

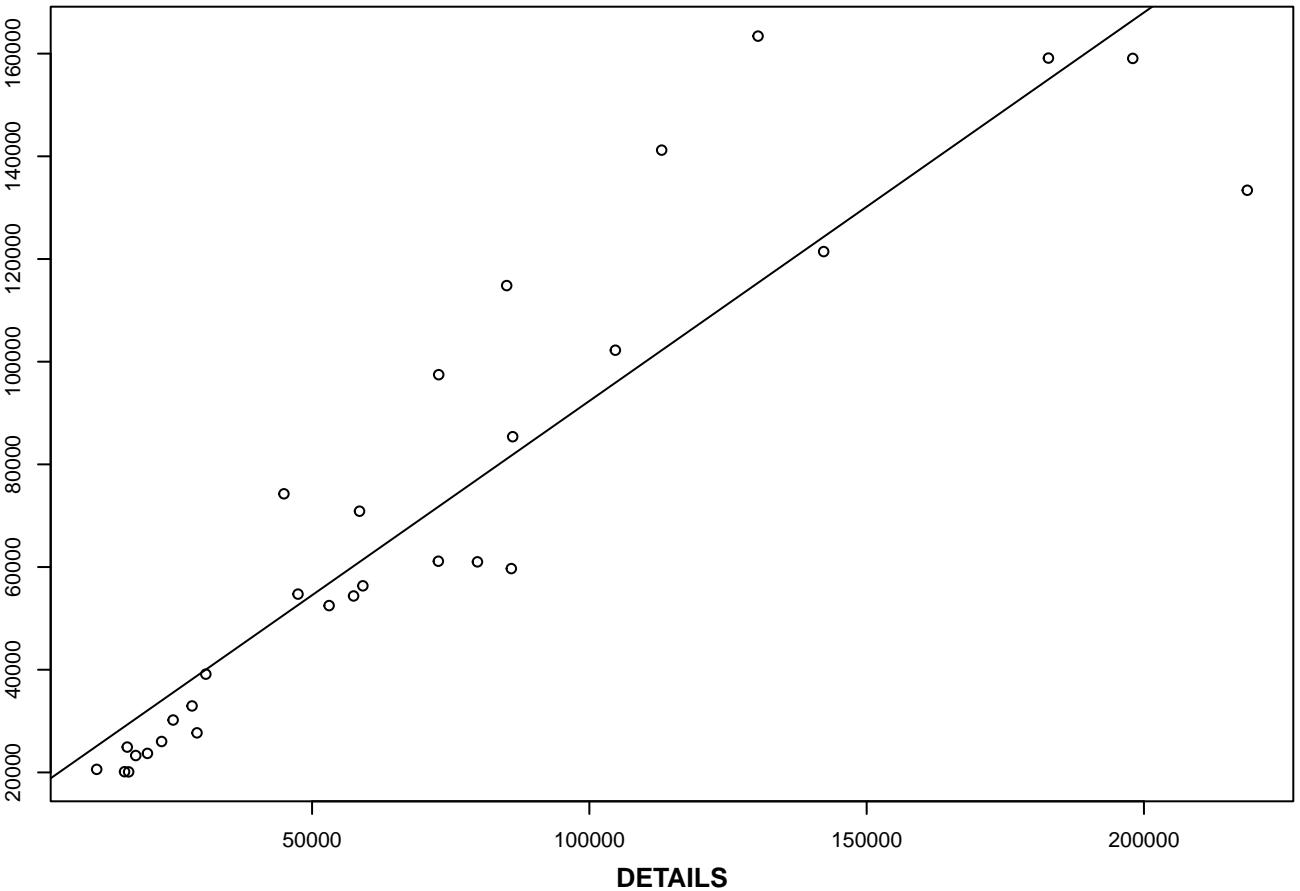
# CONFUSION MATRIX

		Actual	
		D	WW
Predicted	D	86	0
	WW	0	27

## DETAILS

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

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

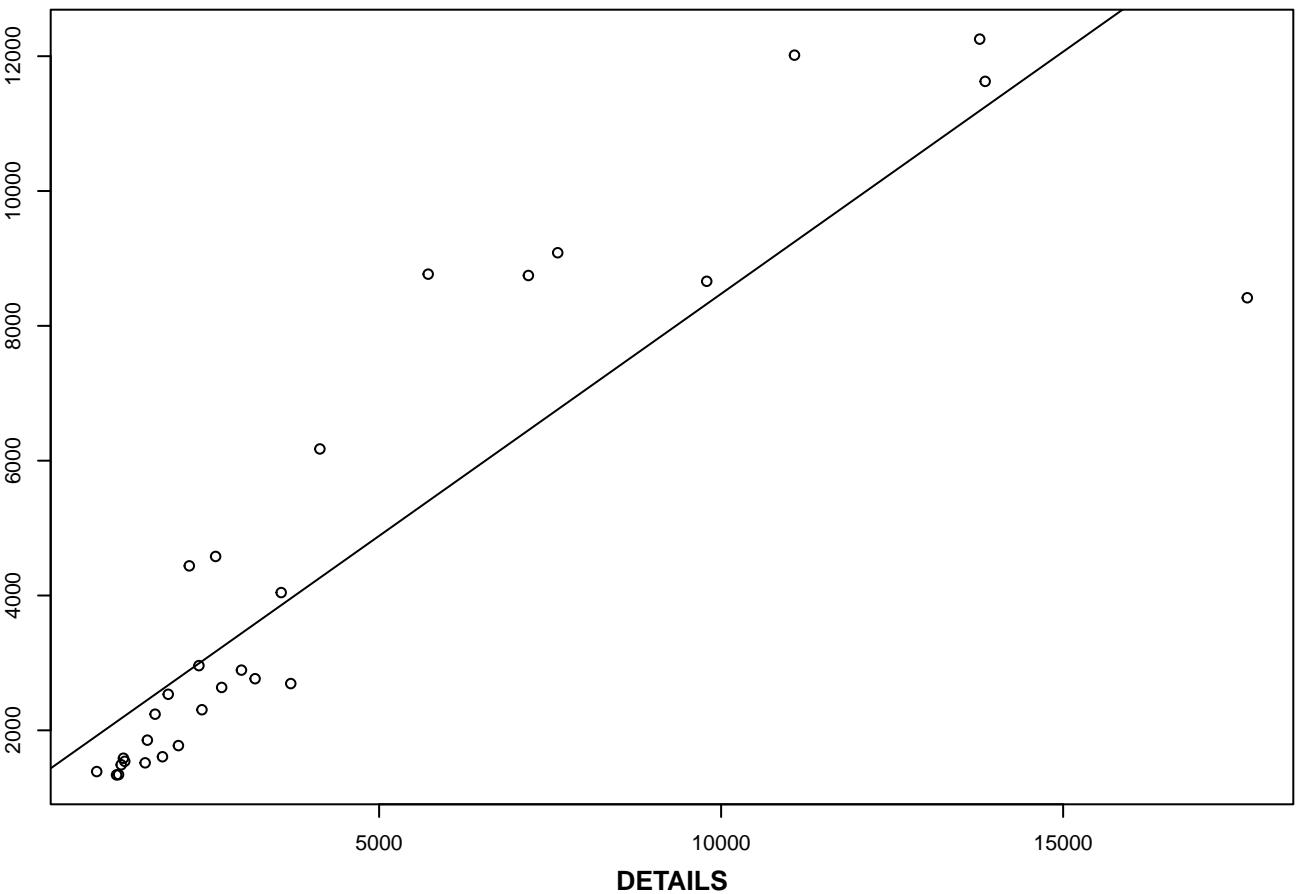


RMSE	NRMSE	MAE	NMAE
22922.958	32.3 %	15188.516	21.4 %

R<sup>2</sup>

0.837

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



**RMSE**  
2046.094

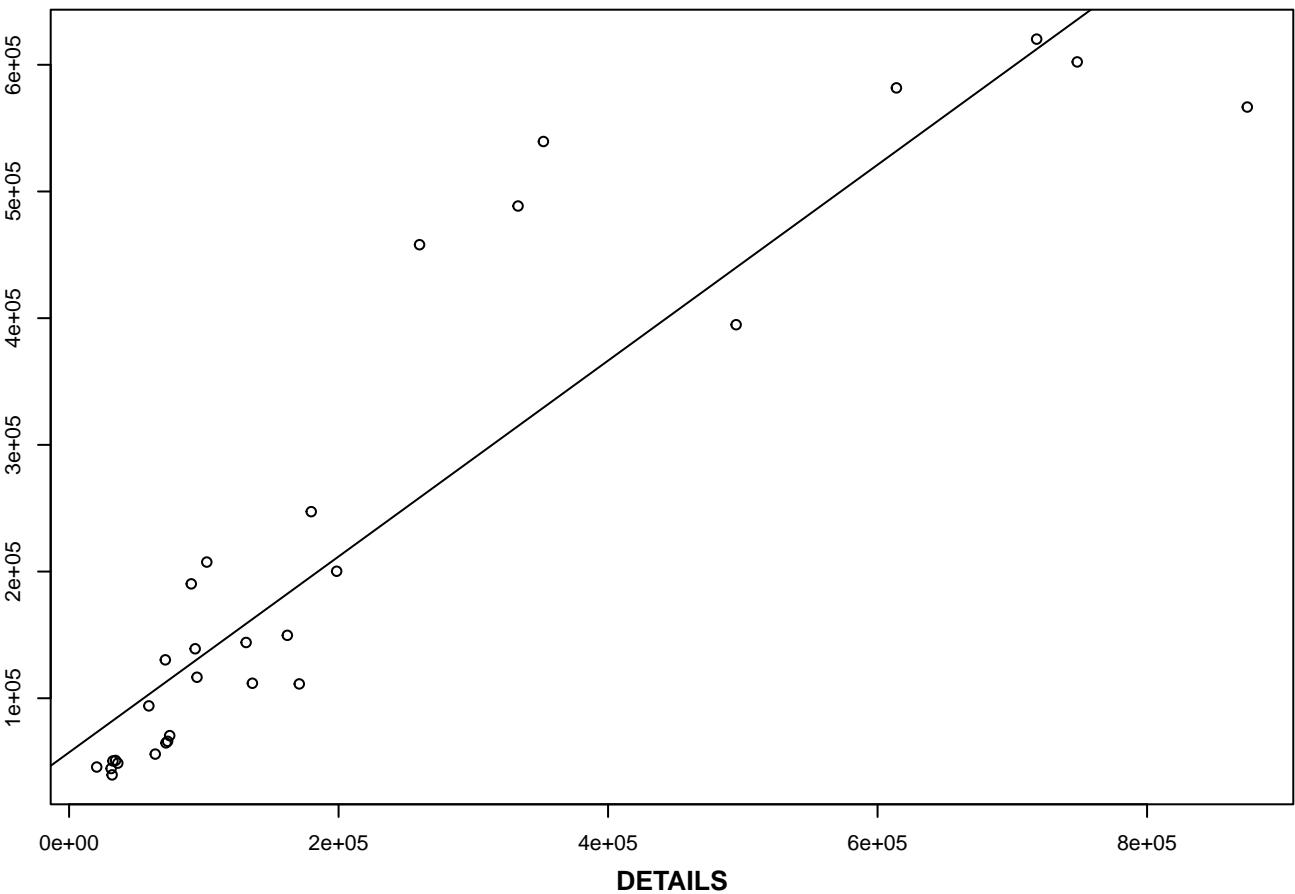
**NRMSE**  
45.7 %

**MAE**  
1127.533

**NMAE**  
25.2 %

**R<sup>2</sup>**  
0.788

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



**RMSE**  
95585.802

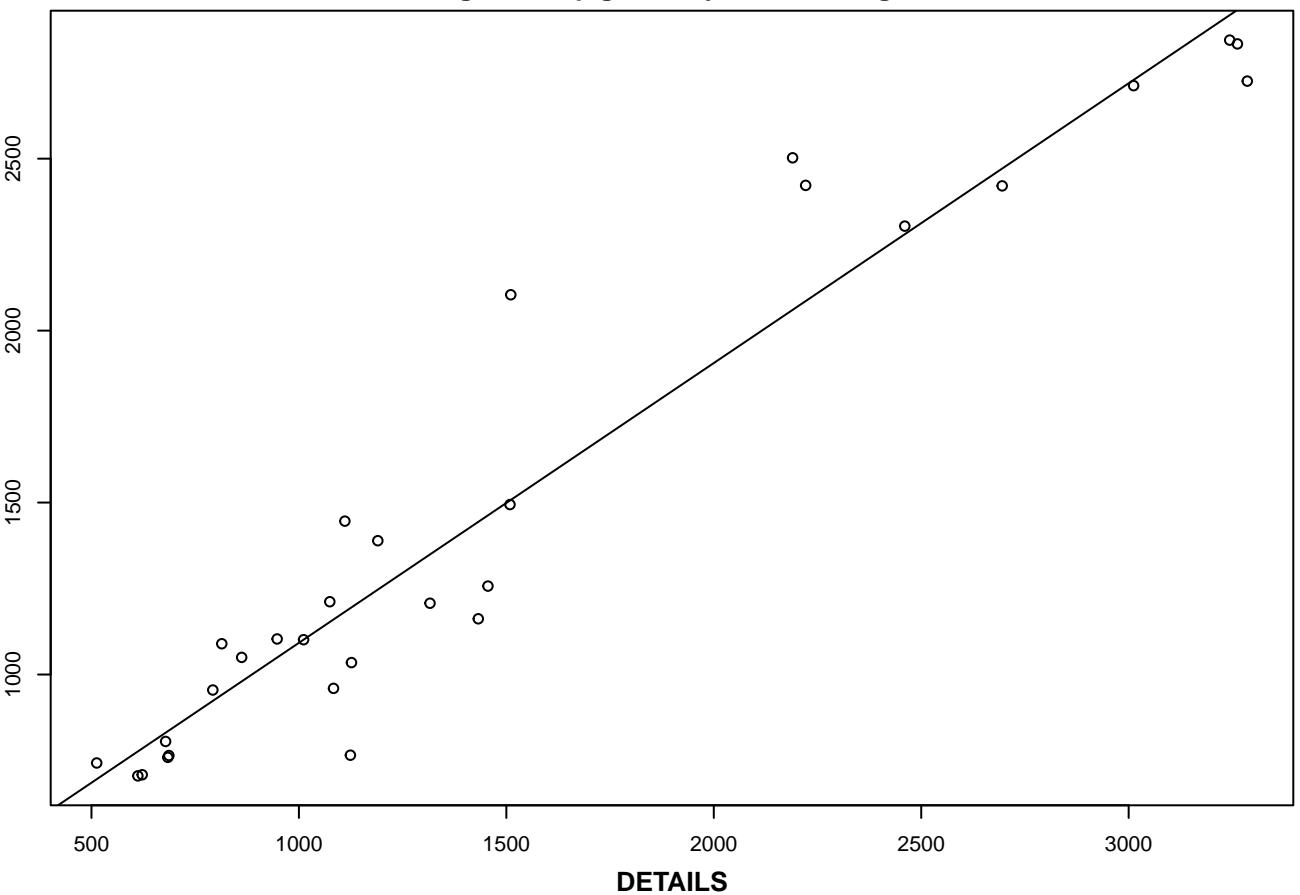
**NRMSE**  
45.1 %

**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

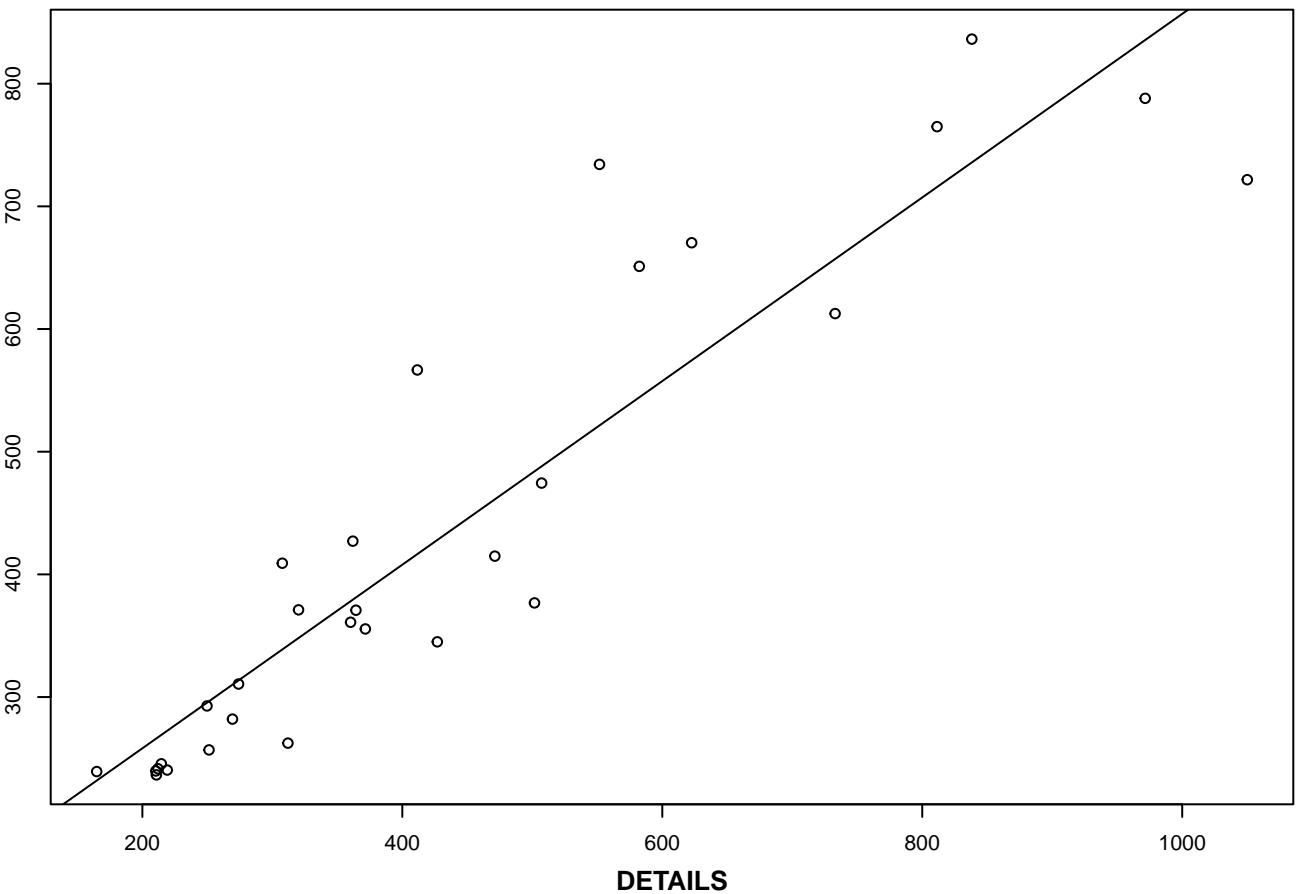
**NMAE**

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

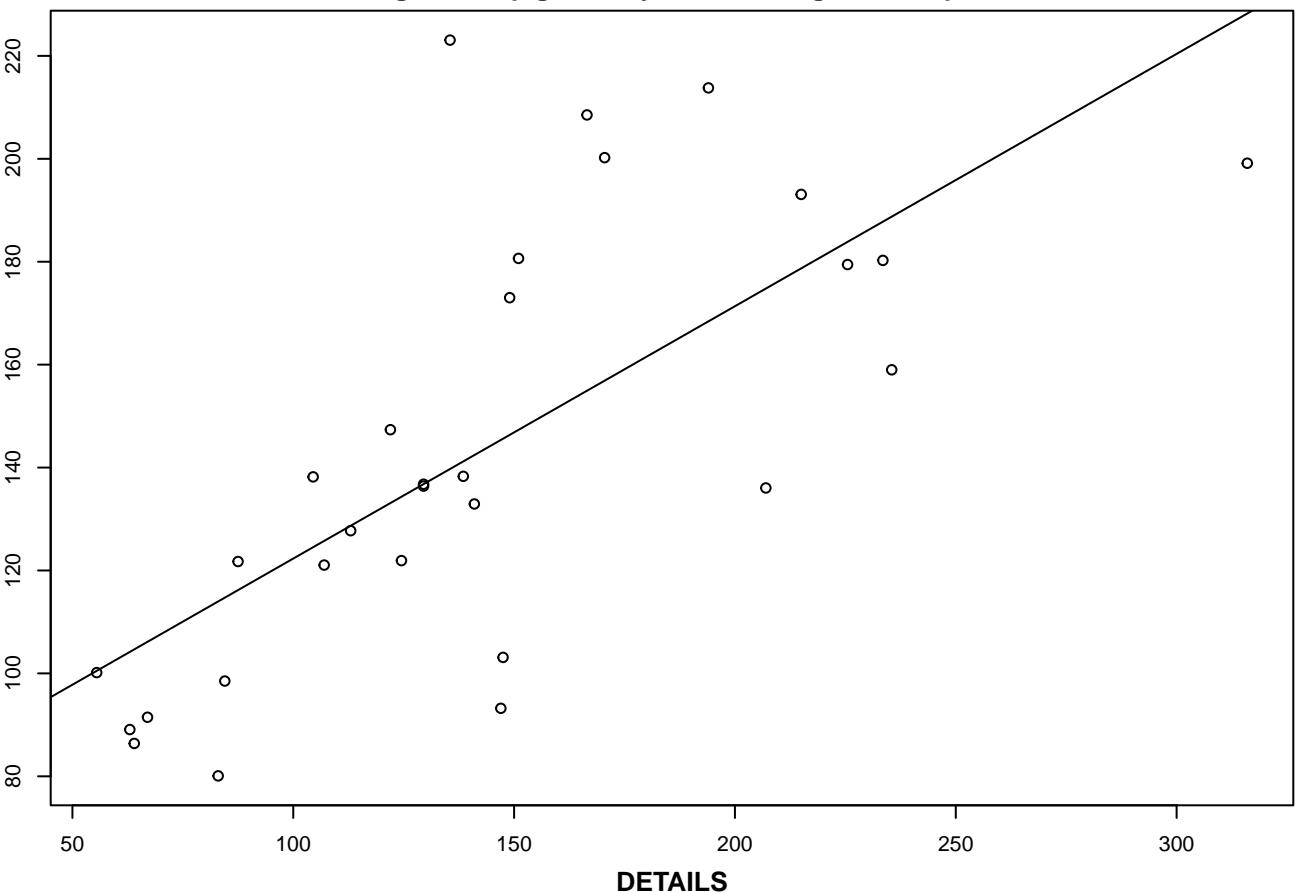
**NMAE**

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

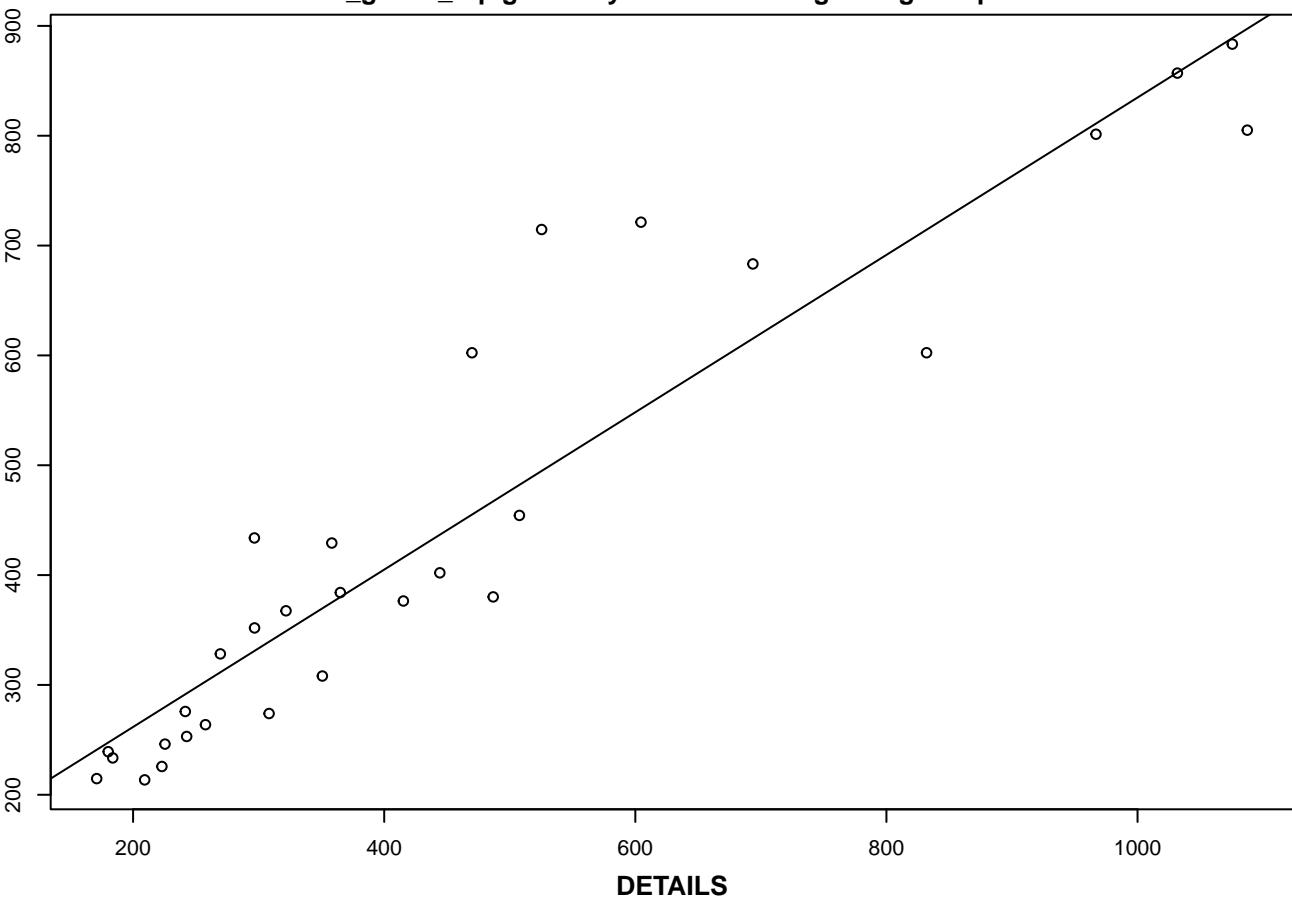
**NMAE**

23.2 %

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

0.495

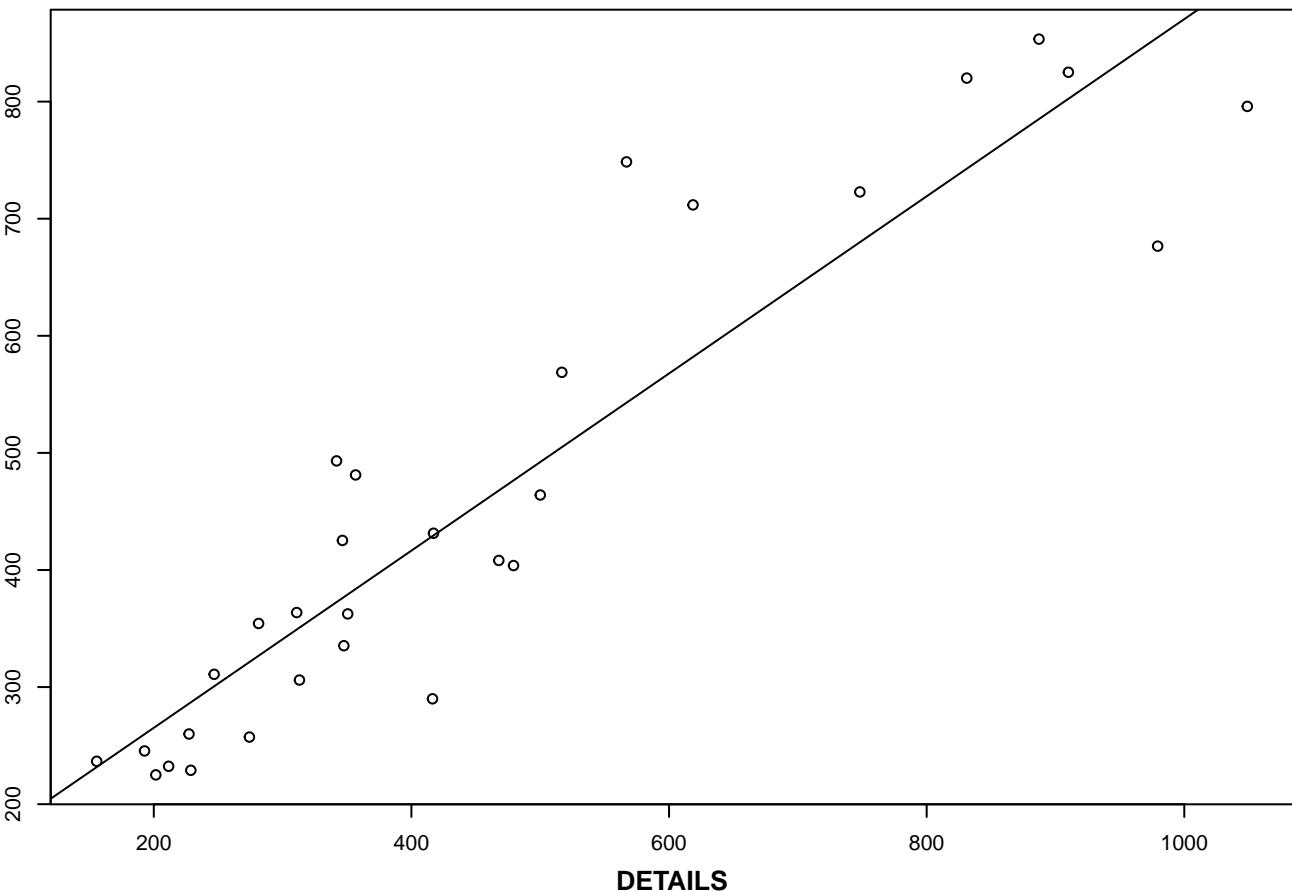
loocv\_genes\_top.geometry.fluo.minrectangle.length.a..px..csv



R^2

0.874

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



**RMSE**

100.774

**NRMSE**

21.9 %

**MAE**

71.748

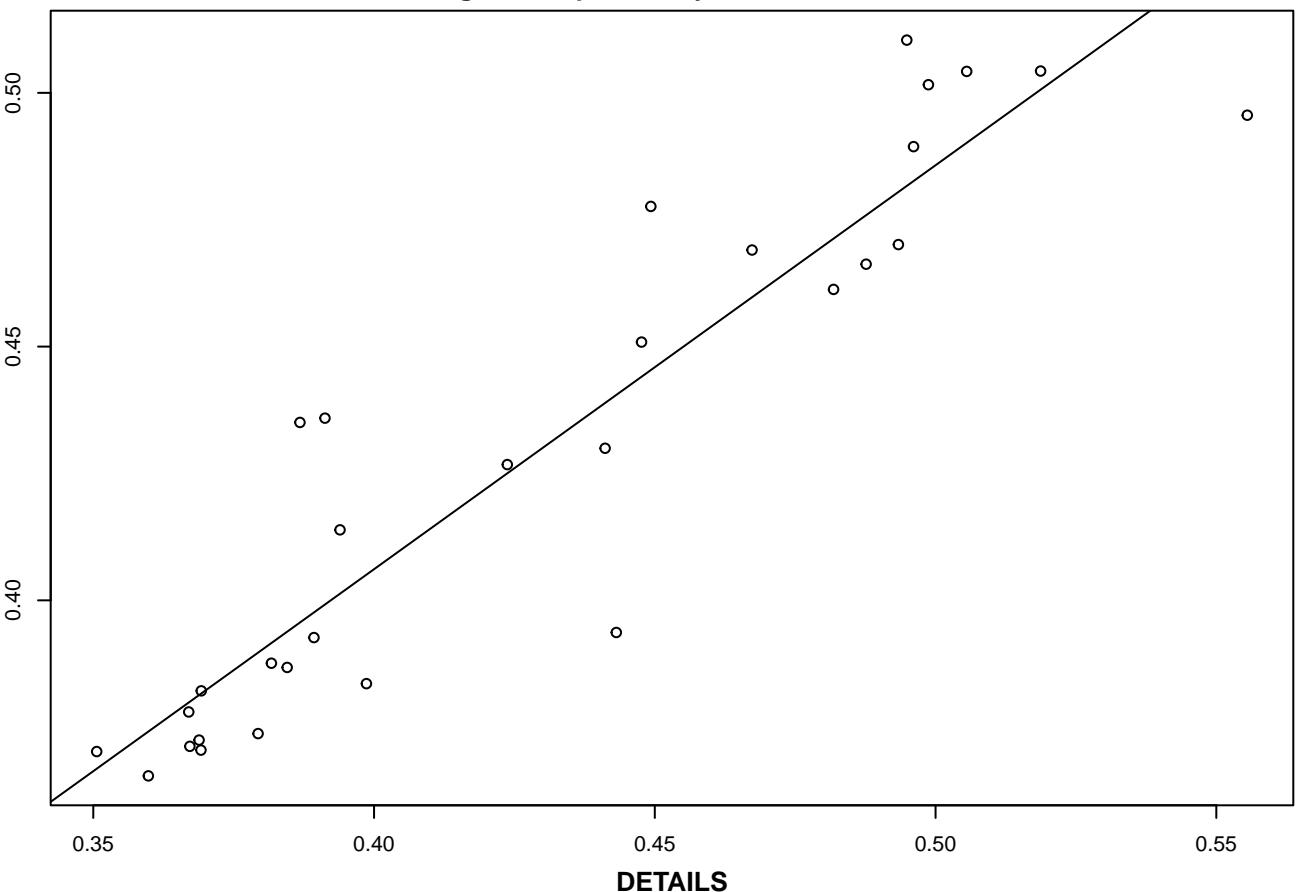
**NMAE**

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

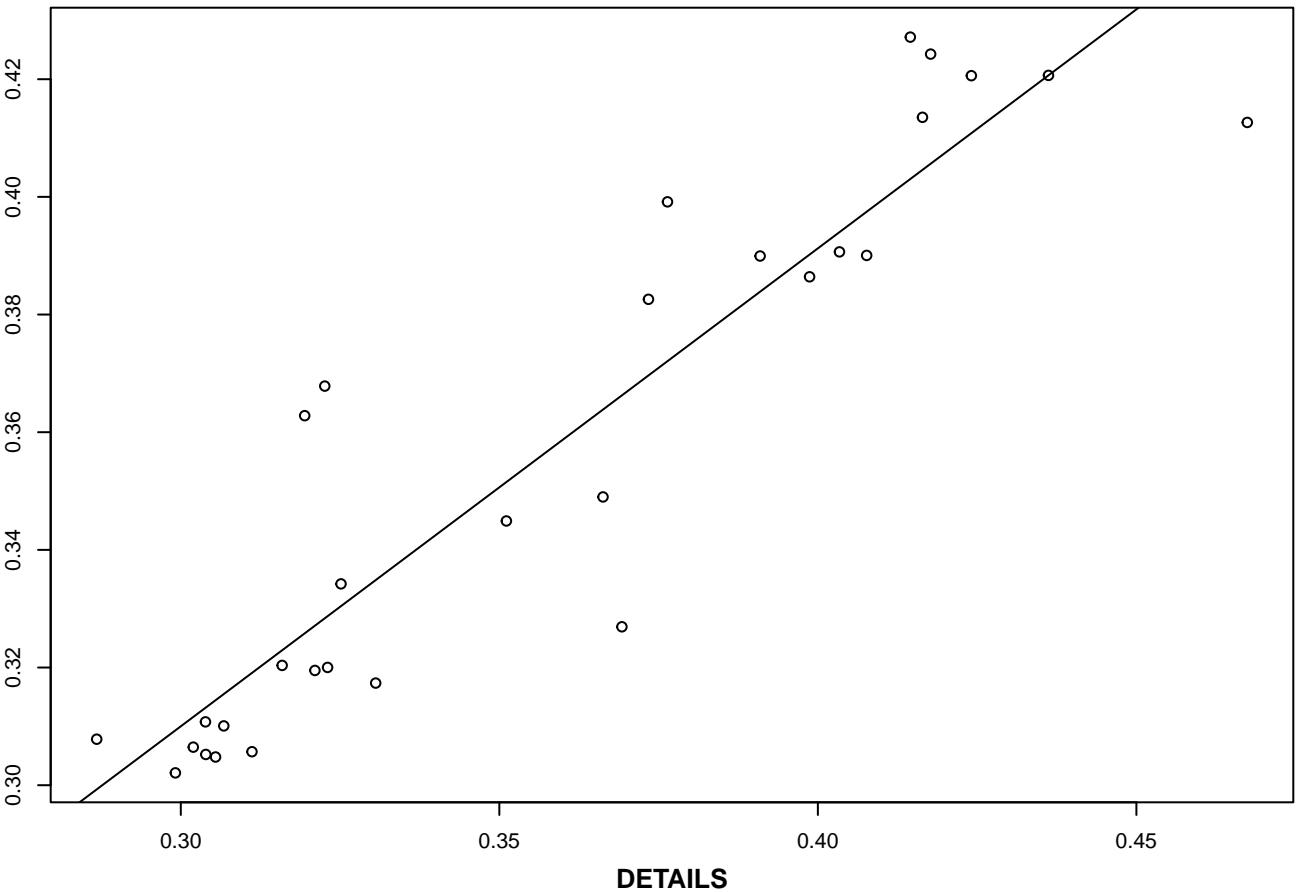
**NMAE**

3.6 %

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

0.857

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



**RMSE**

0.02

**NRMSE**

5.5 %

**MAE**

0.013

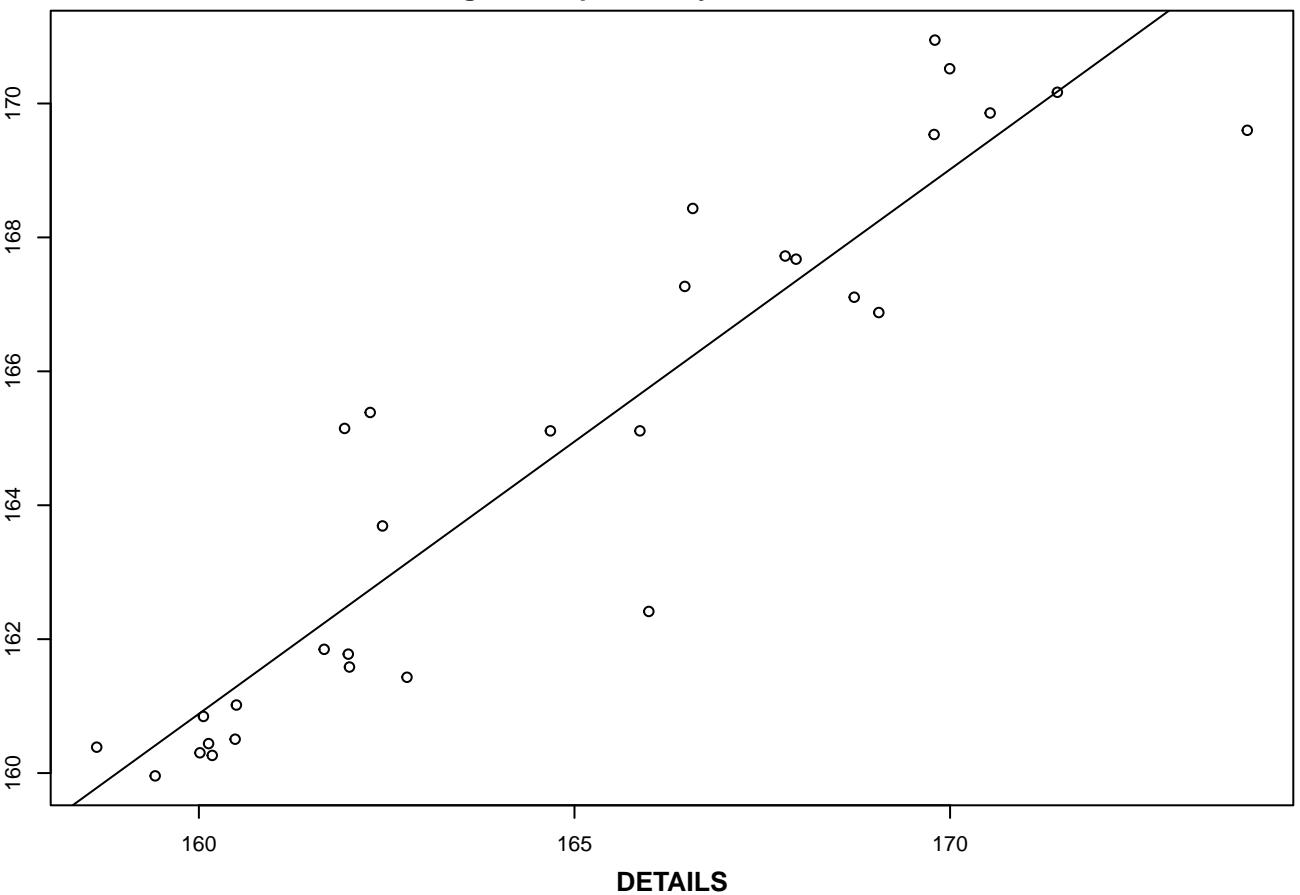
**NMAE**

3.8 %

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

0.846

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



**RMSE**

1.588

**NRMSE**

1 %

**MAE**

1.127

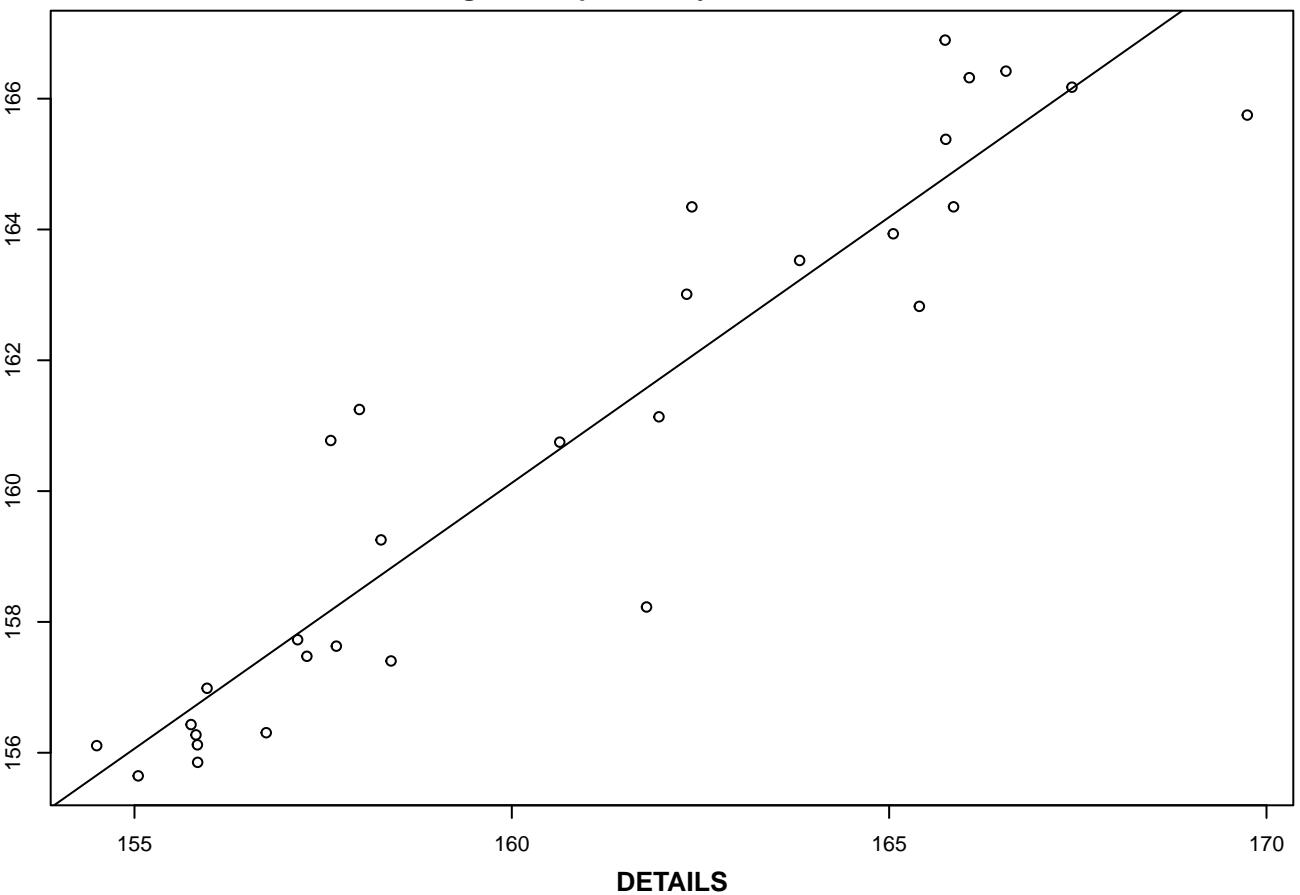
**NMAE**

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

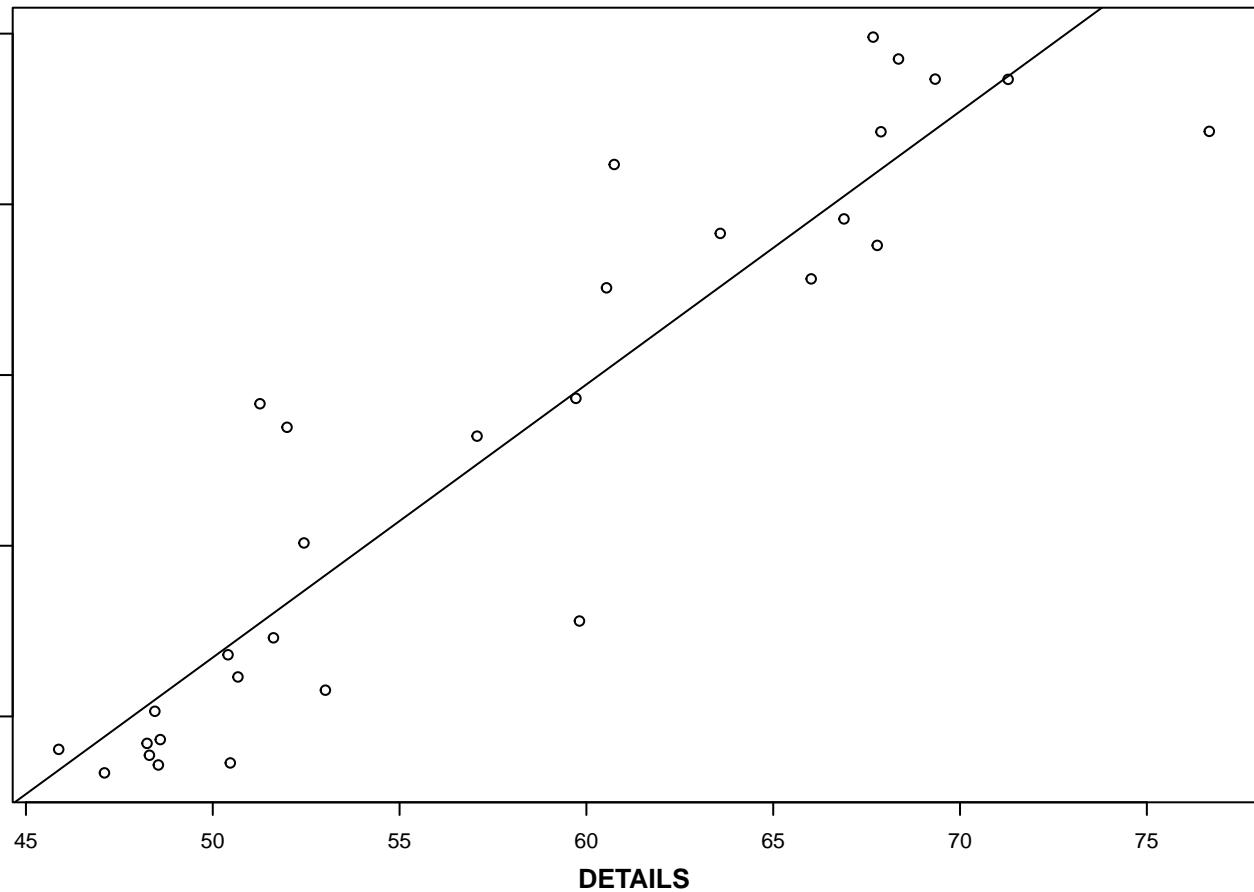
**NMAE**

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

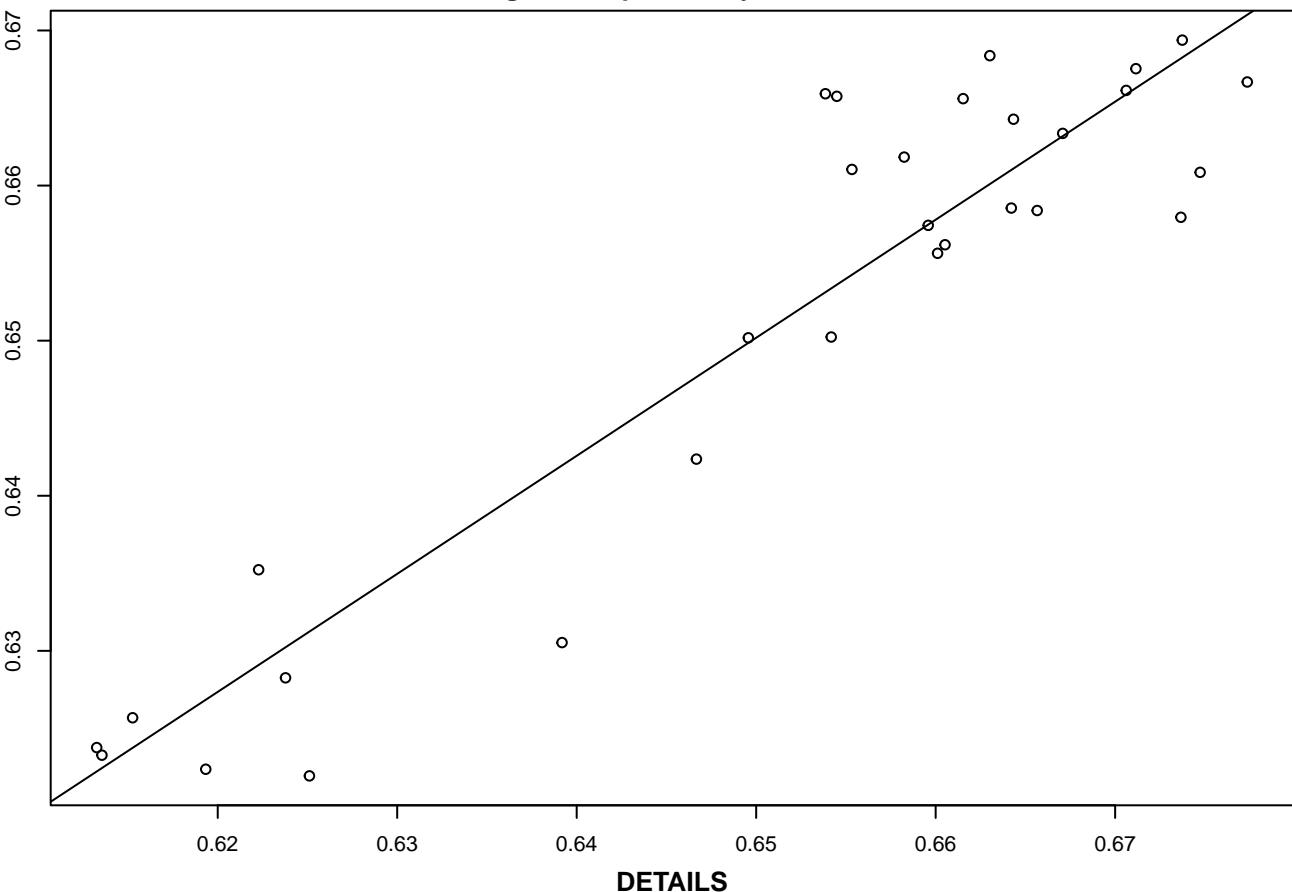
**NMAE**

4.3 %

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

0.848

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



**RMSE**

0.008

**NRMSE**

1.2 %

**MAE**

0.006

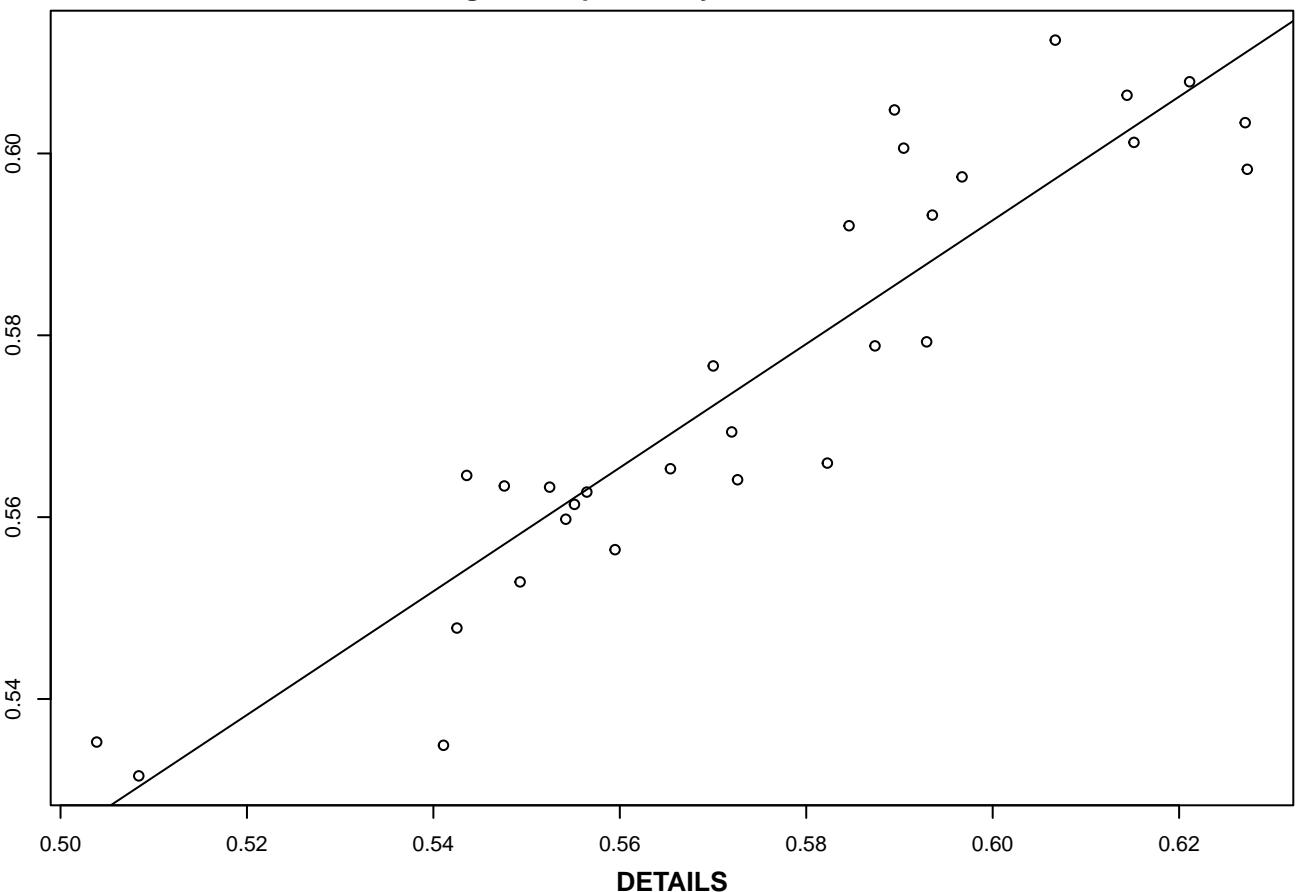
**NMAE**

1 %

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

0.868

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



**RMSE**

0.013

**NRMSE**

2.3 %

**MAE**

0.011

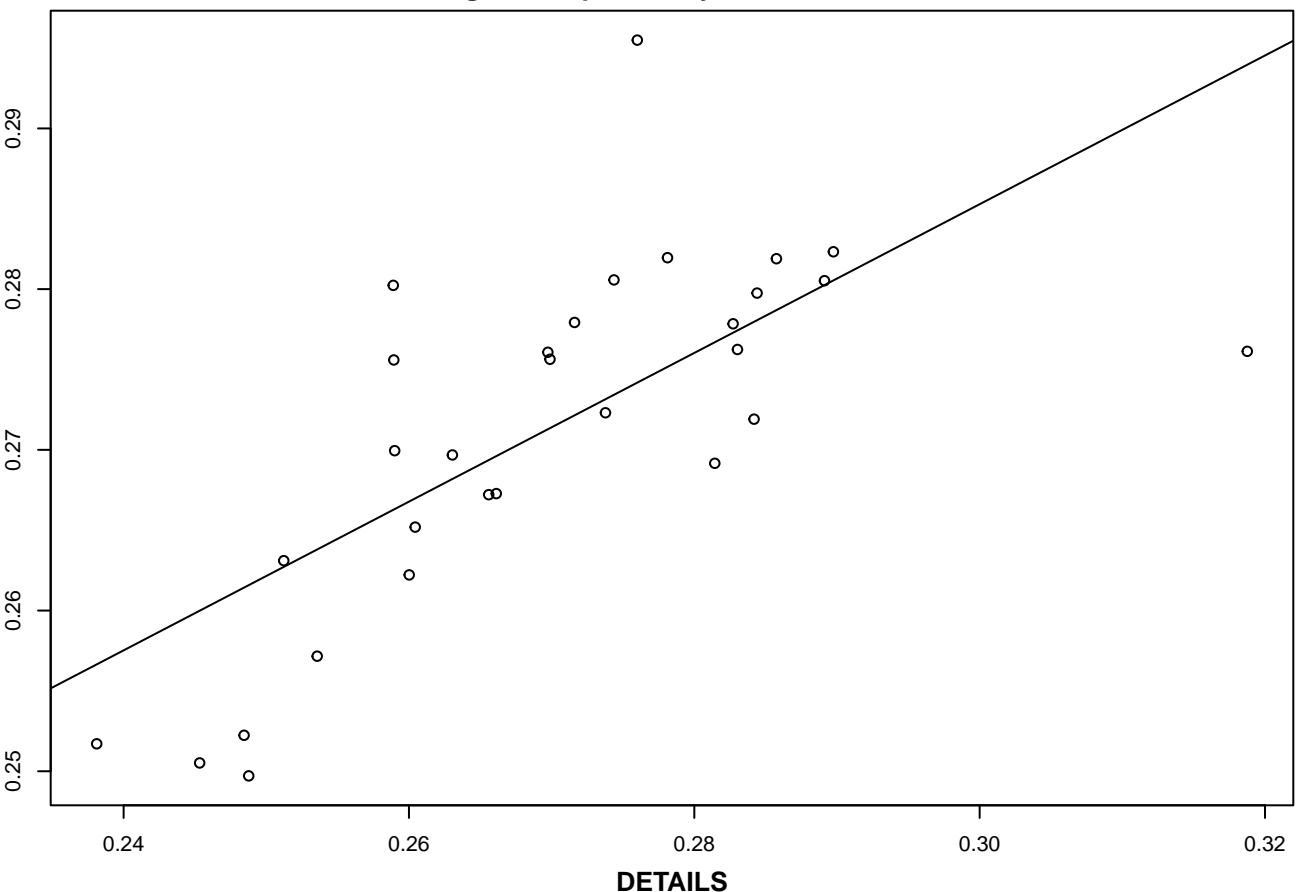
**NMAE**

1.9 %

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

0.853

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



**RMSE**

0.012

**NRMSE**

4.4 %

**MAE**

0.009

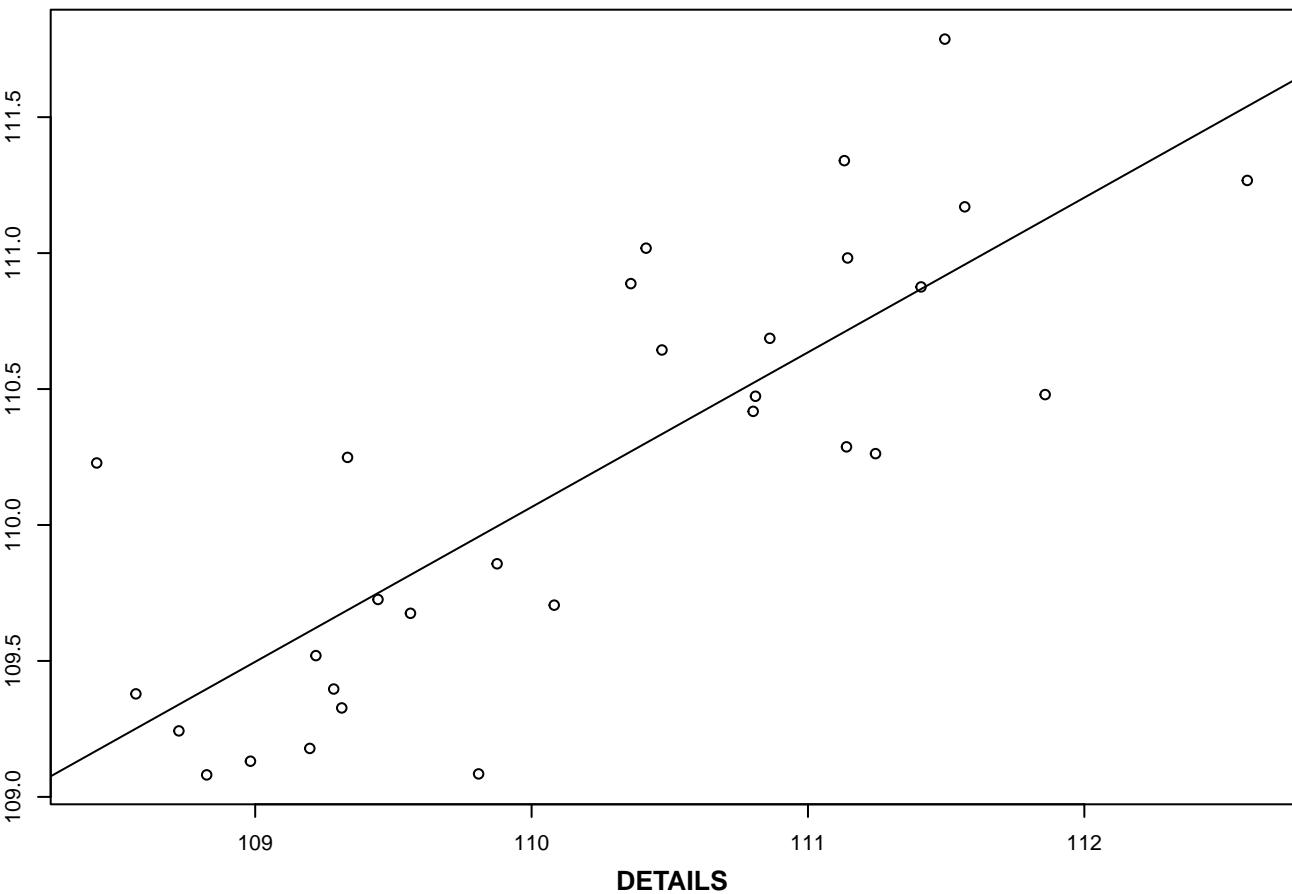
**NMAE**

3.2 %

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

0.497

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



RMSE	NRMSE	MAE	NMAE
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0.655

0.6 %

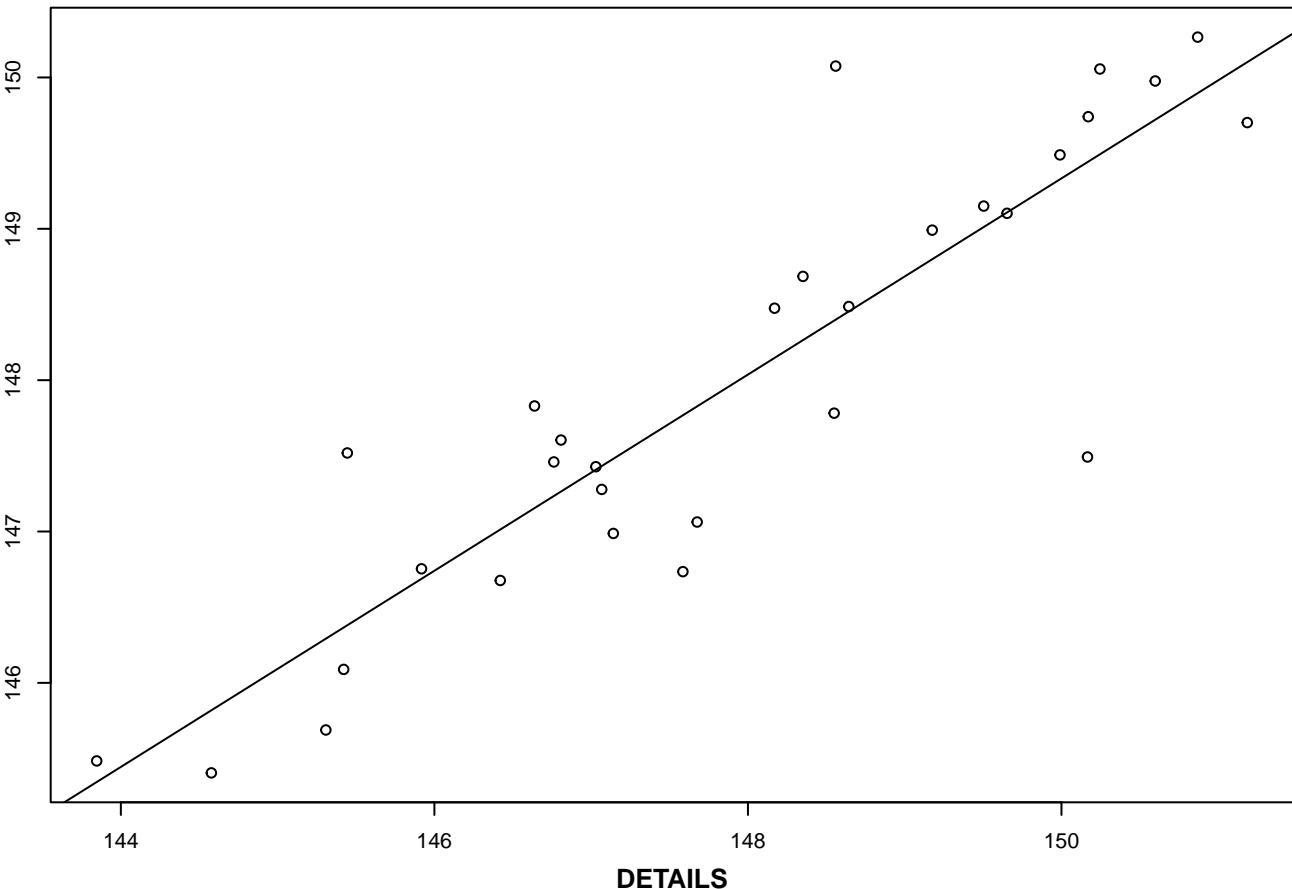
0.491

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

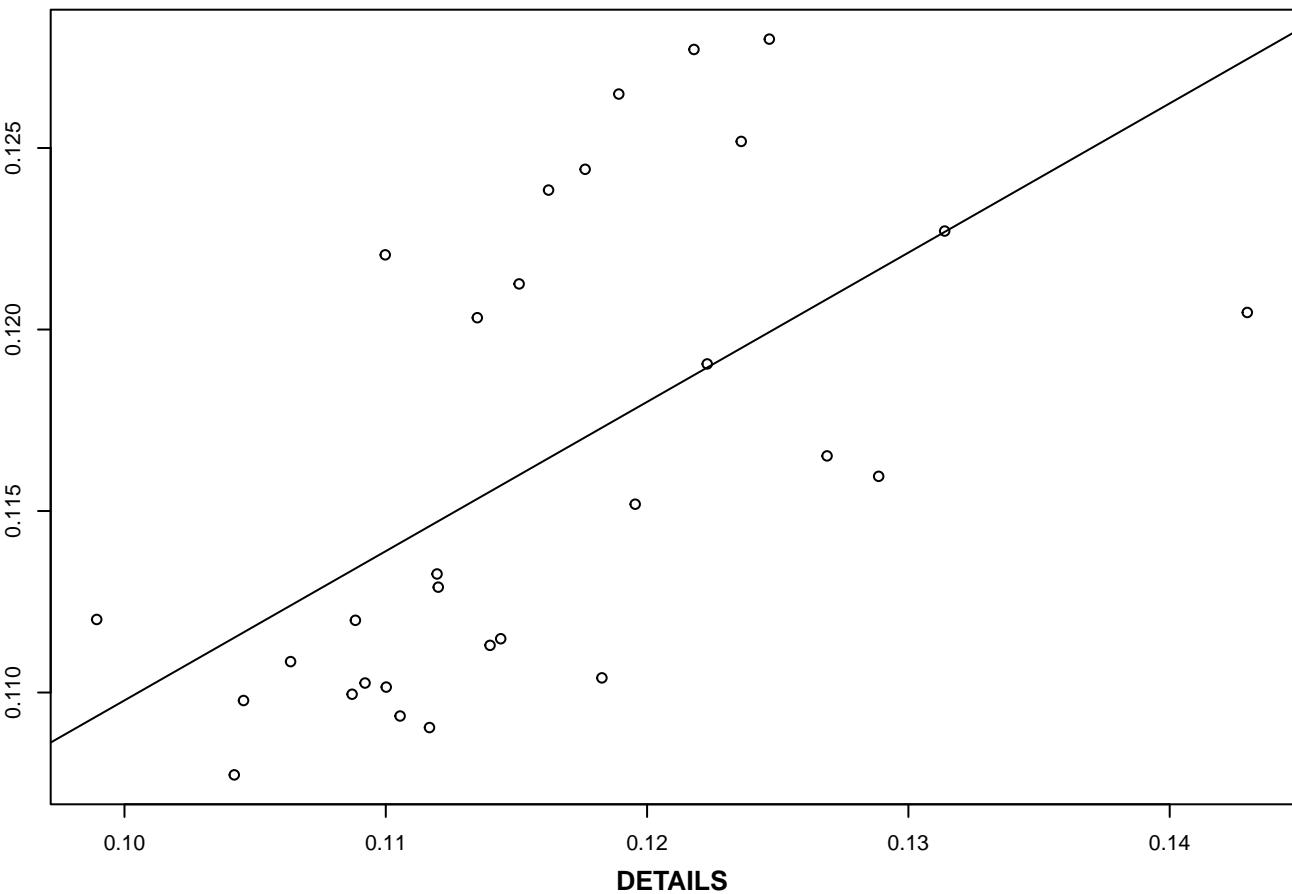
**NMAE**

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

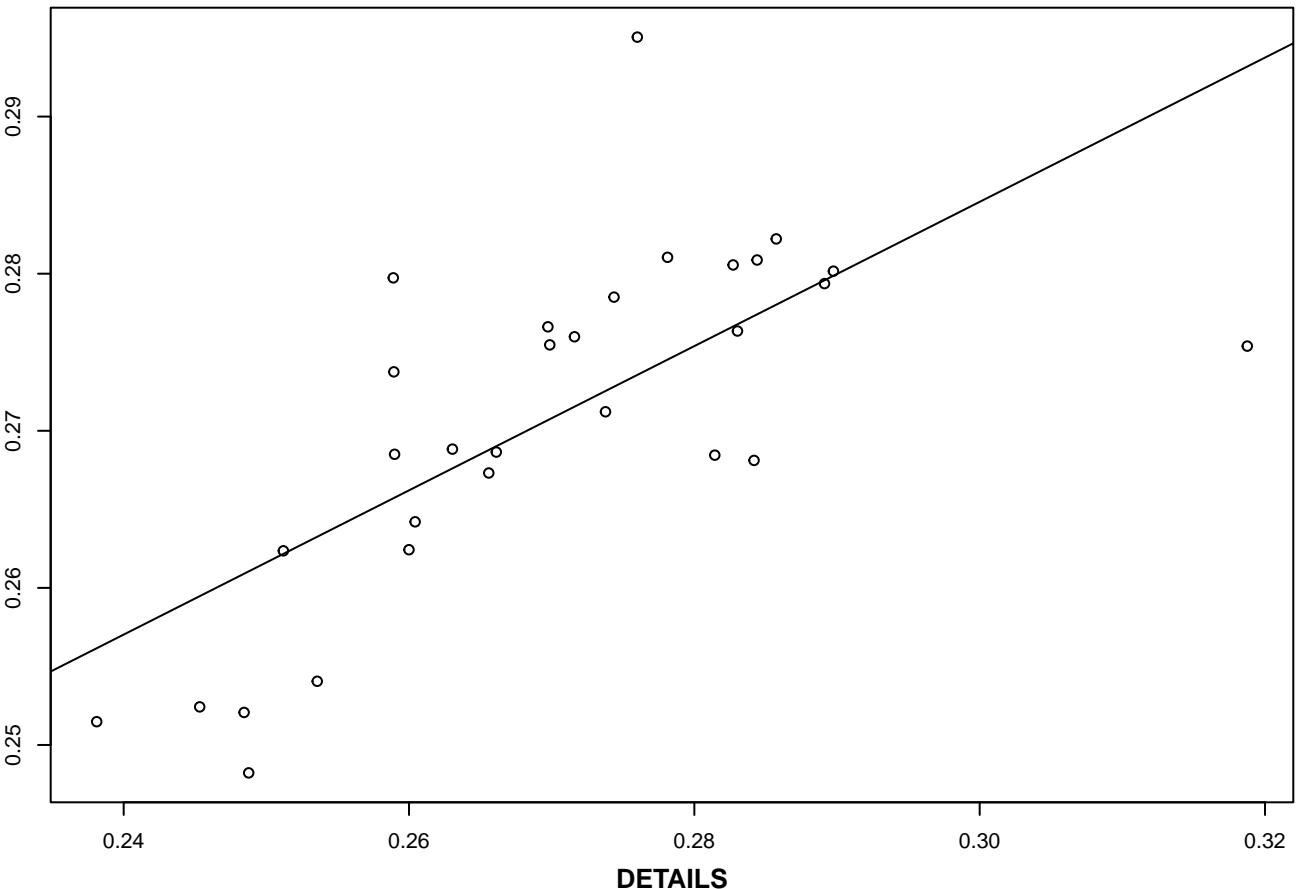
**NMAE**

4.9 %

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

0.341

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



**RMSE**

0.012

**NRMSE**

4.4 %

**MAE**

0.008

**NMAE**

3.1 %

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

0.488