

TICTOC RNAseq

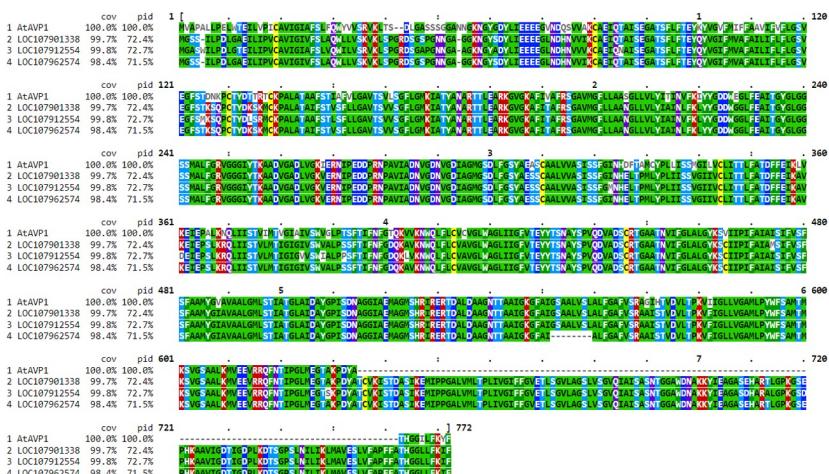


TICTOC RNAseq

59918 genes in 48 samples. Of the 54267 genes passed filter (see above), 0 were converted to Ensembl gene IDs in our database. The remaining 54267 genes were kept in the data using original IDs.

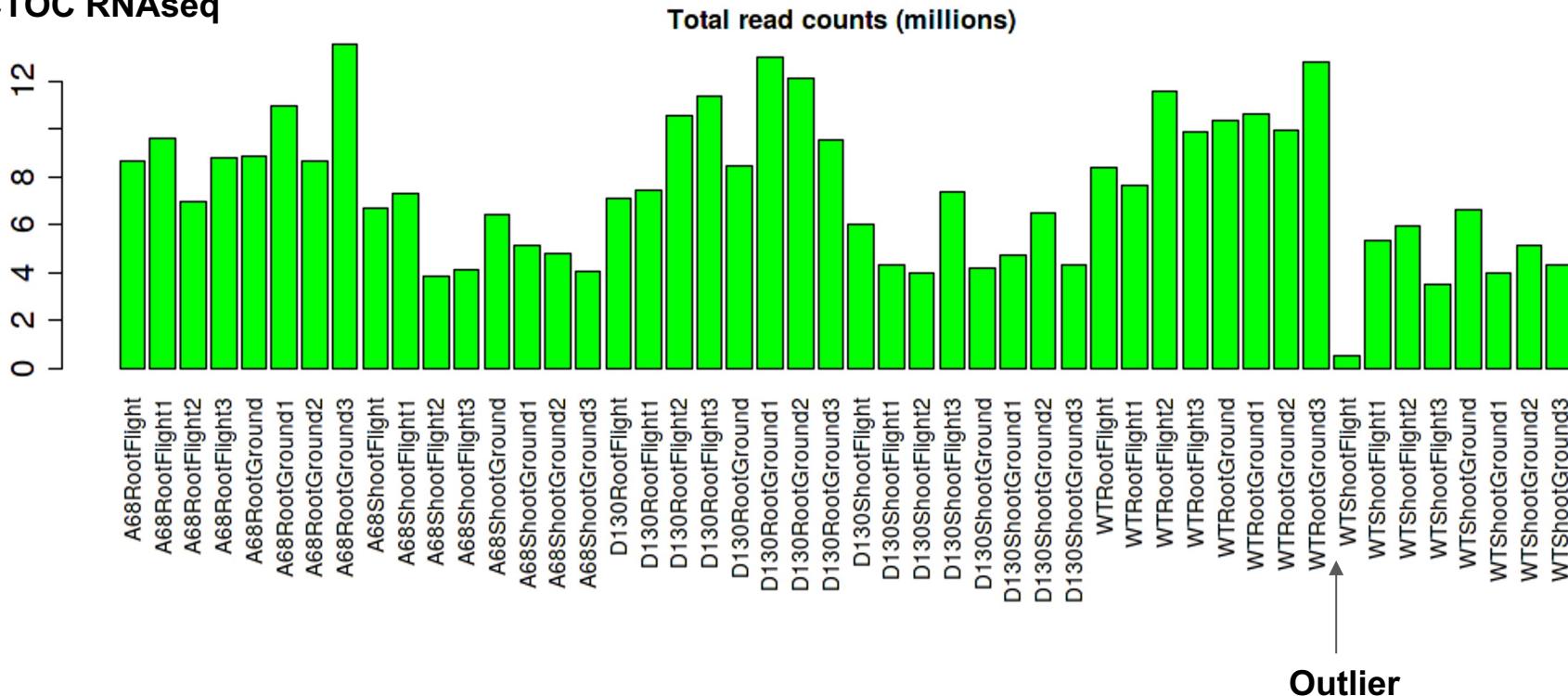
Study_design	A68RF1_S5_L004	A68RF2_S6_L004	A68RF3_S7_L004	A68RF4_S8_L004	A68RG1_S9_L004	A68RG2_S10_L004	
Geno-Treatment1-Tissue	A68RF	A68RF	A68RF	A68RF	A68RG	A68RG	
Treatment	Flight	Flight	Flight	Flight	Ground	Ground	C
Geno-Tissue	A68R	A68R	A68R	A68R	A68R	A68R	
Genotype	A68	A68	A68	A68	A68	A68	
Tissue	Root	Root	Root	Root	Root	Root	F
ID	A68.R.F1_S5_L004	A68.R.F2_S6_L004	A68.R.F3_S7_L004	A68.R.F4_S8_L004	A68.R.G1_S9_L004	A68.R.G2_S	
Gohir.A01G000301.v2.1	4	5	1	4	1		
Gohir.A01G000401.v2.1	55	51	48	76	27		
Gohir.A01G000500.v2.1	42	48	40	41	38		
Gohir.A01G000600.v2.1	93	114	93	96	153		
Gohir.A01G000800.v2.1	20	0	1	11	88		
Gohir.A01G000900.v2.1	0	0	0	0	0		
Gohir.A01G001000.v2.1	20	49	20	24	21		
Gohir.A01G001100.v2.1	269	319	192	277	257		
Gohir.A01G001200.v2.1	13	14	17	14	20		
Gohir.A01G001300.v2.1	335	320	247	335	1098		
Gohir.A01G001400.v2.1	188	155	152	208	286		
Gohir.A01G001500.v2.1	98	137	127	145	29		
Gohir.A01G001700.v2.1	73	39	50	76	7		
Gohir.A01G001800.v2.1	1	0	0	0	0		
Gohir.A01G001900.v2.1	125	114	31	75	48		

Over Expression of AVP in A68 and D130 lines.



AVP alignment with EBI COFFEE

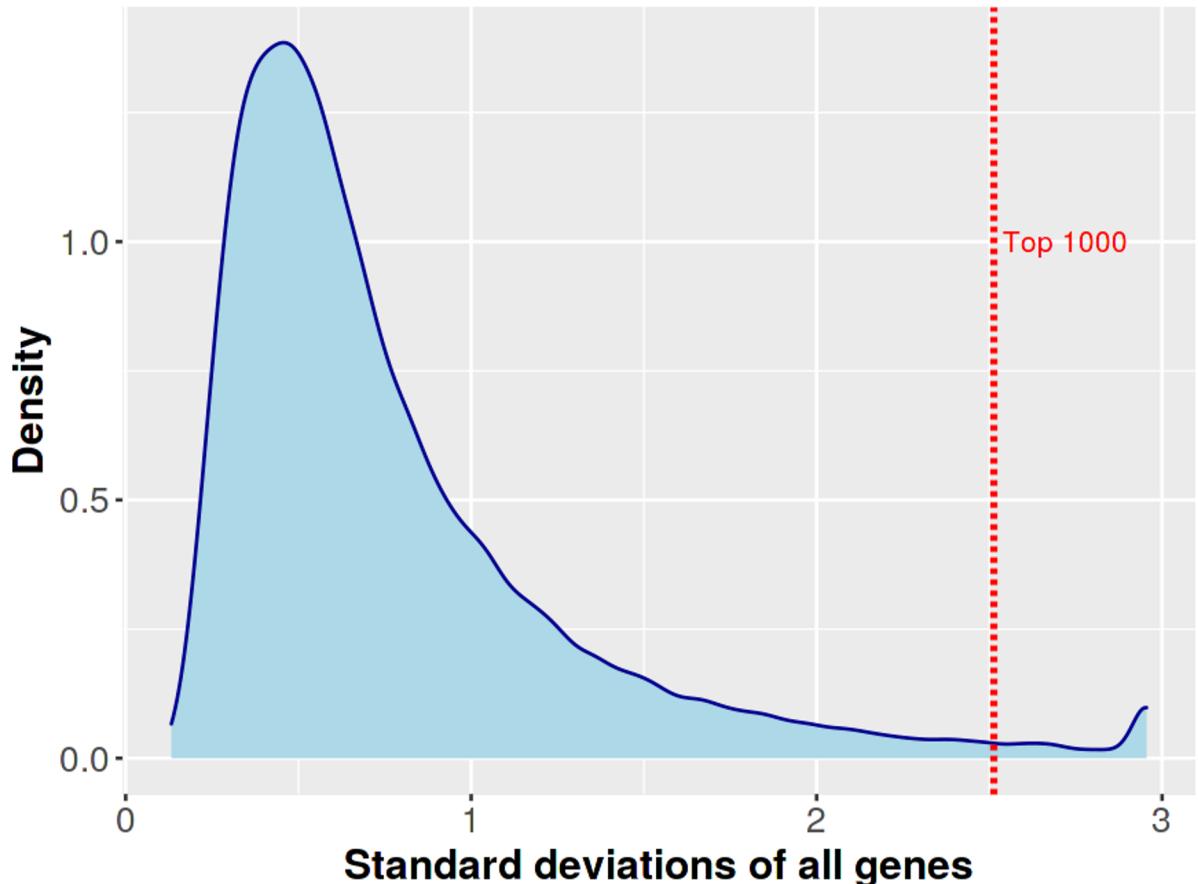
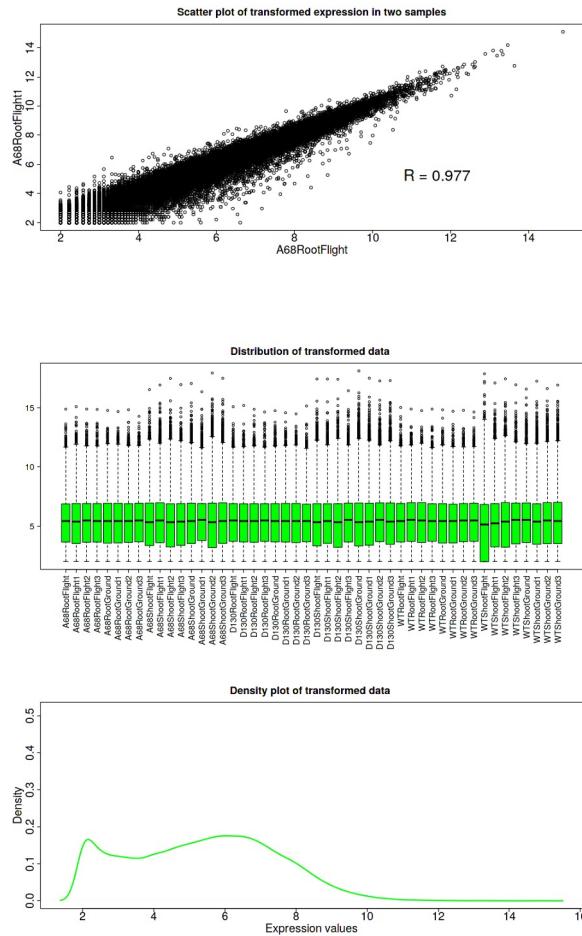
TICTOC RNAseq



Comment: The A68 and D130 have similar differentially expressed loci in orbit

1 sample outlier: WT Shoot flight low sequencing depth -> influence on the 3rd principle component

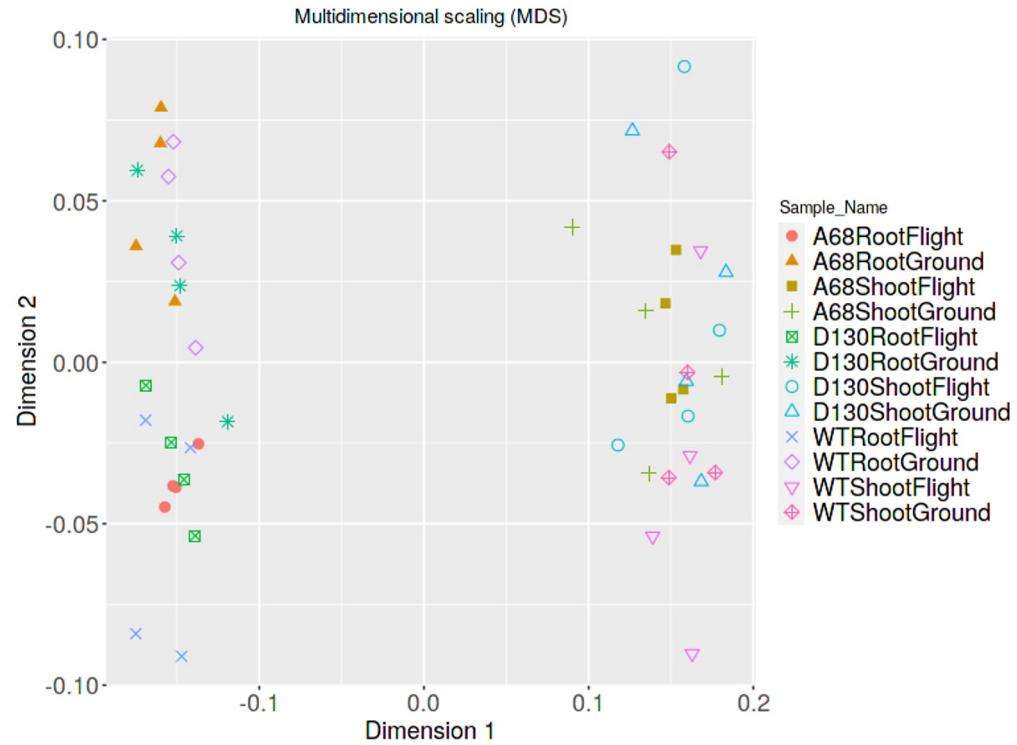
TICTOC RNAseq



MDS

Pearson sample correlation matrix

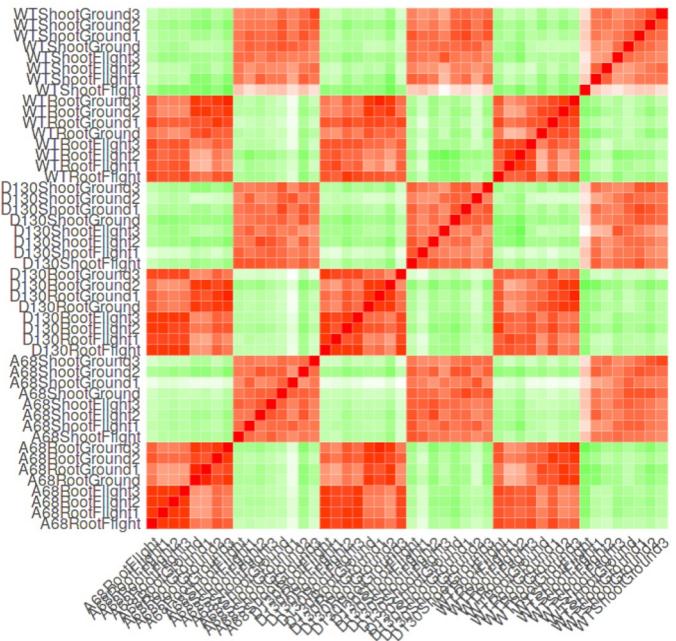
Ground



Flight

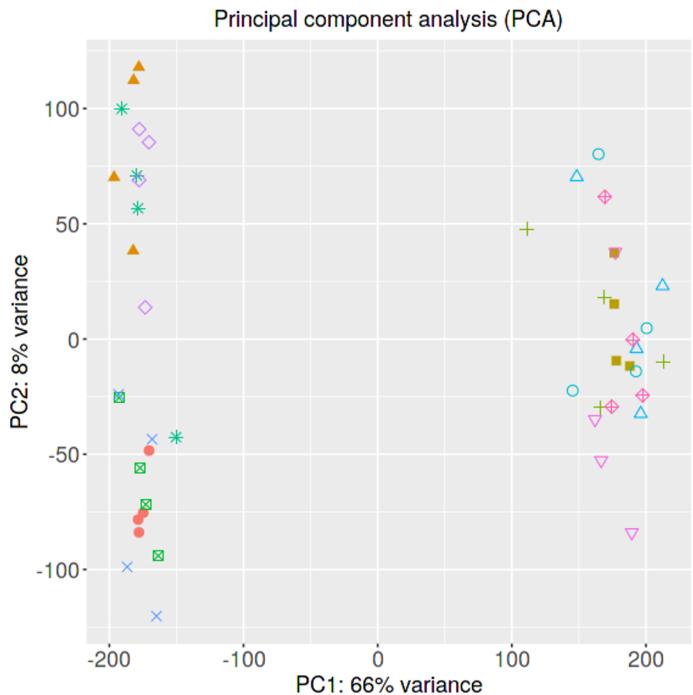
Root

Shoot



PC 1 (Tissue) and PC 2 (Treatment)

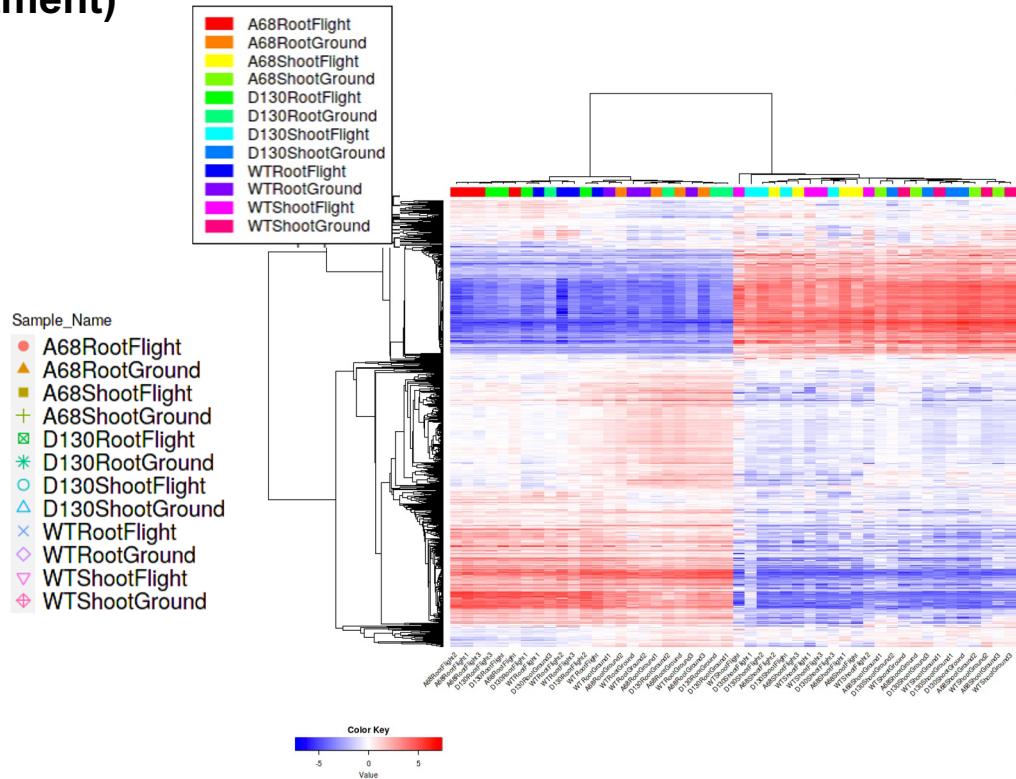
Ground



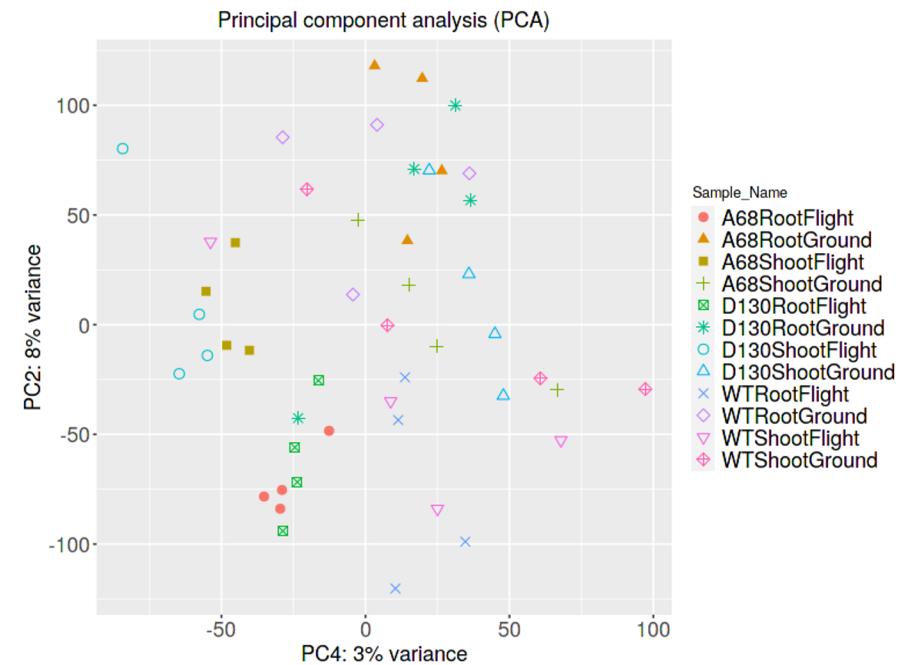
Flight

Root

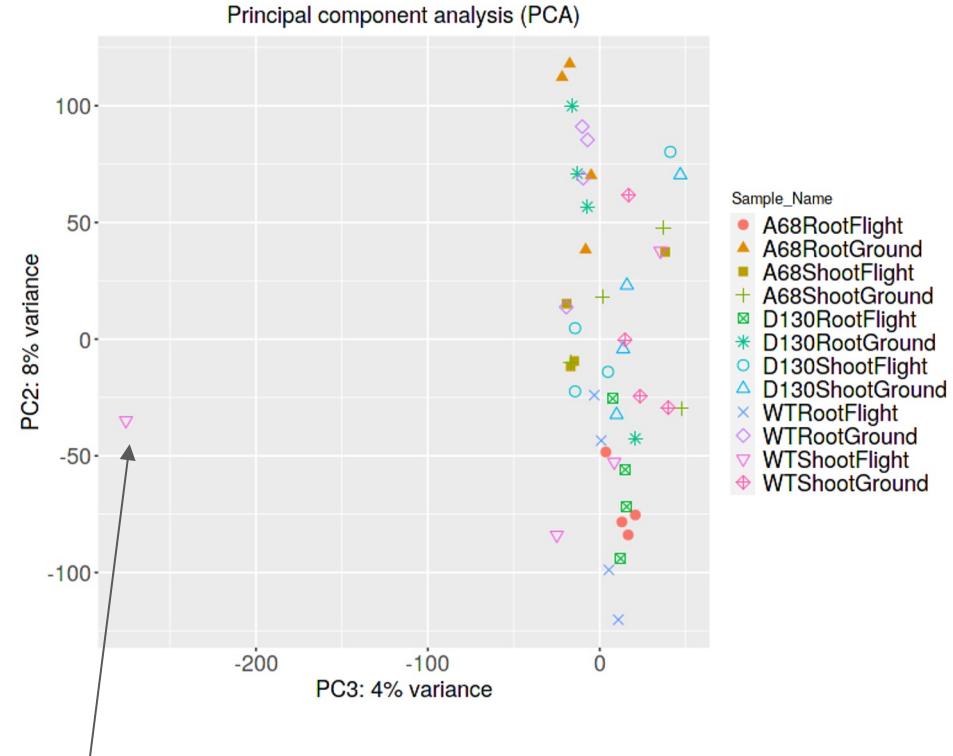
Shoot



PC 2 (Treatment) and PC 4?



PC 2 (Treatment) and PC 3?



Outlier

Comparisons	Up	Down
WTShootGround-D130ShootGround	3	3
WTShootGround-A68ShootGround	3	3
WTShootFlight-WTShootGround	844	877
WTRootGround-D130RootGround	2	11
WTRootGround-A68RootGround	9	6
WTRootFlight-WTRootGround	4461	2697
D130ShootFlight-D130ShootGround	1352	2228
D130RootFlight-D130RootGround	2000	2051
A68ShootFlight-A68ShootGround	458	1258
A68RootFlight-A68RootGround	4954	6163

Identifying Differential Expressed Genes (DEGs). See next tab for details.

Method:

DESeq2 ▾

FDR cutoff

Min fold change

Identifying Differential Expressed Genes (DEGs). See next tab for details.

Method:

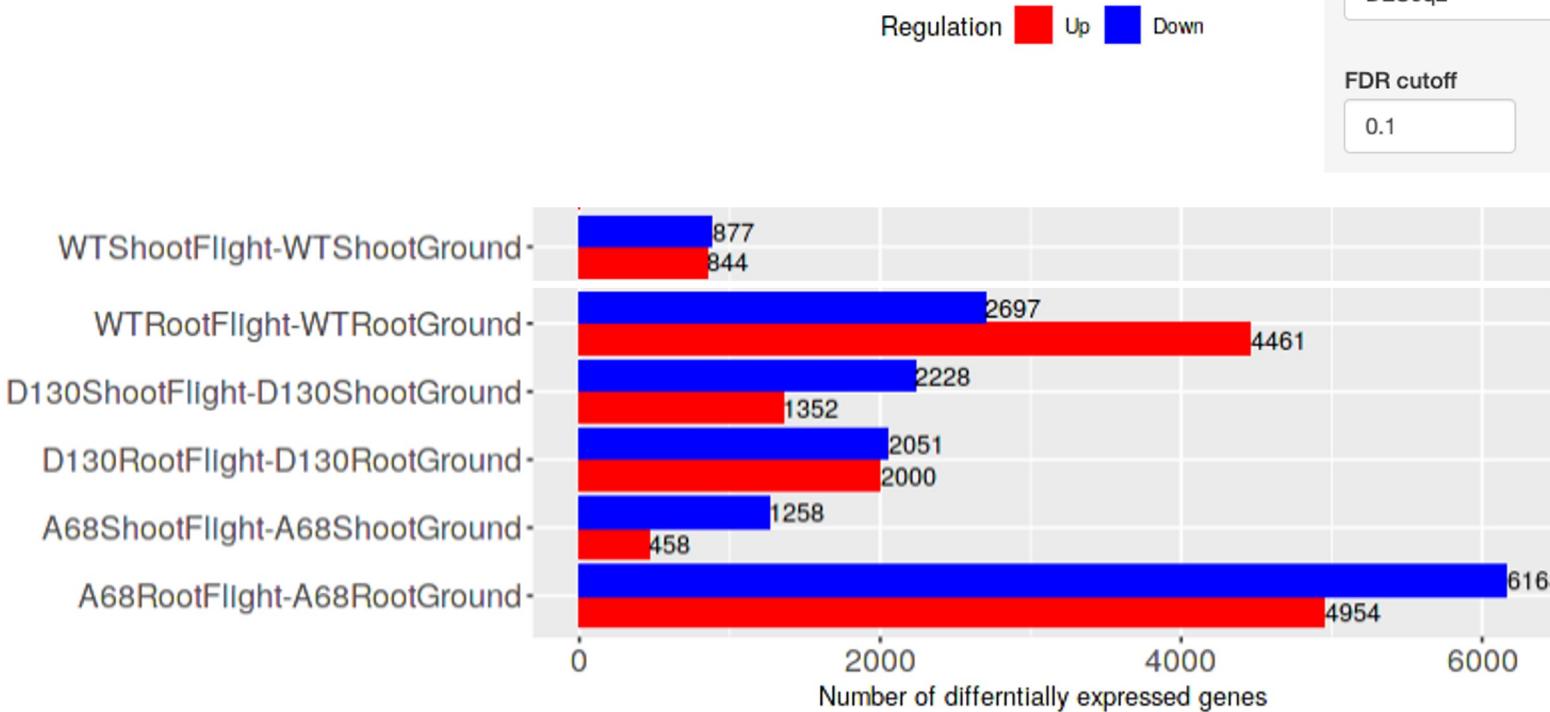
DESeq2

FDR cutoff

0.1

Min fold change

2



Identifying Differential Expressed Genes (DEGs). See next tab for details.

Method:

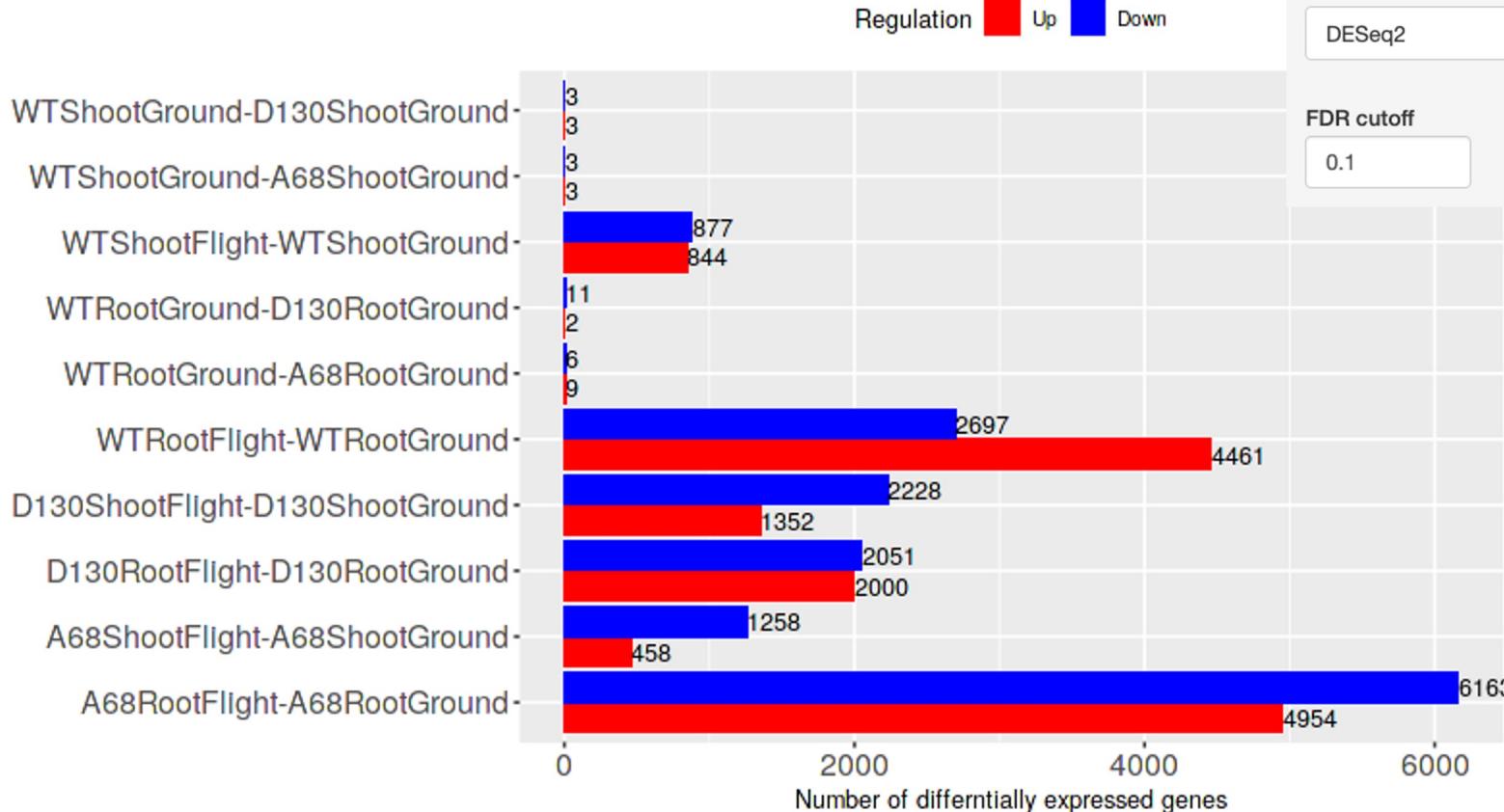
DESeq2

FDR cutoff

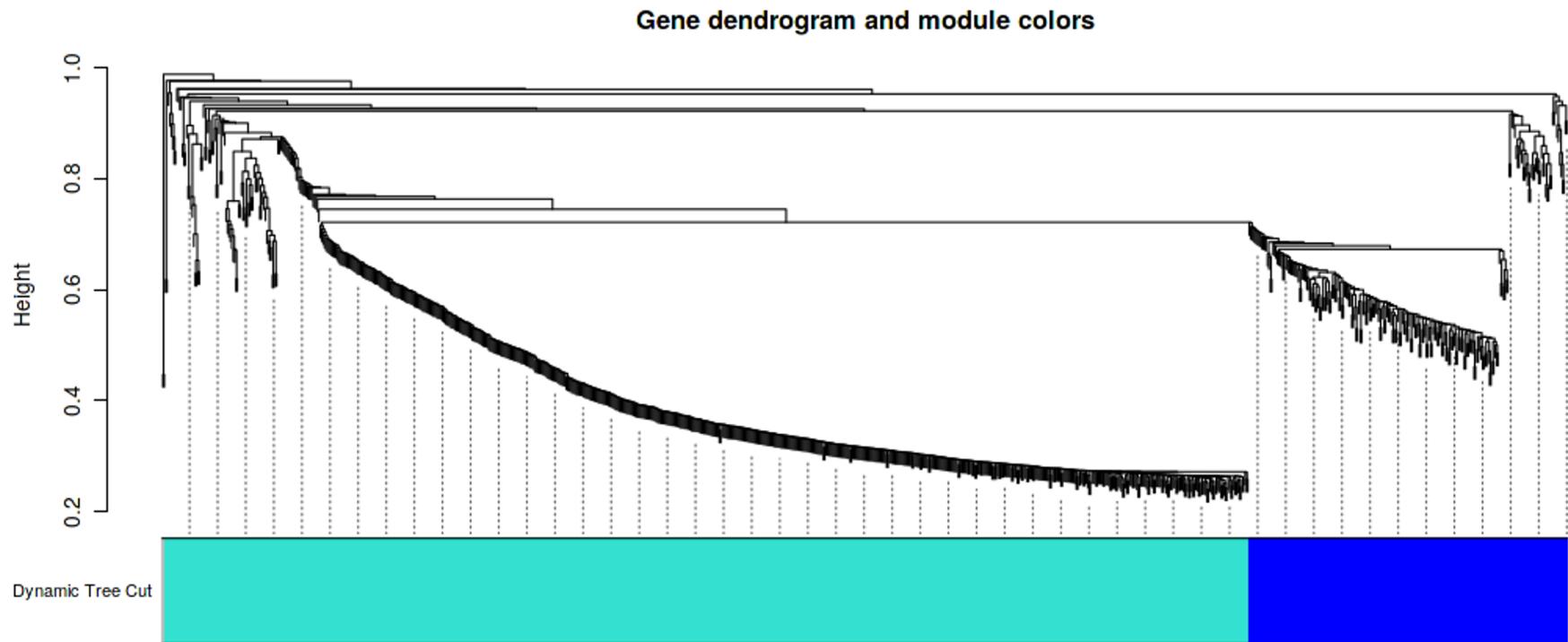
0.1

Min fold change

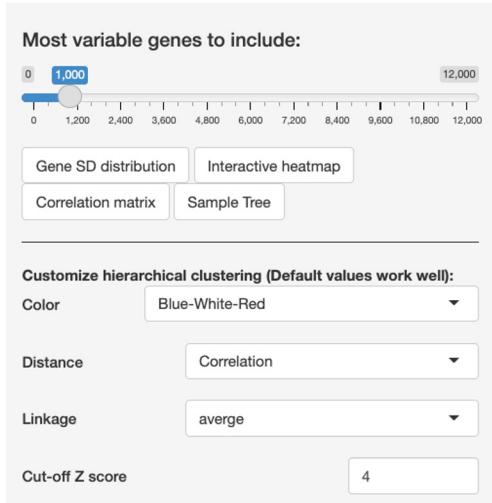
2



2 cluster in WGCNA when all genotypes are used.



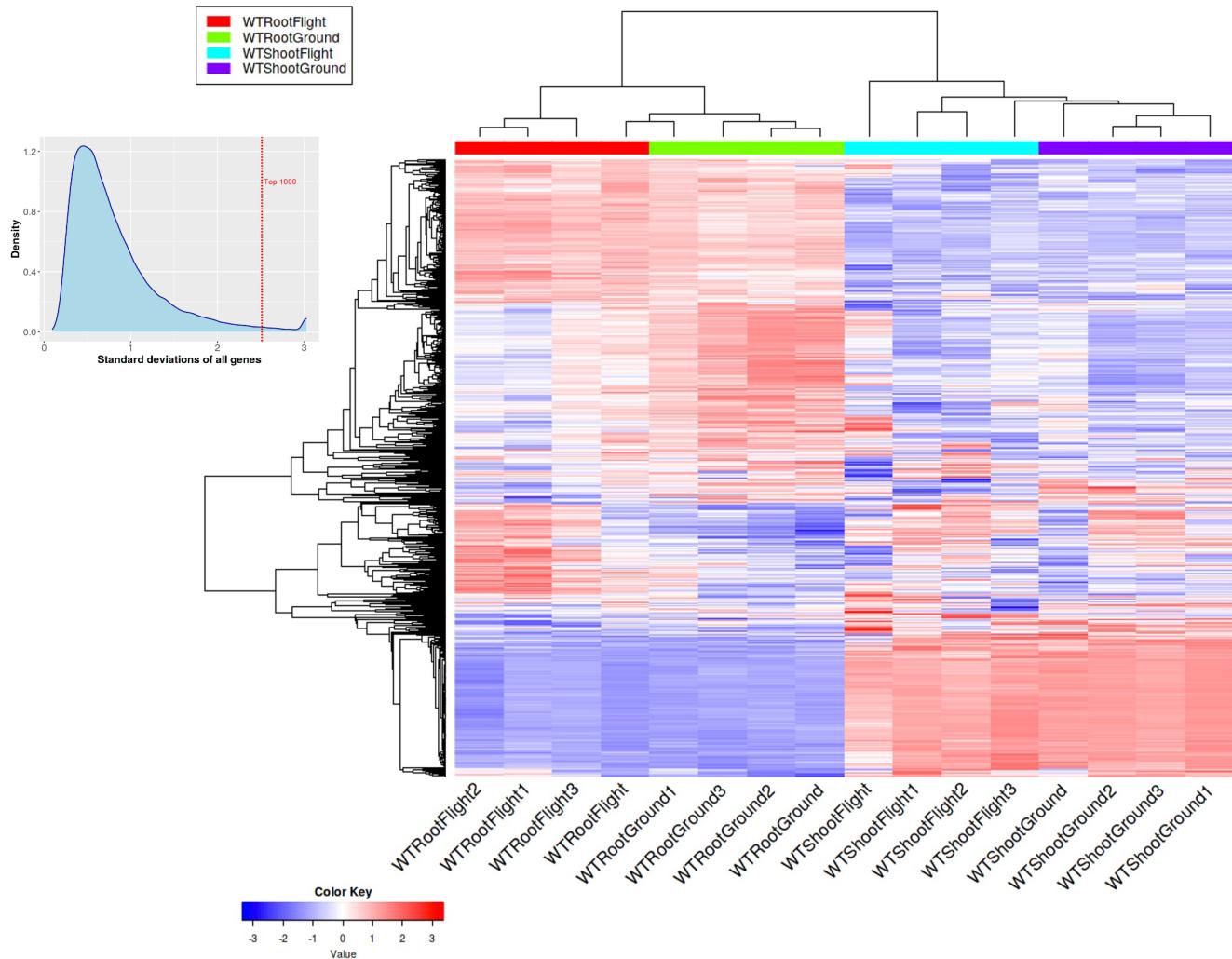
Just WT Cotton



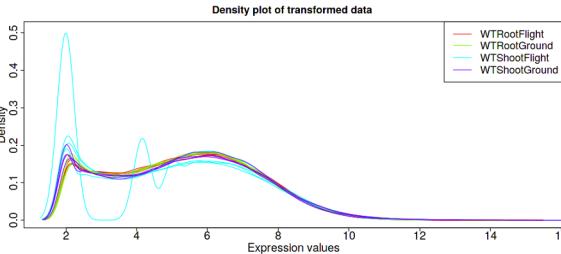
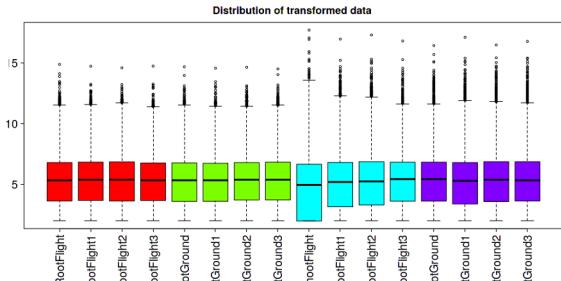
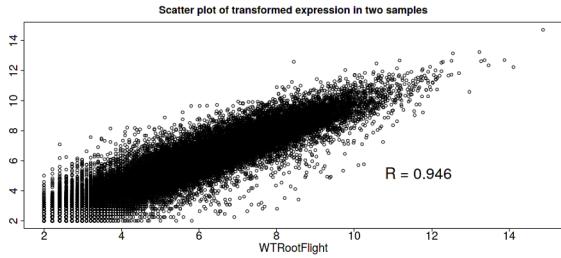
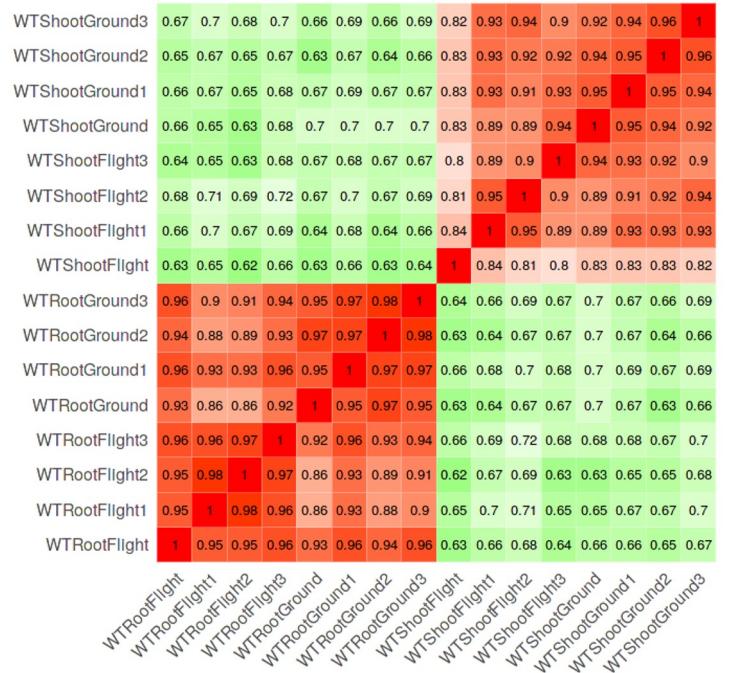
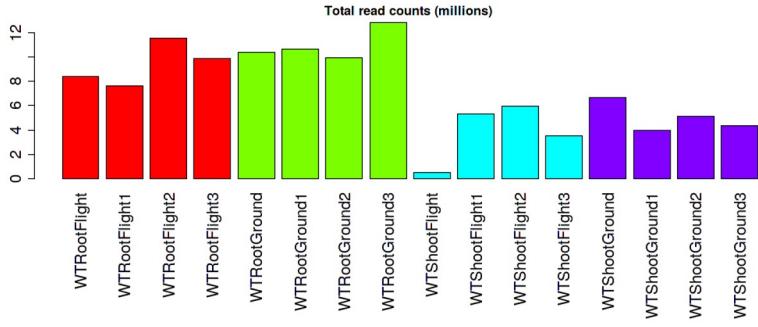
Center genes (subtract mean)

Normalize genes (divide by SD)

Center samples (subtract mean)

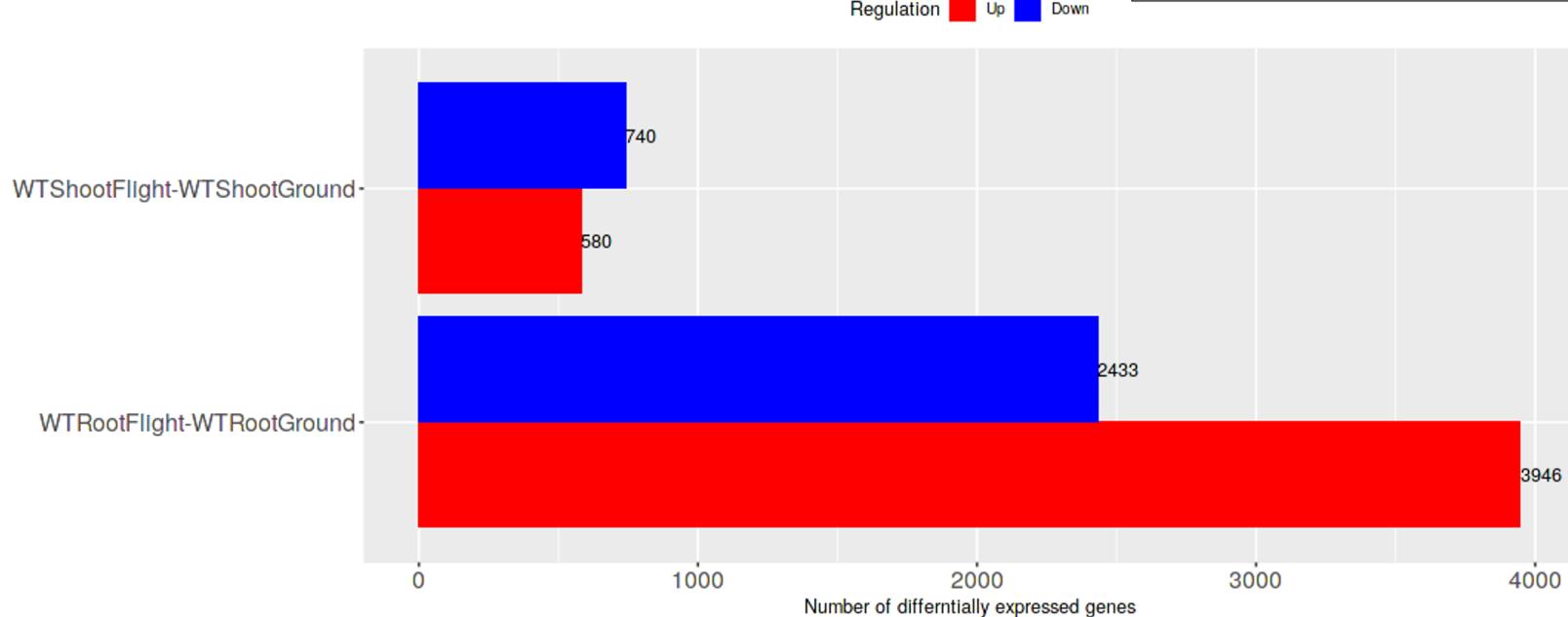
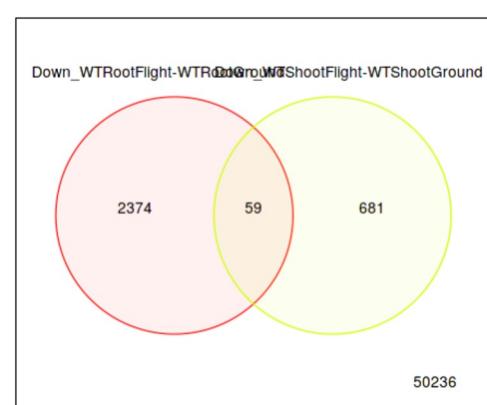
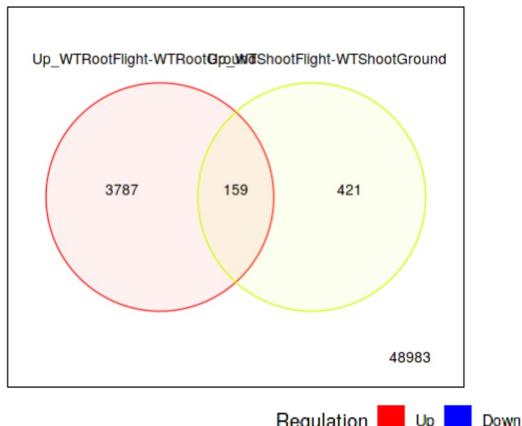


Just WT Cotton

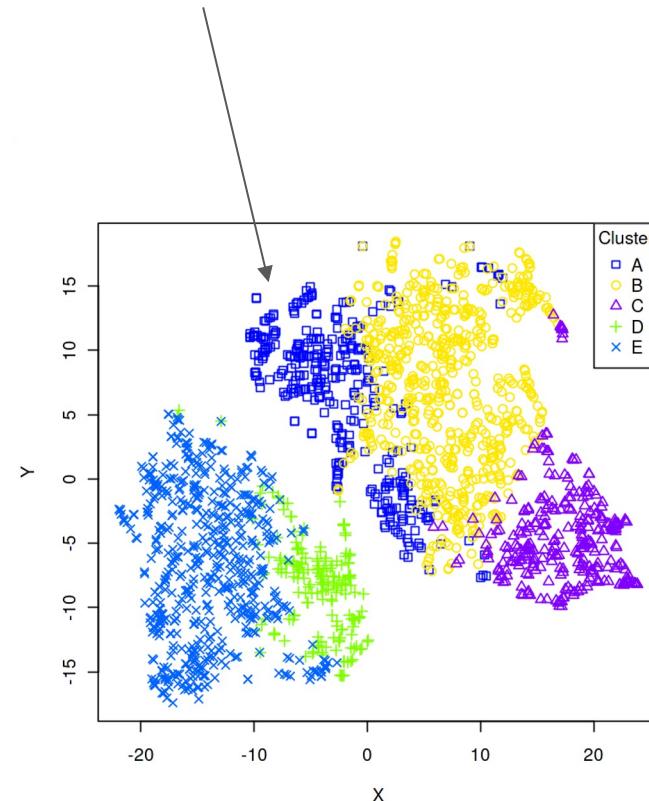


TICTOC RNAseq just WT roots and shoots

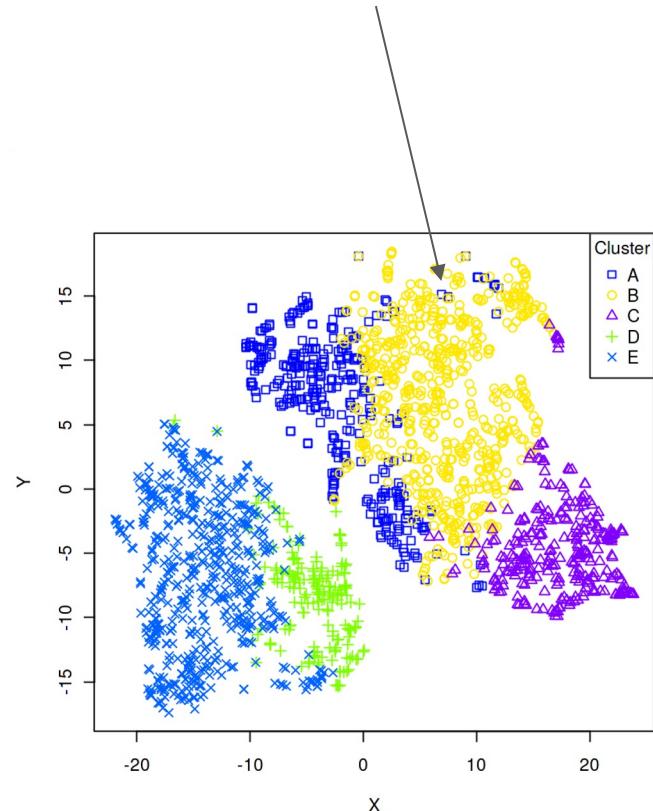
Comparisons	Up	Down
WTShootFlight-WTShootGround	580	740
WTRootFlight-WTRootGround	3946	243



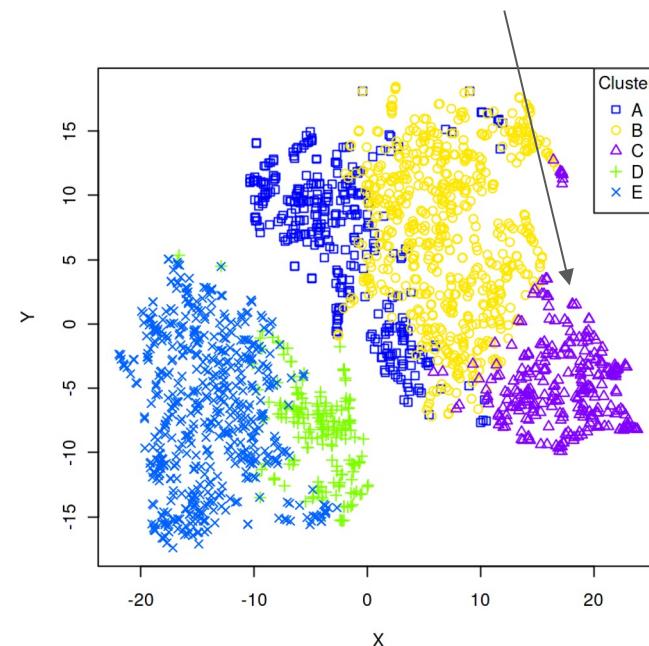
Cluster	adj.Pval	nGenes	Pathways
A	2.3e-18	21	Photosynthesis
	4.3e-07	39	Oxidation-reduction process
	3.5e-05	7	Fatty acid biosynthetic process
	1.5e-04	3	Respiratory electron transport chain
	1.6e-03	4	Cellular glucan metabolic process
	1.8e-03	3	Polysaccharide catabolic process
	1.8e-03	12	Carbohydrate metabolic process
	1.8e-03	2	Peroxisome fission
	4.8e-03	2	Glutamine biosynthetic process
	6.0e-03	3	DNA-templated transcription-initiation
	6.3e-03	3	Cellulose biosynthetic process
	7.4e-03	2	Riboflavin biosynthetic process
	9.5e-03	5	Protein folding



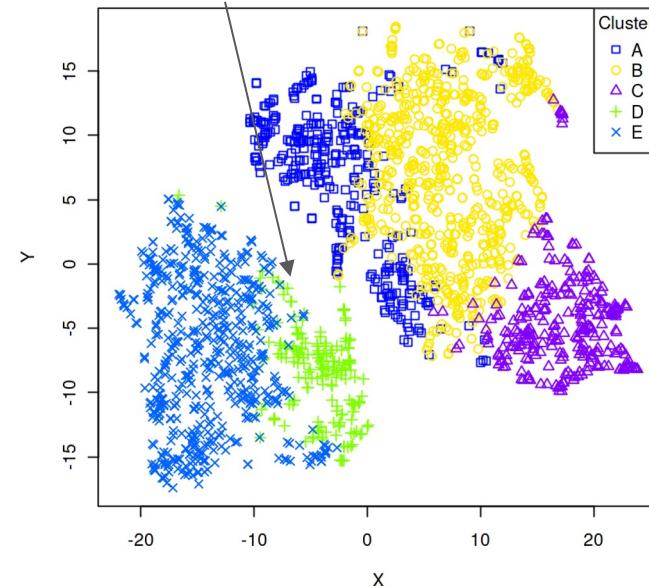
B	4.9e-14	22	Photosynthesis
	5.4e-12	70	Oxidation-reduction process
	1.0e-06	33	Metabolic process
	2.9e-04	3	Photosystem II assembly
	3.2e-04	4	Photosynthetic electron transport chain
	3.7e-04	5	Photosynthesis-light reaction
	9.0e-04	9	Protein folding
	9.0e-04	7	Fatty acid biosynthetic process
	9.0e-04	7	Recognition of pollen
	1.8e-03	18	Proteolysis
	3.4e-03	2	Chlorophyll biosynthetic process
	4.6e-03	2	Potassium ion transport
	4.6e-03	4	Lipid biosynthetic process
	4.6e-03	2	Thiamine biosynthetic process
	4.6e-03	2	Carotenoid biosynthetic process



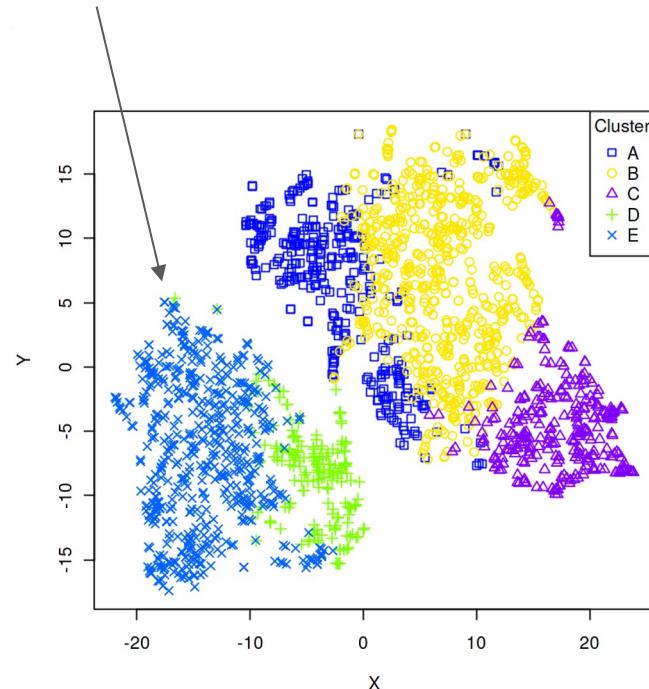
C	2.8e-76	37	Photosynthesis-light harvesting
	1.9e-48	39	Photosynthesis
	2.4e-07	35	Oxidation-reduction process
	3.0e-06	7	Glycolytic process
	1.2e-05	3	Glycine catabolic process
	4.8e-05	2	Pyruvate metabolic process
	5.6e-05	6	Fatty acid biosynthetic process
	3.4e-04	3	Sucrose metabolic process
	1.1e-03	2	Photosystem II stabilization
	1.3e-03	4	ATP synthesis coupled proton transport
	1.7e-03	2	Phosphorylation
	2.5e-03	2	Gluconeogenesis
	2.7e-03	3	Lipid biosynthetic process
	5.4e-03	3	Glycerol ether metabolic process
	1.0e-02	12	Metabolic process



D	7.2e-17	41	Oxidation-reduction process
	1.1e-03	2	Arginine catabolic process
	6.1e-03	2	Spermidine biosynthetic process
	6.1e-03	2	Terpenoid biosynthetic process

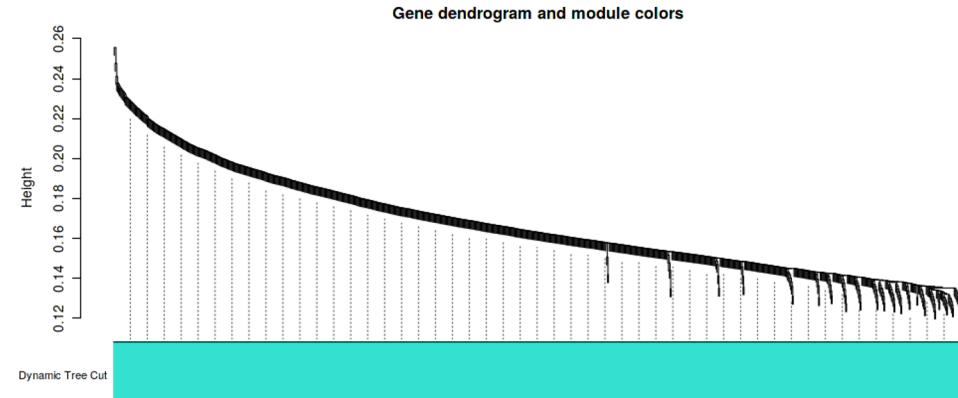


E	6.7e-35	38	Response to oxidative stress
	1.7e-34	103	Oxidation-reduction process
	2.3e-17	34	Transport
	1.6e-08	10	Response to biotic stimulus
	9.6e-08	4	Plant-type cell wall organization
	4.7e-07	29	Transmembrane transport
	7.5e-07	10	Defense response
	2.0e-05	4	Cellular ion homeostasis
	5.3e-05	13	Signal transduction
	3.3e-04	5	Cellulose biosynthetic process
	8.6e-04	2	Plant-type secondary cell wall biogenesis
	5.8e-03	2	Nicotianamine biosynthetic process
	6.8e-03	5	Multicellular organism development
	9.9e-03	2	Glutamine biosynthetic process



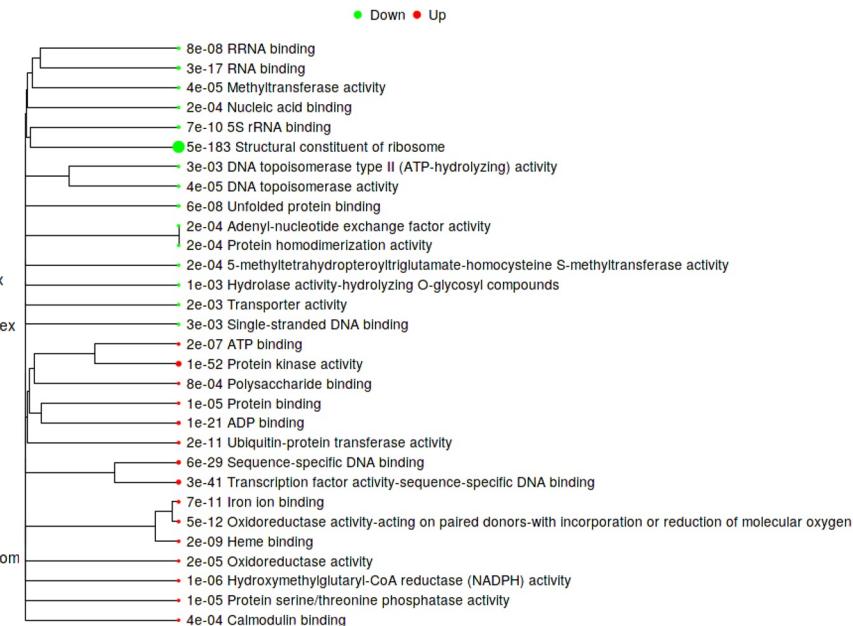
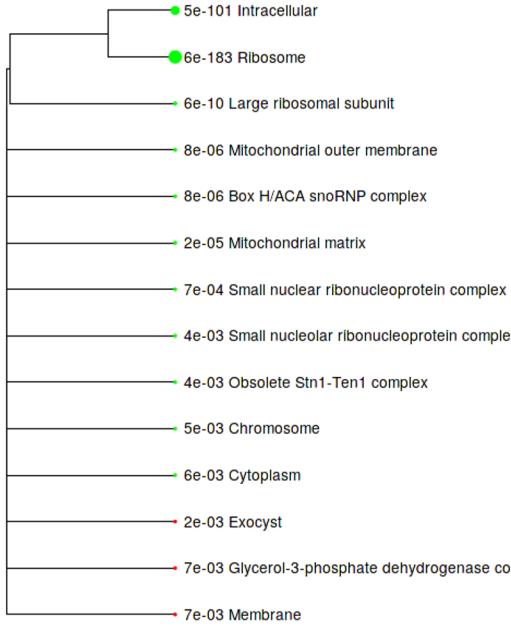
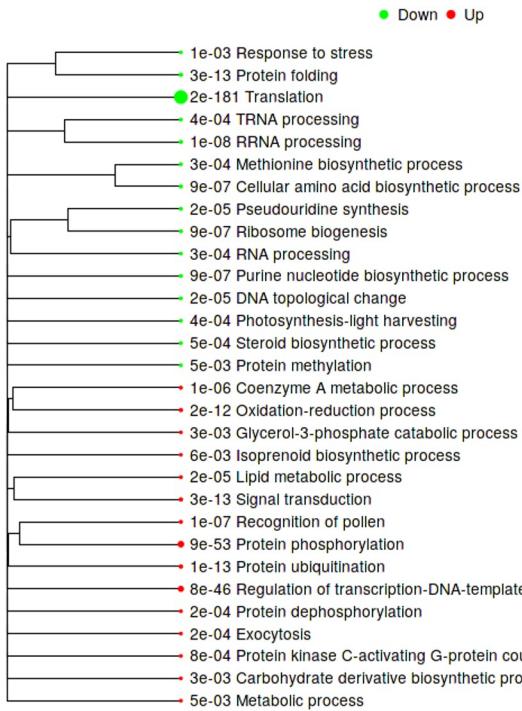
TICTOC RNAseq just WT roots and shoots

adj.Pval	Genes	Pathways
6.1e-64	41	Photosynthesis-light harvesting
3.1e-54	61	Photosynthesis
1.9e-38	149	Oxidation-reduction process
2.2e-32	114	Membrane
3.6e-31	35	Photosystem II
3.6e-31	19	Photosystem I reaction center
3.8e-27	26	Photosystem I
1.7e-24	20	Photosystem II oxygen evolving complex
2.5e-24	66	Heme binding
1.7e-22	18	Extrinsic component of membrane
6.4e-22	33	Peroxidase activity
7.1e-22	34	Response to oxidative stress
2.4e-19	71	Oxidoreductase activity
1.1e-10	8	Fructose-bisphosphate aldolase activity
5.0e-10	7	Thylakoid membrane

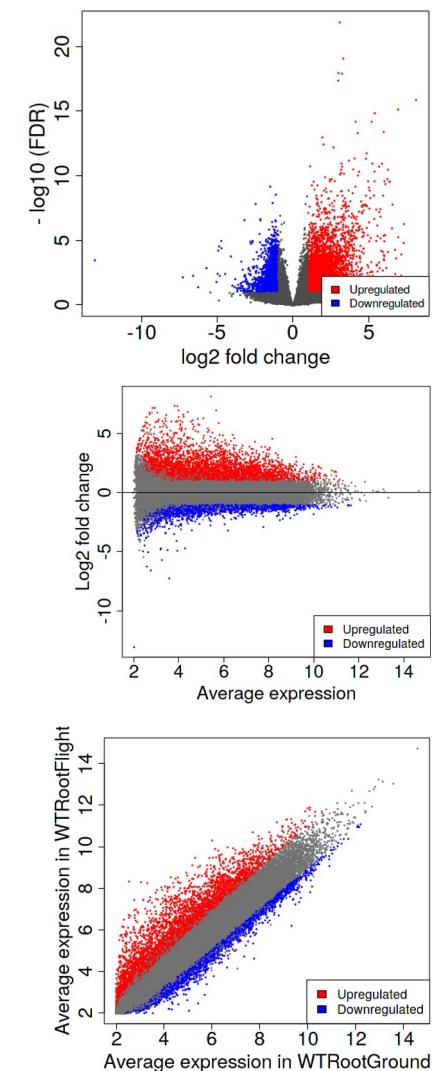
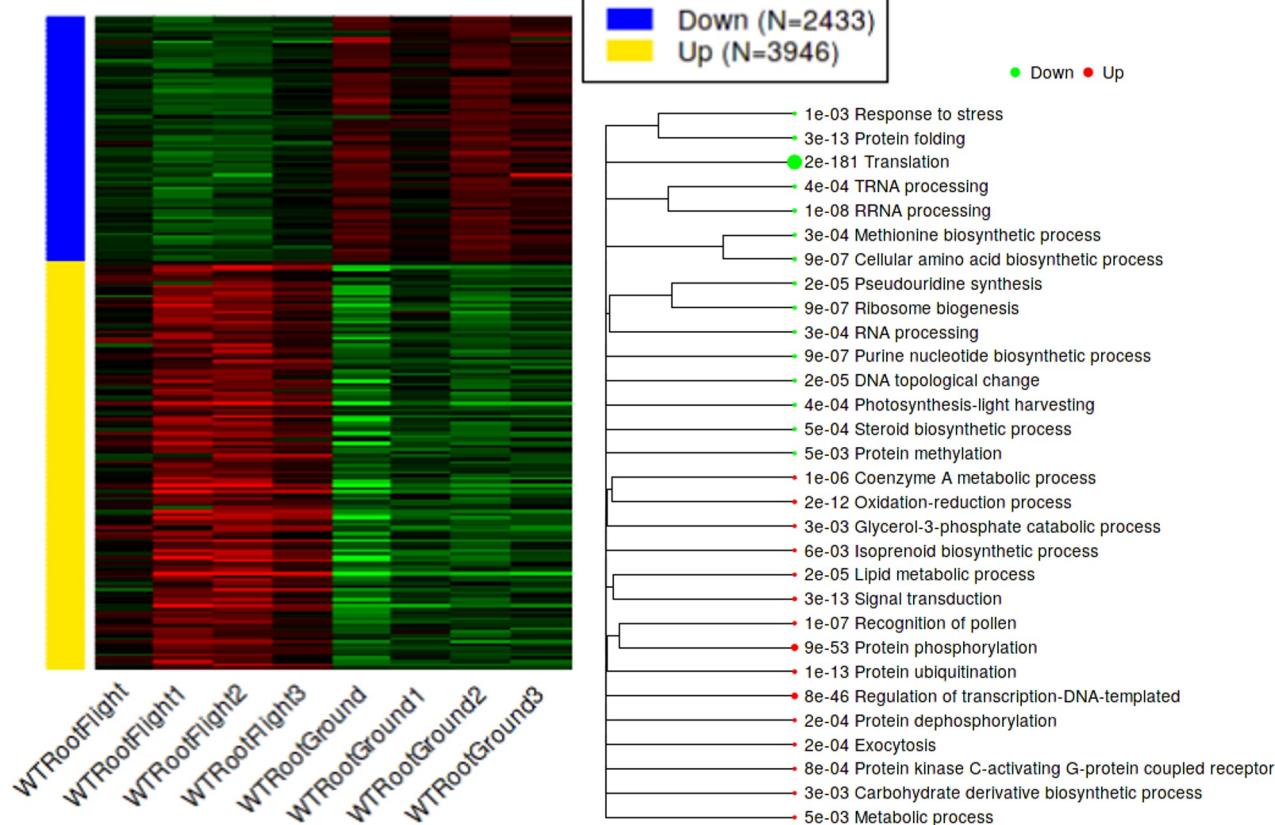


TICTOC RNAseq just WT Root

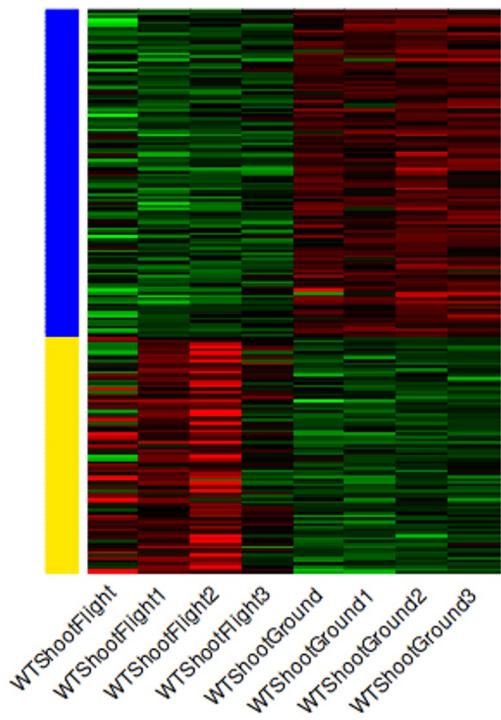
● Down ● Up



TICTOC RNAseq just WT Root



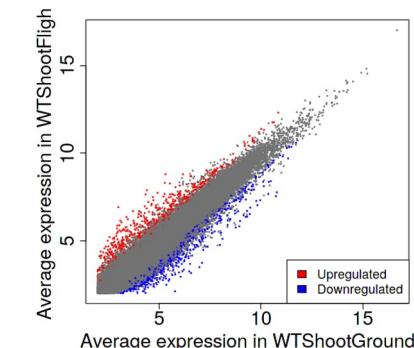
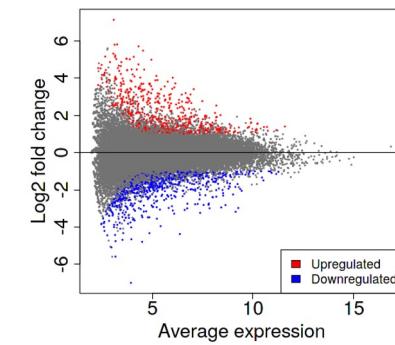
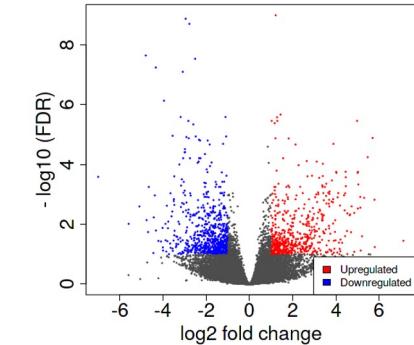
TICTOC RNAseq just WT Shoot



Down (N=740)
Up (N=580)

● Down ● Up

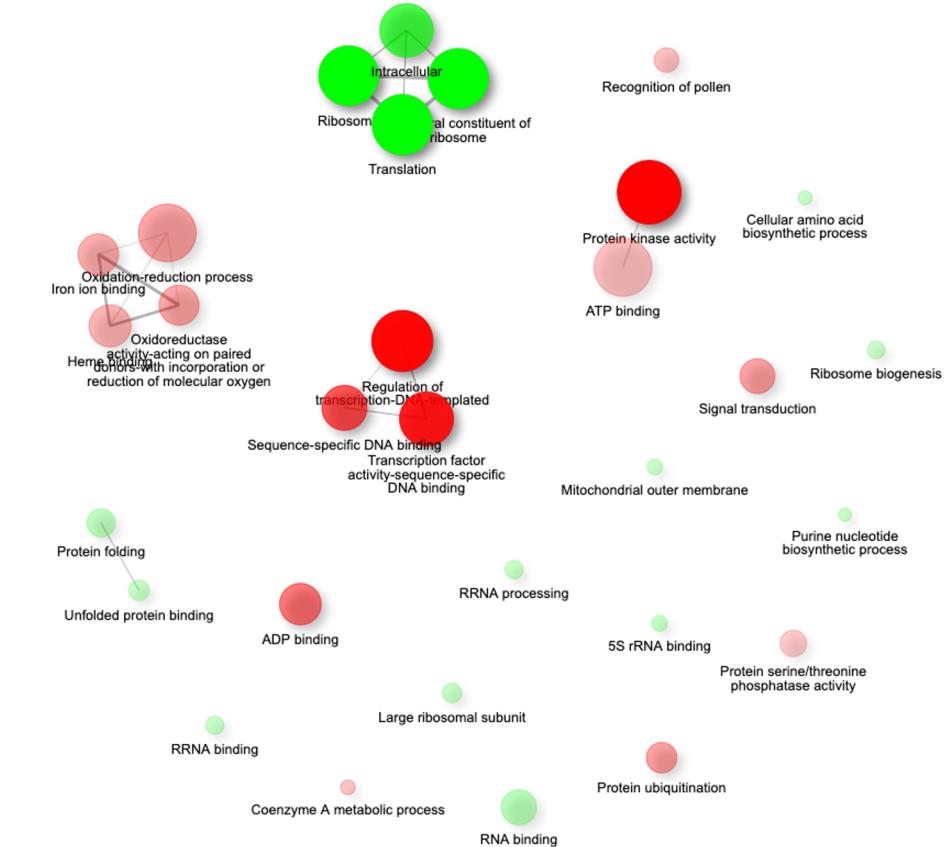
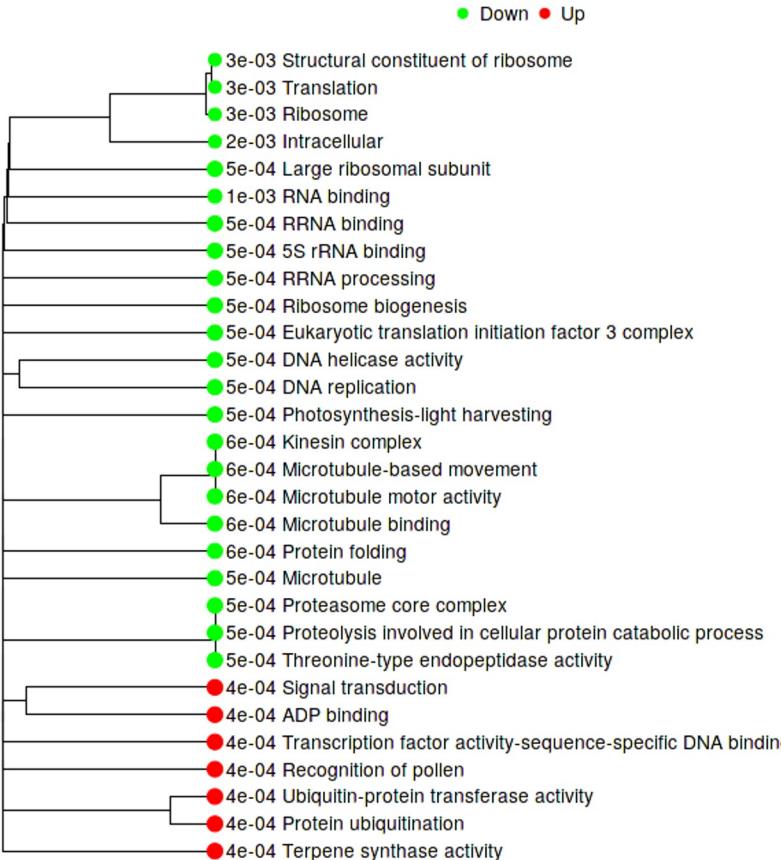
- 9e-03 Steroid biosynthetic process
- 2e-03 Oxidation-reduction process
- 5e-03 Protein repair
- 9e-03 Fatty acid biosynthetic process
- 4e-03 Drug transmembrane transport
- 1e-04 Transmembrane transport
- 9e-03 Transport
- 9e-03 Ion transport
- 4e-03 Lipid biosynthetic process
- 4e-03 Phospholipid transport
- 9e-03 Anion transport
- 9e-03 Carbohydrate metabolic process
- 8e-04 Oxidation-reduction process
- 5e-06 Coenzyme A metabolic process
- 2e-05 Protein ubiquitination
- 1e-04 RNA processing
- 1e-04 Protein folding
- 1e-04 Regulation of transcription-DNA-templated
- 5e-04 Protein dephosphorylation
- 7e-03 Proteolysis involved in cellular protein catabolic process



TICTOC RNAseq just WT Root

GSEA preranked fgsea

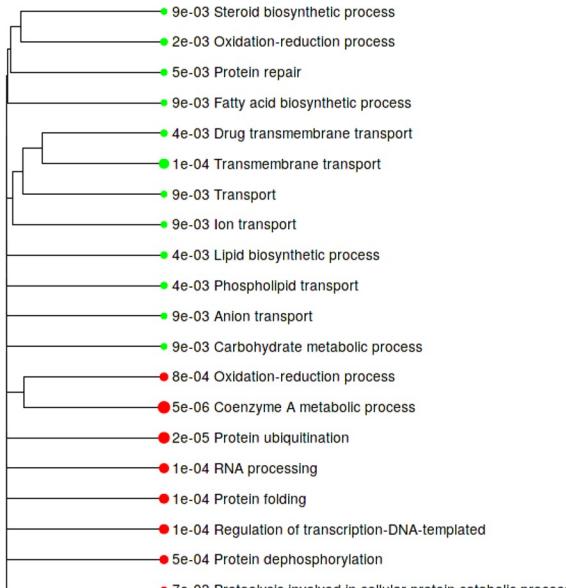
Top 300 including all GoCellular site, GoBiological process and Molecular function



TICTOC RNAseq just WT Shoot

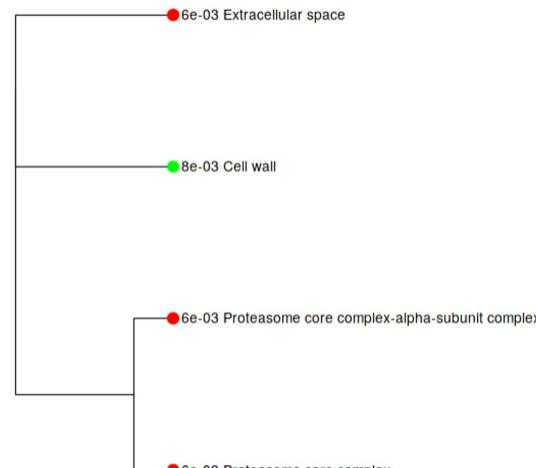
GoBiological process

● Down ● Up



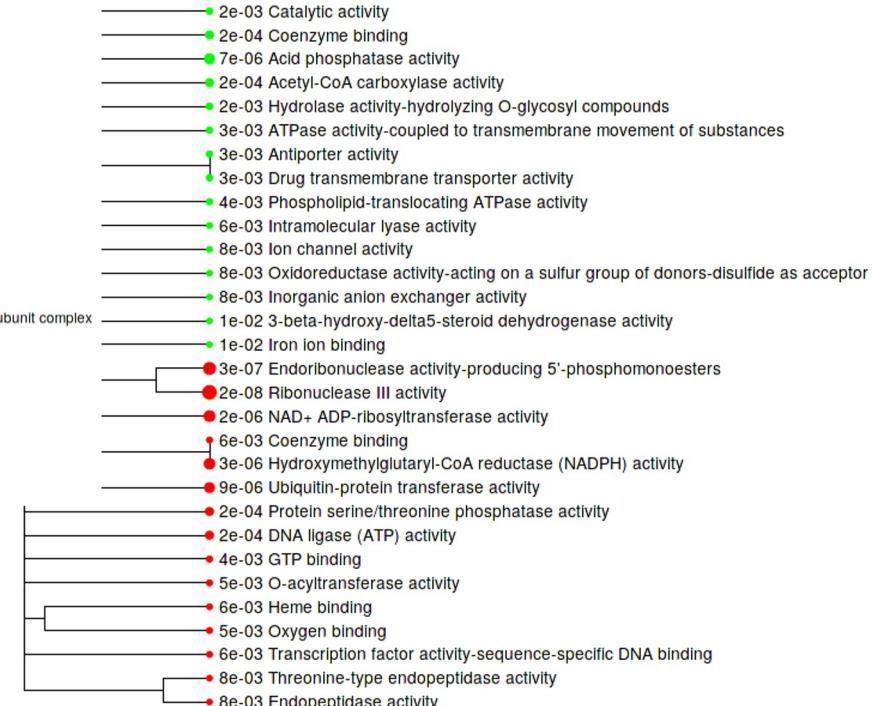
GoCellular site

● Down ● Up



Molecular function

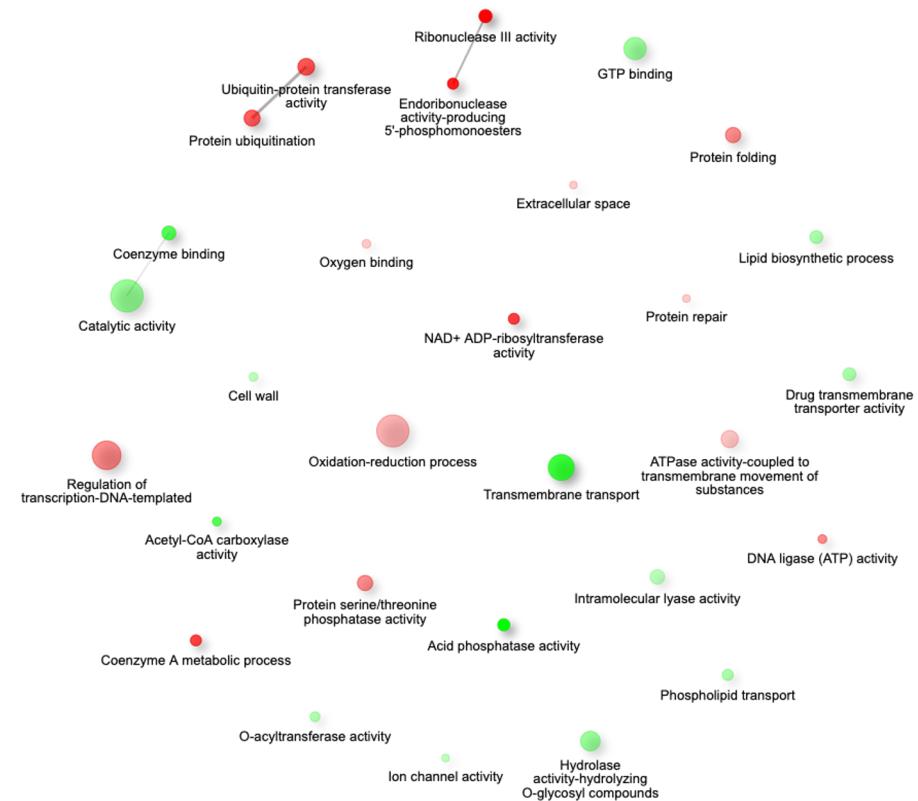
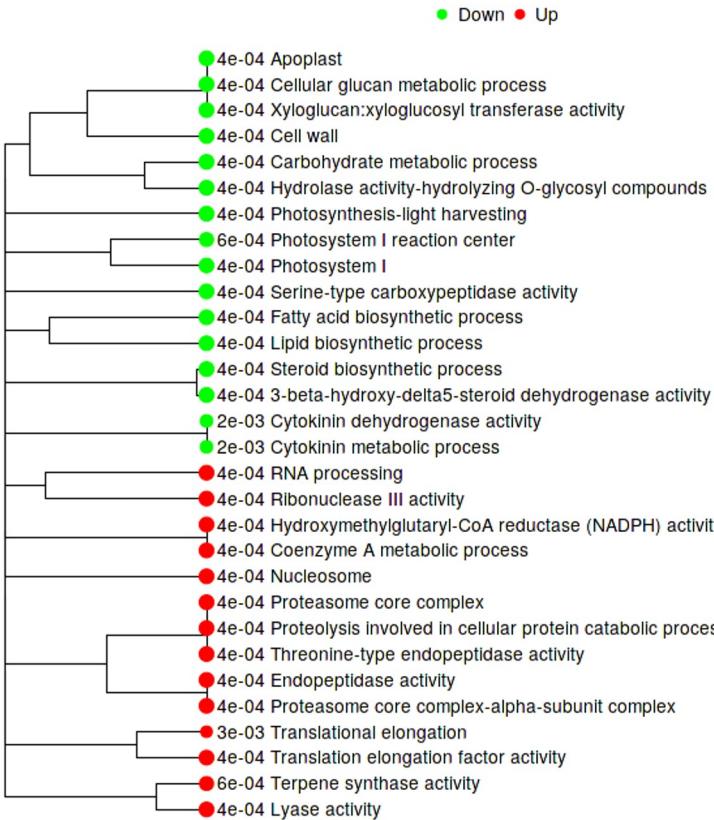
● Down ● Up



TICTOC RNAseq just WT Shoot

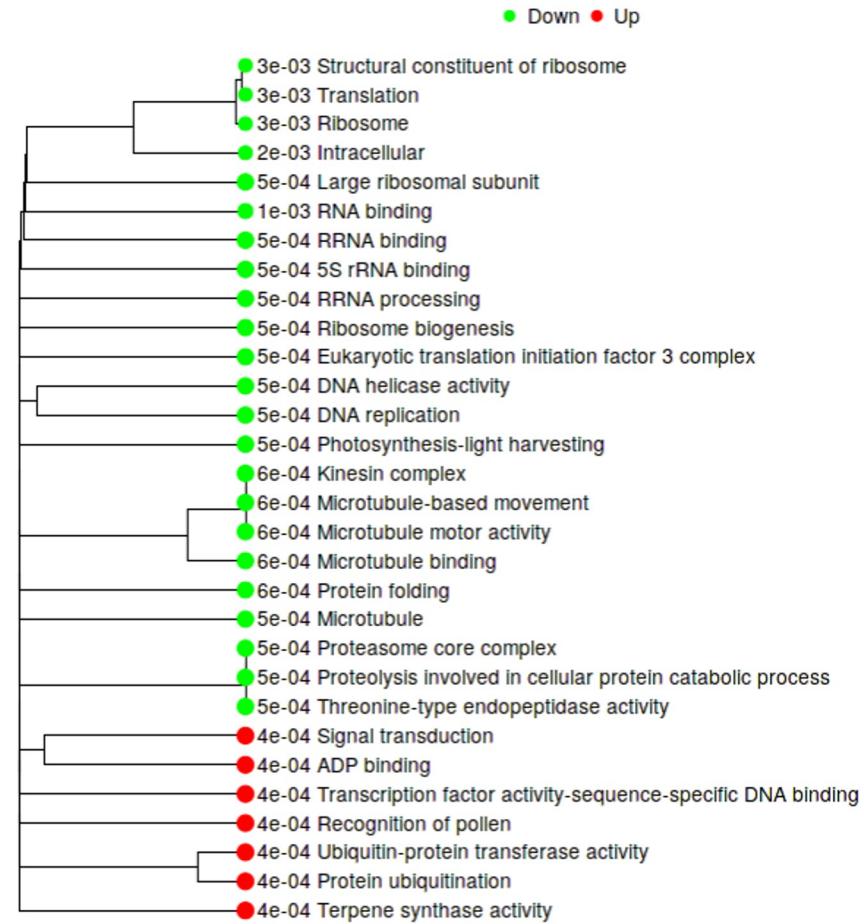
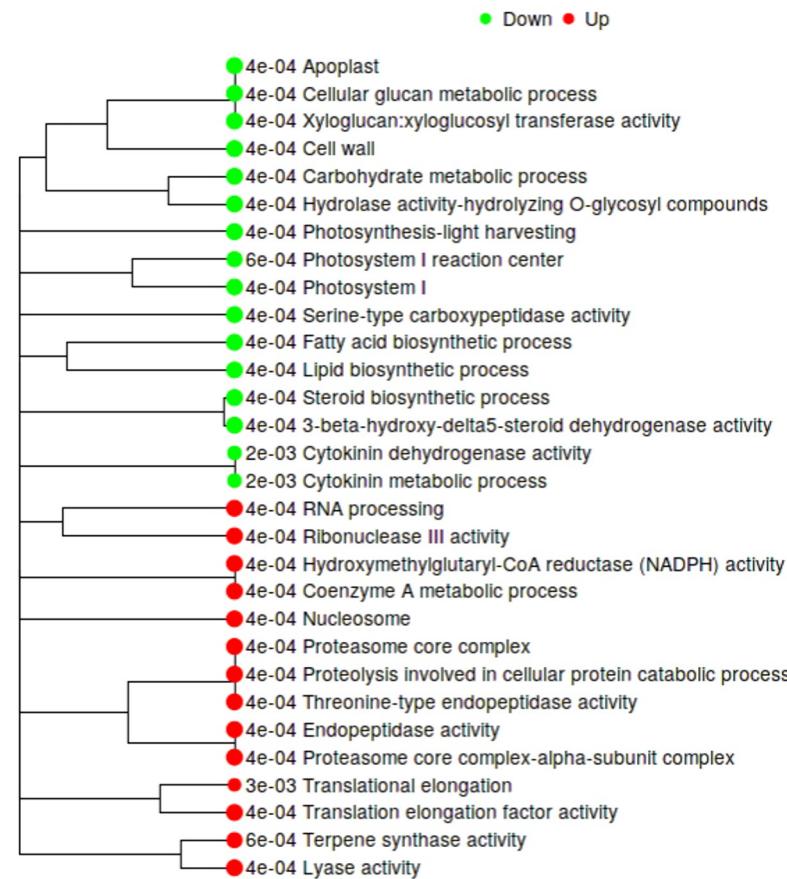
GSEA preranked fgsea

Top 300 including all GoCellular site, GoBiological process and Molecular function

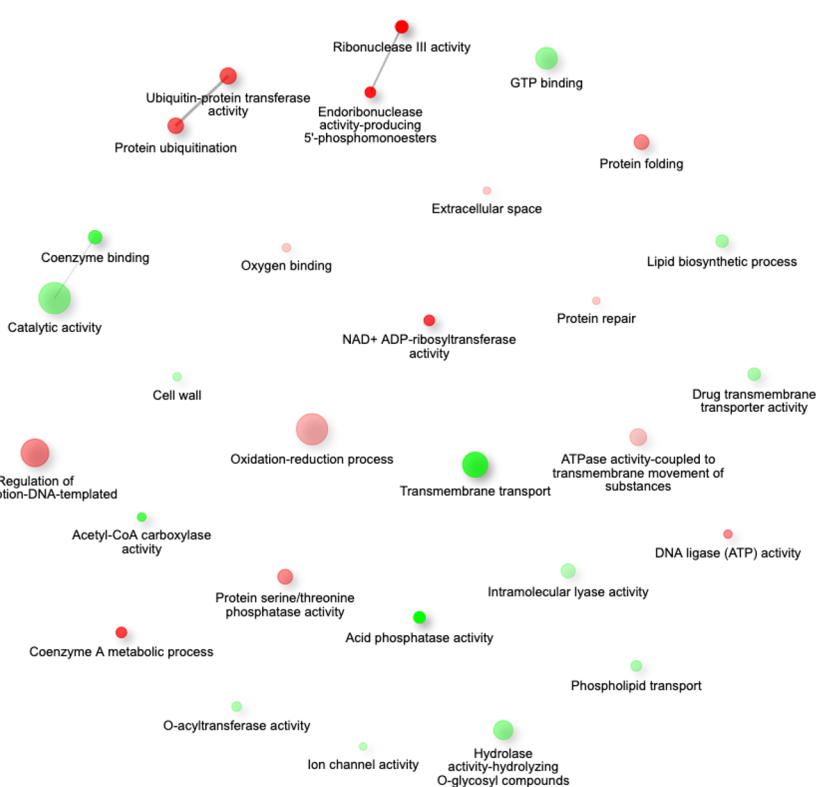


TICTOC RNAseq just WT Shoot

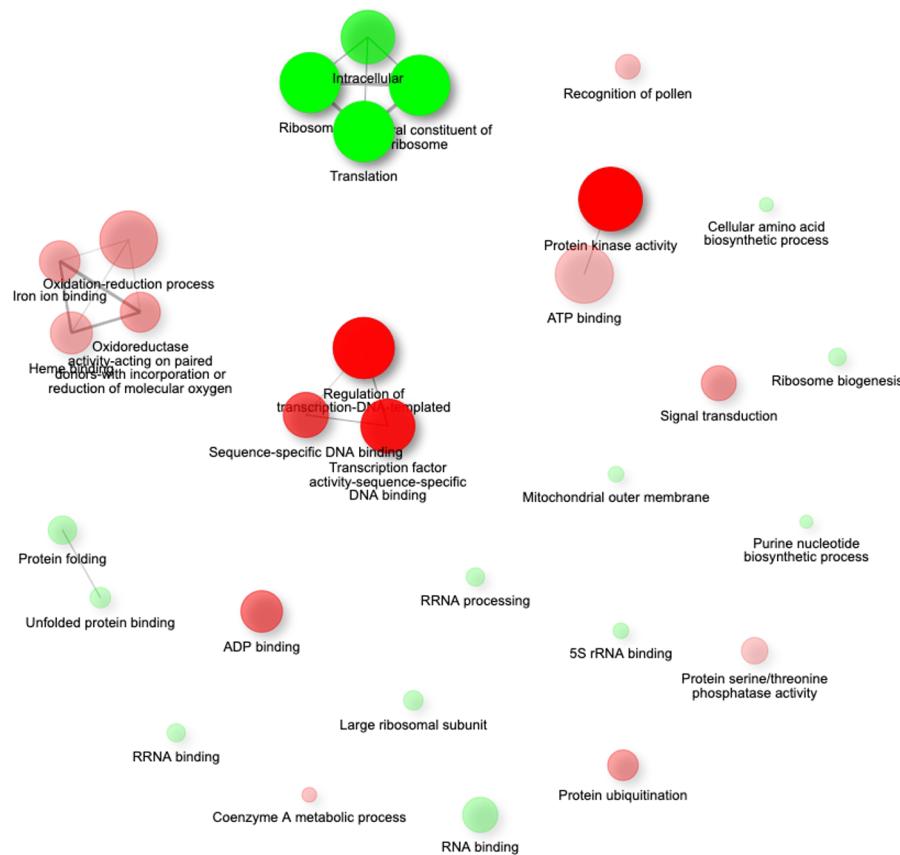
TICTOC RNAseq just WT Root



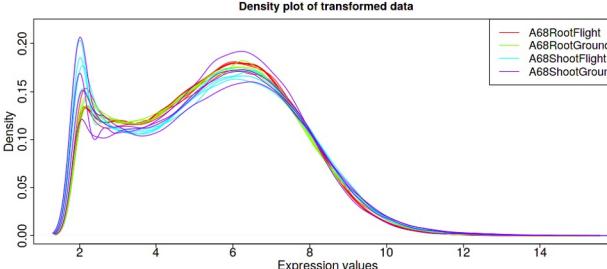
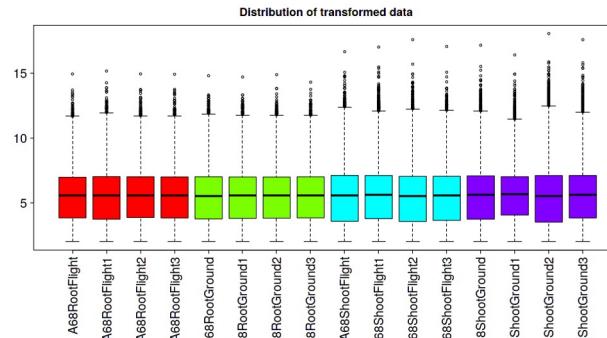
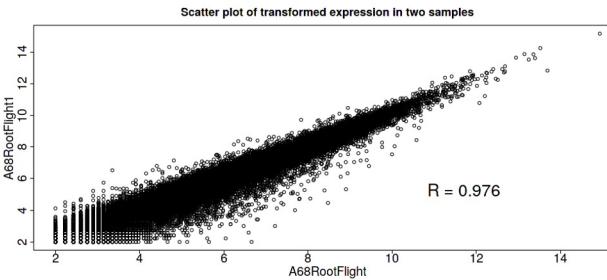
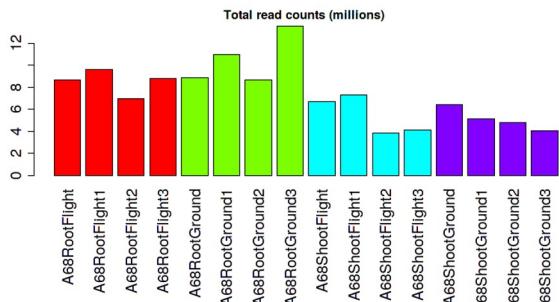
TICTOC RNAseq just WT Shoot



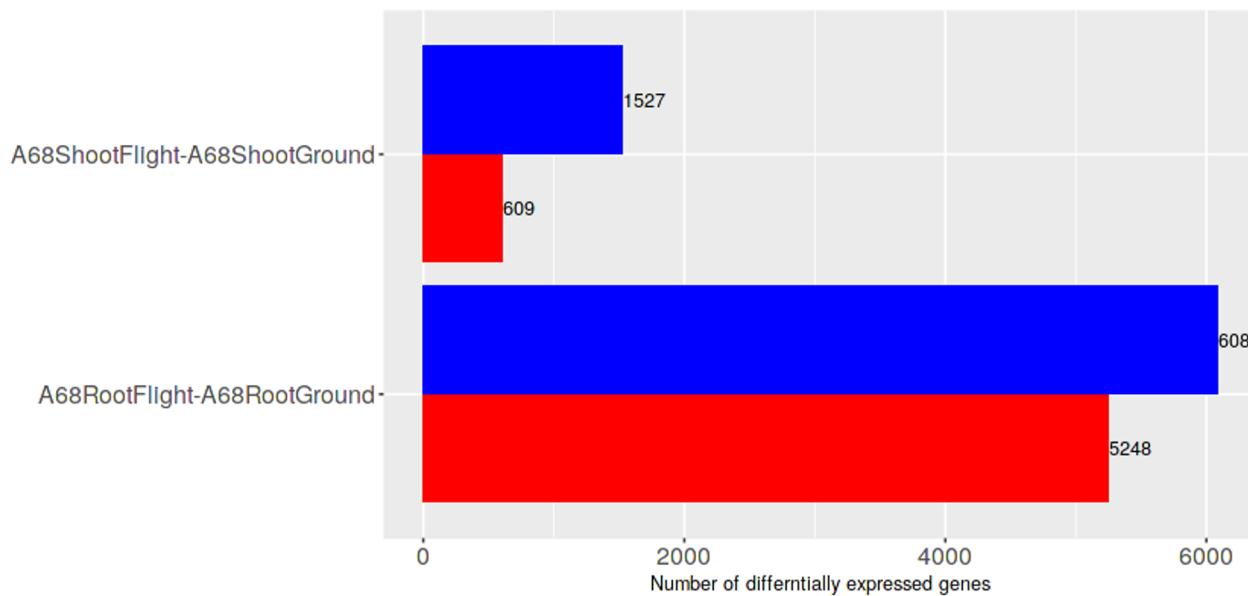
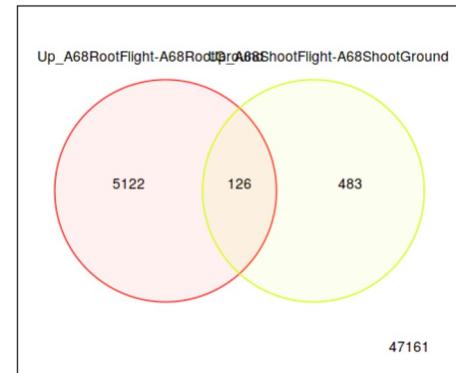
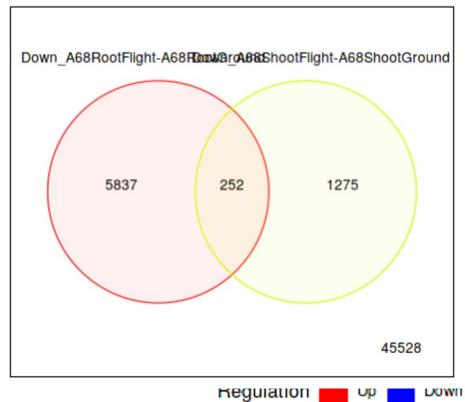
TICTOC RNAseq just WT Root



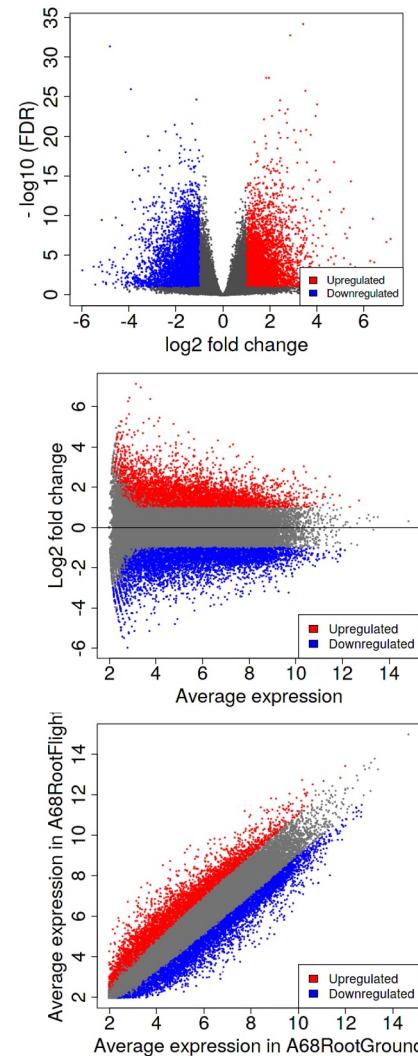
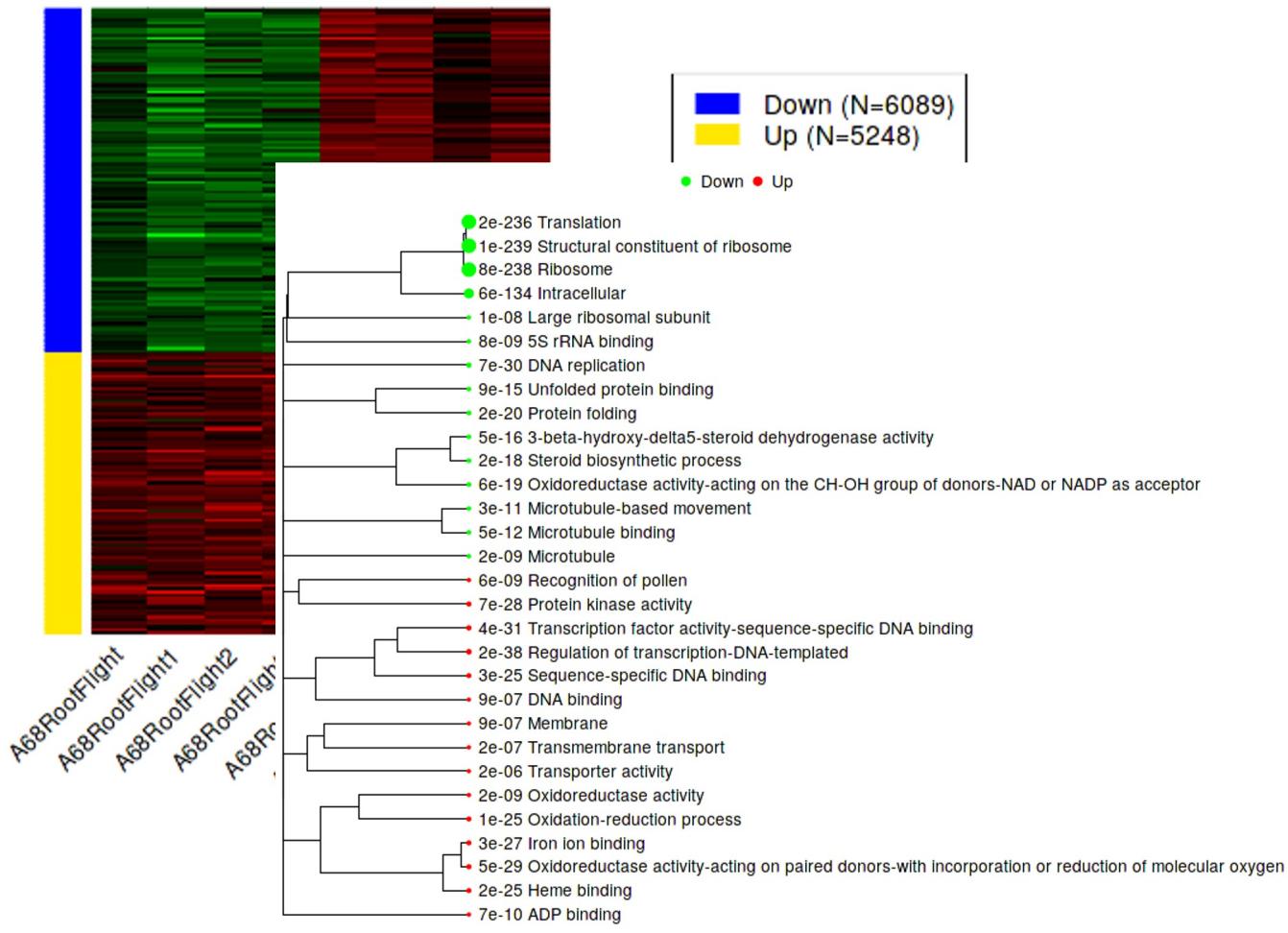
TICTOC RNAseq just A68 Root and shoot



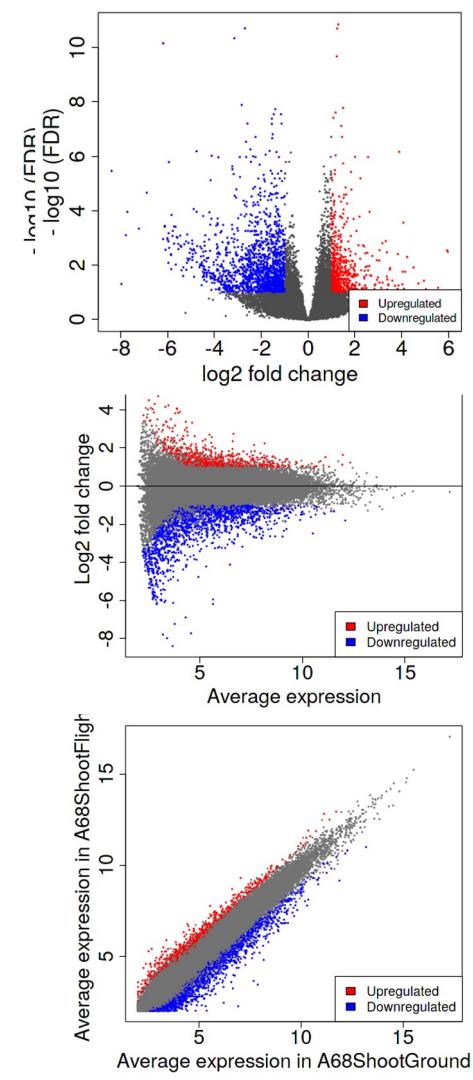
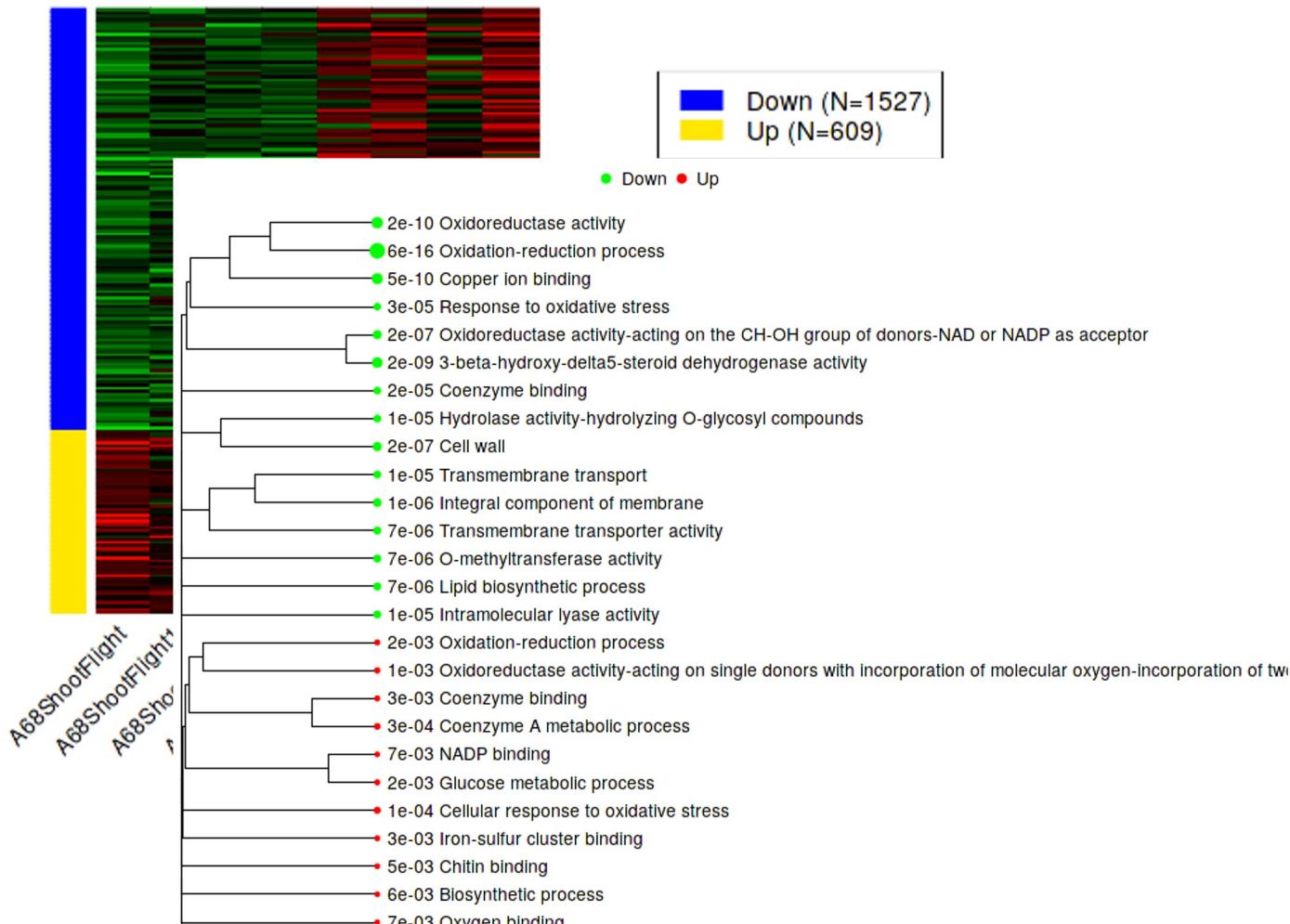
TICTOC RNAseq just A68 Root and shoot



TICTOC RNAseq just A68 Root

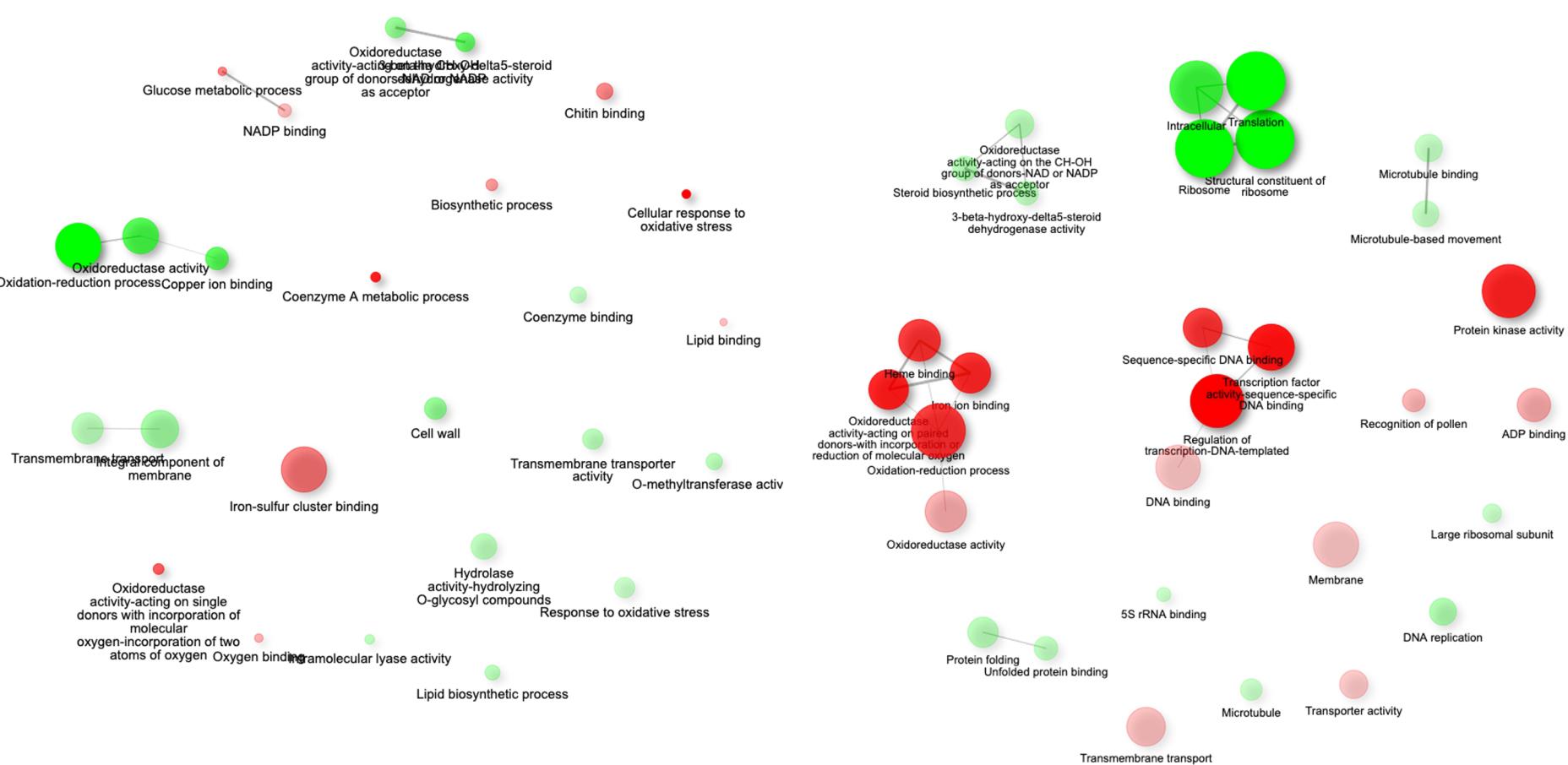


TICTOC RNAseq just A68 Shoot



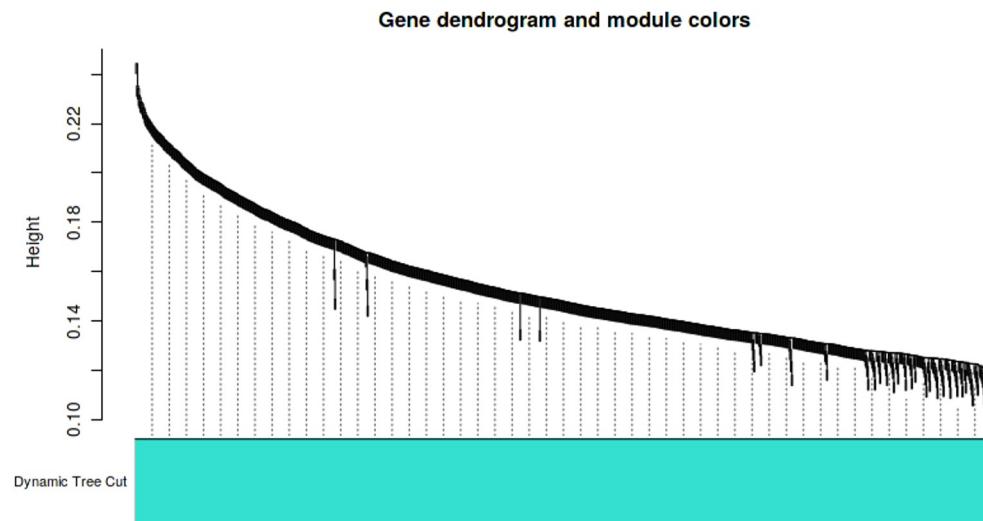
TICTOC RNAseq just A68 Shoot

TICTOC RNAseq just A68 Root

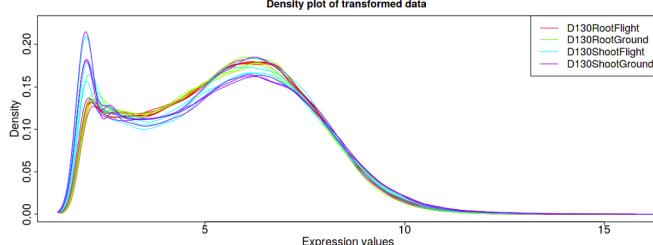
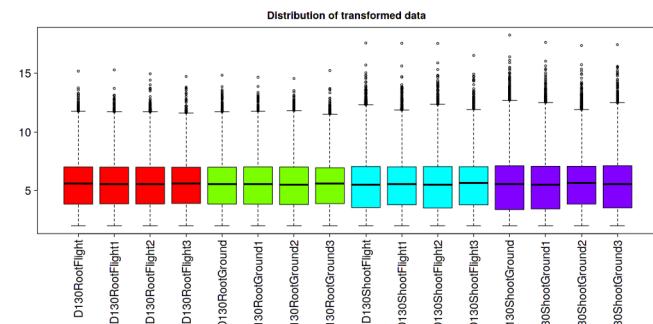
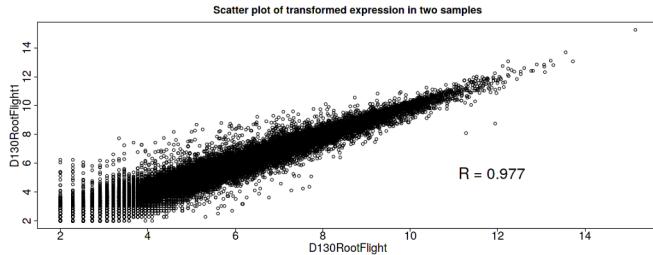
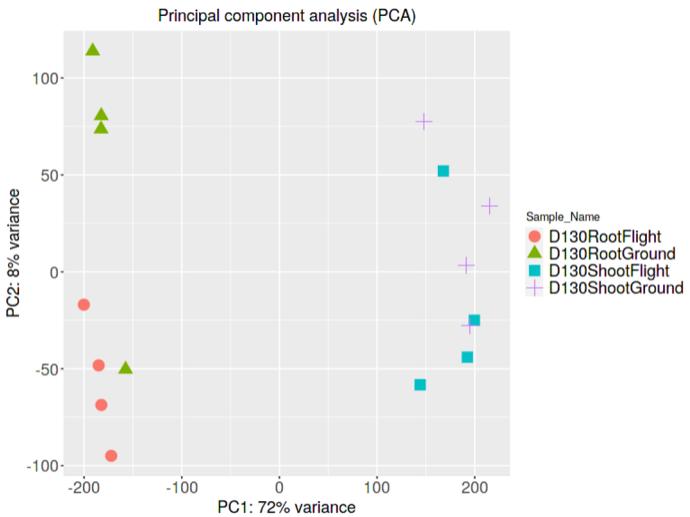
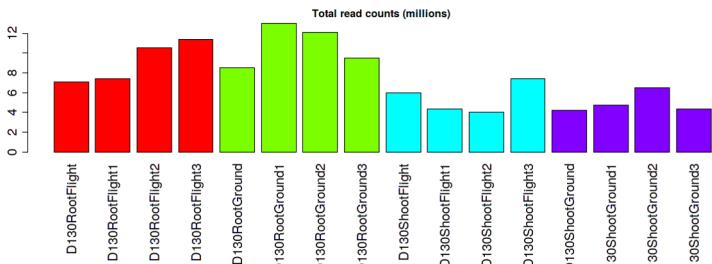


TICTOC RNAseq just A68 Roots and Shoot

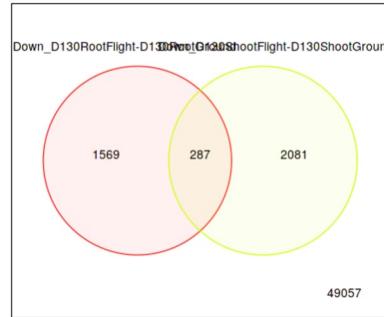
adj.Pval	Genes	Pathways
1.9e-57	38	Photosynthesis-light harvesting
5.6e-52	59	Photosynthesis
3.9e-40	151	Oxidation-reduction process
7.4e-22	34	Response to oxidative stress
4.2e-06	10	Response to biotic stimulus
2.9e-05	25	Transport
3.7e-05	40	Metabolic process
1.2e-04	10	Fatty acid biosynthetic process
1.2e-04	3	Plant-type cell wall organization
1.3e-04	10	Defense response
2.2e-04	4	Cellular ion homeostasis
5.1e-04	3	Glycine catabolic process
6.6e-04	2	Pyruvate metabolic process
9.7e-04	8	Glycolytic process
1.2e-03	4	Sucrose metabolic process



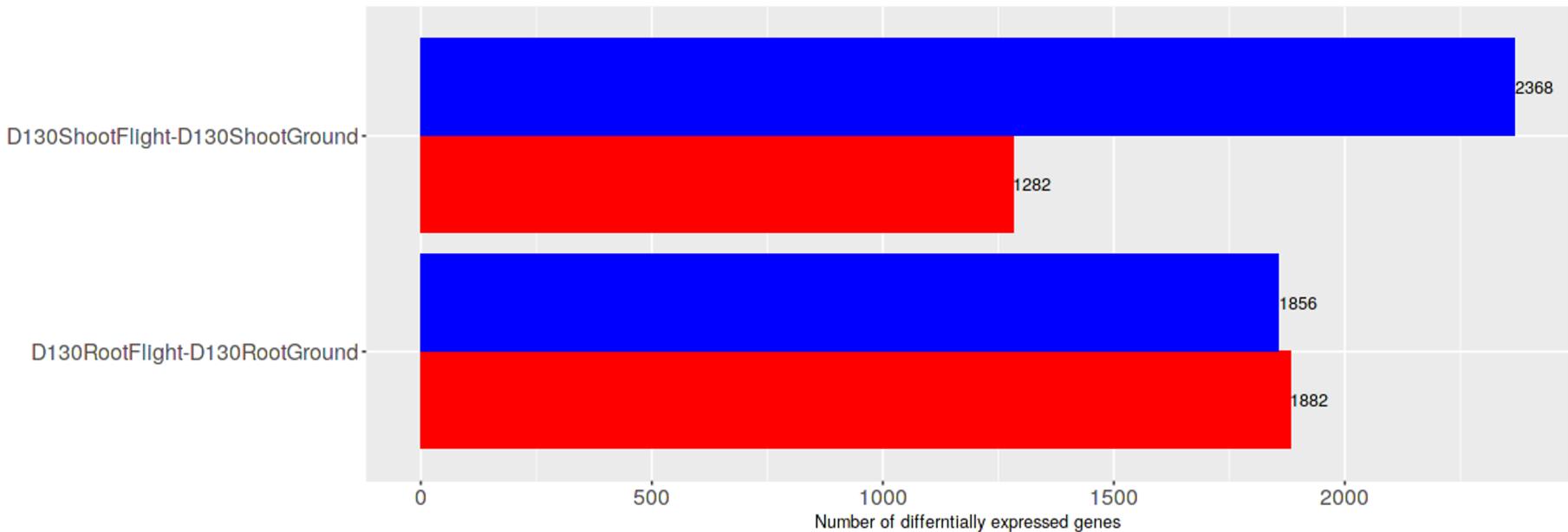
TICTOC RNAseq just D130 Roots and Shoot



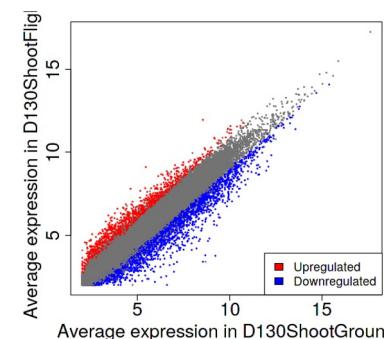
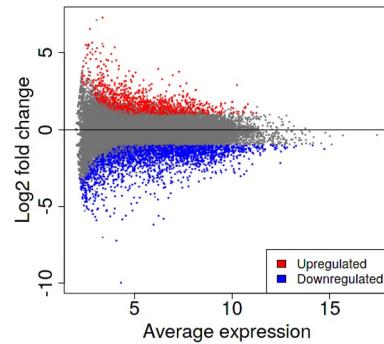
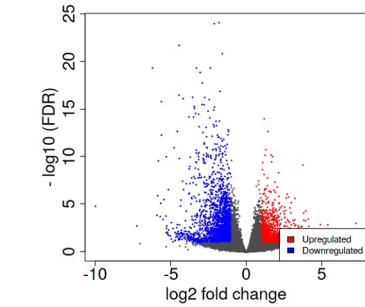
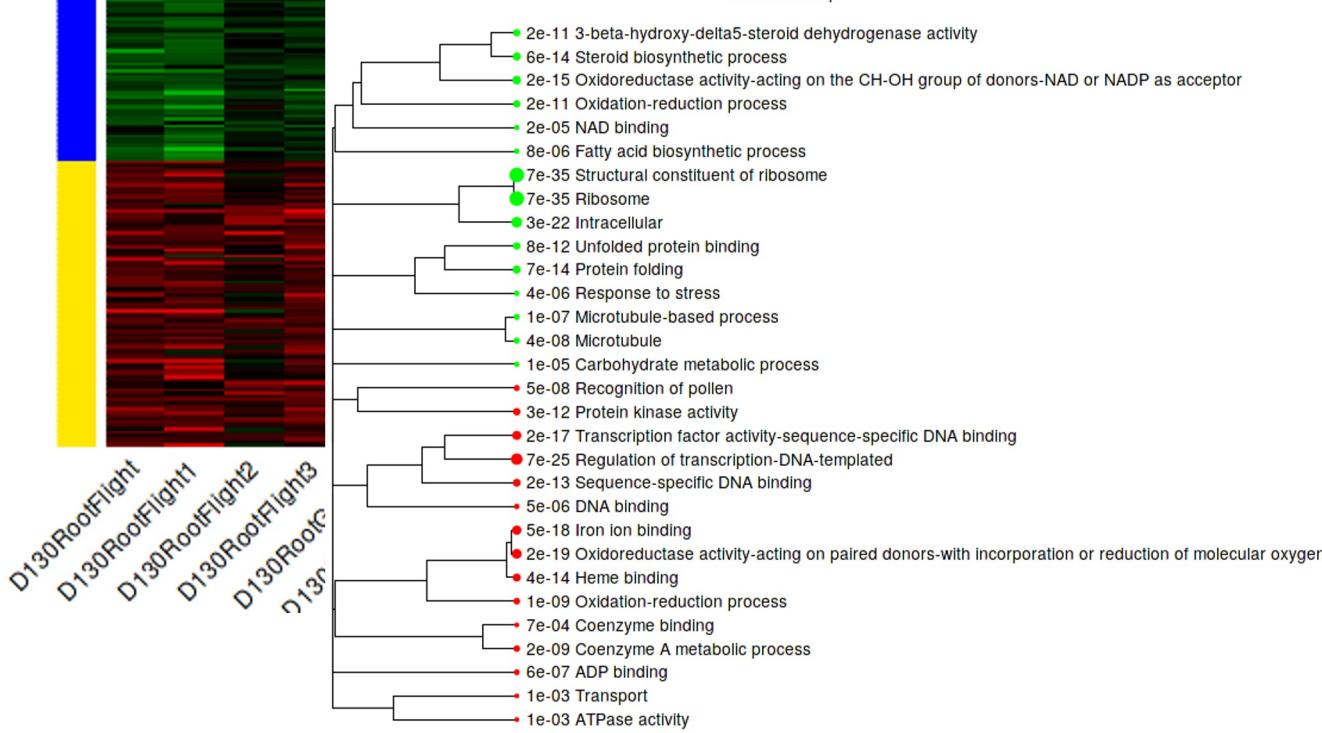
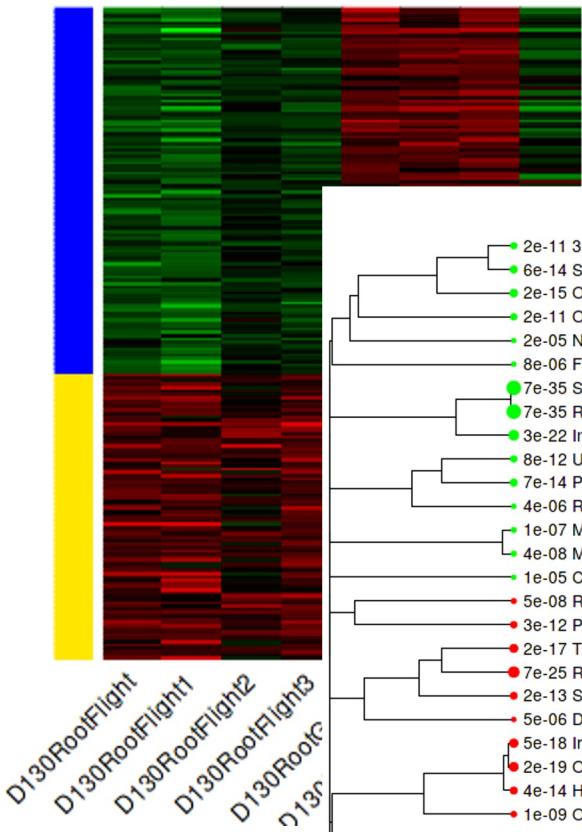
TICTOC RNAseq just D130 Roots and Shoot



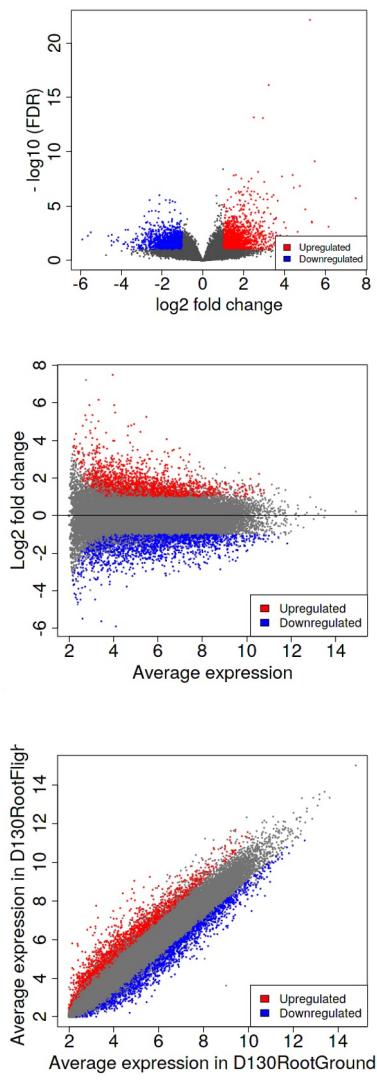
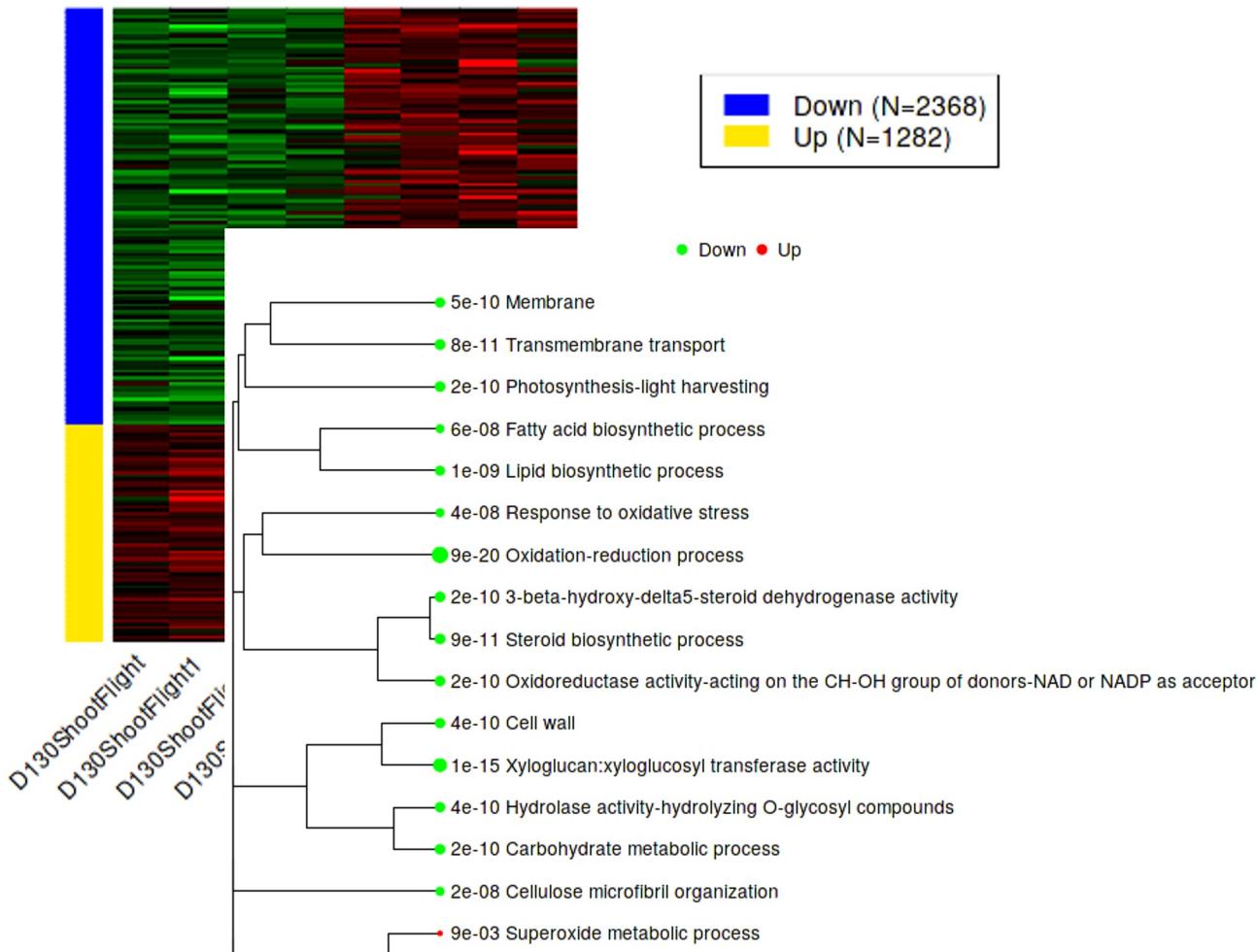
Regulation ■ Up ■ Down



TICTOC RNAseq just D130 Roots

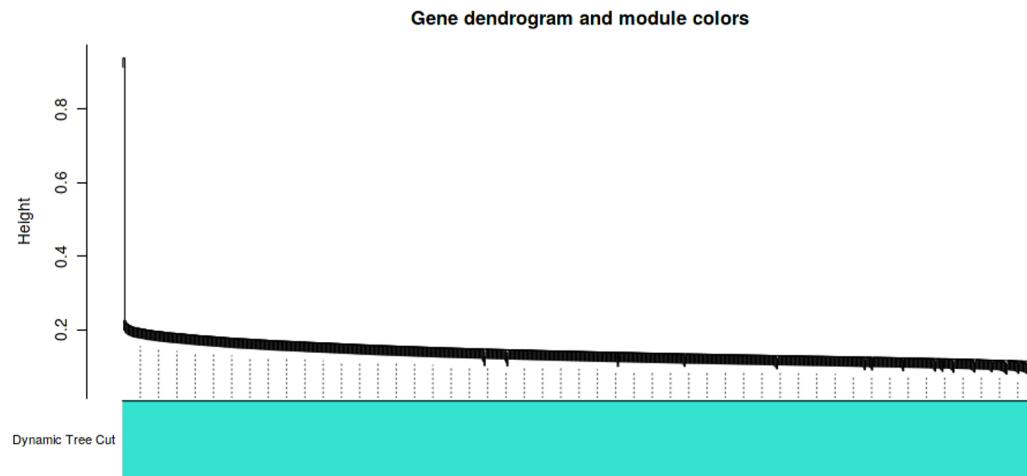


TICTOC RNAseq just D130 Shoot

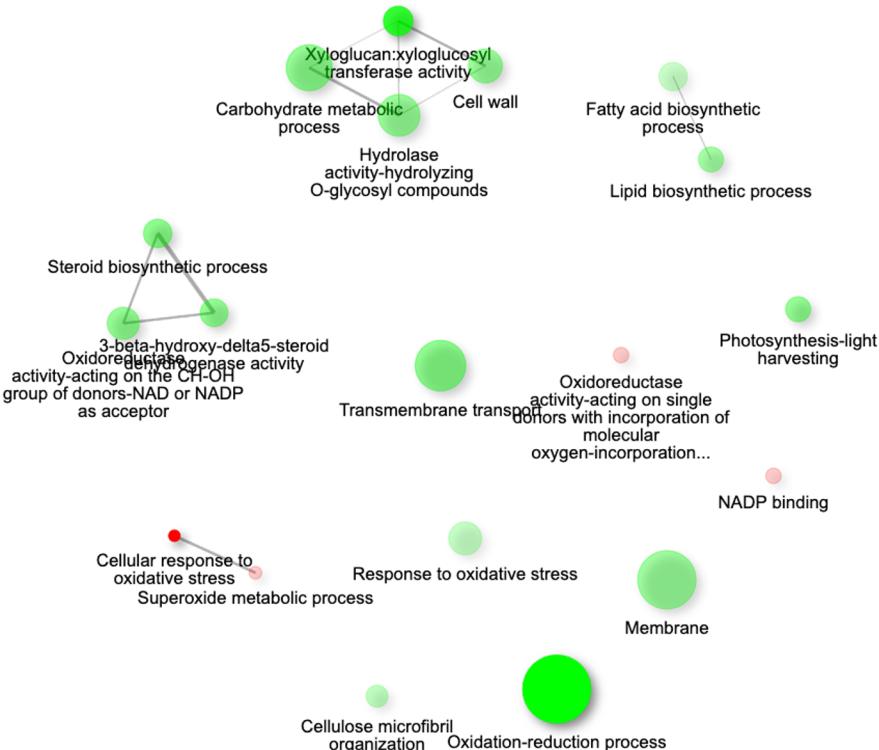


TICTOC RNAseq just D130 Roots and Shoot

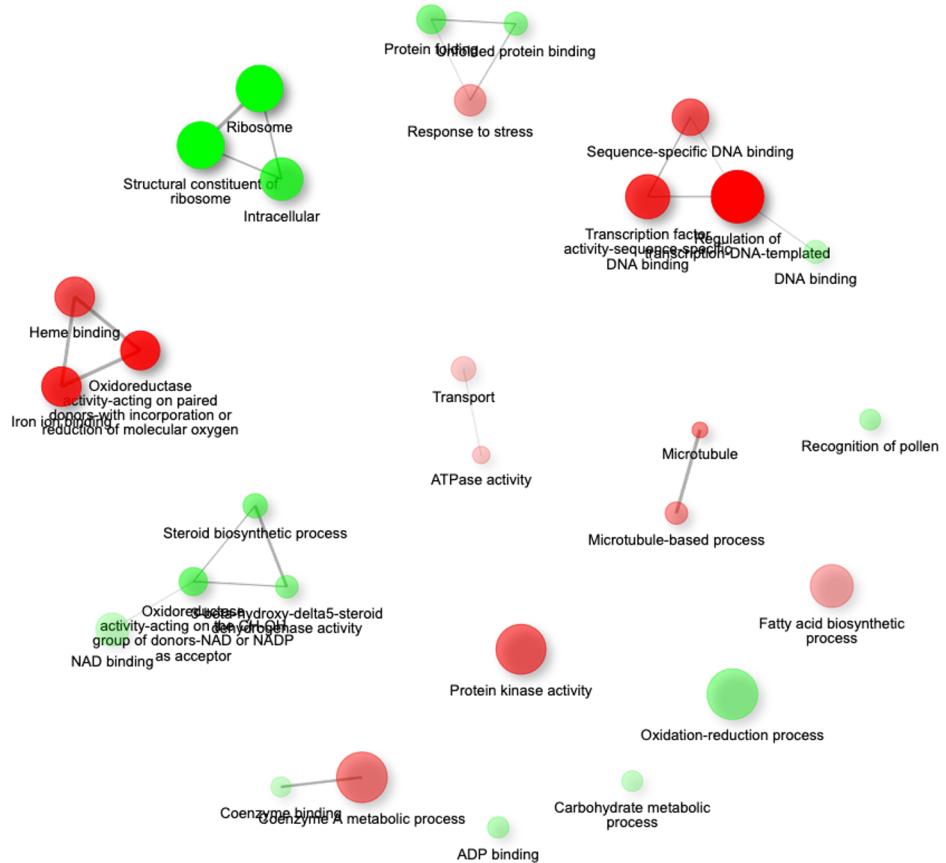
adj.Pval	Genes	Pathways
2.9e-59	39	Photosynthesis-light harvesting
1.7e-47	56	Photosynthesis
1.9e-43	157	Oxidation-reduction process
5.7e-35	118	Membrane
1.2e-28	18	Photosystem I reaction center
3.8e-27	70	Heme binding
5.3e-26	31	Photosystem II
1.1e-25	25	Photosystem I
6.3e-23	77	Oxidoreductase activity
7.1e-22	33	Peroxidase activity
7.9e-22	34	Response to oxidative stress
2.6e-16	15	Photosystem II oxygen evolving complex
3.5e-14	13	Extrinsic component of membrane
6.2e-12	42	Iron ion binding
4.6e-11	38	Oxidoreductase activity-acting on paired donors-with incorporation or reduction of molecular oxygen



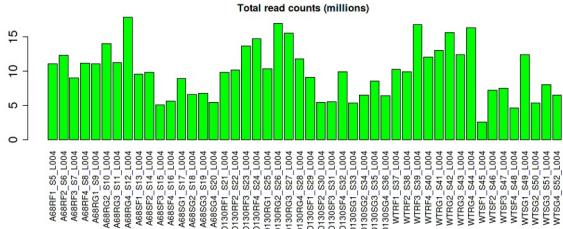
TICTOC RNAseq just D130 Shoot



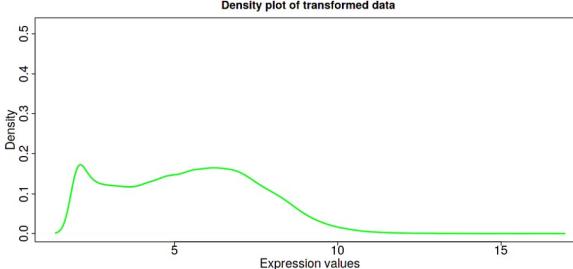
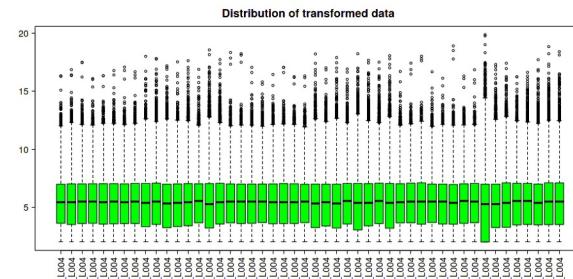
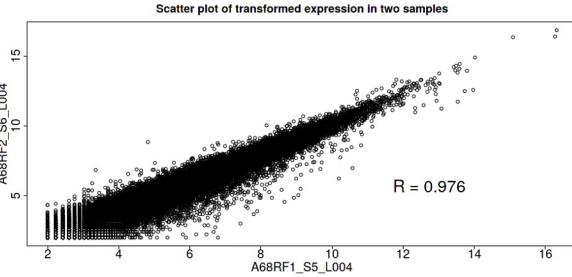
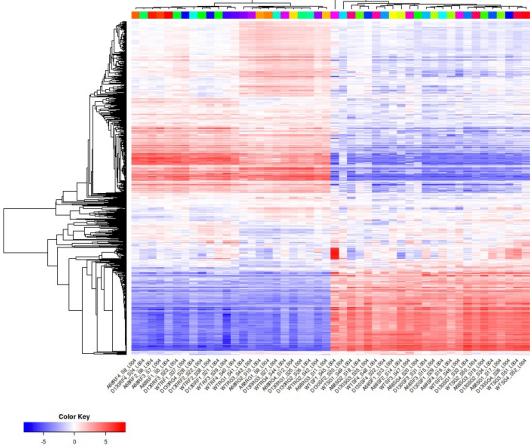
TICTOC RNAseq just D130 Root



Alignment Version 2



92479 genes in 48 samples. Of the 61955 genes passed filter (see above), 0 were converted to Ensembl gene IDs in our database. The remaining 61955 genes were kept in the data using original IDs.



Gene dendrogram and module colors

