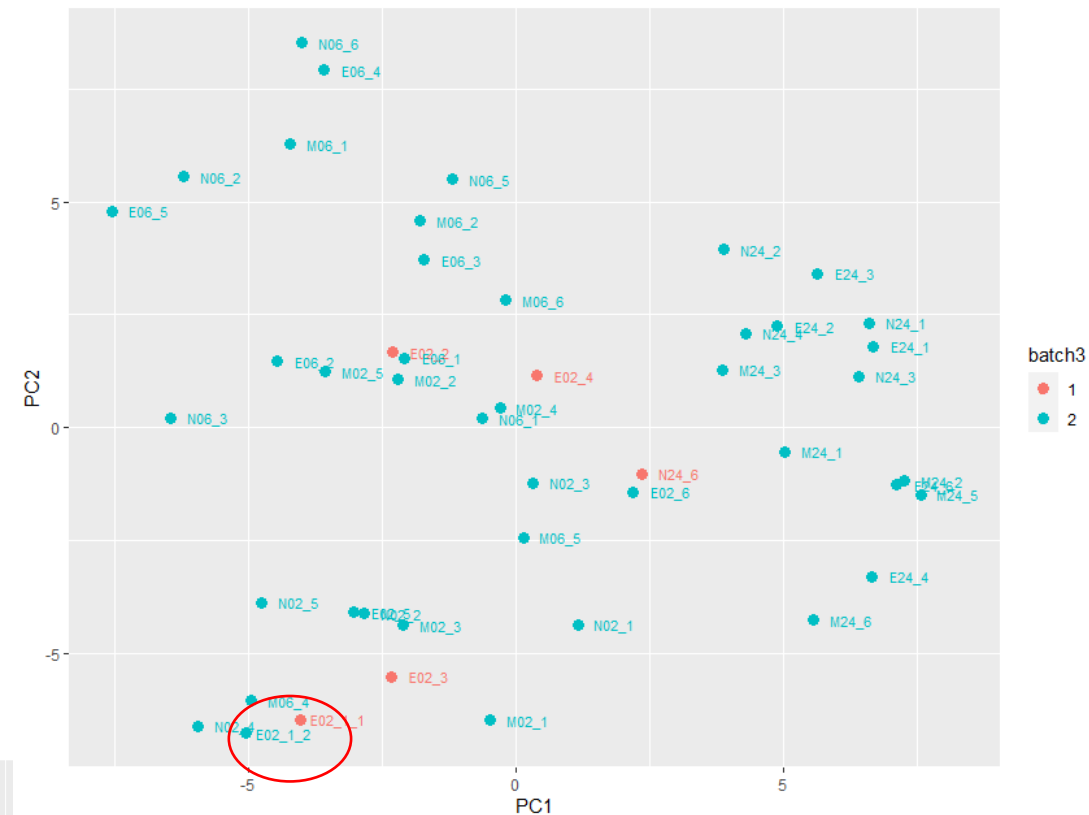
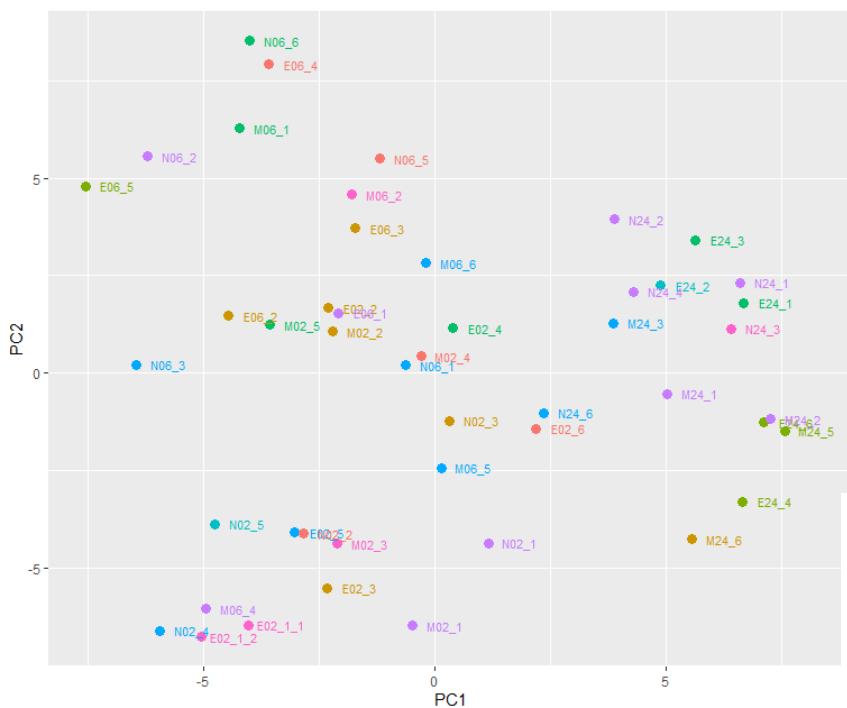
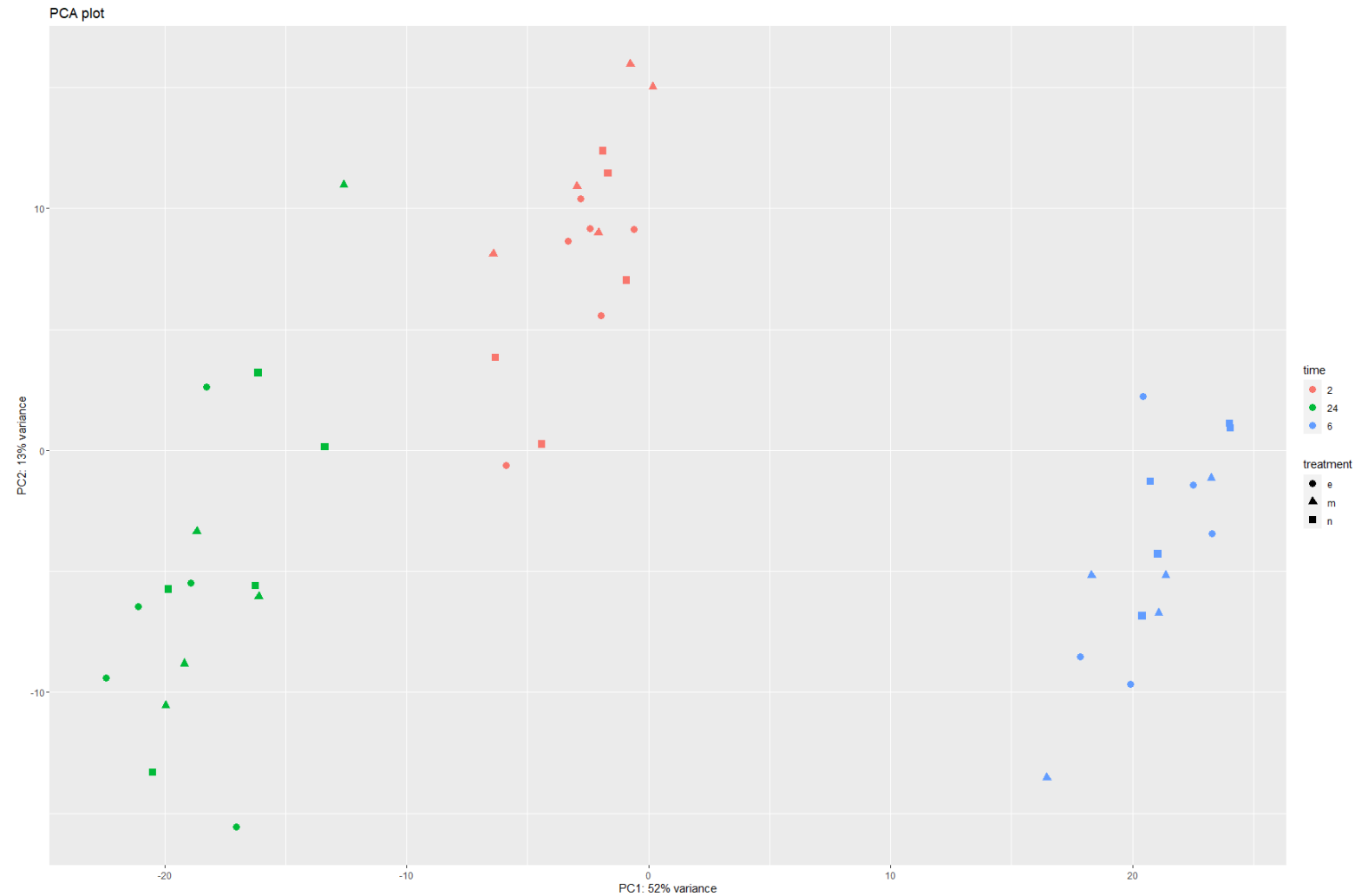


Arabidopsis RNAseq results

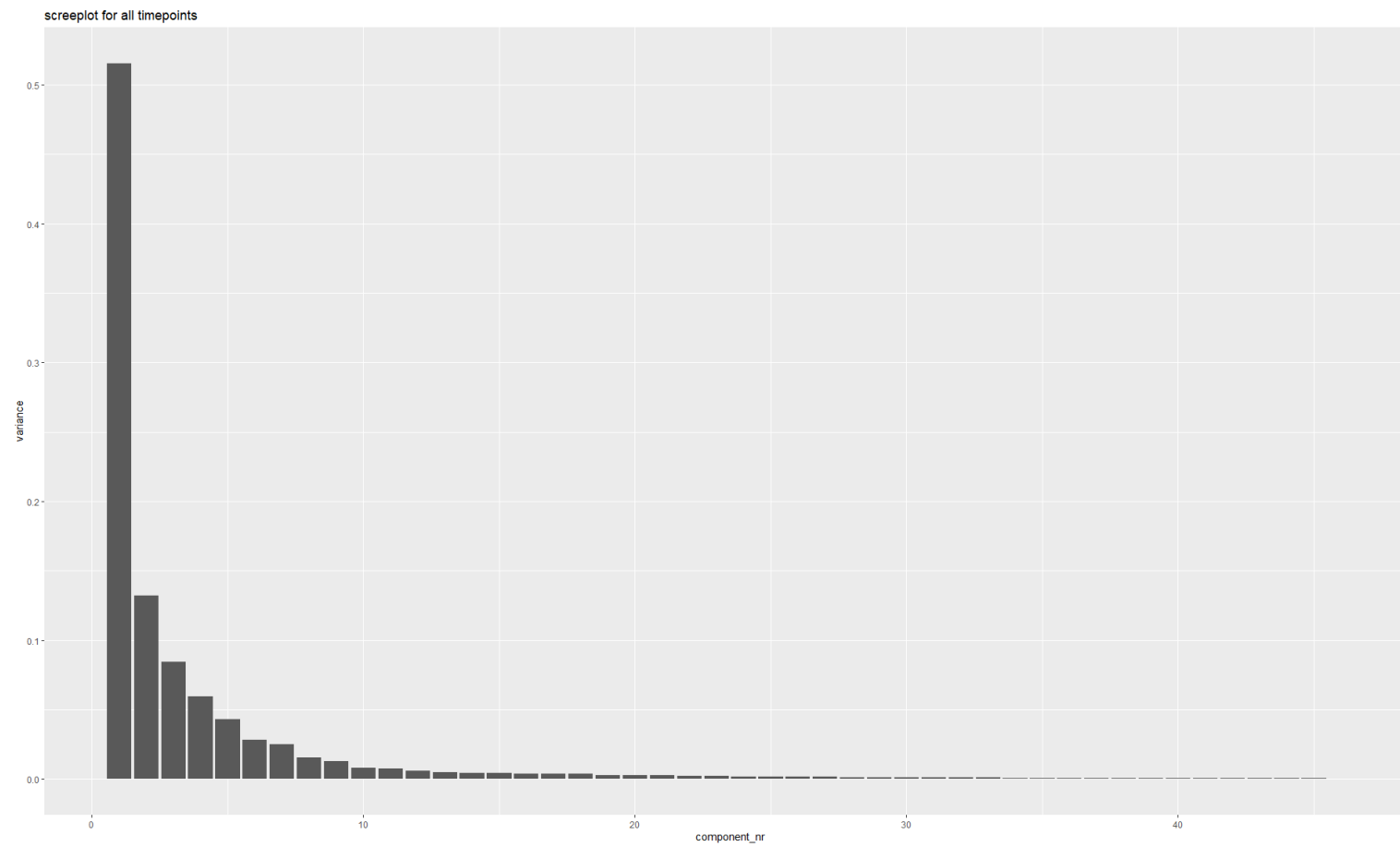
Check for batch effects



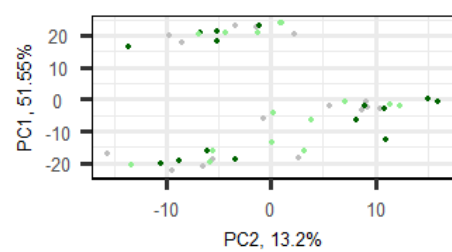
PCA biplot, taking 500 top variance genes



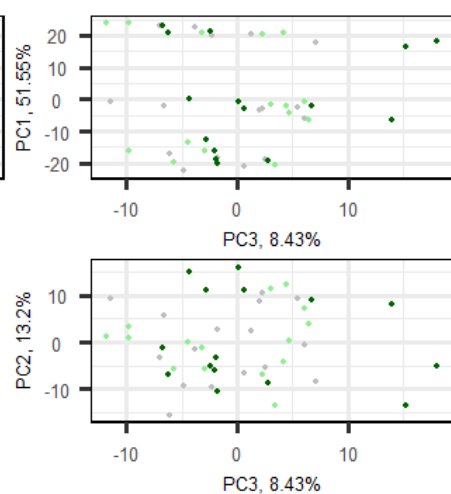
Scree plot



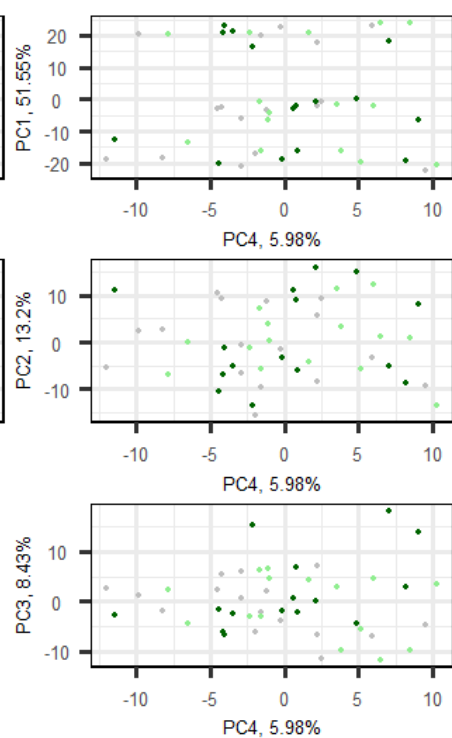
**PC1,
51.55%**



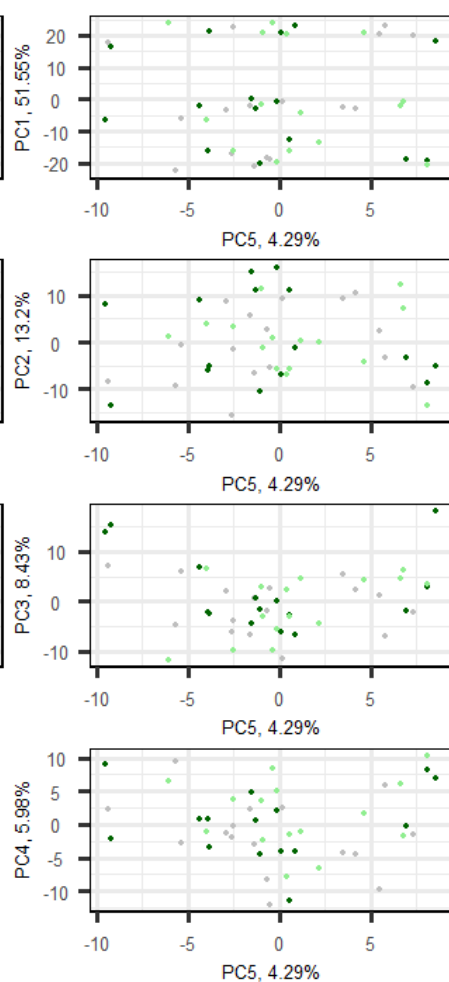
**PC2,
13.2%**



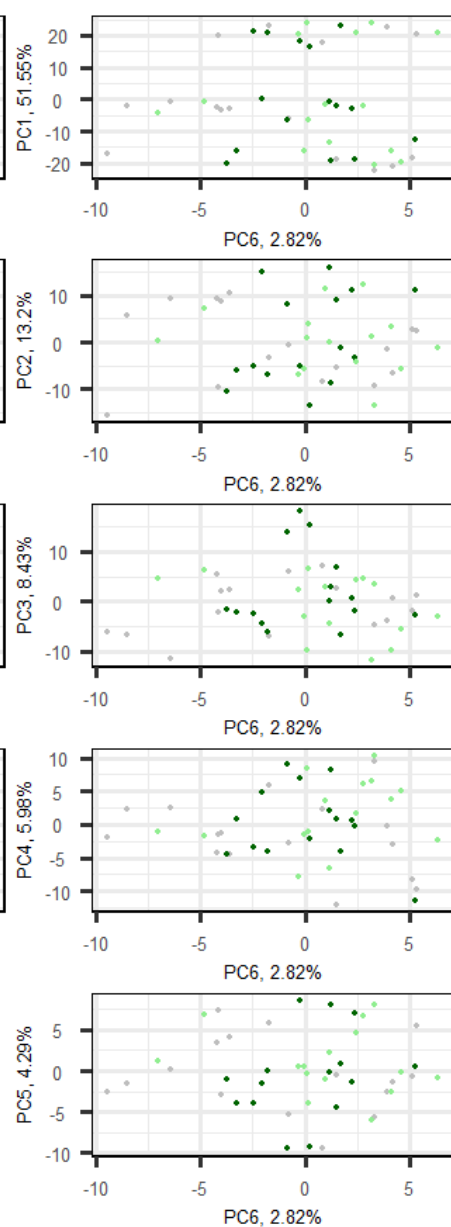
**PC3,
8.43%**



**PC4,
5.98%**



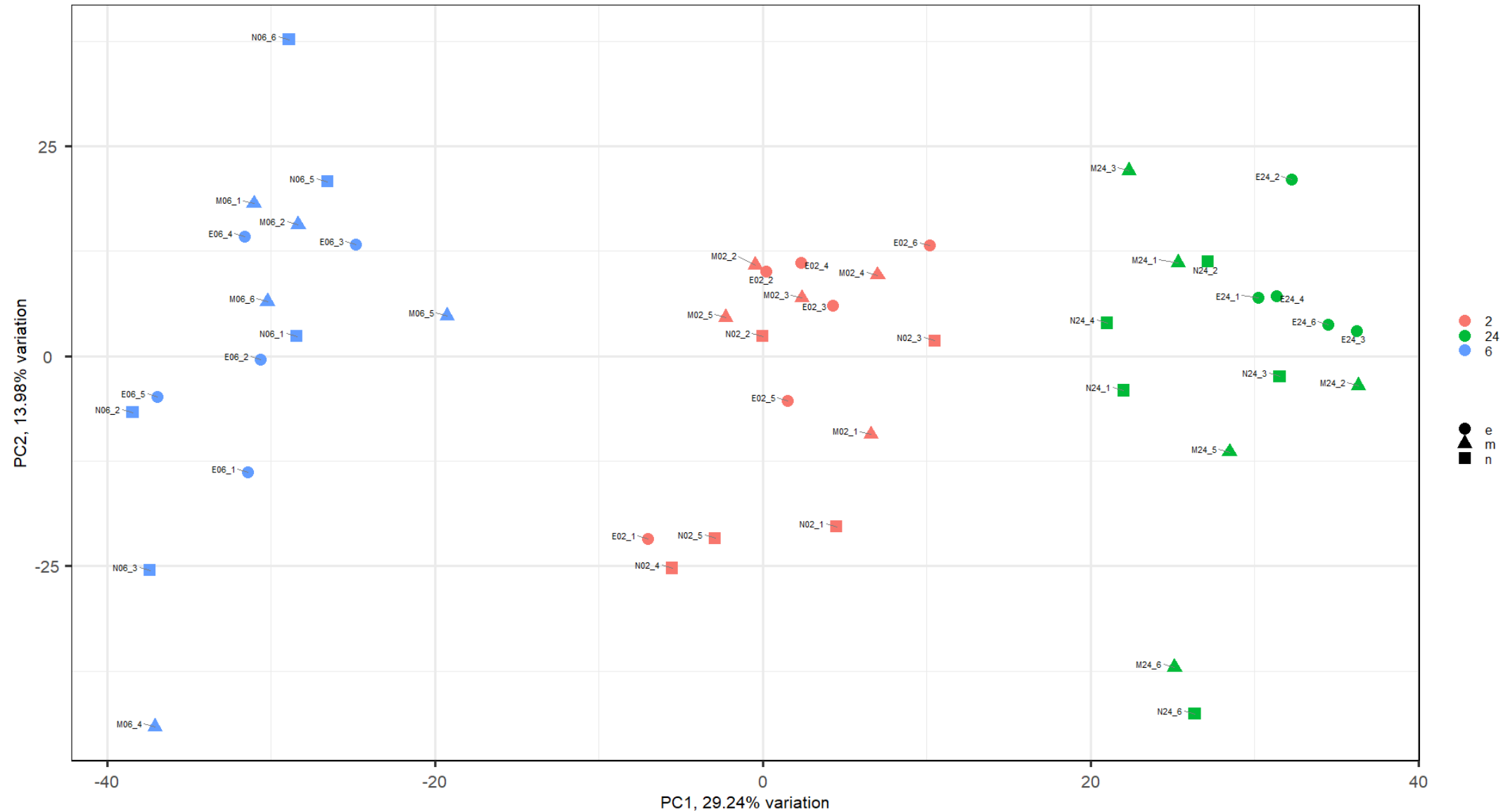
**PC5,
4.29%**



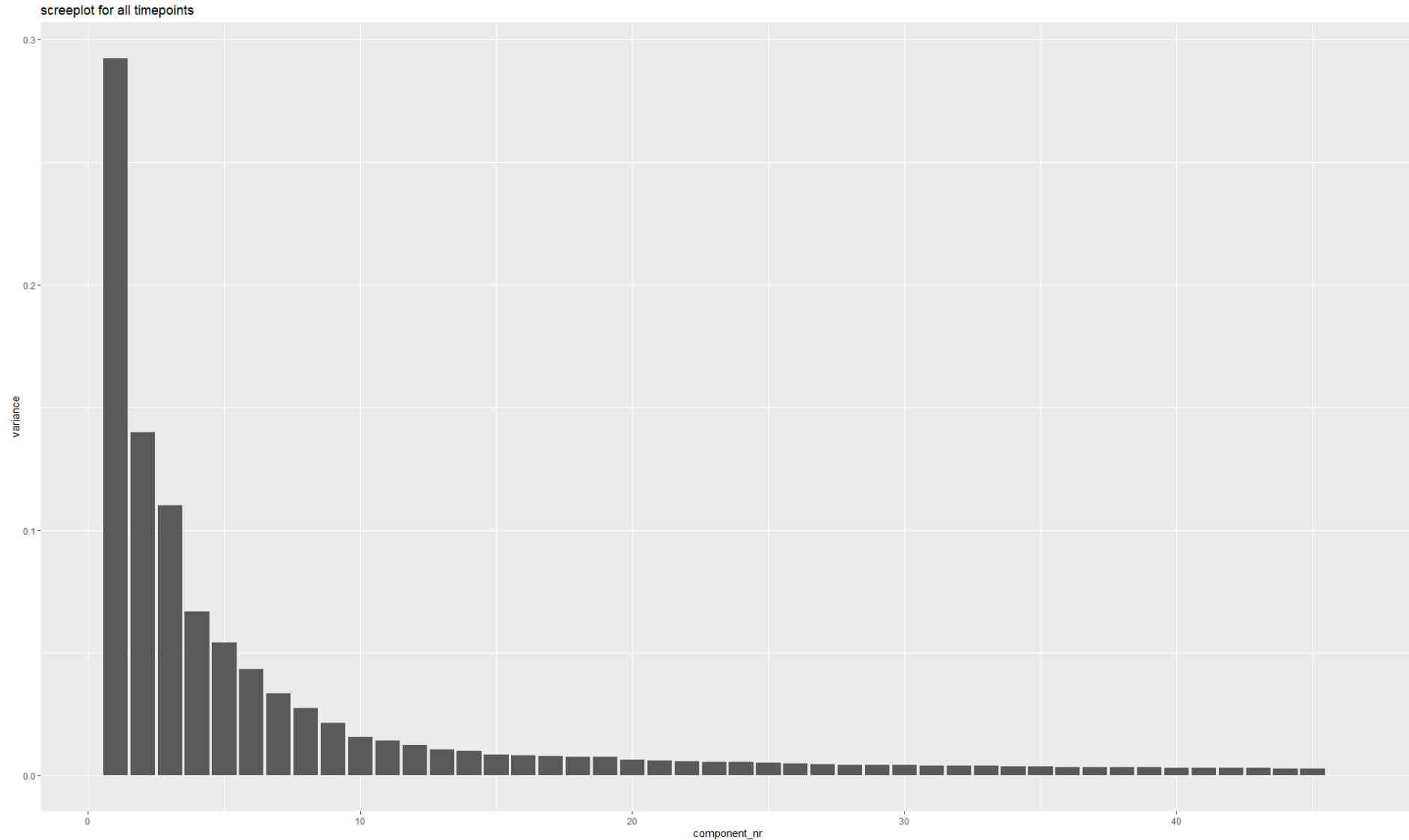
**PC6,
2.82%**

Elbow method says PC6

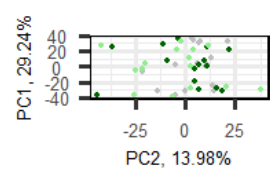
PCA biplot, taking 50% most variable genes



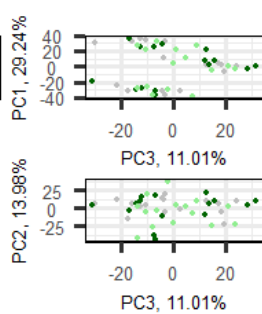
Scree plot top 50% variance genes



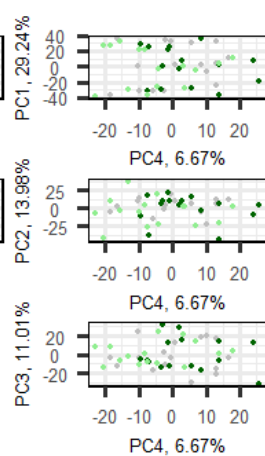
**PC1,
29.24%**



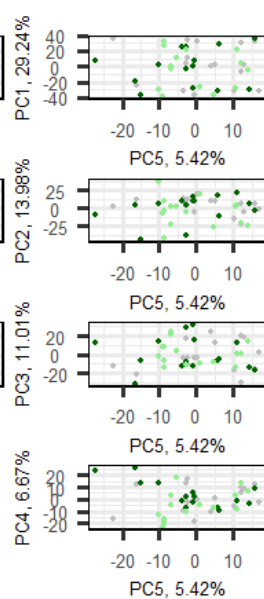
**PC2,
13.98%**



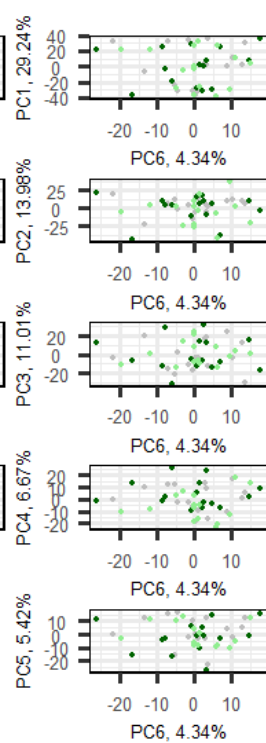
**PC3,
11.01%**



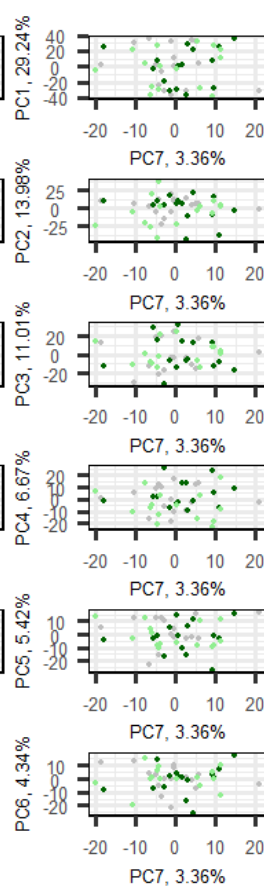
**PC4,
6.67%**



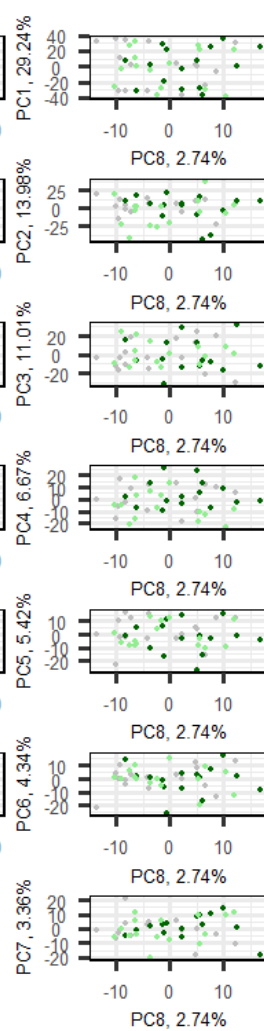
**PC5,
5.42%**



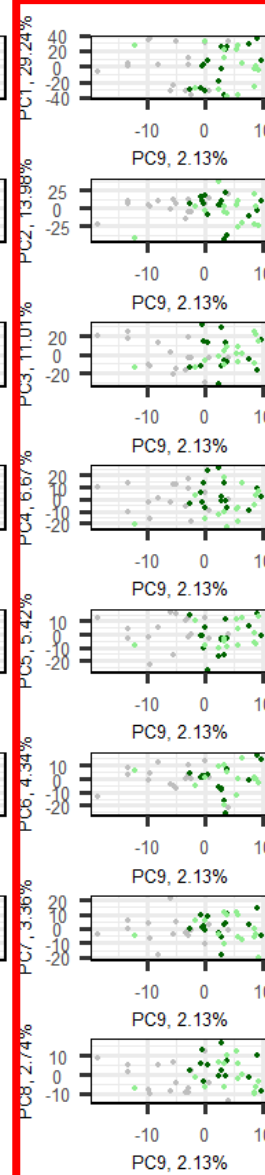
**PC6,
4.34%**



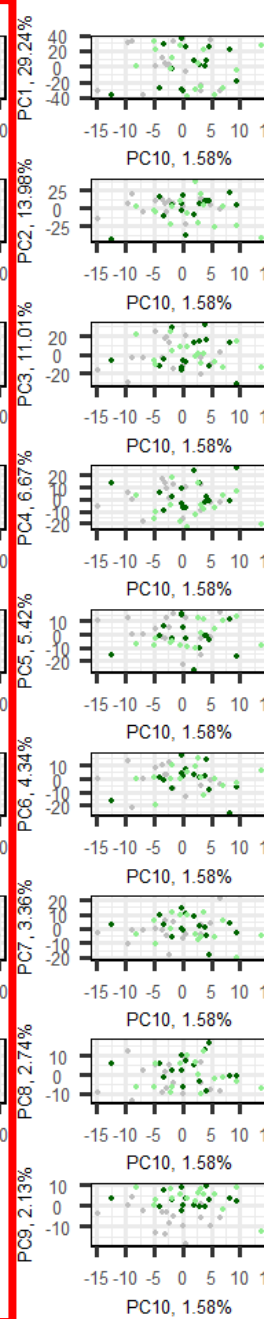
**PC7,
3.36%**



**PC8,
2.74%**



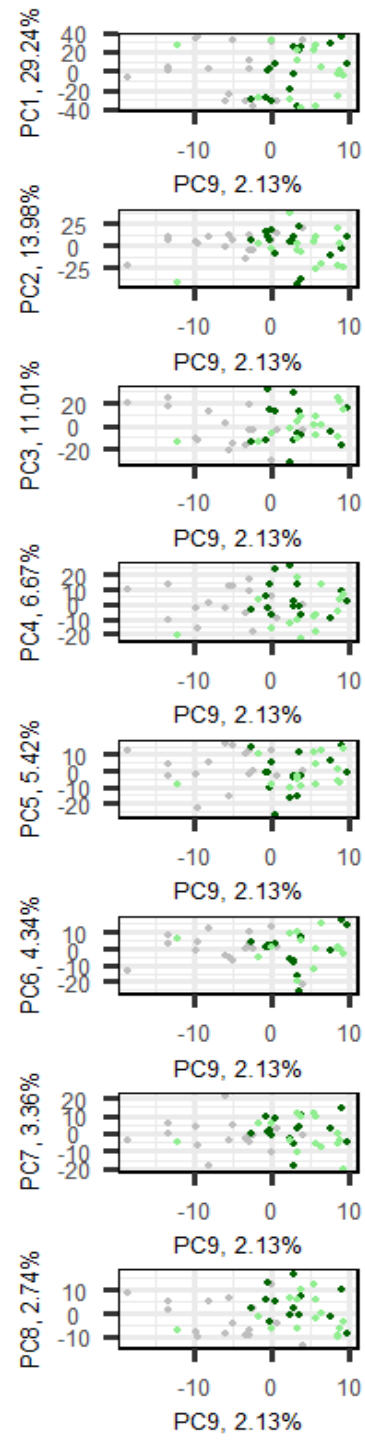
**PC9,
2.13%**



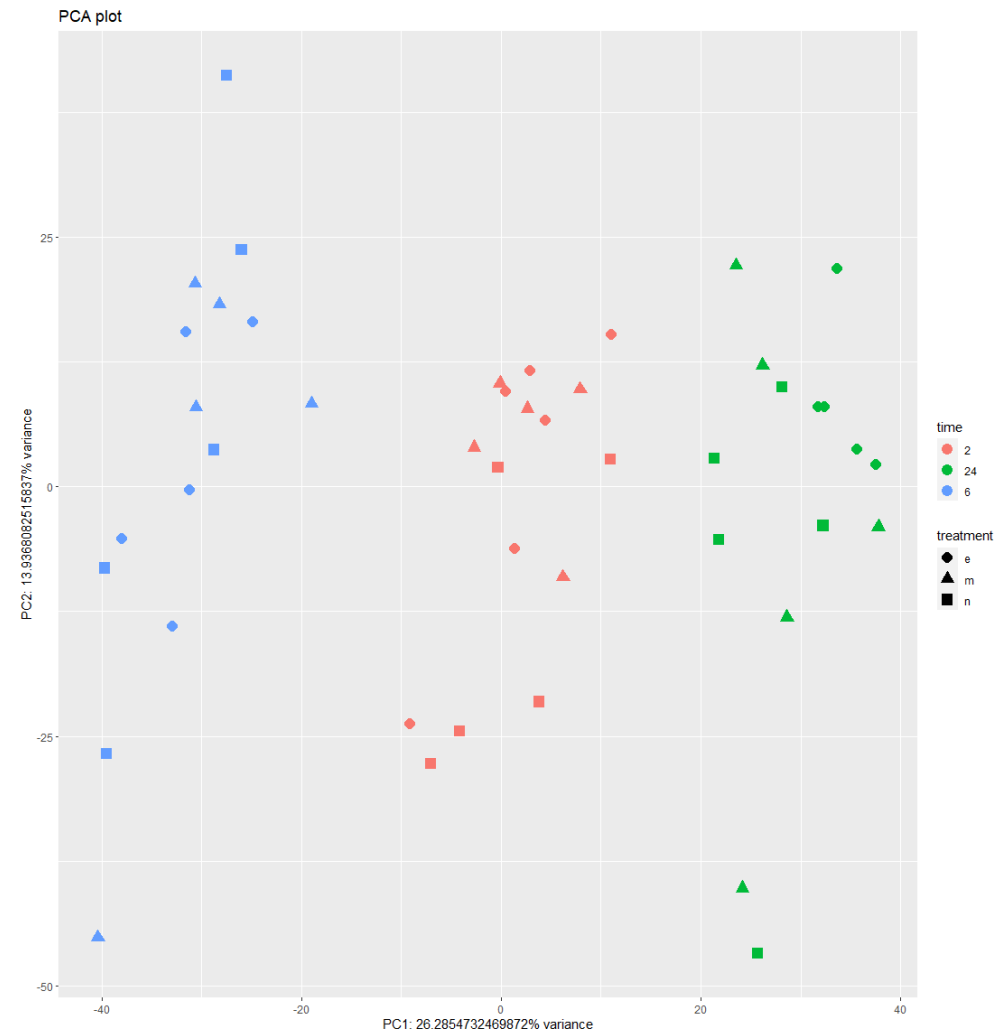
**PC10,
1.58%**



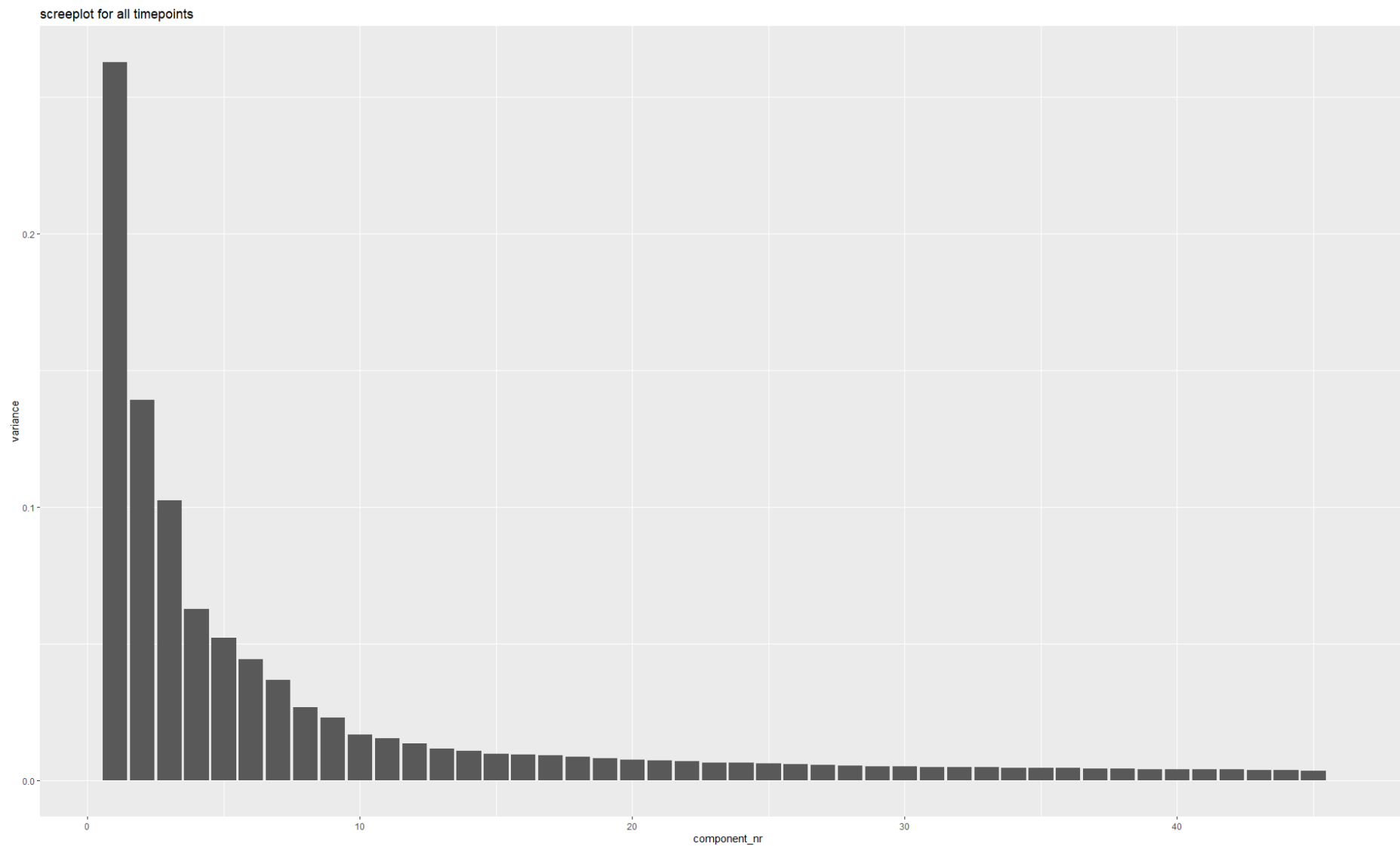
Gray = EtOH carrier
Lightgreen = nM solA
Darkgreen = uM solA



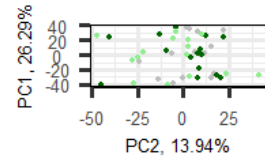
PCA plot lower 10% of variance removed



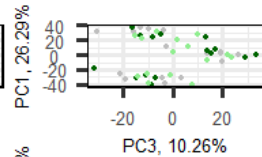
Scree plot doesn't change so much



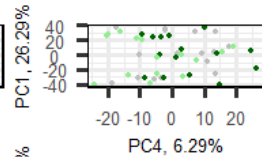
**PC1,
26.29%**



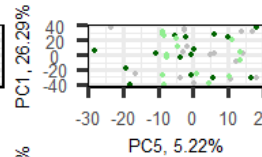
**PC2,
13.94%**



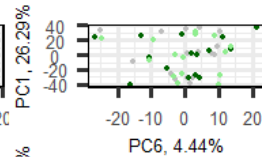
**PC3,
10.26%**



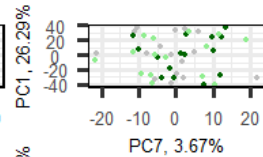
**PC4,
6.29%**



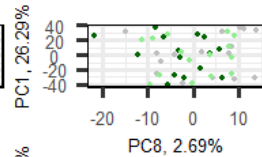
**PC5,
5.22%**



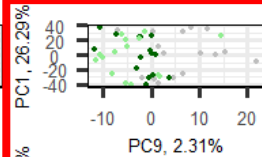
**PC6,
4.44%**



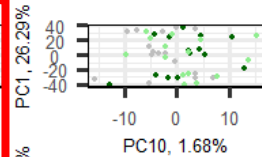
**PC7,
3.67%**



**PC8,
2.69%**

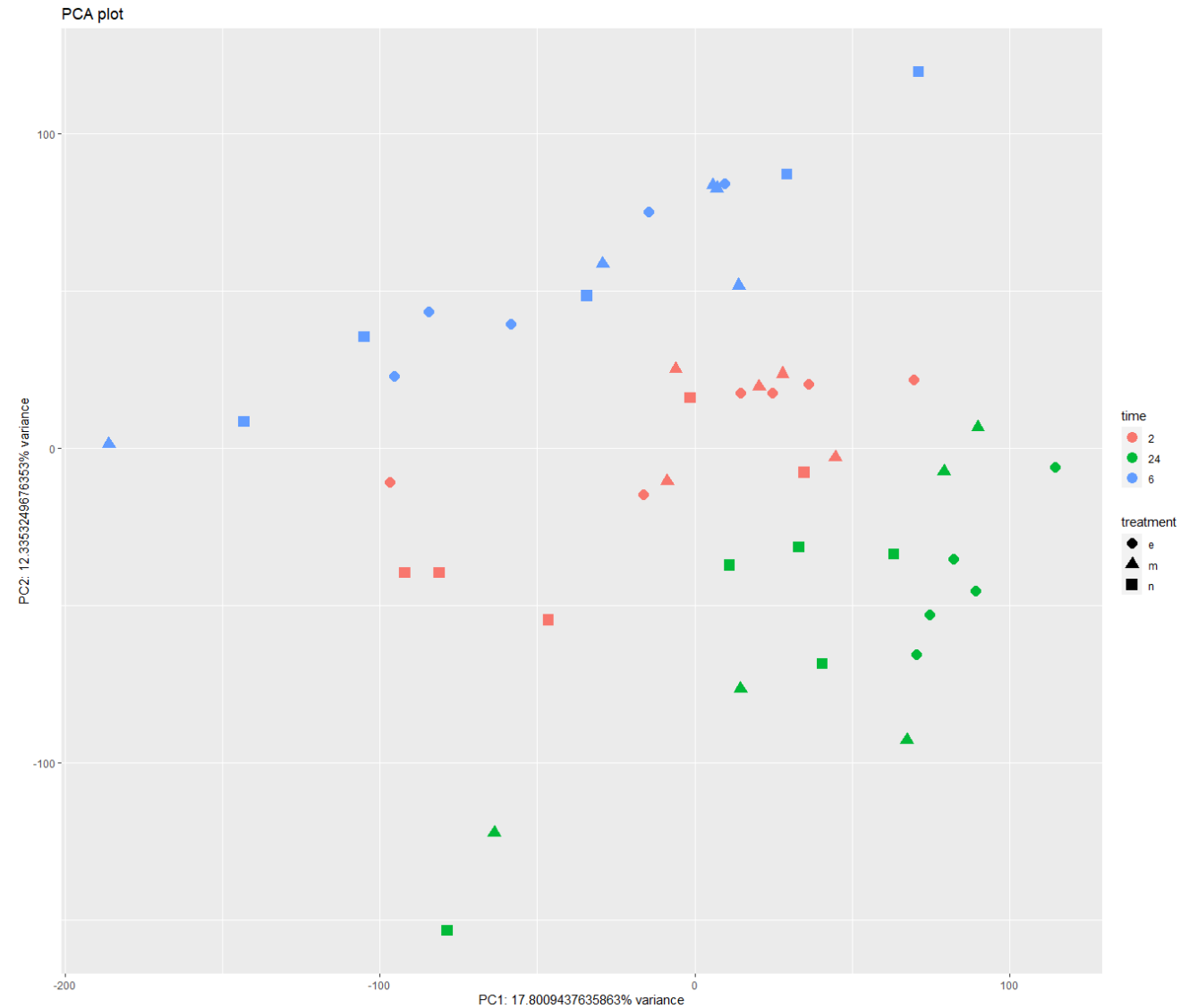


**PC9,
2.31%**

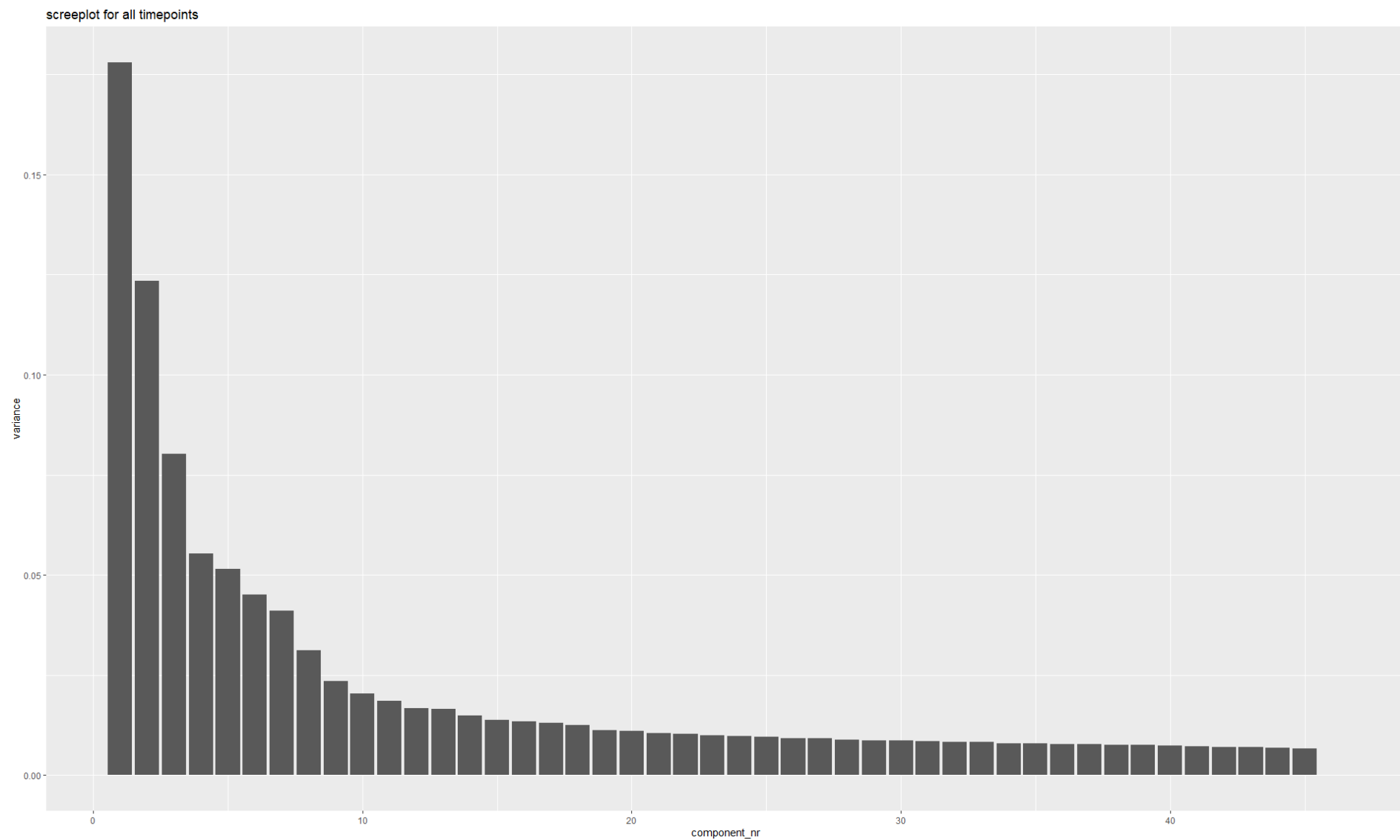


**PC10,
1.68%**

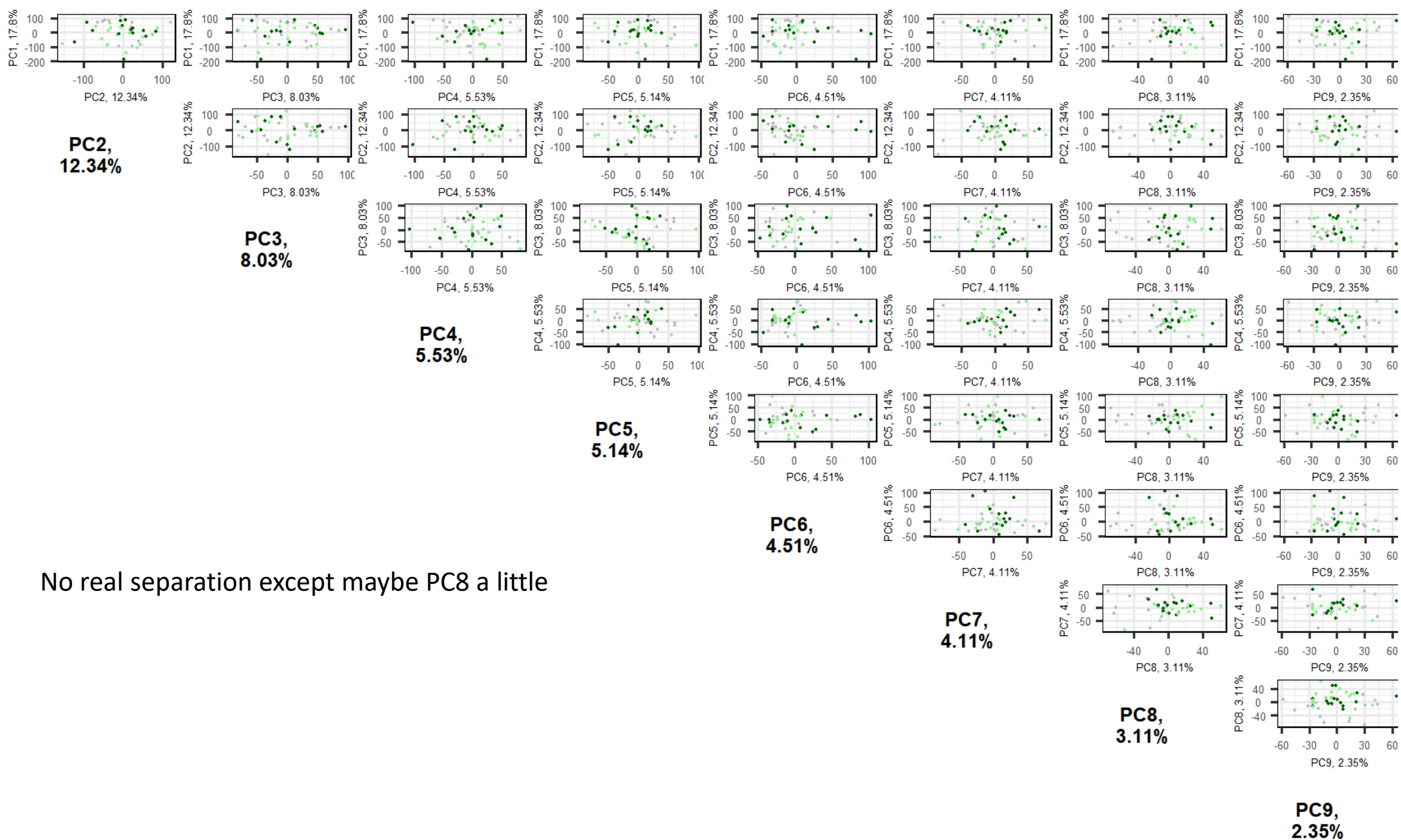
PCA plot, remvar 10%, *scaled*



Scree plot *scaled*

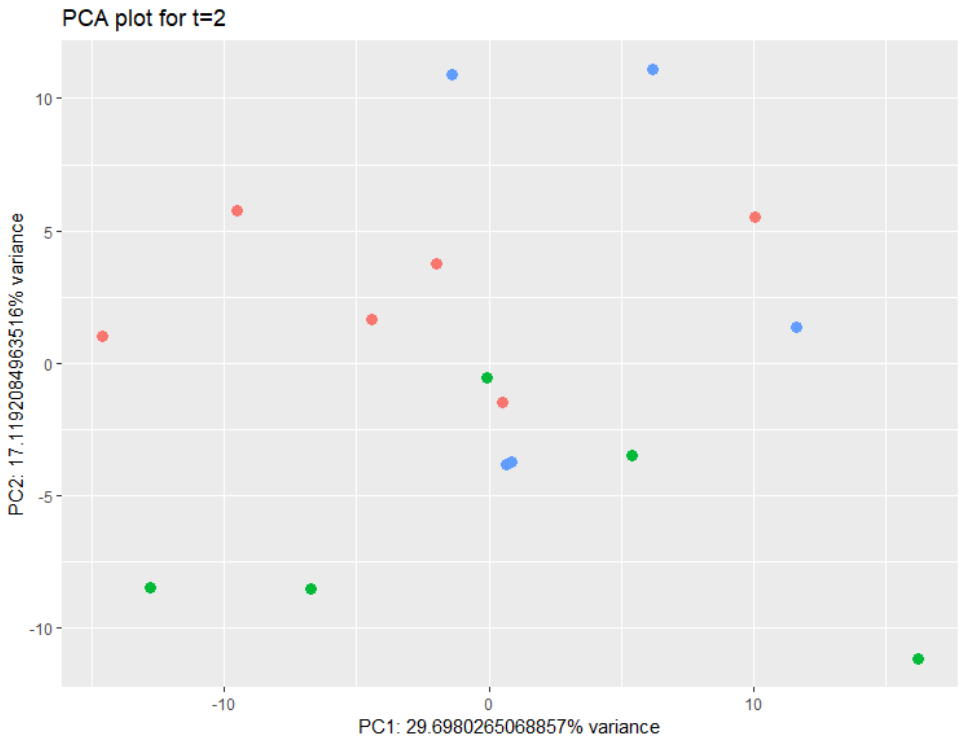


**PC1,
17.8%**

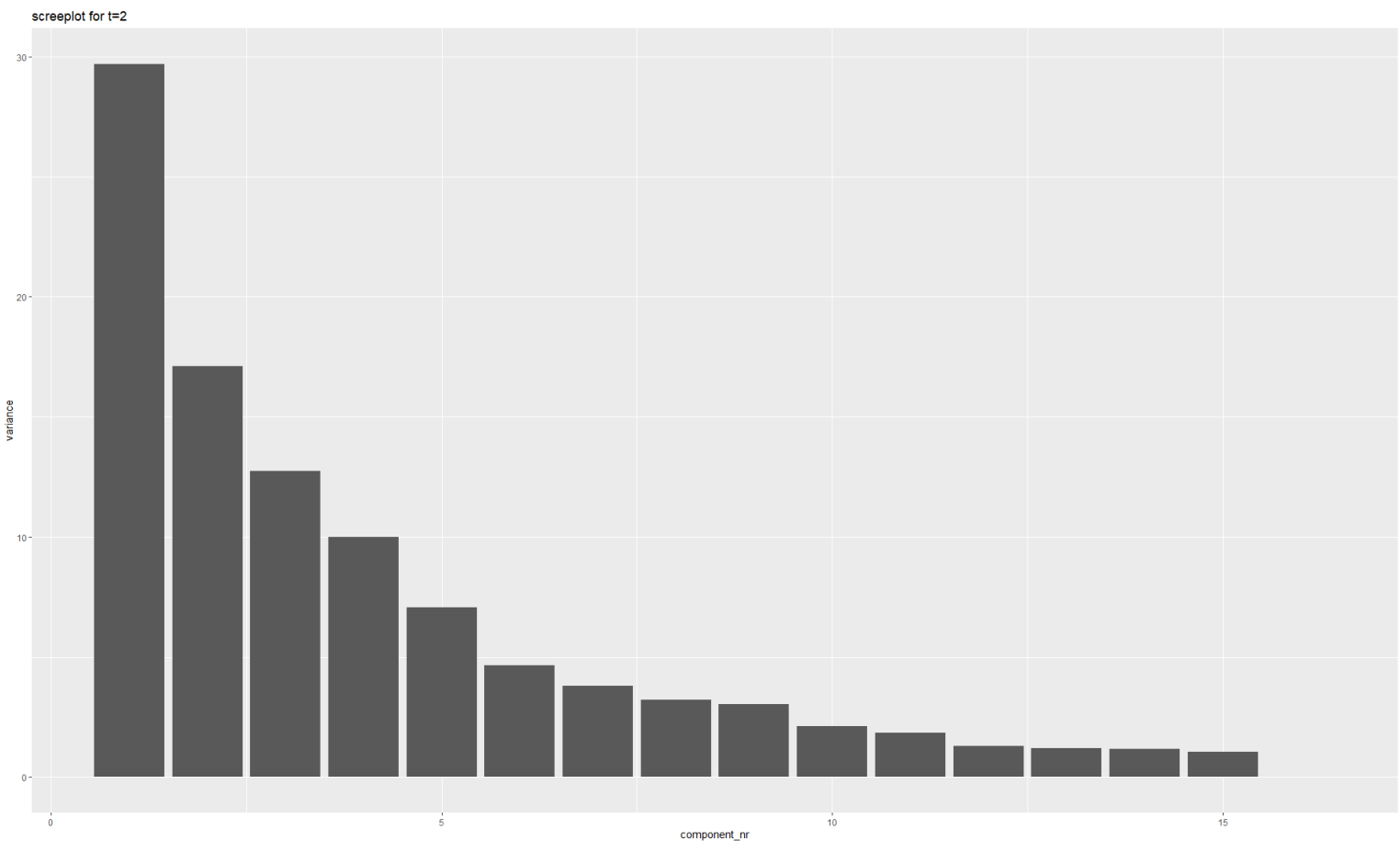


Biplot and screeplot t=2

non-scaled, 500 top variance genes

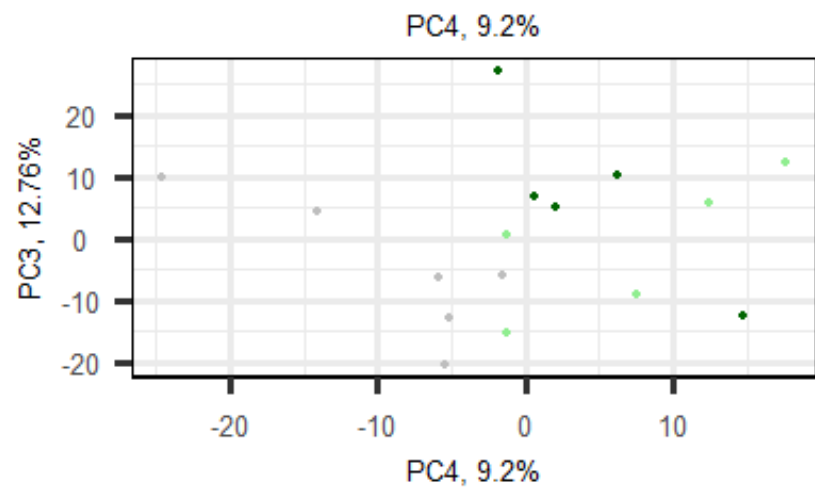
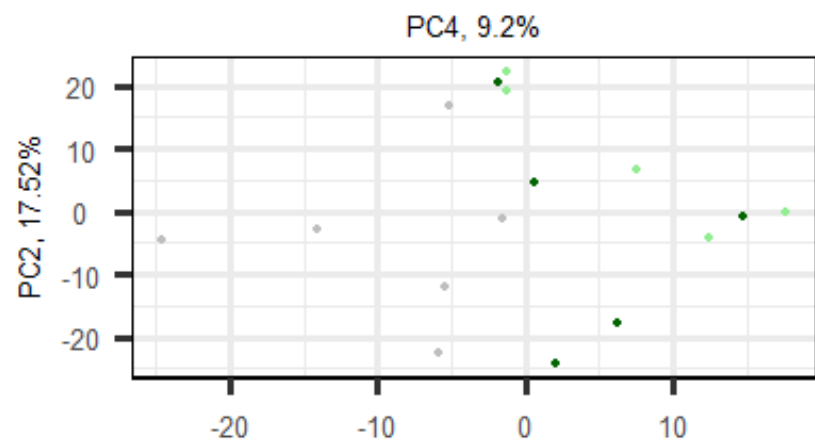
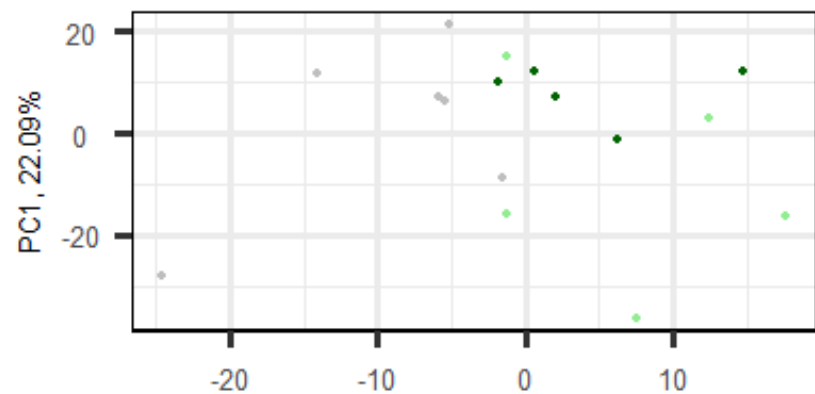


No further interesting biplots

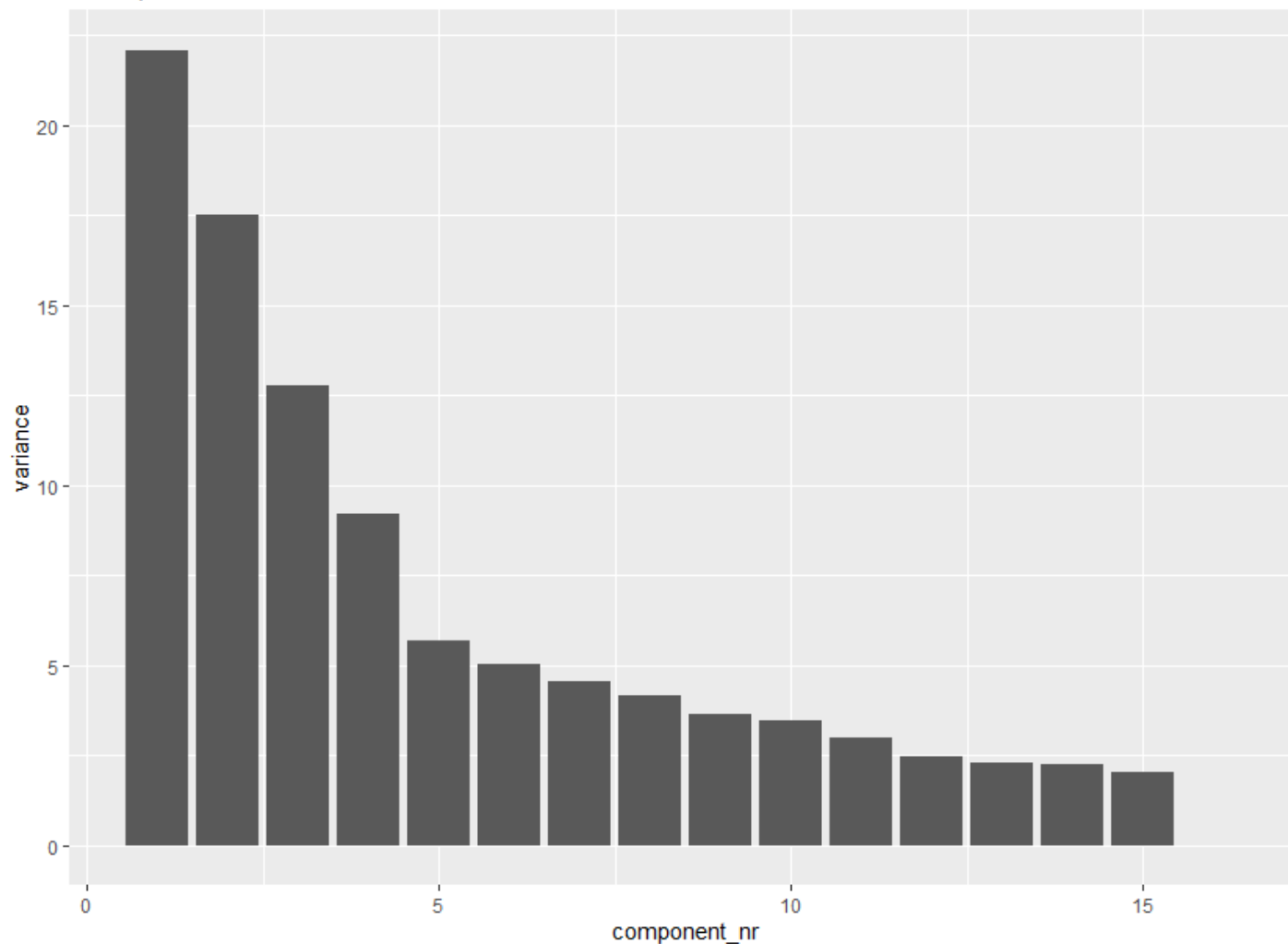


Biplot and screeplot t=2

non-scaled, 50% top variance genes

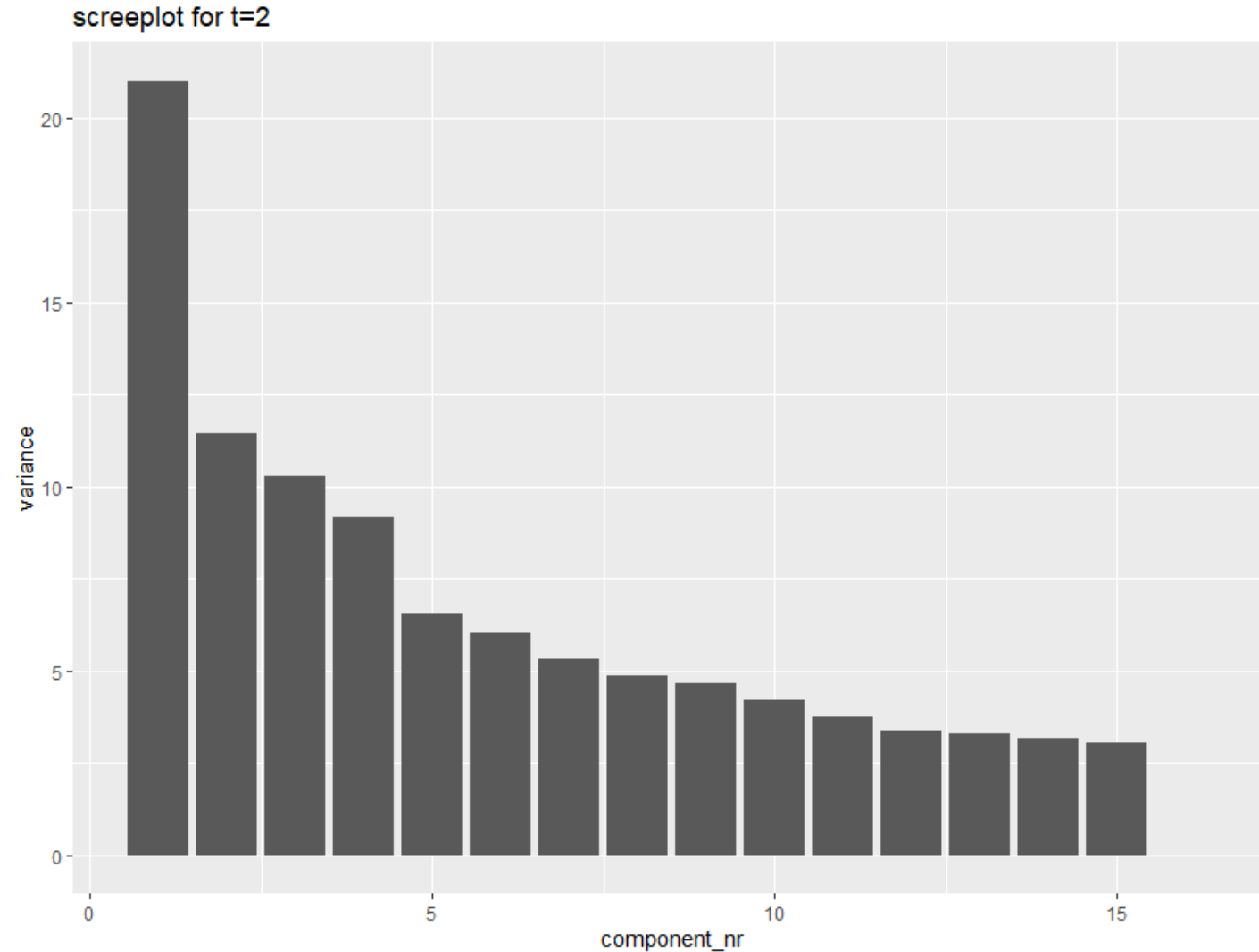
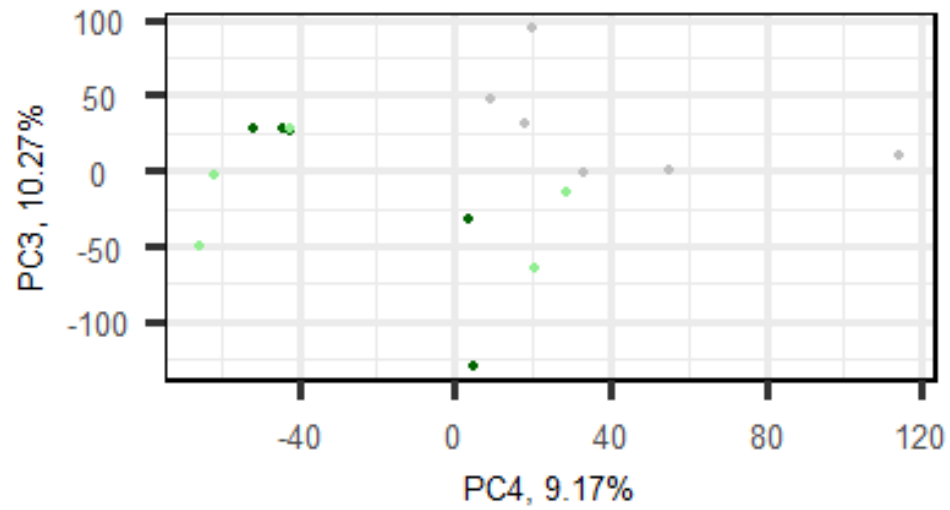


screeplot for t=2



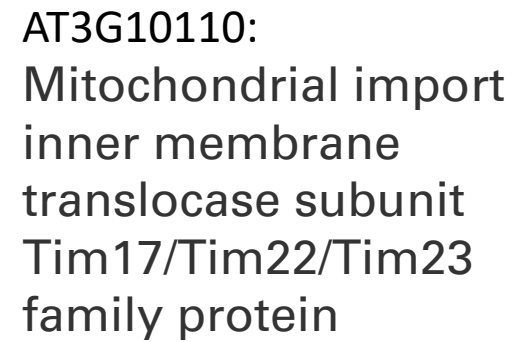
Biplot and screeplot t=2

scaled, 90% top variance genes



PC1, PC2, PC3, PC4, PC5

PC1, PC2, PC3, PC4, PC5



Top 0.1% variables

Permanova on t=2 subdataset

Call:

```
adonis(formula = counts_norm_vst_2_t ~ treatment, data = xp_design_2, permutations = 9999, method = "euclidean")
```

Permutation: free

Number of permutations: 9999

Terms added sequentially (first to last)

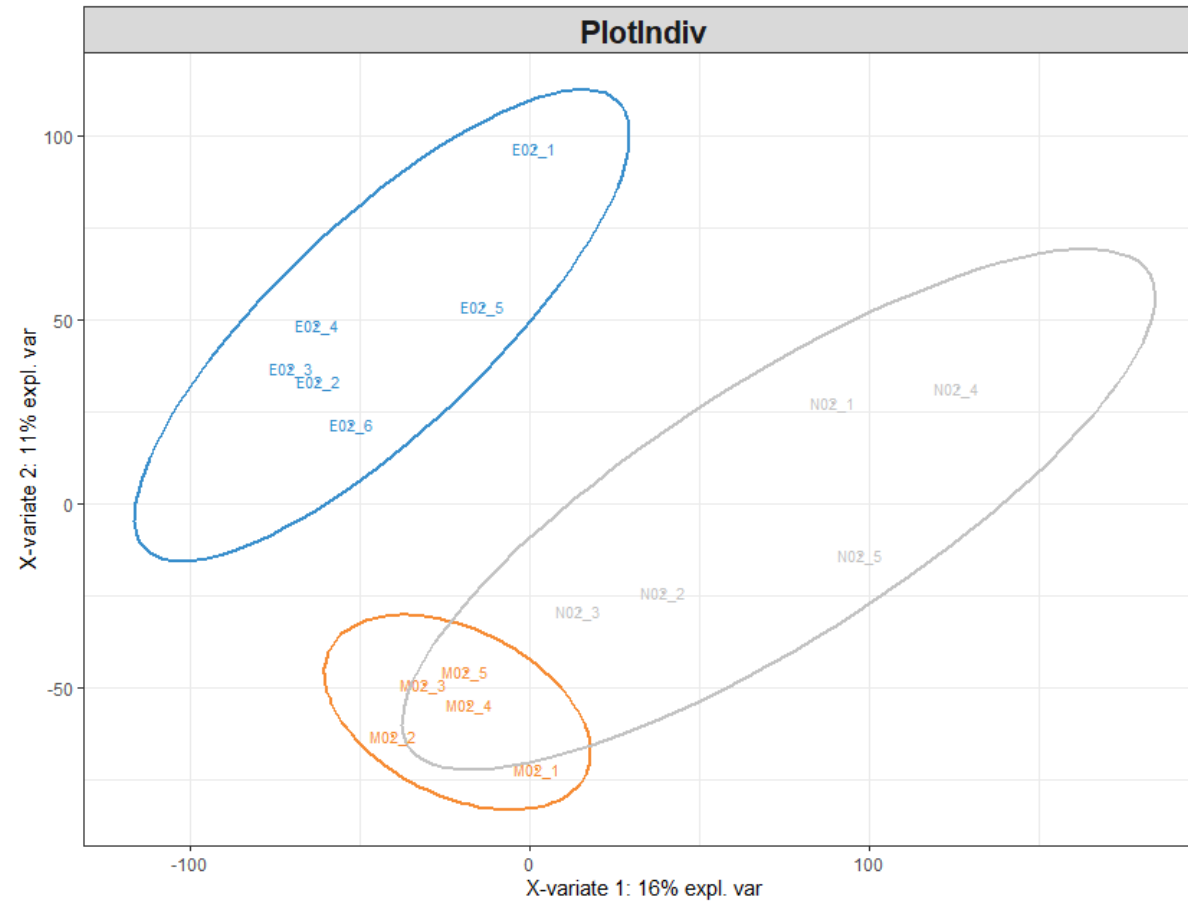
	Df	SumsOfSqs	MeanSqs	F.Model	R2
treatment	2	4016.2	2008.1	1.4526	0.18266
Residuals	13	17971.4	1382.4		0.81734
Total	15	21987.6			1.00000

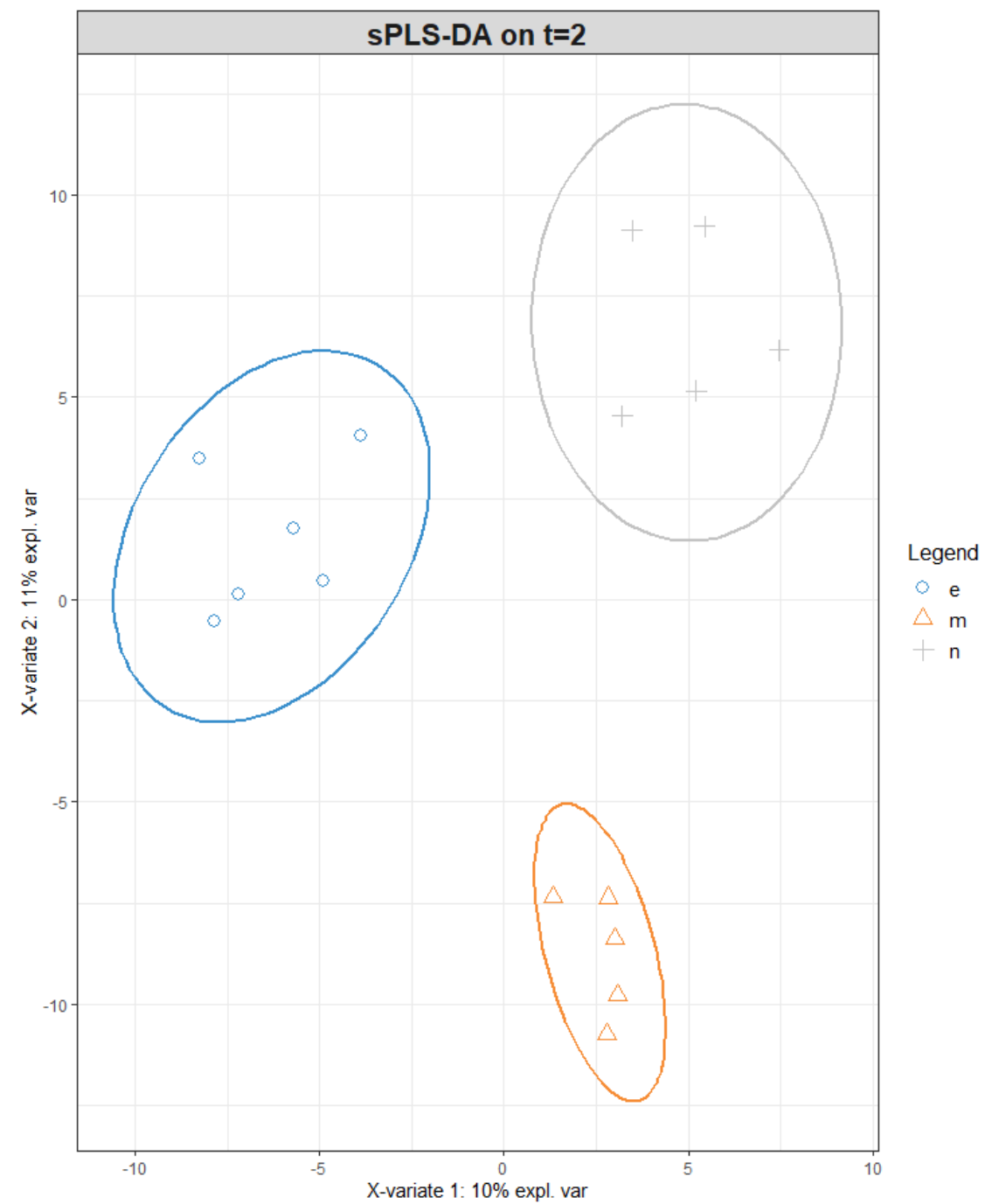
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Pr(>F)
0.0404 *

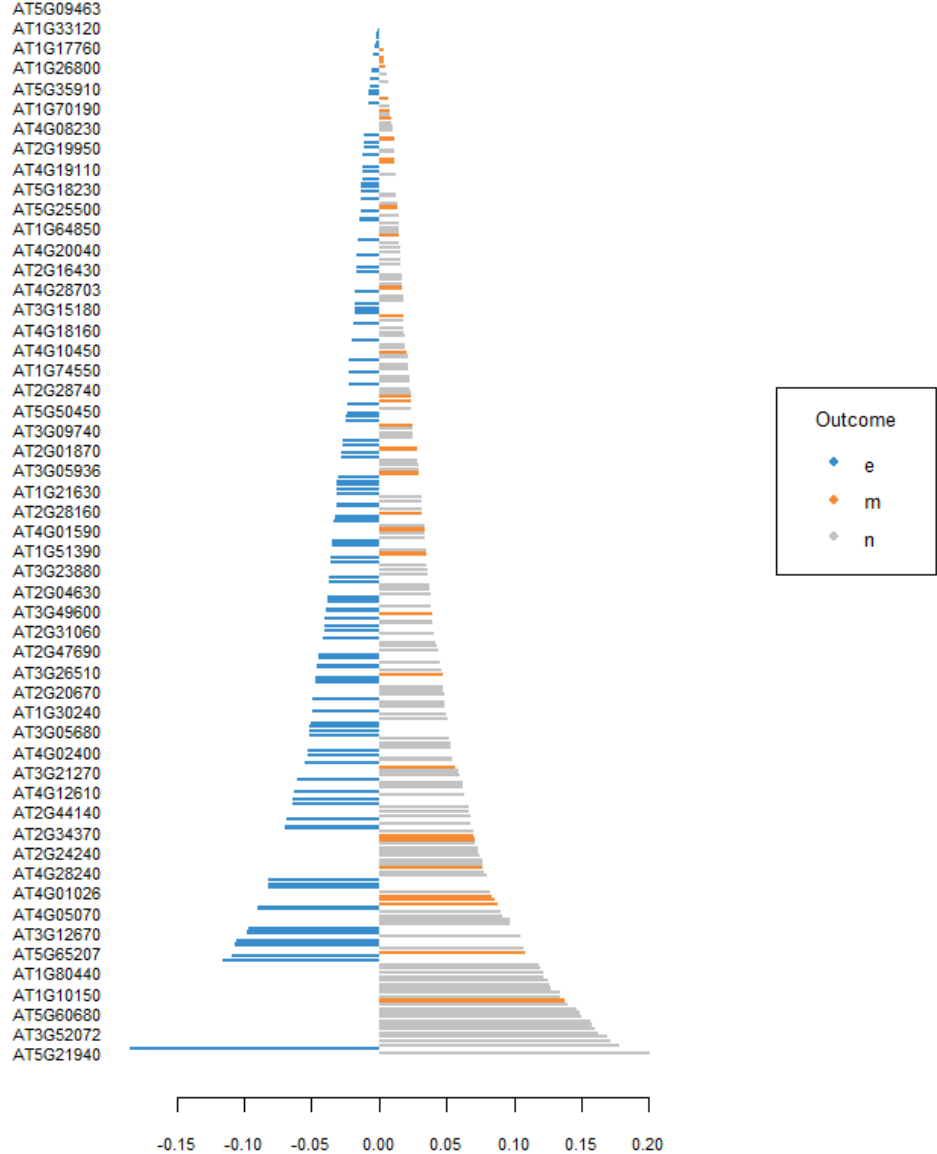
The other two timepoints do not show a significant effect of treatment

PLS-DA on treatment at t=2

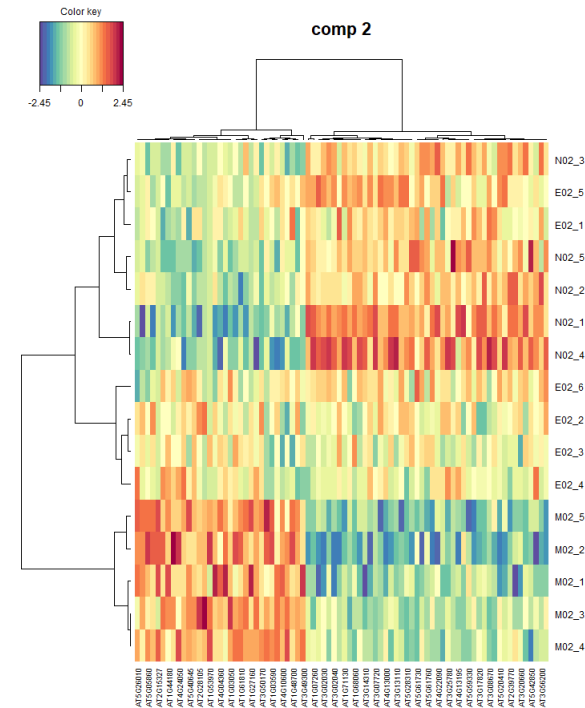
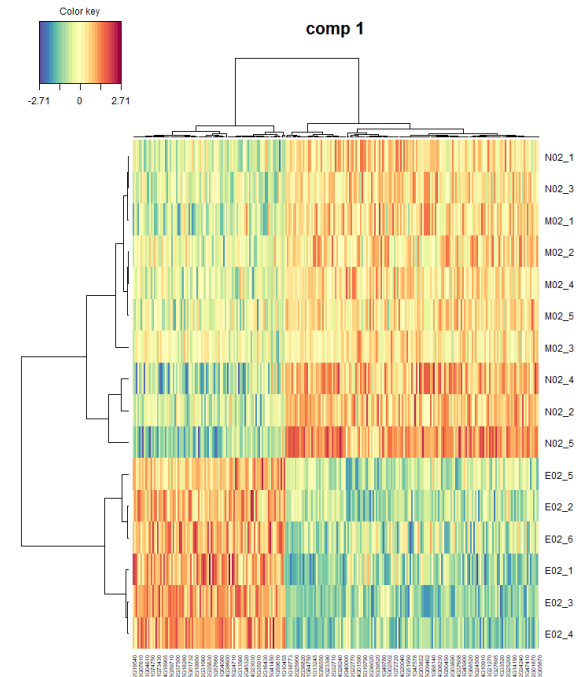
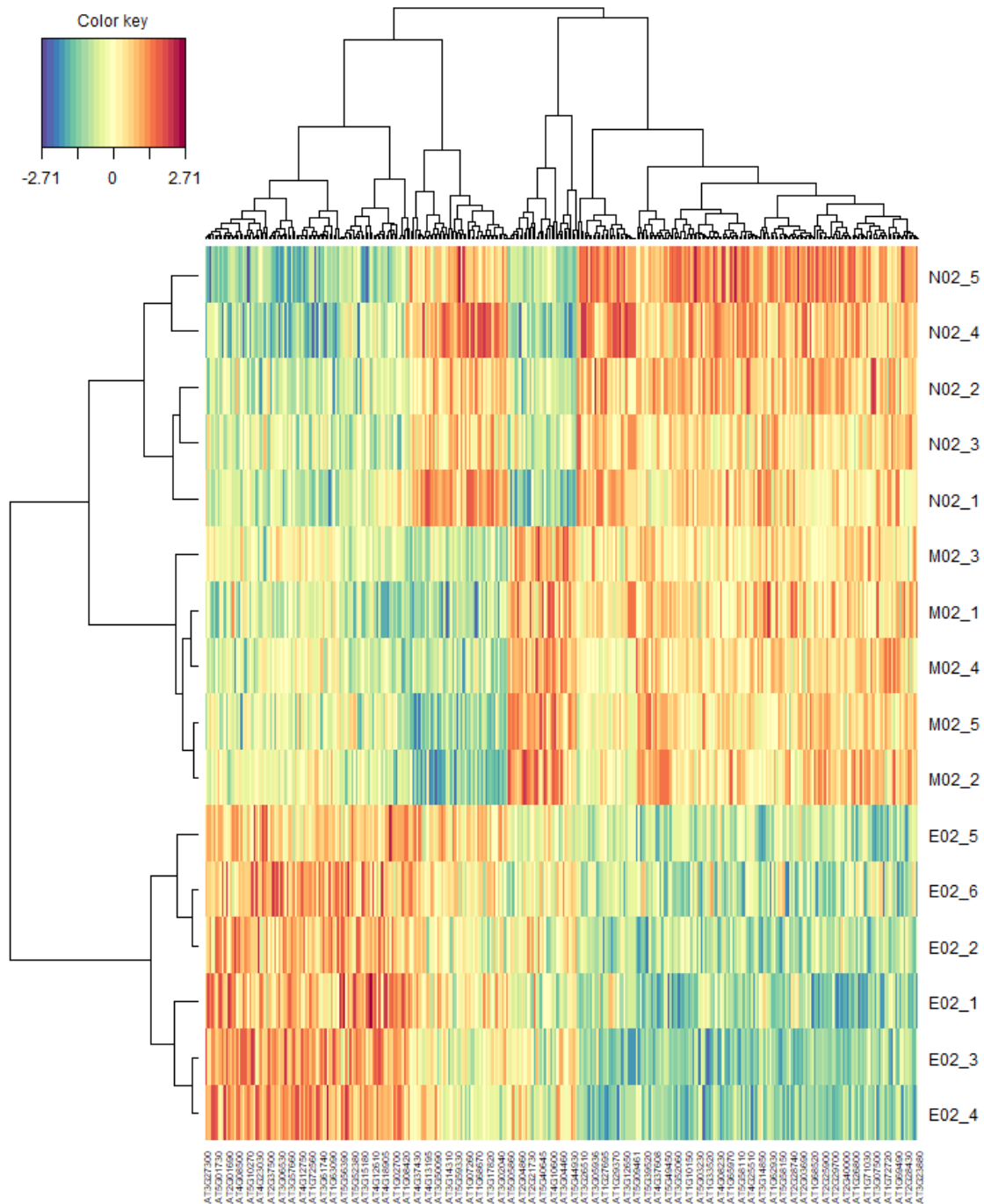




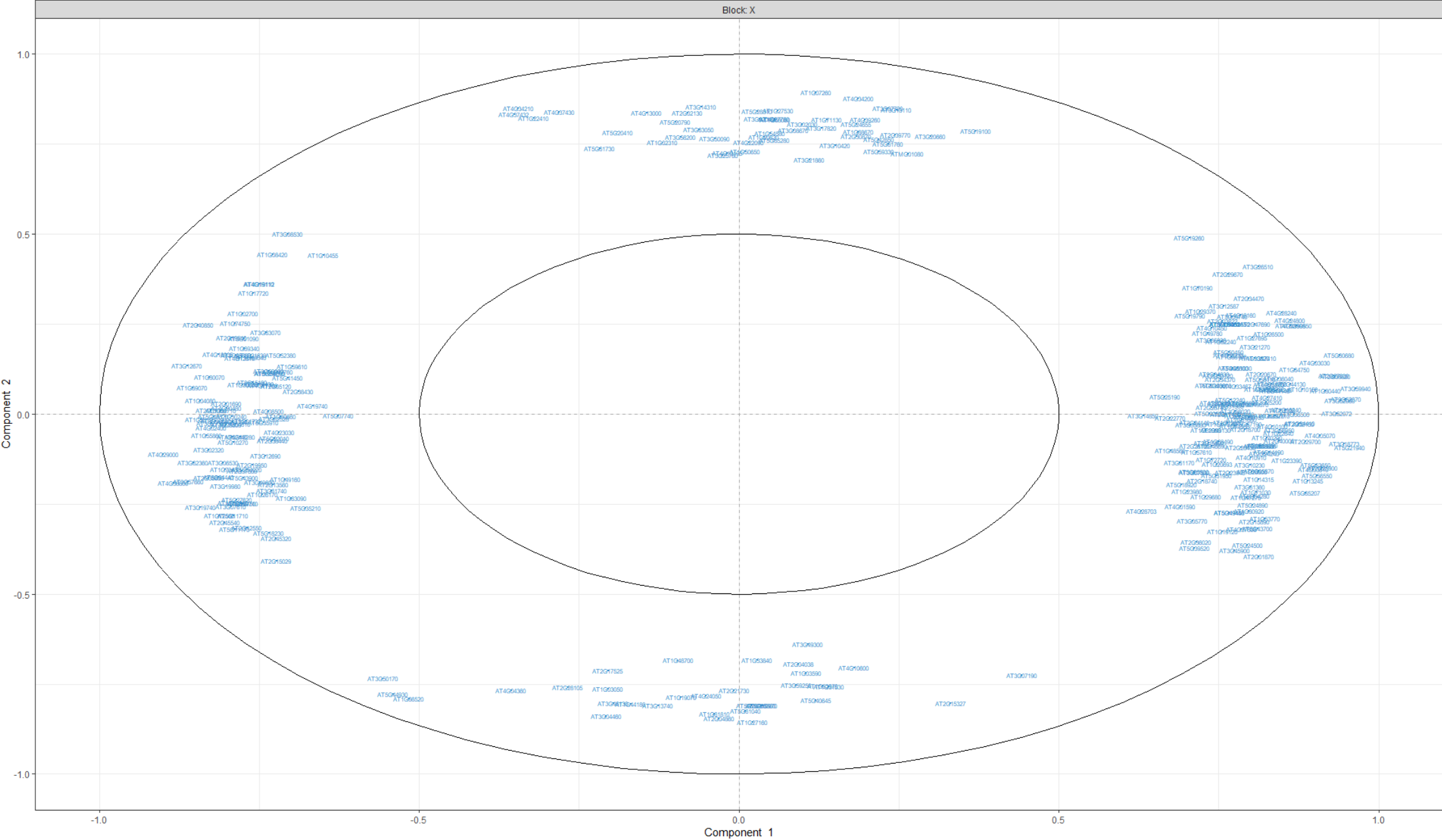
Loadings on comp 1



Euclidean
distance,
complete
linkage

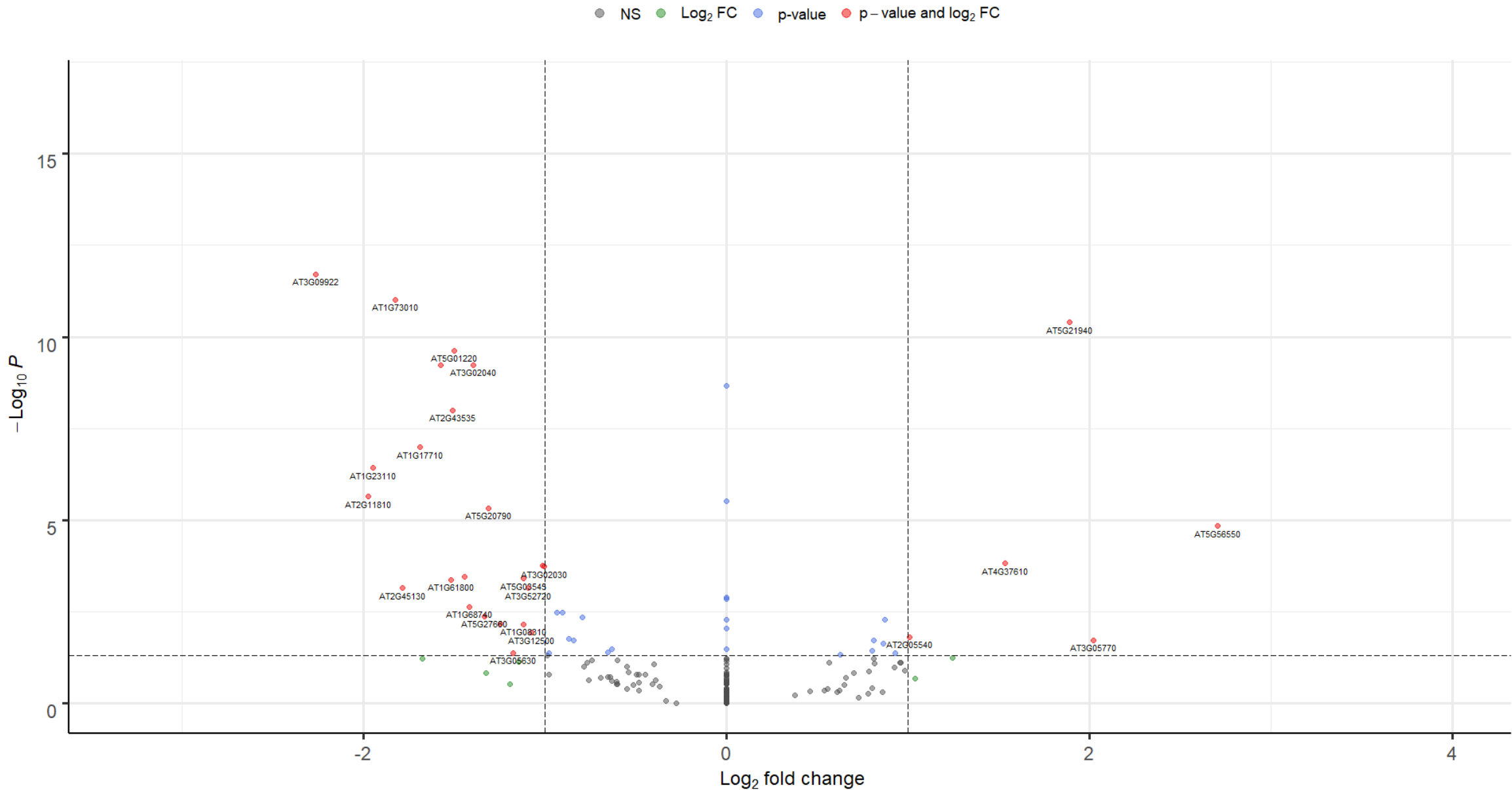


Correlation Circle Plots

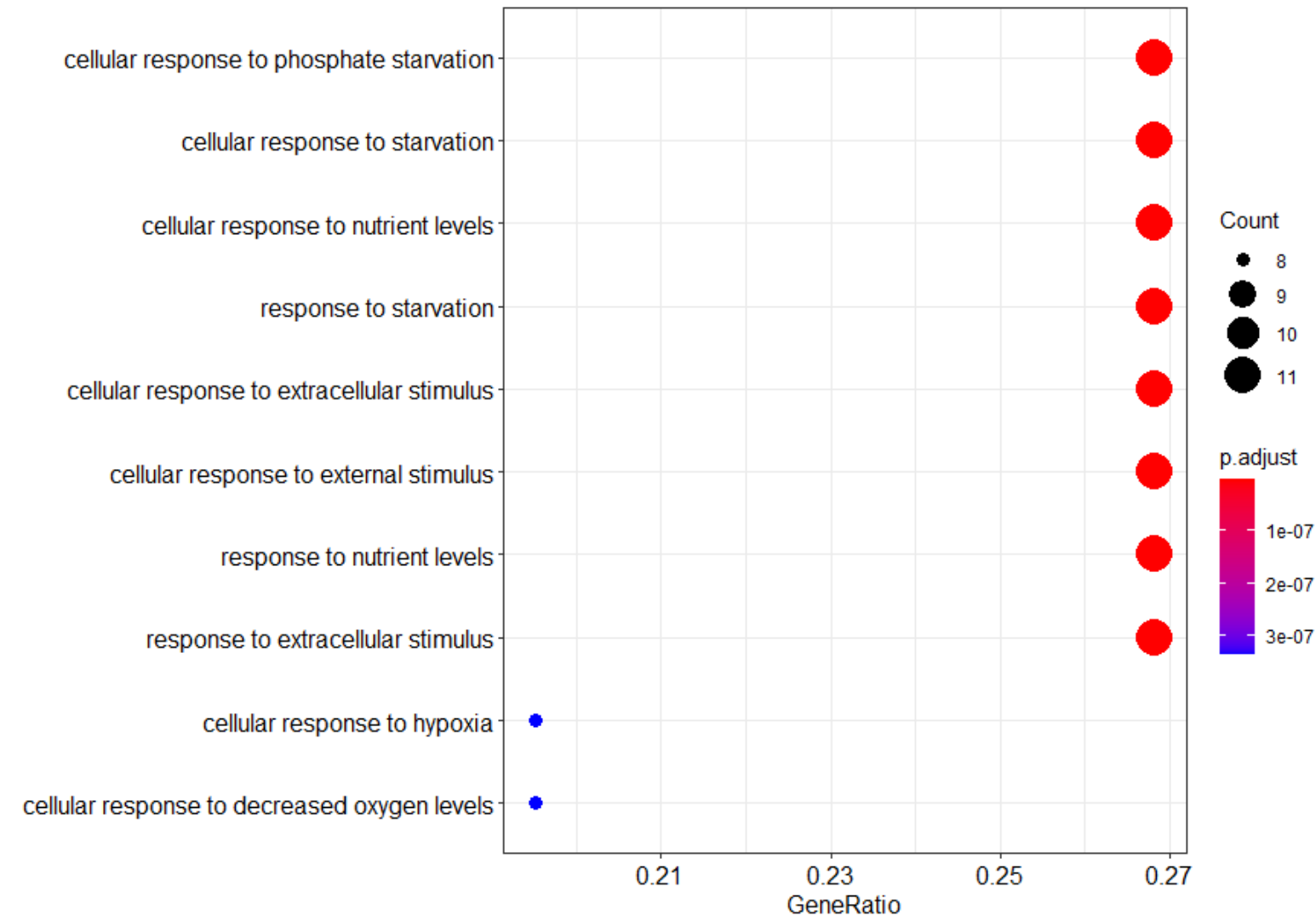


DEGs t=2 1.5uM soIA treatment

LFC>1, padj <0.05

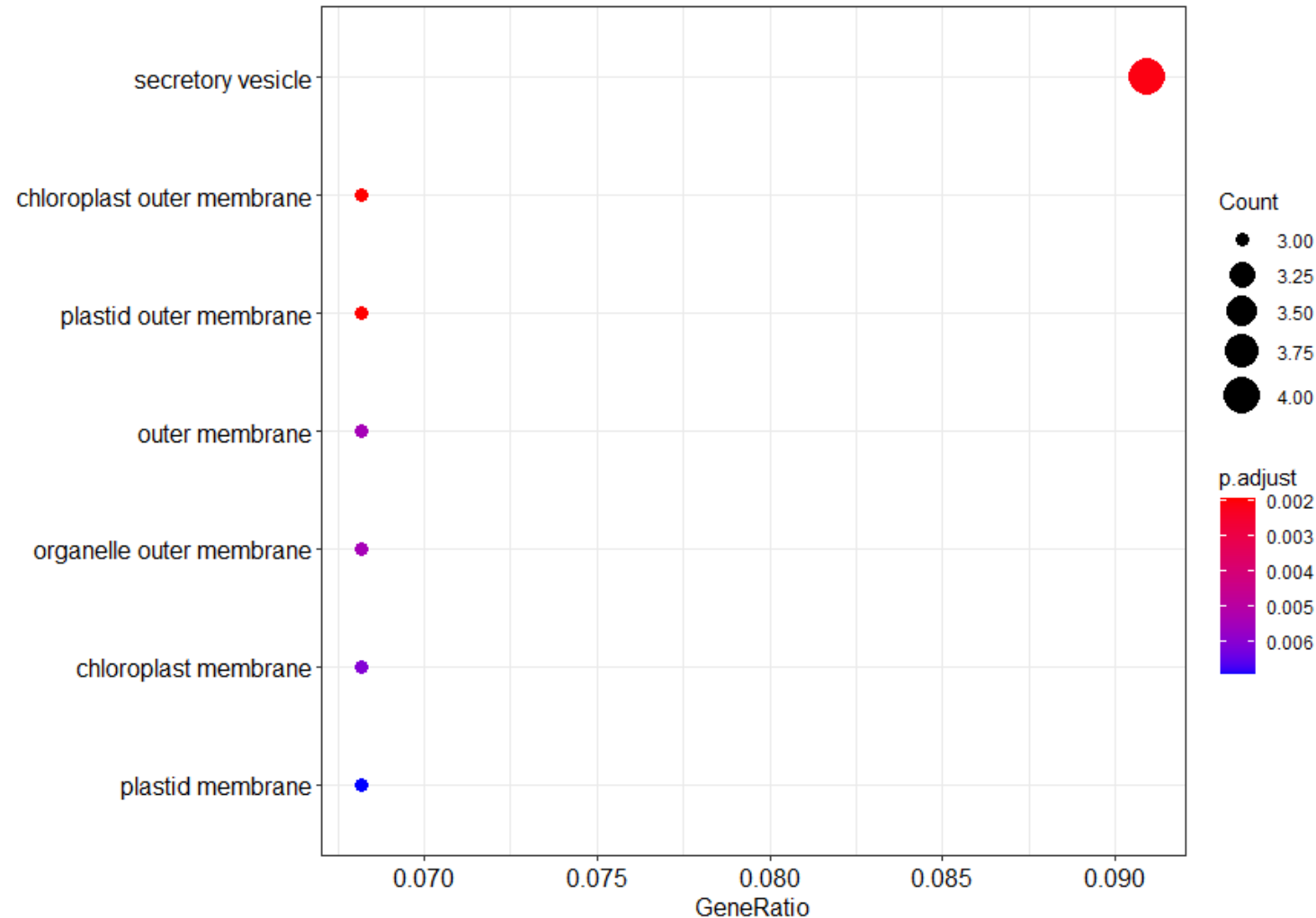


GO terms biological processes (1.5uM solA treatment)

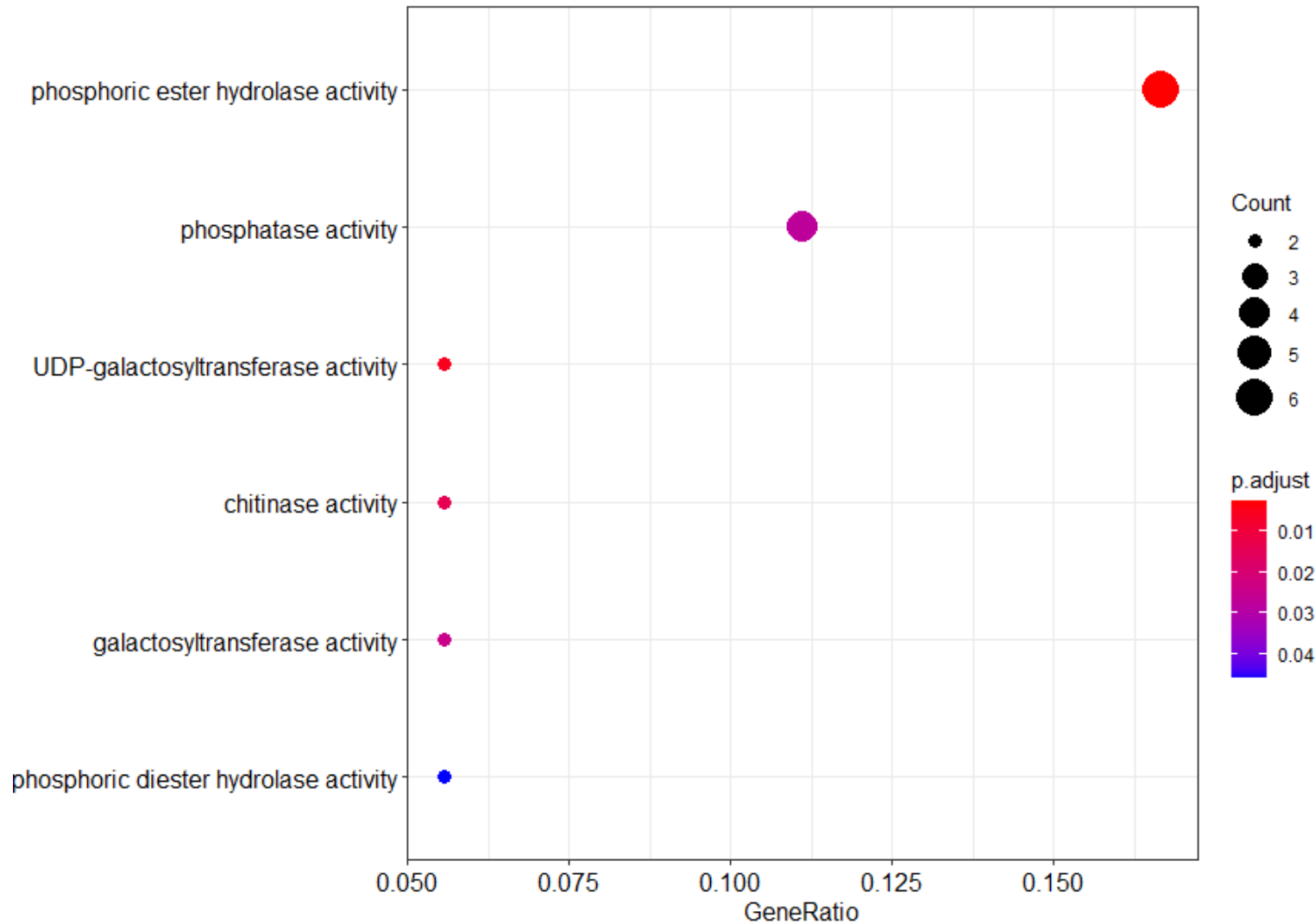


ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue
GO:0016036	cellular response to phosphate starvation	11/41	74/21510	1.0689E-18	2.65086E-16	1.75524E-16
GO:0009267	cellular response to starvation	11/41	146/21510	2.55078E-15	3.16297E-13	2.09433E-13
GO:0031669	cellular response to nutrient levels	11/41	168/21510	1.22276E-14	1.01081E-12	6.69298E-13
GO:0042594	response to starvation	11/41	181/21510	2.79755E-14	1.73448E-12	1.14847E-12
GO:0031668	cellular response to extracellular stimulus	11/41	203/21510	9.93831E-14	4.9294E-12	3.26395E-12
GO:0071496	cellular response to external stimulus	11/41	209/21510	1.36964E-13	5.66116E-12	3.74848E-12
GO:0031667	response to nutrient levels	11/41	227/21510	3.39289E-13	1.20205E-11	7.95926E-12
GO:0009991	response to extracellular stimulus	11/41	263/21510	1.69223E-12	5.24591E-11	3.47352E-11
GO:0071456	cellular response to hypoxia	8/41	238/21510	1.39283E-08	3.35177E-07	2.21934E-07
GO:0036294	cellular response to decreased oxygen levels	8/41	240/21510	1.48667E-08	3.35177E-07	2.21934E-07
GO:0071453	cellular response to oxygen levels	8/41	240/21510	1.48667E-08	3.35177E-07	2.21934E-07
GO:0009247	glycolipid biosynthetic process	5/41	47/21510	2.82643E-08	5.84129E-07	3.86775E-07
GO:0001666	response to hypoxia	8/41	264/21510	3.11705E-08	5.94637E-07	3.93732E-07
GO:0036293	response to decreased oxygen levels	8/41	268/21510	3.50191E-08	5.9591E-07	3.94575E-07
GO:0070482	response to oxygen levels	8/41	269/21510	3.60429E-08	5.9591E-07	3.94575E-07
GO:0006664	glycolipid metabolic process	5/41	51/21510	4.30427E-08	6.27917E-07	4.15768E-07
GO:1903509	liposaccharide metabolic process	5/41	51/21510	4.30427E-08	6.27917E-07	4.15768E-07
GO:0046467	membrane lipid biosynthetic process	5/41	88/21510	6.81697E-07	9.39227E-06	6.21899E-06
GO:0019375	galactolipid biosynthetic process	3/41	13/21510	1.81408E-06	2.36785E-05	1.56785E-05
GO:0006643	membrane lipid metabolic process	5/41	109/21510	1.9742E-06	2.44801E-05	1.62092E-05
GO:0019374	galactolipid metabolic process	3/41	15/21510	2.8784E-06	3.39925E-05	2.25078E-05
GO:0055062	phosphate ion homeostasis	3/41	19/21510	6.09763E-06	6.57483E-05	4.35346E-05
GO:0072506	trivalent inorganic anion homeostasis	3/41	19/21510	6.09763E-06	6.57483E-05	4.35346E-05
GO:0006020	inositol metabolic process	3/41	21/21510	8.34715E-06	7.96189E-05	5.27188E-05
GO:0055083	monovalent inorganic anion homeostasis	3/41	21/21510	8.34715E-06	7.96189E-05	5.27188E-05
GO:0072505	divalent inorganic anion homeostasis	3/41	21/21510	8.34715E-06	7.96189E-05	5.27188E-05
GO:0043647	inositol phosphate metabolic process	3/41	34/21510	3.69148E-05	0.000339069	0.000224511
GO:0055081	anion homeostasis	3/41	44/21510	8.06269E-05	0.000714124	0.00047285
GO:0046434	organophosphate catabolic process	3/41	55/21510	0.000157406	0.001346096	0.000891303
GO:0019751	polyol metabolic process	3/41	62/21510	0.000224824	0.001858548	0.001230617
GO:0006644	phospholipid metabolic process	4/41	199/21510	0.000550644	0.004405149	0.002916822
GO:0009395	phospholipid catabolic process	2/41	22/21510	0.000799283	0.006194443	0.004101584
GO:1901137	carbohydrate derivative biosynthetic process	5/41	420/21510	0.001164404	0.008750673	0.005794164
GO:0016998	cell wall macromolecule catabolic process	2/41	30/21510	0.001490688	0.010873257	0.00719961
GO:0006979	response to oxidative stress	5/41	454/21510	0.001641863	0.011434234	0.007571054
GO:0006650	glycerophospholipid metabolic process	3/41	123/21510	0.001659808	0.011434234	0.007571054
GO:0046173	polyol biosynthetic process	2/41	33/21510	0.001802856	0.012084006	0.008001294
GO:0006066	alcohol metabolic process	3/41	134/21510	0.00211956	0.013629648	0.009024724
GO:0006817	phosphate ion transport	2/41	36/21510	0.002143372	0.013629648	0.009024724
GO:0000302	response to reactive oxygen species	3/41	154/21510	0.003142975	0.019486448	0.012902741
GO:1901615	organic hydroxy compound metabolic process	4/41	323/21510	0.003262818	0.019736073	0.013068028
GO:0046486	glycerolipid metabolic process	3/41	158/21510	0.003378175	0.019947319	0.013207902
GO:1901617	organic hydroxy compound biosynthetic process	3/41	195/21510	0.006071397	0.035016427	0.02318575
GO:0044262	cellular carbohydrate metabolic process	4/41	401/21510	0.006993185	0.038793072	0.025686414
GO:0042542	response to hydrogen peroxide	2/41	66/21510	0.007039065	0.038793072	0.025686414
GO:0009409	response to cold	4/41	413/21510	0.007744249	0.041751601	0.027645372
GO:0046165	alcohol biosynthetic process	2/41	74/21510	0.008778966	0.046323055	0.030672312
GO:0009873	ethylene-activated signaling pathway	2/41	76/21510	0.009241066	0.047745506	0.031614172

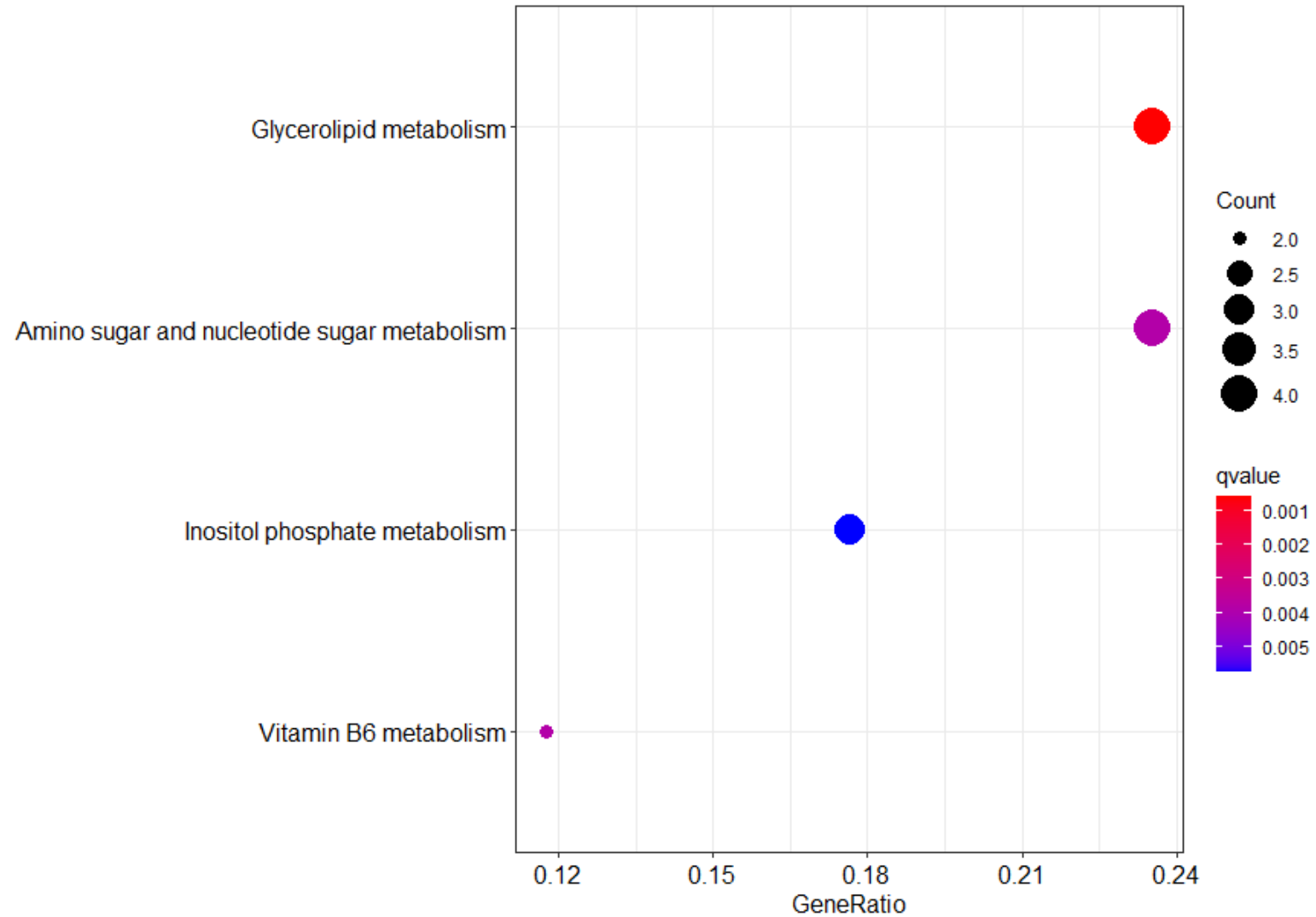
GO terms cellular compartment (1.5uM solA treatment)



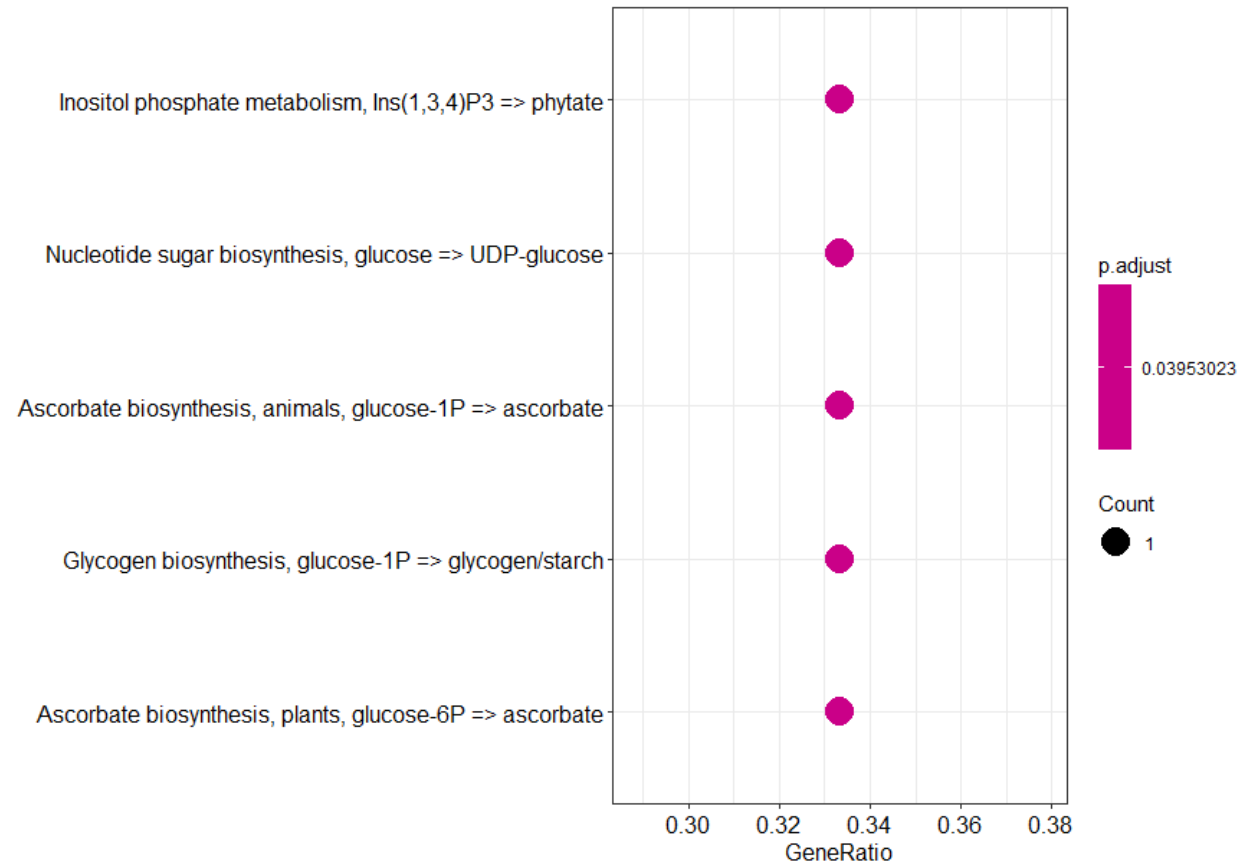
GO terms molecular function (1.5uM solA treatment)



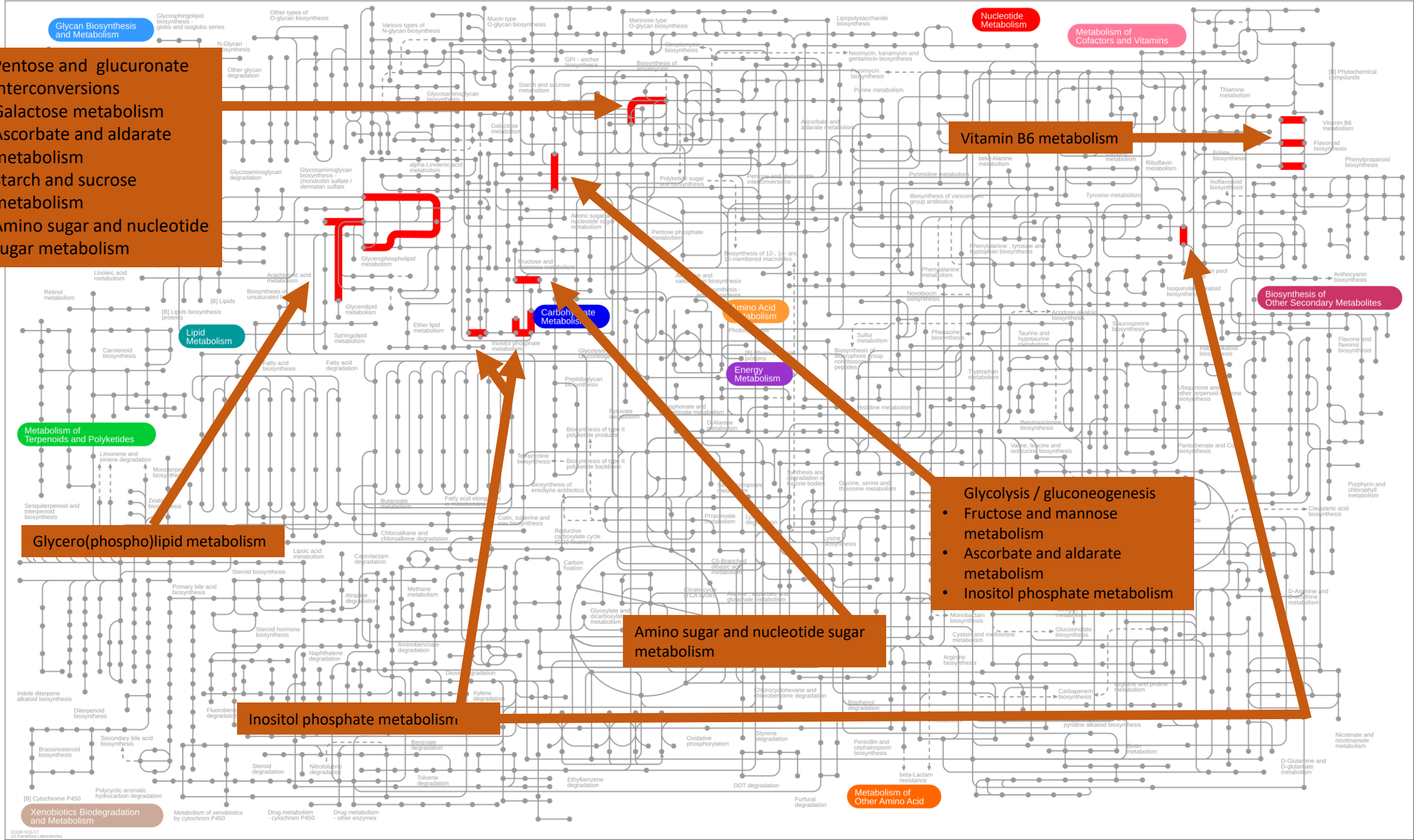
KEGG analysis



KEGG module analysis



- Pentose and glucuronate interconversions
- Galactose metabolism
- Ascorbate and aldarate metabolism
- Starch and sucrose metabolism
- Amino sugar and nucleotide sugar metabolism



Metabolism of Terpenoids and Polyketides

Glycero(phospho)lipid metabolism

Lipid Metabolism

Carbohydrate Metabolism

Amino Acid Metabolism

Energy Metabolism

Nucleotide Metabolism

Metabolism of Colofactors and Vitamins

Vitamin B6 metabolism

Biosynthesis of Other Secondary Metabolites

Glycolysis / gluconeogenesis

- Fructose and mannose metabolism
- Ascorbate and aldarate metabolism
- Inositol phosphate metabolism

Amino sugar and nucleotide sugar metabolism

Inositol phosphate metabolism

Metabolism of Other Amino Acid

Metabolism of
Terpenoids and Polyketides

Glycero-
phospholipid
metabolism

Glycolysis/ascorbate
/aldarate
metabolism

Biosynthesis of
Other Secondary Metabolites

Biosynthesis of
Cofactor and Vitamins

