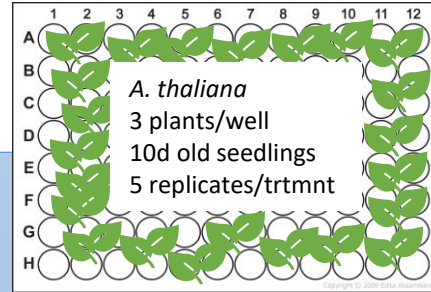


Arabidopsis RNAseq results

Goal of experiment: what is the role of solanoeclepin A in the plant?

Experimental set-up



Treatments:

1.5 nM solA

1.5 uM solA

1% EtOH carrier

Timepoints:

t = 2h

t = 2h

t = 2h

t = 6h

t = 6h

t = 6h

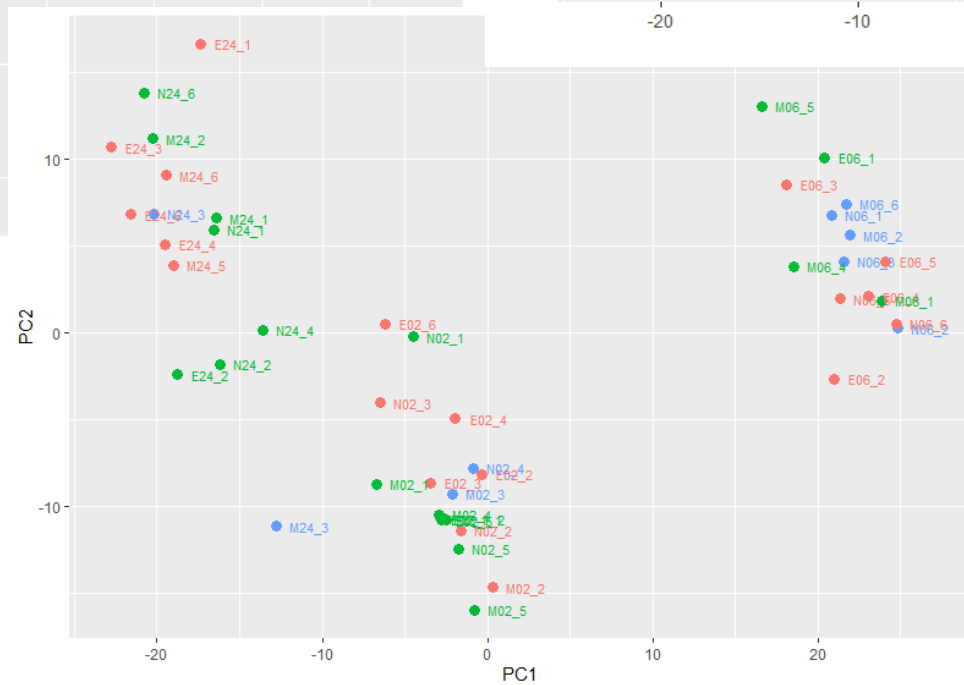
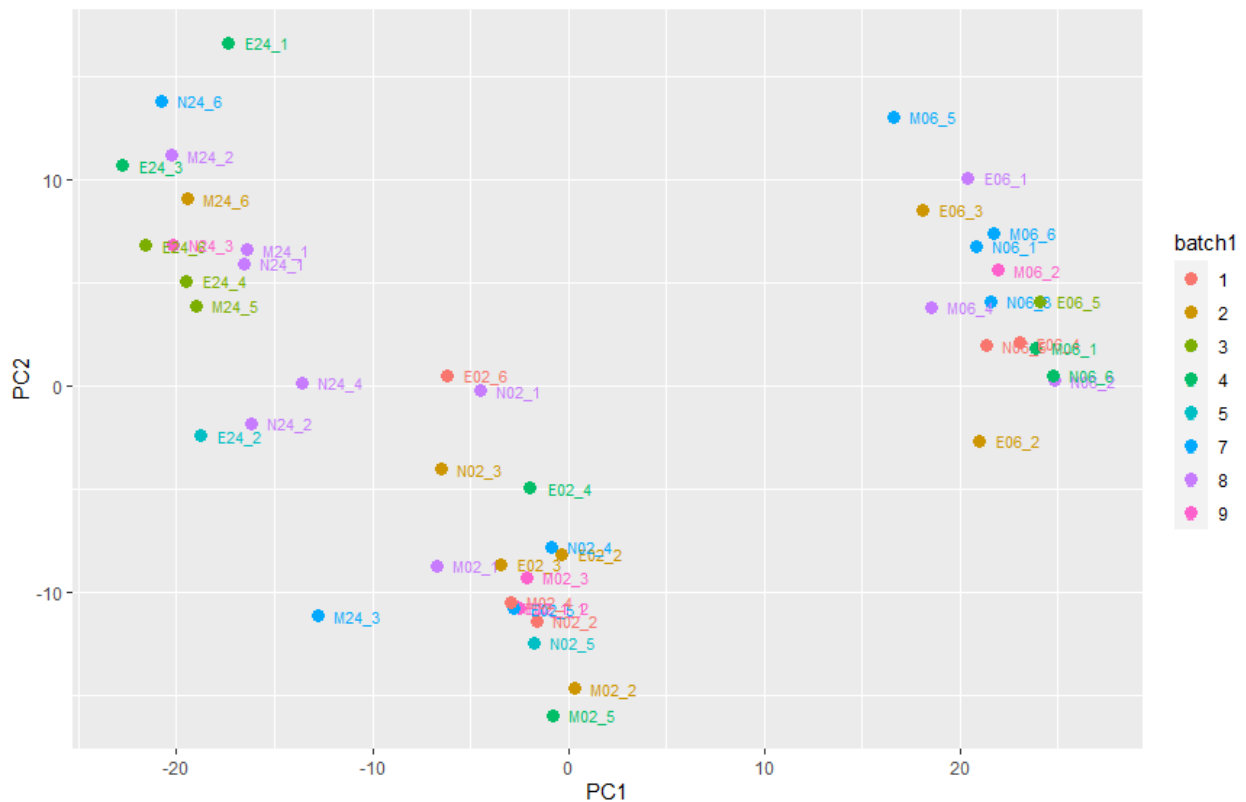
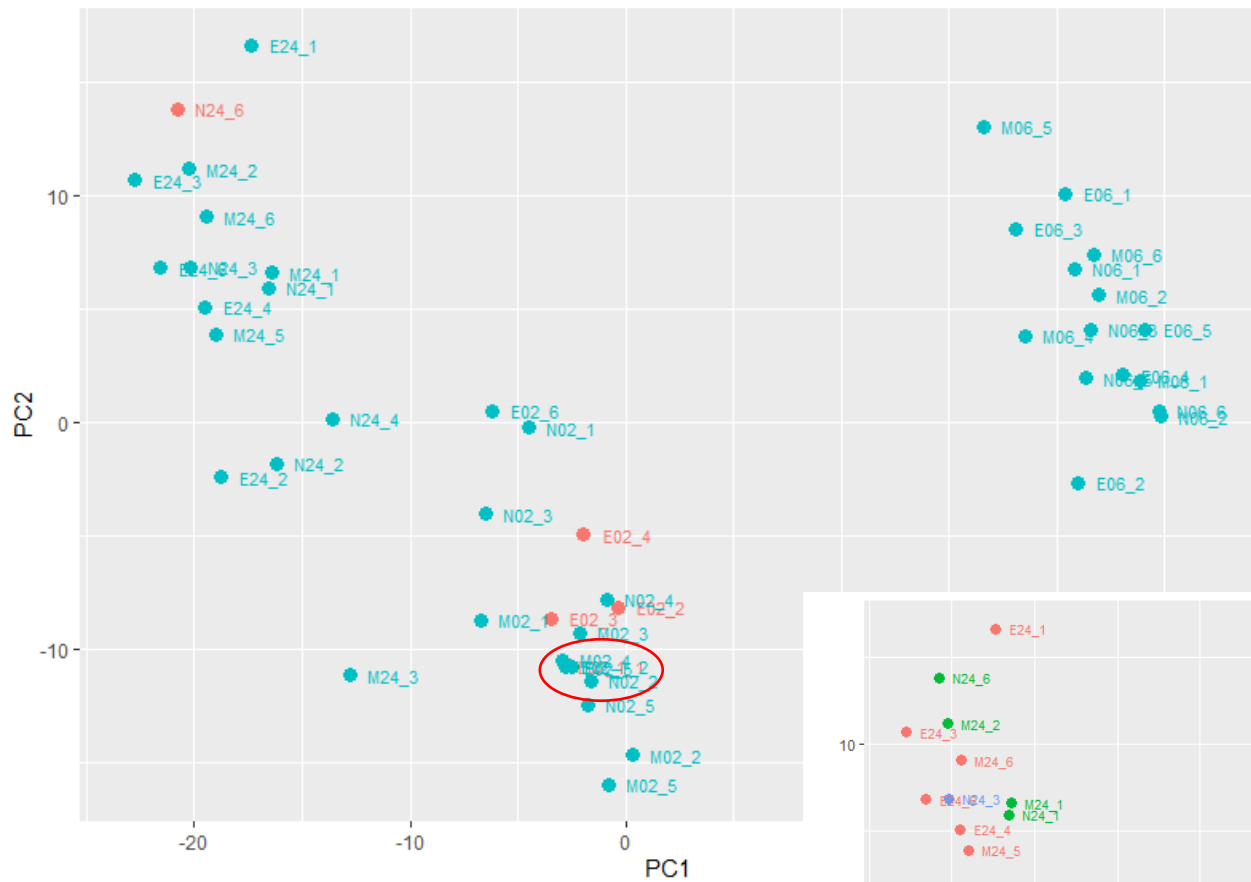
t = 24h

t = 24h

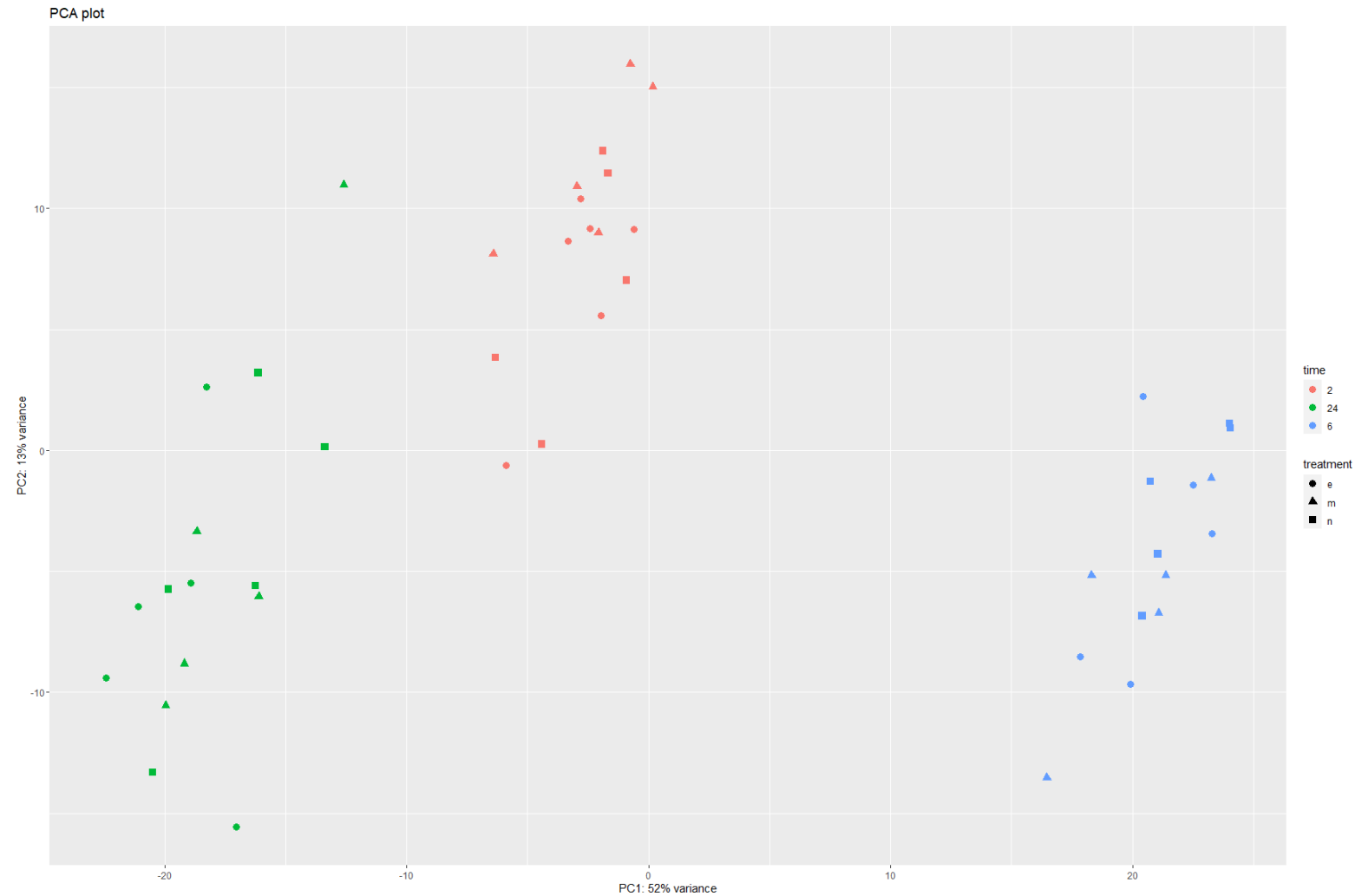
t = 24h

total: 45 samples

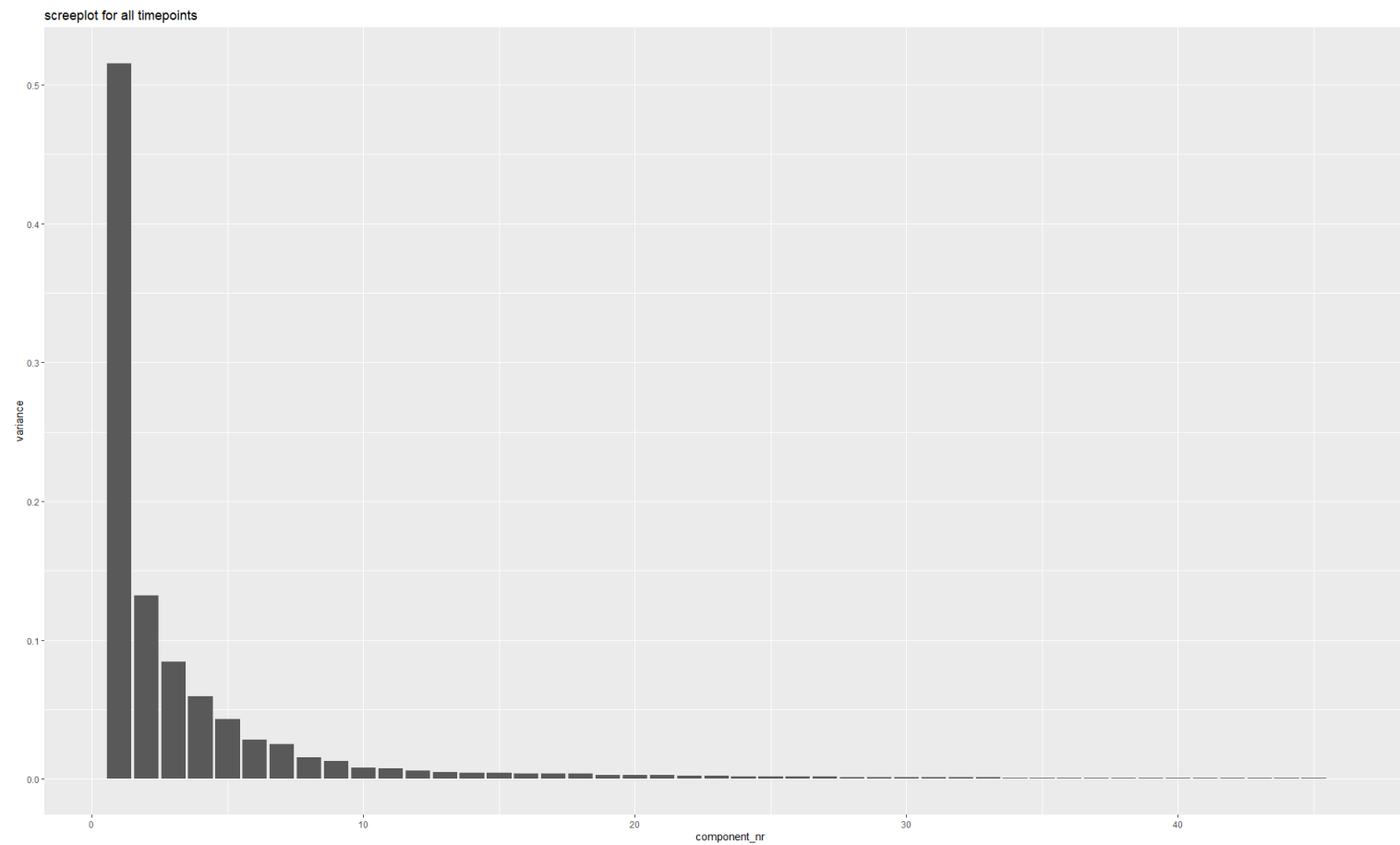
Check for batch effects



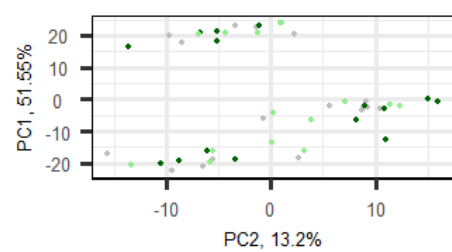
PCA biplot, taking 500 top variance genes



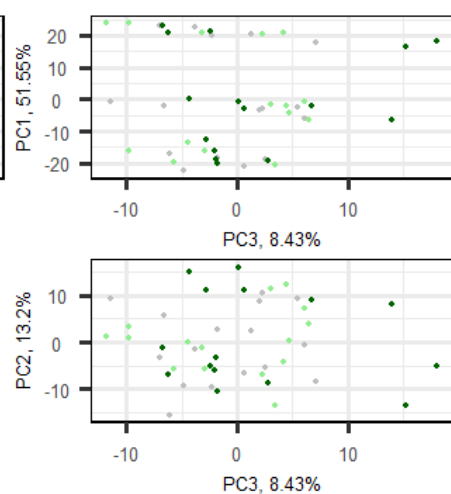
Scree plot



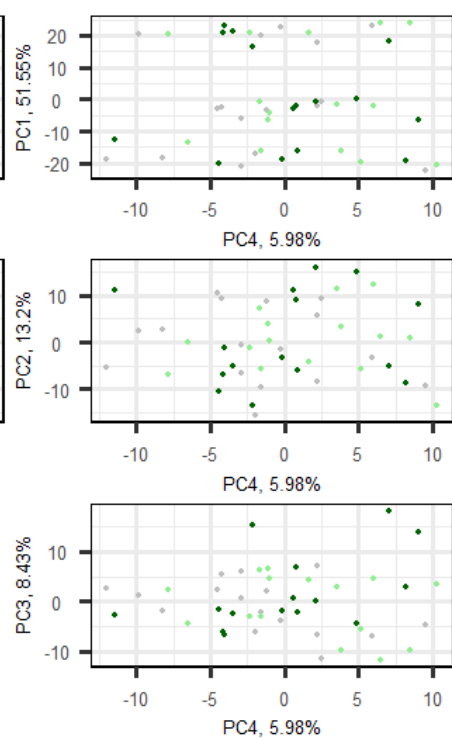
**PC1,
51.55%**



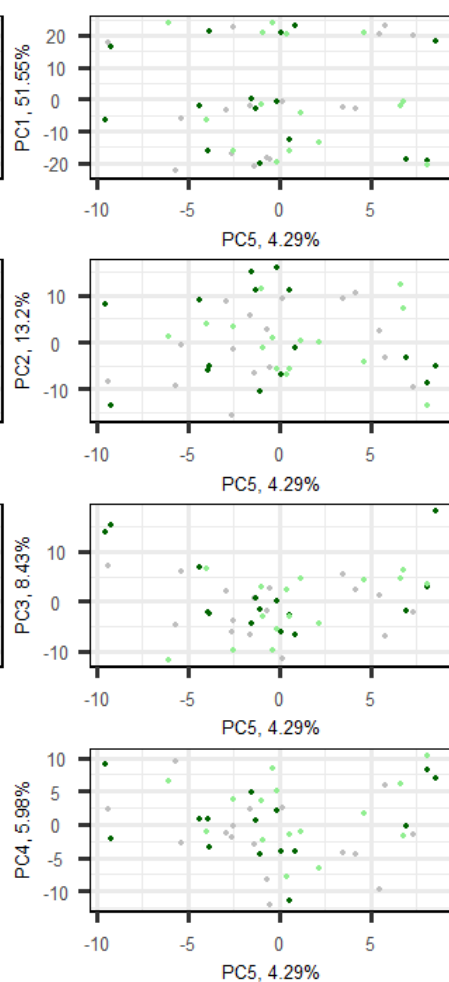
**PC2,
13.2%**



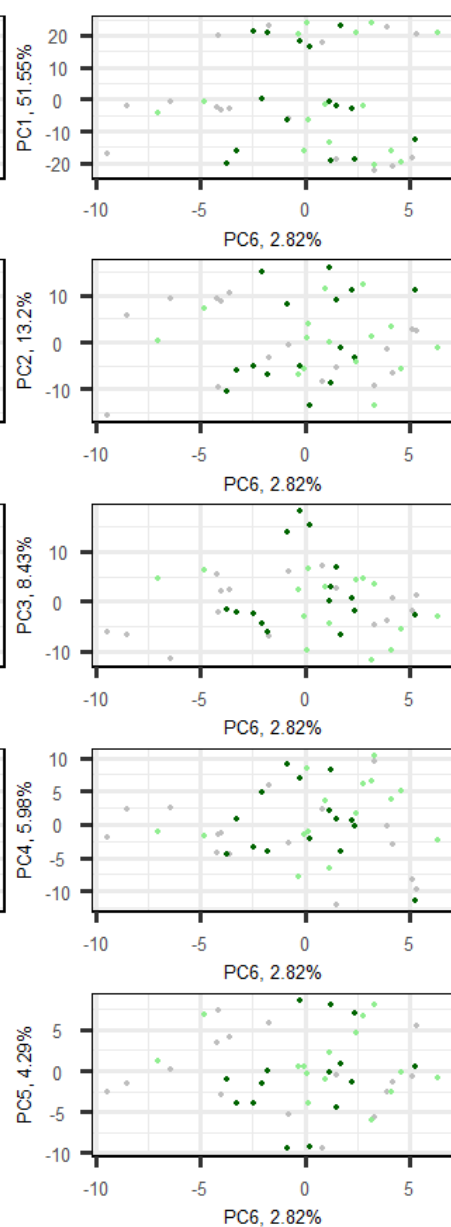
**PC3,
8.43%**



**PC4,
5.98%**



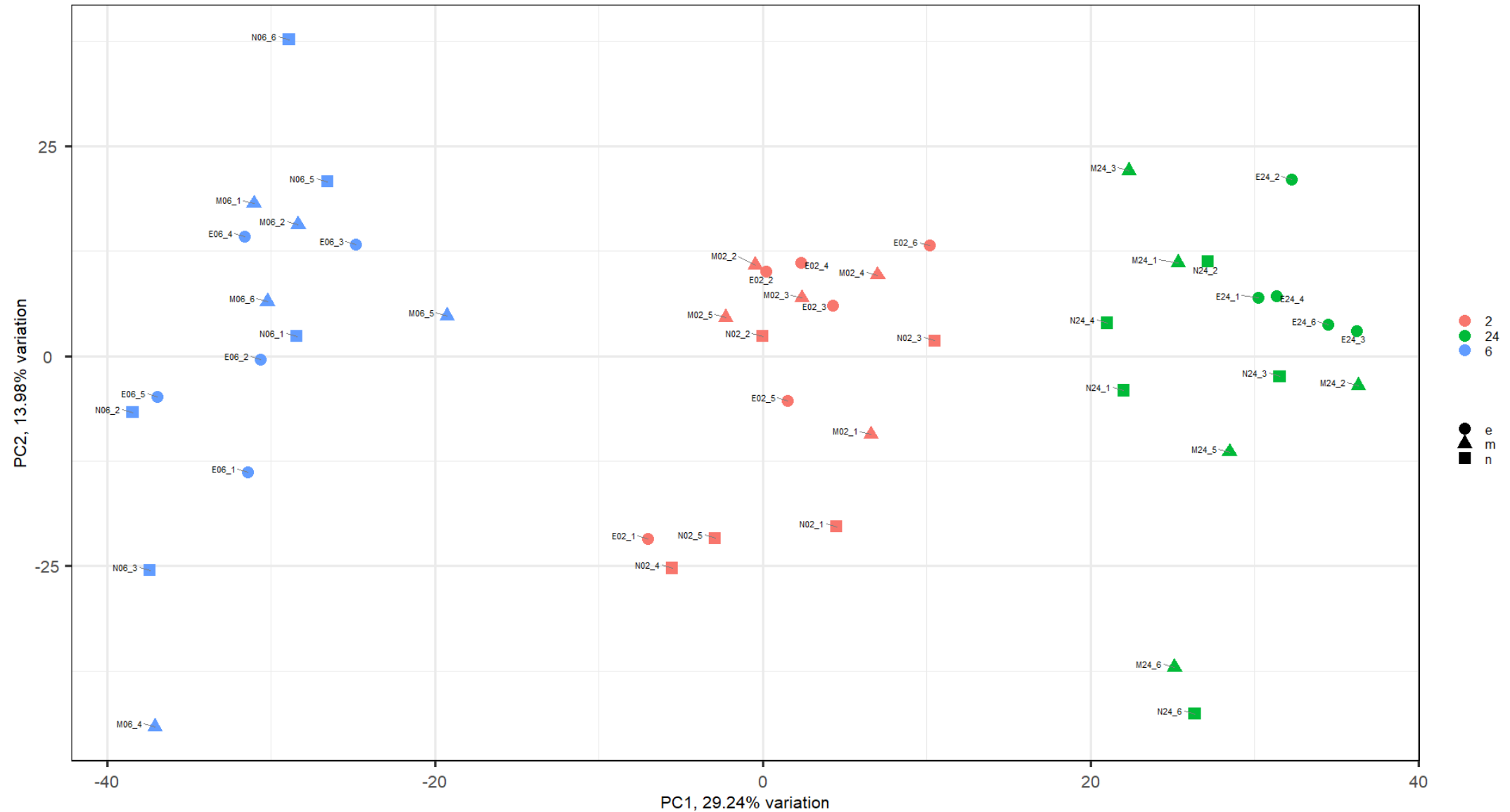
**PC5,
4.29%**



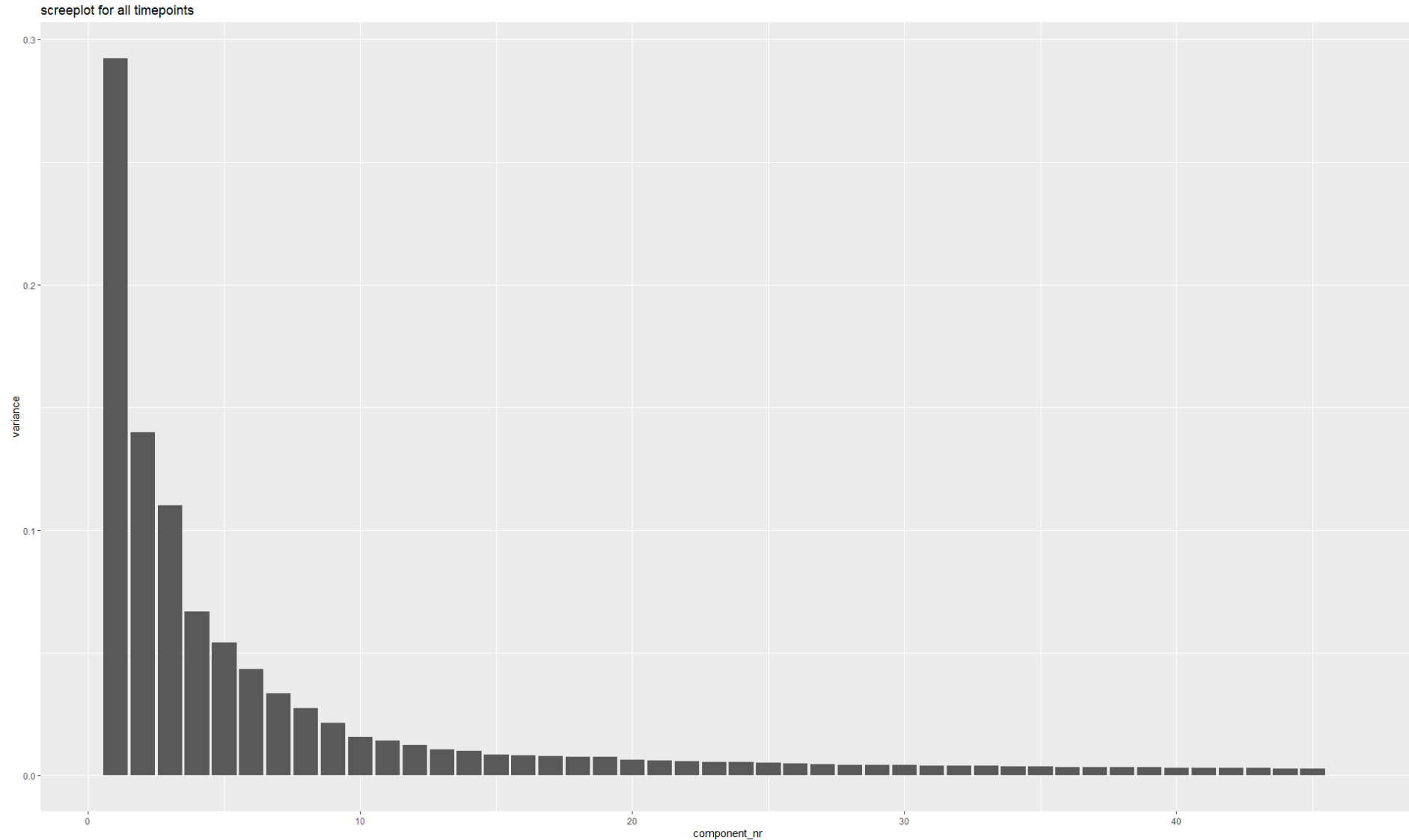
**PC6,
2.82%**

Elbow method says PC6

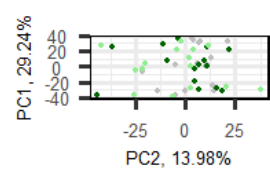
PCA biplot, taking 50% most variable genes



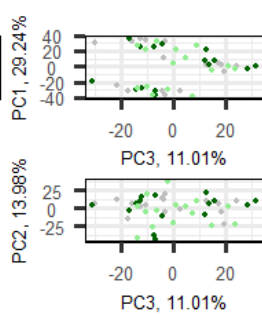
Scree plot top 50% variance genes



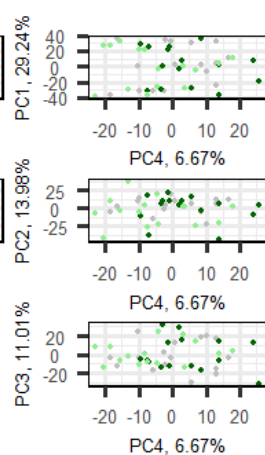
**PC1,
29.24%**



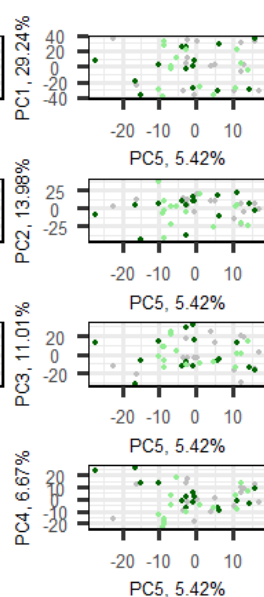
**PC2,
13.98%**



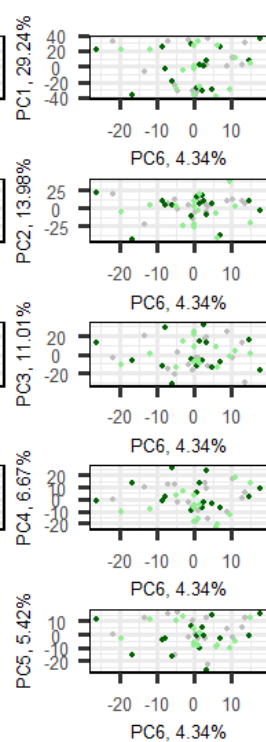
**PC3,
11.01%**



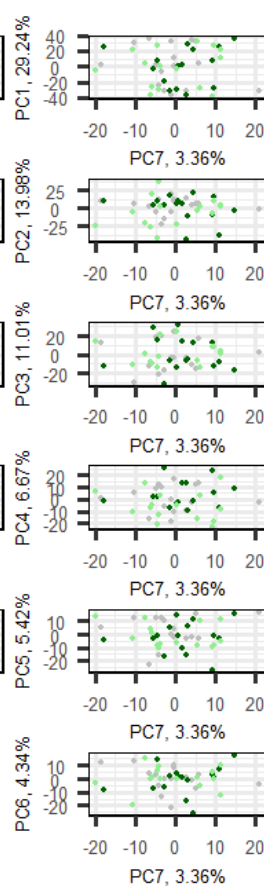
**PC4,
6.67%**



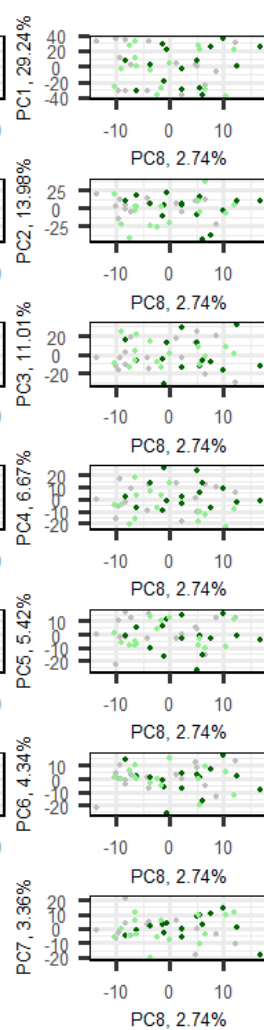
**PC5,
5.42%**



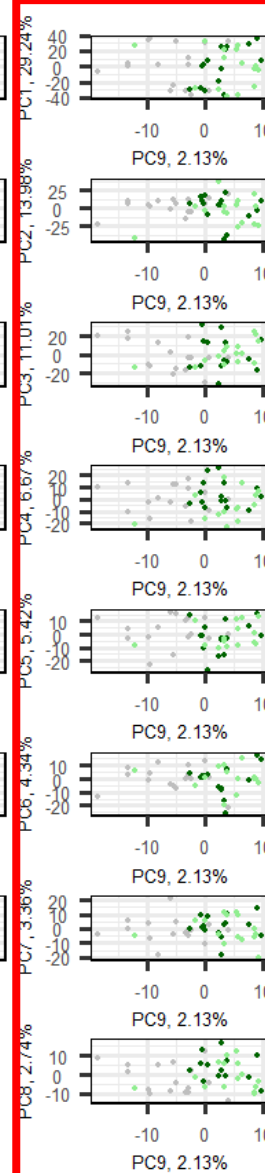
**PC6,
4.34%**



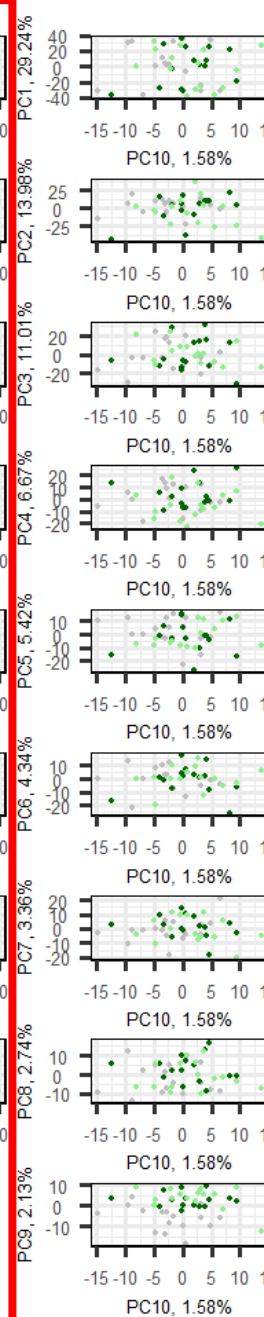
**PC7,
3.36%**



**PC8,
2.74%**



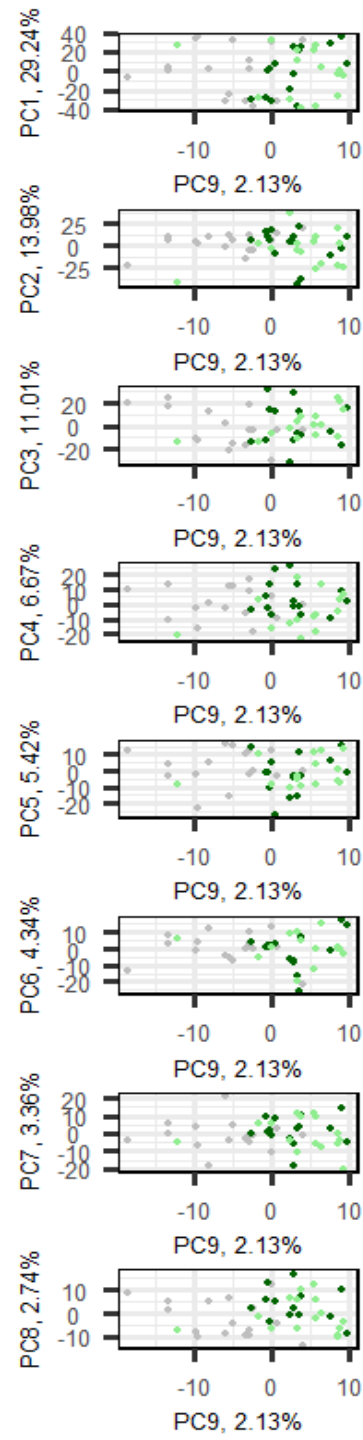
**PC9,
2.13%**



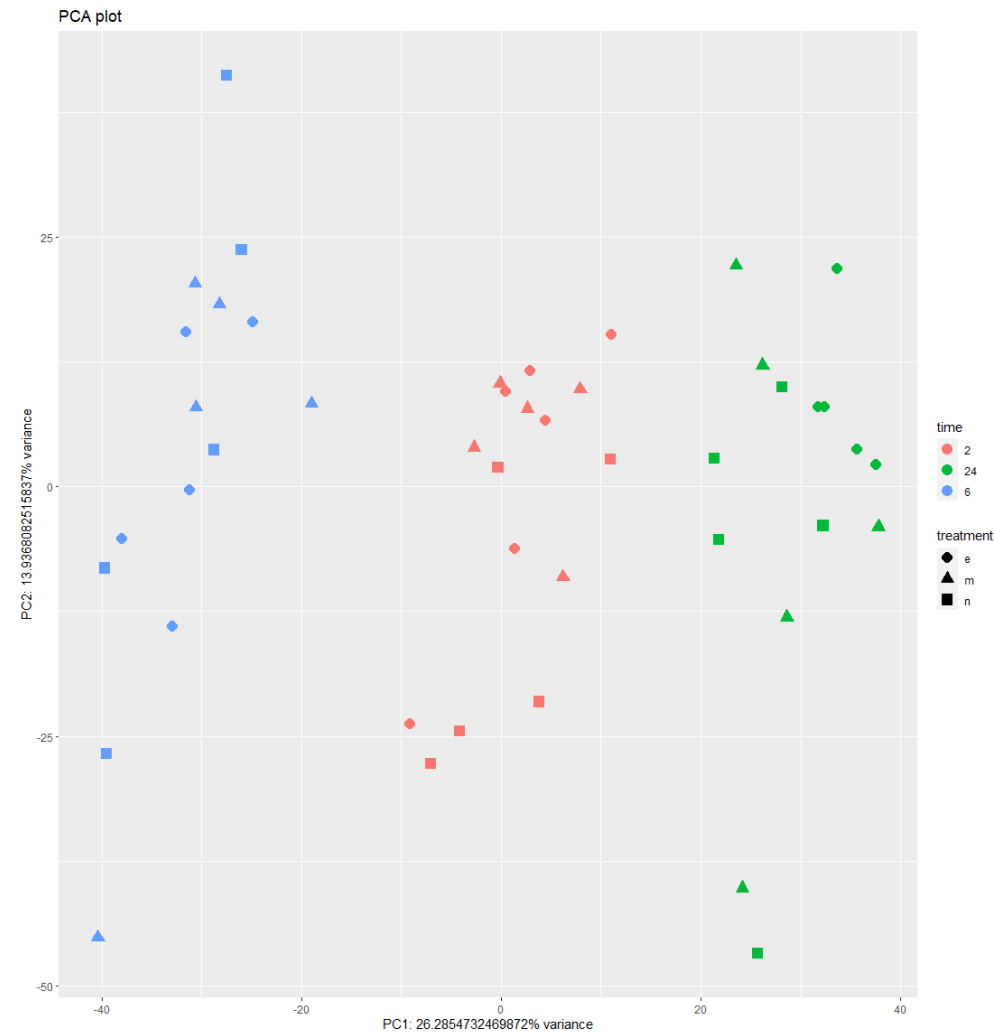
**PC10,
1.58%**



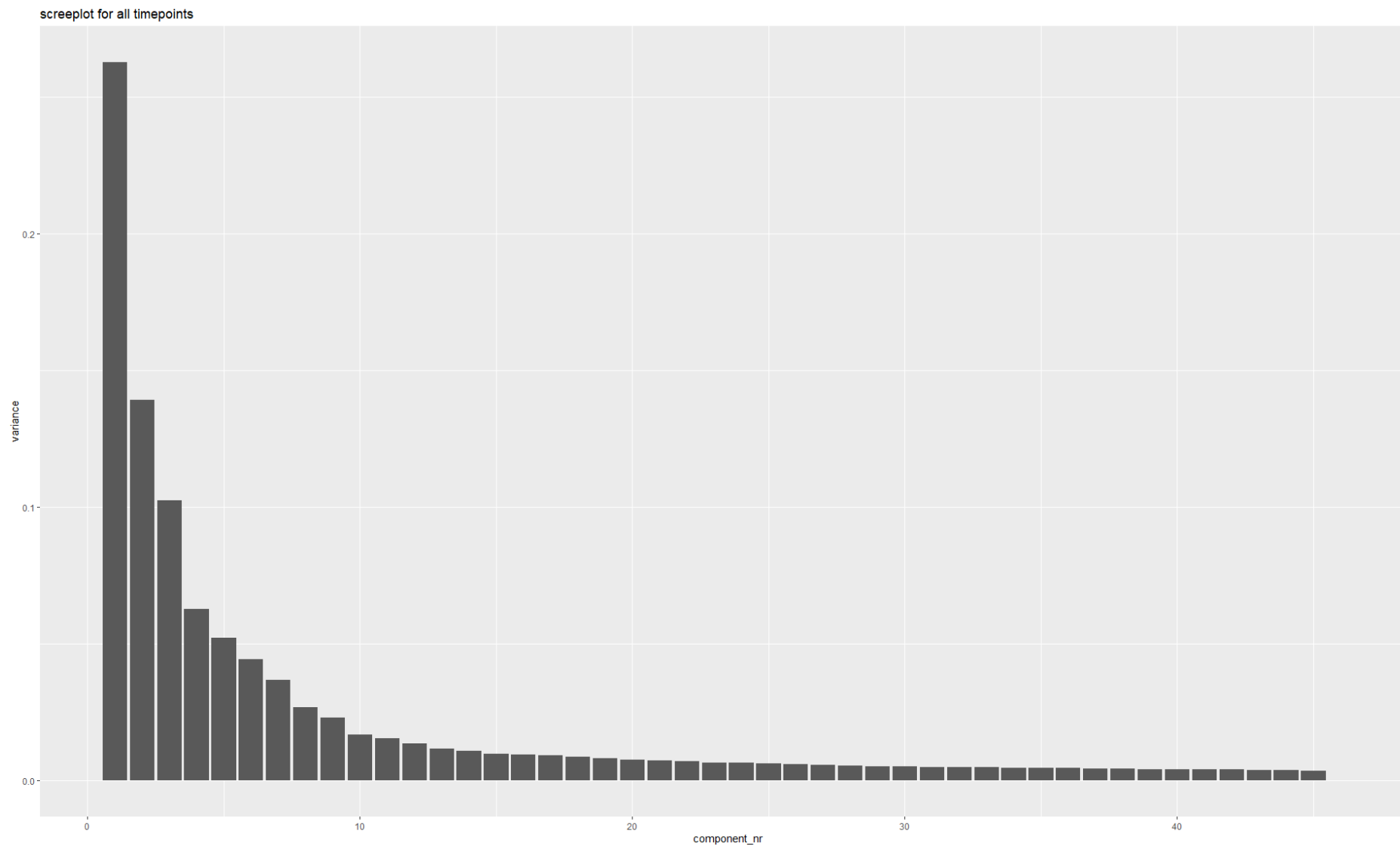
Gray = EtOH carrier
Lightgreen = nM solA
Darkgreen = uM solA



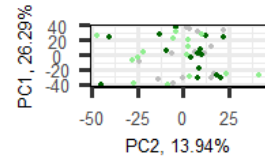
PCA plot lower 10% of variance removed



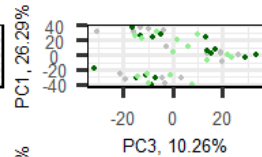
Scree plot doesn't change so much



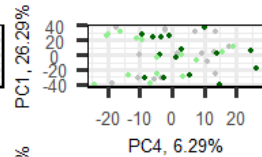
**PC1,
26.29%**



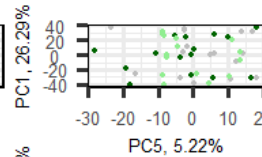
**PC2,
13.94%**



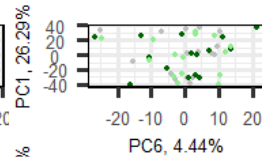
**PC3,
10.26%**



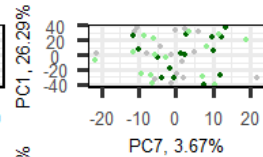
**PC4,
6.29%**



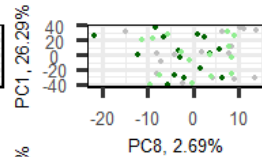
**PC5,
5.22%**



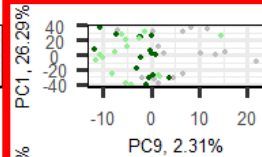
**PC6,
4.44%**



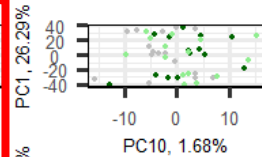
**PC7,
3.67%**



**PC8,
2.69%**

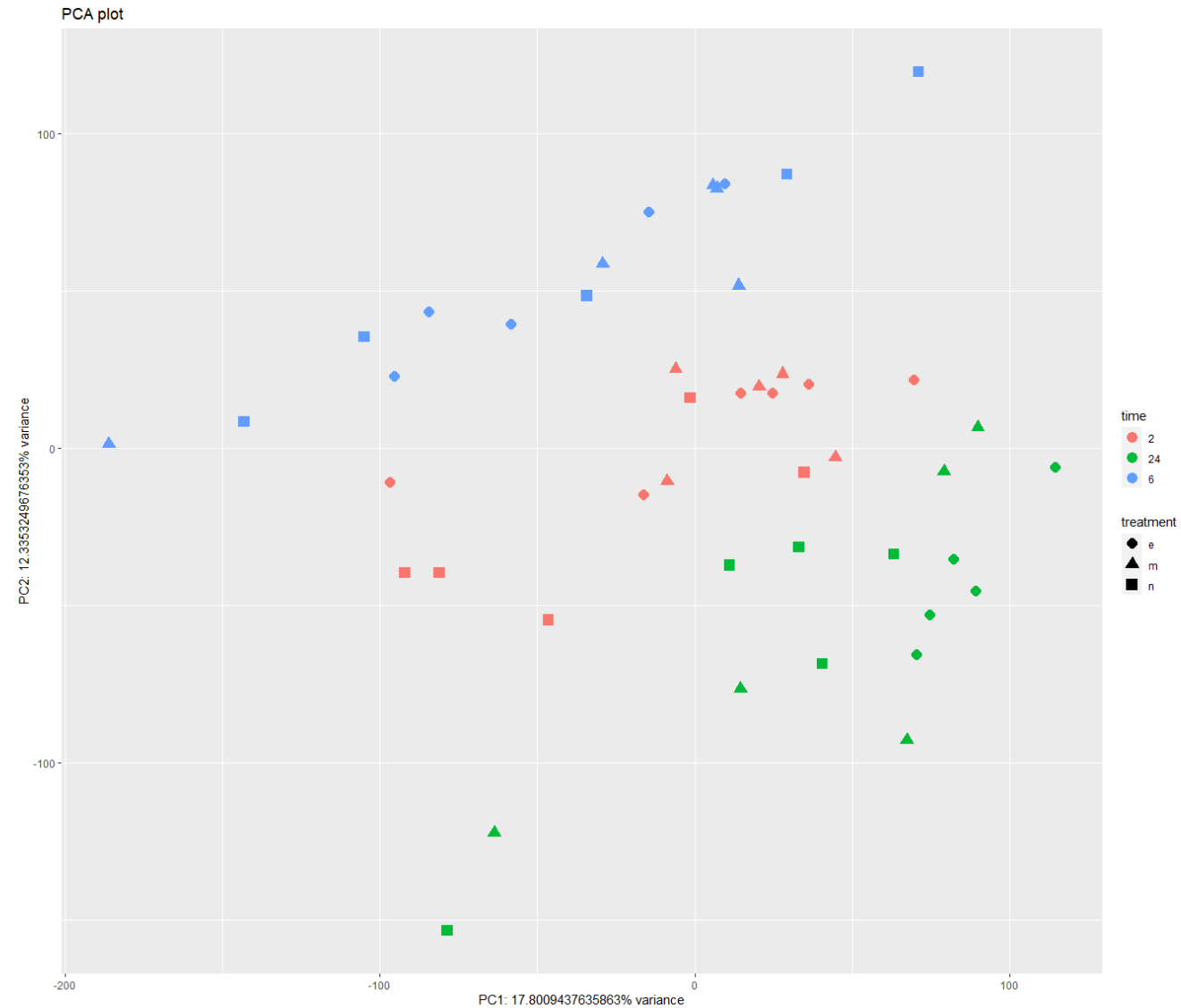


**PC9,
2.31%**

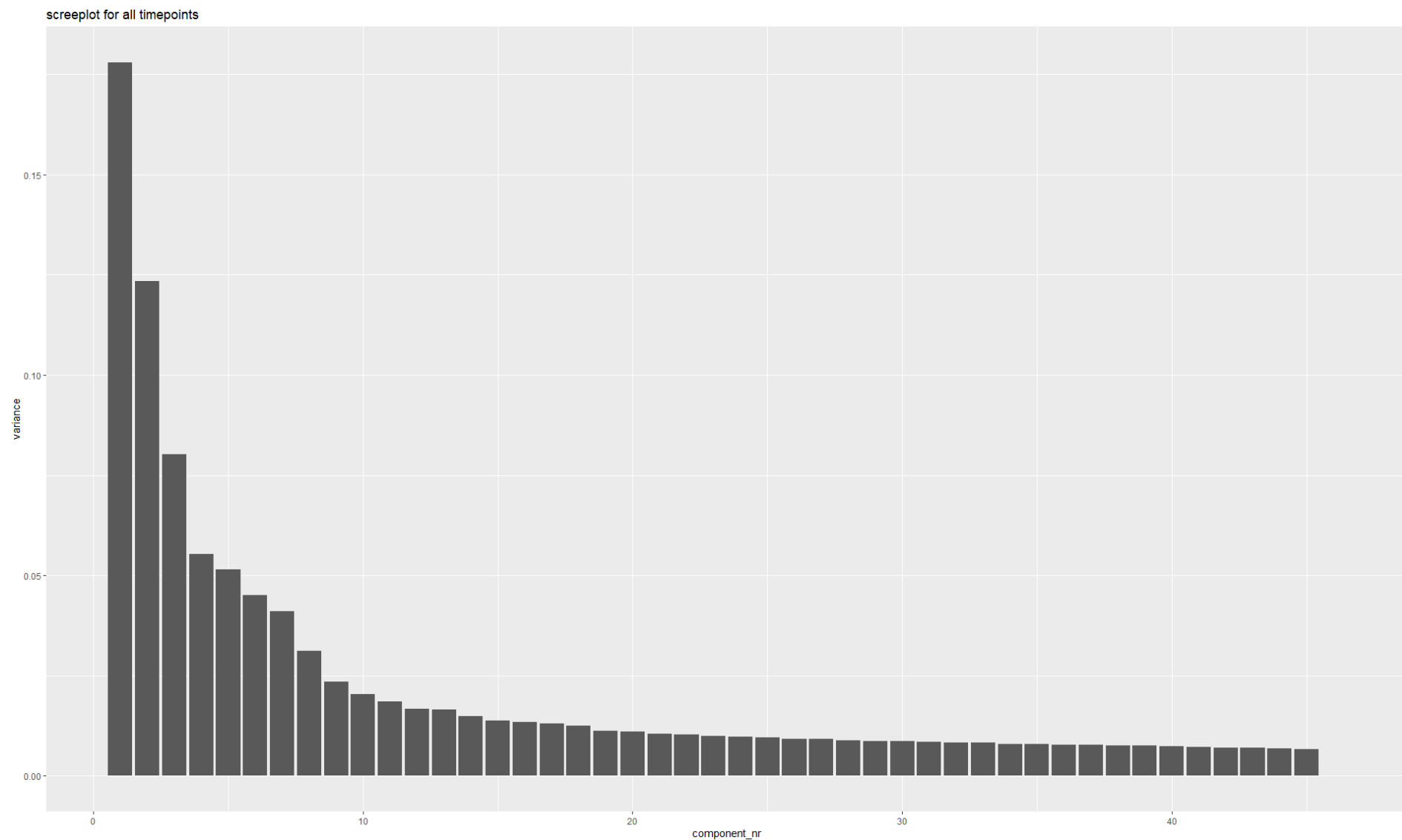


**PC10,
1.68%**

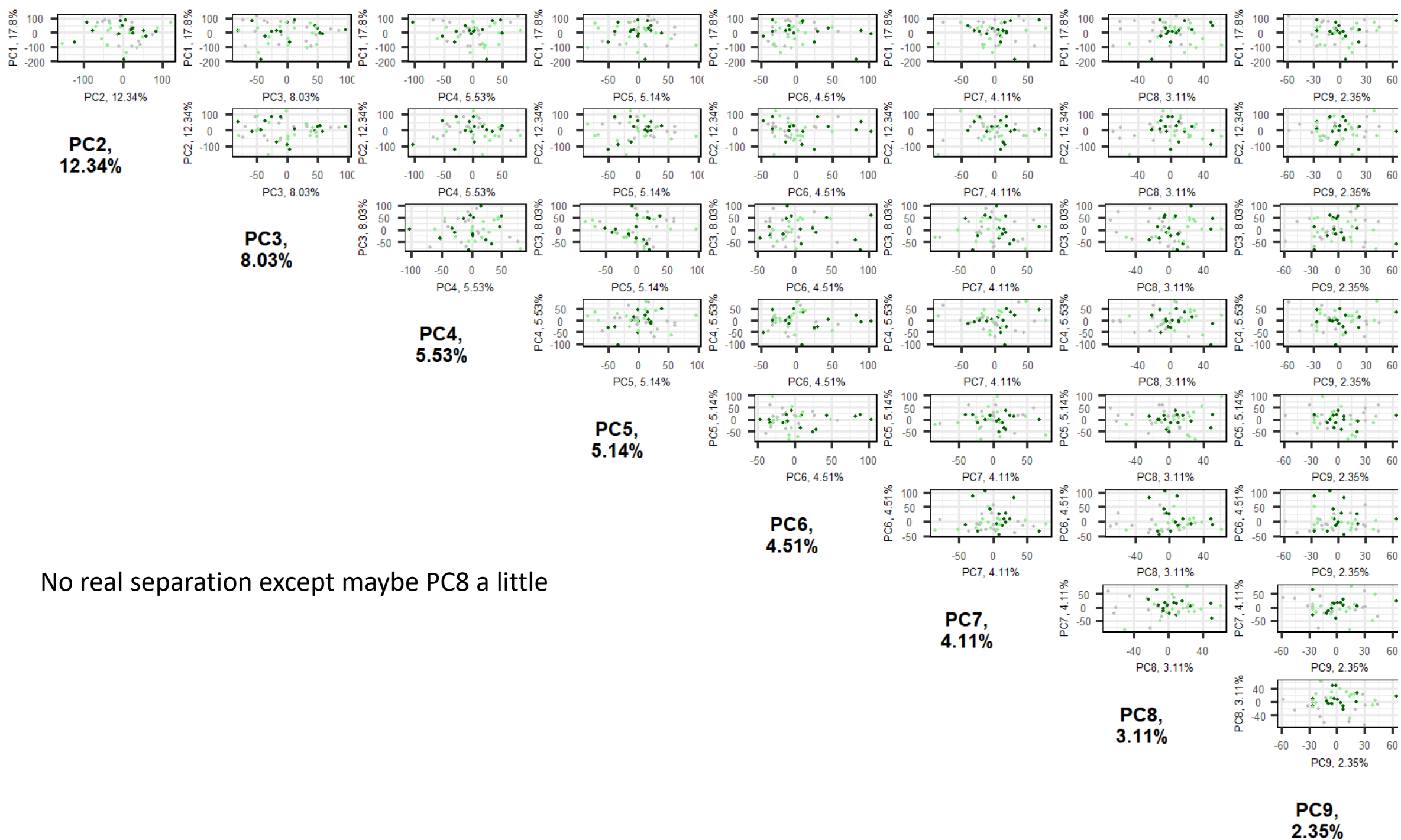
PCA plot, remvar 10%, *scaled*



Scree plot *scaled*

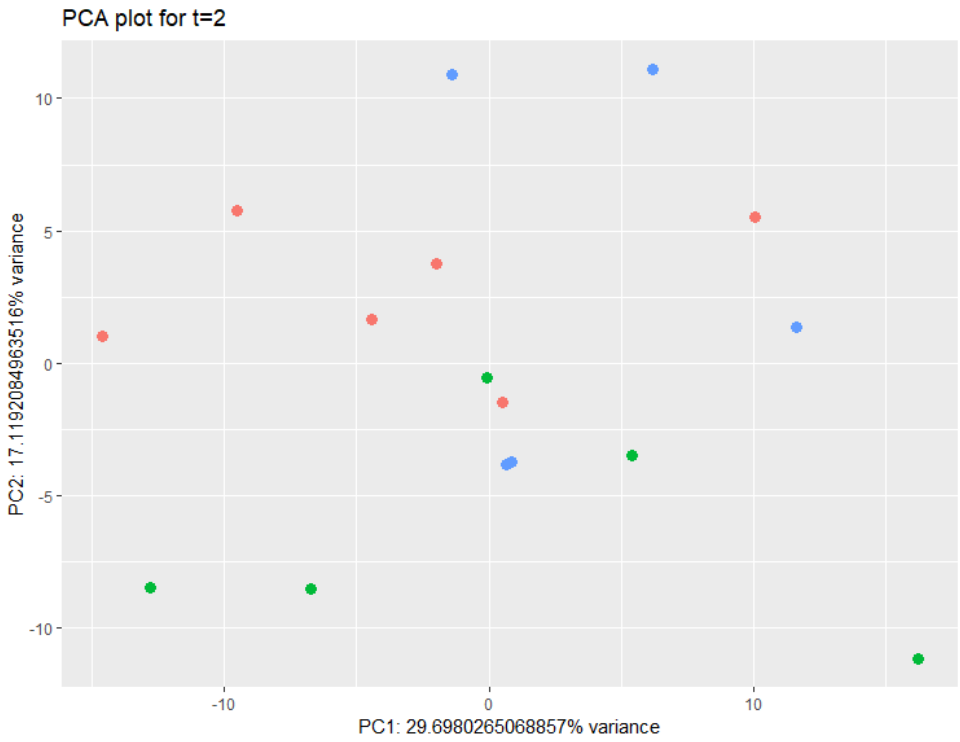


**PC1,
17.8%**

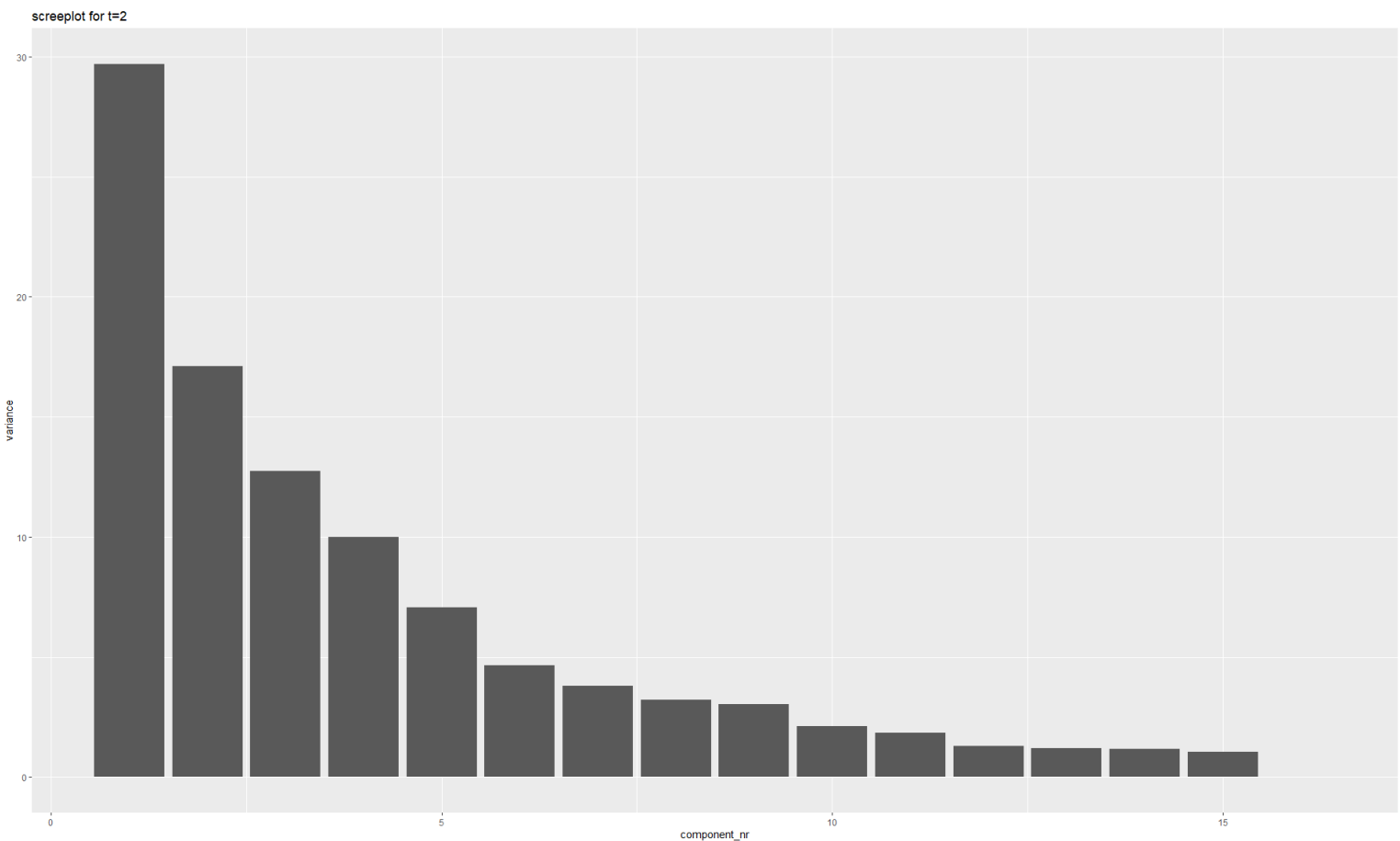


Biplot and screeplot t=2

non-scaled, 500 top variance genes

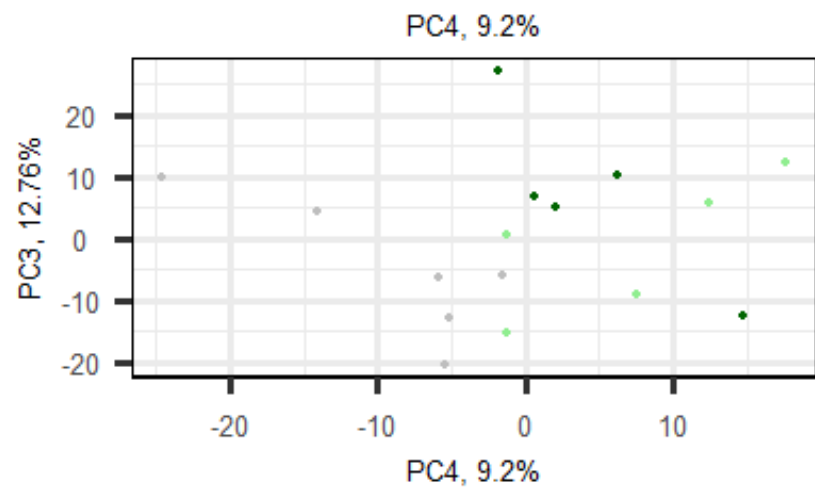
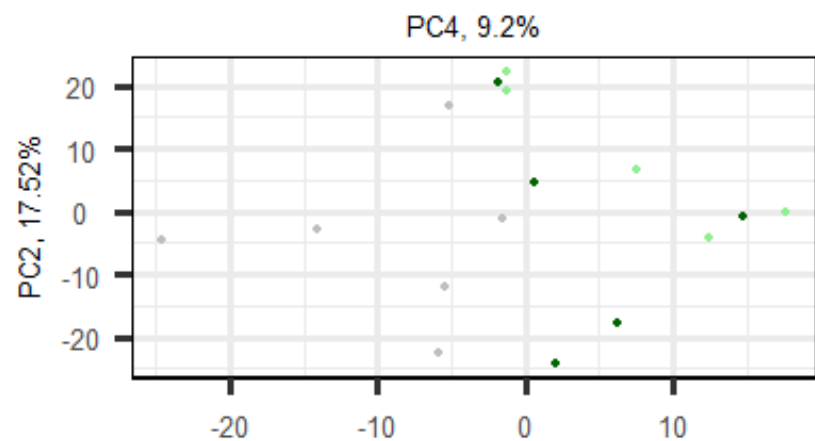
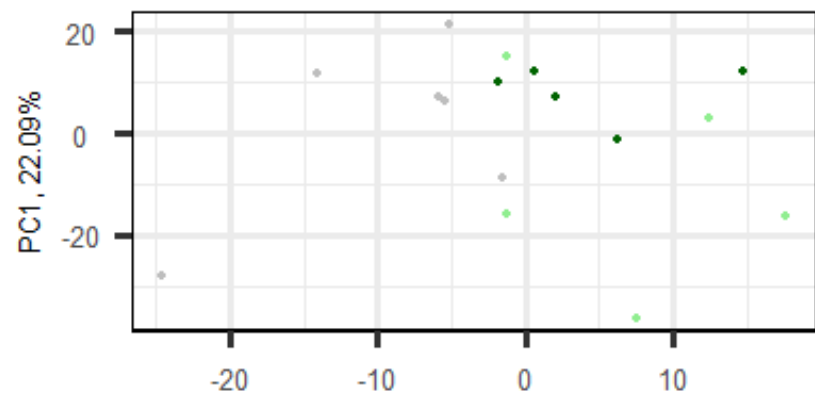


No further interesting biplots

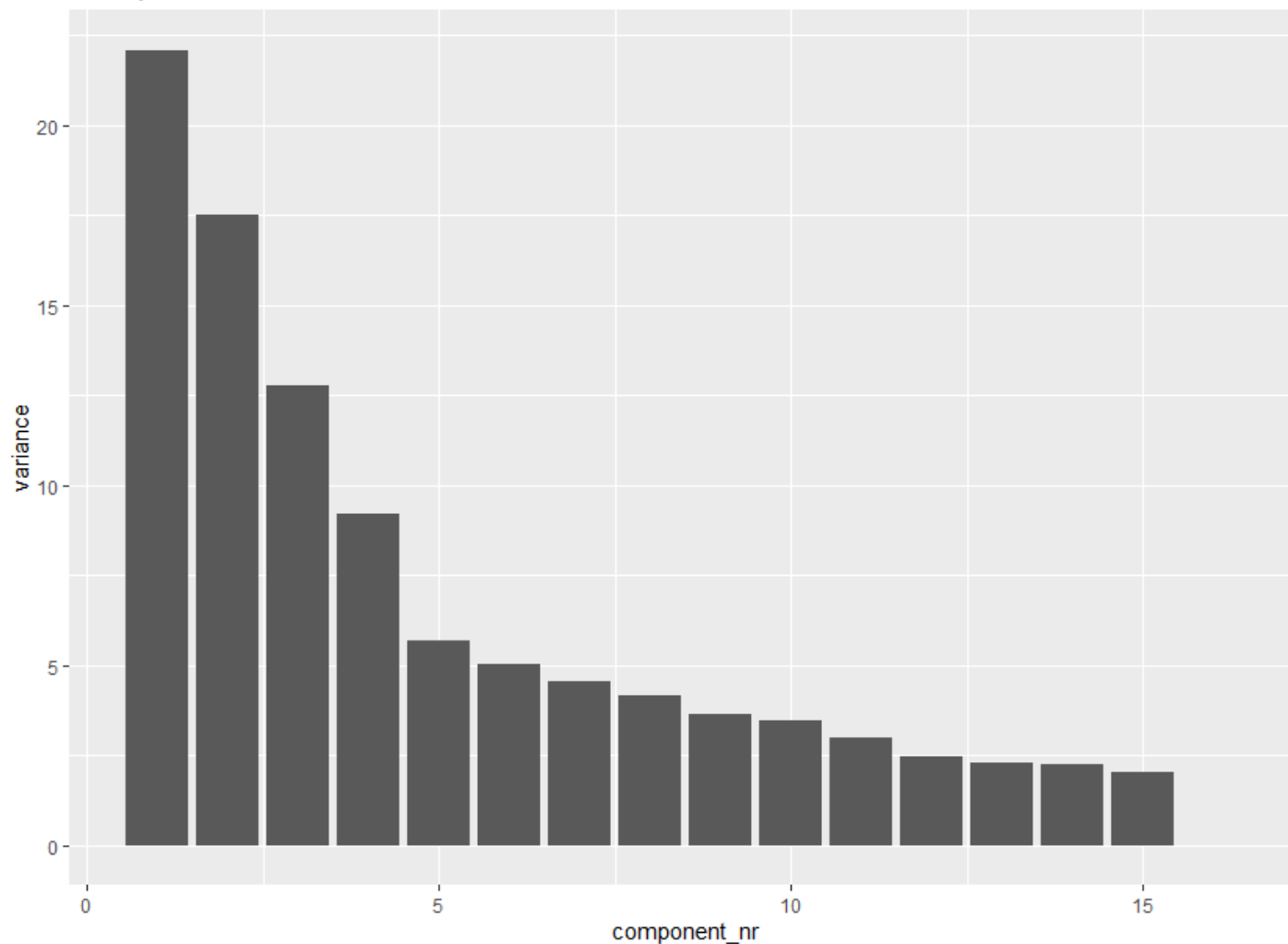


Biplot and screeplot t=2

non-scaled, 50% top variance genes

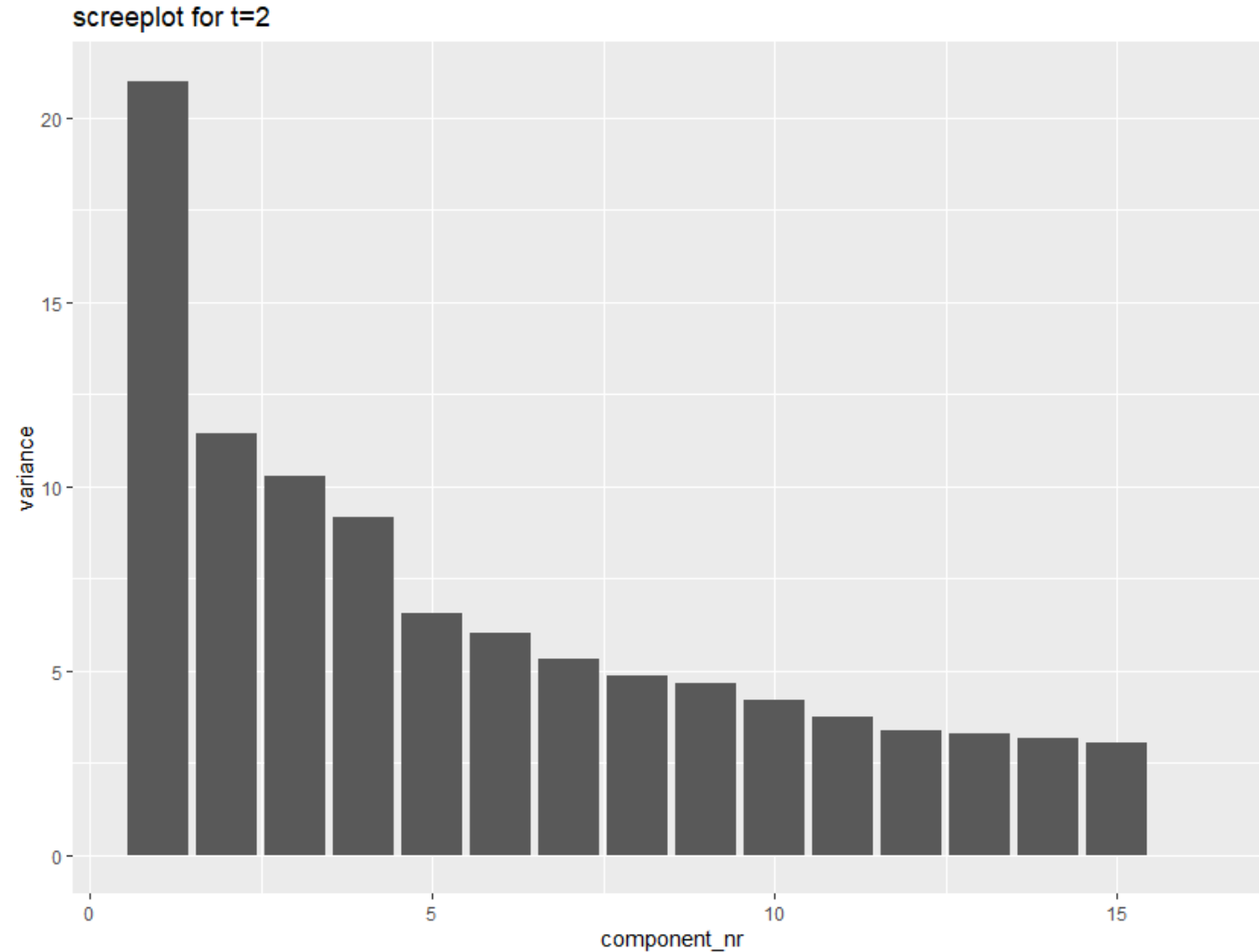
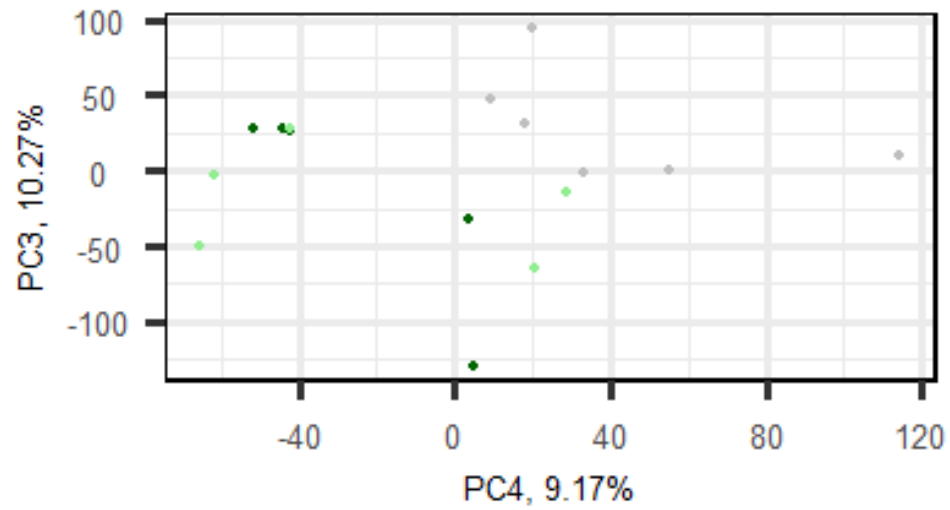


screeplot for t=2



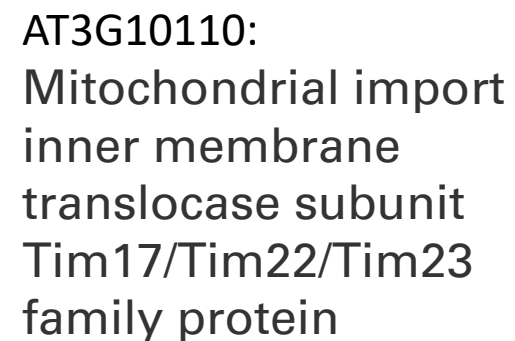
Biplot and screeplot t=2

scaled, 90% top variance genes



PC1, PC2, PC3, PC4, PC5

PC1, PC2, PC3, PC4, PC5



AT3G10110:
Mitochondrial import
inner membrane
translocase subunit
Tim17/Tim22/Tim23
family protein

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)

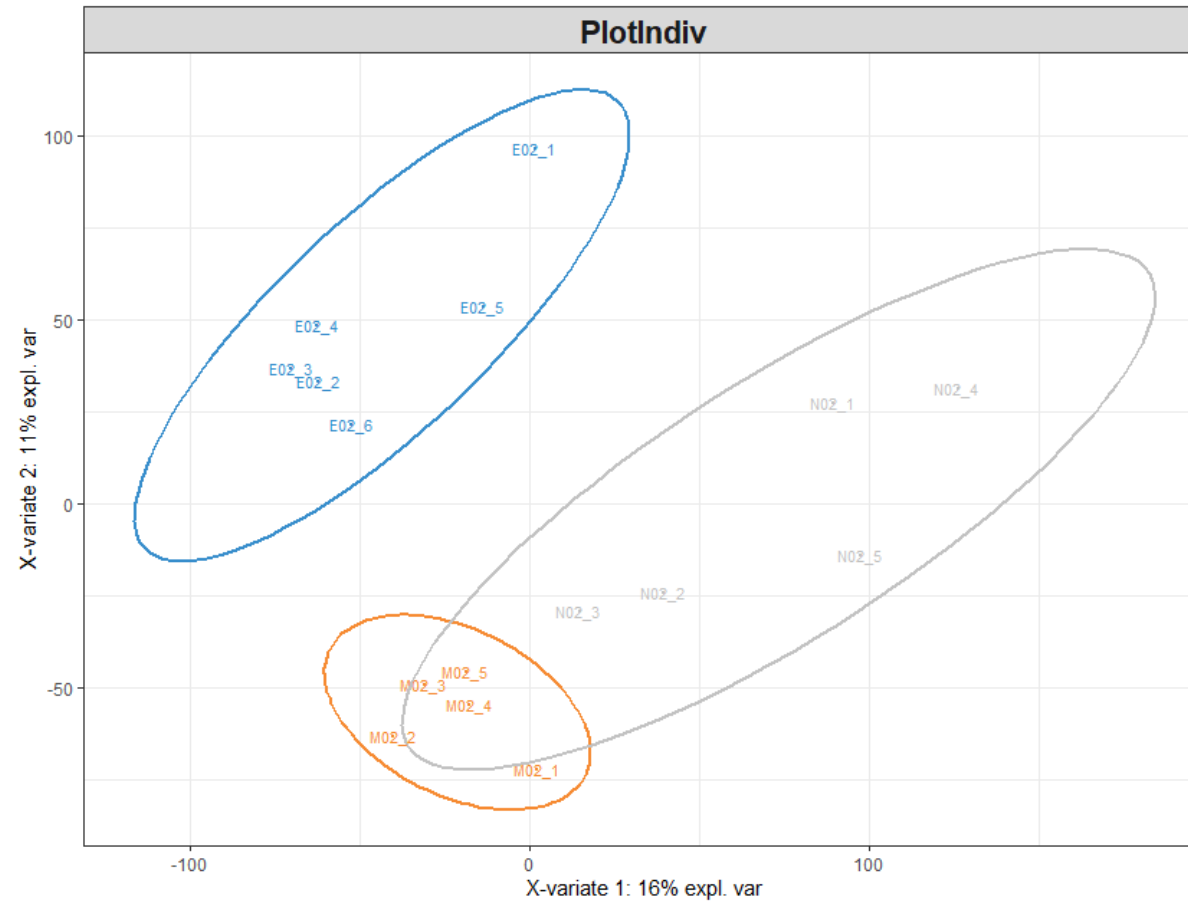
	Df	SumsOfSqs	MeanSqs	F.Model	R2
treatment	2	4016.2	2008.1	1.4526	0.18266
Residuals	13	17971.4	1382.4		0.81734
Total	15	21987.6			1.00000

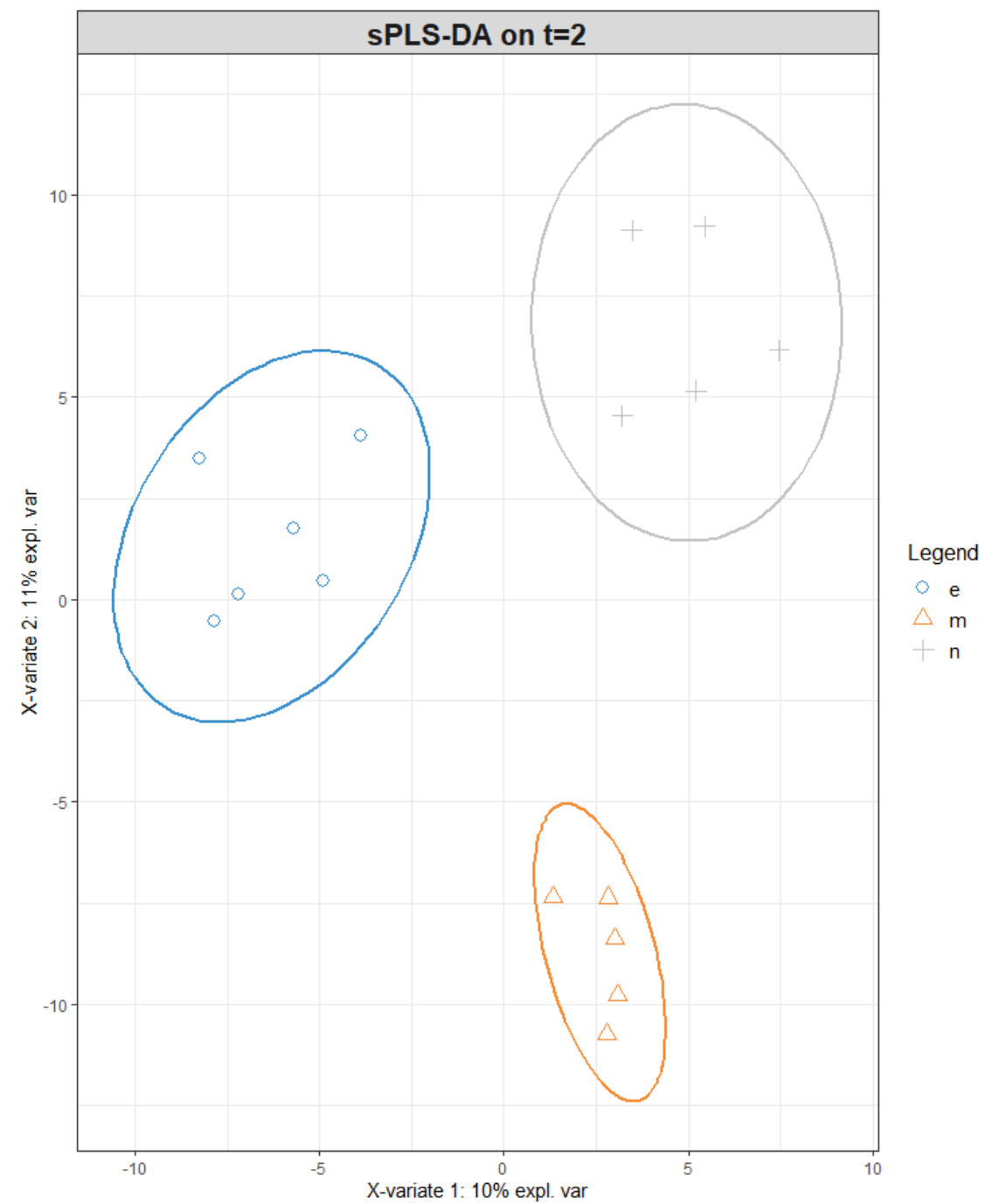
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Pr(>F)
0.0404 *

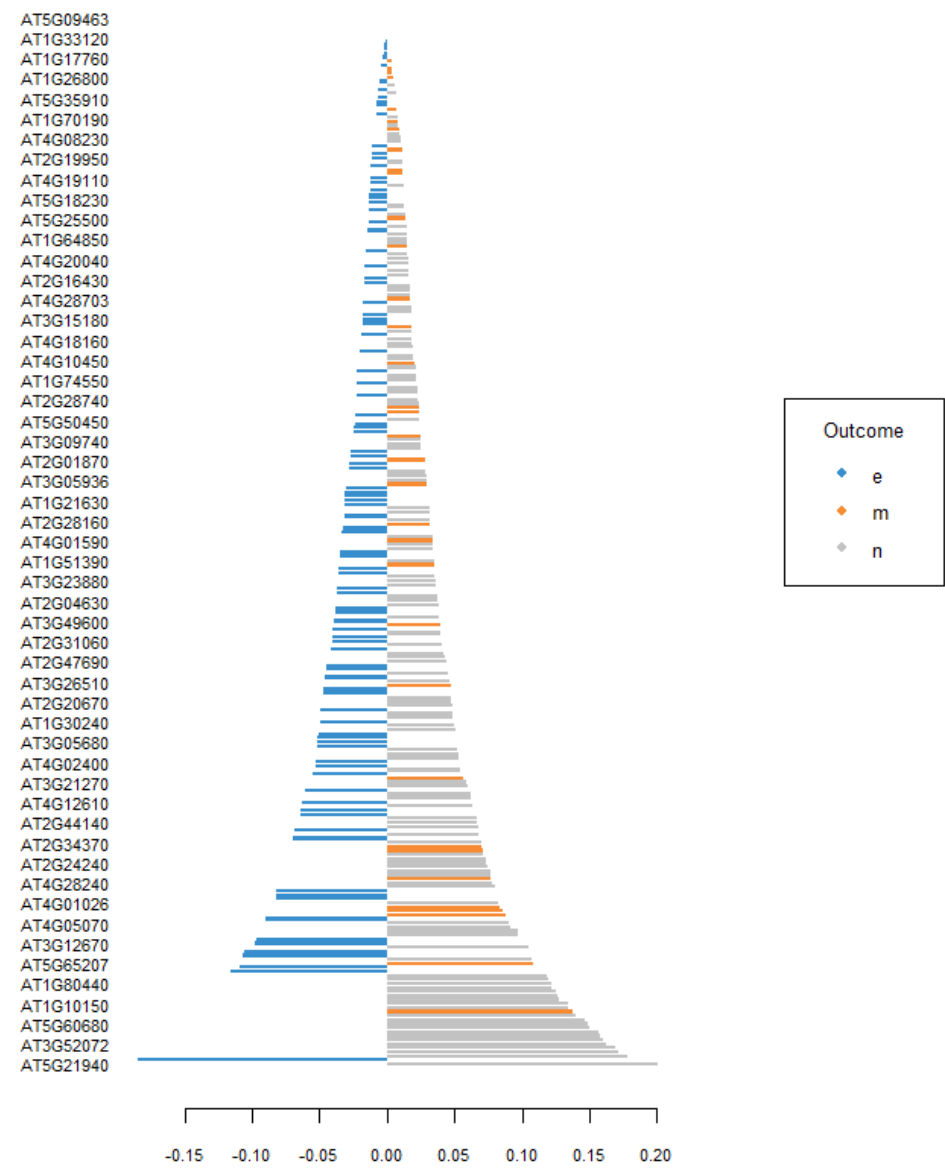
The other two timepoints do not show a significant effect of treatment

PLS-DA on treatment at t=2

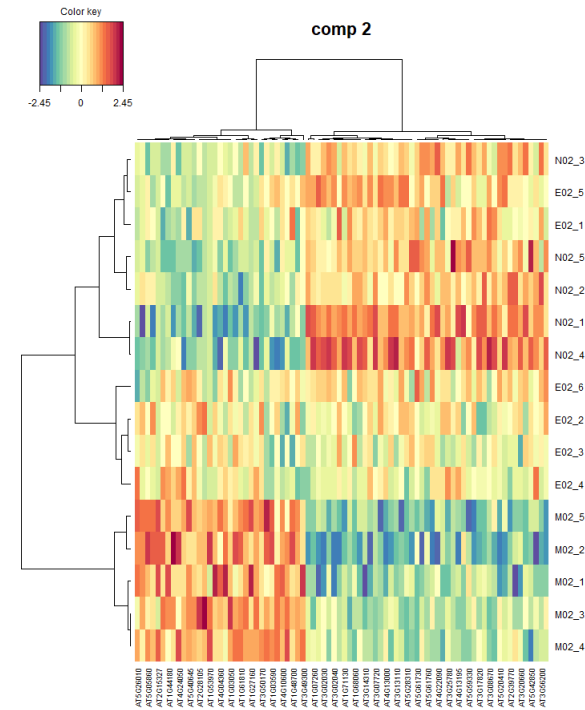
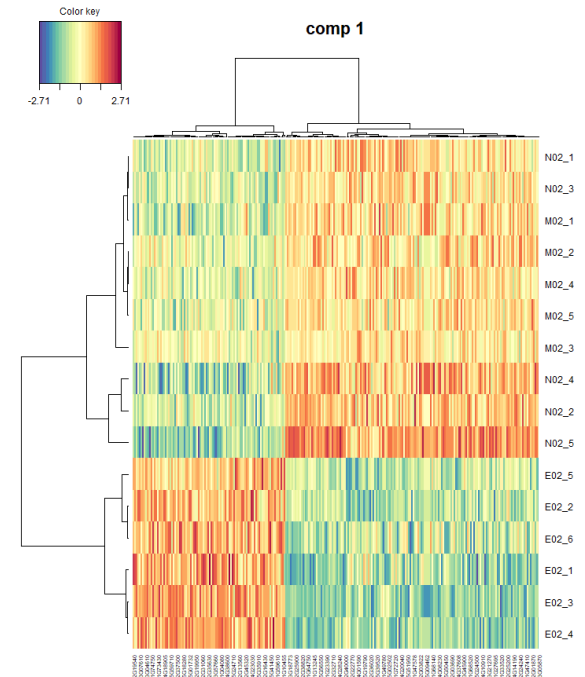
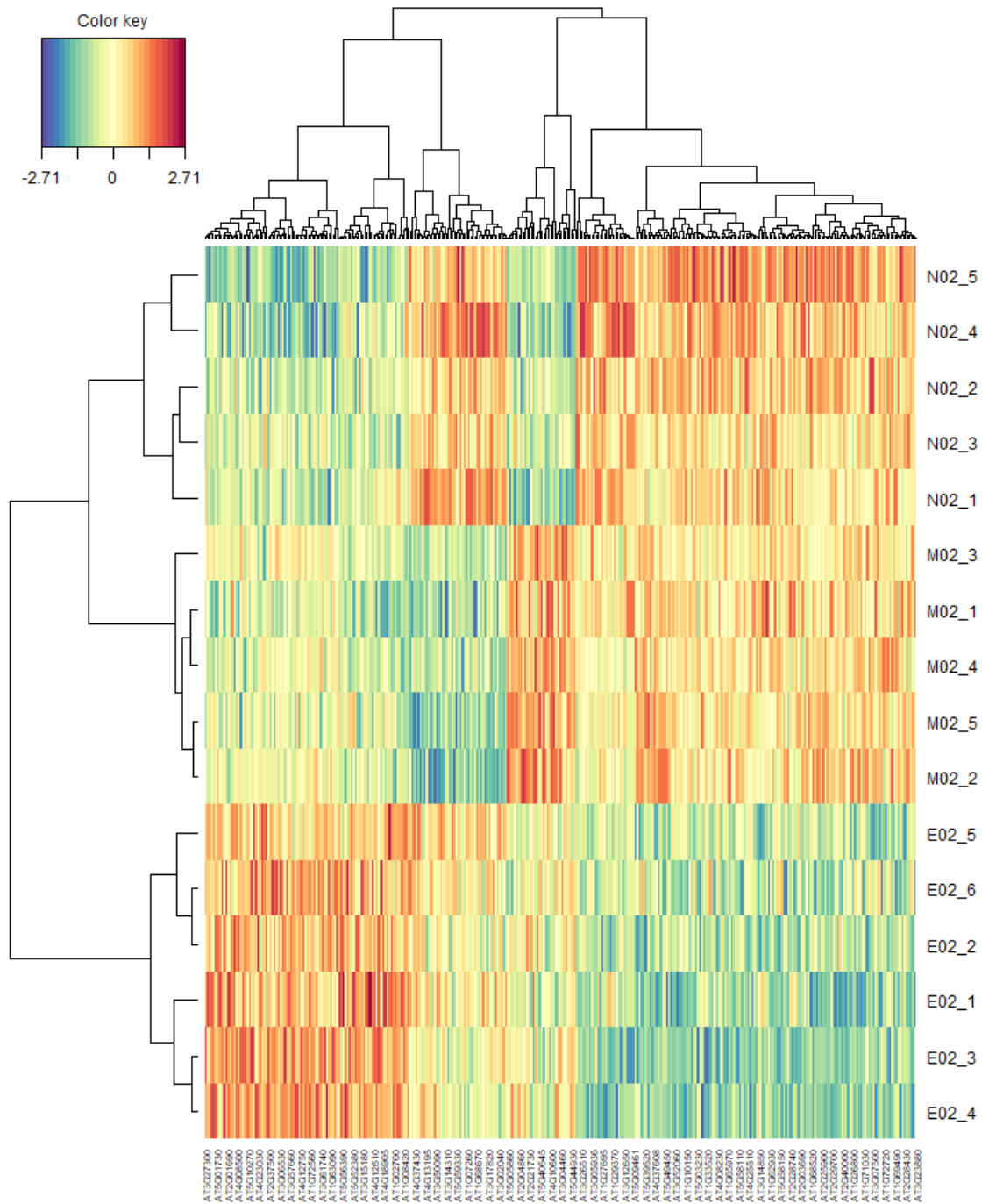




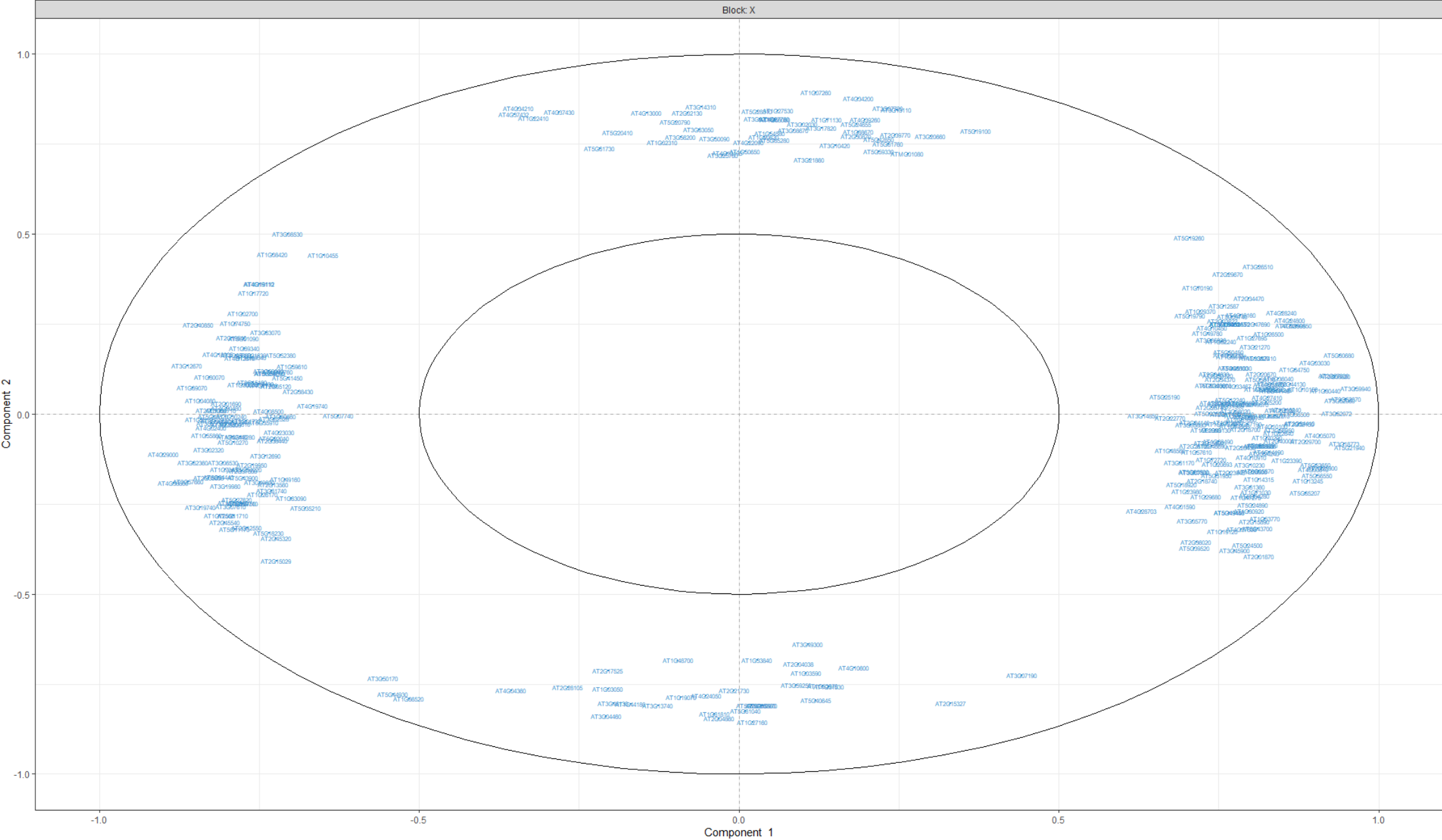
Loadings on comp 1



Euclidean distance, complete linkage

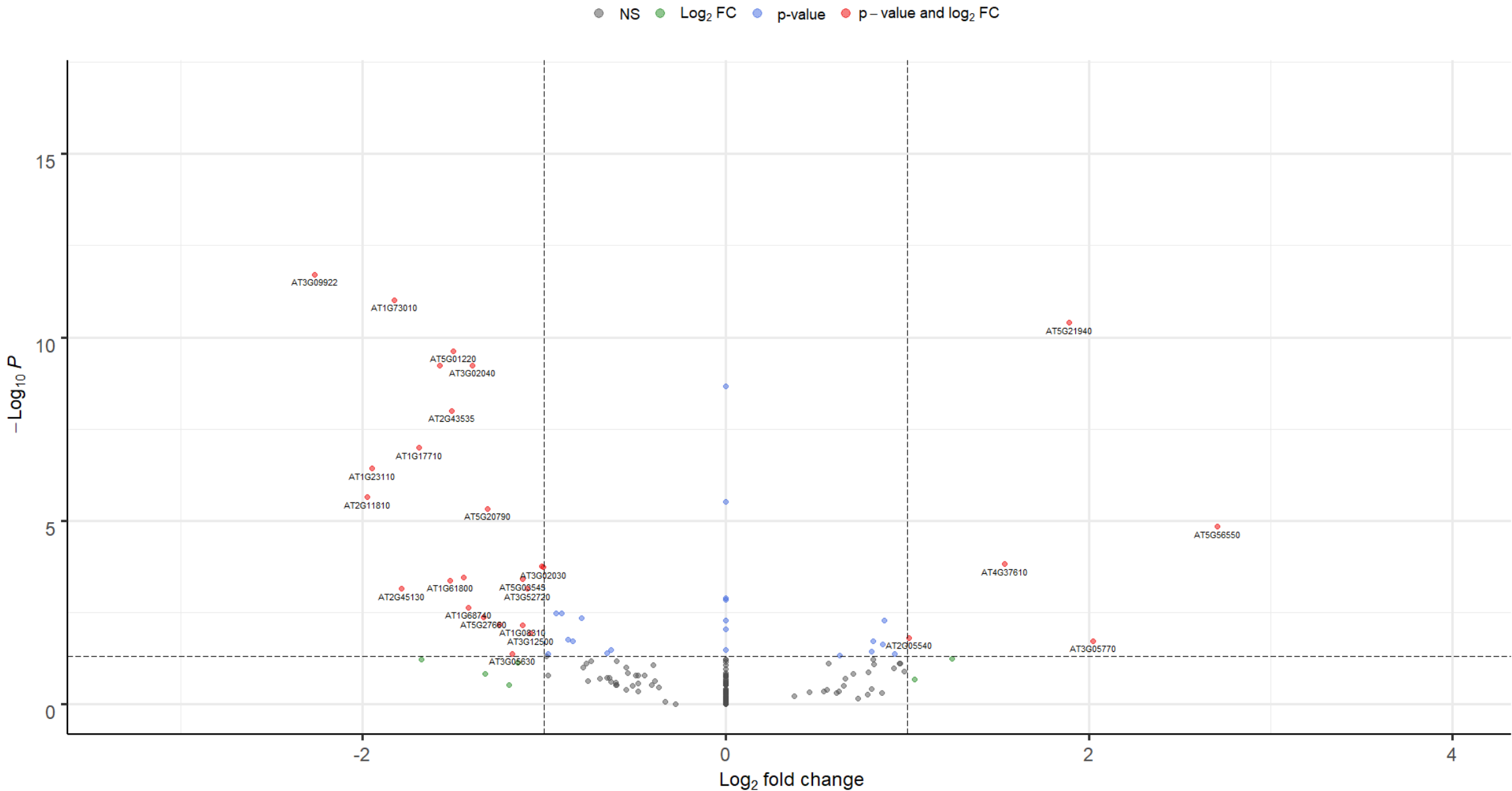


Correlation Circle Plots



DEGs t=2 1.5uM solA treatment

LFC>1, padj <0.05

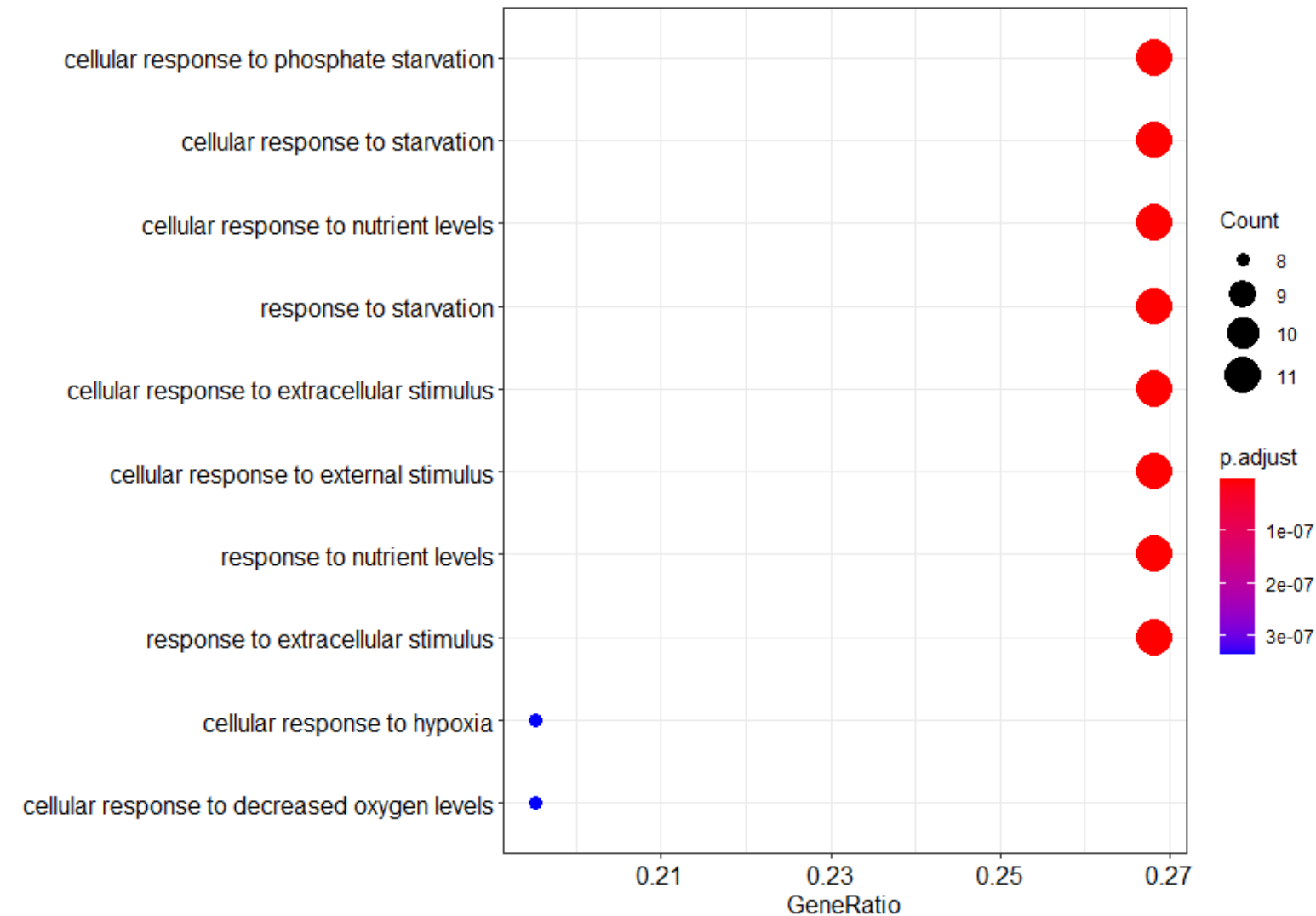


List of DEGs t=2 uM solA

AT3G10020			AT3g10020/T22K18_16 [Source:UniProtKB/TrEMBL;Acc:Q9SR67]		1.004336836
AT3G12500	ATHCHIB	P19171	Basic endochitinase B [Source:UniProtKB/Swiss-Prot;Acc:P19171]	CHI-B	-1.236010429
AT3G17790	ATACP5	Q9SCX8	Purple acid phosphatase 17 [Source:UniProtKB/Swiss-Prot;Acc:Q9SCX8]	PAP17	-1.005809063
AT3G47420	ATPS3	Q9C5L3	Putative glycerol-3-phosphate transporter 1 [Source:UniProtKB/Swiss-Prot;Acc:Q9C5L3]	ATPS3	-1.646532146
AT3G49780	ATPSK4	Q9M2Y0	Phytosulfokines 3 [Source:UniProtKB/Swiss-Prot;Acc:Q9M2Y0]	PSK3	1.60636832
AT3G52720	CAH1	O04846	Alpha carbonic anhydrase 1, chloroplastic [Source:UniProtKB/Swiss-Prot;Acc:O04846]	ACA1	-1.202621961
AT4G04610	APR1	P92979	5'-adenylylsulfate reductase 1, chloroplastic [Source:UniProtKB/Swiss-Prot;Acc:P92979]	APR1	-1.100538168
AT4G12480	pEARL1	Q39176	PEARL1 [Source:UniProtKB/TrEMBL;Acc:A0A178V1J0]	EARL1	1.162259704
AT4G15540		F4JK59	WAT1-related protein At4g15540 [Source:UniProtKB/Swiss-Prot;Acc:F4JK59]		-0.878675337
AT4G23000			Calcineurin-like metallo-phosphoesterase superfamily protein [Source:TAIR;Acc:AT4G23000]		-1.415861652
AT4G23670			AT4G23670 protein [Source:UniProtKB/TrEMBL;Acc:Q9SUR0]		-0.893855981
AT4G33030	SQD1	O48917	UDP-sulfoquinovose synthase, chloroplastic [Source:UniProtKB/Swiss-Prot;Acc:O48917]	SQD1	-1.049079414
AT4G33770		O81893	Inositol-tetrakisphosphate 1-kinase 2 [Source:UniProtKB/Swiss-Prot;Acc:O81893]	ITPK2	-1.172947467
AT4G37610	BT5	Q6EJ98	BTB/POZ and TAZ domain-containing protein 5 [Source:UniProtKB/Swiss-Prot;Acc:Q6EJ98]	BT5	1.661451623
AT4G39800	MI-1-P SYNTHASE	P42801	Inositol-3-phosphate synthase isozyme 1 [Source:UniProtKB/Swiss-Prot;Acc:P42801]	IPS1	-0.982384888
AT5G01220	SQD2	Q8S4F6	Sulfoquinovosyl transferase SQD2 [Source:UniProtKB/Swiss-Prot;Acc:Q8S4F6]	SQD2	-1.557363036
AT5G03545	AT4		At5g03545 [Source:UniProtKB/TrEMBL;Acc:Q9LZD2]	AT4	-1.224258377
AT5G11740	AGP15	Q9LYF6	ATAGP15 [Source:UniProtKB/TrEMBL;Acc:C0SVP3]	AGP15	-0.745428519
AT5G20150	ATSPX1	Q8LBH4	SPX domain-containing protein 1 [Source:UniProtKB/Swiss-Prot;Acc:Q8LBH4]	SPX1	-1.428983371
AT5G20410	MGD2	O82730	Monogalactosyldiacylglycerol synthase 2, chloroplastic [Source:UniProtKB/Swiss-Prot;Acc:O82730]	MGD2	-1.576923084
AT5G20790			unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_pr		-1.393963321
AT5G21940			At5g21940 [Source:UniProtKB/TrEMBL;Acc:Q9C593]		1.957075301
AT5G27660		Q3E6S8	DEG14 [Source:UniProtKB/TrEMBL;Acc:A0A178UPC0]		-1.503761964
AT5G52310	COR78	Q06738	Low-temperature-induced 78 kDa protein [Source:UniProtKB/Swiss-Prot;Acc:Q06738]	RD29A	1.253092441
AT5G56550	OXS3		Emb [Source:UniProtKB/TrEMBL;Acc:Q9LVB9]	OXS3	2.893596785

ensembl_gene_id	tair_symbol	uniprotswissprot	description	external_gene	log2-foldChange
AT1G08310			Alpha/beta-Hydrolases superfamily protein [Source:UniProtKB/TrEMBL;Acc:A8MRK8]		-1.277711493
AT1G17710		Q9FZ62	Inorganic pyrophosphatase 2 [Source:UniProtKB/Swiss-Prot;Acc:Q9FZ62]		-1.776029063
AT1G23110			Fold protein [Source:UniProtKB/TrEMBL;Acc:Q6DSU0]		-2.058859974
AT1G25560	TEM1	Q9C6M5	AP2/ERF and B3 domain-containing transcription repressor TEM1 [Source:UniProtKB/Swiss-P	TEM1	1.098769965
AT1G61800	GPT2	Q94B38	glucose-6-phosphate/phosphate translocator 2 [Source:TAIR;Acc:AT1G61800]	GPT2	-1.664566686
AT1G68740	PHO1;H1	Q93ZF5	Phosphate transporter PHO1 homolog 1 [Source:UniProtKB/Swiss-Prot;Acc:Q93ZF5]	PHO1-H1	-1.58572287
AT1G68840	RAV2	P82280	TEM2 [Source:UniProtKB/TrEMBL;Acc:A0A178WNP0]	RAV2	0.936876341
AT1G71030	ATMYBL2		At1g71030/F23N20_2 [Source:UniProtKB/TrEMBL;Acc:Q9C9A5]	ATMYBL2	0.945811473
AT1G73010	ATPS2	Q67YC0	Inorganic pyrophosphatase 1 [Source:UniProtKB/Swiss-Prot;Acc:Q67YC0]	PS2	-1.887939364
AT1G80920	J8	Q9SAG8	Chaperone protein dnaJ 8, chloroplastic [Source:UniProtKB/Swiss-Prot;Acc:Q9SAG8]	ATJ8	0.982576924
AT2G05510			At2g05510 [Source:UniProtKB/TrEMBL;Acc:Q9SL16]		1.129810875
AT2G05540			At2g05540/T20G20.11 [Source:UniProtKB/TrEMBL;Acc:Q9SL13]		1.161021999
AT2G11810	MGDC	Q9SI93	Monogalactosyldiacylglycerol synthase 3, chloroplastic [Source:UniProtKB/Swiss-Prot;Acc:Q9	MGD3	-2.097899334
AT2G36120	DOT1	Q9SIH2	Glycine-rich protein DOT1 [Source:UniProtKB/Swiss-Prot;Acc:Q9SIH2]	DOT1	0.74785726
AT2G43535		Q8RYE7	Defensin-like protein 196 [Source:UniProtKB/Swiss-Prot;Acc:Q8RYE7]	ATTI4	-1.577075618
AT2G43620		O22841	Endochitinase At2g43620 [Source:UniProtKB/Swiss-Prot;Acc:O22841]		1.976899989
AT2G45130	ATSPX3	Q5PP62	SPX domain-containing protein 3 [Source:UniProtKB/Swiss-Prot;Acc:Q5PP62]	SPX3	-1.969757074
AT3G02030			Transferase [Source:UniProtKB/TrEMBL;Acc:A0A119LSS3]		-1.094482452
AT3G02040	SRG3	Q9SGA2	Glycerophosphodiester phosphodiesterase GDPD1, chloroplastic [Source:UniProtKB/Swiss-P	GDPD1	-1.450111222
AT3G02870	VTC4	Q9M8S8	Inositol-phosphate phosphatase [Source:UniProtKB/Swiss-Prot;Acc:Q9M8S8]	VTC4	-1.015018403
AT3G03250	UGP	Q9M9P3	UTP--glucose-1-phosphate uridylyltransferase [Source:UniProtKB/TrEMBL;Acc:A0A119LT02]	UGP	-0.7794926
AT3G05630	PLDP2	Q9M9W8	Phospholipase D zeta 2 [Source:UniProtKB/Swiss-Prot;Acc:Q9M9W8]	PLPZETA2	-1.408708811
AT3G05770			F10A16.6 protein [Source:UniProtKB/TrEMBL;Acc:Q9M9L9]		2.341366514
AT3G09922	IPS1		induced by phosphate starvation1 [Source:TAIR;Acc:AT3G09922]	IPS1	-2.334640936

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

P starvation

Hypoxia

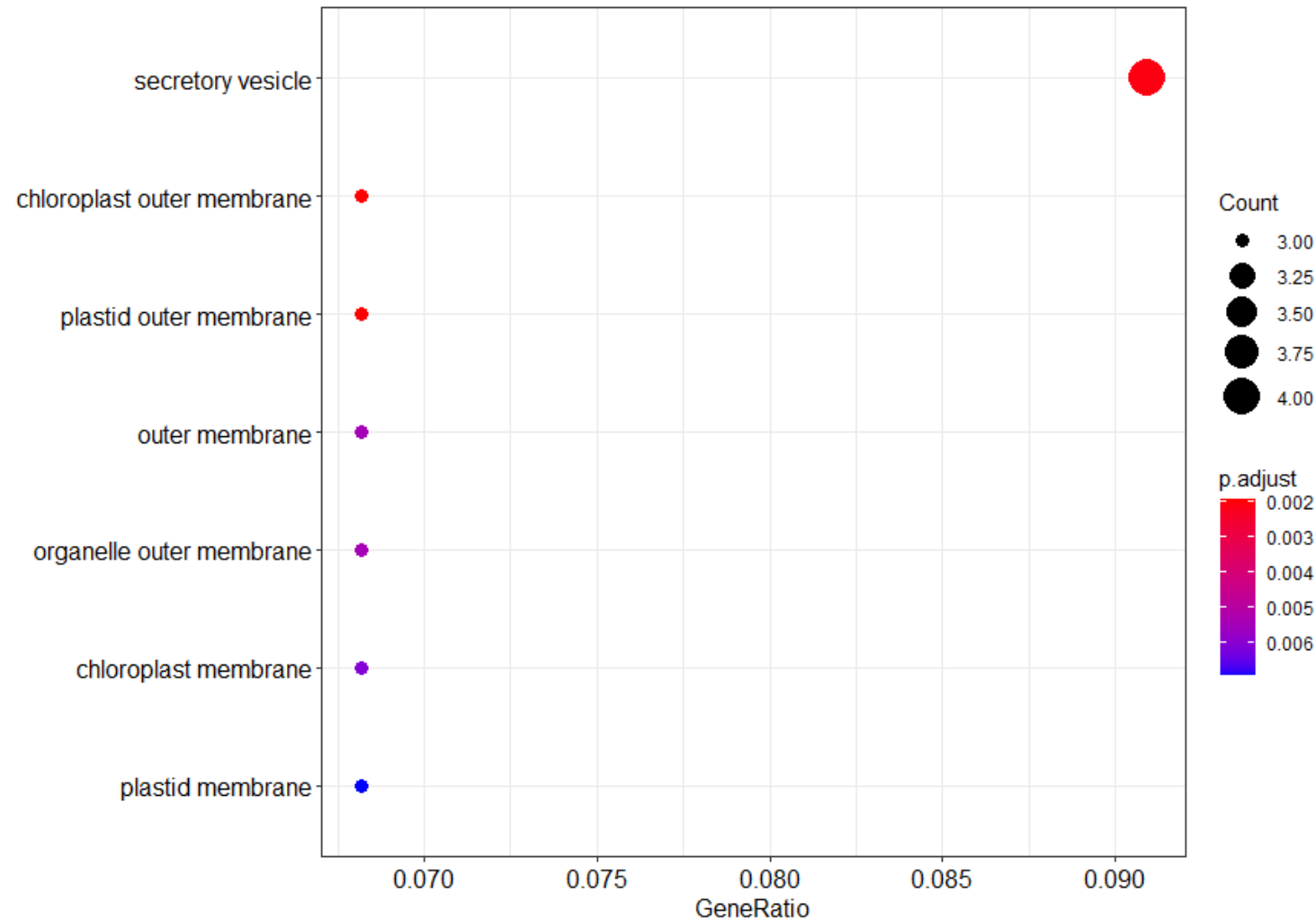
Lipid metabolism

Response to fungus

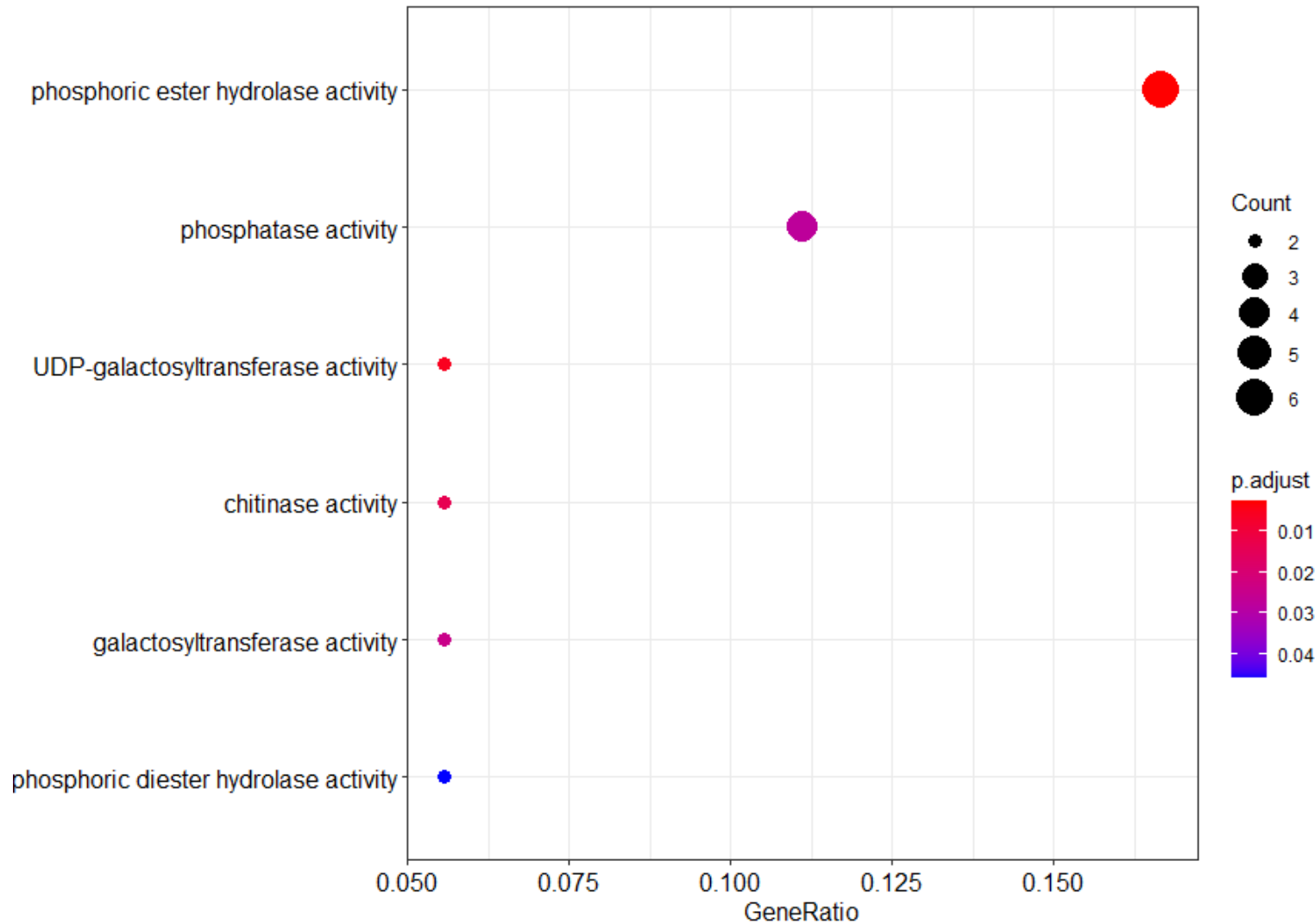
Other biotic stress response

ID	Description	Gen	BgRatio	pvalue	p.adjust	qvalue	geneID
GO:0016036	cellular response to phosphate starvation	11/41	74/21510	1.0689E-18	2.65086E-16	1.75524E-16	PHO1;H1/AtPPsPase1/ATMGD3/ATSPX3/AtUGP1/PDLZ2/SQD1/SQD2/AT4/ATSPX1/ATMGD2
GO:0009267	cellular response to starvation	11/41	146/21510	2.55078E-15	3.16297E-13	2.09433E-13	PHO1;H1/AtPPsPase1/ATMGD3/ATSPX3/AtUGP1/PDLZ2/SQD1/SQD2/AT4/ATSPX1/ATMGD2
GO:0031669	cellular response to nutrient levels	11/41	168/21510	1.22276E-14	1.01081E-12	6.69298E-13	PHO1;H1/AtPPsPase1/ATMGD3/ATSPX3/AtUGP1/PDLZ2/SQD1/SQD2/AT4/ATSPX1/ATMGD2
GO:0042594	response to starvation	11/41	181/21510	2.79755E-14	1.73448E-12	1.14847E-12	PHO1;H1/AtPPsPase1/ATMGD3/ATSPX3/AtUGP1/PDLZ2/SQD1/SQD2/AT4/ATSPX1/ATMGD2
GO:0031668	cellular response to extracellular stimulus	11/41	203/21510	9.93831E-14	4.9294E-12	3.26395E-12	PHO1;H1/AtPPsPase1/ATMGD3/ATSPX3/AtUGP1/PDLZ2/SQD1/SQD2/AT4/ATSPX1/ATMGD2
GO:0071496	cellular response to external stimulus	11/41	209/21510	1.36964E-13	5.66116E-12	3.74848E-12	PHO1;H1/AtPPsPase1/ATMGD3/ATSPX3/AtUGP1/PDLZ2/SQD1/SQD2/AT4/ATSPX1/ATMGD2
GO:0031667	response to nutrient levels	11/41	227/21510	3.39289E-13	1.20205E-11	7.95926E-12	PHO1;H1/AtPPsPase1/ATMGD3/ATSPX3/AtUGP1/PDLZ2/SQD1/SQD2/AT4/ATSPX1/ATMGD2
GO:0009991	response to extracellular stimulus	11/41	263/21510	1.69223E-12	5.24591E-11	3.47352E-11	PHO1;H1/AtPPsPase1/ATMGD3/ATSPX3/AtUGP1/PDLZ2/SQD1/SQD2/AT4/ATSPX1/ATMGD2
GO:0071456	cellular response to hypoxia	8/41	238/21510	1.39283E-08	3.35177E-07	2.21934E-07	AtTEM1/AtRAV2/AtPPsPase1/AtGDPD1/NA/ATPSK3/ATSPX1/NA
GO:0036294	cellular response to decreased oxygen levels	8/41	240/21510	1.48667E-08	3.35177E-07	2.21934E-07	AtTEM1/AtRAV2/AtPPsPase1/AtGDPD1/NA/ATPSK3/ATSPX1/NA
GO:0071453	cellular response to oxygen levels	8/41	240/21510	1.48667E-08	3.35177E-07	2.21934E-07	AtTEM1/AtRAV2/AtPPsPase1/AtGDPD1/NA/ATPSK3/ATSPX1/NA
GO:0009247	glycolipid biosynthetic process	5/41	47/21510	2.82643E-08	5.84129E-07	3.86775E-07	ATMGD3/PDLZ2/SQD1/SQD2/ATMGD2
GO:0001666	response to hypoxia	8/41	264/21510	3.11705E-08	5.94637E-07	3.93732E-07	AtTEM1/AtRAV2/AtPPsPase1/AtGDPD1/NA/ATPSK3/ATSPX1/NA
GO:0036293	response to decreased oxygen levels	8/41	268/21510	3.50191E-08	5.9591E-07	3.94575E-07	AtTEM1/AtRAV2/AtPPsPase1/AtGDPD1/NA/ATPSK3/ATSPX1/NA
GO:0070482	response to oxygen levels	8/41	269/21510	3.60429E-08	5.9591E-07	3.94575E-07	AtTEM1/AtRAV2/AtPPsPase1/AtGDPD1/NA/ATPSK3/ATSPX1/NA
GO:0006664	glycolipid metabolic process	5/41	51/21510	4.30427E-08	6.27917E-07	4.15768E-07	ATMGD3/PDLZ2/SQD1/SQD2/ATMGD2
GO:1903509	liposaccharide metabolic process	5/41	51/21510	4.30427E-08	6.27917E-07	4.15768E-07	ATMGD3/PDLZ2/SQD1/SQD2/ATMGD2
GO:0046467	membrane lipid biosynthetic process	5/41	88/21510	6.81697E-07	9.39227E-06	6.21899E-06	ATMGD3/PDLZ2/SQD1/SQD2/ATMGD2
GO:0019375	galactolipid biosynthetic process	3/41	13/21510	1.81408E-06	2.36785E-05	1.56785E-05	ATMGD3/PDLZ2/ATMGD2
GO:0006643	membrane lipid metabolic process	5/41	109/21510	1.9742E-06	2.44801E-05	1.62092E-05	ATMGD3/PDLZ2/SQD1/SQD2/ATMGD2
GO:0019374	galactolipid metabolic process	3/41	15/21510	2.8784E-06	3.39925E-05	2.25078E-05	ATMGD3/PDLZ2/ATMGD2
GO:0055062	phosphate ion homeostasis	3/41	19/21510	6.09763E-06	6.57483E-05	4.35346E-05	AtGDPD1/ATACP5/AtG3Pp1
GO:0072506	trivalent inorganic anion homeostasis	3/41	19/21510	6.09763E-06	6.57483E-05	4.35346E-05	AtGDPD1/ATACP5/AtG3Pp1
GO:0006020	inositol metabolic process	3/41	21/21510	8.34715E-06	7.96189E-05	5.27188E-05	VTC4/AtITPK2/ATIPS1
GO:0055083	monovalent inorganic anion homeostasis	3/41	21/21510	8.34715E-06	7.96189E-05	5.27188E-05	AtGDPD1/ATACP5/AtG3Pp1
GO:0072505	divalent inorganic anion homeostasis	3/41	21/21510	8.34715E-06	7.96189E-05	5.27188E-05	AtGDPD1/ATACP5/AtG3Pp1
GO:0043647	inositol phosphate metabolic process	3/41	34/21510	3.69148E-05	0.000339069	0.000224511	VTC4/AtITPK2/ATIPS1
GO:0055081	anion homeostasis	3/41	44/21510	8.06269E-05	0.000714124	0.00047285	AtGDPD1/ATACP5/AtG3Pp1
GO:0046434	organophosphate catabolic process	3/41	55/21510	0.000157406	0.001346096	0.000891303	AtGDPD1/VTC4/PDLZ2
GO:0019751	polyol metabolic process	3/41	62/21510	0.000224824	0.001858548	0.001230617	VTC4/AtITPK2/ATIPS1
GO:0006644	phospholipid metabolic process	4/41	199/21510	0.000550644	0.004405149	0.002916822	AtGDPD1/VTC4/PDLZ2/ATIPS1
GO:0009395	phospholipid catabolic process	2/41	22/21510	0.000799283	0.006194443	0.004101584	AtGDPD1/PDLZ2
GO:1901137	carbohydrate derivative biosynthetic process	5/41	420/21510	0.001164404	0.008750673	0.005794164	ATMGD3/PDLZ2/SQD1/SQD2/ATMGD2
GO:0016998	cell wall macromolecule catabolic process	2/41	30/21510	0.001490688	0.010873257	0.00719961	NA/ATHCHIB
GO:0006979	response to oxidative stress	5/41	454/21510	0.001641863	0.011434234	0.007571054	NA/ATACP5/BT5/COR78/ATOXS3
GO:0006650	glycerophospholipid metabolic process	3/41	123/21510	0.001659808	0.011434234	0.007571054	AtGDPD1/VTC4/ATIPS1
GO:0046173	polyol biosynthetic process	2/41	33/21510	0.001802856	0.012084006	0.008001294	VTC4/ATIPS1
GO:0006066	alcohol metabolic process	3/41	134/21510	0.00211956	0.013629648	0.009024724	VTC4/AtITPK2/ATIPS1
GO:0006817	phosphate ion transport	2/41	36/21510	0.002143372	0.013629648	0.009024724	PHO1;H1/AT4
GO:0000302	response to reactive oxygen species	3/41	154/21510	0.003142975	0.019486448	0.012902741	ATACP5/BT5/COR78
GO:1901615	organic hydroxy compound metabolic process	4/41	323/21510	0.003262818	0.019736073	0.013068028	ATMYBL2/VTC4/AtITPK2/ATIPS1
GO:0046486	glycerolipid metabolic process	3/41	158/21510	0.003378175	0.019947319	0.013207902	AtGDPD1/VTC4/ATIPS1
GO:1901617	organic hydroxy compound biosynthetic process	3/41	195/21510	0.006071397	0.035016427	0.02318575	ATMYBL2/VTC4/ATIPS1
GO:0044262	cellular carbohydrate metabolic process	4/41	401/21510	0.006993185	0.038793072	0.025686414	VTC4/AtUGP1/AtITPK2/ATIPS1
GO:0042542	response to hydrogen peroxide	2/41	66/21510	0.007039065	0.038793072	0.025686414	ATACP5/BT5
GO:0009409	response to cold	4/41	413/21510	0.007744249	0.041751601	0.027645372	VTC4/EARL1/BT5/COR78
GO:0046165	alcohol biosynthetic process	2/41	74/21510	0.008778966	0.046323055	0.030672312	VTC4/ATIPS1
GO:0009873	ethylene-activated signaling pathway	2/41	76/21510	0.009241066	0.047745506	0.031614172	AtTEM1/ATHCHIB

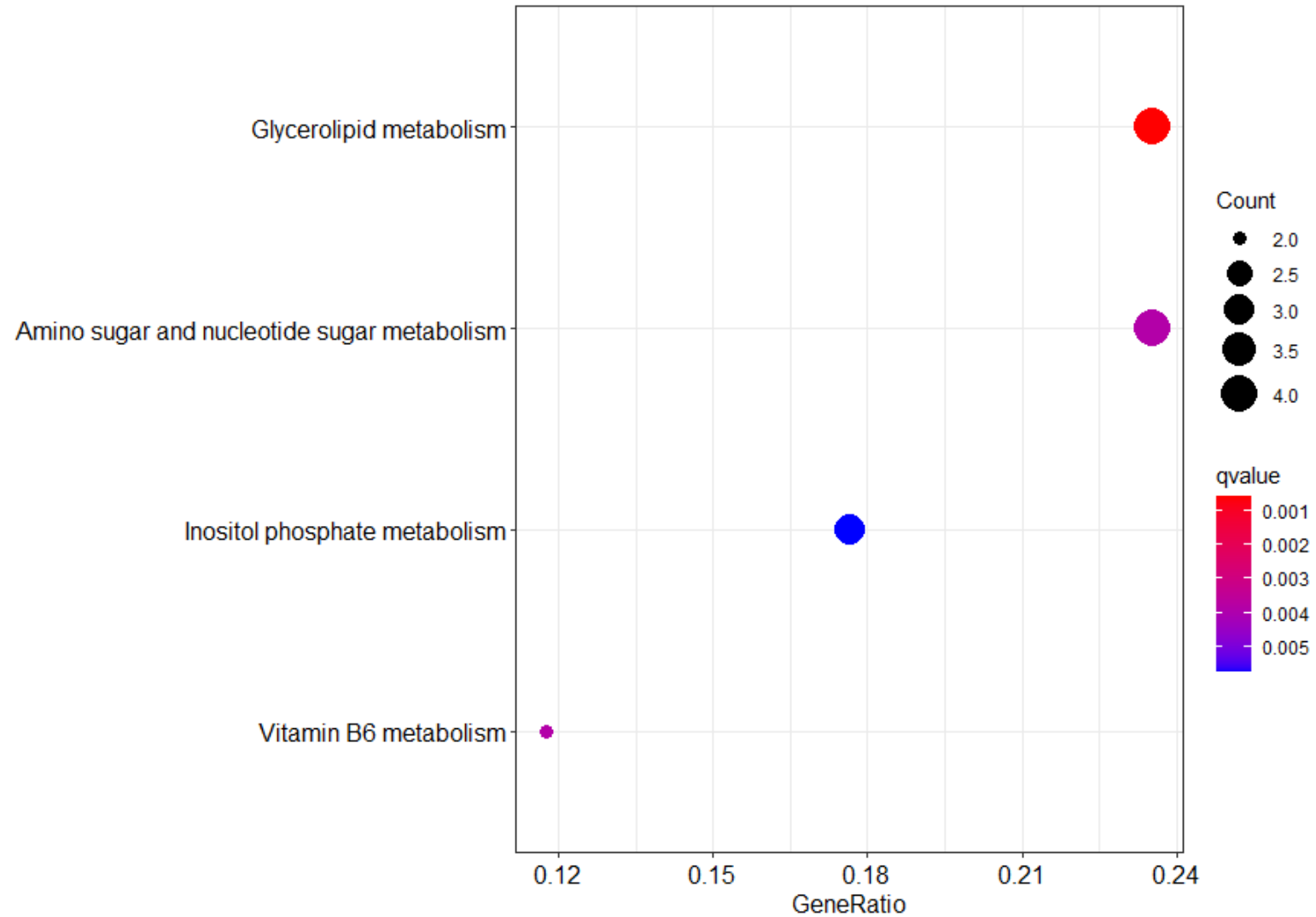
GO terms cellular compartment (1.5uM solA treatment)



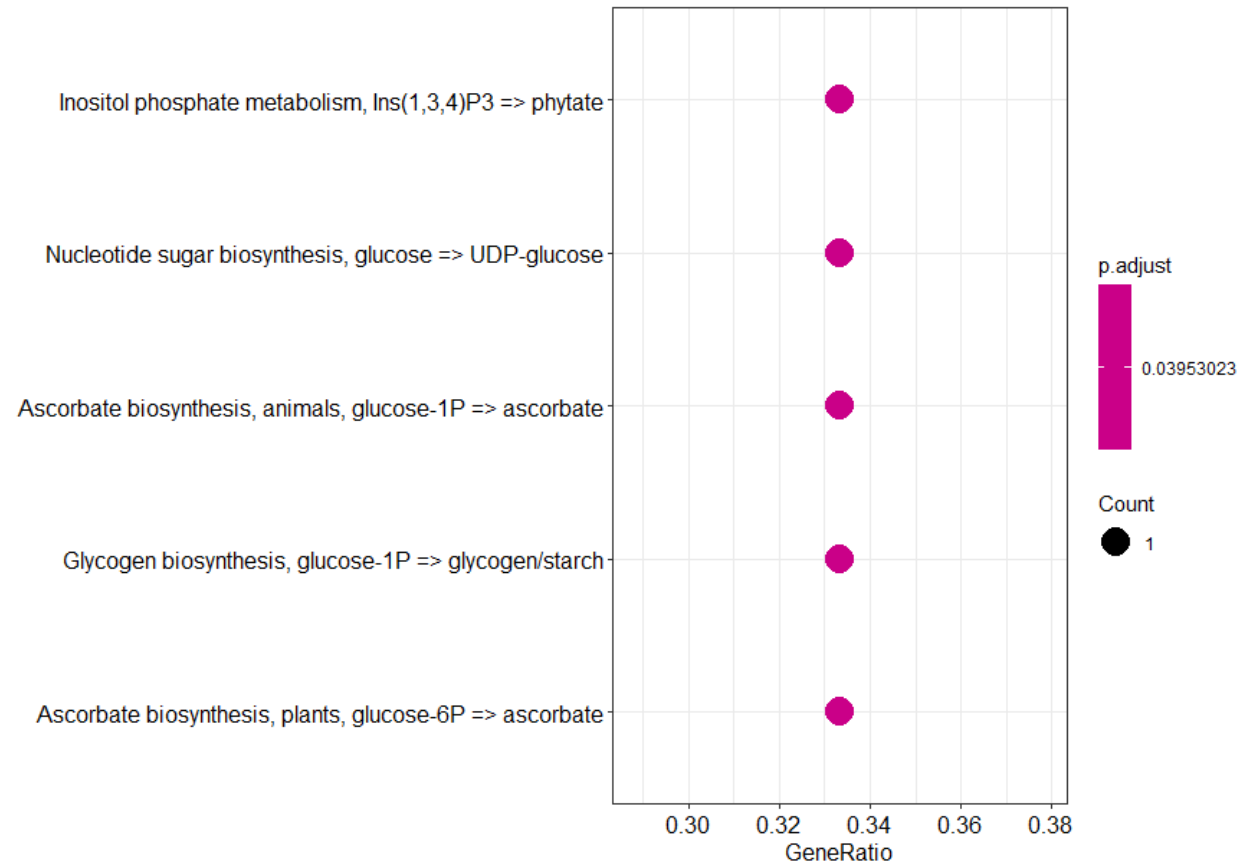
GO terms molecular function (1.5uM solA treatment)



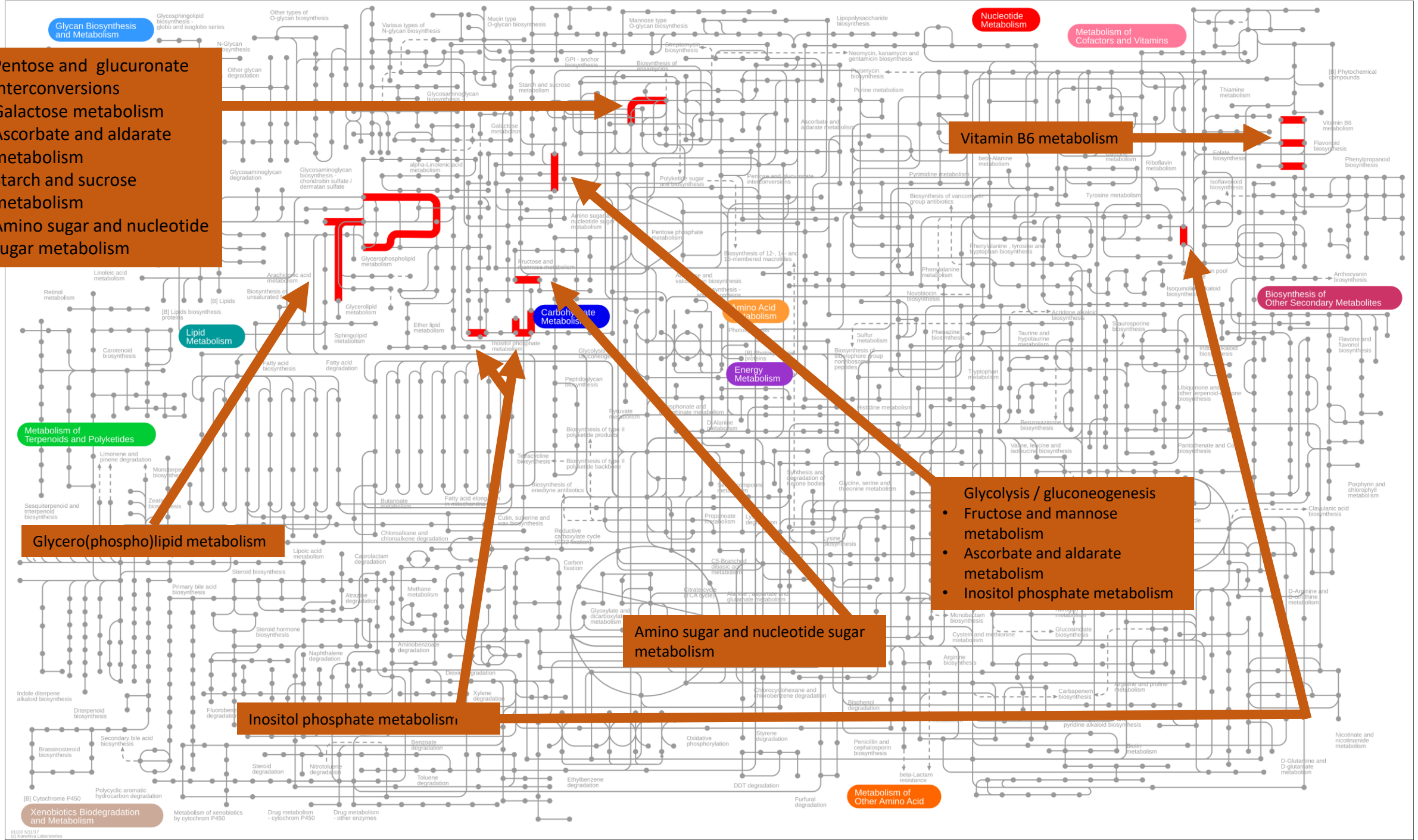
KEGG analysis



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

Vitamin B6 metabolism

Biosynthesis of Other Secondary Metabolites

Amino sugar and nucleotide sugar metabolism

Inositol phosphate metabolism

Glycolysis / gluconeogenesis

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

Metabolism of Other Amino Acid

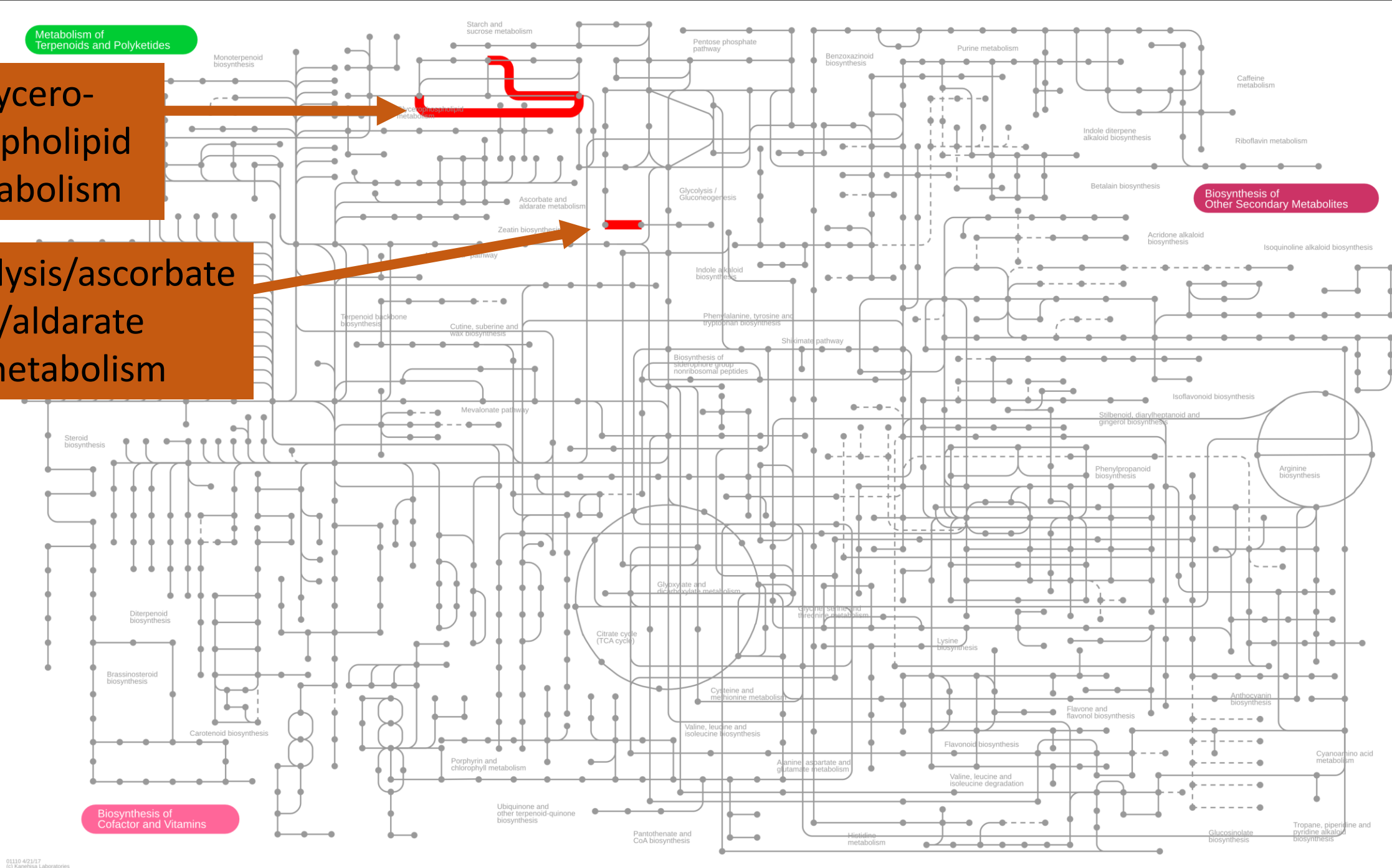
Metabolism of
Terpenoids and Polyketides

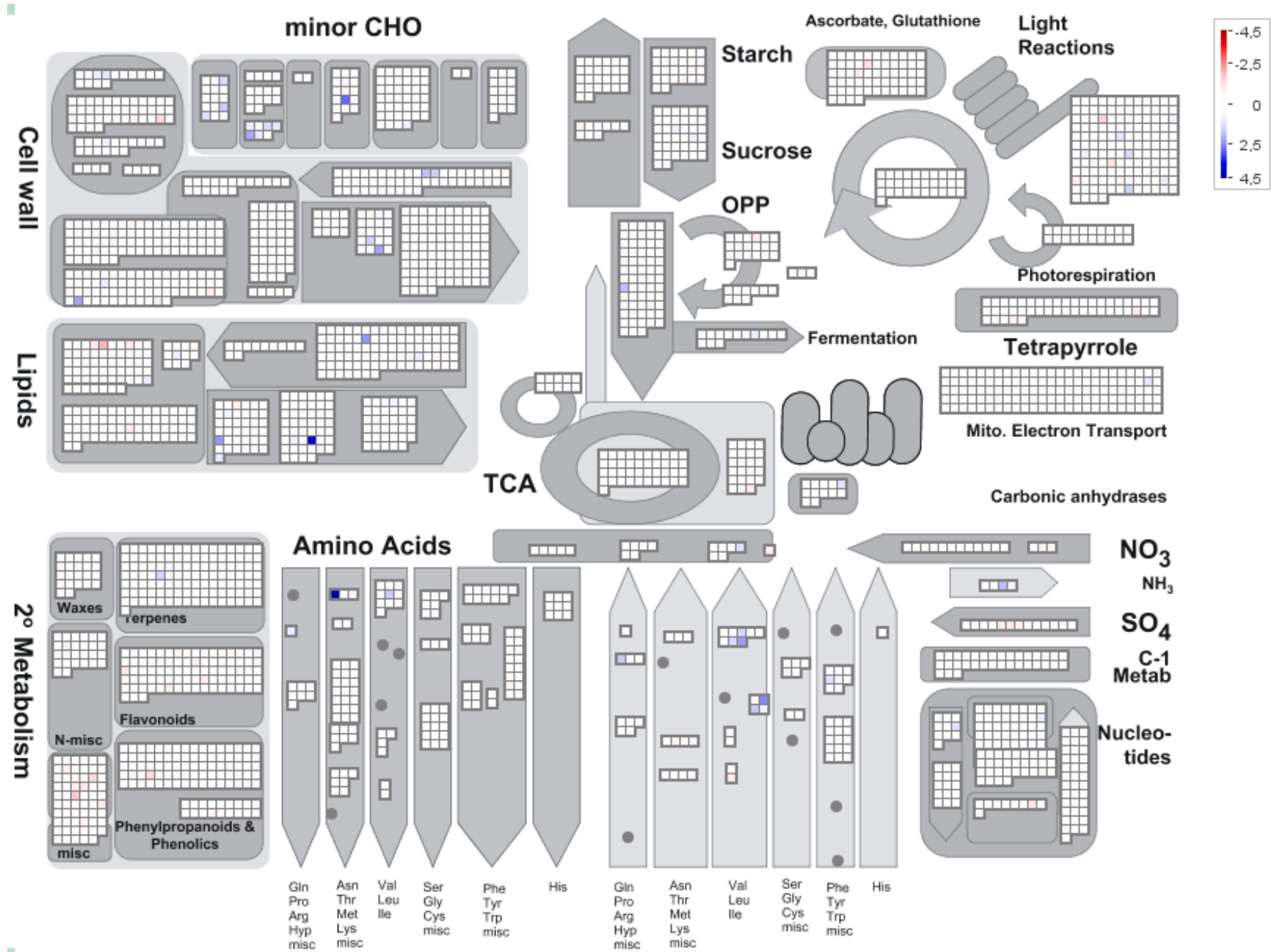
Glycero-
phospholipid
metabolism

Glycolysis/ascorbate
/aldarate
metabolism

Biosynthesis of
Other Secondary Metabolites

Biosynthesis of
Cofactor and Vitamins

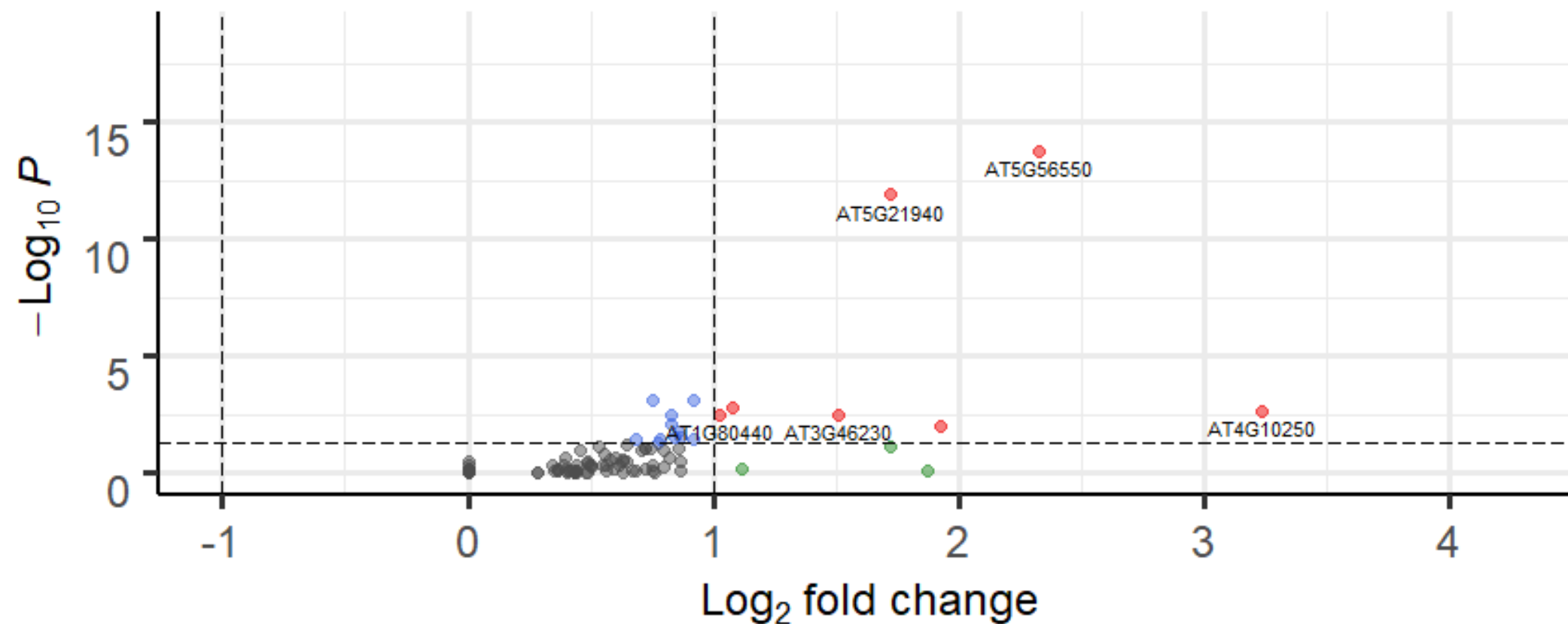




DEGs t=2 1.5nM solA treatment

LFC>1, padj <0.05

● NS ● Log₂ FC ● p-value ● p-value and log₂ FC

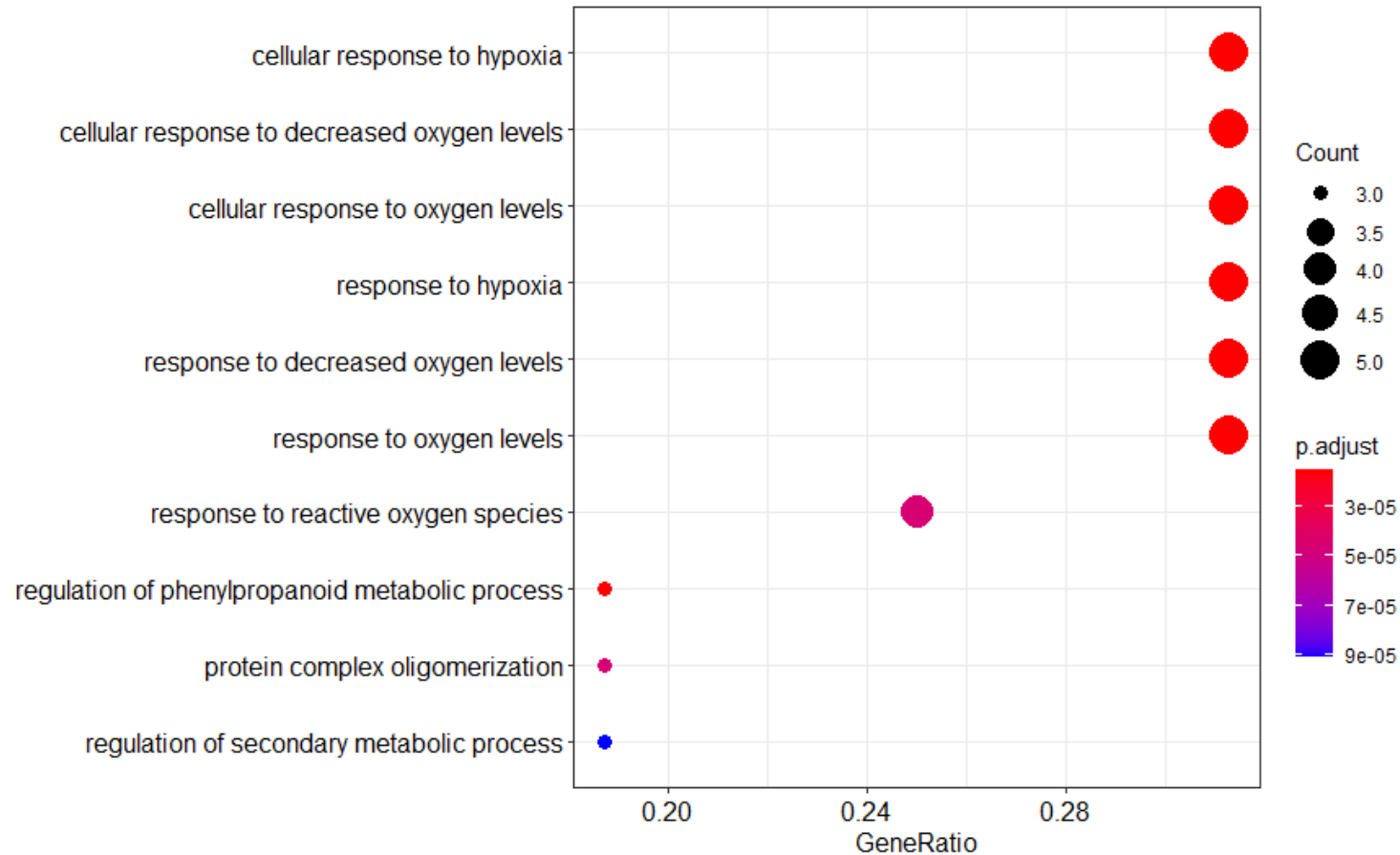


Total = 28775 variables

DEGs nM solA t=2

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AT1G70700	JAZ9	Q8W4J8	TIFY7 [Source:UniProtKB/TrEMBL;Acc:A0A178WMP7]	JAZ9	TAIR Gene Name
AT1G80440		Q9M8L2	F-box/kelch-repeat protein At1g80440 [Source:UniProtKB/Swiss-Prot;Acc:Q9M8L2]		
AT2G20670			Expressed protein [Source:UniProtKB/TrEMBL;Acc:Q9SIU5]		
AT2G25900	ATCTH	O82307	Zinc finger CCCH domain-containing protein 23 [Source:UniProtKB/Swiss-Prot;Acc:O82307]	ATCTH	TAIR Gene Name
AT2G44130		O80582	F-box/kelch-repeat protein At2g44130 [Source:UniProtKB/Swiss-Prot;Acc:O80582]		
AT3G18773		Q9LS99	RING-H2 finger protein ATL77 [Source:UniProtKB/Swiss-Prot;Acc:Q9LS99]	ATL77	UniProtKB Gene Name
AT3G26510			Octicosapeptide/Phox/Bem1p family protein [Source:UniProtKB/TrEMBL;Acc:Q27GK5]		
AT3G46230	ATHSP17.4	P19036	17.4 kDa class I heat shock protein [Source:UniProtKB/Swiss-Prot;Acc:P19036]	HSP17.4A	UniProtKB Gene Name
AT3G50970	LTi30	P42758	Dehydrin Xero 2 [Source:UniProtKB/Swiss-Prot;Acc:P42758]	XERO2	UniProtKB Gene Name
AT3G59940		Q9M1Y1	F-box/kelch-repeat protein SKIP20 [Source:UniProtKB/Swiss-Prot;Acc:Q9M1Y1]	SKIP20	UniProtKB Gene Name
AT4G10250	ATHSP22.0	Q38806	22.0 kDa heat shock protein [Source:UniProtKB/Swiss-Prot;Acc:Q38806]	HSP22.0	UniProtKB Gene Name
AT4G27410	RD26	Q93VY3	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein [Source:Uni	RD26	TAIR Gene Name
AT4G32480			AT4g32480/F8B4_180 [Source:UniProtKB/TrEMBL;Acc:Q9SUU4]		
AT5G12020	HSP17.6II	P29830	17.6 kDa class II heat shock protein [Source:UniProtKB/Swiss-Prot;Acc:P29830]	HSP17.6	UniProtKB Gene Name
AT5G19120			AT5g19120/T24G5_20 [Source:UniProtKB/TrEMBL;Acc:Q93VG3]		
AT5G21940			At5g21940 [Source:UniProtKB/TrEMBL;Acc:Q9C593]		
AT5G52310	COR78	Q06738	Low-temperature-induced 78 kDa protein [Source:UniProtKB/Swiss-Prot;Acc:Q06738]	RD29A	UniProtKB Gene Name
AT5G56550	OXS3		Emb [Source:UniProtKB/TrEMBL;Acc:Q9LVB9]	OXS3	TAIR Gene Name

GO terms biological processes (1.5nM solA treatment)




 P starvation

 Hypoxia

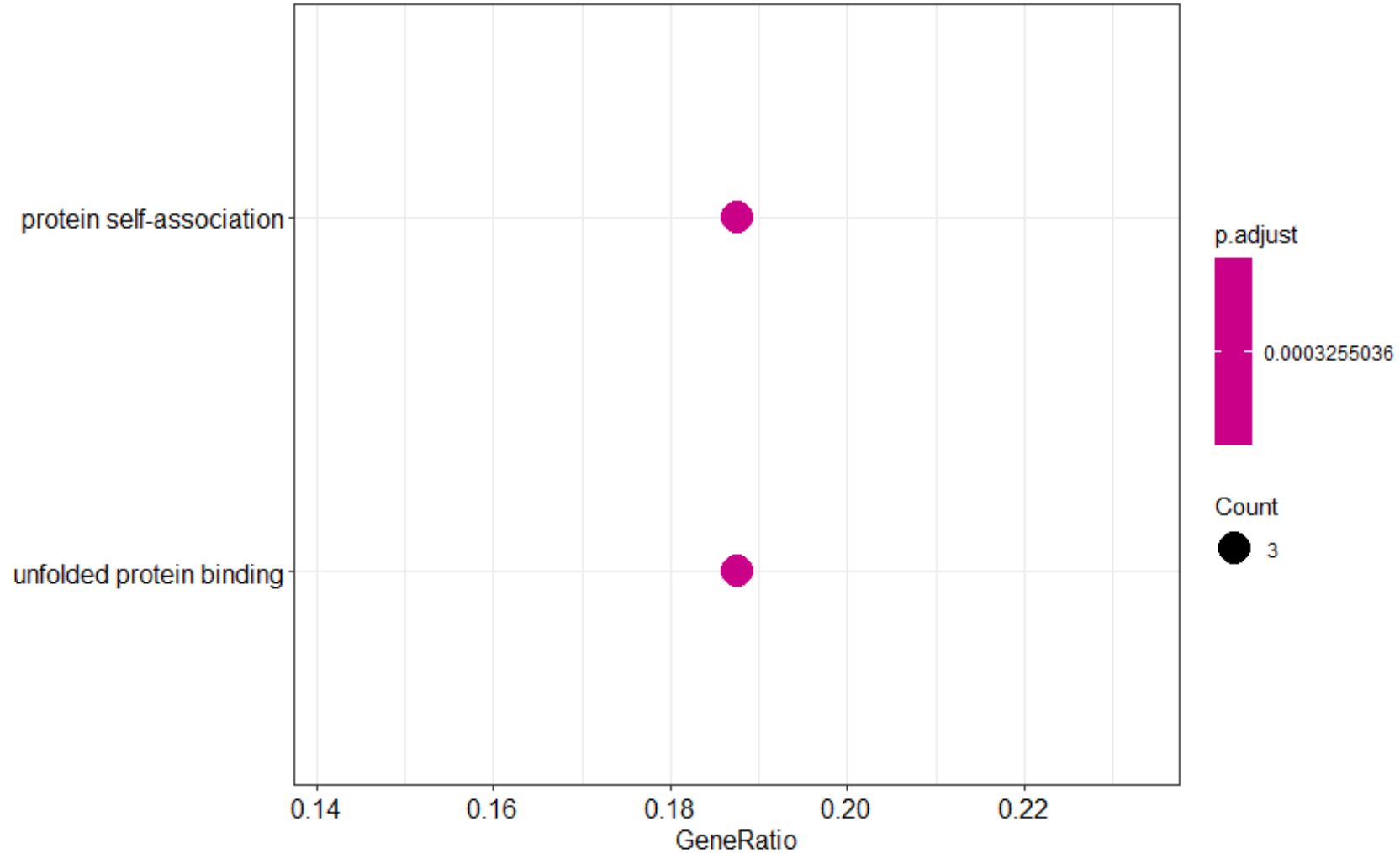
 Lipid metabolism

 Response to fungus

 Other biotic stress
response

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
GO:2000762	regulation of phenylpropanoid metabolic process	3/16	19/21510	3.24826E-07	1.54008E-05	7.76076E-06	KFB20/KFB39/AtKFB50
GO:0071456	cellular response to hypoxia	5/16	238/21510	6.28815E-07	1.54008E-05	7.76076E-06	ATHSP17.4/ATHSP22.0/NA/HSP17.6II/NA
GO:0036294	cellular response to decreased oxygen levels	5/16	240/21510	6.55353E-07	1.54008E-05	7.76076E-06	ATHSP17.4/ATHSP22.0/NA/HSP17.6II/NA
GO:0071453	cellular response to oxygen levels	5/16	240/21510	6.55353E-07	1.54008E-05	7.76076E-06	ATHSP17.4/ATHSP22.0/NA/HSP17.6II/NA
GO:0001666	response to hypoxia	5/16	264/21510	1.04865E-06	1.54446E-05	7.78286E-06	ATHSP17.4/ATHSP22.0/NA/HSP17.6II/NA
GO:0036293	response to decreased oxygen levels	5/16	268/21510	1.12924E-06	1.54446E-05	7.78286E-06	ATHSP17.4/ATHSP22.0/NA/HSP17.6II/NA
GO:0070482	response to oxygen levels	5/16	269/21510	1.15013E-06	1.54446E-05	7.78286E-06	ATHSP17.4/ATHSP22.0/NA/HSP17.6II/NA
GO:0000302	response to reactive oxygen species	4/16	154/21510	4.30065E-06	4.58467E-05	2.3103E-05	ATHSP17.4/ATHSP22.0/HSP17.6II/COR78
GO:0051259	protein complex oligomerization	3/16	44/21510	4.38958E-06	4.58467E-05	2.3103E-05	ATHSP17.4/ATHSP22.0/HSP17.6II
GO:0043455	regulation of secondary metabolic process	3/16	57/21510	9.64088E-06	9.06243E-05	4.56673E-05	KFB20/KFB39/AtKFB50
GO:0006979	response to oxidative stress	5/16	454/21510	1.47677E-05	0.000117626	5.92739E-05	ATHSP17.4/ATHSP22.0/HSP17.6II/COR78/ATOXS3
GO:0042542	response to hydrogen peroxide	3/16	66/21510	1.5016E-05	0.000117626	5.92739E-05	ATHSP17.4/ATHSP22.0/HSP17.6II
GO:0080036	regulation of cytokinin-activated signaling pathway	2/16	16/21510	6.18719E-05	0.000447381	0.000225444	KFB20/AtKFB50
GO:0009698	phenylpropanoid metabolic process	3/16	122/21510	9.44518E-05	0.000634176	0.000319574	KFB20/KFB39/AtKFB50
GO:0006457	protein folding	3/16	176/21510	0.00027883	0.001747334	0.000880516	ATHSP17.4/ATHSP22.0/HSP17.6II
GO:0009651	response to salt stress	4/16	465/21510	0.000319174	0.001875148	0.000944923	ATHSP17.4/ATHSP22.0/HSP17.6II/COR78
GO:0009636	response to toxic substance	3/16	196/21510	0.000382286	0.002113818	0.001065194	ATHSP17.4/ATHSP22.0/HSP17.6II
GO:0009408	response to heat	3/16	234/21510	0.000641007	0.00334748	0.00168686	ATHSP17.4/ATHSP22.0/HSP17.6II
GO:0046677	response to antibiotic	3/16	250/21510	0.000776673	0.003799437	0.00191461	ATHSP17.4/ATHSP22.0/HSP17.6II
GO:0009736	cytokinin-activated signaling pathway	2/16	57/21510	0.000808391	0.003799437	0.00191461	KFB20/AtKFB50
GO:0071368	cellular response to cytokinin stimulus	2/16	62/21510	0.000955737	0.004278063	0.002155799	KFB20/AtKFB50
GO:0009966	regulation of signal transduction	3/16	298/21510	0.001289566	0.005501483	0.002772304	JAZ9/KFB20/AtKFB50
GO:0023051	regulation of signaling	3/16	303/21510	0.001352723	0.005501483	0.002772304	JAZ9/KFB20/AtKFB50
GO:0010646	regulation of cell communication	3/16	307/21510	0.001404634	0.005501483	0.002772304	JAZ9/KFB20/AtKFB50
GO:0019748	secondary metabolic process	3/16	360/21510	0.002214245	0.008325563	0.004195412	KFB20/KFB39/AtKFB50
GO:0009968	negative regulation of signal transduction	2/16	103/21510	0.002608184	0.008611019	0.004339259	KFB20/AtKFB50
GO:0009735	response to cytokinin	2/16	104/21510	0.002658173	0.008611019	0.004339259	KFB20/AtKFB50
GO:0009414	response to water deprivation	3/16	384/21510	0.002659516	0.008611019	0.004339259	LTI30/ANAC072/COR78
GO:0010648	negative regulation of cell communication	2/16	107/21510	0.002810852	0.008611019	0.004339259	KFB20/AtKFB50
GO:0023057	negative regulation of signaling	2/16	107/21510	0.002810852	0.008611019	0.004339259	KFB20/AtKFB50
GO:0009415	response to water	3/16	393/21510	0.002839804	0.008611019	0.004339259	LTI30/ANAC072/COR78
GO:0042493	response to drug	3/16	465/21510	0.004557974	0.013389049	0.006747001	ATHSP17.4/ATHSP22.0/HSP17.6II
GO:0009608	response to symbiont	1/16	12/21510	0.008891918	0.025328494	0.012763519	COR78
GO:0061014	positive regulation of mRNA catabolic process	1/16	13/21510	0.009629556	0.026622889	0.01341579	ATCTH
GO:0009611	response to wounding	2/16	215/21510	0.010881981	0.028414061	0.014318396	JAZ9/COR78
GO:0048585	negative regulation of response to stimulus	2/16	215/21510	0.010881981	0.028414061	0.014318396	KFB20/AtKFB50
GO:0043488	regulation of mRNA stability	1/16	16/21510	0.011839381	0.030078427	0.015157102	ATCTH
GO:0010555	response to mannitol	1/16	17/21510	0.012574962	0.031106484	0.01567516	COR78
GO:0043487	regulation of RNA stability	1/16	20/21510	0.014778625	0.034729768	0.017501003	ATCTH
GO:1903313	positive regulation of mRNA metabolic process	1/16	20/21510	0.014778625	0.034729768	0.017501003	ATCTH
GO:1902074	response to salt	1/16	21/21510	0.015512154	0.03556445	0.017921615	COR78
GO:0061013	regulation of mRNA catabolic process	1/16	22/21510	0.016245171	0.03635824	0.018321621	ATCTH
GO:0009269	response to desiccation	1/16	24/21510	0.017709671	0.038714163	0.019508817	COR78

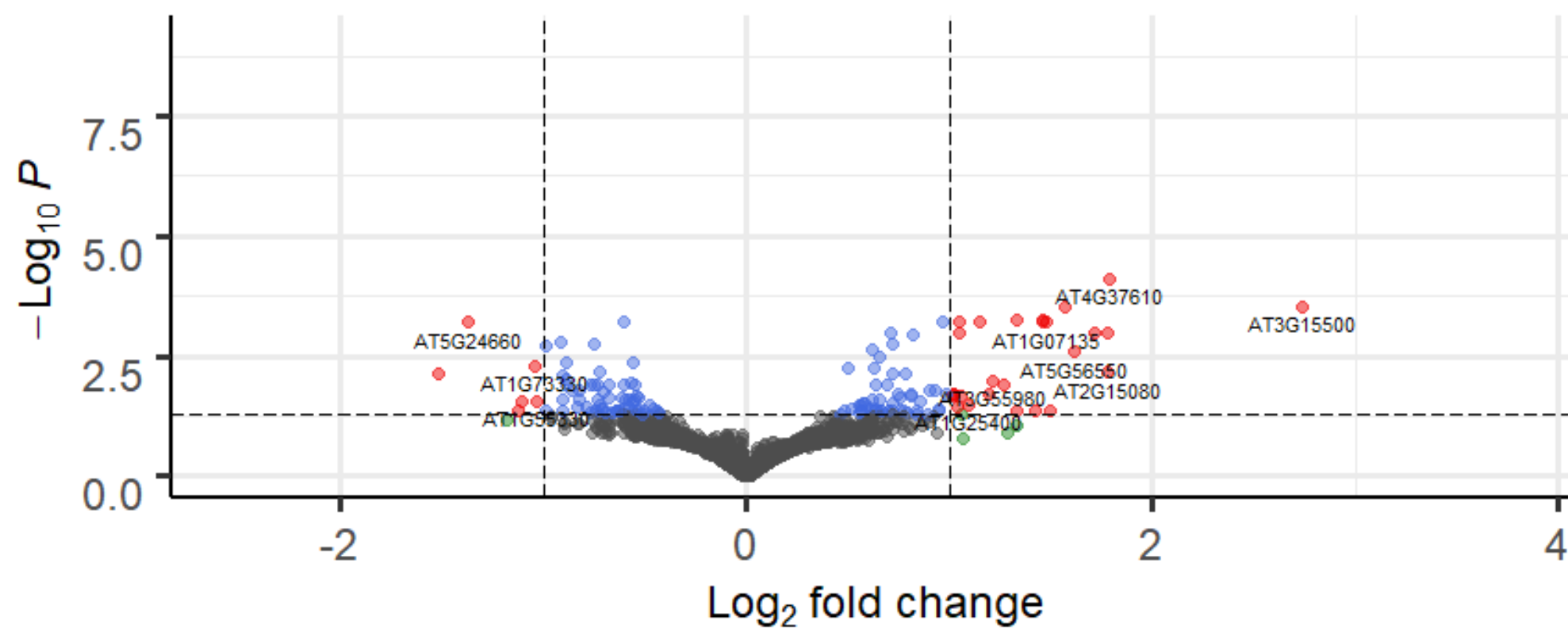
GO terms molecular function (nM solA)



DEGs t=6 1.5nM solA treatment

LFC>1, padj <0.05

● NS ● Log₂ FC ● p-value ● p-value and log₂ FC



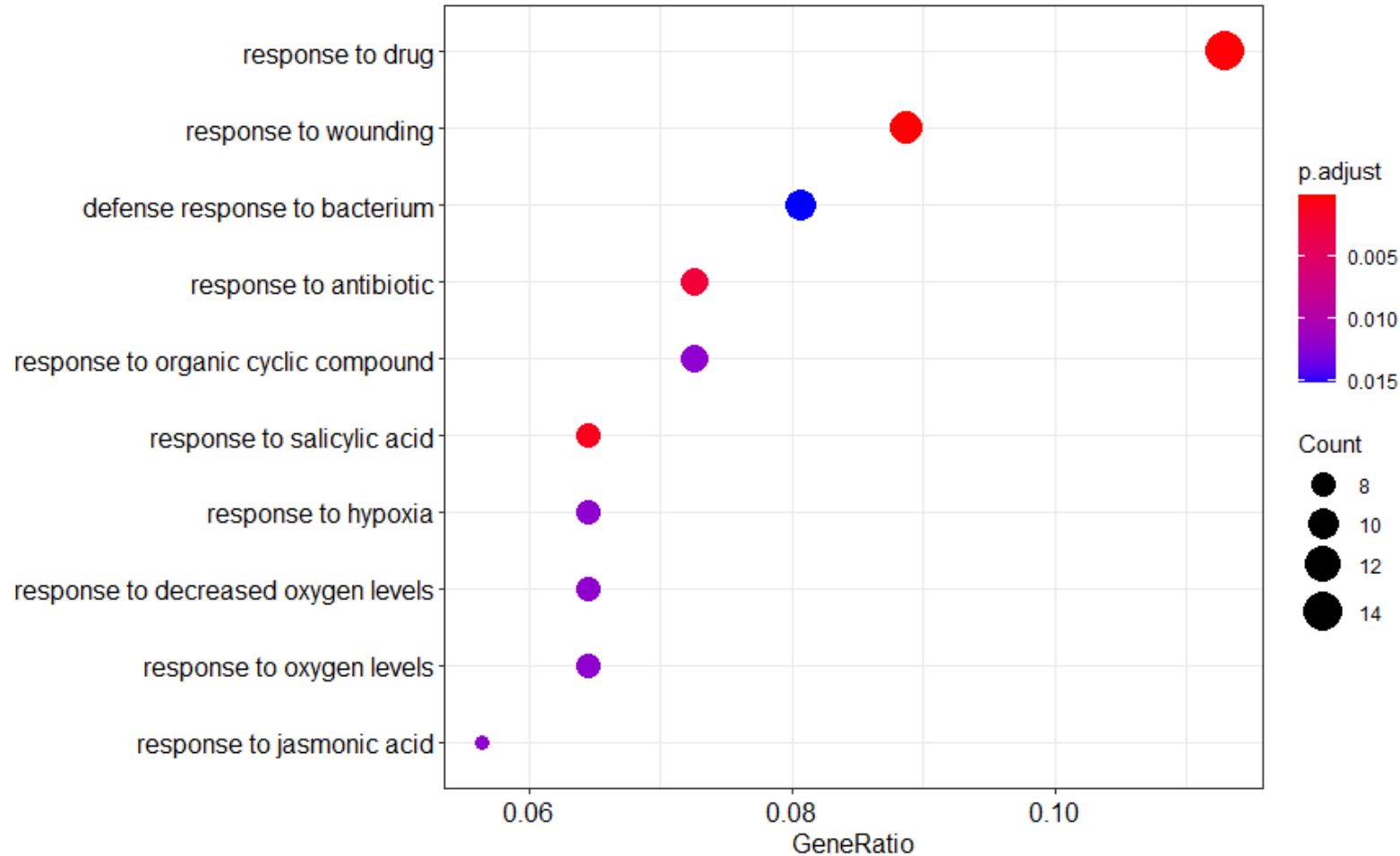
Total = 28775 variables

AT4G24350			Phosphorylase superfamily protein [Source:UniProtKB/TrEMBL;Acc:Q94K59]		1.245413
AT1G25400			At1g25400 [Source:UniProtKB/TrEMBL;Acc:Q9C6L0]		1.301688
AT1G72920			Similar to part of disease resistance protein [Source:UniProtKB/TrEMBL;Acc:Q9SSN4]		1.37793
AT3G55980	SZF1	Q93ZS9	Salt-inducible zinc finger 1 [Source:UniProtKB/TrEMBL;Acc:A0A1I9LNJ4]	SZF1	1.382687
AT2G29300		Q42182	NAD(P)-binding Rossmann-fold superfamily protein [Source:UniProtKB/TrEMBL;Acc:F4IKL5]		1.43942
AT2G38470	WRKY33	Q8S8P5	WRKY33 [Source:UniProtKB/TrEMBL;Acc:A0A384L4W4]	WRKY33	1.440581
AT5G45340	CYP707A3	Q9FH76	Abscisic acid 8'-hydroxylase 3 [Source:UniProtKB/Swiss-Prot;Acc:Q9FH76]	CYP707A3	1.577441
AT1G70700	TIFY7	Q8W4J8	TIFY7 [Source:UniProtKB/TrEMBL;Acc:A0A178WMP7]	JAZ9	1.589908
AT1G70700	JAZ9	Q8W4J8	TIFY7 [Source:UniProtKB/TrEMBL;Acc:A0A178WMP7]	JAZ9	1.589908
AT1G07135			At1g07135 [Source:UniProtKB/TrEMBL;Acc:Q9LMK6]		1.599406
AT2G15042			Leucine-rich repeat (LRR) family protein [Source:TAIR;Acc:AT2G15042]		1.620845
AT3G44260		Q9LXM2	Probable CCR4-associated factor 1 homolog 9 [Source:UniProtKB/Swiss-Prot;Acc:Q9LXM2]	CAF1-9	1.683874
AT1G69490	NAP	O49255	NAP [Source:UniProtKB/TrEMBL;Acc:A0A178W8K0]	NAC029	1.723998
AT5G56550	OXS3		Emb [Source:UniProtKB/TrEMBL;Acc:Q9LVB9]	OXS3	1.793827
AT2G40000	HSPRO2	O04203	Nematode resistance protein-like HSPRO2 [Source:UniProtKB/Swiss-Prot;Acc:O04203]	HSPRO2	1.804376
AT1G80840	WRKY40	Q9SAH7	Probable WRKY transcription factor 40 [Source:UniProtKB/Swiss-Prot;Acc:Q9SAH7]	WRKY40	1.885608
AT4G37610	BT5	Q6EJ98	BTB/POZ and TAZ domain-containing protein 5 [Source:UniProtKB/Swiss-Prot;Acc:Q6EJ98]	BT5	1.904929
AT4G24570	DIC2	Q9SB52	DIC2 [Source:UniProtKB/TrEMBL;Acc:A0A178URN9]	PUMP4	1.949921
AT2G15080	AtRLP19	Q9ZUK3	Receptor-like protein 19 [Source:UniProtKB/Swiss-Prot;Acc:Q9ZUK3]	AtRLP19	2.001687
AT2G15080	AtRLP19	Q9ZUK7	Receptor-like protein 19 [Source:UniProtKB/Swiss-Prot;Acc:Q9ZUK3]	AtRLP19	2.001687
AT3G15500	ATNAC3	Q9LDY8	NAC3 [Source:UniProtKB/TrEMBL;Acc:A0A178VLD3]	NAC055	2.936594

DEGs n=140 (nM solA, t=6). Only top up and down DEGs shown

AT1G73630		Q9C9U8	Probable calcium-binding protein CML26 [Source:UniProtKB/Swiss-Prot;Acc:Q9C9U8]	CML26	-1.728939
AT5G24660	LSU2	Q9FIR9	Protein RESPONSE TO LOW SULFUR 2 [Source:UniProtKB/Swiss-Prot;Acc:Q9FIR9]	LSU2	-1.503484
AT4G02970	AT7SL-1			AT7SL-1	-1.386661
AT2G30540		O04341	Monothiol glutaredoxin-S9 [Source:UniProtKB/Swiss-Prot;Acc:O04341]	GRXS9	-1.319458
AT1G55330	AGP21	Q9C8A4	ATAGP21 [Source:UniProtKB/TrEMBL;Acc:A0A178W6X6]	AGP21	-1.23028
AT4G04925			At4g04925 [Source:UniProtKB/TrEMBL;Acc:Q8LFB8]		-1.205431
AT1G73330	ATDR4		Dr4 protein [Source:UniProtKB/TrEMBL;Acc:Q39091]	ATDR4	-1.17622
AT1G53541			unknown protein; Ha. [Source:TAIR;Acc:AT1G53541]		-1.103702
AT5G21020			At5g21020 [Source:UniProtKB/TrEMBL;Acc:Q3E985]		-1.093016
AT3G47350	ATHSD2	Q9STY8	Hydroxysteroid dehydrogenase 2 [Source:UniProtKB/TrEMBL;Acc:F4JBH8]	ATHSD2	-1.072252
AT5G49480	ATCP1	Q9FDX6	Calcium-binding protein CP1 [Source:UniProtKB/Swiss-Prot;Acc:Q9FDX6]	ATCP1	-1.034493
AT1G07600	MT1A	P43392	Metallothionein-like protein 1A [Source:UniProtKB/Swiss-Prot;Acc:P43392]	MT1A	-1.025865
AT4G38840			At4g38840 [Source:UniProtKB/TrEMBL;Acc:Q9T0J2]		-1.015934
AT1G07590		Q940Q2	Pentatricopeptide repeat-containing protein At1g07590, mitochondrial [Source:UniProtKB/S		-1.015802
AT1G78100		Q9C9S2	AUF1 [Source:UniProtKB/TrEMBL;Acc:A0A178VZX8]		-1.007006
AT3G24000		Q9LIQ7	Pentatricopeptide repeat-containing protein At3g24000, mitochondrial [Source:UniProtKB/S	PCMP-H87	-0.991851
AT1G20430			Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q94B54]		-0.971929
AT1G11630		Q9SAB4	Pentatricopeptide repeat-containing protein At1g11630, mitochondrial [Source:UniProtKB/S		-0.956785
AT5G43790		Q9FG85	Pentatricopeptide repeat-containing protein At5g43790 [Source:UniProtKB/Swiss-Prot;Acc:C	PCMP-E30	-0.943562
AT5G57785			At5g57785 [Source:UniProtKB/TrEMBL;Acc:Q8GY06]		-0.940849

GO terms biological processes(1.5nM solA t=6)



GO terms biological processes(1.5nM solA t=6)

 P starvation

 Hypoxia

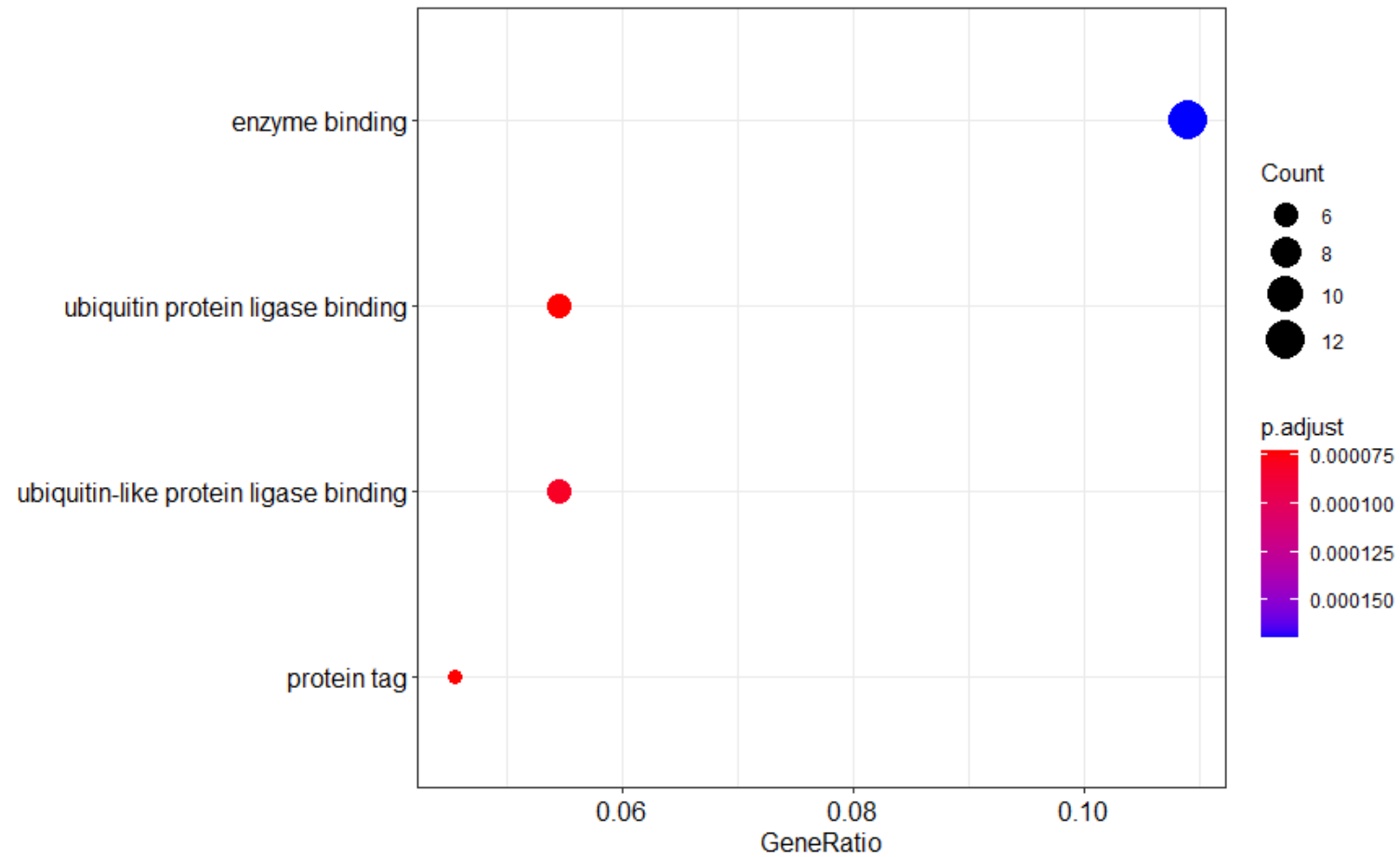
 Lipid metabolism

 Response to fungus

 Other biotic stress response

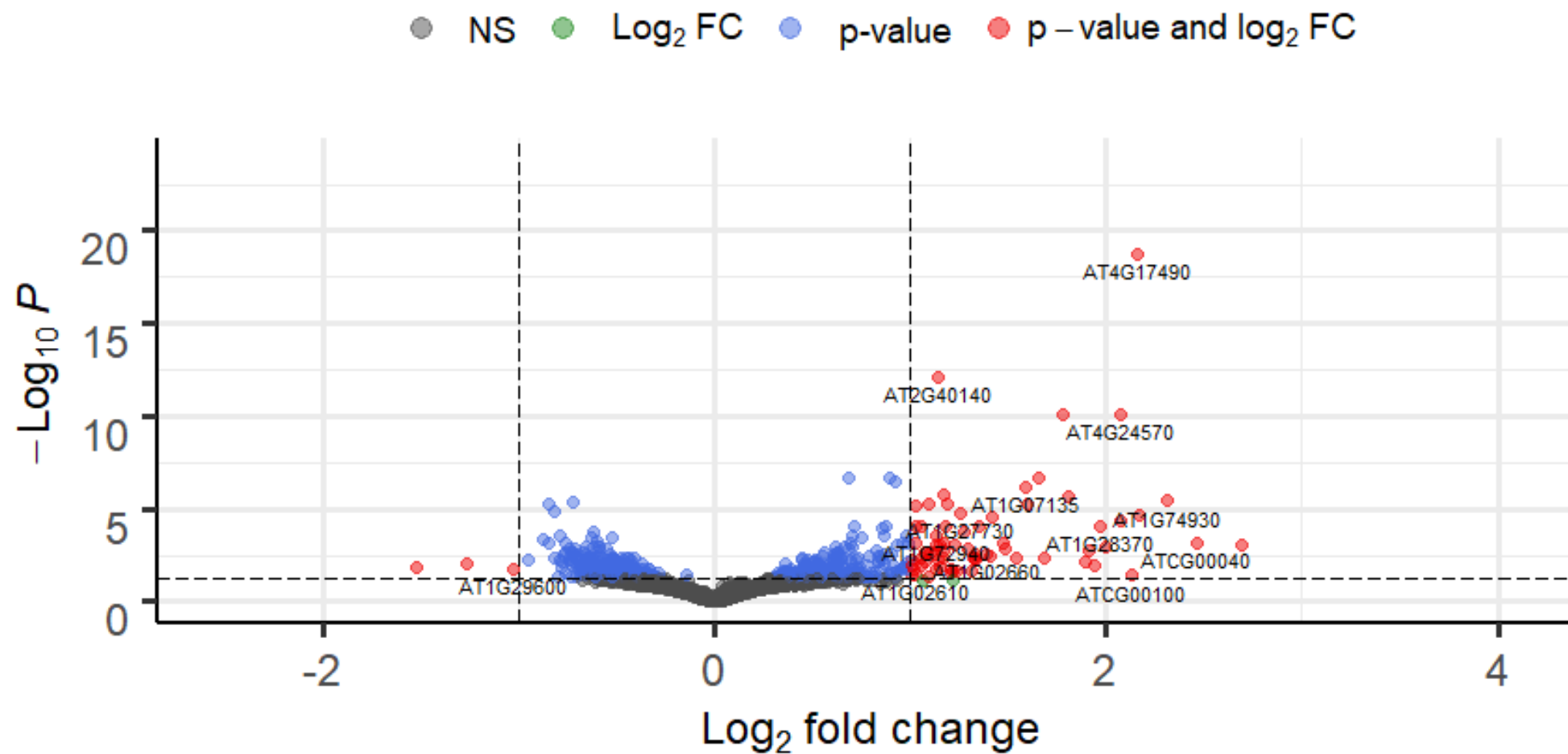
ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
GO:0009611	response to wounding	11/124	215/21510	4.85179E-08	3.09544E-05	2.87022E-05	OPCL1/JAZ9/NA/RGLG4/ATWRKY40/AtCAF1a/NA/ACS6/NA/atnudt8/NA
GO:0042493	response to drug	14/124	465/21510	4.98856E-07	0.000159135	0.000147556	GAI/DHAR2/ATWRKY40/ATWRKY33/ATHSPRO2/GAPC/DRT100/NA/ATSZF1/UBI10/DIC2/ATWF
GO:0009751	response to salicylic acid	8/124	160/21510	4.16988E-06	0.000886795	0.000822272	GAI/DHAR2/ATWRKY40/ATHSPRO2/NA/UBI10/BT5/BT1
GO:0046677	response to antibiotic	9/124	250/21510	1.48834E-05	0.002373909	0.002201183	GAI/DHAR2/ATWRKY40/ATHSPRO2/GAPC/NA/UBI10/BT5/BT1
GO:0014070	response to organic cyclic compound	9/124	325/21510	0.000113849	0.012049245	0.011172538	ATCSLD5/GAI/DHAR2/ATWRKY40/ATHSPRO2/NA/UBI10/BT5/BT1
GO:0001666	response to hypoxia	8/124	264/21510	0.000149517	0.012049245	0.011172538	NA/ACBP/NA/ATHSPRO2/ATSZF1/DIC2/NA/CYP707A3
GO:0009753	response to jasmonic acid	7/124	198/21510	0.000152863	0.012049245	0.011172538	GAI/JAZ9/RGLG4/ANAC055/NA/ACS6/ATWRKY11
GO:0036293	response to decreased oxygen levels	8/124	268/21510	0.000165708	0.012049245	0.011172538	NA/ACBP/NA/ATHSPRO2/ATSZF1/DIC2/NA/CYP707A3
GO:0070482	response to oxygen levels	8/124	269/21510	0.000169974	0.012049245	0.011172538	NA/ACBP/NA/ATHSPRO2/ATSZF1/DIC2/NA/CYP707A3
GO:0042742	defense response to bacterium	10/124	440/21510	0.000237242	0.015136036	0.014034734	VAD1/RGLG4/ATWRKY40/ATWRKY33/ATHSPRO2/AtCAF1a/ATWRKY11/LSU2/ATHS83/ADF4
GO:0009867	jasmonic acid mediated signaling pathway	5/124	104/21510	0.000342366	0.019857256	0.018412436	GAI/JAZ9/RGLG4/ANAC055/ATWRKY11
GO:0071395	cellular response to jasmonic acid stimulus	5/124	108/21510	0.000407462	0.020570632	0.019073907	GAI/JAZ9/RGLG4/ANAC055/ATWRKY11
GO:0071456	cellular response to hypoxia	7/124	238/21510	0.00046713	0.020570632	0.019073907	NA/NA/ATHSPRO2/ATSZF1/DIC2/NA/CYP707A3
GO:0036294	cellular response to decreased oxygen levels	7/124	240/21510	0.000491022	0.020570632	0.019073907	NA/NA/ATHSPRO2/ATSZF1/DIC2/NA/CYP707A3
GO:0071453	cellular response to oxygen levels	7/124	240/21510	0.000491022	0.020570632	0.019073907	NA/NA/ATHSPRO2/ATSZF1/DIC2/NA/CYP707A3
GO:0010243	response to organonitrogen compound	7/124	242/21510	0.000515878	0.020570632	0.019073907	MNS5/ATWRKY40/ATWRKY33/ATSZF1/ATRMA1/ATWRKY11/BT5
GO:0042542	response to hydrogen peroxide	4/124	66/21510	0.000575301	0.021590703	0.020019757	DHAR2/GAPC/BT5/BT1
GO:0010200	response to chitin	5/124	138/21510	0.001235459	0.043790172	0.040603988	ATWRKY40/ATWRKY33/ATSZF1/ATWRKY11/BT5
GO:1901698	response to nitrogen compound	7/124	290/21510	0.001481332	0.049191612	0.045612417	MNS5/ATWRKY40/ATWRKY33/ATSZF1/ATRMA1/ATWRKY11/BT5
GO:0006334	nucleosome assembly	3/124	40/21510	0.001581033	0.049191612	0.045612417	NAP1;4/HTB11/HTB4
GO:0009615	response to virus	4/124	87/21510	0.00161916	0.049191612	0.045612417	ATWRKY40/ATHSP70/NA/ATSGS3

GO terms mol function(1.5nM solA t=6)



DEGs t=24 1.5uM solA treatment

LFC>1, padj <0.05



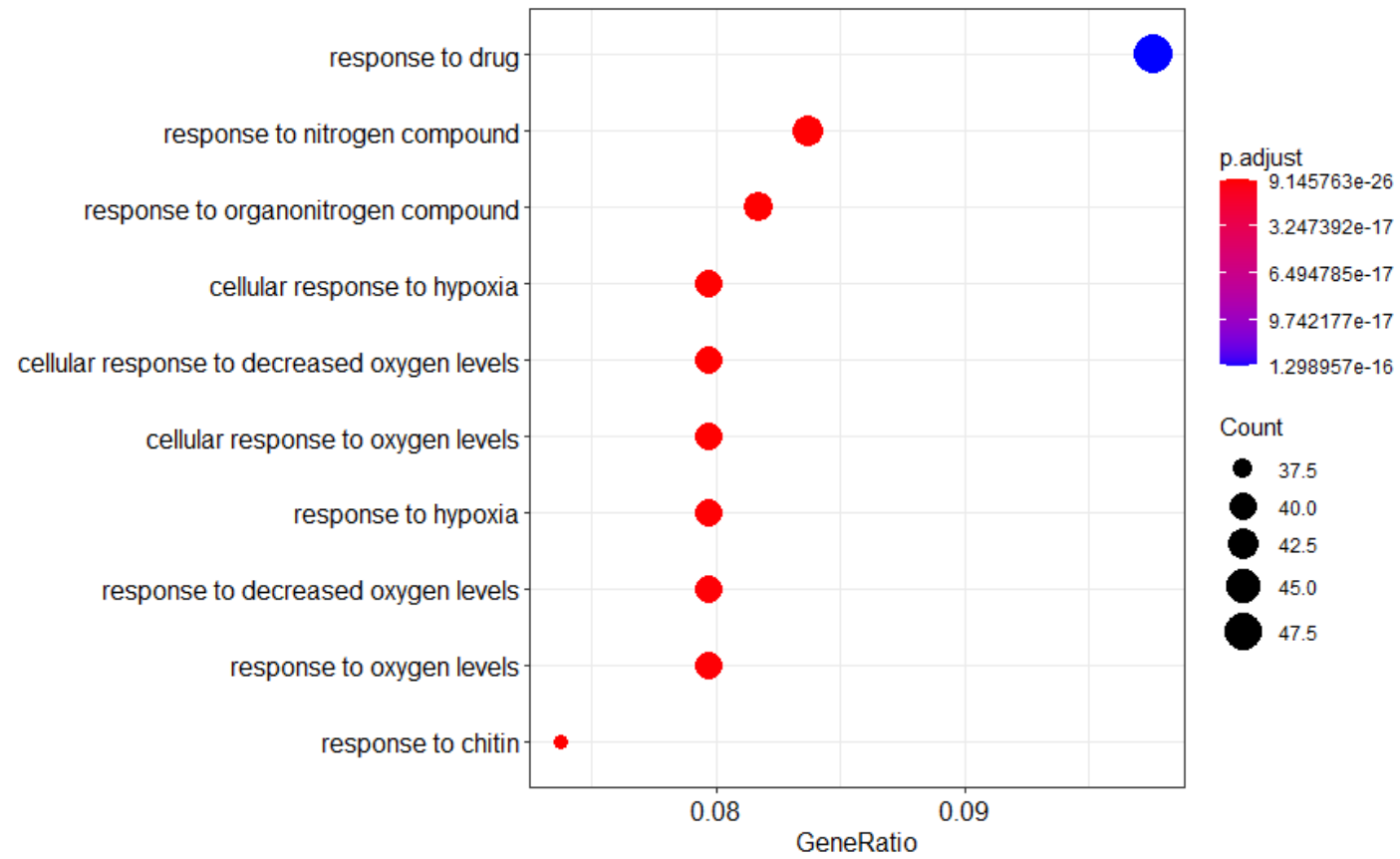
Total = 28775 variables

AT1G07135			At1g07135 [Source:UniProtKB/TrEMBL;Acc:Q9LMK6]		1.664546392
AT1G72910			Similar to part of disease resistance protein [Source:UniProtKB/TrEMBL;Acc:Q9SSN5]		1.676595233
AT5G47230	ERF5	O80341	ERF5 [Source:UniProtKB/TrEMBL;Acc:A0A178UKK9]	ERF5	1.699557764
AT3G14440	NCED3	Q9LRR7	9-cis-epoxycarotenoid dioxygenase NCED3, chloroplastic [Source:UniProtKB/Swiss-Prot;Acc:NCED3]	NCED3	1.699667574
ATCG00540	PETA	P56771	Cytochrome f [Source:UniProtKB/Swiss-Prot;Acc:P56771]	PETA	1.733425364
AT3G55980	SZF1	Q93ZS9	Salt-inducible zinc finger 1 [Source:UniProtKB/TrEMBL;Acc:A0A1I9LNJ4]	SZF1	1.734755148
AT4G29780			Nuclease [Source:UniProtKB/TrEMBL;Acc:Q84J48]		1.839852684
ATCG01110	NDHH	P56753	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic [Source:UniProtKB/Swiss-Prot;Ac	NDHH	1.90594745
AT4G13395	DVL10		DVL10 [Source:UniProtKB/TrEMBL;Acc:Q6IM91]	DVL10	1.91017745
ATCG00180	RPOC1	P56763	DNA-directed RNA polymerase subunit beta' [Source:UniProtKB/Swiss-Prot;Acc:P56763]	RPOC1	2.111847985
AT1G28370	ERF11	Q9C5I3	ERF domain protein 11 [Source:TAIR;Acc:AT1G28370]	ERF11	2.113898096
AT4G24570	DIC2	Q9SB52	DIC2 [Source:UniProtKB/TrEMBL;Acc:A0A178URN9]	PUMP4	2.141213749
ATCG00710	PSBH	P56780	Photosystem II reaction center protein H [Source:UniProtKB/Swiss-Prot;Acc:P56780]	PSBH	2.154453903
ATCG00560	PSBL	P60129	Photosystem II reaction center protein L [Source:UniProtKB/Swiss-Prot;Acc:P60129]	PSBL	2.190085684
AT4G17490	ATERF6	Q8VZ91	Ethylene-responsive transcription factor 6 [Source:UniProtKB/Swiss-Prot;Acc:Q8VZ91]	ERF6	2.204142362
ATCG00580	PSBE	P56779	Cytochrome b559 subunit alpha [Source:UniProtKB/TrEMBL;Acc:A0A1B1W4W2]	PSBE	2.21257386
ATCG00520	YCF4	P56788	Photosystem I assembly protein Ycf4 [Source:UniProtKB/Swiss-Prot;Acc:P56788]	YCF4	2.271502994
ATCG00570	PSBF	P62095	Cytochrome b559 subunit beta [Source:UniProtKB/TrEMBL;Acc:A0A1B1W4V6]	PSBF	2.309710483
AT1G74930	ORA47	Q9S7L5	Ethylene-responsive transcription factor ERF018 [Source:UniProtKB/Swiss-Prot;Acc:Q9S7L5]	ERF018	2.451437717
ATCG00040	MATK	P56784	maturase K [Source:TAIR;Acc:ATCG00040]	MATK	2.693451635
ATCG00500	ACCD	P56765	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic [Source:Uni	ACCD	2.948774657






DEG’s t=24 uM
solA. N=792.
Only top up and
down shown

ensembl_	tair_syn	uniprot	description	external	log2FoldCl
AT4G15200	AFH3	O23373	formin 3 [Source:TAIR;Acc:AT4G15200]	AFH3	-1.87309098
AT5G49340	TBL4	Q9FJ06	Protein trichome birefringence-like 4 [Source:UniProtKB/Swiss-Prot;Acc:Q9FJ06]	TBL4	-1.54480367
AT3G30720	QQS	Q3E7K4	Protein QQS [Source:UniProtKB/Swiss-Prot;Acc:Q3E7K4]	QQS	-1.45465771
AT1G29600		Q9C7P1	Zinc finger C-x8-C-x5-C-x3-H type family protein [Source:TAIR;Acc:AT1G29600]		-1.24948181
AT2G12170			BEST Arabidopsis thaliana protein match is: Transcriptional factor B3 family protein (TAIR:AT		-1.11614955
AT3G09450			F3L24.34 protein [Source:UniProtKB/TrEMBL;Acc:Q9S710]		-1.0935199
AT4G25434	ATNUDT10	Q6NPD7	nudix hydrolase homolog 10 [Source:TAIR;Acc:AT4G25434]	ATNUDT10	-0.98525547
AT5G03830			CDK inhibitor P21 binding protein [Source:UniProtKB/TrEMBL;Acc:F4KI15]		-0.95737776
AT4G01915			unknown protein; Ha. [Source:TAIR;Acc:AT4G01915]		-0.93523029
AT3G17225			Plant invertase/pectin methylesterase inhibitor superfamily protein [Source:UniProtKB/TrE		-0.92587169
AT4G21400	CRK28	O65405	Cysteine-rich receptor-like protein kinase 28 [Source:UniProtKB/Swiss-Prot;Acc:O65405]	CRK28	-0.91240228
AT1G13150	CYP86C4		Cytochrome P450, family 86, subfamily C, polypeptide 4 [Source:UniProtKB/TrEMBL;Acc:Q9S	CYP86C4	-0.91229153
AT3G62750	BGLU8	Q67XN2	Beta glucosidase 8 [Source:UniProtKB/TrEMBL;Acc:A0A1I9LTV6]	BGLU8	-0.90258011
AT1G80980			At1g80980 [Source:UniProtKB/TrEMBL;Acc:Q9SAG2]		-0.8801196
AT4G00040		O81305	Type III polyketide synthase C [Source:UniProtKB/Swiss-Prot;Acc:O81305]		-0.87937844
AT1G29560			Zinc finger C-x8-C-x5-C-x3-H type family protein [Source:UniProtKB/TrEMBL;Acc:B3H4U9]		-0.87858756
AT3G44960			Shugoshin [Source:UniProtKB/TrEMBL;Acc:A0A1I9LT08]		-0.86724774
AT3G47675			Ternary complex factor MIP1 leucine-zipper protein [Source:UniProtKB/TrEMBL;Acc:Q8L5Z2]		-0.86293723
AT1G02010	SEC1A	Q9C5P7	secretory 1A [Source:TAIR;Acc:AT1G02010]	SEC1A	-0.86001208
AT4G27370	VIIIB	F4JIU4	P-loop containing nucleoside triphosphate hydrolases superfamily protein [Source:TAIR;Acc	VIIIB	-0.85735348

Biol. Processes (1.5uM solA t=24)

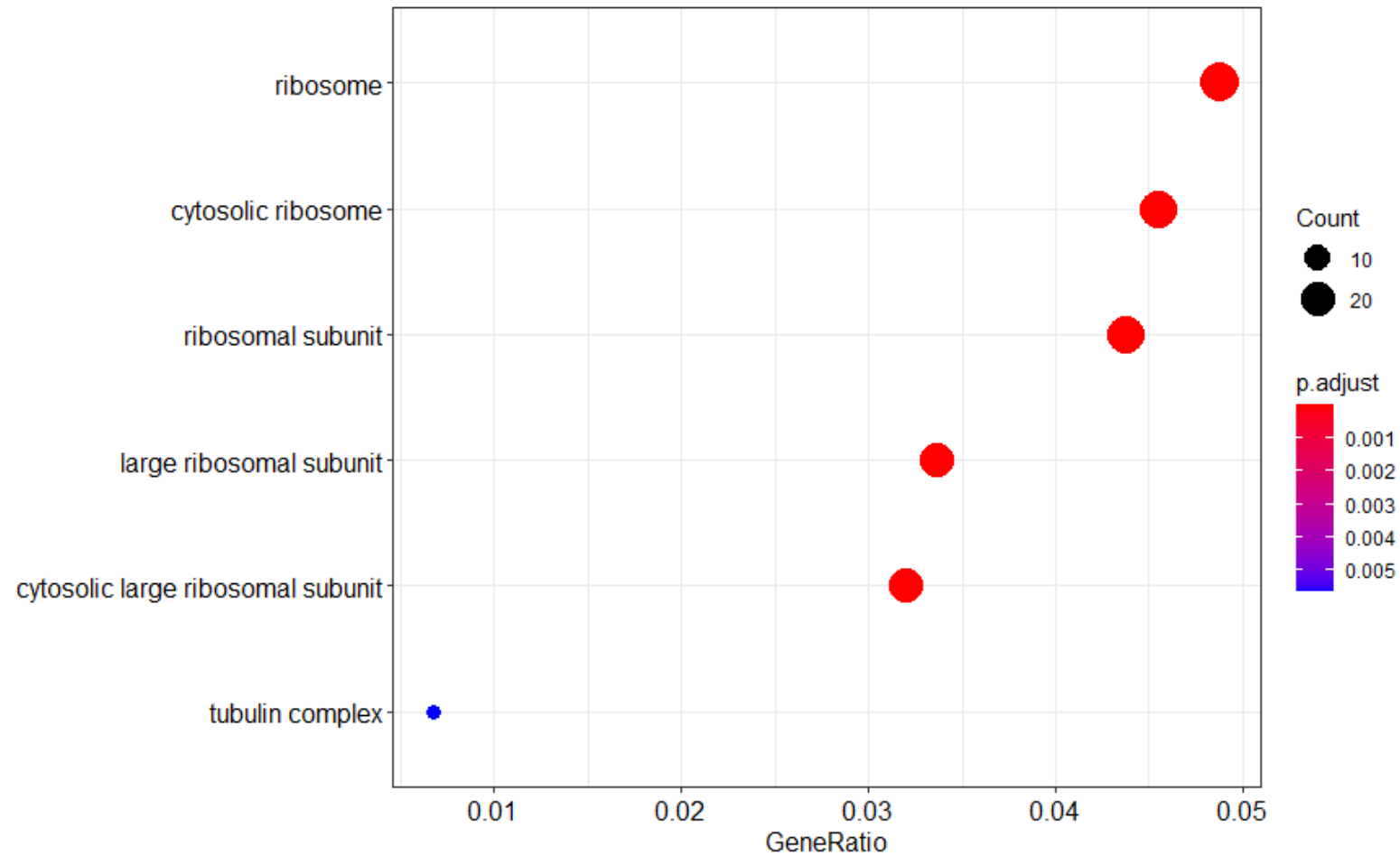


Biol. Processes (1.5uM solA t=24)

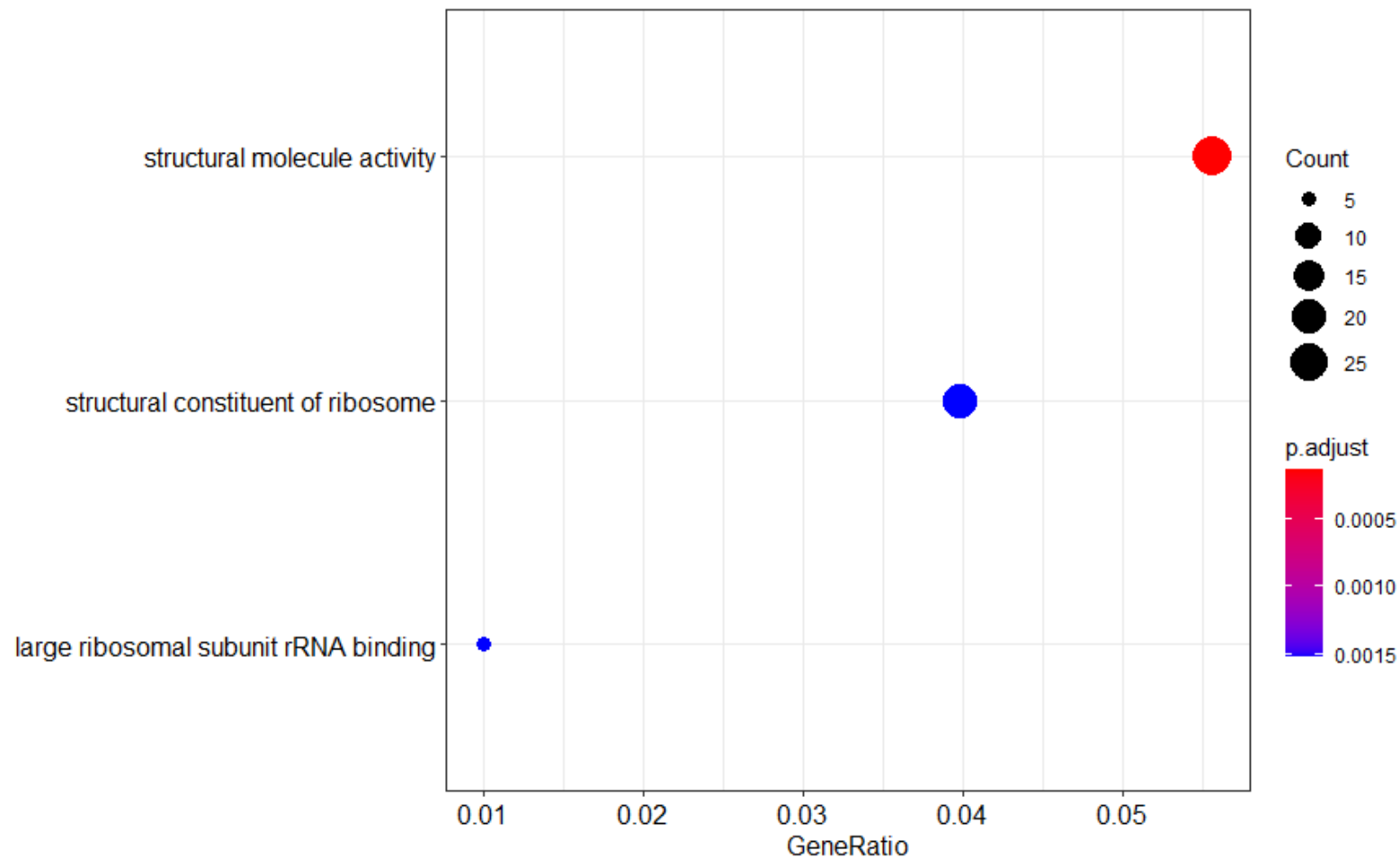
-  P starvation
-  Hypoxia
-  Lipid metabolism
-  Response to fungus
-  Other biotic stress response

ID	Description	Gene	BgRatio	pvalue	p.adjust	qvalue	geneID
GO:0010200	response to chitin	37/502	138/21510	6.78973E-29	9.14576E-26	8.29776E-26	STZ/ATMYC2/ATBZIP60/ADOF1/ATCMPG1/ATWRKY40/AtLYK5/ATL
GO:0010243	response to organonitrogen compound	41/502	242/21510	1.49013E-23	1.0036E-20	9.10546E-21	ATGLR3.4/MNSS5/STZ/ATMYC2/ATBZIP60/ADOF1/AtFBS1/AtHrd1B/
GO:0071456	cellular response to hypoxia	40/502	238/21510	7.19327E-23	2.67612E-20	2.42798E-20	NA/NA/STZ/ATGA2OX2/UKL3/AtFBS1/NA/NA/NA/NA/ATMKK9/N
GO:0036294	cellular response to decreased oxygen levels	40/502	240/21510	9.93362E-23	2.67612E-20	2.42798E-20	NA/NA/STZ/ATGA2OX2/UKL3/AtFBS1/NA/NA/NA/NA/ATMKK9/N
GO:0071453	cellular response to oxygen levels	40/502	240/21510	9.93362E-23	2.67612E-20	2.42798E-20	NA/NA/STZ/ATGA2OX2/UKL3/AtFBS1/NA/NA/NA/NA/ATMKK9/N
GO:1901698	response to nitrogen compound	42/502	290/21510	2.18576E-21	4.90703E-19	4.45205E-19	ATGLR3.4/MNSS5/STZ/ATMYC2/ATBZIP60/ADOF1/AtFBS1/AtHrd1B/
GO:0001666	response to hypoxia	40/502	264/21510	3.74764E-21	7.21153E-19	6.54287E-19	NA/NA/STZ/ATGA2OX2/UKL3/AtFBS1/NA/NA/NA/NA/ATMKK9/N
GO:0036293	response to decreased oxygen levels	40/502	268/21510	6.59418E-21	1.11029E-18	1.00735E-18	NA/NA/STZ/ATGA2OX2/UKL3/AtFBS1/NA/NA/NA/NA/ATMKK9/N
GO:0070482	response to oxygen levels	40/502	269/21510	7.58223E-21	1.13481E-18	1.02959E-18	NA/NA/STZ/ATGA2OX2/UKL3/AtFBS1/NA/NA/NA/NA/ATMKK9/N
GO:0042493	response to drug	49/502	465/21510	9.64333E-19	1.29896E-16	1.17852E-16	STZ/ATMYC2/ATBZIP60/ADOF1/AtFBS1/ATCMPG1/ATLOX4/ATWR
GO:0009611	response to wounding	23/502	215/21510	1.41587E-09	1.7338E-07	1.57304E-07	ATGLR3.4/WAKL7/AtJAZ1/STZ/ATMYC2/NA/AtFBS1/ATLOX4/NA/A
GO:0042742	defense response to bacterium	30/502	440/21510	1.84731E-07	2.07361E-05	1.88134E-05	VAD1/AtJAZ1/ATLFNR2/ATWRKY40/TET8/NHL13/ATWRKY33/ATHS
GO:0009651	response to salt stress	27/502	465/21510	1.50658E-05	0.001561049	0.001416307	ATCSLD5/STZ/NSL1/OTS1/AtFBS1/ATMKK9/AtSOT1/ATWRKY33/AT
GO:0002376	immune system process	25/502	415/21510	1.68456E-05	0.001620783	0.001470503	ATLFNR2/NSL1/ATMEK4/HUB2/ATSOT16/ATWRKY40/AtLYK5/AtPU
GO:0080134	regulation of response to stress	22/502	366/21510	5.53446E-05	0.004969944	0.004509128	PLIP2/AtJAZ1/ATMYC2/ATWRKY40/EVR/IDL7/ATERF-4/JAI3/ANAC
GO:0031347	regulation of defense response	17/502	247/21510	7.55864E-05	0.006363434	0.005773412	PLIP2/AtJAZ1/ATMYC2/ATWRKY40/EVR/ATERF-4/JAI3/ATSYP122/A
GO:0006955	immune response	22/502	377/21510	8.54458E-05	0.006770321	0.006142572	ATLFNR2/NSL1/ATMEK4/HUB2/ATSOT16/AtLYK5/ATWRKY33/ATHS
GO:0045087	innate immune response	21/502	364/21510	0.000144166	0.010788397	0.00978809	ATLFNR2/NSL1/ATMEK4/HUB2/ATSOT16/AtLYK5/ATWRKY33/ATHS
GO:0000027	ribosomal large subunit assembly	6/502	39/21510	0.000265999	0.018857909	0.017109391	ARP1/NA/NA/NA/MRPL11/RPL12C
GO:0009414	response to water deprivation	21/502	384/21510	0.00029793	0.020065586	0.018205092	ATCSLD5/STZ/ATMYC2/AtPUB23/ATWRKY33/ATCAMP25/ATNCED
GO:0042273	ribosomal large subunit biogenesis	9/502	94/21510	0.00035099	0.022513512	0.020426045	ARP1/NA/NA/NA/NA/NA/MRPL11/RPL12C/NA
GO:0009415	response to water	21/502	393/21510	0.000404903	0.024791122	0.022492472	ATCSLD5/STZ/ATMYC2/AtPUB23/ATWRKY33/ATCAMP25/ATNCED
GO:0034728	nucleosome organization	7/502	59/21510	0.000432178	0.025133057	0.022802703	NA/HTB11/ATINO80/H2B/ATSWC6/HTB4/NA
GO:0006979	response to oxidative stress	23/502	454/21510	0.00046268	0.025133057	0.022802703	STZ/ATMYC2/ATLOX4/ATNTRA/AtOZF1/ATHSPRO2/IDL7/GATL10/A
GO:0042255	ribosome assembly	8/502	78/21510	0.000466464	0.025133057	0.022802703	ARP1/NA/NA/NA/NA/NA/MRPL11/RPL12C
GO:0051865	protein autoubiquitination	4/502	17/21510	0.000547853	0.02838301	0.025751319	AtPUB23/AtRDUF1/AtPUB22/AtRDUF2
GO:0032350	regulation of hormone metabolic process	7/502	62/21510	0.000586738	0.029271684	0.026557594	SPL10/NSL1/ATCAMP25/APD1/ATH1/CBP60G/SPL2
GO:0009753	response to jasmonic acid	13/502	198/21510	0.000803159	0.038637674	0.035055163	AtJAZ1/ATMYC2/AtFBS1/ATSOT16/ATERF-4/JAI3/ATBT2/ATSYP122
GO:0010337	regulation of salicylic acid metabolic process	4/502	19/21510	0.000859804	0.039936425	0.036233493	NSL1/ATCAMP25/APD1/CBP60G
GO:0009620	response to fungus	18/502	335/21510	0.000963753	0.043272496	0.039260241	ATLFNR2/ATMKK9/ATWRKY40/CBP1/AP2C1/ATL2G/ATWRKY33/AT
GO:0009612	response to mechanical stimulus	4/502	20/21510	0.001055076	0.044412095	0.040294176	ATGLR3.4/ATCAL4/ACS6/AtCML24
GO:0044247	cellular polysaccharide catabolic process	4/502	20/21510	0.001055076	0.044412095	0.040294176	ATPHS2/ATPTPKIS1/ATISA3/ATLDA
GO:0071824	protein-DNA complex subunit organization	9/502	110/21510	0.001104651	0.045089834	0.040909075	NA/NA/HTB11/ATINO80/PTF2/H2B/ATSWC6/HTB4/NA

Cellular comp. (1.5uM solA t=24)

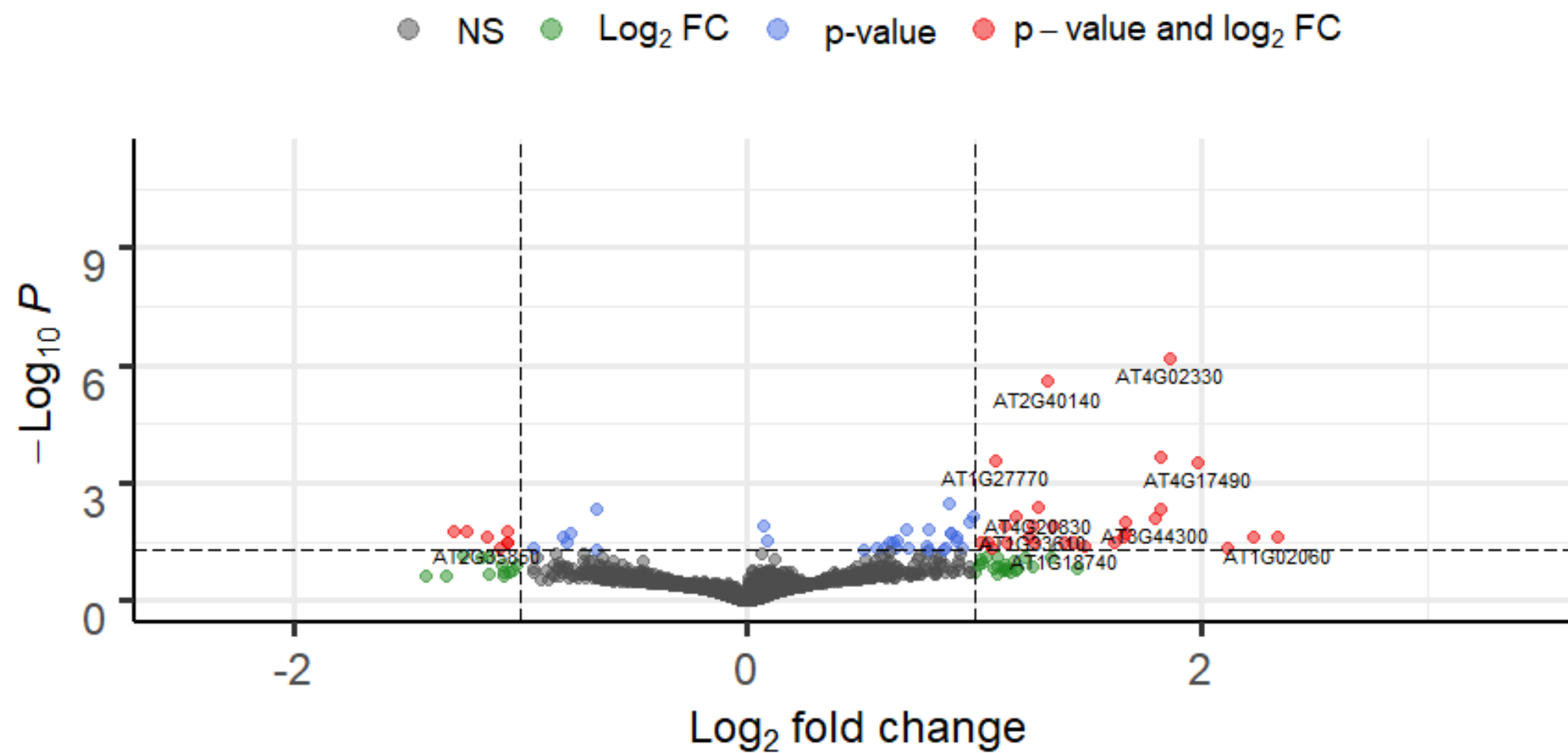


Mol. function(1.5uM solA t=24)



DEGs t=24 1.5nM solA treatment

LFC>1, padj <0.05



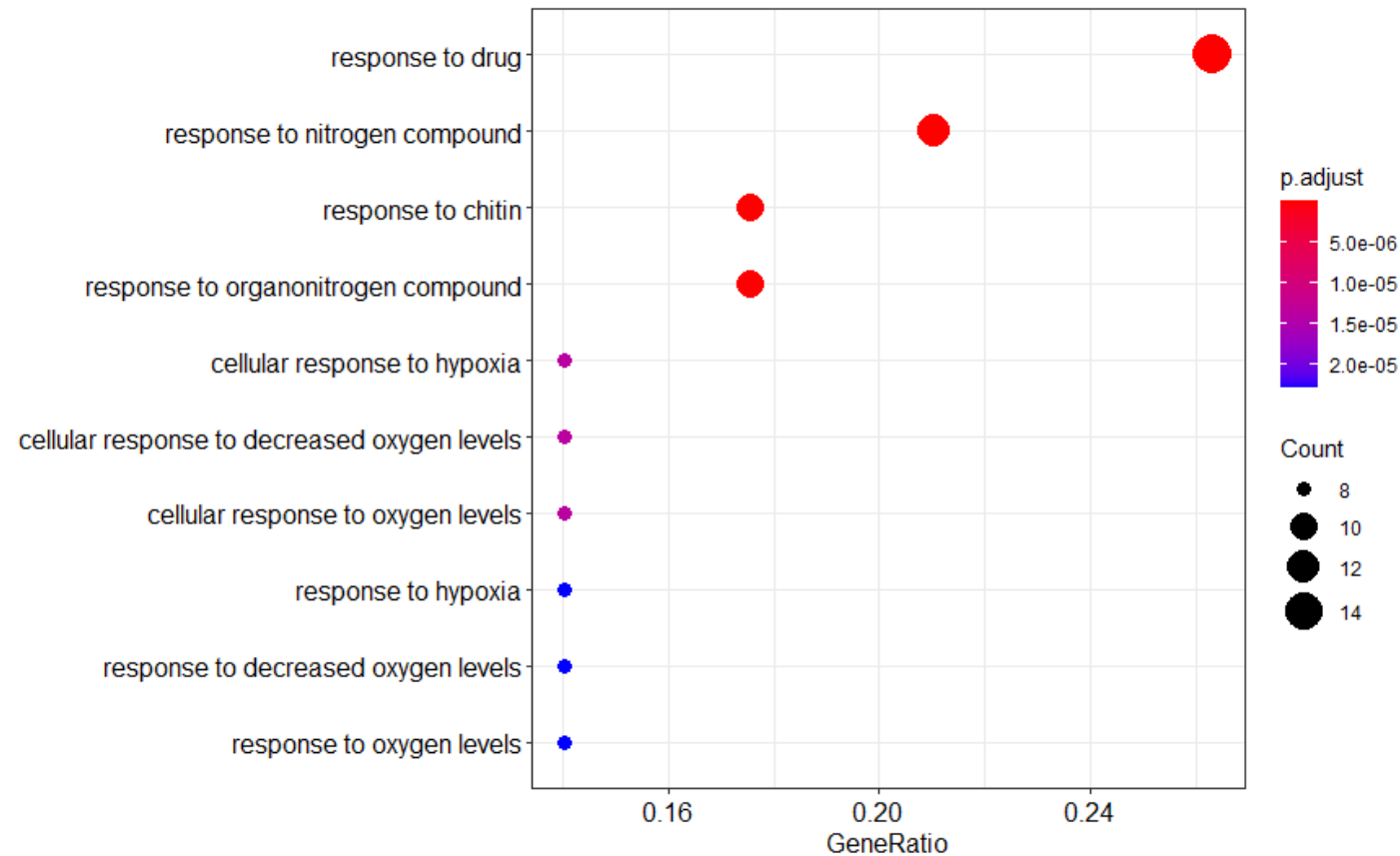
Total = 28775 variables






AT2G23810	TET8	Q8S8Q6	TET8 [Source:UniProtKB/TrEMBL;Acc:A0A178VYI5]	TET8	1.441421287
AT5G06320	NHL3	Q9FNH6	NHL3 [Source:UniProtKB/TrEMBL;Acc:A0A178UB58]	NHL3	1.502033714
AT2G22500	UCP5	Q9SJY5	Mitochondrial uncoupling protein 5 [Source:UniProtKB/Swiss-Prot;Acc:Q9SJY5]	PUMP5	1.528301907
AT1G18740			At1g18740/F6A14_15 [Source:UniProtKB/TrEMBL;Acc:Q9M9U5]		1.641884203
AT4G36430		O23237	Peroxidase 49 [Source:UniProtKB/Swiss-Prot;Acc:O23237]	PER49	1.685298763
AT5G45400	RPA70C	Q9FHJ6	Replication protein A 70 kDa DNA-binding subunit C [Source:UniProtKB/Swiss-Prot;Acc:Q9FHJ6]	RPA1C	1.767239243
AT3G55980	SZF1	Q93ZS9	Salt-inducible zinc finger 1 [Source:UniProtKB/TrEMBL;Acc:A0A1I9LNJ4]	SZF1	1.884617906
AT2G33580		O22808	Protein LYK5 [Source:UniProtKB/Swiss-Prot;Acc:O22808]	LYK5	1.913648592
AT4G23690		Q9SUQ8	Dirigent protein 6 [Source:UniProtKB/Swiss-Prot;Acc:Q9SUQ8]	DIR6	1.922790845
AT1G72520	LOX4	Q9FNX8	Lipoxygenase 4, chloroplastic [Source:UniProtKB/Swiss-Prot;Acc:Q9FNX8]	LOX4	1.931485146
AT4G29780			Nuclease [Source:UniProtKB/TrEMBL;Acc:Q84J48]		1.95609139
AT4G02330	ATPMEPCR	Q8RXX7	Probable pectinesterase/pectinesterase inhibitor 41 [Source:UniProtKB/Swiss-Prot;Acc:Q8RXX7]	PME41	1.956515596
AT4G24570	DIC2	Q9SB52	DIC2 [Source:UniProtKB/TrEMBL;Acc:A0A178URN9]	PUMP4	2.015290423
AT3G44300	NIT2	P32962	NIT2 [Source:UniProtKB/TrEMBL;Acc:A0A384LD03]	NIT2	2.017583715
AT4G17490	ATERF6	Q8VZ91	Ethylene-responsive transcription factor 6 [Source:UniProtKB/Swiss-Prot;Acc:Q8VZ91]	ERF6	2.144845007
AT3G56400	WRKY70	Q9LY00	Probable WRKY transcription factor 70 [Source:UniProtKB/Swiss-Prot;Acc:Q9LY00]	WRKY70	2.461179921
AT3G48360	BT2	Q94BN0	BTB/POZ and TAZ domain-containing protein 2 [Source:UniProtKB/Swiss-Prot;Acc:Q94BN0]	BT2	2.563155694
AT1G28370	ERF11	Q9C5I3	ERF domain protein 11 [Source:TAIR;Acc:AT1G28370]	ERF11	2.581466378
AT1G02060		O81908	Pentatricopeptide repeat-containing protein At1g02060, chloroplastic [Source:UniProtKB/Swiss-Prot;Acc:O81908]		2.711584845
AT1G17744			Uncharacterized protein At1g17740 [Source:UniProtKB/TrEMBL;Acc:Q94AG7]		3.581026001

DEGs t=24 nM
solA. N= 62

ensembl_	tair_syn	unipro	description	external	log2FoldCh
AT5G53050			Alpha/beta-Hydrolases superfamily protein [Source:UniProtKB/TrEMBL;Acc:Q9LVU7]		-1.389355931
AT2G35850			Transmembrane protein [Source:UniProtKB/TrEMBL;Acc:Q9SJ65]		-1.318830719
AT5G38140	NF-YC12	Q58CM8	Nuclear transcription factor Y subunit C-10 [Source:UniProtKB/Swiss-Prot;Acc:Q58CM8]	NFYC10	-1.280131545
AT4G01595			Protein kinase superfamily protein [Source:UniProtKB/TrEMBL;Acc:F4JG28]		-1.227396705
AT3G05930	GLP8	P93000	GLP8 [Source:UniProtKB/TrEMBL;Acc:A0A384KAA2]	GLP8	-1.188137947
AT1G27370	SPL10	Q8S9L0	Squamosa promoter-binding-like protein 10 [Source:UniProtKB/Swiss-Prot;Acc:Q8S9L0]	SPL10	-0.928648384
AT4G36980			FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXpressed in: root		-0.917672138
AT5G53420			CCT motif family protein [Source:UniProtKB/TrEMBL;Acc:Q8L602]		-0.885359587
AT1G73170			P-loop containing nucleoside triphosphate hydrolases superfamily protein [Source:TAIR;Acc:AT1G73170]		-0.726604106

Biol. Process (1.5nM solA, t=24)



-  P starvation
-  Hypoxia
-  Lipid metabolism
-  Response to fungus
-  Other biotic stress response

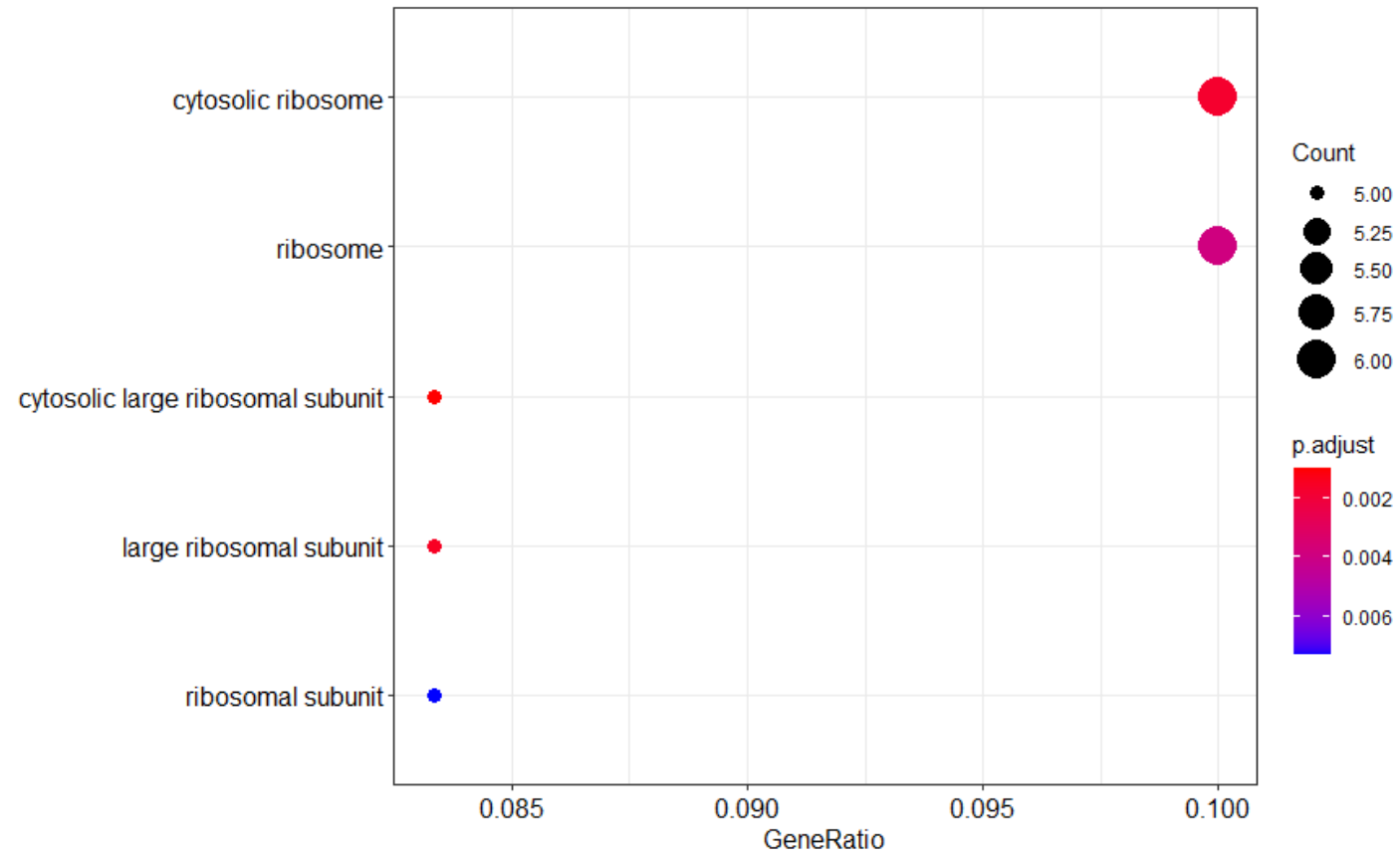
Biol.
Processes
(1.5nM solA
t=24)

ID	Description	Gen	BgRatio	pvalue	p.adjust	qvalue	geneID
GO:0042493	response to drug	15/57	465/21510	8.08153E-13	3.4993E-10	2.73071E-10	ATBZIP60/ATLOX4/ATPUMP5/AtLYK5/ATWRKY33/ATSZF2/ATBT2/ANAC062
GO:0010200	response to chitin	10/57	138/21510	2.837E-12	6.1421E-10	4.79303E-10	ATBZIP60/AtLYK5/ATWRKY33/ATSZF2/ANAC062/ATSZF1/ATWRKY70/ATERF6
GO:1901698	response to nitrogen compound	12/57	290/21510	1.18391E-11	1.70878E-09	1.33346E-09	ATBZIP60/AtLYK5/ATWRKY33/ATSZF2/AtNIT2/ATBT2/ANAC062/ATSZF1/AT
GO:0010243	response to organonitrogen compound	10/57	242/21510	7.33007E-10	7.9348E-08	6.19198E-08	ATBZIP60/AtLYK5/ATWRKY33/ATSZF2/ANAC062/ATSZF1/ATWRKY70/ATERF6
GO:0071456	cellular response to hypoxia	8/57	238/21510	2.06838E-07	1.36384E-05	1.06428E-05	ATPUMP5/ATSZF2/ATSZF1/ATWRKY70/DIC2/NA/NHL3/NRP
GO:0036294	cellular response to decreased oxygen levels	8/57	240/21510	2.20482E-07	1.36384E-05	1.06428E-05	ATPUMP5/ATSZF2/ATSZF1/ATWRKY70/DIC2/NA/NHL3/NRP
GO:0071453	cellular response to oxygen levels	8/57	240/21510	2.20482E-07	1.36384E-05	1.06428E-05	ATPUMP5/ATSZF2/ATSZF1/ATWRKY70/DIC2/NA/NHL3/NRP
GO:0001666	response to hypoxia	8/57	264/21510	4.54989E-07	2.27054E-05	1.77183E-05	ATPUMP5/ATSZF2/ATSZF1/ATWRKY70/DIC2/NA/NHL3/NRP
GO:0036293	response to decreased oxygen levels	8/57	268/21510	5.09815E-07	2.27054E-05	1.77183E-05	ATPUMP5/ATSZF2/ATSZF1/ATWRKY70/DIC2/NA/NHL3/NRP
GO:0070482	response to oxygen levels	8/57	269/21510	5.24373E-07	2.27054E-05	1.77183E-05	ATPUMP5/ATSZF2/ATSZF1/ATWRKY70/DIC2/NA/NHL3/NRP
GO:0006979	response to oxidative stress	8/57	454/21510	2.47185E-05	0.000973009	0.000759295	ATLOX4/ATBT2/ATWRKY70/ATERF6/AT-HSFA4A/AtBBE19/NA/ATFC-I
GO:0000302	response to reactive oxygen species	5/57	154/21510	5.4664E-05	0.00197246	0.001539224	ATLOX4/ATBT2/ATWRKY70/ATERF6/AT-HSFA4A
GO:0042742	defense response to bacterium	7/57	440/21510	0.000156305	0.005206154	0.004062661	TET8/ATWRKY33/ATWRKY70/CRK10/ADR1-L2/NHL3/BIR1
GO:0009620	response to fungus	6/57	335/21510	0.000253741	0.007847859	0.006124135	AP2C1/ATWRKY33/ATSZF2/ATWRKY70/AtPME41/AtBBE19
GO:0008272	sulfate transport	2/57	11/21510	0.000373681	0.010181022	0.007944835	ATPUMP5/DIC2
GO:0042435	indole-containing compound biosynthetic process	3/57	53/21510	0.000376204	0.010181022	0.007944835	ATWRKY33/AtNIT2/ATWRKY70
GO:0010120	camalexin biosynthetic process	2/57	14/21510	0.000615121	0.013339169	0.010409319	ATWRKY33/ATWRKY70
GO:0052317	camalexin metabolic process	2/57	14/21510	0.000615121	0.013339169	0.010409319	ATWRKY33/ATWRKY70
GO:0050832	defense response to fungus	5/57	265/21510	0.000678441	0.013339169	0.010409319	AP2C1/ATWRKY33/ATSZF2/ATWRKY70/AtBBE19
GO:0009700	indole phytoalexin biosynthetic process	2/57	15/21510	0.000708547	0.013339169	0.010409319	ATWRKY33/ATWRKY70
GO:0046217	indole phytoalexin metabolic process	2/57	15/21510	0.000708547	0.013339169	0.010409319	ATWRKY33/ATWRKY70
GO:0052314	phytoalexin metabolic process	2/57	15/21510	0.000708547	0.013339169	0.010409319	ATWRKY33/ATWRKY70
GO:0052315	phytoalexin biosynthetic process	2/57	15/21510	0.000708547	0.013339169	0.010409319	ATWRKY33/ATWRKY70
GO:0009409	response to cold	6/57	413/21510	0.000766928	0.013836651	0.010797532	NA/ATWRKY33/ATSZF2/ATBT2/ANAC062/AtPME41
GO:0035435	phosphate ion transmembrane transport	2/57	16/21510	0.000808391	0.01400133	0.010926041	ATPUMP5/DIC2
GO:0009873	ethylene-activated signaling pathway	3/57	76/21510	0.001081328	0.017723483	0.01383065	ATERF11/ATWRKY70/ATERF6
GO:0042430	indole-containing compound metabolic process	3/57	77/21510	0.001123061	0.017723483	0.01383065	ATWRKY33/AtNIT2/ATWRKY70
GO:0015743	malate transport	2/57	19/21510	0.001146091	0.017723483	0.01383065	ATPUMP5/DIC2
GO:0071369	cellular response to ethylene stimulus	3/57	83/21510	0.001394882	0.020245647	0.01579884	ATERF11/ATWRKY70/ATERF6
GO:0015740	C4-dicarboxylate transport	2/57	21/21510	0.001402701	0.020245647	0.01579884	ATPUMP5/DIC2
GO:0072348	sulfur compound transport	2/57	22/21510	0.001540349	0.021515202	0.016789546	ATPUMP5/DIC2
GO:0014070	response to organic cyclic compound	5/57	325/21510	0.001680906	0.022098529	0.01724475	ATCSLD5/ATBT2/ATWRKY70/AtPME41/NHL3
GO:0009403	toxin biosynthetic process	2/57	23/21510	0.001684184	0.022098529	0.01724475	ATWRKY33/ATWRKY70
GO:0009814	defense response, incompatible interaction	4/57	201/21510	0.001985377	0.025284357	0.019730834	ATWRKY33/ANAC062/ATWRKY70/NHL3
GO:0006855	drug transmembrane transport	2/57	26/21510	0.002152474	0.026226672	0.020466176	ATPUMP5/DIC2
GO:0000160	phosphorelay signal transduction system	3/57	97/21510	0.002180509	0.026226672	0.020466176	ATERF11/ATWRKY70/ATERF6
GO:0098661	inorganic anion transmembrane transport	2/57	27/21510	0.002320726	0.027158772	0.021193547	ATPUMP5/DIC2
GO:0009611	response to wounding	4/57	215/21510	0.002533388	0.028872899	0.022531179	ATLOX4/AP2C1/ATBT2/NHL3
GO:0006835	dicarboxylic acid transport	2/57	29/21510	0.00267527	0.029702359	0.023178454	ATPUMP5/DIC2
GO:0045087	innate immune response	5/57	364/21510	0.002749083	0.029758822	0.023222516	AtLYK5/ATWRKY33/ANAC062/ATWRKY70/NHL3
GO:0006563	L-serine metabolic process	2/57	30/21510	0.002861498	0.030220212	0.023582565	ATCS-C/PSAT1
GO:0006955	immune response	5/57	377/21510	0.003195323	0.032942257	0.025706733	AtLYK5/ATWRKY33/ANAC062/ATWRKY70/NHL3
GO:0071897	DNA biosynthetic process	2/57	33/21510	0.003455626	0.034797348	0.027154367	ATBT2/ATRPA70C
GO:0006817	phosphate ion transport	2/57	36/21510	0.004102259	0.040369963	0.031502997	ATPUMP5/DIC2
GO:0046677	response to antibiotic	4/57	250/21510	0.004343561	0.041794713	0.032614812	ATLOX4/ATBT2/ATWRKY70/NHL3
GO:0030968	endoplasmic reticulum unfolded protein response	2/57	38/21510	0.004562103	0.042943276	0.033511101	ATBZIP60/ANAC062
GO:0002376	immune system process	5/57	415/21510	0.004798917	0.044211301	0.034500614	AtLYK5/ATWRKY33/ANAC062/ATWRKY70/NHL3
GO:0009070	serine family amino acid biosynthetic process	2/57	41/21510	0.005294384	0.047759757	0.037269678	ATCS-C/PSAT1

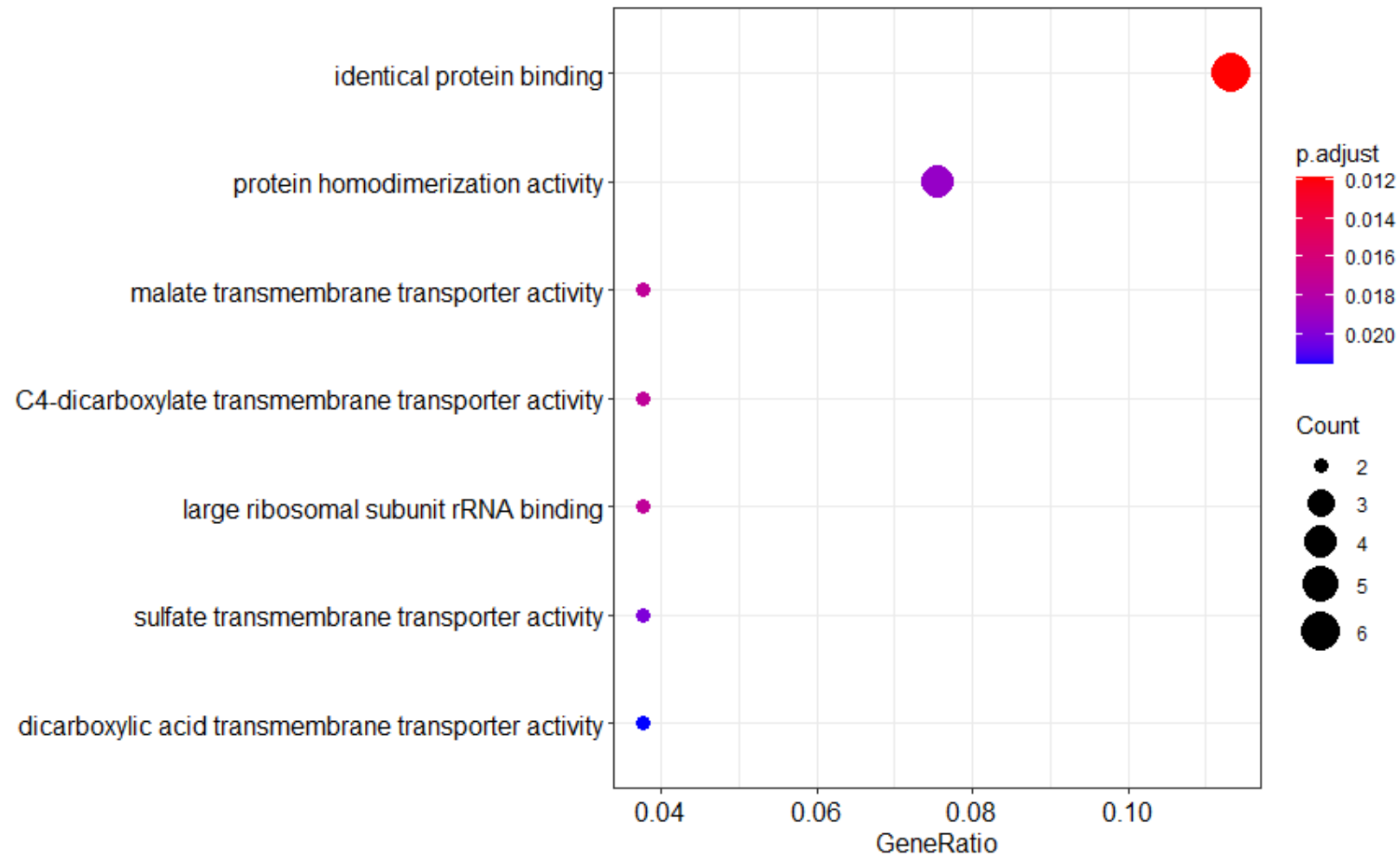
Biol. Process (1.5nM solA, t=24)

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:0042493	response to drug	15/57	465/21510	8.08E-13	3.50E-10	2.73E-10	ATBZIP60/	15
GO:0010200	response to chitin	Oct-57	138/21510	2.84E-12	6.14E-10	4.79E-10	ATBZIP60/	10
GO:1901698	response to nitrogen compound	Dec-57	290/21510	1.18E-11	1.71E-09	1.33E-09	ATBZIP60/	12
GO:0010243	response to organonitrogen compound	Oct-57	242/21510	7.33E-10	7.93E-08	6.19E-08	ATBZIP60/	10
GO:0071456	cellular response to hypoxia	Aug-57	238/21510	2.07E-07	1.36E-05	1.06E-05	ATPUMP5	8
GO:0036294	cellular response to decreased oxygen levels	Aug-57	240/21510	2.20E-07	1.36E-05	1.06E-05	ATPUMP5	8
GO:0071453	cellular response to oxygen levels	Aug-57	240/21510	2.20E-07	1.36E-05	1.06E-05	ATPUMP5	8
GO:0001666	response to hypoxia	Aug-57	264/21510	4.55E-07	2.27E-05	1.77E-05	ATPUMP5	8
GO:0036293	response to decreased oxygen levels	Aug-57	268/21510	5.10E-07	2.27E-05	1.77E-05	ATPUMP5	8
GO:0070482	response to oxygen levels	Aug-57	269/21510	5.24E-07	2.27E-05	1.77E-05	ATPUMP5	8
GO:0006979	response to oxidative stress	Aug-57	454/21510	2.47E-05	9.73E-04	7.59E-04	ATLOX4/A	8
GO:0000302	response to reactive oxygen species	May-57	154/21510	5.47E-05	0.00197246	0.001539	ATLOX4/A	5
GO:0042742	defense response to bacterium	Jul-57	440/21510	1.56E-04	0.005206154	0.004063	TET8/ATW	7
GO:0009620	response to fungus	Jun-57	335/21510	2.54E-04	0.007847859	0.006124	AP2C1/AT	6
GO:0008272	sulfate transport	Feb-57	11/21510	3.74E-04	0.010181022	0.007945	ATPUMP5	2
GO:0042435	indole-containing compound biosynthetic proce	Mar-57	53/21510	3.76E-04	0.010181022	0.007945	ATWRKY3	3
GO:0010120	camalexin biosynthetic process	Feb-57	14/21510	6.15E-04	0.013339169	0.010409	ATWRKY3	2
GO:0052317	camalexin metabolic process	Feb-57	14/21510	6.15E-04	0.013339169	0.010409	ATWRKY3	2
GO:0050832	defense response to fungus	May-57	265/21510	6.78E-04	0.013339169	0.010409	AP2C1/AT	5
GO:0009700	indole phytoalexin biosynthetic process	Feb-57	15/21510	7.09E-04	0.013339169	0.010409	ATWRKY3	2
GO:0046217	indole phytoalexin metabolic process	Feb-57	15/21510	7.09E-04	0.013339169	0.010409	ATWRKY3	2
GO:0052314	phytoalexin metabolic process	Feb-57	15/21510	7.09E-04	0.013339169	0.010409	ATWRKY3	2
GO:0052315	phytoalexin biosynthetic process	Feb-57	15/21510	7.09E-04	0.013339169	0.010409	ATWRKY3	2
GO:0009409	response to cold	Jun-57	413/21510	7.67E-04	0.013836651	0.010798	NA/ATWR	6
GO:0035435	phosphate ion transmembrane transport	Feb-57	16/21510	8.08E-04	0.01400133	0.010926	ATPUMP5	2
GO:0009873	ethylene-activated signaling pathway	Mar-57	76/21510	0.001081	0.017723483	0.013831	ATERF11//	3
GO:0042430	indole-containing compound metabolic process	Mar-57	77/21510	0.001123	0.017723483	0.013831	ATWRKY3	3
GO:0015743	malate transport	Feb-57	19/21510	0.001146	0.017723483	0.013831	ATPUMP5	2
GO:0071369	cellular response to ethylene stimulus	Mar-57	83/21510	0.001395	0.020245647	0.015799	ATERF11//	3
GO:0015740	C4-dicarboxylate transport	Feb-57	21/21510	0.001403	0.020245647	0.015799	ATPUMP5	2
GO:0072348	sulfur compound transport	Feb-57	22/21510	0.00154	0.021515202	0.01679	ATPUMP5	2
GO:0014070	response to organic cyclic compound	May-57	325/21510	0.001681	0.022098529	0.017245	ATCSLD5//	5
GO:0009403	toxin biosynthetic process	Feb-57	23/21510	0.001684	0.022098529	0.017245	ATWRKY3	2
GO:0009814	defense response, incompatible interaction	Apr-57	201/21510	0.001985	0.025284357	0.019731	ATWRKY3	4
GO:0006855	drug transmembrane transport	Feb-57	26/21510	0.002152	0.026226672	0.020466	ATPUMP5	2
GO:0000160	phosphorelay signal transduction system	Mar-57	97/21510	0.002181	0.026226672	0.020466	ATERF11//	3
GO:0098661	inorganic anion transmembrane transport	Feb-57	27/21510	0.002321	0.027158772	0.021194	ATPUMP5	2
GO:0009611	response to wounding	Apr-57	215/21510	0.002534	0.028872899	0.022531	ATLOX4/A	4
GO:0006835	dicarboxylic acid transport	Feb-57	29/21510	0.002675	0.029702359	0.023178	ATPUMP5	2
GO:0045087	innate immune response	May-57	364/21510	0.002749	0.029758822	0.023223	AtLYK5/AT	5
GO:0006563	L-serine metabolic process	Feb-57	30/21510	0.002861	0.030220212	0.023583	ATCS-C/P5	2
GO:0006955	immune response	May-57	377/21510	0.003195	0.032942257	0.025707	AtLYK5/AT	5
GO:0071897	DNA biosynthetic process	Feb-57	33/21510	0.003456	0.034797348	0.027154	ATBT2/AT	2
GO:0006817	phosphate ion transport	Feb-57	36/21510	0.004102	0.040369963	0.031503	ATPUMP5	2
GO:0046677	response to antibiotic	Apr-57	250/21510	0.004344	0.041794713	0.032615	ATLOX4/A	4
GO:0030968	endoplasmic reticulum unfolded protein respor	Feb-57	38/21510	0.004562	0.042943276	0.033511	ATBZIP60/	2
GO:0002376	immune system process	May-57	415/21510	0.004799	0.044211301	0.034501	AtLYK5/AT	5
GO:0009070	serine family amino acid biosynthetic process	Feb-57	41/21510	0.005294	0.047759757	0.03727	ATCS-C/P5	2

Cell comp. (1.5nM, t=24)



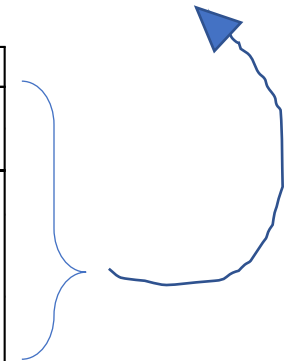
Molecular function (1.5nM, t=24)



Murray, Shane L, Ingle, Robert A, ...
 Basal resistance against
Pseudomonas syringae in
 arabidopsis involves WRKY53 and
 a protein with homology to a
 nematode resistance protein.

MOLECULAR
 PLANT-MICROBE
 INTERACTIONS

Interesting genes



t	treatment	log2FoldC	tair_symb	description	external_	notes
24	uM	1.381319	HSPRO2	Nematode resistance protein-like HSPRO2	HSPRO2	In <i>B. Vulgaris</i> , infers resistance against SCN
6	nM	1.804376	HSPRO2	Nematode resistance protein-like HSPRO2	HSPRO2	
24	nM	1.126698	WRKY33	WRKY33 [Source:UniProtKB/TrEMBL;Acc:A0A384L4W4]	WRKY33	Member of the plant WRKY transcription factor family. Regulates the antagonistic relationship between defense pathways mediating responses to <i>P. Syringae</i> and necrotrophic fungal pathogens. Located in the nucleus. Involved in resposne to various abiotic stresses - especially salt stress
24	uM	1.099936	WRKY33	WRKY33 [Source:UniProtKB/TrEMBL;Acc:A0A384L4W4]	WRKY33	
6	nM	1.440581	WRKY33	WRKY33 [Source:UniProtKB/TrEMBL;Acc:A0A384L4W4]	WRKY33	
24	nM	2.581466	ERF11	ERF domain protein 11 [Source:TAIR;Acc:AT1G28370]	ERF11	close relative of OXS3 (see below)
24	uM	2.113898	ERF11	ERF domain protein 11 [Source:TAIR;Acc:AT1G28370]	ERF11	
24	uM	2.204142	ATERF6	Ethylene-responsive transcription factor 6	ERF6	
24	nM	2.144845	ATERF6	Ethylene-responsive transcription factor 6	ERF6	increases resistance to oxidative stress
6	nM	1.185339		At5g21940 [Source:UniProtKB/TrEMBL;Acc:Q9C593]		
2	nM	1.775879		At5g21940 [Source:UniProtKB/TrEMBL;Acc:Q9C593]		
2	uM	1.957075		At5g21940 [Source:UniProtKB/TrEMBL;Acc:Q9C593]		increases resistance to oxidative stress
6	nM	1.793827	OXS3	Emb [Source:UniProtKB/TrEMBL;Acc:Q9LVB9]	OXS3	
2	nM	2.389844	OXS3	Emb [Source:UniProtKB/TrEMBL;Acc:Q9LVB9]	OXS3	
2	uM	2.893597	OXS3	Emb [Source:UniProtKB/TrEMBL;Acc:Q9LVB9]	OXS3	
24	uM	1.734755	SZF1	Salt-inducible zinc finger 1	SZF1	
24	nM	1.884618	SZF1	Salt-inducible zinc finger 1	SZF1	
6	nM	1.382687	SZF1	Salt-inducible zinc finger 1	SZF1	
24	uM	2.141214	DIC2	DIC2 [Source:UniProtKB/TrEMBL;Acc:A0A178URN9]	PUMP4	
24	nM	2.01529	DIC2	DIC2 [Source:UniProtKB/TrEMBL;Acc:A0A178URN9]	PUMP4	
6	nM	1.949921	DIC2	DIC2 [Source:UniProtKB/TrEMBL;Acc:A0A178URN9]	PUMP4	
24	uM	1.839853		Nuclease [Source:UniProtKB/TrEMBL;Acc:Q84J48]		
24	nM	1.956091		Nuclease [Source:UniProtKB/TrEMBL;Acc:Q84J48]		
6	nM	1.182935		Nuclease [Source:UniProtKB/TrEMBL;Acc:Q84J48]		

Summary biological processes GO terms

Possible explanations of hypoxia GO terms (1):

- High metabolic activity
→ *solA is growth hormone?*
- Hypoxia during pathogen infection
 - Hypoxia at site of infection
 - Slow oxygen diffusion in tumorigenic tissues
 → *solA is signaling molecule, mimicking/warning for pathogens?*

Hypoxia response in Arabidopsis roots infected by *Plasmodiophora brassicae* supports the c [BMC Plant Biol. 2016]

Arabidopsis RAP2.2 plays an important role in plant resistance to *Botrytis cinerea* and ethylene responses. [New Phytol. 2012]

AP2/ERF Family Transcription Factors ORA59 and RAP2.3 Interact in the Nucleus and Function Together [Front Plant Sci. 2018]

Distinct branches of the N-end rule pathway modulate the plant immune response. [New Phytol. 2019]

Nitric oxide sensing in plants is mediated by proteolytic control of group VII ERF transcription factors. [Mol Cell. 2014]

Ethylene-mediated nitric oxide depletion pre-adapts plants to hypoxia stress. [Nat Commun. 2019]

Botrytis cinerea induces local hypoxia in Arabidopsis leaves. [New Phytol. 2020]

cellular response to decreased oxygen levels	5
cellular response to hypoxia	5
cellular response to oxygen levels	5
response to decreased oxygen levels	5
response to hypoxia	5
response to oxygen levels	5
response to drug	4
response to oxidative stress	4
response to wounding	4
defense response to bacterium	3
response to antibiotic	3
response to chitin	3
response to hydrogen peroxide	3
response to nitrogen compound	3
response to organonitrogen compound	3
response to reactive oxygen species	3