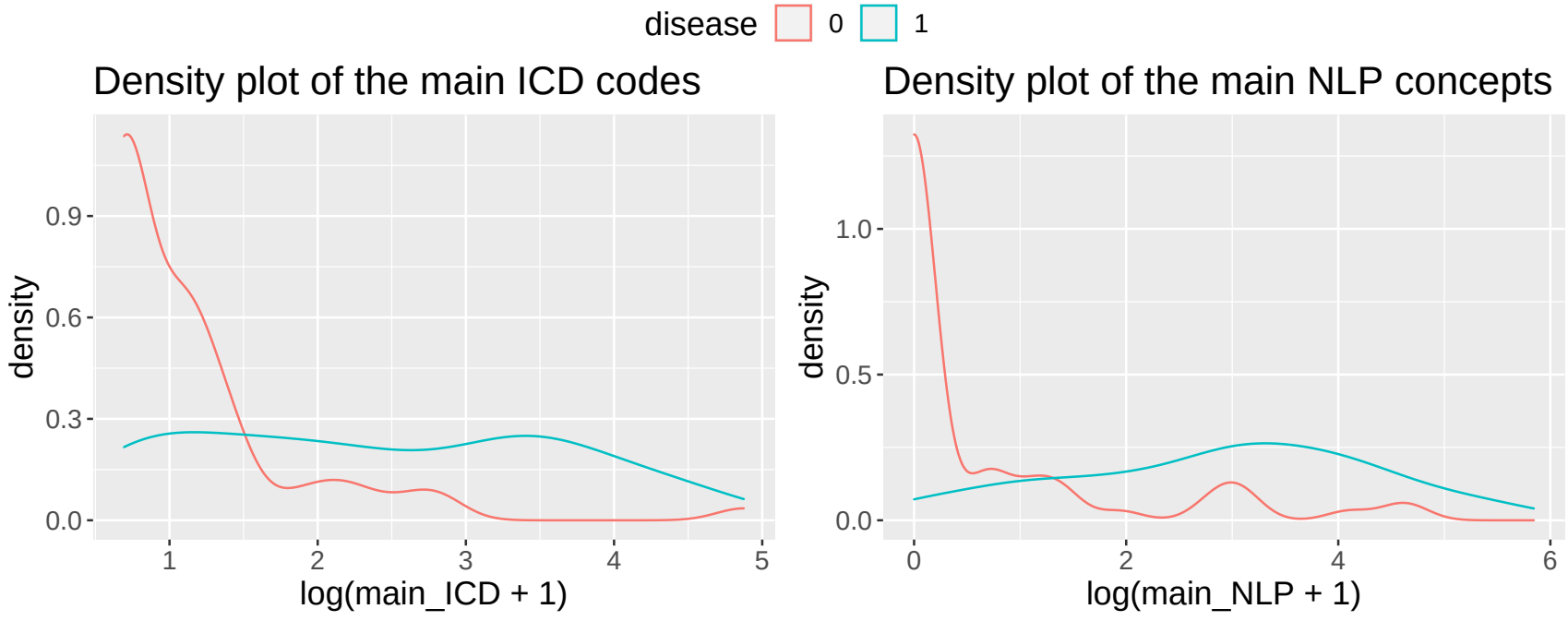
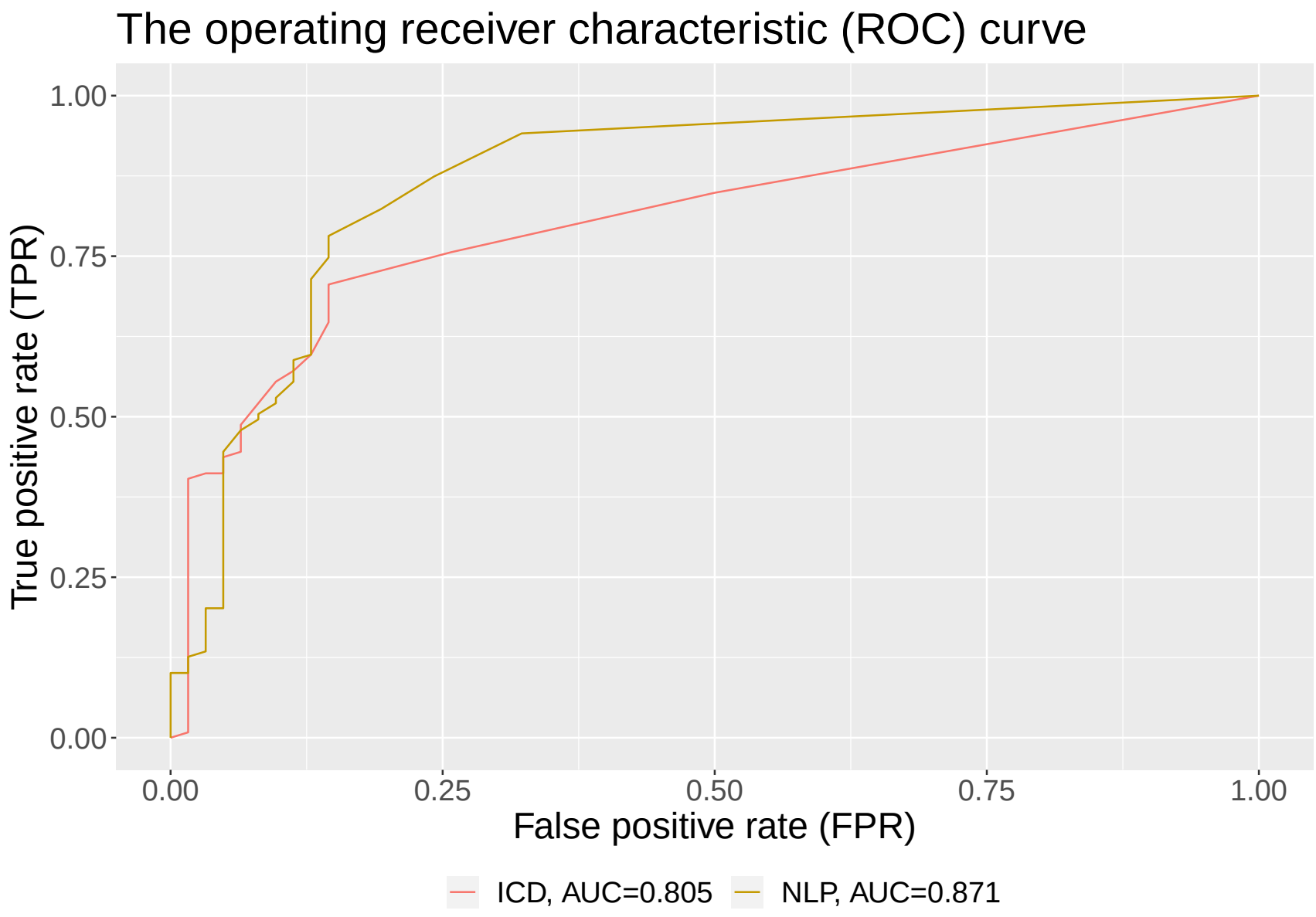
Module 3: Semi-supervised learning (PheCAP)

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"
```

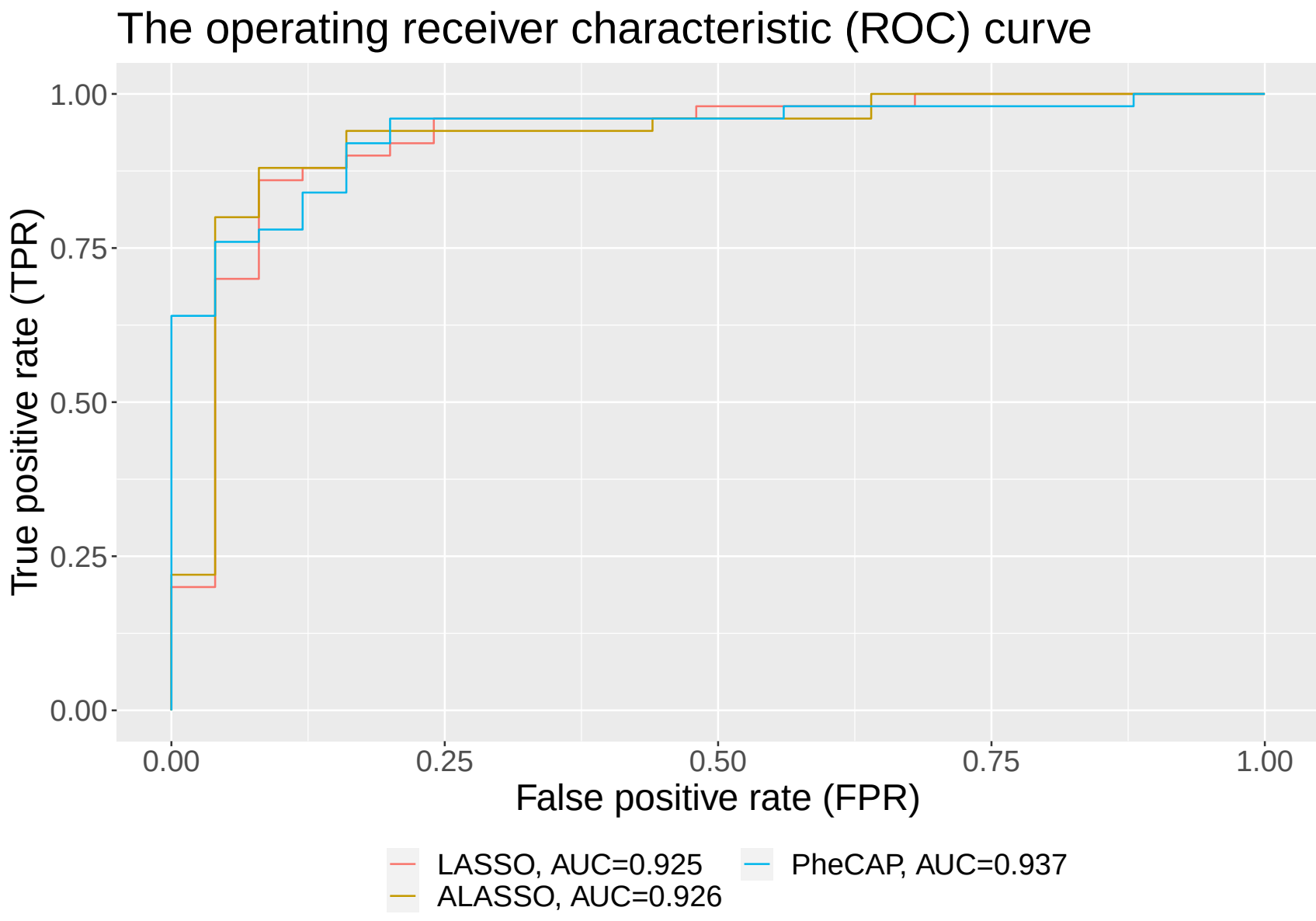
Step 2: Orthogonalization + supervised learning

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

```
phecap_lasso
```

```
## Phenotyping model:
## $lasso_cv
##            (Intercept)                main_ICD                main_NLP
##              1.9258667               0.2157399               1.1666409
## healthcare_utilization                   NLP56                   NLP93
##             -0.9772753               0.0000000              -0.3242900
##                 NLP274                  NLP306
##              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 0.6637589 0.6066667 0.1 0.86 0.9450549 0.7627119 0.9005236
```

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

```
##      cutoff pos.rate FPR  TPR       PPV       NPV        F1
## 1 0.7120506     0.62 0.1 0.88 0.9462366 0.7894737 0.9119171
```

```
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,
  surrogates = surrogates,
  feature_selected = feature_selected,
  nsim = 600,
  ntrain = c(50, 70, 90)
)
```

Supervised learning vs. PheCAP for different training size