Manuscript table1

Deisiany

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# Table 1

# Load TIR1/AFB1, Aux/IAAs, and ARFs so we can bind all together.  
TIR <- read.csv("../final\_trees/AFB\_input/2023\_0919\_AFB\_Gm\_ortholog.csv")  
  
  
IAA <- read.csv("../final\_trees/IAA\_input/IAA\_Gm\_ortholog.csv")  
IAA2 <- read.csv("../final\_trees/IAA\_input/LABELS2\_20230917.csv") %>% .[30:90, ]  
IAA2 <- IAA2 %>% select(tair\_locus, ensembl\_gene\_id, Class)  
  
IAA\_ortho <- merge(IAA, IAA2, by = "tair\_locus", all = TRUE)  
IAA\_ortho <- IAA\_ortho %>% rename(`Gene ID` = ensembl\_gene\_id.x,  
 `Transcript ID` = tair\_locus,  
 Orthology = ortholog\_name,  
 `Class/Clade` = Class) %>%   
 select(`Transcript ID`, Orthology, `Class/Clade`)   
IAA\_ortho$Family <- "IAA"  
  
  
expression\_data <- read\_csv("FINAL\_manuscript\_gene\_INFO.csv") %>% select(-c(Average\_Expression, `...22`))

## New names:  
## Rows: 221 Columns: 22  
## ── Column specification  
## ──────────────────────────────────────────────────────── Delimiter: "," chr  
## (6): ensembl\_gene\_id, ortholog\_number, tair\_locus, class, name, Family dbl  
## (16): AM, OF, IAM, IBM, RootTip, Cotyledon, Hypocotyl, SAM6D, SAM17D, SA...  
## ℹ Use `spec()` to retrieve the full column specification for this data. ℹ  
## Specify the column types or set `show\_col\_types = FALSE` to quiet this message.  
## • `` -> `...22`

comb\_expr\_df <- merge(IAA\_ortho, expression\_data, by.x = "Transcript ID", by.y = "tair\_locus", all =TRUE)  
  
comb\_expr\_df <- comb\_expr\_df %>% mutate(Class = coalesce(`Class/Clade`, class))  
  
comb\_expr\_df <- comb\_expr\_df %>%   
 select(-c(class, `Class/Clade`, Orthology, Family.x))  
  
# populate NA's in class in accordance to their ensembl gene ID. if the same ID they belong to the same class  
comb\_expr\_df2 <- comb\_expr\_df %>%  
 group\_by(ensembl\_gene\_id) %>%  
 mutate(Class = if (all(is.na(Class))) NA else na.omit(Class)) %>%  
 ungroup()  
  
  
# separate Class into Class and Clade  
comb\_expr\_df2 <- comb\_expr\_df2 %>% separate(Class, c('Class', 'Clade'),sep = " - ")

## Warning: Expected 2 pieces. Missing pieces filled with `NA` in 120 rows [1, 2, 9, 10,  
## 13, 17, 18, 19, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 38, 39, ...].

# Now combine TIR df to get their new clades.  
df <- merge(comb\_expr\_df2, TIR, by.x = "ensembl\_gene\_id", by.y = "ensembl\_gene\_id", all = TRUE)  
  
df <- df %>% mutate(Clade = coalesce(Clade.x, Clade.y))  
  
df <- df %>% select(-c(Clade.x, Clade.y, class, tair\_locus, ortholog\_name, name.x, name.y)) %>% rename(Orthology = ortholog\_number)  
  
df <- df %>%   
 group\_by(ensembl\_gene\_id) %>%   
 mutate(Clade = if(all(is.na(Clade))) NA else na.omit(Clade)) %>%   
 ungroup()  
  
# I can add clades to ARFs as I have not saved that as csv file when I built trees.   
df <- df %>% mutate(Clade = ifelse(grepl("ARF", .$Family.y) & grepl("A", .$Class), "II",  
 ifelse(grepl("ARF", .$Family.y) & grepl("B", .$Class), "I",  
 ifelse(grepl("ARF", .$Family.y) & grepl("C", .$Class), "III", Clade))))  
  
  
  
df2 <-  
 df %>% mutate(Class = ifelse(grepl("Glyma.02G218100", .$ensembl\_gene\_id), "A", Class),  
 Clade =  
 ifelse(grepl("Glyma.02G218100", .$ensembl\_gene\_id), "I", Clade))  
  
  
df2 <- df2 %>% rename(Family = Family.y, `Gene ID` = ensembl\_gene\_id) %>% drop\_na()  
  
# save Table 1 for manuscript  
df2 %>% select(`Gene ID`, Orthology, `Transcript ID`, Class, Clade, Family) %>% arrange(Family, Clade, Class, Orthology) %>% write\_csv("Table1.csv")  
  
# write\_csv(df2, "20230919\_expression\_heatmap.csv")

# Heatmap

# Source:  
# https://stackoverflow.com/questions/43051525/how-to-draw-pheatmap-plot-to-screen-and-also-save-to-file  
save\_pheatmap\_pdf <- function(x, filename, width=7, height=4) {  
 stopifnot(!missing(x))  
 stopifnot(!missing(filename))  
 pdf(filename, width=width, height=height)  
 grid::grid.newpage()  
 grid::grid.draw(x$gtable)  
 dev.off()  
}  
  
# https://davetang.org/muse/2018/05/15/making-a-heatmap-in-r-with-the-pheatmap-package/

# Make a heatmap label by uniting orthology column and gene ID column  
heatmap\_df <- df2 %>%   
 relocate(`Gene ID`, .after = `Transcript ID`) %>%   
 unite("heatmap\_label", `Gene ID`:Orthology, sep = "|", remove = TRUE)  
  
  
# Genes with an median expression across tissues that are less than 2 TPM, will be excluded from downtream analysis  
heatmap\_df2 <- heatmap\_df %>%   
 mutate(expr\_median = round(apply(heatmap\_df[,c(4:17)], 1, median), digits = 4)) %>%   
 subset(., expr\_median>= 2) %>% dplyr::filter(., Class != "COI1")  
  
 # we kept 133 genes for downstream normalization

# Normalization by transcript

Expr\_data\_Norm <- heatmap\_df2 %>% relocate(c(Class, Clade), .after = Family) %>% select(-expr\_median)  
  
# Normalize data by performing a z-score transformation on selected columns.  
  
# Iterate through each row of the 'Expr\_data\_Norm' data frame.  
for (j in 1:nrow(Expr\_data\_Norm)) {  
 # Iterate through columns starting from the 6th column to the last column.  
for (i in 6:ncol(Expr\_data\_Norm)) {   
   
 # Calculate the z-score normalization for each cell in the data frame.  
 # 1. Subtract the mean of the selected row (columns 6 to the last column).  
 # 2. Divide by the standard deviation of the selected row.  
 Expr\_data\_Norm[j,i]<-   
 (Expr\_data\_Norm[j,i]-rowMeans(Expr\_data\_Norm[j,6:ncol(Expr\_data\_Norm)]))/  
 sd(Expr\_data\_Norm[j,6:ncol(Expr\_data\_Norm)])   
}  
}  
  
Expr\_data\_Norm <-Expr\_data\_Norm %>% drop\_na() %>% column\_to\_rownames(., var = "heatmap\_label")

# Build heatmap with normalized data

# Specify colors  
Class\_df1\_colors = list(Family = c(ARF = "Purple", IAA = "yellow", `AFB/TIR1`="lightblue"), Class = c(A="purple", B="lightseagreen", C="orange", TIR1="green", `AFB2/3`="blue", `AFB4/5`="yellow", COI1="pink", AFB6="pink2"))

(expr\_analysis <- pheatmap::pheatmap(mat = Expr\_data\_Norm[,5:18], annotation\_row = Expr\_data\_Norm[,c(2,3)], annotation\_colors = Class\_df1\_colors[1],  
 fontsize = 6,   
 fontsize\_row = 5,  
 cellwidth = 6,  
 cellheight = 5,   
 clustering\_distance\_rows = "euclidean",  
 treeheight\_row = 300,   
 cutree\_rows = 6,   
 # main = "Expression analysis - normalized by transcripts",  
 color = c("grey80", "white", "mistyrose2", "lightpink", "lightblue", "turquoise", "lightslateblue")))

A diagram of a number of data

Description automatically generated with medium confidence

save\_pheatmap\_pdf(expr\_analysis, "20230926\_FINAL\_NORM\_by\_Transcript.pdf", height = 12, width = 9)

## quartz\_off\_screen   
## 2

Z-score normalization standardizes the data such that the mean of each row becomes 0 and the standard deviation becomes 1. The resulting values can be positive or negative and represent how many standard deviations a data point is from the mean of its row.

In the context of z-score normalization:

Values close to 0 represent gene expression levels similar to the mean of their respective rows. Negative values represent gene expression levels below the mean of their respective rows. Positive values represent gene expression levels above the mean of their respective rows.

So, in your heatmap, the -1 represents genes that have expression levels approximately 1 standard deviation below the mean of their respective rows.

These genes are relatively lower in expression compared to the mean expression of those genes across the samples or conditions under analysis.

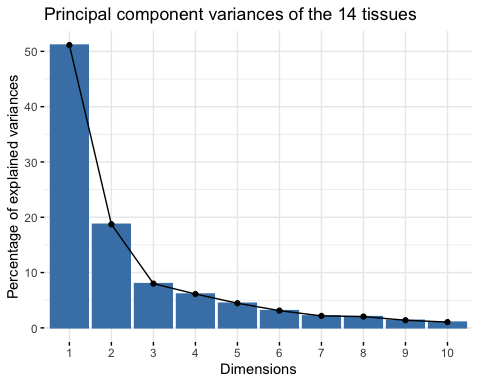
# Principal component analysis

Using the full data set in which data median expression was greater than 2. In our PCA we are not using the normalized data. That is beacause we are already transforming our data once by using scale = true, which is known to change the range of the data whereas normalized changes its shape distribution.

pca\_data <- heatmap\_df2 %>% relocate(c(Class, Clade), .after = Family) %>% select(-expr\_median)  
  
  
  
# for analysis with all tissues   
pca <- prcomp(pca\_data[, -(1:5)],   
 scale. = T, center = T)  
summary(pca)

## Importance of components:  
## PC1 PC2 PC3 PC4 PC5 PC6 PC7  
## Standard deviation 2.6757 1.6196 1.05841 0.92601 0.79038 0.66102 0.55083  
## Proportion of Variance 0.5114 0.1874 0.08002 0.06125 0.04462 0.03121 0.02167  
## Cumulative Proportion 0.5114 0.6988 0.77878 0.84003 0.88465 0.91586 0.93753  
## PC8 PC9 PC10 PC11 PC12 PC13 PC14  
## Standard deviation 0.53473 0.43946 0.38317 0.32336 0.26775 0.2275 0.14373  
## Proportion of Variance 0.02042 0.01379 0.01049 0.00747 0.00512 0.0037 0.00148  
## Cumulative Proportion 0.95796 0.97175 0.98224 0.98971 0.99483 0.9985 1.00000

factoextra::fviz\_eig(pca, main = "Principal component variances of the 14 tissues")



ggsave("20230927\_PCscreePlot\_allTissues.png", dpi = 1000, width = 10, height = 8)

## PC1 and PC2 for all 14 tissues

Family <- pca\_data$Family  
  
# extract the loading so we can change the arrows more easily  
PCA\_loadings <- data.frame(Variables=rownames(pca$rotation), pca$rotation)  
  
  
comb\_pca\_df <- cbind(pca\_data, pca$x[, 1:4])

### PC1 and PC2 outside ellipse labels for the 14 tissues

PC1\_2all <- ggbiplot::ggbiplot(pca, obs.scale = 1, var.scale = .5,   
 varname.adjust = 3,  
 groups = Family, var.axes = F, varname.size = 2,   
 ellipse = TRUE, circle = FALSE, ellipse.prob = .70)

## ------------------------------------------------------------------------------

## You have loaded plyr after dplyr - this is likely to cause problems.  
## If you need functions from both plyr and dplyr, please load plyr first, then dplyr:  
## library(plyr); library(dplyr)

## ------------------------------------------------------------------------------

##   
## Attaching package: 'plyr'

## The following objects are masked from 'package:plotly':  
##   
## arrange, mutate, rename, summarise

## The following objects are masked from 'package:dplyr':  
##   
## arrange, count, desc, failwith, id, mutate, rename, summarise,  
## summarize

## The following object is masked from 'package:purrr':  
##   
## compact

##   
## Attaching package: 'scales'

## The following object is masked from 'package:viridis':  
##   
## viridis\_pal

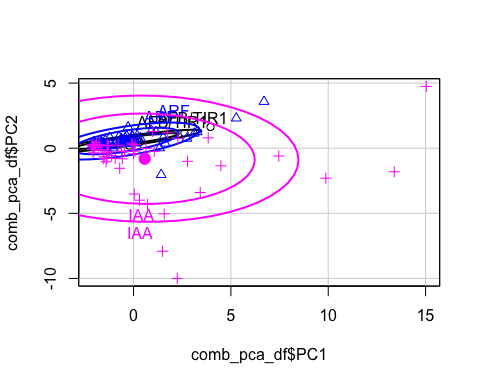
## The following object is masked from 'package:purrr':  
##   
## discard

## The following object is masked from 'package:readr':  
##   
## col\_factor

# Extract components so we can select out   
PC1\_2all$data

## xvar yvar groups  
## 1 -1.304753081 0.253967120 ARF  
## 2 -1.934745295 0.185928231 IAA  
## 3 -1.616343442 -0.113511655 IAA  
## 4 0.071187241 0.274717011 IAA  
## 5 7.459612561 -0.600002016 IAA  
## 6 -0.749858791 0.859463281 ARF  
## 7 -0.005956317 -0.427960267 IAA  
## 8 -1.524808613 0.431662229 AFB/TIR1  
## 9 1.574336185 -5.041777156 IAA  
## 10 -1.125575851 -0.558512920 IAA  
## 11 -0.578750074 -0.811787304 IAA  
## 12 -0.102457801 0.788703488 AFB/TIR1  
## 13 -1.734416069 0.129024379 AFB/TIR1  
## 14 0.542400680 -0.670223439 IAA  
## 15 2.276729634 0.750445550 IAA  
## 16 -0.307178253 0.330600703 ARF  
## 17 0.923944787 1.334152162 ARF  
## 18 -1.417357564 0.157370925 ARF  
## 19 -0.428112834 0.500704876 ARF  
## 20 1.418306200 -2.036229235 ARF  
## 21 1.623282025 0.380380191 ARF  
## 22 -2.129452835 -0.114441199 IAA  
## 23 3.425337748 -3.402760865 IAA  
## 24 0.306505583 0.466557952 AFB/TIR1  
## 25 13.392512855 -1.806412389 IAA  
## 26 -1.395820127 0.019944454 ARF  
## 27 -0.071996269 0.256945271 IAA  
## 28 -0.636996614 0.476207228 AFB/TIR1  
## 29 3.120519585 1.142973848 ARF  
## 30 -0.431602510 0.803815826 ARF  
## 31 -1.866388546 0.375426589 ARF  
## 32 1.337994430 0.015559355 ARF  
## 33 6.702648045 3.579346703 ARF  
## 34 -2.050727705 0.494196522 ARF  
## 35 -0.617206008 -0.218288936 IAA  
## 36 15.037892920 4.746237323 IAA  
## 37 -0.488627623 0.398718486 AFB/TIR1  
## 38 3.271439778 1.250223968 ARF  
## 39 5.275584046 2.305407189 ARF  
## 40 -1.369724965 -0.788772964 IAA  
## 41 -0.667462730 0.526307555 ARF  
## 42 -0.350550067 0.913360463 ARF  
## 43 0.191018481 0.098979610 ARF  
## 44 -0.450954600 0.394826074 ARF  
## 45 -1.955375052 0.413220346 AFB/TIR1  
## 46 -1.668697519 0.421500106 AFB/TIR1  
## 47 -1.422813511 0.323815463 ARF  
## 48 0.144182276 0.393931829 ARF  
## 49 2.741786531 0.753157423 ARF  
## 50 1.148171748 1.245116561 ARF  
## 51 -2.105944003 0.202653740 ARF  
## 52 0.639274022 -0.023380766 IAA  
## 53 -2.063221418 0.141276678 IAA  
## 54 -1.837152604 0.261934275 AFB/TIR1  
## 55 -0.632126448 0.732872508 ARF  
## 56 -1.068012274 0.168806405 ARF  
## 57 -1.789096929 -0.140394034 IAA  
## 58 -1.329711750 0.231182561 IAA  
## 59 3.834394420 0.793449297 IAA  
## 60 -1.552833562 0.395883644 ARF  
## 61 -2.130228985 0.229001671 IAA  
## 62 1.062351513 -0.241185818 IAA  
## 63 -0.468794376 -0.249922455 IAA  
## 64 0.077758331 0.524357821 AFB/TIR1  
## 65 -2.084695899 0.369234056 AFB/TIR1  
## 66 -0.856921604 0.507222423 AFB/TIR1  
## 67 -1.508225563 -0.662268126 IAA  
## 68 -1.559775037 -0.800512633 IAA  
## 69 -2.018657725 0.043427973 IAA  
## 70 -1.909610168 0.277764356 ARF  
## 71 4.485099923 -1.351421276 IAA  
## 72 2.771186411 -1.008109821 IAA  
## 73 -1.778294112 0.262406297 IAA  
## 74 -0.711451800 -1.541788959 IAA  
## 75 0.304514187 -3.991108850 IAA  
## 76 2.243284561 -9.997776235 IAA  
## 77 -1.044218657 0.004571344 ARF  
## 78 -0.860081508 0.223425301 ARF  
## 79 -1.540300976 0.174794131 ARF  
## 80 -0.075389131 0.937109194 ARF  
## 81 -1.455953728 0.582823128 ARF  
## 82 -2.063880601 0.149412964 ARF  
## 83 -0.902465346 0.479261947 ARF  
## 84 1.526821368 0.804159673 ARF  
## 85 -1.705462800 0.589012162 ARF  
## 86 -1.600893255 0.192216165 ARF  
## 87 -1.791100183 0.339552665 ARF  
## 88 -1.737520983 0.145743103 ARF  
## 89 -1.679057092 -0.108332600 IAA  
## 90 -1.994650072 0.350064536 ARF  
## 91 -0.056763350 0.882006175 ARF  
## 92 0.344926556 0.780242803 ARF  
## 93 -0.446664212 0.458750897 ARF  
## 94 -0.564238437 0.443802208 ARF  
## 95 0.988840347 1.281462617 IAA  
## 96 -0.793439779 0.229054413 IAA  
## 97 -1.900821570 0.435235820 IAA  
## 98 -1.372216366 -0.353257233 IAA  
## 99 -1.413117840 -1.040984678 IAA  
## 100 -1.362338626 0.207864794 IAA  
## 101 -1.285762155 0.171175760 IAA  
## 102 -1.166597927 0.338183452 ARF  
## 103 -0.098539817 0.642577969 ARF  
## 104 -0.230981637 0.201050662 AFB/TIR1  
## 105 0.071596867 -0.228022083 IAA  
## 106 0.156497195 0.696034794 ARF  
## 107 -1.219875713 0.814553891 ARF  
## 108 -1.297431165 -0.285475152 IAA  
## 109 -1.979546144 0.237586347 IAA  
## 110 1.748018509 1.187868663 IAA  
## 111 -0.603884550 0.638749151 ARF  
## 112 -1.676009054 0.418512190 ARF  
## 113 -1.955130698 0.355458289 ARF  
## 114 -1.994415698 0.311126791 ARF  
## 115 -0.353407486 0.428375254 ARF  
## 116 0.180816068 0.960752443 ARF  
## 117 3.952871915 1.625931704 AFB/TIR1  
## 118 -1.649072111 0.285122668 ARF  
## 119 -2.107793036 0.262895090 IAA  
## 120 -0.279830679 1.613426920 ARF  
## 121 -0.598906053 0.577784192 ARF  
## 122 -2.099471731 0.273681105 ARF  
## 123 2.615232113 1.164031145 AFB/TIR1  
## 124 -2.073025165 -0.349419050 IAA  
## 125 0.719480304 -4.324426296 IAA  
## 126 0.034697877 -3.518281284 IAA  
## 127 -1.545395901 0.285127917 ARF  
## 128 0.193178086 0.633239300 AFB/TIR1  
## 129 -0.088423804 0.385551512 IAA  
## 130 -1.883285723 0.267885408 ARF  
## 131 1.484478940 -7.913429916 IAA  
## 132 -0.941227933 -0.781215430 IAA  
## 133 9.877340758 -2.300225618 IAA

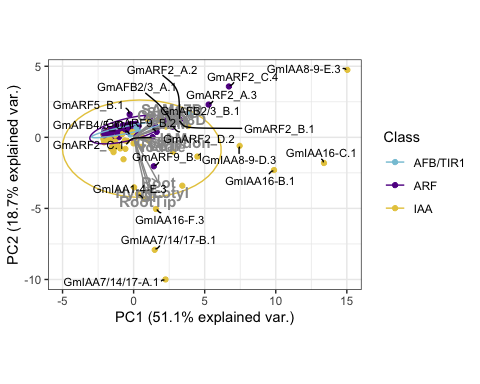
build <- ggplot\_build(PC1\_2all)$data  
points <- build[[1]]  
  
# co-ordinates of the ellipses  
ell\_points <- car::dataEllipse(comb\_pca\_df$PC1,   
 comb\_pca\_df$PC2,   
 as.factor(comb\_pca\_df$Family), levels=c(.7, .9))



# add geom\_point with ellipses point   
  
ell\_ARF <- as.data.frame(ell\_points$ARF$`0.7`)  
  
ell\_IAA <- as.data.frame(ell\_points$IAA$`0.7`)  
  
ell\_TIR <- as.data.frame(ell\_points$`AFB/TIR1`$`0.7`)  
  
# Find which points are outside (!) the ellipse, and add this to the data  
library(sp)  
dat\_TIR <- data.frame(  
 points[2:3],   
 in.ell\_TIR = as.logical(point.in.polygon(points$x, points$y, ell\_TIR$x, ell\_TIR$y))  
)  
  
dat\_IAA <- data.frame(  
 points[2:3],   
 in.ell\_IAA = as.logical(point.in.polygon(points$x, points$y, ell\_IAA$x, ell\_IAA$y))   
)   
  
dat\_ARF <- data.frame(  
 points[2:3],   
 in.ell\_ARF = as.logical(point.in.polygon(points$x, points$y, ell\_ARF$x, ell\_ARF$y))  
)  
# as.logical(point..) equals to TRUE indicated points are inside ellipses  
  
# Combining data points for labeling  
transcript\_expr\_logic <- cbind(comb\_pca\_df, dat\_TIR, dat\_IAA, dat\_ARF) %>% select(., - c(x, y))  
  
  
expr\_logic <- transcript\_expr\_logic %>% mutate(., in\_ell = case\_when(Family=="ARF" & `in.ell\_ARF` == TRUE ~ "TRUE",  
 Family=="IAA" & `in.ell\_IAA` == TRUE ~ "TRUE",  
 Family=="AFB/TIR1" & `in.ell\_TIR` == TRUE ~ "TRUE")) %>%  
 mutate(in\_ell = coalesce(in\_ell, "FALSE"))  
  
expr\_logic[which(expr\_logic$in\_ell == FALSE),]

## Transcript ID heatmap\_label Family Class Clade  
## 5 Glyma.01G098000.3 Glyma.01G098000|GmIAA8-9-D.3 IAA A I  
## 9 Glyma.02G142500.3 Glyma.02G142500|GmIAA16-F.3 IAA C III  
## 20 Glyma.03G070500.1 Glyma.03G070500|GmARF9\_B.1 ARF B I  
## 21 Glyma.03G070500.2 Glyma.03G070500|GmARF9\_B.2 ARF B I  
## 25 Glyma.03G247400.1 Glyma.03G247400|GmIAA16-C.1 IAA C III  
## 29 Glyma.04G200600.1 Glyma.04G200600|GmARF2\_B.1 ARF B I  
## 32 Glyma.05G200800.1 Glyma.05G200800|GmARF2\_C.1 ARF B I  
## 33 Glyma.05G200800.4 Glyma.05G200800|GmARF2\_C.4 ARF B I  
## 36 Glyma.06G091700.3 Glyma.06G091700|GmIAA8-9-E.3 IAA A I  
## 38 Glyma.06G164900.2 Glyma.06G164900|GmARF2\_A.2 ARF B I  
## 39 Glyma.06G164900.3 Glyma.06G164900|GmARF2\_A.3 ARF B I  
## 49 Glyma.08G008100.2 Glyma.08G008100|GmARF2\_D.2 ARF B I  
## 76 Glyma.10G180100.1 Glyma.10G180100|GmIAA7/14/17-A.1 IAA C III  
## 104 Glyma.14G179500.1 Glyma.14G179500|GmAFB4/5\_C.1 AFB/TIR1 AFB4/5 IV  
## 117 Glyma.16G050500.1 Glyma.16G050500|GmAFB2/3\_B.1 AFB/TIR1 AFB2/3 II  
## 120 Glyma.17G256500.1 Glyma.17G256500|GmARF5\_B.1 ARF A II  
## 123 Glyma.19G100200.1 Glyma.19G100200|GmAFB2/3\_A.1 AFB/TIR1 AFB2/3 II  
## 125 Glyma.19G161000.3 Glyma.19G161000|GmIAA1-4-E.3 IAA B II  
## 131 Glyma.20G210400.1 Glyma.20G210400|GmIAA7/14/17-B.1 IAA C III  
## 133 Glyma.20G225000.1 Glyma.20G225000|GmIAA16-B.1 IAA C III  
## AM OF IAM IBM RootTip Cotyledon  
## 5 68.216252 51.350688 53.553189 96.275020 32.628226 78.301786  
## 9 14.688070 529.887081 73.110411 28.516509 43.238091 0.202364  
## 20 14.963834 9.149436 10.014337 18.303006 6.361899 6.335987  
## 21 45.008611 32.497606 40.924358 42.192675 8.439588 8.282666  
## 25 123.752976 182.226043 143.672394 136.882838 68.294552 100.483878  
## 29 59.132821 34.776950 54.023677 104.014185 5.893899 15.036259  
## 32 23.736932 7.300337 13.387625 33.516112 4.197497 21.693739  
## 33 106.794815 41.848269 90.206750 89.149798 3.924654 25.580965  
## 36 120.096829 73.349658 80.928913 112.799969 14.116324 123.198735  
## 38 62.736767 31.362845 56.712867 104.850125 1.621706 14.695636  
## 39 78.161251 91.333242 102.461124 95.846621 1.569549 29.653419  
## 49 41.952212 22.684099 48.464588 54.600720 2.166574 14.976262  
## 76 7.941917 536.895072 6.035997 7.033665 214.246604 30.729826  
## 104 21.750232 21.417969 15.854160 17.435871 11.207461 8.506090  
## 117 55.698420 35.061948 32.831068 58.586254 13.107811 27.899216  
## 120 7.845772 2.581028 3.311743 17.662479 0.302999 1.222648  
## 123 42.087683 43.031580 27.129734 42.689001 13.615904 12.545145  
## 125 4.478037 404.803343 44.077715 17.846549 72.730750 41.028328  
## 131 4.160975 265.136463 15.528614 13.540402 130.804062 41.664671  
## 133 83.900583 259.425512 113.461714 100.588102 53.025576 53.477803  
## Hypocotyl SAM6D SAM17D SAM38D Callus Leaf Root  
## 5 172.112449 101.538840 108.035003 57.568952 3.602672 72.181052 53.728970  
## 9 114.709942 7.356839 6.637677 7.455989 1.051705 20.562404 67.383610  
## 20 4.159165 21.230577 13.709403 9.639602 2.603449 42.803542 126.598709  
## 21 7.071054 47.672295 55.806546 37.757871 0.685890 8.647167 43.277837  
## 25 215.724837 75.229555 108.926253 87.081914 65.420159 178.440543 98.055423  
## 29 13.614824 40.036100 67.500984 33.565553 5.088175 22.636836 12.527492  
## 32 20.950298 31.857638 31.063118 16.461606 4.368482 44.030052 25.338768  
## 33 38.494199 75.216825 290.336670 100.526085 25.977418 0.000000 0.000000  
## 36 118.328990 229.139072 393.546142 181.391747 71.756006 45.788590 20.983248  
## 38 13.618860 48.102339 51.456817 31.907033 8.665198 27.396630 14.501406  
## 39 18.983798 38.298793 237.526834 76.153152 6.048278 3.674760 1.606524  
## 49 26.934453 45.899996 104.119336 30.814124 3.509392 48.206033 26.688307  
## 76 350.297556 2.600212 4.426392 5.209396 2.744771 20.850299 94.160633  
## 104 17.456177 22.806197 19.605122 9.950014 12.500697 19.094595 14.355242  
## 117 27.176499 82.133333 87.939197 38.297183 47.396469 32.138566 17.503017  
## 120 1.046225 28.072725 24.136925 7.085973 69.182090 2.954026 4.491654  
## 123 19.247151 60.919431 75.317808 31.290701 44.433814 27.410816 21.526502  
## 125 177.214792 3.197441 2.314000 2.924909 0.843634 6.919914 6.338750  
## 131 633.844120 1.661192 0.821472 1.444420 0.244966 0.972353 62.263900  
## 133 102.248657 92.557209 144.677356 86.120903 10.711991 21.058177 104.233361  
## Nodule PC1 PC2 PC3 PC4 in.ell\_TIR  
## 5 22.341412 7.4596126 -0.60000202 2.0307657 0.4458205 FALSE  
## 9 1.533396 1.5743362 -5.04177716 -0.6172365 0.6633938 FALSE  
## 20 27.491901 1.4183062 -2.03622924 5.7800703 1.3629861 FALSE  
## 21 3.279099 1.6232820 0.38038019 0.1987720 1.1554167 FALSE  
## 25 5.415049 13.3925129 -1.80641239 2.1698302 -5.4199946 FALSE  
## 29 10.758737 3.1205196 1.14297385 0.1671277 1.3202221 FALSE  
## 32 21.300657 1.3379944 0.01555935 2.7843694 0.4682530 FALSE  
## 33 0.000000 6.7026480 3.57934670 -3.3730284 1.3243790 FALSE  
## 36 22.794609 15.0378929 4.74623732 -1.3006126 -0.9309800 FALSE  
## 38 9.673077 3.2714398 1.25022397 0.2925031 0.9717274 FALSE  
## 39 0.000000 5.2755840 2.30540719 -2.8806692 1.9555757 FALSE  
## 49 8.836310 2.7417865 0.75315742 0.9842749 0.4962433 FALSE  
## 76 5.269519 2.2432846 -9.99777623 -1.0514431 -0.9241382 FALSE  
## 104 3.394860 -0.2309816 0.20105066 0.5268626 -0.5560466 FALSE  
## 117 8.945171 3.9528719 1.62593170 0.5054186 -1.6929049 FALSE  
## 120 0.392173 -0.2798307 1.61342692 0.2055221 -3.4292754 FALSE  
## 123 7.313215 2.6152321 1.16403114 0.5868563 -1.5858479 FALSE  
## 125 0.000000 0.7194803 -4.32442630 -2.0960569 -0.4665481 FALSE  
## 131 0.495348 1.4844789 -7.91342992 -2.4573024 -0.8906494 FALSE  
## 133 53.539749 9.8773408 -2.30022562 3.5022307 4.6373748 FALSE  
## in.ell\_IAA in.ell\_ARF in\_ell  
## 5 FALSE FALSE FALSE  
## 9 FALSE FALSE FALSE  
## 20 TRUE FALSE FALSE  
## 21 TRUE FALSE FALSE  
## 25 FALSE FALSE FALSE  
## 29 TRUE FALSE FALSE  
## 32 TRUE FALSE FALSE  
## 33 FALSE FALSE FALSE  
## 36 FALSE FALSE FALSE  
## 38 TRUE FALSE FALSE  
## 39 FALSE FALSE FALSE  
## 49 TRUE FALSE FALSE  
## 76 FALSE FALSE FALSE  
## 104 TRUE TRUE FALSE  
## 117 TRUE FALSE FALSE  
## 120 TRUE FALSE FALSE  
## 123 TRUE FALSE FALSE  
## 125 FALSE FALSE FALSE  
## 131 FALSE FALSE FALSE  
## 133 FALSE FALSE FALSE

PC1\_2all +   
 geom\_segment(PCA\_loadings, mapping=aes(x=0, y=0, # Change the size of arrows   
 xend=(PC1\*8.75), yend=(PC2\*8.75)),   
 arrow = arrow(length = unit(1/2, "picas")), color="gray60") +  
 annotate("text", x=(PCA\_loadings$PC1\*8.75), #add the tissue names to it manually  
 y=(PCA\_loadings$PC2\*8.75),   
 label=PCA\_loadings$Variables, size=4, color="gray60", fontface="bold") +  
 theme(panel.background = element\_rect(fill = "white", linewidth = 1))+   
 theme\_bw()+  
 scale\_color\_manual(values=c("#86C5D8", "#620093", "#E7C94C"))+  
 ggrepel::geom\_text\_repel(data = expr\_logic %>%   
 as\_tibble(rownames = "name") %>%   
 filter(as.logical(in\_ell == FALSE)),   
 aes(PC1, PC2, label=sub(".\*\\|", "", heatmap\_label)),   
 size=3, max.overlaps = 100, min.segment.length = 0,   
 segment.curvature = -0.1) +  
 labs(color = "Class") +   
 theme\_bw()



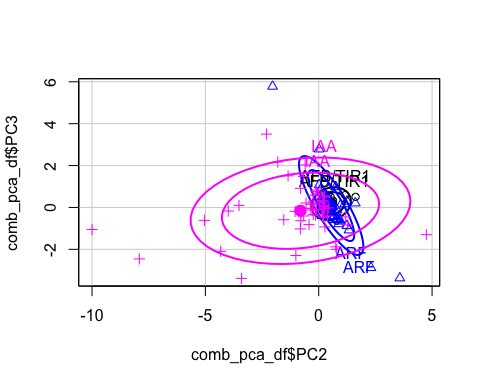
ggsave("20230927\_PC1\_2\_allTissues.png", dpi = 1000, width = 10, height = 8)  
ggsave("20230927\_PC1\_2\_allTissues.pdf", dpi = 1000, width = 10, height = 8)

### PC2 and PC3 outside ellipse labels for the 14 tissues

PC2\_3all <- ggbiplot::ggbiplot(pca, obs.scale = 1, var.scale = .5, choices = c(2, 3),  
 varname.adjust = 3,  
 groups = Family, var.axes = F, varname.size = 2,   
 ellipse = TRUE, circle = FALSE, ellipse.prob = .70)  
   
  
# Extract components so we can select out   
PC2\_3all$data

## xvar yvar groups  
## 1 0.253967120 0.192765997 ARF  
## 2 0.185928231 0.323910990 IAA  
## 3 -0.113511655 0.829138289 IAA  
## 4 0.274717011 -0.929827851 IAA  
## 5 -0.600002016 2.030765709 IAA  
## 6 0.859463281 -0.543671987 ARF  
## 7 -0.427960267 -0.820157717 IAA  
## 8 0.431662229 0.097838721 AFB/TIR1  
## 9 -5.041777156 -0.617236529 IAA  
## 10 -0.558512920 0.212488063 IAA  
## 11 -0.811787304 -1.025141950 IAA  
## 12 0.788703488 -0.633363301 AFB/TIR1  
## 13 0.129024379 0.388439486 AFB/TIR1  
## 14 -0.670223439 1.484374427 IAA  
## 15 0.750445550 -1.880148999 IAA  
## 16 0.330600703 0.213426698 ARF  
## 17 1.334152162 -1.082153419 ARF  
## 18 0.157370925 -0.395001161 ARF  
## 19 0.500704876 0.080303779 ARF  
## 20 -2.036229235 5.780070252 ARF  
## 21 0.380380191 0.198771991 ARF  
## 22 -0.114441199 -0.085693178 IAA  
## 23 -3.402760865 -3.388444330 IAA  
## 24 0.466557952 0.166835894 AFB/TIR1  
## 25 -1.806412389 2.169830163 IAA  
## 26 0.019944454 1.074396091 ARF  
## 27 0.256945271 0.489833024 IAA  
## 28 0.476207228 -0.051671359 AFB/TIR1  
## 29 1.142973848 0.167127745 ARF  
## 30 0.803815826 -0.548952095 ARF  
## 31 0.375426589 0.157488574 ARF  
## 32 0.015559355 2.784369433 ARF  
## 33 3.579346703 -3.373028396 ARF  
## 34 0.494196522 0.018029747 ARF  
## 35 -0.218288936 0.162561278 IAA  
## 36 4.746237323 -1.300612613 IAA  
## 37 0.398718486 0.569404529 AFB/TIR1  
## 38 1.250223968 0.292503137 ARF  
## 39 2.305407189 -2.880669155 ARF  
## 40 -0.788772964 -0.633847587 IAA  
## 41 0.526307555 0.141808591 ARF  
## 42 0.913360463 -0.656456898 ARF  
## 43 0.098979610 0.889037817 ARF  
## 44 0.394826074 0.286525824 ARF  
## 45 0.413220346 -0.086074243 AFB/TIR1  
## 46 0.421500106 0.078045033 AFB/TIR1  
## 47 0.323815463 0.576287661 ARF  
## 48 0.393931829 0.899632729 ARF  
## 49 0.753157423 0.984274929 ARF  
## 50 1.245116561 -0.873135543 ARF  
## 51 0.202653740 0.140445647 ARF  
## 52 -0.023380766 0.649133026 IAA  
## 53 0.141276678 -0.125741994 IAA  
## 54 0.261934275 0.016357767 AFB/TIR1  
## 55 0.732872508 -0.587549057 ARF  
## 56 0.168806405 0.710504593 ARF  
## 57 -0.140394034 -0.360521593 IAA  
## 58 0.231182561 0.257918902 IAA  
## 59 0.793449297 -1.998468838 IAA  
## 60 0.395883644 0.150013982 ARF  
## 61 0.229001671 0.049754903 IAA  
## 62 -0.241185818 -0.345426570 IAA  
## 63 -0.249922455 0.580533544 IAA  
## 64 0.524357821 0.502244955 AFB/TIR1  
## 65 0.369234056 0.114997043 AFB/TIR1  
## 66 0.507222423 -0.214148722 AFB/TIR1  
## 67 -0.662268126 -0.406399893 IAA  
## 68 -0.800512633 0.914386871 IAA  
## 69 0.043427973 0.206015394 IAA  
## 70 0.277764356 0.074614796 ARF  
## 71 -1.351421276 1.509715283 IAA  
## 72 -1.008109821 -2.292586475 IAA  
## 73 0.262406297 -0.029598759 IAA  
## 74 -1.541788959 -0.587753821 IAA  
## 75 -3.991108850 -0.171191334 IAA  
## 76 -9.997776235 -1.051443078 IAA  
## 77 0.004571344 0.531597276 ARF  
## 78 0.223425301 -0.109188343 ARF  
## 79 0.174794131 0.317995304 ARF  
## 80 0.937109194 -0.594875791 ARF  
## 81 0.582823128 0.004808883 ARF  
## 82 0.149412964 0.324427333 ARF  
## 83 0.479261947 -0.173718424 ARF  
## 84 0.804159673 0.857615531 ARF  
## 85 0.589012162 -0.146999936 ARF  
## 86 0.192216165 0.092837656 ARF  
## 87 0.339552665 0.275671087 ARF  
## 88 0.145743103 0.204583749 ARF  
## 89 -0.108332600 0.749279943 IAA  
## 90 0.350064536 -0.025807891 ARF  
## 91 0.882006175 -0.788482703 ARF  
## 92 0.780242803 -0.264669941 ARF  
## 93 0.458750897 0.352511287 ARF  
## 94 0.443802208 -0.049101215 ARF  
## 95 1.281462617 -0.833524403 IAA  
## 96 0.229054413 0.559131560 IAA  
## 97 0.435235820 -0.022773811 IAA  
## 98 -0.353257233 0.152202391 IAA  
## 99 -1.040984678 -0.188391551 IAA  
## 100 0.207864794 -0.465096502 IAA  
## 101 0.171175760 -0.417437561 IAA  
## 102 0.338183452 0.239714138 ARF  
## 103 0.642577969 -0.433940124 ARF  
## 104 0.201050662 0.526862594 AFB/TIR1  
## 105 -0.228022083 0.297046621 IAA  
## 106 0.696034794 -0.401907770 ARF  
## 107 0.814553891 -0.125386206 ARF  
## 108 -0.285475152 -0.122534533 IAA  
## 109 0.237586347 0.097778388 IAA  
## 110 1.187868663 -0.453351398 IAA  
## 111 0.638749151 -0.442597992 ARF  
## 112 0.418512190 -0.204069007 ARF  
## 113 0.355458289 0.229584716 ARF  
## 114 0.311126791 0.219278723 ARF  
## 115 0.428375254 0.457407776 ARF  
## 116 0.960752443 0.101790408 ARF  
## 117 1.625931704 0.505418632 AFB/TIR1  
## 118 0.285122668 -0.017733146 ARF  
## 119 0.262895090 -0.064799773 IAA  
## 120 1.613426920 0.205522094 ARF  
## 121 0.577784192 -0.221521206 ARF  
## 122 0.273681105 0.113040052 ARF  
## 123 1.164031145 0.586856325 AFB/TIR1  
## 124 -0.349419050 -0.048212877 IAA  
## 125 -4.324426296 -2.096056941 IAA  
## 126 -3.518281284 0.098701172 IAA  
## 127 0.285127917 0.193201295 ARF  
## 128 0.633239300 0.321861245 AFB/TIR1  
## 129 0.385551512 -0.405549799 IAA  
## 130 0.267885408 0.074216762 ARF  
## 131 -7.913429916 -2.457302433 IAA  
## 132 -0.781215430 -0.258947266 IAA  
## 133 -2.300225618 3.502230742 IAA

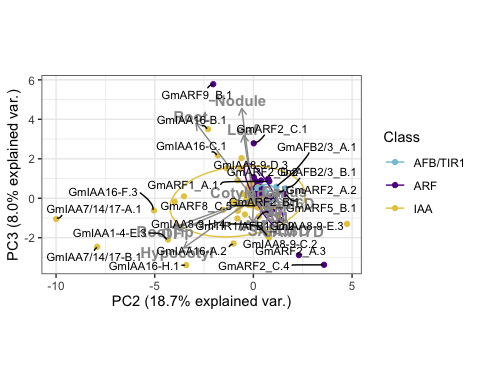
build <- ggplot\_build(PC2\_3all)$data  
points <- build[[1]]  
  
# co-ordinates of the ellipses  
ell\_points <- car::dataEllipse(comb\_pca\_df$PC2,   
 comb\_pca\_df$PC3,   
 as.factor(comb\_pca\_df$Family), levels=c(.7, .9))



# add geom\_point with ellipses point   
  
ell\_ARF <- as.data.frame(ell\_points$ARF$`0.7`)  
  
ell\_IAA <- as.data.frame(ell\_points$IAA$`0.7`)  
  
ell\_TIR <- as.data.frame(ell\_points$`AFB/TIR1`$`0.7`)  
  
# Find which points are outside (!) the ellipse, and add this to the data  
  
dat\_TIR <- data.frame(  
 points[2:3],   
 in.ell\_TIR = as.logical(point.in.polygon(points$x, points$y, ell\_TIR$x, ell\_TIR$y))  
)  
  
dat\_IAA <- data.frame(  
 points[2:3],   
 in.ell\_IAA = as.logical(point.in.polygon(points$x, points$y, ell\_IAA$x, ell\_IAA$y))   
)   
  
dat\_ARF <- data.frame(  
 points[2:3],   
 in.ell\_ARF = as.logical(point.in.polygon(points$x, points$y, ell\_ARF$x, ell\_ARF$y))  
)  
# as.logical(point..) equals to TRUE indicated points are inside ellipses  
  
# Combining data points for labeling  
transcript\_expr\_logic2 <- cbind(comb\_pca\_df, dat\_TIR, dat\_IAA, dat\_ARF) %>% select(., - c(x, y))  
  
  
expr\_logic2 <- transcript\_expr\_logic2 %>% mutate(., in\_ell = case\_when(Family=="ARF" & `in.ell\_ARF` == TRUE ~ "TRUE",  
 Family=="IAA" & `in.ell\_IAA` == TRUE ~ "TRUE",  
 Family=="AFB/TIR1" & `in.ell\_TIR` == TRUE ~ "TRUE")) %>%  
 mutate(in\_ell = coalesce(in\_ell, "FALSE"))  
  
expr\_logic2[which(expr\_logic2$in\_ell == FALSE),]

## Transcript ID heatmap\_label Family Class Clade  
## 5 Glyma.01G098000.3 Glyma.01G098000|GmIAA8-9-D.3 IAA A I  
## 9 Glyma.02G142500.3 Glyma.02G142500|GmIAA16-F.3 IAA C III  
## 12 Glyma.02G152800.2 Glyma.02G152800|GmTIR1/AFB1\_D.2 AFB/TIR1 TIR1/AFB1 I  
## 15 Glyma.02G218100.4 Glyma.02G218100|GmIAA8-9-H.4 IAA A I  
## 18 Glyma.02G239600.5 Glyma.02G239600|GmARF8\_C.5 ARF A II  
## 20 Glyma.03G070500.1 Glyma.03G070500|GmARF9\_B.1 ARF B I  
## 23 Glyma.03G158700.1 Glyma.03G158700|GmIAA16-H.1 IAA C III  
## 25 Glyma.03G247400.1 Glyma.03G247400|GmIAA16-C.1 IAA C III  
## 29 Glyma.04G200600.1 Glyma.04G200600|GmARF2\_B.1 ARF B I  
## 32 Glyma.05G200800.1 Glyma.05G200800|GmARF2\_C.1 ARF B I  
## 33 Glyma.05G200800.4 Glyma.05G200800|GmARF2\_C.4 ARF B I  
## 36 Glyma.06G091700.3 Glyma.06G091700|GmIAA8-9-E.3 IAA A I  
## 38 Glyma.06G164900.2 Glyma.06G164900|GmARF2\_A.2 ARF B I  
## 39 Glyma.06G164900.3 Glyma.06G164900|GmARF2\_A.3 ARF B I  
## 49 Glyma.08G008100.2 Glyma.08G008100|GmARF2\_D.2 ARF B I  
## 59 Glyma.08G273500.2 Glyma.08G273500|GmIAA8-9-C.2 IAA A I  
## 72 Glyma.10G162400.2 Glyma.10G162400|GmIAA16-A.2 IAA C III  
## 76 Glyma.10G180100.1 Glyma.10G180100|GmIAA7/14/17-A.1 IAA C III  
## 84 Glyma.12G164100.1 Glyma.12G164100|GmARF1\_A.1 ARF B I  
## 117 Glyma.16G050500.1 Glyma.16G050500|GmAFB2/3\_B.1 AFB/TIR1 AFB2/3 II  
## 120 Glyma.17G256500.1 Glyma.17G256500|GmARF5\_B.1 ARF A II  
## 123 Glyma.19G100200.1 Glyma.19G100200|GmAFB2/3\_A.1 AFB/TIR1 AFB2/3 II  
## 125 Glyma.19G161000.3 Glyma.19G161000|GmIAA1-4-E.3 IAA B II  
## 131 Glyma.20G210400.1 Glyma.20G210400|GmIAA7/14/17-B.1 IAA C III  
## 133 Glyma.20G225000.1 Glyma.20G225000|GmIAA16-B.1 IAA C III  
## AM OF IAM IBM RootTip Cotyledon  
## 5 68.216252 51.350688 53.553189 96.275020 32.628226 78.301786  
## 9 14.688070 529.887081 73.110411 28.516509 43.238091 0.202364  
## 12 22.069192 16.181094 21.004047 22.849022 12.164769 15.200032  
## 15 58.683503 91.015780 54.923525 50.038109 25.887821 8.588162  
## 18 13.757865 13.859804 8.771196 7.354321 6.099923 14.166313  
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## 36 120.096829 73.349658 80.928913 112.799969 14.116324 123.198735  
## 38 62.736767 31.362845 56.712867 104.850125 1.621706 14.695636  
## 39 78.161251 91.333242 102.461124 95.846621 1.569549 29.653419  
## 49 41.952212 22.684099 48.464588 54.600720 2.166574 14.976262  
## 59 60.235552 42.618679 62.597901 70.694115 15.151090 25.020319  
## 72 50.429036 62.648515 44.799041 49.047824 54.886130 14.549869  
## 76 7.941917 536.895072 6.035997 7.033665 214.246604 30.729826  
## 84 29.907851 25.658848 21.848792 33.978092 12.158648 15.573356  
## 117 55.698420 35.061948 32.831068 58.586254 13.107811 27.899216  
## 120 7.845772 2.581028 3.311743 17.662479 0.302999 1.222648  
## 123 42.087683 43.031580 27.129734 42.689001 13.615904 12.545145  
## 125 4.478037 404.803343 44.077715 17.846549 72.730750 41.028328  
## 131 4.160975 265.136463 15.528614 13.540402 130.804062 41.664671  
## 133 83.900583 259.425512 113.461714 100.588102 53.025576 53.477803  
## Hypocotyl SAM6D SAM17D SAM38D Callus Leaf Root  
## 5 172.112449 101.538840 108.035003 57.568952 3.602672 72.181052 53.728970  
## 9 114.709942 7.356839 6.637677 7.455989 1.051705 20.562404 67.383610  
## 12 20.202937 29.352679 33.917530 17.176745 17.838179 0.000000 0.000000  
## 15 51.413131 79.581114 54.407495 42.568039 6.383128 0.000000 0.000000  
## 18 33.826894 0.000000 11.829332 13.561473 1.551810 0.000000 0.000000  
## 20 4.159165 21.230577 13.709403 9.639602 2.603449 42.803542 126.598709  
## 23 382.933284 20.163323 39.919056 73.535631 0.583159 6.250057 14.892682  
## 25 215.724837 75.229555 108.926253 87.081914 65.420159 178.440543 98.055423  
## 29 13.614824 40.036100 67.500984 33.565553 5.088175 22.636836 12.527492  
## 32 20.950298 31.857638 31.063118 16.461606 4.368482 44.030052 25.338768  
## 33 38.494199 75.216825 290.336670 100.526085 25.977418 0.000000 0.000000  
## 36 118.328990 229.139072 393.546142 181.391747 71.756006 45.788590 20.983248  
## 38 13.618860 48.102339 51.456817 31.907033 8.665198 27.396630 14.501406  
## 39 18.983798 38.298793 237.526834 76.153152 6.048278 3.674760 1.606524  
## 49 26.934453 45.899996 104.119336 30.814124 3.509392 48.206033 26.688307  
## 59 166.602217 77.910628 90.255018 63.645599 6.462795 11.030950 6.618096  
## 72 258.563372 52.919869 43.482386 62.182188 12.401001 7.425099 12.077243  
## 76 350.297556 2.600212 4.426392 5.209396 2.744771 20.850299 94.160633  
## 84 22.344234 27.195518 37.963940 21.692550 51.460680 19.141297 21.871309  
## 117 27.176499 82.133333 87.939197 38.297183 47.396469 32.138566 17.503017  
## 120 1.046225 28.072725 24.136925 7.085973 69.182090 2.954026 4.491654  
## 123 19.247151 60.919431 75.317808 31.290701 44.433814 27.410816 21.526502  
## 125 177.214792 3.197441 2.314000 2.924909 0.843634 6.919914 6.338750  
## 131 633.844120 1.661192 0.821472 1.444420 0.244966 0.972353 62.263900  
## 133 102.248657 92.557209 144.677356 86.120903 10.711991 21.058177 104.233361  
## Nodule PC1 PC2 PC3 PC4 in.ell\_TIR  
## 5 22.341412 7.4596126 -0.60000202 2.0307657 0.445820518 FALSE  
## 9 1.533396 1.5743362 -5.04177716 -0.6172365 0.663393838 FALSE  
## 12 0.000000 -0.1024578 0.78870349 -0.6333633 -0.606570751 FALSE  
## 15 0.000000 2.2767296 0.75044555 -1.8801490 0.882776840 FALSE  
## 18 0.000000 -1.4173576 0.15737092 -0.3950012 -0.059740809 FALSE  
## 20 27.491901 1.4183062 -2.03622924 5.7800703 1.362986140 FALSE  
## 23 2.016265 3.4253377 -3.40276087 -3.3884443 0.846071762 FALSE  
## 25 5.415049 13.3925129 -1.80641239 2.1698302 -5.419994579 FALSE  
## 29 10.758737 3.1205196 1.14297385 0.1671277 1.320222051 TRUE  
## 32 21.300657 1.3379944 0.01555935 2.7843694 0.468252980 FALSE  
## 33 0.000000 6.7026480 3.57934670 -3.3730284 1.324379018 FALSE  
## 36 22.794609 15.0378929 4.74623732 -1.3006126 -0.930979975 FALSE  
## 38 9.673077 3.2714398 1.25022397 0.2925031 0.971727378 FALSE  
## 39 0.000000 5.2755840 2.30540719 -2.8806692 1.955575677 FALSE  
## 49 8.836310 2.7417865 0.75315742 0.9842749 0.496243282 FALSE  
## 59 1.380951 3.8343944 0.79344930 -1.9984688 0.825223890 FALSE  
## 72 0.000000 2.7711864 -1.00810982 -2.2925865 -0.002501458 FALSE  
## 76 5.269519 2.2432846 -9.99777623 -1.0514431 -0.924138217 FALSE  
## 84 7.347936 1.5268214 0.80415967 0.8576155 -2.169356529 FALSE  
## 117 8.945171 3.9528719 1.62593170 0.5054186 -1.692904946 FALSE  
## 120 0.392173 -0.2798307 1.61342692 0.2055221 -3.429275402 FALSE  
## 123 7.313215 2.6152321 1.16403114 0.5868563 -1.585847922 FALSE  
## 125 0.000000 0.7194803 -4.32442630 -2.0960569 -0.466548138 FALSE  
## 131 0.495348 1.4844789 -7.91342992 -2.4573024 -0.890649441 FALSE  
## 133 53.539749 9.8773408 -2.30022562 3.5022307 4.637374786 FALSE  
## in.ell\_IAA in.ell\_ARF in\_ell  
## 5 FALSE FALSE FALSE  
## 9 FALSE FALSE FALSE  
## 12 TRUE TRUE FALSE  
## 15 FALSE FALSE FALSE  
## 18 TRUE FALSE FALSE  
## 20 FALSE FALSE FALSE  
## 23 FALSE FALSE FALSE  
## 25 FALSE FALSE FALSE  
## 29 TRUE FALSE FALSE  
## 32 FALSE FALSE FALSE  
## 33 FALSE FALSE FALSE  
## 36 FALSE FALSE FALSE  
## 38 TRUE FALSE FALSE  
## 39 FALSE FALSE FALSE  
## 49 TRUE FALSE FALSE  
## 59 FALSE FALSE FALSE  
## 72 FALSE FALSE FALSE  
## 76 FALSE FALSE FALSE  
## 84 TRUE FALSE FALSE  
## 117 TRUE FALSE FALSE  
## 120 TRUE FALSE FALSE  
## 123 TRUE FALSE FALSE  
## 125 FALSE FALSE FALSE  
## 131 FALSE FALSE FALSE  
## 133 FALSE FALSE FALSE

PC2\_3all +   
 geom\_segment(PCA\_loadings, mapping=aes(x=0, y=0, # Change the size of arrows   
 xend=(PC2\*8), yend=(PC3\*8)),   
 arrow = arrow(length = unit(1/2, "picas")), color="gray60") +  
 annotate("text", x=(PCA\_loadings$PC2\*8.75), #add the tissue names to it manually  
 y=(PCA\_loadings$PC3\*8.75),   
 label=PCA\_loadings$Variables, size=4, color="gray60", fontface="bold") +  
 theme(panel.background = element\_rect(fill = "white", linewidth = 1))+   
 theme\_bw()+  
 scale\_color\_manual(values=c("#86C5D8", "#620093", "#E7C94C"))+  
 ggrepel::geom\_text\_repel(data = expr\_logic2 %>%   
 as\_tibble(rownames = "name") %>%   
 filter(as.logical(in\_ell == FALSE)),   
 aes(PC2, PC3, label=sub(".\*\\|", "", heatmap\_label)),   
 size=3, max.overlaps = 100, min.segment.length = 0,   
 segment.curvature = -0.1) +  
 labs(color = "Class") +   
 theme\_bw()



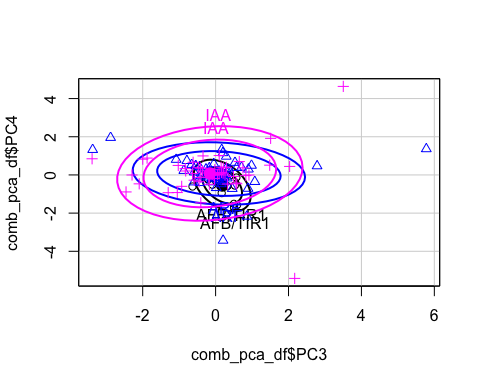
ggsave("20230927\_PC2\_3\_allTissues.png", dpi = 1000, width = 10, height = 8)  
ggsave("20230927\_PC2\_3\_allTissues.pdf", dpi = 1000, width = 10, height = 8)

## PC3 and PC4 for all 14 tissues

PC3\_4all <- ggbiplot::ggbiplot(pca, obs.scale = 1, var.scale = .5, choices = c(3,4),   
 varname.adjust = 3,  
 groups = Family, var.axes = F, varname.size = 2,   
 ellipse = TRUE, circle = FALSE, ellipse.prob = .70)  
  
  
# Extract components so we can select out   
PC3\_4all$data

## xvar yvar groups  
## 1 0.192765997 -0.329157357 ARF  
## 2 0.323910990 -0.475687016 IAA  
## 3 0.829138289 -0.036476522 IAA  
## 4 -0.929827851 -0.596814655 IAA  
## 5 2.030765709 0.445820518 IAA  
## 6 -0.543671987 0.467432769 ARF  
## 7 -0.820157717 0.205971511 IAA  
## 8 0.097838721 0.071591356 AFB/TIR1  
## 9 -0.617236529 0.663393838 IAA  
## 10 0.212488063 0.372205118 IAA  
## 11 -1.025141950 0.497830190 IAA  
## 12 -0.633363301 -0.606570751 AFB/TIR1  
## 13 0.388439486 -0.027544084 AFB/TIR1  
## 14 1.484374427 0.510884280 IAA  
## 15 -1.880148999 0.882776840 IAA  
## 16 0.213426698 -0.342539454 ARF  
## 17 -1.082153419 0.807398759 ARF  
## 18 -0.395001161 -0.059740809 ARF  
## 19 0.080303779 -0.243991322 ARF  
## 20 5.780070252 1.362986140 ARF  
## 21 0.198771991 1.155416668 ARF  
## 22 -0.085693178 0.034427672 IAA  
## 23 -3.388444330 0.846071762 IAA  
## 24 0.166835894 -0.952600938 AFB/TIR1  
## 25 2.169830163 -5.419994579 IAA  
## 26 1.074396091 -0.353111432 ARF  
## 27 0.489833024 -0.078333073 IAA  
## 28 -0.051671359 -0.075470037 AFB/TIR1  
## 29 0.167127745 1.320222051 ARF  
## 30 -0.548952095 0.475445406 ARF  
## 31 0.157488574 0.046630592 ARF  
## 32 2.784369433 0.468252980 ARF  
## 33 -3.373028396 1.324379018 ARF  
## 34 0.018029747 -0.672254946 ARF  
## 35 0.162561278 0.130306707 IAA  
## 36 -1.300612613 -0.930979975 IAA  
## 37 0.569404529 -0.135589979 AFB/TIR1  
## 38 0.292503137 0.971727378 ARF  
## 39 -2.880669155 1.955575677 ARF  
## 40 -0.633847587 0.080138588 IAA  
## 41 0.141808591 0.005907838 ARF  
## 42 -0.656456898 0.540261125 ARF  
## 43 0.889037817 -0.709455025 ARF  
## 44 0.286525824 0.333019125 ARF  
## 45 -0.086074243 -0.512682037 AFB/TIR1  
## 46 0.078045033 -0.027875326 AFB/TIR1  
## 47 0.576287661 0.380679666 ARF  
## 48 0.899632729 0.298409644 ARF  
## 49 0.984274929 0.496243282 ARF  
## 50 -0.873135543 0.226144958 ARF  
## 51 0.140445647 -0.084054512 ARF  
## 52 0.649133026 0.701903529 IAA  
## 53 -0.125741994 0.095581276 IAA  
## 54 0.016357767 -0.335554133 AFB/TIR1  
## 55 -0.587549057 0.144105430 ARF  
## 56 0.710504593 0.391861533 ARF  
## 57 -0.360521593 0.209868199 IAA  
## 58 0.257918902 -0.003108430 IAA  
## 59 -1.998468838 0.825223890 IAA  
## 60 0.150013982 -0.471664728 ARF  
## 61 0.049754903 0.022310438 IAA  
## 62 -0.345426570 0.996380369 IAA  
## 63 0.580533544 -0.463754306 IAA  
## 64 0.502244955 -1.514606539 AFB/TIR1  
## 65 0.114997043 -0.155428110 AFB/TIR1  
## 66 -0.214148722 -0.225376445 AFB/TIR1  
## 67 -0.406399893 -0.132299390 IAA  
## 68 0.914386871 -0.003733875 IAA  
## 69 0.206015394 0.088858545 IAA  
## 70 0.074614796 -0.126598662 ARF  
## 71 1.509715283 1.915691304 IAA  
## 72 -2.292586475 -0.002501458 IAA  
## 73 -0.029598759 -0.187635626 IAA  
## 74 -0.587753821 -0.275831866 IAA  
## 75 -0.171191334 -0.490329128 IAA  
## 76 -1.051443078 -0.924138217 IAA  
## 77 0.531597276 0.648999766 ARF  
## 78 -0.109188343 -0.208434682 ARF  
## 79 0.317995304 -0.168331019 ARF  
## 80 -0.594875791 -0.375545404 ARF  
## 81 0.004808883 0.018108365 ARF  
## 82 0.324427333 0.078558501 ARF  
## 83 -0.173718424 0.362553950 ARF  
## 84 0.857615531 -2.169356529 ARF  
## 85 -0.146999936 0.007800111 ARF  
## 86 0.092837656 -0.001694144 ARF  
## 87 0.275671087 0.014778960 ARF  
## 88 0.204583749 -0.247017881 ARF  
## 89 0.749279943 0.370701122 IAA  
## 90 -0.025807891 -0.090310742 ARF  
## 91 -0.788482703 0.744876265 ARF  
## 92 -0.264669941 0.300848696 ARF  
## 93 0.352511287 0.291391237 ARF  
## 94 -0.049101215 0.579170451 ARF  
## 95 -0.833524403 0.330486790 IAA  
## 96 0.559131560 -0.426860938 IAA  
## 97 -0.022773811 0.273444399 IAA  
## 98 0.152202391 0.406918506 IAA  
## 99 -0.188391551 -0.132620836 IAA  
## 100 -0.465096502 0.378210247 IAA  
## 101 -0.417437561 0.354610124 IAA  
## 102 0.239714138 -0.372805353 ARF  
## 103 -0.433940124 -0.408984924 ARF  
## 104 0.526862594 -0.556046556 AFB/TIR1  
## 105 0.297046621 0.399860511 IAA  
## 106 -0.401907770 0.093790074 ARF  
## 107 -0.125386206 -0.371265410 ARF  
## 108 -0.122534533 0.019319698 IAA  
## 109 0.097778388 0.057486747 IAA  
## 110 -0.453351398 -0.355495023 IAA  
## 111 -0.442597992 0.413317924 ARF  
## 112 -0.204069007 0.144534631 ARF  
## 113 0.229584716 -0.081833467 ARF  
## 114 0.219278723 -0.136465251 ARF  
## 115 0.457407776 -0.717654679 ARF  
## 116 0.101790408 0.189752408 ARF  
## 117 0.505418632 -1.692904946 AFB/TIR1  
## 118 -0.017733146 -0.152751925 ARF  
## 119 -0.064799773 0.081077732 IAA  
## 120 0.205522094 -3.429275402 ARF  
## 121 -0.221521206 -0.123086248 ARF  
## 122 0.113040052 -0.006051997 ARF  
## 123 0.586856325 -1.585847922 AFB/TIR1  
## 124 -0.048212877 -0.018020025 IAA  
## 125 -2.096056941 -0.466548138 IAA  
## 126 0.098701172 1.015184517 IAA  
## 127 0.193201295 0.035834145 ARF  
## 128 0.321861245 -0.590150626 AFB/TIR1  
## 129 -0.405549799 -1.459565623 IAA  
## 130 0.074216762 0.099160724 ARF  
## 131 -2.457302433 -0.890649441 IAA  
## 132 -0.258947266 0.101572514 IAA  
## 133 3.502230742 4.637374786 IAA

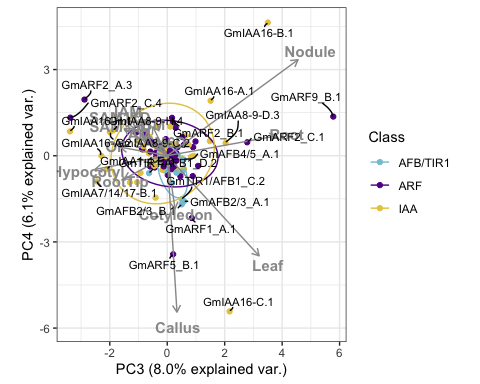
build <- ggplot\_build(PC3\_4all)$data  
points <- build[[1]]  
  
# co-ordinates of the ellipses  
ell\_points <- car::dataEllipse(comb\_pca\_df$PC3,   
 comb\_pca\_df$PC4,   
 as.factor(comb\_pca\_df$Family), levels=c(.7, .9))



# add geom\_point with ellipses point   
  
ell\_ARF <- as.data.frame(ell\_points$ARF$`0.7`)  
  
ell\_IAA <- as.data.frame(ell\_points$IAA$`0.7`)  
  
ell\_TIR <- as.data.frame(ell\_points$`AFB/TIR1`$`0.7`)  
  
# Find which points are outside (!) the ellipse, and add this to the data  
  
dat\_TIR <- data.frame(  
 points[2:3],   
 in.ell\_TIR = as.logical(point.in.polygon(points$x, points$y, ell\_TIR$x, ell\_TIR$y))  
)  
  
dat\_IAA <- data.frame(  
 points[2:3],   
 in.ell\_IAA = as.logical(point.in.polygon(points$x, points$y, ell\_IAA$x, ell\_IAA$y))   
)   
  
dat\_ARF <- data.frame(  
 points[2:3],   
 in.ell\_ARF = as.logical(point.in.polygon(points$x, points$y, ell\_ARF$x, ell\_ARF$y))  
)  
# as.logical(point..) equals to TRUE indicated points are inside ellipses  
  
# Combining data points for labeling  
transcript\_expr\_logic3 <- cbind(comb\_pca\_df, dat\_TIR, dat\_IAA, dat\_ARF) %>% select(., - c(x, y))  
  
  
expr\_logic3 <- transcript\_expr\_logic3 %>% mutate(., in\_ell = case\_when(Family=="ARF" & `in.ell\_ARF` == TRUE ~ "TRUE",  
 Family=="IAA" & `in.ell\_IAA` == TRUE ~ "TRUE",  
 Family=="AFB/TIR1" & `in.ell\_TIR` == TRUE ~ "TRUE")) %>%  
 mutate(in\_ell = coalesce(in\_ell, "FALSE"))  
  
expr\_logic3[which(expr\_logic3$in\_ell == FALSE),]

## Transcript ID heatmap\_label Family Class Clade  
## 5 Glyma.01G098000.3 Glyma.01G098000|GmIAA8-9-D.3 IAA A I  
## 12 Glyma.02G152800.2 Glyma.02G152800|GmTIR1/AFB1\_D.2 AFB/TIR1 TIR1/AFB1 I  
## 15 Glyma.02G218100.4 Glyma.02G218100|GmIAA8-9-H.4 IAA A I  
## 20 Glyma.03G070500.1 Glyma.03G070500|GmARF9\_B.1 ARF B I  
## 23 Glyma.03G158700.1 Glyma.03G158700|GmIAA16-H.1 IAA C III  
## 25 Glyma.03G247400.1 Glyma.03G247400|GmIAA16-C.1 IAA C III  
## 29 Glyma.04G200600.1 Glyma.04G200600|GmARF2\_B.1 ARF B I  
## 32 Glyma.05G200800.1 Glyma.05G200800|GmARF2\_C.1 ARF B I  
## 33 Glyma.05G200800.4 Glyma.05G200800|GmARF2\_C.4 ARF B I  
## 37 Glyma.06G095400.1 Glyma.06G095400|GmAFB4/5\_A.1 AFB/TIR1 AFB4/5 IV  
## 39 Glyma.06G164900.3 Glyma.06G164900|GmARF2\_A.3 ARF B I  
## 59 Glyma.08G273500.2 Glyma.08G273500|GmIAA8-9-C.2 IAA A I  
## 64 Glyma.10G021500.2 Glyma.10G021500|GmTIR1/AFB1\_C.2 AFB/TIR1 TIR1/AFB1 I  
## 71 Glyma.10G162400.1 Glyma.10G162400|GmIAA16-A.1 IAA C III  
## 72 Glyma.10G162400.2 Glyma.10G162400|GmIAA16-A.2 IAA C III  
## 84 Glyma.12G164100.1 Glyma.12G164100|GmARF1\_A.1 ARF B I  
## 117 Glyma.16G050500.1 Glyma.16G050500|GmAFB2/3\_B.1 AFB/TIR1 AFB2/3 II  
## 120 Glyma.17G256500.1 Glyma.17G256500|GmARF5\_B.1 ARF A II  
## 123 Glyma.19G100200.1 Glyma.19G100200|GmAFB2/3\_A.1 AFB/TIR1 AFB2/3 II  
## 125 Glyma.19G161000.3 Glyma.19G161000|GmIAA1-4-E.3 IAA B II  
## 131 Glyma.20G210400.1 Glyma.20G210400|GmIAA7/14/17-B.1 IAA C III  
## 133 Glyma.20G225000.1 Glyma.20G225000|GmIAA16-B.1 IAA C III  
## AM OF IAM IBM RootTip Cotyledon Hypocotyl  
## 5 68.216252 51.350688 53.553189 96.27502 32.628226 78.301786 172.112449  
## 12 22.069192 16.181094 21.004047 22.84902 12.164769 15.200032 20.202937  
## 15 58.683503 91.015780 54.923525 50.03811 25.887821 8.588162 51.413131  
## 20 14.963834 9.149436 10.014337 18.30301 6.361899 6.335987 4.159165  
## 23 62.978354 188.282417 63.415971 50.27380 93.913232 11.797675 382.933284  
## 25 123.752976 182.226043 143.672394 136.88284 68.294552 100.483878 215.724837  
## 29 59.132821 34.776950 54.023677 104.01418 5.893899 15.036259 13.614824  
## 32 23.736932 7.300337 13.387625 33.51611 4.197497 21.693739 20.950298  
## 33 106.794815 41.848269 90.206750 89.14980 3.924654 25.580965 38.494199  
## 37 16.624289 16.028732 15.517072 13.11757 3.675868 9.842971 17.361197  
## 39 78.161251 91.333242 102.461124 95.84662 1.569549 29.653419 18.983798  
## 59 60.235552 42.618679 62.597901 70.69411 15.151090 25.020319 166.602217  
## 64 19.724328 16.170619 18.096732 18.50347 10.239295 14.506518 14.635121  
## 71 60.897385 87.148645 58.213890 60.41856 39.516020 28.827155 119.352820  
## 72 50.429036 62.648515 44.799041 49.04782 54.886130 14.549869 258.563372  
## 84 29.907851 25.658848 21.848792 33.97809 12.158648 15.573356 22.344234  
## 117 55.698420 35.061948 32.831068 58.58625 13.107811 27.899216 27.176499  
## 120 7.845772 2.581028 3.311743 17.66248 0.302999 1.222648 1.046225  
## 123 42.087683 43.031580 27.129734 42.68900 13.615904 12.545145 19.247151  
## 125 4.478037 404.803343 44.077715 17.84655 72.730750 41.028328 177.214792  
## 131 4.160975 265.136463 15.528614 13.54040 130.804062 41.664671 633.844120  
## 133 83.900583 259.425512 113.461714 100.58810 53.025576 53.477803 102.248657  
## SAM6D SAM17D SAM38D Callus Leaf Root Nodule  
## 5 101.538840 108.035003 57.568952 3.602672 72.181052 53.728970 22.341412  
## 12 29.352679 33.917530 17.176745 17.838179 0.000000 0.000000 0.000000  
## 15 79.581114 54.407495 42.568039 6.383128 0.000000 0.000000 0.000000  
## 20 21.230577 13.709403 9.639602 2.603449 42.803542 126.598709 27.491901  
## 23 20.163323 39.919056 73.535631 0.583159 6.250057 14.892682 2.016265  
## 25 75.229555 108.926253 87.081914 65.420159 178.440543 98.055423 5.415049  
## 29 40.036100 67.500984 33.565553 5.088175 22.636836 12.527492 10.758737  
## 32 31.857638 31.063118 16.461606 4.368482 44.030052 25.338768 21.300657  
## 33 75.216825 290.336670 100.526085 25.977418 0.000000 0.000000 0.000000  
## 37 17.568729 22.163578 11.157726 12.838756 8.101368 7.946719 7.208545  
## 39 38.298793 237.526834 76.153152 6.048278 3.674760 1.606524 0.000000  
## 59 77.910628 90.255018 63.645599 6.462795 11.030950 6.618096 1.380951  
## 64 12.243954 22.316362 15.443247 25.621399 26.106051 5.641934 3.205496  
## 71 55.456636 78.452259 42.917887 2.247079 23.957562 65.117084 21.527670  
## 72 52.919869 43.482386 62.182188 12.401001 7.425099 12.077243 0.000000  
## 84 27.195518 37.963940 21.692550 51.460680 19.141297 21.871309 7.347936  
## 117 82.133333 87.939197 38.297183 47.396469 32.138566 17.503017 8.945171  
## 120 28.072725 24.136925 7.085973 69.182090 2.954026 4.491654 0.392173  
## 123 60.919431 75.317808 31.290701 44.433814 27.410816 21.526502 7.313215  
## 125 3.197441 2.314000 2.924909 0.843634 6.919914 6.338750 0.000000  
## 131 1.661192 0.821472 1.444420 0.244966 0.972353 62.263900 0.495348  
## 133 92.557209 144.677356 86.120903 10.711991 21.058177 104.233361 53.539749  
## PC1 PC2 PC3 PC4 in.ell\_TIR in.ell\_IAA  
## 5 7.45961256 -0.60000202 2.0307657 0.445820518 FALSE FALSE  
## 12 -0.10245780 0.78870349 -0.6333633 -0.606570751 FALSE TRUE  
## 15 2.27672963 0.75044555 -1.8801490 0.882776840 FALSE FALSE  
## 20 1.41830620 -2.03622924 5.7800703 1.362986140 FALSE FALSE  
## 23 3.42533775 -3.40276087 -3.3884443 0.846071762 FALSE FALSE  
## 25 13.39251285 -1.80641239 2.1698302 -5.419994579 FALSE FALSE  
## 29 3.12051959 1.14297385 0.1671277 1.320222051 FALSE TRUE  
## 32 1.33799443 0.01555935 2.7843694 0.468252980 FALSE FALSE  
## 33 6.70264804 3.57934670 -3.3730284 1.324379018 FALSE FALSE  
## 37 -0.48862762 0.39871849 0.5694045 -0.135589979 FALSE TRUE  
## 39 5.27558405 2.30540719 -2.8806692 1.955575677 FALSE FALSE  
## 59 3.83439442 0.79344930 -1.9984688 0.825223890 FALSE FALSE  
## 64 0.07775833 0.52435782 0.5022450 -1.514606539 FALSE FALSE  
## 71 4.48509992 -1.35142128 1.5097153 1.915691304 FALSE FALSE  
## 72 2.77118641 -1.00810982 -2.2925865 -0.002501458 FALSE FALSE  
## 84 1.52682137 0.80415967 0.8576155 -2.169356529 FALSE FALSE  
## 117 3.95287191 1.62593170 0.5054186 -1.692904946 FALSE FALSE  
## 120 -0.27983068 1.61342692 0.2055221 -3.429275402 FALSE FALSE  
## 123 2.61523211 1.16403114 0.5868563 -1.585847922 FALSE FALSE  
## 125 0.71948030 -4.32442630 -2.0960569 -0.466548138 FALSE FALSE  
## 131 1.48447894 -7.91342992 -2.4573024 -0.890649441 FALSE FALSE  
## 133 9.87734076 -2.30022562 3.5022307 4.637374786 FALSE FALSE  
## in.ell\_ARF in\_ell  
## 5 FALSE FALSE  
## 12 TRUE FALSE  
## 15 FALSE FALSE  
## 20 FALSE FALSE  
## 23 FALSE FALSE  
## 25 FALSE FALSE  
## 29 FALSE FALSE  
## 32 FALSE FALSE  
## 33 FALSE FALSE  
## 37 TRUE FALSE  
## 39 FALSE FALSE  
## 59 FALSE FALSE  
## 64 FALSE FALSE  
## 71 FALSE FALSE  
## 72 FALSE FALSE  
## 84 FALSE FALSE  
## 117 FALSE FALSE  
## 120 FALSE FALSE  
## 123 FALSE FALSE  
## 125 FALSE FALSE  
## 131 FALSE FALSE  
## 133 FALSE FALSE

PC3\_4all +   
 geom\_segment(PCA\_loadings, mapping=aes(x=0, y=0, # Change the size of arrows   
 xend=(PC3\*8), yend=(PC4\*8)),   
 arrow = arrow(length = unit(1/2, "picas")), color="gray60") +  
 annotate("text", x=(PCA\_loadings$PC3\*8.75), #add the tissue names to it manually  
 y=(PCA\_loadings$PC4\*8.75),   
 label=PCA\_loadings$Variables, size=4, color="gray60", fontface="bold") +  
 theme(panel.background = element\_rect(fill = "white", linewidth = 1))+   
 theme\_bw()+  
 scale\_color\_manual(values=c("#86C5D8", "#620093", "#E7C94C")) +  
 ggrepel::geom\_text\_repel(data = expr\_logic3 %>%   
 as\_tibble(rownames = "name") %>%   
 filter(as.logical(in\_ell == FALSE)),   
 aes(PC3, PC4, label=sub(".\*\\|", "", heatmap\_label)),   
 size=3, max.overlaps = 100, min.segment.length = 0,   
 segment.curvature = -0.1) +  
 labs(color = "Class") +   
 theme\_bw()



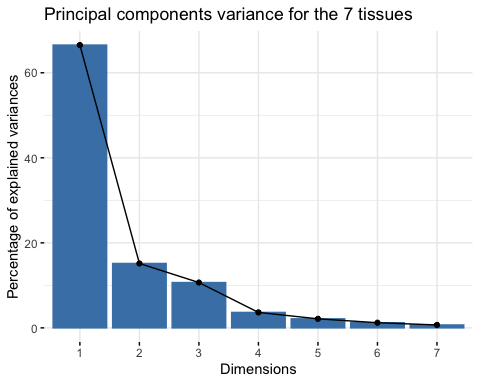
ggsave("20230927\_PC3\_4\_allTissues.png", dpi = 1000, width = 10, height = 8)  
ggsave("20230927\_PC3\_4\_allTissues.pdf", dpi = 1000, width = 10, height = 8)

# PCA with only tissues of interest

pca2 <- prcomp(pca\_data[, -c(1:5, 7:10, 16, 18:19)],   
 scale. = T, center = T)  
summary(pca2)

## Importance of components:  
## PC1 PC2 PC3 PC4 PC5 PC6 PC7  
## Standard deviation 2.1579 1.0299 0.8640 0.50467 0.38576 0.29139 0.21916  
## Proportion of Variance 0.6652 0.1515 0.1066 0.03638 0.02126 0.01213 0.00686  
## Cumulative Proportion 0.6652 0.8167 0.9234 0.95975 0.98101 0.99314 1.00000

factoextra::fviz\_eig(pca2, main = "Principal components variance for the 7 tissues")



ggsave("20230927\_PCscreePlot\_7Tissues.png", dpi = 1000, width = 10, height = 8)

joint\_pca\_df <- cbind(pca\_data, pca2$x[, 1:4])  
head(joint\_pca\_df)

## Transcript ID heatmap\_label Family Class Clade AM  
## 1 Glyma.01G002100.1 Glyma.01G002100|GmARF7/19\_F.1 ARF A II 10.166688  
## 2 Glyma.01G019400.1 Glyma.01G019400|GmIAA8-9-B.1 IAA A I 4.023220  
## 3 Glyma.01G019400.2 Glyma.01G019400|GmIAA8-9-B.2 IAA A I 3.945653  
## 4 Glyma.01G019400.3 Glyma.01G019400|GmIAA8-9-B.3 IAA A I 22.514233  
## 5 Glyma.01G098000.3 Glyma.01G098000|GmIAA8-9-D.3 IAA A I 68.216252  
## 6 Glyma.01G103500.1 Glyma.01G103500|GmARF9\_A.1 ARF B I 23.365836  
## OF IAM IBM RootTip Cotyledon Hypocotyl SAM6D  
## 1 11.093702 9.940766 11.778406 6.055558 6.293037 12.466244 8.948254  
## 2 7.572444 0.000000 1.479181 3.679860 1.003818 8.866408 2.983280  
## 3 0.000000 6.009114 7.650699 2.217478 2.098637 11.260883 9.399142  
## 4 35.850834 20.735453 26.681081 16.122488 4.029864 88.717989 25.081359  
## 5 51.350688 53.553189 96.275020 32.628226 78.301786 172.112449 101.538840  
## 6 7.195187 14.135920 28.240802 4.918282 2.088168 2.353419 26.594544  
## SAM17D SAM38D Callus Leaf Root Nodule PC1  
## 1 8.096833 5.745906 9.251965 4.882454 6.893253 1.926212 -1.0501429  
## 2 7.873006 3.443632 6.039812 10.540945 5.246408 0.577947 -1.3485364  
## 3 0.000000 2.491927 0.946290 11.828802 22.566715 1.890763 -1.2849928  
## 4 26.514627 29.093086 17.719987 6.167892 0.000000 0.000000 0.1258125  
## 5 108.035003 57.568952 3.602672 72.181052 53.728970 22.341412 6.2978744  
## 6 33.652046 16.405528 1.091669 0.000000 0.000000 0.000000 -0.3140464  
## PC2 PC3 PC4  
## 1 0.10515442 0.1357363 -0.16679473  
## 2 0.03516704 0.3910160 0.02172556  
## 3 -0.03259973 0.4674483 -0.06753696  
## 4 -0.19841417 -0.6187942 0.41436903  
## 5 -1.83724237 1.5164566 -1.17162708  
## 6 0.76188043 -0.2984882 0.15505685

Family <- joint\_pca\_df$Family  
  
# extract the loading so we can change the arrows more easily later while ploting  
PCA\_loadings2 <- data.frame(Variables=rownames(pca2$rotation), pca2$rotation)

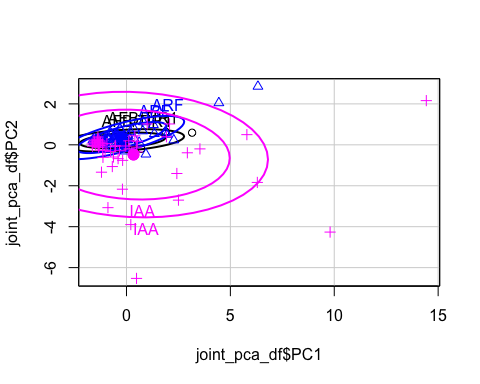
# Plot  
library(ggrepel)  
PC1\_2\_7tissues <- ggbiplot::ggbiplot(pca2, obs.scale = 1, var.scale = .5, choices = c(1, 2),  
 varname.adjust = 3,  
 groups = Family, var.axes = F, varname.size = 2,   
 ellipse = TRUE, circle = FALSE, ellipse.prob = .70)

## withdraw lables outside ellipses to label outliers

# Extract components so we can select out   
PC1\_2\_7tissues$data

## xvar yvar groups  
## 1 -1.05014286 0.10515442 ARF  
## 2 -1.34853637 0.03516704 IAA  
## 3 -1.28499278 -0.03259973 IAA  
## 4 0.12581250 -0.19841417 IAA  
## 5 6.29787441 -1.83724237 IAA  
## 6 -0.31404635 0.76188043 ARF  
## 7 0.50539968 -0.34300647 IAA  
## 8 -1.12869949 0.37674443 AFB/TIR1  
## 9 -0.68221161 -1.06192064 IAA  
## 10 -1.32267878 -0.05614018 IAA  
## 11 -1.33942303 -0.12354575 IAA  
## 12 0.06210206 0.41382610 AFB/TIR1  
## 13 -1.32261153 0.16146909 AFB/TIR1  
## 14 0.40306612 0.43976369 IAA  
## 15 2.07329850 1.01893547 IAA  
## 16 -0.05373907 -0.19219653 ARF  
## 17 0.81044975 1.11700892 ARF  
## 18 -0.78784060 -0.12083822 ARF  
## 19 -0.24435712 0.14788376 ARF  
## 20 -0.07853023 -0.30909424 ARF  
## 21 1.29528965 0.98161007 ARF  
## 22 -1.65539096 0.04406573 IAA  
## 23 2.50142090 -2.70244068 IAA  
## 24 0.70690012 -0.19818565 AFB/TIR1  
## 25 9.79977762 -4.26352971 IAA  
## 26 -0.99159124 -0.23057025 ARF  
## 27 -0.03794509 -0.05712991 IAA  
## 28 -0.35471399 0.37697535 AFB/TIR1  
## 29 1.85976056 0.61742415 ARF  
## 30 -0.31860769 0.79593666 ARF  
## 31 -1.34000604 0.23346430 ARF  
## 32 0.93454507 -0.45975448 ARF  
## 33 6.32619943 2.85428889 ARF  
## 34 -1.62029102 0.22580682 ARF  
## 35 -0.52375557 -0.05145862 IAA  
## 36 14.43049528 2.15899012 IAA  
## 37 -0.43602126 0.15912727 AFB/TIR1  
## 38 1.95569813 0.50580340 ARF  
## 39 4.44562780 2.04813145 ARF  
## 40 -1.20335584 -1.33745677 IAA  
## 41 -0.10578553 0.24206119 ARF  
## 42 0.35581526 0.80233487 ARF  
## 43 -0.18778513 0.04913286 ARF  
## 44 -0.08921436 0.44159097 ARF  
## 45 -1.45080932 0.22207205 AFB/TIR1  
## 46 -1.14906764 0.28259178 AFB/TIR1  
## 47 -0.99845260 0.22602501 ARF  
## 48 0.05595252 0.23517727 ARF  
## 49 2.27842210 0.23014394 ARF  
## 50 1.34307083 0.54381981 ARF  
## 51 -1.55156504 0.16357844 ARF  
## 52 0.51958352 0.17260396 IAA  
## 53 -1.36883544 0.27331654 IAA  
## 54 -1.38601667 0.12704175 AFB/TIR1  
## 55 -0.47630116 0.55667830 ARF  
## 56 -0.84258221 0.27501312 ARF  
## 57 -1.56272647 0.22850724 IAA  
## 58 -0.94247516 0.05578545 IAA  
## 59 3.53507221 -0.19876183 IAA  
## 60 -1.07587306 0.22563162 ARF  
## 61 -1.46220344 0.13643709 IAA  
## 62 0.47369476 -0.11275080 IAA  
## 63 -0.18575199 -0.75842052 IAA  
## 64 0.01141647 -0.20362431 AFB/TIR1  
## 65 -1.42021154 0.20580527 AFB/TIR1  
## 66 -0.17447944 0.17662980 AFB/TIR1  
## 67 -1.14563503 -0.26383478 IAA  
## 68 -1.49981620 -0.02775860 IAA  
## 69 -1.54348979 0.12874603 IAA  
## 70 -1.39507835 0.16168347 ARF  
## 71 2.92945855 -0.38908091 IAA  
## 72 2.42394340 -1.40080513 IAA  
## 73 -1.15099418 0.04204640 IAA  
## 74 -0.62584455 -0.59554073 IAA  
## 75 -0.40410313 -0.67555222 IAA  
## 76 0.20859279 -3.89840357 IAA  
## 77 -0.84786884 0.39304286 ARF  
## 78 -0.28107091 -0.14129573 ARF  
## 79 -0.79489435 0.01134430 ARF  
## 80 -0.42946116 0.30503427 ARF  
## 81 -0.86565058 0.26459088 ARF  
## 82 -1.57421557 0.13997225 ARF  
## 83 -0.58850376 0.33976118 ARF  
## 84 0.60982840 0.11755926 ARF  
## 85 -0.95270455 0.41027661 ARF  
## 86 -1.18400893 0.03642123 ARF  
## 87 -1.35845402 0.18832650 ARF  
## 88 -1.32330825 0.07623100 ARF  
## 89 -1.32211008 0.09616199 IAA  
## 90 -1.33857165 0.22631146 ARF  
## 91 0.18759733 0.63062446 ARF  
## 92 0.37773397 0.28877357 ARF  
## 93 -0.28033129 0.18223673 ARF  
## 94 -0.49772951 0.50936896 ARF  
## 95 0.99582518 1.01924752 IAA  
## 96 -0.55223302 -0.06070833 IAA  
## 97 -1.37434561 0.37953170 IAA  
## 98 -1.28152736 0.19095485 IAA  
## 99 -1.13207935 -0.61127542 IAA  
## 100 -1.25672736 0.12918250 IAA  
## 101 -1.41443268 -0.02383471 IAA  
## 102 -1.00237591 0.08053528 ARF  
## 103 0.07271378 0.24466668 ARF  
## 104 -0.16199629 0.02332871 AFB/TIR1  
## 105 0.11133693 0.19479841 IAA  
## 106 0.08787857 0.41799993 ARF  
## 107 -0.76288272 0.57895723 ARF  
## 108 -1.03198092 -0.27146457 IAA  
## 109 -1.39231781 0.23943824 IAA  
## 110 1.92371297 0.39438069 IAA  
## 111 -0.58154082 0.43897284 ARF  
## 112 -1.35296511 0.21805555 ARF  
## 113 -1.39891628 0.16435444 ARF  
## 114 -1.47279337 0.21819497 ARF  
## 115 -0.37176747 0.12804991 ARF  
## 116 0.78469153 0.67534859 ARF  
## 117 3.15794243 0.59153383 AFB/TIR1  
## 118 -1.10801710 0.21113642 ARF  
## 119 -1.40473569 0.19705245 IAA  
## 120 -0.82324378 0.57202079 ARF  
## 121 -0.44612445 0.38556844 ARF  
## 122 -1.54287005 0.30454921 ARF  
## 123 1.88822437 0.64531129 AFB/TIR1  
## 124 -1.63443659 -0.06758392 IAA  
## 125 -0.19442276 -2.16841690 IAA  
## 126 -0.89218238 -3.07007360 IAA  
## 127 -1.14683163 0.16640283 ARF  
## 128 0.22854712 0.06134928 AFB/TIR1  
## 129 -0.33759214 -0.28989506 IAA  
## 130 -1.26104706 0.28590134 ARF  
## 131 0.48333718 -6.52671369 IAA  
## 132 -0.76649931 -0.32242524 IAA  
## 133 5.79424460 0.49697177 IAA

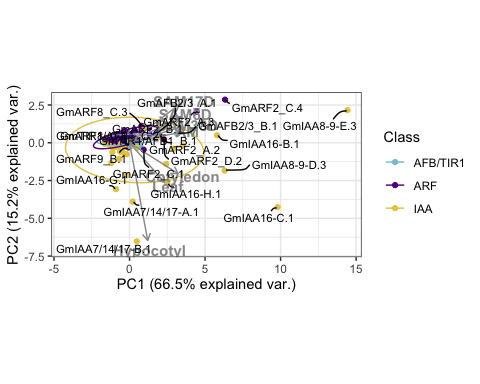
build <- ggplot\_build(PC1\_2\_7tissues)$data  
points <- build[[1]]  
  
# co-ordinates of the ellipses  
ell\_points <- car::dataEllipse(joint\_pca\_df$PC1,   
 joint\_pca\_df$PC2,   
 as.factor(joint\_pca\_df$Family), levels=c(.7, .9))



# add geom\_point with ellipses point   
  
ell\_ARF <- as.data.frame(ell\_points$ARF$`0.7`)  
  
ell\_IAA <- as.data.frame(ell\_points$IAA$`0.7`)  
  
ell\_TIR <- as.data.frame(ell\_points$`AFB/TIR1`$`0.7`)  
  
# Find which points are outside (!) the ellipse, and add this to the data  
library(sp)  
dat\_TIR <- data.frame(  
 points[2:3],   
 in.ell\_TIR = as.logical(point.in.polygon(points$x, points$y, ell\_TIR$x, ell\_TIR$y))  
)  
  
dat\_IAA <- data.frame(  
 points[2:3],   
 in.ell\_IAA = as.logical(point.in.polygon(points$x, points$y, ell\_IAA$x, ell\_IAA$y))   
)   
  
dat\_ARF <- data.frame(  
 points[2:3],   
 in.ell\_ARF = as.logical(point.in.polygon(points$x, points$y, ell\_ARF$x, ell\_ARF$y))  
)  
# as.logical(point..) equals to TRUE indicated points are inside ellipses  
  
# Combining data points for labeling  
#Combine data points coordinates with PCs and expression data containing gene names will help us to have only genes of interest names, or at list the majority of them.  
transcript\_expr\_logical <- cbind(joint\_pca\_df, dat\_TIR, dat\_IAA, dat\_ARF) %>% select(., - c(x, y))  
  
  
expr\_logical <- transcript\_expr\_logical %>% mutate(., in\_ell = case\_when(Family=="ARF" & `in.ell\_ARF` == TRUE ~ "TRUE",  
 Family=="IAA" & `in.ell\_IAA` == TRUE ~ "TRUE",  
 Family=="AFB/TIR1" & `in.ell\_TIR` == TRUE ~ "TRUE")) %>%  
 mutate(in\_ell = coalesce(in\_ell, "FALSE"))  
  
expr\_logical[which(expr\_logical$in\_ell == FALSE),]

## Transcript ID heatmap\_label Family Class Clade  
## 5 Glyma.01G098000.3 Glyma.01G098000|GmIAA8-9-D.3 IAA A I  
## 16 Glyma.02G239600.1 Glyma.02G239600|GmARF8\_C.1 ARF A II  
## 17 Glyma.02G239600.3 Glyma.02G239600|GmARF8\_C.3 ARF A II  
## 20 Glyma.03G070500.1 Glyma.03G070500|GmARF9\_B.1 ARF B I  
## 23 Glyma.03G158700.1 Glyma.03G158700|GmIAA16-H.1 IAA C III  
## 24 Glyma.03G209400.1 Glyma.03G209400|GmTIR1/AFB1\_B.1 AFB/TIR1 TIR1/AFB1 I  
## 25 Glyma.03G247400.1 Glyma.03G247400|GmIAA16-C.1 IAA C III  
## 29 Glyma.04G200600.1 Glyma.04G200600|GmARF2\_B.1 ARF B I  
## 32 Glyma.05G200800.1 Glyma.05G200800|GmARF2\_C.1 ARF B I  
## 33 Glyma.05G200800.4 Glyma.05G200800|GmARF2\_C.4 ARF B I  
## 36 Glyma.06G091700.3 Glyma.06G091700|GmIAA8-9-E.3 IAA A I  
## 38 Glyma.06G164900.2 Glyma.06G164900|GmARF2\_A.2 ARF B I  
## 39 Glyma.06G164900.3 Glyma.06G164900|GmARF2\_A.3 ARF B I  
## 49 Glyma.08G008100.2 Glyma.08G008100|GmARF2\_D.2 ARF B I  
## 64 Glyma.10G021500.2 Glyma.10G021500|GmTIR1/AFB1\_C.2 AFB/TIR1 TIR1/AFB1 I  
## 76 Glyma.10G180100.1 Glyma.10G180100|GmIAA7/14/17-A.1 IAA C III  
## 117 Glyma.16G050500.1 Glyma.16G050500|GmAFB2/3\_B.1 AFB/TIR1 AFB2/3 II  
## 123 Glyma.19G100200.1 Glyma.19G100200|GmAFB2/3\_A.1 AFB/TIR1 AFB2/3 II  
## 126 Glyma.19G161100.1 Glyma.19G161100|GmIAA16-G.1 IAA C III  
## 131 Glyma.20G210400.1 Glyma.20G210400|GmIAA7/14/17-B.1 IAA C III  
## 133 Glyma.20G225000.1 Glyma.20G225000|GmIAA16-B.1 IAA C III  
## AM OF IAM IBM RootTip Cotyledon  
## 5 68.216252 51.350688 53.553189 96.275020 32.628226 78.301786  
## 16 18.062407 8.153791 22.217284 25.144304 6.595787 17.054927  
## 17 37.168779 5.439277 41.924483 51.089719 6.308382 0.000000  
## 20 14.963834 9.149436 10.014337 18.303006 6.361899 6.335987  
## 23 62.978354 188.282417 63.415971 50.273803 93.913232 11.797675  
## 24 25.967032 26.377921 14.286116 20.719333 9.445604 22.549691  
## 25 123.752976 182.226043 143.672394 136.882838 68.294552 100.483878  
## 29 59.132821 34.776950 54.023677 104.014185 5.893899 15.036259  
## 32 23.736932 7.300337 13.387625 33.516112 4.197497 21.693739  
## 33 106.794815 41.848269 90.206750 89.149798 3.924654 25.580965  
## 36 120.096829 73.349658 80.928913 112.799969 14.116324 123.198735  
## 38 62.736767 31.362845 56.712867 104.850125 1.621706 14.695636  
## 39 78.161251 91.333242 102.461124 95.846621 1.569549 29.653419  
## 49 41.952212 22.684099 48.464588 54.600720 2.166574 14.976262  
## 64 19.724328 16.170619 18.096732 18.503468 10.239295 14.506518  
## 76 7.941917 536.895072 6.035997 7.033665 214.246604 30.729826  
## 117 55.698420 35.061948 32.831068 58.586254 13.107811 27.899216  
## 123 42.087683 43.031580 27.129734 42.689001 13.615904 12.545145  
## 126 6.156592 108.404702 30.826540 8.523381 43.829775 4.519645  
## 131 4.160975 265.136463 15.528614 13.540402 130.804062 41.664671  
## 133 83.900583 259.425512 113.461714 100.588102 53.025576 53.477803  
## Hypocotyl SAM6D SAM17D SAM38D Callus Leaf Root  
## 5 172.112449 101.538840 108.035003 57.568952 3.602672 72.181052 53.728970  
## 16 16.326781 22.517324 12.659333 10.229414 2.716798 21.320212 7.310538  
## 17 23.986700 52.872850 68.490459 26.447317 6.139986 0.000000 3.626608  
## 20 4.159165 21.230577 13.709403 9.639602 2.603449 42.803542 126.598709  
## 23 382.933284 20.163323 39.919056 73.535631 0.583159 6.250057 14.892682  
## 24 20.867913 28.476275 25.128377 20.548182 11.542469 26.686917 5.465411  
## 25 215.724837 75.229555 108.926253 87.081914 65.420159 178.440543 98.055423  
## 29 13.614824 40.036100 67.500984 33.565553 5.088175 22.636836 12.527492  
## 32 20.950298 31.857638 31.063118 16.461606 4.368482 44.030052 25.338768  
## 33 38.494199 75.216825 290.336670 100.526085 25.977418 0.000000 0.000000  
## 36 118.328990 229.139072 393.546142 181.391747 71.756006 45.788590 20.983248  
## 38 13.618860 48.102339 51.456817 31.907033 8.665198 27.396630 14.501406  
## 39 18.983798 38.298793 237.526834 76.153152 6.048278 3.674760 1.606524  
## 49 26.934453 45.899996 104.119336 30.814124 3.509392 48.206033 26.688307  
## 64 14.635121 12.243954 22.316362 15.443247 25.621399 26.106051 5.641934  
## 76 350.297556 2.600212 4.426392 5.209396 2.744771 20.850299 94.160633  
## 117 27.176499 82.133333 87.939197 38.297183 47.396469 32.138566 17.503017  
## 123 19.247151 60.919431 75.317808 31.290701 44.433814 27.410816 21.526502  
## 126 334.804651 0.817625 0.938549 2.175286 0.045598 1.253888 31.879730  
## 131 633.844120 1.661192 0.821472 1.444420 0.244966 0.972353 62.263900  
## 133 102.248657 92.557209 144.677356 86.120903 10.711991 21.058177 104.233361  
## Nodule PC1 PC2 PC3 PC4 in.ell\_TIR  
## 5 22.341412 6.29787441 -1.8372424 1.5164566 -1.17162708 FALSE  
## 16 0.657995 -0.05373907 -0.1921965 0.8084196 -0.30166116 FALSE  
## 17 0.000000 0.81044975 1.1170089 -0.7546656 0.42743184 FALSE  
## 20 27.491901 -0.07853023 -0.3090942 1.7082831 0.36298038 FALSE  
## 23 2.016265 2.50142090 -2.7024407 -2.7850869 1.95425693 FALSE  
## 24 1.007309 0.70690012 -0.1981856 0.8944149 -0.24184281 FALSE  
## 25 5.415049 9.79977762 -4.2635297 5.7326293 1.19531413 FALSE  
## 29 10.758737 1.85976056 0.6174242 0.3612860 0.76750320 FALSE  
## 32 21.300657 0.93454507 -0.4597545 1.6269670 -0.09431274 FALSE  
## 33 0.000000 6.32619943 2.8542889 -2.3102058 1.29013983 FALSE  
## 36 22.794609 14.43049528 2.1589901 -1.5310904 -2.57494825 FALSE  
## 38 9.673077 1.95569813 0.5058034 0.6227889 0.85277438 FALSE  
## 39 0.000000 4.44562780 2.0481314 -1.4582800 0.62005161 FALSE  
## 49 8.836310 2.27842210 0.2301439 1.2286204 0.63434759 FALSE  
## 64 3.205496 0.01141647 -0.2036243 0.9369297 0.04368445 FALSE  
## 76 5.269519 0.20859279 -3.8984036 -0.9846724 -0.43448129 FALSE  
## 117 8.945171 3.15794243 0.5915338 0.5657640 -0.06986253 FALSE  
## 123 7.313215 1.88822437 0.6453113 0.4537617 0.33399282 FALSE  
## 126 15.878389 -0.89218238 -3.0700736 -1.9027957 0.34702454 FALSE  
## 131 0.495348 0.48333718 -6.5267137 -3.4003668 -0.81527683 FALSE  
## 133 53.539749 5.79424460 0.4969718 -0.8400912 -0.23361517 FALSE  
## in.ell\_IAA in.ell\_ARF in\_ell  
## 5 FALSE FALSE FALSE  
## 16 TRUE FALSE FALSE  
## 17 TRUE FALSE FALSE  
## 20 TRUE FALSE FALSE  
## 23 FALSE FALSE FALSE  
## 24 TRUE FALSE FALSE  
## 25 FALSE FALSE FALSE  
## 29 TRUE FALSE FALSE  
## 32 TRUE FALSE FALSE  
## 33 FALSE FALSE FALSE  
## 36 FALSE FALSE FALSE  
## 38 TRUE FALSE FALSE  
## 39 FALSE FALSE FALSE  
## 49 TRUE FALSE FALSE  
## 64 TRUE FALSE FALSE  
## 76 FALSE FALSE FALSE  
## 117 TRUE FALSE FALSE  
## 123 TRUE FALSE FALSE  
## 126 FALSE FALSE FALSE  
## 131 FALSE FALSE FALSE  
## 133 FALSE FALSE FALSE

ggbiplot::ggbiplot(pca2, obs.scale = 1, var.scale = .5, choices = c(1, 2),  
 varname.adjust = 3,  
 groups = Family, var.axes = F, varname.size = 2,   
 ellipse = TRUE, circle = FALSE, ellipse.prob = .70) +   
 geom\_segment(PCA\_loadings2, mapping=aes(x=0, y=0, # Change the size of arrows   
 xend=(PC1\*8), yend=(PC2\*8)),   
 arrow = arrow(length = unit(1/2, "picas")), color="gray60") +  
 annotate("text", x=(PCA\_loadings2$PC1\*8.75), #add the tissue names to it manually  
 y=(PCA\_loadings2$PC2\*8.75),   
 label=PCA\_loadings2$Variables, size=4, color="gray60", fontface="bold") +  
 theme(panel.background = element\_rect(fill = "white", linewidth = 1))+   
 theme\_bw()+  
 scale\_color\_manual(values=c("#86C5D8", "#620093", "#E7C94C")) +  
 ggrepel::geom\_text\_repel(data = expr\_logical %>%   
 as\_tibble(rownames = "name") %>%   
 filter(as.logical(in\_ell == FALSE)),   
 aes(PC1, PC2, label=sub(".\*\\|", "", heatmap\_label)),   
 size=3, max.overlaps = 100, min.segment.length = 0,   
 segment.curvature = -0.1) +  
 labs(color = "Class") +   
 theme\_bw()



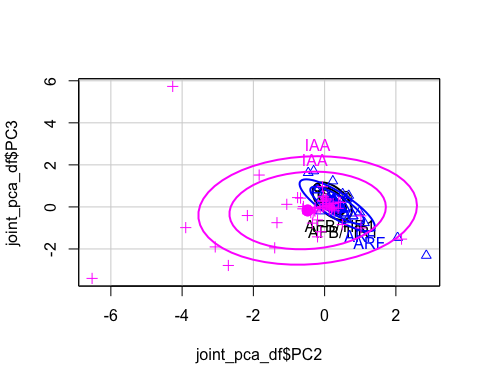
ggsave("20230927\_PC1\_2\_7Tissues.png", dpi = 1000, width = 10, height = 8)  
ggsave("20230927\_PC1\_2\_7Tissues.pdf", dpi = 1000, width = 10, height = 8)

## PC2 and PC3 outside ellipse labels

PC2\_3tissues <- ggbiplot::ggbiplot(pca2, obs.scale = 1, var.scale = .5, choices = c(2, 3),  
 varname.adjust = 3,  
 groups = Family, var.axes = F, varname.size = 2,   
 ellipse = TRUE, circle = FALSE, ellipse.prob = .70)   
   
  
# Extract components so we can select out   
PC2\_3tissues$data

## xvar yvar groups  
## 1 0.10515442 0.135736327 ARF  
## 2 0.03516704 0.391015981 IAA  
## 3 -0.03259973 0.467448263 IAA  
## 4 -0.19841417 -0.618794158 IAA  
## 5 -1.83724237 1.516456612 IAA  
## 6 0.76188043 -0.298488215 ARF  
## 7 -0.34300647 -0.771942835 IAA  
## 8 0.37674443 -0.019034277 AFB/TIR1  
## 9 -1.06192064 0.123263847 IAA  
## 10 -0.05614018 0.296718025 IAA  
## 11 -0.12354575 -0.074216901 IAA  
## 12 0.41382610 -0.307513791 AFB/TIR1  
## 13 0.16146909 0.118751120 AFB/TIR1  
## 14 0.43976369 0.210544795 IAA  
## 15 1.01893547 -1.002175172 IAA  
## 16 -0.19219653 0.808419635 ARF  
## 17 1.11700892 -0.754665609 ARF  
## 18 -0.12083822 -0.198053390 ARF  
## 19 0.14788376 0.203702144 ARF  
## 20 -0.30909424 1.708283097 ARF  
## 21 0.98161007 -0.249254037 ARF  
## 22 0.04406573 0.048238640 IAA  
## 23 -2.70244068 -2.785086871 IAA  
## 24 -0.19818565 0.894414856 AFB/TIR1  
## 25 -4.26352971 5.732629313 IAA  
## 26 -0.23057025 0.800391367 ARF  
## 27 -0.05712991 0.024957986 IAA  
## 28 0.37697535 -0.074310120 AFB/TIR1  
## 29 0.61742415 0.361286016 ARF  
## 30 0.79593666 -0.433613208 ARF  
## 31 0.23346430 0.101766304 ARF  
## 32 -0.45975448 1.626967022 ARF  
## 33 2.85428889 -2.310205824 ARF  
## 34 0.22580682 0.024556471 ARF  
## 35 -0.05145862 0.264364967 IAA  
## 36 2.15899012 -1.531090403 IAA  
## 37 0.15912727 0.141906335 AFB/TIR1  
## 38 0.50580340 0.622788860 ARF  
## 39 2.04813145 -1.458279986 ARF  
## 40 -1.33745677 -0.750021960 IAA  
## 41 0.24206119 0.377262769 ARF  
## 42 0.80233487 -0.439075999 ARF  
## 43 0.04913286 0.051104600 ARF  
## 44 0.44159097 0.071044809 ARF  
## 45 0.22207205 -0.047741305 AFB/TIR1  
## 46 0.28259178 -0.031576561 AFB/TIR1  
## 47 0.22602501 0.161153854 ARF  
## 48 0.23517727 0.291896516 ARF  
## 49 0.23014394 1.228620351 ARF  
## 50 0.54381981 -0.346616692 ARF  
## 51 0.16357844 0.061513280 ARF  
## 52 0.17260396 0.134356933 IAA  
## 53 0.27331654 -0.185967868 IAA  
## 54 0.12704175 0.051140263 AFB/TIR1  
## 55 0.55667830 -0.286010626 ARF  
## 56 0.27501312 0.222705920 ARF  
## 57 0.22850724 -0.007314077 IAA  
## 58 0.05578545 0.335059268 IAA  
## 59 -0.19876183 -1.424143572 IAA  
## 60 0.22563162 0.022943597 ARF  
## 61 0.13643709 -0.009929315 IAA  
## 62 -0.11275080 -1.179610247 IAA  
## 63 -0.75842052 0.443021793 IAA  
## 64 -0.20362431 0.936929695 AFB/TIR1  
## 65 0.20580527 0.214269342 AFB/TIR1  
## 66 0.17662980 0.040059182 AFB/TIR1  
## 67 -0.26383478 -0.027750940 IAA  
## 68 -0.02775860 0.504784255 IAA  
## 69 0.12874603 0.067089129 IAA  
## 70 0.16168347 0.144718515 ARF  
## 71 -0.38908091 -0.270753178 IAA  
## 72 -1.40080513 -1.946238594 IAA  
## 73 0.04204640 0.165611508 IAA  
## 74 -0.59554073 0.021079016 IAA  
## 75 -0.67555222 0.418826607 IAA  
## 76 -3.89840357 -0.984672374 IAA  
## 77 0.39304286 -0.039468673 ARF  
## 78 -0.14129573 0.280245925 ARF  
## 79 0.01134430 0.650288391 ARF  
## 80 0.30503427 -0.302086741 ARF  
## 81 0.26459088 0.360448967 ARF  
## 82 0.13997225 0.032561259 ARF  
## 83 0.33976118 0.035765053 ARF  
## 84 0.11755926 0.440653982 ARF  
## 85 0.41027661 -0.100032400 ARF  
## 86 0.03642123 0.131115667 ARF  
## 87 0.18832650 0.112977921 ARF  
## 88 0.07623100 0.060351273 ARF  
## 89 0.09616199 0.093041365 IAA  
## 90 0.22631146 0.075836951 ARF  
## 91 0.63062446 -0.618197885 ARF  
## 92 0.28877357 0.291349997 ARF  
## 93 0.18223673 0.286799671 ARF  
## 94 0.50936896 -0.107640571 ARF  
## 95 1.01924752 -0.425150473 IAA  
## 96 -0.06070833 0.962239600 IAA  
## 97 0.37953170 -0.067668928 IAA  
## 98 0.19095485 -0.106174638 IAA  
## 99 -0.61127542 -0.090989128 IAA  
## 100 0.12918250 -0.136450892 IAA  
## 101 -0.02383471 -0.002678882 IAA  
## 102 0.08053528 0.228044041 ARF  
## 103 0.24466668 -0.211148378 ARF  
## 104 0.02332871 0.603415593 AFB/TIR1  
## 105 0.19479841 -0.088816512 IAA  
## 106 0.41799993 0.024403946 ARF  
## 107 0.57895723 -0.099986924 ARF  
## 108 -0.27146457 -0.198514723 IAA  
## 109 0.23943824 0.163541169 IAA  
## 110 0.39438069 0.232333327 IAA  
## 111 0.43897284 -0.116129991 ARF  
## 112 0.21805555 -0.051162129 ARF  
## 113 0.16435444 0.183674413 ARF  
## 114 0.21819497 0.118174410 ARF  
## 115 0.12804991 0.315839653 ARF  
## 116 0.67534859 0.544740295 ARF  
## 117 0.59153383 0.565764005 AFB/TIR1  
## 118 0.21113642 0.022927865 ARF  
## 119 0.19705245 -0.047540345 IAA  
## 120 0.57202079 -0.045815482 ARF  
## 121 0.38556844 -0.100377639 ARF  
## 122 0.30454921 -0.025405134 ARF  
## 123 0.64531129 0.453761721 AFB/TIR1  
## 124 -0.06758392 0.007290830 IAA  
## 125 -2.16841690 -0.410351711 IAA  
## 126 -3.07007360 -1.902795711 IAA  
## 127 0.16640283 0.079576472 ARF  
## 128 0.06134928 0.790073247 AFB/TIR1  
## 129 -0.28989506 -0.151673820 IAA  
## 130 0.28590134 0.055831155 ARF  
## 131 -6.52671369 -3.400366836 IAA  
## 132 -0.32242524 -0.282003528 IAA  
## 133 0.49697177 -0.840091171 IAA

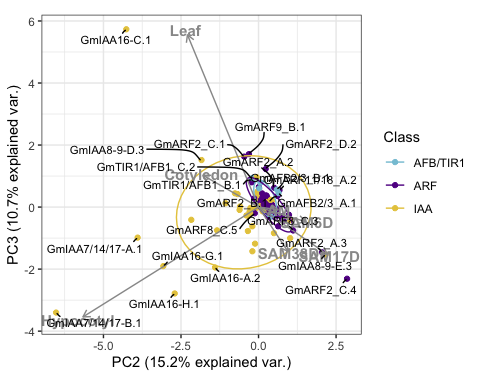
build <- ggplot\_build(PC2\_3tissues)$data  
points <- build[[1]]  
  
# co-ordinates of the ellipses  
ell\_points <- car::dataEllipse(joint\_pca\_df$PC2,   
 joint\_pca\_df$PC3,   
 as.factor(joint\_pca\_df$Family), levels=c(.7, .9))



# add geom\_point with ellipses point   
  
ell\_ARF <- as.data.frame(ell\_points$ARF$`0.7`)  
  
ell\_IAA <- as.data.frame(ell\_points$IAA$`0.7`)  
  
ell\_TIR <- as.data.frame(ell\_points$`AFB/TIR1`$`0.7`)  
  
# Find which points are outside (!) the ellipse, and add this to the data  
library(sp)  
dat\_TIR <- data.frame(  
 points[2:3],   
 in.ell\_TIR = as.logical(point.in.polygon(points$x, points$y, ell\_TIR$x, ell\_TIR$y))  
)  
  
dat\_IAA <- data.frame(  
 points[2:3],   
 in.ell\_IAA = as.logical(point.in.polygon(points$x, points$y, ell\_IAA$x, ell\_IAA$y))   
)   
  
dat\_ARF <- data.frame(  
 points[2:3],   
 in.ell\_ARF = as.logical(point.in.polygon(points$x, points$y, ell\_ARF$x, ell\_ARF$y))  
)  
# as.logical(point..) equals to TRUE indicated points are inside ellipses  
  
# Combining data points for labeling  
transcript\_expr\_logical2 <- cbind(joint\_pca\_df, dat\_TIR, dat\_IAA, dat\_ARF) %>% select(., - c(x, y))  
  
  
expr\_logical2 <- transcript\_expr\_logical2 %>% mutate(., in\_ell = case\_when(Family=="ARF" & `in.ell\_ARF` == TRUE ~ "TRUE",  
 Family=="IAA" & `in.ell\_IAA` == TRUE ~ "TRUE",  
 Family=="AFB/TIR1" & `in.ell\_TIR` == TRUE ~ "TRUE")) %>%  
 mutate(in\_ell = coalesce(in\_ell, "FALSE"))  
  
expr\_logical2[which(expr\_logical2$in\_ell == FALSE),]

## Transcript ID heatmap\_label Family Class Clade  
## 5 Glyma.01G098000.3 Glyma.01G098000|GmIAA8-9-D.3 IAA A I  
## 17 Glyma.02G239600.3 Glyma.02G239600|GmARF8\_C.3 ARF A II  
## 18 Glyma.02G239600.5 Glyma.02G239600|GmARF8\_C.5 ARF A II  
## 20 Glyma.03G070500.1 Glyma.03G070500|GmARF9\_B.1 ARF B I  
## 23 Glyma.03G158700.1 Glyma.03G158700|GmIAA16-H.1 IAA C III  
## 24 Glyma.03G209400.1 Glyma.03G209400|GmTIR1/AFB1\_B.1 AFB/TIR1 TIR1/AFB1 I  
## 25 Glyma.03G247400.1 Glyma.03G247400|GmIAA16-C.1 IAA C III  
## 29 Glyma.04G200600.1 Glyma.04G200600|GmARF2\_B.1 ARF B I  
## 32 Glyma.05G200800.1 Glyma.05G200800|GmARF2\_C.1 ARF B I  
## 33 Glyma.05G200800.4 Glyma.05G200800|GmARF2\_C.4 ARF B I  
## 36 Glyma.06G091700.3 Glyma.06G091700|GmIAA8-9-E.3 IAA A I  
## 38 Glyma.06G164900.2 Glyma.06G164900|GmARF2\_A.2 ARF B I  
## 39 Glyma.06G164900.3 Glyma.06G164900|GmARF2\_A.3 ARF B I  
## 49 Glyma.08G008100.2 Glyma.08G008100|GmARF2\_D.2 ARF B I  
## 64 Glyma.10G021500.2 Glyma.10G021500|GmTIR1/AFB1\_C.2 AFB/TIR1 TIR1/AFB1 I  
## 72 Glyma.10G162400.2 Glyma.10G162400|GmIAA16-A.2 IAA C III  
## 76 Glyma.10G180100.1 Glyma.10G180100|GmIAA7/14/17-A.1 IAA C III  
## 116 Glyma.16G023600.2 Glyma.16G023600|GmARF11/18\_A.2 ARF B I  
## 117 Glyma.16G050500.1 Glyma.16G050500|GmAFB2/3\_B.1 AFB/TIR1 AFB2/3 II  
## 123 Glyma.19G100200.1 Glyma.19G100200|GmAFB2/3\_A.1 AFB/TIR1 AFB2/3 II  
## 126 Glyma.19G161100.1 Glyma.19G161100|GmIAA16-G.1 IAA C III  
## 131 Glyma.20G210400.1 Glyma.20G210400|GmIAA7/14/17-B.1 IAA C III  
## AM OF IAM IBM RootTip Cotyledon  
## 5 68.216252 51.350688 53.553189 96.275020 32.628226 78.301786  
## 17 37.168779 5.439277 41.924483 51.089719 6.308382 0.000000  
## 18 13.757865 13.859804 8.771196 7.354321 6.099923 14.166313  
## 20 14.963834 9.149436 10.014337 18.303006 6.361899 6.335987  
## 23 62.978354 188.282417 63.415971 50.273803 93.913232 11.797675  
## 24 25.967032 26.377921 14.286116 20.719333 9.445604 22.549691  
## 25 123.752976 182.226043 143.672394 136.882838 68.294552 100.483878  
## 29 59.132821 34.776950 54.023677 104.014185 5.893899 15.036259  
## 32 23.736932 7.300337 13.387625 33.516112 4.197497 21.693739  
## 33 106.794815 41.848269 90.206750 89.149798 3.924654 25.580965  
## 36 120.096829 73.349658 80.928913 112.799969 14.116324 123.198735  
## 38 62.736767 31.362845 56.712867 104.850125 1.621706 14.695636  
## 39 78.161251 91.333242 102.461124 95.846621 1.569549 29.653419  
## 49 41.952212 22.684099 48.464588 54.600720 2.166574 14.976262  
## 64 19.724328 16.170619 18.096732 18.503468 10.239295 14.506518  
## 72 50.429036 62.648515 44.799041 49.047824 54.886130 14.549869  
## 76 7.941917 536.895072 6.035997 7.033665 214.246604 30.729826  
## 116 21.273921 9.543860 18.469447 22.065738 1.482088 5.689943  
## 117 55.698420 35.061948 32.831068 58.586254 13.107811 27.899216  
## 123 42.087683 43.031580 27.129734 42.689001 13.615904 12.545145  
## 126 6.156592 108.404702 30.826540 8.523381 43.829775 4.519645  
## 131 4.160975 265.136463 15.528614 13.540402 130.804062 41.664671  
## Hypocotyl SAM6D SAM17D SAM38D Callus Leaf Root  
## 5 172.112449 101.538840 108.035003 57.568952 3.602672 72.181052 53.728970  
## 17 23.986700 52.872850 68.490459 26.447317 6.139986 0.000000 3.626608  
## 18 33.826894 0.000000 11.829332 13.561473 1.551810 0.000000 0.000000  
## 20 4.159165 21.230577 13.709403 9.639602 2.603449 42.803542 126.598709  
## 23 382.933284 20.163323 39.919056 73.535631 0.583159 6.250057 14.892682  
## 24 20.867913 28.476275 25.128377 20.548182 11.542469 26.686917 5.465411  
## 25 215.724837 75.229555 108.926253 87.081914 65.420159 178.440543 98.055423  
## 29 13.614824 40.036100 67.500984 33.565553 5.088175 22.636836 12.527492  
## 32 20.950298 31.857638 31.063118 16.461606 4.368482 44.030052 25.338768  
## 33 38.494199 75.216825 290.336670 100.526085 25.977418 0.000000 0.000000  
## 36 118.328990 229.139072 393.546142 181.391747 71.756006 45.788590 20.983248  
## 38 13.618860 48.102339 51.456817 31.907033 8.665198 27.396630 14.501406  
## 39 18.983798 38.298793 237.526834 76.153152 6.048278 3.674760 1.606524  
## 49 26.934453 45.899996 104.119336 30.814124 3.509392 48.206033 26.688307  
## 64 14.635121 12.243954 22.316362 15.443247 25.621399 26.106051 5.641934  
## 72 258.563372 52.919869 43.482386 62.182188 12.401001 7.425099 12.077243  
## 76 350.297556 2.600212 4.426392 5.209396 2.744771 20.850299 94.160633  
## 116 0.823623 51.901613 58.246322 22.000399 0.000000 23.922628 7.371101  
## 117 27.176499 82.133333 87.939197 38.297183 47.396469 32.138566 17.503017  
## 123 19.247151 60.919431 75.317808 31.290701 44.433814 27.410816 21.526502  
## 126 334.804651 0.817625 0.938549 2.175286 0.045598 1.253888 31.879730  
## 131 633.844120 1.661192 0.821472 1.444420 0.244966 0.972353 62.263900  
## Nodule PC1 PC2 PC3 PC4 in.ell\_TIR  
## 5 22.341412 6.29787441 -1.8372424 1.5164566 -1.17162708 FALSE  
## 17 0.000000 0.81044975 1.1170089 -0.7546656 0.42743184 FALSE  
## 18 0.000000 -0.78784060 -0.1208382 -0.1980534 -0.30047323 FALSE  
## 20 27.491901 -0.07853023 -0.3090942 1.7082831 0.36298038 FALSE  
## 23 2.016265 2.50142090 -2.7024407 -2.7850869 1.95425693 FALSE  
## 24 1.007309 0.70690012 -0.1981856 0.8944149 -0.24184281 FALSE  
## 25 5.415049 9.79977762 -4.2635297 5.7326293 1.19531413 FALSE  
## 29 10.758737 1.85976056 0.6174242 0.3612860 0.76750320 FALSE  
## 32 21.300657 0.93454507 -0.4597545 1.6269670 -0.09431274 FALSE  
## 33 0.000000 6.32619943 2.8542889 -2.3102058 1.29013983 FALSE  
## 36 22.794609 14.43049528 2.1589901 -1.5310904 -2.57494825 FALSE  
## 38 9.673077 1.95569813 0.5058034 0.6227889 0.85277438 FALSE  
## 39 0.000000 4.44562780 2.0481314 -1.4582800 0.62005161 FALSE  
## 49 8.836310 2.27842210 0.2301439 1.2286204 0.63434759 FALSE  
## 64 3.205496 0.01141647 -0.2036243 0.9369297 0.04368445 FALSE  
## 72 0.000000 2.42394340 -1.4008051 -1.9462386 0.94710249 FALSE  
## 76 5.269519 0.20859279 -3.8984036 -0.9846724 -0.43448129 FALSE  
## 116 1.267483 0.78469153 0.6753486 0.5447403 0.07576599 FALSE  
## 117 8.945171 3.15794243 0.5915338 0.5657640 -0.06986253 FALSE  
## 123 7.313215 1.88822437 0.6453113 0.4537617 0.33399282 FALSE  
## 126 15.878389 -0.89218238 -3.0700736 -1.9027957 0.34702454 FALSE  
## 131 0.495348 0.48333718 -6.5267137 -3.4003668 -0.81527683 FALSE  
## in.ell\_IAA in.ell\_ARF in\_ell  
## 5 FALSE FALSE FALSE  
## 17 TRUE FALSE FALSE  
## 18 TRUE FALSE FALSE  
## 20 FALSE FALSE FALSE  
## 23 FALSE FALSE FALSE  
## 24 TRUE TRUE FALSE  
## 25 FALSE FALSE FALSE  
## 29 TRUE FALSE FALSE  
## 32 TRUE FALSE FALSE  
## 33 FALSE FALSE FALSE  
## 36 FALSE FALSE FALSE  
## 38 TRUE FALSE FALSE  
## 39 FALSE FALSE FALSE  
## 49 TRUE FALSE FALSE  
## 64 TRUE TRUE FALSE  
## 72 FALSE FALSE FALSE  
## 76 FALSE FALSE FALSE  
## 116 TRUE FALSE FALSE  
## 117 TRUE FALSE FALSE  
## 123 TRUE FALSE FALSE  
## 126 FALSE FALSE FALSE  
## 131 FALSE FALSE FALSE

PC2\_3tissues +   
 geom\_segment(PCA\_loadings2, mapping=aes(x=0, y=0, # Change the size of arrows   
 xend=(PC2\*7), yend=(PC3\*7)),   
 arrow = arrow(length = unit(1/2, "picas")), color="gray60") +  
 annotate("text", x=(PCA\_loadings2$PC2\*7.2), #add the tissue names to it manually  
 y=(PCA\_loadings2$PC3\*7.2),   
 label=PCA\_loadings2$Variables, size=4, color="gray60", fontface="bold") +  
 theme(panel.background = element\_rect(fill = "white", linewidth = 1))+   
 theme\_bw()+  
 scale\_color\_manual(values=c("#86C5D8", "#620093", "#E7C94C")) +  
 ggrepel::geom\_text\_repel(data = expr\_logical2 %>%   
 as\_tibble(rownames = "name") %>%   
 filter(as.logical(in\_ell == FALSE)),   
 aes(PC2, PC3, label=sub(".\*\\|", "", heatmap\_label)),   
 size=3, max.overlaps = 100, min.segment.length = 0,   
 segment.curvature = -0.1) +  
 labs(color = "Class") +   
 theme\_bw()



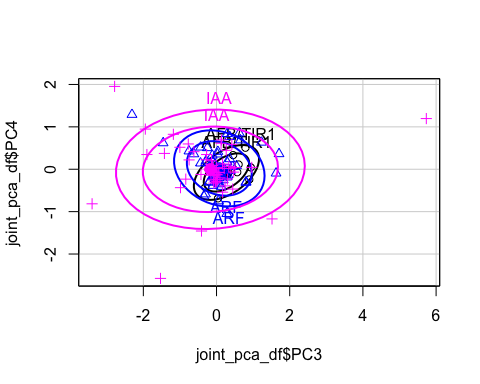
ggsave("20230927\_PC2\_3\_7Tissues.png", dpi = 1000, width = 10, height = 8)  
ggsave("20230927\_PC2\_3\_7Tissues.pdf", dpi = 1000, width = 10, height = 8)

## PC3 and PC4 outside ellipse labels

PC3\_4tissues <- ggbiplot::ggbiplot(pca2, obs.scale = 1, var.scale = .5, choices = c(3,4),   
 varname.adjust = 3,  
 groups = Family, var.axes = F, varname.size = 2,   
 ellipse = TRUE, circle = FALSE, ellipse.prob = .70)  
   
  
# Extract components so we can select out   
PC3\_4tissues$data

## xvar yvar groups  
## 1 0.135736327 -0.166794726 ARF  
## 2 0.391015981 0.021725559 IAA  
## 3 0.467448263 -0.067536958 IAA  
## 4 -0.618794158 0.414369028 IAA  
## 5 1.516456612 -1.171627082 IAA  
## 6 -0.298488215 0.155056850 ARF  
## 7 -0.771942835 0.596692174 IAA  
## 8 -0.019034277 -0.085791352 AFB/TIR1  
## 9 0.123263847 0.612851368 IAA  
## 10 0.296718025 -0.229885278 IAA  
## 11 -0.074216901 -0.327047811 IAA  
## 12 -0.307513791 -0.426101201 AFB/TIR1  
## 13 0.118751120 -0.092852907 AFB/TIR1  
## 14 0.210544795 0.019512657 IAA  
## 15 -1.002175172 0.518106927 IAA  
## 16 0.808419635 -0.301661161 ARF  
## 17 -0.754665609 0.427431840 ARF  
## 18 -0.198053390 -0.300473230 ARF  
## 19 0.203702144 -0.032318665 ARF  
## 20 1.708283097 0.362980383 ARF  
## 21 -0.249254037 0.504865466 ARF  
## 22 0.048238640 -0.079805461 IAA  
## 23 -2.785086871 1.954256930 IAA  
## 24 0.894414856 -0.241842809 AFB/TIR1  
## 25 5.732629313 1.195314126 IAA  
## 26 0.800391367 -0.312065182 ARF  
## 27 0.024957986 -0.239320843 IAA  
## 28 -0.074310120 0.116710951 AFB/TIR1  
## 29 0.361286016 0.767503195 ARF  
## 30 -0.433613208 0.518572902 ARF  
## 31 0.101766304 -0.077183564 ARF  
## 32 1.626967022 -0.094312744 ARF  
## 33 -2.310205824 1.290139828 ARF  
## 34 0.024556471 -0.195978255 ARF  
## 35 0.264364967 0.445650978 IAA  
## 36 -1.531090403 -2.574948254 IAA  
## 37 0.141906335 -0.156514601 AFB/TIR1  
## 38 0.622788860 0.852774381 ARF  
## 39 -1.458279986 0.620051612 ARF  
## 40 -0.750021960 0.220037571 IAA  
## 41 0.377262769 -0.033857714 ARF  
## 42 -0.439075999 0.142648481 ARF  
## 43 0.051104600 -0.749801388 ARF  
## 44 0.071044809 -0.068042055 ARF  
## 45 -0.047741305 -0.140250716 AFB/TIR1  
## 46 -0.031576561 -0.264358663 AFB/TIR1  
## 47 0.161153854 -0.163854323 ARF  
## 48 0.291896516 -0.187321330 ARF  
## 49 1.228620351 0.634347589 ARF  
## 50 -0.346616692 -0.633762872 ARF  
## 51 0.061513280 -0.348275075 ARF  
## 52 0.134356933 0.691566165 IAA  
## 53 -0.185967868 -0.030659800 IAA  
## 54 0.051140263 -0.104071856 AFB/TIR1  
## 55 -0.286010626 0.197392945 ARF  
## 56 0.222705920 -0.018660135 ARF  
## 57 -0.007314077 -0.117126136 IAA  
## 58 0.335059268 0.067574118 IAA  
## 59 -1.424143572 0.373460488 IAA  
## 60 0.022943597 -0.306222560 ARF  
## 61 -0.009929315 -0.125112574 IAA  
## 62 -1.179610247 0.824300448 IAA  
## 63 0.443021793 -0.467603321 IAA  
## 64 0.936929695 0.043684449 AFB/TIR1  
## 65 0.214269342 -0.060390329 AFB/TIR1  
## 66 0.040059182 -0.686082095 AFB/TIR1  
## 67 -0.027750940 -0.304216067 IAA  
## 68 0.504784255 0.041205637 IAA  
## 69 0.067089129 -0.073136425 IAA  
## 70 0.144718515 -0.017263227 ARF  
## 71 -0.270753178 0.346803341 IAA  
## 72 -1.946238594 0.947102490 IAA  
## 73 0.165611508 -0.541531009 IAA  
## 74 0.021079016 -0.130540709 IAA  
## 75 0.418826607 0.586608071 IAA  
## 76 -0.984672374 -0.434481291 IAA  
## 77 -0.039468673 0.111993163 ARF  
## 78 0.280245925 -1.048339856 ARF  
## 79 0.650288391 0.687757199 ARF  
## 80 -0.302086741 -0.586239367 ARF  
## 81 0.360448967 0.244664502 ARF  
## 82 0.032561259 -0.154052291 ARF  
## 83 0.035765053 0.418059786 ARF  
## 84 0.440653982 0.061925950 ARF  
## 85 -0.100032400 -0.385496367 ARF  
## 86 0.131115667 -0.408555161 ARF  
## 87 0.112977921 -0.153389597 ARF  
## 88 0.060351273 -0.210476652 ARF  
## 89 0.093041365 -0.201897919 IAA  
## 90 0.075836951 -0.127619481 ARF  
## 91 -0.618197885 0.360031756 ARF  
## 92 0.291349997 0.839323391 ARF  
## 93 0.286799671 0.170762865 ARF  
## 94 -0.107640571 0.185923451 ARF  
## 95 -0.425150473 -0.122584160 IAA  
## 96 0.962239600 0.043951364 IAA  
## 97 -0.067668928 -0.140894757 IAA  
## 98 -0.106174638 0.088468230 IAA  
## 99 -0.090989128 0.016103825 IAA  
## 100 -0.136450892 0.200696132 IAA  
## 101 -0.002678882 0.039279304 IAA  
## 102 0.228044041 -0.121129223 ARF  
## 103 -0.211148378 -0.307775202 ARF  
## 104 0.603415593 0.112023704 AFB/TIR1  
## 105 -0.088816512 -0.250014529 IAA  
## 106 0.024403946 0.355643287 ARF  
## 107 -0.099986924 -0.179283342 ARF  
## 108 -0.198514723 0.001283642 IAA  
## 109 0.163541169 0.122506596 IAA  
## 110 0.232333327 -0.392657919 IAA  
## 111 -0.116129991 0.326223430 ARF  
## 112 -0.051162129 -0.151720388 ARF  
## 113 0.183674413 -0.252281288 ARF  
## 114 0.118174410 -0.100612169 ARF  
## 115 0.315839653 -0.141738678 ARF  
## 116 0.544740295 0.075765990 ARF  
## 117 0.565764005 -0.069862526 AFB/TIR1  
## 118 0.022927865 -0.260894094 ARF  
## 119 -0.047540345 -0.066857327 IAA  
## 120 -0.045815482 -0.223146203 ARF  
## 121 -0.100377639 0.160113846 ARF  
## 122 -0.025405134 -0.135980283 ARF  
## 123 0.453761721 0.333992817 AFB/TIR1  
## 124 0.007290830 -0.286482378 IAA  
## 125 -0.410351711 -1.457000005 IAA  
## 126 -1.902795711 0.347024541 IAA  
## 127 0.079576472 -0.140137191 ARF  
## 128 0.790073247 0.507465423 AFB/TIR1  
## 129 -0.151673820 -0.141425041 IAA  
## 130 0.055831155 -0.099674050 ARF  
## 131 -3.400366836 -0.815276835 IAA  
## 132 -0.282003528 0.225510060 IAA  
## 133 -0.840091171 -0.233615166 IAA

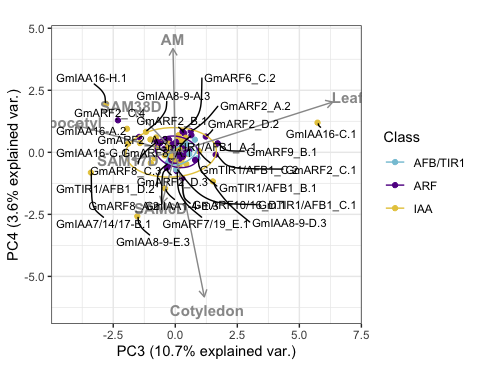
build <- ggplot\_build(PC3\_4tissues)$data  
points <- build[[1]]  
  
# co-ordinates of the ellipses  
ell\_points <- car::dataEllipse(joint\_pca\_df$PC3,   
 joint\_pca\_df$PC4,   
 as.factor(joint\_pca\_df$Family), levels=c(.7, .9))



# add geom\_point with ellipses point   
  
ell\_ARF <- as.data.frame(ell\_points$ARF$`0.7`)  
  
ell\_IAA <- as.data.frame(ell\_points$IAA$`0.7`)  
  
ell\_TIR <- as.data.frame(ell\_points$`AFB/TIR1`$`0.7`)  
  
# Find which points are outside (!) the ellipse, and add this to the data  
library(sp)  
dat\_TIR <- data.frame(  
 points[2:3],   
 in.ell\_TIR = as.logical(point.in.polygon(points$x, points$y, ell\_TIR$x, ell\_TIR$y))  
)  
  
dat\_IAA <- data.frame(  
 points[2:3],   
 in.ell\_IAA = as.logical(point.in.polygon(points$x, points$y, ell\_IAA$x, ell\_IAA$y))   
)   
  
dat\_ARF <- data.frame(  
 points[2:3],   
 in.ell\_ARF = as.logical(point.in.polygon(points$x, points$y, ell\_ARF$x, ell\_ARF$y))  
)  
# as.logical(point..) equals to TRUE indicated points are inside ellipses  
  
# Combining data points for labeling  
transcript\_expr\_logical3 <- cbind(joint\_pca\_df, dat\_TIR, dat\_IAA, dat\_ARF) %>% select(., - c(x, y))  
  
  
expr\_logical3 <- transcript\_expr\_logical3 %>% mutate(., in\_ell = case\_when(Family=="ARF" & `in.ell\_ARF` == TRUE ~ "TRUE",  
 Family=="IAA" & `in.ell\_IAA` == TRUE ~ "TRUE",  
 Family=="AFB/TIR1" & `in.ell\_TIR` == TRUE ~ "TRUE")) %>%  
 mutate(in\_ell = coalesce(in\_ell, "FALSE"))  
  
expr\_logical3[which(expr\_logical3$in\_ell == FALSE),]

## Transcript ID heatmap\_label Family Class Clade  
## 5 Glyma.01G098000.3 Glyma.01G098000|GmIAA8-9-D.3 IAA A I  
## 12 Glyma.02G152800.2 Glyma.02G152800|GmTIR1/AFB1\_D.2 AFB/TIR1 TIR1/AFB1 I  
## 17 Glyma.02G239600.3 Glyma.02G239600|GmARF8\_C.3 ARF A II  
## 20 Glyma.03G070500.1 Glyma.03G070500|GmARF9\_B.1 ARF B I  
## 23 Glyma.03G158700.1 Glyma.03G158700|GmIAA16-H.1 IAA C III  
## 24 Glyma.03G209400.1 Glyma.03G209400|GmTIR1/AFB1\_B.1 AFB/TIR1 TIR1/AFB1 I  
## 25 Glyma.03G247400.1 Glyma.03G247400|GmIAA16-C.1 IAA C III  
## 29 Glyma.04G200600.1 Glyma.04G200600|GmARF2\_B.1 ARF B I  
## 32 Glyma.05G200800.1 Glyma.05G200800|GmARF2\_C.1 ARF B I  
## 33 Glyma.05G200800.4 Glyma.05G200800|GmARF2\_C.4 ARF B I  
## 36 Glyma.06G091700.3 Glyma.06G091700|GmIAA8-9-E.3 IAA A I  
## 38 Glyma.06G164900.2 Glyma.06G164900|GmARF2\_A.2 ARF B I  
## 39 Glyma.06G164900.3 Glyma.06G164900|GmARF2\_A.3 ARF B I  
## 43 Glyma.07G130400.1 Glyma.07G130400|GmARF7/19\_E.1 ARF A II  
## 49 Glyma.08G008100.2 Glyma.08G008100|GmARF2\_D.2 ARF B I  
## 50 Glyma.08G008100.3 Glyma.08G008100|GmARF2\_D.3 ARF B I  
## 62 Glyma.09G203300.3 Glyma.09G203300|GmIAA8-9-A.3 IAA A I  
## 64 Glyma.10G021500.2 Glyma.10G021500|GmTIR1/AFB1\_C.2 AFB/TIR1 TIR1/AFB1 I  
## 66 Glyma.10G021500.1 Glyma.10G021500|GmTIR1/AFB1\_C.1 AFB/TIR1 TIR1/AFB1 I  
## 72 Glyma.10G162400.2 Glyma.10G162400|GmIAA16-A.2 IAA C III  
## 78 Glyma.11G145500.1 Glyma.11G145500|GmARF10/16\_D.1 ARF C III  
## 79 Glyma.11G204200.1 Glyma.11G204200|GmARF8\_A.1 ARF A II  
## 80 Glyma.11G204200.2 Glyma.11G204200|GmARF8\_A.2 ARF A II  
## 92 Glyma.13G221400.2 Glyma.13G221400|GmARF6\_C.2 ARF A II  
## 125 Glyma.19G161000.3 Glyma.19G161000|GmIAA1-4-E.3 IAA B II  
## 126 Glyma.19G161100.1 Glyma.19G161100|GmIAA16-G.1 IAA C III  
## 128 Glyma.19G206800.1 Glyma.19G206800|GmTIR1/AFB1\_A.1 AFB/TIR1 TIR1/AFB1 I  
## 131 Glyma.20G210400.1 Glyma.20G210400|GmIAA7/14/17-B.1 IAA C III  
## AM OF IAM IBM RootTip Cotyledon Hypocotyl  
## 5 68.216252 51.350688 53.55319 96.275020 32.628226 78.301786 172.112449  
## 12 22.069192 16.181094 21.00405 22.849022 12.164769 15.200032 20.202937  
## 17 37.168779 5.439277 41.92448 51.089719 6.308382 0.000000 23.986700  
## 20 14.963834 9.149436 10.01434 18.303006 6.361899 6.335987 4.159165  
## 23 62.978354 188.282417 63.41597 50.273803 93.913232 11.797675 382.933284  
## 24 25.967032 26.377921 14.28612 20.719333 9.445604 22.549691 20.867913  
## 25 123.752976 182.226043 143.67239 136.882838 68.294552 100.483878 215.724837  
## 29 59.132821 34.776950 54.02368 104.014185 5.893899 15.036259 13.614824  
## 32 23.736932 7.300337 13.38762 33.516112 4.197497 21.693739 20.950298  
## 33 106.794815 41.848269 90.20675 89.149798 3.924654 25.580965 38.494199  
## 36 120.096829 73.349658 80.92891 112.799969 14.116324 123.198735 118.328990  
## 38 62.736767 31.362845 56.71287 104.850125 1.621706 14.695636 13.618860  
## 39 78.161251 91.333242 102.46112 95.846621 1.569549 29.653419 18.983798  
## 43 18.550414 8.914698 15.95095 18.729053 15.689098 23.181993 16.710000  
## 49 41.952212 22.684099 48.46459 54.600720 2.166574 14.976262 26.934453  
## 50 41.903106 15.801812 23.41788 55.329663 4.236413 28.260708 18.724678  
## 62 36.472556 37.373970 38.15859 43.541833 11.505870 0.000000 117.295863  
## 64 19.724328 16.170619 18.09673 18.503468 10.239295 14.506518 14.635121  
## 66 14.419899 9.741531 6.79071 12.735183 6.157738 17.688606 17.203871  
## 72 50.429036 62.648515 44.79904 49.047824 54.886130 14.549869 258.563372  
## 78 15.909573 17.106814 12.58611 12.520897 6.758486 30.401493 8.543969  
## 79 19.241075 21.103199 0.00000 3.055660 3.172375 0.000000 5.721453  
## 80 13.373647 0.000000 35.09998 44.159391 4.581945 10.261290 31.902014  
## 92 34.943626 18.239549 27.73661 43.916594 1.658267 1.279513 28.990865  
## 125 4.478037 404.803343 44.07771 17.846549 72.730750 41.028328 177.214792  
## 126 6.156592 108.404702 30.82654 8.523381 43.829775 4.519645 334.804651  
## 128 29.377480 13.907445 22.73580 26.728168 6.489989 7.571060 13.364493  
## 131 4.160975 265.136463 15.52861 13.540402 130.804062 41.664671 633.844120  
## SAM6D SAM17D SAM38D Callus Leaf Root Nodule  
## 5 101.538840 108.035003 57.568952 3.602672 72.181052 53.728970 22.341412  
## 12 29.352679 33.917530 17.176745 17.838179 0.000000 0.000000 0.000000  
## 17 52.872850 68.490459 26.447317 6.139986 0.000000 3.626608 0.000000  
## 20 21.230577 13.709403 9.639602 2.603449 42.803542 126.598709 27.491901  
## 23 20.163323 39.919056 73.535631 0.583159 6.250057 14.892682 2.016265  
## 24 28.476275 25.128377 20.548182 11.542469 26.686917 5.465411 1.007309  
## 25 75.229555 108.926253 87.081914 65.420159 178.440543 98.055423 5.415049  
## 29 40.036100 67.500984 33.565553 5.088175 22.636836 12.527492 10.758737  
## 32 31.857638 31.063118 16.461606 4.368482 44.030052 25.338768 21.300657  
## 33 75.216825 290.336670 100.526085 25.977418 0.000000 0.000000 0.000000  
## 36 229.139072 393.546142 181.391747 71.756006 45.788590 20.983248 22.794609  
## 38 48.102339 51.456817 31.907033 8.665198 27.396630 14.501406 9.673077  
## 39 38.298793 237.526834 76.153152 6.048278 3.674760 1.606524 0.000000  
## 43 16.764956 21.488396 10.756881 24.155359 2.997797 25.928328 7.688516  
## 49 45.899996 104.119336 30.814124 3.509392 48.206033 26.688307 8.836310  
## 50 55.230644 26.660841 30.862812 6.303453 0.000000 0.000000 0.216233  
## 62 30.426647 41.114157 30.034268 6.427166 0.000000 30.080385 5.435140  
## 64 12.243954 22.316362 15.443247 25.621399 26.106051 5.641934 3.205496  
## 66 28.663983 21.325627 11.737596 3.718783 4.726063 2.093318 0.000000  
## 72 52.919869 43.482386 62.182188 12.401001 7.425099 12.077243 0.000000  
## 78 9.310248 10.078082 10.215456 0.759723 4.047713 2.691333 0.596545  
## 79 0.000000 0.000000 17.832069 0.000000 18.572984 3.488127 1.310676  
## 80 32.214786 40.620313 0.000000 17.181705 0.000000 0.000000 0.000000  
## 92 22.677736 46.861420 20.641988 2.961649 19.960475 4.115777 1.477684  
## 125 3.197441 2.314000 2.924909 0.843634 6.919914 6.338750 0.000000  
## 126 0.817625 0.938549 2.175286 0.045598 1.253888 31.879730 15.878389  
## 128 20.598762 24.312187 18.931187 13.373494 25.380331 5.994108 3.091861  
## 131 1.661192 0.821472 1.444420 0.244966 0.972353 62.263900 0.495348  
## PC1 PC2 PC3 PC4 in.ell\_TIR in.ell\_IAA  
## 5 6.29787441 -1.83724237 1.51645661 -1.17162708 FALSE FALSE  
## 12 0.06210206 0.41382610 -0.30751379 -0.42610120 FALSE TRUE  
## 17 0.81044975 1.11700892 -0.75466561 0.42743184 FALSE TRUE  
## 20 -0.07853023 -0.30909424 1.70828310 0.36298038 FALSE FALSE  
## 23 2.50142090 -2.70244068 -2.78508687 1.95425693 FALSE FALSE  
## 24 0.70690012 -0.19818565 0.89441486 -0.24184281 FALSE TRUE  
## 25 9.79977762 -4.26352971 5.73262931 1.19531413 FALSE FALSE  
## 29 1.85976056 0.61742415 0.36128602 0.76750320 FALSE TRUE  
## 32 0.93454507 -0.45975448 1.62696702 -0.09431274 FALSE TRUE  
## 33 6.32619943 2.85428889 -2.31020582 1.29013983 FALSE FALSE  
## 36 14.43049528 2.15899012 -1.53109040 -2.57494825 FALSE FALSE  
## 38 1.95569813 0.50580340 0.62278886 0.85277438 FALSE TRUE  
## 39 4.44562780 2.04813145 -1.45827999 0.62005161 FALSE TRUE  
## 43 -0.18778513 0.04913286 0.05110460 -0.74980139 FALSE TRUE  
## 49 2.27842210 0.23014394 1.22862035 0.63434759 FALSE TRUE  
## 50 1.34307083 0.54381981 -0.34661669 -0.63376287 FALSE TRUE  
## 62 0.47369476 -0.11275080 -1.17961025 0.82430045 FALSE FALSE  
## 64 0.01141647 -0.20362431 0.93692969 0.04368445 FALSE TRUE  
## 66 -0.17447944 0.17662980 0.04005918 -0.68608210 FALSE TRUE  
## 72 2.42394340 -1.40080513 -1.94623859 0.94710249 FALSE FALSE  
## 78 -0.28107091 -0.14129573 0.28024593 -1.04833986 FALSE FALSE  
## 79 -0.79489435 0.01134430 0.65028839 0.68775720 FALSE TRUE  
## 80 -0.42946116 0.30503427 -0.30208674 -0.58623937 FALSE TRUE  
## 92 0.37773397 0.28877357 0.29135000 0.83932339 FALSE TRUE  
## 125 -0.19442276 -2.16841690 -0.41035171 -1.45700001 FALSE FALSE  
## 126 -0.89218238 -3.07007360 -1.90279571 0.34702454 FALSE FALSE  
## 128 0.22854712 0.06134928 0.79007325 0.50746542 FALSE TRUE  
## 131 0.48333718 -6.52671369 -3.40036684 -0.81527683 FALSE FALSE  
## in.ell\_ARF in\_ell  
## 5 FALSE FALSE  
## 12 TRUE FALSE  
## 17 FALSE FALSE  
## 20 FALSE FALSE  
## 23 FALSE FALSE  
## 24 TRUE FALSE  
## 25 FALSE FALSE  
## 29 FALSE FALSE  
## 32 FALSE FALSE  
## 33 FALSE FALSE  
## 36 FALSE FALSE  
## 38 FALSE FALSE  
## 39 FALSE FALSE  
## 43 FALSE FALSE  
## 49 FALSE FALSE  
## 50 FALSE FALSE  
## 62 FALSE FALSE  
## 64 TRUE FALSE  
## 66 FALSE FALSE  
## 72 FALSE FALSE  
## 78 FALSE FALSE  
## 79 FALSE FALSE  
## 80 FALSE FALSE  
## 92 FALSE FALSE  
## 125 FALSE FALSE  
## 126 FALSE FALSE  
## 128 FALSE FALSE  
## 131 FALSE FALSE

PC3\_4tissues +   
 geom\_segment(PCA\_loadings2, mapping=aes(x=0, y=0, # Change the size of arrows   
 xend=(PC3\*8), yend=(PC4\*8)),   
 arrow = arrow(length = unit(1/2, "picas")), color="gray60") +  
 annotate("text", x=(PCA\_loadings2$PC3\*8.75), #add the tissue names to it manually  
 y=(PCA\_loadings2$PC4\*8.75),   
 label=PCA\_loadings2$Variables, size=4, color="gray60", fontface="bold") +  
 theme(panel.background = element\_rect(fill = "white", linewidth = 1))+   
 theme\_bw()+  
 scale\_color\_manual(values=c("#86C5D8", "#620093", "#E7C94C")) +  
 ggrepel::geom\_text\_repel(data = expr\_logical3 %>%   
 as\_tibble(rownames = "name") %>%   
 filter(as.logical(in\_ell == FALSE)),   
 aes(PC3, PC4, label=sub(".\*\\|", "", heatmap\_label)),   
 size=3, max.overlaps = 100, min.segment.length = 0,   
 segment.curvature = -0.1) +  
 labs(color = "Class") +   
 theme\_bw()



ggsave("20230927\_PC3\_4\_7Tissues.png", dpi = 1000, width = 10, height = 8)  
ggsave("20230927\_PC3\_4\_7Tissues.pdf", dpi = 1000, width = 10, height = 8)

# Principal component comparisons.

We observe here the differences between our principal component analysis with all 14 tissues from databases, and with only the 7 tissues that are part of aerial architecture. It is visible that our principal component analysis is minimally affected by the exclusion of tissues herein analysed, hence we are confident to display only the aerial tissues we are interested in. We also observe that root, hypocotyl, nodule, and open flower fall along the same direction, implying that these tissues are correlated. As we move to principal components that accounts for smaller amounts of variation, we notice an improvement in the discrimination of the correlation between root, nodule and hypocotyl tissues. On the other hand root tips, and open flower correlation to hypocotyl shifts more when looking at PC3 and PC4, with a very small discrimination between these tissues. We can speculate that this correlation could be due to these tissues being at approximate similar developmental stages, and therefore exhibit similar patterns of gene expression as they respond to common developmental cues. It also shows the redundancy of auxin response genes as they have overlap in functional roles. Further investigation of these genes are important to gain more insightful information of which genes are important in growth and development of these tissues, and if different pair of auxin regulatory genes are important during this process.