

```
Call:
glm(formula = dy_payer ~ dx_pay_count + dx_payer, family = "binomial",
    data = DTtrain)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.2198	-0.1228	-0.1228	-0.1228	3.1275

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-4.88318	0.04104	-118.972	< 2e-16 ***
dx_pay_count	0.45323	0.10275	4.411	1.03e-05 ***
dx_payerTRUE	4.53863	0.19722	23.013	< 2e-16 ***

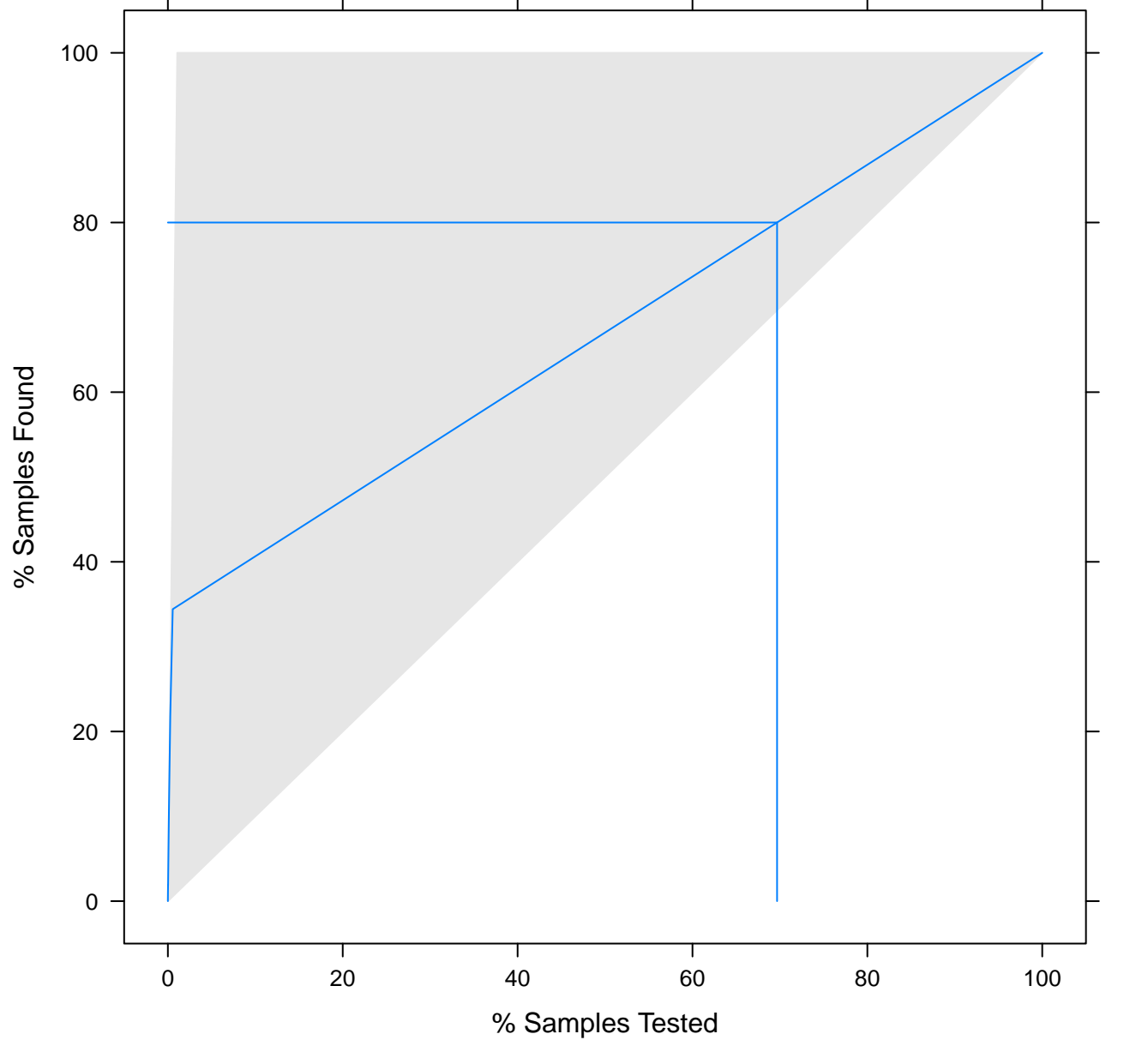
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

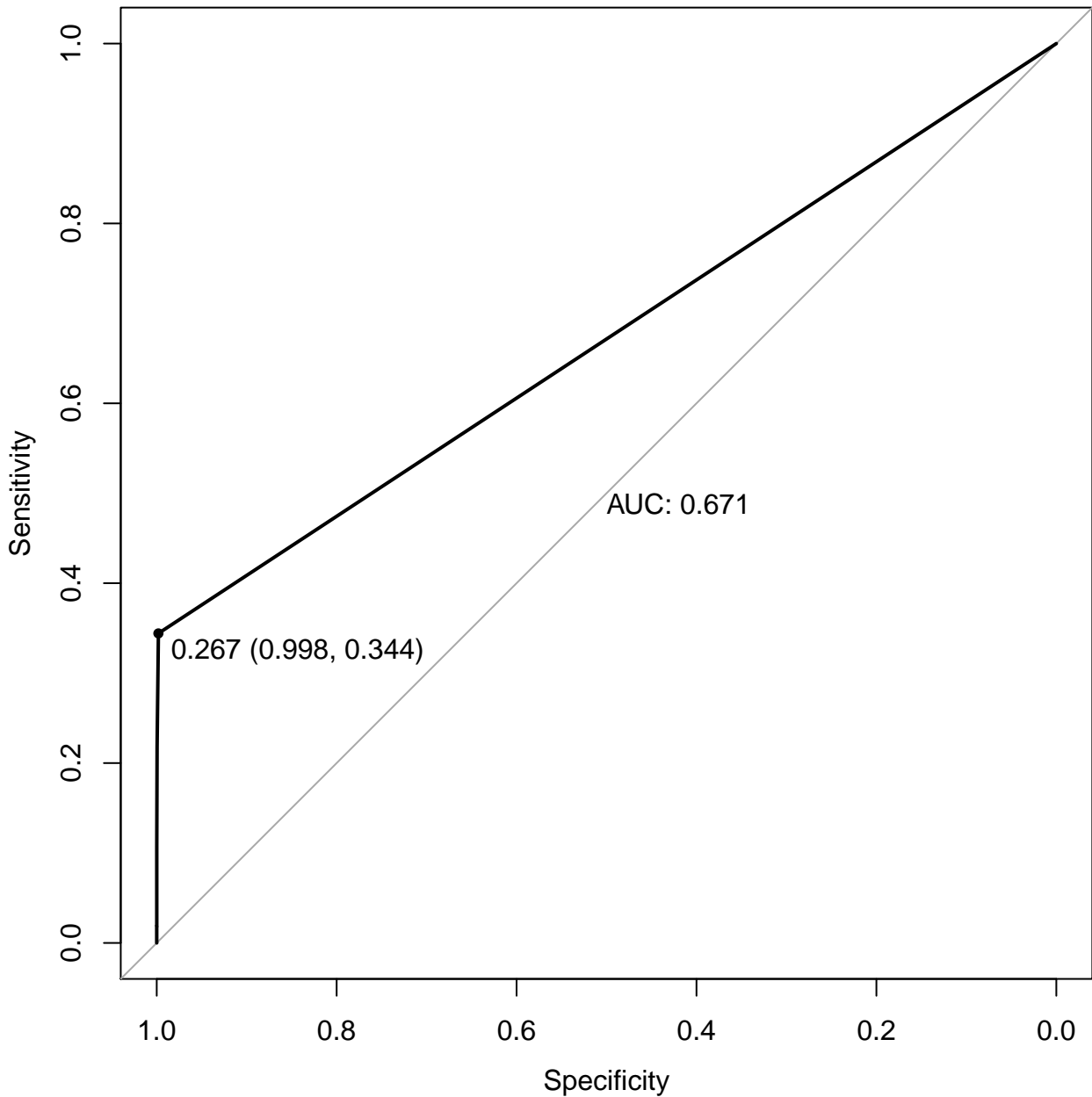
Null deviance: 9543.4 on 80000 degrees of freedom
Residual deviance: 7599.5 on 79998 degrees of freedom
AIC: 7605.5

Number of Fisher Scoring iterations: 7

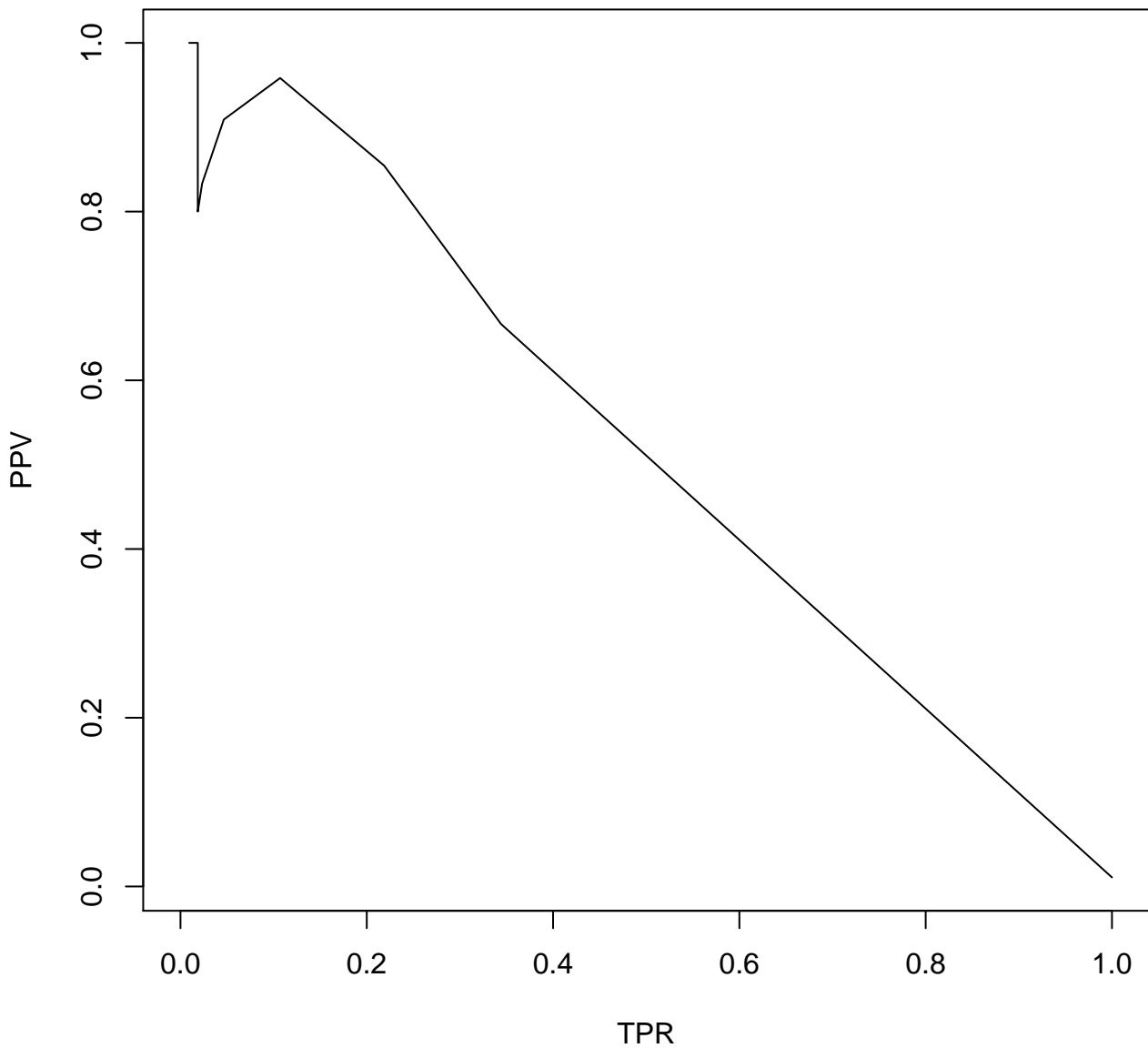
Lift chart



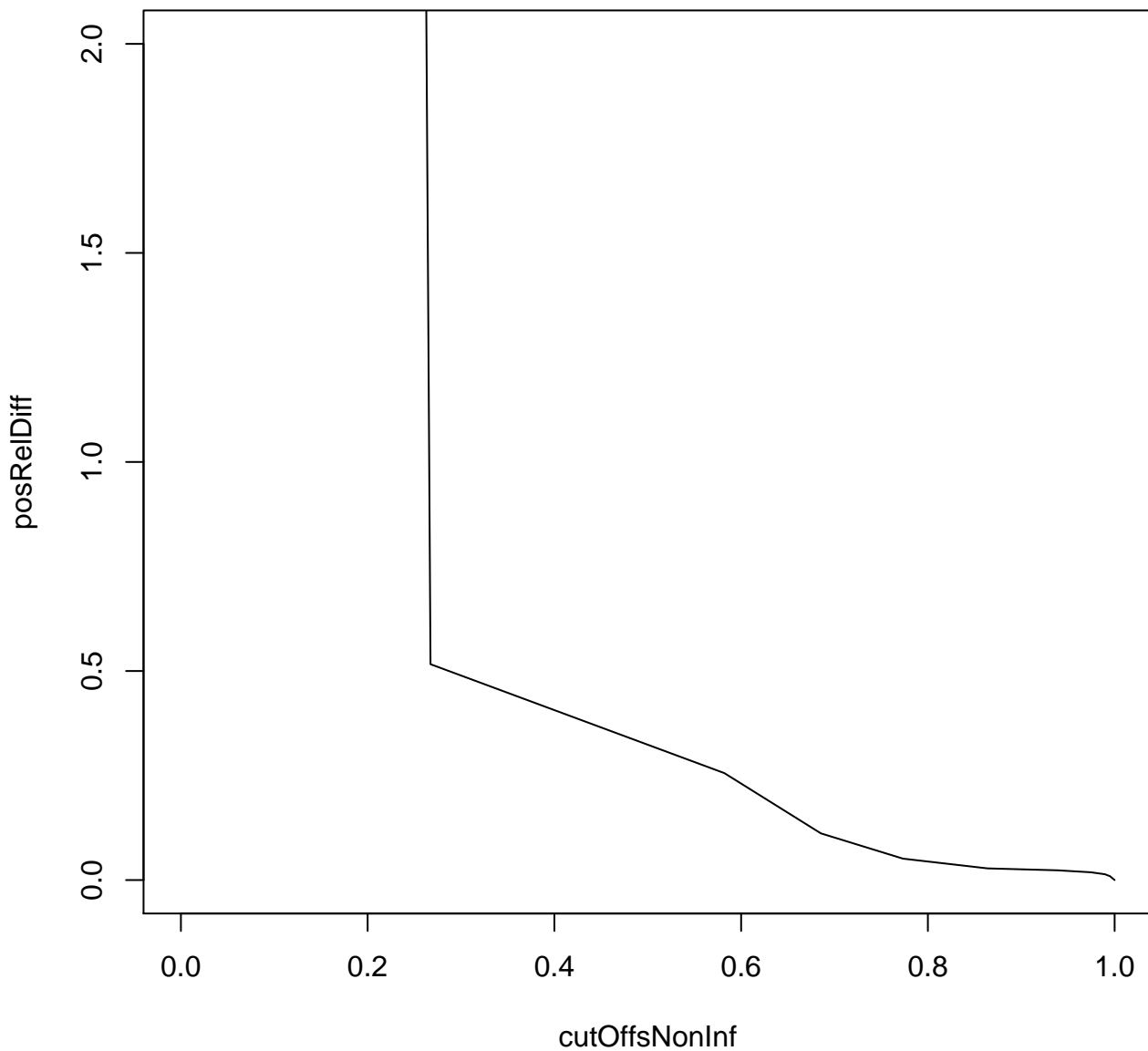
ROC curve



Sensitivity vs. Precision



predicted positives / actual positives



```
[1] "1st matrix - threshold based on the ROC curve"  
[2] "0.26732928651714"  
[3] "2nd matrix - threshold based on the predicted vs. actual count of positives"  
[4] "0.26732928651714"
```

Confusion Matrix and Statistics

	Reference	
Prediction	FALSE	TRUE
FALSE	19747	141
TRUE	37	74

Accuracy : 0.9911

95% CI : (0.9897, 0.9924)

No Information Rate : 0.9892

P-Value [Acc > NIR] : 0.005133

Kappa : 0.45

McNemar's Test P-Value : 1.162e-14

Sensitivity : 0.34419

Specificity : 0.99813

Pos Pred Value : 0.66667

Neg Pred Value : 0.99291

Prevalence : 0.01075

Detection Rate : 0.00370

Detection Prevalence : 0.00555

Balanced Accuracy : 0.67116

'Positive' Class : TRUE

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