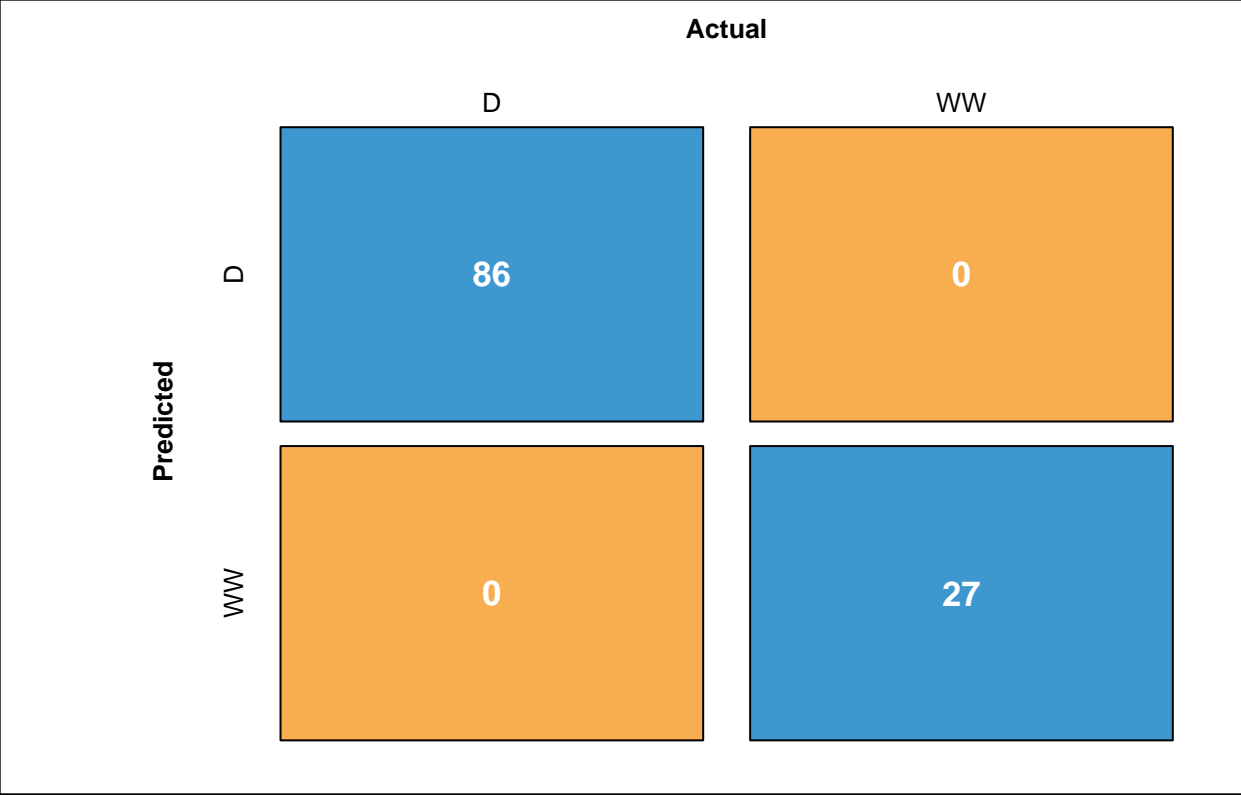


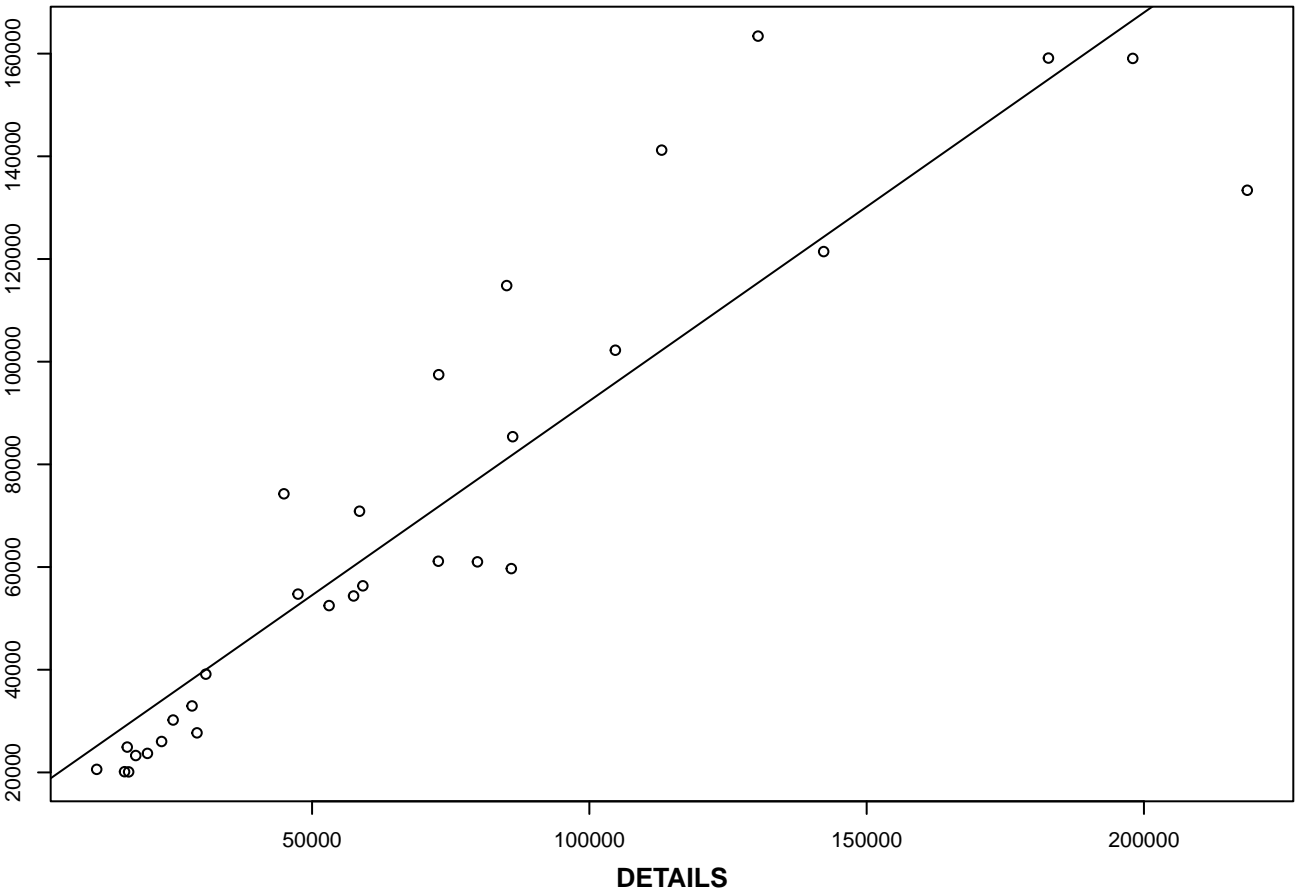
# CONFUSION MATRIX



## DETAILS

Sensitivity	Specificity	Precision	Recall	F1
1	1	1	1	1
Accuracy		Kappa		
1		1		

loocv\_genes\_top.geometry.fluo.area.px.2..csv



**RMSE**

22922.958

**NRMSE**

32.3 %

**MAE**

15188.516

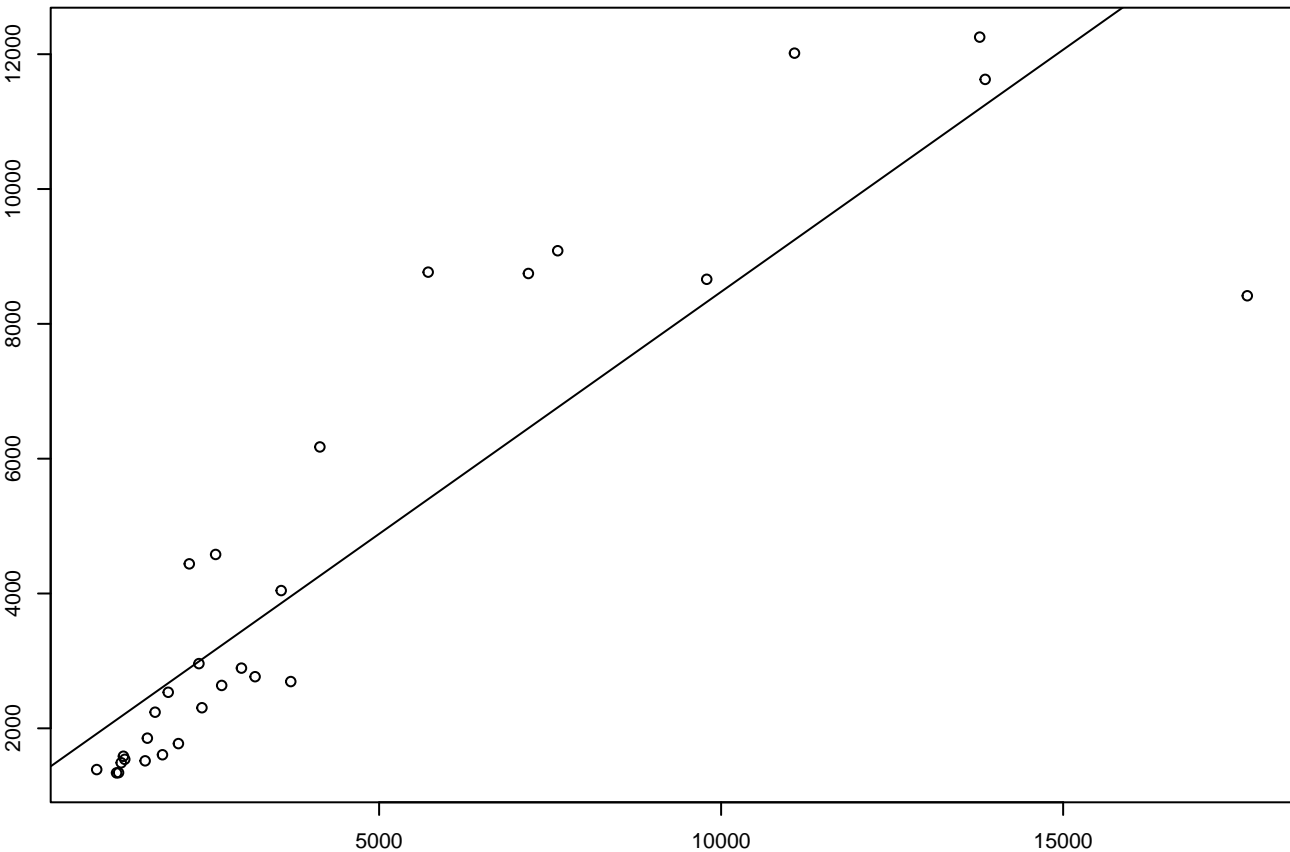
**NMAE**

21.4 %

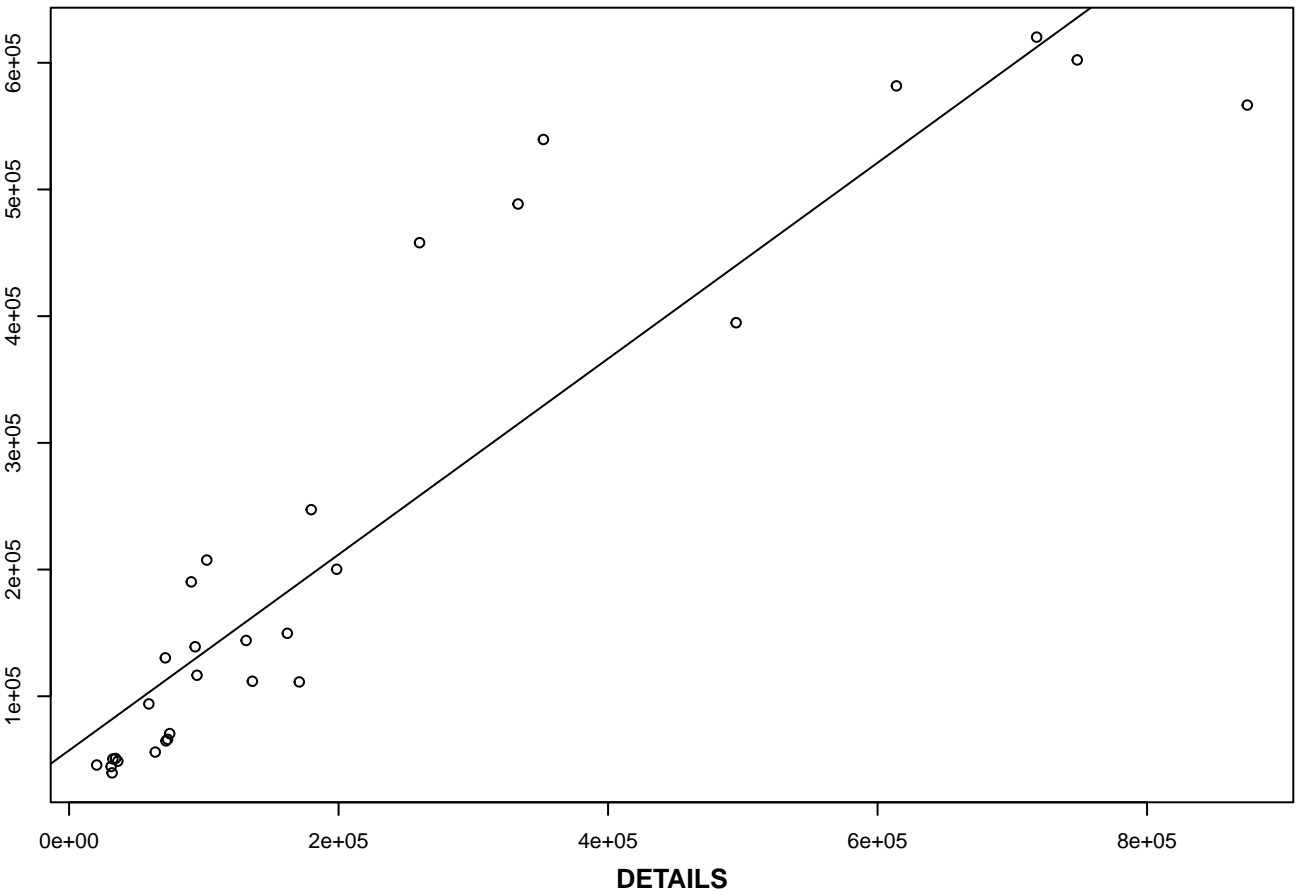
**R^2**

0.837

loocv\_genes\_top.geometry.fluo.border.length..px..csv



loocv\_genes\_top.geometry.fluo.hull.area.px.csv



**RMSE**

95585.802

**NRMSE**

45.1 %

**MAE**

62925.18

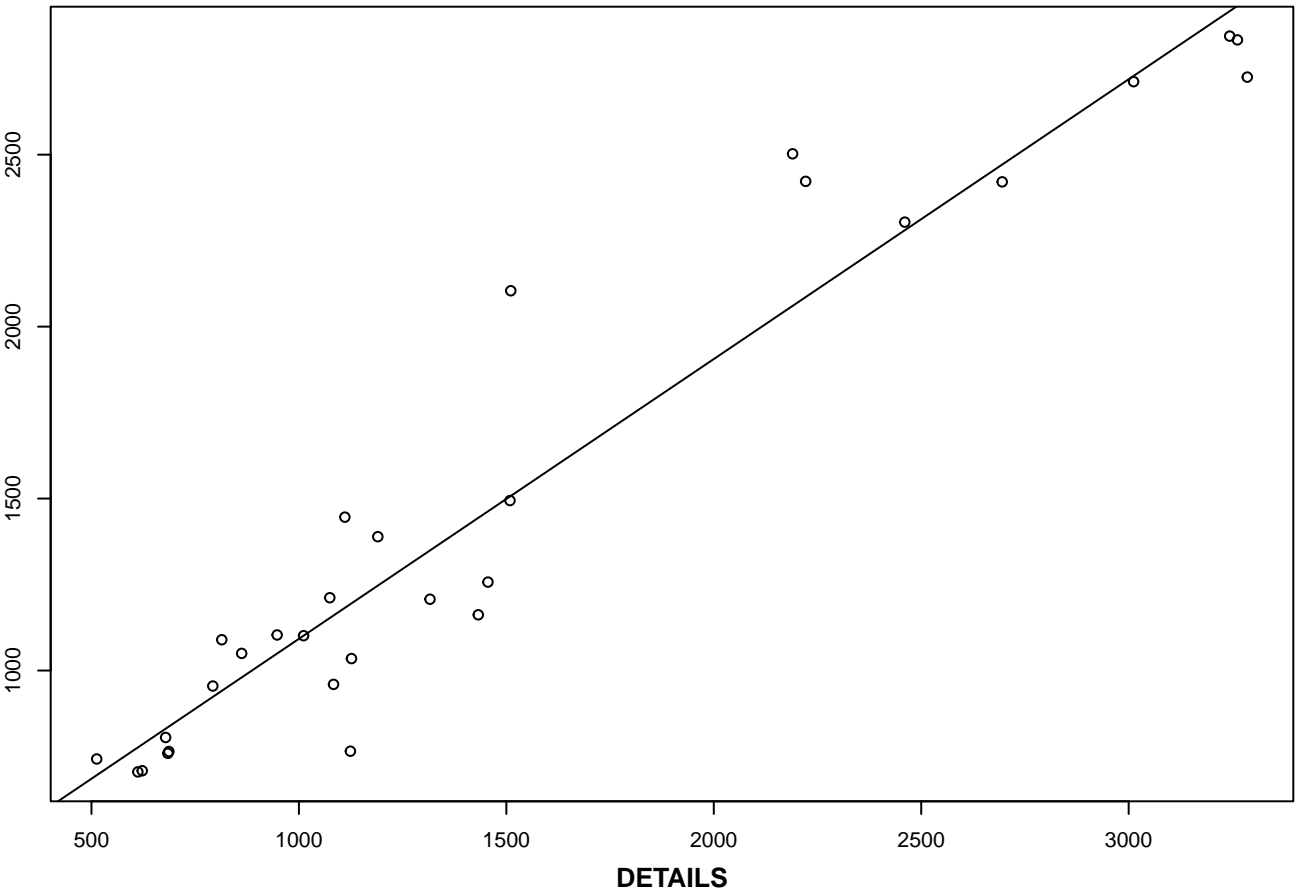
**NMAE**

29.7 %

**R<sup>2</sup>**

0.841

loocv\_genes\_top.geometry.fluo.hull.length.csv



**RMSE**

261.461

**NRMSE**

17.6 %

**MAE**

220.778

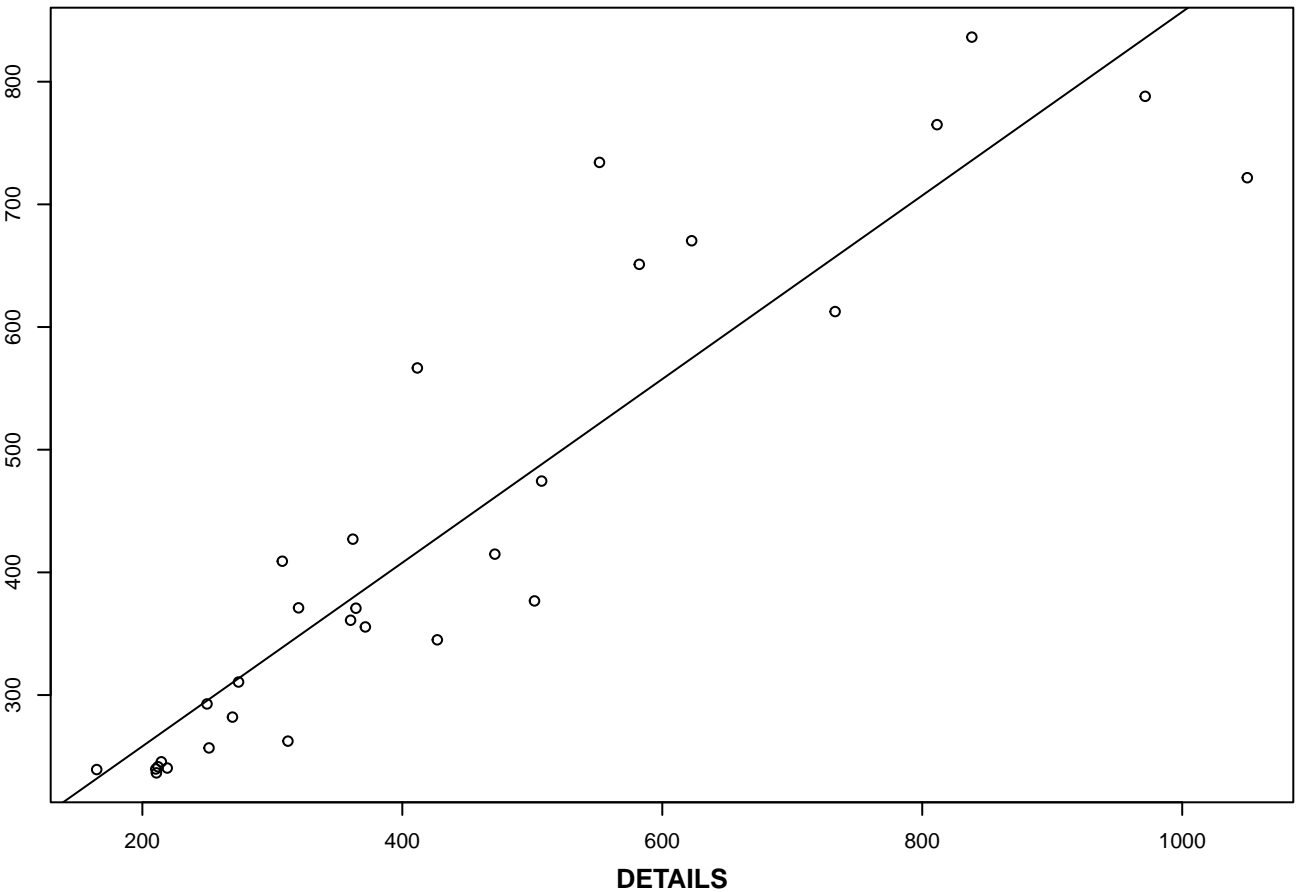
**NMAE**

14.9 %

**R<sup>2</sup>**

0.921

loocv\_genes\_top.geometry.fluo.hull.pc2.px.csv



**RMSE**

96.894

**NRMSE**

22.1 %

**MAE**

67.67

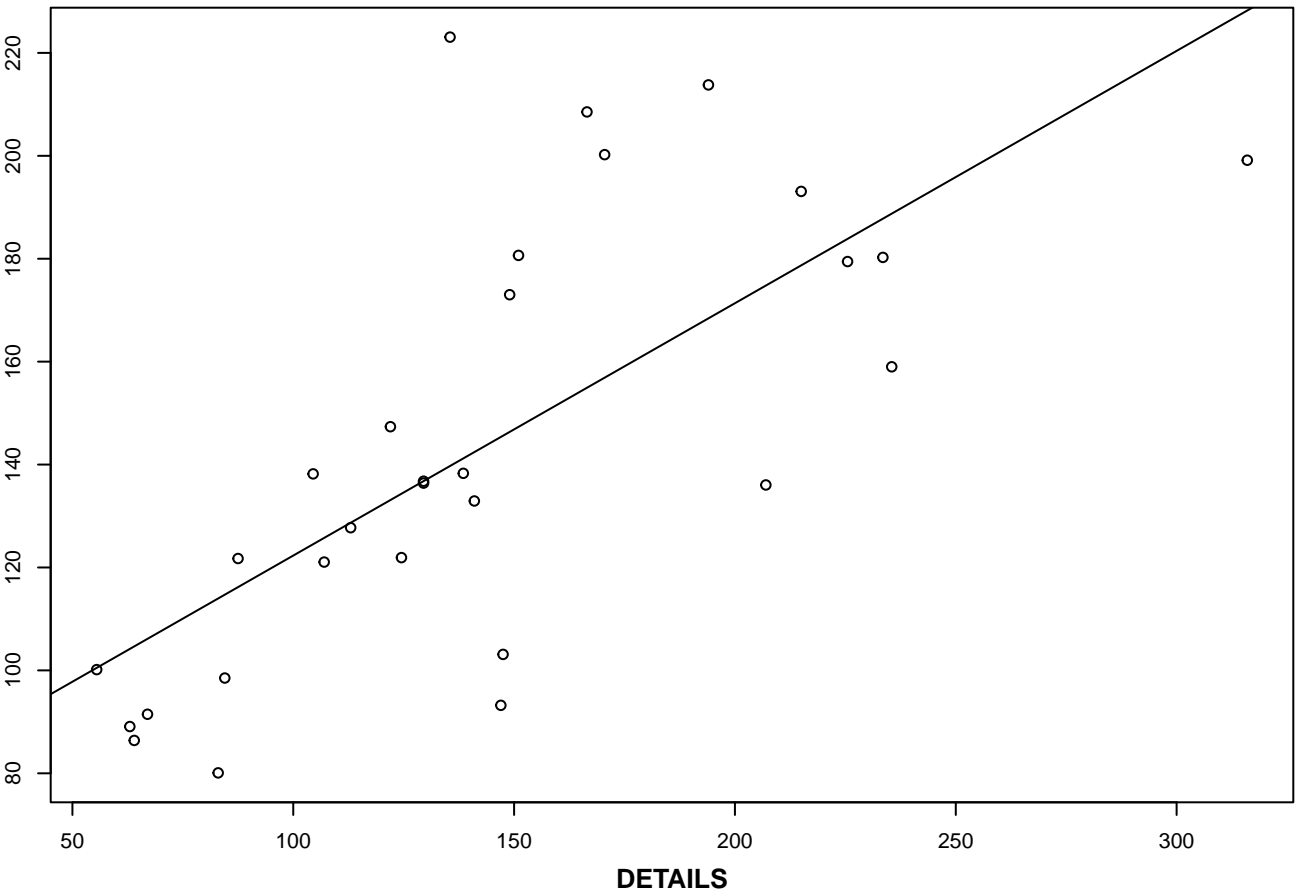
**NMAE**

15.4 %

**R<sup>2</sup>**

0.839

loocv\_genes\_top.geometry.fluo.leaf.length.mean.px.csv



**RMSE**

42.632

**NRMSE**

29.7 %

**MAE**

33.269

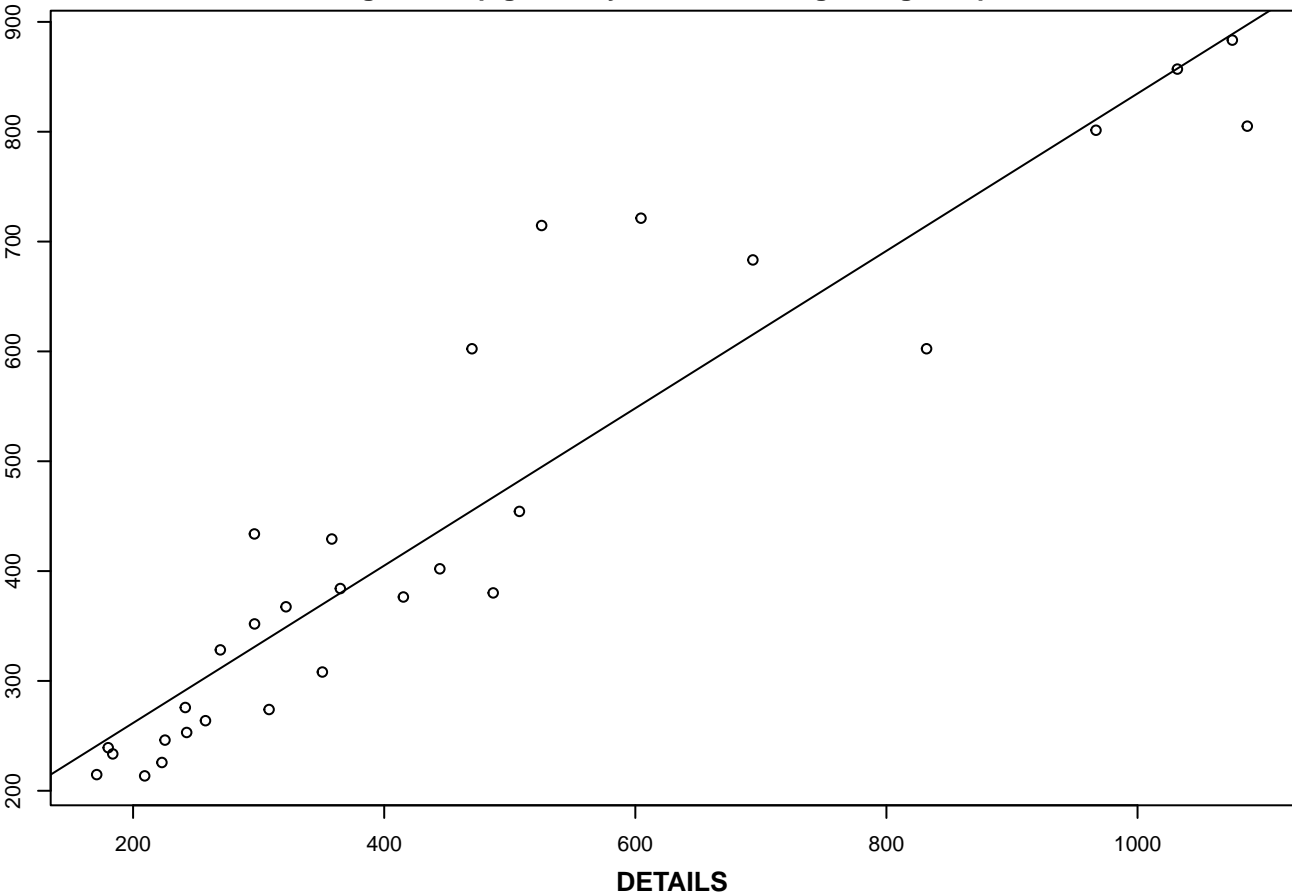
**NMAE**

23.2 %

**R<sup>2</sup>**

0.495

loocv\_genes\_top.geometry.fluo.minrectangle.length.a.px.csv



**RMSE**

109.135

**NRMSE**

24 %

**MAE**

80.976

**NMAE**

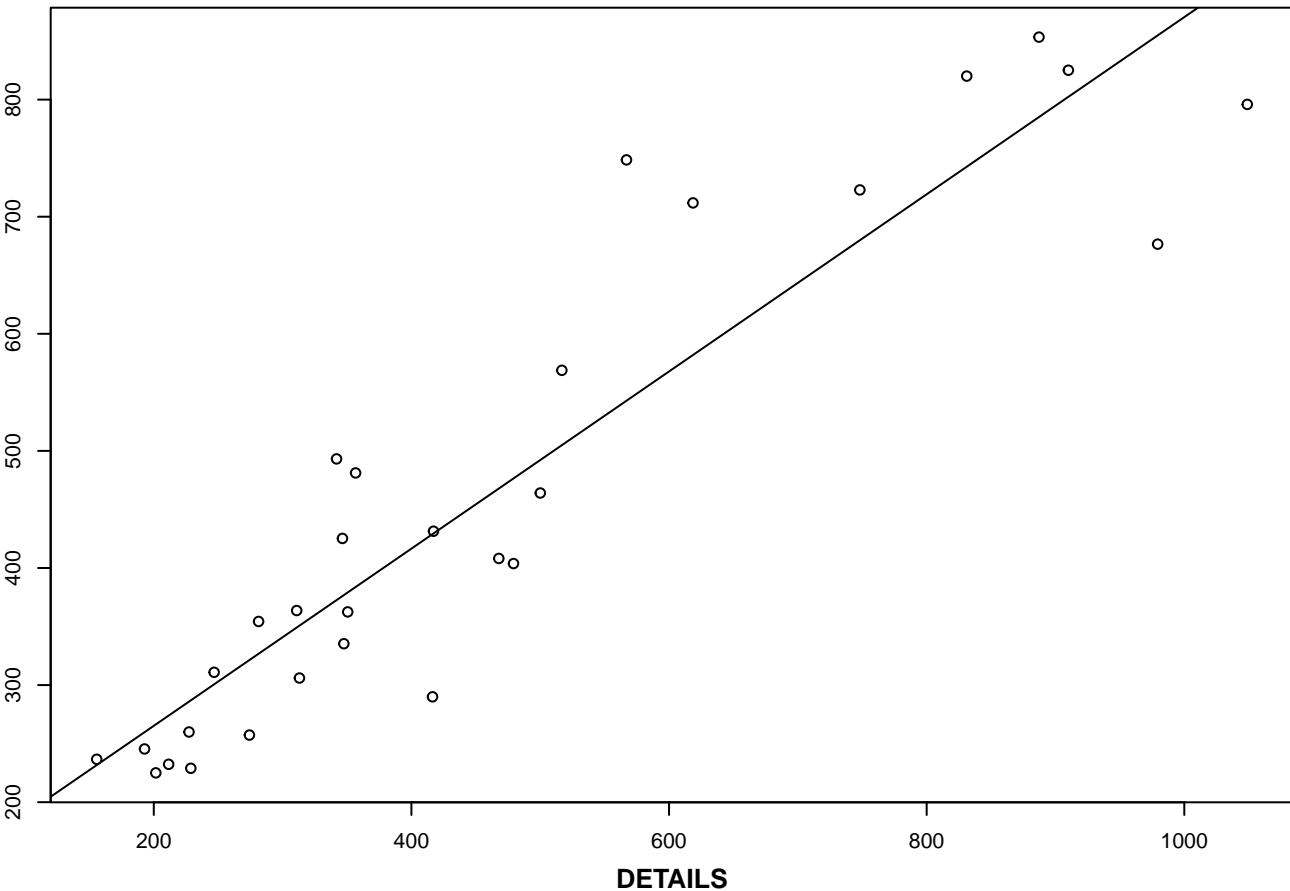
17.8 %

**R<sup>2</sup>**

0.874



loocv\_genes\_top.geometry.fluo.minrectangle.length.b.px.csv



**RMSE**

100.774

**NRMSE**

21.9 %

**MAE**

71.748

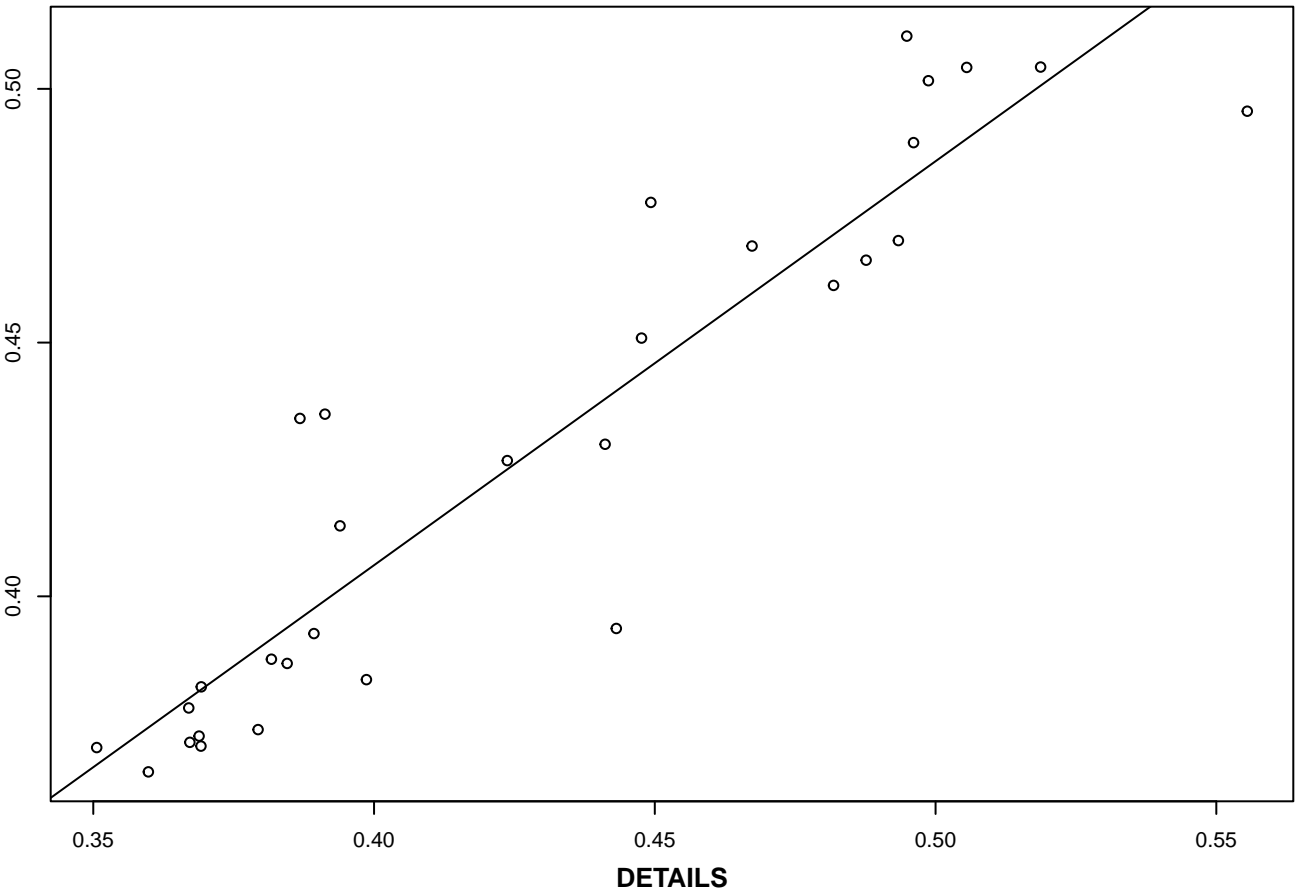
**NMAE**

15.6 %

**R<sup>2</sup>**

0.848

loocv\_genes\_top.intensity.fluo.hsv.v.mean.csv



**RMSE**

0.022

**NRMSE**

5.2 %

**MAE**

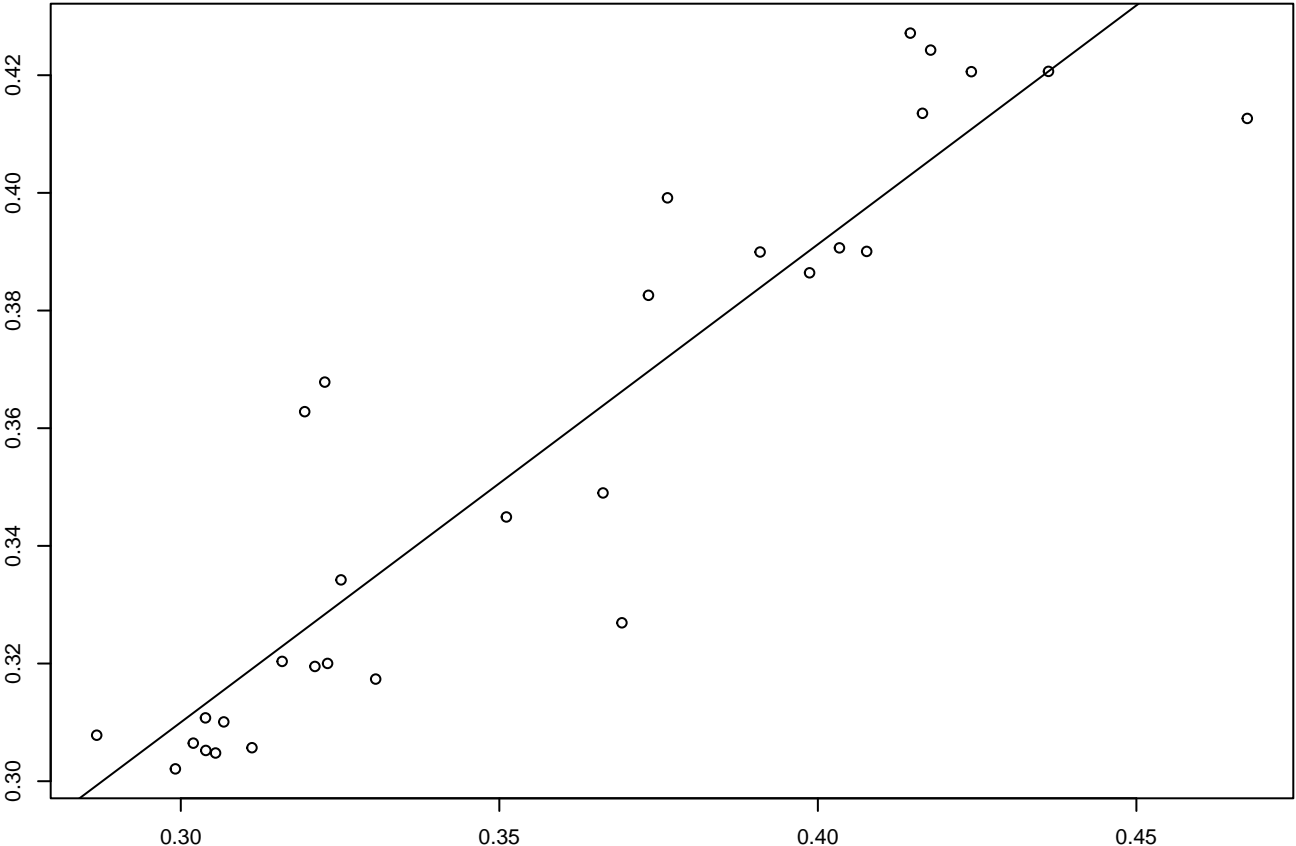
0.016

**NMAE**

3.6 %

**R<sup>2</sup>**

0.857



**DETAILS**

**RMSE**

0.02

**NRMSE**

5.5 %

**MAE**

0.013

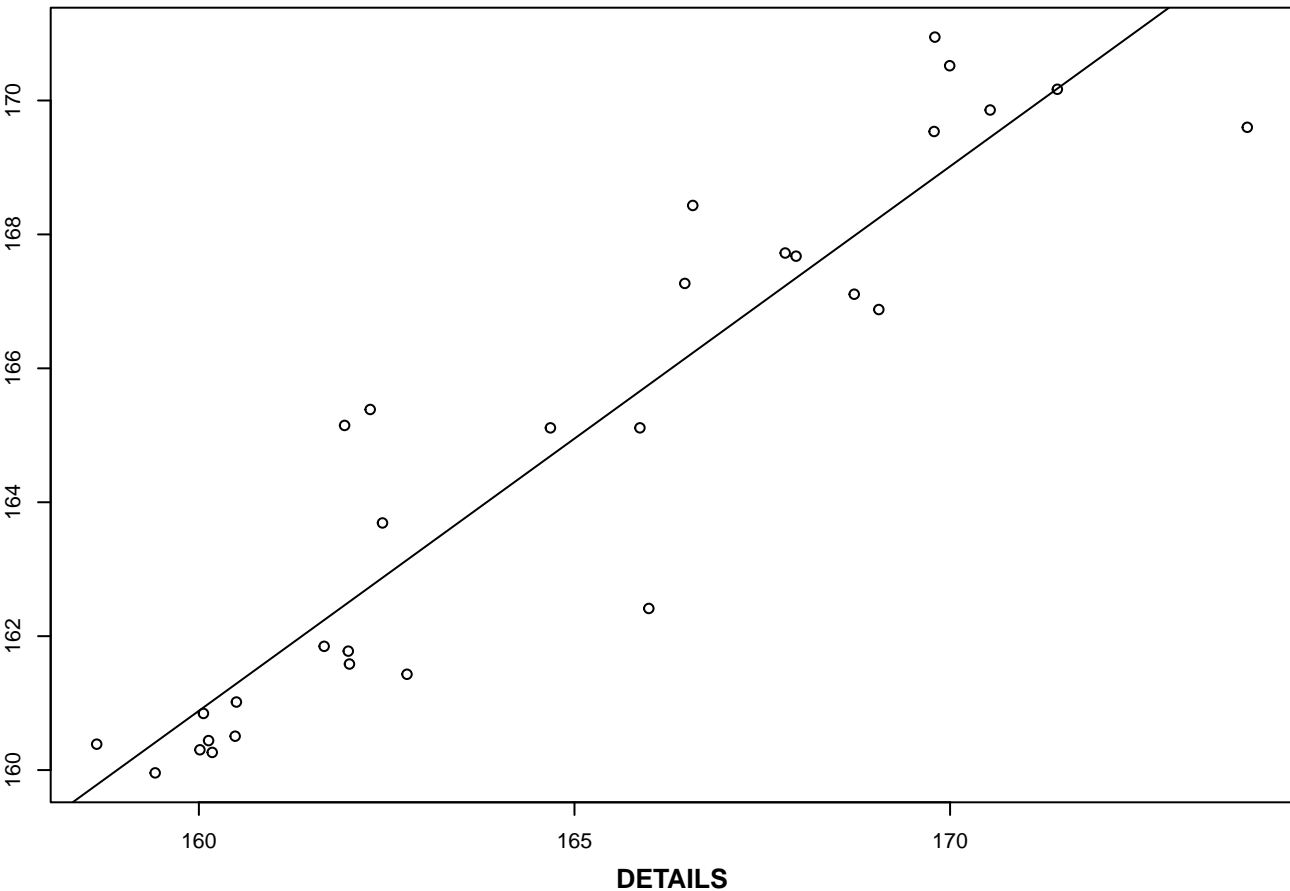
**NMAE**

3.8 %

**R^2**

0.846

loocv\_genes\_top.intensity.fluo.lab.a.mean.csv



**RMSE**

1.588

**NRMSE**

1 %

**MAE**

1.127

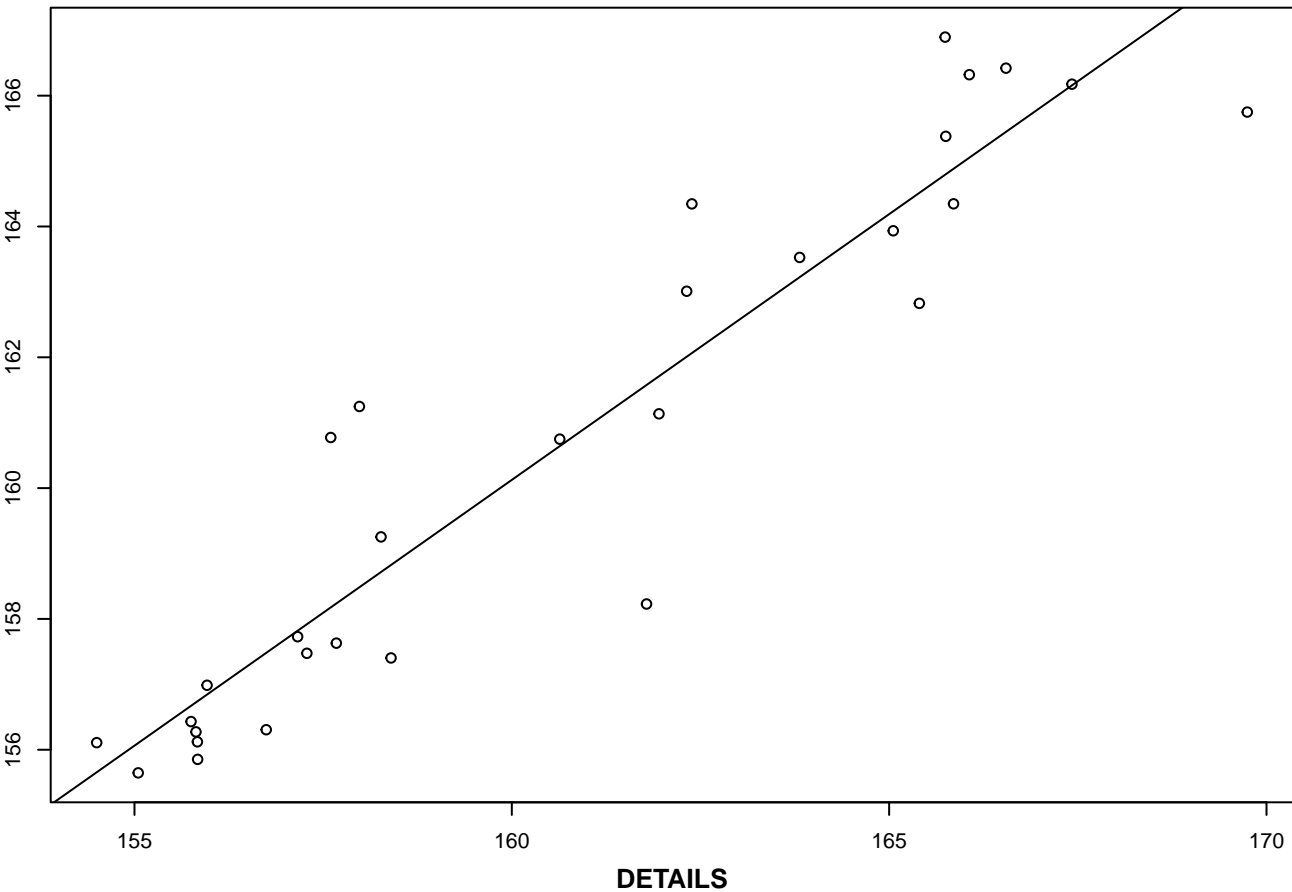
**NMAE**

0.7 %

**R<sup>2</sup>**

0.863

loocv\_genes\_top.intensity.fluo.lab.b.mean.csv



**RMSE**

1.581

**NRMSE**

1 %

**MAE**

1.137

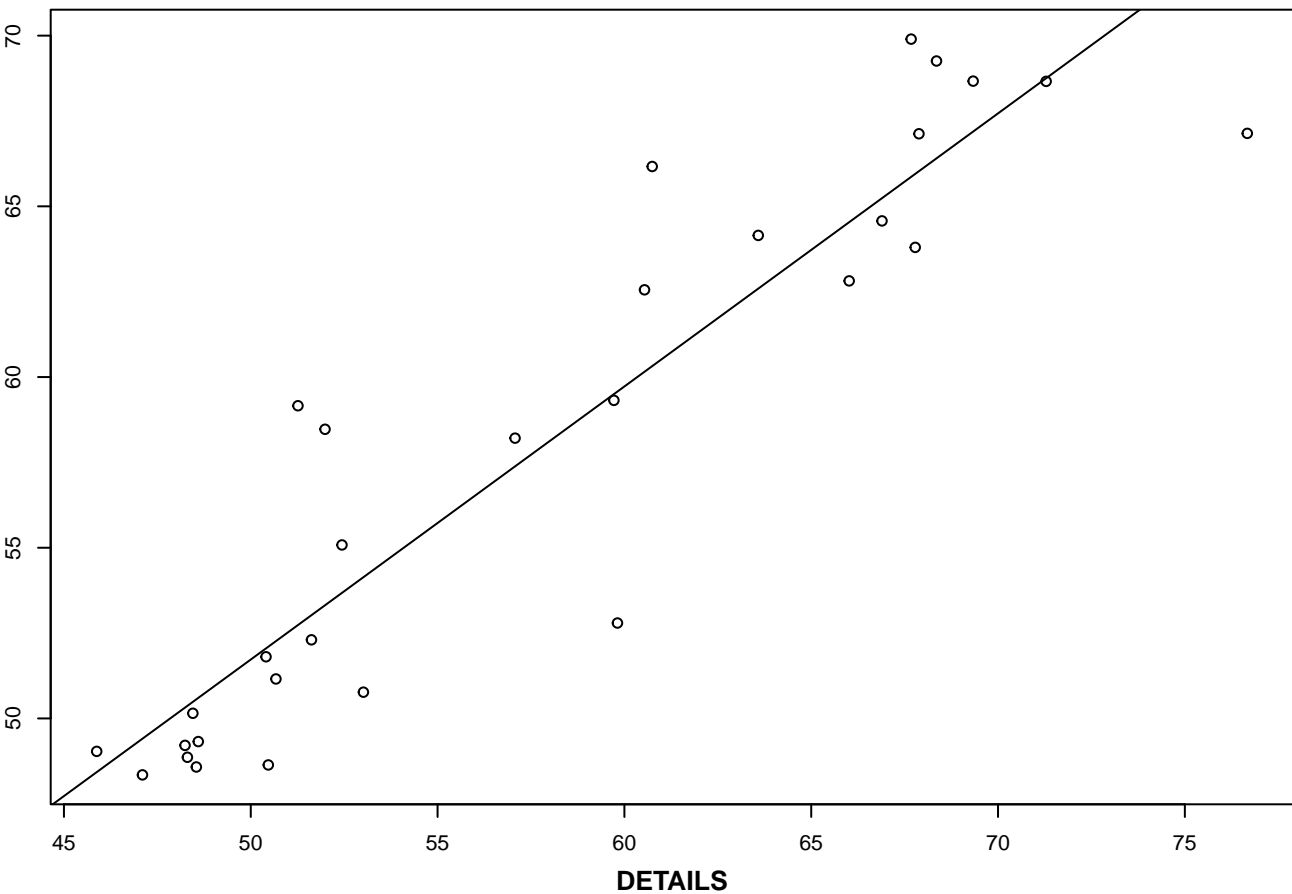
**NMAE**

0.7 %

**R<sup>2</sup>**

0.878

loocv\_genes\_top.intensity.fluo.lab.l.mean.csv



**RMSE**

3.46

**NRMSE**

6 %

**MAE**

2.494

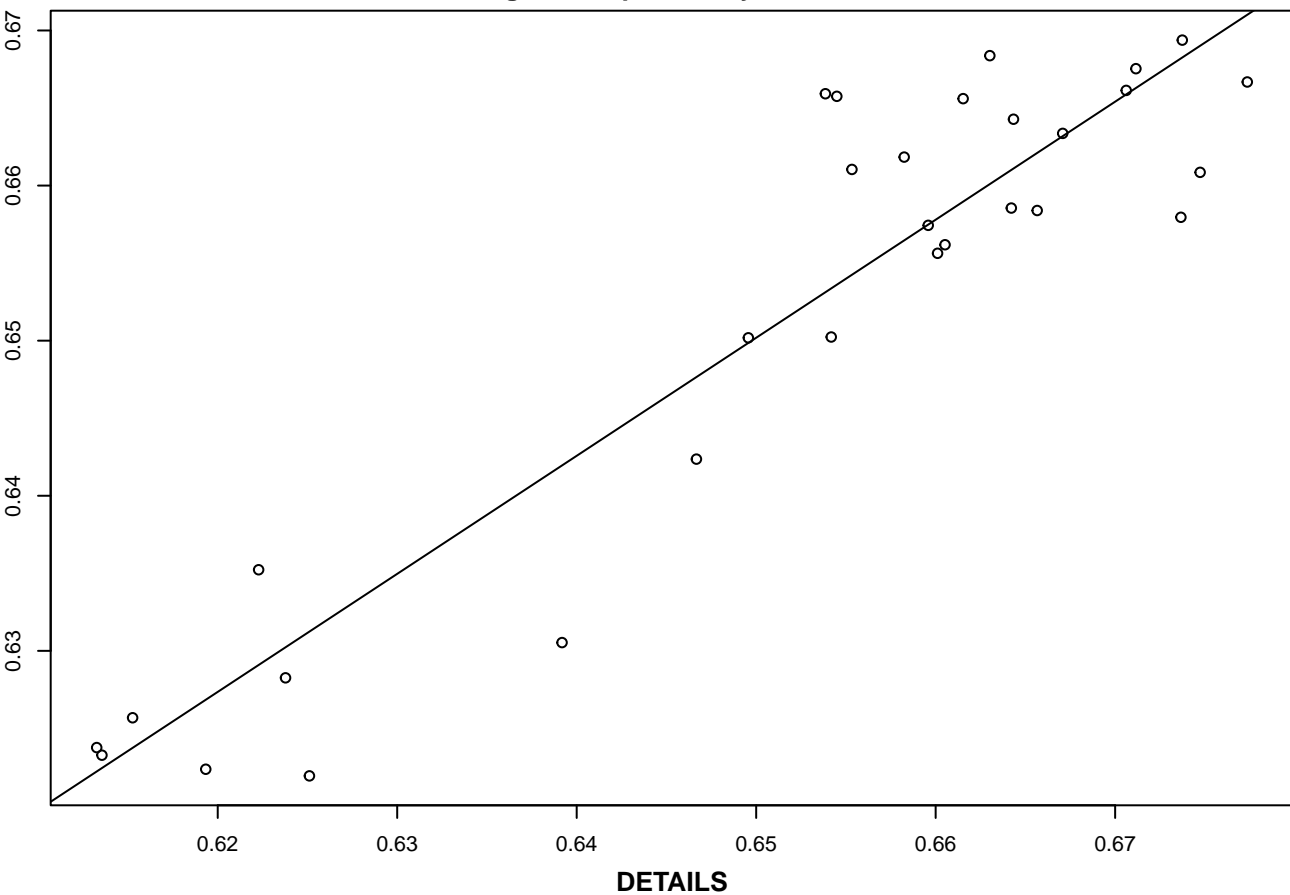
**NMAE**

4.3 %

**R<sup>2</sup>**

0.848

loocv\_genes\_top.intensity.nir.mean.csv



**RMSE**

0.008

**NRMSE**

1.2 %

**MAE**

0.006

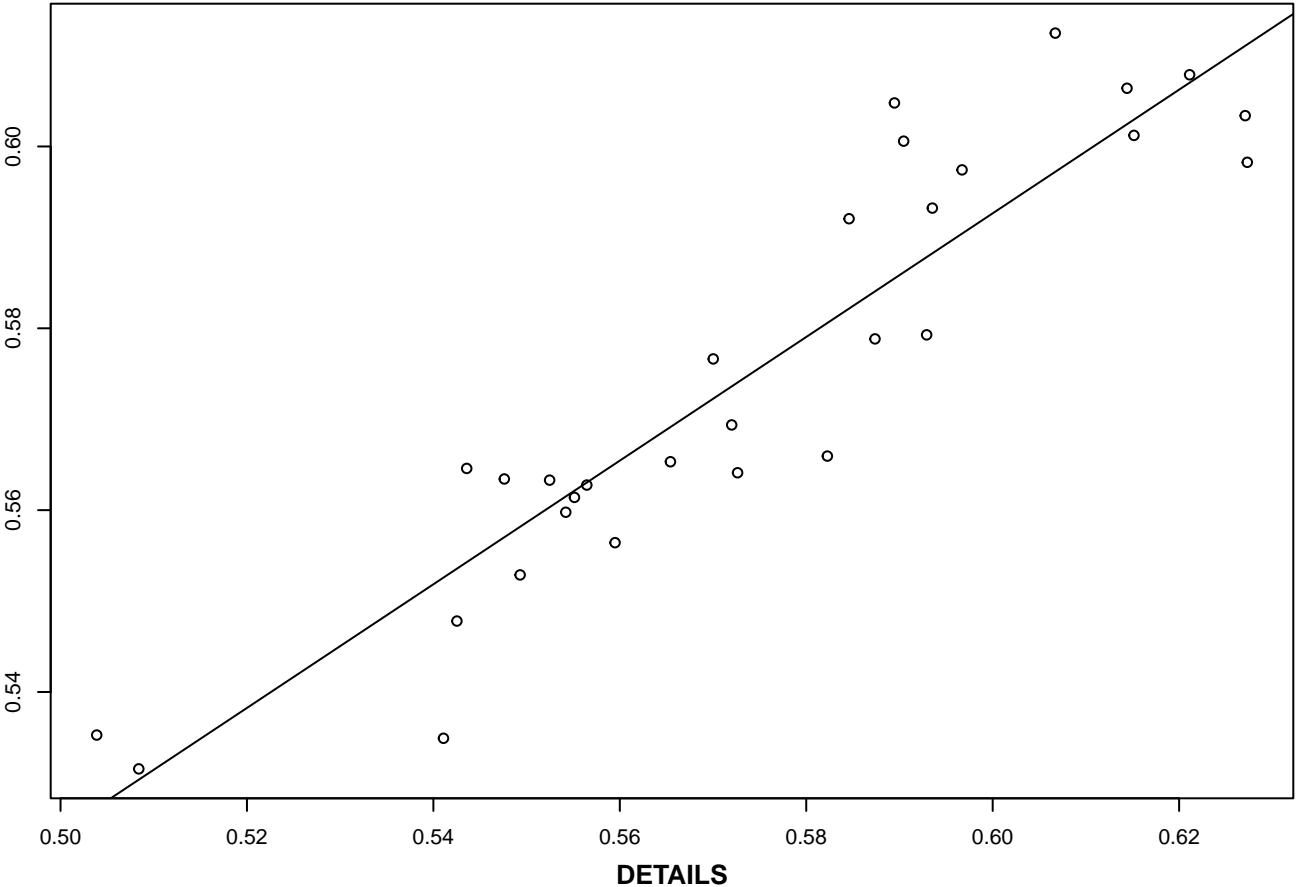
**NMAE**

1 %

**R<sup>2</sup>**

0.868

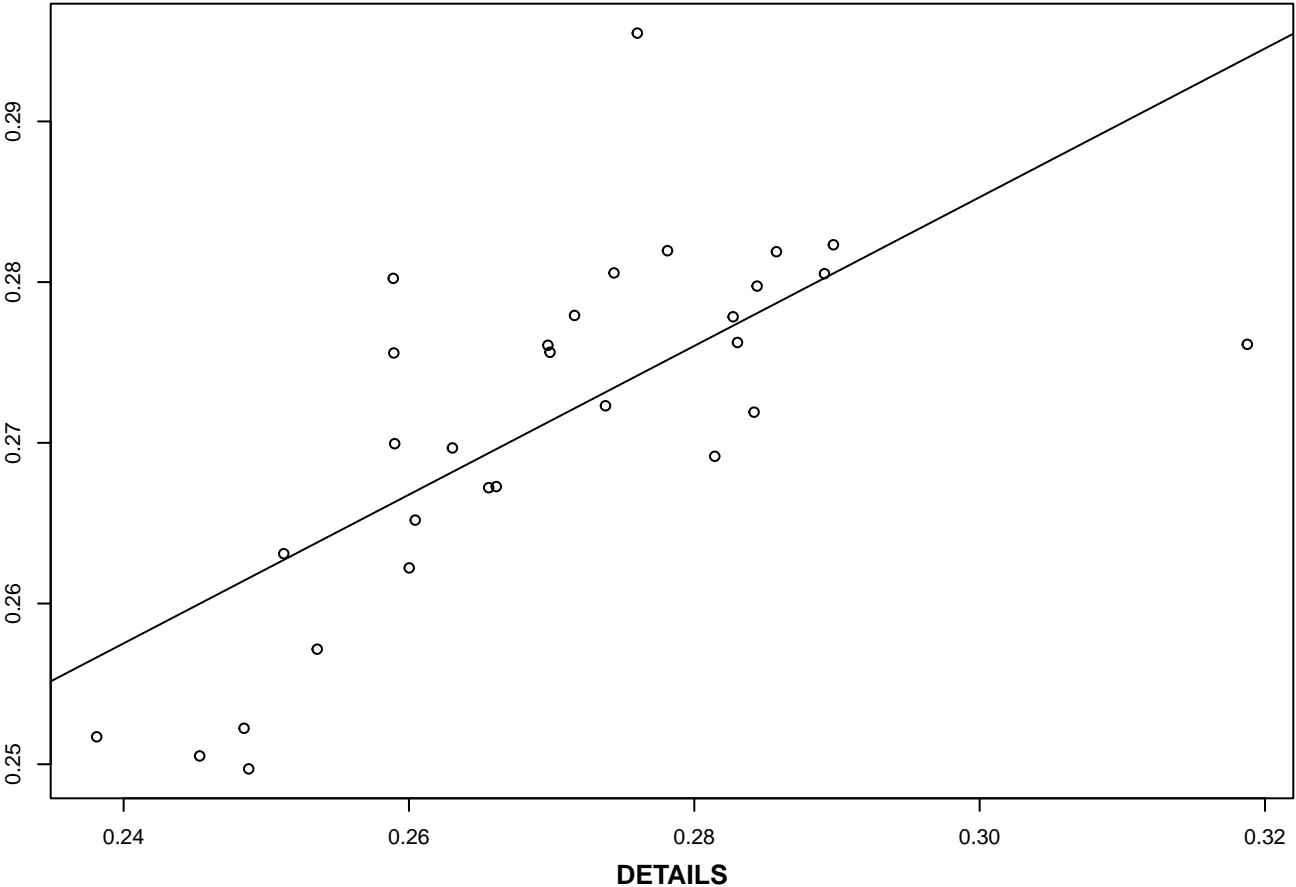
loocv\_genes\_top.intensity.vis.hsv.s.mean.csv



RMSE	NRMSE	MAE	NMAE
0.013	2.3 %	0.011	1.9 %
R^2			
0.853			

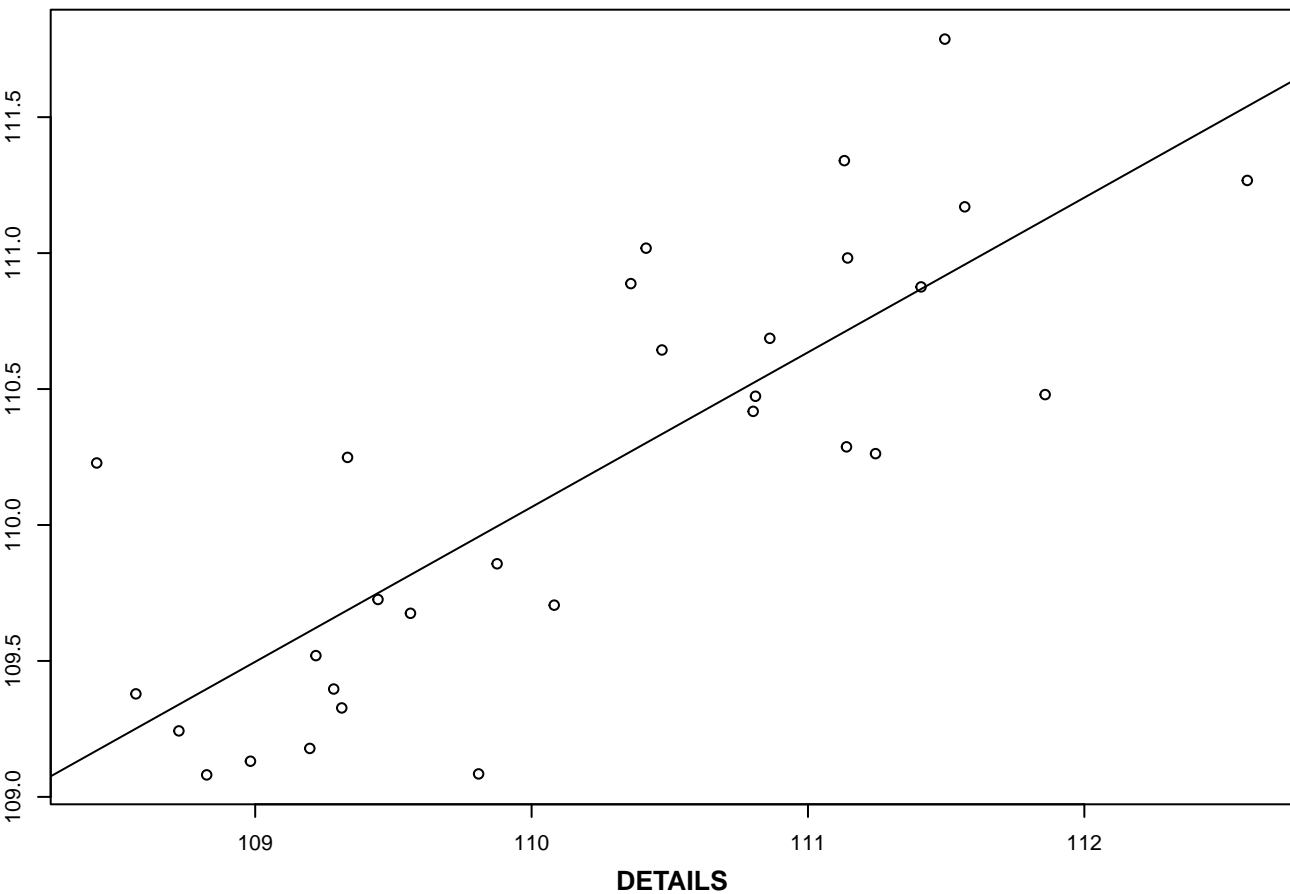


loocv\_genes\_top.intensity.vis.hsv.v.mean.csv



RMSE	NRMSE	MAE	NMAE
0.012	4.4 %	0.009	3.2 %
R^2			
0.497			

loocv\_genes\_top.intensity.vis.lab.a.mean.csv



**RMSE**

0.655

**NRMSE**

0.6 %

**MAE**

0.491

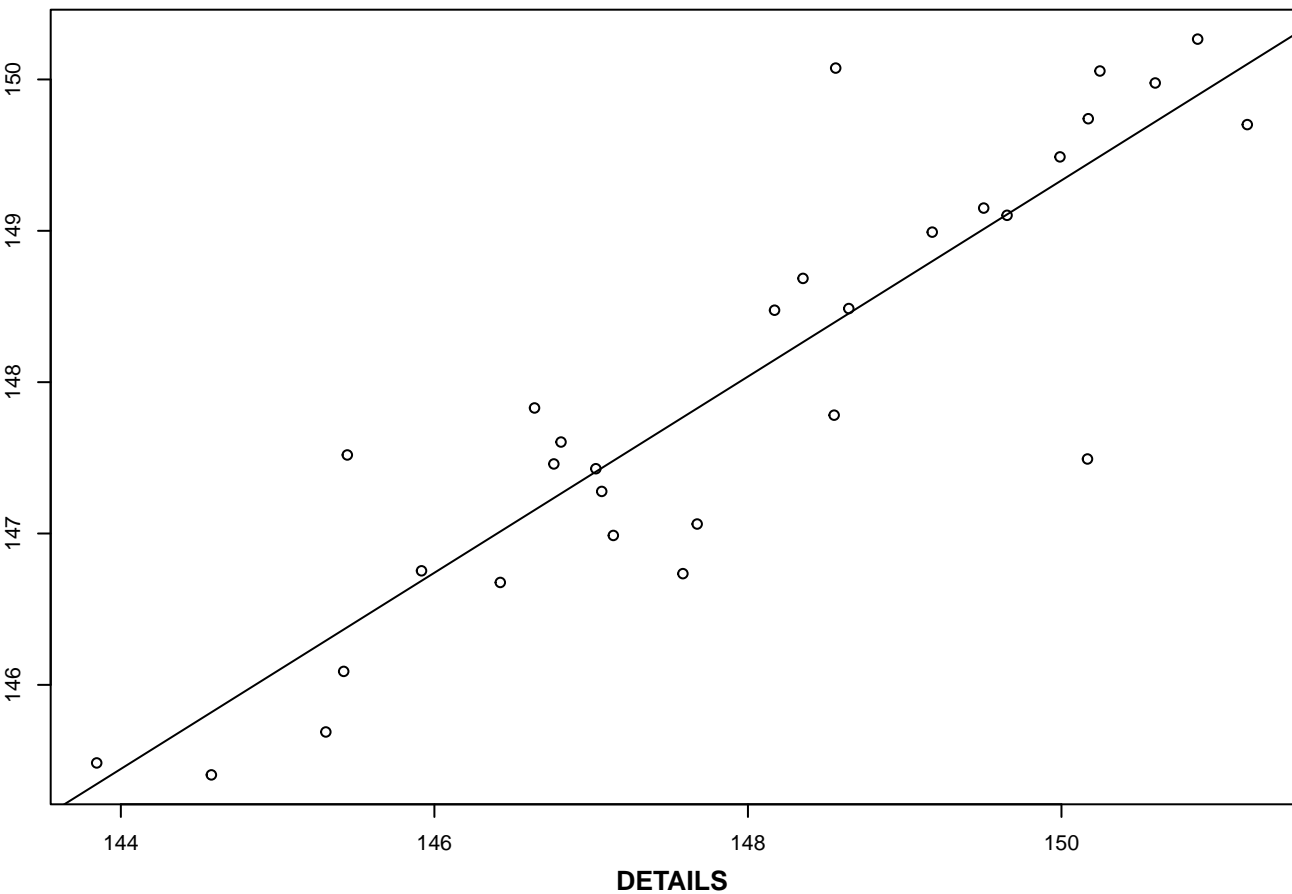
**NMAE**

0.4 %

**R<sup>2</sup>**

0.647

loocv\_genes\_top.intensity.vis.lab.b.mean.csv



**RMSE**

0.949

**NRMSE**

0.6 %

**MAE**

0.742

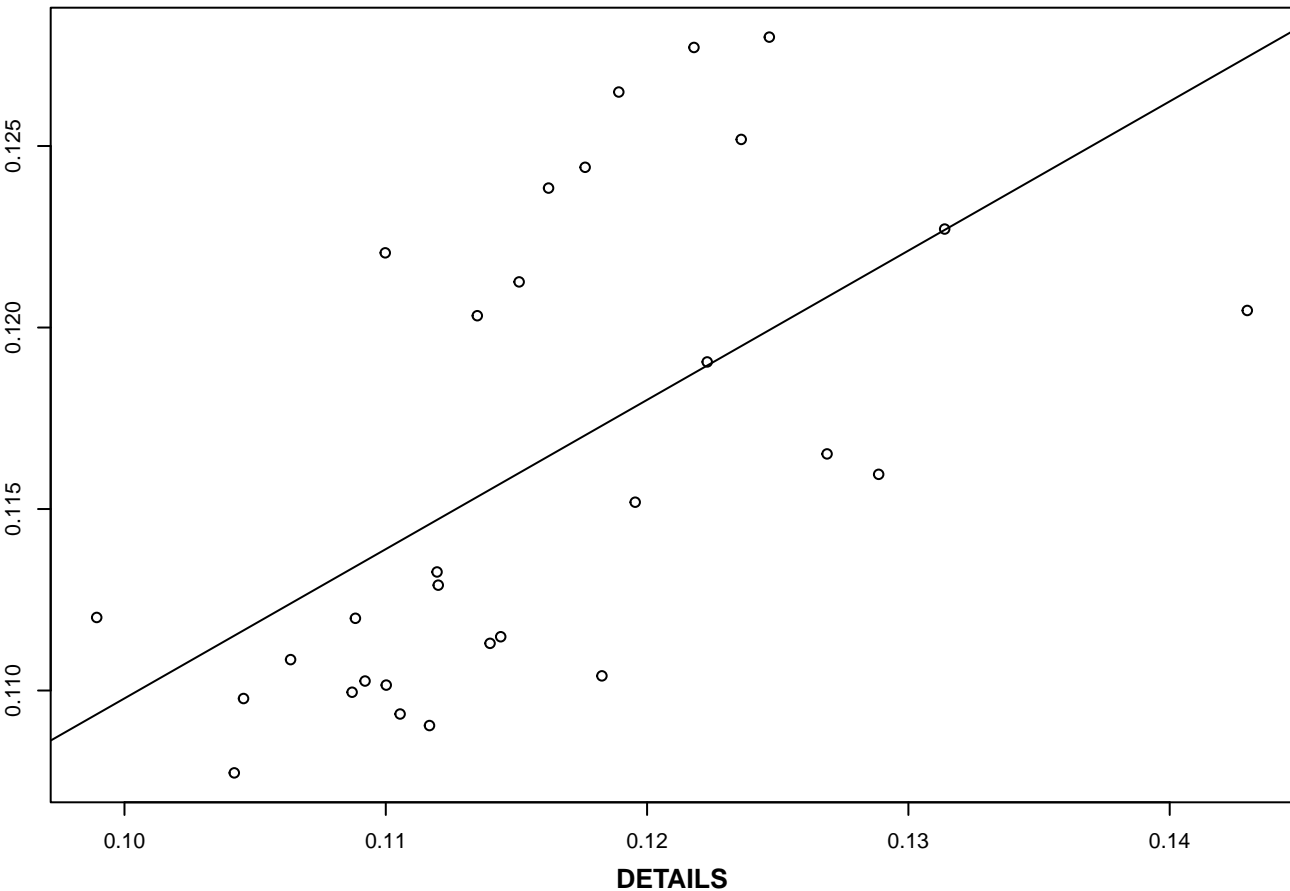
**NMAE**

0.5 %

**R<sup>2</sup>**

0.791

loocv\_genes\_top.intensity.vis.rgb.blue.mean.csv



**RMSE**

0.007

**NRMSE**

6.4 %

**MAE**

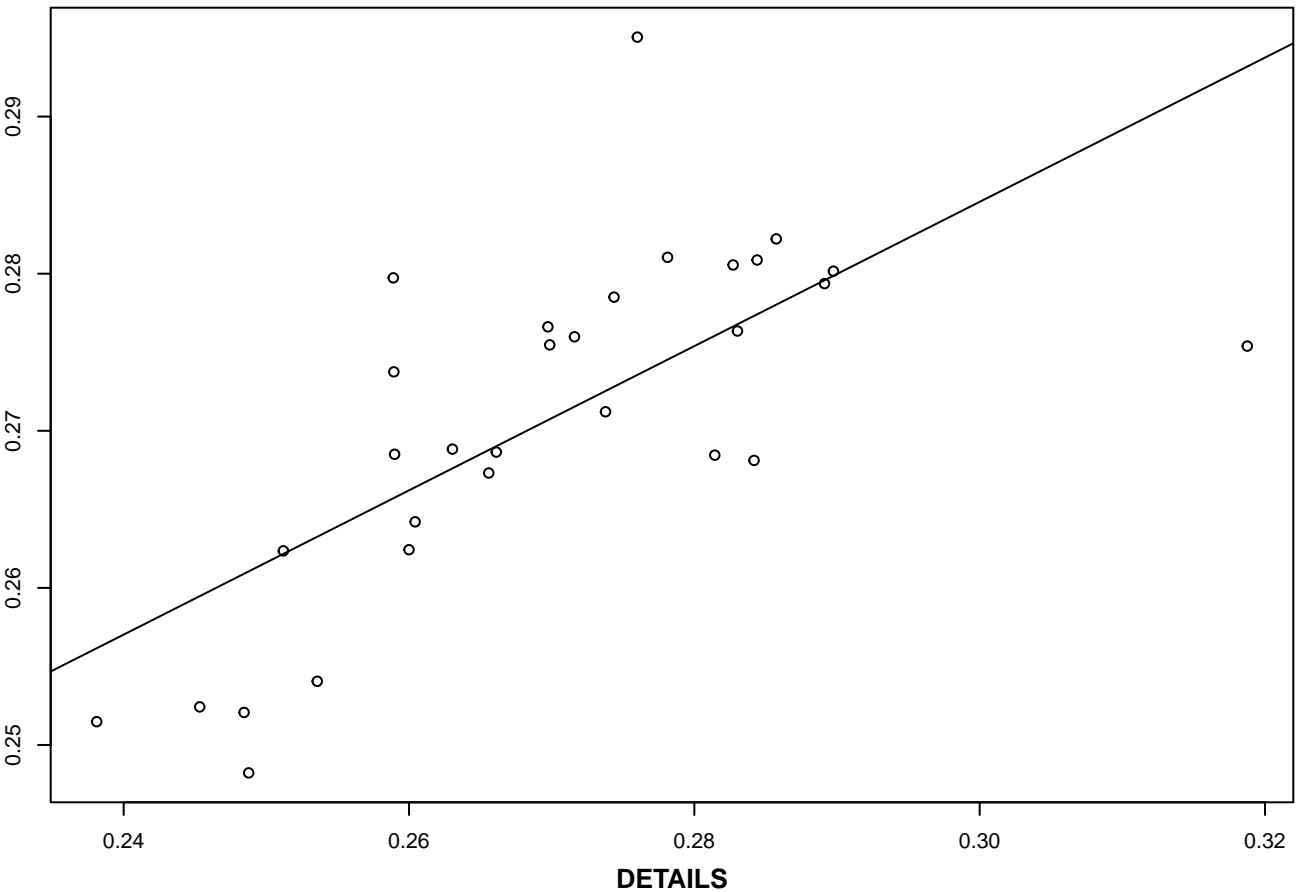
0.006

**NMAE**

4.9 %

**R<sup>2</sup>**

0.341

**RMSE**

0.012

**NRMSE**

4.4 %

**MAE**

0.008

**NMAE**

3.1 %

**R<sup>2</sup>**

0.488