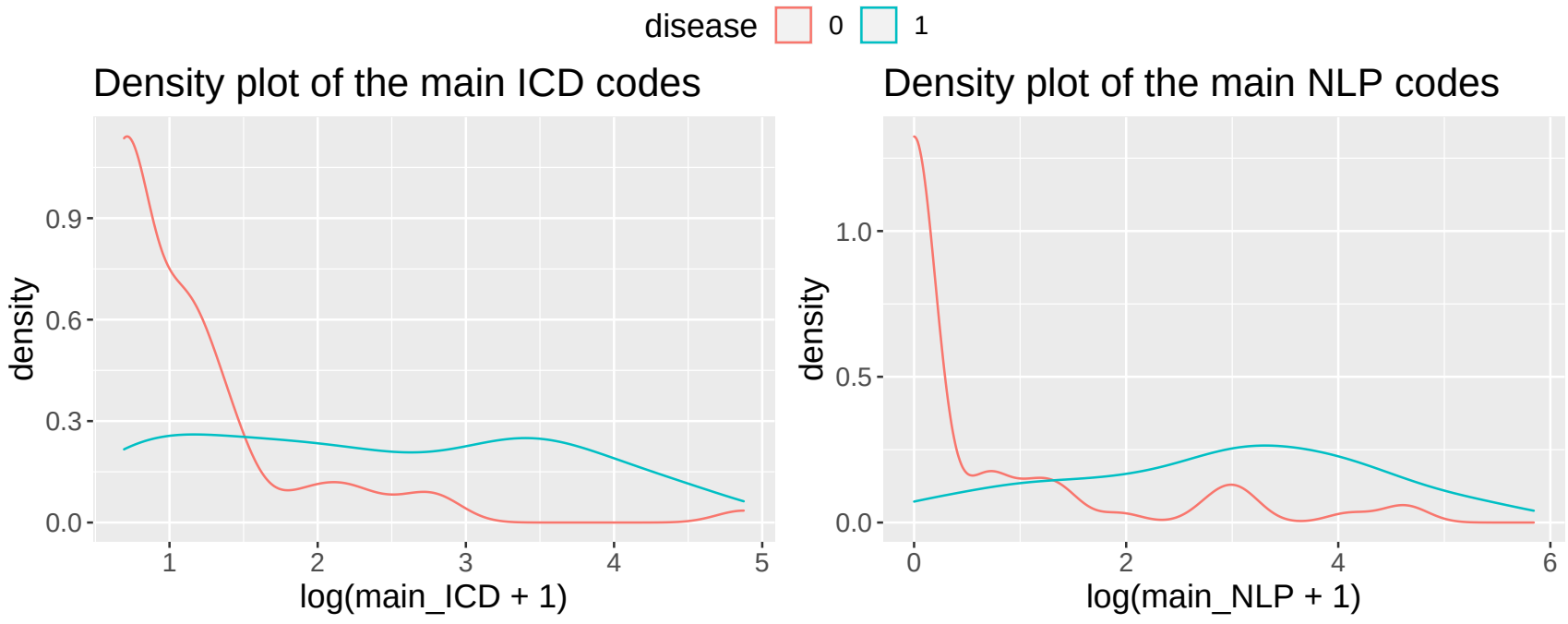
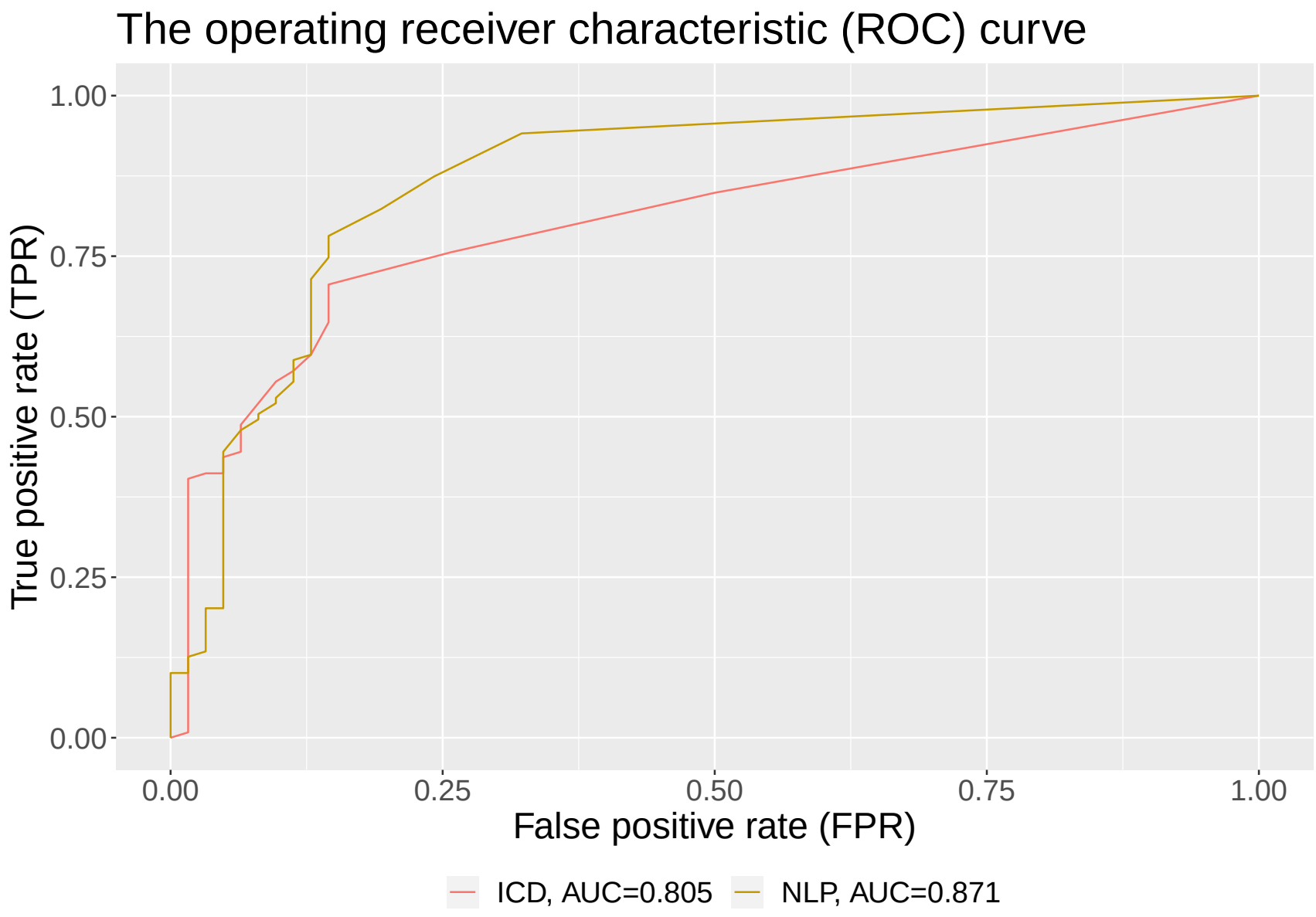
Module 3: Semi-supervised learning (PheCAP)

Surrogates for CAD



The more the disease-related codes and NLP mentions, the more **likely** the patient has the disease.

ROC Surrogates



Step 1: SAFE

```
surrogates <- list(
  PhecapSurrogate(
    variable_names = "main_ICD",
    lower_cutoff = 1, upper_cutoff = 10),
  PhecapSurrogate(
    variable_names = "main_NLP",
    lower_cutoff = 1, upper_cutoff = 10))

feature_selected <- phecap_run_feature_extraction(data, surrogates)
feature_selected
```

```
## Feature(s) selected by surrogate-assisted feature extraction (SAFE)
## [1] "main_ICD" "main_NLP" "NLP56"    "NLP93"    "NLP274"   "NLP306"
```

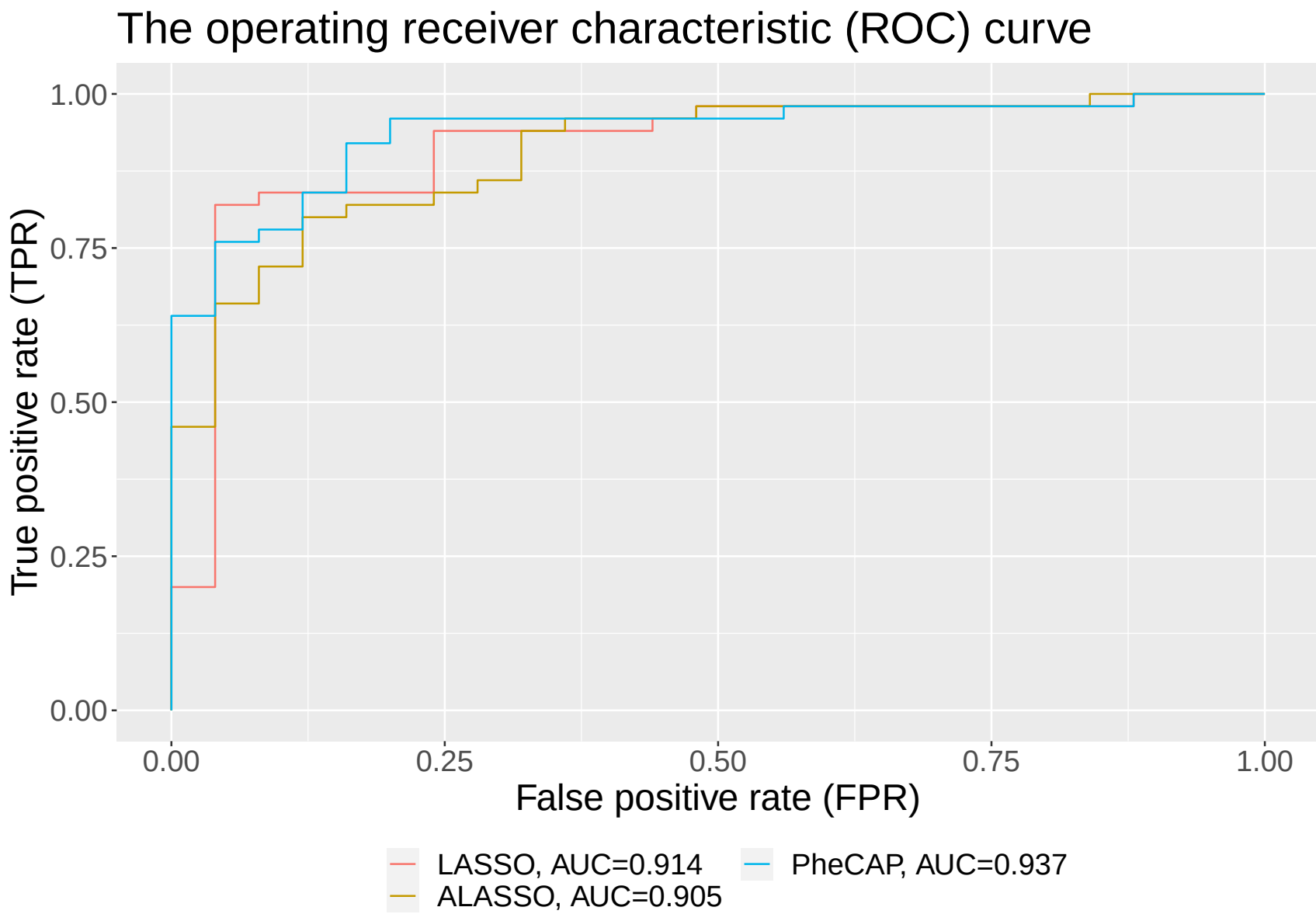
Step 2: Orthogonalization + supervised learning

```
phecap_lasso <- phecap_train_phenotyping_model(data, surrogates, feature_selected,
                                               method = "lasso_cv")
```

```
phecap_lasso
```

```
## Phenotyping model:
## $lasso_cv
##             (Intercept)                main_ICD                main_NLP healthcare_utilization
##               1.9258667                0.2157399                1.1666409               -0.9772753
##                   NLP56                    NLP93                   NLP274                   NLP306
##               0.0000000               -0.3242900                0.0000000                0.0000000
##
## AUC on training data: 0.93
## Average AUC on random splits: 0.889
```

Supervised learning (LASSO, ALASSO) vs. PheCAP



Supervised learning (LASSO, ALASSO) vs. PheCAP at FPR = 0.10

```
get_roc_parameter(0.1, roc_full_lasso)
```

```
##      cutoff  pos.rate FPR  TPR       PPV       NPV        F1
## 1 0.8573308 0.5933333 0.1 0.84 0.9438202 0.7377049 0.8888889
```

```
get_roc_parameter(0.1, roc_full_alasso)
```

```
##      cutoff  pos.rate FPR  TPR       PPV       NPV        F1
## 1 0.9228109 0.5133333 0.1 0.72 0.9350649 0.6164384 0.8135593
```

```
roc_full_phecap <- get_roc(y_true = test_y, y_score = y_hat_phecap) %>% data.frame()
get_roc_parameter(0.1, roc_full_phecap)
```

```
##      cutoff  pos.rate FPR  TPR      PPV       NPV       F1
## 1 0.8342308 0.5533333 0.1 0.78 0.939759 0.6716418 0.852459
```

Supervised learning vs. PheCAP for different training size

- Randomly sample training size $= 50, 70, 90$
- Use the remaining data as the test set
- Repeat 600 times

```
auc_phecap <- validate_phecap(dat = labeled_data,
                              orig_data = ehr_data,
                              surrogates = surrogates,
                              feature_selected = feature_selected,
                              nsim = 600,
                              n.train = c(50, 70, 90))
```

Supervised learning vs. PheCAP for different training size