

$\Delta\Delta G$ Report

April 1, 2016

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1 All data comparison

1.1 Case comparison tables

prediction_set_id	score_method	TopX	n	FC	R	MAE
zemu-values	zemu-paper	1	566	0.70	0.58	1.10
zemu-psbrub_1.6	Rescore-Talaris2014	50	566	0.74	0.56	1.02
		3	566	0.68	0.49	1.26
			566	0.21	0.03	140.48
james-backrub-rscript-full	Unrescored-Talaris	10	566	0.58	-0.01	54.55

Table 1.1: complete dataset. Abbreviations: FC = fraction correct, R = Pearson's R

prediction_set_id	score_method	TopX	n	FC	R	MAE
zemu-values	zemu-paper	1	566	0.71	0.58	1.03
zemu-psbrub_1.6	Rescore-Talaris2014	50	566	0.75	0.56	1.04
		3	566	0.69	0.49	1.10
			566	0.47	0.03	25.91
james-backrub-rscript-full	Unrescored-Talaris	10	566	0.62	-0.01	27.78

Table 1.2: complete dataset (scaled). Abbreviations: FC = fraction correct, R = Pearson's R

prediction_set_id	score_method	TopX	n	FC	R	MAE
zemu-values	zemu-paper	1	34	0.65	0.69	1.55
zemu-psbrub_1.6	Rescore-Talaris2014	3	34	0.56	0.68	1.64
		50	34	0.62	0.66	1.61
		3	34	0.38	0.33	83.49
james-backrub-rscript-full	Unrescored-Talaris	10	34	0.62	0.20	44.78

Table 1.3: cases with G or P. Abbreviations: FC = fraction correct, R = Pearson's R

prediction_set_id	score_method	TopX	n	FC	R	MAE
zemu-values	zemu-paper	1	532	0.71	0.56	1.07
zemu-psbrub_1.6	Rescore-Talaris2014	50	532	0.74	0.55	0.98
		3	532	0.68	0.48	1.24
		3	532	0.20	0.02	144.12
james-backrub-rscript-full	Unrescored-Talaris	10	532	0.57	-0.02	55.17

Table 1.4: cases without G or P. Abbreviations: FC = fraction correct, R = Pearson's R

prediction_set_id	score_method	TopX	n	FC	R	MAE
zemu-values	zemu-paper	1	488	0.71	0.57	1.08
zemu-psbrub_1.6	Rescore-Talaris2014	50	488	0.75	0.54	0.98
		3	488	0.68	0.47	1.25
			488	0.17	0.04	78.03
james-backrub-rscript-full	Unrescored-Talaris	10	488	0.60	-0.02	43.18

Table 1.5: large-to-small mutations. Abbreviations: FC = fraction correct, R = Pearson's R

prediction_set_id	score_method	TopX	n	FC	R	MAE
zemu-values	zemu-paper	1	113	0.76	0.62	1.56
zemu-psbrub_1.6	Rescore-Talaris2014	50	113	0.75	0.55	1.60
		3	113	0.73	0.52	1.78
			113	0.22	0.19	33.59
james-backrub-rscript-full	Unrescored-Talaris	10	113	0.50	0.11	21.47

Table 1.6: multiple mutations. Abbreviations: FC = fraction correct, R = Pearson's R

prediction_set_id	score_method	TopX	n	FC	R	MAE
zemu-psbrub_1.6	Rescore-Talaris2014	50	453	0.73	0.56	0.87
zemu-values	zemu-paper	1	453	0.69	0.54	0.99
zemu-psbrub_1.6	Rescore-Talaris2014	3	453	0.66	0.45	1.13
james-backrub-rscript-full	Unrescored-Talaris		453	0.21	0.02	167.14
		10	453	0.59	-0.02	62.80

Table 1.7: single mutations. Abbreviations: FC = fraction correct, R = Pearson's R

prediction_set_id	score_method	TopX	n	FC	R	MAE
zemu-psbrub_1.6	Rescore-Talaris2014	50	62	0.68	0.53	0.97
zemu-values	zemu-paper	1	62	0.65	0.48	1.09
zemu-psbrub_1.6	Rescore-Talaris2014	3	62	0.69	0.35	1.14
james-backrub-rscript-full	Unrescored-Talaris	10	62	0.48	-0.15	144.14
		3	62	0.37	-0.07	623.45

Table 1.8: small-to-large mutations. Abbreviations: FC = fraction correct, R = Pearson's R

1.2 All data plots

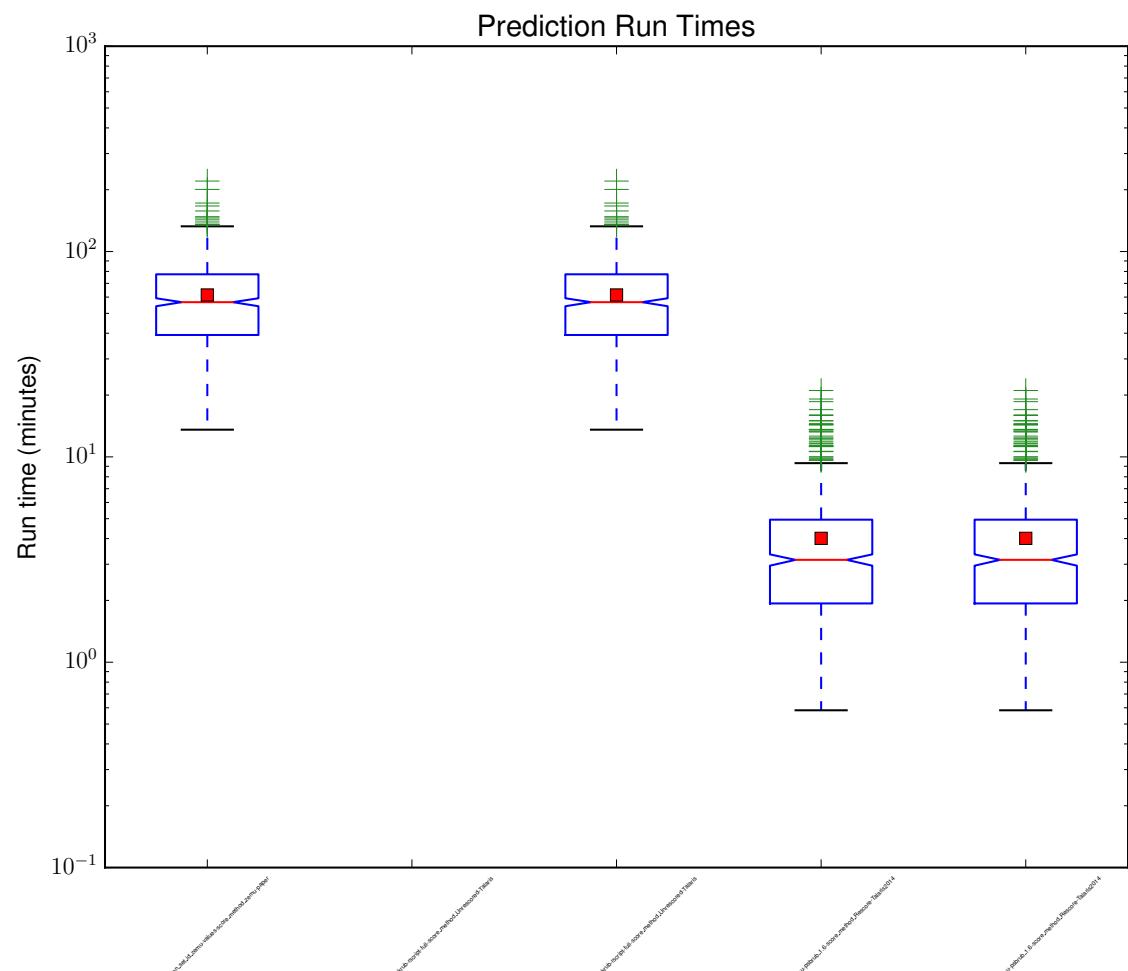


Figure 1.1: Run times

2 topx_50-prediction_set_id_zemu-psbrub_1.6-score_method_Rescore-Talaris2014

zemu-psbrub_1.6 Backrub ddG (Pooja and Samuel) on ZEMu with kT of 1.6 (ZEMu)

Prediction set scoring credit: Kyle Barlow

2.1 Data tables

The predicted DDG value per case is computed using the 50 lowest-scoring mutant structures and the 50 lowest-scoring wildtype structures.

Derived mutations in analysis are omitted):

The stability classification cutoffs are: Experimental=1.00 kcal/mol, Predicted=1.00 energy units.

2.1.1 Breakdown by volume

A case is considered a small-to-large (resp. large-to-small) mutation if all of the wildtype residues have a smaller (resp. larger) van der Waals volume than the corresponding mutant residue. The order is defined as G < A < S < C < P < D < T < N < V < E < Q < H < ILM < FK < Y < R < W so some cases are considered to have no change in volume e.g. MET → LEU.

Not enough data for analysis of mutations no change in volume (at least 8 cases are required).

Statistic name	Value	p-value
Fraction correct	0.68	
Fraction correct (fuzzy)	0.69	
Gamma correlation coef.	0.19	
Kolmogorov-Smirnov test (XY)	0.18	(2-tailed p-value= 2.57×10^{-01})
MAE	0.97	
Pearson's R	0.53	(2-tailed p-value= 9.59×10^{-06})
Spearman's R	0.29	(2-tailed p-value= 2.28×10^{-02})
X-axis Kolmogorov-Smirnov test	0.13	(p-value= 2.29×10^{-01})
X-axis normality test	2.18	(2-sided chi ² p-value= 3.36×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.19	(p-value= 1.97×10^{-02})
Y-axis normality test	37.64	(2-sided chi ² p-value= 6.71×10^{-09})
n	62.00	
num_null_cases	0.00	

Table 2.1: Statistics - small-to-large mutations (62 cases)

Statistic name	Value	p-value
Fraction correct	0.75	
Fraction correct (fuzzy)	0.77	
Gamma correlation coef.	0.39	
Kolmogorov-Smirnov test (XY)	0.19	(2-tailed p-value= 4.42×10^{-08})
MAE	0.98	
Pearson's R	0.54	(2-tailed p-value= 5.24×10^{-39})
Spearman's R	0.58	(2-tailed p-value= 7.41×10^{-45})
X-axis Kolmogorov-Smirnov test	0.36	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	92.92	(2-sided chi ² p-value= 6.64×10^{-21})
Y-axis Kolmogorov-Smirnov test	0.40	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	198.70	(2-sided chi ² p-value= 7.13×10^{-44})
n	488.00	
num_null_cases	0.00	

Table 2.2: Statistics - large-to-small mutations (488 cases)

2.1.2 Separating out mutations involving glycine or proline.

This cases may involve changes to secondary structure so we separate them out here.

Statistic name	Value	p-value
Fraction correct	0.62	
Fraction correct (fuzzy)	0.64	
Gamma correlation coef.	0.49	
Kolmogorov-Smirnov test (XY)	0.24	(2-tailed p-value= 2.65×10^{-01})
MAE	1.61	
Pearson's R	0.66	(2-tailed p-value= 1.83×10^{-05})
Spearman's R	0.65	(2-tailed p-value= 3.13×10^{-05})
X-axis Kolmogorov-Smirnov test	0.52	(p-value= 4.57×10^{-09})
X-axis normality test	0.66	(2-sided chi ² p-value= 7.21×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.34	(p-value= 5.48×10^{-04})
Y-axis normality test	5.33	(2-sided chi ² p-value= 6.96×10^{-02})
n	34.00	
num_null_cases	0.00	

Table 2.3: Statistics - cases with G or P (34 cases)

Statistic name	Value	p-value
Fraction correct	0.74	
Fraction correct (fuzzy)	0.76	
Gamma correlation coef.	0.39	
Kolmogorov-Smirnov test (XY)	0.17	(2-tailed p-value= 5.42×10^{-07})
MAE	0.98	
Pearson's R	0.55	(2-tailed p-value= 2.45×10^{-43})
Spearman's R	0.58	(2-tailed p-value= 3.12×10^{-48})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	57.49	(2-sided chi ² p-value= 3.28×10^{-13})
Y-axis Kolmogorov-Smirnov test	0.37	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	239.14	(2-sided chi ² p-value= 1.18×10^{-52})
n	532.00	
num_null_cases	0.00	

Table 2.4: Statistics - cases without G or P (532 cases)

2.1.3 Number of mutations

Statistic name	Value	p-value
Fraction correct	0.73	
Fraction correct (fuzzy)	0.74	
Gamma correlation coef.	0.33	
Kolmogorov-Smirnov test (XY)	0.20	(2-tailed p-value= 1.69×10^{-08})
MAE	0.87	
Pearson's R	0.56	(2-tailed p-value= 2.12×10^{-39})
Spearman's R	0.49	(2-tailed p-value= 9.78×10^{-29})
X-axis Kolmogorov-Smirnov test	0.32	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	116.40	(2-sided chi ² p-value= 5.29×10^{-26})
Y-axis Kolmogorov-Smirnov test	0.37	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	165.57	(2-sided chi ² p-value= 1.11×10^{-36})
n	453.00	
num_null_cases	0.00	

Table 2.5: Statistics - single mutations (453 cases)

Statistic name	Value	p-value
Fraction correct	0.75	
Fraction correct (fuzzy)	0.77	
Gamma correlation coef.	0.48	
Kolmogorov-Smirnov test (XY)	0.12	(2-tailed p-value= 4.21×10^{-01})
MAE	1.60	
Pearson's R	0.55	(2-tailed p-value= 2.20×10^{-10})
Spearman's R	0.69	(2-tailed p-value= 3.26×10^{-17})
X-axis Kolmogorov-Smirnov test	0.45	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	4.54	(2-sided chi ² p-value= 1.03×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.40	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	18.32	(2-sided chi ² p-value= 1.05×10^{-04})
n	113.00	
num_null_cases	0.00	

Table 2.6: Statistics - multiple mutations (113 cases)

2.1.4 Entire dataset using a scaling factor of 1/0.917 to improve the fraction correct metric.

Warning: Results in this section use an averaged scaling factor to improve the value for the fraction correct metric. This scalar will vary over benchmark runs so these results should not be interpreted as performance results; they should be considered as what could be obtained if the predicted values were scaled by a "magic" value.

Statistic name	Value	p-value
Fraction correct	0.75	
Fraction correct (fuzzy)	0.76	
Gamma correlation coef.	0.40	
Kolmogorov-Smirnov test (XY)	0.16	(2-tailed p-value= 9.82×10^{-07})
MAE	1.04	
Pearson's R	0.56	(2-tailed p-value= 4.65×10^{-48})
Spearman's R	0.58	(2-tailed p-value= 2.77×10^{-52})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	52.55	(2-sided chi ² p-value= 3.88×10^{-12})
Y-axis Kolmogorov-Smirnov test	0.36	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	238.24	(2-sided chi ² p-value= 1.85×10^{-52})
n	566.00	
num_null_cases	0.00	

Table 2.7: Statistics - complete dataset (scaled) (566 cases)

2.1.5 Entire dataset

Overall statistics

Statistic name	Value	p-value
Fraction correct	0.74	
Fraction correct (fuzzy)	0.75	
Gamma correlation coef.	0.40	
Kolmogorov-Smirnov test (XY)	0.16	(2-tailed p-value= 5.11×10^{-07})
MAE	1.02	
Pearson's R	0.56	(2-tailed p-value= 4.65×10^{-48})
Spearman's R	0.58	(2-tailed p-value= 2.77×10^{-52})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	52.55	(2-sided chi ² p-value= 3.88×10^{-12})
Y-axis Kolmogorov-Smirnov test	0.36	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	238.24	(2-sided chi ² p-value= 1.85×10^{-52})
n	566.00	
num_null_cases	0.00	

Table 2.8: Statistics - complete dataset (566 cases)

2.2 Main plots

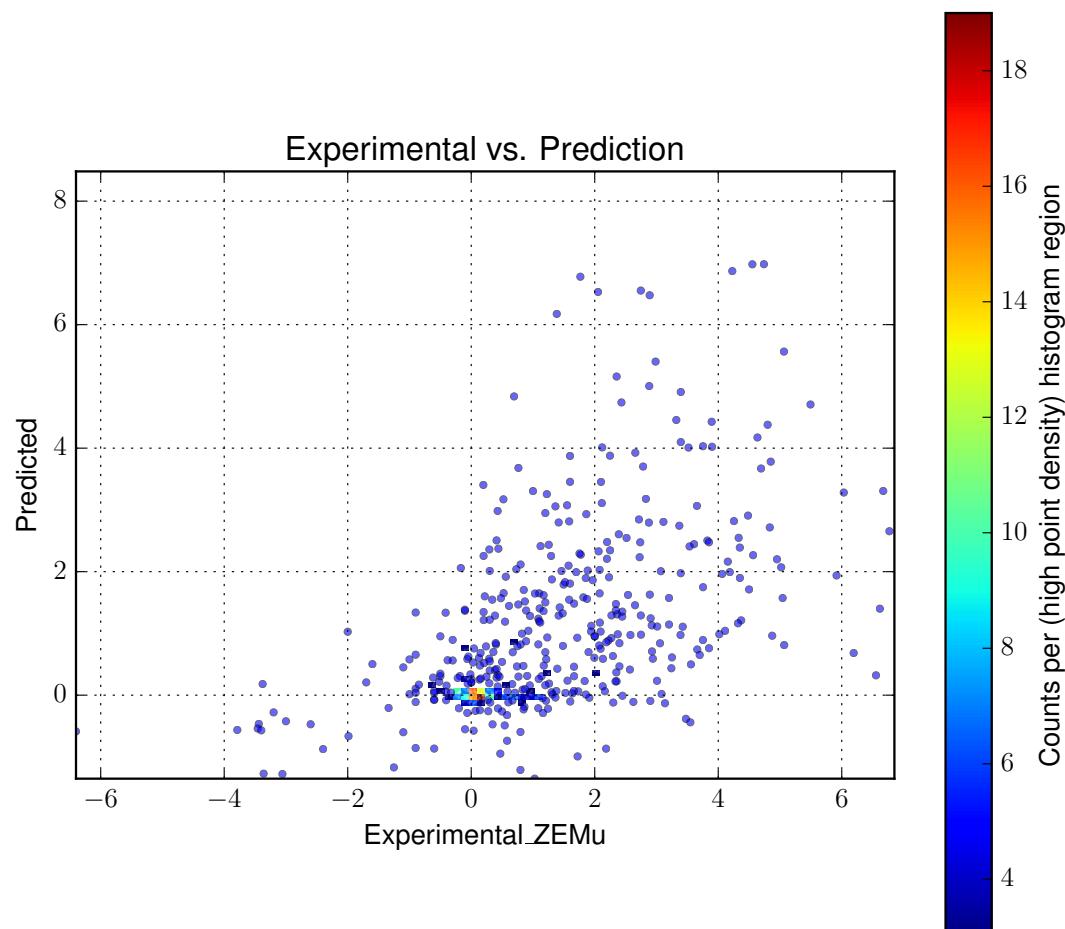
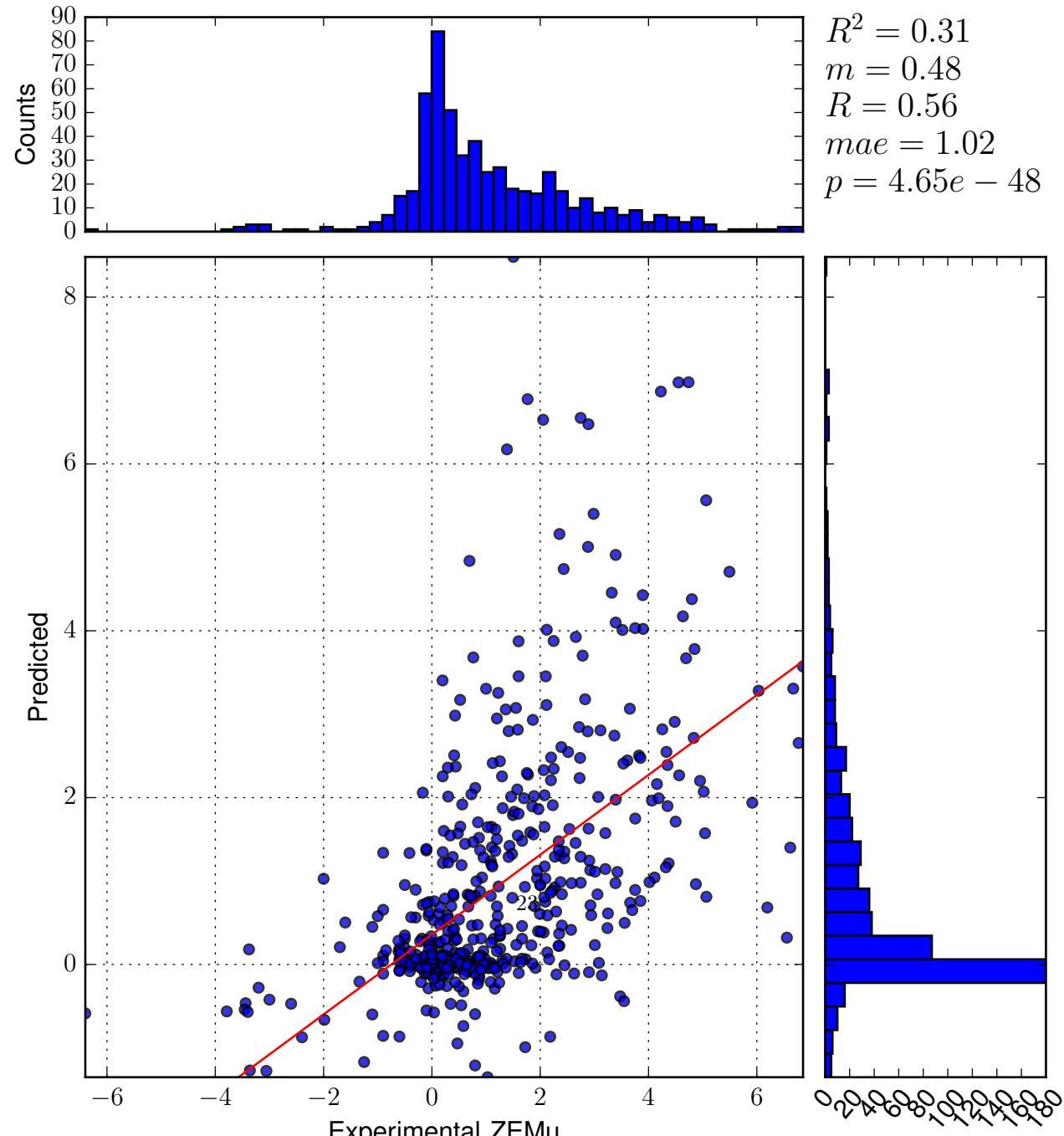
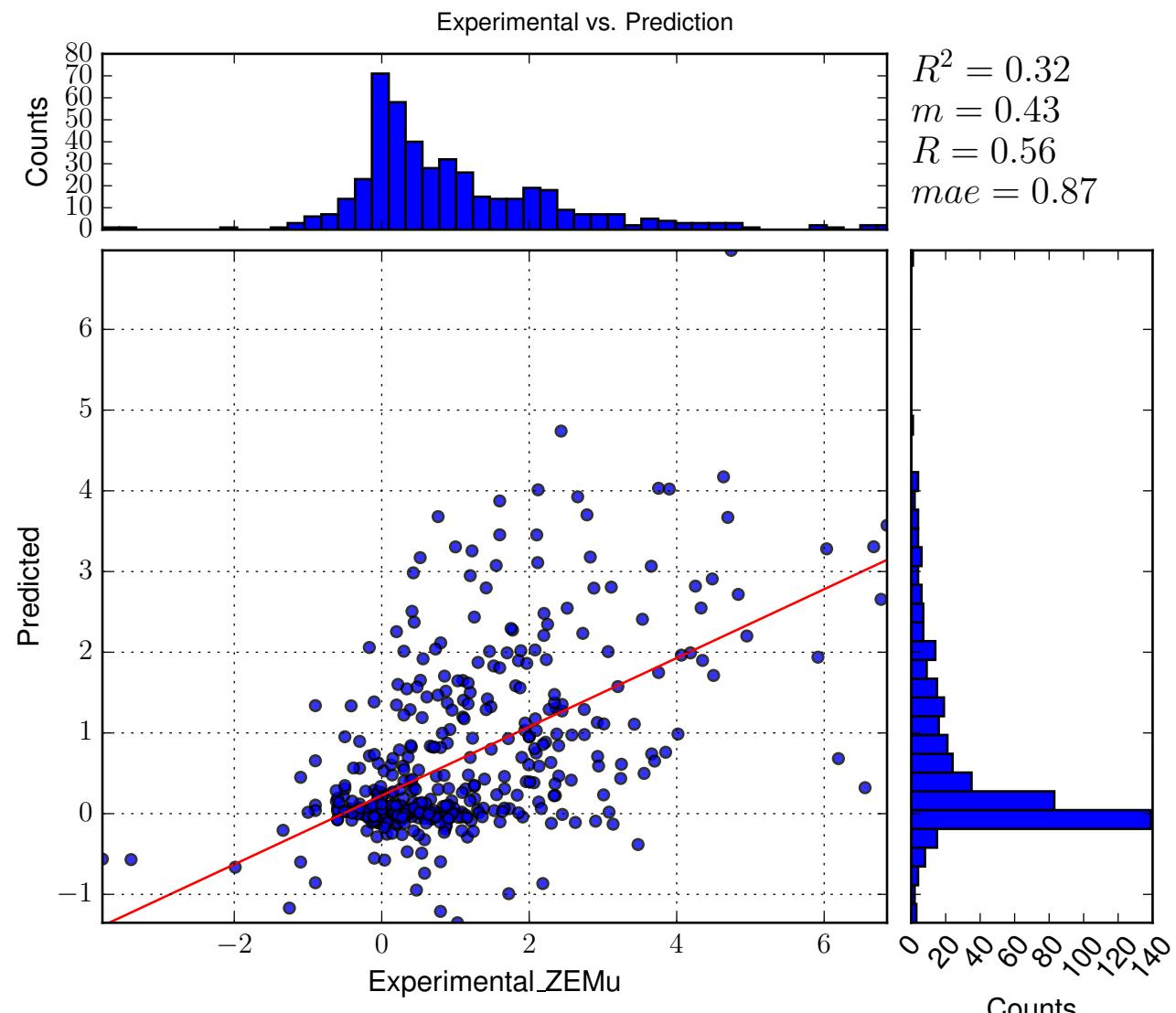


Figure 2.1: Experimental vs. Predicted scatterplot (with density binning)

Experimental vs. Prediction





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Figure 2.3: Single mutations data subset

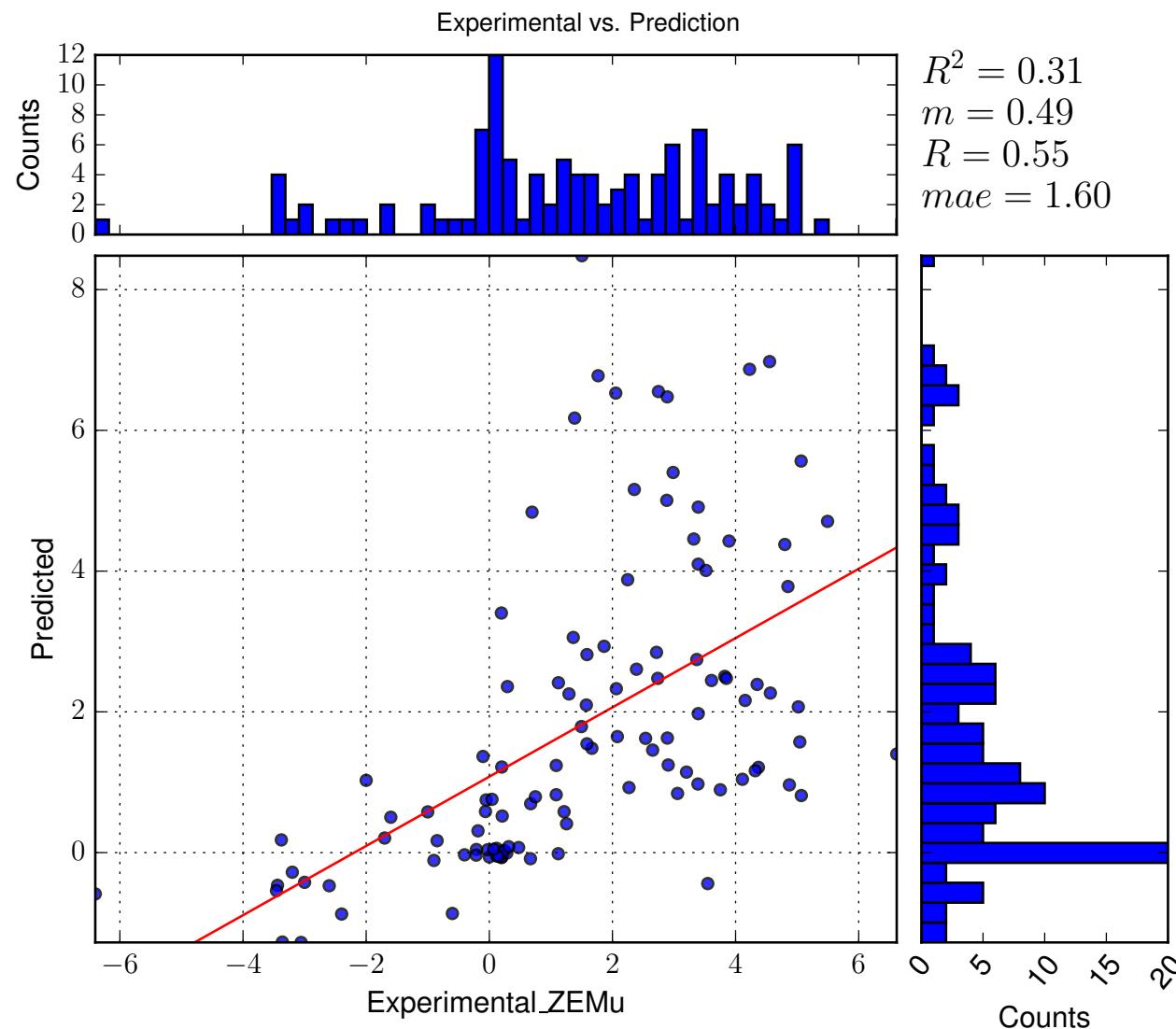
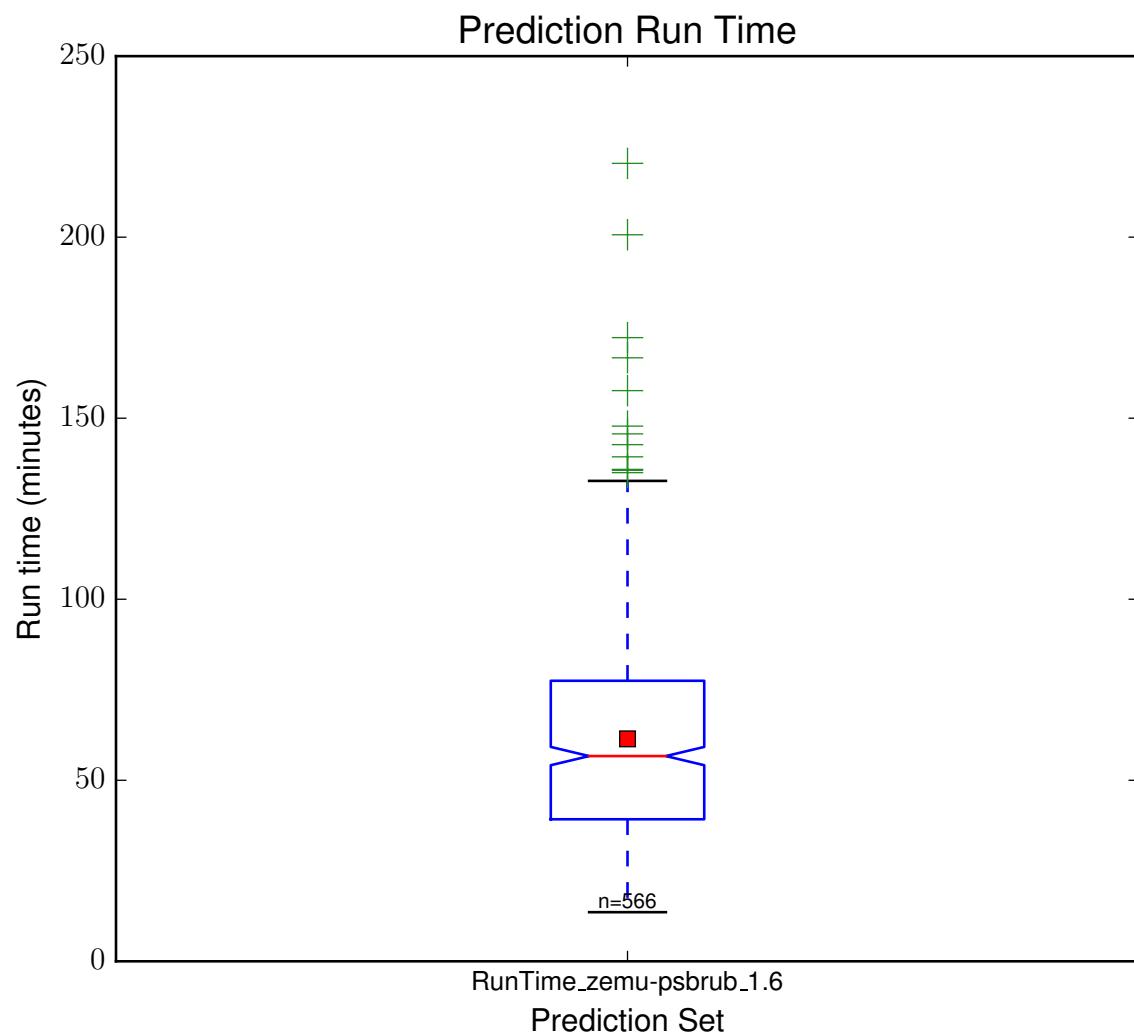


Figure 2.4: Multiple mutations data subset



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Figure 2.5: Run time

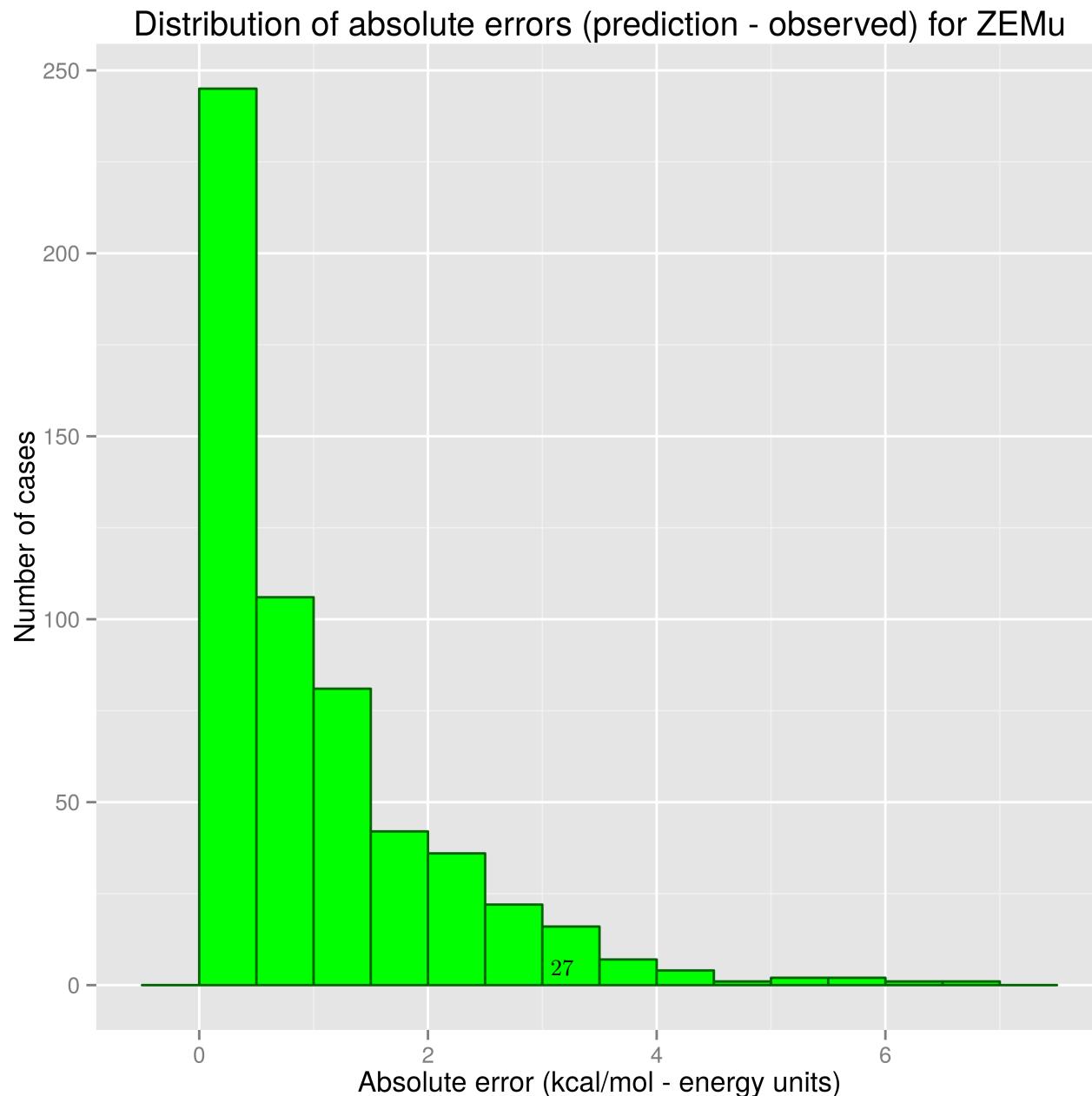


Figure 2.6: Absolute error histogram

2.3 Adjustments

Optimization of the cutoffs for the fraction correct metric

Optimum cutoff for fraction correct metric at varying experimental cutoffs for ZF

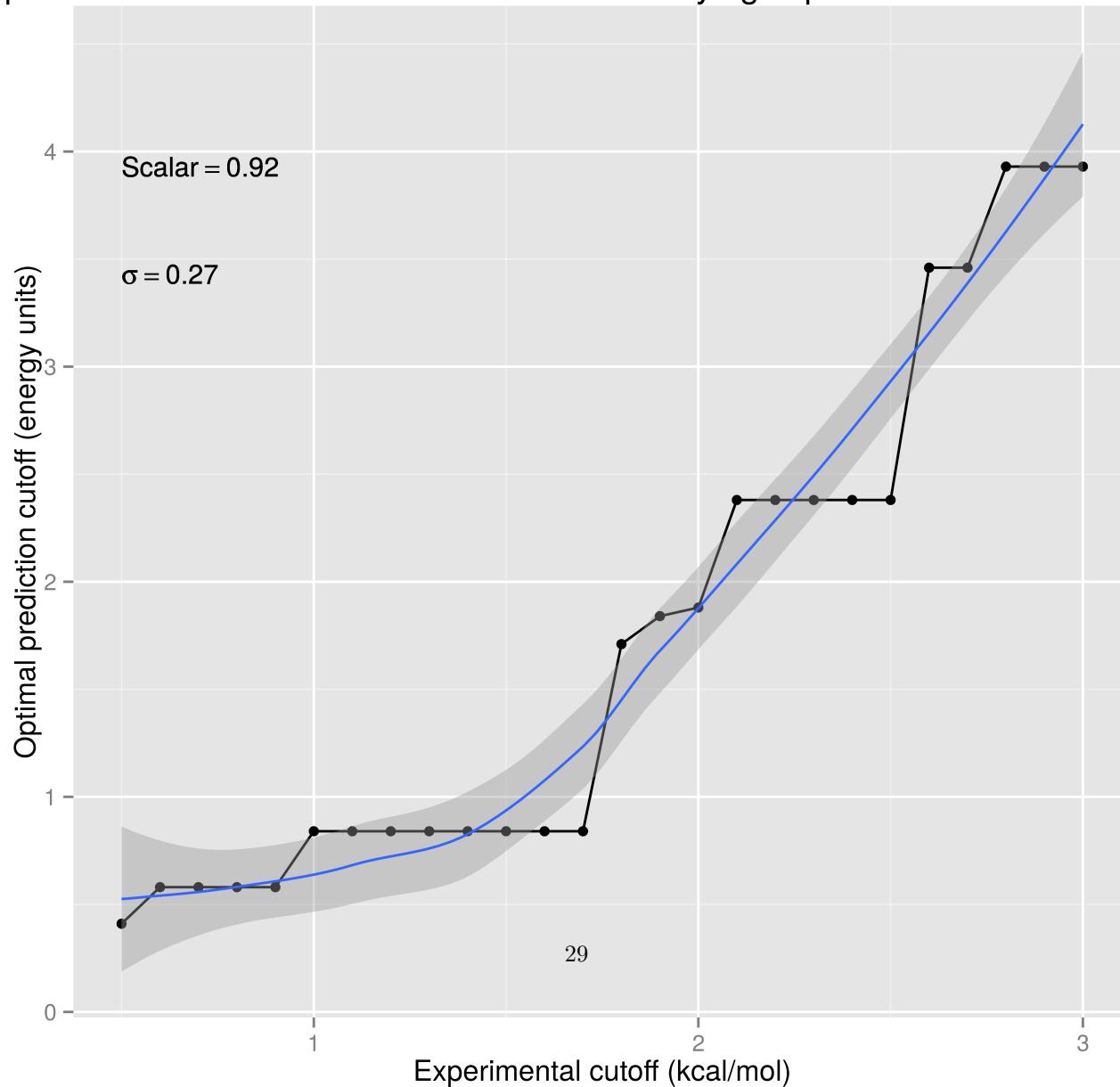


Figure 2.7: Scalar adjustment calculation plot

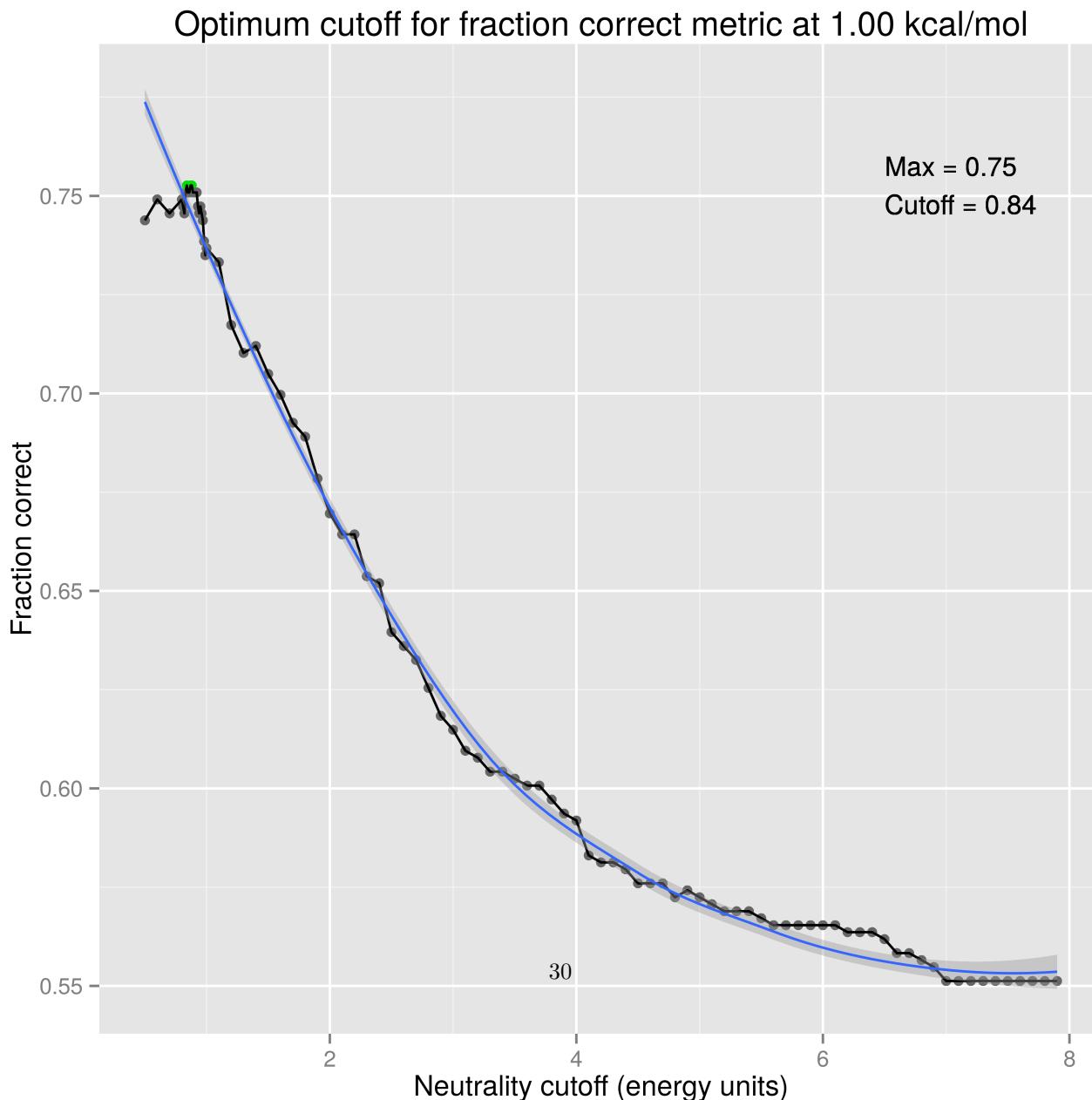


Figure 2.8: Optimal predictive cutoff plot

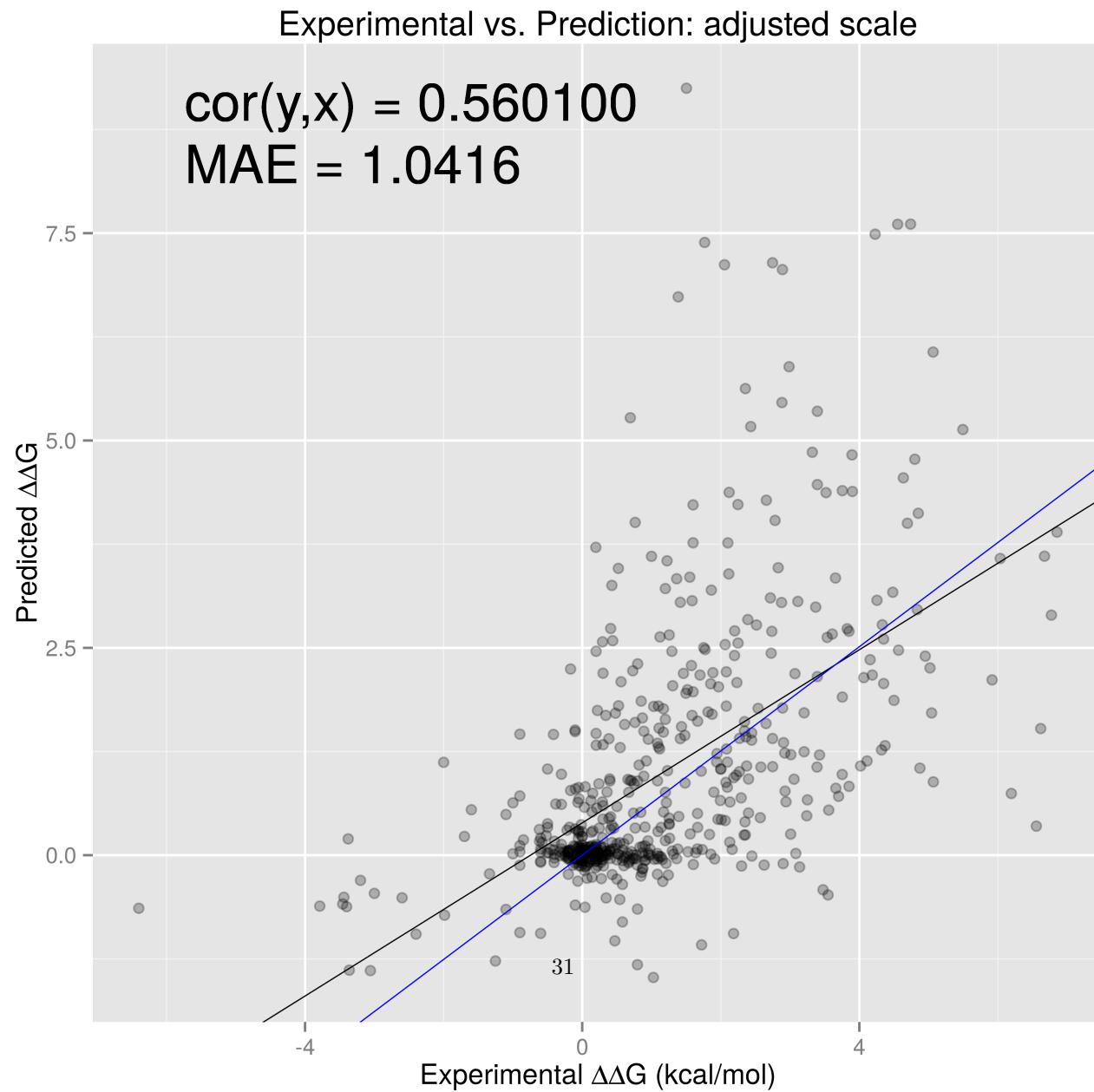


Figure 2.9: Main adj. scatterplot

Distribution of absolute errors (prediction - observed) for ZEMu

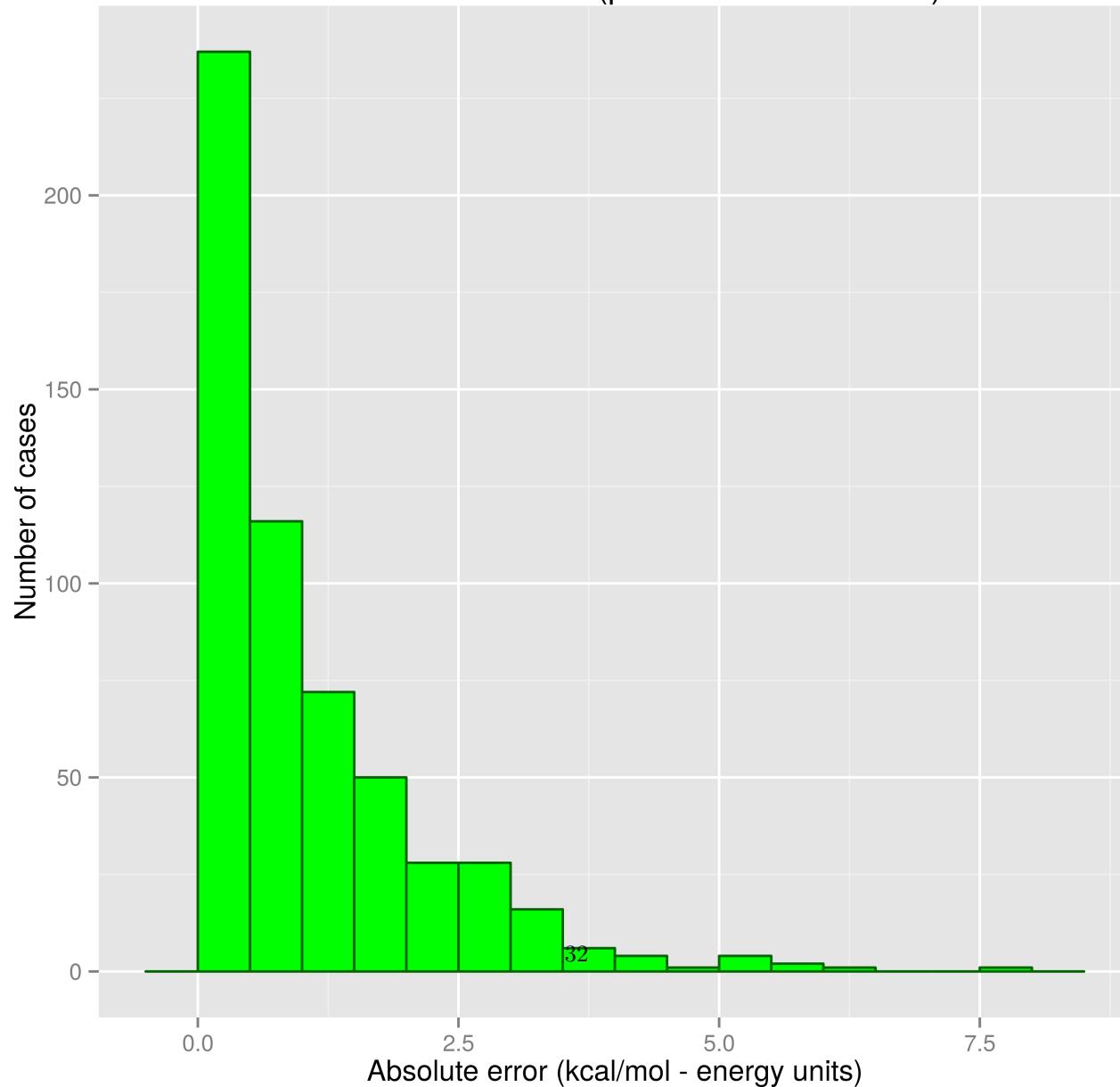
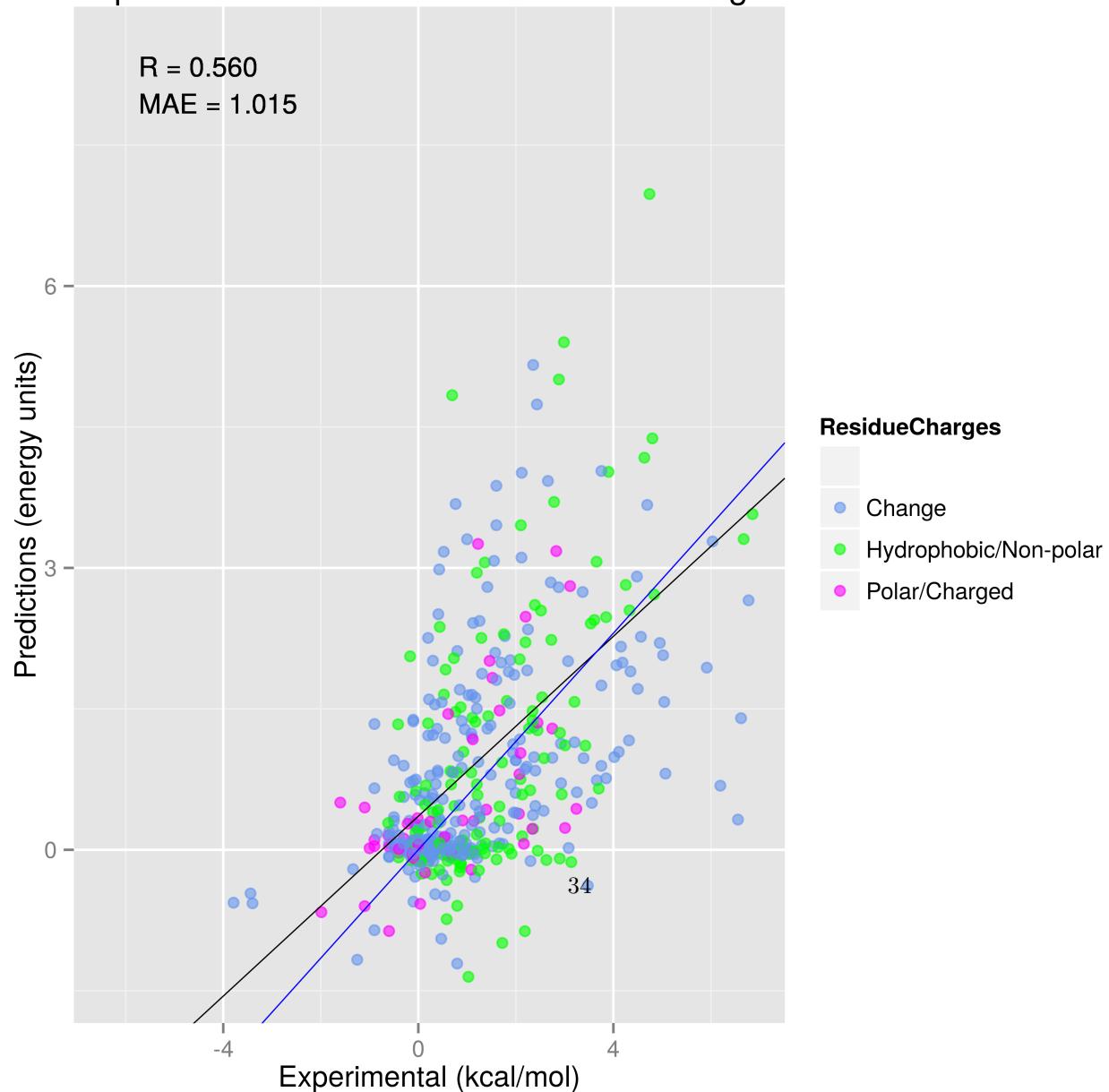


Figure 2.10: Absolute errors adjusted with scalar

2.4 Residue context

Experimental vs. Prediction - Residue charges



Experimental vs. Prediction - Exposure (cutoff = 0.25)

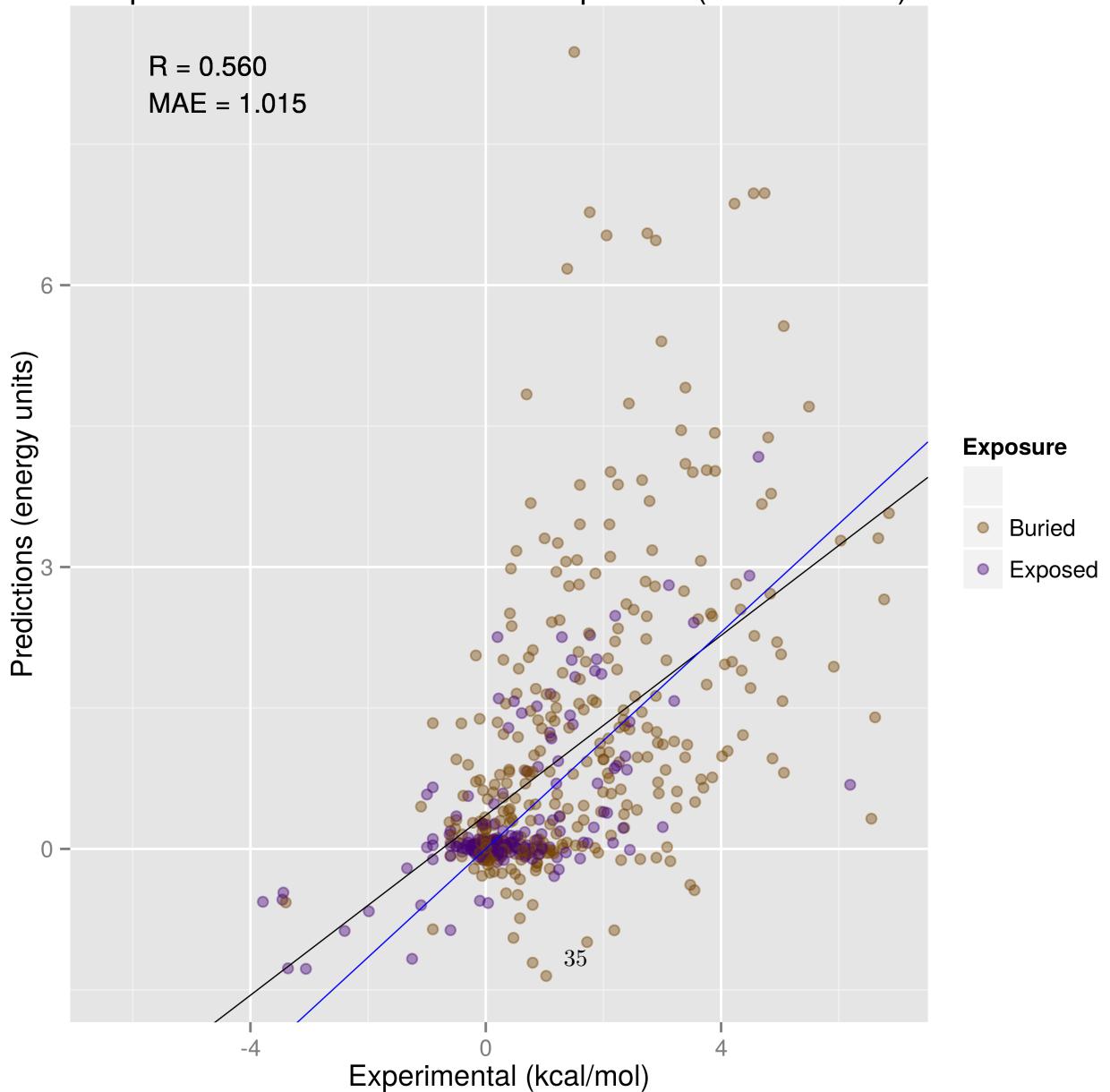


Figure 2.12: Experimental vs. Prediction - Exposure (cutoff = 0.25)

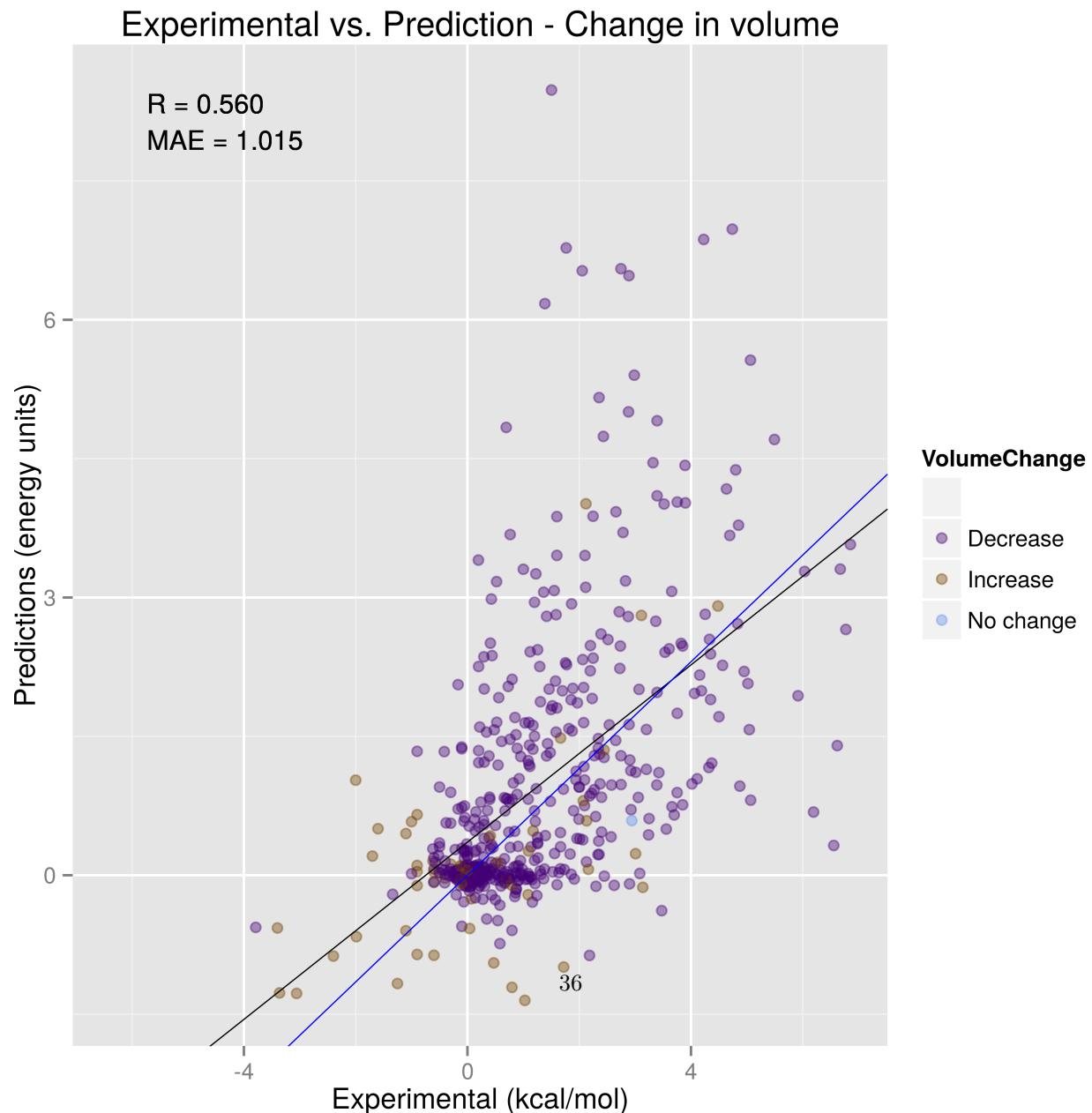


Figure 2.13: Experimental vs. Prediction - Change in volume

Experimental vs. Prediction - Wildtype residue s.s.

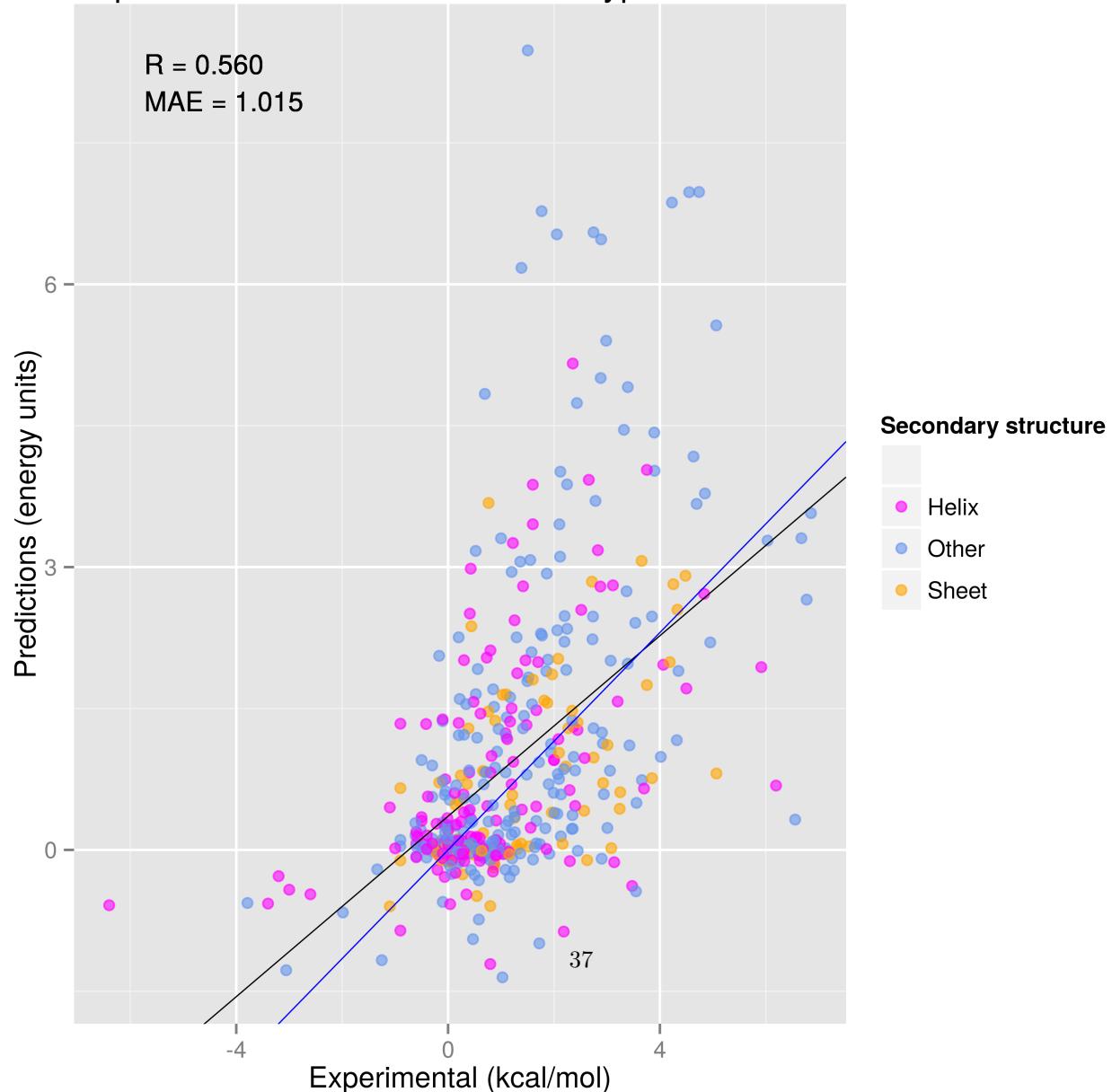
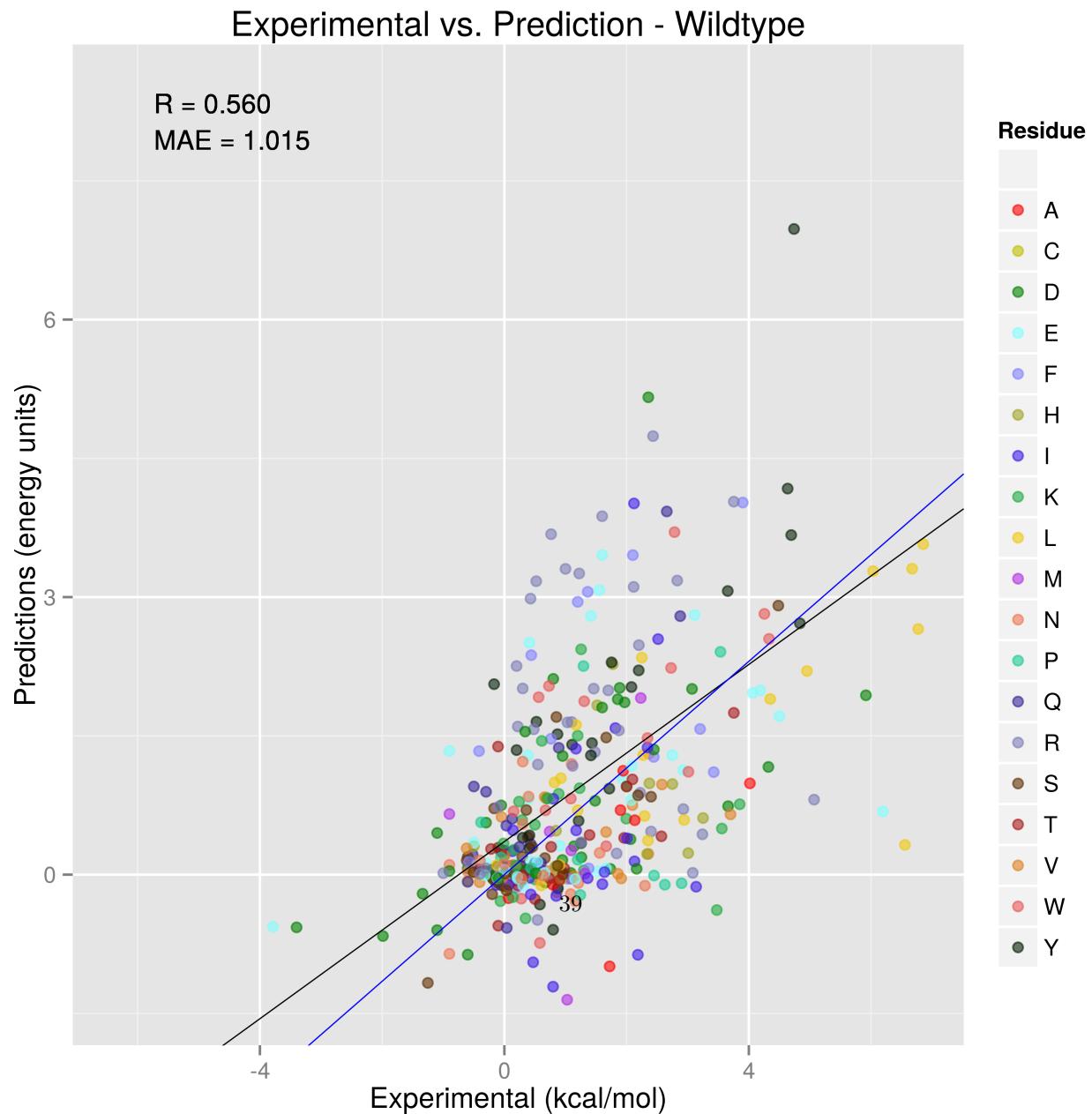


Figure 2.14: Experimental vs. Prediction - Wildtype residue s.s.

2.5 Residue types



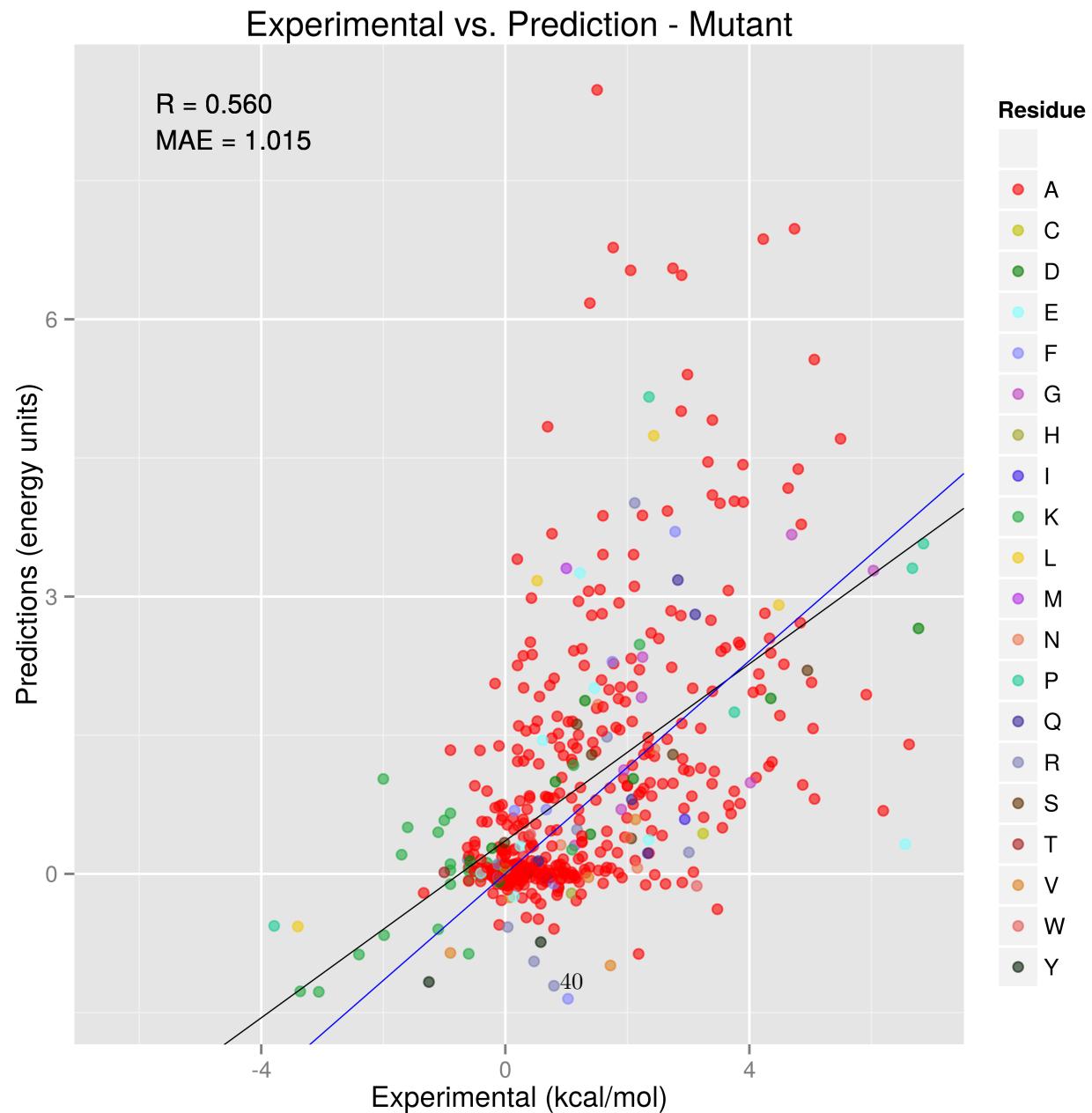


Figure 2.16: Experimental vs. Prediction - Mutant

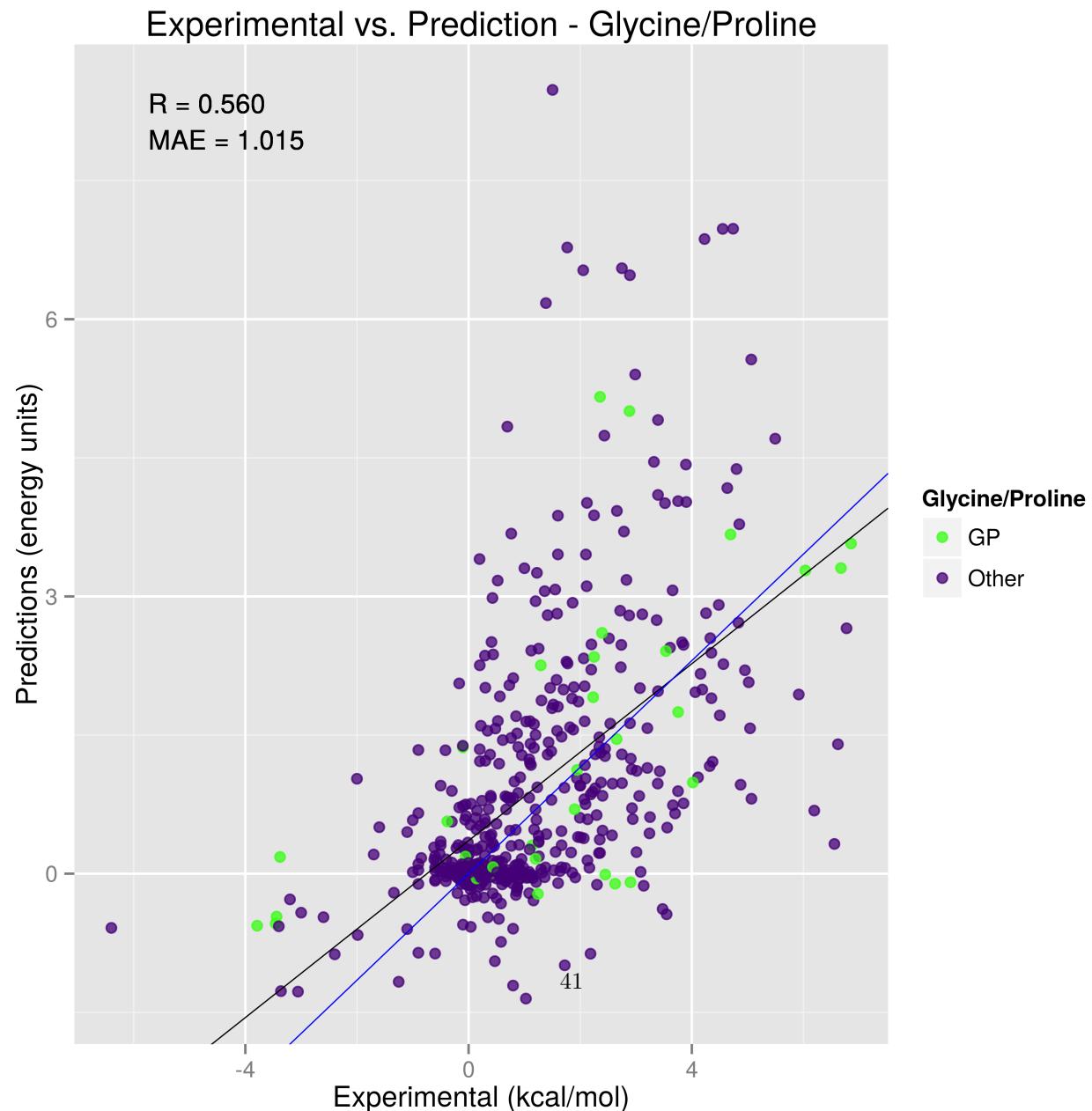
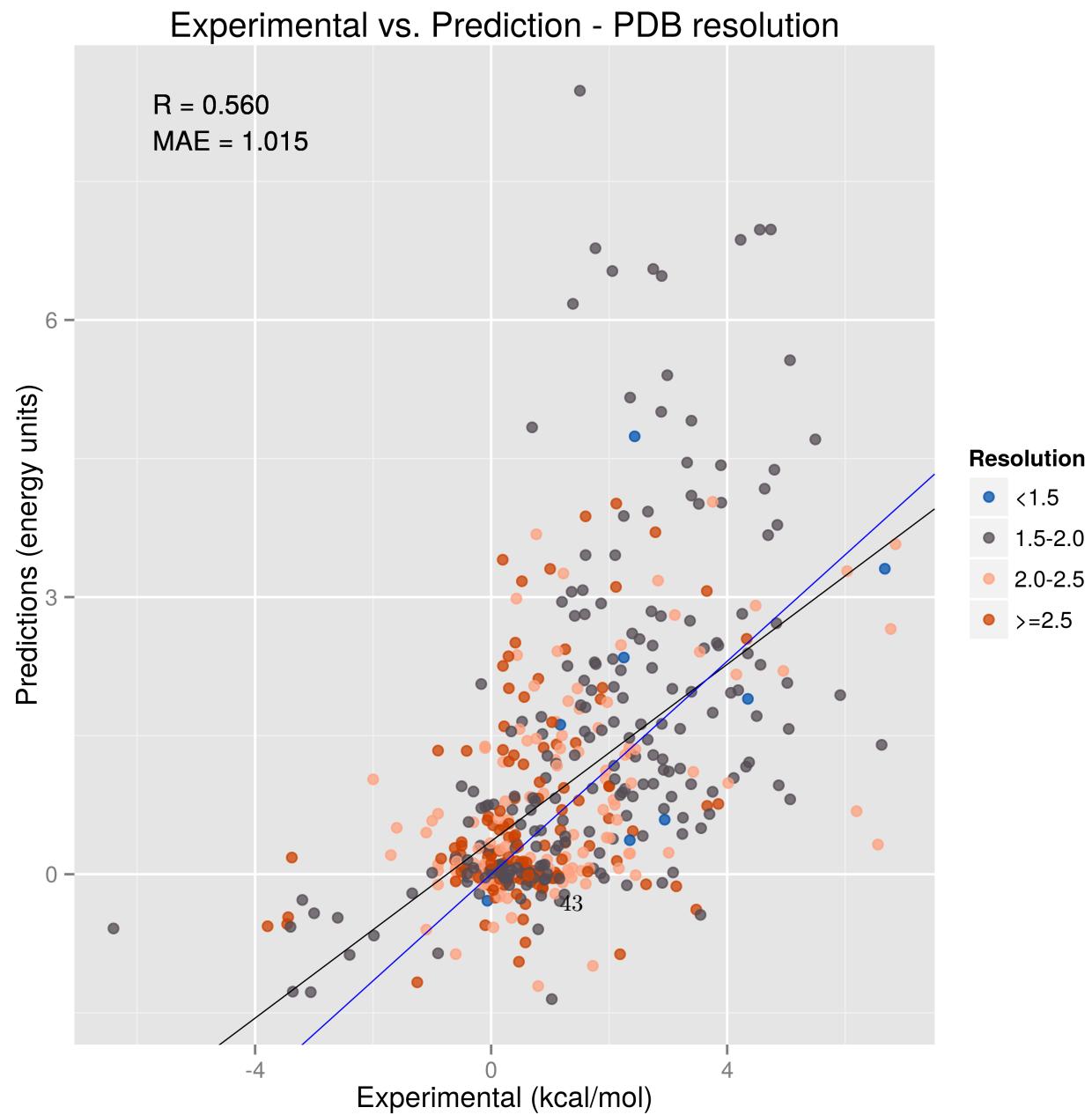


Figure 2.17: Experimental vs. Prediction - Glycine/Proline

2.6 Chain properties



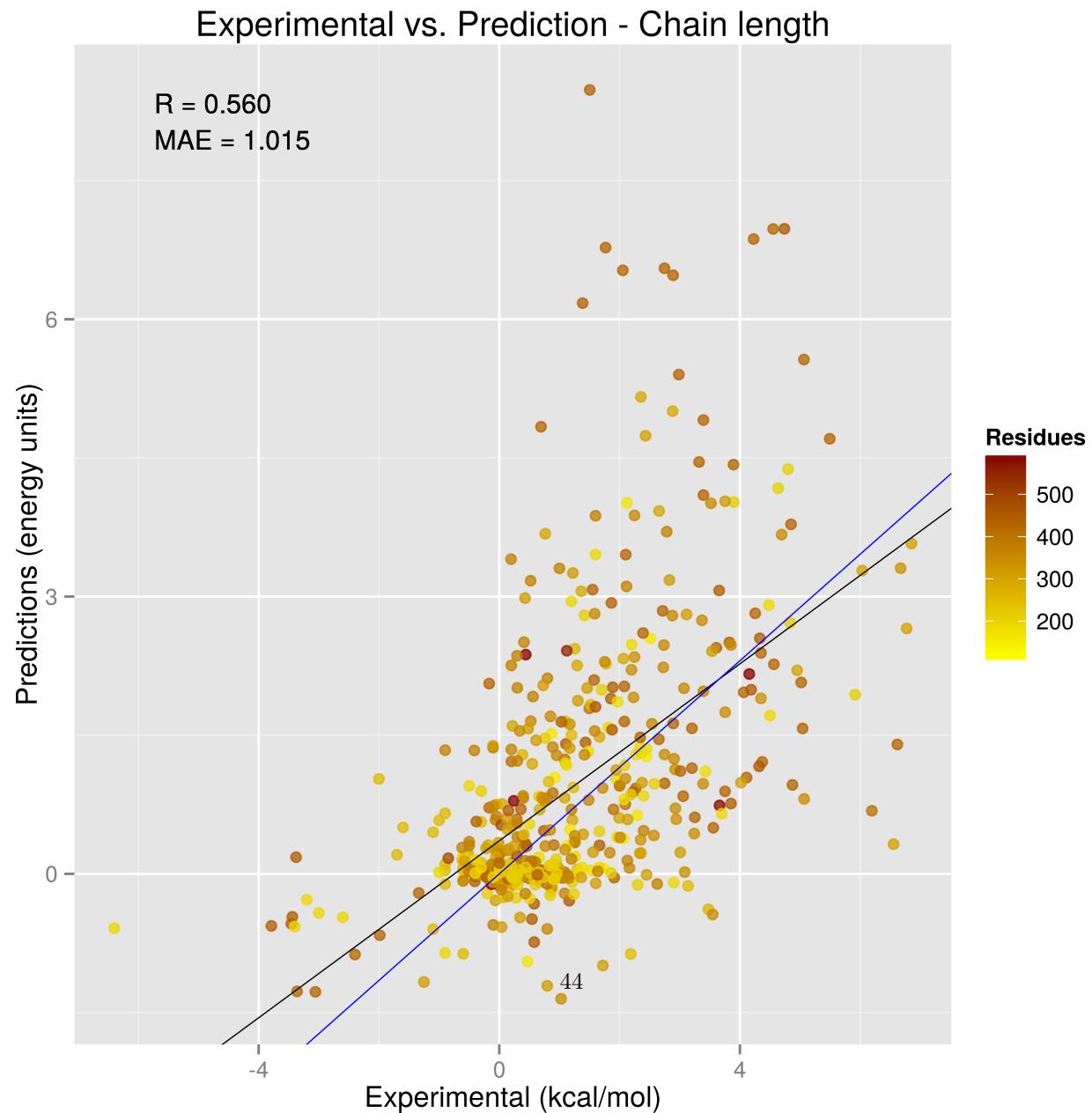
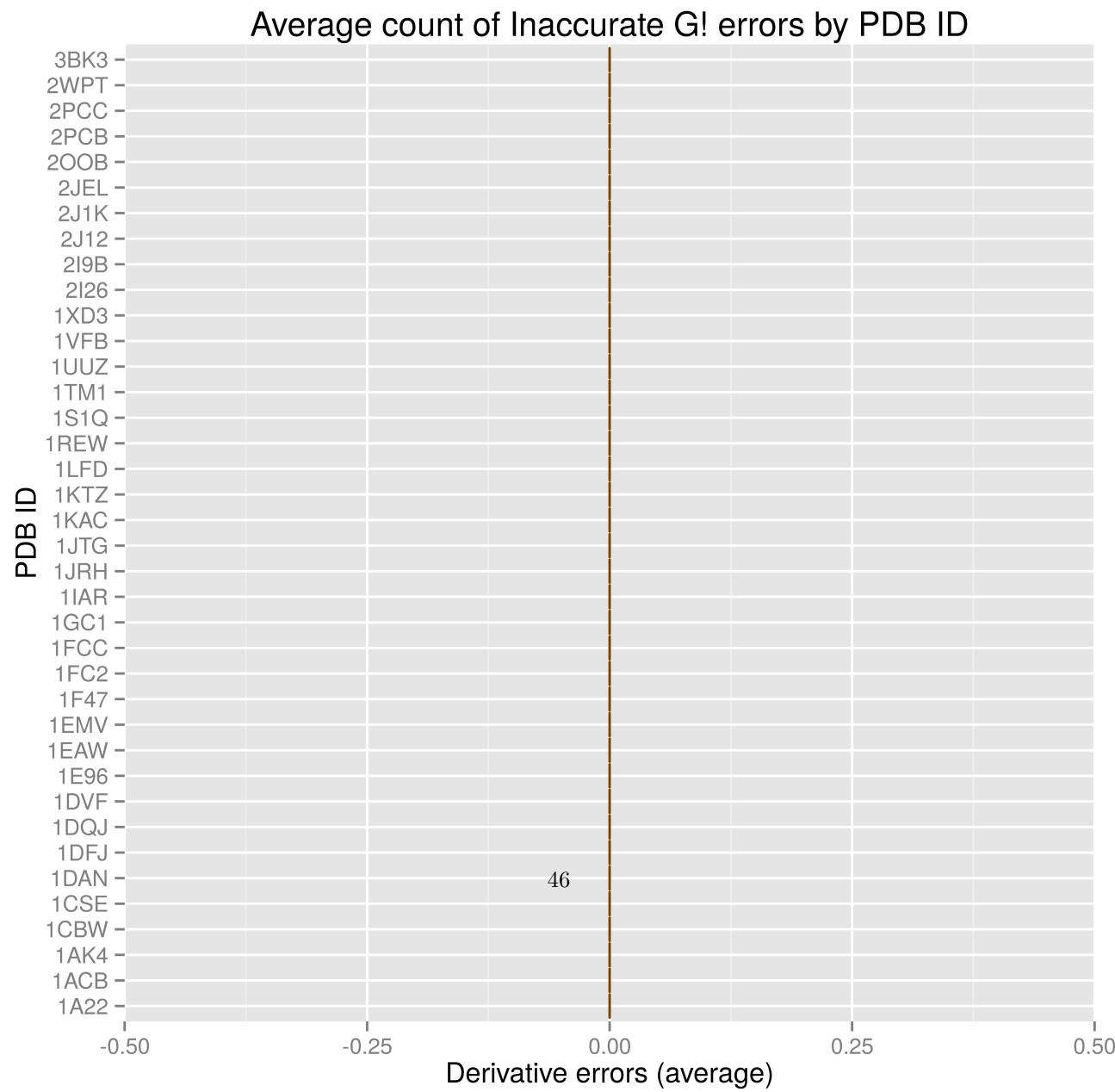


Figure 2.19: Experimental vs. Prediction - Chain length

2.7 Errors / debugging



3 `topx_1-prediction_set_id_zemu-values-score_method_zemu-paper`

zemu-values ZEMu author values (ZEMu)

Prediction set scoring credit: ZEMu authors

3.1 Data tables

The predicted DDG value per case is computed using the 1 lowest-scoring mutant structures and the 1 lowest-scoring wildtype structures.

Derived mutations in analysis are omitted):

The stability classification cutoffs are: Experimental=1.00 kcal/mol, Predicted=1.00 energy units.

3.1.1 Breakdown by volume

A case is considered a small-to-large (resp. large-to-small) mutation if all of the wildtype residues have a smaller (resp. larger) van der Waals volume than the corresponding mutant residue. The order is defined as G < A < S < C < P < D < T < N < V < E < Q < H < ILM < FK < Y < R < W so some cases are considered to have no change in volume e.g. MET → LEU.

Not enough data for analysis of mutations no change in volume (at least 8 cases are required).

Statistic name	Value	p-value
Fraction correct	0.65	
Fraction correct (fuzzy)	0.67	
Gamma correlation coef.	0.17	
Kolmogorov-Smirnov test (XY)	0.18	(2-tailed p-value= 2.57×10^{-01})
MAE	1.09	
Pearson's R	0.48	(2-tailed p-value= 8.65×10^{-05})
Spearman's R	0.24	(2-tailed p-value= 6.45×10^{-02})
X-axis Kolmogorov-Smirnov test	0.13	(p-value= 2.29×10^{-01})
X-axis normality test	2.18	(2-sided chi ² p-value= 3.36×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.15	(p-value= 1.07×10^{-01})
Y-axis normality test	59.66	(2-sided chi ² p-value= 1.11×10^{-13})
n	62.00	
num_null_cases	0.00	

Table 3.1: Statistics - small-to-large mutations (62 cases)

Statistic name	Value	p-value
Fraction correct	0.71	
Fraction correct (fuzzy)	0.72	
Gamma correlation coef.	0.37	
Kolmogorov-Smirnov test (XY)	0.18	(2-tailed p-value= 1.37×10^{-07})
MAE	1.08	
Pearson's R	0.57	(2-tailed p-value= 4.53×10^{-43})
Spearman's R	0.53	(2-tailed p-value= 2.06×10^{-37})
X-axis Kolmogorov-Smirnov test	0.36	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	92.92	(2-sided chi ² p-value= 6.64×10^{-21})
Y-axis Kolmogorov-Smirnov test	0.25	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	153.78	(2-sided chi ² p-value= 4.04×10^{-34})
n	488.00	
num_null_cases	0.00	

Table 3.2: Statistics - large-to-small mutations (488 cases)

3.1.2 Separating out mutations involving glycine or proline.

This cases may involve changes to secondary structure so we separate them out here.

Statistic name	Value	p-value
Fraction correct	0.65	
Fraction correct (fuzzy)	0.64	
Gamma correlation coef.	0.55	
Kolmogorov-Smirnov test (XY)	0.24	(2-tailed p-value= 2.65×10^{-01})
MAE	1.55	
Pearson's R	0.69	(2-tailed p-value= 5.16×10^{-06})
Spearman's R	0.73	(2-tailed p-value= 8.11×10^{-07})
X-axis Kolmogorov-Smirnov test	0.52	(p-value= 4.57×10^{-09})
X-axis normality test	0.66	(2-sided chi ² p-value= 7.21×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.34	(p-value= 4.31×10^{-04})
Y-axis normality test	14.61	(2-sided chi ² p-value= 6.72×10^{-04})
n	34.00	
num_null_cases	0.00	

Table 3.3: Statistics - cases with G or P (34 cases)

Statistic name	Value	p-value
Fraction correct	0.71	
Fraction correct (fuzzy)	0.72	
Gamma correlation coef.	0.37	
Kolmogorov-Smirnov test (XY)	0.17	(2-tailed p-value= 1.35×10^{-07})
MAE	1.07	
Pearson's R	0.56	(2-tailed p-value= 9.10×10^{-45})
Spearman's R	0.53	(2-tailed p-value= 3.70×10^{-39})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	57.49	(2-sided chi ² p-value= 3.28×10^{-13})
Y-axis Kolmogorov-Smirnov test	0.22	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	171.27	(2-sided chi ² p-value= 6.46×10^{-38})
n	532.00	
num_null_cases	0.00	

Table 3.4: Statistics - cases without G or P (532 cases)

3.1.3 Number of mutations

Statistic name	Value	p-value
Fraction correct	0.69	
Fraction correct (fuzzy)	0.70	
Gamma correlation coef.	0.30	
Kolmogorov-Smirnov test (XY)	0.19	(2-tailed p-value= 8.34×10^{-08})
MAE	0.99	
Pearson's R	0.54	(2-tailed p-value= 3.07×10^{-35})
Spearman's R	0.44	(2-tailed p-value= 5.54×10^{-23})
X-axis Kolmogorov-Smirnov test	0.32	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	116.40	(2-sided chi ² p-value= 5.29×10^{-26})
Y-axis Kolmogorov-Smirnov test	0.23	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	169.06	(2-sided chi ² p-value= 1.95×10^{-37})
n	453.00	
num_null_cases	0.00	

Table 3.5: Statistics - single mutations (453 cases)

Statistic name	Value	p-value
Fraction correct	0.76	
Fraction correct (fuzzy)	0.77	
Gamma correlation coef.	0.50	
Kolmogorov-Smirnov test (XY)	0.11	(2-tailed p-value= 5.24×10^{-01})
MAE	1.56	
Pearson's R	0.62	(2-tailed p-value= 1.66×10^{-13})
Spearman's R	0.70	(2-tailed p-value= 7.66×10^{-18})
X-axis Kolmogorov-Smirnov test	0.45	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	4.54	(2-sided chi ² p-value= 1.03×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.41	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	11.63	(2-sided chi ² p-value= 2.99×10^{-03})
n	113.00	
num_null_cases	0.00	

Table 3.6: Statistics - multiple mutations (113 cases)

3.1.4 Entire dataset using a scaling factor of 1/1.274 to improve the fraction correct metric.

Warning: Results in this section use an averaged scaling factor to improve the value for the fraction correct metric. This scalar will vary over benchmark runs so these results should not be interpreted as performance results; they should be considered as what could be obtained if the predicted values were scaled by a "magic" value.

Statistic name	Value	p-value
Fraction correct	0.71	
Fraction correct (fuzzy)	0.72	
Gamma correlation coef.	0.38	
Kolmogorov-Smirnov test (XY)	0.19	(2-tailed p-value= 5.17×10^{-09})
MAE	1.03	
Pearson's R	0.58	(2-tailed p-value= 6.86×10^{-52})
Spearman's R	0.55	(2-tailed p-value= 2.69×10^{-45})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	52.55	(2-sided chi ² p-value= 3.88×10^{-12})
Y-axis Kolmogorov-Smirnov test	0.25	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	191.99	(2-sided chi ² p-value= 2.04×10^{-42})
n	566.00	
num_null_cases	0.00	

Table 3.7: Statistics - complete dataset (scaled) (566 cases)

3.1.5 Entire dataset

Overall statistics

Statistic name	Value	p-value
Fraction correct	0.70	
Fraction correct (fuzzy)	0.71	
Gamma correlation coef.	0.38	
Kolmogorov-Smirnov test (XY)	0.17	(2-tailed p-value= 2.62×10^{-07})
MAE	1.10	
Pearson's R	0.58	(2-tailed p-value= 6.86×10^{-52})
Spearman's R	0.55	(2-tailed p-value= 2.69×10^{-45})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	52.55	(2-sided chi ² p-value= 3.88×10^{-12})
Y-axis Kolmogorov-Smirnov test	0.22	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	191.99	(2-sided chi ² p-value= 2.04×10^{-42})
n	566.00	
num_null_cases	0.00	

Table 3.8: Statistics - complete dataset (566 cases)

3.2 Main plots

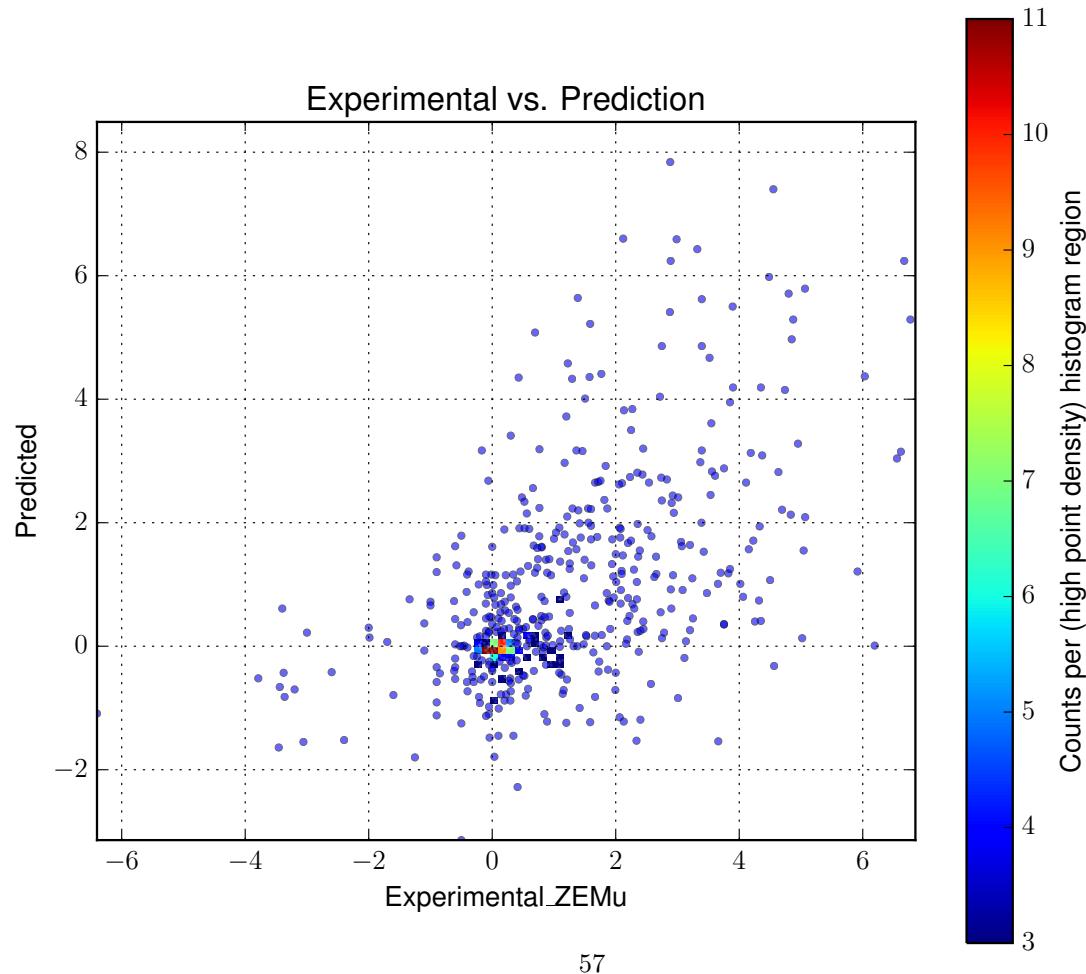
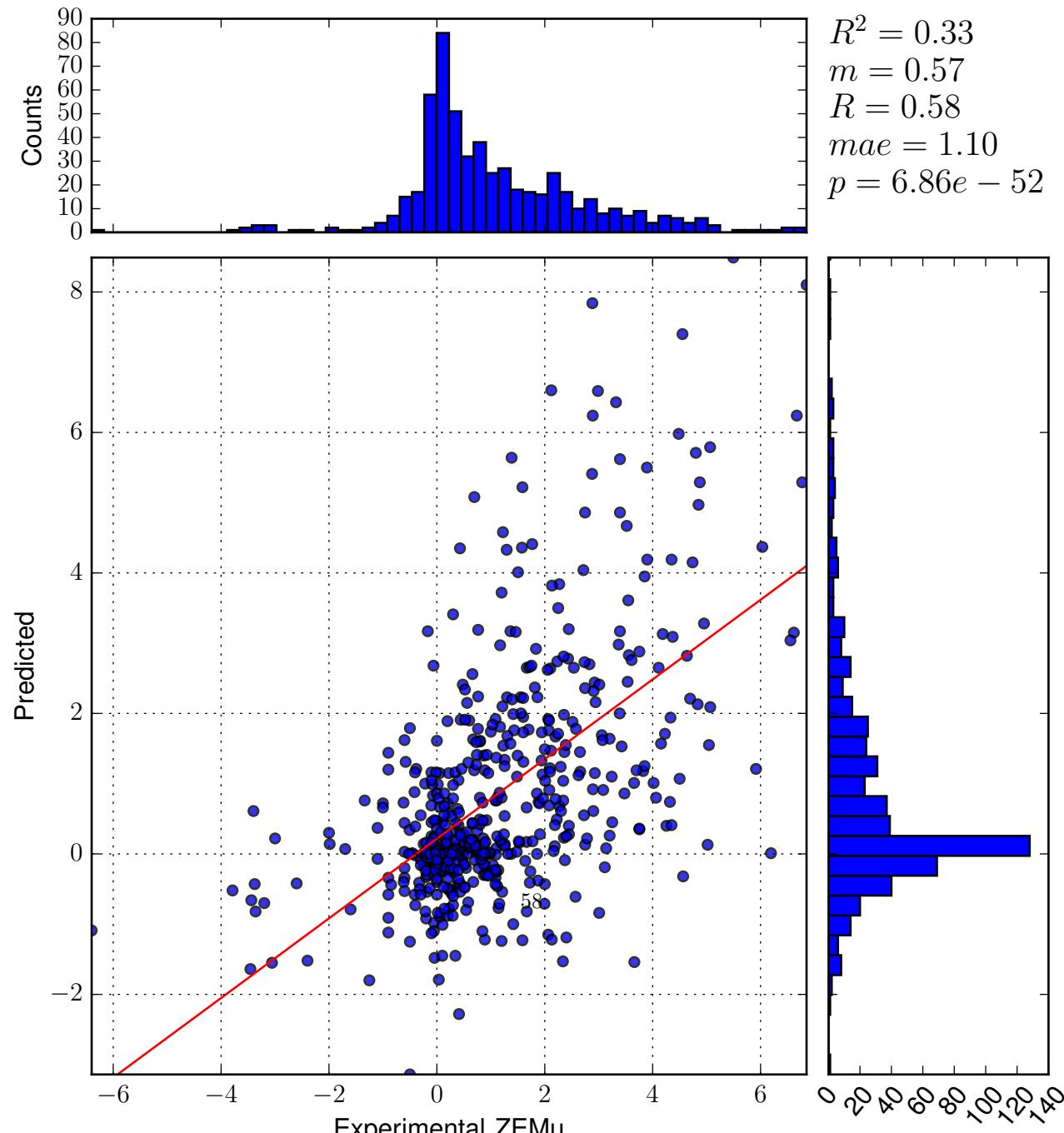
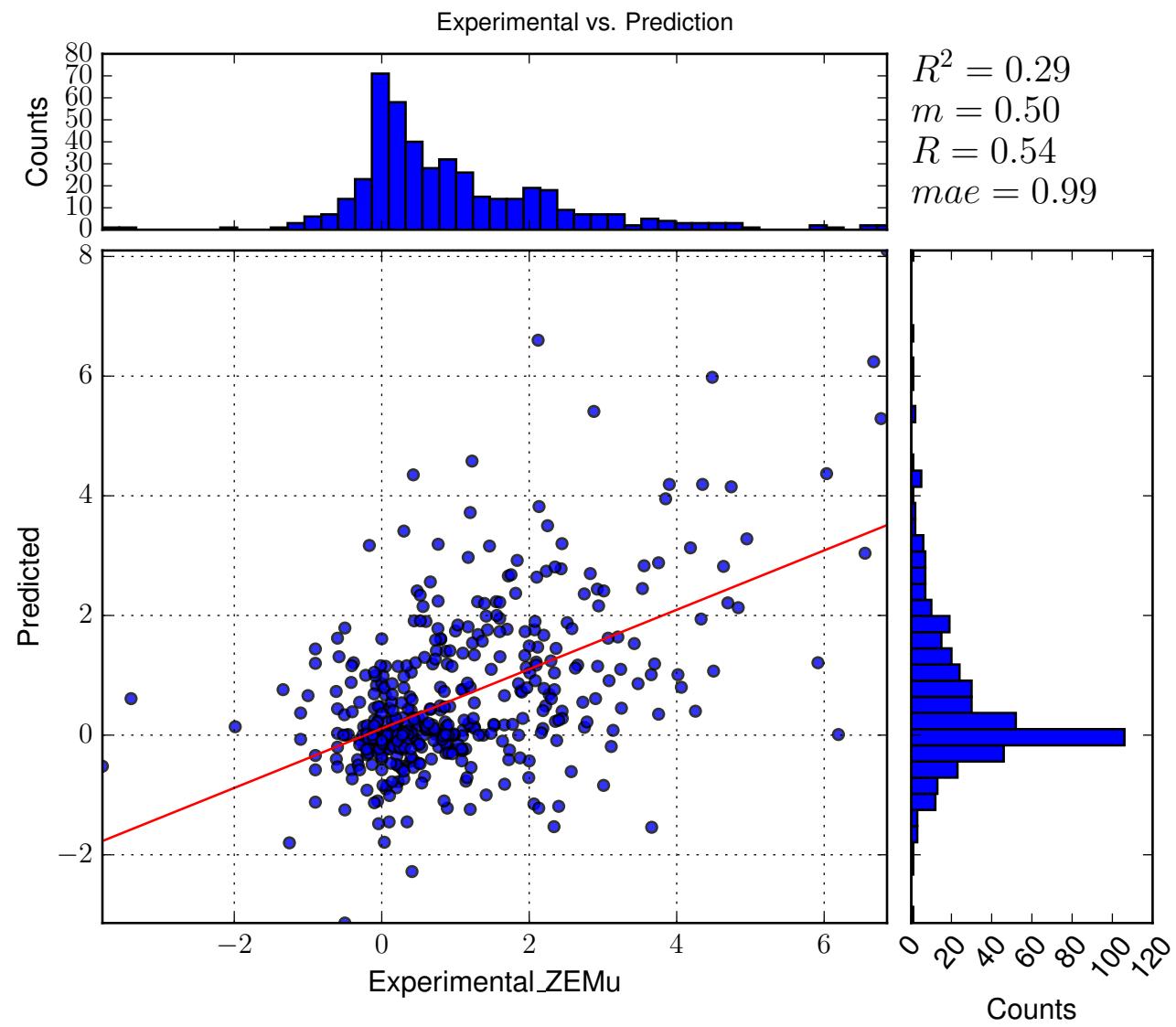
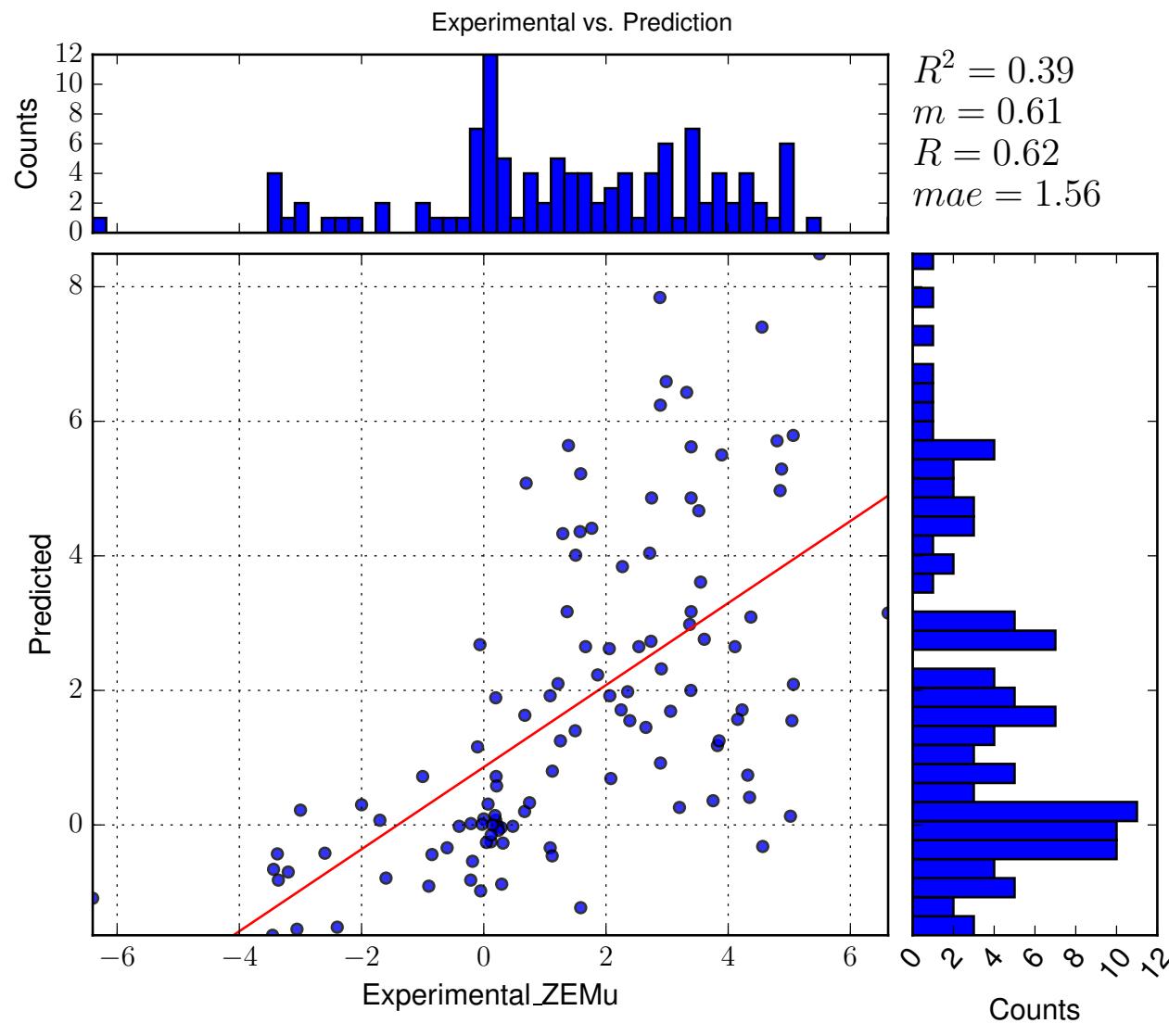


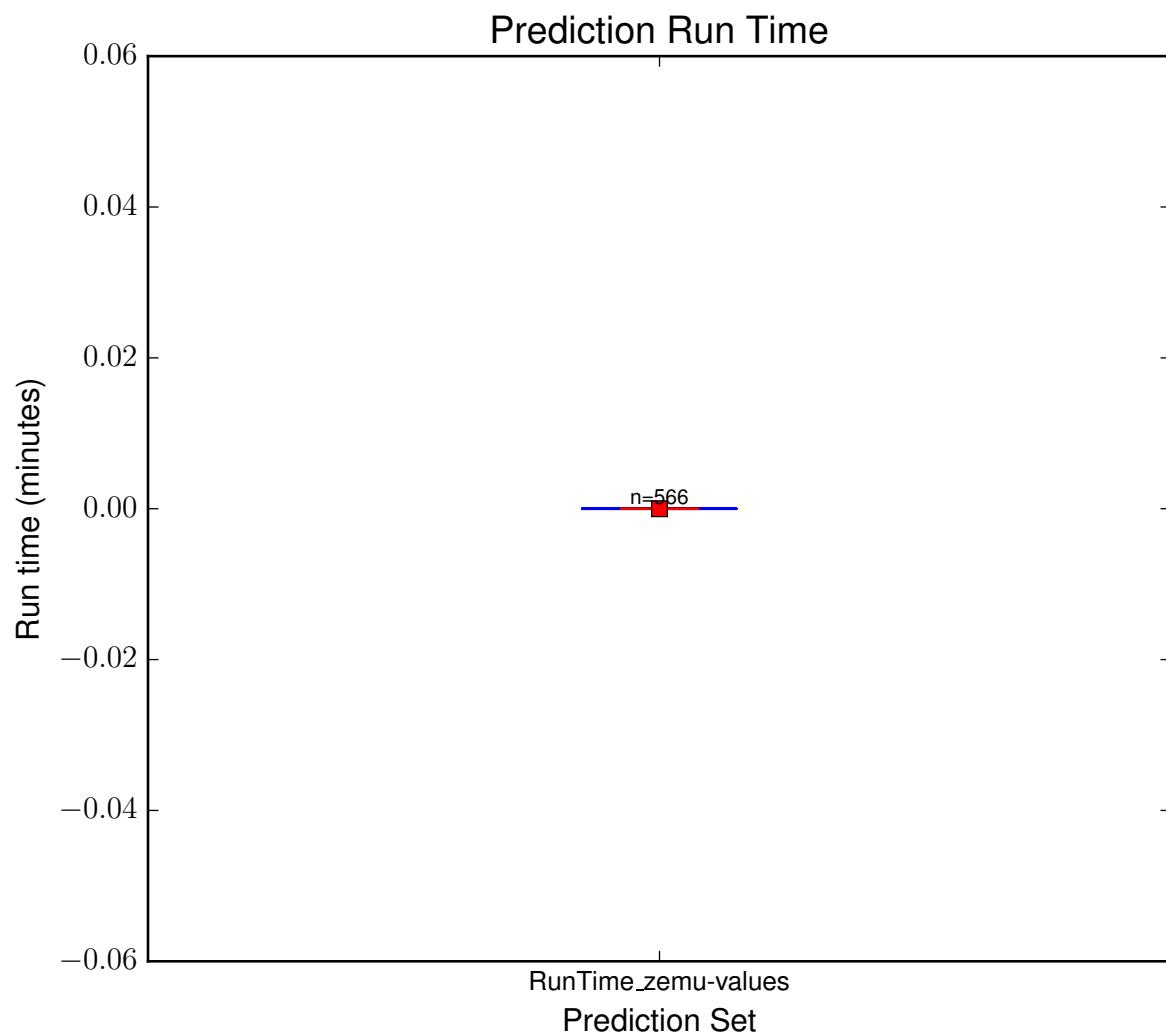
Figure 3.1: Experimental vs. Predicted scatterplot (with density binning)

Experimental vs. Prediction









61
Figure 3.5: Run time

Distribution of absolute errors (prediction - observed) for ZEMu

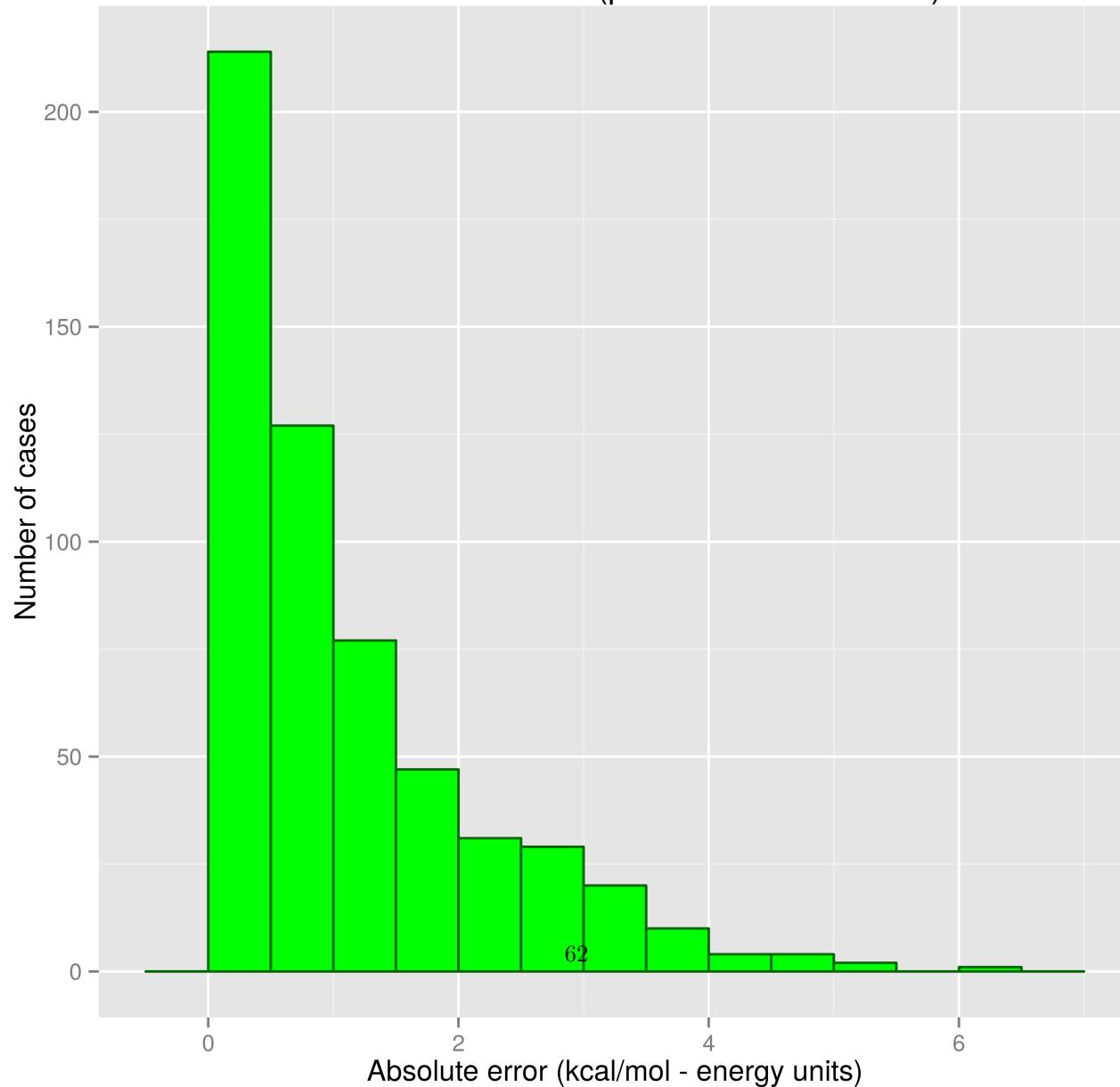


Figure 3.6: Absolute error histogram

3.3 Adjustments

Optimization of the cutoffs for the fraction correct metric

Optimum cutoff for fraction correct metric at varying experimental cutoffs for ZF

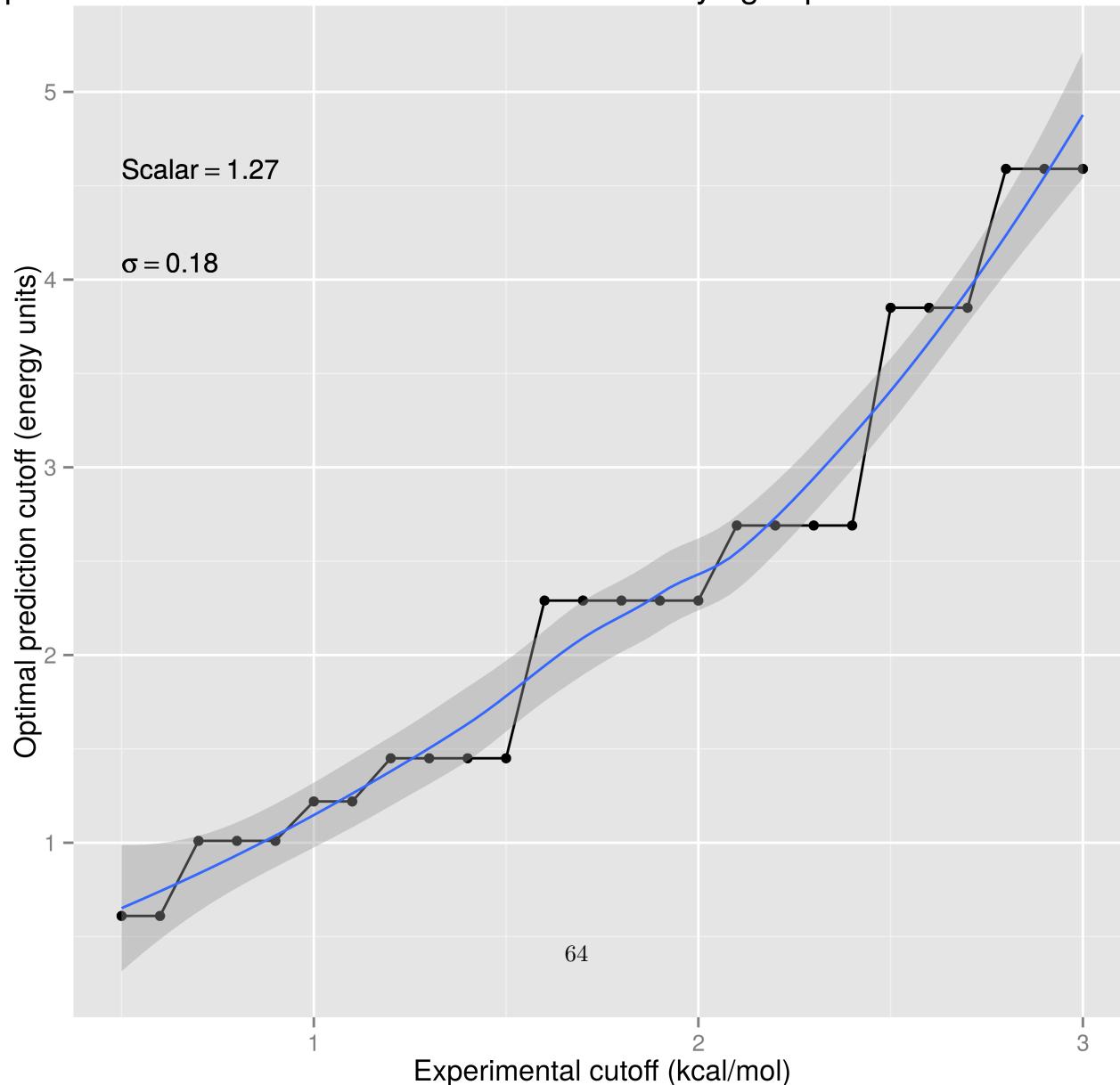


Figure 3.7: Scalar adjustment calculation plot

Optimum cutoff for fraction correct metric at 1.00 kcal/mol

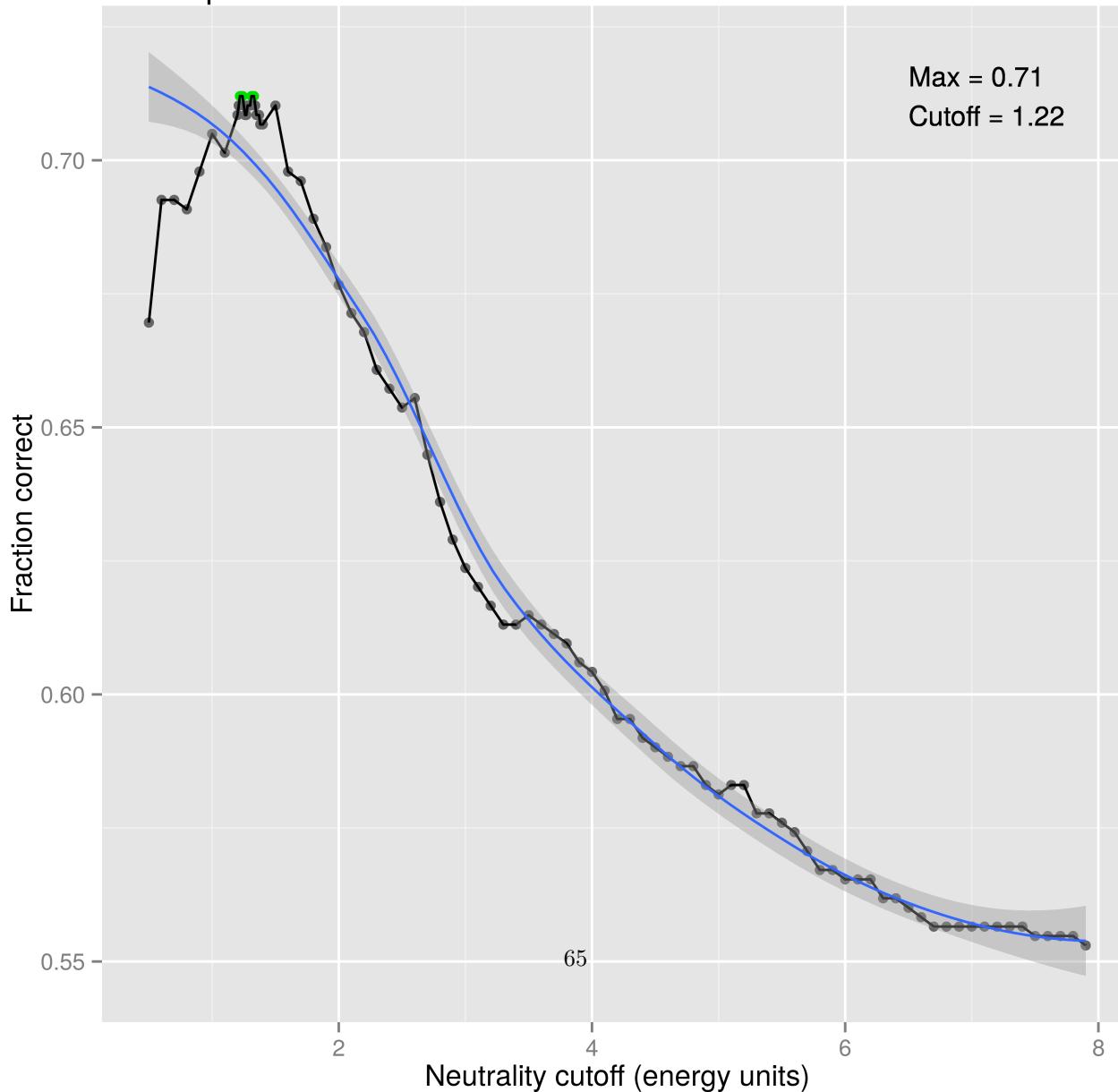


Figure 3.8: Optimal predictive cutoff plot

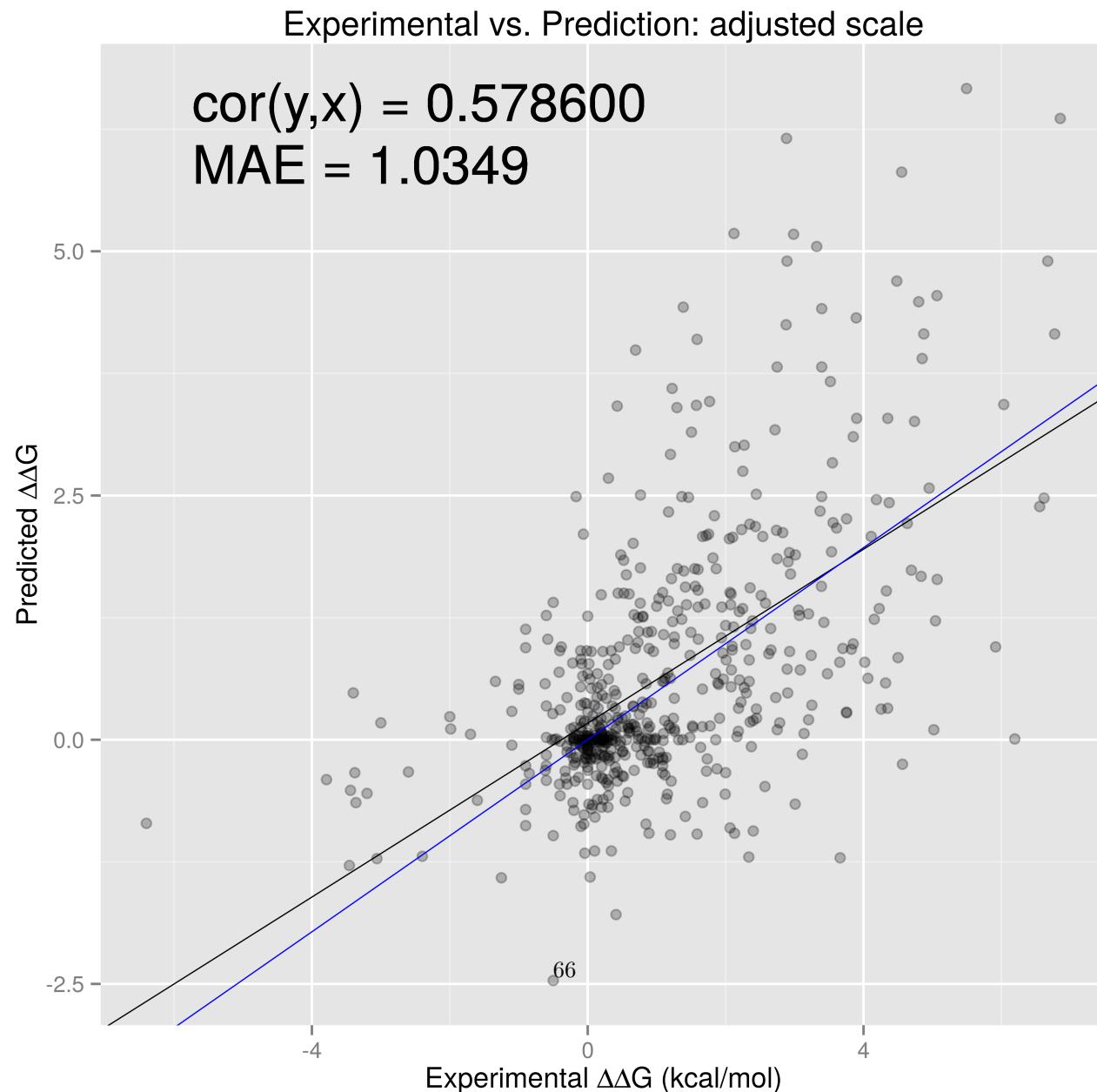


Figure 3.9: Main adj. scatterplot

Distribution of absolute errors (prediction - observed) for ZEMu

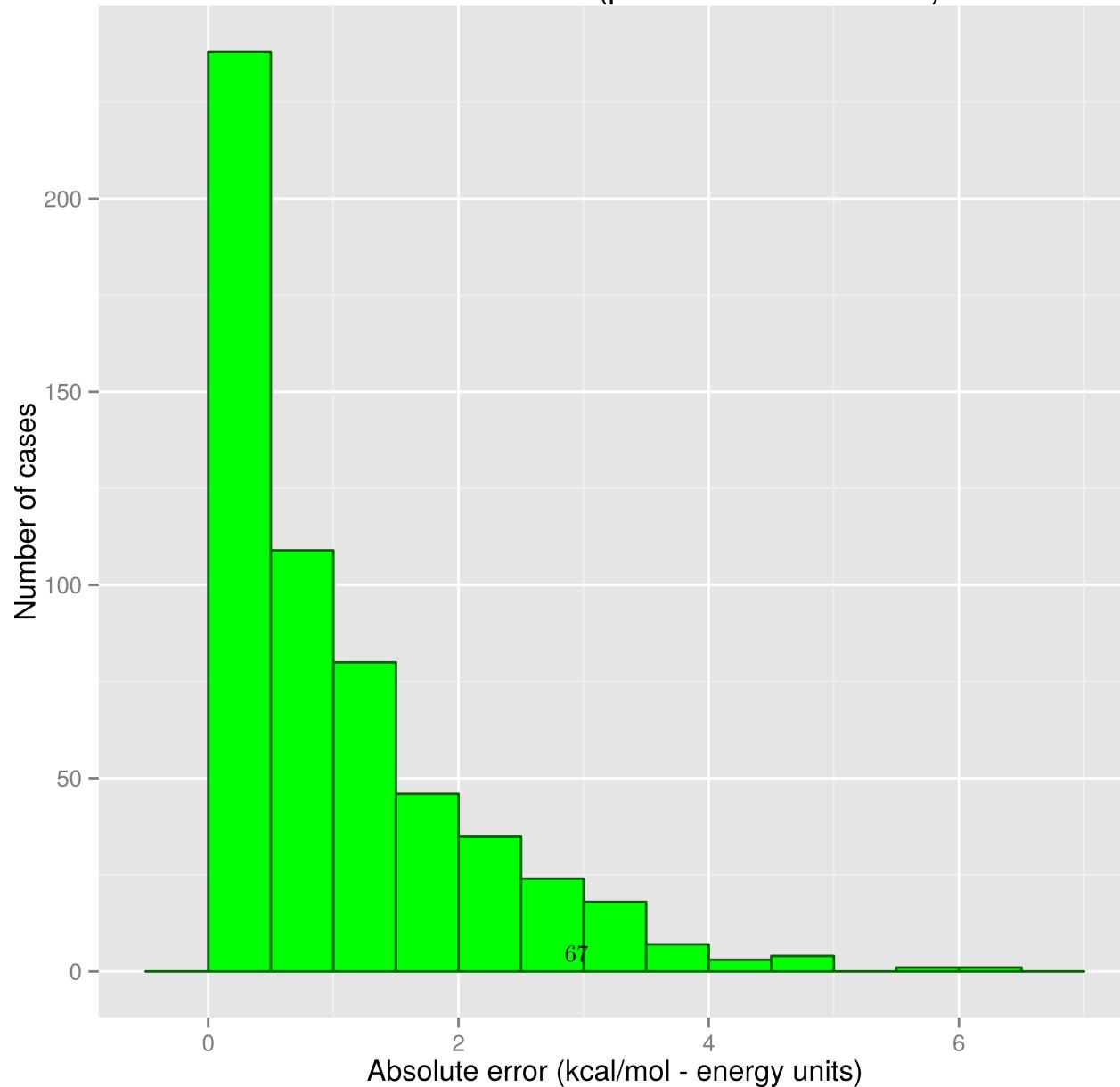
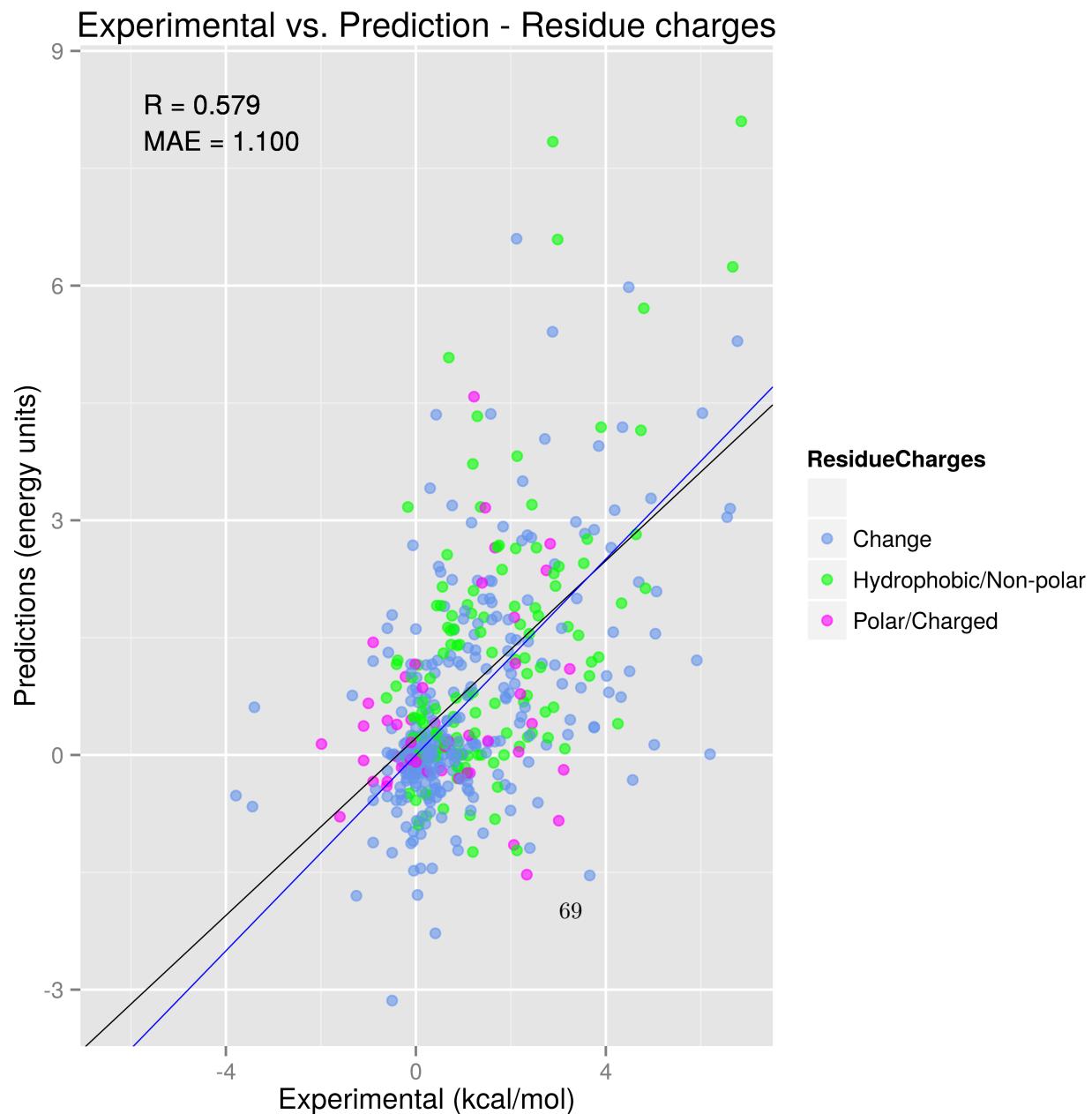


Figure 3.10: Absolute errors adjusted with scalar

3.4 Residue context



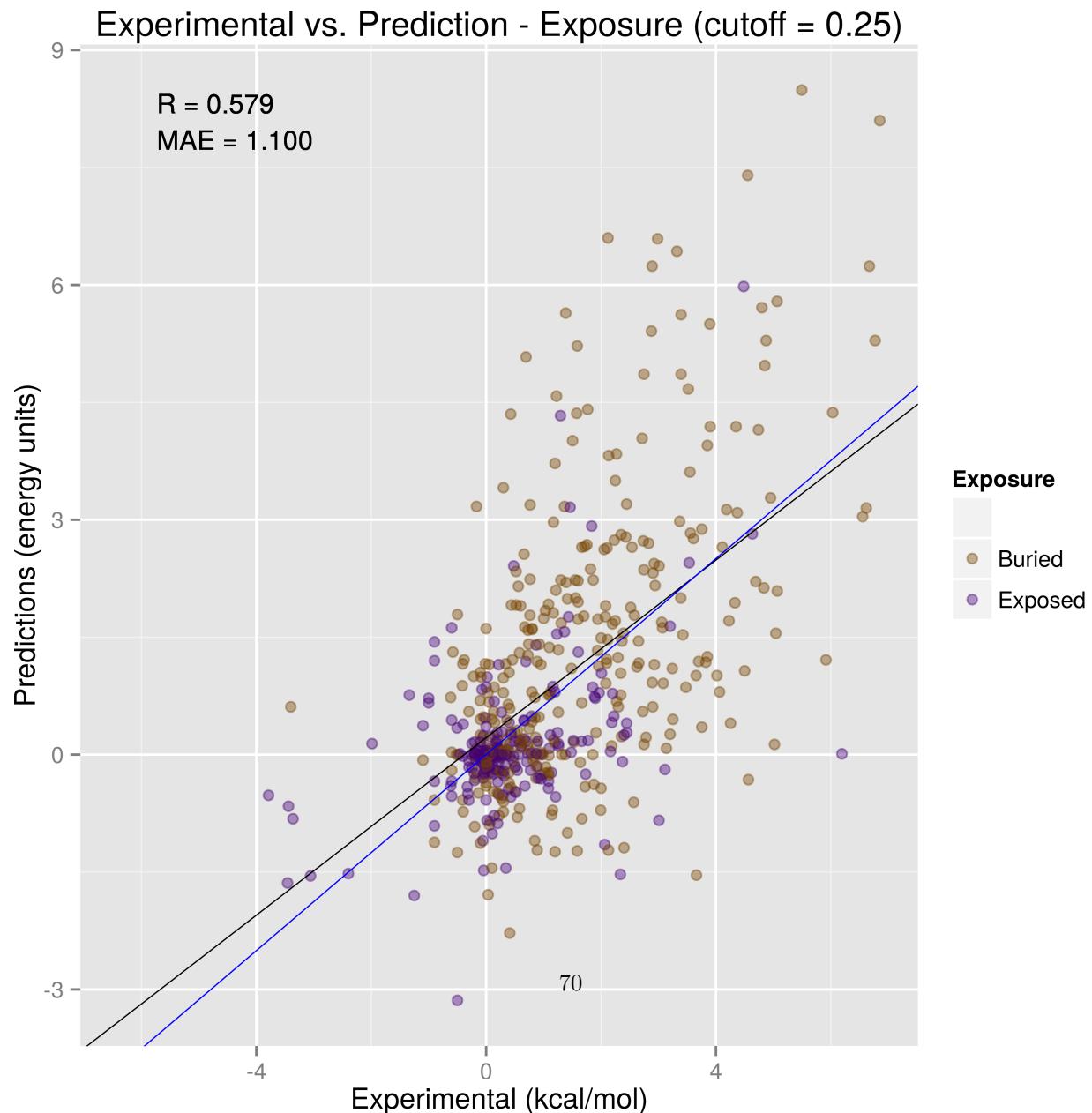


Figure 3.12: Experimental vs. Prediction - Exposure (cutoff = 0.25)

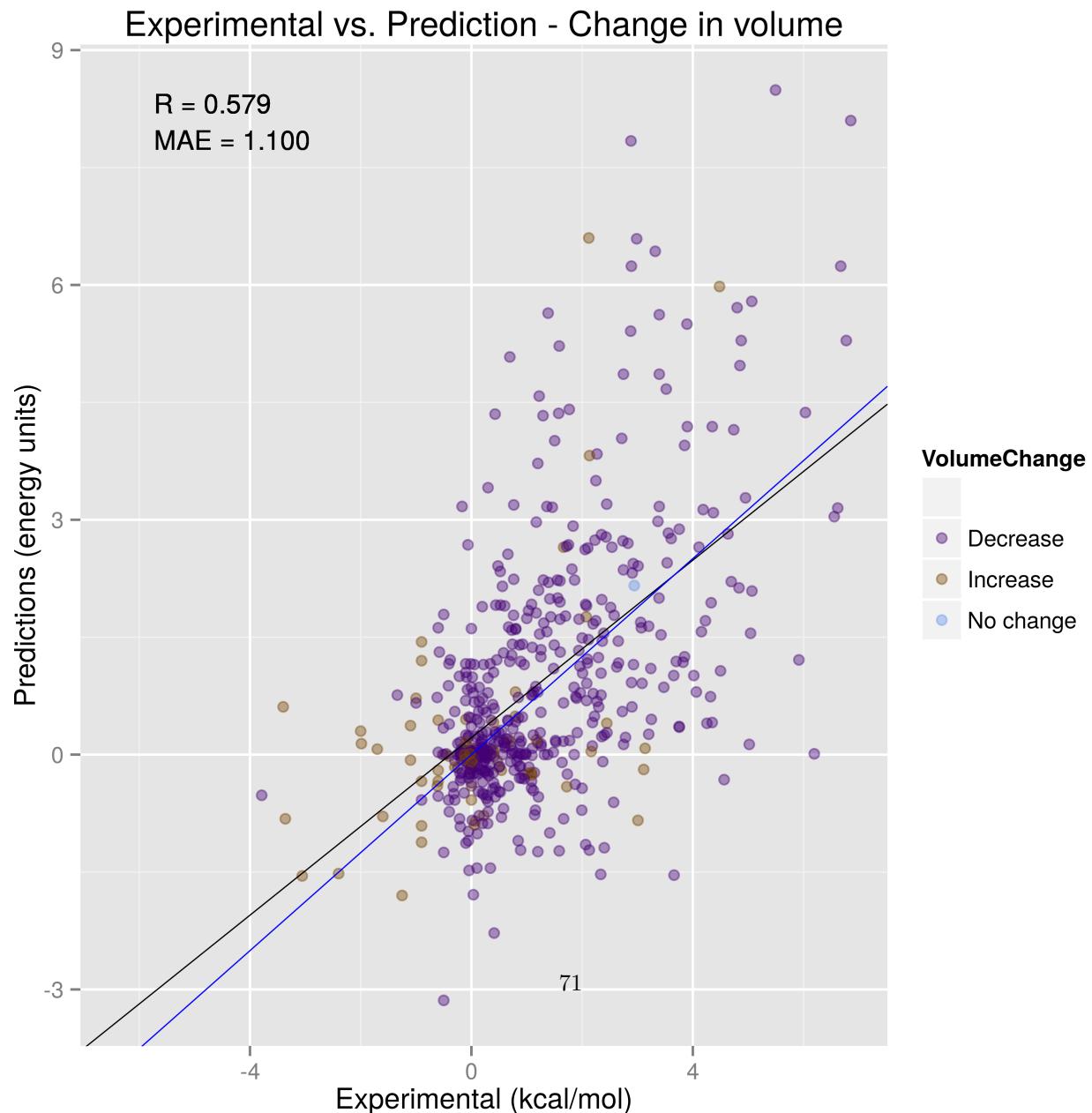


Figure 3.13: Experimental vs. Prediction - Change in volume

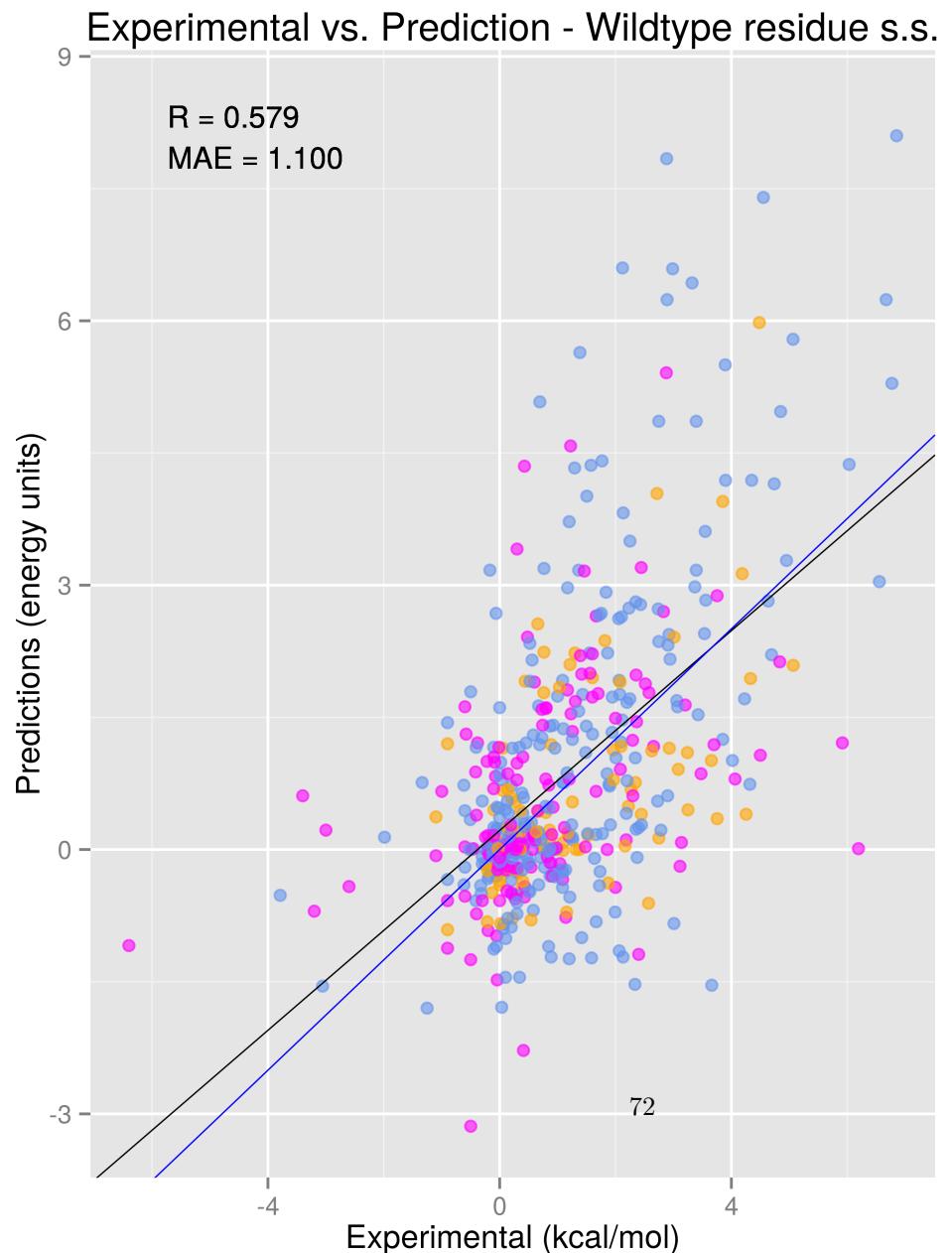
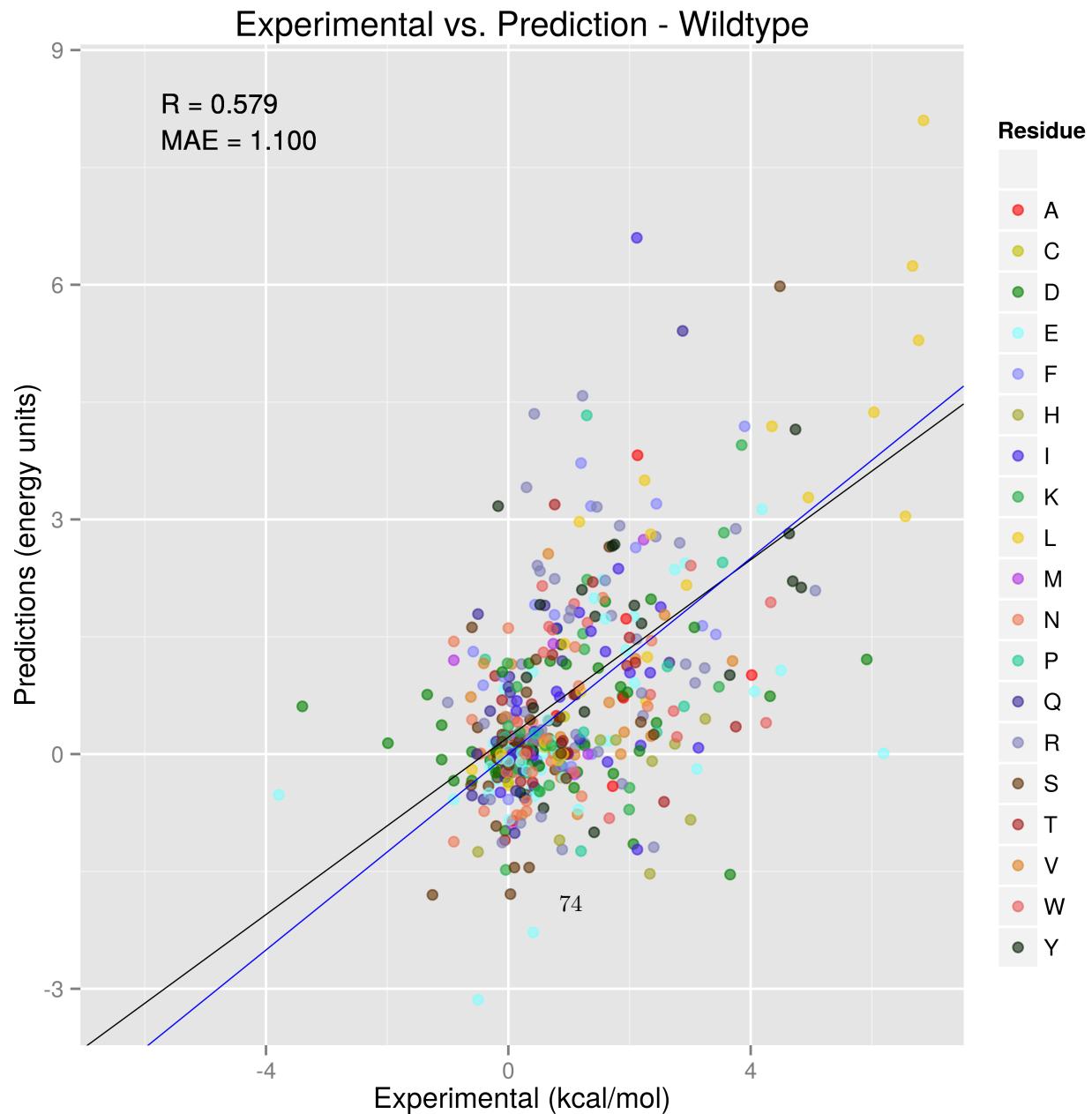


Figure 3.14: Experimental vs. Prediction - Wildtype residue s.s.

3.5 Residue types



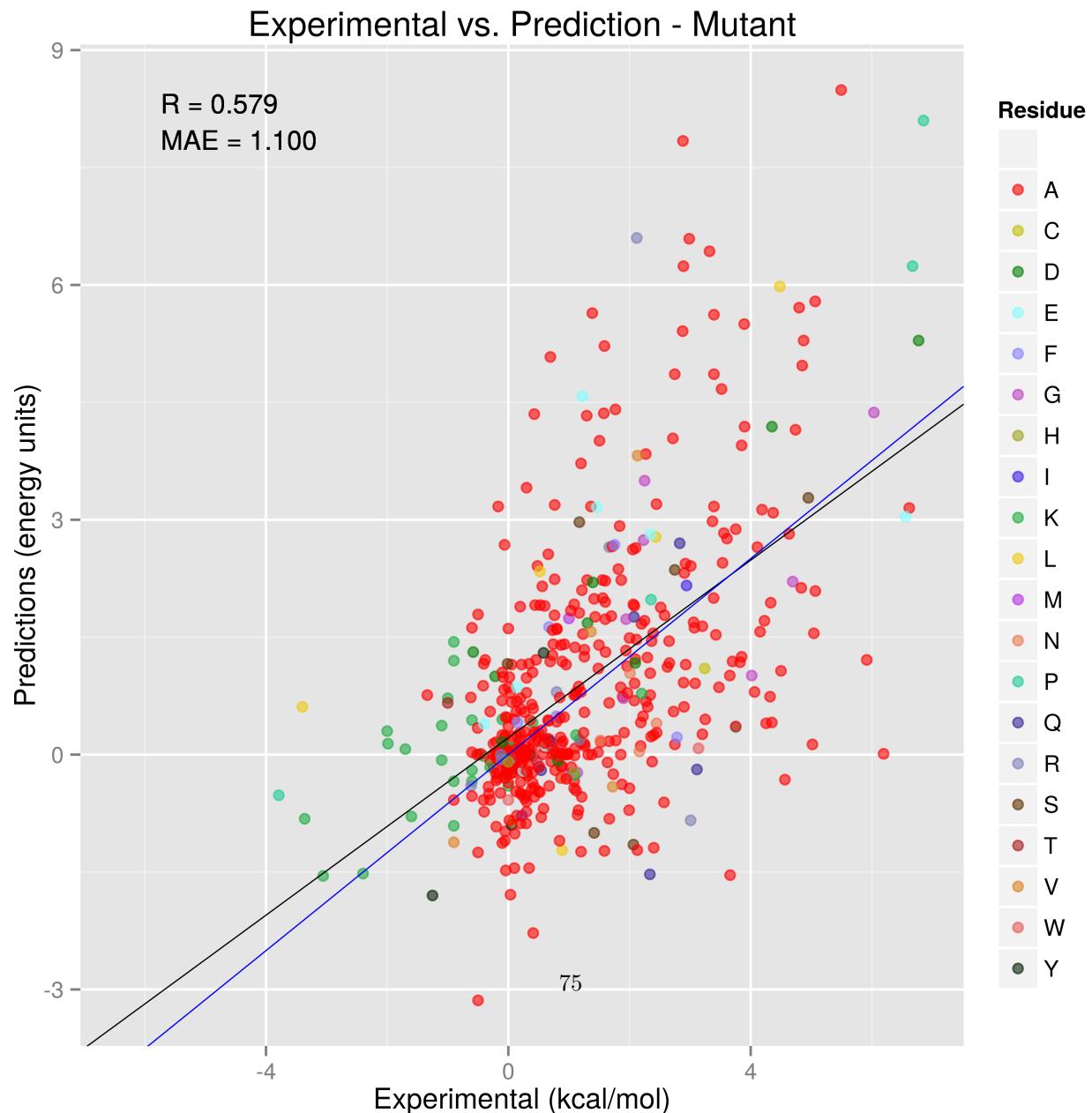


Figure 3.16: Experimental vs. Prediction - Mutant

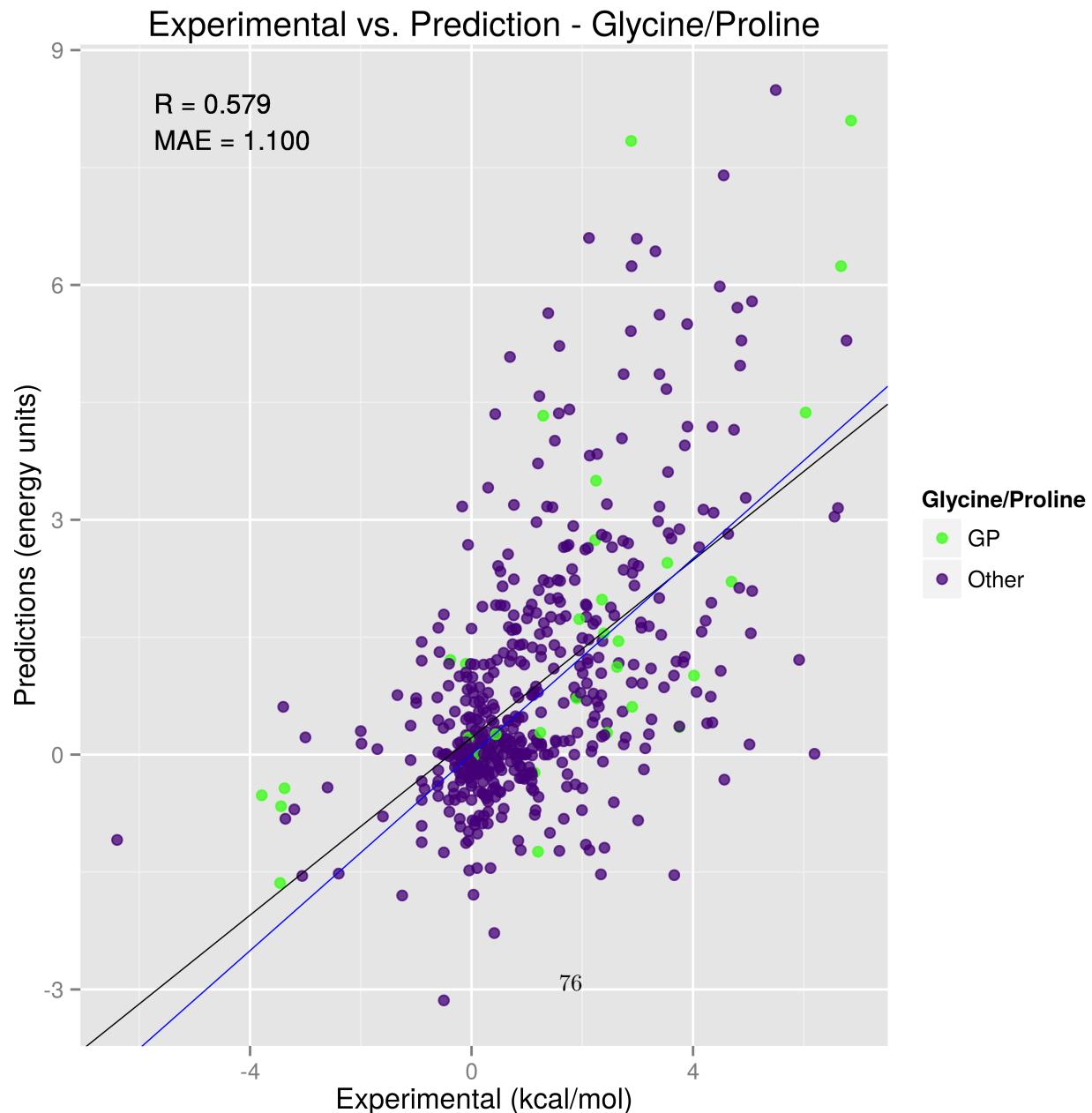
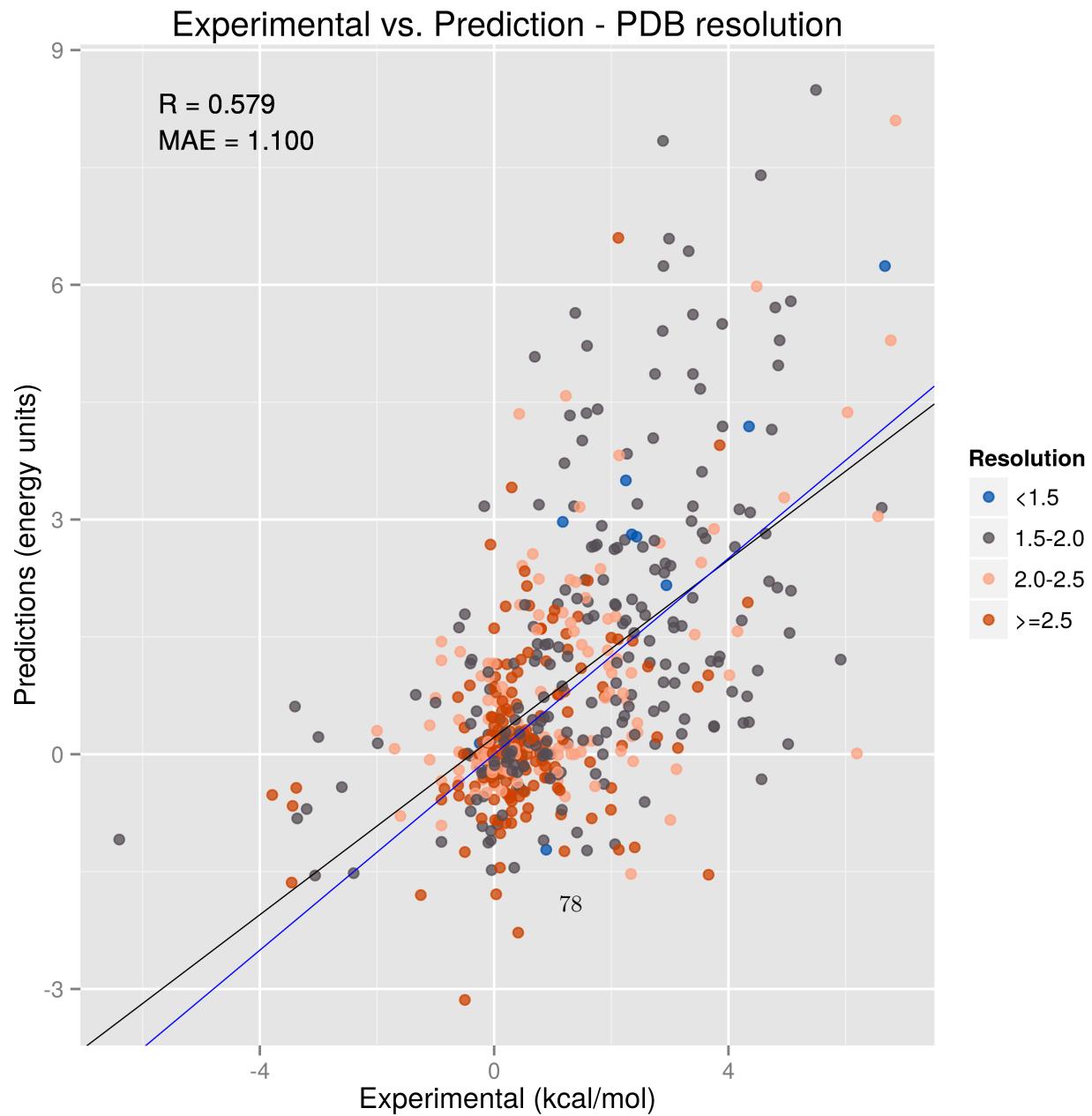


Figure 3.17: Experimental vs. Prediction - Glycine/Proline

3.6 Chain properties



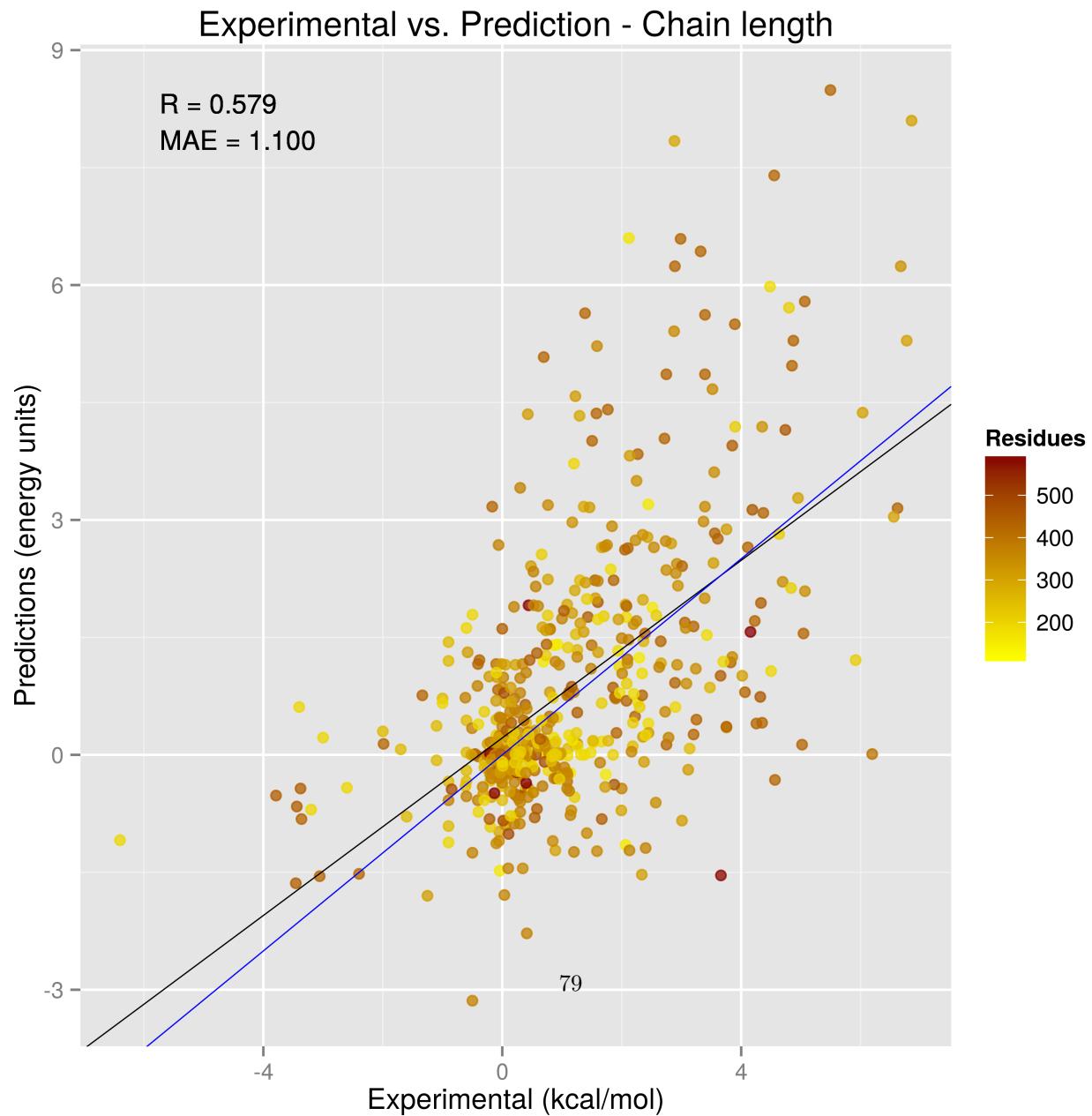
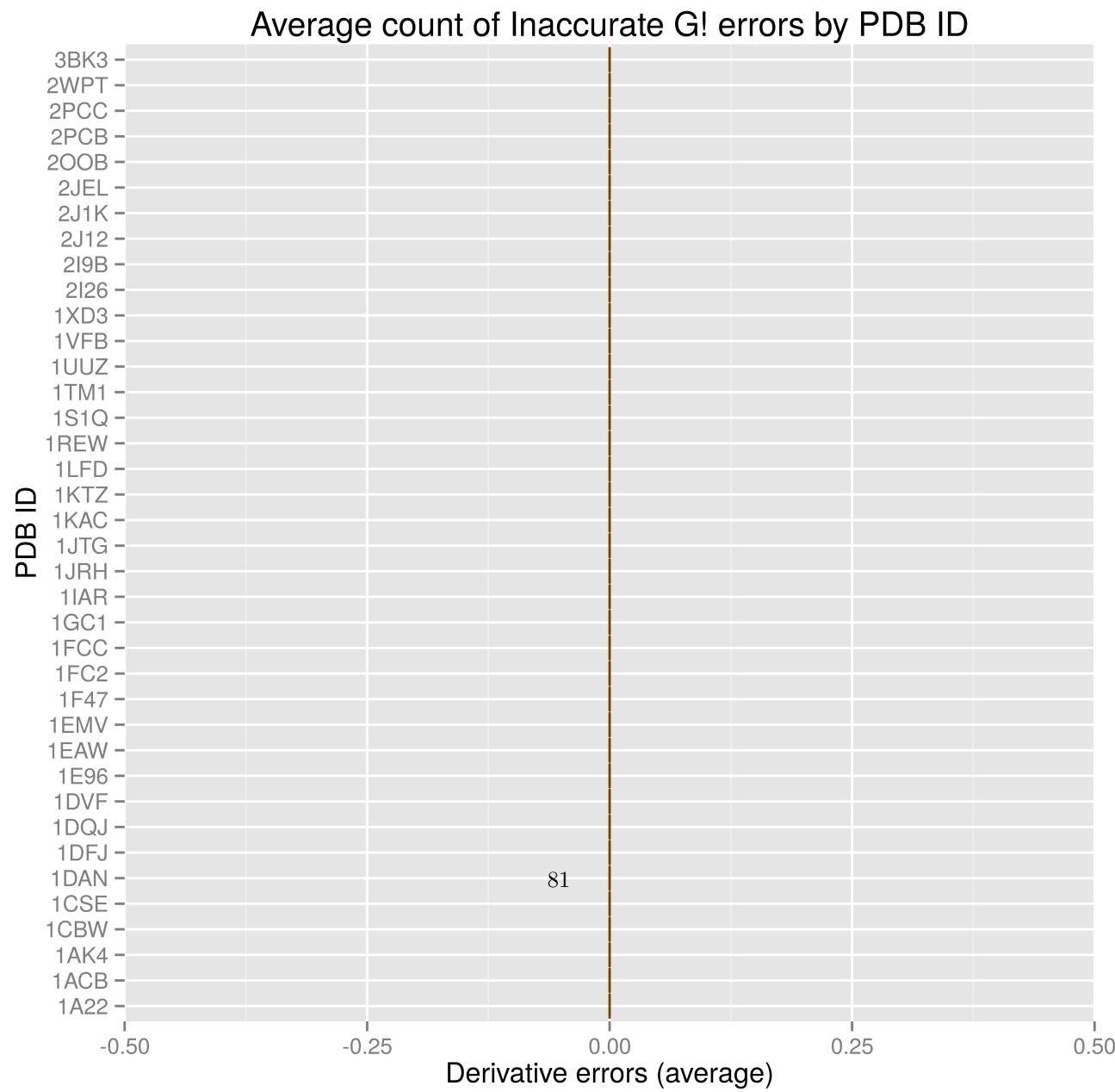


Figure 3.19: Experimental vs. Prediction - Chain length

3.7 Errors / debugging



4 topx_3-prediction_set_id_zemu-psbrub_1.6-score_method_Rescore-Talaris2014

zemu-psbrub_1.6 Backrub ddG (Pooja and Samuel) on ZEMu with kT of 1.6 (ZEMu)

Prediction set scoring credit: Kyle Barlow

4.1 Data tables

The predicted DDG value per case is computed using the 3 lowest-scoring mutant structures and the 3 lowest-scoring wildtype structures as in the paper by Kellogg et al.

Derived mutations in analysis are omitted):

The stability classification cutoffs are: Experimental=1.00 kcal/mol, Predicted=1.00 energy units.

4.1.1 Breakdown by volume

A case is considered a small-to-large (resp. large-to-small) mutation if all of the wildtype residues have a smaller (resp. larger) van der Waals volume than the corresponding mutant residue. The order is defined as G < A < S < C < P < D < T < N < V < E < Q < H < ILM < FK < Y < R < W so some cases are considered to have no change in volume e.g. MET → LEU.

Not enough data for analysis of mutations no change in volume (at least 8 cases are required).

Statistic name	Value	p-value
Fraction correct	0.69	
Fraction correct (fuzzy)	0.71	
Gamma correlation coef.	0.17	
Kolmogorov-Smirnov test (XY)	0.10	(2-tailed p-value= 9.20×10^{-01})
MAE	1.14	
Pearson's R	0.35	(2-tailed p-value= 5.31×10^{-03})
Spearman's R	0.25	(2-tailed p-value= 5.04×10^{-02})
X-axis Kolmogorov-Smirnov test	0.13	(p-value= 2.29×10^{-01})
X-axis normality test	2.18	(2-sided chi ² p-value= 3.36×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.10	(p-value= 5.58×10^{-01})
Y-axis normality test	10.20	(2-sided chi ² p-value= 6.11×10^{-03})
n	62.00	
num_null_cases	0.00	

Table 4.1: Statistics - small-to-large mutations (62 cases)

Statistic name	Value	p-value
Fraction correct	0.68	
Fraction correct (fuzzy)	0.69	
Gamma correlation coef.	0.34	
Kolmogorov-Smirnov test (XY)	0.17	(2-tailed p-value= 1.66×10^{-06})
MAE	1.25	
Pearson's R	0.47	(2-tailed p-value= 9.66×10^{-28})
Spearman's R	0.51	(2-tailed p-value= 1.19×10^{-33})
X-axis Kolmogorov-Smirnov test	0.36	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	92.92	(2-sided chi ² p-value= 6.64×10^{-21})
Y-axis Kolmogorov-Smirnov test	0.27	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	116.72	(2-sided chi ² p-value= 4.52×10^{-26})
n	488.00	
num_null_cases	0.00	

Table 4.2: Statistics - large-to-small mutations (488 cases)

4.1.2 Separating out mutations involving glycine or proline.

This cases may involve changes to secondary structure so we separate them out here.

Statistic name	Value	p-value
Fraction correct	0.56	
Fraction correct (fuzzy)	0.58	
Gamma correlation coef.	0.48	
Kolmogorov-Smirnov test (XY)	0.21	(2-tailed p-value= 4.22×10^{-01})
MAE	1.64	
Pearson's R	0.68	(2-tailed p-value= 1.11×10^{-05})
Spearman's R	0.66	(2-tailed p-value= 1.82×10^{-05})
X-axis Kolmogorov-Smirnov test	0.52	(p-value= 4.57×10^{-09})
X-axis normality test	0.66	(2-sided chi ² p-value= 7.21×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.37	(p-value= 9.48×10^{-05})
Y-axis normality test	3.64	(2-sided chi ² p-value= 1.62×10^{-01})
n	34.00	
num_null_cases	0.00	

Table 4.3: Statistics - cases with G or P (34 cases)

Statistic name	Value	p-value
Fraction correct	0.68	
Fraction correct (fuzzy)	0.69	
Gamma correlation coef.	0.35	
Kolmogorov-Smirnov test (XY)	0.15	(2-tailed p-value= 9.88×10^{-06})
MAE	1.24	
Pearson's R	0.48	(2-tailed p-value= 3.58×10^{-32})
Spearman's R	0.51	(2-tailed p-value= 1.43×10^{-36})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	57.49	(2-sided chi ² p-value= 3.28×10^{-13})
Y-axis Kolmogorov-Smirnov test	0.23	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	135.86	(2-sided chi ² p-value= 3.15×10^{-30})
n	532.00	
num_null_cases	0.00	

Table 4.4: Statistics - cases without G or P (532 cases)

4.1.3 Number of mutations

Statistic name	Value	p-value
Fraction correct	0.66	
Fraction correct (fuzzy)	0.68	
Gamma correlation coef.	0.31	
Kolmogorov-Smirnov test (XY)	0.18	(2-tailed p-value= 1.15×10^{-06})
MAE	1.13	
Pearson's R	0.45	(2-tailed p-value= 2.01×10^{-24})
Spearman's R	0.46	(2-tailed p-value= 1.53×10^{-24})
X-axis Kolmogorov-Smirnov test	0.32	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	116.40	(2-sided chi ² p-value= 5.29×10^{-26})
Y-axis Kolmogorov-Smirnov test	0.22	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	125.84	(2-sided chi ² p-value= 4.72×10^{-28})
n	453.00	
num_null_cases	0.00	

Table 4.5: Statistics - single mutations (453 cases)

Statistic name	Value	p-value
Fraction correct	0.73	
Fraction correct (fuzzy)	0.74	
Gamma correlation coef.	0.40	
Kolmogorov-Smirnov test (XY)	0.09	(2-tailed p-value= 7.49×10^{-01})
MAE	1.78	
Pearson's R	0.52	(2-tailed p-value= 3.05×10^{-09})
Spearman's R	0.58	(2-tailed p-value= 1.15×10^{-11})
X-axis Kolmogorov-Smirnov test	0.45	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	4.54	(2-sided chi ² p-value= 1.03×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.44	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	7.23	(2-sided chi ² p-value= 2.70×10^{-02})
n	113.00	
num_null_cases	0.00	

Table 4.6: Statistics - multiple mutations (113 cases)

4.1.4 Entire dataset using a scaling factor of 1/1.465 to improve the fraction correct metric.

Warning: Results in this section use an averaged scaling factor to improve the value for the fraction correct metric. This scalar will vary over benchmark runs so these results should not be interpreted as performance results; they should be considered as what could be obtained if the predicted values were scaled by a "magic" value.

Statistic name	Value	p-value
Fraction correct	0.69	
Fraction correct (fuzzy)	0.69	
Gamma correlation coef.	0.35	
Kolmogorov-Smirnov test (XY)	0.17	(2-tailed p-value= 1.87×10^{-07})
MAE	1.10	
Pearson's R	0.49	(2-tailed p-value= 1.70×10^{-35})
Spearman's R	0.52	(2-tailed p-value= 1.49×10^{-40})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	52.55	(2-sided chi ² p-value= 3.88×10^{-12})
Y-axis Kolmogorov-Smirnov test	0.25	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	136.64	(2-sided chi ² p-value= 2.13×10^{-30})
n	566.00	
num_null_cases	0.00	

Table 4.7: Statistics - complete dataset (scaled) (566 cases)

4.1.5 Entire dataset

Overall statistics

Statistic name	Value	p-value
Fraction correct	0.68	
Fraction correct (fuzzy)	0.69	
Gamma correlation coef.	0.35	
Kolmogorov-Smirnov test (XY)	0.15	(2-tailed p-value= 6.39×10^{-06})
MAE	1.26	
Pearson's R	0.49	(2-tailed p-value= 1.70×10^{-35})
Spearman's R	0.52	(2-tailed p-value= 1.49×10^{-40})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	52.55	(2-sided chi ² p-value= 3.88×10^{-12})
Y-axis Kolmogorov-Smirnov test	0.23	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	136.64	(2-sided chi ² p-value= 2.13×10^{-30})
n	566.00	
num_null_cases	0.00	

Table 4.8: Statistics - complete dataset (566 cases)

4.2 Main plots

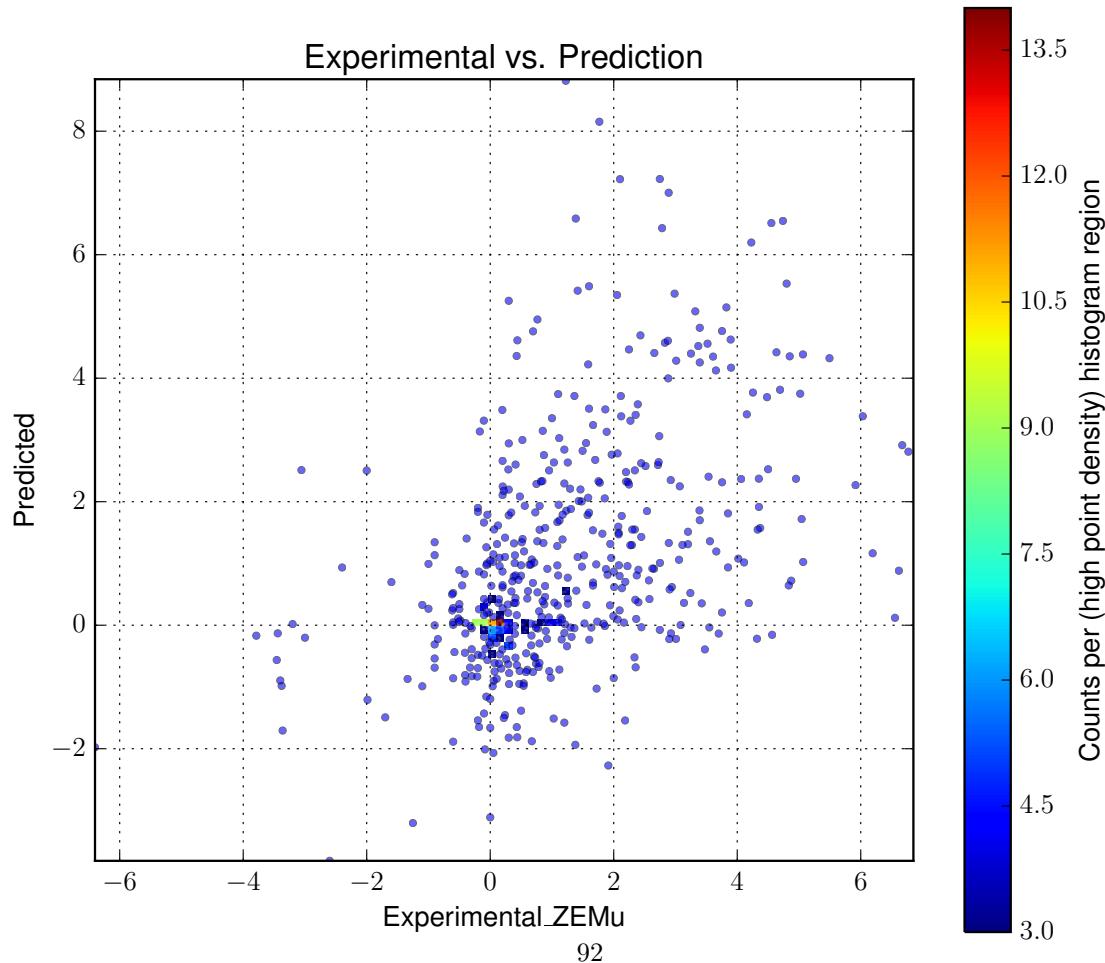
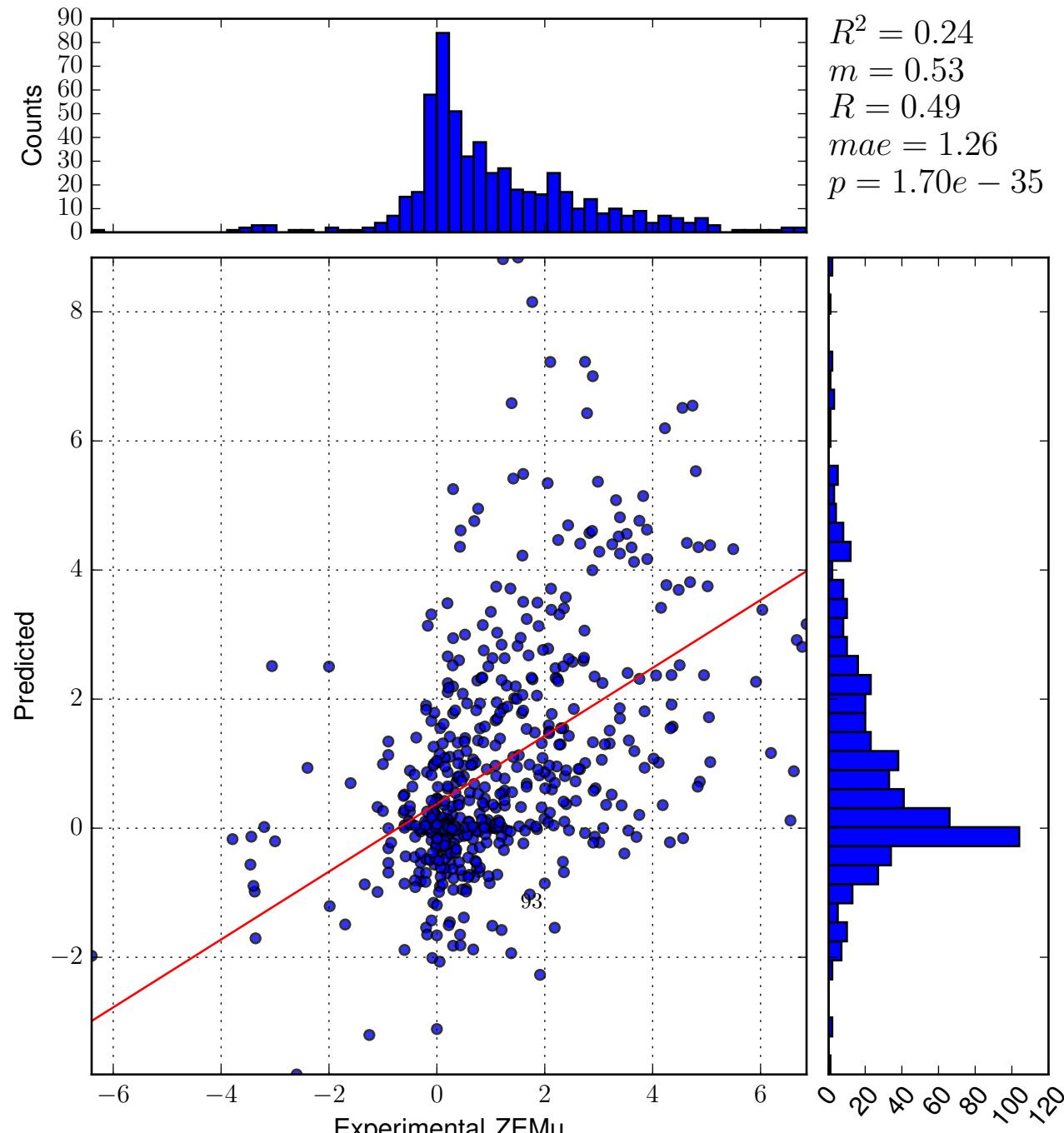


Figure 4.1: Experimental vs. Predicted scatterplot (with density binning)

Experimental vs. Prediction



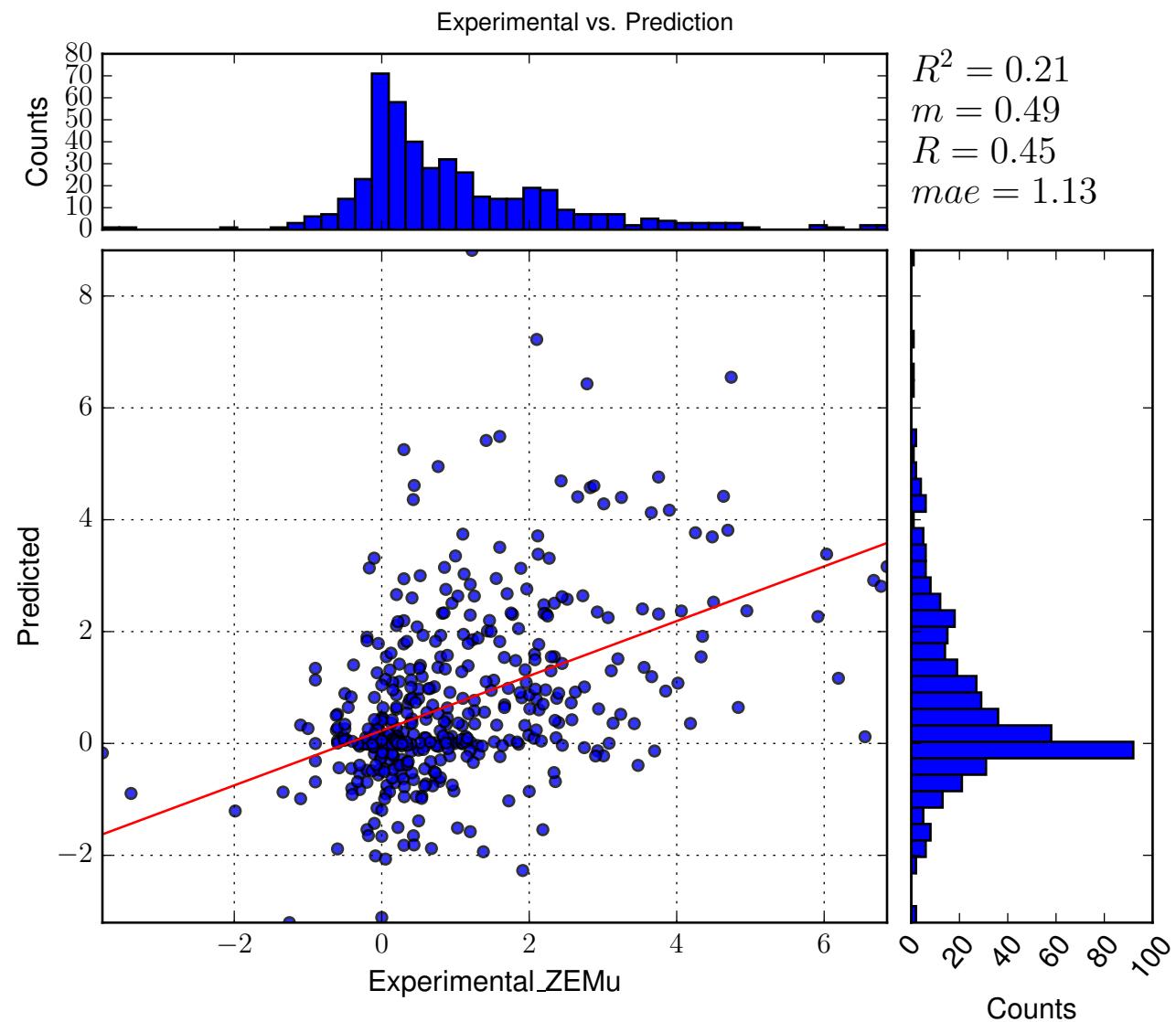
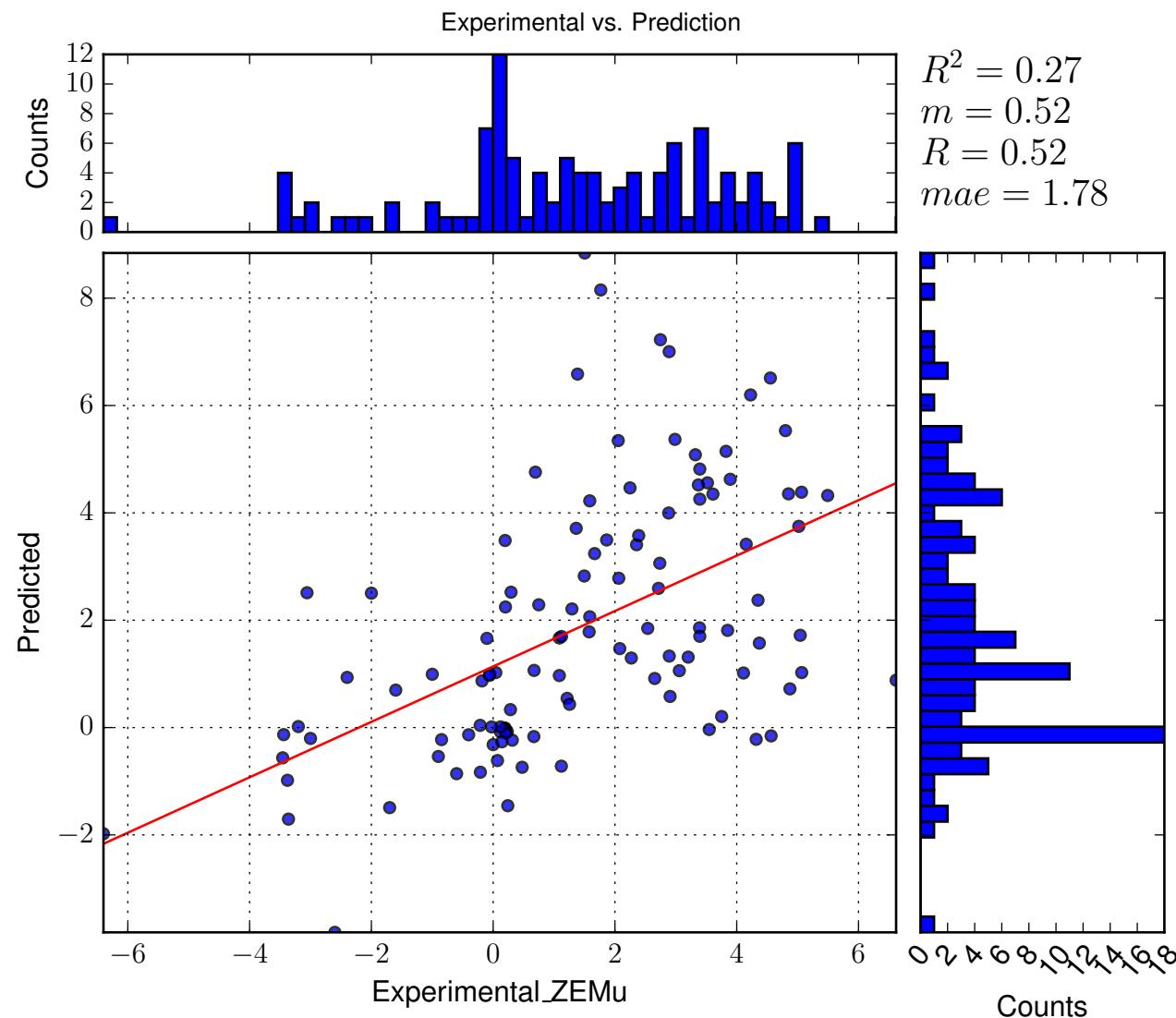
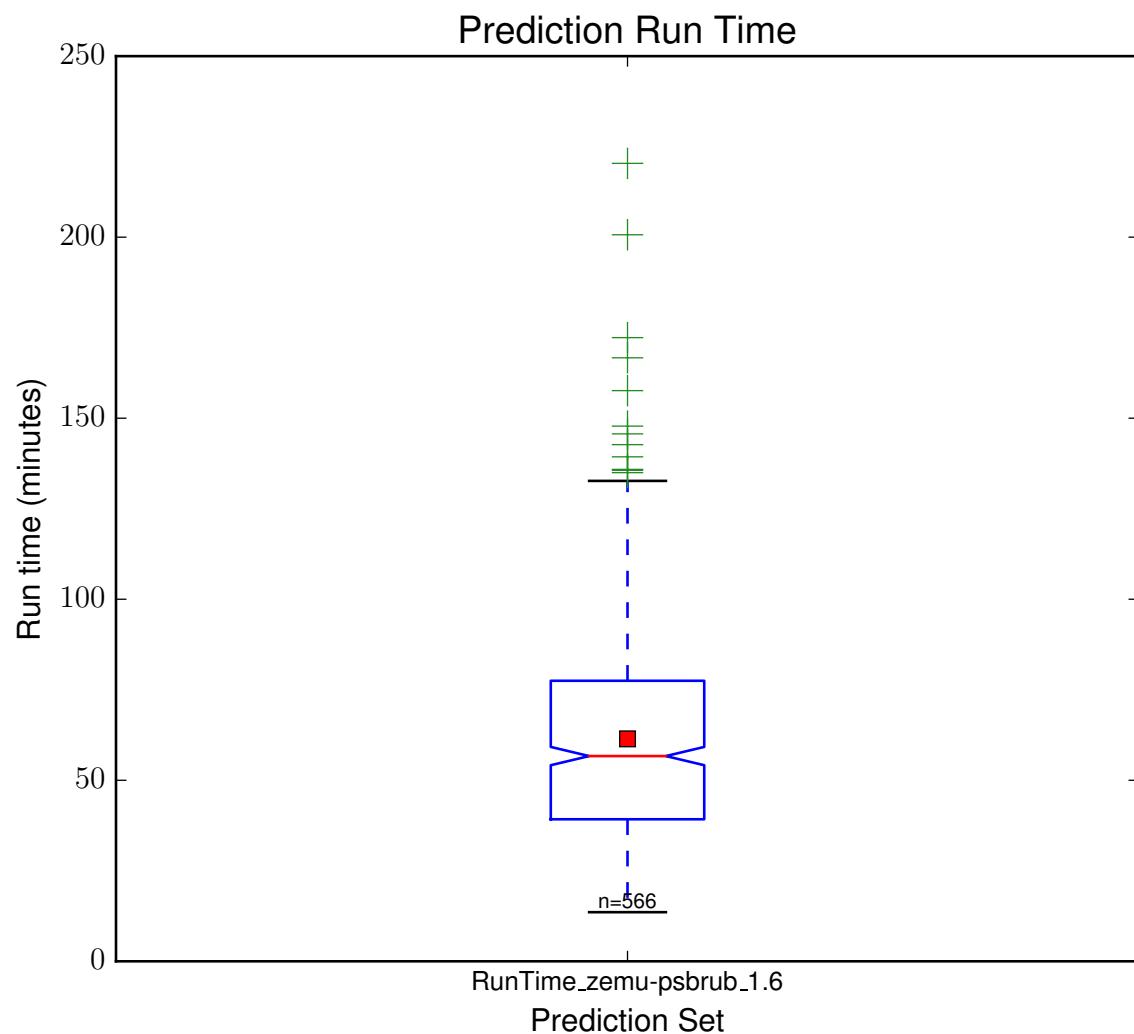


Figure 4.3: Single mutations data subset



95
 Figure 4.4: Multiple mutations data subset



96
Figure 4.5: Run time

Distribution of absolute errors (prediction - observed) for ZEMu

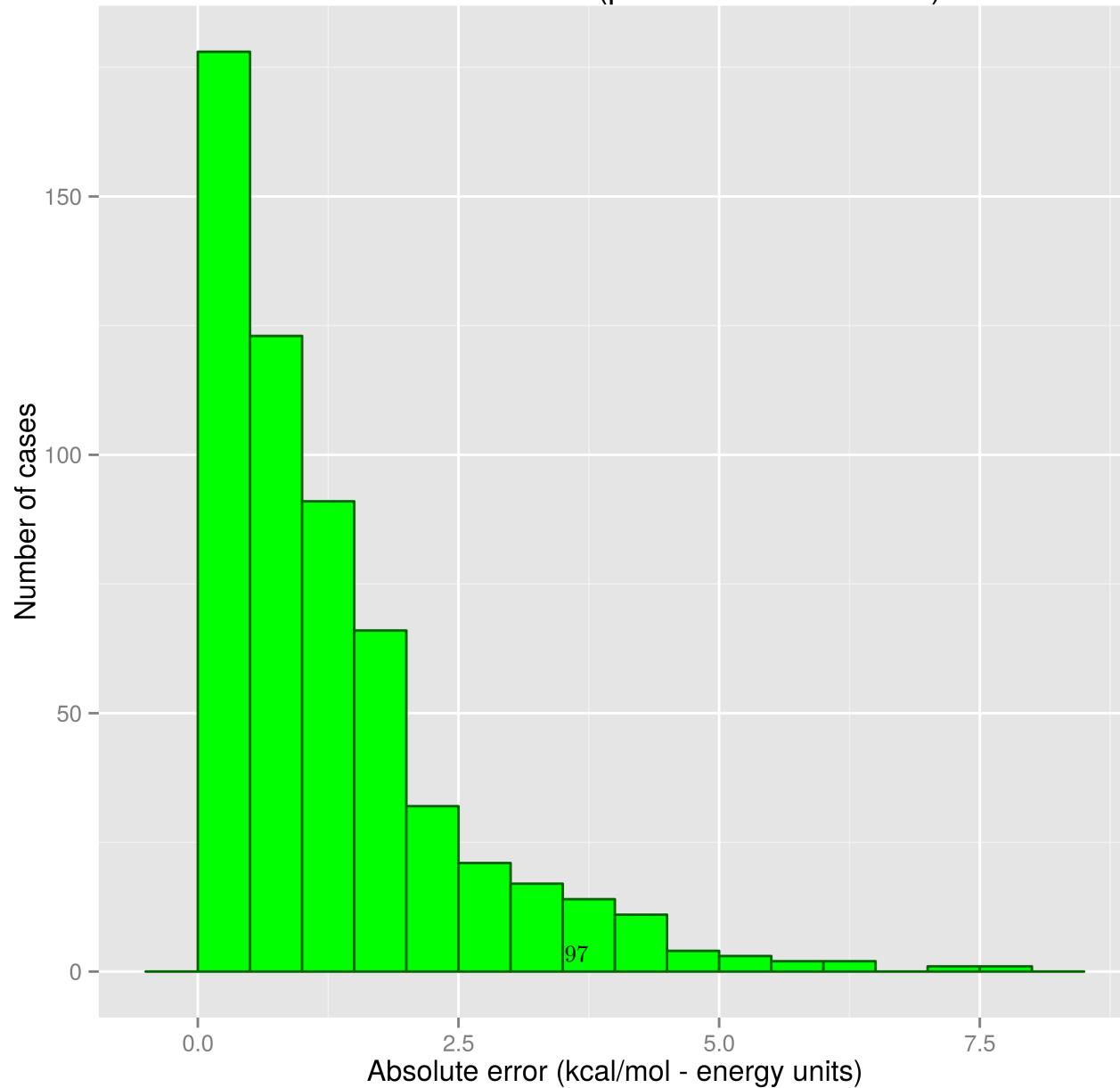


Figure 4.6: Absolute error histogram

4.3 Adjustments

Optimization of the cutoffs for the fraction correct metric

Optimum cutoff for fraction correct metric at varying experimental cutoffs for ZF

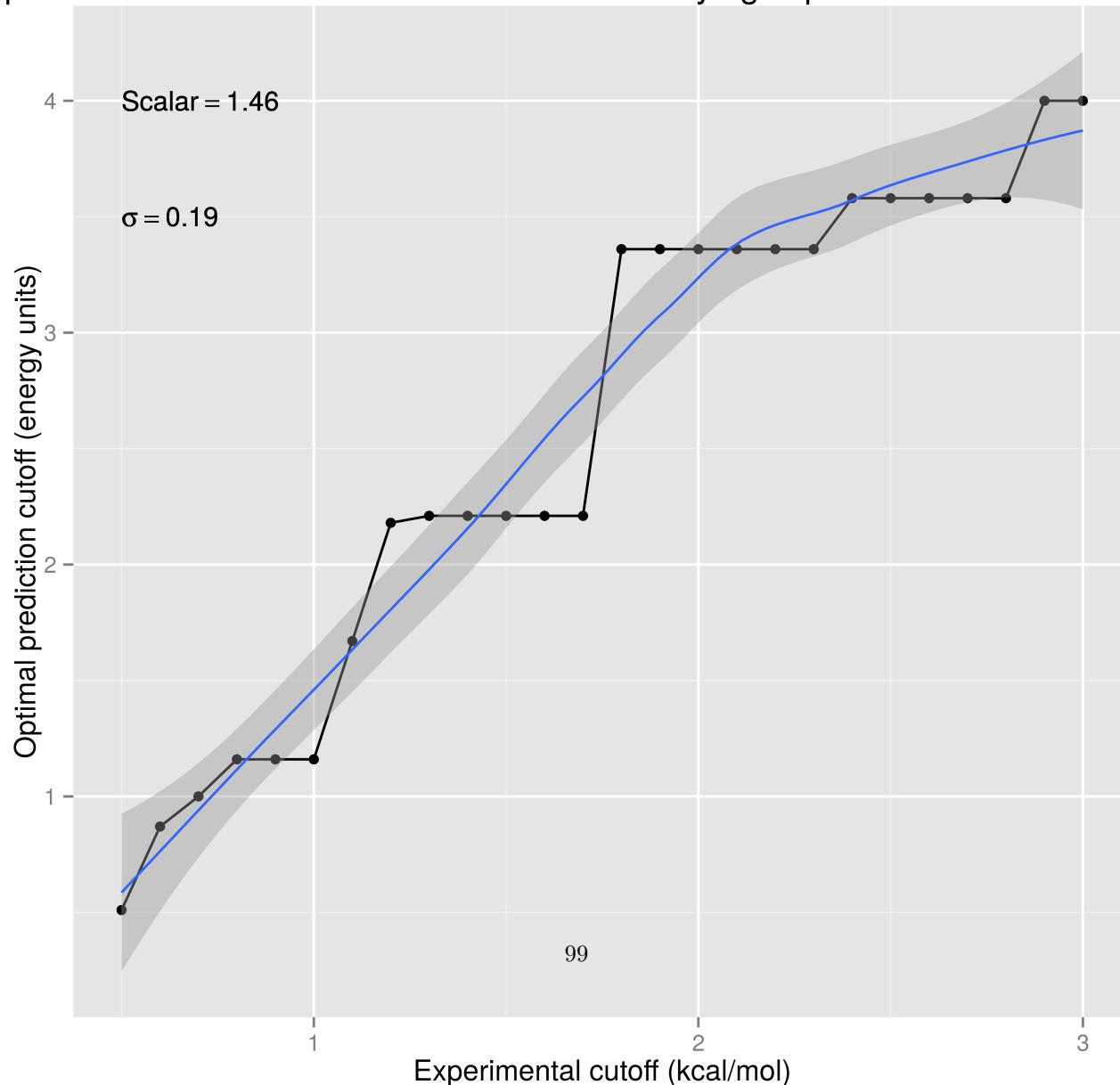


Figure 4.7: Scalar adjustment calculation plot

Optimum cutoff for fraction correct metric at 1.00 kcal/mol

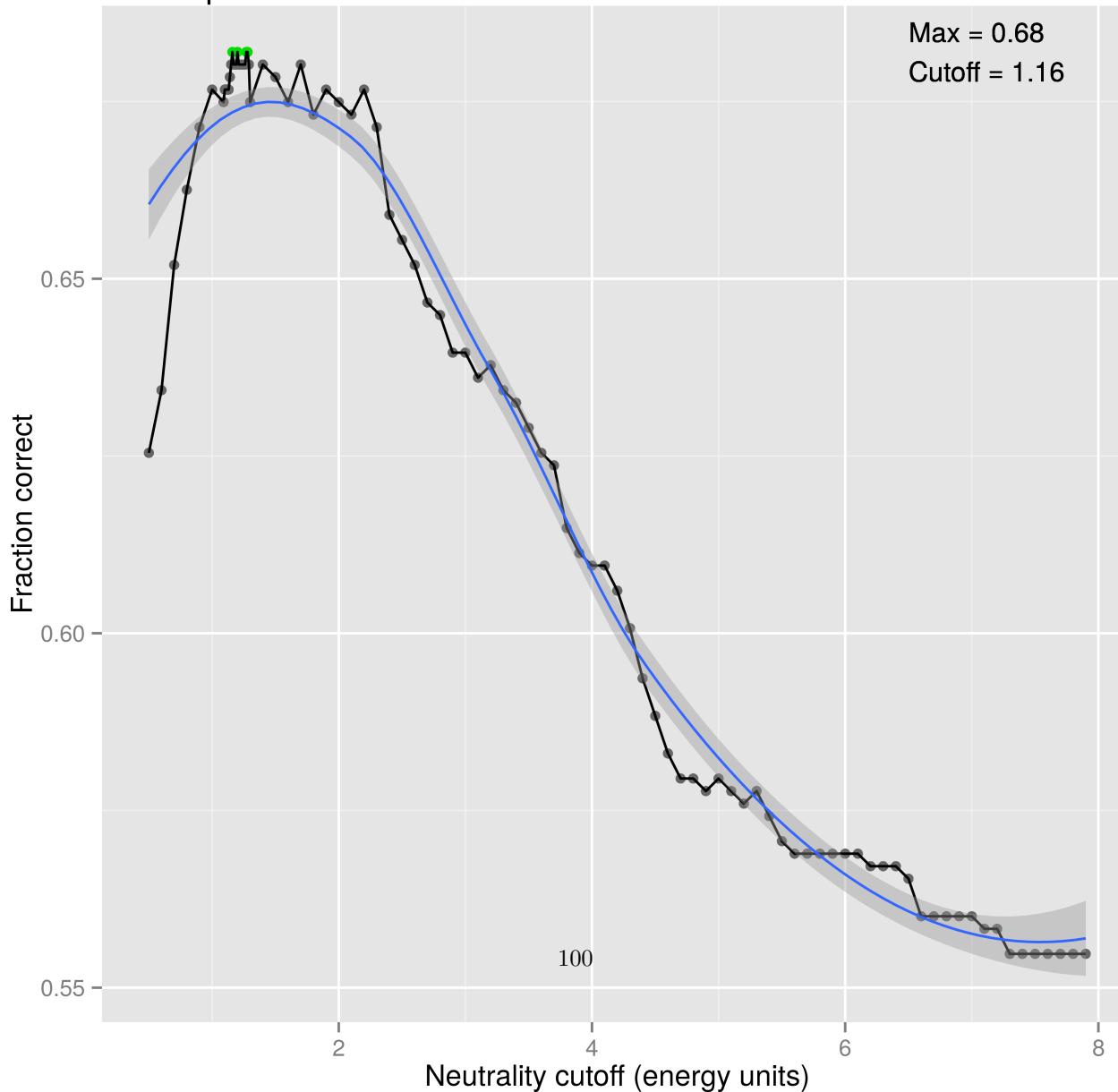


Figure 4.8: Optimal predictive cutoff plot

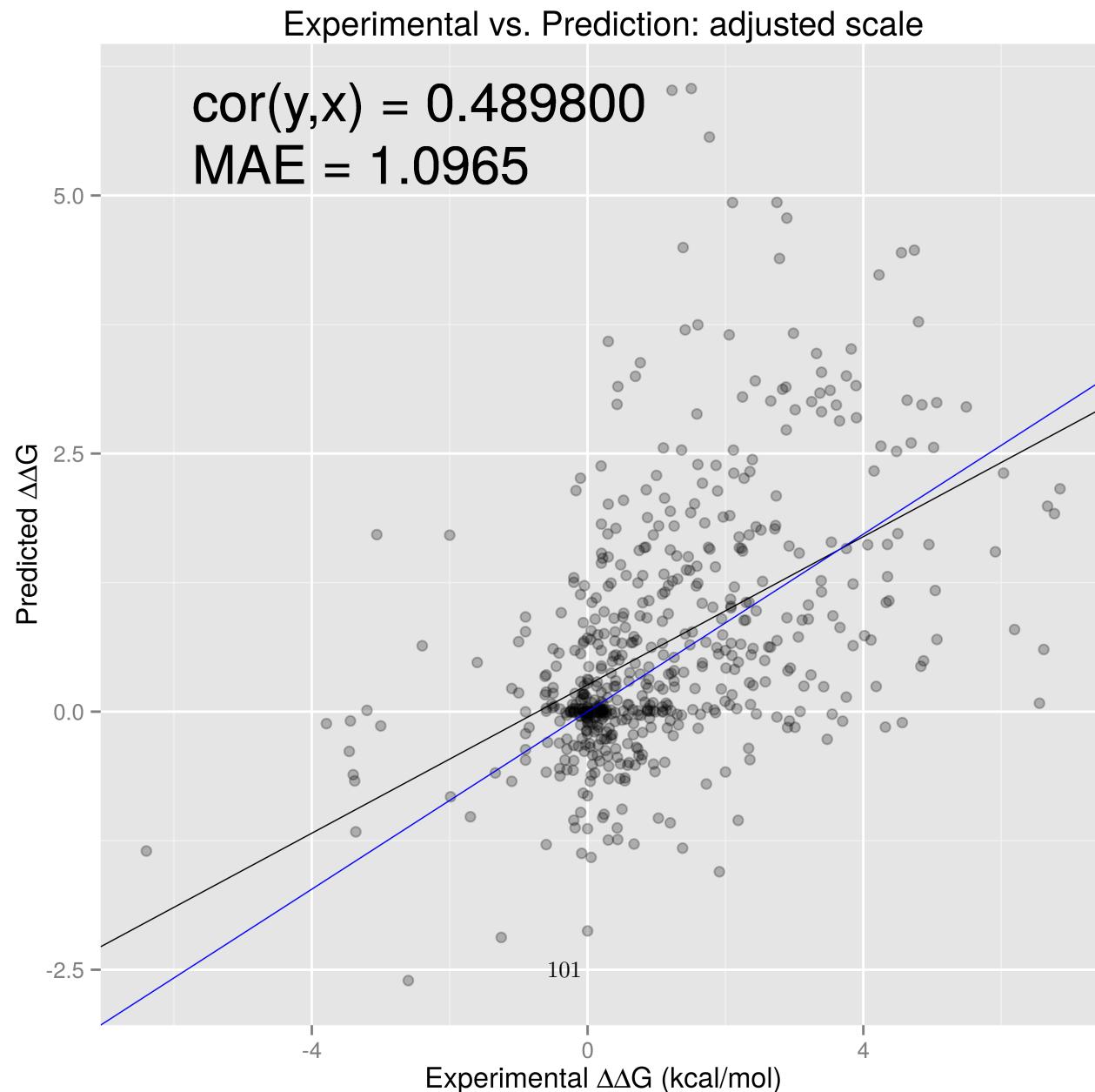


Figure 4.9: Main adj. scatterplot

Distribution of absolute errors (prediction - observed) for ZEMu

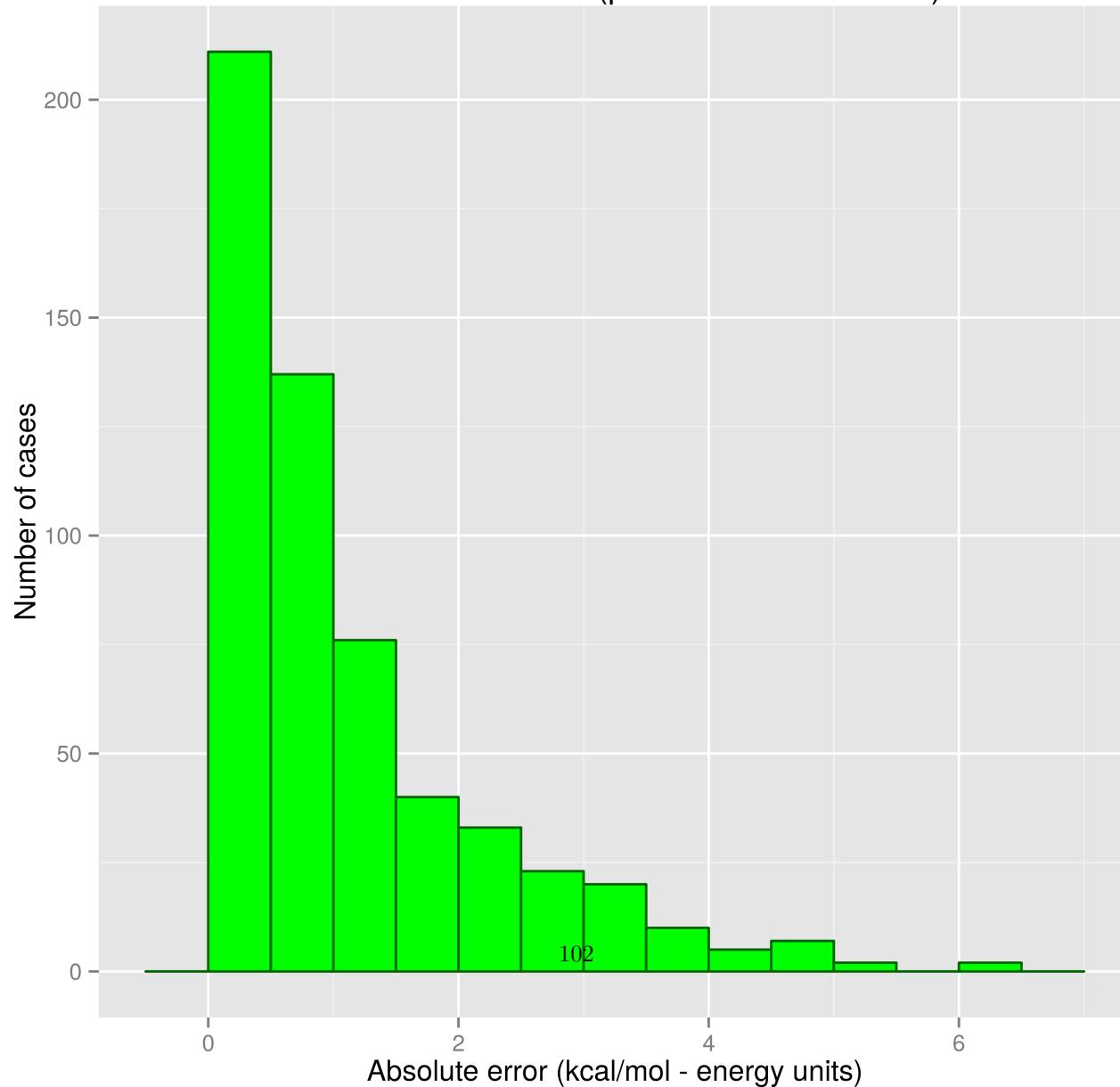
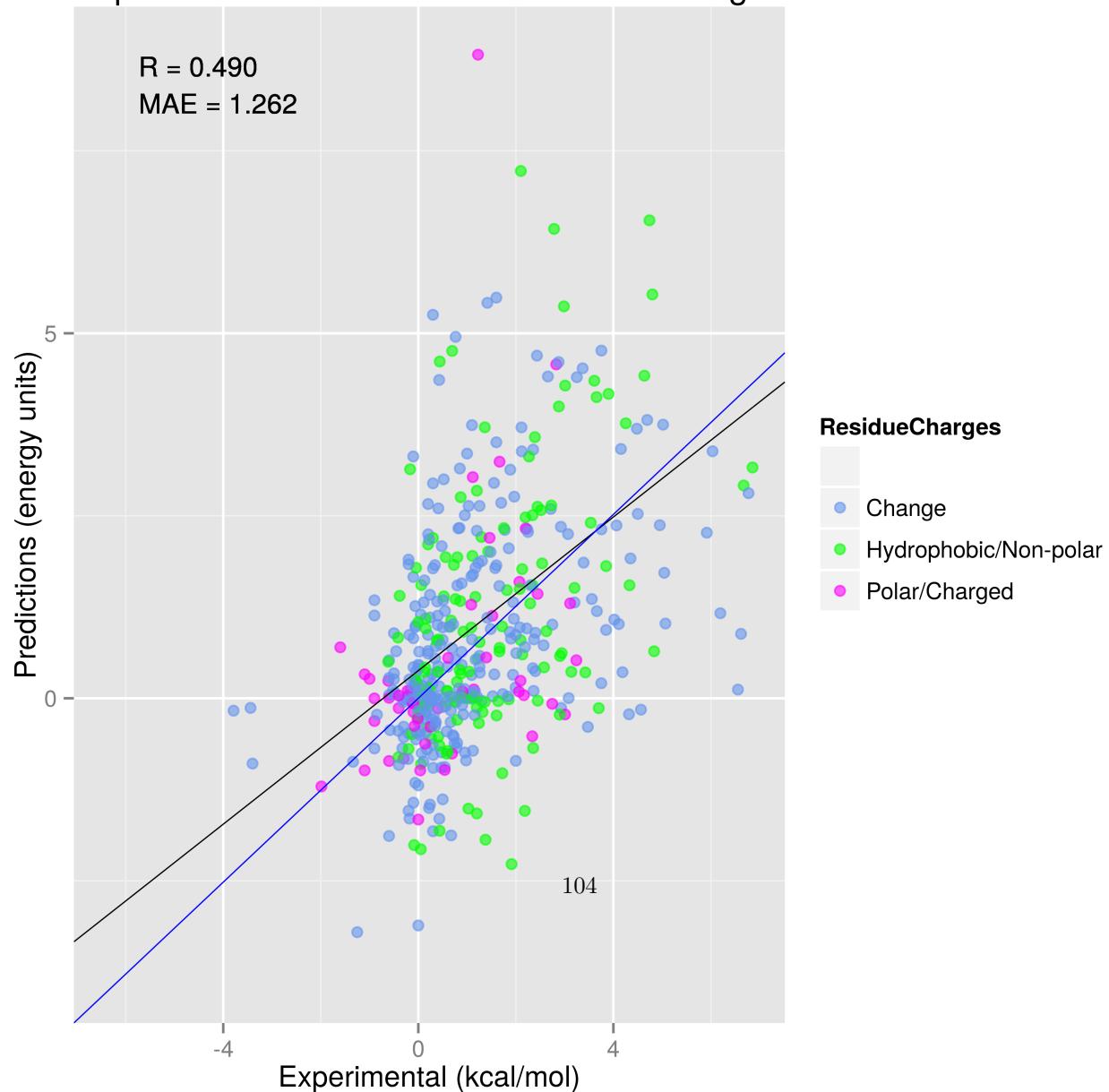


Figure 4.10: Absolute errors adjusted with scalar

4.4 Residue context

Experimental vs. Prediction - Residue charges



Experimental vs. Prediction - Exposure (cutoff = 0.25)

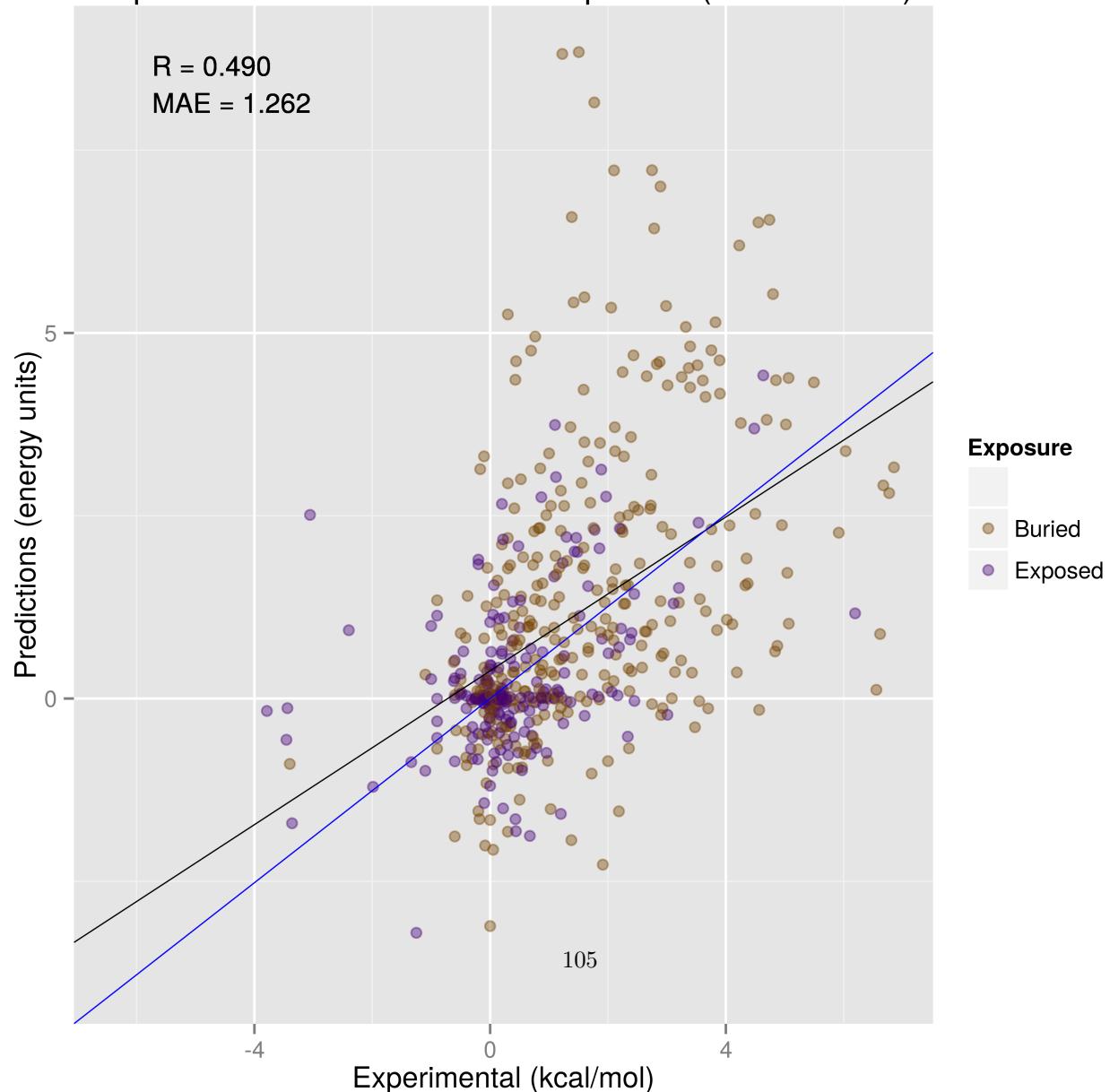


Figure 4.12: Experimental vs. Prediction - Exposure (cutoff = 0.25)

Experimental vs. Prediction - Change in volume

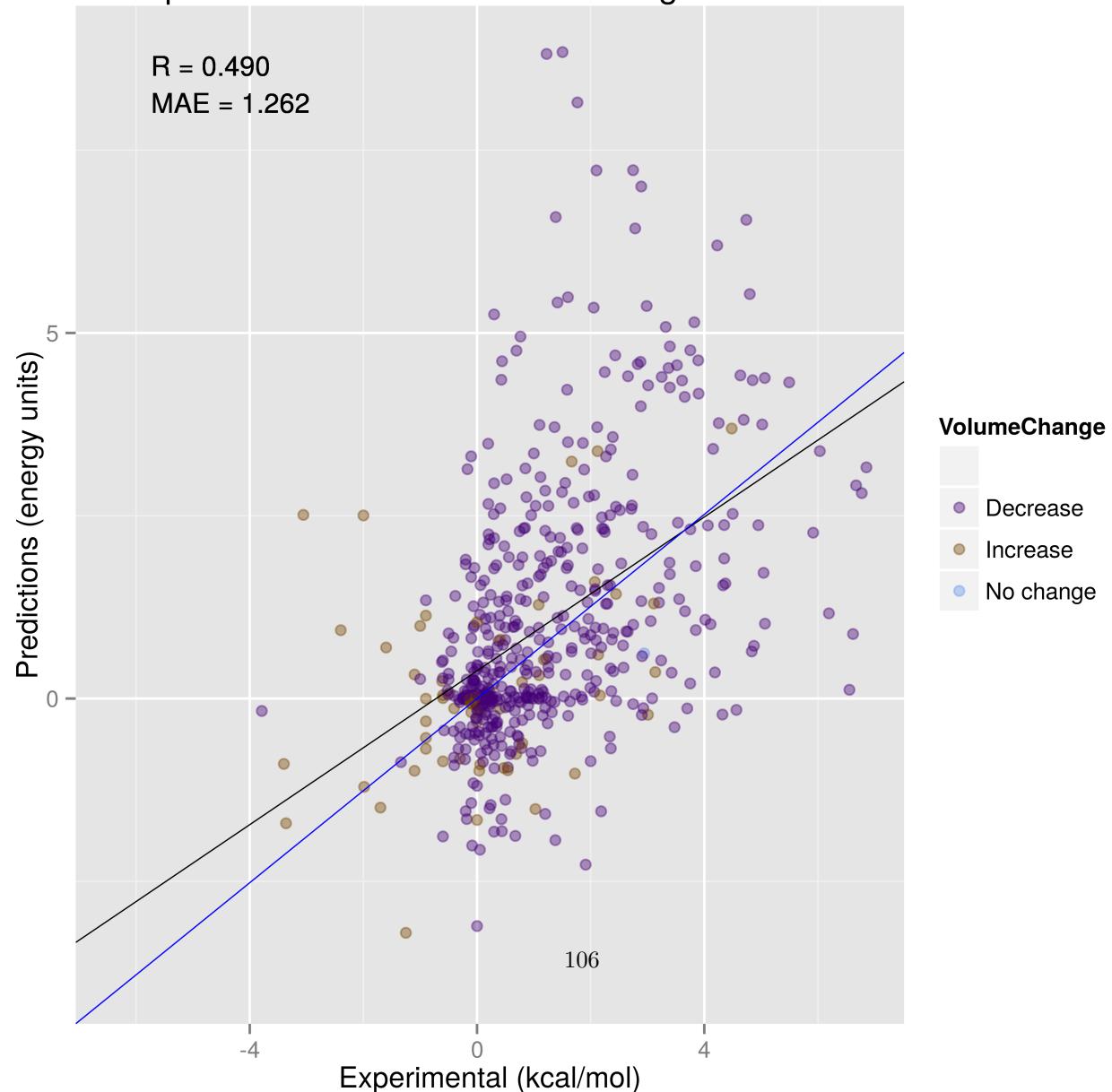


Figure 4.13: Experimental vs. Prediction - Change in volume

Experimental vs. Prediction - Wildtype residue s.s.

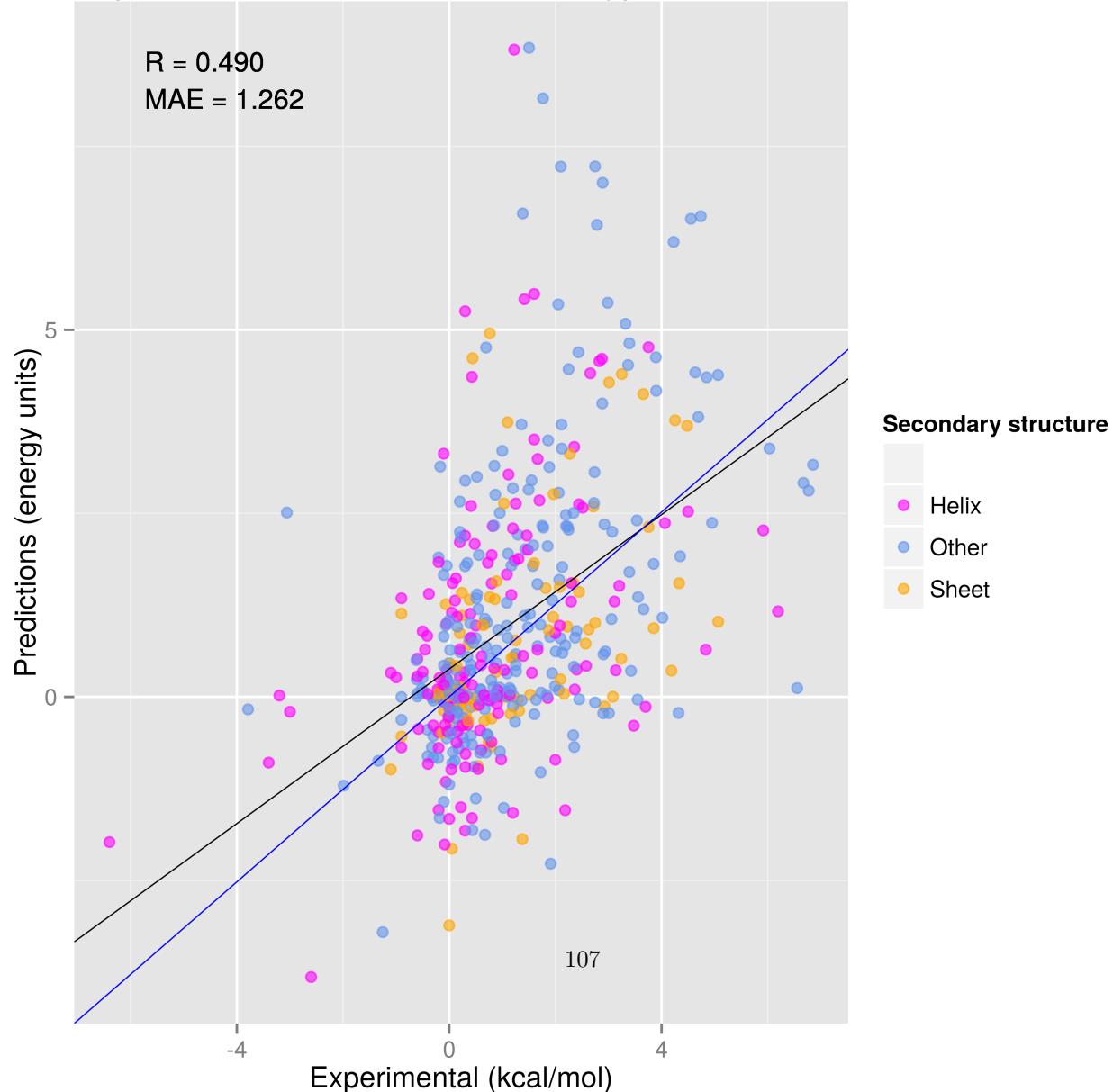
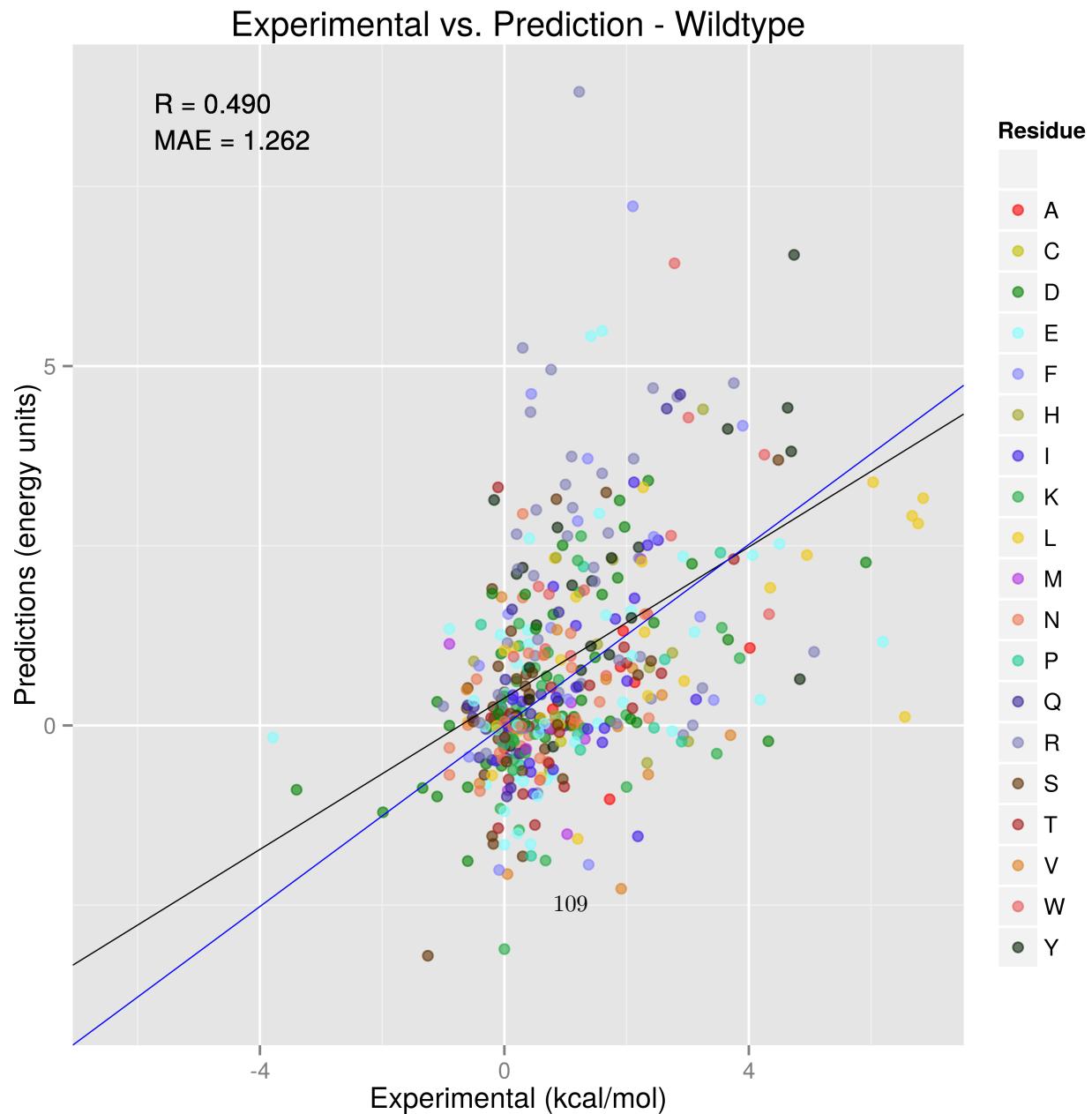


Figure 4.14: Experimental vs. Prediction - Wildtype residue s.s.

4.5 Residue types



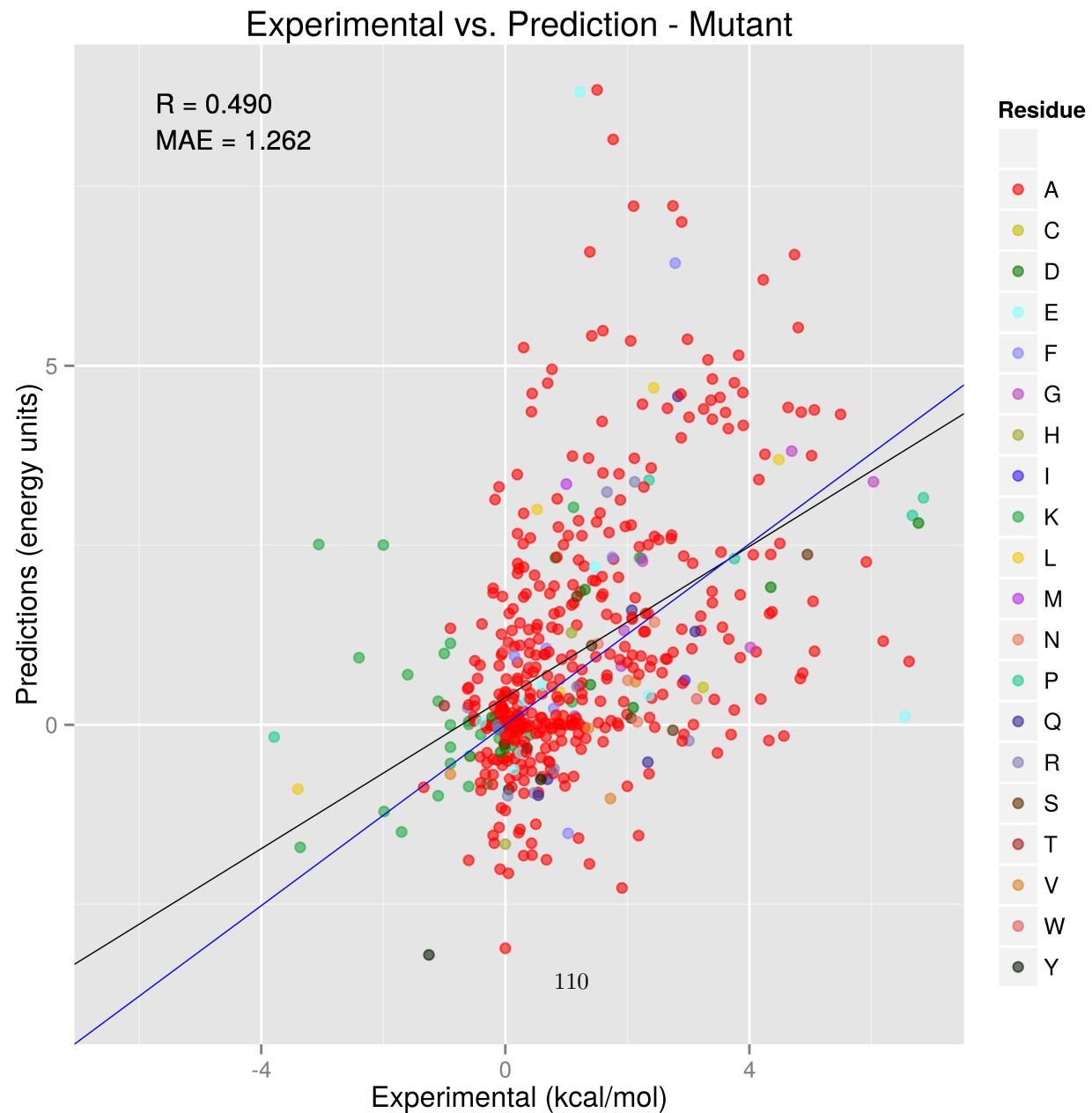


Figure 4.16: Experimental vs. Prediction - Mutant

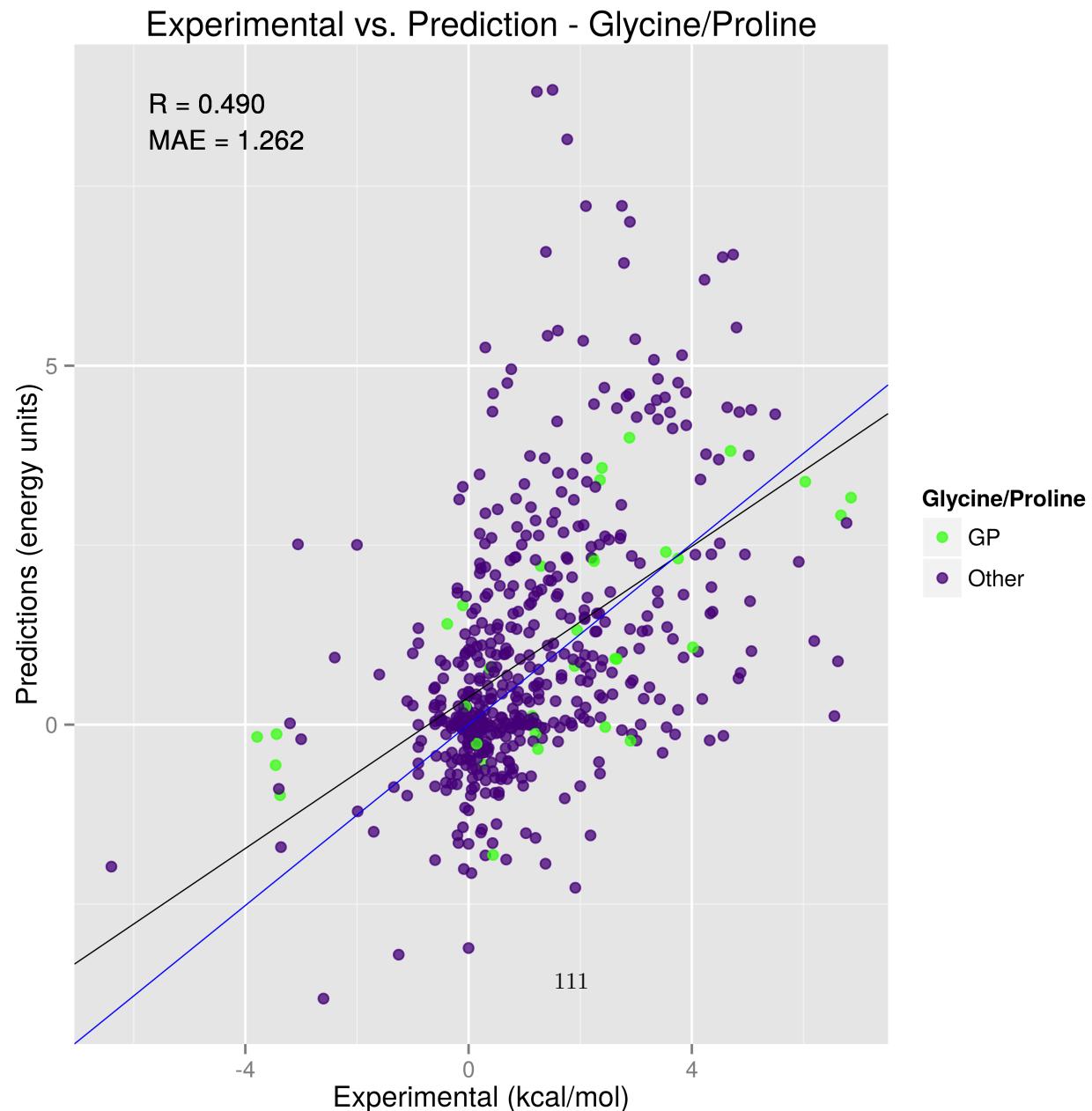
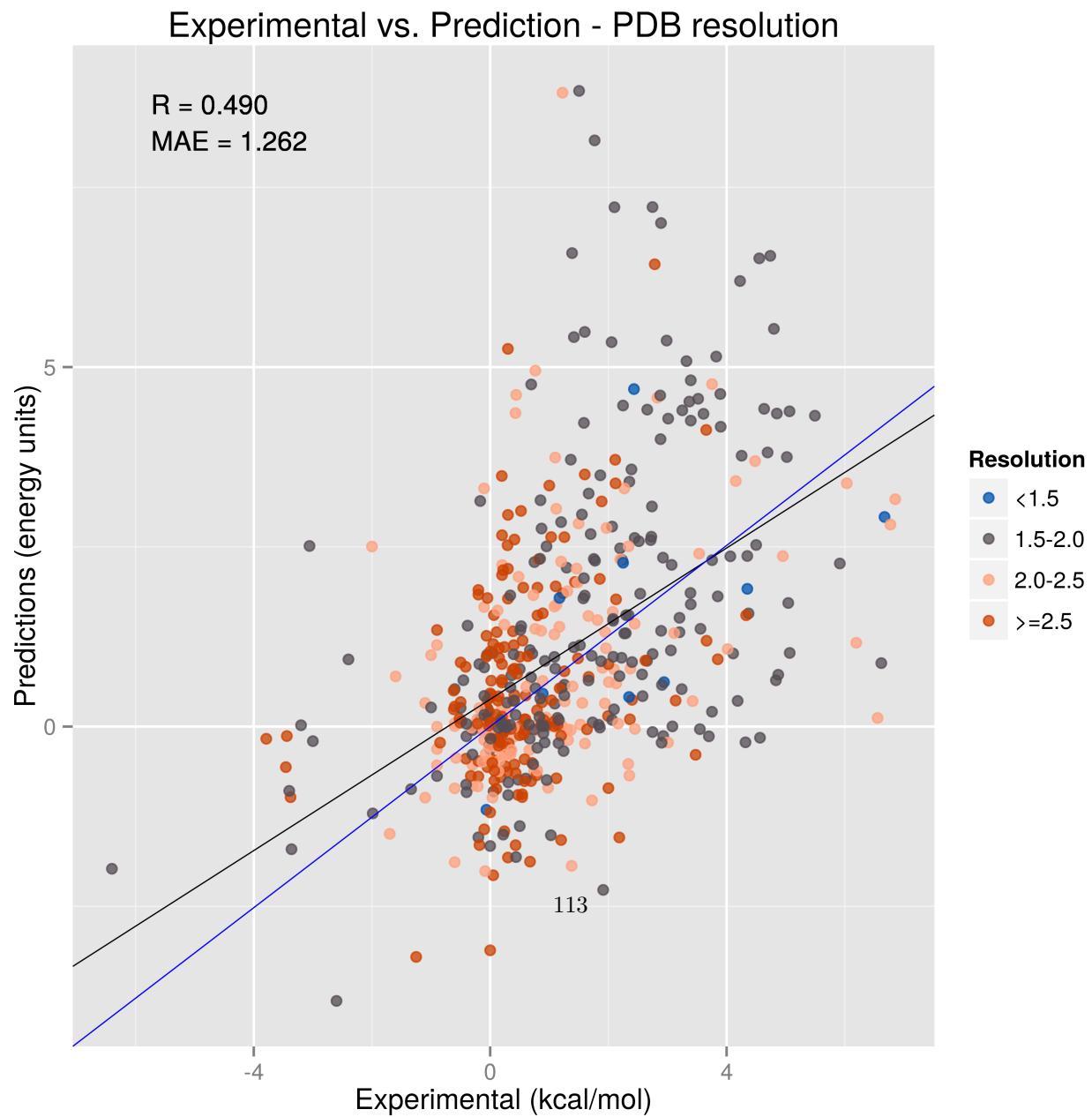


Figure 4.17: Experimental vs. Prediction - Glycine/Proline

4.6 Chain properties



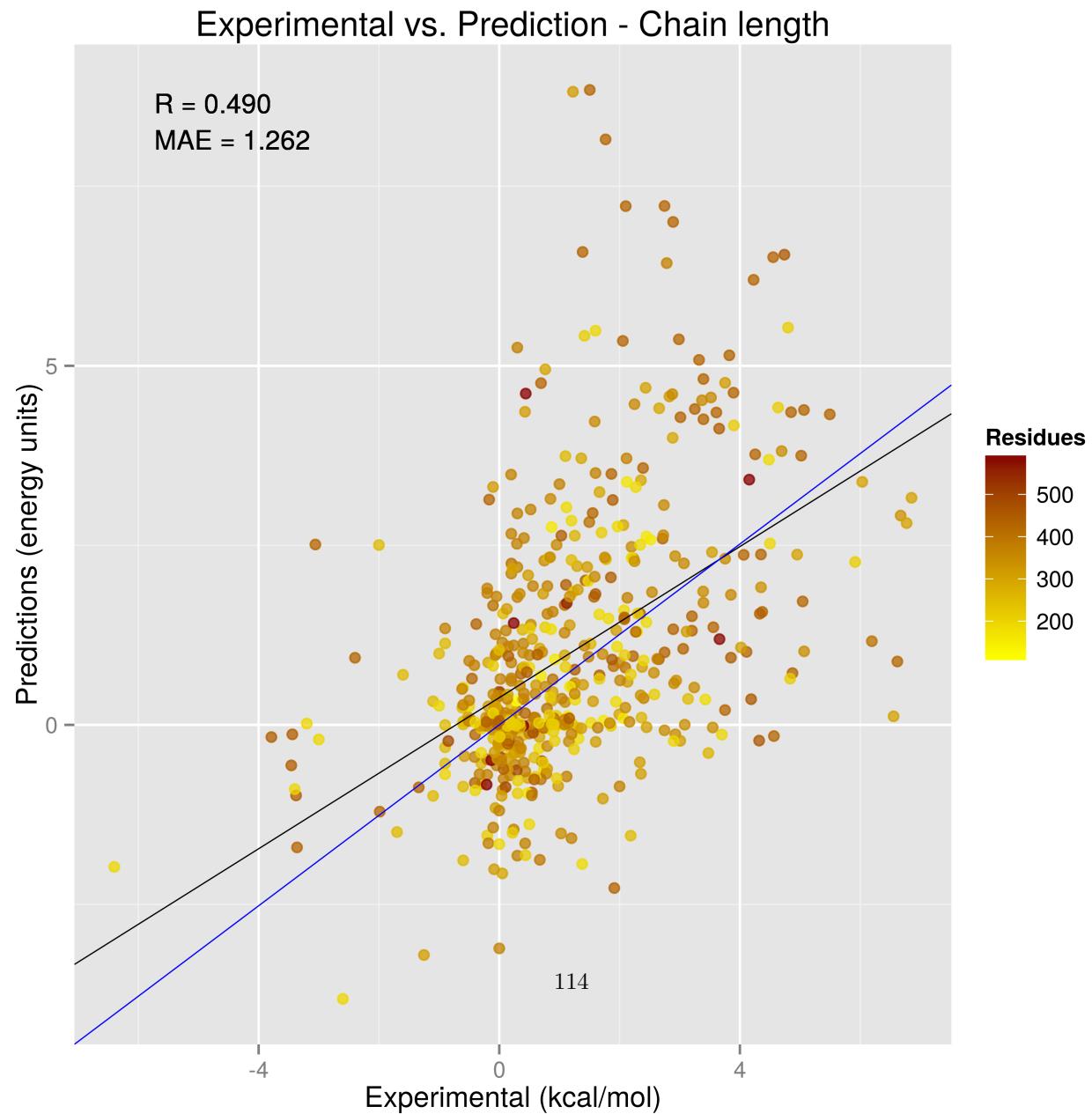
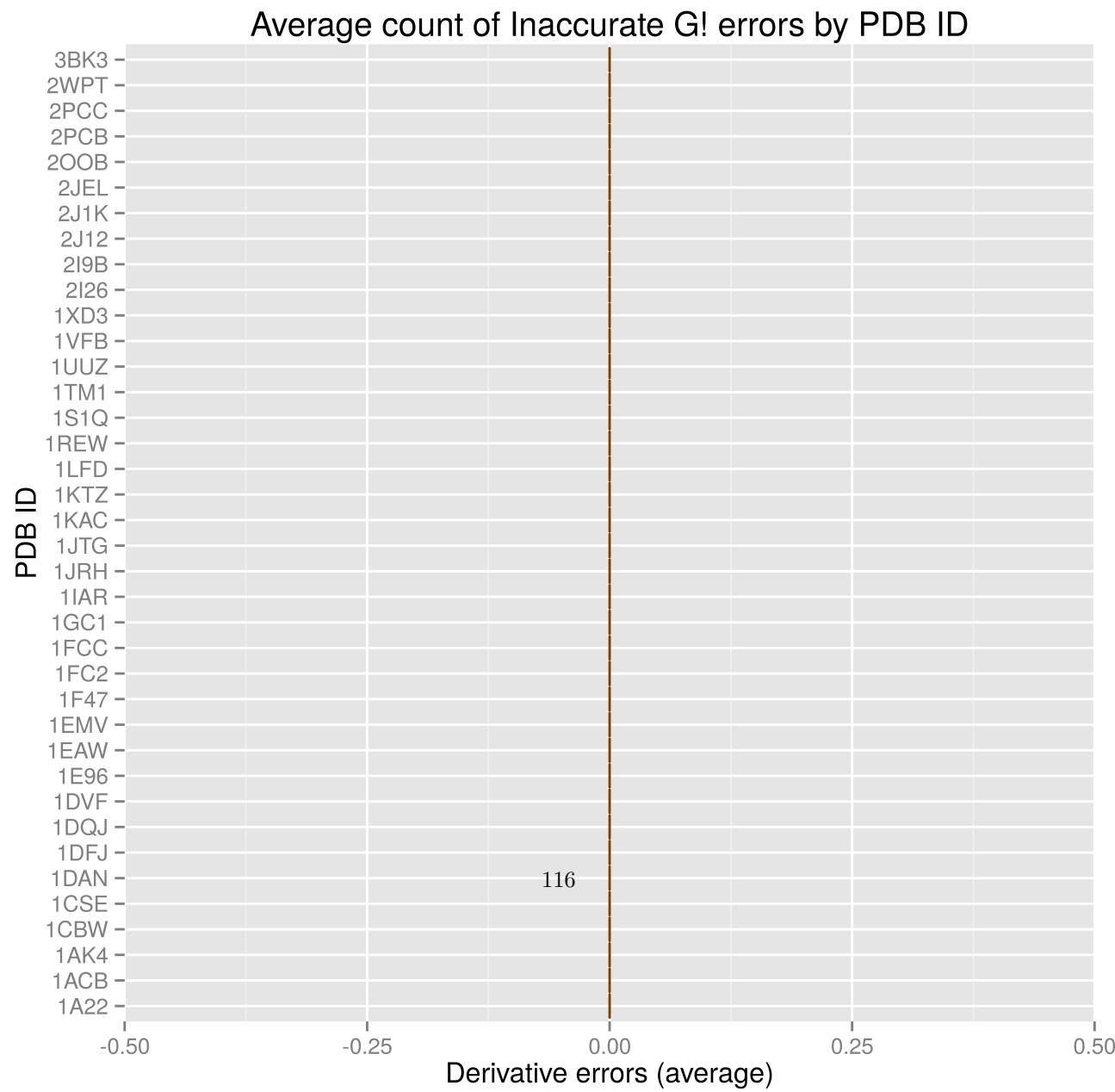


Figure 4.19: Experimental vs. Prediction - Chain length

4.7 Errors / debugging



5 topx_10-prediction_set_id_james-backrub-rscript-full-score_method_Unrescored-Talaris

james-backrub-rscript-full First full ZEMu run (ZEMu)

Prediction set scoring credit: James Lucas

5.1 Data tables

The predicted DDG value per case is computed using the 10 lowest-scoring mutant structures and the 10 lowest-scoring wildtype structures.

Derived mutations in analysis are omitted):

The stability classification cutoffs are: Experimental=1.00 kcal/mol, Predicted=1.00 energy units.

5.1.1 Breakdown by volume

A case is considered a small-to-large (resp. large-to-small) mutation if all of the wildtype residues have a smaller (resp. larger) van der Waals volume than the corresponding mutant residue. The order is defined as G < A < S < C < P < D < T < N < V < E < Q < H < ILM < FK < Y < R < W so some cases are considered to have no change in volume e.g. MET → LEU.

Not enough data for analysis of mutations no change in volume (at least 8 cases are required).

Statistic name	Value	p-value
Fraction correct	0.48	
Fraction correct (fuzzy)	0.49	
Gamma correlation coef.	0.06	
Kolmogorov-Smirnov test (XY)	0.16	(2-tailed p-value= 3.65×10^{-01})
MAE	144.14	
Pearson's R	-0.15	(2-tailed p-value= 2.53×10^{-01})
Spearman's R	0.08	(2-tailed p-value= 5.22×10^{-01})
X-axis Kolmogorov-Smirnov test	0.13	(p-value= 2.29×10^{-01})
X-axis normality test	2.18	(2-sided chi ² p-value= 3.36×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.13	(p-value= 2.16×10^{-01})
Y-axis normality test	96.17	(2-sided chi ² p-value= 1.31×10^{-21})
n	62.00	
num_null_cases	0.00	

Table 5.1: Statistics - small-to-large mutations (62 cases)

Statistic name	Value	p-value
Fraction correct	0.60	
Fraction correct (fuzzy)	0.60	
Gamma correlation coef.	0.17	
Kolmogorov-Smirnov test (XY)	0.20	(2-tailed p-value= 6.18×10^{-09})
MAE	43.18	
Pearson's R	-0.02	(2-tailed p-value= 6.23×10^{-01})
Spearman's R	0.25	(2-tailed p-value= 3.13×10^{-08})
X-axis Kolmogorov-Smirnov test	0.36	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	92.92	(2-sided chi ² p-value= 6.64×10^{-21})
Y-axis Kolmogorov-Smirnov test	0.25	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	611.36	(2-sided chi ² p-value= 1.76×10^{-133})
n	488.00	
num_null_cases	0.00	

Table 5.2: Statistics - large-to-small mutations (488 cases)

5.1.2 Separating out mutations involving glycine or proline.

This cases may involve changes to secondary structure so we separate them out here.

Statistic name	Value	p-value
Fraction correct	0.62	
Fraction correct (fuzzy)	0.62	
Gamma correlation coef.	0.27	
Kolmogorov-Smirnov test (XY)	0.15	(2-tailed p-value= 8.25×10^{-01})
MAE	44.78	
Pearson's R	0.20	(2-tailed p-value= 2.49×10^{-01})
Spearman's R	0.39	(2-tailed p-value= 2.08×10^{-02})
X-axis Kolmogorov-Smirnov test	0.52	(p-value= 4.57×10^{-09})
X-axis normality test	0.66	(2-sided chi ² p-value= 7.21×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.48	(p-value= 1.41×10^{-07})
Y-axis normality test	37.81	(2-sided chi ² p-value= 6.17×10^{-09})
n	34.00	
num_null_cases	0.00	

Table 5.3: Statistics - cases with G or P (34 cases)

Statistic name	Value	p-value
Fraction correct	0.57	
Fraction correct (fuzzy)	0.58	
Gamma correlation coef.	0.16	
Kolmogorov-Smirnov test (XY)	0.19	(2-tailed p-value= 1.50×10^{-08})
MAE	55.17	
Pearson's R	-0.02	(2-tailed p-value= 6.90×10^{-01})
Spearman's R	0.23	(2-tailed p-value= 5.05×10^{-08})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	57.49	(2-sided chi ² p-value= 3.28×10^{-13})
Y-axis Kolmogorov-Smirnov test	0.22	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	556.94	(2-sided chi ² p-value= 1.15×10^{-121})
n	532.00	
num_null_cases	0.00	

Table 5.4: Statistics - cases without G or P (532 cases)

5.1.3 Number of mutations

Statistic name	Value	p-value
Fraction correct	0.59	
Fraction correct (fuzzy)	0.60	
Gamma correlation coef.	0.17	
Kolmogorov-Smirnov test (XY)	0.17	(2-tailed p-value= 3.31×10^{-06})
MAE	62.80	
Pearson's R	-0.02	(2-tailed p-value= 6.51×10^{-01})
Spearman's R	0.25	(2-tailed p-value= 7.50×10^{-08})
X-axis Kolmogorov-Smirnov test	0.32	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	116.40	(2-sided chi ² p-value= 5.29×10^{-26})
Y-axis Kolmogorov-Smirnov test	0.21	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	455.76	(2-sided chi ² p-value= 1.08×10^{-99})
n	453.00	
num_null_cases	0.00	

Table 5.5: Statistics - single mutations (453 cases)

Statistic name	Value	p-value
Fraction correct	0.50	
Fraction correct (fuzzy)	0.51	
Gamma correlation coef.	0.20	
Kolmogorov-Smirnov test (XY)	0.18	(2-tailed p-value= 5.11×10^{-02})
MAE	21.47	
Pearson's R	0.11	(2-tailed p-value= 2.54×10^{-01})
Spearman's R	0.27	(2-tailed p-value= 3.48×10^{-03})
X-axis Kolmogorov-Smirnov test	0.45	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	4.54	(2-sided chi ² p-value= 1.03×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.35	(p-value= 6.77×10^{-13})
Y-axis normality test	106.24	(2-sided chi ² p-value= 8.53×10^{-24})
n	113.00	
num_null_cases	0.00	

Table 5.6: Statistics - multiple mutations (113 cases)

5.1.4 Entire dataset using a scaling factor of 1/1.991 to improve the fraction correct metric.

Warning: Results in this section use an averaged scaling factor to improve the value for the fraction correct metric. This scalar will vary over benchmark runs so these results should not be interpreted as performance results; they should be considered as what could be obtained if the predicted values were scaled by a "magic" value.

Statistic name	Value	p-value
Fraction correct	0.62	
Fraction correct (fuzzy)	0.63	
Gamma correlation coef.	0.17	
Kolmogorov-Smirnov test (XY)	0.19	(2-tailed p-value= 2.42×10^{-09})
MAE	27.78	
Pearson's R	-0.01	(2-tailed p-value= 9.01×10^{-01})
Spearman's R	0.25	(2-tailed p-value= 1.68×10^{-09})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	52.55	(2-sided chi ² p-value= 3.88×10^{-12})
Y-axis Kolmogorov-Smirnov test	0.21	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	592.40	(2-sided chi ² p-value= 2.30×10^{-129})
n	566.00	
num_null_cases	0.00	

Table 5.7: Statistics - complete dataset (scaled) (566 cases)

5.1.5 Entire dataset

Overall statistics

Statistic name	Value	p-value
Fraction correct	0.58	
Fraction correct (fuzzy)	0.58	
Gamma correlation coef.	0.17	
Kolmogorov-Smirnov test (XY)	0.17	(2-tailed p-value= 1.33×10^{-07})
MAE	54.55	
Pearson's R	-0.01	(2-tailed p-value= 9.01×10^{-01})
Spearman's R	0.25	(2-tailed p-value= 1.68×10^{-09})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	52.55	(2-sided chi ² p-value= 3.88×10^{-12})
Y-axis Kolmogorov-Smirnov test	0.24	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	592.40	(2-sided chi ² p-value= 2.30×10^{-129})
n	566.00	
num_null_cases	0.00	

Table 5.8: Statistics - complete dataset (566 cases)

5.2 Main plots

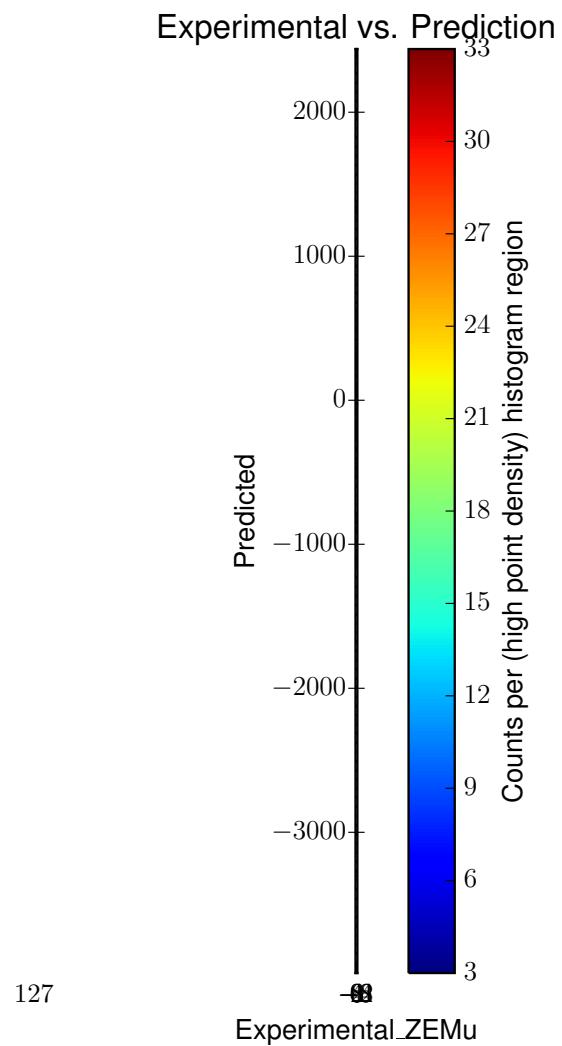
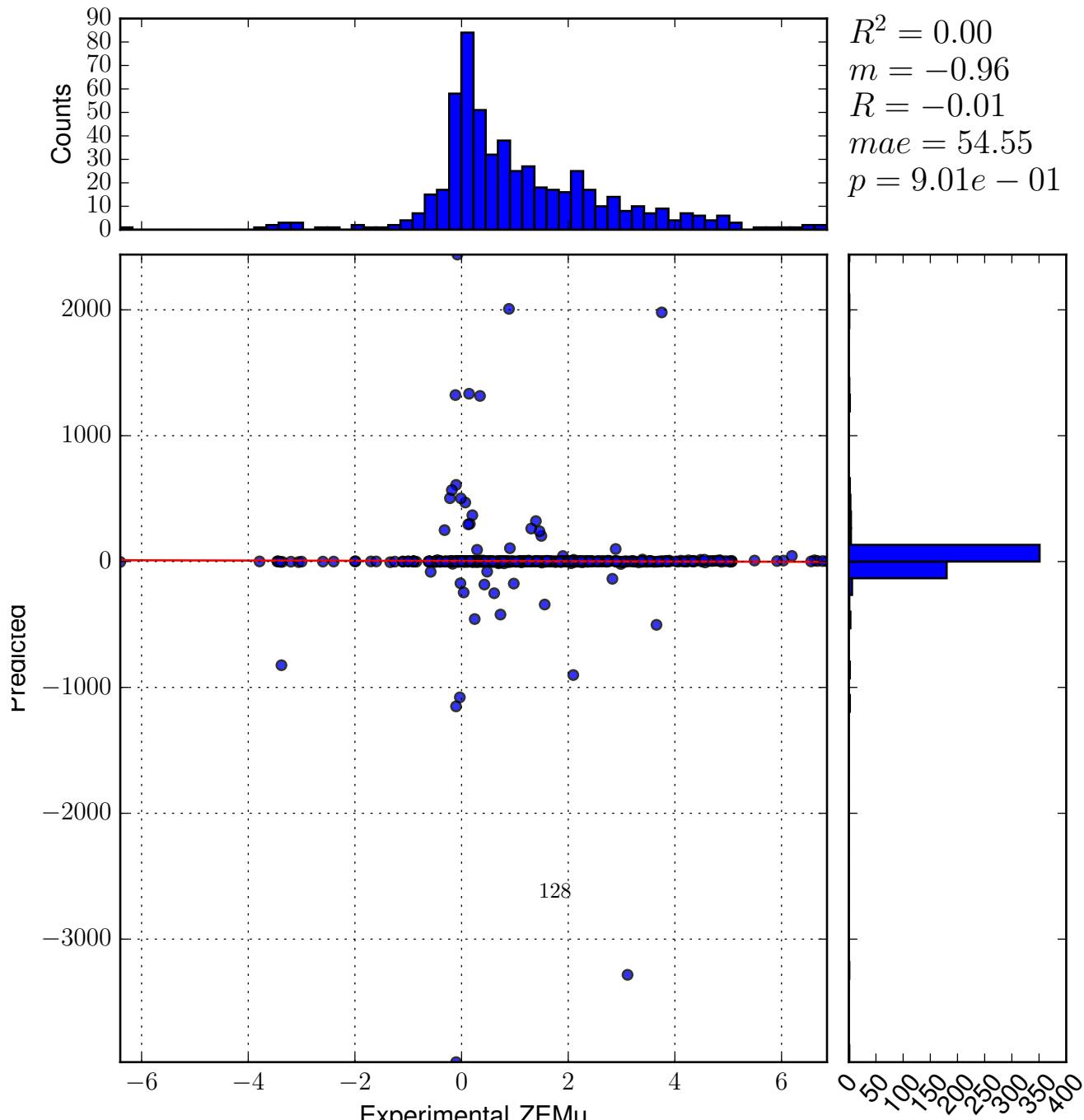


Figure 5.1: Experimental vs. Predicted scatterplot (with density binning)

Experimental vs. Prediction



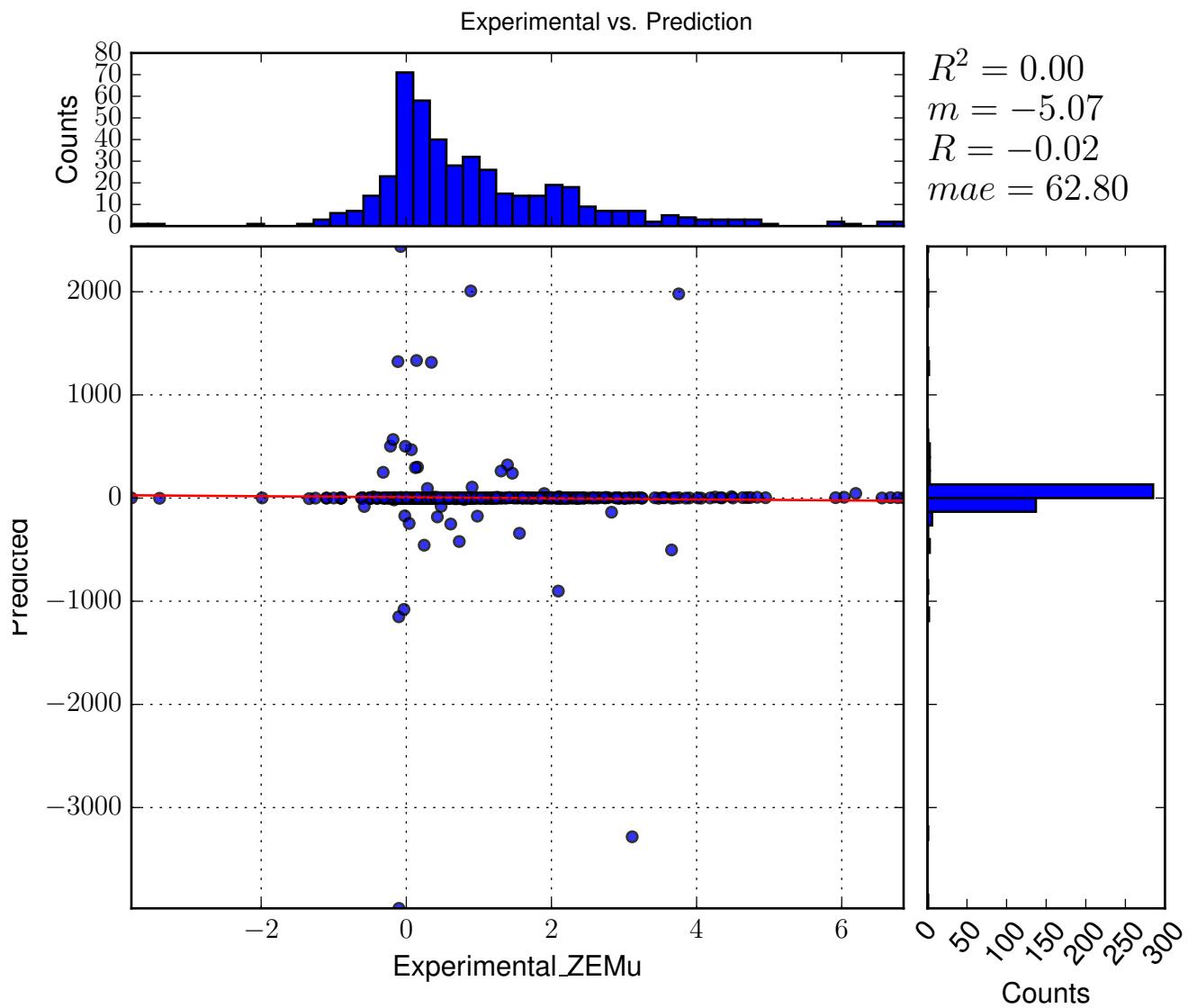


Figure 5.3: Single mutations data subset

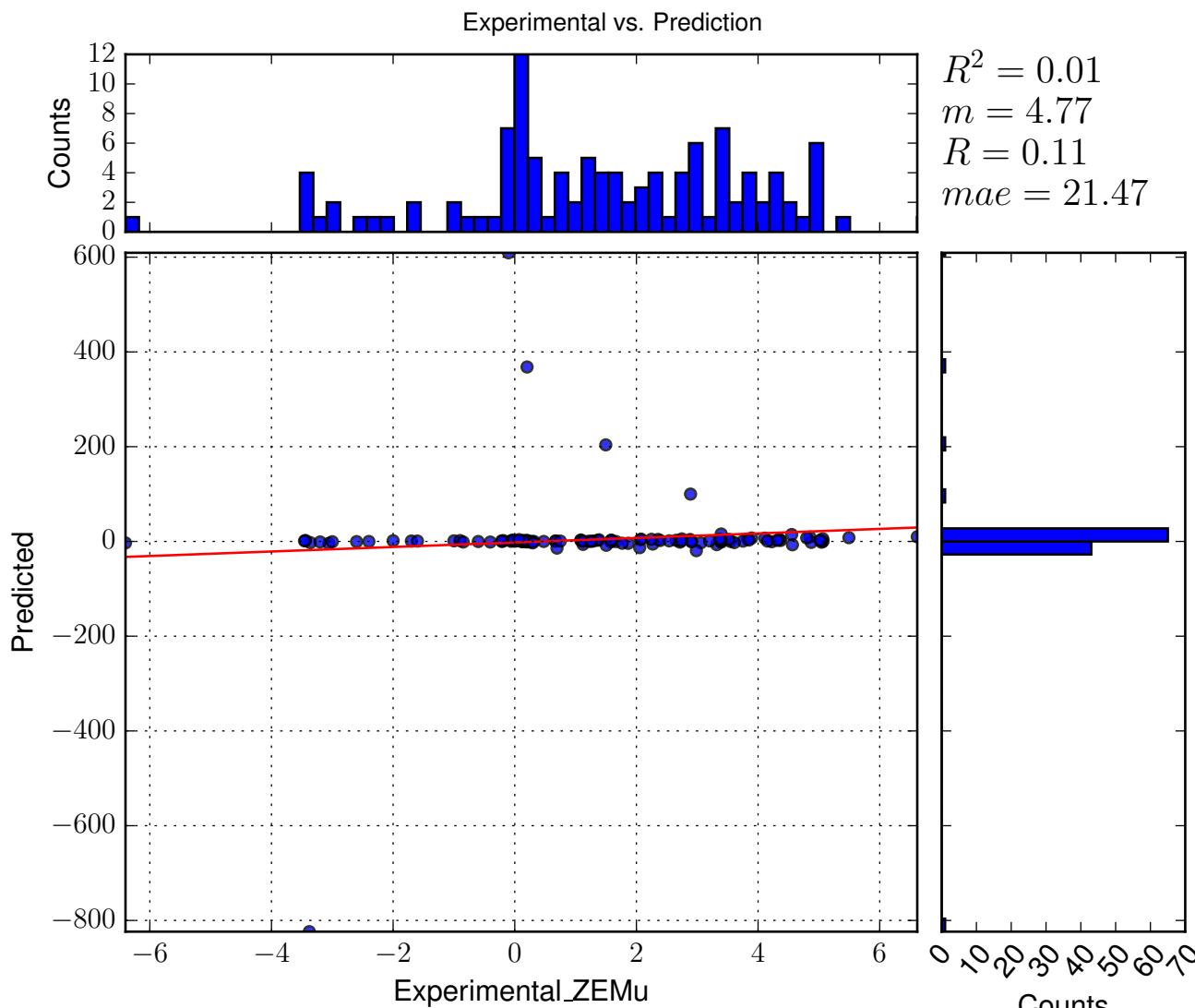
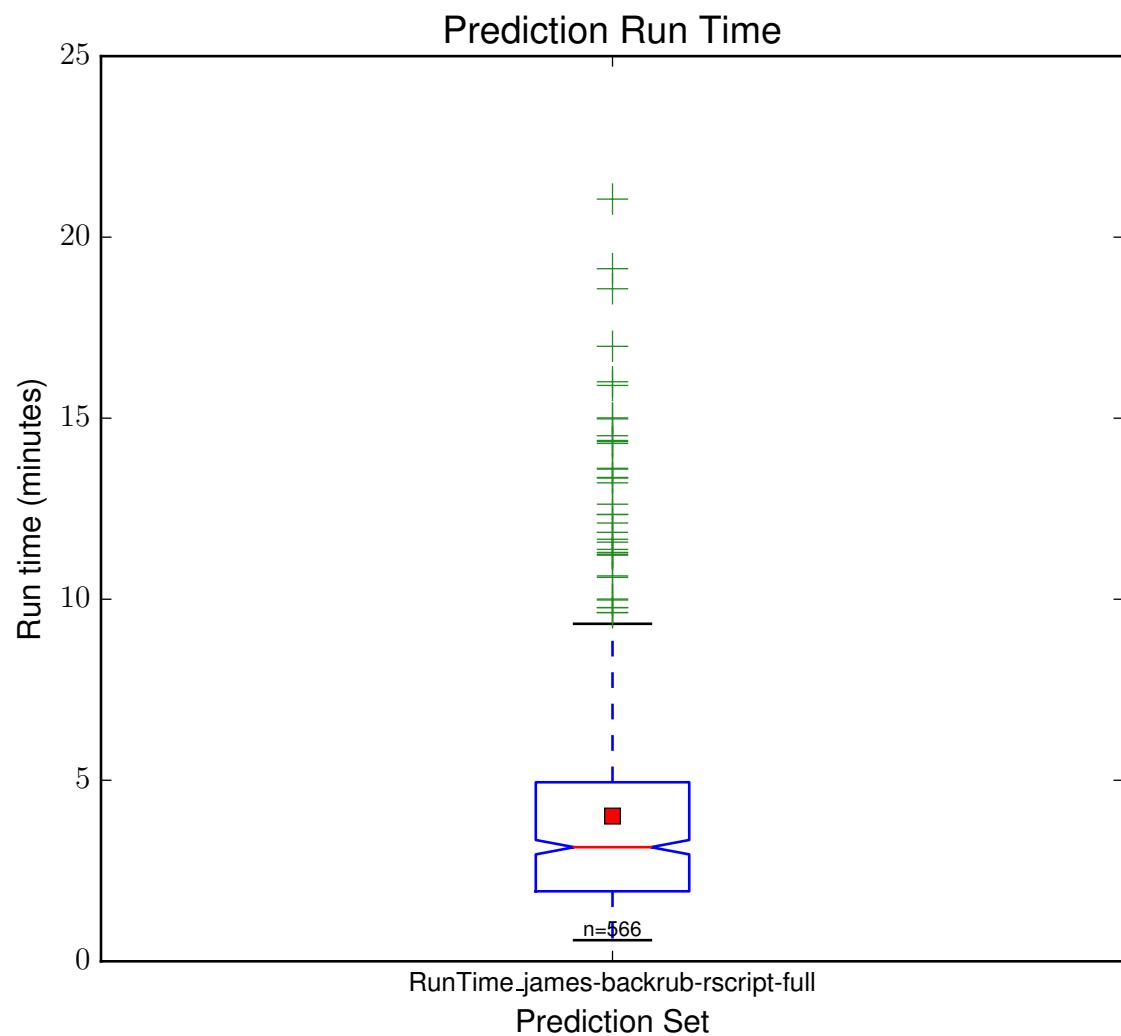


Figure 5.4: Multiple mutations data subset



131
Figure 5.5: Run time

Distribution of absolute errors (prediction - observed) for ZEMu

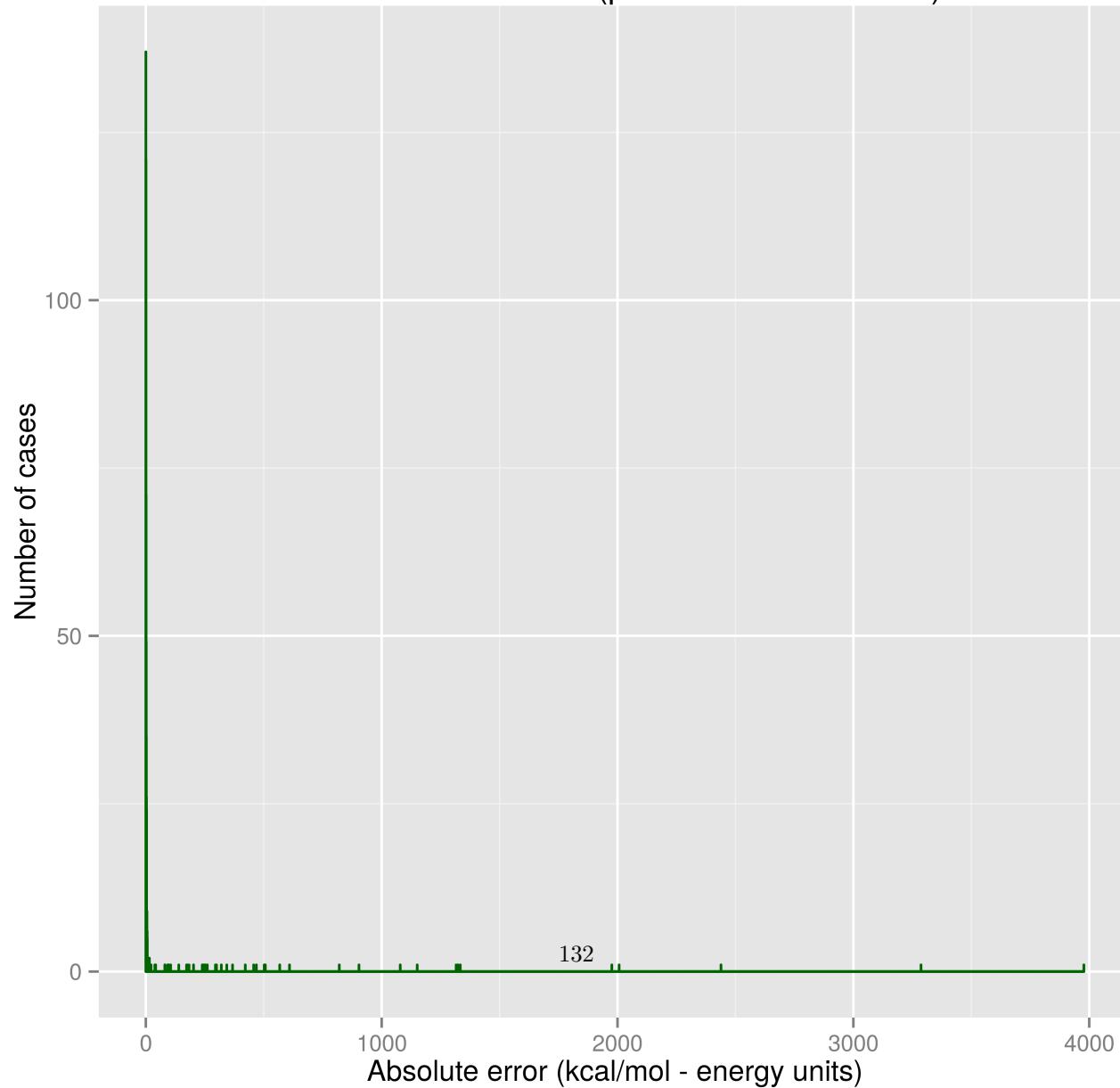


Figure 5.6: Absolute error histogram

5.3 Adjustments

Optimization of the cutoffs for the fraction correct metric

Optimum cutoff for fraction correct metric at varying experimental cutoffs for ZF

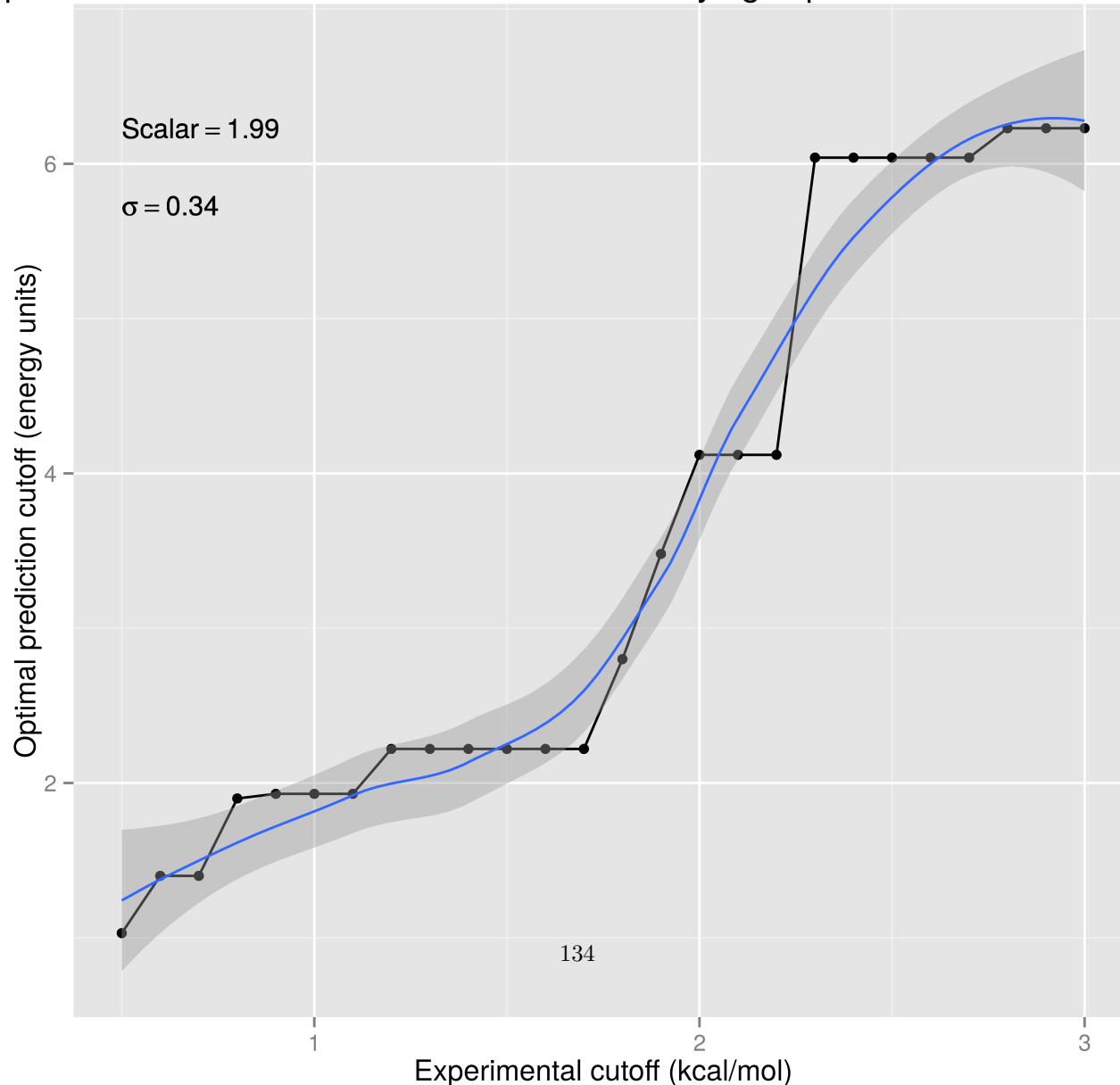


Figure 5.7: Scalar adjustment calculation plot

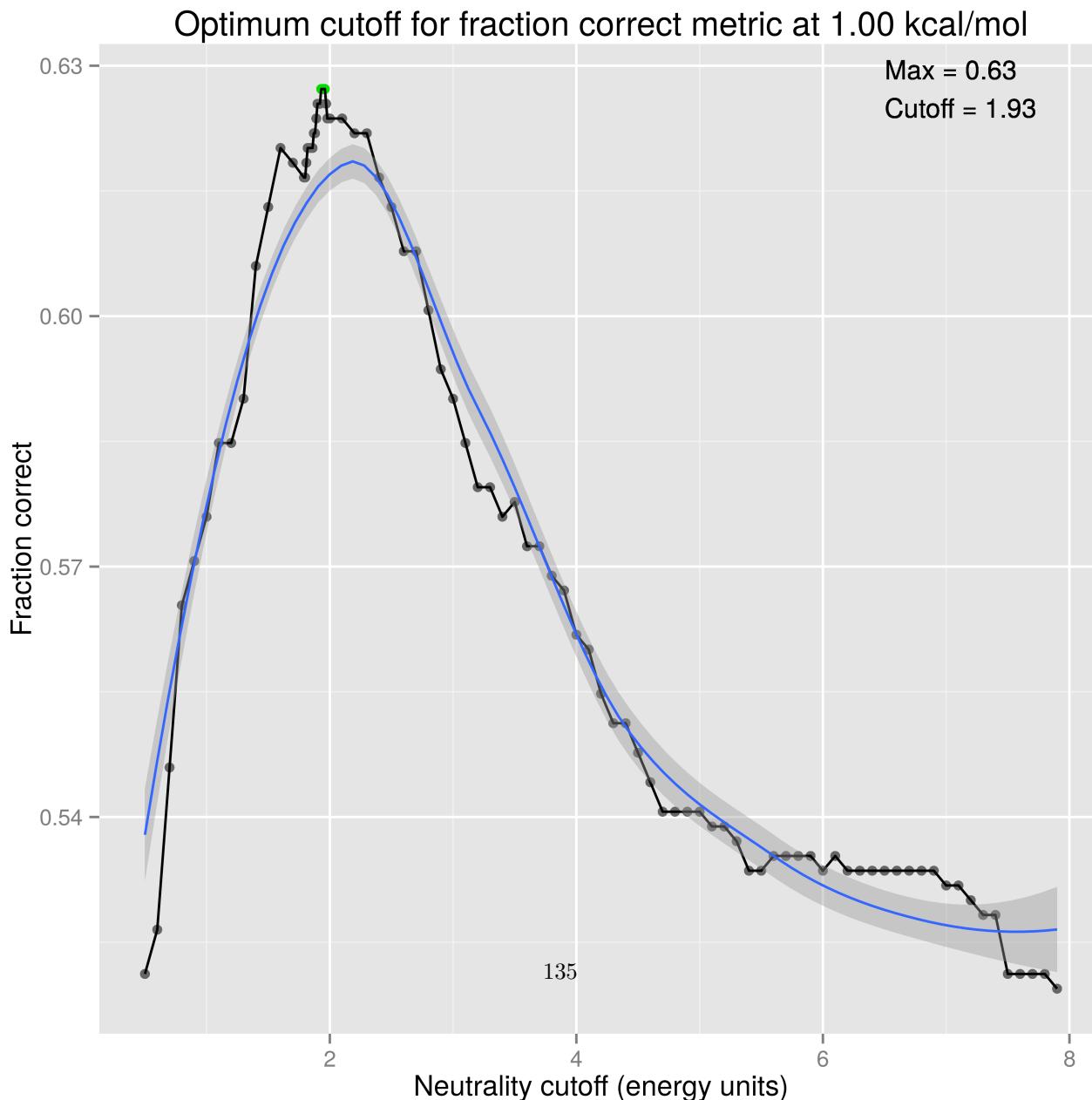


Figure 5.8: Optimal predictive cutoff plot

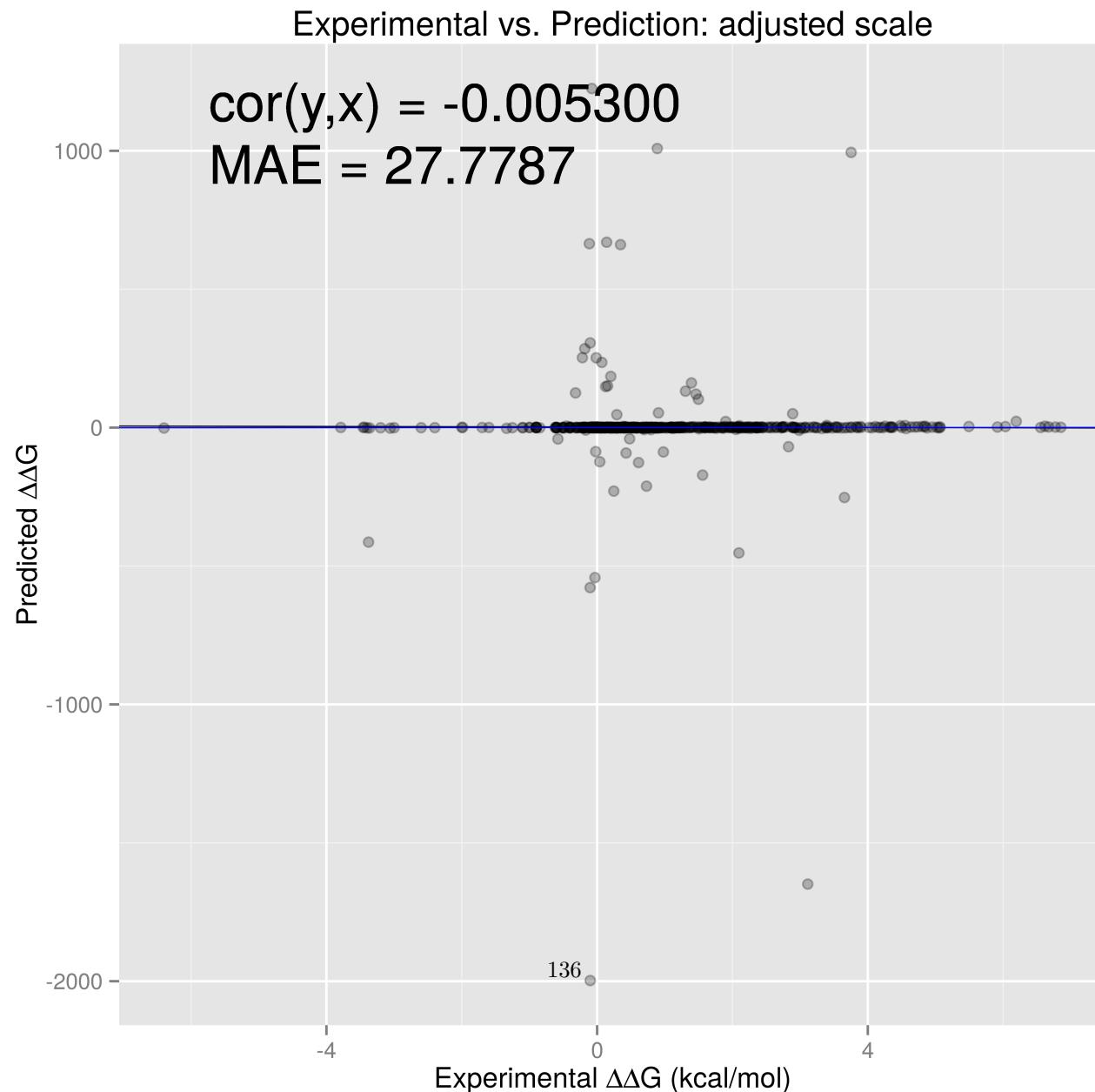


Figure 5.9: Main adj. scatterplot

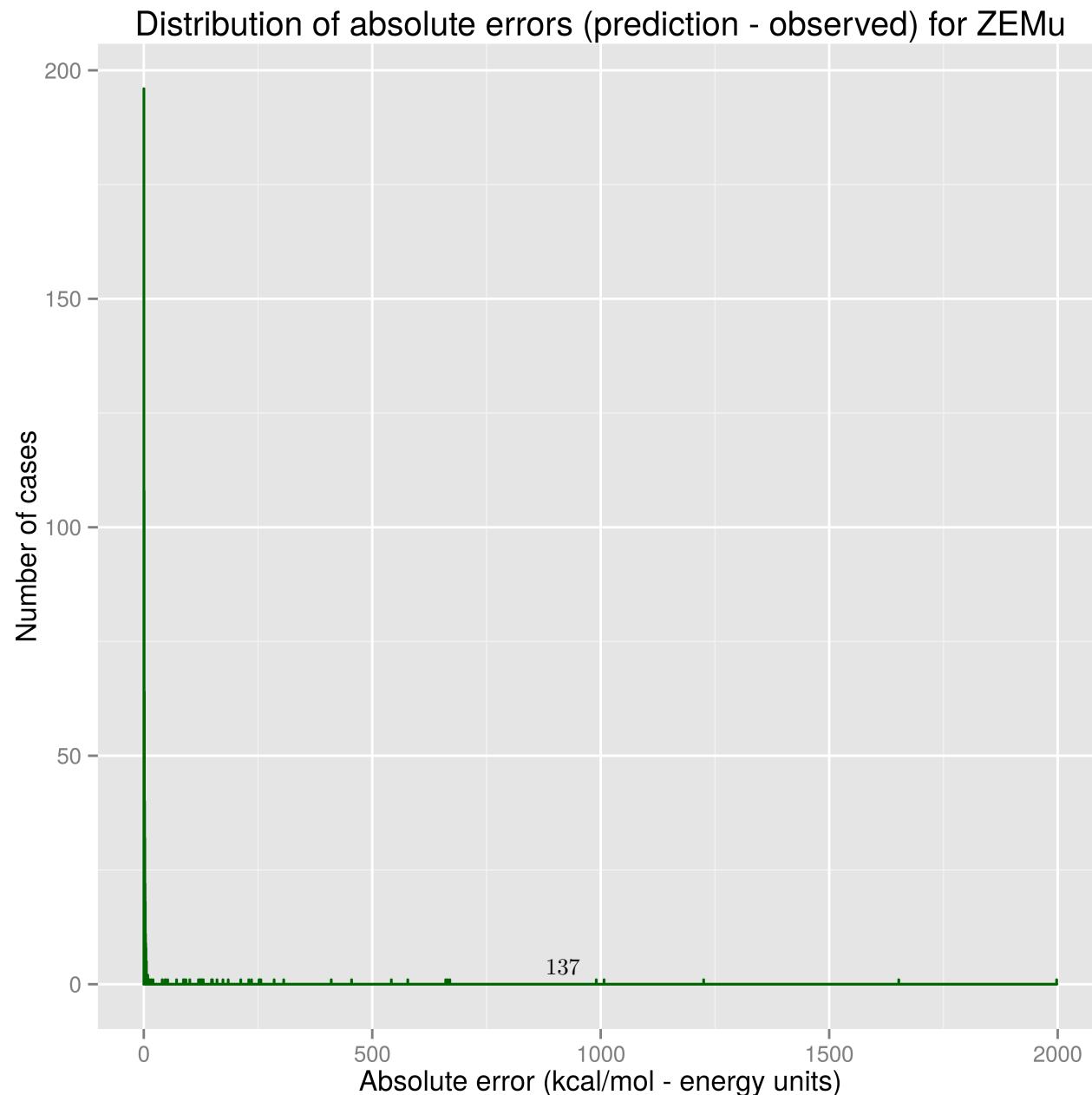
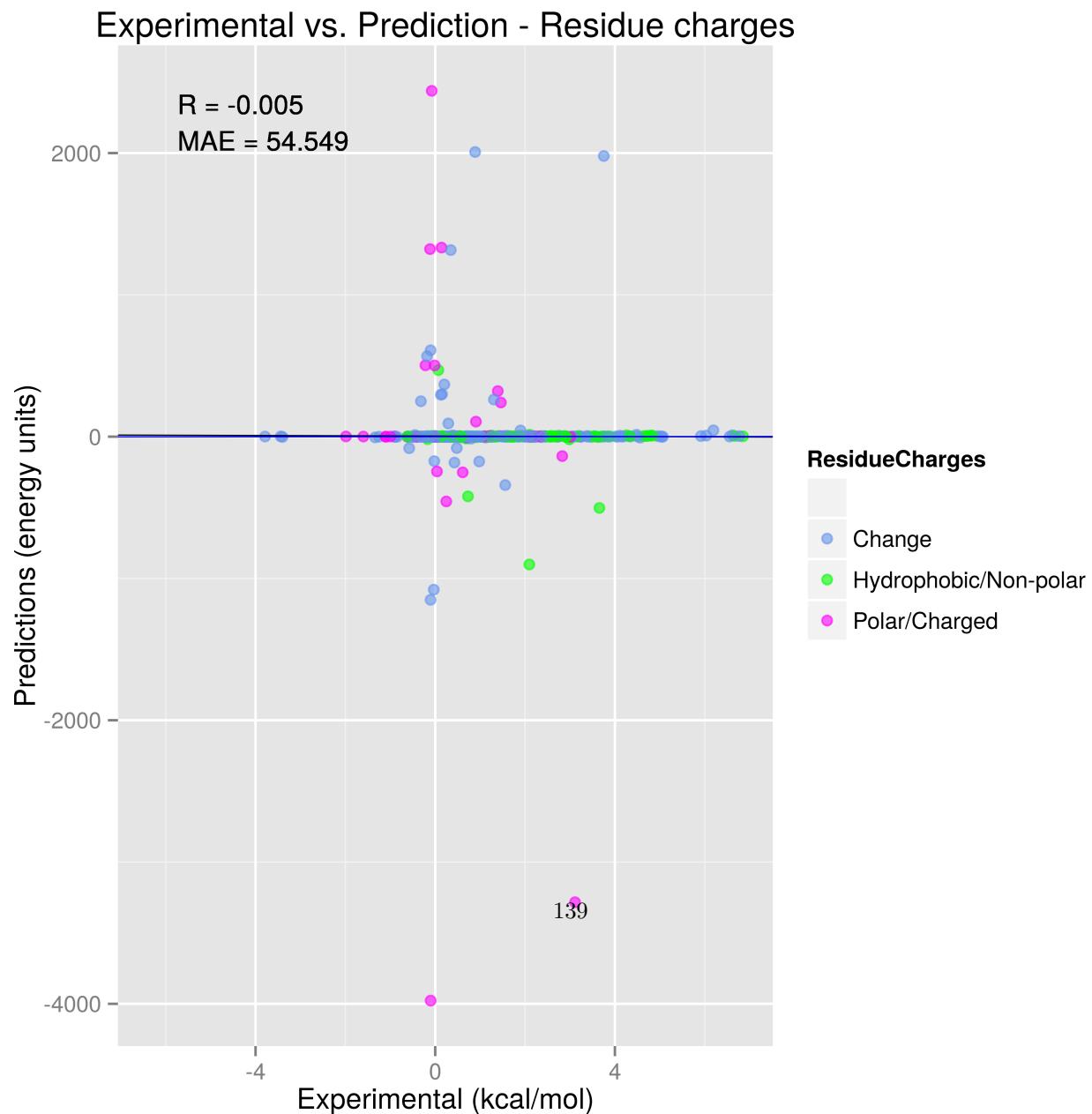


Figure 5.10: Absolute errors adjusted with scalar

5.4 Residue context



Experimental vs. Prediction - Exposure (cutoff = 0.25)

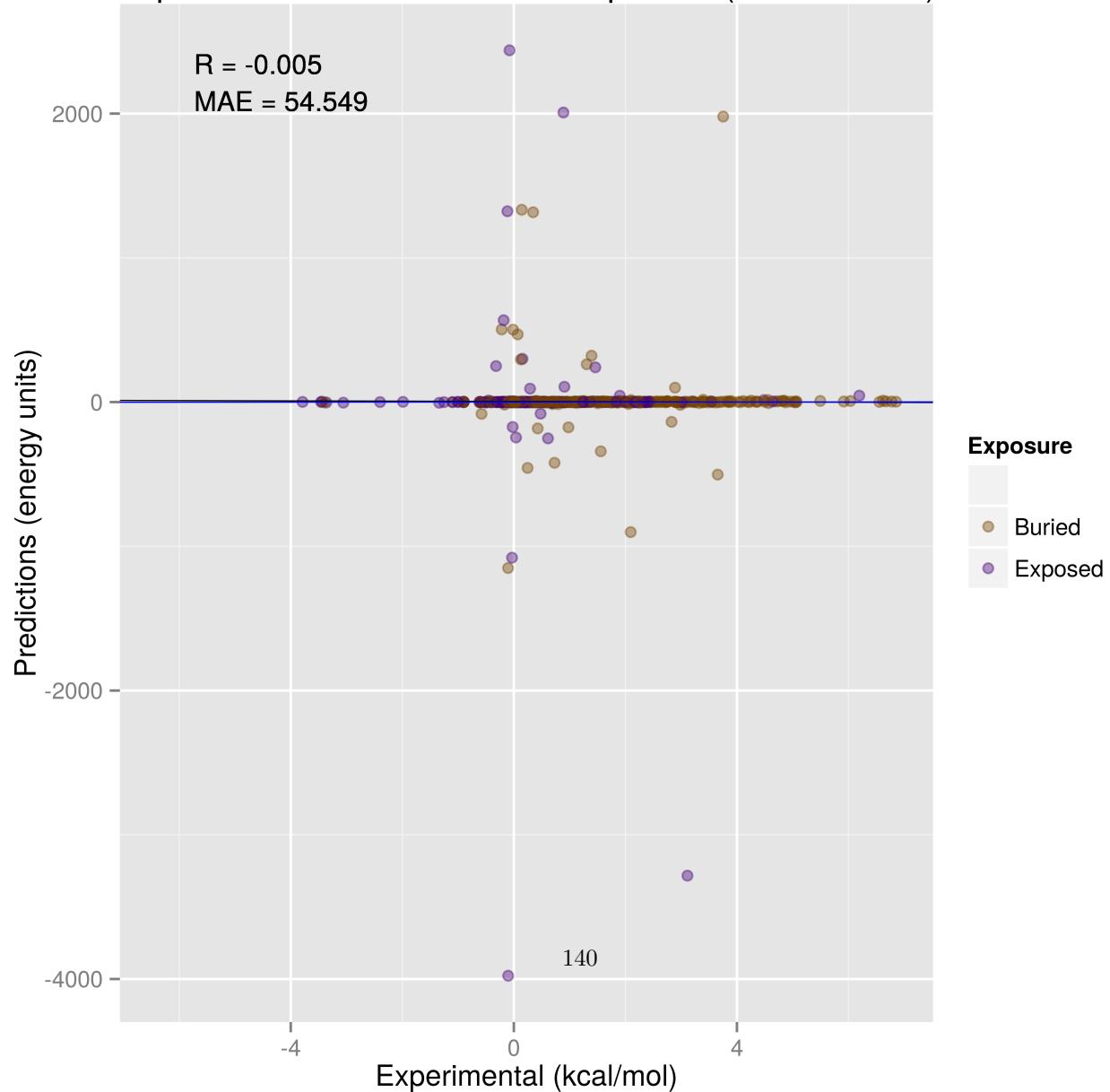


Figure 5.12: Experimental vs. Prediction - Exposure (cutoff = 0.25)

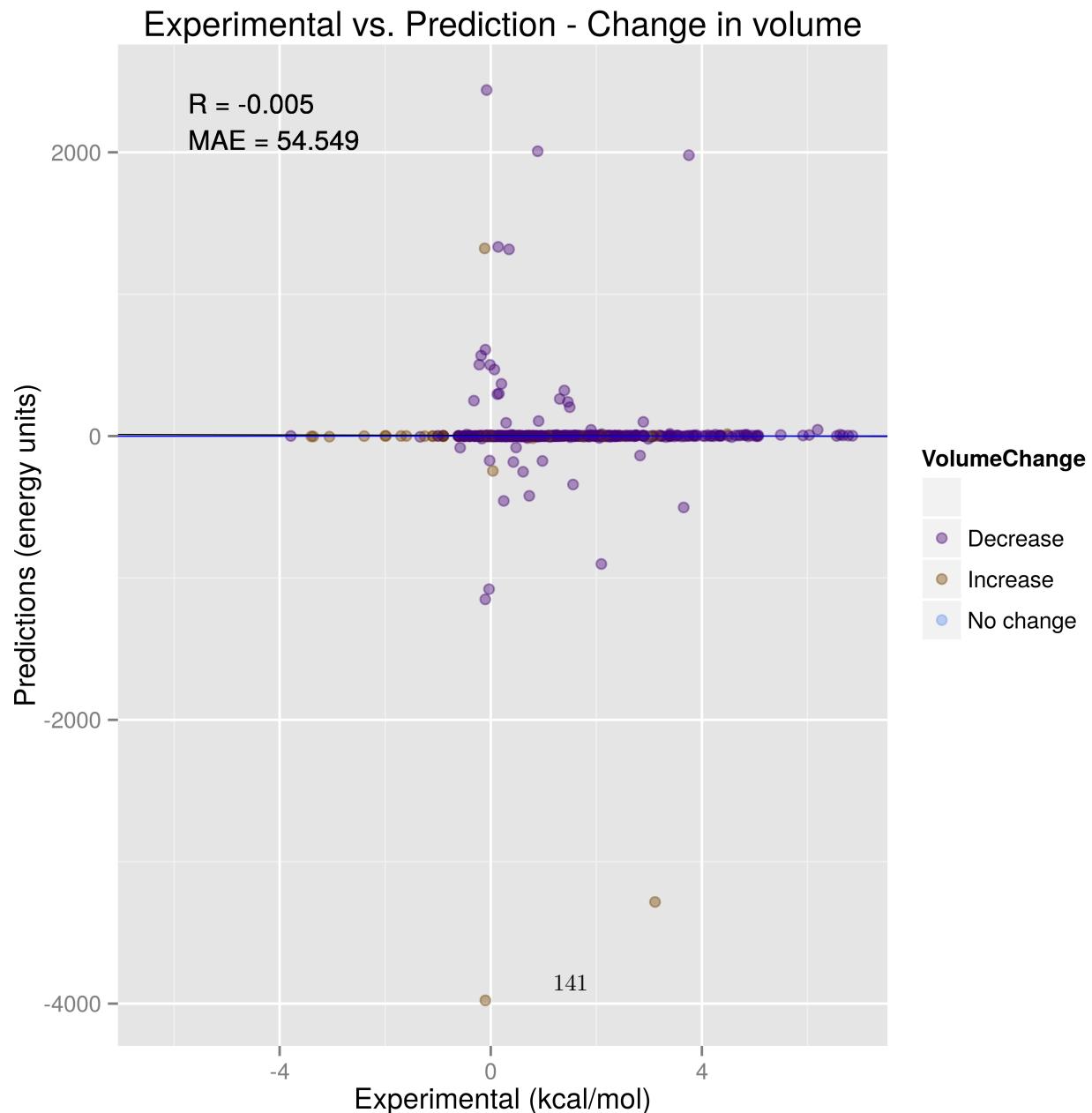


Figure 5.13: Experimental vs. Prediction - Change in volume

Experimental vs. Prediction - Wildtype residue s.s.

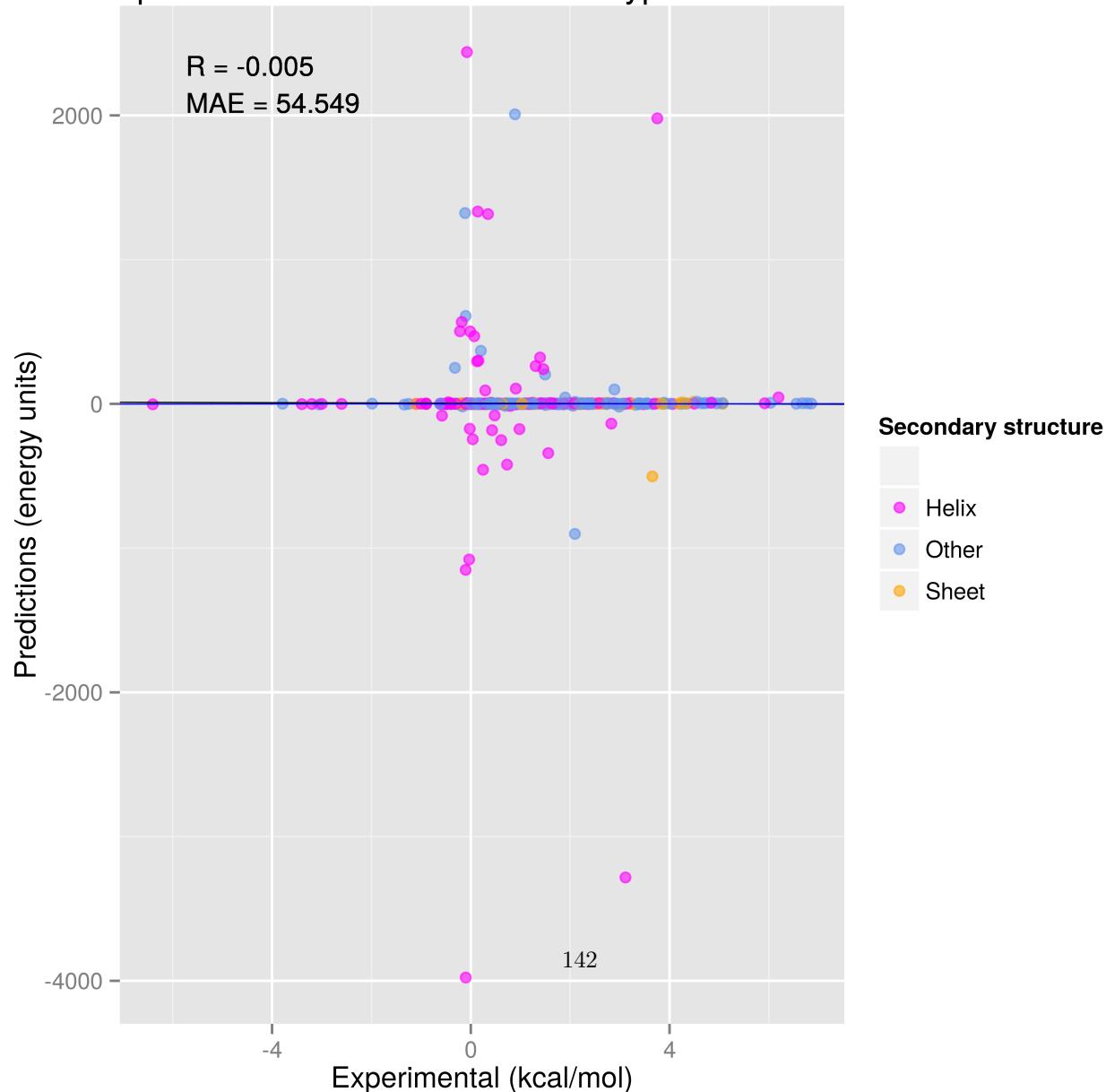
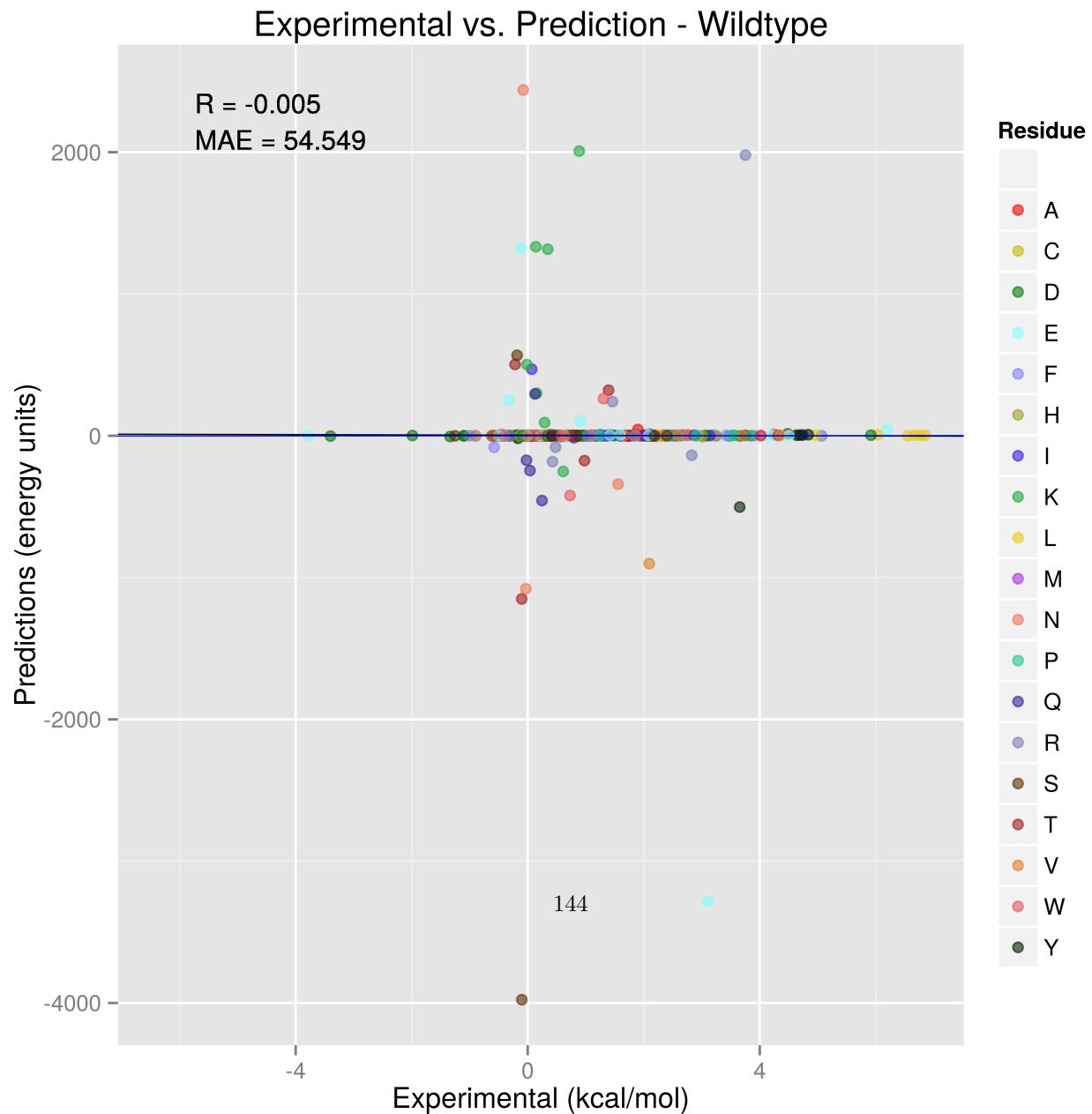


Figure 5.14: Experimental vs. Prediction - Wildtype residue s.s.

5.5 Residue types



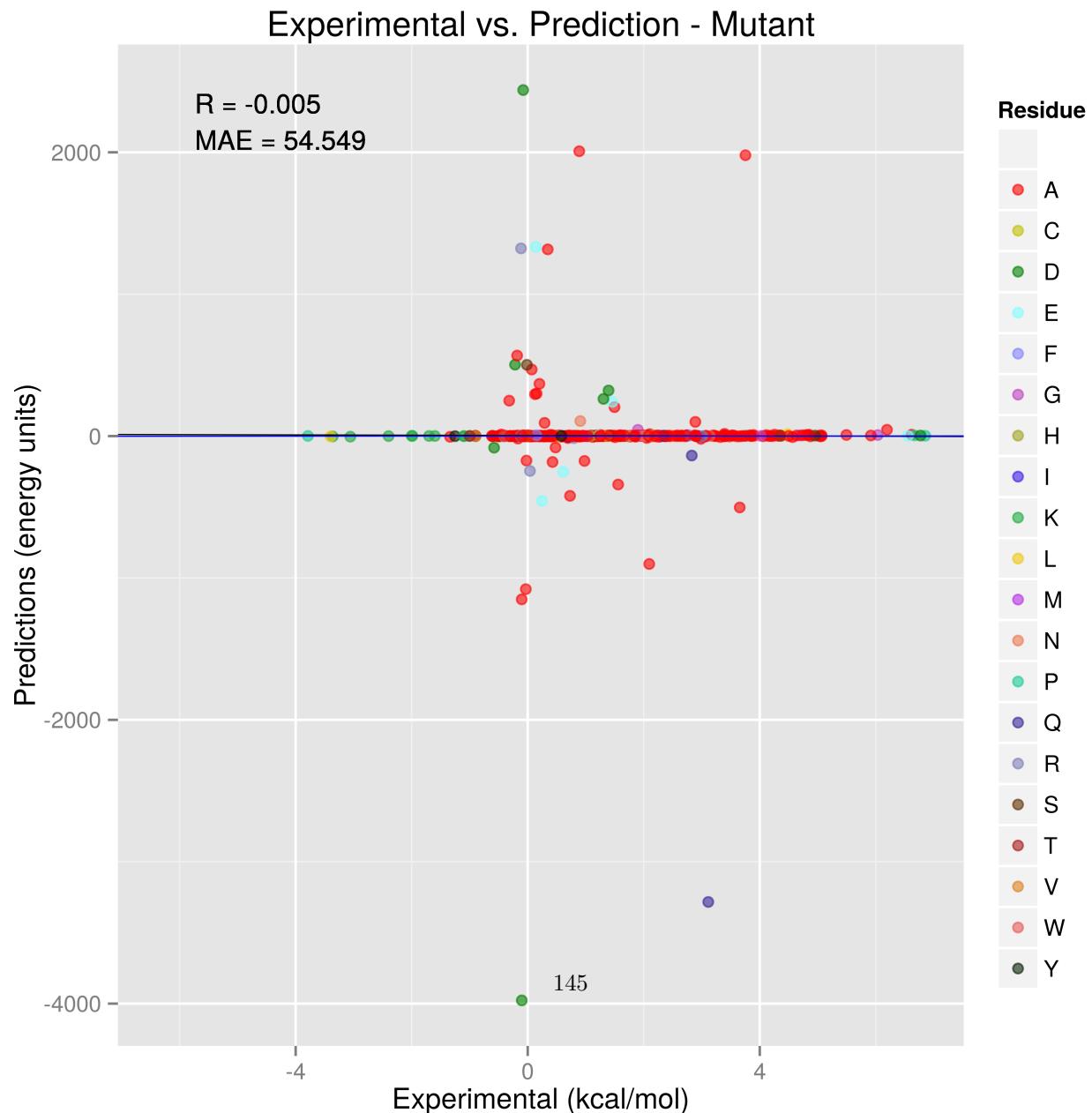


Figure 5.16: Experimental vs. Prediction - Mutant

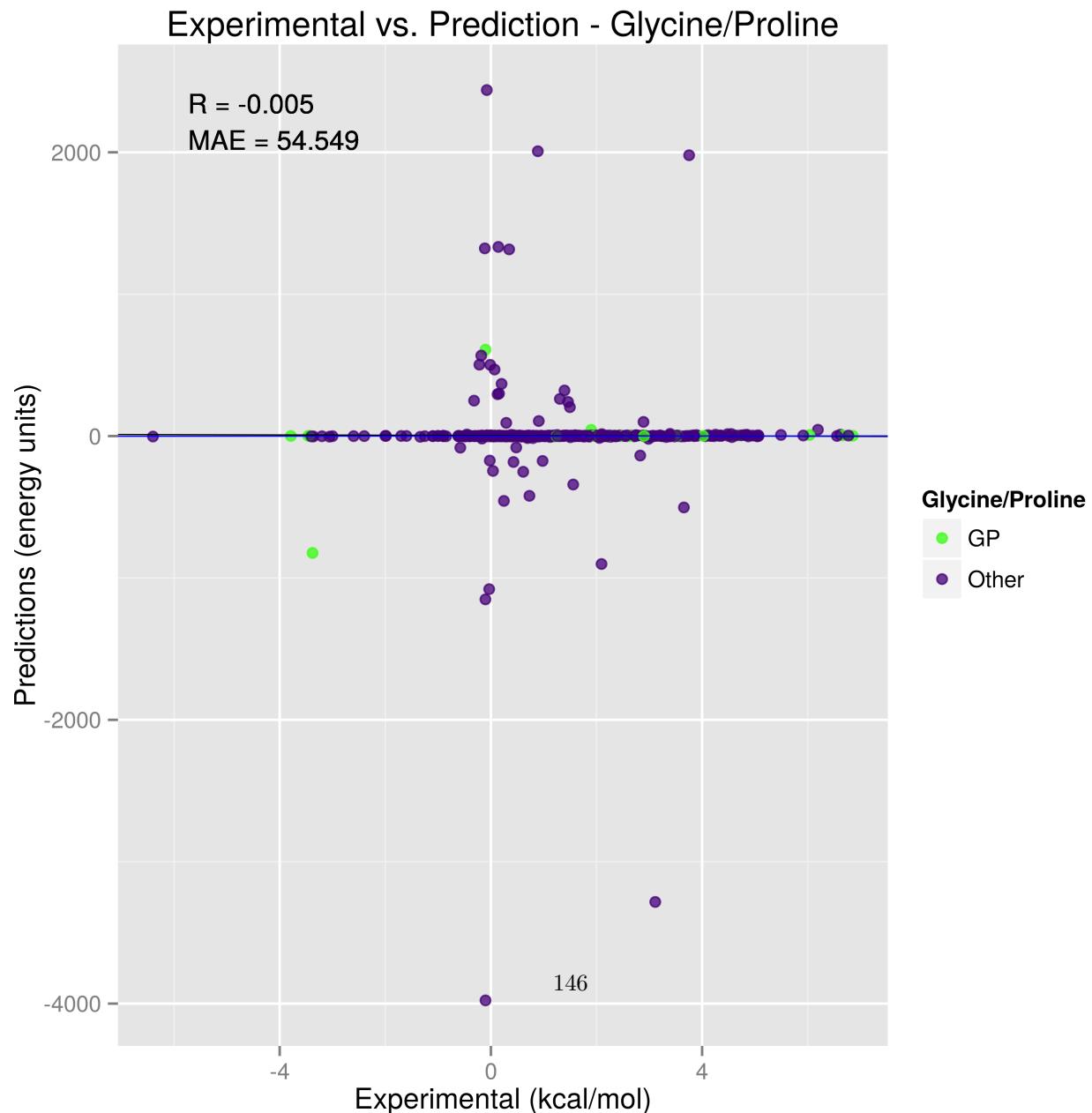
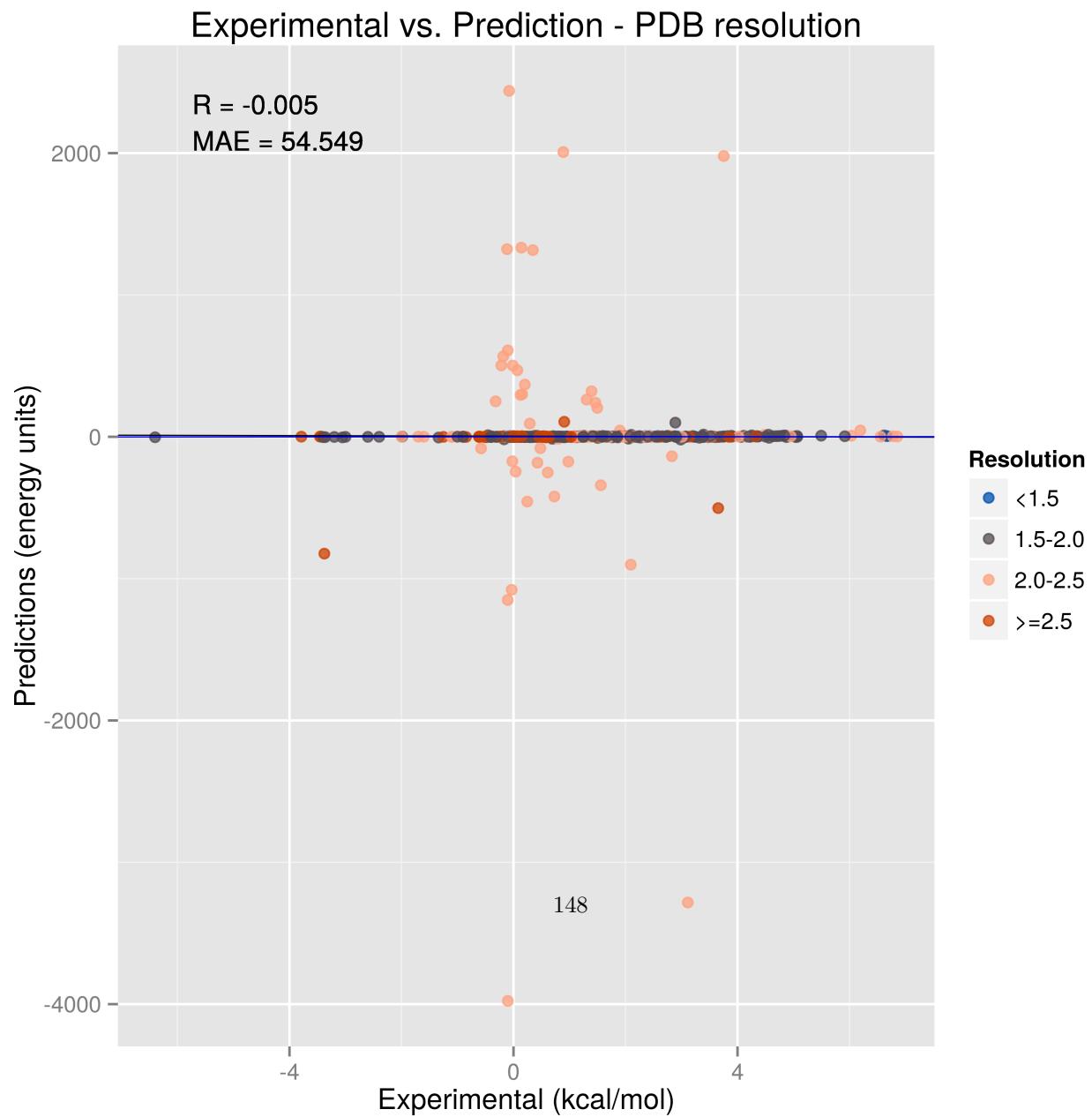


Figure 5.17: Experimental vs. Prediction - Glycine/Proline

5.6 Chain properties



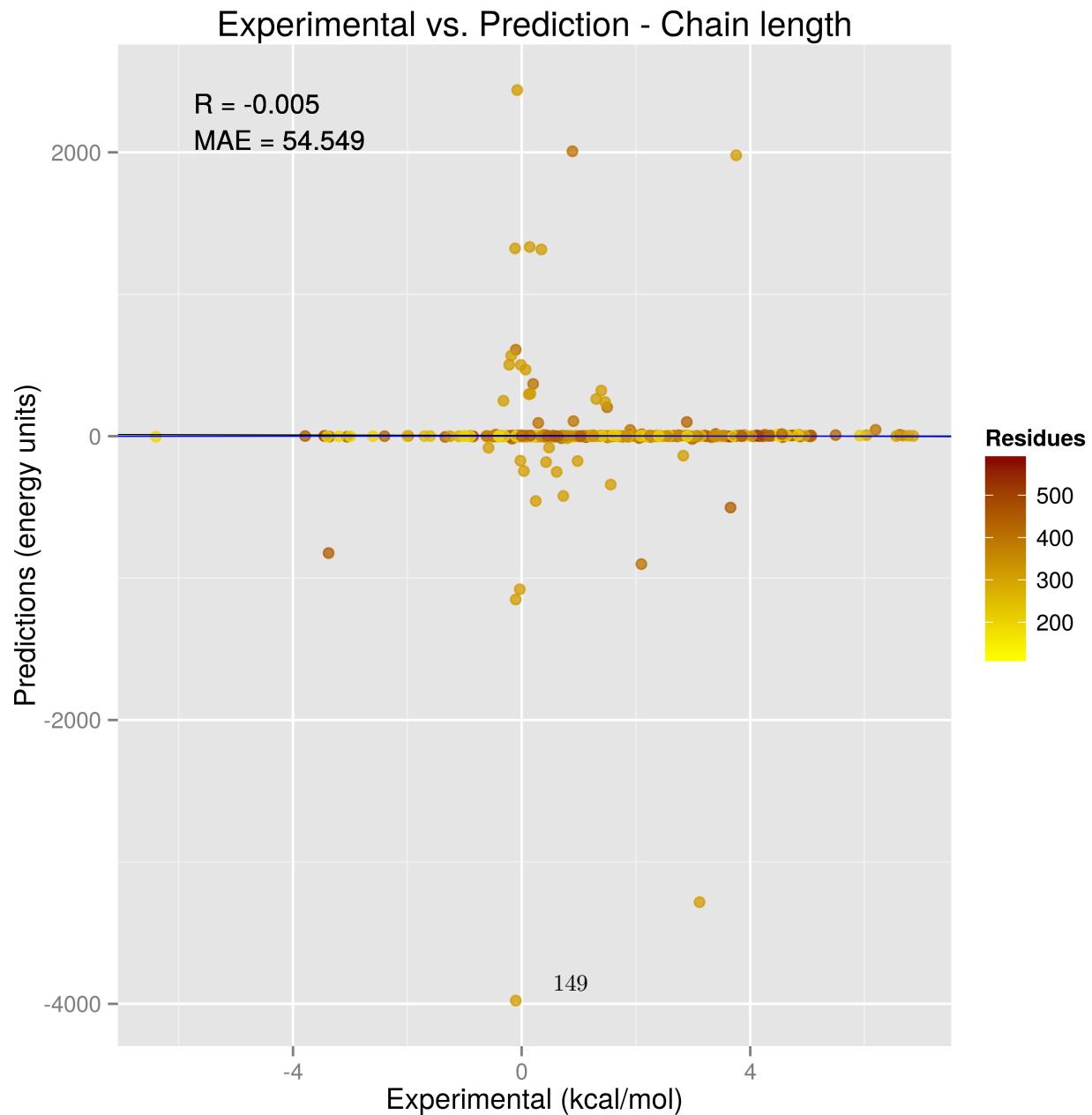
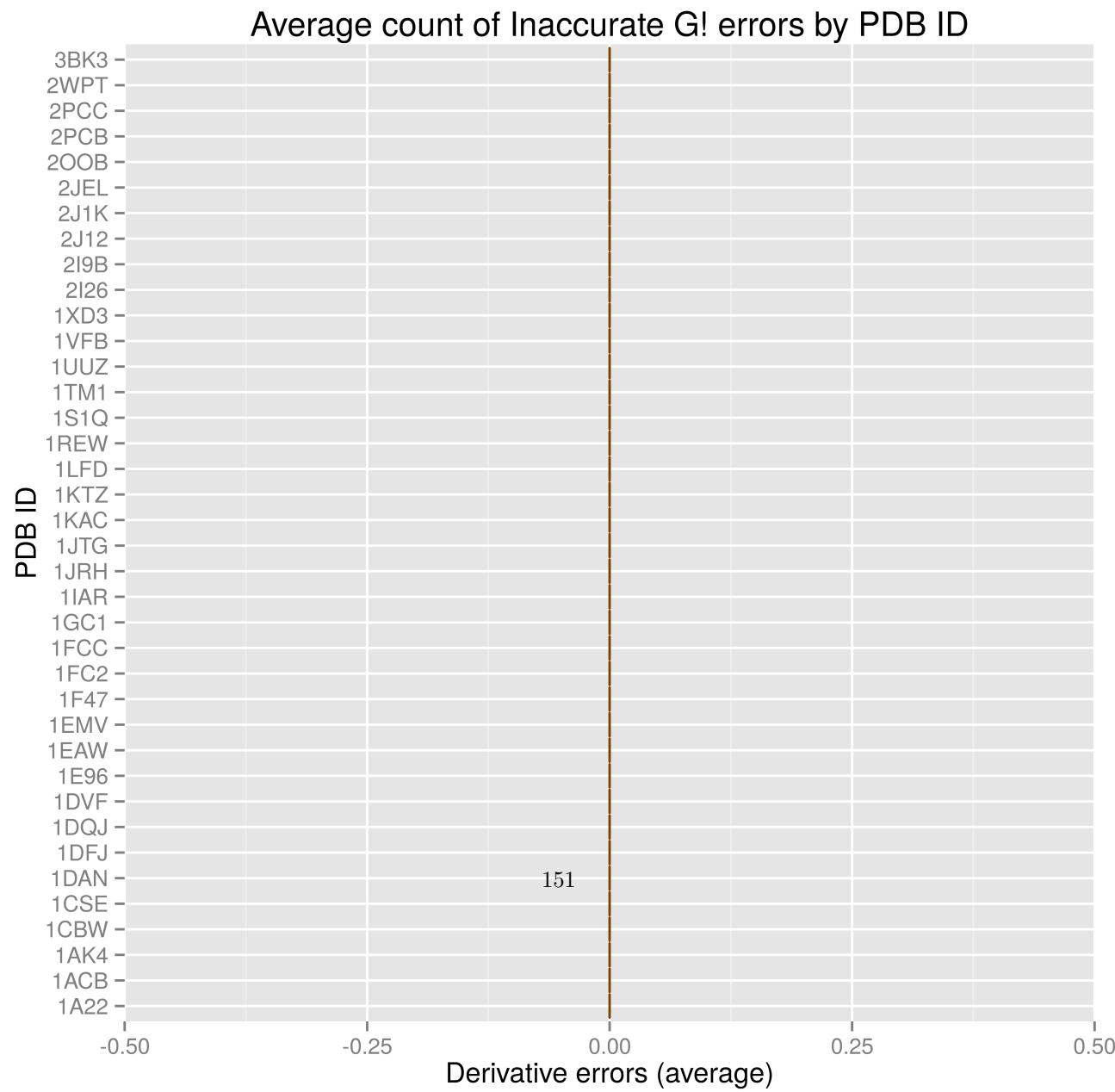


Figure 5.19: Experimental vs. Prediction - Chain length

5.7 Errors / debugging



6 topx_3-prediction_set_id_james-backrub-rscript-full-score_method_Unrescored-Talaris

james-backrub-rscript-full First full ZEMu run (ZEMu)

Prediction set scoring credit: James Lucas

6.1 Data tables

The predicted DDG value per case is computed using the 3 lowest-scoring mutant structures and the 3 lowest-scoring wildtype structures as in the paper by Kellogg et al.

Derived mutations in analysis are omitted):

The stability classification cutoffs are: Experimental=1.00 kcal/mol, Predicted=1.00 energy units.

6.1.1 Breakdown by volume

A case is considered a small-to-large (resp. large-to-small) mutation if all of the wildtype residues have a smaller (resp. larger) van der Waals volume than the corresponding mutant residue. The order is defined as G < A < S < C < P < D < T < N < V < E < Q < H < ILM < FK < Y < R < W so some cases are considered to have no change in volume e.g. MET → LEU.

Not enough data for analysis of mutations no change in volume (at least 8 cases are required).

Statistic name	Value	p-value
Fraction correct	0.37	
Fraction correct (fuzzy)	0.39	
Gamma correlation coef.	0.12	
Kolmogorov-Smirnov test (XY)	0.48	(2-tailed p-value= 4.75×10^{-07})
MAE	623.45	
Pearson's R	-0.07	(2-tailed p-value= 5.65×10^{-01})
Spearman's R	0.17	(2-tailed p-value= 1.90×10^{-01})
X-axis Kolmogorov-Smirnov test	0.13	(p-value= 2.29×10^{-01})
X-axis normality test	2.18	(2-sided chi ² p-value= 3.36×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.50	(p-value= 6.88×10^{-15})
Y-axis normality test	123.23	(2-sided chi ² p-value= 1.75×10^{-27})
n	62.00	
num_null_cases	0.00	

Table 6.1: Statistics - small-to-large mutations (62 cases)

Statistic name	Value	p-value
Fraction correct	0.17	
Fraction correct (fuzzy)	0.18	
Gamma correlation coef.	0.12	
Kolmogorov-Smirnov test (XY)	0.78	(2-tailed p-value= 2.40×10^{-130})
MAE	78.03	
Pearson's R	0.04	(2-tailed p-value= 3.62×10^{-01})
Spearman's R	0.17	(2-tailed p-value= 2.39×10^{-04})
X-axis Kolmogorov-Smirnov test	0.36	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	92.92	(2-sided chi ² p-value= 6.64×10^{-21})
Y-axis Kolmogorov-Smirnov test	0.54	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	760.49	(2-sided chi ² p-value= 7.29×10^{-166})
n	488.00	
num_null_cases	0.00	

Table 6.2: Statistics - large-to-small mutations (488 cases)

6.1.2 Separating out mutations involving glycine or proline.

This cases may involve changes to secondary structure so we separate them out here.

Statistic name	Value	p-value
Fraction correct	0.38	
Fraction correct (fuzzy)	0.38	
Gamma correlation coef.	0.46	
Kolmogorov-Smirnov test (XY)	0.47	(2-tailed p-value= 6.23×10^{-04})
MAE	83.49	
Pearson's R	0.33	(2-tailed p-value= 5.33×10^{-02})
Spearman's R	0.63	(2-tailed p-value= 7.28×10^{-05})
X-axis Kolmogorov-Smirnov test	0.52	(p-value= 4.57×10^{-09})
X-axis normality test	0.66	(2-sided chi ² p-value= 7.21×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.36	(p-value= 1.52×10^{-04})
Y-axis normality test	80.24	(2-sided chi ² p-value= 3.76×10^{-18})
n	34.00	
num_null_cases	0.00	

Table 6.3: Statistics - cases with G or P (34 cases)

Statistic name	Value	p-value
Fraction correct	0.20	
Fraction correct (fuzzy)	0.20	
Gamma correlation coef.	0.09	
Kolmogorov-Smirnov test (XY)	0.74	(2-tailed p-value= 1.94×10^{-130})
MAE	144.12	
Pearson's R	0.02	(2-tailed p-value= 7.09×10^{-01})
Spearman's R	0.13	(2-tailed p-value= 2.71×10^{-03})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	57.49	(2-sided chi ² p-value= 3.28×10^{-13})
Y-axis Kolmogorov-Smirnov test	0.54	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	1156.11	(2-sided chi ² p-value= 9.01×10^{-252})
n	532.00	
num_null_cases	0.00	

Table 6.4: Statistics - cases without G or P (532 cases)

6.1.3 Number of mutations

Statistic name	Value	p-value
Fraction correct	0.21	
Fraction correct (fuzzy)	0.21	
Gamma correlation coef.	0.22	
Kolmogorov-Smirnov test (XY)	0.75	(2-tailed p-value= 8.20×10^{-112})
MAE	167.14	
Pearson's R	0.02	(2-tailed p-value= 7.45×10^{-01})
Spearman's R	0.32	(2-tailed p-value= 6.58×10^{-12})
X-axis Kolmogorov-Smirnov test	0.32	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	116.40	(2-sided chi ² p-value= 5.29×10^{-26})
Y-axis Kolmogorov-Smirnov test	0.51	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	959.68	(2-sided chi ² p-value= 4.05×10^{-209})
n	453.00	
num_null_cases	0.00	

Table 6.5: Statistics - single mutations (453 cases)

Statistic name	Value	p-value
Fraction correct	0.22	
Fraction correct (fuzzy)	0.23	
Gamma correlation coef.	-0.10	
Kolmogorov-Smirnov test (XY)	0.69	(2-tailed p-value= 1.18×10^{-24})
MAE	33.59	
Pearson's R	0.19	(2-tailed p-value= 4.65×10^{-02})
Spearman's R	-0.16	(2-tailed p-value= 9.34×10^{-02})
X-axis Kolmogorov-Smirnov test	0.45	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	4.54	(2-sided chi ² p-value= 1.03×10^{-01})
Y-axis Kolmogorov-Smirnov test	0.61	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	243.29	(2-sided chi ² p-value= 1.48×10^{-53})
n	113.00	
num_null_cases	0.00	

Table 6.6: Statistics - multiple mutations (113 cases)

6.1.4 Entire dataset using a scaling factor of 1/5.645 to improve the fraction correct metric.

Warning: Results in this section use an averaged scaling factor to improve the value for the fraction correct metric. This scalar will vary over benchmark runs so these results should not be interpreted as performance results; they should be considered as what could be obtained if the predicted values were scaled by a "magic" value.

Statistic name	Value	p-value
Fraction correct	0.47	
Fraction correct (fuzzy)	0.48	
Gamma correlation coef.	0.12	
Kolmogorov-Smirnov test (XY)	0.66	(2-tailed p-value= 3.27×10^{-108})
MAE	25.91	
Pearson's R	0.03	(2-tailed p-value= 5.17×10^{-01})
Spearman's R	0.17	(2-tailed p-value= 4.50×10^{-05})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	52.55	(2-sided chi ² p-value= 3.88×10^{-12})
Y-axis Kolmogorov-Smirnov test	0.37	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	1236.20	(2-sided chi ² p-value= 3.65×10^{-269})
n	566.00	
num_null_cases	0.00	

Table 6.7: Statistics - complete dataset (scaled) (566 cases)

6.1.5 Entire dataset

Overall statistics

Statistic name	Value	p-value
Fraction correct	0.21	
Fraction correct (fuzzy)	0.21	
Gamma correlation coef.	0.12	
Kolmogorov-Smirnov test (XY)	0.73	(2-tailed p-value= 1.23×10^{-132})
MAE	140.48	
Pearson's R	0.03	(2-tailed p-value= 5.17×10^{-01})
Spearman's R	0.17	(2-tailed p-value= 4.50×10^{-05})
X-axis Kolmogorov-Smirnov test	0.31	(p-value= $0.00 \times 10^{+00}$)
X-axis normality test	52.55	(2-sided chi ² p-value= 3.88×10^{-12})
Y-axis Kolmogorov-Smirnov test	0.52	(p-value= $0.00 \times 10^{+00}$)
Y-axis normality test	1236.20	(2-sided chi ² p-value= 3.65×10^{-269})
n	566.00	
num_null_cases	0.00	

Table 6.8: Statistics - complete dataset (566 cases)

6.2 Main plots

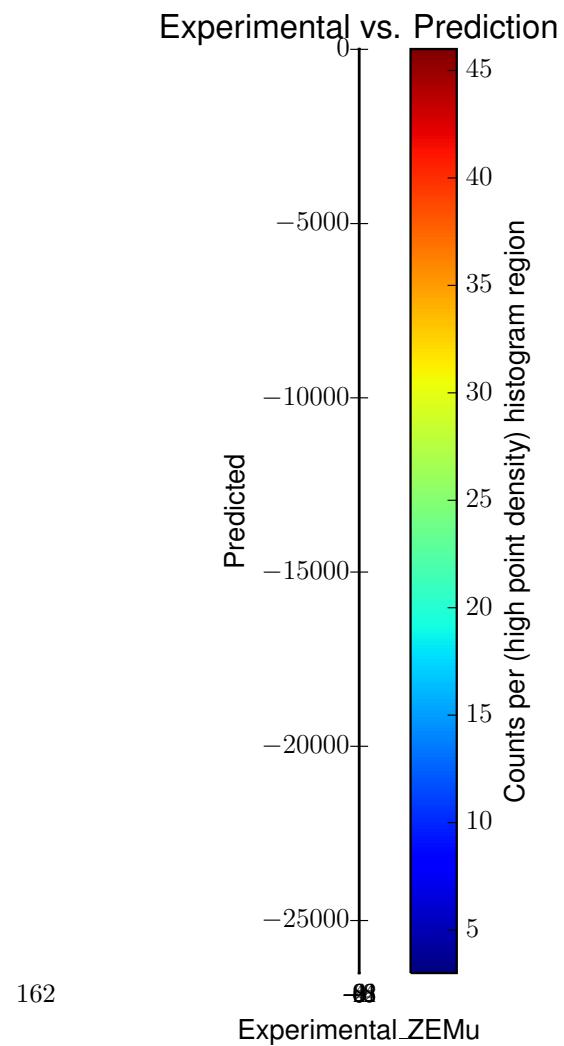
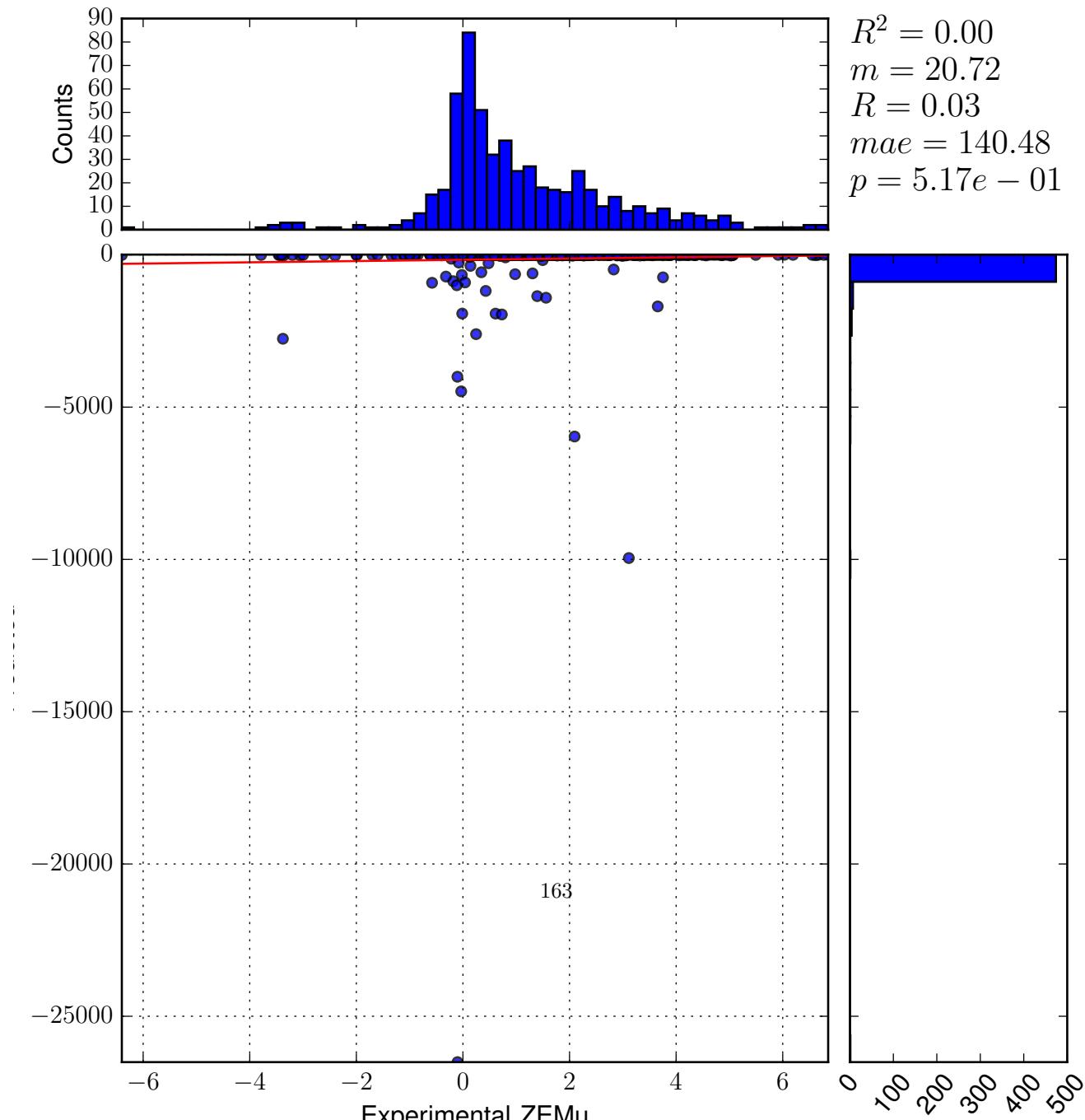
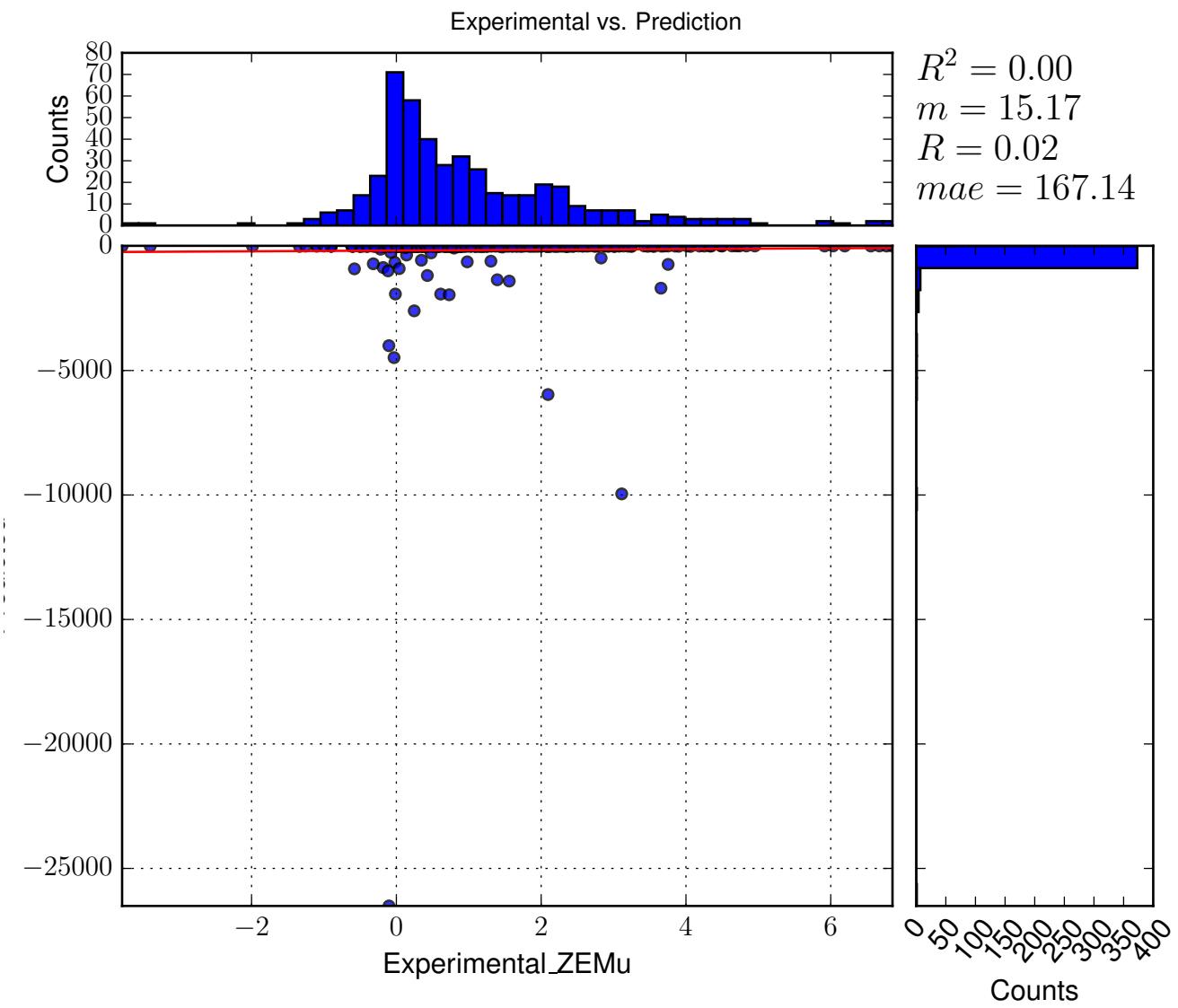


Figure 6.1: Experimental vs. Predicted scatterplot (with density binning)

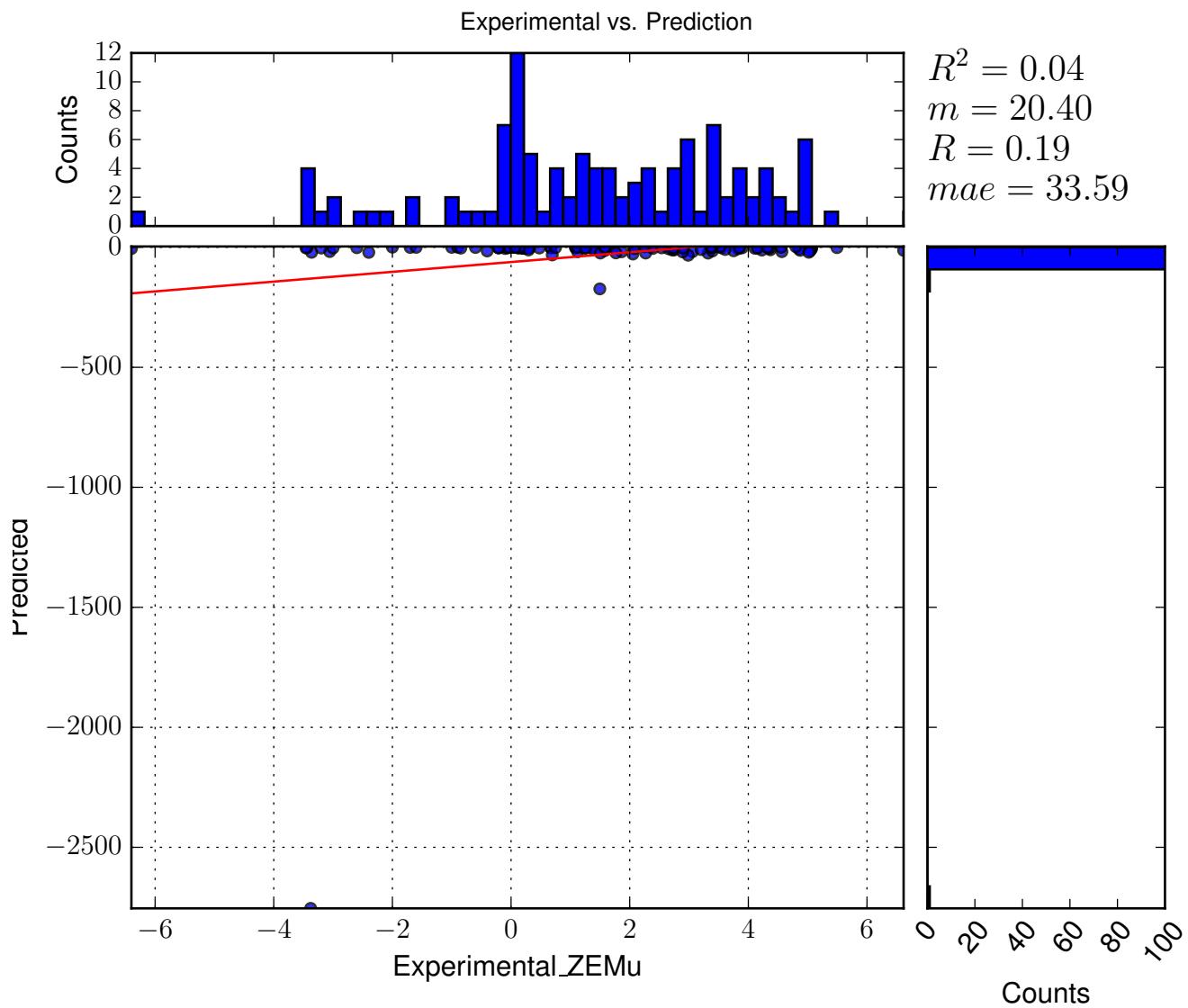
Experimental vs. Prediction



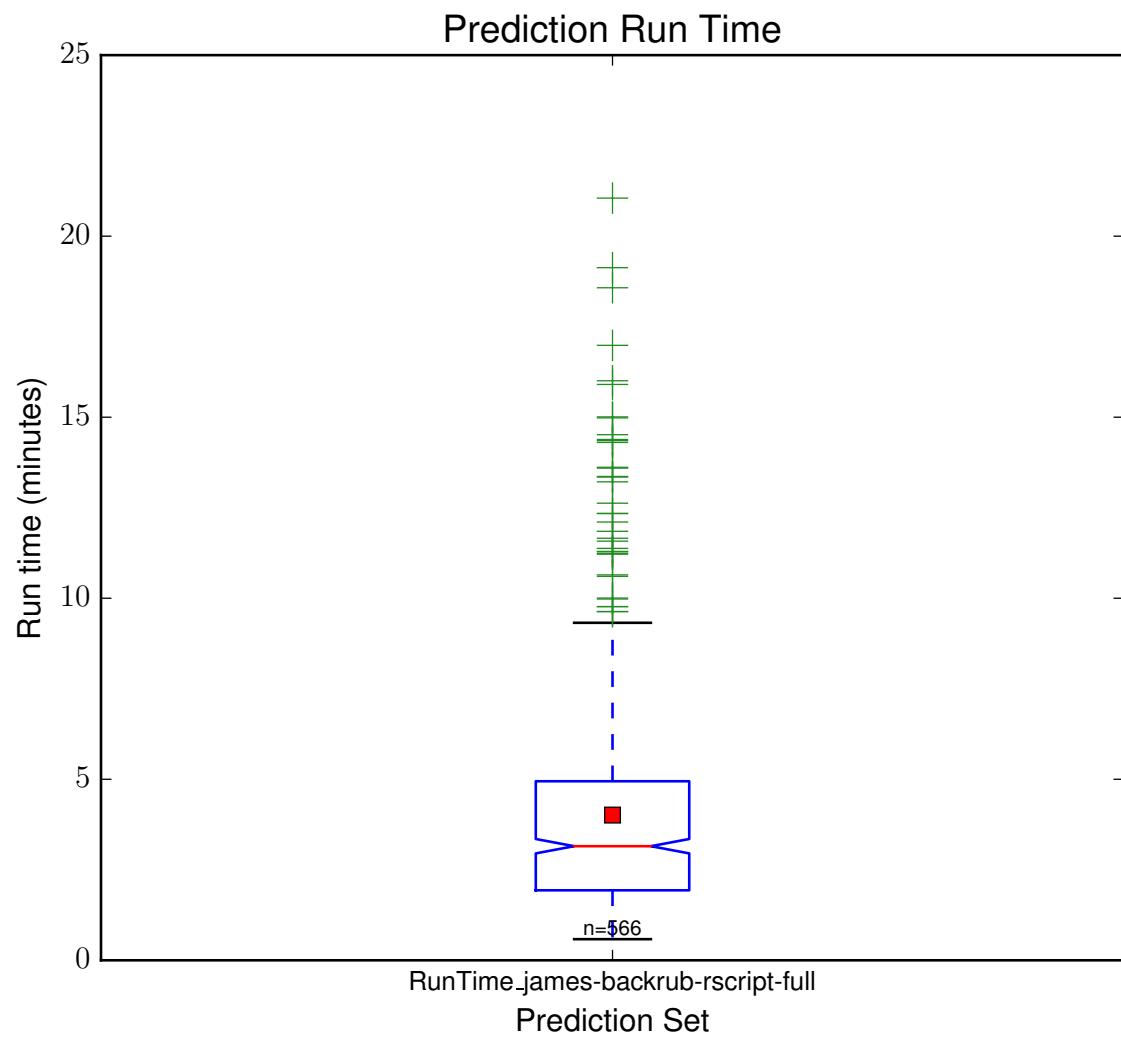


164

Figure 6.3: Single mutations data subset



165
 Figure 6.4: Multiple mutations data subset



166
Figure 6.5: Run time

Distribution of absolute errors (prediction - observed) for ZEMu

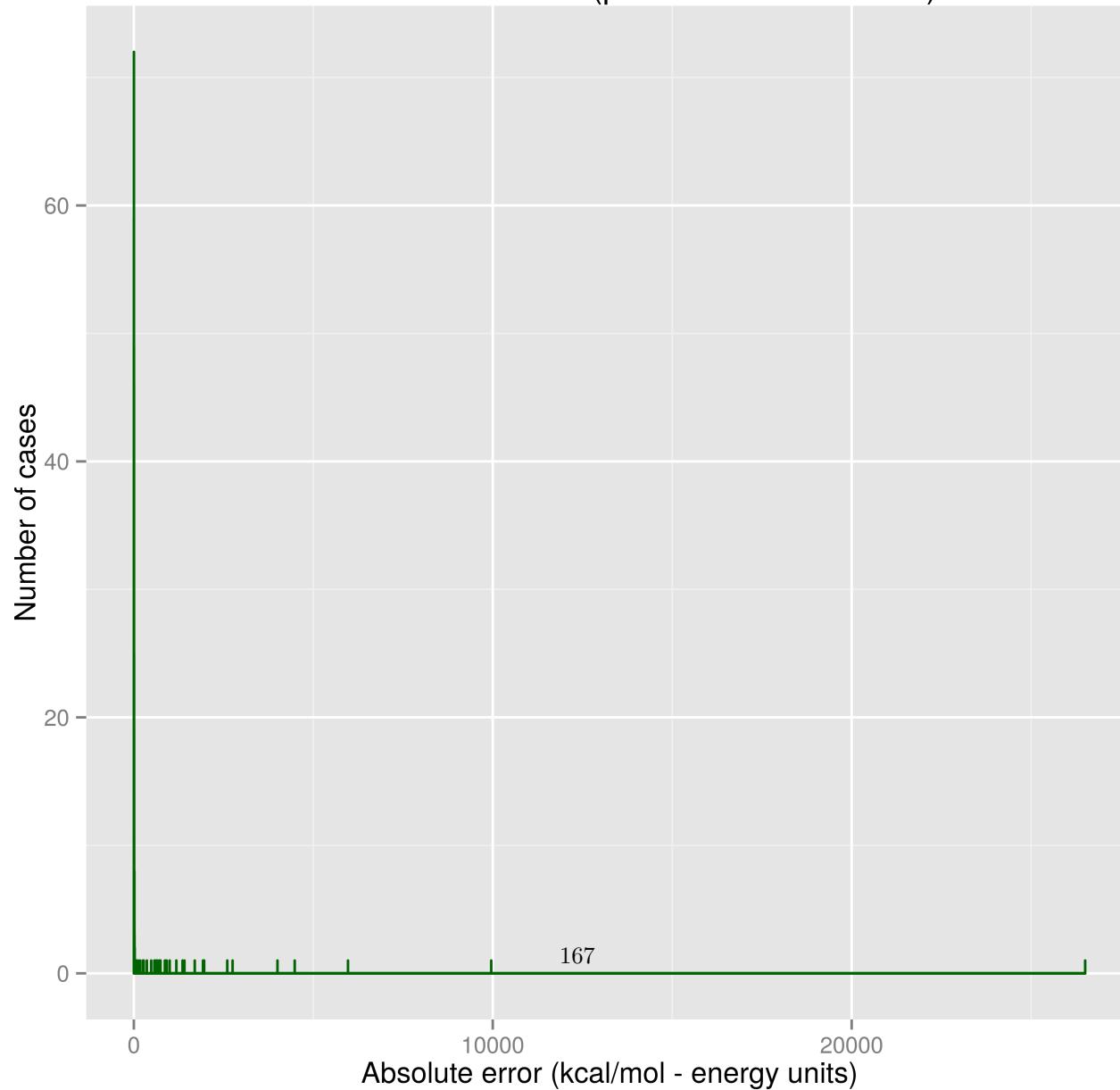


Figure 6.6: Absolute error histogram

6.3 Adjustments

Optimization of the cutoffs for the fraction correct metric

Optimum cutoff for fraction correct metric at varying experimental cutoffs for Z

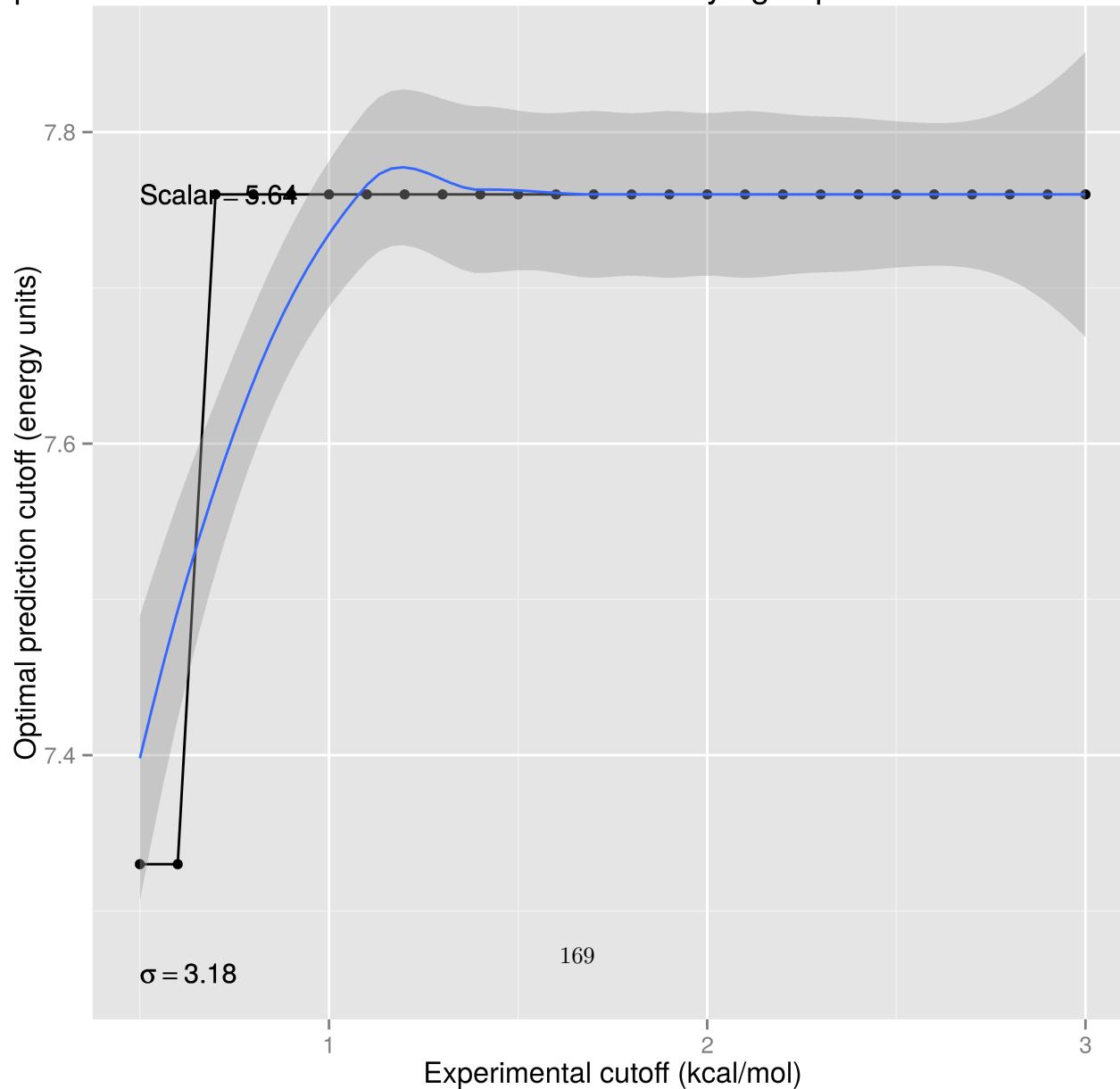


Figure 6.7: Scalar adjustment calculation plot

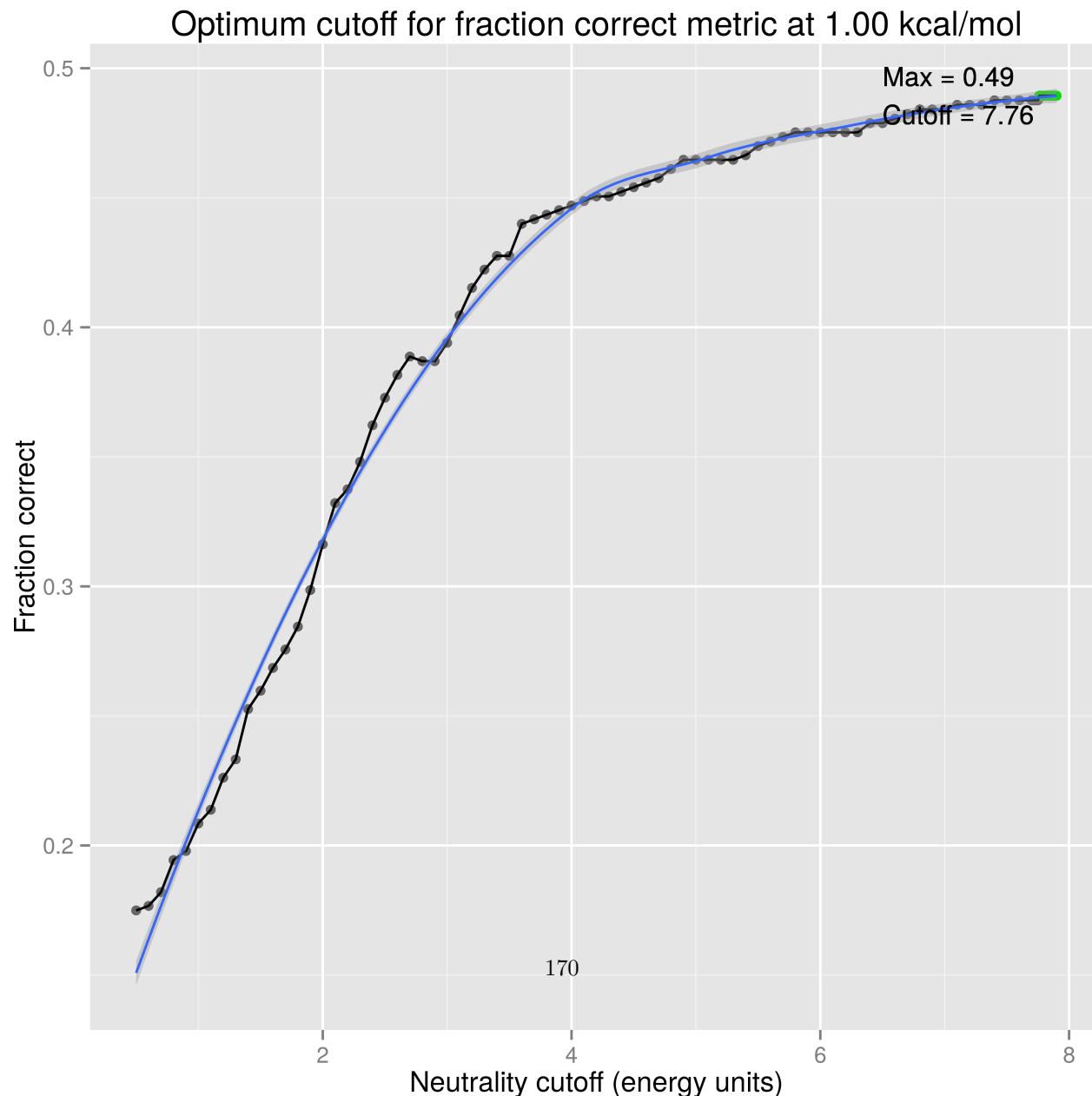


Figure 6.8: Optimal predictive cutoff plot

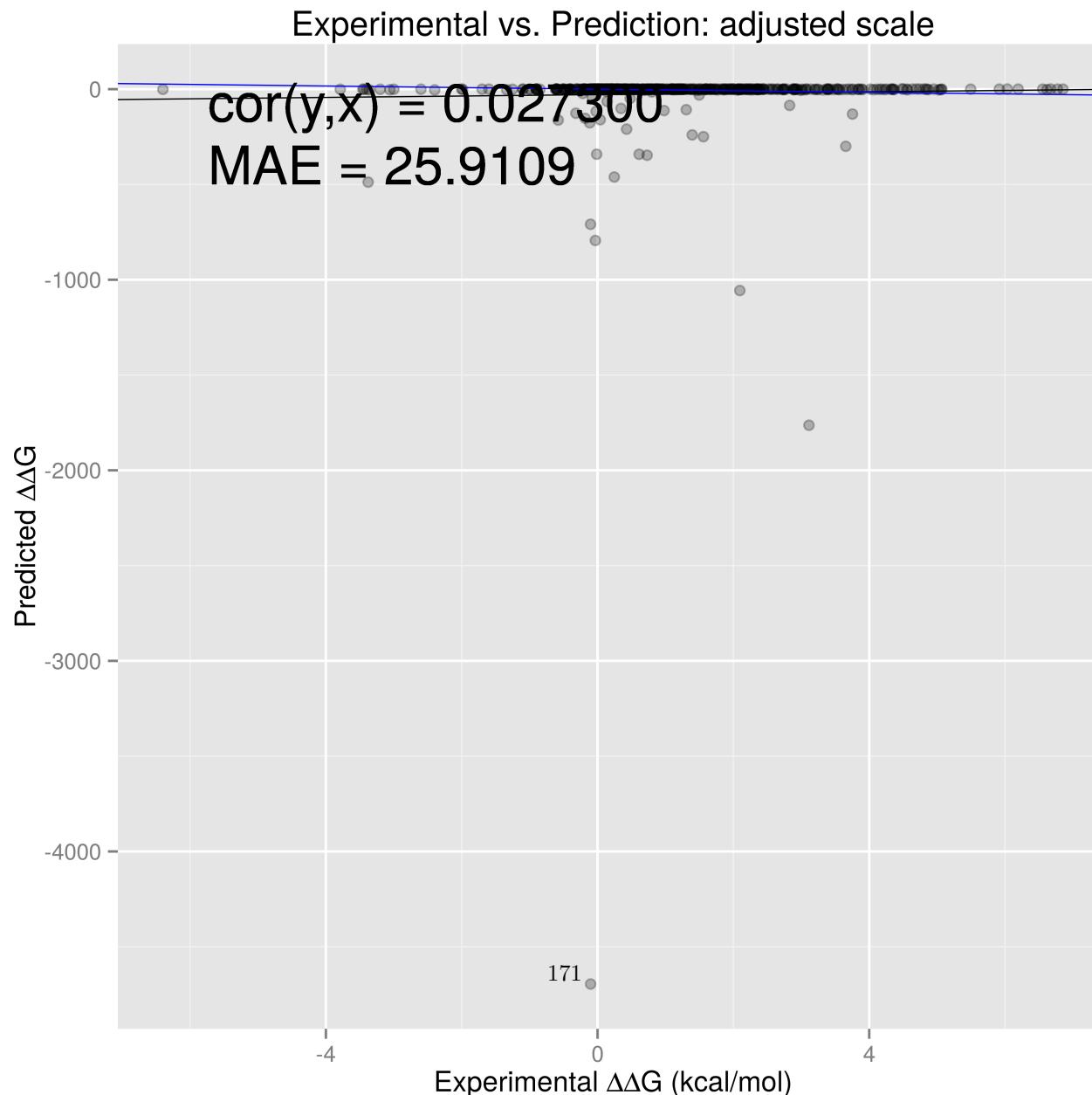


Figure 6.9: Main adj. scatterplot

Distribution of absolute errors (prediction - observed) for ZEMu

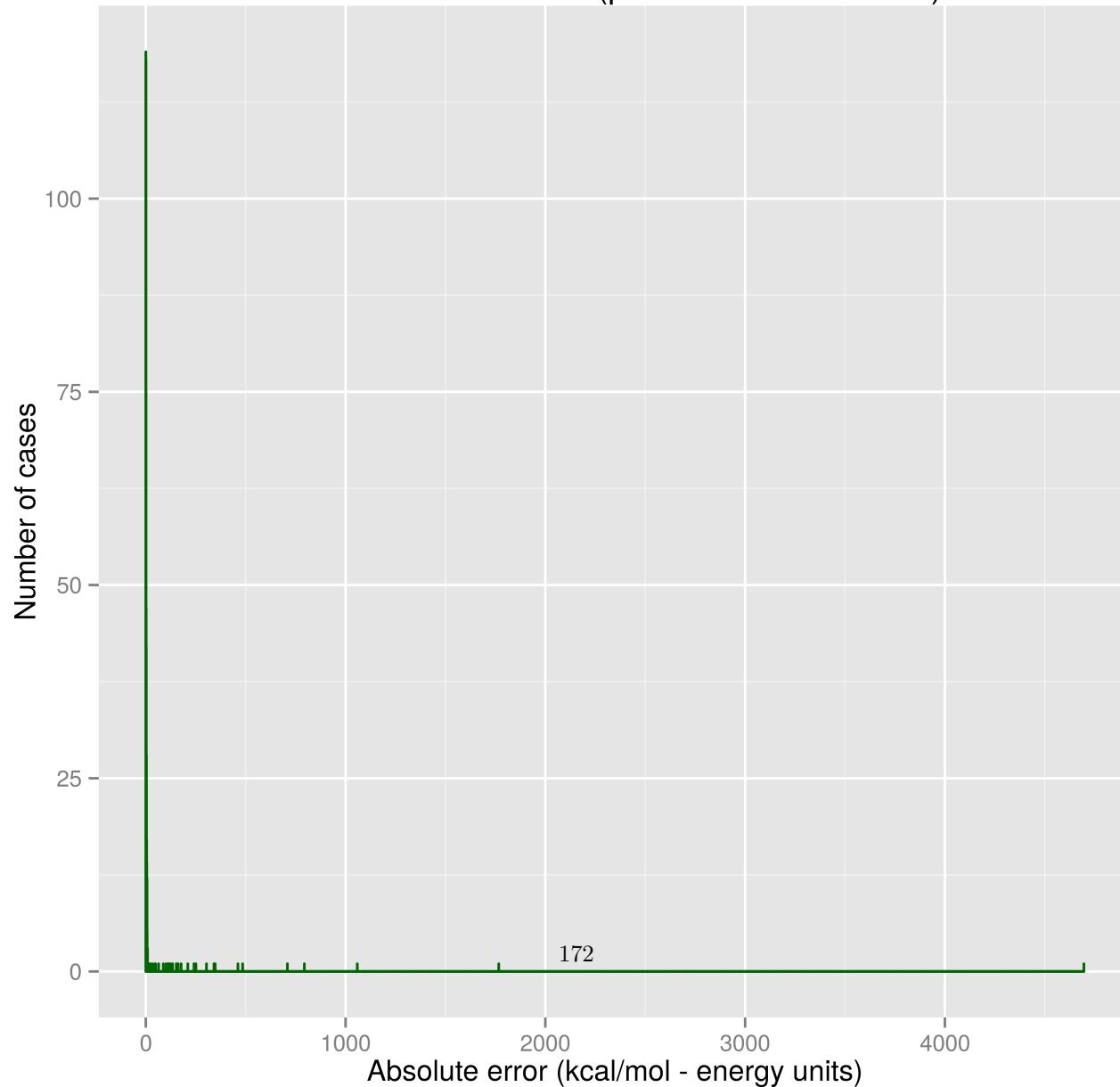
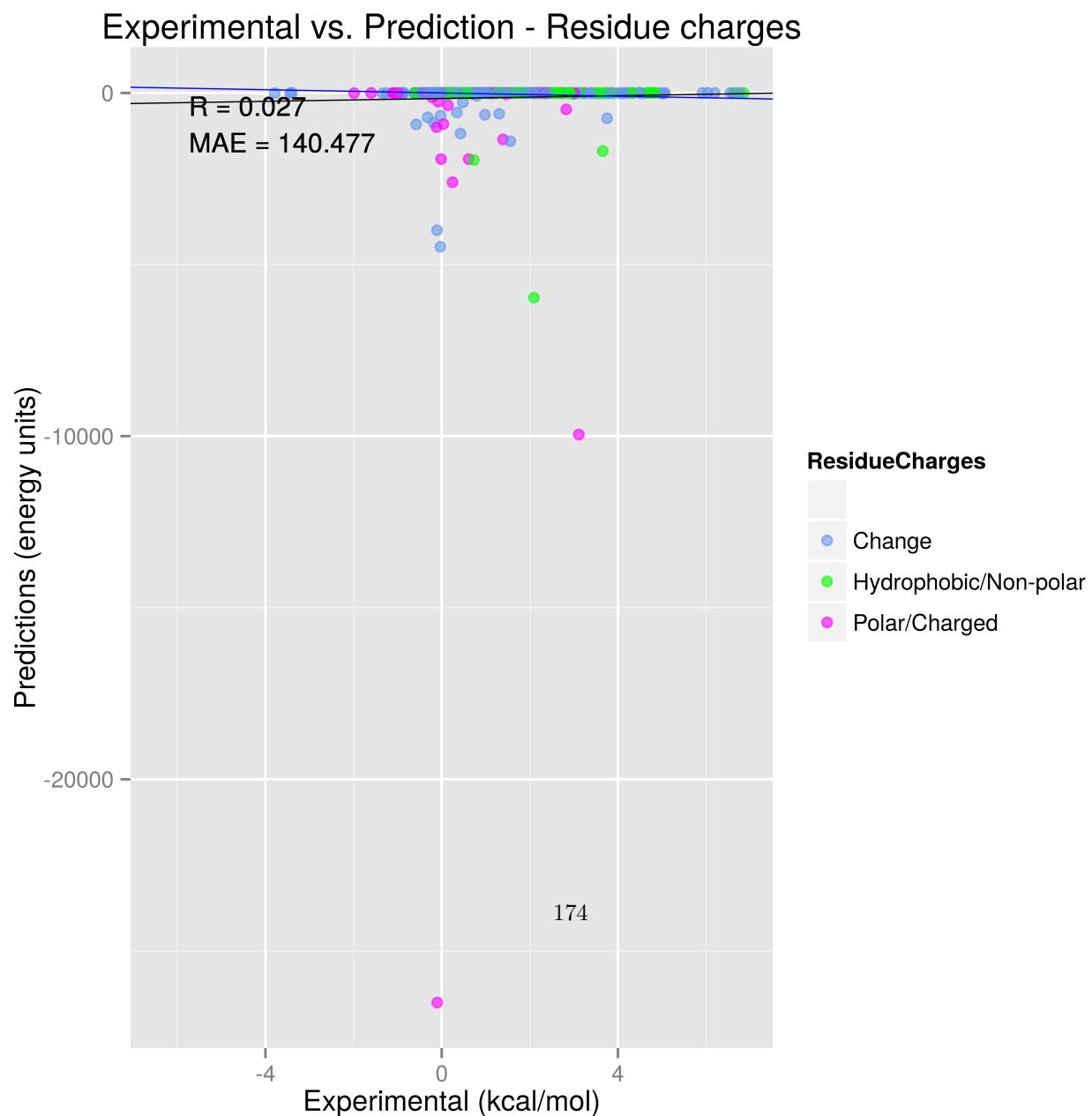


Figure 6.10: Absolute errors adjusted with scalar

6.4 Residue context



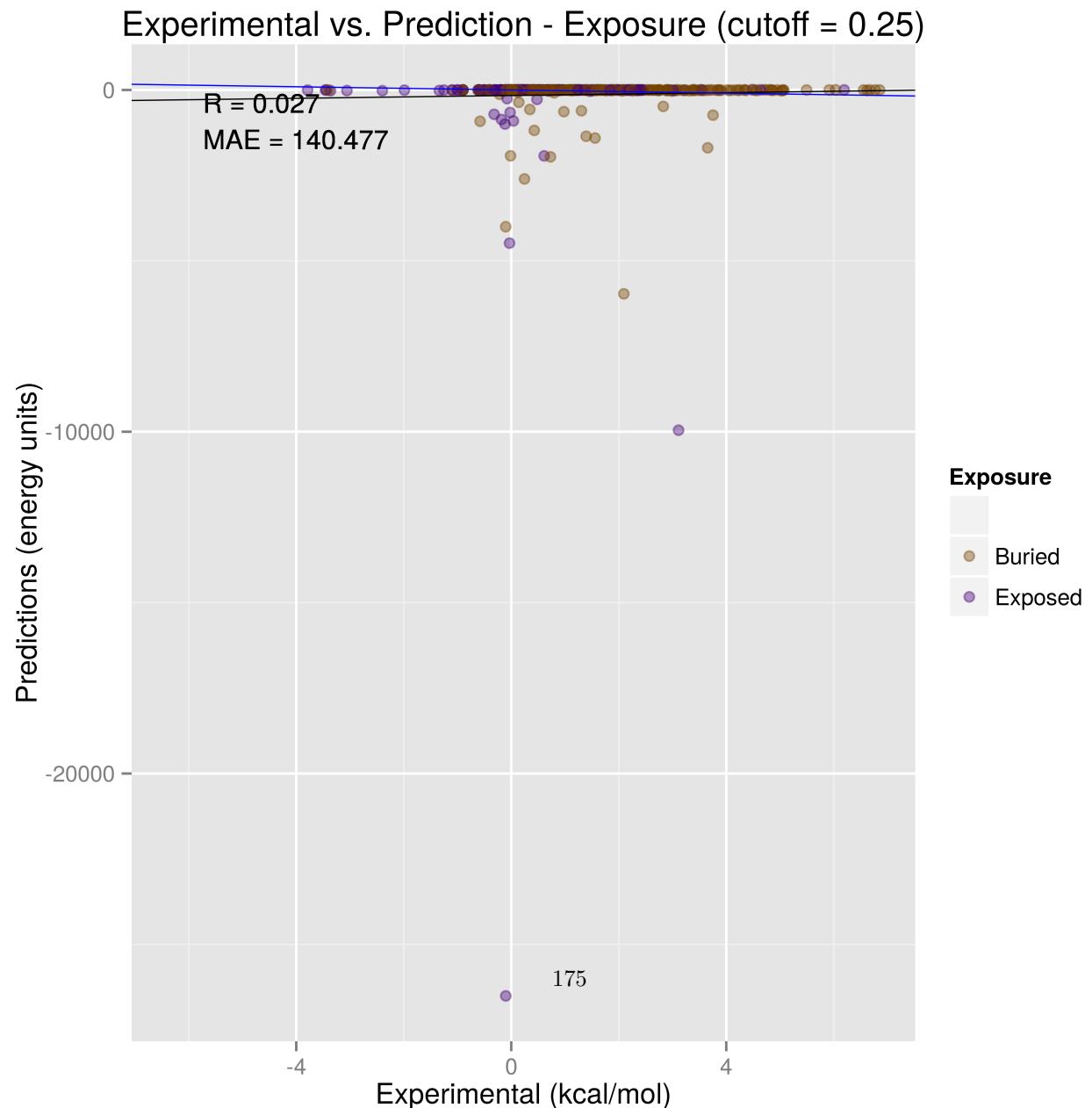


Figure 6.12: Experimental vs. Prediction - Exposure (cutoff = 0.25)

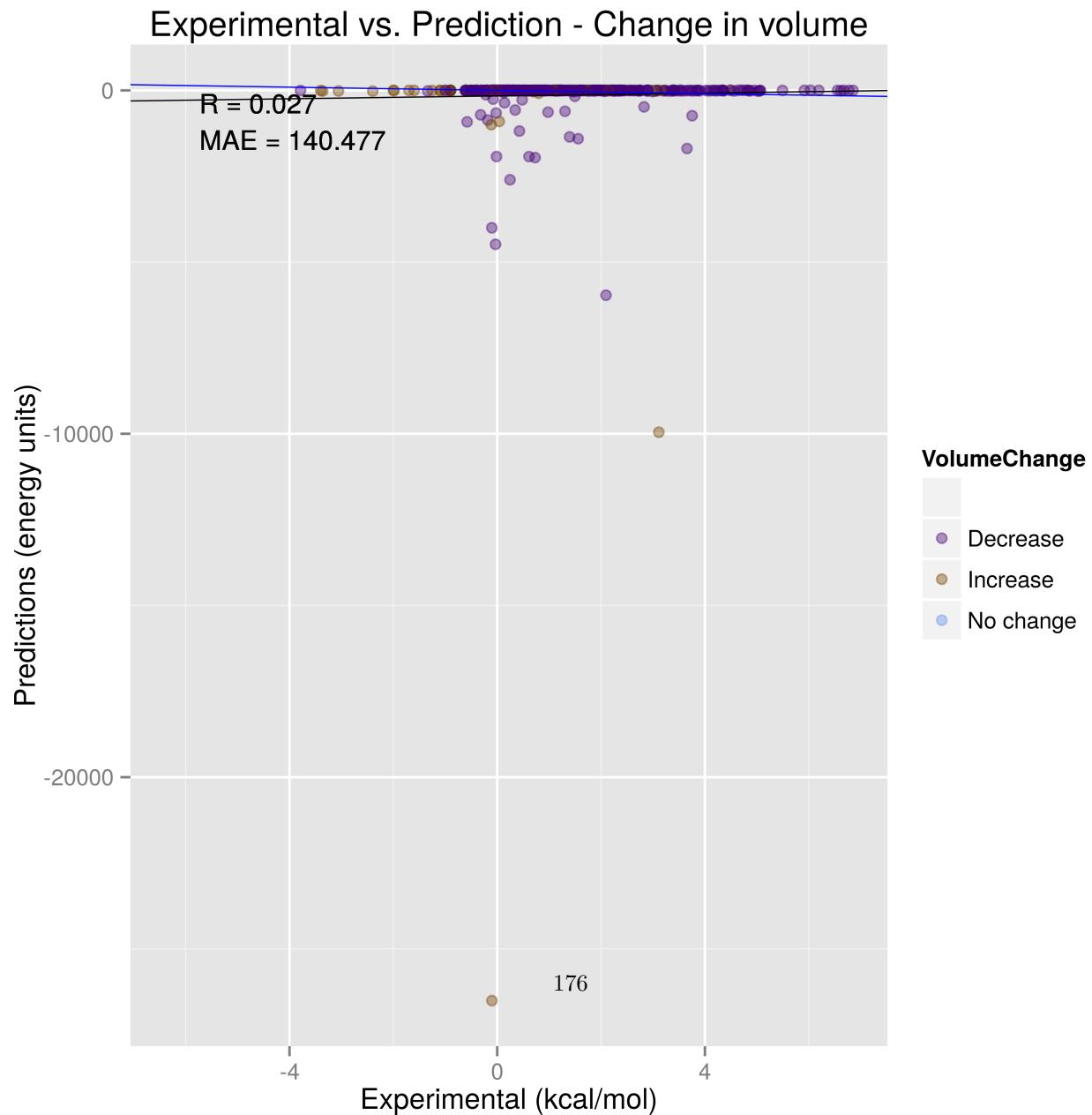


Figure 6.13: Experimental vs. Prediction - Change in volume

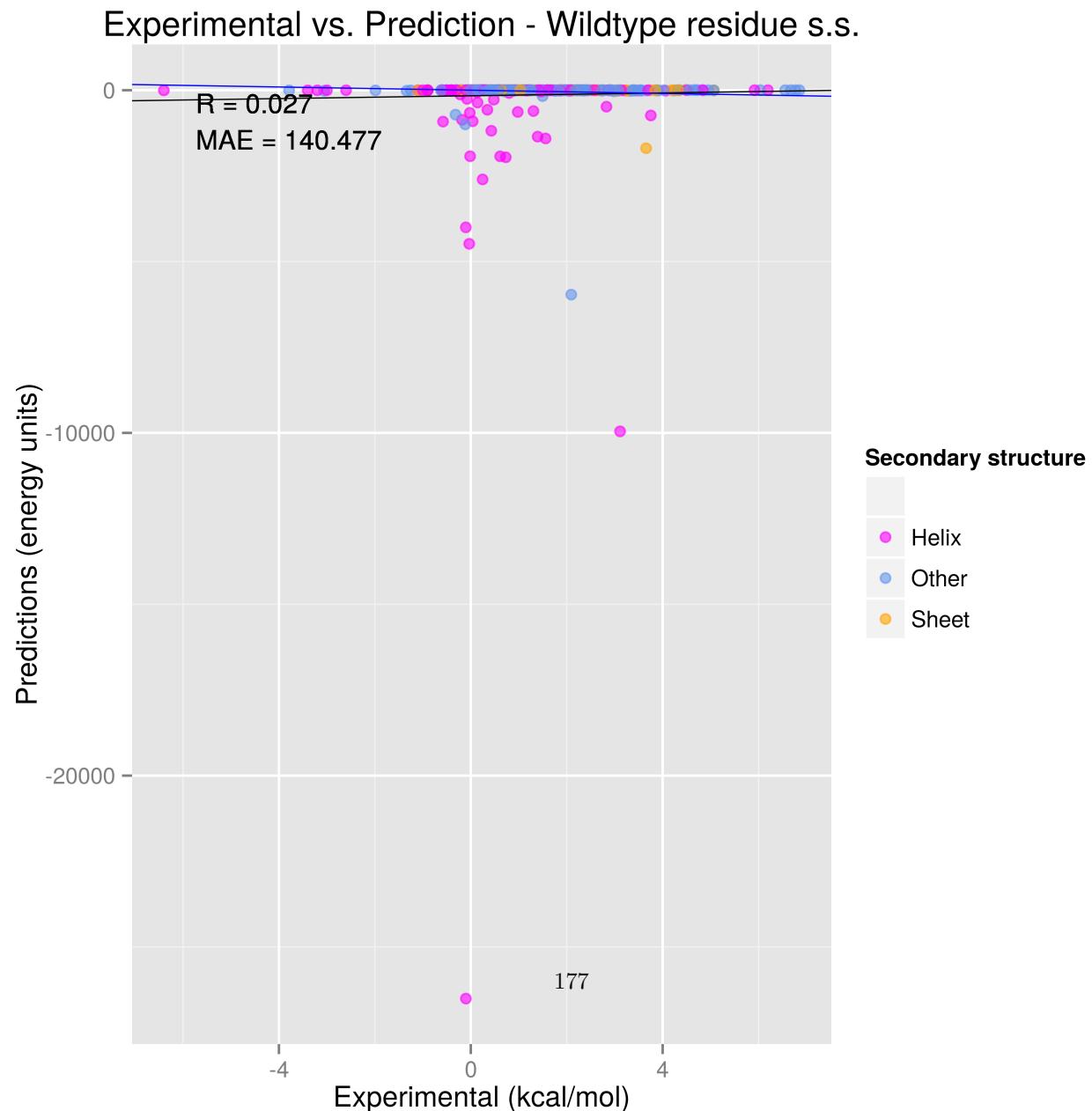
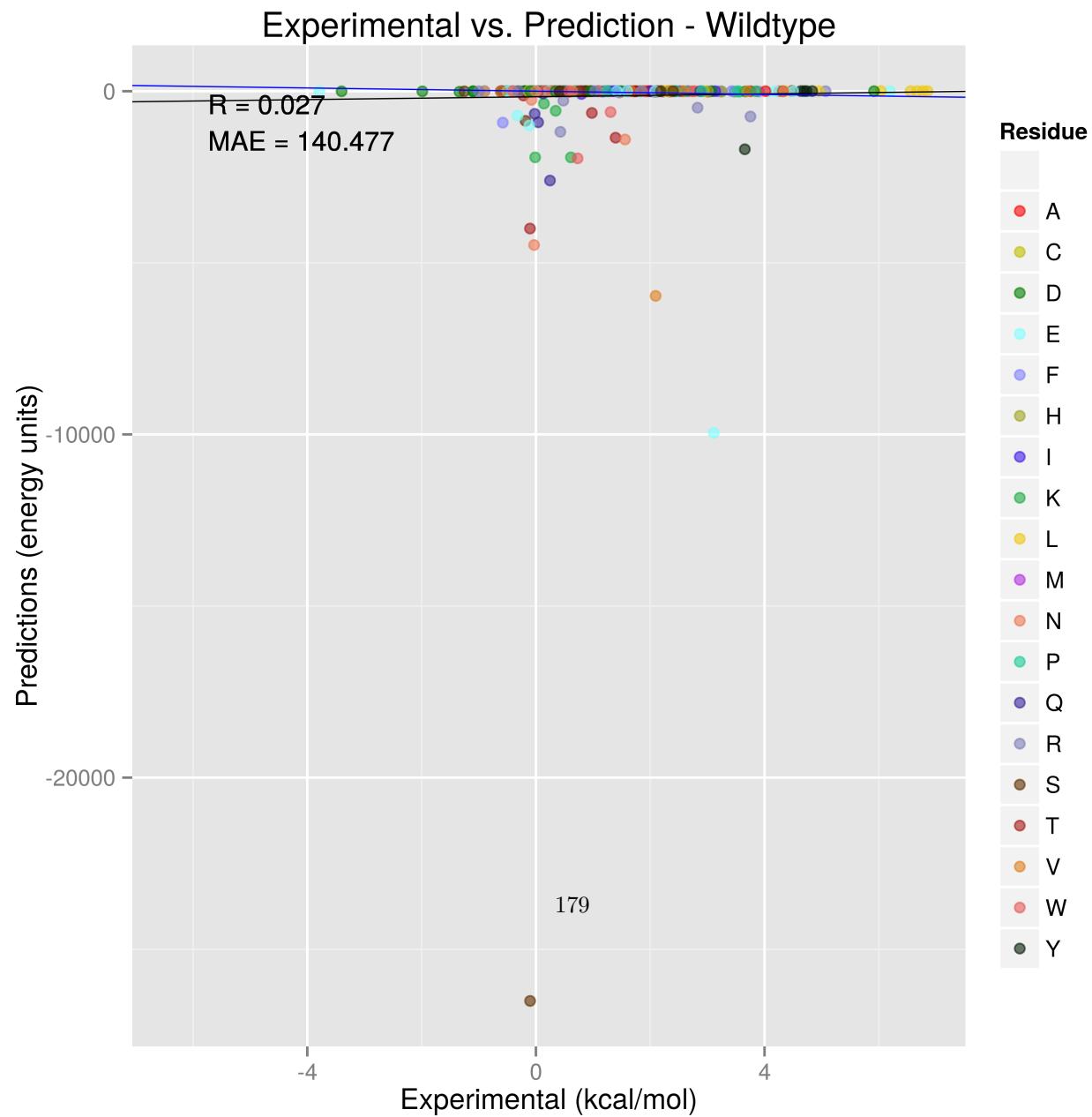


Figure 6.14: Experimental vs. Prediction - Wildtype residue s.s.

6.5 Residue types



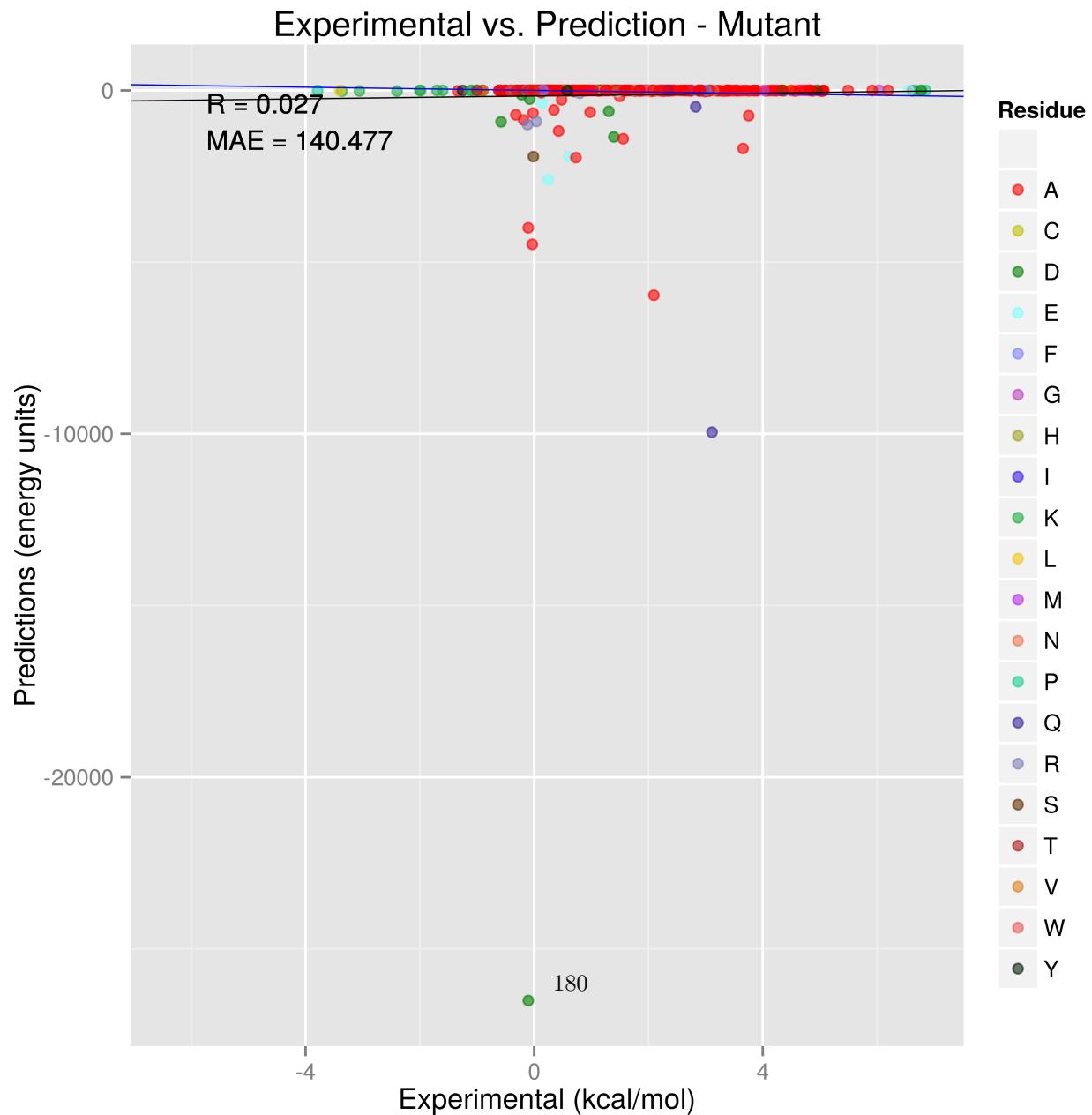


Figure 6.16: Experimental vs. Prediction - Mutant

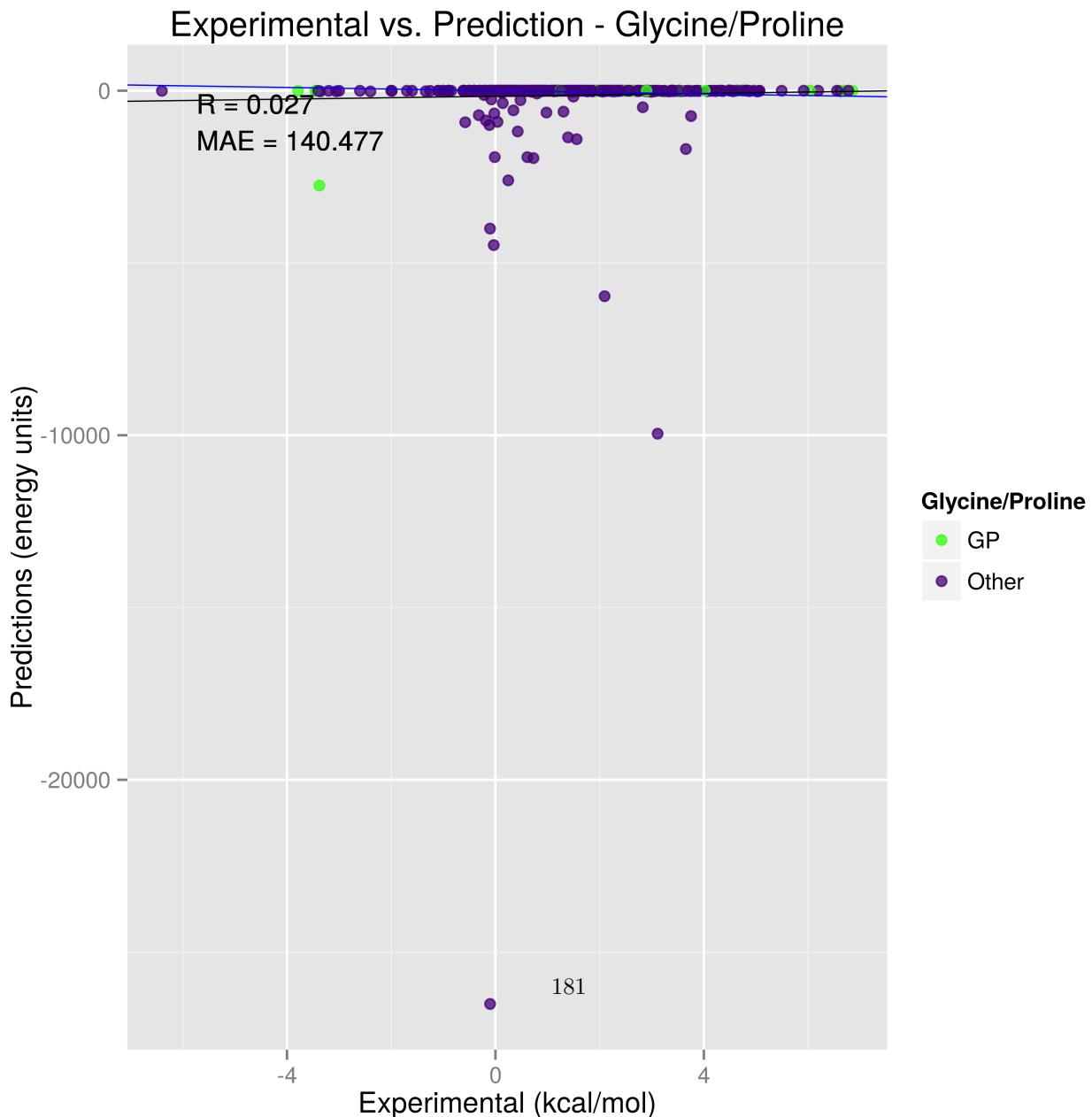
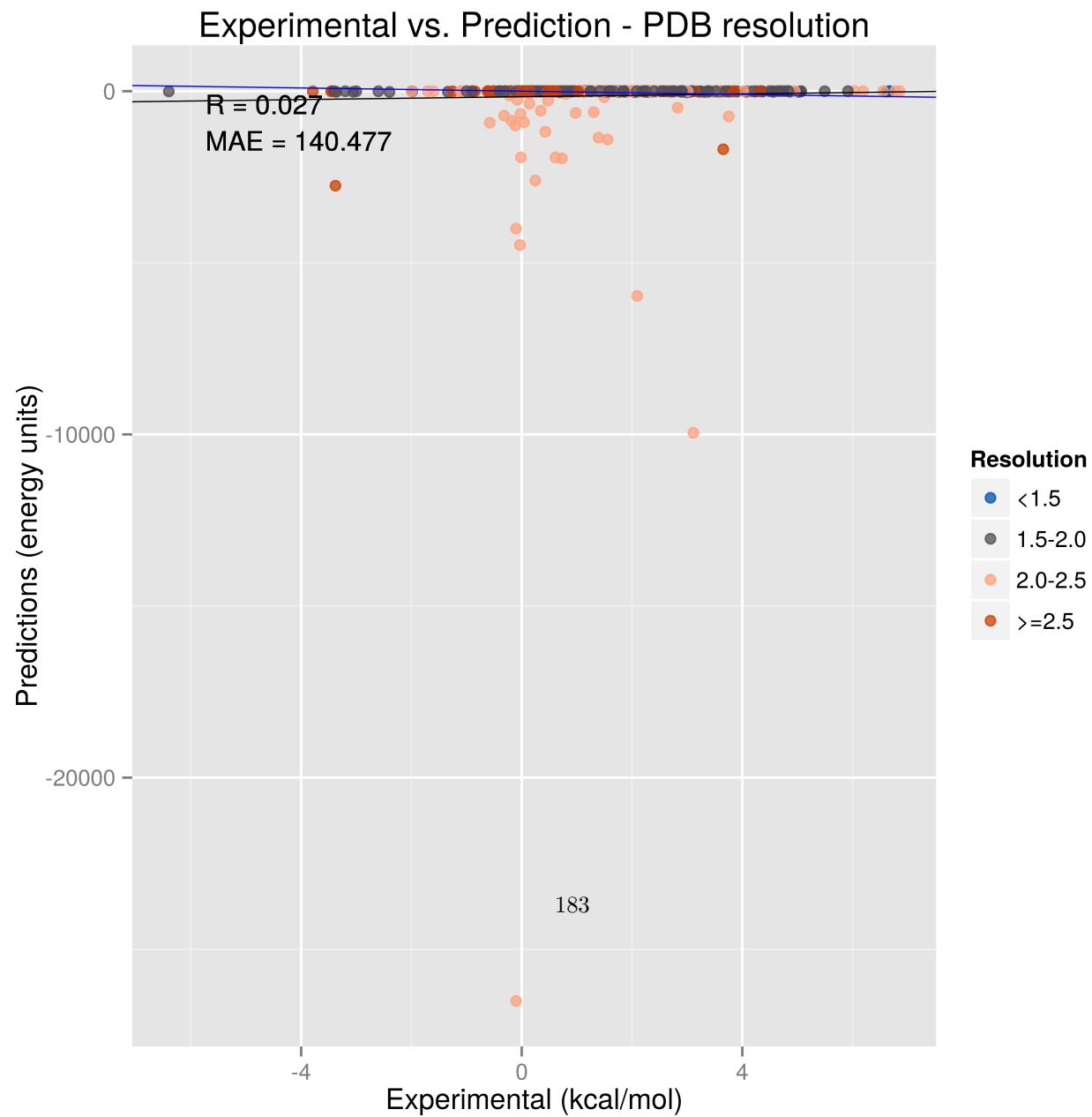


Figure 6.17: Experimental vs. Prediction - Glycine/Proline

6.6 Chain properties



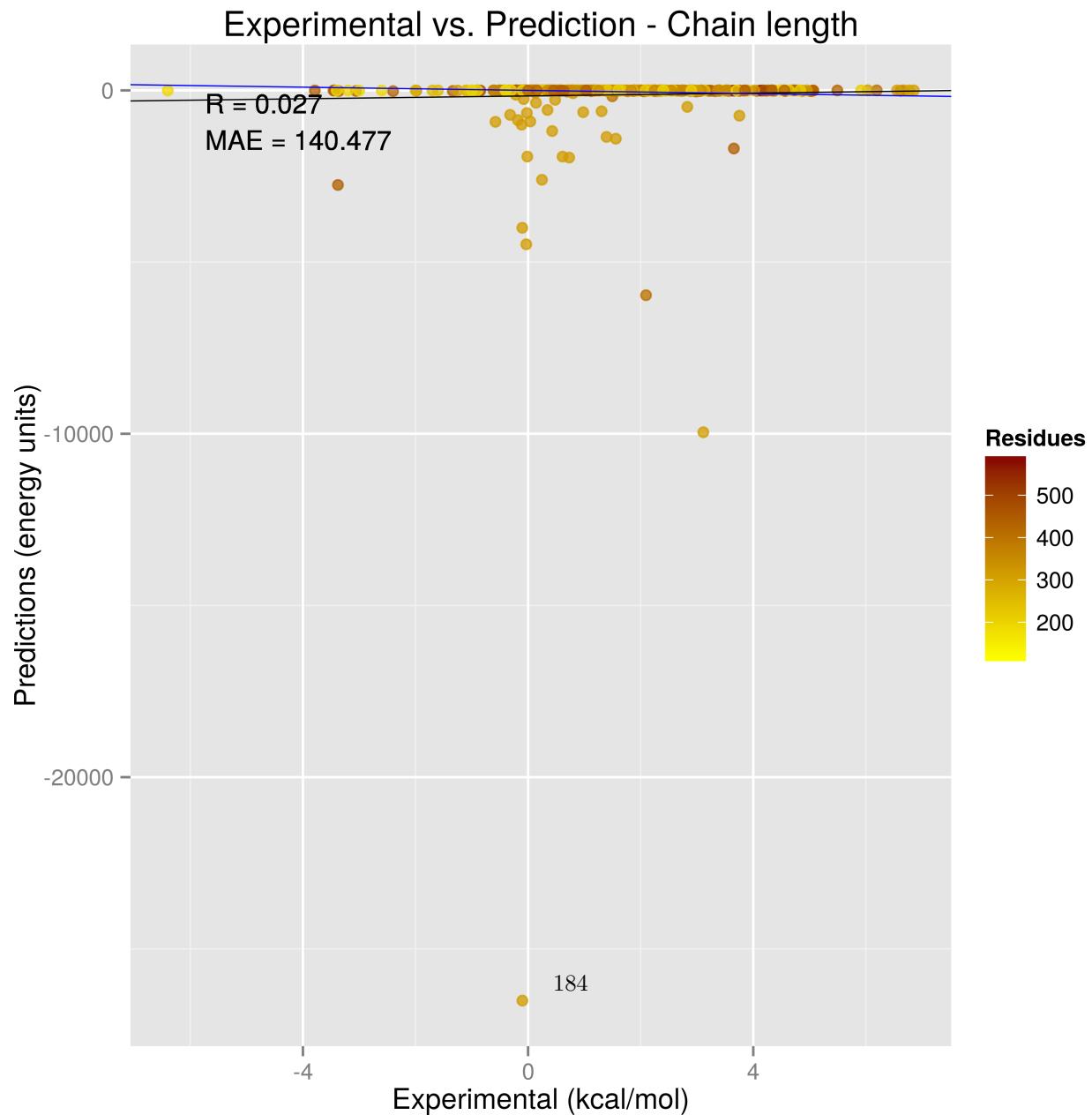


Figure 6.19: Experimental vs. Prediction - Chain length

6.7 Errors / debugging

