

Evaluate testing data (multi-class)

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Labels: 0: Basal 1: LumA 2: LumB 3: Her2

0. Load Data

```
library(tidyverse)
library(ggrepel)
library(caret)
library(pROC)
source("~/ml-pipeline/ML_performanceCheck/PerformanceUtils.R")

home <- "~/ml-pipeline/tests"
project_name <- "test_multiclass_1"
training_data <- "test_multiclass_tcga_brca.csv"
label_name <- "pam50_RNAseq"

## output path for analyzed data
outfile <- paste0(home, "/results/", project_name)
```

300 of samples were used

100 of full features

10 runs, each run contains 3 CVs.

Labels:

Var1	Freq
0	50
1	149
2	74
3	27

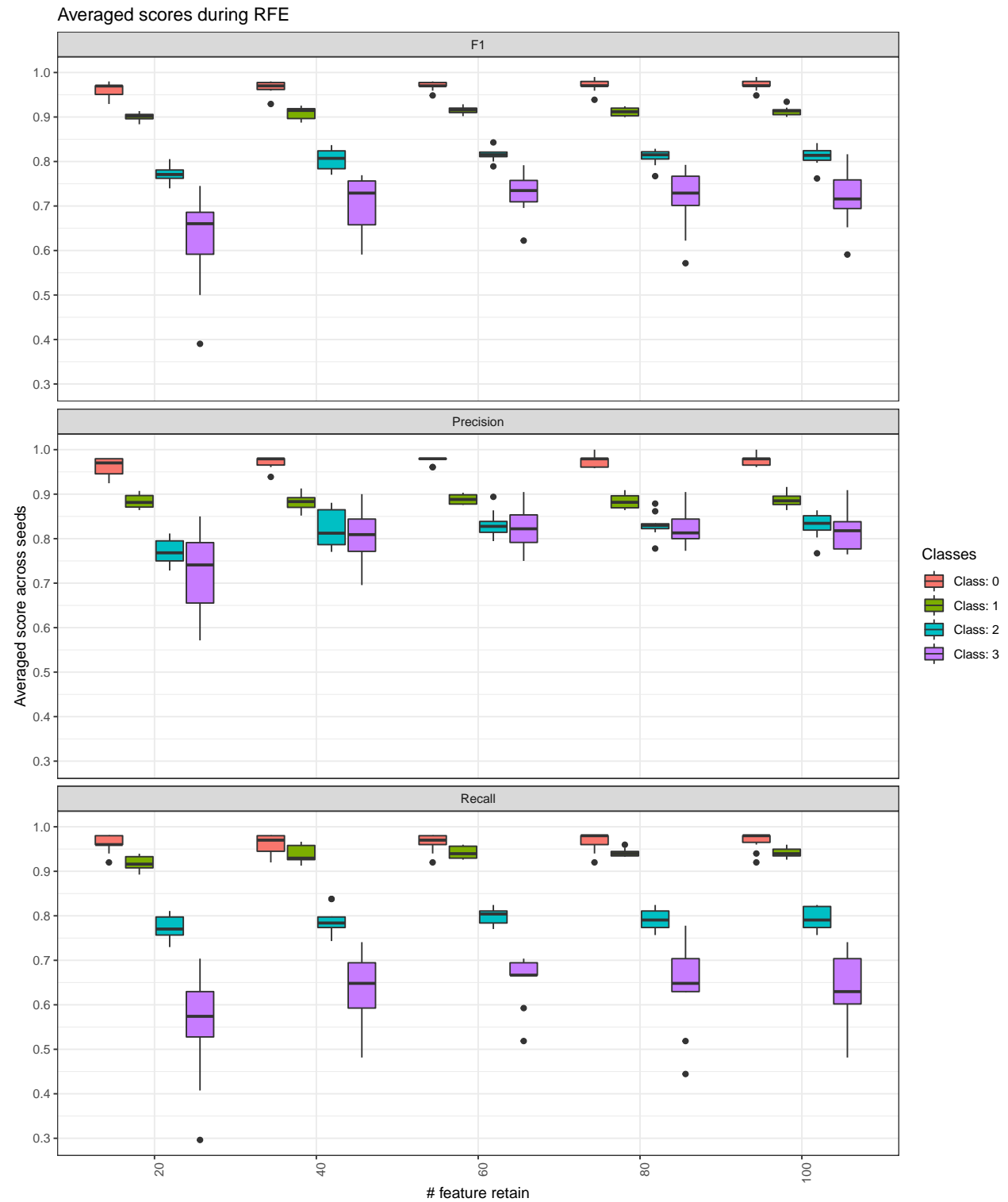
1. Scores

average = T: scores are based on pre-validation (combine predictions from all CVs per job and then calculate a single score per job).

average = F: report all the scores from each CV across entire jobs.

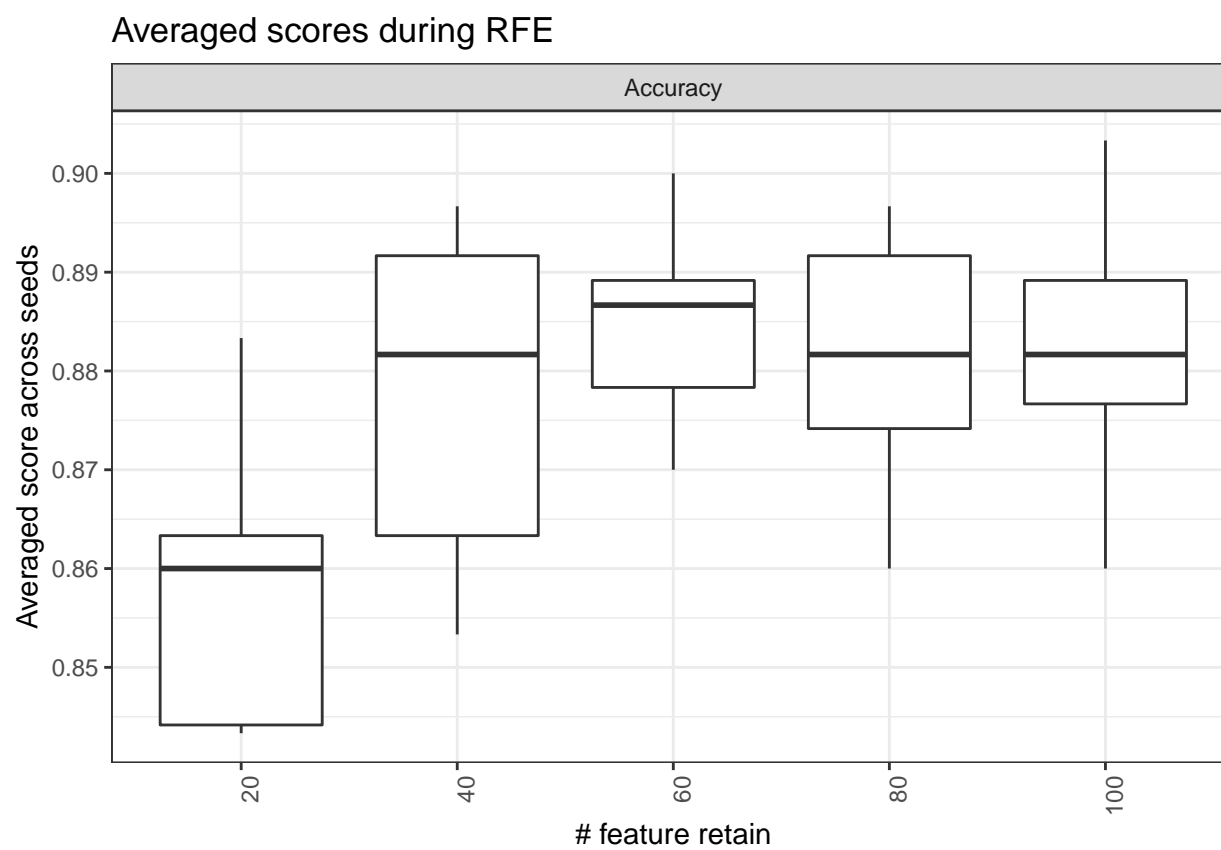
1. Scores

1.1 uncalibrated average



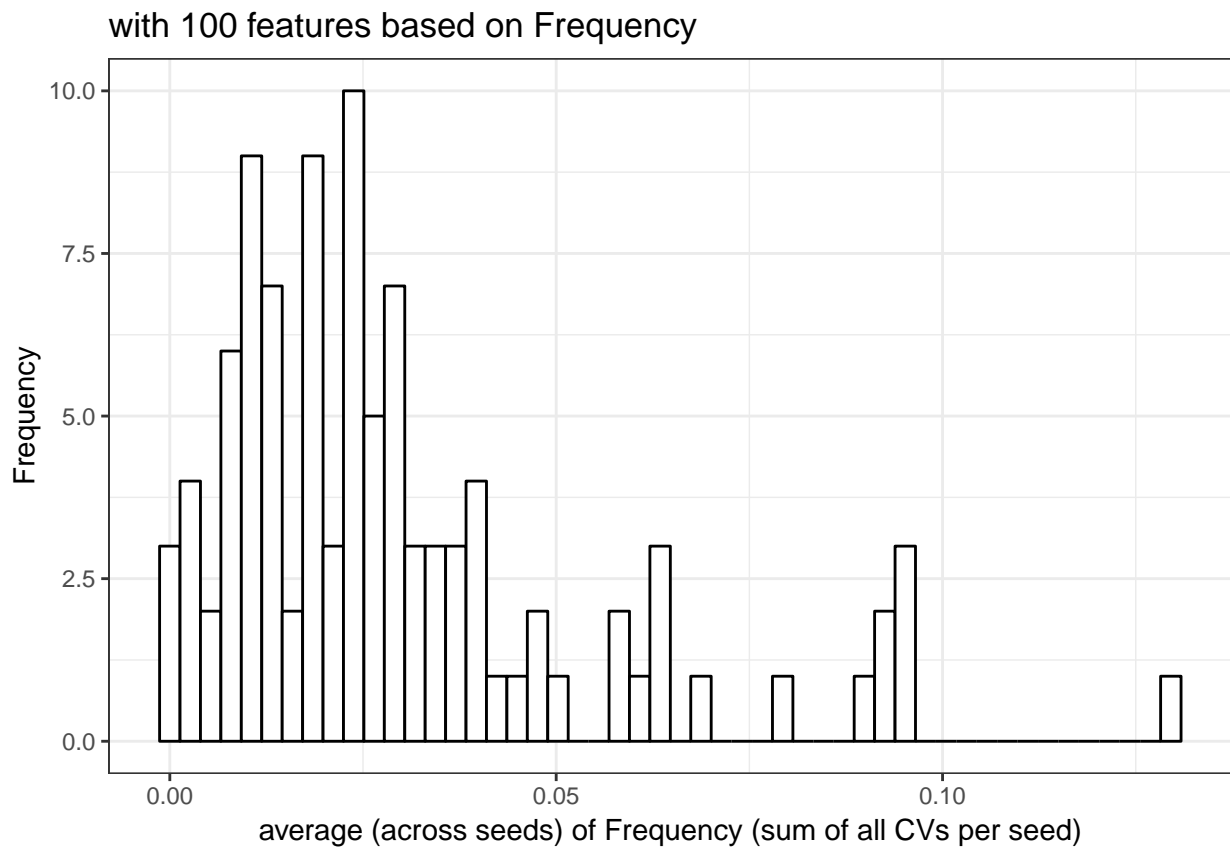
```
plt$overall +  
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
```

```
scale_y_continuous(breaks = seq(0, 1, 0.01))
```

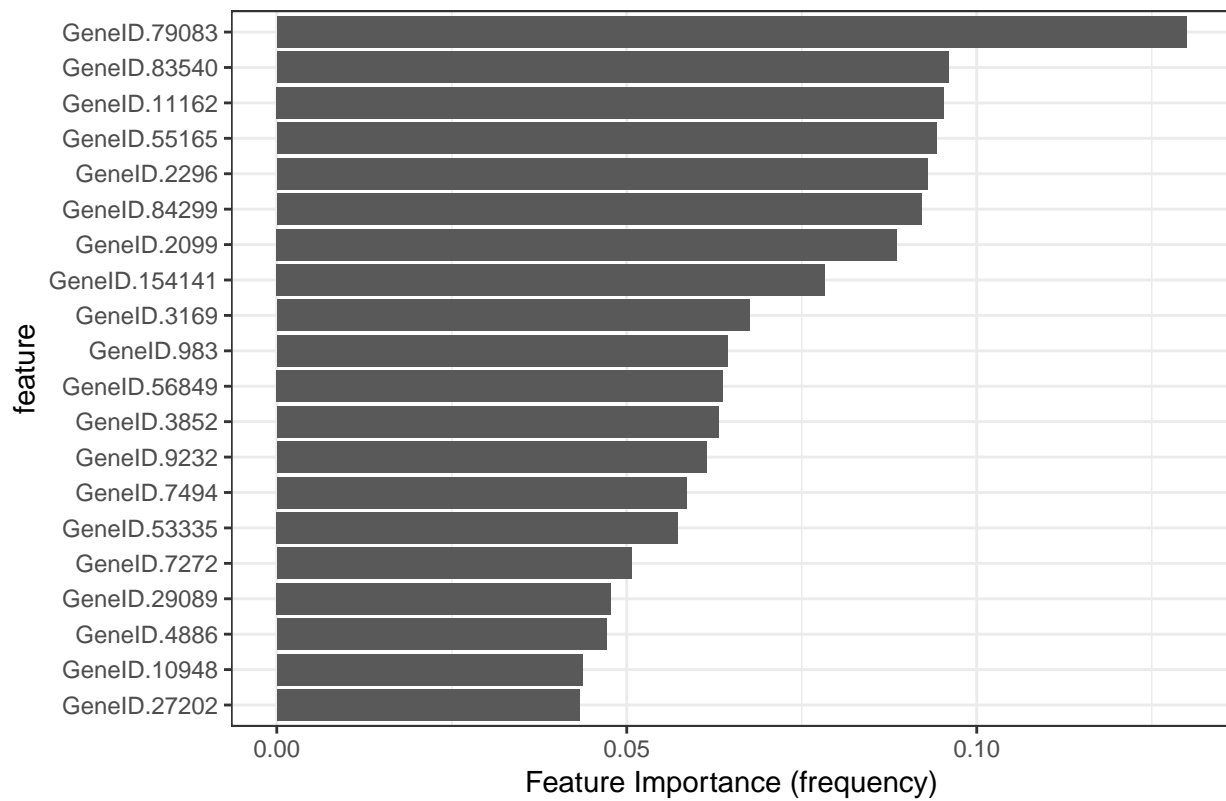


metrics	max_med	size
Accuracy	0.887	60
F1	0.859	60
Precision	0.881	60
Recall	0.839	60

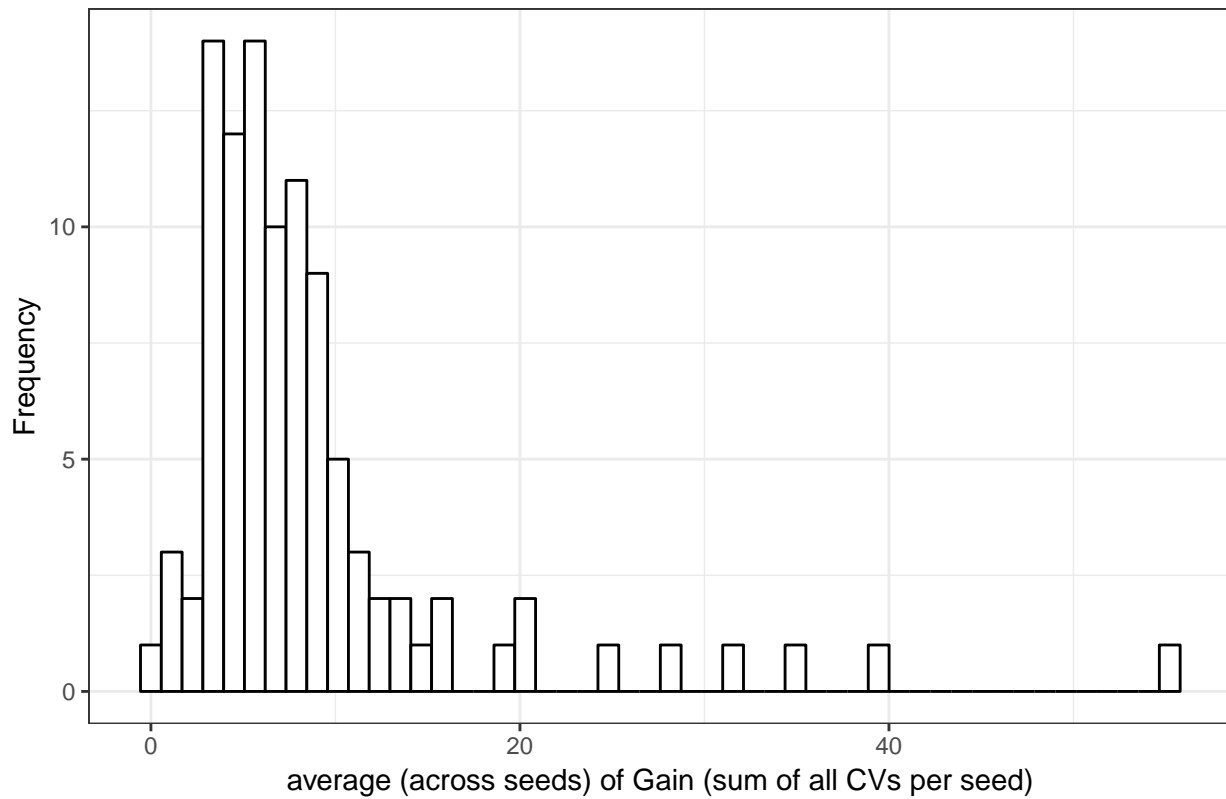
3. Important Features



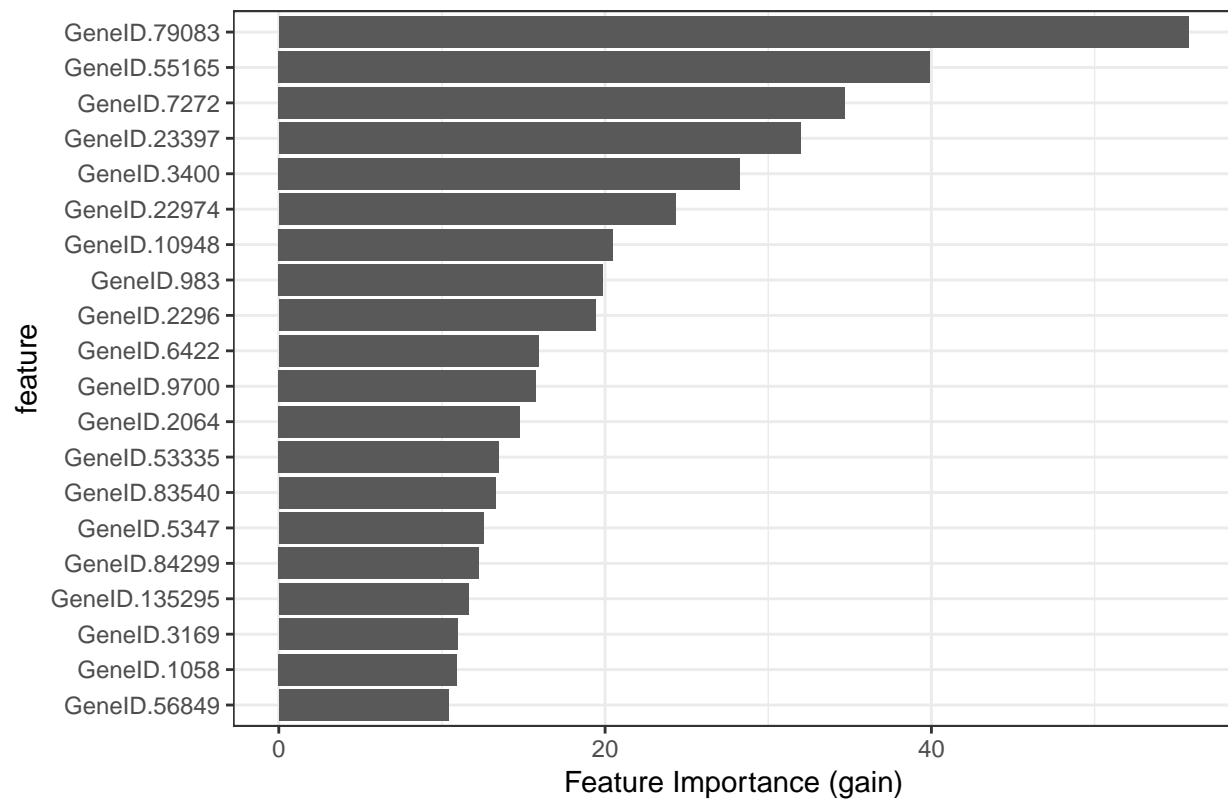
Top 20 features at 100 feature set based on Frequency



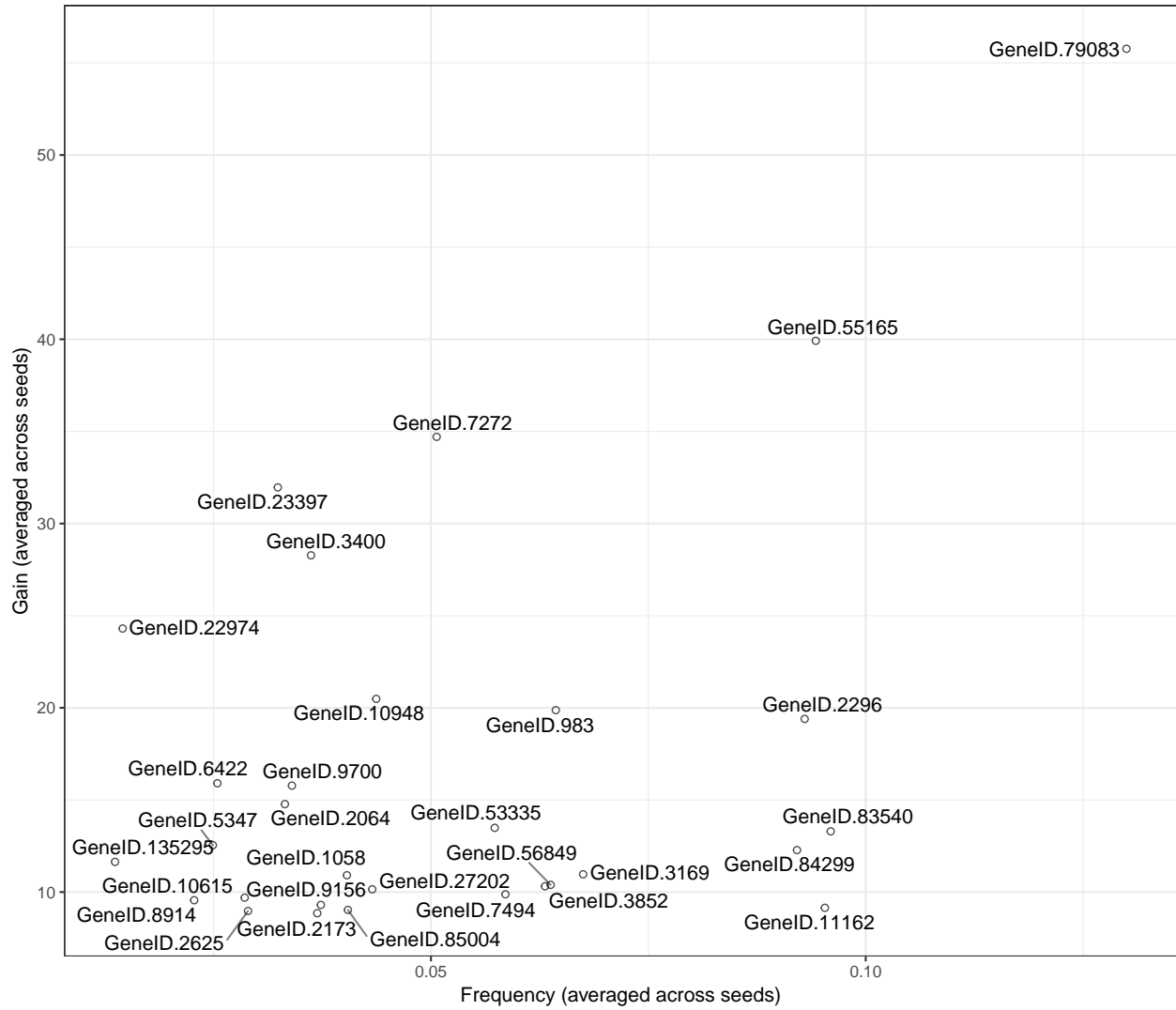
with 100 features based on Gain



Top 20 features at 100 feature set based on Gain



Top 30 features at 100 feature set



4. Hyper-parameters

