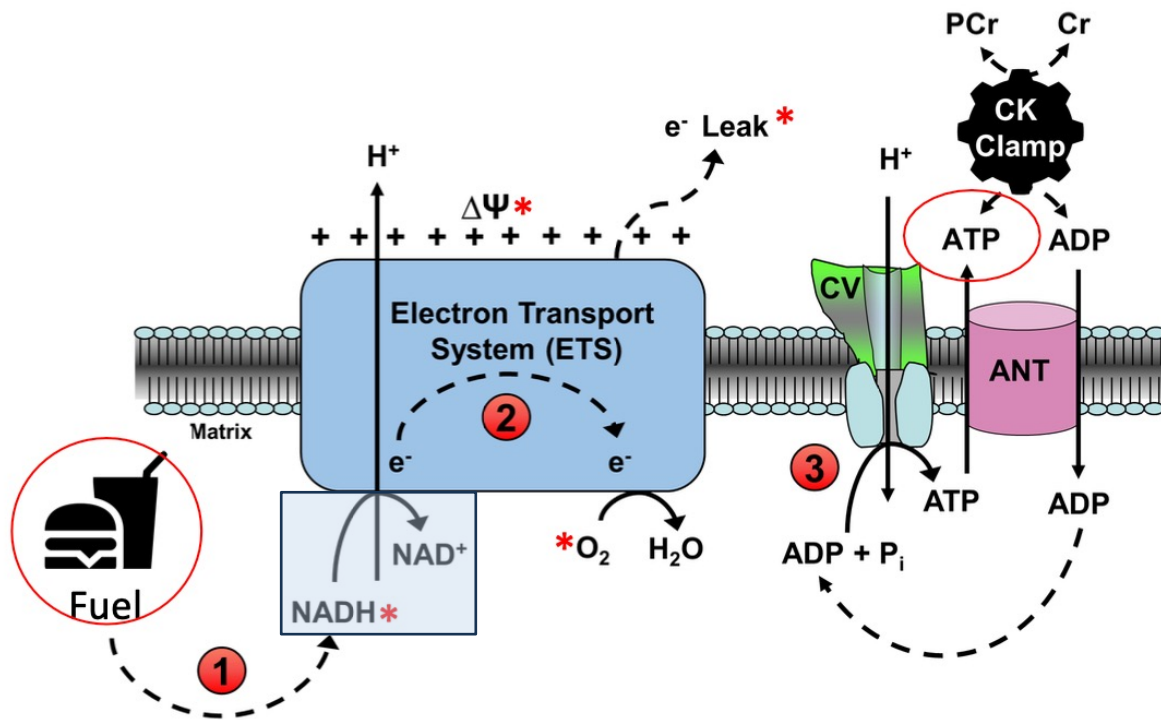




Redox

Group B: Cynthia Yan, Jenny Yan, Athena Ru



1. Matrix Dehydrogenases
2. Electron Transport System (ETS)
3. ATP Synthesis

Redox

NADH autofluorescence of the mitochondria; an indicator of how well mitochondrial dehydrogenase enzymes can produce reducing equivalents from a given fuel

Outcome Variables

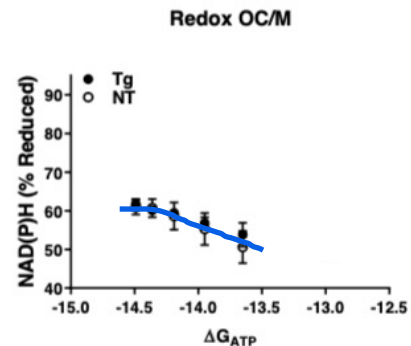
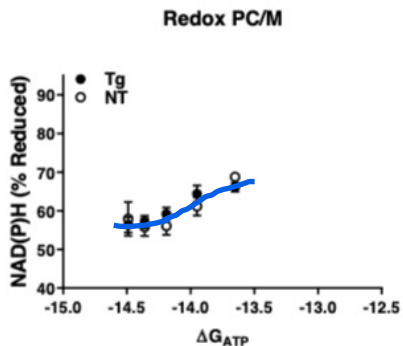
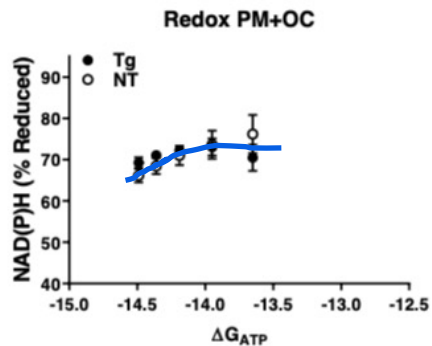
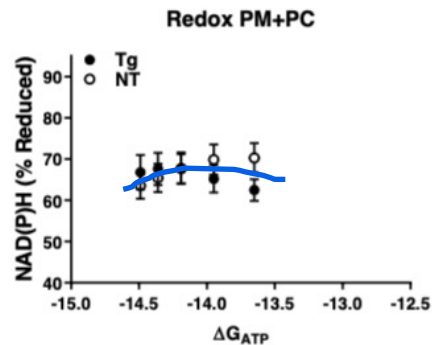
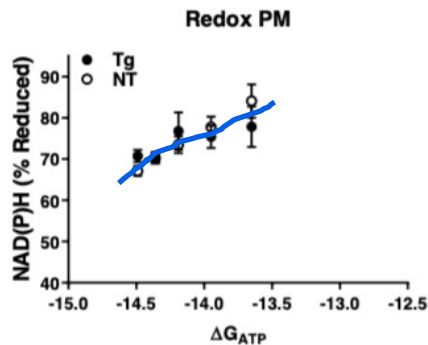
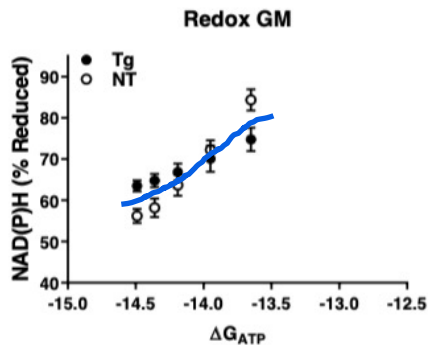
JO_2 – Oxygen Flux

dPsi – Mito Membrane Potential

Redox – NADH

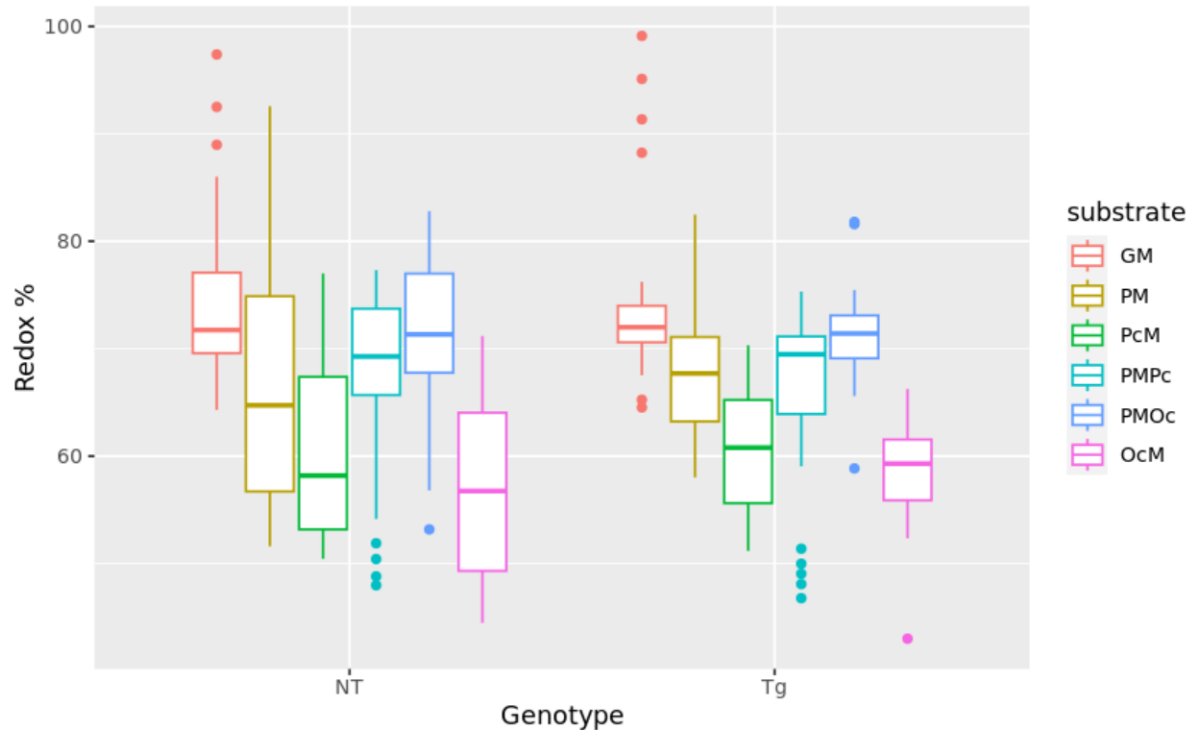
e^- Leak – ROS Production

Client's Graphs



Shape of Redox Variable by Genotype

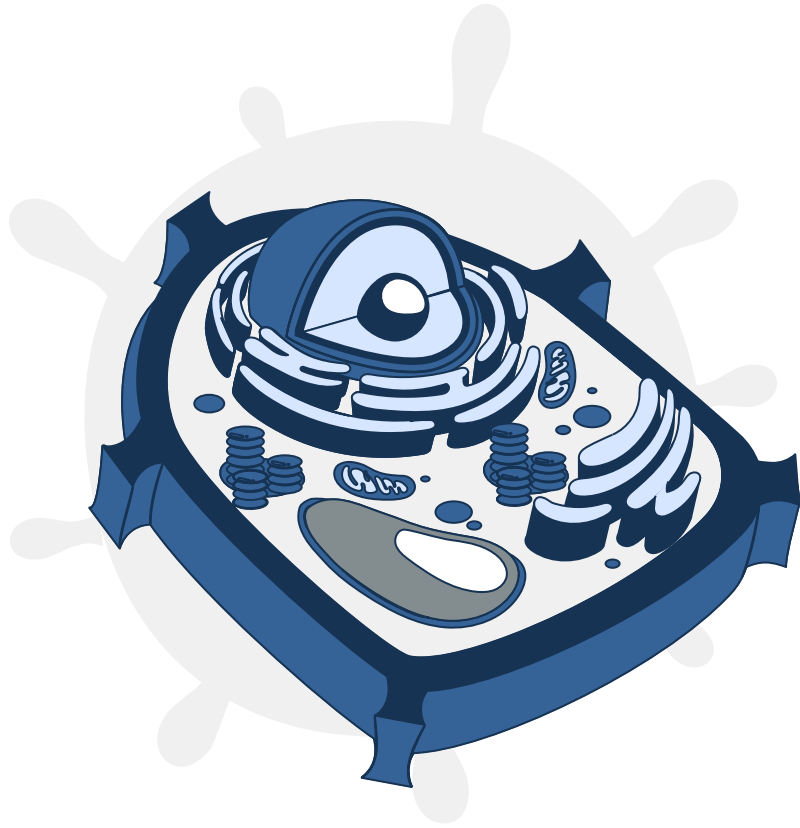
Colored by Substrate



Difference Between Genotypes

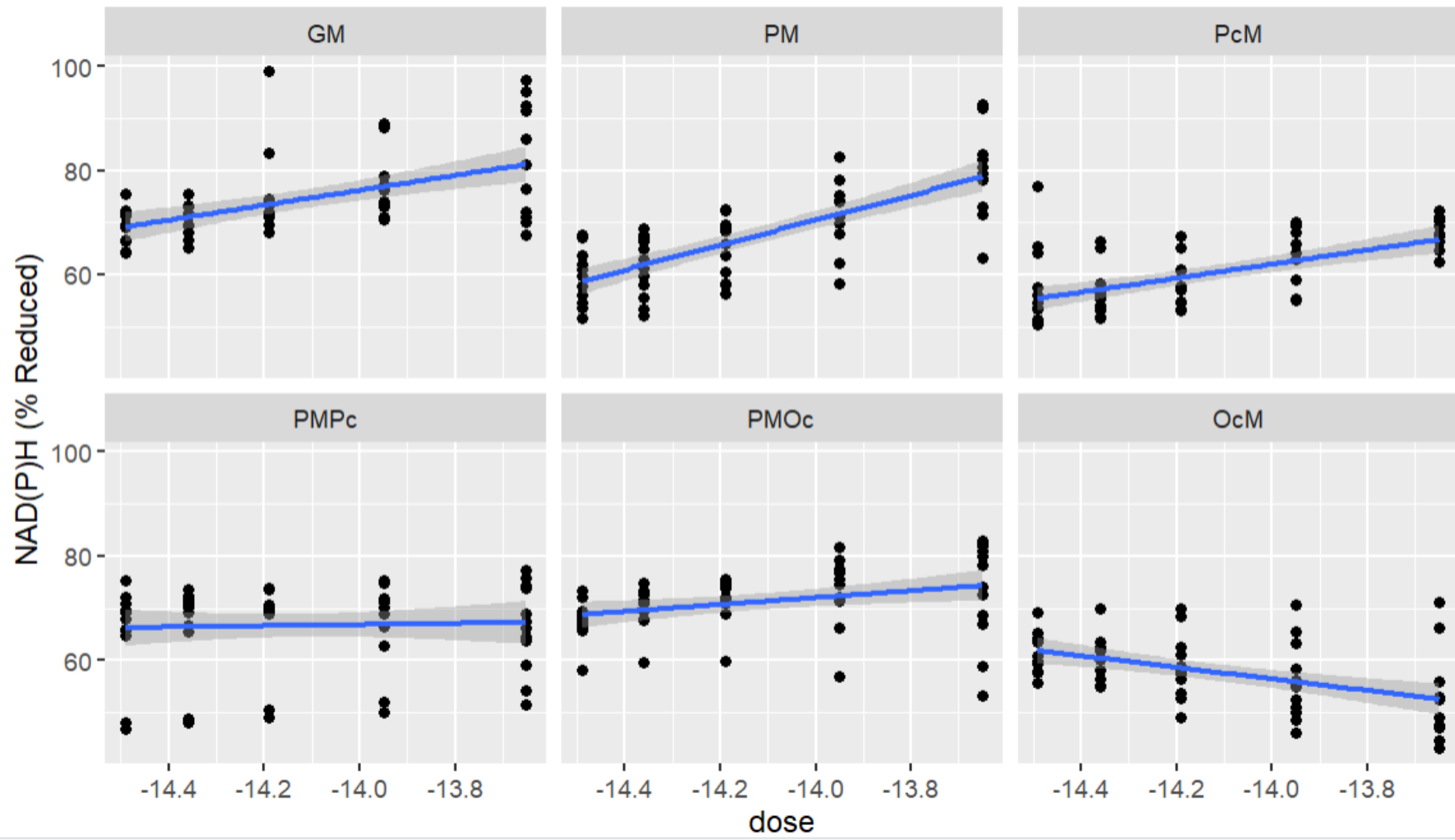
Table 1: ANOVA Results for Genotype and Substrate Interaction

Term	Df	Sum-Sq	MeanSq	Statistic	P Value
Genotype	1	4.049	4.049	0.0663643	0.797
Substrate	5	11872.874	2374.574810	38.922	<0.001
Genotype:substrate	5	70.245	14.048978	0.230	0.949
Residuals	347	21170.135	61.009	NA	NA

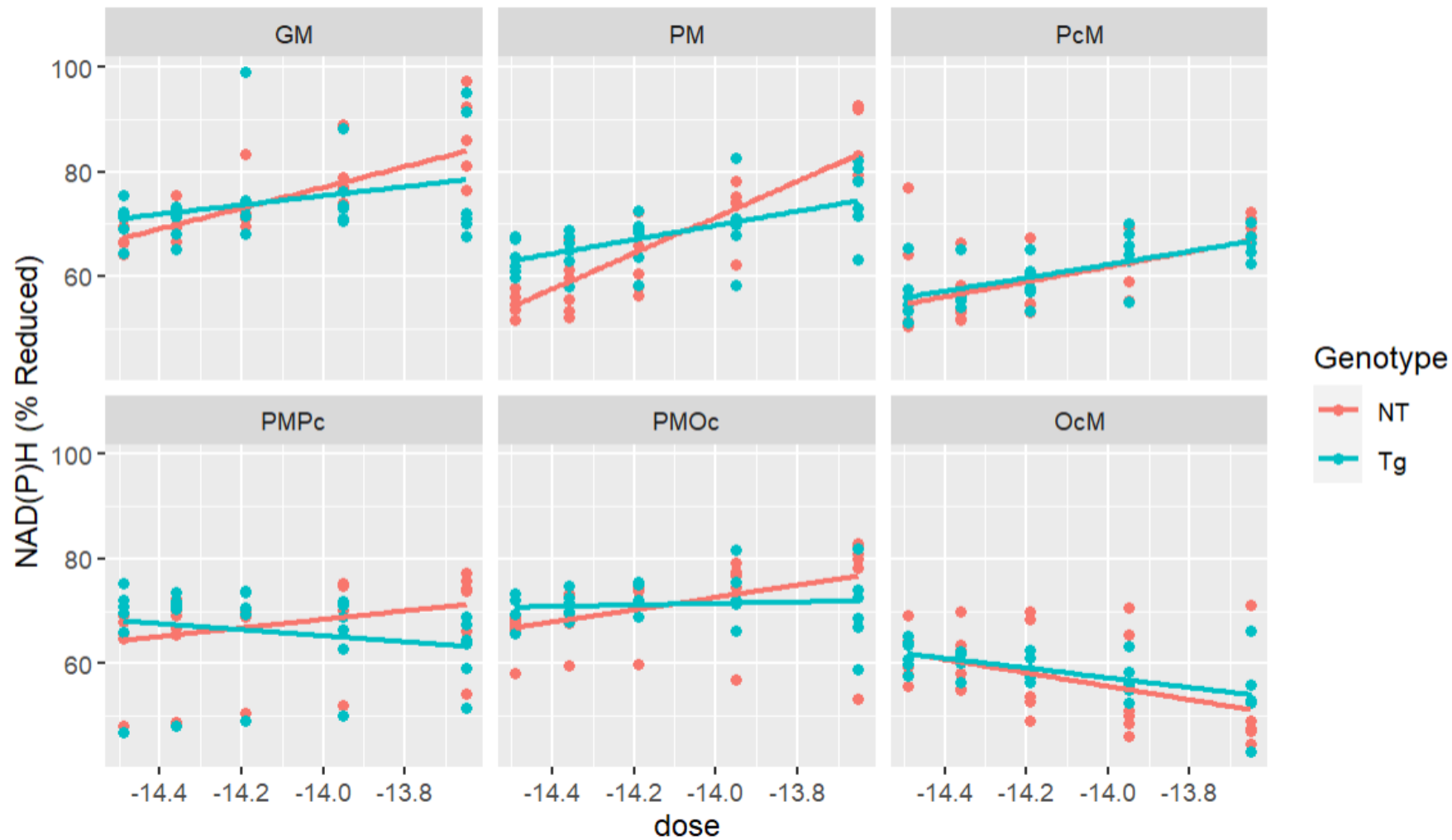


Modelling by Substrate (6 models)

Substrate:

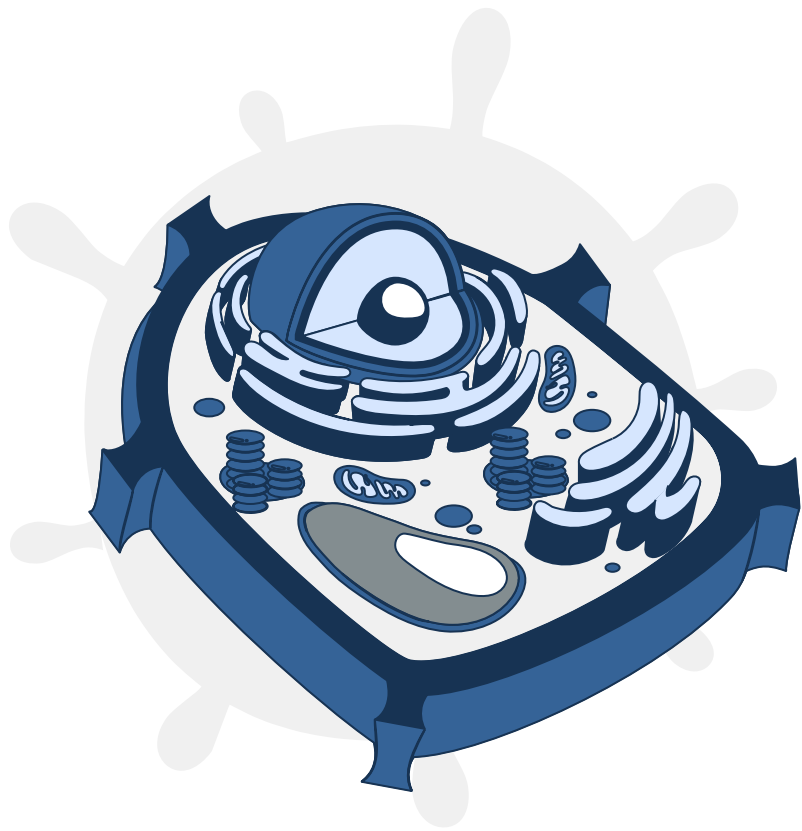


Substrate:



Interaction Effects Model

```
summary_list <- redox %>%  
  drop_na() %>%  
  group_by(substrate) %>%  
  do(model_summary = {  
    fit <- lm(y ~ poly(dose, 2) * geno, data = .)  
    summary(fit)$r.squared  
  })
```



One-for-All Models

Interaction Effects Model

Call:

```
lm(formula = y ~ substrate * poly(dose, 2) * geno, data = redox)
```

Residual standard error: 6.497 on 323 degrees of freedom

Multiple R-squared: 0.5883, Adjusted R-squared: 0.5436

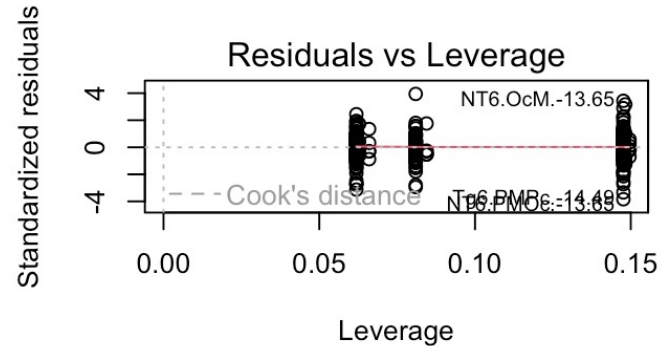
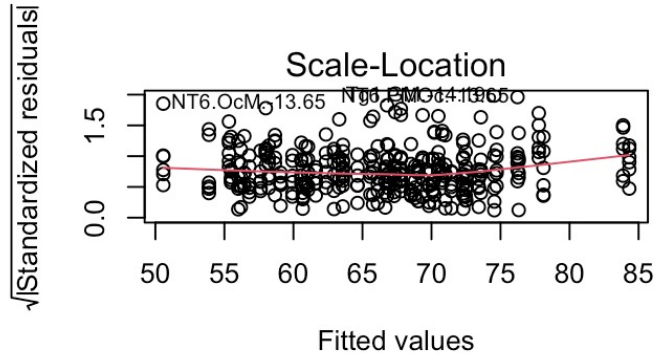
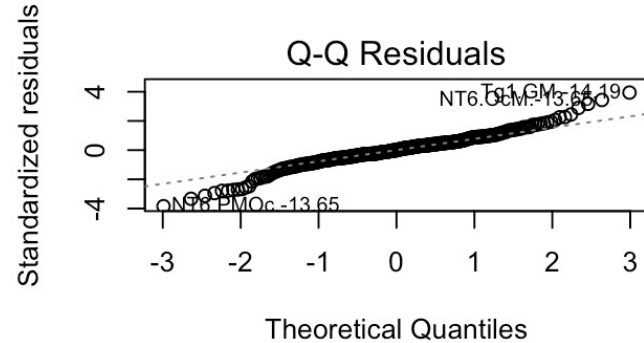
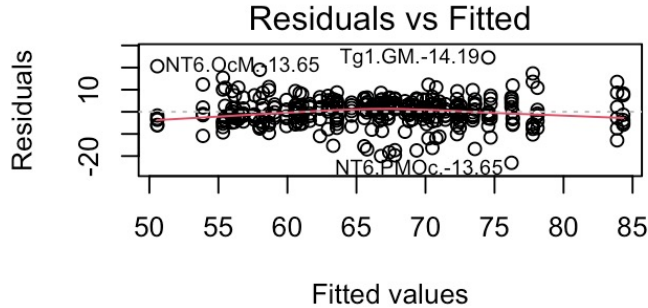
F-statistic: 13.19 on 35 and 323 DF, p-value: < 2.2e-16

Statistically Significant ($p < 0.05$) Variables:

all substrate main effects (baseline=GM), dose¹,

substratePM:dose¹, substratePMPc:dose¹, substrateOcM:dose¹

Model Diagnostics



GAM Model

Call:

```
lm(formula = y ~ substrate + poly(dose, 2) + geno, data = redox)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	74.2543	1.0313	71.999	< 2e-16	***
substratePM	-6.9131	1.3501	-5.121	5.04e-07	***
substratePcM	-14.0843	1.3558	-10.388	< 2e-16	***
substratePMPc	-7.7147	1.3501	-5.714	2.36e-08	***
substratePMOc	-3.2206	1.3501	-2.386	0.0176	*
substrateOcM	-16.5495	1.3501	-12.258	< 2e-16	***
poly(dose, 2)1	-45.5302	7.3998	-6.153	2.08e-09	***
poly(dose, 2)2	5.6503	7.3983	0.764	0.4455	
genoTg	0.2375	0.7806	0.304	0.7611	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

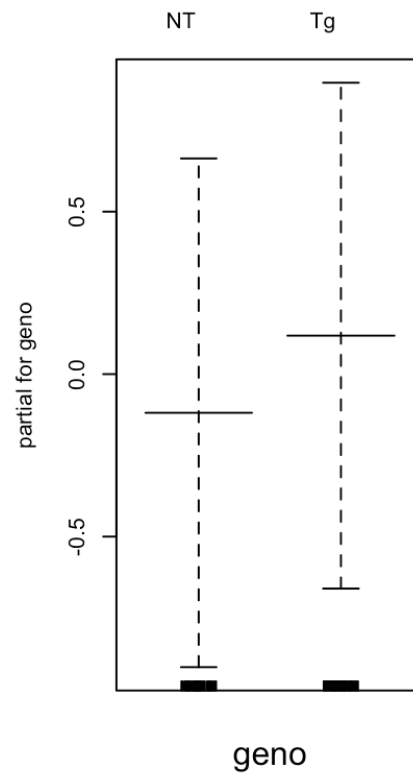
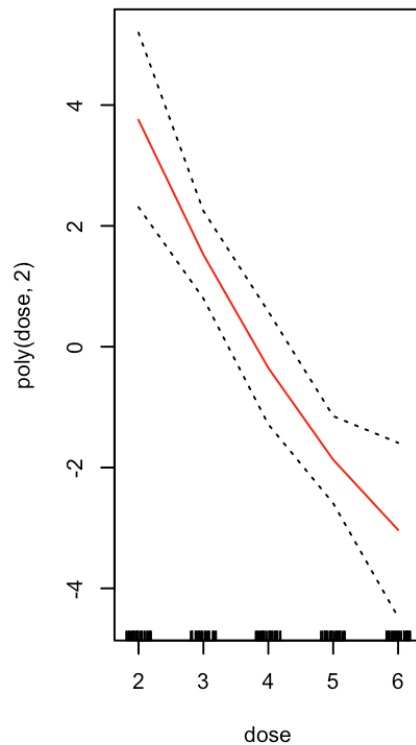
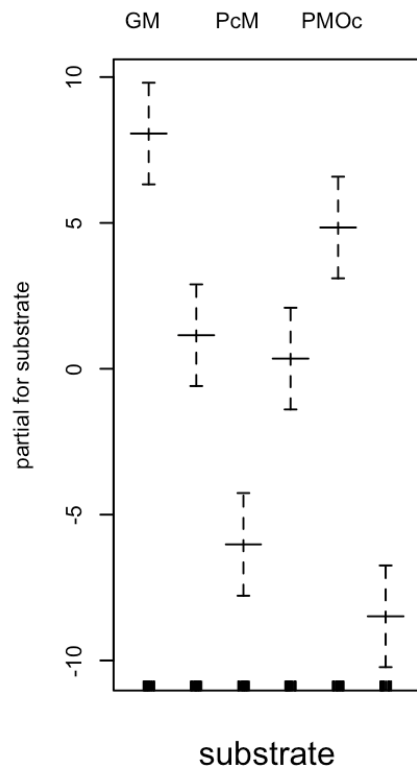
Residual standard error: 7.395 on 350 degrees of freedom

(1 observation deleted due to missingness)

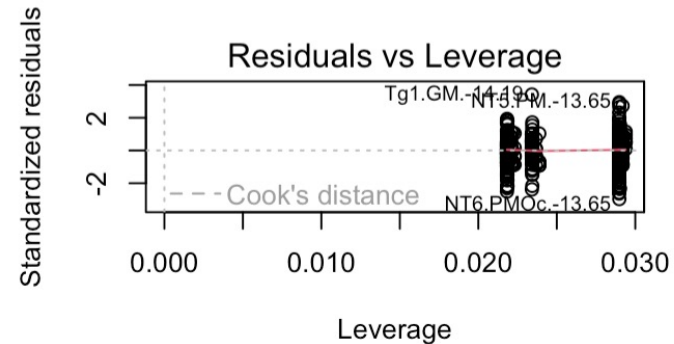
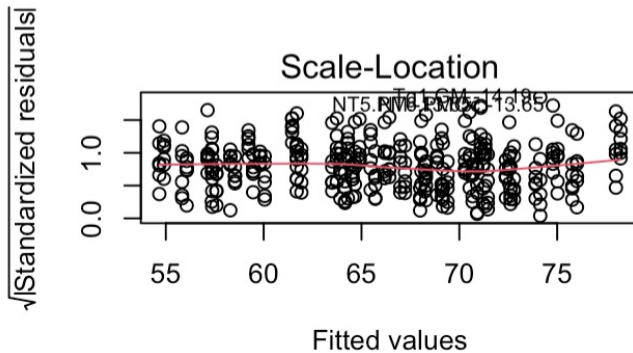
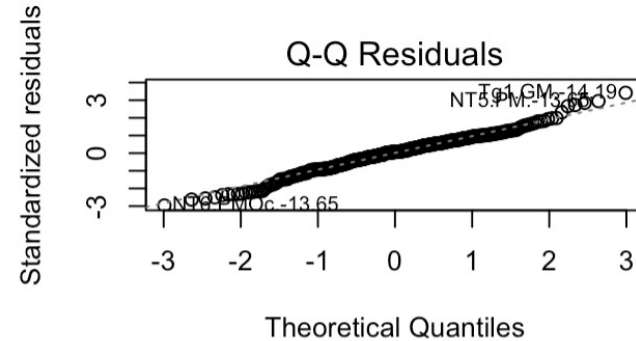
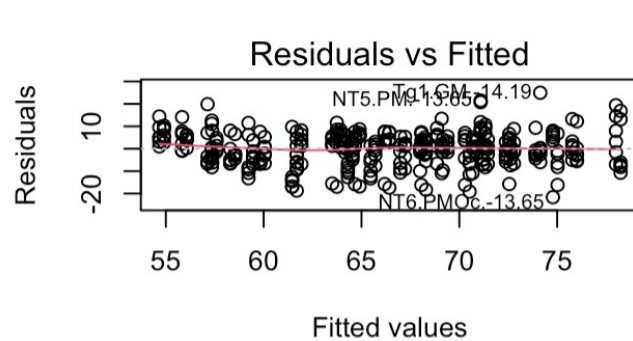
Multiple R-squared: 0.4221, Adjusted R-squared: 0.4089

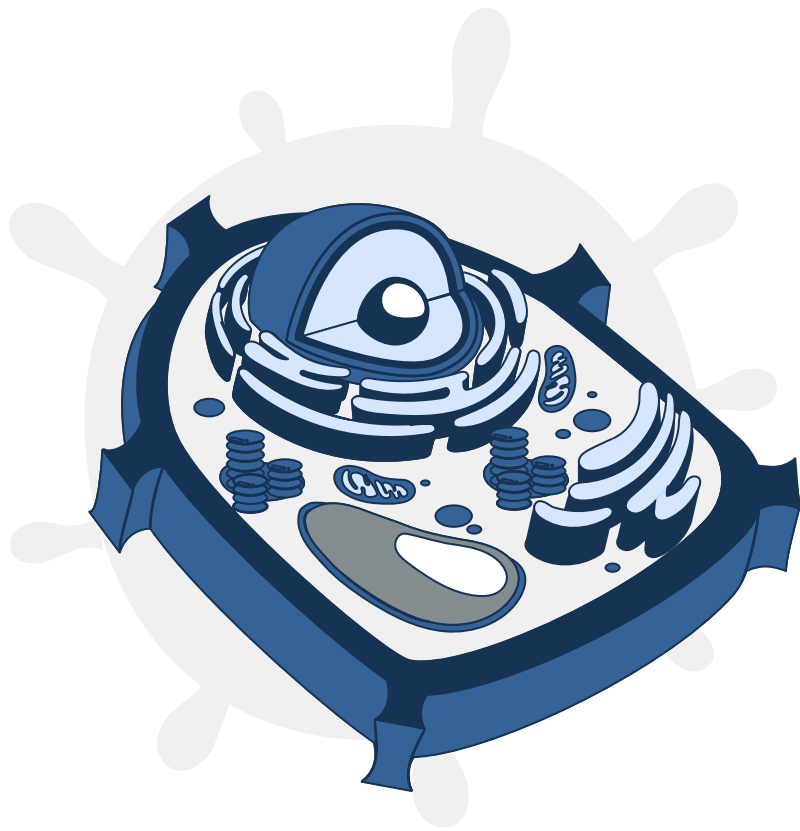
F-statistic: 31.96 on 8 and 350 DF, p-value: < 2.2e-16

GAM Plots



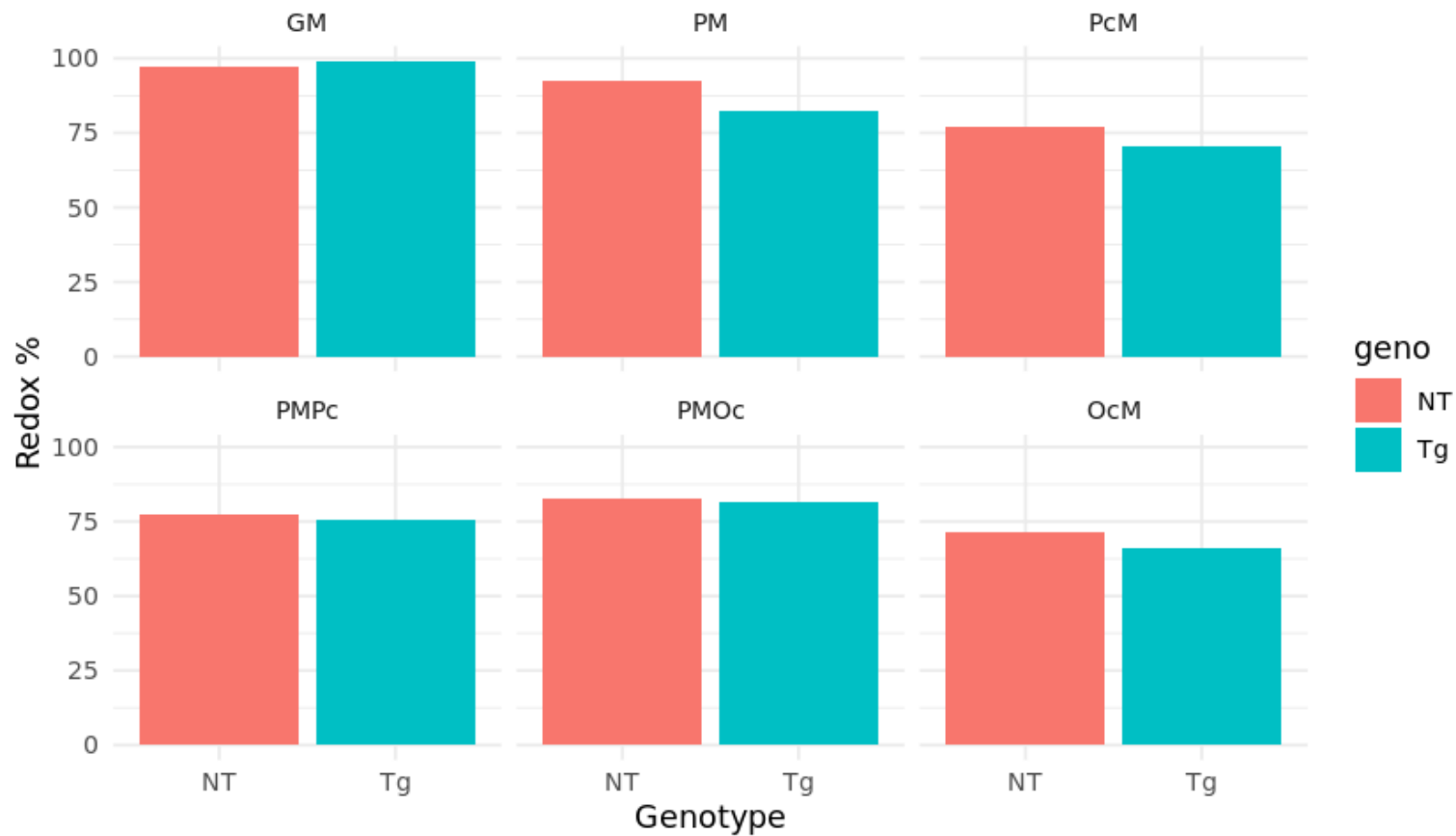
Model Diagnostics



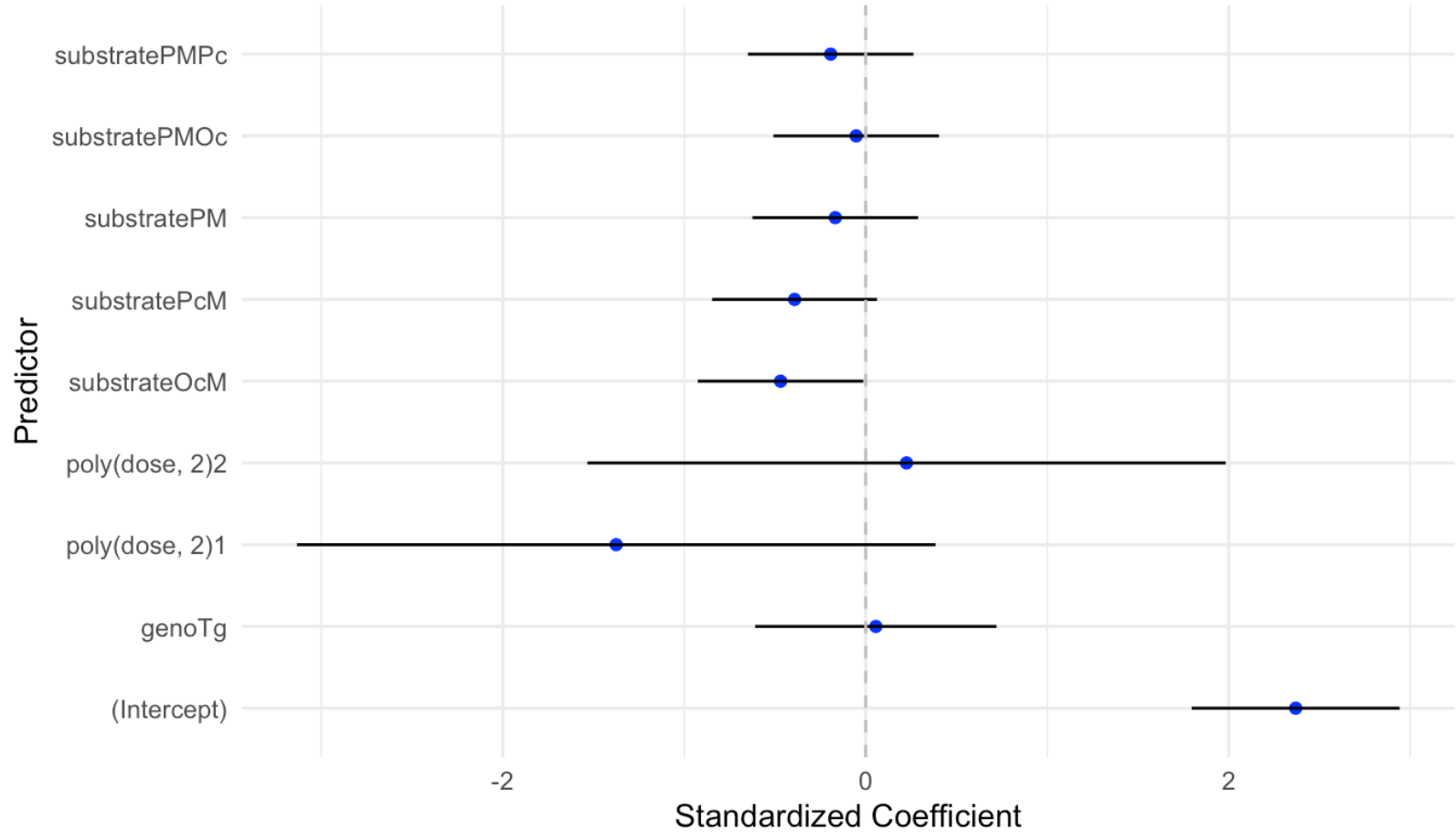


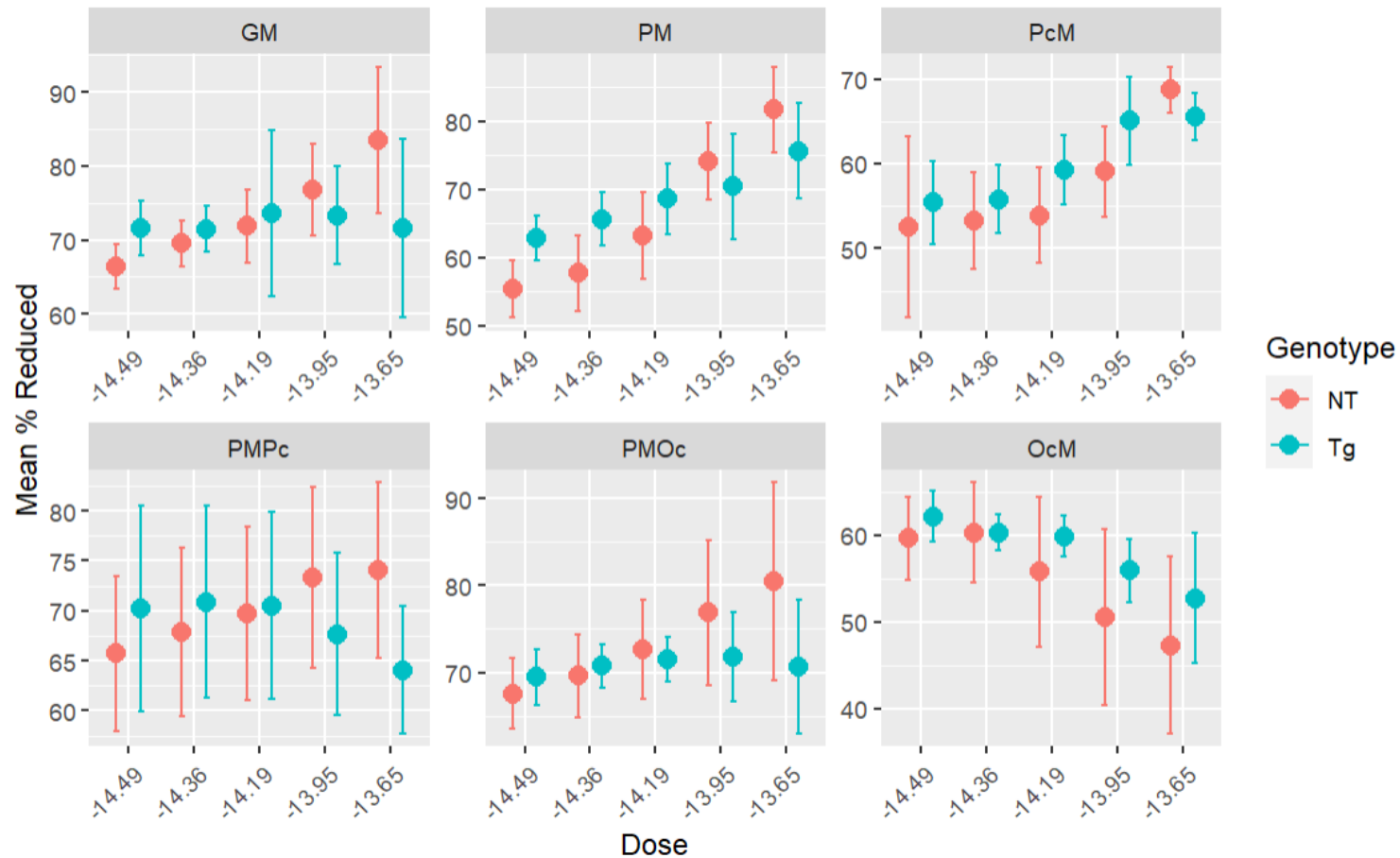
Visualization Recommendations

Mean Redox % by Genotype and Substrate



Effects of Predictors in GAM





Conclusions

- NA Redox response data (1 row) was removed
- We investigated outliers for each substrate in our boxplots
- Batch effects existed on substrates
- The dose response relationship is a quadratic polynomial
- There is no significant difference between the genotypes