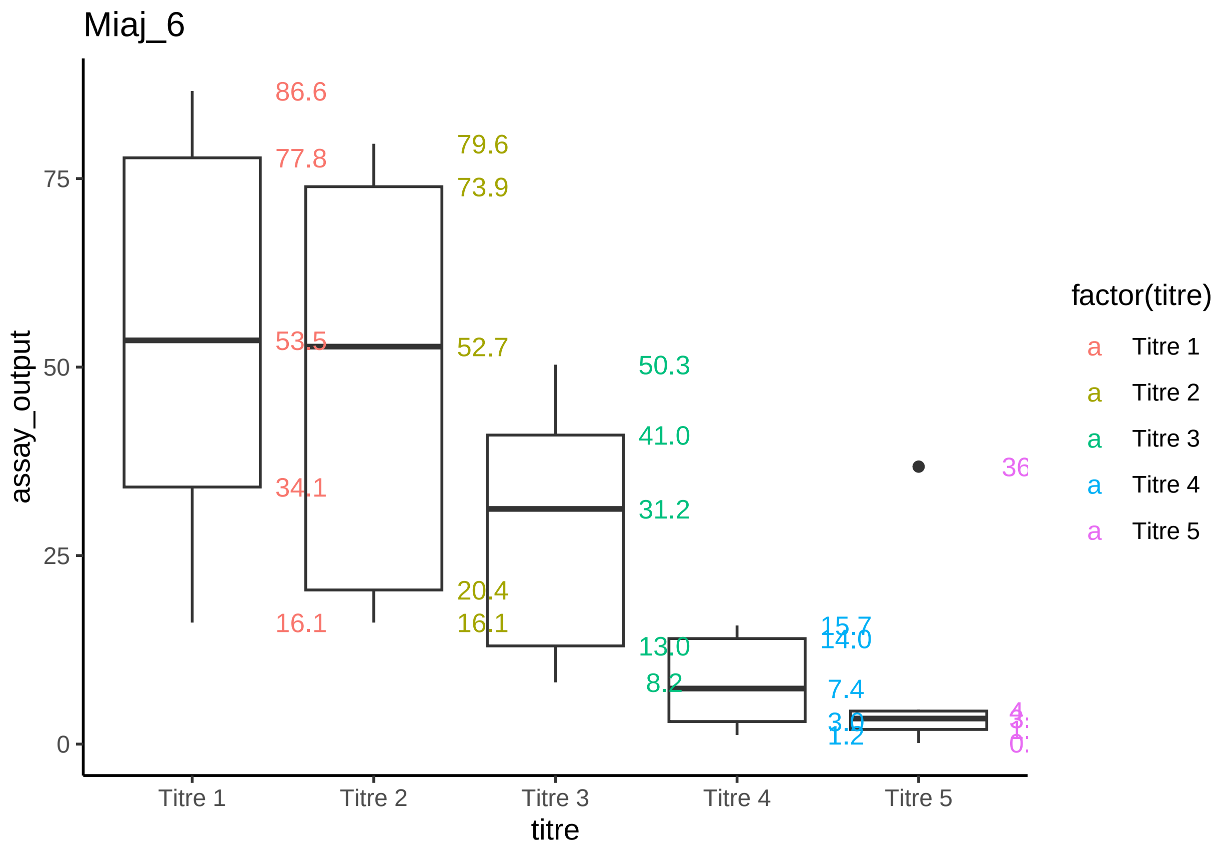

Lise_1
assay_output
60
40
20
0
63.1
57.1
51.0
36.6
22.1
36.2
29.2
22.1
18.2
14.2
10.5
6.8
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[72]]
```

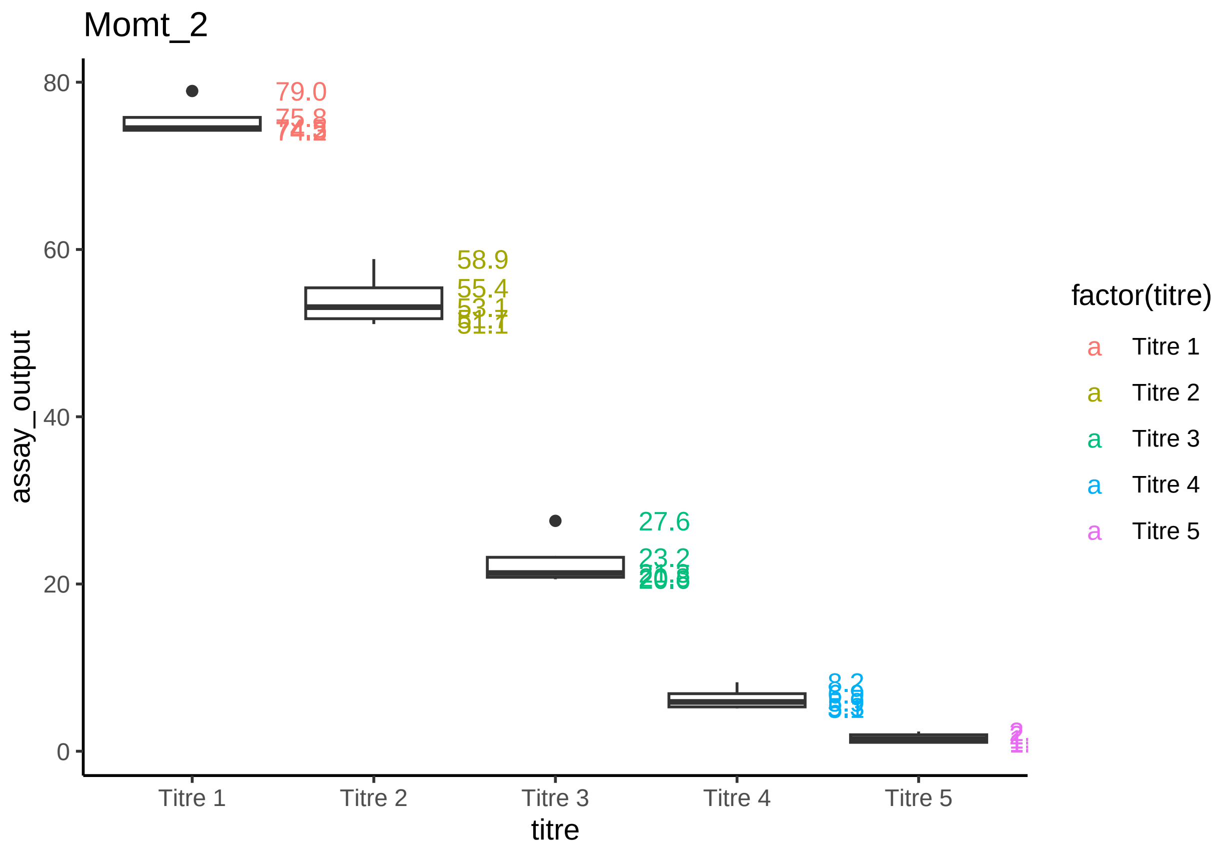


Melw_1
assay_output
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
89.5
88.0
76.3
62.8
56.0
68.4
66.9
45.7
23.3
17.7
30.3
28.8
17.5
6.0
4.2
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

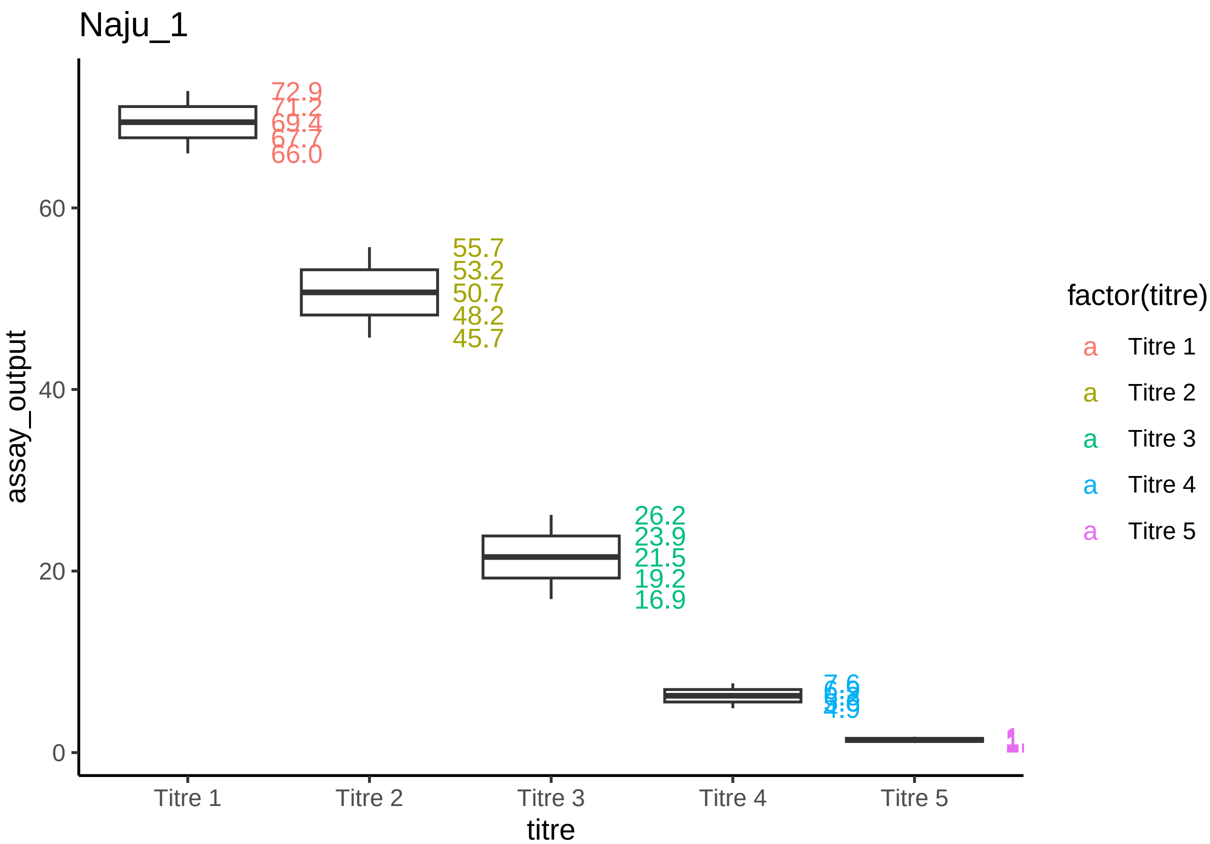

```
##
## [[73]]
```


Miaj_6
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
86.6
77.8
53.5
34.1
16.1
79.6
73.9
52.7
20.4
16.1
50.3
41.0
31.2
13.0
8.2
15.7
14.0
7.4
3.0
1.2
75
50
25
0

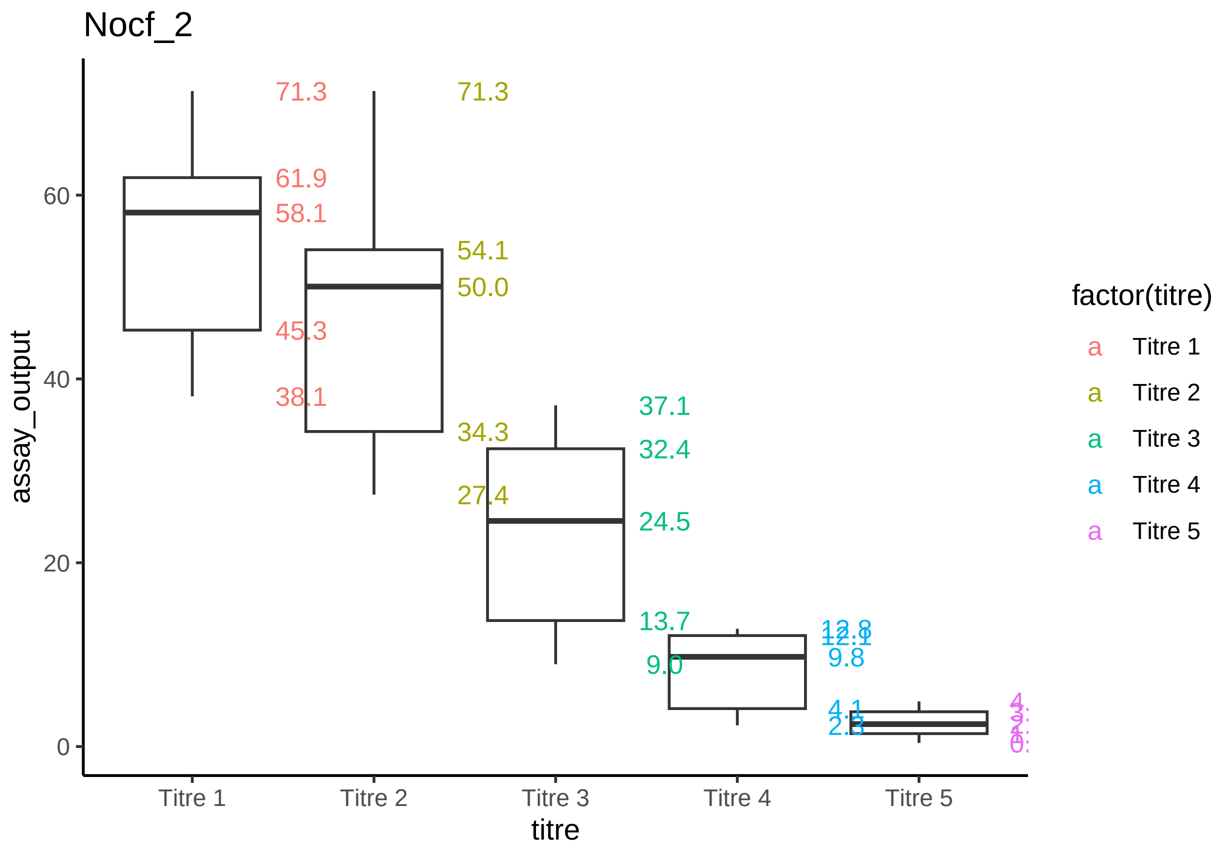
```
##
## [[74]]
```


Momt_2
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
79.0
58.9
55.4
27.6
23.2
8.2

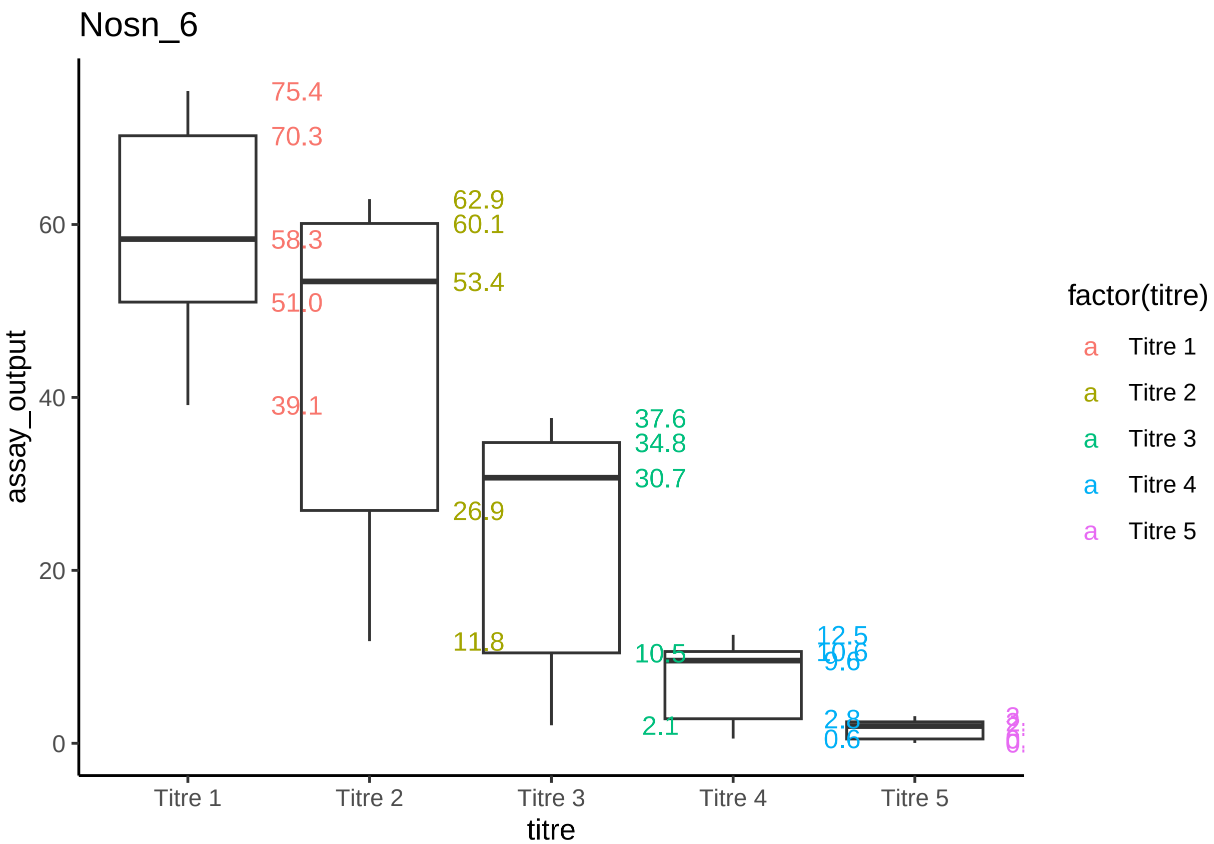
```
##
## [[75]]
```


Naju_1
72.9
71.2
69.4
67.7
66.0
55.7
53.2
50.7
48.2
45.7
26.2
23.9
21.5
19.2
16.9
7.6
4.9
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

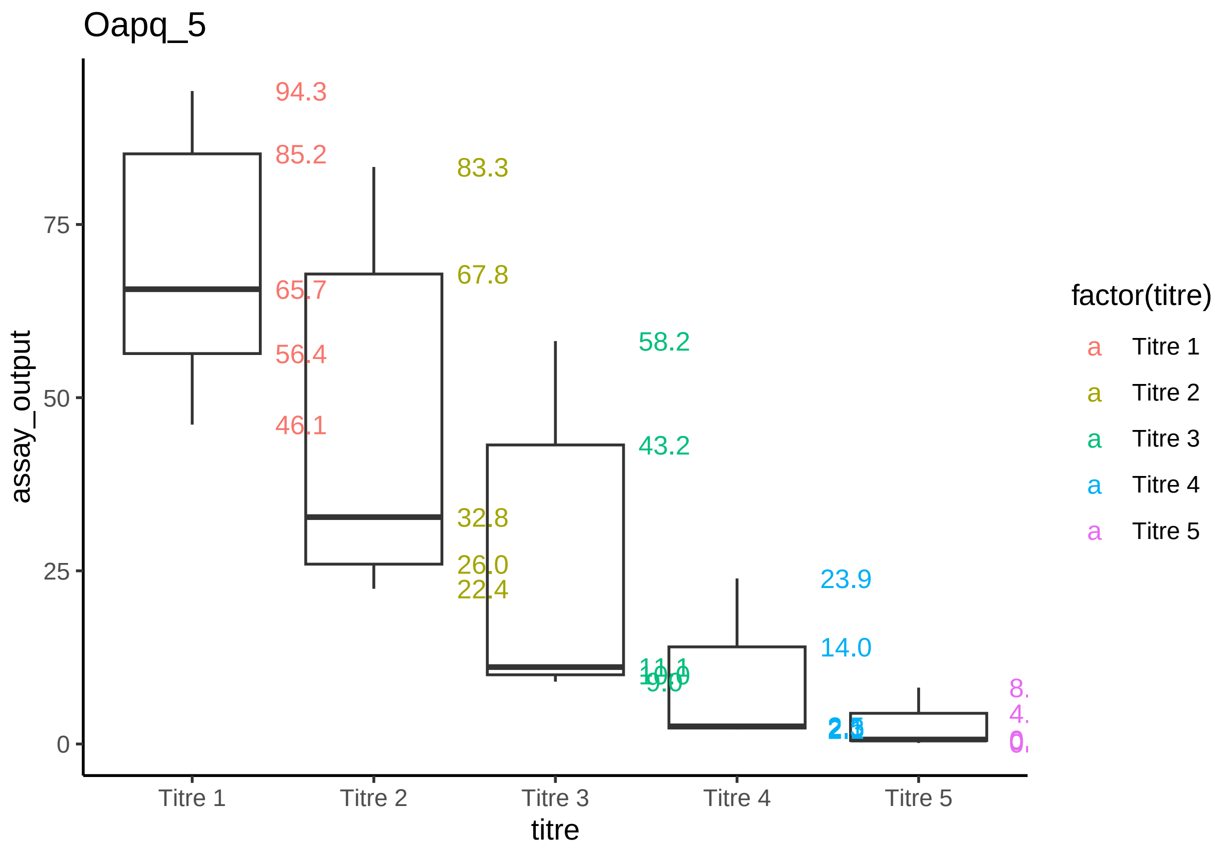
```
##
## [[76]]
```


Nocf_2
71.3
61.9
58.1
45.3
38.1
71.3
54.1
50.0
34.3
27.4
37.1
32.4
24.5
13.7
9.0
12.8
12.1
9.8
4.1
2.3
assay_output
60
40
20
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[77]]
```

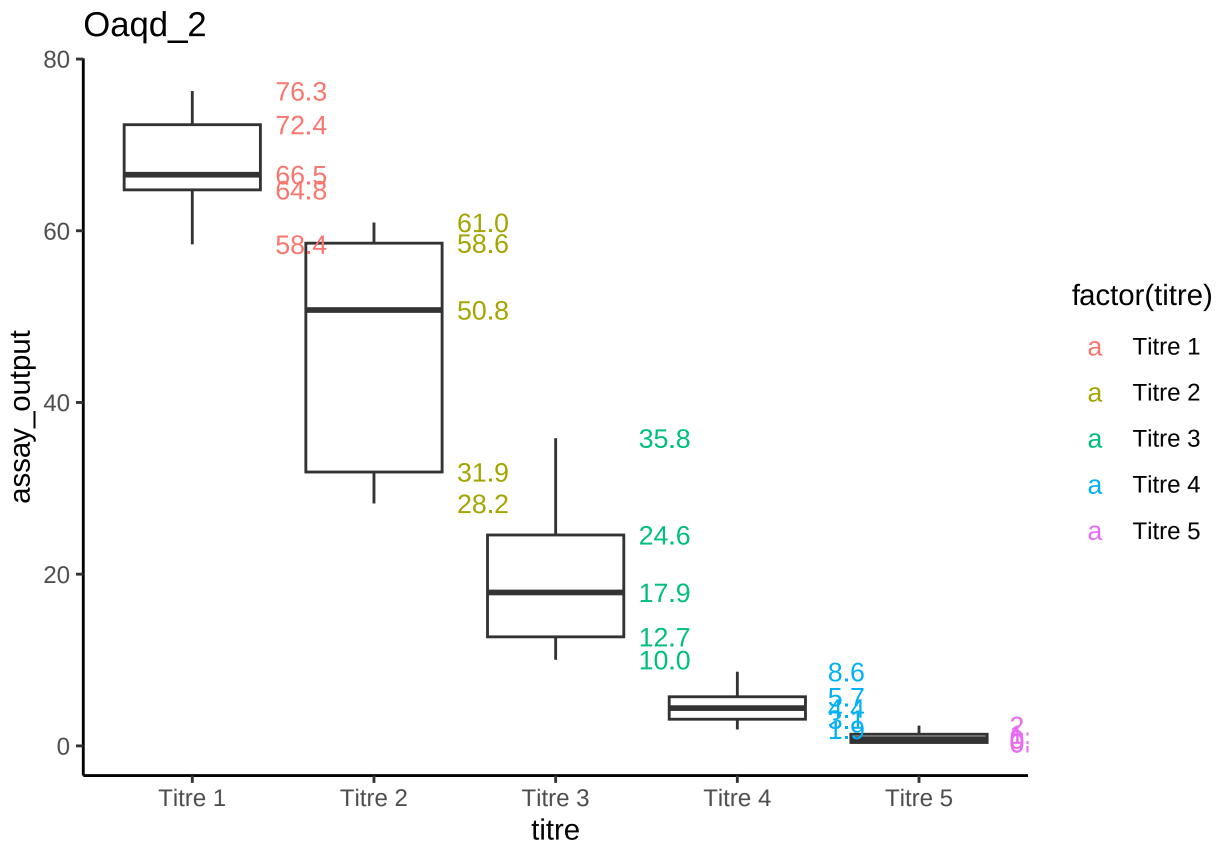

Nosn_6
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
20
40
60
75.4
70.3
58.3
51.0
39.1
62.9
60.1
53.4
26.9
11.8
37.6
34.8
30.7
10.5
2.1
12.5
10.6
9.6
2.8
0.6
factor(titre)

```
##
## [[78]]
```

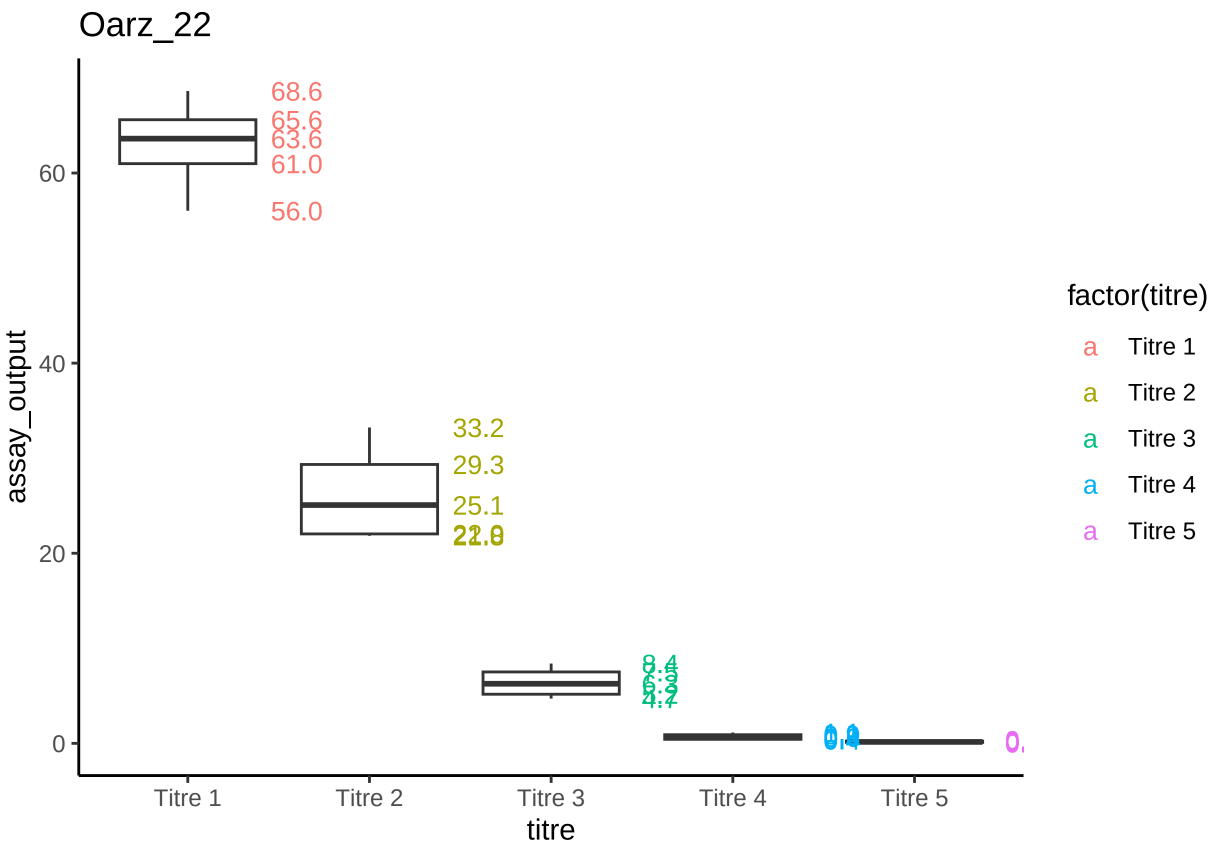


Oapq_5
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
25
50
75
94.3
85.2
65.7
56.4
46.1
83.3
67.8
32.8
26.0
22.4
58.2
43.2
23.9
14.0
factor(titre)

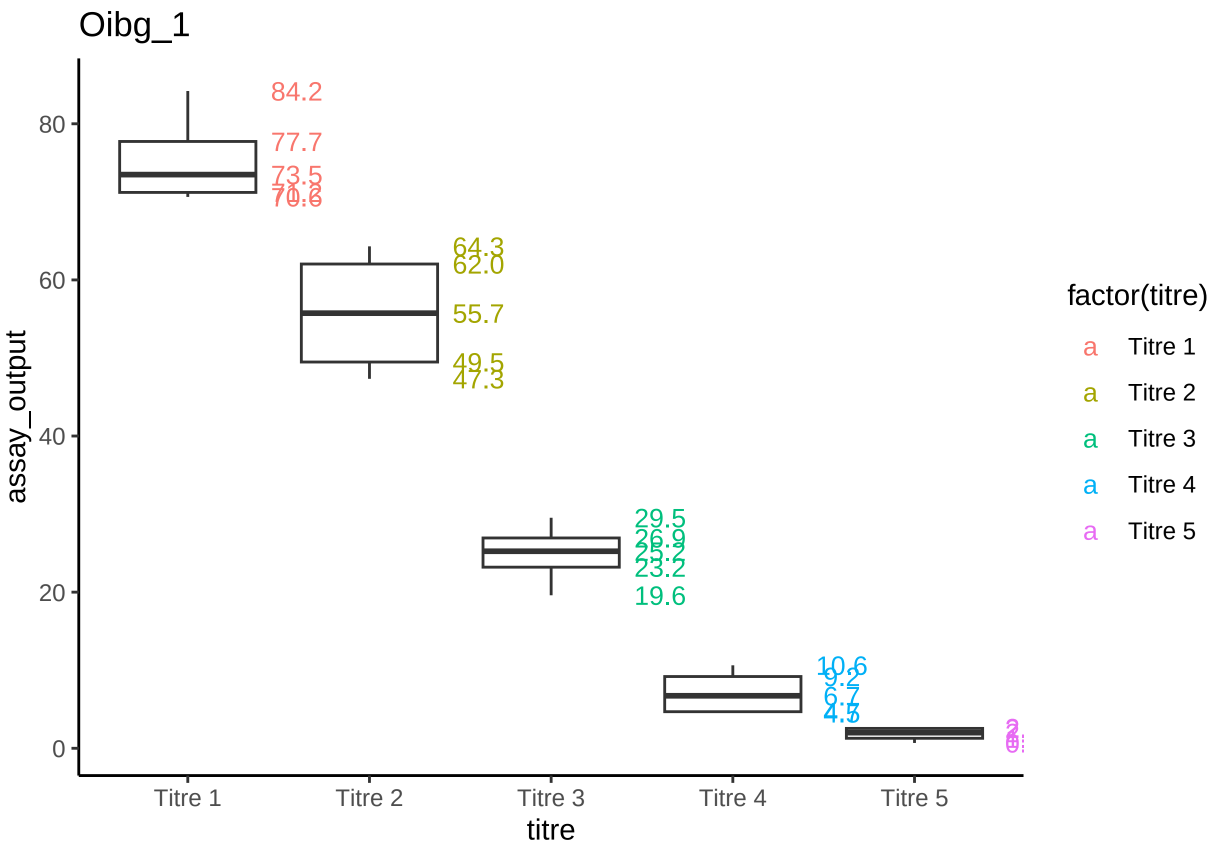

```
##
## [[79]]
```


Oaqd_2
assay_output
80
60
40
20
0
76.3
72.4
66.5
64.8
58.4
61.0
58.6
50.8
31.9
28.2
35.8
24.6
17.9
12.7
10.0
8.6
5.7
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[80]]
```

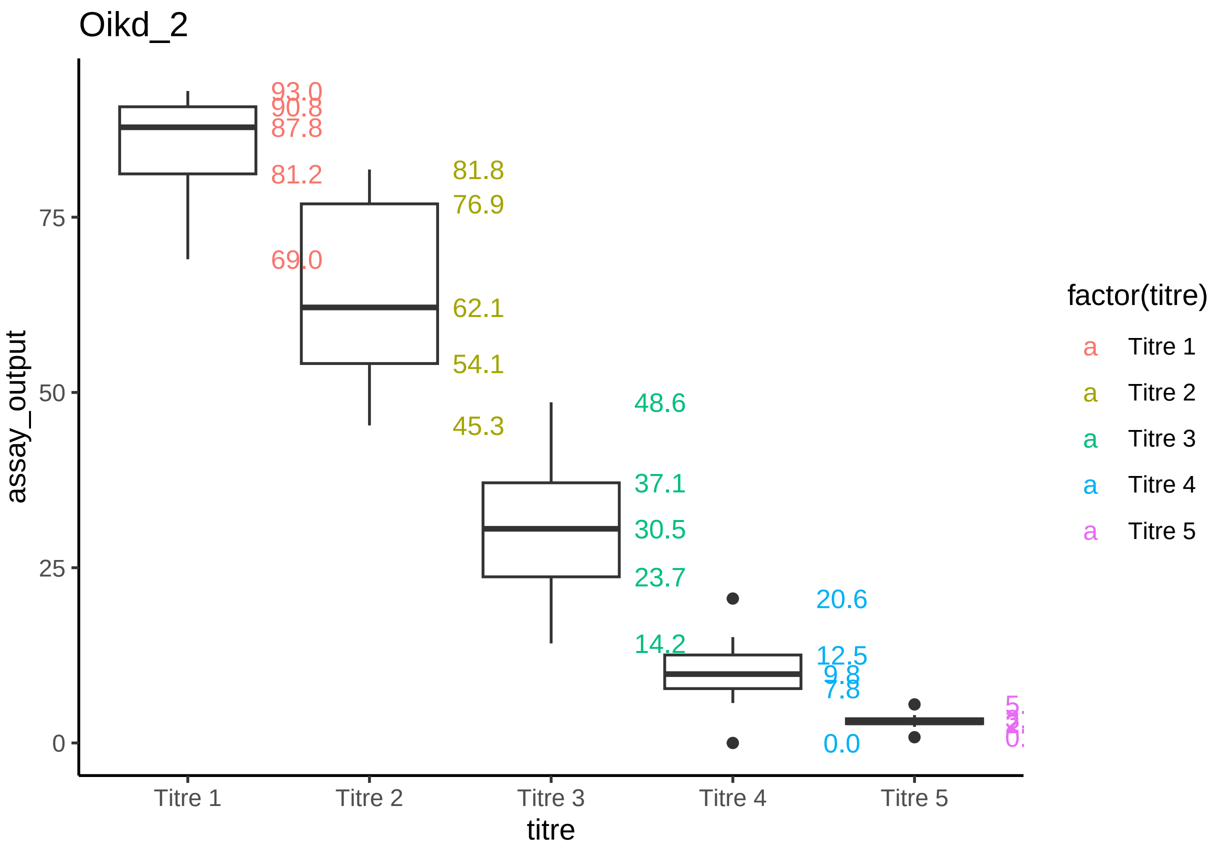

Oarz_22
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
68.6
65.6
63.6
61.0
56.0
33.2
29.3
25.1


```
##
## [[81]]
```

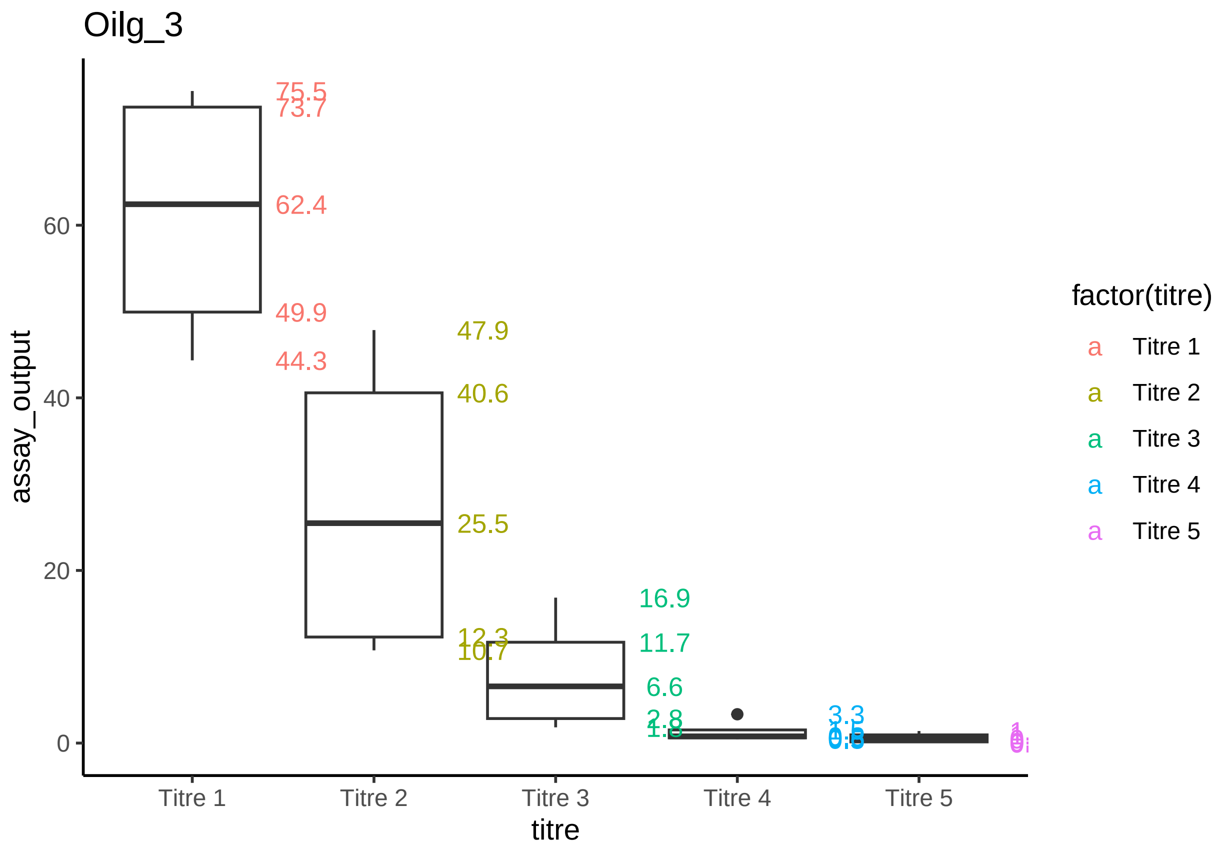


Oibg_1
assay_output
titre
80
60
40
20
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
84.2
77.7
73.5
64.3
62.0
55.7
49.5
47.3
29.5
23.2
19.6
10.6
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[82]]
```

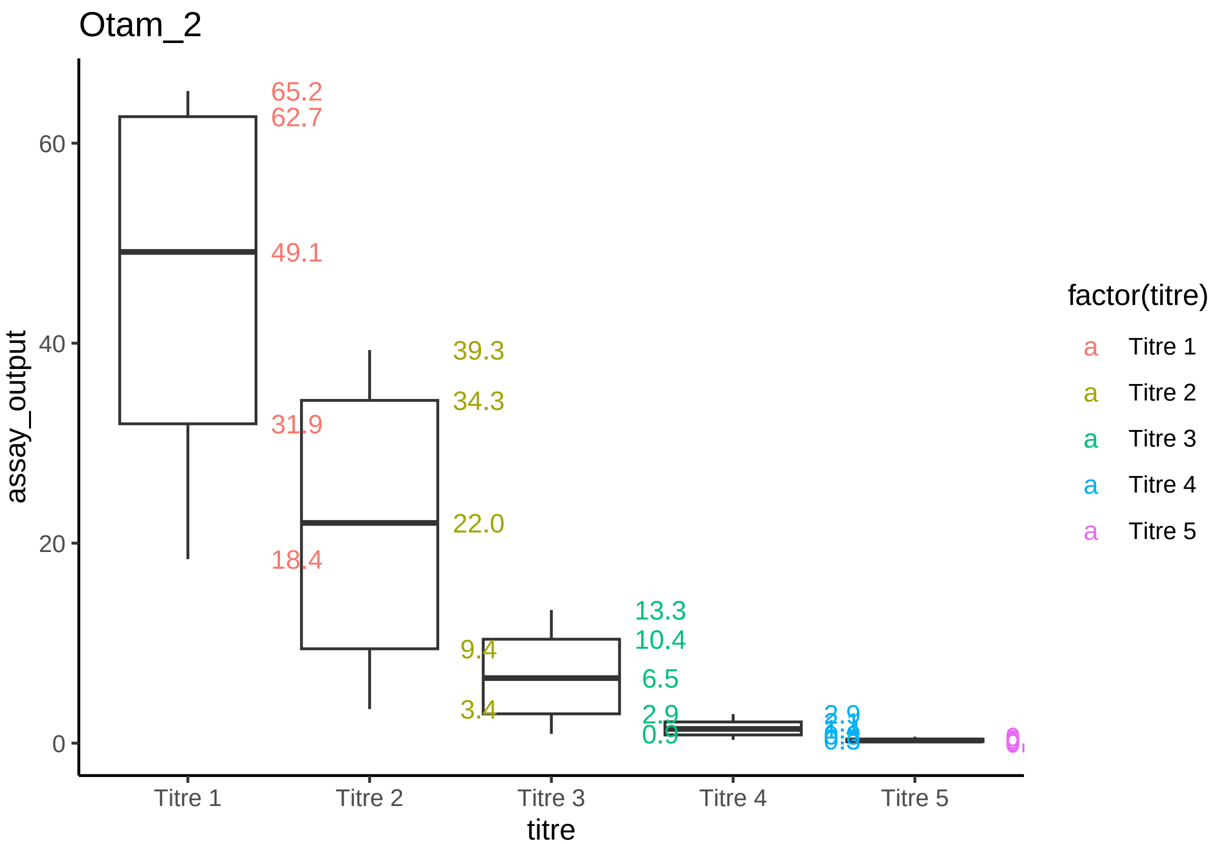

Oikd_2
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
93.0
90.8
87.8
81.2
69.0
81.8
76.9
62.1
54.1
45.3
48.6
37.1
30.5
23.7
14.2
20.6
12.5
9.8
7.8
0.0
75
50
25
0

```
##
## [[83]]
```

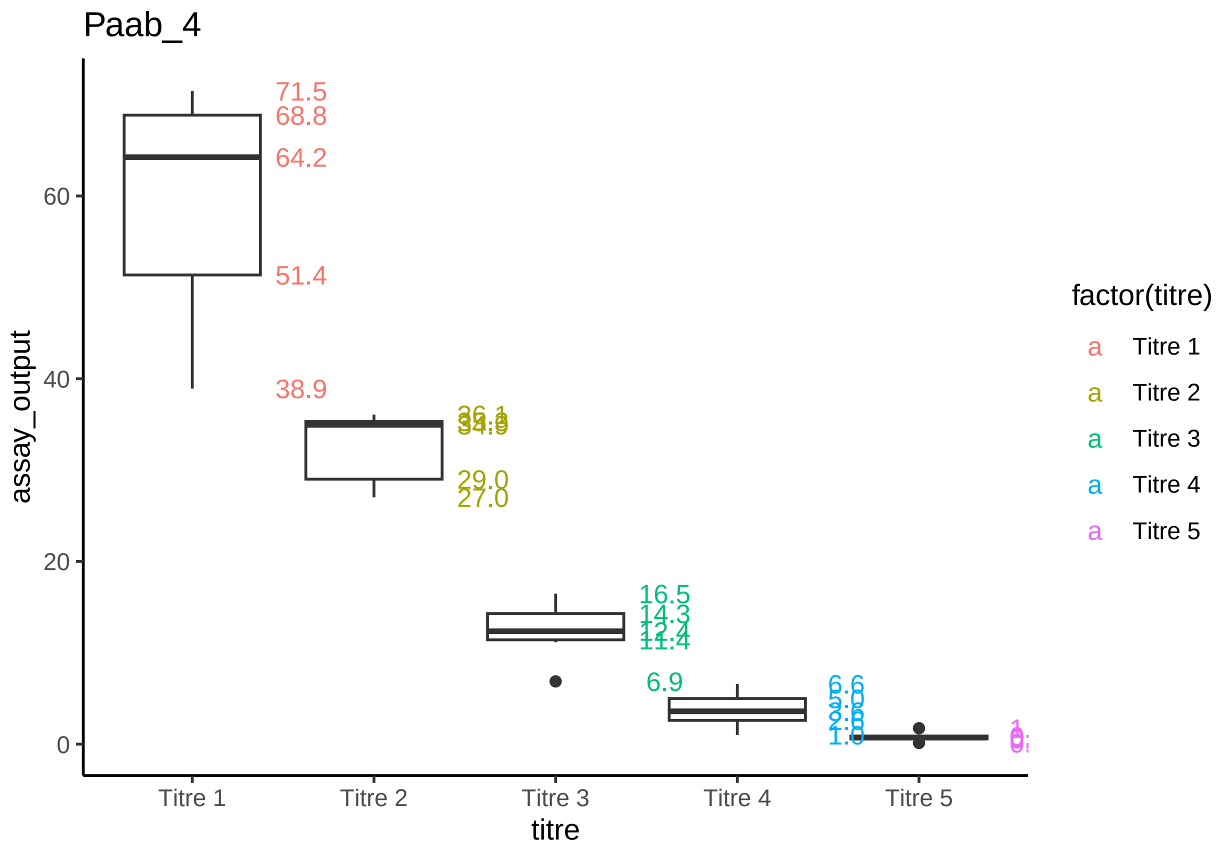


Oilg_3
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
75.5
73.7
62.4
49.9
44.3
47.9
40.6
25.5
12.3
10.7
16.9
11.7
6.6
2.8
1.8
3.3


```
##
## [[84]]
```

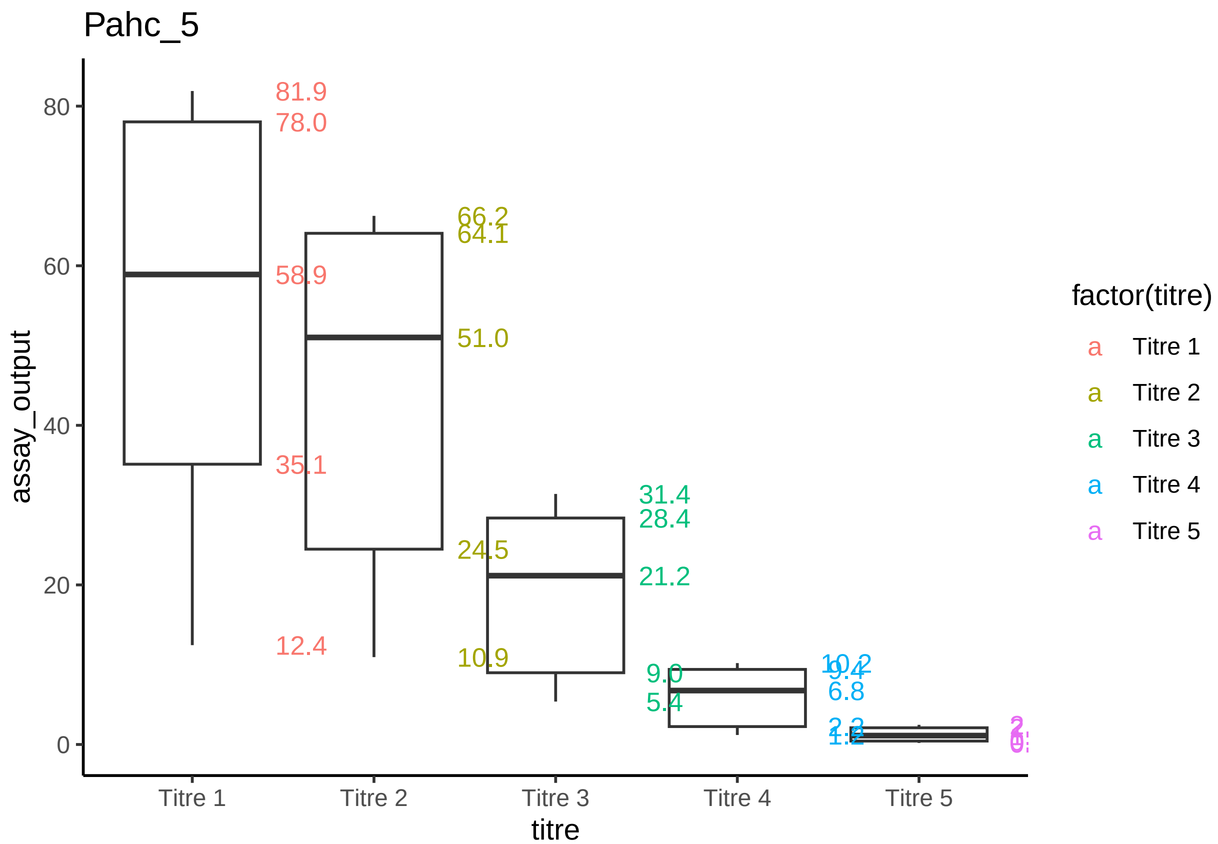

Otam_2
65.2
62.7
49.1
31.9
18.4
39.3
34.3
22.0
9.4
3.4
13.3
10.4
6.5
2.9
0.9
2.9
0.5
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[85]]
```

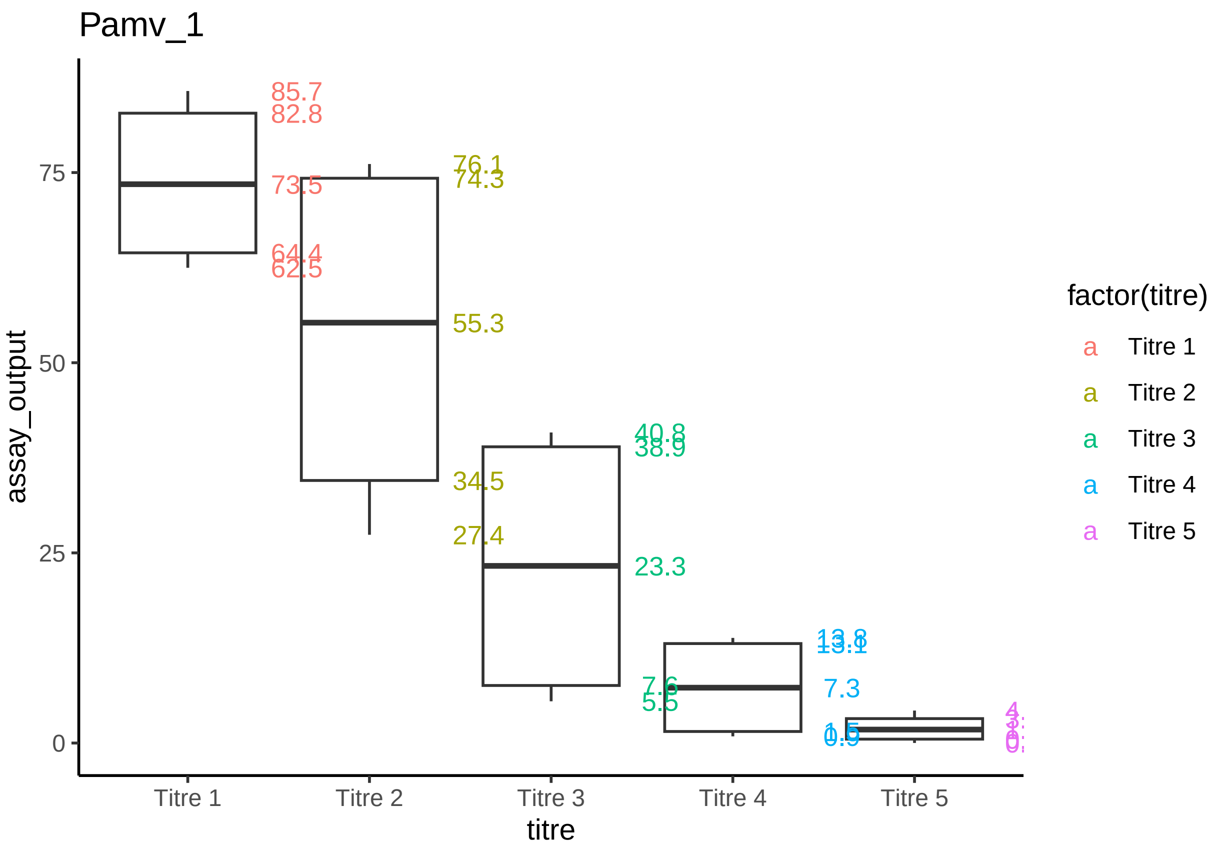


Paab_4
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
71.5
68.8
64.2
51.4
38.9
29.0
27.0
16.5
14.3
11.4
6.9
6.6
1.0


```
##
## [[86]]
```

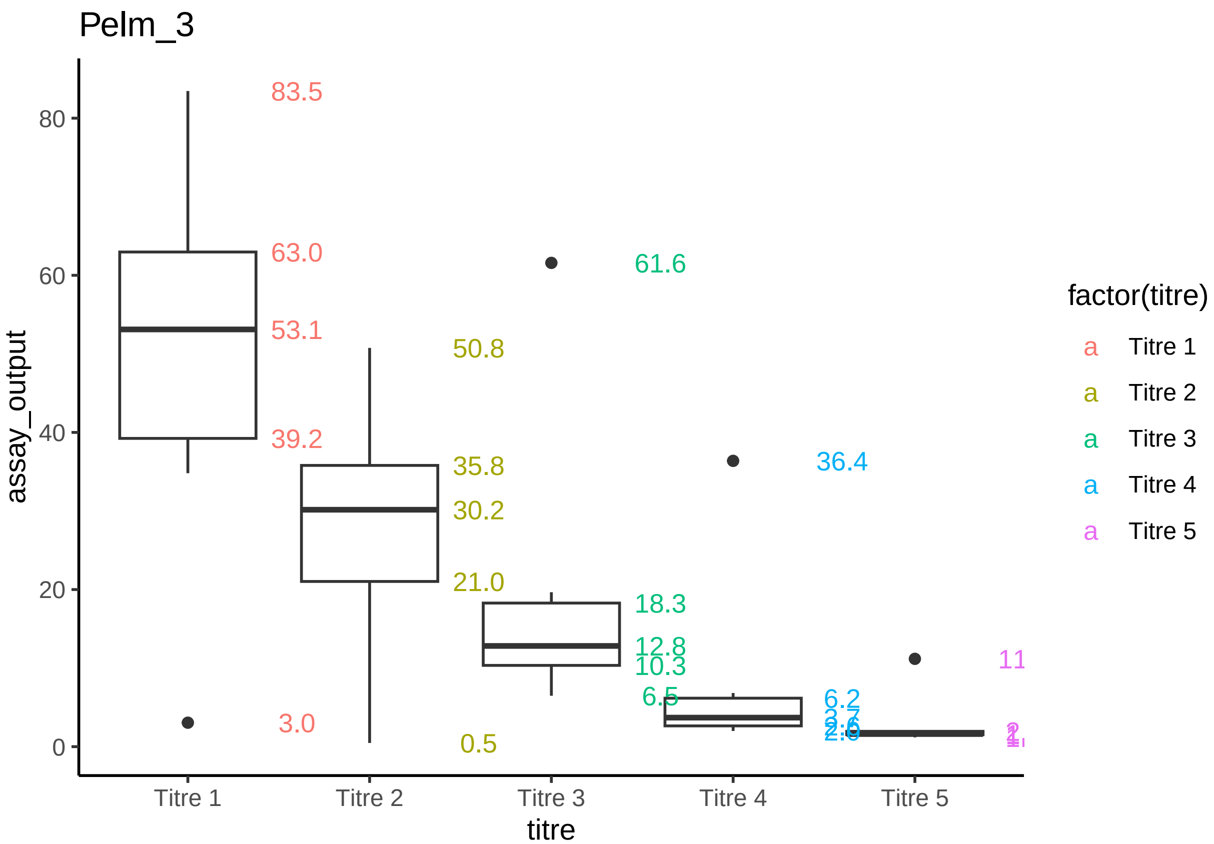

Pahc_5
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
81.9
78.0
58.9
35.1
12.4
66.2
64.1
51.0
24.5
10.9
31.4
28.4
21.2
9.0
5.4
6.8

```
##
## [[87]]
```

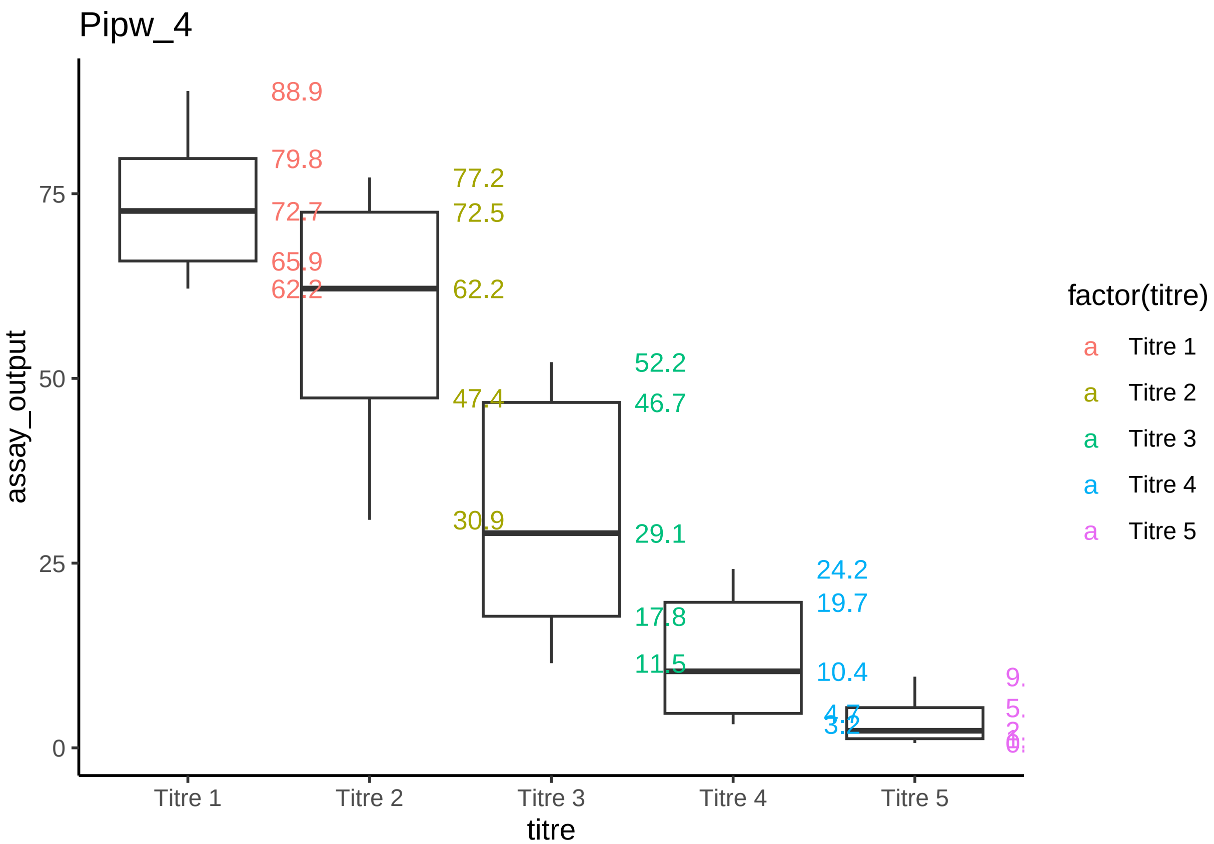


Pamv_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
85.7
82.8
73.5
64.4
62.5
76.1
74.3
55.3
34.5
27.4
40.8
38.9
23.3
7.6
5.5
13.8
13.1
7.3
1.5
0.9
0
25
50
75


```
##
## [[88]]
```

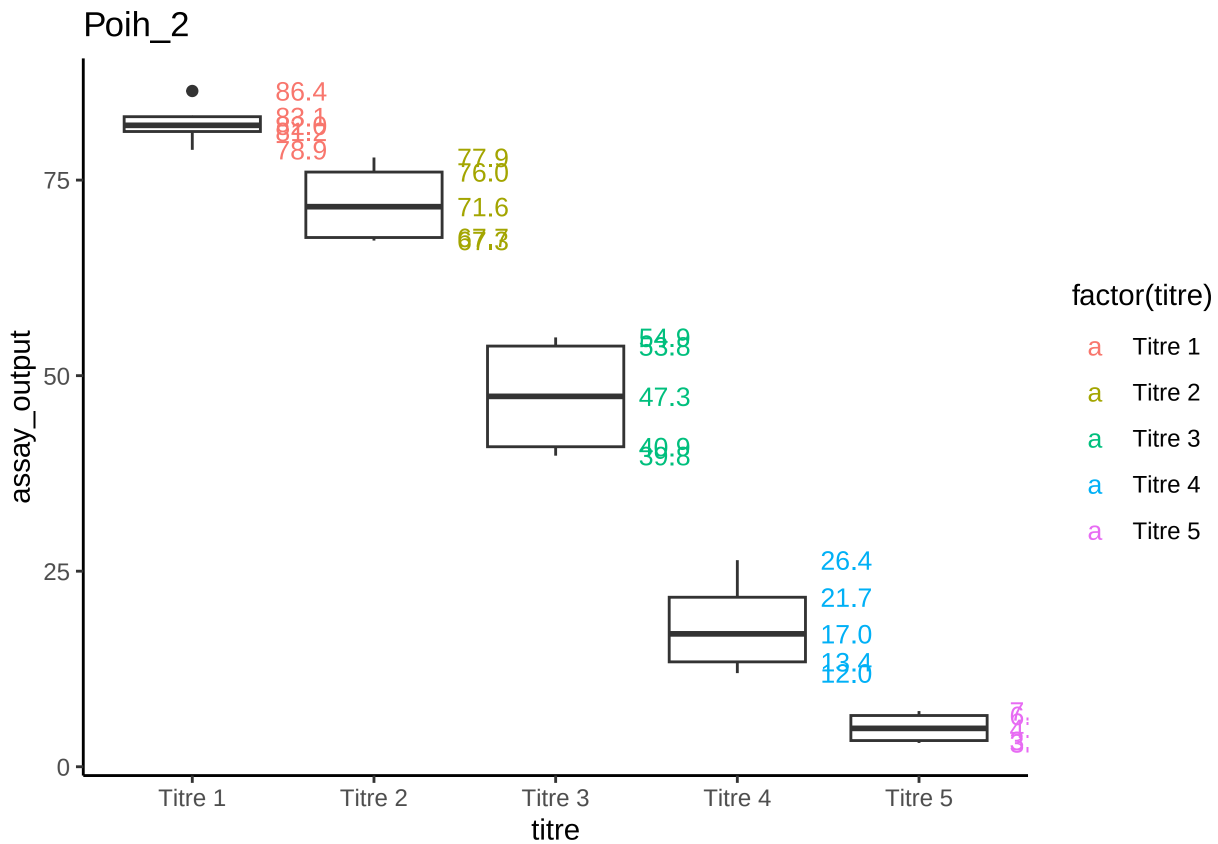

Pelm_3
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
83.5
63.0
53.1
39.2
3.0
50.8
35.8
30.2
21.0
0.5
61.6
18.3
12.8
10.3
6.5
36.4
6.2
11

```
##
## [[89]]
```

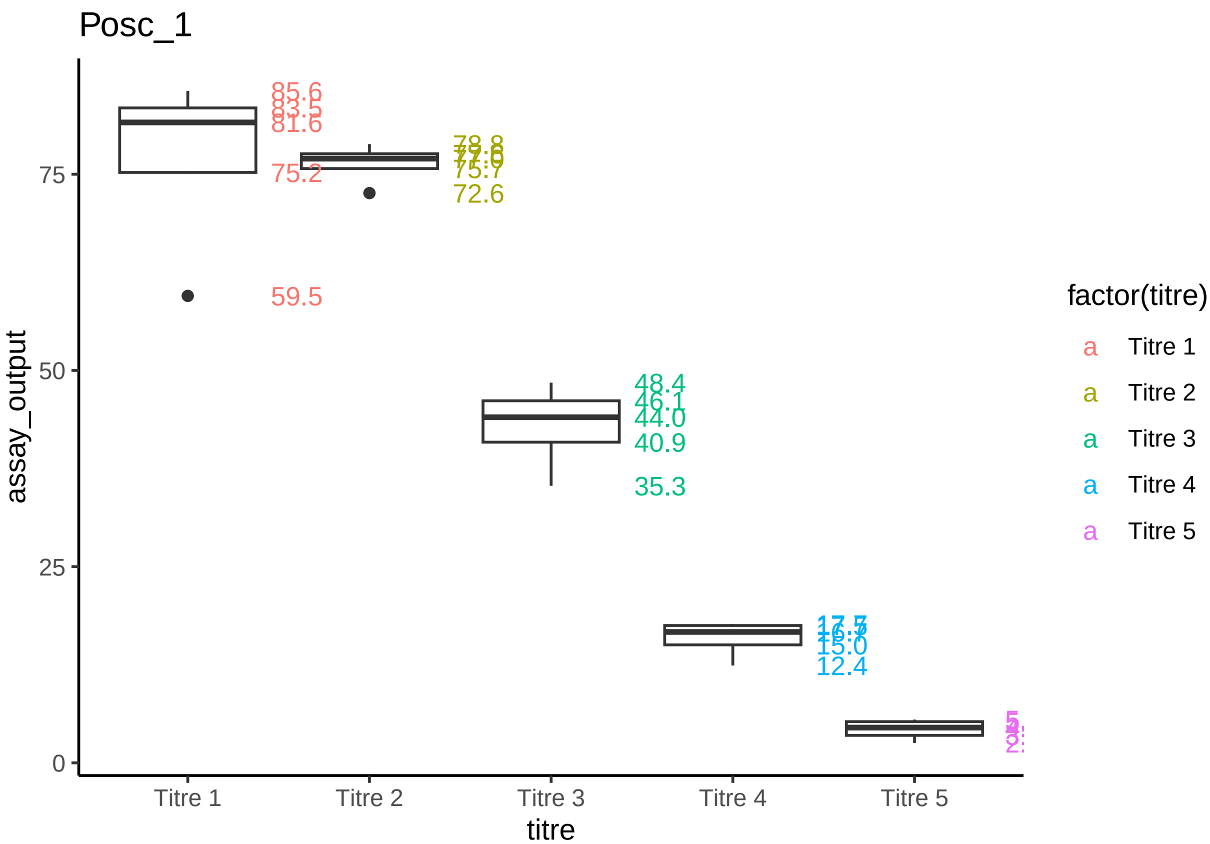


Pipw_4
88.9
79.8
72.7
65.9
62.2
77.2
72.5
62.2
47.4
30.9
52.2
46.7
29.1
17.8
11.5
24.2
19.7
10.4
4.7
3.2
75
50
25
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

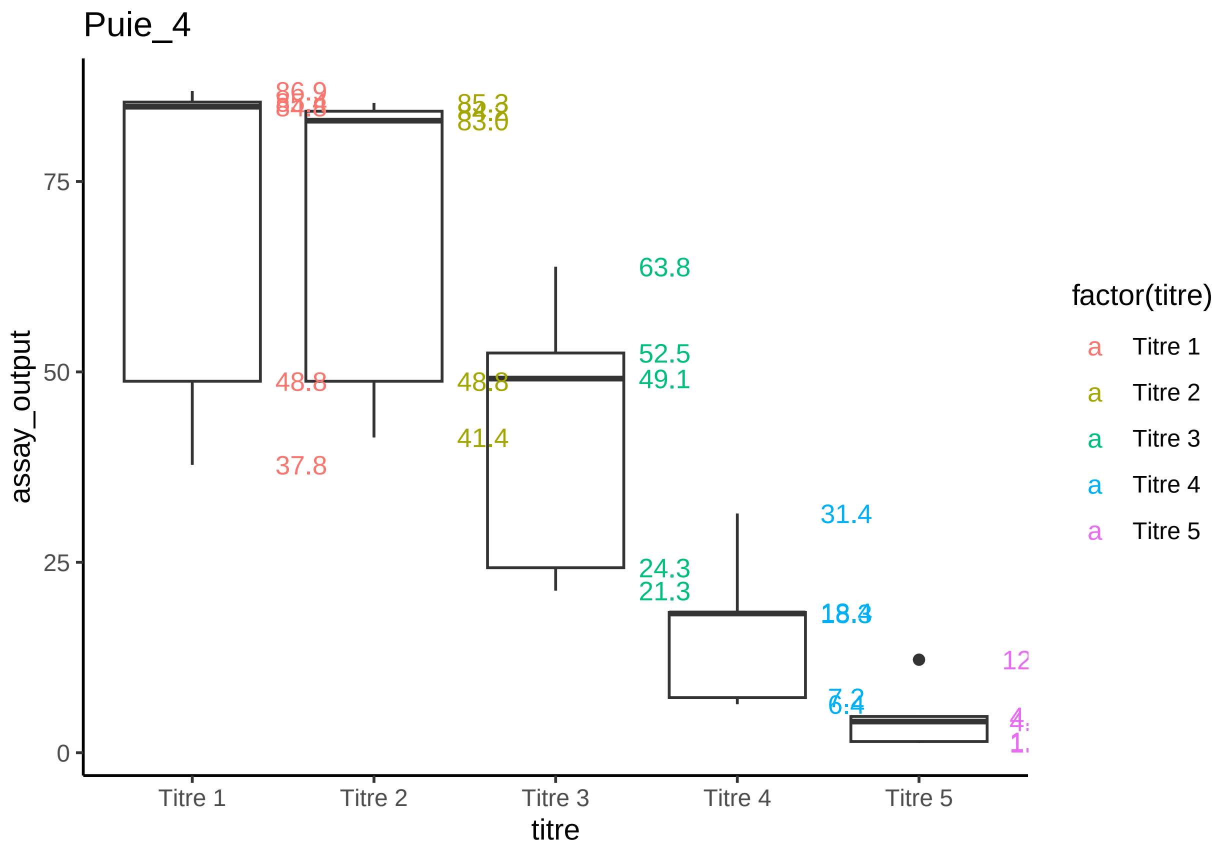

```
##
## [[90]]
```


Poih_2
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
86.4
71.6
47.3
26.4
21.7
17.0

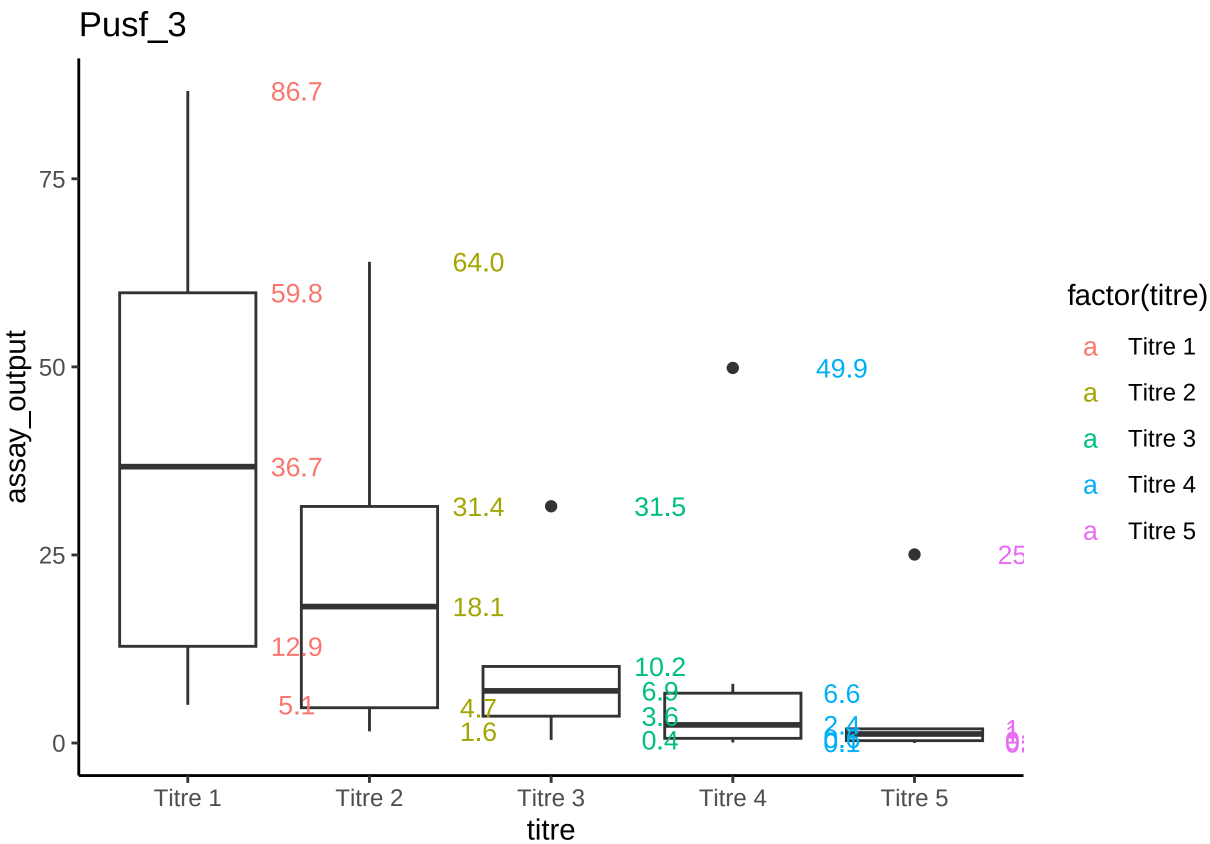
```
##
## [[91]]
```


Posc_1
assay_output
titre
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
85.6
83.5
81.6
75.2
59.5
78.8
75.7
72.6
48.4
46.1
44.0
40.9
35.3
15.0
12.4
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

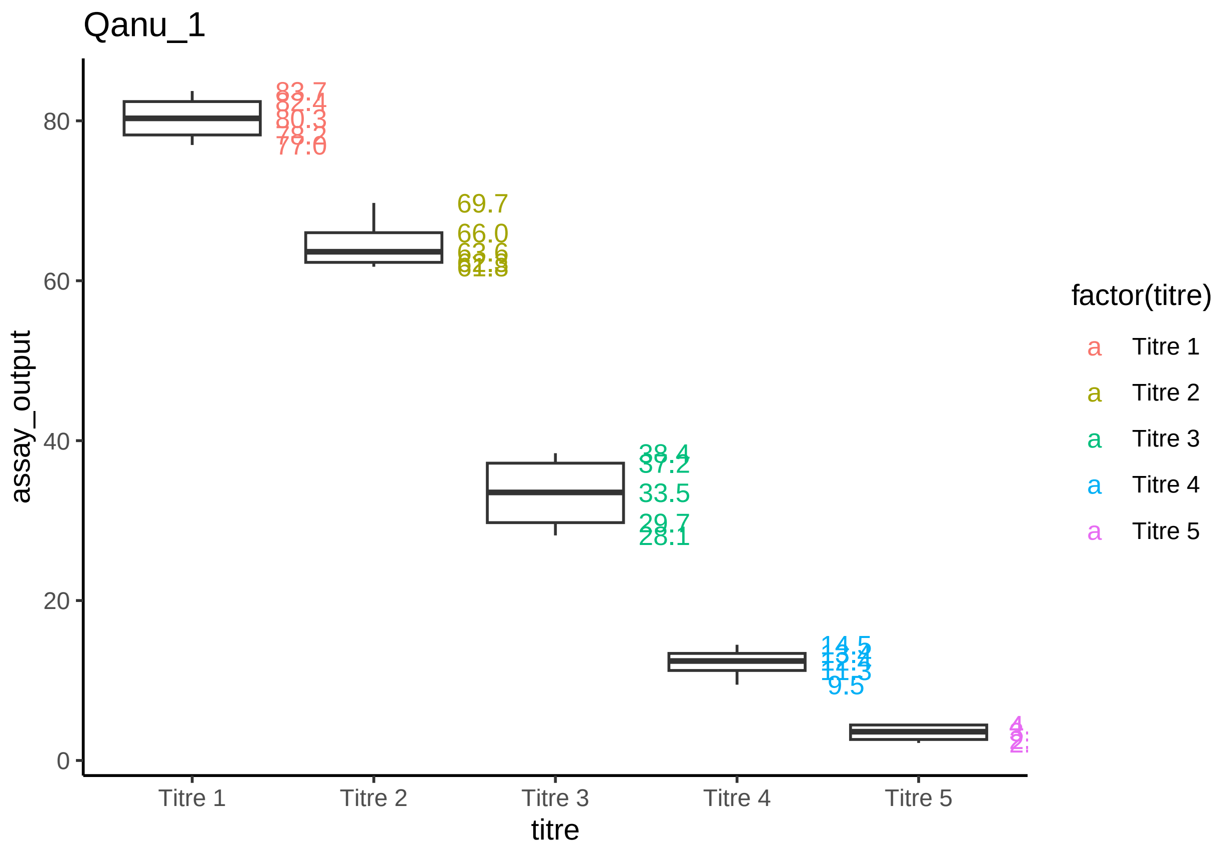
```
##
## [[92]]
```


Puie_4
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
25
50
75
63.8
52.5
49.1
24.3
21.3
31.4
37.8
41.4

```
##
## [[93]]
```

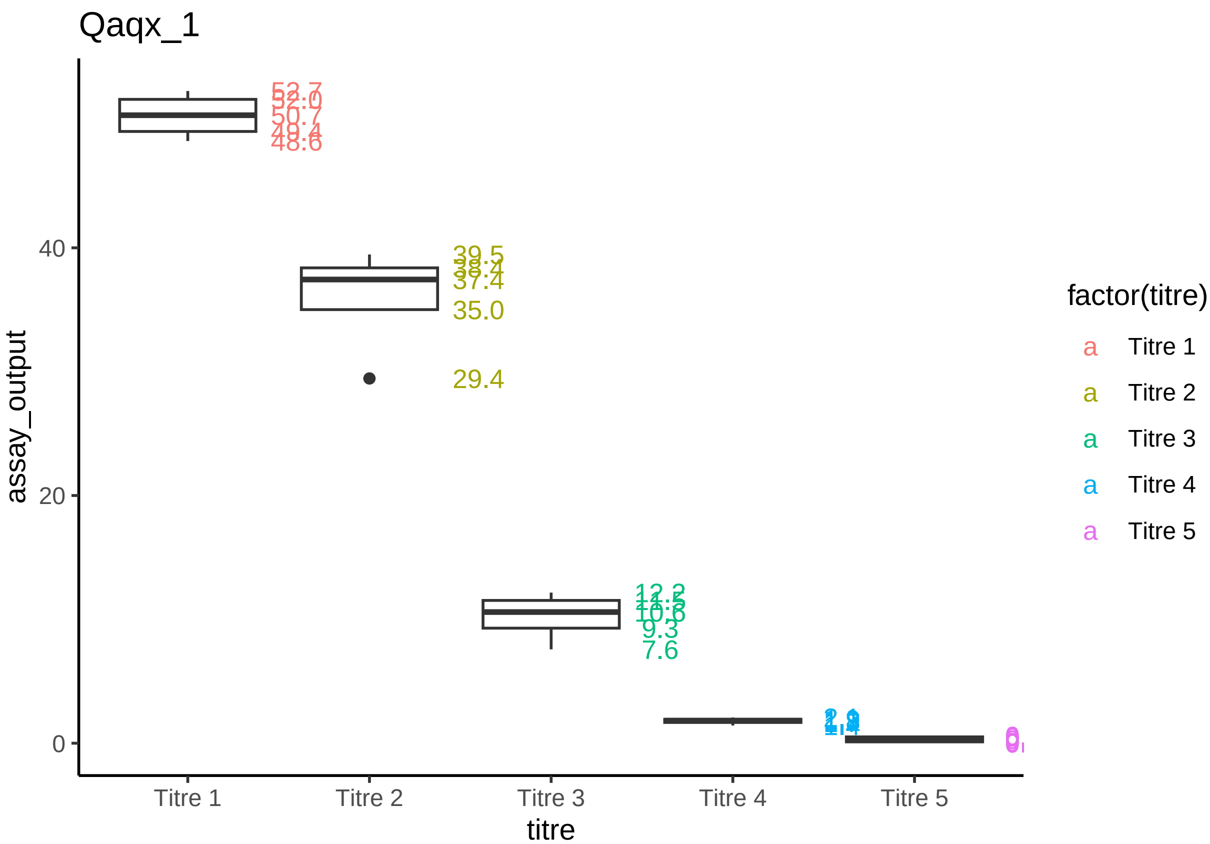

Pusf_3
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
86.7
59.8
36.7
12.9
5.1
64.0
31.4
18.1
4.7
1.6
31.5
10.2
6.9
3.6
0.4
49.9
6.6
2.4
0.1
25
0
25
50
75

```
##
## [[94]]
```

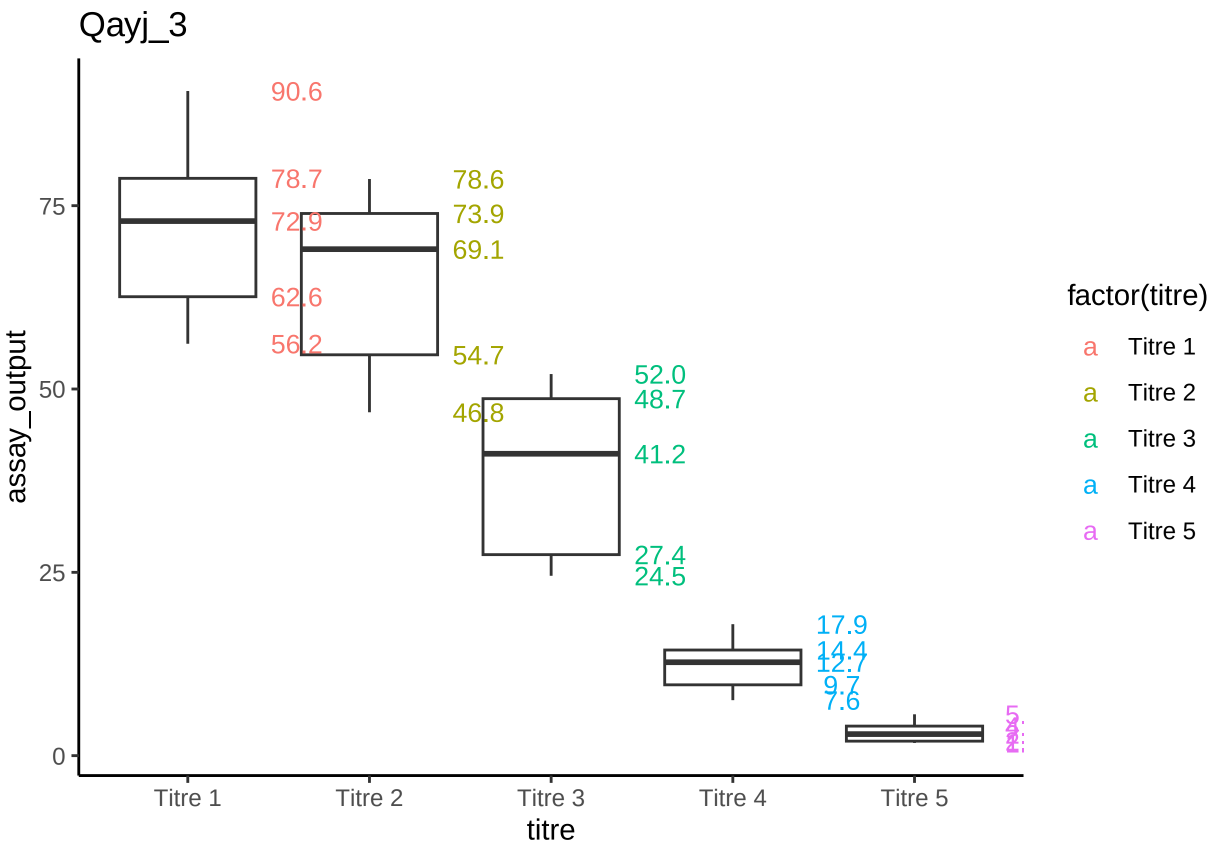


Qanu_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
69.7
66.0
33.5
9.5

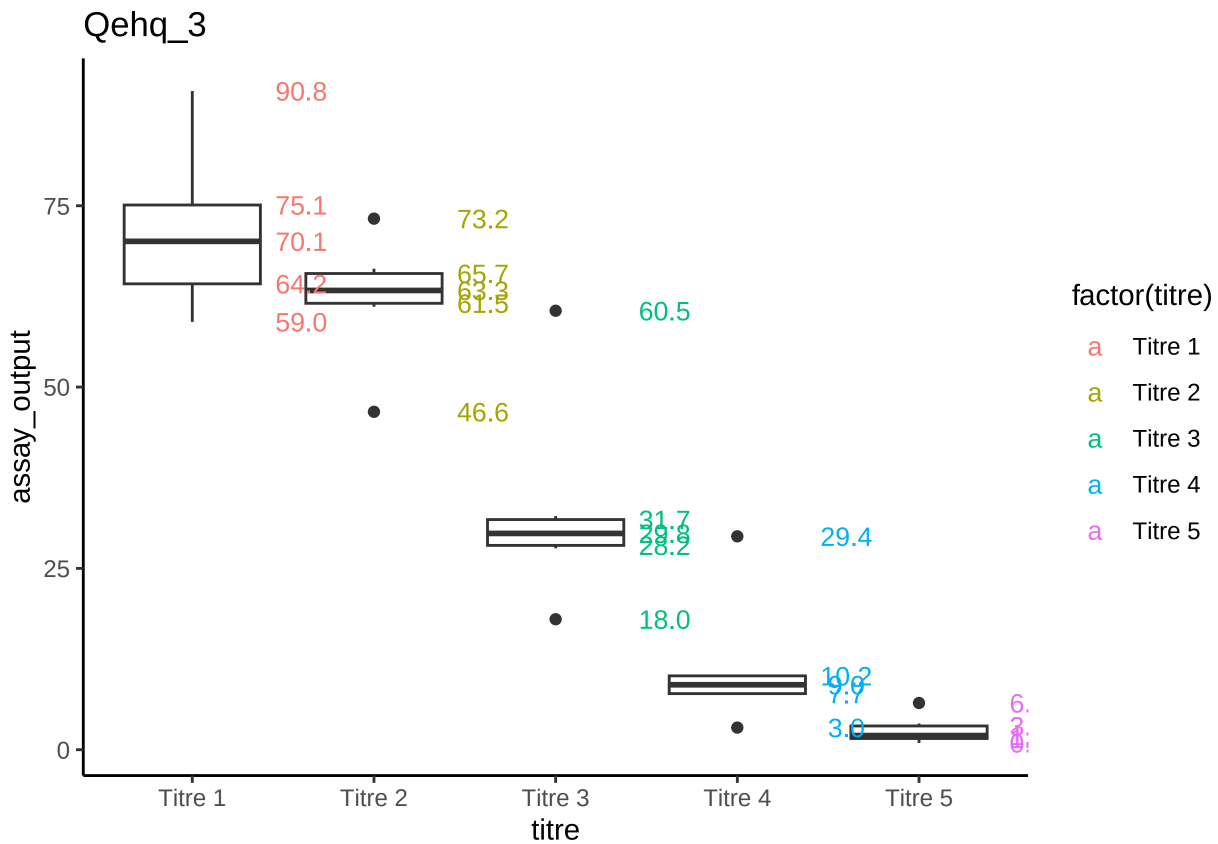

```
##
## [[95]]
```


Qaqx_1
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
35.0
29.4
7.6

```
##
## [[96]]
```

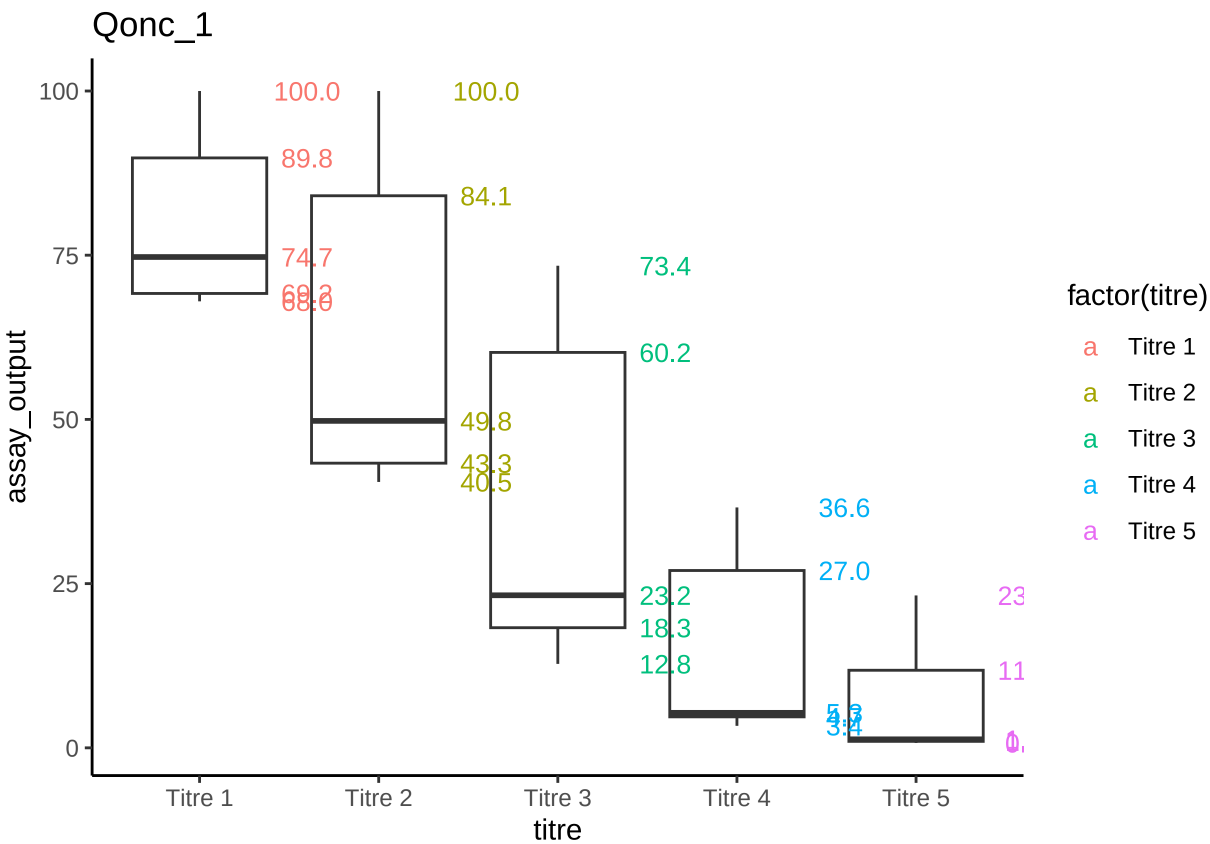

Qayj_3
90.6
78.7
72.9
62.6
56.2
78.6
73.9
69.1
54.7
46.8
52.0
48.7
41.2
27.4
24.5
17.9
14.4
12.7
9.7
7.6
75
50
25
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[97]]
```



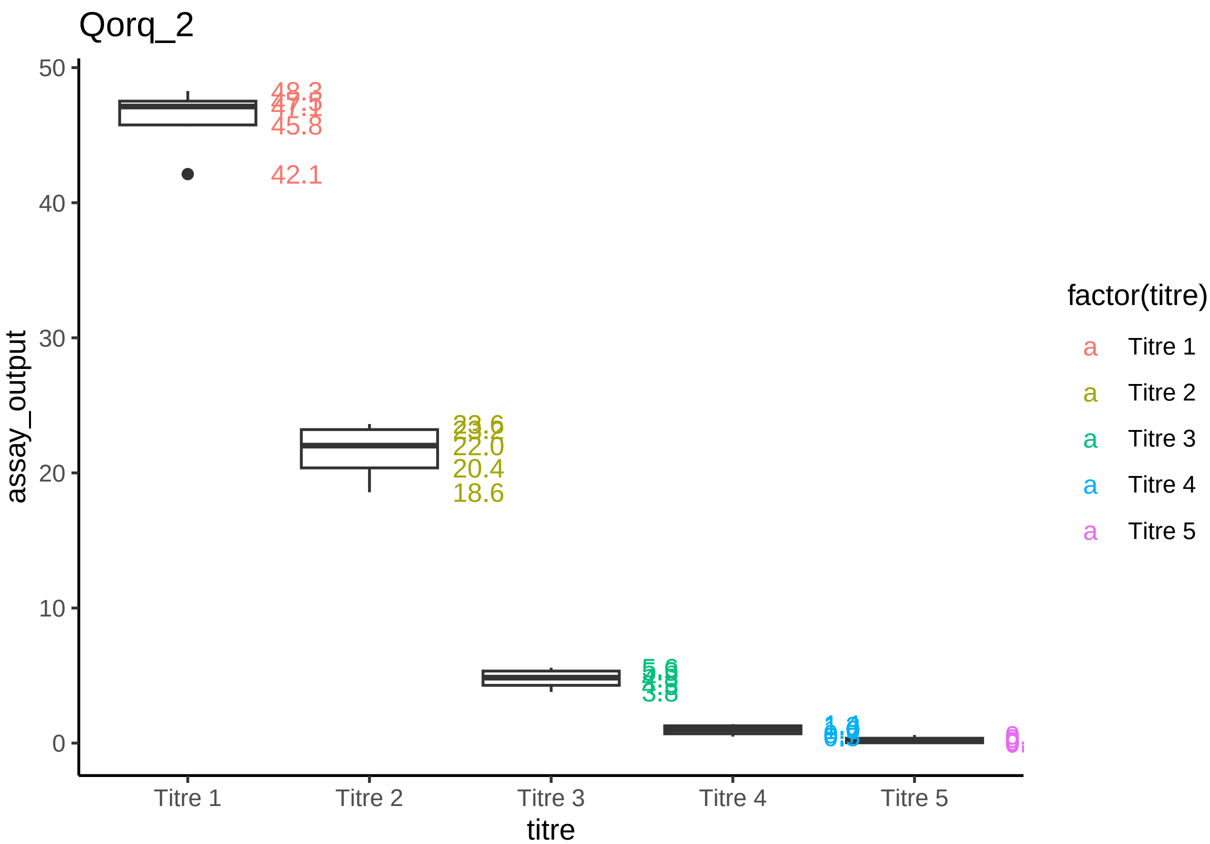
Qehq_3
90.8
75.1
70.1
64.2
59.0
73.2
65.7
63.3
61.5
46.6
60.5
31.7
29.8
28.2
18.0
29.4
10.2
9.0
7.7
3.0
assay_output
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[98]]
```



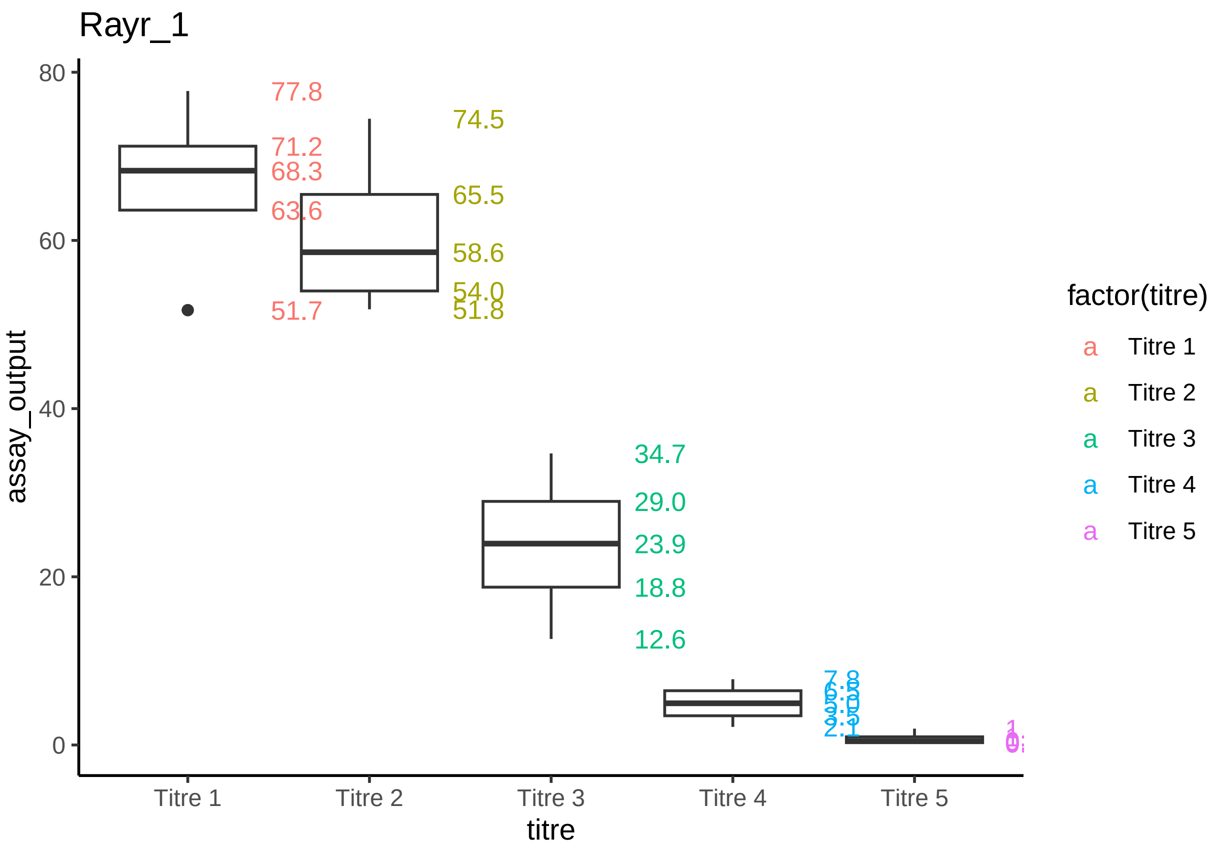
Qonc_1
100
75
50
25
0
assay_output
100.0
89.8
74.7
69.2
68.6
100.0
84.1
49.8
43.3
40.5
73.4
60.2
23.2
18.3
12.8
36.6
27.0
5.3
4.3
3.4
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[99]]
```

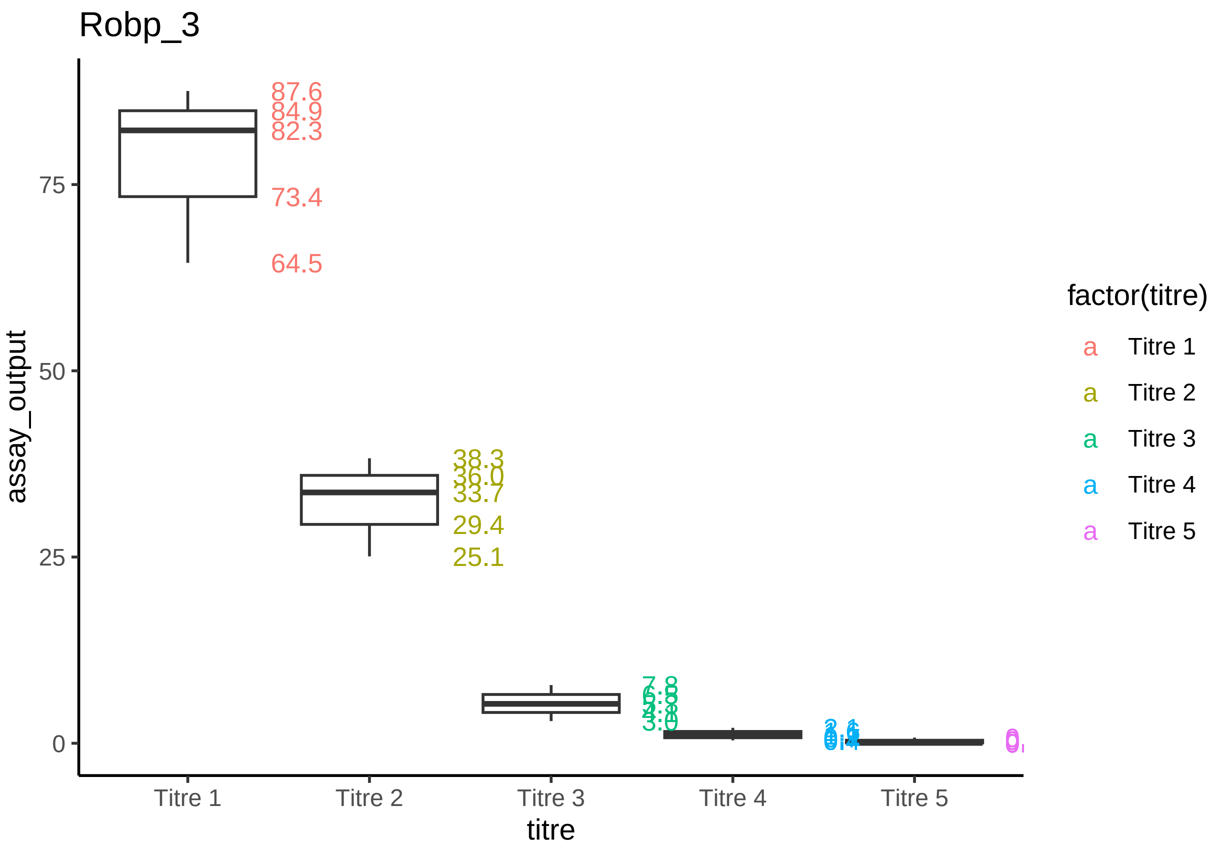


Qorq_2
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
50
40
30
20
10
0
42.1
45.8
20.4
18.6
factor(titre)


```
##
## [[100]]
```

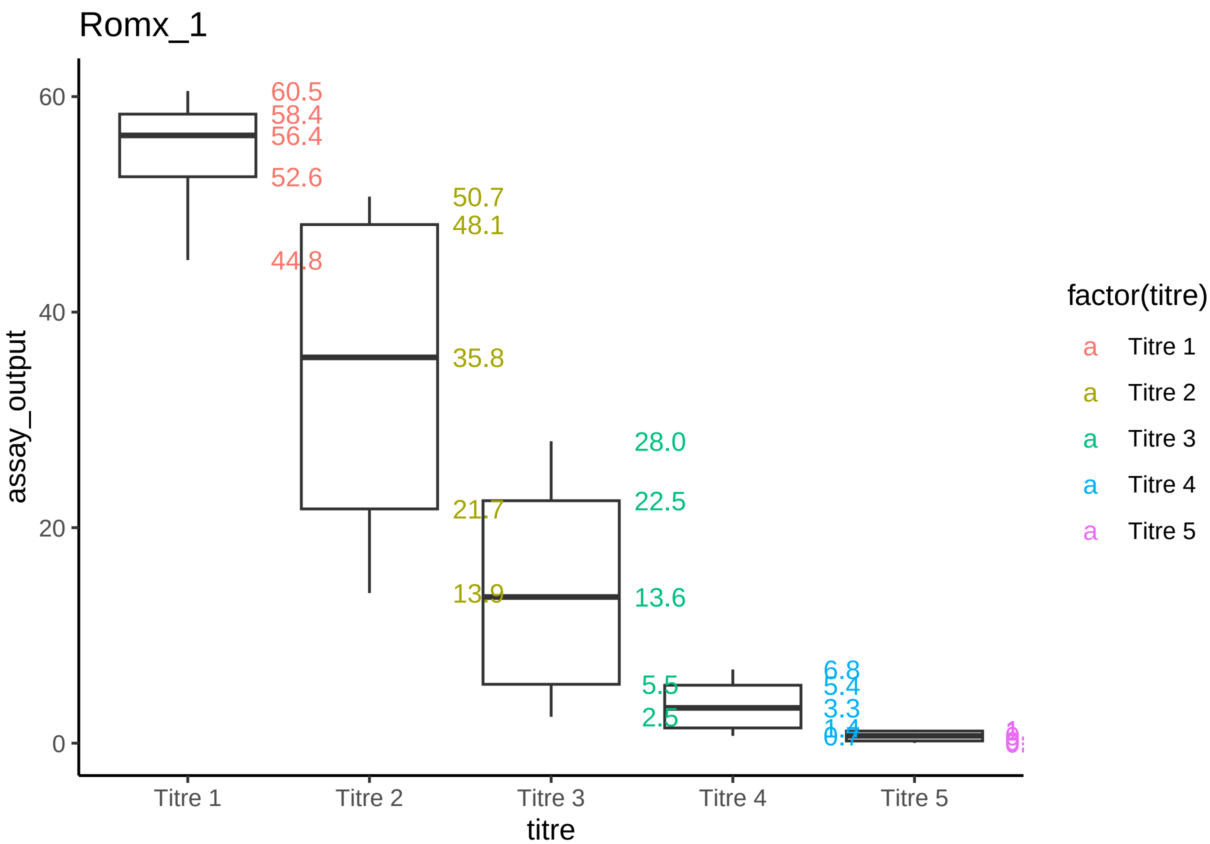

Rayr_1
80
60
40
20
0
assay_output
77.8
71.2
68.3
63.6
51.7
74.5
65.5
58.6
54.0
51.8
34.7
29.0
23.9
18.8
12.6
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[101]]
```

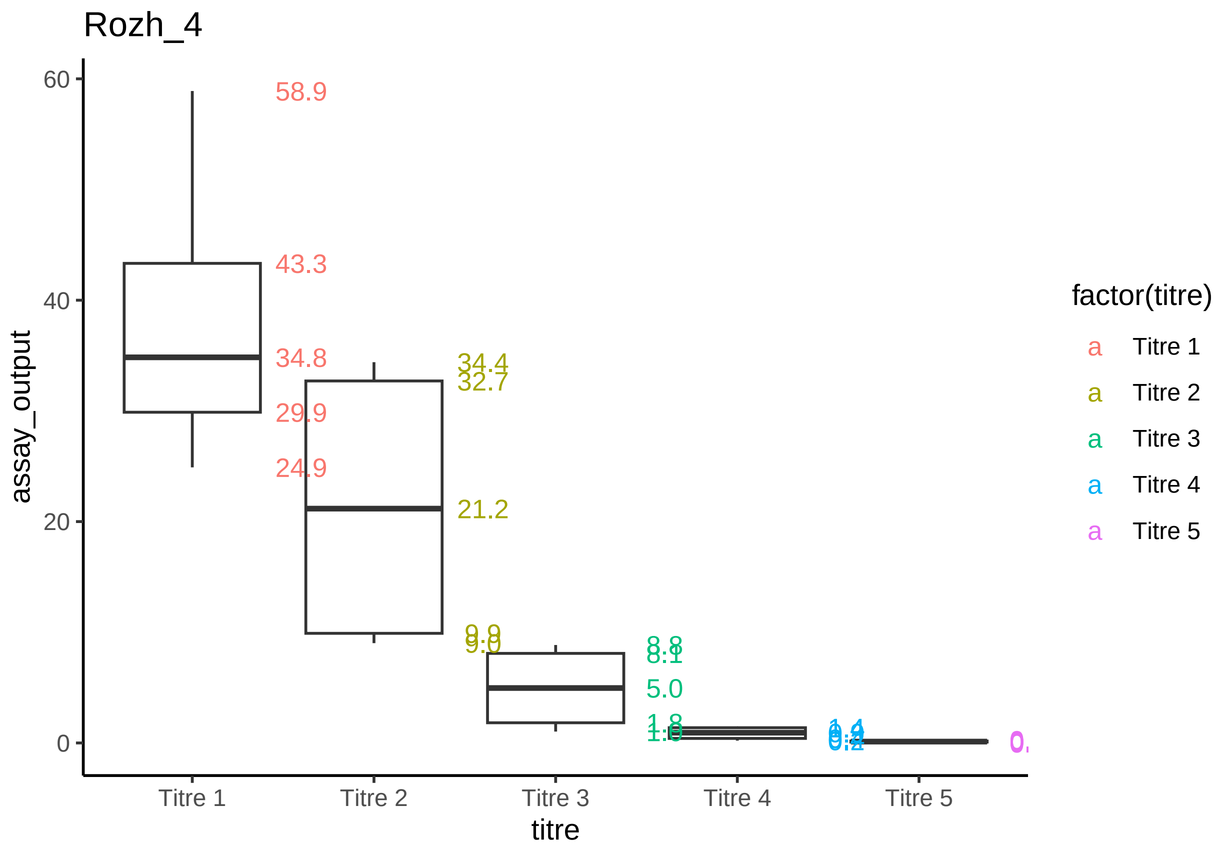


Robp_3
87.6
84.9
82.3
73.4
64.5
38.3
36.0
33.7
29.4
25.1
7.8
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5
assay_output
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre


```
##
## [[102]]
```

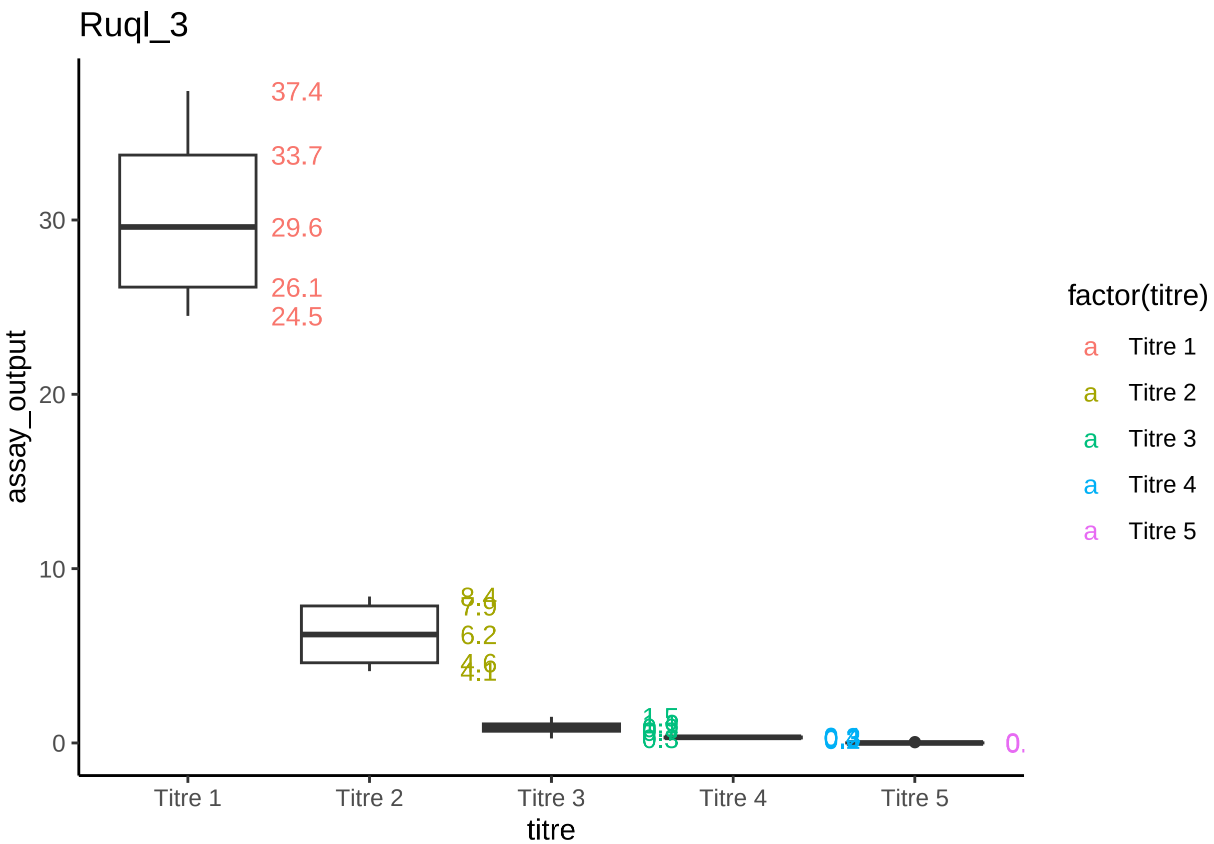

Romx_1
assay_output
60
40
20
0
60.5
58.4
56.4
52.6
44.8
50.7
48.1
35.8
21.7
13.9
28.0
22.5
13.6
5.5
2.5
6.8
5.4
3.3
1.4
0.7
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[103]]
```



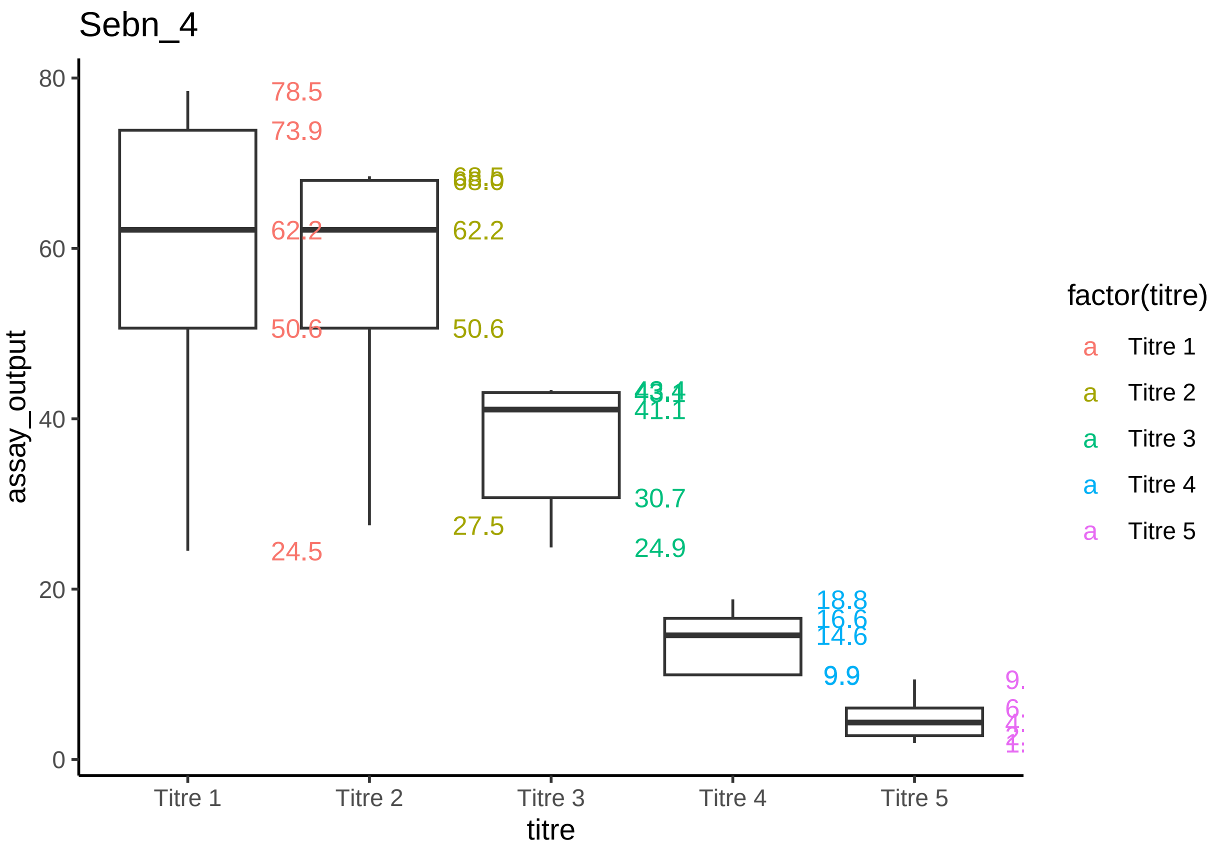
Rozh_4
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
58.9
43.3
34.8
29.9
24.9
34.4
32.7
21.2
5.0
factor(titre)


```
##
## [[104]]
```



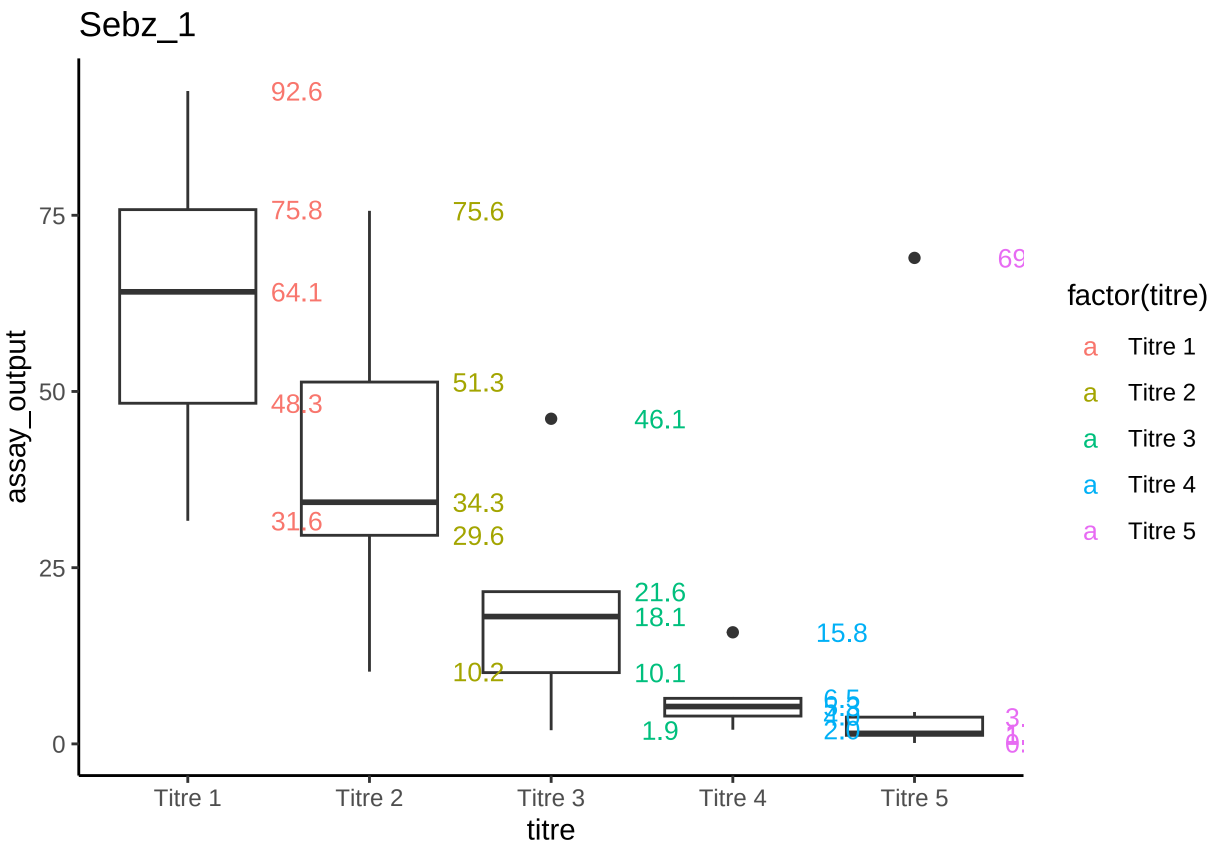
Ruql_3
37.4
33.7
29.6
26.1
24.5
8.4
7.9
6.2
4.6
4.1
1.5
0.5
0.
30
20
10
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[105]]
```

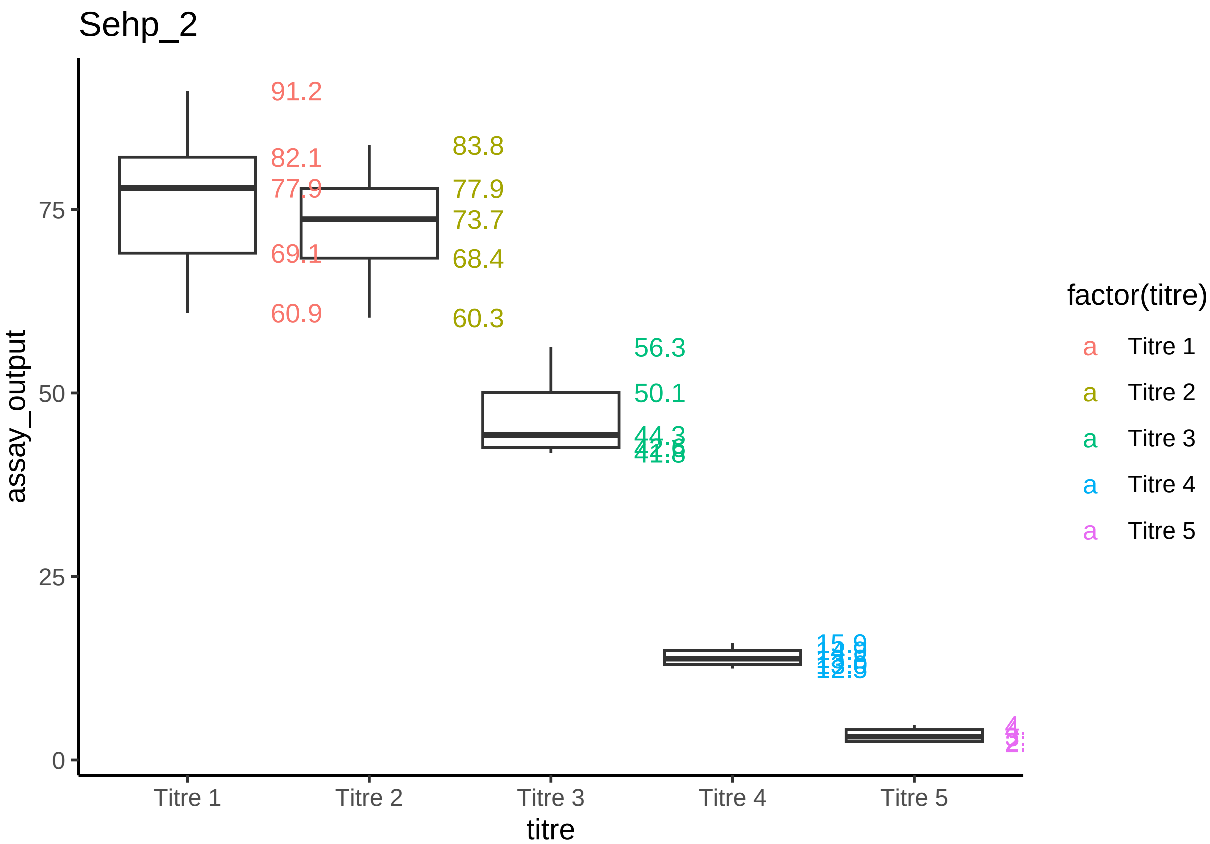


Sebn_4
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
78.5
73.9
62.2
50.6
24.5
62.2
50.6
27.5
41.1
30.7
24.9
18.8
16.6
14.6
9.9

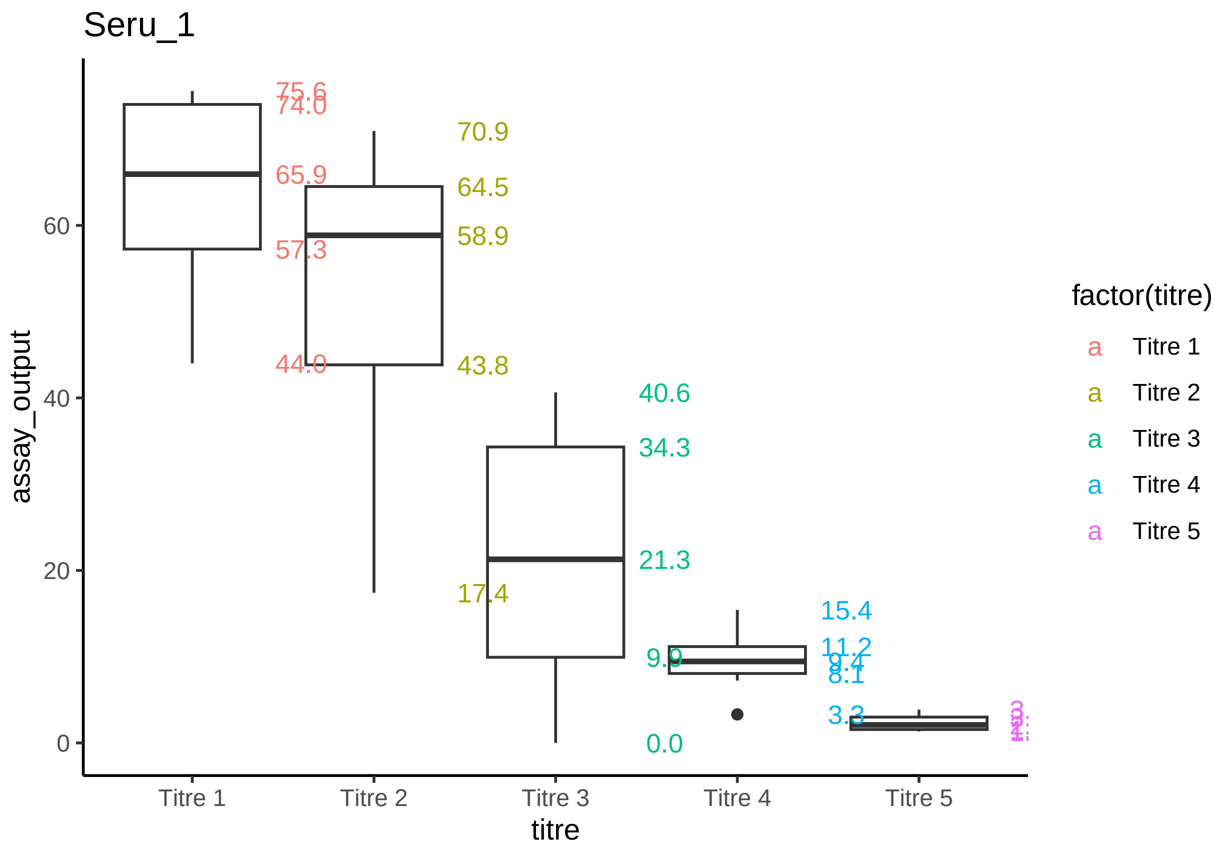

```
##
## [[106]]
```


Sebz_1
assay_output
75
50
25
0
92.6
75.8
64.1
48.3
31.6
75.6
51.3
34.3
29.6
10.2
46.1
21.6
18.1
10.1
1.9
15.8
6.5
2.0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[107]]
```

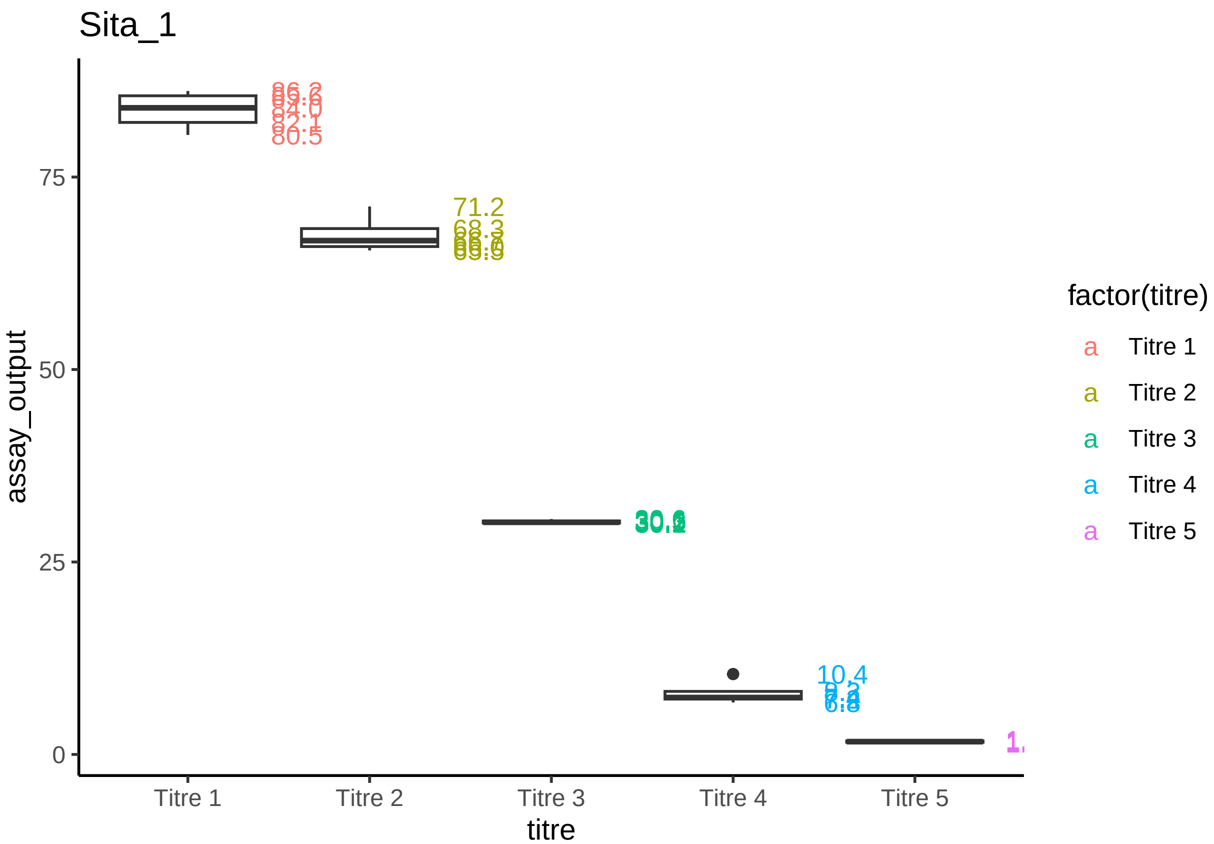

Sehp_2
91.2
82.1
77.9
69.1
60.9
83.8
77.9
73.7
68.4
60.3
56.3
50.1
assay_output
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[108]]
```

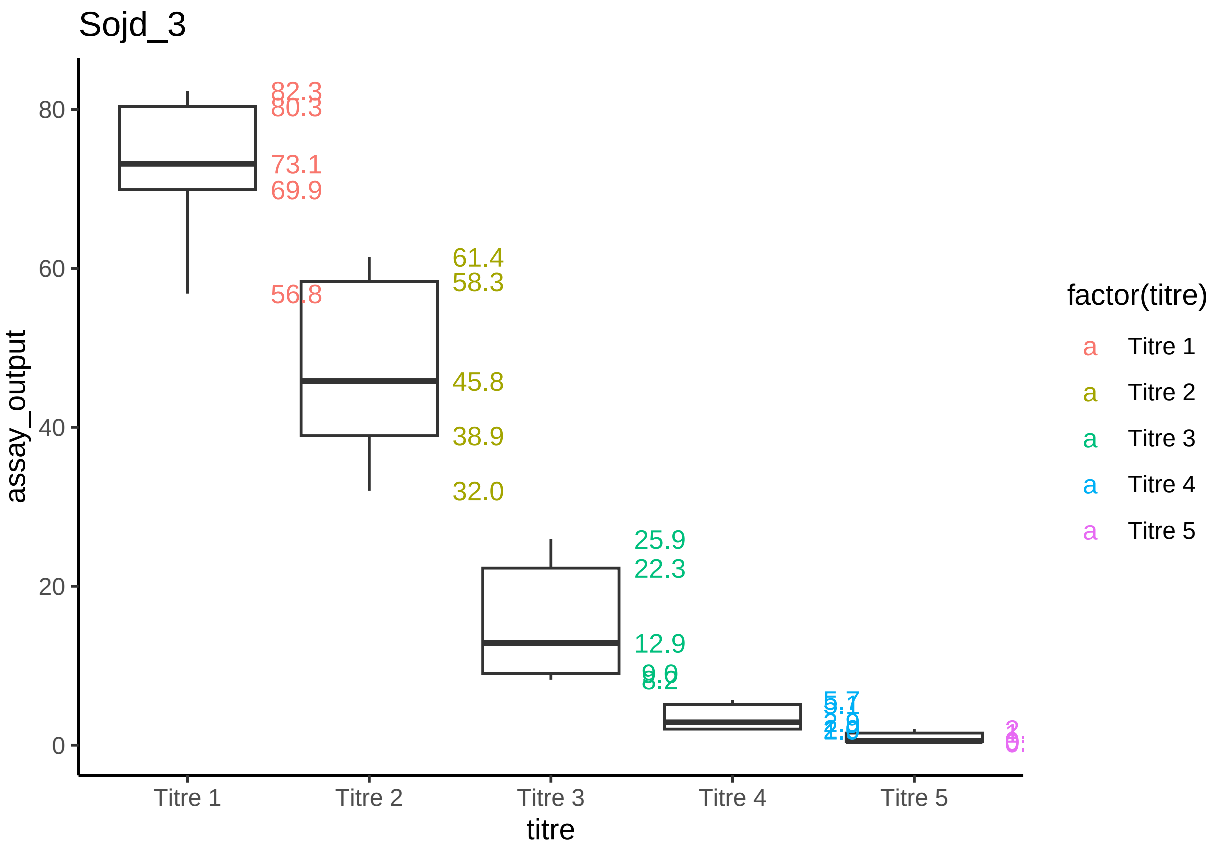


Seru_1
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
75.6
74.0
65.9
57.3
44.0
70.9
64.5
58.9
43.8
17.4
40.6
34.3
21.3
9.9
0.0
15.4
11.2
9.4
8.1
3.3

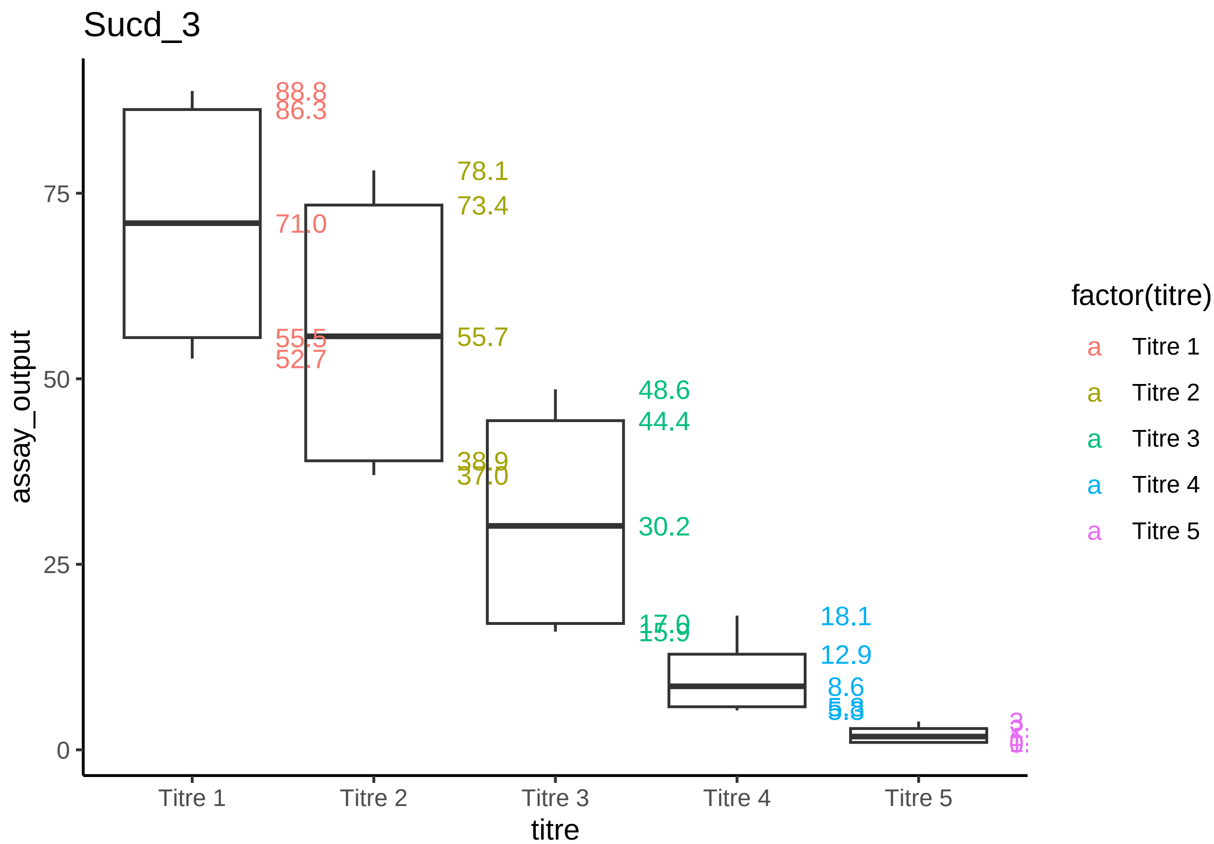

```
##
## [[109]]
```


Sita_1
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
71.2
68.3
10.4

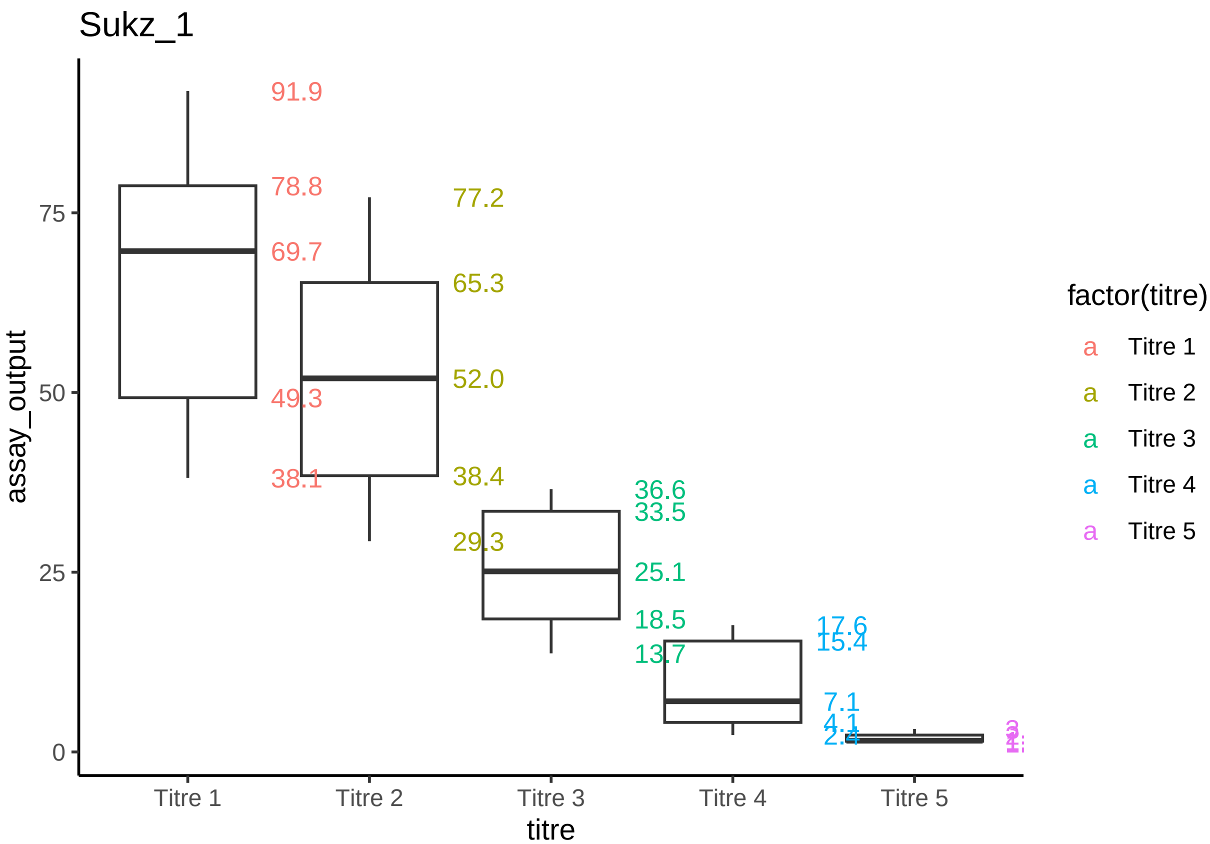
```
##
## [[110]]
```


Sojd_3
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5
82.3
80.3
73.1
69.9
56.8
61.4
58.3
45.8
38.9
32.0
25.9
22.3
12.9


```
##
## [[111]]
```

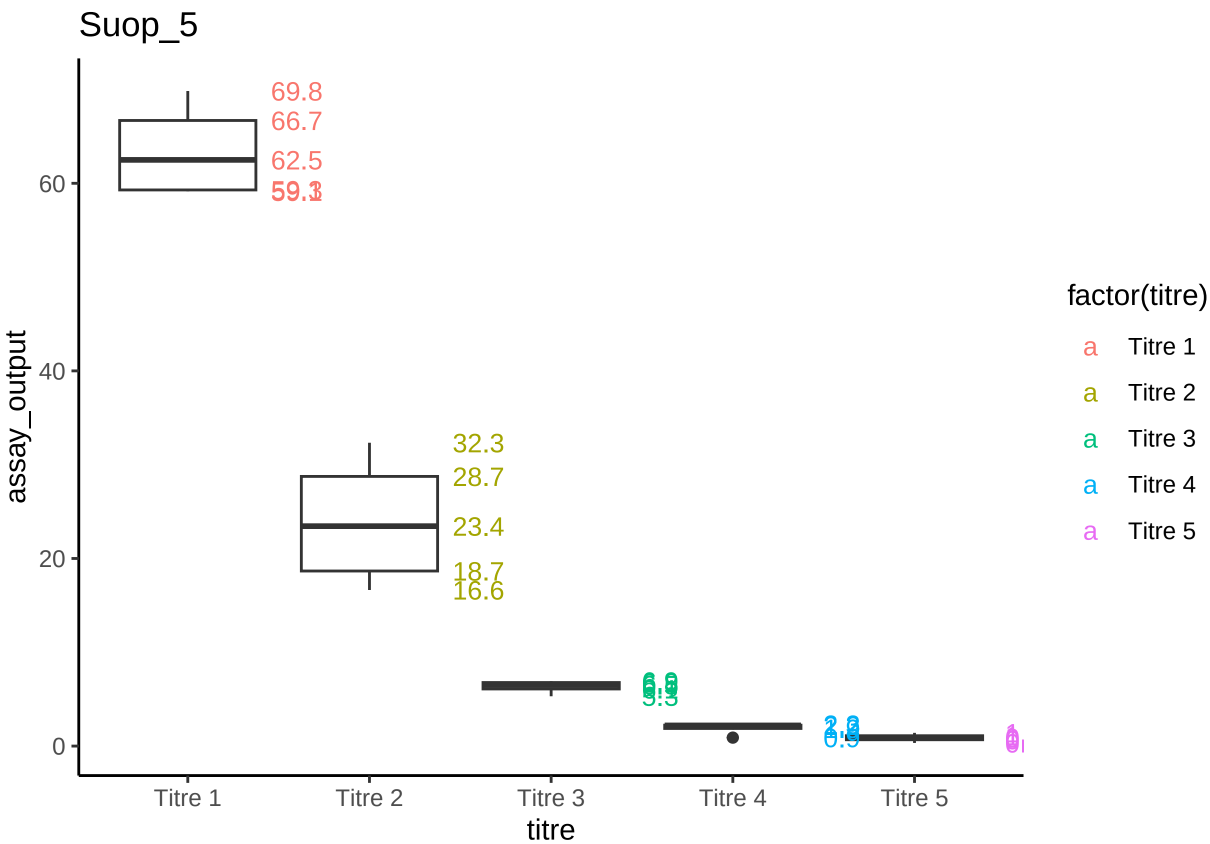

Sucd_3
assay_output
titre
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
88.8
86.3
71.0
55.5
52.7
78.1
73.4
55.7
38.9
37.0
48.6
44.4
30.2
17.0
15.9
18.1
12.9
8.6
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[112]]
```



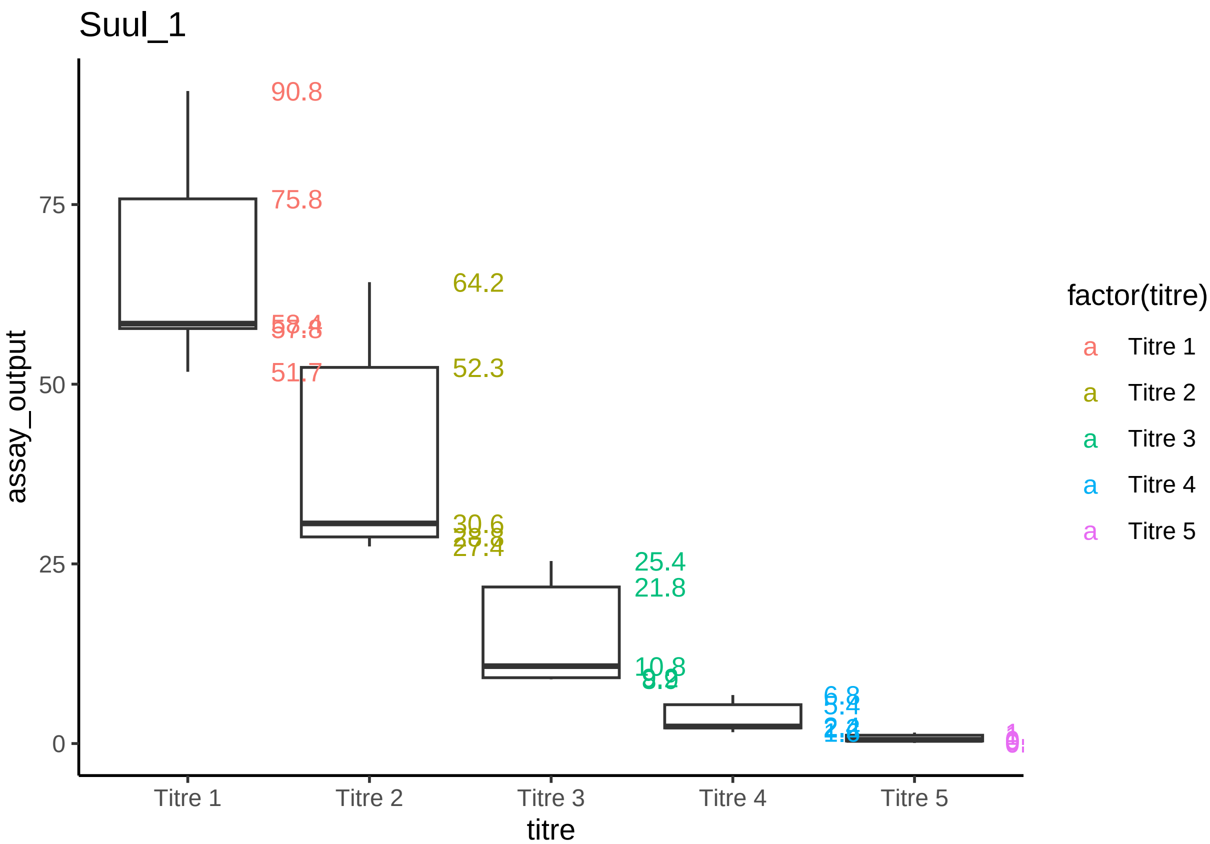
Sukz_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
25
50
75
91.9
78.8
69.7
49.3
38.1
77.2
65.3
52.0
38.4
29.3
36.6
33.5
25.1
18.5
13.7
17.6
15.4
7.1
4.1
2.4
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[113]]
```



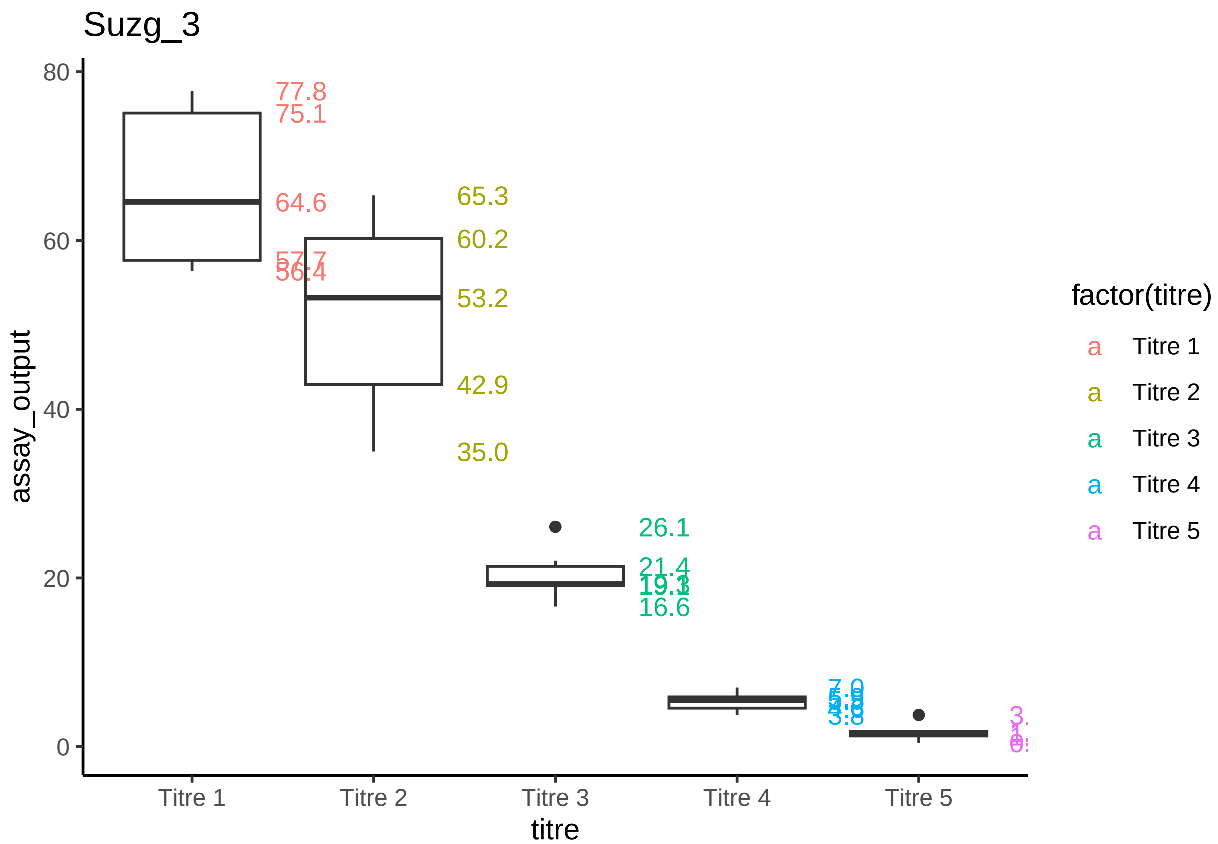
Suop_5
69.8
66.7
62.5
32.3
28.7
23.4
18.7
16.6
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[114]]
```



Suul_1
90.8
75.8
58.4
57.8
51.7
64.2
52.3
30.6
28.8
28.2
27.4
25.4
21.8
10.8
8.9
8.8
6.8
5.4
2.4
2.2
1.8
assay_output
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

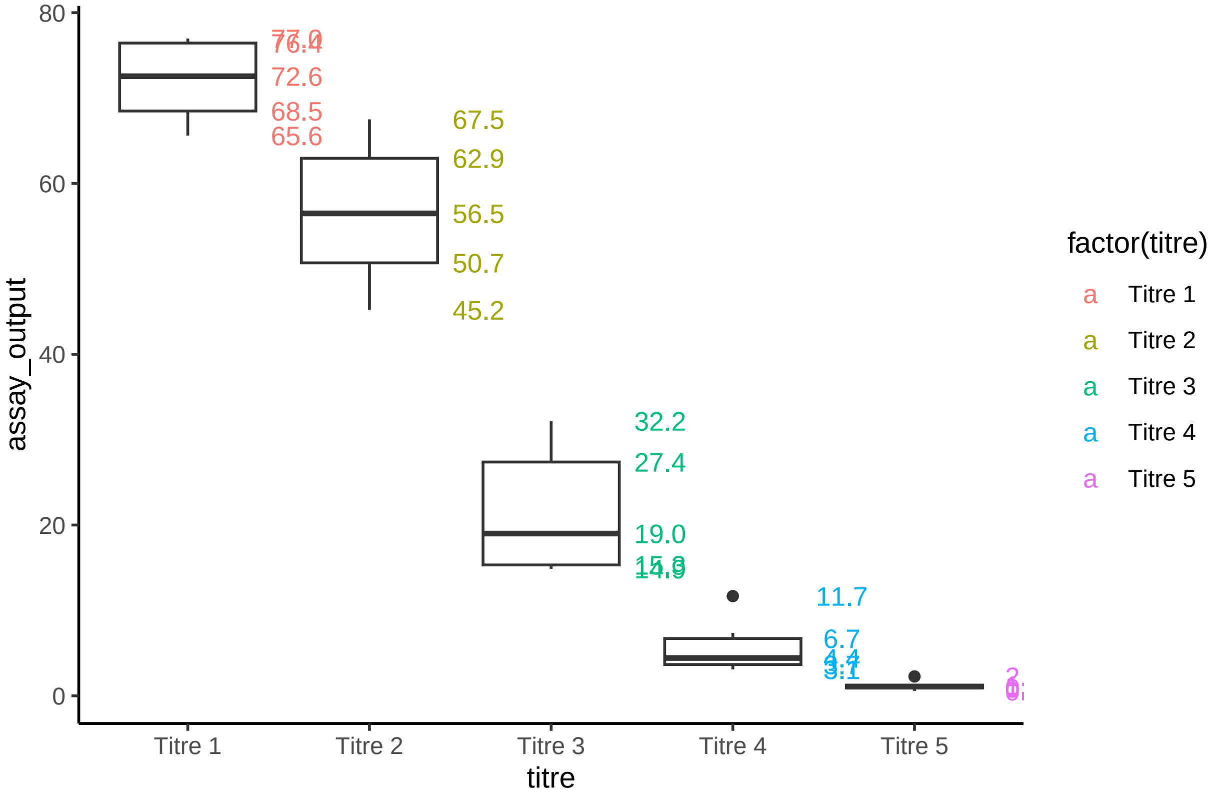

```
##
## [[115]]
```



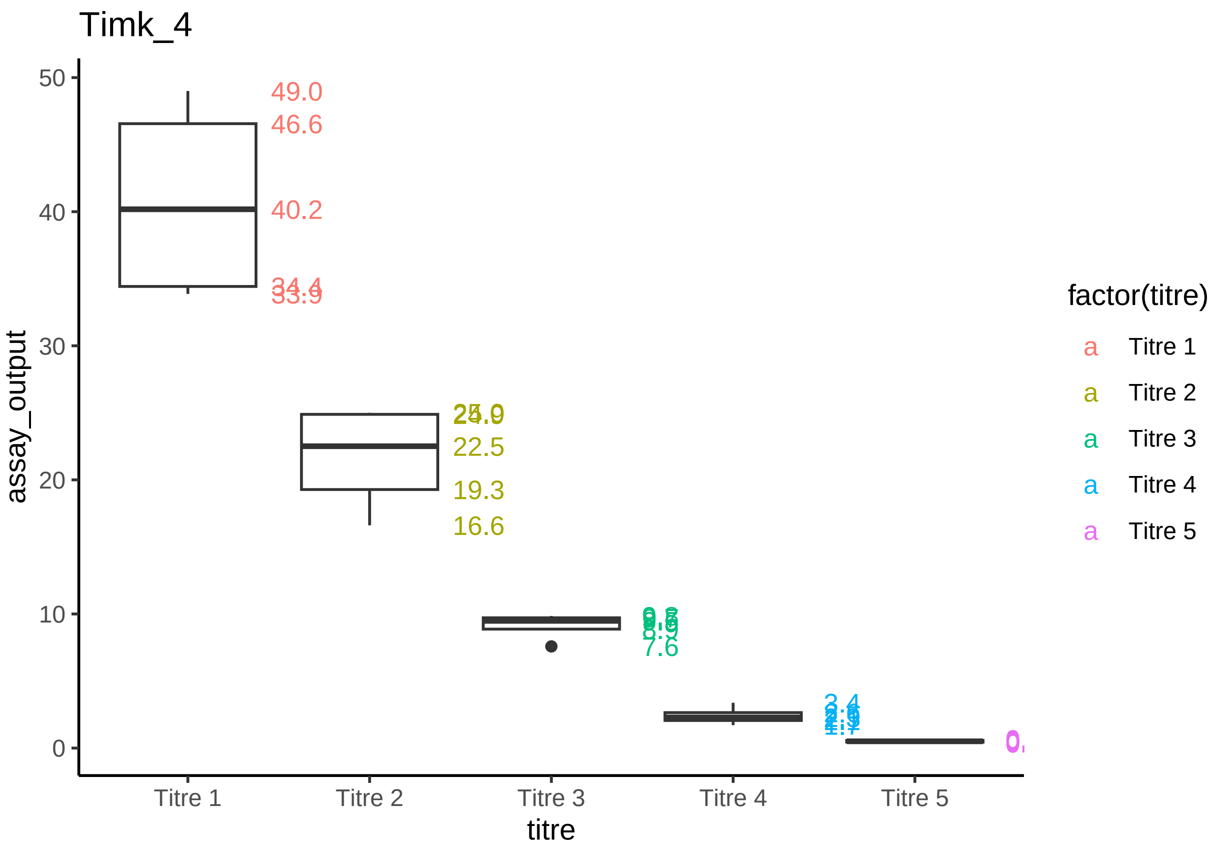
Suzg_3
80
60
40
20
0
assay_output
77.8
75.1
64.6
57.7
56.4
65.3
60.2
53.2
42.9
35.0
26.1
21.4
19.1
16.6
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[116]]
```

Terl_1

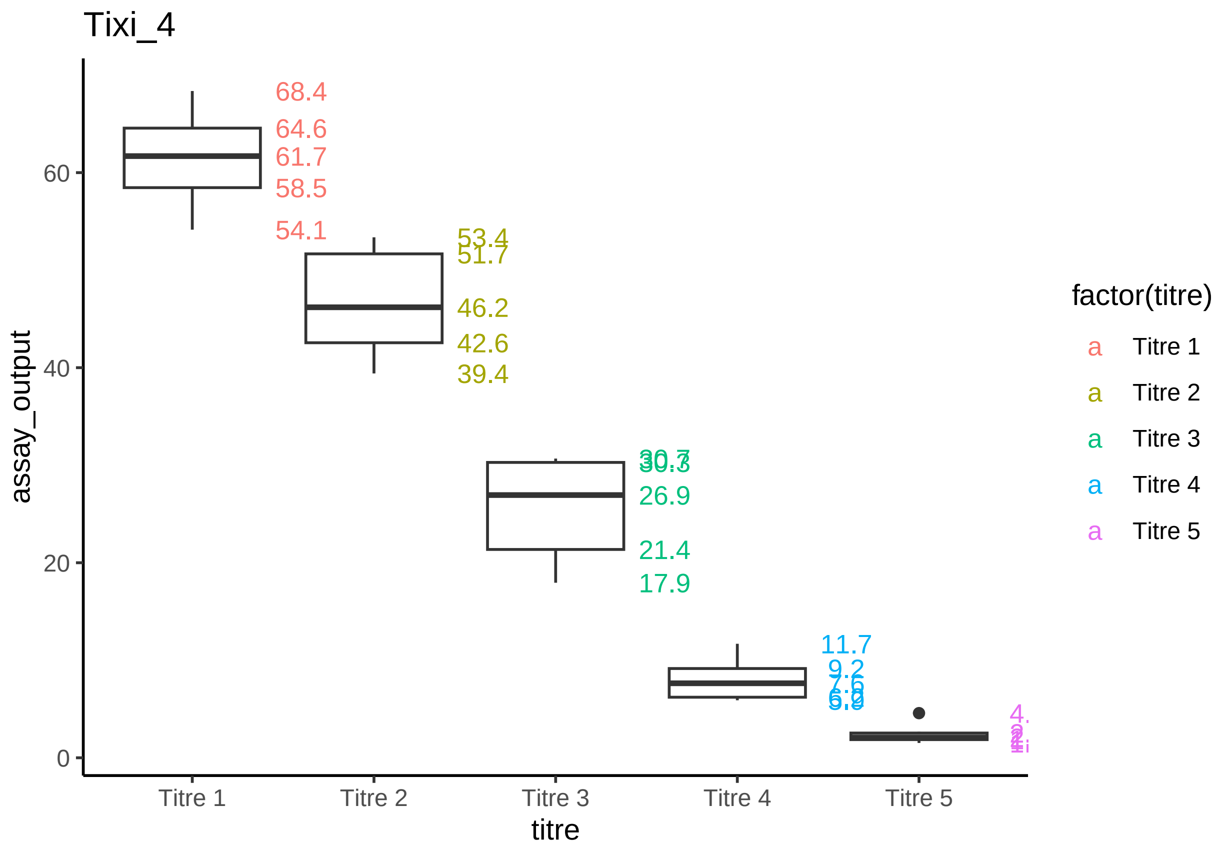

Terl_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
77.0
76.4
72.6
68.5
65.6
67.5
62.9
56.5
50.7
45.2
32.2
27.4
19.0
15.3
14.9
11.7
6.7
4.4
3.1

```
##
## [[117]]
```



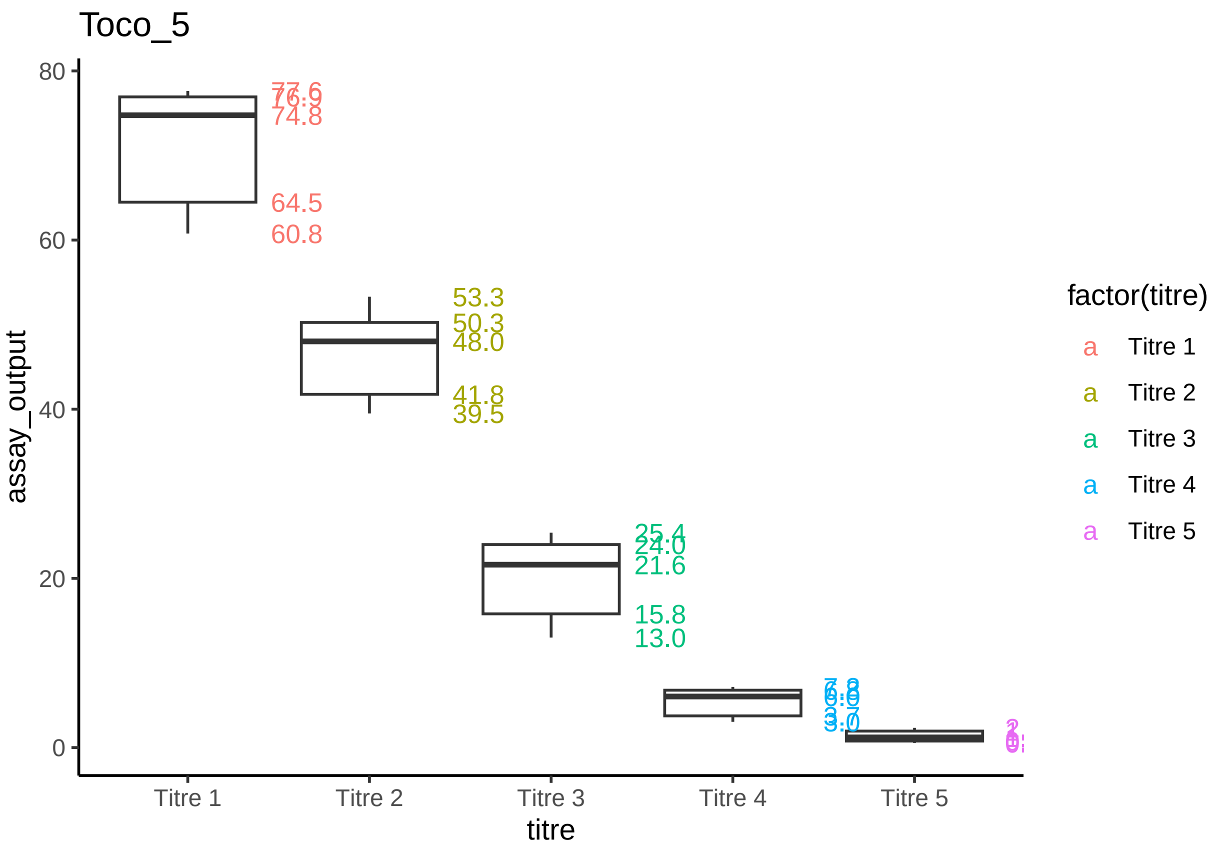
Timk_4
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
49.0
46.6
40.2
22.5
19.3
16.6
7.6


```
##
## [[118]]
```

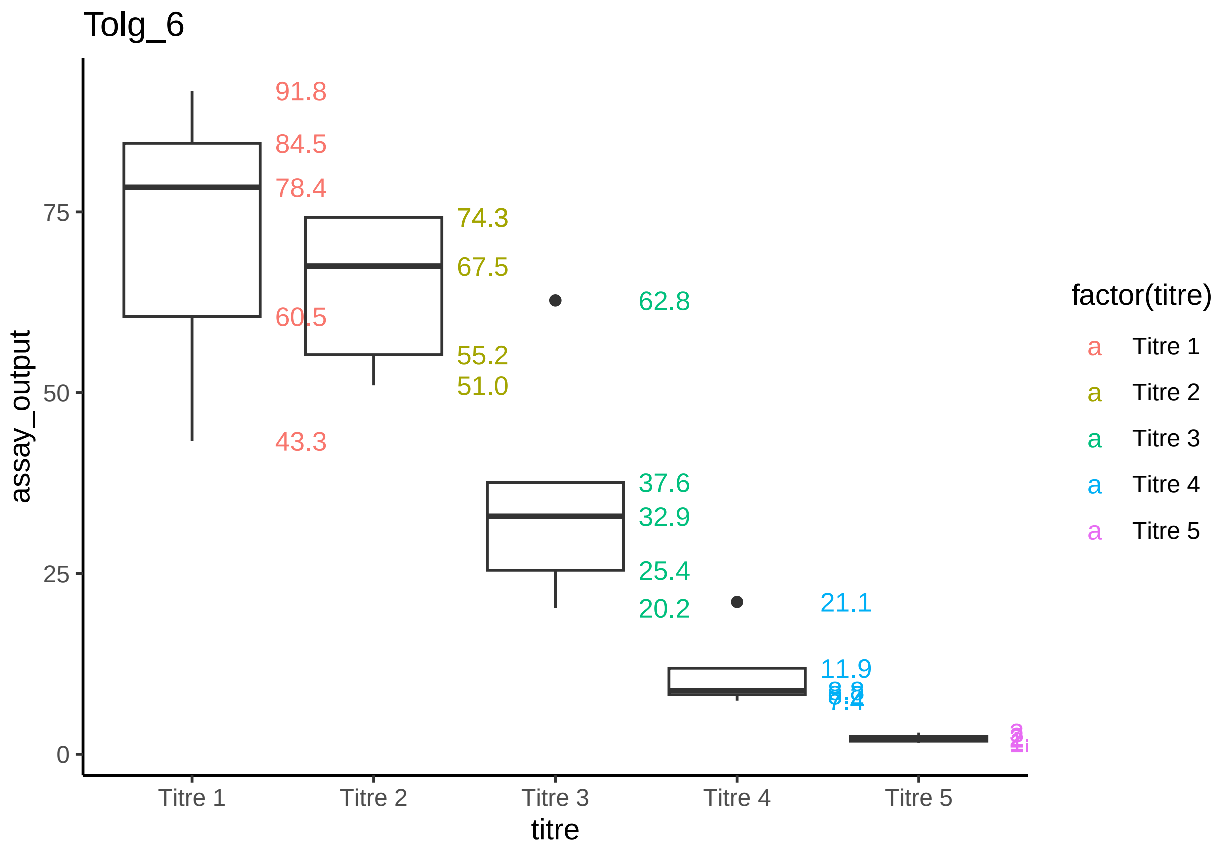


Tixi_4
68.4
64.6
61.7
58.5
54.1
53.4
51.7
46.2
42.6
39.4
30.3
26.9
21.4
17.9
11.7
9.2
7.6
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

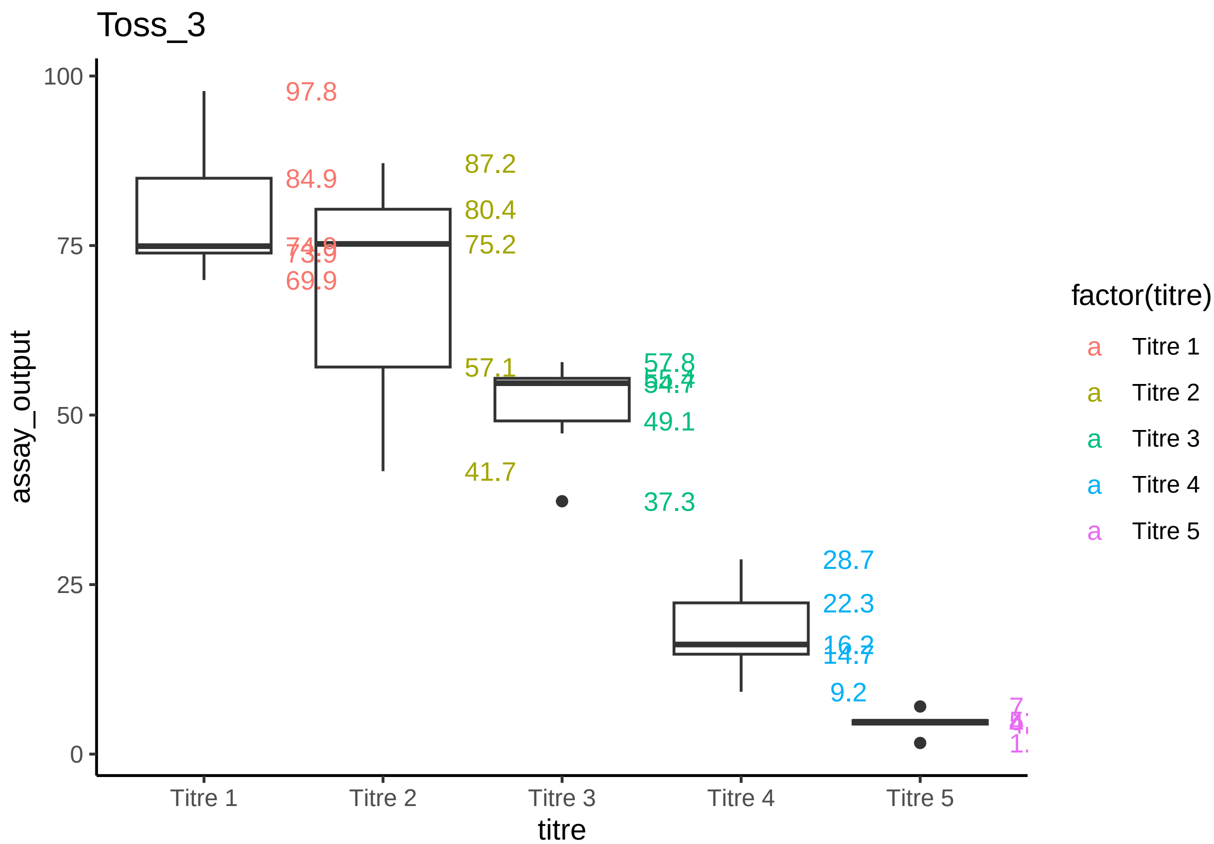

```
##
## [[119]]
```


Toco_5
80
60
40
20
0
assay_output
77.6
76.9
74.8
64.5
60.8
53.3
50.3
48.0
41.8
39.5
25.4
24.0
21.6
15.8
13.0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

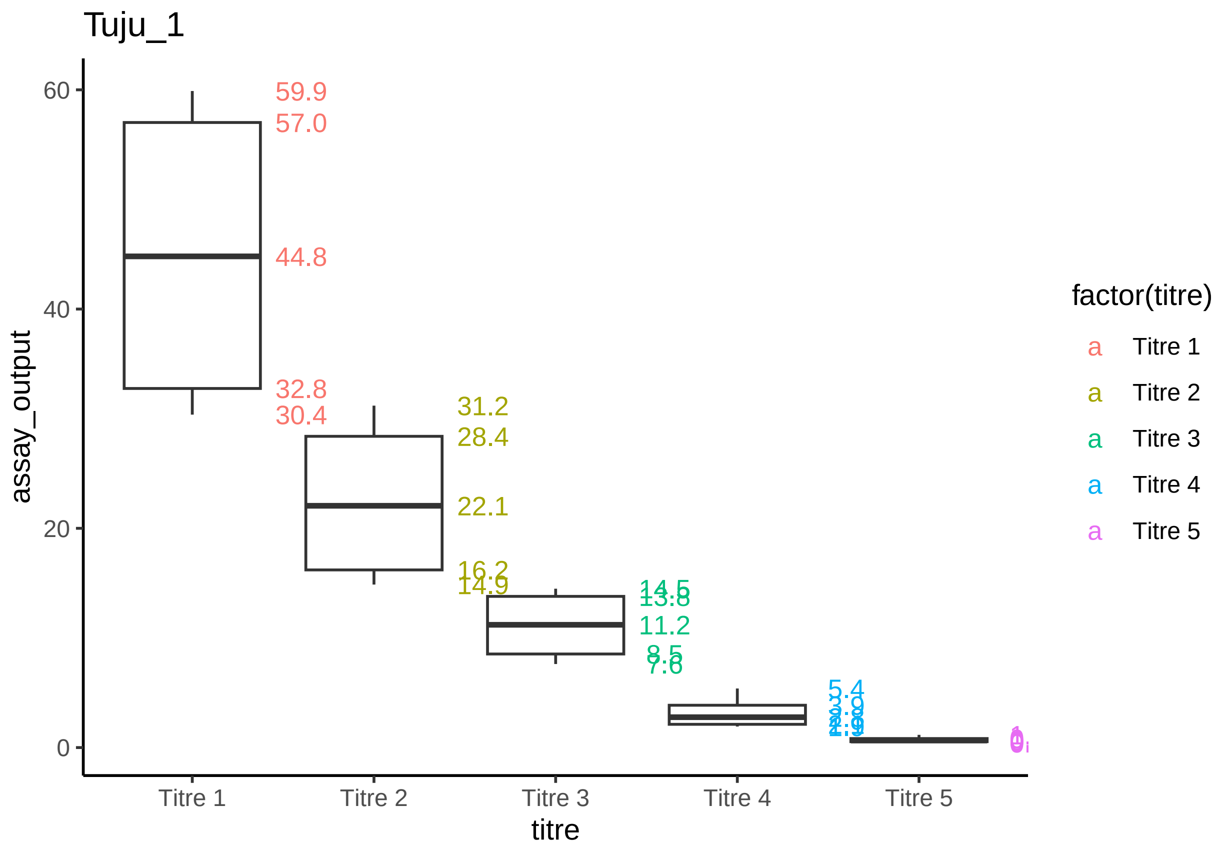
```
##
## [[120]]
```


Tolg_6
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
91.8
84.5
78.4
60.5
43.3
74.3
67.5
55.2
51.0
62.8
37.6
32.9
25.4
20.2
21.1
11.9
0
25
50
75

```
##
## [[121]]
```

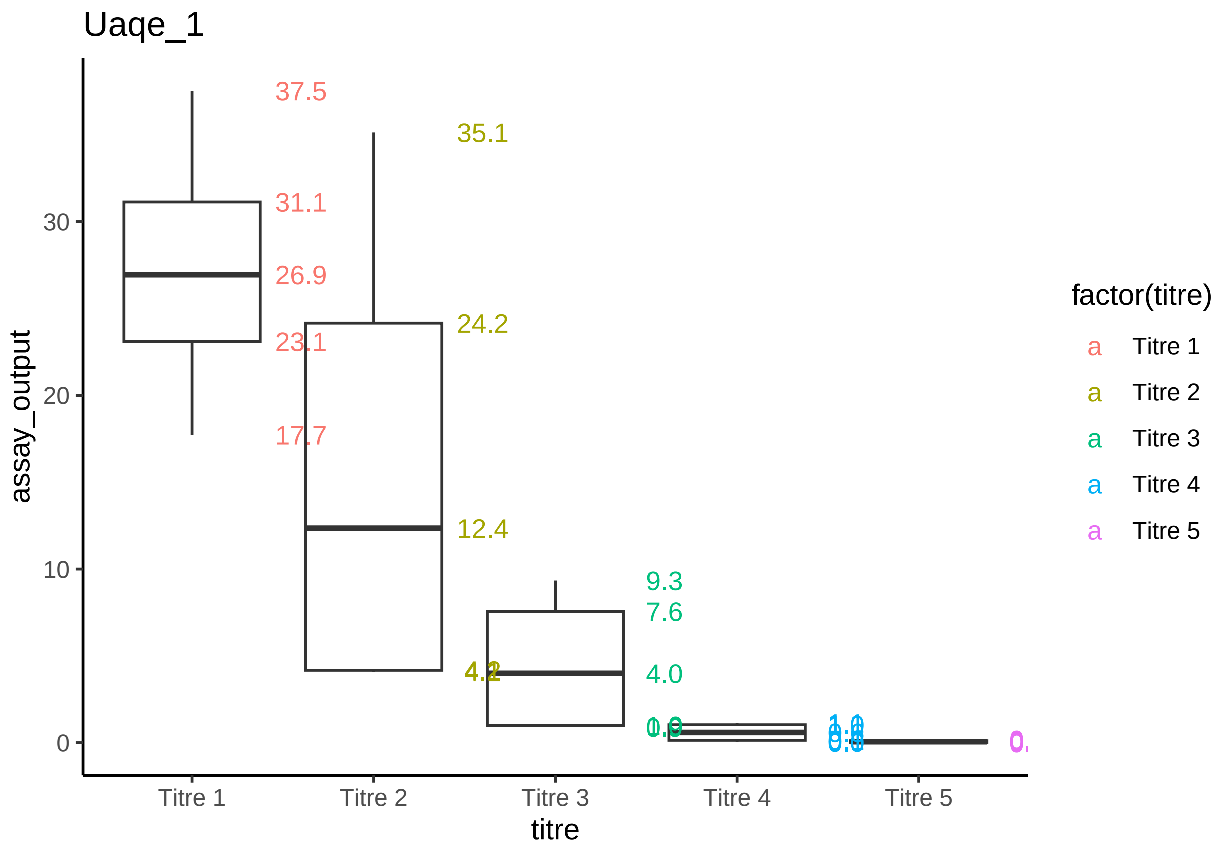

Toss_3
100
75
50
25
0
assay_output
97.8
84.9
74.9
73.9
69.9
87.2
80.4
75.2
57.1
41.7
57.8
54.7
54.7
49.1
37.3
28.7
22.3
16.2
14.7
9.2
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[122]]
```

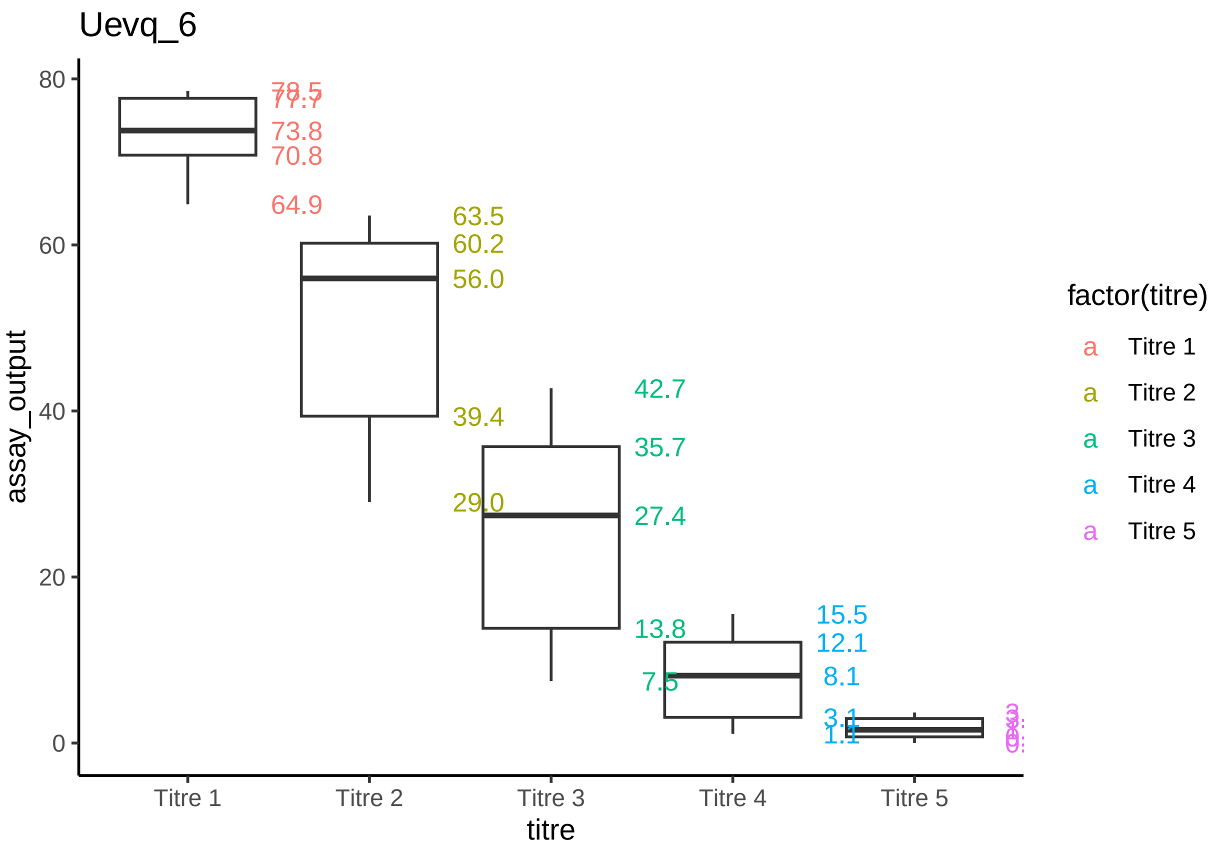


Tuju_1
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
59.9
57.0
44.8
32.8
30.4
31.2
28.4
22.1
16.2
14.9
14.5
13.8
11.2
8.5
7.6
5.4

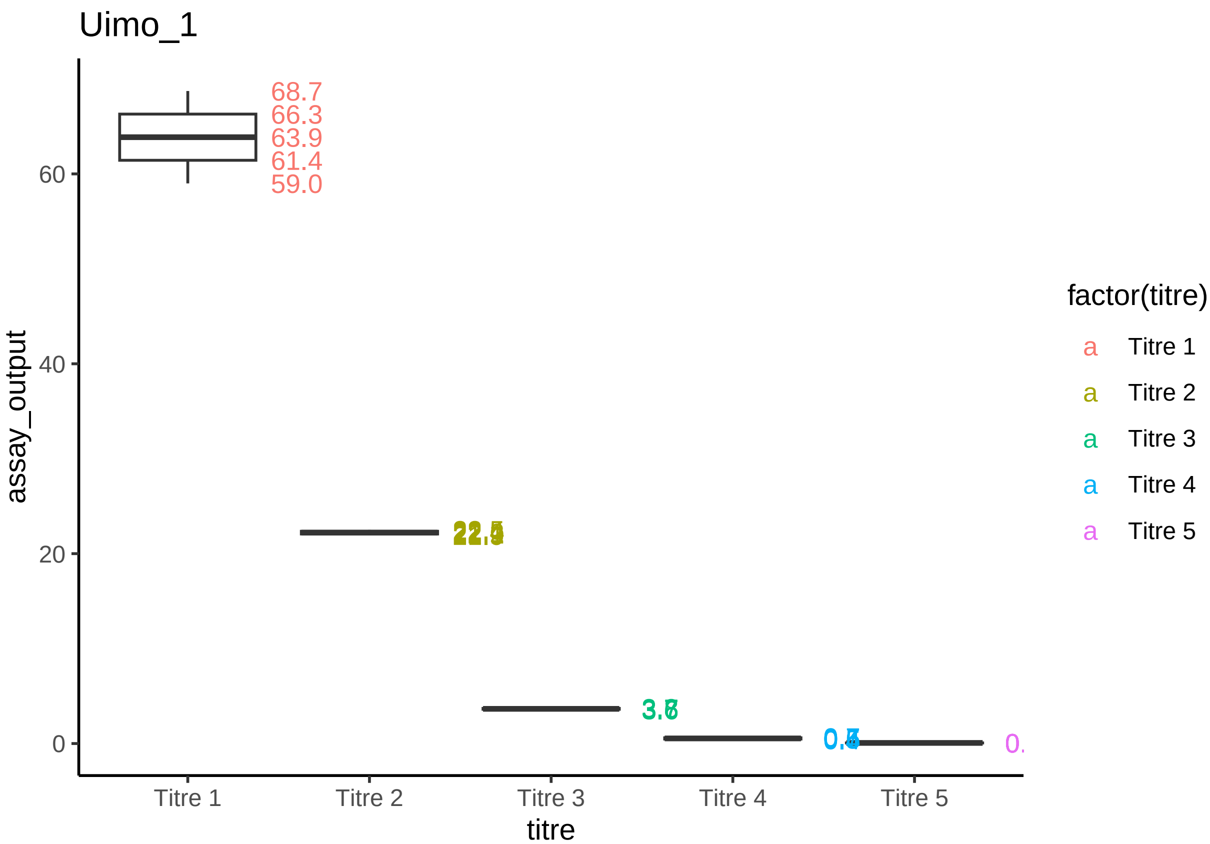

```
##
## [[123]]
```


Uaqe_1
37.5
35.1
31.1
26.9
24.2
23.1
17.7
12.4
9.3
7.6
4.0
30
20
10
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

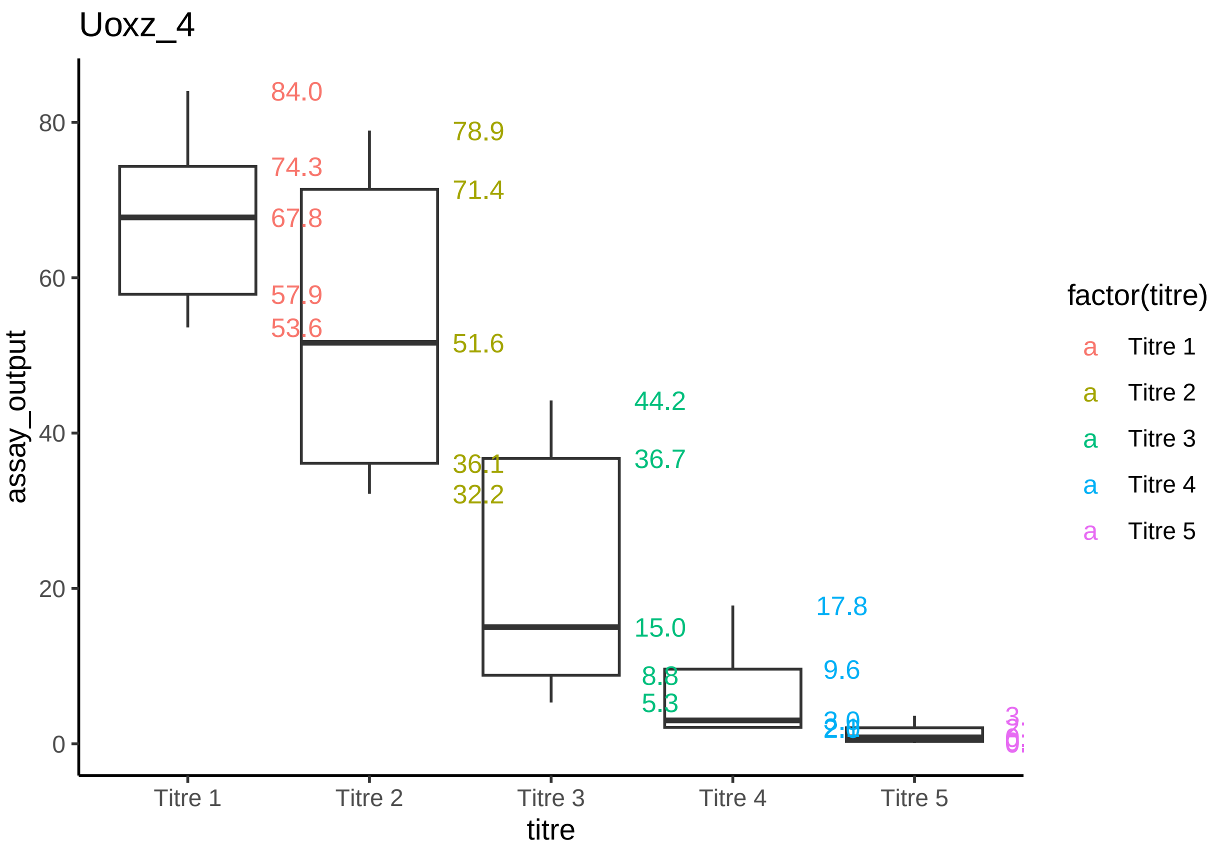
```
##
## [[124]]
```


Uevq_6
assay_output
80
60
40
20
0
78.5
77.7
73.8
70.8
64.9
63.5
60.2
56.0
39.4
29.0
42.7
35.7
27.4
13.8
7.5
15.5
12.1
8.1
3.1
1.1
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

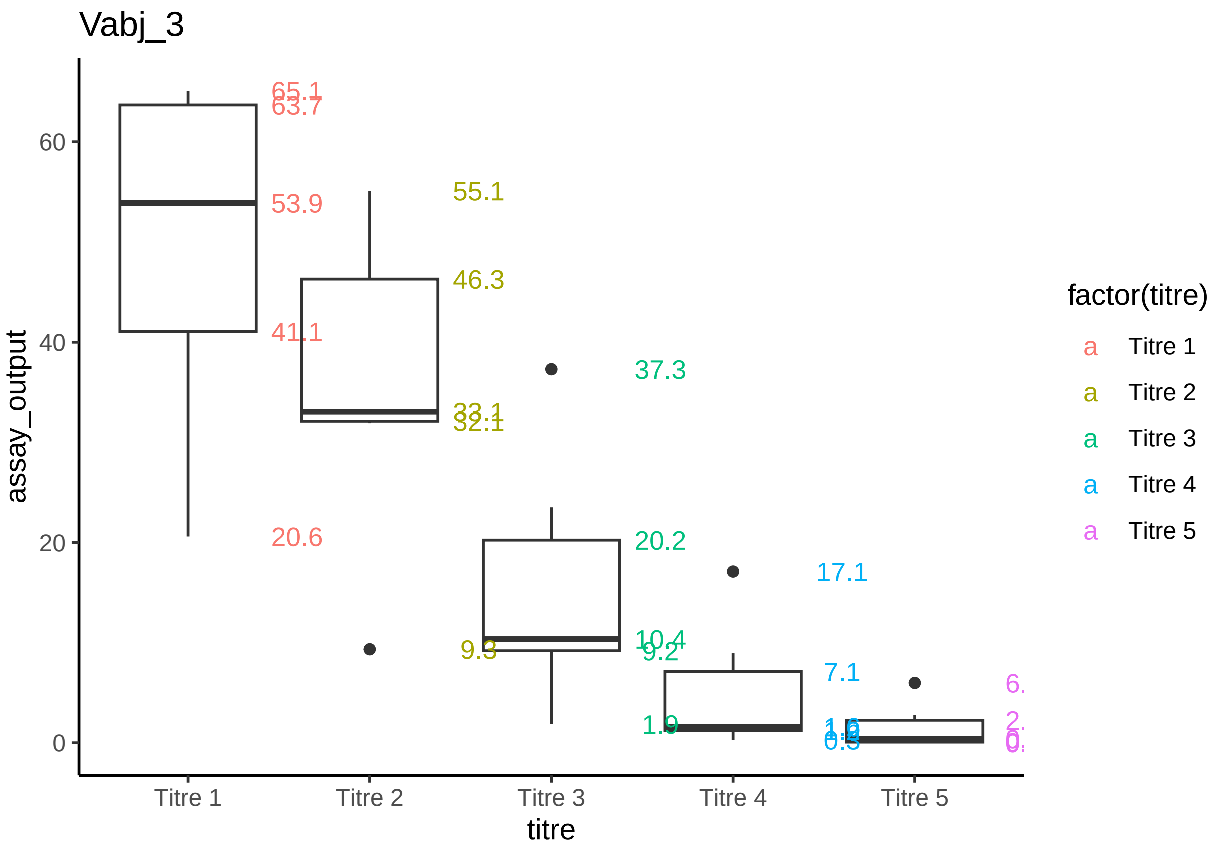
```
##
## [[125]]
```


Uimo_1
68.7
66.3
63.9
61.4
59.0
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5
assay_output
60
40
20
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre

```
##
## [[126]]
```

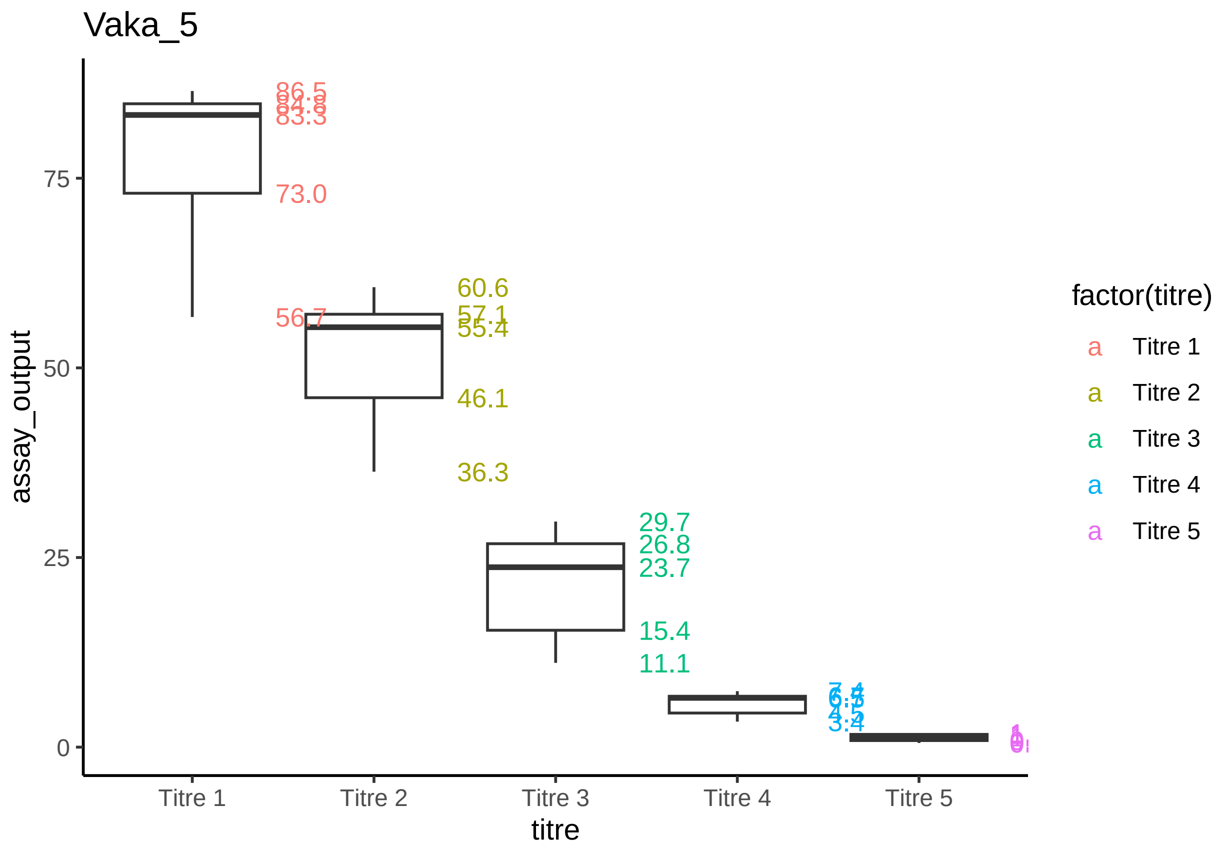

Uoxz_4
assay_output
80
60
40
20
0
84.0
74.3
67.8
57.9
53.6
78.9
71.4
51.6
36.1
32.2
44.2
36.7
15.0
8.8
5.3
17.8
9.6
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[127]]
```



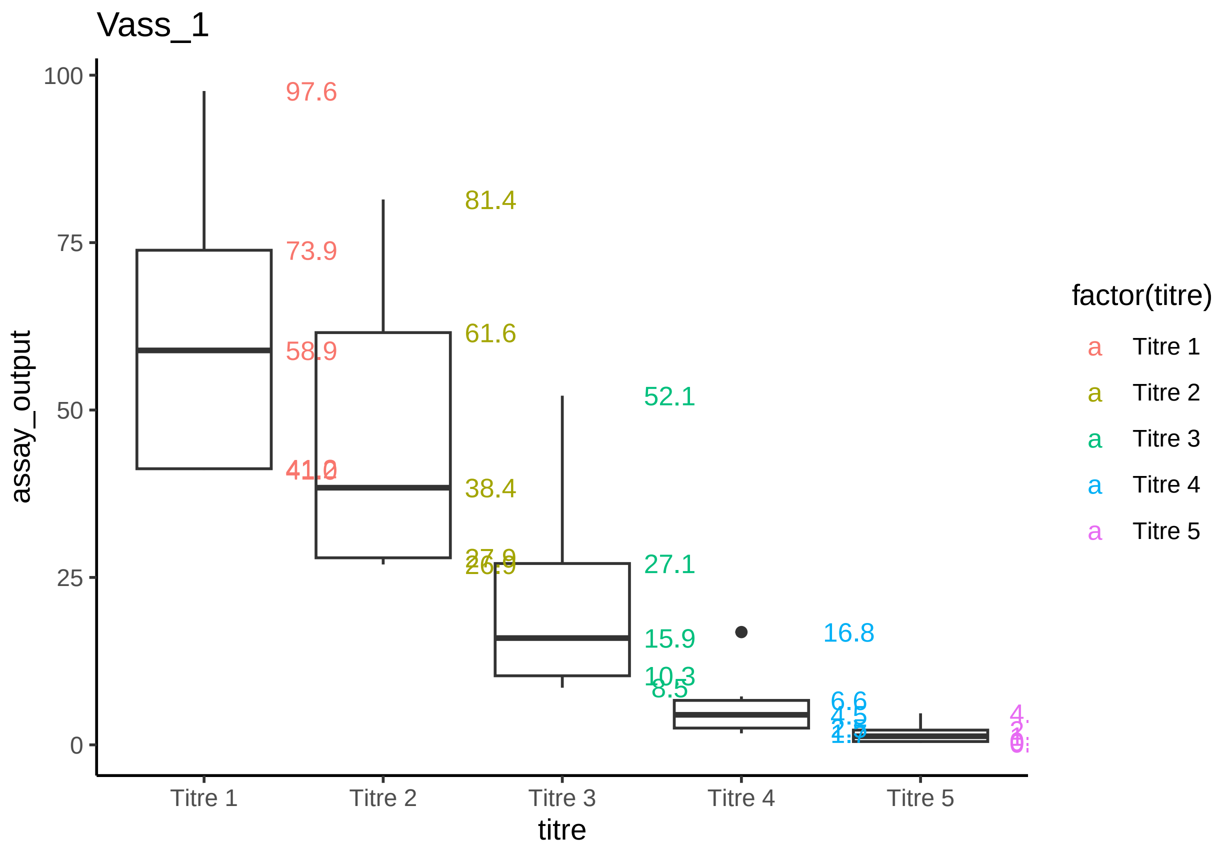
Vabj_3
assay_output
titre
60
40
20
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
65.1
63.7
53.9
41.1
20.6
55.1
46.3
33.1
32.1
9.3
37.3
20.2
10.4
9.2
1.9
17.1
7.1
0.5
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[128]]
```



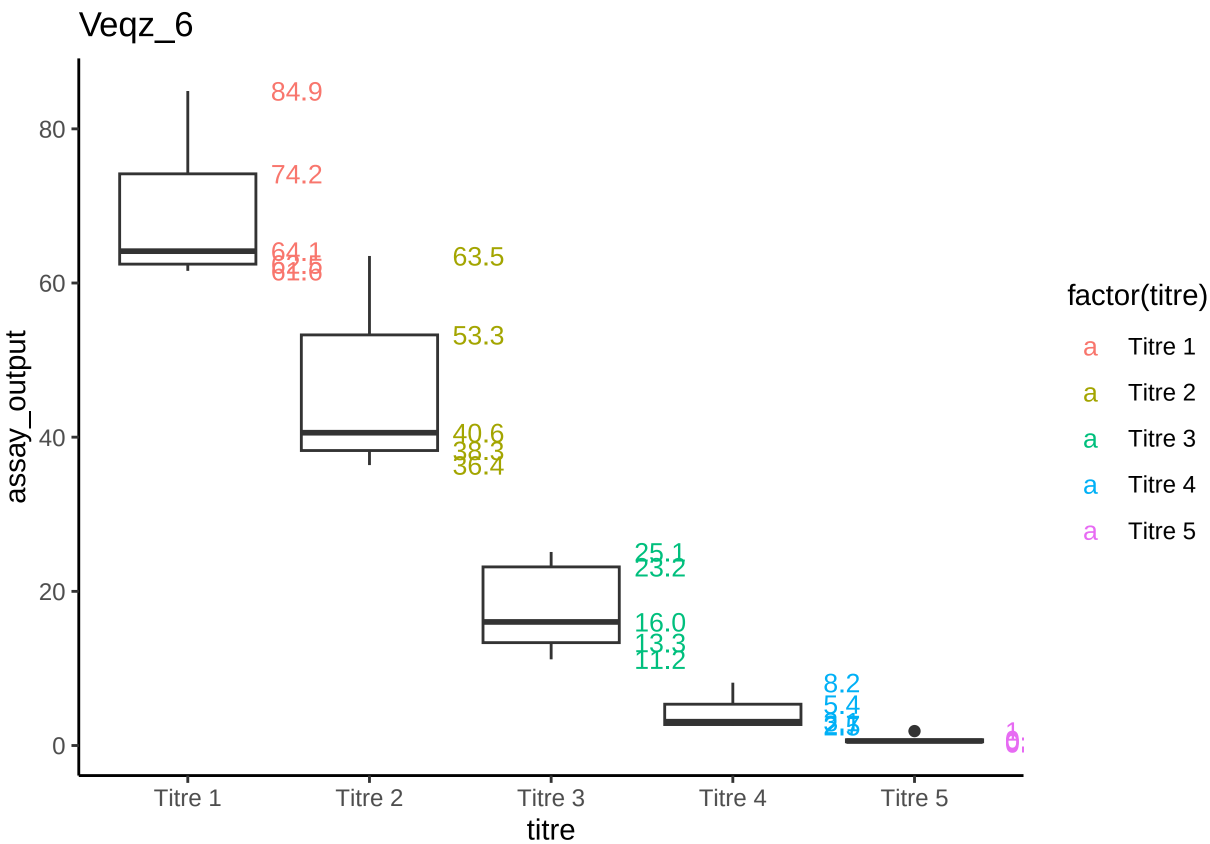
Vaka_5
86.5
84.8
83.3
73.0
56.7
60.6
57.1
55.4
46.1
36.3
29.7
26.8
23.7
15.4
11.1
3.4
75
50
25
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[129]]
```

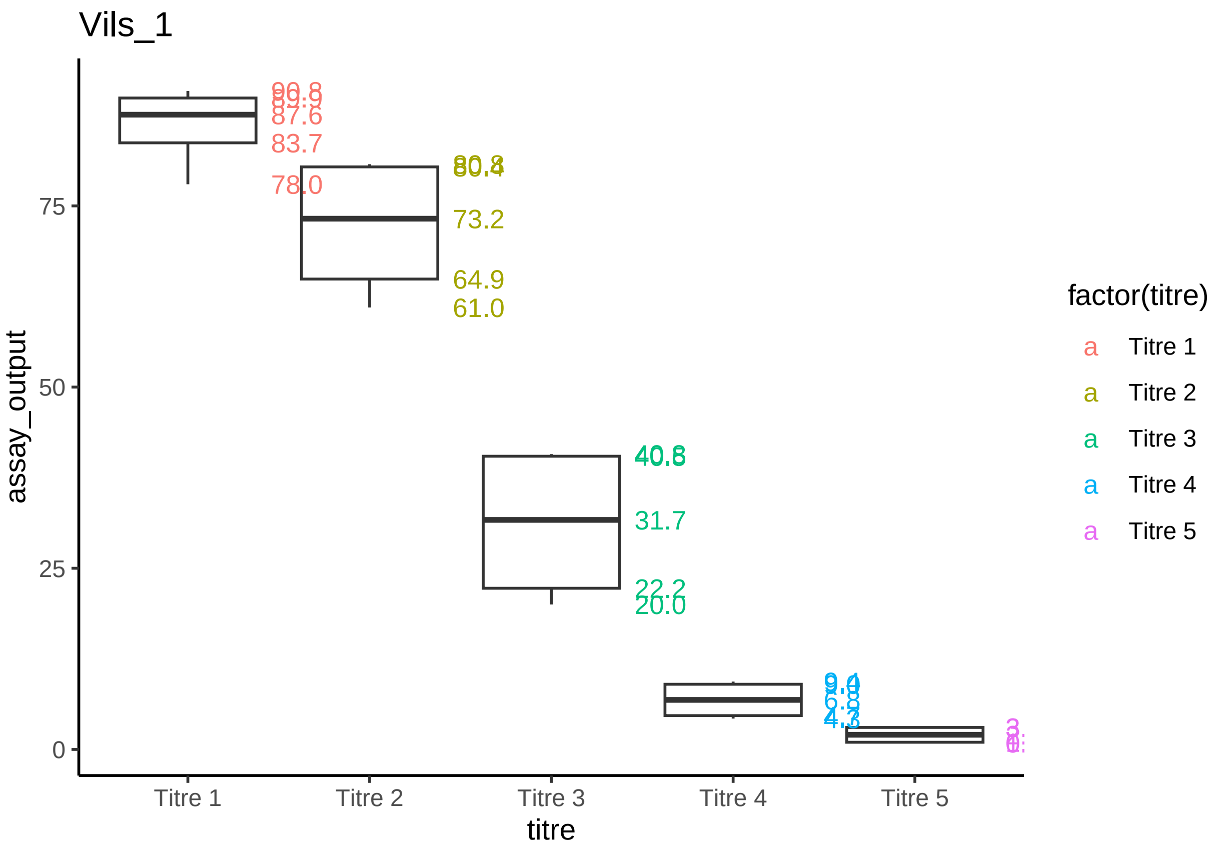


Vass_1
100
75
50
25
0
assay_output
97.6
73.9
58.9
41.0
81.4
61.6
38.4
27.9
26.5
52.1
27.1
15.9
10.3
8.5
16.8
6.6
4.5
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

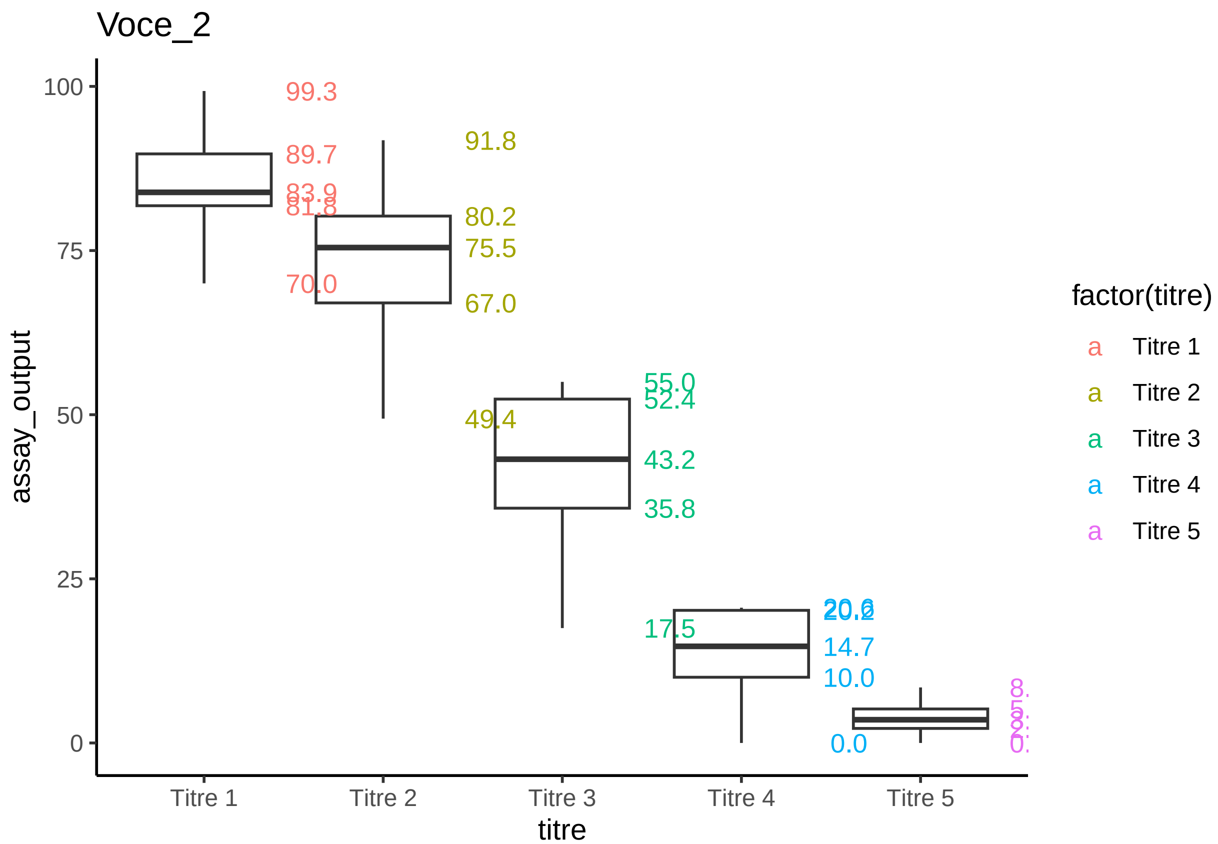

```
##
## [[130]]
```


Veqz_6
assay_output
80
60
40
20
0
84.9
74.2
64.1
63.5
53.3
40.6
36.4
25.1
23.2
16.0
13.3
11.2
8.2
5.4
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

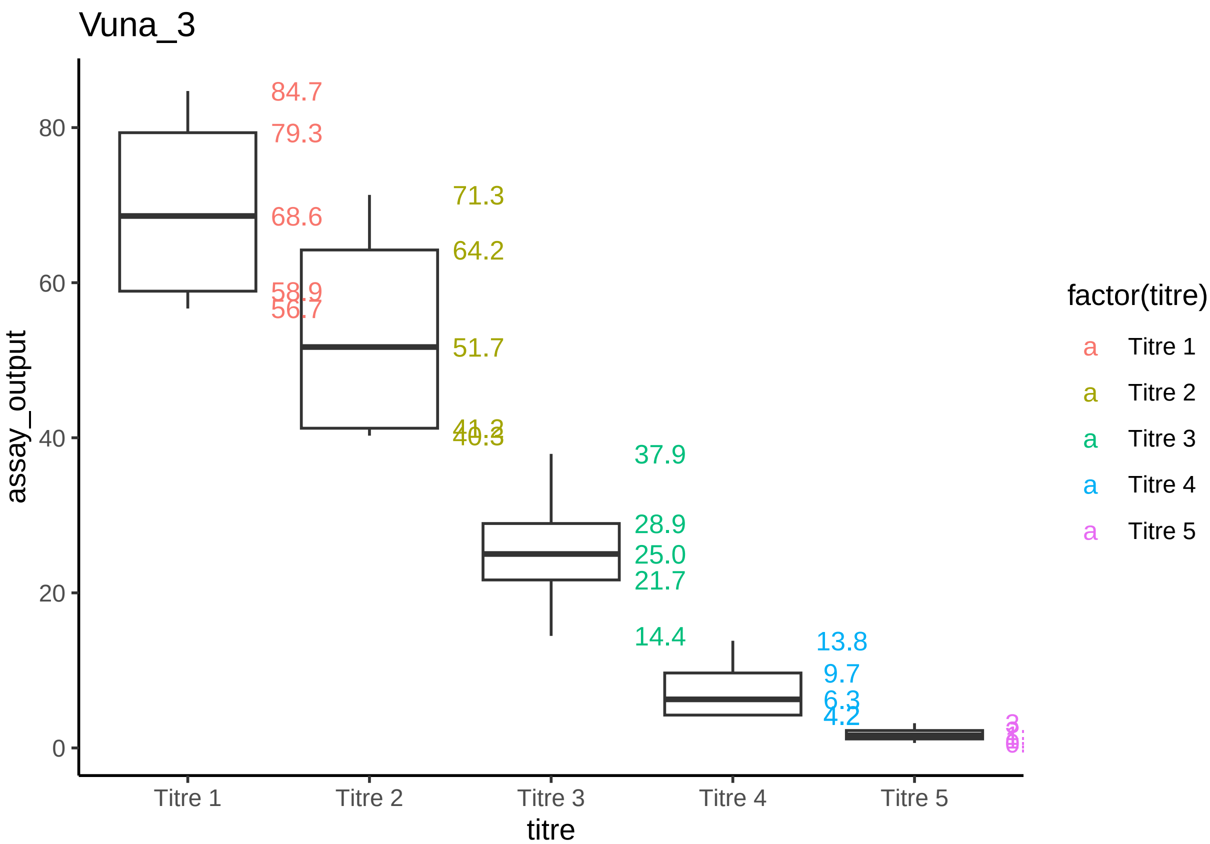
```
##
## [[131]]
```


Vils_1
assay_output
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
87.6
83.7
78.0
73.2
64.9
61.0
31.7
20.0
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[132]]
```

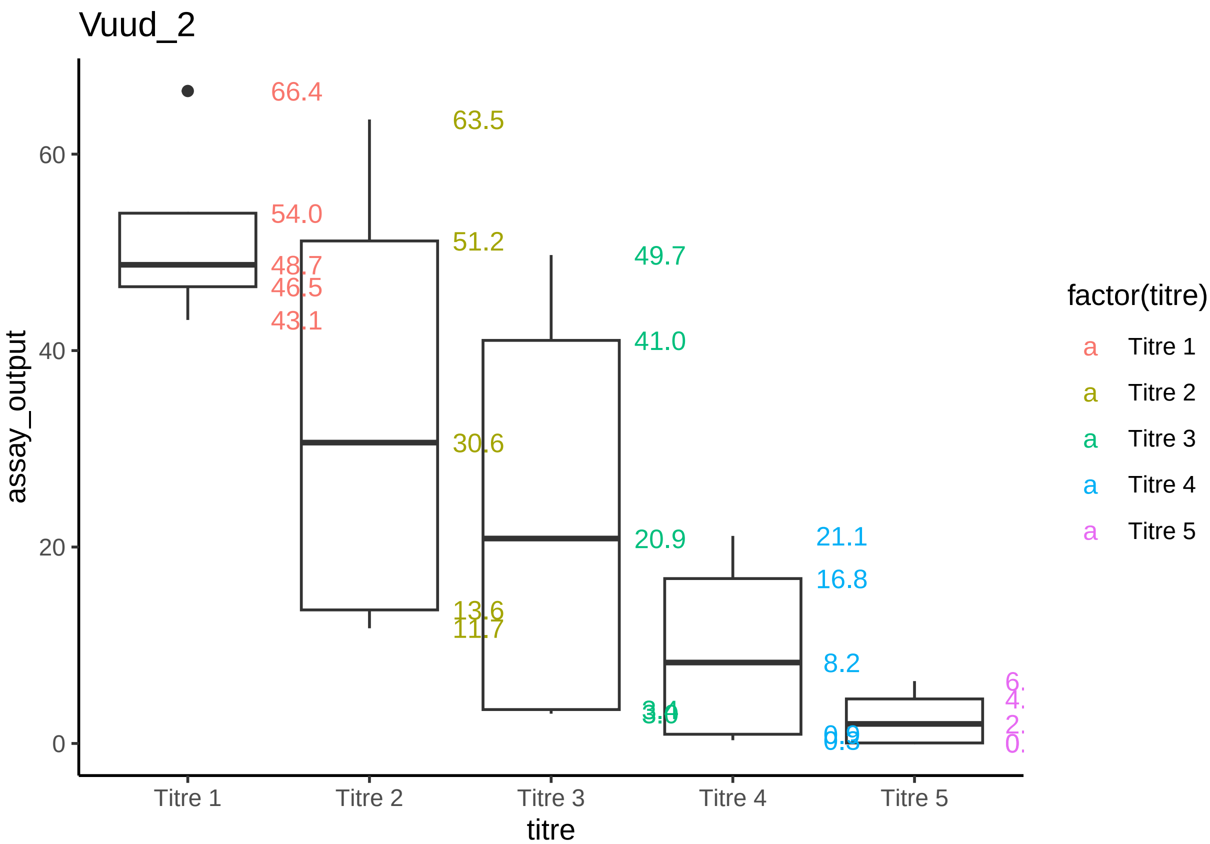

Voce_2
100
75
50
25
0
assay_output
99.3
89.7
83.9
81.8
70.0
91.8
80.2
75.5
67.0
49.4
55.0
52.4
43.2
35.8
17.5
20.6
20.2
14.7
10.0
0.0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[133]]
```

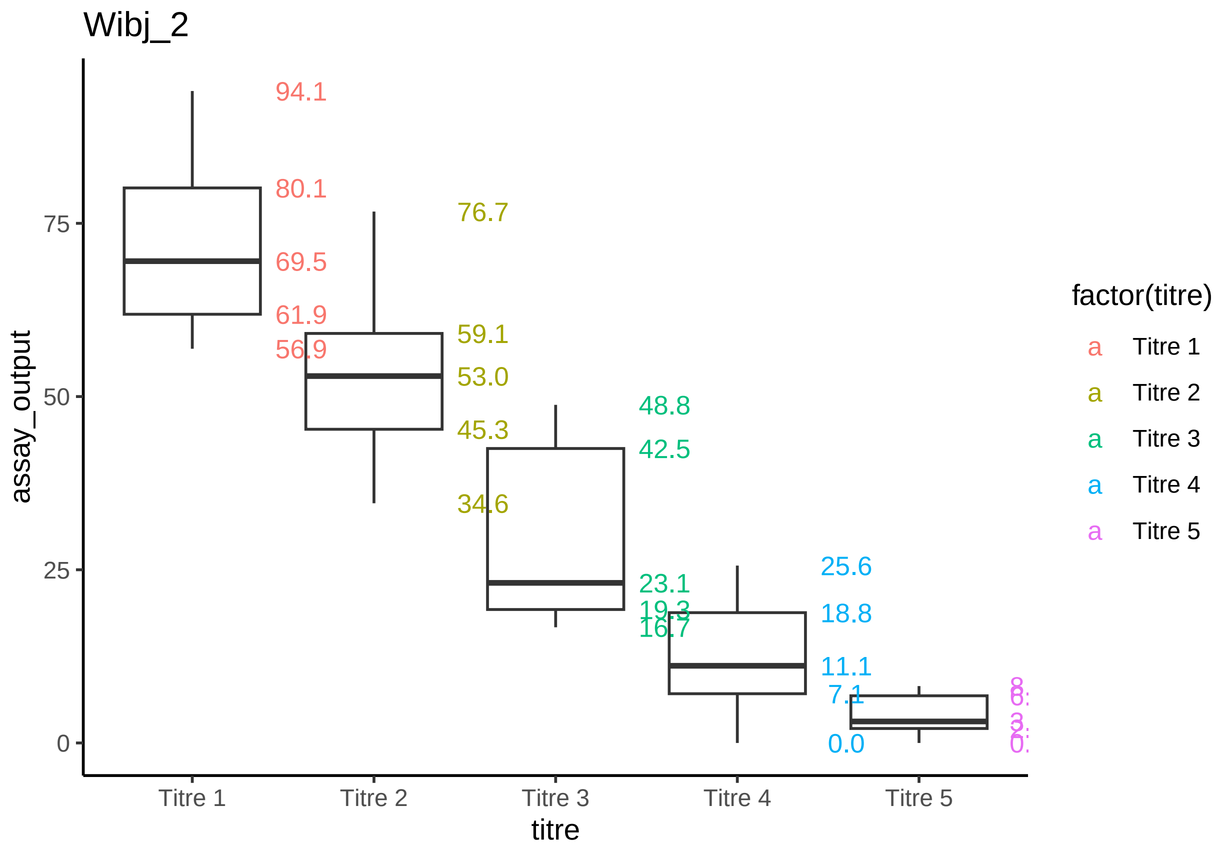


Vuna_3
84.7
79.3
68.6
58.9
56.7
71.3
64.2
51.7
41.3
40.3
37.9
28.9
25.0
21.7
14.4
13.8
9.7
6.3
4.2
80
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[134]]
```

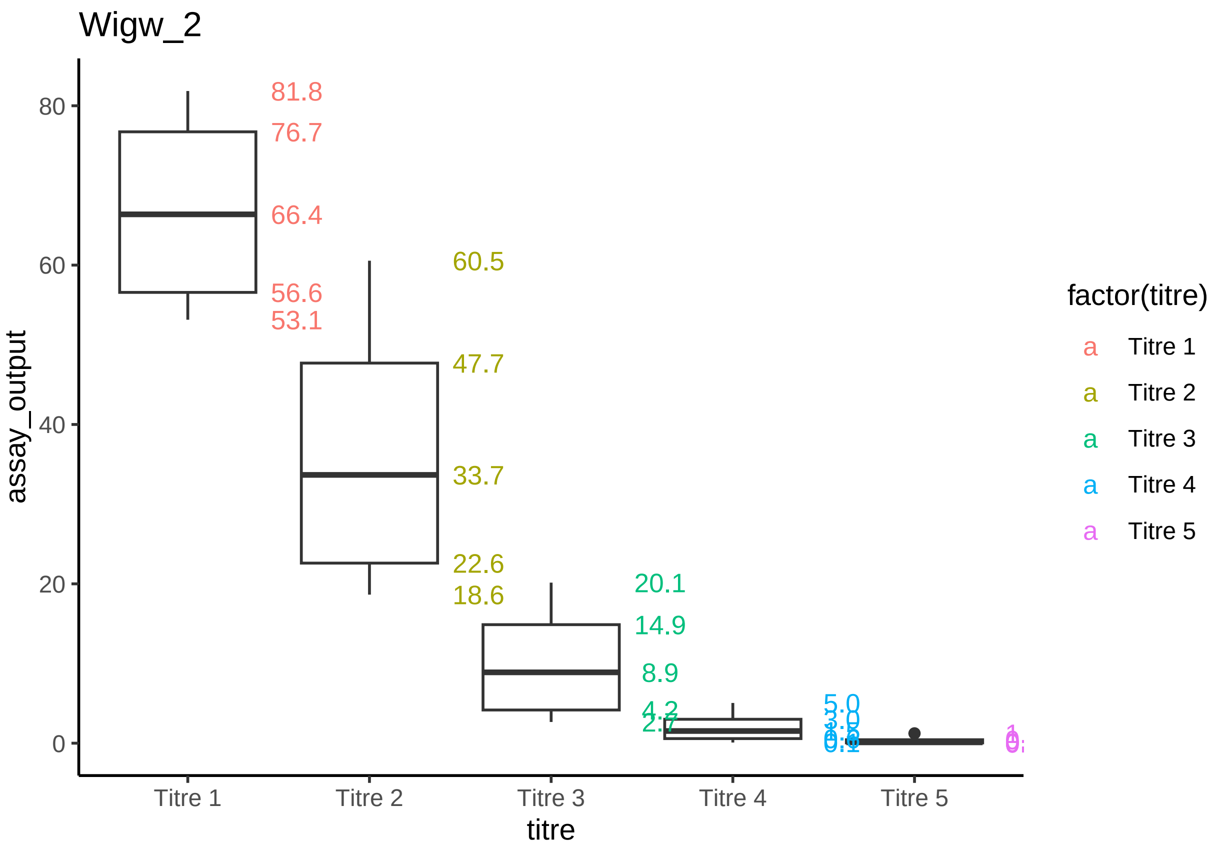

Vuud_2
66.4
63.5
54.0
51.2
48.7
46.5
43.1
49.7
41.0
30.6
20.9
21.1
16.8
13.6
11.7
8.2
3.4
3.0
0.9
0.3
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[135]]
```



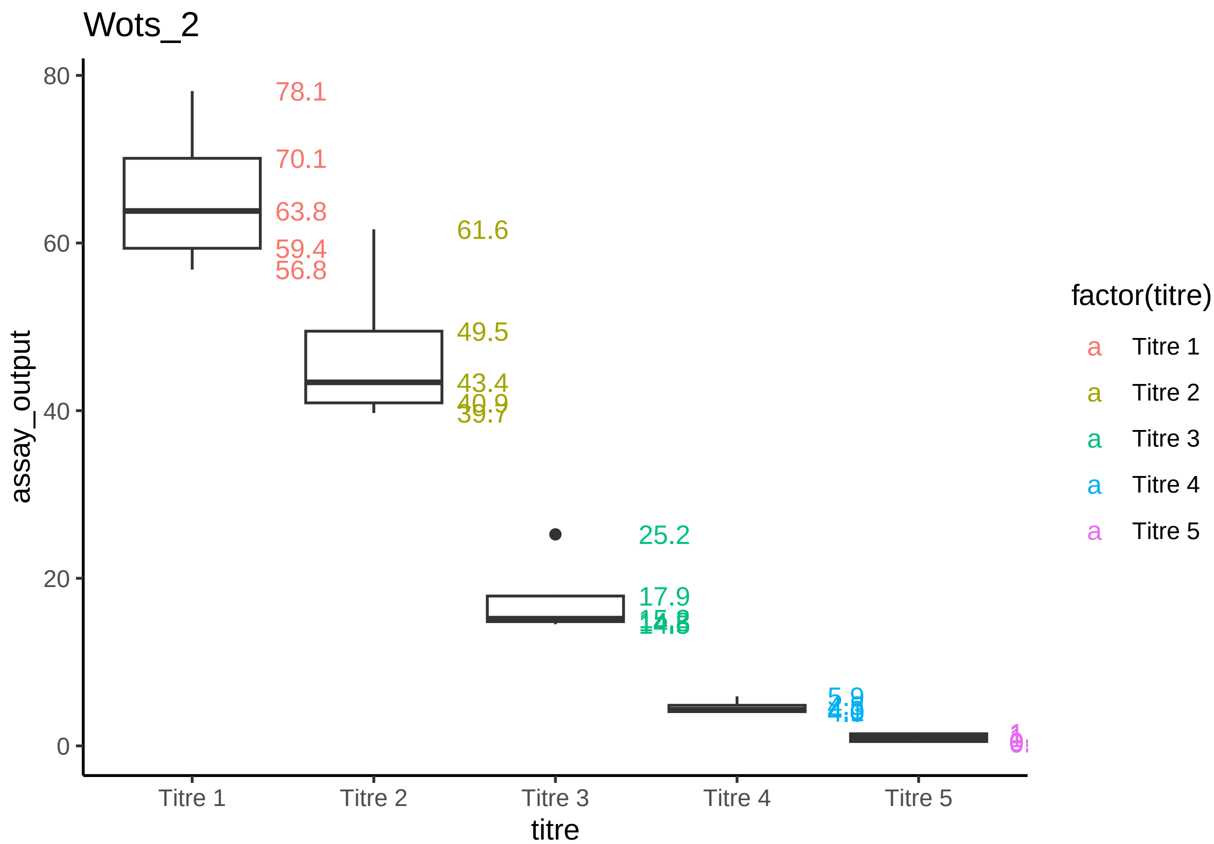
Wibj_2
94.1
80.1
69.5
61.9
56.9
76.7
59.1
53.0
45.3
34.6
48.8
42.5
23.1
19.3
16.7
25.6
18.8
11.1
7.1
0.0
assay_output
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[136]]
```

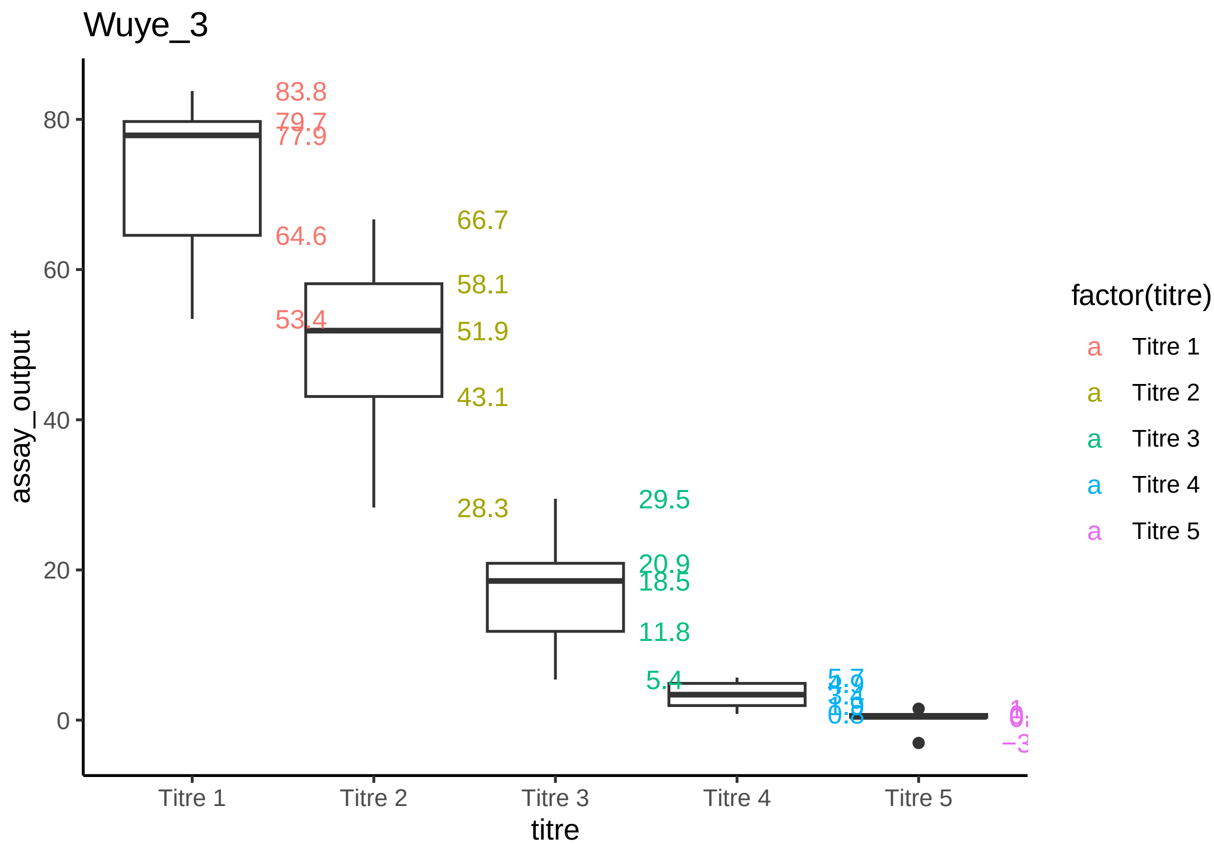


Wigw_2
81.8
76.7
66.4
56.6
53.1
60.5
47.7
33.7
22.6
18.6
20.1
14.9
8.9
5.0
80
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

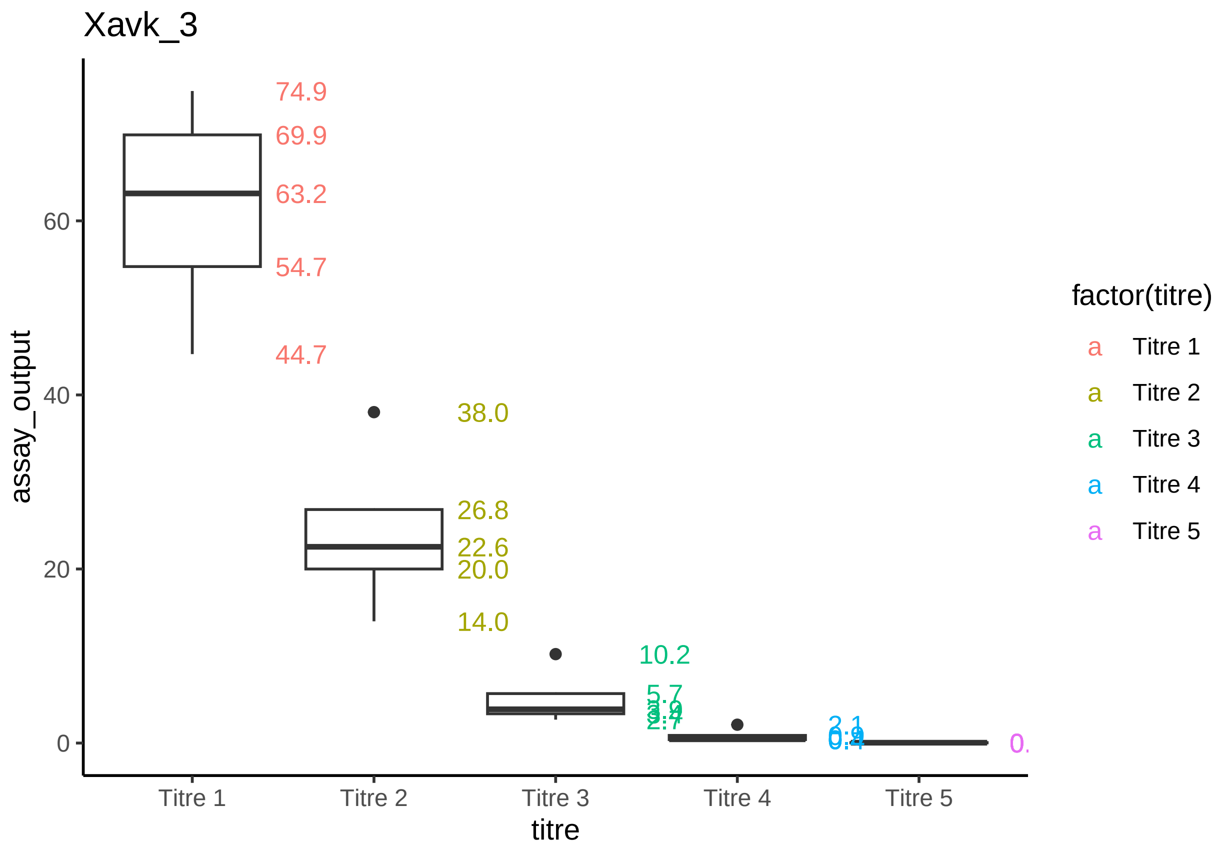

```
##
## [[137]]
```


Wots_2
80
60
40
20
0
assay_output
78.1
70.1
63.8
59.4
56.8
61.6
49.5
43.4
40.9
39.7
25.2
17.9
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[138]]
```

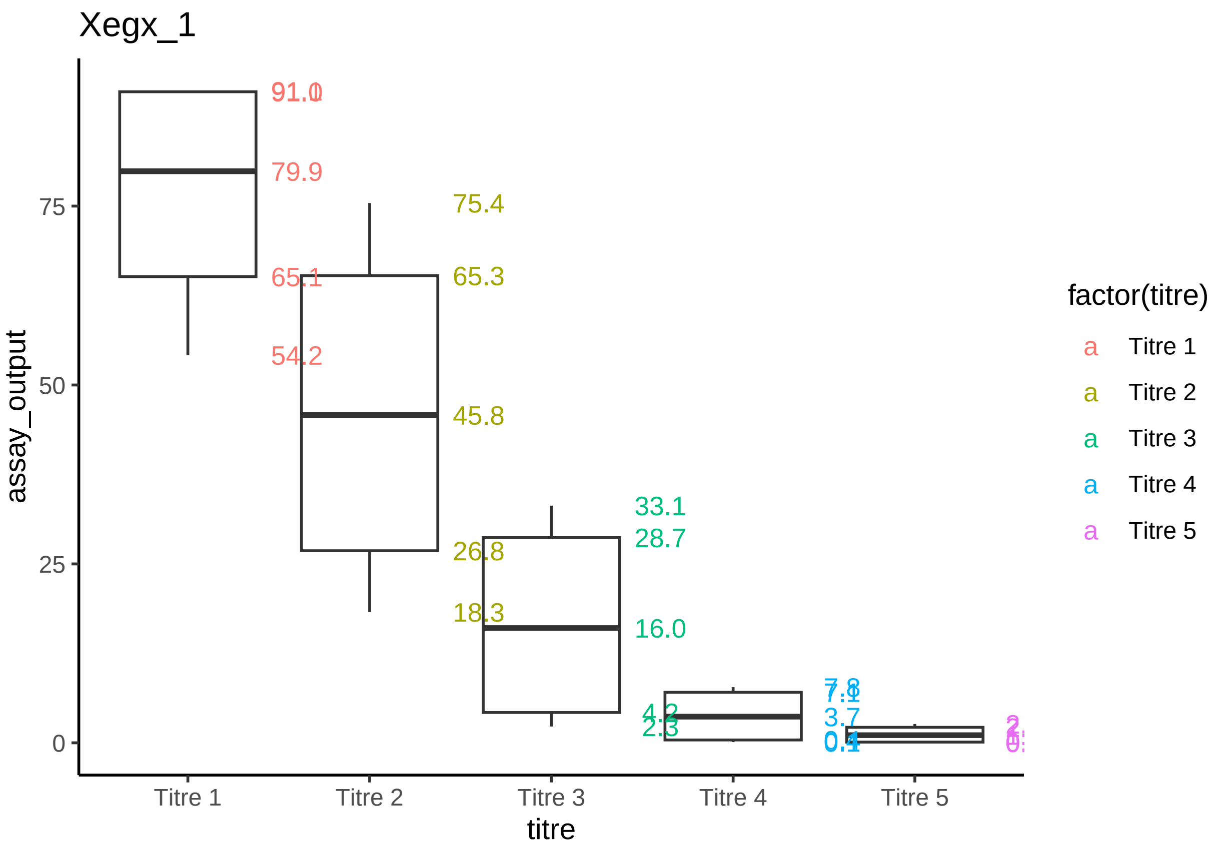

Wuye_3
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
83.8
79.7
77.9
64.6
53.4
66.7
58.1
51.9
43.1
28.3
29.5
20.9
18.5
11.8
5.4

```
##
## [[139]]
```

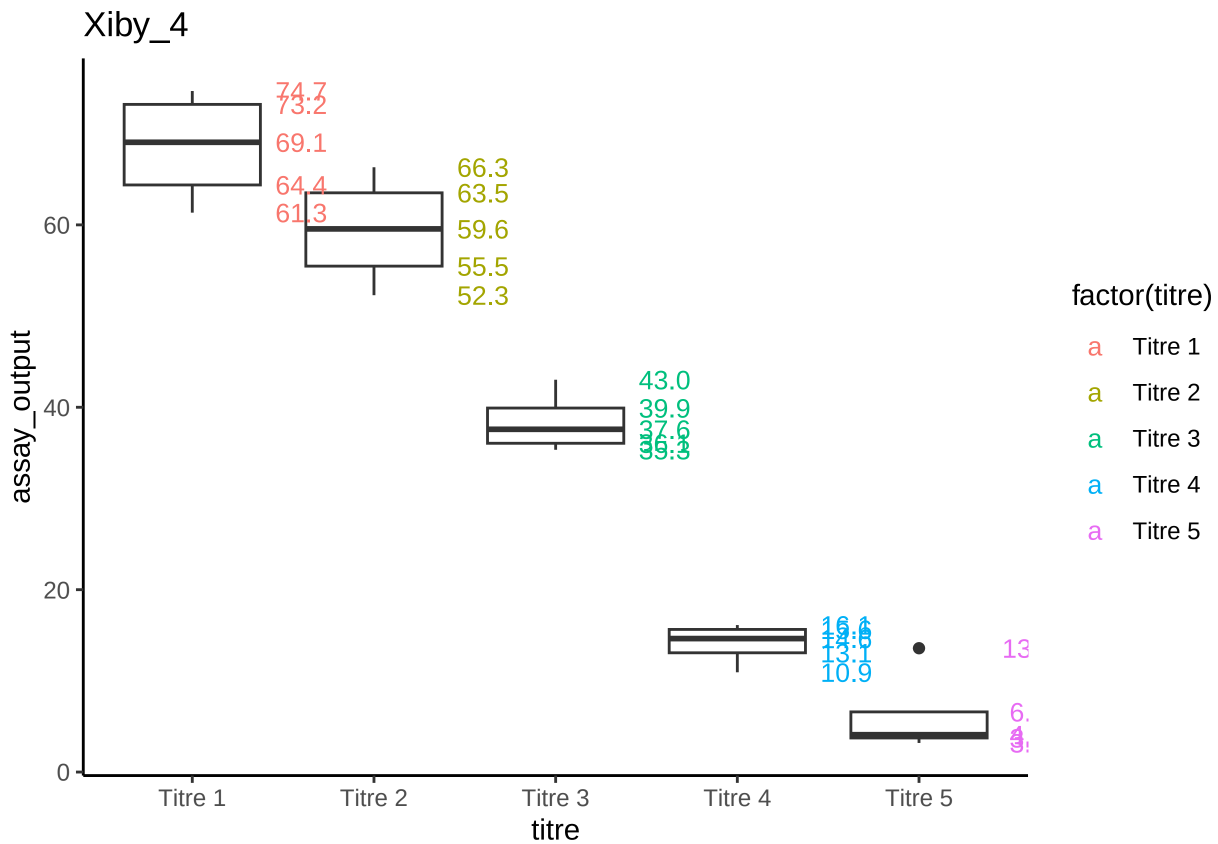


Xavk_3
74.9
69.9
63.2
54.7
44.7
38.0
26.8
22.6
20.0
14.0
10.2
5.7
2.7
2.1
0.
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[140]]
```

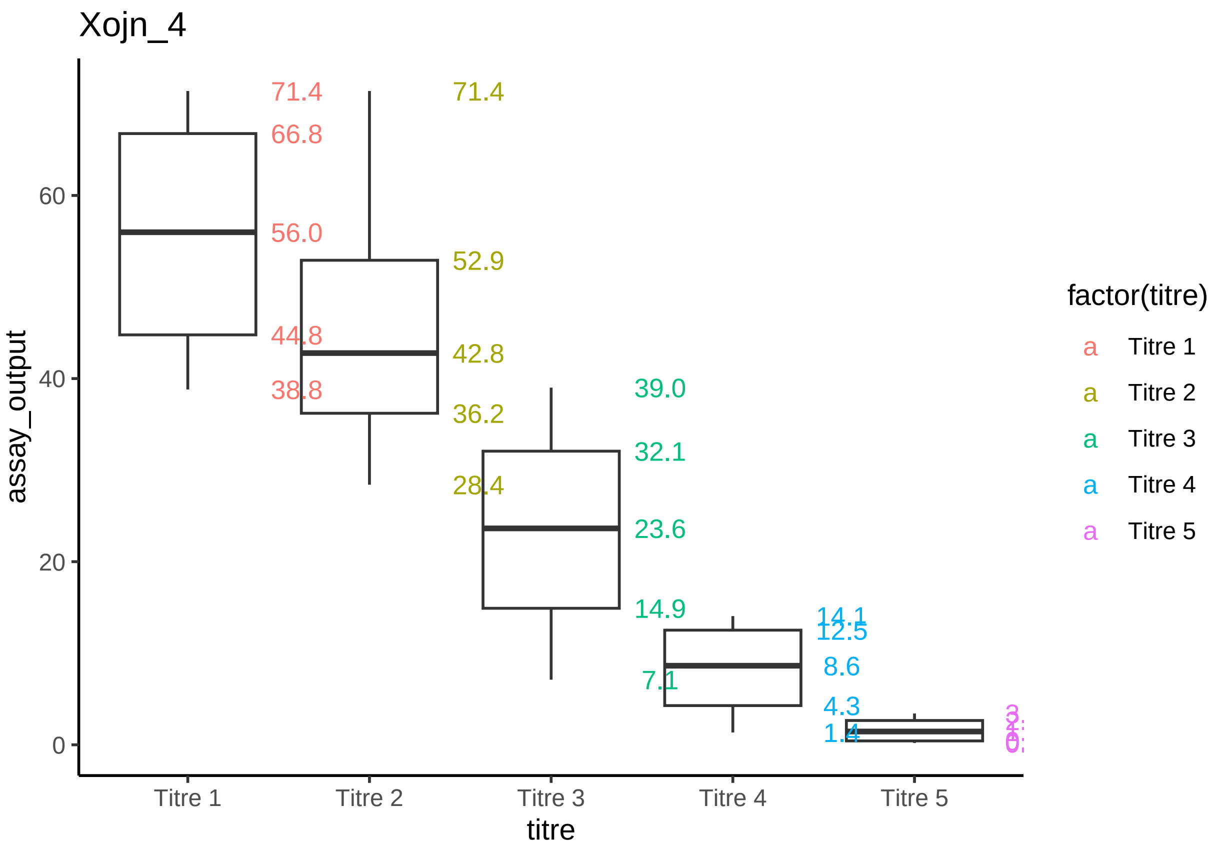

Xegx_1
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
91.0
79.9
65.1
54.2
75.4
65.3
45.8
26.8
18.3
33.1
28.7
16.0
4.2
2.3
7.8
7.1
3.7
0.4
0
25
50
75

```
##
## [[141]]
```

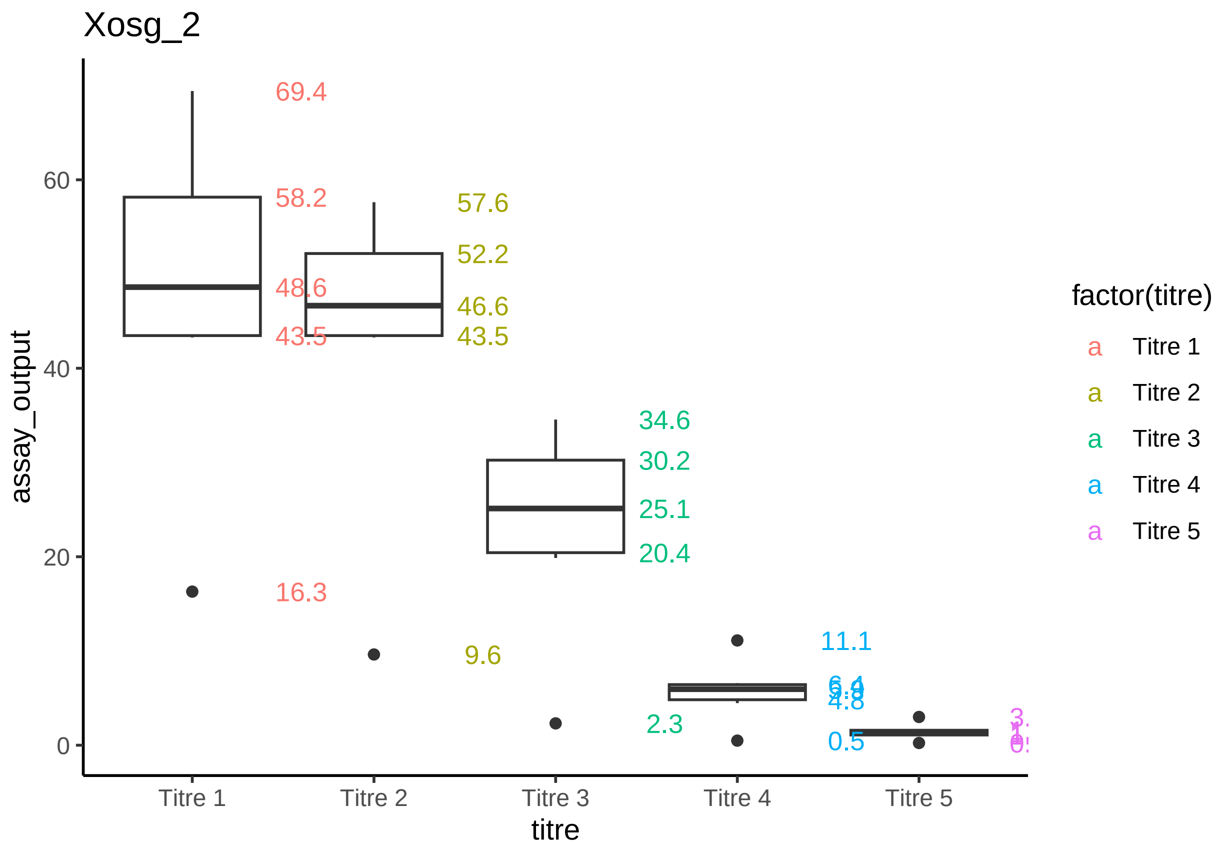


Xiby_4
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
0
20
40
60
74.7
73.2
69.1
64.4
61.3
66.3
63.5
59.6
55.5
52.3
43.0
39.9
37.6
10.9
factor(titre)

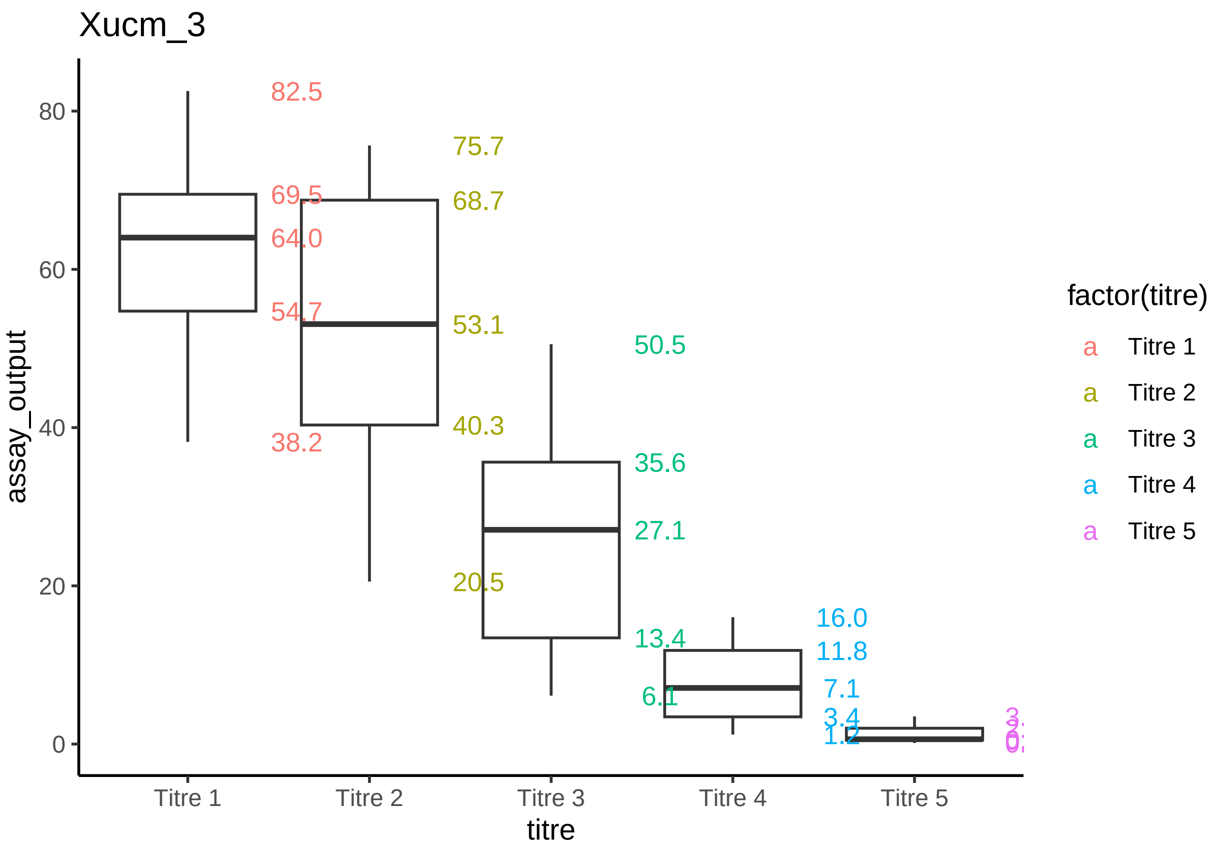

```
##
## [[142]]
```


Xojn_4
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
71.4
66.8
56.0
44.8
38.8
71.4
52.9
42.8
36.2
28.4
39.0
32.1
23.6
14.9
7.1
14.1
12.5
8.6
4.3
1.4

```
##
## [[143]]
```

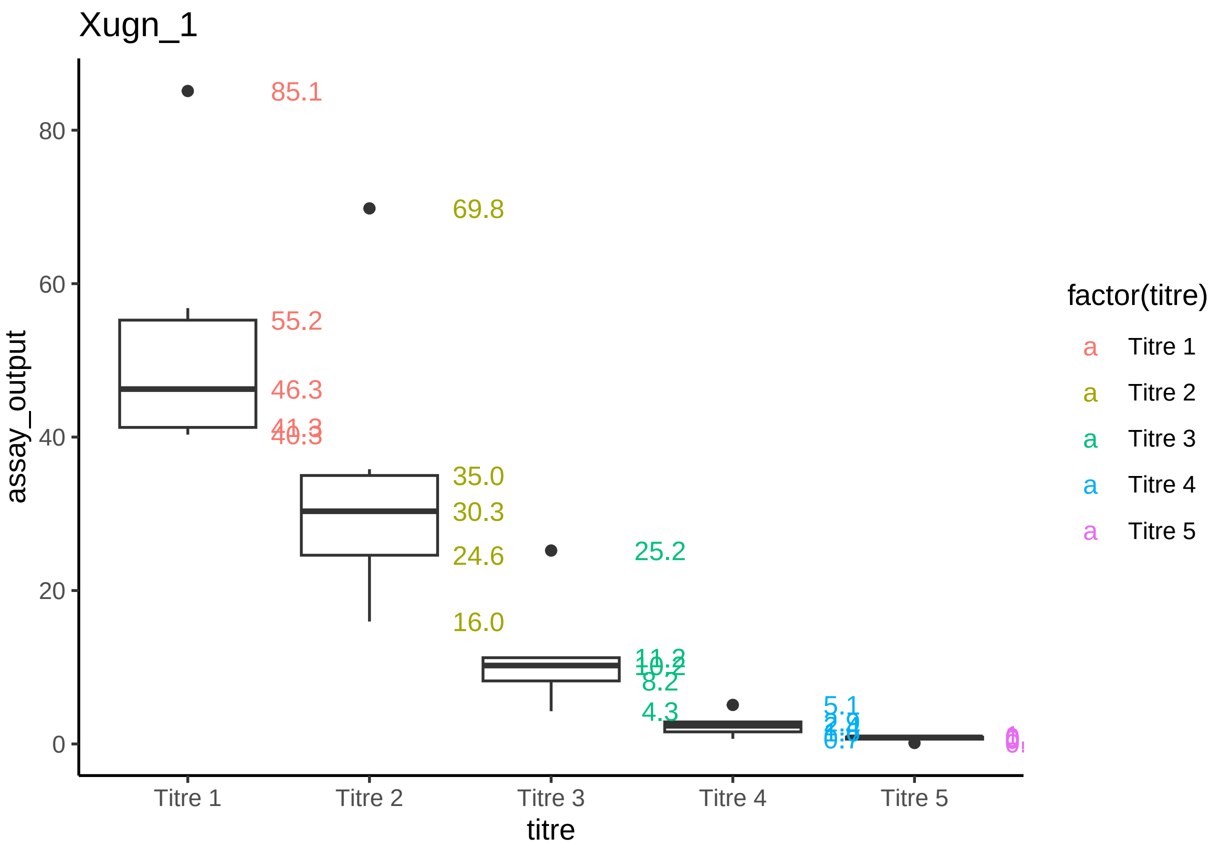

Xosg_2
69.4
58.2
57.6
52.2
48.6
46.6
43.5
43.5
34.6
30.2
25.1
20.4
16.3
9.6
11.1
2.3
0.5
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[144]]
```

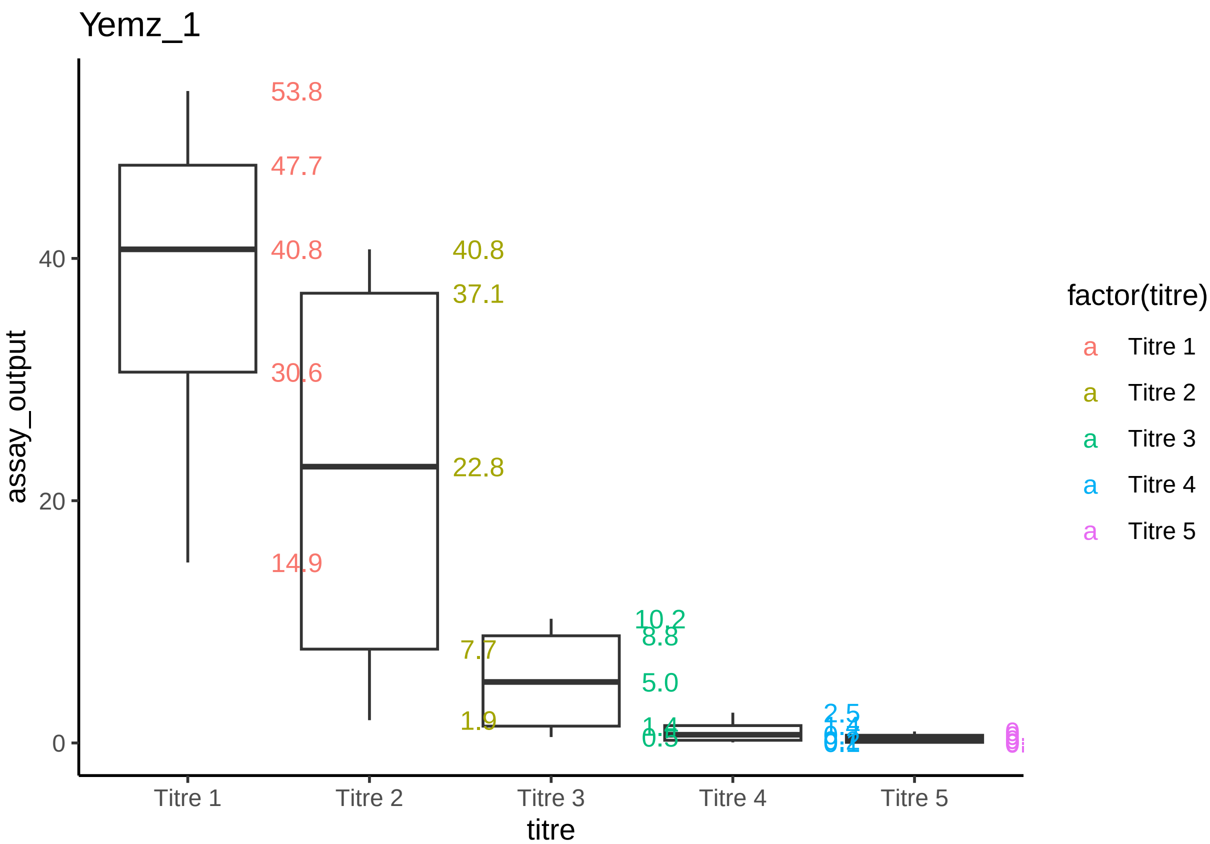


Xucm_3
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
82.5
69.5
64.0
54.7
38.2
75.7
68.7
53.1
40.3
20.5
50.5
35.6
27.1
13.4
6.1
16.0
11.8
7.1
3.4
1.2


```
##
## [[145]]
```

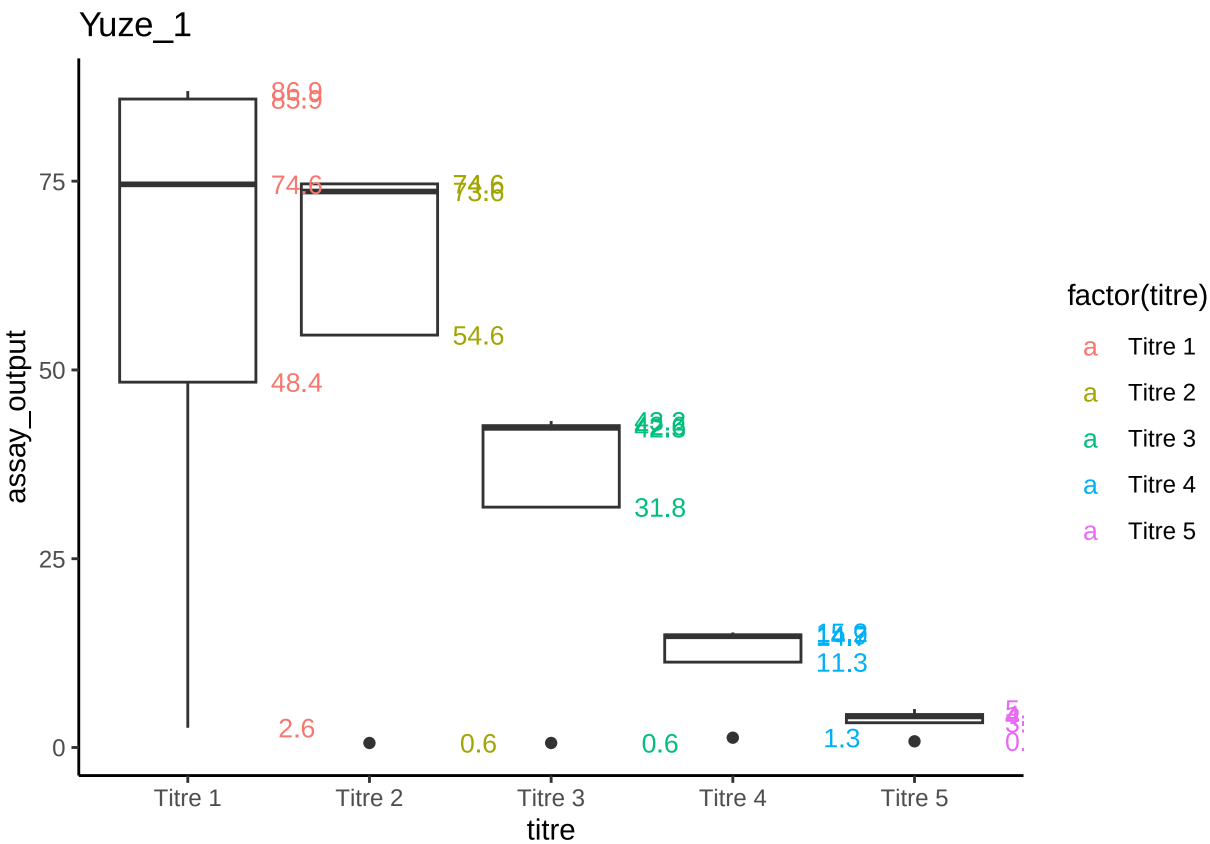

Xugn_1
85.1
69.8
55.2
46.3
41.3
40.3
35.0
30.3
24.6
25.2
16.0
11.3
10.2
8.2
4.3
5.1
0.7
80
60
40
20
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[146]]
```

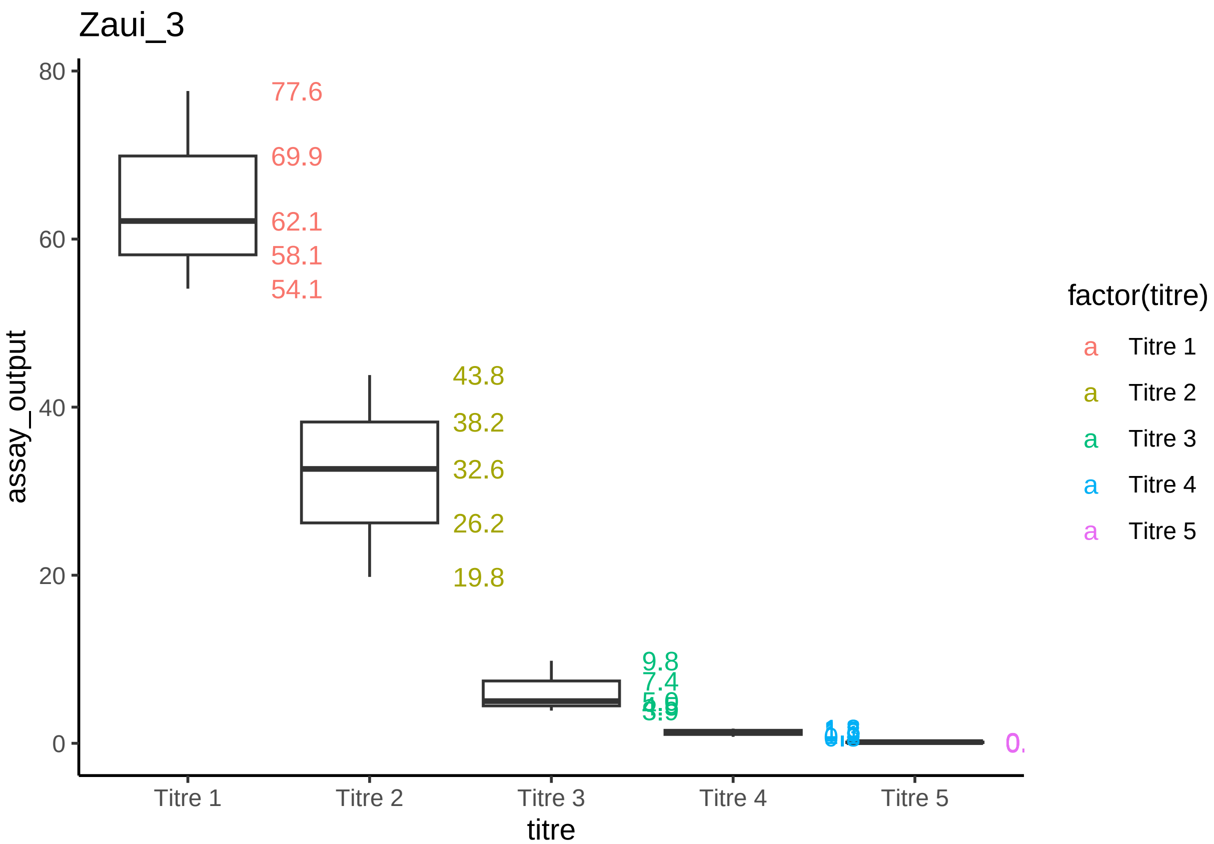


Yemz_1
assay_output
titre
factor(titre)
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
53.8
47.7
40.8
30.6
14.9
40.8
37.1
22.8
7.7
1.9
10.2
8.8
5.0
2.5

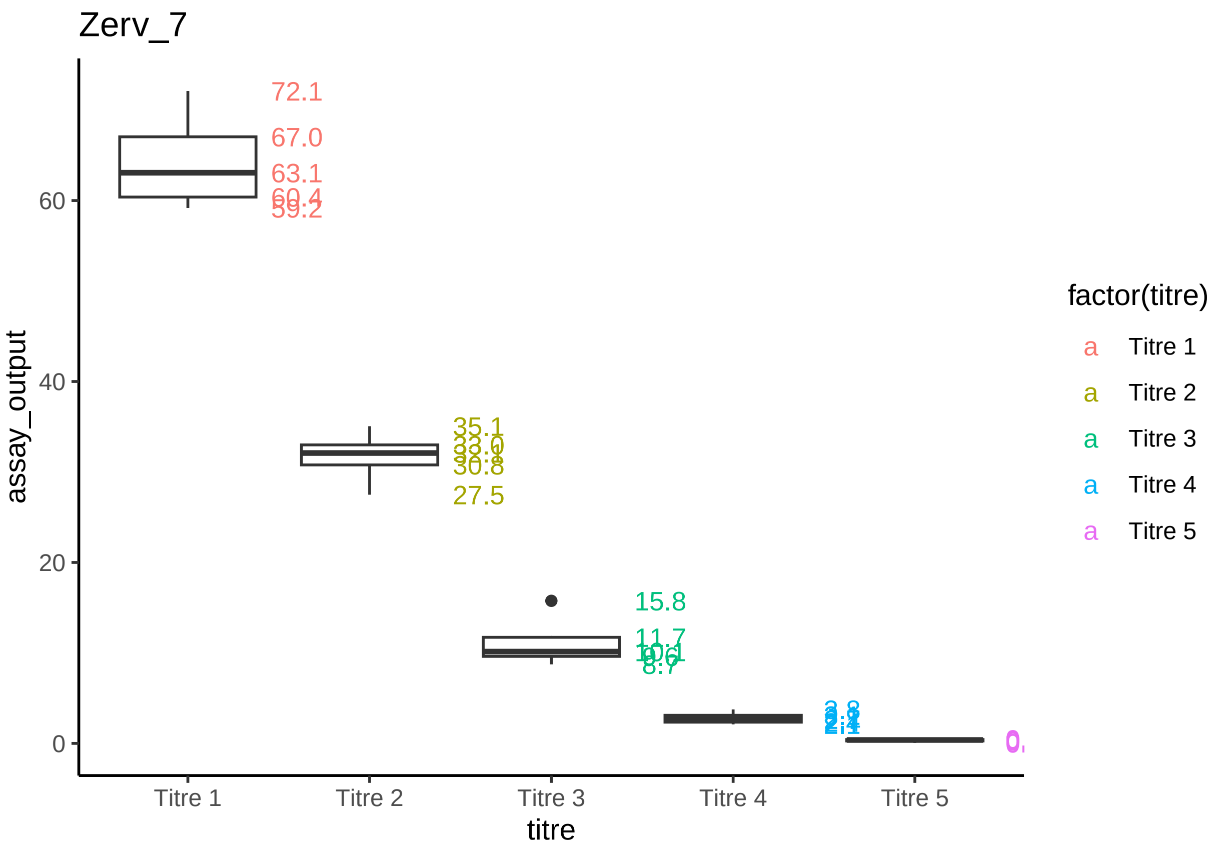

```
##
## [[147]]
```


Yuze_1
86.9
85.9
74.6
48.4
2.6
74.6
73.6
54.6
0.6
42.8
42.3
31.8
0.6
15.0
14.9
11.3
1.3
assay_output
75
50
25
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[148]]
```

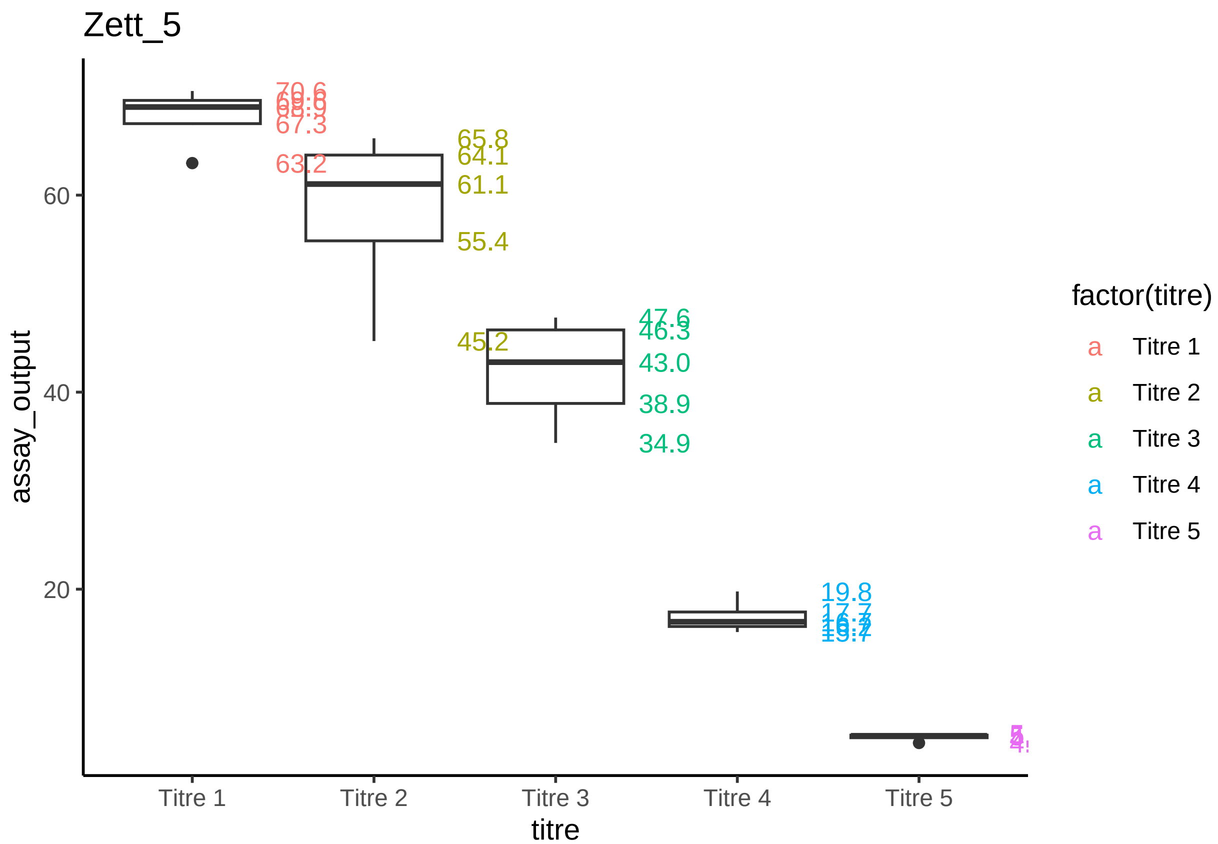

Zaui_3
80
60
40
20
0
assay_output
77.6
69.9
62.1
58.1
54.1
43.8
38.2
32.6
26.2
19.8
9.8
7.4
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5

```
##
## [[149]]
```



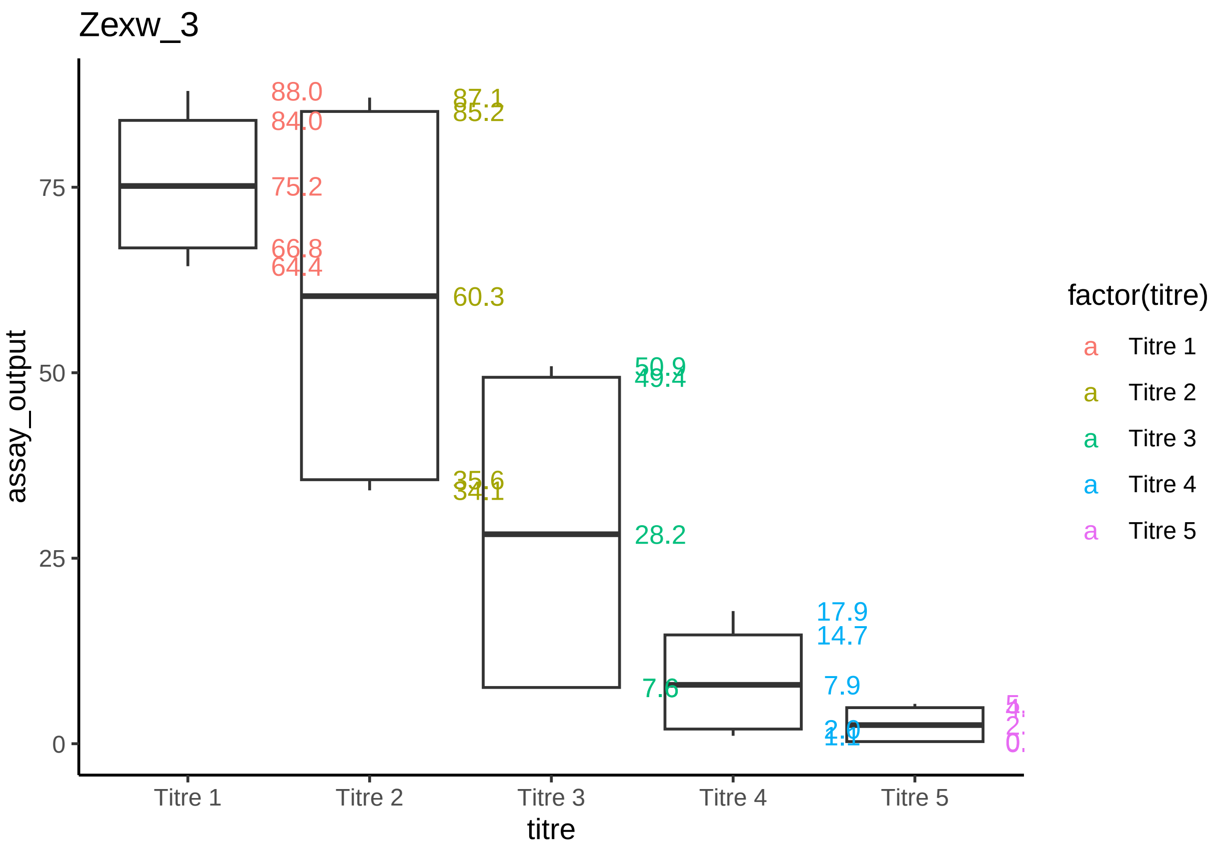
Zerv_7
72.1
67.0
63.1
59.2
35.1
27.5
15.8
11.7
8.7
assay_output
60
40
20
0
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[150]]
```



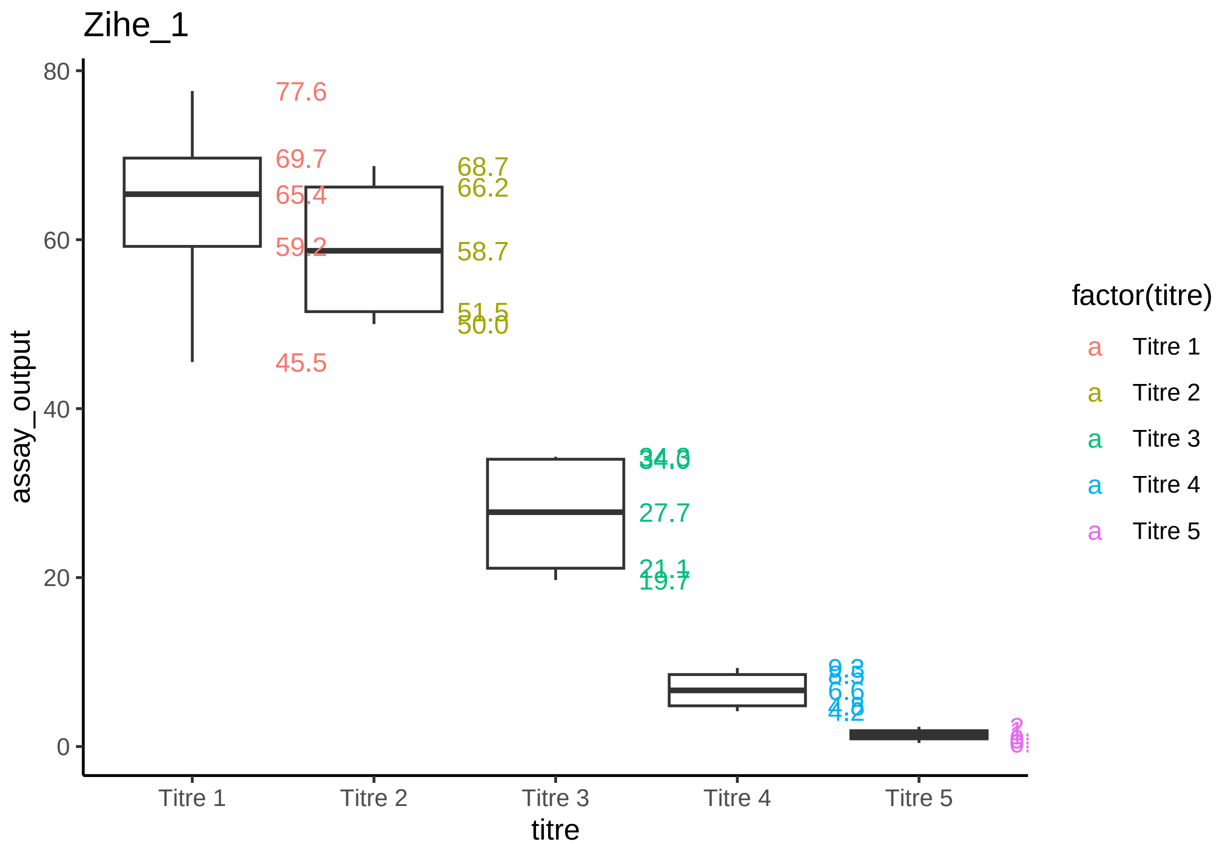
Zett_5
assay_output
titre
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
factor(titre)
70.6
67.3
63.2
65.8
64.1
61.1
55.4
45.2
47.6
46.3
43.0
38.9
34.9
19.8
60
40
20


```
##
## [[151]]
```



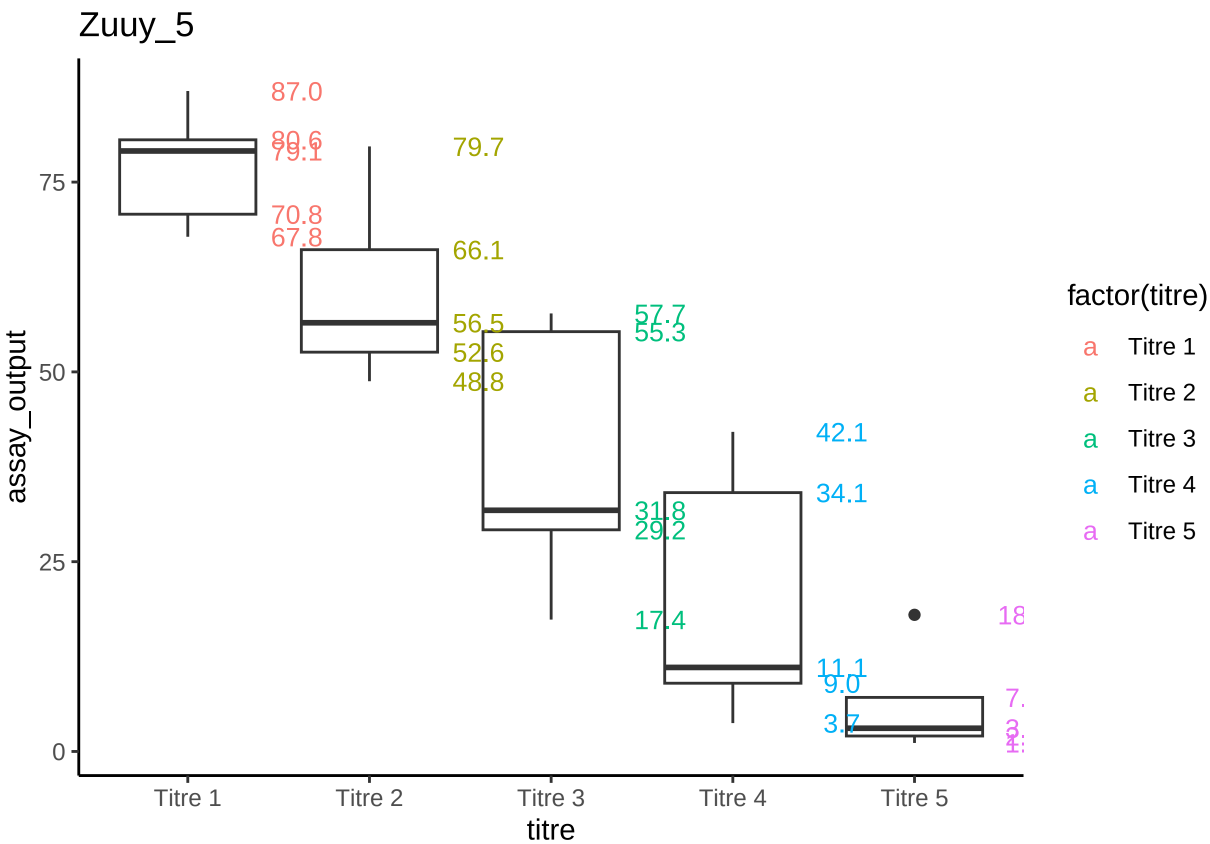
Zexw_3
88.0
84.0
75.2
66.8
64.4
87.1
85.2
60.3
35.6
34.1
50.9
49.4
28.2
7.6
17.9
14.7
7.9
2.0
1.1
75
50
25
0
assay_output
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)
a Titre 1
a Titre 2
a Titre 3
a Titre 4
a Titre 5


```
##
## [[152]]
```



Zihe_1
80
60
40
20
0
assay_output
77.6
69.7
65.4
59.2
45.5
68.7
66.2
58.7
51.5
50.0
34.3
34.0
27.7
21.1
19.7
Titre 1
Titre 2
Titre 3
Titre 4
Titre 5
titre
factor(titre)


```
##
## [[153]]
```




```
#names(box_plot_vector)=vector_data_per_cell_line$cell_line
```

### dealing with outliers

Now i want to get rid of outliers, however i can't just get rid of all outlier values because they might actually be biologically relevant, have to check with other values in the replicates or screen,

creating outlier function which determines if the value is outlier by $(1.5 \times IQR + UQ)$ or $1.5 \times IQR - LQ$

```
is_outlier <- function(x) {
  return(x < quantile(x, 0.25) - 1.5 * IQR(x) | x > quantile(x, 0.75) + 1.5 * IQR(x))
}
```

this is a function that applies outlier per titre (checks if value is a outlier compared to other values in other screens)

```
outlier_function=function(i){
  i %>%
  group_by(titre) %>%
  mutate(outlier = ifelse(is_outlier(assay_output), assay_output, as.numeric(NA)))
}
```

use this to remove outlying observations. per screen (per cell) there are 5 titres (with 2 replicates ), if at least 3 of these points are outliers that set of points for that replicate is removed (whole observation may be outlier )

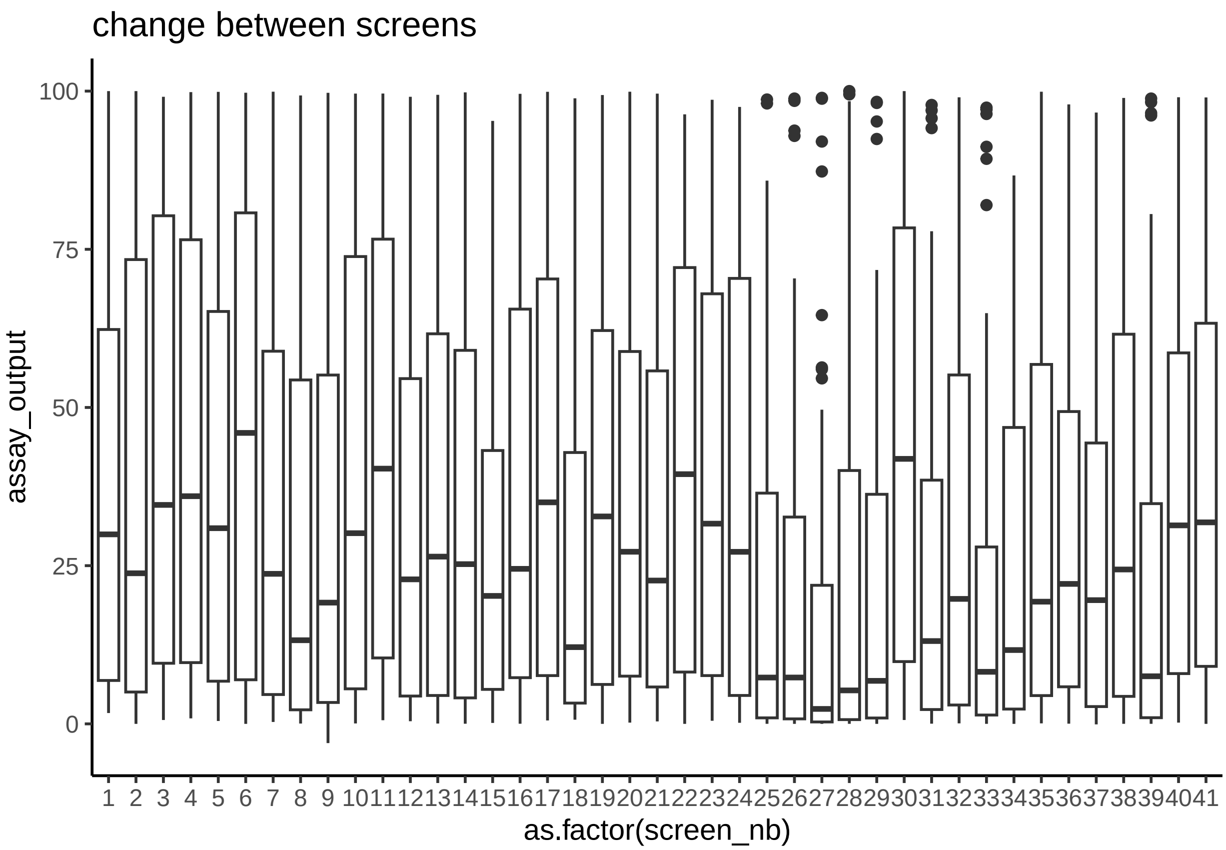
```
all_outliers=purrr::map(vector_data_per_cell_line$data,outlier_function)
HIV1_vector_data=bind_rows(all_outliers)%>%group_by(cell_line,screen_nb,replicate)%>%filter(((sum(is.na
```

### normalising between the screens

In order to get rid of any batch effects from the screening process, we want to find the zscore to normalise within the screen, this makes it more comparable between screens

plot the boxplot for each screen, before normalisation

```
ggplot(data = HIV1_vector_data,aes(y=assay_output, x=as.factor(screen_nb),group = screen_nb,))+
  geom_boxplot()+
  ggtitle('change between screens')+
  theme_classic()
```

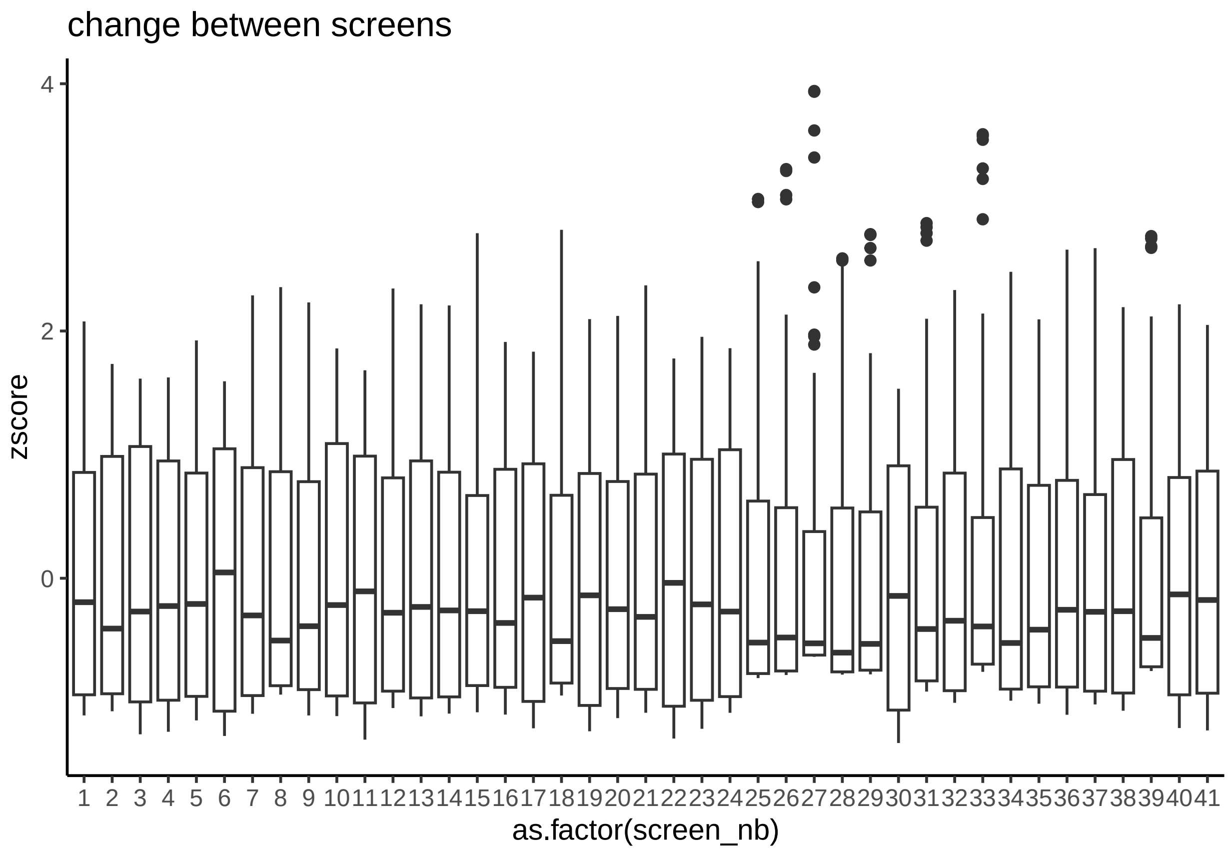



okay going to apply zscore to all values to standardise between screens to try and get rid of any batch effects to allow proper comparison

```
#HIV_vector_group_data = HIV1_vector_data%>%summarise(mean_output=mean(assay_output),sd_output=sd(assay_
HIV1_vector_data=HIV1_vector_data%>%
  group_by(screen_nb)%>%
  mutate(zscore=((((assay_output-mean(assay_output))/sd(assay_output)))))%>%
  ungroup()
```

making box plot for after normalisation

```
ggplot(data = HIV1_vector_data,aes(y=zscore, x=as.factor(screen_nb),group = screen_nb,))+
  geom_boxplot()+
  ggtitle('change between screens')+
  theme_classic()
```




### finding parameters

so now i have the normalised max mean percentage (in z score) A bit worried that by normalising it and getting rid of the difference it might affect results

finding now the area under the curve using AUC function

```
HIV1_vector_data=HIV1_vector_data%>%group_by(batch,cell_line,screen,screen_nb,replicate)%>%
  mutate(area_under_curve=AUC(infection_volume_ul,(zscore)))%>%
  ungroup()
```

updating the df list per cell line

```
vector_data_per_cell_line=HIV1_vector_data%>%nest_by(cell_line,.keep = T)
```

## fitting the curves

##logarithmic

Here we use a logarithmic

$$a + b \times log_2(x - c)$$

with 3 parameters, a- y offset b- slope and c- x offset, to help plot the graph in our analysis a higher a and b should correspond to more permissive/susceptible and a lower c would correspond to less permissive. However this depends on how the data is fitted, the fit may mean these values aren't directly correlated with those phenotype

```
logarithmic_func <- function(x, a, b,c) {
  a + b * log2(x-c)
}
```

this is the function for fitting. using a robust nlsLM function, fits the data using start points, having to choose good starting volumes, saves coefs to the database. There is also error handling using tryCatch- giving error message and instead adds NA

Plotting function, using ggplot, use logarithmic function to create predicted list of values, these values are then fed into geom line to be the fitted line. then add the parameters onto the graph averaged for each cell line

```
apply_plot_log=function(i){
i <- i %>%
    mutate(predicted = logarithmic_func(infection_volume_ul, i$a, i$b,i$c))

  # Create the plot
  p=ggplot(data = i, aes(x = infection_volume_ul, y = zscore, group = interaction(screen_nb,replicate))
    geom_point(aes(color=screen_nb),color = "blue", size = 2, alpha = 0.6) + # Actual data points
    geom_line(aes(y = predicted,color=screen_nb), color = "red", size = 1) + # Fitted line
    ggtitle(unique(i$cell_line)) + # Dynamic title
    labs(x = "Infection Volume (uL)", y = "Mean Z-Score") +
    theme_classic()

    params_text <- paste0(
    "Parameters:\n",
    "a = ", round(mean(i$a, na.rm = TRUE), 2), "\n",
    "b = ", round(mean(i$b, na.rm = TRUE), 2), "\n",
    "d = ", round(mean(i$c, na.rm = TRUE), 2), "\n"
  )

  p + annotate("text",
               x = Inf, y = -Inf,
               label = params_text,
               hjust = 1.1, vjust = -0.1,
               size = 3)
}
```

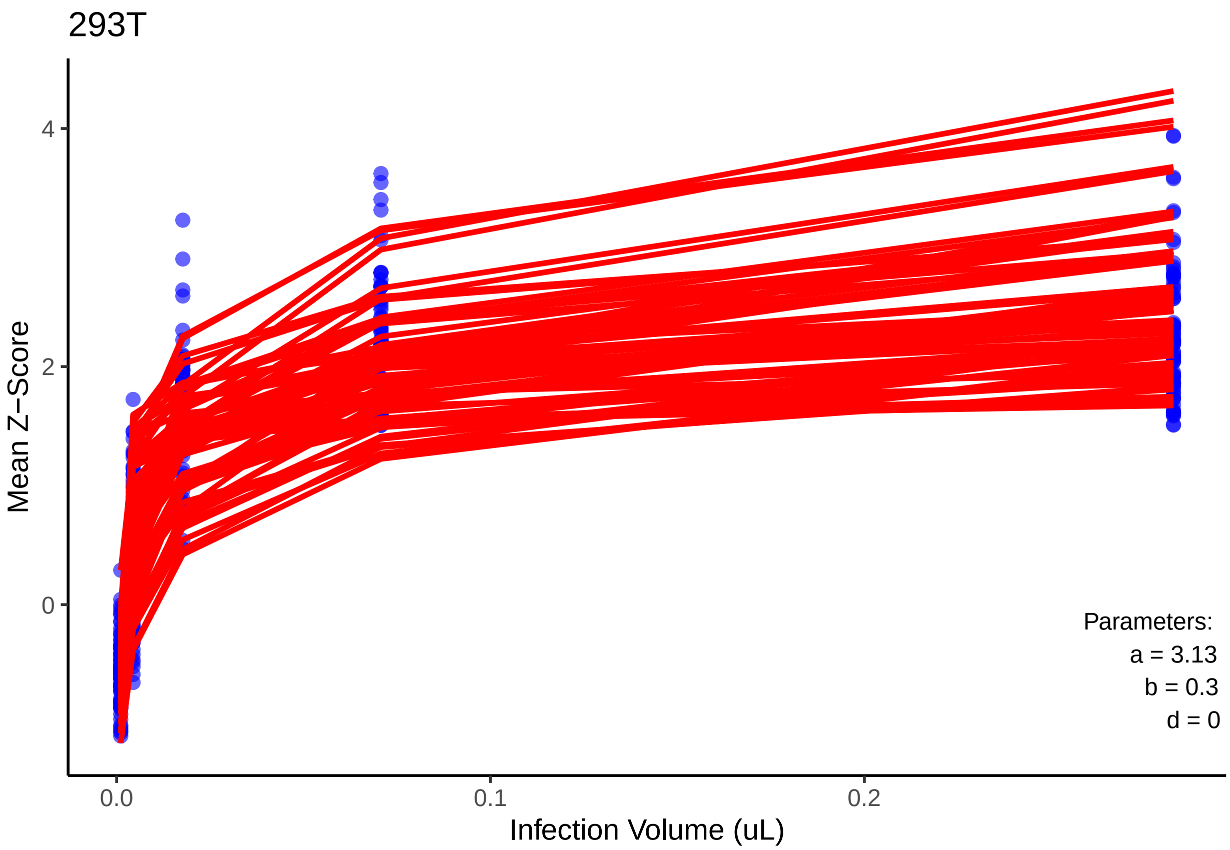
```
logarithmic_plot_vector=purrr::map(vector_data_per_cell_line$data,apply_plot_log)
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

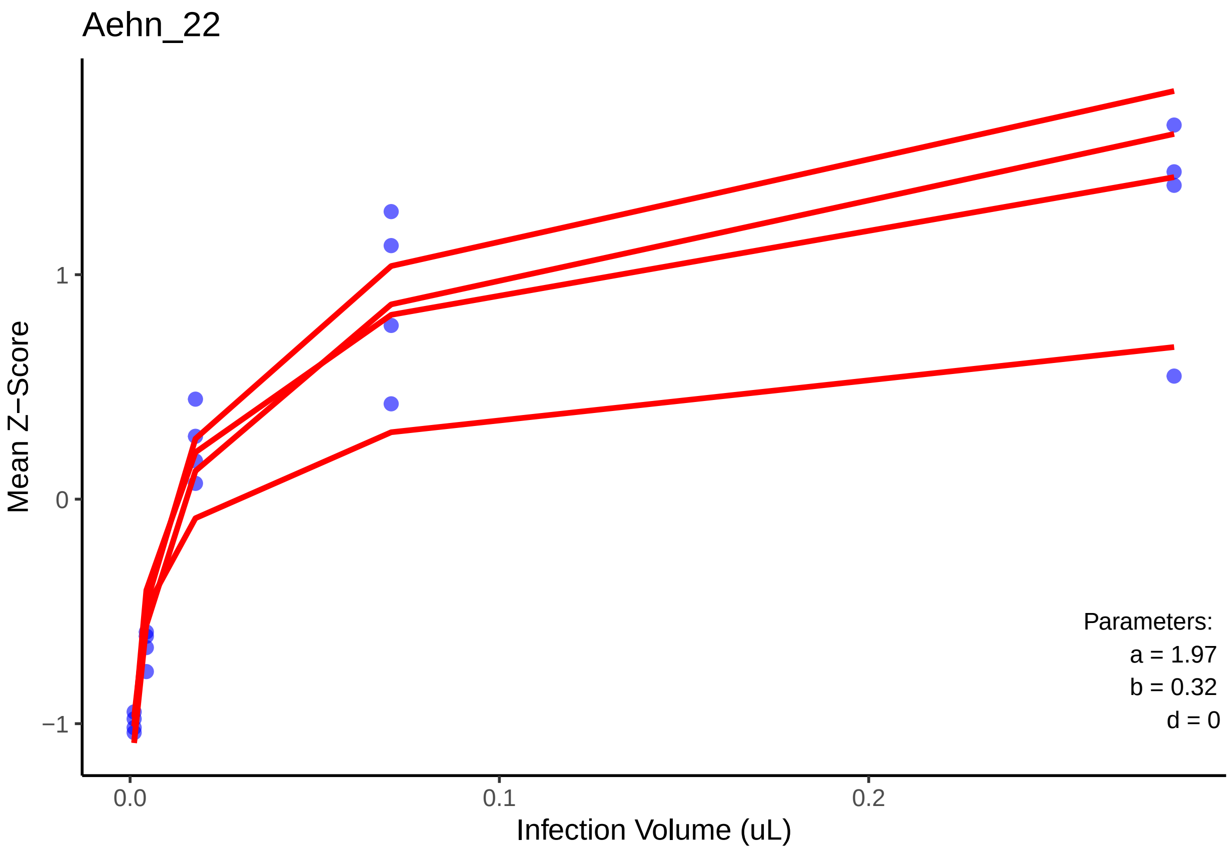
```
names(logarithmic_plot_vector)=vector_data_per_cell_line$cell_line
logarithmic_plot_vector
```

```
## $`293T`
```

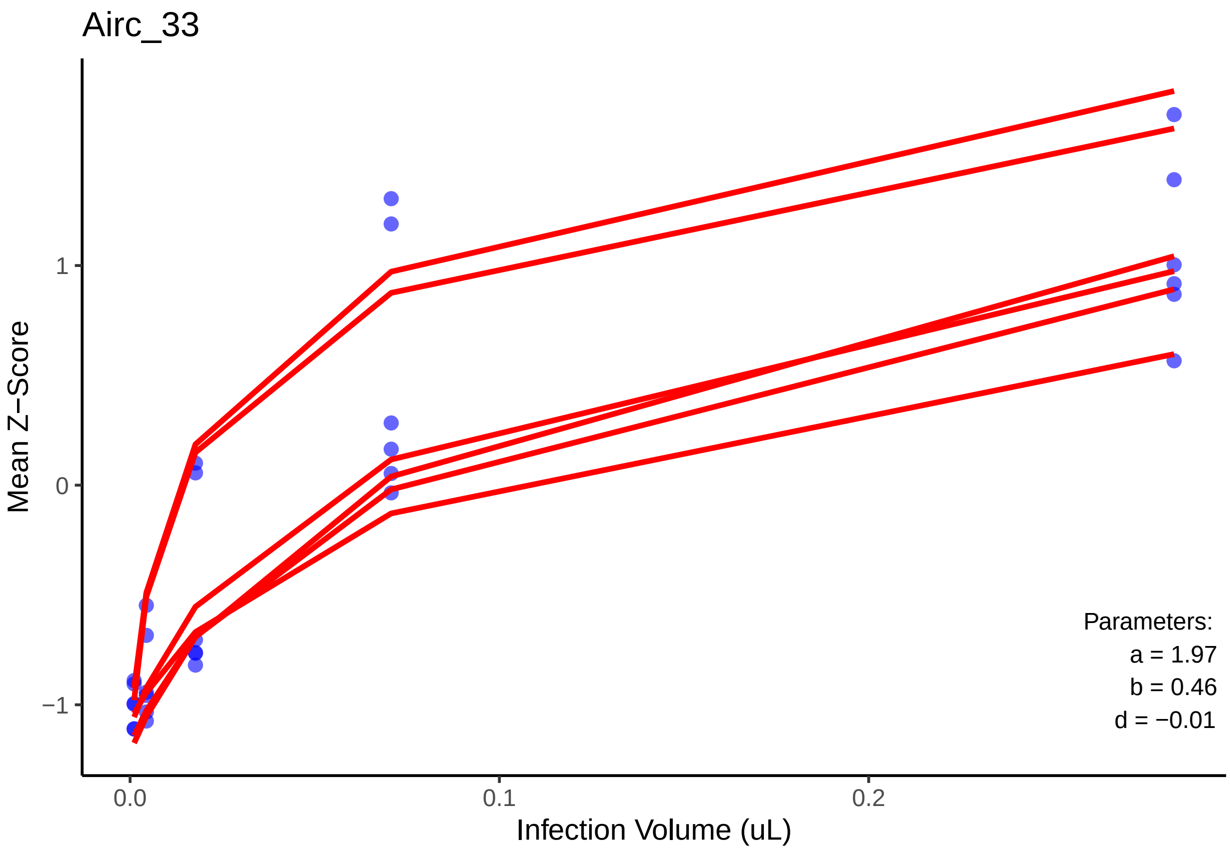
```
## Warning: Removed 15 rows containing missing values or values outside the scale range
## (`geom_line()`).
```


293T
Mean Z−Score
4
2
0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 3.13
b = 0.3
d = 0

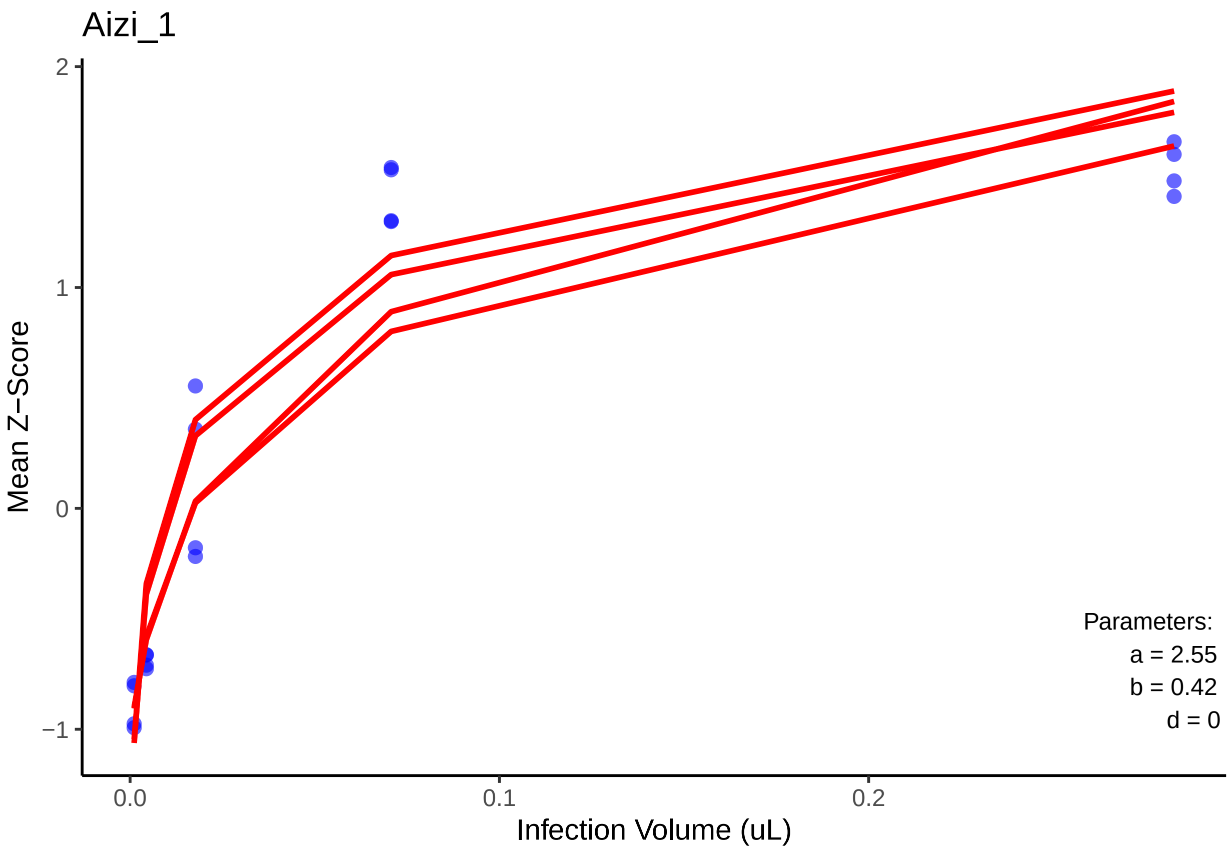
```
##
## $Aehn_22
```


Aehn_22
Mean Z−Score
Infection Volume (uL)
1
0
−1
0.0
0.1
0.2
Parameters:
a = 1.97
b = 0.32
d = 0

```
##
## $Airc_33
```

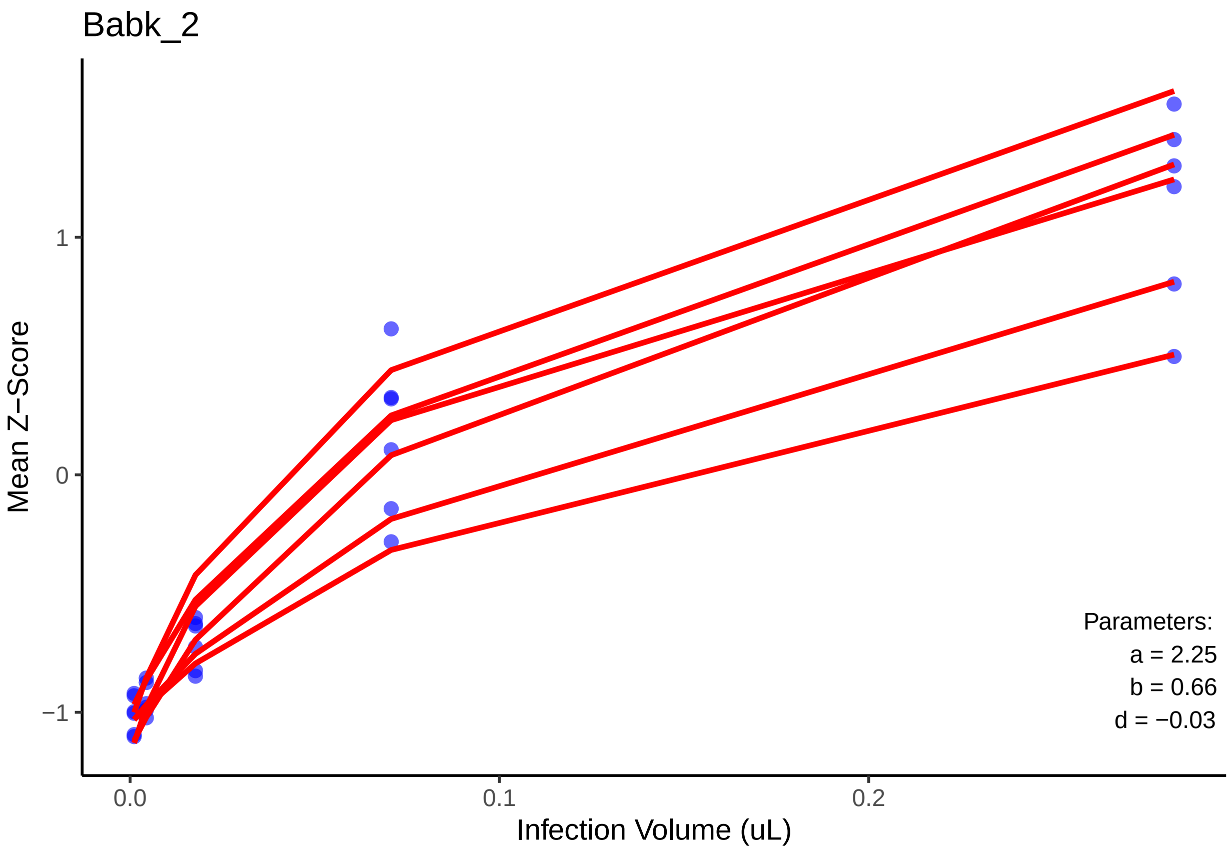

Airc_33
Mean Z−Score
Infection Volume (uL)
Parameters:
a = 1.97
b = 0.46
d = −0.01
1
0
−1
0.0
0.1
0.2

```
##
## $Aizi_1
```



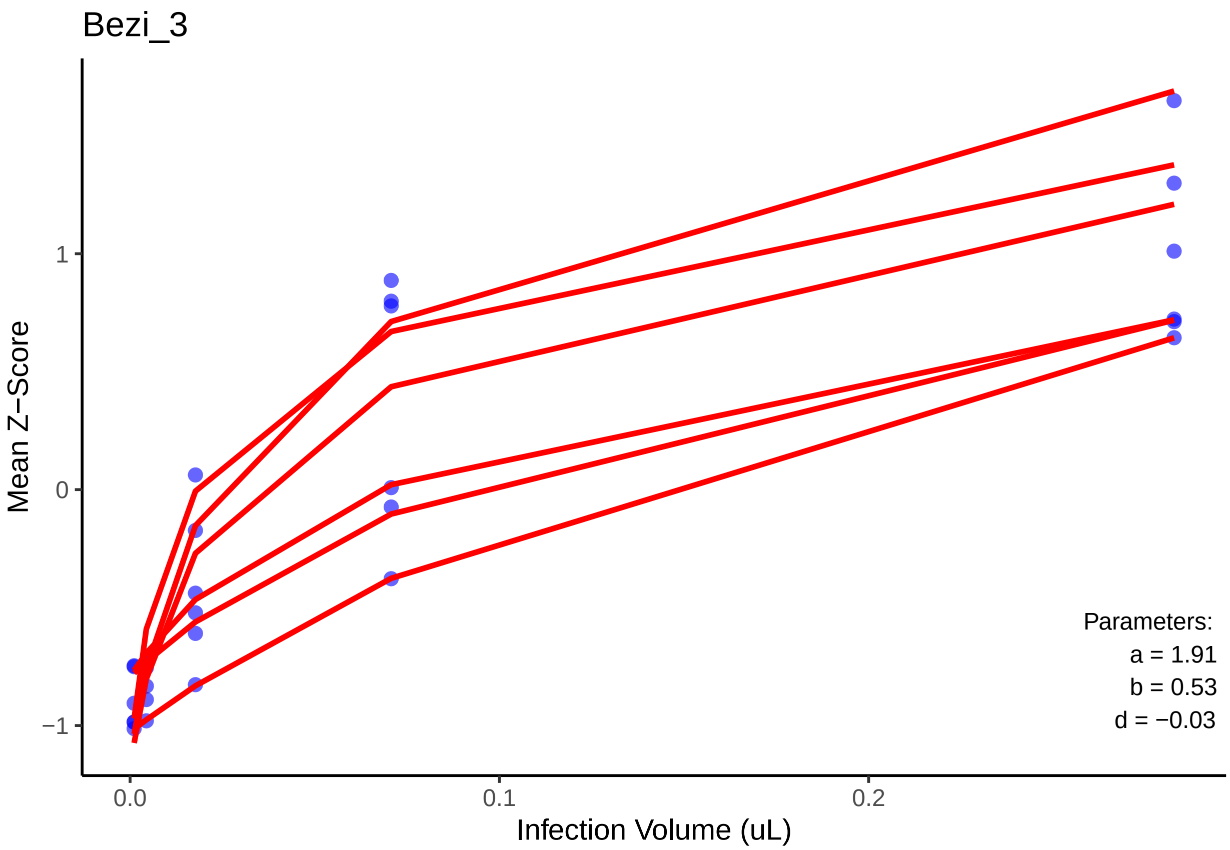
Aizi_1
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.55
b = 0.42
d = 0


```
##
## $Babk_2
```

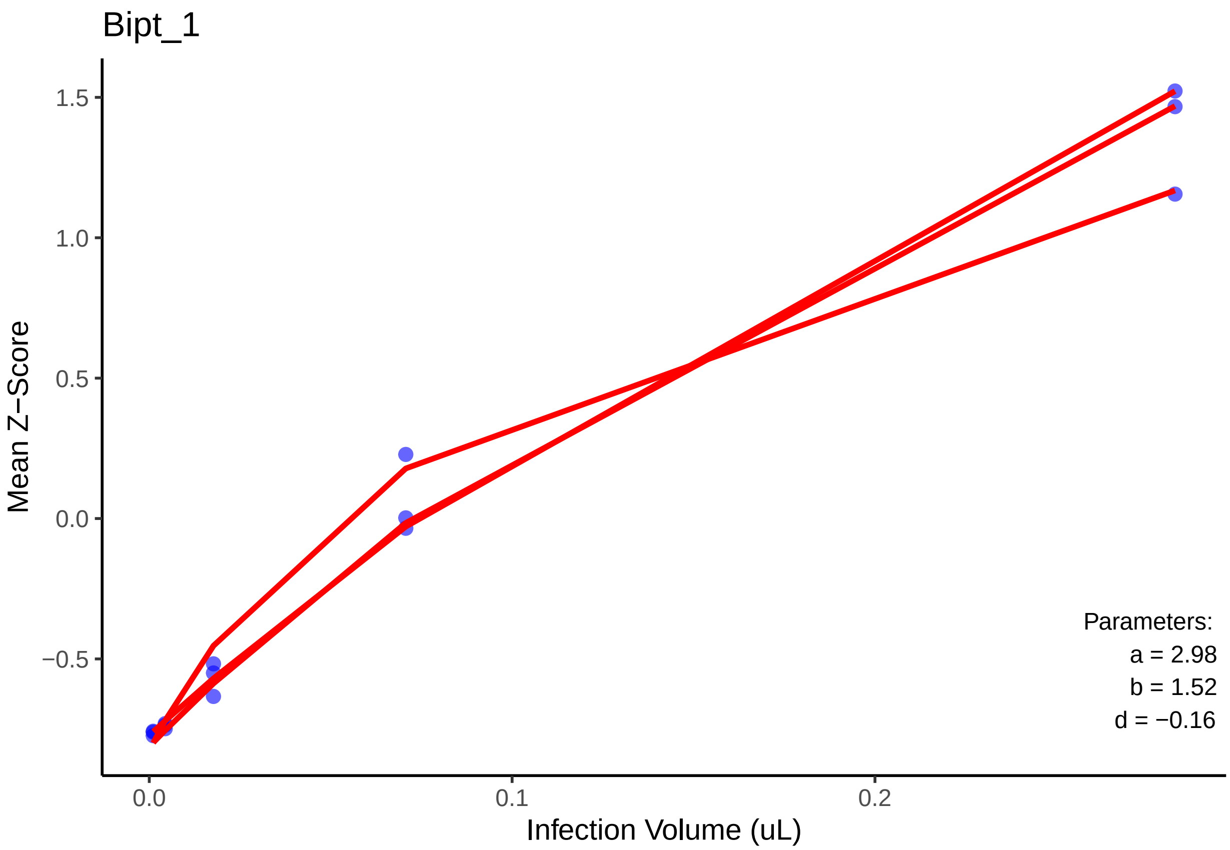


Babk_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.25
b = 0.66
d = −0.03

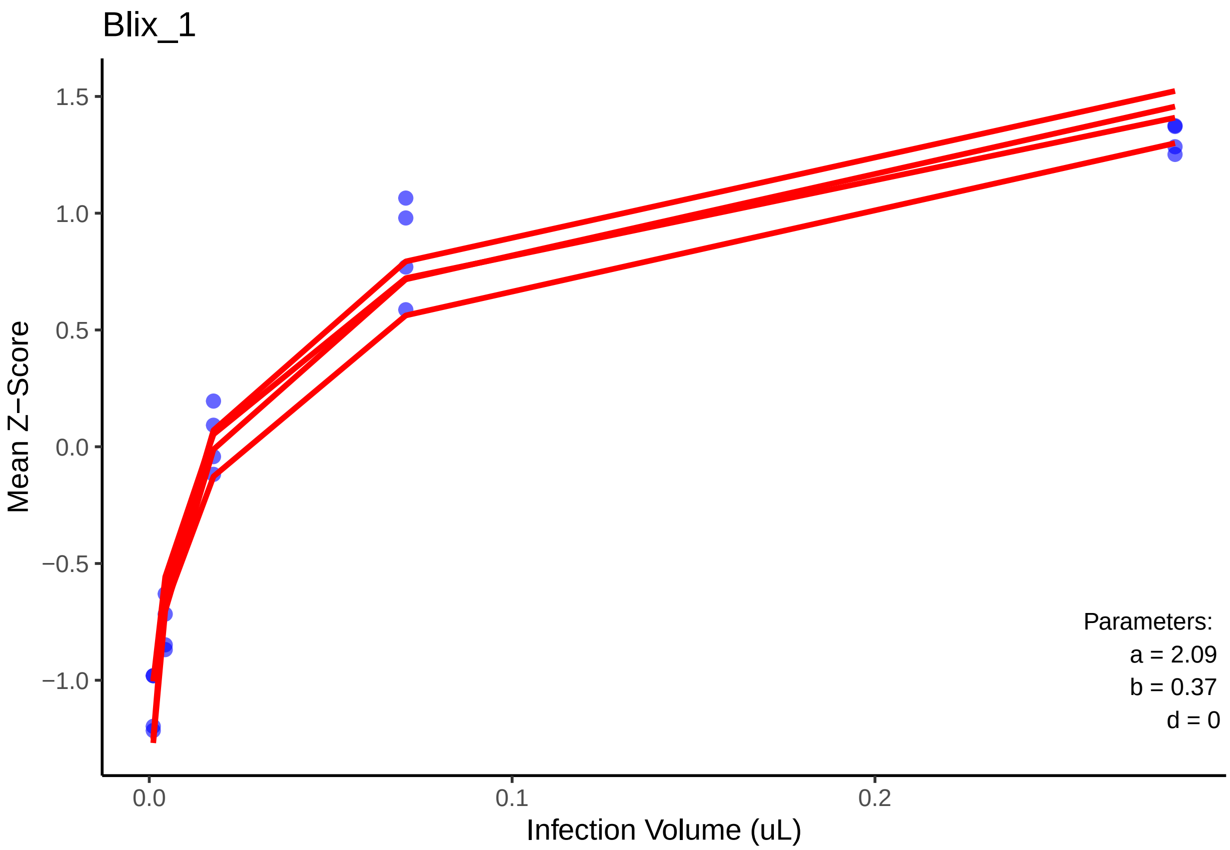

```
##
## $Bezi_3
```


Bezi_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.91
b = 0.53
d = −0.03

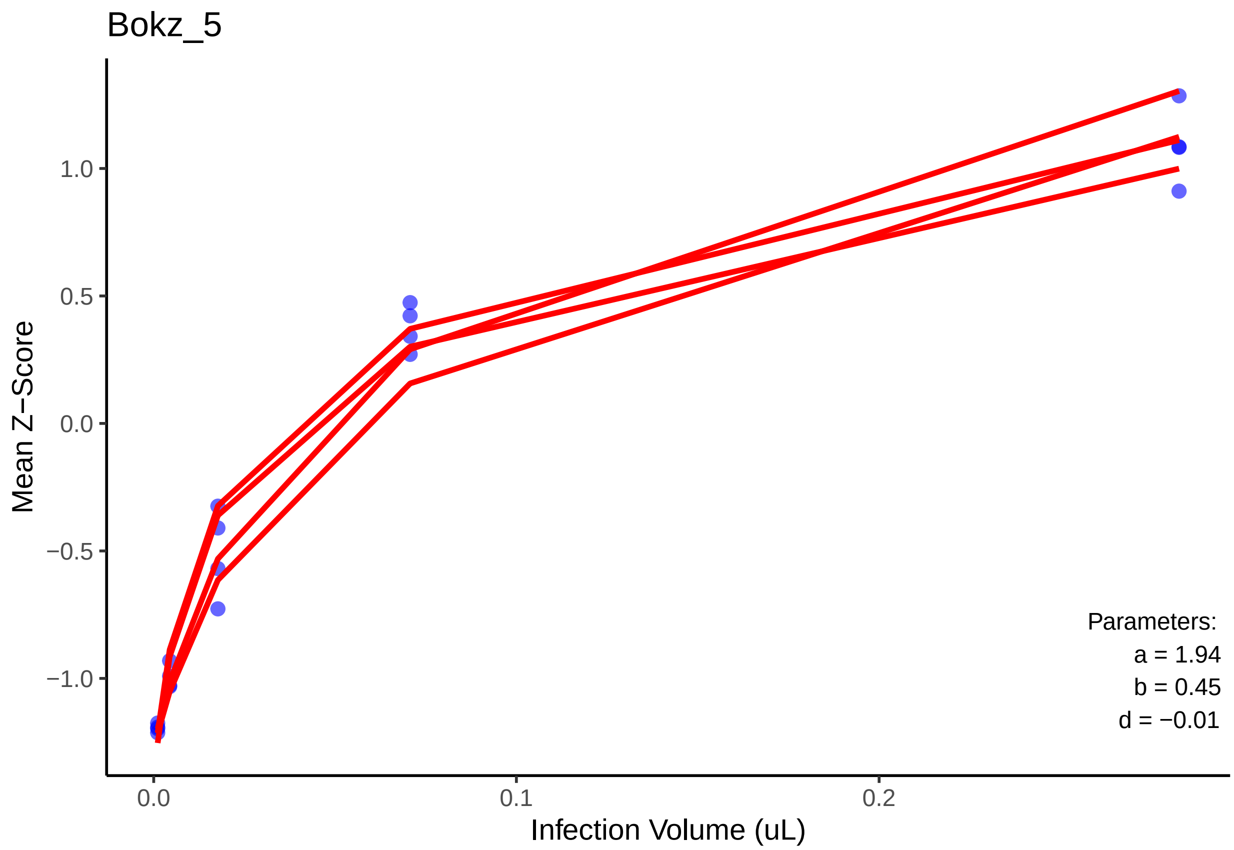
```
##
## $Bipt_1
```


Bipt_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.98
b = 1.52
d = −0.16

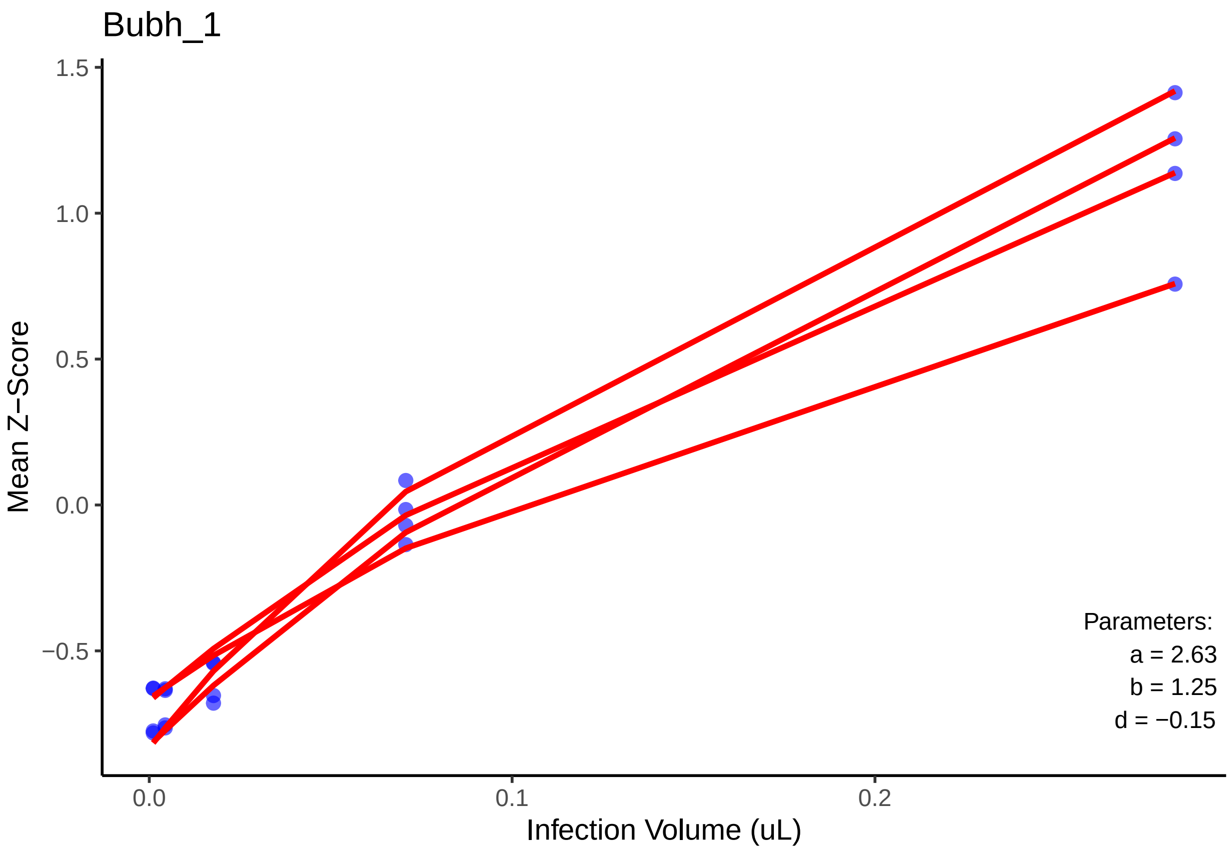
```
##
## $Blix_1
```


Blix_1
1.5
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.09
b = 0.37
d = 0

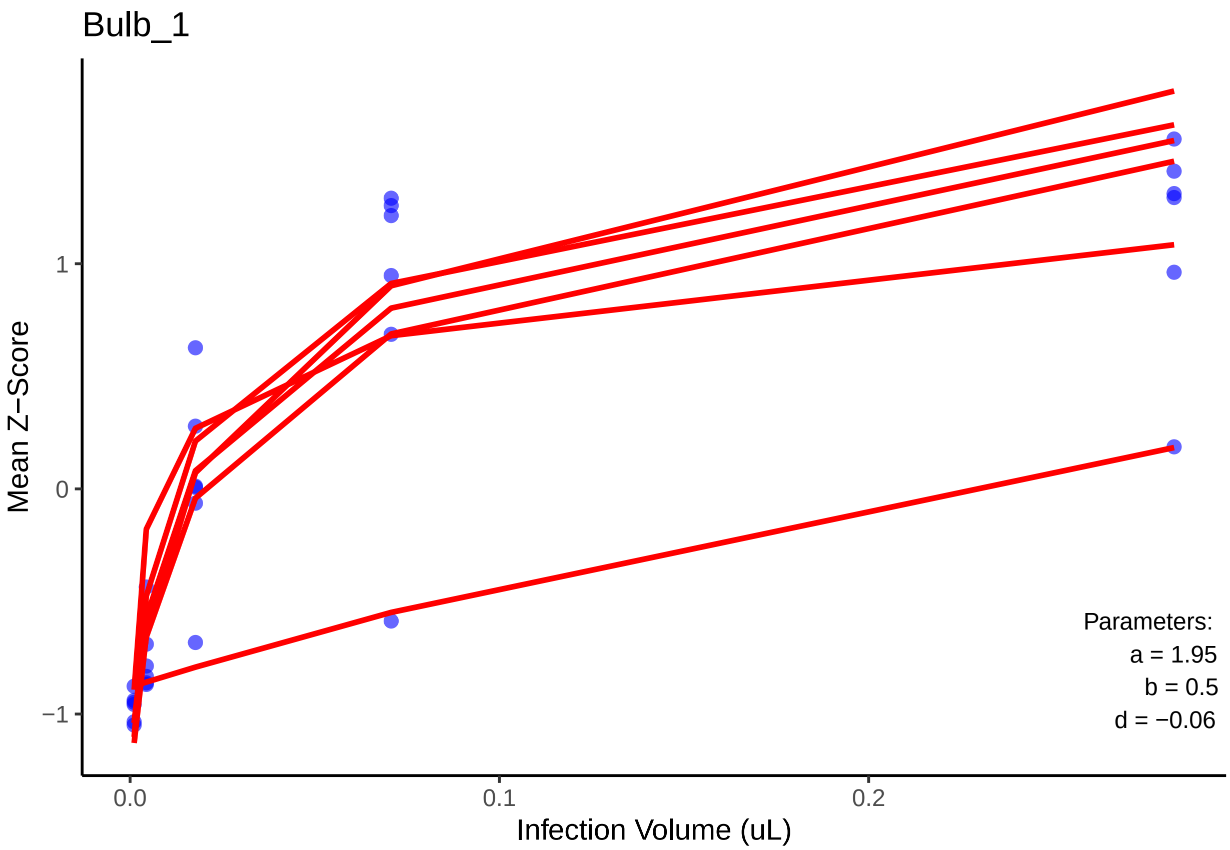
```
##
## $Bokz_5
```


Bokz_5
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.94
b = 0.45
d = −0.01

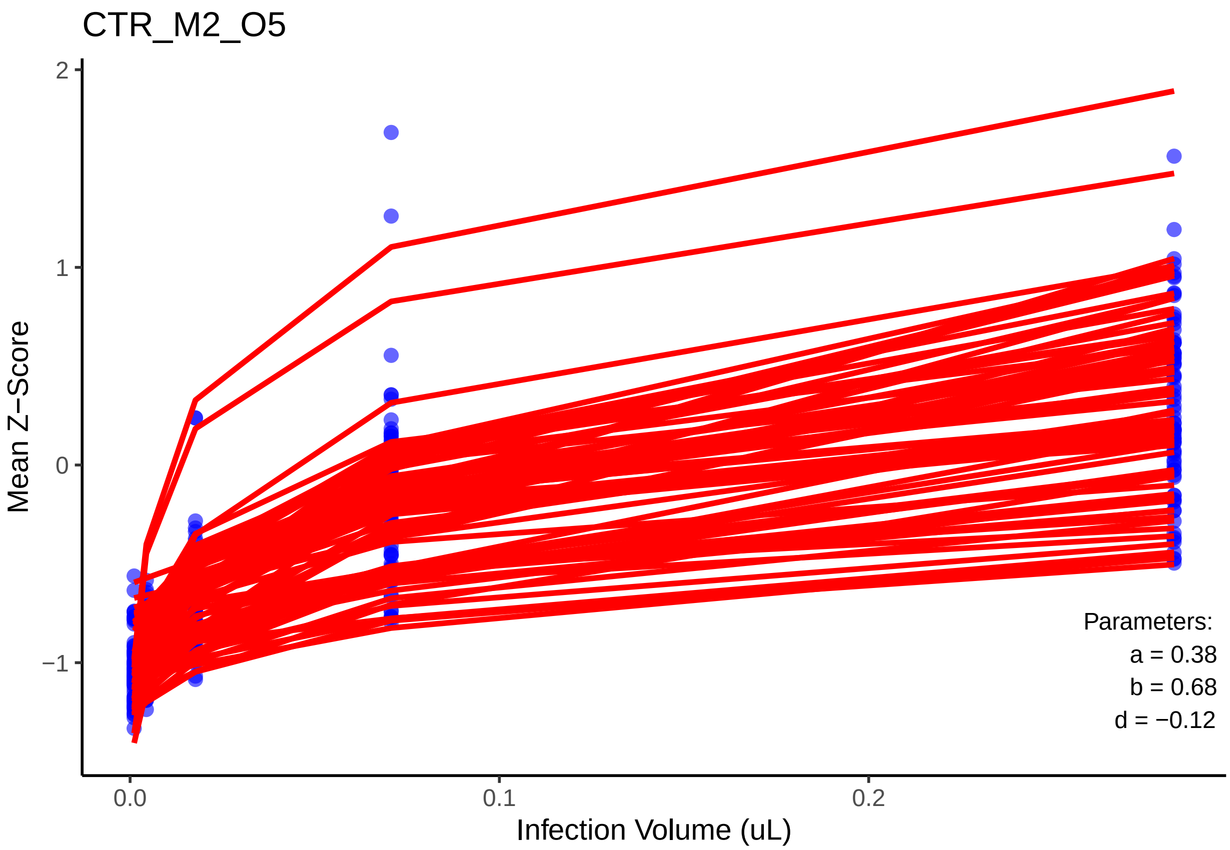
```
##
## $Bubh_1
```


Bubh_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.63
b = 1.25
d = −0.15

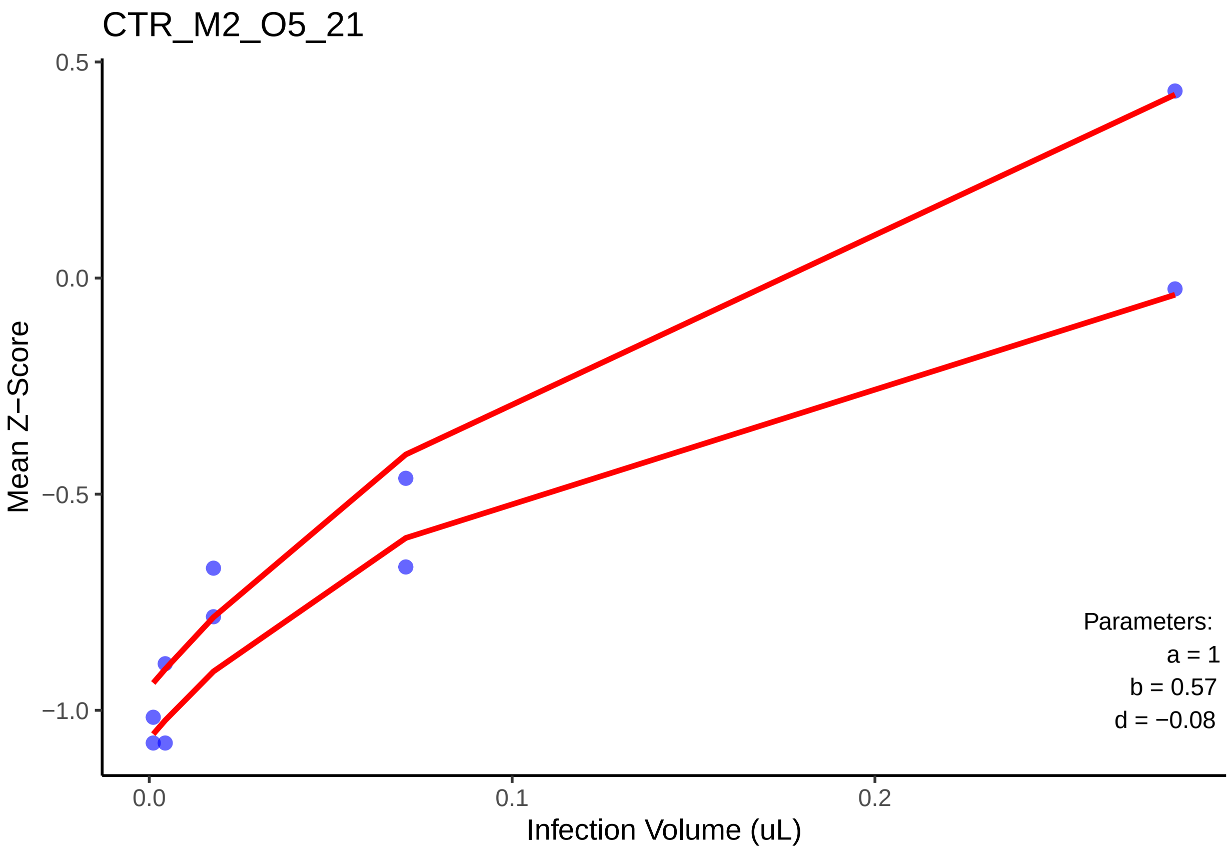
```
##
## $Bulb_1
```


Bulb_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.95
b = 0.5
d = −0.06

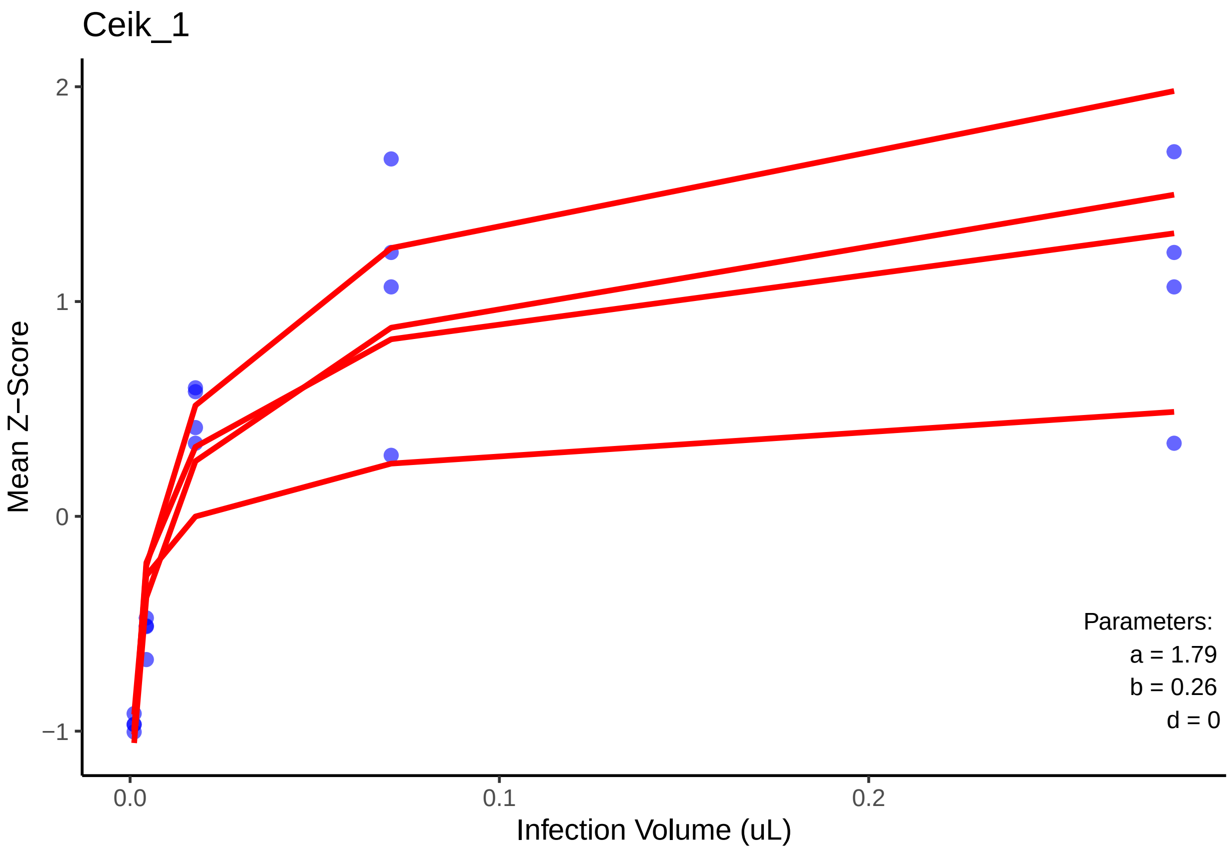
```
##
## $CTR_M2_05
```


CTR_M2_O5
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 0.38
b = 0.68
d = −0.12

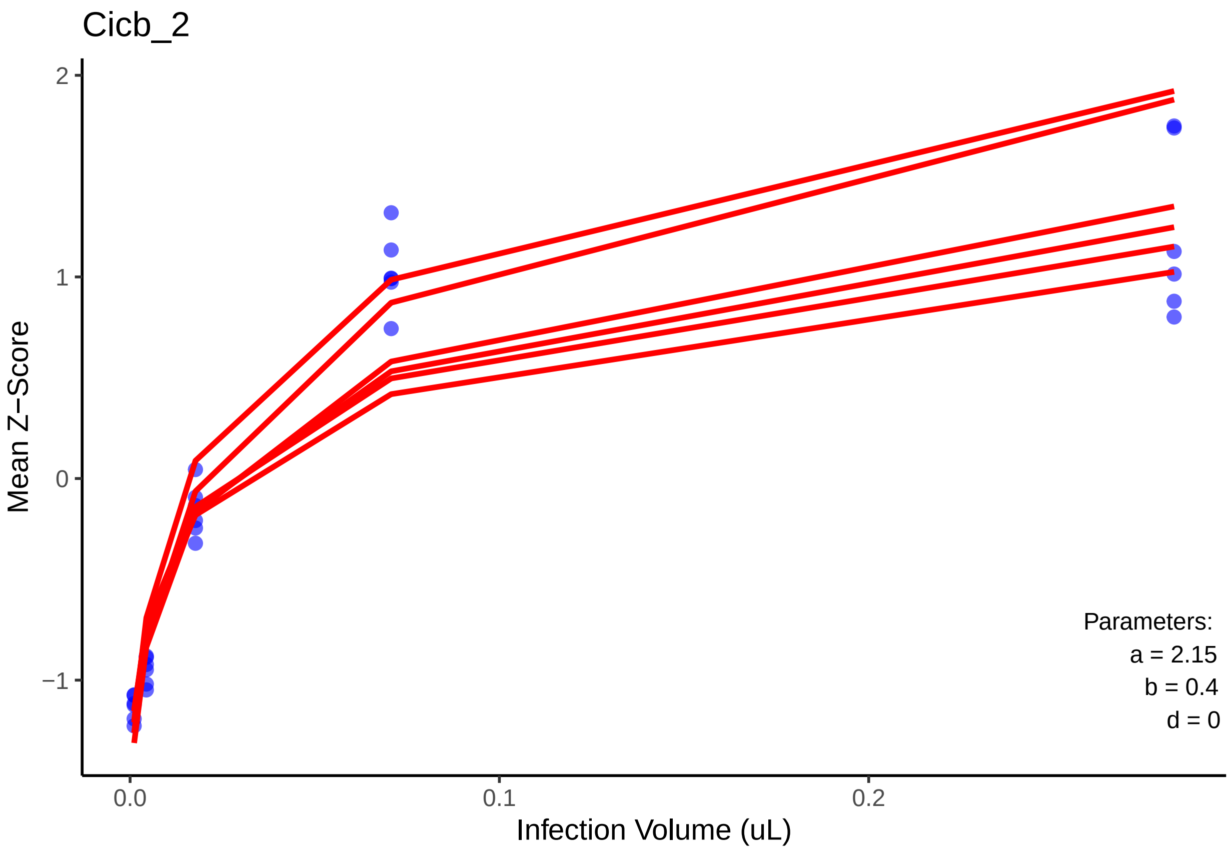
```
##
## $CTR_M2_O5_21
```


CTR_M2_O5_21
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1
b = 0.57
d = −0.08

```
##
## $Ceik_1
```

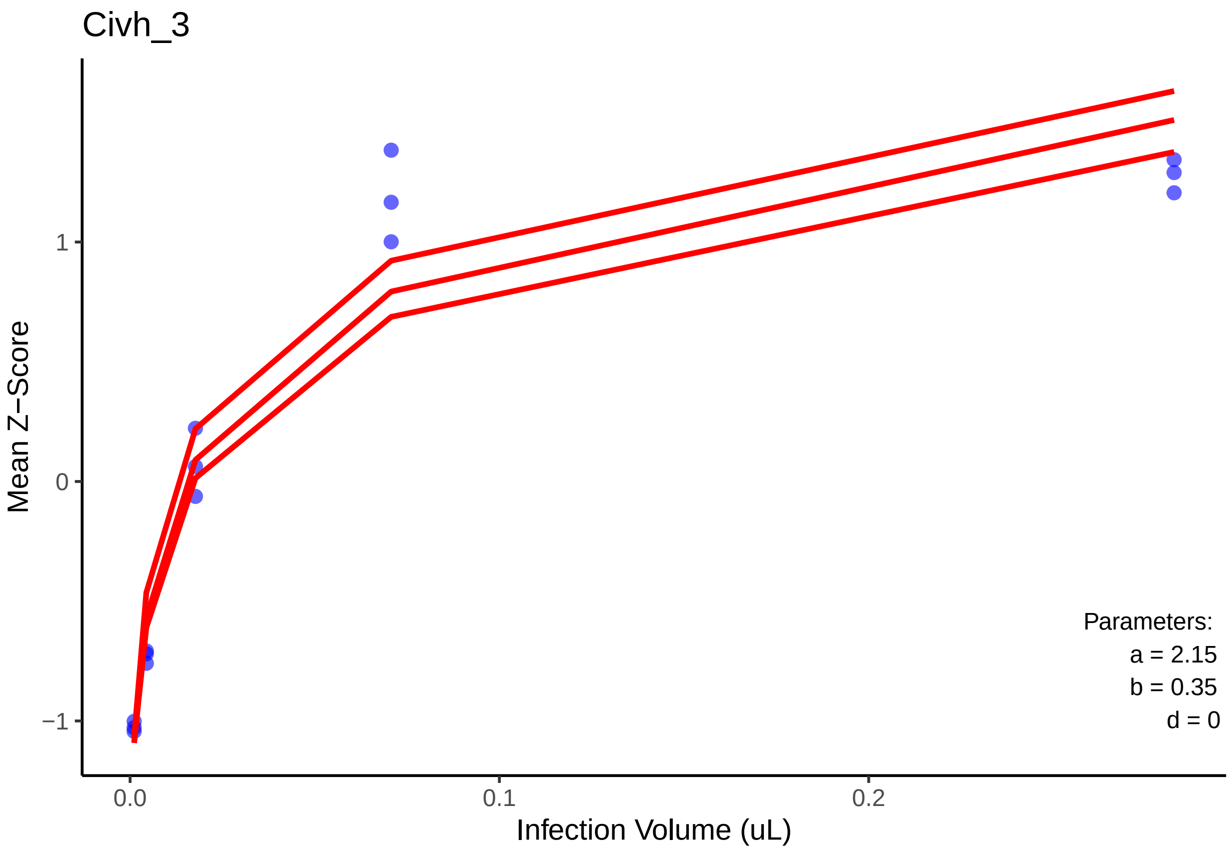

Ceik_1
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 1.79
b = 0.26
d = 0

```
##
## $Cicb_2
```

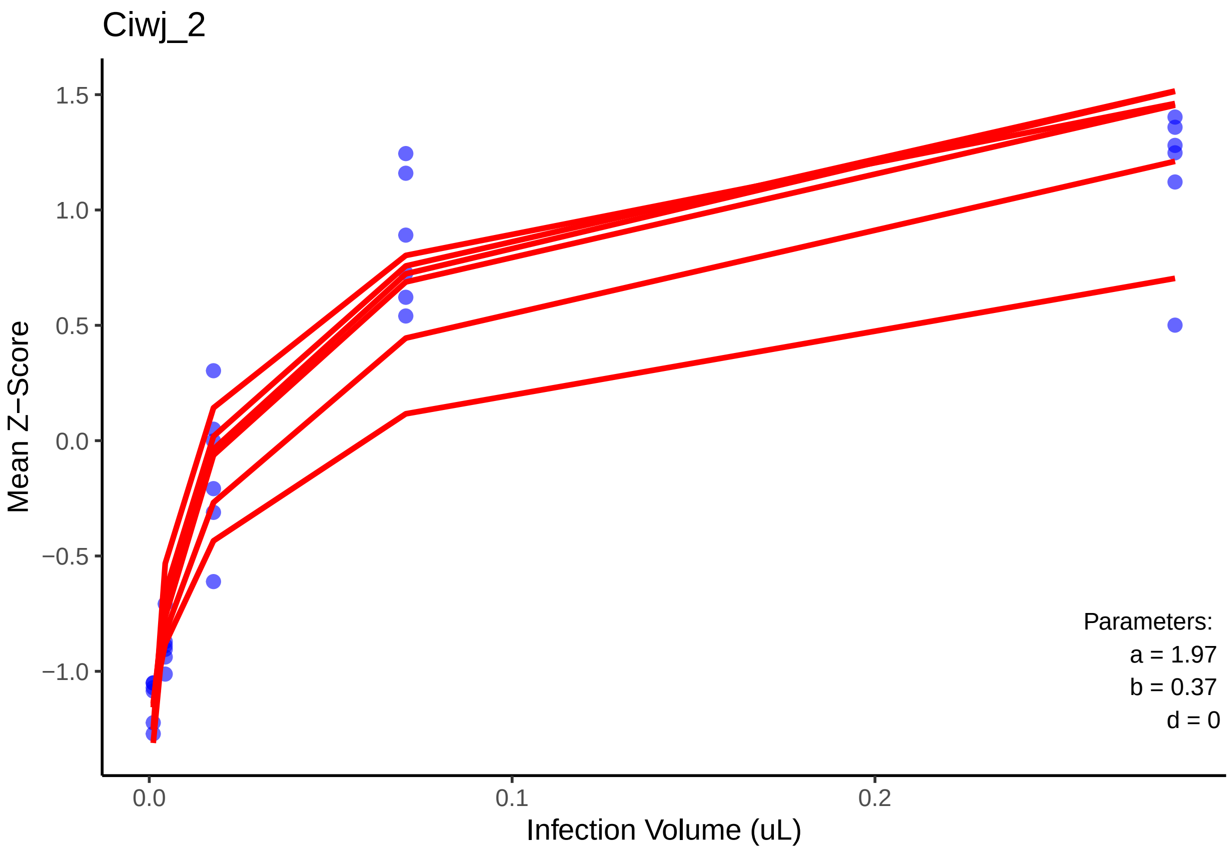


Cicb_2
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.15
b = 0.4
d = 0

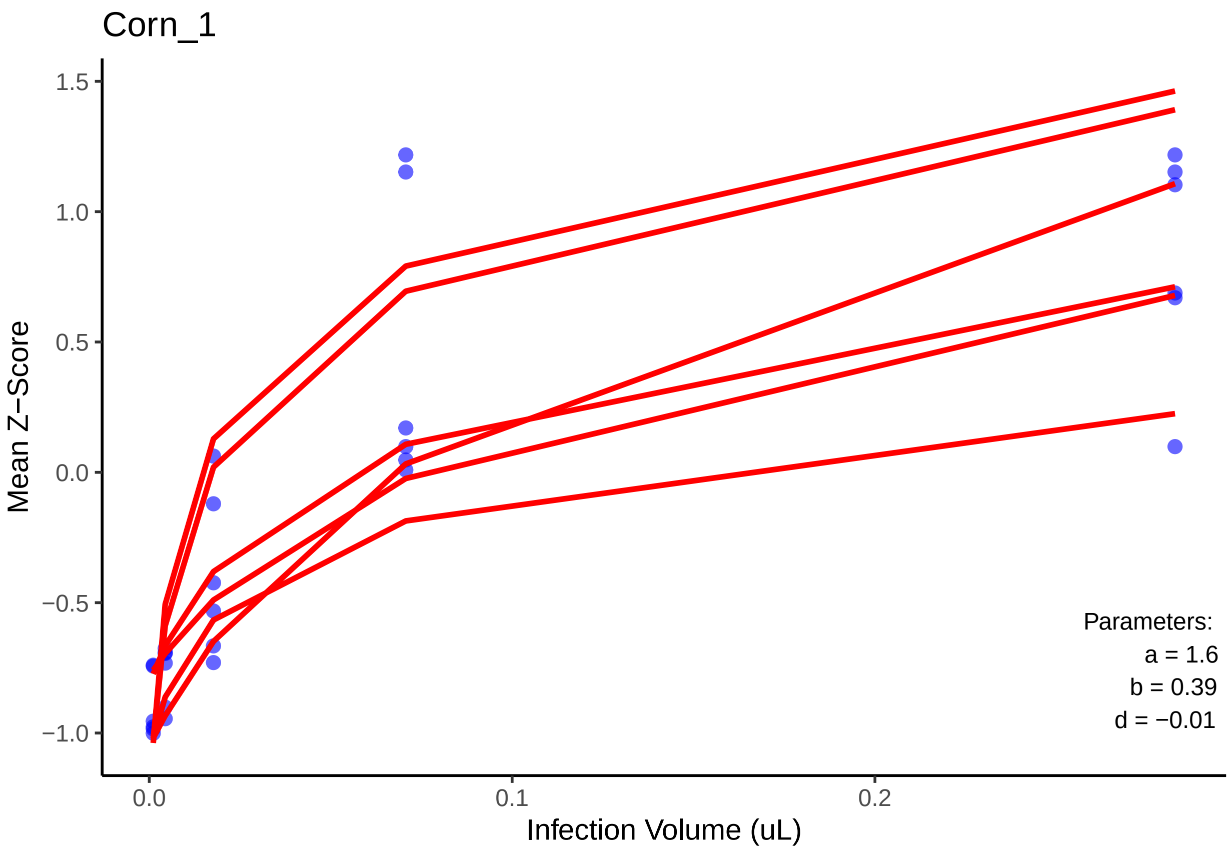

```
##
## $Civh_3
```


Civh_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.15
b = 0.35
d = 0

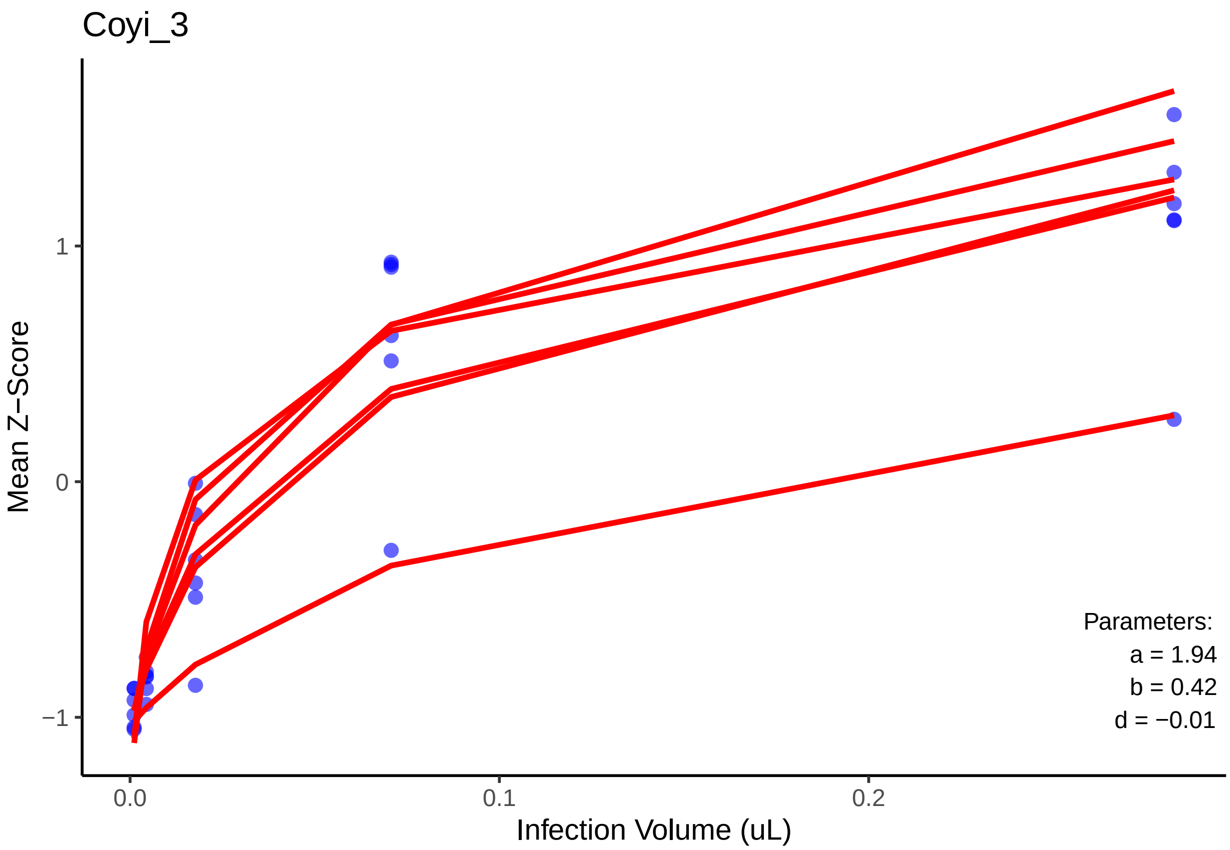
```
##
## $Ciwj_2
```


Ciwj_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.97
b = 0.37
d = 0

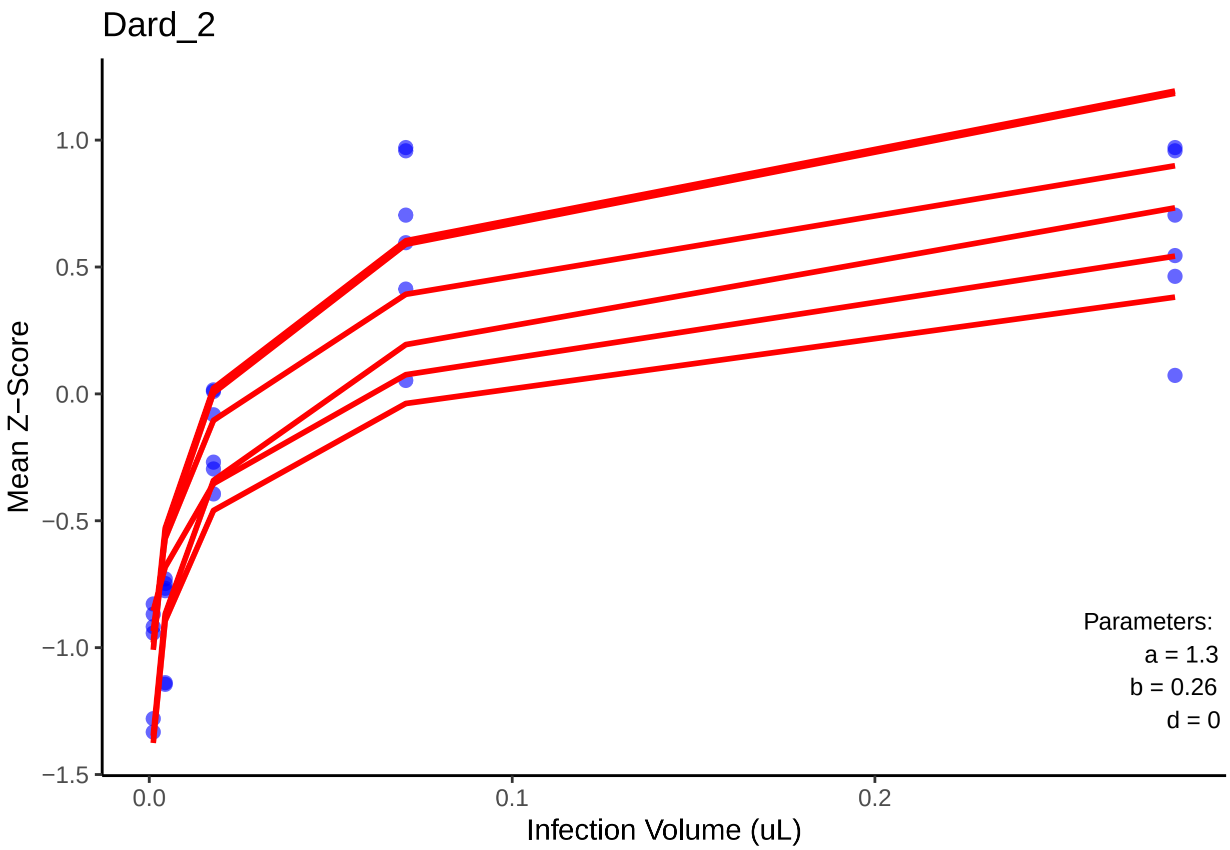
```
##
## $Corn_1
```


Corn_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.6
b = 0.39
d = −0.01

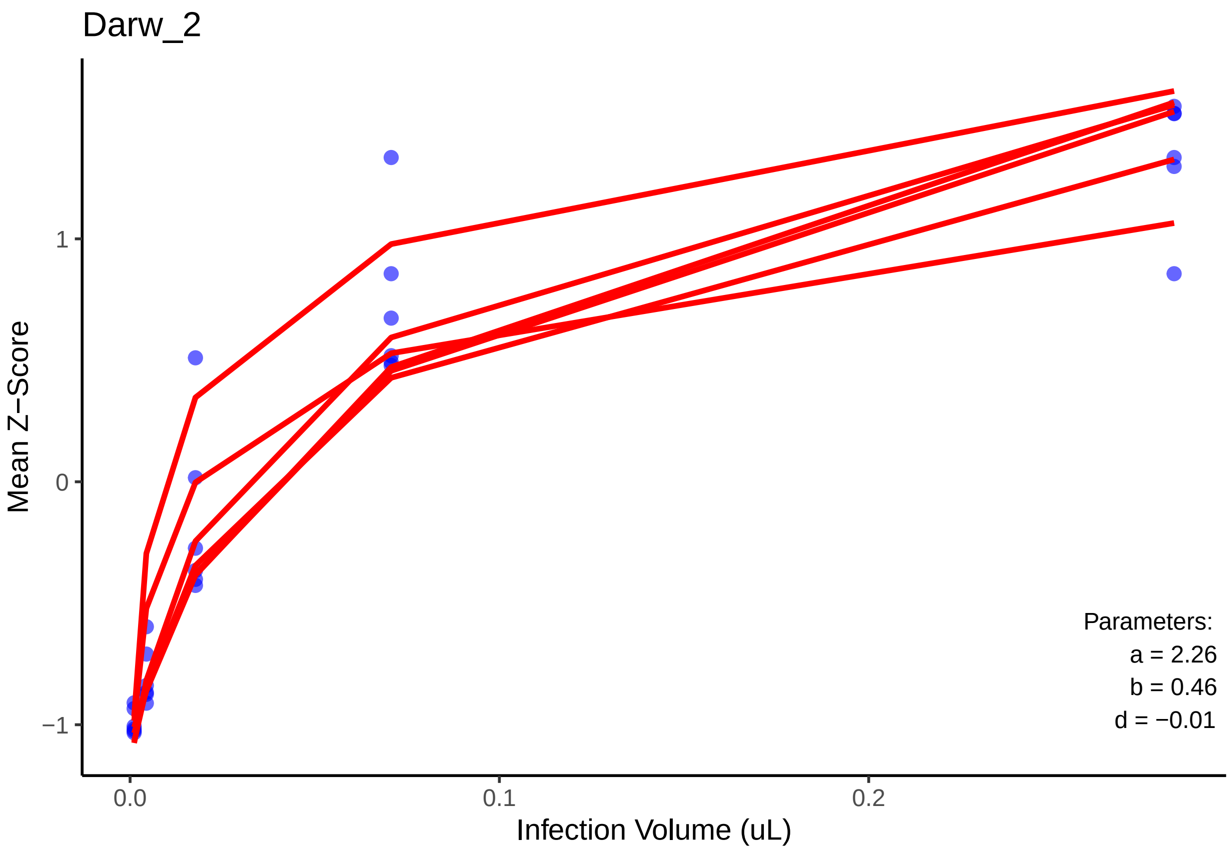
```
##
## $Coyi_3
```


Coyi_3
Mean Z−Score
Infection Volume (uL)
1
0
−1
0.0
0.1
0.2
Parameters:
a = 1.94
b = 0.42
d = −0.01

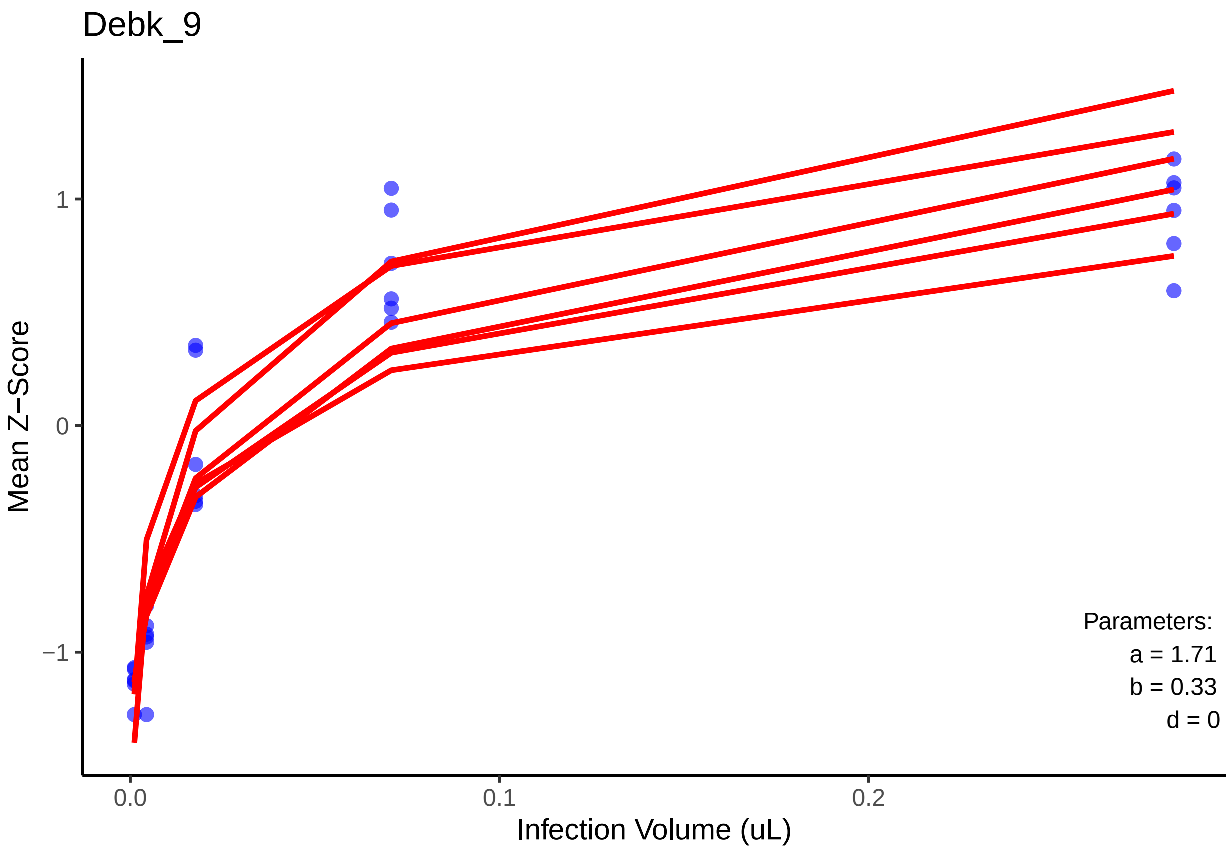
```
##
## $Dard_2
```


Dard_2
Mean Z−Score
Infection Volume (uL)
1.0
0.5
0.0
−0.5
−1.0
−1.5
0.0
0.1
0.2
Parameters:
a = 1.3
b = 0.26
d = 0

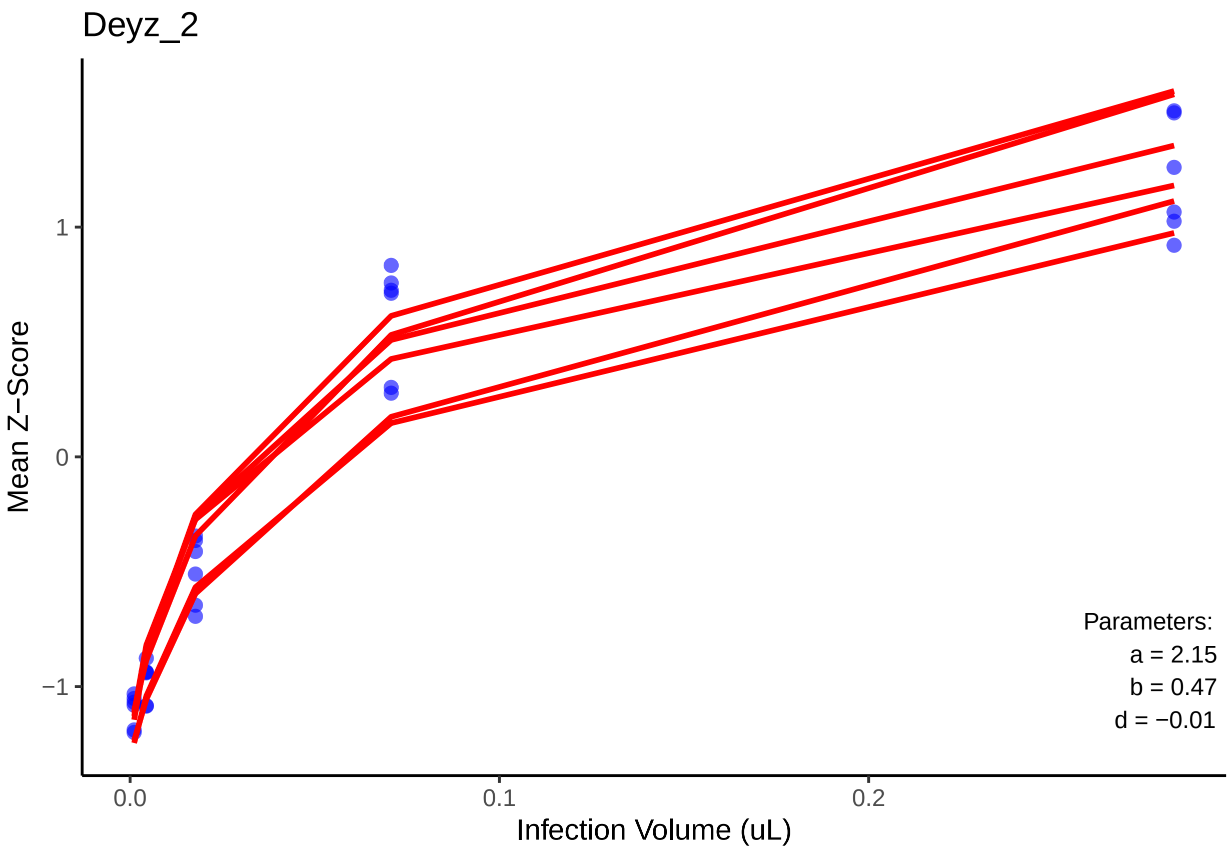
```
##
## $Darw_2
```


Darw_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.26
b = 0.46
d = −0.01

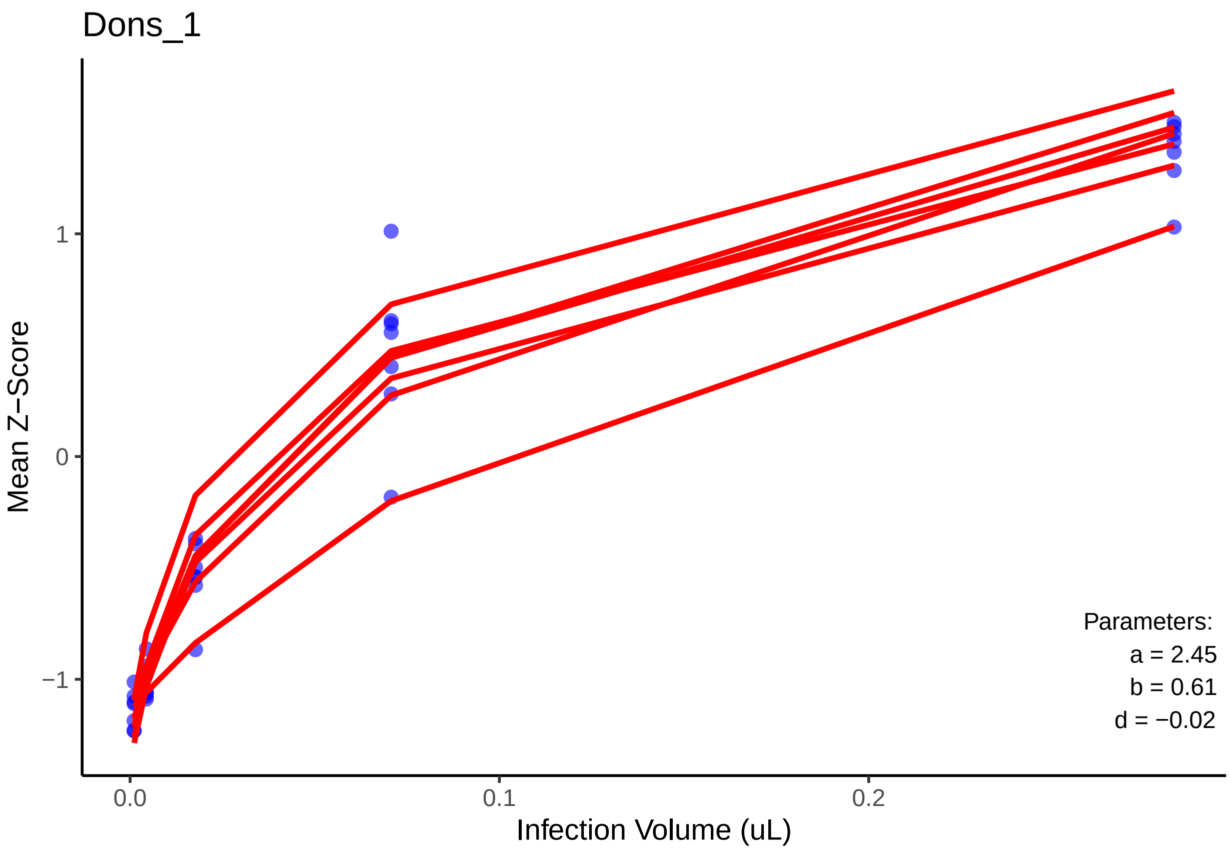
```
##
## $Debk_9
```


Debk_9
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.71
b = 0.33
d = 0

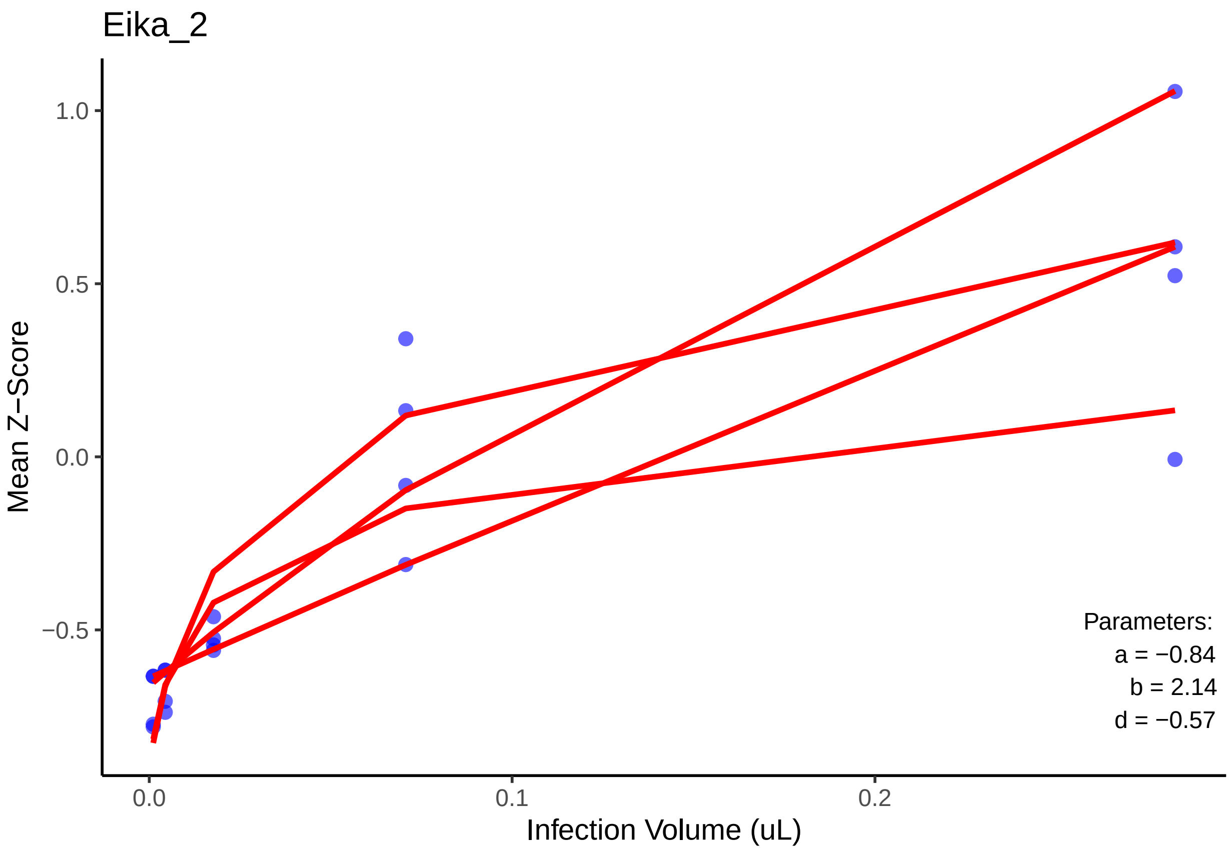
```
##
## $Deyz_2
```


Deyz_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.15
b = 0.47
d = −0.01

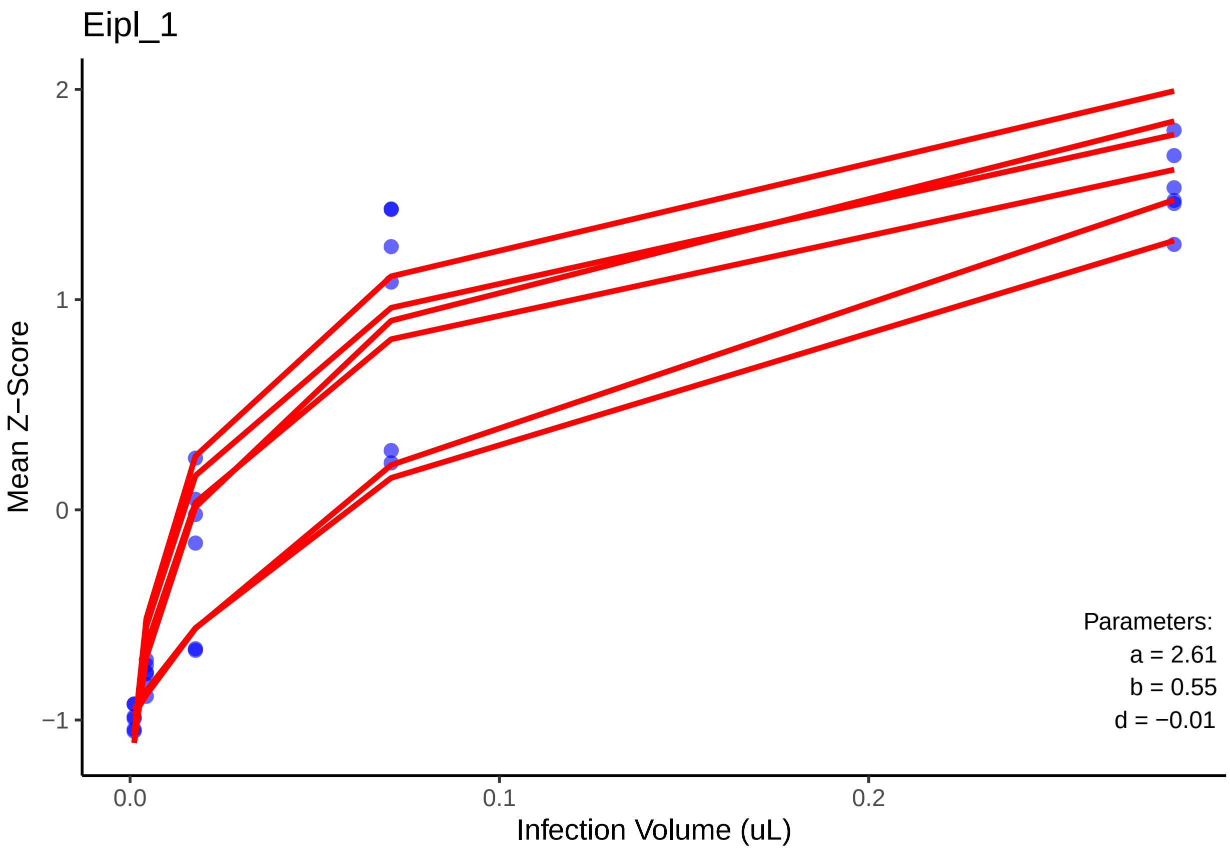
```
##
## $Dons_1
```


Dons_1
Mean Z−Score
Infection Volume (uL)
Parameters:
a = 2.45
b = 0.61
d = −0.02
1
0
−1
0.0
0.1
0.2

```
##
## $Eika_2
```


Eika_2
1.0
0.5
0.0
−0.5
Mean Z−Score
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = −0.84
b = 2.14
d = −0.57

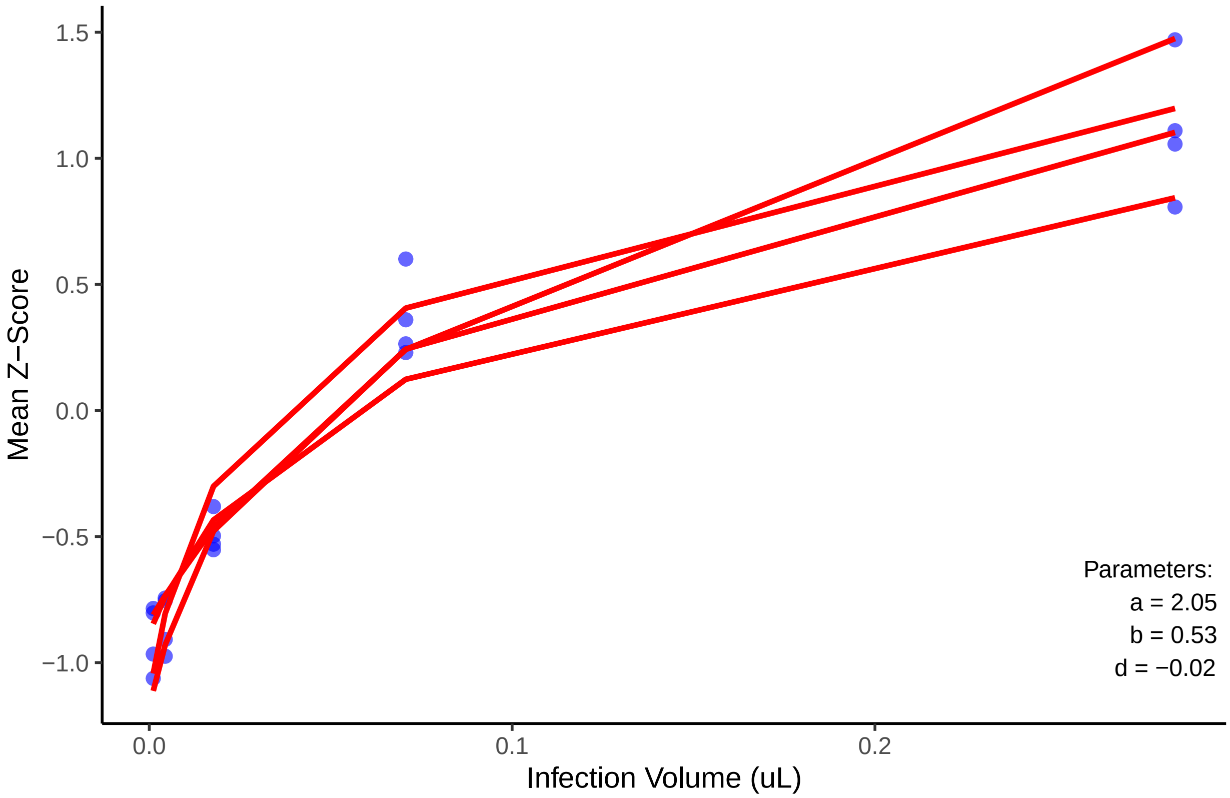
```
##
## $Eipl_1
```



Eipl_1
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.61
b = 0.55
d = −0.01

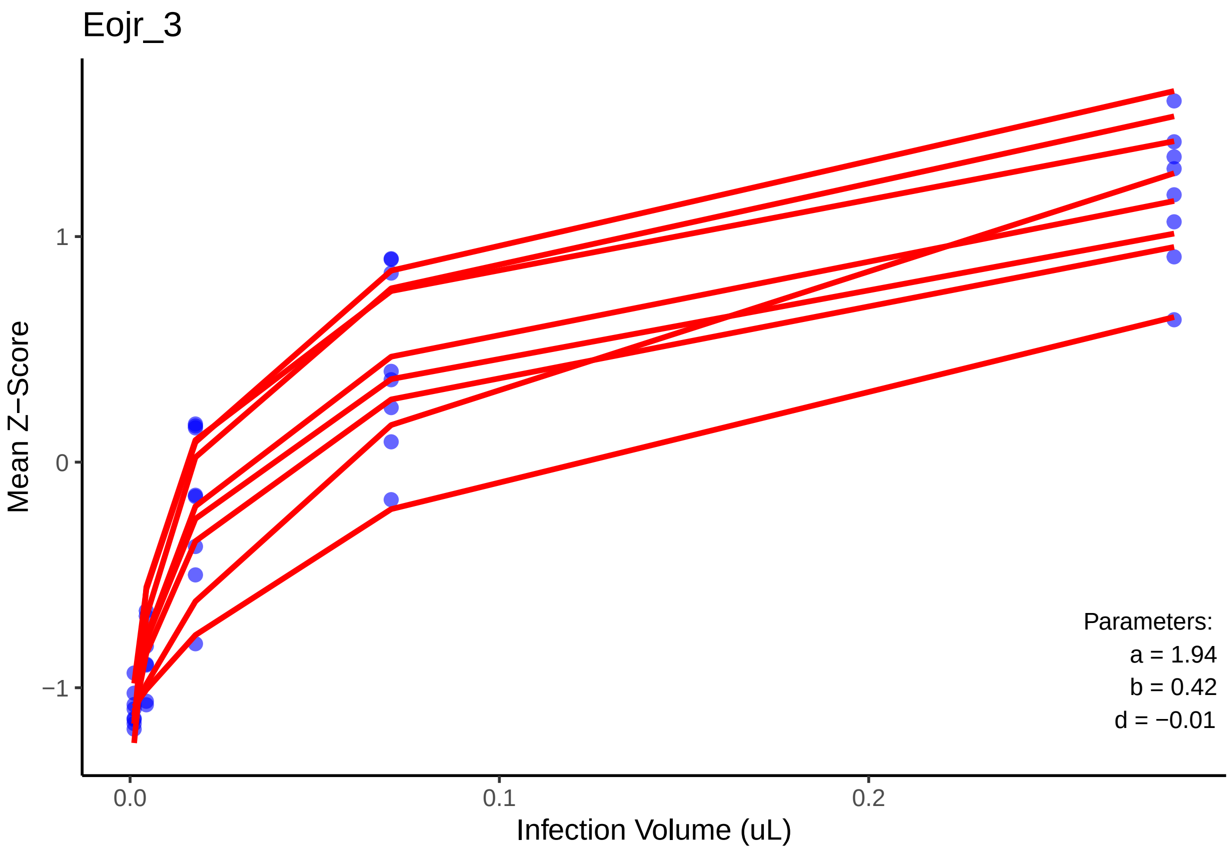

```
##
## $Eiwy_1
```

Eiwy_1

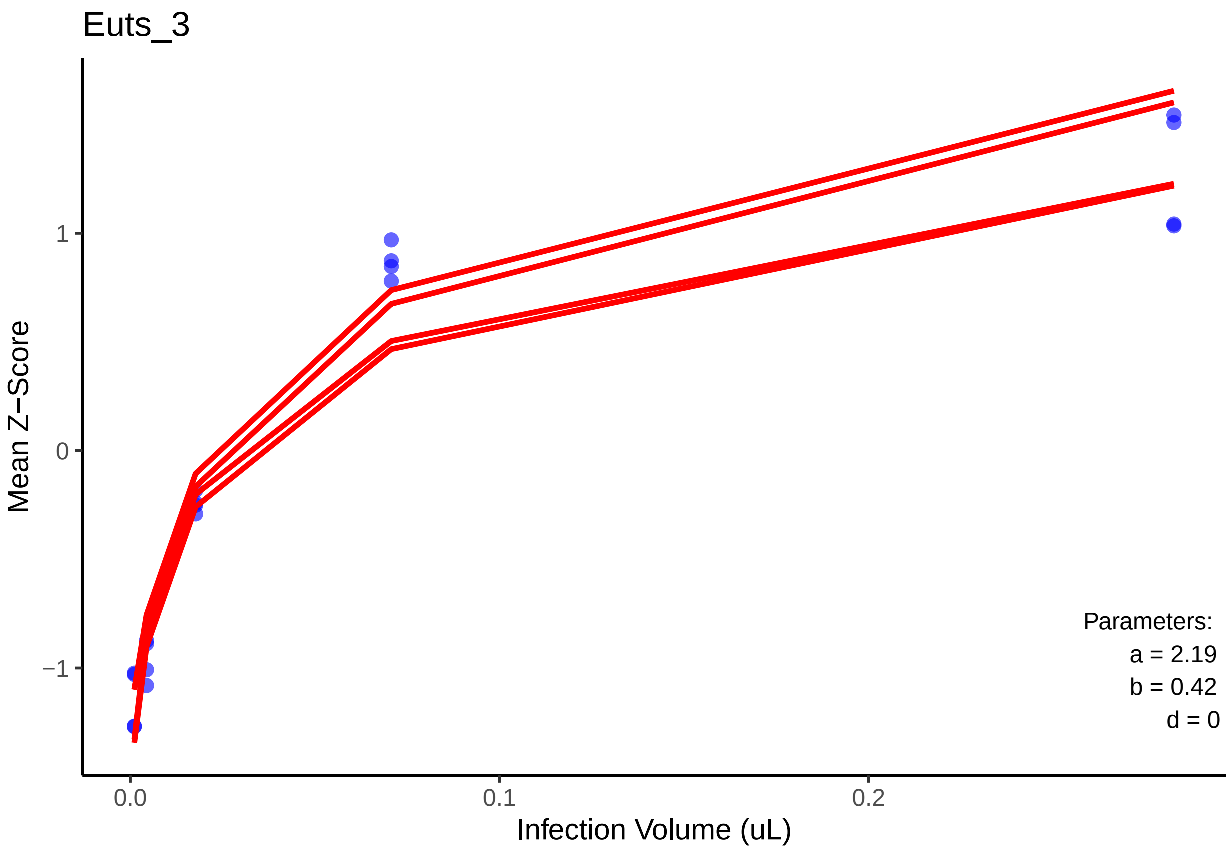


Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.05
b = 0.53
d = −0.02

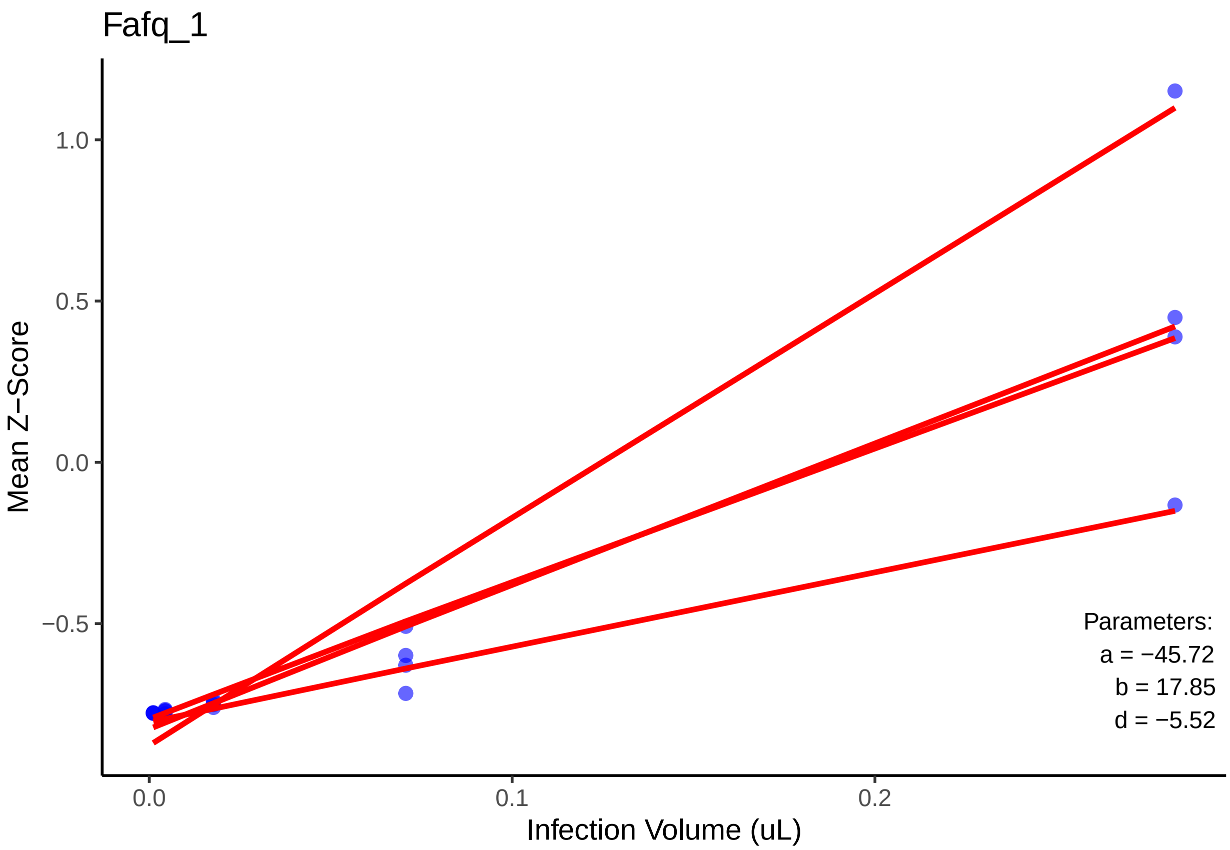

```
##
## $Eojr_3
```


Eojr_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.94
b = 0.42
d = −0.01

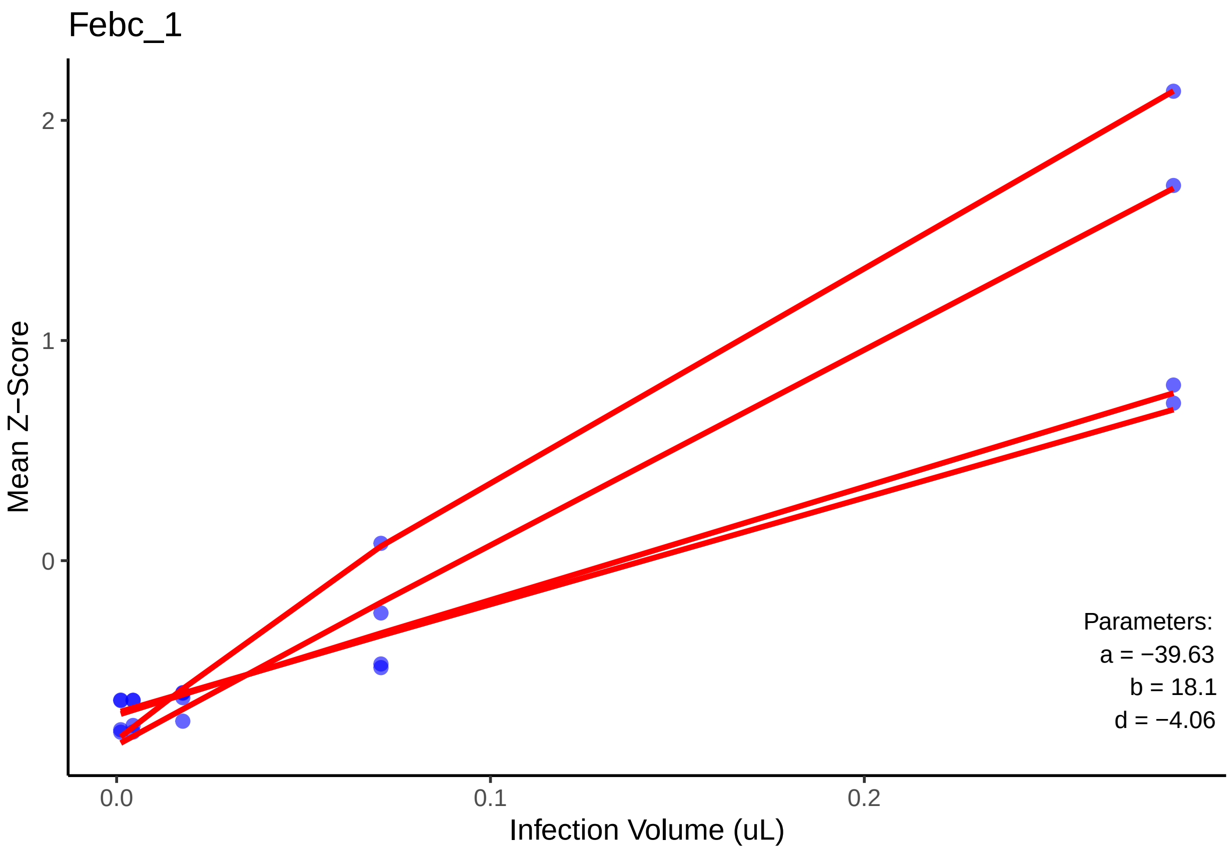
```
##
## $Euts_3
```


Euts_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.19
b = 0.42
d = 0

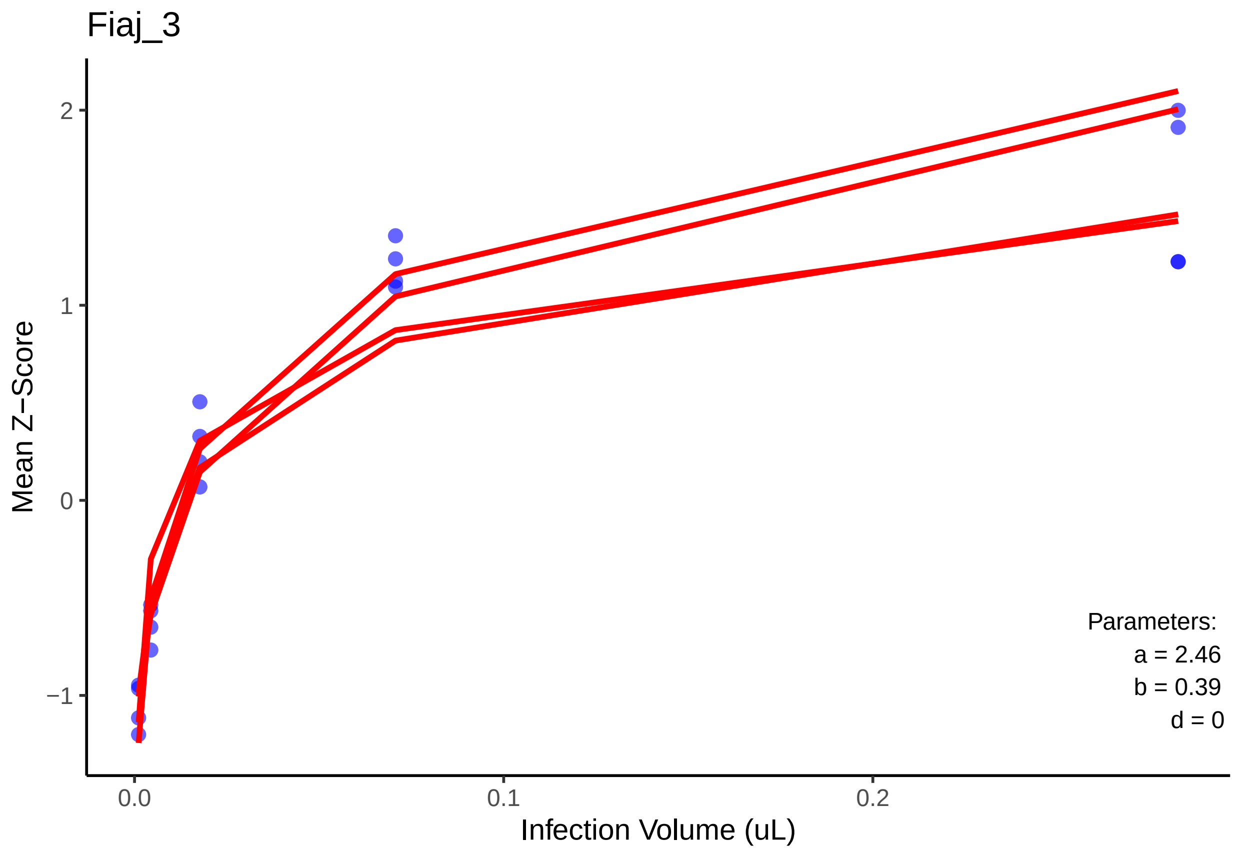
```
##
## $Fafq_1
```


Fafq_1
Mean Z−Score
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = −45.72
b = 17.85
d = −5.52

```
##
## $Febc_1
```

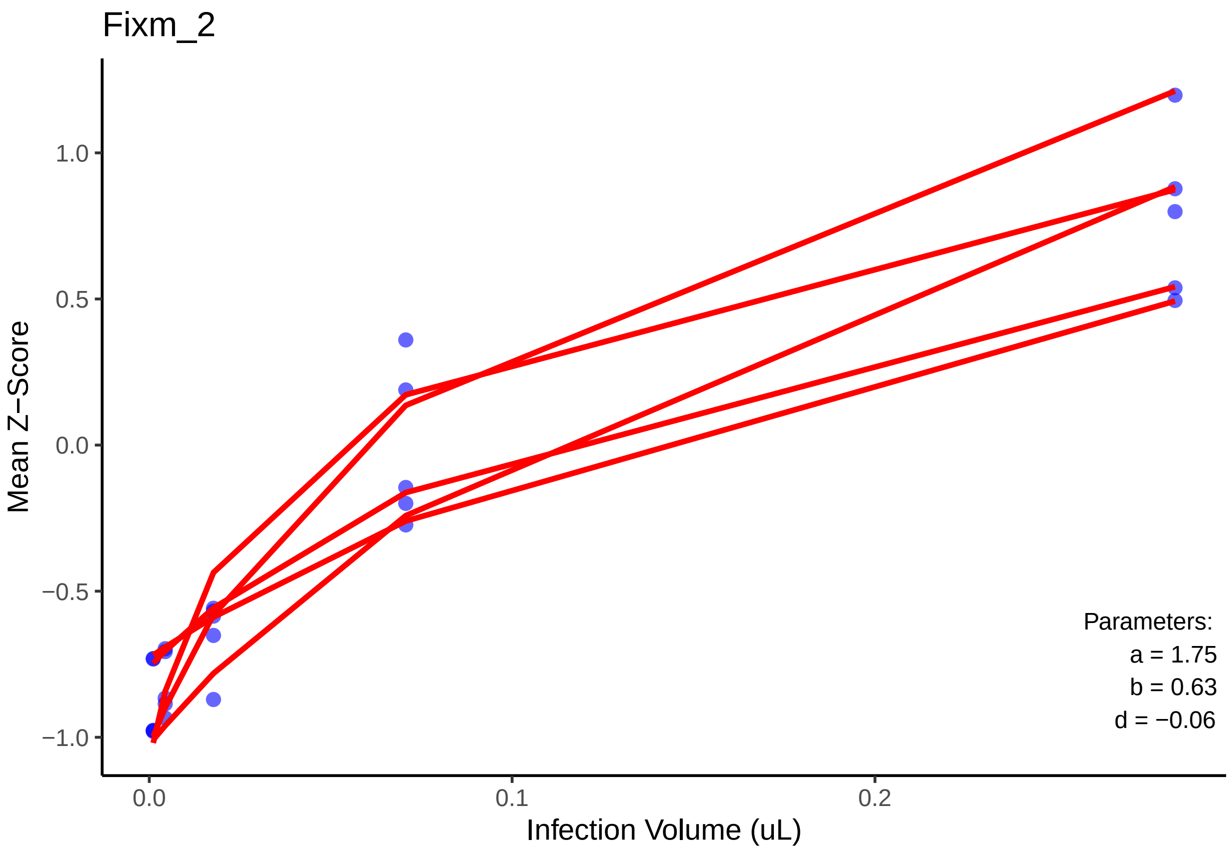

Febc_1
Mean Z−Score
2
1
0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = −39.63
b = 18.1
d = −4.06

```
##
## $Fiaj_3
```

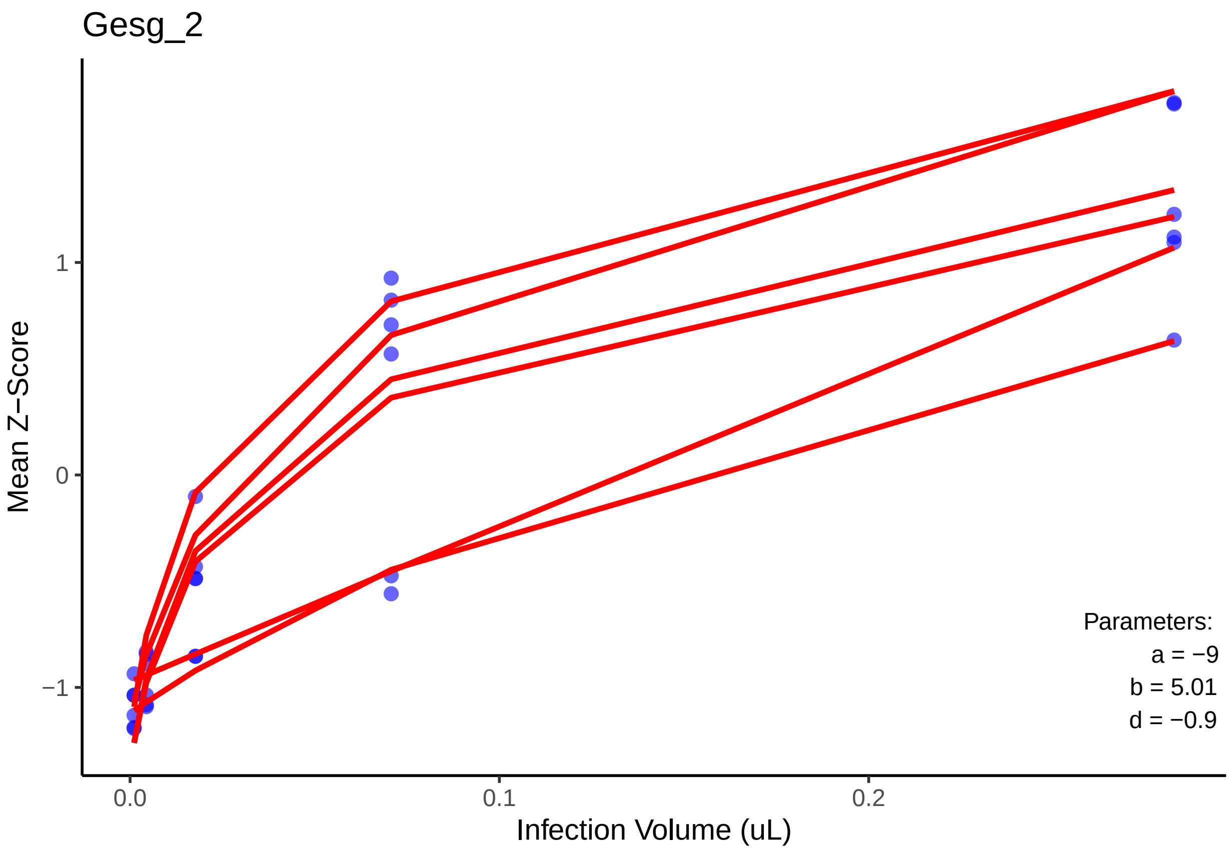


Fiaj_3
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.46
b = 0.39
d = 0

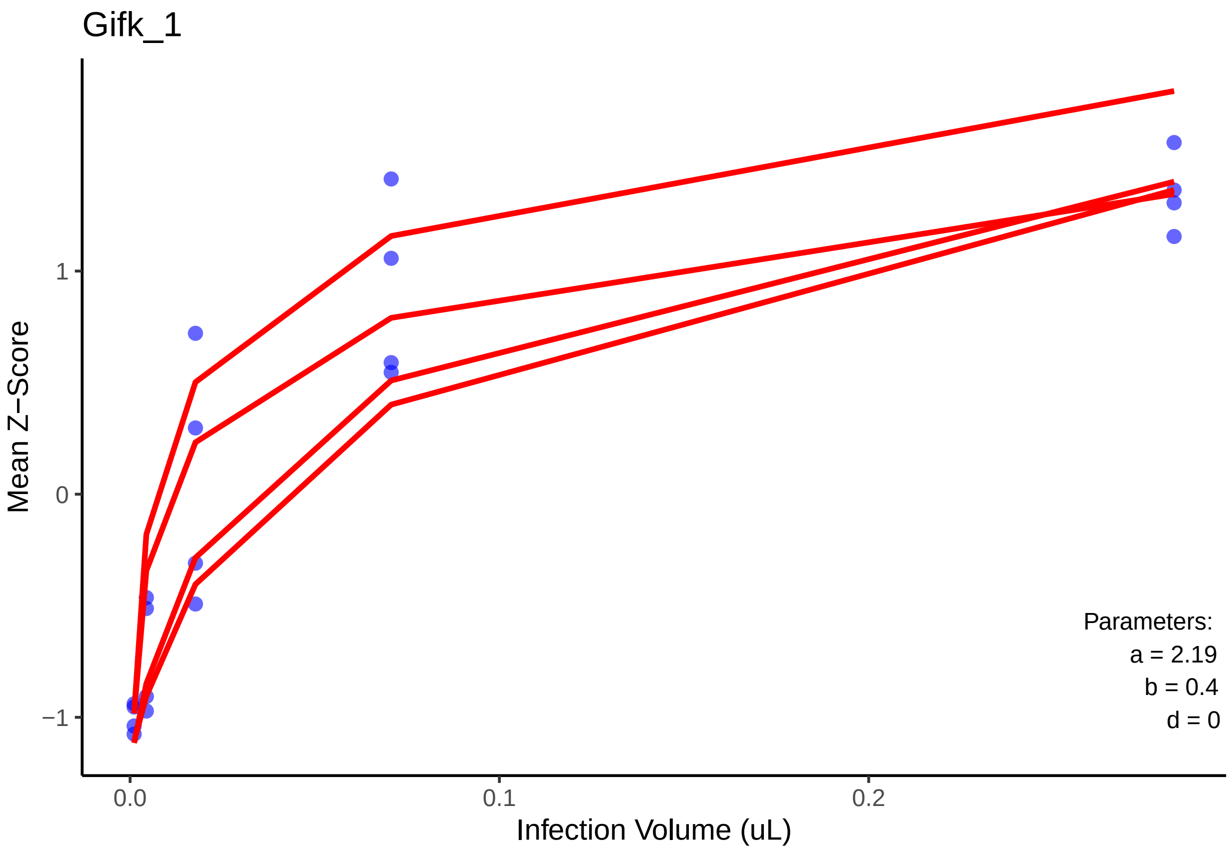

```
##
## $Fixm_2
```


Fixm_2
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.75
b = 0.63
d = −0.06

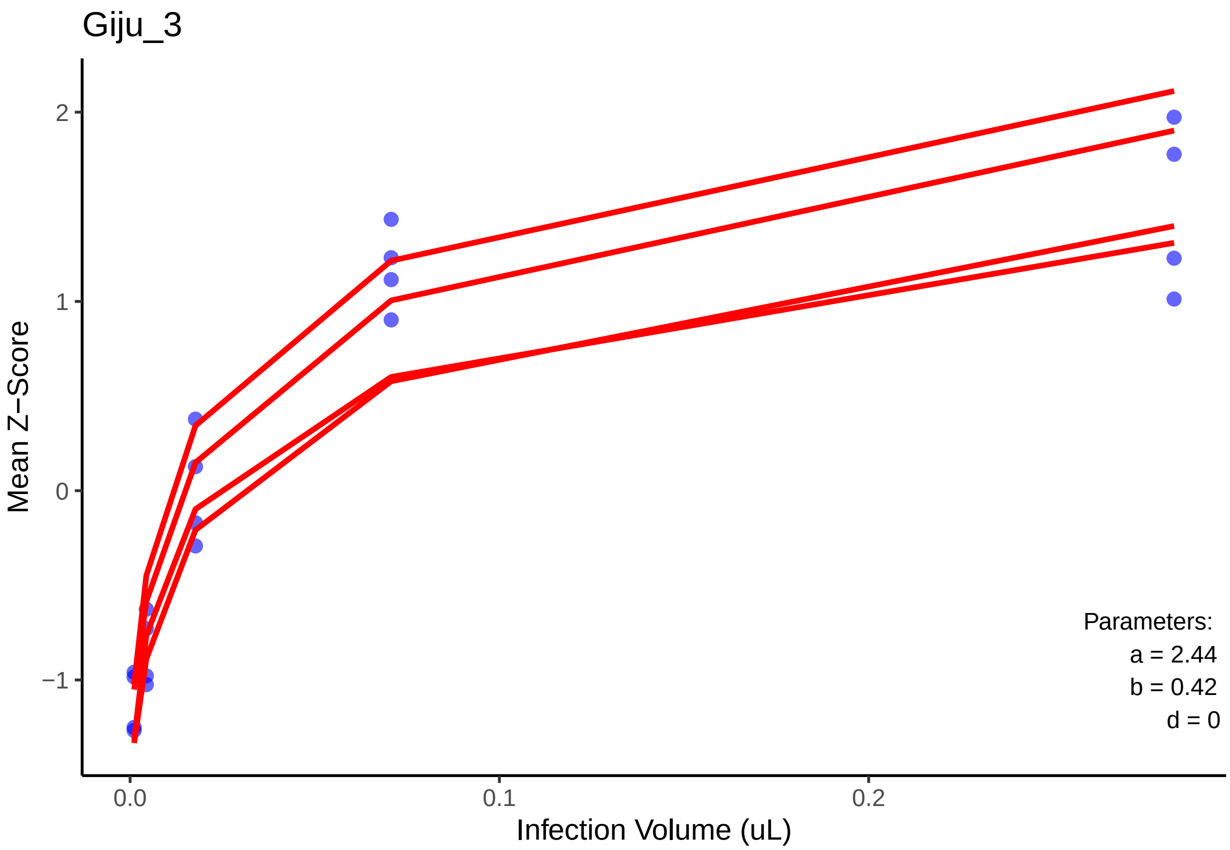
```
##
## $Gesg_2
```


Gesg_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = −9
b = 5.01
d = −0.9

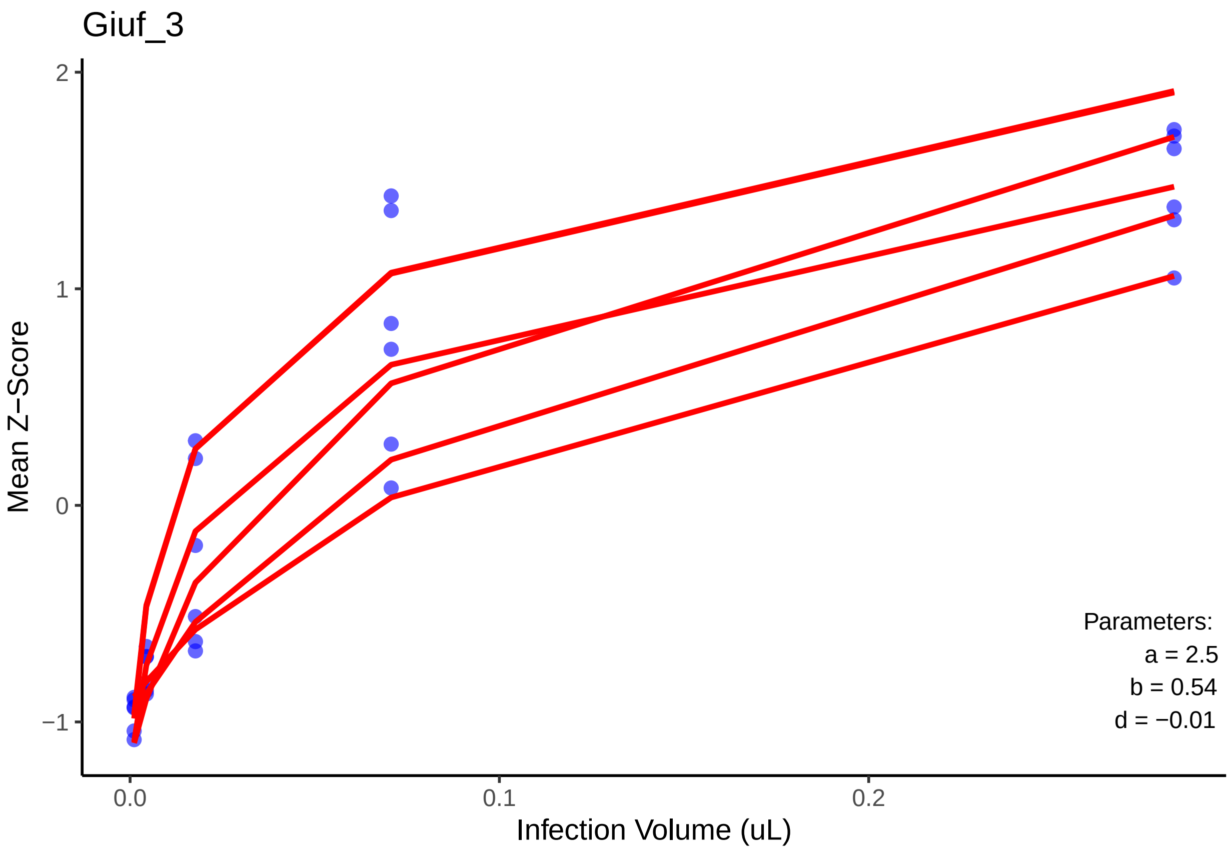
```
##
## $Gifk_1
```


Gifk_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.19
b = 0.4
d = 0

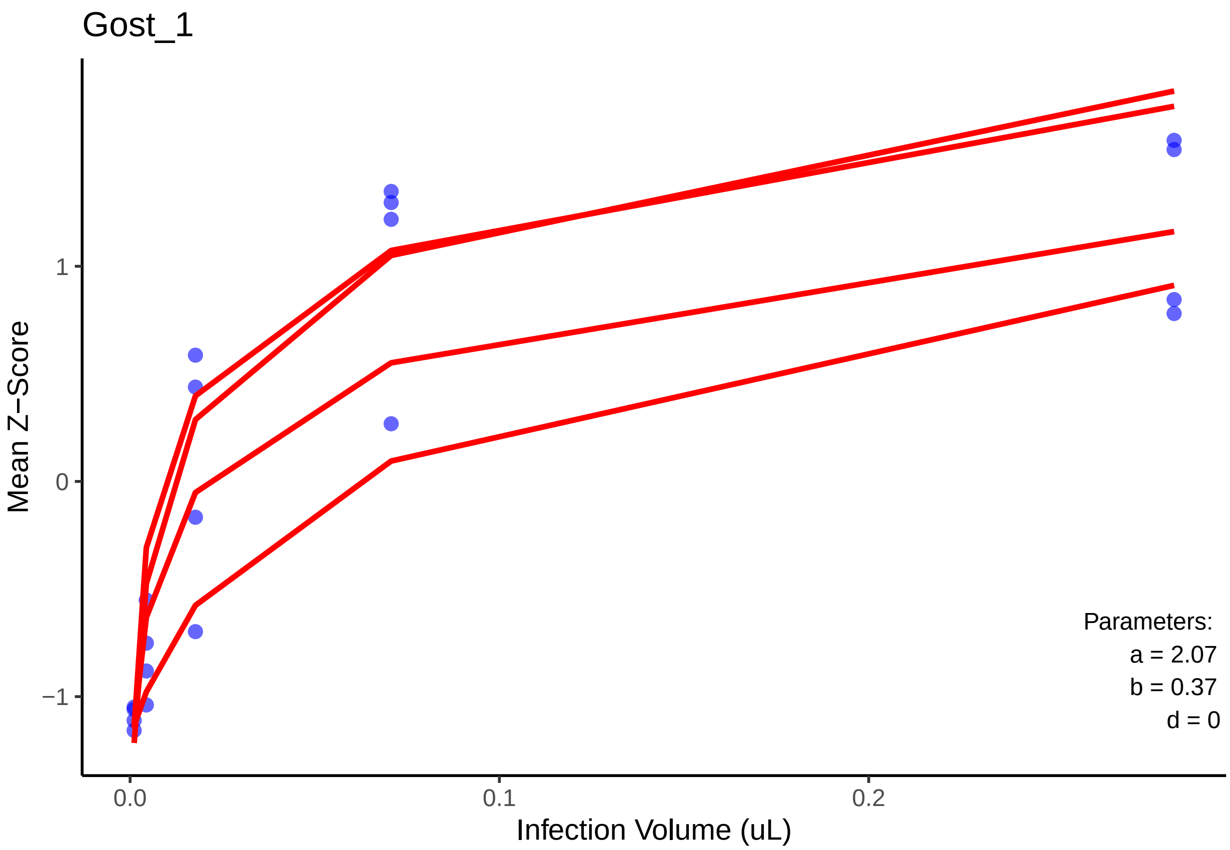
```
##
## $Giju_3
```


Giju_3
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.44
b = 0.42
d = 0

```
##
## $Giuf_3
```

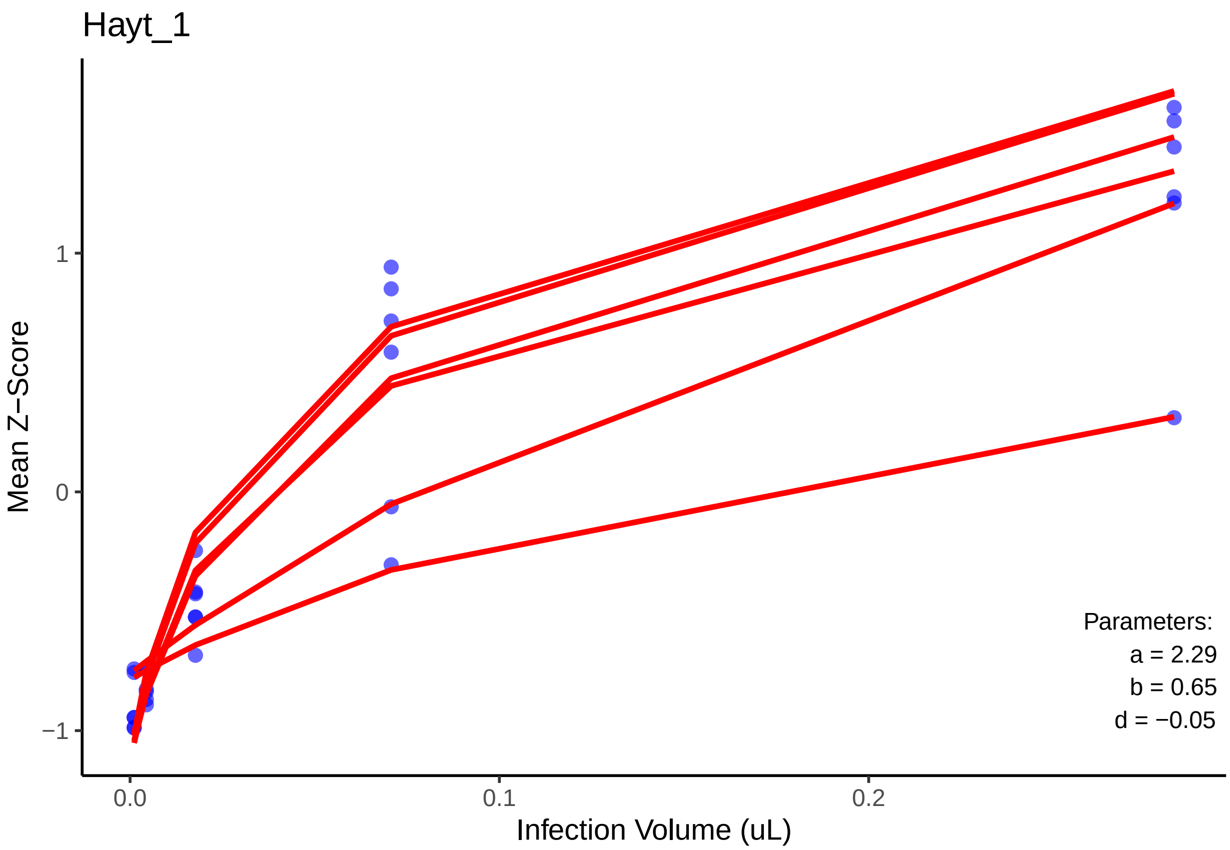

Giuf_3
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.5
b = 0.54
d = −0.01

```
##
## $Gost_1
```

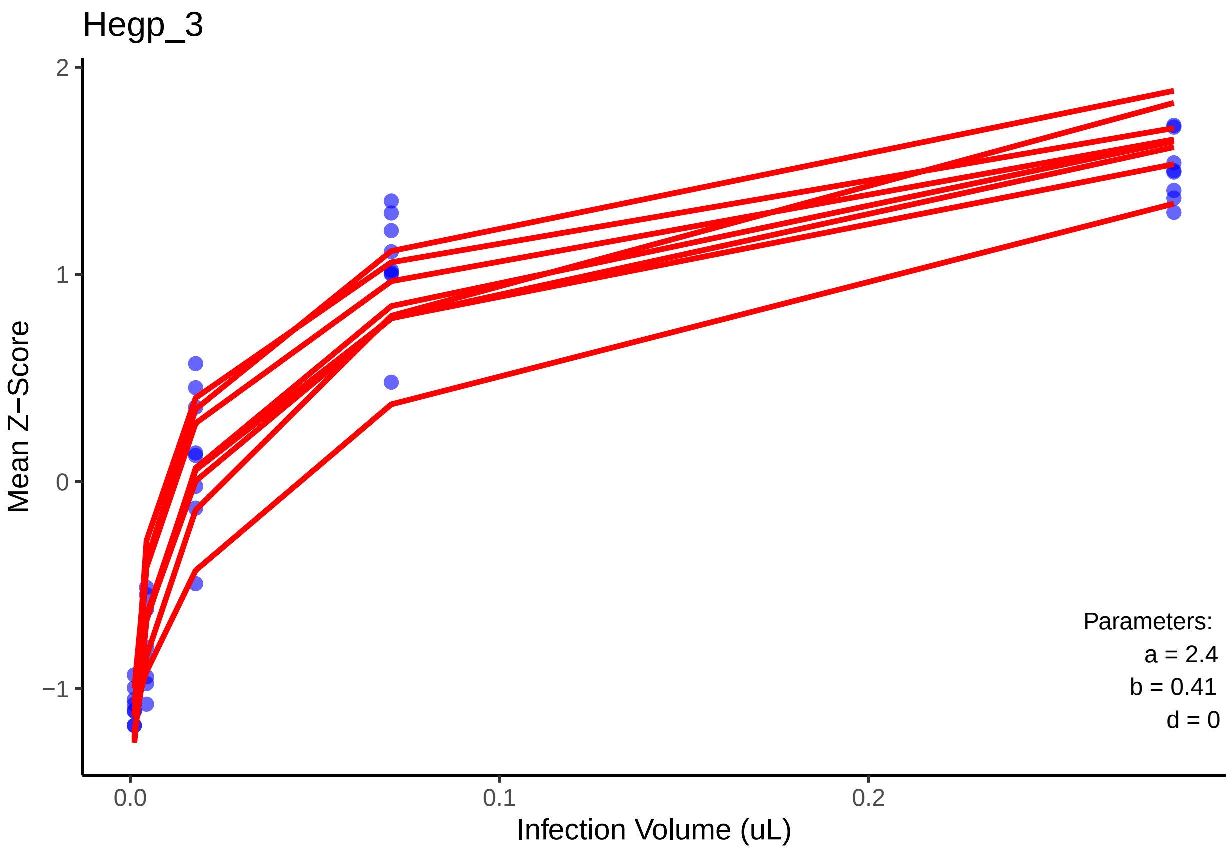


Gost_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.07
b = 0.37
d = 0

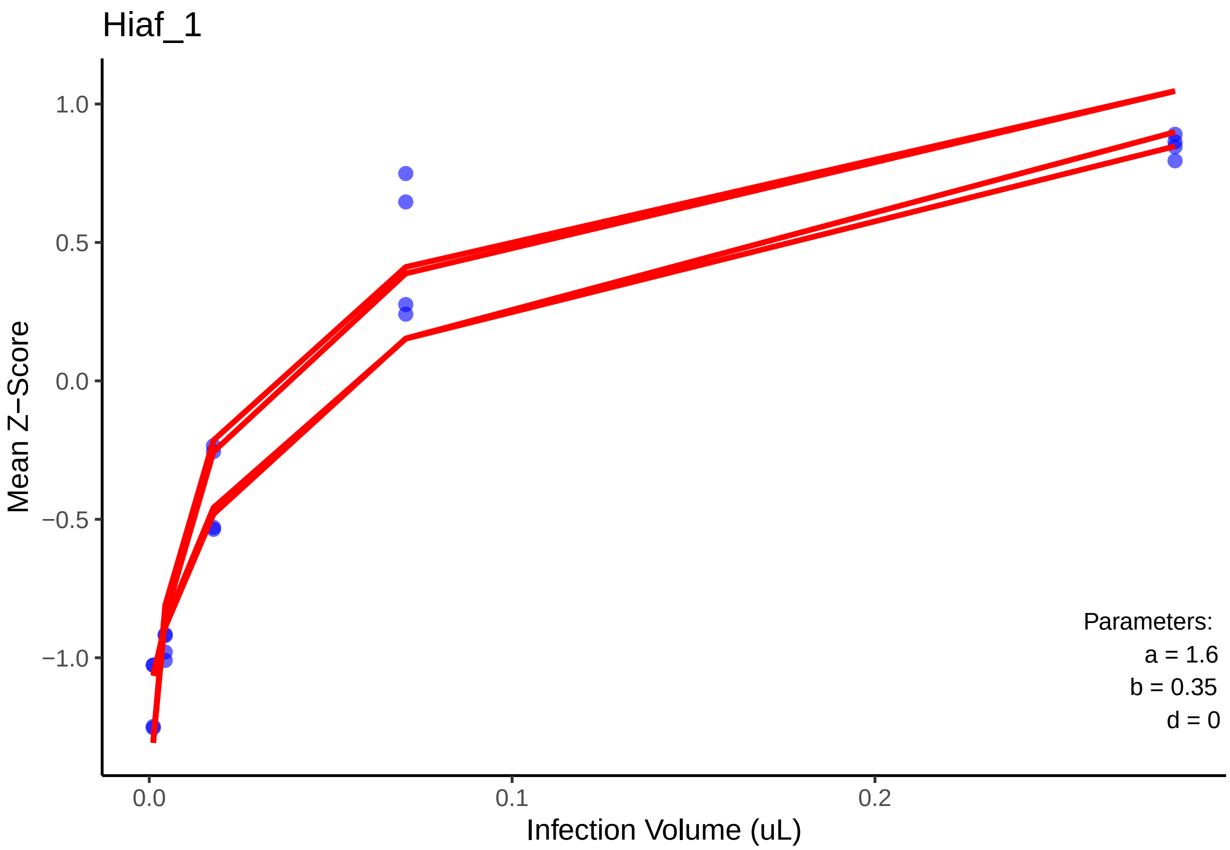

```
##
## $Hayt_1
```


Hayt_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.29
b = 0.65
d = −0.05

```
##
## $Hegp_3
```

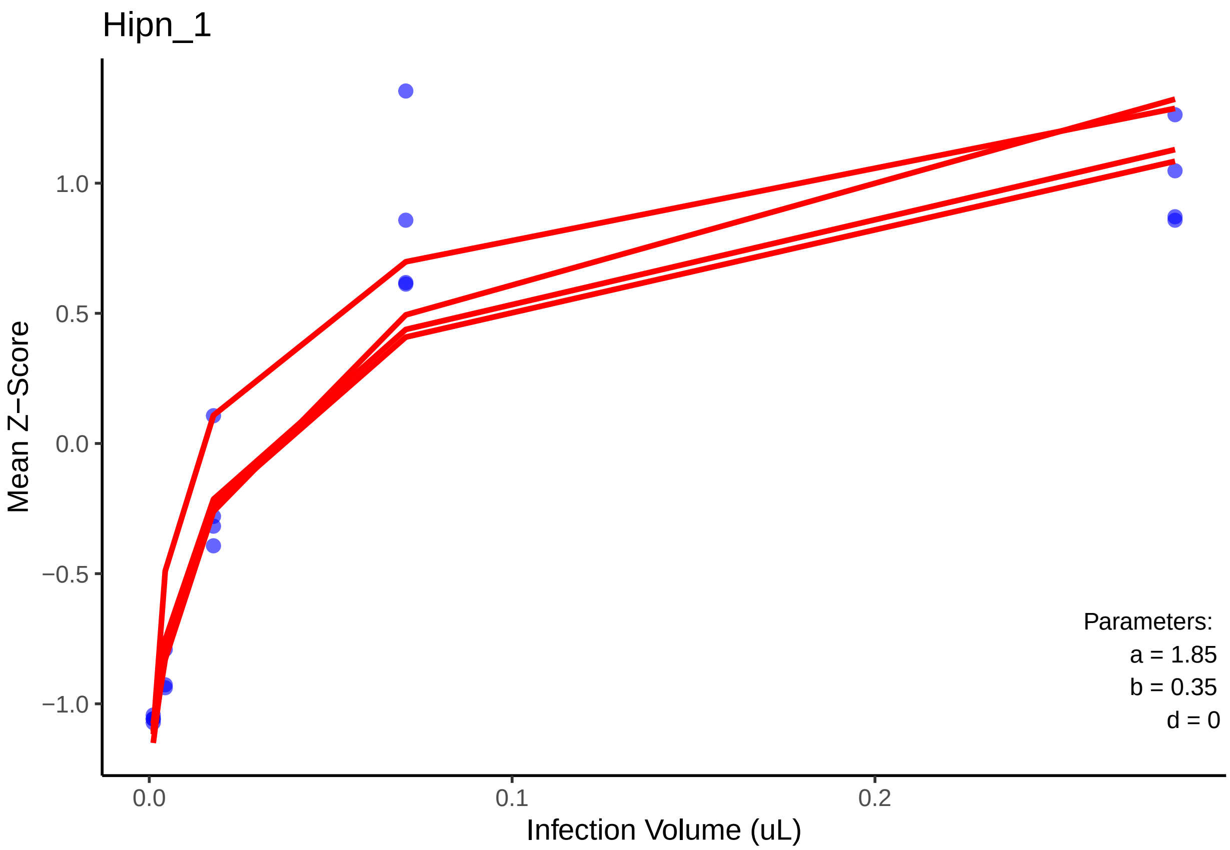

Hegp_3
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.4
b = 0.41
d = 0

```
##
## $Hiaf_1
```

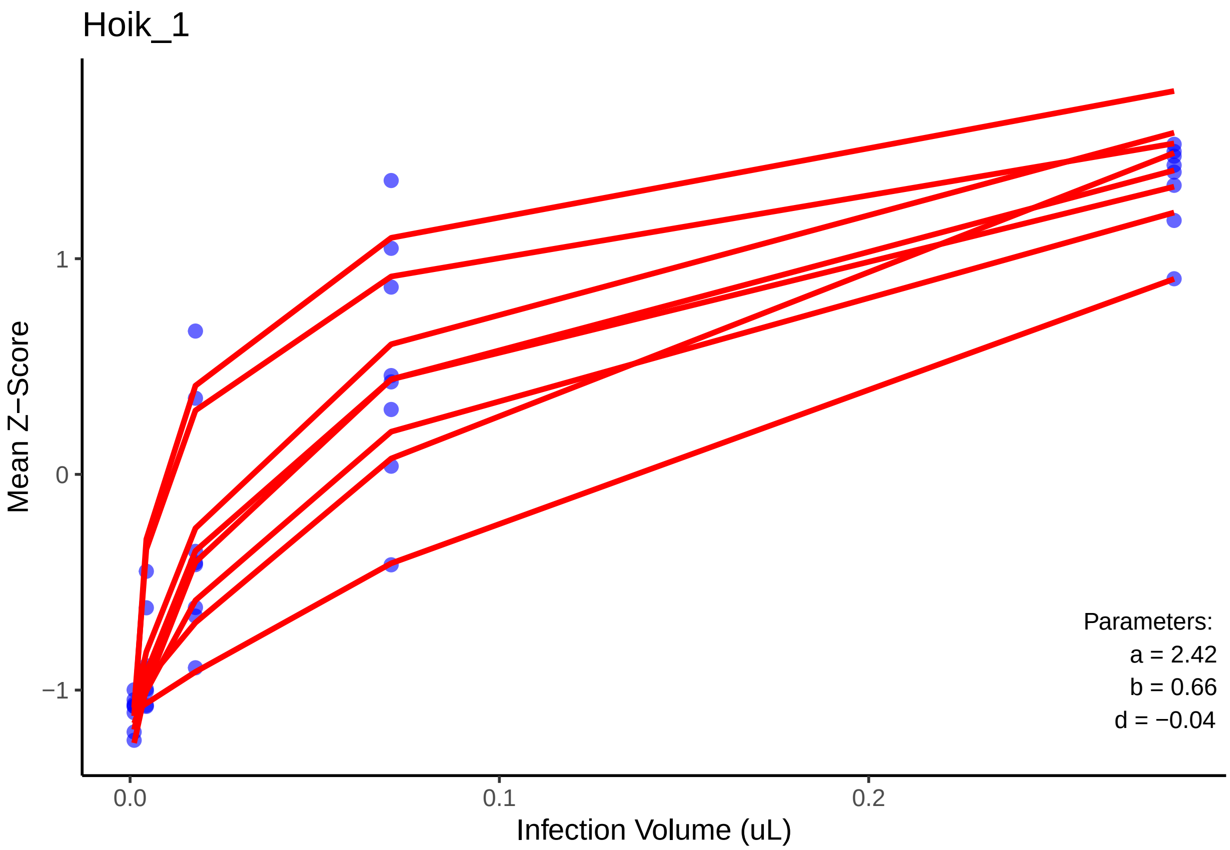


Hiaf_1
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.6
b = 0.35
d = 0

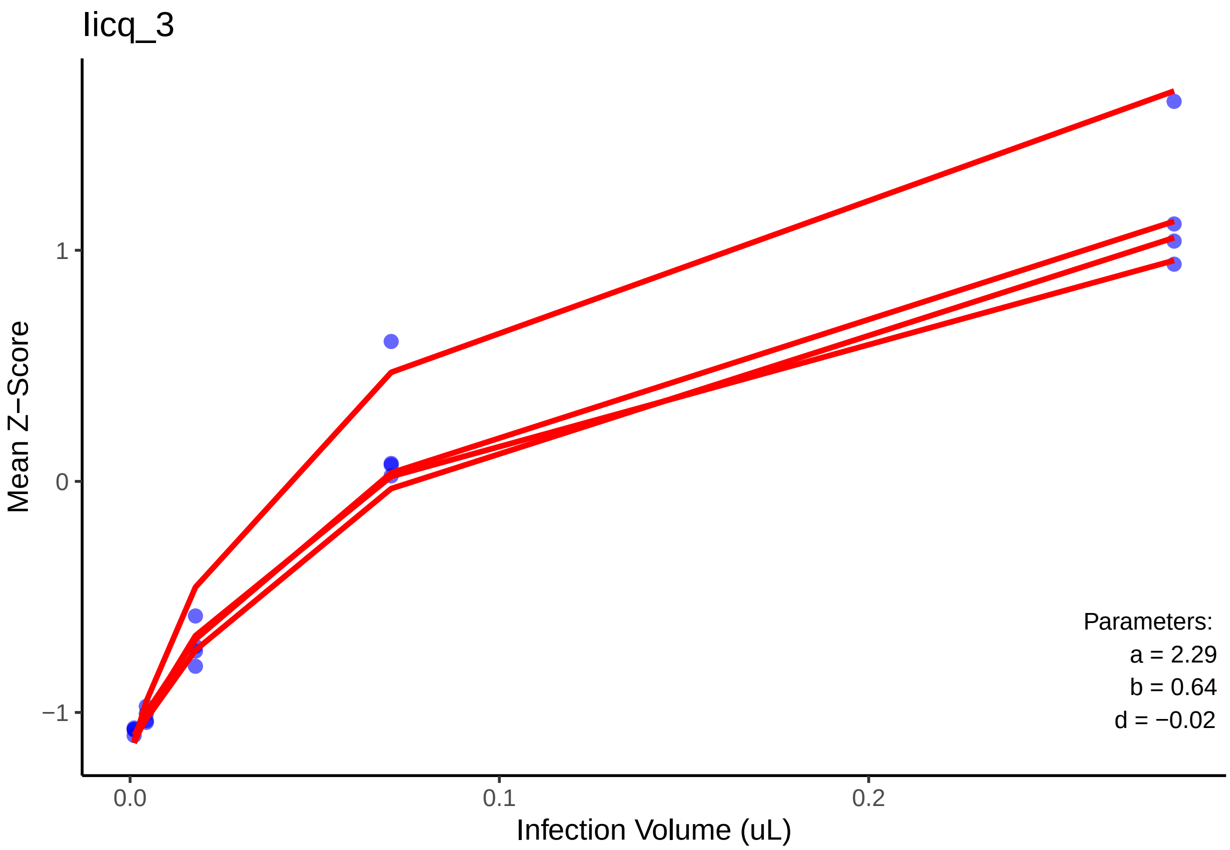

```
##
## $Hipn_1
```


Hipn_1
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.85
b = 0.35
d = 0

```
##
## $Hoik_1
```

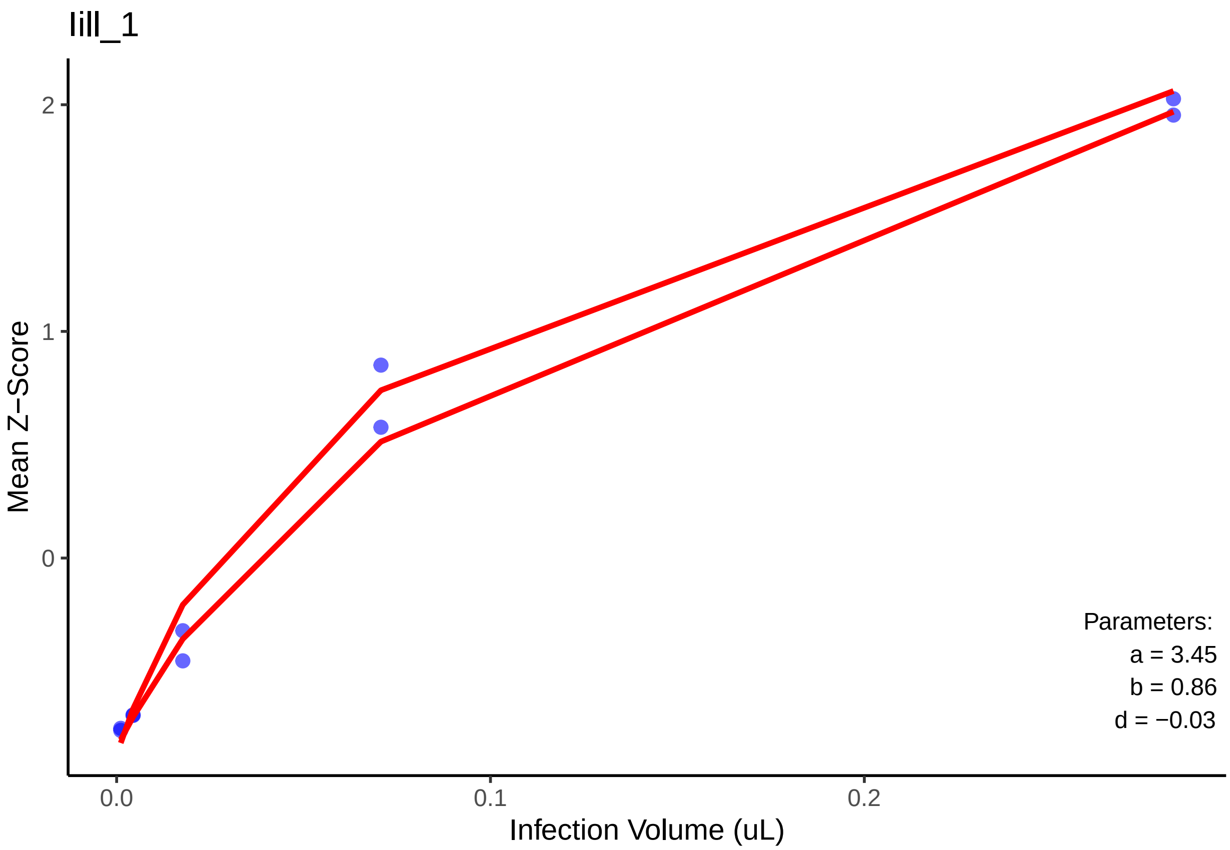

Hoik_1
Mean Z−Score
Infection Volume (uL)
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.42
b = 0.66
d = −0.04

```
##
## $Iicq_3
```



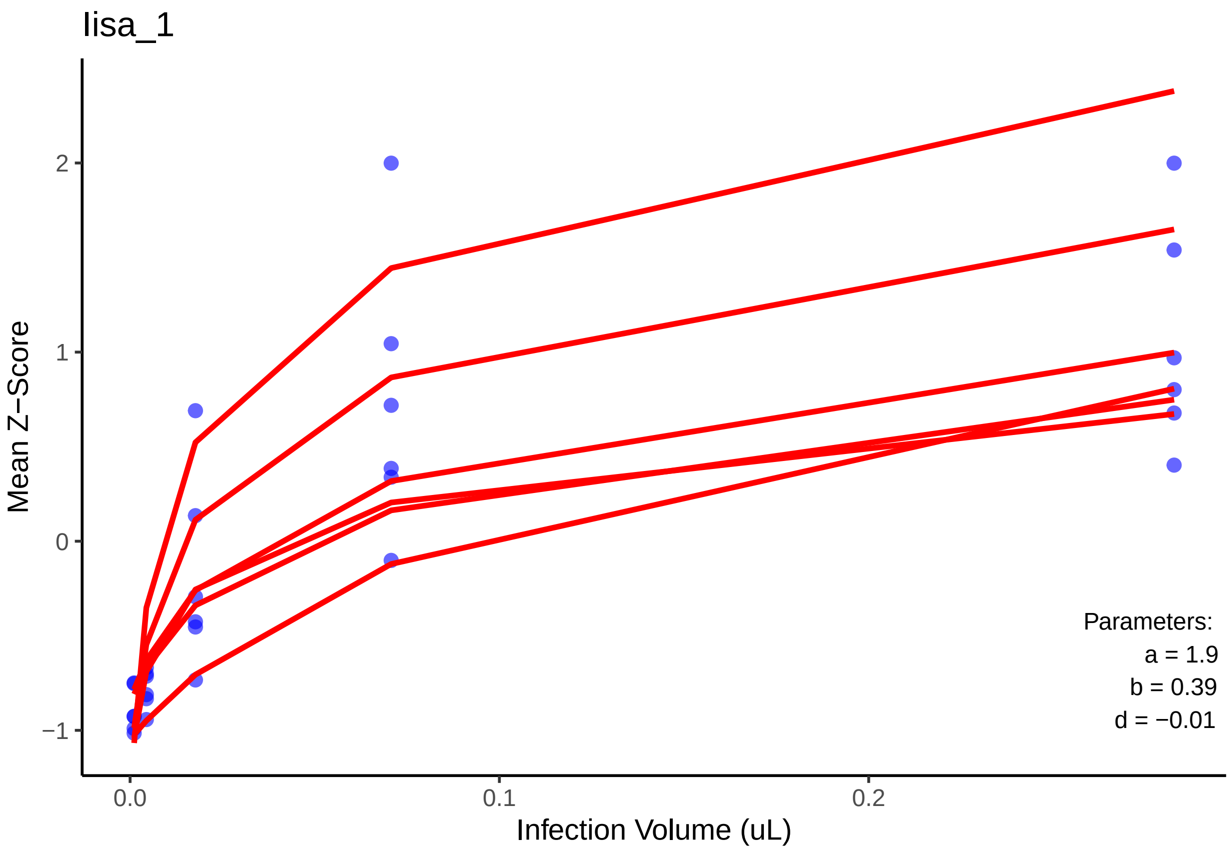
Iicq_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.29
b = 0.64
d = −0.02


```
##
## $Iill_1
```

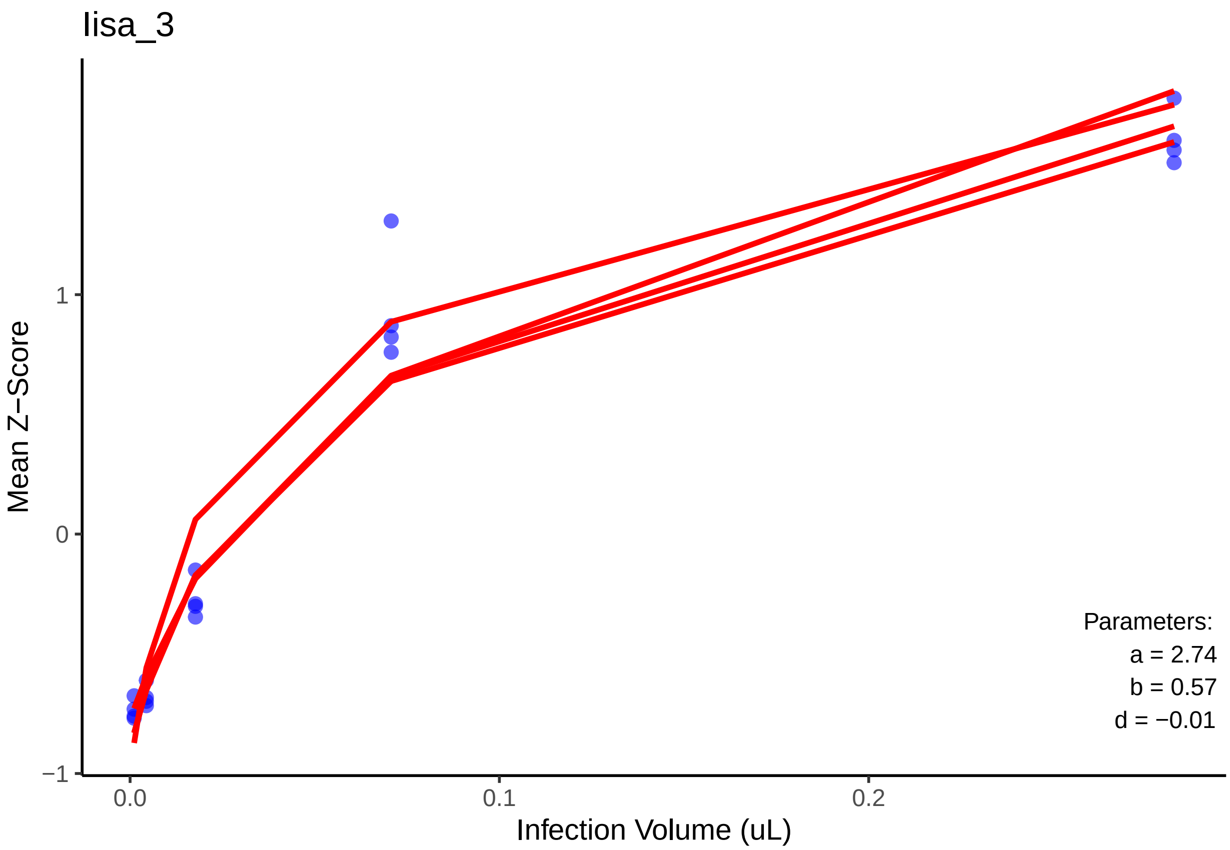


Iill_1
Mean Z−Score
2
1
0
Parameters:
a = 3.45
b = 0.86
d = −0.03
0.0
0.1
0.2
Infection Volume (uL)

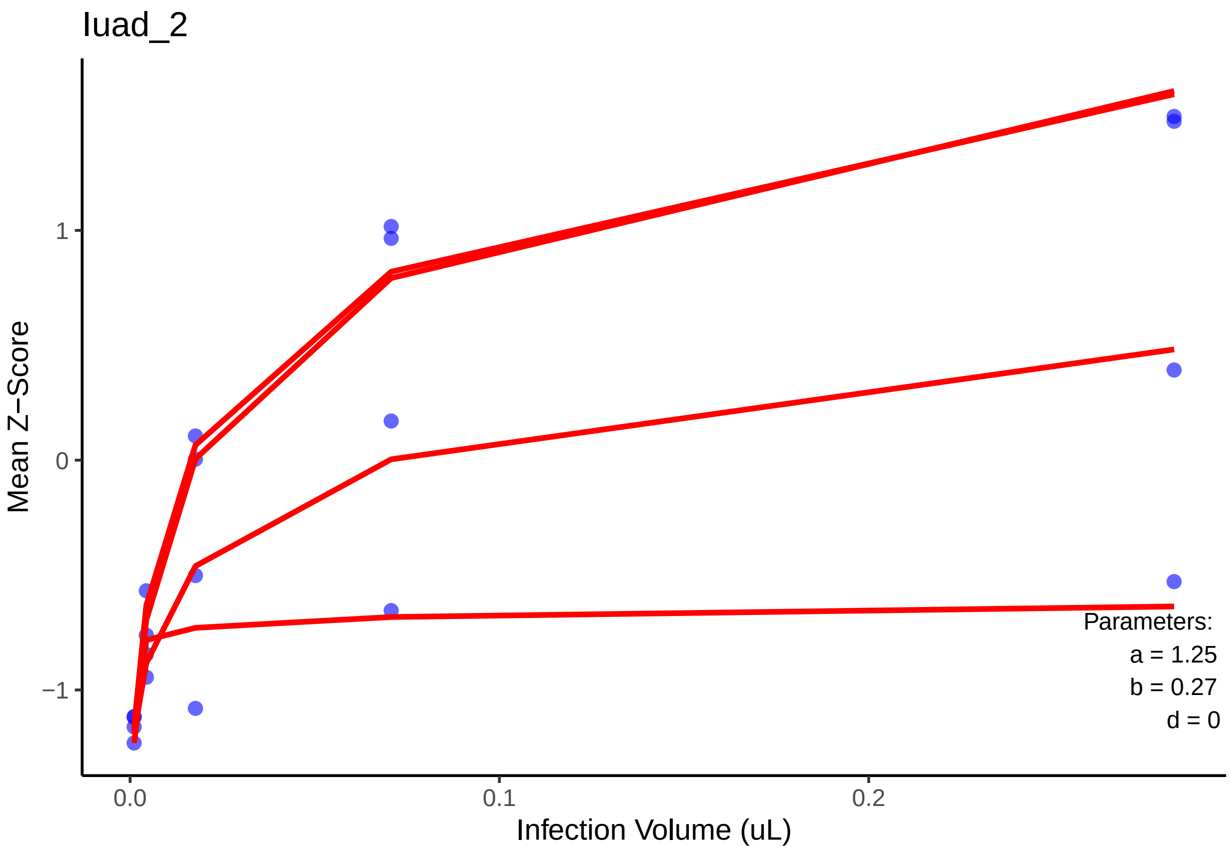

```
##
## $Iisa_1
```


Iisa_1
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.9
b = 0.39
d = −0.01

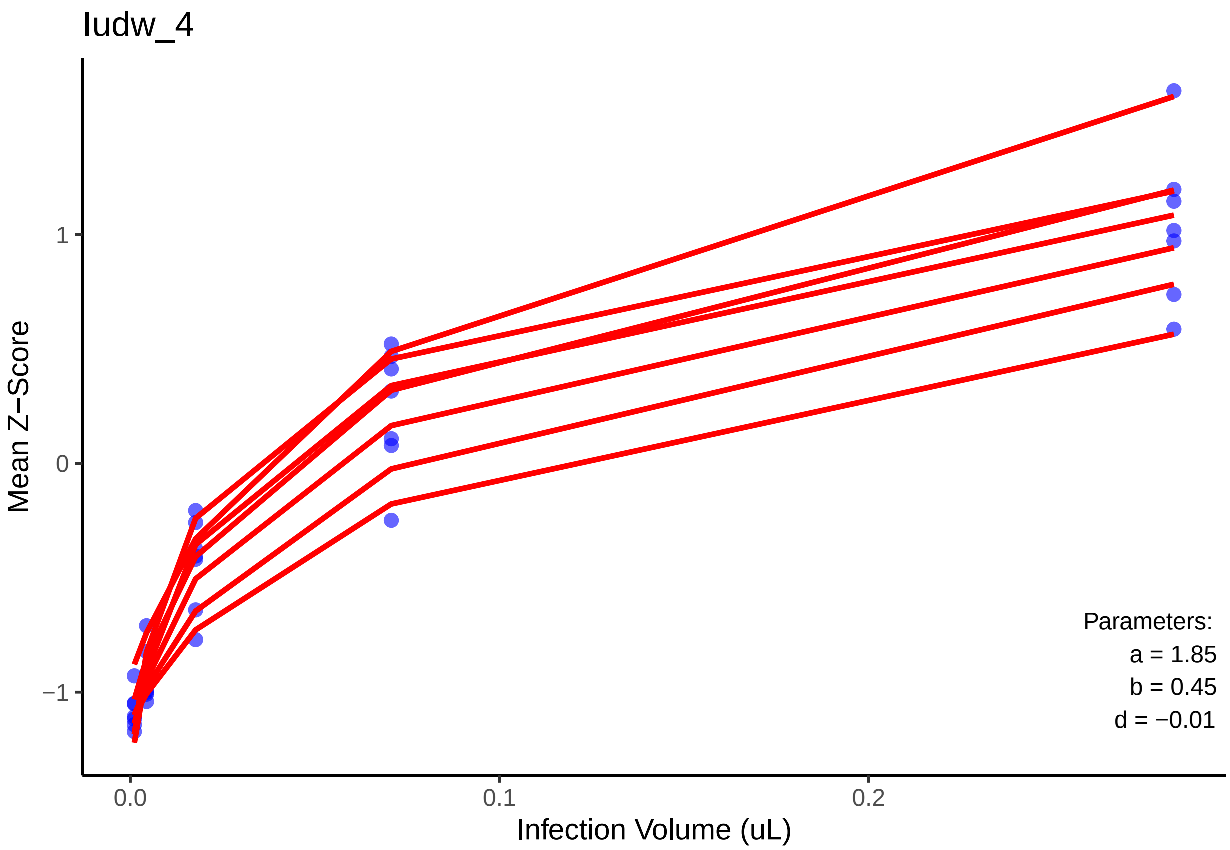
```
##
## $Iisa_3
```


lisa_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.74
b = 0.57
d = −0.01

```
##
## $luad_2
```

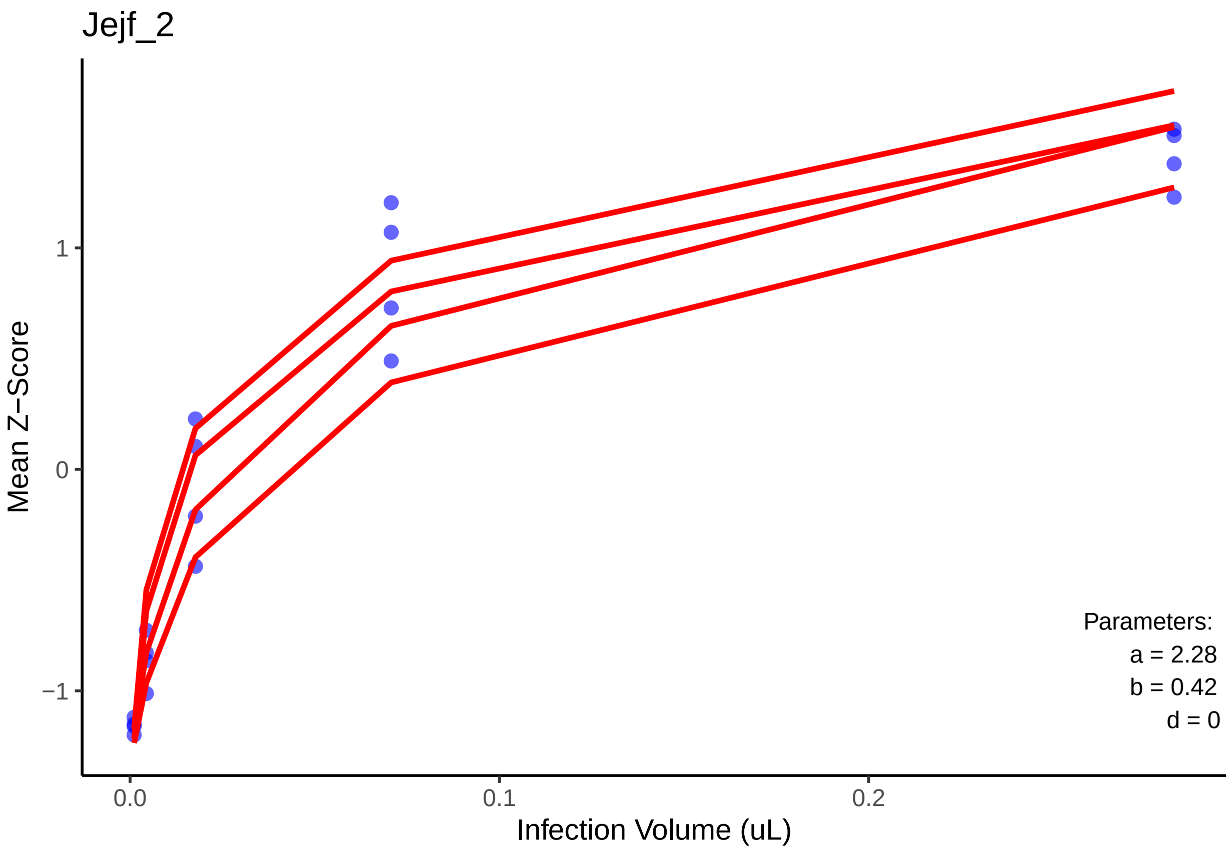

Iuad_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.25
b = 0.27
d = 0

```
##
## $Iudw_4
```

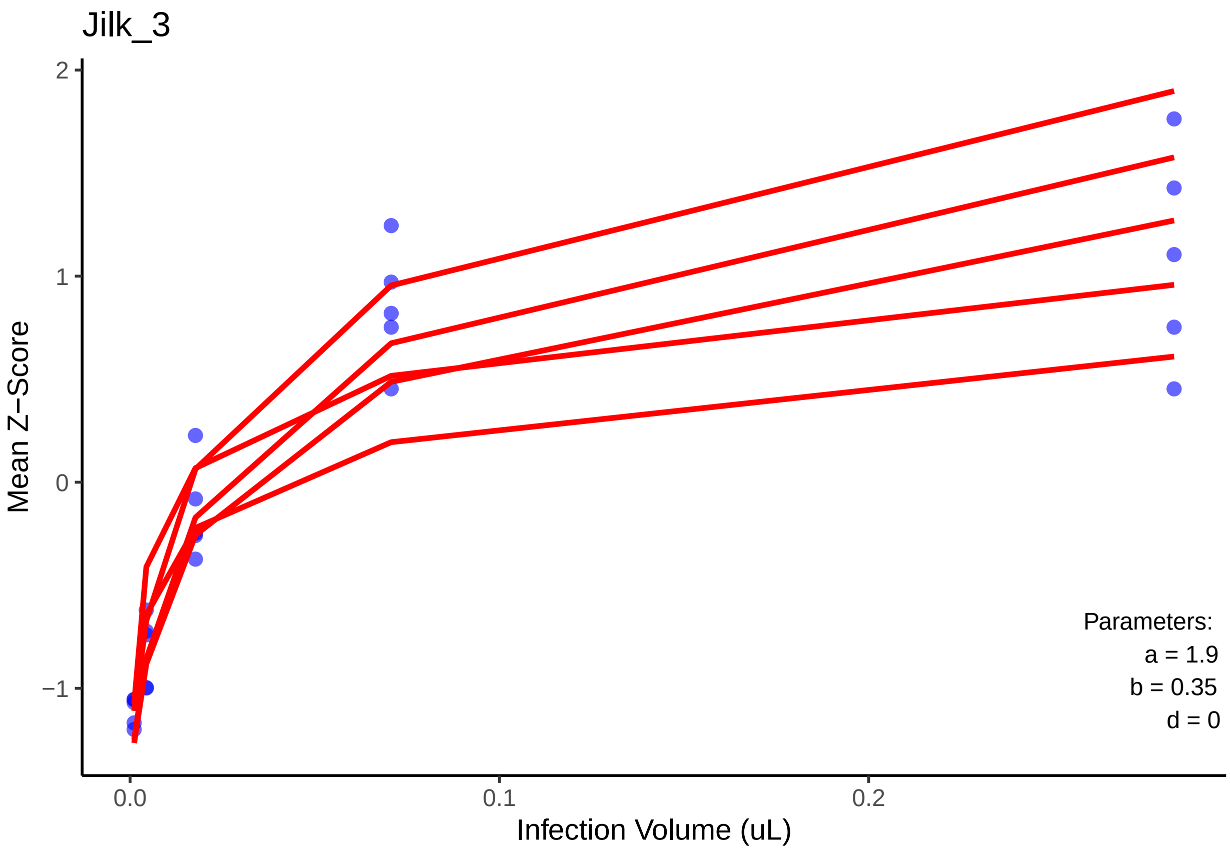


Iudw_4
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.85
b = 0.45
d = −0.01

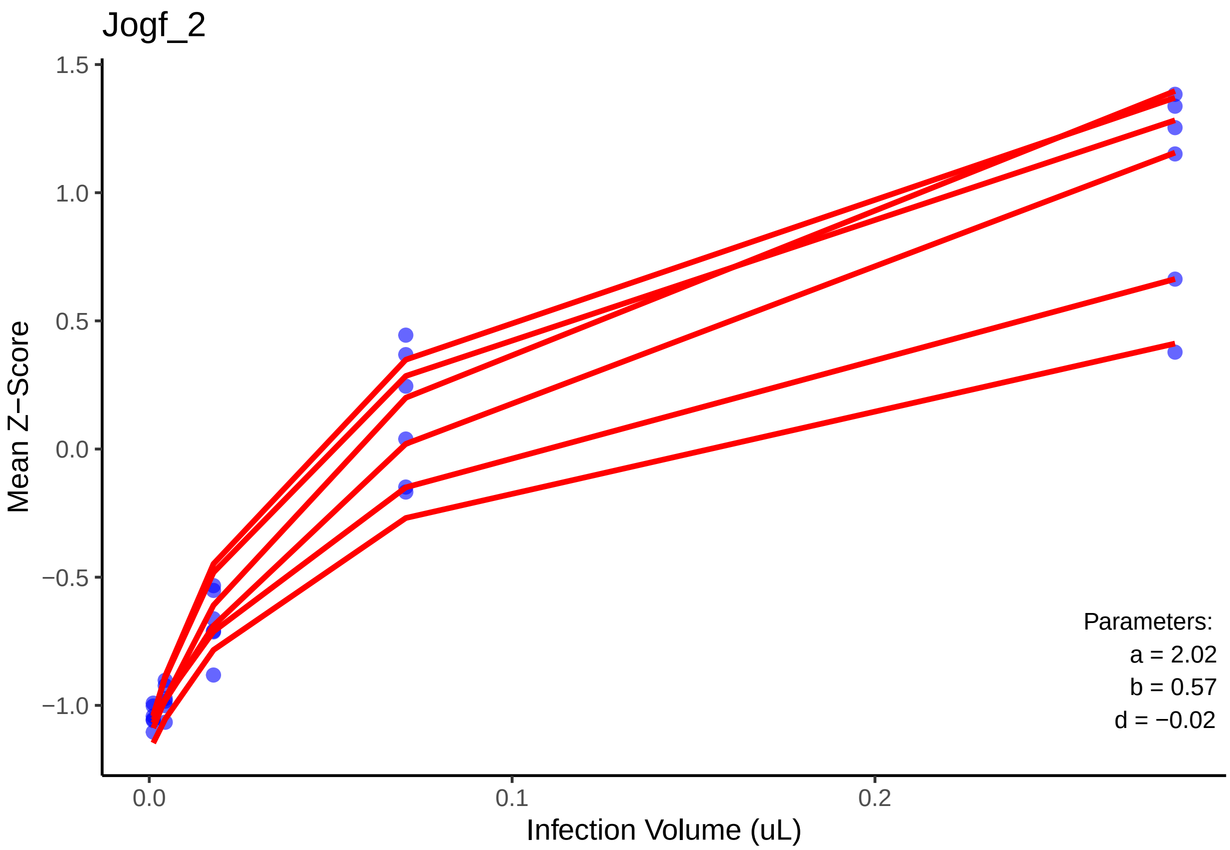

```
##
## $Jejf_2
```


Jejf_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.28
b = 0.42
d = 0

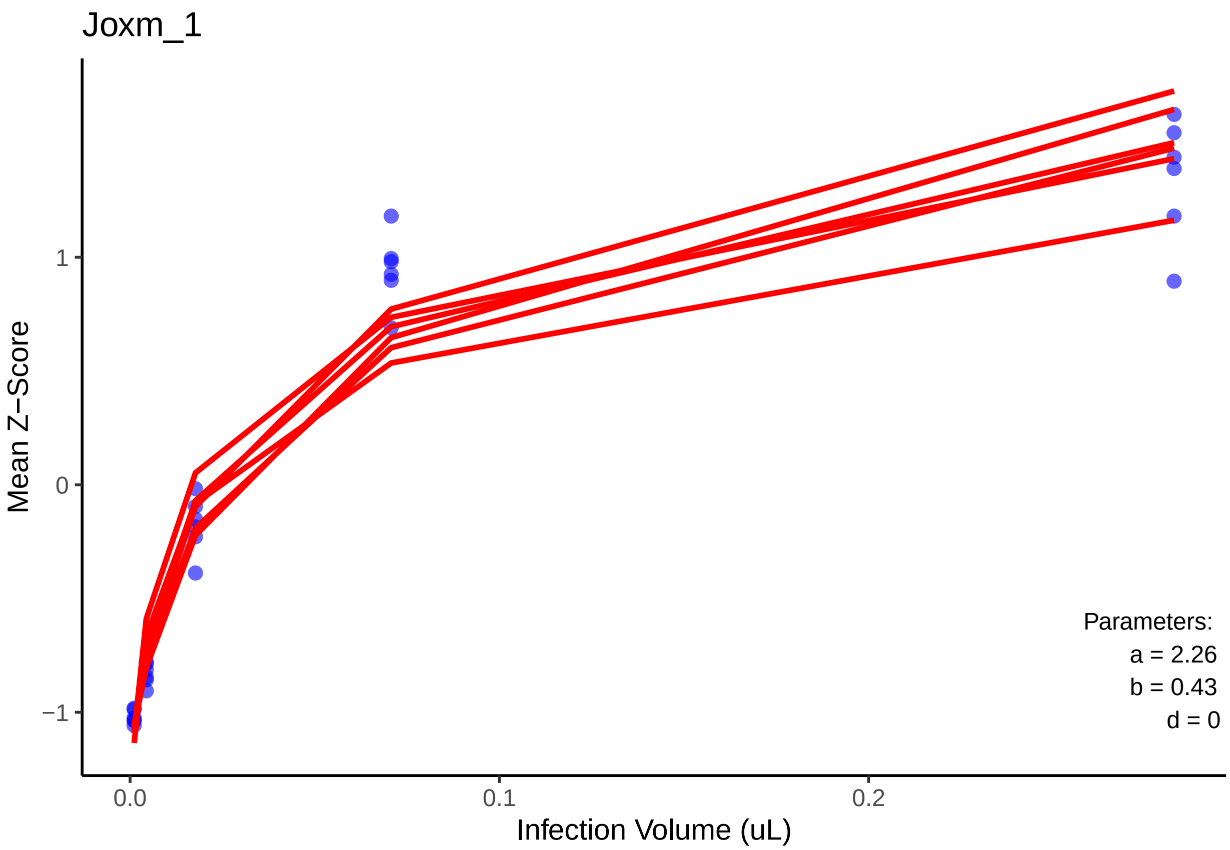
```
##
## $Jilk_3
```


Jilk_3
Mean Z−Score
Infection Volume (uL)
Parameters:
a = 1.9
b = 0.35
d = 0
2
1
0
−1
0.0
0.1
0.2

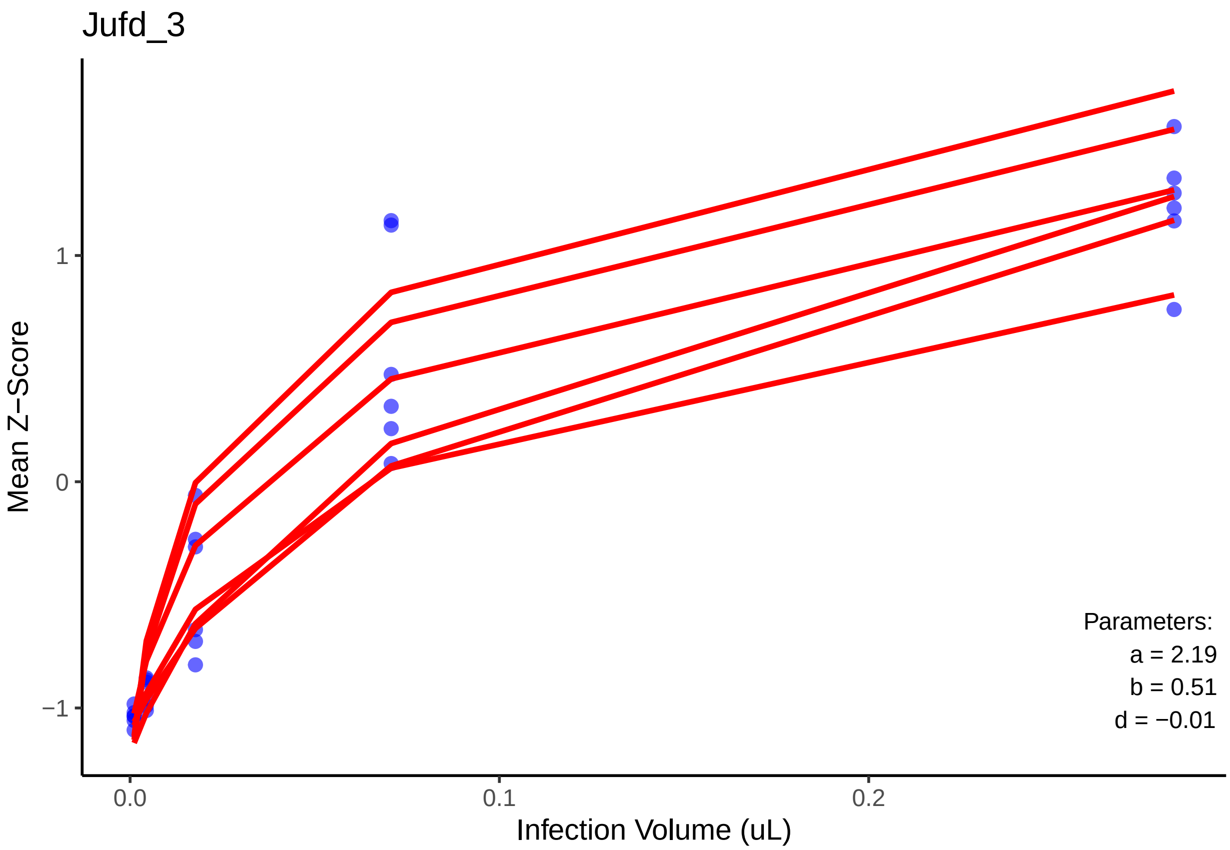
```
##
## $Jogf_2
```


Jogf_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.02
b = 0.57
d = −0.02

```
##
## $Joxm_1
```

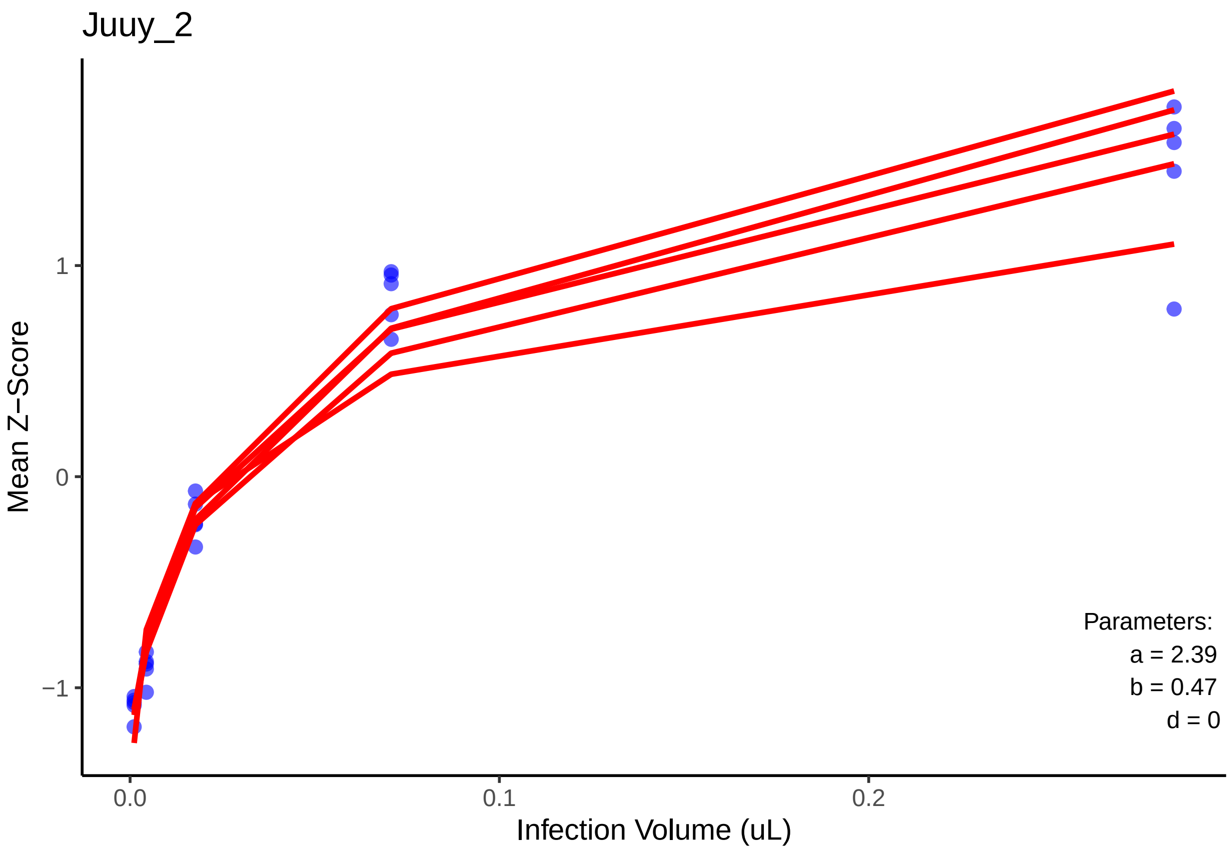

Joxm_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.26
b = 0.43
d = 0

```
##
## $Jufd_3
```

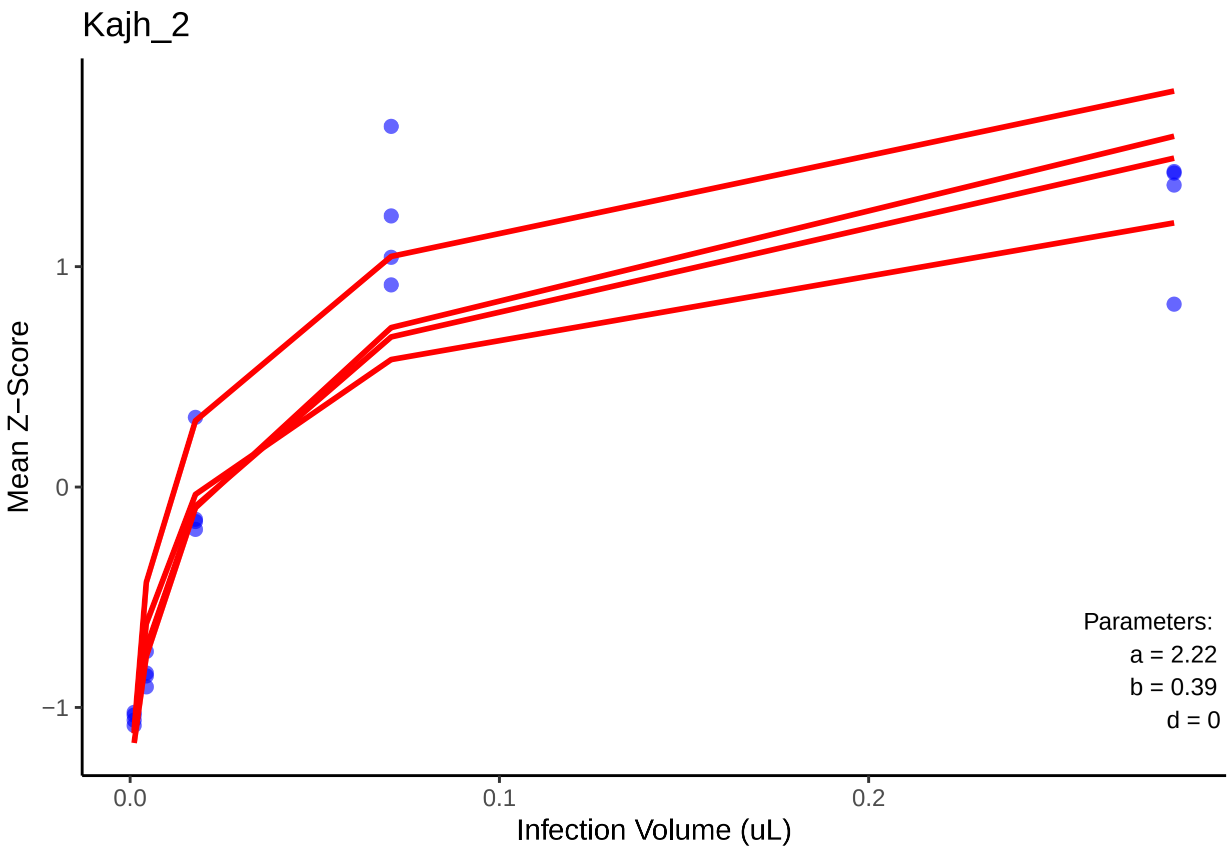


Jufd_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.19
b = 0.51
d = −0.01


```
##
## $Juuy_2
```

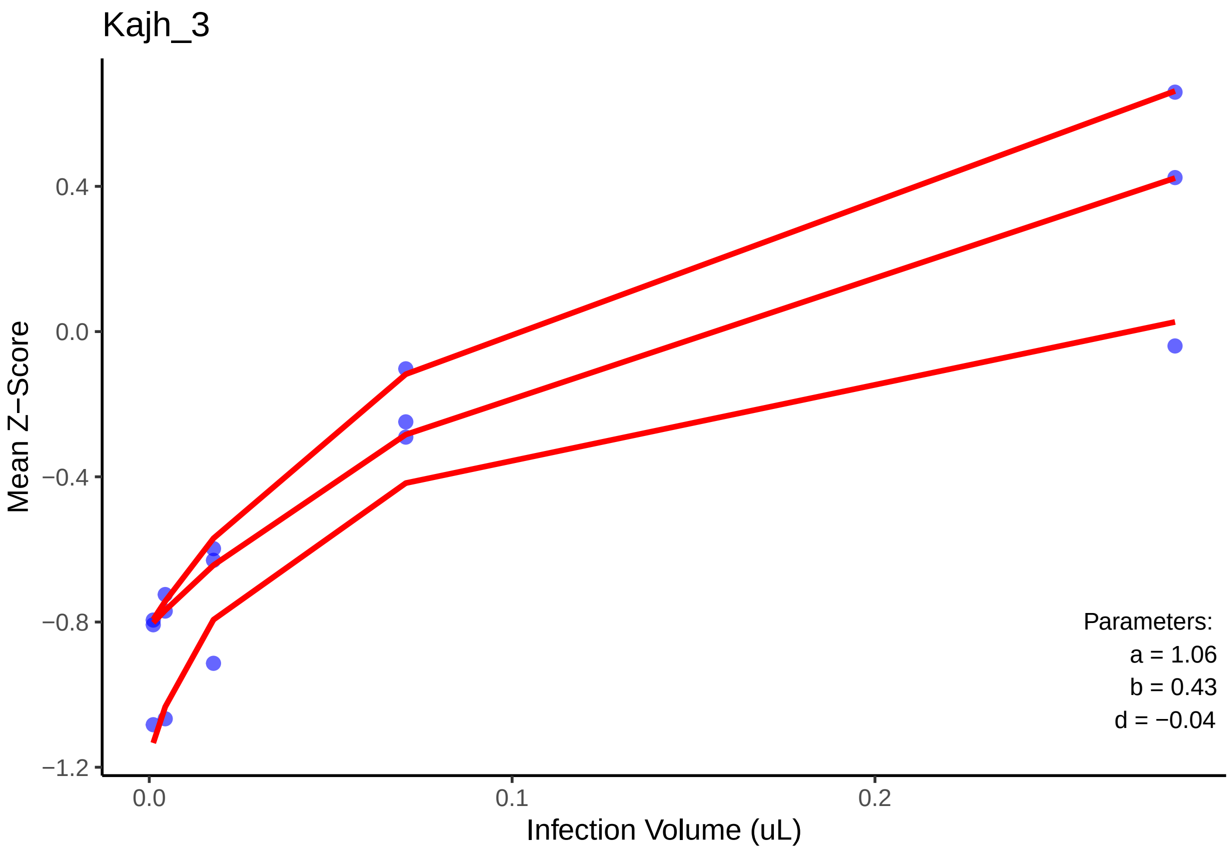

Juuy_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.39
b = 0.47
d = 0

```
##
## $Kajh_2
```

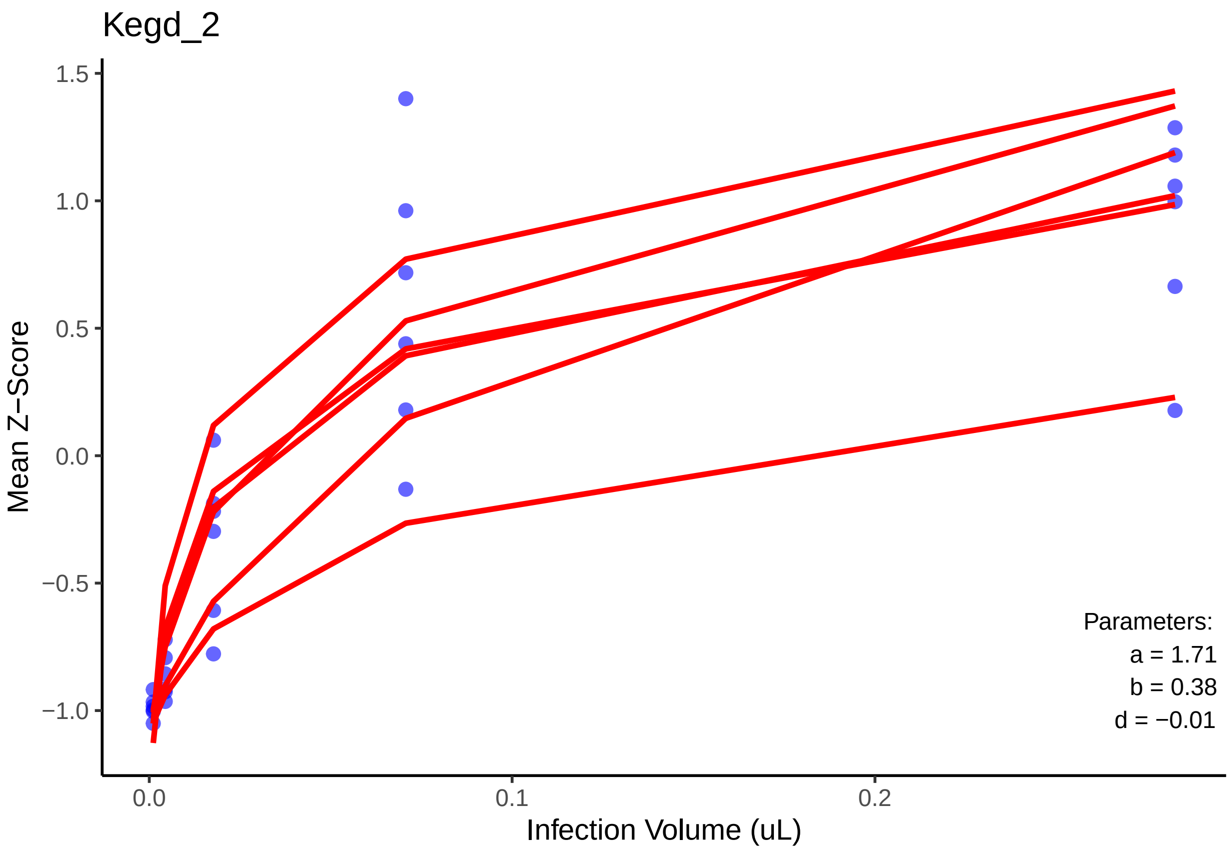


Kajh_2
Mean Z−Score
Infection Volume (uL)
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.22
b = 0.39
d = 0

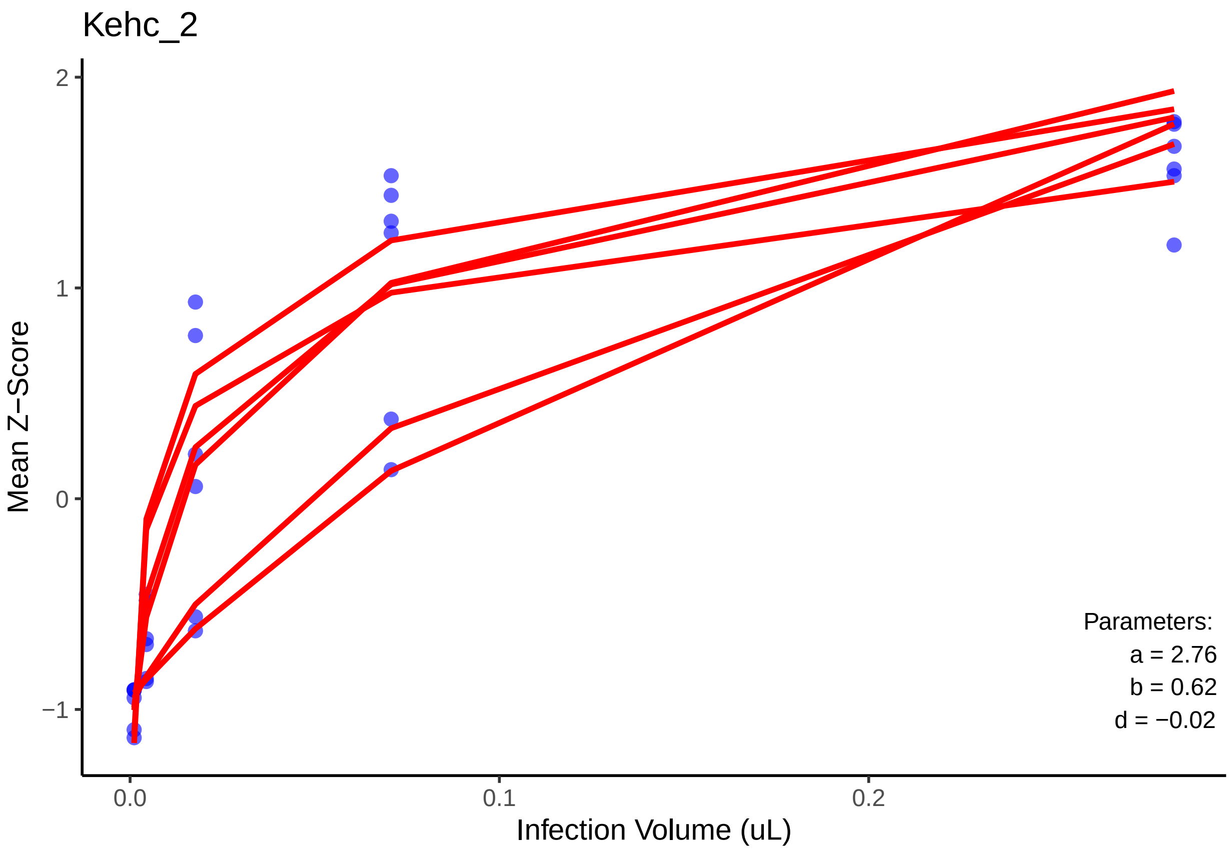

```
##
## $Kajh_3
```


Kajh_3
Mean Z−Score
0.4
0.0
−0.4
−0.8
−1.2
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.06
b = 0.43
d = −0.04

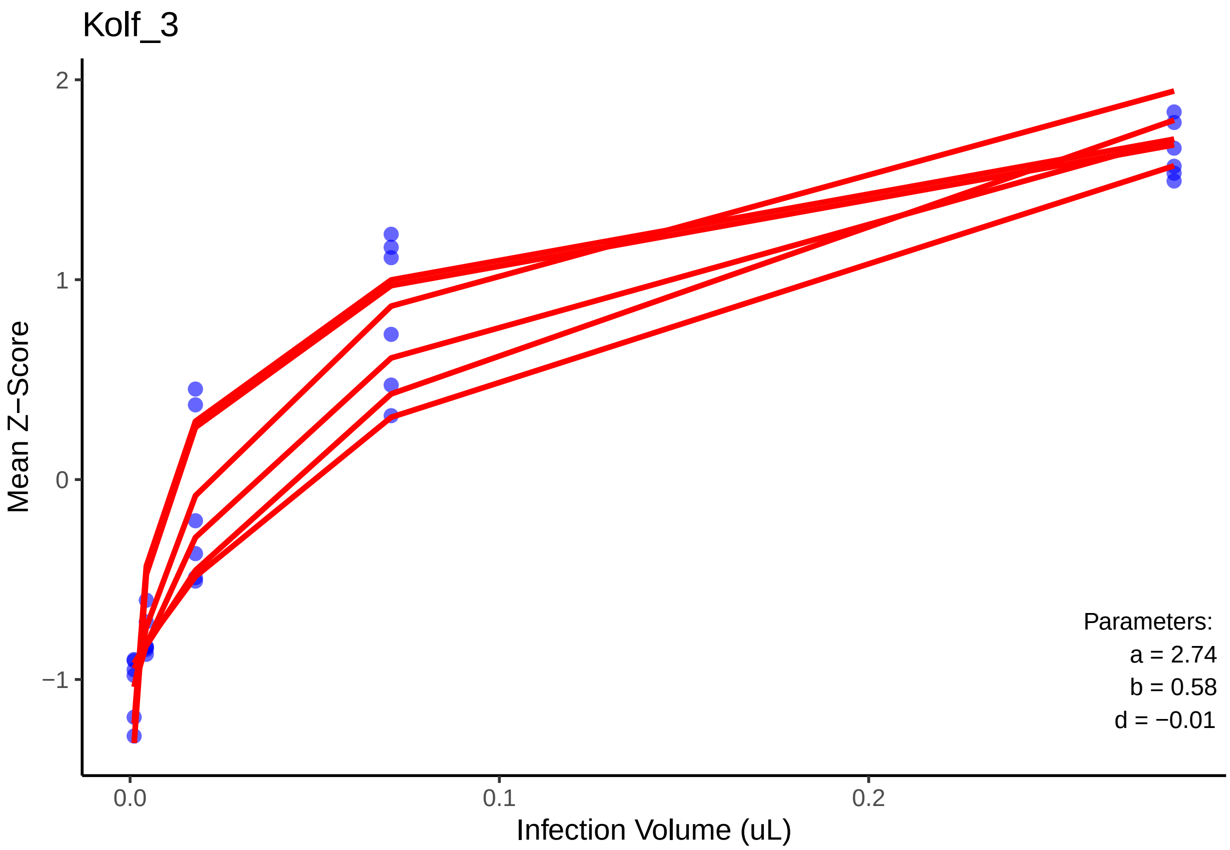
```
##
## $Kegd_2
```


Kegd_2
Mean Z−Score
Infection Volume (uL)
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Parameters:
a = 1.71
b = 0.38
d = −0.01

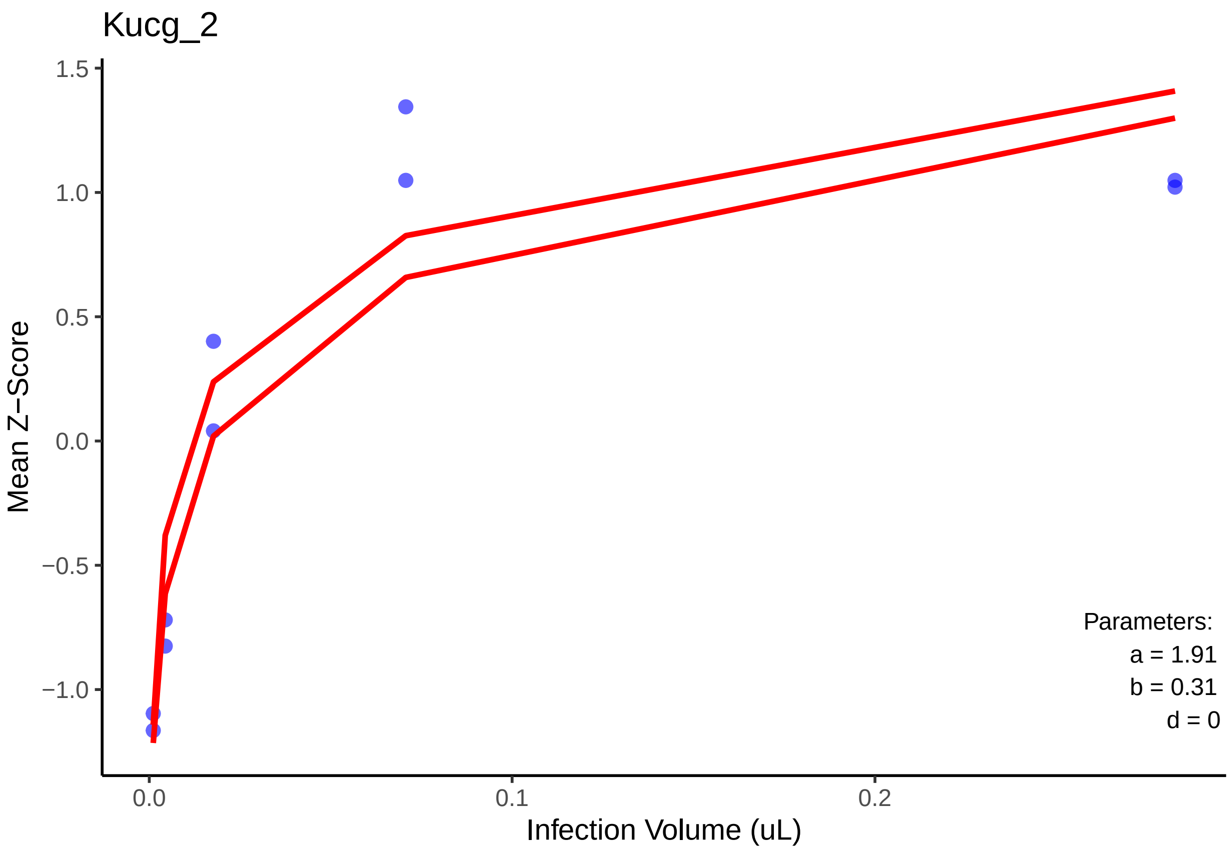
```
##
## $Kehc_2
```


Kehc_2
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.76
b = 0.62
d = −0.02

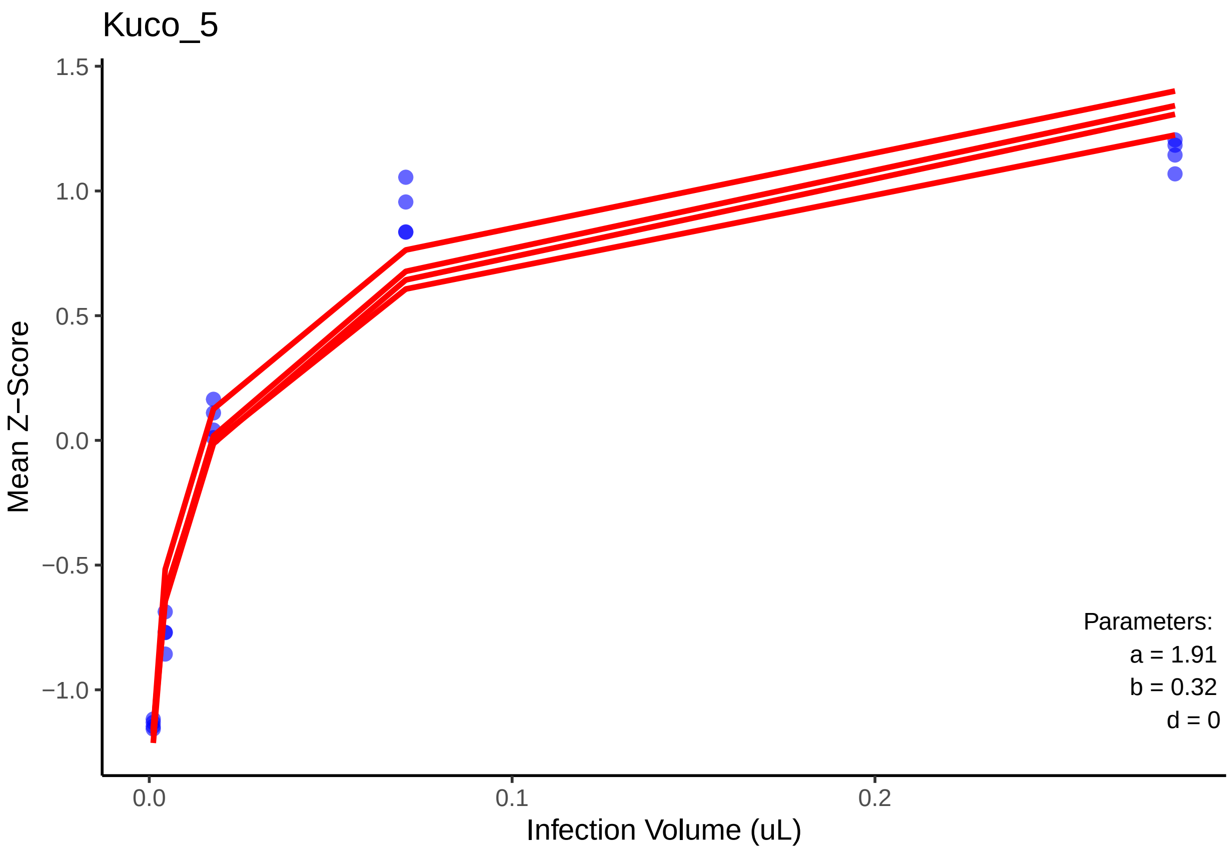
```
##
## $Kolf_3
```


Kolf_3
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.74
b = 0.58
d = −0.01

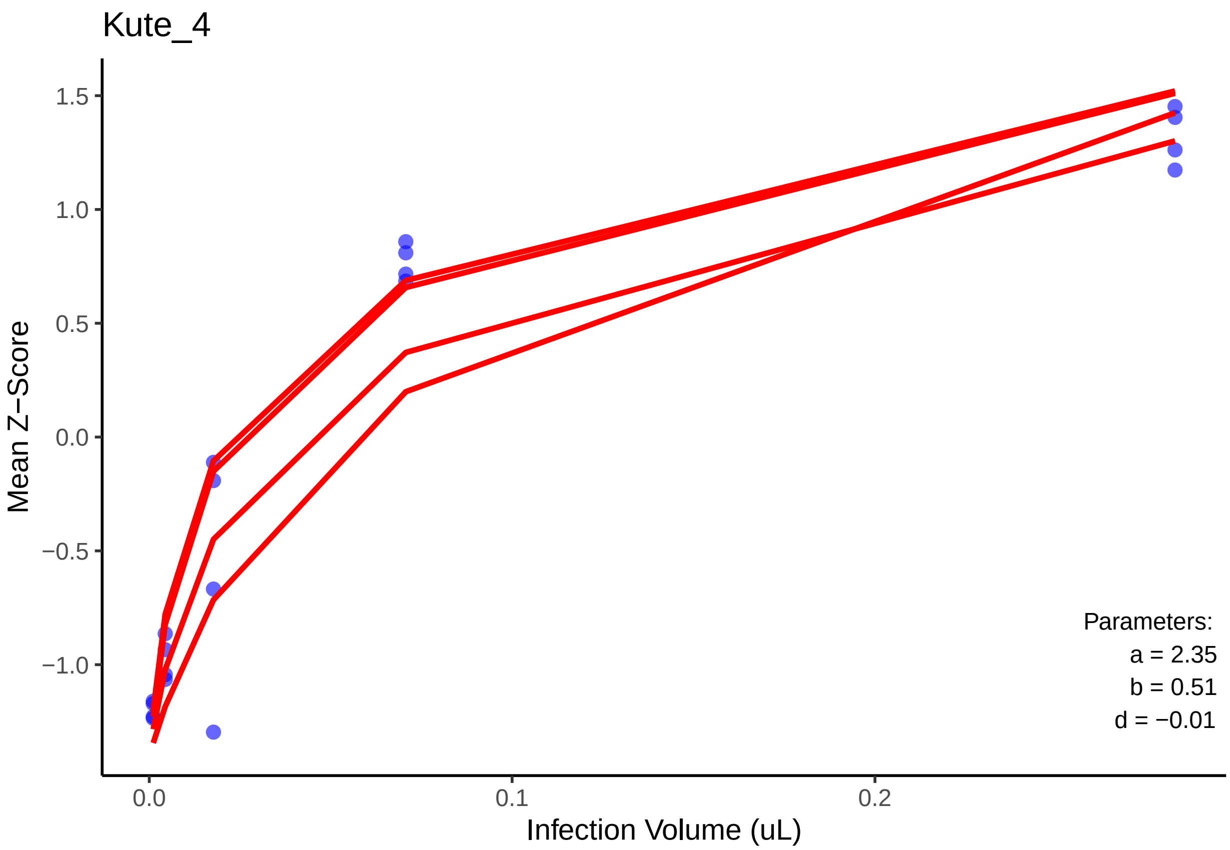
```
##
## $Kucg_2
```


Kucg_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
Parameters:
a = 1.91
b = 0.31
d = 0
0.0
0.1
0.2
Infection Volume (uL)

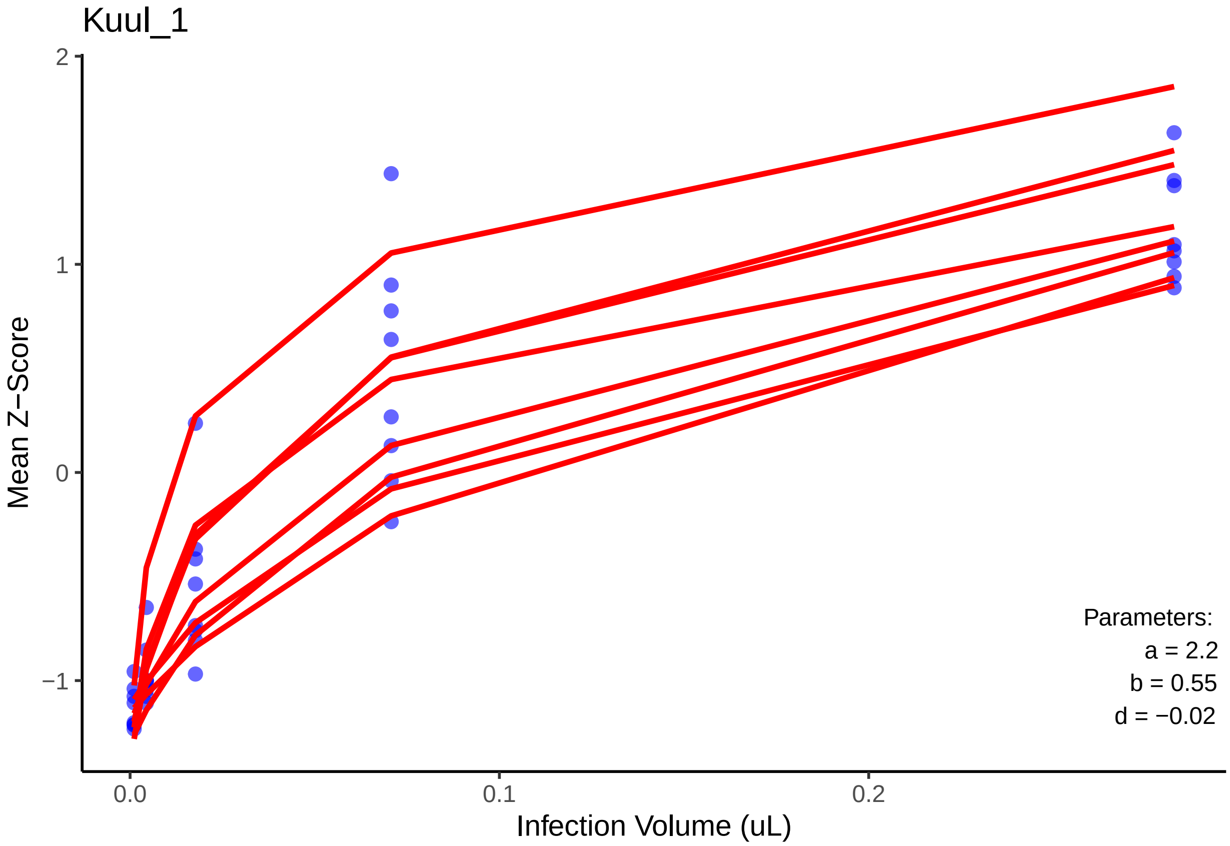
```
##
## $Kuco_5
```


Kuco_5
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
Parameters:
a = 1.91
b = 0.32
d = 0
0.0
0.1
0.2
Infection Volume (uL)

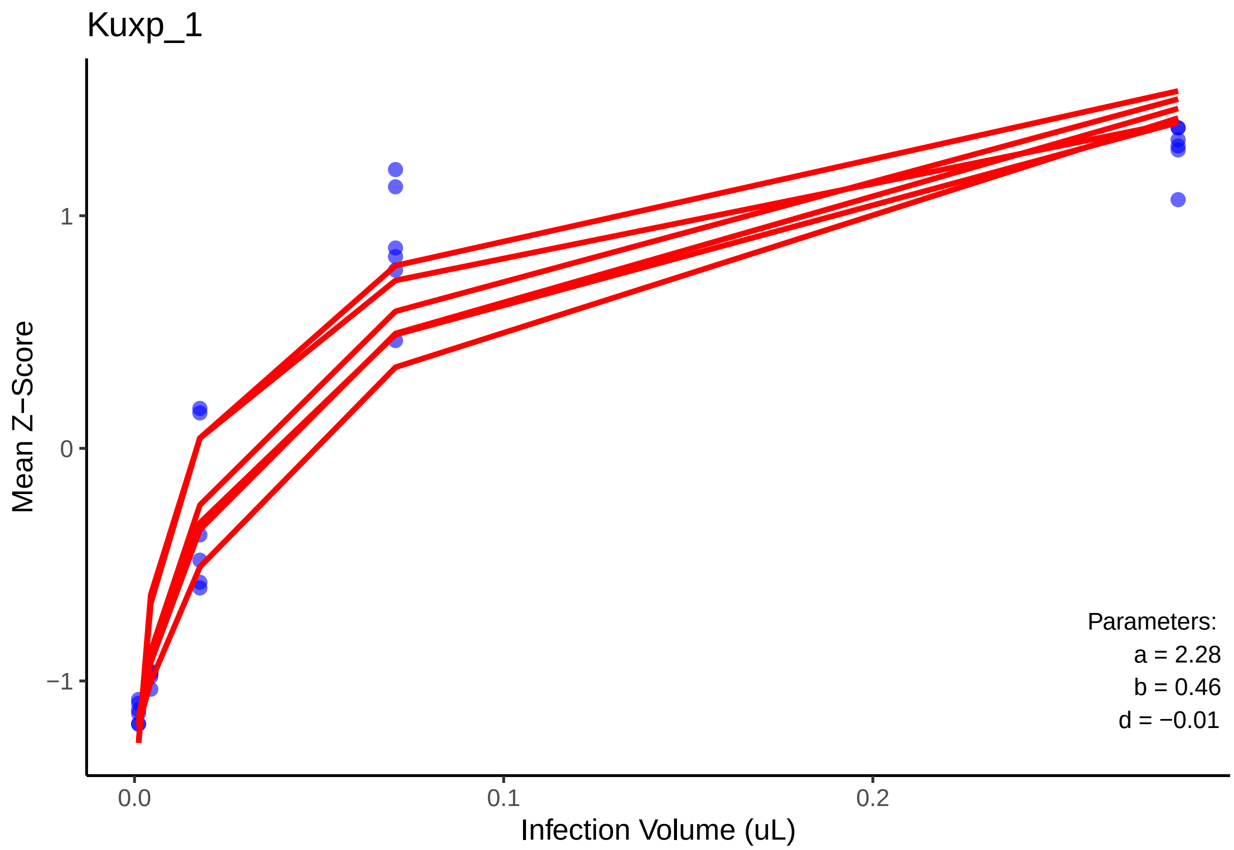
```
##
## $Kute_4
```


Kute_4
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.35
b = 0.51
d = −0.01

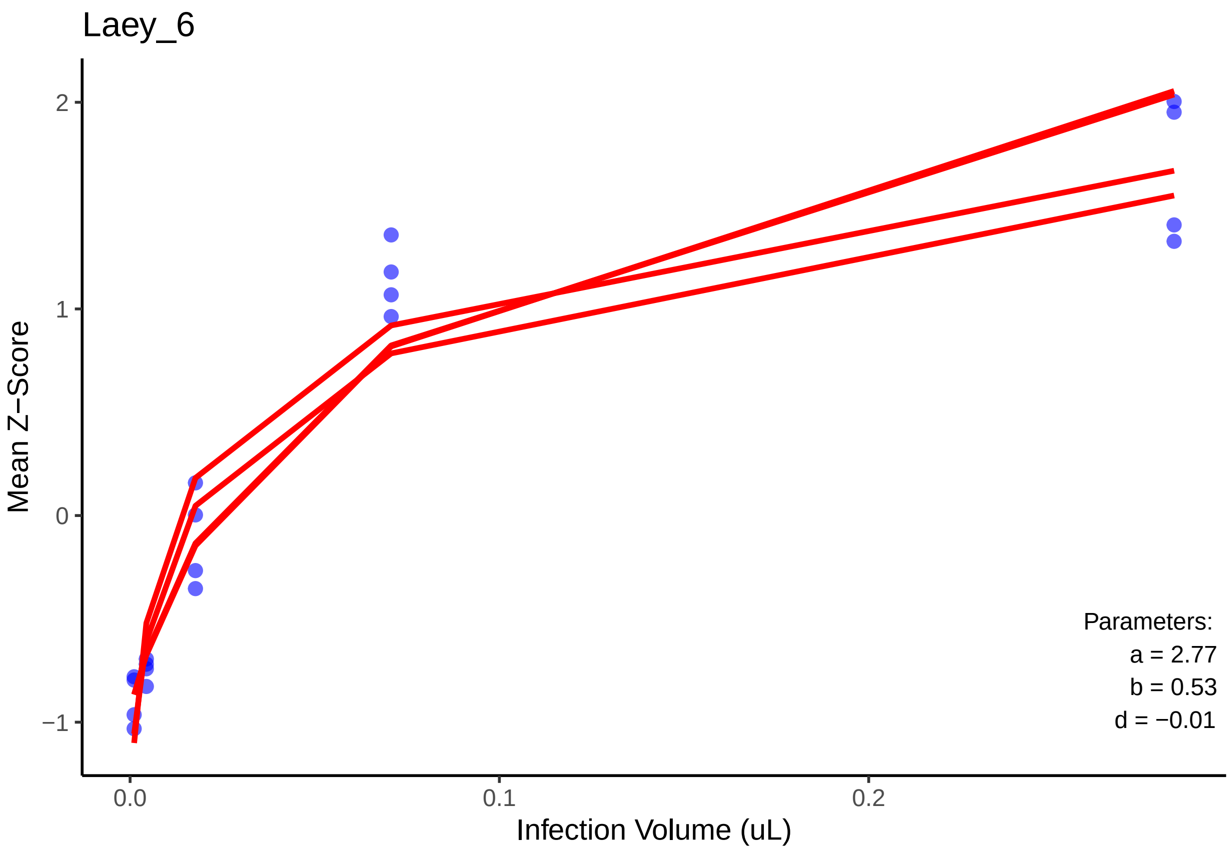
```
##
## $Kuul_1
```


Kuul_1
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.2
b = 0.55
d = −0.02

```
##
## $Kuxp_1
```

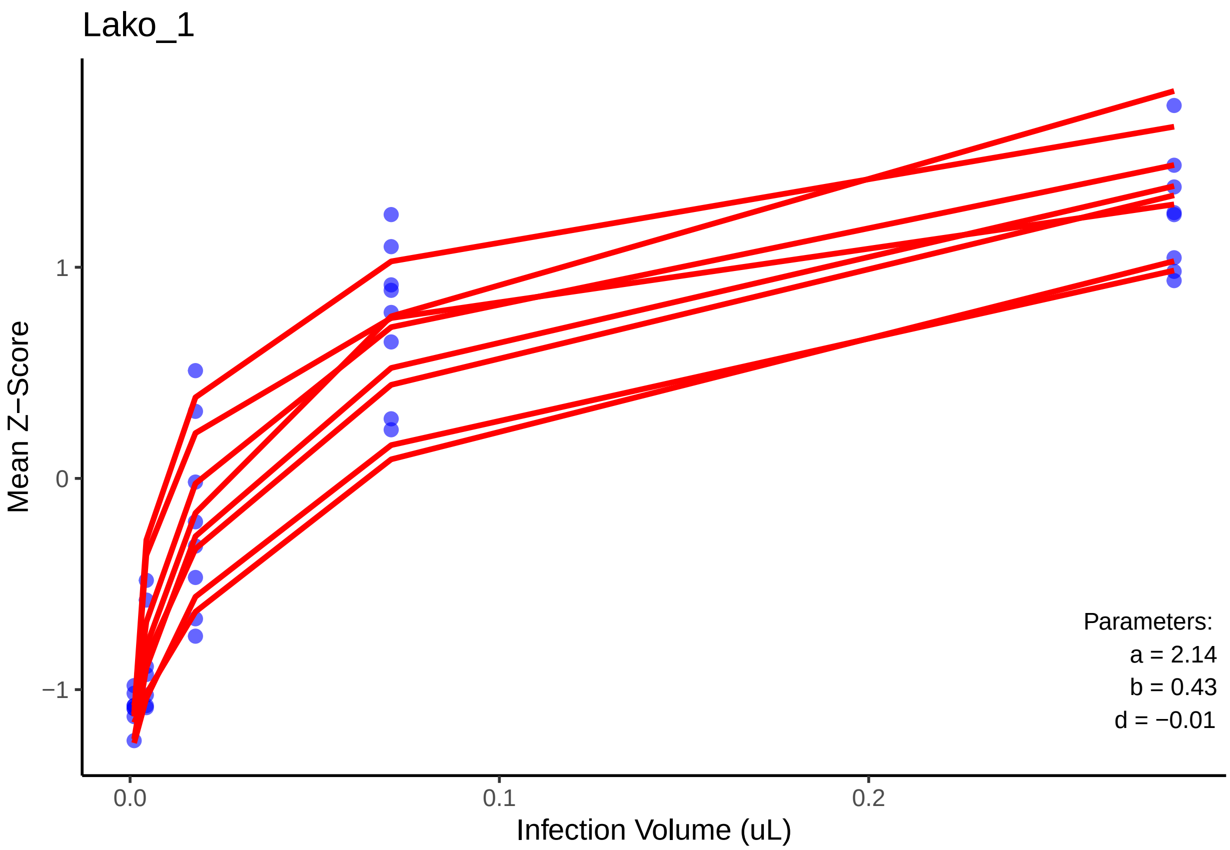

Kuxp_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.28
b = 0.46
d = −0.01

```
##
## $Laey_6
```

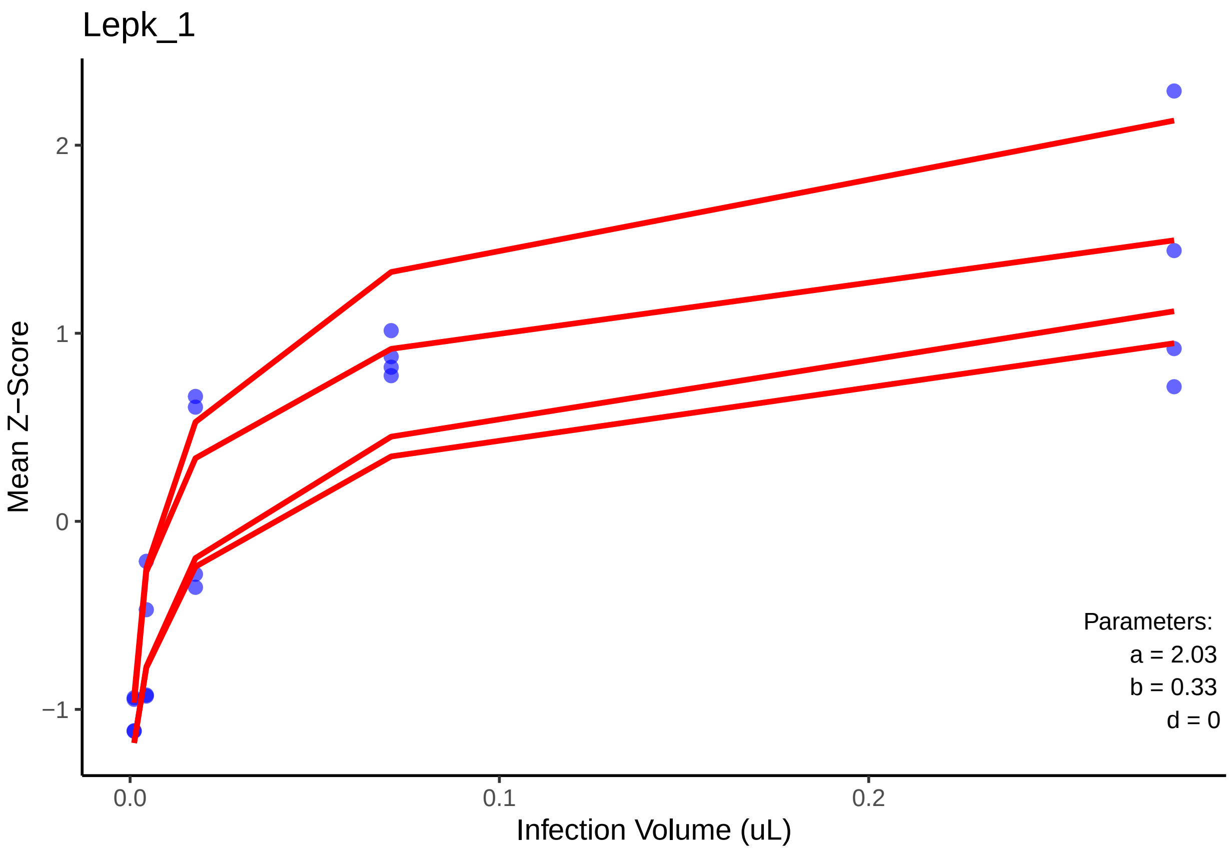


Laey_6
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.77
b = 0.53
d = −0.01


```
##
## $Lako_1
```

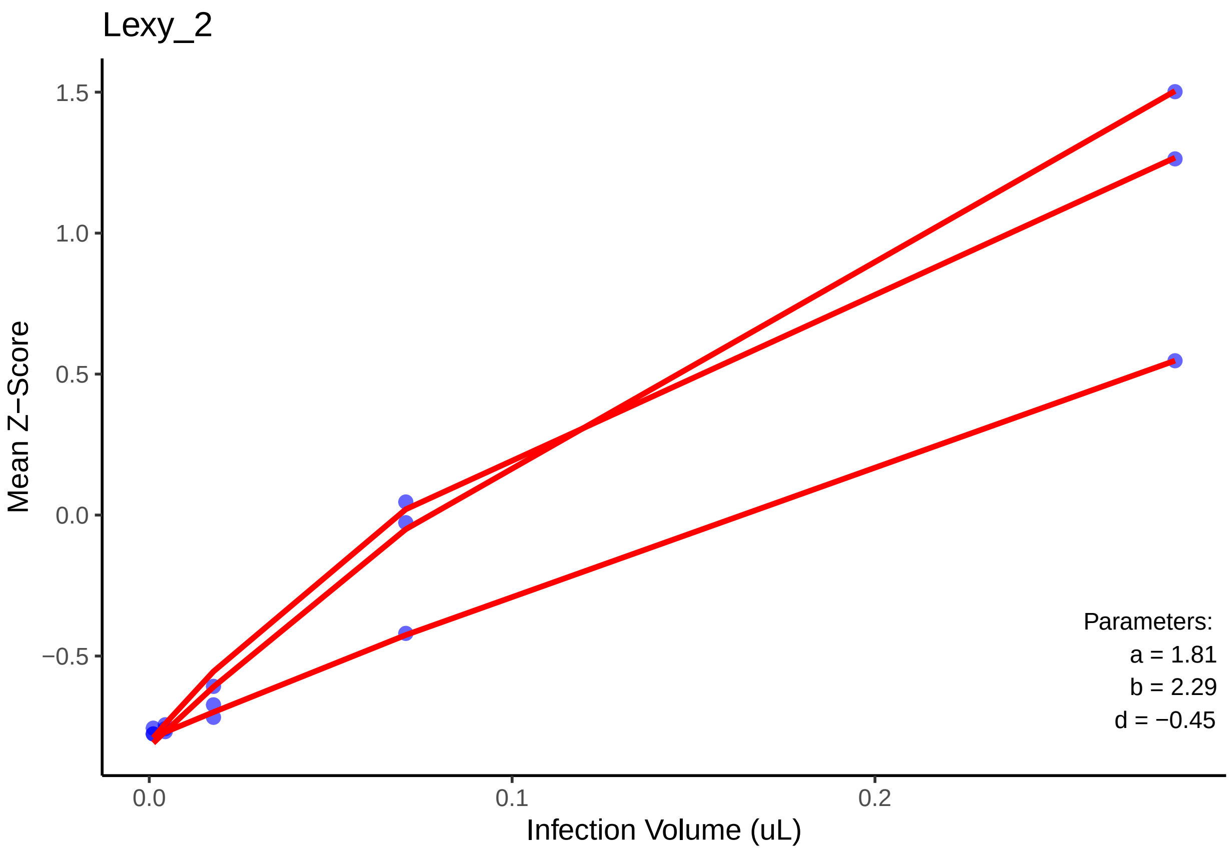

Lako_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.14
b = 0.43
d = −0.01

```
##
## $Lepk_1
```

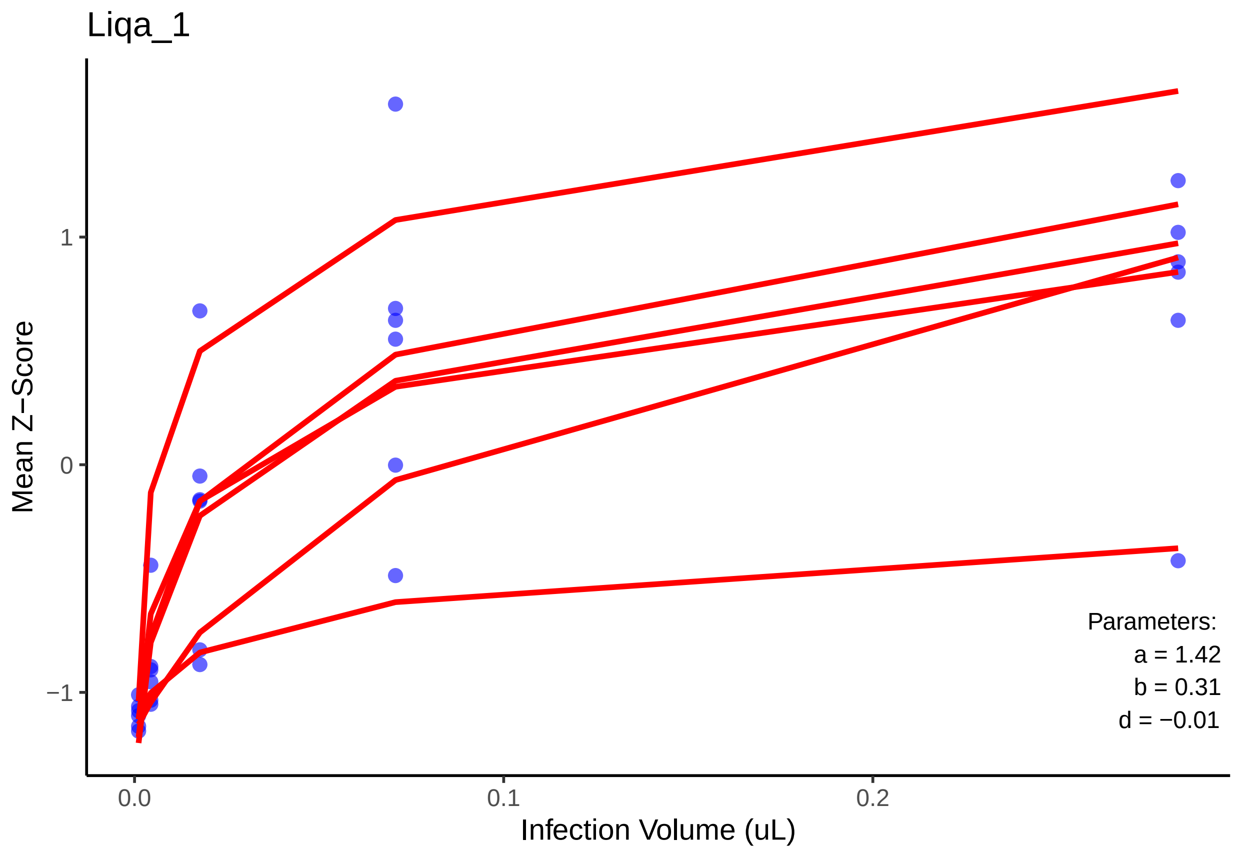


Lepk_1
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.03
b = 0.33
d = 0

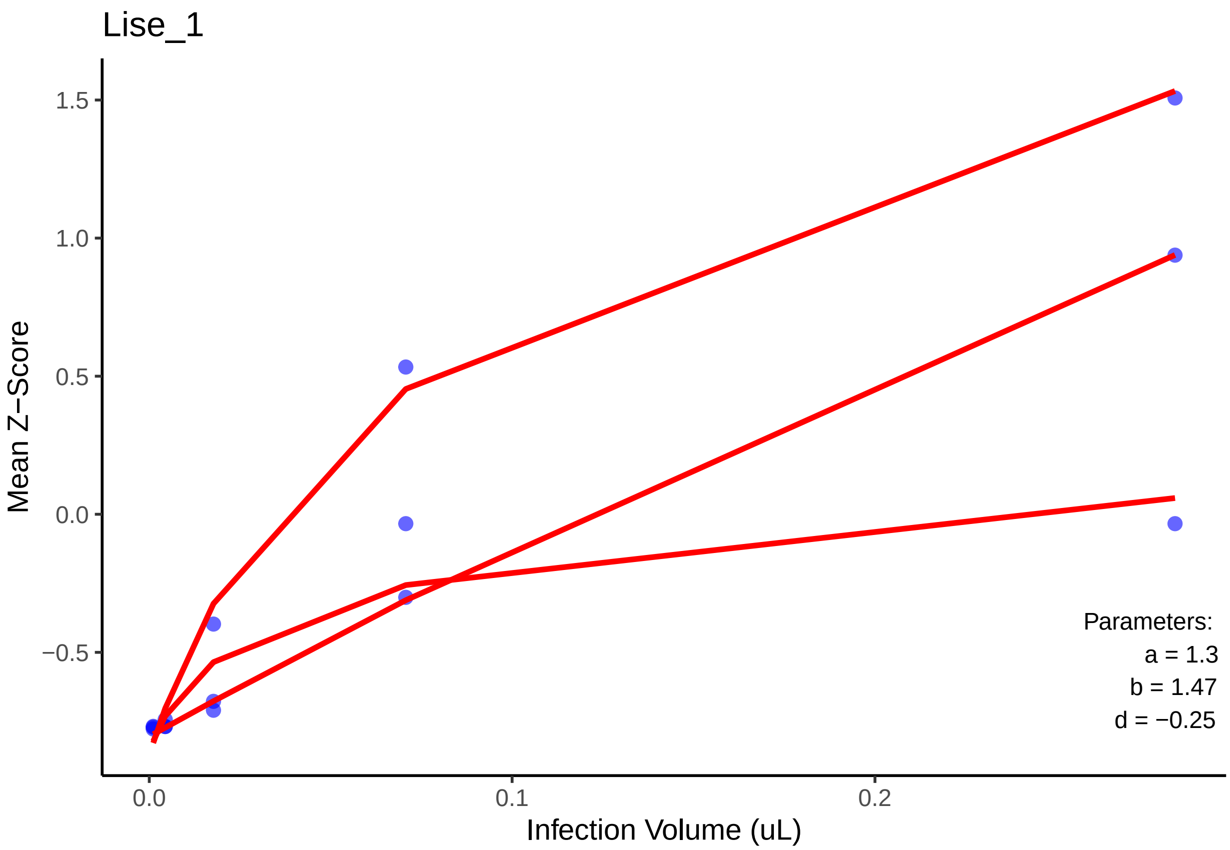

```
##
## $Lexy_2
```


Lexy_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.81
b = 2.29
d = −0.45

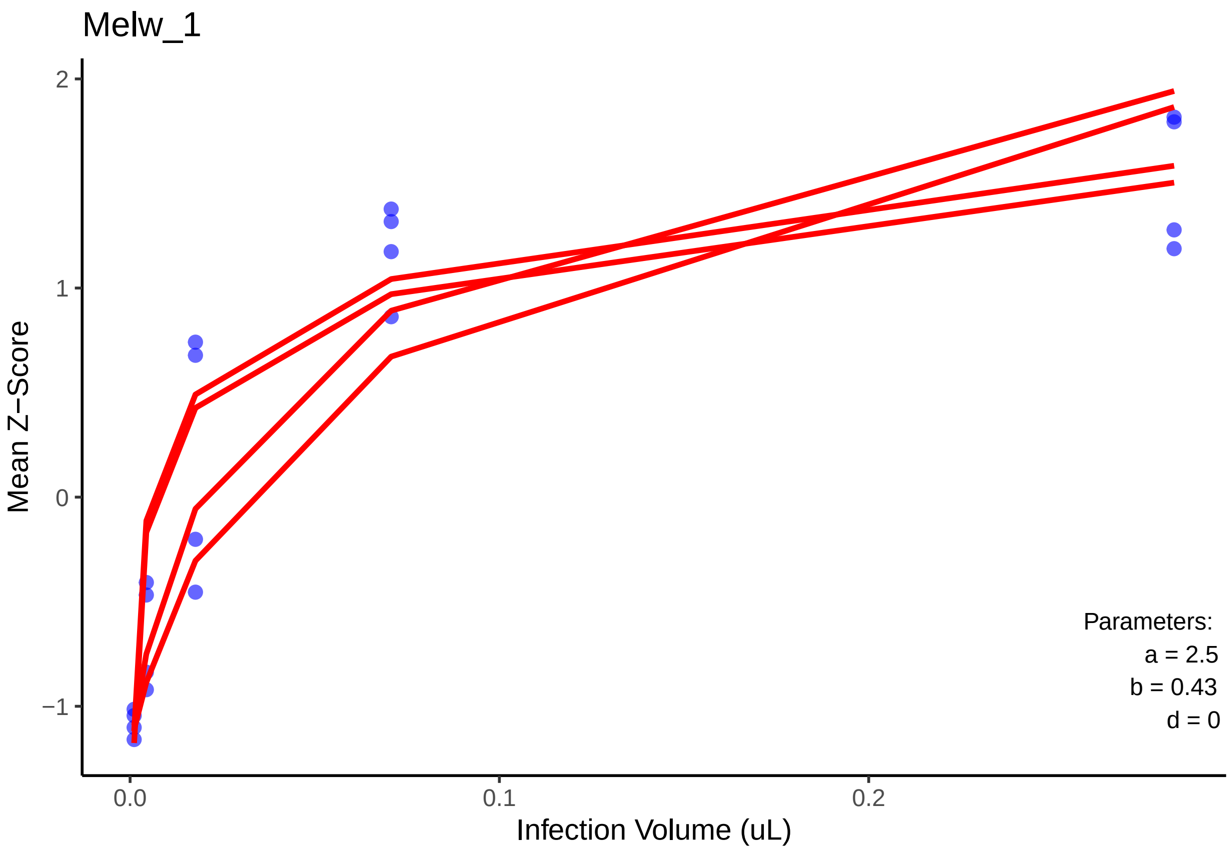
```
##
## $Liqa_1
```


Liqa_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.42
b = 0.31
d = −0.01

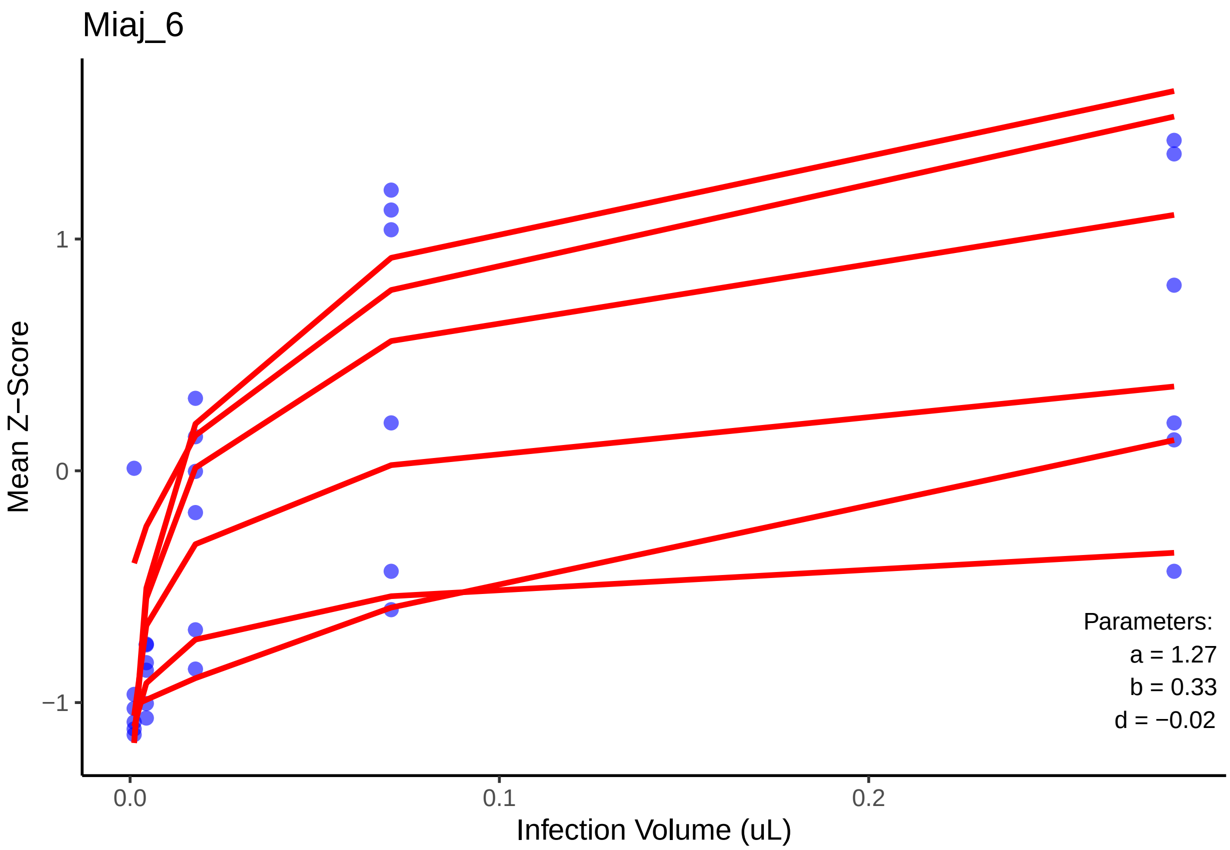
```
##
## $Lise_1
```


Lise_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.3
b = 1.47
d = −0.25

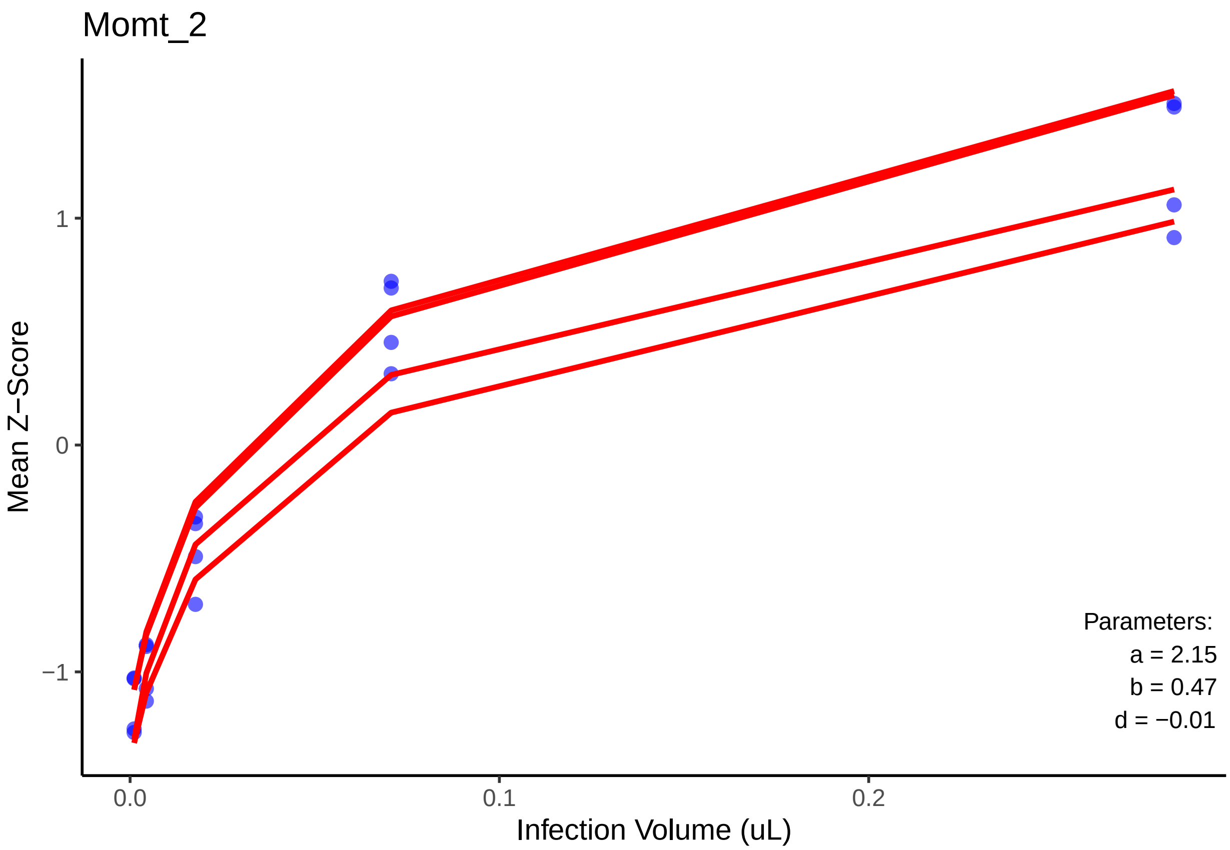
```
##
## $Melw_1
```


Melw_1
Mean Z−Score
Infection Volume (uL)
Parameters:
a = 2.5
b = 0.43
d = 0
2
1
0
−1
0.0
0.1
0.2

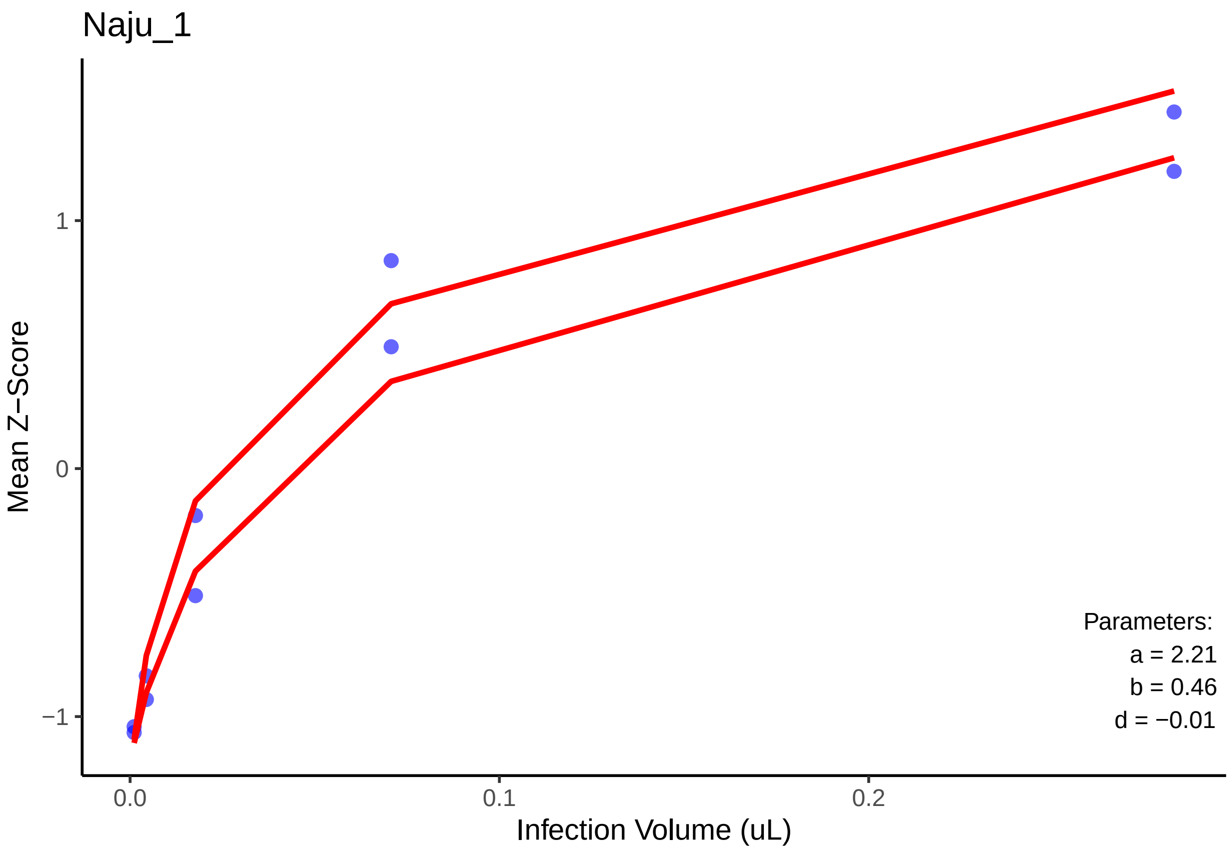
```
##
## $Miaj_6
```


Miaj_6
Mean Z−Score
Infection Volume (uL)
Parameters:
a = 1.27
b = 0.33
d = −0.02
1
0
−1
0.0
0.1
0.2

```
##
## $Momt_2
```

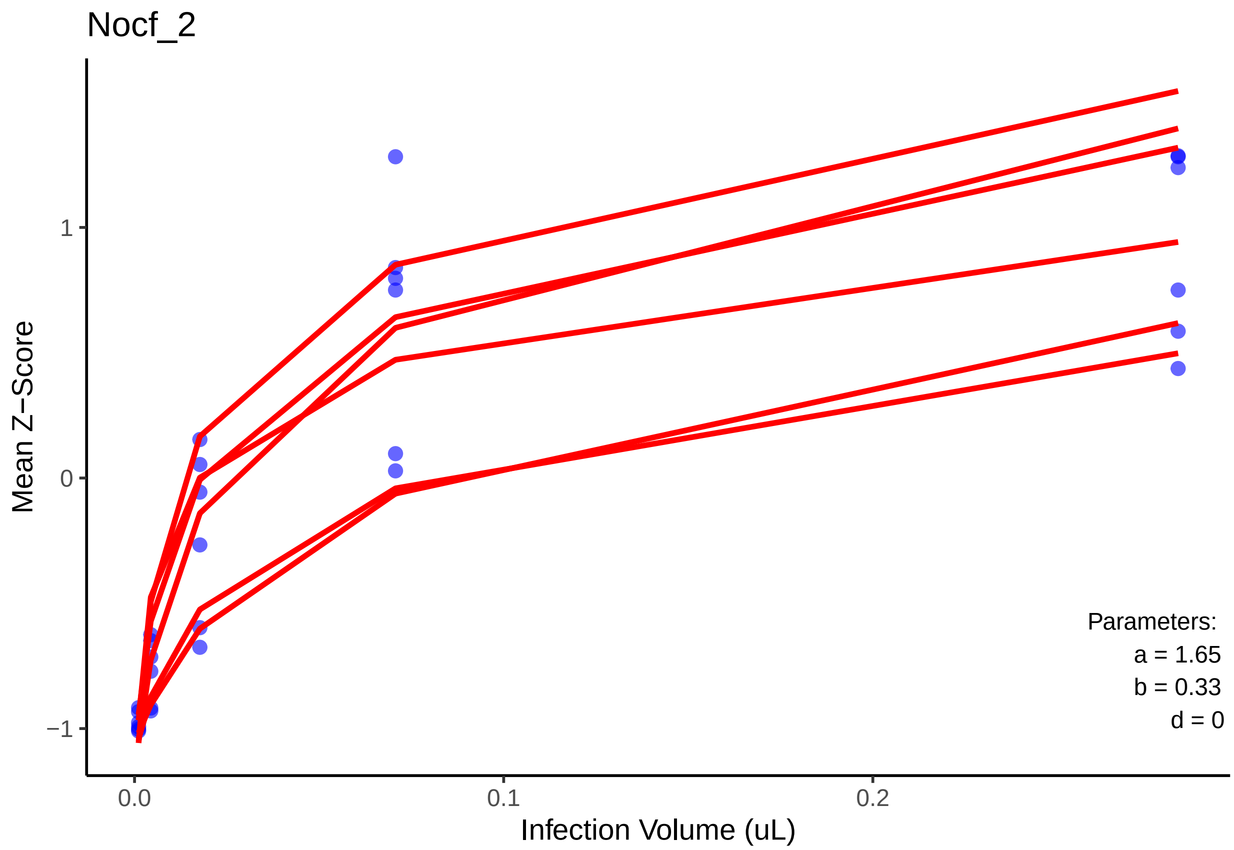

Momt_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.15
b = 0.47
d = −0.01

```
##
## $Naju_1
```

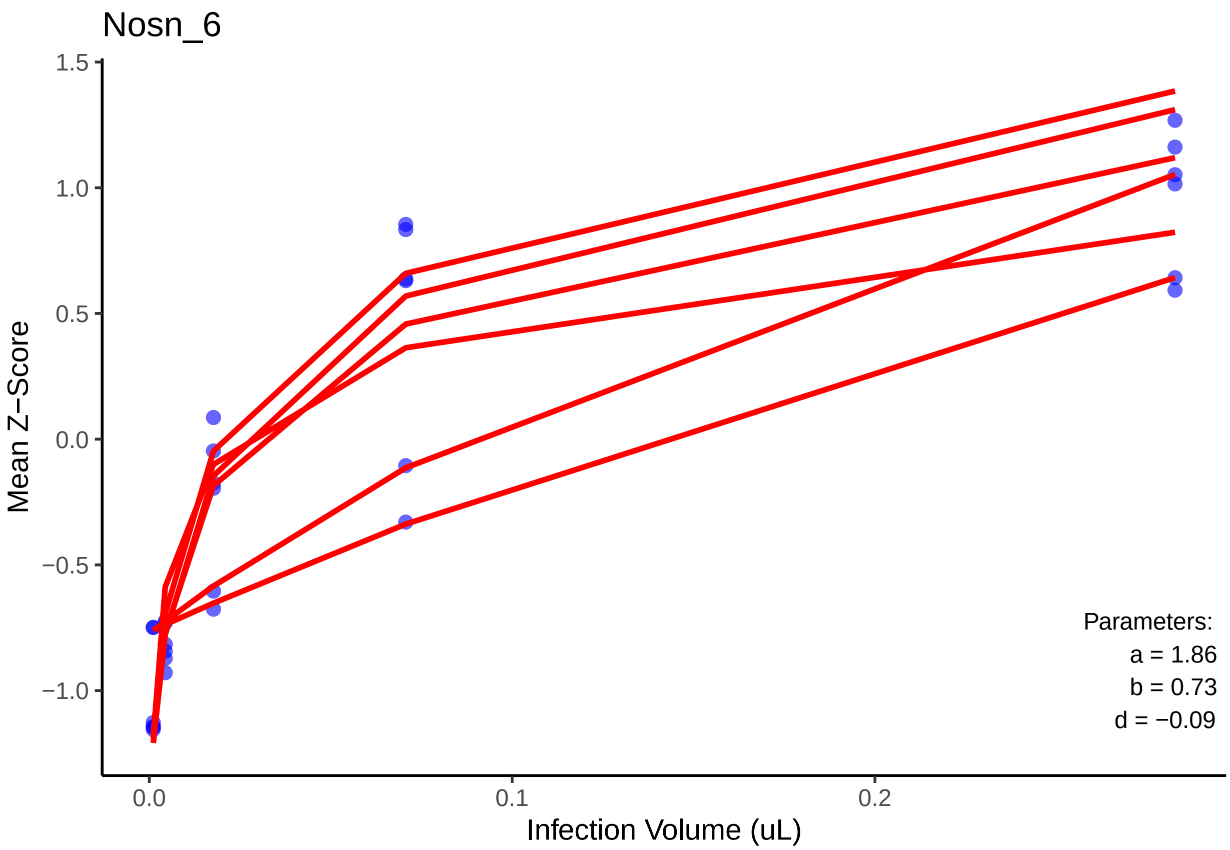


Naju_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.21
b = 0.46
d = −0.01

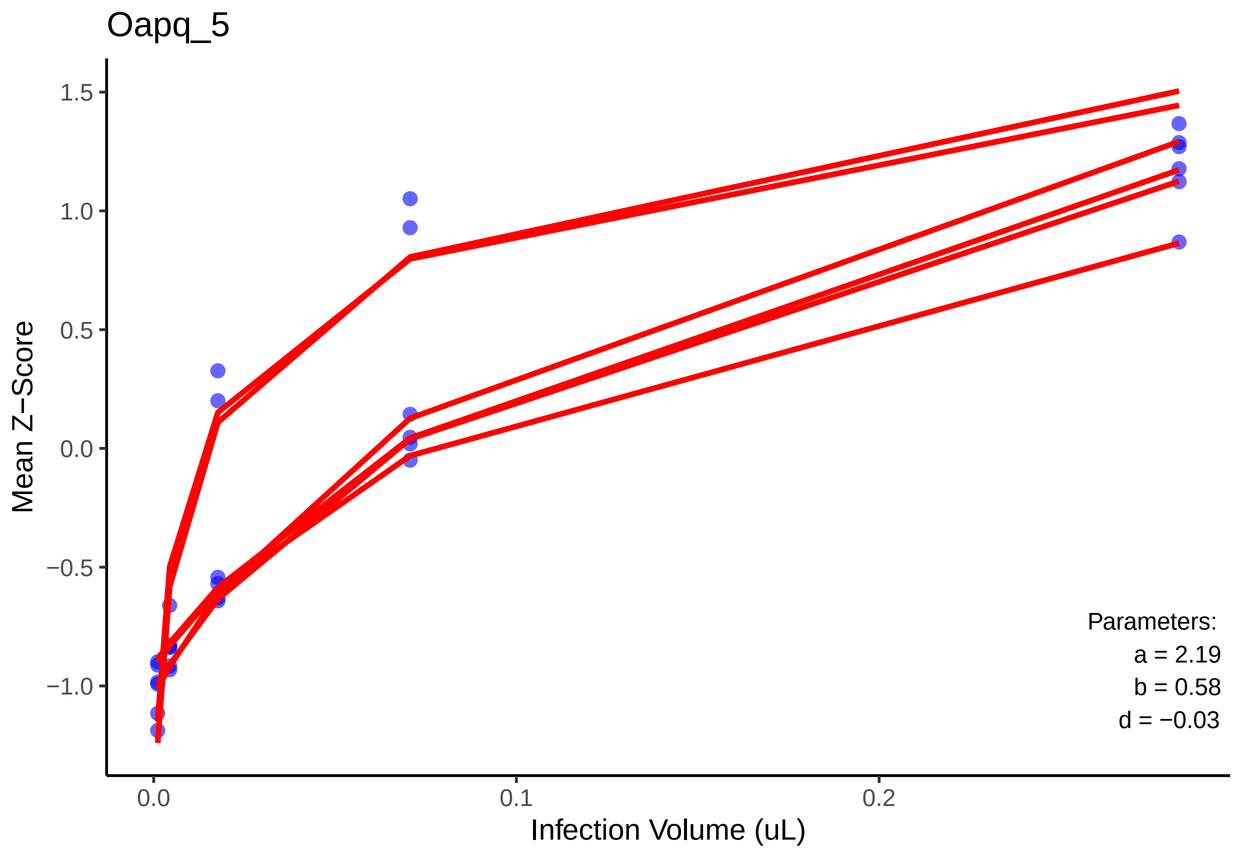

```
##
## $Nocf_2
```


Nocf_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.65
b = 0.33
d = 0

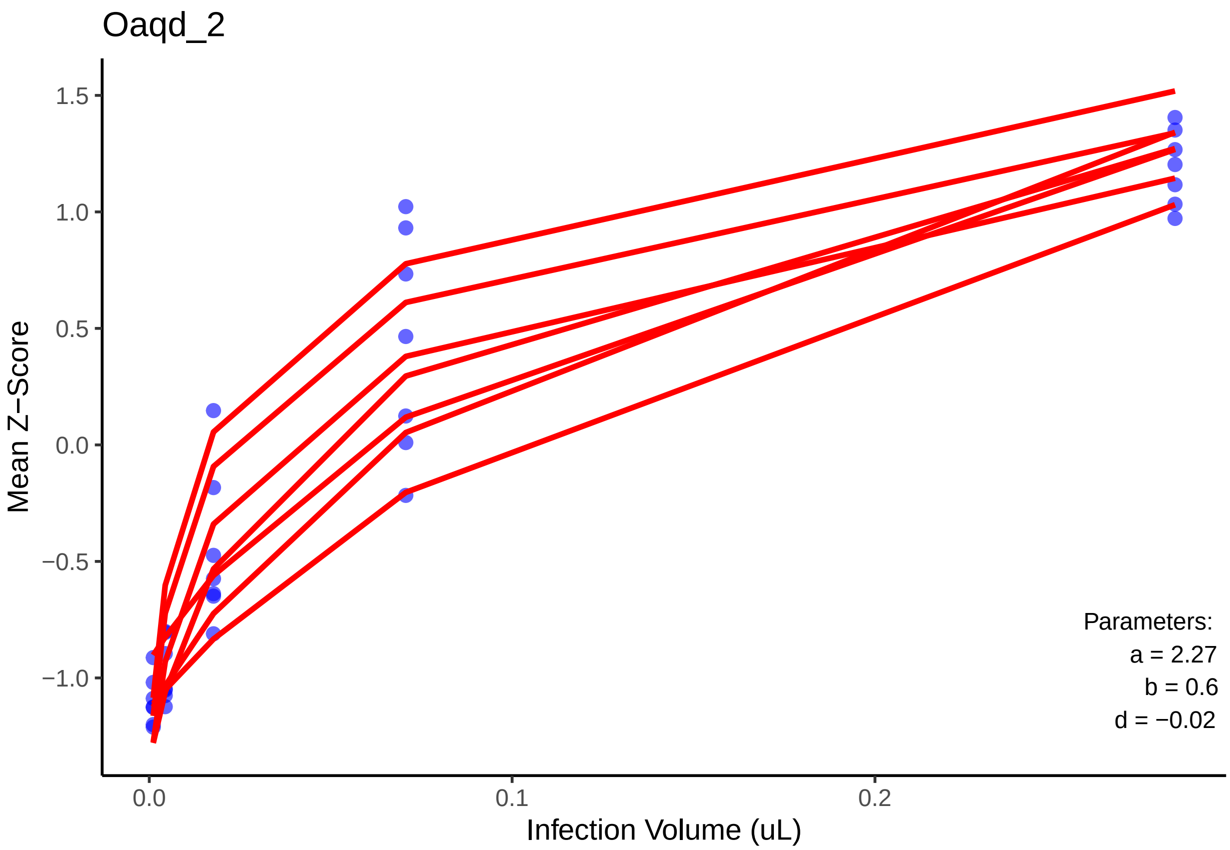
```
##
## $Nosn_6
```


Nosn_6
1.5
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.86
b = 0.73
d = −0.09

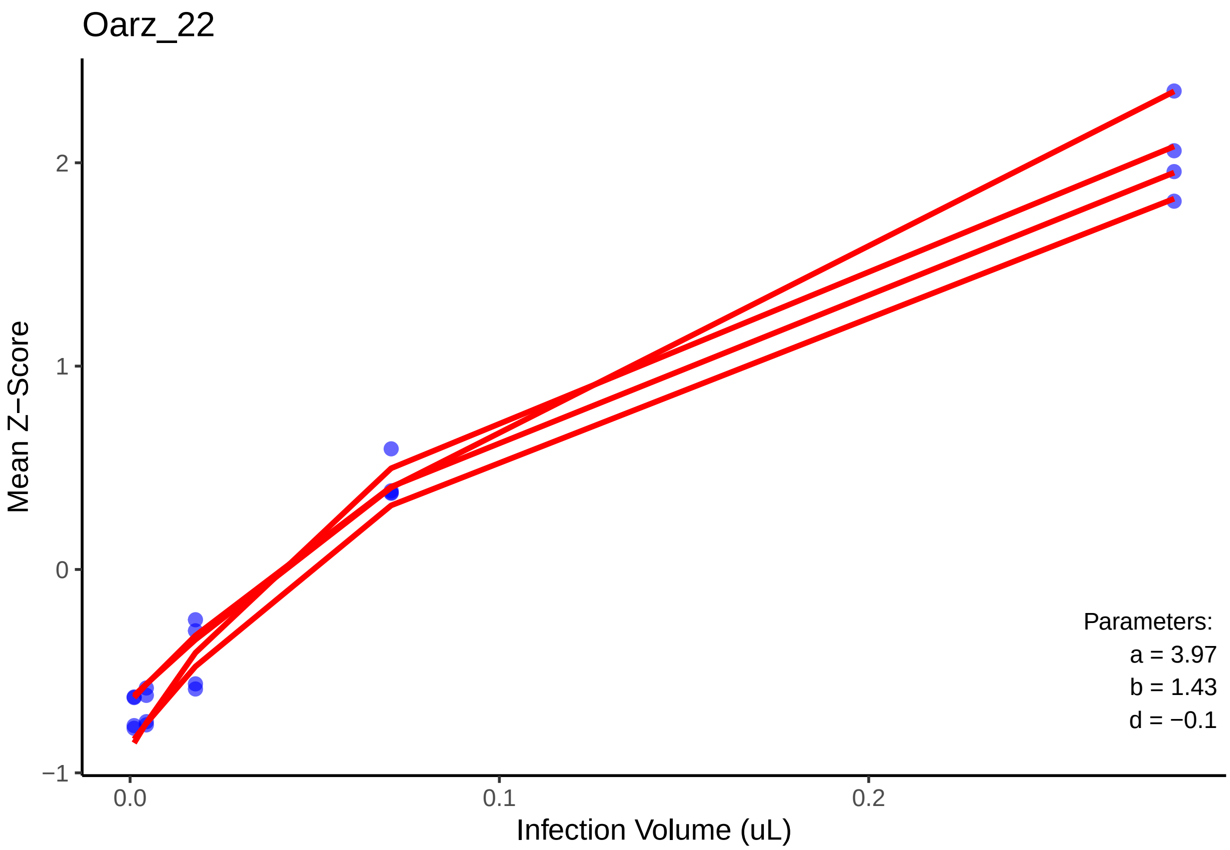
```
##
## $Oapq_5
```


Oapq_5
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.19
b = 0.58
d = −0.03

```
##
## $Oaqd_2
```

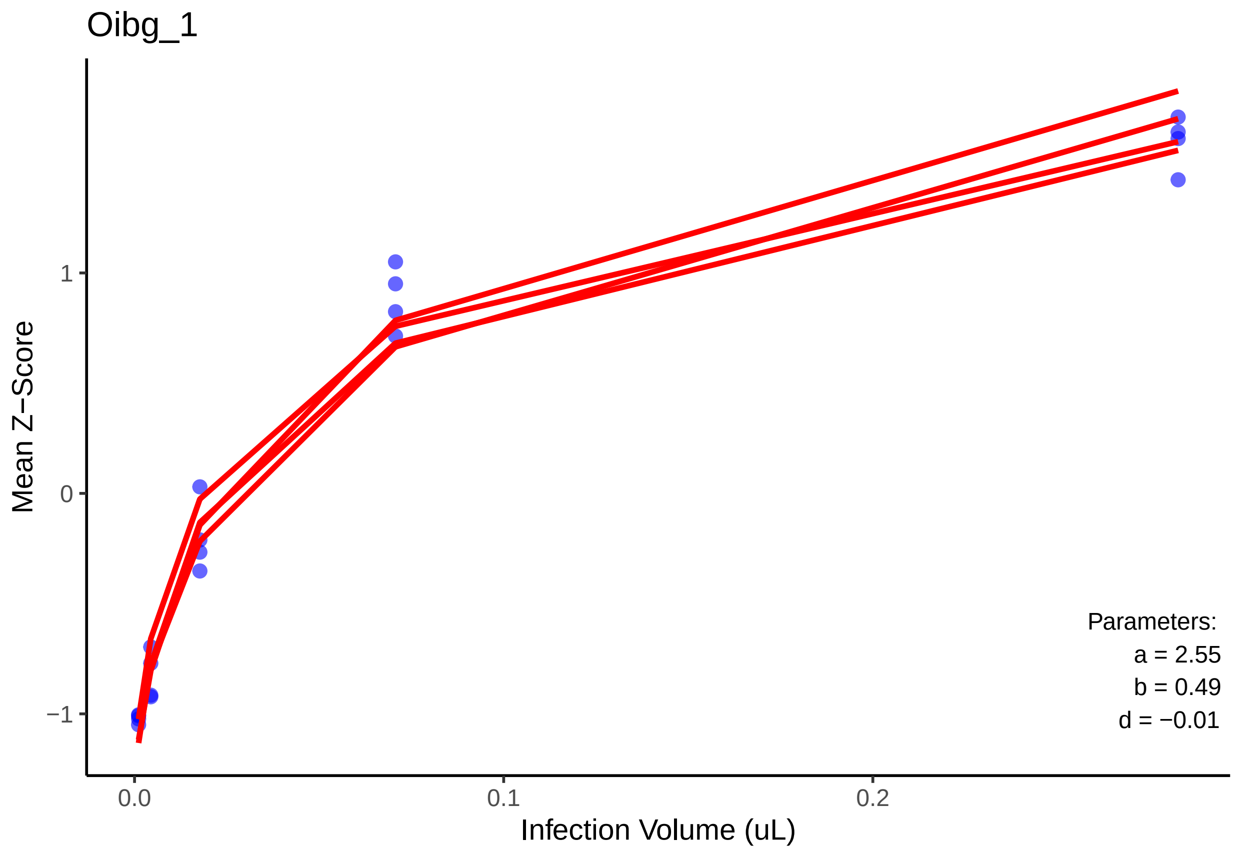

Oaqd_2
Mean Z−Score
Infection Volume (uL)
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Parameters:
a = 2.27
b = 0.6
d = −0.02

```
##
## $Oarz_22
```

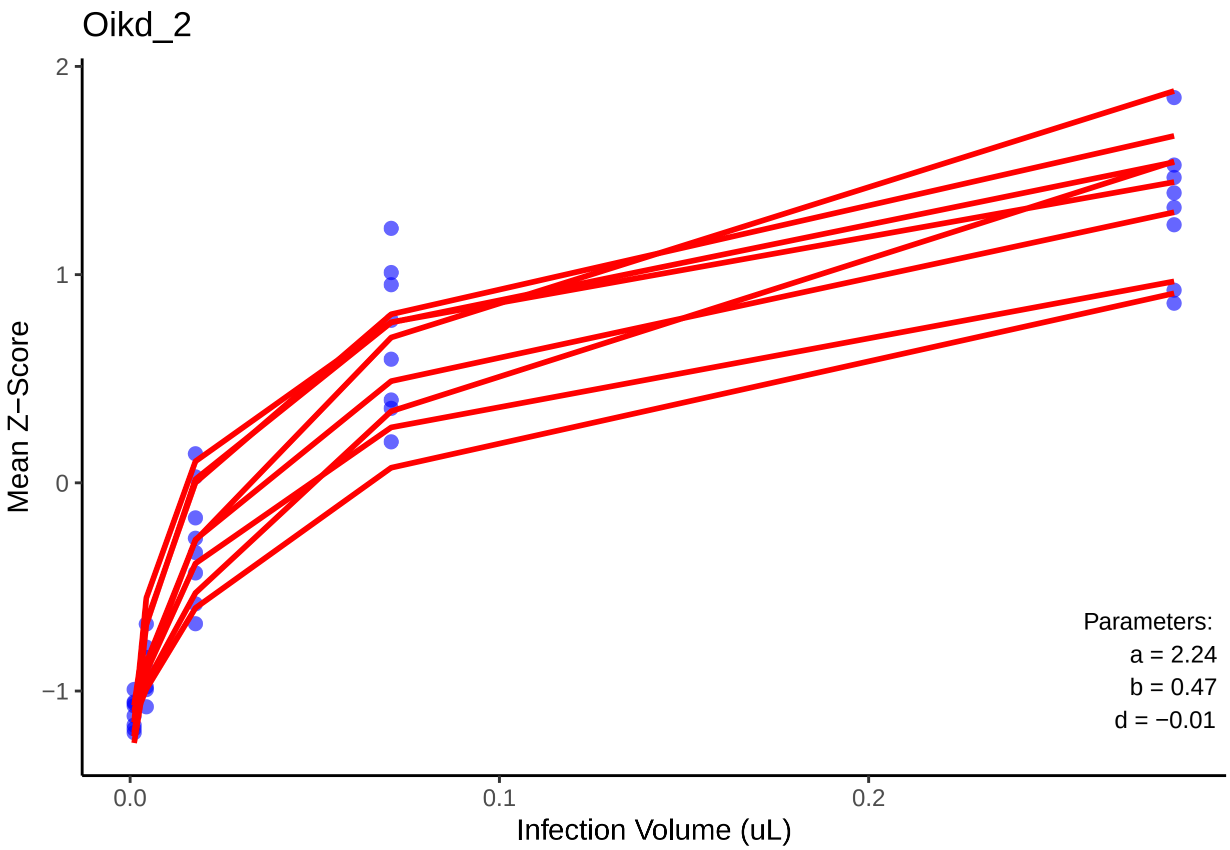


Oarz_22
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 3.97
b = 1.43
d = −0.1


```
##
## $Oibg_1
```

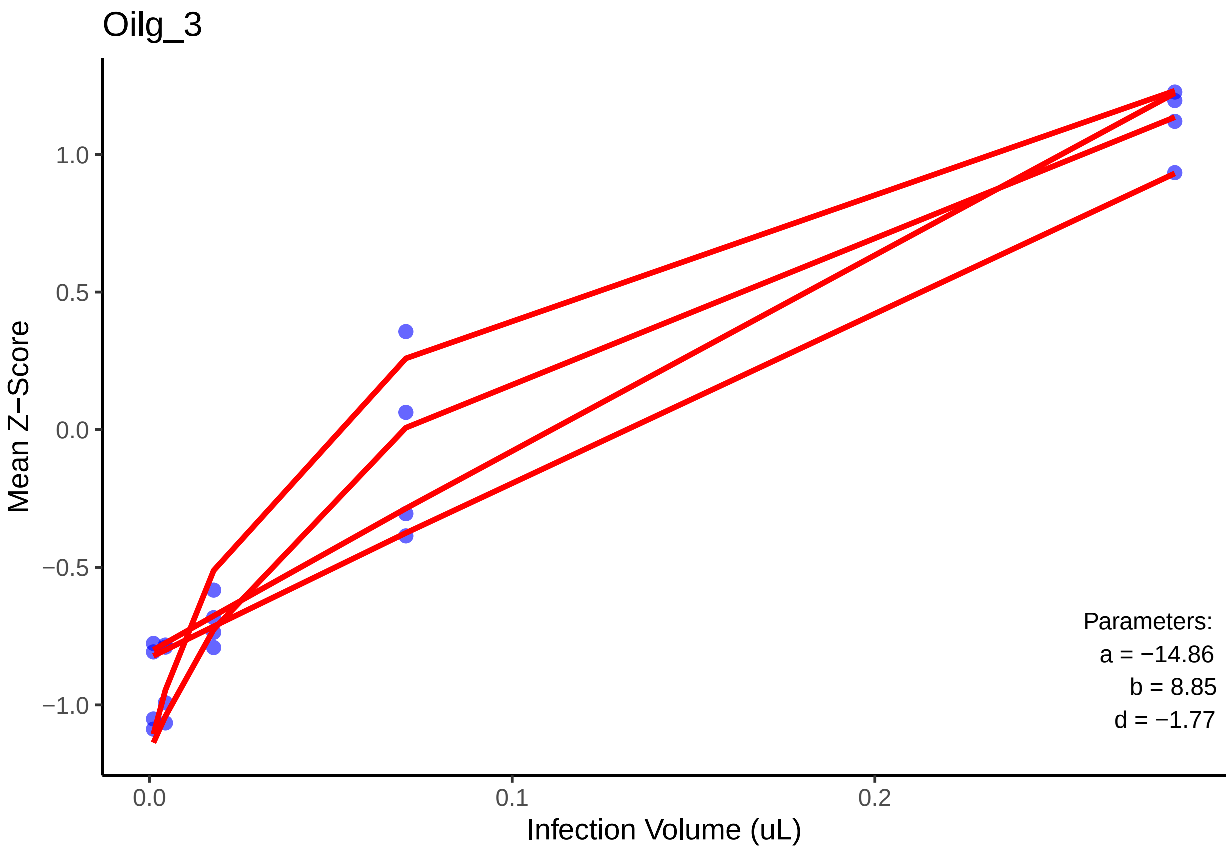

Oibg_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.55
b = 0.49
d = −0.01

```
##
## $Oikd_2
```

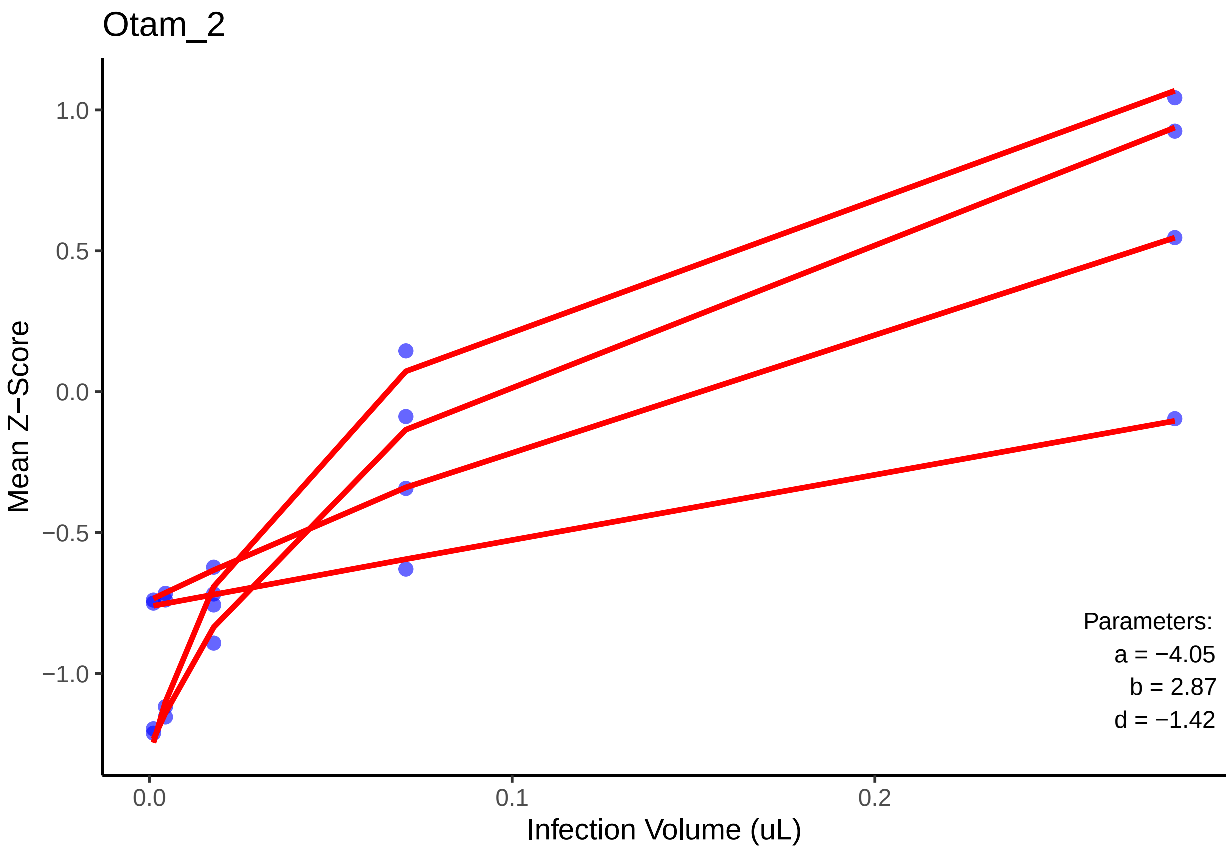


Oikd_2
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.24
b = 0.47
d = −0.01

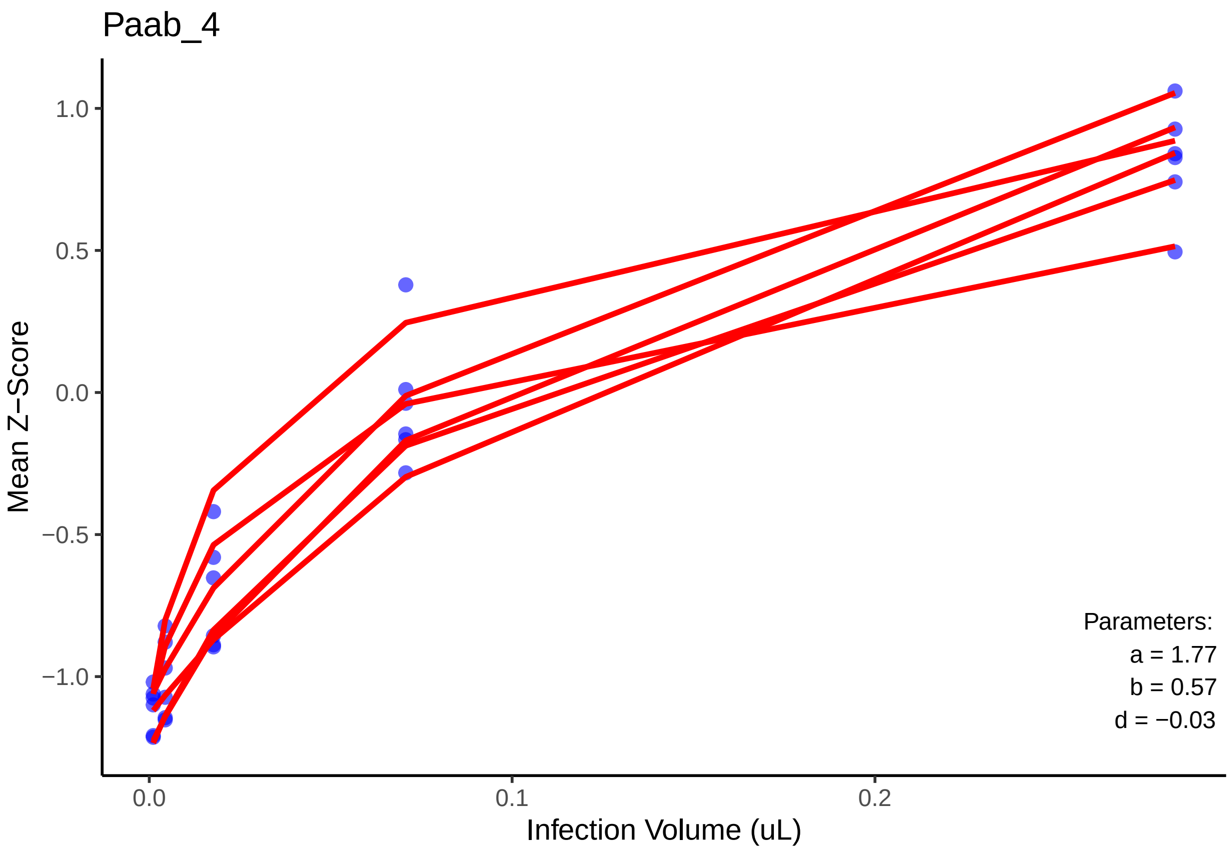

```
##
## $Oilg_3
```


Oilg_3
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = −14.86
b = 8.85
d = −1.77

```
##
## $Otam_2
```

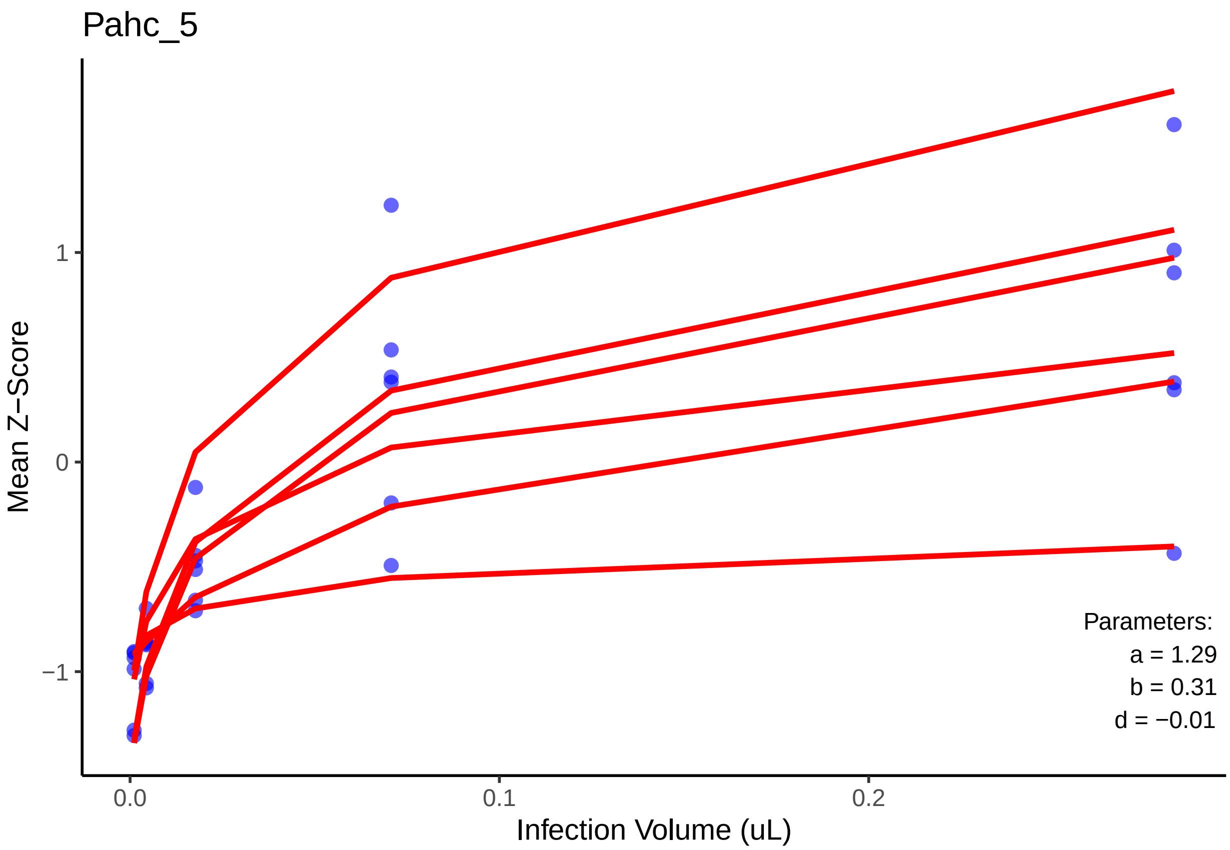

Otam_2
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = −4.05
b = 2.87
d = −1.42

```
##
## $Paab_4
```



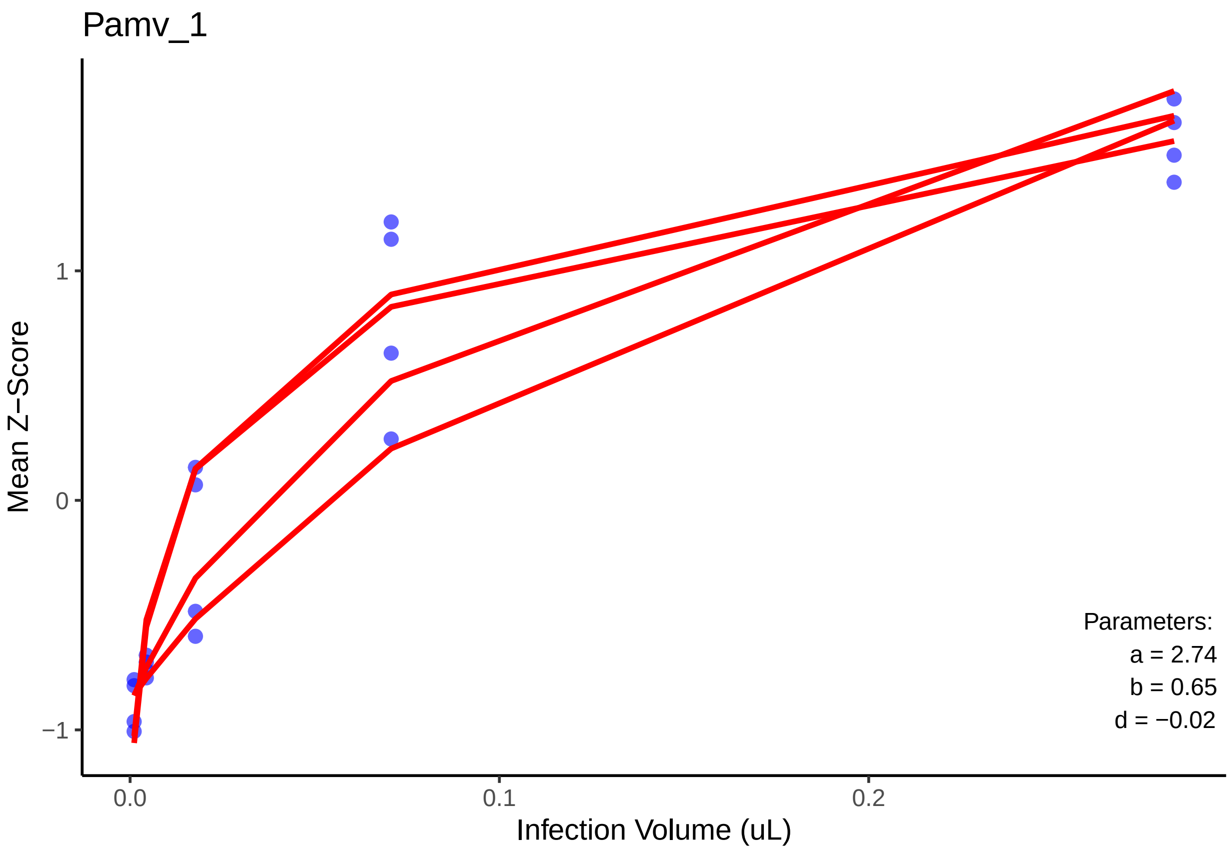
Paab_4
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.77
b = 0.57
d = −0.03


```
##
## $Pahc_5
```

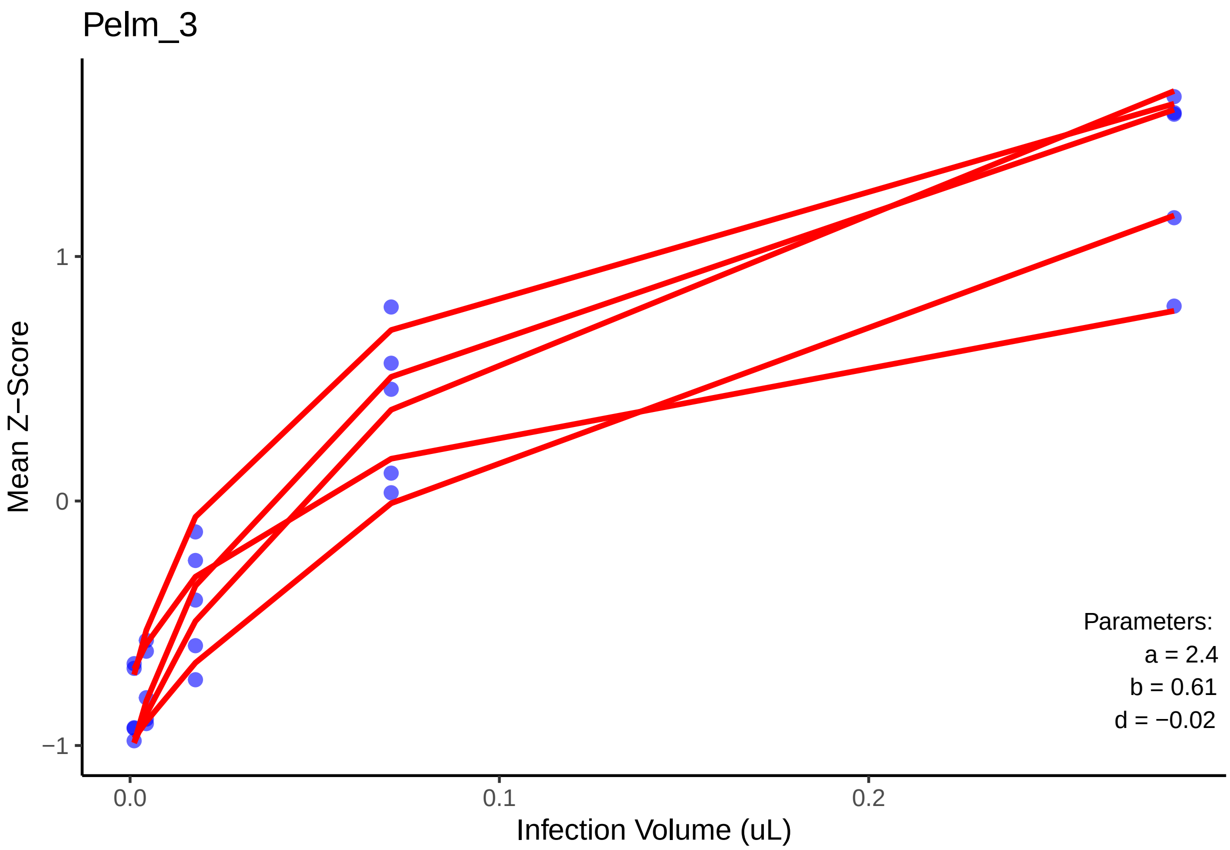


Pahc_5
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.29
b = 0.31
d = −0.01

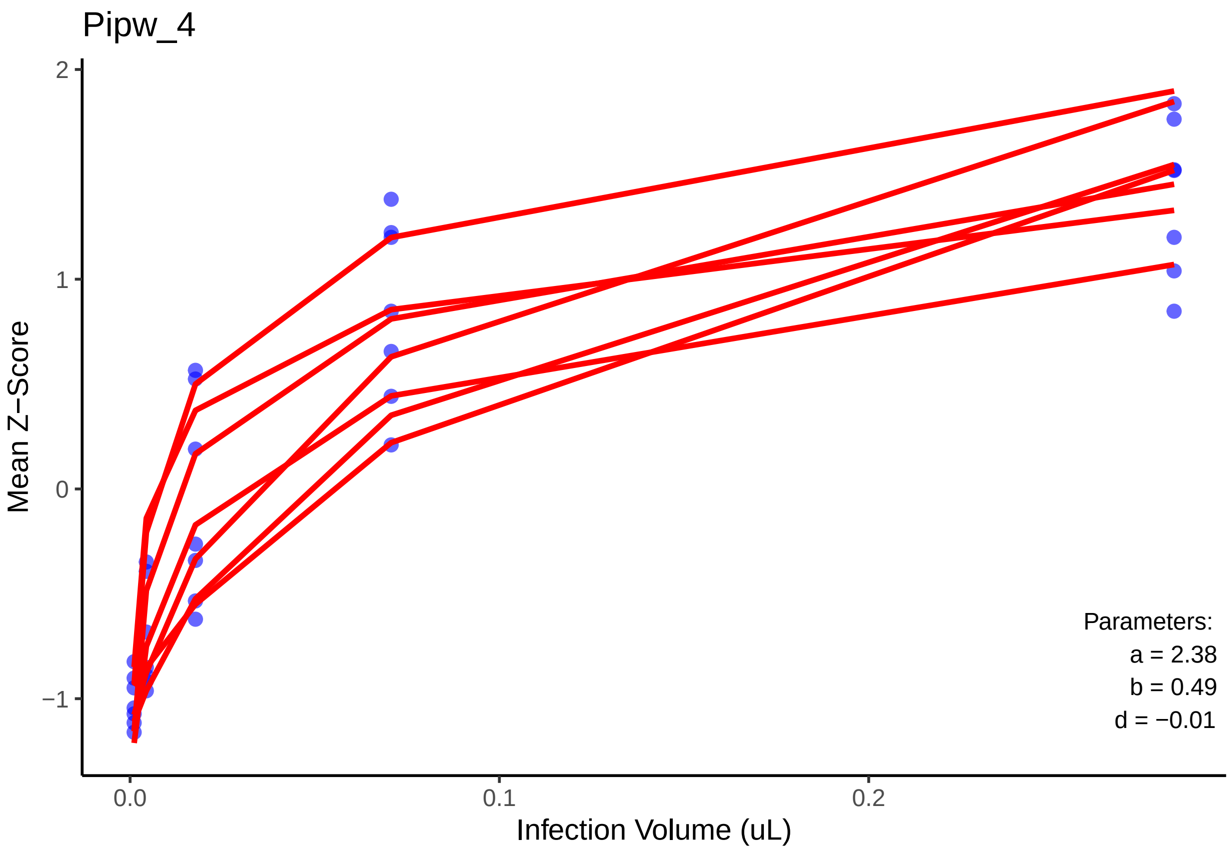

```
##
## $Pamv_1
```


Pamv_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.74
b = 0.65
d = −0.02

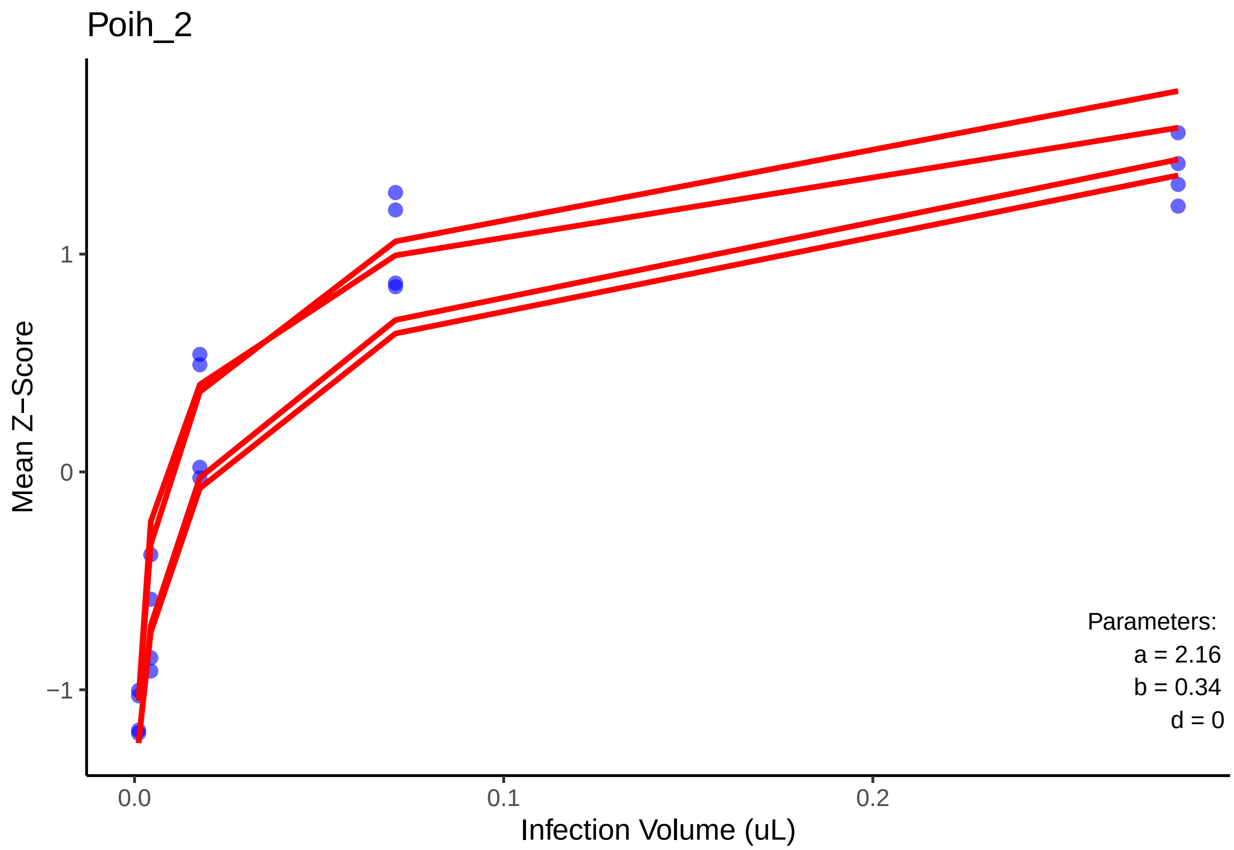
```
##
## $Pelm_3
```


Pelm_3
Mean Z−Score
Infection Volume (uL)
Parameters:
a = 2.4
b = 0.61
d = −0.02
1
0
−1
0.0
0.1
0.2

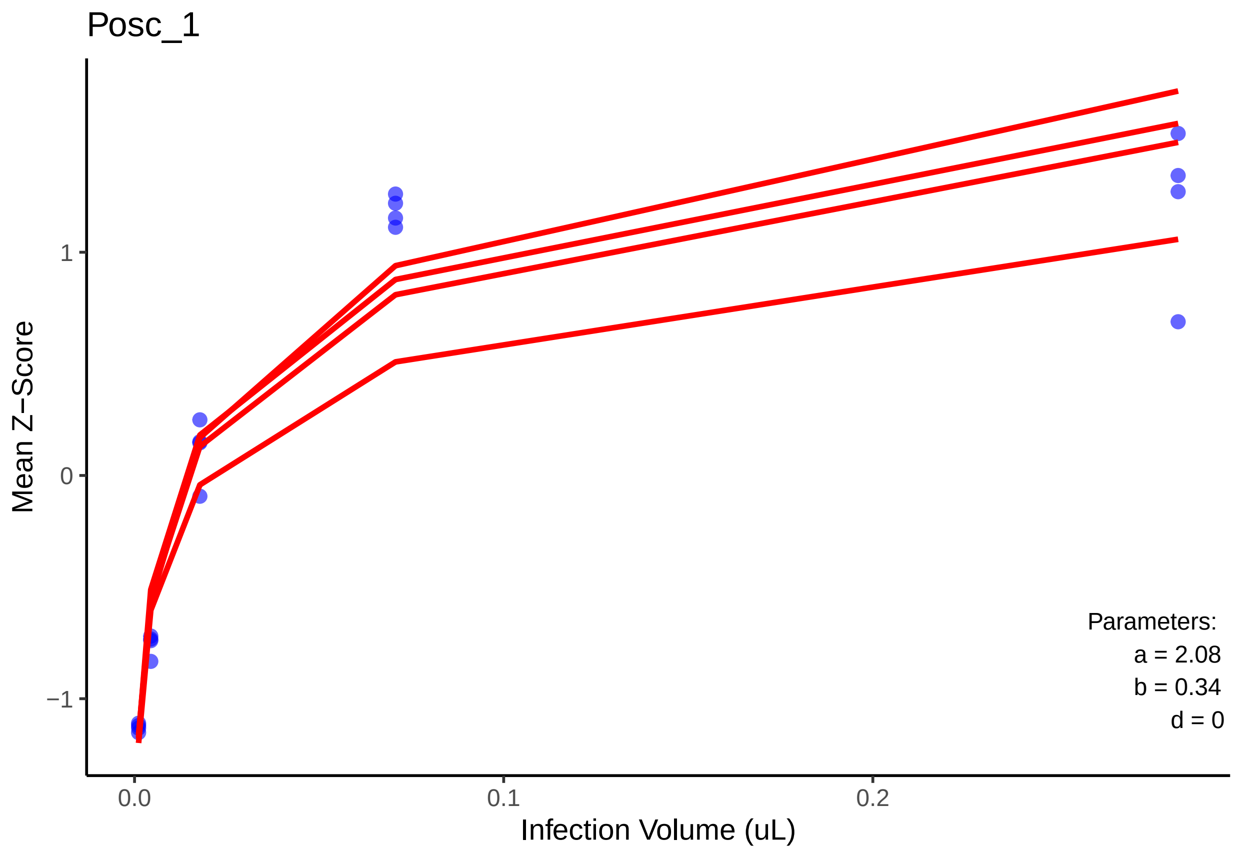
```
##
## $Pipw_4
```


Pipw_4
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.38
b = 0.49
d = −0.01

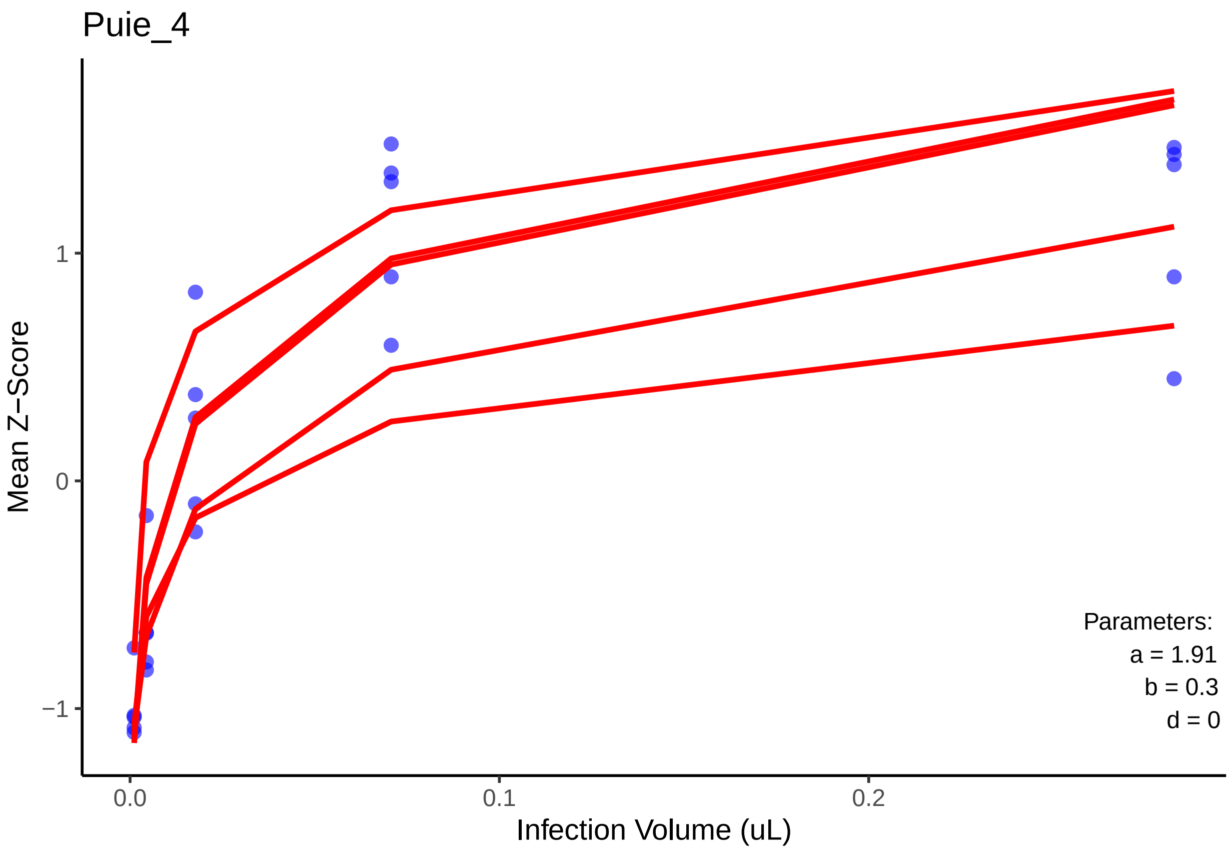
```
##
## $Poih_2
```


Poih_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.16
b = 0.34
d = 0

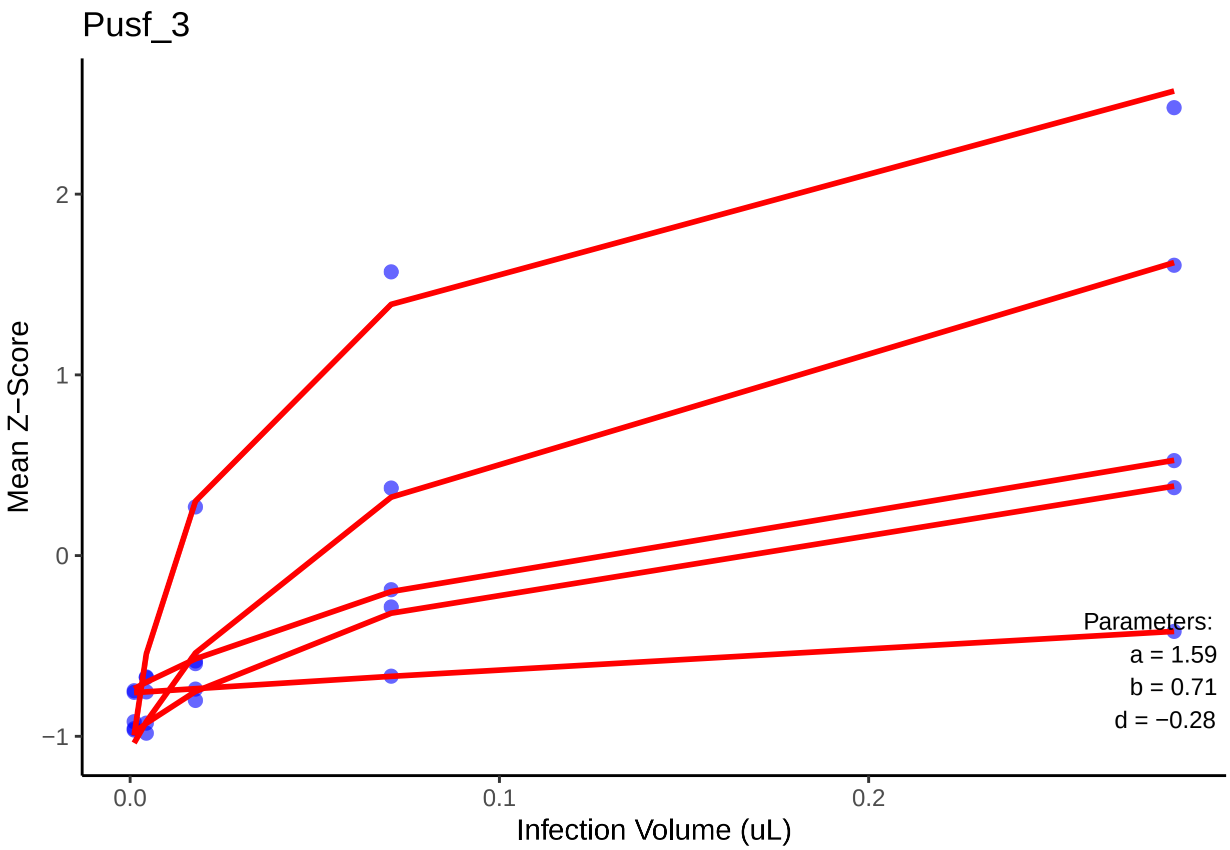
```
##
## $Posc_1
```


Posc_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.08
b = 0.34
d = 0

```
##
## $Puie_4
```


Puie_4
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.91
b = 0.3
d = 0

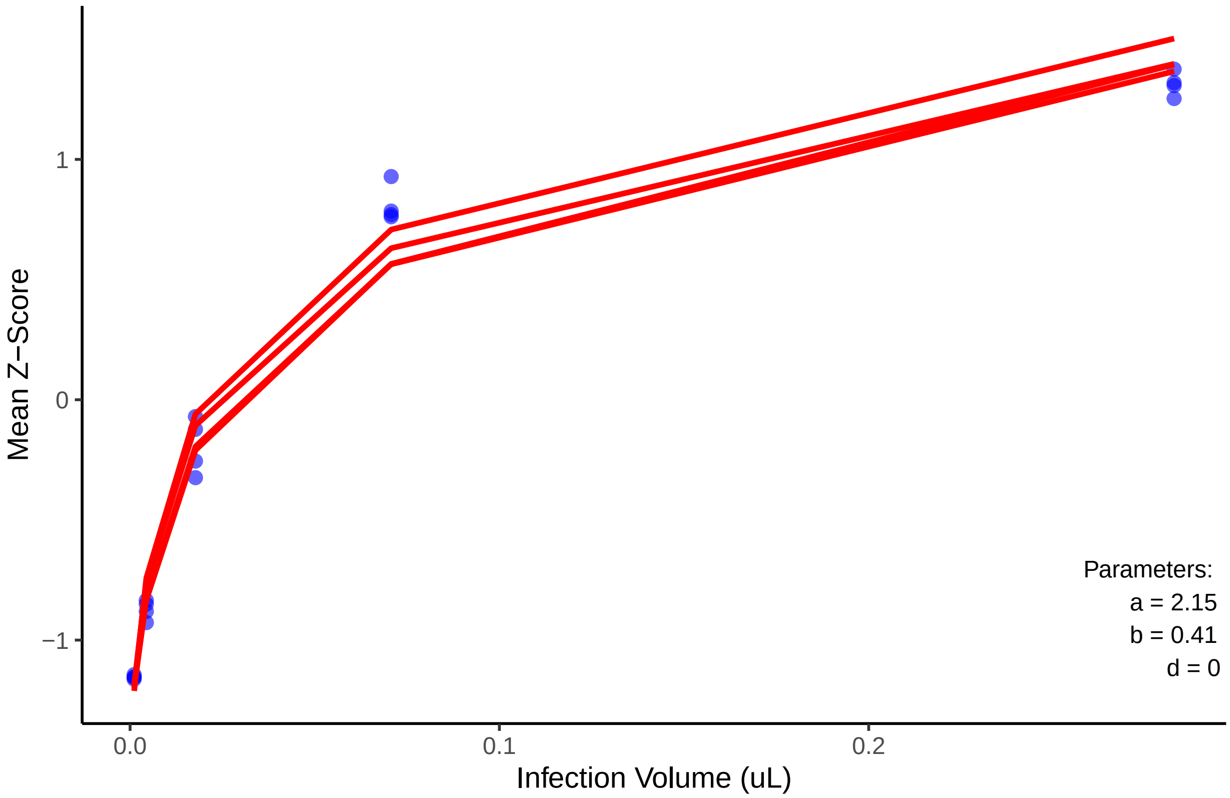
```
##
## $Pusf_3
```



Pusf_3
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 1.59
b = 0.71
d = −0.28

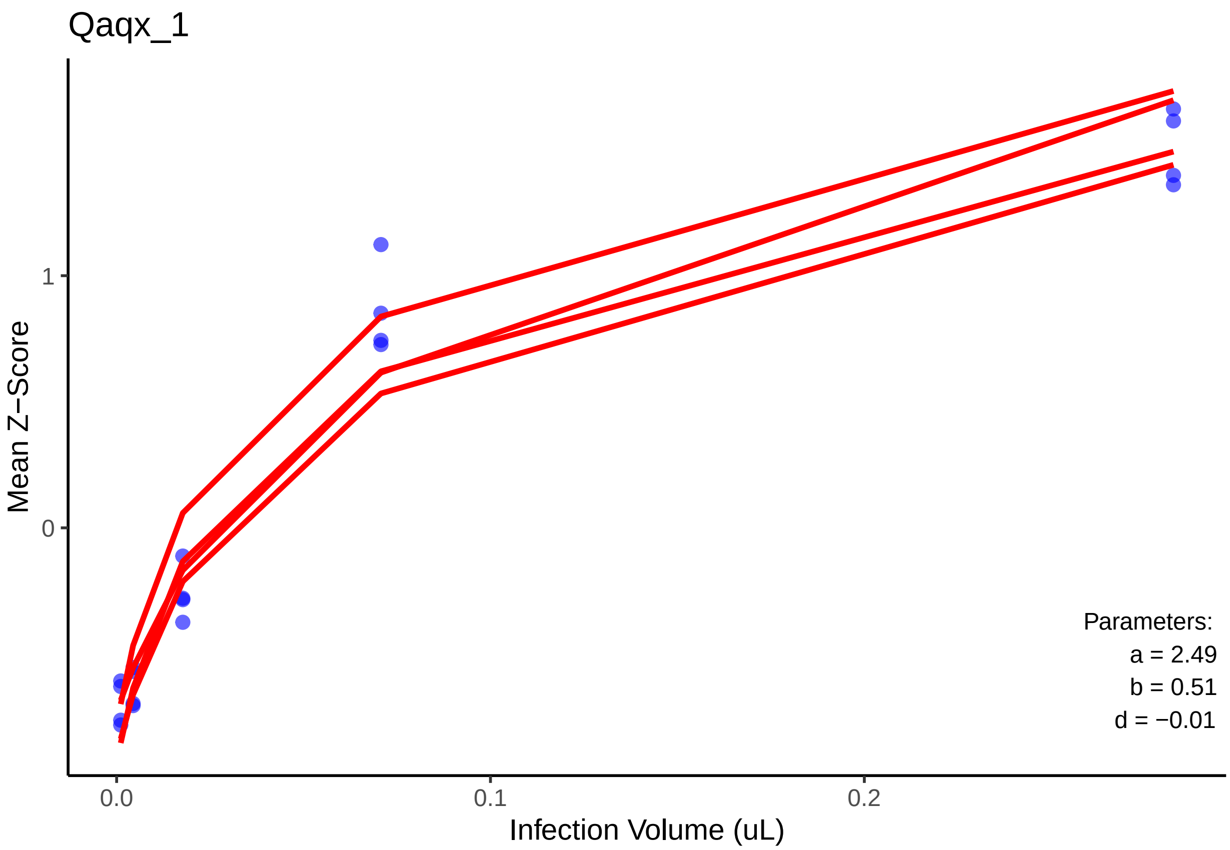

```
##
## $Qanu_1
```

Qanu_1



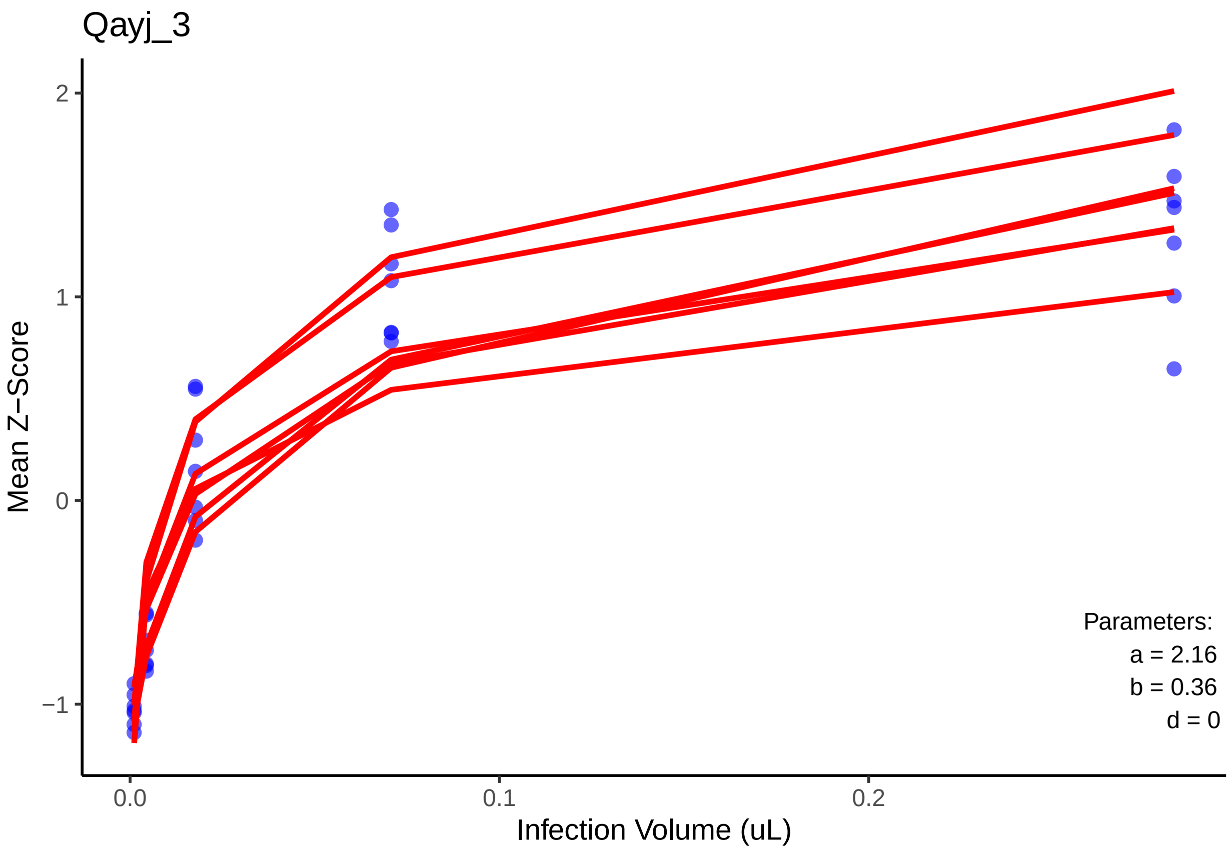
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.15
b = 0.41
d = 0


```
##
## $Qaqx_1
```



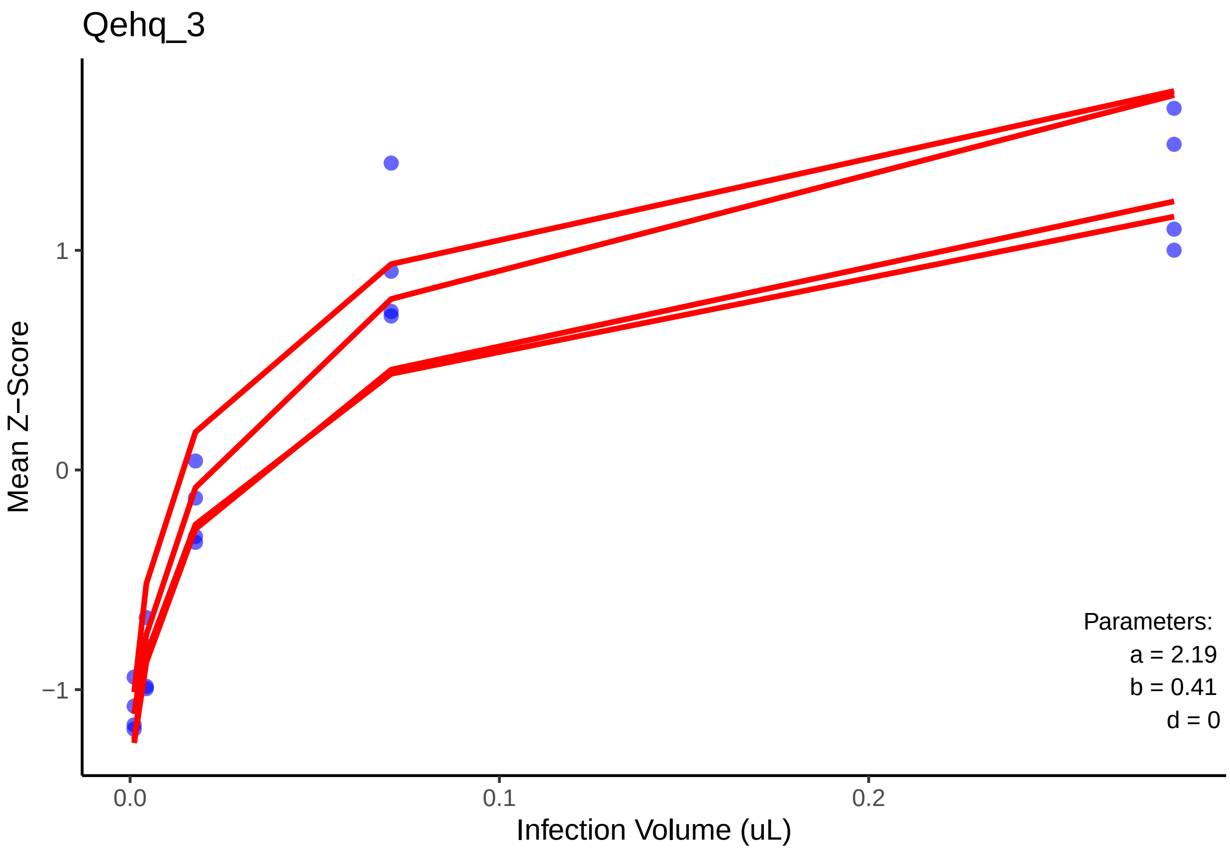
Qaqx_1
Mean Z−Score
1
0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.49
b = 0.51
d = −0.01


```
##
## $Qayj_3
```



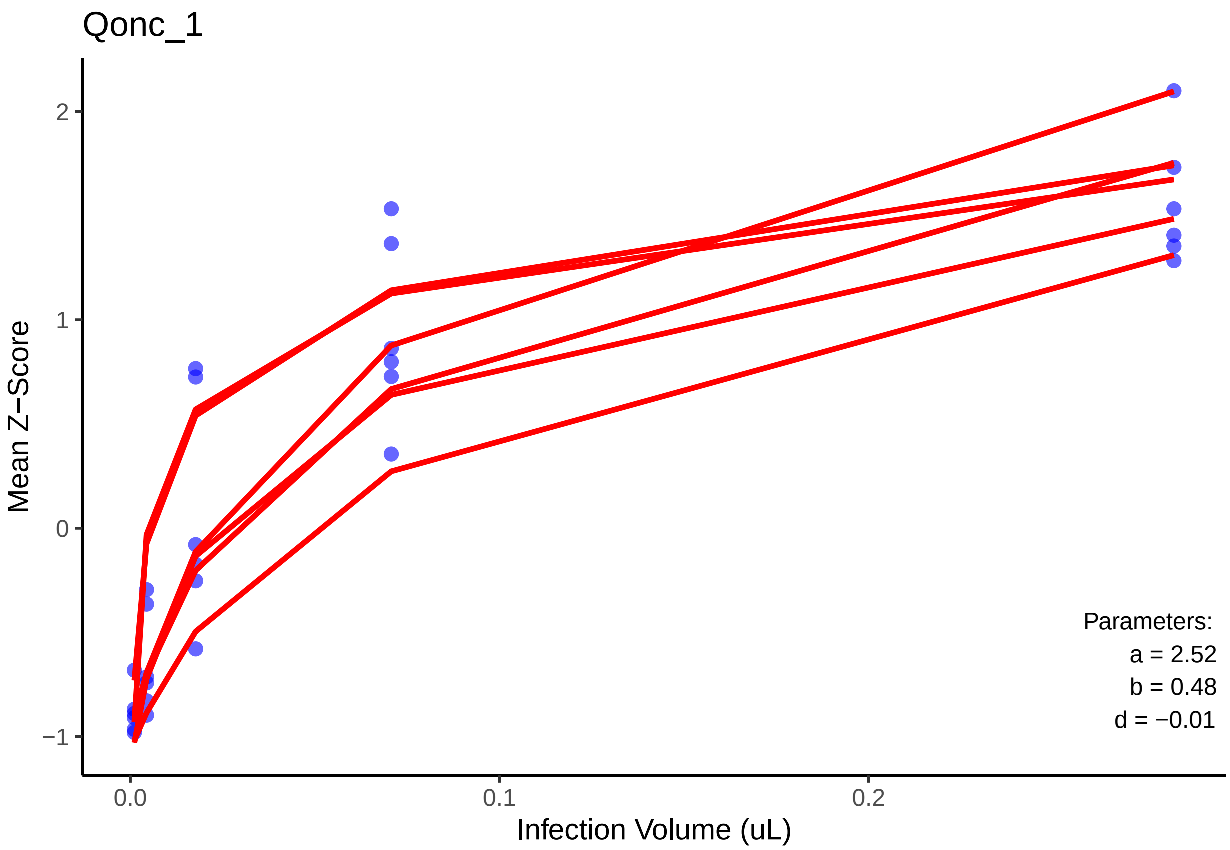
Qayj_3
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.16
b = 0.36
d = 0


```
##
## $Qehq_3
```

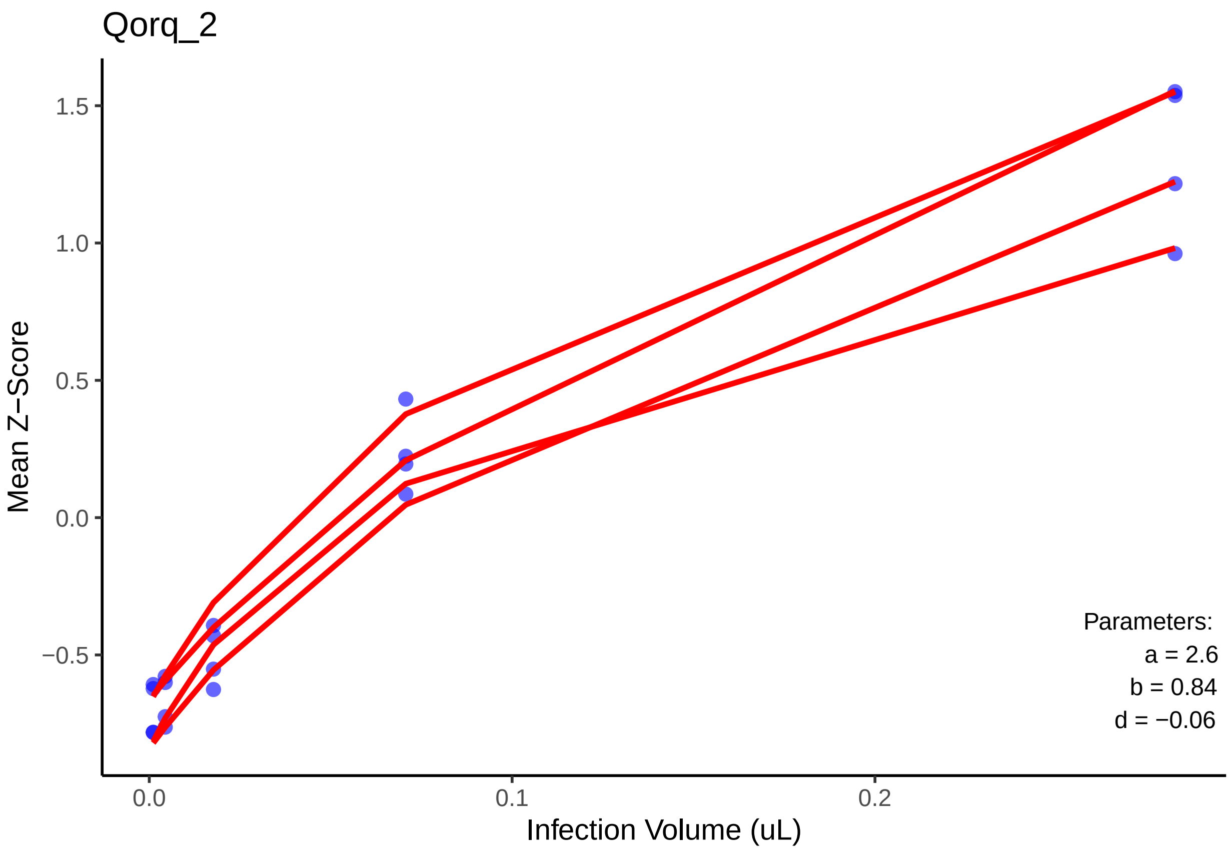


Qehq_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.19
b = 0.41
d = 0

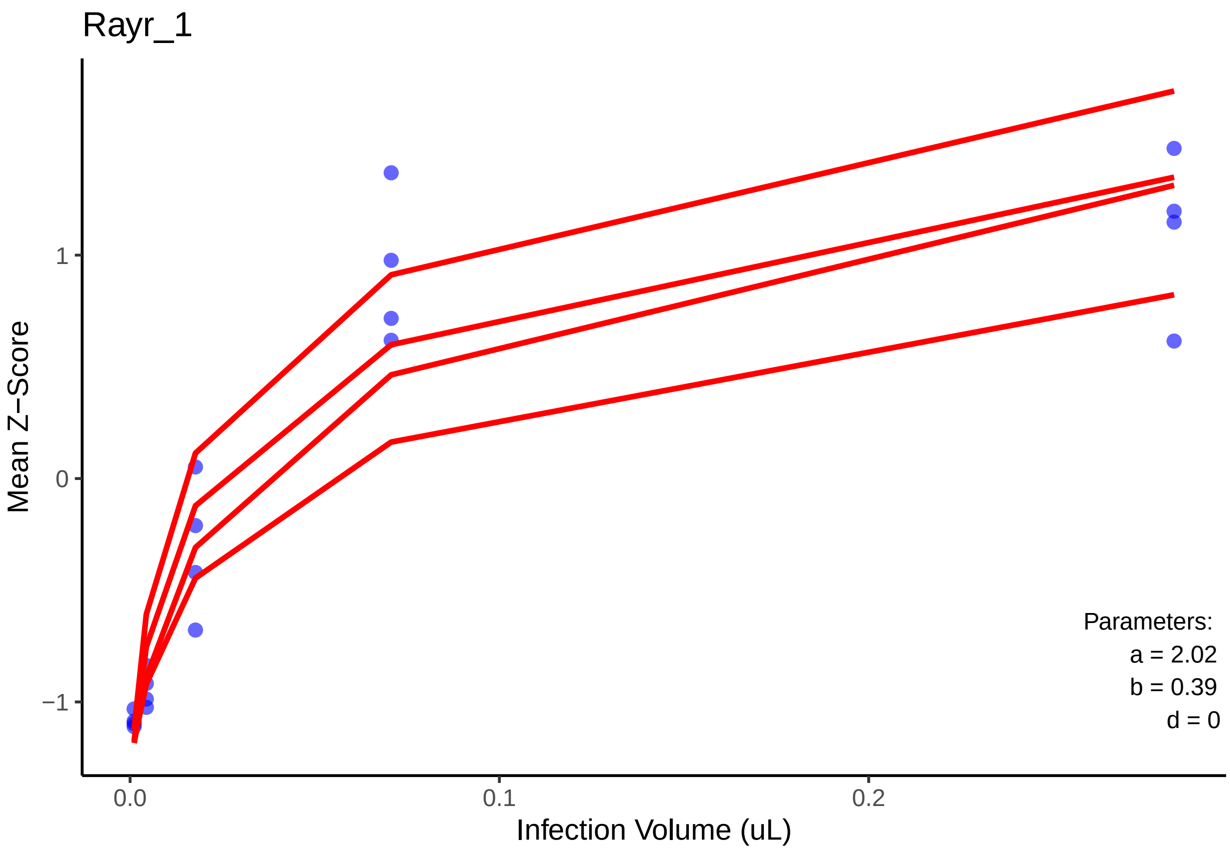

```
##
## $Qonc_1
```


Qonc_1
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.52
b = 0.48
d = −0.01

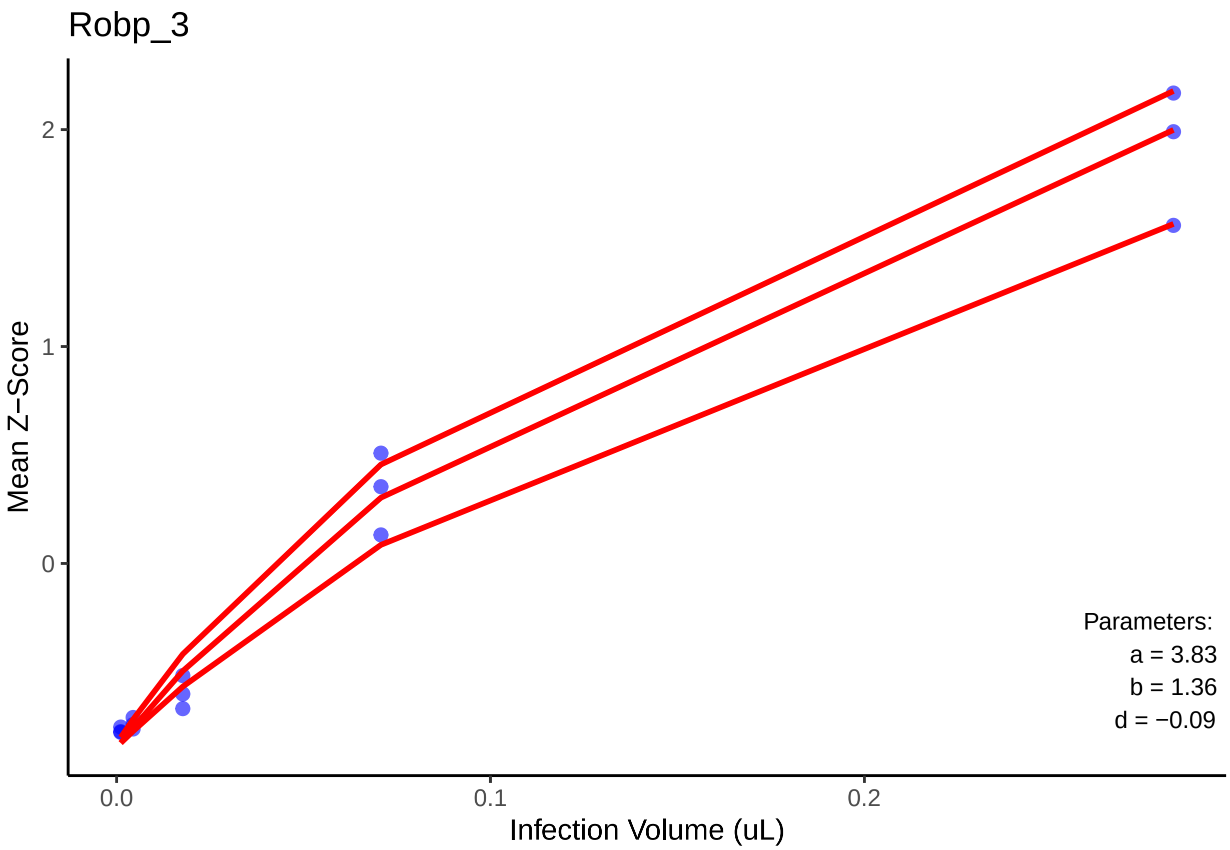
```
##
## $Qorq_2
```


Qorq_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.6
b = 0.84
d = −0.06

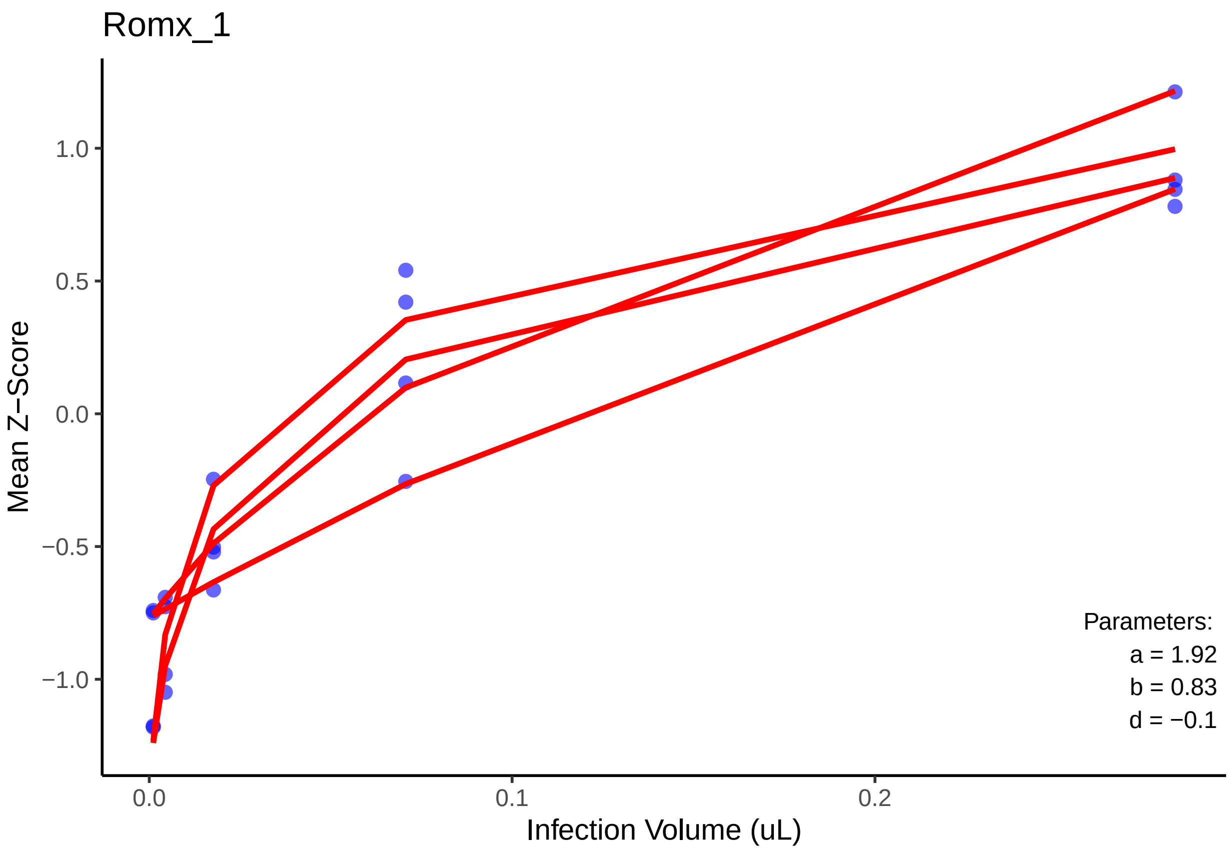
```
##
## $Rayr_1
```


Rayr_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.02
b = 0.39
d = 0

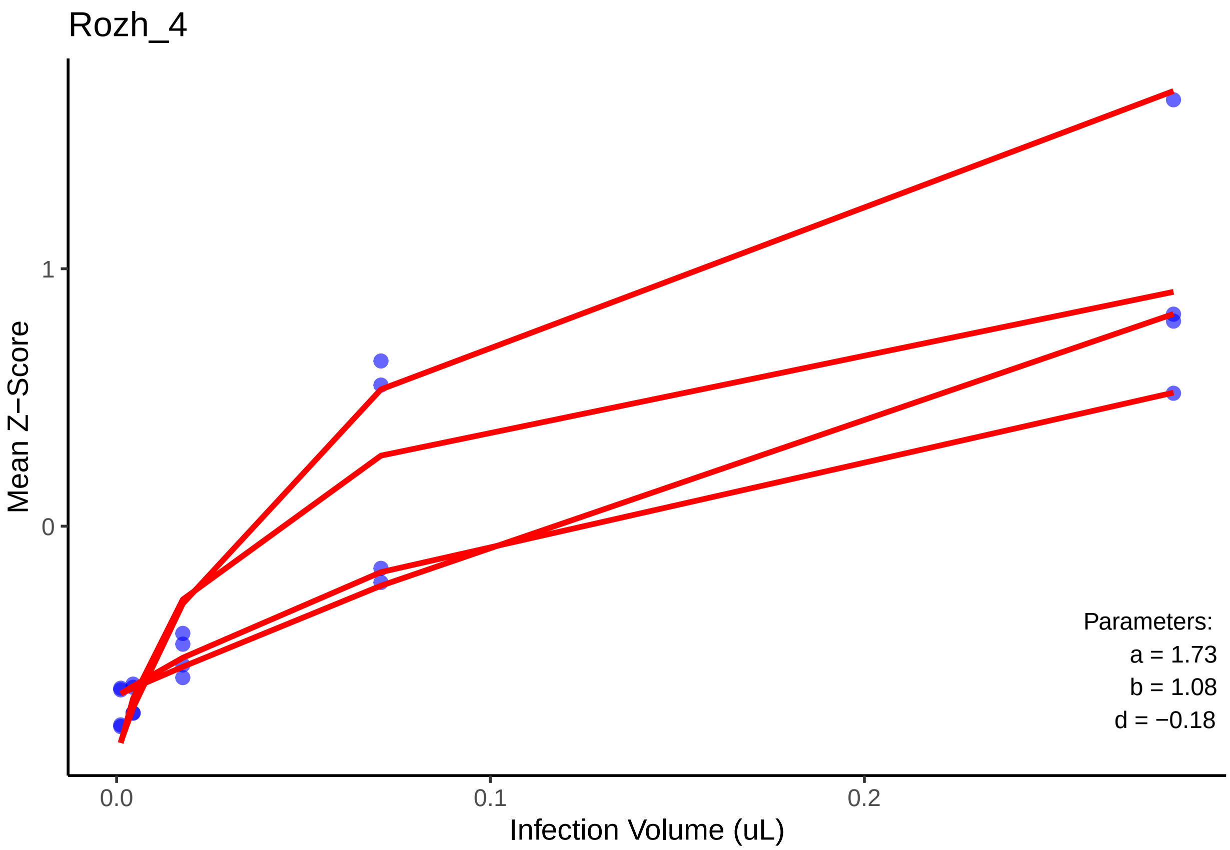
```
##
## $Robp_3
```


Robp_3
Mean Z−Score
Infection Volume (uL)
2
1
0
0.0
0.1
0.2
Parameters:
a = 3.83
b = 1.36
d = −0.09

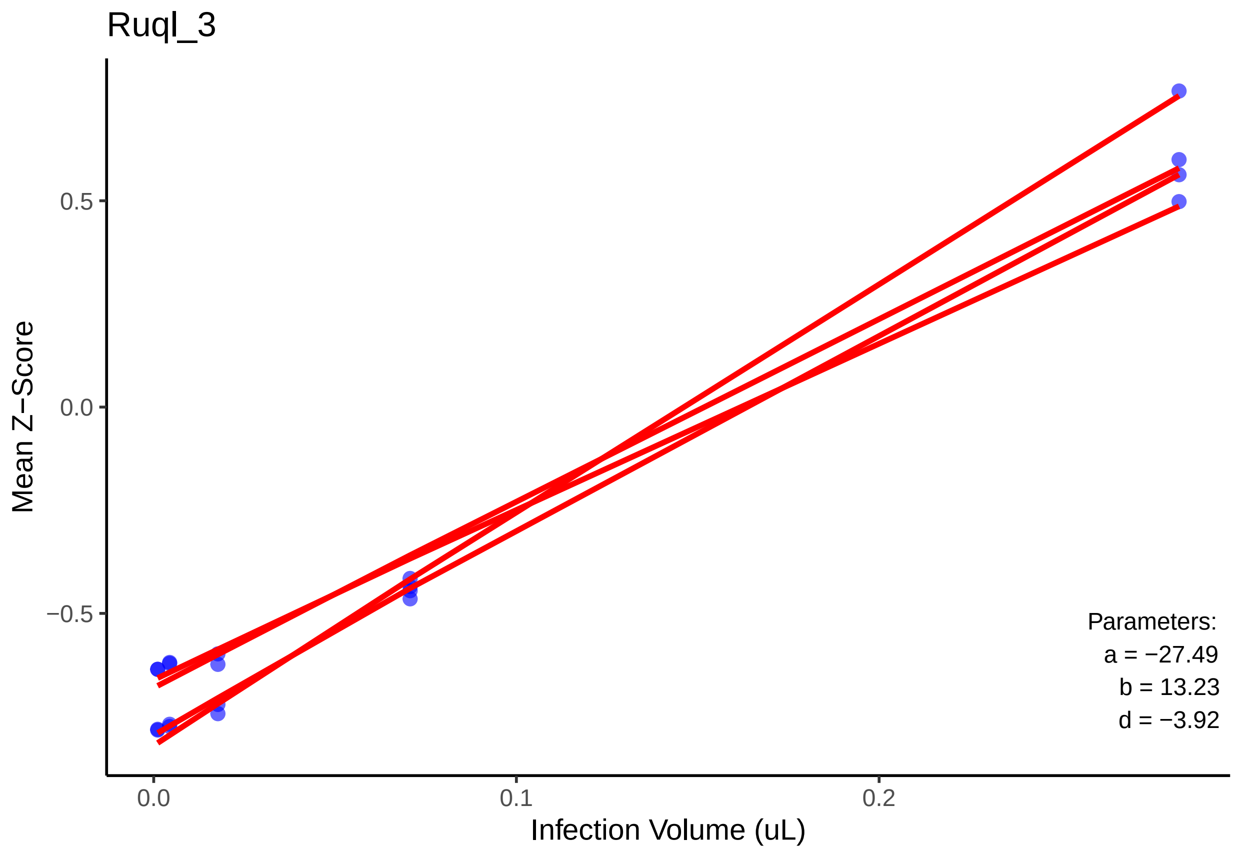
```
##
## $Romx_1
```


Romx_1
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.92
b = 0.83
d = −0.1

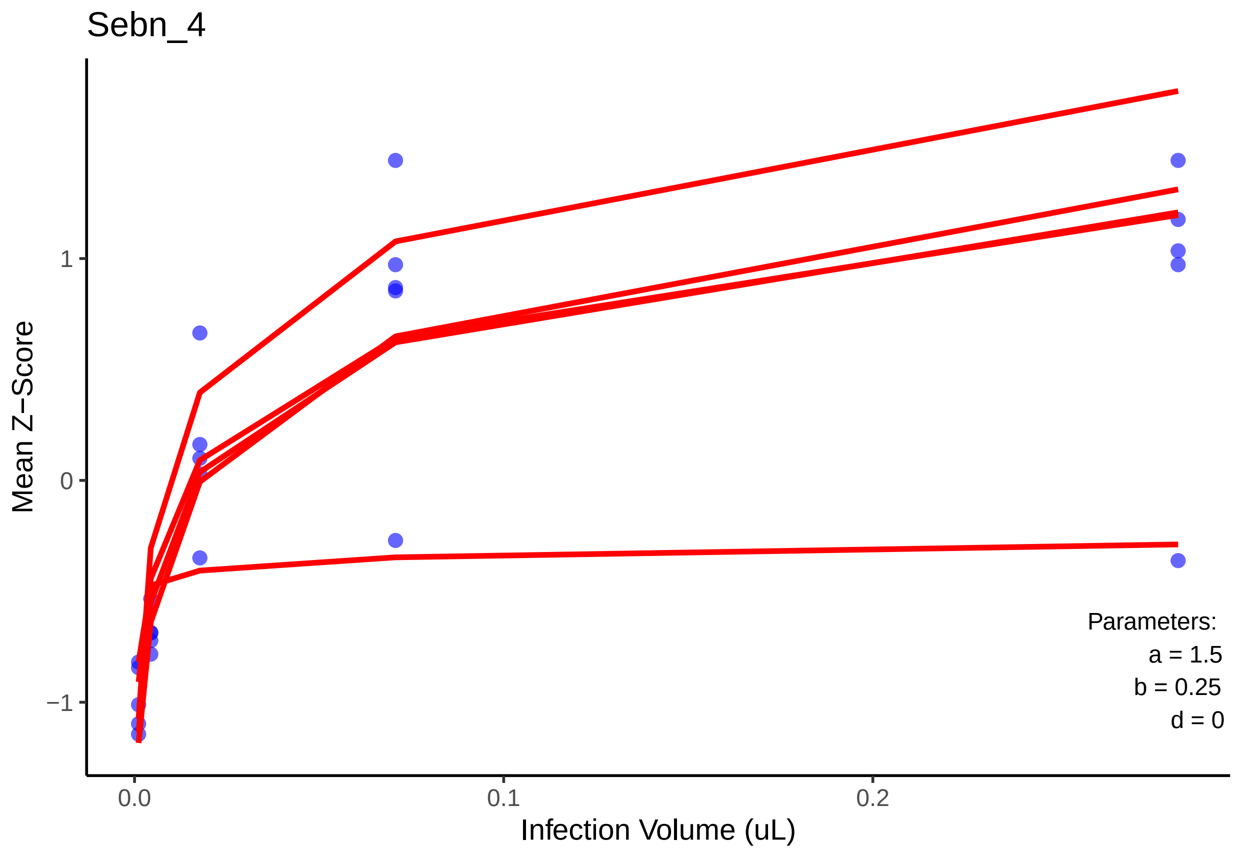
```
##
## $Rozh_4
```


Rozh_4
Mean Z−Score
Infection Volume (uL)
Parameters:
a = 1.73
b = 1.08
d = −0.18
1
0
0.0
0.1
0.2

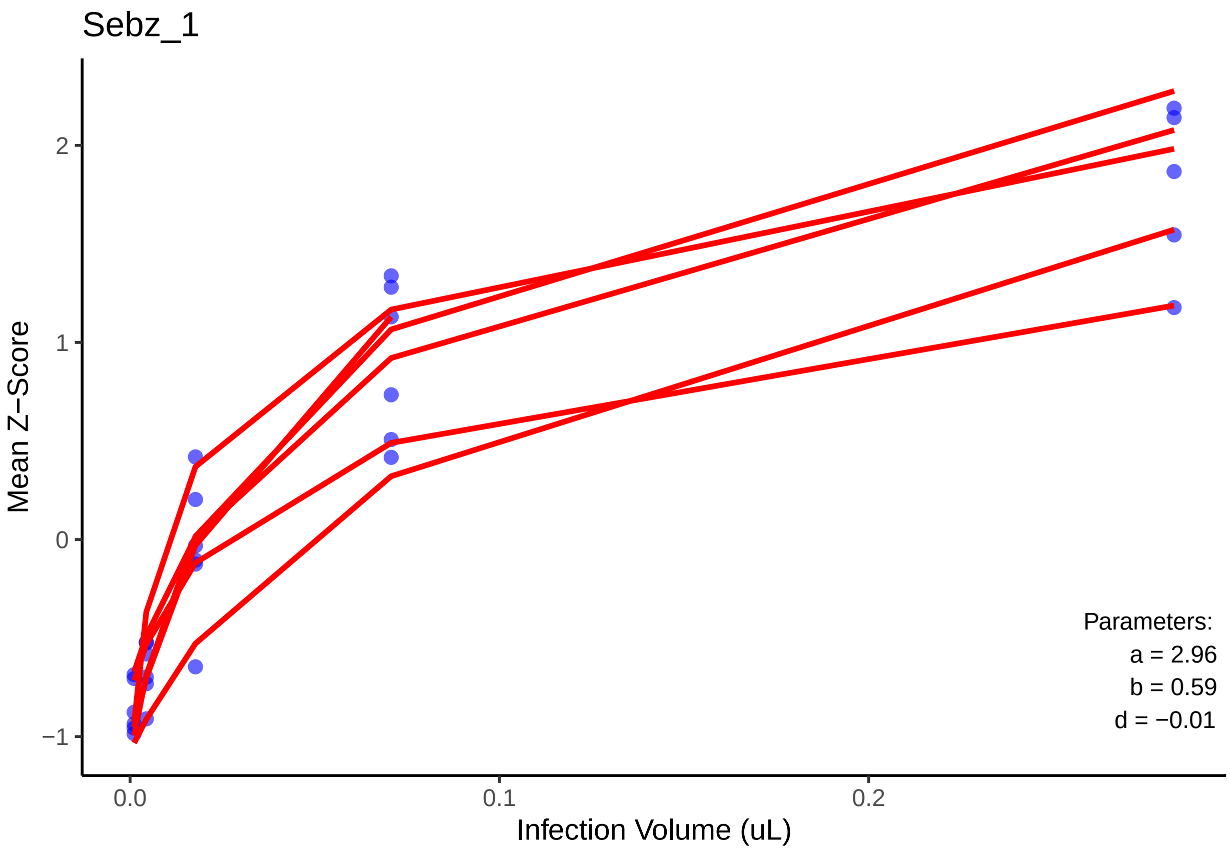
```
##
## $Ruql_3
```


Ruql_3
Mean Z−Score
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = −27.49
b = 13.23
d = −3.92

```
##
## $Sebn_4
```

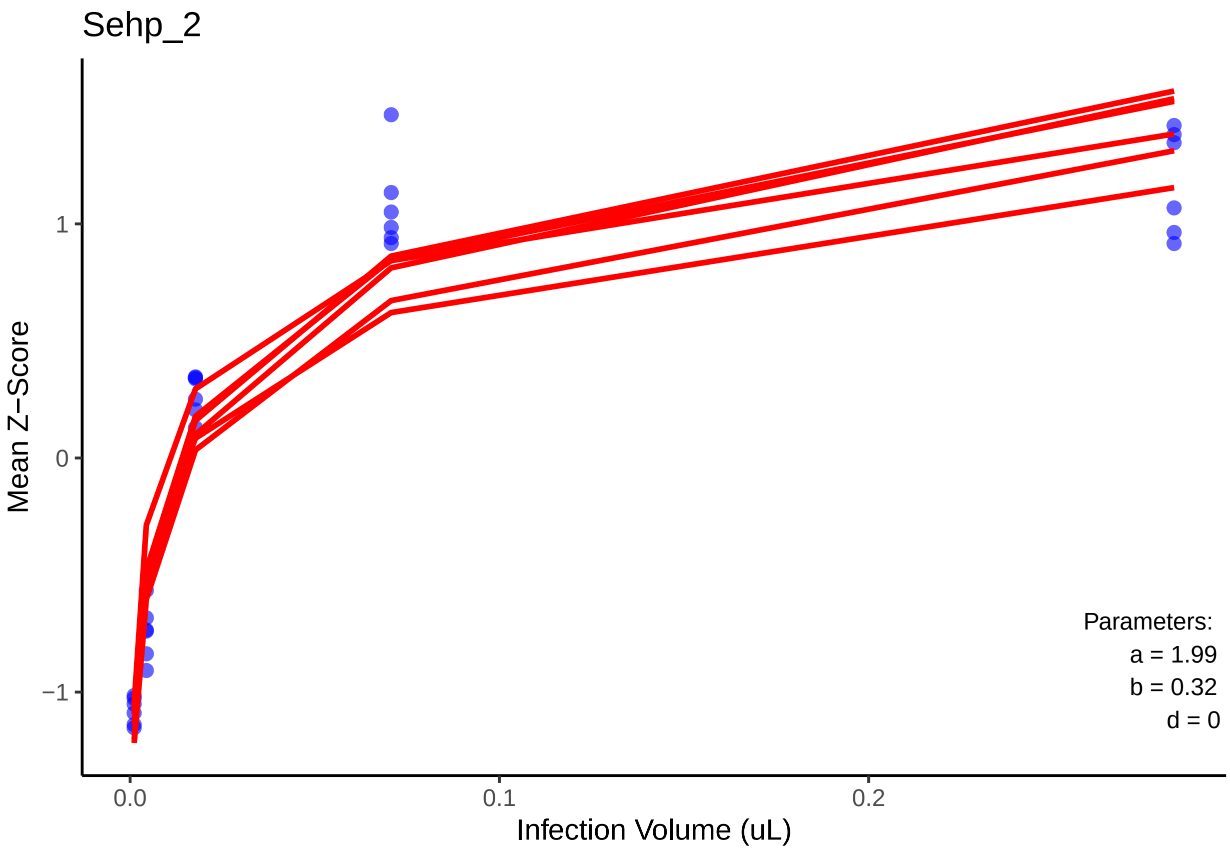

Sebn_4
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.5
b = 0.25
d = 0

```
##
## $Sebz_1
```

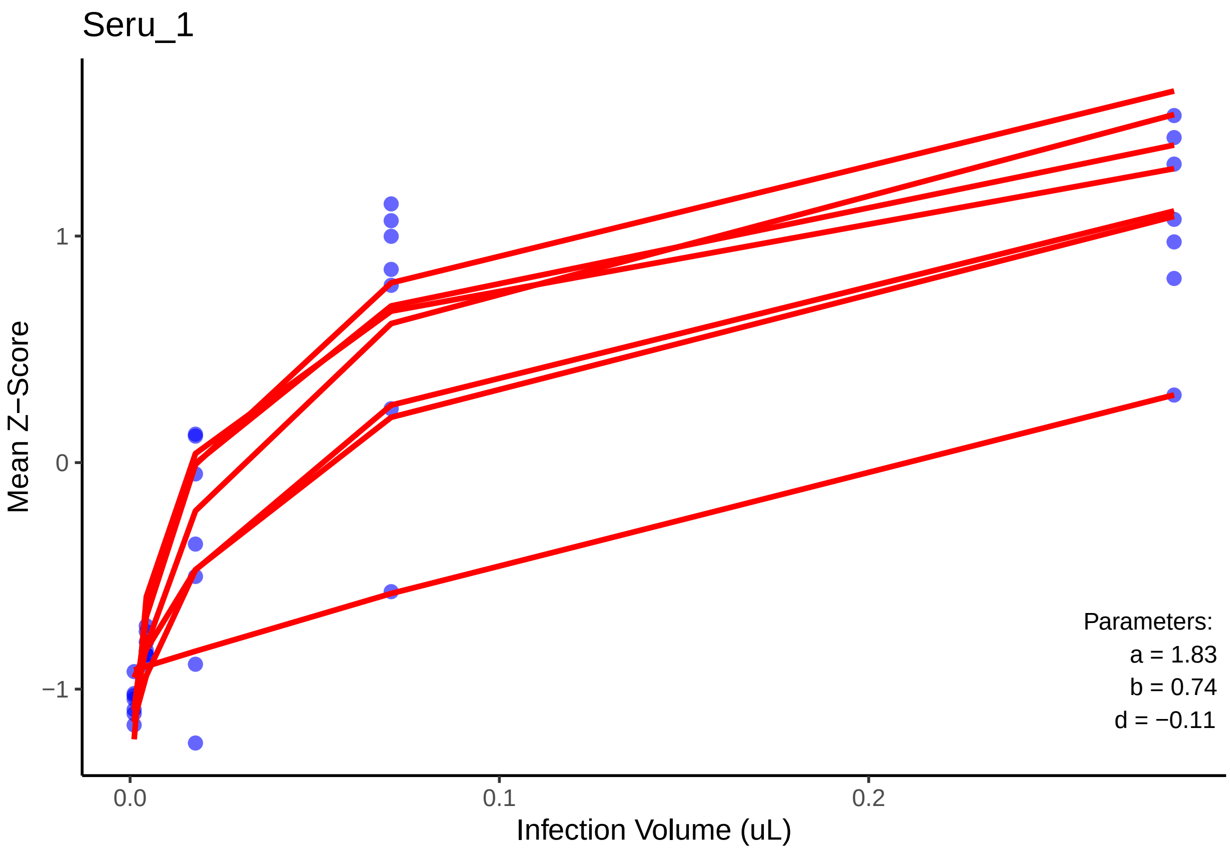


Sebz_1
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.96
b = 0.59
d = −0.01

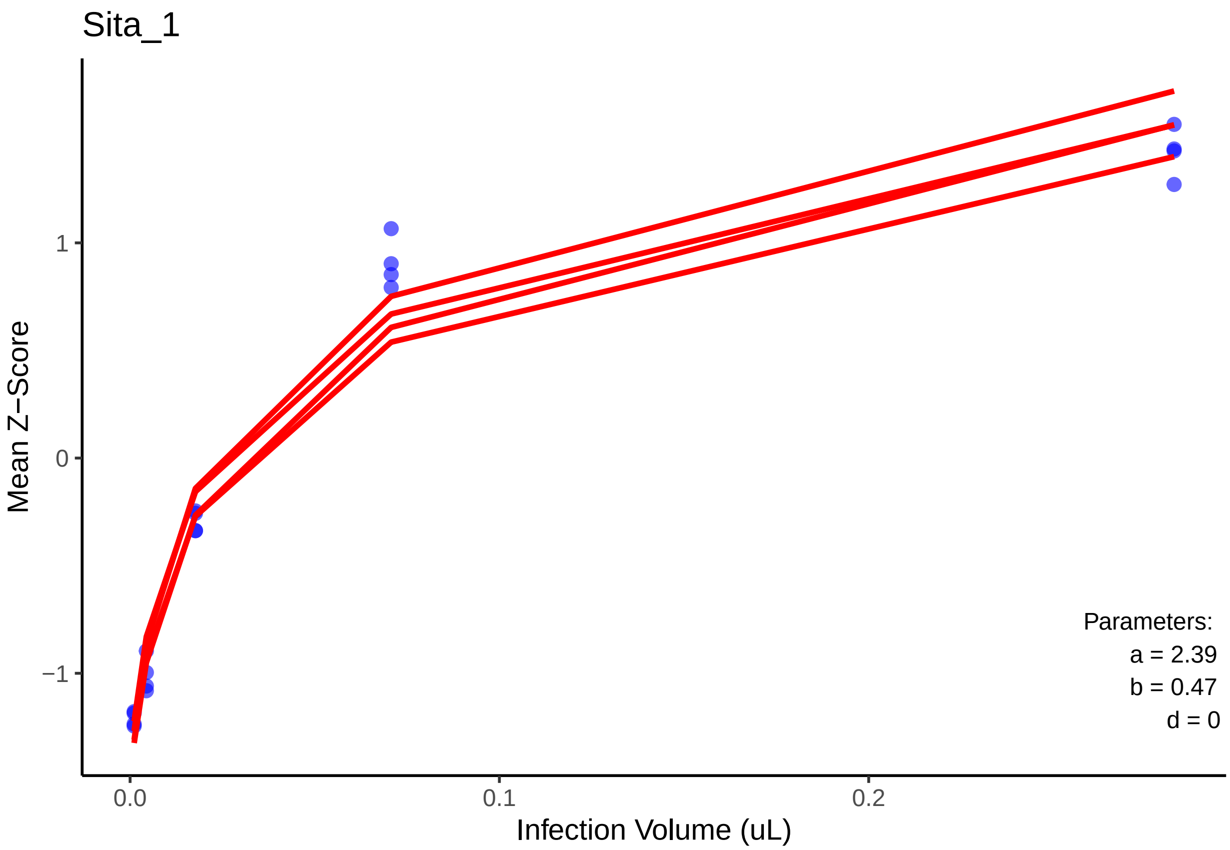

```
##
## $Sehp_2
```


Sehp_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.99
b = 0.32
d = 0

```
##
## $Seru_1
```

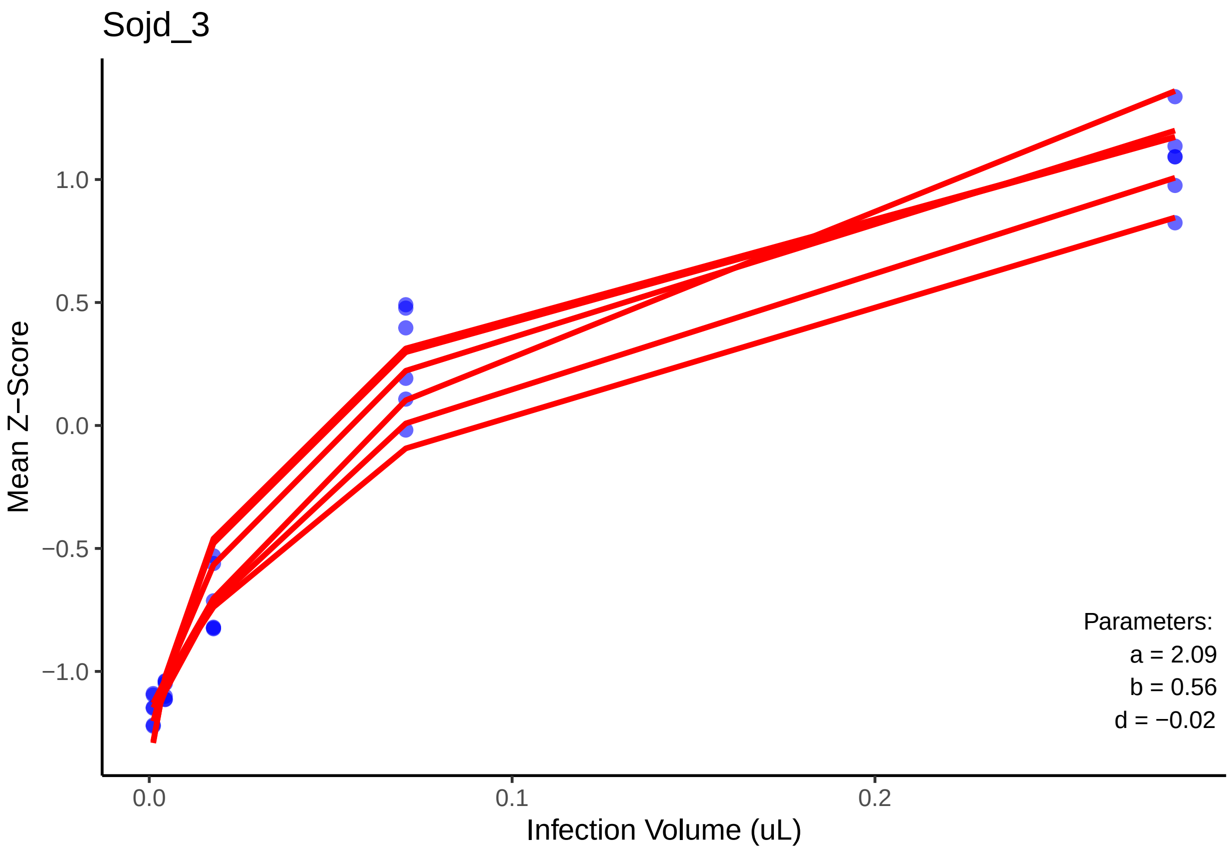

Seru_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.83
b = 0.74
d = −0.11

```
##
## $Sita_1
```

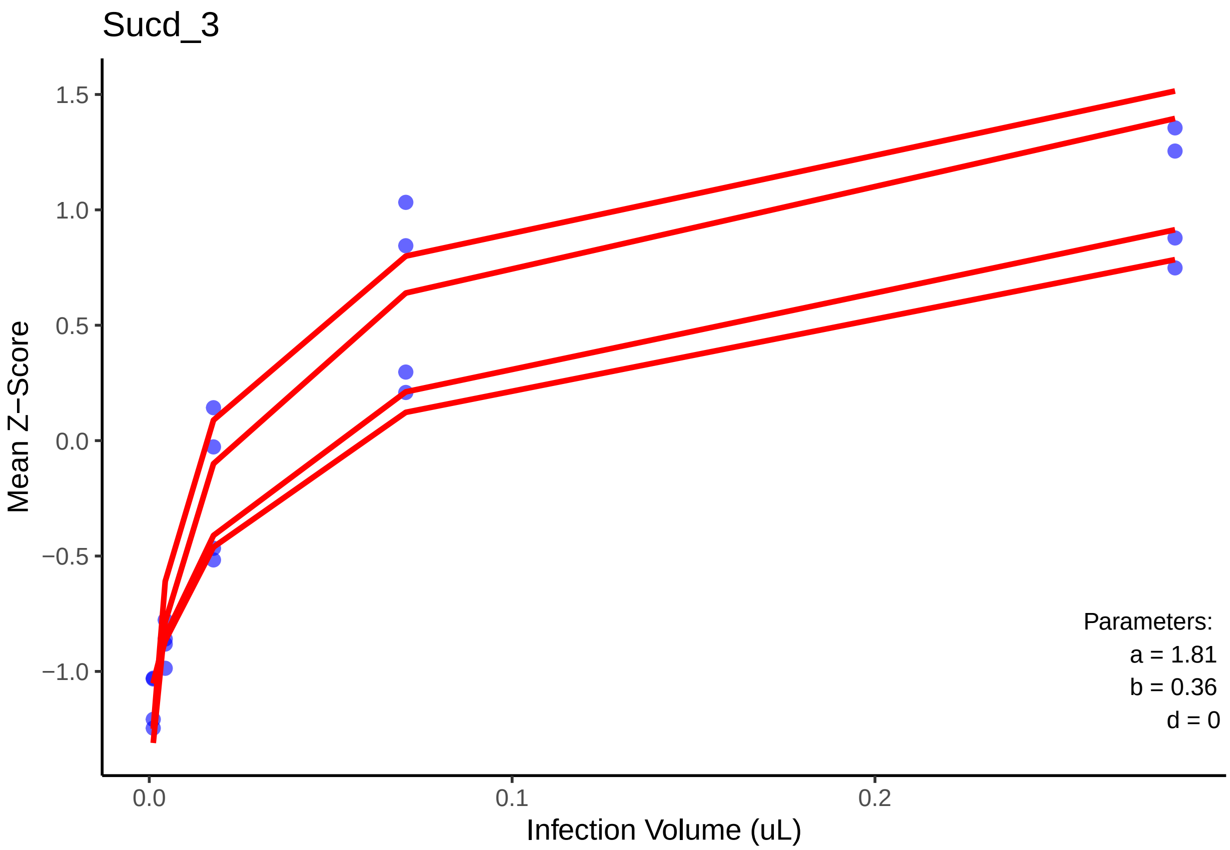


Sita_1
Mean Z−Score
Infection Volume (uL)
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.39
b = 0.47
d = 0


```
##
## $Sojd_3
```

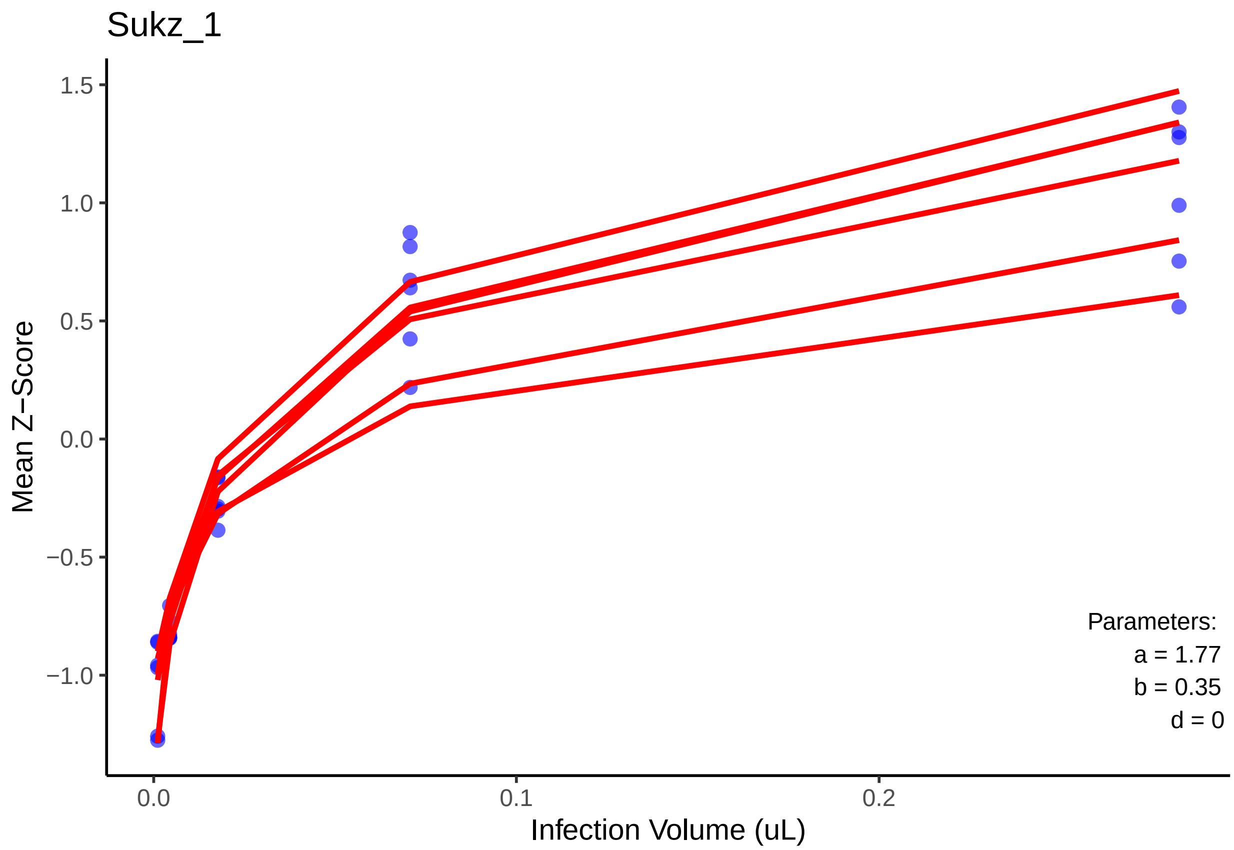

Sojd_3
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.09
b = 0.56
d = −0.02

```
##
## $Sucd_3
```

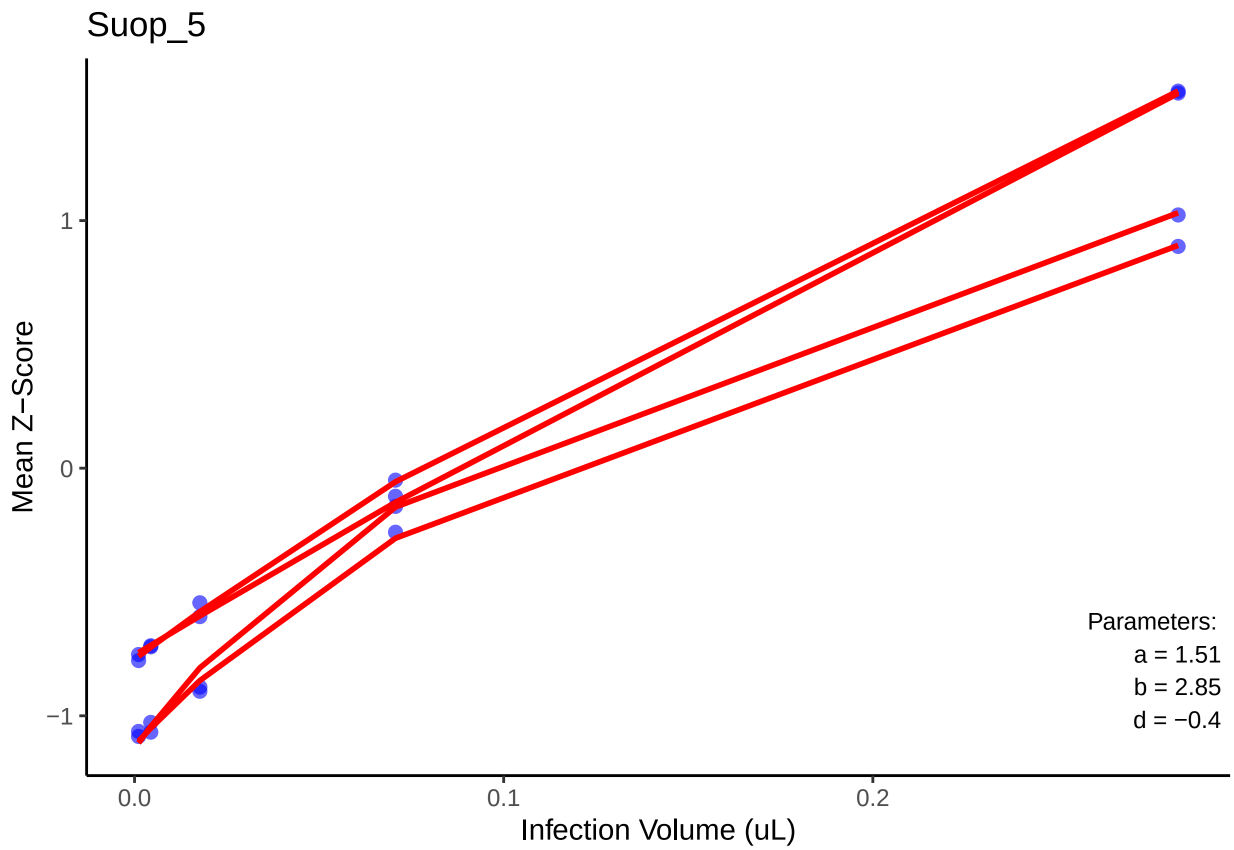


Sucd_3
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.81
b = 0.36
d = 0

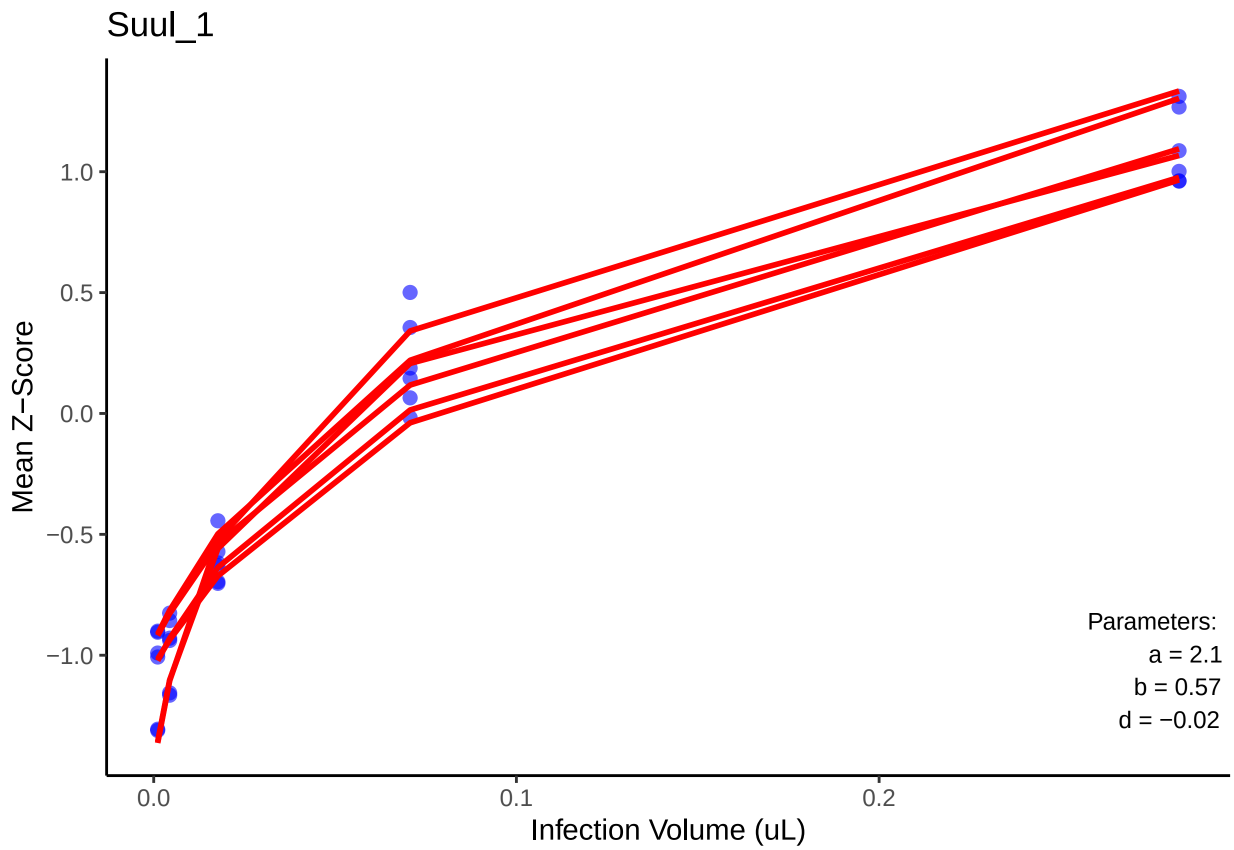

```
##
## $Sukz_1
```


Sukz_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.77
b = 0.35
d = 0

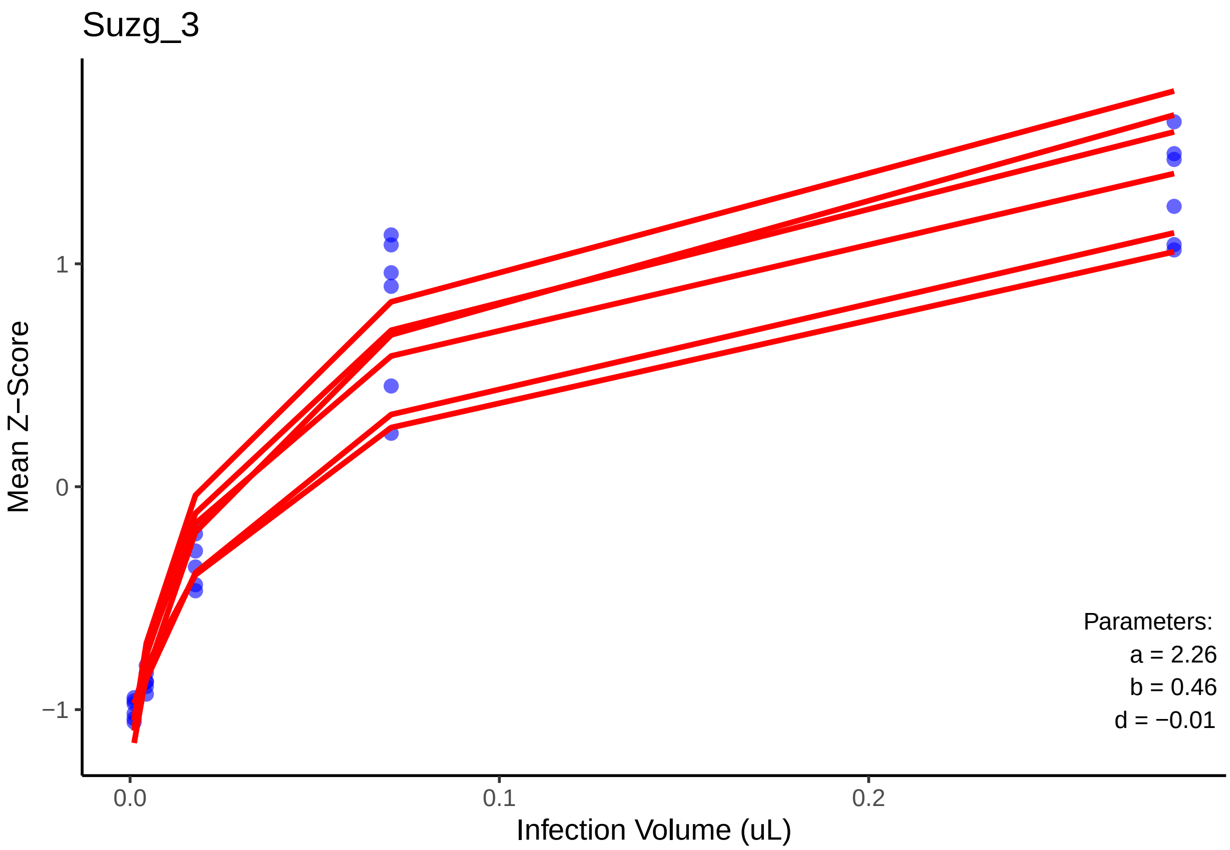
```
##
## $Suop_5
```


Suop_5
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.51
b = 2.85
d = −0.4

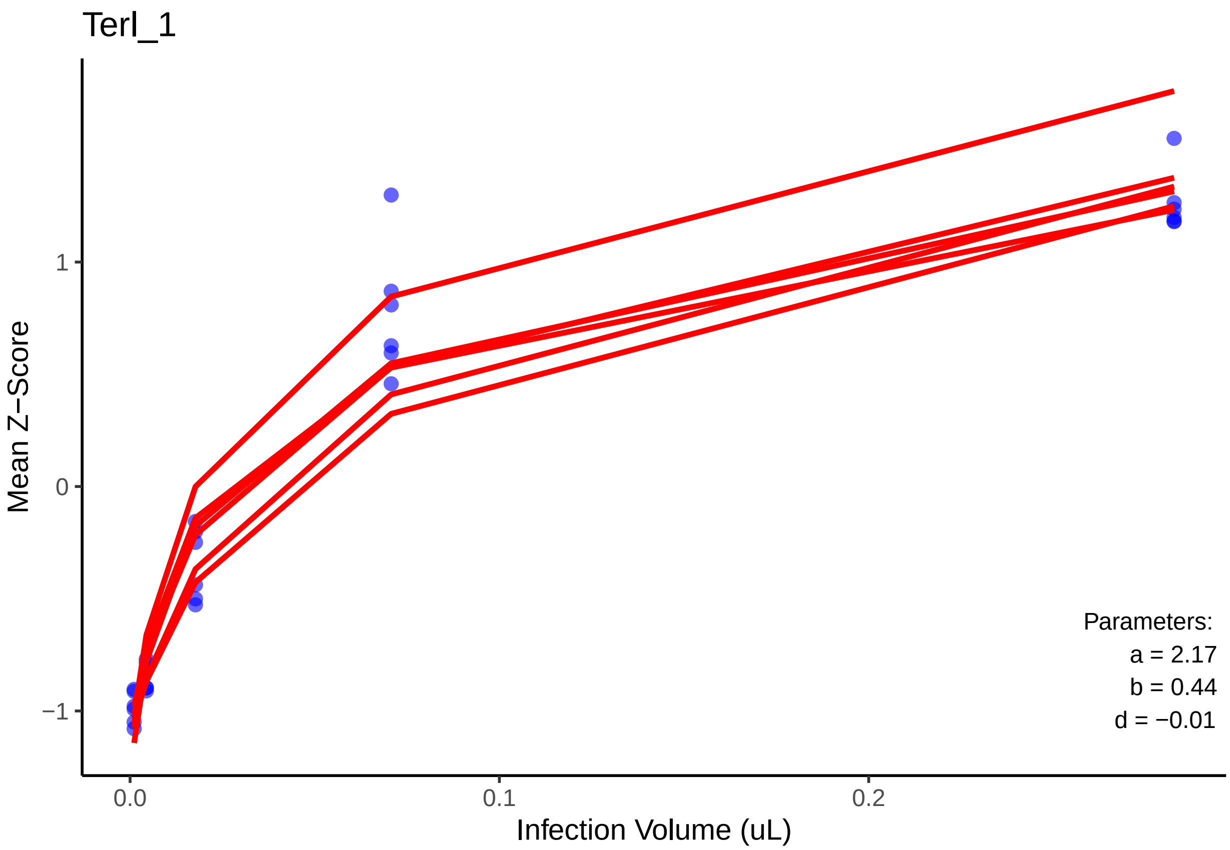
```
##
## $Suul_1
```


Suul_1
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.1
b = 0.57
d = −0.02

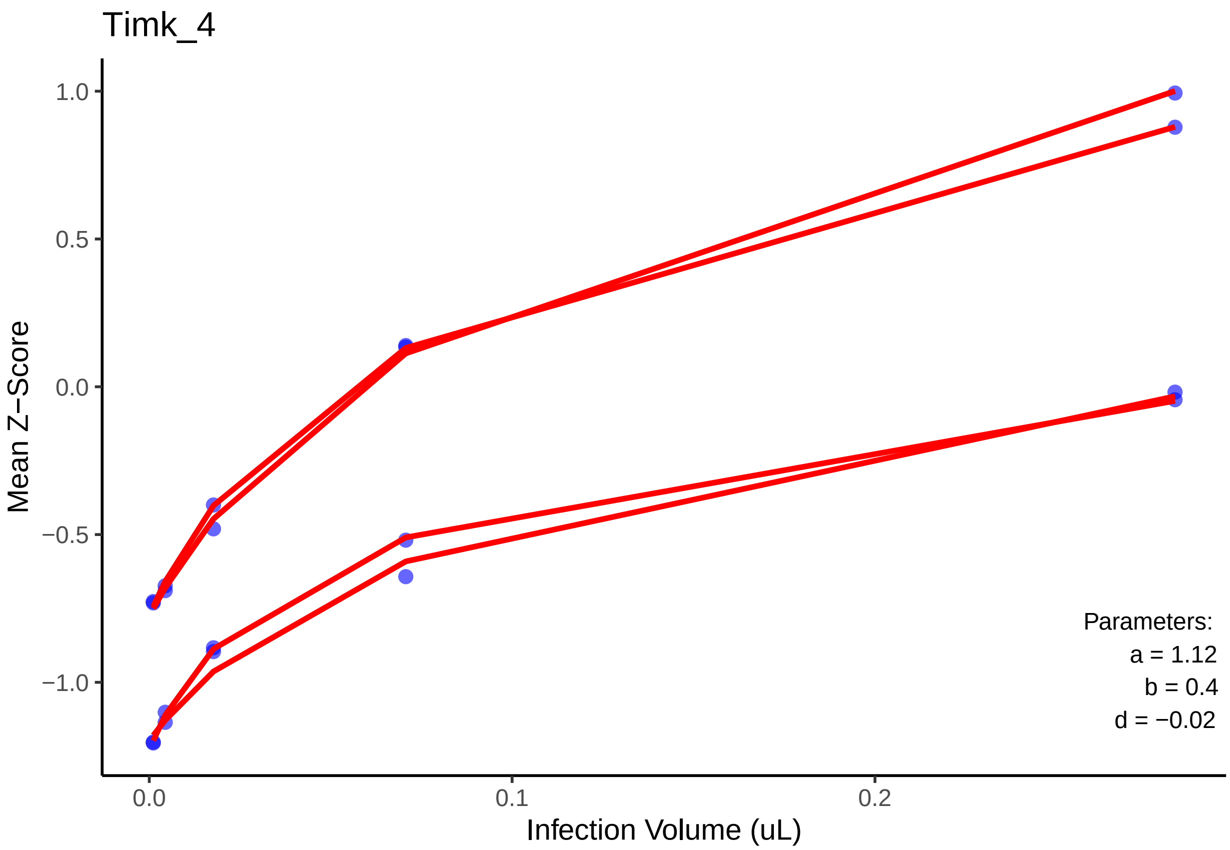
```
##
## $Suzg_3
```


Suzg_3
Mean Z−Score
Infection Volume (uL)
Parameters:
a = 2.26
b = 0.46
d = −0.01
1
0
−1
0.0
0.1
0.2

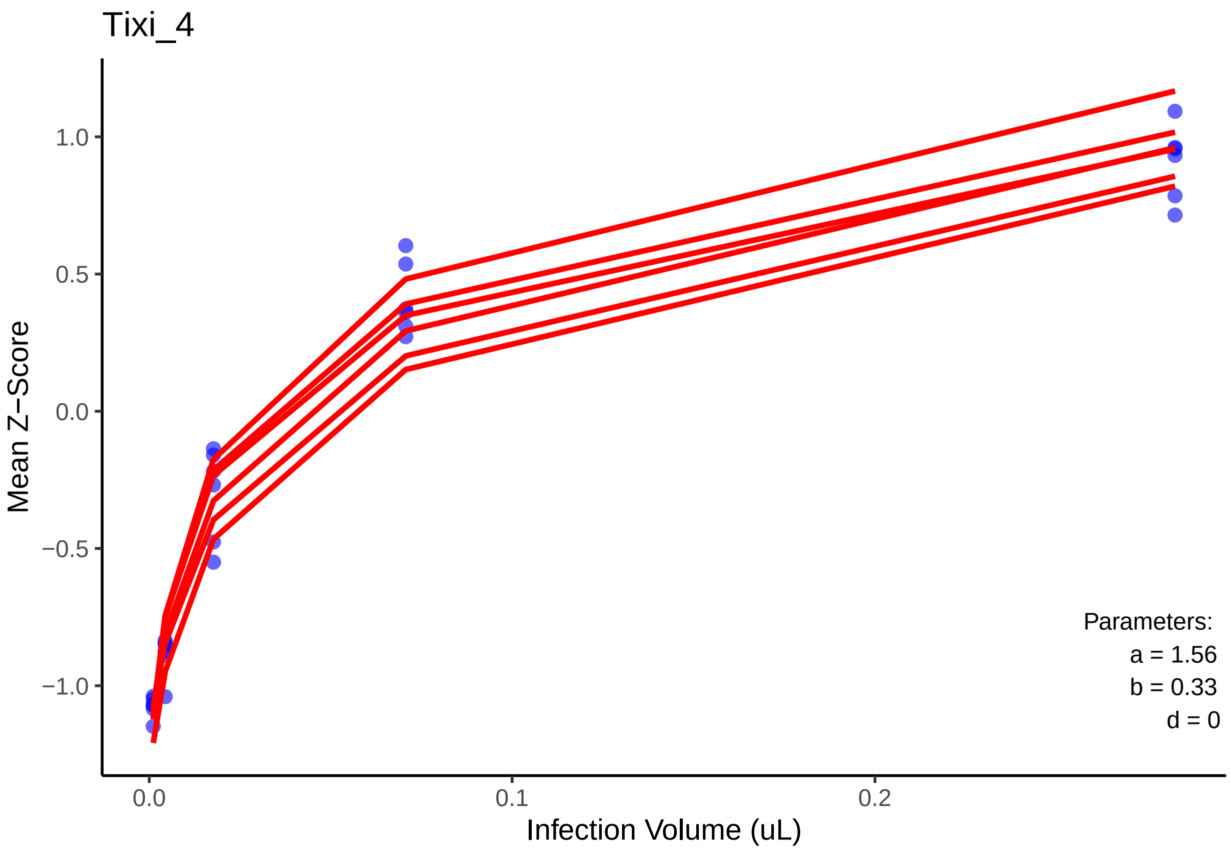
```
##
## $Terl_1
```


Terl_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.17
b = 0.44
d = −0.01

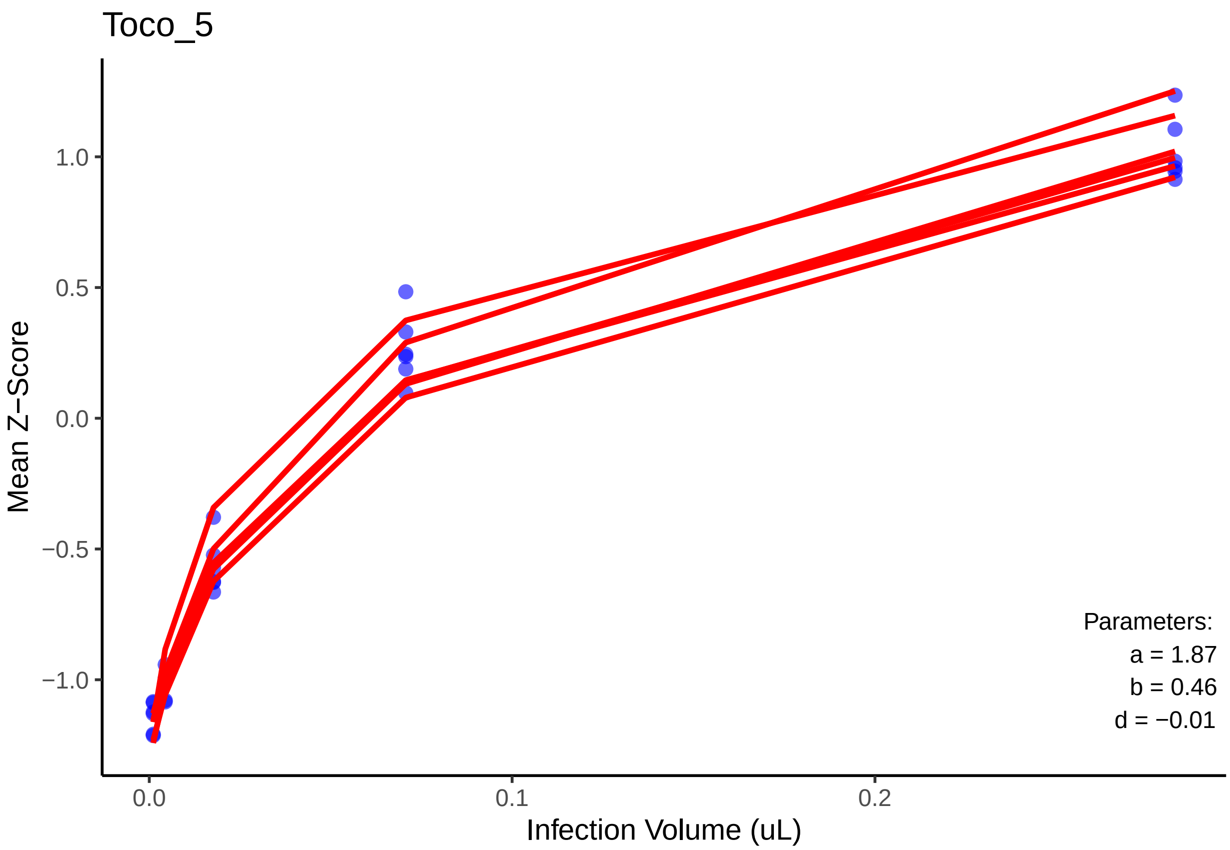
```
##
## $Timk_4
```


Timk_4
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.12
b = 0.4
d = −0.02

```
##
## $Tixi_4
```

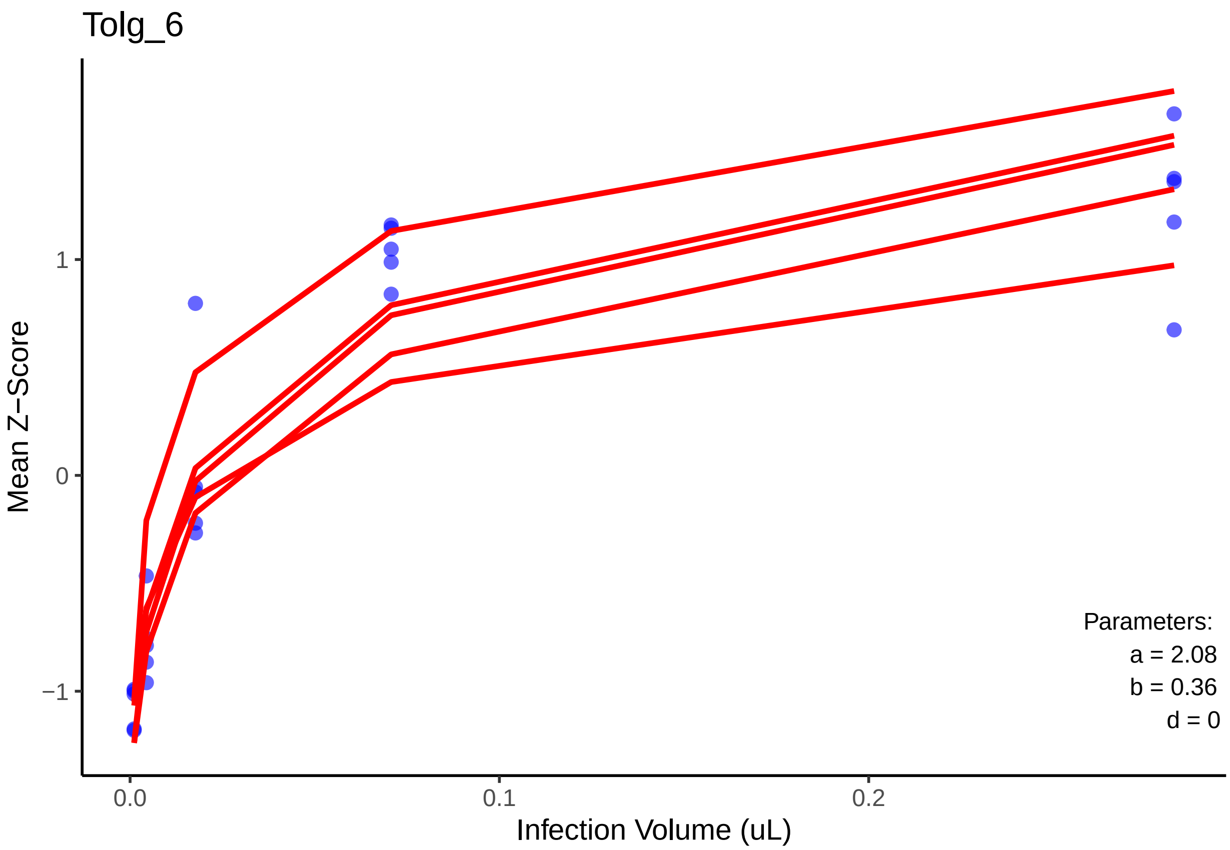

Tixi_4
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
Parameters:
a = 1.56
b = 0.33
d = 0
0.0
0.1
0.2
Infection Volume (uL)

```
##
## $Toco_5
```



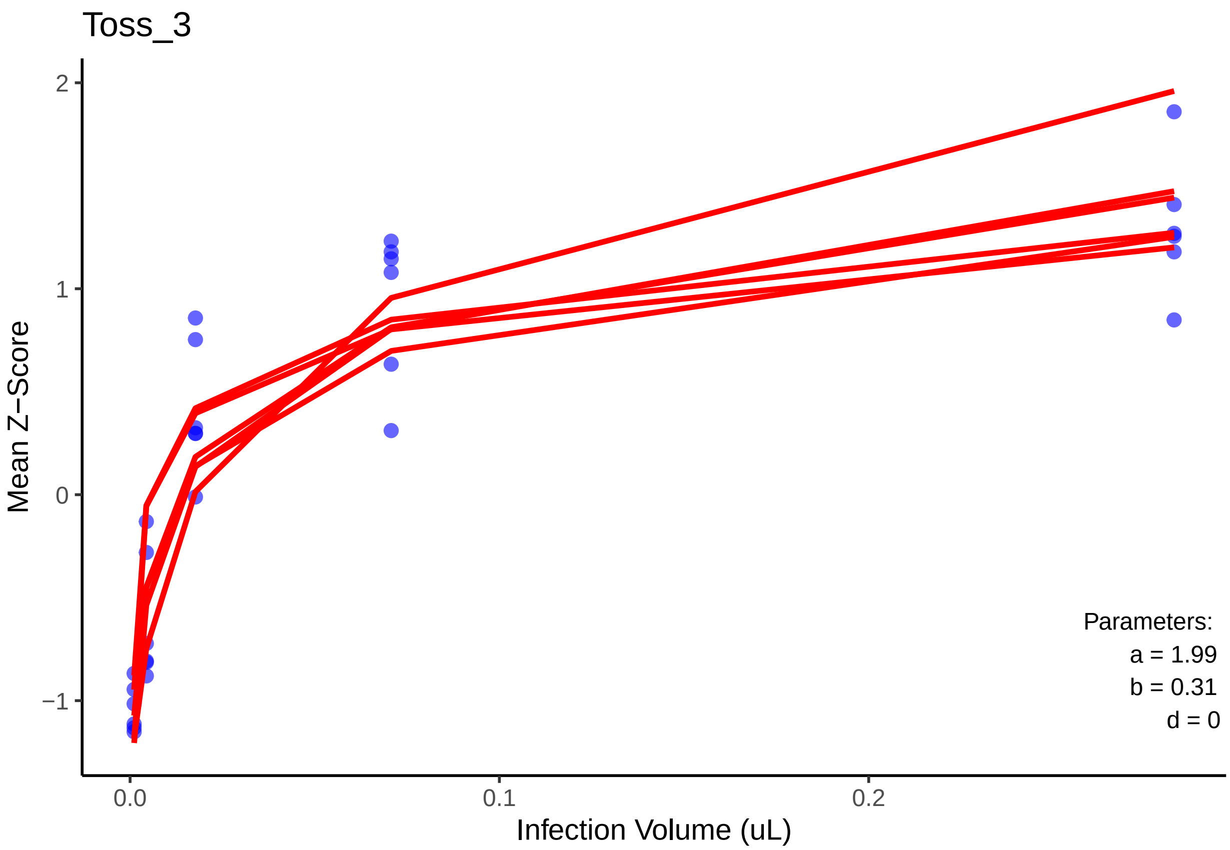
Toco_5
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.87
b = 0.46
d = −0.01


```
##
## $Tolg_6
```

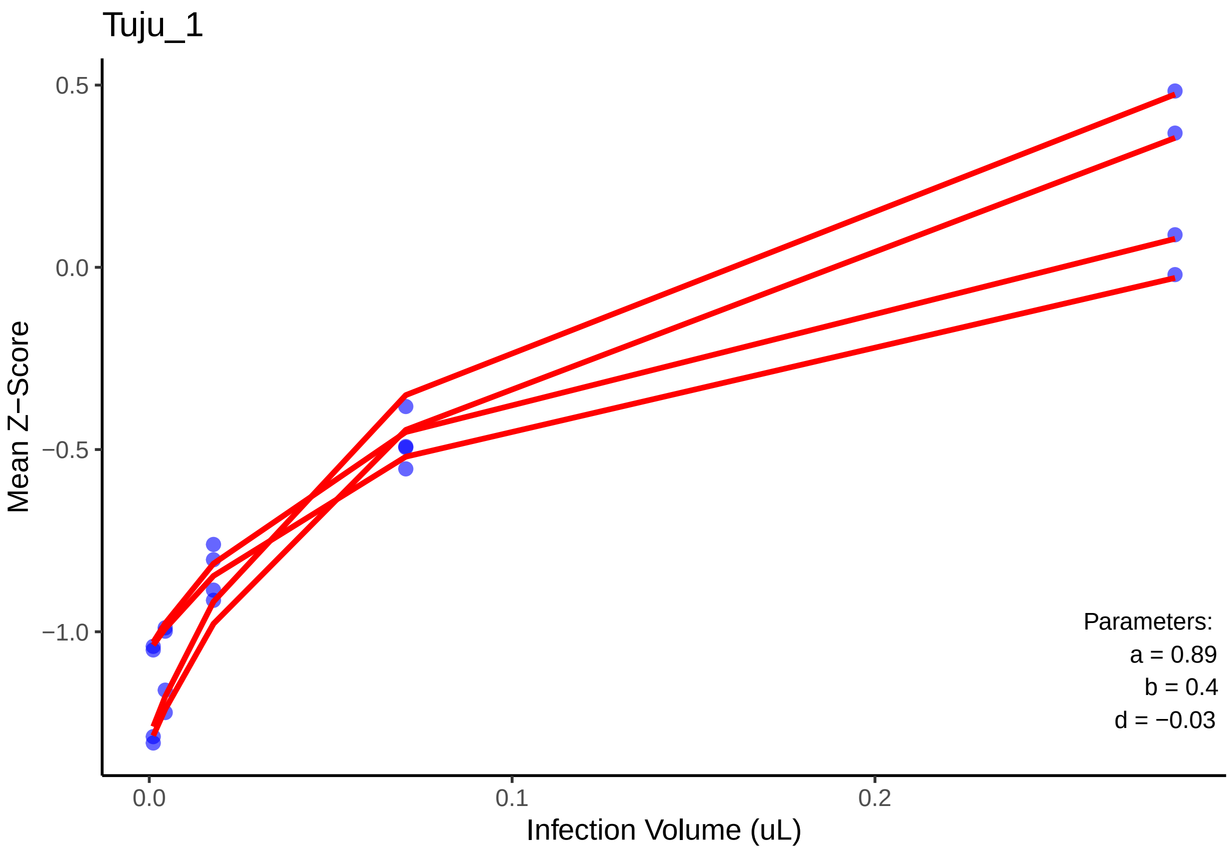


Tolg_6
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.08
b = 0.36
d = 0

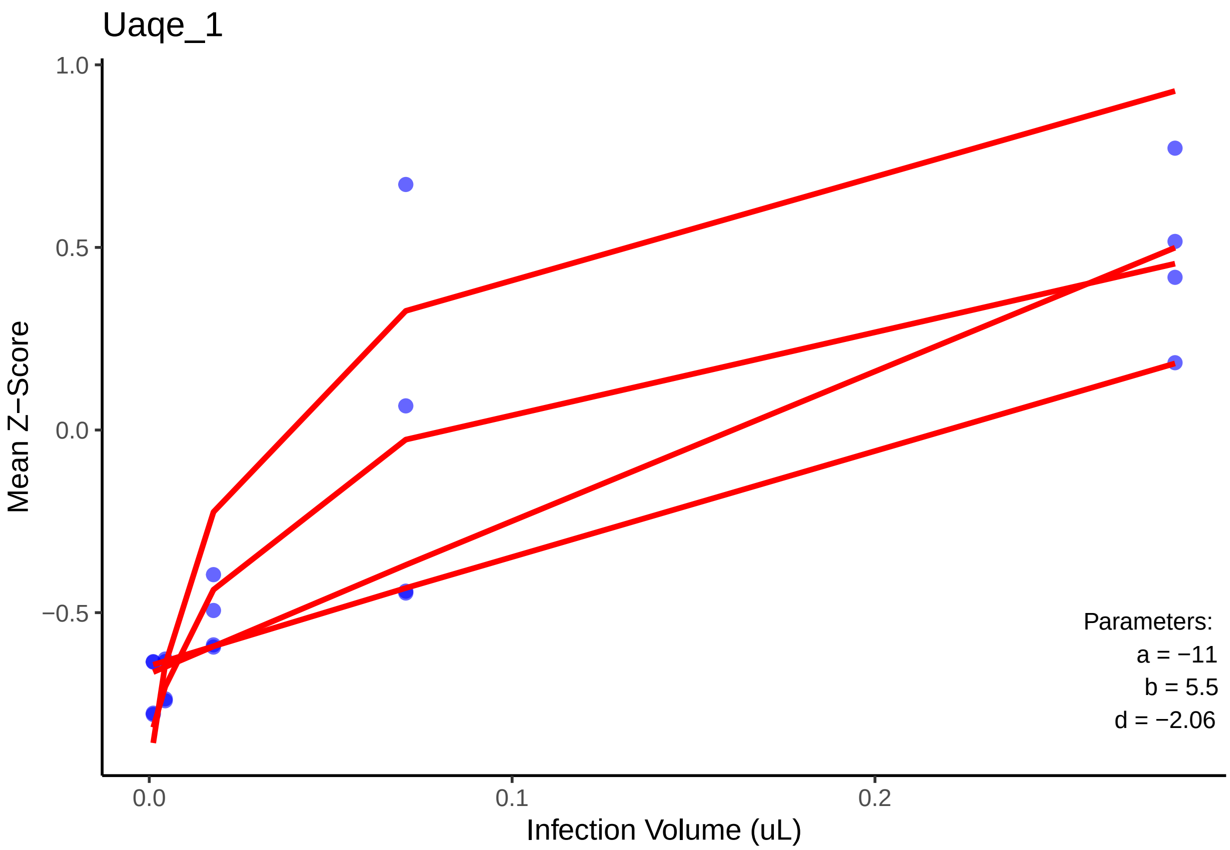

```
##
## $Toss_3
```


Toss_3
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 1.99
b = 0.31
d = 0

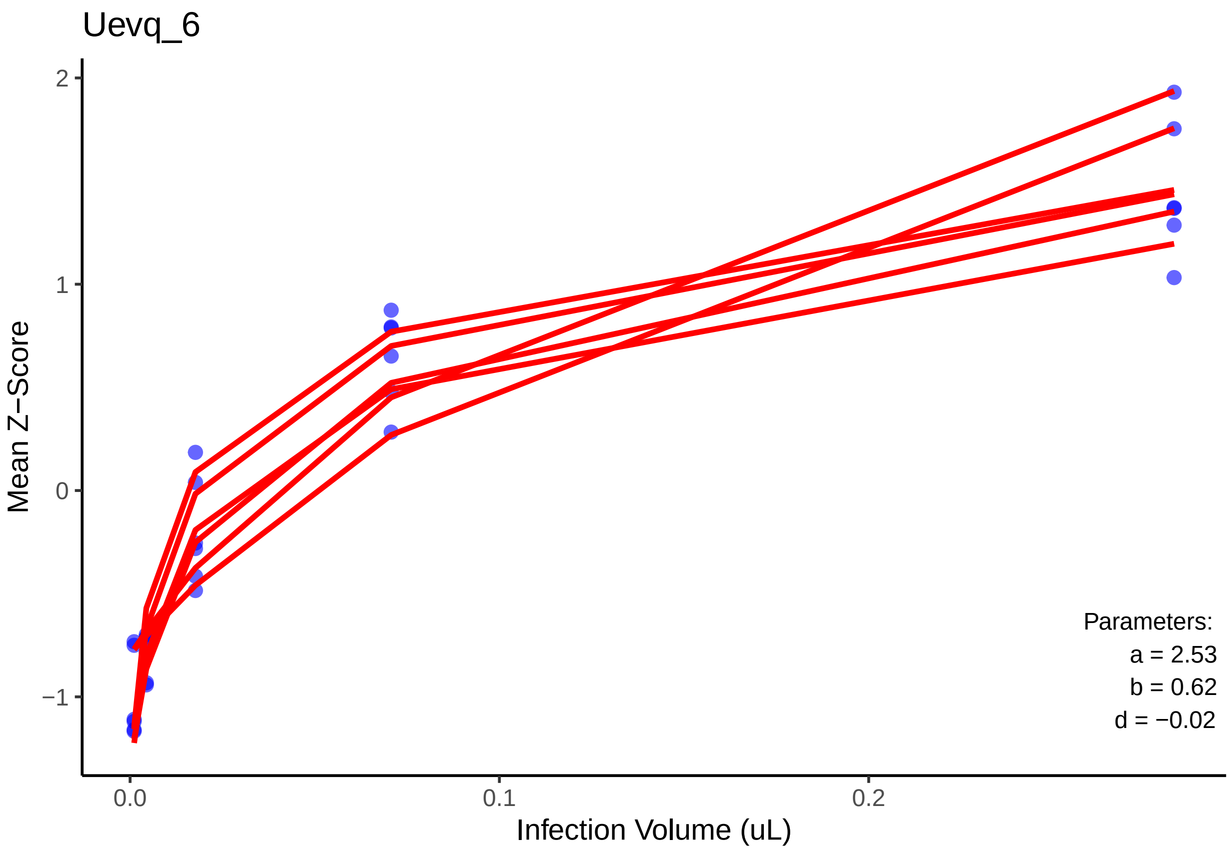
```
##
## $Tuju_1
```


Tuju_1
Mean Z−Score
Infection Volume (uL)
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Parameters:
a = 0.89
b = 0.4
d = −0.03

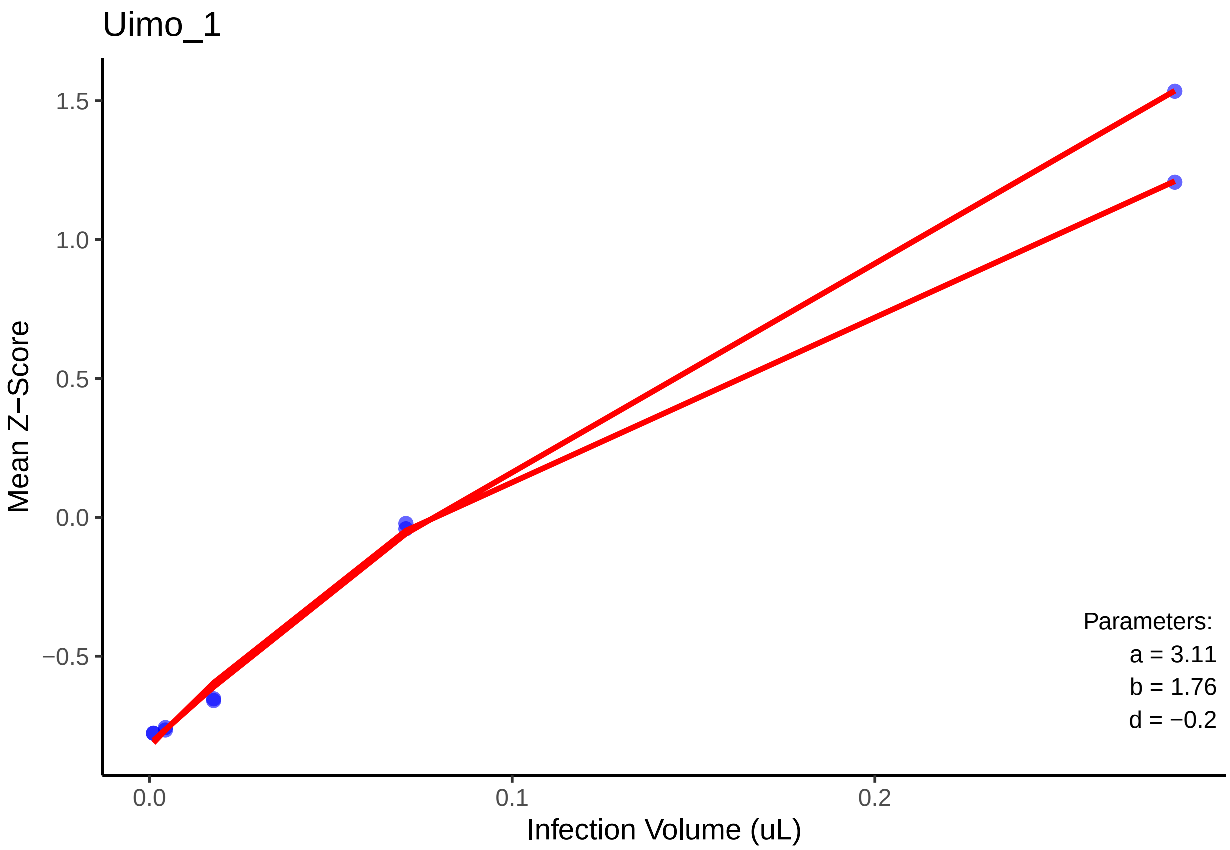
```
##
## $Uaqe_1
```


Uaqe_1
1.0
0.5
0.0
−0.5
Mean Z−Score
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = −11
b = 5.5
d = −2.06

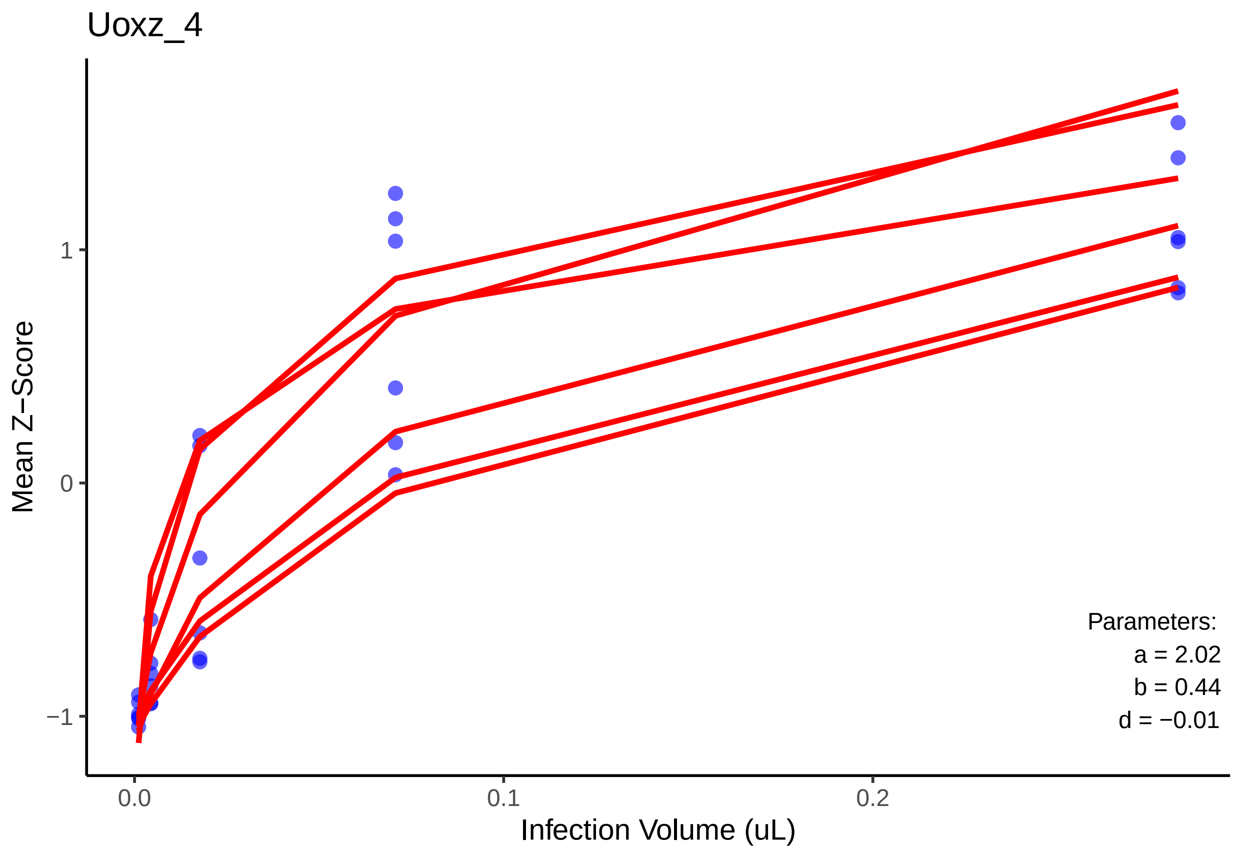
```
##
## $Uevq_6
```


Uevq_6
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.53
b = 0.62
d = −0.02

```
##
## $Uimo_1
```

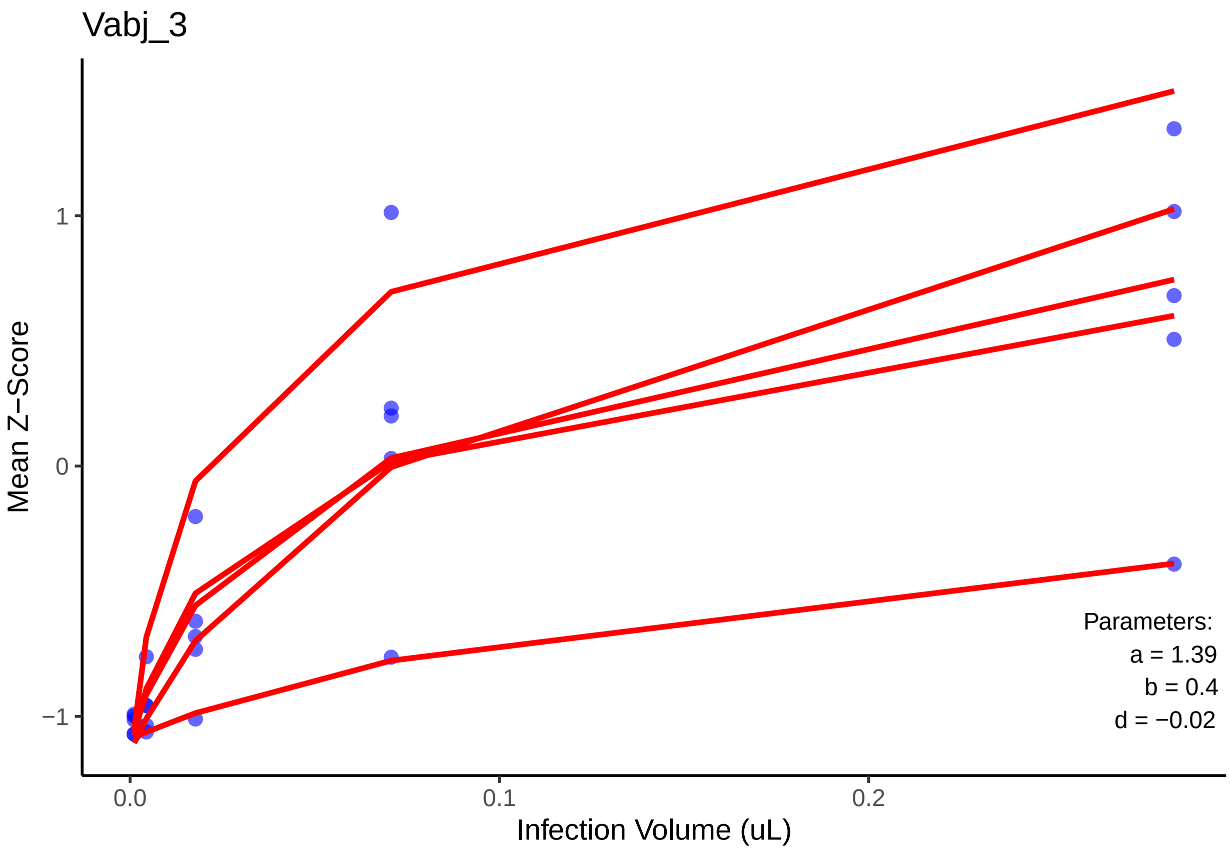

Uimo_1
Mean Z−Score
Infection Volume (uL)
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Parameters:
a = 3.11
b = 1.76
d = −0.2

```
##
## $Uoxz_4
```

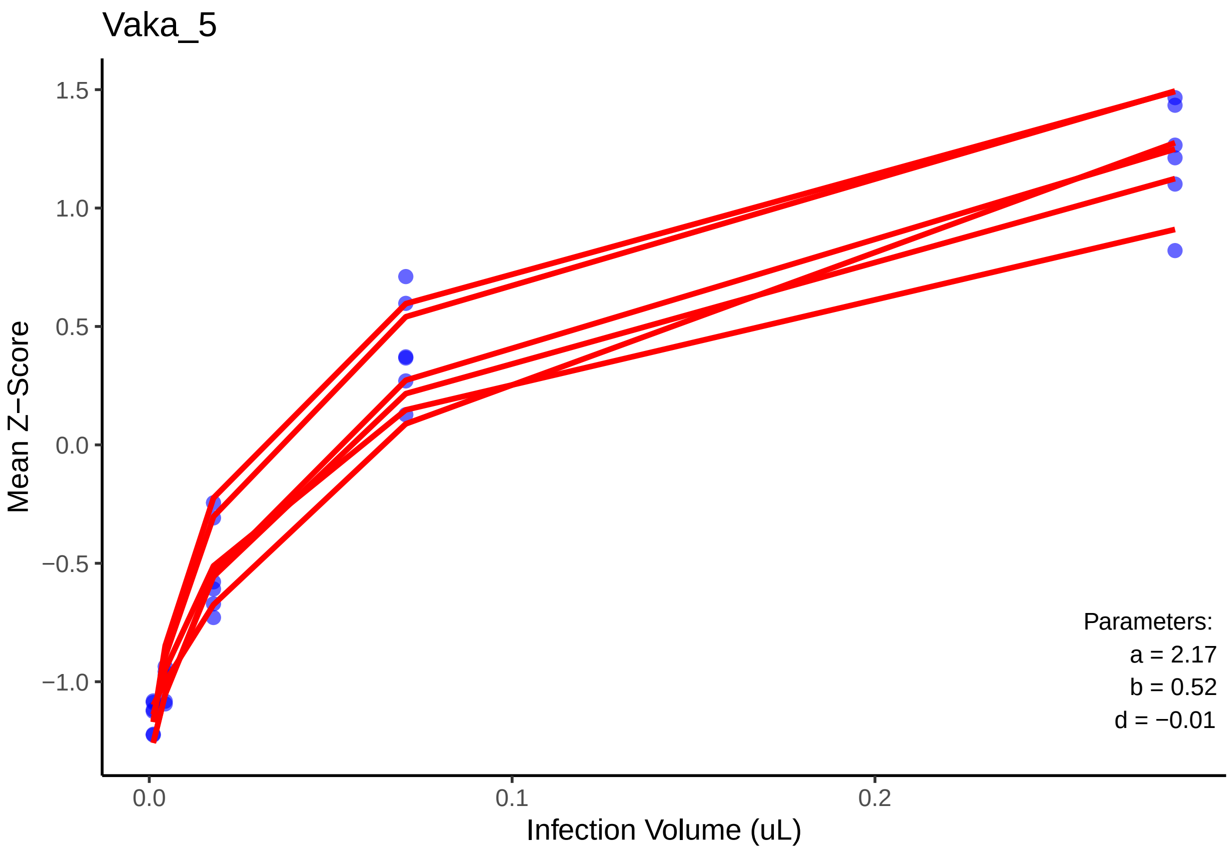


Uoxz_4
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.02
b = 0.44
d = −0.01

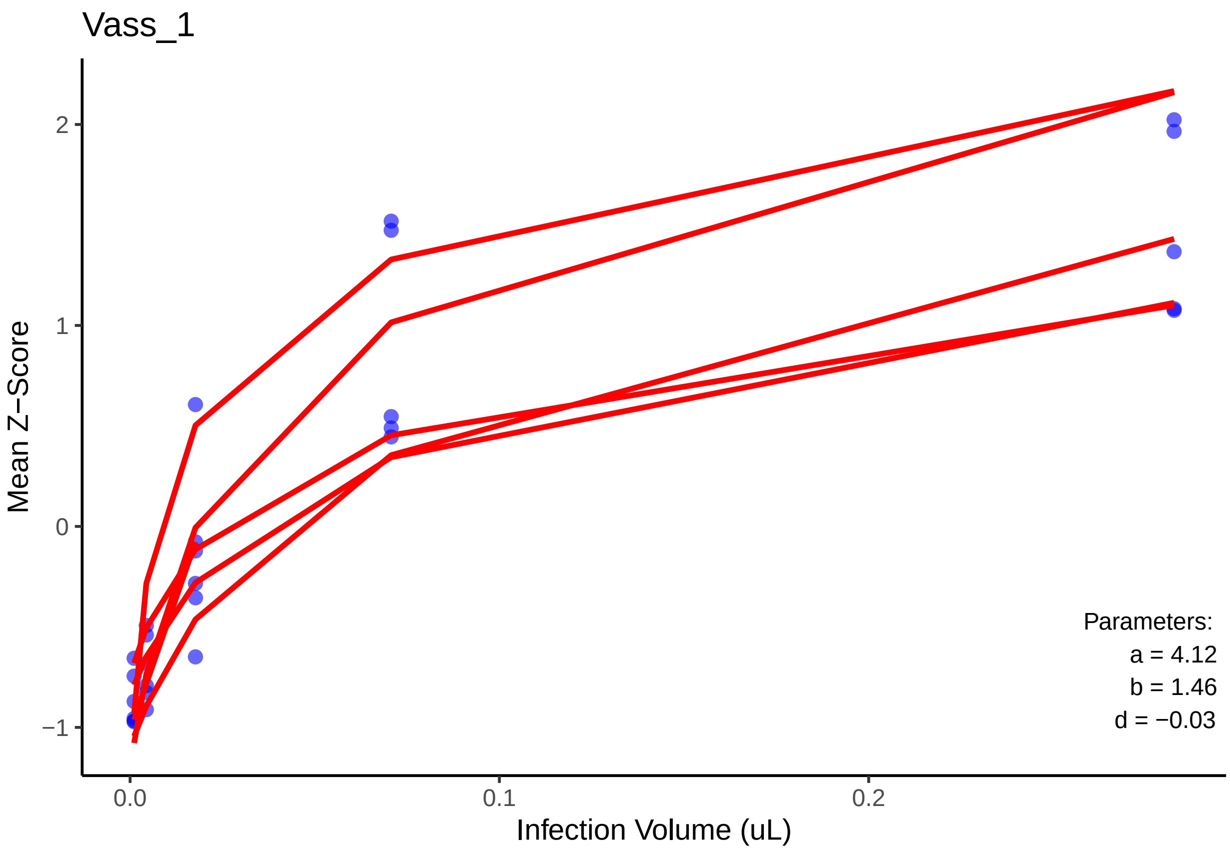

```
##
## $Vabj_3
```


Vabj_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.39
b = 0.4
d = −0.02

```
##
## $Vaka_5
```

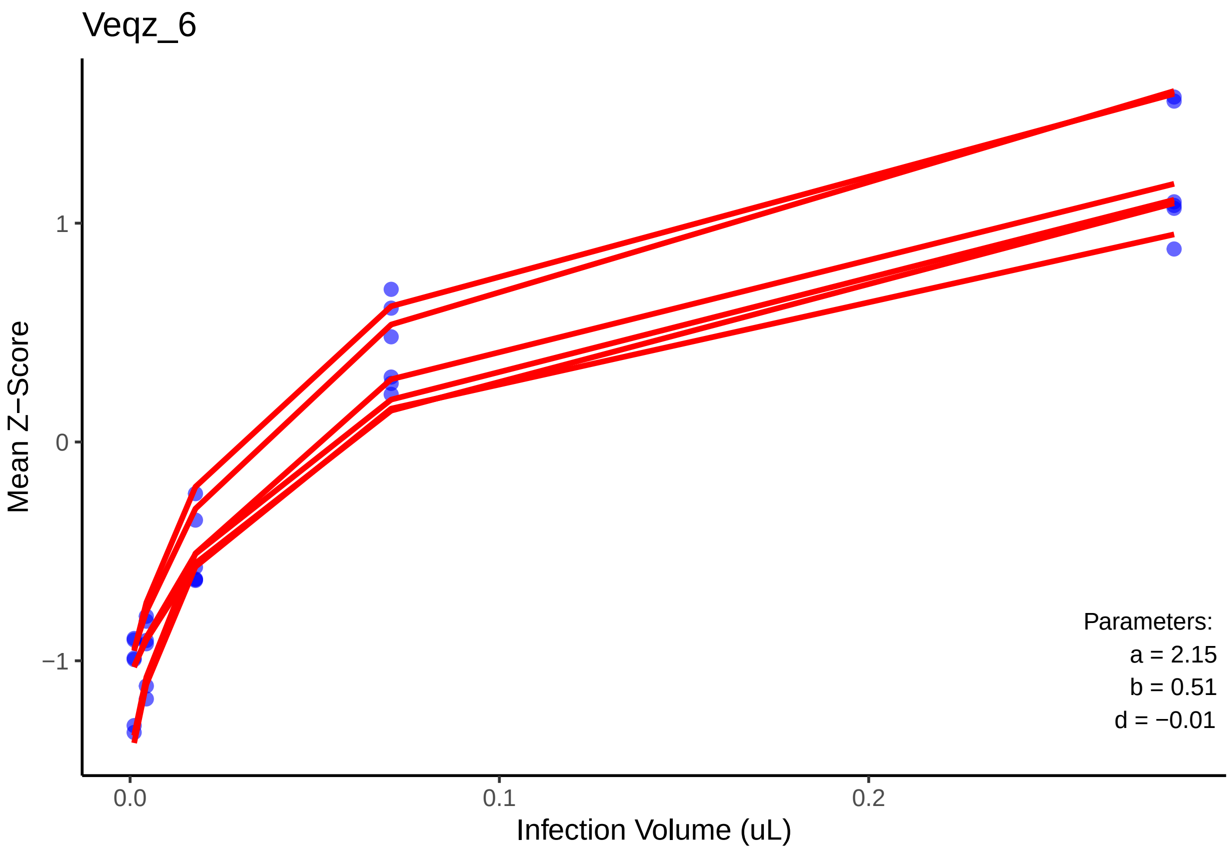

Vaka_5
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.17
b = 0.52
d = −0.01

```
##
## $Vass_1
```

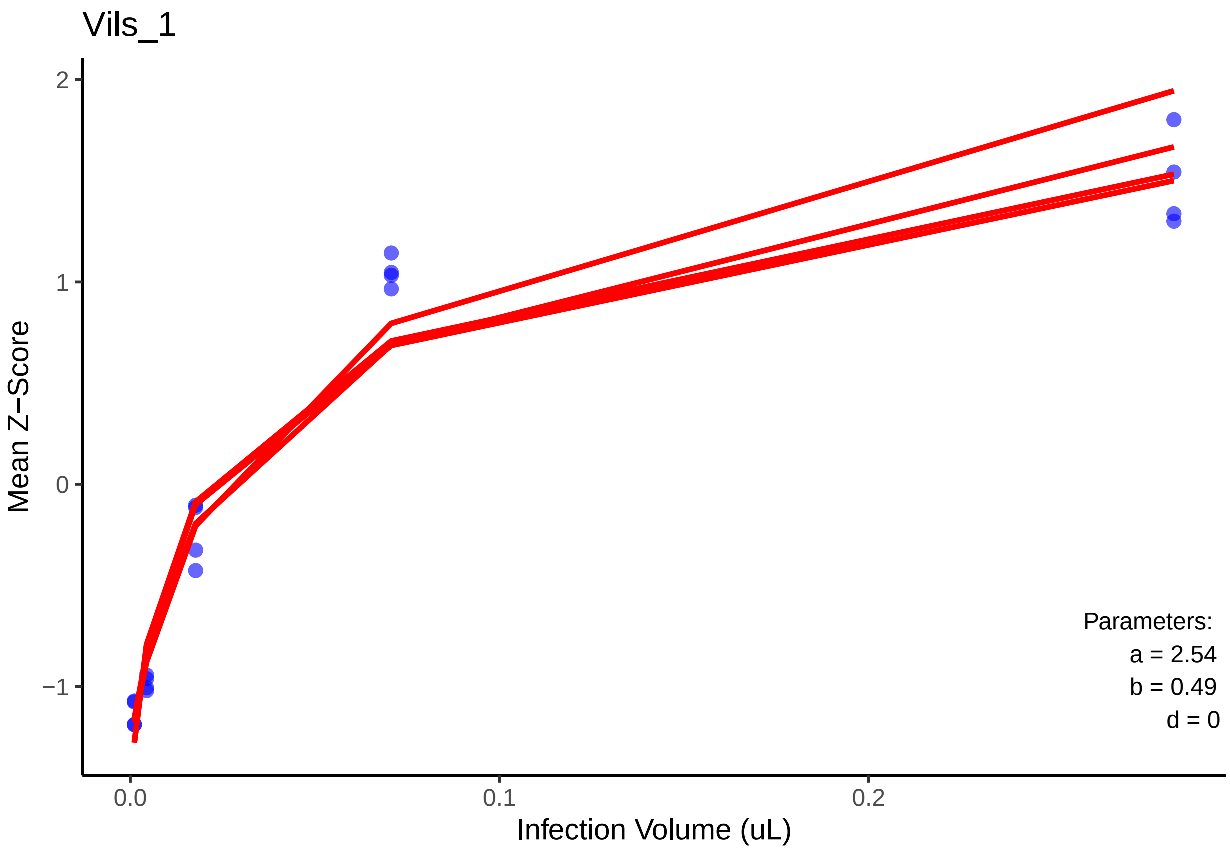


Vass_1
Mean Z−Score
Infection Volume (uL)
Parameters:
a = 4.12
b = 1.46
d = −0.03


```
##
## $Veqz_6
```

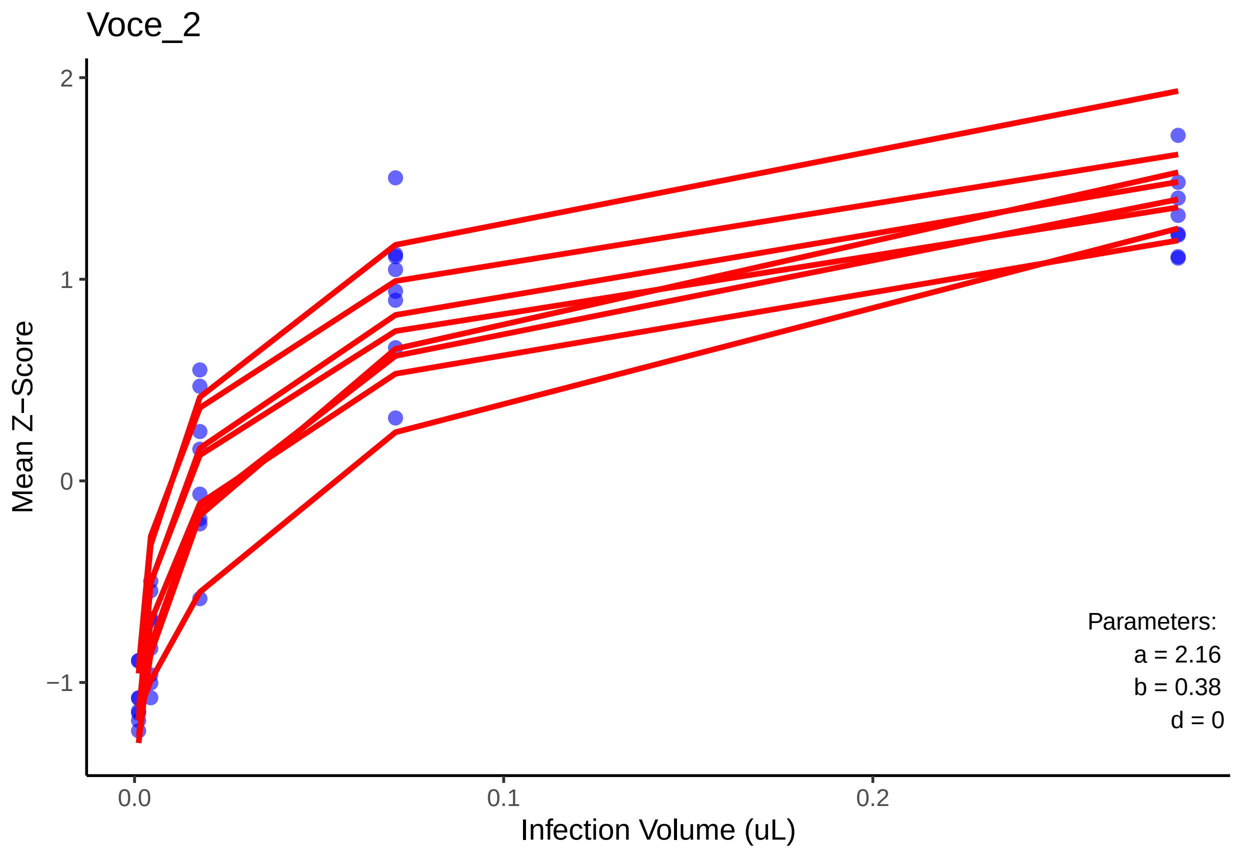

Veqz_6
Mean Z−Score
Infection Volume (uL)
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.15
b = 0.51
d = −0.01

```
##
## $Vils_1
```

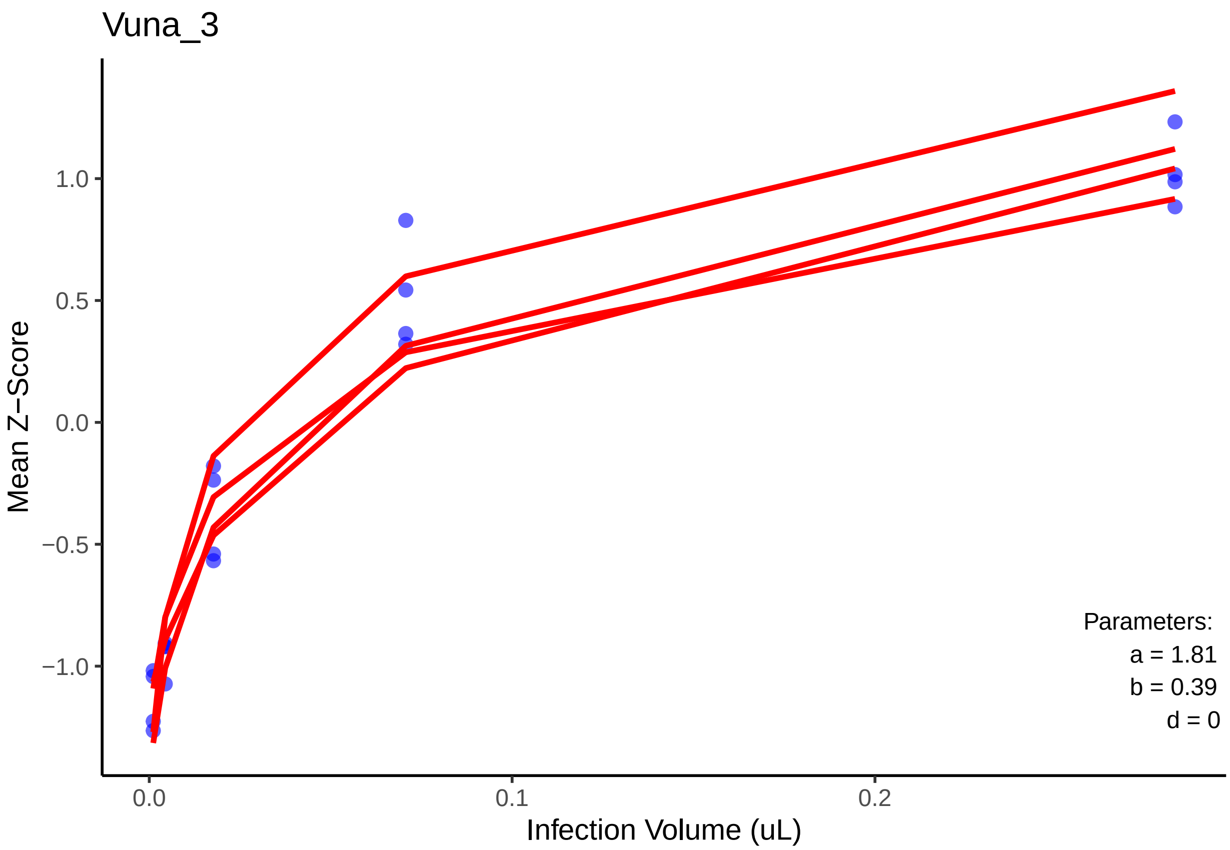


Vils_1
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.54
b = 0.49
d = 0


```
##
## $Voce_2
```

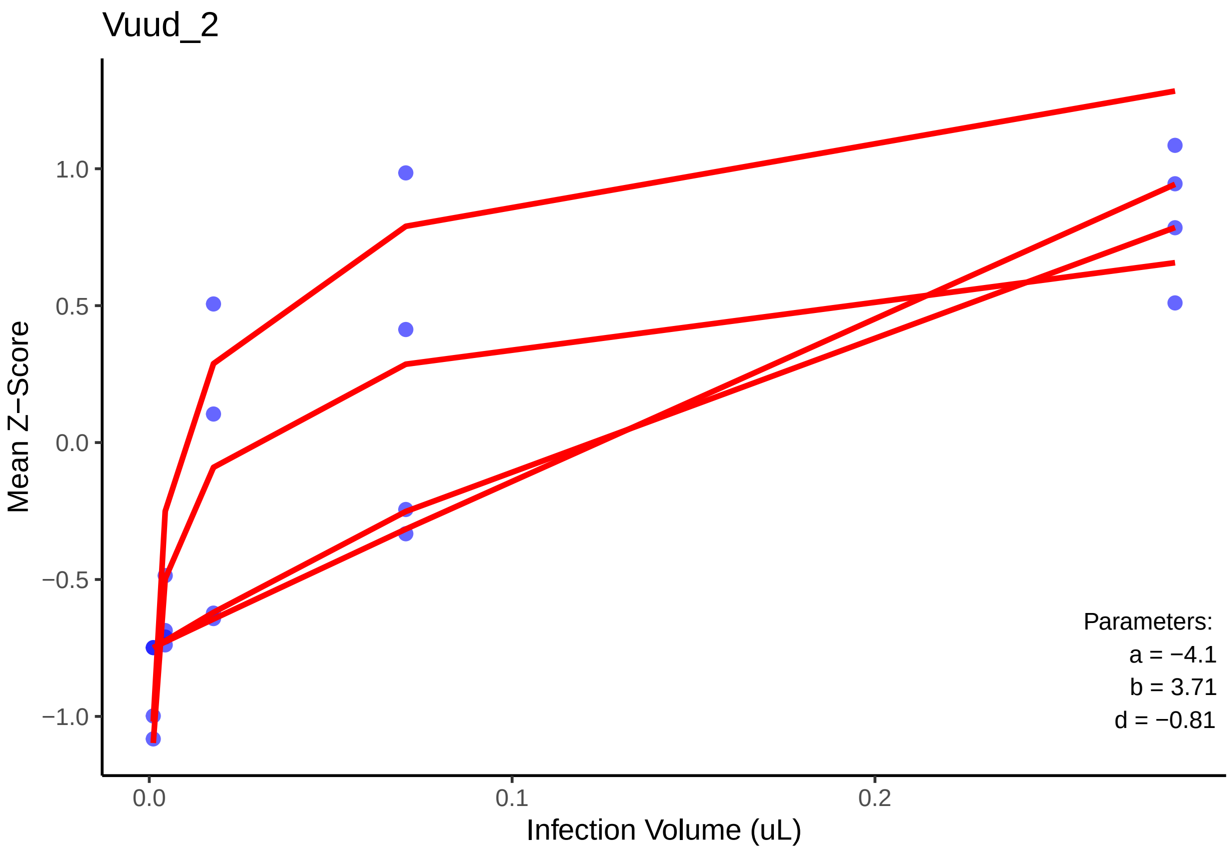

Voce_2
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.16
b = 0.38
d = 0

```
##
## $Vuna_3
```



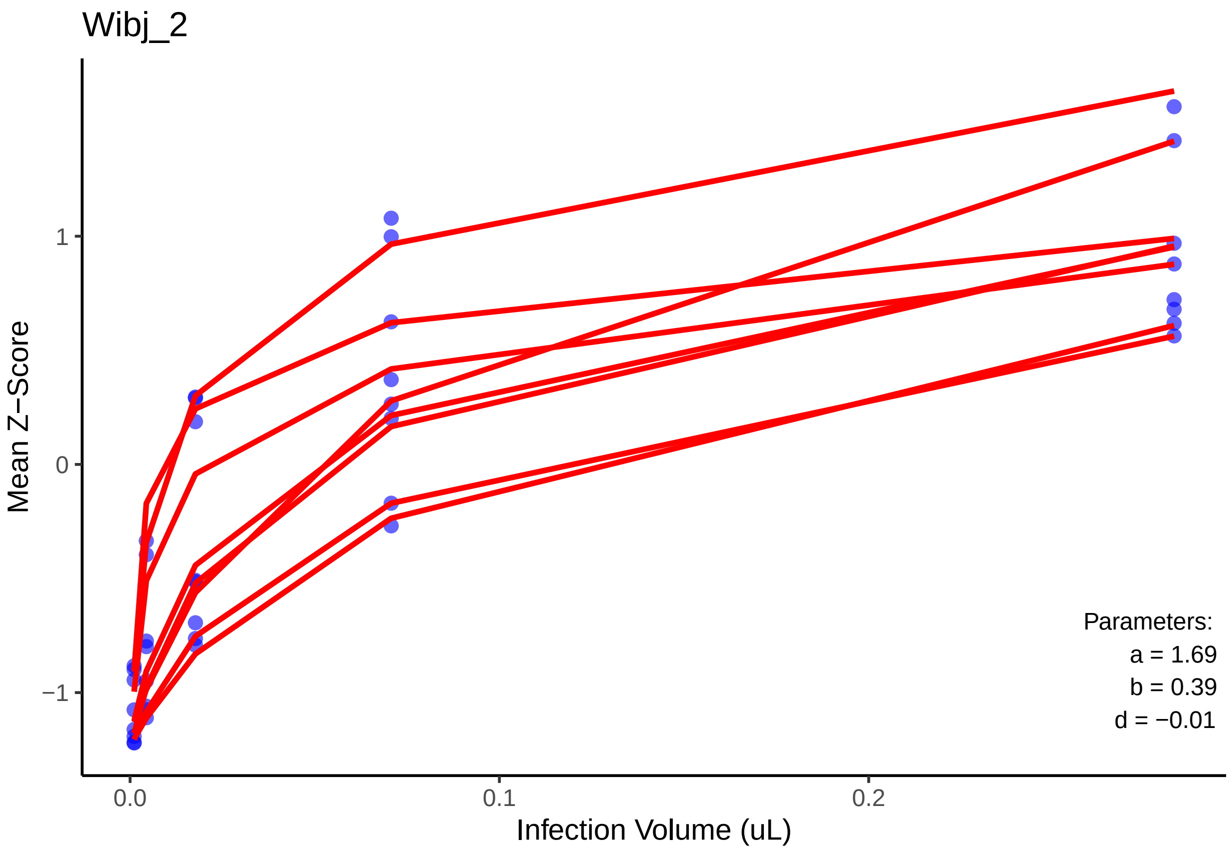
Vuna_3
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.81
b = 0.39
d = 0


```
##
## $Vuud_2
```

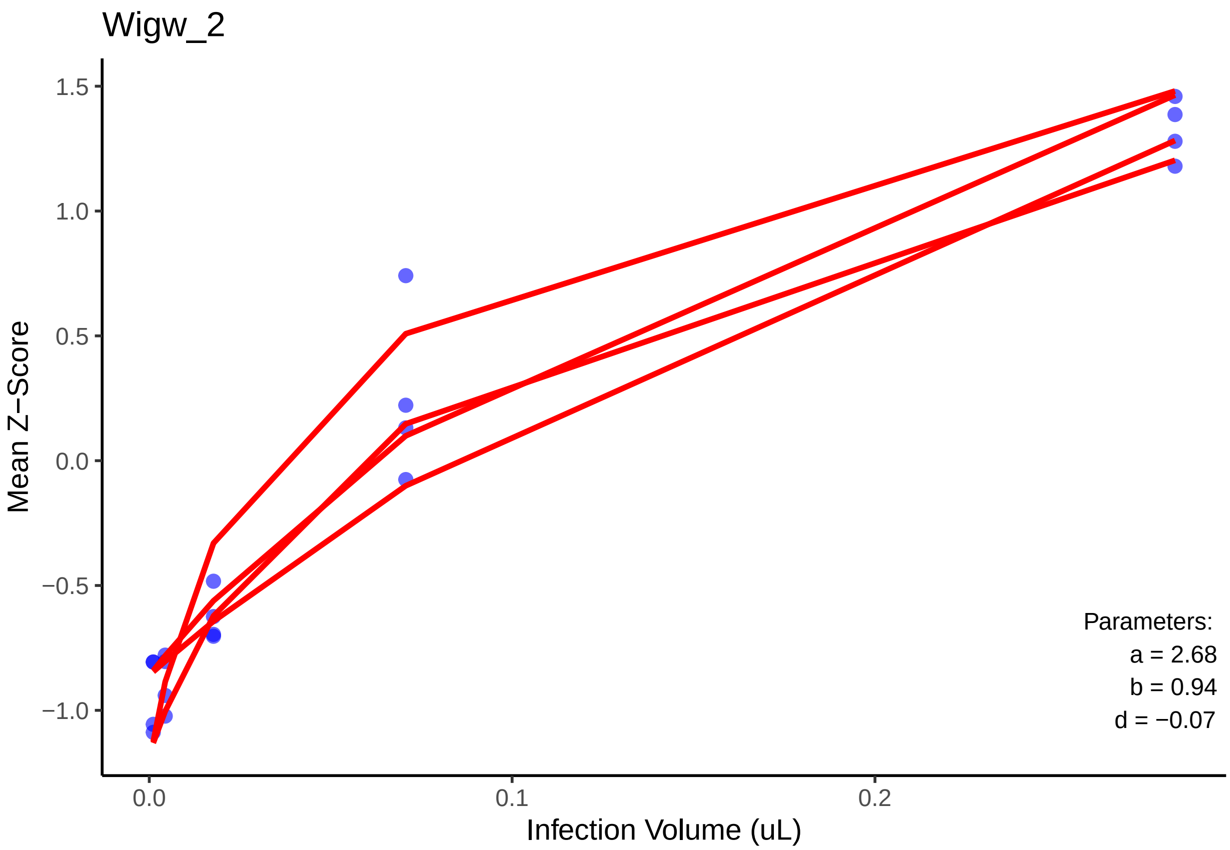


Vuud_2
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = −4.1
b = 3.71
d = −0.81

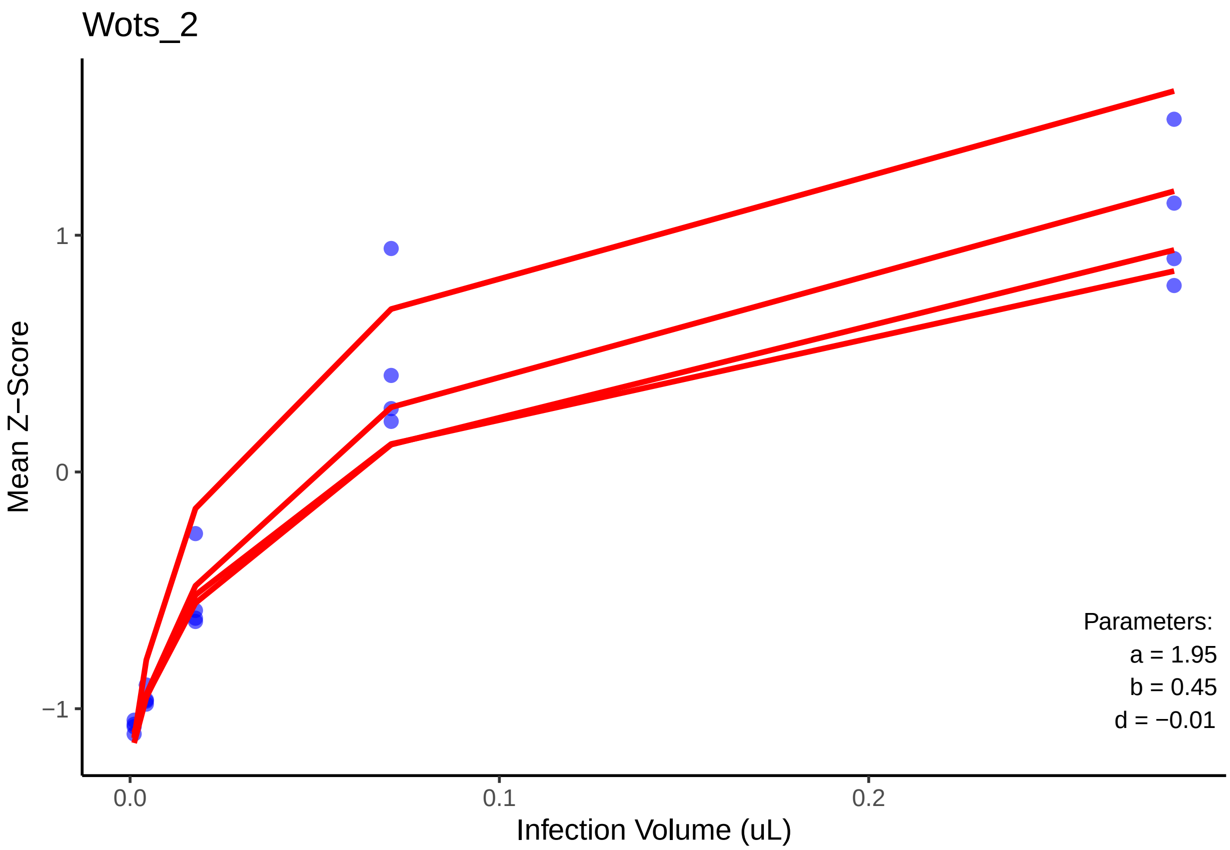

```
##
## $Wibj_2
```


Wibj_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.69
b = 0.39
d = −0.01

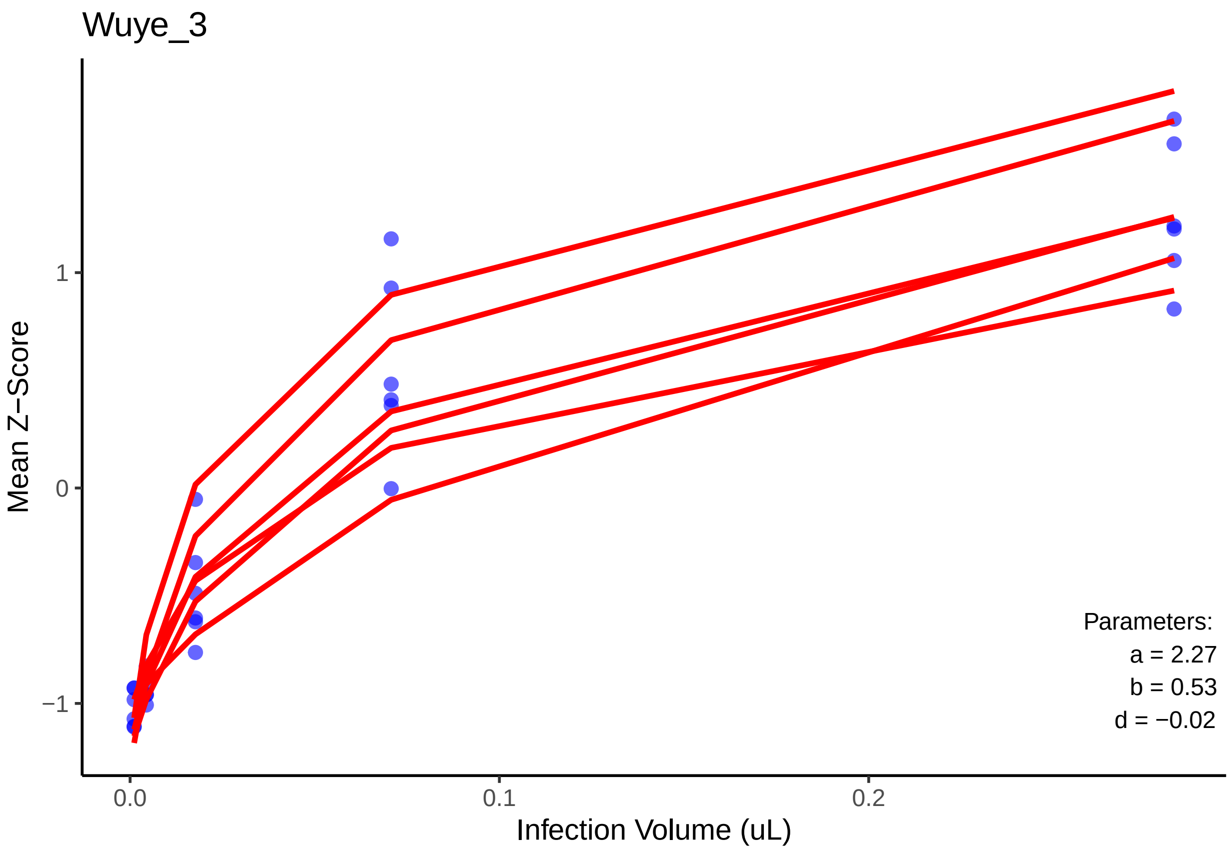
```
##
## $Wigw_2
```


Wigw_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.68
b = 0.94
d = −0.07

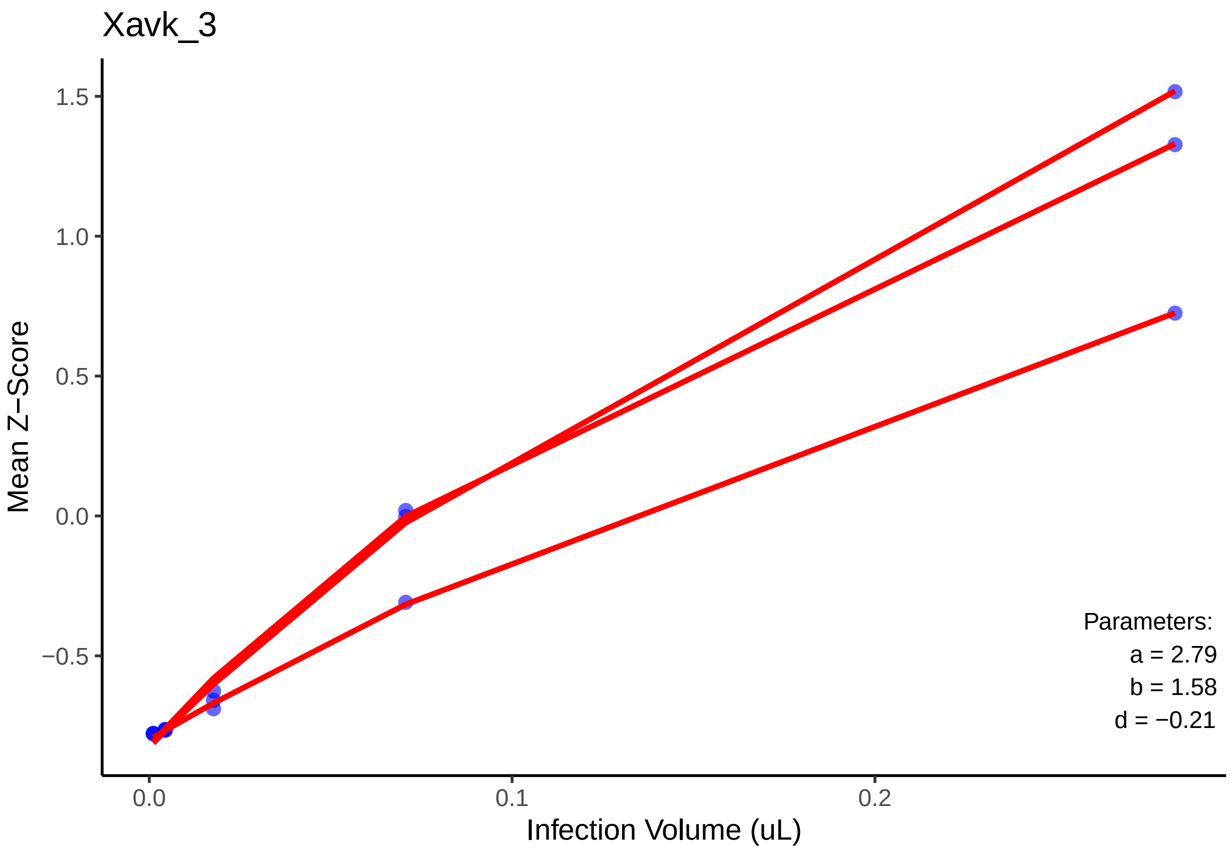
```
##
## $Wots_2
```


Wots_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.95
b = 0.45
d = −0.01

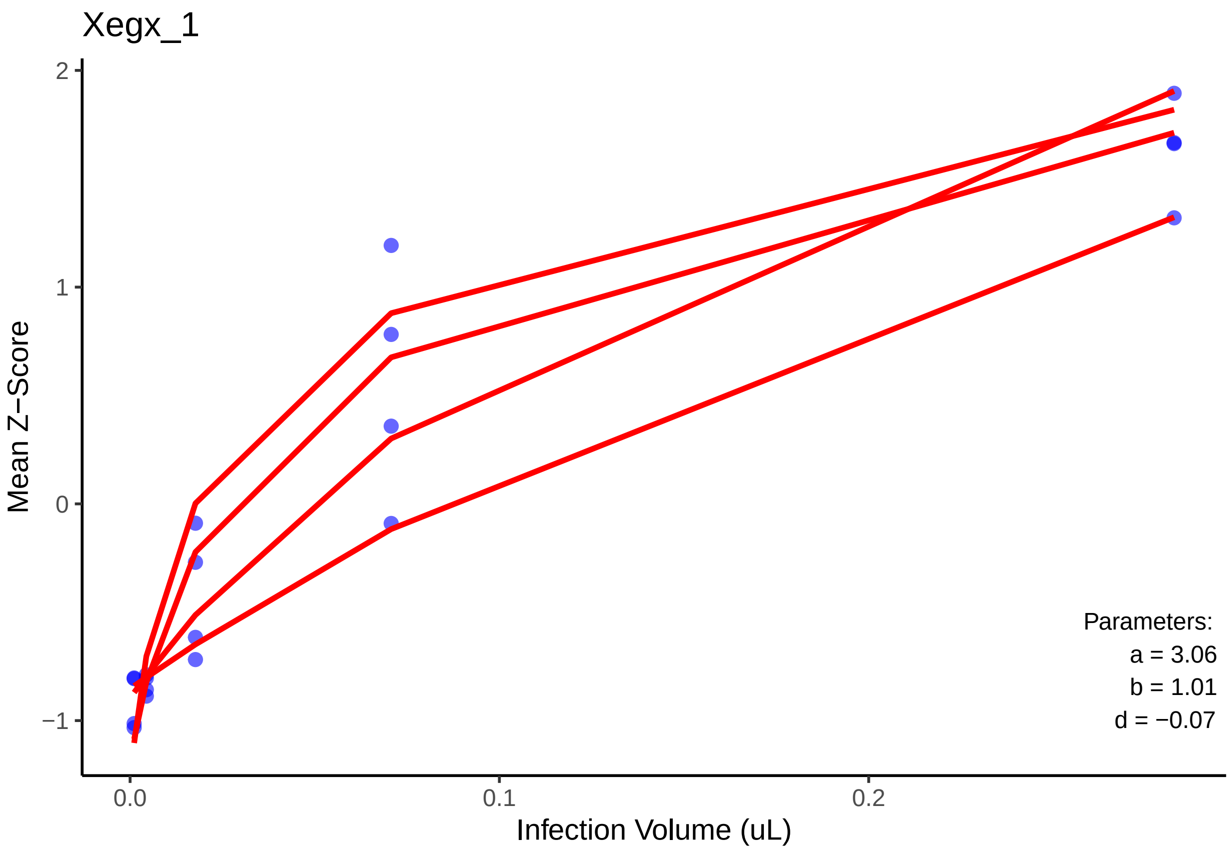
```
##
## $Wuye_3
```


Wuye_3
Mean Z−Score
Infection Volume (uL)
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.27
b = 0.53
d = −0.02

```
##
## $Xavk_3
```

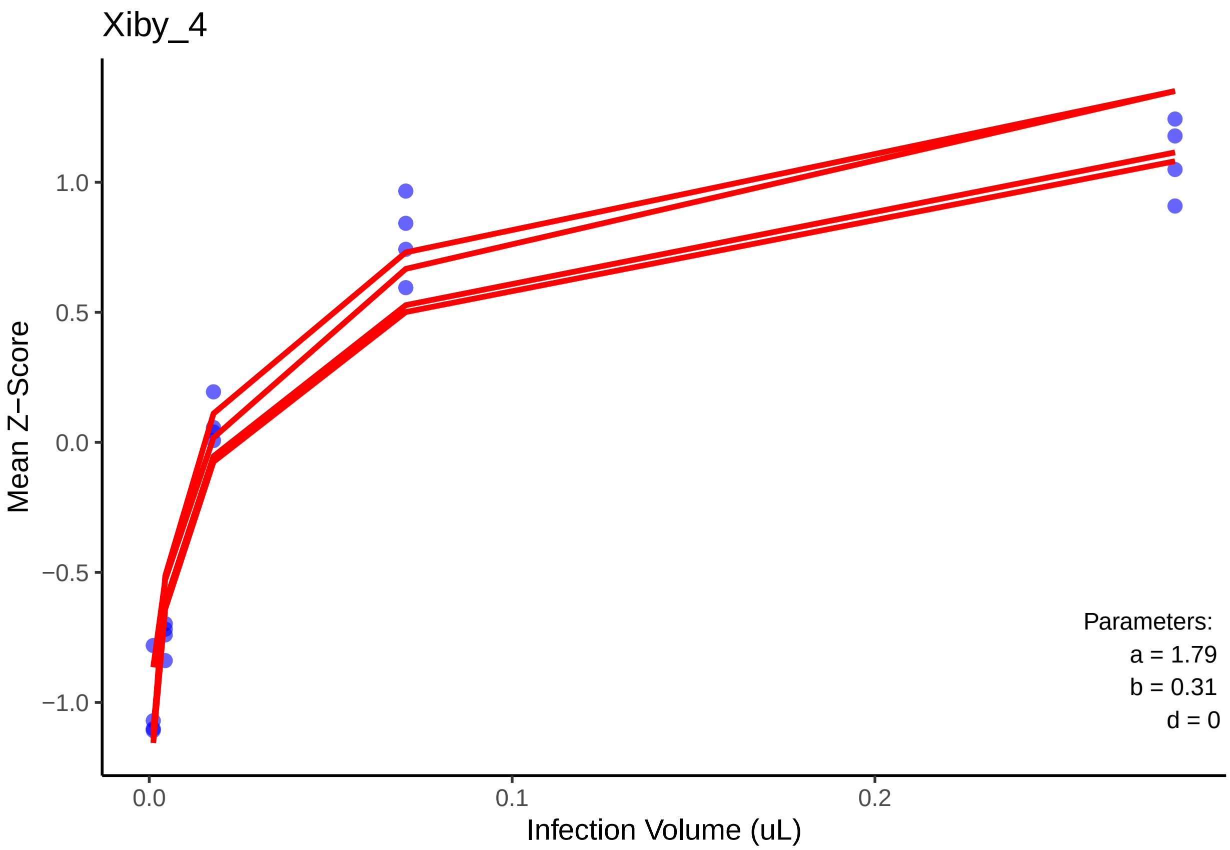

Xavk_3
1.5
1.0
0.5
0.0
−0.5
Mean Z−Score
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.79
b = 1.58
d = −0.21

```
##
## $Xegx_1
```

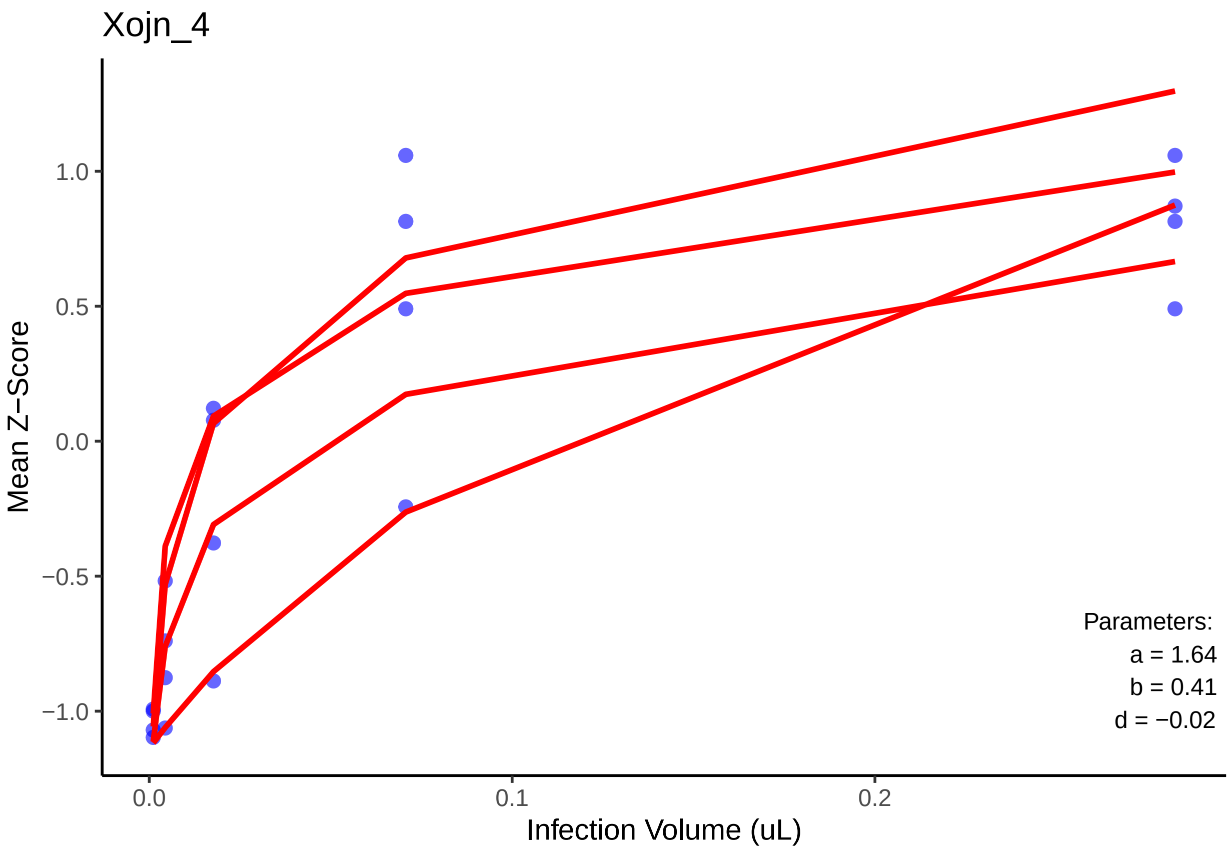


Xegx_1
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 3.06
b = 1.01
d = −0.07

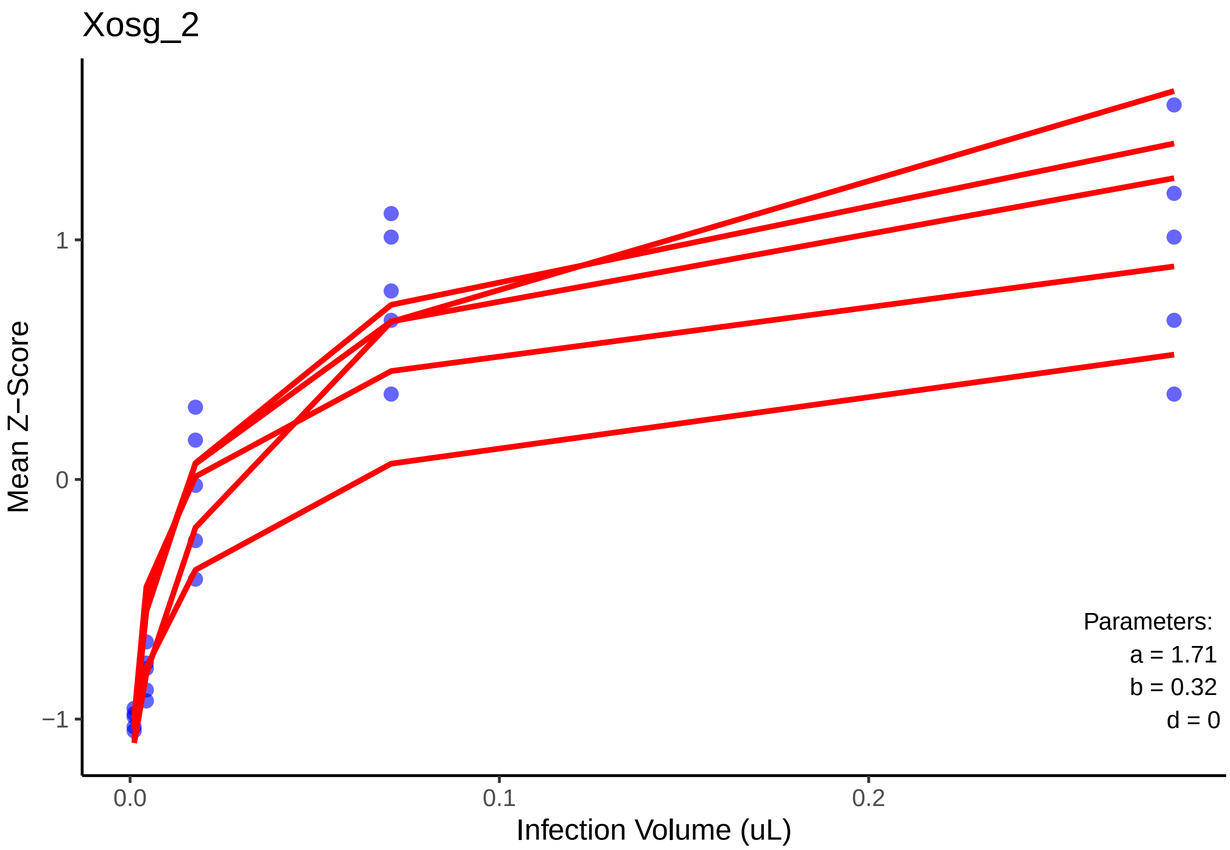

```
##
## $Xiby_4
```


Xiby_4
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.79
b = 0.31
d = 0

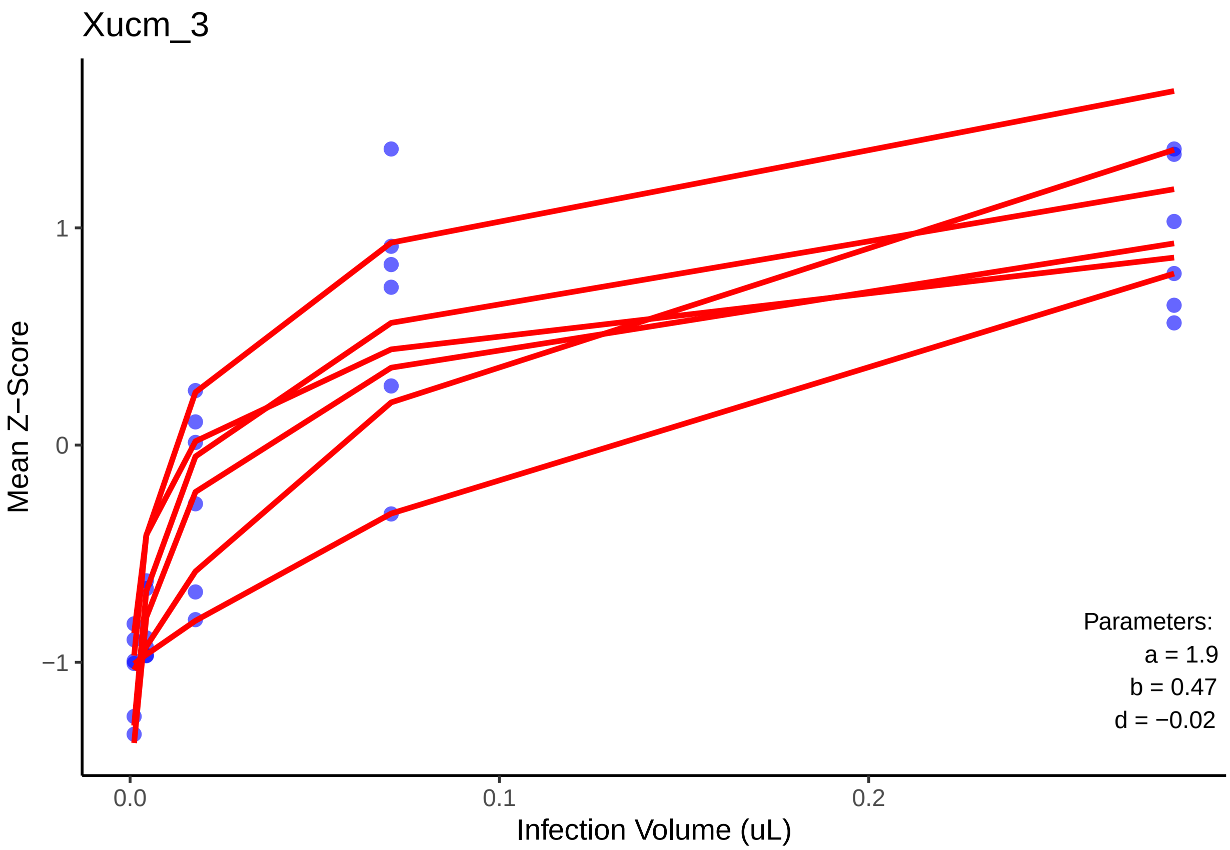
```
##
## $Xojn_4
```


Xojn_4
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.64
b = 0.41
d = −0.02

```
##
## $Xosg_2
```


Xosg_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.71
b = 0.32
d = 0

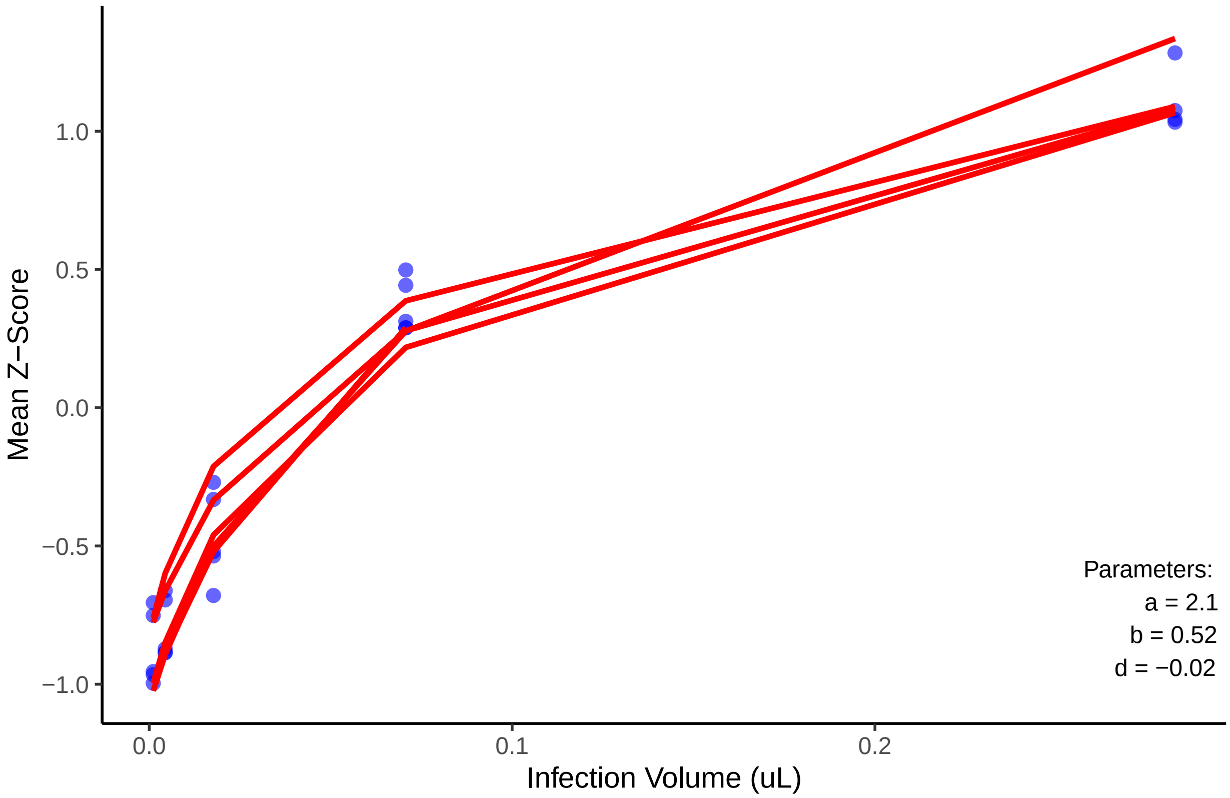
```
##
## $Xucm_3
```



Xucm_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.9
b = 0.47
d = −0.02

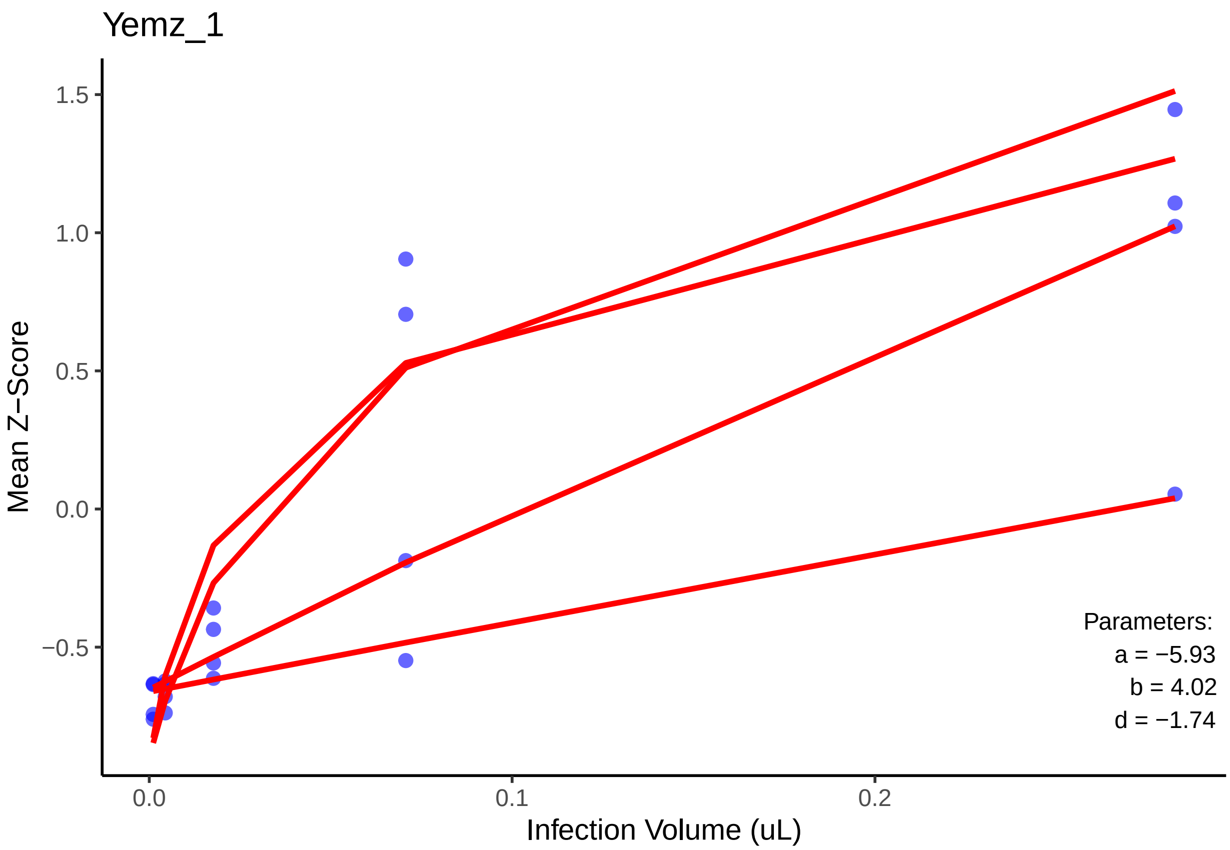

```
##
## $Xugn_1
```

Xugn_1

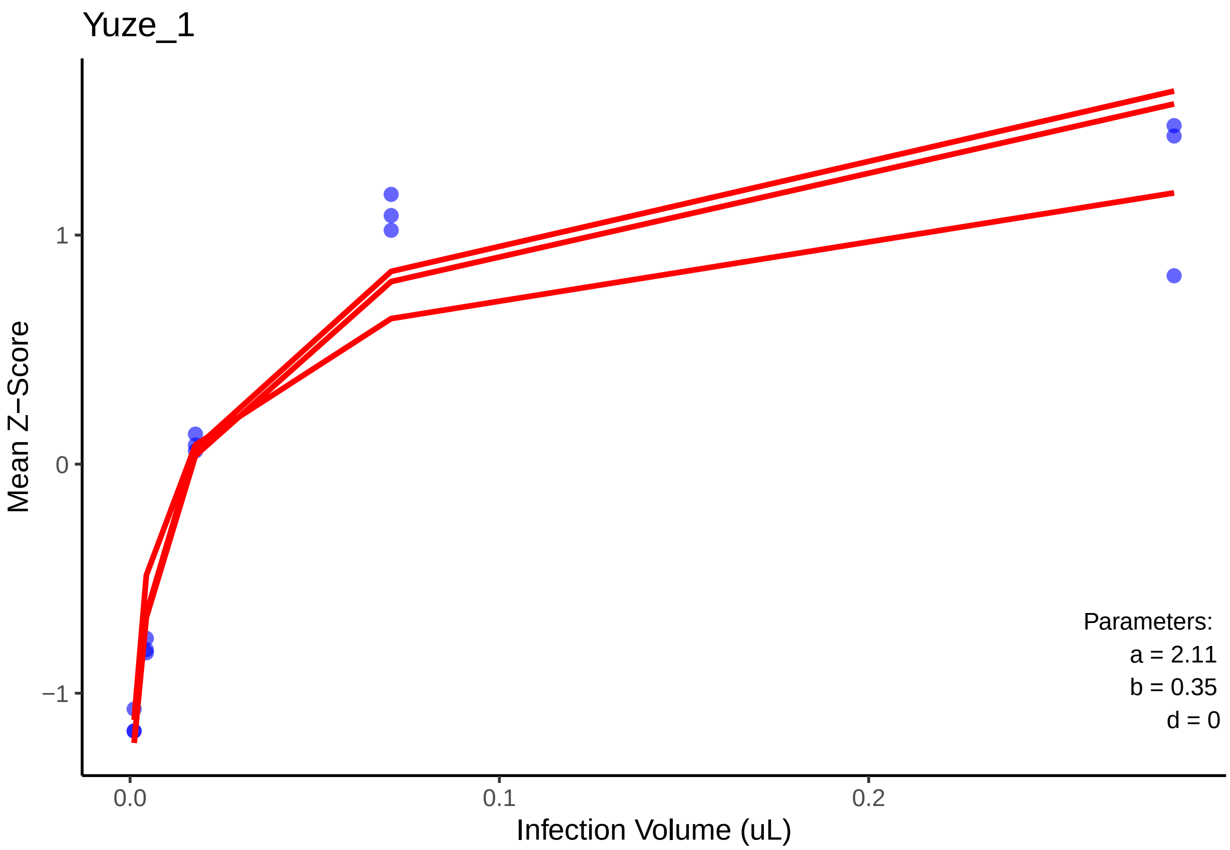


Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.1
b = 0.52
d = −0.02

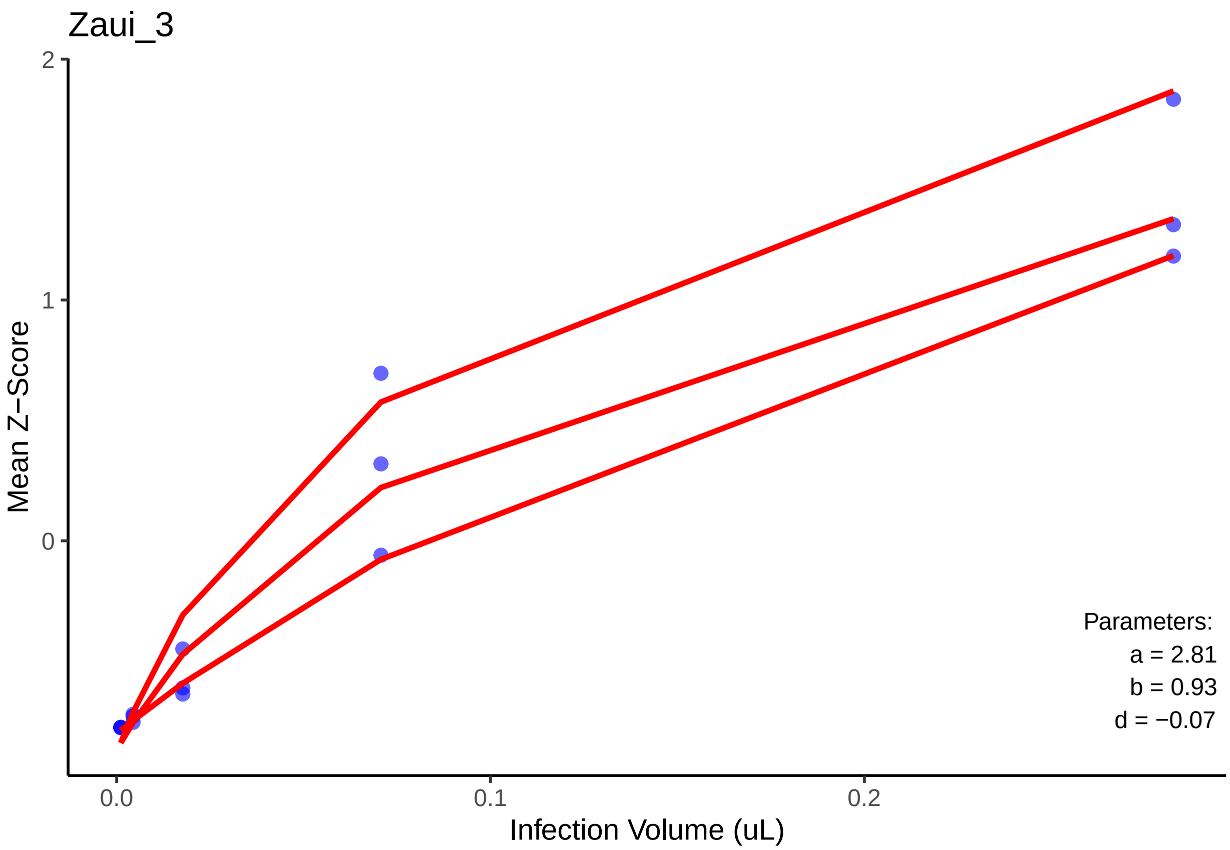

```
##
## $Yemz_1
```


Yemz_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = −5.93
b = 4.02
d = −1.74

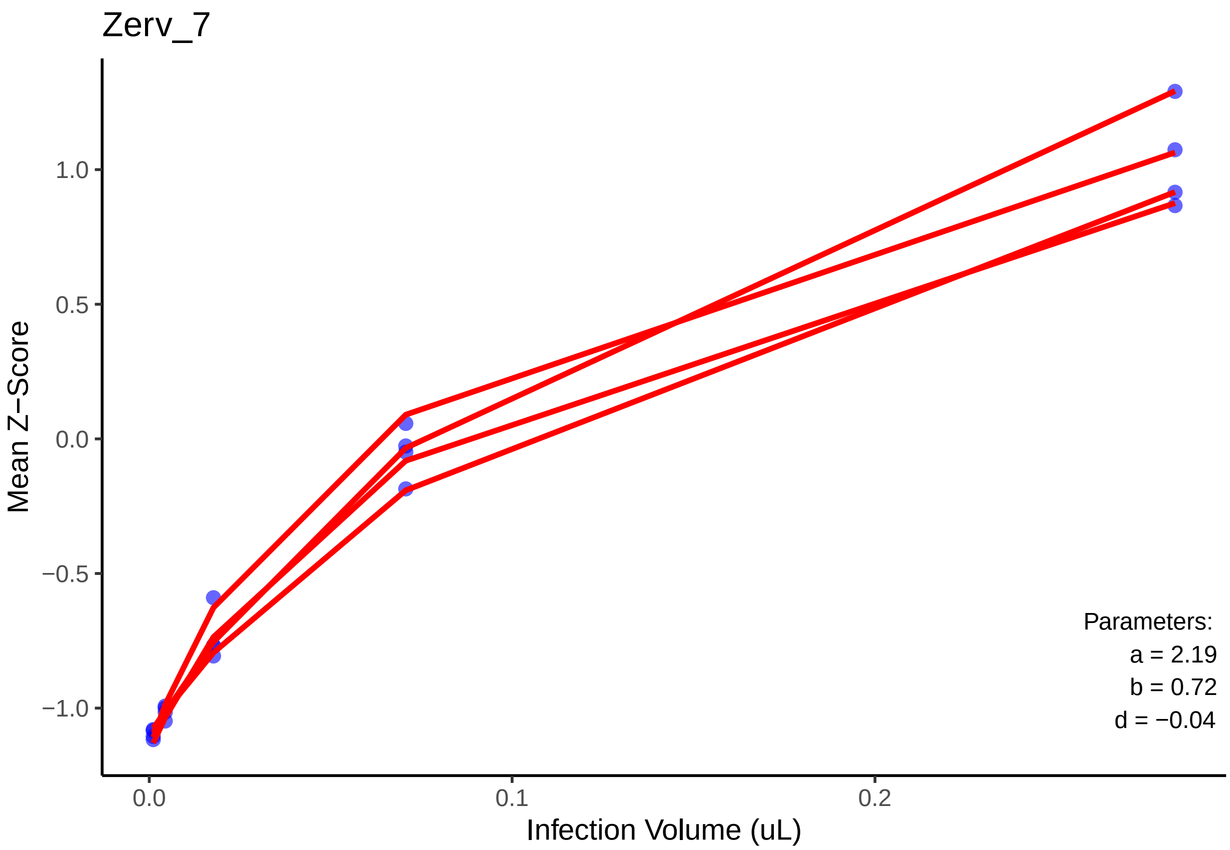
```
##
## $Yuze_1
```


Yuze_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.11
b = 0.35
d = 0

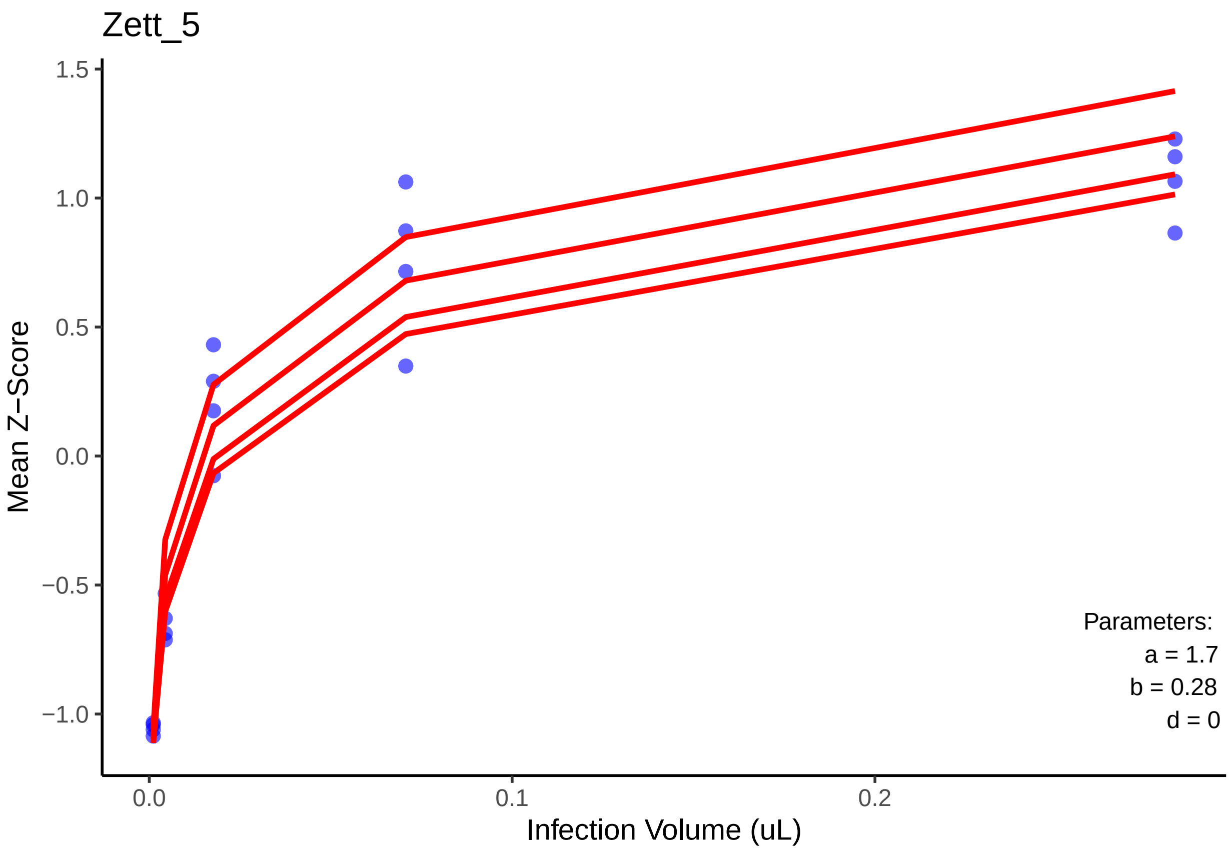
```
##
## $Zaui_3
```


Zaui_3
2
1
0
Mean Z−Score
Parameters:
a = 2.81
b = 0.93
d = −0.07
0.0
0.1
0.2
Infection Volume (uL)

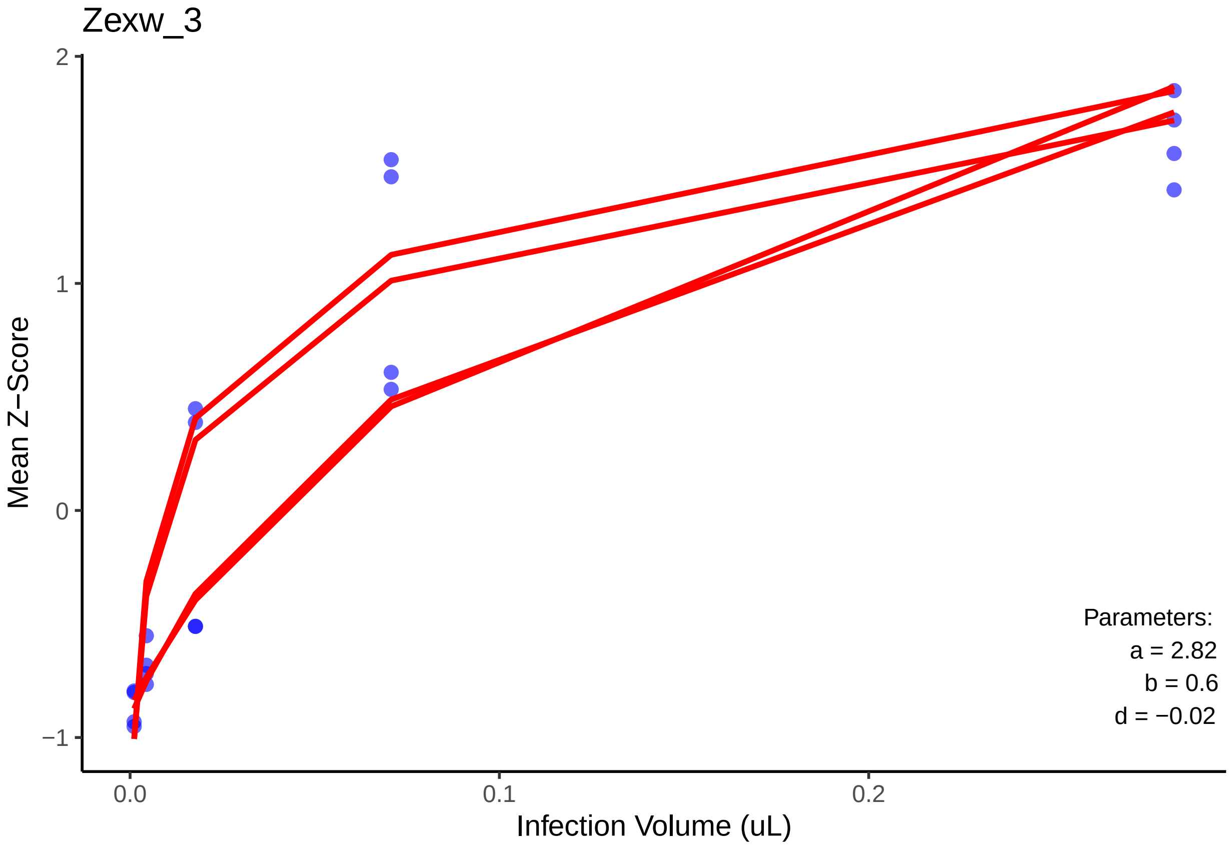
```
##
## $Zerv_7
```


Zerv_7
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 2.19
b = 0.72
d = −0.04

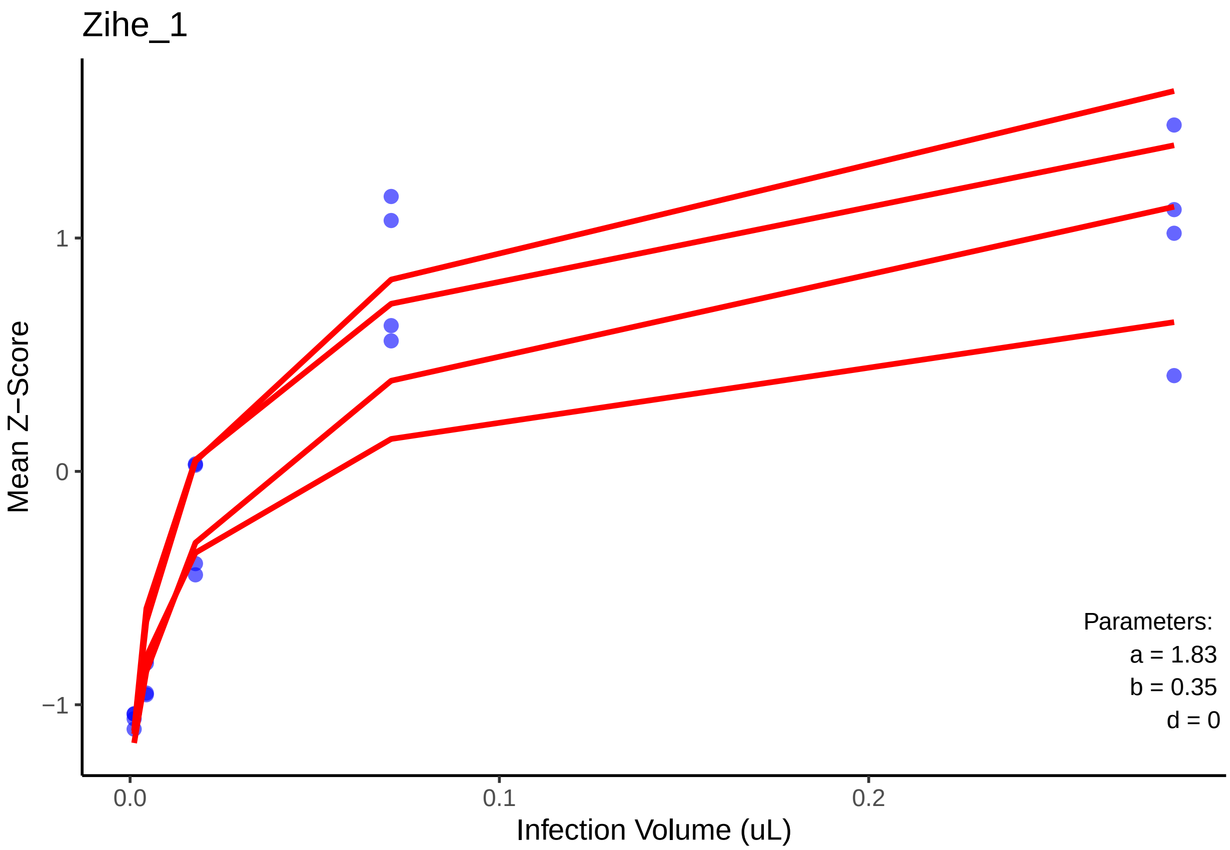
```
##
## $Zett_5
```


Zett_5
Mean Z−Score
Infection Volume (uL)
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Parameters:
a = 1.7
b = 0.28
d = 0

```
##
## $Zexw_3
```

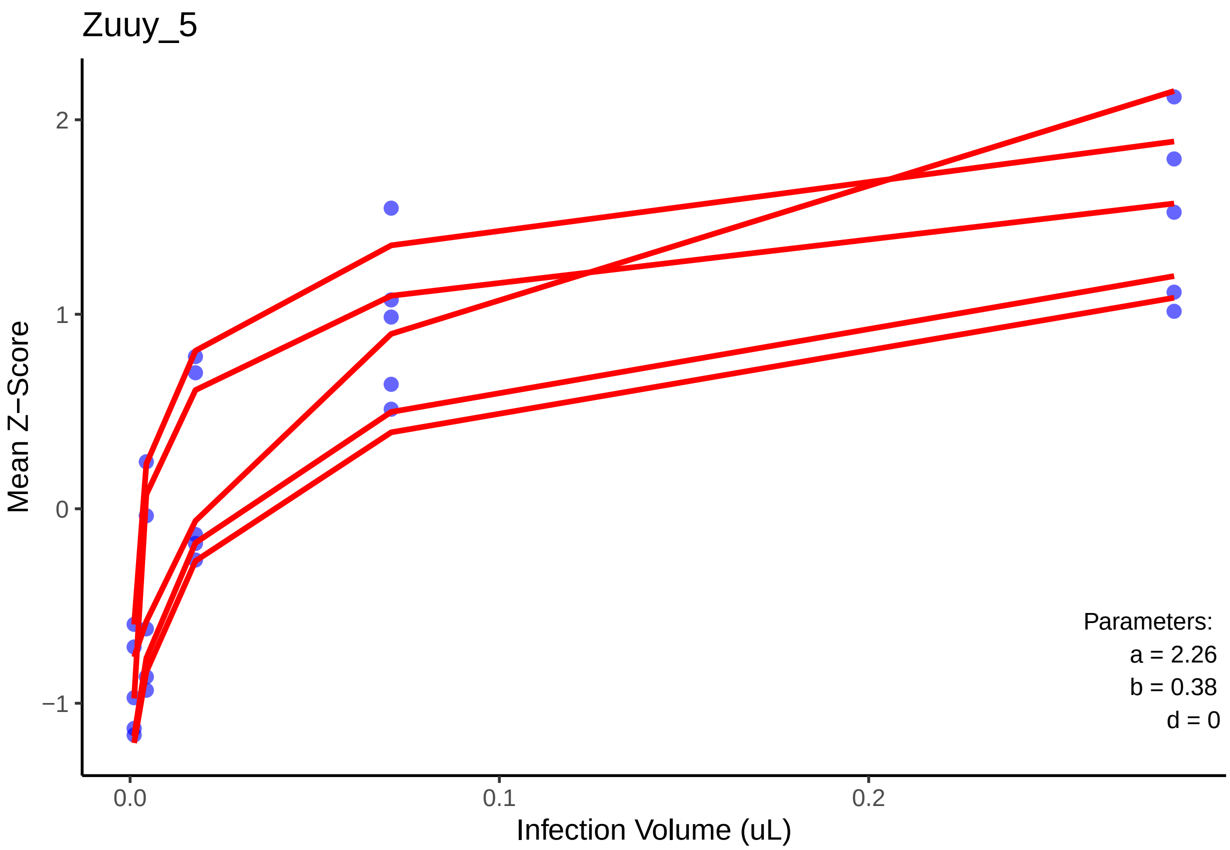

Zexw_3
Mean Z−Score
Infection Volume (uL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
a = 2.82
b = 0.6
d = −0.02

```
##
## $Zihe_1
```



Zihe_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (uL)
Parameters:
a = 1.83
b = 0.35
d = 0


```
##
## $Zuuy_5
```




## logistic

Decided to use to use a 4 parameter logistic,

$$c + \frac{d - c}{1 + e^{b(x-e)}}$$

c - min,d-max, b-slope, e- x offset a higher c and d and b should correspond to an increase in permissiveness, an increase in e should correspond with lower permissiveness , however the fitting of the graph may not fit completely accurately, e.g parameters such as b and c may be extra large/small to allow a more accurate fit compared to what the values actually represent. So said parameters may have to be reevaluated later in the analysis

I use Drc (dose response package ) as they provide a robust 4 parameter fitting with drm function, i then take the coefficients out of the model and store them, per replicate

```
# Correct 4PL formula (parentheses fix)
logistic_func <- function(x, b, d, e,c){
 c+ ((d-c)/(1 + exp(b*(x - e))))# Fixed denominator placement
}

# Robust fitting function
logistic_fit <- function(data) {
    fitted_data <- data %>%
        group_by(screen_nb,replicate) %>%  # Verify these columns exist in your data
        group_modify(~ {
            tryCatch({ # Fit with drm, explicitly stating NO log transformation
                model <- drm(zscore ~ infection_volume_ul, fct = L.4(), data = .x)
                coefs <- coef(model)
```

```
                .x %>%
                    mutate(
                        logis_b = coefs["b:(Intercept)"],
                        logis_e = coefs["e:(Intercept)"],
                        logis_c = coefs["c:(Intercept)"],
                        logis_d = coefs["d:(Intercept)"]
                    )
            }, error = function(e) {
                warning(paste("drc error for screen_nb:", .x$screen_nb[1], ":", e$message))
                .x %>%
                    mutate(logis_b = NA, logis_e = NA, logis_d = NA)
            })
        }) %>%
        ungroup()
    return(fitted_data)
}

# Apply to cell line data
vector_data_per_cell_line <- purrr::map(vector_data_per_cell_line$data,logistic_fit)%>%bind_rows()%>%ne
```

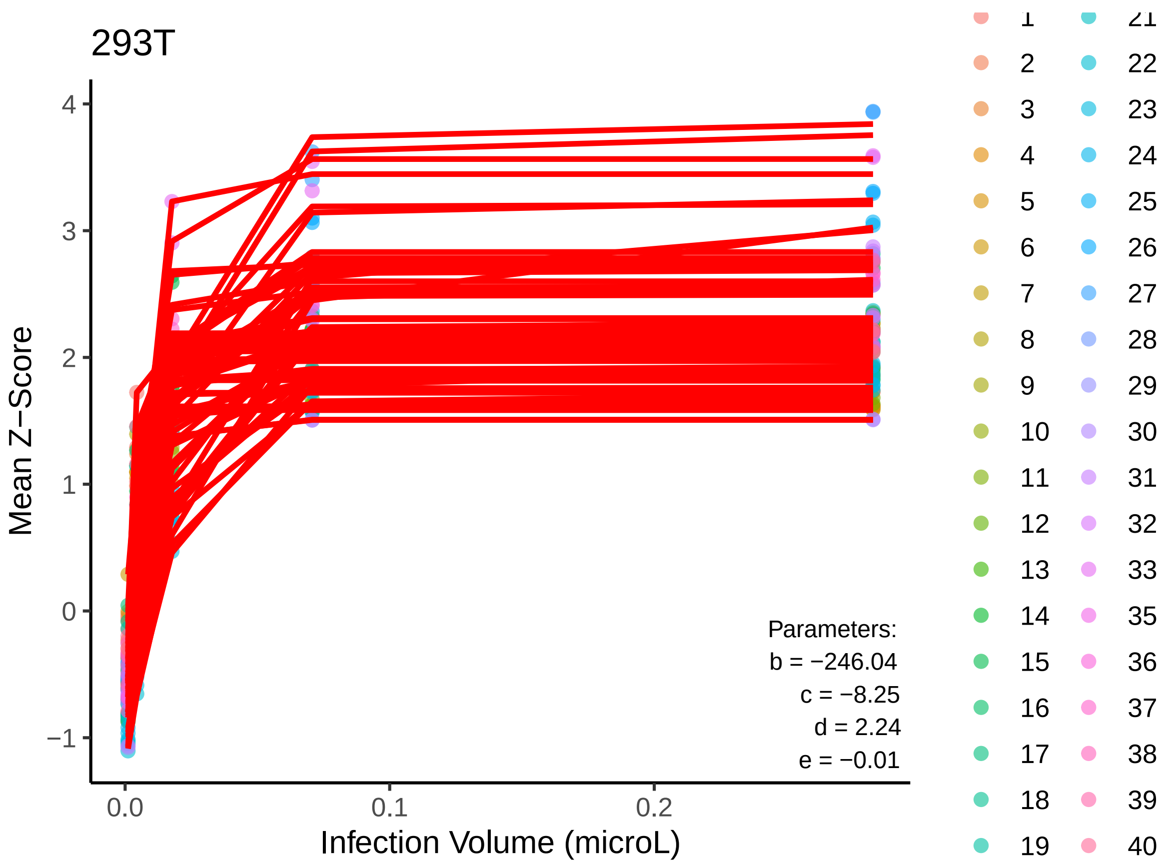
similar to plot logarithmic, i create predicted then use ggplot to plot the line over the actual points to assess the fit, and use the parameters to see if the values i get for each parameter make biological sense

```
apply_plot_logistic <- function(i) {
  # Generate predictions using row-wise parameters
  plot_data <- i %>%
    mutate(
      predicted = logistic_func(
        x = infection_volume_ul,
        b = logis_b,
        c = logis_c,
        d = logis_d,
        e = logis_e
      )
    )

  # Create base plot
  p <- ggplot(plot_data, aes(x = infection_volume_ul, y = zscore)) +
    # Actual data points
    geom_point(
      aes(color = factor(screen_nb)),  # Color by screen_nb
      size = 2,
      alpha = 0.6,
      show.legend = T
    ) +
    # Fitted curves
    geom_line(
      aes(y = predicted, group = interaction(screen_nb, replicate)),
      color = "red",
      linewidth = 1
    ) +
    # Labels and theme
    labs(
      title = unique(plot_data$cell_line),
```

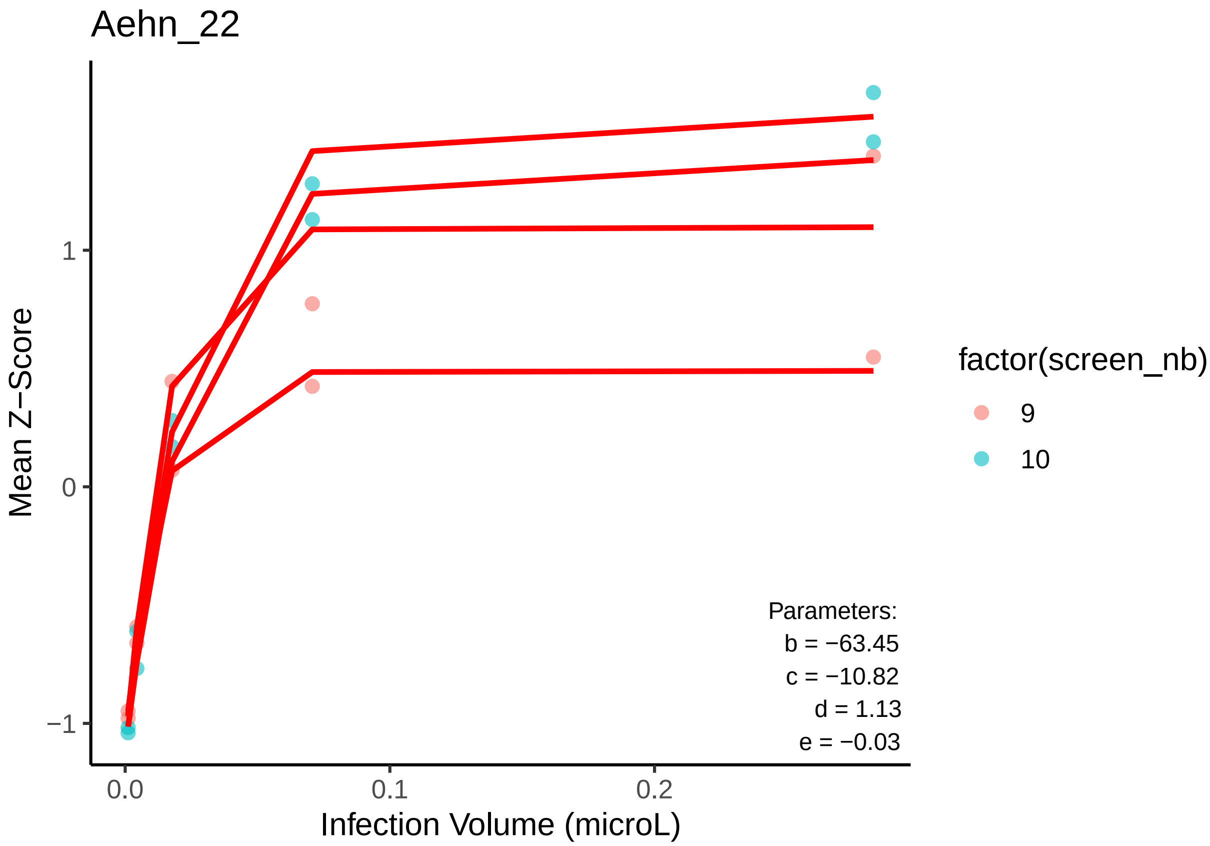
```
      x = "Infection Volume (microL)",
      y = "Mean Z-Score"
    ) +
    theme_classic(base_size = 12)

  # Add regression parameters annotation
  params_text <- paste0(
    "Parameters:\n",
    "b = ", round(mean(plot_data$logis_b, na.rm = TRUE), 2), "\n",
    "c = ", round(mean(plot_data$logis_c, na.rm = TRUE), 2), "\n",
    "d = ", round(mean(plot_data$logis_d, na.rm = TRUE), 2), "\n",
    "e = ", round(mean(plot_data$logis_e, na.rm = TRUE), 2)
  )

  p + annotate("text",
               x = Inf, y = -Inf,
               label = params_text,
               hjust = 1.1, vjust = -0.1,
               size = 3)
}
```

```
logistic_plot_vector=purrr::map(vector_data_per_cell_line$data,apply_plot_logistic)
names(logistic_plot_vector)=vector_data_per_cell_line$cell_line
logistic_plot_vector
```

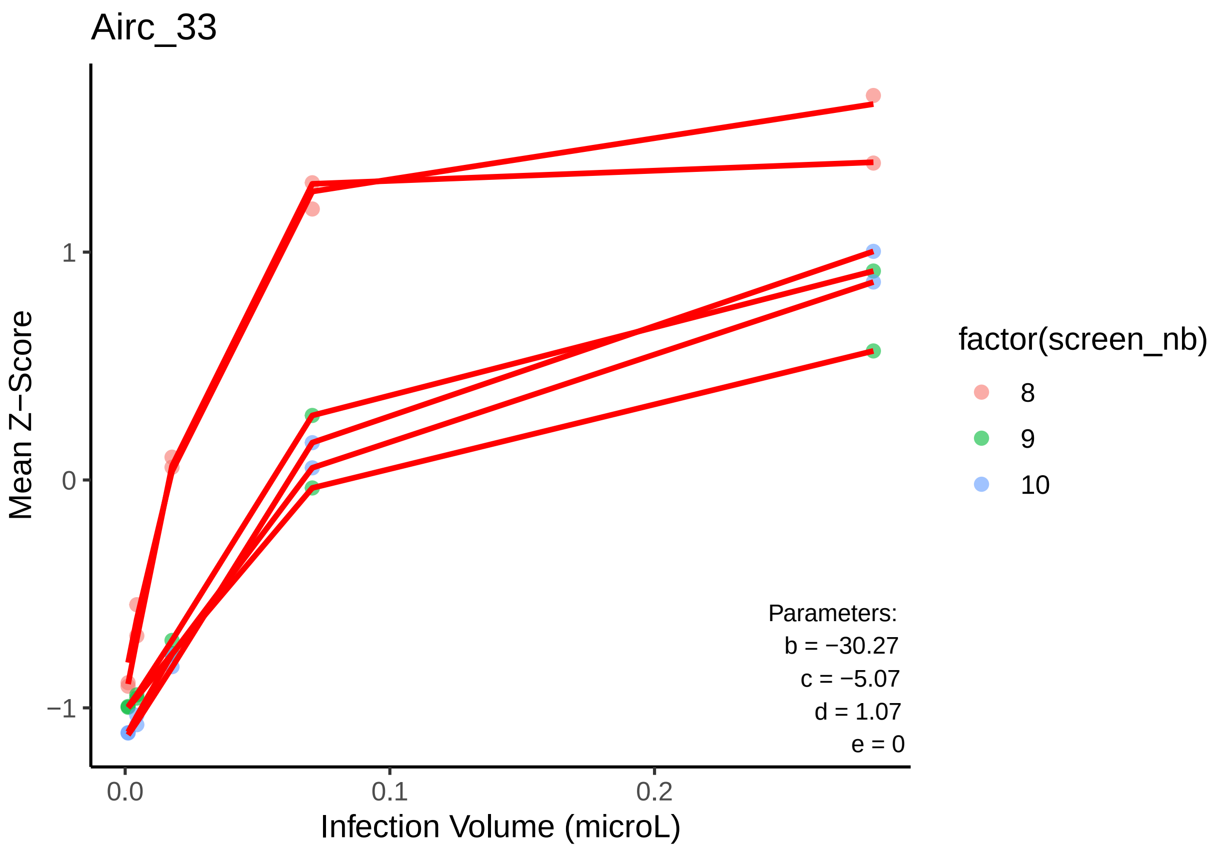
```
## $`293T`
```



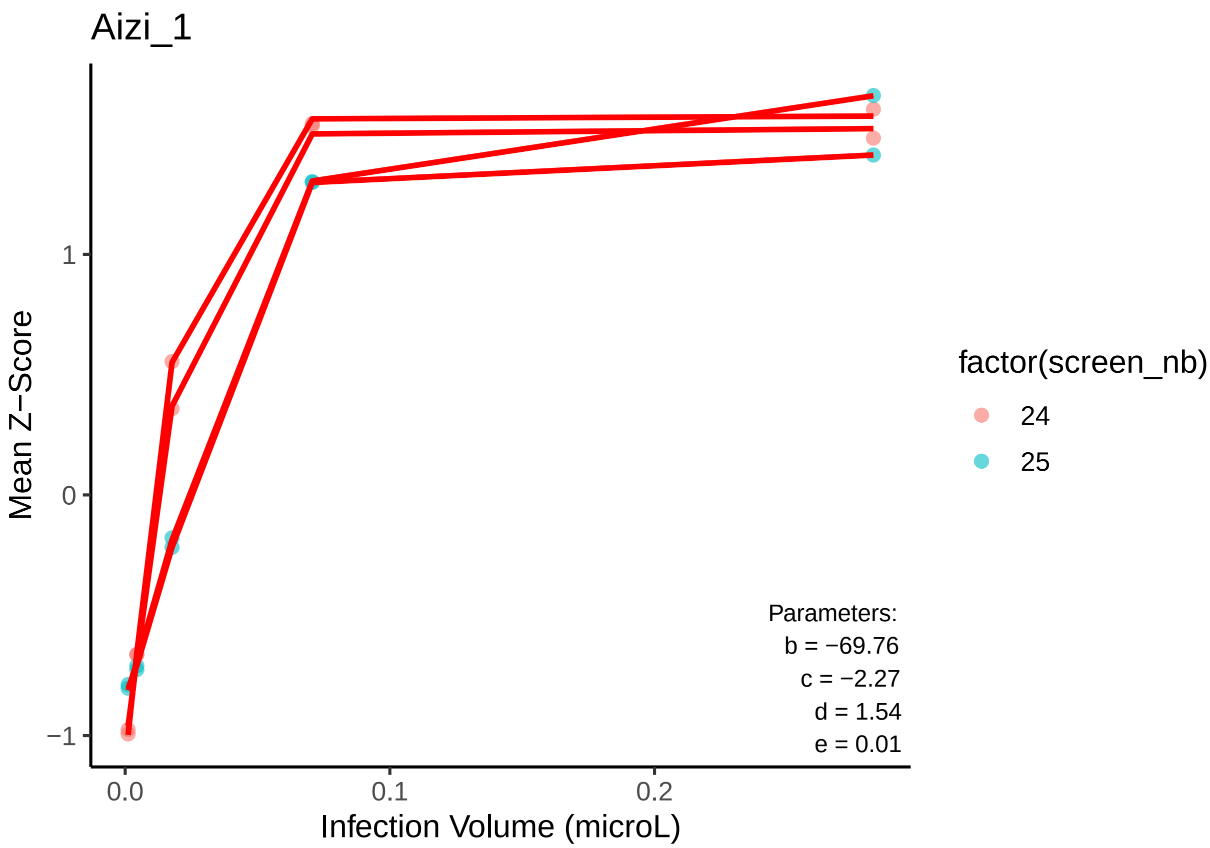
```
##
## $Aehn_22
```



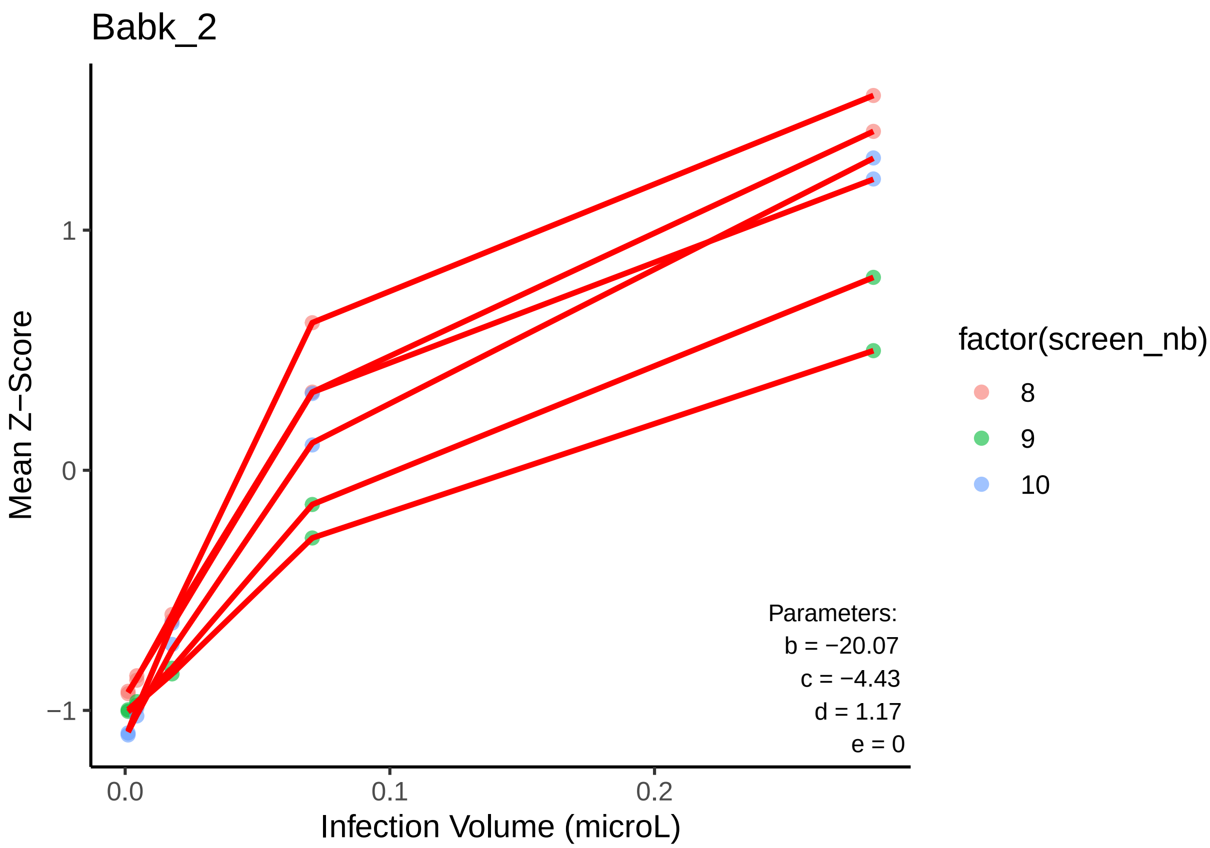

```
##
## $Airc_33
```


Airc_33
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −30.27
c = −5.07
d = 1.07
e = 0
factor(screen_nb)
8
9
10

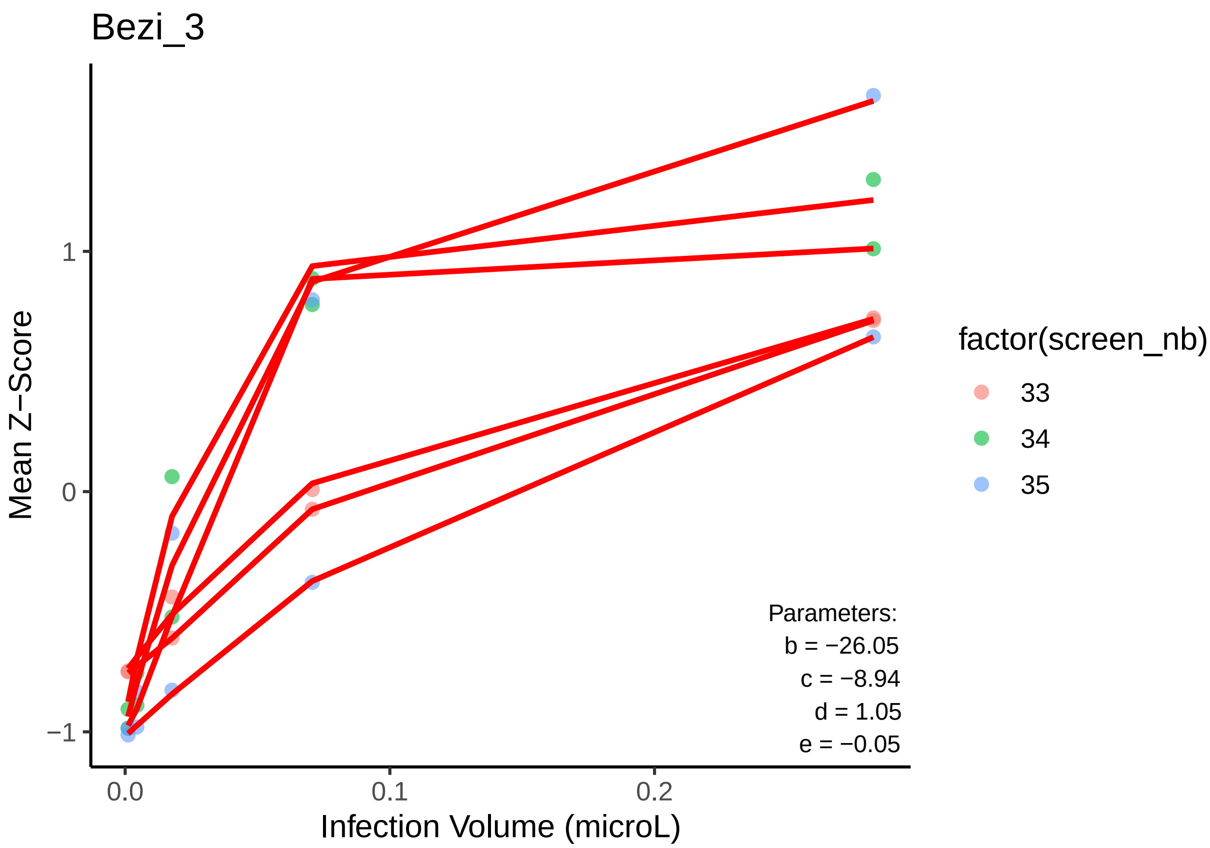
```
##
## $Aizi_1
```


Aizi_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −69.76
c = −2.27
d = 1.54
e = 0.01
factor(screen_nb)
24
25

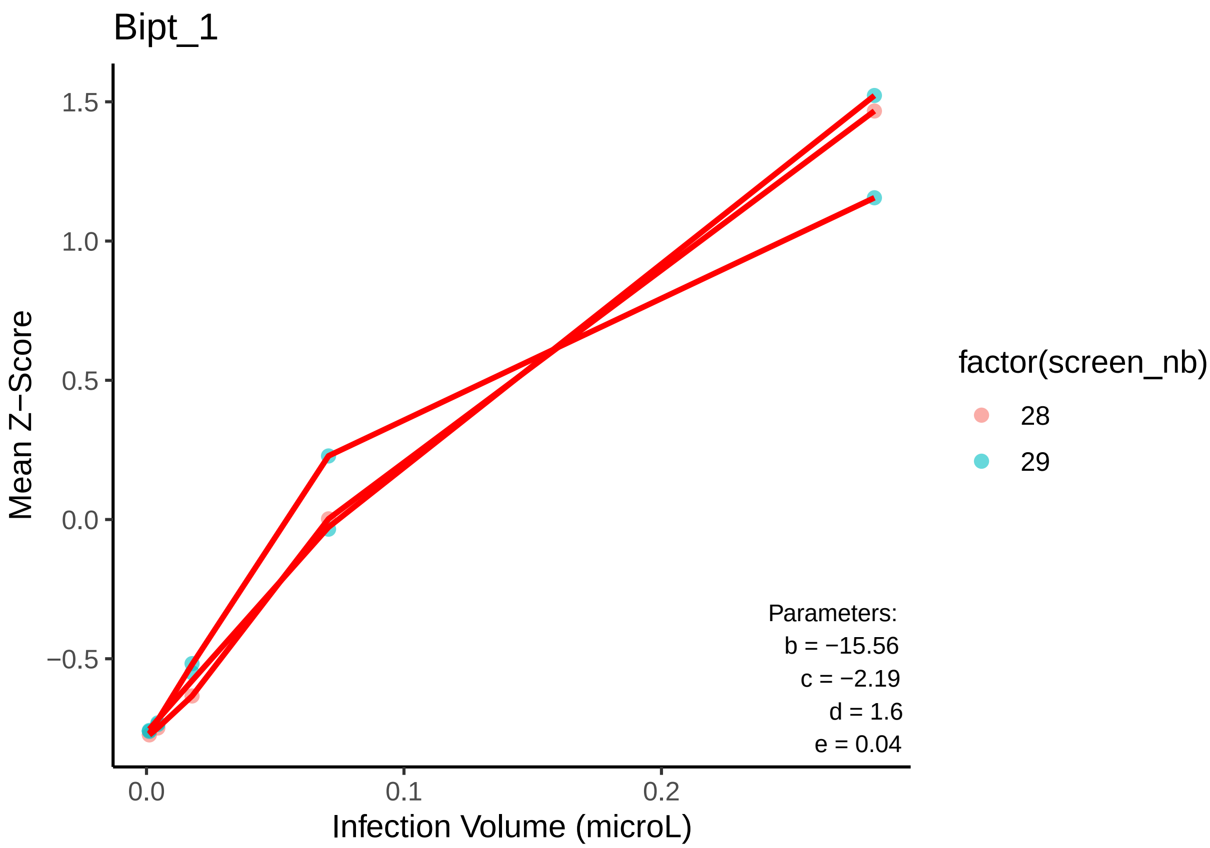
```
##
## $Babk_2
```


Babk_2
Mean Z−Score
Infection Volume (microL)
1
0
−1
0.0
0.1
0.2
factor(screen_nb)
8
9
10
Parameters:
b = −20.07
c = −4.43
d = 1.17
e = 0

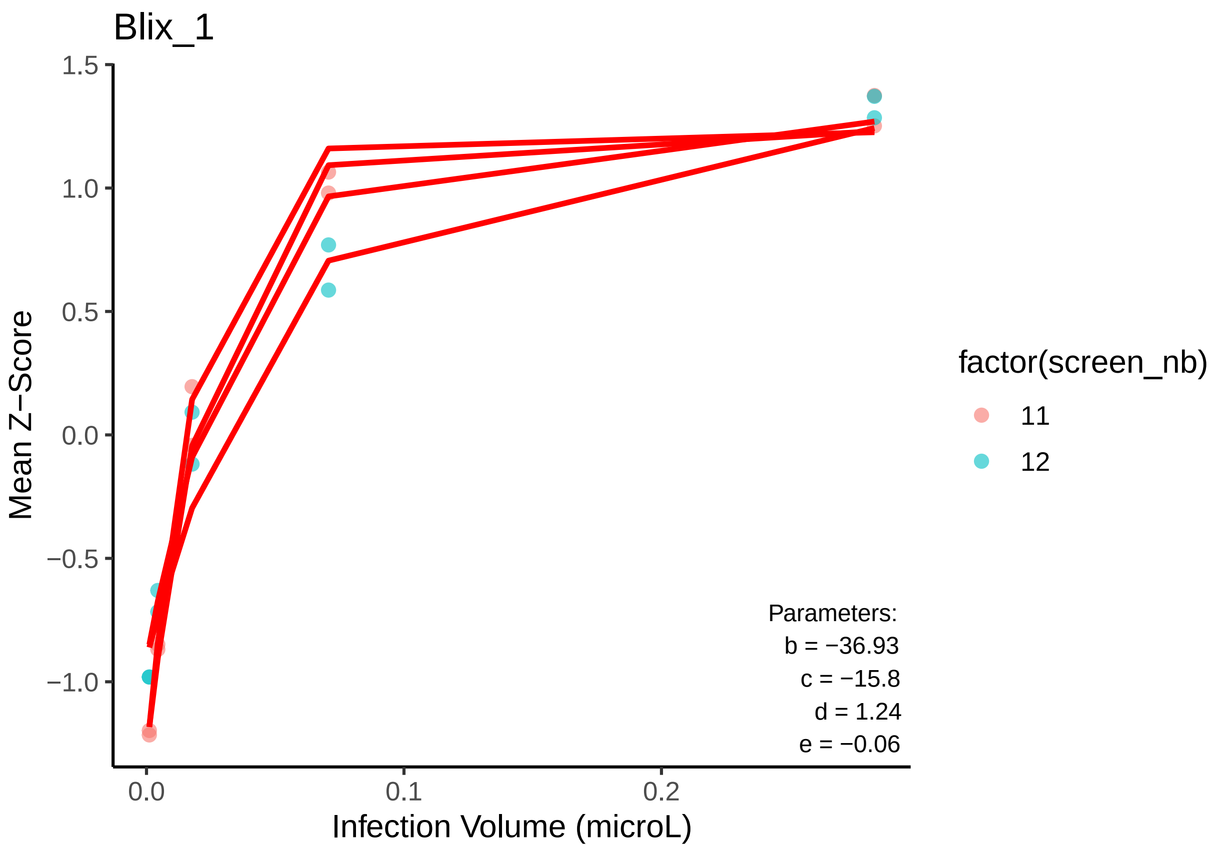
```
##
## $Bezi_3
```


Bezi_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −26.05
c = −8.94
d = 1.05
e = −0.05
factor(screen_nb)
33
34
35

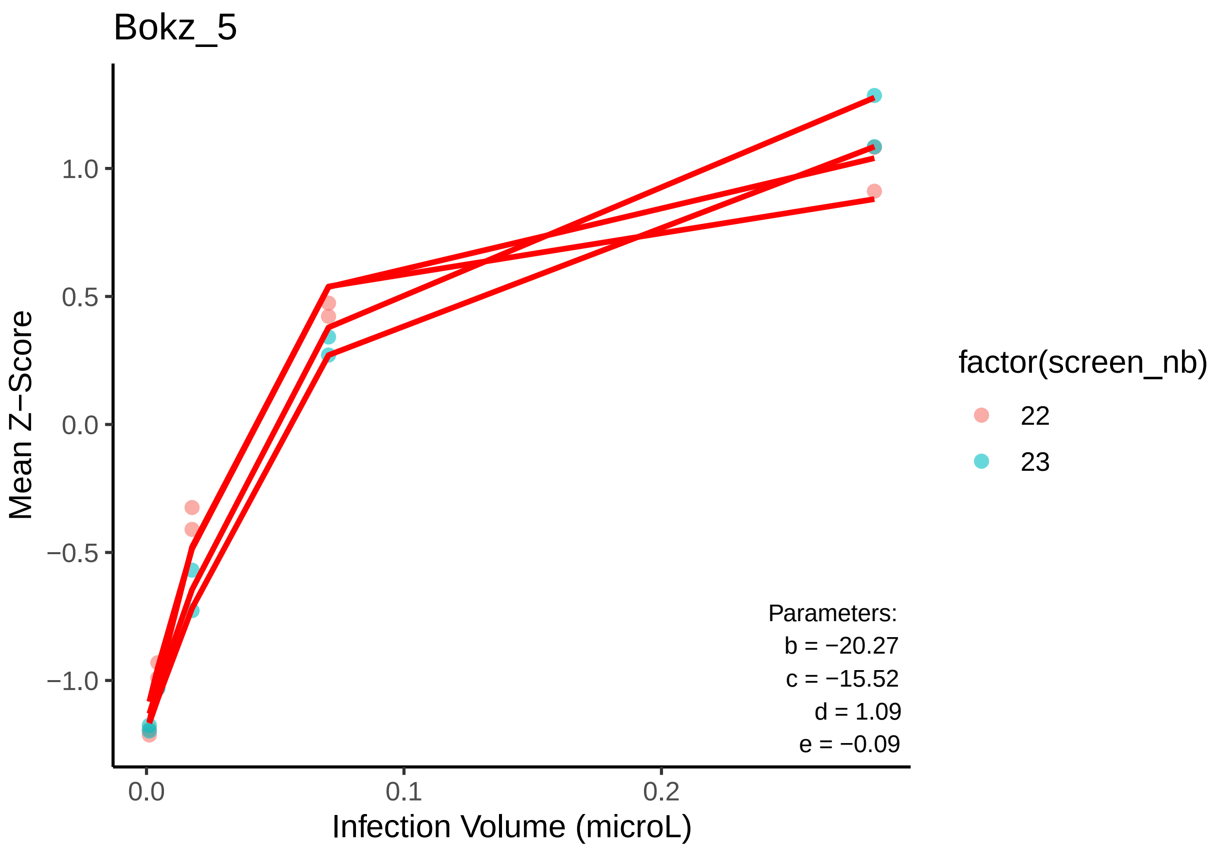
```
##
## $Bipt_1
```


Bipt_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −15.56
c = −2.19
d = 1.6
e = 0.04
factor(screen_nb)
28
29

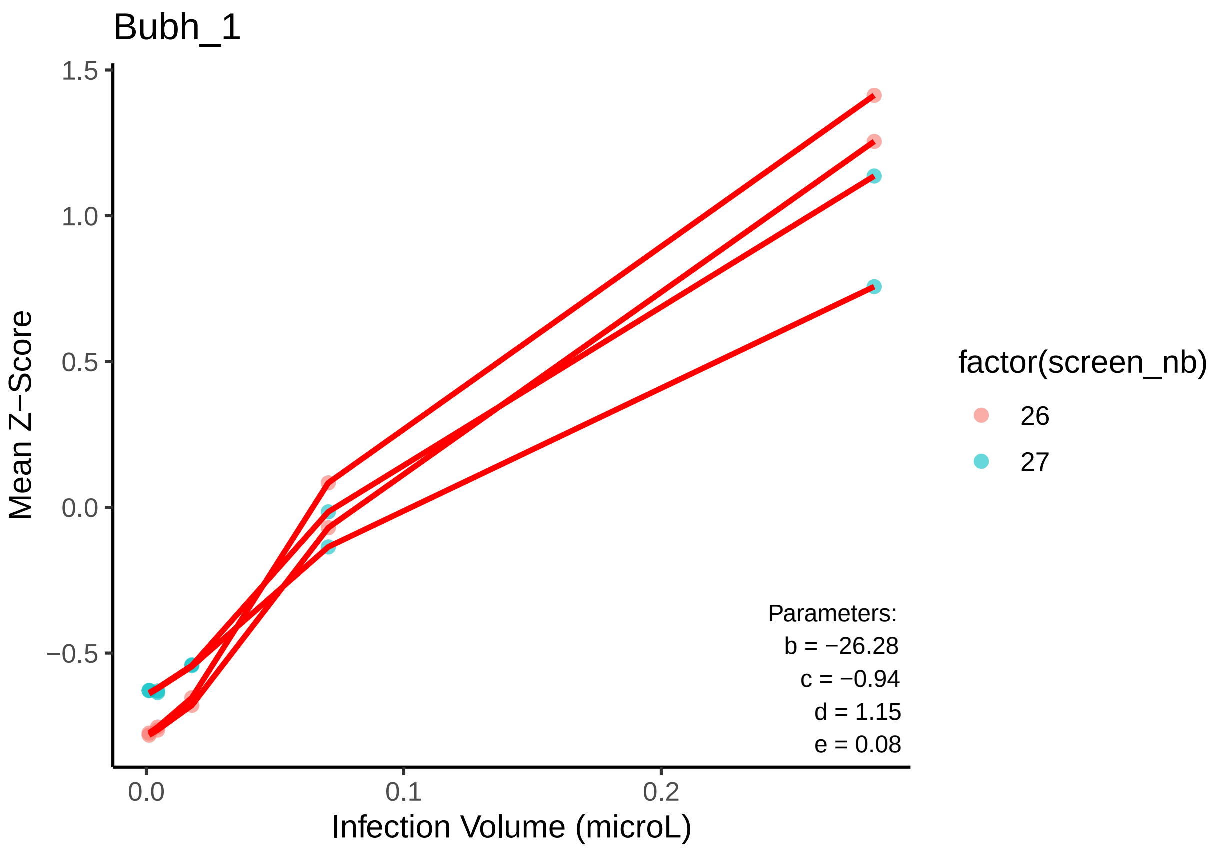
```
##
## $Blix_1
```


Blix_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −36.93
c = −15.8
d = 1.24
e = −0.06
factor(screen_nb)
11
12

```
##
## $Bokz_5
```

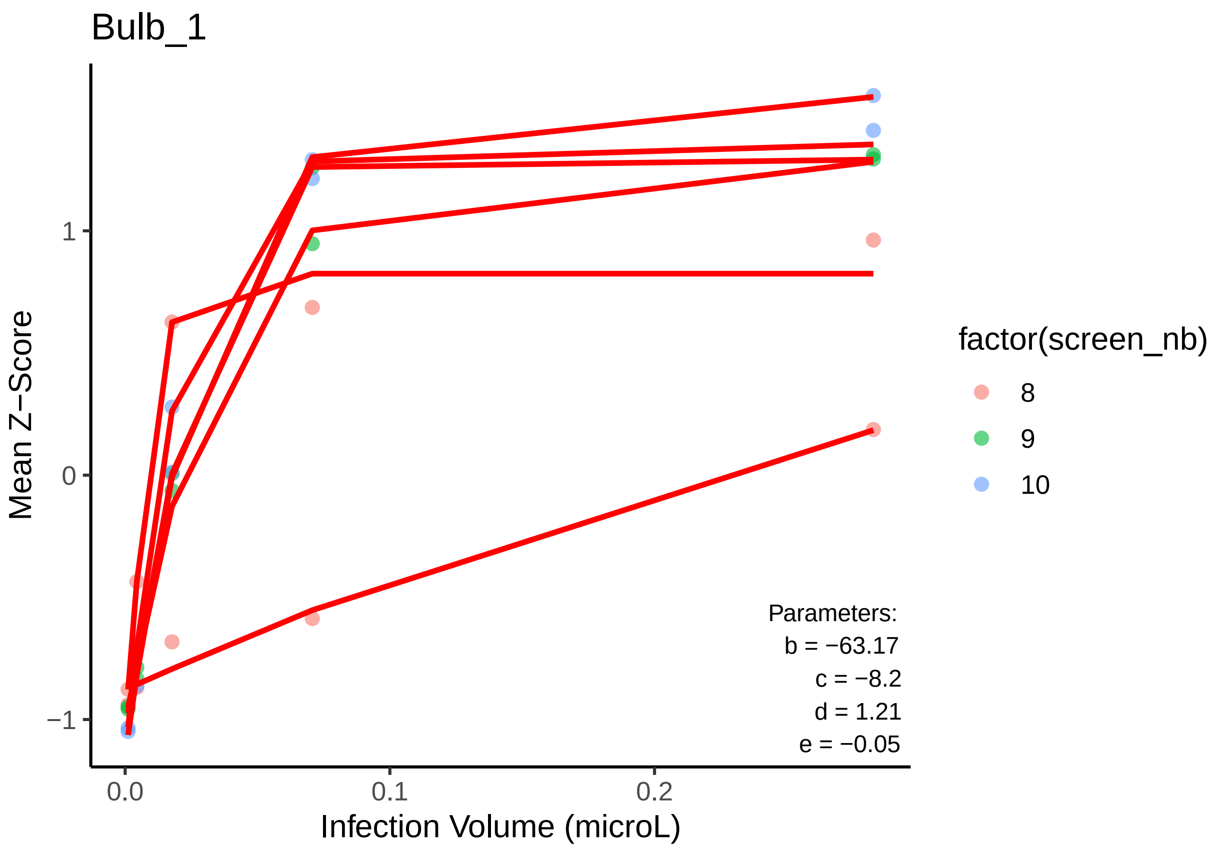

Bokz_5
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
22
23
Parameters:
b = −20.27
c = −15.52
d = 1.09
e = −0.09

```
##
## $Bubh_1
```

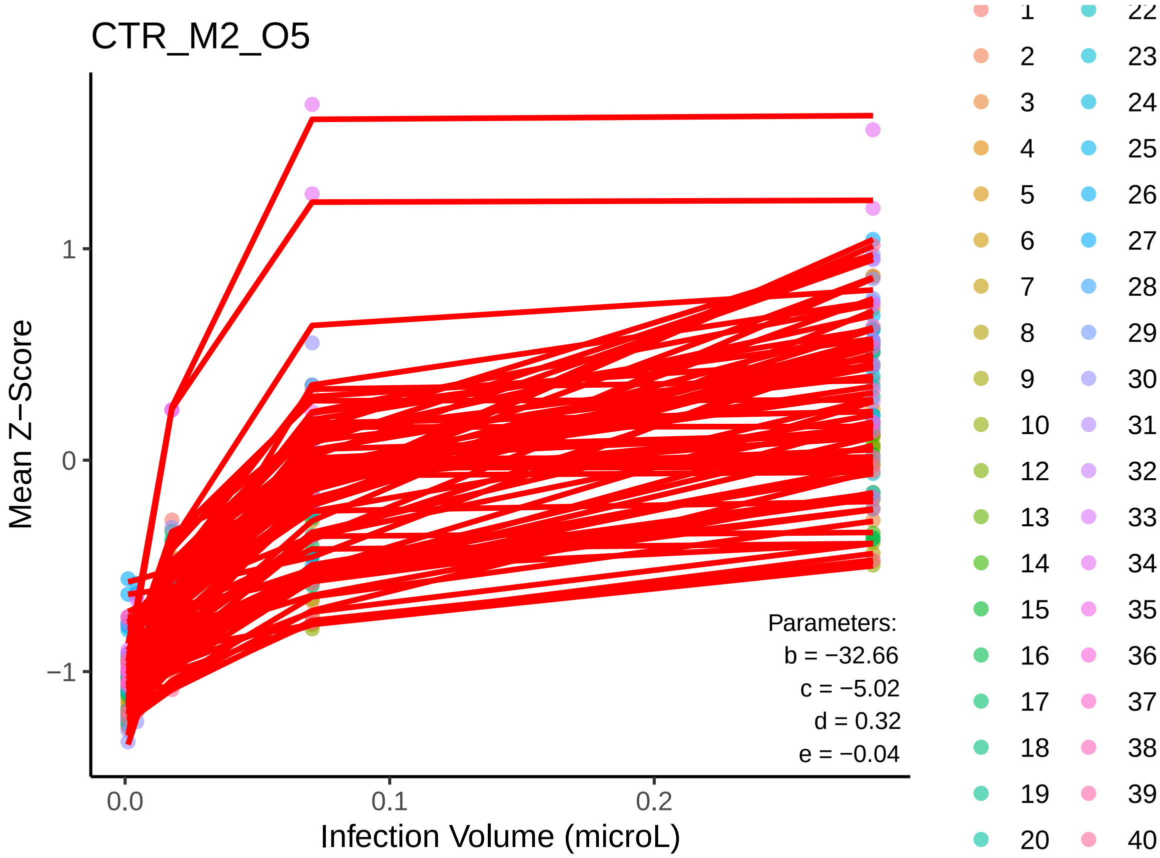


Bubh_1
1.5
1.0
0.5
0.0
−0.5
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
26
27
Parameters:
b = −26.28
c = −0.94
d = 1.15
e = 0.08


```
##
## $Bulb_1
```

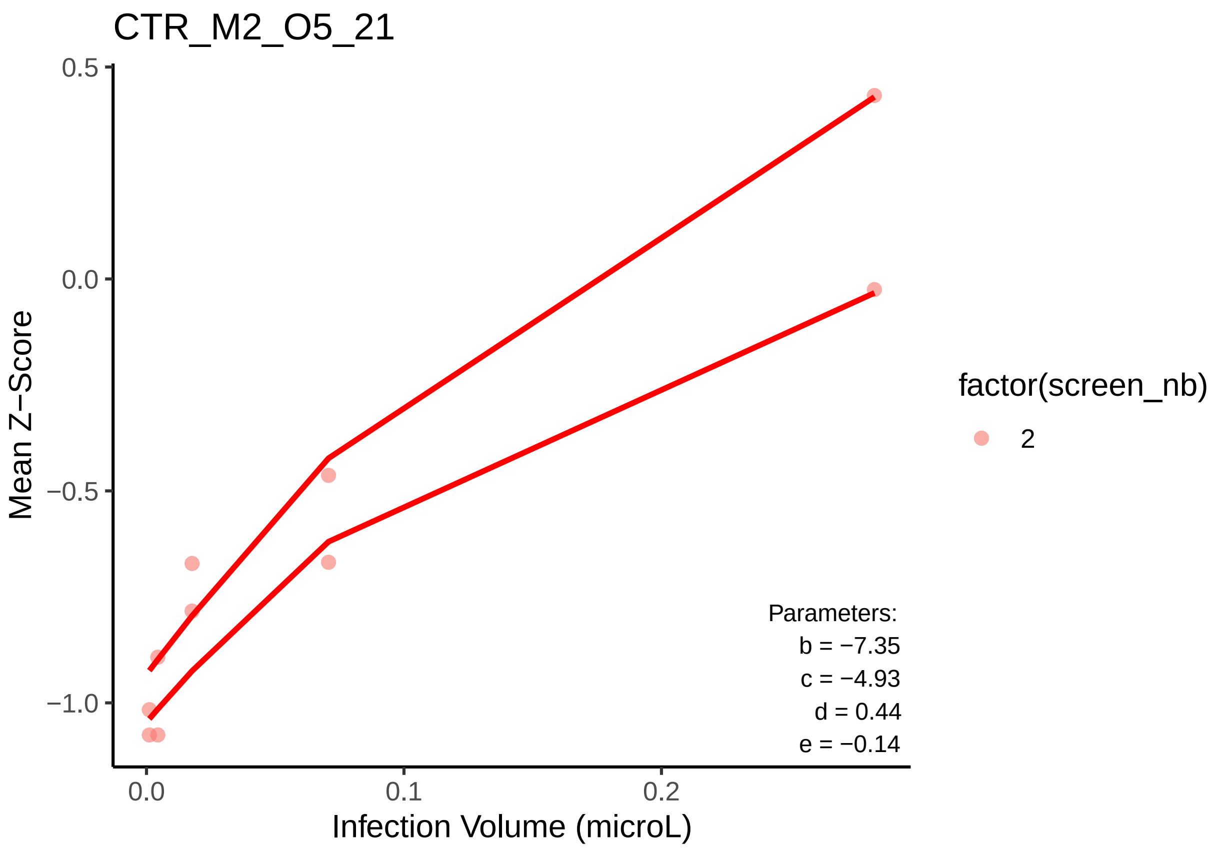

Bulb_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
8
9
10
Parameters:
b = −63.17
c = −8.2
d = 1.21
e = −0.05

```
##
## $CTR_M2_05
```

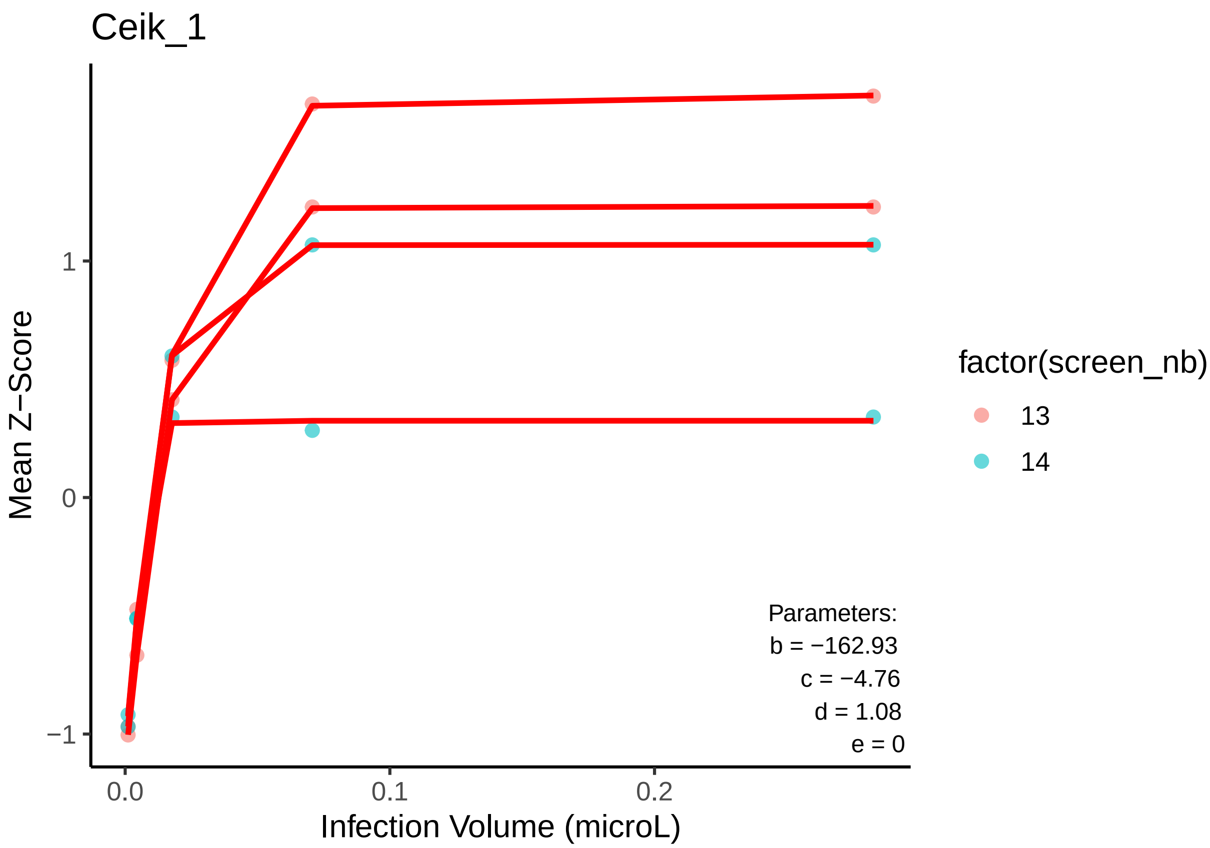


CTR_M2_O5
Mean Z−Score
Infection Volume (microL)
Parameters:
b = −32.66
c = −5.02
d = 0.32
e = −0.04
1
2
3
4
5
6
7
8
9
10
12
13
14
15
16
17
18
19
20
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40


```
##
## $CTR_M2_O5_21
```

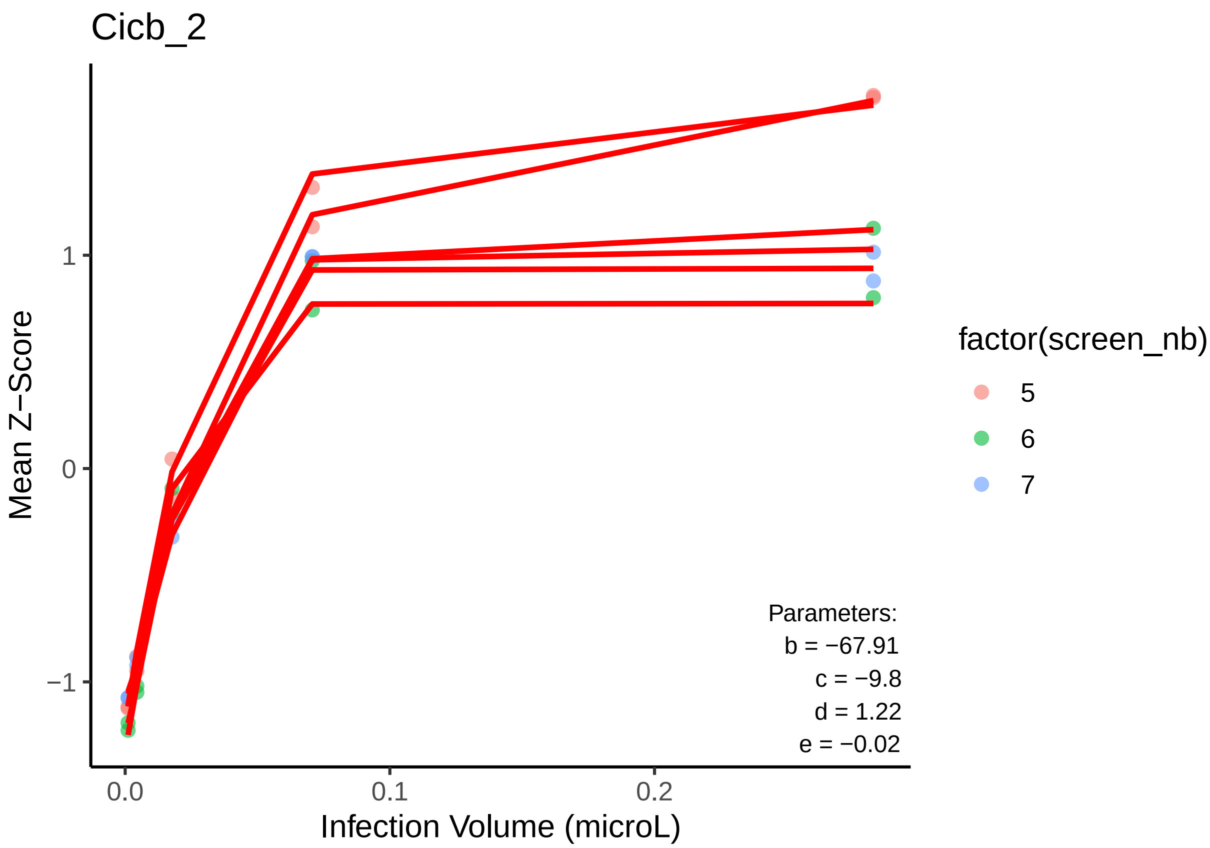

CTR_M2_O5_21
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
2
Parameters:
b = −7.35
c = −4.93
d = 0.44
e = −0.14

```
##
## $Ceik_1
```

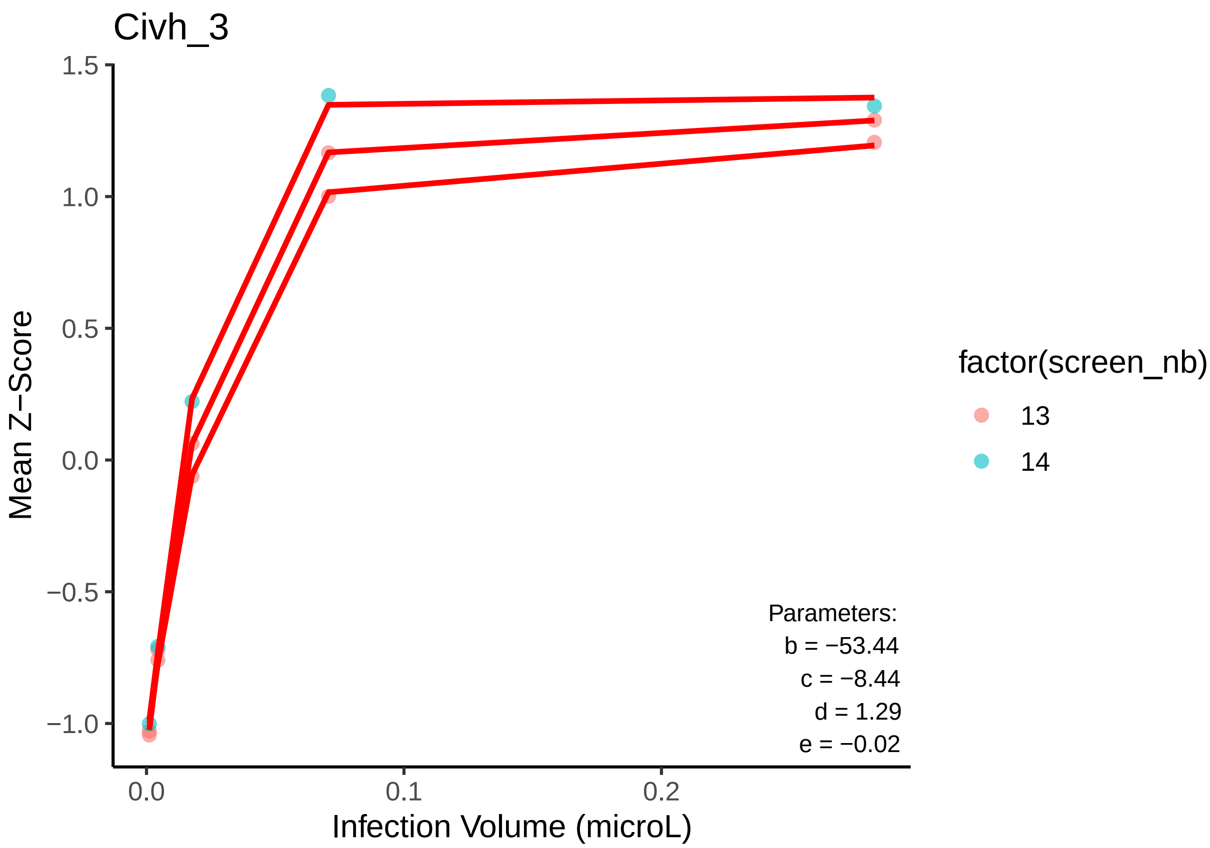


Ceik_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −162.93
c = −4.76
d = 1.08
e = 0
factor(screen_nb)
13
14

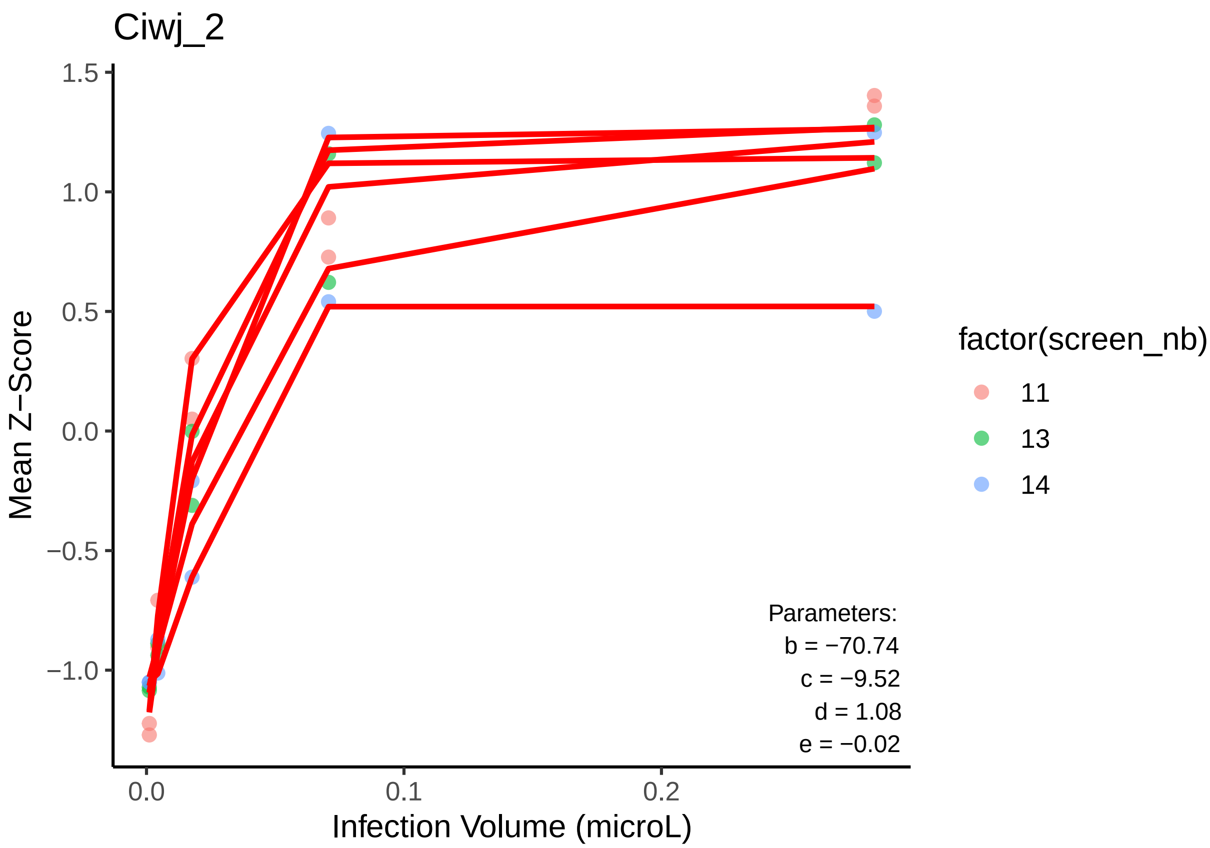

```
##
## $Cicb_2
```


Cicb_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
5
6
7
Parameters:
b = −67.91
c = −9.8
d = 1.22
e = −0.02

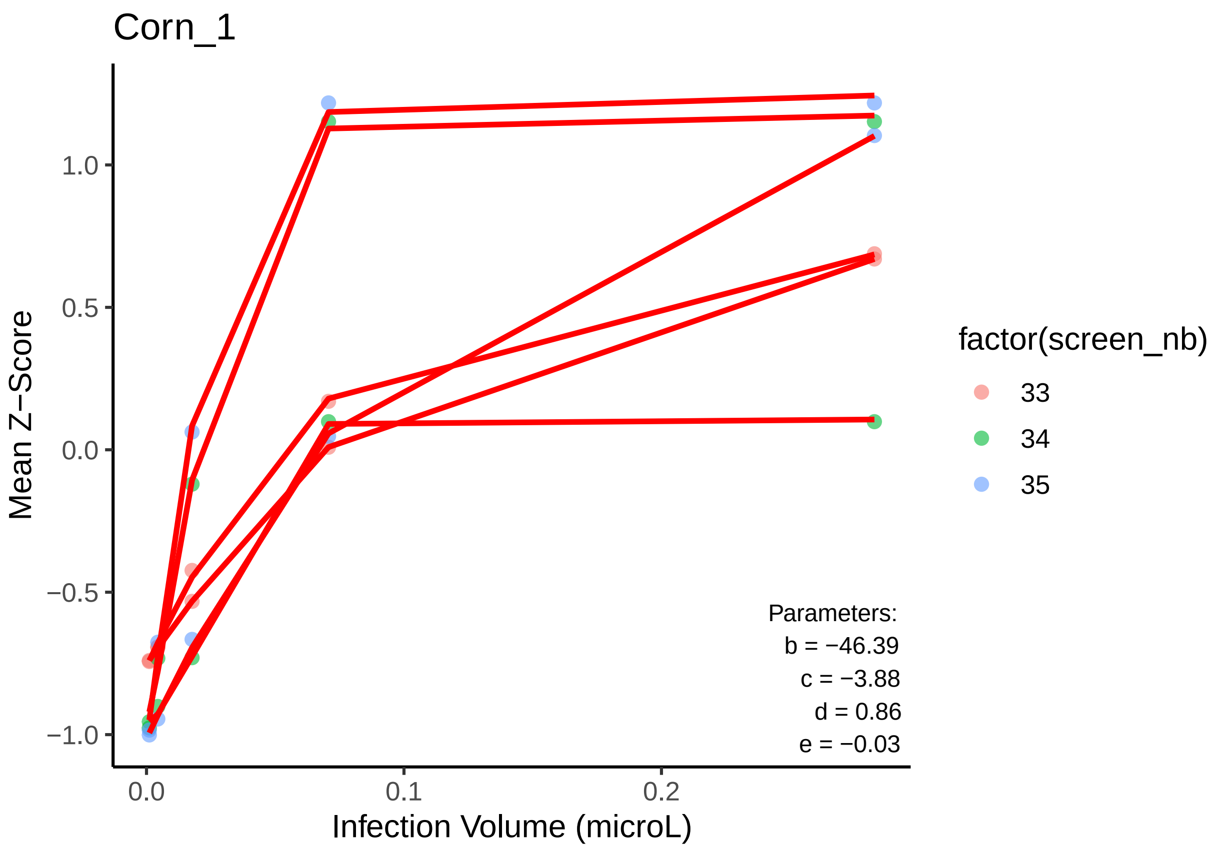
```
##
## $Civh_3
```


Civh_3
1.5
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
Parameters:
b = −53.44
c = −8.44
d = 1.29
e = −0.02
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
13
14

```
##
## $Ciwj_2
```

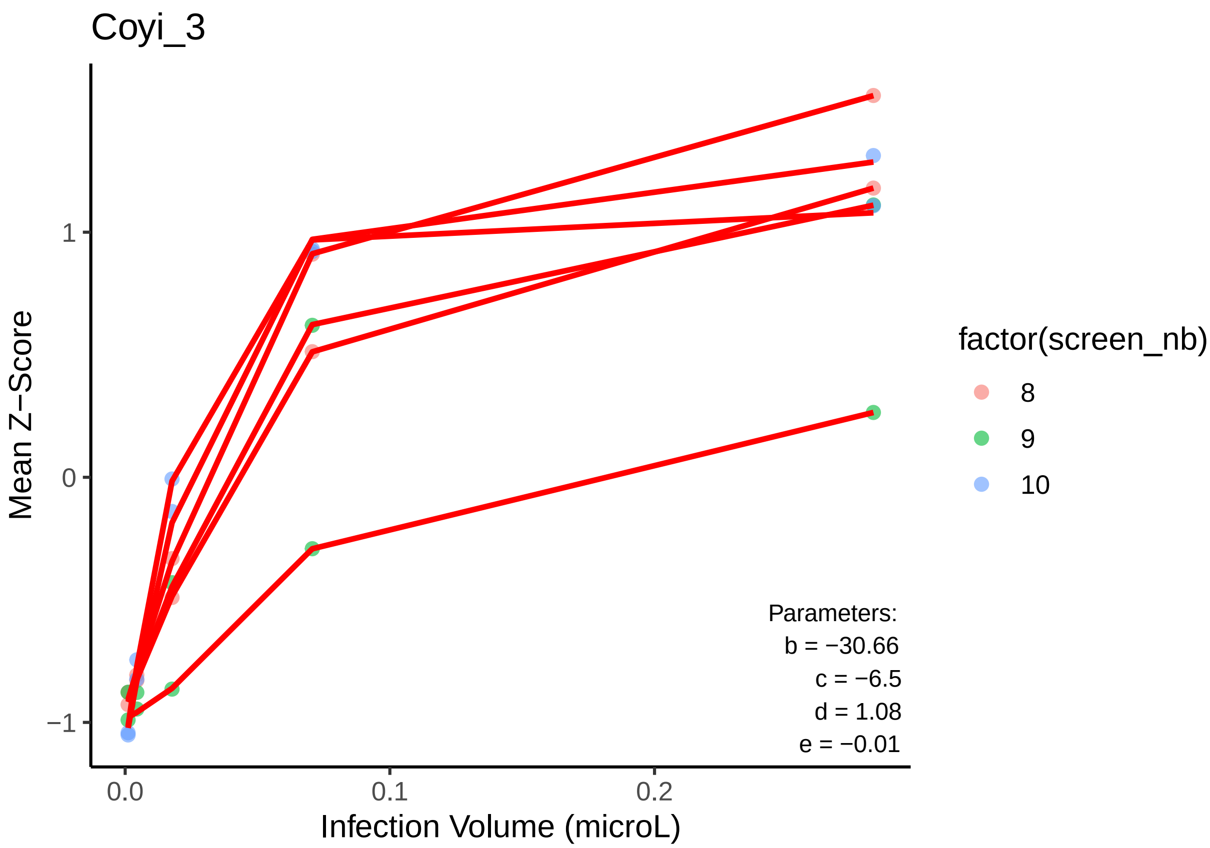

Ciwj_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −70.74
c = −9.52
d = 1.08
e = −0.02
factor(screen_nb)
11
13
14

```
##
## $Corn_1
```

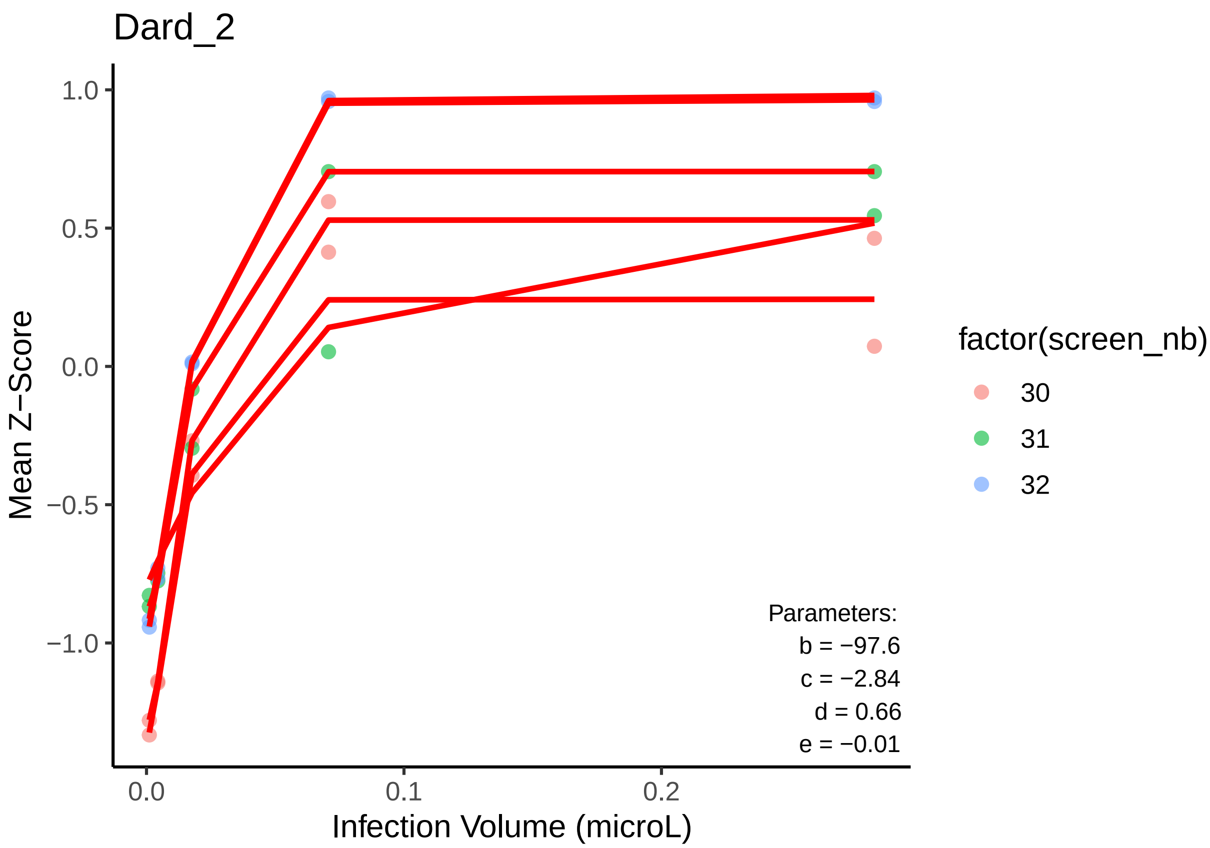


Corn_1
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
33
34
35
Parameters:
b = −46.39
c = −3.88
d = 0.86
e = −0.03


```
##
## $Coyi_3
```

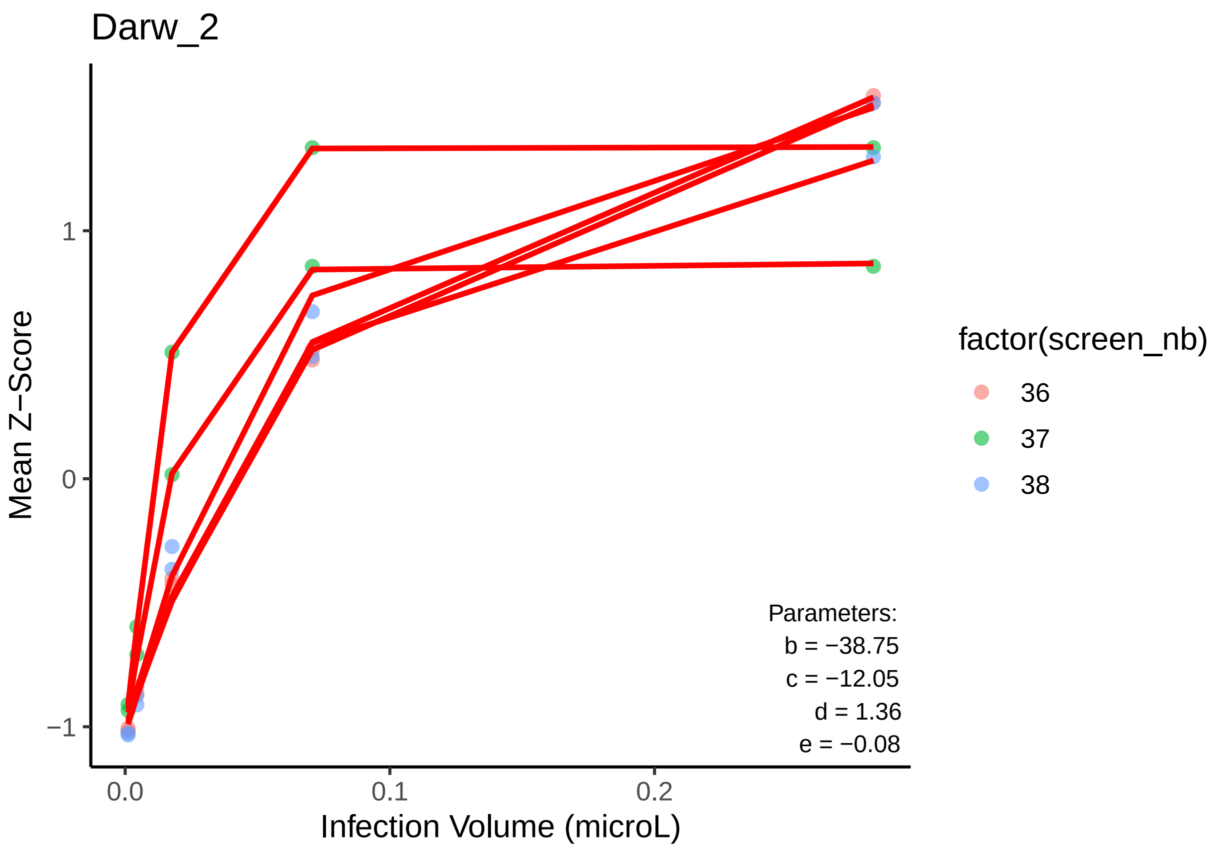

Coyi_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
8
9
10
Parameters:
b = −30.66
c = −6.5
d = 1.08
e = −0.01

```
##
## $Dard_2
```

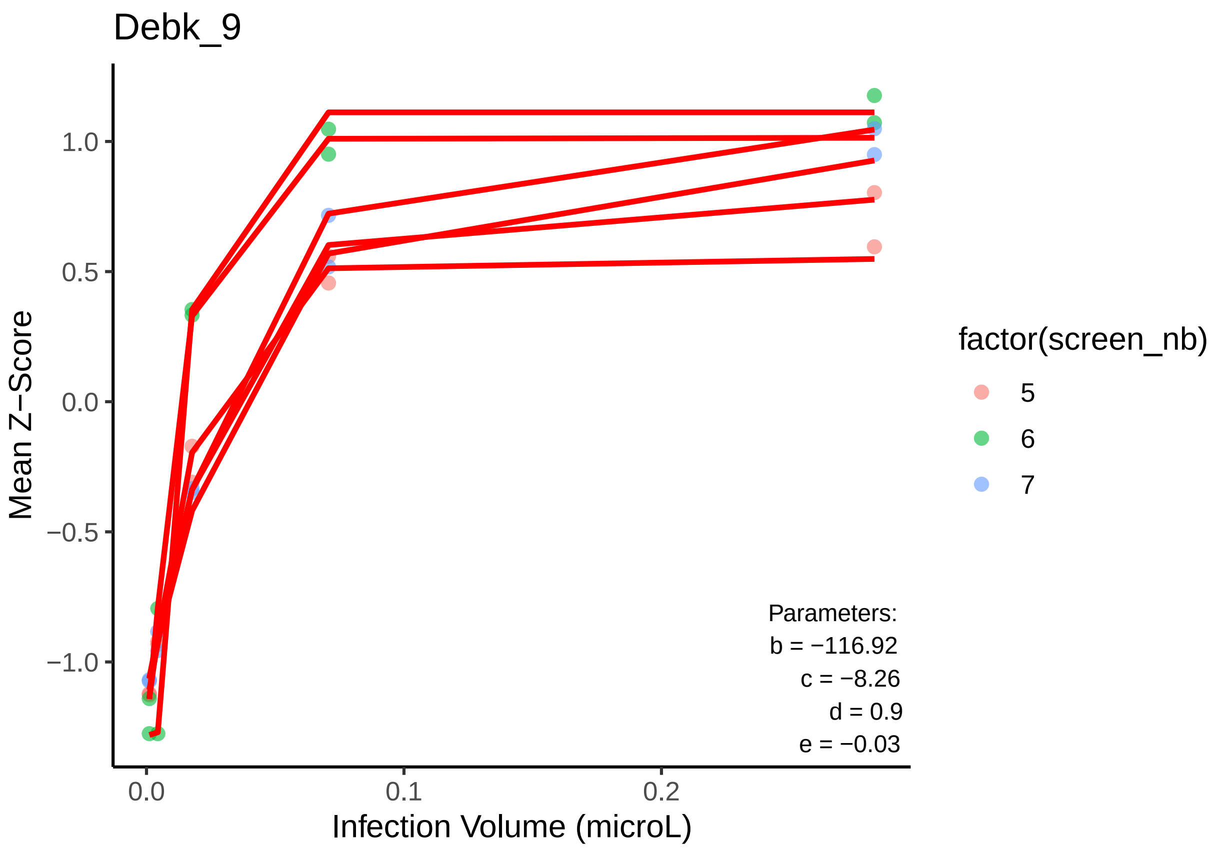


Dard_2
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −97.6
c = −2.84
d = 0.66
e = −0.01
factor(screen_nb)
30
31
32


```
##
## $Darw_2
```

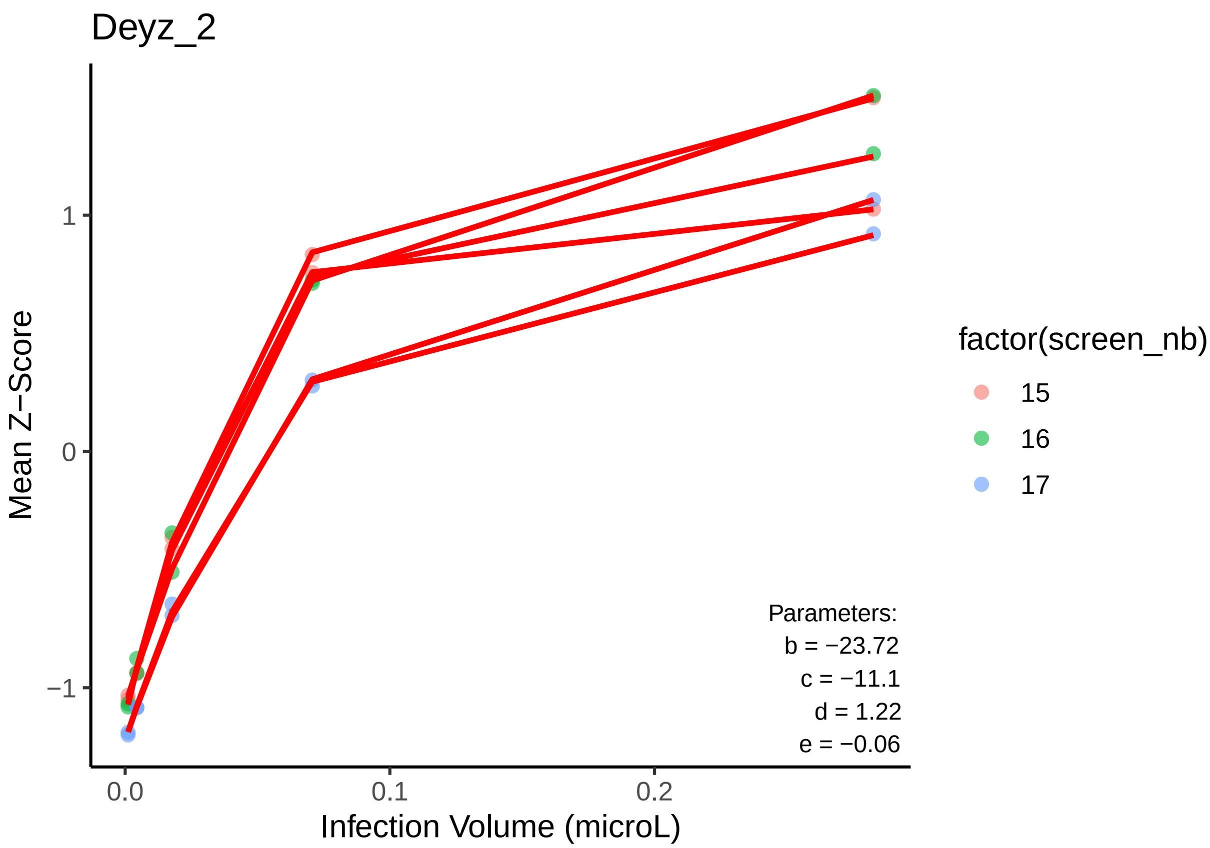

Darw_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −38.75
c = −12.05
d = 1.36
e = −0.08
factor(screen_nb)
36
37
38

```
##
## $Debk_9
```

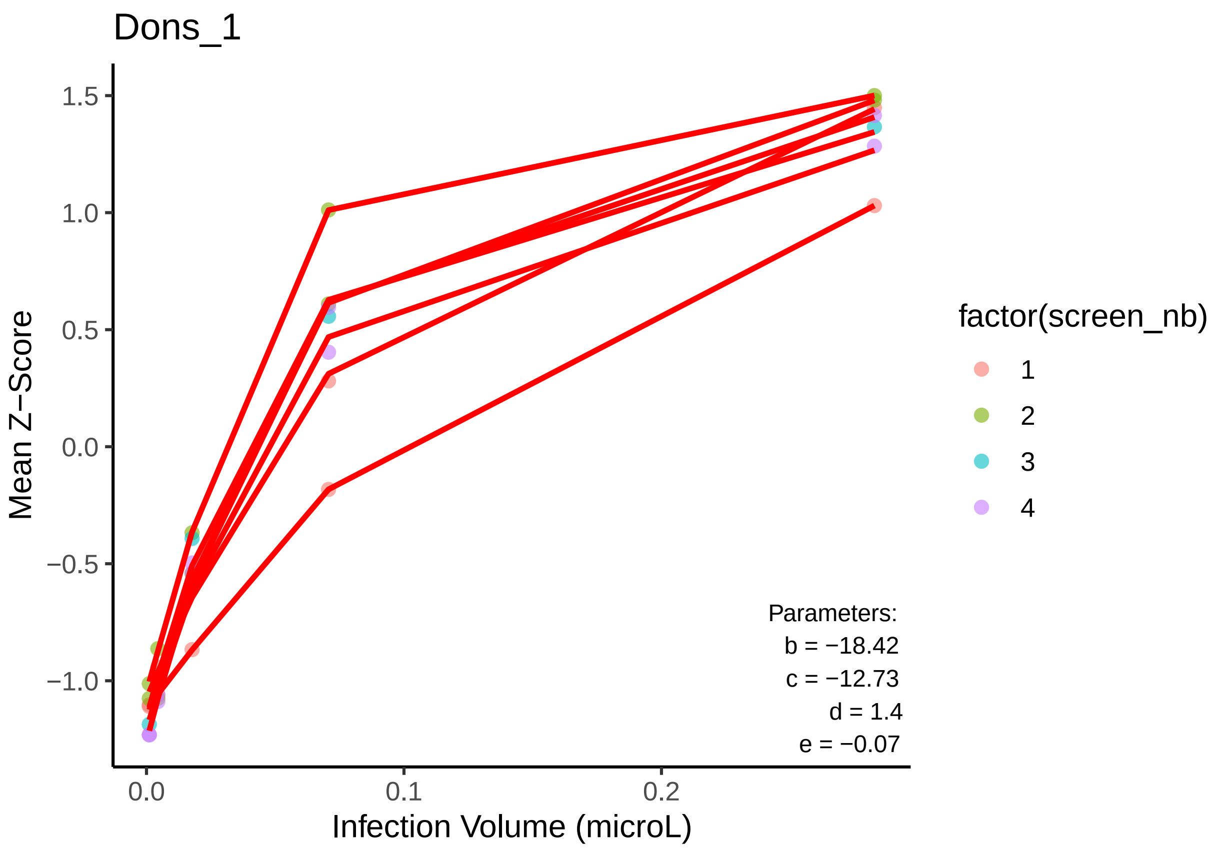


Debk_9
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −116.92
c = −8.26
d = 0.9
e = −0.03
factor(screen_nb)
5
6
7

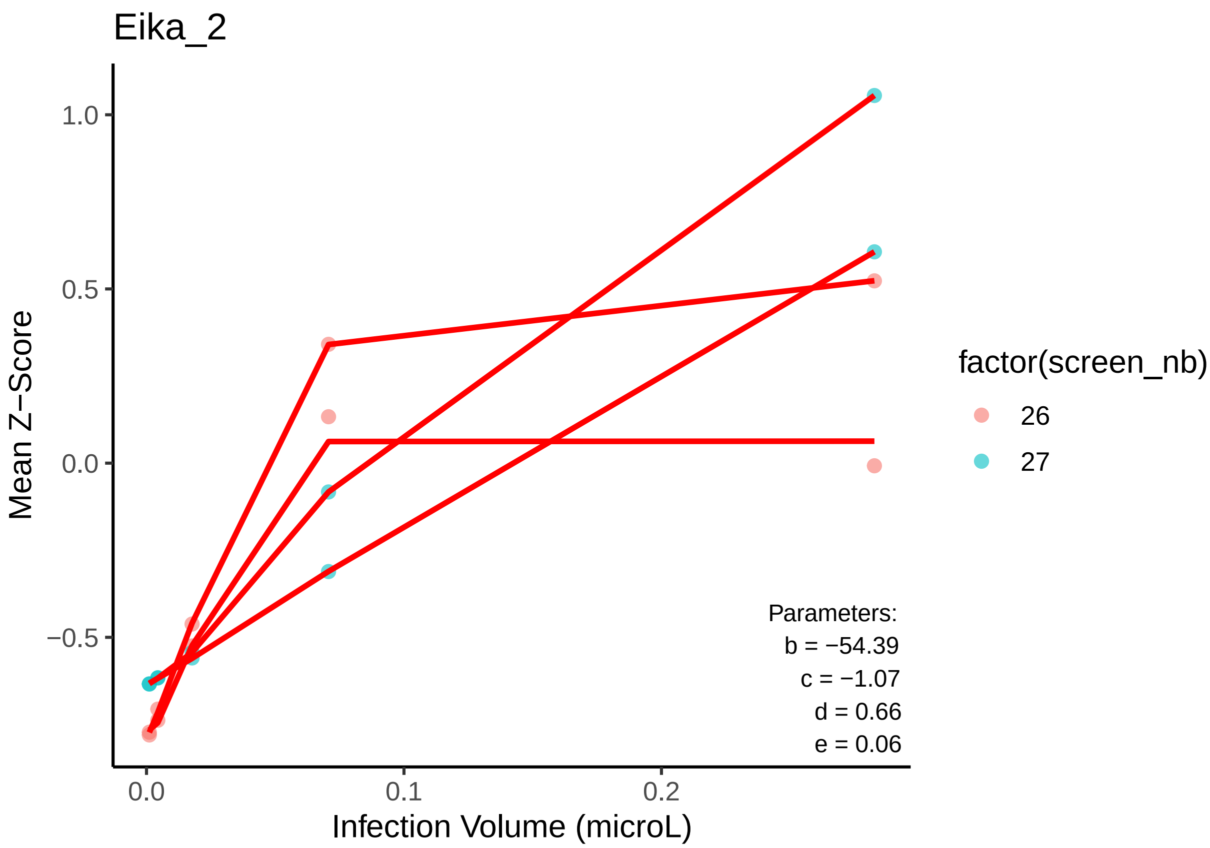

```
##
## $Deyz_2
```


Deyz_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −23.72
c = −11.1
d = 1.22
e = −0.06
factor(screen_nb)
15
16
17

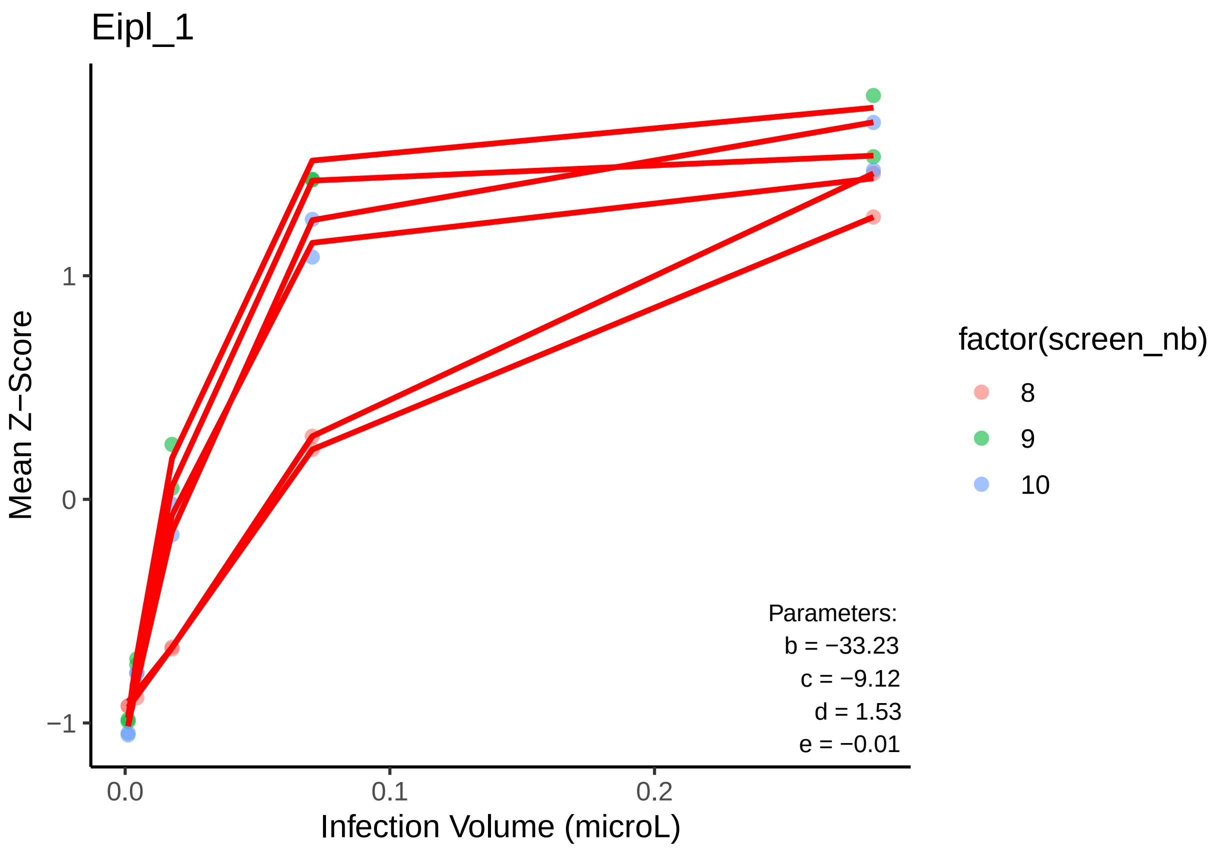
```
##
## $Dons_1
```


Dons_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −18.42
c = −12.73
d = 1.4
e = −0.07
factor(screen_nb)
1
2
3
4

```
##
## $Eika_2
```

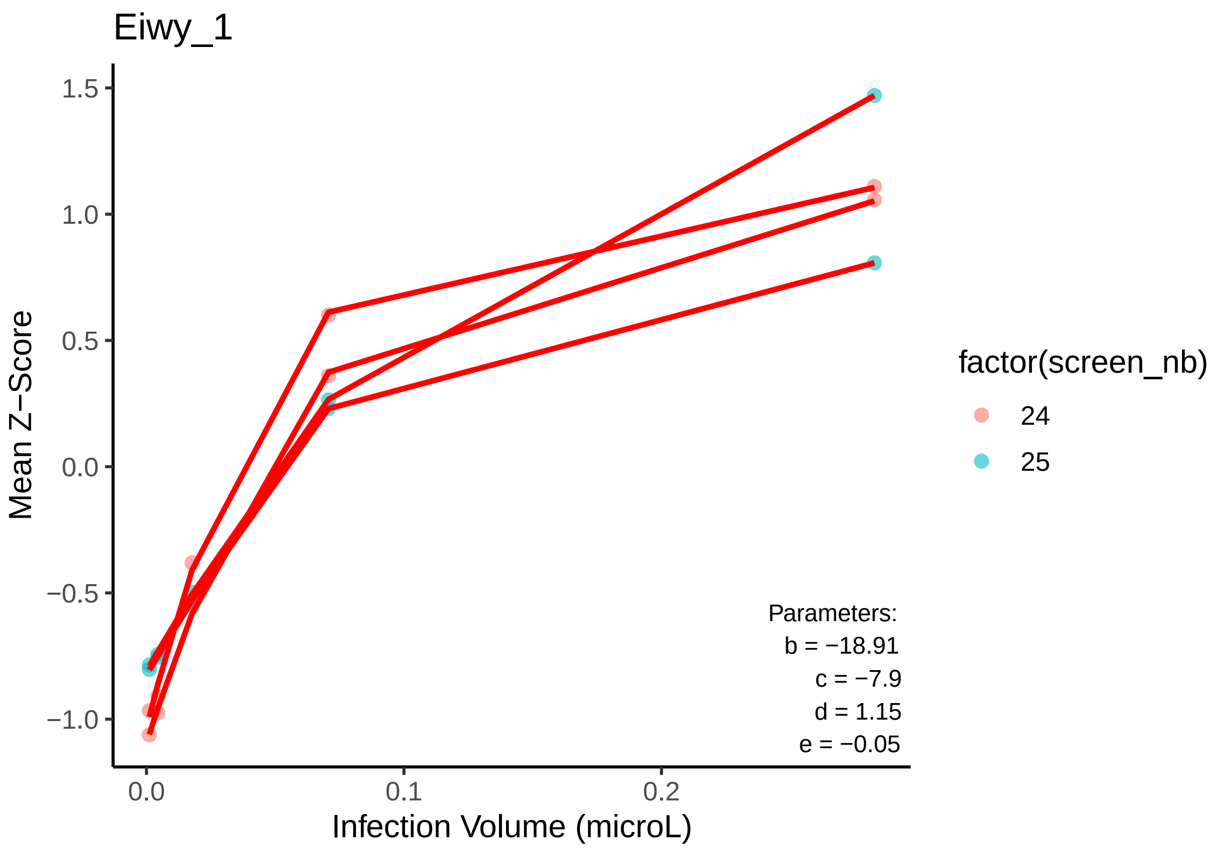

Eika_2
Mean Z−Score
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
26
27
Parameters:
b = −54.39
c = −1.07
d = 0.66
e = 0.06

```
##
## $Eipl_1
```

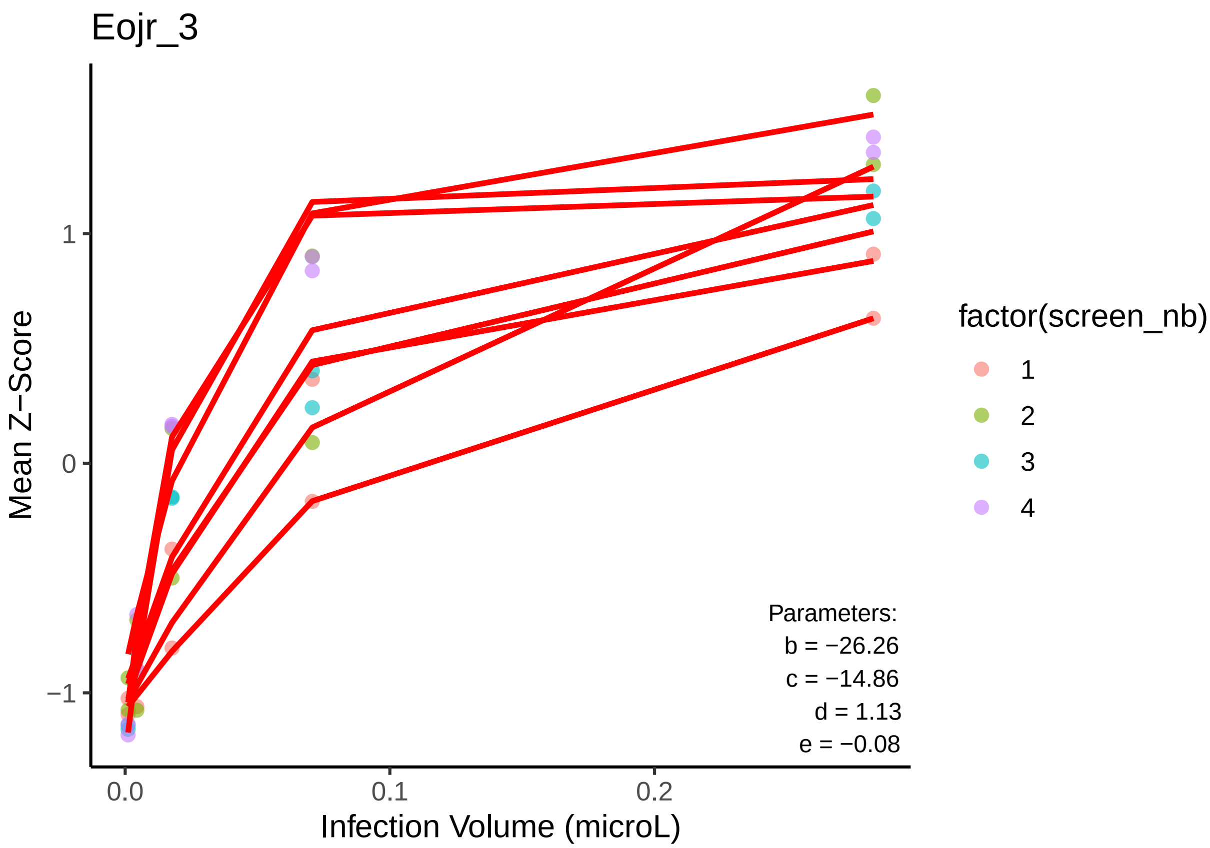


Eipl_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
8
9
10
Parameters:
b = −33.23
c = −9.12
d = 1.53
e = −0.01


```
##
## $Eiwy_1
```

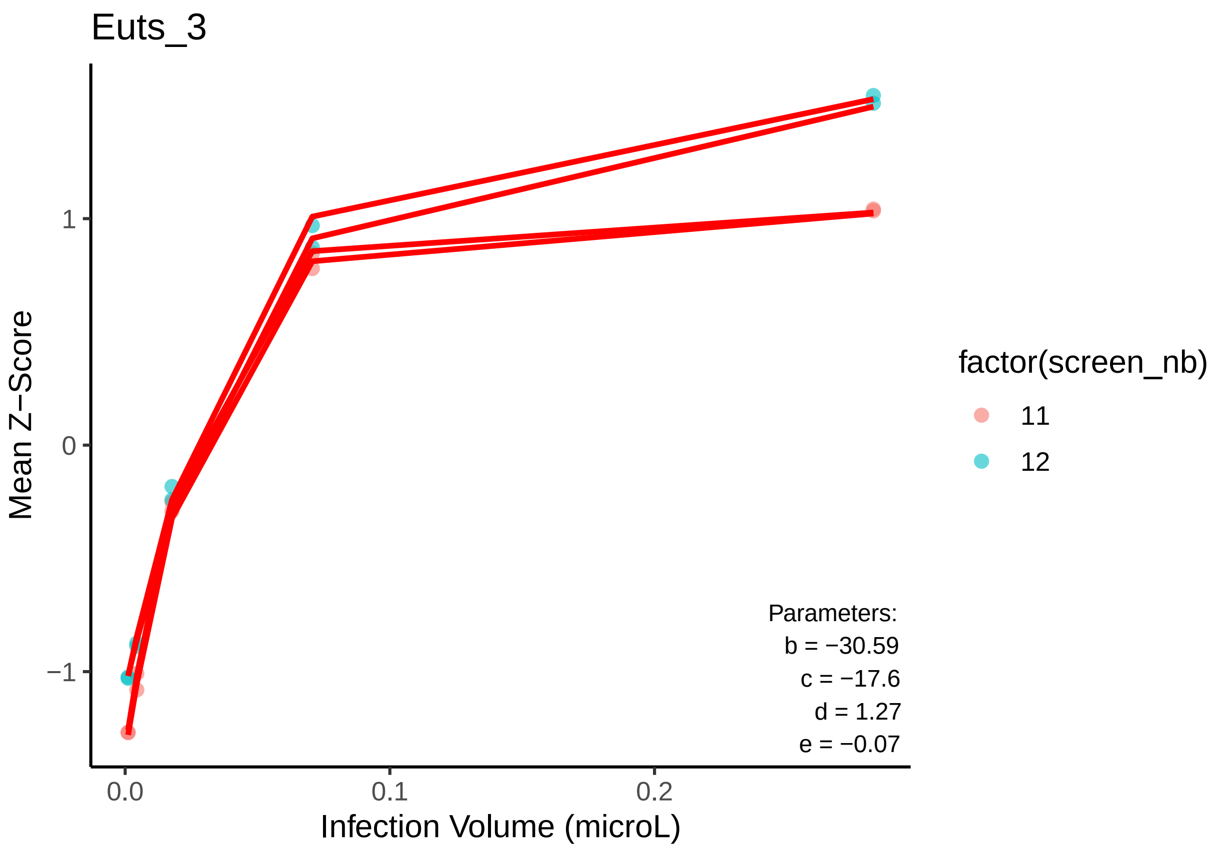

Eiwy_1
1.5
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −18.91
c = −7.9
d = 1.15
e = −0.05
factor(screen_nb)
24
25

```
##
## $Eojr_3
```

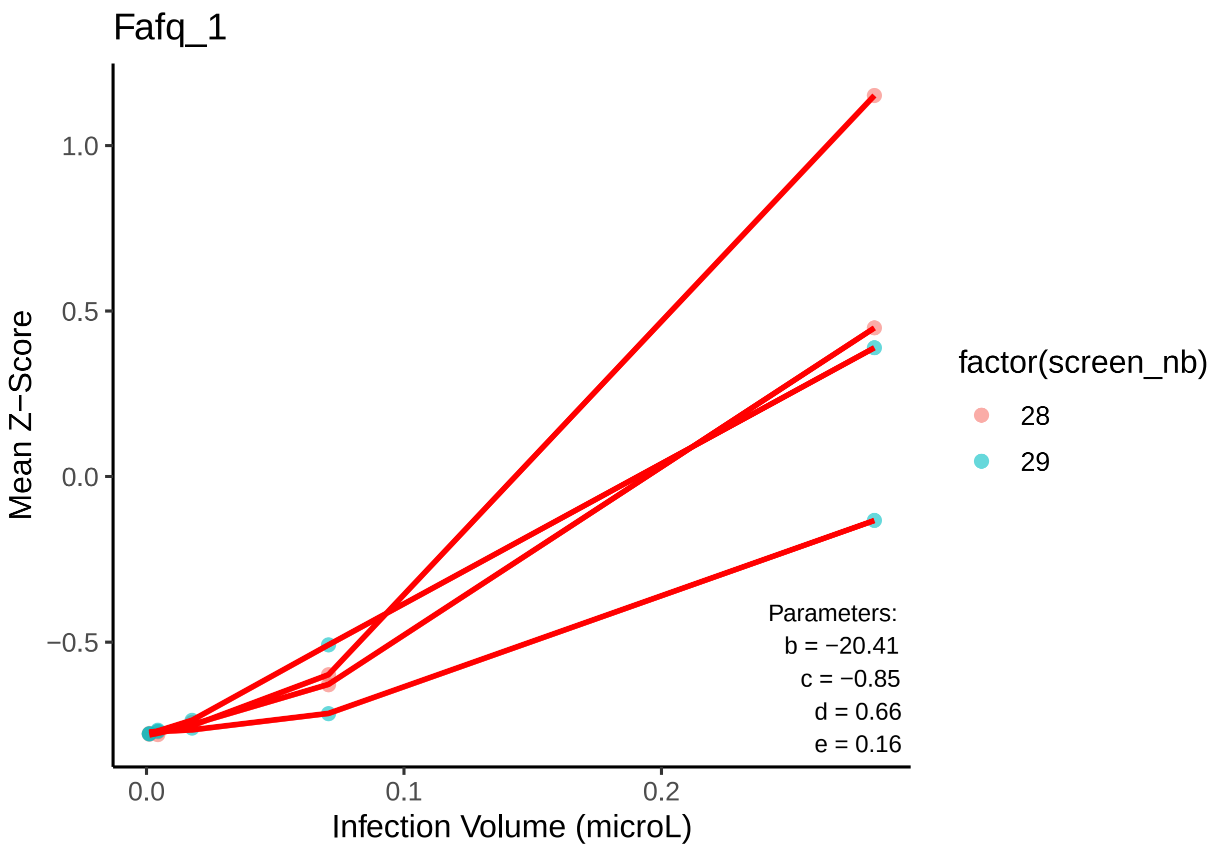


Eojr_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
1
2
3
4
Parameters:
b = −26.26
c = −14.86
d = 1.13
e = −0.08

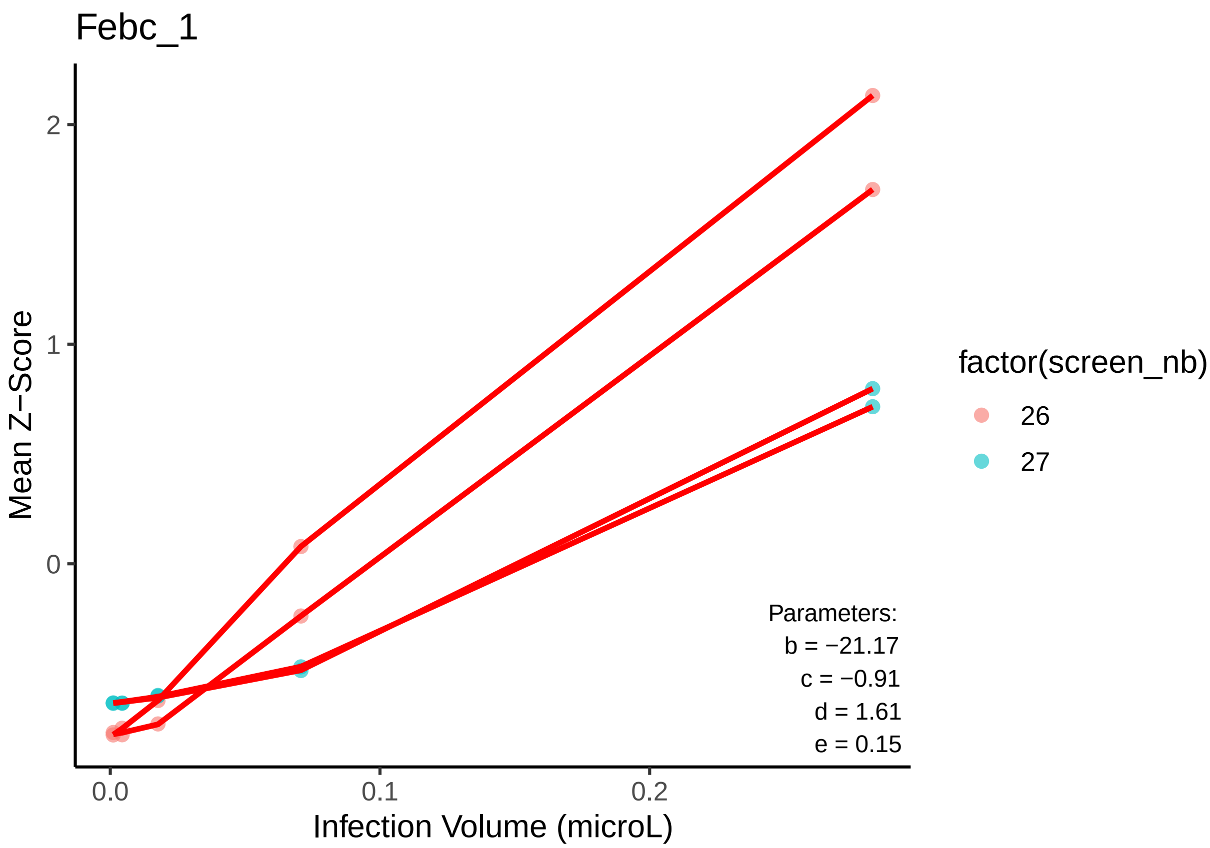

```
##
## $Euts_3
```


Euts_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −30.59
c = −17.6
d = 1.27
e = −0.07
factor(screen_nb)
11
12

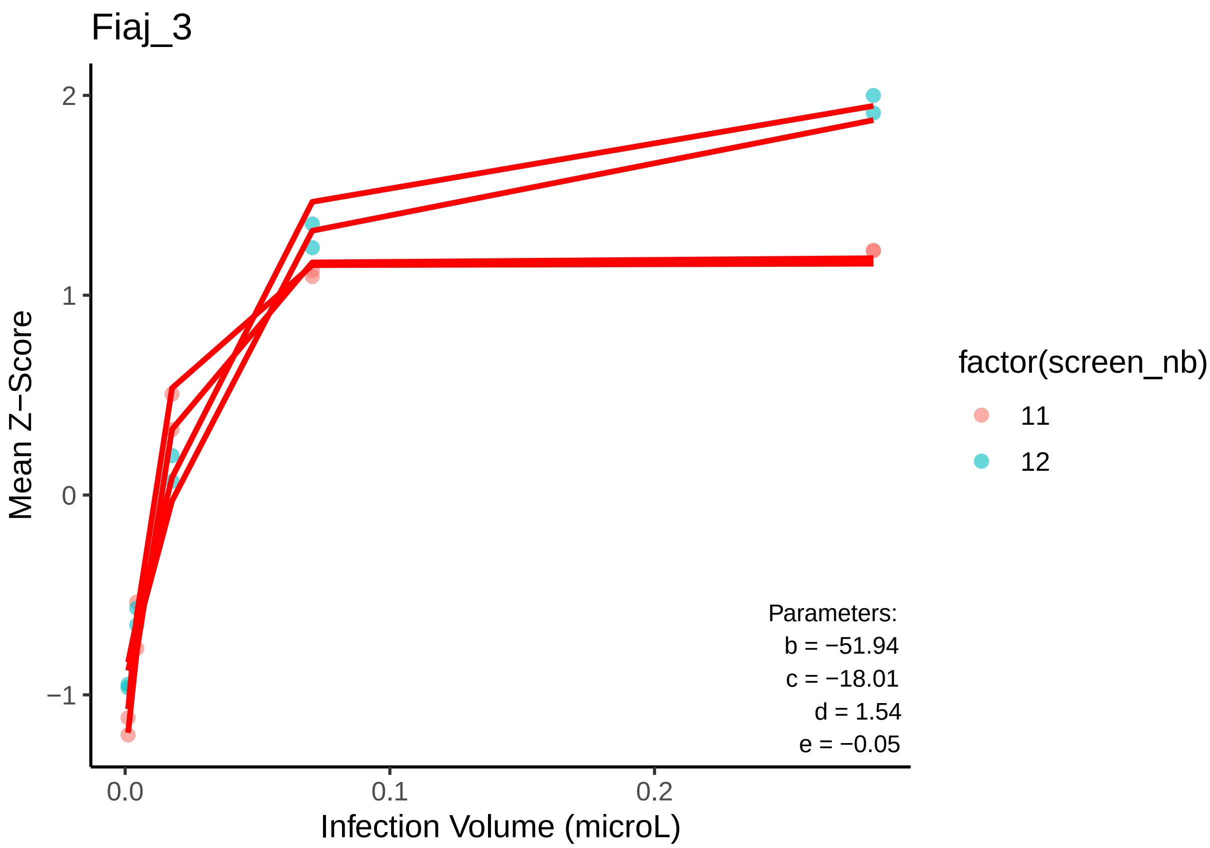
```
##
## $Fafq_1
```


Fafq_1
Mean Z−Score
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −20.41
c = −0.85
d = 0.66
e = 0.16
factor(screen_nb)
28
29

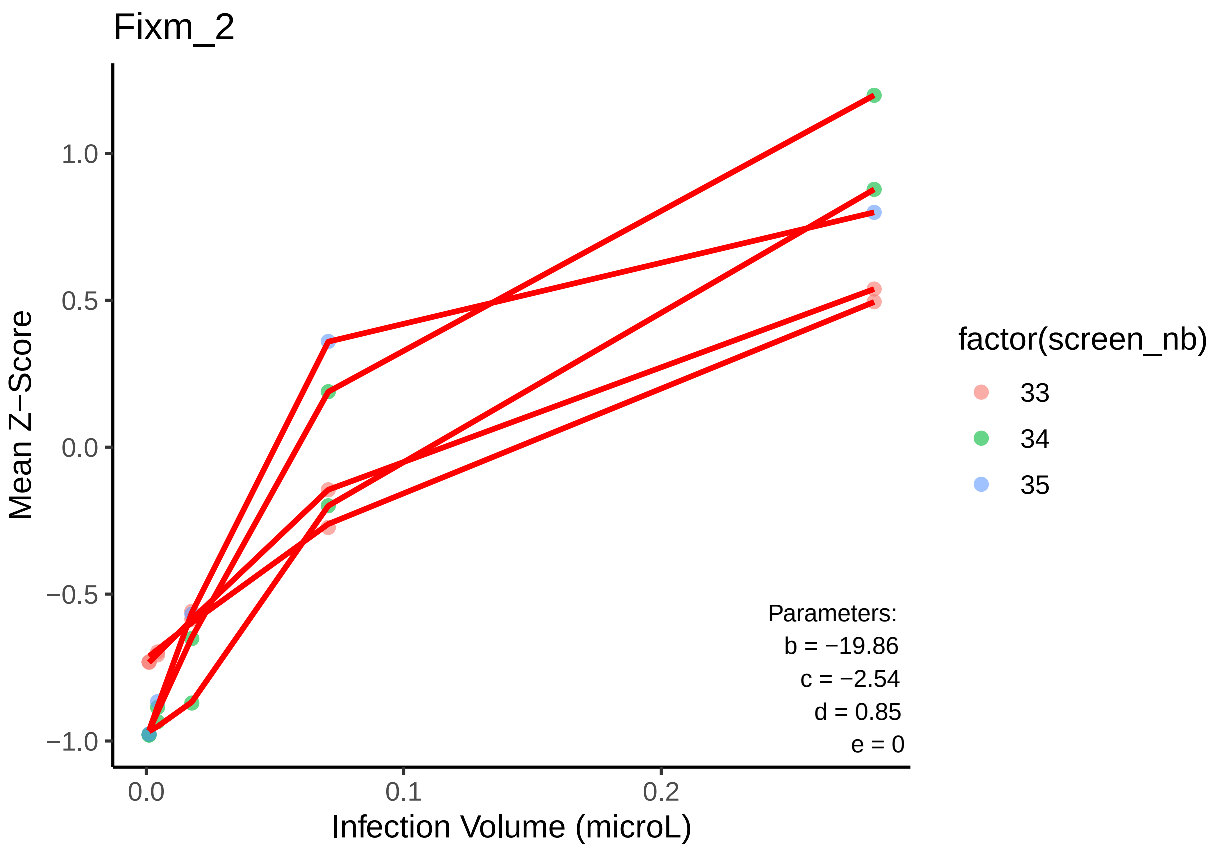
```
##
## $Febc_1
```


Febc_1
Mean Z−Score
Infection Volume (microL)
factor(screen_nb)
26
27
Parameters:
b = −21.17
c = −0.91
d = 1.61
e = 0.15
0.0
0.1
0.2
0
1
2

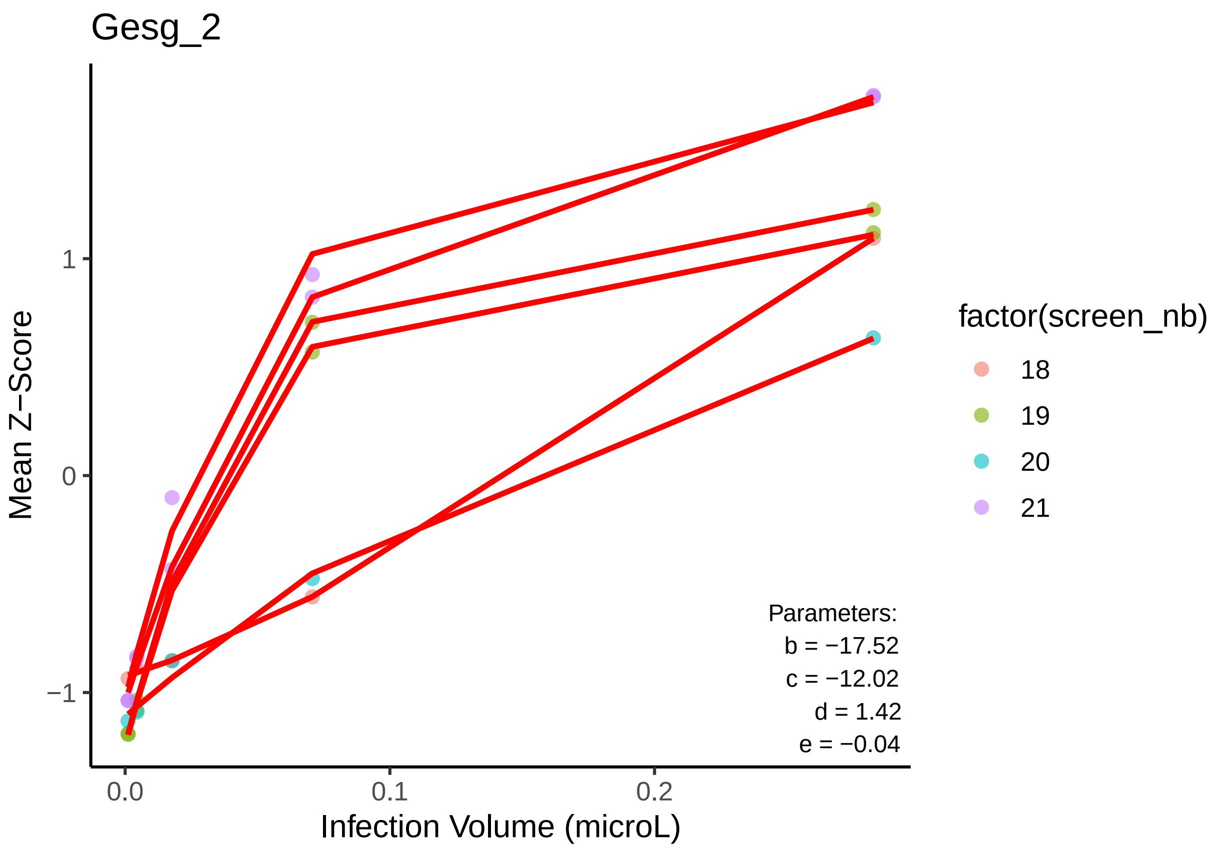
```
##
## $Fiaj_3
```


Fiaj_3
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −51.94
c = −18.01
d = 1.54
e = −0.05
factor(screen_nb)
11
12

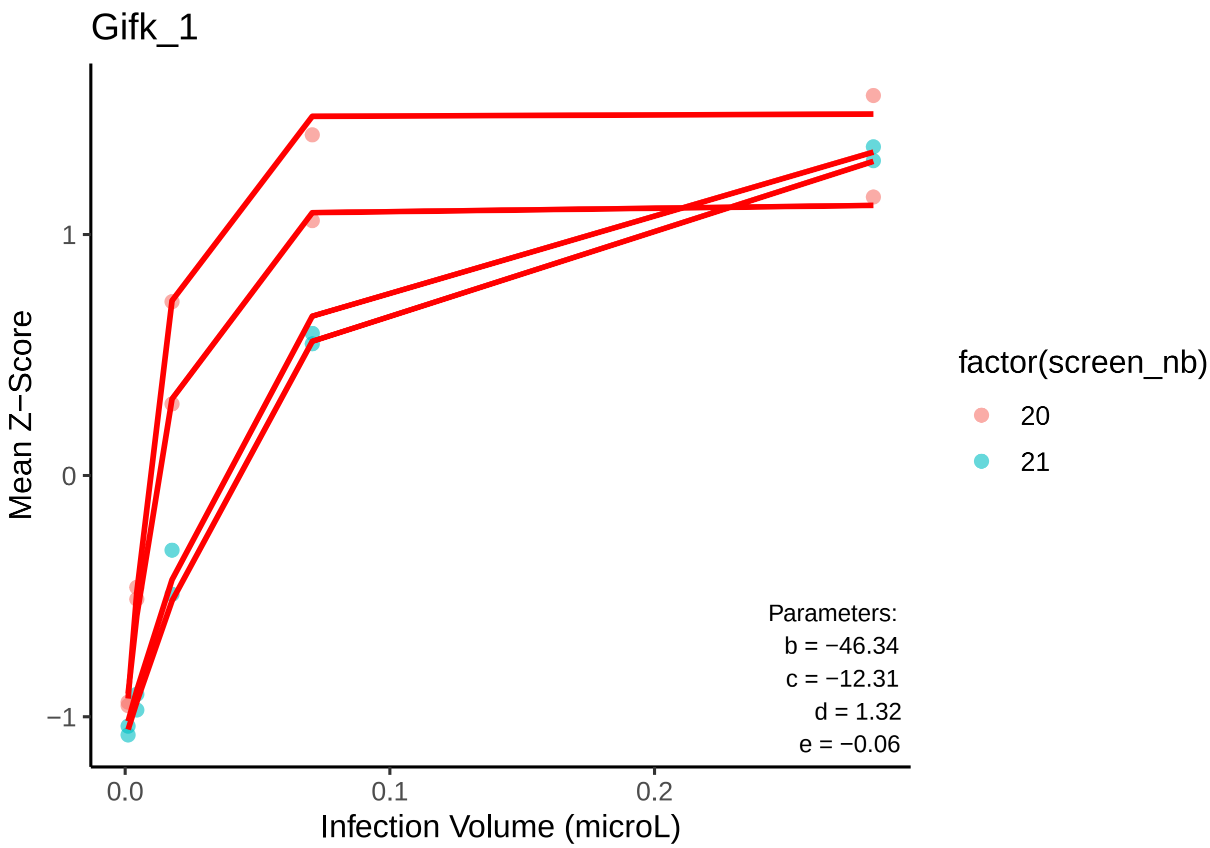
```
##
## $Fixm_2
```


Fixm_2
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
33
34
35
Parameters:
b = −19.86
c = −2.54
d = 0.85
e = 0

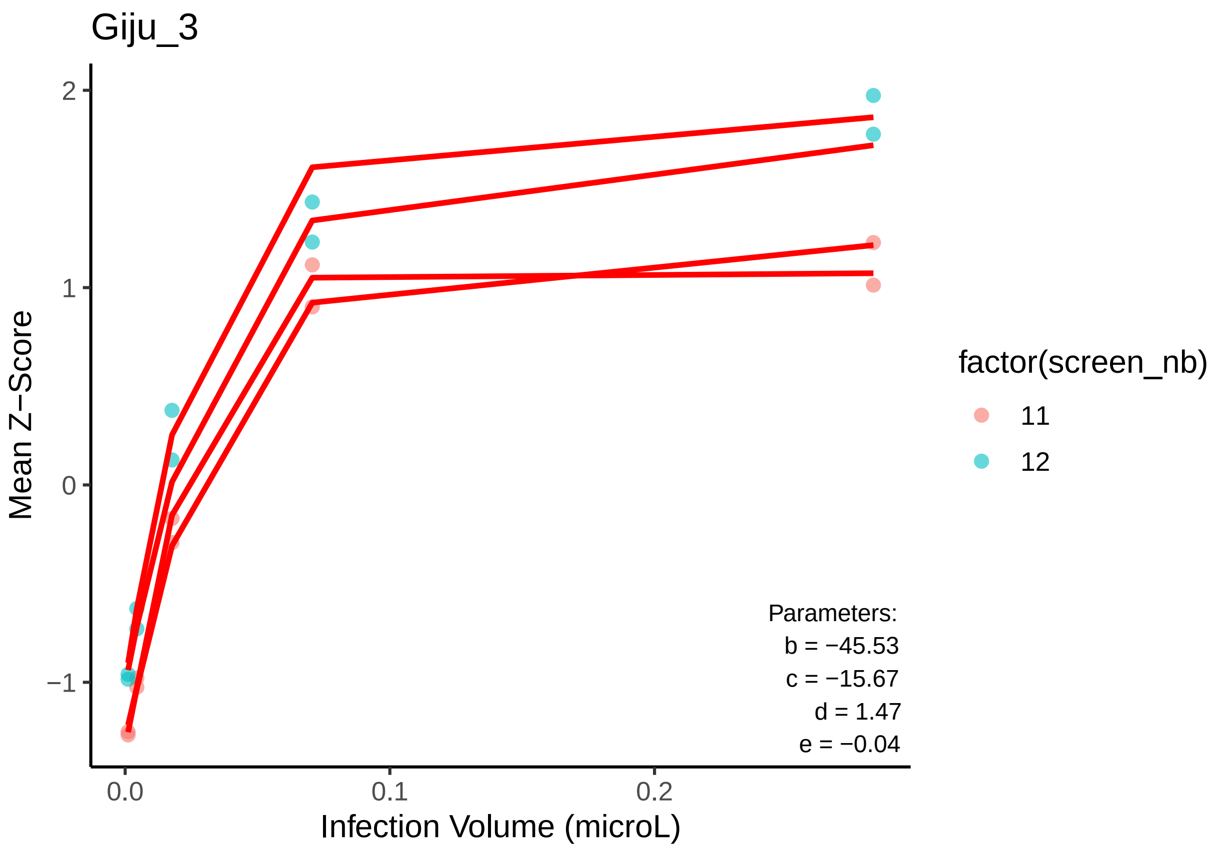
```
##
## $Gesg_2
```


Gesg_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
18
19
20
21
Parameters:
b = −17.52
c = −12.02
d = 1.42
e = −0.04

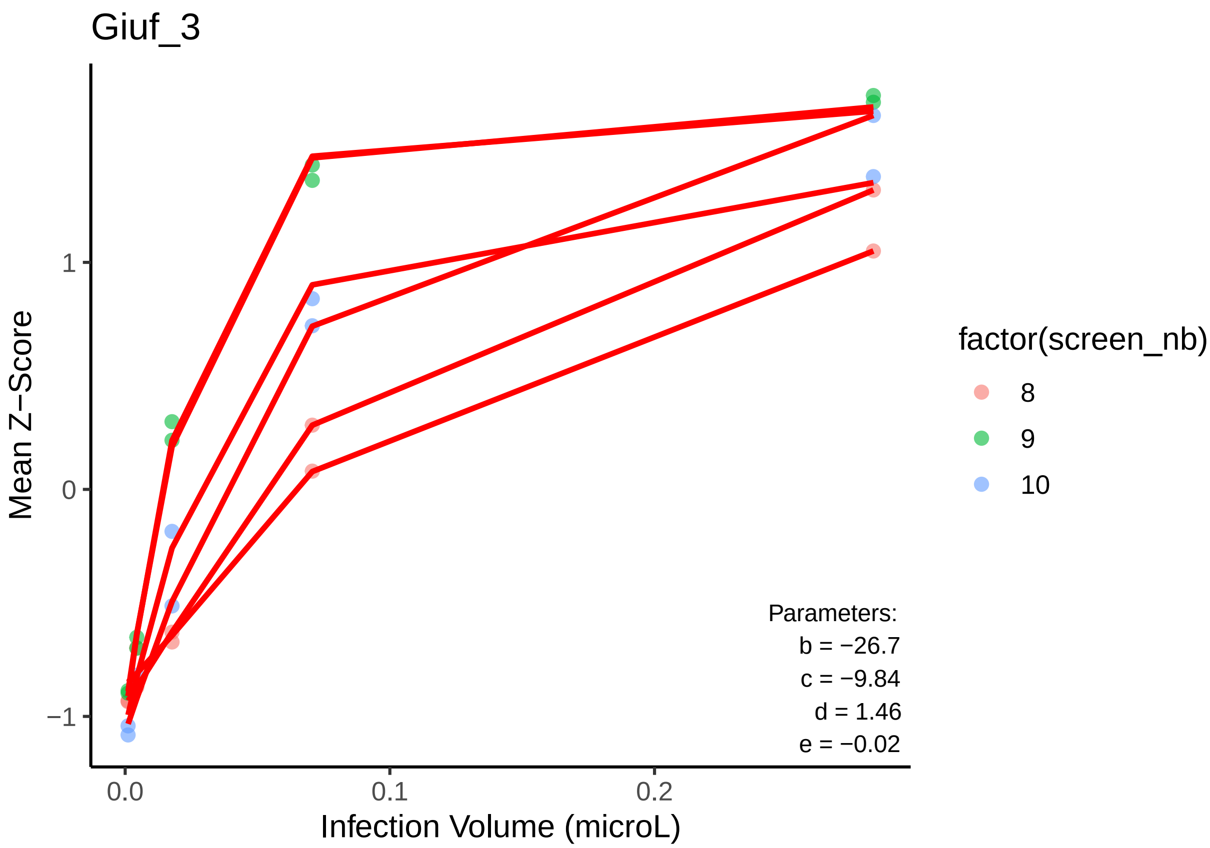
```
##
## $Gifk_1
```


Gifk_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
20
21
Parameters:
b = −46.34
c = −12.31
d = 1.32
e = −0.06

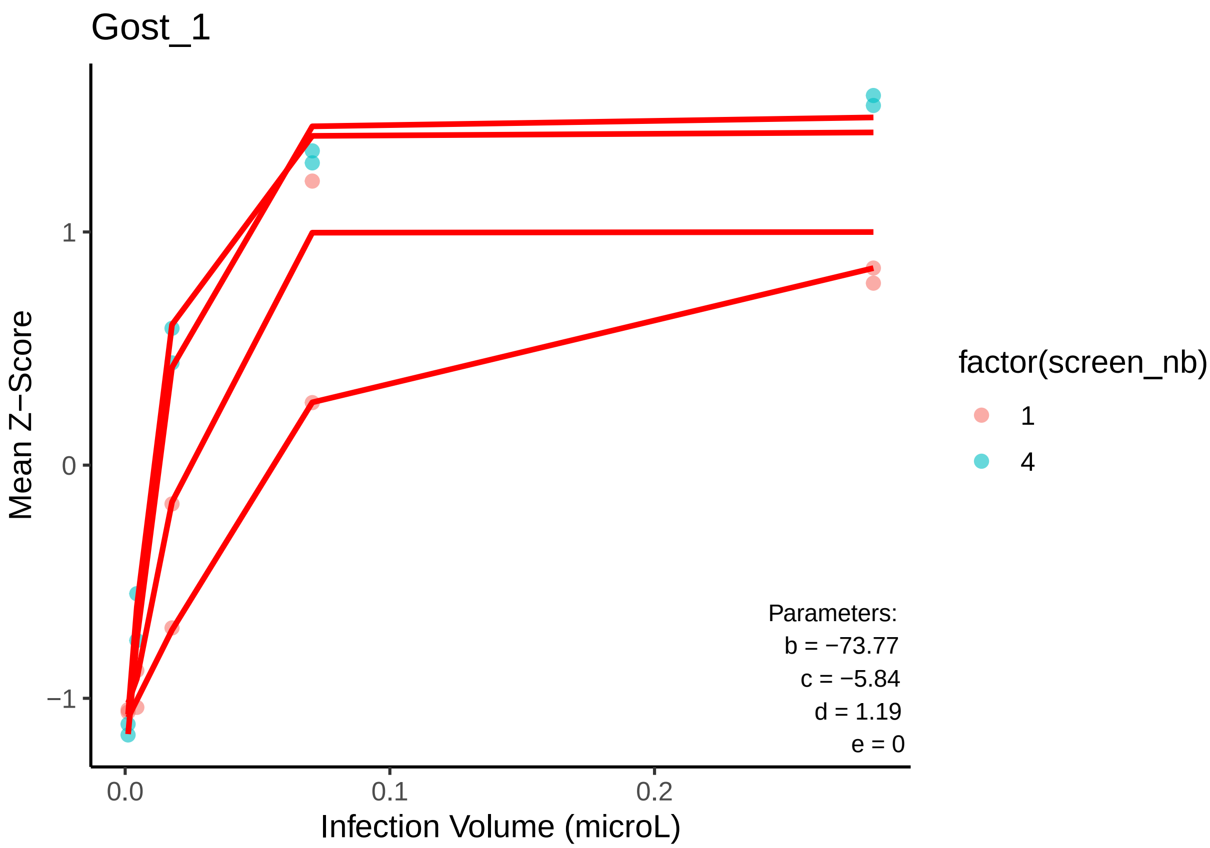
```
##
## $Giju_3
```


Giju_3
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
11
12
Parameters:
b = −45.53
c = −15.67
d = 1.47
e = −0.04

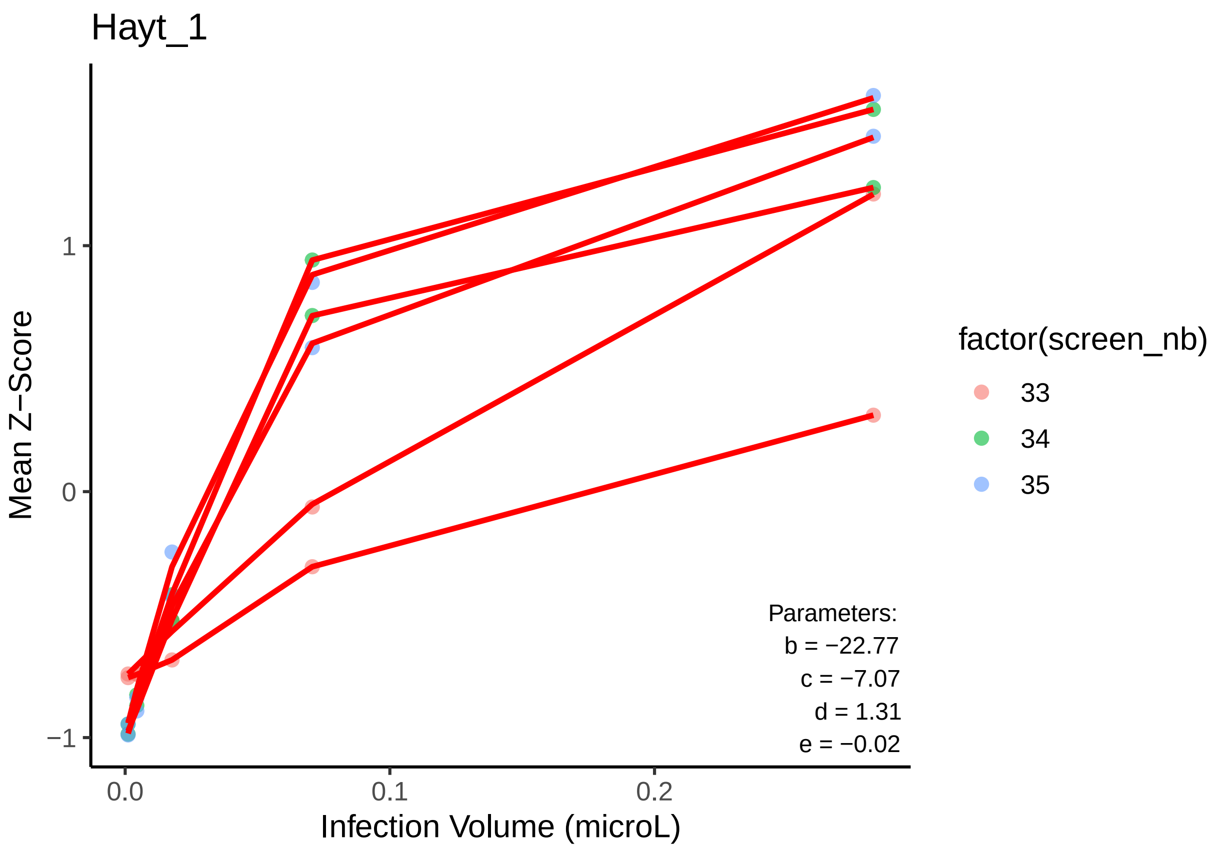
```
##
## $Giuf_3
```


Giuf_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −26.7
c = −9.84
d = 1.46
e = −0.02
factor(screen_nb)
8
9
10

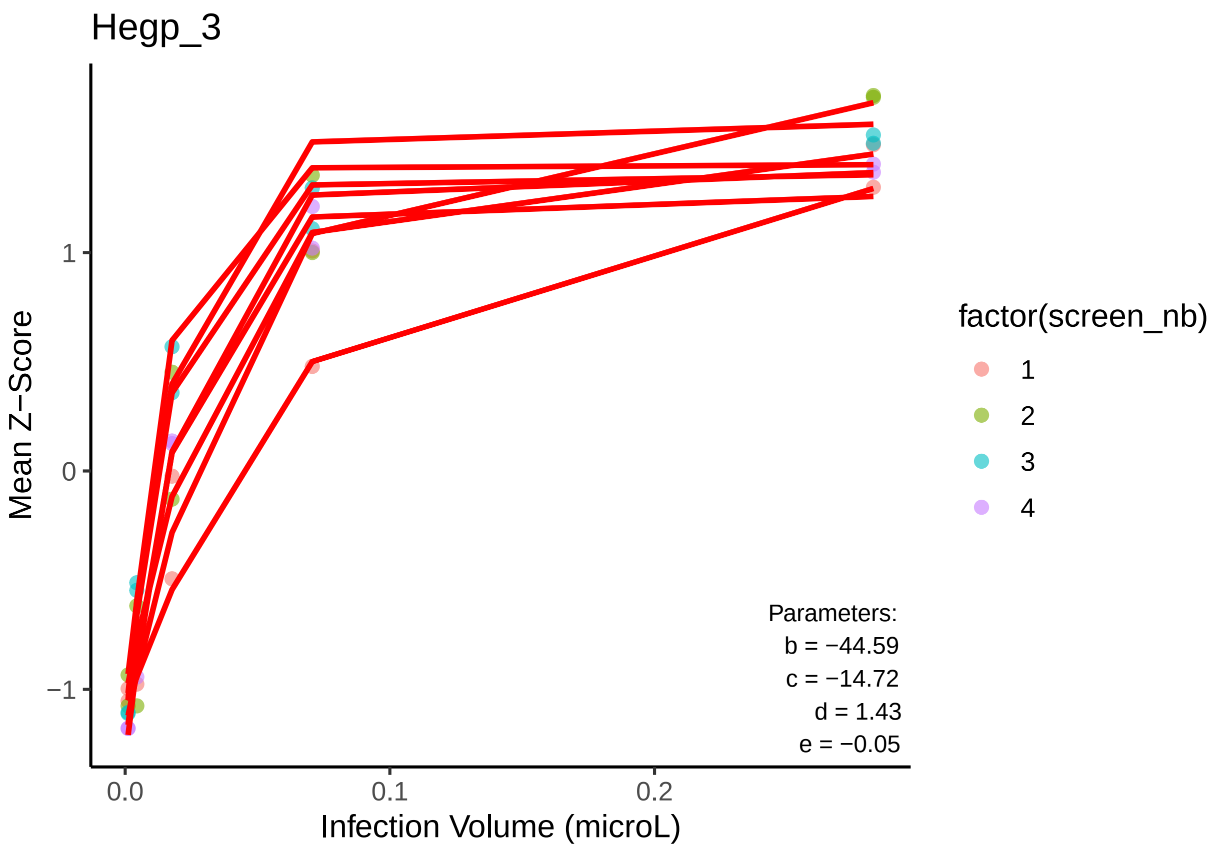
```
##
## $Gost_1
```


Gost_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −73.77
c = −5.84
d = 1.19
e = 0
factor(screen_nb)
1
4

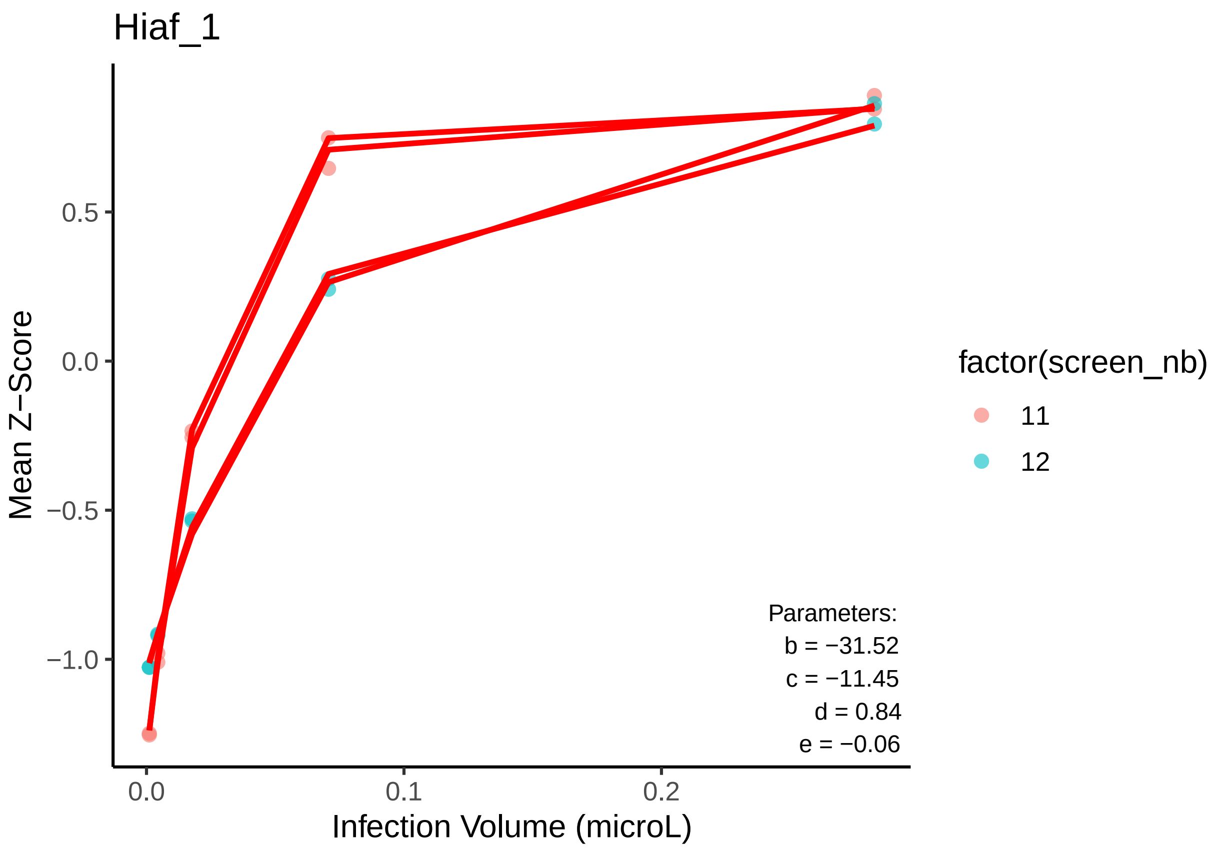
```
##
## $Hayt_1
```


Hayt_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
33
34
35
Parameters:
b = −22.77
c = −7.07
d = 1.31
e = −0.02

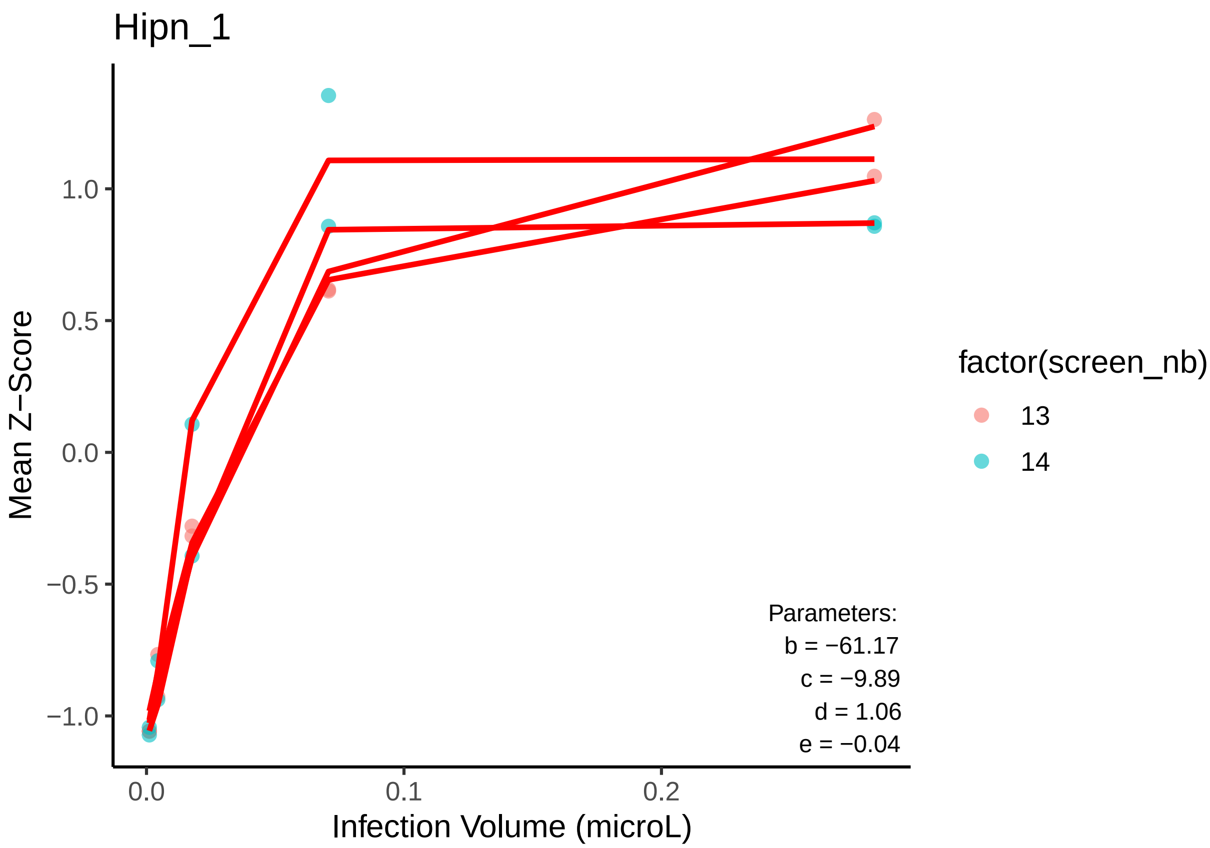
```
##
## $Hegp_3
```


Hegp_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
1
2
3
4
Parameters:
b = −44.59
c = −14.72
d = 1.43
e = −0.05

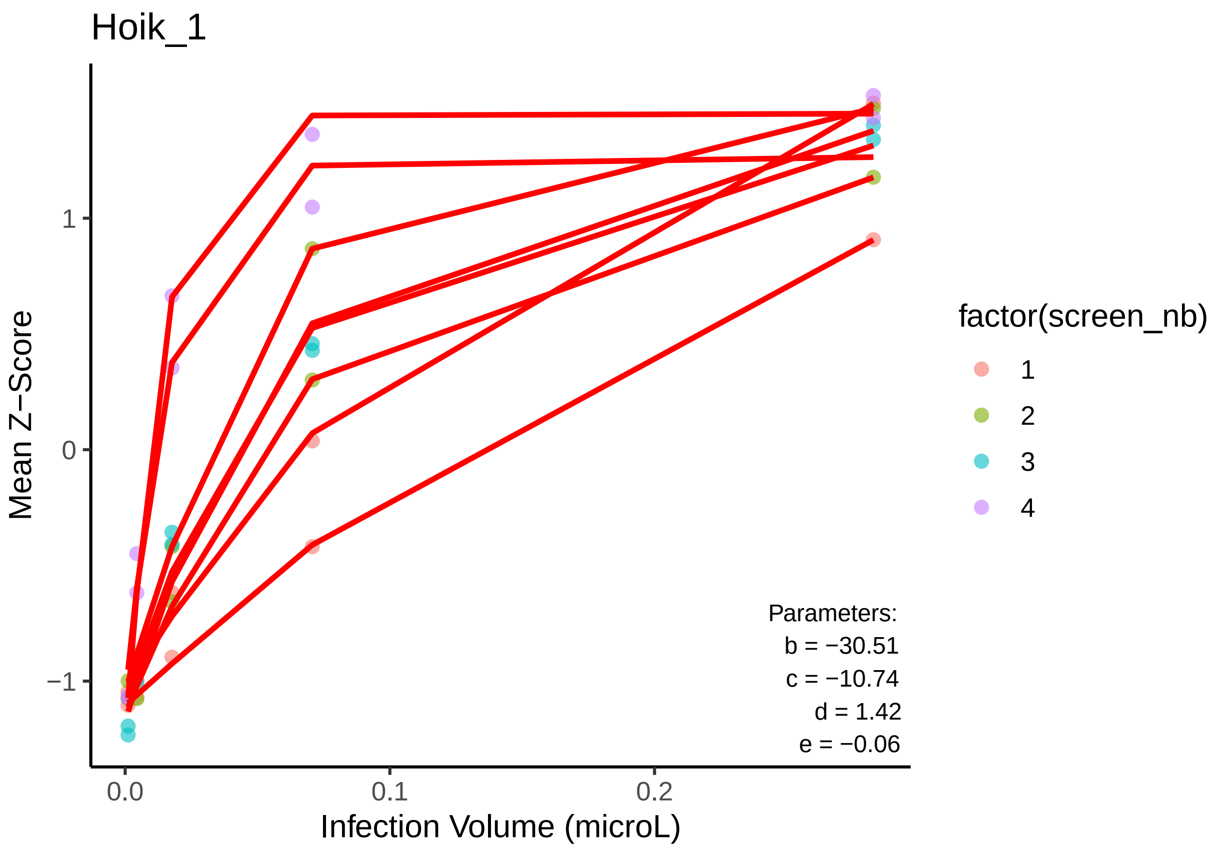
```
##
## $Hiaf_1
```


Hiaf_1
Mean Z−Score
0.5
0.0
−0.5
−1.0
Parameters:
b = −31.52
c = −11.45
d = 0.84
e = −0.06
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
11
12

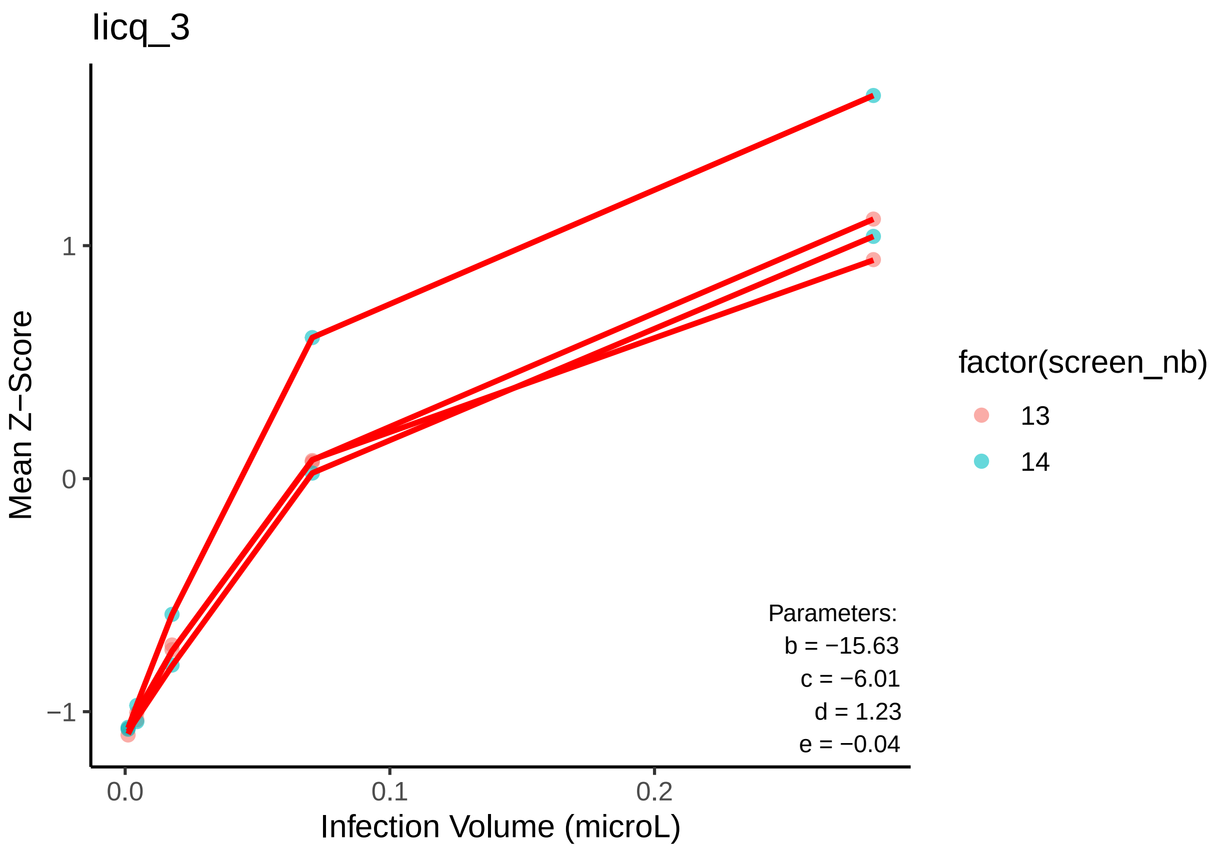
```
##
## $Hipn_1
```


Hipn_1
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −61.17
c = −9.89
d = 1.06
e = −0.04
factor(screen_nb)
13
14

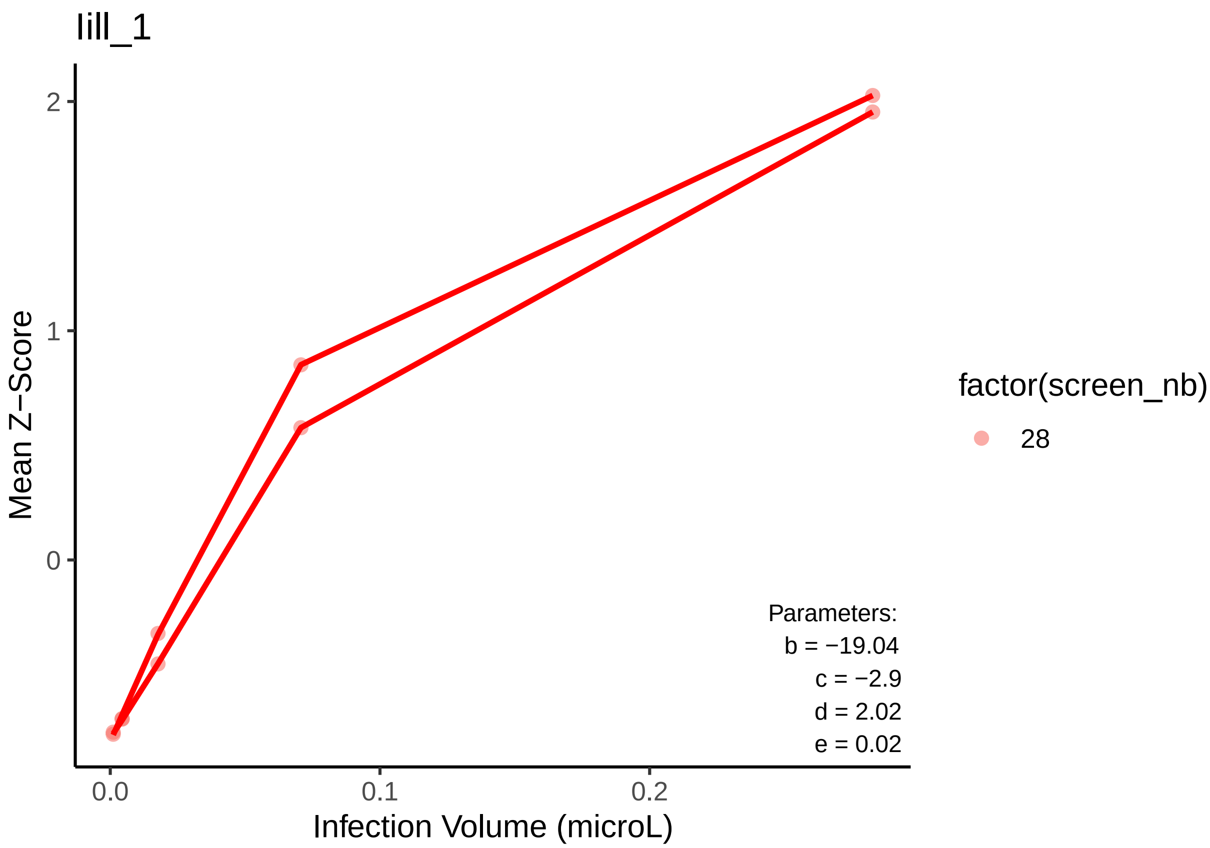
```
##
## $Hoik_1
```


Hoik_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
1
2
3
4
Parameters:
b = −30.51
c = −10.74
d = 1.42
e = −0.06

```
##
## $Iicq_3
```

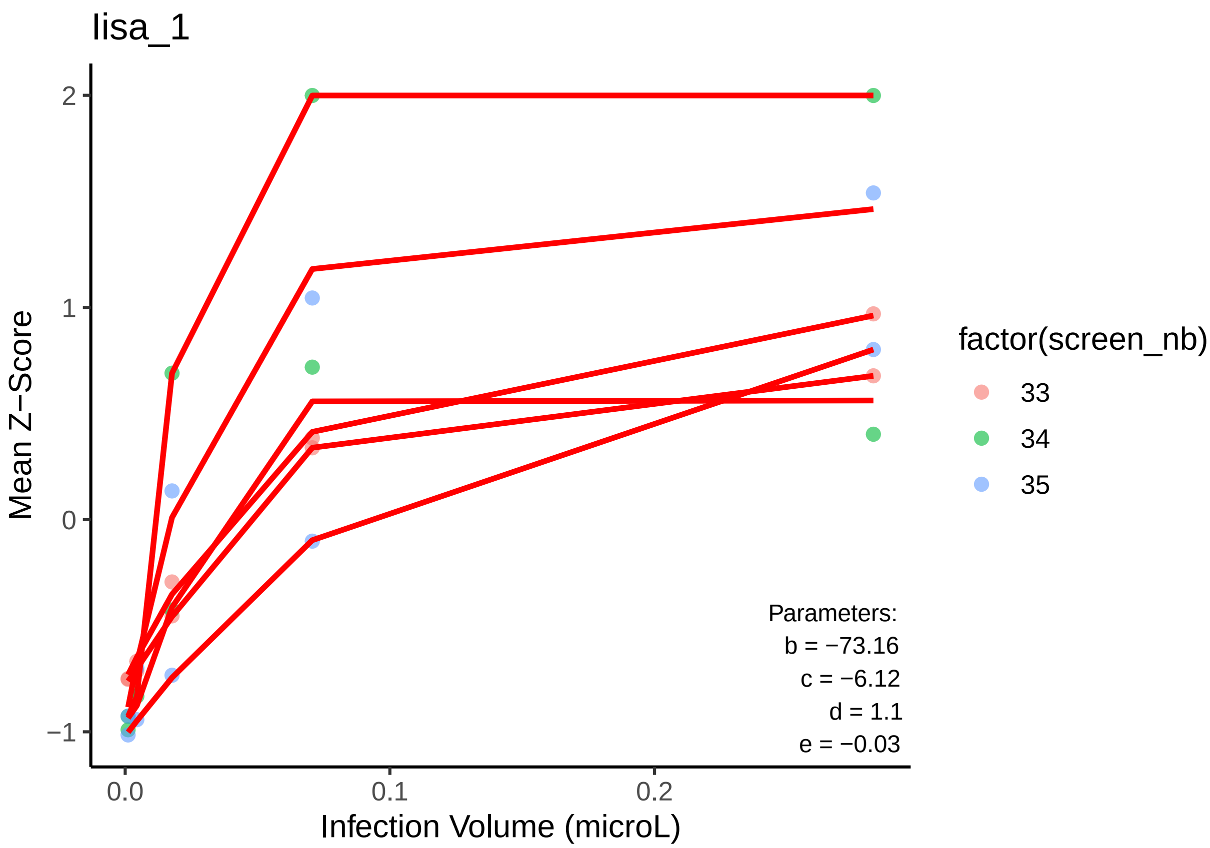

Iicq_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −15.63
c = −6.01
d = 1.23
e = −0.04
factor(screen_nb)
13
14

```
##
## $Iill_1
```


Iill_1
Mean Z−Score
2
1
0
Parameters:
b = −19.04
c = −2.9
d = 2.02
e = 0.02
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
28

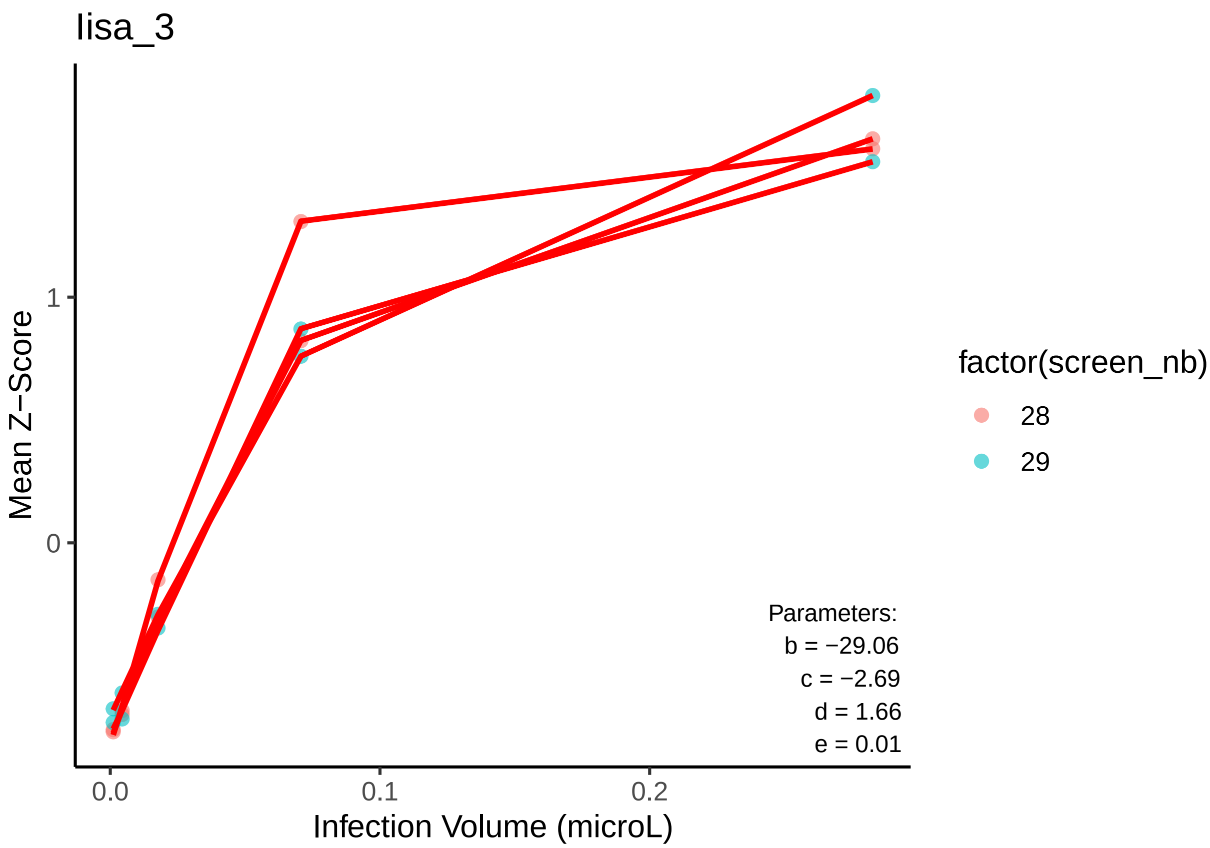
```
##
## $Iisa_1
```

Iisa_1

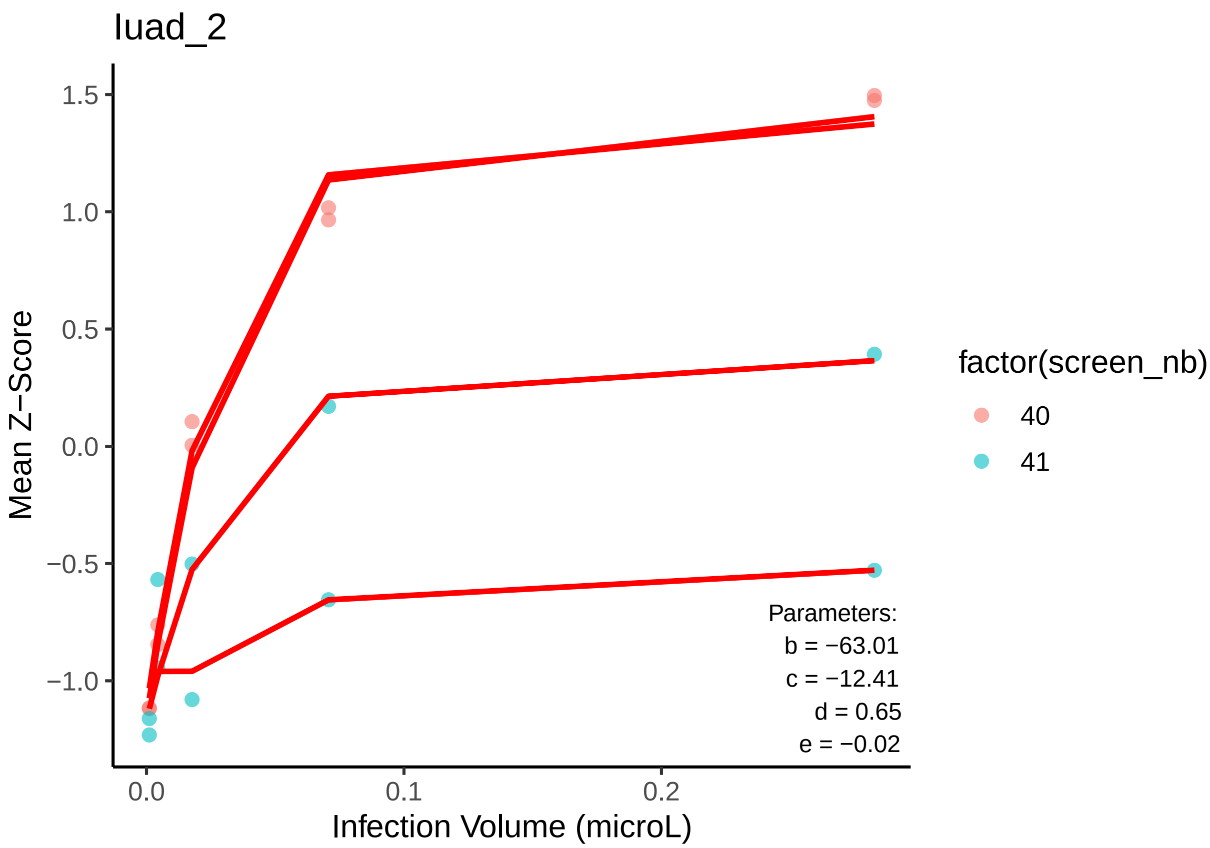


Iisa_1
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −73.16
c = −6.12
d = 1.1
e = −0.03
factor(screen_nb)
33
34
35


```
##
## $Iisa_3
```

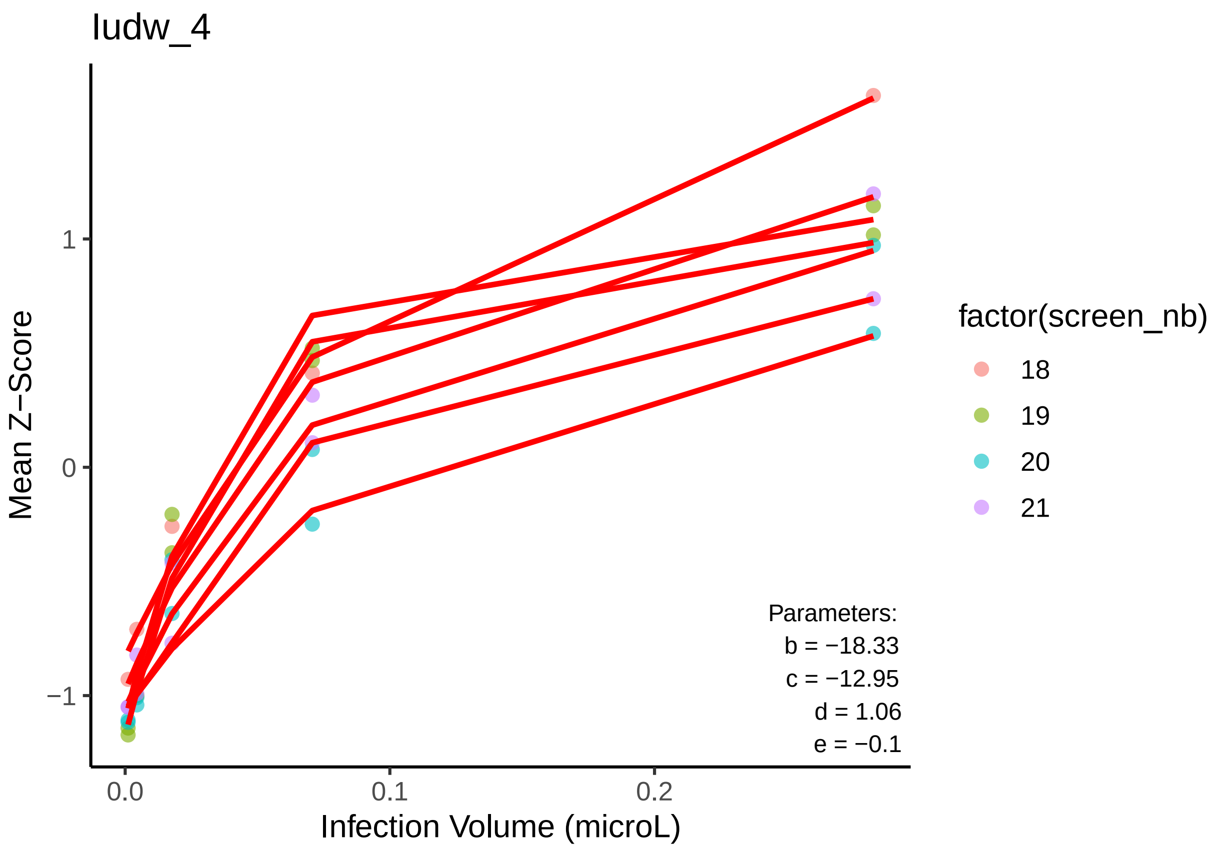

lisa_3
Mean Z−Score
1
0
Parameters:
b = −29.06
c = −2.69
d = 1.66
e = 0.01
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
28
29

```
##
## $luad_2
```

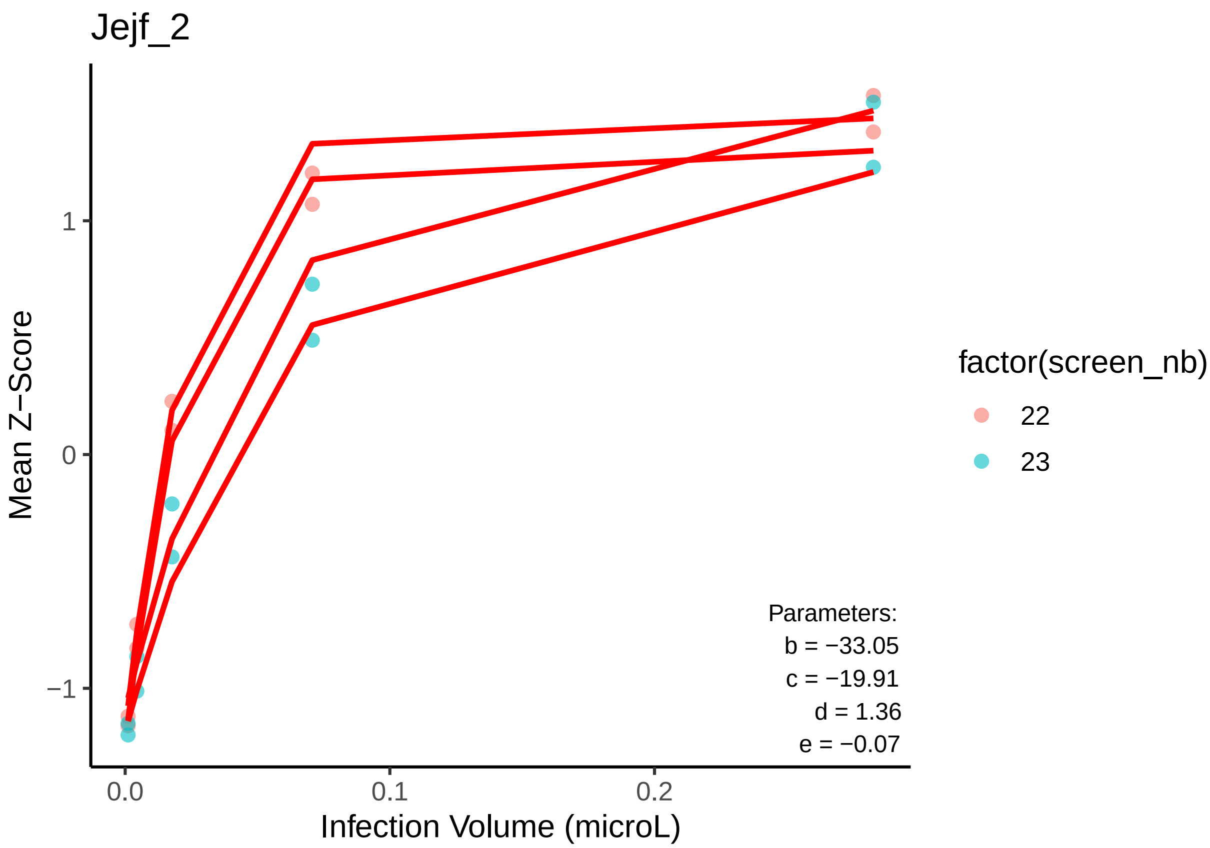


Iuad_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
40
41
Parameters:
b = −63.01
c = −12.41
d = 0.65
e = −0.02

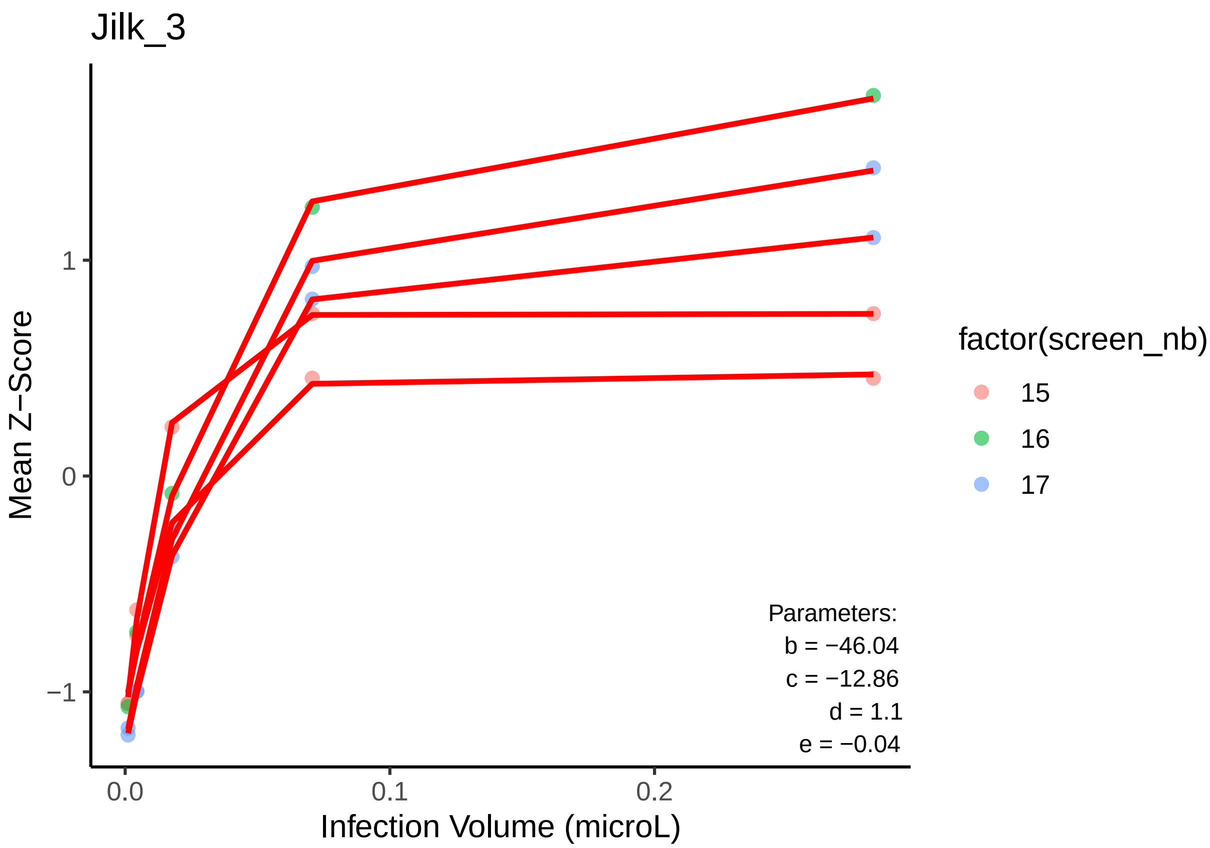

```
##
## $Iudw_4
```


Iudw_4
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −18.33
c = −12.95
d = 1.06
e = −0.1
factor(screen_nb)
18
19
20
21

```
##
## $Jejf_2
```

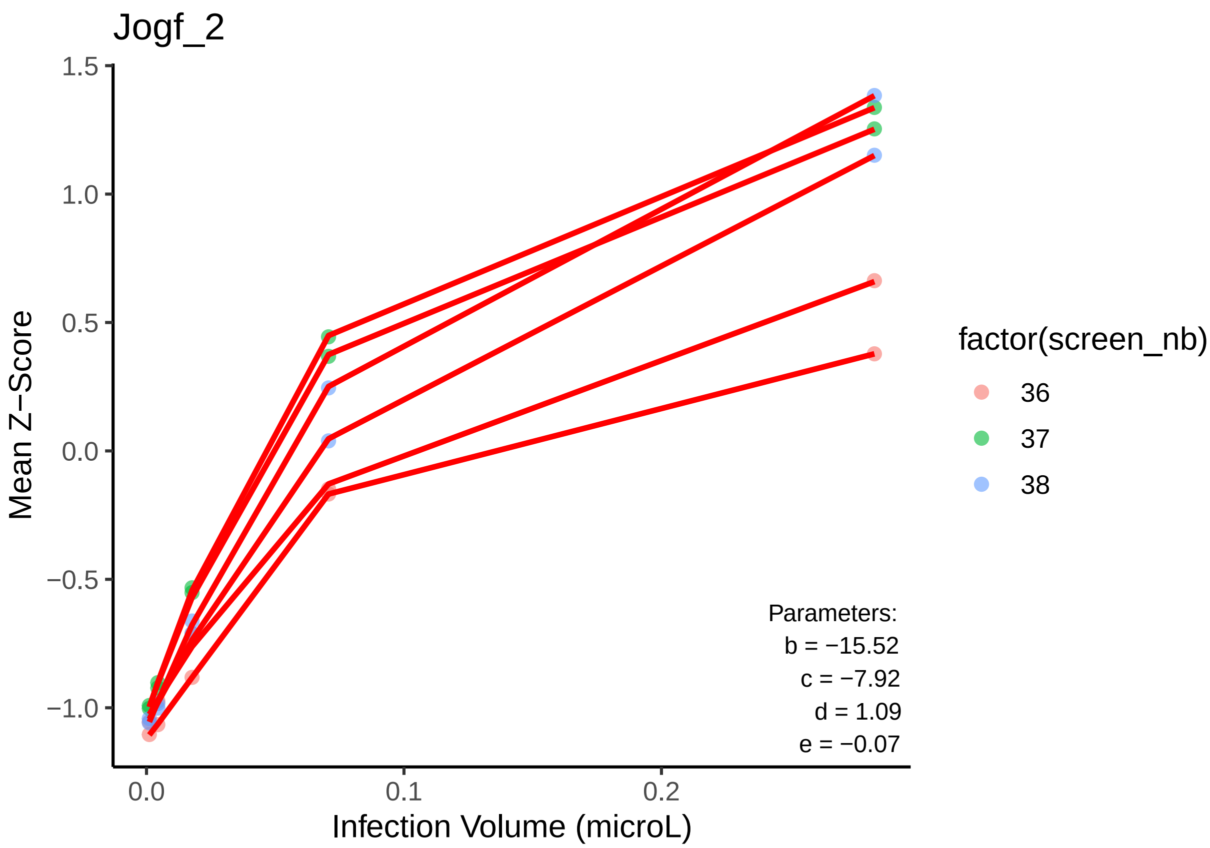

Jejf_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −33.05
c = −19.91
d = 1.36
e = −0.07
factor(screen_nb)
22
23

```
##
## $Jilk_3
```

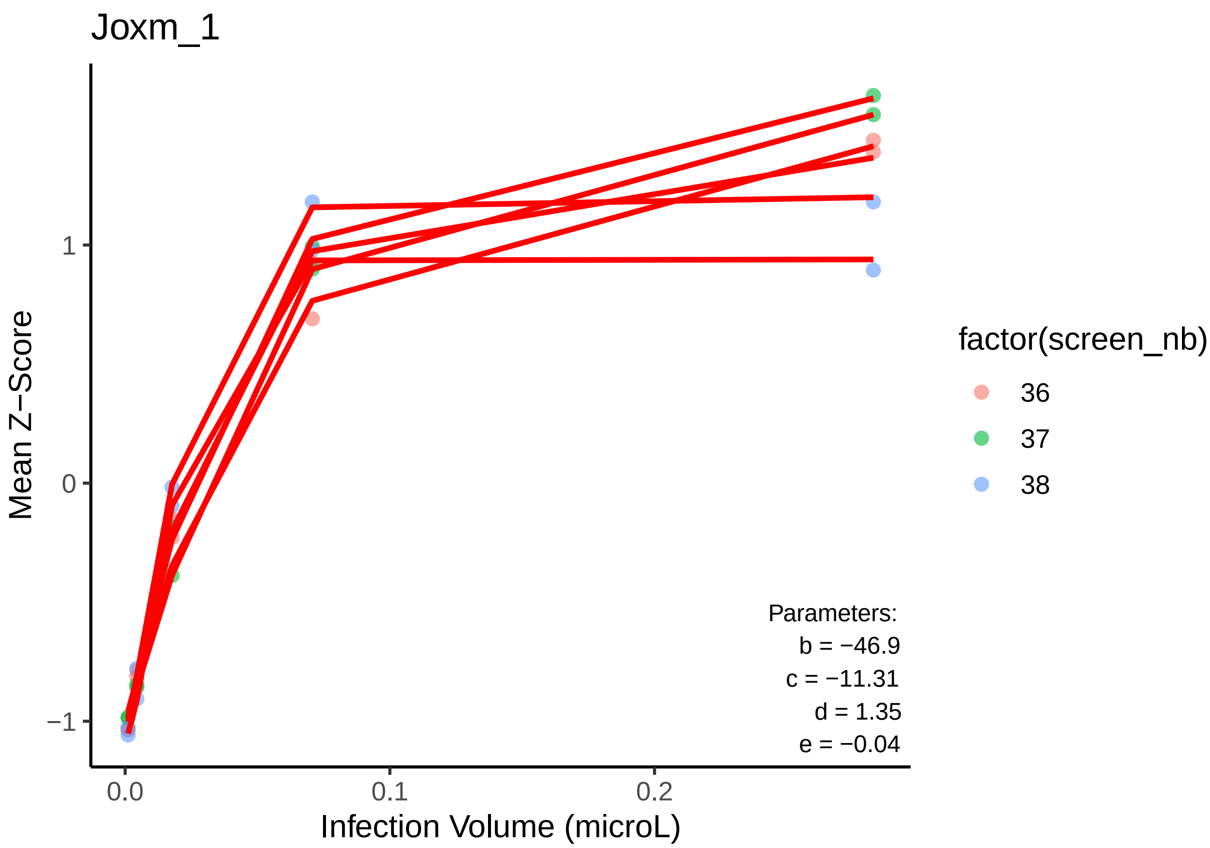


Jilk_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −46.04
c = −12.86
d = 1.1
e = −0.04
factor(screen_nb)
15
16
17


```
##
## $Jogf_2
```

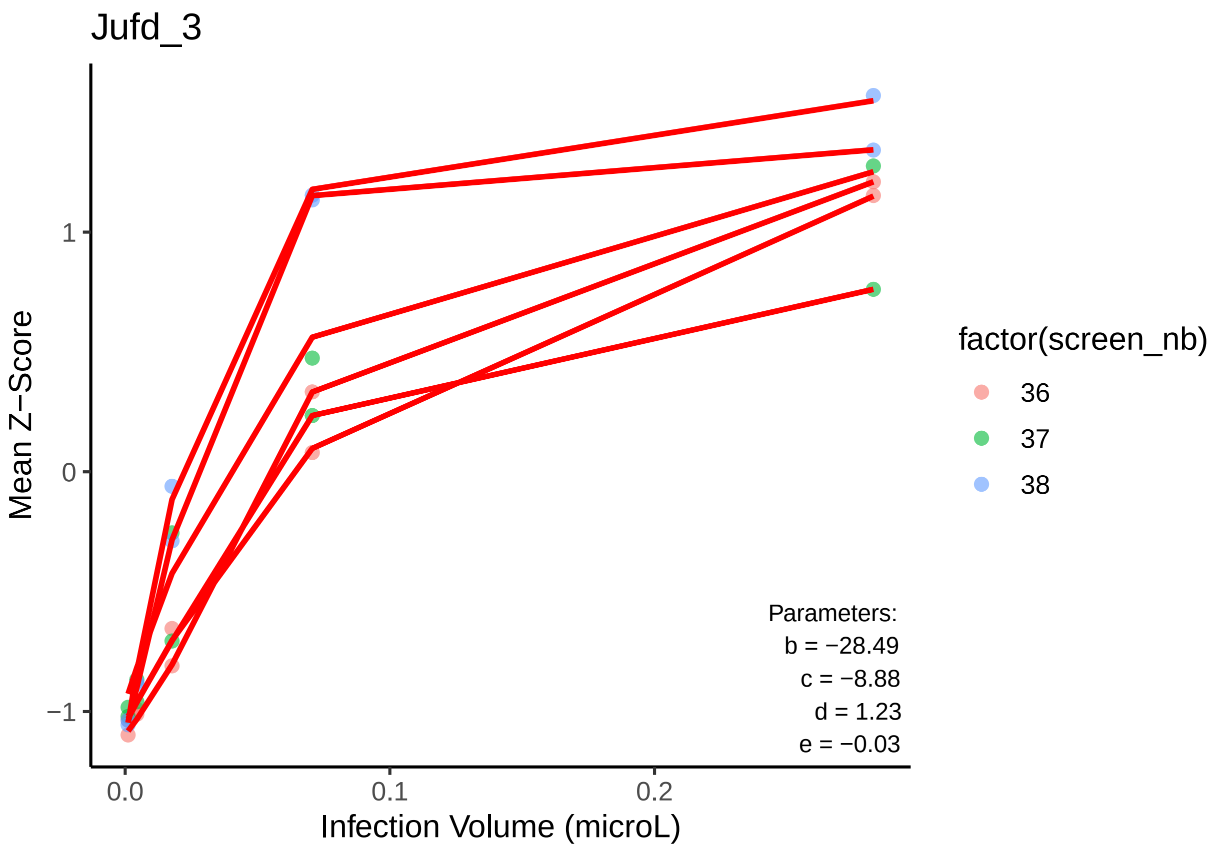

Jogf_2
1.5
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −15.52
c = −7.92
d = 1.09
e = −0.07
factor(screen_nb)
36
37
38

```
##
## $Joxm_1
```



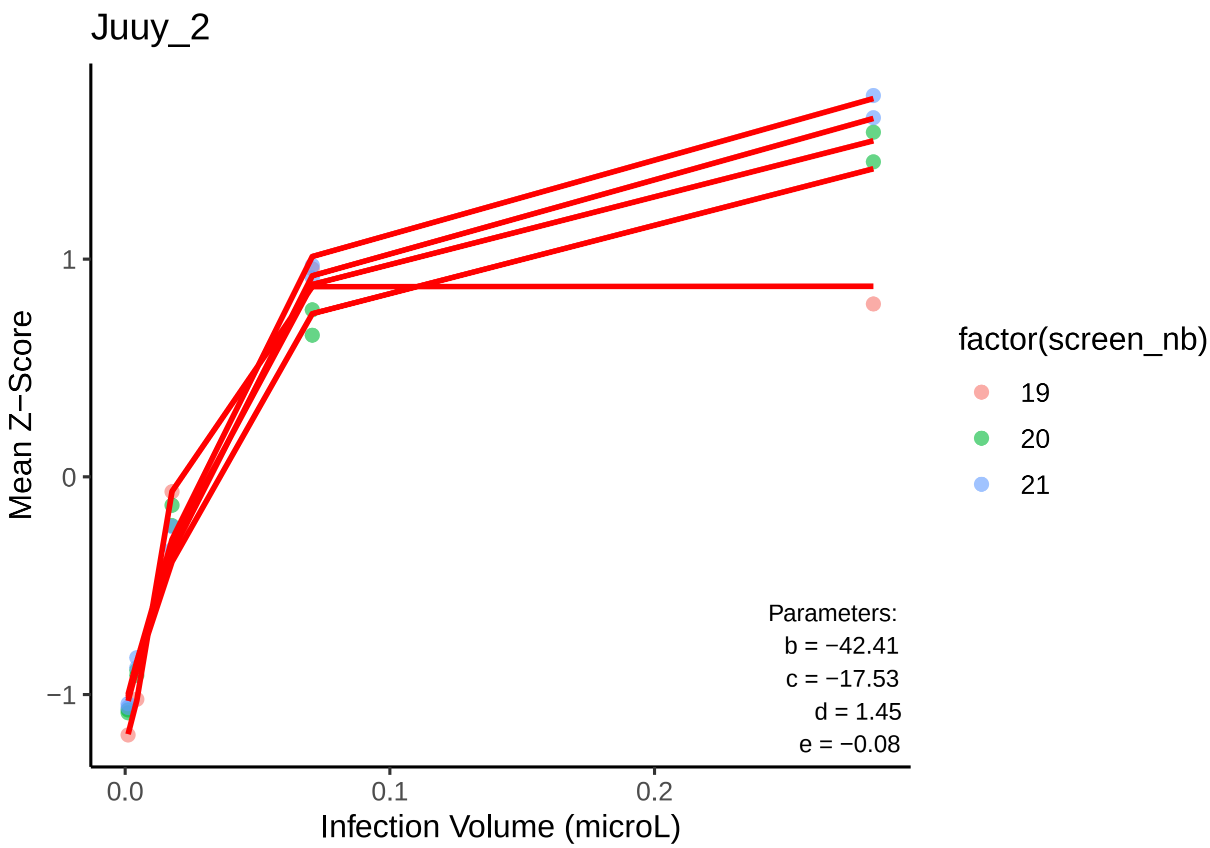
Joxm_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −46.9
c = −11.31
d = 1.35
e = −0.04
factor(screen_nb)
36
37
38


```
##
## $Jufd_3
```

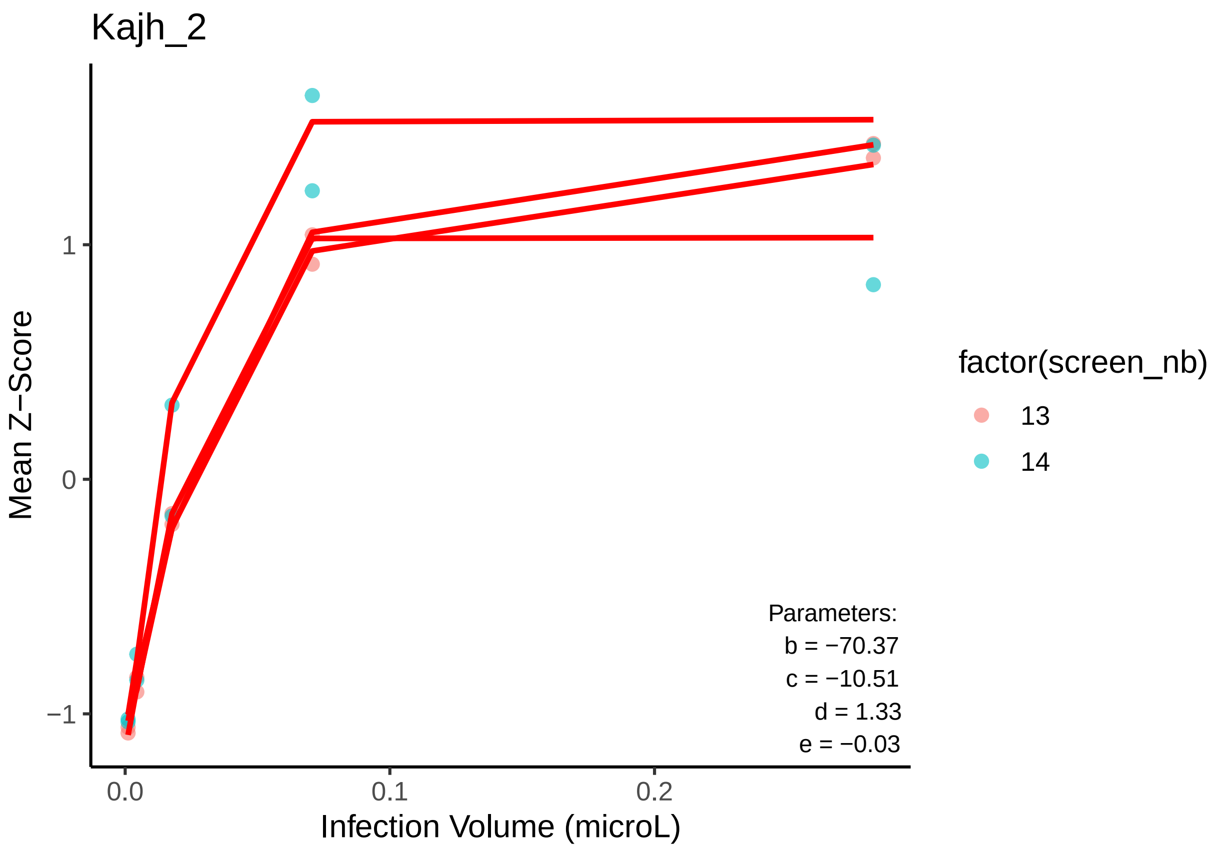


Jufd_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −28.49
c = −8.88
d = 1.23
e = −0.03
factor(screen_nb)
36
37
38

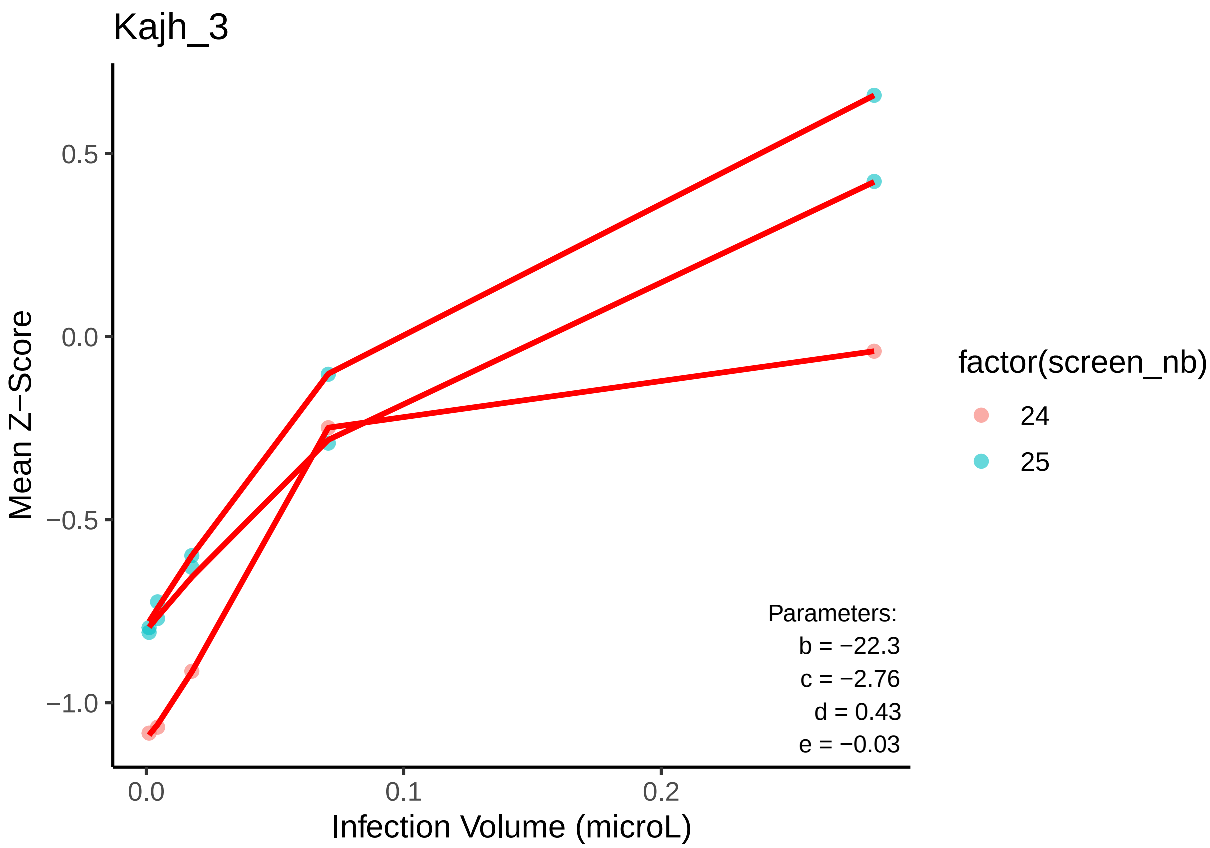

```
##
## $Juuy_2
```


Juuy_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −42.41
c = −17.53
d = 1.45
e = −0.08
factor(screen_nb)
19
20
21

```
##
## $Kajh_2
```

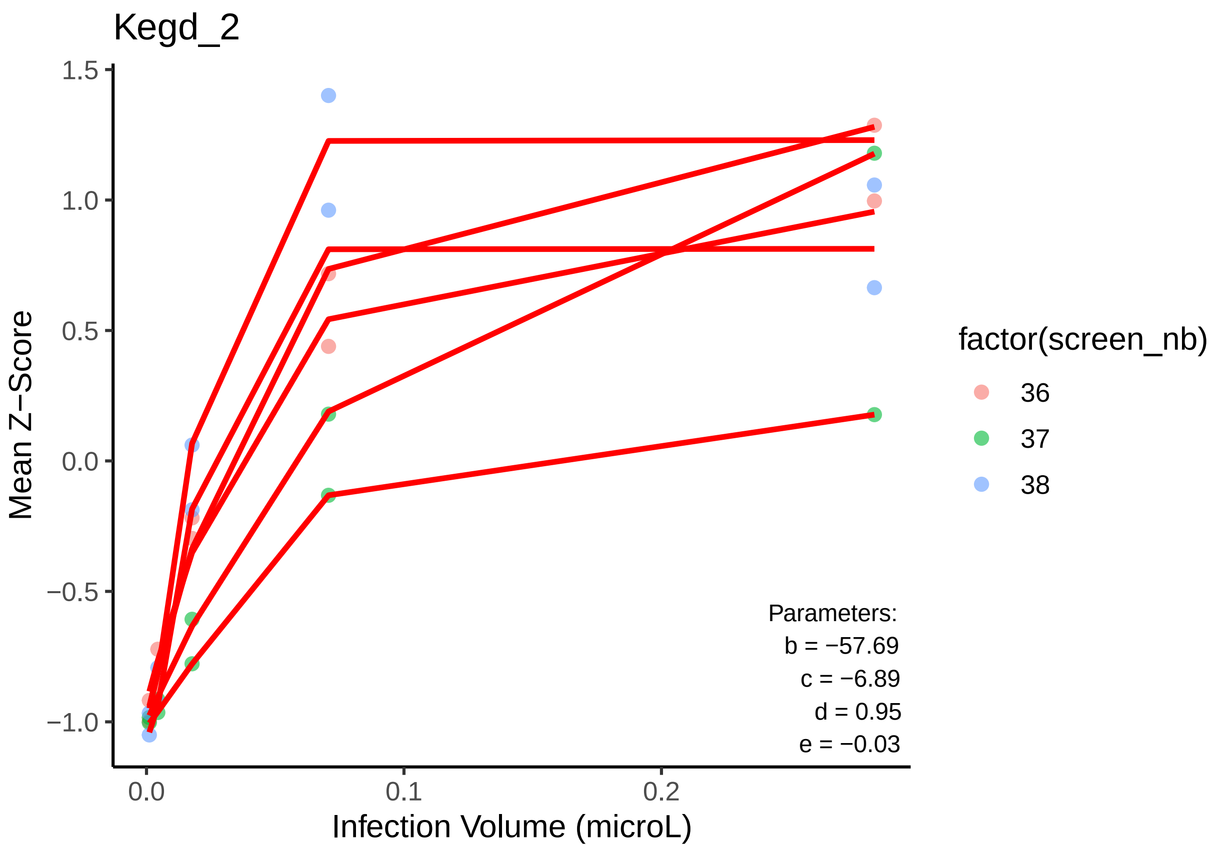

Kajh_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −70.37
c = −10.51
d = 1.33
e = −0.03
factor(screen_nb)
13
14

```
##
## $Kajh_3
```

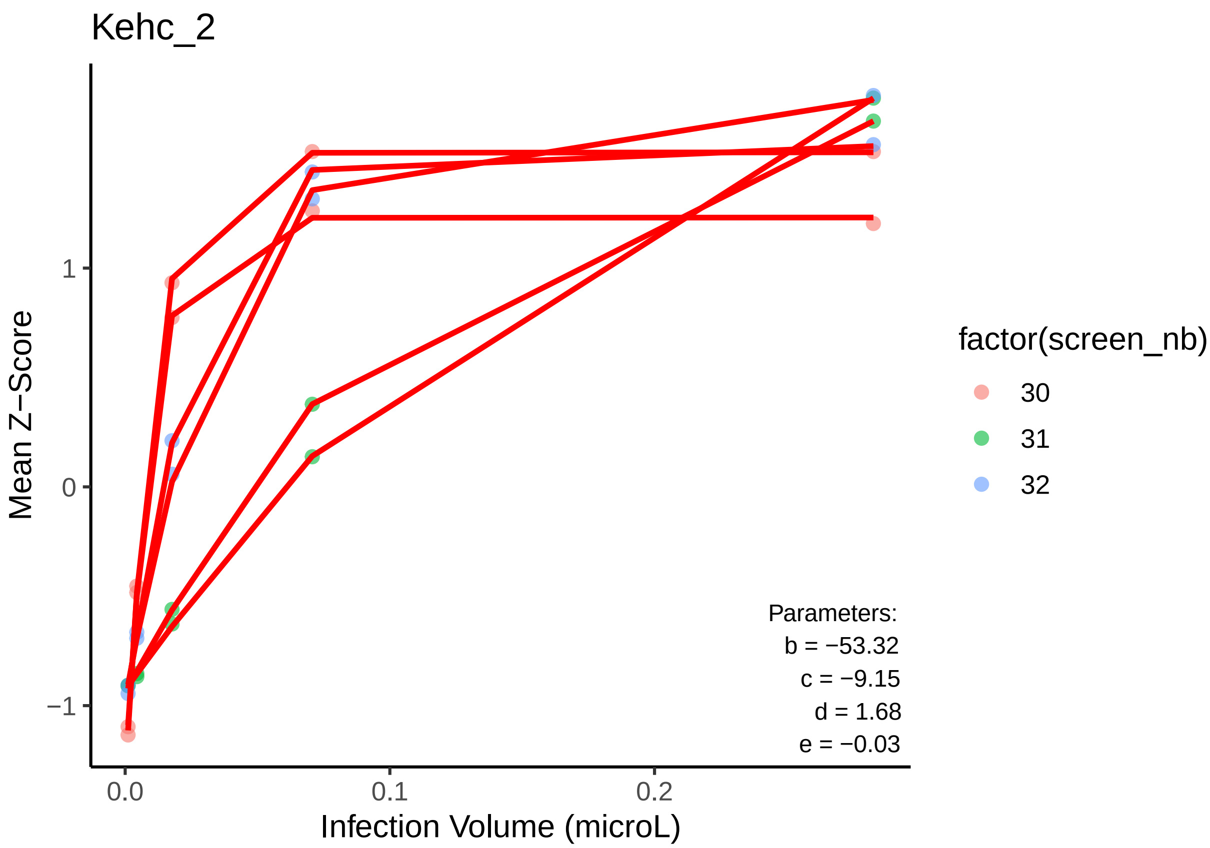


Kajh_3
Mean Z−Score
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
24
25
Parameters:
b = −22.3
c = −2.76
d = 0.43
e = −0.03

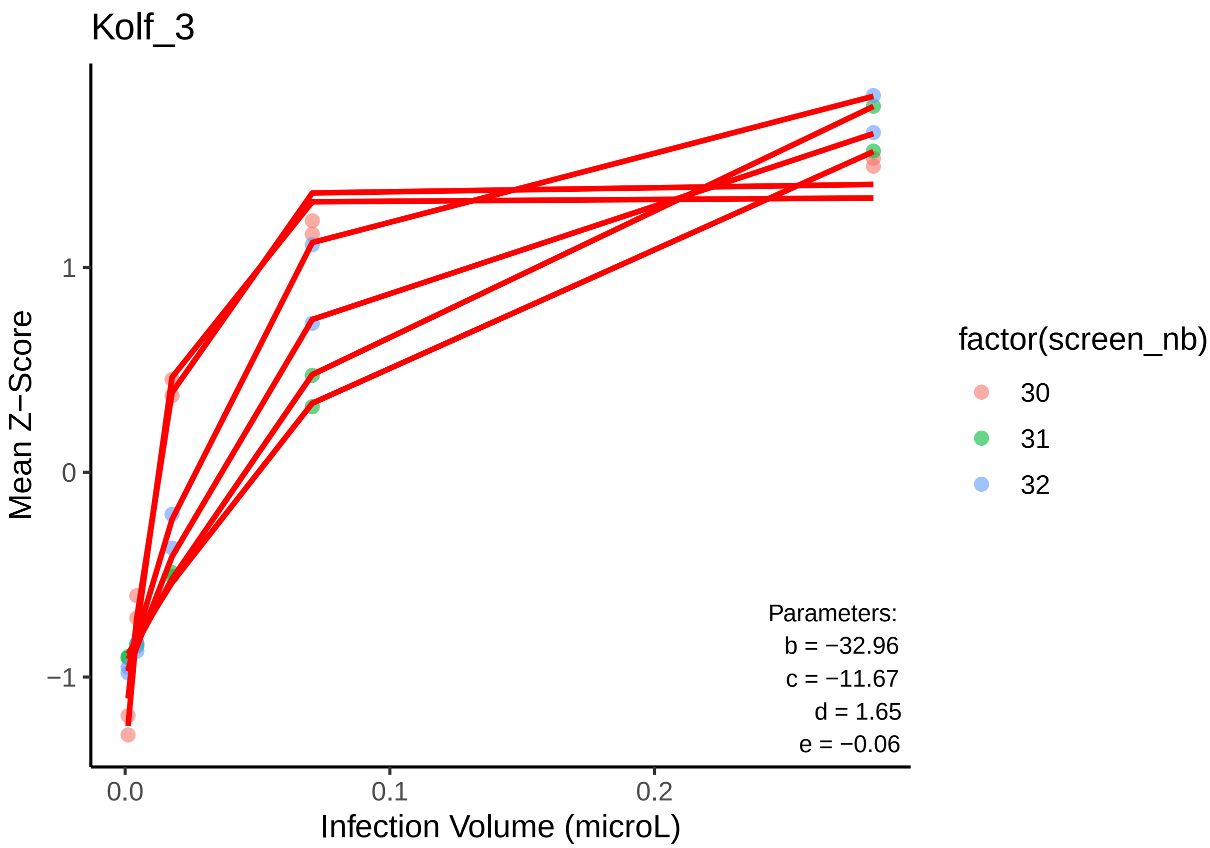

```
##
## $Kegd_2
```


Kegd_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −57.69
c = −6.89
d = 0.95
e = −0.03
factor(screen_nb)
36
37
38

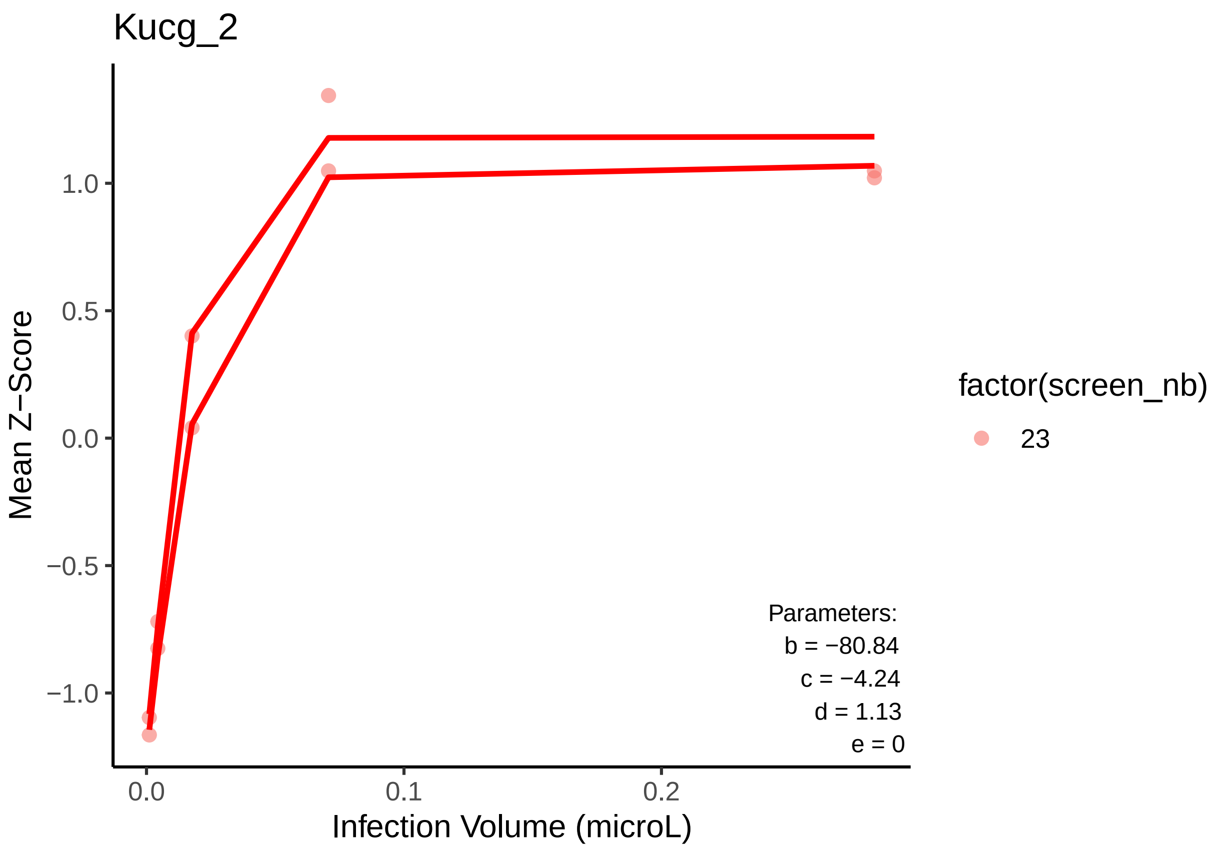
```
##
## $Kehc_2
```


Kehc_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −53.32
c = −9.15
d = 1.68
e = −0.03
factor(screen_nb)
30
31
32

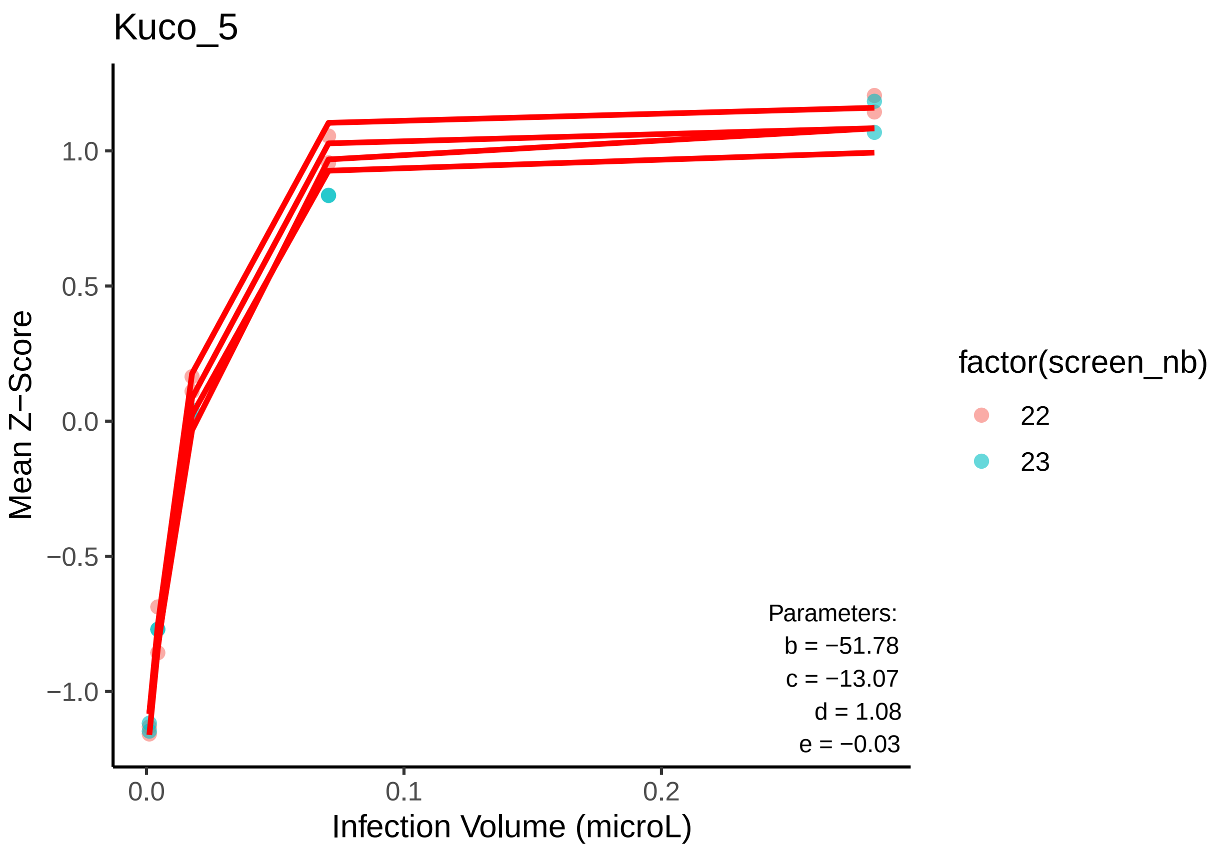
```
##
## $Kolf_3
```


Kolf_3
Mean Z−Score
Infection Volume (microL)
factor(screen_nb)
30
31
32
Parameters:
b = −32.96
c = −11.67
d = 1.65
e = −0.06
1
0
−1
0.0
0.1
0.2

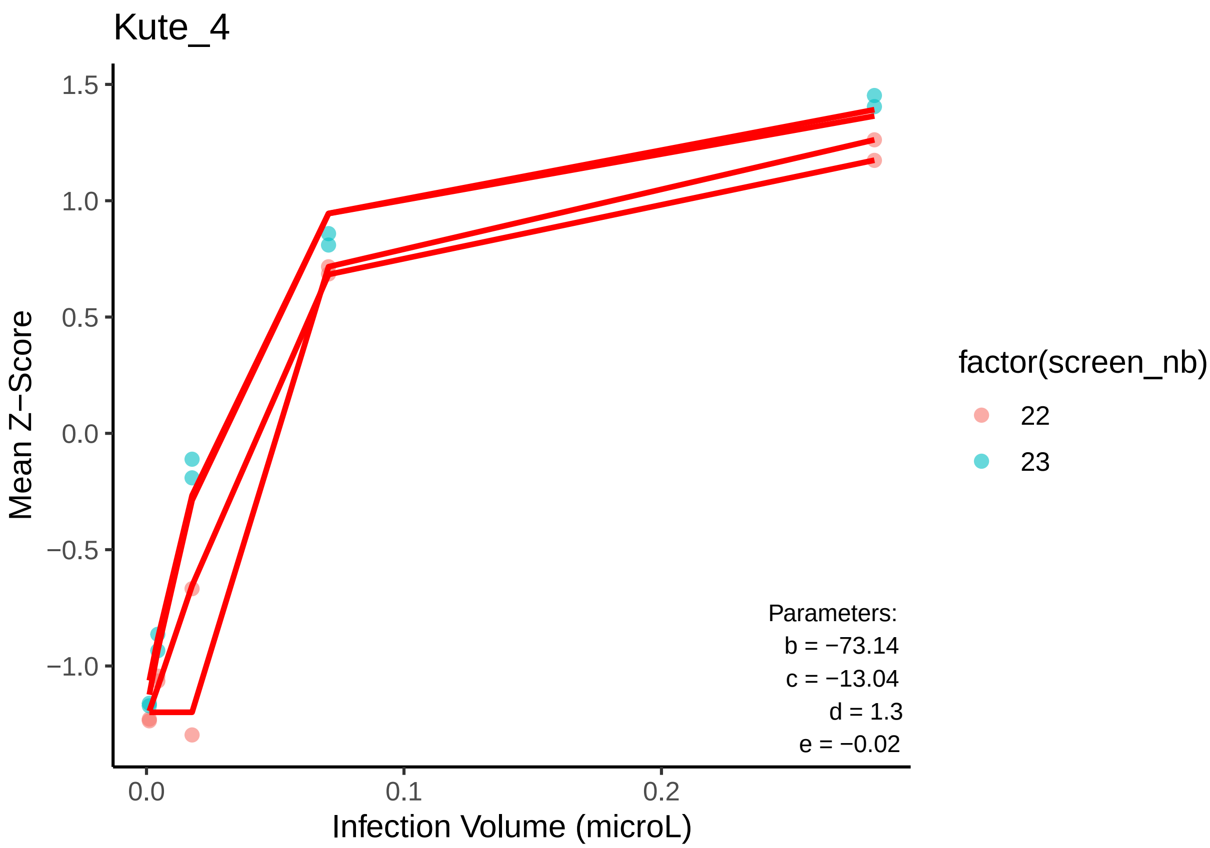
```
##
## $Kucg_2
```


Kucg_2
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −80.84
c = −4.24
d = 1.13
e = 0
factor(screen_nb)
23

```
##
## $Kuco_5
```

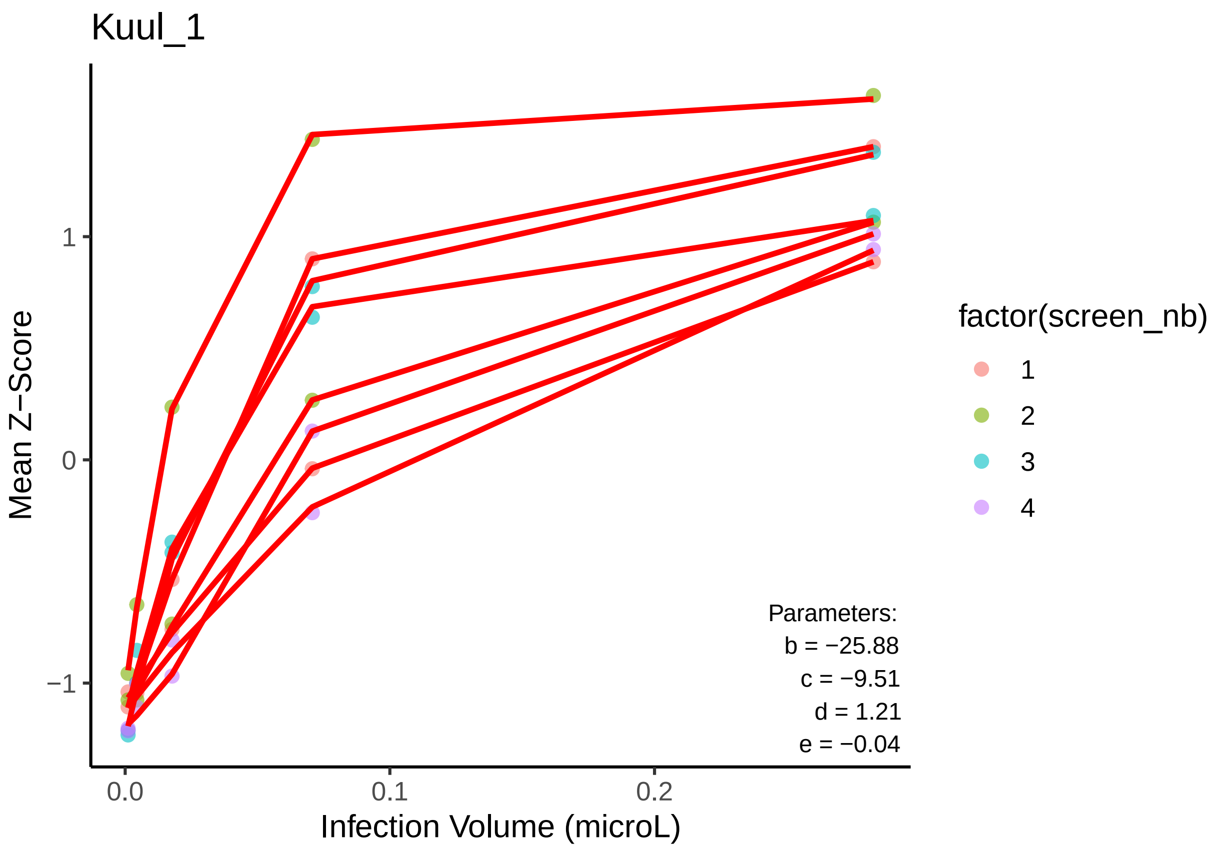

Kuco_5
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −51.78
c = −13.07
d = 1.08
e = −0.03
factor(screen_nb)
22
23

```
##
## $Kute_4
```

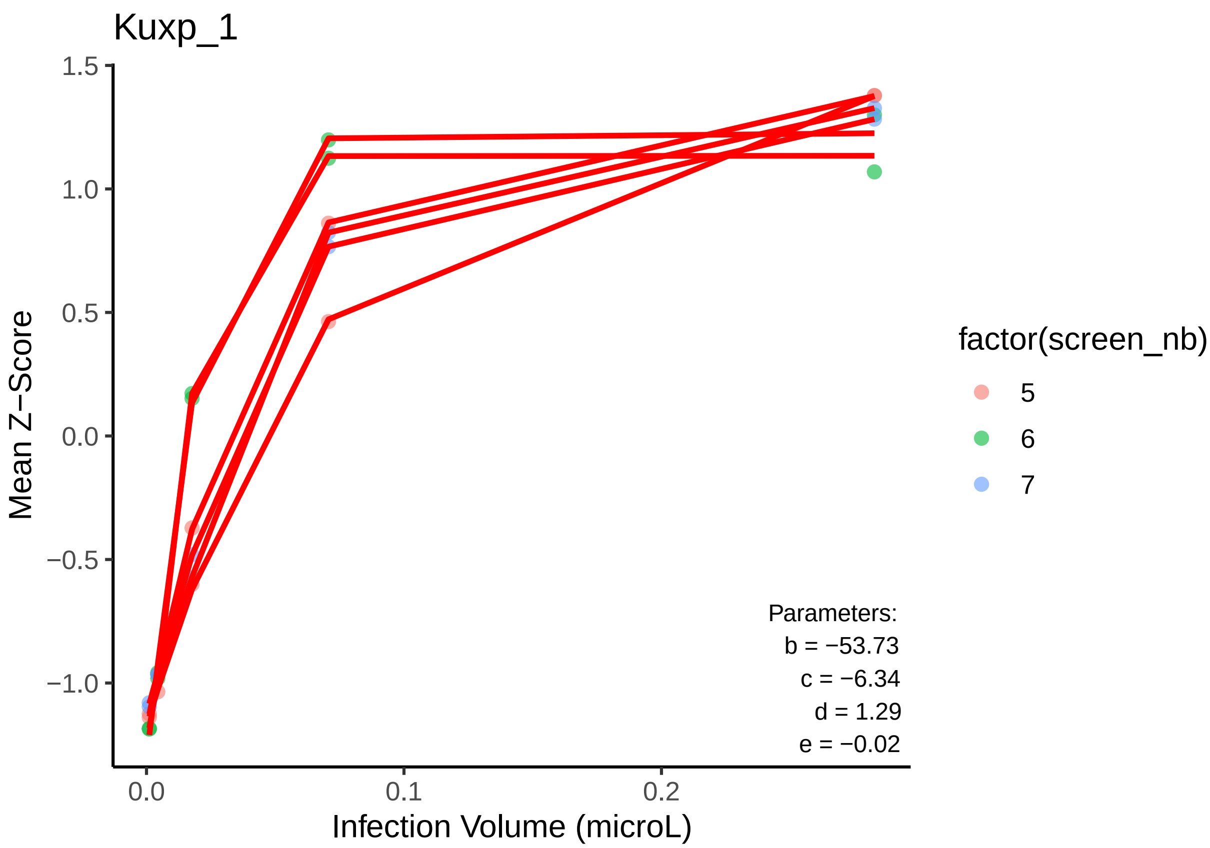


Kute_4
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −73.14
c = −13.04
d = 1.3
e = −0.02
factor(screen_nb)
22
23

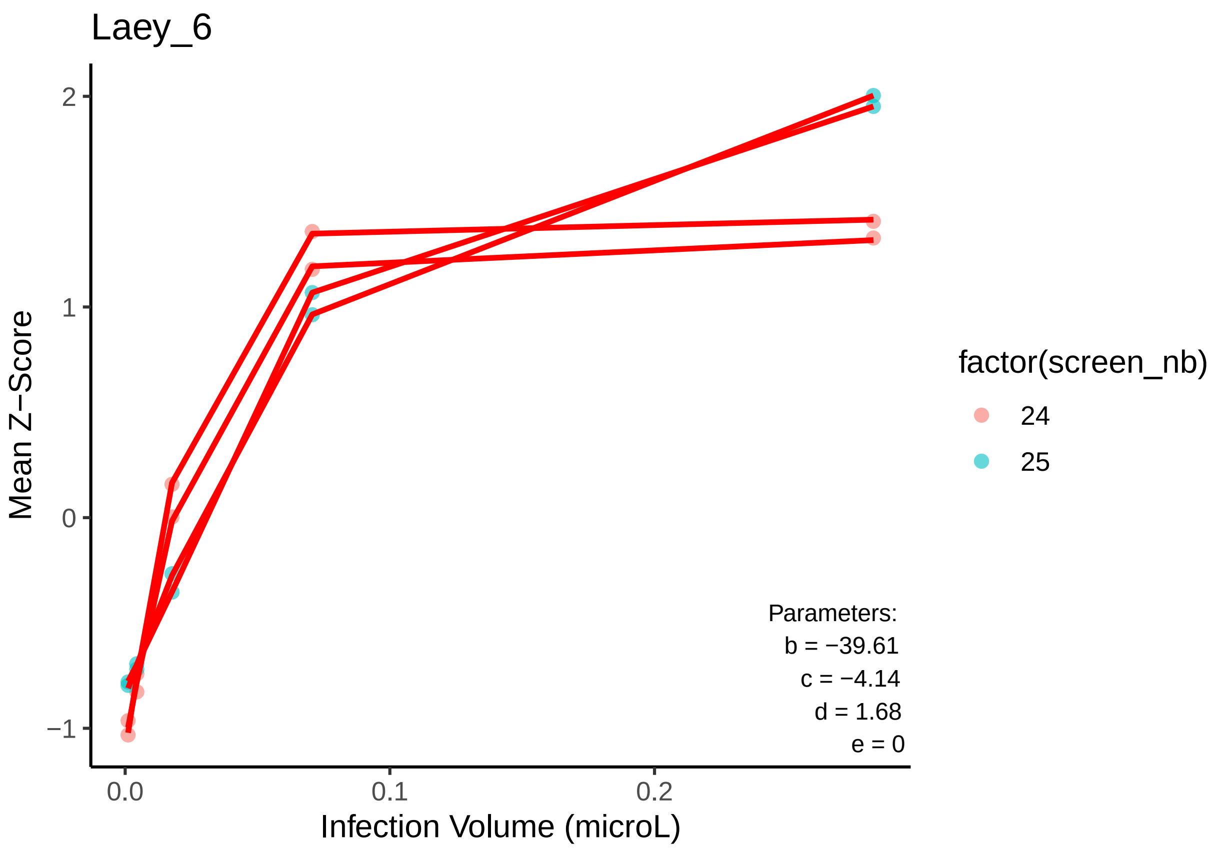

```
##
## $Kuul_1
```


Kuul_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −25.88
c = −9.51
d = 1.21
e = −0.04
factor(screen_nb)
1
2
3
4

```
##
## $Kuxp_1
```

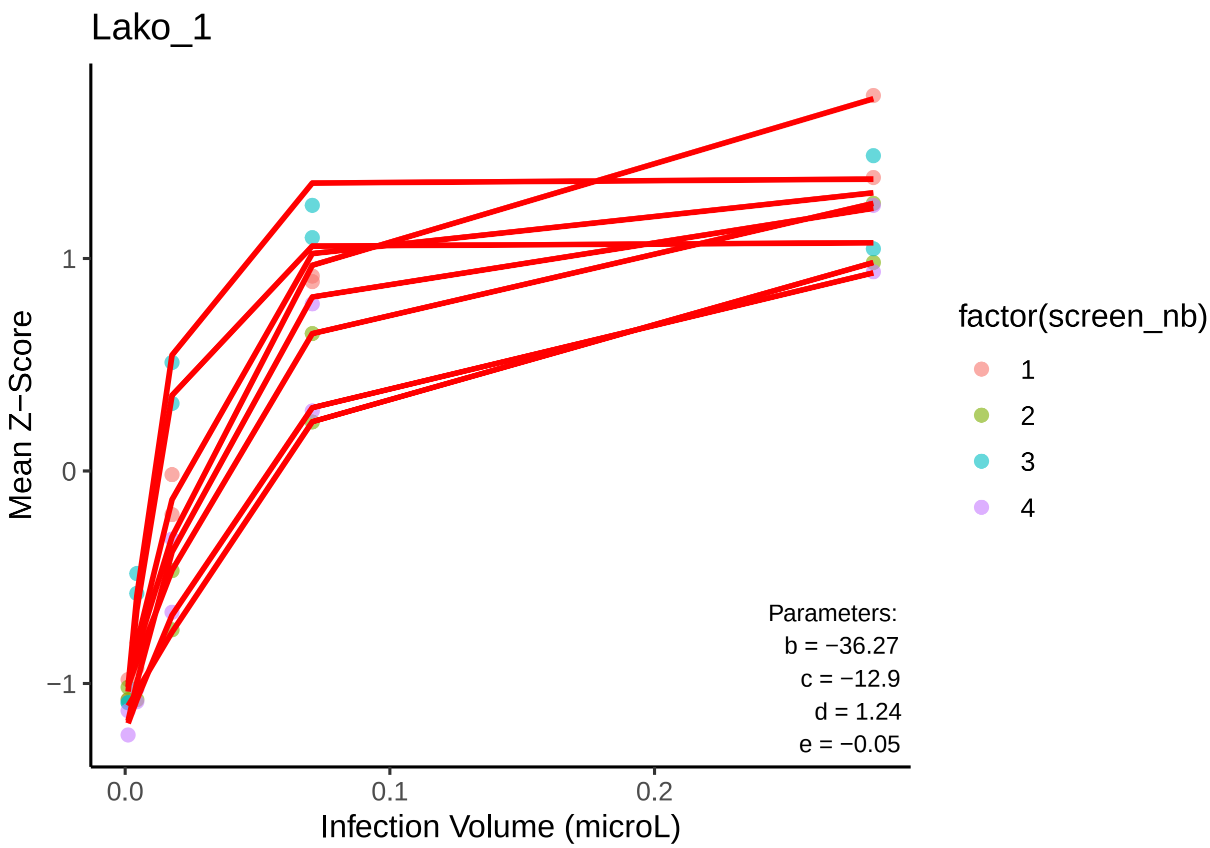

Kuxp_1
1.5
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −53.73
c = −6.34
d = 1.29
e = −0.02
factor(screen_nb)
5
6
7

```
##
## $Laey_6
```

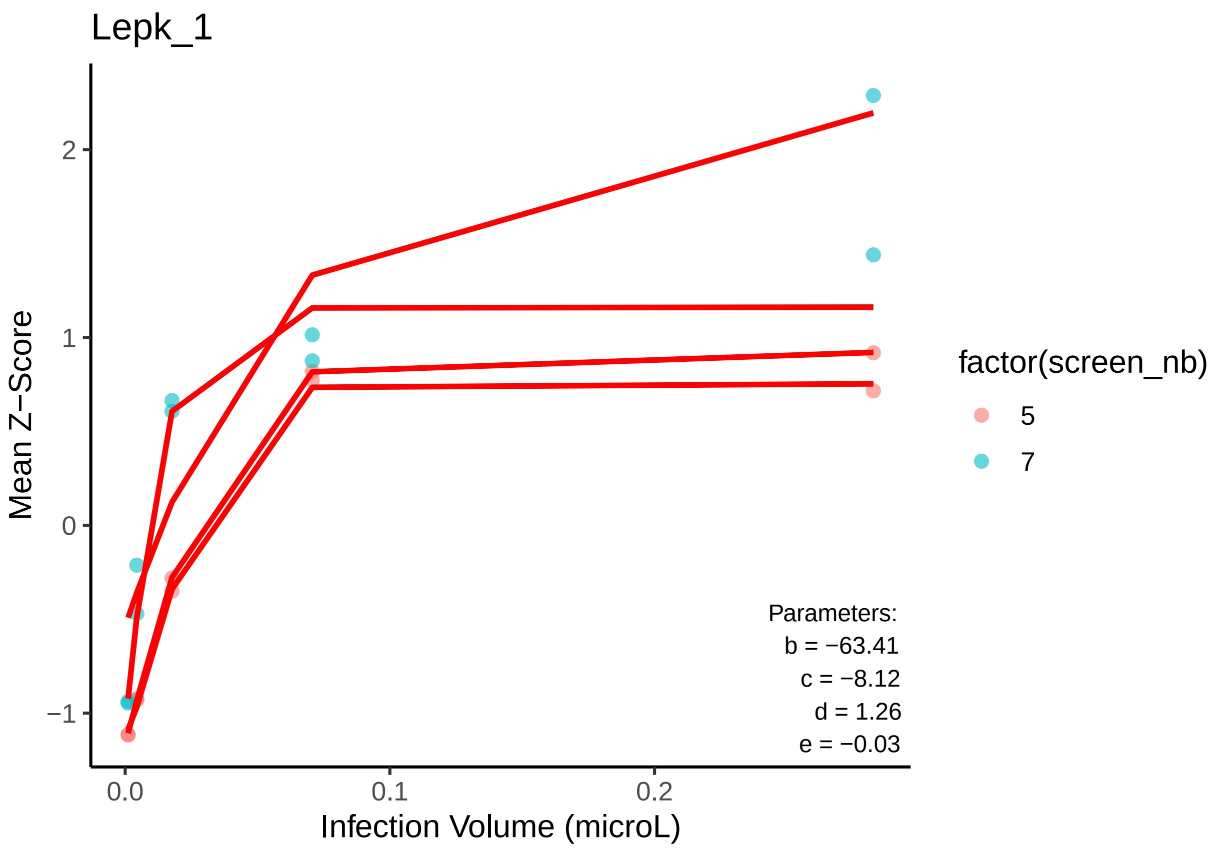


Laey_6
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −39.61
c = −4.14
d = 1.68
e = 0
factor(screen_nb)
24
25

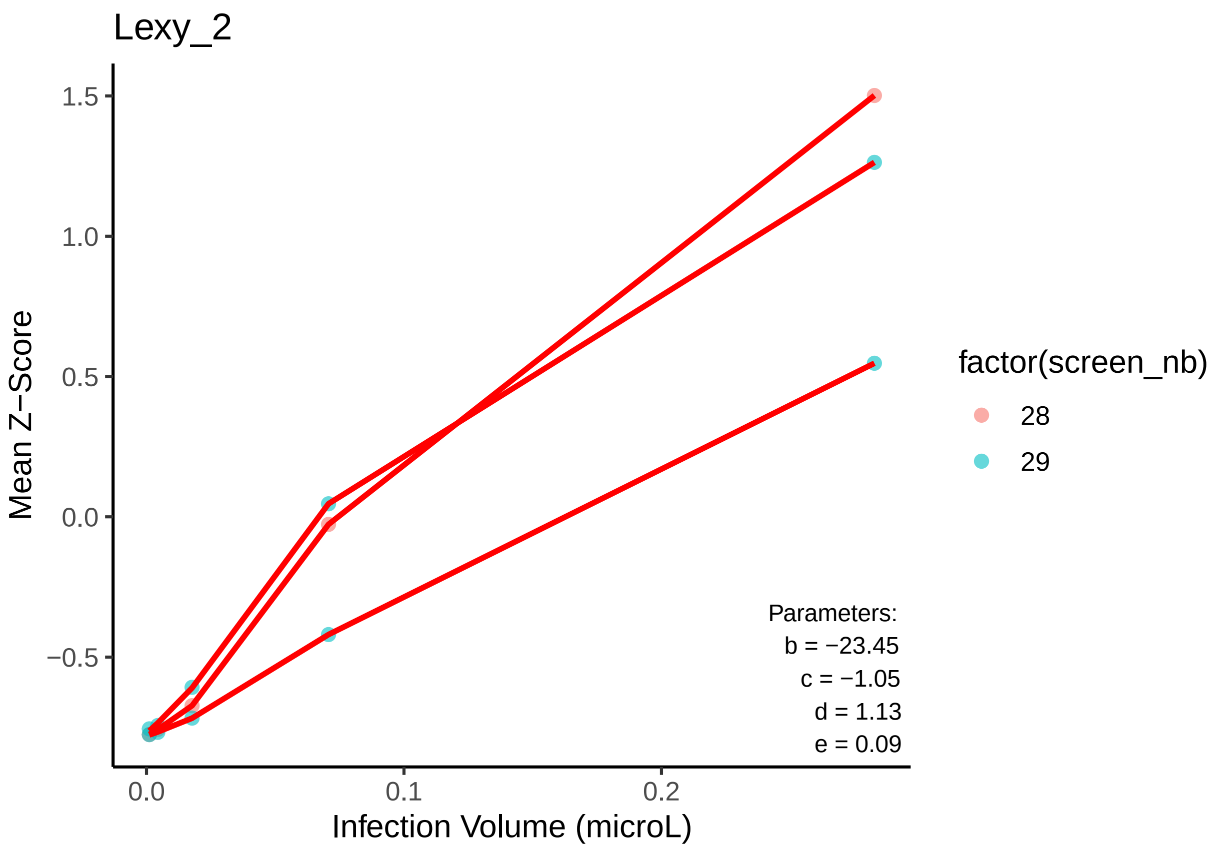

```
##
## $Lako_1
```


Lako_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
1
2
3
4
Parameters:
b = −36.27
c = −12.9
d = 1.24
e = −0.05

```
##
## $Lepk_1
```

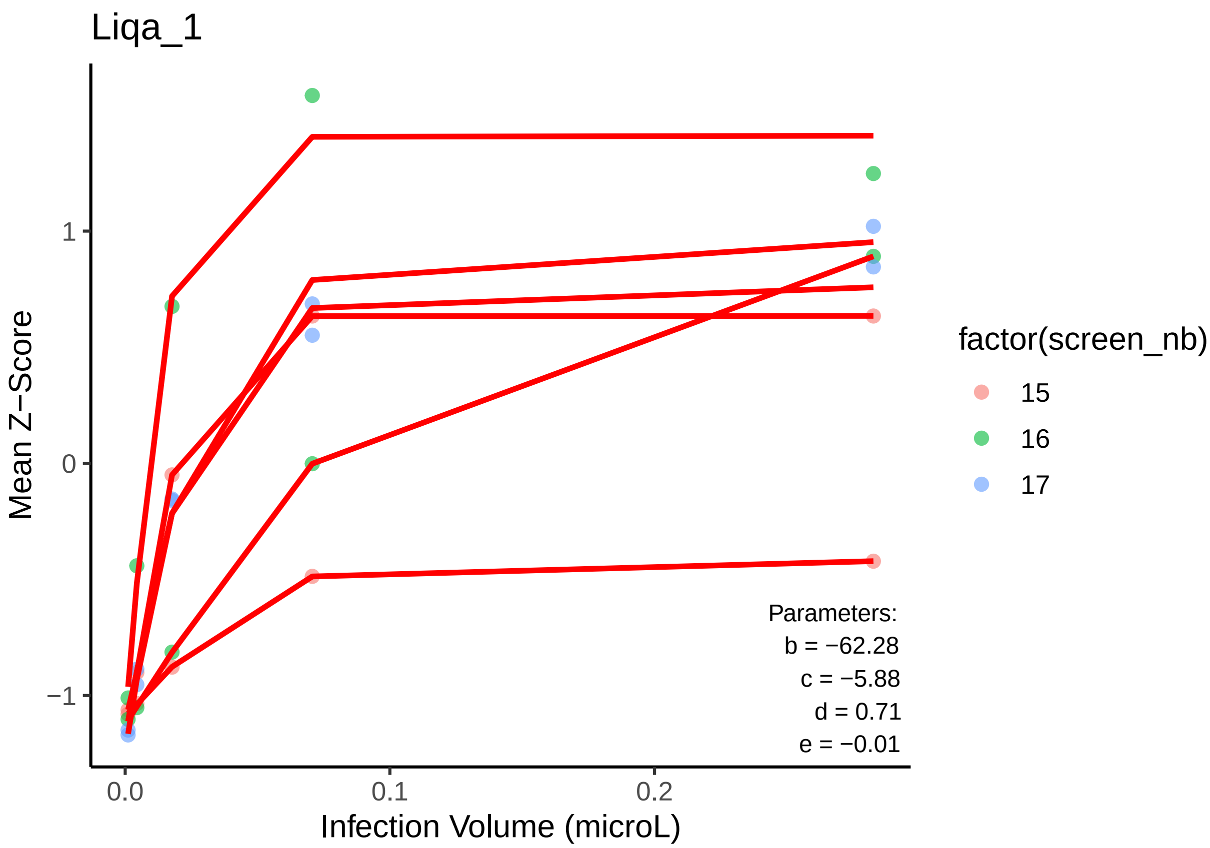

Lepk_1
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −63.41
c = −8.12
d = 1.26
e = −0.03
factor(screen_nb)
5
7

```
##
## $Lexy_2
```

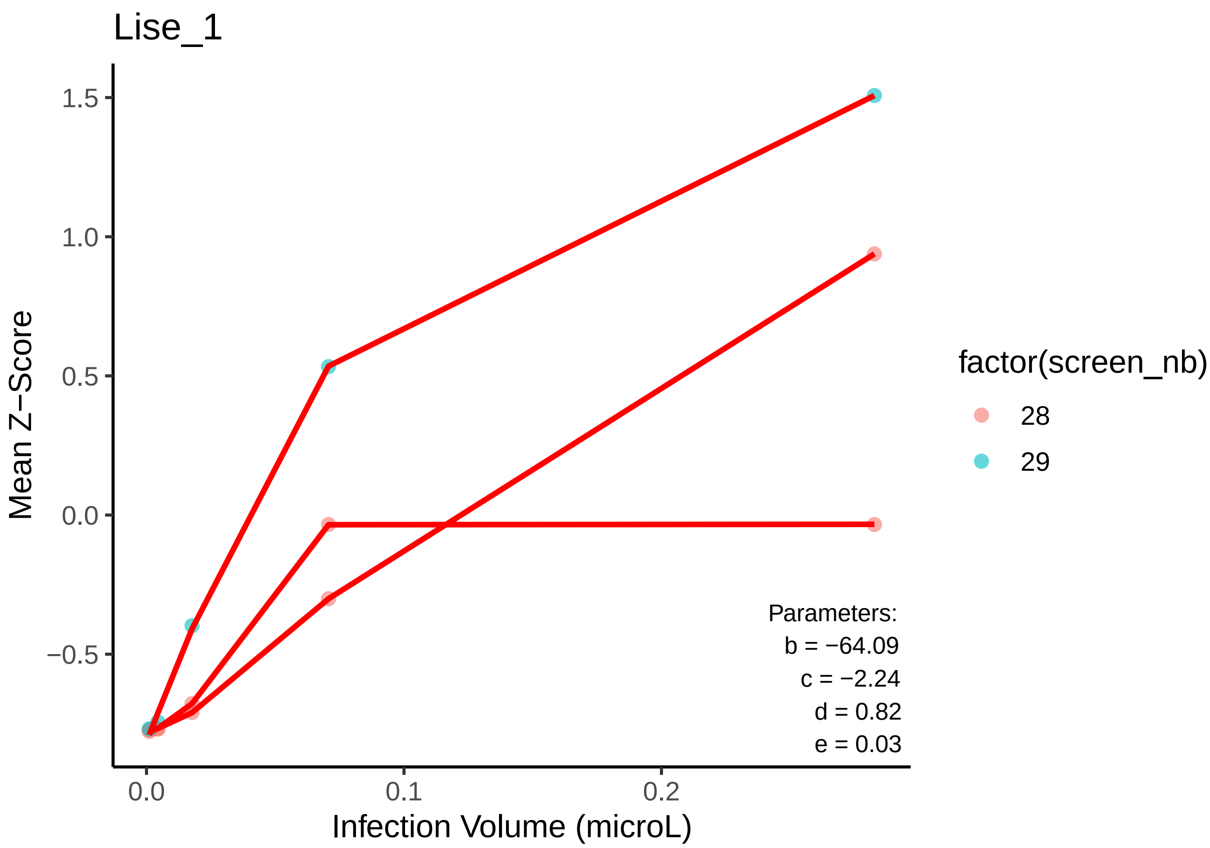


Lexy_2
1.5
1.0
0.5
0.0
−0.5
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −23.45
c = −1.05
d = 1.13
e = 0.09
factor(screen_nb)
28
29

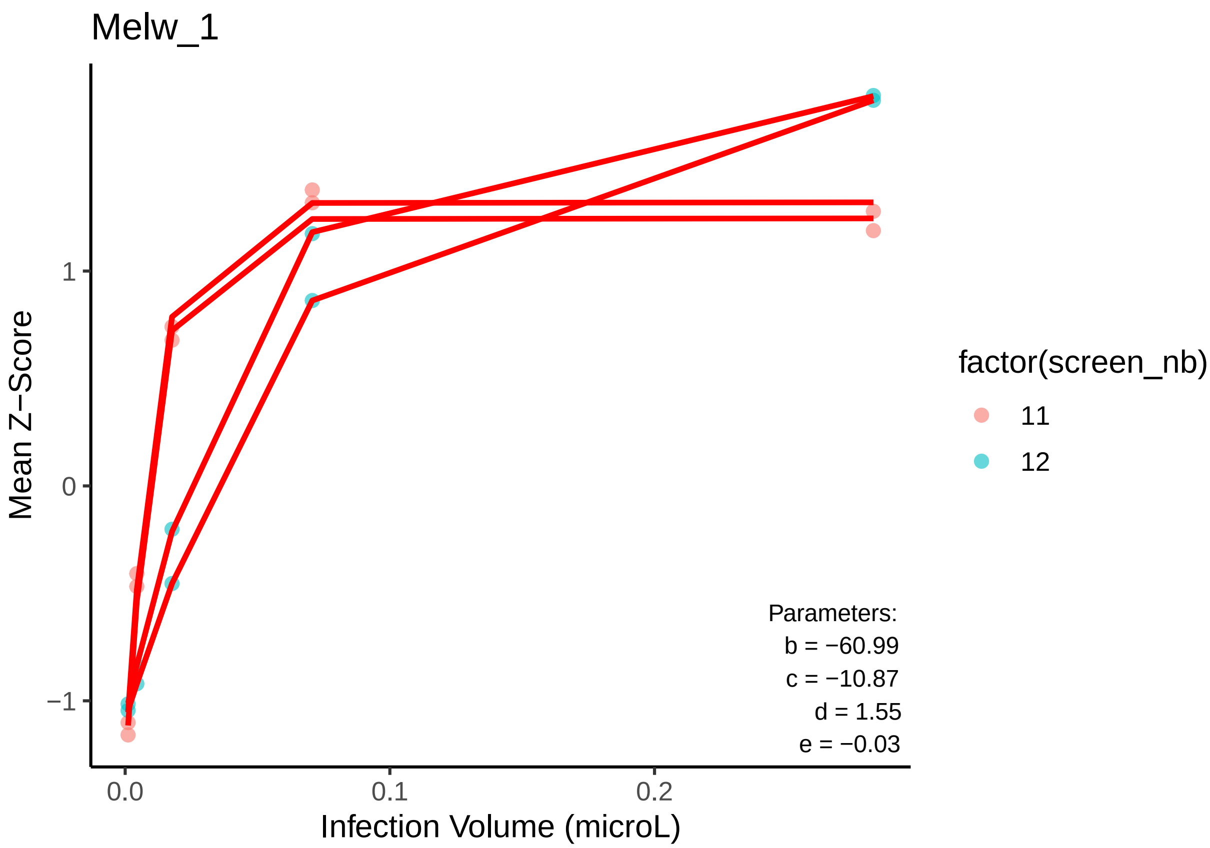

```
##
## $Liqa_1
```


Liqa_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −62.28
c = −5.88
d = 0.71
e = −0.01
factor(screen_nb)
15
16
17

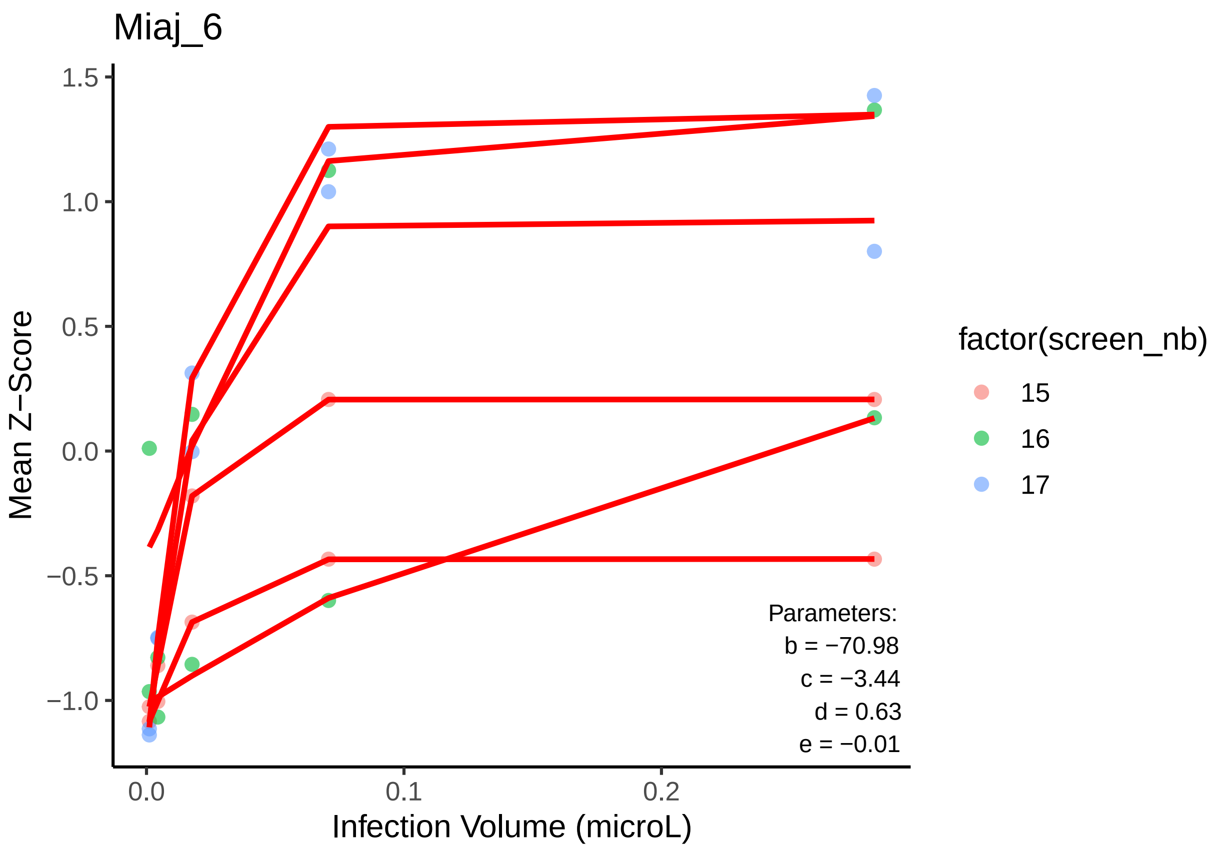
```
##
## $Lise_1
```


Lise_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
28
29
Parameters:
b = −64.09
c = −2.24
d = 0.82
e = 0.03

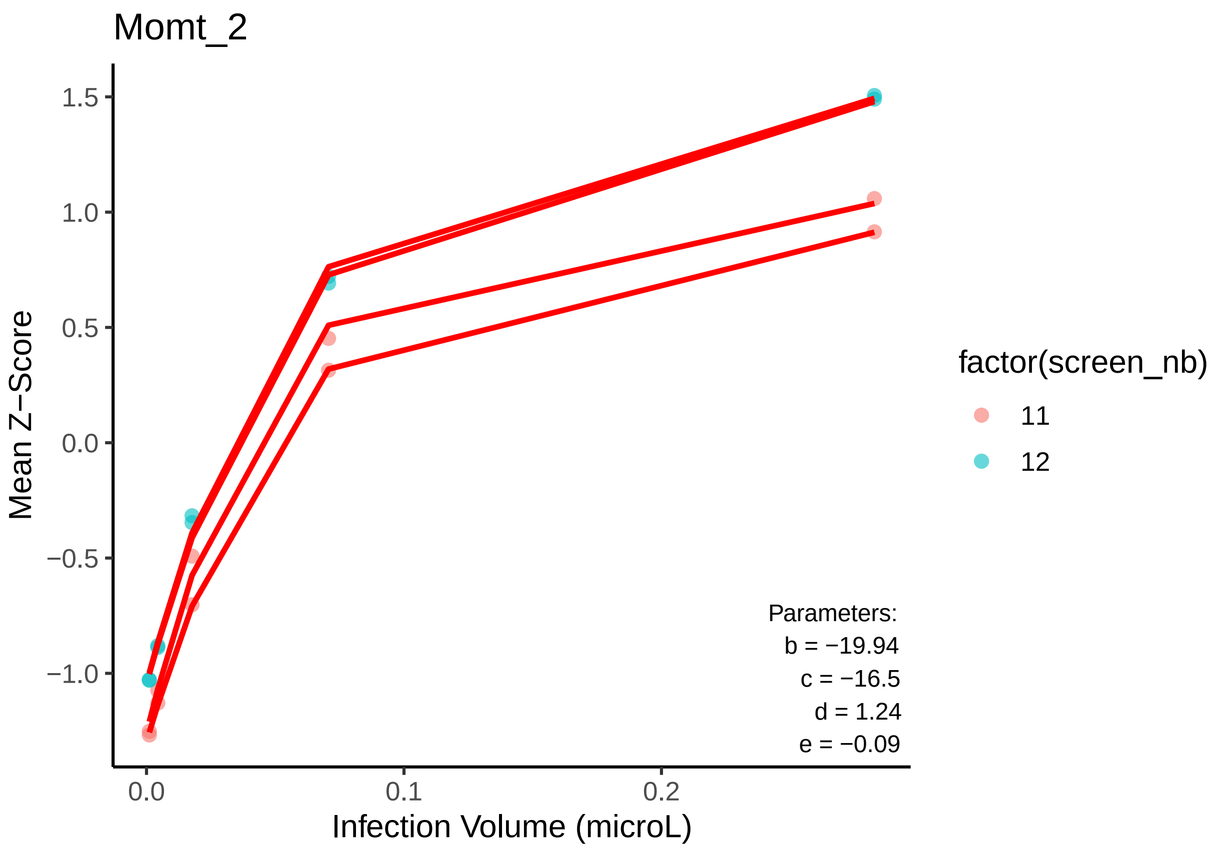
```
##
## $Melw_1
```


Melw_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −60.99
c = −10.87
d = 1.55
e = −0.03
factor(screen_nb)
11
12

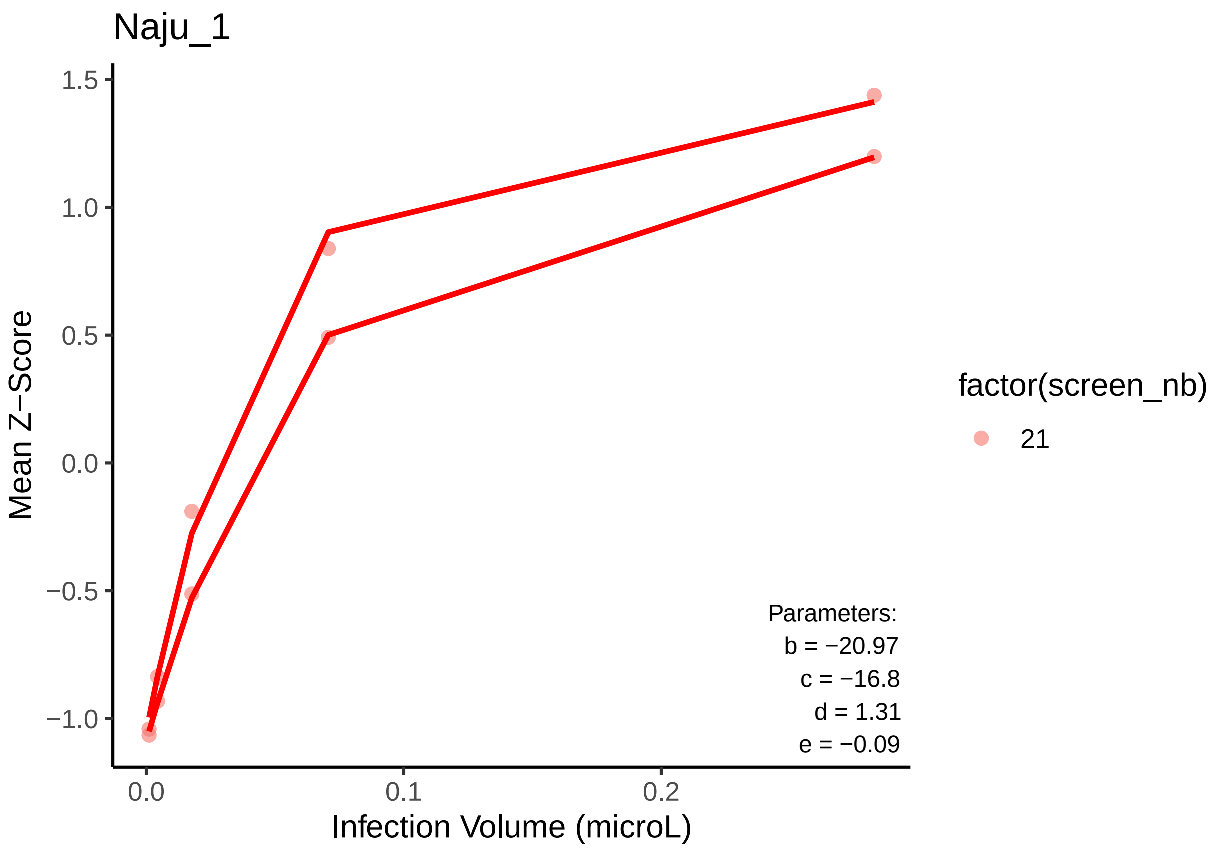
```
##
## $Miaj_6
```


Miaj_6
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
15
16
17
Parameters:
b = −70.98
c = −3.44
d = 0.63
e = −0.01

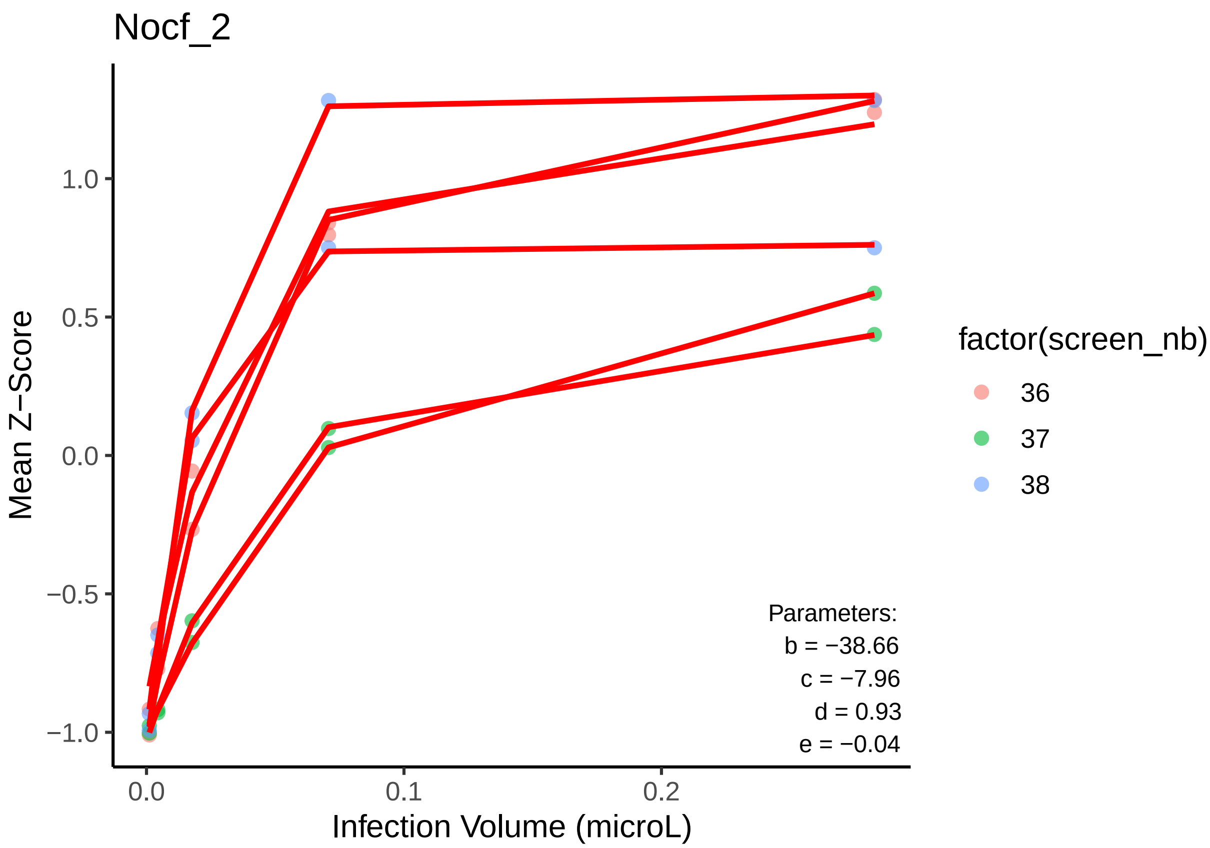
```
##
## $Momt_2
```


Momt_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −19.94
c = −16.5
d = 1.24
e = −0.09
factor(screen_nb)
11
12

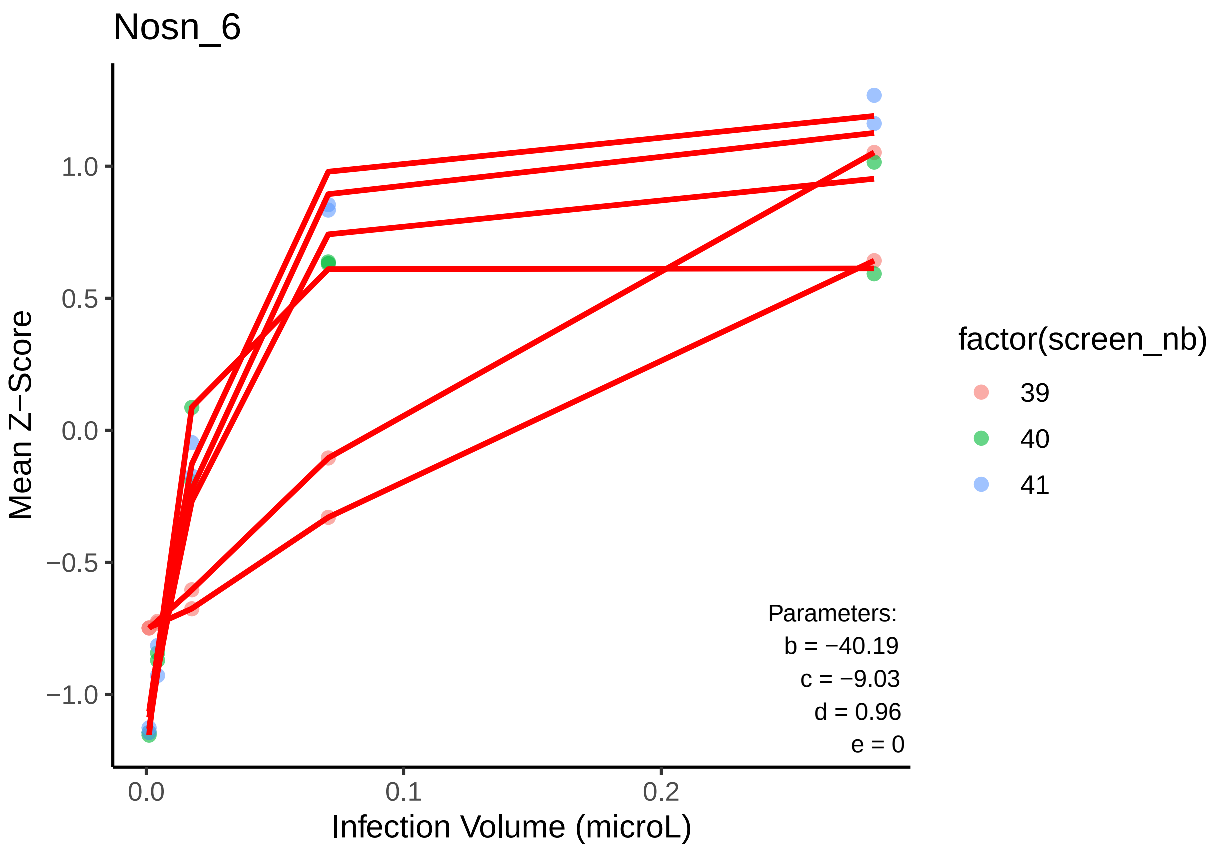
```
##
## $Naju_1
```


Naju_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −20.97
c = −16.8
d = 1.31
e = −0.09
factor(screen_nb)
21

```
##
## $Nocf_2
```

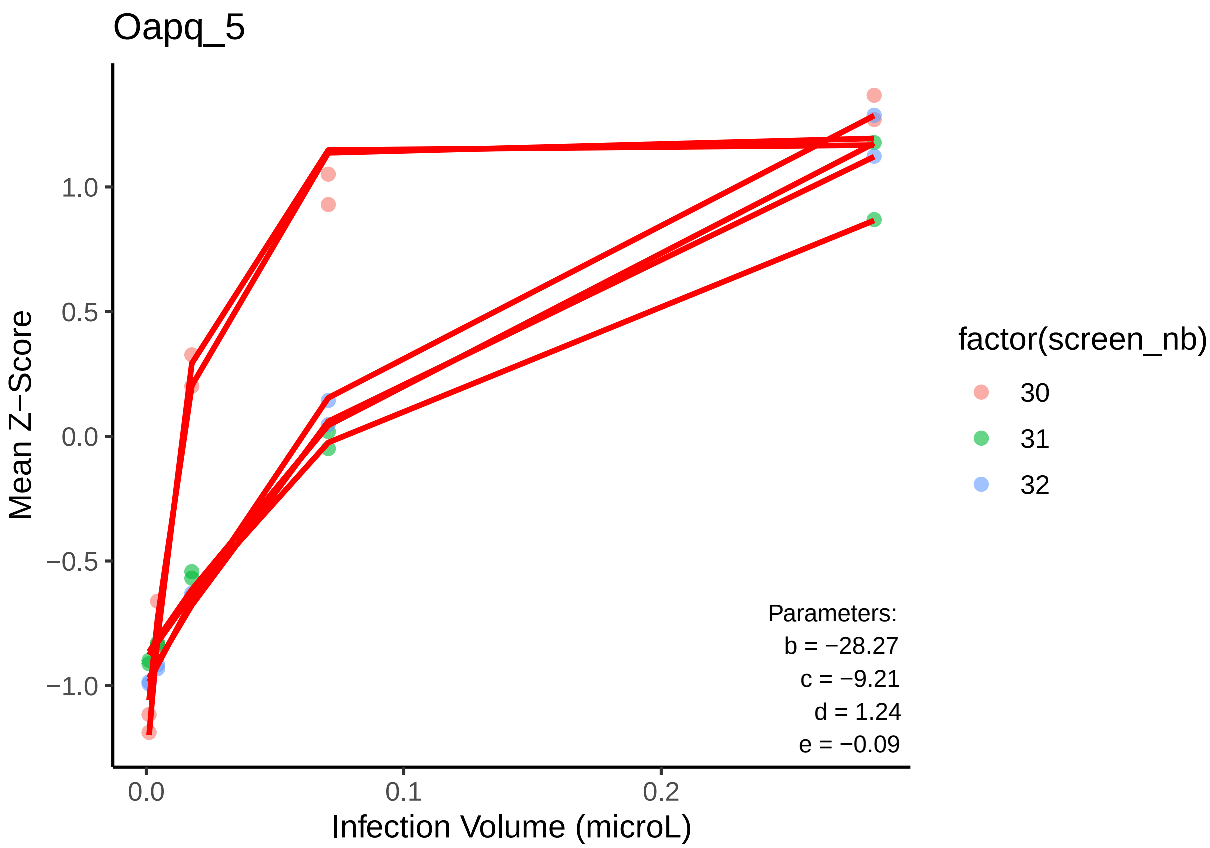

Nocf_2
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −38.66
c = −7.96
d = 0.93
e = −0.04
factor(screen_nb)
36
37
38

```
##
## $Nosn_6
```



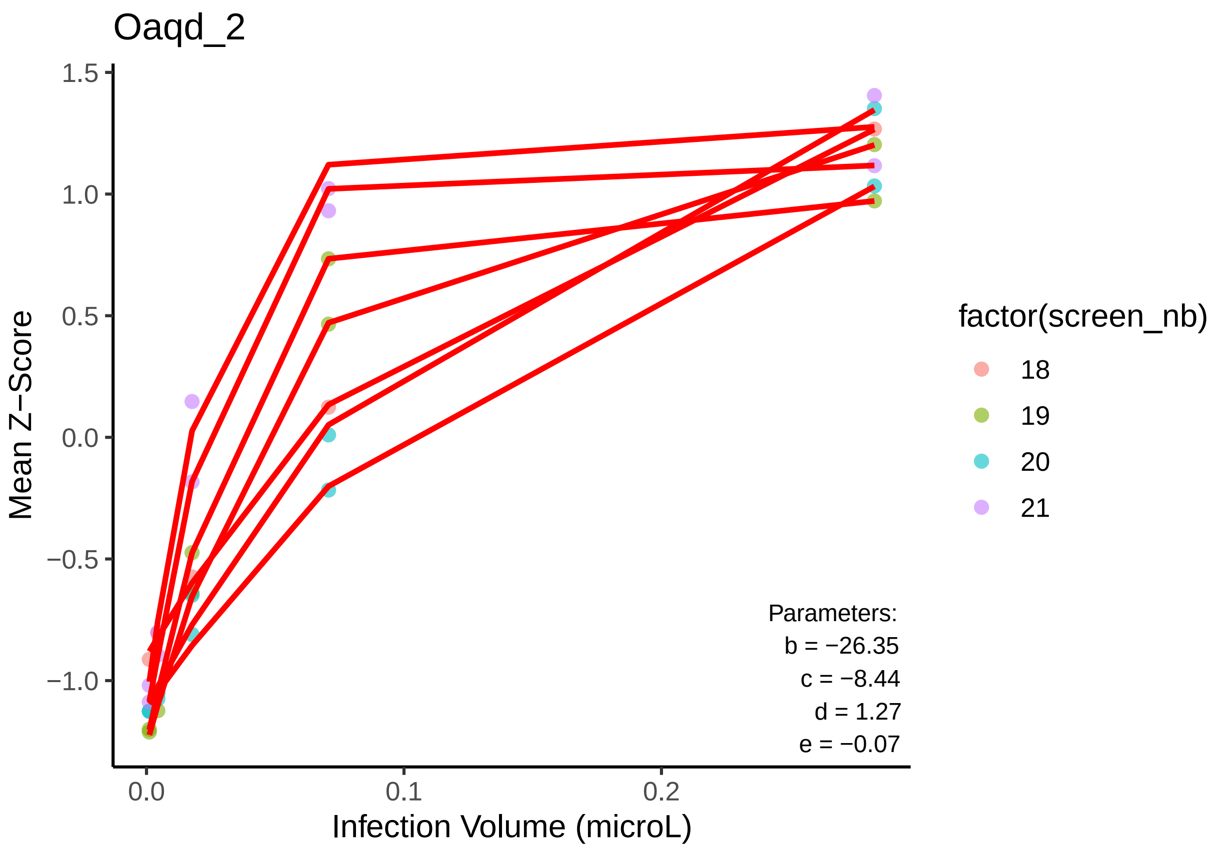
Nosn_6
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −40.19
c = −9.03
d = 0.96
e = 0
factor(screen_nb)
39
40
41


```
##
## $Oapq_5
```



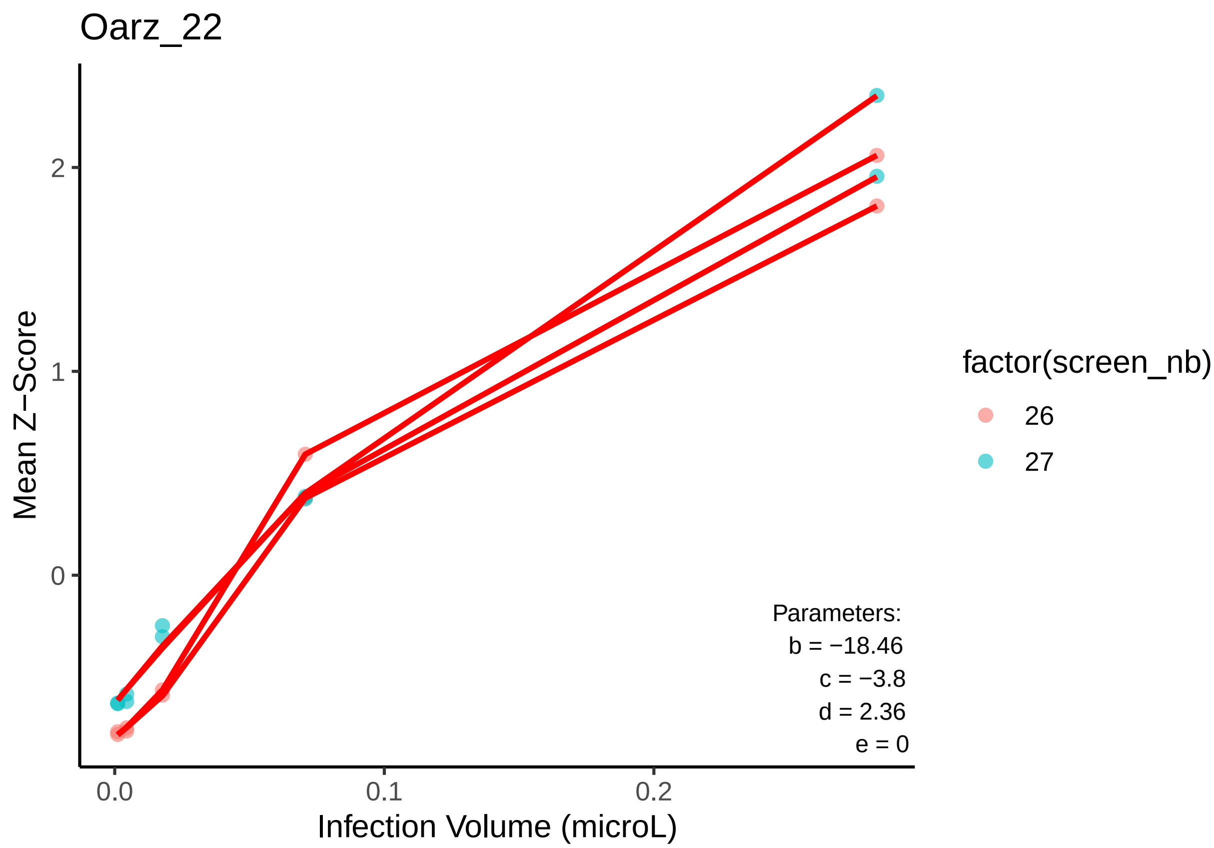
Oapq_5
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
30
31
32
Parameters:
b = −28.27
c = −9.21
d = 1.24
e = −0.09


```
##
## $Oaqd_2
```

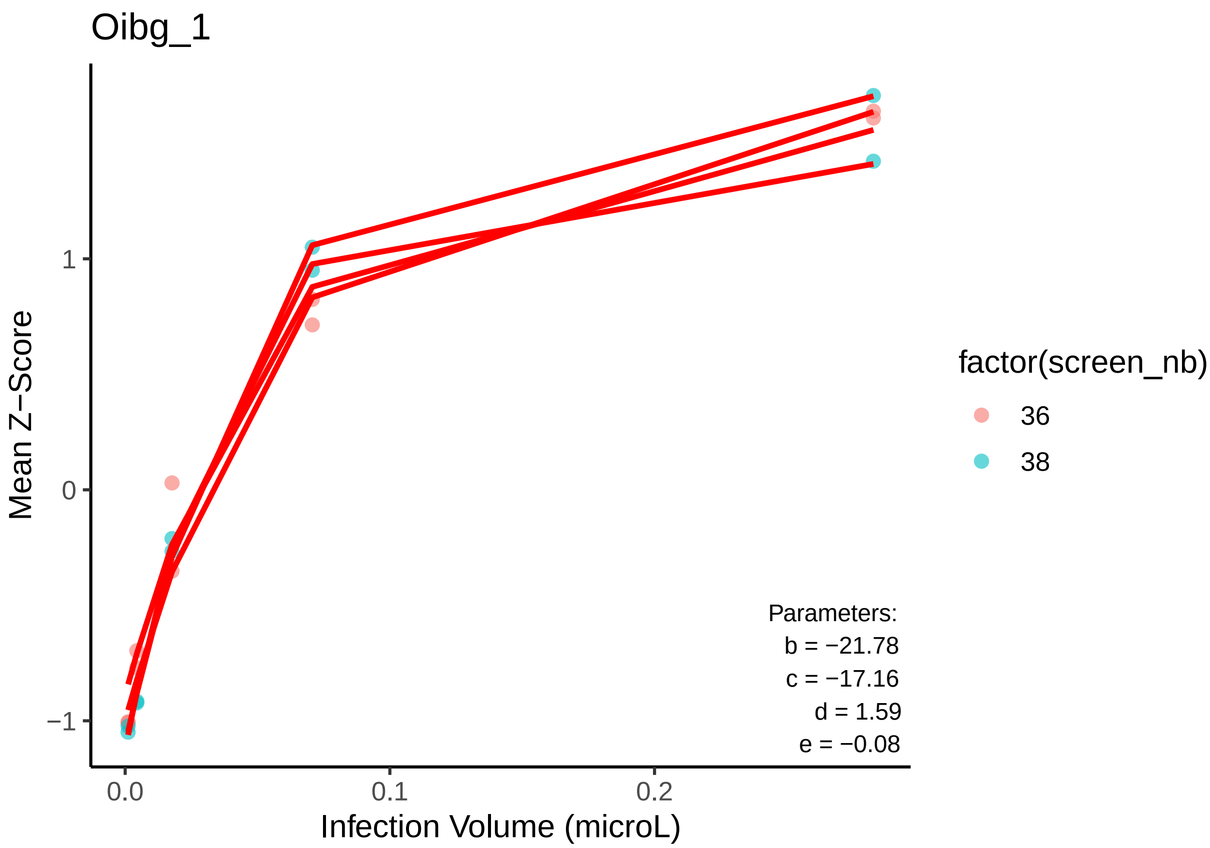


Oaqd_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −26.35
c = −8.44
d = 1.27
e = −0.07
factor(screen_nb)
18
19
20
21

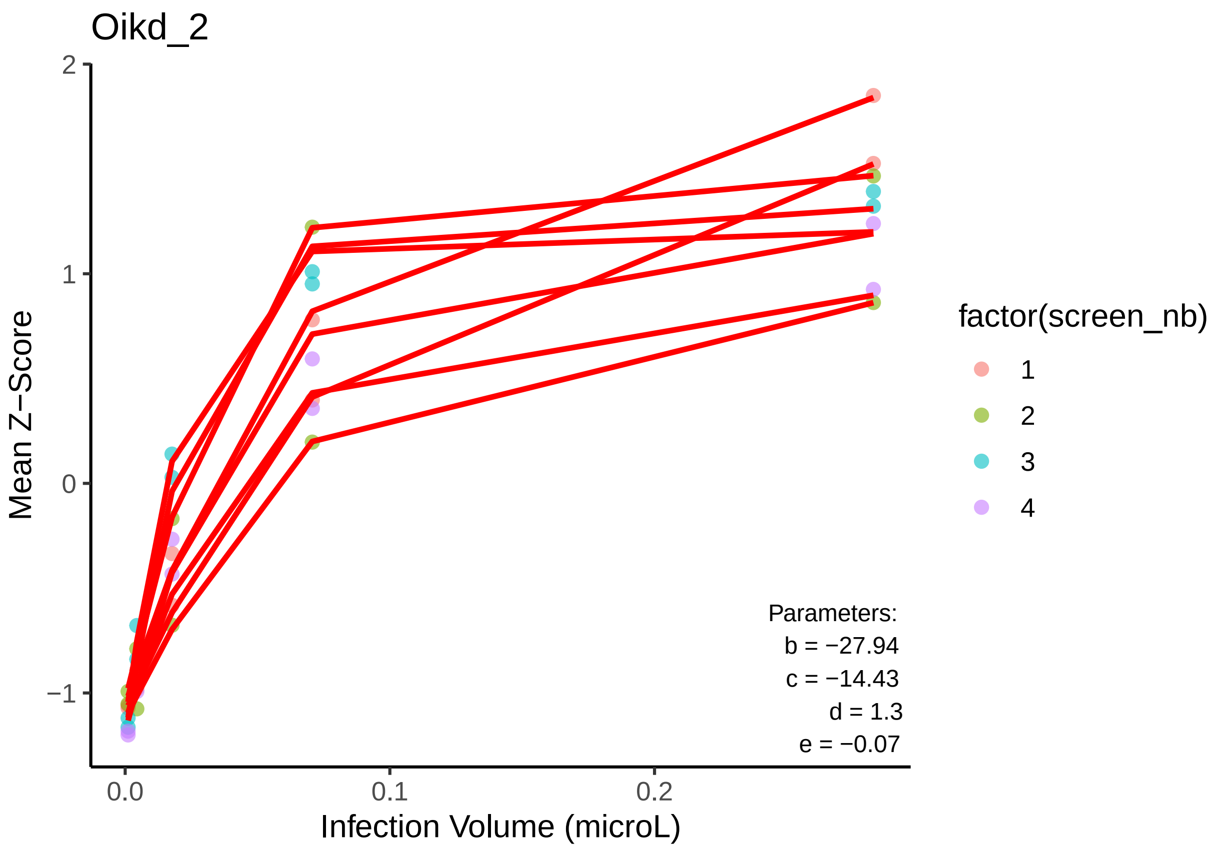

```
##
## $Oarz_22
```


Oarz_22
Mean Z−Score
2
1
0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −18.46
c = −3.8
d = 2.36
e = 0
factor(screen_nb)
26
27

```
##
## $Oibg_1
```

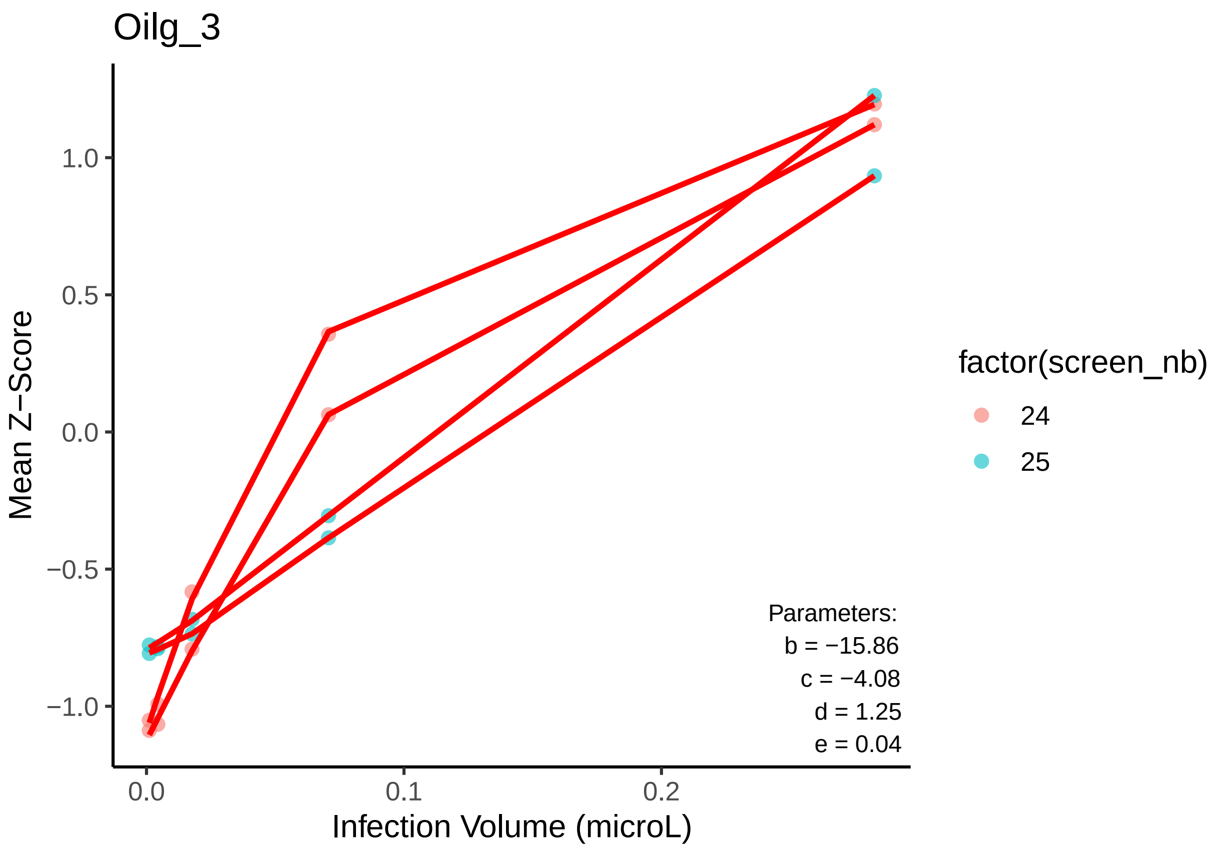

Oibg_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −21.78
c = −17.16
d = 1.59
e = −0.08
factor(screen_nb)
36
38

```
##
## $Oikd_2
```



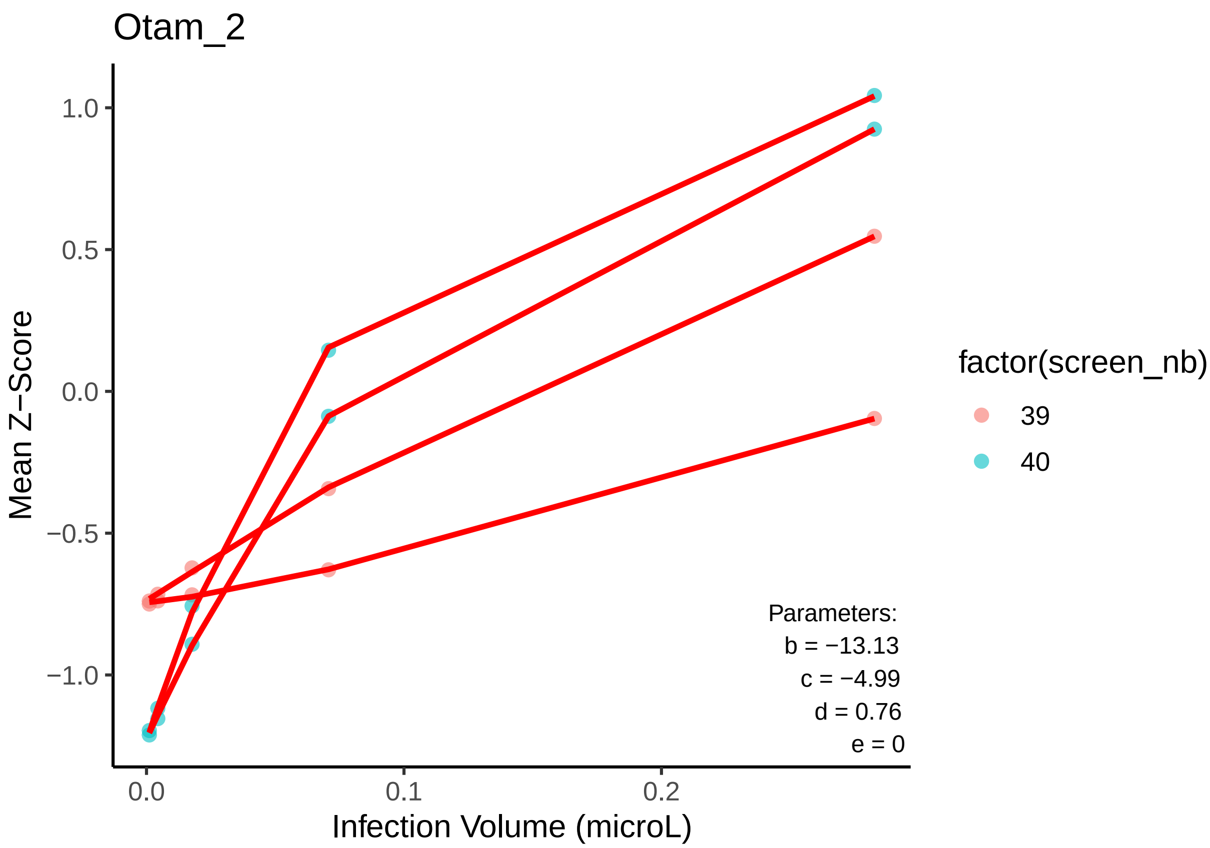
Oikd_2
Mean Z−Score
Infection Volume (microL)
2
1
0
−1
0.0
0.1
0.2
factor(screen_nb)
1
2
3
4
Parameters:
b = −27.94
c = −14.43
d = 1.3
e = −0.07


```
##
## $Oilg_3
```

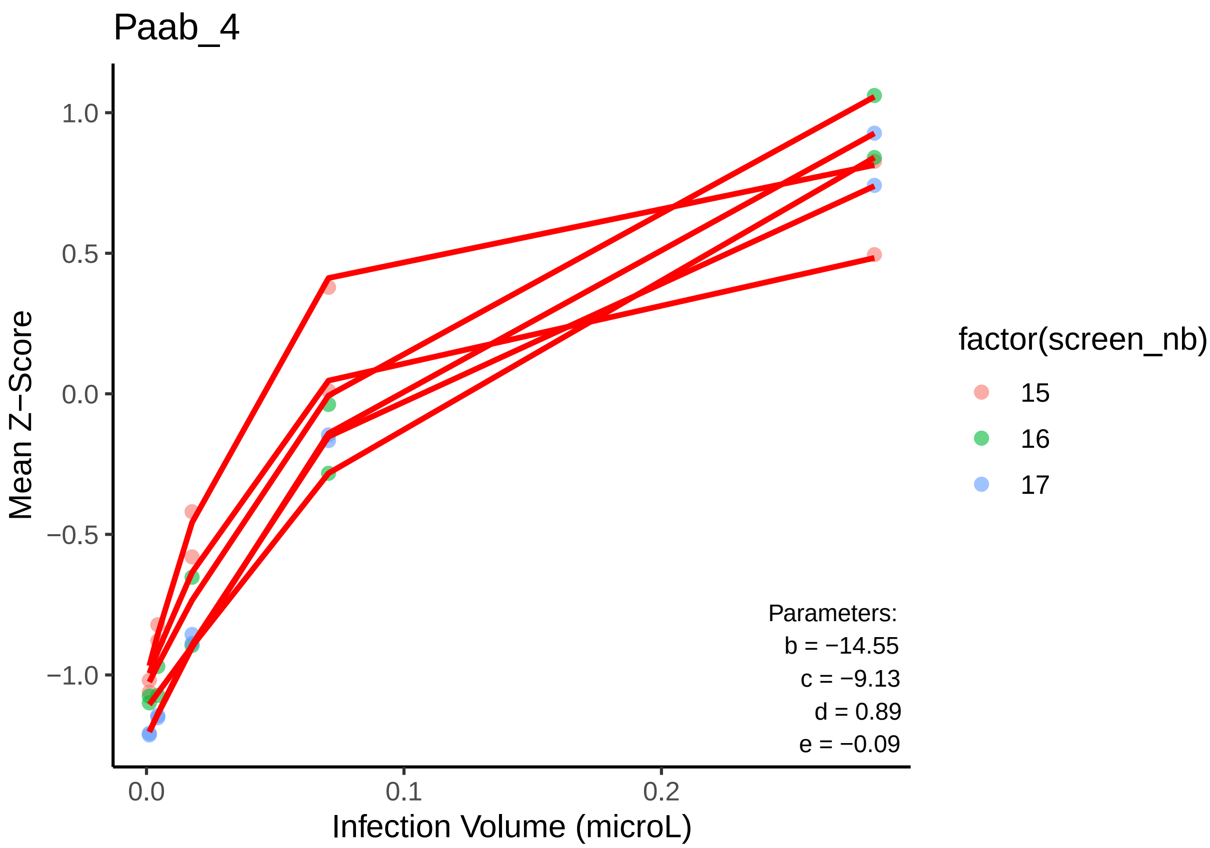


Oilg_3
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −15.86
c = −4.08
d = 1.25
e = 0.04
factor(screen_nb)
24
25

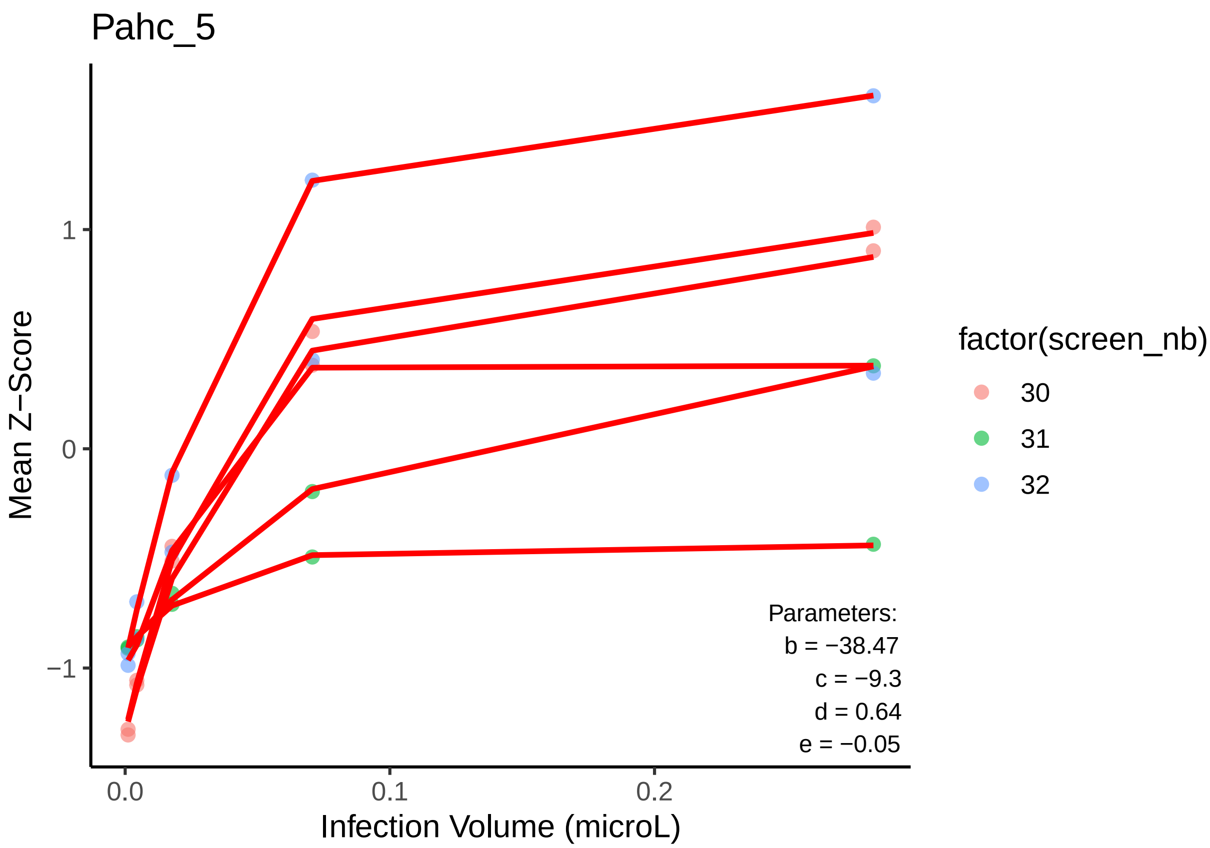

```
##
## $Otam_2
```


Otam_2
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
39
40
Parameters:
b = −13.13
c = −4.99
d = 0.76
e = 0

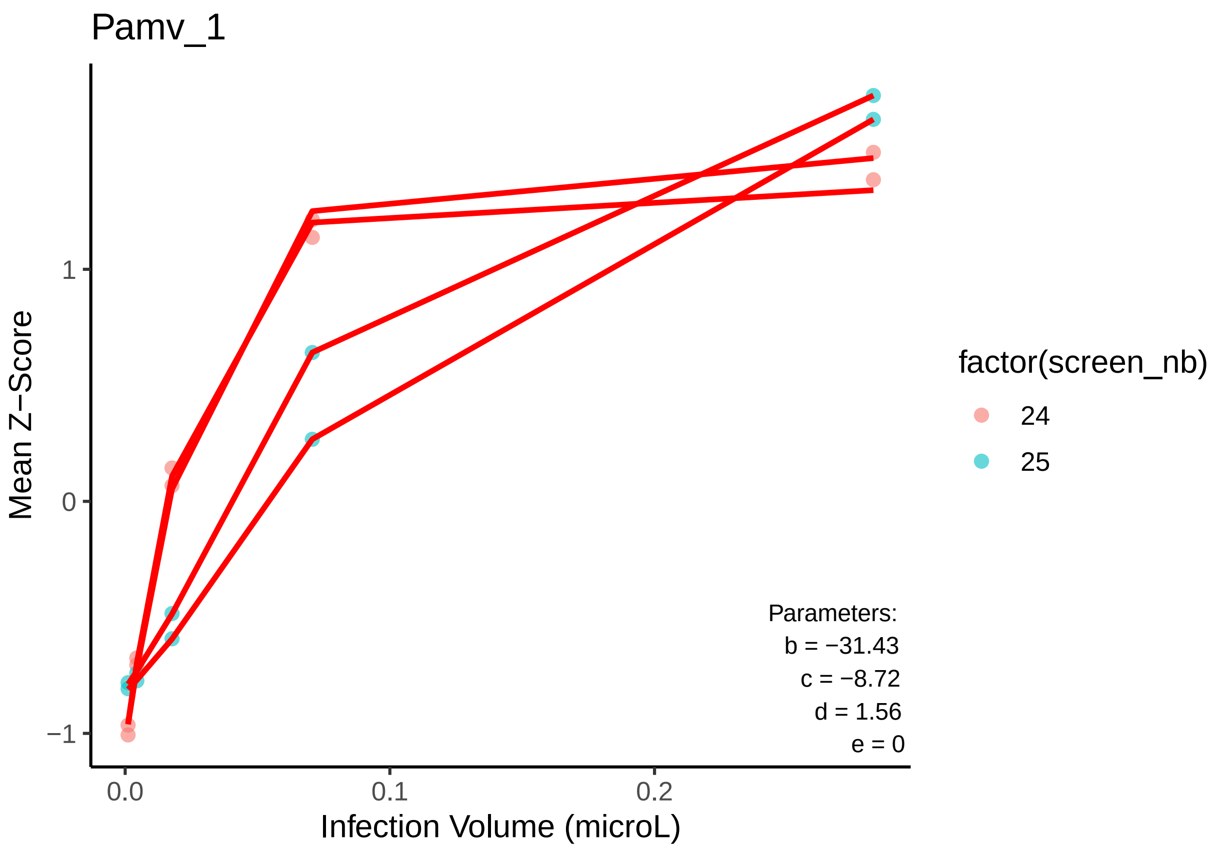
```
##
## $Paab_4
```


Paab_4
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
Parameters:
b = −14.55
c = −9.13
d = 0.89
e = −0.09
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
15
16
17

```
##
## $Pahc_5
```

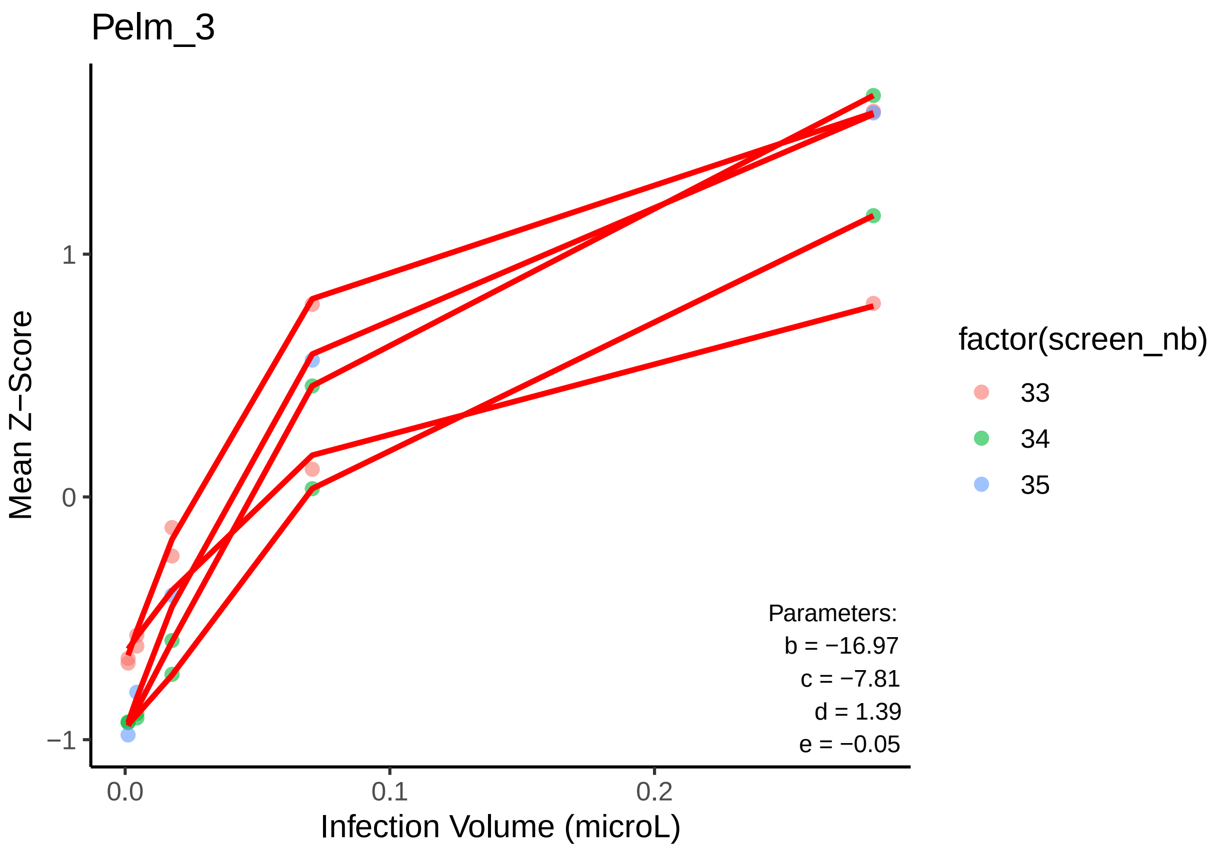

Pahc_5
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −38.47
c = −9.3
d = 0.64
e = −0.05
factor(screen_nb)
30
31
32

```
##
## $Pamv_1
```



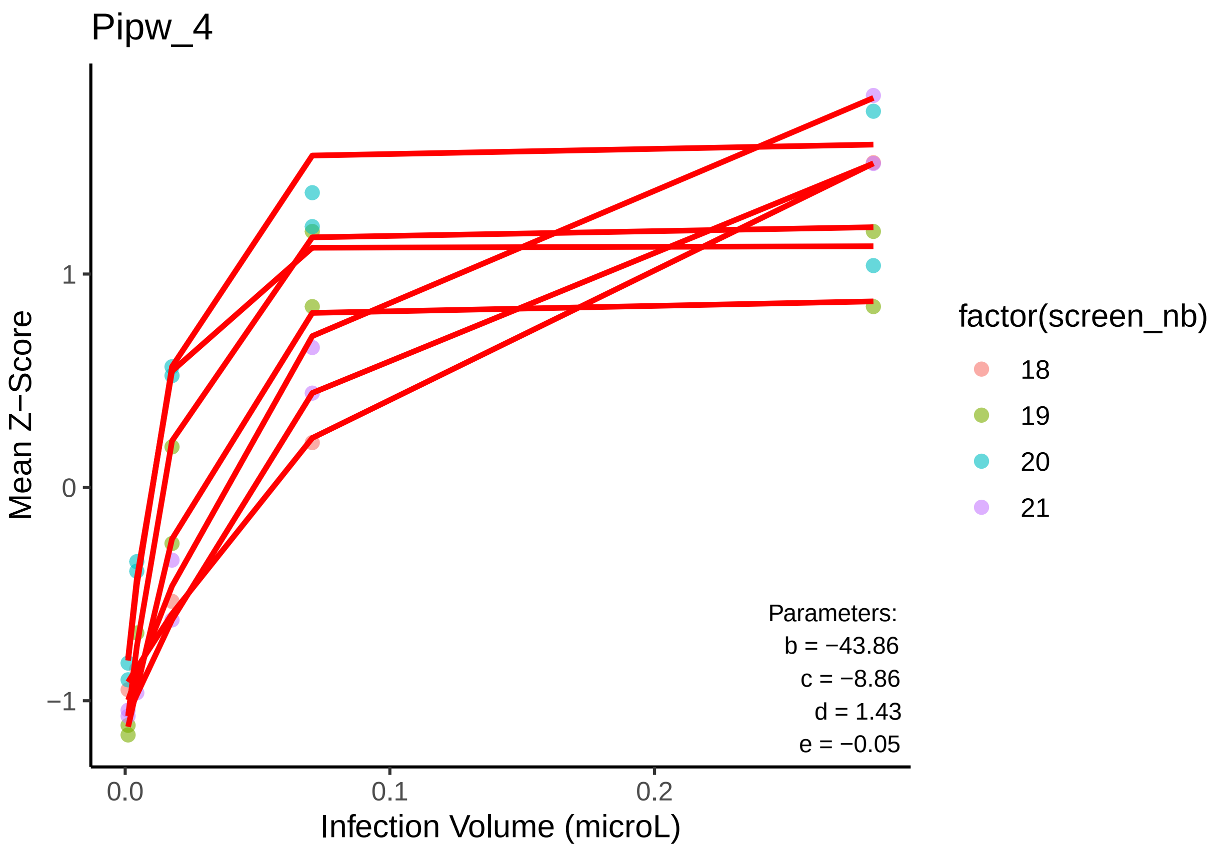
Pamv_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
24
25
Parameters:
b = −31.43
c = −8.72
d = 1.56
e = 0


```
##
## $Pelm_3
```

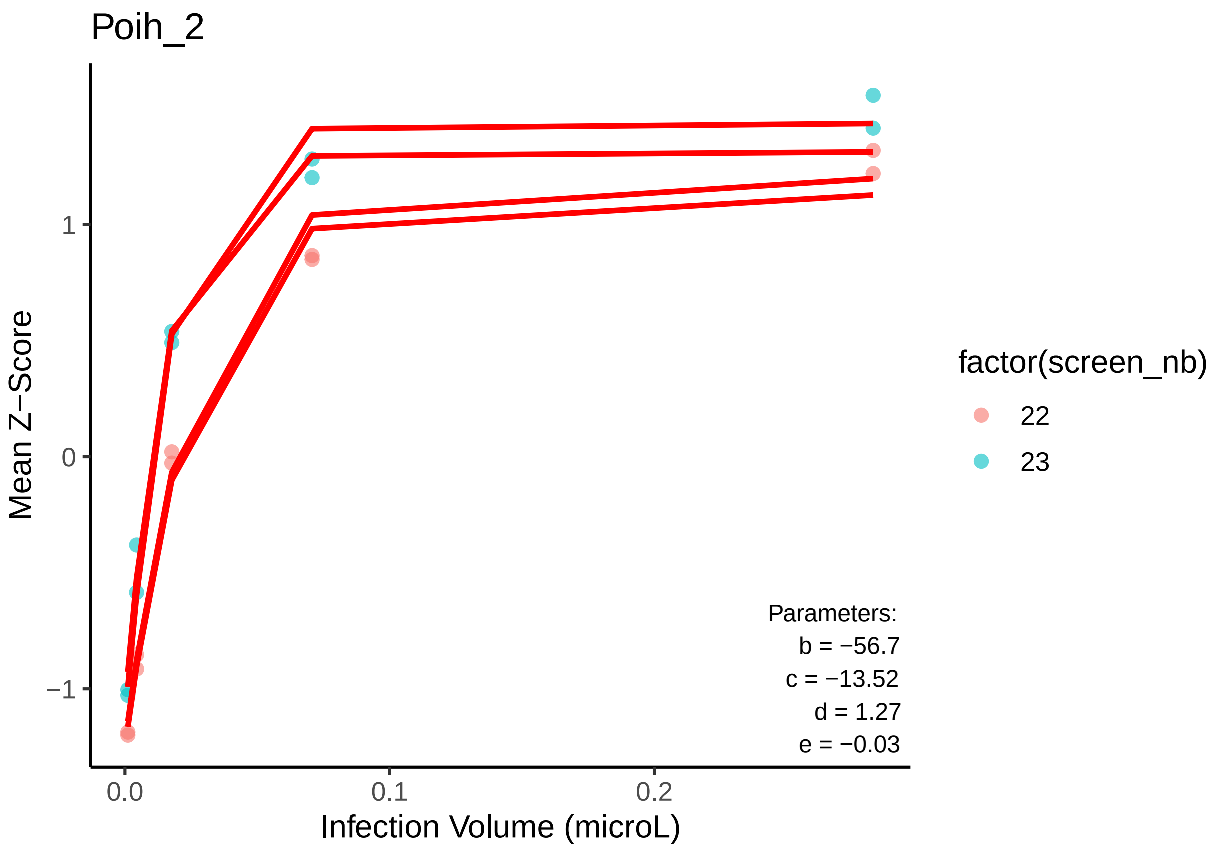


Pelm_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
33
34
35
Parameters:
b = −16.97
c = −7.81
d = 1.39
e = −0.05


```
##
## $Pipw_4
```

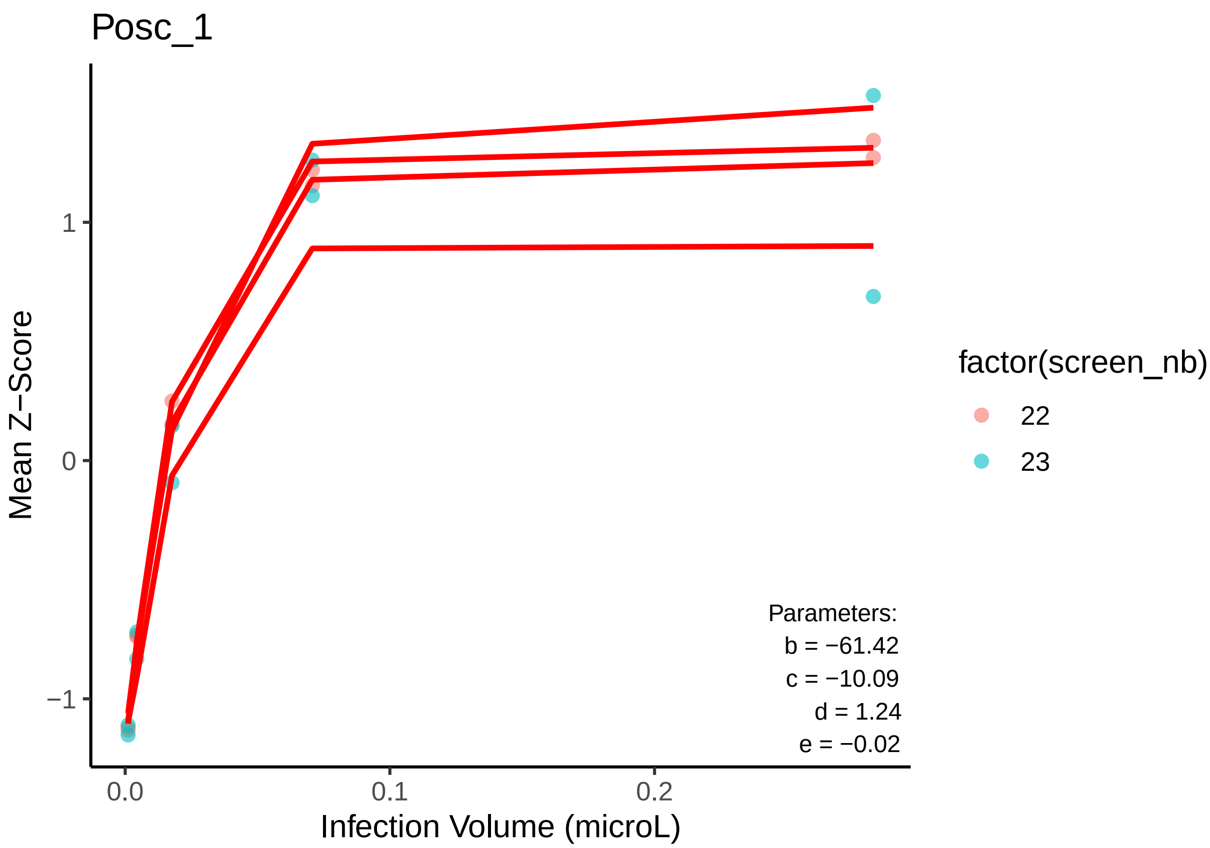

Pipw_4
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
18
19
20
21
Parameters:
b = −43.86
c = −8.86
d = 1.43
e = −0.05

```
##
## $Poih_2
```

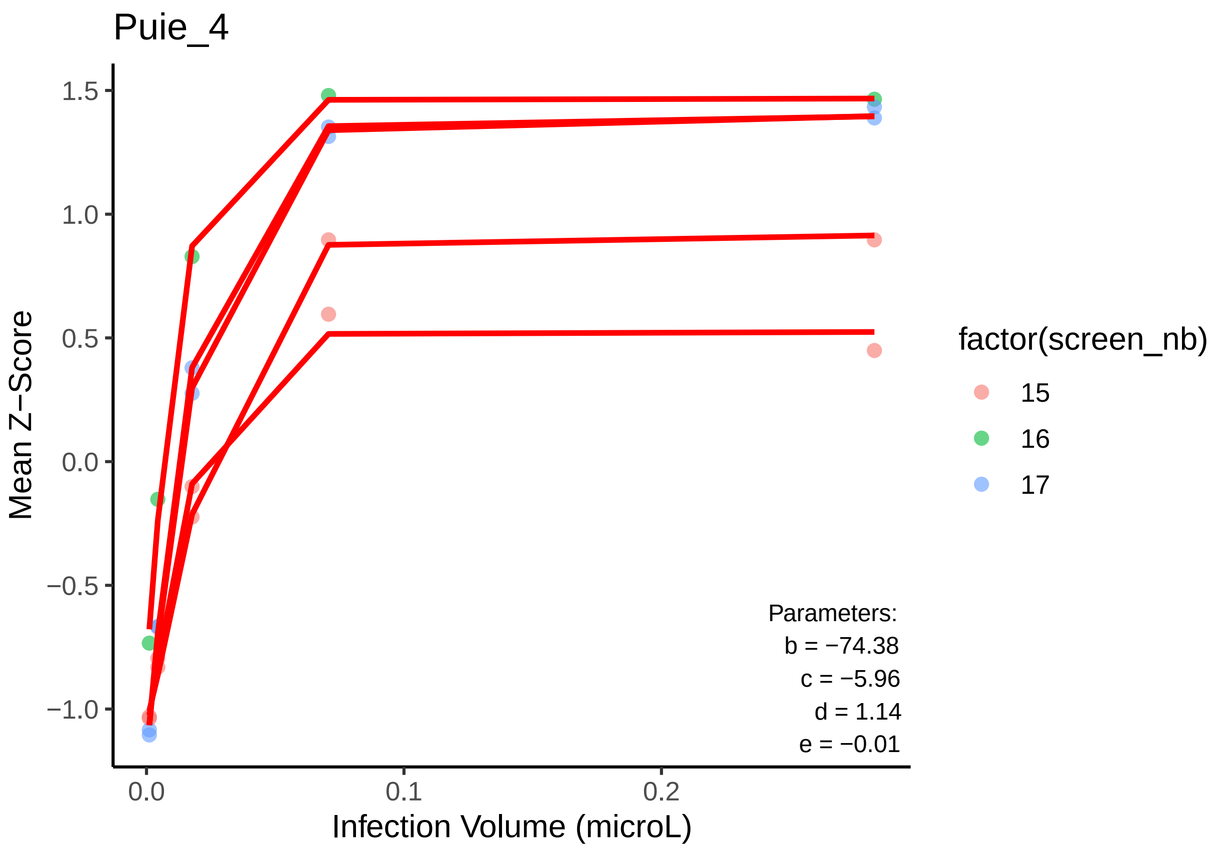


Poih_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −56.7
c = −13.52
d = 1.27
e = −0.03
factor(screen_nb)
22
23

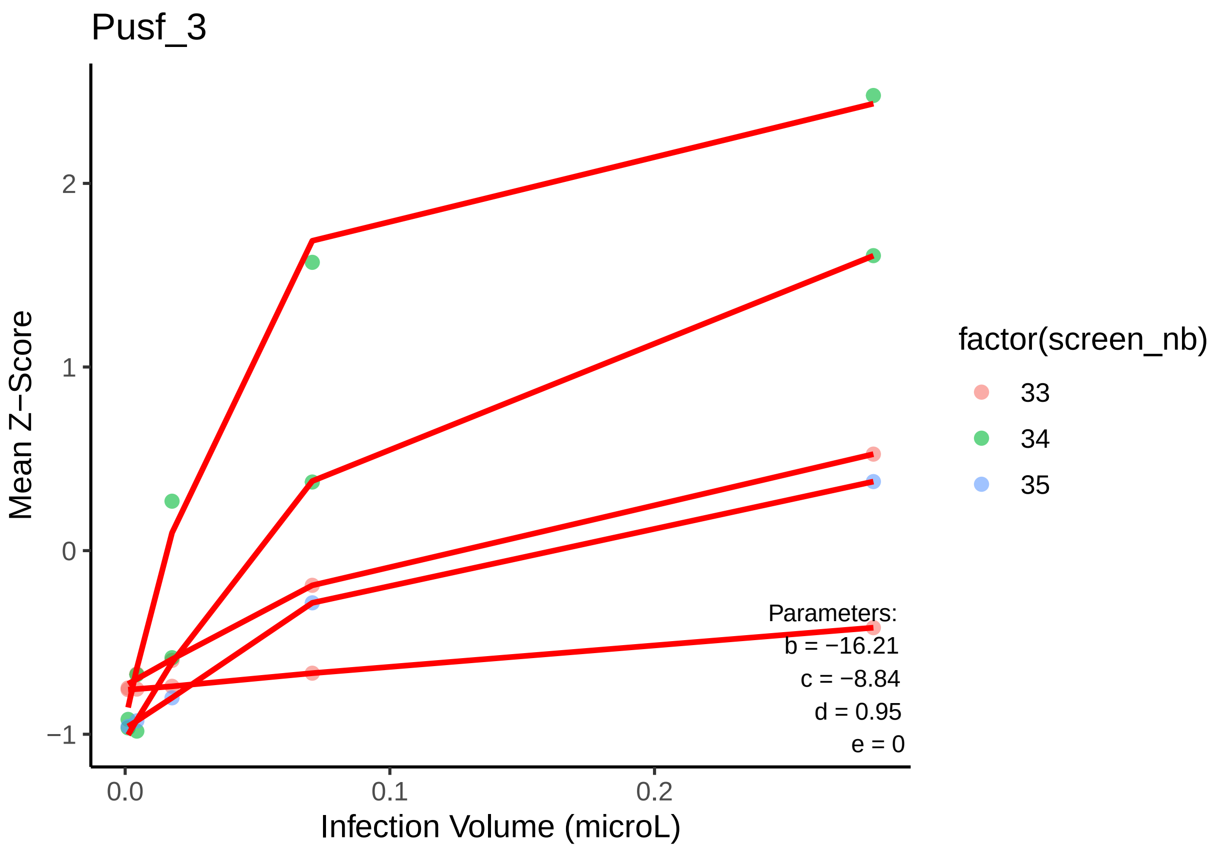

```
##
## $Posc_1
```


Posc_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
22
23
Parameters:
b = −61.42
c = −10.09
d = 1.24
e = −0.02

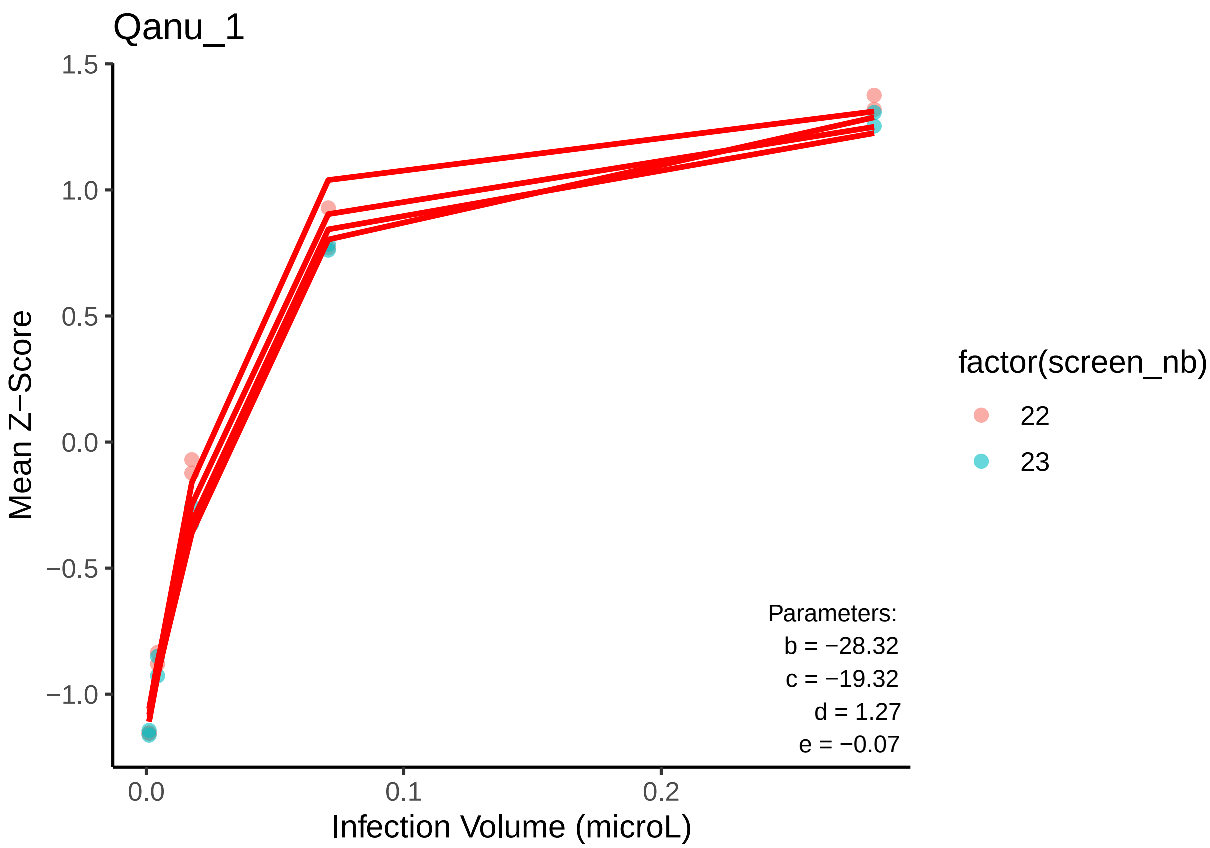
```
##
## $Puie_4
```


Puie_4
1.5
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −74.38
c = −5.96
d = 1.14
e = −0.01
factor(screen_nb)
15
16
17

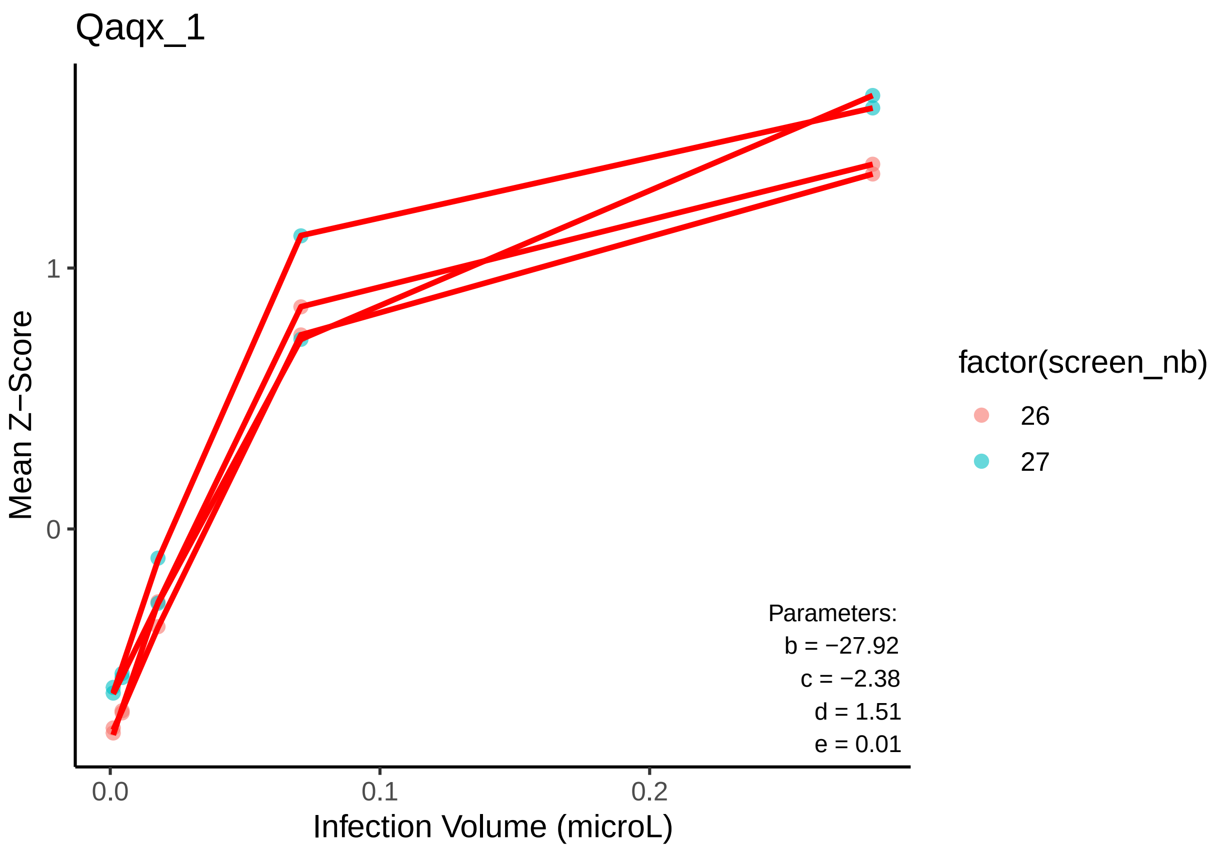
```
##
## $Pusf_3
```


Pusf_3
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
33
34
35
Parameters:
b = −16.21
c = −8.84
d = 0.95
e = 0

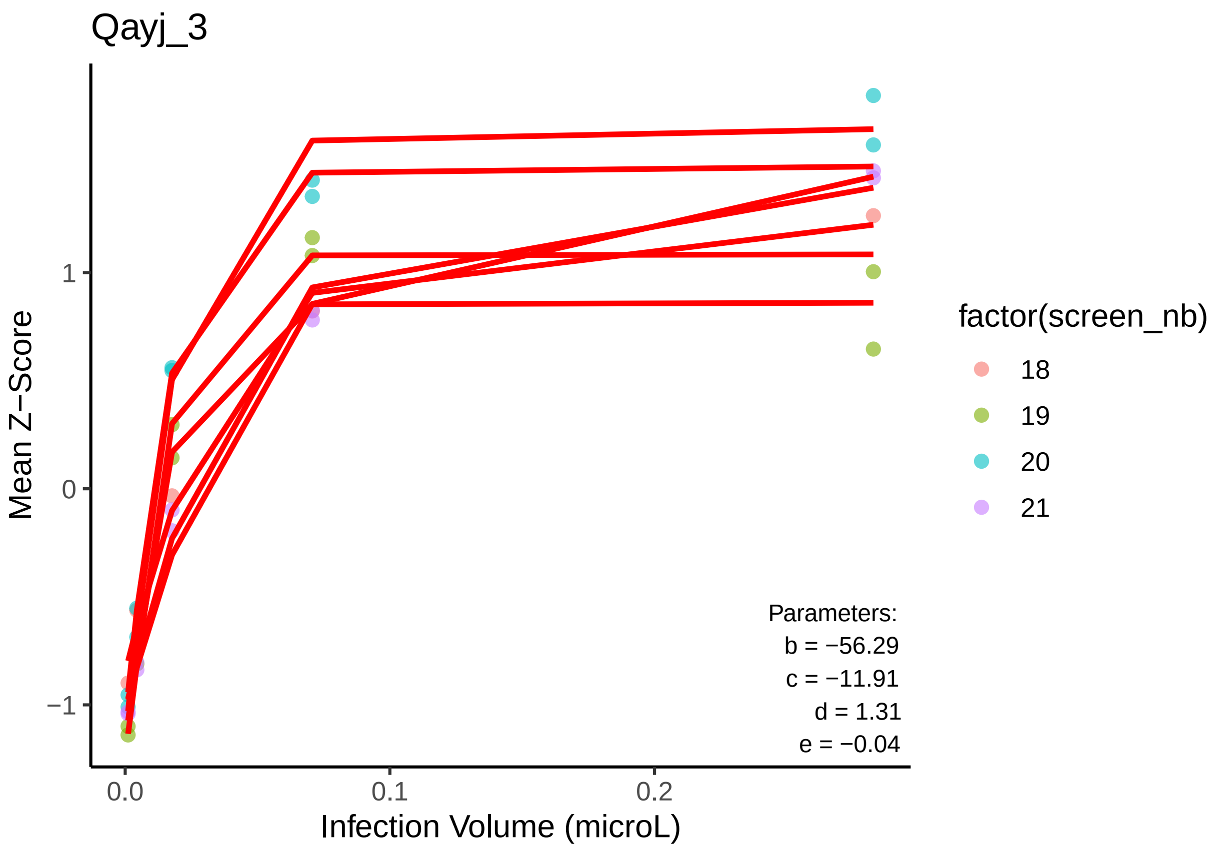
```
##
## $Qanu_1
```


Qanu_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −28.32
c = −19.32
d = 1.27
e = −0.07
factor(screen_nb)
22
23

```
##
## $Qaqx_1
```

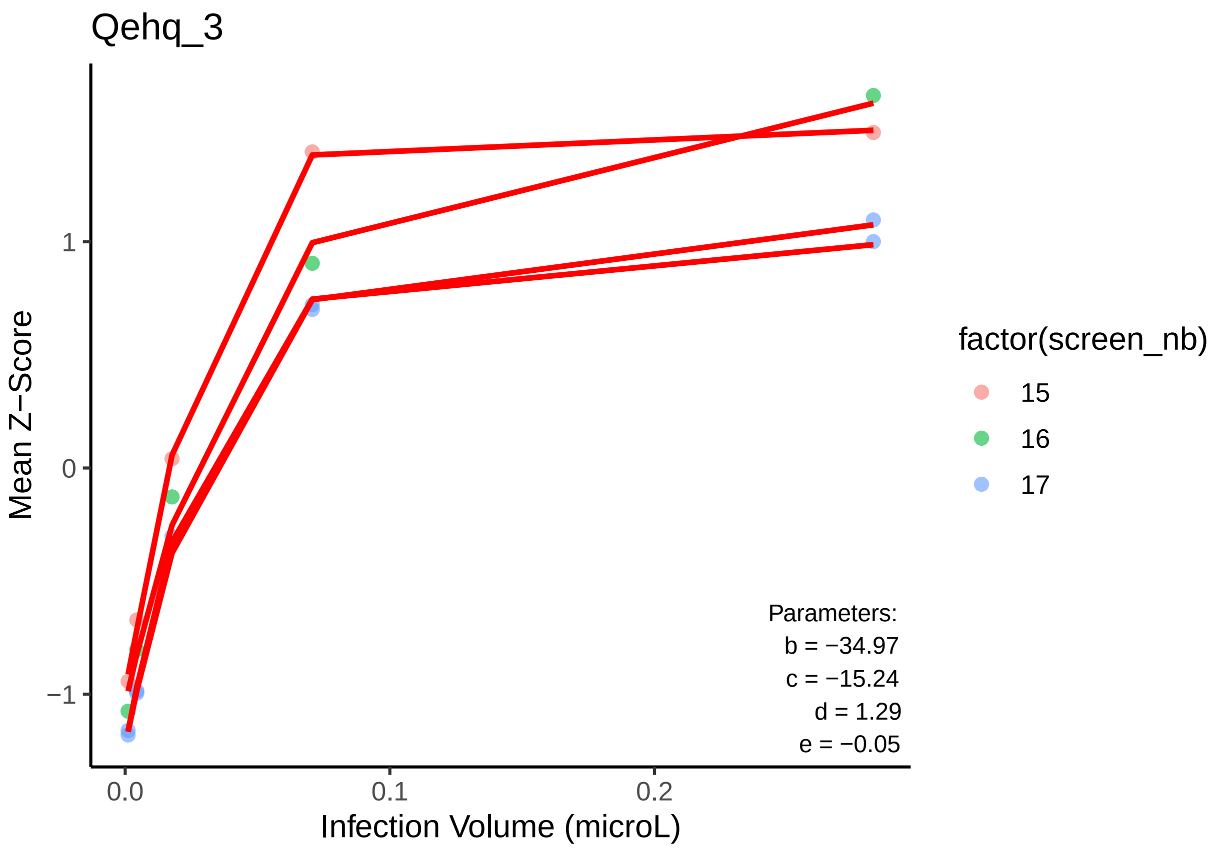

Qaqx_1
Mean Z−Score
1
0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −27.92
c = −2.38
d = 1.51
e = 0.01
factor(screen_nb)
26
27

```
##
## $Qayj_3
```

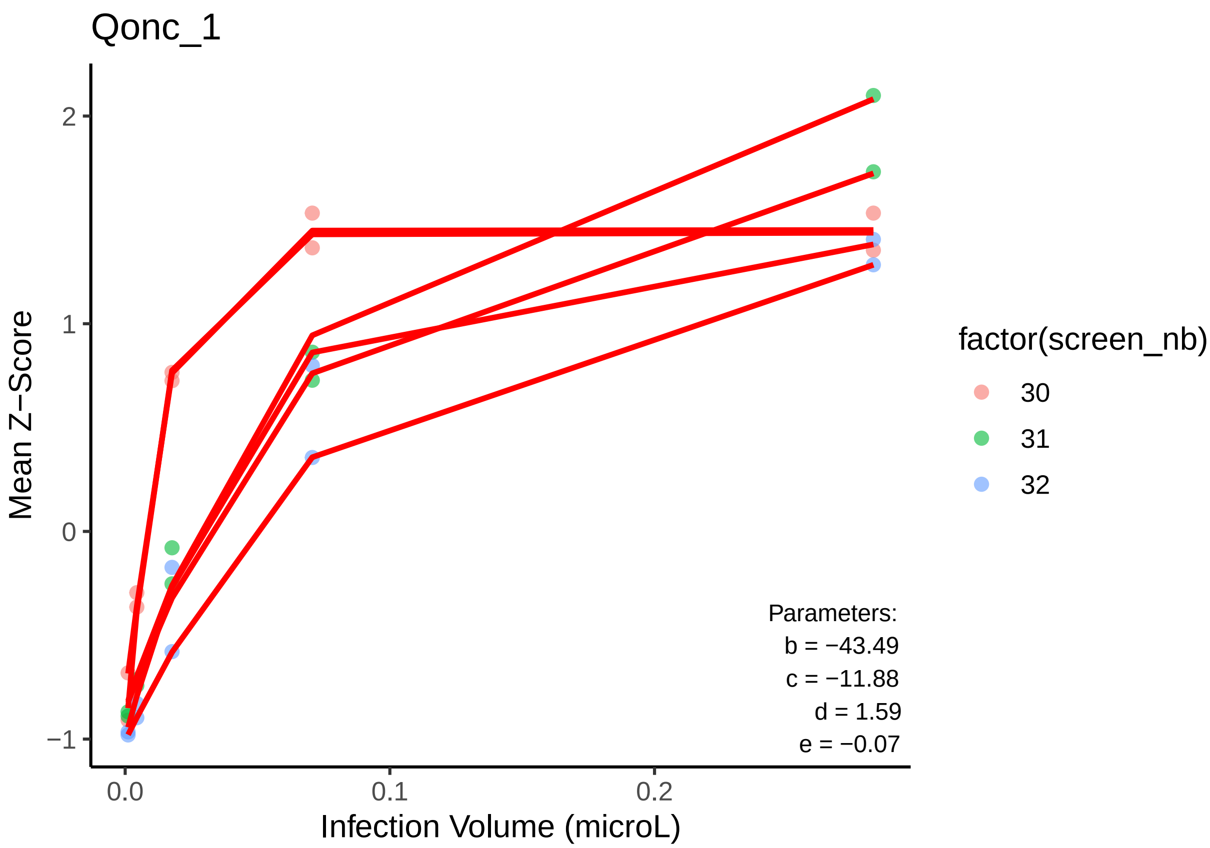


Qayj_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
18
19
20
21
Parameters:
b = −56.29
c = −11.91
d = 1.31
e = −0.04

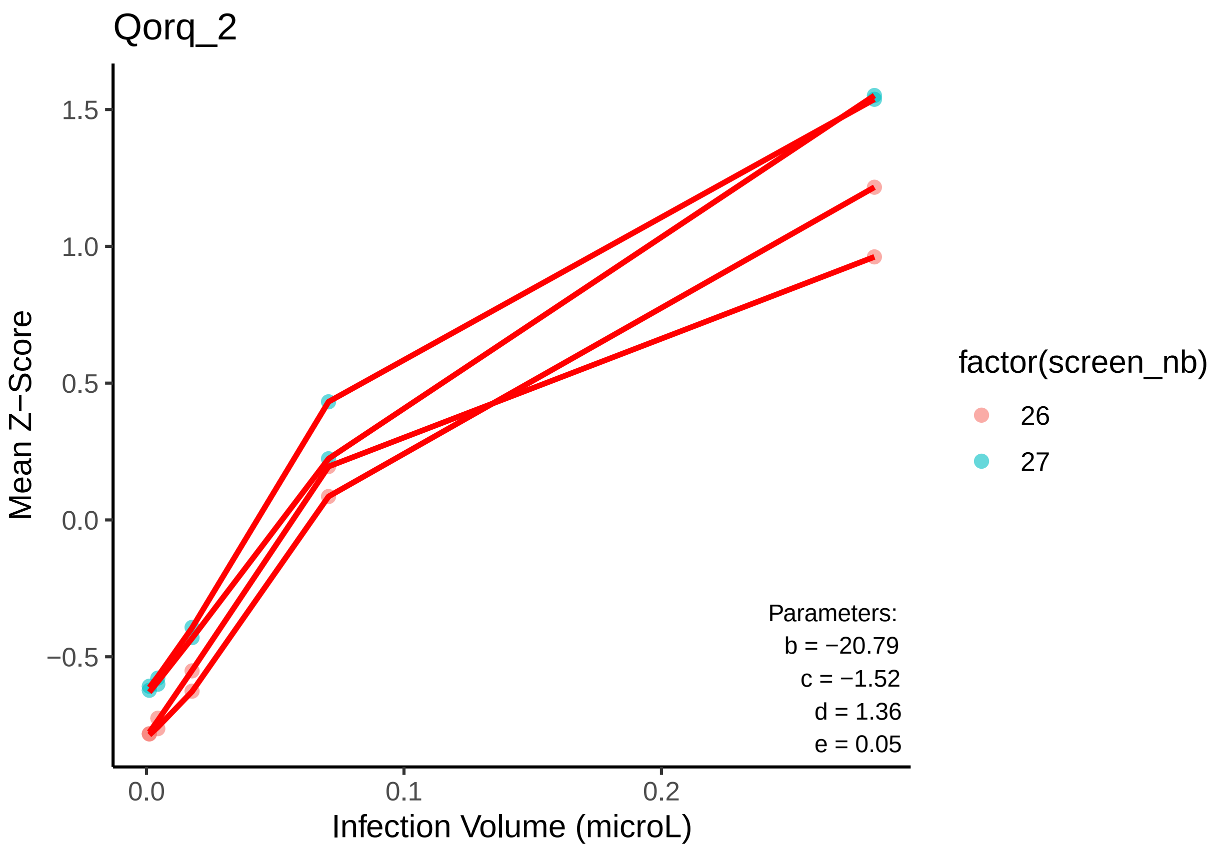

```
##
## $Qehq_3
```


Qehq_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −34.97
c = −15.24
d = 1.29
e = −0.05
factor(screen_nb)
15
16
17

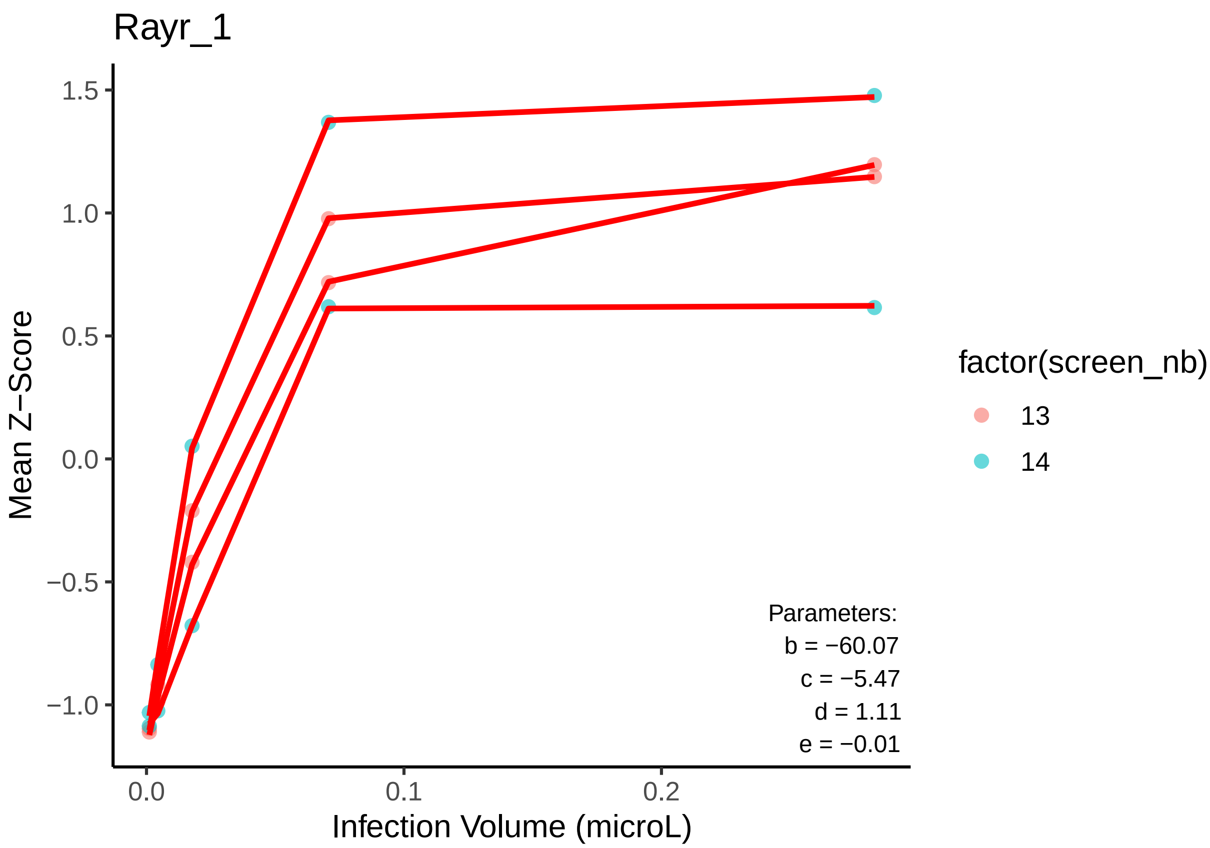
```
##
## $Qonc_1
```


Qonc_1
2
1
0
−1
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −43.49
c = −11.88
d = 1.59
e = −0.07
factor(screen_nb)
30
31
32

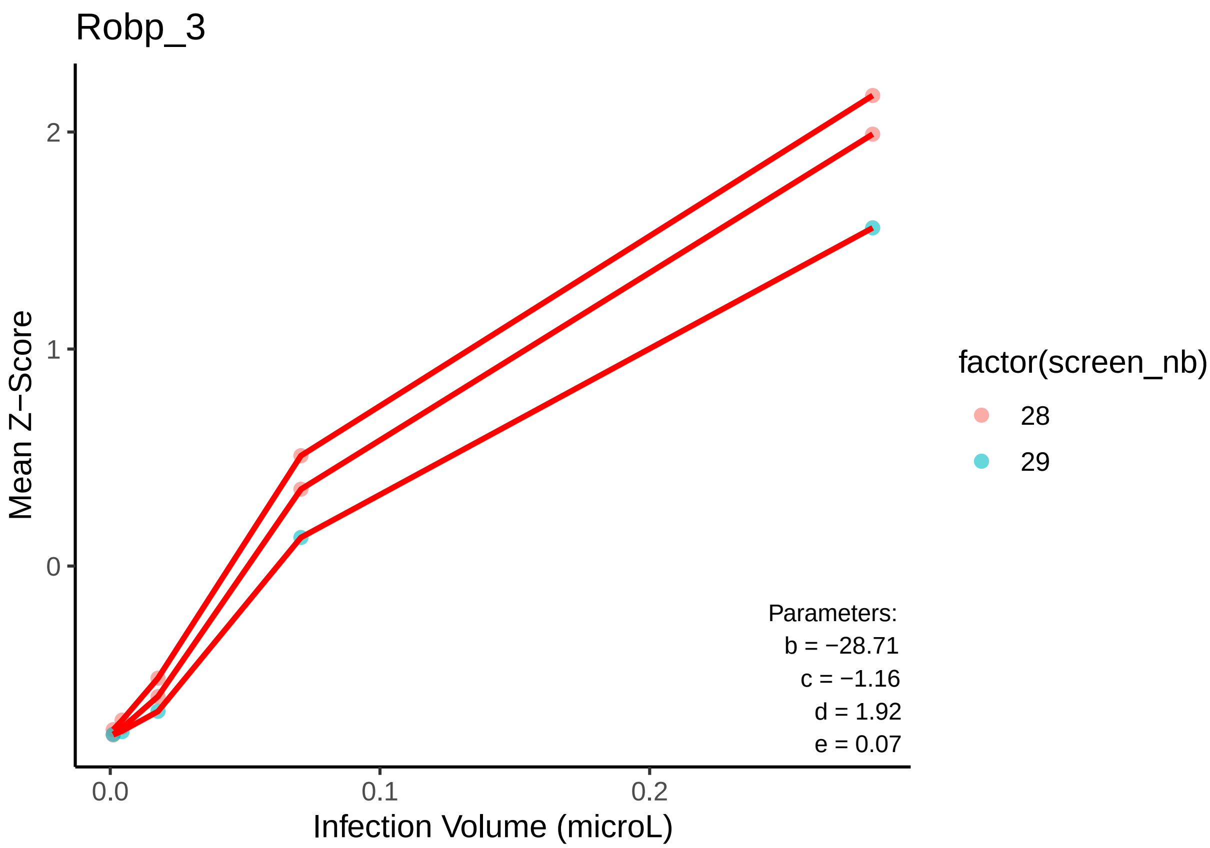
```
##
## $Qorq_2
```


Qorq_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −20.79
c = −1.52
d = 1.36
e = 0.05
factor(screen_nb)
26
27

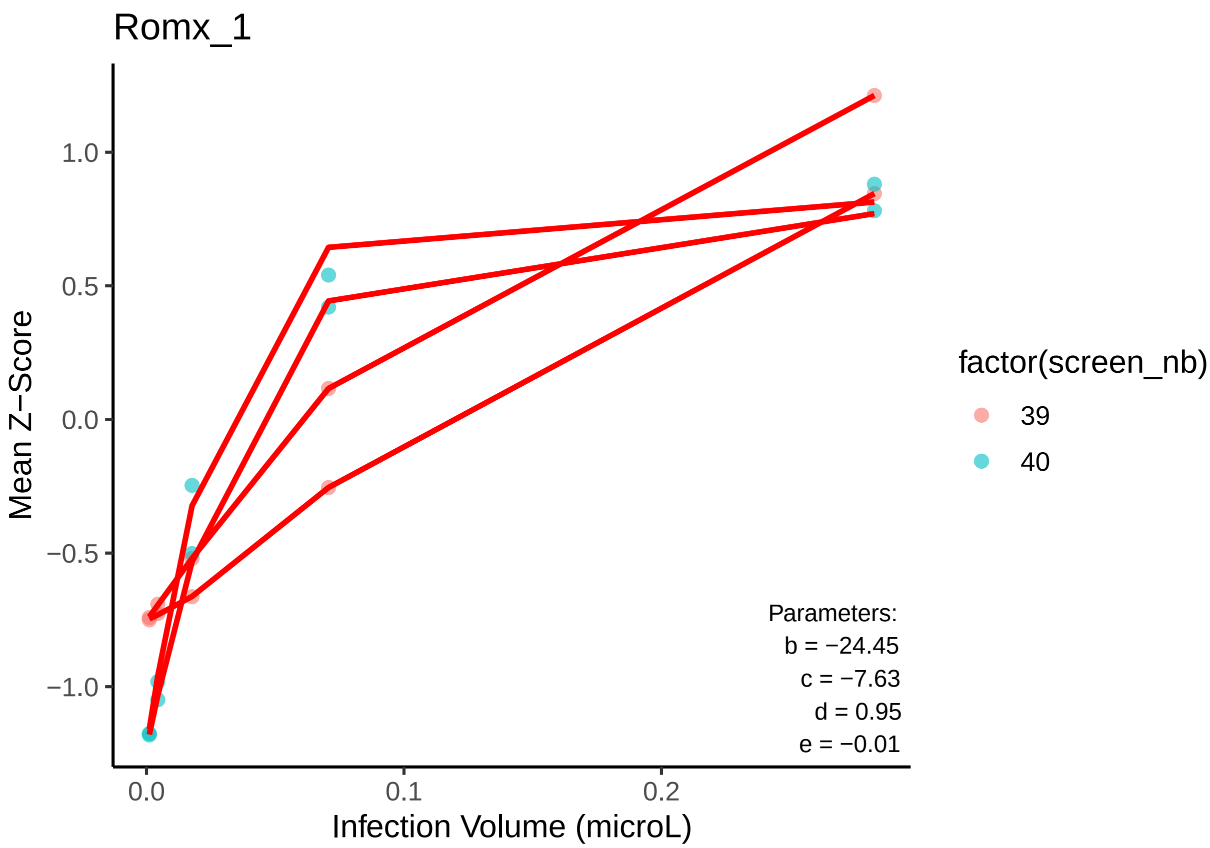
```
##
## $Rayr_1
```


Rayr_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −60.07
c = −5.47
d = 1.11
e = −0.01
factor(screen_nb)
13
14

```
##
## $Robp_3
```

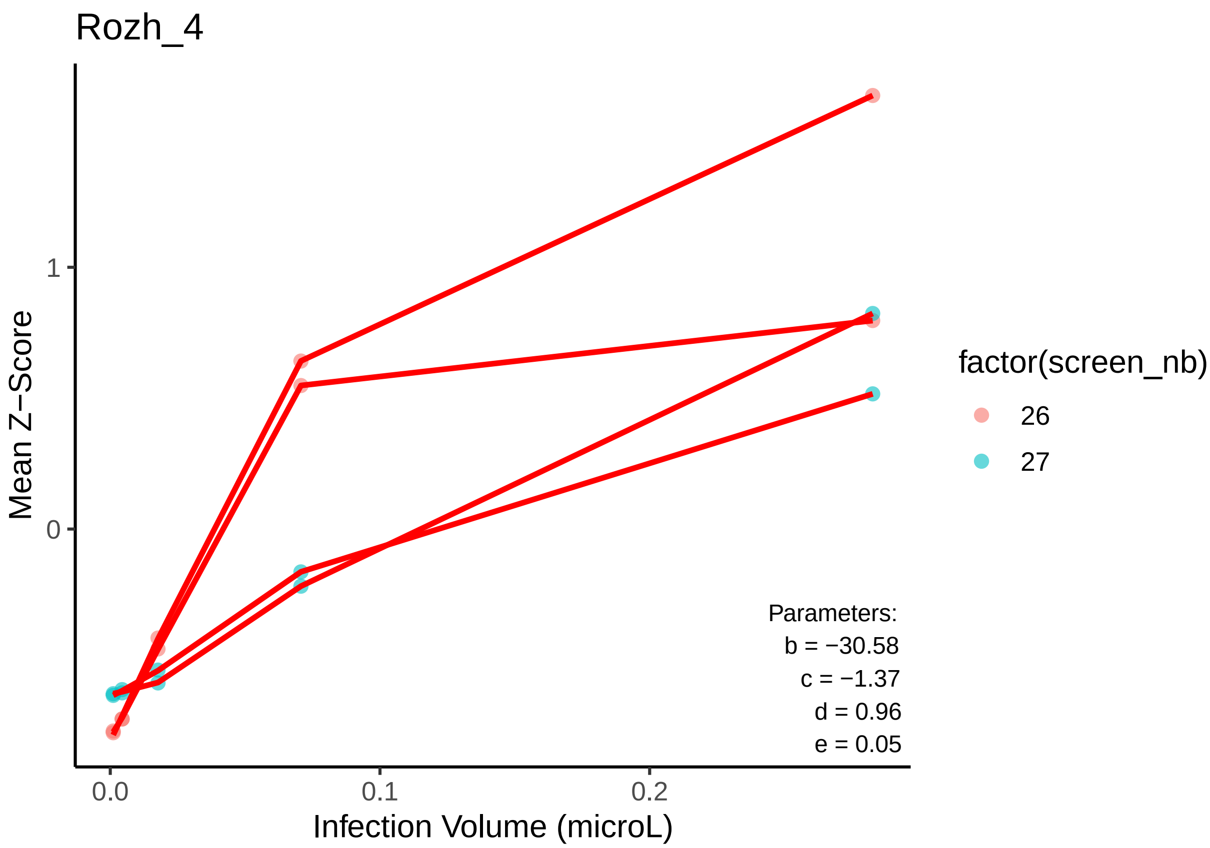

Robp_3
Mean Z−Score
2
1
0
factor(screen_nb)
28
29
Parameters:
b = −28.71
c = −1.16
d = 1.92
e = 0.07
0.0
0.1
0.2
Infection Volume (microL)

```
##
## $Romx_1
```

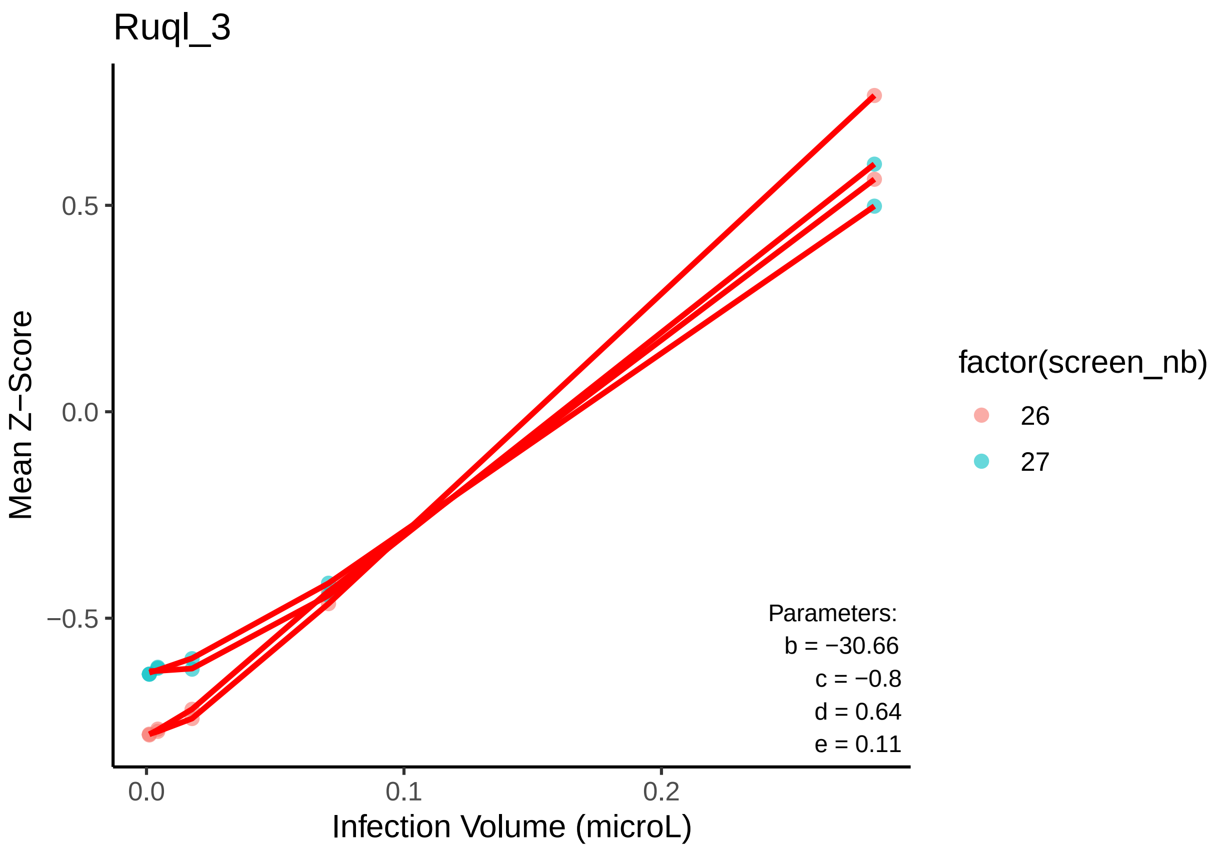


Romx_1
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −24.45
c = −7.63
d = 0.95
e = −0.01
factor(screen_nb)
39
40


```
##
## $Rozh_4
```

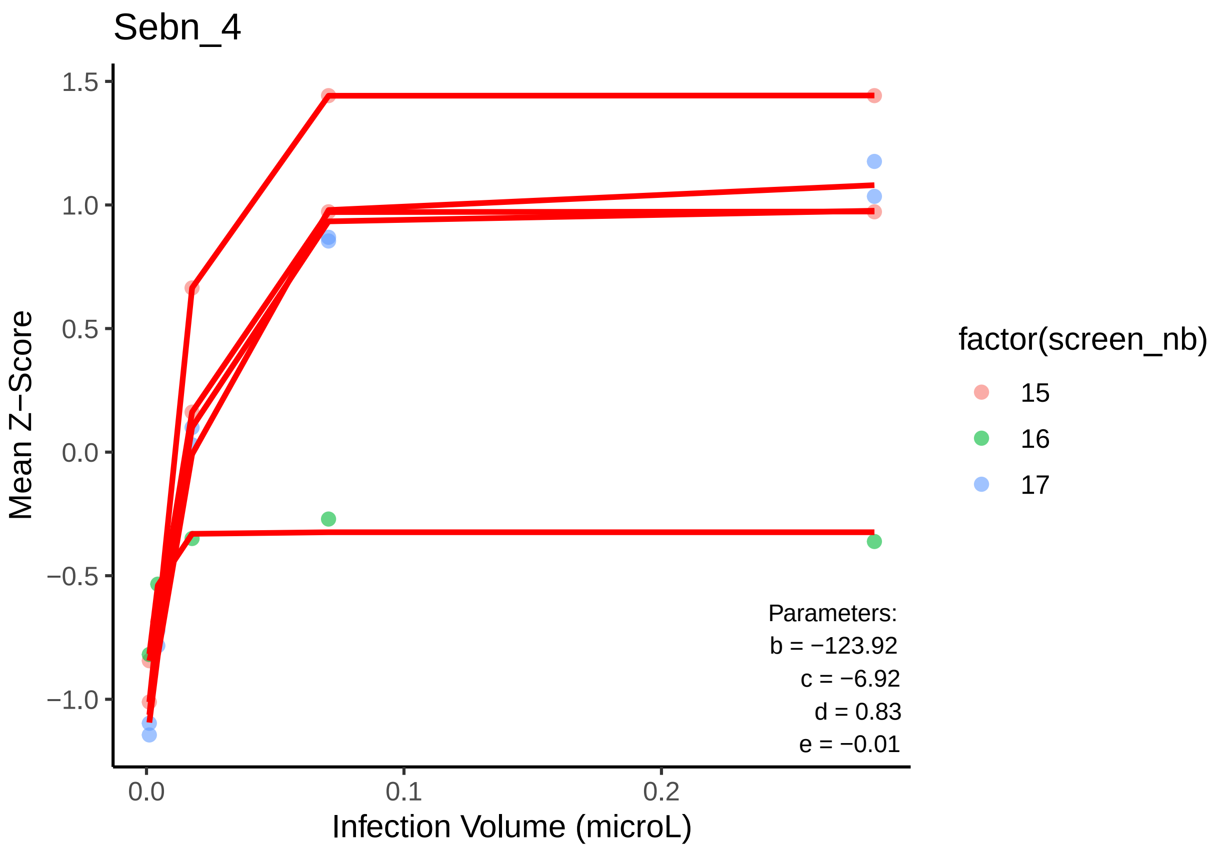

Rozh_4
Mean Z−Score
1
0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
26
27
Parameters:
b = −30.58
c = −1.37
d = 0.96
e = 0.05

```
##
## $Ruql_3
```



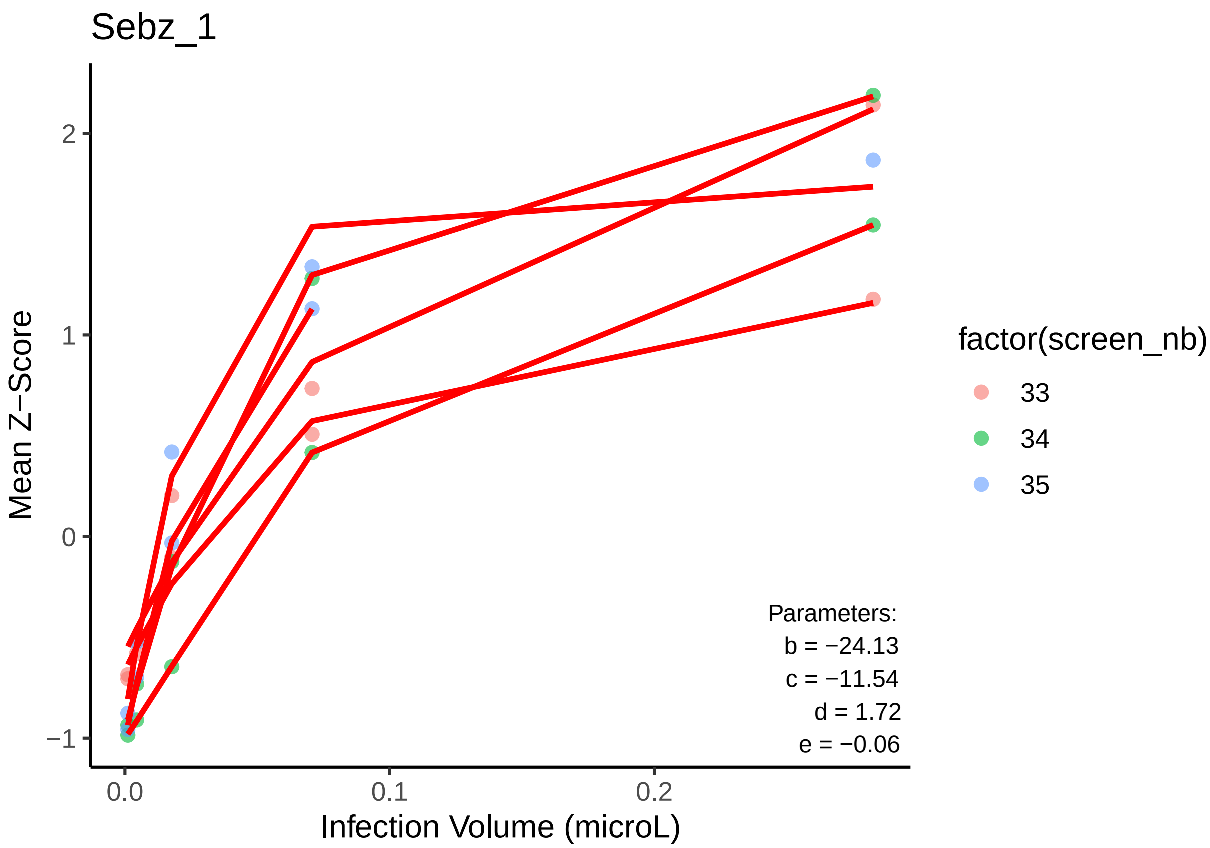
Ruql_3
Mean Z−Score
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −30.66
c = −0.8
d = 0.64
e = 0.11
factor(screen_nb)
26
27


```
##
## $Sebn_4
```

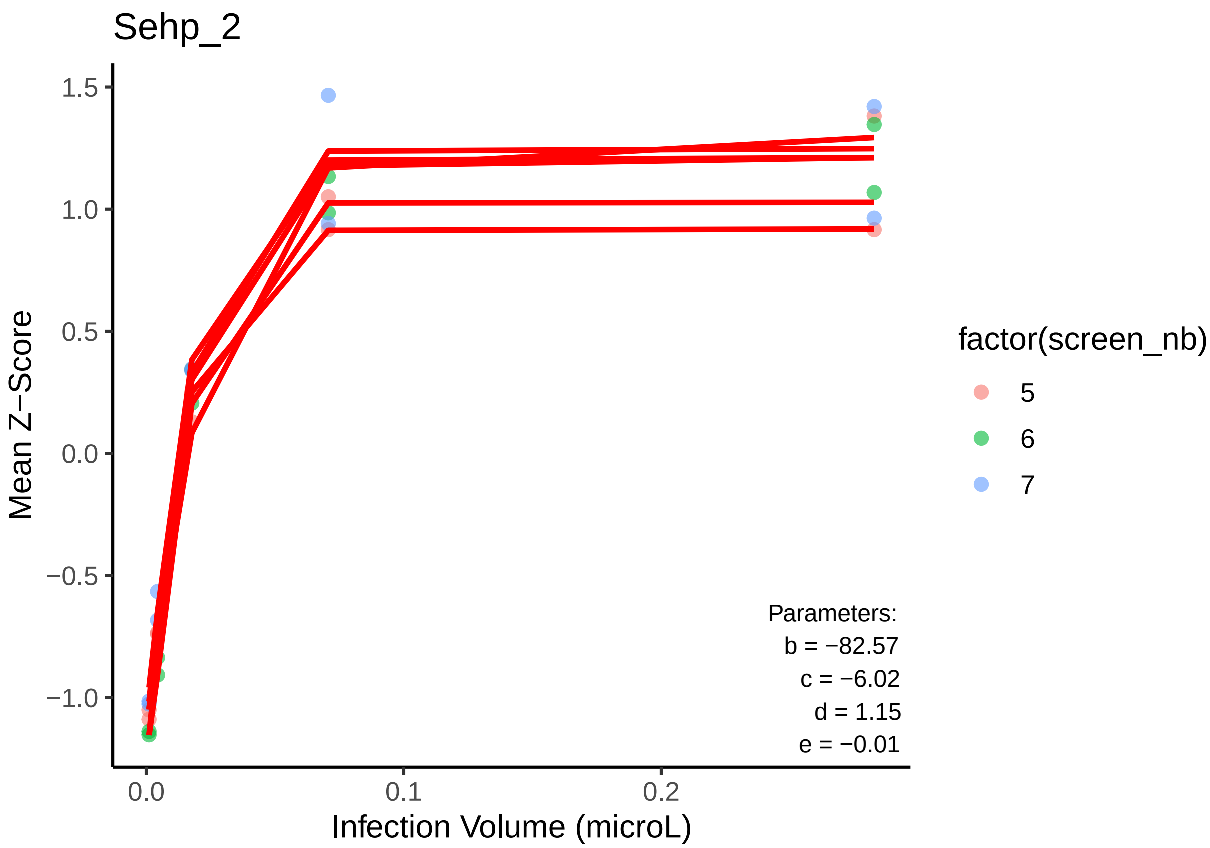


Sebn_4
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −123.92
c = −6.92
d = 0.83
e = −0.01
factor(screen_nb)
15
16
17

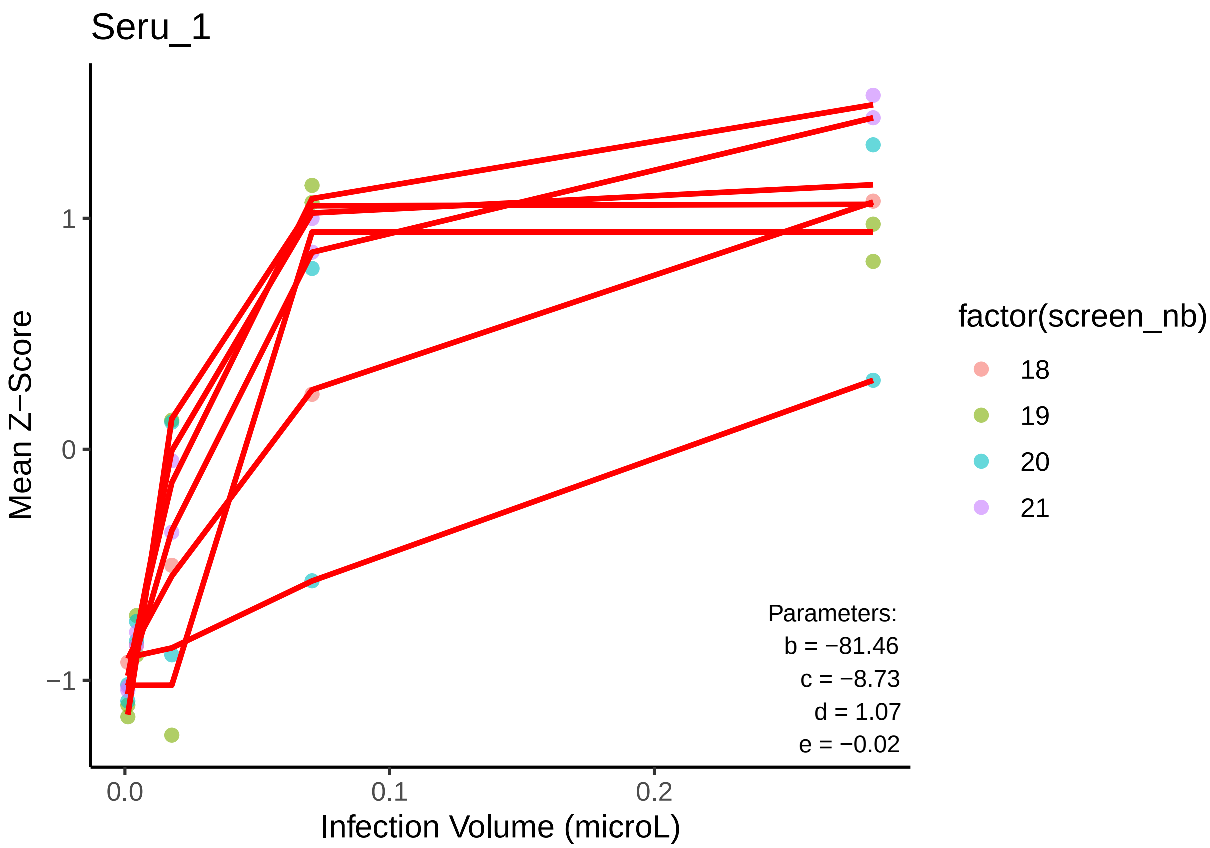

```
##
## $Sebz_1
```


Sebz_1
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
33
34
35
Parameters:
b = −24.13
c = −11.54
d = 1.72
e = −0.06

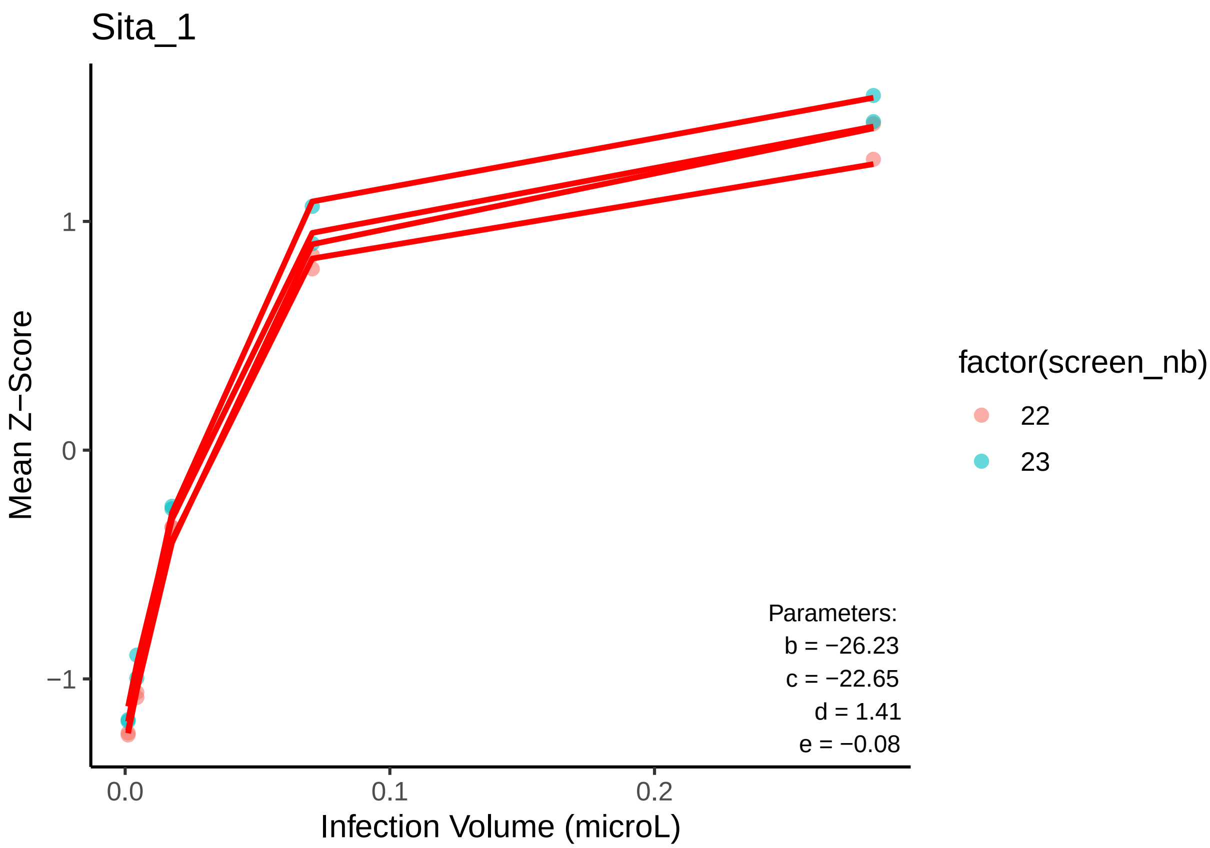
```
##
## $Sehp_2
```


Sehp_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −82.57
c = −6.02
d = 1.15
e = −0.01
factor(screen_nb)
5
6
7

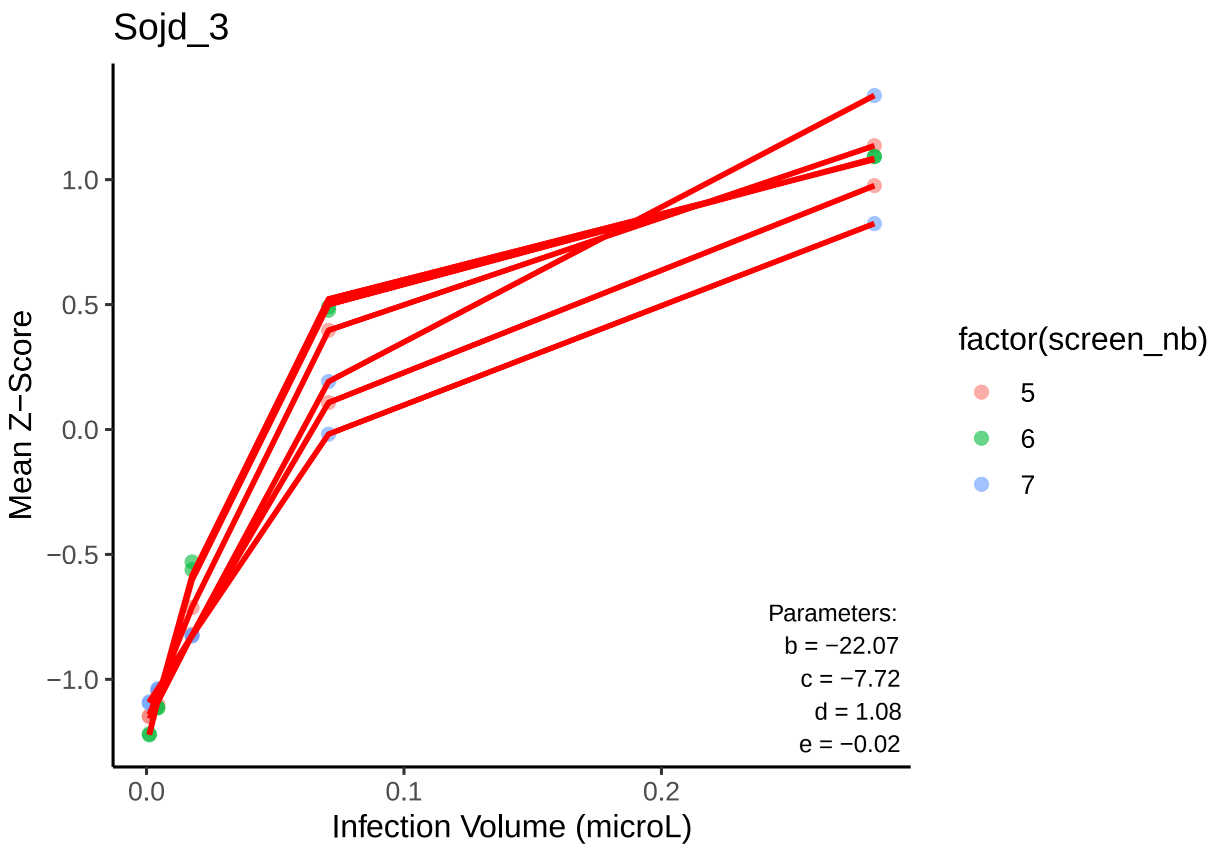
```
##
## $Seru_1
```


Seru_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −81.46
c = −8.73
d = 1.07
e = −0.02
factor(screen_nb)
18
19
20
21

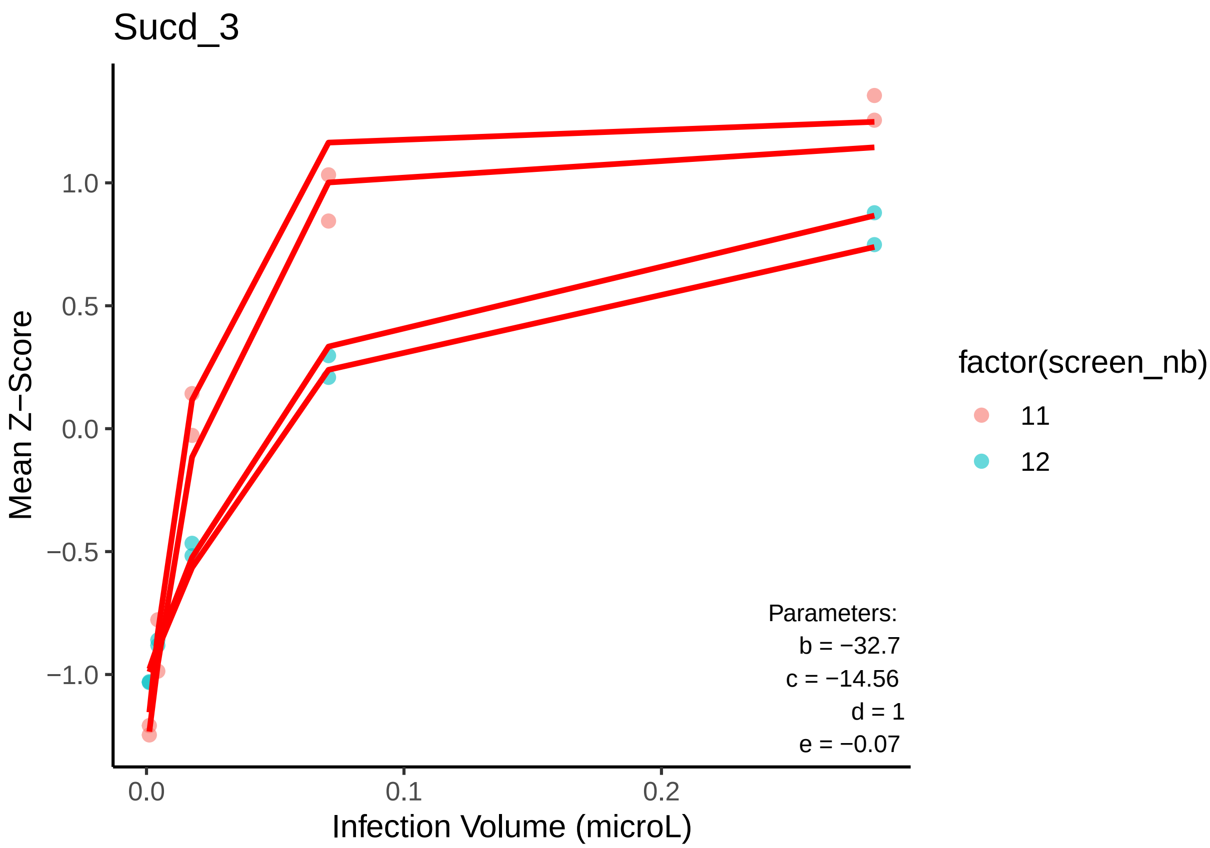
```
##
## $Sita_1
```


Sita_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −26.23
c = −22.65
d = 1.41
e = −0.08
factor(screen_nb)
22
23

```
##
## $Sojd_3
```

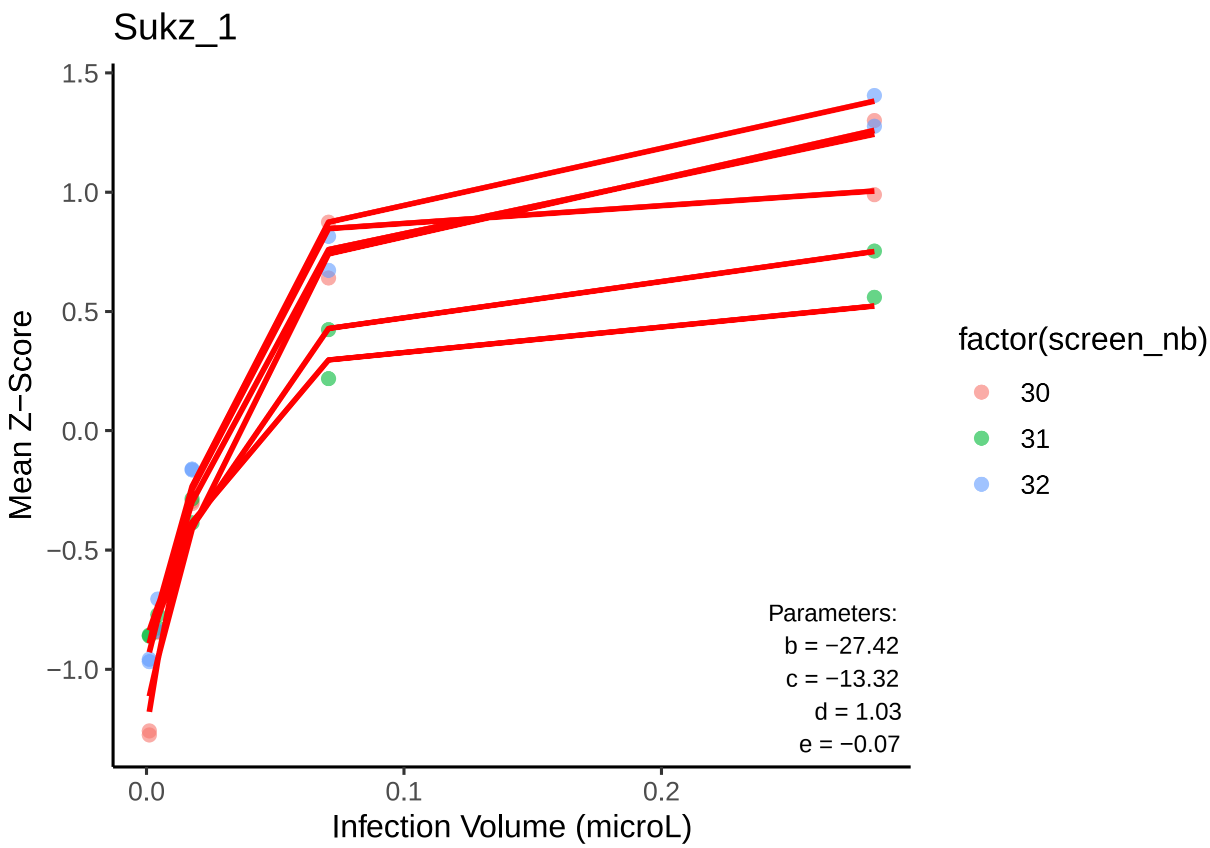

Sojd_3
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
Parameters:
b = −22.07
c = −7.72
d = 1.08
e = −0.02
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
5
6
7

```
##
## $Sucd_3
```

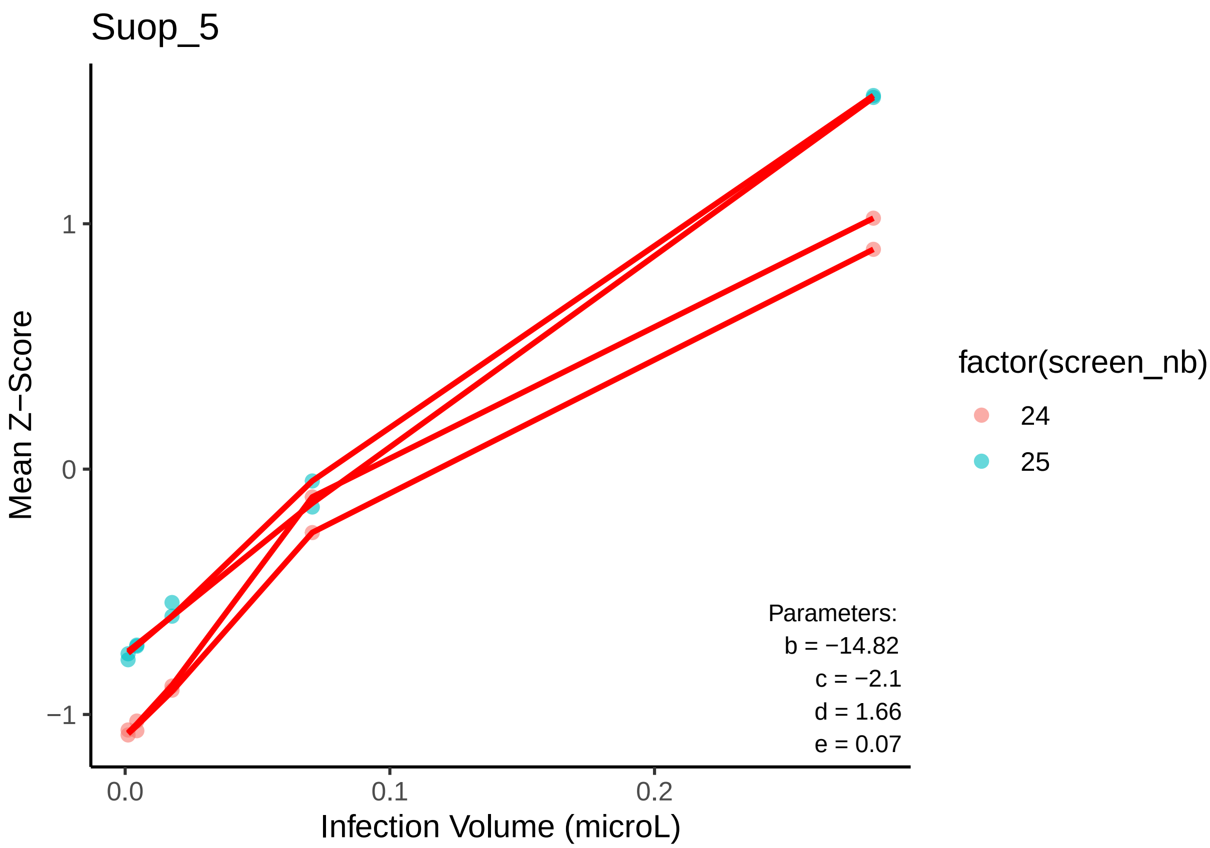


Sucd_3
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −32.7
c = −14.56
d = 1
e = −0.07
factor(screen_nb)
11
12


```
##
## $Sukz_1
```

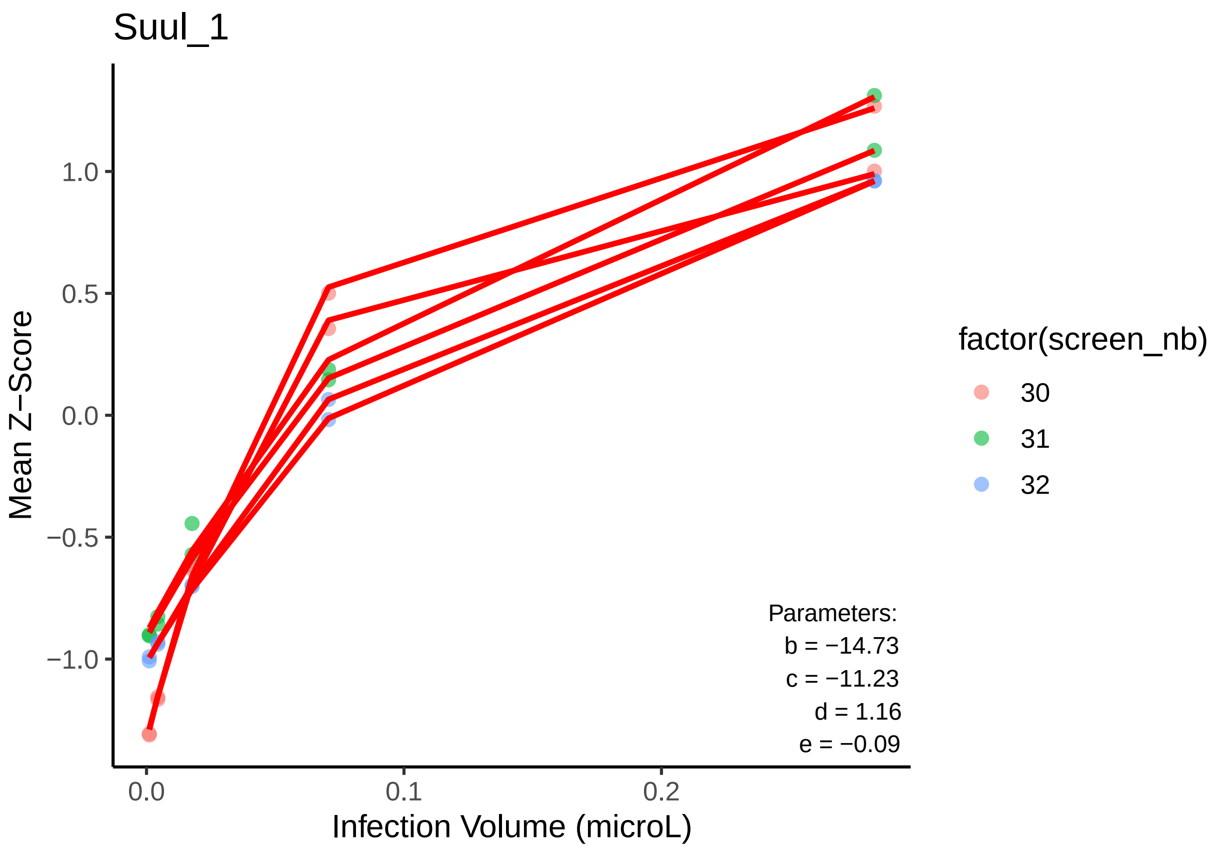

Sukz_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −27.42
c = −13.32
d = 1.03
e = −0.07
factor(screen_nb)
30
31
32

```
##
## $Suop_5
```



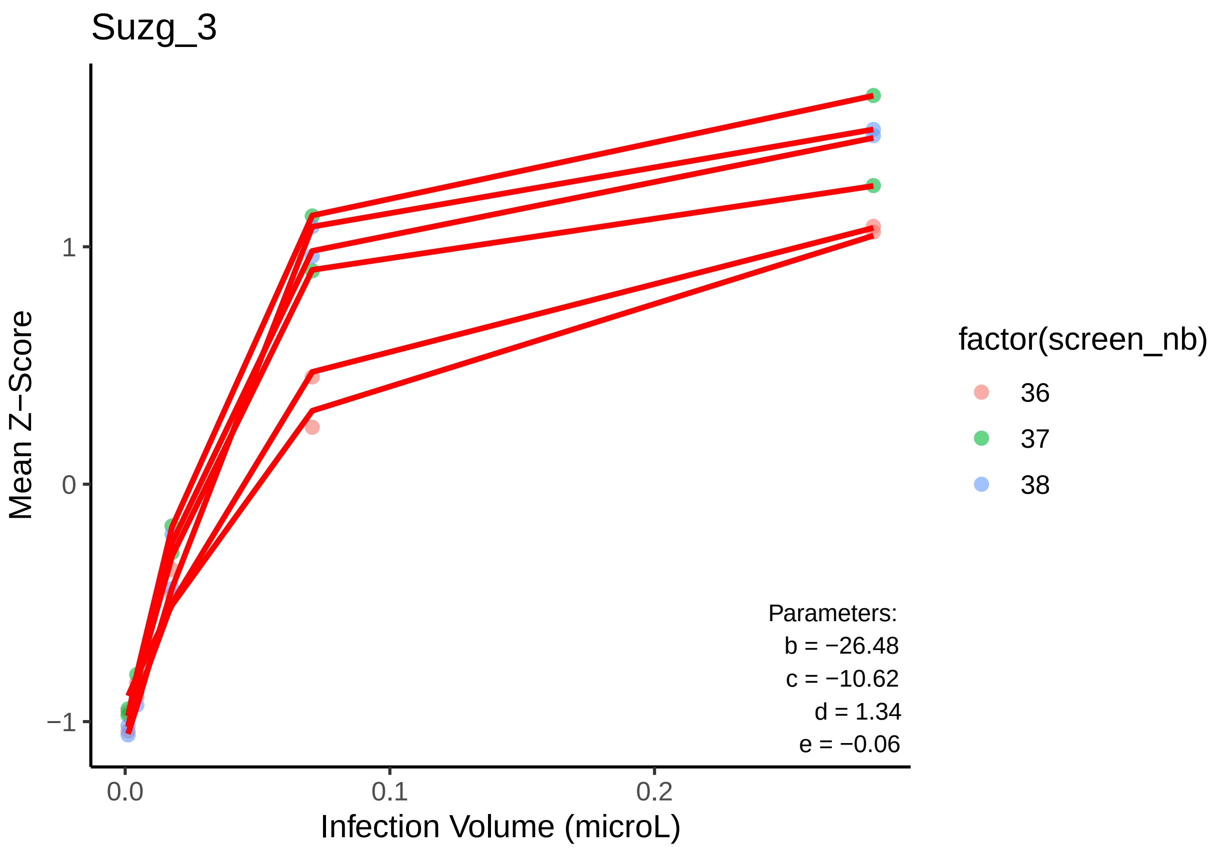
Suop_5
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
24
25
Parameters:
b = −14.82
c = −2.1
d = 1.66
e = 0.07


```
##
## $Suul_1
```



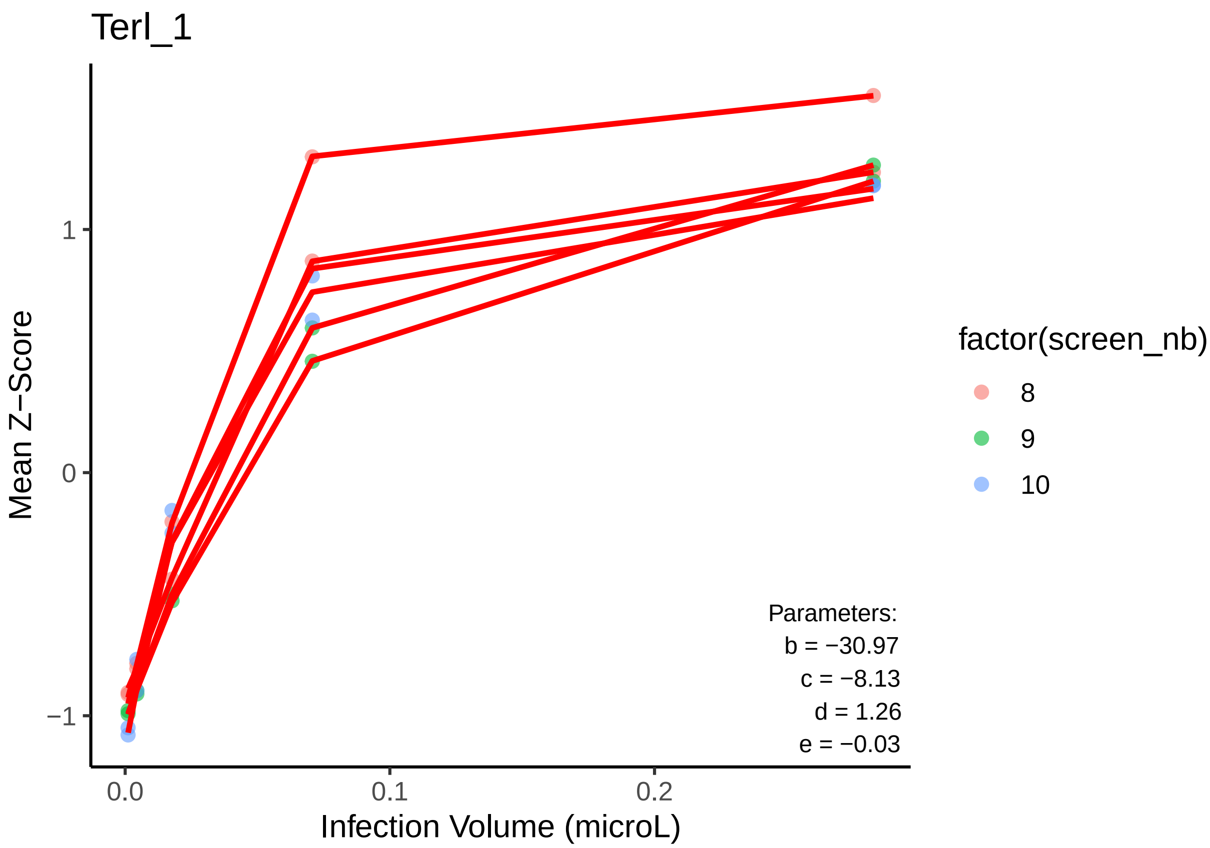
Suul_1
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
30
31
32
Parameters:
b = −14.73
c = −11.23
d = 1.16
e = −0.09


```
##
## $Suzg_3
```



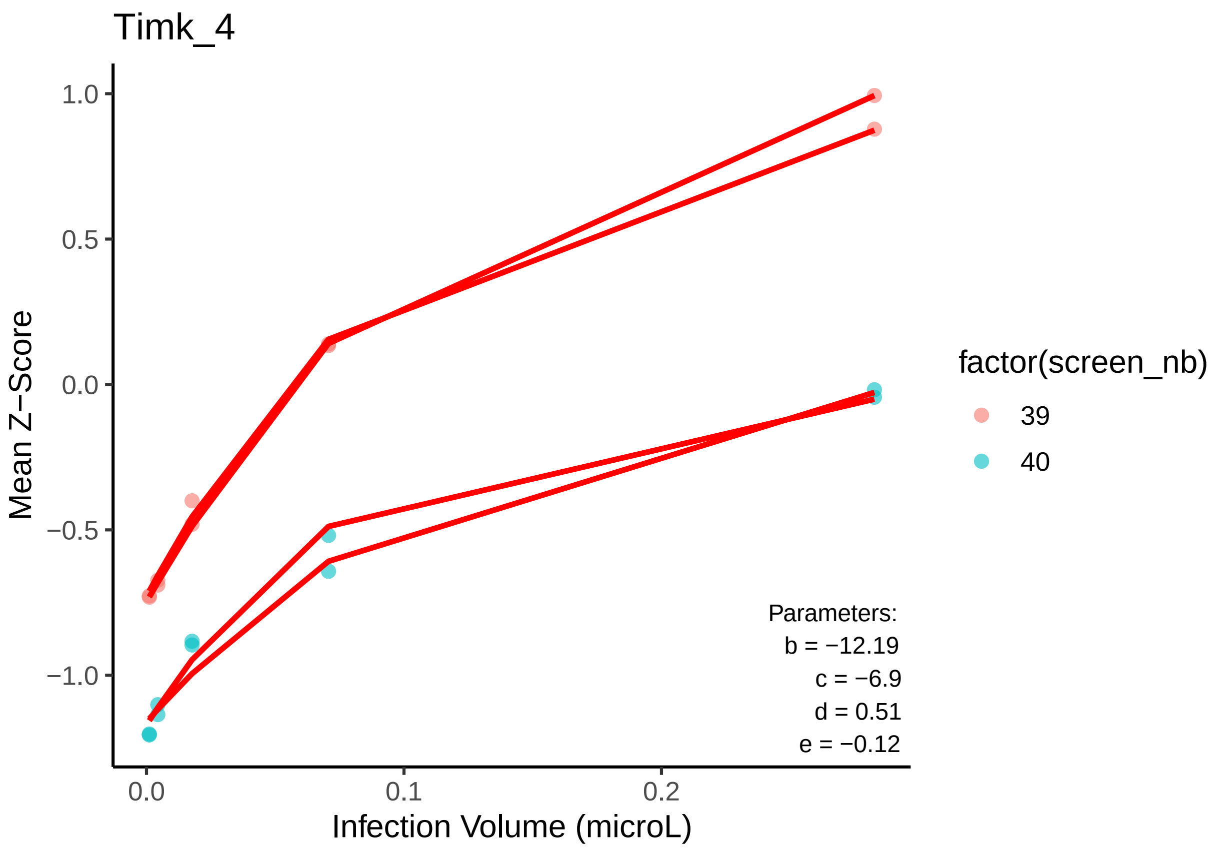
Suzg_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
36
37
38
Parameters:
b = −26.48
c = −10.62
d = 1.34
e = −0.06


```
##
## $Terl_1
```



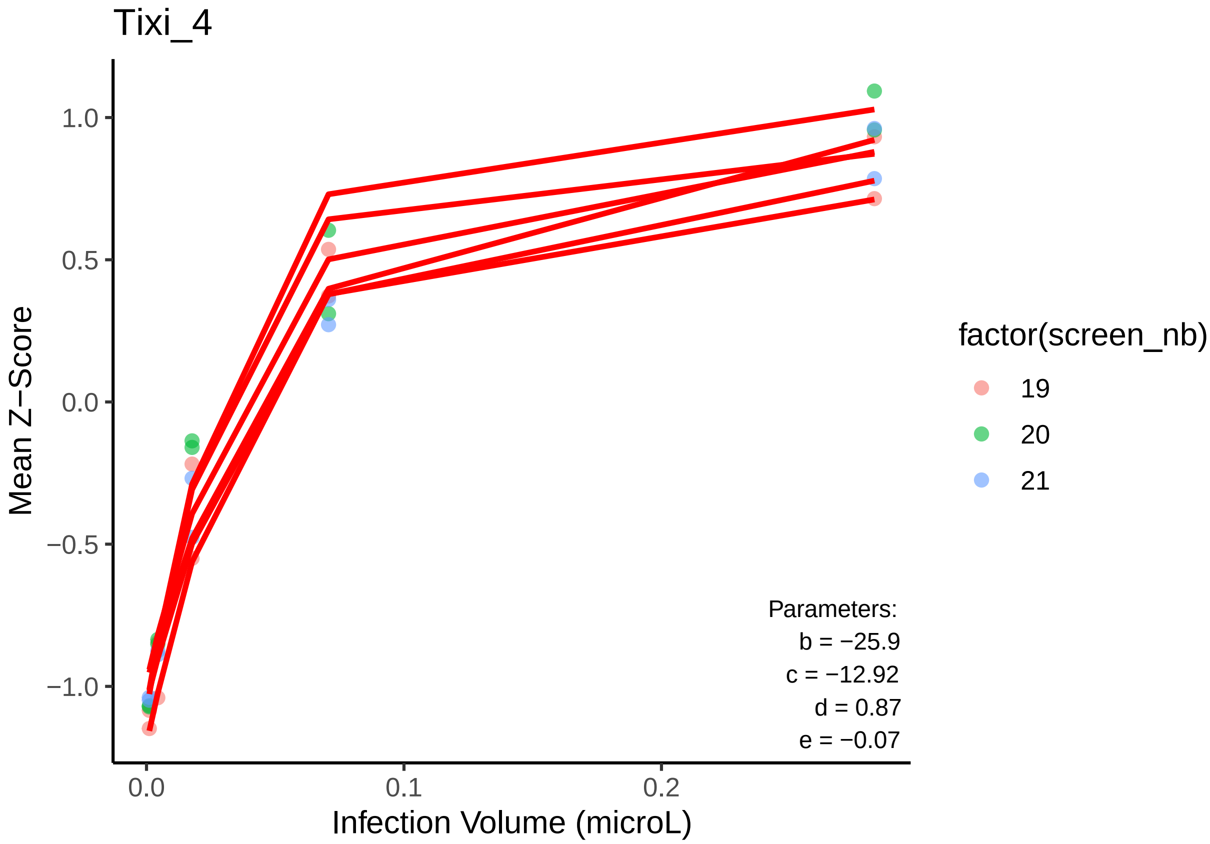
Terl_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
8
9
10
Parameters:
b = −30.97
c = −8.13
d = 1.26
e = −0.03


```
##
## $Timk_4
```



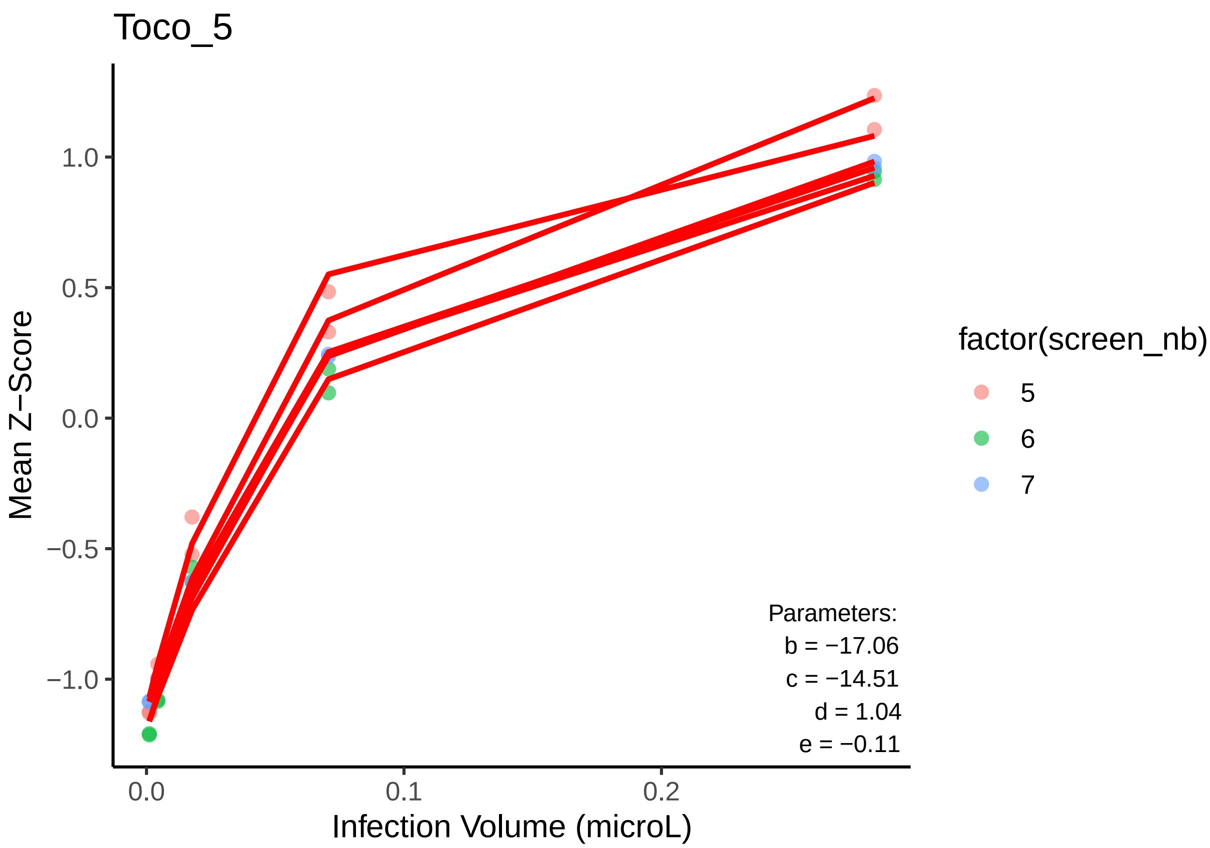
Timk_4
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −12.19
c = −6.9
d = 0.51
e = −0.12
factor(screen_nb)
39
40


```
##
## $Tixi_4
```

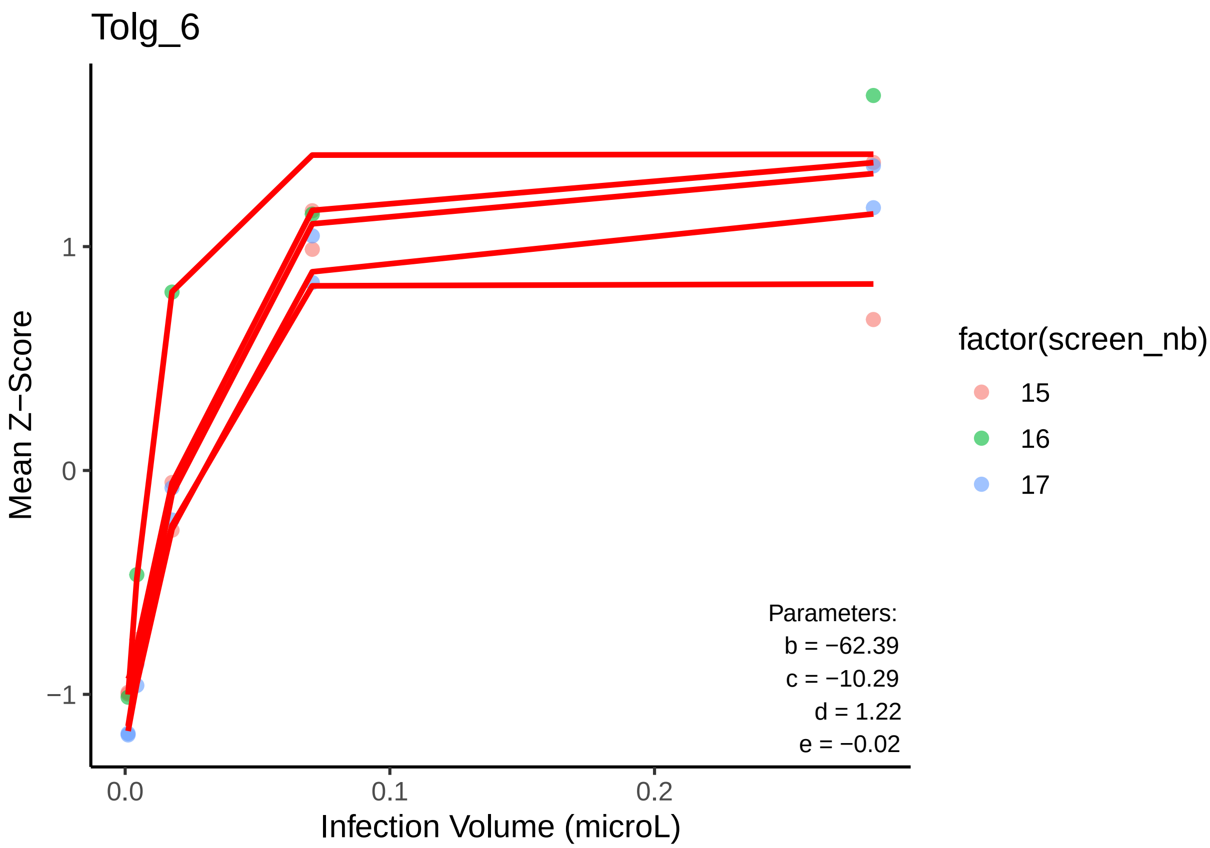


Tixi_4
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
19
20
21
Parameters:
b = −25.9
c = −12.92
d = 0.87
e = −0.07


```
##
## $Toco_5
```

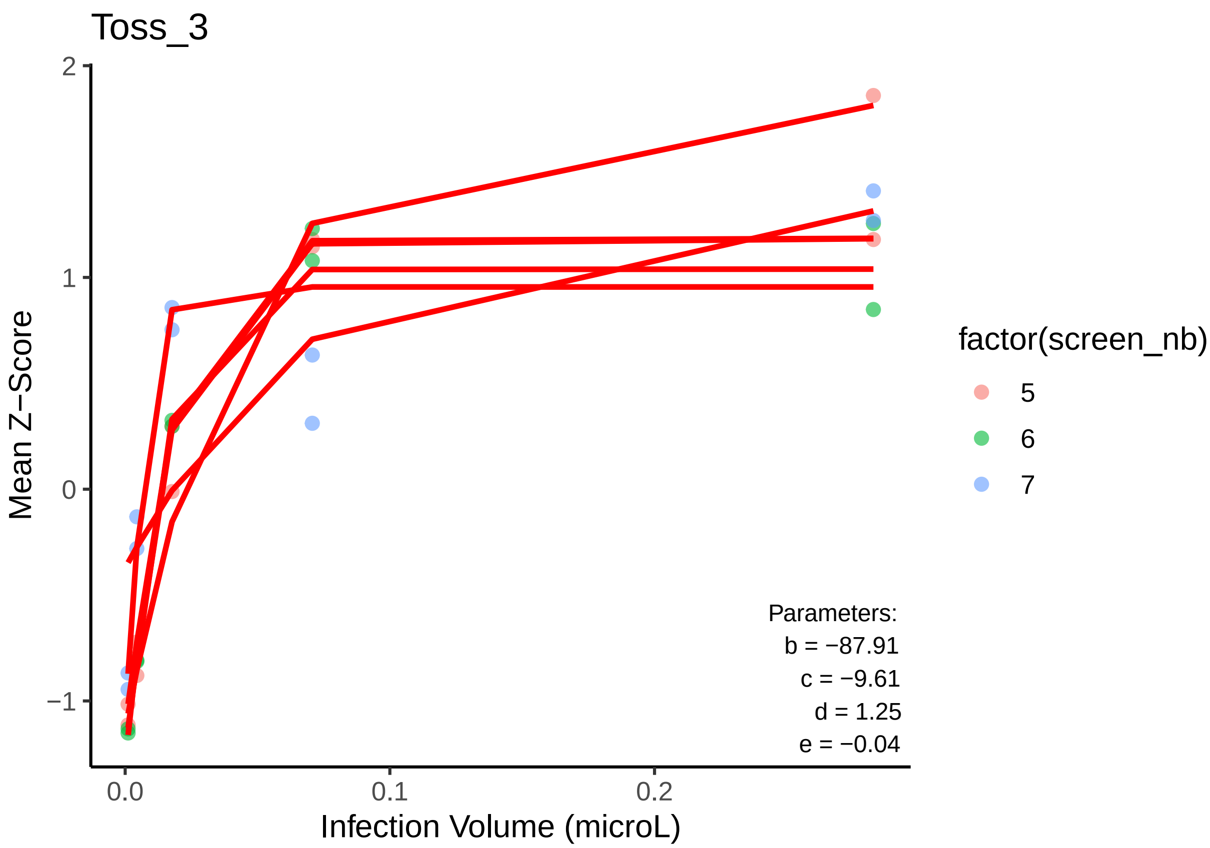

Toco_5
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
5
6
7
Parameters:
b = −17.06
c = −14.51
d = 1.04
e = −0.11

```
##
## $Tolg_6
```



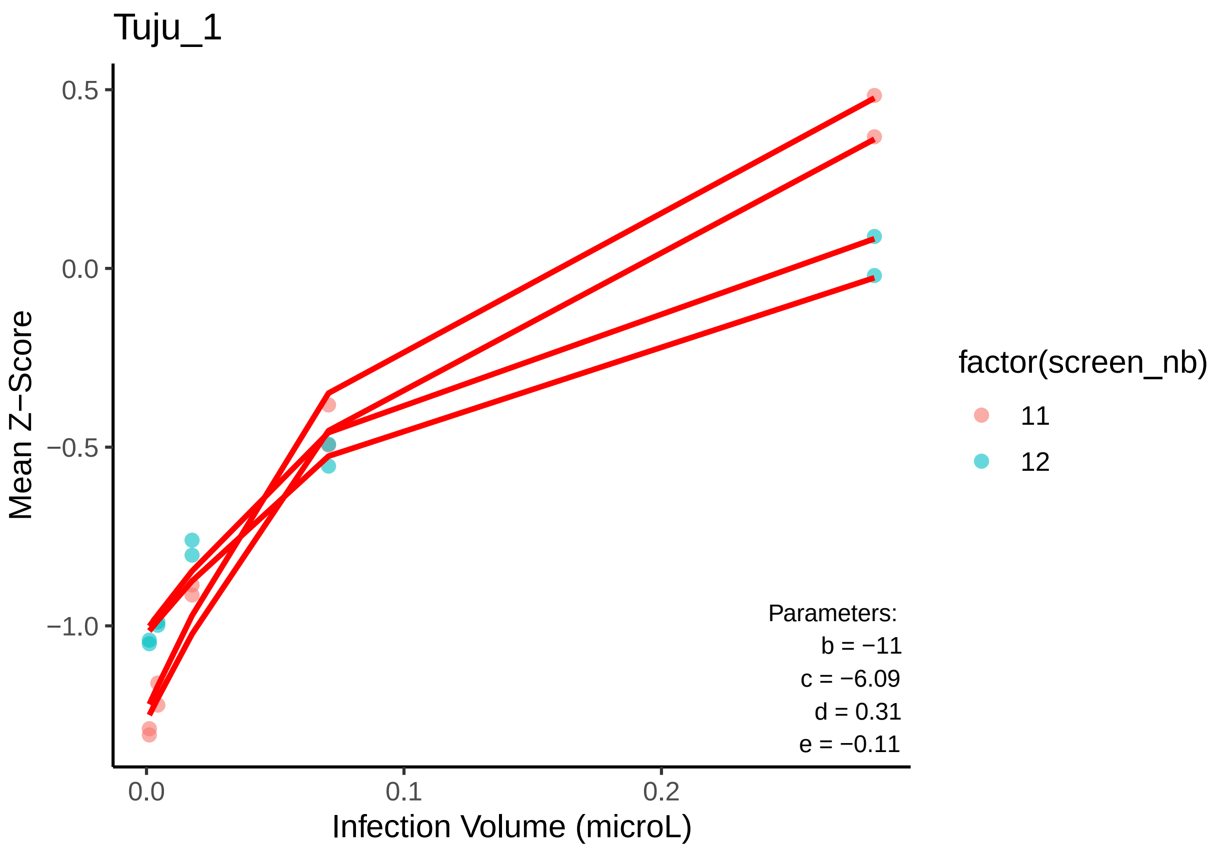
Tolg_6
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −62.39
c = −10.29
d = 1.22
e = −0.02
factor(screen_nb)
15
16
17


```
##
## $Toss_3
```



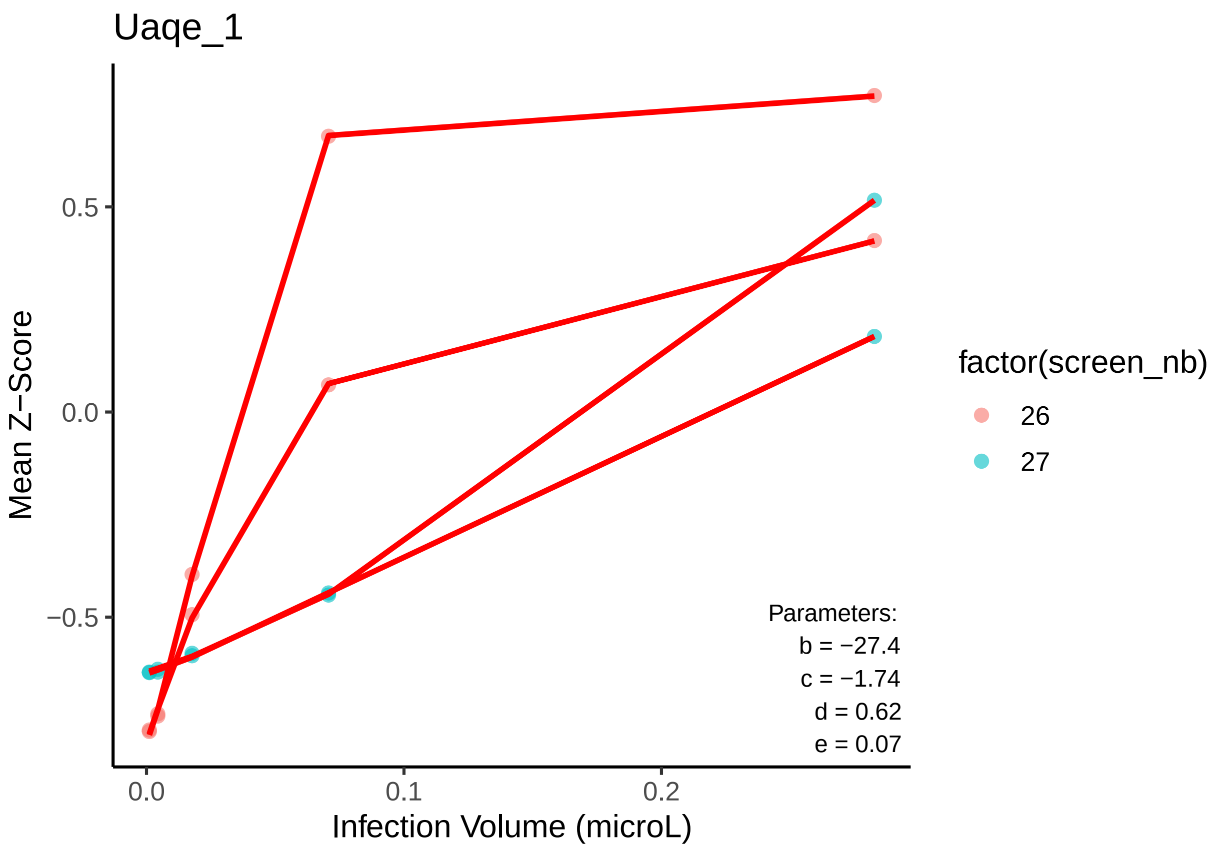
Toss_3
Mean Z−Score
Infection Volume (microL)
factor(screen_nb)
5
6
7
Parameters:
b = −87.91
c = −9.61
d = 1.25
e = −0.04


```
##
## $Tuju_1
```

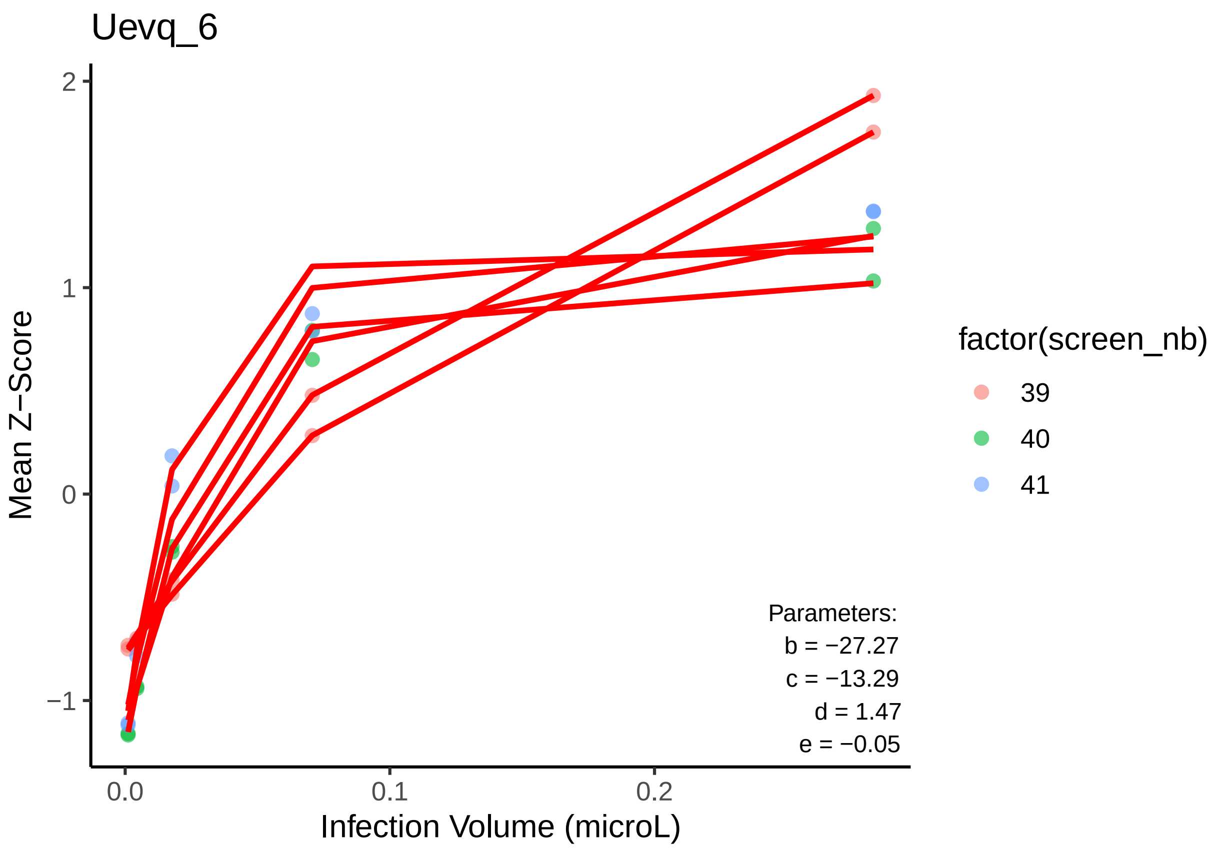


Tuju_1
Mean Z−Score
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −11
c = −6.09
d = 0.31
e = −0.11
factor(screen_nb)
11
12

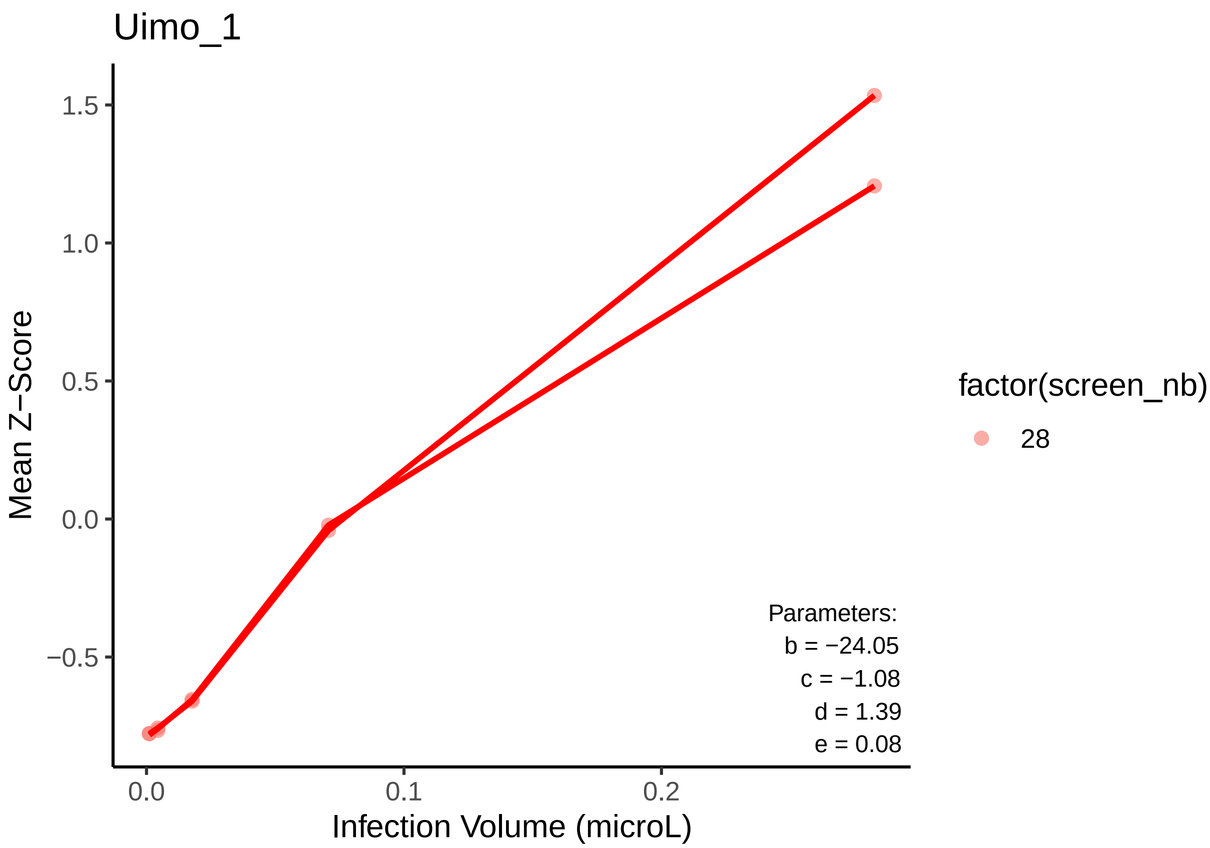

```
##
## $Uaqe_1
```


Uaqe_1
Mean Z−Score
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
26
27
Parameters:
b = −27.4
c = −1.74
d = 0.62
e = 0.07

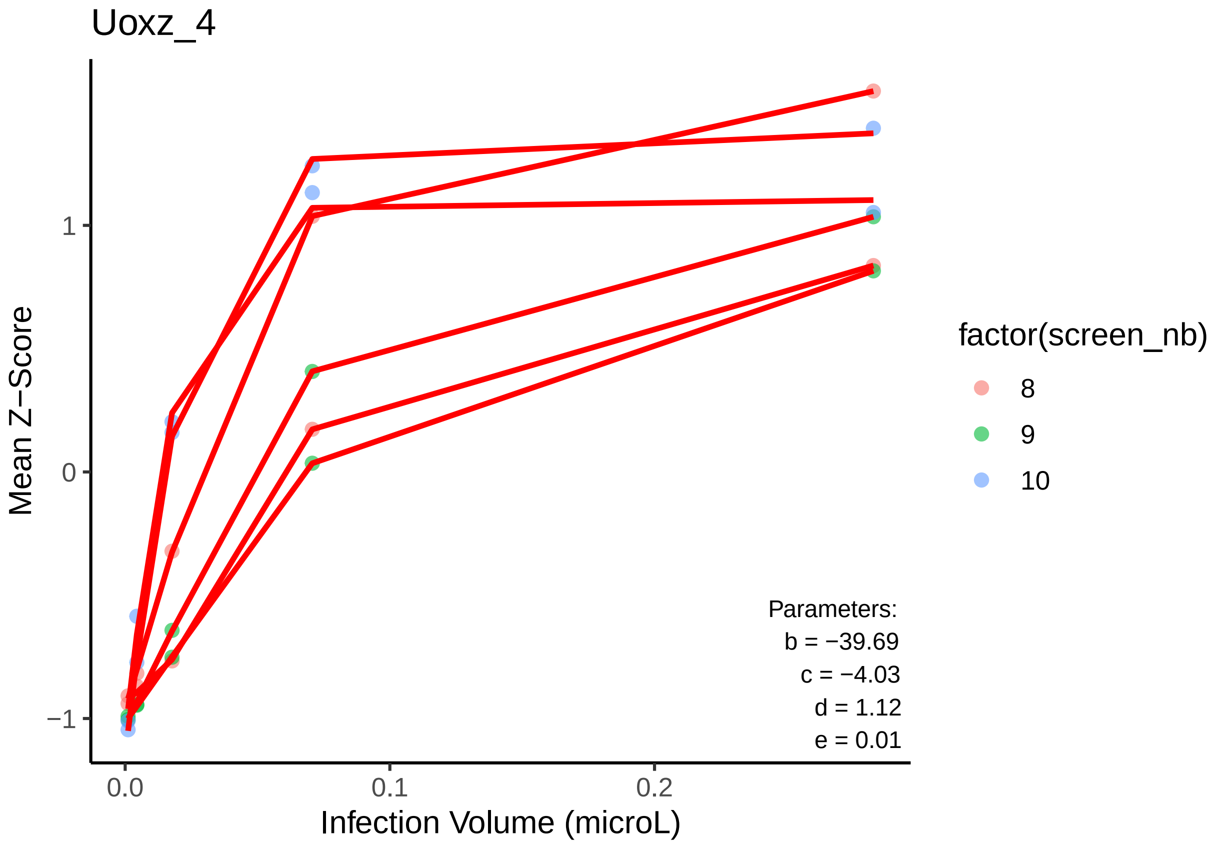
```
##
## $Uevq_6
```


Uevq_6
Mean Z−Score
Infection Volume (microL)
2
1
0
−1
0.0
0.1
0.2
Parameters:
b = −27.27
c = −13.29
d = 1.47
e = −0.05
factor(screen_nb)
39
40
41

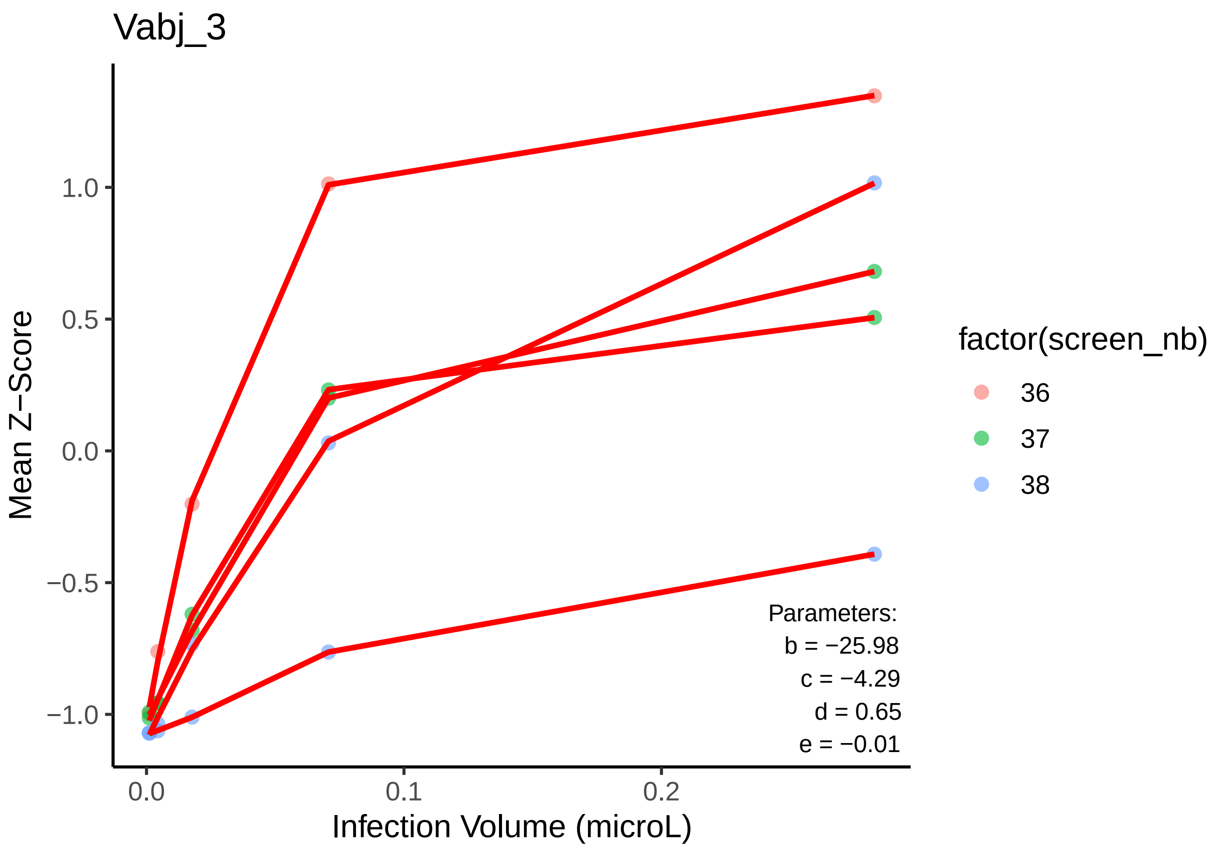
```
##
## $Uimo_1
```


Uimo_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
Parameters:
b = −24.05
c = −1.08
d = 1.39
e = 0.08
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
28

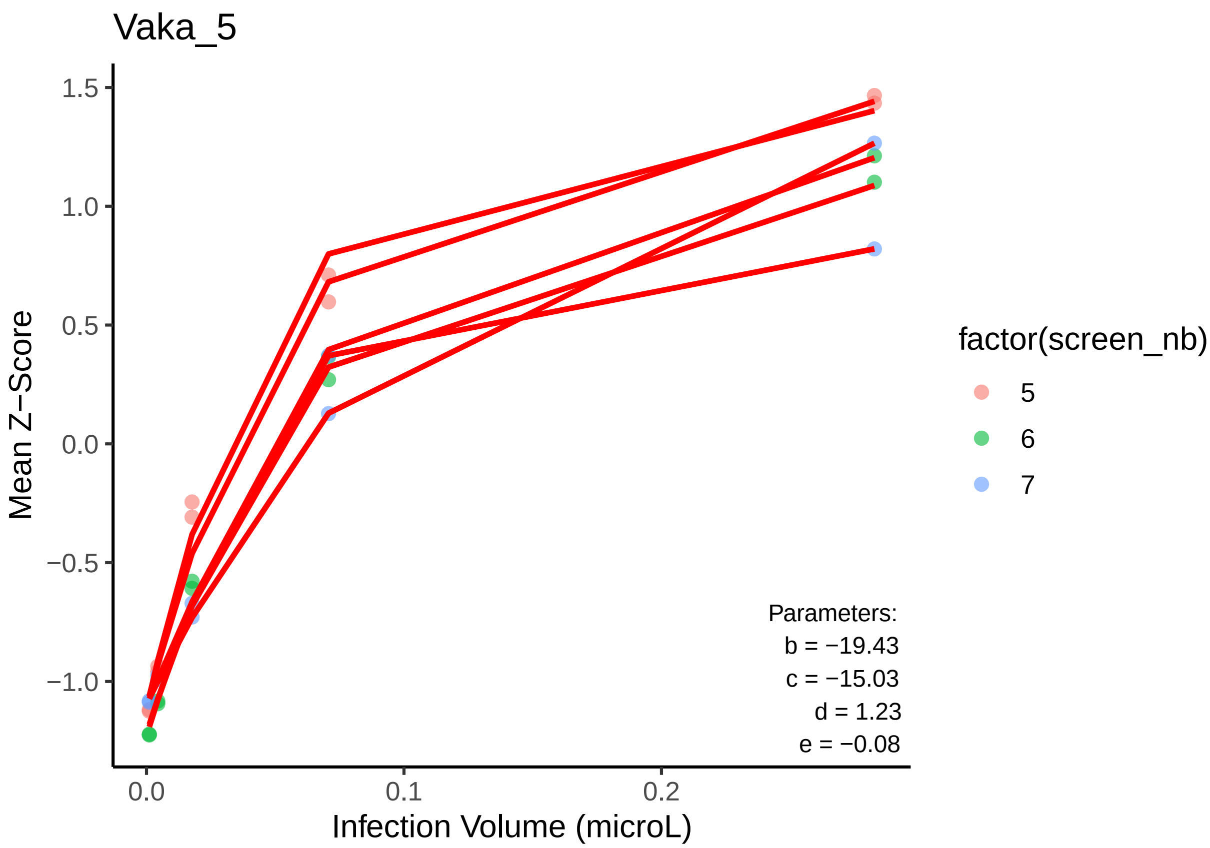
```
##
## $Uoxz_4
```


Uoxz_4
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
8
9
10
Parameters:
b = −39.69
c = −4.03
d = 1.12
e = 0.01

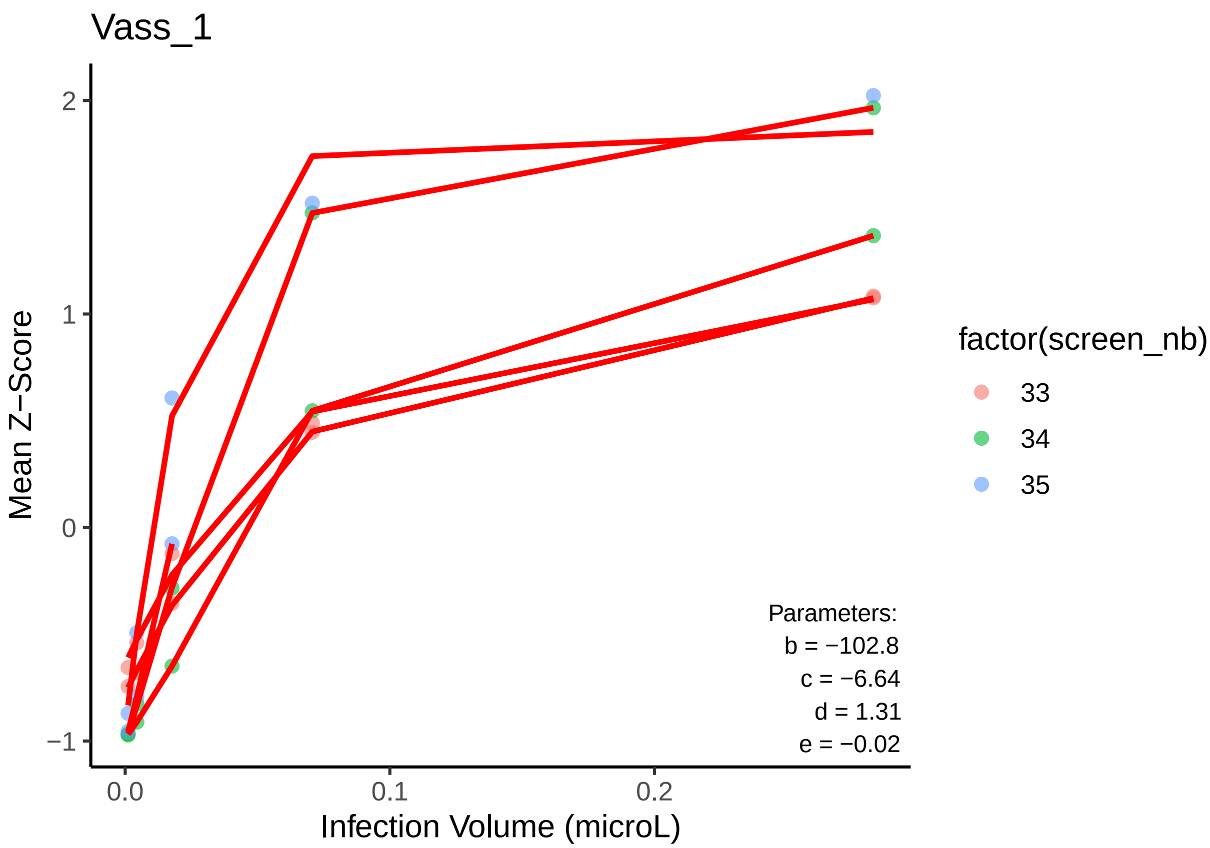
```
##
## $Vabj_3
```


Vabj_3
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −25.98
c = −4.29
d = 0.65
e = −0.01
factor(screen_nb)
36
37
38

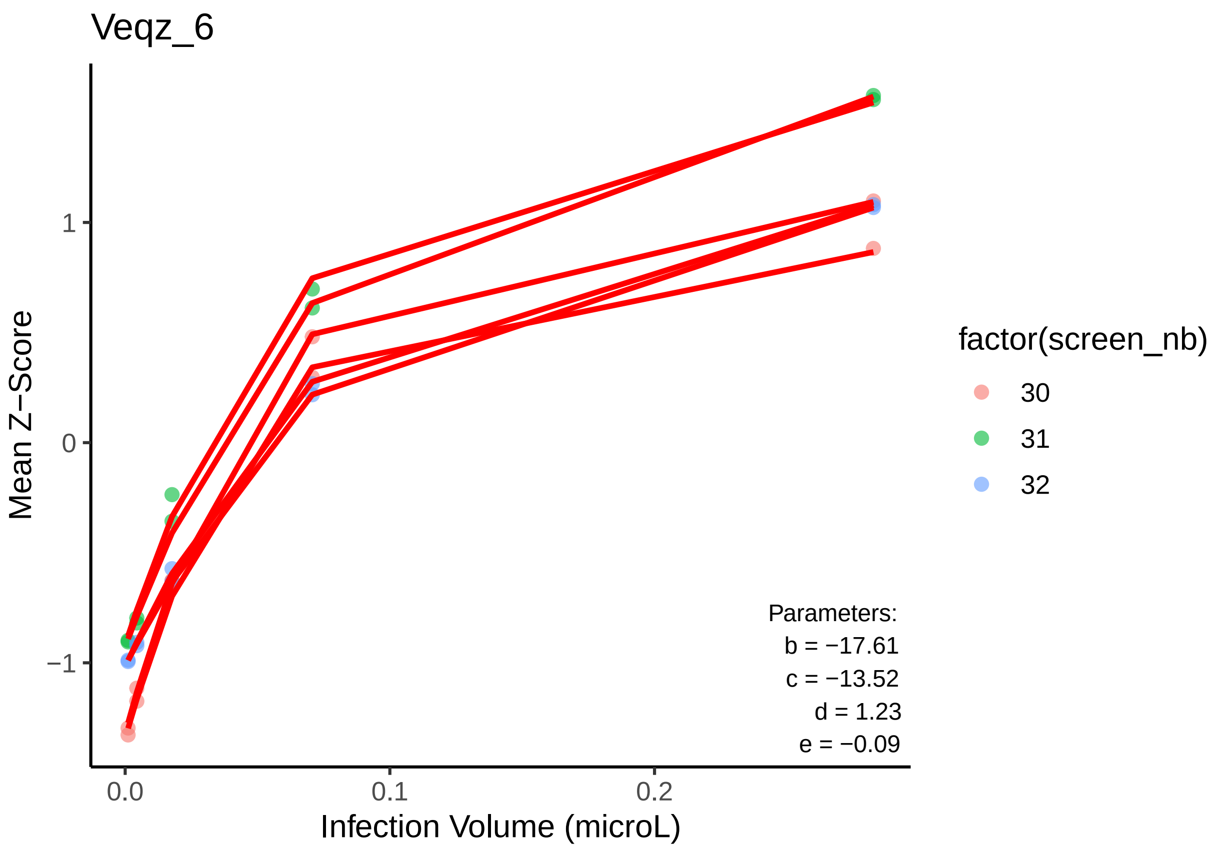
```
##
## $Vaka_5
```


Vaka_5
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
5
6
7
Parameters:
b = −19.43
c = −15.03
d = 1.23
e = −0.08

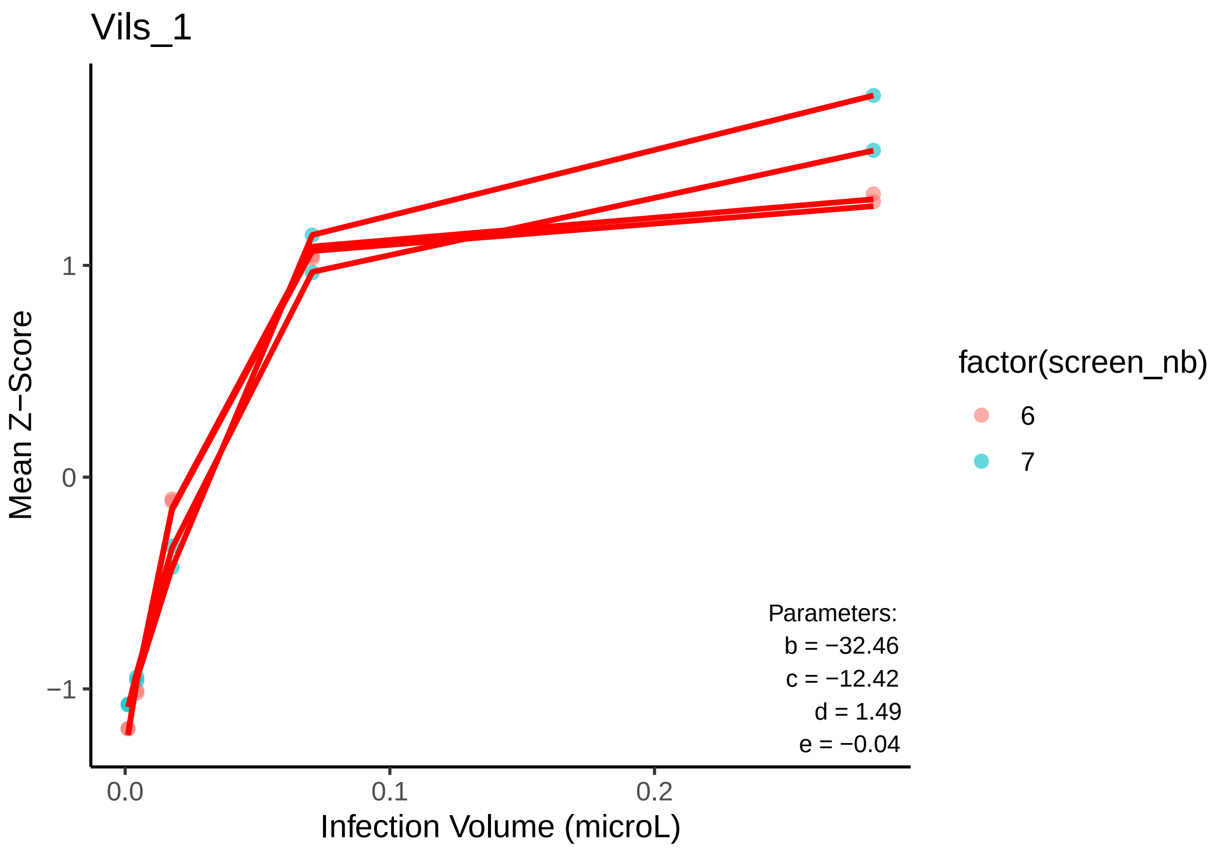
```
##
## $Vass_1
```


Vass_1
Mean Z−Score
2
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
33
34
35
Parameters:
b = −102.8
c = −6.64
d = 1.31
e = −0.02

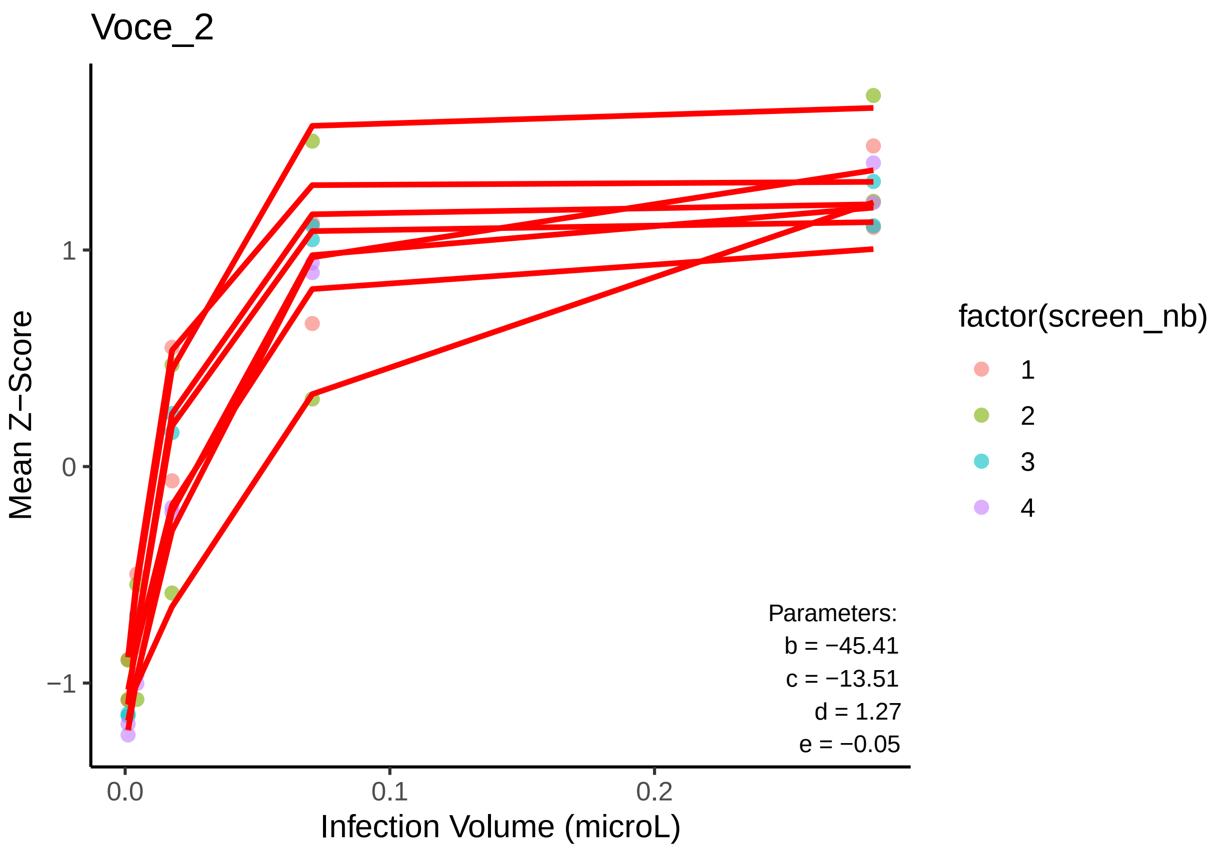
```
##
## $Veqz_6
```


Veqz_6
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −17.61
c = −13.52
d = 1.23
e = −0.09
factor(screen_nb)
30
31
32

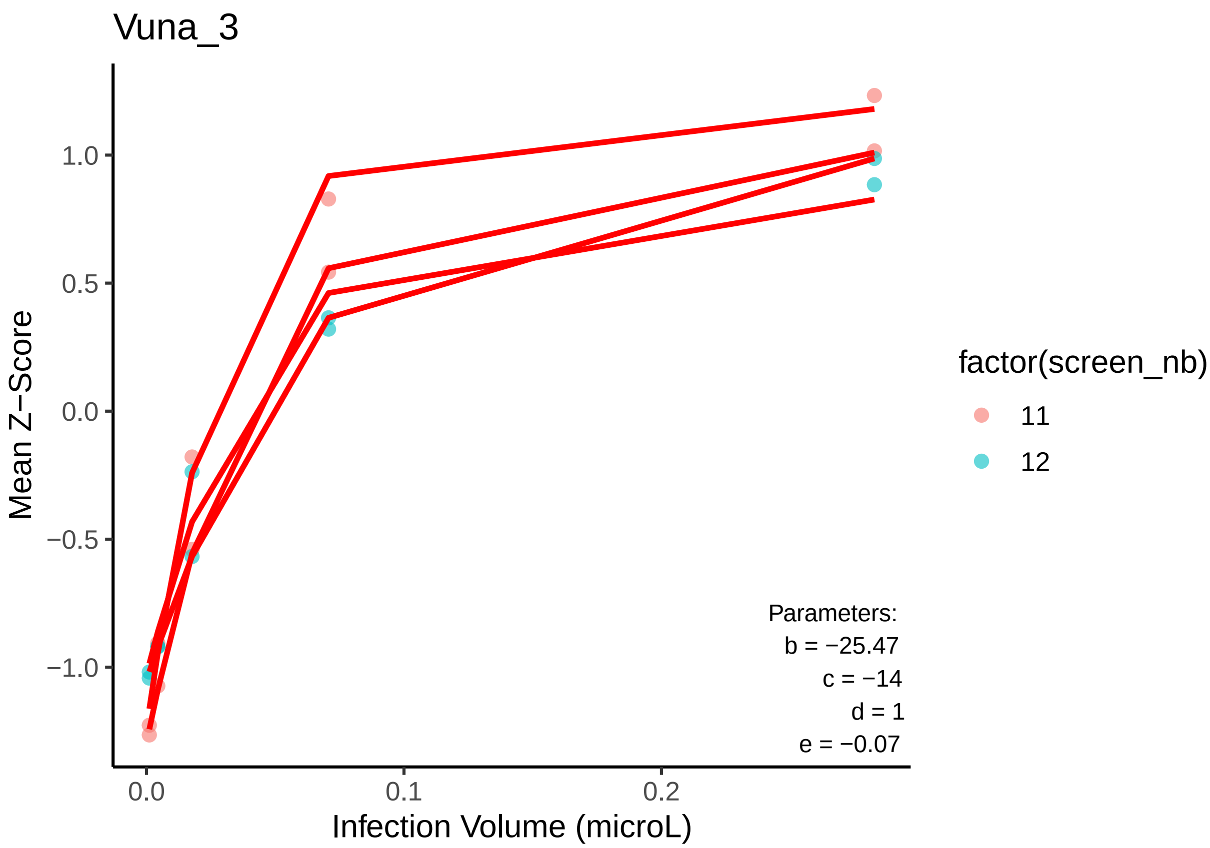
```
##
## $Vils_1
```


Vils_1
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −32.46
c = −12.42
d = 1.49
e = −0.04
factor(screen_nb)
6
7

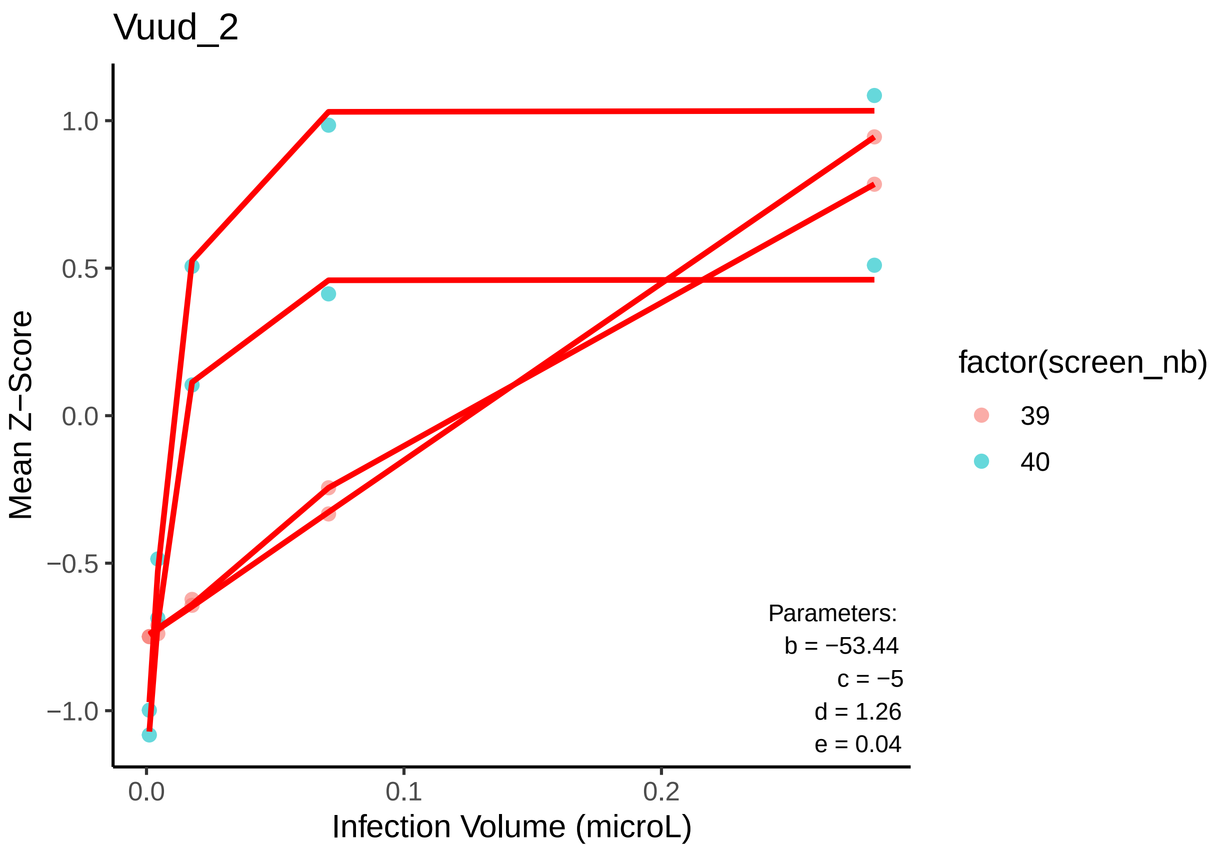
```
##
## $Voce_2
```


Voce_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
1
2
3
4
Parameters:
b = −45.41
c = −13.51
d = 1.27
e = −0.05

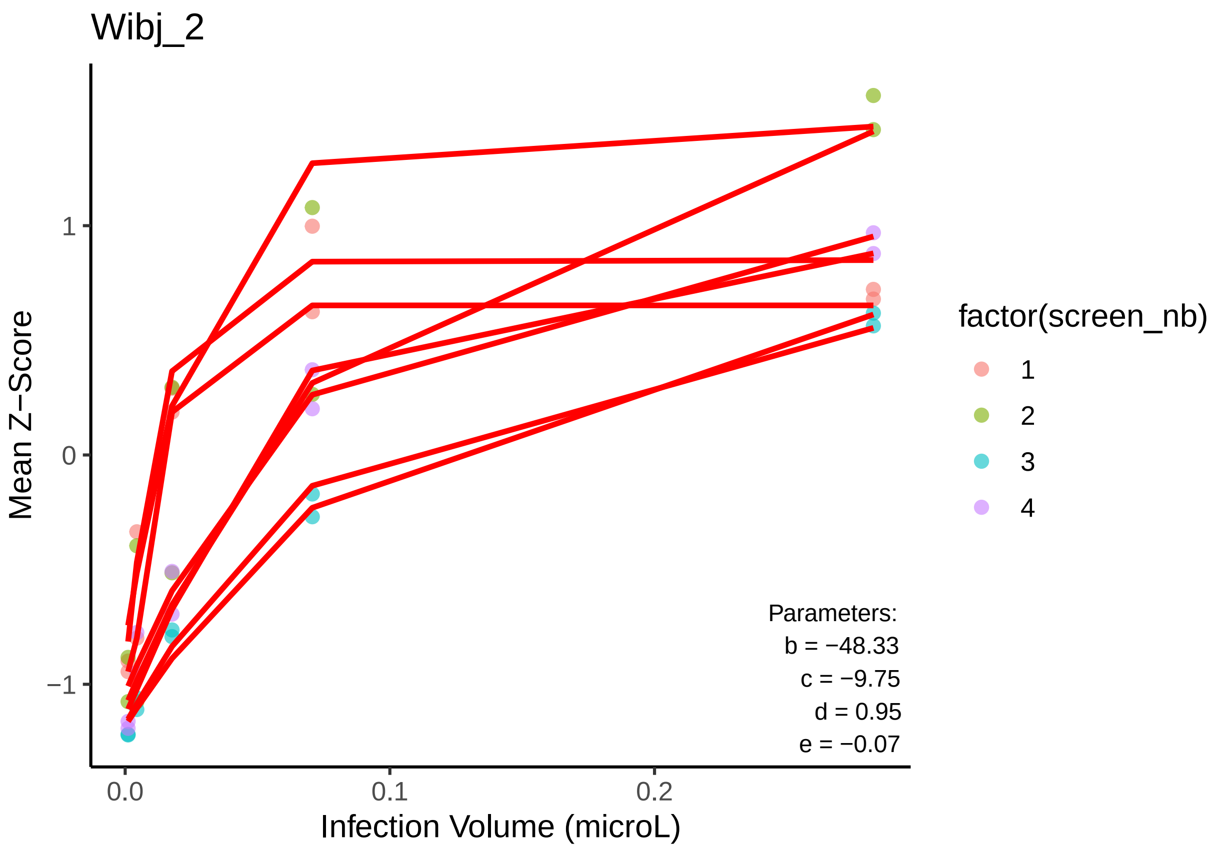
```
##
## $Vuna_3
```


Vuna_3
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −25.47
c = −14
d = 1
e = −0.07
factor(screen_nb)
11
12

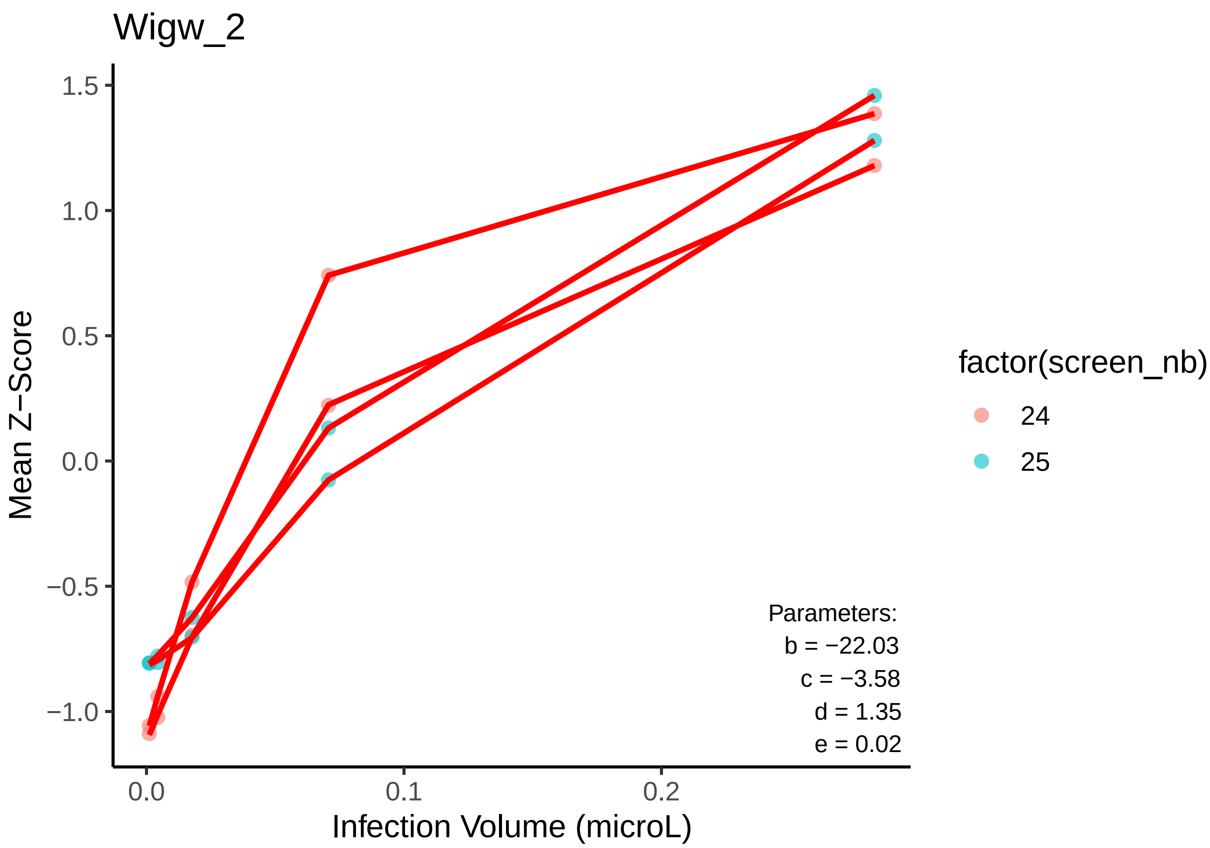
```
##
## $Vuud_2
```


Vuud_2
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −53.44
c = −5
d = 1.26
e = 0.04
factor(screen_nb)
39
40

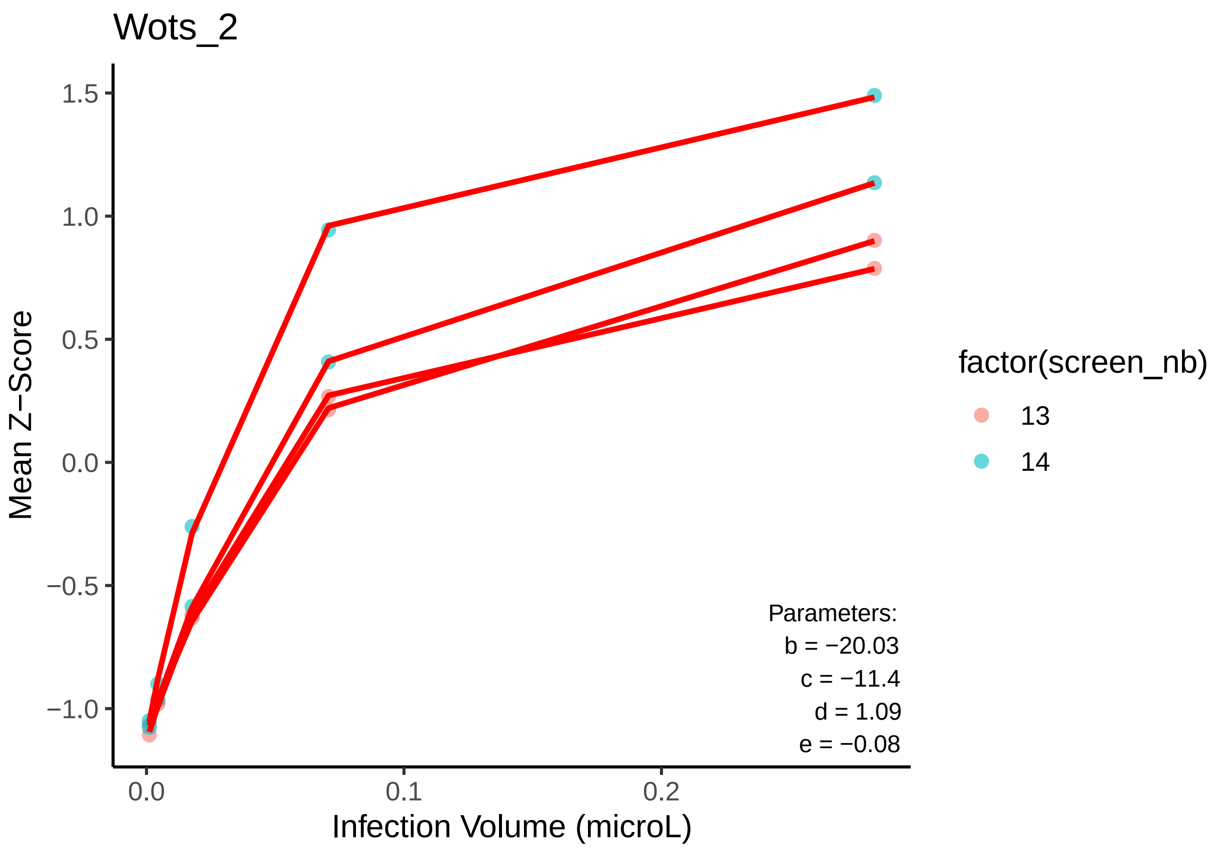
```
##
## $Wibj_2
```


Wibj_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
1
2
3
4
Parameters:
b = −48.33
c = −9.75
d = 0.95
e = −0.07

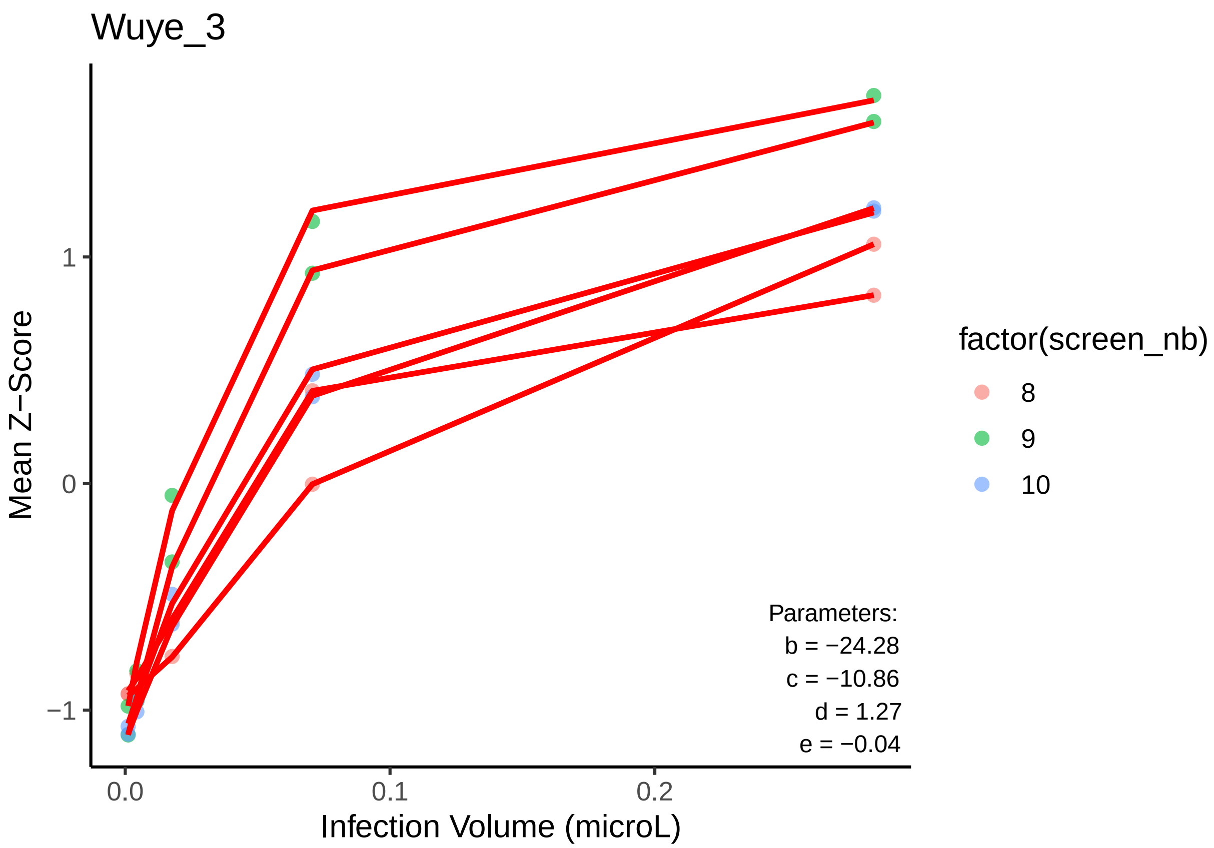
```
##
## $Wigw_2
```


Wigw_2
1.5
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
24
25
Parameters:
b = −22.03
c = −3.58
d = 1.35
e = 0.02

```
##
## $Wots_2
```

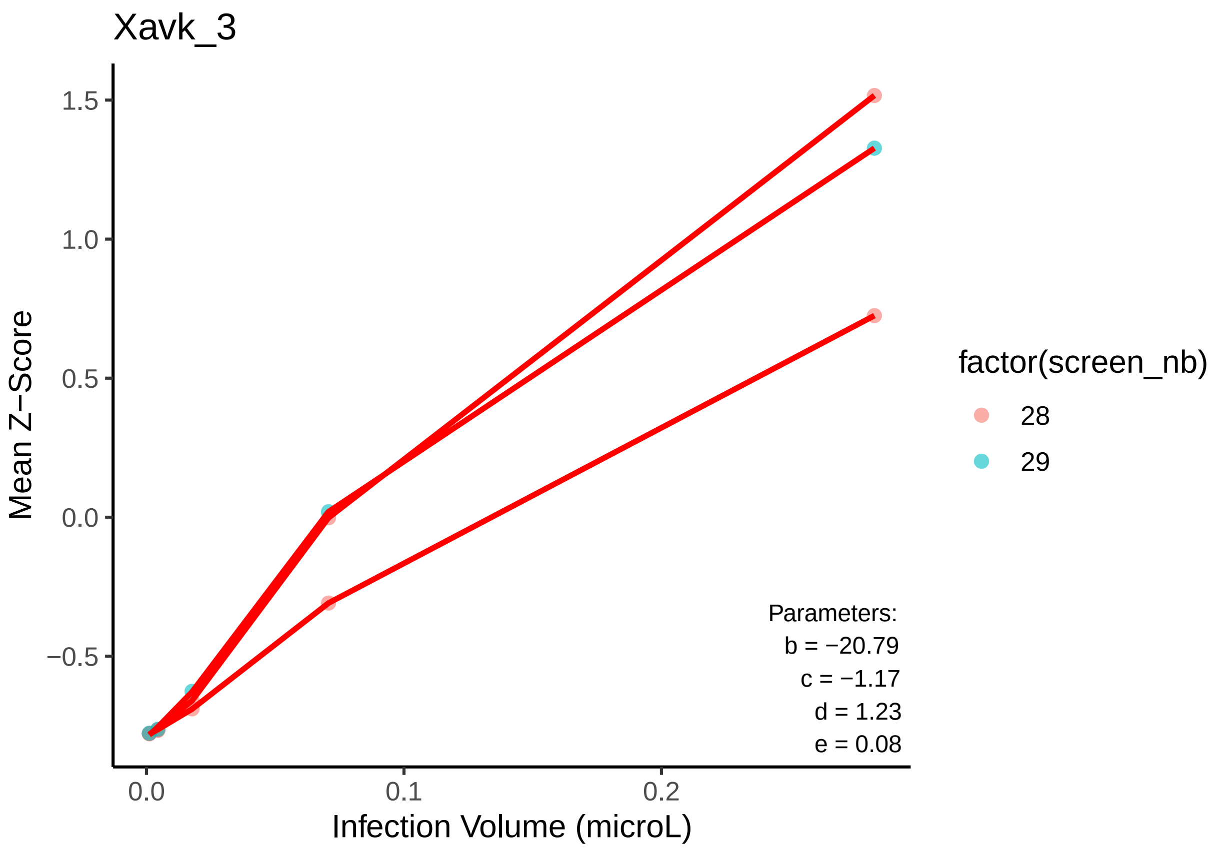

Wots_2
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −20.03
c = −11.4
d = 1.09
e = −0.08
factor(screen_nb)
13
14

```
##
## $Wuye_3
```

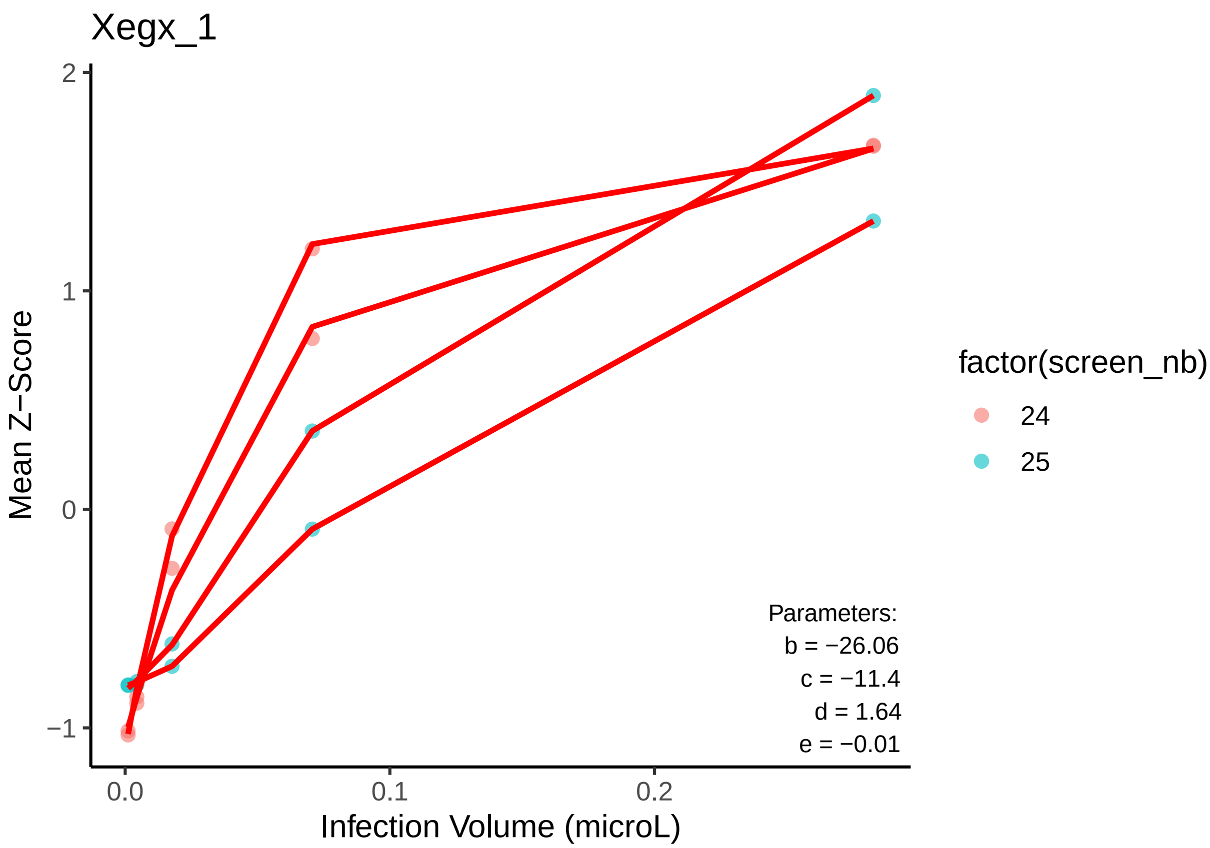


Wuye_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
8
9
10
Parameters:
b = −24.28
c = −10.86
d = 1.27
e = −0.04

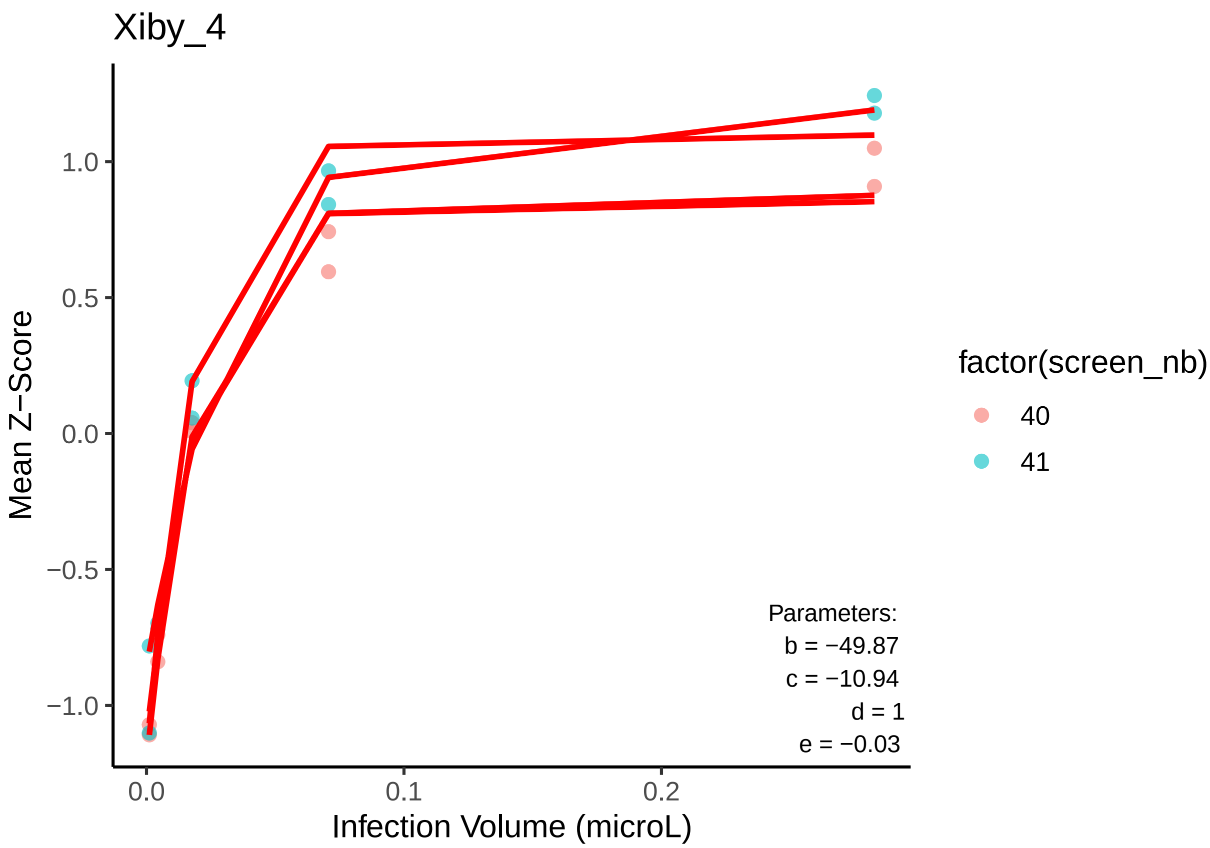

```
##
## $Xavk_3
```


Xavk_3
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −20.79
c = −1.17
d = 1.23
e = 0.08
factor(screen_nb)
28
29

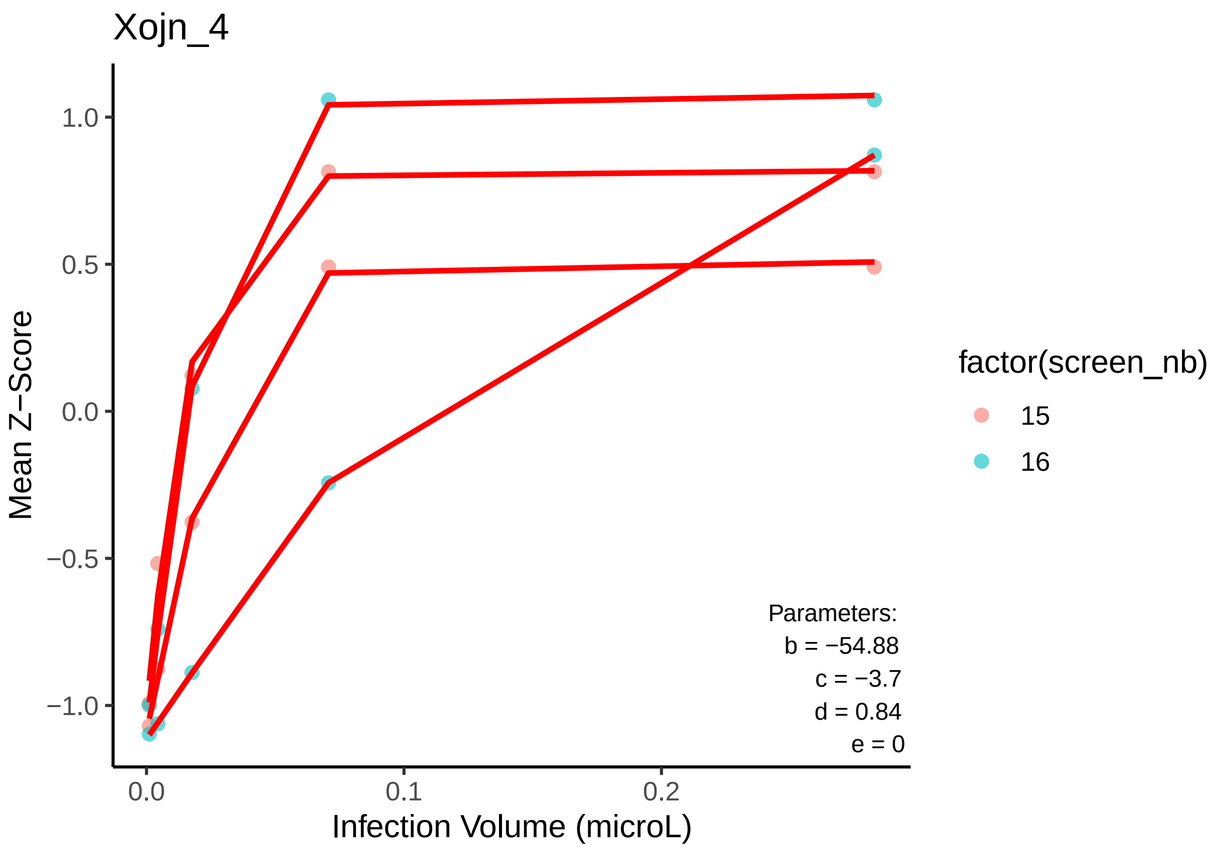
```
##
## $Xegx_1
```


Xegx_1
Mean Z−Score
Infection Volume (microL)
factor(screen_nb)
24
25
Parameters:
b = −26.06
c = −11.4
d = 1.64
e = −0.01
2
1
0
−1
0.0
0.1
0.2

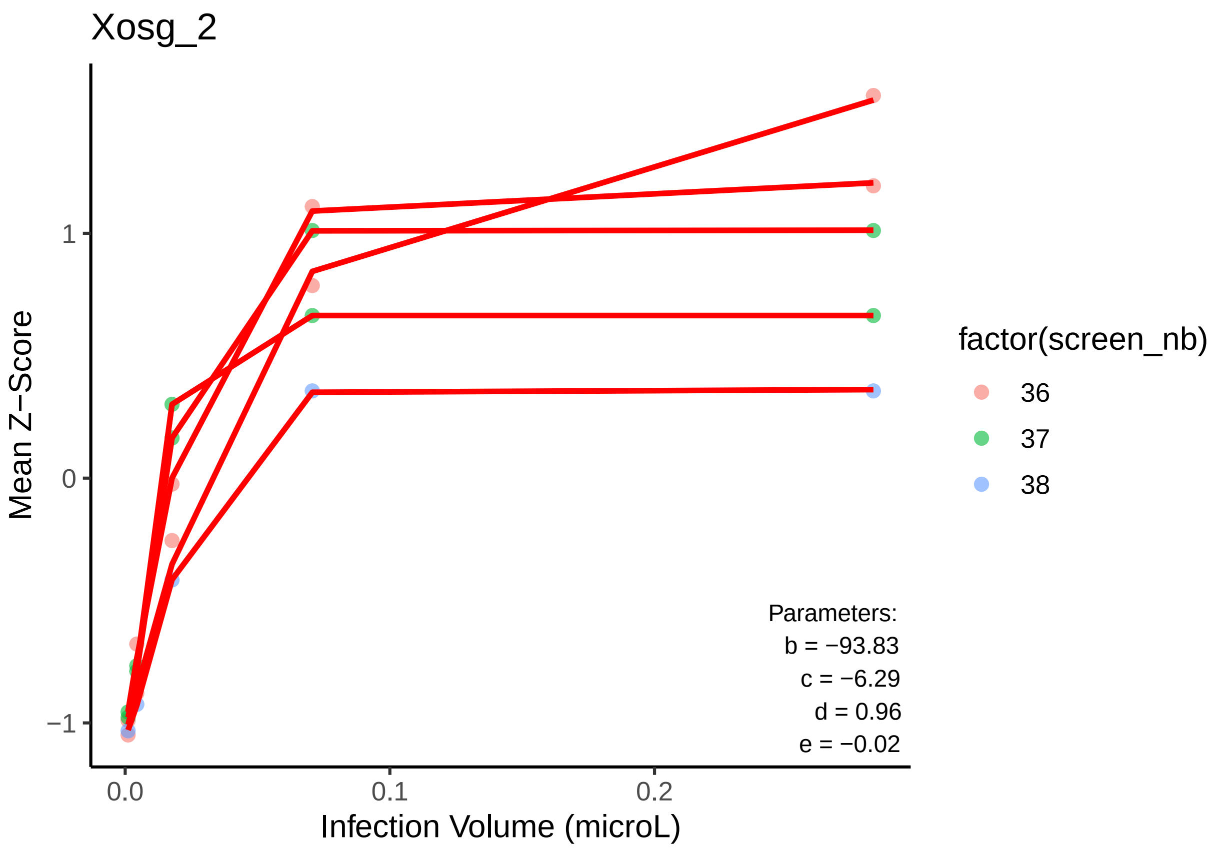
```
##
## $Xiby_4
```


Xiby_4
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −49.87
c = −10.94
d = 1
e = −0.03
factor(screen_nb)
40
41

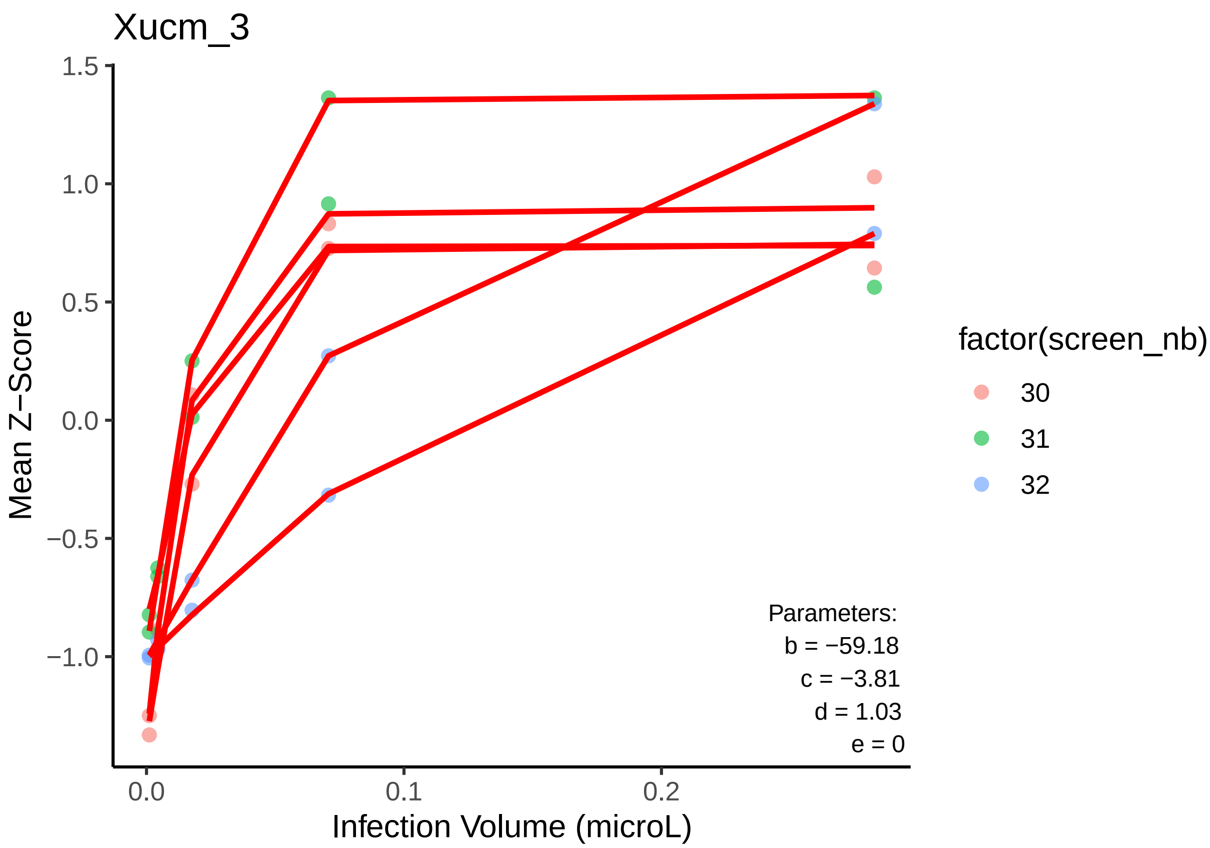
```
##
## $Xojn_4
```


Xojn_4
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
15
16
Parameters:
b = −54.88
c = −3.7
d = 0.84
e = 0

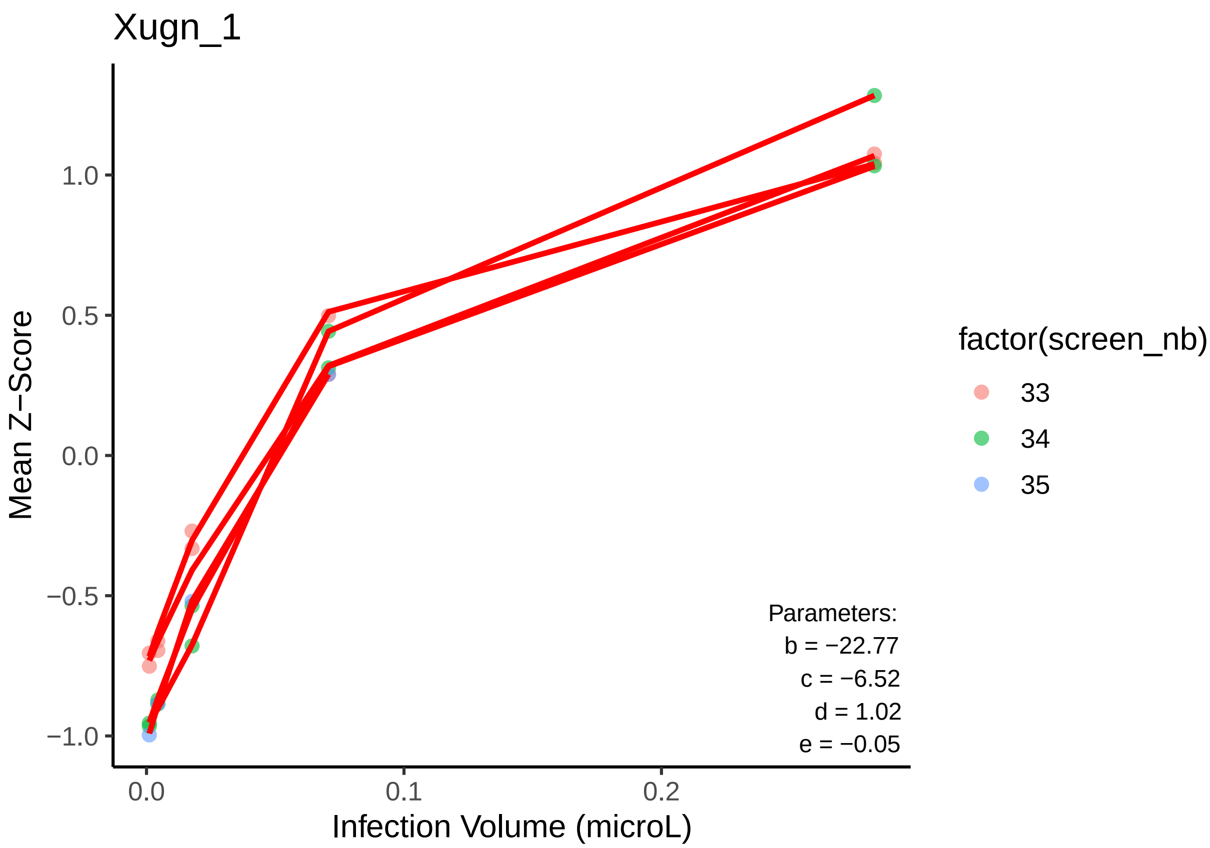
```
##
## $Xosg_2
```


Xosg_2
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −93.83
c = −6.29
d = 0.96
e = −0.02
factor(screen_nb)
36
37
38

```
##
## $Xucm_3
```

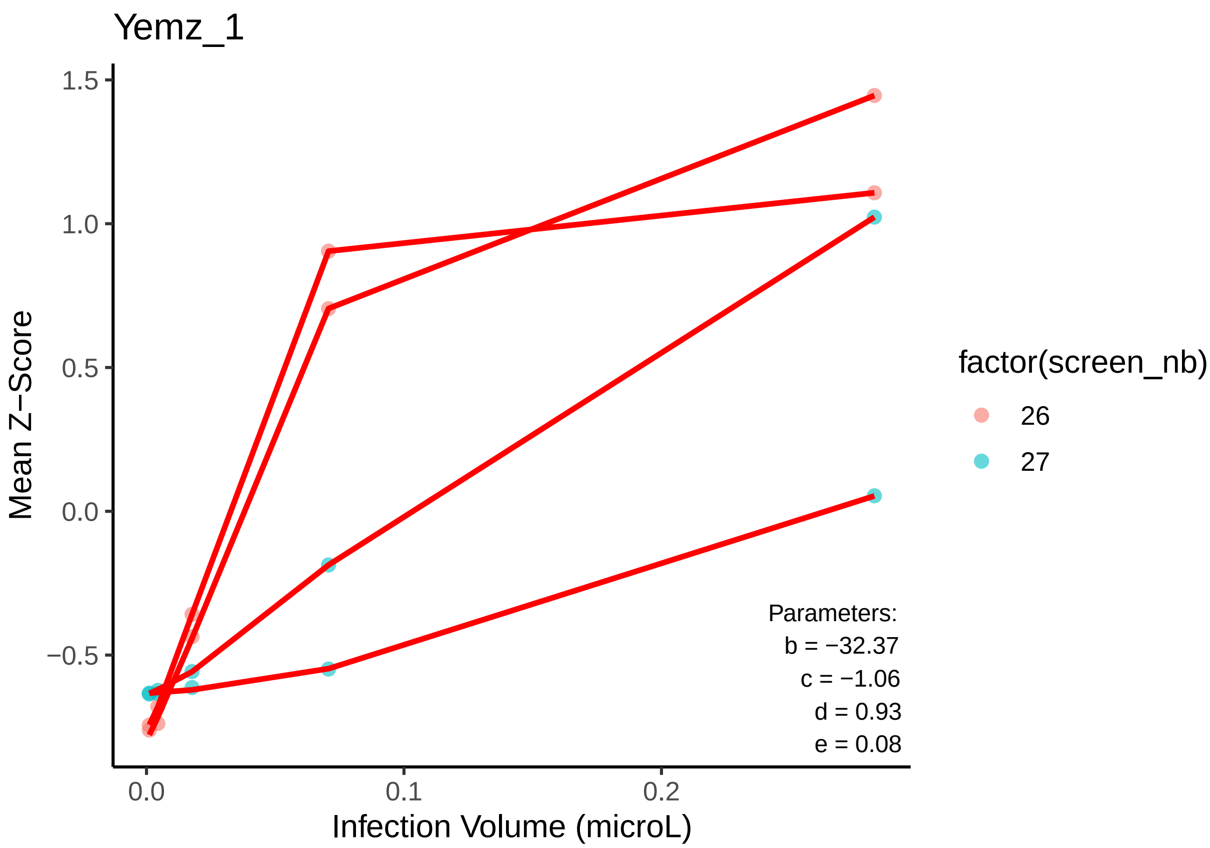

Xucm_3
1.5
1.0
0.5
0.0
−0.5
−1.0
Mean Z−Score
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −59.18
c = −3.81
d = 1.03
e = 0
factor(screen_nb)
30
31
32

```
##
## $Xugn_1
```

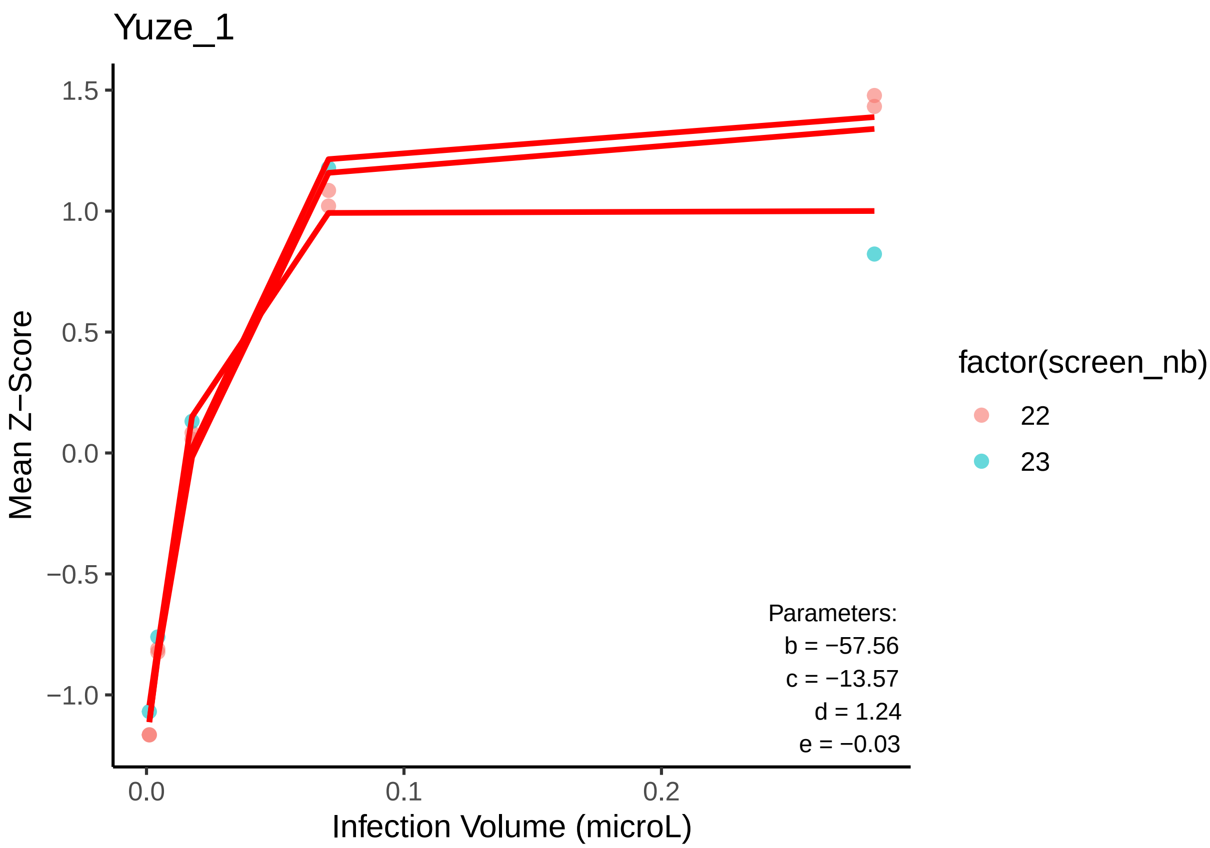


Xugn_1
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −22.77
c = −6.52
d = 1.02
e = −0.05
factor(screen_nb)
33
34
35

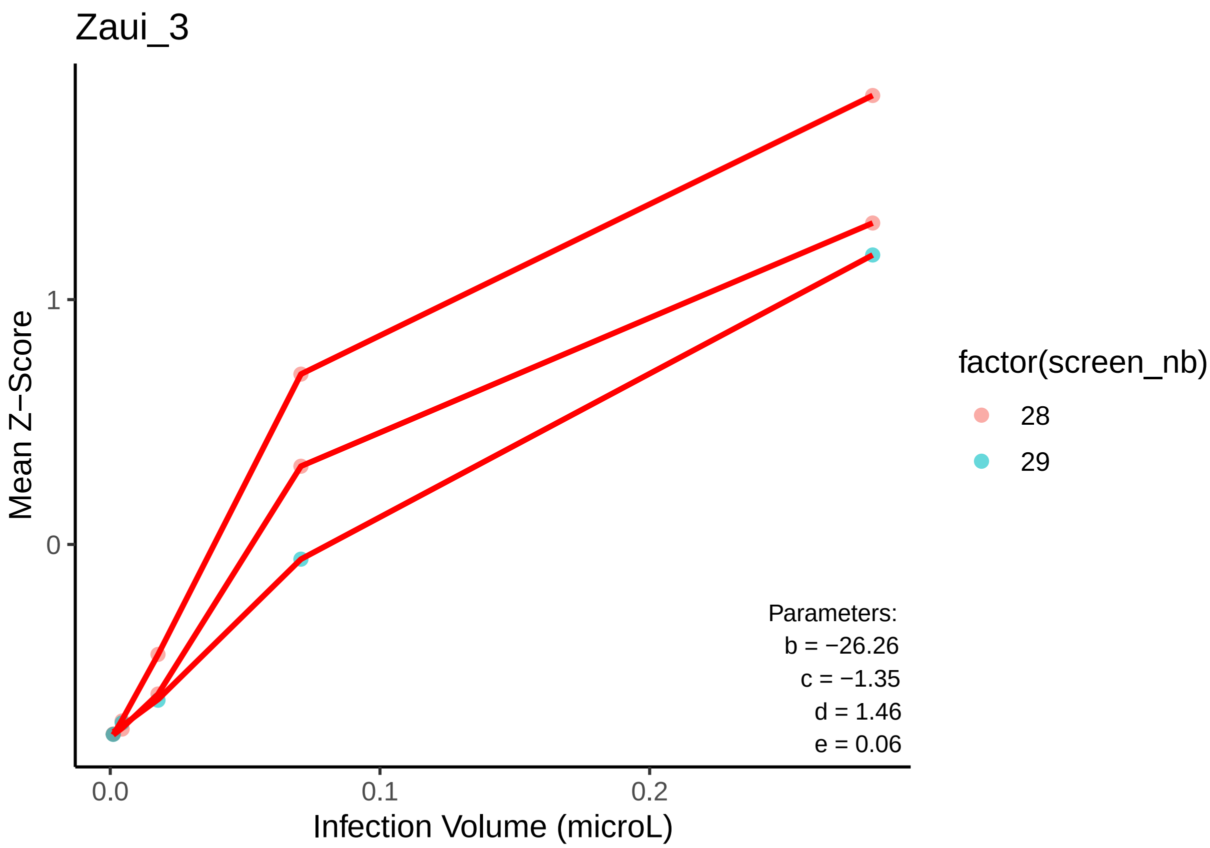

```
##
## $Yemz_1
```


Yemz_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
26
27
Parameters:
b = −32.37
c = −1.06
d = 0.93
e = 0.08

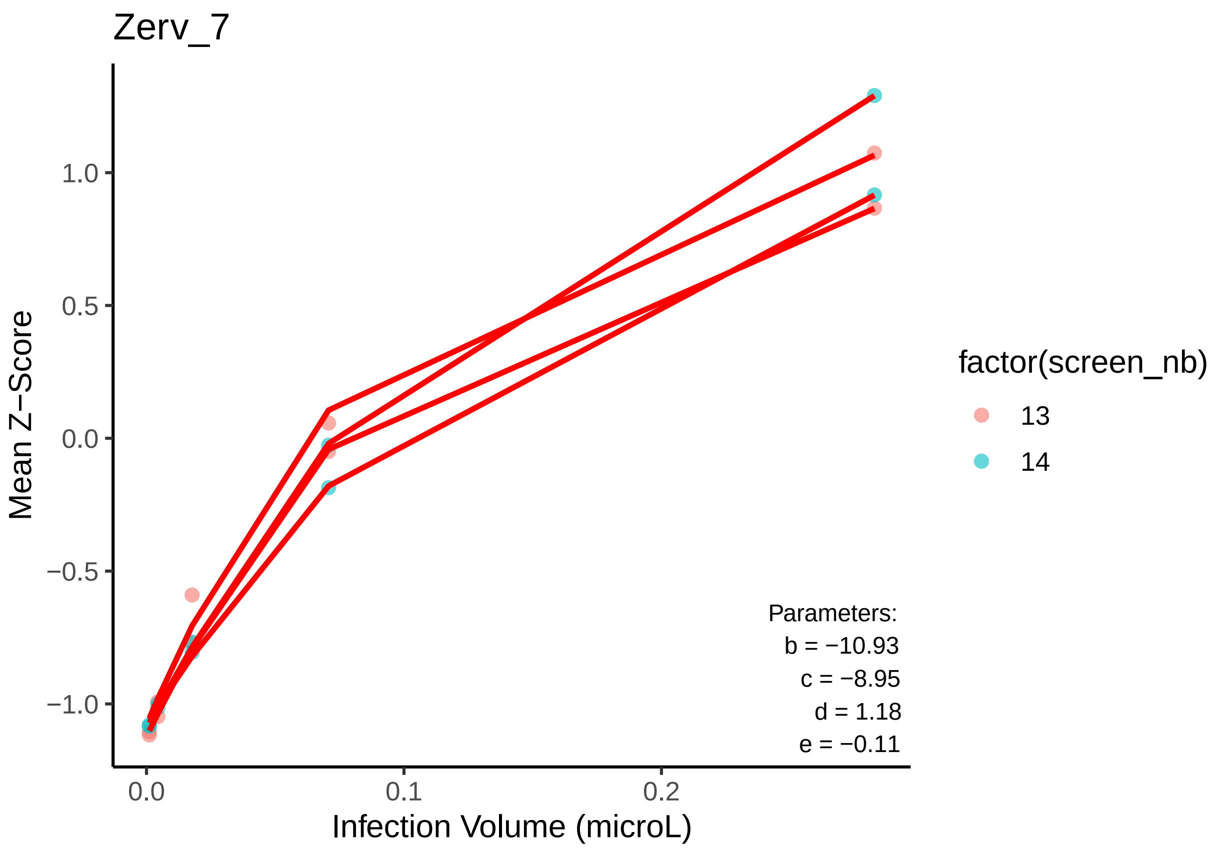
```
##
## $Yuze_1
```


Yuze_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
22
23
Parameters:
b = −57.56
c = −13.57
d = 1.24
e = −0.03

```
##
## $Zaui_3
```

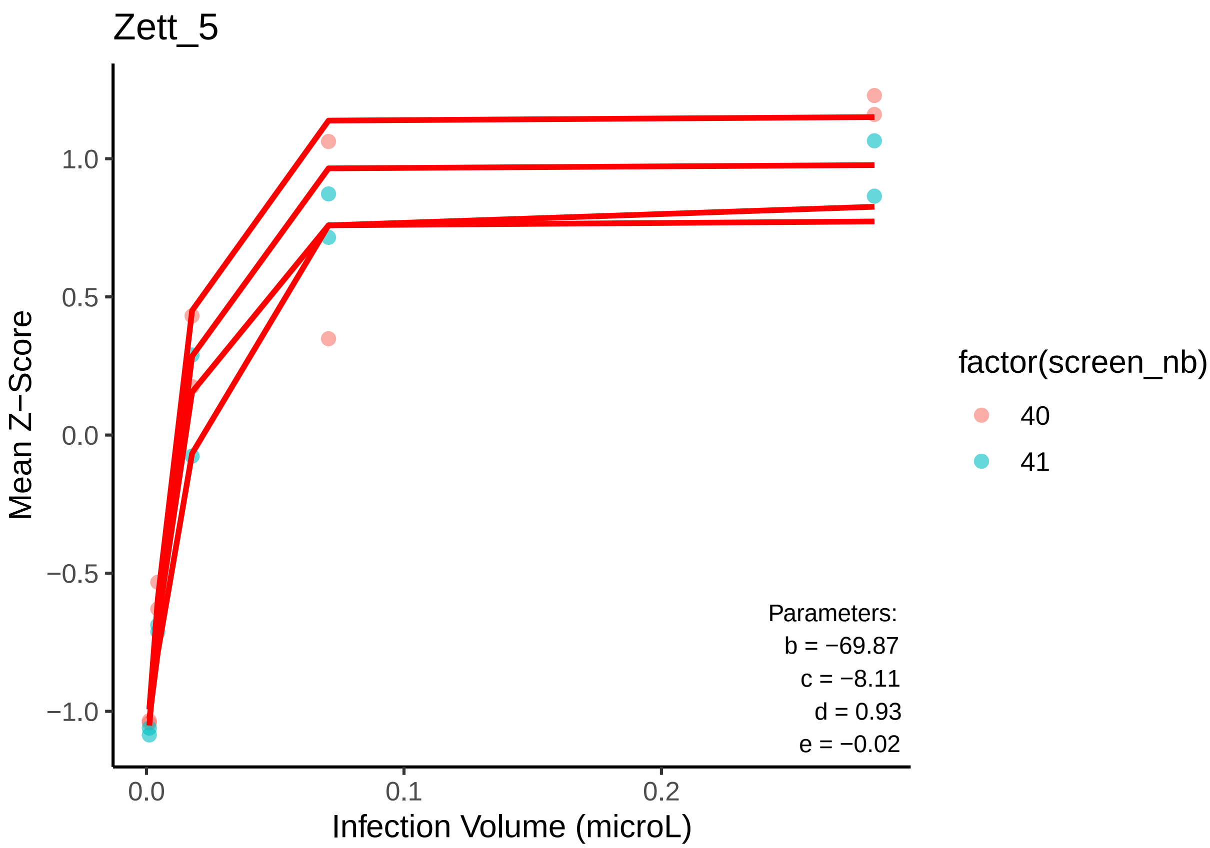

Zaui_3
Mean Z−Score
1
0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
28
29
Parameters:
b = −26.26
c = −1.35
d = 1.46
e = 0.06

```
##
## $Zerv_7
```

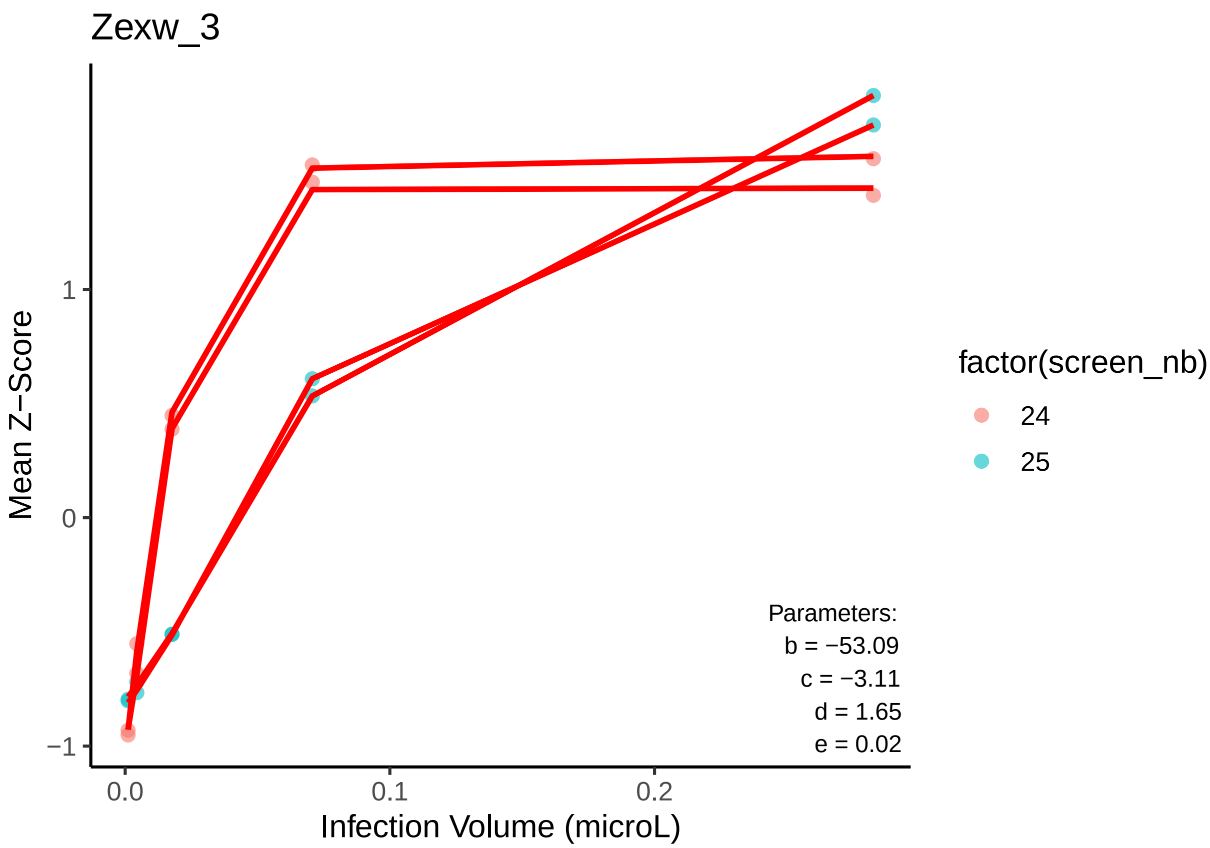


Zerv_7
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
factor(screen_nb)
13
14
Parameters:
b = −10.93
c = −8.95
d = 1.18
e = −0.11

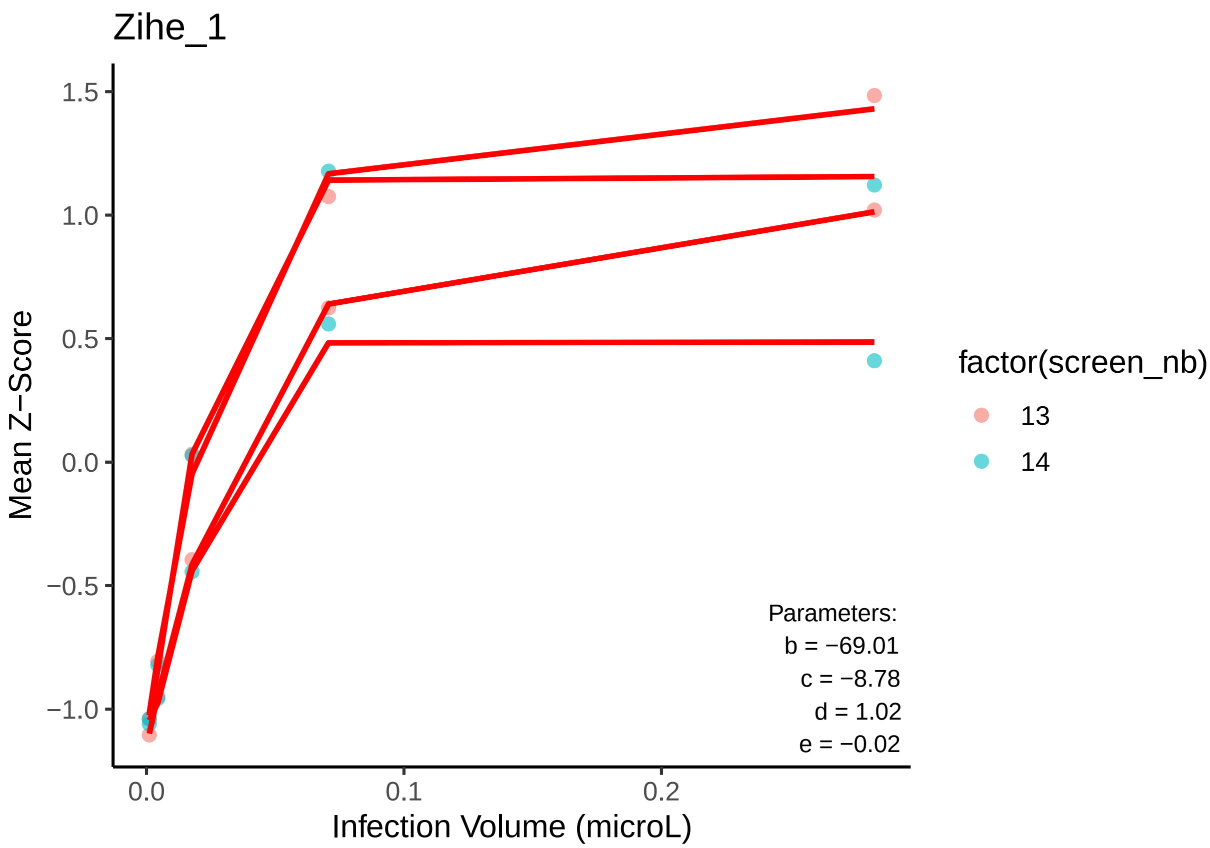

```
##
## $Zett_5
```


Zett_5
Mean Z−Score
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −69.87
c = −8.11
d = 0.93
e = −0.02
factor(screen_nb)
40
41

```
##
## $Zexw_3
```

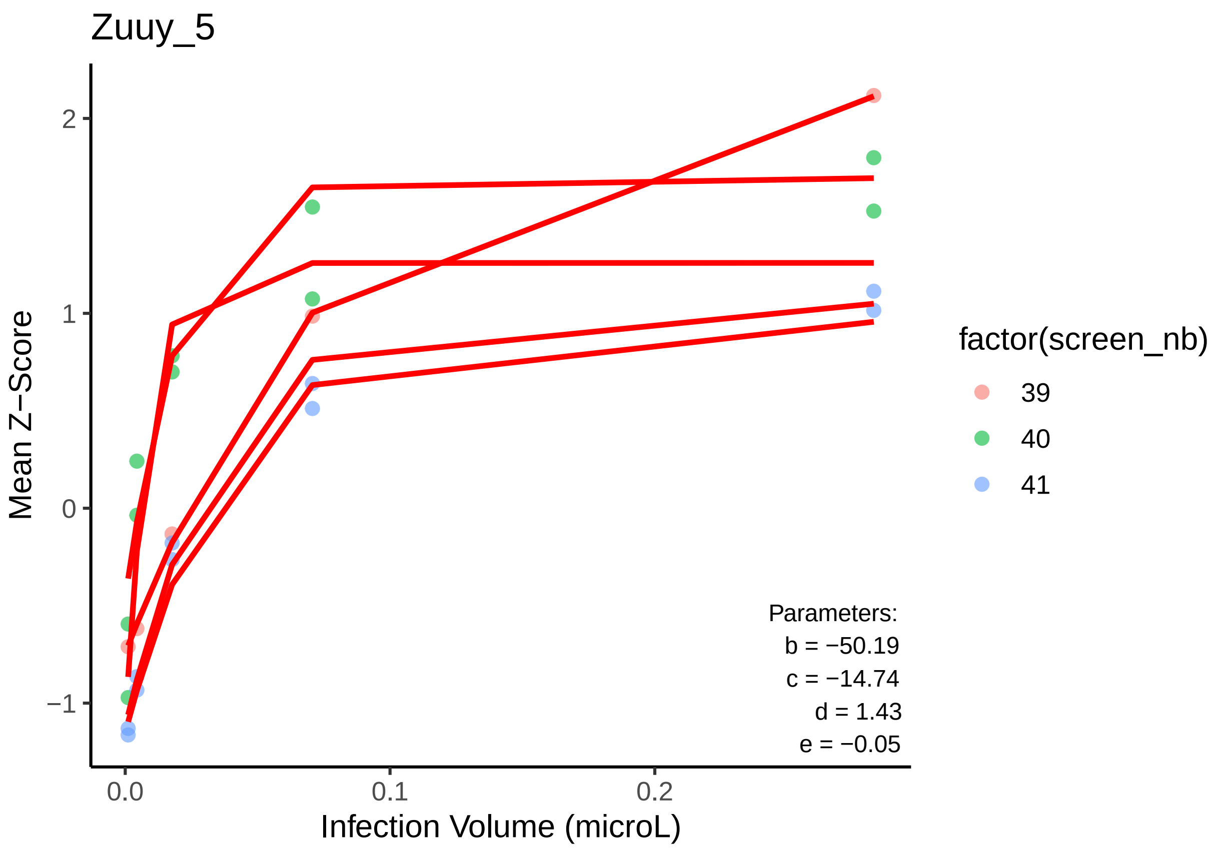

Zexw_3
Mean Z−Score
1
0
−1
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −53.09
c = −3.11
d = 1.65
e = 0.02
factor(screen_nb)
24
25

```
##
## $Zihe_1
```



Zihe_1
Mean Z−Score
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0
0.1
0.2
Infection Volume (microL)
Parameters:
b = −69.01
c = −8.78
d = 1.02
e = −0.02
factor(screen_nb)
13
14


```
##
## $Zuuy_5
```




## averaging and cleaning data

I now bind rows from the cell line dataframe list to get a dataframe containing all my parameters, i then group it and summarise it to get the mean for all the parameters across replicates

```
HIV1_vector_data=vector_data_per_cell_line%>%unnest()
```

```
## Warning: `cols` is now required when using `unnest()`.
## i Please use `cols = c(data)`.
```

```
HIV1_vector_data_mean=HIV1_vector_data%>%
  group_by(batch,cell_line,screen,screen_nb,titre,infection_volume_ul)%>%
  summarise(assay_output=mean(assay_output),
            zscore=mean(zscore),a_log=mean(a),
            b_log=mean(b),c_log=mean(c),
            logis_b=mean(logis_b),
            logis_d=mean(logis_d),
            logis_c=mean(logis_c),
            logis_e=mean(logis_e),
            area_under_curve=mean(area_under_curve))%>%
  ungroup()
```

```
## `summarise()` has grouped output by 'batch', 'cell_line', 'screen',
## 'screen_nb', 'titre'. You can override using the `.groups` argument.
```

```
HIV1_vector_data_mean <- HIV1_vector_data_mean %>%
  mutate(across(c(zscore, a_log, b_log,c_log, logis_b, logis_d,logis_c,logis_e, area_under_curve), as.nu
```

i then create a dataframe containing the parameter information for each cell screen, so one row per screen and cell line

```
HIV1_vector_data_PCA=unique(HIV1_vector_data_mean%>%
                              group_by(cell_line,screen_nb)%>%
                              summarise(assay_output=max(zscore),
                                        a_log=a_log,
                                        b_log=(b_log),
                                        c_log=c_log,
                                        logis_b=logis_b,
                                        logis_d=logis_d,
                                        logis_c=logis_c,
                                        logis_e=logis_e,
                                        area_under_curve=area_under_curve))
```

```
## Warning: Returning more (or less) than 1 row per `summarise()` group was deprecated in
## dplyr 1.1.0.
## i Please use `reframe()` instead.
## i When switching from `summarise()` to `reframe()`, remember that `reframe()`
##   always returns an ungrouped data frame and adjust accordingly.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## `summarise()` has grouped output by 'cell_line', 'screen_nb'. You can override
## using the `.groups` argument.
```

Then averaging between screens,so i get a dataframe with each cell line by itself with its parameters

```
HIV1_vector_data_PCA_sum <- HIV1_vector_data_PCA %>%
  group_by(cell_line) %>%
  summarise(
    assay_output      = mean(assay_output, na.rm = TRUE),
    a_log             = mean(a_log, na.rm = TRUE),
    b_log             = mean(b_log, na.rm = TRUE),
    c_log             = mean(c_log, na.rm = TRUE),
    logis_b           = -mean(logis_b, na.rm = TRUE),
    logis_d           = mean(logis_d, na.rm = TRUE),
    logis_c           = mean(logis_c, na.rm = TRUE),
    logis_e           = mean(logis_e, na.rm = TRUE),
    area_under_curve  = abs(mean(area_under_curve, na.rm = TRUE))
  )
```

i Then rescale it for the PCA, allowing the different parameters to be included(by scaling it one parameter with a different range doesn't have a skewing effect on the data)

i then turn it into a matrix to set the row names as the cell names,

```
HIV1_vector_data_PCA_1=HIV1_vector_data_PCA_sum%>%mutate_if(is.numeric,scale)



HIV1_vector_data_PCA_1=subset(HIV1_vector_data_PCA_1, select=-cell_line)

HIV1_vector_data_PCA_1=as.matrix(HIV1_vector_data_PCA_1)

row.names(HIV1_vector_data_PCA_1)=HIV1_vector_data_PCA_sum$cell_line
```

here i am checking the correlation but there is a visualization for this later

```r
HIV1_vector_data_PCA_1=as.data.frame(HIV1_vector_data_PCA_1)
cor(x=HIV1_vector_data_PCA_1$c_log,y=HIV1_vector_data_PCA_1$area_under_curve)
```

```
## [1] 0.3553378
```

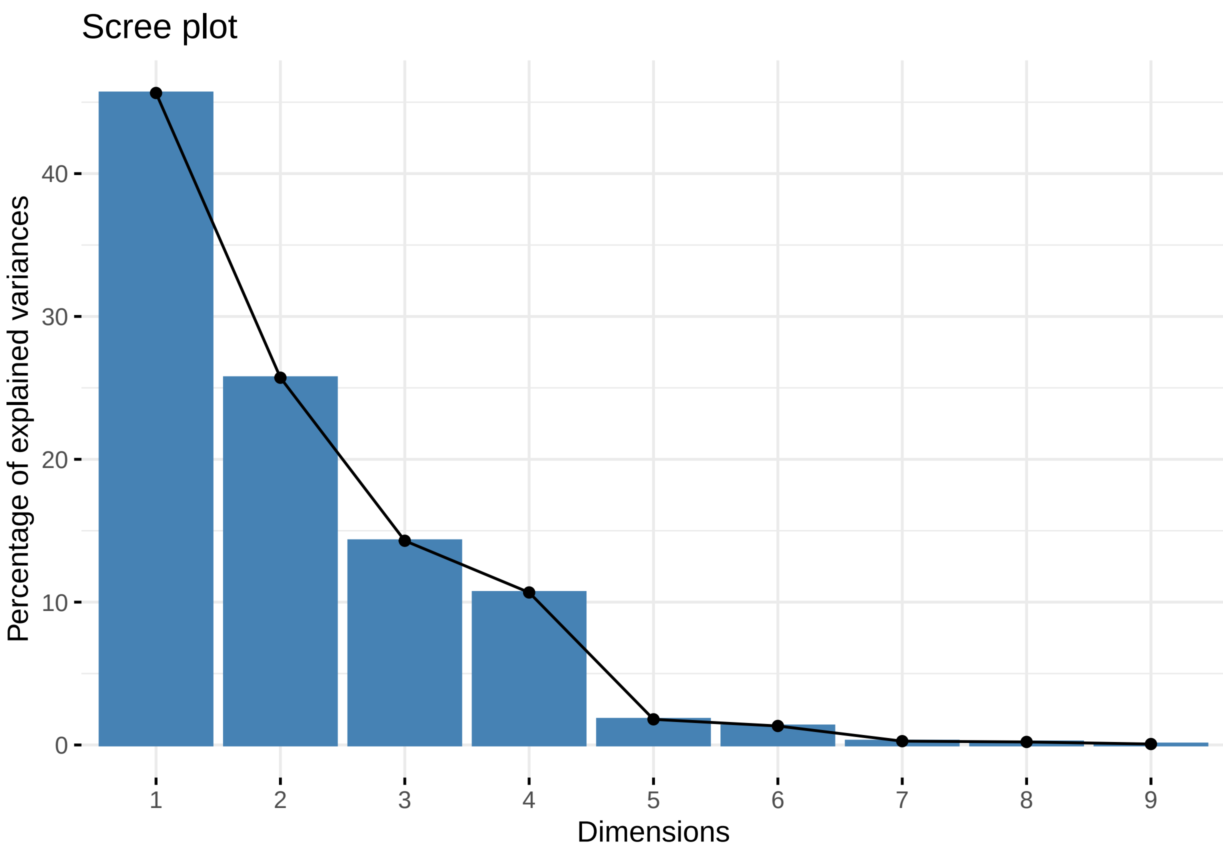
#PCA

i used prcomp for my pca analysis, also used factoextra which gives me some more tools to help visualise the data, it generates an object that allows me to visualise data

```r
PCA=prcomp(x = HIV1_vector_data_PCA_1)
```

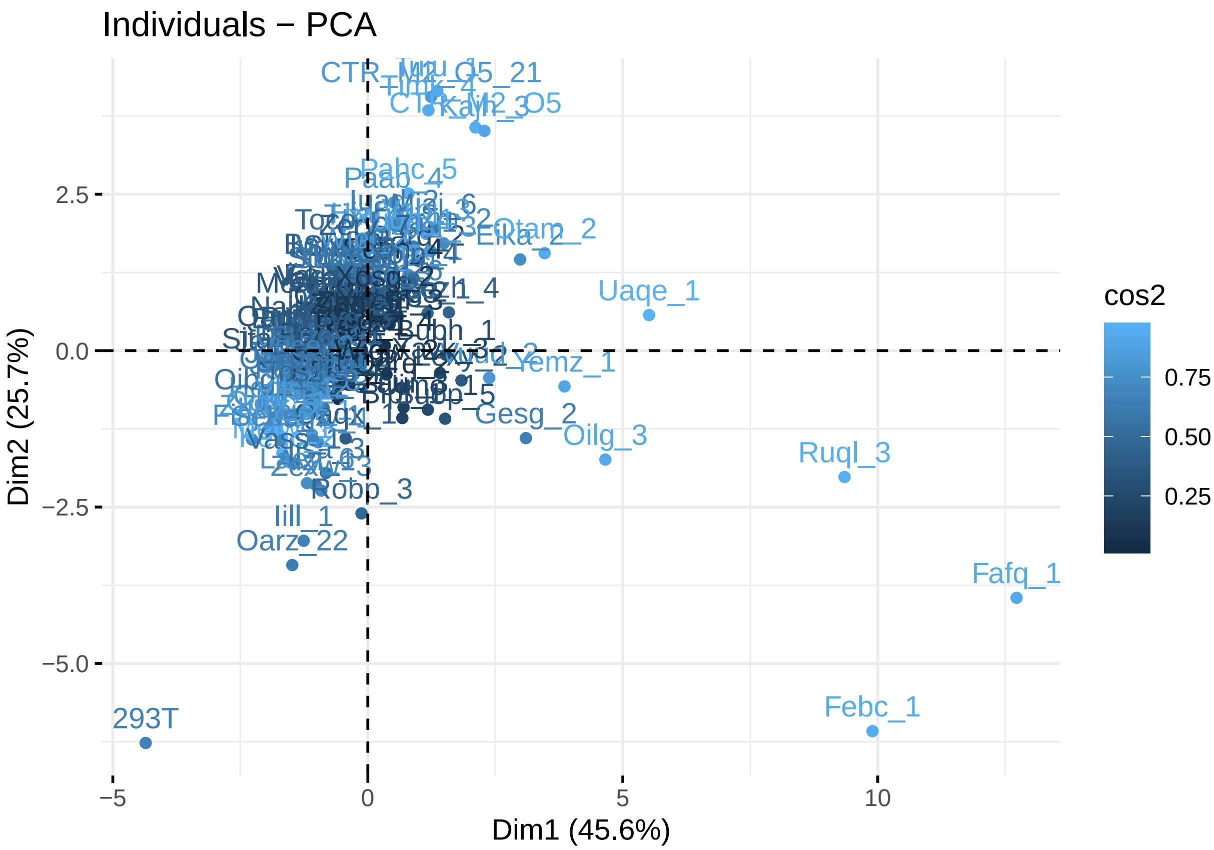
I generate a graph to show me my contributions for each principle component, normally majority of difference in variance is explained by PC1 and PC2

```r
library(factoextra)
fviz_eig(PCA)
```



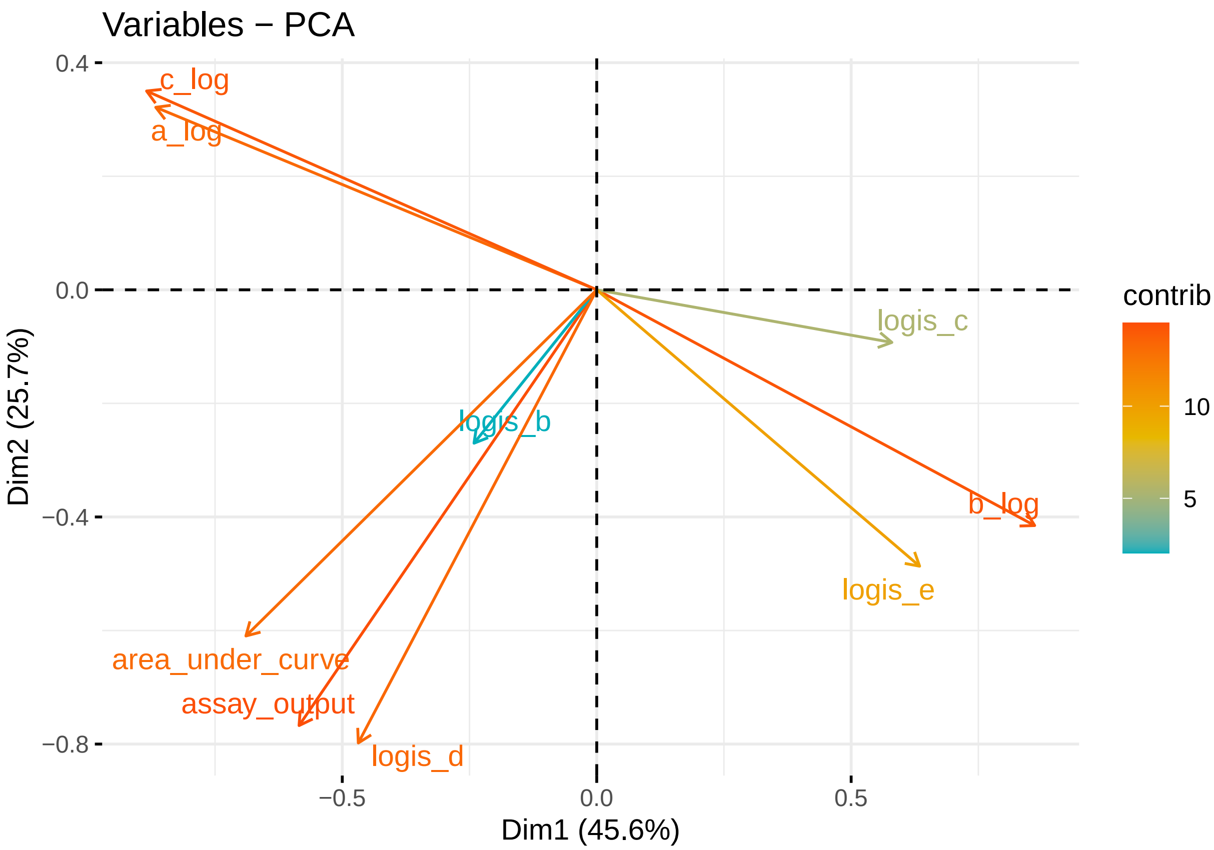

This is a plot of the points on my graph by PC1 and PC2 , can visualise the spread

```r
fviz_pca_ind(PCA,col.ind = "cos2",repel = F)
```



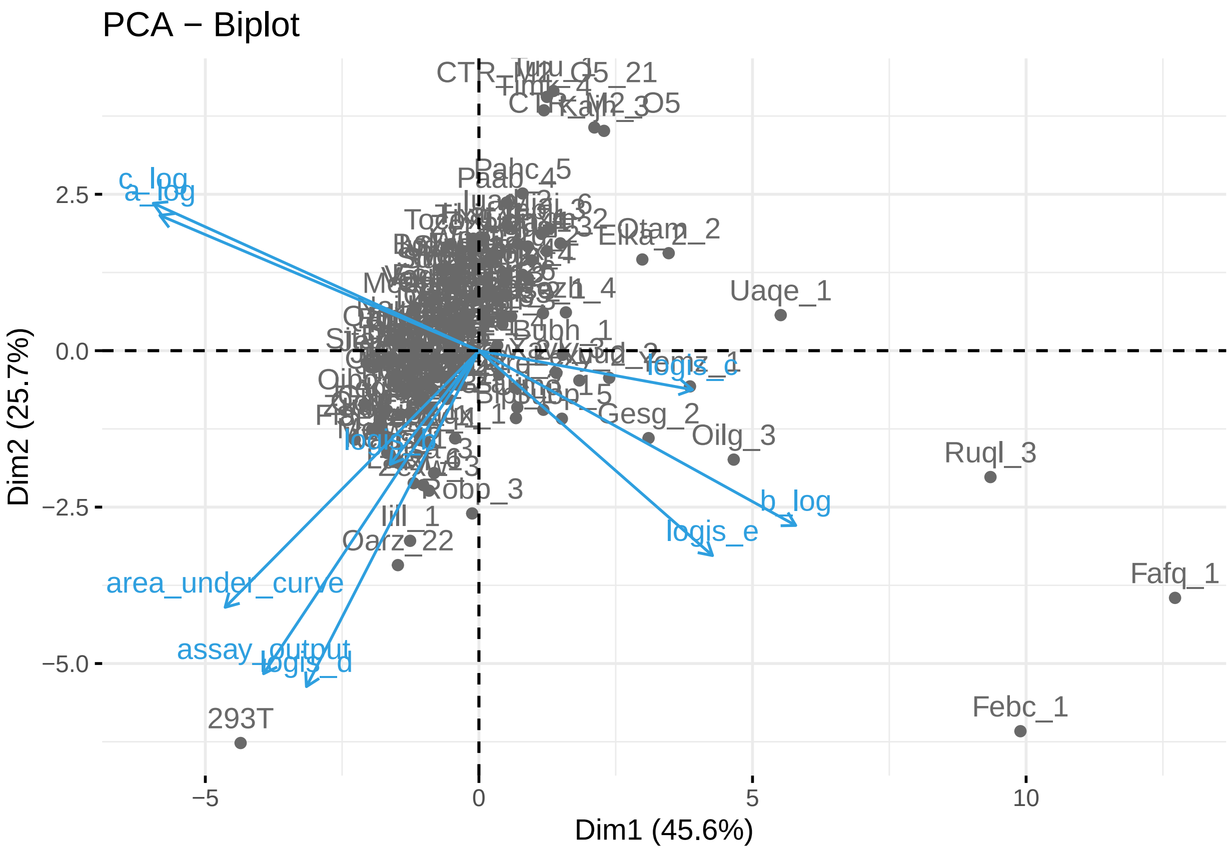

This shows how each of my parameters contribute to the variance explained in PC1 and PC2, the more direction a parameter points to the more that parameter contributes to the. variance explained by that Principle component. Contributions are shown by colour, with blue meaning it has little contribution to the variance in the PCs

```
fviz_pca_var(PCA,
             col.var = "contrib", # Color by contributions to the PC
             gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
             repel = TRUE )
```




Overlays data points with the parameters to see how each datapiont is in parameter and can see which parameters are causing the split

```
fviz_pca_biplot(PCA, repel=F,
                col.var = "#2E9FDF", # Variables color
                col.ind = "#696969"  # Individuals color
                )
```



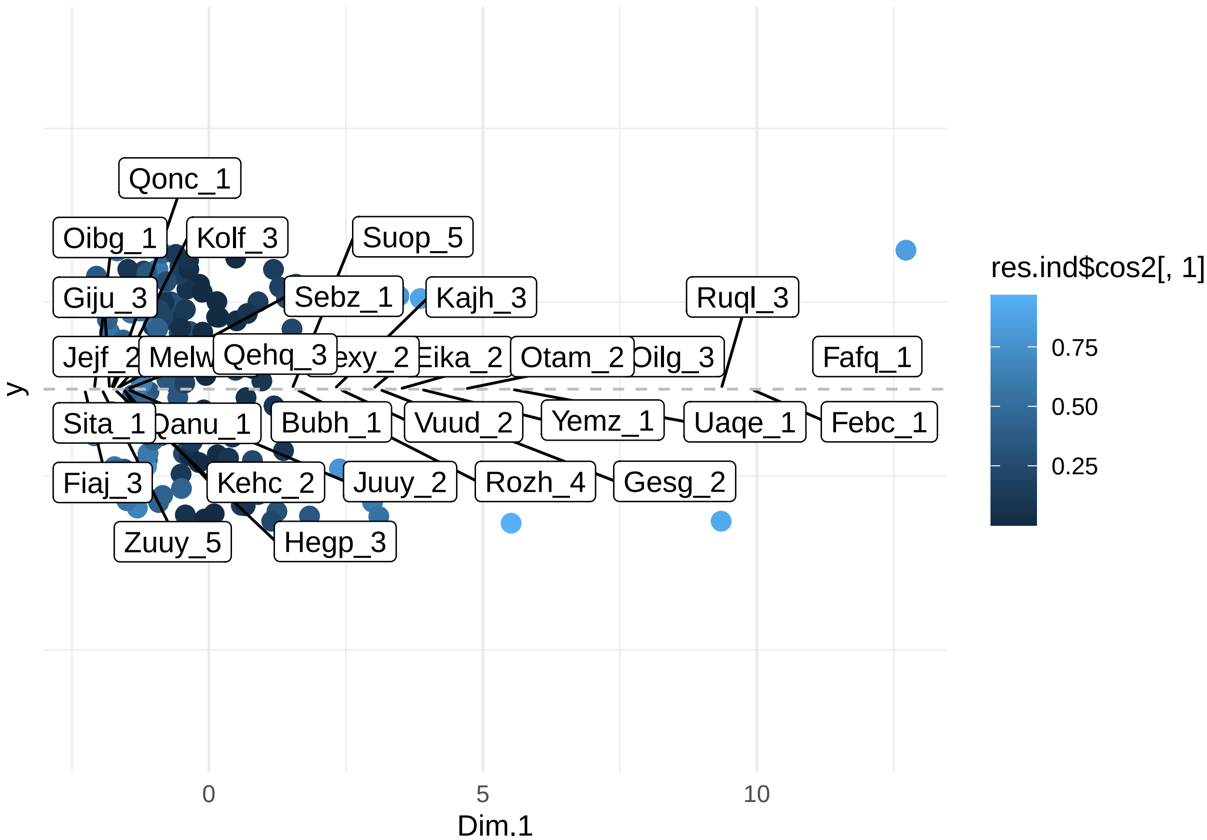

In this snippet i get rid of positive and negative controls for dataset as it would affect the quantiles i use to determine extremes and would take up other cell lines in that quantile e.g the top 10%.

I then plot a graph showing how data is organised only on the PC with the highest percentage of variance (PC1), this gives me a linear graph of points. I added jitter to make the points more readable but the y axis in the graph doesn't represent anything at all

```
res.ind <- get_pca_ind(PCA)
dim(res.ind$coord)
```

```
## [1] 153   9
```

```
ind_coord <- as.data.frame(res.ind$coord)
ind_coord=ind_coord[-which(row.names(ind_coord)==('293T')|row.names(ind_coord)=='CTR_M2_05'|row.names(in
res.ind$cos2=res.ind$cos2[-which(row.names(res.ind$cos2)==('293T')|row.names(res.ind$cos2)=='CTR_M2_05'

ggplot(data = ind_coord,aes(x=Dim.1,y = 0,label=row.names(ind_coord)))+
  geom_point(size = 3,aes(colour = res.ind$cos2[,1]), position = position_jitter(height = 0.02,width =
  geom_label_repel(aes(label=ifelse(Dim.1 < quantile(Dim.1, 0.1) | Dim.1 > quantile(Dim.1, 0.9),row.name
  geom_hline(yintercept = 0, linetype = "dashed", color = "gray")+
  theme_minimal() +
  coord_cartesian(ylim = c(-0.05, 0.05))+
  theme(axis.ticks.y = element_blank(),
        axis.text.y  = element_blank(),
        panel.grid.major.y = element_blank())
```



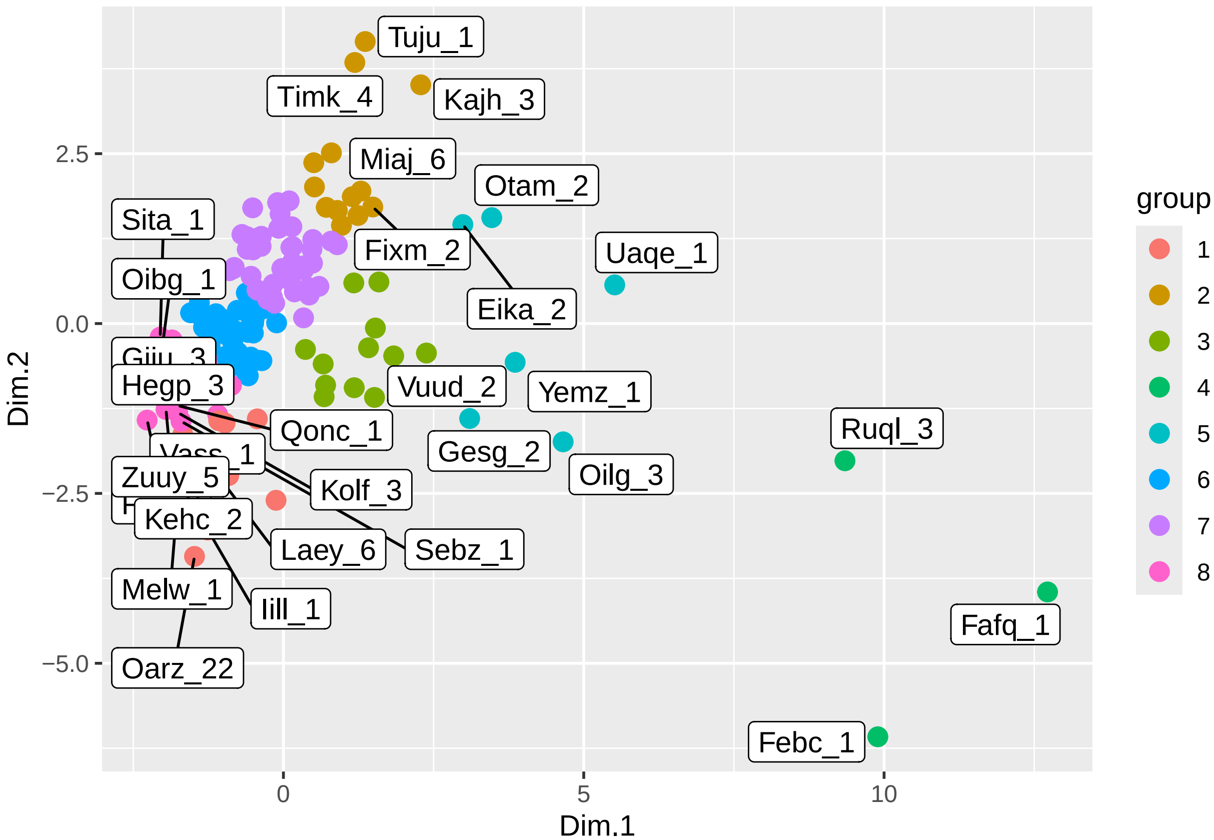

#classification

Here i work on my classification, because the PC1 is only about 50% means that i can't trust it properly classify my data, but just in case i keep the upper and lower 10% of the points for dimension 1

but i also create a weighted score, combining both PC1 and PC2 to properly split up my data. I try to use it by taking the percentages of PC1 and PC2 and rescaling it to 100% and then multiplying the PC by its scaled percentage. When you look at the directions of parameters and the spread of the cell lines, assay output and area under curve seem to account for most of the variation, so by weighting the PC, you can classify more accurately the top and bottom quantiles.

I also plot the points with k means clustering alogirthm, and i label based on the top quantiles for my combined score, i save the top and bottom 10% to their own dataframes for storage

```
susceptible_vector_cell=ind_coord[(ind_coord$Dim.1 < quantile(ind_coord$Dim.1, 0.1)),]
Resistant_vector_cell=ind_coord[(ind_coord$Dim.1 > quantile(ind_coord$Dim.1, 0.9)),]

HIV_vector_data_susceptible=HIV1_vector_data_PCA_1[match(row.names(susceptible_vector_cell),(HIV1_vecto
HIV_vector_data_resistant=HIV1_vector_data_PCA_1[match(row.names(Resistant_vector_cell),(HIV1_vector_da

set.seed(45)
clusters <- kmeans(ind_coord[, c("Dim.1", "Dim.2")], centers = 8)
ind_coord$group <- as.factor(clusters$cluster)
ind_coord$pc_combined=0.70*ind_coord$Dim.1+ 0.30*ind_coord$Dim.2

ggplot(data = ind_coord,aes(x=Dim.1,y = Dim.2,label=row.names(ind_coord)))+
  geom_point(size = 3,aes(colour = group))+
  geom_label_repel(aes(label=ifelse(pc_combined < quantile(pc_combined, 0.1) | pc_combined > quantile(pc
```




```
susceptible_vector_cell=ind_coord[(ind_coord$pc_combined < quantile(ind_coord$pc_combined, 0.1)),]
Resistant_vector_cell=ind_coord[(ind_coord$pc_combined > quantile(ind_coord$pc_combined, 0.9)),]


HIV1_vector_data_notable <- as.data.frame(rbind(HIV_vector_data_resistant, HIV_vector_data_susceptible)
  mutate(phenotype = ifelse(row.names(.) %in% row.names(HIV_vector_data_resistant),
                            "resistant",
                            "susceptible"))
```

here i create the classification based on the clusters, i set the clusters and choose the most extreme groups, NOTE- k means code changes every time so i set the seed. if the seed is changed this code would have to be changed also

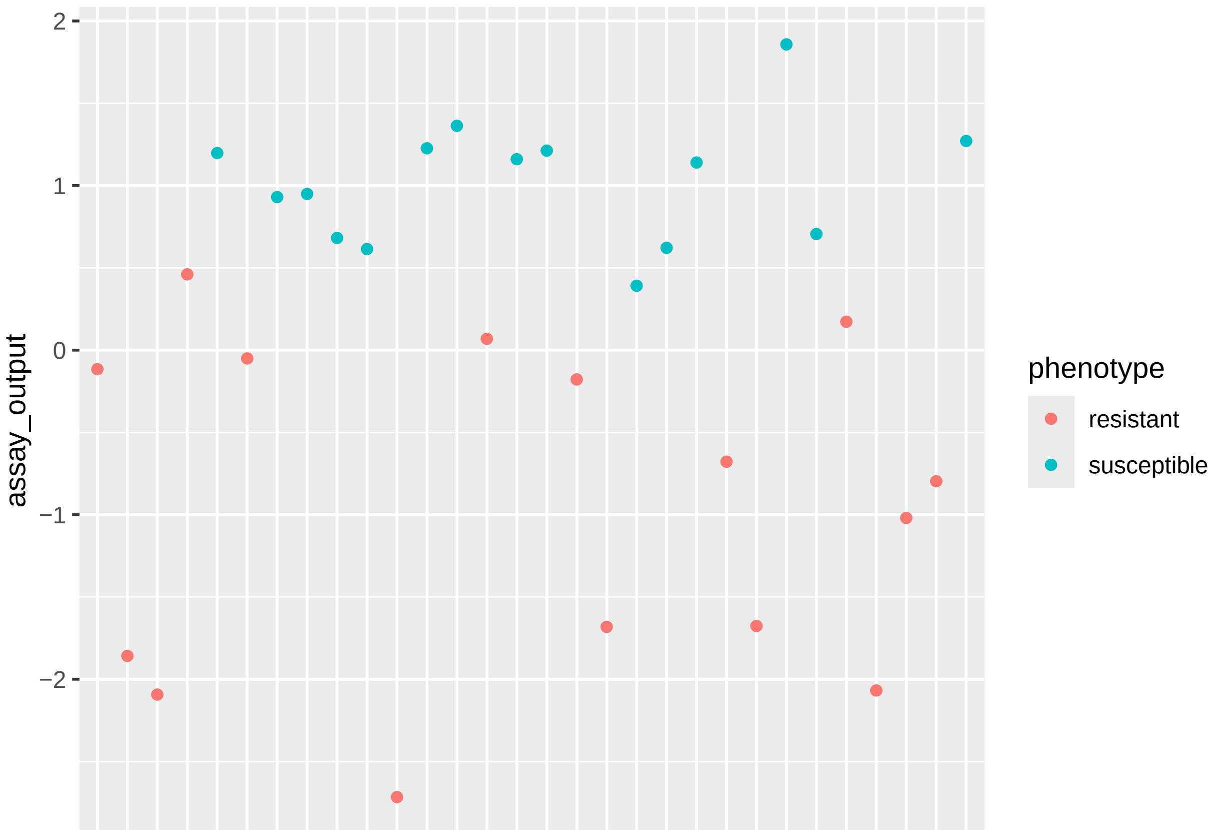
```
susceptible_vector_clusters=ind_coord[(ind_coord$group==1),]
Resistant_vector_clusters=ind_coord[(ind_coord$group==5|ind_coord$group==6|ind_coord$group==3),]
```

### visualising data split

here i visualise the extremes i found, and see the split between them in a graph, can see how well the separation is by splitting between the parameters, can also see how well parameters align to biological expectations

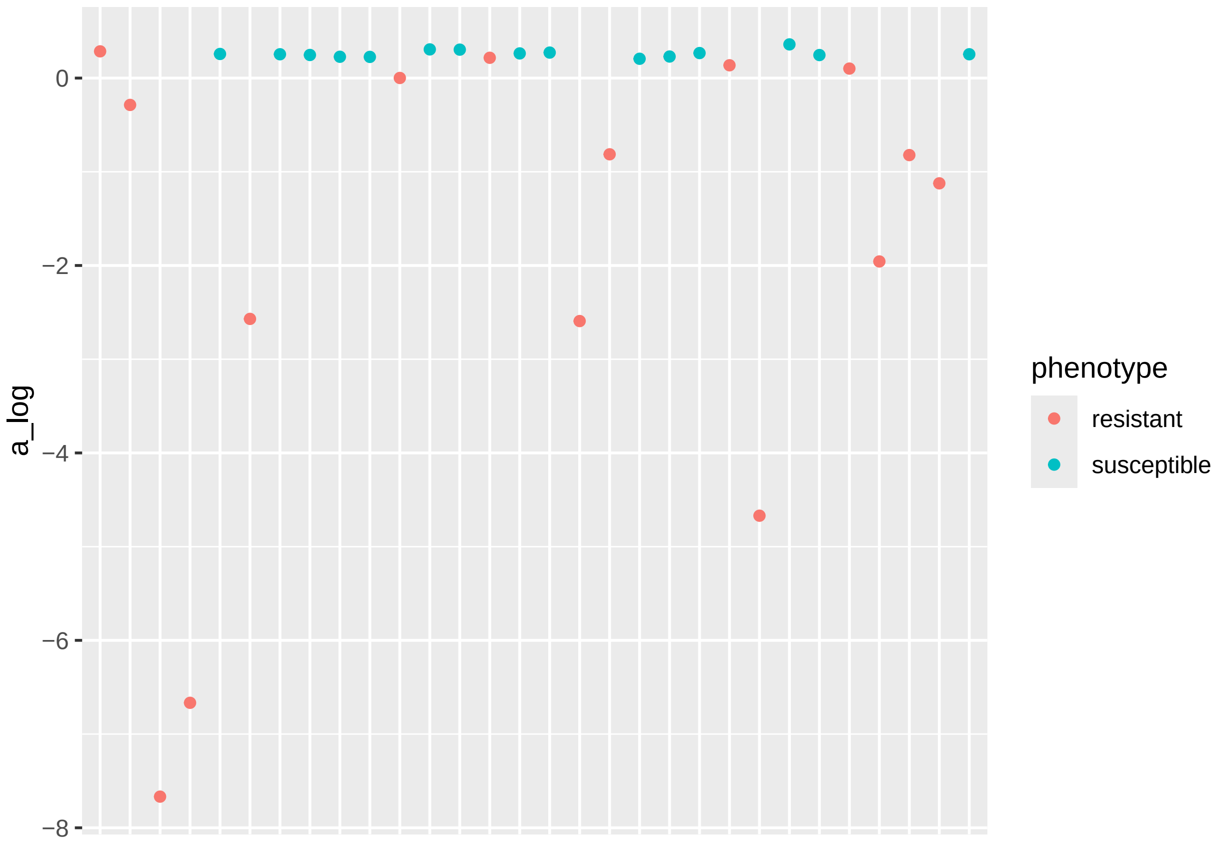
here i look at assay output(zscore) there is a solid split between the susceptible and resistant with suscpetibles consistenly having higher output (which is the max output seen)

```
ggplot(HIV1_vector_data_notable,aes(x=row.names(HIV1_vector_data_notable),y=assay_output,colour = pheno
  geom_point()+
  theme(axis.title.x=element_blank(),
        axis.text.x=element_blank(),
        axis.ticks.x=element_blank())
```

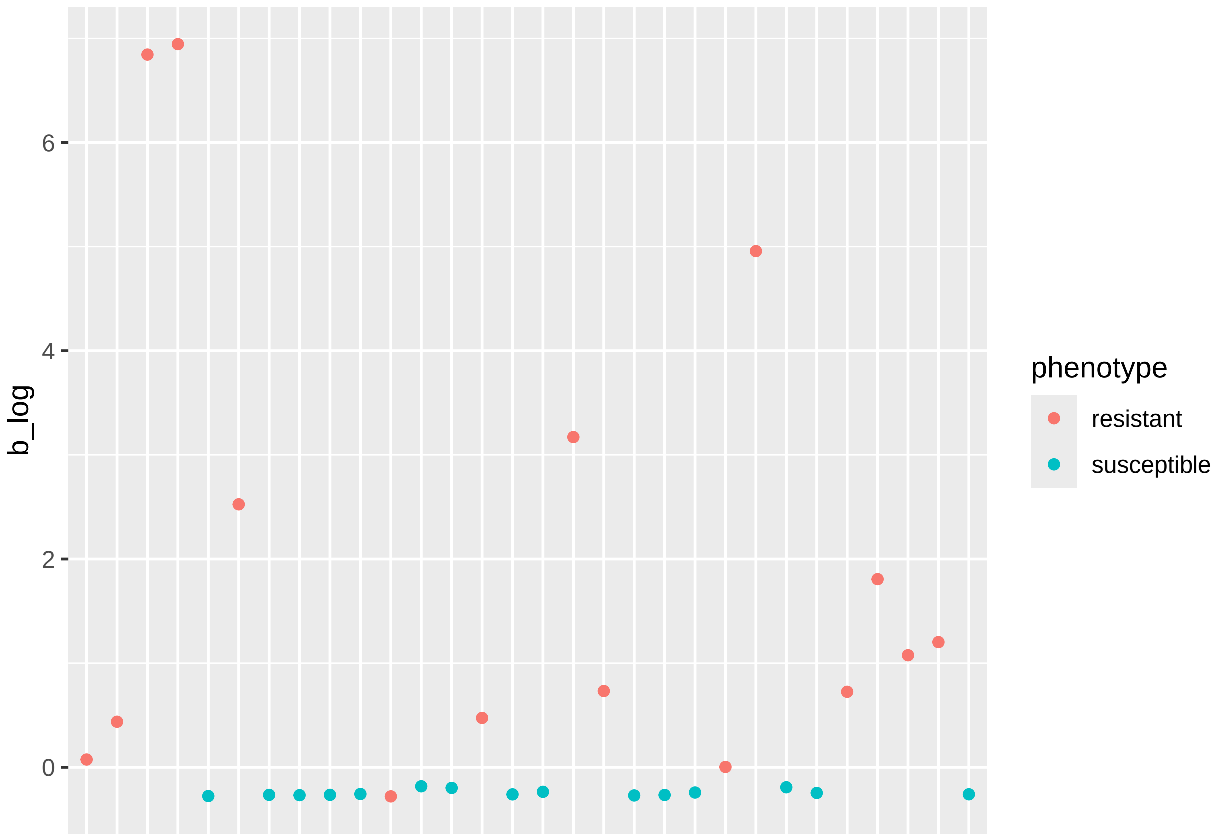



this looks at the a log (the y offset in our logarithmic function), there is a clear difference between the values with the resistant having lower y offsets which is what you would expect though some are near 0 but all the susceptible are above zero meaning showing they would be more permissible

```
ggplot(HIV1_vector_data_notable,aes(x=row.names(HIV1_vector_data_notable),y=a_log,colour = phenotype))+
  geom_point()+
  theme(axis.title.x=element_blank(),
        axis.text.x=element_blank(),
        axis.ticks.x=element_blank())
```

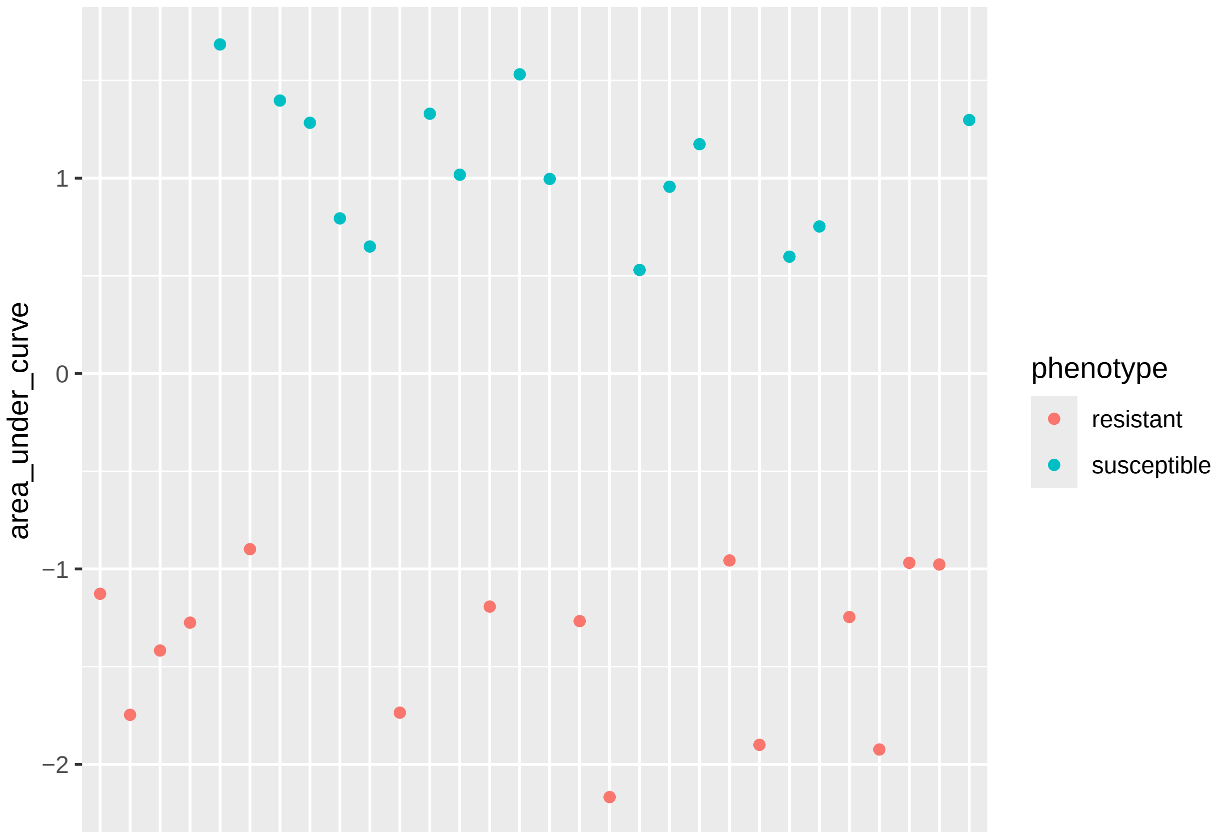



```
ggplot(HIV1_vector_data_notable,aes(x=row.names(HIV1_vector_data_notable),y=b_log,colour = phenotype))+
  geom_point()+
  theme(axis.title.x=element_blank(),
        axis.text.x=element_blank(),
        axis.ticks.x=element_blank())
```

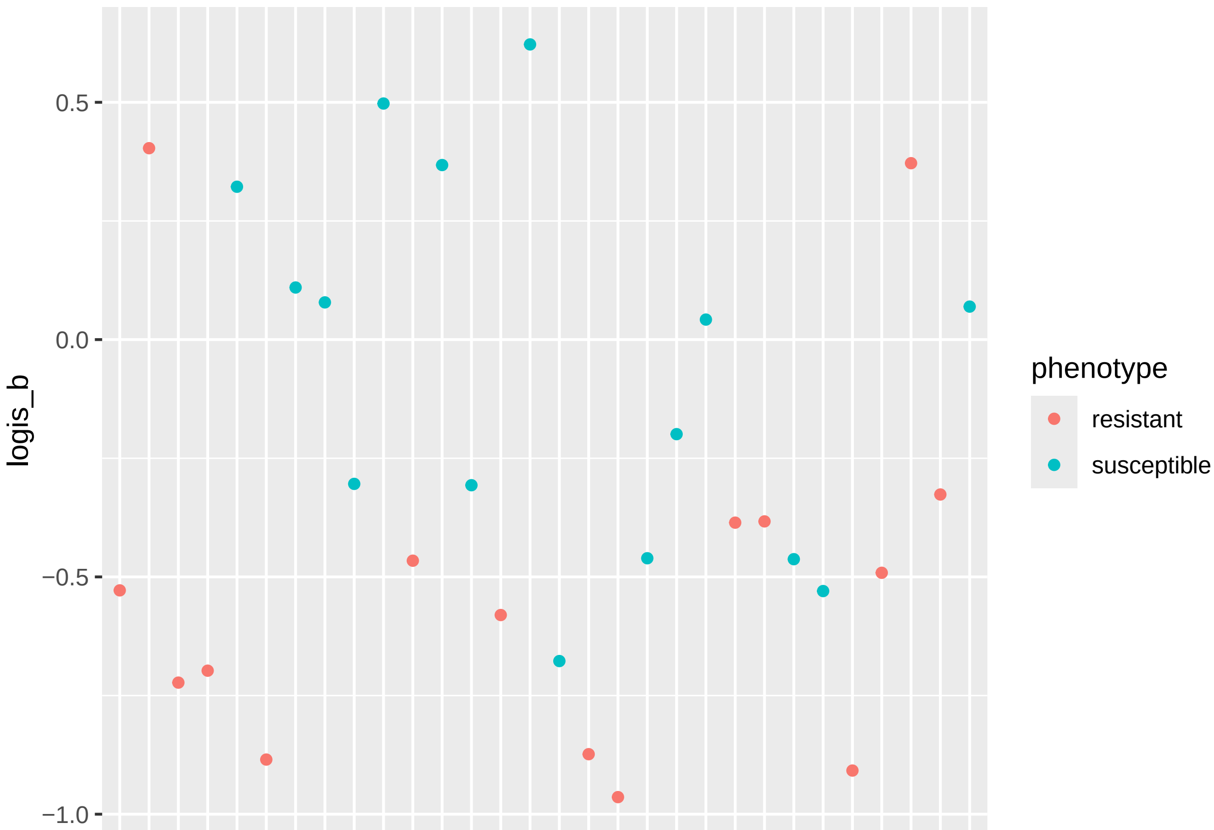



This also has a clear split which biologically makes sense, though biologically having a high absolute AUC doesn't neccesarily mean that it is a extremely susceptible, but it does imply something about the dynamics of the and how it responds vector

```
ggplot(HIV1_vector_data_notable,aes(x=row.names(HIV1_vector_data_notable),y=area_under_curve,colour = ph
  geom_point()+
  theme(axis.title.x=element_blank(),
        axis.text.x=element_blank(),
        axis.ticks.x=element_blank())
```



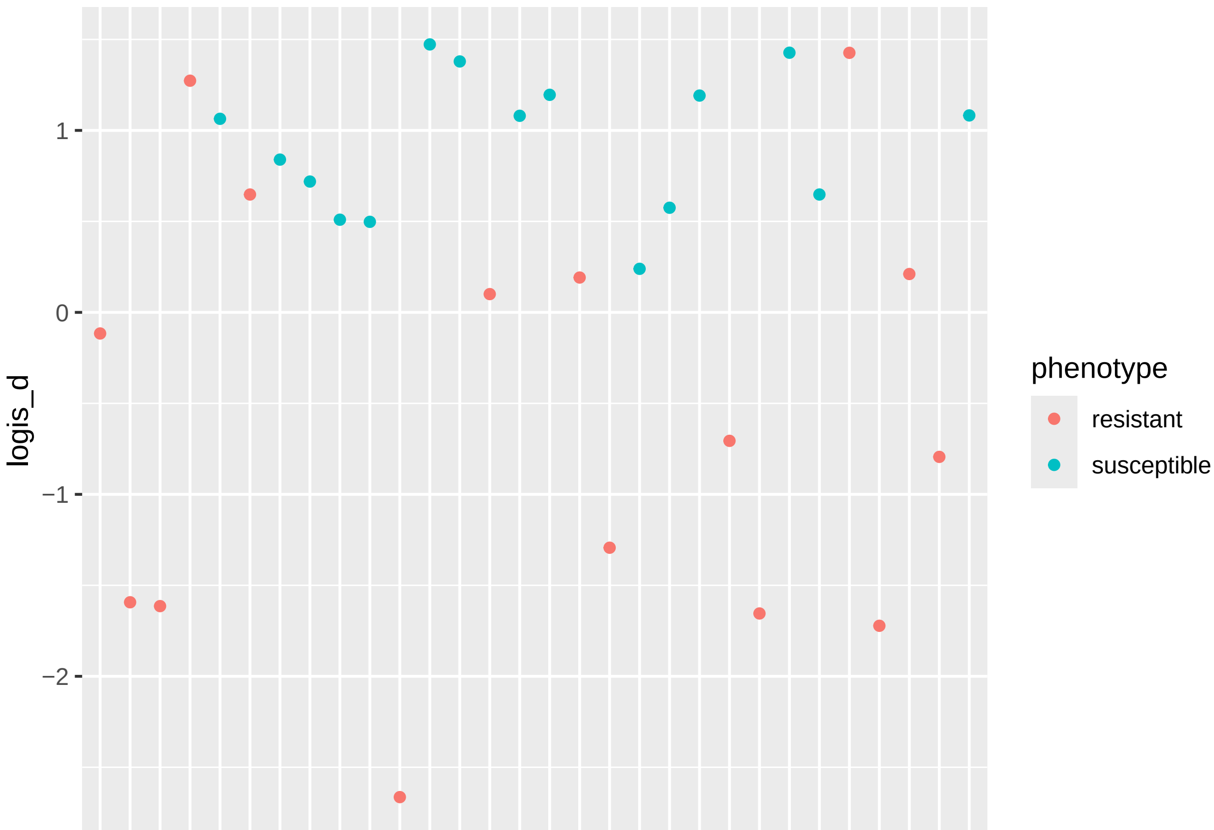

```r
ggplot(HIV1_vector_data_notable,aes(x=row.names(HIV1_vector_data_notable),y=logis_b,colour = phenotype)
  geom_point()+
  theme(axis.title.x=element_blank(),
        axis.text.x=element_blank(),
        axis.ticks.x=element_blank())
```




logis_d is the max from the 4 parameter logistic, it mostly would align with the assay output, but the logistic may find a higher max depending on the shape of the fitted curve, e.g if the curve was increasing but hadn't reached a plateau the model would model a theorised plateau that may be higher than assay output, so in this way it measures both the max output and the dynamics of the gfp production

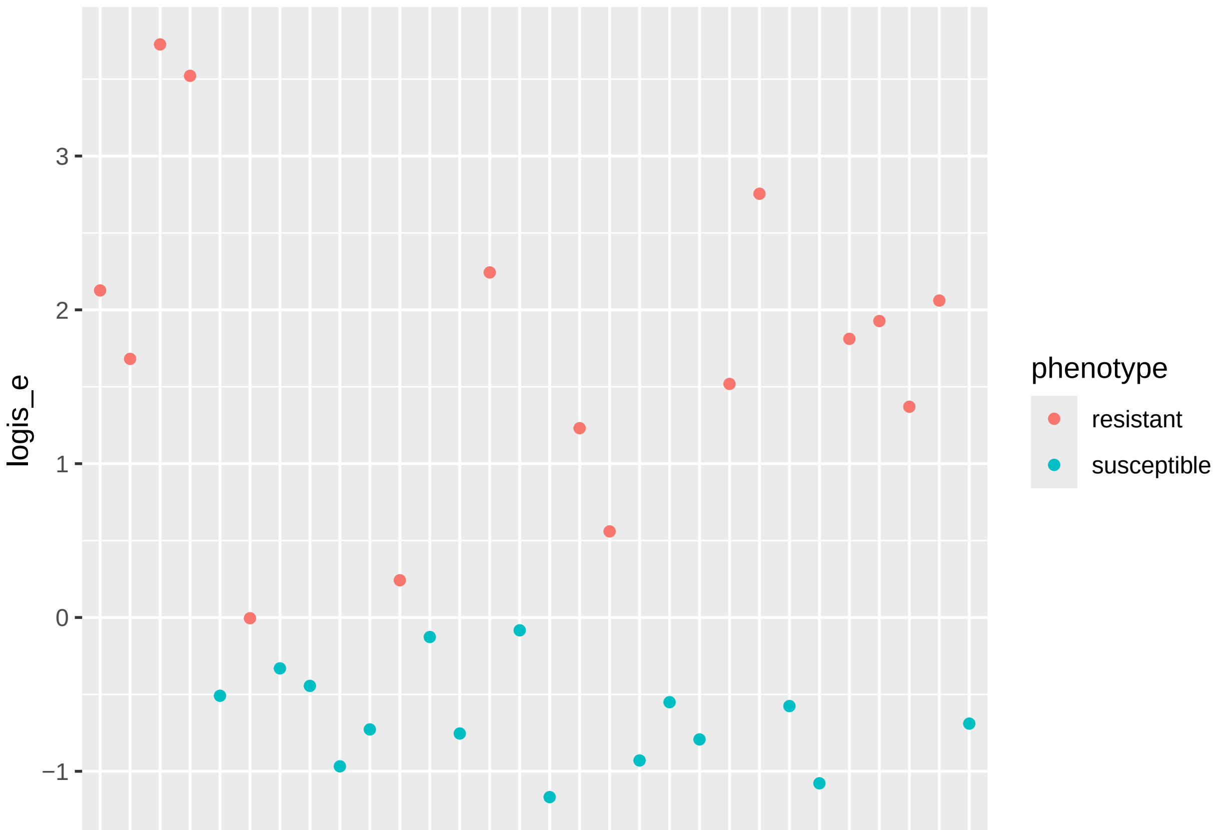
we see a good split except for one cell line Febc which is resistant but has a high value. This could mean the curve of that cell followed a more gradual increase but still was modelled a high theorised plateau.

```
ggplot(HIV1_vector_data_notable,aes(x=row.names(HIV1_vector_data_notable),y=logis_d,colour = phenotype))
  geom_point()+
  theme(axis.title.x=element_blank(),
        axis.text.x=element_blank(),
        axis.ticks.x=element_blank())
```



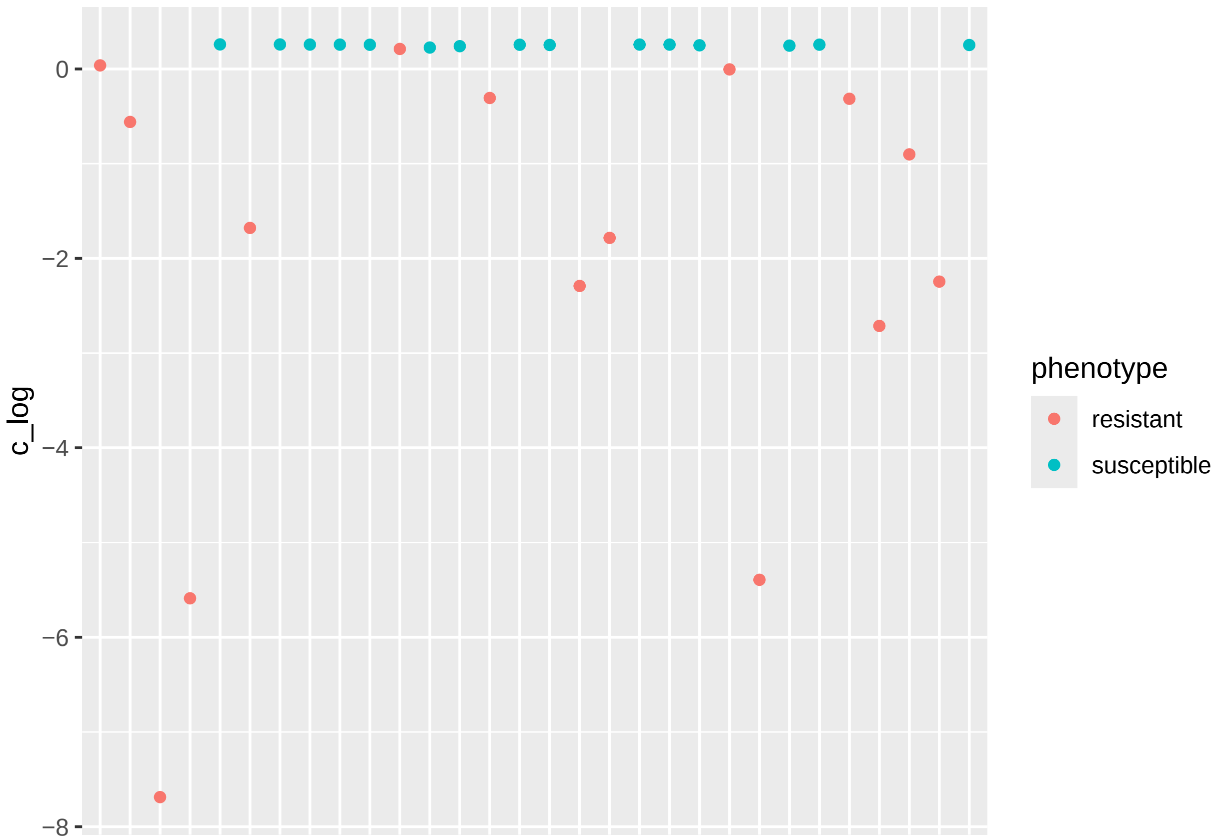

Logis e works as the x offset, so having a high logis e shifts the graph to the right which would theoretically make it more resistant . the graph is not as split, with a lot of overlap between susceptible and resistant but many of the resistant have higher logis e than susceptible which would be expected.

```
ggplot(HIV1_vector_data_notable,aes(x=row.names(HIV1_vector_data_notable),y=logis_e,colour = phenotype))
  geom_point()+
  theme(axis.title.x=element_blank(),
        axis.text.x=element_blank(),
        axis.ticks.x=element_blank())
```




c log is the x offset in the logarithmic model, this means that theoretically the susceptible would have lower c log but this is not what is seen, instead we see the opposite that only the resistant have low c log, However c_log is highly correlated with a_log which does fit what would be expected. It could be that due to a quirk in the modelling, the shape of the highly susceptible affected the way c log was modeled to have a correct fit, compared to the more flat growth of the resistant curves which may have been modeled to have much lower c_log.

```
ggplot(HIV1_vector_data_notable,aes(x=row.names(HIV1_vector_data_notable),y=c_log,colour = phenotype))+
  geom_point()+
  theme(axis.title.x=element_blank(),
        axis.text.x=element_blank(),
        axis.ticks.x=element_blank())
```




### ranking list

Here i rank and gain the top cell lines in each parameter to see which cell lines appear the most,this is another way of separating the data but i dont prefer it

```
vector_ranking=list()
for(col in names(HIV1_vector_data_PCA_1[,c(1:3,6,7,9)])) {

  # Extract the column values
  vec <- HIV1_vector_data_PCA_1[[col]]

  # Calculate the 10th and 90th quantiles (ignoring NAs)
  low_quant  <- quantile(vec, 0.1, na.rm = TRUE)
  high_quant <- quantile(vec, 0.9, na.rm = TRUE)

  # Identify rows where the value is either below the 10th percentile or above the 90th percentile
  extreme_idx <- which(vec < low_quant | vec > high_quant)

  # Subset the original data frame for these extreme values
  subset_data <- HIV1_vector_data_PCA_1[extreme_idx, ]

  # Add a phenotype column: if the value is below the 10th percentile, call it "resistant",
  # if above the 90th percentile, label it "susceptible"
  # (This uses the current column's values from the subset.)
  subset_data$phenotype <- ifelse(vec[extreme_idx] < low_quant, "resistant", "susceptible")
  subset_data$cell_line=rownames(subset_data)
  rownames(subset_data) <- NULL
```

```r
  # Store the subset in the vector_ranking list using the column name as the key
  vector_ranking[[col]] <- subset_data
}

for(col in names(HIV1_vector_data_PCA_1[,c(4,5,8)])) {

  # Extract the column values
  vec <- HIV1_vector_data_PCA_1[[col]]

  # Calculate the 10th and 90th quantiles (ignoring NAs)
  low_quant  <- quantile(vec, 0.1, na.rm = TRUE)
  high_quant <- quantile(vec, 0.9, na.rm = TRUE)

  # Identify rows where the value is either below the 10th percentile or above the 90th percentile
  extreme_idx <- which(vec < low_quant | vec > high_quant)

  # Subset the original data frame for these extreme values
  subset_data <- HIV1_vector_data_PCA_1[extreme_idx, ]

  # Add a phenotype column: if the value is below the 10th percentile, call it "resistant",
  # if above the 90th percentile, label it "susceptible"
  # (This uses the current column's values from the subset.)
  subset_data$phenotype <- ifelse(vec[extreme_idx] < low_quant, "susceptible","resistant")
  subset_data$cell_line=rownames(subset_data)
  rownames(subset_data) <- NULL

  # Store the subset in the vector_ranking list using the column name as the key
  vector_ranking[[col]] <- subset_data
}
```

```r
vector_ranking_df=bind_rows(vector_ranking)
cell_line_counts <- vector_ranking_df %>%
  count(cell_line,phenotype)

# 3. Get the cell lines that appear more than 9 times.
common_vector_cell_lines <- cell_line_counts[cell_line_counts$n>2,]

# 4. Filter the original data to include only those common_vector cell lines.
most_common_vector <- inner_join(vector_ranking_df,common_vector_cell_lines,join_by(x$cell_line==y$cell_

# Optionally, view the result:
unique(most_common_vector)
```

```
##    assay_output         a_log       b_log       c_log     logis_b     logis_d
## 1    3.24097893  0.3748034774 -0.30781438  0.26138590  6.67223990  3.17627500
## 2   -2.57523359 -0.0879936874 -0.11119842  0.07599256 -0.29951576 -2.63097122
## 3   -2.85411206  0.0171429525 -0.20613934  0.14320224 -1.15564974 -2.26783460
## 4   -1.40992169  0.0658324205 -0.32986337  0.25897950  1.83518570 -1.61186269
## 5   -1.85840178 -0.2863665039  0.43734457 -0.55976652  0.40332070 -1.59302648
## 6   -2.09287464 -7.6676476946  6.84457353 -7.68744361 -0.72271654 -1.61416545
## 7    2.36916357  0.4193862857 -0.08536256  0.21435862 -0.76819494  2.51267355
## 8    1.38929740  0.3037583952 -0.20473071  0.24231684 -0.43622101  1.43180882
## 9   -1.37827486  0.0570889699 -0.32799989  0.25949518  0.68907729 -1.62212331
## 10  -2.71602072  0.0013993340 -0.27986231  0.21113800 -0.46586836 -2.66384223
```

```
## 11   1.22633192  0.3060168663 -0.18304142  0.22607237  0.36780635  1.47261332
## 12   1.36286095  0.3035023592 -0.19860596  0.24027786 -0.30682589  1.37907413
## 13   1.43988187  0.3075732782 -0.22072534  0.24961443 -0.08653376  1.47590502
## 14  -1.39445273  0.0850566514 -0.30911863  0.25317759  0.66486663 -1.45685588
## 15  -1.73242591  0.0619139941 -0.30066114  0.22611018  0.95296422 -1.70405913
## 16   2.52913979  0.5054921755  0.14637025  0.11908930 -0.78743269  3.52827716
## 17   1.21211365  0.2723062888 -0.23580085  0.25313008 -0.67732479  1.19557544
## 18  -1.68158912 -0.8132760111  0.73215632 -1.78352495 -0.96399161 -1.29327586
## 19  -1.59239517  0.0639166064 -0.30910632  0.25265297 -0.12438428 -1.67003051
## 20   1.86819223  0.4628868862  0.11585090  0.11820841 -0.39688066  1.92577528
## 21  -1.67647306 -4.6698456853  4.95673736 -5.39322724 -0.38305668 -1.65468700
## 22  -1.45993359  0.0514286500 -0.34824396  0.26083884  3.49534120 -1.67281892
## 23   1.85760367  0.3595578882 -0.19246268  0.24587119 -0.46265959  1.42704415
## 24  -2.12726256  0.0367872400 -0.27495988  0.22544646 -0.99518913 -2.05062439
## 25  -2.77665484 -0.0007974928 -0.27401590  0.22080205 -1.03461904 -2.67770617
## 26  -2.06828665 -1.9568383087  1.80640660 -2.71304016 -0.49132411 -1.72225360
## 27   1.51534046  0.5971670379  0.21784745  0.20771823  2.54338422  0.55271857
## 28   1.33229906  0.3556537449 -0.02365003  0.15300191 -0.53547278  1.35242026
## 29   1.36239158  0.3156877808 -0.19259045  0.23579691  0.36020012  1.40192866
## 31   0.65215884  0.3577270850  0.20193453  0.01691024 -0.83989282  1.17188901
## 36   0.46029706 -6.6663853870  6.94478242 -5.58865183 -0.69762344  1.27314742
## 52   0.55718702  0.3634516355  0.28083267 -0.02947392 -0.60231356  0.60727133
## 54   0.12840515  0.3179874209  0.17324594 -0.01181657 -0.71696573  0.21919760
## 57   3.24097893  0.3748034774 -0.30781438  0.26138590  6.67223990  3.17627500
## 59  -0.28206288  0.1474555485 -0.33066477  0.26119292  4.00029372 -0.33059901
## 61  -1.85840178 -0.2863665039  0.43734457 -0.55976652  0.40332070 -1.59302648
## 62  -2.09287464 -7.6676476946  6.84457353 -7.68744361 -0.72271654 -1.61416545
## 63   0.46029706 -6.6663853870  6.94478242 -5.58865183 -0.69762344  1.27314742
## 64  -0.05052663 -2.5698552174  2.52514515 -1.67860286 -0.88485676  0.64777719
## 66   0.04819839  0.1665838352 -0.31204175  0.26069700  1.27986811 -0.19676331
## 67   0.06878914  0.2167553886  0.47359174 -0.30664353 -0.58032373  0.10046606
## 69  -0.17807664 -2.5928096321  3.17100719 -2.29107048 -0.87353800  0.19152622
## 70  -1.68158912 -0.8132760111  0.73215632 -1.78352495 -0.96399161 -1.29327586
## 72   0.09438870  0.1739567374 -0.31785954  0.26058283  1.15602044  0.00965968
## 73  -1.67647306 -4.6698456853  4.95673736 -5.39322724 -0.38305668 -1.65468700
## 75   0.01926630  0.1801361881 -0.30676506  0.26039653  1.33727150 -0.11852813
## 76   0.17260198  0.1013427982  0.72491903 -0.31511514 -0.90806671  1.42640360
## 77   0.46108104  0.1802200625 -0.31109608  0.26028477  1.51428686  0.18707478
## 78  -2.06828665 -1.9568383087  1.80640660 -2.71304016 -0.49132411 -1.72225360
## 82  -0.79663115 -1.1231189555  1.20168263 -2.24497106 -0.32634908 -0.79409691
##        logis_c      logis_e area_under_curve   phenotype    cell_line n
## 1   0.04505523  0.345586931        4.7274676 susceptible         293T 4
## 2   0.78717776 -0.315687810       -1.8792011   resistant    CTR_M2_O5 4
## 3   0.78266138 -2.236166817       -1.1502481   resistant CTR_M2_O5_21 3
## 4   1.22438116  0.395132973       -0.6222876   resistant       Dard_2 4
## 5   1.59782705  1.681207451       -1.7463770   resistant       Eika_2 5
## 6   1.64470105  3.725626638       -1.4174523   resistant       Fafq_1 5
## 7   1.21075476  0.879023564        1.1674719 susceptible       Iill_1 4
## 8   1.25511634  0.686906345        1.1487306 susceptible       Iisa_3 4
## 9  -0.79636031  0.019445941       -0.9541170   resistant       Iuad_2 4
## 10  1.31682276  0.241950524       -1.7353425   resistant       Kajh_3 4
## 11 -0.10937860 -0.126953081        1.3297774 susceptible       Kehc_2 4
## 12 -0.64112753 -0.754235686        1.0176264 susceptible       Kolf_3 3
## 13  0.94886744  0.444008505        1.5340430 susceptible       Laey_6 4
```

```
## 14  0.58125381  0.321340421       -0.7298805   resistant       Liqa_1 3
## 15  1.09769605  0.374412810       -0.9742222   resistant       Miaj_6 3
## 16  1.02116571  0.488407311        0.7882949 susceptible     Oarz_22 3
## 17 -1.79889938 -1.167779192        0.9959481 susceptible      Oibg_1 3
## 18  0.76919060  0.559721593       -2.1674507   resistant      Otam_2 4
## 19 -0.14114231 -0.515159392       -1.2007986   resistant      Pahc_5 3
## 20  1.59002928  1.995830815        0.1920732 susceptible      Robp_3 4
## 21  1.65398666  2.754689436       -1.9000064   resistant      Ruql_3 5
## 22  0.38515513  0.316469877       -0.5032298   resistant      Sebn_4 6
## 23 -0.58471376 -0.575847350        0.5981263 susceptible      Sebz_1 3
## 24  0.36700953 -1.853139886       -2.0241708   resistant      Timk_4 4
## 25  0.53858240 -1.763225675       -1.2587220   resistant      Tuju_1 4
## 26  1.45710477  1.927259027       -1.9239447   resistant      Uaqe_1 5
## 27  0.04826202  0.004393533        1.0115718 susceptible      Vass_1 3
## 28 -0.58428260  0.348187762        0.4598859 susceptible      Xegx_1 3
## 29  1.16730007  0.955117249        1.3658417 susceptible      Zexw_3 4
## 31  1.41337320  1.529270897       -0.6694225 susceptible      Bipt_1 5
## 36  1.63109434  3.521387835       -1.2747026   resistant      Febc_1 3
## 52  1.59490788  2.171862647       -0.8661276 susceptible      Uimo_1 4
## 54  1.56910714  2.084708589       -1.1012058 susceptible      Xavk_3 4
## 57  0.04505523  0.345586931        4.7274676   resistant        293T 3
## 59  0.81885650  0.420738436        0.9293527   resistant      Ceik_1 3
## 61  1.59782705  1.681207451       -1.7463770 susceptible      Eika_2 3
## 62  1.64470105  3.725626638       -1.4174523 susceptible      Fafq_1 3
## 63  1.63109434  3.521387835       -1.2747026 susceptible      Febc_1 4
## 64 -0.26892680 -0.005039933       -0.8988614 susceptible      Gesg_2 3
## 66  0.92778720  0.440295599        0.9516241   resistant      Kucg_2 3
## 67  1.60563476  2.243183738       -1.1927011 susceptible      Lexy_2 3
## 69  0.96112383  1.230846284       -1.2667539 susceptible      Oilg_3 3
## 70  0.76919060  0.559721593       -2.1674507 susceptible      Otam_2 3
## 72  0.53414350  0.364156552        1.1870694   resistant      Puie_4 3
## 73  1.65398666  2.754689436       -1.9000064 susceptible      Ruql_3 3
## 75  0.55267657  0.356658125        0.9796917   resistant      Sehp_2 3
## 76  1.37997093  1.811536597       -1.2458728 susceptible      Suop_5 5
## 77 -0.20648674 -0.204807949        0.9660652   resistant      Toss_3 3
## 78  1.45710477  1.927259027       -1.9239447 susceptible      Uaqe_1 3
## 82  1.59916664  2.060554373       -0.9771668 susceptible      Yemz_1 3
```

```
common_vector_list=unique(most_common_vector)
```