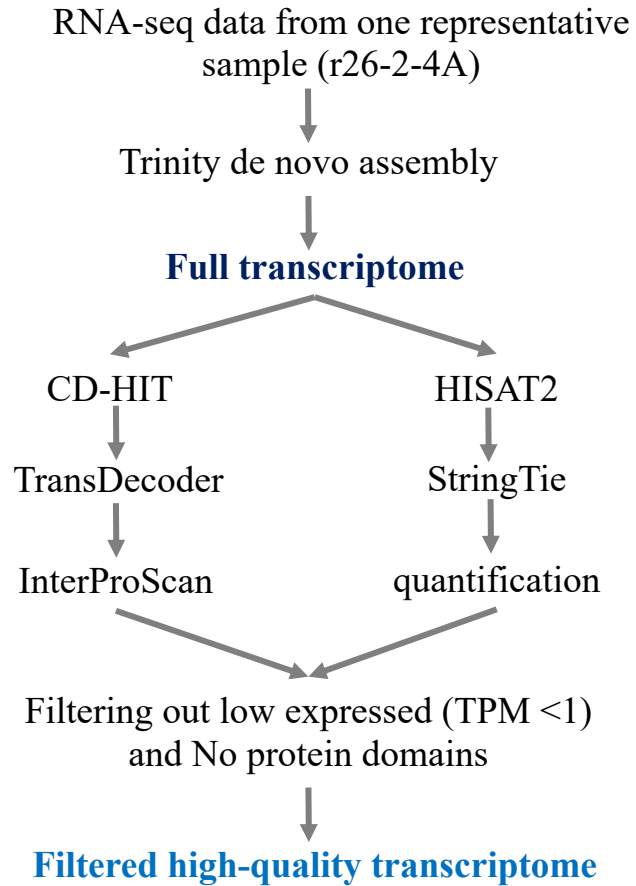
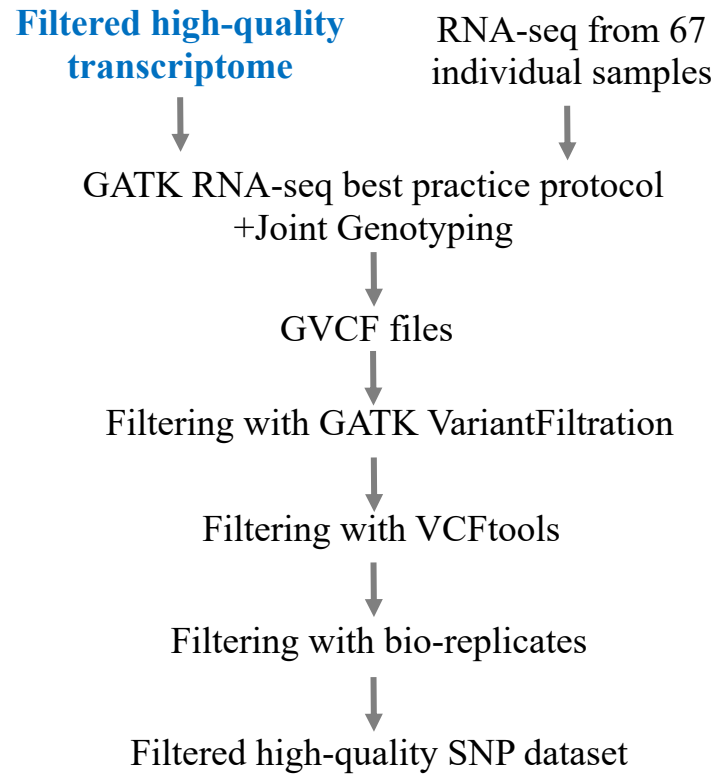


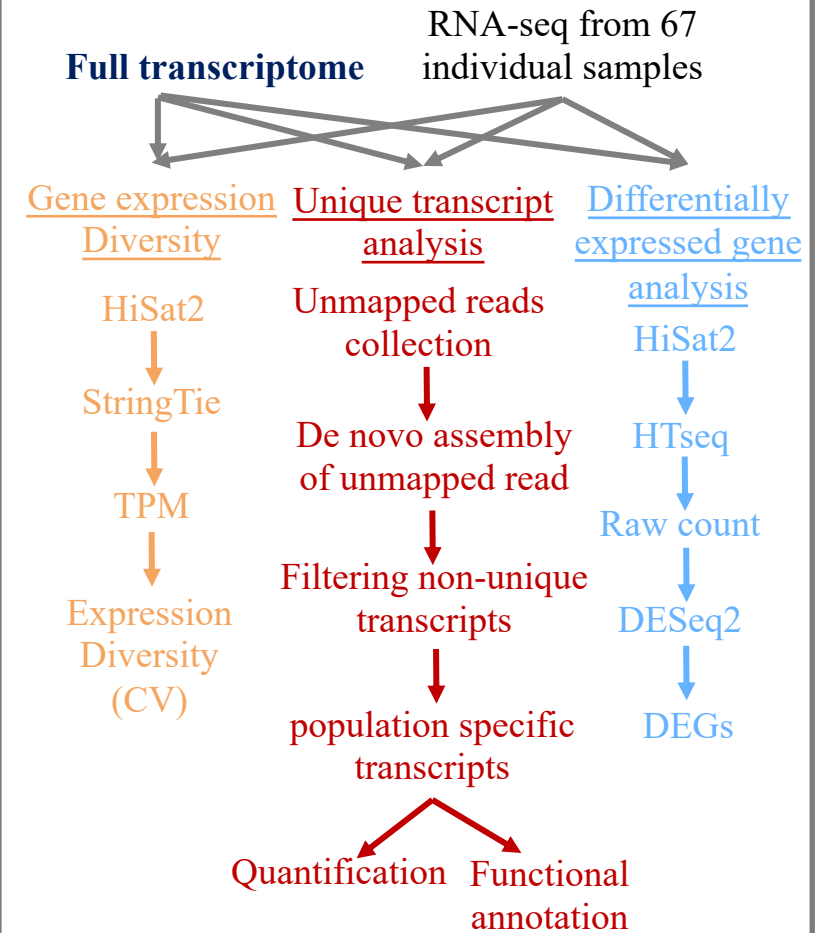
Reference transcriptome establishment



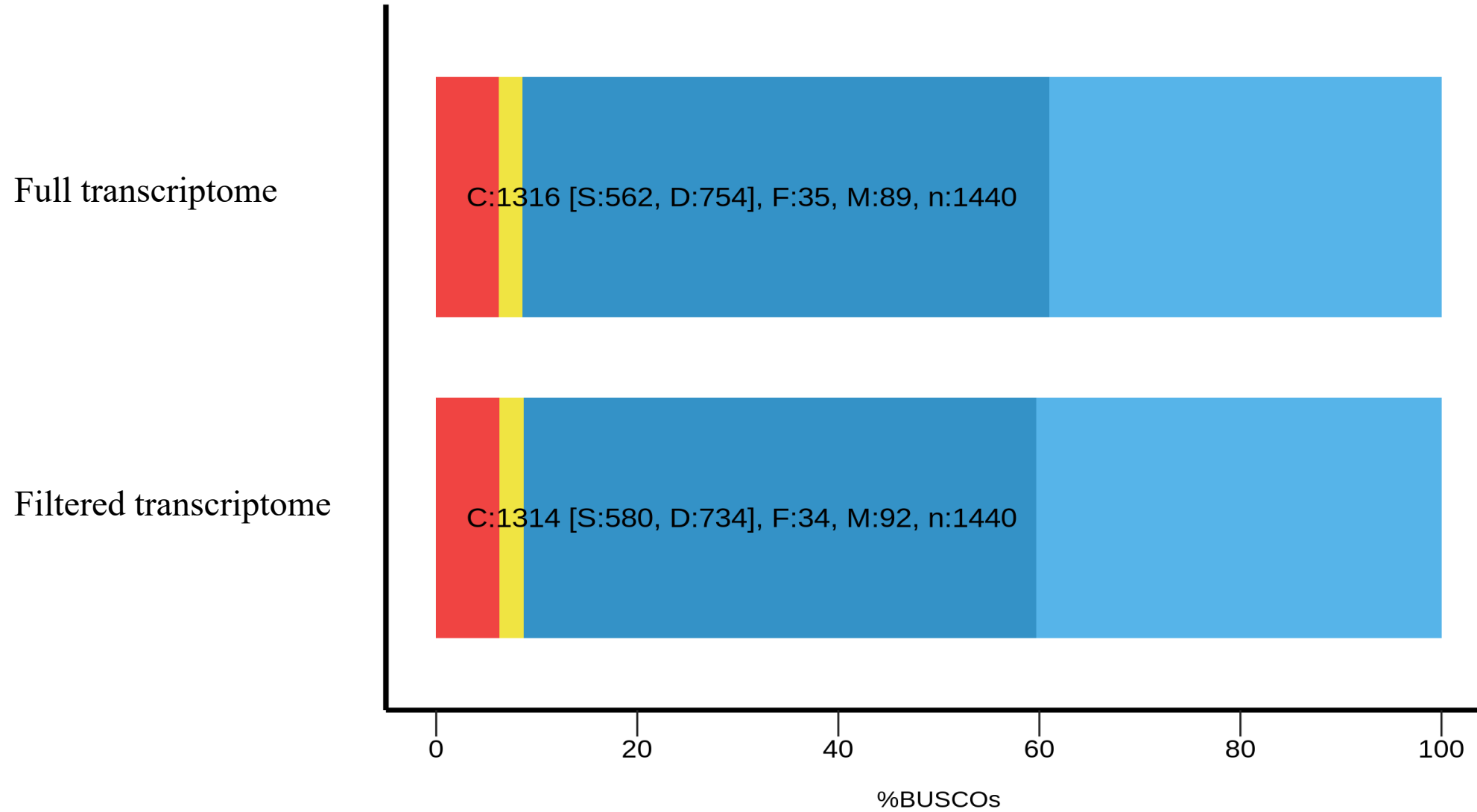
SNP calling

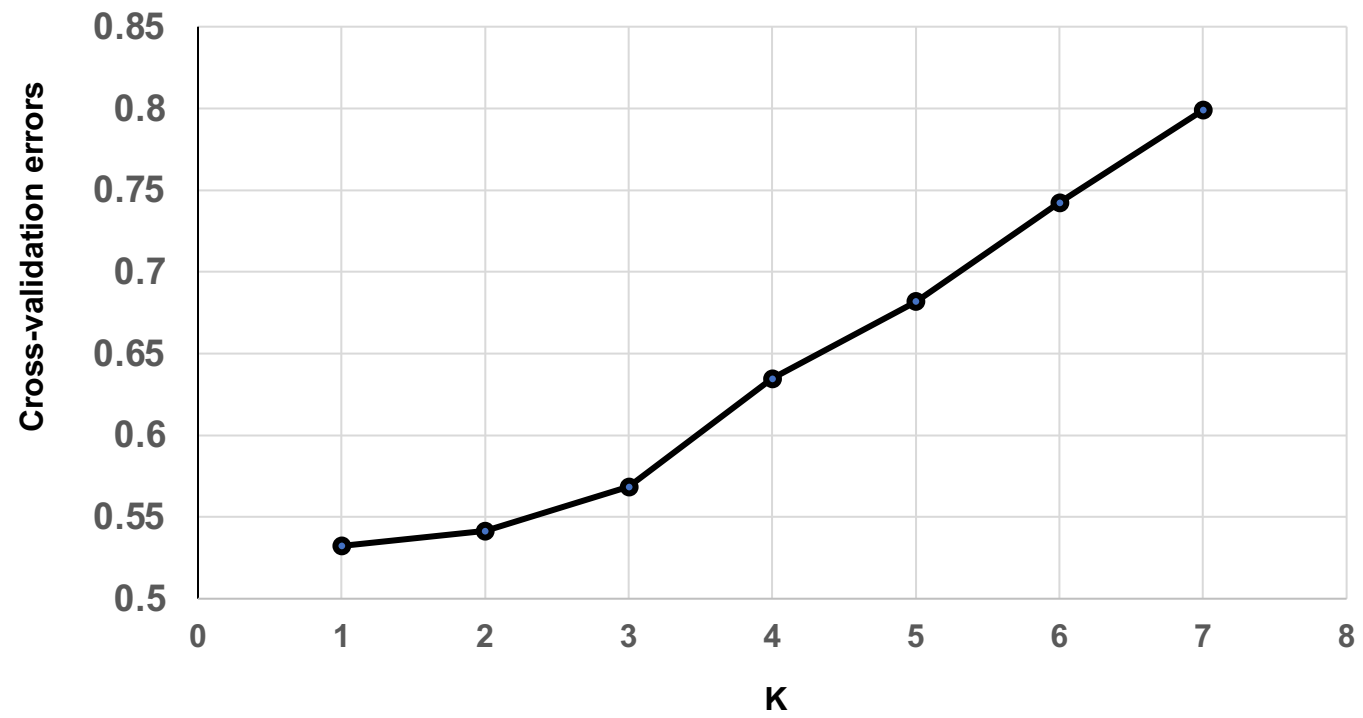


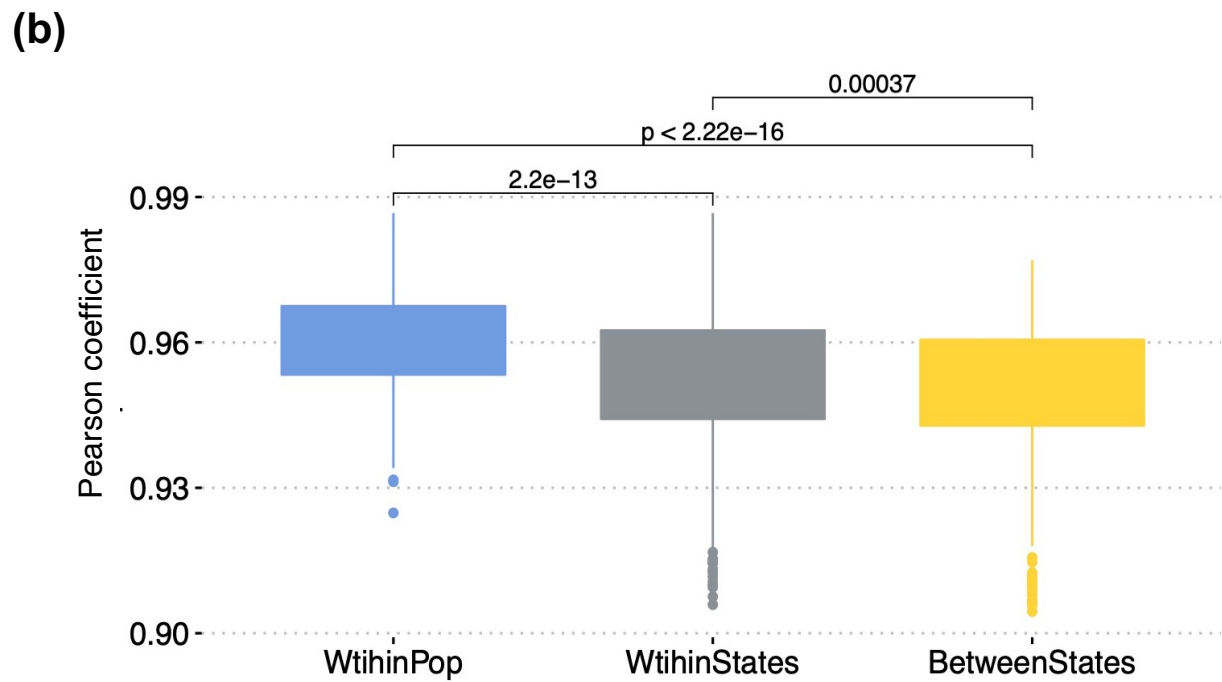
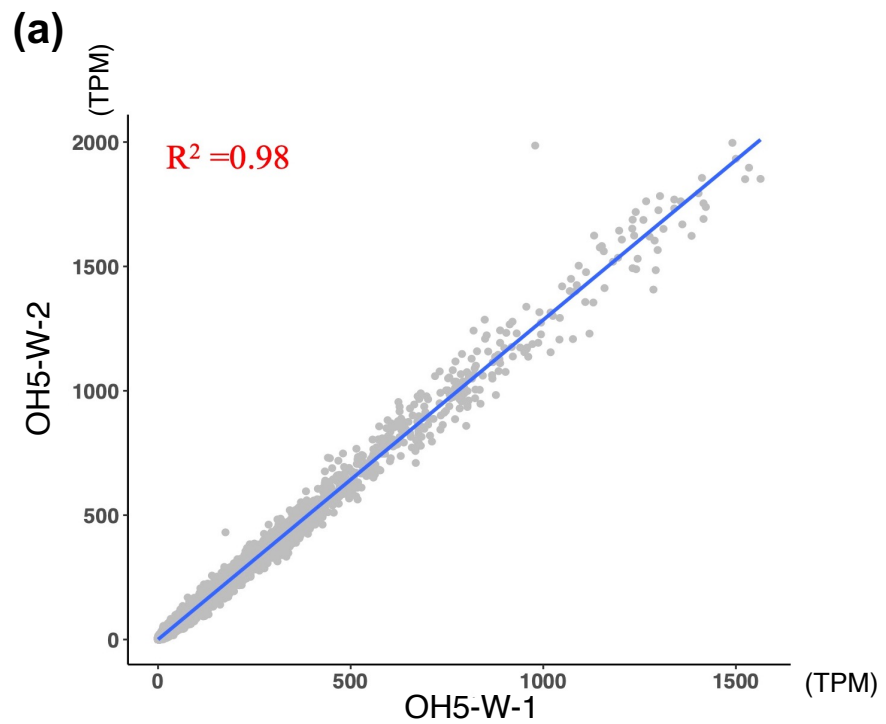
Gene expression analysis



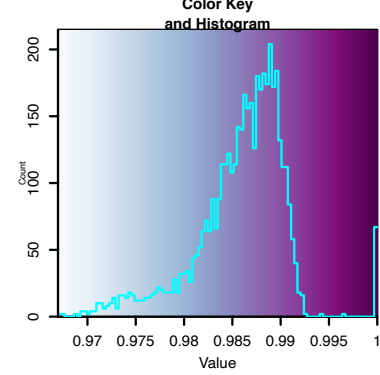
BUSCO Assessment Results



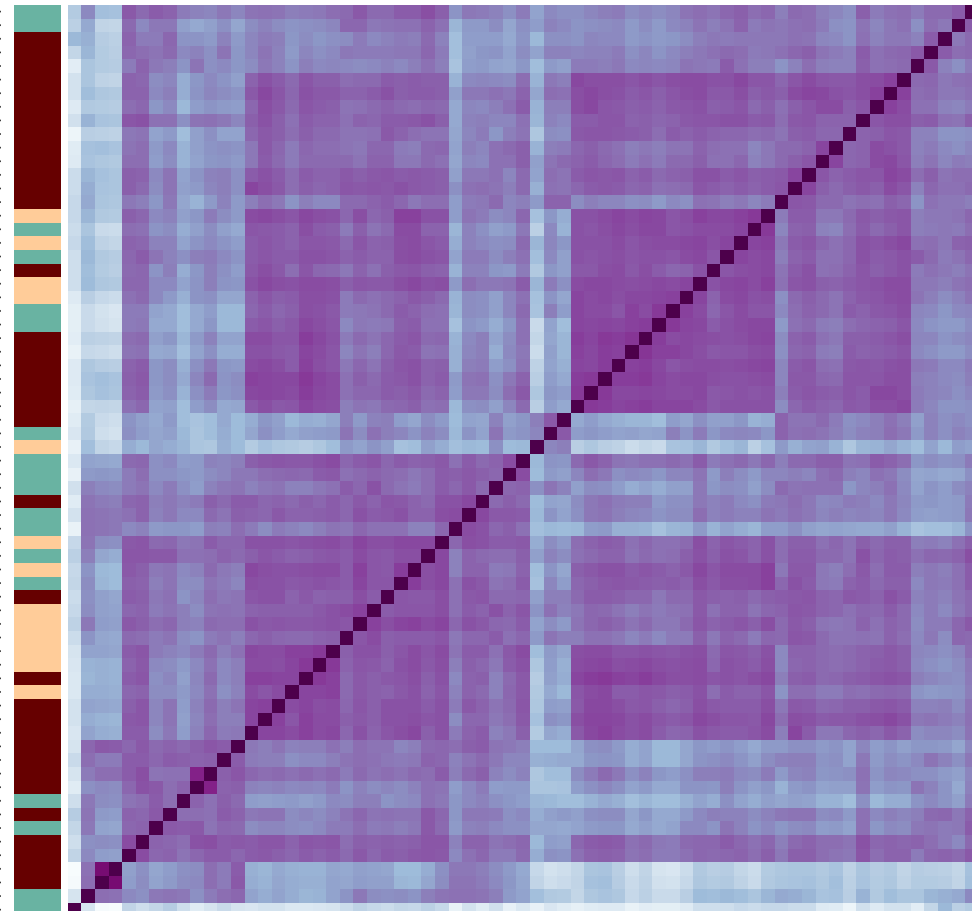
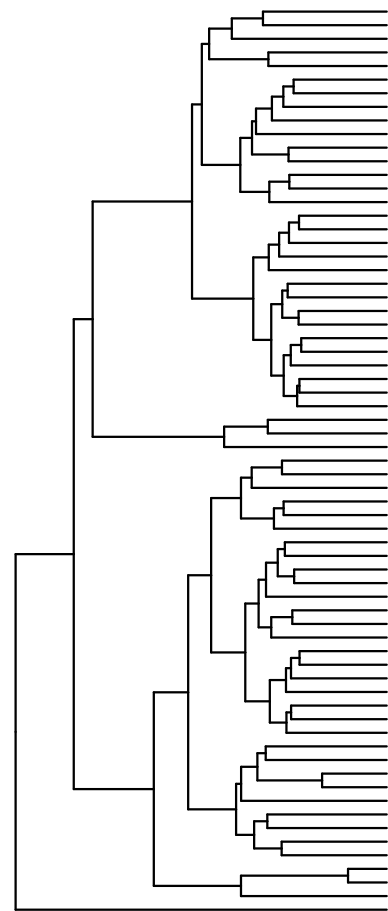
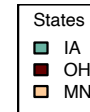
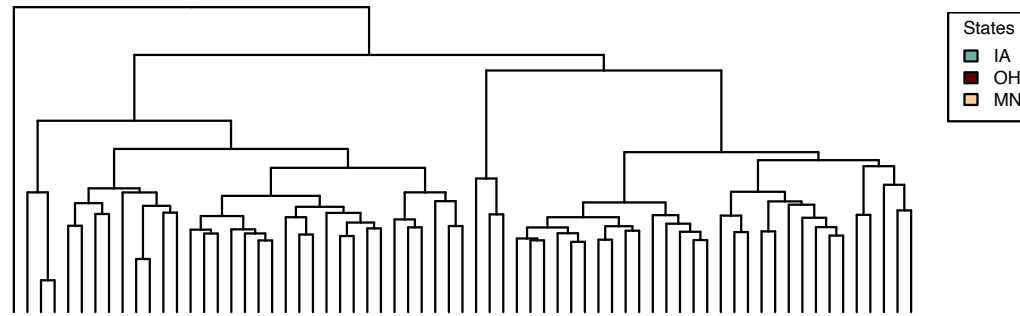




(c)

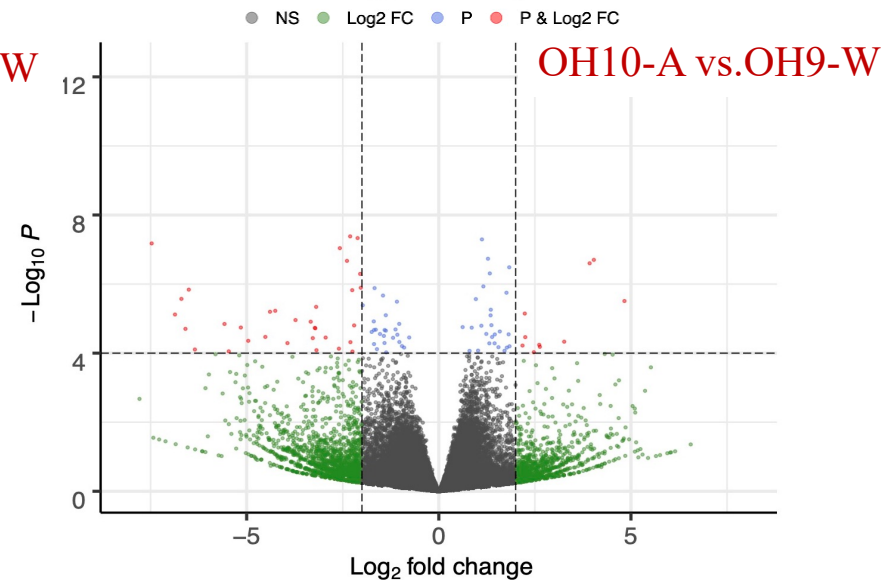
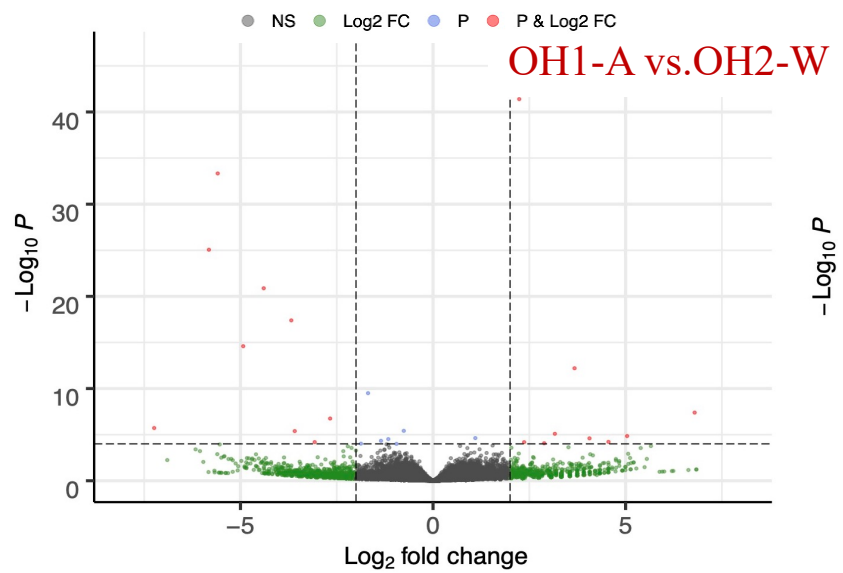
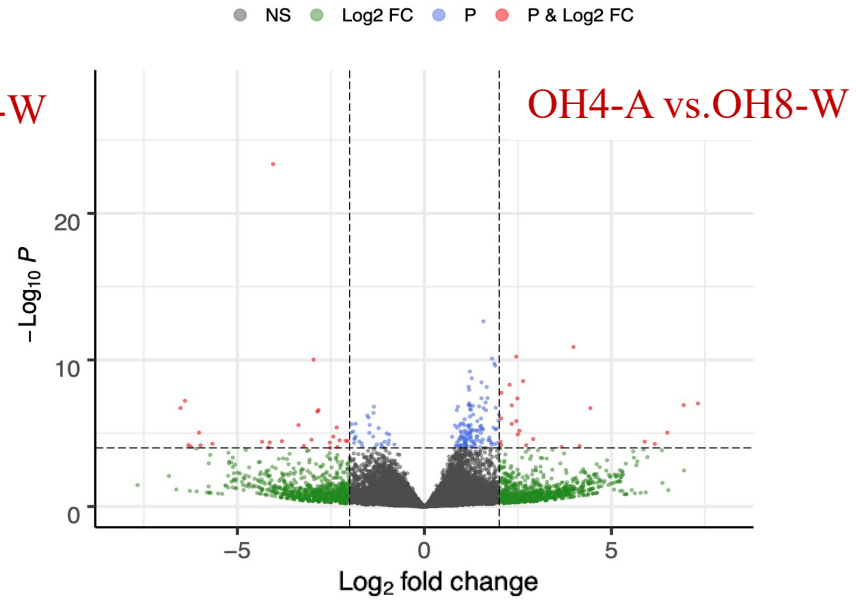
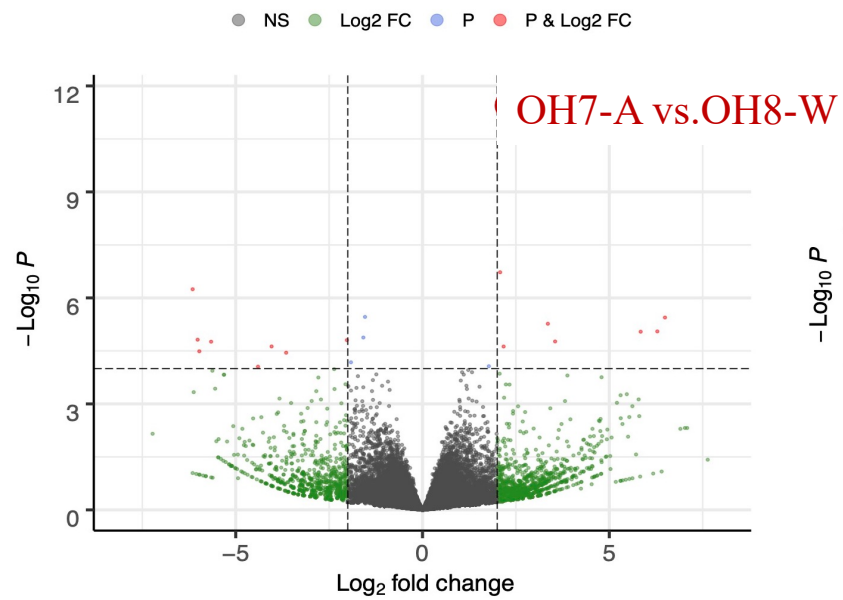


The Pearson correlation of each sample

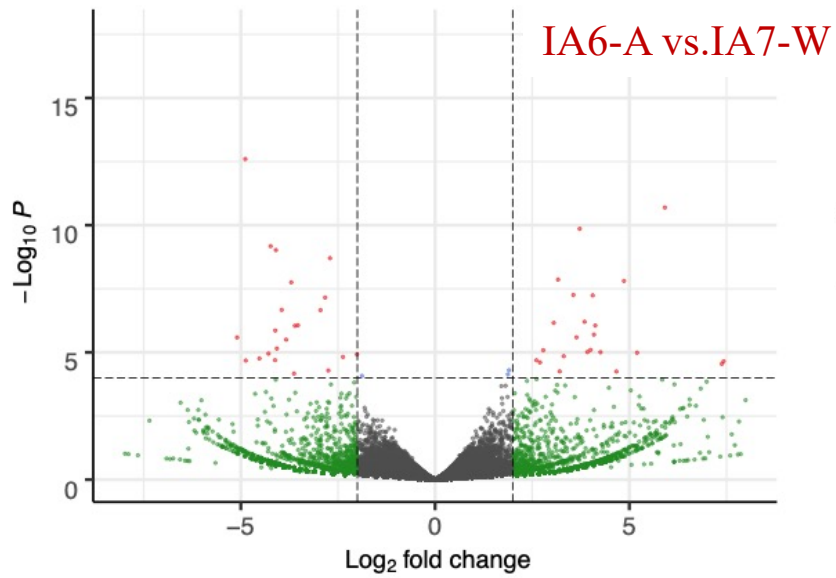


IA6-A-2 *
IA4-A-1 *
OH7-A-4 *
OH8-W-3
OH8-W-1
OH9-W-4
OH3-W-5
OH2-W-1
OH7-A-1 *
OH6-W-3
OH1-A-3 *
OH1-A-2 *
OH2-W-2
OH3-W-2
OH9-W-2
MN2-W-3
IA1-A-4 *
MN2-W-4
IA7-W-1
OH1-A-1 *
MN2-W-1
MN3-A-1 *
IA3-W-3
IA3-W-1
OH10-A-3 *
OH10-A-2 *
OH2-W-3
OH2-W-4
OH3-W-4
OH9-W-3
OH9-W-1
IA1-A-1 *
MN2-W-2
IA3-W-2
IA2-W-2
IA1-A-3
OH10-A-1 *
IA1-A-2 *
IA2-W-1 *
MN1-W-4
IA4-A-2 *
MN3-A-3 *
IA3-W-4
OH6-W-2
MN1-W-2
MN1-W-1
MN2-W-5
MN1-W-3
MN3-A-2 *
OH10-A-4 *
MN3-A-4 *
OH6-W-1
OH3-W-3
OH3-W-1
OH4-A-1 *
OH7-A-2 *
OH4-A-4 *
OH4-A-3 *
IA7-W-2
OH4-A-2 *
IA5-W-1
OH8-W-2
OH7-A-3 *
OH5-W-2
OH5-W-1
IA5-W-2
IA6-A-1 *

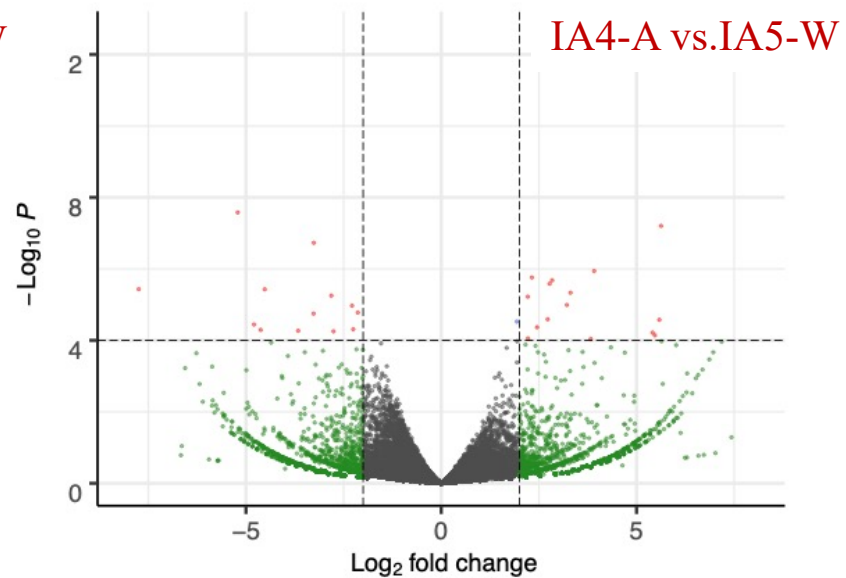
Supplemental Figure S4



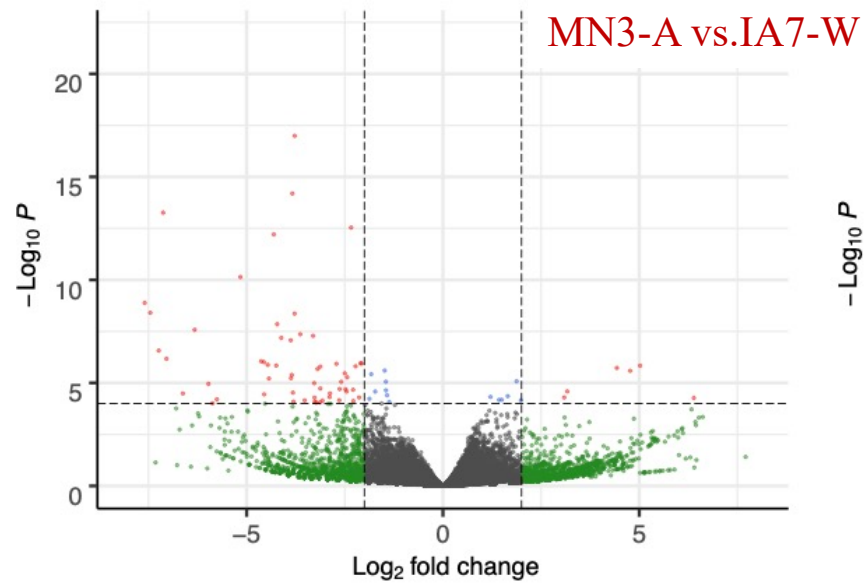
● NS ● Log2 FC ● P ● P & Log2 FC



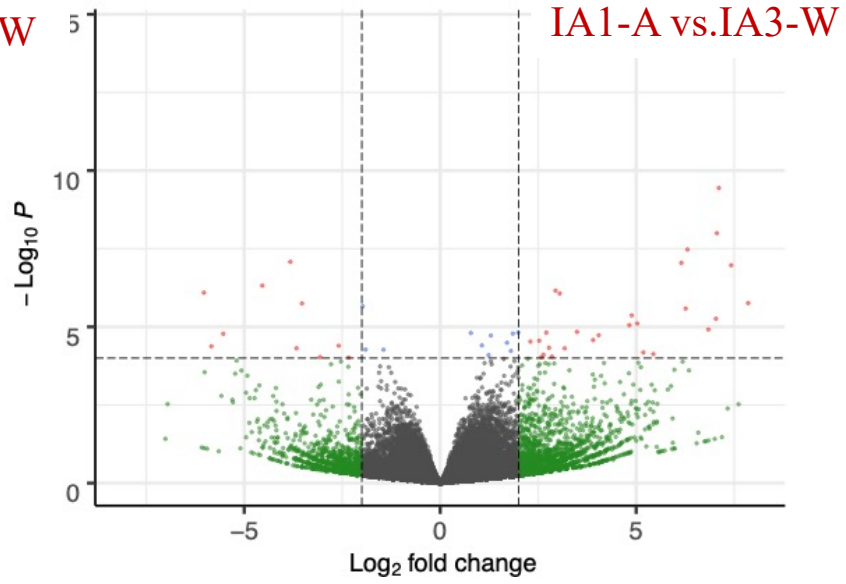
● NS ● Log2 FC ● P ● P & Log2 FC



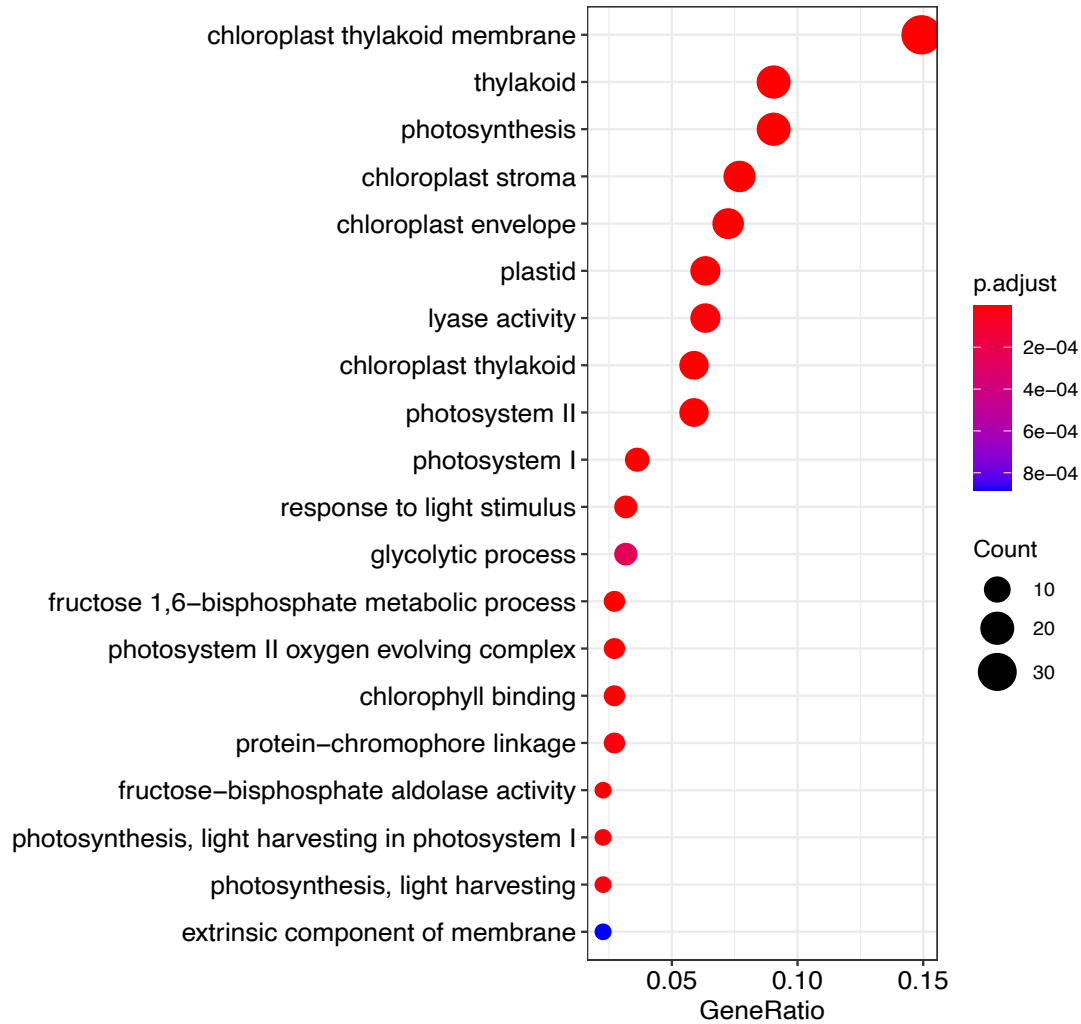
● NS ● Log2 FC ● P ● P & Log2 FC



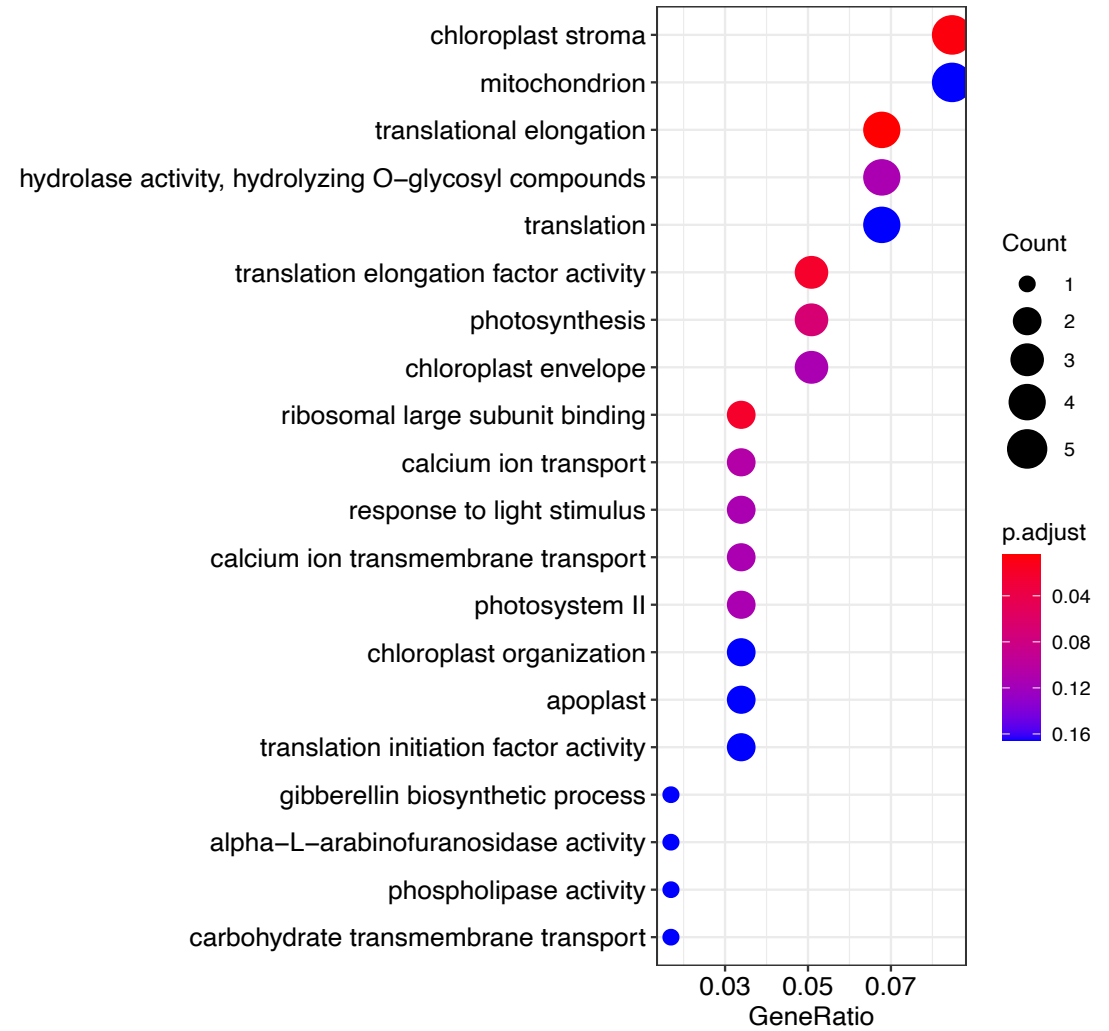
● NS ● Log2 FC ● P ● P & Log2 FC



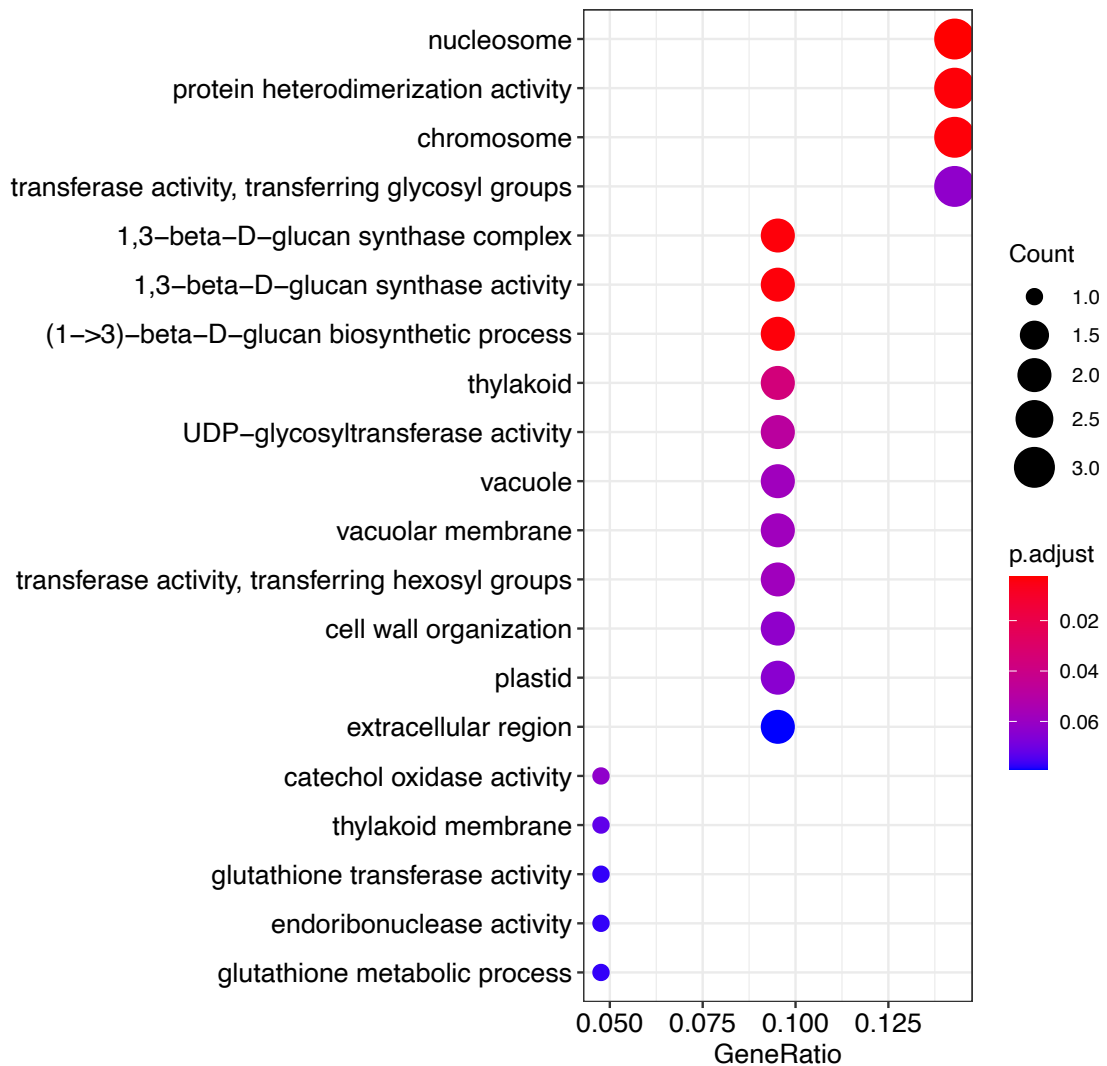
OH4-A upregulated genes



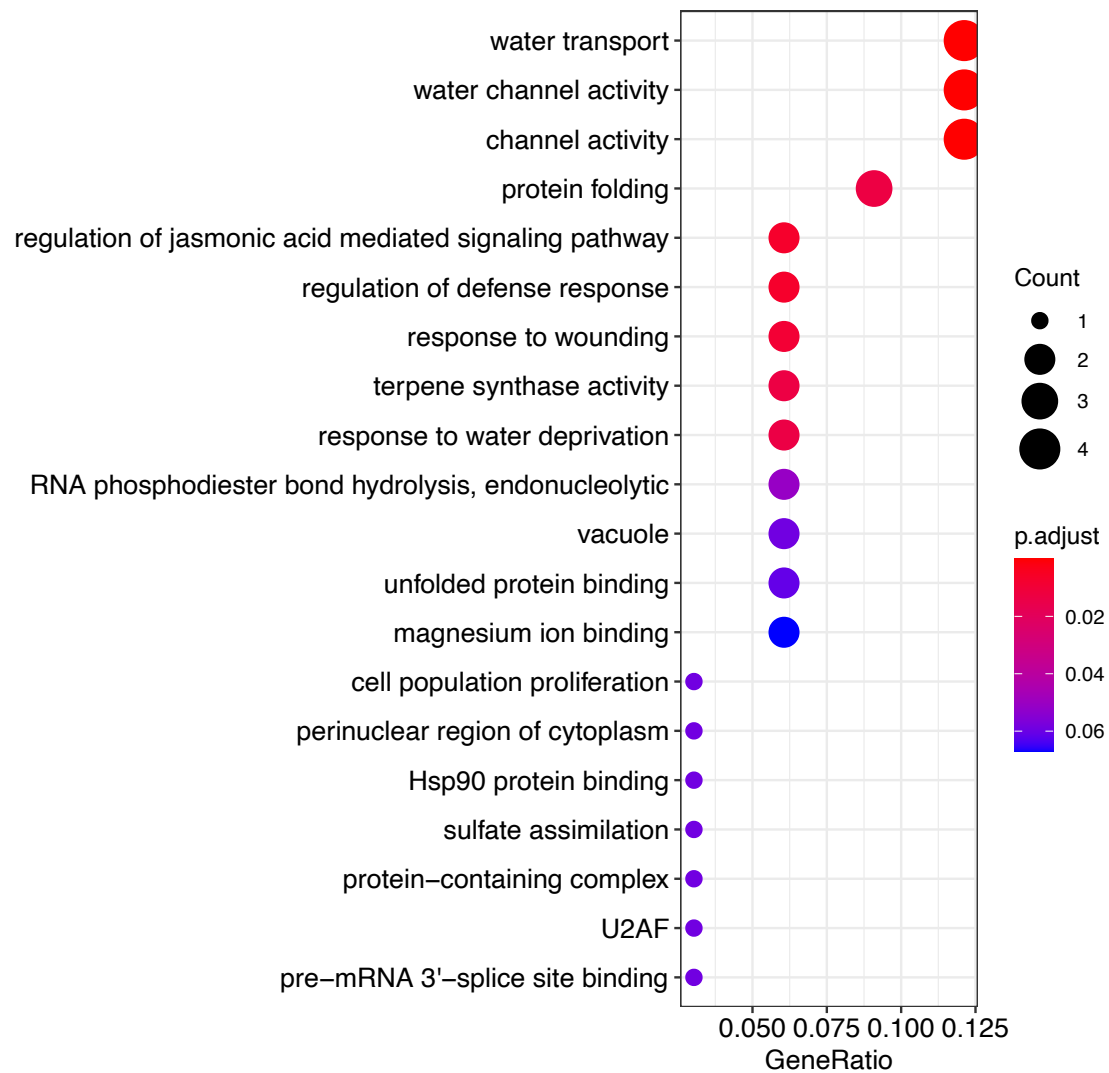
OH10-A upregulated genes



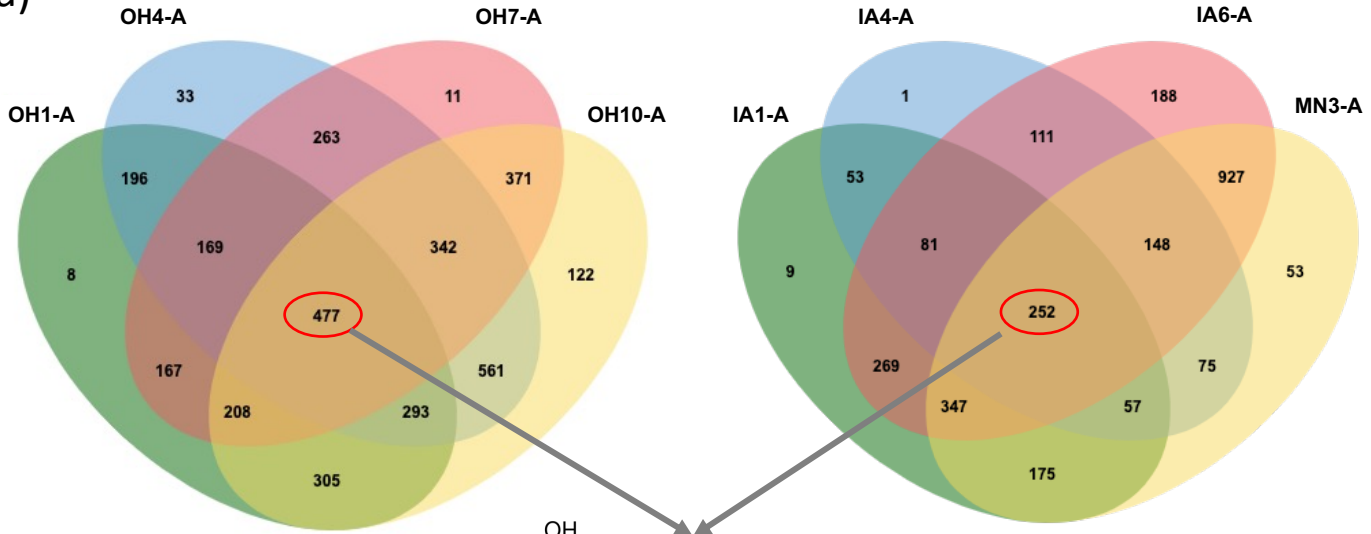
IA4-A upregulated genes



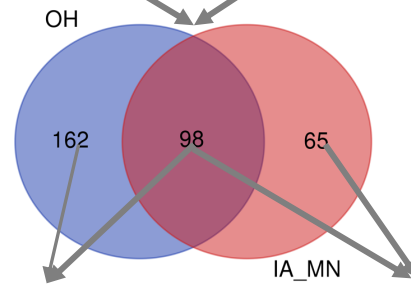
IA6-A upregulated genes



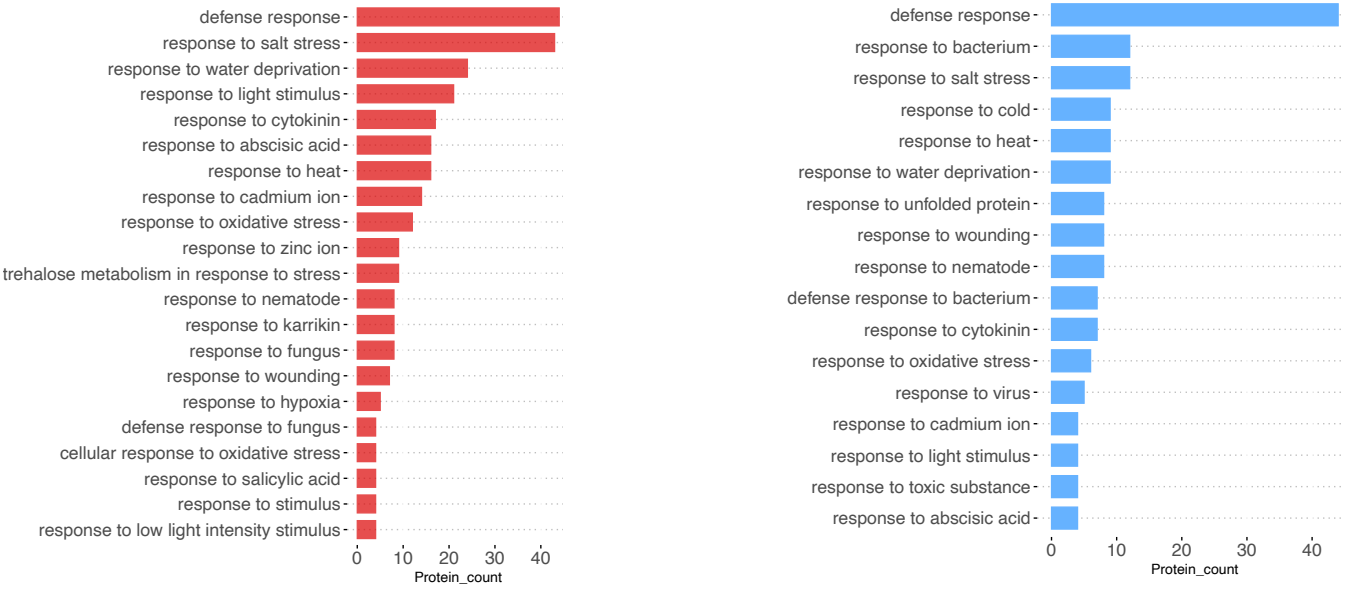
(a)

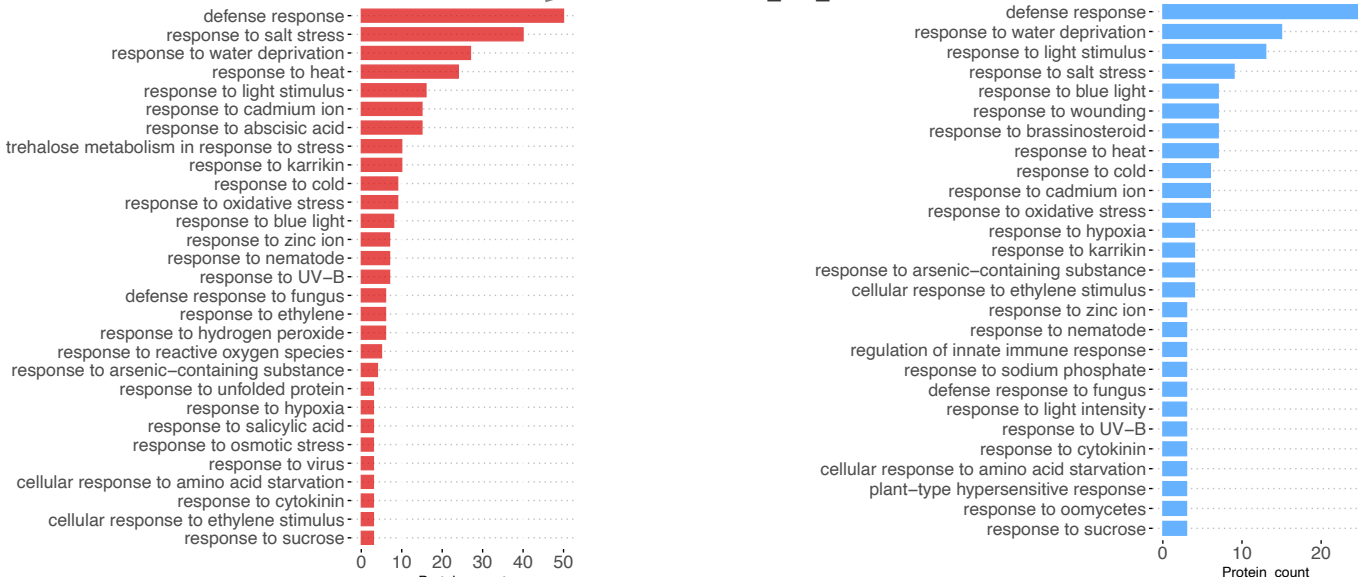
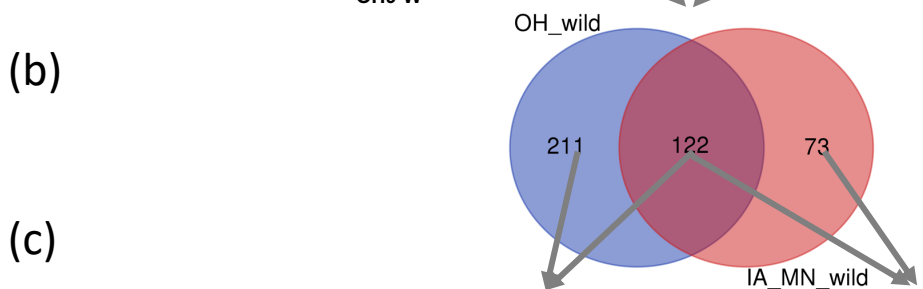
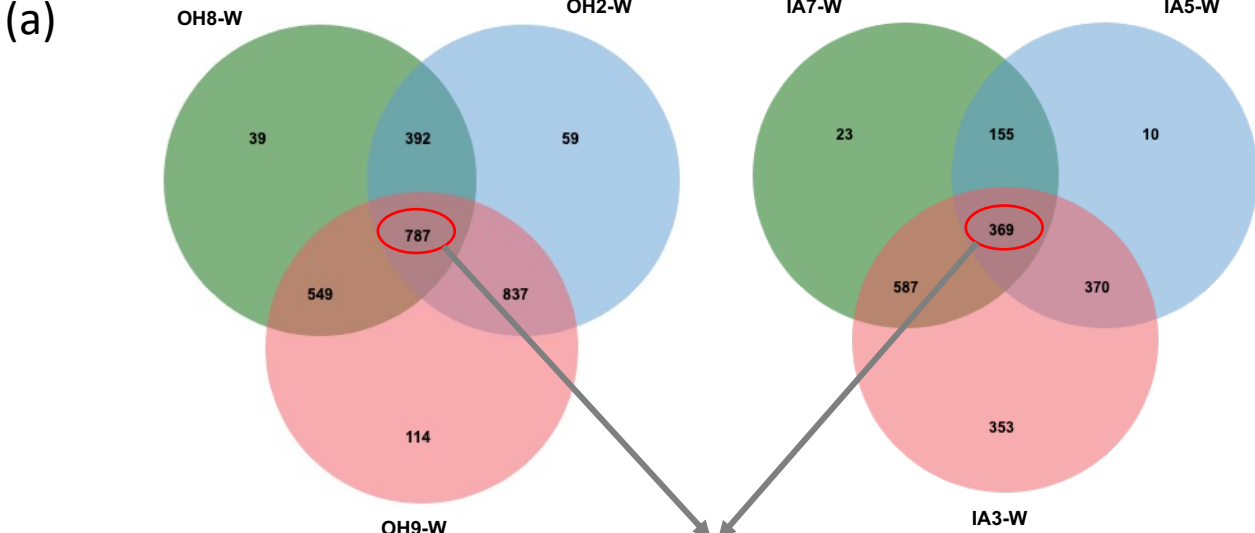


(b)



(c)



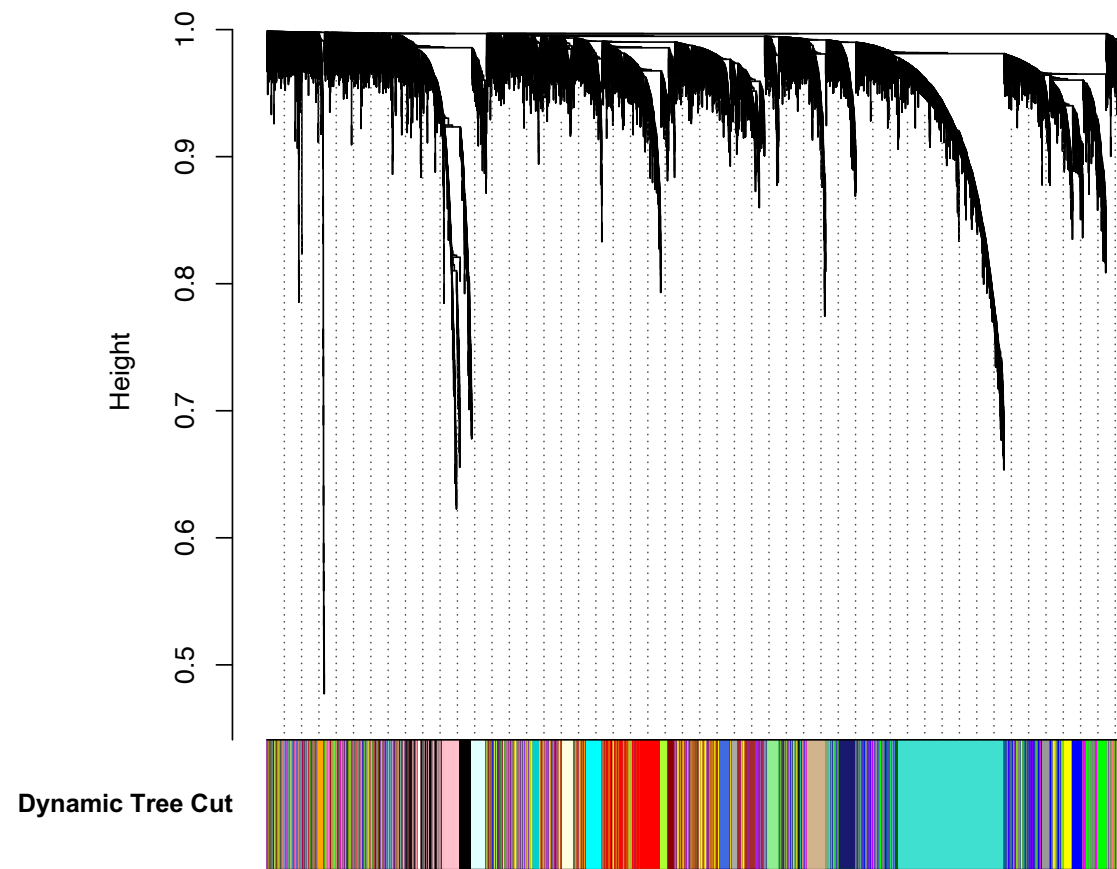
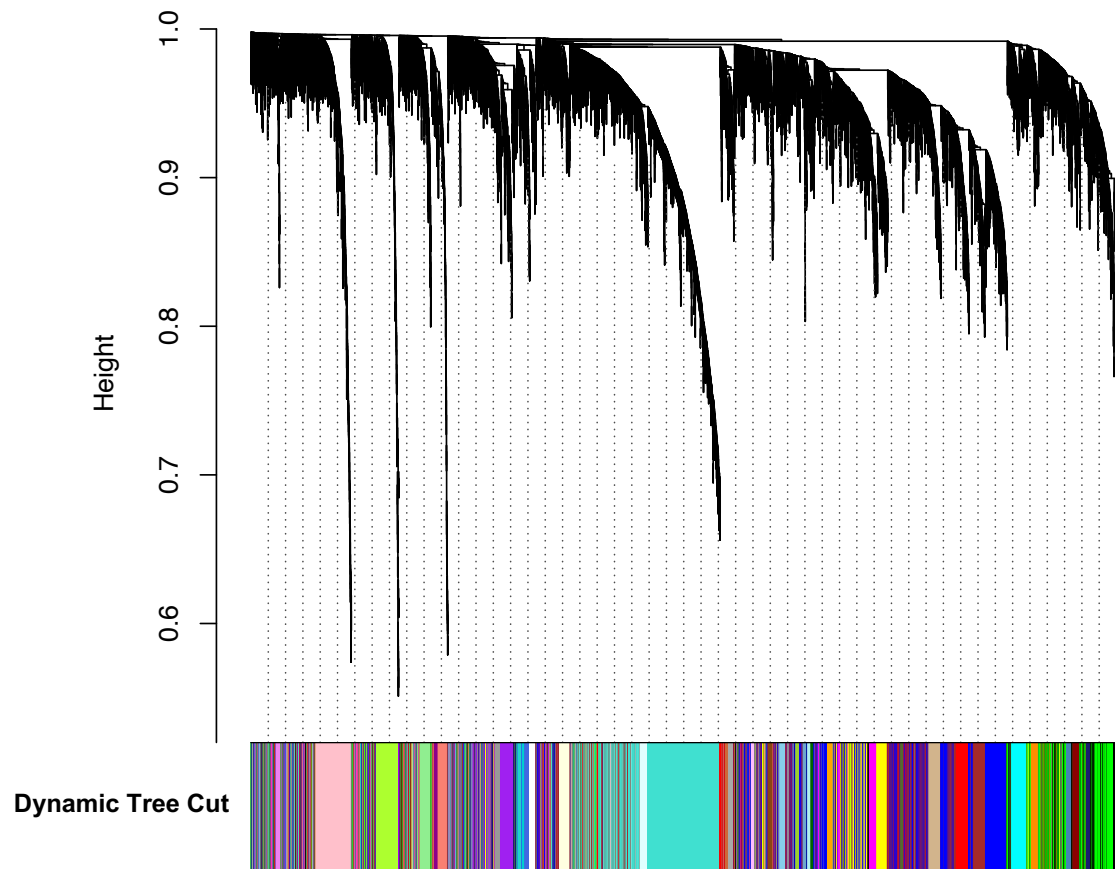


Supplemental Figure S9

(a)

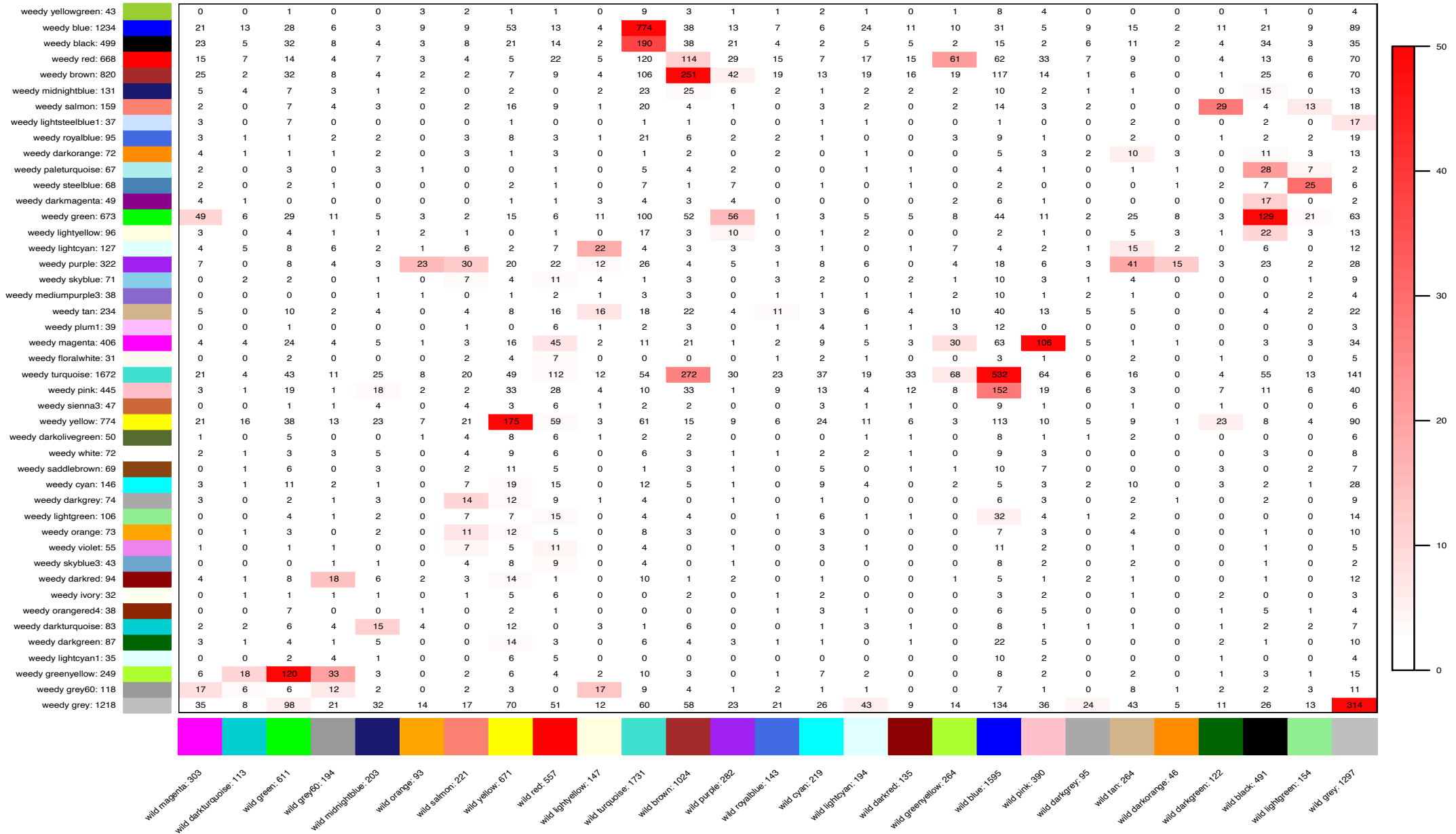
Weedy

Wild



(b)

Correspondence of weedy and wild modules



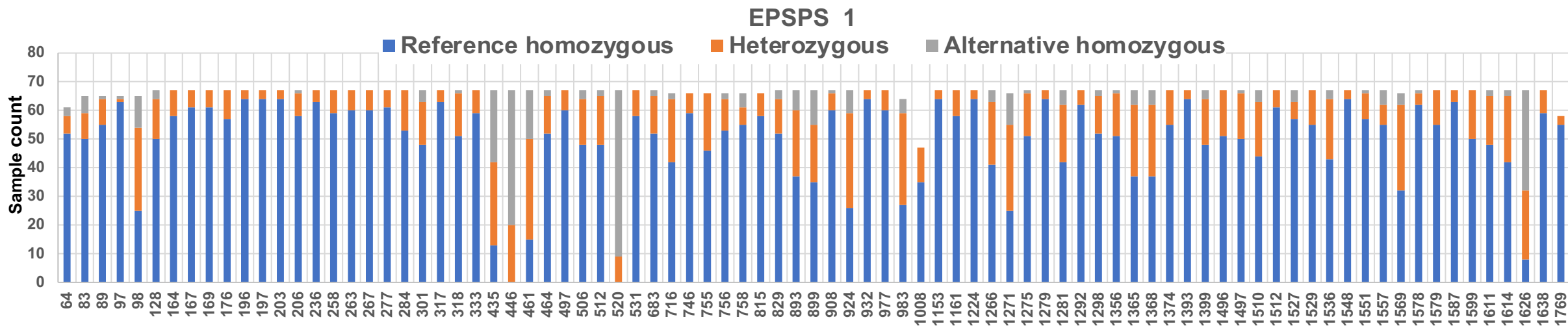
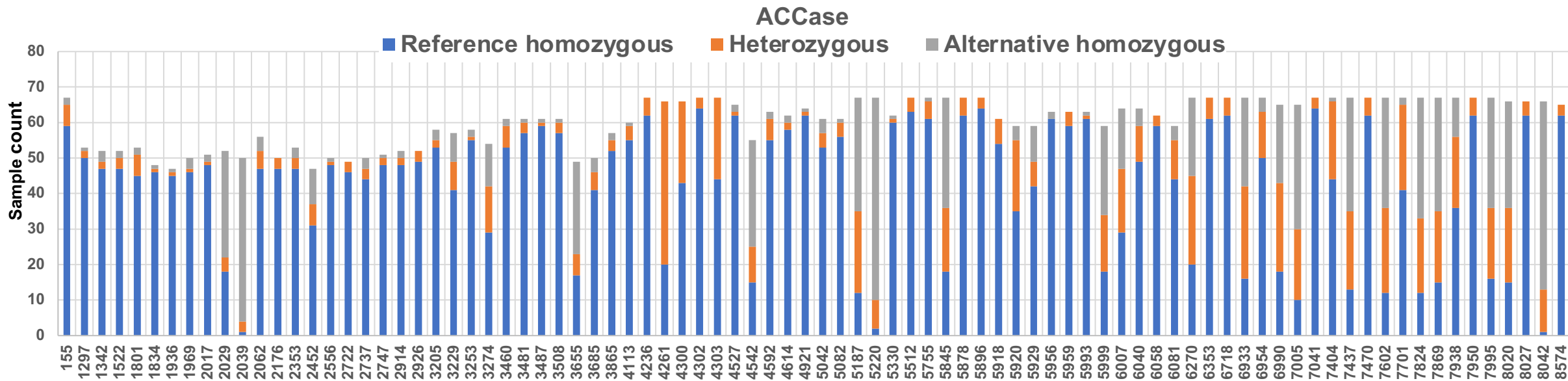
(c)

Conserved modules

Gene module	Representative GO annotation
Blue	Ribosome biogenesis
Brown	DNA replication
Black	Ribosome biogenesis
Green	Photosynthesis
Green yellow	Calcium ion binding
Magenta	Motor activity
Turquoise	DNA repair
Yellow	Autophagy

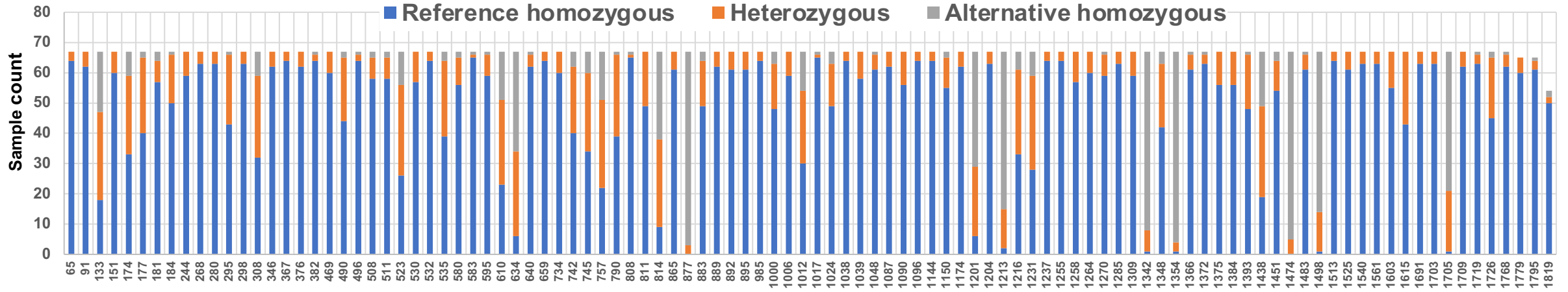
Variable modules

Gene module	Representative GO annotation
Yellow green	Autophagy
Royal blue	branched-chain amino acid biosynthetic process
Plum1	peptidyl-serine phosphorylation
Floral white	xenobiotic transport
Cyan	cellulose biosynthetic process
Dark Green	transcription factor binding
Light cyan1	endoplasmic reticulum
Medium purple3	Golgi transport

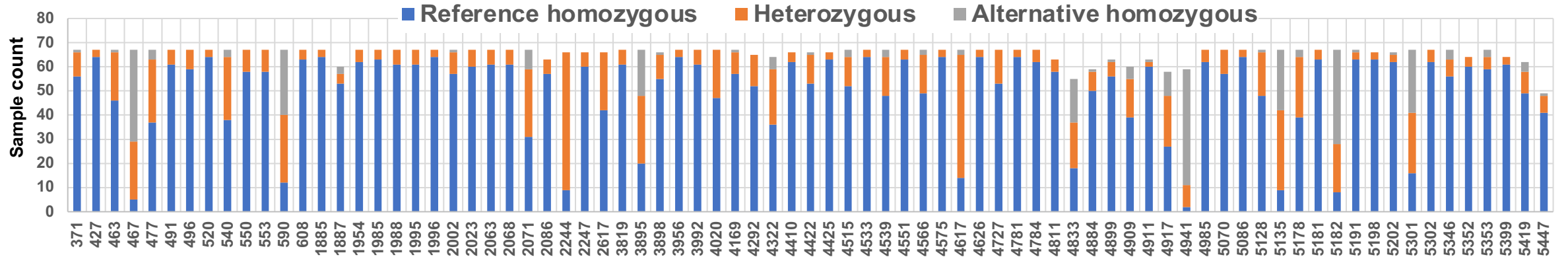


Supplemental Figure S11

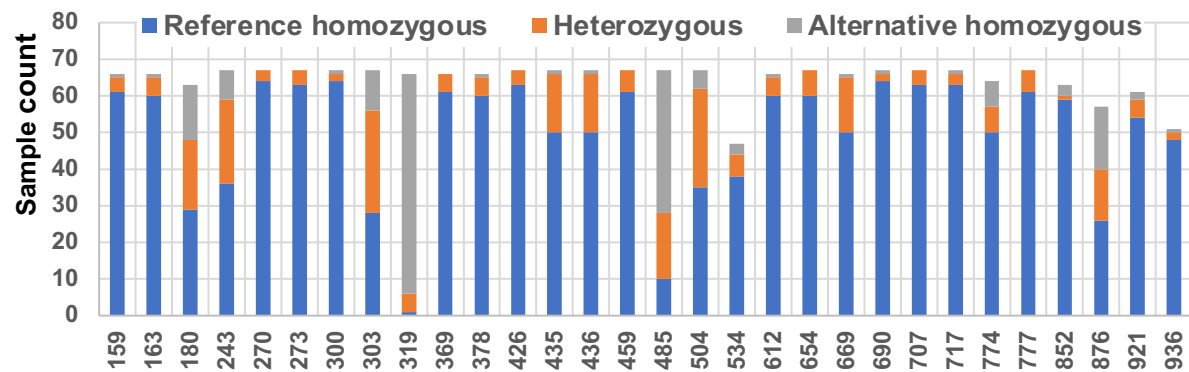
EPSPS_2



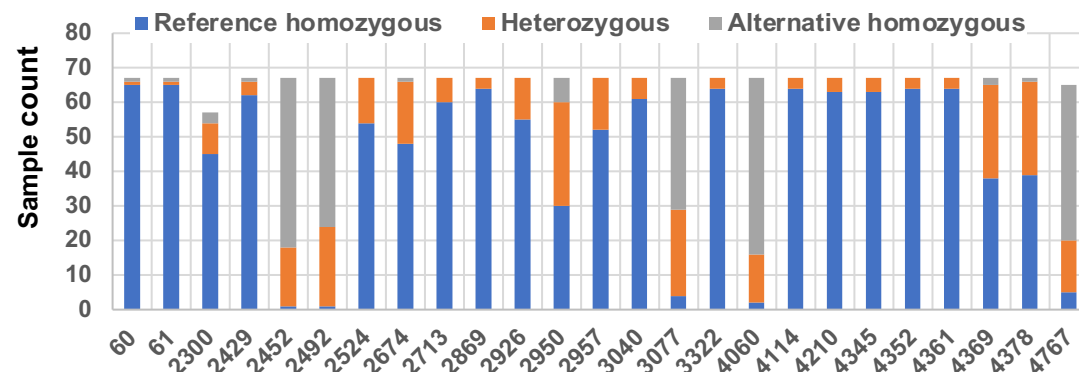
GS



HPPD



PDS



PPO

