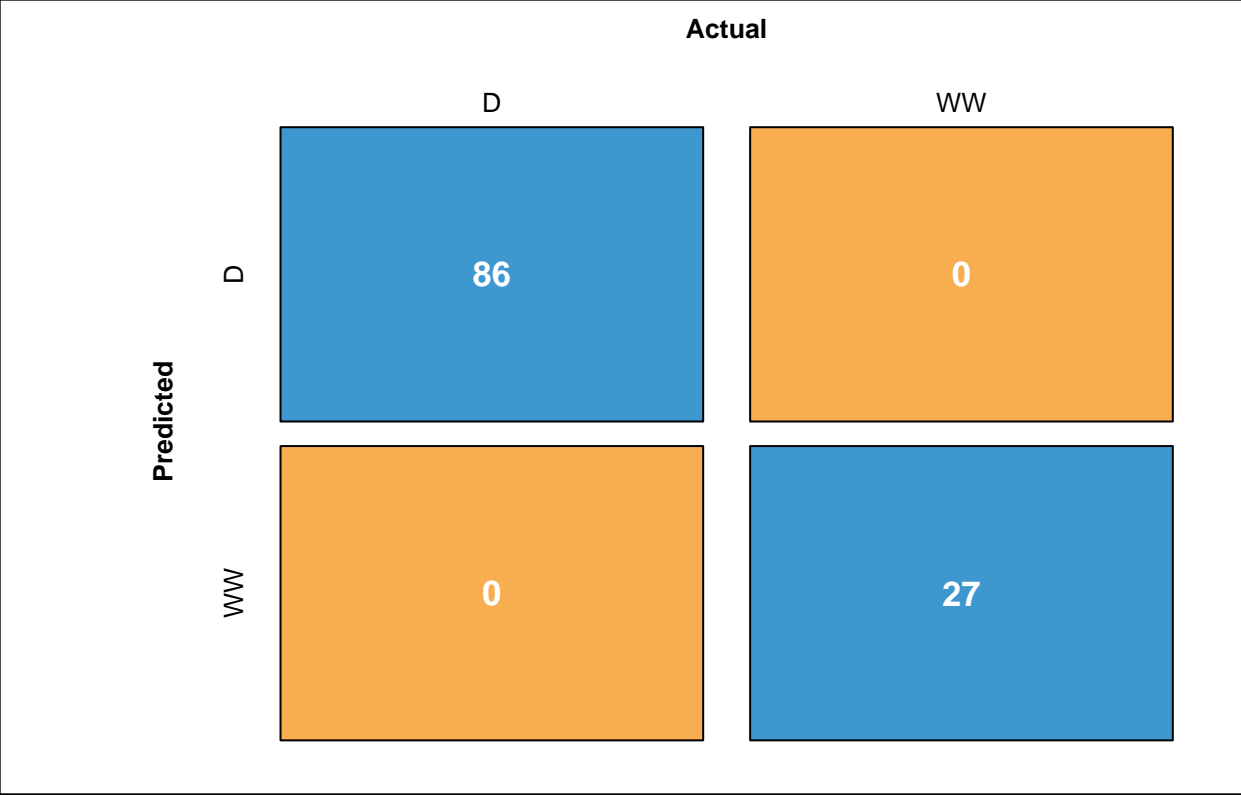


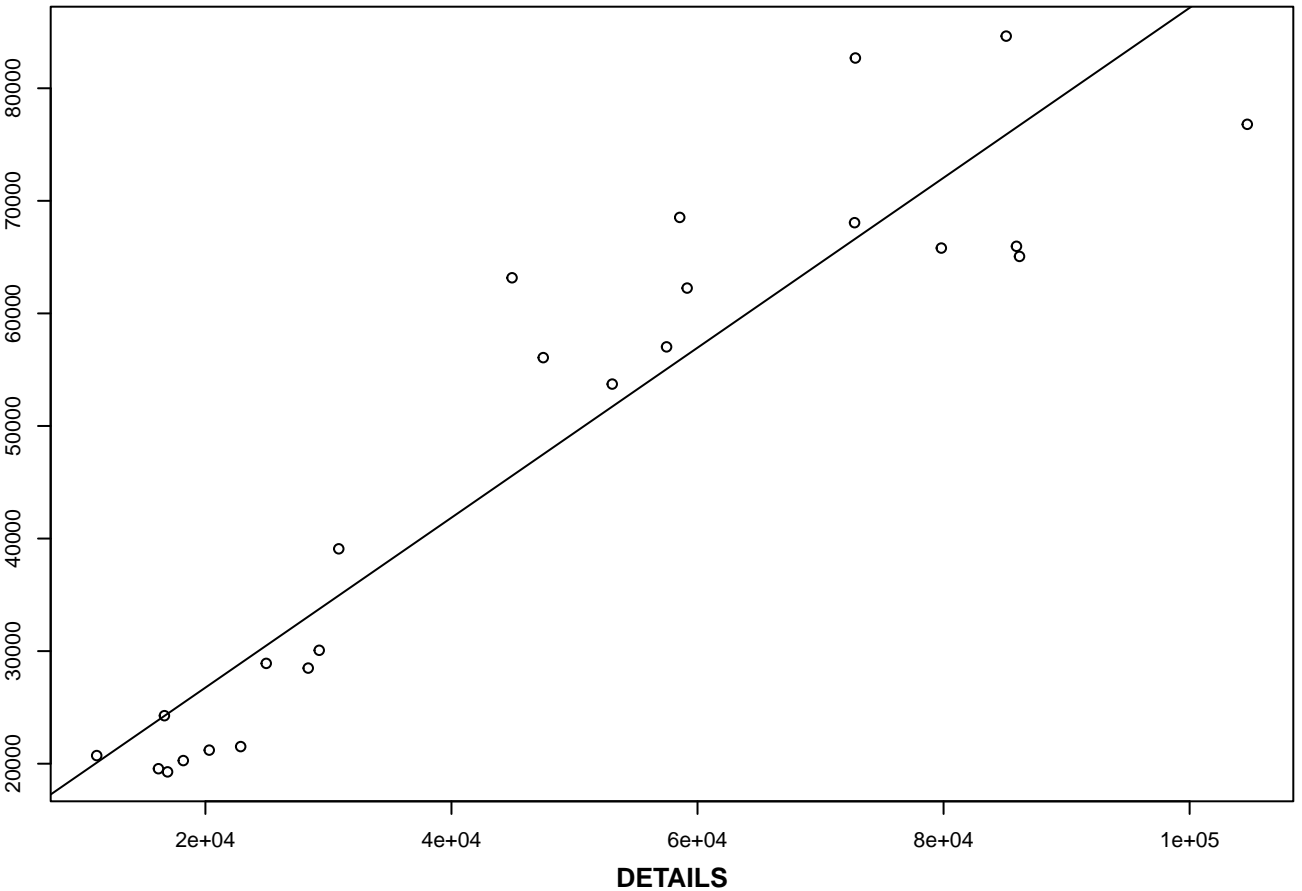
# CONFUSION MATRIX



## 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**

10629.894

**NRMSE**

22.3 %

**MAE**

7475.126

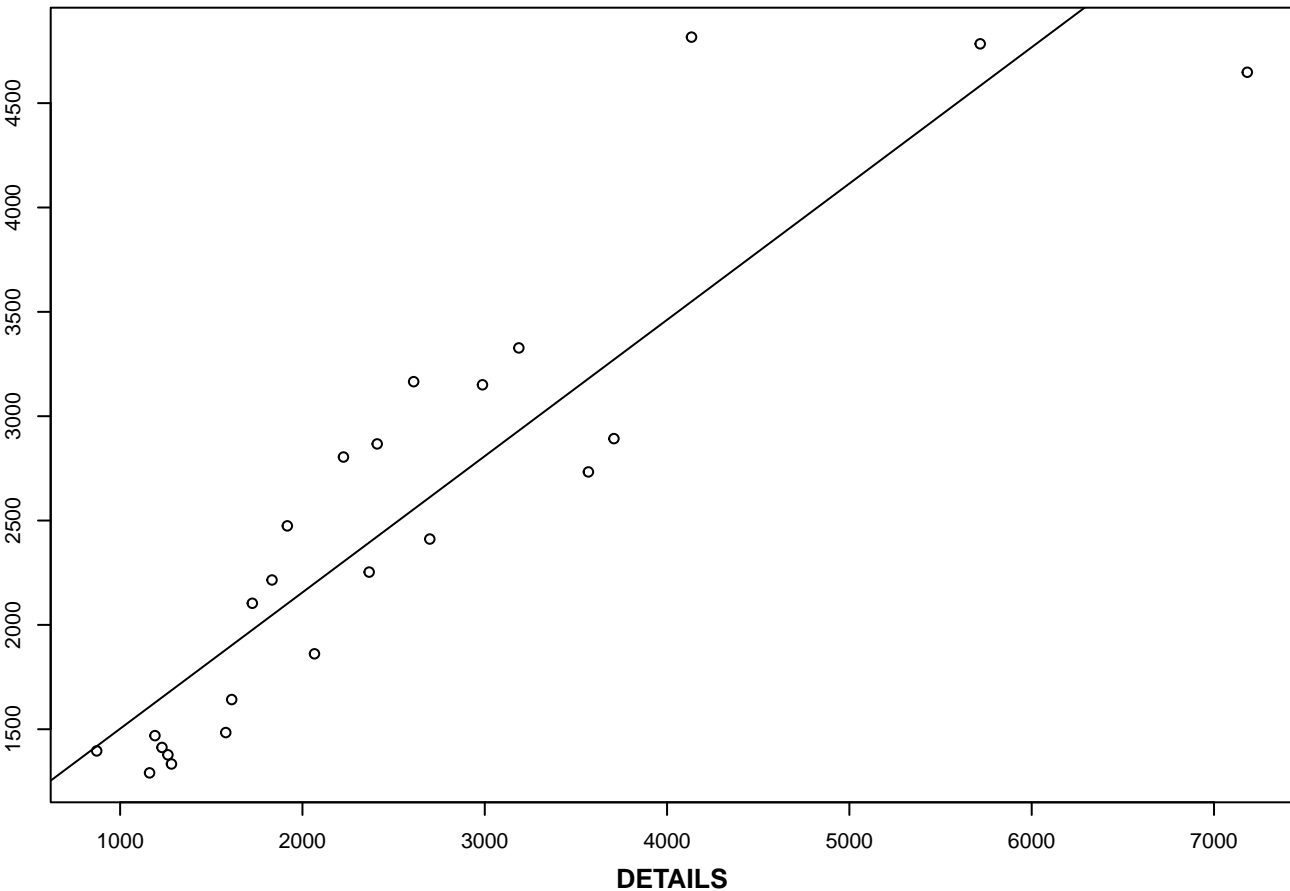
**NMAE**

15.7 %

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

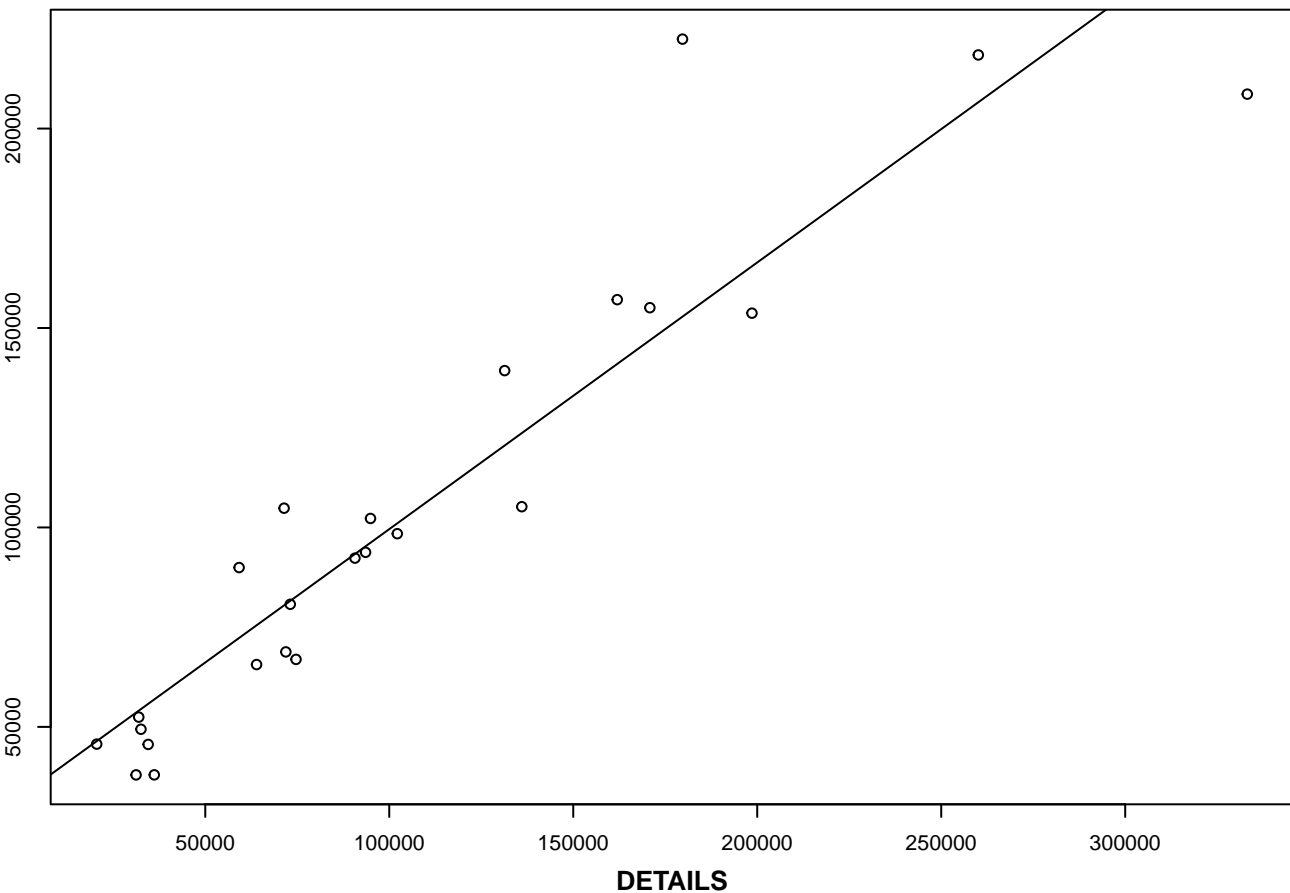
0.866

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



RMSE	NRMSE	MAE	NMAE
682.819	27.1 %	459.526	18.2 %
R^2			
0.821			

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



**RMSE**

33004.079

**NRMSE**

31 %

**MAE**

20530.222

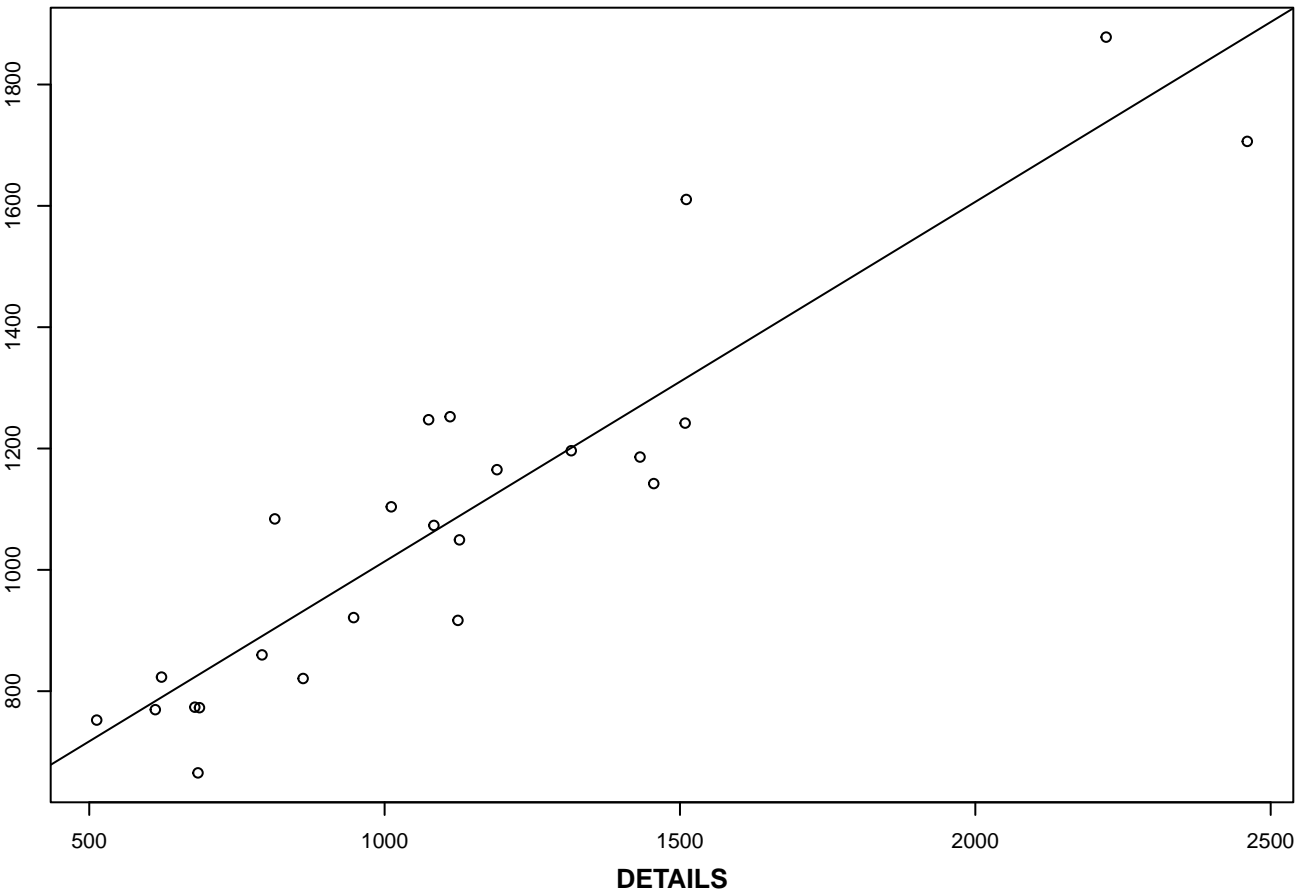
**NMAE**

19.3 %

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

0.857

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



**RMSE**

229.904

**NRMSE**

20.6 %

**MAE**

169.735

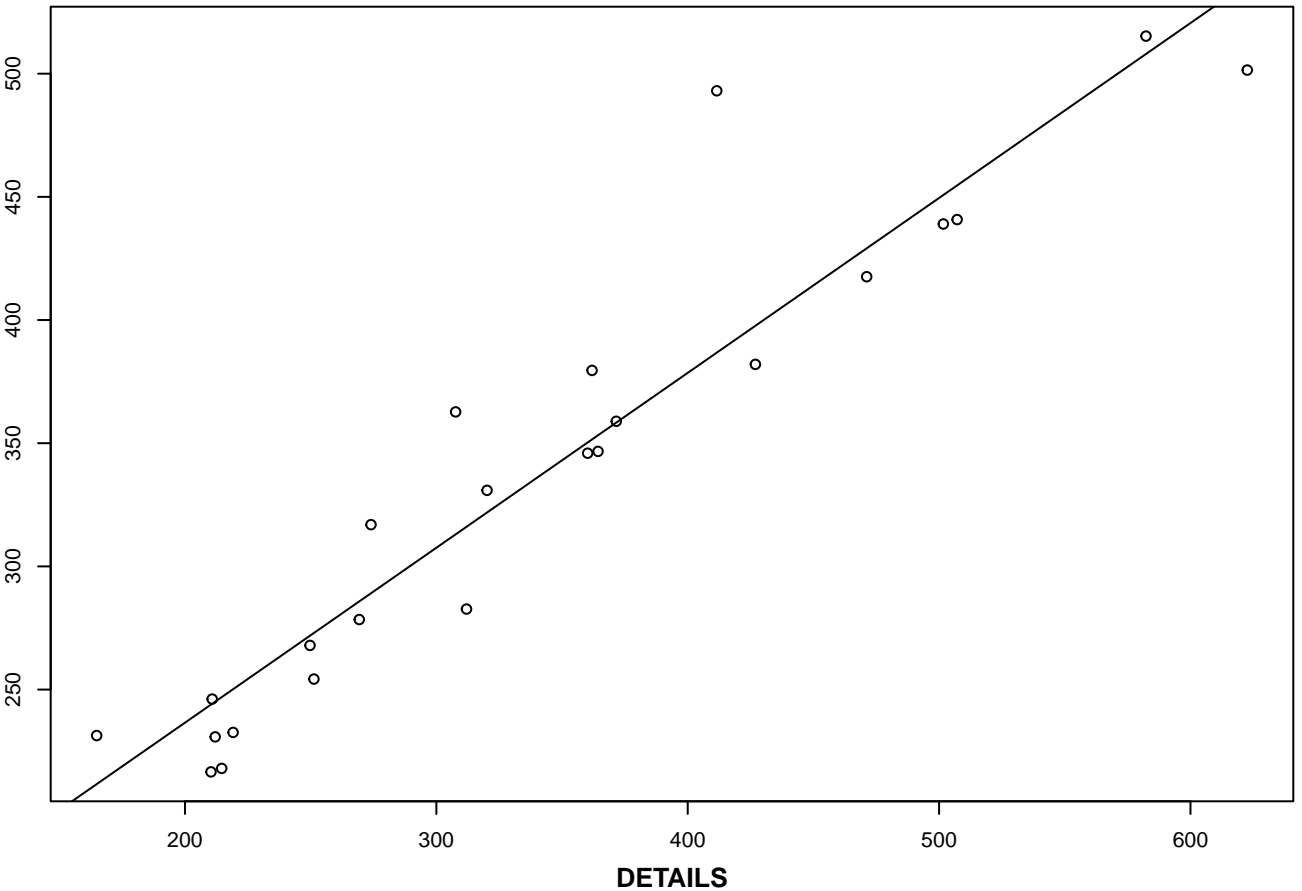
**NMAE**

15.2 %

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

0.84

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



**RMSE**

46.794

**NRMSE**

13.7 %

**MAE**

36.311

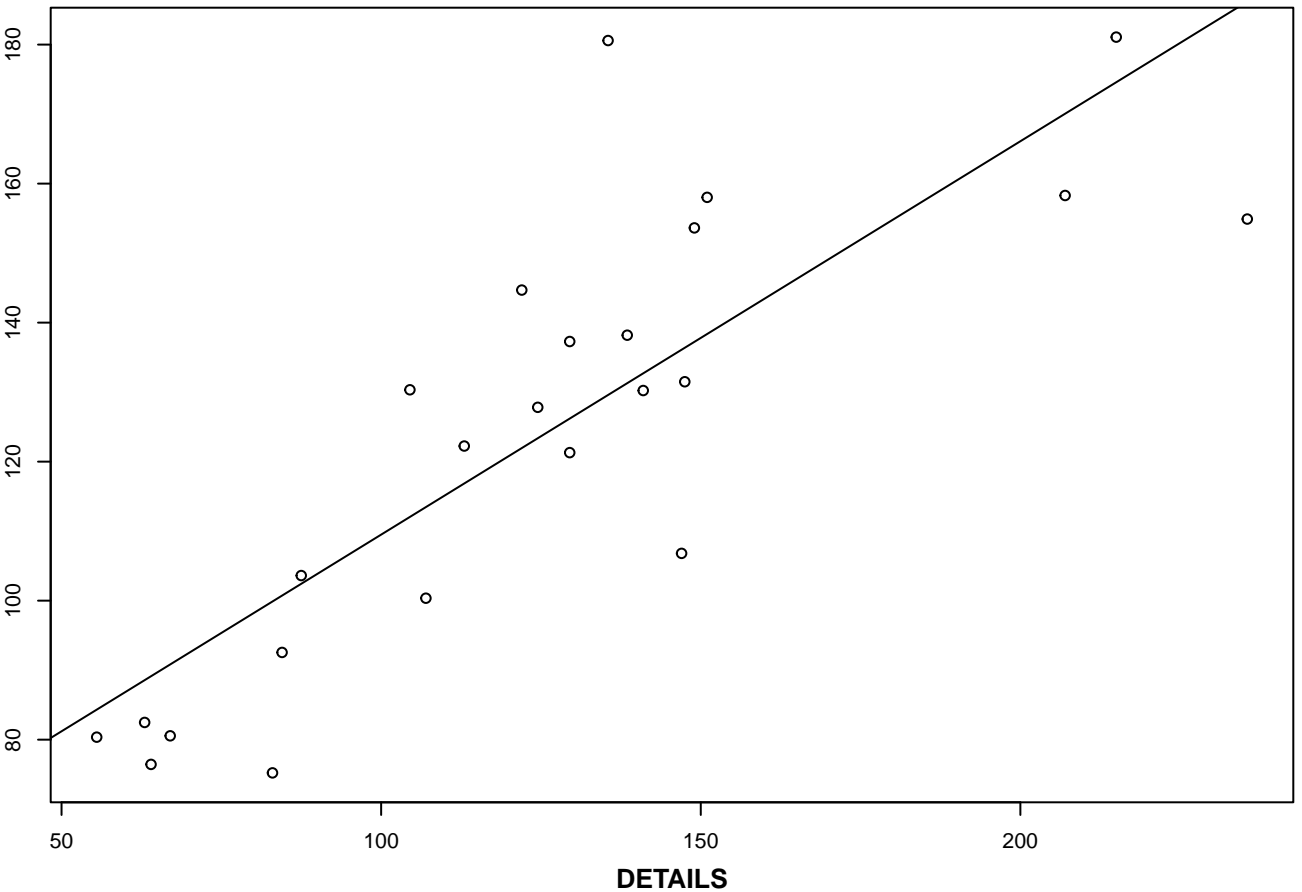
**NMAE**

10.6 %

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

0.895

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



**RMSE**

26.835

**NRMSE**

21.5 %

**MAE**

19.718

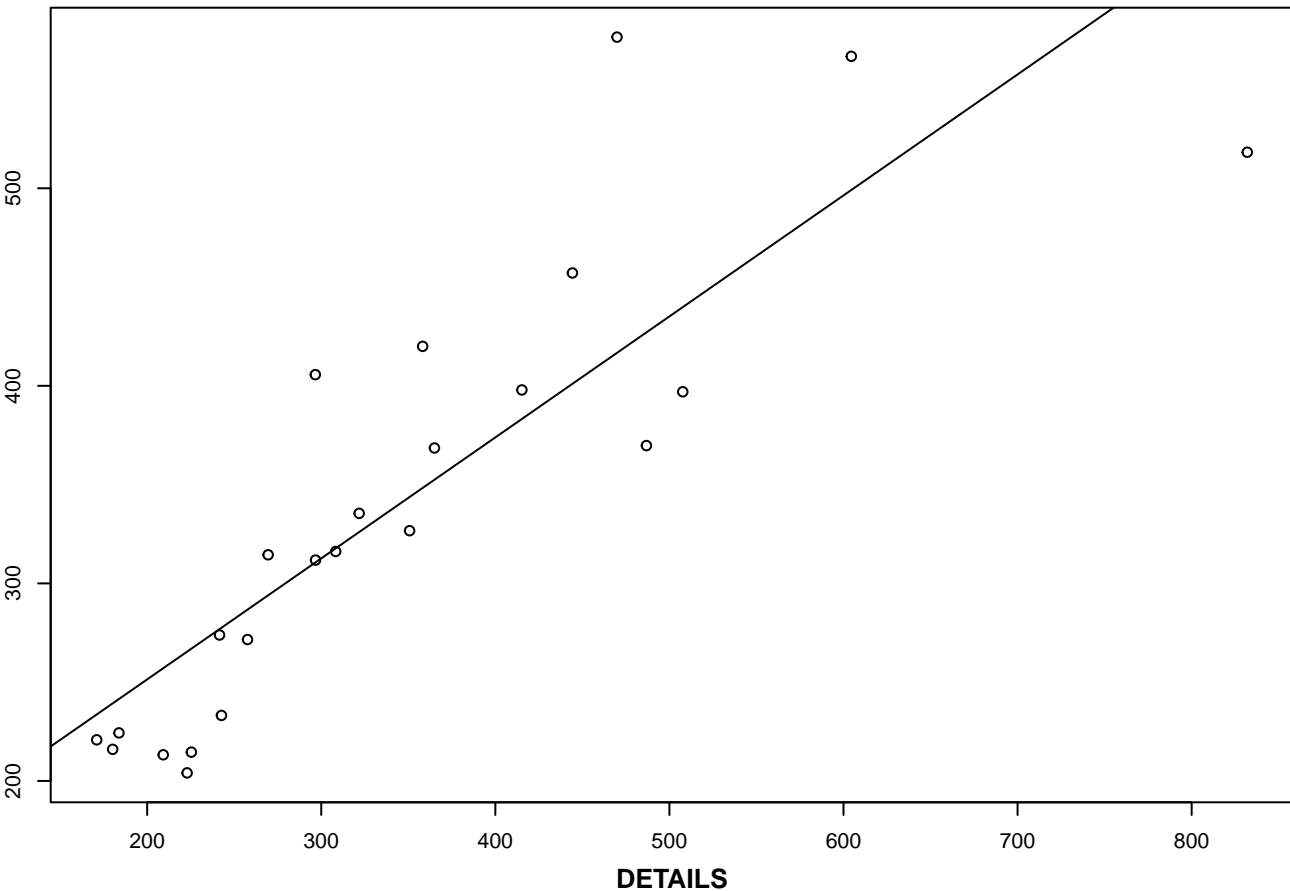
**NMAE**

15.8 %

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

0.685

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



**RMSE**

82.573

**NRMSE**

24 %

**MAE**

50.477

**NMAE**

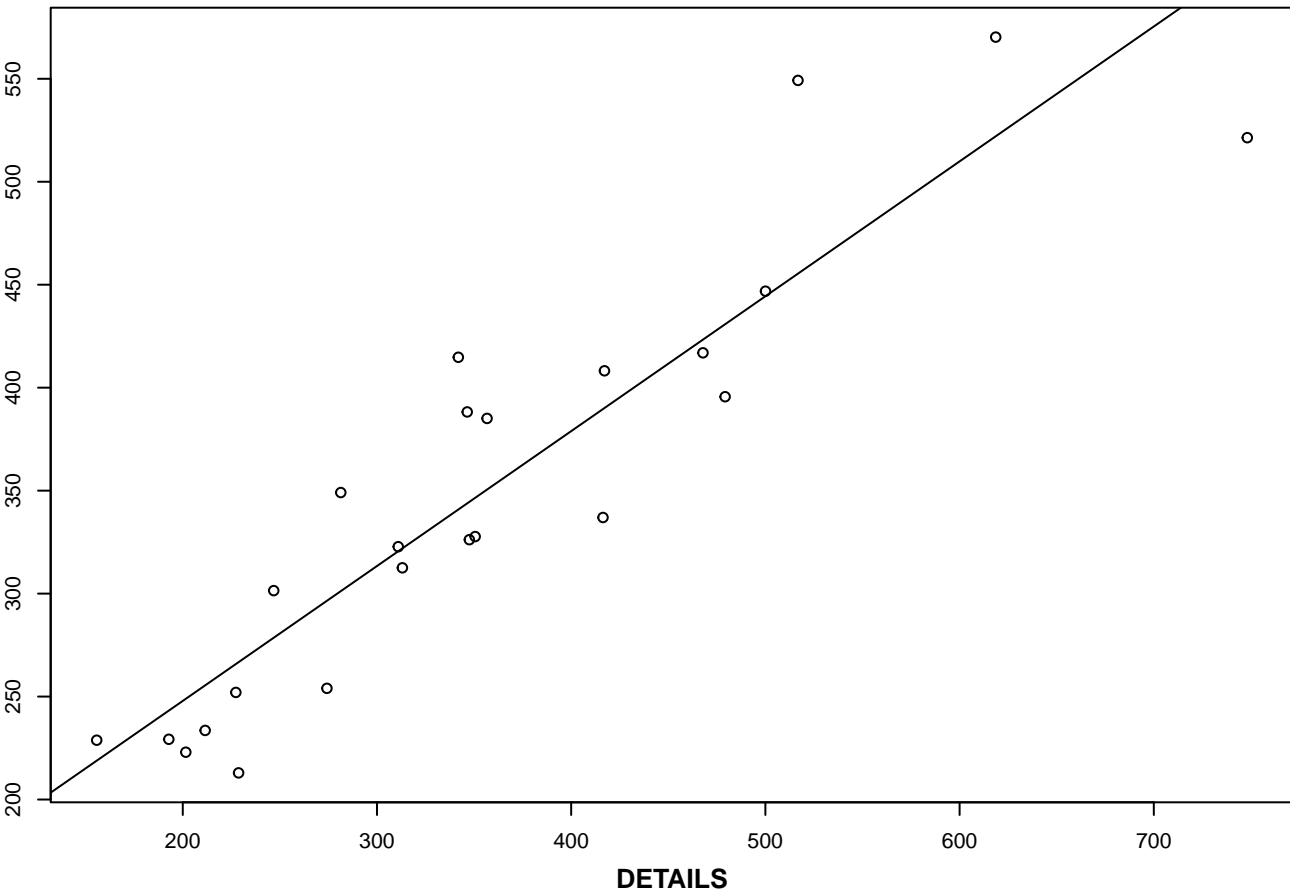
14.7 %

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

0.722



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



**RMSE**

64.241

**NRMSE**

18 %

**MAE**

46.641

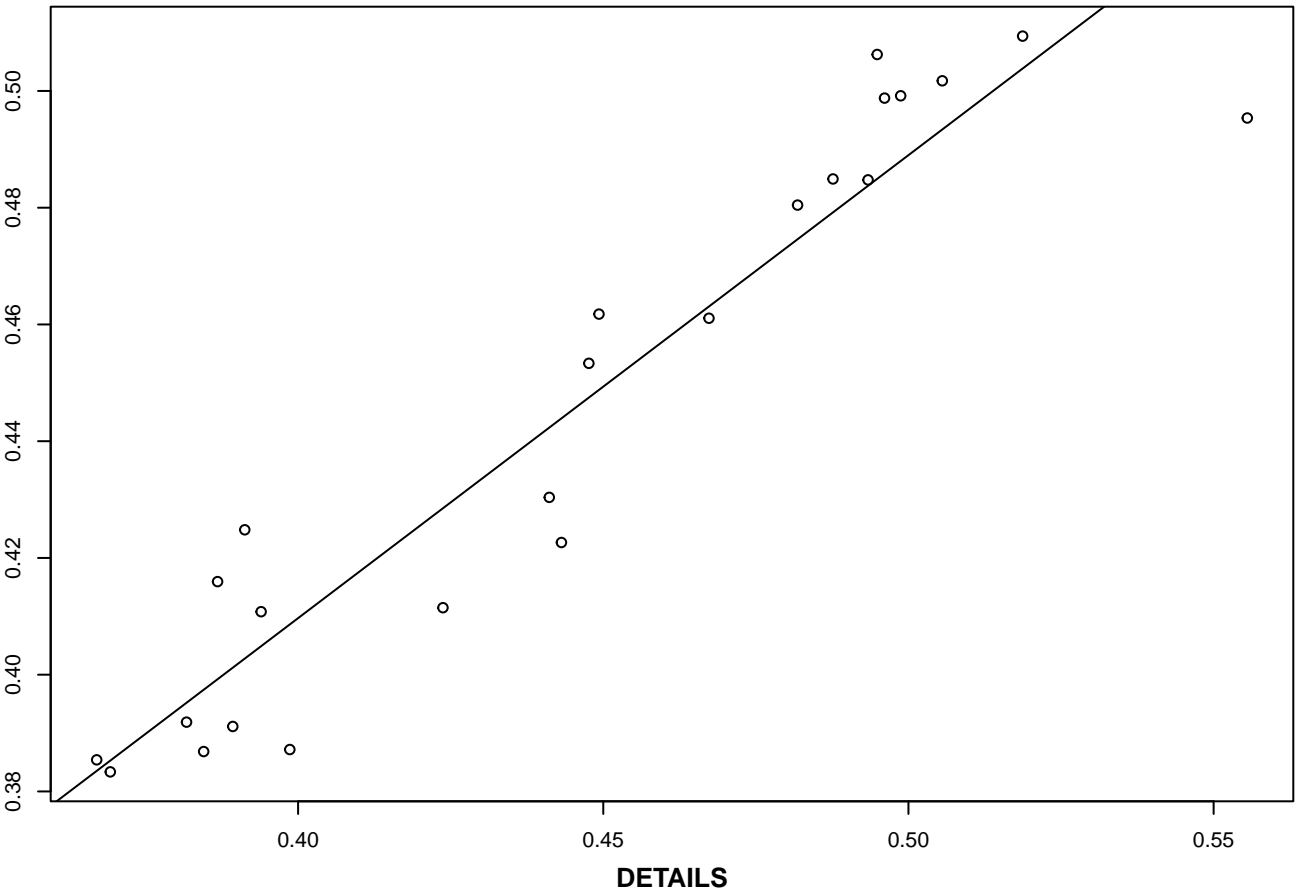
**NMAE**

13.1 %

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

0.832

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



**RMSE**

0.018

**NRMSE**

4.1 %

**MAE**

0.013

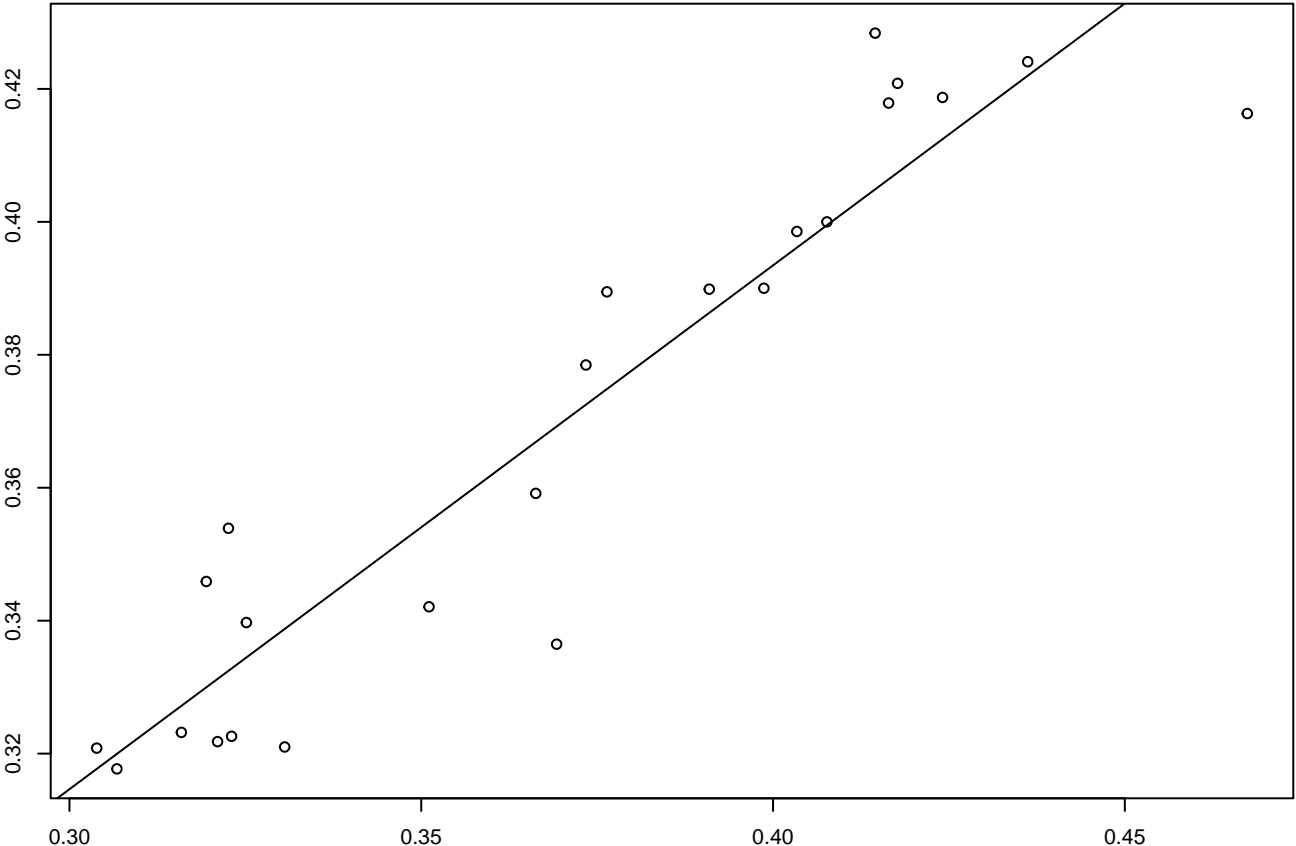
**NMAE**

2.9 %

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

0.899

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



DETAILS

**RMSE**

0.017

**NRMSE**

4.6 %

**MAE**

0.012

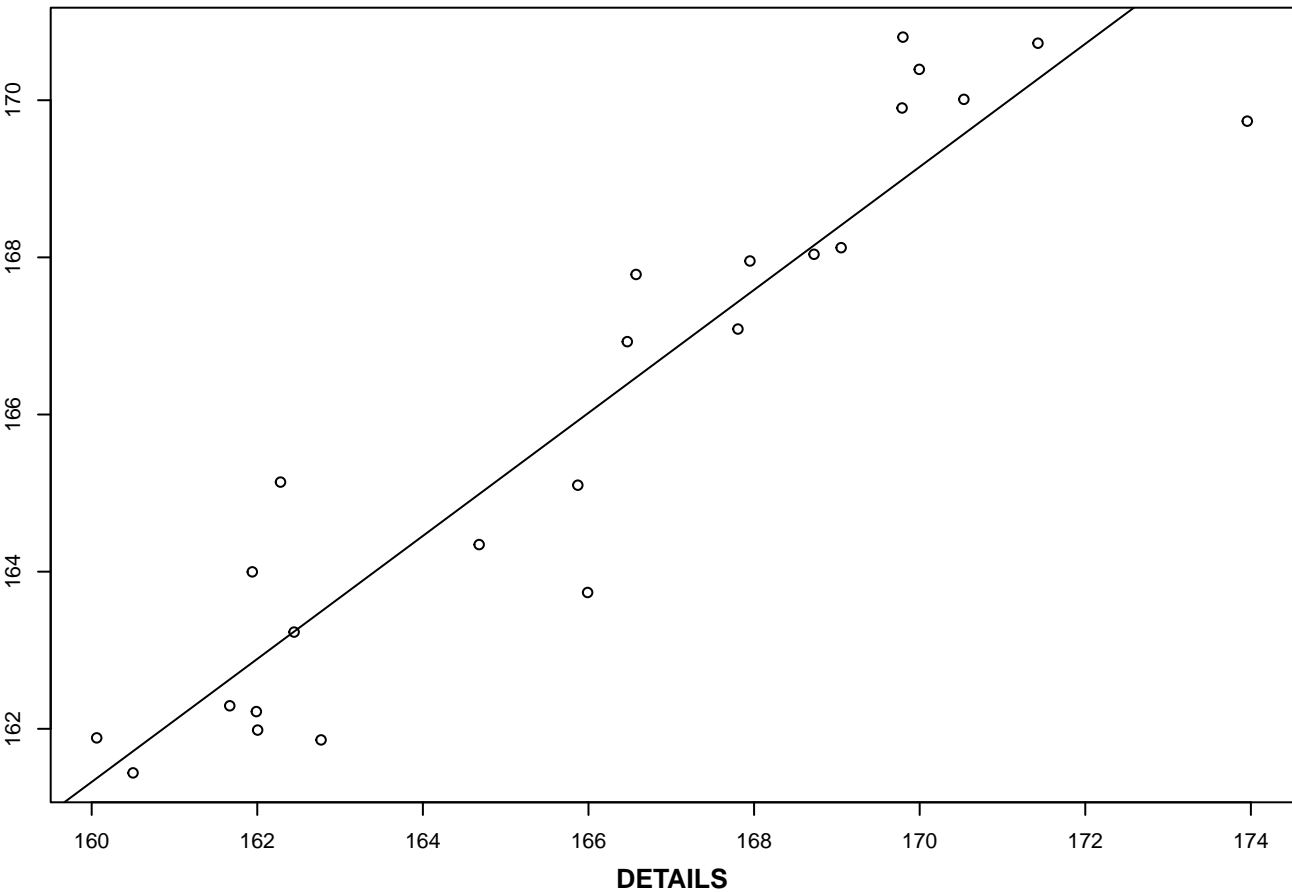
**NMAE**

3.3 %

**R^2**

0.873

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



**RMSE**

1.408

**NRMSE**

0.8 %

**MAE**

1.024

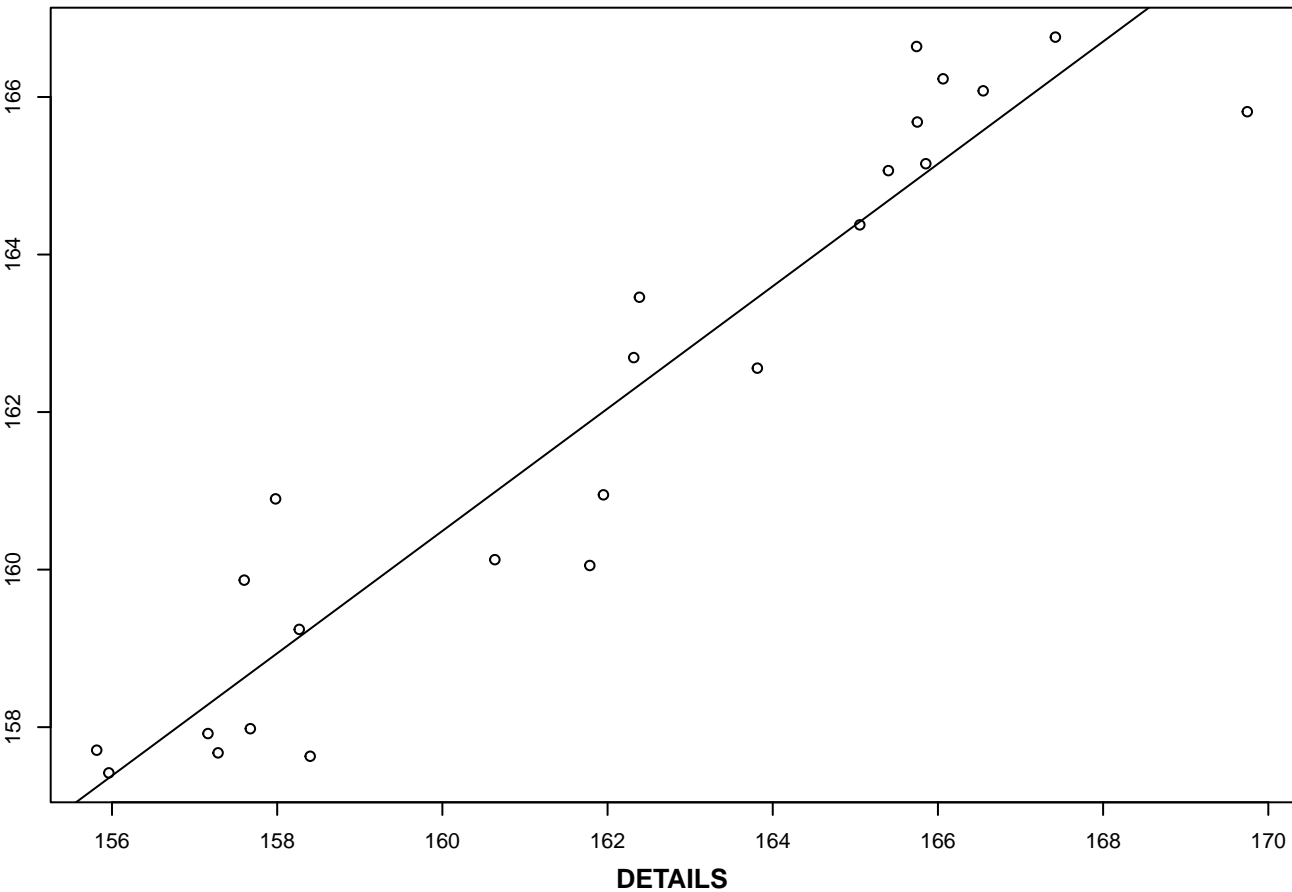
**NMAE**

0.6 %

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

0.875

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



**RMSE**

1.397

**NRMSE**

0.9 %

**MAE**

1.066

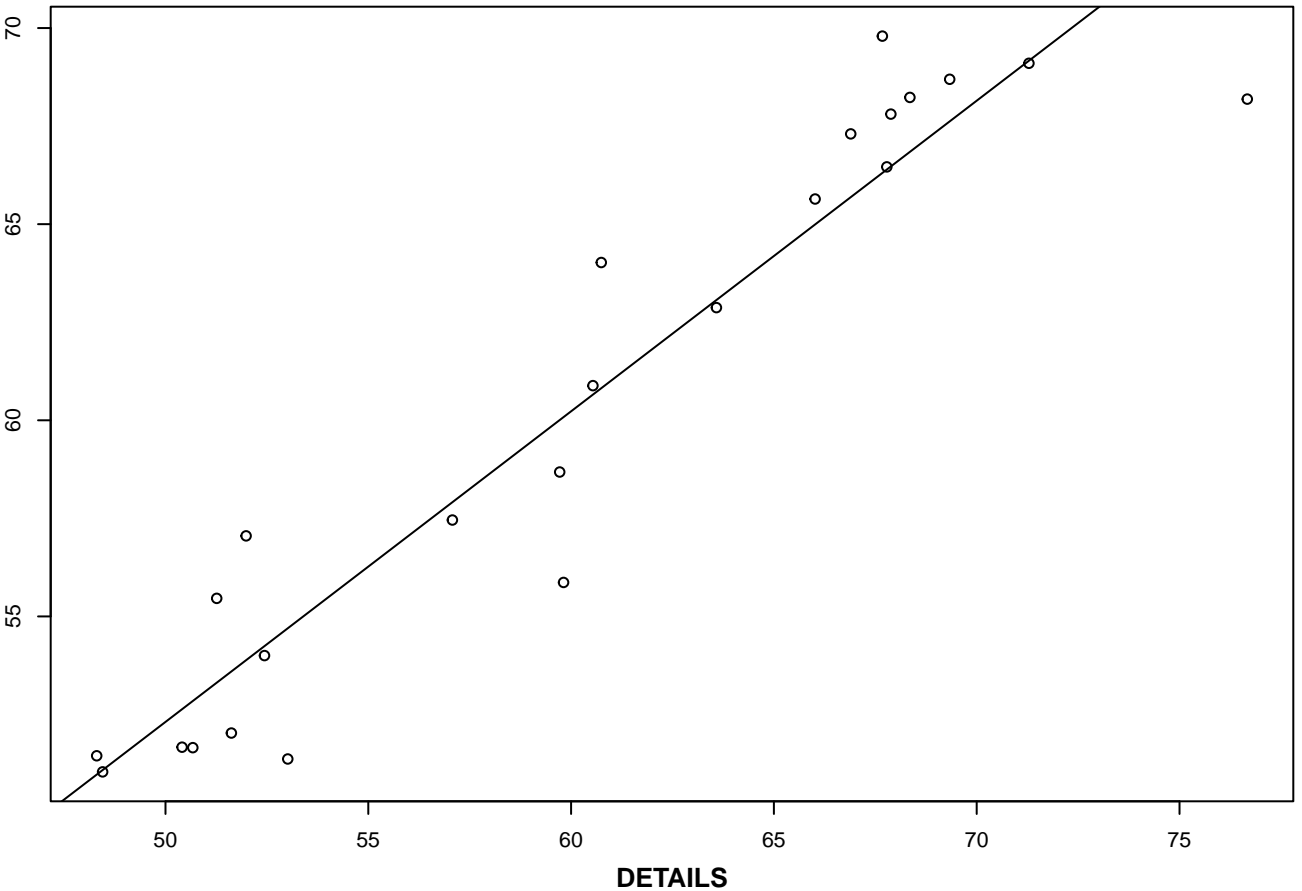
**NMAE**

0.7 %

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

0.899

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



**RMSE**

2.736

**NRMSE**

4.6 %

**MAE**

1.929

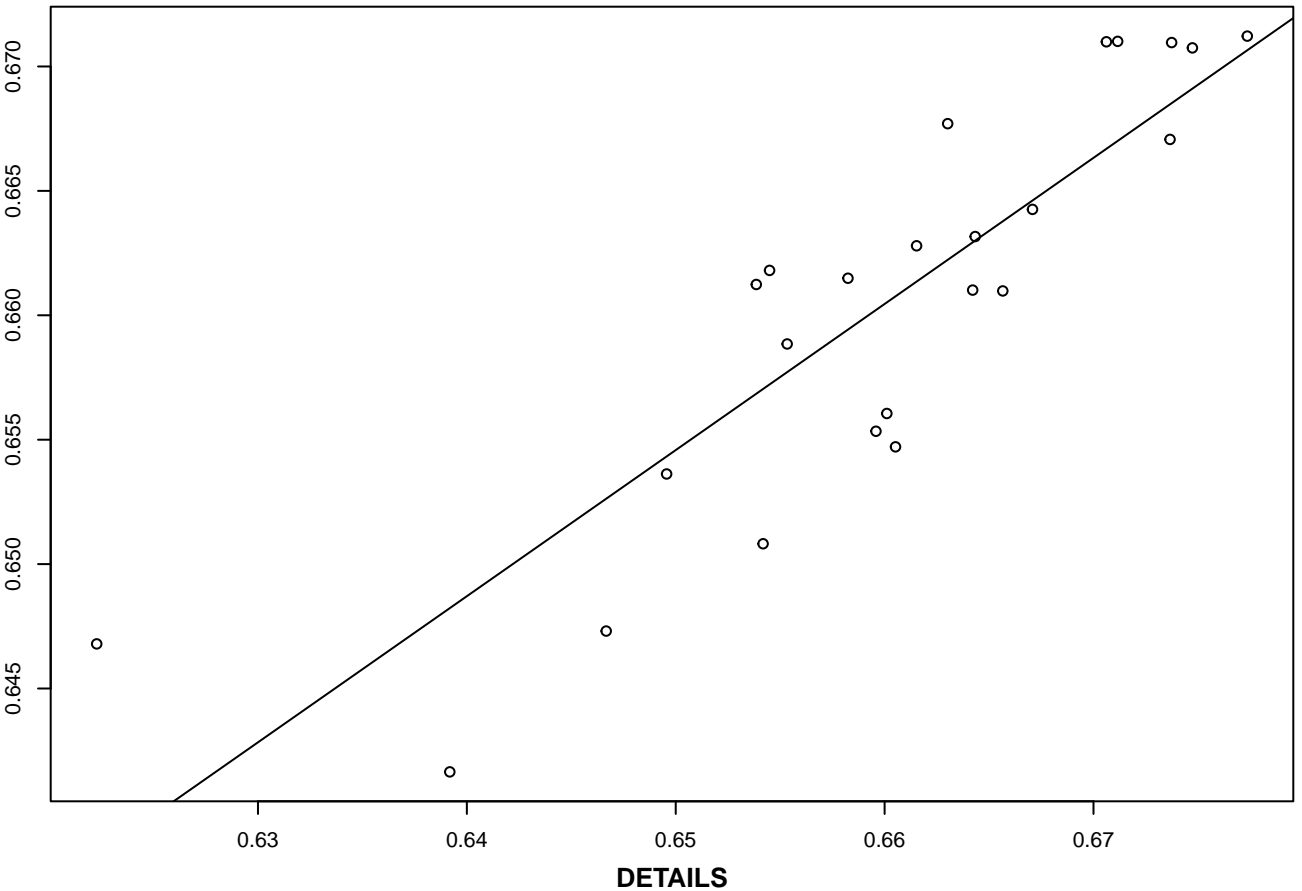
**NMAE**

3.2 %

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

0.903

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



**RMSE**

0.006

**NRMSE**

1 %

**MAE**

0.005

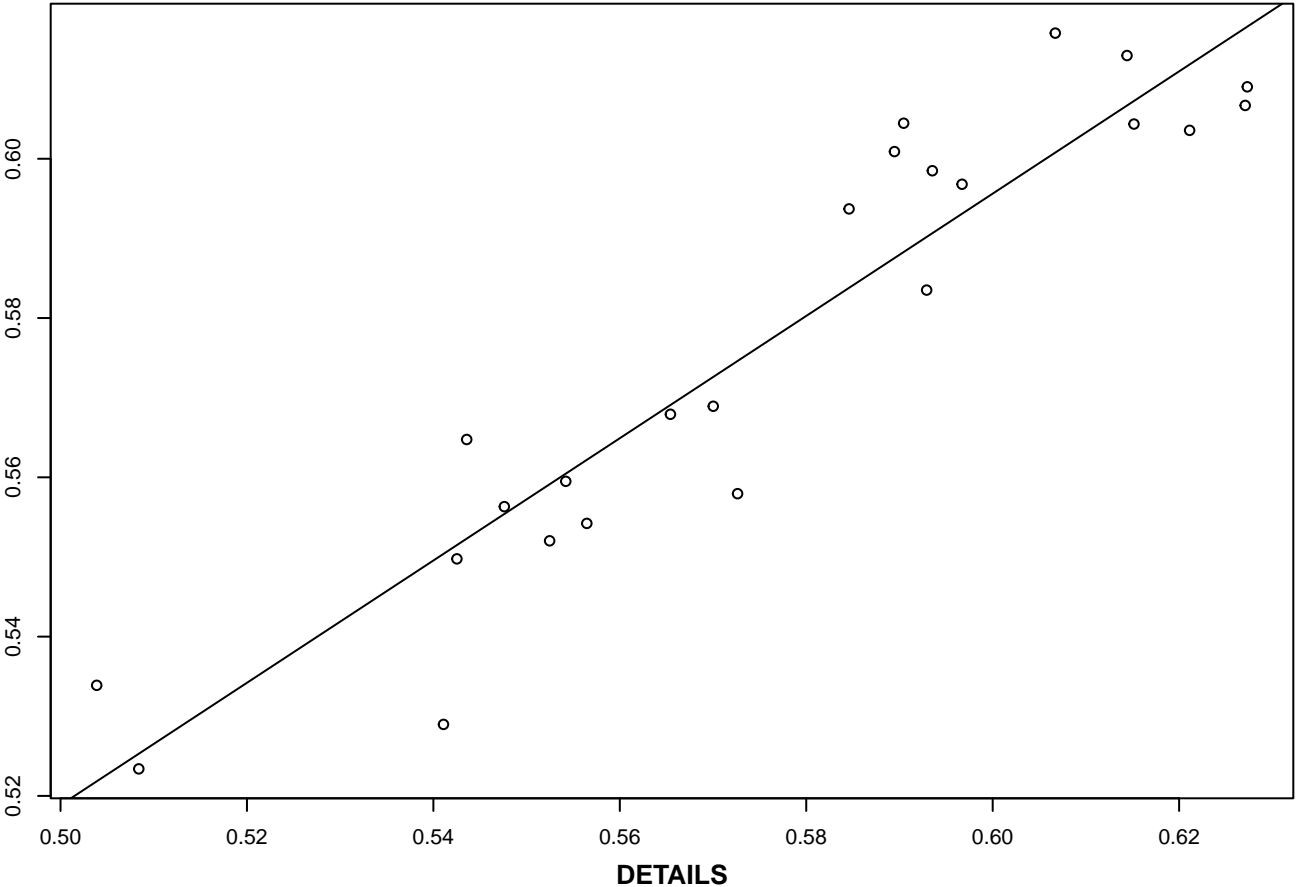
**NMAE**

0.7 %

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

0.754

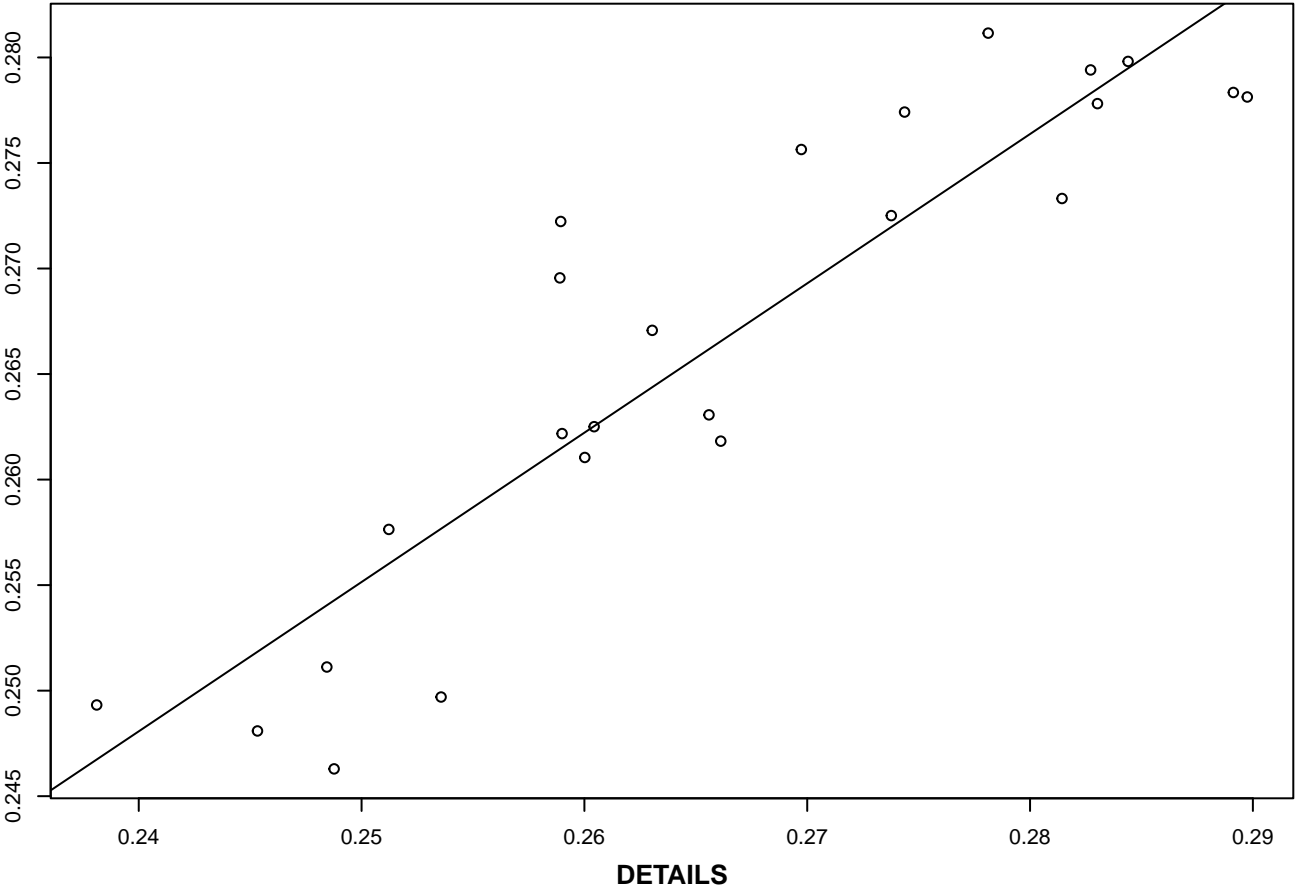
loocv\_genes\_top.intensity.vis.hsv.s.mean.csv



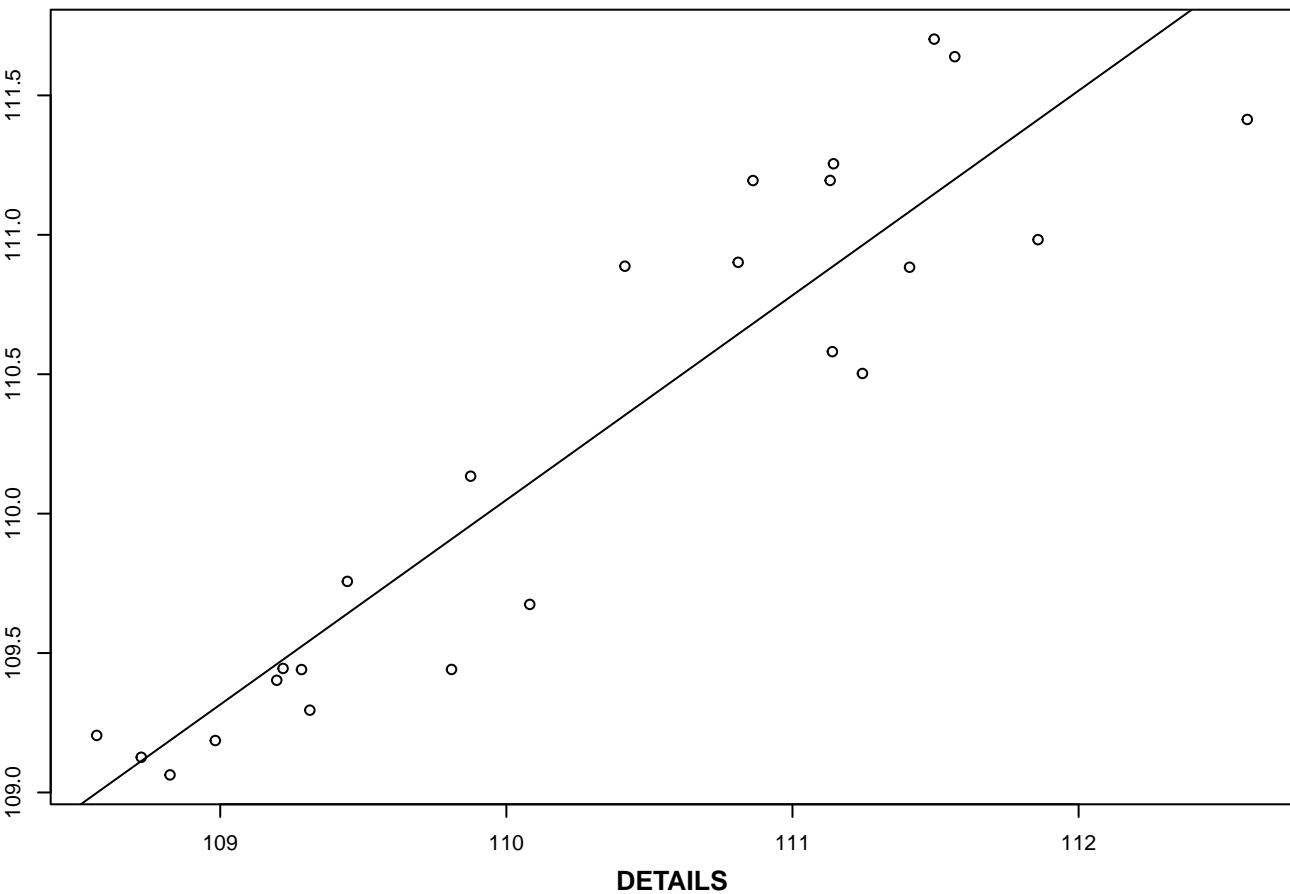
RMSE	NRMSE	MAE	NMAE
0.013	2.2 %	0.01	1.8 %
R^2			
0.877			



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



<b>RMSE</b>	<b>NRMSE</b>	<b>MAE</b>	<b>NMAE</b>
0.006	2.4 %	0.005	2 %
<b>R^2</b>			
0.818			

**RMSE**

0.454

**NRMSE**

0.4 %

**MAE**

0.361

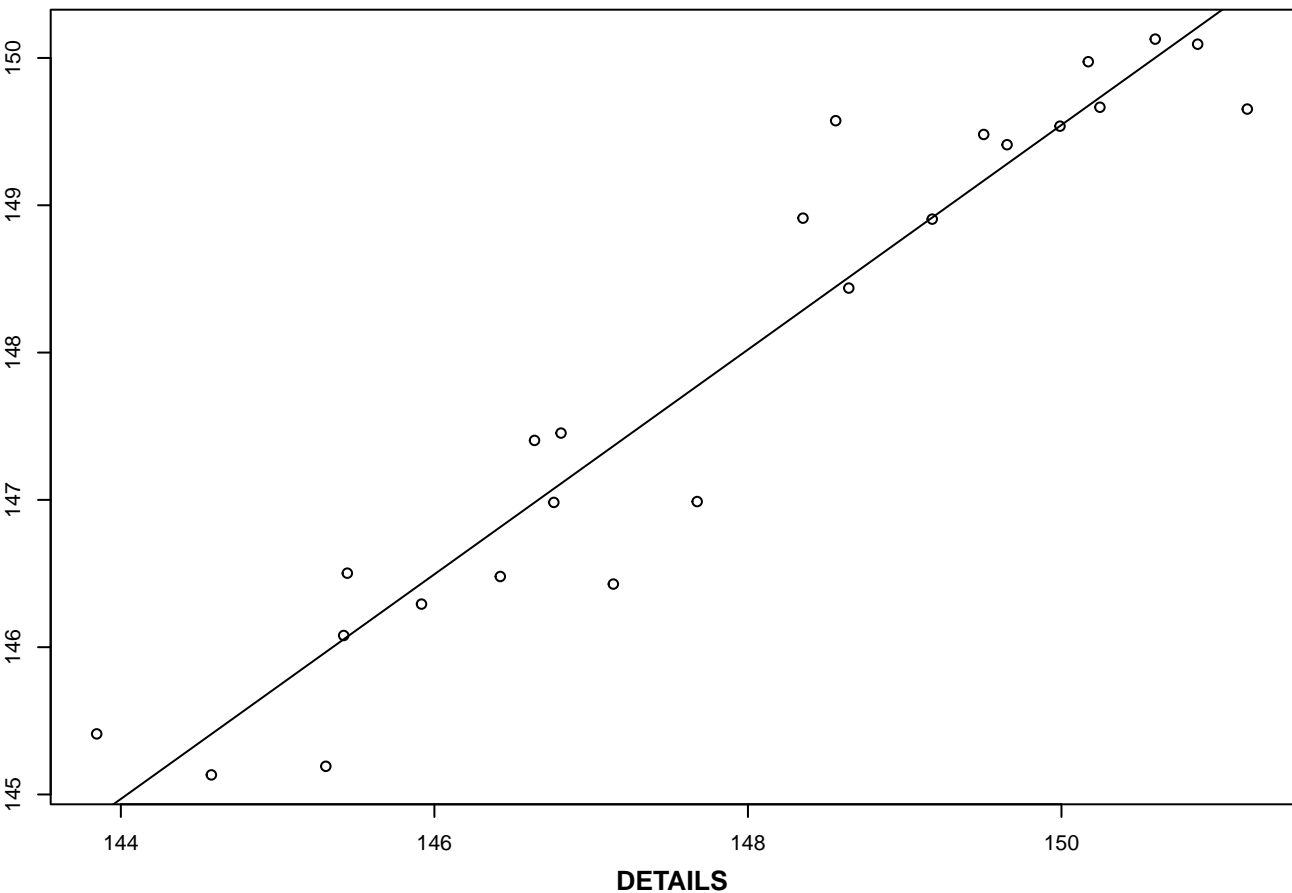
**NMAE**

0.3 %

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

0.856

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



**RMSE**

0.7

**NRMSE**

0.5 %

**MAE**

0.573

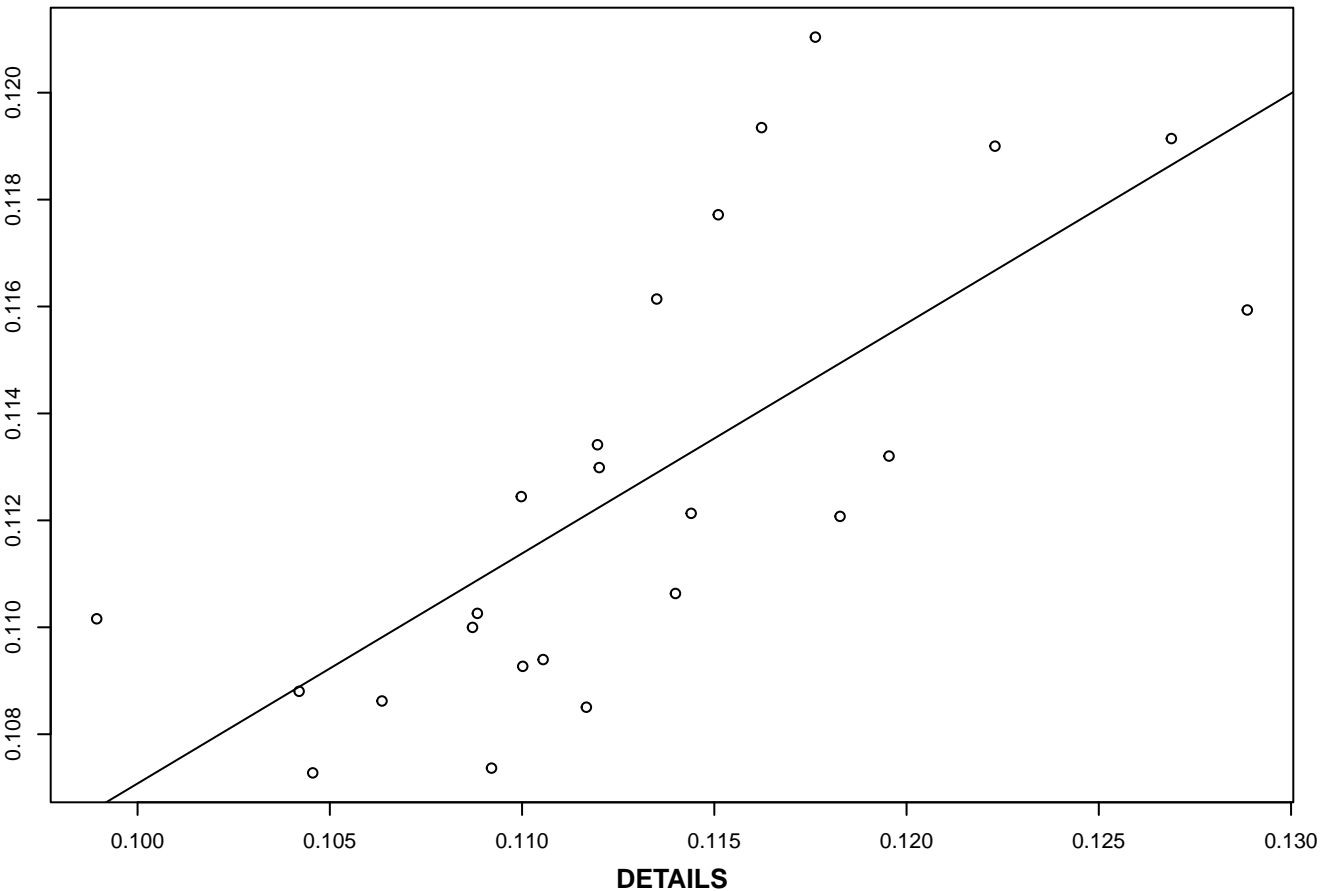
**NMAE**

0.4 %

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

0.917

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



**RMSE**

0.005

**NRMSE**

4.3 %

**MAE**

0.004

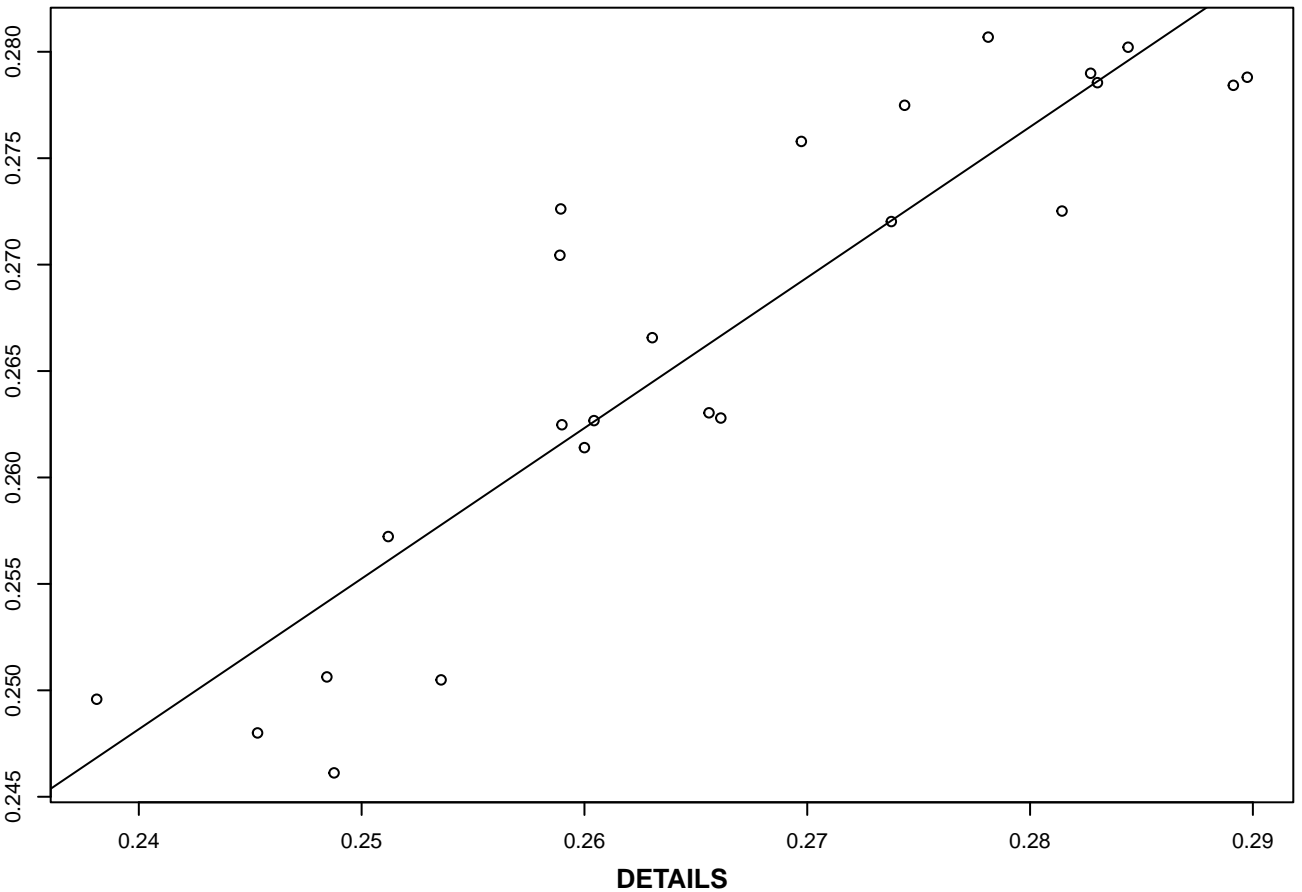
**NMAE**

3.3 %

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

0.516

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



**RMSE**

0.006

**NRMSE**

2.4 %

**MAE**

0.005

**NMAE**

2 %

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

0.817