

Model 10 Predictions

Ethan Allavarpu (UID: 405287603)

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CREATE YOUR OWN COPY OF THE FILE IF YOU WANT TO CHANGE THINGS!!!!

Transforming and Cleaning the Data

```
training <- read.csv("training.csv", stringsAsFactors = TRUE)
training$class <- factor(training$class)
levels(training$class) <- c("NG", "OG", "TSG")
outlier <- function(data) {
  low <- mean(data) - 3 * sd(data)
  high <- mean(data) + 3 * sd(data)
  which(data < low | data > high)
}
# library(ggplot2)
# scatter <- function(var) {
#   ggplot(training, aes_string(var, "class")) +
#     geom_jitter(width = 0.05, height = 0.1, size = 0.1,
#                 colour = rgb(0, 0, 0, alpha = 1 / 3))
# }
# scat_plot <- lapply(names(training)[-99], scatter)
# library(gridExtra)
# grid.arrange(grobs = scat_plot[1:20], ncol = 4)
# grid.arrange(grobs = scat_plot[21:40], ncol = 4)
# grid.arrange(grobs = scat_plot[41:60], ncol = 4)
# grid.arrange(grobs = scat_plot[61:80], ncol = 4)
# grid.arrange(grobs = scat_plot[81:98], ncol = 4)
outlier_index <- sort(table(unlist(lapply(training[,-99], outlier))), decreasing = TRUE)
outlier_index[1:100]
```

915	1280	2918	517	1914	2182	3052	1173	2215	3049	259	740	1749	1979	2998	417
24	24	24	22	22	22	20	19	19	19	18	18	18	18	18	17
441	806	2297	422	635	1258	1570	2278	2518	2729	80	150	2694	169	276	341
17	17	17	16	16	16	16	16	16	16	15	15	15	14	14	14
1528	1556	1726	1809	1911	1955	2071	2624	2641	3120	3142	73	277	364	751	1244
14	14	14	14	14	14	14	14	14	14	14	13	13	13	13	13
1330	2329	2787	343	1138	1171	1188	1372	1460	2031	2251	2968	2983	3166	352	634
13	13	13	12	12	12	12	12	12	12	12	12	12	12	11	11
907	923	1096	1858	2636	588	1137	1317	1463	1561	1740	1991	2487	2540	2555	2621
11	11	11	11	11	10	10	10	10	10	10	10	10	10	10	10
2815	3029	74	144	657	789	857	1267	1610	1932	2022	2093	2142	2534	2666	2721

```

      10    10    9    9    9    9    9    9    9    9    9    9    9    9    9    9
2848 2900 3027 155
      9    9    9    8

training <- training[-as.numeric(names(outlier_index)[1:50]),]
sort(training$Missense_TO_Silent_Ratio, decreasing = TRUE)[1:10]

[1] 384.98658 172.91420 135.59623 71.09712 23.21809 21.81193 20.37791
[8] 19.42402 19.38769 15.84808

training <- training[-which(training$Missense_TO_Silent_Ratio > 100), ]
sort(training$Missense_KB_Ratio, decreasing = TRUE)[1:10]

[1] 2063.9413 1296.6625 1060.0601 952.3810 931.4227 726.8519 594.7603
[8] 593.3610 581.5085 516.8084

training <- training[-which(training$Missense_KB_Ratio > 2000), ]
sort(training$LOF_TO_Silent_Ratio, decreasing = TRUE)[1:10]

[1] 81.177835 9.030120 6.470238 5.582840 4.741460 4.558252 4.176630
[8] 4.058140 4.039062 4.021930

training <- training[-which(training$LOF_TO_Silent_Ratio > 5), ]
sort(training$Gene_expression_Z_score, decreasing = TRUE)[1:10]

[1] 19.720 9.210 7.080 6.883 6.590 6.280 5.321 5.316 3.161 2.767

training <- training[-which(training$Gene_expression_Z_score > 4), ]
sort(training$dN_to_dS_ratio, decreasing = TRUE)[1:10]

[1] 20.950 3.649 3.446 3.372 2.574 2.194 2.183 2.102 1.921 1.744

training <- training[-which(training$dN_to_dS_ratio > 5), ]
sort(training$Silent_KB_Ratio, decreasing = TRUE)[1:10]

[1] 474.4745 193.1684 174.0558 171.0362 166.4971 160.2273 158.7697 148.5800
[9] 143.6782 135.2657

training <- training[-which(training$Silent_KB_Ratio > 200), ]
sort(training$Lost_start_and_stop_fraction, decreasing = TRUE)[1:10]

[1] 0.333 0.167 0.118 0.087 0.074 0.071 0.071 0.068 0.067 0.067

training <- training[-which(training$Lost_start_and_stop_fraction > 0.2), ]
sort(training$Synonymous_Zscore, decreasing = FALSE)[1:10]

[1] -20.5110 -10.9780 -10.2960 -9.7346 -9.3720 -8.8090 -8.4062 -8.3918
[9] -8.1076 -8.1076

training <- training[-which(training$Synonymous_Zscore < -15), ]
numeric_training <- training[,-99]

n_zeroes <- rep(NA, nrow(numeric_training))

for(i in seq_len(nrow(numeric_training))){  

  row_i_zeroes <- 0  

  for(j in seq_len(ncol(numeric_training))){  

    if(round(numeric_training[i,j], digits = 5) == 0){  

      row_i_zeroes <- row_i_zeroes + 1  

    }  

  }
}

```

```

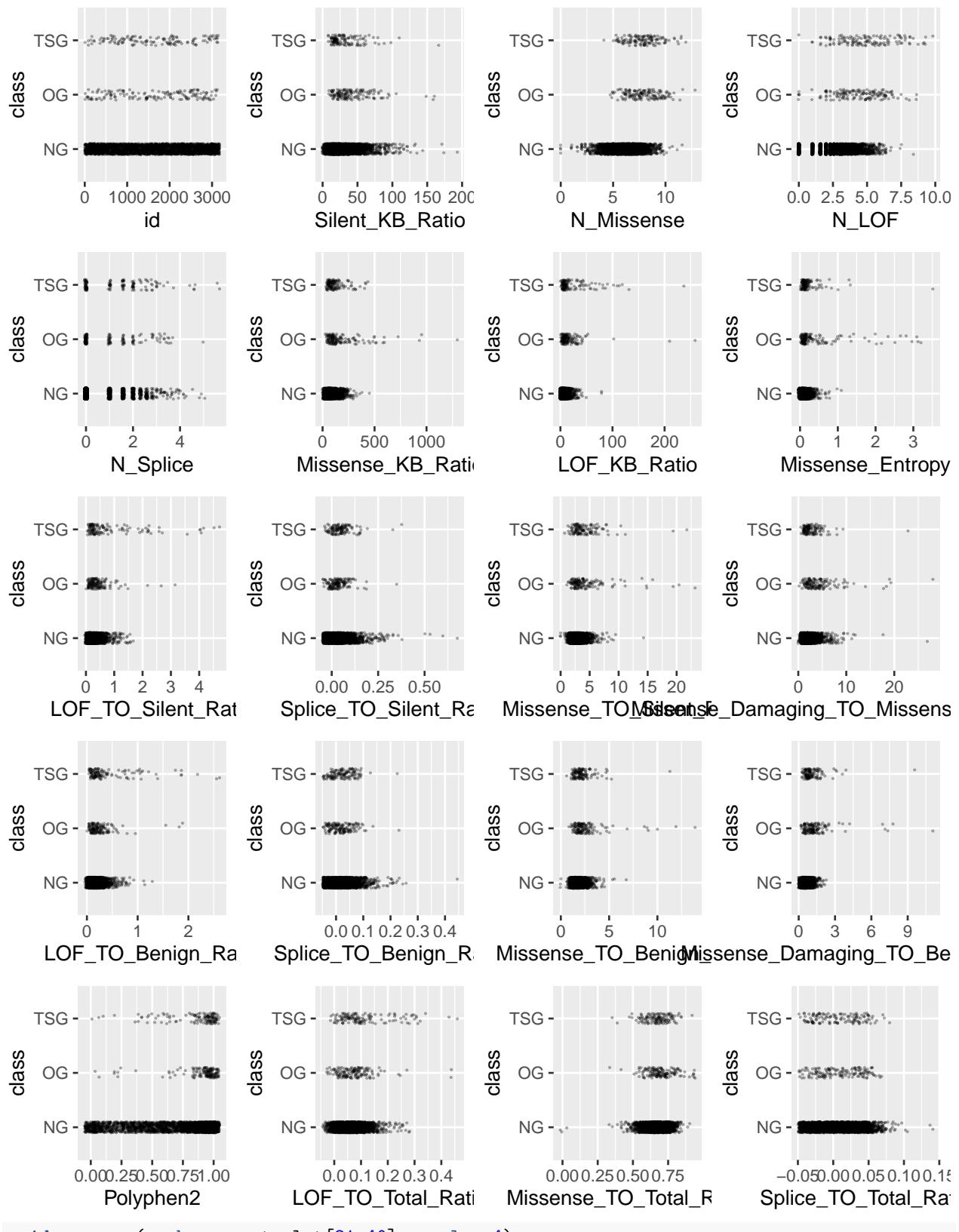
    }
    n_zeroes[i] <- row_i_zeroes
}
training <- training[n_zeroes <= 50, ]
# Remove 1 of 2 variables that have r value of 1 or -1 (i.e. perfectly correlated)
perf_corr <- which(abs(cor(training[,-99])) == 1, arr.ind = TRUE)
which(perf_corr[,1] != perf_corr[,2])

Minus_Cell_proliferation_rate_CRISPR_KD      Cell_proliferation_rate_CRISPR_KD
43                                         44

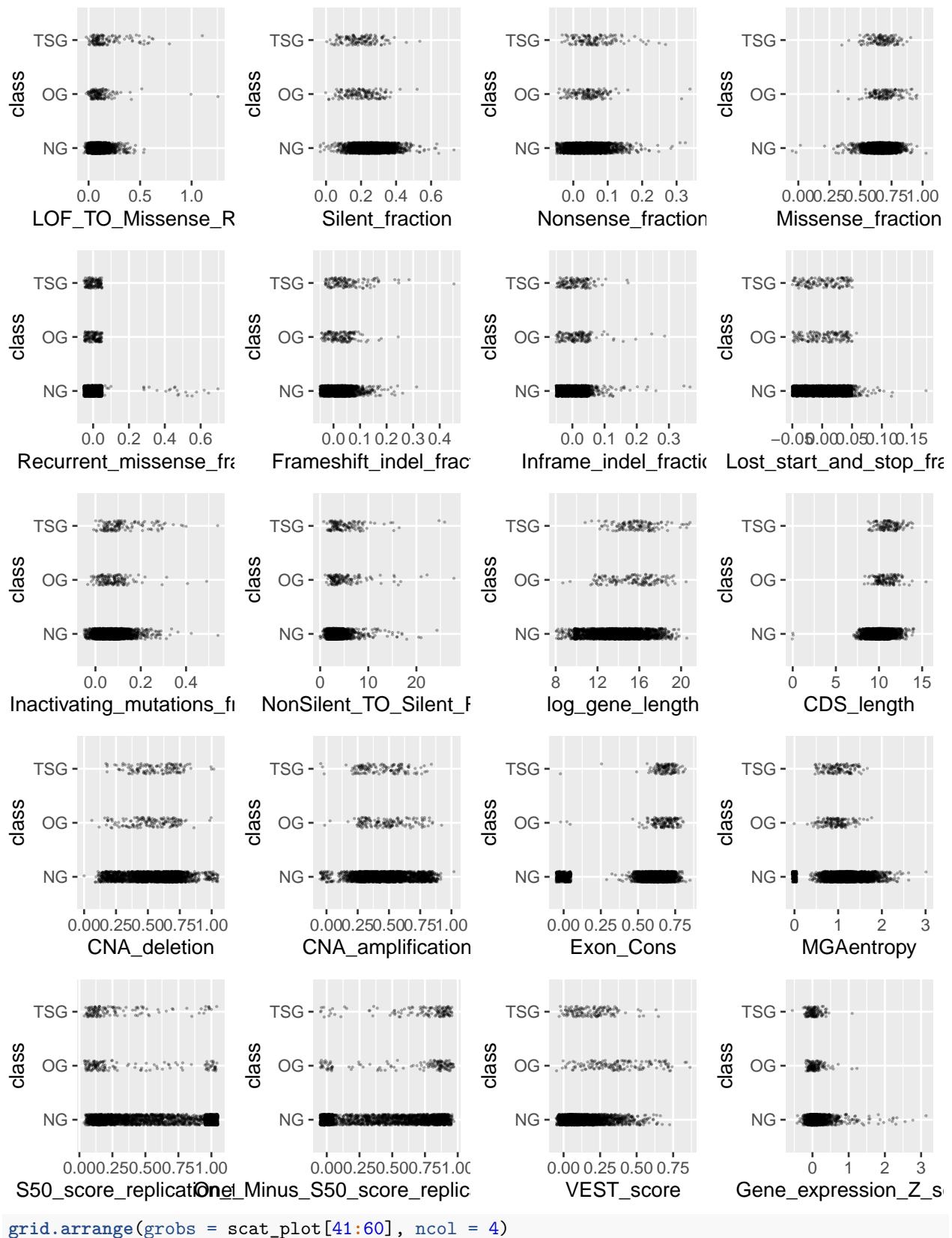
training <- training[, -43]

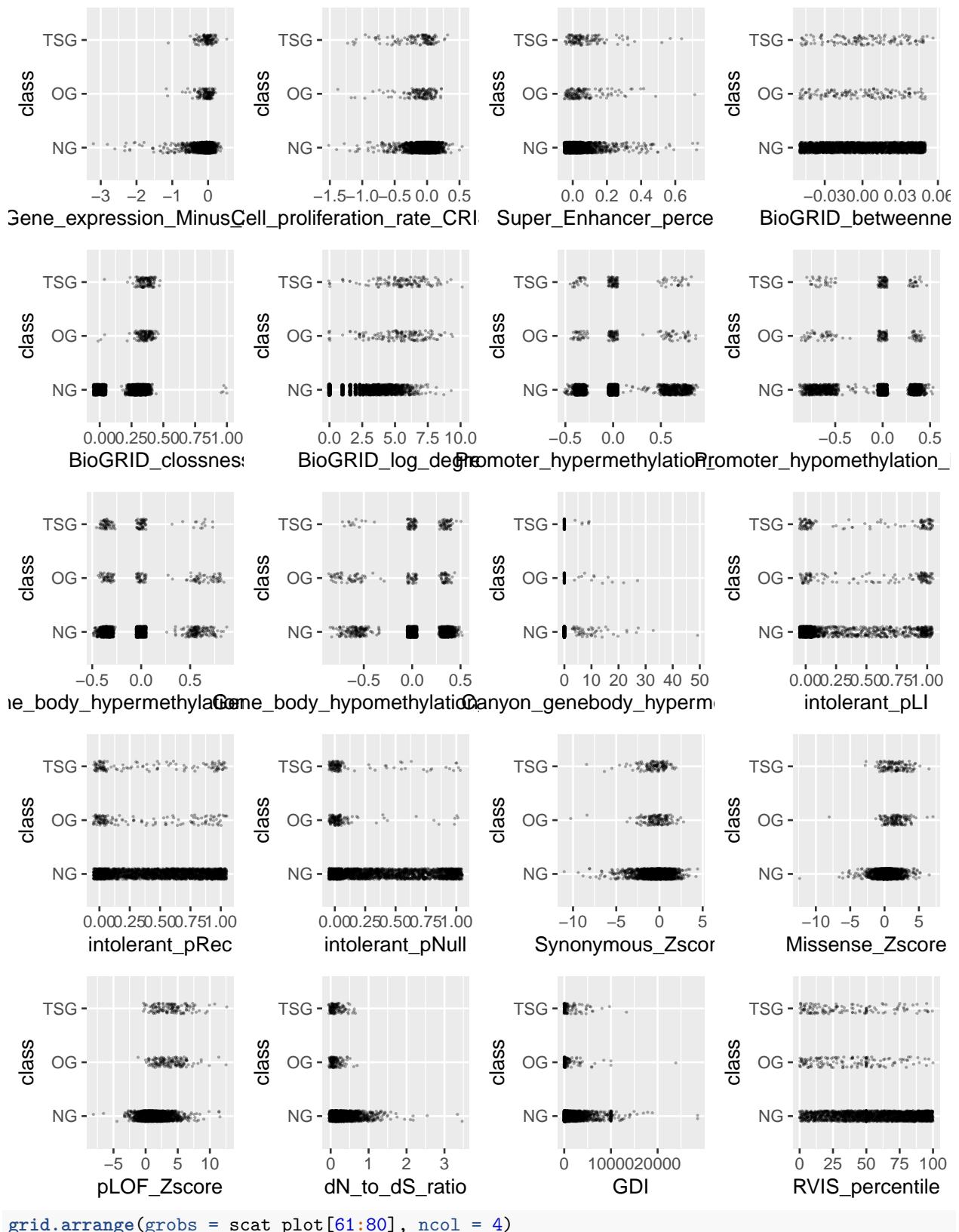
library(ggplot2)
scatter <- function(var) {
  ggplot(training, aes_string(var, "class")) +
    geom_jitter(width = 0.05, height = 0.1, size = 0.1,
                colour = rgb(0, 0, 0, alpha = 1 / 3))
}
scat_plot <- lapply(names(training)[-98], scatter)
library(gridExtra)
grid.arrange(grobs = scat_plot[1:20], ncol = 4)

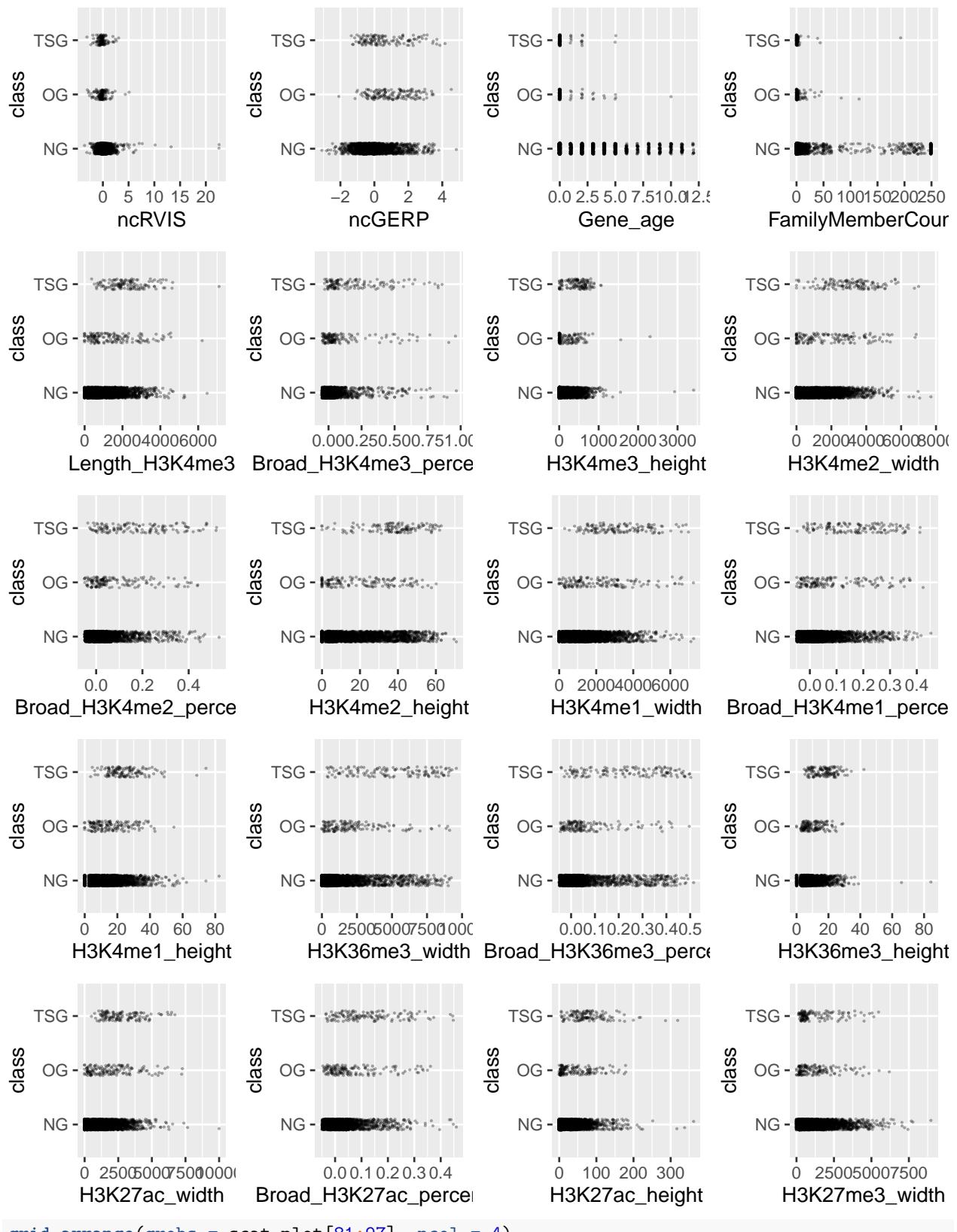
```



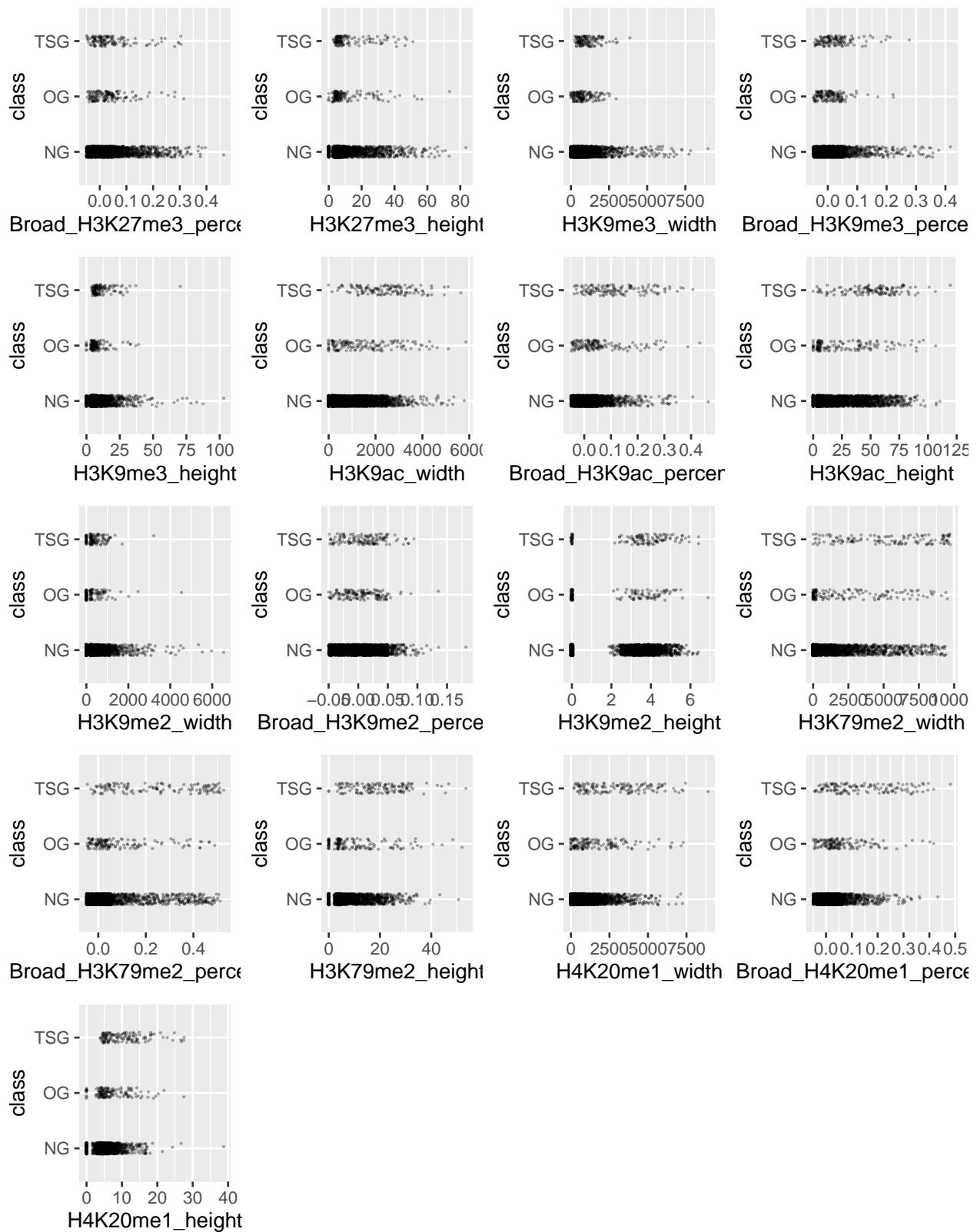
```
grid.arrange(grobs = scat_plot[21:40], ncol = 4)
```







```
grid.arrange(grobs = scat_plot[81:97], ncol = 4)
```



```

Attaching package: 'dplyr'
The following object is masked from 'package:gridExtra':
  combine

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

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

#function to calculate wca
score <- function (conf_mat) {
  print(sum(diag(conf_mat) * c(1, 20, 20)))
  print(sum(diag(conf_mat) * c(1, 20, 20)) / sum(apply(conf_mat, 2, sum) * c(1, 20, 20)))
}

# Set new threshold to account for unbalanced data
classify <- function(probs, k) {
  if (any(probs[2:3] > k)) {
    subset <- probs[2:3]
    output <- which(subset == max(subset))
    if (length(output) > 1) {
      output <- sample(1:2, 1)
    }
  } else {
    output <- 0
  }
  output
}

```

Multinom (Logistic Regression)

```
library(dplyr)
library(caret)

Loading required package: lattice
set.seed(12)
mn <- nnet::multinom(class ~ ., data = training, model = TRUE)

# weights:  297 (196 variable)
initial  value 3326.598010
iter  10 value 1352.245526
iter  20 value 1217.290354
iter  30 value 1085.878928
iter  40 value 942.253816
iter  50 value 839.781152
iter  60 value 772.029605
iter  70 value 678.667906
iter  80 value 550.944852
iter  90 value 446.725235
iter 100 value 355.375074
final  value 355.375074
stopped after 100 iterations

tidymn <- broom::tidy(mn) %>% arrange(p.value)
tidymn <- tidymn %>% filter(p.value < 0.05 / nrow(tidymn))
terms <- unique(tidymn$term)[-1]
terms

[1] "Missense_Entropy"
[2] "LOF_T0_Silent_Ratio"
[3] "Splice_T0_Silent_Ratio"
[4] "LOF_T0_Benign_Ratio"
[5] "Splice_T0_Benign_Ratio"
[6] "Missense_Damaging_T0_Benign_Ratio"
[7] "Polyphen2"
[8] "LOF_T0_Total_Ratio"
[9] "Missense_T0_Total_Ratio"
[10] "Splice_T0_Total_Ratio"
[11] "LOF_T0_Missense_Ratio"
[12] "Silent_fraction"
[13] "Nonsense_fraction"
[14] "Missense_fraction"
[15] "Recurrent_missense_fraction"
[16] "Frameshift_indel_fraction"
[17] "Inframe_indel_fraction"
[18] "Lost_start_and_stop_fraction"
[19] "Inactivating_mutations_fraction"
[20] "CNA_deletion"
[21] "CNA_amplification"
[22] "Exon_Cons"
[23] "MGAentropy"
[24] "S50_score_replication_timing"
[25] "One_Minus_S50_score_replication_timing"
[26] "VEST_score"
```

```

[27] "Gene_expression_Z_score"
[28] "Gene_expression_Minus_Z_score"
[29] "Cell_proliferation_rate_CRISPR_KD"
[30] "Super_Enhancer_percentage"
[31] "BioGRID_betweenness"
[32] "BioGRID_closeness"
[33] "Promoter_hypermethylation_in_cancer"
[34] "Promoter_hypomethylation_in_cancer"
[35] "Gene_body_hypermethylation_in_cancer"
[36] "Gene_body_hypomethylation_in_cancer"
[37] "intolerant_pLI"
[38] "intolerant_pRec"
[39] "intolerant_pNull"
[40] "dN_to_dS_ratio"
[41] "Broad_H3K4me3_percentage"
[42] "Broad_H3K4me2_percentage"
[43] "Broad_H3K4me1_percentage"
[44] "Broad_H3K36me3_percentage"
[45] "Broad_H3K27ac_percentage"
[46] "Broad_H3K27me3_percentage"
[47] "Broad_H3K9me3_percentage"
[48] "Broad_H3K9ac_percentage"
[49] "Broad_H3K9me2_percentage"
[50] "Broad_H3K79me2_percentage"
[51] "Broad_H4K20me1_percentage"
[52] "Missense_T0_Benign_Ratio"
[53] "Missense_T0_Silent_Ratio"
[54] "N_Missense"
[55] "CDS_length"
[56] "ncGERP"
[57] "NonSilent_T0_Silent_Ratio"
[58] "ncRVIS"
[59] "BioGRID_log_degree"
[60] "N_LOF"
[61] "N_Splice"
[62] "Missense_Damaging_T0_Missense_Benign_Ratio"
[63] "Missense_Zscore"
[64] "H3K9me2_height"

library(dplyr)
sig <- logical(97)
names(sig) <- names(training)[-98]
k <- 1
diffs <- logical(97)
for (var in names(training)[-98]) {
  model <- aov(training[[var]] ~ factor(training$class))
  sig[k] <- summary(model)[[1]][1, 5]
  diff[sig[k]] <- all(TukeyHSD(model)$`factor(training$class)`[, 4] < 0.05 / 97)
  k <- k + 1
}
sort(sig[diffs])

```

```

  Broad_H4K20me1_percentage
  2.563341e-146
  VEST_score

```

	1.141090e-121
Broad_H3K9ac_percentage	7.096289e-111
	H3K79me2_height
	1.252905e-110
	H3K79me2_width
	5.618333e-110
	Missense_Entropy
	1.254512e-109
Broad_H3K79me2_percentage	4.654407e-107
Missense_Damaging_T0_Benign_Ratio	1.510740e-106
	Broad_H3K4me2_percentage
	1.195197e-105
	H4K20me1_width
	6.869405e-105
Broad_H3K36me3_percentage	8.244495e-104
	H3K36me3_width
	4.633126e-103
	H4K20me1_height
	1.332273e-101
LOF_T0_Silent_Ratio	4.745882e-101
	Broad_H3K27ac_percentage
	5.173854e-97
Broad_H3K4me1_percentage	1.023092e-95
	LOF_KB_Ratio
	4.040183e-93
	Missense_KB_Ratio
	4.866503e-89
	H3K4me1_width
	6.433999e-80
LOF_T0_Benign_Ratio	1.552250e-78
	Broad_H3K4me3_percentage
	3.171192e-78
	H3K36me3_height
	2.795995e-75
	H3K4me2_width
	9.456016e-74
	H3K9ac_width
	1.107951e-71
Missense_Damaging_T0_Missense_Benign_Ratio	2.508133e-68
	H3K9ac_height
	1.751625e-65
Missense_T0_Benign_Ratio	5.840566e-64
	H3K27ac_width
	2.548087e-63
Length_H3K4me3	

```

    1.108383e-60
H3K27ac_height
2.528240e-58
LOF_TO_Total_Ratio
8.428823e-48
LOF_TO_Missense_Ratio
1.945822e-42
H3K4me1_height
6.778589e-42
Frameshift_indel_fraction
5.027810e-34

score <- function (conf_mat) {
  sum(diag(conf_mat) * c(1, 20, 20)) / sum(apply(conf_mat, 2, sum) * c(1, 20, 20))
}

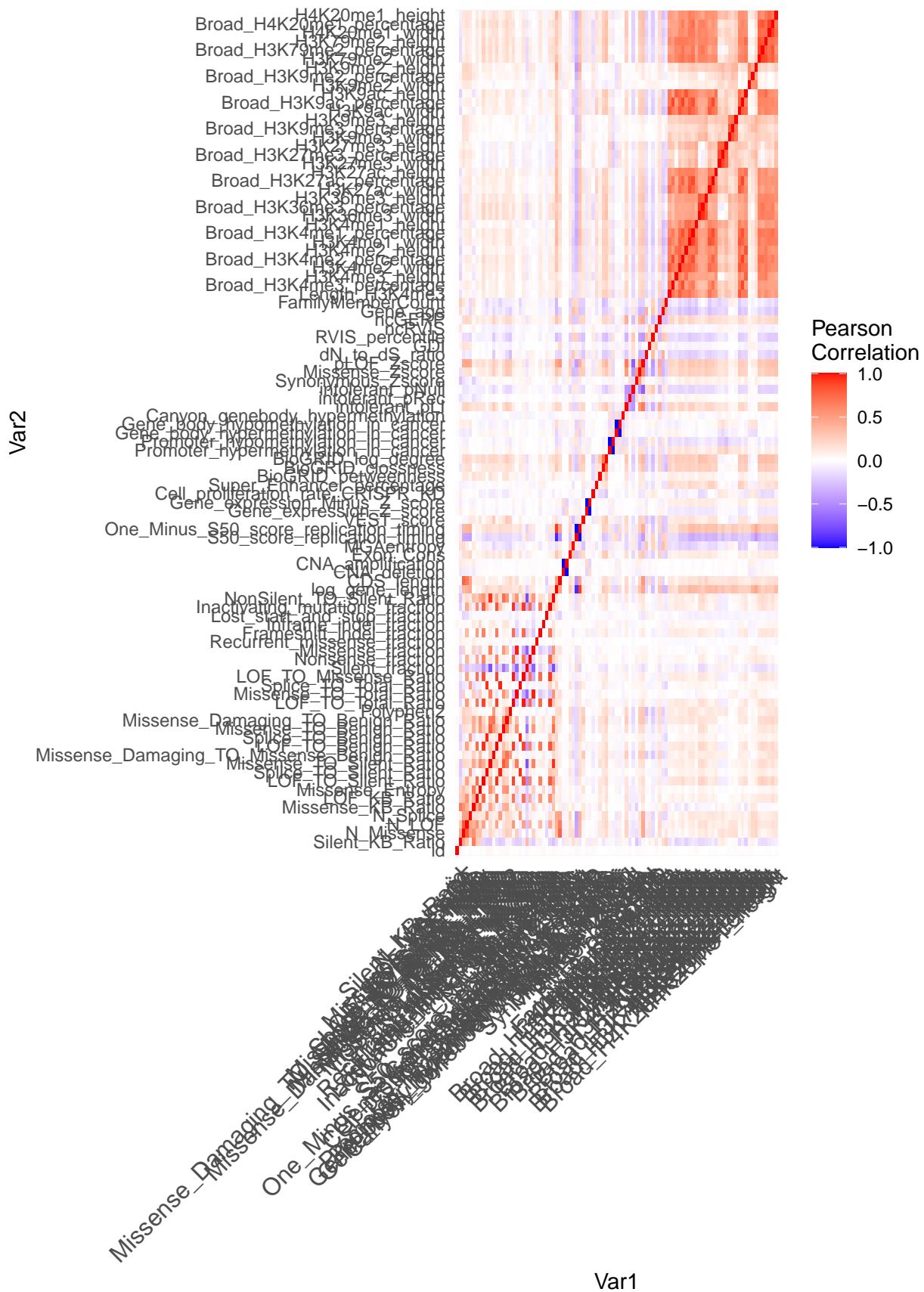
sig_terms <- names(sort(sig[diffs]))
combo_terms <- table(c(terms, sig_terms)) == 2
final_terms <- names(combo_terms[combo_terms])
term_mat <- cor(training %>% select(all_of(final_terms)))

ind_terms <- final_terms[-c(1, 3, 4, 5, 10, 11, 13, 14, 15, 17)]
vars <- training
cor_mtx = round(cor(vars[, names(vars) != "class"]), 2)
library(reshape2)
#reshape it
melted_cor_mtx <- melt(cor_mtx)

#draw the heatmap
cor_heatmap = ggplot(data = melted_cor_mtx, aes(x=Var1, y=Var2, fill=value)) + geom_tile()
cor_heatmap = cor_heatmap +
scale_fill_gradient2(low = "blue", high = "red", mid = "white", midpoint = 0, limit = c(-1,1), space =
theme_minimal() +
theme(axis.text.x = element_text(angle = 45, vjust = 1, size = 12, hjust = 1))

cor_heatmap

```



```
which(abs(cor_mtx) > 0.75, arr.ind = TRUE)
```

	row	col
id	1	1
Silent_KB_Ratio	2	2
N_Missense	3	3
N_LOF	4	3
CDS_length	32	3
N_Missense	3	4
N_LOF	4	4
N_Splice	5	5
Missense_KB_Ratio	6	6
LOF_KB_Ratio	7	7
Missense_Entropy	8	8
LOF_TO_Silent_Ratio	9	9
LOF_TO_Benign_Ratio	13	9
LOF_TO_Total_Ratio	18	9
LOF_TO_Missense_Ratio	21	9
Inactivating_mutations_fraction	29	9
Splice_TO_Silent_Ratio	10	10
Splice_TO_Benign_Ratio	14	10
Splice_TO_Total_Ratio	20	10
Missense_TO_Silent_Ratio	11	11
Missense_TO_Benign_Ratio	15	11
NonSilent_TO_Silent_Ratio	30	11
Missense_Damaging_TO_Missense_Benign_Ratio	12	12
LOF_TO_Silent_Ratio	9	13
LOF_TO_Benign_Ratio	13	13
LOF_TO_Total_Ratio	18	13
LOF_TO_Missense_Ratio	21	13
Inactivating_mutations_fraction	29	13
Splice_TO_Silent_Ratio	10	14
Splice_TO_Benign_Ratio	14	14
Splice_TO_Total_Ratio	20	14
Missense_TO_Silent_Ratio	11	15
Missense_TO_Benign_Ratio	15	15
Missense_Damaging_TO_Benign_Ratio	16	16
Polyphen2	17	17
LOF_TO_Silent_Ratio	9	18
LOF_TO_Benign_Ratio	13	18
LOF_TO_Total_Ratio	18	18
LOF_TO_Missense_Ratio	21	18
Inactivating_mutations_fraction	29	18
Missense_TO_Total_Ratio	19	19
Missense_fraction	24	19
Splice_TO_Silent_Ratio	10	20
Splice_TO_Benign_Ratio	14	20
Splice_TO_Total_Ratio	20	20
LOF_TO_Silent_Ratio	9	21
LOF_TO_Benign_Ratio	13	21
LOF_TO_Total_Ratio	18	21
LOF_TO_Missense_Ratio	21	21
Inactivating_mutations_fraction	29	21
Silent_fraction	22	22

NonSilent_T0_Silent_Ratio	30	22
Nonsense_fraction	23	23
Missense_T0_Total_Ratio	19	24
Missense_fraction	24	24
Recurrent_missense_fraction	25	25
Frameshift_indel_fraction	26	26
Inframe_indel_fraction	27	27
Lost_start_and_stop_fraction	28	28
LOF_T0_Silent_Ratio	9	29
LOF_T0_Benign_Ratio	13	29
LOF_T0_Total_Ratio	18	29
LOF_T0_Missense_Ratio	21	29
Inactivating_mutations_fraction	29	29
Missense_T0_Silent_Ratio	11	30
Silent_fraction	22	30
NonSilent_T0_Silent_Ratio	30	30
log_gene_length	31	31
S50_score_replication_timing	37	31
One_Minus_S50_score_replication_timing	38	31
N_Missense	3	32
CDS_length	32	32
CNA_deletion	33	33
CNA_amplification	34	33
CNA_deletion	33	34
CNA_amplification	34	34
Exon_Cons	35	35
MGAentropy	36	36
log_gene_length	31	37
S50_score_replication_timing	37	37
One_Minus_S50_score_replication_timing	38	37
log_gene_length	31	38
S50_score_replication_timing	37	38
One_Minus_S50_score_replication_timing	38	38
VEST_score	39	39
Gene_expression_Z_score	40	40
Gene_expression_Minus_Z_score	41	40
Gene_expression_Z_score	40	41
Gene_expression_Minus_Z_score	41	41
Cell_proliferation_rate_CRISPR_KD	42	42
Super_Enhancer_percentage	43	43
BioGRID_betweenness	44	44
BioGRID_closeness	45	45
BioGRID_log_degree	46	46
Promoter_hypermethylation_in_cancer	47	47
Promoter_hypomethylation_in_cancer	48	47
Promoter_hypermethylation_in_cancer	47	48
Promoter_hypomethylation_in_cancer	48	48
Gene_body_hypermethylation_in_cancer	49	49
Gene_body_hypomethylation_in_cancer	50	49
Gene_body_hypermethylation_in_cancer	49	50
Gene_body_hypomethylation_in_cancer	50	50
Canyon_genebody_hypermethylation	51	51
intolerant_pLI	52	52
intolerant_pRec	53	53

intolerant_pNull	54	54
Synonymous_Zscore	55	55
Missense_Zscore	56	56
pLOF_Zscore	57	57
dN_to_dS_ratio	58	58
GDI	59	59
RVIS_percentile	60	60
ncRVIS	61	61
ncGERP	62	62
Gene_age	63	63
FamilyMemberCount	64	64
Length_H3K4me3	65	65
H3K4me2_width	68	65
H3K9ac_width	86	65
Broad_H3K4me3_percentage	66	66
Broad_H3K4me2_percentage	69	66
Broad_H3K9ac_percentage	87	66
H3K4me3_height	67	67
H3K9ac_height	88	67
Length_H3K4me3	65	68
H3K4me2_width	68	68
Broad_H3K4me2_percentage	69	68
H3K4me2_height	70	68
H3K4me1_width	71	68
H3K9ac_width	86	68
Broad_H3K4me3_percentage	66	69
H3K4me2_width	68	69
Broad_H3K4me2_percentage	69	69
Broad_H3K4me1_percentage	72	69
Broad_H3K27ac_percentage	78	69
Broad_H3K9ac_percentage	87	69
H3K4me2_width	68	70
H3K4me2_height	70	70
H3K9ac_height	88	70
H3K4me2_width	68	71
H3K4me1_width	71	71
Broad_H3K4me1_percentage	72	71
H3K27ac_width	77	71
Broad_H3K27ac_percentage	78	71
H3K9ac_width	86	71
Broad_H3K9ac_percentage	87	71
Broad_H3K4me2_percentage	69	72
H3K4me1_width	71	72
Broad_H3K4me1_percentage	72	72
Broad_H3K27ac_percentage	78	72
Broad_H3K9ac_percentage	87	72
H3K4me1_height	73	73
H3K36me3_width	74	74
Broad_H3K36me3_percentage	75	74
H3K36me3_height	76	74
H3K36me3_width	74	75
Broad_H3K36me3_percentage	75	75
H3K36me3_height	76	75
H3K36me3_width	74	76

Broad_H3K36me3_percentage	75	76
H3K36me3_height	76	76
H3K4me1_width	71	77
H3K27ac_width	77	77
Broad_H3K27ac_percentage	78	77
H3K9ac_width	86	77
Broad_H3K4me2_percentage	69	78
H3K4me1_width	71	78
Broad_H3K4me1_percentage	72	78
H3K27ac_width	77	78
Broad_H3K27ac_percentage	78	78
Broad_H3K9ac_percentage	87	78
H3K27ac_height	79	79
H3K27me3_width	80	80
Broad_H3K27me3_percentage	81	80
H3K27me3_height	82	80
H3K27me3_width	80	81
Broad_H3K27me3_percentage	81	81
H3K27me3_height	82	81
H3K27me3_width	80	82
Broad_H3K27me3_percentage	81	82
H3K27me3_height	82	82
H3K9me3_width	83	83
Broad_H3K9me3_percentage	84	83
H3K9me3_width	83	84
Broad_H3K9me3_percentage	84	84
H3K9me3_height	85	85
Length_H3K4me3	65	86
H3K4me2_width	68	86
H3K4me1_width	71	86
H3K27ac_width	77	86
H3K9ac_width	86	86
Broad_H3K9ac_percentage	87	86
Broad_H3K4me3_percentage	66	87
Broad_H3K4me2_percentage	69	87
H3K4me1_width	71	87
Broad_H3K4me1_percentage	72	87
Broad_H3K27ac_percentage	78	87
H3K9ac_width	86	87
Broad_H3K9ac_percentage	87	87
H3K4me3_height	67	88
H3K4me2_height	70	88
H3K9ac_height	88	88
H3K9me2_width	89	89
Broad_H3K9me2_percentage	90	90
H3K9me2_height	91	91
H3K79me2_width	92	92
Broad_H3K79me2_percentage	93	92
H3K79me2_height	94	92
Broad_H4K20me1_percentage	96	92
H3K79me2_width	92	93
Broad_H3K79me2_percentage	93	93
H3K79me2_height	94	93
Broad_H4K20me1_percentage	96	93

```

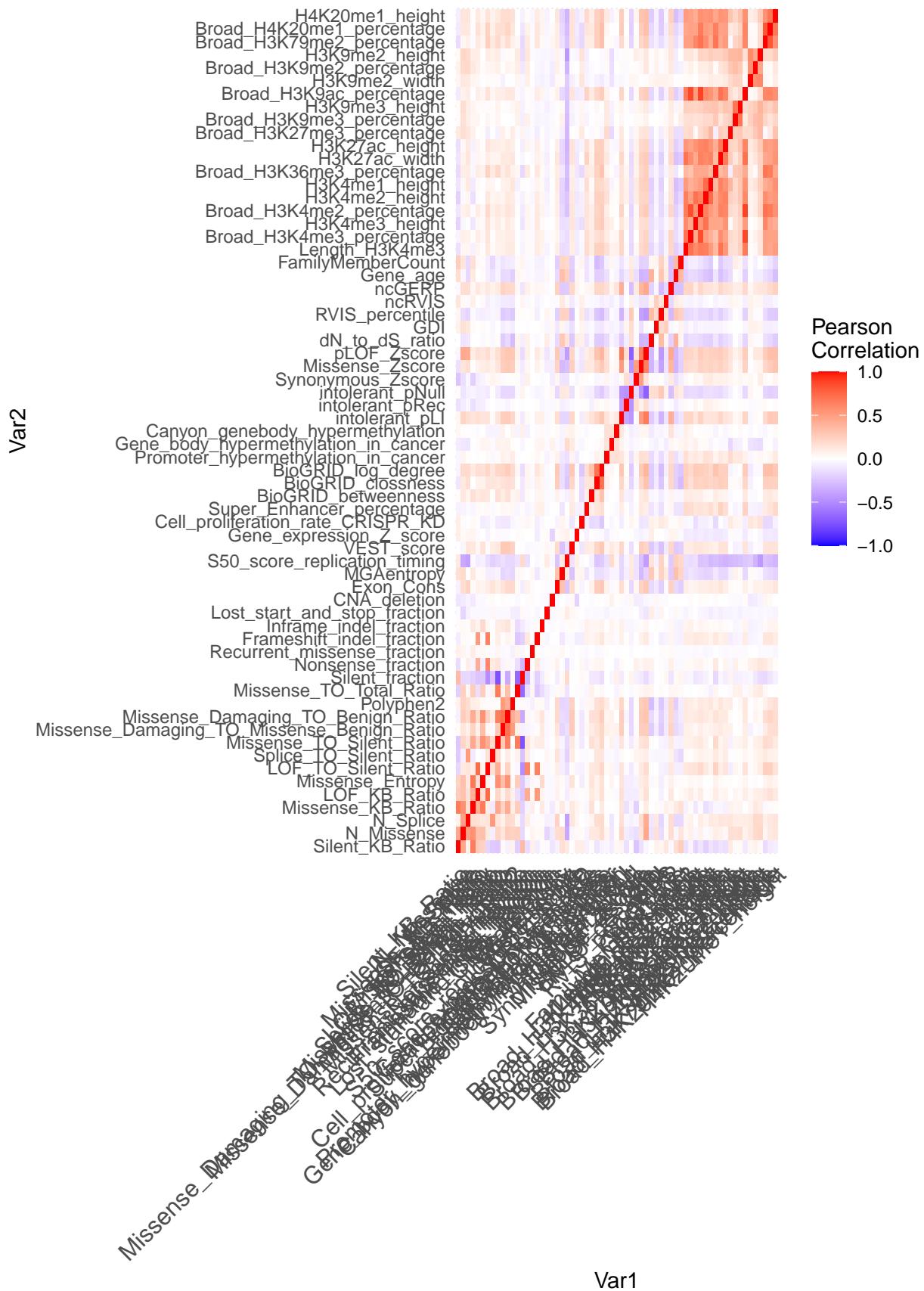
H3K79me2_width                                92  94
Broad_H3K79me2_percentage                     93  94
H3K79me2_height                               94  94
H4K20me1_width                                95  95
Broad_H4K20me1_percentage                     96  95
H3K79me2_width                                92  96
Broad_H3K79me2_percentage                     93  96
H4K20me1_width                                95  96
Broad_H4K20me1_percentage                     96  96
H4K20me1_height                               97  97

# Eliminate all but one of a set of variables highly correlated with one another
vars <- vars[, -c(1, 4, 32, 13, 18, 21, 29, 14, 20, 15, 30,
                 15, 24, 31, 38, 34, 41, 48, 50, 68, 86, 88,
                 71, 72, 78, 74, 76, 80, 82, 83, 92, 94, 95)]
cor_mtx = round(cor(vars[, names(vars) != "class"]), 2)
library(reshape2)
#reshape it
melted_cor_mtx <- melt(cor_mtx)

#draw the heatmap
cor_heatmap = ggplot(data = melted_cor_mtx, aes(x=Var1, y=Var2, fill=value)) + geom_tile()
cor_heatmap = cor_heatmap +
scale_fill_gradient2(low = "blue", high = "red", mid = "white", midpoint = 0, limit = c(-1,1), space =
theme_minimal() +
theme(axis.text.x = element_text(angle = 45, vjust = 1, size = 12, hjust = 1))

cor_heatmap

```



```
which(abs(cor_mtx) > 0.6, arr.ind = TRUE)
```

	row	col
Silent_KB_Ratio	1	1
Missense_KB_Ratio	4	1
N_Missense	2	2
N_Splice	3	3
Silent_KB_Ratio	1	4
Missense_KB_Ratio	4	4
Missense_Entropy	6	4
LOF_KB_Ratio	5	5
LOF_TO_Silent_Ratio	7	5
Missense_KB_Ratio	4	6
Missense_Entropy	6	6
LOF_KB_Ratio	5	7
LOF_TO_Silent_Ratio	7	7
Nonsense_fraction	15	7
Frameshift_indel_fraction	17	7
Splice_TO_Silent_Ratio	8	8
Missense_TO_Silent_Ratio	9	9
Missense_Damaging_TO_Benign_Ratio	11	9
Missense_TO_Total_Ratio	13	9
Silent_fraction	14	9
Missense_Damaging_TO_Missense_Benign_Ratio	10	10
Missense_Damaging_TO_Benign_Ratio	11	10
Missense_TO_Silent_Ratio	9	11
Missense_Damaging_TO_Missense_Benign_Ratio	10	11
Missense_Damaging_TO_Benign_Ratio	11	11
Polyphen2	12	12
Missense_TO_Silent_Ratio	9	13
Missense_TO_Total_Ratio	13	13
Silent_fraction	14	13
Missense_TO_Silent_Ratio	9	14
Missense_TO_Total_Ratio	13	14
Silent_fraction	14	14
LOF_TO_Silent_Ratio	7	15
Nonsense_fraction	15	15
Recurrent_missense_fraction	16	16
LOF_TO_Silent_Ratio	7	17
Frameshift_indel_fraction	17	17
Inframe_indel_fraction	18	18
Lost_start_and_stop_fraction	19	19
CNA_deletion	20	20
Exon_Cons	21	21
MGAentropy	22	22
S50_score_replication_timing	23	23
VEST_score	24	24
Gene_expression_Z_score	25	25
Cell_proliferation_rate_CRISPR_KD	26	26
Super_Enhancer_percentage	27	27
BioGRID_betweenness	28	28
BioGRID_clossness	29	29
BioGRID_log_degree	30	29
BioGRID_clossness	29	30

BioGRID_log_degree	30	30
Promoter_hypermethylation_in_cancer	31	31
Gene_body_hypermethylation_in_cancer	32	32
Canyon_genebody_hypermethylation	33	33
intolerant_pLI	34	34
pLOF_Zscore	39	34
intolerant_pRec	35	35
intolerant_pNull	36	36
pLOF_Zscore	39	36
Synonymous_Zscore	37	37
Missense_Zscore	38	38
pLOF_Zscore	39	38
intolerant_pLI	34	39
intolerant_pNull	36	39
Missense_Zscore	38	39
pLOF_Zscore	39	39
dN_to_dS_ratio	40	40
GDI	41	41
RVIS_percentile	42	42
ncRVIS	43	43
ncGERP	44	44
Gene_age	45	45
FamilyMemberCount	46	46
Length_H3K4me3	47	47
Broad_H3K4me3_percentage	48	47
Broad_H3K4me2_percentage	50	47
H3K4me2_height	51	47
H3K27ac_width	54	47
Broad_H3K9ac_percentage	59	47
Length_H3K4me3	47	48
Broad_H3K4me3_percentage	48	48
Broad_H3K4me2_percentage	50	48
Broad_H3K9ac_percentage	59	48
H3K4me3_height	49	49
H3K4me2_height	51	49
Broad_H3K79me2_percentage	63	49
Length_H3K4me3	47	50
Broad_H3K4me3_percentage	48	50
Broad_H3K4me2_percentage	50	50
H3K4me2_height	51	50
H3K27ac_width	54	50
H3K27ac_height	55	50
Broad_H3K9ac_percentage	59	50
Broad_H3K79me2_percentage	63	50
Broad_H4K20me1_percentage	64	50
Length_H3K4me3	47	51
H3K4me3_height	49	51
Broad_H3K4me2_percentage	50	51
H3K4me2_height	51	51
H3K4me1_height	52	51
H3K27ac_height	55	51
H3K4me2_height	51	52
H3K4me1_height	52	52
H3K27ac_width	54	52

Broad_H3K36me3_percentage	53	53
Broad_H3K79me2_percentage	63	53
Broad_H4K20me1_percentage	64	53
Length_H3K4me3	47	54
Broad_H3K4me2_percentage	50	54
H3K4me1_height	52	54
H3K27ac_width	54	54
H3K27ac_height	55	54
Broad_H3K9ac_percentage	59	54
Broad_H3K4me2_percentage	50	55
H3K4me2_height	51	55
H3K27ac_width	54	55
H3K27ac_height	55	55
Broad_H3K9ac_percentage	59	55
Broad_H3K27me3_percentage	56	56
Broad_H3K9me3_percentage	57	57
H3K9me3_height	58	57
Broad_H3K9me3_percentage	57	58
H3K9me3_height	58	58
Length_H3K4me3	47	59
Broad_H3K4me3_percentage	48	59
Broad_H3K4me2_percentage	50	59
H3K27ac_width	54	59
H3K27ac_height	55	59
Broad_H3K9ac_percentage	59	59
Broad_H3K79me2_percentage	63	59
Broad_H4K20me1_percentage	64	59
H3K9me2_width	60	60
Broad_H3K9me2_percentage	61	61
H3K9me2_height	62	62
H3K4me3_height	49	63
Broad_H3K4me2_percentage	50	63
Broad_H3K36me3_percentage	53	63
Broad_H3K9ac_percentage	59	63
Broad_H3K79me2_percentage	63	63
Broad_H4K20me1_percentage	64	63
Broad_H3K4me2_percentage	50	64
Broad_H3K36me3_percentage	53	64
Broad_H3K9ac_percentage	59	64
Broad_H3K79me2_percentage	63	64
Broad_H4K20me1_percentage	64	64
H4K20me1_height	65	64
Broad_H4K20me1_percentage	64	65
H4K20me1_height	65	65

```

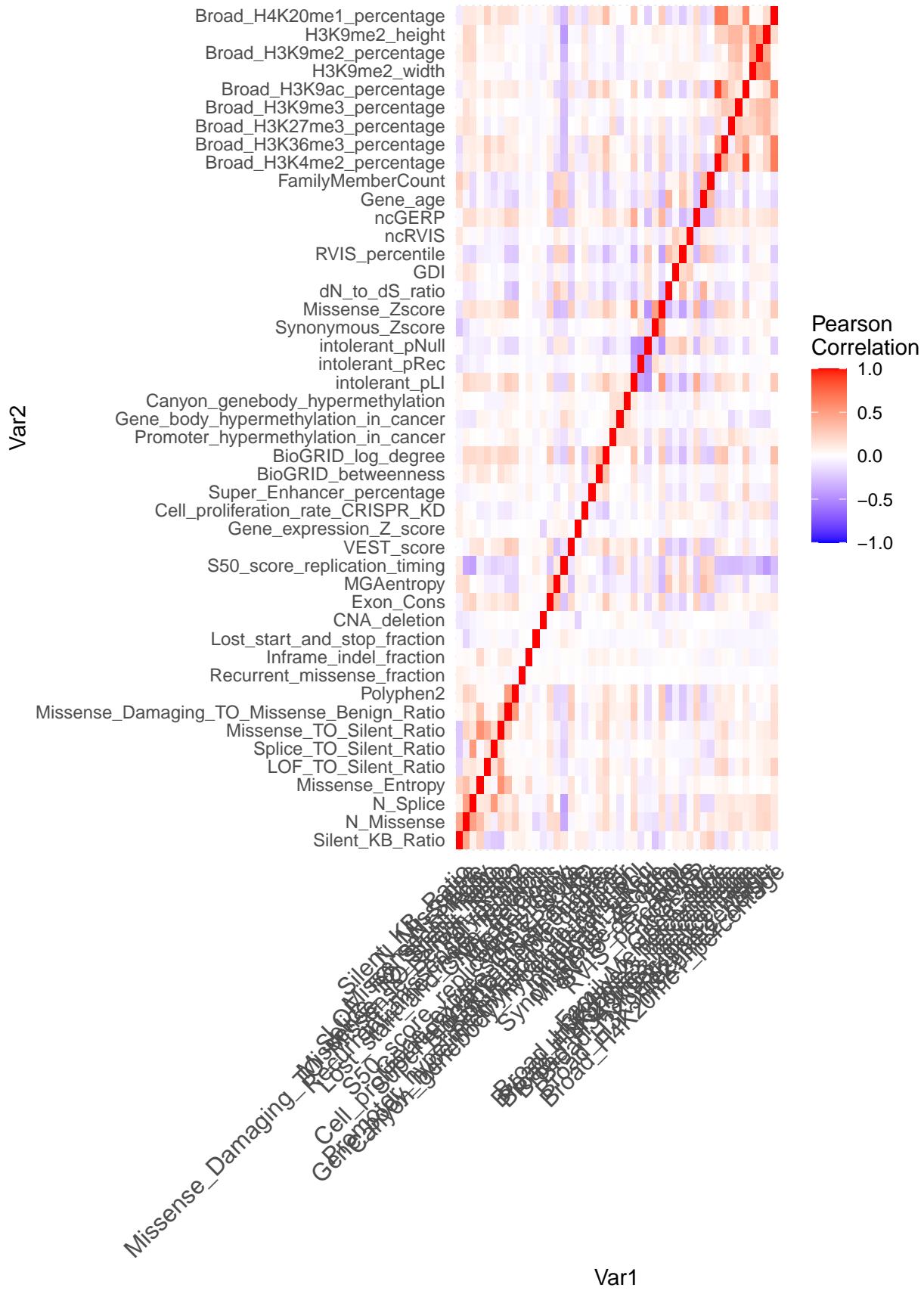
# Eliminate all but one of a set of variables highly correlated with one another
vars <- vars[, -c(4, 5, 15, 17, 11, 13, 14, 29, 39, 47,
               48, 51, 49, 54, 55, 52, 58, 63, 65)]
cor_mtx = round(cor(vars[, names(vars) != "class"]), 2)
library(reshape2)
#reshape it
melted_cor_mtx <- melt(cor_mtx)

#draw the heatmap

```

```
cor_heatmap = ggplot(data = melted_cor_mtx, aes(x=Var1, y=Var2, fill=value)) + geom_tile()
cor_heatmap = cor_heatmap +
  scale_fill_gradient2(low = "blue", high = "red", mid = "white", midpoint = 0, limit = c(-1,1), space =
    theme_minimal() +
    theme(axis.text.x = element_text(angle = 45, vjust = 1, size = 12, hjust = 1))

cor_heatmap
```



```

set.seed(12)
mn <- nnet::multinom(class ~ ., data = vars, model = TRUE)

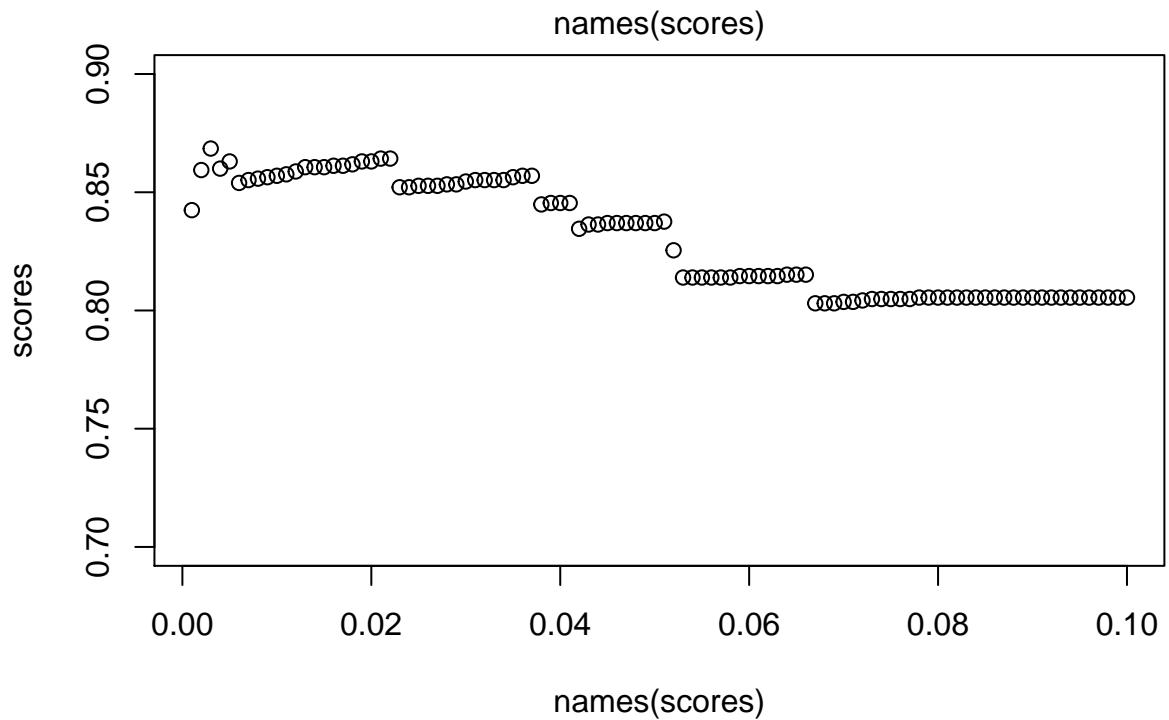
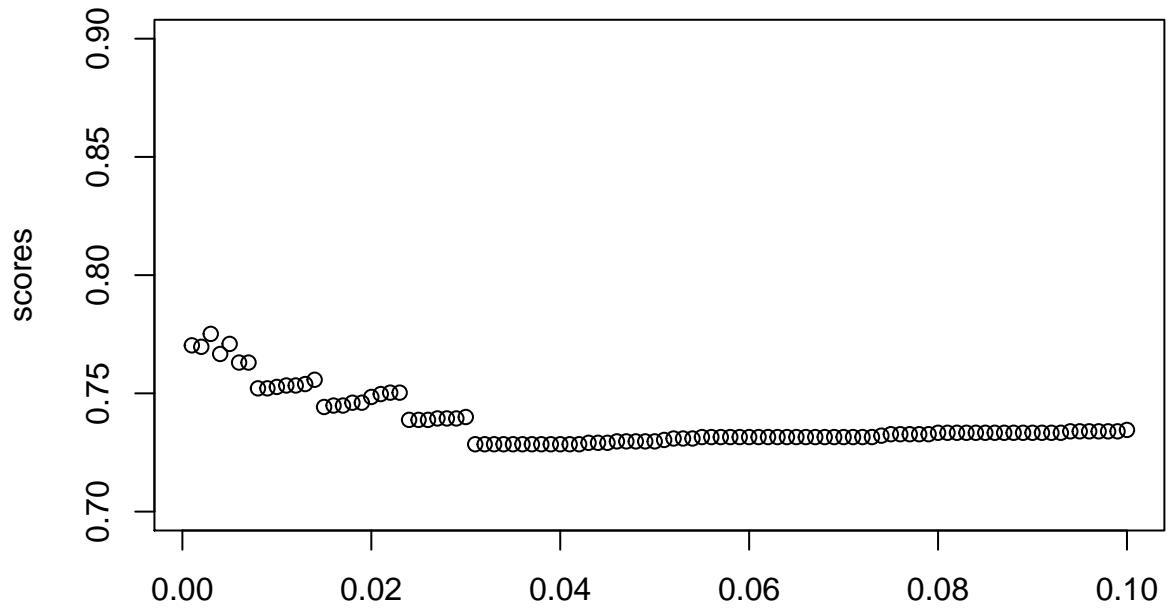
# weights: 144 (94 variable)
initial value 3326.598010
iter 10 value 2203.553663
iter 20 value 1768.520559
iter 30 value 1279.557302
iter 40 value 560.047897
iter 50 value 369.893402
iter 60 value 362.666406
iter 70 value 360.813749
iter 80 value 359.828020
iter 90 value 359.519184
iter 100 value 359.410338
final value 359.410338
stopped after 100 iterations

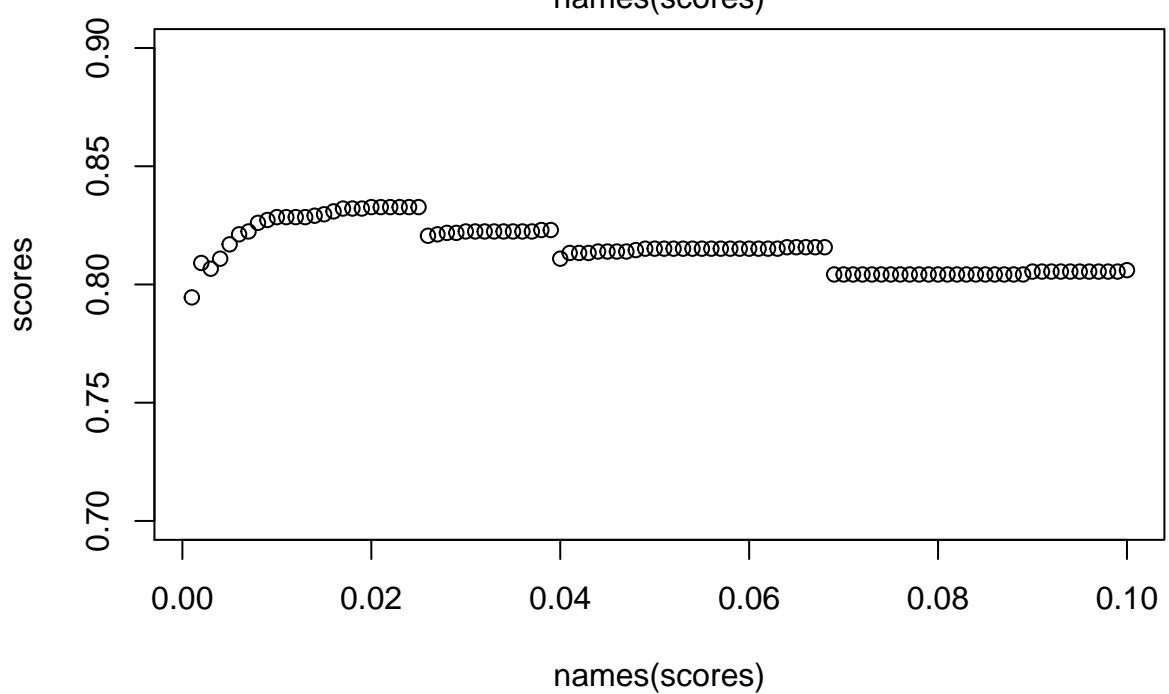
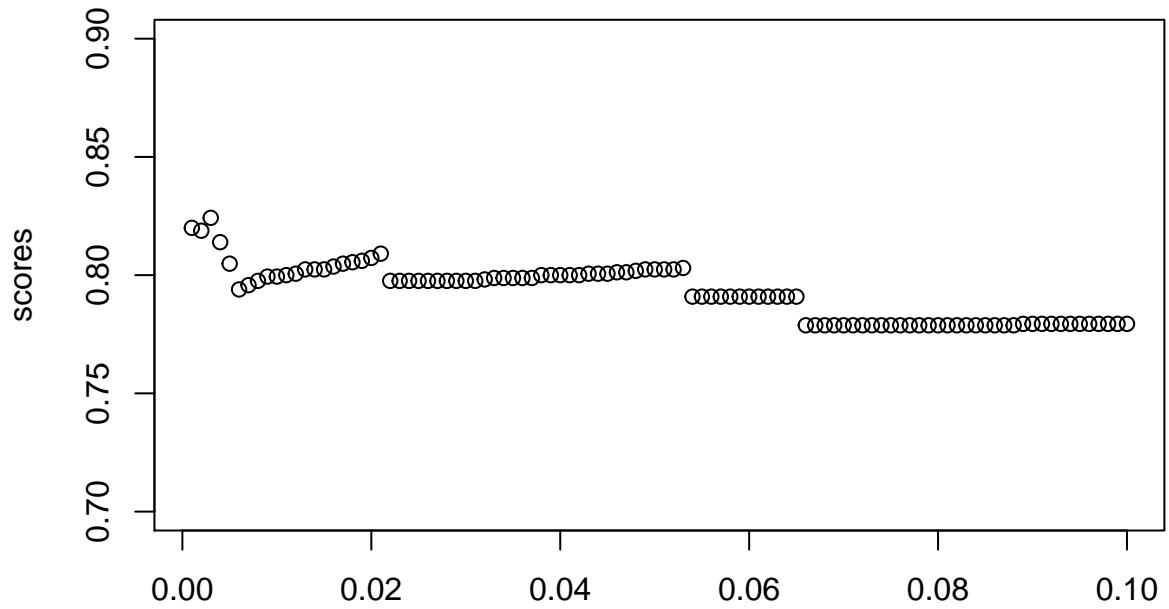
tidymn <- broom::tidy(mn) %>% arrange(p.value)
tidymn <- tidymn %>% filter(p.value < 0.05 / nrow(tidymn))
terms <- unique(tidymn$term)[-1]

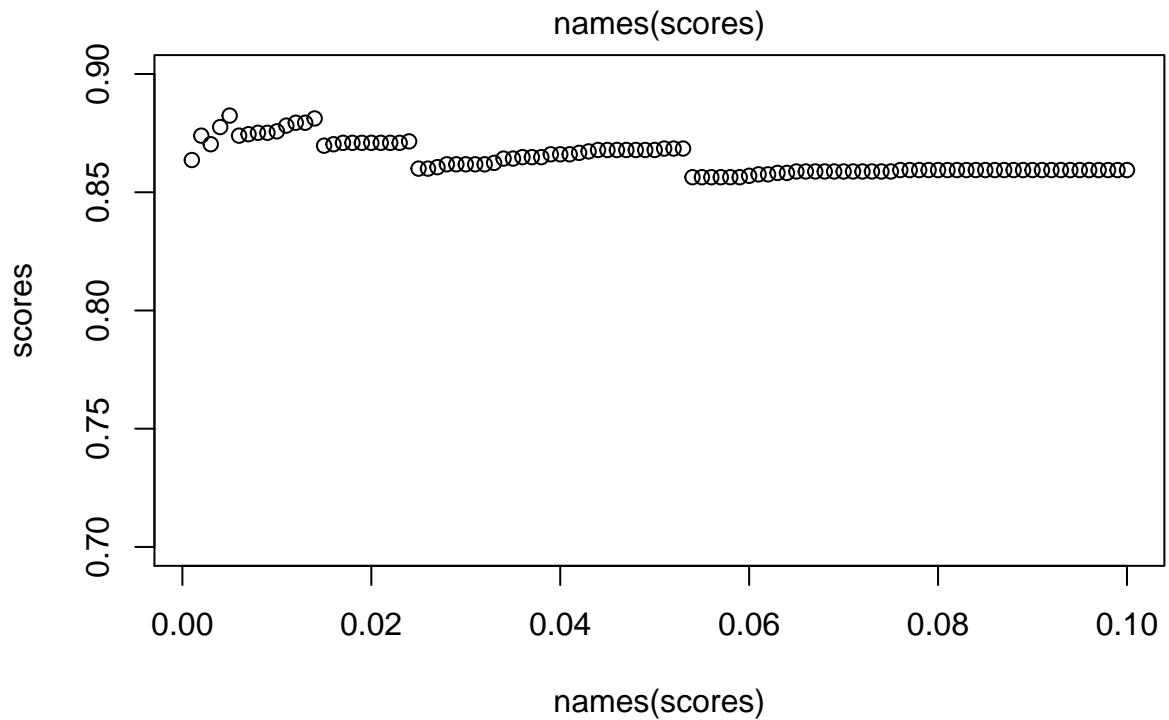
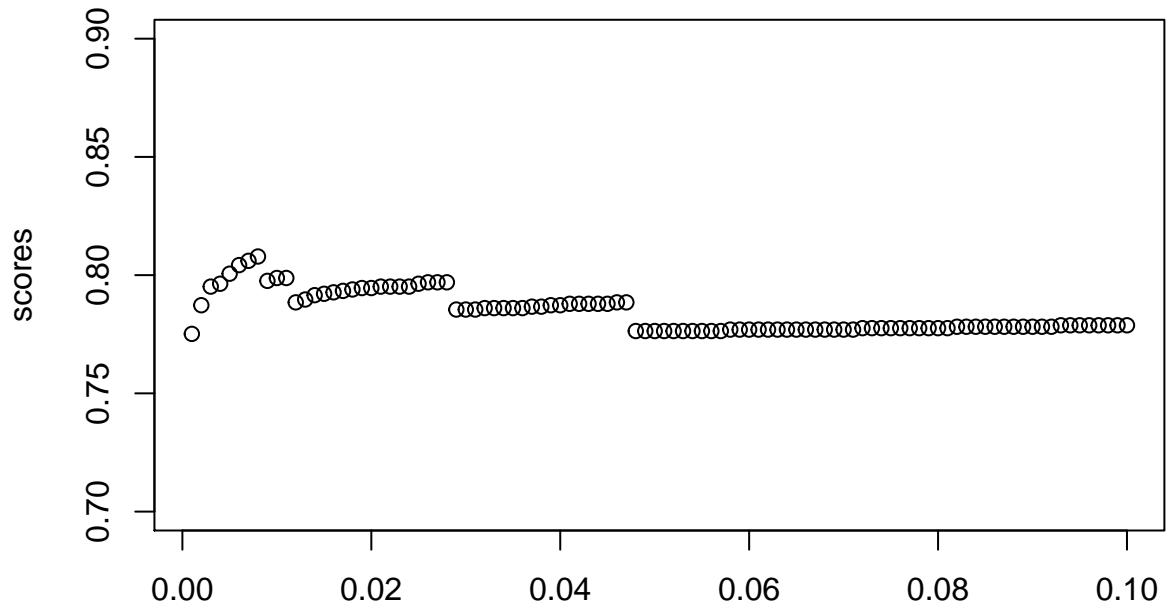
vars <- training %>% select(all_of(terms), class)
set.seed(91232)
thresh_list <- list()
length(thresh_list) <- 10
j <- 1
for (rand in ceiling(runif(10, min = 1, max = 10000000))) {
  set.seed(rand)
  vars_test <- createDataPartition(vars$class, p = 0.8,
                                    list = FALSE)
  vars_train <- vars[vars_test, ]
  vars_test <- vars[-vars_test, ]

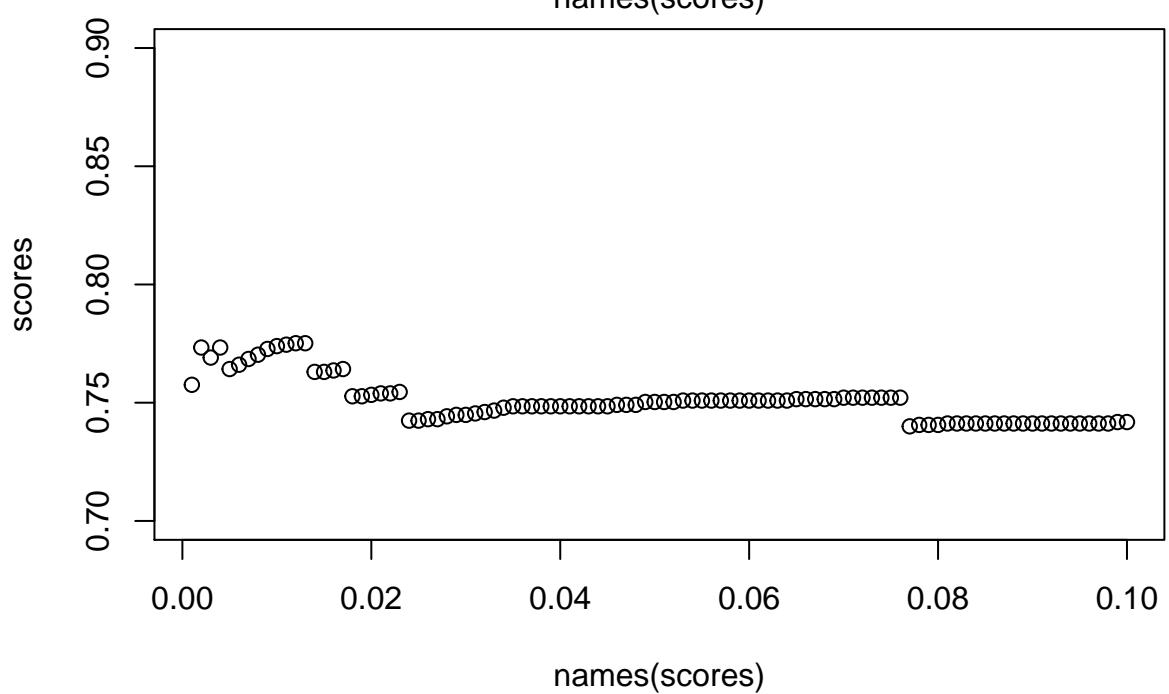
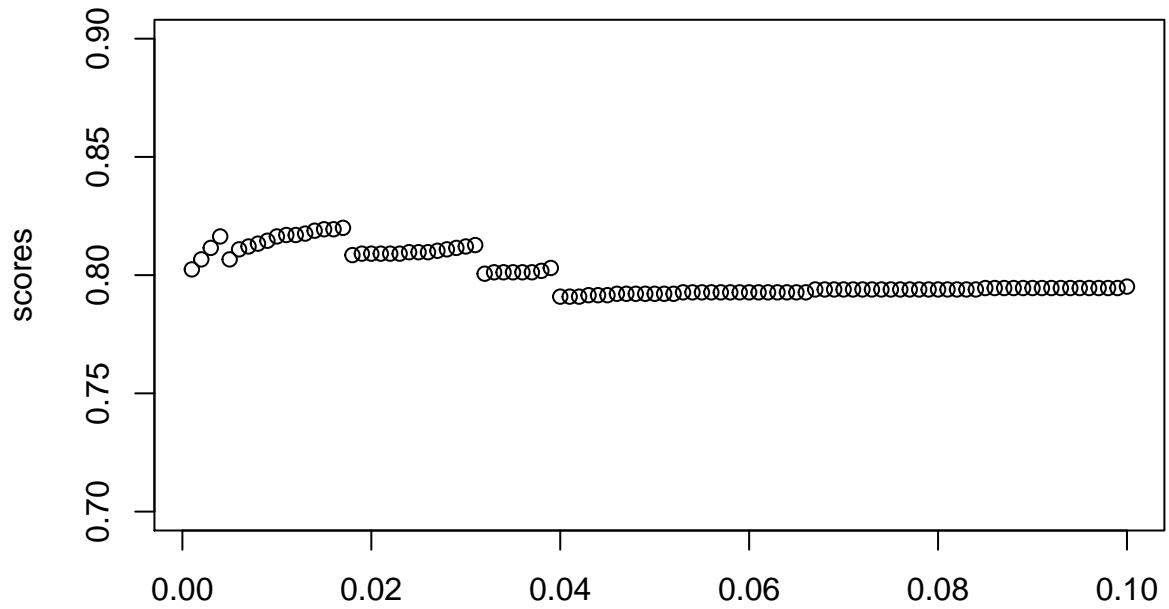
  train_cont <- trainControl(method = "cv", number = 5, classProbs = TRUE, savePredictions = TRUE)
  lda_ft <- train(class ~ ., data = vars_train, method = "lda", preProc = c("center", "scale"),
                  trControl = train_cont)
  preds <- predict(lda_ft, newdata = vars_test, type = "prob")
  scores <- numeric(100)
  for (i in seq(from = 0.001, to = 0.1, by = 0.001)) {
    lda_mod <- table("pred"=apply(preds, 1, classify, k = i), "obs" = vars_test$class)
    lda_mod
    scores[i*1000] <- score(lda_mod)
  }
  names(scores) <- seq(from = 0.001, to = 0.1, by = 0.001)
  plot(scores ~ names(scores), ylim = c(0.7, 0.9),)
  best_thresh <- names(scores)[scores == max(scores)]
  max(scores)
  thresh_list[[j]] <- best_thresh
  j <- j + 1
}

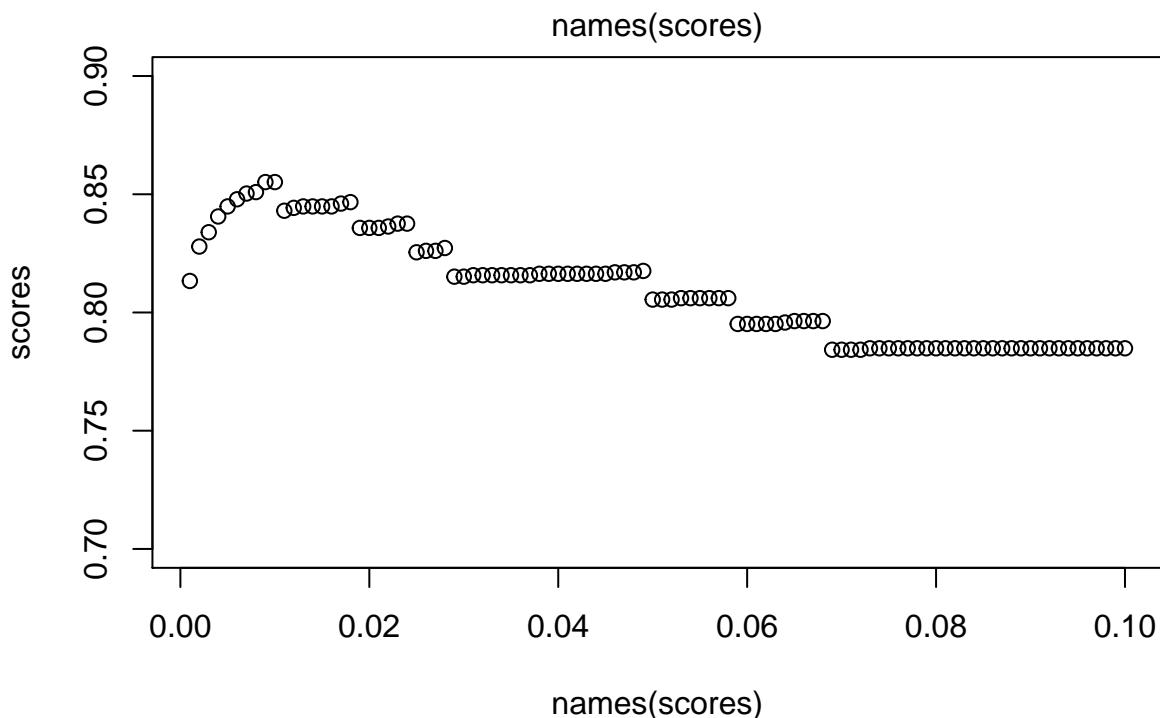
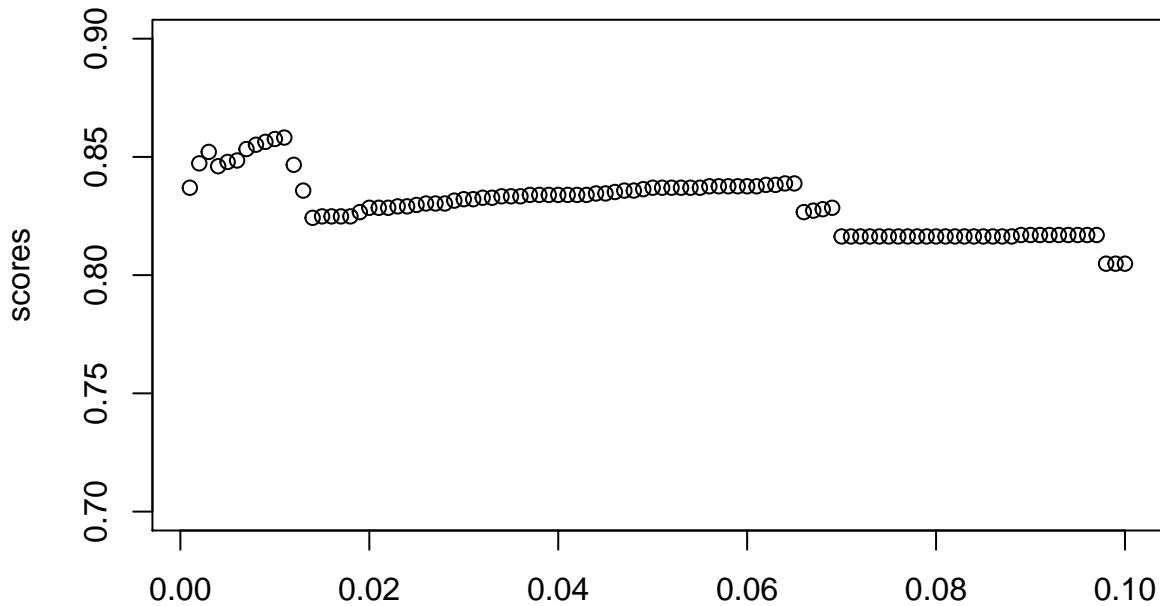
```











```
mean(as.numeric(unlist(thresh_list)))
```

```
[1] 0.01347059
```

```
median(as.numeric(unlist(thresh_list)))
```

```
[1] 0.012
```

```
set.seed(42)
vars_test <- createDataPartition(vars$class, p = 0.8,
                                list = FALSE)
vars_train <- vars[vars_test, ]
```

```

vars_test <- vars[-vars_test, ]
train_cont <- trainControl(method = "cv", number = 5, classProbs = TRUE, savePredictions = TRUE)
lda_ft <- train(class ~ ., data = vars_train, method = "lda", preProc = c("center", "scale"),
                 trControl = train_cont)
preds <- predict(lda_ft, newdata = vars_test, type = "prob")
lda_mod <- table("pred"=apply(preds, 1, classify, k = 0.01), "obs" = vars_test$class)
lda_mod

obs
pred NG OG TSG
  0 509   2   4
  1 16   22   4
  2 25   5   18

score(lda_mod)

[1] 0.7933333

tests <- read.csv("test.csv")
preds <- predict(lda_ft, newdata = tests, type = "prob")
preds <- apply(preds, 1, classify, k = 0.01)
names(preds) <- tests$id
csv_file <- data.frame(id = tests$id,
                        class = preds)
write.csv(csv_file, "modelpredictions10.csv", row.names = FALSE)
model_2_beta <- read.csv("modelpredictions2_beta.csv")
table("BEST MOD" = model_2_beta$class, csv_file$class)

BEST MOD      0      1      2
  0 1096    25    17
  1    10    65     5
  2    15     8   122

```