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| FIGURE 3FIGURE 3 rm(list = ls(all = TRUE))> ####Work Path Setting> setwd("C:/Users/23983/Desktop/R results")> ####Data import> #It is recommended to use UTF-8 csv format to import data> data <- read.csv("trainTotal data (+ disaggregated information) (10 risk factors).csv",header = TRUE)> test <- read.csv("vadTotal data (+ disaggregated information) (10 risk factors).csv",header = TRUE)> ###############Training set model training and probability derivation###############> fit.full <- glm(END ~ V2+V3+V8+V17+V20+V21, data =test, family = 'binomial') > fit.full <- glm(END ~ V2+V3+V8+V17+V20+V21, data =train, family = 'binomial') > train$predict <- predict(object = fit.full, type = "response", newdata = train)> test$predict <- predict(object = fit.full,type = "response", newdata = test)> ###############Differentiation-ROC curve plotting###############> library(pROC)> roc.train <- roc(train$END,train$predict,ci=TRUE,polt=TRUE)> plot(roc.train,+ col = 'red', #Setting the curve colour+ legacy.axes = TRUE, #So that the x-axis becomes1-Specificity+ xlab = '1-Specificity',+ print.auc = TRUE)> roc.train> roc.test <- roc(test$END,test$predict,ci=TRUE,polt=TRUE)> plot(roc.test,+ col = '#00468BFF', #Setting the curve colour+ legacy.axes = TRUE, #So that the x-axis becomes1-Specificity+ xlab = '1-Specificity',+ print.auc = TRUE)> roc.test |