

**Analysis of Factors Affecting Potato Gene Expression Levels Under
Multivariate Conditions**

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Abstract

Potato is one of the world's leading non-cereal staple crops, known for its high nutritional value, and is an important food source in many countries. Given the importance of potato in the global diet, the present study attempted to find ways in which potato production could be maximized. This study hope to investigate how variables such as planting environment, fertilization strategy, and time affect the expression level of 63 genes during potato cultivation, and to obtain the most suitable planting method for potato growth. This study combined 15 growing environments (combinations of growing regions and potato varieties) and 11 fertilization strategies with two observations per potato plant at different times, utilizing longitudinal analyses, multiple linear regression models, and hierarchical cluster analysis.

The research revealed that the growing environment, potato variety, sampling days, and fertilization strategies, as well as the complex interplay between these factors, substantially influenced gene expression levels. Among these, genetic determinants were identified as the most impactful, closely followed by environmental and temporal considerations. Furthermore, this study, while maintaining the same total amount of fertilization, adjusted the proportions of the two fertilizations and discovered that secondary fertilization significantly enhances the expression levels of various genes in potatoes. This indicates that an appropriate strategy for secondary fertilization plays a crucial role in promoting gene expression in potato cultivation. And all 63 genes showed a strong positive growth trend when the fertilization strategy was 60:180.

Introduction

Potatoes, as one of the world's primary food crops, not only serve as an essential food source but also offer the nutritional benefits of both vegetables and fruits, playing a crucial role in the food security of numerous countries. Despite the relative ease of potato cultivation, maximizing yield necessitates ongoing research into variety selection, planting environments, and other influential factors. It is important that changes in gene expression in potatoes are closely linked to their yields, so some advice on growing potatoes can be obtained by studying changes in gene expression (Kabir 2004). For instance, it is known that the amount of fertilization impacts potato growth, but excessive fertilization in the initial application can lead to potato death, while too much in the second application can contaminate the soil. Thus, by observing the changes in potato gene expression level over time and fertilizer application, it is possible to find the most appropriate fertilization strategy to improve potato survival and yield. This underscores the importance of in-depth exploration into factors affecting gene expression.

This research is dedicated to analyzing various factors influencing potato gene expression levels, intending to offer a scientific foundation for potato cultivation. By examining potatoes from 15 different varieties and cultivation area combinations, this paper employs longitudinal analysis to map the trends of gene expression levels under varying fertilization methods over time. Data were then converted to a long format for analysis using a multivariate linear regression model, thoroughly examining how variables such as planting region, potato variety, fertilization amounts (including first

and second applications), and sampling days, as well as their interactions, impact the expression of 63 different genes. The study concludes with an analysis of residuals to reaffirm the primary factors affecting potato gene expression levels.

Data

This dataset encompasses information such as potato identification numbers, varieties, planting locations, fertilization methods, timing, and the expression levels of 63 genes. During the data preprocessing stage, an initial data cleaning is conducted. Given that there are 15 different combinations of potato varieties and planting locations, these two variables were merged into a new variable, named 'syc' (All combinations of planting areas and potato varieties are shown in Table 1). Additionally, due to the presence of six distinct fertilization treatments (trt) and the absence of treatment data in some records, the datasets with a total fertilization amount of 106 were categorized as trt3, and those with a total of 200 were classified as trt4.

Considering that the combination of Charlottetown 2014 and Russet Burbank was only observed once on the 42nd day, with no further data available to explore changes in potato gene expression levels for this variety and land combination over time, this study will exclude this combination. Additionally, some potatoes were observed three times, with a short interval between the second and third observations. Given that such a brief interval is unlikely to result in significant changes in potato gene expression levels, this study will disregard parts of the data that include the third observation.

The research aims to investigate the impact of different fertilization methods and time

on gene expression levels. Considering that different treatments primarily differentiate based on the total amount of fertilizer used, ten distinct fertilization strategies were defined by combining the first and second fertilization applications, and these strategies were named ‘fertilization_Strategies’. To accommodate the study’s need for long-format data, the dataset was converted into a long format for subsequent analysis.

	Russet Burbank	Jemseg	Shepody	Atlantic	Classic Russet
Off-Carberry 2014	24	0	0	0	0
On-Carberry 2014	24	0	0	0	0
PŽribonka 2014	0	0	0	0	24
Charlottetown 2014	20	0	0	0	0
Fredericton MAT2014	12	12	12	0	0
Fredericton GE2012	20	0	20	20	0
Fredericton PK2014	8	0	4	0	0

Table 1: The combinations of planting regions and potato varieties

Method

Multi-linear regression

Multiple linear regression is a statistical technique that employs multiple explanatory variables to predict the outcome of a response variable. The objective of multiple linear regression is to model the linear relationship between the independent variables and the response variable. The formula is shown below.

$$Y_i = \beta_0 + \beta_1x_1 + \beta_2x_2 + \dots + \beta_nx_n + \epsilon$$

Considering the influence of multiple variables in the dataset on gene expression levels, a multiple linear regression model is utilized for analysis. The analysis employs data transformed into a long format, with gene expression level as the dependent variable. Independent variables include the genes, treatments, block, syc, fertilization strategies (fertilization_Strategies), days after leaf sampling (DAP_for_leaf_sampling), and interaction terms between fertilization strategies and genes, as well as between genes and days after leaf sampling.

Longitudinal Analysis

Longitudinal studies involve repeatedly observing the same variables over a certain period, allowing researchers to continuously examine the same individuals to identify any changes that may occur over time. In this study, gene expression levels were observed at two distinct time points. Given that changes in gene expression are minimal over closely spaced intervals, the data processing categorized observation days into two groups: those less than 50 days were classified into one category, and those greater than 50 days into another. Considering the aim of this study is to explore the effects of fertilization and time on gene expression, a longitudinal analysis method was employed to examine the data.

Agglomerative Hierarchical Clustering

Hierarchical clustering is an analytical method that groups objects based on similarity. In this method, different clusters form a hierarchical structure and can be visualized

through dendrograms. Agglomerative hierarchical clustering employs a bottom-up approach. Initially, each object forms its own cluster, and then progressively, the most similar pairs of clusters are merged until all objects are consolidated into a predetermined number of clusters. In this study, the model's residual data were analyzed through hierarchical clustering. By calculating the distance matrix between genes and performing hierarchical clustering, a dendrogram is generated. By cutting the dendrogram, the clustering results for each gene are obtained. This study particularly focuses on the smaller clusters at the bottom of the clustering tree. Since residuals represent unobserved variability within the model, analyzing them in conjunction with the results of the model offers unique insights. If certain genes are grouped together in the residual clustering tree and exhibit similar coefficients or response patterns in the model output, this suggests that these genes have similar responses to various factors. This method reveals whether the patterns of gene expression response to different treatments or conditions are similar, thereby aiding in the assessment of how each gene performs under specific experimental conditions.

Analysis

This section will elaborate on how to analyze the data using the aforementioned methods and identify the significant factors affecting the variation in potato gene expression levels.

Plot data

Firstly, for the sake of facilitating data analysis, the data converted into a long format

is visualized. By plotting line graphs of various genes over time, a preliminary classification can be made. In these line graphs, the horizontal axis represents time, while the vertical axis indicates the gene expression levels, and different colored lines represent combinations of fertilization methods (trt) and areas (block), that is, an experimental unit (plot). In the first type of graph, all lines show a downward trend over time, indicating that regardless of the fertilization method, the expression levels of these genes decrease with time. The lines in the second type of graph all show an upward trend, suggesting that regardless of the fertilization method, the expression levels of these genes increase over time. The third type of graph shows lines without a clear trend, indicating that the expression levels of these genes fluctuate over time, without a clear pattern of increase or decrease. The image of gene St.LIP serves as an excellent example of the first category, while the image of gene St.Unk1 represents the second category. Such visualizations may indicate that time is a significant factor affecting the expression levels of these genes, whereas the impact of fertilization strategies on their expression levels might be minimal. Conversely, genes like St.MSRB, which are categorized under the third type of images, could suggest that different fertilization methods significantly affect their expression levels.

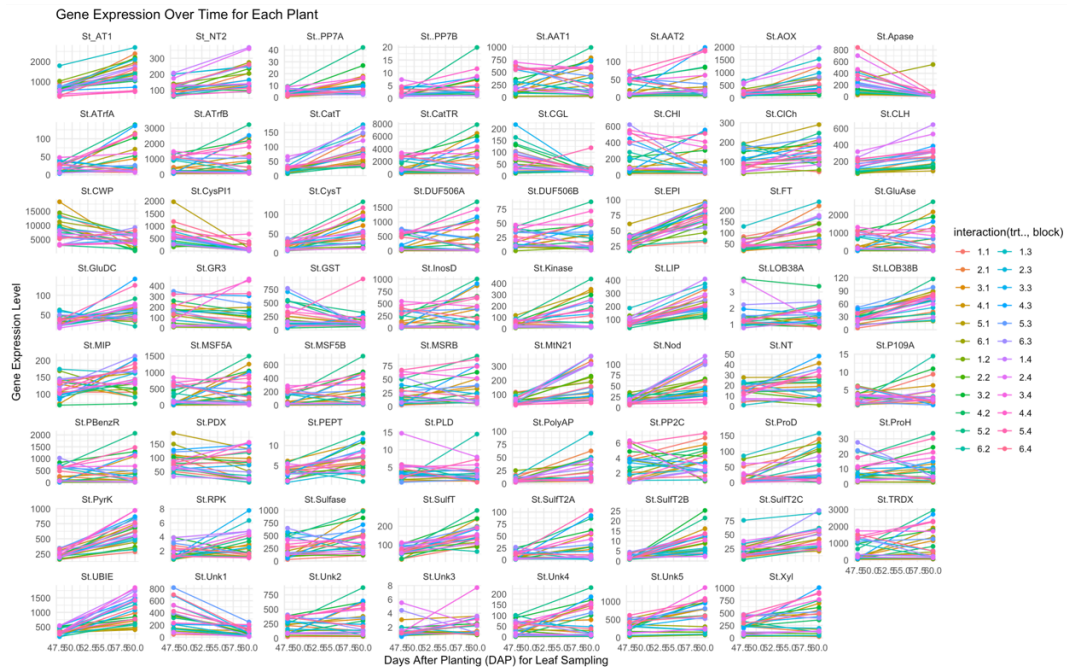


Figure 1: The plot of the data

Fitting multi-linear regression model and create the ANOVA table.

Model 1:

Y (gene expression) \sim gene + syc + trt + block + fertilization_Strategies + DAP_for_leaf_sampling

This model uses gene expression levels as the dependent variable, with genes, syc (the combination of variety and planting location), trt (treatment), block, fertilization strategies, and days after leaf sampling (DAP_for_leaf_sampling) as independent variables. The results show that time, all genes except for St.CHI and St.ClCh, the combination of variety and planting location, and the 240:0 fertilization strategy significantly affect changes in gene expression levels, as their p-values are all less than 0.05. Notably, the coefficient for time is negative, indicating that gene expression levels decrease over time. Furthermore, the fertilization strategy fertilization_Strategies240:0 has a significant positive impact on gene expression, highlighting fertilization strategy

as a key factor.

By integrating the results from the ANOVA table with multiple linear regression (figure 5), a comprehensive understanding of the model and the impact of various variables on gene expression levels can be achieved. Thus, an ANOVA table for this model was created. Showing that gene, the combination of planting location and variety (syc), fertilization treatment (trt), fertilization strategies, and days after leaf sampling (DAP_for_leaf_sampling) are significant factors affecting gene expression ($p < 0.05$). Notably, the gene variable has the largest sum of squares (Sum Sq), indicating that gene type is the primary factor influencing changes in gene expression levels, while the effects of fertilization treatment and days after leaf sampling are comparatively smaller.

```
Call:
lm(formula = expression ~ gene + syc + trt + block + fertilization_Strategies +
    DAP_for_leaf_sampling, data = data)

Residuals:
    Min       1Q   Median       3Q      Max
-12355   -460    -37     233   90148

Coefficients: (1 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  2260.452    144.332   15.661 < 2e-16 ***
geneSt_NT2  -2495.412    170.805  -14.610 < 2e-16 ***
geneSt_PP7A -2878.602    170.805  -16.853 < 2e-16 ***
geneSt_PP7B -2899.309    170.805  -16.974 < 2e-16 ***
geneSt_AAT1 -2198.380    170.805  -12.871 < 2e-16 ***
geneSt_AAT2 -2852.354    170.805  -16.700 < 2e-16 ***
geneSt_AOX  -1827.734    170.805  -10.701 < 2e-16 ***
geneSt_Apase -1843.063    170.805  -10.790 < 2e-16 ***
geneSt_ATrFA -2884.707    170.805  -16.889 < 2e-16 ***
geneSt_ATrFB -2447.532    170.805  -14.329 < 2e-16 ***
geneSt_CatT -2756.510    170.805  -16.138 < 2e-16 ***
geneSt_CatTR -1434.028    170.805   -8.396 < 2e-16 ***
geneSt_CGL  -2791.927    170.805  -16.346 < 2e-16 ***
geneSt_CHI   -52.643    170.805   -0.308  0.7579
geneSt_CLCh -129.121    170.805   -0.756  0.4497
geneSt_CLH  -2705.404    170.805  -15.839 < 2e-16 ***
geneSt_CWP   8909.676    170.805  52.163 < 2e-16 ***
geneSt_CysP11 -2694.328    170.805  -15.774 < 2e-16 ***
geneSt_CysT  -2862.506    170.805  -16.759 < 2e-16 ***
geneSt_DUF506A -1882.445    170.805  -11.021 < 2e-16 ***
geneSt_DUF506B -2879.825    170.805  -16.860 < 2e-16 ***
geneSt_EPI  -2828.617    170.805  -16.561 < 2e-16 ***
geneSt_FT   -2657.804    170.805  -15.560 < 2e-16 ***
geneSt_GluAse -2527.588    170.805  -14.798 < 2e-16 ***
geneSt_GluDC -2268.162    170.805  -13.279 < 2e-16 ***
geneSt_GR3  -1781.151    170.805  -10.428 < 2e-16 ***
geneSt_GST  -2665.768    170.805  -15.607 < 2e-16 ***
geneSt_InosD -1946.938    170.805  -11.399 < 2e-16 ***
```

Figure 2: summary of model 1

```
geneSt_Kinase -2822.179    170.805  -16.523 < 2e-16 ***
geneSt_LIP   -2514.544    170.805  -14.722 < 2e-16 ***
geneSt_LOB38A -2914.192    170.805  -17.062 < 2e-16 ***
geneSt_LOB38B -2825.901    170.805  -16.545 < 2e-16 ***
geneSt_MEP   -2457.419    170.805  -14.387 < 2e-16 ***
geneSt_MSF5A -1759.532    170.805  -10.301 < 2e-16 ***
geneSt_MSF5B -2538.006    170.805  -14.859 < 2e-16 ***
geneSt_MSRB  -2834.120    170.805  -16.593 < 2e-16 ***
geneSt_MZN1  -2662.427    170.805  -15.588 < 2e-16 ***
geneSt_Nod   -2851.204    170.805  -16.693 < 2e-16 ***
geneSt_NT    -2879.710    170.805  -16.860 < 2e-16 ***
geneSt_P109A -2911.653    170.805  -17.047 < 2e-16 ***
geneSt_PBenzR -2114.740    170.805  -12.381 < 2e-16 ***
geneSt_PDX   -2880.366    170.805  -16.395 < 2e-16 ***
geneSt_PEPF  -2906.769    170.805  -17.018 < 2e-16 ***
geneSt_PLD   -2918.132    170.805  -17.085 < 2e-16 ***
geneSt_PolyAP -2888.996    170.805  -16.914 < 2e-16 ***
geneSt_PP2C  -2905.546    170.805  -17.011 < 2e-16 ***
geneSt_ProD  -2763.759    170.805  -16.181 < 2e-16 ***
geneSt_ProH  -2903.149    170.805  -16.997 < 2e-16 ***
geneSt_PyrK  -2050.328    170.805  -12.004 < 2e-16 ***
geneSt_RPK   -2916.883    170.805  -17.077 < 2e-16 ***
geneSt_Sulfase -2709.720    170.805  -14.898 < 2e-16 ***
geneSt_SulfT -2544.725    170.805  -14.898 < 2e-16 ***
geneSt_SulfT2A -2753.892    170.805  -16.123 < 2e-16 ***
geneSt_SulfT2B -2878.507    170.805  -16.853 < 2e-16 ***
geneSt_SulfT2C -2890.855    170.805  -16.925 < 2e-16 ***
geneSt_TRDX  -1197.144    170.805   -7.009  2.47e-12 ***
geneSt_UBIE  -1926.975    170.805  -11.282 < 2e-16 ***
geneSt_Unk1  -2772.514    170.805  -16.232 < 2e-16 ***
geneSt_Unk2  -2609.799    170.805  -15.279 < 2e-16 ***
geneSt_Unk3  -2913.900    170.805  -17.060 < 2e-16 ***
geneSt_Unk4  -2853.492    170.805  -16.706 < 2e-16 ***
geneSt_Unk5  -1951.301    170.805  -11.424 < 2e-16 ***
geneSt_Xyl   -2446.791    170.805  -14.325 < 2e-16 ***
sycFredericton GE2012_Atlantic 1162.604    83.184  13.976 < 2e-16 ***
sycFredericton GE2012_Russet Burbank 845.824    83.184  10.168 < 2e-16 ***
sycFredericton GE2012_Shepody 887.020    83.261  10.654 < 2e-16 ***
```

Figure 3: summary of model 1

sycFredericton MAT2014_Jemseg	696.936	103.794	6.715	1.93e-11	***
sycFredericton MAT2014_Russet Burbank	660.089	103.794	6.360	2.06e-10	***
sycFredericton MAT2014_Shepody	798.598	103.794	7.694	1.48e-14	***
sycFredericton PK2014_Russet Burbank	903.863	125.467	7.204	6.02e-13	***
sycFredericton PK2014_Shepody	1297.900	147.950	8.773	< 2e-16	***
sycOff-Carberry 2014_Russet Burbank	390.314	91.759	4.254	2.11e-05	***
sycOn-Carberry 2014_Russet Burbank	543.540	91.444	5.944	2.82e-09	***
sycPZribonka 2014_Classic Russet	497.900	92.821	5.364	8.21e-08	***
trt2	-123.600	348.696	-0.354	0.7230	
trt3	-37.032	255.347	-0.145	0.8847	
trt4	7.316	281.865	0.026	0.9793	
trt5	67.285	79.178	0.850	0.3954	
trt6	-208.307	286.506	-0.727	0.4672	
block2	-70.757	44.418	-1.593	0.1112	
block3	-60.469	44.103	-1.371	0.1704	
block4	-46.737	44.073	-1.060	0.2889	
fertilization_Strategies60.0	176.750	348.246	0.508	0.6118	
fertilization_Strategies106.0	142.255	265.414	0.536	0.5920	
fertilization_Strategies120.0	288.968	262.142	1.102	0.2703	
fertilization_Strategies180.0	321.968	282.513	1.140	0.2544	
fertilization_Strategies200.0	522.520	307.406	1.700	0.0892	
fertilization_Strategies240.0	613.421	99.867	6.142	8.26e-10	***
fertilization_Strategies60.120	115.305	263.163	0.438	0.6613	
fertilization_Strategies60.120	68.787	282.052	0.244	0.8073	
fertilization_Strategies60.180	167.920	255.347	0.658	0.5108	
fertilization_Strategies60.180	NA	NA	NA	NA	
DAP_for_leaf_sampling1	-218.748	36.770	-5.949	2.73e-09	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1					
Residual standard error: 2351 on 23785 degrees of freedom					
Multiple R-squared: 0.3218, Adjusted R-squared: 0.3192					
F-statistic: 124 on 91 and 23785 DF, p-value: < 2.2e-16					

Figure 4: summary of model 1.

Analysis of Variance Table

Response: expression	Df	Sum Sq	Mean Sq	F value	Pr(>F)
gene	62	5.8710e+10	946938879	171.2829	< 2.2e-16 ***
syc	11	2.7407e+09	249153242	45.0670	< 2.2e-16 ***
trt	5	4.5307e+08	90613026	16.3901	3.499e-16 ***
block	3	1.5396e+07	5131965	0.9283	0.426
fertilization_Strategies	9	2.6813e+08	29792621	5.3889	2.097e-07 ***
DAP_for_leaf_sampling	1	1.9566e+08	195664211	35.3919	2.734e-09 ***
Residuals	23785	1.3150e+11	5528509		

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

Figure 5: ANOVA table of model 1

Model 2:

Y (gene expression) ~ gene + syc + fertilization_Strategies + DAP_for_leaf_sampling + gene * DAP_for_leaf_sampling + gene * fertilization_Strategies

Given that the block variable did not show a significant impact on gene expression levels in model1, it was decided to exclude the block variable in the development of the new model, model2, and to incorporate interaction terms between variables. Considering that different fertilization strategies reflect the total amount of fertilization, the trt variable was also excluded in the new model. Additionally, since the interaction between trt and block did not significantly affect gene expression (figure 4), this interaction term was not considered in model2 (the full summary of the model 2 is shown in appendix). The analysis of model2 revealed that all genes had a highly significant impact, while the effects of the fertilization strategies 60:0, 120:0, 200:0, and 240:0 were not significant (figure 6), and other strategies significantly affected gene expression. It is important to note that under a p-value threshold of 0.05, only the

interaction term of gene St.CWP with all the fertilization strategies reached the level of significance. Additionally, the interaction of genes St.CHI and St.TRDX with all the other fertilization strategies except the 200:0 fertilization strategy showed significance. This phenomenon did not occur in the interaction of other genes with fertilization strategies. Further investigation of the gene St.CWP shows that the coefficients for its interaction with all fertilization strategies involving a non-zero second application are positive. This suggests that these interactions have a positive effect on the dependent variable, meaning that the expression level of this gene increases when the second application of fertilizer is non-zero. These results highlight the potential effects of specific fertilization strategies on regulating the expression of this gene.

The newly generated ANOVA table further confirmed that genes, the combination of location and year, fertilization strategies, and sampling time significantly influence gene expression levels (figure 7). Particularly noteworthy is that the interactions between genes and sampling time, as well as between genes and fertilization strategies, have a significant impact on gene expression levels, highlighting the importance of considering such interactions in the experimental design phase.

fertilization_Strategies60.0	-380.74	379.11	-1.004	0.315234
fertilization_Strategies106.0	-1709.67	499.52	-3.423	0.000621 ***
fertilization_Strategies120.0	51.79	457.59	0.113	0.909889
fertilization_Strategies180.0	-1352.69	340.01	-3.978	6.96e-05 ***
fertilization_Strategies200.0	807.03	691.72	1.167	0.243343
fertilization_Strategies240.0	-278.48	469.46	-0.593	0.553064
fertilization_Strategies60.60	-2692.89	523.14	-5.148	2.66e-07 ***
fertilization_Strategies60.120	-2718.71	473.71	-5.739	9.63e-09 ***
fertilization_Strategies0.180	-3968.33	1531.60	-2.591	0.009577 **
fertilization_Strategies60.180	-2826.65	495.91	-5.700	1.21e-08 ***

Figure 6: The impact of fertilization strategies in the model

Analysis of Variance Table

Response: expression

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
gene	62	5.1907e+10	837204833	213.4574	< 2.2e-16 ***
syc	10	2.2520e+09	225195729	57.4169	< 2.2e-16 ***
fertilization_Strategies	9	6.6568e+08	73964939	18.8584	< 2.2e-16 ***
DAP_for_leaf_sampling	1	1.9816e+08	198159310	50.5236	1.215e-12 ***
gene:DAP_for_leaf_sampling	62	1.9114e+09	30828314	7.8601	< 2.2e-16 ***
gene:fertilization_Strategies	620	2.2470e+10	36242233	9.2405	< 2.2e-16 ***
Residuals	20844	8.1753e+10	3922118		

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

Figure 7: ANOVA table of model 2

Residuals vs Fitted and QQ plot

To strengthen the statistical foundation of the model, a logarithmic transformation was applied to the original data. The primary purpose of this transformation was to reduce the skewness of the data, thus bringing the distribution of residuals closer to a normal distribution, which is one of the key assumptions relied upon by most linear regression models. After the logarithmic transformation, residual vs. fitted value plots and QQ plots were drawn.

By evaluating the effects of the transformation, the heavy-tailed nature displayed by the QQ plot and the outliers observed in the residual plot complement each other, both suggesting the possible presence of anomalies or extreme values in the data (figure 8). However, the residual plot did not reveal any significant heteroscedasticity or non-linear trends, implying that although the data may not strictly adhere to a normal distribution, the use of a linear model is still an appropriate choice.

In the scatter plot of residuals versus fitted values, different genes are categorized by color, where each color represents a gene (figure 9). Points of different colors (i.e., different genes) are concentrated within specific ranges of fitted values. For example, most black points are primarily located on the right side of the plot, corresponding to fitted values between 6 and 10, while most blue points are on the left side, corresponding to fitted values between 0 and 2. This indicates that under certain environmental or experimental conditions, some genes exhibit higher expression levels (higher fitted values), while others show lower expression levels (lower fitted values). Moreover, these variations further demonstrate significant differences in the expression

levels of different genes under specific experimental conditions.

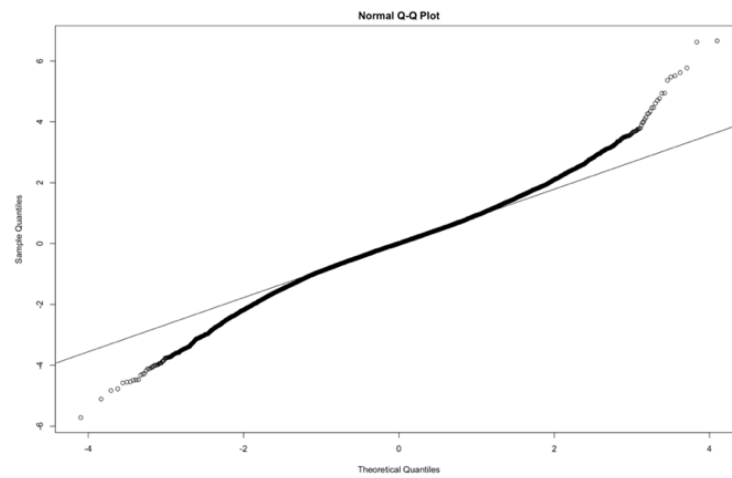


Figure 8: QQ plot of the model

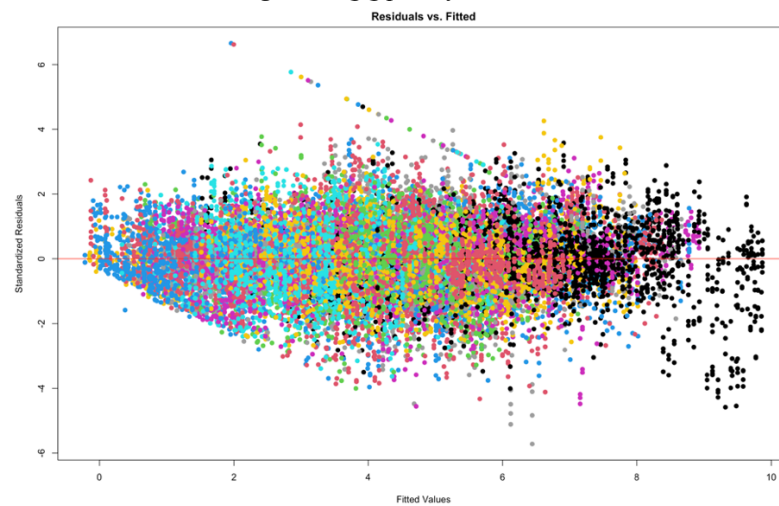


Figure 9: Residuals vs. Fitted

Hierarchical Clustering

The model residuals were clustered to form a dendrogram, full dendrogram is presented in the appendix. In Model 2 results, the direct impacts of fertilization strategies 60.0, 120.0, 200.0, and 240.0 are not significant, however, the interactions of certain genes with these fertilization strategies are significant. Further analysis reveals that among the interactions with the 60:0 fertilization strategy, only St.CHI, St.Clch, St.CWP, and St.TRDX show significant interactions; notably, the interaction coefficients for St.CHI and St.ClCh are positive, and these two genes are grouped together in a small cluster at

the bottom of the dendrogram (Figure 12). Similarly, St.CWP and St.TRDX are also categorized together in the same small cluster at the bottom of the dendrogram. When the number of clusters is set to 7, these four genes will be grouped into the same small cluster. This phenomenon is also observed in the interactions of genes with fertilization strategies 120:0 and 240:0. Analysis of the genes significantly interacting with the 120:0 and 240:0 fertilization strategies reveals that some of these genes are grouped into the same small cluster at the bottom of the clustering tree. For example, genes St.AAT1 and St.Apase, which significantly interact with the 240:0 fertilization strategy, have positive coefficients and are classified into the same small cluster (Figure 13). Similarly, genes St.DUF506A and St.Unk5 (Figure 11), St.GluDC, St.MSF5B and St.Pyrk (Figure 10), St.CWP, St.GR3 and St.TRDX also exhibit the same clustering pattern.

These genes exhibited consistent responses to environmental changes, with their residuals also being grouped into the same small cluster at the bottom of the dendrogram. This further suggests that these genes have similar response patterns to environmental variables, which typically implies that they may have related functions or participate in similar biological processes. Such findings help to deepen the understanding of their roles in cellular mechanisms and physiological responses.

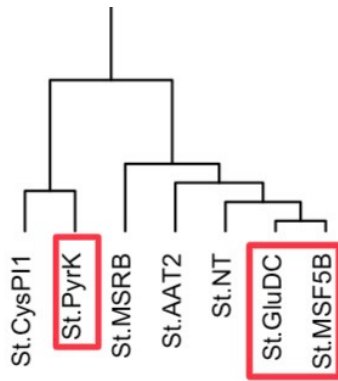


Figure 10: Small cluster of genes *St. GluDC*, *St.MSF5B* and *St.PyrK*

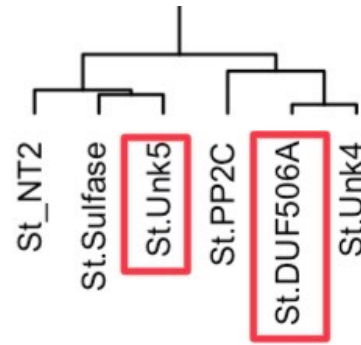


Figure 11: Small cluster of genes *St.DUF506A* and *St.Unk5*

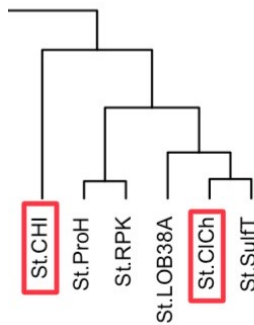


Figure 12: Small cluster of genes *St.CHI* and *St.ClCh*



Figure 13: Small cluster of genes *St.AAT1* and *St.Apase*

Conclusion

In this study, various factors affecting gene expression levels were analyzed in depth using multiple linear regression models. Preliminary statistical tests, including QQ plots, plots of residuals and fitted values, verified the applicability of the model and the normal distribution of the residuals, ensuring the accuracy of the subsequent analysis. In addition, by clustering the model residuals, this study successfully revealed potential population patterns in gene expression. The similar response patterns of genes under specific environmental conditions were indicated by the analysis of small clusters at the bottom of the clustered dendrogram, which provided new insights into the environmental sensitivity of gene expression.

Overall, the planting environment, fertilization strategies, sampling days, and their

interactions (gene and fertilization strategies, gene and sampling days), significantly affect the variation in gene expression levels. In this model, the coefficient for time (DAP_for_leaf_sampling) is positive, but the coefficients for the interaction between time and individual genes are negative. This indicates that although there is a general trend of increasing gene expression levels over time when no fertilization is applied, this growth trend does not apply to all genes. Specifically, the expression levels of most genes actually decrease over time. From the analysis of planting regions and potato varieties, although all combinations positively influence gene expression, the Shepody variety planted in the Fredericton PK2014 area shows the most significant positive impact. Following closely is the Atlantic variety planted in the Fredericton GE2012 area, which also exhibits a strong positive effect.

Further investigation of fertilization strategies reveals that in scenarios of a single application, fertilization amounts of 106 and 180 significantly impact gene expression levels, with all genes except St.ClCh showing positive coefficients in interaction with these fertilization strategies. This implies that if only one fertilization can be applied, keeping the total amount at 106 or 180 might maximize growth indicators in potatoes. If applying fertilization twice, the first application should be kept at 60, with total amounts controlled at 120, 180, or 240, to maximize positive expression across all genes. Notably, when the fertilization strategies are set at 60:60 and 60:180, the interaction coefficients for all genes, including St.ClCh, are positive, indicating that these two fertilization methods should be prioritized in the potato cultivation process. From another perspective, by comparing the effects of single and multiple

fertilizations, this study also provides some practical recommendations for potato fertilization strategies. St.CWP, which stands for Cell Wall Protein, plays a crucial role in plant growth and development (Parenteau 2020). Research indicates that St.CWP is not only involved in the formation of cell walls and the elongation of cells but also significantly impacts resilience to adverse conditions. Specifically, this gene inhibits cell elongation, thereby reducing stem internode length and plant height, which enhances the plant's lodging resistance. Additionally, it promotes the synthesis of cellulose and the thickening of secondary walls. The increased thickness of cell walls and higher cellulose content further enhance the plant's resistance to diseases and pests, potentially leading to increased seed and biomass yields (Fan 2018). This study found that although the interaction coefficient of this gene with the fertilization strategy of 120:0 is negative, it is positive with the 60:60 strategy. This indicates that, given the same total amount of fertilization, a second application significantly boosts the expression level of this gene. A similar effect was observed in other genes such as St.AOX, St.CLH, St_NT2, St.FT, St.LIP, and St.MtN21. These genes are Primary amine oxidase, Chlorophyllase, Low-affinity nitrate transporter, Flowering locus T protein, Chloroplast lipocalin, and Nodulin MtN21 family protein. The increased expression levels of these genes play a positive role in the growth process of potatoes (Parenteau 2020). In these cases, interaction coefficients with strategies involving a nonzero second fertilization are positive, while those with a zero second application are negative, demonstrating that compared to a single application, a second fertilization positively influences the growth and health of potatoes. Therefore, the

fertilization strategy most recommended by this study is 60:60, followed by 60:180.

Both of these fertilization methods can significantly enhance the gene expression levels in potatoes. Meanwhile, the use of a 200:0 fertilization strategy is not recommended, as this approach leads to a significant decrease in the expression of most genes.

To further investigate, these methods can be used to explore the relationships between fertilization methods, planting environments, and potato varieties. Instead of simply combining planting regions and potato varieties, a more comprehensive model could be fitted to determine the most suitable planting regions and fertilization methods for each potato variety.

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[Learning%3A-with-in-R-Witten/b5e5a7eee59dd740897c0c3d1ada96c2e2a7e0a7](https://www.semanticscholar.org/paper/An-Introduction-to-Statistical-Learning%3A-with-in-R-Witten/b5e5a7eee59dd740897c0c3d1ada96c2e2a7e0a7)

I would like to express my profound gratitude to Professor Gu Hong for her guidance and support throughout the year on the honors project and this thesis.

Appendix

R code

Since some of the data cleaning was not done in R Studio, the data was imported directly from the pre-processed ‘data_clean’ dataset. Additionally, this code can also be applied to other response variables with only minor modifications required.

Therefore, the detailed steps for fitting model 1 are not shown below. If necessary, only the code for fitting model 2 needs to be adjusted.

1. Convert data formats and data cleaning:

```
```{r}
library(tidyr)
```



```

library(dplyr)
data <- read.csv('~/Desktop/data_clean.csv', header =
 TRUE)
gene_cols <- grep("^St[. _]", names(data), value = TRUE)

data_long <- pivot_longer(data,
 cols = all_of(gene_cols),
 names_to = "gene",
 values_to = "expression")

data_long <- data_long %>%
 select(gene, everything()) %>%
 arrange(gene, sample.ID)

data_long <- data_long %>%
 select(gene, expression, everything())

#Export the data converted to long format
write.csv(data_long,
 "/Users/linxiyou/Documents/datalong.csv", row.names =
 FALSE)
...

```

## 2. Preprocess variables and build the model:

```

```{r}
# Import the data converted to long format
data <-
  read.csv("/Users/linxiyou/Documents/datalong.csv",
  header = TRUE)

# Preprocess each variable
data$syc <- paste(data$Site.year, data$cultivar, sep =
  "_")
data$syc <- as.factor(data$syc)
data$first <- as.factor(data$N.source.at.planting.kg.ha)
data$second <- as.factor(data$N.source.2nd.appl..kg.ha)
data$fertilization_Strategies <- interaction(data$first,
  data$second)
data$DAP_for_leaf_sampling <-
  ifelse(data$DAP.for.leaf.sampling < 50, "0", "1")
data$DAP_for_leaf_sampling <-
  as.factor(data$DAP_for_leaf_sampling)

```

```

data$gene <- as.factor(data$gene)
data$trt <- as.factor(data$trt..)
data$block <- as.factor(data$block)

# Since the interaction between trt and block was not
  significant, the new model omitted these two
  variables.
model <- lm(expression ~ gene + syc +
  fertilization_Strategies + DAP_for_leaf_sampling +
    gene * DAP_for_leaf_sampling + gene *
  fertilization_Strategies, data = data)

# Due to the length of the output, the model fitting
  results were saved into a txt document.
sink("model.txt")
print(model)
sink()
#create the ANOVA table of the model 1
model_anova <- anova(model)
print(model_anova)
` ``

```

3. Create the Residuals vs Fitted plot and QQ plot

```

` `` {r}
# Perform logarithmic transformation on the original data
data$expression_log <- log(data$expression)
model_log <- lm(expression_log ~ gene + syc +
  fertilization_Strategies + DAP_for_leaf_sampling
    +
  gene*DAP_for_leaf_sampling+gene*fertilization_Strategies,
  data = data)
model_log_anova<-anova(model_log)
print(model_log_anova)

#plot of the residual
par(mar=c(4, 4, 2, 2))
plot(resid(model_log))

#Residuals vs Fitted plot and Use different colors for the
  scatter points to distinguish between genes.
plot(fitted(model_log), resid(model_log), col=data$gene,
  main="Residuals vs. Fitted", ylab="Standardized
  Residuals", xlab="Fitted Values", pch=19)

```

```

abline(h=0, col="red")

#qq plot
qqnorm(resid(model_log))
qqline(resid(model_log))
` ``

4. Cluster
library(pheatmap)
library(reshape2)

gene_counts <- table(data$gene, data$DAP_for_leaf_sampling)
residuals_data <- resid(model)
n <- nrow(gene_counts)
time_points <- 2
summary(residuals_data)

#Add the residual of the model to the data
data$residuals = residuals_data
aggregate_residuals <- aggregate(residuals ~ gene +
DAP_for_leaf_sampling, data, mean)

#Calculate distance between genes
residuals_wide <- dcast(aggregate_residuals, gene ~
DAP_for_leaf_sampling, value.var = "residuals")

residuals_dist <- dist(as.matrix(residuals_wide[,-1]))
hc <- hclust(residuals_dist)
plot(hc, hang=-1)

#Assume that the number of clusters is set to 3 and view
the output
k <- 3
clusters <- cutree(hc, k)
residuals_wide$cluster <- clusters
cat("Number of genes in each cluster:\n")
print(table(residuals_wide$cluster))
cat("\nGenes in each cluster:\n")
for (i in 1:k) {
  cat(sprintf("Cluster %d:\n", i))
  print(residuals_wide$gene[residuals_wide$cluster == i])
}
plot(hc, labels=residuals_wide$gene, cex=0.6, hang=-1,
main="Cluster Dendrogram")

```

Output

1. The full output of the model 2

Call:
`lm(formula = expression ~ gene + syc + fertilization_Strategies + DAP_for_leaf_sampling + gene * DAP_for_leaf_sampling + gene * Fertilization_Strategies, data = data)`

Residuals:

Min	1Q	Median	3Q	Max
-29277	-266	-33	160	70713

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2632.31	287.81	9.146	< 2e-16 ***
geneSt_Nt2	-2659.49	398.45	-6.675	2.53e-11 ***
geneSt_PP7A	-3217.74	398.45	-8.076	7.03e-16 ***
geneSt_PP7B	-3221.76	398.45	-8.086	6.48e-16 ***
geneSt_AAT1	-2760.96	398.45	-6.929	4.34e-12 ***
geneSt_AAT2	-3187.76	398.45	-8.000	1.30e-15 ***
geneSt_AOX	-1346.90	398.45	-3.380	0.000725 ***
geneSt_Apase	-2579.88	398.45	-6.475	9.68e-11 ***
geneSt_ATrfA	-3211.62	398.45	-8.060	7.97e-16 ***
geneSt_ATrfB	-2923.62	398.45	-7.338	2.25e-13 ***
geneSt_CatT	-3077.47	398.45	-7.724	1.18e-14 ***
geneSt_CatTR	-1978.99	398.45	-4.967	6.80e-07 ***
geneSt_CGL	-3067.09	398.45	-7.698	1.44e-14 ***
geneSt_CHI	-1340.83	398.45	-3.365	0.000766 ***
geneSt_ClCh	-1383.16	398.45	-3.471	0.000519 ***
geneSt_CLH	-2946.69	398.45	-7.395	1.46e-13 ***
geneSt_CWP	9623.29	398.45	24.152	< 2e-16 ***
geneSt_CysP11	-2995.67	398.45	-7.518	5.75e-14 ***
geneSt_CysT	-3191.36	398.45	-8.009	1.21e-15 ***
geneSt_DUF506A	-2408.51	398.45	-6.045	1.52e-09 ***
geneSt_DUF506B	-3199.20	398.45	-8.029	1.03e-15 ***
geneSt_EPI	-3154.62	398.45	-7.917	2.54e-15 ***
geneSt_FF	-2889.66	398.45	-7.252	4.23e-13 ***
geneSt_GluAse	-3081.44	398.45	-7.734	1.00e-14 ***
geneSt_GluDC	-2862.00	398.45	-7.183	7.03e-13 ***
geneSt_GR3	-2589.39	398.45	-6.499	8.27e-11 ***
geneSt_GST	-2923.87	398.45	-7.338	2.24e-13 ***
geneSt_InosD	-2660.77	398.45	-6.678	2.48e-11 ***
geneSt_Kinase	-3190.59	398.45	-8.008	1.22e-15 ***
geneSt_LIP	-2718.69	398.45	-6.823	9.12e-12 ***
geneSt_LOB38A	-3225.09	398.45	-8.094	6.05e-16 ***
geneSt_LOB38B	-3180.12	398.45	-7.981	1.52e-15 ***
geneSt_MIP	-2868.24	398.45	-7.199	6.27e-13 ***
geneSt_MSFA	-2594.09	398.45	-6.510	7.64e-11 ***
geneSt_MSFSB	-3087.17	398.45	-7.748	9.72e-15 ***
geneSt_MSRR	-3172.11	398.45	-7.961	1.78e-15 ***
geneSt_MN21	-2890.33	398.45	-7.254	4.17e-13 ***
geneSt_Nod	-3156.44	398.45	-7.922	2.44e-15 ***
geneSt_P109A	-3180.85	398.45	-7.983	1.49e-15 ***
geneSt_P109B	-3223.44	398.45	-8.050	6.26e-16 ***
geneSt_PBenzR	-2980.68	398.45	-7.481	7.65e-14 ***
geneSt_PDX	-3154.50	398.45	-7.917	2.54e-15 ***
geneSt_PEPT	-3224.31	398.45	-8.092	6.15e-16 ***
geneSt_PLD	-3227.87	398.45	-8.101	5.71e-16 ***
geneSt_PolyAP	-3187.32	398.45	-7.999	1.31e-15 ***
geneSt_PP2C	-3201.24	398.45	-8.034	9.86e-16 ***
geneSt_ProD	-2958.64	398.45	-7.425	1.16e-13 ***
geneSt_PyrK	-3218.95	398.45	-8.079	6.86e-16 ***
geneSt_RPK	-2602.22	398.45	-6.531	6.67e-11 ***
geneSt_Sulfase	-3225.98	398.45	-8.096	5.94e-16 ***
geneSt_SulFT	-3023.03	398.45	-7.587	3.40e-14 ***
geneSt_SulFT2A	-2990.55	398.45	-7.506	6.34e-14 ***
geneSt_SulFT2B	-3148.80	398.45	-7.903	2.85e-15 ***
geneSt_SulFT2C	-3210.23	398.45	-8.057	8.20e-16 ***
geneSt_TRDX	-3198.41	398.45	-8.027	1.04e-15 ***
geneSt_UBIE	-2146.84	398.45	-5.388	7.19e-08 ***
geneSt_Unk1	-2165.79	398.45	-5.436	5.52e-08 ***
geneSt_Unk2	-3132.75	398.45	-7.862	3.93e-15 ***
geneSt_Unk3	-3026.98	398.45	-7.597	3.15e-14 ***
geneSt_Unk4	-3227.15	398.45	-8.099	5.80e-16 ***
geneSt_Unk5	-3195.07	398.45	-8.019	1.12e-15 ***
geneSt_Xyl	-2830.87	398.45	-7.105	1.24e-12 ***
sycFredericton GE2012_Atlantic	-2965.03	398.45	-7.441	1.03e-13 ***
sycFredericton GE2012_Russet Burbank	1163.15	75.63	15.379	< 2e-16 ***
sycFredericton GE2012_Shepody	846.37	75.63	11.191	< 2e-16 ***
sycFredericton MAT2014_Jemseg	888.53	75.70	11.737	< 2e-16 ***
sycFredericton MAT2014_Russet Burbank	712.56	94.15	7.568	3.93e-14 ***
sycFredericton MAT2014_Shepody	675.72	94.15	7.177	7.36e-13 ***
sycFredericton PK2014_Russet Burbank	814.23	94.15	8.648	< 2e-16 ***
sycFredericton PK2014_Shepody	875.23	112.45	7.787	7.38e-15 ***
sycOff-Carberry 2014_Russet Burbank	1269.15	133.13	9.533	< 2e-16 ***
sycOn-Carberry 2014_Russet Burbank	320.60	79.17	4.050	5.13e-05 ***

Figure 14: Summary of the model 2 (1)

sycPzribonka 2014_Classic Russet	426.34	80.03	5.327	1.01e-07 ***	geneSt_LOB38B:DAP_for_leaf_sampling1	-1137.82	335.94	-3.387	0.000708 ***
Fertilization_Strategies60.0	-380.74	379.11	-1.004	0.315234	geneSt_MIP:DAP_for_leaf_sampling1	-1130.02	335.94	-3.364	0.000770 ***
Fertilization_Strategies106.0	-1789.67	499.52	-3.423	0.000621 ***	geneSt_MSFA:DAP_for_leaf_sampling1	-1752.11	335.94	-5.216	1.85e-07 ***
Fertilization_Strategies120.0	51.79	457.59	0.113	0.909889	geneSt_MSFSB:DAP_for_leaf_sampling1	-1267.56	335.94	-3.773	0.000162 ***
Fertilization_Strategies180.0	-1352.69	340.01	-3.978	6.96e-05 ***	geneSt_MSRR:DAP_for_leaf_sampling1	-1178.19	335.94	-3.507	0.000454 ***
Fertilization_Strategies200.0	807.03	691.72	1.167	0.243343	geneSt_MN21:DAP_for_leaf_sampling1	-1065.78	335.94	-3.173	0.001513 ***
Fertilization_Strategies240.0	-278.48	469.46	-0.593	0.553064	geneSt_Nod:DAP_for_leaf_sampling1	-1125.41	335.94	-3.350	0.000809 ***
Fertilization_Strategies60.120	-2692.89	523.14	-5.148	2.66e-07 ***	geneSt_NT:DAP_for_leaf_sampling1	-1154.47	335.94	-3.437	0.000590 ***
Fertilization_Strategies60.180	-2718.71	473.71	-5.739	9.63e-09 ***	geneSt_P109A:DAP_for_leaf_sampling1	-1156.13	335.94	-3.441	0.000580 ***
Fertilization_Strategies60.180	-3968.33	1531.60	-2.591	0.009577 ***	geneSt_PBenzR:DAP_for_leaf_sampling1	-1408.39	335.94	-4.192	2.77e-05 ***
DAP_for_leaf_sampling1	-2826.65	495.91	-5.700	1.21e-08 ***	geneSt_PDX:DAP_for_leaf_sampling1	-1160.01	335.94	-3.453	0.000555 ***
geneSt_Nt2:DAP_for_leaf_sampling1	997.98	238.01	4.193	2.76e-05 ***	geneSt_PEPT:DAP_for_leaf_sampling1	-1157.52	335.94	-3.446	0.000571 ***
geneSt_PP7A:DAP_for_leaf_sampling1	-1111.34	335.94	-3.308	0.000941 ***	geneSt_PLD:DAP_for_leaf_sampling1	-1157.51	335.94	-3.446	0.000571 ***
geneSt_PP7B:DAP_for_leaf_sampling1	-1147.00	335.94	-3.414	0.000641 ***	geneSt_PolyAP:DAP_for_leaf_sampling1	-1135.39	335.94	-3.380	0.000727 ***
geneSt_AAT1:DAP_for_leaf_sampling1	-1154.43	335.94	-3.436	0.000591 ***	geneSt_PP2C:DAP_for_leaf_sampling1	-1165.41	335.94	-3.469	0.000523 ***
geneSt_AAT2:DAP_for_leaf_sampling1	-1367.50	335.94	-4.071	4.70e-05 ***	geneSt_ProD:DAP_for_leaf_sampling1	-1089.47	335.94	-3.243	0.001184 ***
geneSt_AOX:DAP_for_leaf_sampling1	-1185.22	335.94	-3.528	0.000419 ***	geneSt_PyrK:DAP_for_leaf_sampling1	-1162.46	335.94	-3.460	0.000541 ***
geneSt_Apase:DAP_for_leaf_sampling1	-1172.81	335.94	-3.491	0.000482 ***	geneSt_Sulfase:DAP_for_leaf_sampling1	-1143.66	335.94	-3.404	0.000664 ***
geneSt_ATrfA:DAP_for_leaf_sampling1	-1869.50	335.94	-5.565	2.65e-08 ***	geneSt_SulFT:DAP_for_leaf_sampling1	-1156.99	335.94	-3.444	0.000574 ***
geneSt_ATrfB:DAP_for_leaf_sampling1	-1154.89	335.94	-3.438	0.000588 ***	geneSt_SulFT2A:DAP_for_leaf_sampling1	-1168.86	335.94	-3.479	0.000504 ***
geneSt_CatT:DAP_for_leaf_sampling1	-1183.57	335.94	-3.523	0.000427 ***	geneSt_SulFT2B:DAP_for_leaf_sampling1	-1169.67	335.94	-3.482	0.000499 ***
geneSt_CatTR:DAP_for_leaf_sampling1	-1123.88	335.94	-3.345	0.000823 ***	geneSt_SulFT2C:DAP_for_leaf_sampling1	-1163.07	335.94	-3.462	0.000537 ***
geneSt_CGL:DAP_for_leaf_sampling1	-1364.76	335.94	-4.063	4.87e-05 ***	geneSt_TRDX:DAP_for_leaf_sampling1	-1142.60	335.94	-3.401	0.000672 ***
geneSt_CHI:DAP_for_leaf_sampling1	-1193.02	335.94	-3.551	0.000384 ***	geneSt_UBIE:DAP_for_leaf_sampling1	-2100.27	335.94	-6.252	4.13e-10 ***
geneSt_ClCh:DAP_for_leaf_sampling1	-2858.22	335.94	-8.508	< 2e-16 ***	geneSt_Unk1:DAP_for_leaf_sampling1	-902.81	335.94	-2.685	0.007258 ***
geneSt_CLH:DAP_for_leaf_sampling1	1371.75	335.94	4.083	4.46e-05 ***	geneSt_Unk2:DAP_for_leaf_sampling1	-1232.41	335.94	-3.669	0.000245 ***
geneSt_CWP:DAP_for_leaf_sampling1	-1183.70	335.94	-3.524	0.000427 ***	geneSt_Unk3:DAP_for_leaf_sampling1	-1235.93	335.94	-3.679	0.000235 ***
geneSt_CysP11:DAP_for_leaf_sampling1	-1453.92	335.94	-4.328	1.51e-05 ***	geneSt_Unk4:DAP_for_leaf_sampling1	-1156.97	335.94	-3.444	0.000574 ***
geneSt_CysT:DAP_for_leaf_sampling1	-1367.22	335.94	-4.070	4.72e-05 ***	geneSt_Unk5:DAP_for_leaf_sampling1	-1189.89	335.94	-3.542	0.000398 ***
geneSt_DUF506A:DAP_for_leaf_sampling1	-1163.86	335.94	-3.464	0.000532 ***	geneSt_Xyl:DAP_for_leaf_sampling1	-1199.59	335.94	-3.571	0.000357 ***
geneSt_DUF506B:DAP_for_leaf_sampling1	-2126.44	335.94	-6.330	2.50e-10 ***	geneSt_FF:DAP_for_leaf_sampling1	-1249.44	335.94	-3.719	0.000200 ***
geneSt_EPI:DAP_for_leaf_sampling1	-1184.21	335.94	-3.525	0.000424 ***	geneSt_GluAse:DAP_for_leaf_sampling1	-1133.67	335.94	-3.375	0.000740 ***
geneSt_FF:DAP_for_leaf_sampling1	-1133.67	335.94	-3.375	0.000740 ***	geneSt_GluDC:DAP_for_leaf_sampling1	-1102.80	335.94	-3.283	0.001030 ***
geneSt_GluAse:DAP_for_leaf_sampling1	-1138.09	335.94	-3.388	0.000706 ***	geneSt_GR3:DAP_for_leaf_sampling1	-1389.87	335.94	-4.137	3.53e-05 ***
geneSt_GluDC:DAP_for_leaf_sampling1	-1149.86	335.94	-3.443	0.000621 ***	geneSt_GST:DAP_for_leaf_sampling1	-1930.14	335.94	-5.745	9.28e-09 ***
geneSt_GR3:DAP_for_leaf_sampling1	-1389.87	335.94	-4.137	3.53e-05 ***	geneSt_InosD:DAP_for_leaf_sampling1	-1181.37	335.94	-3.517	0.000438 ***
geneSt_GST:DAP_for_leaf_sampling1	-1930.14	335.94	-5.745	9.28e-09 ***	geneSt_Kinase:DAP_for_leaf_sampling1	-1683.84	335.94	-5.012	5.42e-07 ***
geneSt_InosD:DAP_for_leaf_sampling1	-1181.37	335.94	-3.517	0.000438 ***	geneSt_LIP:DAP_for_leaf_sampling1	-1187.34	335.94	-3.534	0.000410 ***
geneSt_Kinase:DAP_for_leaf_sampling1	-1683.84	335.94	-5.012	5.42e-07 ***	geneSt_LOB38A:DAP_for_leaf_sampling1	-1058.67	335.94	-3.151	0.001627 ***
geneSt_LIP:DAP_for_leaf_sampling1	-1187.34	335.94	-3.534	0.000410 ***	geneSt_LOB38B:DAP_for_leaf_sampling1	-1157.68	335.94	-3.446	0.000570 ***
geneSt_LOB38A:DAP_for_leaf_sampling1	-1058.67	335.94	-3.151	0.001627 ***					

Figure 15: Summary of the model 2 (2)

geneSt.CatTR:fertilization_Strategies60.0	131.85	535.51	0.246	0.805518	geneSt.Sulfase:fertilization_Strategies60.0	329.52	535.51	0.615	0.533336
geneSt.CGI:fertilization_Strategies60.0	481.34	535.51	0.899	0.368739	geneSt.SulfT:fertilization_Strategies60.0	547.61	535.51	1.023	0.306502
geneSt.CHI:fertilization_Strategies60.0	1965.75	535.51	3.671	0.000242	geneSt.SulfT2A:fertilization_Strategies60.0	510.17	535.51	0.953	0.340755
geneSt.CLCh:fertilization_Strategies60.0	3347.99	535.51	6.252	4.12e-10	geneSt.SulfT2B:fertilization_Strategies60.0	428.06	535.51	0.799	0.424087
geneSt.CLH:fertilization_Strategies60.0	331.04	535.51	0.618	0.536464	geneSt.SulfT2C:fertilization_Strategies60.0	400.78	535.51	0.748	0.454217
geneSt.CWP:fertilization_Strategies60.0	-4957.76	535.51	-9.258	< 2e-16	geneSt.TRDx:fertilization_Strategies60.0	1139.38	535.51	2.128	0.033375 *
geneSt.CysPII:fertilization_Strategies60.0	533.89	535.51	0.997	0.318781	geneSt.URIE:fertilization_Strategies60.0	298.72	535.51	0.558	0.576966
geneSt.CysT:fertilization_Strategies60.0	430.26	535.51	0.803	0.421712	geneSt.Unk1:fertilization_Strategies60.0	483.35	535.51	0.903	0.366742
geneSt.DUF506A:fertilization_Strategies60.0	864.77	535.51	1.615	0.106355	geneSt.Unk2:fertilization_Strategies60.0	510.62	535.51	0.954	0.340330
geneSt.DUF506B:fertilization_Strategies60.0	433.50	535.51	0.810	0.418224	geneSt.Unk3:fertilization_Strategies60.0	422.39	535.51	0.789	0.430253
geneSt.EPI:fertilization_Strategies60.0	412.40	535.51	0.770	0.441245	geneSt.Unk4:fertilization_Strategies60.0	435.27	535.51	0.813	0.416326
geneSt.FT:fertilization_Strategies60.0	338.61	535.51	0.632	0.527190	geneSt.Unk5:fertilization_Strategies60.0	726.60	535.51	1.357	0.174840
geneSt.GluAse:fertilization_Strategies60.0	443.05	535.51	0.827	0.408050	geneSt.Xyl:fertilization_Strategies60.0	594.38	535.51	1.110	0.267033
geneSt.GluDC:fertilization_Strategies60.0	714.48	535.51	1.334	0.182148	geneSt.NT2:fertilization_Strategies106.0	1793.74	704.89	2.545	0.010944 *
geneSt.GR3:fertilization_Strategies60.0	963.09	535.51	1.798	0.072115	geneSt.PP7A:fertilization_Strategies106.0	1730.49	704.89	2.455	0.014097 *
geneSt.GST:fertilization_Strategies60.0	265.92	535.51	0.497	0.619486	geneSt.PP7B:fertilization_Strategies106.0	1734.74	704.89	2.461	0.013862 *
geneSt.InoS:fertilization_Strategies60.0	821.04	535.51	1.533	0.125237	geneSt.AAT1:fertilization_Strategies106.0	1746.65	704.89	2.478	0.013223 *
geneSt.Kinase:fertilization_Strategies60.0	437.71	535.51	0.817	0.413717	geneSt.AAT2:fertilization_Strategies106.0	1739.79	704.89	2.468	0.013588 *
geneSt.LIP:fertilization_Strategies60.0	279.73	535.51	0.522	0.601422	geneSt.AOX:fertilization_Strategies106.0	1186.38	704.89	1.683	0.092377 *
geneSt.LOB38A:fertilization_Strategies60.0	423.38	535.51	0.791	0.429170	geneSt.Apase:fertilization_Strategies106.0	1810.04	704.89	2.568	0.010240 *
geneSt.LOB38B:fertilization_Strategies60.0	440.58	535.51	0.823	0.410668	geneSt.ATrfa:fertilization_Strategies106.0	1731.73	704.89	2.457	0.014028 *
geneSt.MIP:fertilization_Strategies60.0	429.23	535.51	0.802	0.422824	geneSt.ATrfb:fertilization_Strategies106.0	1910.75	704.89	2.711	0.006719 **
geneSt.MSF5A:fertilization_Strategies60.0	934.02	535.51	1.744	0.081142	geneSt.CatT:fertilization_Strategies106.0	1639.21	704.89	2.325	0.020056 *
geneSt.MSF5B:fertilization_Strategies60.0	554.81	535.51	1.036	0.300189	geneSt.CatTR:fertilization_Strategies106.0	1937.19	704.89	2.748	0.005997 **
geneSt.MSR8:fertilization_Strategies60.0	435.41	535.51	0.813	0.416179	geneSt.CGI:fertilization_Strategies106.0	1632.31	704.89	2.316	0.020584 *
geneSt.MnN21:fertilization_Strategies60.0	334.83	535.51	0.625	0.531802	geneSt.CHI:fertilization_Strategies106.0	1712.34	704.89	2.429	0.015139 **
geneSt.Nod:fertilization_Strategies60.0	367.66	535.51	0.687	0.492363	geneSt.CLCh:fertilization_Strategies106.0	-2447.06	704.89	-3.472	0.000518 ***
geneSt.NT:fertilization_Strategies60.0	432.04	535.51	0.807	0.419801	geneSt.CLH:fertilization_Strategies106.0	1639.18	704.89	2.325	0.020058 *
geneSt.P109A:fertilization_Strategies60.0	1744.06	535.51	3.192	0.028433	geneSt.CWP:fertilization_Strategies106.0	10551.88	704.89	14.969	< 2e-16 ***
geneSt.PBnzR:fertilization_Strategies60.0	651.78	535.51	1.217	0.223564	geneSt.CysPII:fertilization_Strategies106.0	1746.75	704.89	2.478	0.013218 *
geneSt.PDX:fertilization_Strategies60.0	446.65	535.51	0.834	0.404249	geneSt.CysT:fertilization_Strategies106.0	1736.00	704.89	2.463	0.013794 *
geneSt.PEPT:fertilization_Strategies60.0	423.08	535.51	0.790	0.429499	geneSt.DUF506A:fertilization_Strategies106.0	1941.80	704.89	2.755	0.005878 **
geneSt.PLD:fertilization_Strategies60.0	420.20	535.51	0.785	0.432649	geneSt.DUF506B:fertilization_Strategies106.0	1739.51	704.89	2.468	0.013663 *
geneSt.PolyAP:fertilization_Strategies60.0	382.86	535.51	0.715	0.474645	geneSt.EPI:fertilization_Strategies106.0	1729.15	704.89	2.453	0.014172 *
geneSt.PP2C:fertilization_Strategies60.0	420.52	535.51	0.785	0.432304	geneSt.FT:fertilization_Strategies106.0	1718.31	704.89	2.438	0.014789 *
geneSt.Prod:fertilization_Strategies60.0	232.62	535.51	0.434	0.664003	geneSt.GluAse:fertilization_Strategies106.0	1771.43	704.89	2.513	0.011976 *
geneSt.ProH:fertilization_Strategies60.0	425.37	535.51	0.794	0.427010	geneSt.GluDC:fertilization_Strategies106.0	1664.01	704.89	2.361	0.018251 **
geneSt.PyrK:fertilization_Strategies60.0	585.48	535.51	1.093	0.274264	geneSt.GR3:fertilization_Strategies106.0	1897.01	704.89	2.691	0.007125 **
geneSt.RPK:fertilization_Strategies60.0	417.46	535.51	0.780	0.436568	geneSt.GST:fertilization_Strategies106.0	1737.10	704.89	2.459	0.013953 **

Figure 15: Summary of the model 2 (3)

geneSt.InoS:fertilization_Strategies106.0	2099.37	704.89	2.978	0.002902 **	geneSt.AAT1:fertilization_Strategies120.0	1039.73	645.94	1.610	0.107490
geneSt.Kinase:fertilization_Strategies106.0	1742.62	704.89	2.472	0.013437 *	geneSt.AAT2:fertilization_Strategies120.0	-95.74	645.94	-0.148	0.882170
geneSt.LIP:fertilization_Strategies106.0	1587.86	704.89	2.253	0.024292 *	geneSt.AOX:fertilization_Strategies120.0	-1227.34	645.94	-1.900	0.057434 *
geneSt.LOB38A:fertilization_Strategies106.0	1729.73	704.89	2.454	0.014146 *	geneSt.Apase:fertilization_Strategies120.0	2535.28	645.94	3.925	8.70e-05 ***
geneSt.LOB38B:fertilization_Strategies106.0	1748.33	704.89	2.480	0.013135 *	geneSt.ATrfa:fertilization_Strategies120.0	-194.64	645.94	-0.301	0.763166
geneSt.MIP:fertilization_Strategies106.0	1623.29	704.89	2.303	0.021294 *	geneSt.ATrfb:fertilization_Strategies120.0	-194.49	645.94	-0.301	0.763348
geneSt.MSF5A:fertilization_Strategies106.0	1928.16	704.89	2.735	0.006235 **	geneSt.CatT:fertilization_Strategies120.0	-94.70	645.94	-0.147	0.883446
geneSt.MSF5B:fertilization_Strategies106.0	1775.75	704.89	2.519	0.011770 *	geneSt.CatTR:fertilization_Strategies120.0	-122.40	645.94	-0.189	0.849172
geneSt.MSR8:fertilization_Strategies106.0	1778.24	704.89	2.523	0.011652 *	geneSt.CGI:fertilization_Strategies120.0	-115.76	645.94	-0.179	0.857770
geneSt.MnN21:fertilization_Strategies106.0	1657.84	704.89	2.352	0.018687 *	geneSt.CHI:fertilization_Strategies120.0	7425.82	645.94	11.496	< 2e-16 ***
geneSt.Nod:fertilization_Strategies106.0	1753.28	704.89	2.487	0.012879 *	geneSt.CLCh:fertilization_Strategies120.0	2368.55	645.94	3.667	0.000246 ***
geneSt.NT:fertilization_Strategies106.0	1689.32	704.89	2.397	0.016558 *	geneSt.CLH:fertilization_Strategies120.0	-425.41	645.94	-0.659	0.510162
geneSt.P109A:fertilization_Strategies106.0	1730.32	704.89	2.455	0.014107 *	geneSt.CWP:fertilization_Strategies120.0	-11326.79	645.94	-17.535	< 2e-16 ***
geneSt.PBnzR:fertilization_Strategies106.0	1786.44	704.89	2.534	0.011273 *	geneSt.CysPII:fertilization_Strategies120.0	-264.26	645.94	-0.409	0.682463
geneSt.PDX:fertilization_Strategies106.0	1773.71	704.89	2.516	0.011867 *	geneSt.CysT:fertilization_Strategies120.0	-138.59	645.94	-0.215	0.830111
geneSt.PEPT:fertilization_Strategies106.0	1735.53	704.89	2.462	0.013820 *	geneSt.DUF506A:fertilization_Strategies120.0	2275.34	645.94	3.523	0.000428 ***
geneSt.PLD:fertilization_Strategies106.0	1734.83	704.89	2.461	0.013858 *	geneSt.DUF506B:fertilization_Strategies120.0	-136.32	645.94	-0.211	0.832854
geneSt.PolyAP:fertilization_Strategies106.0	1735.80	704.89	2.463	0.013804 *	geneSt.EPI:fertilization_Strategies120.0	-193.13	645.94	-0.299	0.764946
geneSt.PP2C:fertilization_Strategies106.0	1717.23	704.89	2.436	0.014852 *	geneSt.FT:fertilization_Strategies120.0	-362.53	645.94	-0.561	0.574632
geneSt.Prod:fertilization_Strategies106.0	1701.49	704.89	2.414	0.015794 *	geneSt.GluAse:fertilization_Strategies120.0	68.44	645.94	0.106	0.915618
geneSt.ProH:fertilization_Strategies106.0	1730.03	704.89	2.454	0.014123 *	geneSt.GluDC:fertilization_Strategies120.0	1000.69	645.94	1.549	0.121346
geneSt.PyrK:fertilization_Strategies106.0	1642.94	704.89	2.331	0.019774 *	geneSt.GR3:fertilization_Strategies120.0	2956.44	645.94	4.577	4.74e-06 ***
geneSt.RPK:fertilization_Strategies106.0	1723.27	704.89	2.459	0.013943 *	geneSt.GST:fertilization_Strategies120.0	-354.50	645.94	-0.549	0.583141
geneSt.Sulfase:fertilization_Strategies106.0	1762.08	704.89	2.500	0.012434 *	geneSt.InoS:fertilization_Strategies120.0	1822.99	645.94	2.822	0.004773 **
geneSt.SulfT:fertilization_Strategies106.0	1682.51	704.89	2.387	0.016999 *	geneSt.Kinase:fertilization_Strategies120.0	-22.86	645.94	-0.035	0.971765
geneSt.SulfT2A:fertilization_Strategies106.0	1670.11	704.89	2.369	0.017830 *	geneSt.LIP:fertilization_Strategies120.0	-356.45	645.94	-0.552	0.581071
geneSt.SulfT2B:fertilization_Strategies106.0	1731.99	704.89	2.457	0.014014 *	geneSt.LOB38A:fertilization_Strategies120.0	-201.45	645.94	-0.312	0.755147
geneSt.SulfT2C:fertilization_Strategies106.0	1719.53	704.89	2.439	0.014718 *	geneSt.LOB38B:fertilization_Strategies120.0	-144.69	645.94	-0.224	0.822759
geneSt.TRDx:fertilization_Strategies106.0	1845.47	704.89	2.618	0.008848 **	geneSt.MIP:fertilization_Strategies120.0	178.69	645.94	0.277	0.782057
geneSt.URIE:fertilization_Strategies106.0	1473.55	704.89	2.090	0.036588 *	geneSt.MSF5A:fertilization_Strategies120.0	2510.37	645.94	3.886	0.000102 ***
geneSt.Unk1:fertilization_Strategies106.0	1723.64	704.89	2.445	0.014483 *	geneSt.MSF5B:fertilization_Strategies120.0	705.90	645.94	1.093	0.274483
geneSt.Unk2:fertilization_Strategies106.0	1759.97	704.89	2.497	0.012540 *	geneSt.MSR8:fertilization_Strategies120.0	-83.45	645.94	-0.129	0.897211
geneSt.Unk3:fertilization_Strategies106.0	1731.12	704.89	2.456	0.014062 *	geneSt.Nod:fertilization_Strategies120.0	-254.00	645.94	-0.393	0.694159
geneSt.Unk4:fertilization_Strategies106.0	1740.66	704.89	2.469	0.013541 *	geneSt.NT:fertilization_Strategies120.0	-202.09	645.94	-0.313	0.754392
geneSt.Unk5:fertilization_Strategies106.0	1812.43	704.89	2.571	0.010141 *	geneSt.P109A:fertilization_Strategies120.0	-200.67	645.94	-0.311	0.756064
geneSt.Xyl:fertilization_Strategies106.0	1773.48	704.89	2.516	0.011878 *	geneSt.PBnzR:fertilization_Strategies120.0	1767.22	645.94	2.736	0.006226 **
geneSt.NT2:fertilization_Strategies120.0	-494.35	645.94	-0.765	0.444809	geneSt.PDX:fertilization_Strategies120.0	-144.36	645.94	-0.223	0.823160
geneSt.PP7A:fertilization_Strategies120.0	-140.78	645.94	-0.218	0.827477	geneSt.PEPT:fertilization_Strategies120.0	-191.94	645.94	-0.297	0.766351
geneSt.PP7B:fertilization_Strategies120.0	-179.35	645.94	-0.278	0.781274					

Figure 15: Summary of the model 2 (4)

geneSt.PLD:fertilization_Strategies120.0	-215.10	645.94	-0.333	0.739135	geneSt.DUF506B:fertilization_Strategies180.0	1416.05	480.54	2.947	0.003214	**
geneSt.PolyAP:fertilization_Strategies120.0	-255.94	645.94	-0.396	0.691939	geneSt.EPI:fertilization_Strategies180.0	1380.25	480.54	2.872	0.004079	**
geneSt.PP2C:fertilization_Strategies120.0	-217.08	645.94	-0.336	0.736818	geneSt.FT:fertilization_Strategies180.0	1217.50	480.54	2.534	0.011296	*
geneSt.Prod:fertilization_Strategies120.0	-441.32	645.94	-0.683	0.494472	geneSt.GluAse:fertilization_Strategies180.0	1724.70	480.54	3.589	0.000333	**
geneSt.PyrK:fertilization_Strategies120.0	-186.49	645.94	-0.289	0.772805	geneSt.GlUDC:fertilization_Strategies180.0	2153.09	480.54	4.481	7.48e-06	***
geneSt.RPK:fertilization_Strategies120.0	541.89	645.94	0.839	0.401523	geneSt.GR3:fertilization_Strategies180.0	2914.82	480.54	6.066	1.33e-09	***
geneSt.SulFase:fertilization_Strategies120.0	-216.46	645.94	-0.335	0.737543	geneSt.GST:fertilization_Strategies180.0	1305.37	480.54	2.716	0.006604	**
geneSt.SulFT2B:fertilization_Strategies120.0	-353.95	645.94	-0.548	0.593814	geneSt.InoS:fertilization_Strategies180.0	2606.77	480.54	5.425	5.87e-08	***
geneSt.SulFT2A:fertilization_Strategies120.0	176.30	645.94	0.273	0.784902	geneSt.Kinase:fertilization_Strategies180.0	1500.60	480.54	3.123	0.001794	**
geneSt.SulFT2C:fertilization_Strategies120.0	-124.99	645.94	-0.193	0.846571	geneSt.LIP:fertilization_Strategies180.0	1144.99	480.54	2.383	0.017194	*
geneSt.SulFT2D:fertilization_Strategies120.0	3229.93	645.94	5.000	5.76e-07	geneSt.LOB38A:fertilization_Strategies180.0	1376.15	480.54	2.864	0.004191	**
geneSt.UBI1:fertilization_Strategies120.0	-239.76	645.94	-0.371	0.710503	geneSt.LOB38B:fertilization_Strategies180.0	1473.56	480.54	2.992	0.002779	**
geneSt.Unk1:fertilization_Strategies120.0	-108.33	645.94	-0.168	0.866813	geneSt.MIP:fertilization_Strategies180.0	1529.76	480.54	3.183	0.001457	**
geneSt.Unk2:fertilization_Strategies120.0	203.10	645.94	0.314	0.753203	geneSt.MSF5A:fertilization_Strategies180.0	2732.66	480.54	5.687	1.31e-08	***
geneSt.Unk3:fertilization_Strategies120.0	-202.73	645.94	-0.314	0.753632	geneSt.MSF5B:fertilization_Strategies180.0	1845.65	480.54	3.841	0.000123	**
geneSt.Unk4:fertilization_Strategies120.0	-84.04	645.94	-0.130	0.896481	geneSt.MSRB:fertilization_Strategies180.0	1444.65	480.54	3.006	0.002647	**
geneSt.Unk5:fertilization_Strategies120.0	950.48	645.94	1.471	0.141177	geneSt.MN2I:fertilization_Strategies180.0	1185.86	480.54	2.468	0.013604	*
geneSt.Xyl:fertilization_Strategies120.0	334.84	645.94	0.518	0.604204	geneSt.Mod:fertilization_Strategies180.0	1348.50	480.54	2.806	0.005017	**
geneSt.NT2:fertilization_Strategies180.0	1169.46	480.54	2.434	0.014957	geneSt.NT:fertilization_Strategies180.0	1356.09	480.54	2.822	0.004777	**
geneSt.PP7A:fertilization_Strategies180.0	1415.71	480.54	2.946	0.003222	geneSt.P109A:fertilization_Strategies180.0	1376.10	480.54	2.864	0.004192	**
geneSt.PP7B:fertilization_Strategies180.0	1394.41	480.54	2.902	0.003715	geneSt.PBenzR:fertilization_Strategies180.0	2492.22	480.54	5.186	2.16e-07	***
geneSt.AAT1:fertilization_Strategies180.0	1919.62	480.54	3.995	6.50e-05	geneSt.PDX:fertilization_Strategies180.0	1458.69	480.54	3.035	0.002404	**
geneSt.AAT2:fertilization_Strategies180.0	1436.19	480.54	2.989	0.002805	geneSt.PEPT:fertilization_Strategies180.0	1390.15	480.54	2.893	0.003821	**
geneSt.AOX:fertilization_Strategies180.0	273.67	480.54	0.569	0.569024	geneSt.PLD:fertilization_Strategies180.0	1375.50	480.54	2.862	0.004209	**
geneSt.Apose:fertilization_Strategies180.0	2730.62	480.54	5.682	1.34e-08	geneSt.PolyAP:fertilization_Strategies180.0	1342.45	480.54	2.794	0.005217	**
geneSt.ATrfA:fertilization_Strategies180.0	1399.83	480.54	2.913	0.003583	geneSt.PP2C:fertilization_Strategies180.0	1359.66	480.54	2.829	0.004667	**
geneSt.ATrfB:fertilization_Strategies180.0	1581.90	480.54	3.292	0.000957	geneSt.Prod:fertilization_Strategies180.0	1179.97	480.54	2.455	0.014077	*
geneSt.CatT:fertilization_Strategies180.0	1375.99	480.54	2.863	0.004195	geneSt.ProH:fertilization_Strategies180.0	1387.48	480.54	2.887	0.003889	**
geneSt.CatTR:fertilization_Strategies180.0	1812.17	480.54	3.771	0.000163	geneSt.PyrK:fertilization_Strategies180.0	1771.39	480.54	3.686	0.000228	***
geneSt.CGL:fertilization_Strategies180.0	1334.31	480.54	2.777	0.005496	geneSt.RPK:fertilization_Strategies180.0	1373.63	480.54	2.858	0.004260	**
geneSt.CH1:fertilization_Strategies180.0	4529.12	480.54	9.425	< 2e-16	geneSt.SulFase:fertilization_Strategies180.0	1363.27	480.54	2.837	0.004559	**
geneSt.CLH:fertilization_Strategies180.0	-249.53	480.54	-0.519	0.603583	geneSt.SulFT2A:fertilization_Strategies180.0	1625.23	480.54	3.382	0.000721	***
geneSt.CMP:fertilization_Strategies180.0	1293.80	480.54	2.692	0.007100	geneSt.SulFT2B:fertilization_Strategies180.0	1517.33	480.54	3.158	0.001593	**
geneSt.CysP11:fertilization_Strategies180.0	2996.98	480.54	6.237	4.55e-10	geneSt.SulFT2C:fertilization_Strategies180.0	1414.12	480.54	2.943	0.003256	**
geneSt.CysP12:fertilization_Strategies180.0	1538.00	480.54	3.201	0.001374	geneSt.SulFT2D:fertilization_Strategies180.0	1363.50	480.54	2.837	0.004552	**
geneSt.CysT:fertilization_Strategies180.0	1412.00	480.54	2.938	0.003303	geneSt.TRDY:fertilization_Strategies180.0	3272.55	480.54	6.810	9.99e-12	***
geneSt.DUF506A:fertilization_Strategies180.0	2618.37	480.54	5.449	5.12e-08	geneSt.UBI1:fertilization_Strategies180.0	1103.52	480.54	2.296	0.021662	*
					geneSt.Unk1:fertilization_Strategies180.0	1559.58	480.54	3.245	0.001174	**
					geneSt.Unk2:fertilization_Strategies180.0	1592.48	480.54	3.314	0.000921	**

Figure 15: Summary of the model 2 (5)

geneSt.Unk3:fertilization_Strategies180.0	1379.72	480.54	2.871	0.004093	geneSt.MN2I:fertilization_Strategies200.0	-1102.43	973.17	-1.133	0.257298	
geneSt.Unk4:fertilization_Strategies180.0	1449.06	480.54	3.015	0.002569	geneSt.Mod:fertilization_Strategies200.0	-954.68	973.17	-0.981	0.326601	
geneSt.Unk5:fertilization_Strategies180.0	2357.09	480.54	4.905	9.40e-07	geneSt.NT:fertilization_Strategies200.0	-1094.92	973.17	-1.125	0.260557	
geneSt.Xyl:fertilization_Strategies180.0	1755.89	480.54	3.654	0.000259	geneSt.P109A:fertilization_Strategies200.0	-1102.85	973.17	-1.133	0.257120	
geneSt.NT2:fertilization_Strategies200.0	-711.89	973.17	-0.732	0.464469	geneSt.PBenzR:fertilization_Strategies200.0	-107.40	973.17	-0.110	0.912126	
geneSt.PP7A:fertilization_Strategies200.0	-1053.05	973.17	-1.082	0.279225	geneSt.PDX:fertilization_Strategies200.0	-879.37	973.17	-0.904	0.366207	
geneSt.PP7B:fertilization_Strategies200.0	-1072.78	973.17	-1.102	0.270316	geneSt.PEPT:fertilization_Strategies200.0	-1096.37	973.17	-1.127	0.259924	
geneSt.AAT1:fertilization_Strategies200.0	626.15	973.17	0.643	0.519962	geneSt.PLD:fertilization_Strategies200.0	-1101.03	973.17	-1.131	0.257906	
geneSt.AAT2:fertilization_Strategies200.0	-977.39	973.17	-1.004	0.315226	geneSt.PolyAP:fertilization_Strategies200.0	-1060.10	973.17	-1.089	0.276022	
geneSt.AOX:fertilization_Strategies200.0	-1201.49	973.17	-1.235	0.216984	geneSt.PP2C:fertilization_Strategies200.0	-1100.59	973.17	-1.131	0.258095	
geneSt.Apose:fertilization_Strategies200.0	-1010.92	973.17	-1.039	0.298912	geneSt.Prod:fertilization_Strategies200.0	-1159.36	973.17	-1.191	0.233539	
geneSt.ATrfA:fertilization_Strategies200.0	-950.14	973.17	-0.976	0.328909	geneSt.ProH:fertilization_Strategies200.0	-1076.48	973.17	-1.106	0.268668	
geneSt.ATrfB:fertilization_Strategies200.0	1950.12	973.17	2.004	0.045094	geneSt.PyrK:fertilization_Strategies200.0	-222.34	973.17	-0.228	0.819287	
geneSt.CatT:fertilization_Strategies200.0	-1023.67	973.17	-1.052	0.292858	geneSt.RPK:fertilization_Strategies200.0	-1084.66	973.17	-1.115	0.265047	
geneSt.CatTR:fertilization_Strategies200.0	6892.19	973.17	7.082	1.46e-12	geneSt.SulFase:fertilization_Strategies200.0	-351.69	973.17	-0.361	0.717812	
geneSt.CGL:fertilization_Strategies200.0	-1096.13	973.17	-1.126	0.260030	geneSt.SulFT2A:fertilization_Strategies200.0	-890.55	973.17	-0.915	0.360145	
geneSt.CHI:fertilization_Strategies200.0	-183.96	973.17	-0.189	0.850072	geneSt.SulFT2B:fertilization_Strategies200.0	-1078.50	973.17	-1.108	0.267772	
geneSt.CLH:fertilization_Strategies200.0	-4864.30	973.17	-4.998	5.82e-07	geneSt.SulFT2C:fertilization_Strategies200.0	-1068.80	973.17	-1.098	0.272098	
geneSt.CMP:fertilization_Strategies200.0	-887.85	973.17	-0.912	0.361804	geneSt.TRDY:fertilization_Strategies200.0	1099.49	973.17	1.130	0.258872	
geneSt.CysP11:fertilization_Strategies200.0	18277.61	973.17	18.782	< 2e-16	geneSt.UBI1:fertilization_Strategies200.0	-928.43	973.17	-0.954	0.340081	
geneSt.CysP12:fertilization_Strategies200.0	-825.19	973.17	-0.848	0.396480	geneSt.Unk1:fertilization_Strategies200.0	-1057.21	973.17	-1.086	0.273333	
geneSt.CysT:fertilization_Strategies200.0	-1006.64	973.17	-1.034	0.300963	geneSt.Unk2:fertilization_Strategies200.0	-434.11	973.17	-0.446	0.655548	
geneSt.DUF506A:fertilization_Strategies200.0	-246.53	973.17	-0.253	0.800018	geneSt.Unk3:fertilization_Strategies200.0	-1100.05	973.17	-1.130	0.258329	
geneSt.DUF506B:fertilization_Strategies200.0	-1058.28	973.17	-1.087	0.276845	geneSt.Unk4:fertilization_Strategies200.0	-926.03	973.17	-0.952	0.341331	
geneSt.EPI:fertilization_Strategies200.0	-974.08	973.17	-1.001	0.316870	geneSt.Unk5:fertilization_Strategies200.0	533.08	973.17	0.548	0.583848	
geneSt.FT:fertilization_Strategies200.0	-947.37	973.17	-0.973	0.330320	geneSt.Xyl:fertilization_Strategies200.0	-194.33	973.17	-0.200	0.841730	
geneSt.GluAse:fertilization_Strategies200.0	1003.90	973.17	1.032	0.302283	geneSt.NT2:fertilization_Strategies240.0	12.87	662.78	0.019	0.984510	
geneSt.GR3:fertilization_Strategies200.0	-1078.45	973.17	-1.108	0.267795	geneSt.PP7A:fertilization_Strategies240.0	449.51	662.78	0.678	0.497642	
geneSt.GST:fertilization_Strategies200.0	-836.11	973.17	-0.859	0.390258	geneSt.PP7B:fertilization_Strategies240.0	376.32	662.78	0.568	0.570181	
geneSt.InoS:fertilization_Strategies200.0	355.05	973.17	0.365	0.715239	geneSt.AAT1:fertilization_Strategies240.0	1861.15	662.78	2.808	0.004988	**
geneSt.Kinase:fertilization_Strategies200.0	-1026.22	973.17	-1.055	0.291658	geneSt.AAT2:fertilization_Strategies240.0	535.09	662.78	0.807	0.419482	
geneSt.LIP:fertilization_Strategies200.0	-758.97	973.17	-0.780	0.435463	geneSt.AOX:fertilization_Strategies240.0	-891.95	662.78	-1.346	0.178291	
geneSt.LOB38A:fertilization_Strategies200.0	-1096.36	973.17	-1.127	0.259931	geneSt.Apose:fertilization_Strategies240.0	4564.91	662.78	6.887	5.82e-12	***
geneSt.LOB38B:fertilization_Strategies200.0	-991.31	973.17	-1.019	0.308384	geneSt.ATrfA:fertilization_Strategies240.0	353.76	662.78	0.534	0.535263	
geneSt.MIP:fertilization_Strategies200.0	-18.39	973.17	-0.019	0.984919	geneSt.ATrfB:fertilization_Strategies240.0	429.69	662.78	0.648	0.516786	
geneSt.MSF5A:fertilization_Strategies200.0	1545.67	973.17	1.588	0.112235	geneSt.CatT:fertilization_Strategies240.0	480.69	662.78	0.725	0.468296	
geneSt.MSF5B:fertilization_Strategies200.0	-490.70	973.17	-0.504	0.614103	geneSt.CatTR:fertilization_Strategies240.0	191.54	662.78	0.289	0.772585	
geneSt.MSRB:fertilization_Strategies200.0	-998.73	973.17	-1.026	0.304775	geneSt.CGL:fertilization_Strategies240.0	343.29	662.78	0.518	0.604500	

Figure 15: Summary of the model 2 (6)

geneSt.CH1:fertilization_Strategies240.0	9946.35	662.78	15.007	< 2e-16	***	geneSt.SulFT2A:fertilization_Strategies240.0	824.77	662.78	1.244	0.213366	
geneSt.CLCh:fertilization_Strategies240.0	1680.98	662.78	2.536	0.01211	*	geneSt.SulFT2B:fertilization_Strategies240.0	464.21	662.78	0.700	0.483686	
geneSt.CLH:fertilization_Strategies240.0	172.93	662.78	0.261	0.794159		geneSt.SulFT2C:fertilization_Strategies240.0	311.60	662.78	0.470	0.638263	
geneSt.CWP:fertilization_Strategies240.0	-10013.56	662.78	15.108	< 2e-16	***	geneSt.TRDX:fertilization_Strategies240.0	5780.62	662.78	8.722	< 2e-16	***
geneSt.CysP11:fertilization_Strategies240.0	381.72	662.78	0.576	0.564667		geneSt.UBIE:fertilization_Strategies240.0	281.53	662.78	0.425	0.671807	
geneSt.CysT:fertilization_Strategies240.0	423.51	662.78	0.639	0.522833		geneSt.Unk1:fertilization_Strategies240.0	586.46	662.78	0.885	0.376247	
geneSt.DUF506A:fertilization_Strategies240.0	4050.78	662.78	6.112	1.00e-09	***	geneSt.Unk2:fertilization_Strategies240.0	845.88	662.78	1.276	0.201877	
geneSt.DUF506B:fertilization_Strategies240.0	432.89	662.78	0.653	0.513669		geneSt.Unk3:fertilization_Strategies240.0	340.37	662.78	0.514	0.607572	
geneSt.EPI:fertilization_Strategies240.0	358.92	662.78	0.542	0.588143		geneSt.Unk4:fertilization_Strategies240.0	530.42	662.78	0.800	0.423547	
geneSt.FT:fertilization_Strategies240.0	136.41	662.78	0.206	0.836940		geneSt.Unk5:fertilization_Strategies240.0	2100.30	662.78	3.169	0.001532	**
geneSt.GluA2:fertilization_Strategies240.0	753.98	662.78	1.138	0.255300		geneSt.Xyl:fertilization_Strategies240.0	1023.79	662.78	1.545	0.122435	
geneSt.GluDC:fertilization_Strategies240.0	2764.72	662.78	4.171	3.04e-05	***	geneSt.NT2:fertilization_Strategies60.60	2588.34	738.62	3.504	0.000459	***
geneSt.GR3:fertilization_Strategies240.0	4814.29	662.78	7.264	3.88e-13	***	geneSt.PP7A:fertilization_Strategies60.60	2946.05	738.62	3.989	6.67e-05	***
geneSt.GST:fertilization_Strategies240.0	214.47	662.78	0.324	0.746250		geneSt.PP7B:fertilization_Strategies60.60	2948.42	738.62	3.992	6.58e-05	***
geneSt.InosD:fertilization_Strategies240.0	3240.34	662.78	4.889	1.02e-06	***	geneSt.AAT1:fertilization_Strategies60.60	2875.00	738.62	3.892	9.95e-05	***
geneSt.Kinase:fertilization_Strategies240.0	634.69	662.78	0.958	0.338265		geneSt.AAT2:fertilization_Strategies60.60	2949.11	738.62	3.993	6.55e-05	***
geneSt.LIP:fertilization_Strategies240.0	144.61	662.78	0.218	0.827284		geneSt.AOX:fertilization_Strategies60.60	1603.98	738.62	2.172	0.029897	*
geneSt.LOB38A:fertilization_Strategies240.0	325.26	662.78	0.491	0.623607		geneSt.Apase:fertilization_Strategies60.60	2877.55	738.62	3.896	9.81e-05	***
geneSt.LOB38B:fertilization_Strategies240.0	422.81	662.78	0.638	0.523528		geneSt.AtrfA:fertilization_Strategies60.60	2960.47	738.62	4.008	6.14e-05	***
geneSt.MIP:fertilization_Strategies240.0	957.44	662.78	1.445	0.148592		geneSt.AtrfB:fertilization_Strategies60.60	3233.00	738.62	4.377	1.21e-05	***
geneSt.MSF5A:fertilization_Strategies240.0	3834.52	662.78	5.785	7.32e-09	***	geneSt.CatT:fertilization_Strategies60.60	2835.27	738.62	3.839	0.00124	***
geneSt.MSF5B:fertilization_Strategies240.0	1674.25	662.78	2.526	0.011541	*	geneSt.CatTR:fertilization_Strategies60.60	3501.97	738.62	4.741	2.14e-06	***
geneSt.MSR8:fertilization_Strategies240.0	486.61	662.78	0.734	0.462837		geneSt.CGL:fertilization_Strategies60.60	2884.27	738.62	3.905	9.45e-05	***
geneSt.MN21:fertilization_Strategies240.0	105.37	662.78	0.159	0.873685		geneSt.CHI:fertilization_Strategies60.60	2071.18	738.62	2.804	0.005050	**
geneSt.Nod:fertilization_Strategies240.0	299.51	662.78	0.452	0.651344		geneSt.CLCh:fertilization_Strategies60.60	20.50	738.62	0.028	0.977855	
geneSt.NT:fertilization_Strategies240.0	312.01	662.78	0.471	0.637816		geneSt.CLH:fertilization_Strategies60.60	2990.53	738.62	4.049	5.17e-05	***
geneSt.PI09A:fertilization_Strategies240.0	324.89	662.78	0.490	0.623999		geneSt.CWP:fertilization_Strategies60.60	4307.84	738.62	5.832	5.54e-09	***
geneSt.PbenzR:fertilization_Strategies240.0	3557.86	662.78	5.368	8.04e-08	***	geneSt.CysP11:fertilization_Strategies60.60	3266.05	738.62	4.422	9.83e-06	***
geneSt.PDX:fertilization_Strategies240.0	422.59	662.78	0.638	0.523743		geneSt.DUF506A:fertilization_Strategies60.60	2941.81	738.62	3.983	8.36e-05	***
geneSt.PEPT:fertilization_Strategies240.0	354.04	662.78	0.534	0.593224		geneSt.DUF506B:fertilization_Strategies60.60	2824.79	738.62	3.824	0.000311	***
geneSt.PLD:fertilization_Strategies240.0	315.91	662.78	0.477	0.633620		geneSt.EPI:fertilization_Strategies60.60	2949.93	738.62	3.994	6.52e-05	***
geneSt.PolyAP:fertilization_Strategies240.0	274.96	662.78	0.415	0.678250		geneSt.FT:fertilization_Strategies60.60	2921.97	738.62	3.967	6.65e-05	***
geneSt.ProD:fertilization_Strategies240.0	306.11	662.78	0.462	0.644191		geneSt.GluA5:fertilization_Strategies60.60	2708.60	738.62	3.656	0.000246	***
geneSt.ProH:fertilization_Strategies240.0	87.94	662.78	0.133	0.894444		geneSt.GluDC:fertilization_Strategies60.60	3213.34	738.62	4.350	1.36e-05	***
geneSt.PyrK:fertilization_Strategies240.0	362.62	662.78	0.547	0.584308		geneSt.GR3:fertilization_Strategies60.60	2743.06	738.62	3.714	0.000205	***
geneSt.RPK:fertilization_Strategies240.0	1393.33	662.78	2.102	0.035543	*	geneSt.GST:fertilization_Strategies60.60	2882.30	738.62	3.902	9.56e-05	***
geneSt.SulFase:fertilization_Strategies240.0	314.97	662.78	0.475	0.634628		geneSt.InosD:fertilization_Strategies60.60	2881.62	738.62	3.901	9.59e-05	***
geneSt.SulFT:fertilization_Strategies240.0	165.92	662.78	0.250	0.802324		geneSt.Kinase:fertilization_Strategies60.60	2892.07	738.62	3.915	9.05e-05	***
geneSt.SulFT2A:fertilization_Strategies240.0	1043.54	662.78	1.574	0.115389			2988.66	738.62	4.046	5.22e-05	***

Figure 15: Summary of the model 2 (7)

geneSt.LIP:fertilization_Strategies60.60	2573.45	738.62	3.484	0.000495	***	geneSt.AOX:fertilization_Strategies60.120	1701.44	668.57	2.545	0.010938	*
geneSt.LOB38A:fertilization_Strategies60.60	2949.25	738.62	3.993	6.55e-05	***	geneSt.Apase:fertilization_Strategies60.120	2809.24	668.57	4.202	2.66e-05	***
geneSt.LOB38B:fertilization_Strategies60.60	2955.11	738.62	4.001	6.33e-05	***	geneSt.AtrfA:fertilization_Strategies60.120	3006.01	668.57	4.496	6.95e-06	***
geneSt.MIP:fertilization_Strategies60.60	2718.11	738.62	3.680	0.000234	***	geneSt.AtrfB:fertilization_Strategies60.120	3194.64	668.57	4.778	1.78e-06	***
geneSt.MSF5A:fertilization_Strategies60.60	2880.54	738.62	3.900	9.65e-05	***	geneSt.CatT:fertilization_Strategies60.120	2873.21	668.57	2.498	2.73e-05	***
geneSt.MSF5B:fertilization_Strategies60.60	2971.74	738.62	4.023	5.76e-05	***	geneSt.CatTR:fertilization_Strategies60.120	3222.18	668.57	4.820	1.45e-06	***
geneSt.MSR8:fertilization_Strategies60.60	2937.36	738.62	3.977	7.01e-05	***	geneSt.CGL:fertilization_Strategies60.120	2892.30	668.57	4.326	1.52e-05	***
geneSt.MN21:fertilization_Strategies60.60	2686.01	738.62	3.637	0.000277	***	geneSt.CHI:fertilization_Strategies60.120	2151.91	668.57	3.219	0.001290	**
geneSt.Nod:fertilization_Strategies60.60	2893.23	738.62	3.917	8.99e-05	***	geneSt.CLCh:fertilization_Strategies60.120	-36.37	668.57	-0.054	0.956614	
geneSt.NT:fertilization_Strategies60.60	2922.73	738.62	3.957	7.61e-05	***	geneSt.CLH:fertilization_Strategies60.120	2994.53	668.57	4.479	7.53e-06	***
geneSt.PI09A:fertilization_Strategies60.60	2950.33	738.62	3.994	6.51e-05	***	geneSt.CWP:fertilization_Strategies60.120	3163.05	668.57	4.731	2.25e-06	***
geneSt.PbenzR:fertilization_Strategies60.60	3102.59	738.62	4.200	2.67e-05	***	geneSt.CysP11:fertilization_Strategies60.120	3301.09	668.57	4.938	7.97e-07	***
geneSt.PDX:fertilization_Strategies60.60	2982.25	738.62	4.038	5.42e-05	***	geneSt.DUF506A:fertilization_Strategies60.120	2985.07	668.57	4.465	8.05e-06	***
geneSt.PEPT:fertilization_Strategies60.60	2952.23	738.62	3.997	6.44e-05	***	geneSt.DUF506B:fertilization_Strategies60.120	2937.36	668.57	4.393	1.12e-05	***
geneSt.PLD:fertilization_Strategies60.60	2953.70	738.62	3.999	6.38e-05	***	geneSt.EPI:fertilization_Strategies60.120	2997.08	668.57	4.483	7.40e-06	***
geneSt.PolyAP:fertilization_Strategies60.60	2913.78	738.62	3.945	8.01e-05	***	geneSt.FT:fertilization_Strategies60.120	2969.20	668.57	4.441	8.99e-06	***
geneSt.PP2C:fertilization_Strategies60.60	2931.50	738.62	3.969	7.24e-05	***	geneSt.GluA5:fertilization_Strategies60.120	2751.78	668.57	4.116	3.87e-05	***
geneSt.ProD:fertilization_Strategies60.60	2682.17	738.62	3.631	0.000283	***	geneSt.GluDC:fertilization_Strategies60.120	3180.79	668.57	4.758	1.97e-06	***
geneSt.ProH:fertilization_Strategies60.60	2952.75	738.62	3.998	6.42e-05	***	geneSt.GST:fertilization_Strategies60.120	2793.14	668.57	4.178	2.95e-05	***
geneSt.PyrK:fertilization_Strategies60.60	2847.11	738.62	3.855	0.000116	***	geneSt.InosD:fertilization_Strategies60.120	2942.99	668.57	4.402	1.08e-05	***
geneSt.RPK:fertilization_Strategies60.60	2952.19	738.62	3.997	6.44e-05	***	geneSt.Kinase:fertilization_Strategies60.120	2892.25	668.57	4.326	1.52e-05	***
geneSt.SulFase:fertilization_Strategies60.60	3051.46	738.62	4.131	3.62e-05	***	geneSt.LIP:fertilization_Strategies60.120	2899.32	668.57	4.337	1.45e-05	***
geneSt.SulFT:fertilization_Strategies60.60	2822.78	738.62	3.822	0.000133	***	geneSt.LOB38A:fertilization_Strategies60.120	3042.53	668.57	4.551	5.37e-06	***
geneSt.SulFT2A:fertilization_Strategies60.60	2889.29	738.62	3.912	9.19e-05	***	geneSt.LOB38B:fertilization_Strategies60.120	3052.31	668.57	3.882	0.000104	***
geneSt.SulFT2B:fertilization_Strategies60.60	2941.88	738.62	3.983	6.83e-05	***	geneSt.LOB38C:fertilization_Strategies60.120	2994.59	668.57	4.479	7.53e-06	***
geneSt.SulFT2C:fertilization_Strategies60.60	2930.53	738.62	3.968	7.28e-05	***	geneSt.MIP:fertilization_Strategies60.120	3003.66	668.57	4.493	7.07e-06	***
geneSt.TRDX:fertilization_Strategies60.60	2918.55	738.62	3.951	7.79e-05	***	geneSt.MSF5A:fertilization_Strategies60.120	2738.06	668.57	4.095	4.23e-05	***
geneSt.UBIE:fertilization_Strategies60.60	2289.46	738.62	3.100	0.001940	***	geneSt.MSF5B:fertilization_Strategies60.120	2898.42	668.57	4.335	1.46e-05	***
geneSt.Unk1:fertilization_Strategies60.60	3069.28	738.62	4.155	3.26e-05	***	geneSt.MSR8:fertilization_Strategies60.120	3005.35	668.57	4.495	6.90e-06	***
geneSt.Unk2:fertilization_Strategies60.60	3013.01	738.62	4.079	4.53e-05	***	geneSt.MN21:fertilization_Strategies60.120	2976.60	668.57	4.452	5.54e-06	***
geneSt.Unk3:fertilization_Strategies60.60	2950.99	738.62	3.995	6.48e-05	***	geneSt.Nod:fertilization_Strategies60.120	2712.24	668.57	4.857	4.99e-05	***
geneSt.Unk4:fertilization_Strategies60.60	2971.33	738.62	4.023	5.77e-05	***	geneSt.NT:fertilization_Strategies60.120	2937.23	668.57	4.393	1.12e-05	***
geneSt.Unk5:fertilization_Strategies60.60	3455.72	738.62	4.679	2.90e-06	***	geneSt.PI09A:fertilization_Strategies60.120	2965.67	668.57	4.436	9.21e-06	***
geneSt.Xyl:fertilization_Strategies60.60	3167.95	738.62	4.289	1.80e-05	***	geneSt.PbenzR:fertilization_Strategies60.120	2994.54	668.57	4.479	7.53e-06	***
geneSt.NT2:fertilization_Strategies60.120	2640.64	668.57	3.950	7.85e-05	***	geneSt.PDX:fertilization_Strategies60.120	3118.25	668.57	4.664	3.12e-06	***
geneSt.PP7A:fertilization_Strategies60.120	2987.64	668.57	4.469	7.91e-06	***	geneSt.PEPT:fertilization_Strategies60.120	3012.99	668.57	4.507	6.62e-06	***
geneSt.PP7B:fertilization_Strategies60.120	2993.26	668.57	4.477	7.60e-06	***	geneSt.PLD:fertilization_Strategies60.120	2998.20	668.57	4.484	7.34e-06	***
geneSt.AAT1:fertilization_Strategies60.120	2876.63	668.57	3.983	1.09e-05	***	geneSt.PolyAP:fertilization_Strategies60.120	2999.20	668.57	4.486	7.29e-06	***
geneSt.AAT2:fertilization_Strategies60.120	2997.94	668.57	4.484	7.36e-06	***		2956.44	668.57	4.422	9.82e-06	***

Figure 15: Summary of the model 2 (8)

geneSt_PP2C:fertilization_Strategies60.120	2977.00	668.57	4.453	8.52e-06	***	geneSt_FT:fertilization_Strategies0.180	4086.72	2164.96	1.888	0.059083	.
geneSt_Prod:fertilization_Strategies60.120	2723.21	668.57	4.073	4.65e-05	***	geneSt_GluAse:fertilization_Strategies0.180	4141.04	2164.96	1.913	0.055791	.
geneSt_ProH:fertilization_Strategies60.120	2997.18	668.57	4.483	7.40e-06	***	geneSt_GluDC:fertilization_Strategies0.180	4201.28	2164.96	1.941	0.052321	.
geneSt_PyrK:fertilization_Strategies60.120	2871.13	668.57	4.294	1.76e-05	***	geneSt_GR3:fertilization_Strategies0.180	4452.59	2164.96	2.057	0.039730	*
geneSt_RPK:fertilization_Strategies60.120	2996.90	668.57	4.483	7.41e-06	***	geneSt_GST:fertilization_Strategies0.180	4312.79	2164.96	1.992	0.046373	*
geneSt_SulFase:fertilization_Strategies60.120	3042.36	668.57	4.551	5.38e-06	***	geneSt_InosD:fertilization_Strategies0.180	4282.38	2164.96	1.978	0.047935	*
geneSt_SulFT:fertilization_Strategies60.120	2854.76	668.57	4.270	1.96e-05	***	geneSt_Kinase:fertilization_Strategies0.180	4301.60	2164.96	1.987	0.046943	*
geneSt_SulFT2A:fertilization_Strategies60.120	2935.17	668.57	4.390	1.14e-05	***	geneSt_LIP:fertilization_Strategies0.180	3808.80	2164.96	1.759	0.078541	.
geneSt_SulFT2B:fertilization_Strategies60.120	2987.00	668.57	4.468	7.94e-06	***	geneSt_LOB38A:fertilization_Strategies0.180	4295.28	2164.96	1.984	0.047267	*
geneSt_SulFT2C:fertilization_Strategies60.120	2974.08	668.57	4.448	8.69e-06	***	geneSt_LOB38B:fertilization_Strategies0.180	4248.43	2164.96	1.962	0.049733	*
geneSt_TRDX:fertilization_Strategies60.120	2916.37	668.57	4.362	1.29e-05	***	geneSt_MIP:fertilization_Strategies0.180	3952.70	2164.96	1.826	0.067899	.
geneSt_UBIE:fertilization_Strategies60.120	2294.40	668.57	3.432	0.000091	***	geneSt_MSFA:fertilization_Strategies0.180	4259.79	2164.96	1.968	0.049125	*
geneSt_Unk1:fertilization_Strategies60.120	3091.18	668.57	4.624	3.79e-06	***	geneSt_MSFA5:fertilization_Strategies0.180	4268.41	2164.96	1.972	0.048668	*
geneSt_Unk2:fertilization_Strategies60.120	3020.07	668.57	4.517	6.30e-06	***	geneSt_MSFB:fertilization_Strategies0.180	4275.79	2164.96	1.975	0.048280	*
geneSt_Unk3:fertilization_Strategies60.120	2996.53	668.57	4.482	7.43e-06	***	geneSt_MN21:fertilization_Strategies0.180	3882.54	2164.96	1.793	0.072929	.
geneSt_Unk4:fertilization_Strategies60.120	3013.56	668.57	4.507	6.59e-06	***	geneSt_Nod:fertilization_Strategies0.180	4202.75	2164.96	1.941	0.052238	.
geneSt_Unk5:fertilization_Strategies60.120	3441.98	668.57	5.148	2.65e-07	***	geneSt_NT:fertilization_Strategies0.180	4253.42	2164.96	1.965	0.049465	*
geneSt_Xyl:fertilization_Strategies60.120	3197.25	668.57	4.782	1.74e-06	***	geneSt_P109A:fertilization_Strategies0.180	4293.98	2164.96	1.983	0.047335	*
geneSt_NT2:fertilization_Strategies0.180	3779.57	2164.96	1.746	0.008060	.	geneSt_PBenzR:fertilization_Strategies0.180	4392.16	2164.96	2.029	0.042495	*
geneSt_PP7A:fertilization_Strategies0.180	4279.76	2164.96	1.977	0.048072	*	geneSt_PDX:fertilization_Strategies0.180	4267.10	2164.96	1.971	0.048737	*
geneSt_PP7B:fertilization_Strategies0.180	4289.14	2164.96	1.981	0.047584	*	geneSt_PPT:fertilization_Strategies0.180	4298.03	2164.96	1.985	0.047126	*
geneSt_AA1:fertilization_Strategies0.180	4064.32	2164.96	1.877	0.060487	*	geneSt_PLD:fertilization_Strategies0.180	4297.89	2164.96	1.985	0.047133	*
geneSt_AA2:fertilization_Strategies0.180	4294.86	2164.96	1.984	0.047289	*	geneSt_PolyAP:fertilization_Strategies0.180	4251.20	2164.96	1.964	0.049584	*
geneSt_AOX:fertilization_Strategies0.180	3355.68	2164.96	1.550	0.121156	.	geneSt_PP2C:fertilization_Strategies0.180	4279.16	2164.96	1.977	0.048103	*
geneSt_Apase:fertilization_Strategies0.180	4379.51	2164.96	2.023	0.043094	*	geneSt_ProH:fertilization_Strategies0.180	3992.49	2164.96	1.844	0.065175	*
geneSt_ArFA:fertilization_Strategies0.180	4364.80	2164.96	2.016	0.043800	*	geneSt_ProH1:fertilization_Strategies0.180	4305.52	2164.96	1.989	0.046743	*
geneSt_ArFB:fertilization_Strategies0.180	4153.63	2164.96	1.919	0.055950	*	geneSt_PyrK:fertilization_Strategies0.180	3890.59	2164.96	1.797	0.072337	.
geneSt_CatT:fertilization_Strategies0.180	4122.41	2164.96	1.904	0.056902	*	geneSt_RPK:fertilization_Strategies0.180	4298.01	2164.96	1.985	0.047127	*
geneSt_CatTR:fertilization_Strategies0.180	3449.46	2164.96	1.593	0.111103	.	geneSt_SulFase:fertilization_Strategies0.180	4125.97	2164.96	1.906	0.056689	*
geneSt_CGL:fertilization_Strategies0.180	4303.71	2164.96	1.988	0.046835	*	geneSt_SulFT:fertilization_Strategies0.180	4107.41	2164.96	1.897	0.057811	.
geneSt_CH1:fertilization_Strategies0.180	4220.80	2164.96	1.950	0.051236	*	geneSt_SulFT2A:fertilization_Strategies0.180	4232.69	2164.96	1.955	0.050584	.
geneSt_ClnC:fertilization_Strategies0.180	-28.88	2164.96	-0.013	0.989358	.	geneSt_SulFT2B:fertilization_Strategies0.180	4288.60	2164.96	1.981	0.047612	*
geneSt_ClnH:fertilization_Strategies0.180	4238.62	2164.96	1.958	0.050262	*	geneSt_SulFT2C:fertilization_Strategies0.180	4257.74	2164.96	1.967	0.049234	*
geneSt_CWP:fertilization_Strategies0.180	6111.38	2164.96	2.823	0.004764	**	geneSt_TRDX:fertilization_Strategies0.180	4511.49	2164.96	2.084	0.037183	*
geneSt_CysP11:fertilization_Strategies0.180	4324.31	2164.96	1.997	0.045792	*	geneSt_UBIE:fertilization_Strategies0.180	3070.25	2164.96	1.418	0.156158	.
geneSt_CysT:fertilization_Strategies0.180	4268.98	2164.96	1.972	0.048338	*	geneSt_Unk1:fertilization_Strategies0.180	4285.87	2164.96	1.980	0.047754	*
geneSt_DUF506A:fertilization_Strategies0.180	4448.90	2164.96	2.055	0.039894	*	geneSt_Unk2:fertilization_Strategies0.180	4178.12	2164.96	1.930	0.053633	.
geneSt_DUF506B:fertilization_Strategies0.180	4299.97	2164.96	1.986	0.047026	*	geneSt_Unk3:fertilization_Strategies0.180	4296.63	2164.96	1.985	0.047198	*
geneSt_EPI:fertilization_Strategies0.180	4250.77	2164.96	1.963	0.049607	*	geneSt_Unk4:fertilization_Strategies0.180	4298.19	2164.96	1.985	0.047118	*

Figure 15: Summary of the model 2 (9)

geneSt_Unk5:fertilization_Strategies0.180	4014.68	2164.96	1.854	0.063096	.	geneSt_NT:fertilization_Strategies60.180	3066.93	700.05	4.381	1.19e-05	***
geneSt_Xyl:fertilization_Strategies0.180	4458.62	2164.96	2.059	0.039462	*	geneSt_P109A:fertilization_Strategies60.180	3093.00	700.05	4.418	9.99e-06	***
geneSt_NT2:fertilization_Strategies60.180	2705.93	700.05	3.865	0.000111	***	geneSt_PBenzR:fertilization_Strategies60.180	3317.13	700.05	4.738	2.17e-06	***
geneSt_PP7A:fertilization_Strategies60.180	3087.53	700.05	4.410	1.04e-05	***	geneSt_PDX:fertilization_Strategies60.180	3121.71	700.05	4.459	8.26e-06	***
geneSt_PP7B:fertilization_Strategies60.180	3091.95	700.05	4.417	1.01e-05	***	geneSt_PPT:fertilization_Strategies60.180	3097.14	700.05	4.424	9.72e-06	***
geneSt_AA1:fertilization_Strategies60.180	3013.73	700.05	4.305	1.68e-05	***	geneSt_PLD:fertilization_Strategies60.180	3098.60	700.05	4.426	9.63e-06	***
geneSt_AA2:fertilization_Strategies60.180	3100.01	700.05	4.428	9.54e-06	***	geneSt_PolyAP:fertilization_Strategies60.180	3056.47	700.05	4.364	1.27e-05	***
geneSt_AOX:fertilization_Strategies60.180	1761.28	700.05	2.516	0.011878	*	geneSt_PP2C:fertilization_Strategies60.180	3076.32	700.05	4.394	1.12e-05	***
geneSt_Apase:fertilization_Strategies60.180	2933.75	700.05	4.191	2.79e-05	***	geneSt_ProH:fertilization_Strategies60.180	2824.68	700.05	4.035	5.48e-05	***
geneSt_ArFA:fertilization_Strategies60.180	3106.32	700.05	4.437	9.15e-06	***	geneSt_ProH1:fertilization_Strategies60.180	3099.20	700.05	4.427	9.59e-06	***
geneSt_ArFB:fertilization_Strategies60.180	3434.74	700.05	4.906	9.34e-07	***	geneSt_PyrK:fertilization_Strategies60.180	2986.49	700.05	4.262	2.00e-05	***
geneSt_CatT:fertilization_Strategies60.180	2968.52	700.05	4.240	2.24e-05	***	geneSt_RPK:fertilization_Strategies60.180	3095.84	700.05	4.422	9.81e-06	***
geneSt_CatTR:fertilization_Strategies60.180	3573.40	700.05	5.105	3.34e-07	***	geneSt_SulFase:fertilization_Strategies60.180	3174.23	700.05	4.534	5.81e-06	***
geneSt_CGL:fertilization_Strategies60.180	3005.90	700.05	4.294	1.76e-05	***	geneSt_SulFT:fertilization_Strategies60.180	2964.08	700.05	4.234	2.30e-05	***
geneSt_ClnC:fertilization_Strategies60.180	2242.03	700.05	3.203	0.001363	**	geneSt_SulFT2A:fertilization_Strategies60.180	3037.48	700.05	4.339	1.44e-05	***
geneSt_ClnH:fertilization_Strategies60.180	114.00	700.05	0.163	0.870635	.	geneSt_SulFT2B:fertilization_Strategies60.180	3085.78	700.05	4.408	1.05e-05	***
geneSt_CWP:fertilization_Strategies60.180	3112.49	700.05	4.446	8.78e-06	***	geneSt_SulFT2C:fertilization_Strategies60.180	3071.09	700.05	4.387	1.15e-05	***
geneSt_CysP11:fertilization_Strategies60.180	3183.24	700.05	4.547	5.46e-06	***	geneSt_TRDX:fertilization_Strategies60.180	3098.24	700.05	4.426	9.65e-06	***
geneSt_CysT:fertilization_Strategies60.180	3440.00	700.05	4.914	8.99e-07	***	geneSt_UBIE:fertilization_Strategies60.180	2382.01	700.05	3.603	0.000668	***
geneSt_DUF506A:fertilization_Strategies60.180	3090.71	700.05	4.415	1.01e-05	***	geneSt_Unk1:fertilization_Strategies60.180	3246.05	700.05	4.637	3.56e-06	***
geneSt_DUF506B:fertilization_Strategies60.180	3097.34	700.05	4.424	9.71e-06	***	geneSt_Unk2:fertilization_Strategies60.180	3143.88	700.05	4.491	7.12e-06	***
geneSt_EPI:fertilization_Strategies60.180	3067.63	700.05	4.382	1.18e-05	***	geneSt_Unk3:fertilization_Strategies60.180	3096.04	700.05	4.423	9.80e-06	***
geneSt_FT:fertilization_Strategies60.180	2858.74	700.05	4.004	4.45e-05	***	geneSt_Unk4:fertilization_Strategies60.180	3119.41	700.05	4.456	8.39e-06	***
geneSt_GluAse:fertilization_Strategies60.180	3372.88	700.05	4.818	1.46e-06	***	geneSt_Unk5:fertilization_Strategies60.180	3566.46	700.05	5.095	3.52e-07	***
geneSt_GluDC:fertilization_Strategies60.180	2887.88	700.05	4.125	3.72e-05	***	geneSt_Xyl:fertilization_Strategies60.180	3334.93	700.05	4.764	1.91e-06	***
geneSt_GR3:fertilization_Strategies60.180	3036.84	700.05	4.338	1.44e-05	***	---	---	---	---	---	---
geneSt_GST:fertilization_Strategies60.180	3065.05	700.05	4.378	1.20e-05	***	Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1					
geneSt_InosD:fertilization_Strategies60.180	3020.62	700.05	4.315	1.60e-05	***	Residual standard error: 2138 on 23110 degrees of freedom					
geneSt_Kinase:fertilization_Strategies60.180	3154.81	700.05	4.507	6.62e-06	***	Multiple R-squared: 0.4551, Adjusted R-squared: 0.4371					
geneSt_LIP:fertilization_Strategies60.180	2696.32	700.05	3.852	0.000118	***	F-statistic: 25.2 on 766 and 23110 DF, p-value: < 2.2e-16					
geneSt_LOB38A:fertilization_Strategies60.180	3093.89	700.05	4.420	9.94e-06	***						
geneSt_LOB38B:fertilization_Strategies60.180	3103.15	700.05	4.433	9.35e-06	***						
geneSt_MIP:fertilization_Strategies60.180	2849.29	700.05	4.070	4.71e-05	***						
geneSt_MSFA:fertilization_Strategies60.180	3031.18	700.05	4.330	1.50e-05	***						
geneSt_MSFA5:fertilization_Strategies60.180	3121.84	700.05	4.459	8.25e-06	***						
geneSt_MSFB:fertilization_Strategies60.180	3084.47	700.05	4.406	1.06e-05	***						
geneSt_MN21:fertilization_Strategies60.180	2795.40	700.05	3.993	6.54e-05	***						
geneSt_Nod:fertilization_Strategies60.180	3032.54	700.05	4.332	1.48e-05	***						

Figure 15: Summary of the model 2 (10)

2. The cluster dendrogram

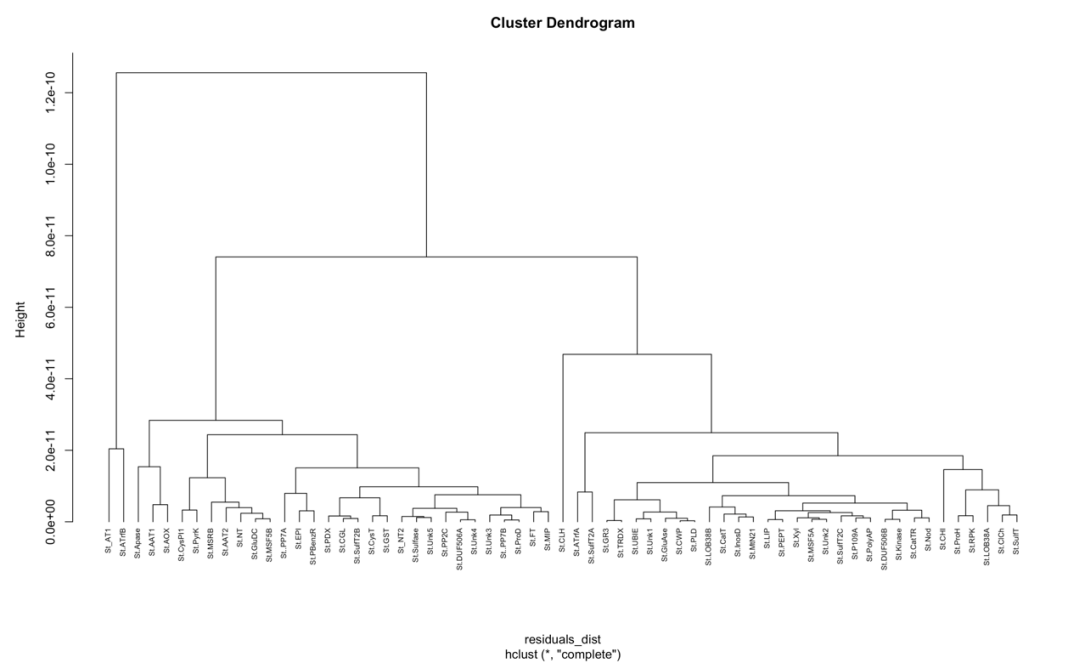


Figure 16: the full cluster dendrogram

3. When the number of clusters is set to three, the clustering results for each gene are obtained.

The focus of this study is on the smaller clusters at the bottom of the cluster dendrogram hence no further analysis is conducted on these results.

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Cluster 1:
[1] St_AT1 St.ATrfB
63 Levels: St_AT1 St_NT2 St..PP7A St..PP7B ... St.Xyl
Cluster 2:
[1] St_NT2 St..PP7A St..PP7B St.AAT1 St.AAT2
[6] St.AOX St.Apase St.CGL St.CysPI1 St.CysT
[11] St.DUF506A St.EPI St.FT St.GluDC St.GST
[16] St.MIP St.MSF5B St.MSRB St.NT St.PBenzR
[21] St.PDX St.PP2C St.ProD St.PyrK St.Sulfase
[26] St.Sulft2B St.Unk3 St.Unk4 St.Unk5
63 Levels: St_AT1 St_NT2 St..PP7A St..PP7B ... St.Xyl
Cluster 3:
[1] St.ATrfA St.CatT St.CatTR St.CHI St.ClCh
[6] St.CLH St.CWP St.DUF506B St.GluAse St.GR3
[11] St.InosD St.Kinase St.LIP St.LOB38A St.LOB38B
[16] St.MSF5A St.MtN21 St.Nod St.P109A St.PEPT
[21] St.PLD St.PolyAP St.ProH St.RPK St.Sulft
[26] St.Sulft2A St.Sulft2C St.TRDX St.UBIE St.Unk1
[31] St.Unk2 St.Xyl
63 Levels: St_AT1 St_NT2 St..PP7A St..PP7B ... St.Xyl

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Figure 17: the result of the cluster