Trends in growth, rwp and photosyn

Objective: To see if CO2 mesophyll resistance (rwp) is realted to total growth traits.

Data limiations: photosynthesis realted traits are from greenhouse and growth characteristics are from field.

Growth data files: Corv_2012_Growth_rep1.csv, Corv_2012_Growth_rep2.csv, Corv_2012_Growth_rep3.csv, GWAS_Clatskanis_july_2013_Height_Diameter.csv

Photosyn data files: datainput_2_27_2015.csv

Local Git directory: setwd("~/GitHub/poplar_GWAS_photosyn")

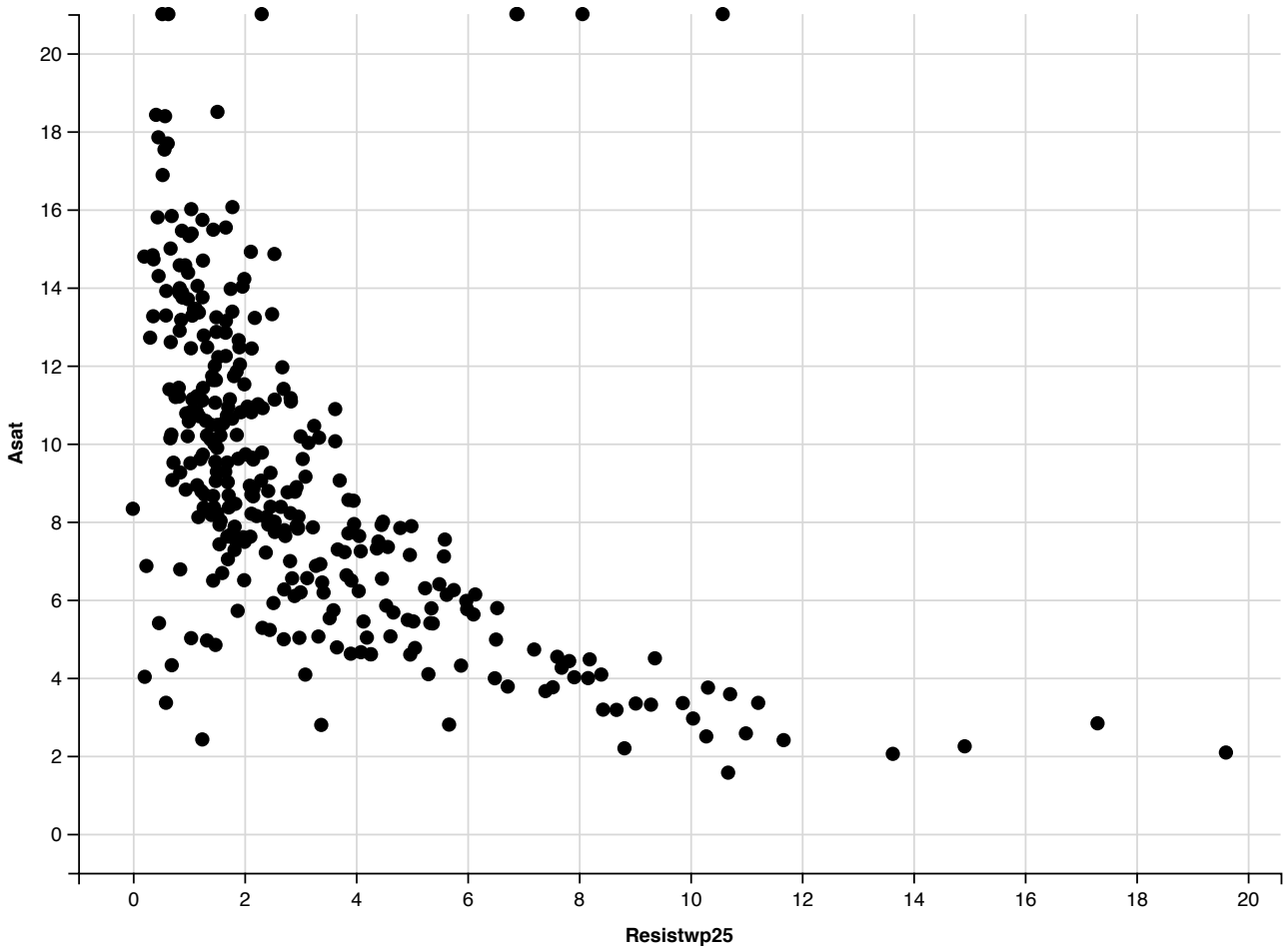
```
##
## Attaching package: 'dplyr'
##
## The following object is masked from 'package:stats':
##
##     filter
##
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

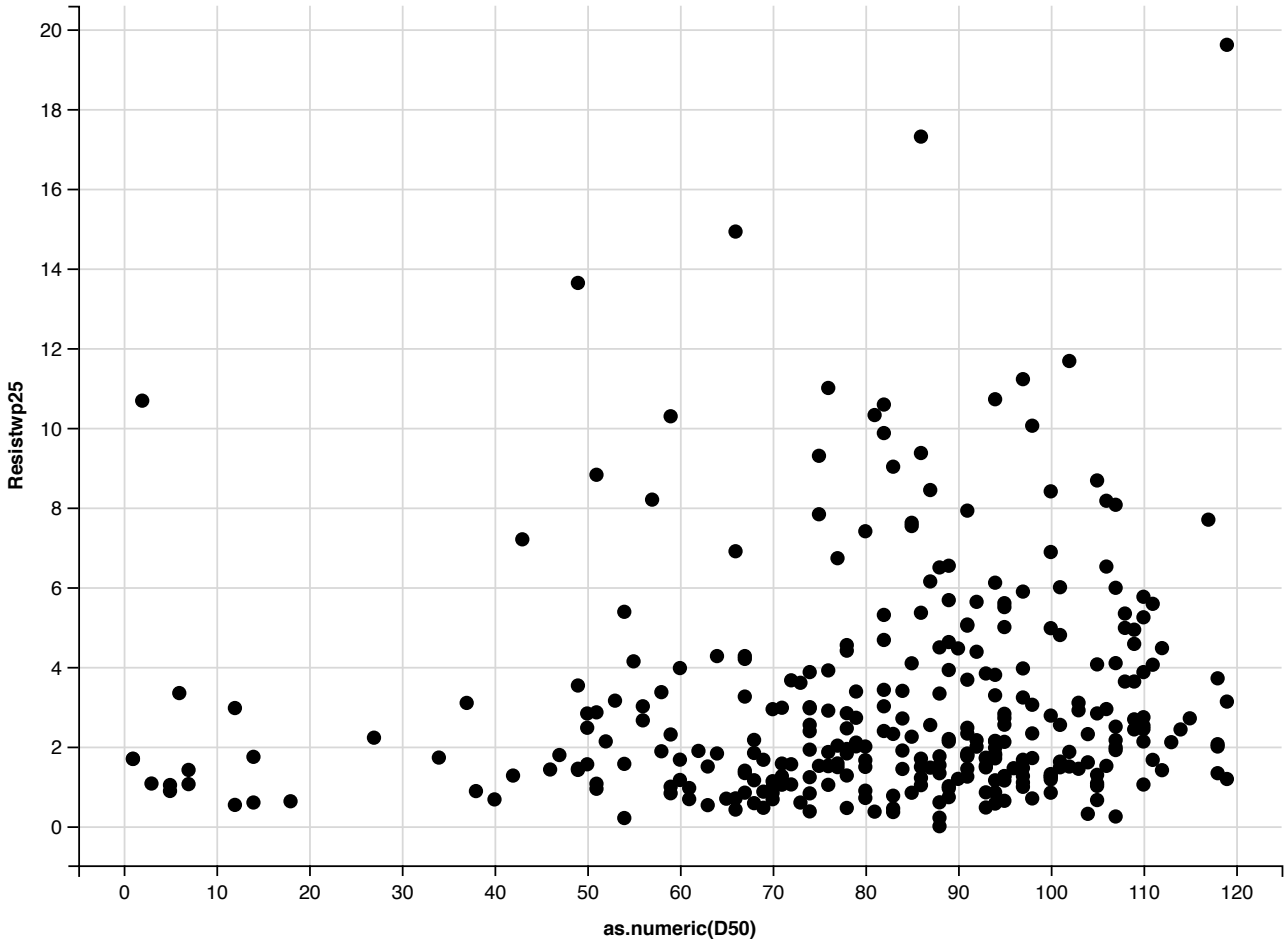
Field Traits
HBS3 Height to the bud scar of year 3 (2011 height)
HBS2 Height to the bud scar of year 2 (2010 height)
HHB height to the highest branch columns F-M are mostly repeated, but with 4 noted trees. What are they for? D20 diameter 20cm
D50 diameter 50cm - for stem taper
BA Branch angle
SB sylleptic branches from last year's growth (2011)
LENT # lenticels in 5cm along trunk
Tephrina 0-4: 0=zero; 1=1-25%; 2=26-50%; 3=51-75%; 4=76-100%
Venturia 0-4: 0=zero; 1=1-25%; 2=26-50%; 3=51-75%; 4=76-100%

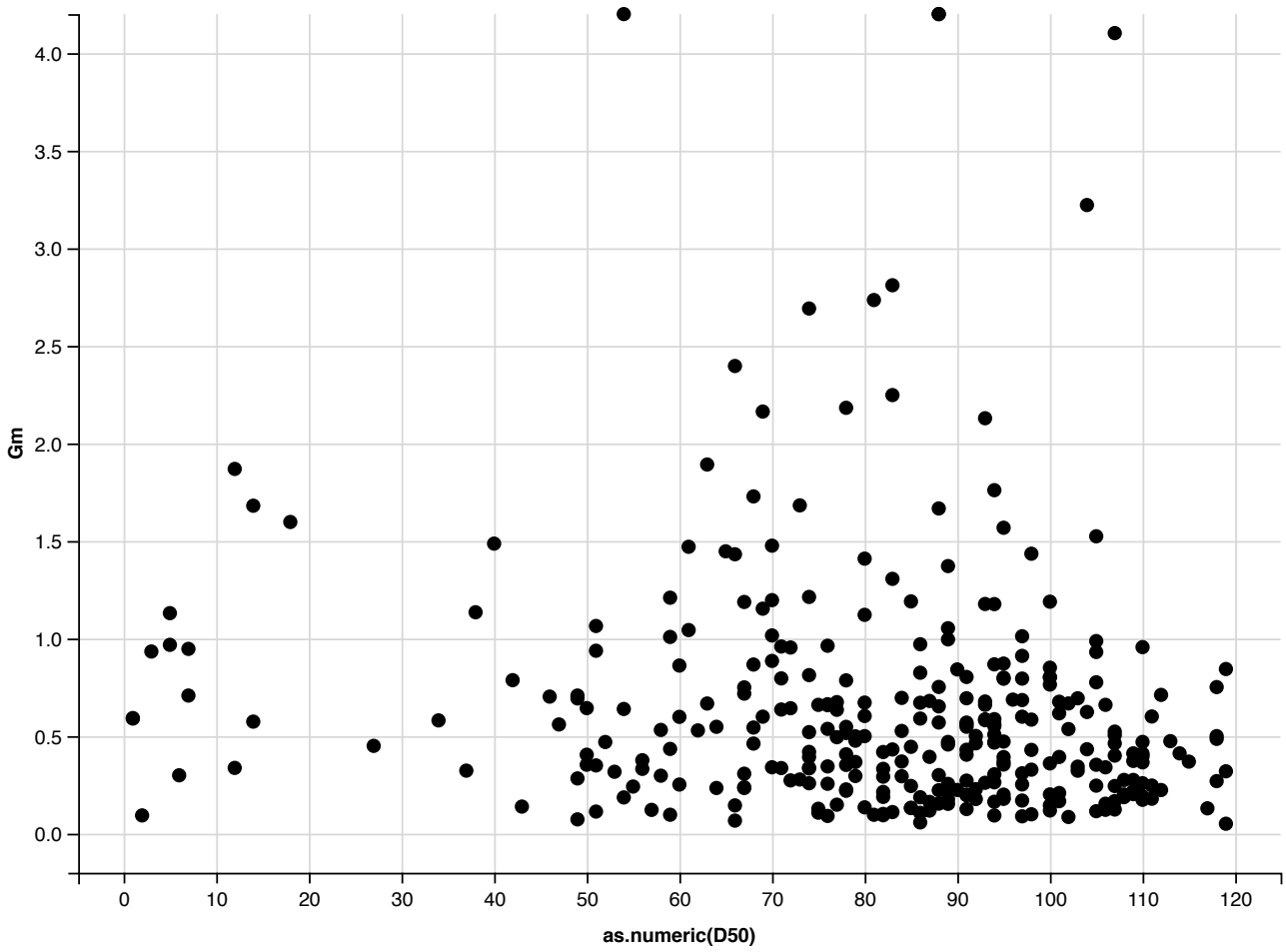
Data manipulation and Gm calculation Note: can only caluclate Gm for samples that have rwp > 0.

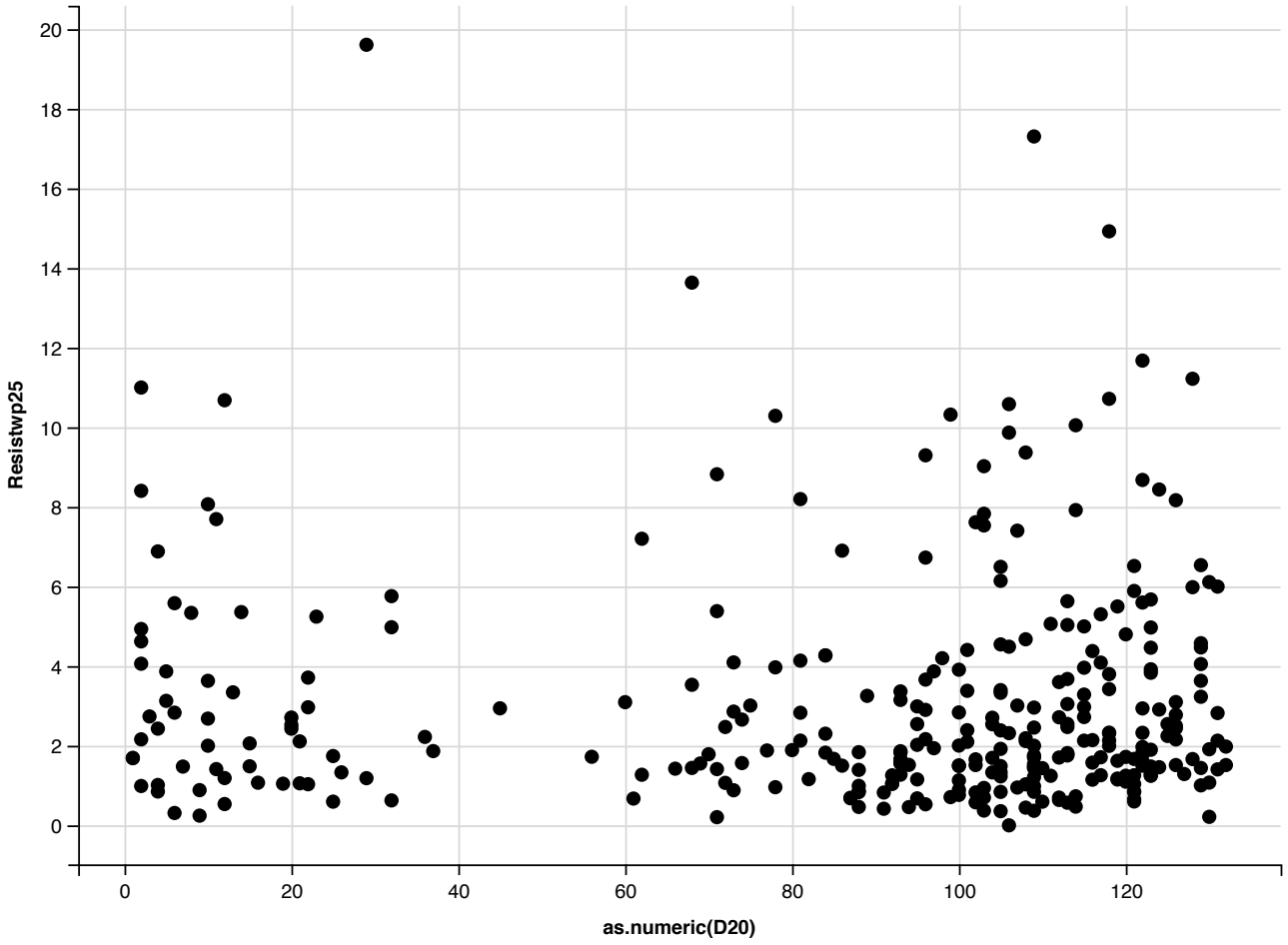
Relationship with Clatskanis Height Diameter data using replilcate 1

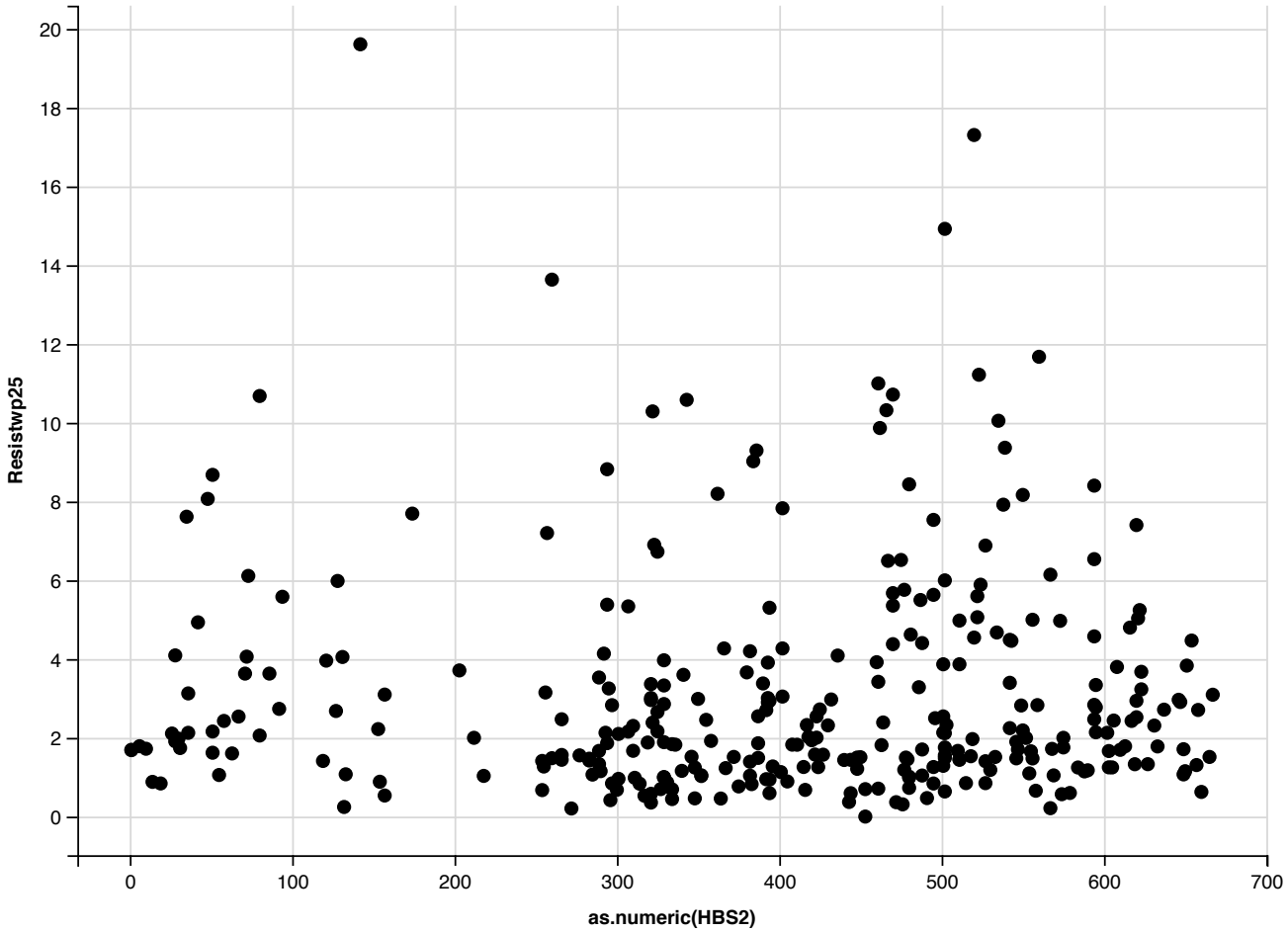
```
## Warning: joining character vector and factor, coercing into character
## vector
```

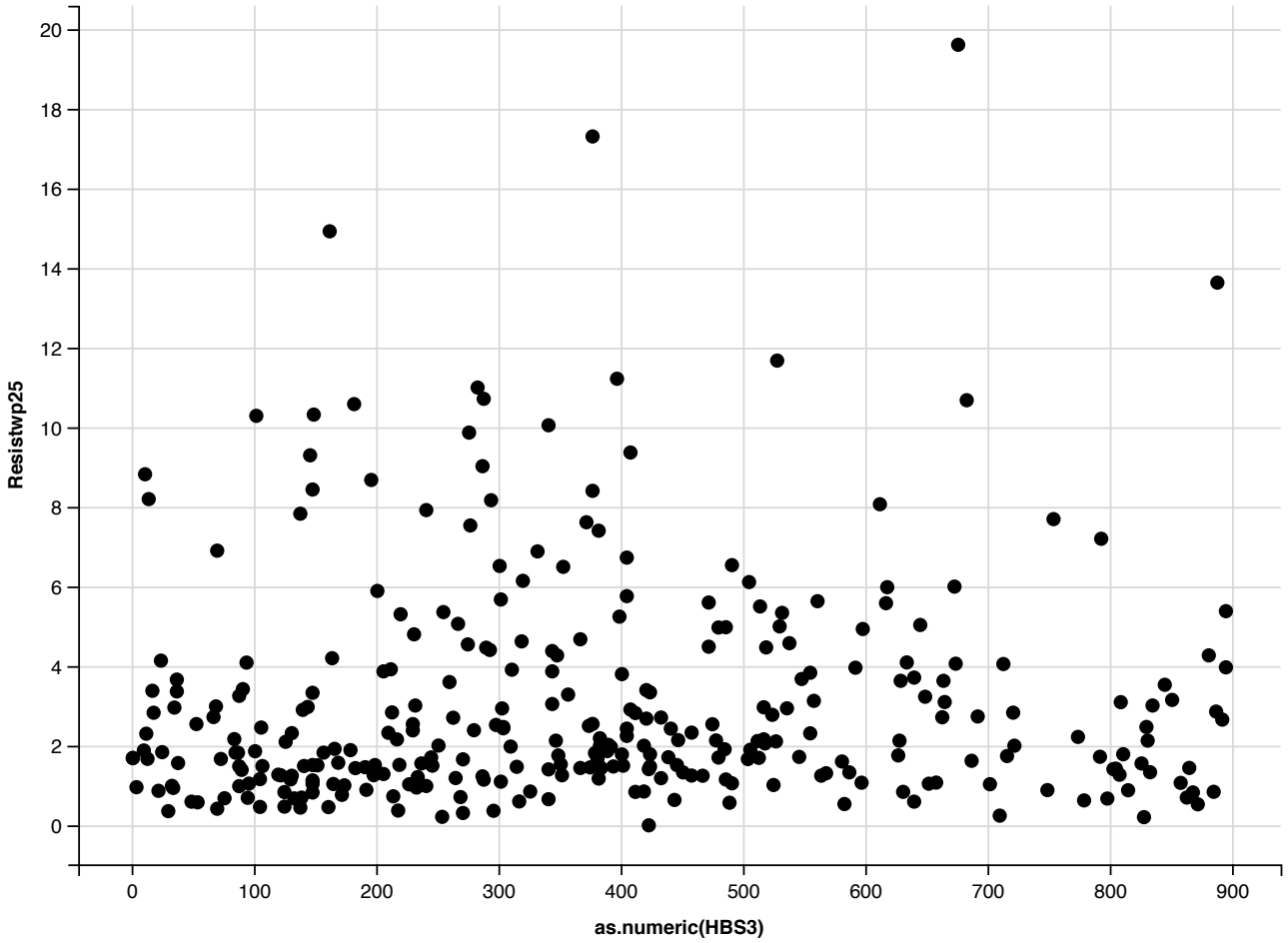

Asat
Resistwp25
0
2
4
6
8
10
12
14
16
18
20


Resistwp25
as.numeric(D50)
0
2
4
6
8
10
12
14
16
18
20
0
10
20
30
40
50
60
70
80
90
100
110
120


Gm
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0
10
20
30
40
50
60
70
80
90
100
110
120
as.numeric(D50)

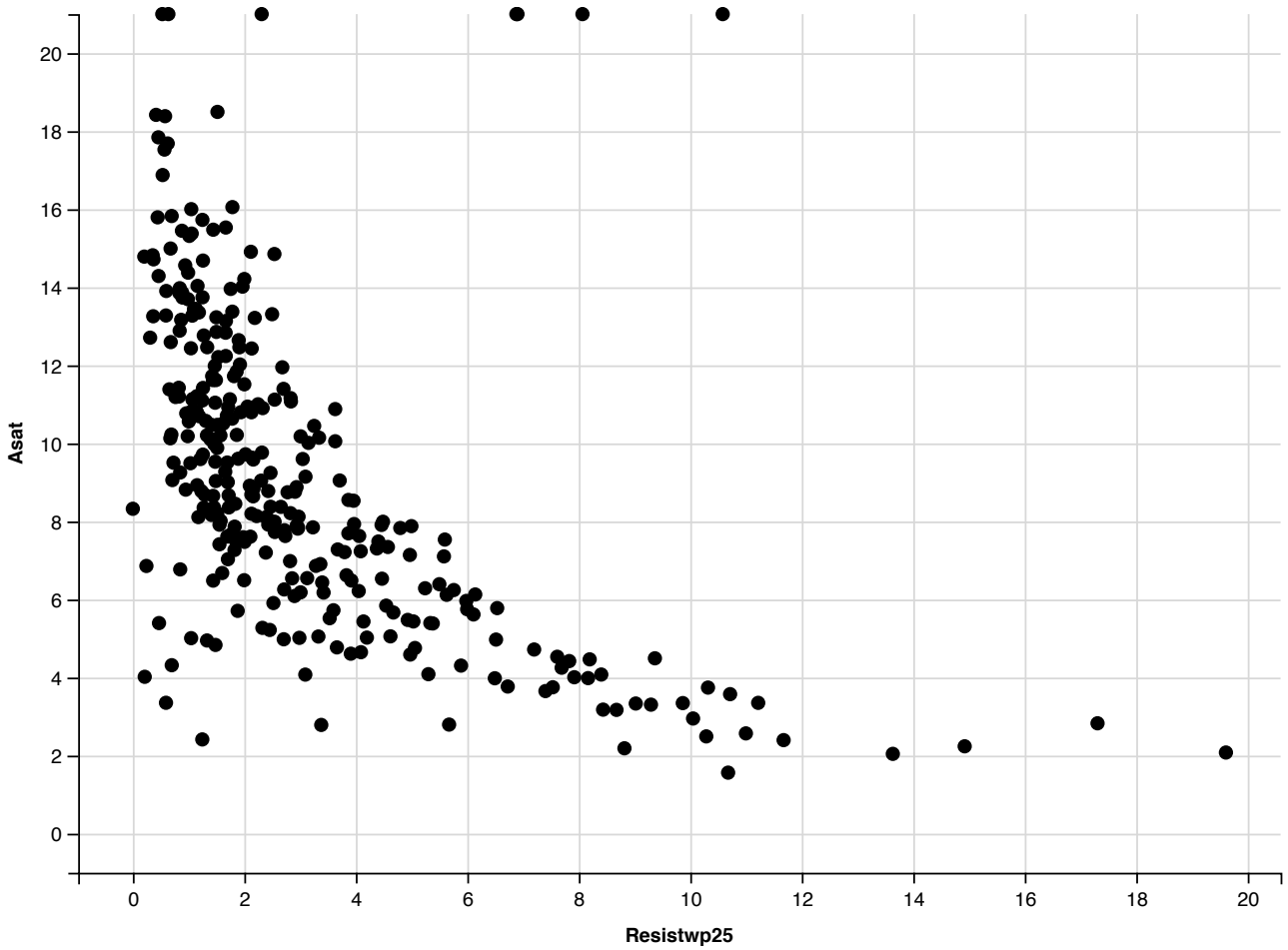

Resistwp25
as.numeric(D20)
0
2
4
6
8
10
12
14
16
18
20
0
20
40
60
80
100
120

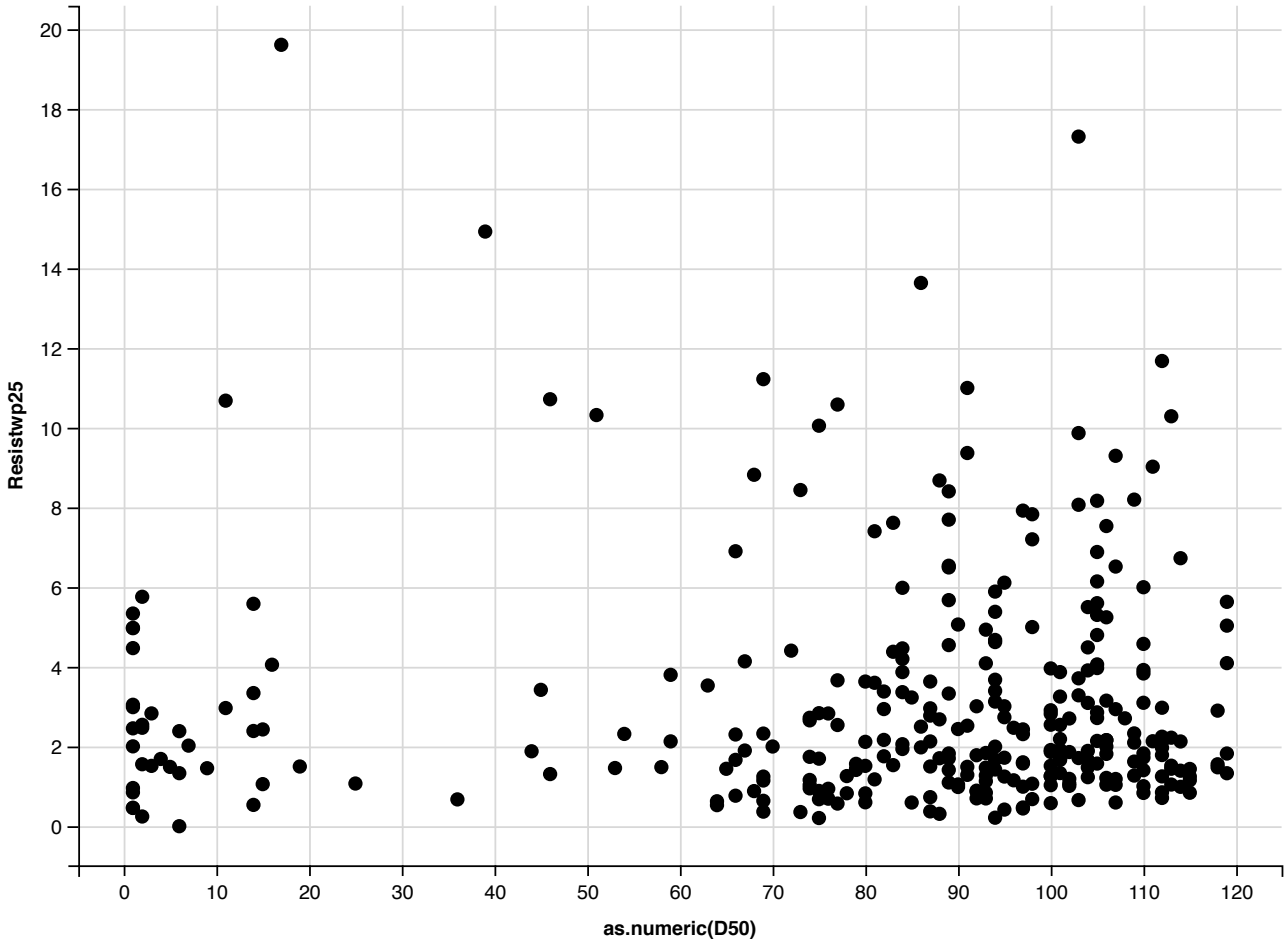

Resistwp25
as.numeric(HBS2)
0
2
4
6
8
10
12
14
16
18
20
0
100
200
300
400
500
600
700

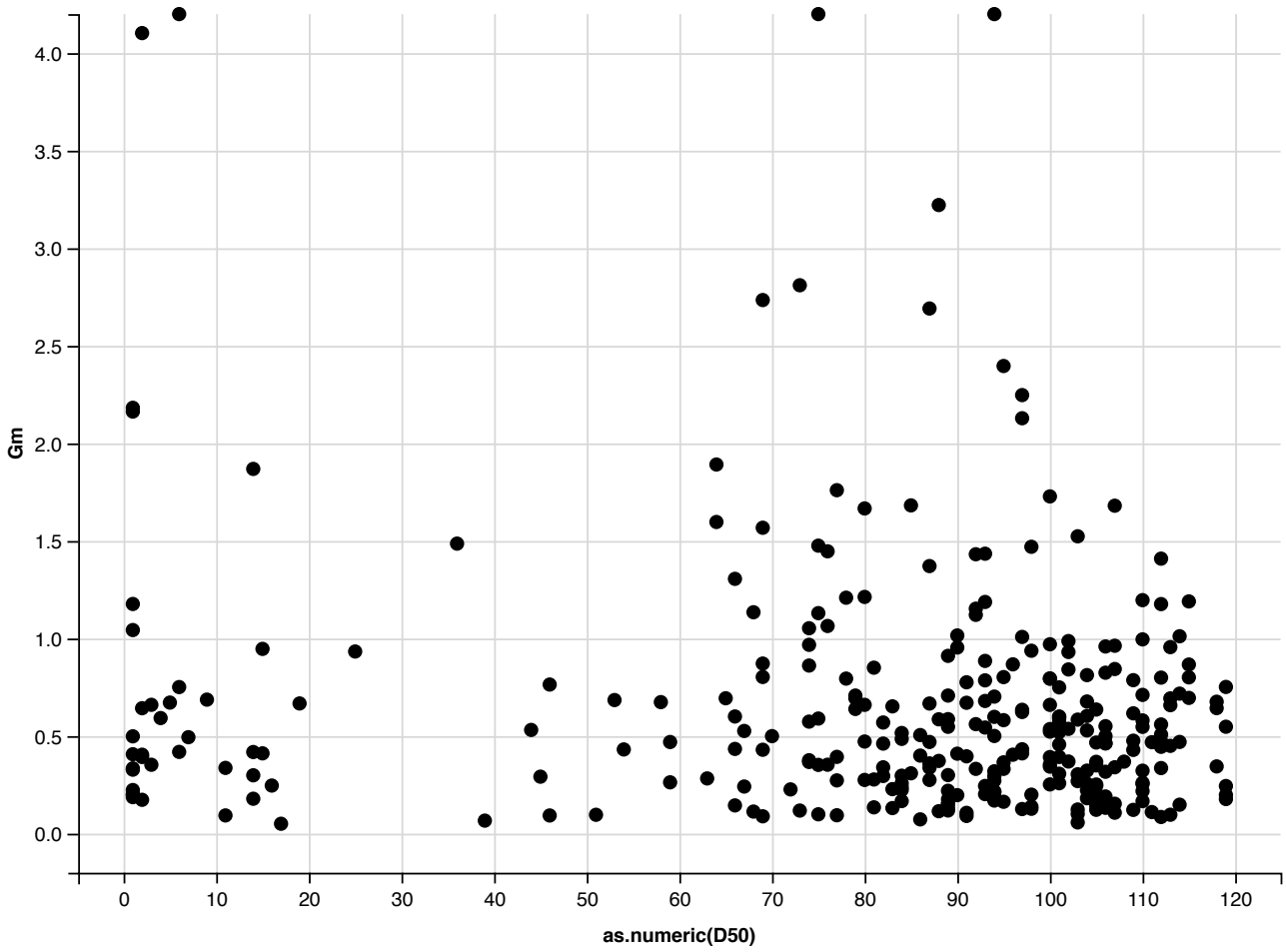


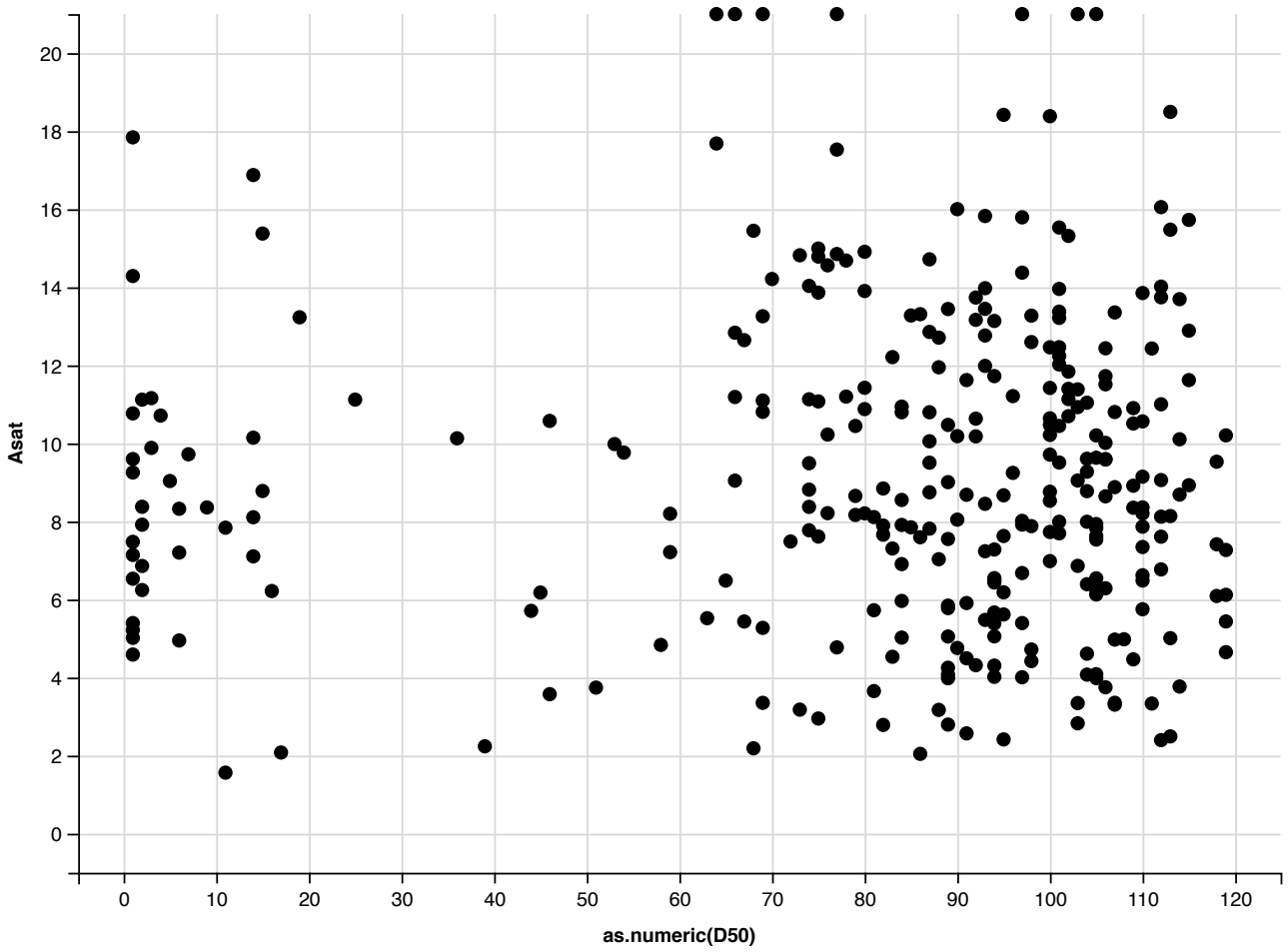
Relationship with Clatskanis Height Diameter data using replilcate 2

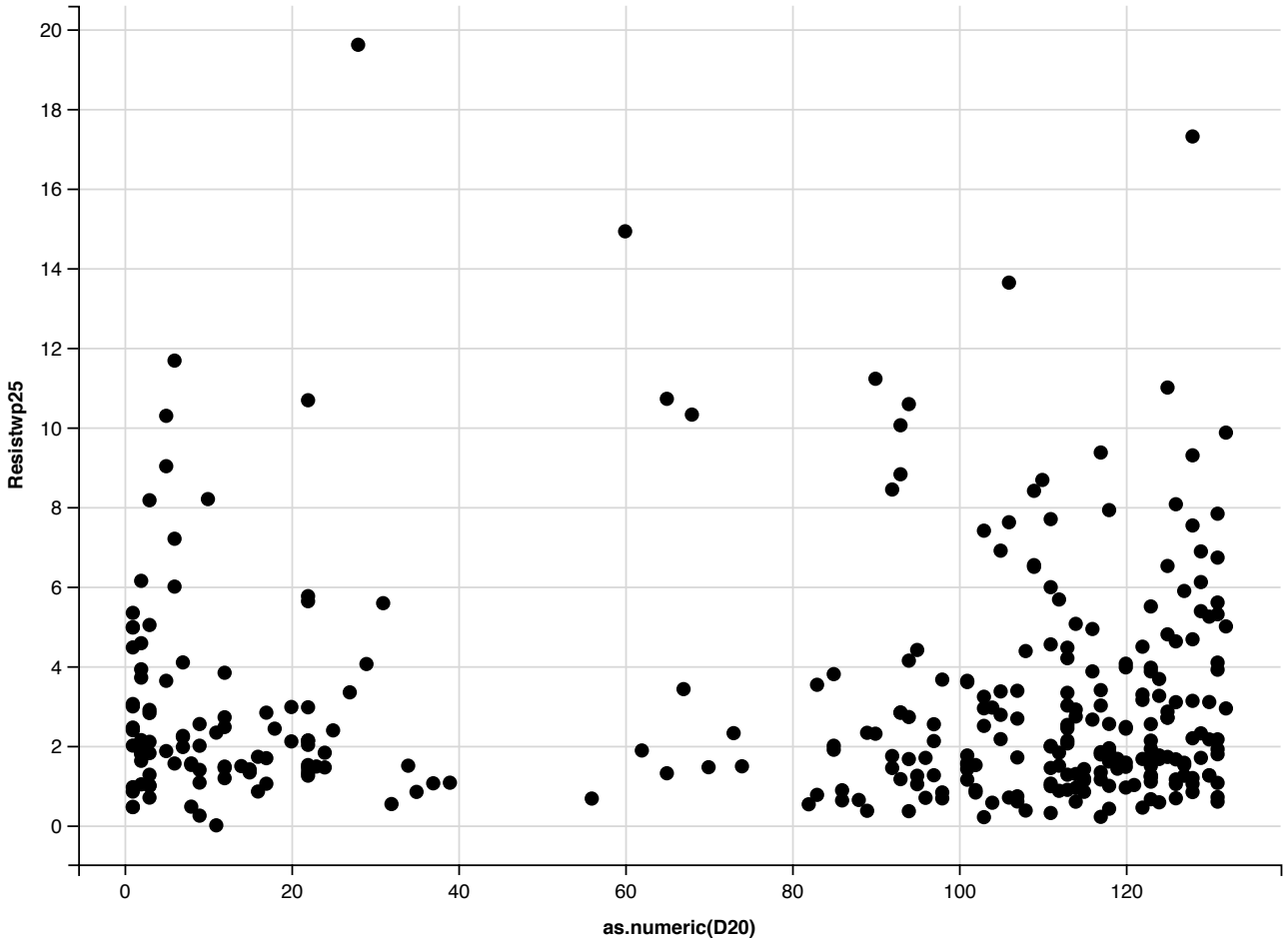
```
## Warning: joining character vector and factor, coercing into character
## vector
```

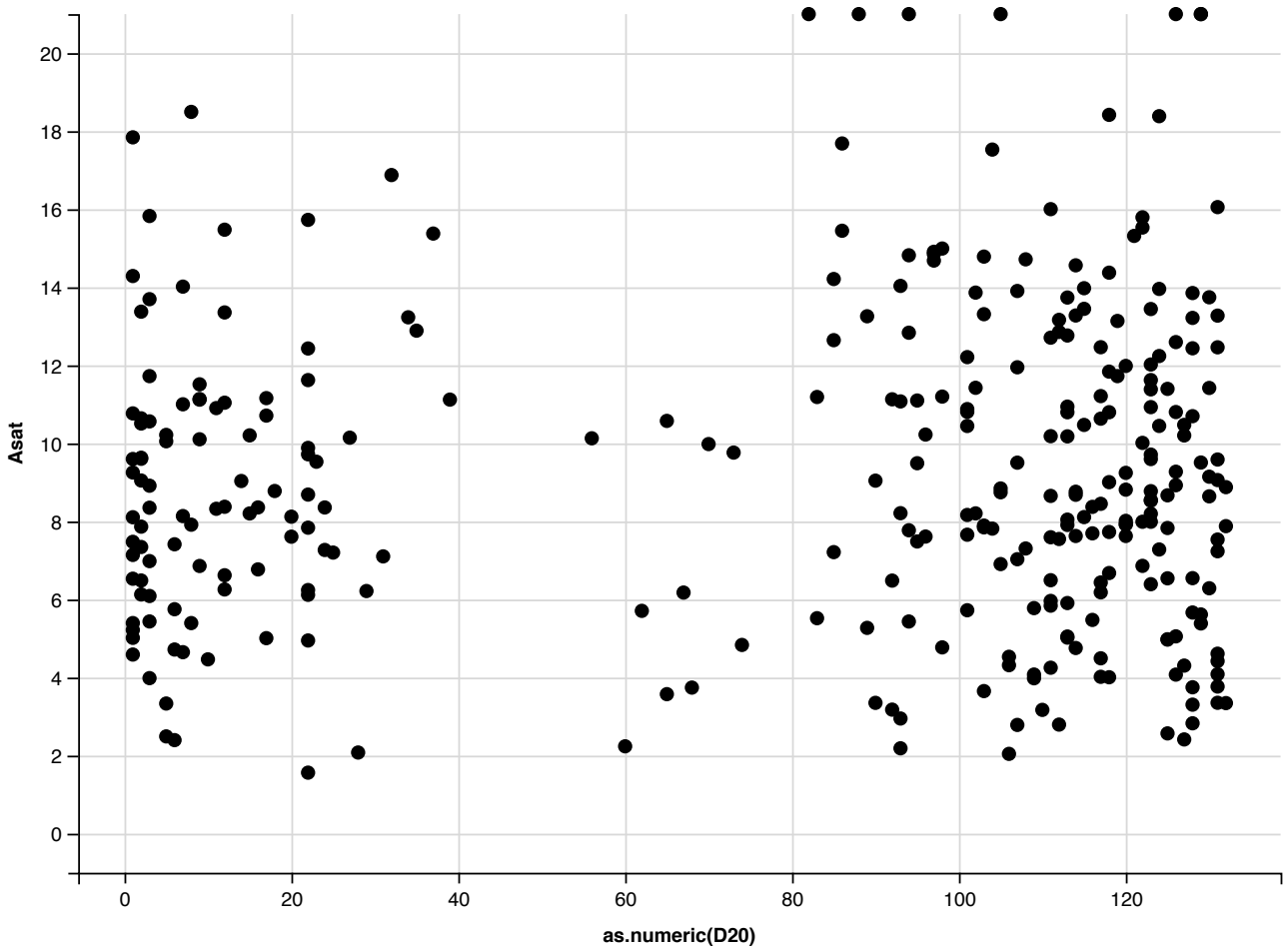

Asat
Resistwp25
0
2
4
6
8
10
12
14
16
18
20

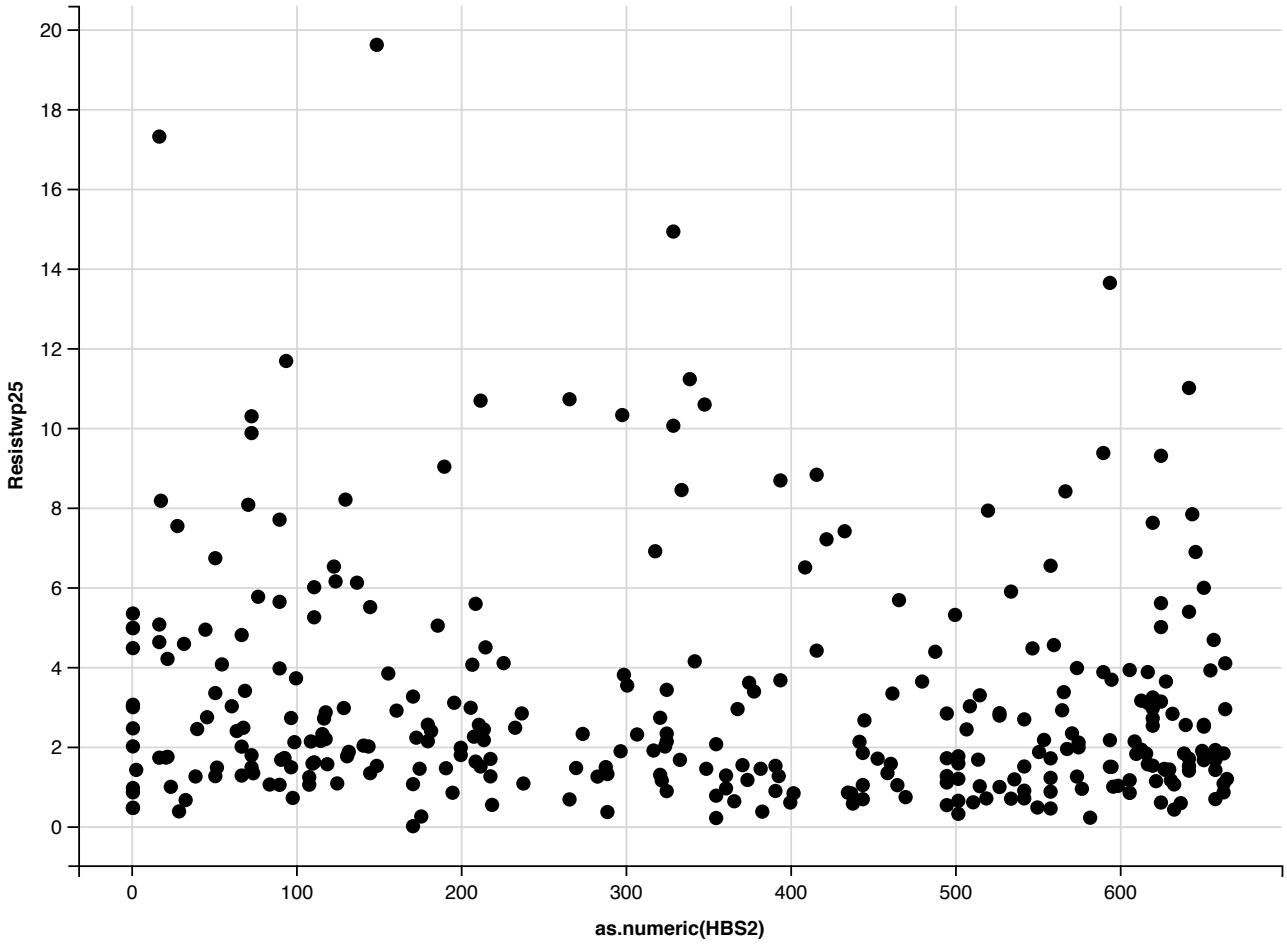

Resistwp25
as.numeric(D50)
0
2
4
6
8
10
12
14
16
18
20
0
10
20
30
40
50
60
70
80
90
100
110
120

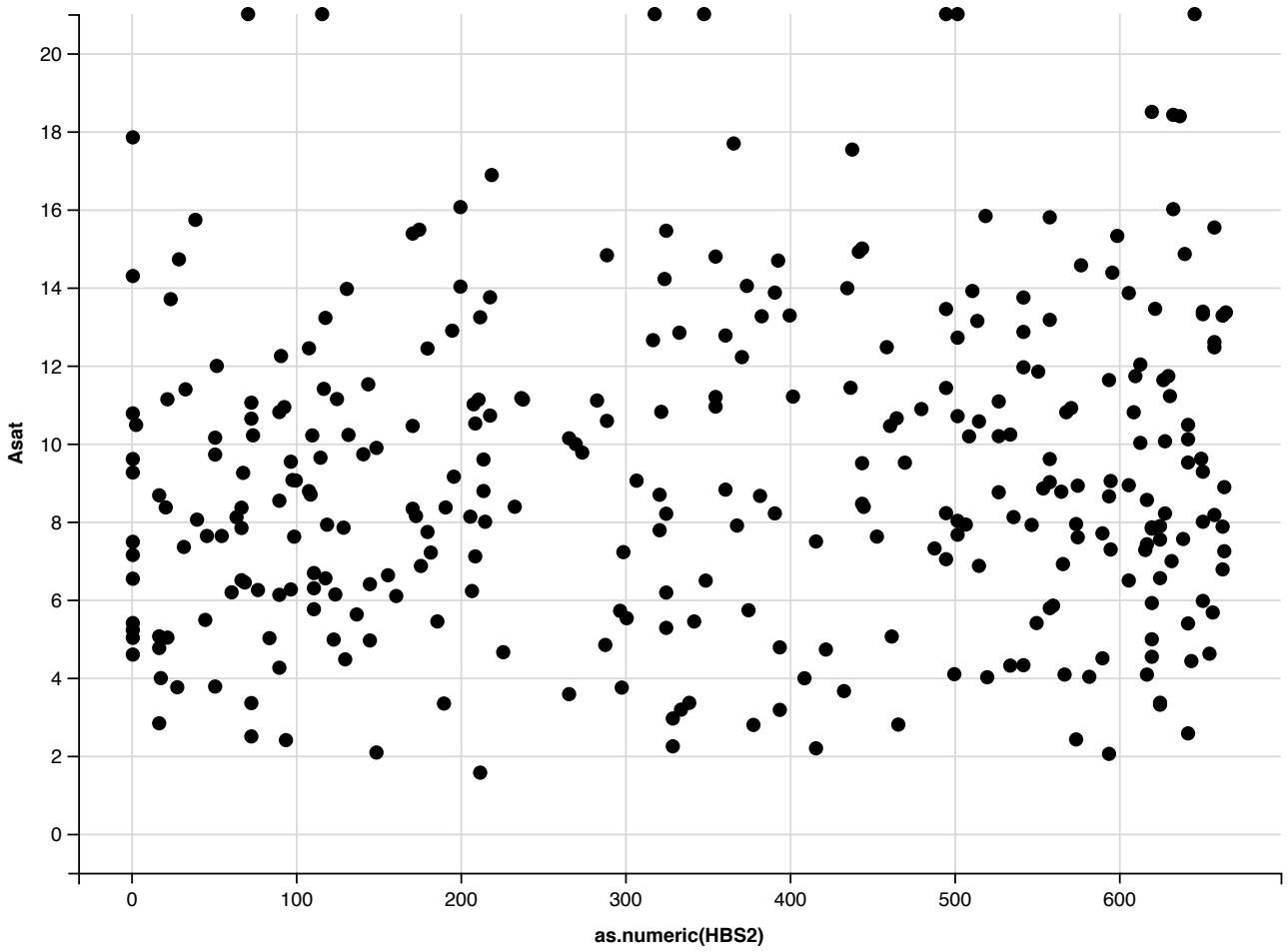

Gm
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0
10
20
30
40
50
60
70
80
90
100
110
120
as.numeric(D50)

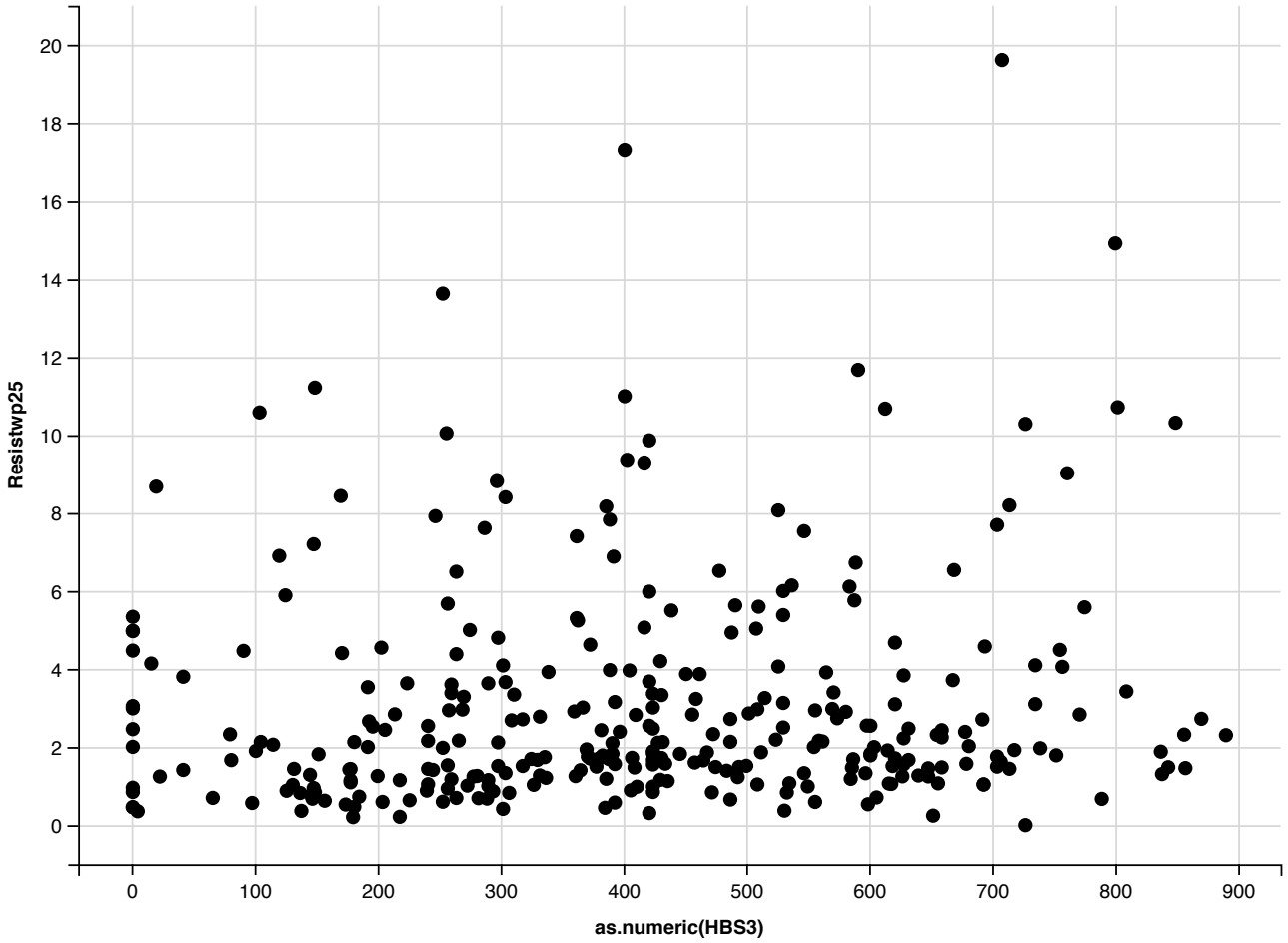

Asat
as.numeric(D50)
0
2
4
6
8
10
12
14
16
18
20
0
10
20
30
40
50
60
70
80
90
100
110
120

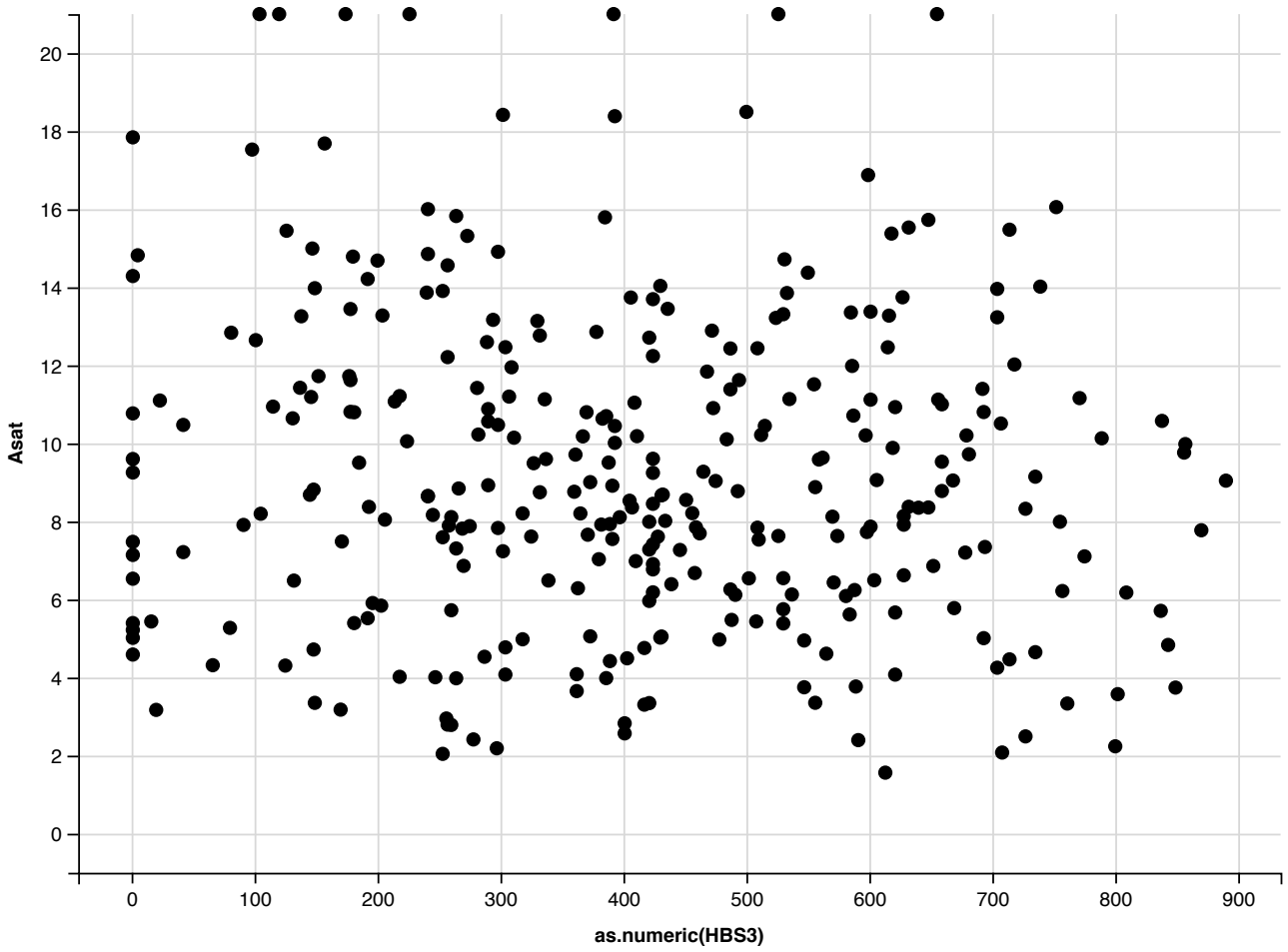

Resistwp25
as.numeric(D20)
0
2
4
6
8
10
12
14
16
18
20
0
20
40
60
80
100
120


Asat
as.numeric(D20)
0
2
4
6
8
10
12
14
16
18
20
0
20
40
60
80
100
120


Resistwp25
as.numeric(HBS2)
0
2
4
6
8
10
12
14
16
18
20
0
100
200
300
400
500
600


Asat
20
18
16
14
12
10
8
6
4
2
0
0
100
200
300
400
500
600
as.numeric(HBS2)


Resistwp25
as.numeric(HBS3)
0
2
4
6
8
10
12
14
16
18
20
0
100
200
300
400
500
600
700
800
900



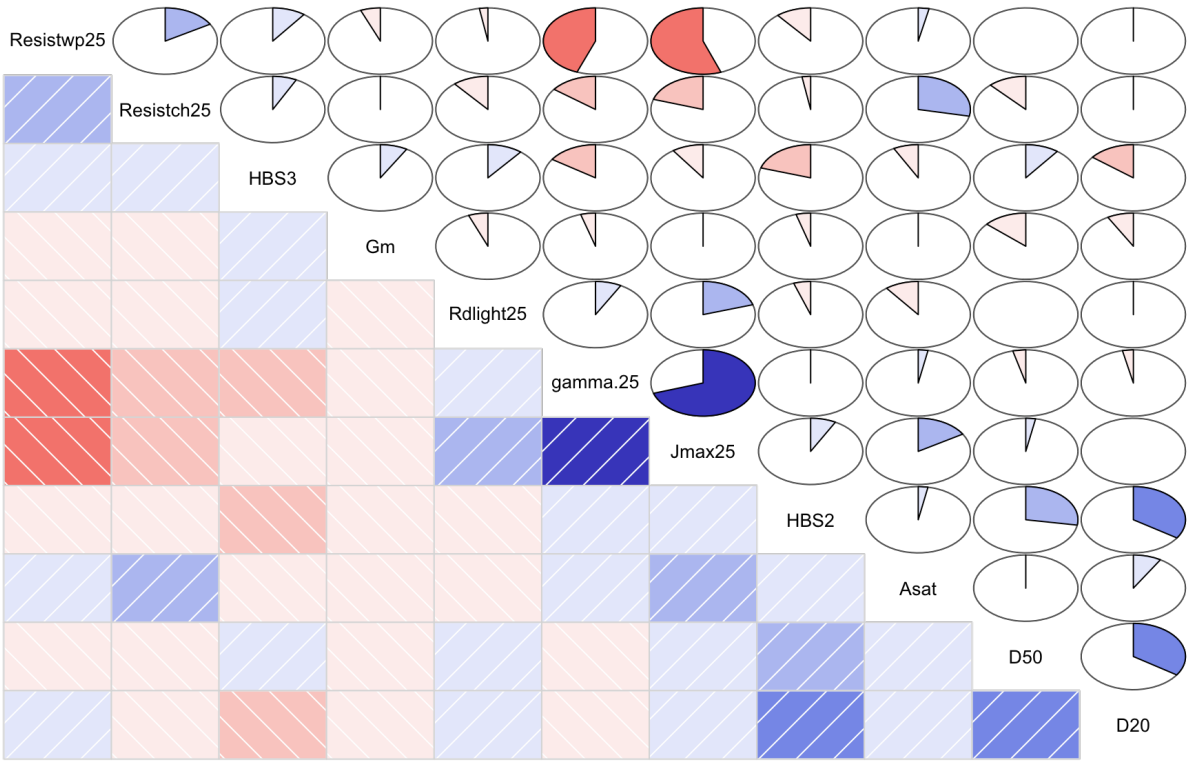
correlegrams Clatskanis Height Diameter data using replilcate 2

```
library(corrgram)

#convert some columns to numeric

datClatHt_2_join<-datClatHt_2_join %>% select(-Duplicate, -id, -Block)
datClatHt_2_join[, c(8:11)] <- sapply(datClatHt_2_join[, c(8:11)], as.numeric)

corrgram(datClatHt_2_join, order=TRUE, lower.panel=panel.shade,
  upper.panel=panel.pie, text.panel=panel.txt,
  main="Clatsk_rep2")
```



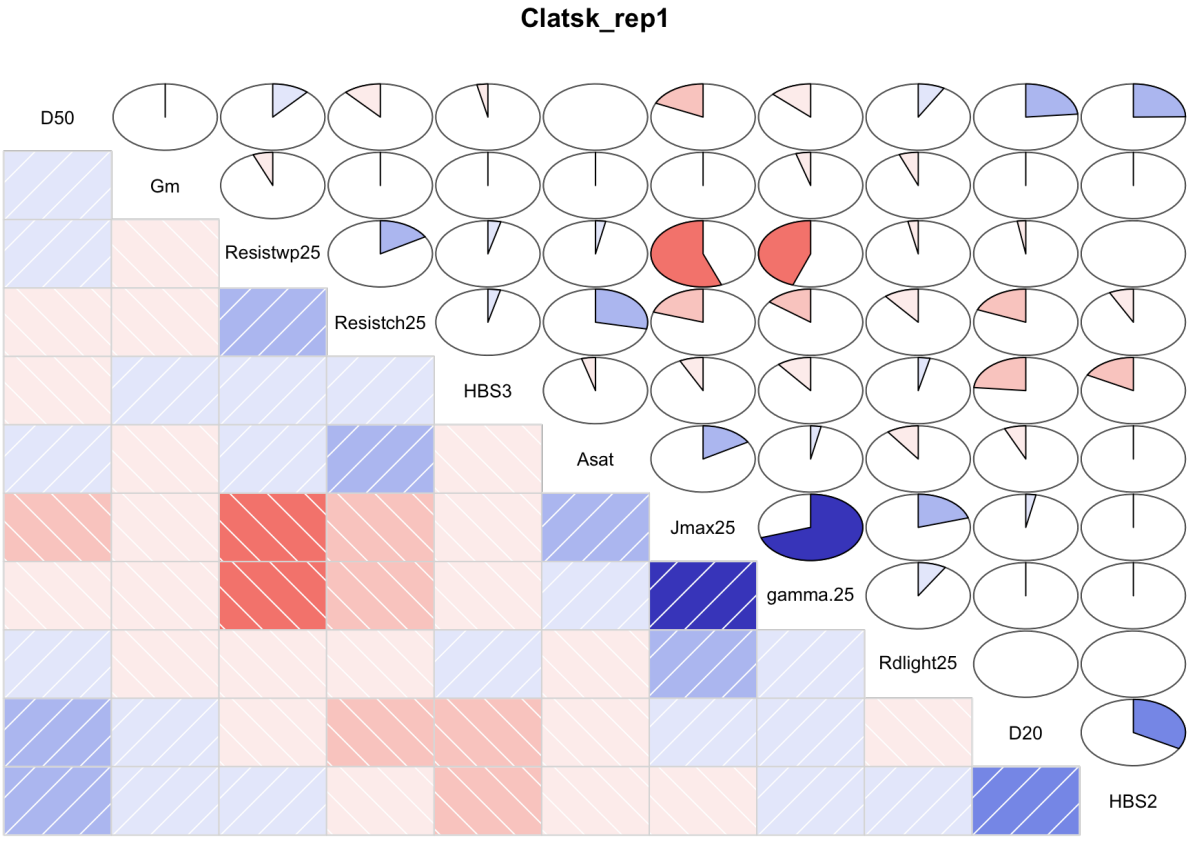
correlegrams Clatskanis Height Diameter data using replilcate 1

```
library(corrgram)

#convert some columns to numeric

datClatHt_1_join<-datClatHt_1_join %>% select(-Duplicate, -id, -Block)
datClatHt_1_join[, c(8:11)] <- sapply(datClatHt_1_join[, c(8:11)], as.numeric)

corrgram(datClatHt_1_join, order=TRUE, lower.panel=panel.shade,
  upper.panel=panel.pie, text.panel=panel.txt,
  main="Clatsk_rep1")
```



correlegrams Corvalis replilcate 1

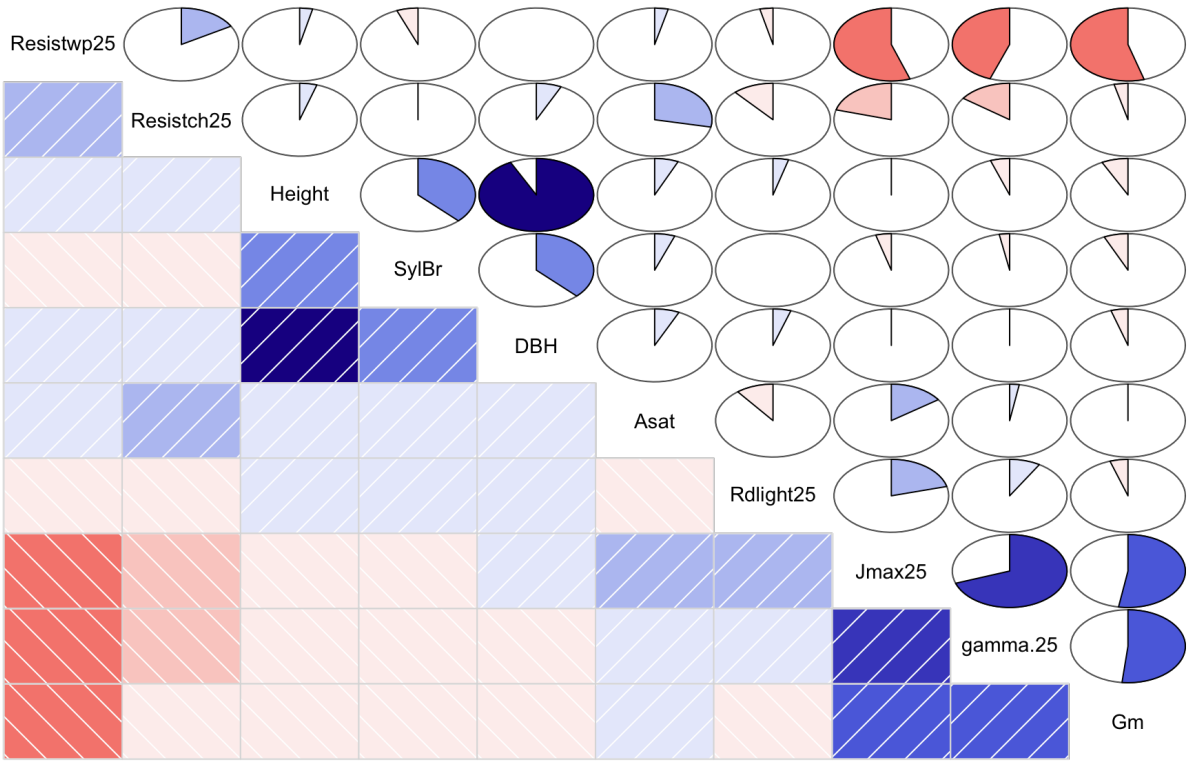
```
datCor_1<-datCor_1 %>% select(id=Geno, Height=Corv_R1_Height_2012, DBH=Corv_R1_DBH_2012, Sy
lBr=SylBr_2012)
datCor_1_join<-inner_join(dat2, datCor_1, by = "id")
```

```
## Warning: joining character vector and factor, coercing into character
## vector
```

```
datCor_1_join<-datCor_1_join %>% select(-Duplicate)
datCor_1_join[, c(9:11)] <- sapply(datCor_1_join[, c(9:11)], as.numeric)

corrgram(datCor_1_join, order=TRUE, lower.panel=panel.shade,
  upper.panel=panel.pie, text.panel=panel.txt,
  main="Corvalis_rep1")
```

Corvalis_rep1



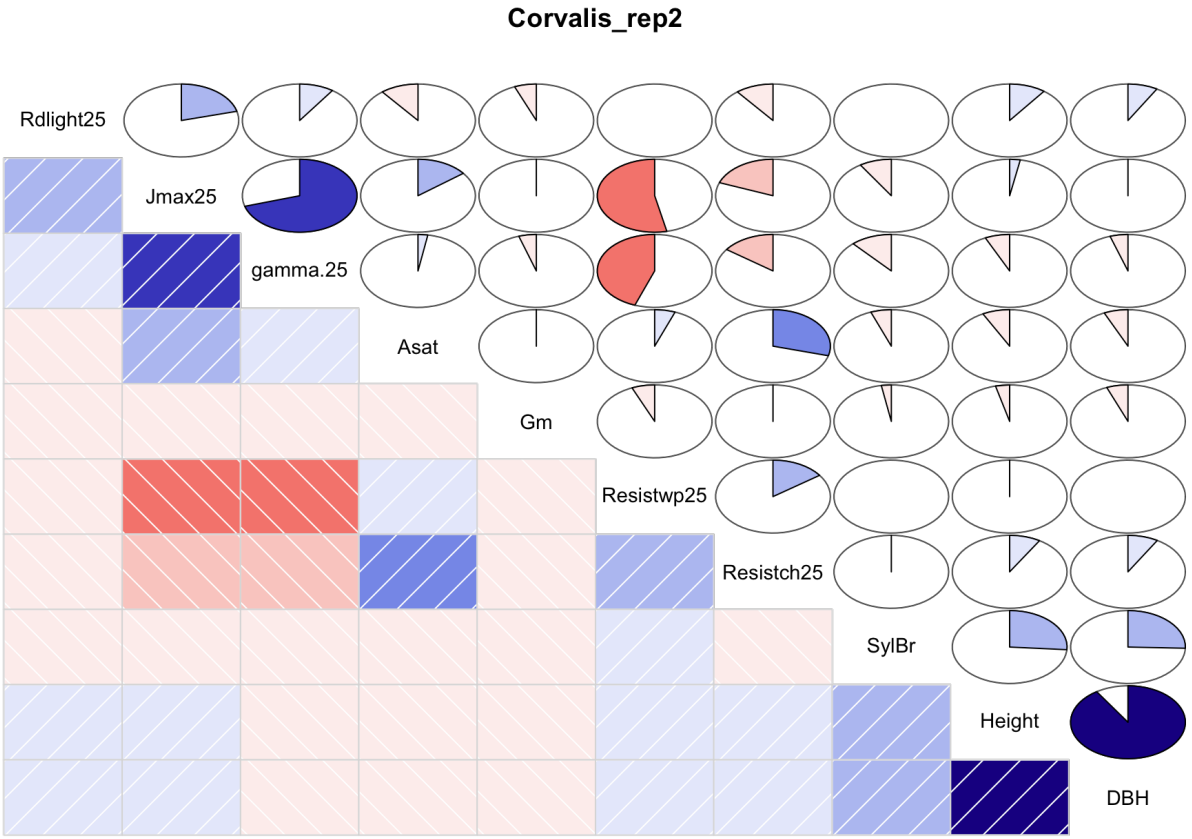
correlegrams Corvalis replilcate 2

```
datCor_2<-datCor_2 %>% select(id=Geno, Height=Corv_R2_Height_2012, DBH=Corv_R3_DBH_2012, Sy
lBr=SylBr_2012)
datCor_2_join<-inner_join(dat2, datCor_2, by = "id")
```

```
## Warning: joining character vector and factor, coercing into character
## vector
```

```
datCor_2_join<-datCor_2_join %>% select(-Duplicate)
datCor_2_join[, c(9:11)] <- sapply(datCor_2_join[, c(9:11)], as.numeric)

corrgram(datCor_2_join, order=TRUE, lower.panel=panel.shade,
  upper.panel=panel.pie, text.panel=panel.txt,
  main="Corvalis_rep2")
```



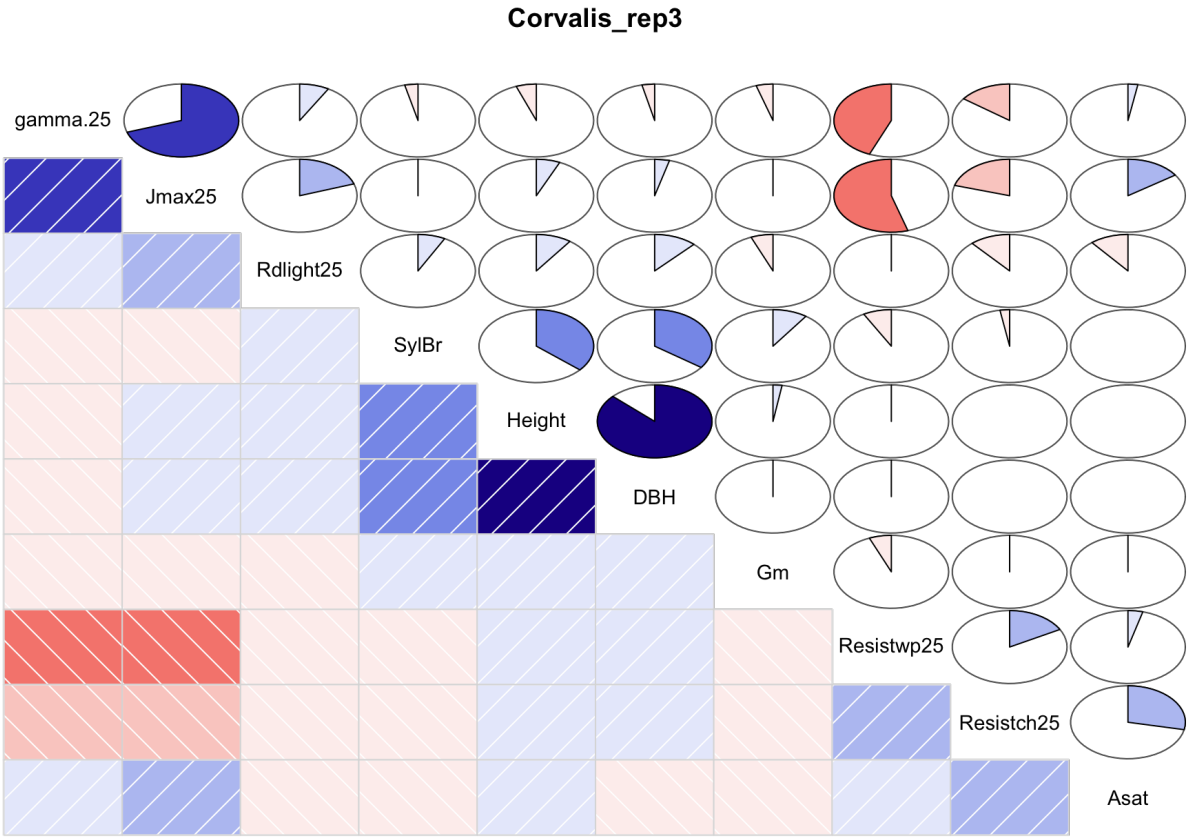
correlegrams Corvalis replilcate 3

```
datCor_3<-datCor_3 %>% select(id=Geno, Height=Corv_R3_Height_2012, DBH=Corv_R3_DBH_2012, Sy
lBr=SylBr_2012)
datCor_3_join<-inner_join(dat2, datCor_3, by = "id")
```

```
## Warning: joining character vector and factor, coercing into character
## vector
```

```
datCor_3_join<-datCor_3_join %>% select(-Duplicate)
datCor_3_join[, c(9:11)] <- sapply(datCor_3_join[, c(9:11)], as.numeric)

corrgram(datCor_3_join, order=TRUE, lower.panel=panel.shade,
  upper.panel=panel.pie, text.panel=panel.txt,
  main="Corvalis_rep3")
```


Corvalis_rep3
gamma.25
Jmax25
Rdlight25
SylBr
Height
DBH
Gm
Resistwp25
Resistch25
Asat