# Descriptive statistics

```
library(magrittr)
library(ggplot2)
library(gridExtra)
library(ggcorrplot)

source("../R/visualizations.R")
source("../R/feature_definitions.R")

training_set <- read.csv("../preprocessed_training_data.csv", row.names = 1, as.is = TRUE)
outcome <- read.csv("../training_outcomes.csv", row.names = 1)[,1]

stopifnot(row.names(training_set) == row.names(outcome))</pre>
```

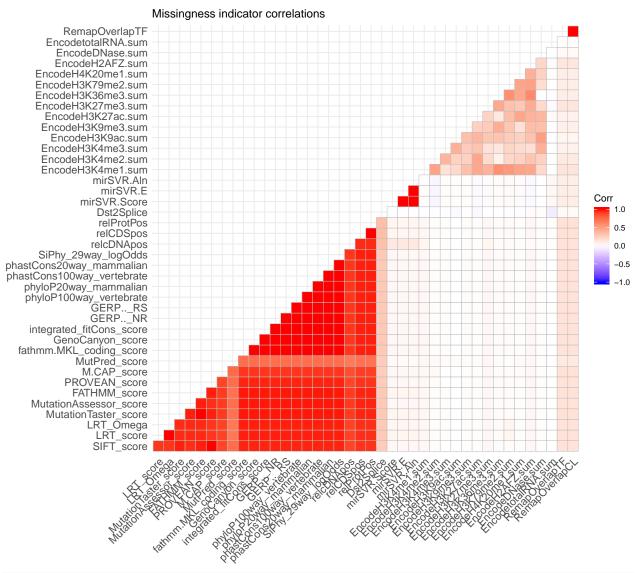
#### Correlations

Plot correlation matrices of missingness indicators against missingness indicators, observed values against observed values, and missingness indicators against observed values.

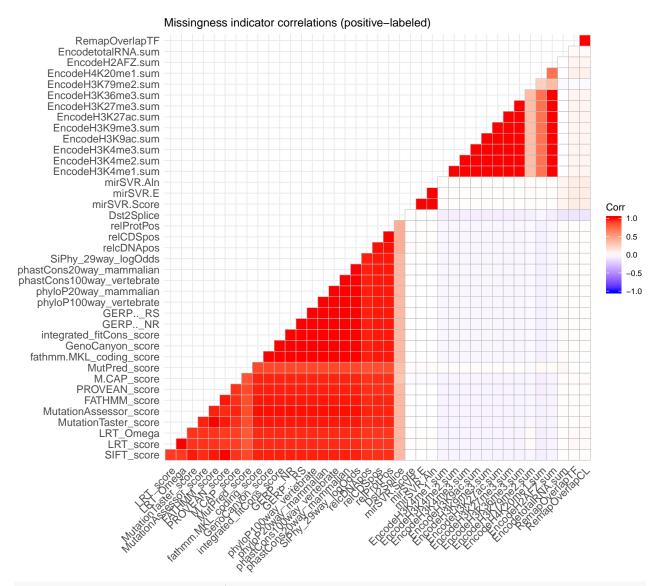
```
positive_data <- training_set[outcome == "positive", ]
negative_data <- training_set[outcome == "negative", ]

# Missingness indicator correlations
plot_missingness_correlations(training_set, numeric_features, "Missingness indicator correlations")</pre>
```

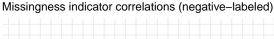
## Warning in cor(miss\_data[, features]): the standard deviation is zero

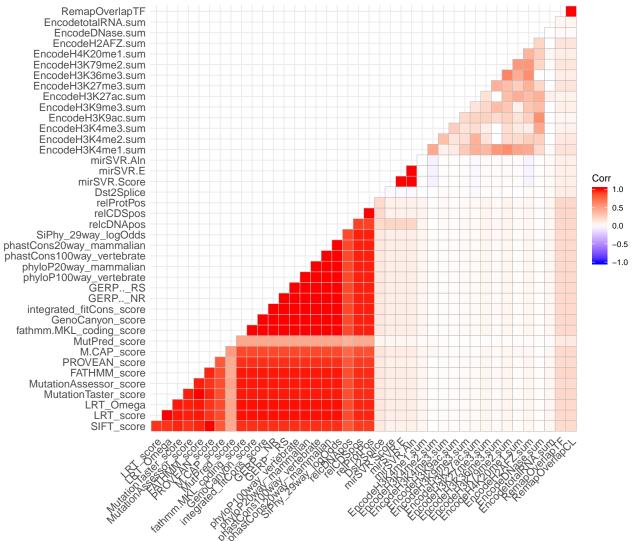


plot\_missingness\_correlations(positive\_data, numeric\_features, "Missingness indicator correlations (pos
## Warning in cor(miss\_data[, features]): the standard deviation is zero



plot\_missingness\_correlations(negative\_data, numeric\_features, "Missingness indicator correlations (neg
## Warning in cor(miss\_data[, features]): the standard deviation is zero

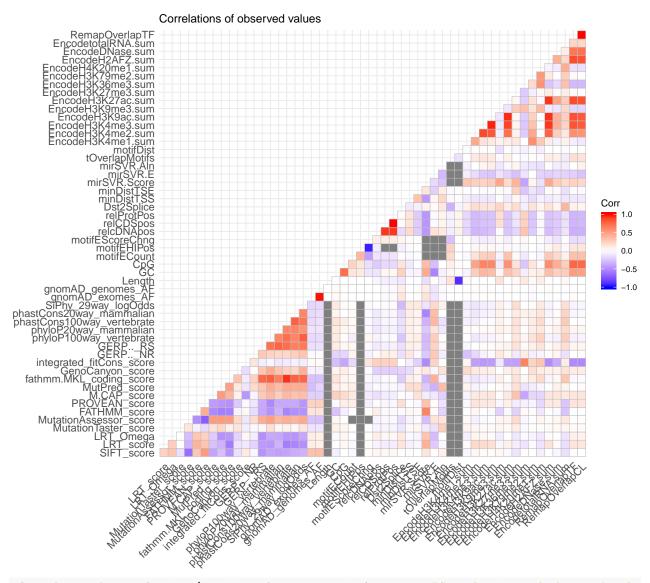




#### # Observed value correlations

plot\_observed\_correlations(training\_set, numeric\_features, "Correlations of observed values")

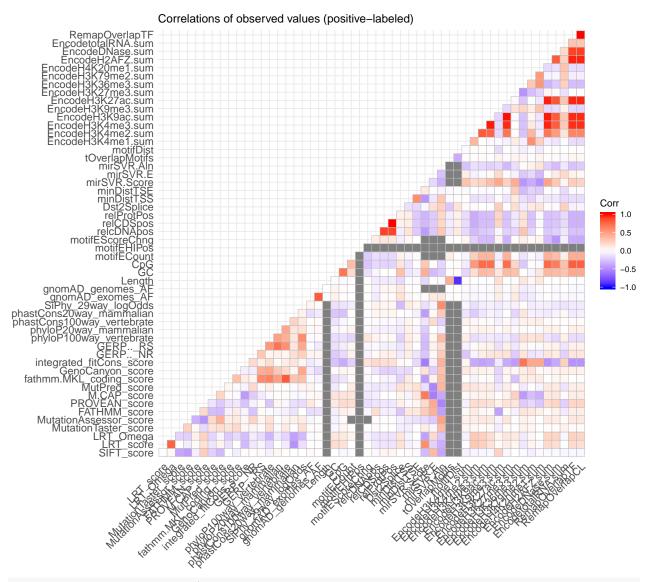
- ## Warning in cor(data[, features], use = "pairwise.complete.obs"): the
- ## standard deviation is zero



plot\_observed\_correlations(positive\_data, numeric\_features, "Correlations of observed values (positive-

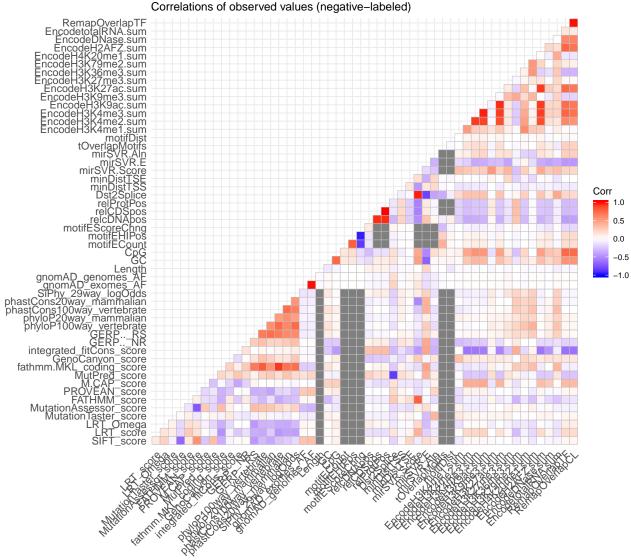
<sup>##</sup> Warning in cor(data[, features], use = "pairwise.complete.obs"): the

<sup>##</sup> standard deviation is zero



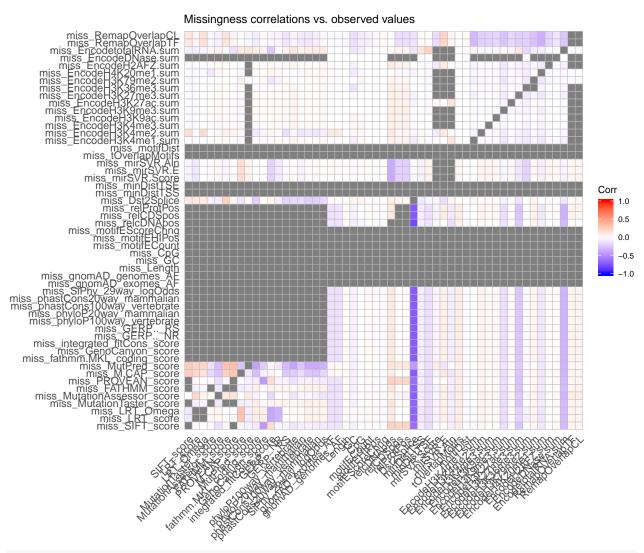
plot\_observed\_correlations(negative\_data, numeric\_features, "Correlations of observed values (negative-

- ## Warning in cor(data[, features], use = "pairwise.complete.obs"): the
- ## standard deviation is zero



# Missingness vs. observed correlations
plot\_missingness\_vs\_observed\_correlations(training\_set, numeric\_features, "Missingness correlations vs.
## Warning in cor(data, miss\_data, use = "pairwise.complete.obs"): the

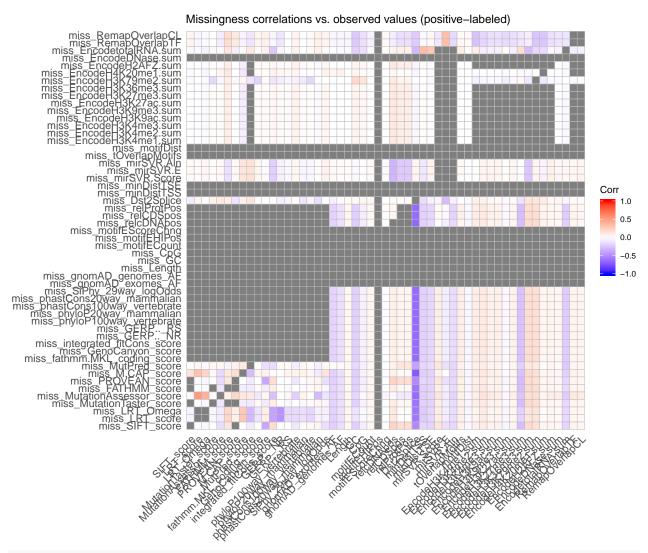
## standard deviation is zero



plot\_missingness\_vs\_observed\_correlations(positive\_data, numeric\_features, "Missingness correlations vs

<sup>##</sup> Warning in cor(data, miss\_data, use = "pairwise.complete.obs"): the

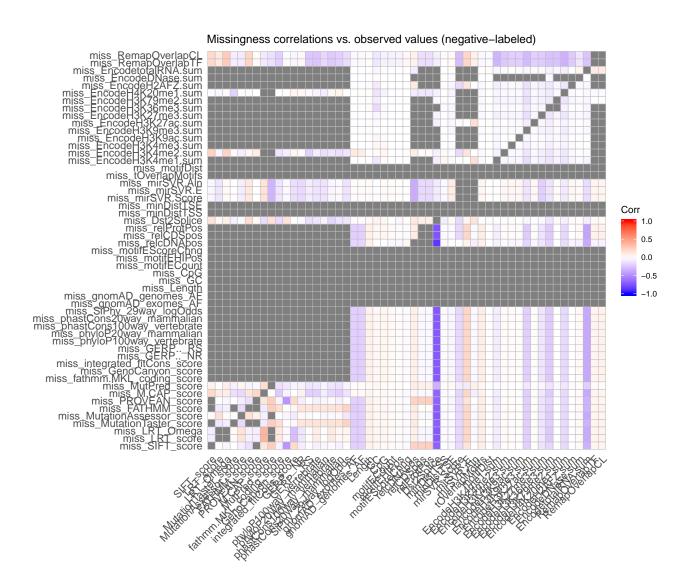
<sup>##</sup> standard deviation is zero



plot\_missingness\_vs\_observed\_correlations(negative\_data, numeric\_features, "Missingness correlations vs

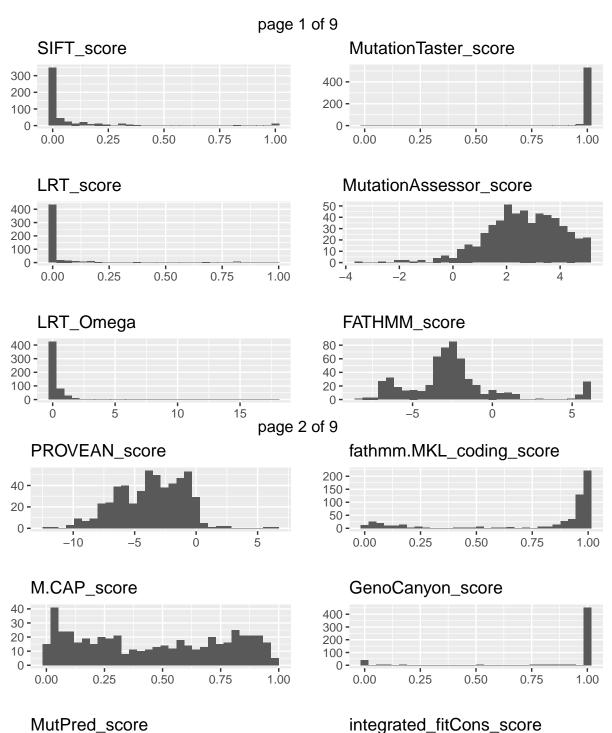
<sup>##</sup> Warning in cor(data, miss\_data, use = "pairwise.complete.obs"): the

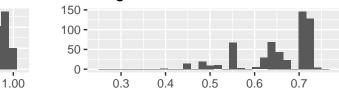
<sup>##</sup> standard deviation is zero



#### Feature value distributions

Next, plot distributions of each feature. Are they normal or linear?





0.75

40 -

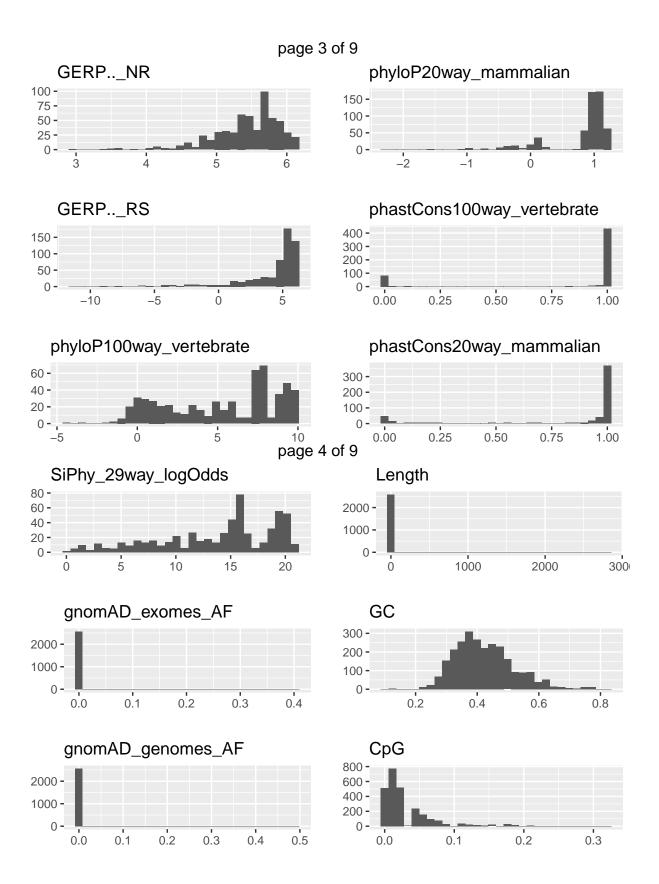
20 -

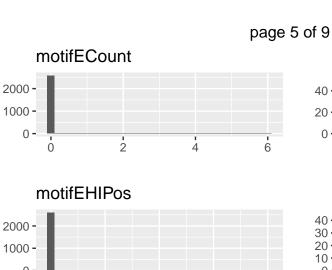
0 -

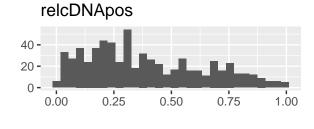
0.00

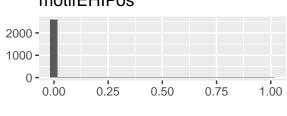
0.25

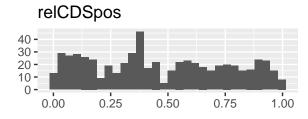
0.50

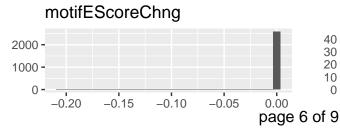


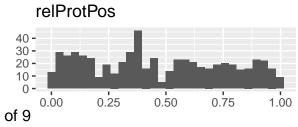


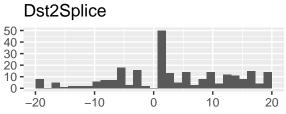


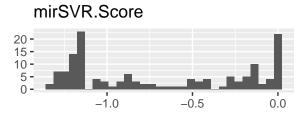


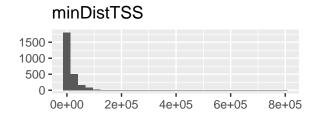


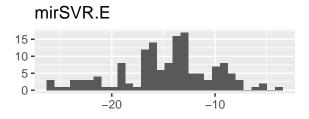


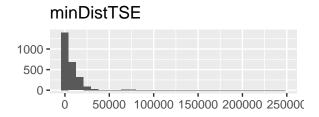


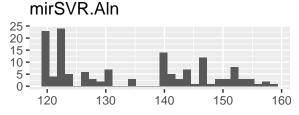




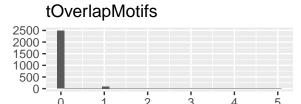




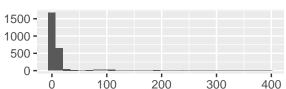




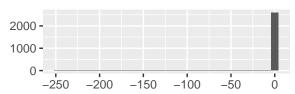




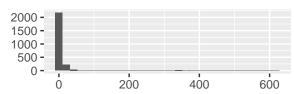
### EncodeH3K4me2.sum



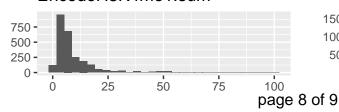
### motifDist



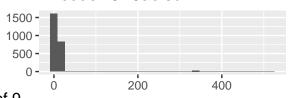
# EncodeH3K4me3.sum



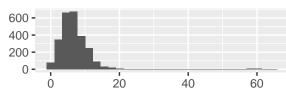
### EncodeH3K4me1.sum



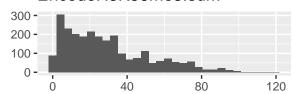
### EncodeH3K9ac.sum



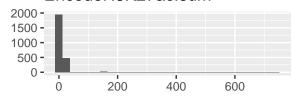
# EncodeH3K9me3.sum



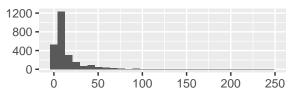
EncodeH3K36me3.sum



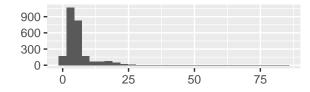
# EncodeH3K27ac.sum



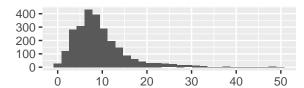
EncodeH3K79me2.sum



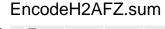
### EncodeH3K27me3.sum

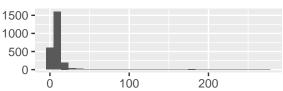


# EncodeH4K20me1.sum

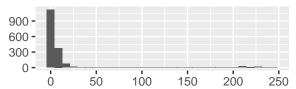




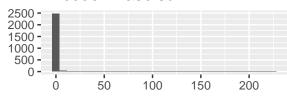




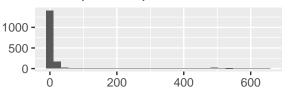
# RemapOverlapTF



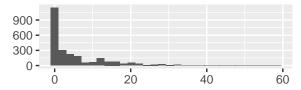
### EncodeDNase.sum



# RemapOverlapCL



#### EncodetotalRNA.sum



They are not, and thus it might be worth considering data transformations. In the case of random forest, however, monotone transformations should have no effect.

#### Categorical level occurrence counts

Print (one-dimensional) contingency tables, i.e. occurrence counts of each level of categorical variables.

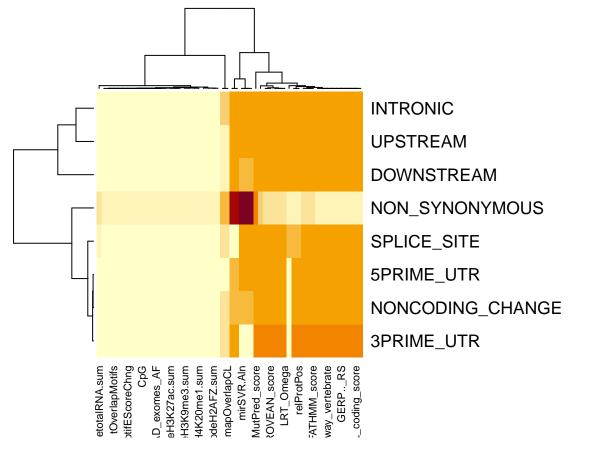
```
for (cat_feat in categorical_features) {
  table(training_set[, cat_feat, drop = FALSE], dnn = cat_feat, useNA = "always") %>% as.data.frame %>%
}
```

```
##
     LRT_pred Freq
## 1
             D
                382
## 2
             N
                162
## 3
             U
                  4
## 4
         <NA> 2044
##
     Dst2SplType Freq
        ACCEPTOR 115
## 1
## 2
           DONOR
                   139
## 3
             <NA> 2338
##
        Consequence.x Freq
## 1
           3PRIME_UTR
## 2
           5PRIME_UTR
                          17
## 3
           DOWNSTREAM
                        458
              INTRONIC
                        794
  5
       NON_SYNONYMOUS
                        580
##
## 6 NONCODING_CHANGE
                          13
## 7
          SPLICE_SITE
                          73
## 8
              UPSTREAM
                        635
```

## 9 <NA> 0

#### Heatmap of feature missingness against consequence

It is likely that missing values are more or less common in some variables depending on the predicted consequence. This can be visualized by a heatmap:



Non-synonymous variants have much less missingness in certain variables and more in others (as expected).

#### Compute number of observed missingness patterns

```
missingness_patterns <- training_set[, c(numeric_features, categorical_features)] %>% is.na
unique_missingness_patterns <- missingness_patterns %>% unique
num_missingness_patterns <- unique_missingness_patterns %>% nrow
print(paste(num_missingness_patterns, "out of", 2^length(c(numeric_features, categorical_features)), "p
```

## [1] "118 out of 72057594037927936 possible missingness patterns."

```
missingness_pattern_factor <- apply(missingness_patterns, MARGIN = 1, function(x) pasteO(as.integer(x),
rows_per_missingness_pattern <- table(missingness_pattern_factor)</pre>
rows_per_missingness_pattern <- rows_per_missingness_pattern %>% as.data.frame
rows_per_missingness_pattern[order(rows_per_missingness_pattern$Freq, decreasing = TRUE),]
##
        missingness_pattern_factor Freq
##
 85
 ##
##
 151
7
##
 86
##
81
 65
3
 ##
              54
74
 ##
              44
87
 32
##
##
 28
8
##
32
 24
##
12
 21
 ##
19
              21
 ##
4
              19
##
75
 19
##
88
 19
##
71
 18
 ##
              16
##
62
 14
 ##
33
              12
 ##
68
              12
##
96
 12
 ##
17
              11
 ##
              11
 ##
               9
##
 9
##
9
 8
 8
##
              7
##
46
 7
##
77
 25
               6
##
##
 6
 6
##
##
 6
63
##
76
 6
##
26
 5
 ##
56
               5
##
72
 5
##
89
 5
 4
##
13
 4
##
 4
##
57
##
 4
##
 4
4
##
 ##
5
               3
 3
##
11
```

3

3

## 28 ## 38

```
3
##
41
3
##
51
##
         3
         3
##
93
##
99
 3
3
##
2
##
1
##
2
2
##
20
2
2
##
23
##
35
2
         2
##
42
         2
##
43
2
##
44
2
##
58
##
61
2
2
##
64
 2
##
2
##
105
##
2
##
2
2
##
##
10
         1
##
14
         1
##
15
1
##
16
1
21
##
         1
##
22
         1
##
24
         1
##
27
1
##
29
1
##
30
1
##
31
1
##
34
         1
36
1
##
##
37
         1
##
40
1
##
47
         1
##
49
         1
54
##
         1
 ##
55
         1
##
59
         1
##
60
         1
##
65
         1
##
67
1
##
70
         1
##
73
1
##
78
         1
##
79
1
##
80
111111111111111111110000000011100011100110001000100011100
         1
##
83
         1
##
84
1
##
91
1
## 94
1
```

```
## 97
1
1
1
1
1
1
1
1
1
1
1
1
1
1
```