

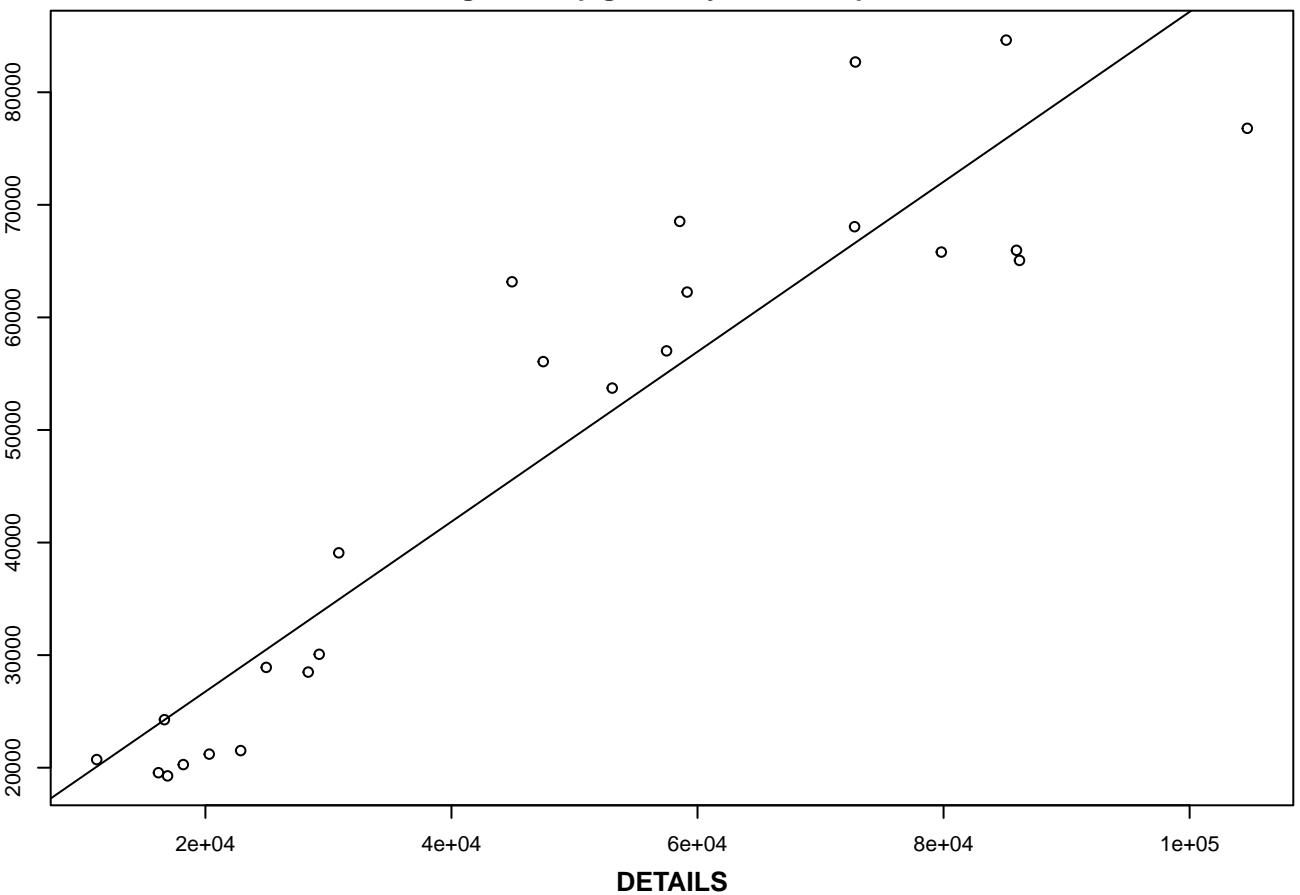
CONFUSION MATRIX

		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

10629.894

NRMSE

22.3 %

MAE

7475.126

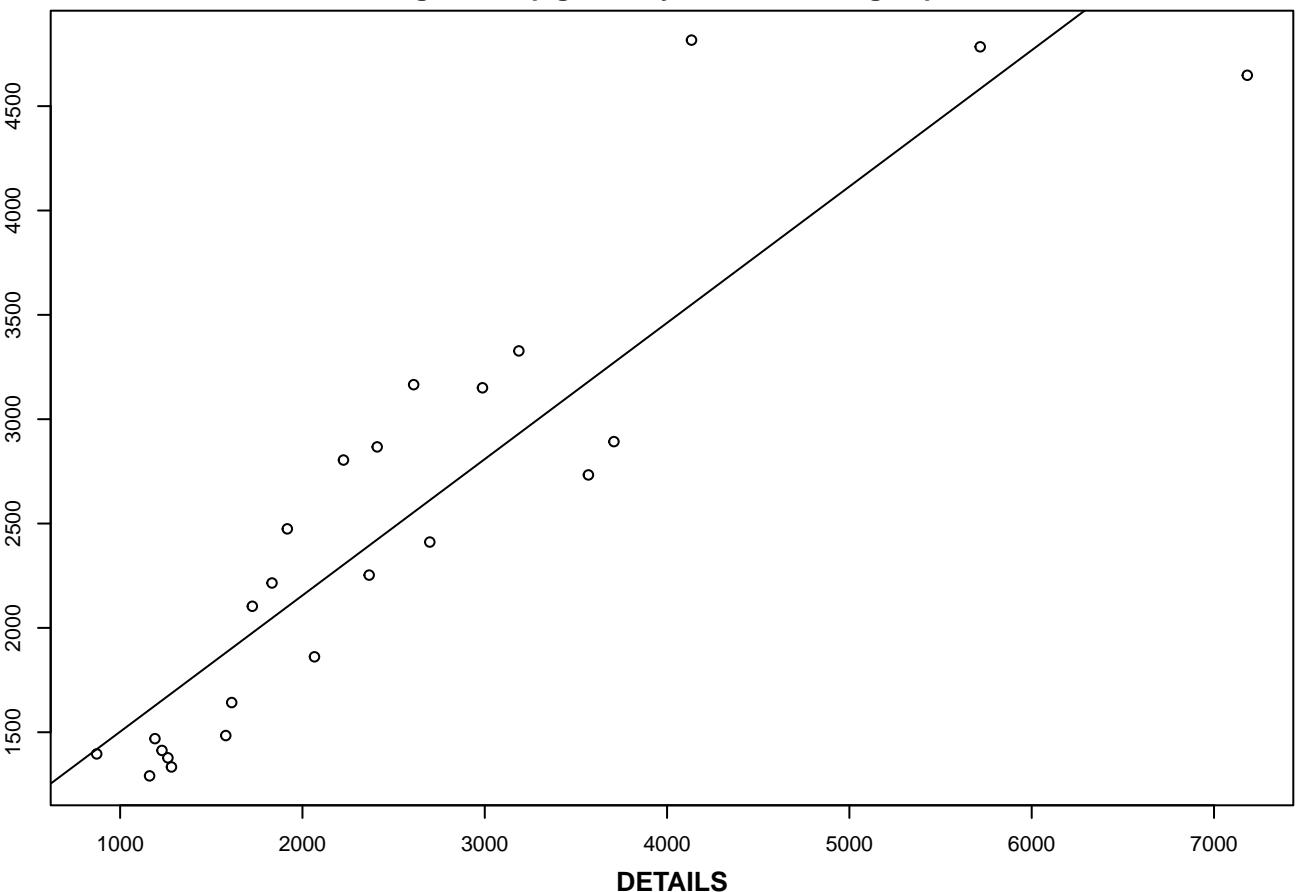
NMAE

15.7 %

R²

0.866

loocv_genes_top.geometry.fluo.border.length..px..csv



RMSE

682.819

NRMSE

27.1 %

MAE

459.526

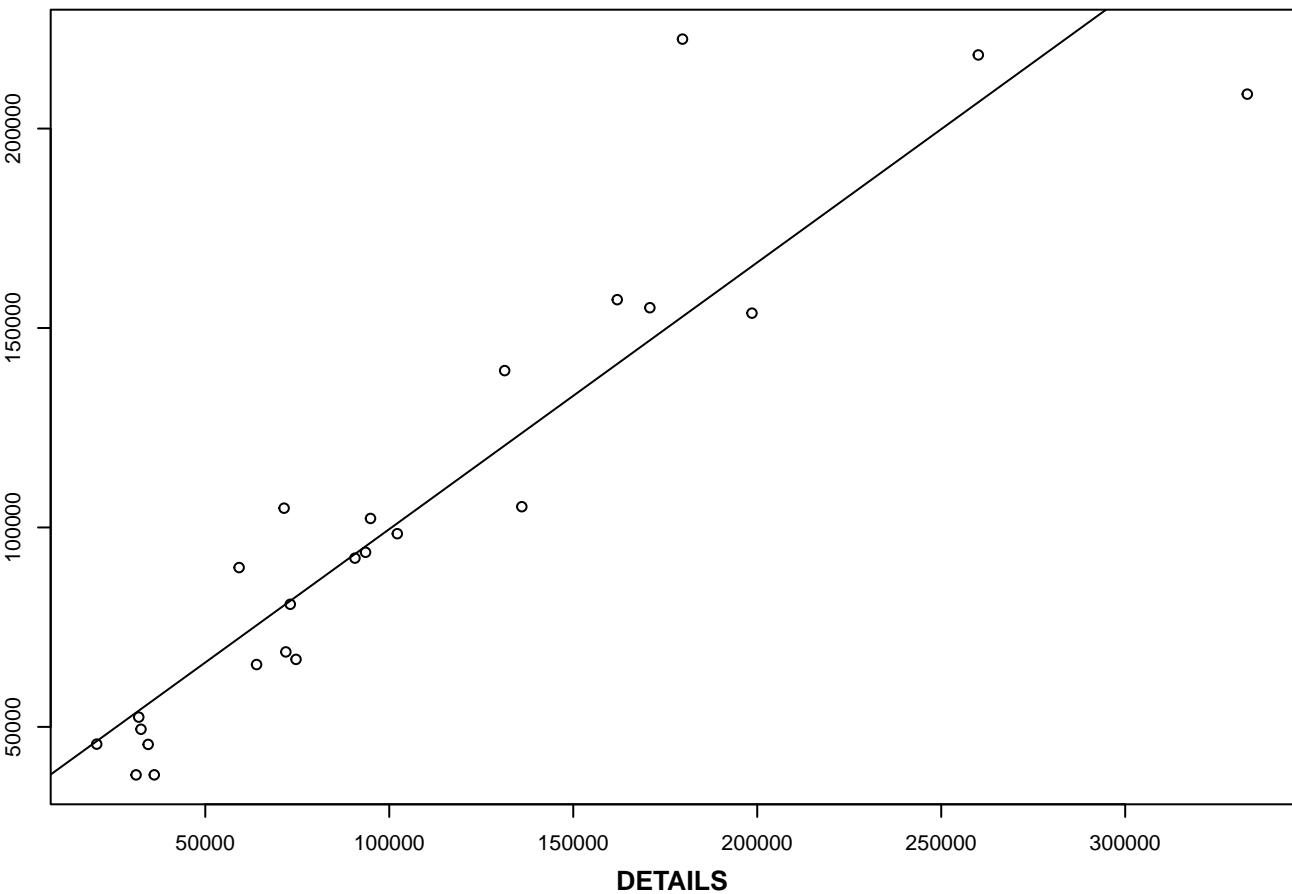
NMAE

18.2 %

R²

0.821

loocv_genes_top.geometry.fluo.hull.area..px..csv



RMSE

33004.079

NRMSE

31 %

MAE

20530.222

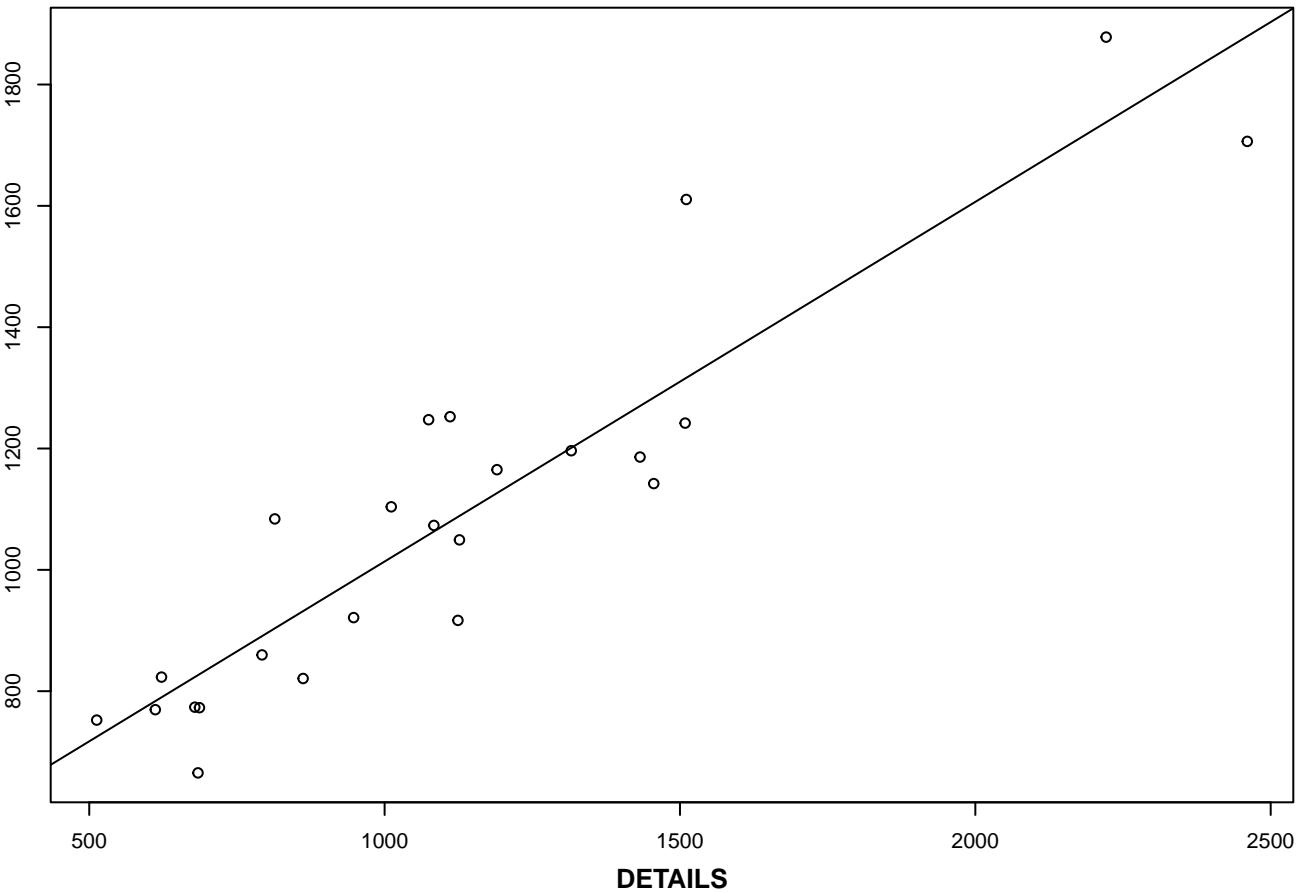
NMAE

19.3 %

R²

0.857

loocv_genes_top.geometry.fluo.hull.length.csv



RMSE

229.904

NRMSE

20.6 %

MAE

169.735

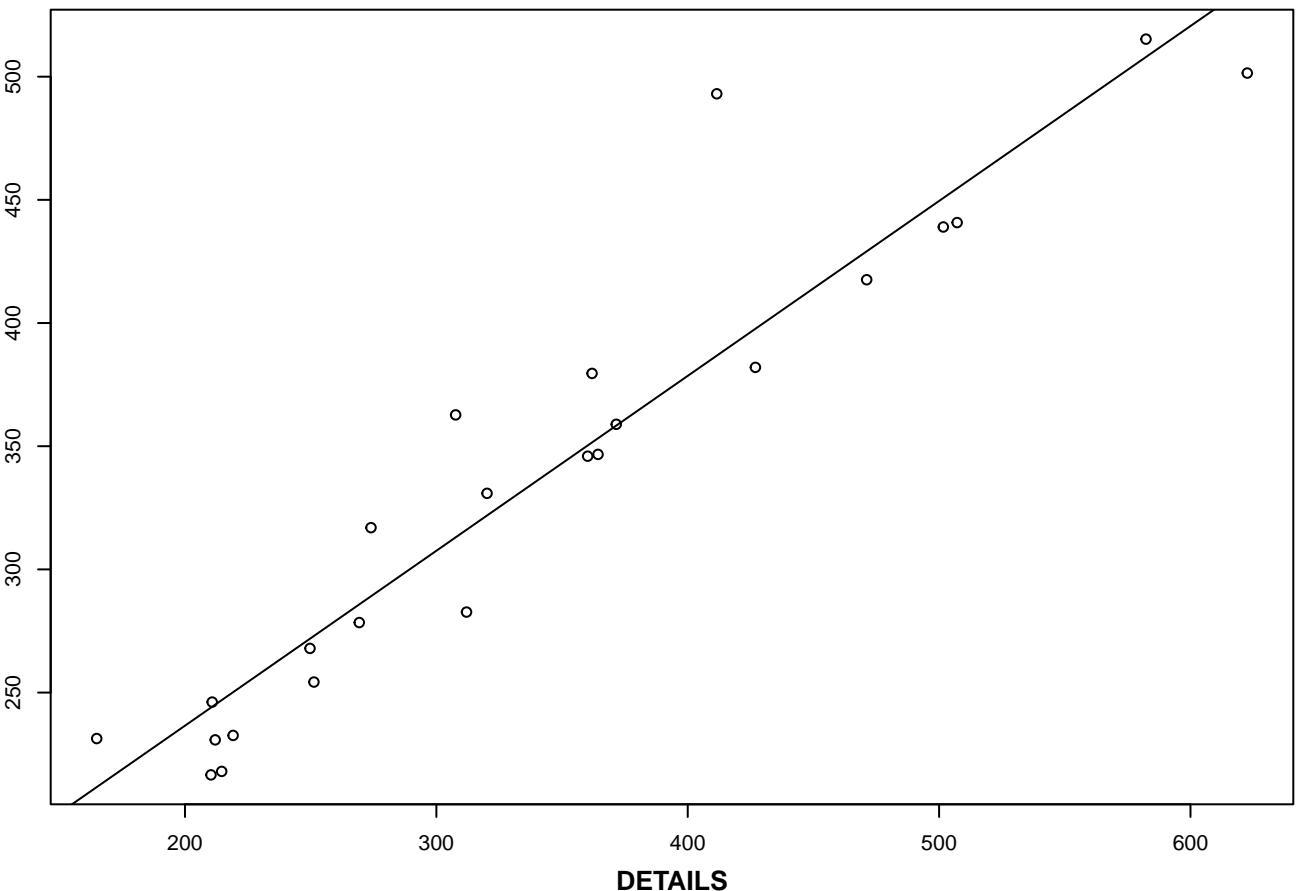
NMAE

15.2 %

R²

0.84

loocv_genes_top.geometry.fluo.hull.pc2..px..csv



RMSE

46.794

NRMSE

13.7 %

MAE

36.311

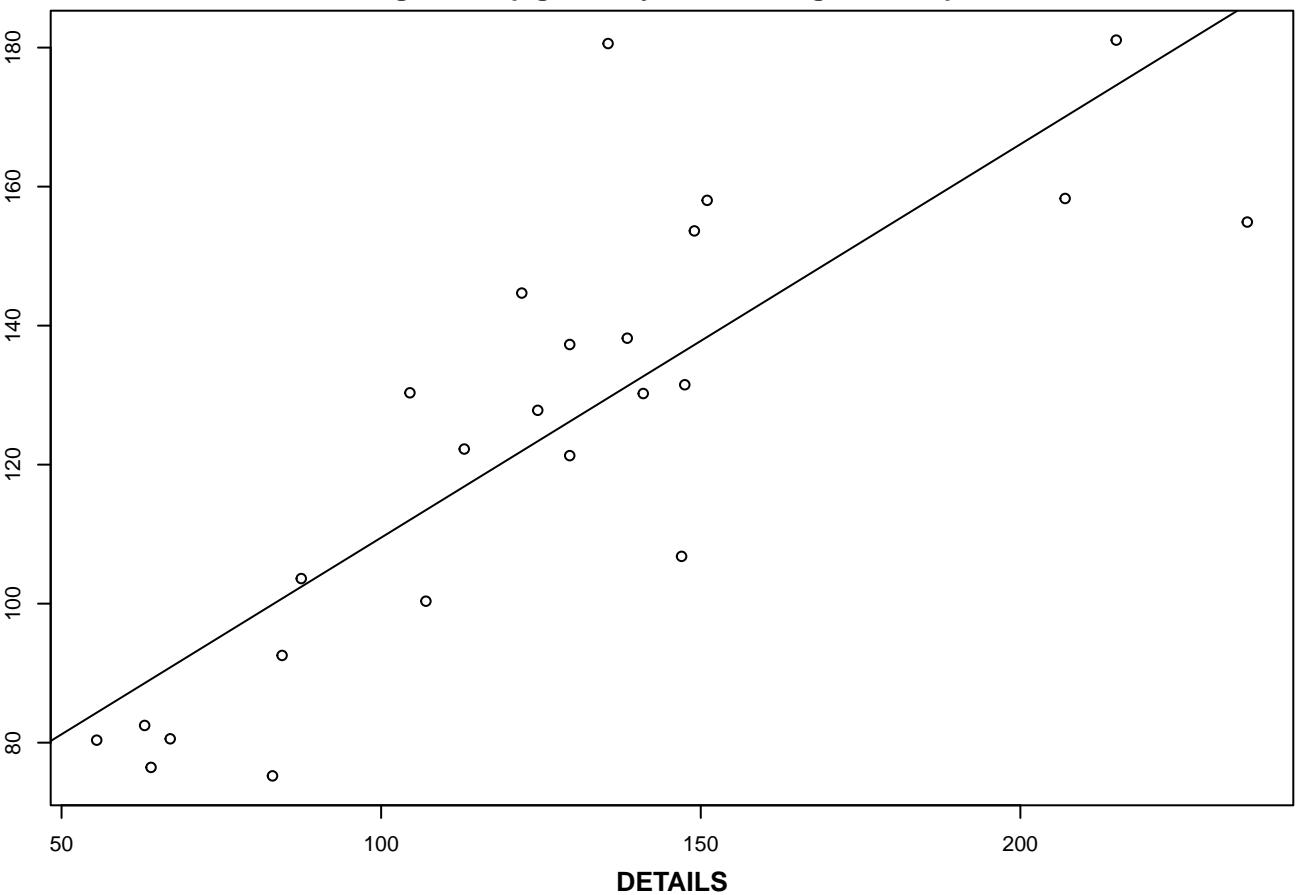
NMAE

10.6 %

R²

0.895

loocv_genes_top.geometry.fluo.leaf.length.mean..px..csv



RMSE

26.835

NRMSE

21.5 %

MAE

19.718

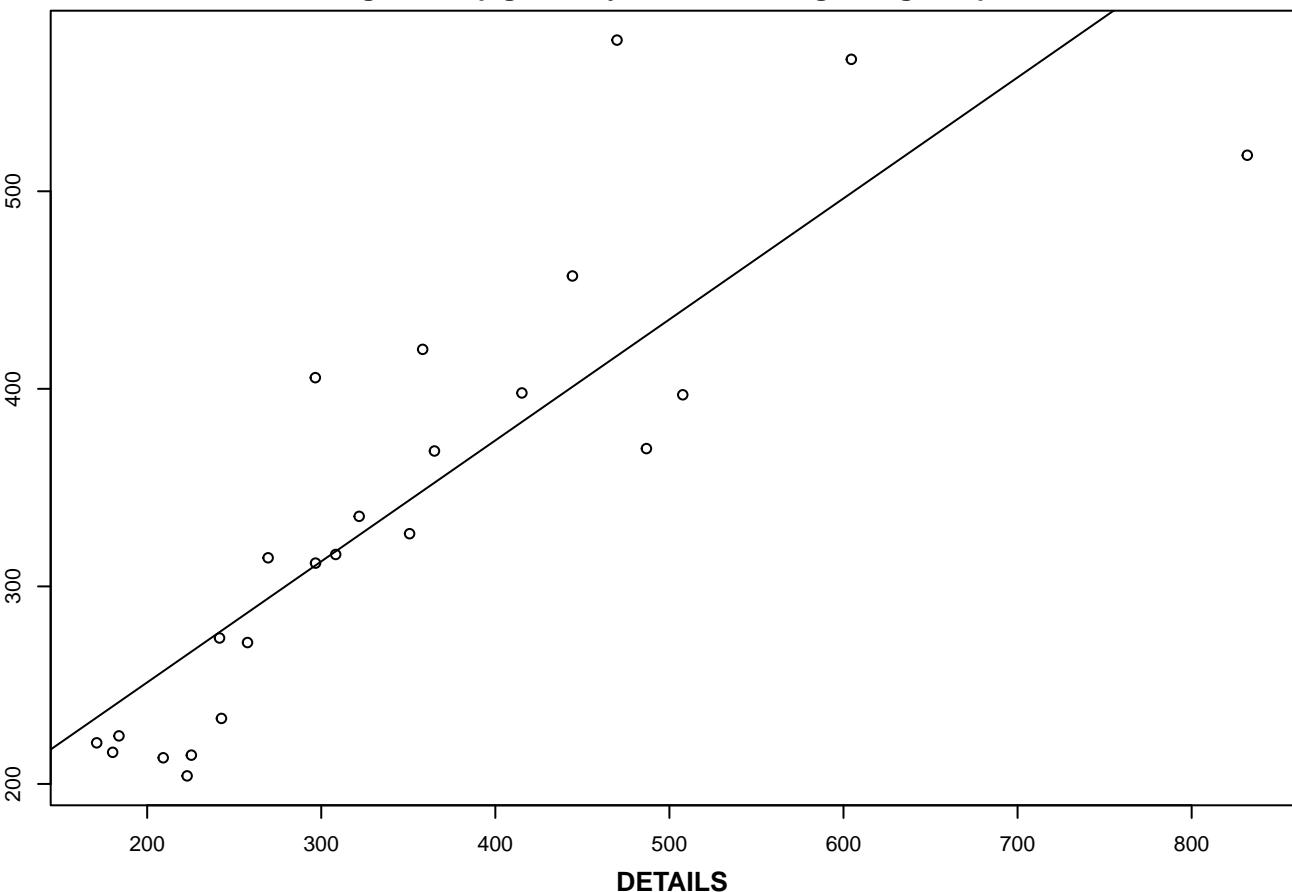
NMAE

15.8 %

R²

0.685

loocv_genes_top.geometry.fluo.minrectangle.length.a..px..csv



RMSE

82.573

NRMSE

24 %

MAE

50.477

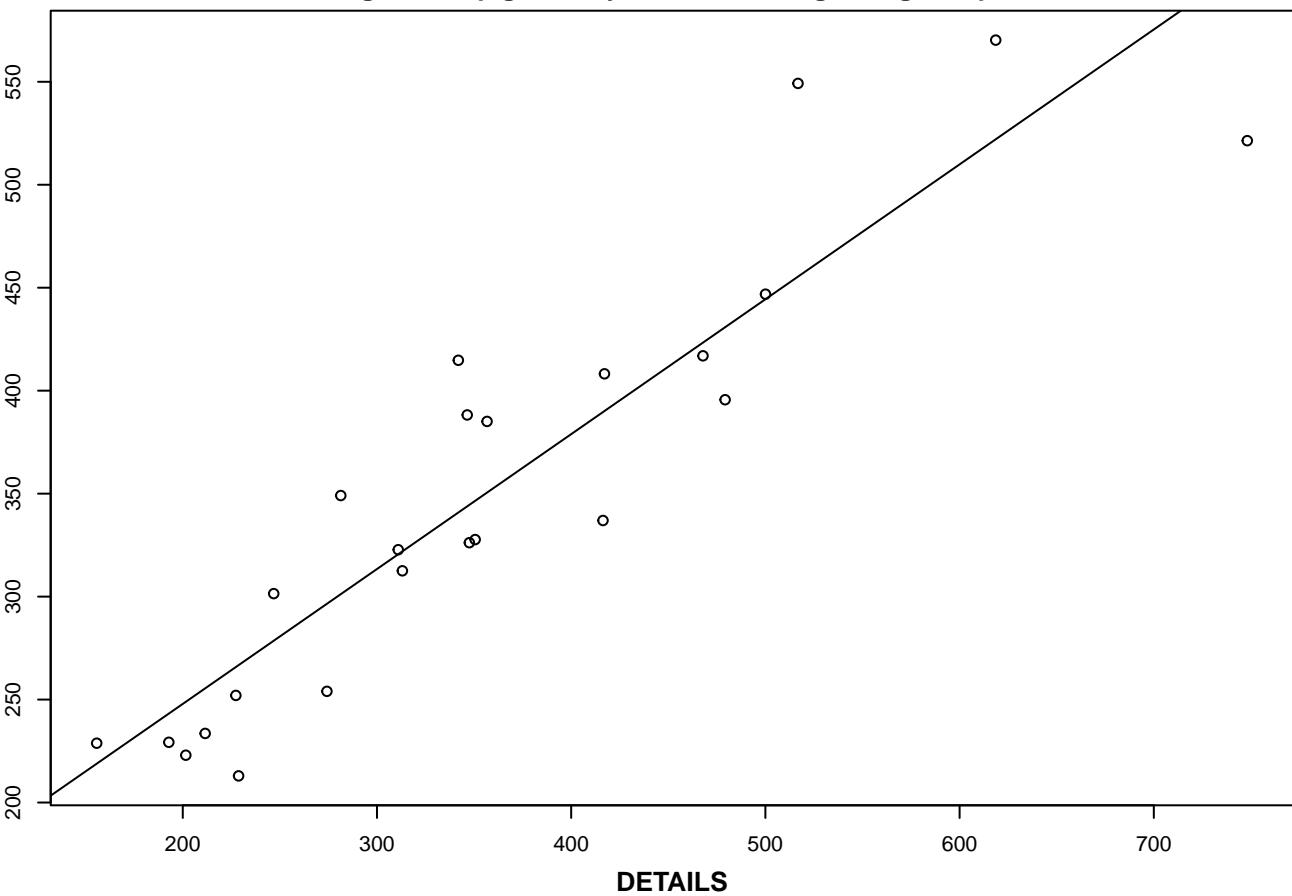
NMAE

14.7 %

R²

0.722

loocv_genes_top.geometry.fluo.minrectangle.length.b..px..csv



RMSE

64.241

NRMSE

18 %

MAE

46.641

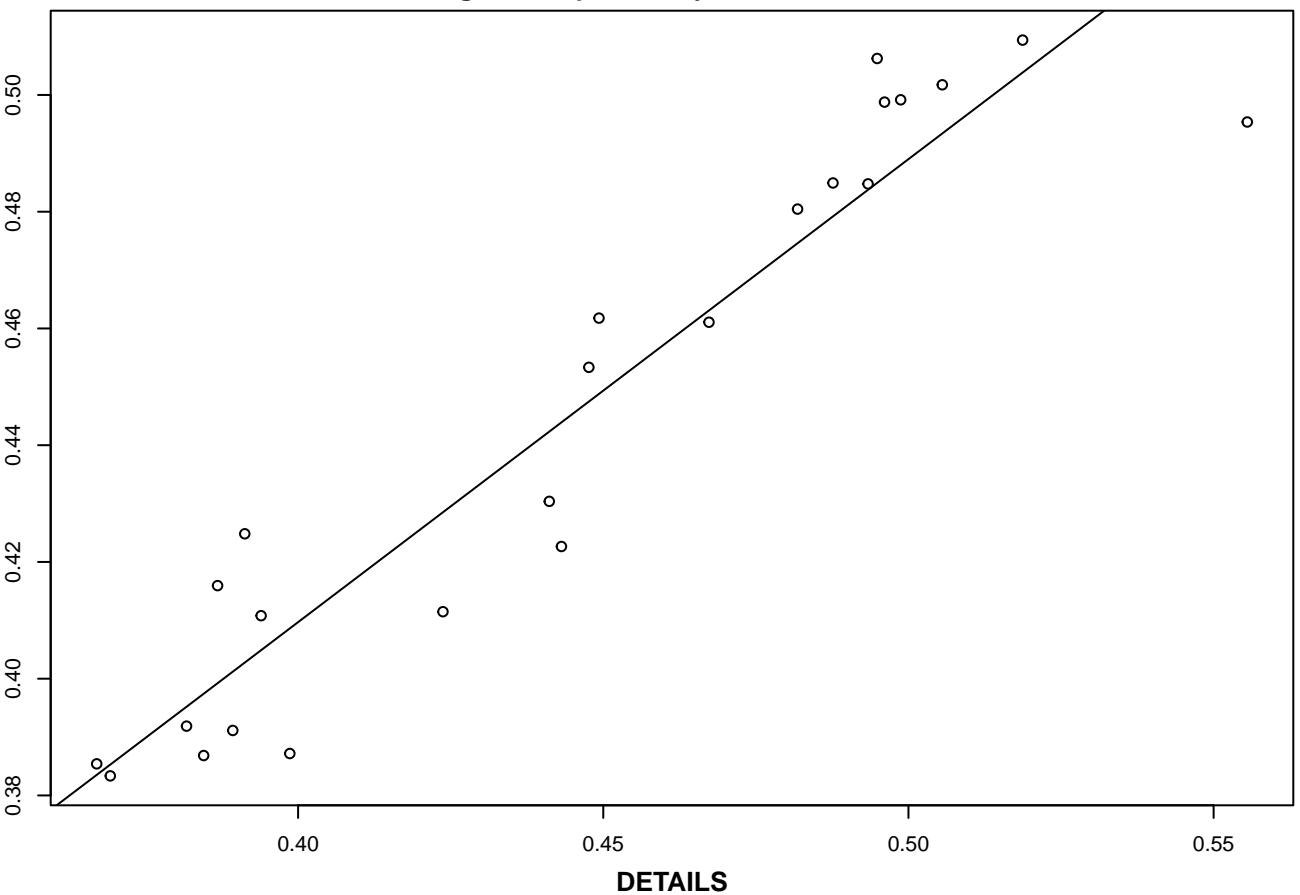
NMAE

13.1 %

R²

0.832

loocv_genes_top.intensity.fluo.hsv.v.mean.csv



RMSE	NRMSE	MAE	NMAE
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0.018

4.1 %

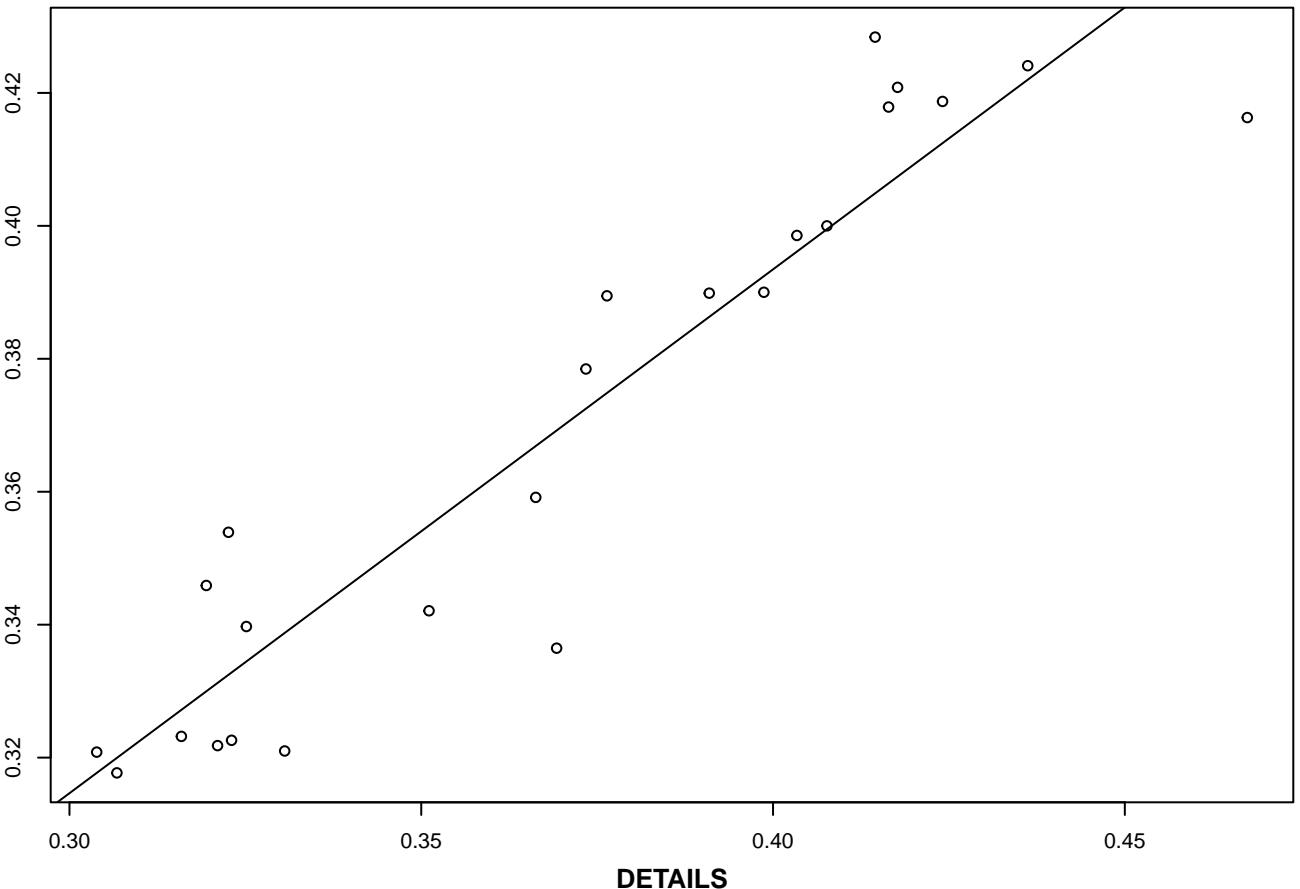
0.013

2.9 %

R^2

0.899

loocv_genes_top.intensity.fluo.intensity.mean.csv



RMSE

0.017

NRMSE

4.6 %

MAE

0.012

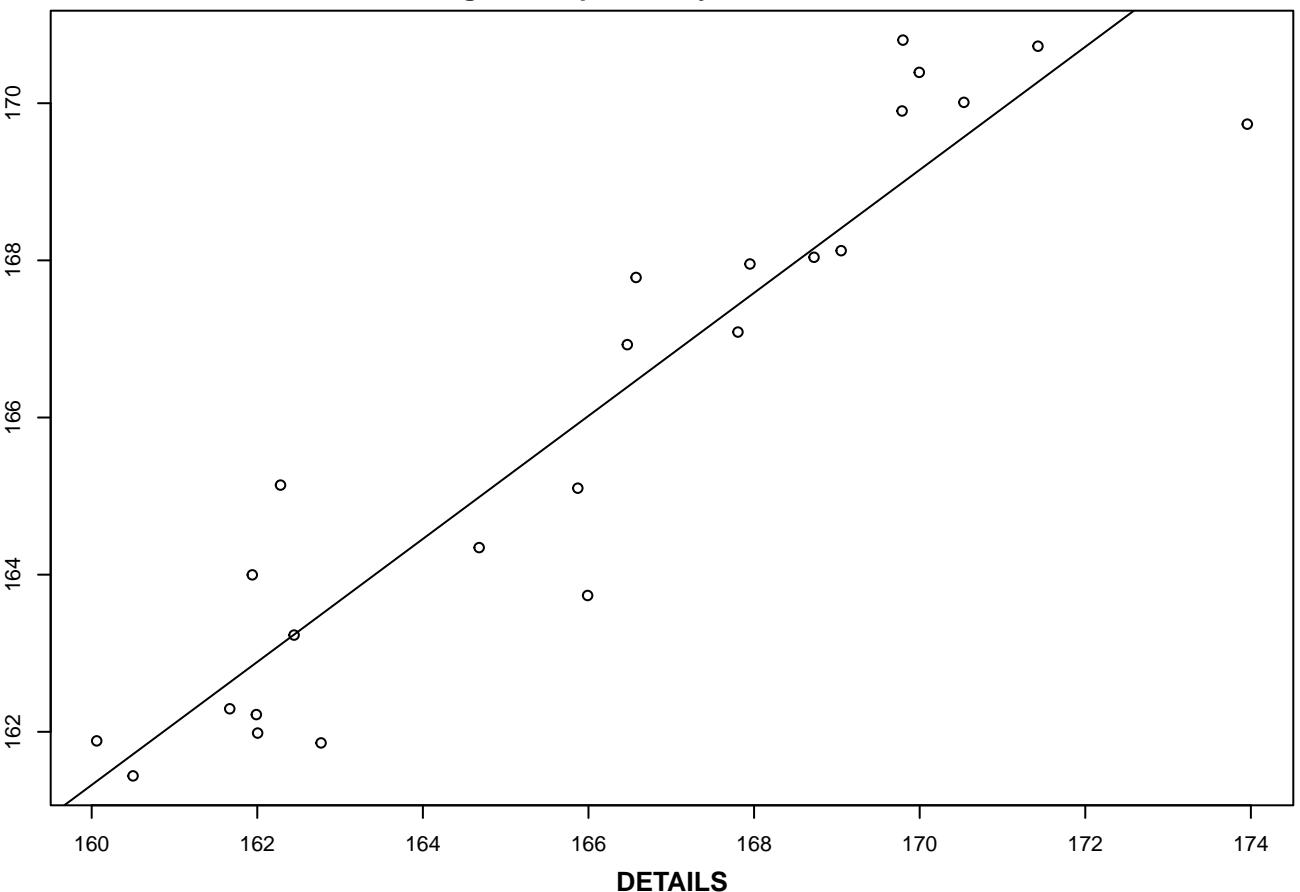
NMAE

3.3 %

R²

0.873

loocv_genes_top.intensity.fluo.lab.a.mean.csv



RMSE

1.408

NRMSE

0.8 %

MAE

1.024

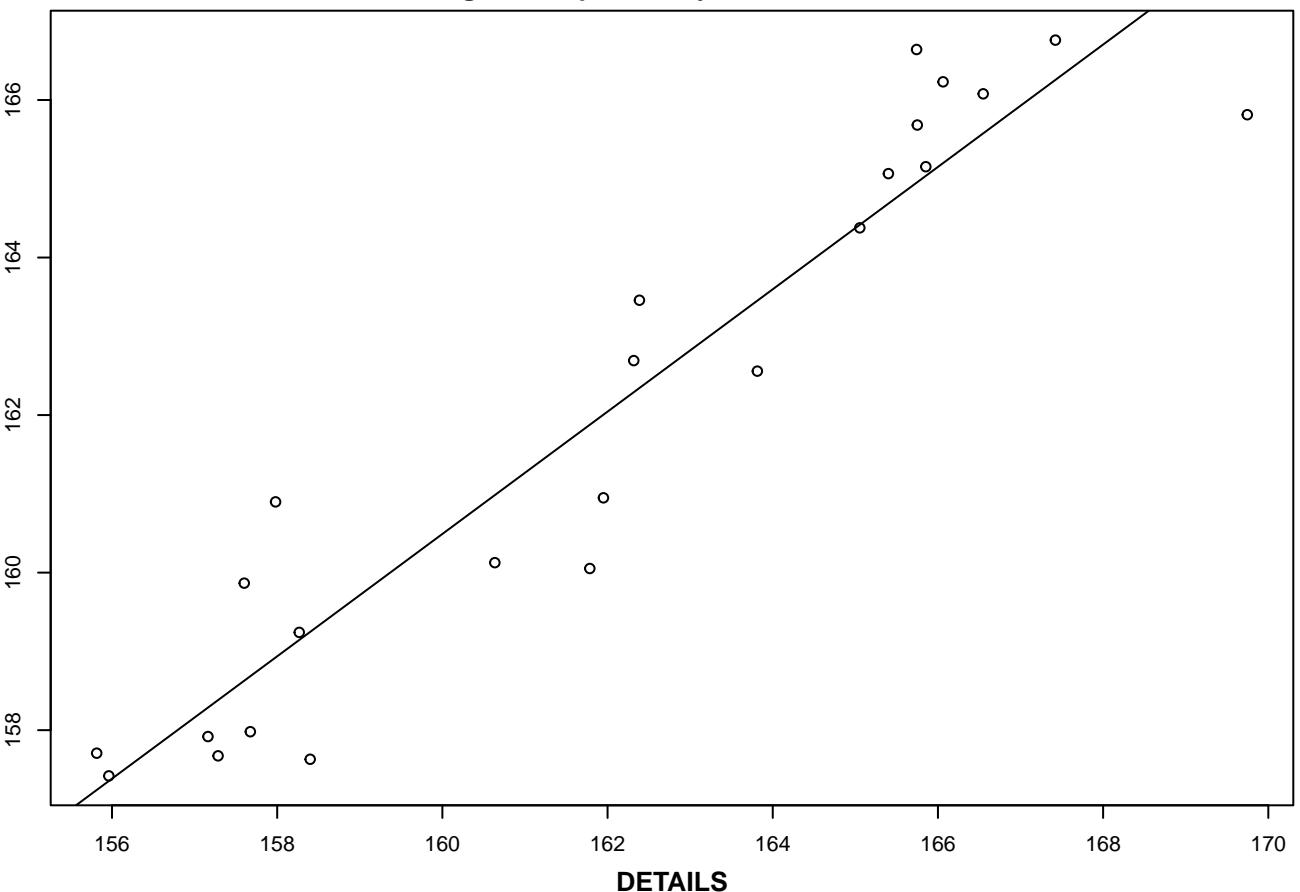
NMAE

0.6 %

R²

0.875

loocv_genes_top.intensity.fluo.lab.b.mean.csv



RMSE

1.397

NRMSE

0.9 %

MAE

1.066

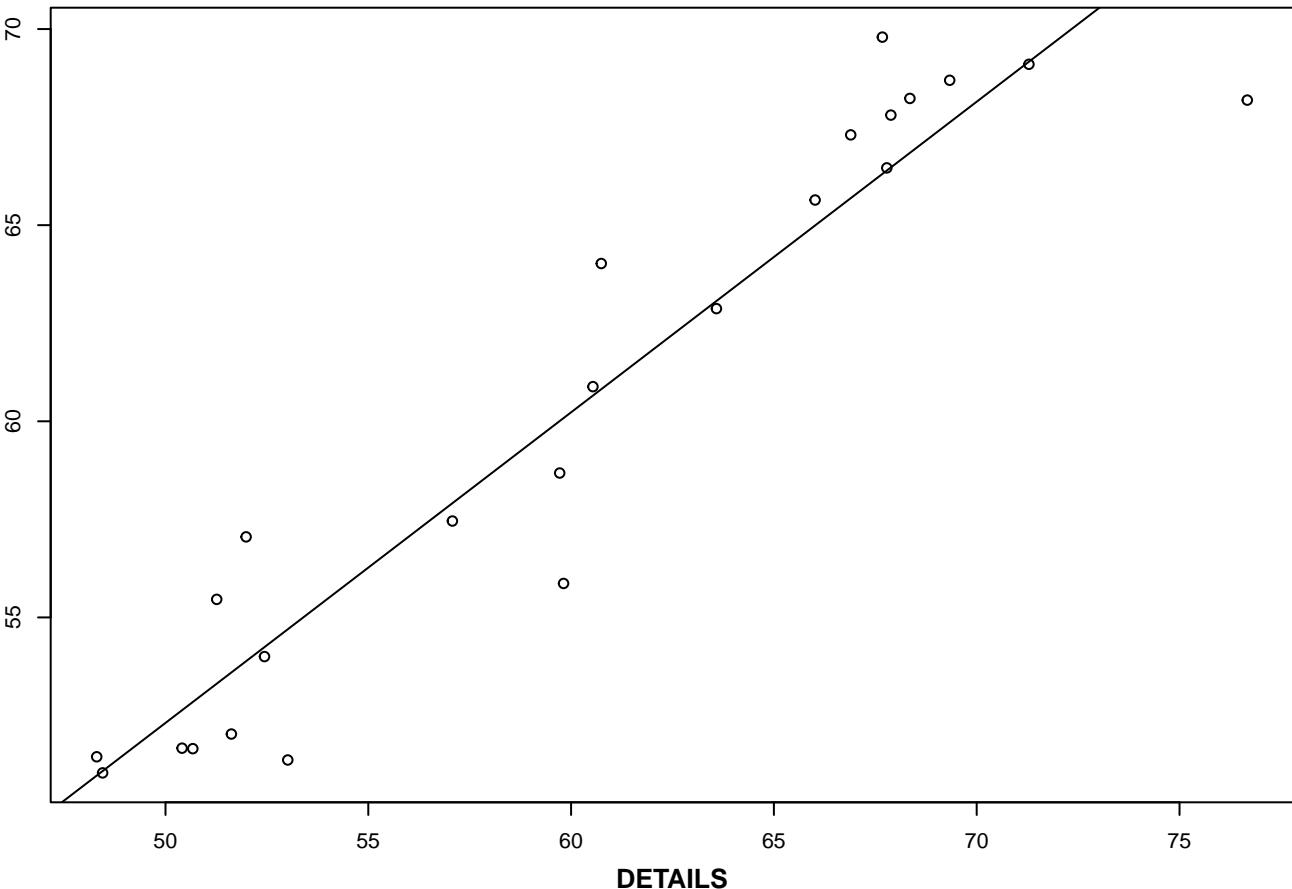
NMAE

0.7 %

R²

0.899

loocv_genes_top.intensity.fluo.lab.l.mean.csv



RMSE

2.736

NRMSE

4.6 %

MAE

1.929

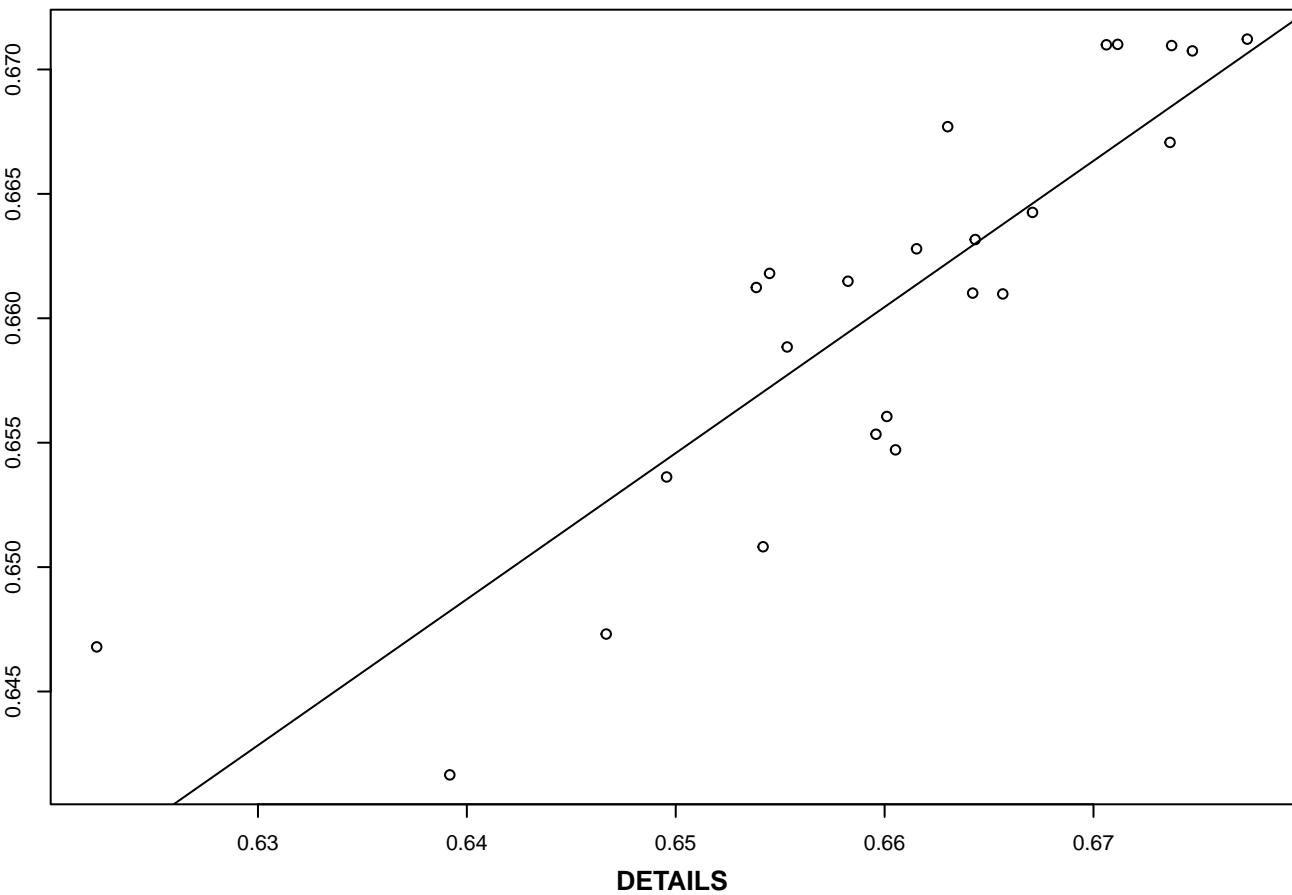
NMAE

3.2 %

R²

0.903

loocv_genes_top.intensity.nir.mean.csv



RMSE

0.006

NRMSE

1 %

MAE

0.005

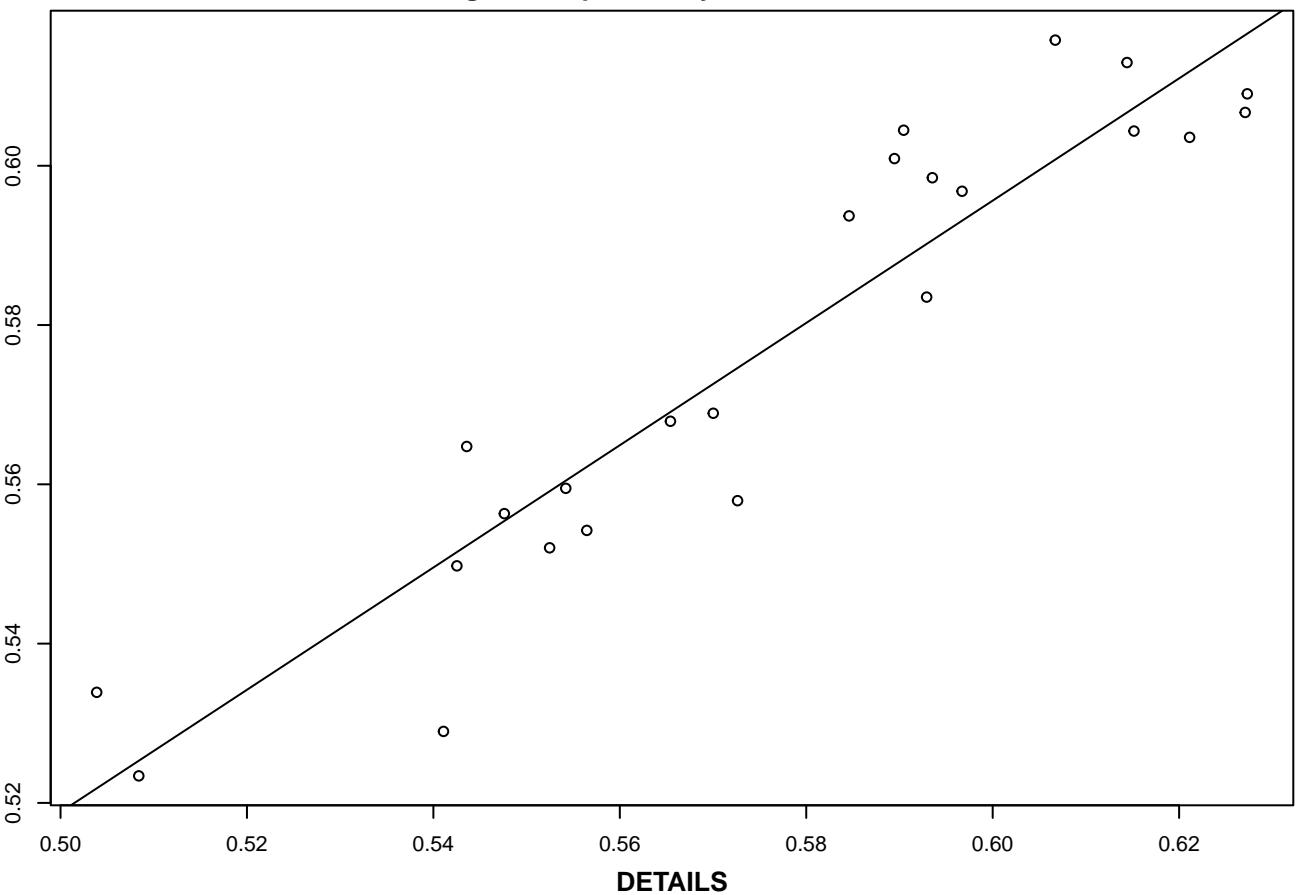
NMAE

0.7 %

R²

0.754

loocv_genes_top.intensity.vis.hsv.s.mean.csv



RMSE

0.013

NRMSE

2.2 %

MAE

0.01

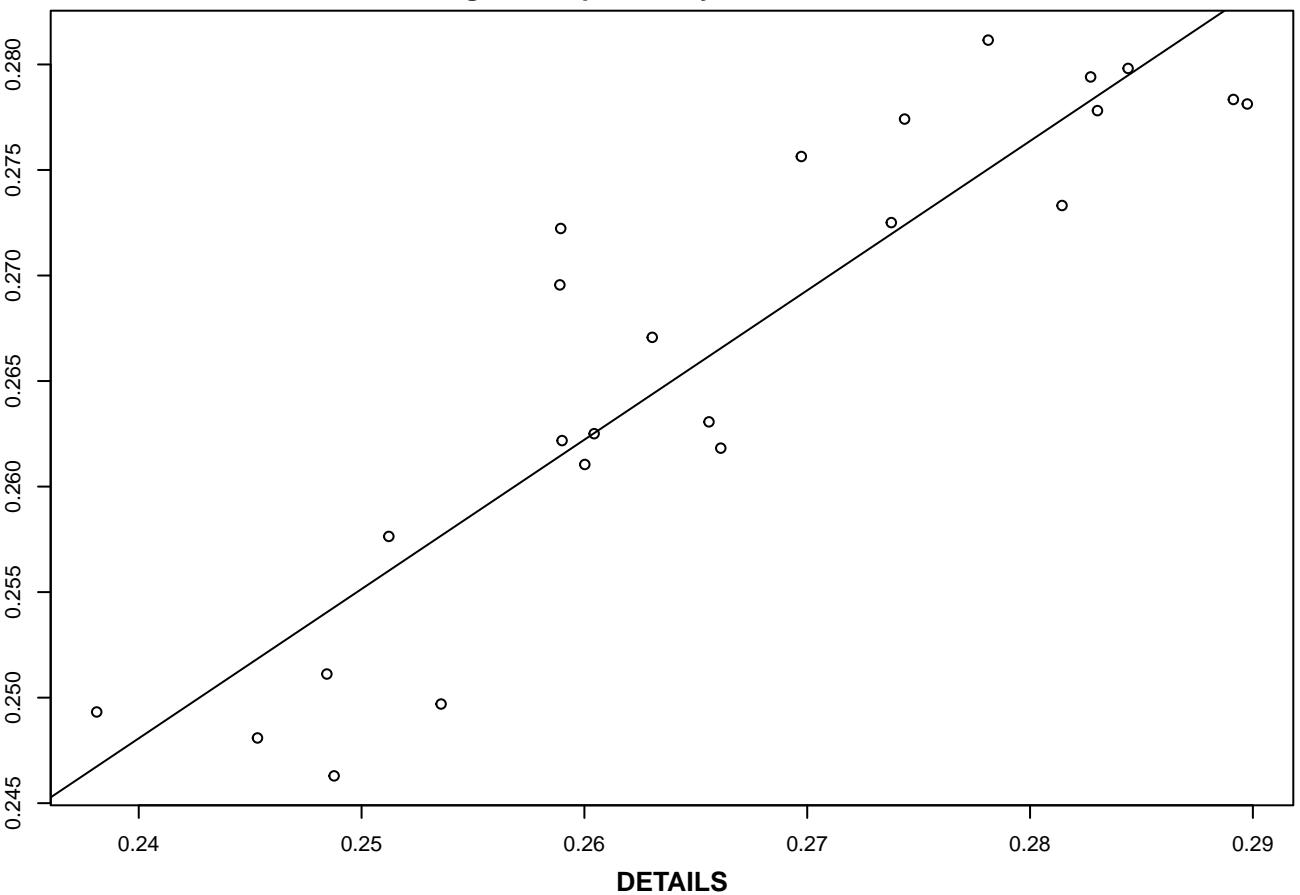
NMAE

1.8 %

R²

0.877

loocv_genes_top.intensity.vis.hsv.v.mean.csv



RMSE

0.006

NRMSE

2.4 %

MAE

0.005

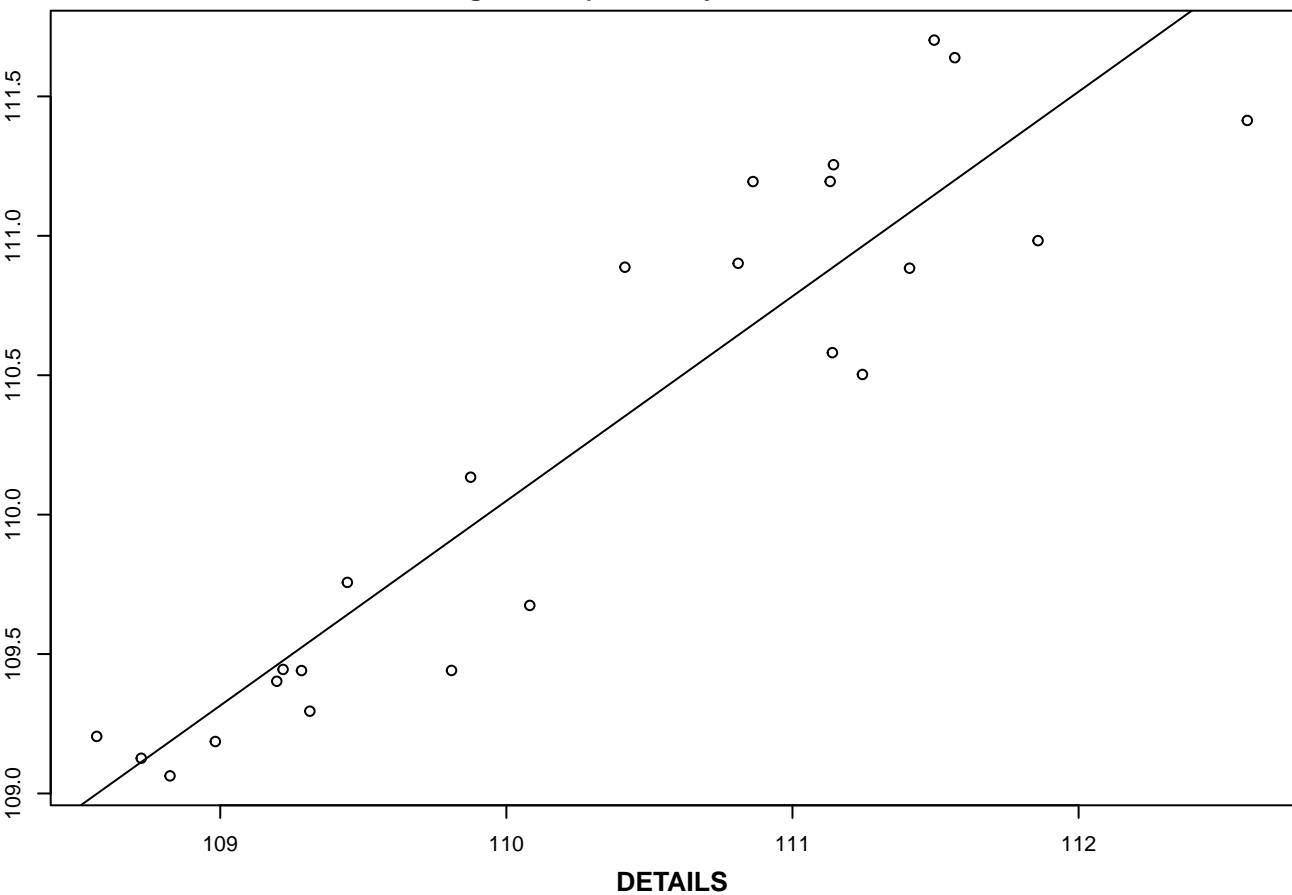
NMAE

2 %

R²

0.818

loocv_genes_top.intensity.vis.lab.a.mean.csv



RMSE

0.454

NRMSE

0.4 %

MAE

0.361

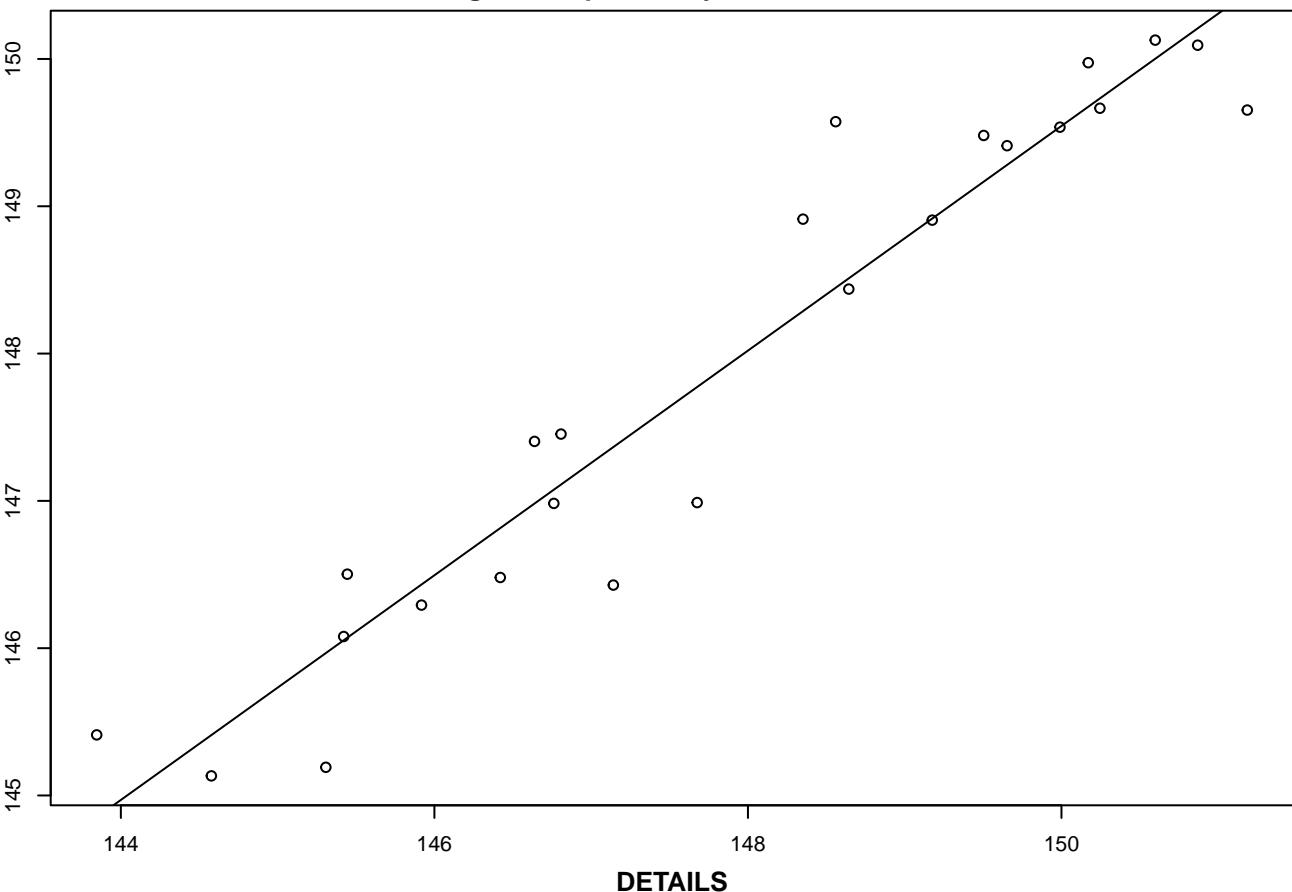
NMAE

0.3 %

R²

0.856

loocv_genes_top.intensity.vis.lab.b.mean.csv



RMSE

0.7

NRMSE

0.5 %

MAE

0.573

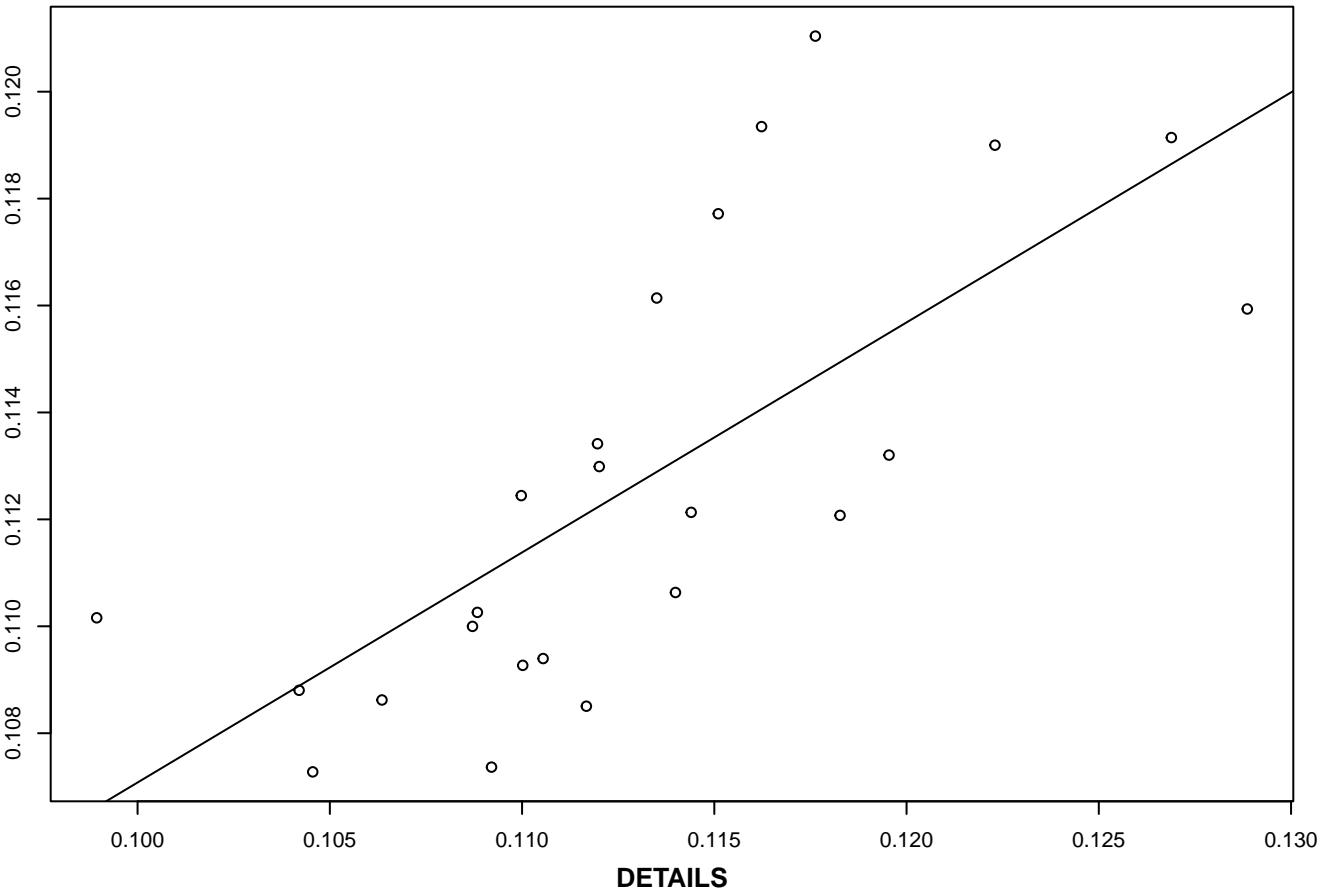
NMAE

0.4 %

R²

0.917

loocv_genes_top.intensity.vis.rgb.blue.mean.csv



RMSE

0.005

NRMSE

4.3 %

MAE

0.004

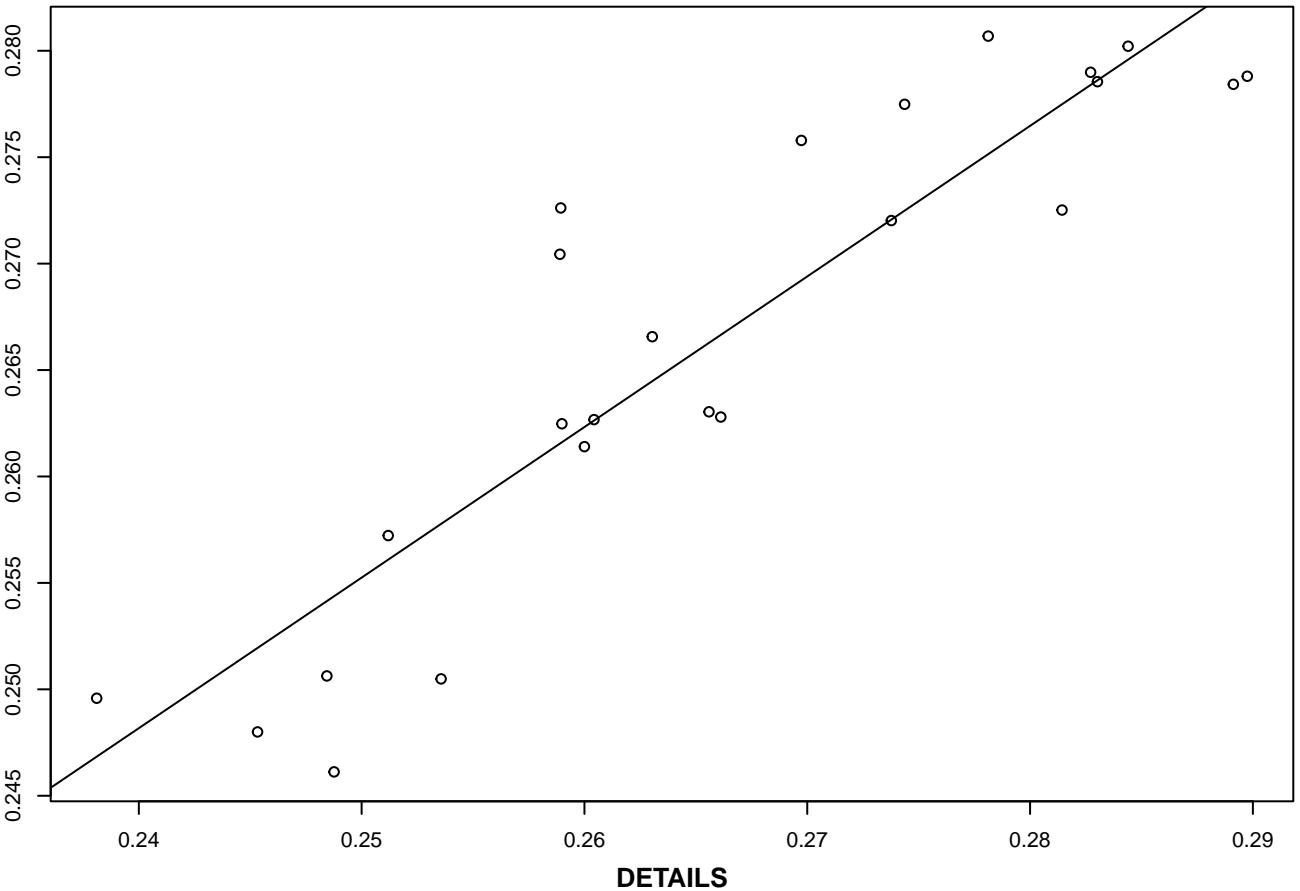
NMAE

3.3 %

R²

0.516

loocv_genes_top.intensity.vis.rgb.green.mean.csv



RMSE

0.006

NRMSE

2.4 %

MAE

0.005

NMAE

2 %

R²

0.817