

Cluster Analysis of Wasps

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Introduction

```
> ggparcoord(data.frame(d[[1]]), columns=1:30, alphaLines=0, boxplot=TRUE, scale="globalminmax") + coord
```

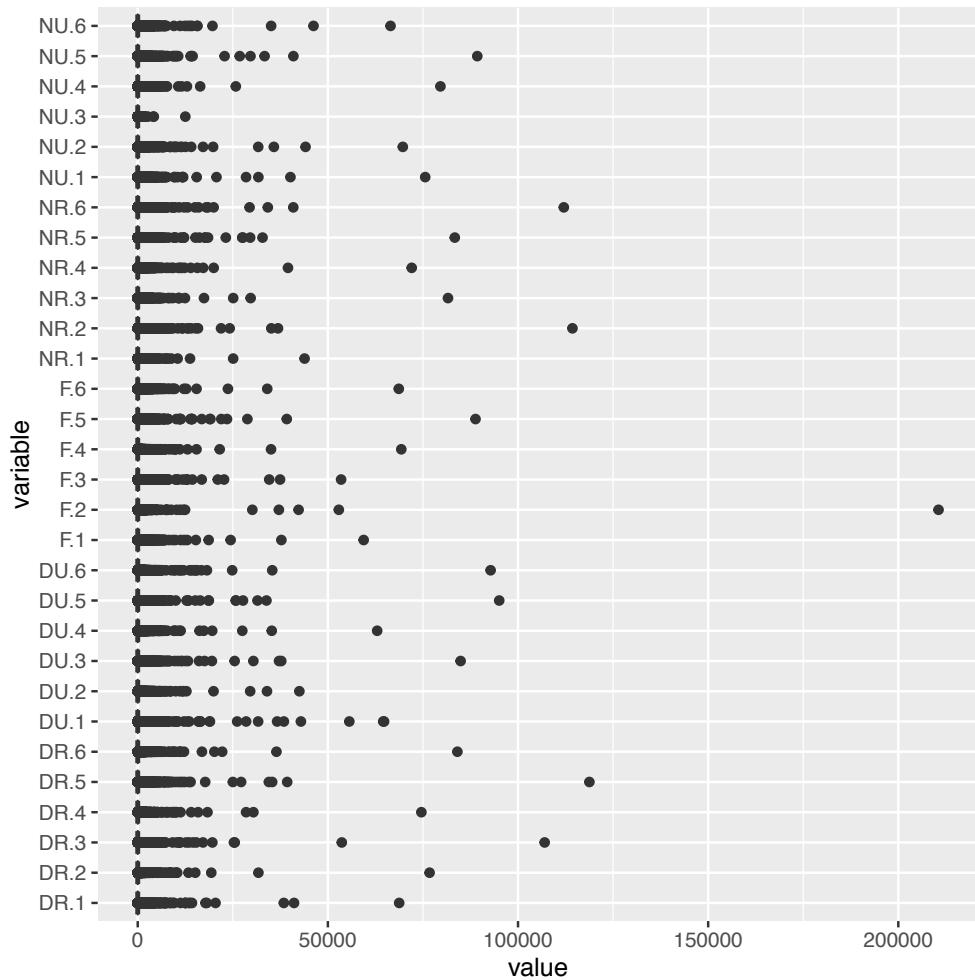


Figure 1: Boxplot of all samples.

```
> myVec = c("DR", "DU", "F", "NR", "NU")
> myCol = c(which(colnames(countTable) == grep('DR', colnames(countTable), value=TRUE)), which(colnames(countTable) == grep('DU', colnames(countTable), value=TRUE)), which(colnames(countTable) == grep('F', colnames(countTable), value=TRUE)), which(colnames(countTable) == grep('NR', colnames(countTable), value=TRUE)), which(colnames(countTable) == grep('NU', colnames(countTable), value=TRUE)))
> # estimate normalization factors
> d = calcNormFactors(d)
```

```
> plotMDS(d, labels=colnames(countTable), col = c("red", "orange", "green", "blue", "purple"))[factor(listcon
```

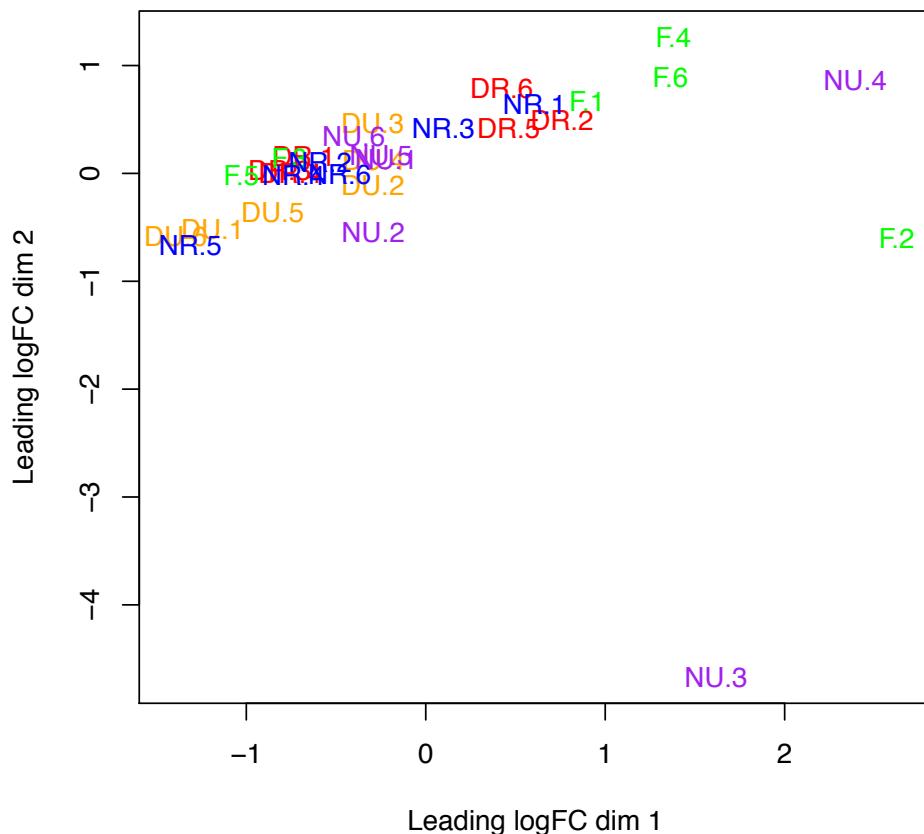


Figure 2: MDS of all samples. NU.3 looks very poor. F.2 does as well. Possibly NU.4 is poor.

```
> # estimate tagwise dispersion  
> d = estimateCommonDisp(d)  
> d = estimateTagwiseDisp(d)  
> # Now, str(d) has raw read counts, norm factors, lib.size, and more
```

```
> plotMeanVar(d, show.tagwise.vars=TRUE, NBline=TRUE)
```

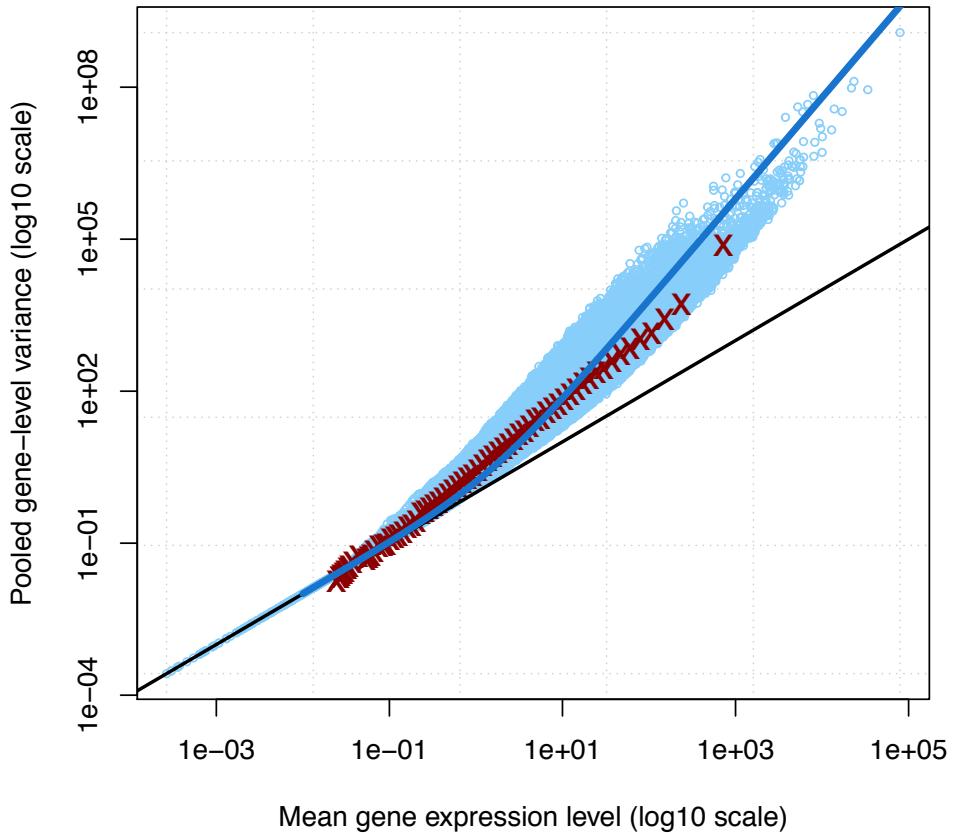


Figure 3: This function is useful for exploring the mean-variance relationship in the data. Raw variances are, for each gene, the pooled variance of the counts from each sample, divided by a scaling factor (by default the effective library size). The function will plot the average raw variance for genes split into nbins bins by overall expression level. The averages are taken on the square-root scale as for count data the arithmetic mean is upwardly biased. A line showing the Poisson mean-variance relationship (mean equals variance) is always shown.

```
> plotBCV(d)
```

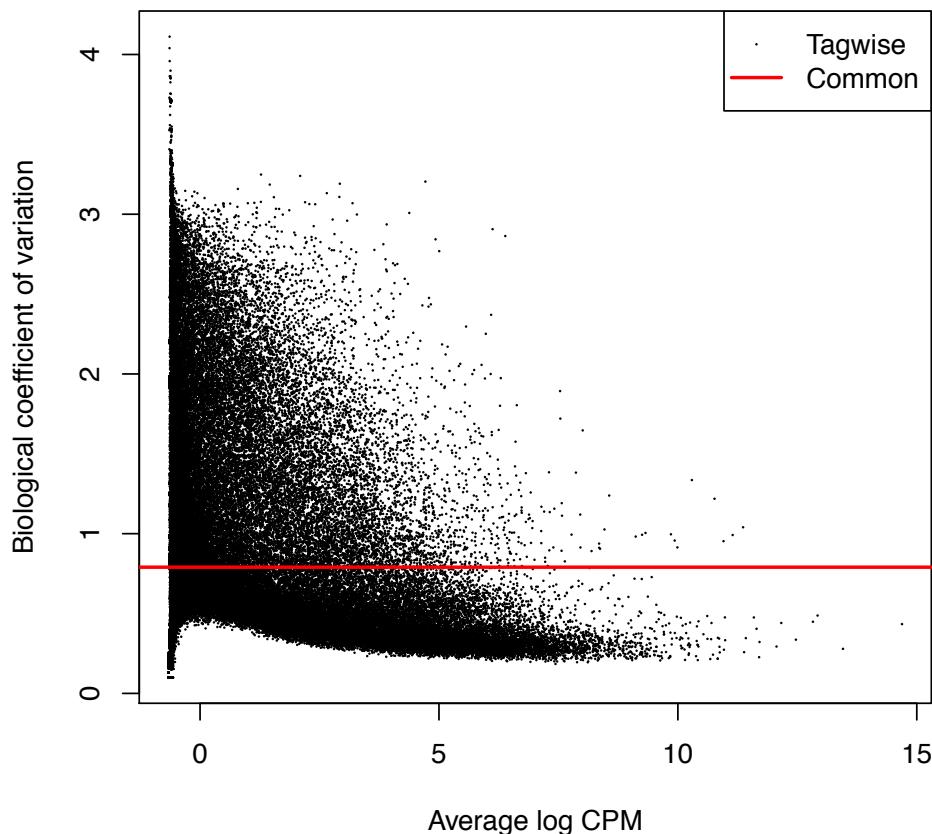


Figure 4: Plots the tagwise biological coefficient of variation (square root of dispersions) against log2-CPM.

```
> # Test for differential expression
> # Compute genewise exact tests for differences in the means between two groups of negative-binomially
> de = exactTest(d, pair=c("NU", "DR"))
> #Use the topTags function to present a tabular summary of the differential expression statistics (note
> tt = topTags(de, n=nrow(d))
> head(tt$table)
```

	logFC	logCPM	PValue	FDR
34808	6.068273	1.3124579	1.791310e-06	0.2824735
89828	6.155402	0.2691713	7.118592e-06	0.5612689
38343	-9.117725	2.5869741	1.211436e-05	0.6367751
79792	7.738891	4.0912902	1.885500e-05	0.7079621
84117	2.056710	3.6192123	2.244776e-05	0.7079621
81034	7.833797	2.8494281	2.811878e-05	0.7390131

```
> # Inspect the depth-adjusted reads per million for some of the top differentially expressed genes (just
> nc = cpm(d, normalized.lib.sizes=TRUE)
> rn = rownames(tt$table)
```

```
> # Sorted in order of lowest FDR from DE comparison
> head(nc[rn,order(listcond)],5)
```

	DR.1	DR.2	DR.3	DR.4	DR.5	DR.6	DU.1
34808	2.792674	0.000000	0.000000	5.683925	2.207572	5.265151	1.710986
89828	1.787735	0.000000	3.312755	4.646608	4.305916	2.772979	0.000000
38343	0.000000	0.000000	0.113717	0.000000	0.000000	0.000000	0.000000
79792	12.215306	0.000000	0.000000	0.000000	38.353693	0.000000	48.154032
84117	16.935878	12.97072	22.958857	15.989591	9.229837	14.005301	19.554525
	DU.2	DU.3	DU.4	DU.5	DU.6	F.1	F.2
34808	1.237378	4.686304	1.361842	2.530349	1.999975	2.014017350	0.0000000000
89828	0.000000	0.000000	0.000000	0.000000	0.000000	0.0000000000	0.0000000000
38343	0.000000	0.000000	0.000000	0.000000	0.000000	0.003151827	0.004250863
79792	24.792177	10.810026	35.374421	36.808222	31.779262	5.767843116	4.314625580
84117	8.831191	7.545109	5.132838	16.609549	17.599779	8.065524882	6.648349169
	F.3	F.4	F.5	F.6	NR.1	NR.2	NR.3
34808	1.425218	0.00000	3.222709369	1.10184	2.273195	3.808794	1.608547
89828	0.000000	0.00000	0.000000000	0.00000	0.000000	0.000000	0.000000
38343	0.000000	0.00000	0.002768651	0.00000	0.000000	0.000000	0.000000
79792	23.730171	0.00000	38.423333864	20.29847	32.315742	39.607136	47.310773
84117	18.287364	16.86495	21.116498586	11.23156	5.669349	8.577221	17.609525
	NR.4	NR.5	NR.6	NU.1	NU.2	NU.3	NU.4
34808	4.111939	2.392347	3.14834177	0.0000000	0.000000	0.00000	0.0000000
89828	0.000000	0.000000	0.000000000	0.0000000	0.000000	0.00000	0.0000000
38343	0.000000	0.000000	0.02672616	0.0000000	0.000000	118.5125	28.766266
79792	23.917779	0.000000	15.80050642	0.0000000	0.000000	0.00000	0.0000000
84117	17.424342	17.139455	11.41741600	0.8991105	1.857902	0.00000	6.792142
	NU.5	NU.6					
34808	0.000000	0.000000					
89828	0.000000	0.000000					
38343	0.000000	49.821681					
79792	0.000000	0.000000					
84117	4.286813	6.072133					

```
> deg = rn[tt$table$FDR < .05]
> plotSmear(d, de.tags=deg)
```

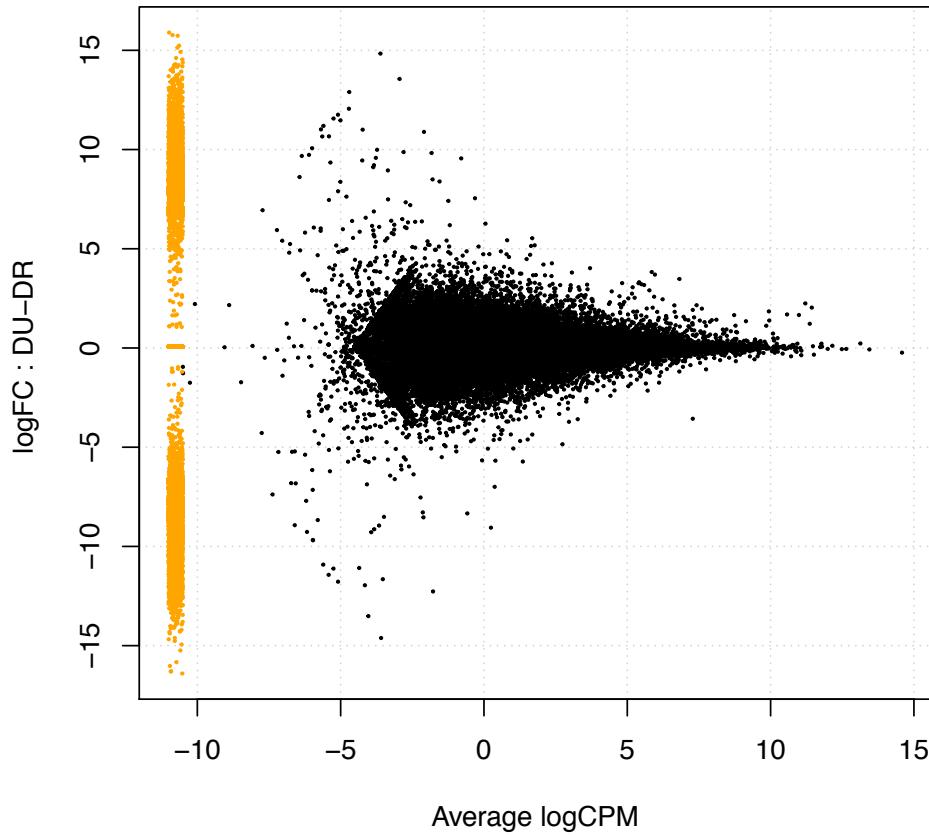


Figure 5: Create a graphical summary, such as an M (log-fold change) versus A (log-average expression) plot, here showing the genes selected as differentially expressed with a 5% false discovery rate. There were none in this dataset!

```
> # Would save file
> write.csv(tt$table, file="toptags_edgeR.csv")
> ##### Is there any step in the edgeR package where genes are eliminated for low mean and/or stdev
>
> d2 <- DGEList(counts=countTable)
> # 38,280 genes (from 157,691).
> #d2 <- d2[rowSums(d2$counts>1)>=ncol(d2)/2,]
> # 52,564 genes (from 157,691). In edgeR, it is recommended to remove features without at least 1 read
> d2 <- d2[rowSums(d2$counts>1)>=6,]
> # Took too long as well
> #d2plot = as.data.frame(d2[[1]])
> #d2plot = gather(d2plot)
> #ggplot(d2plot, aes(factor(value), key)) + geom_boxplot()
>
> # Now positive and negative
```

```

> cpm.d2.new <- cpm(d2, TRUE, TRUE)
> cpm.d2.norm <- betweenLaneNormalization(cpm.d2.new, which="full", round=FALSE)
> d2 = cpm.d2.norm
> RowSD = function(x) {
+   sqrt(rowSums((x - rowMeans(x))^2)/(dim(x)[2] - 1))
+ }
> d2t = d2
> d2 = as.data.frame(d2t)
> d2 = mutate(d2, mean = (DR.1+DR.2+DR.3+DR.4+DR.5+DR.6+DU.1+DU.2+DU.3+DU.4+DU.5+DU.6+F.1+F.2+F.3+F.4+F.5))
> rownames(d2)=rownames(d2t)
> # The first quartile threshold of mean counts across the 5 samples
> q1T = as.numeric(summary(d2$mean)["1st Qu."])
> # (39,427, 31)
> d2q1 = subset(d2,mean>q1T)
> # The first quartile threshold of standard deviation across the 5 samples
> q1Ts = as.numeric(summary(d2q1$stdev)["1st Qu."])
> # L120q1 (29572, 31)
> d2q1 = subset(d2q1,stdev>q1Ts)
> # filt (22992, 31)
> filt = subset(d2,mean<=q1T/stdev<=q1Ts)
> model = loess(mean ~ stdev, data=d2q1)
> # (11855, 32)
> d2q1 = d2q1[which(sign(model$residuals) == 1),]
> d2q1 = d2q1[,1:(ncol(d2q1)-2)]
> d2q1s = t(apply(as.matrix(d2q1), 1, scale))
> colnames(d2q1s)=colnames(d2q1)
> colnames(d2q1)=colnames(d2q1)
> filt = filt[,1:(ncol(filt)-2)]
> colnames(filt)=colnames(d2q1)
> # filt (40709, 32)
> filt = rbind(filt,d2q1[which(sign(model$residuals) == -1),])
> # filt (40709, 32)
> filts = t(apply(as.matrix(filt), 1, scale))
> colnames(filts)=colnames(d2q1)
> colnames(filt)=colnames(d2q1)

```

```
> ggparcoord(d2q1, columns=1:ncol(d2q1), alphaLines=0, boxplot=TRUE, scale="globalminmax") + coord_flip
```

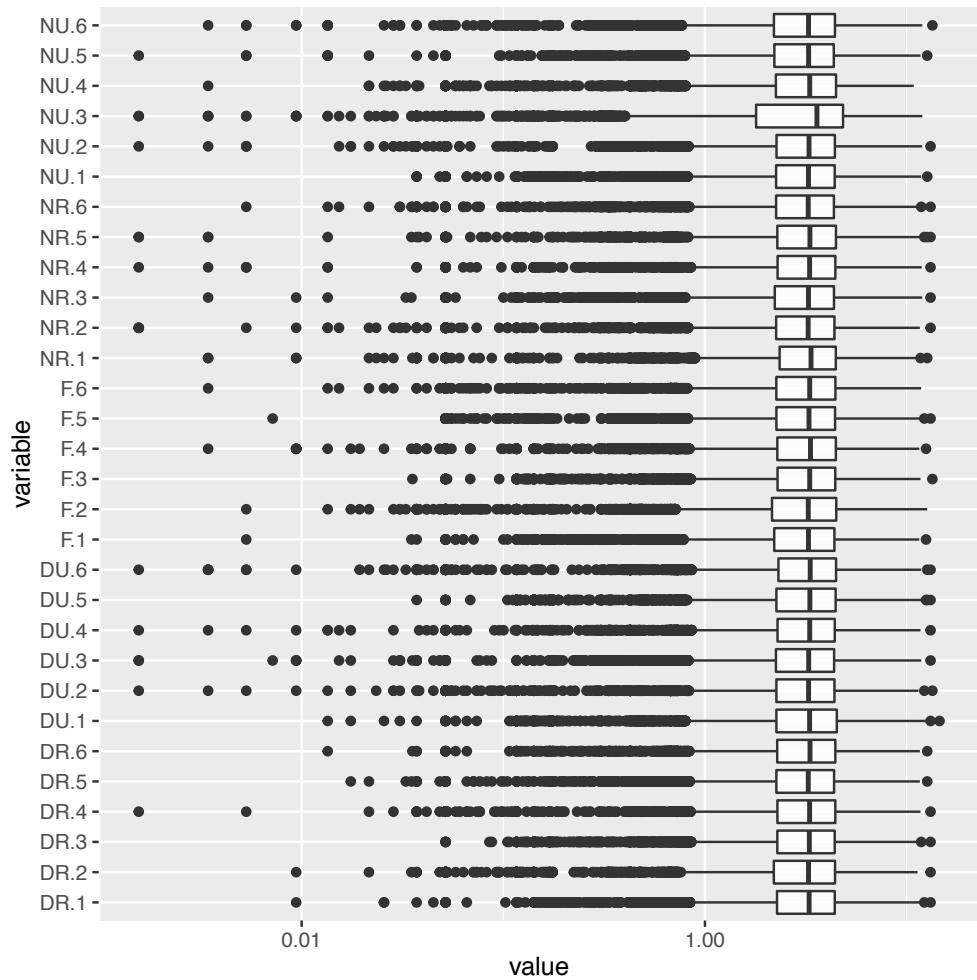


Figure 6: This is d2q1. Looks better than d2q1s.png (only strange one is NU.3)

```
> d2q1s_Plot = as.data.frame(d2q1s)
> ggparcoord(d2q1s_Plot, columns=1:ncol(d2q1s_Plot), alphaLines=0, boxplot=TRUE, scale="globalminmax")
```

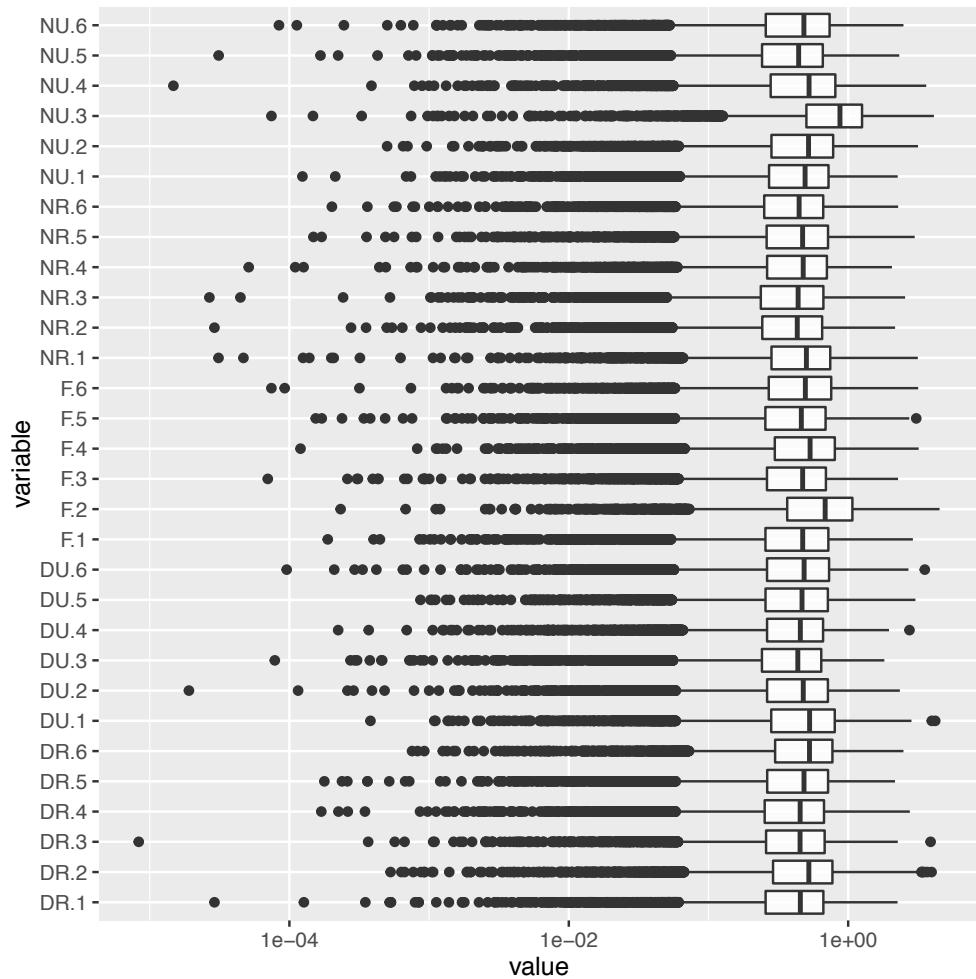


Figure 7: This is d2q1s. Does not look as good as d2q1.png (strange ones are NU.3 and F.2)

```
> # Removing NU.3 and starting over!
> #####
>
> rm(list=ls())
> load("All_wasp.rda")
> countTable = select(countTable,-NU.3)
> d2 <- DGEList(counts=countTable)
> # 38,280 genes (from 157,691).
> #d2 <- d2[rowSums(d2$counts>1)>=ncol(d2)/2,]
> # 52,564 genes (from 157,691). In edgeR, it is recommended to remove features without at least 1 read
> d2 <- d2[rowSums(d2$counts>1)>=5,]
> # Took too long as well
> #d2plot = as.data.frame(d2[[1]])
> #d2plot = gather(d2plot)
> #ggplot(d2plot, aes(factor(value), key)) + geom_boxplot()
>
> # Now positive and negative
```

```

> cpm.d2.new <- cpm(d2, TRUE, TRUE)
> cpm.d2.norm <- betweenLaneNormalization(cpm.d2.new, which="full", round=FALSE)
> d2 = cpm.d2.norm
> RowSD = function(x) {
+   sqrt(rowSums((x - rowMeans(x))^2)/(dim(x)[2] - 1))
+ }
> d2t = d2
> d2 = as.data.frame(d2)
> d2 = mutate(d2, mean = (DR.1+DR.2+DR.3+DR.4+DR.5+DR.6+DU.1+DU.2+DU.3+DU.4+DU.5+DU.6+F.1+F.2+F.3+F.4+F.5))
> rownames(d2)=rownames(d2t)
> # The first quartile threshold of mean counts across the 5 samples
> q1T = as.numeric(summary(d2$mean)["1st Qu."])
> # (41202, 31)
> d2q1 = subset(d2,mean>q1T)
> # The first quartile threshold of standard deviation across the 5 samples
> q1Ts = as.numeric(summary(d2q1$stdev)["1st Qu."])
> # L120q1 (30901, 31)
> d2q1 = subset(d2q1,stdev>q1Ts)
> # filt (24031, 31)
> filt = subset(d2,mean<=q1T/stdev<=q1Ts)
> model = loess(mean ~ stdev, data=d2q1)
> # (12262, 31)
> d2q1 = d2q1[which(sign(model$residuals) == 1),]
> d2q1 = d2q1[,1:(ncol(d2q1)-2)]
> d2q1s = t(apply(as.matrix(d2q1), 1, scale))
> colnames(d2q1s)=colnames(d2q1)
> colnames(d2q1)=colnames(d2q1)
> filt = filt[,1:(ncol(filt)-2)]
> colnames(filt)=colnames(d2q1)
> # filt (42670, 29)
> filt = rbind(filt,d2q1[which(sign(model$residuals) == -1),])
> # filts (42670, 29)
> filts = t(apply(as.matrix(filt), 1, scale))
> colnames(filts)=colnames(d2q1)
> colnames(filt)=colnames(d2q1)

```

```
> ggparcoord(d2q1, columns=1:ncol(d2q1), alphaLines=0, boxplot=TRUE, scale="globalminmax") + coord_flip
```

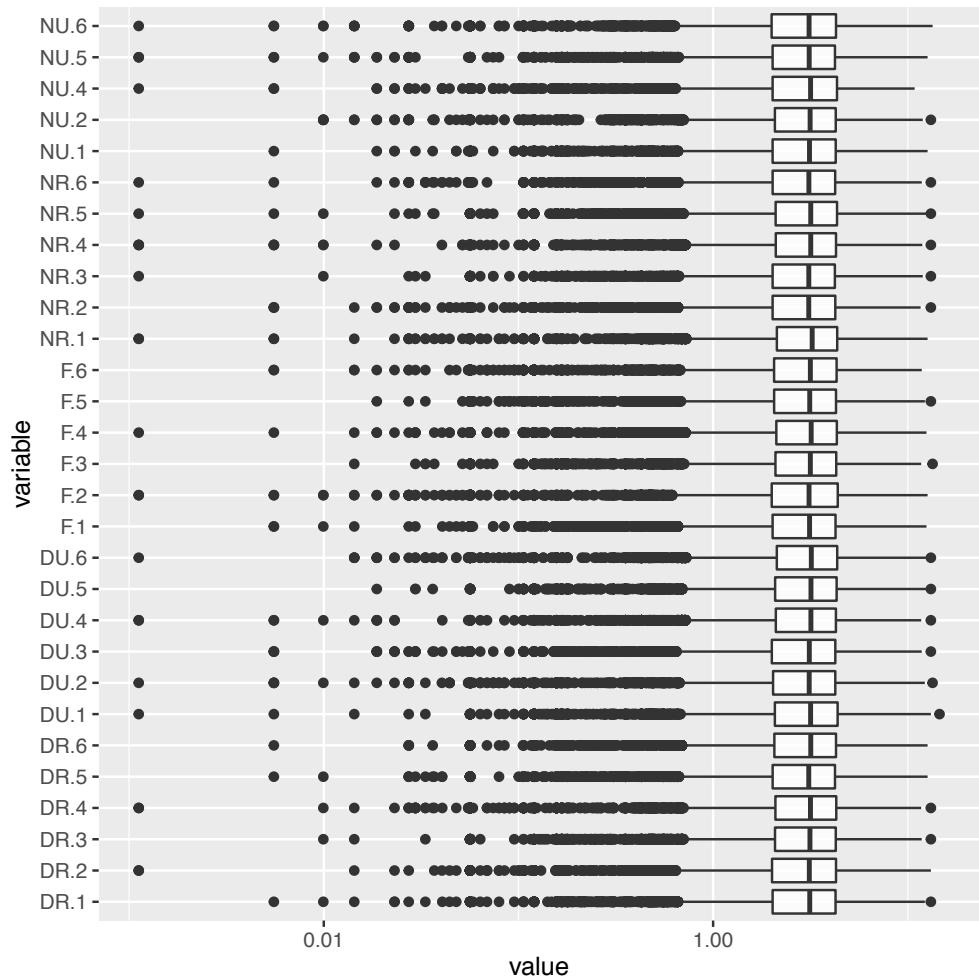


Figure 8: d2q1 NU.3 removed.

```
> d2q1s_Plot = as.data.frame(d2q1s)
> ggparcoord(d2q1s_Plot, columns=1:ncol(d2q1s_Plot), alphaLines=0, boxplot=TRUE, scale="globalminmax")
```

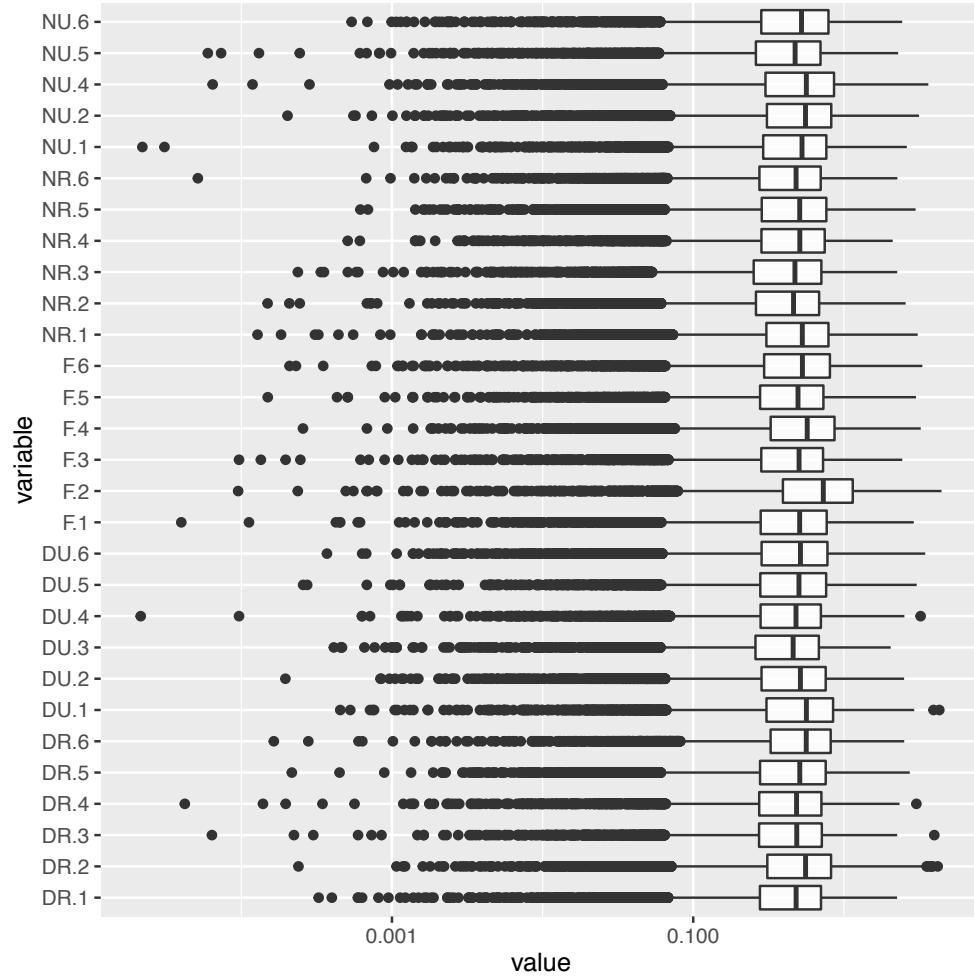


Figure 9: d2q1s NU.3 removed.

```
> ##### Print pairwise scat matrix
> dev.off()
> myVec = c("DR", "DU", "F", "NR", "NU")
> for (i in 1:(length(myVec)-1)){
+   for (j in (i+1):length(myVec)){
+     type1 = myVec[i]
+     type2 = myVec[j]
+     myCol = c(grep(type1, colnames(d2q1)), grep(type2, colnames(d2q1)))
+     jpeg(file = paste(getwd(), "/", type1, "_", type2, "_ALPHA10.jpg", sep=""), height = 700, width =
+       print(scatmat(d2q1, columns=myCol, alpha = 0.01))
+     dev.off()
+     jpeg(file = paste(getwd(), "/", type1, "_", type2, "_ALPHA7.jpg", sep=""), height = 700, width =
+       print(scatmat(d2q1, columns=myCol, alpha = 0.007))
+     dev.off()
+     jpeg(file = paste(getwd(), "/", type1, "_", type2, "_ALPHA3.jpg", sep=""), height = 700, width =
+       print(scatmat(d2q1, columns=myCol, alpha = 0.003))
+     dev.off()
```

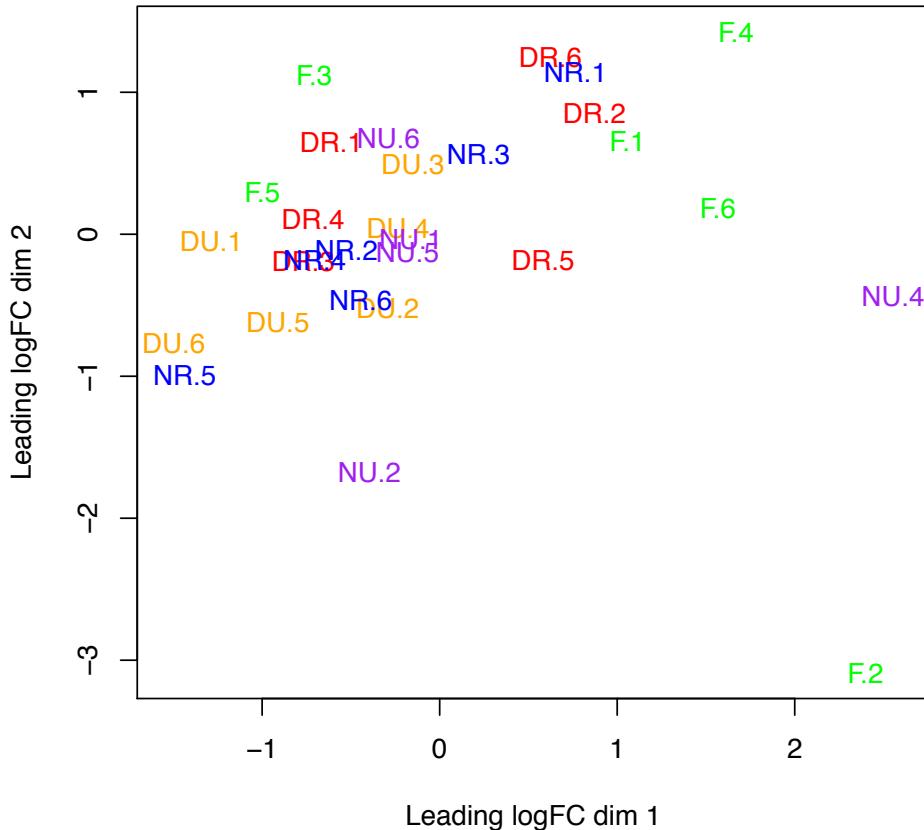
```

+   jpeg(file = paste(getwd(), "/", type1, "_", type2, "_ALPHA1.jpg", sep=""), height = 700, width =
+   print(scatmat(d2q1, columns=myCol, alpha = 0.001))
+   dev.off()
+ }
+ }

> ##### Significance testing for normalized no NU.3 #####
> listcond = c(rep(c("DR","DU","F","NR"),each=6), rep(c("NU"),each=5))
> # create DGEList object
> d = DGEList(counts=countTable, group=listcond)
> # estimate normalization factors
> d = calcNormFactors(d)

> plotMDS(d, labels=colnames(countTable), col = c("red","orange","green","blue","purple"))[factor(listcond)

```



```
> plotMeanVar(d, show.tagwise.vars=TRUE, NBline=TRUE)
```

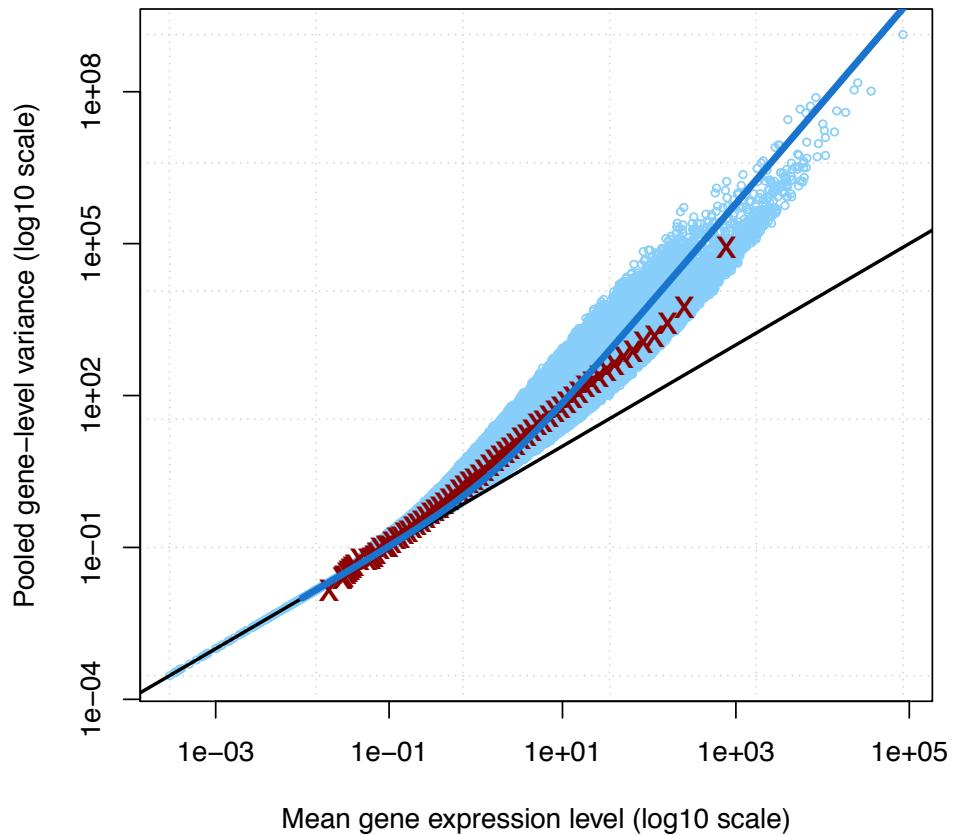


Figure 11: MDS plot NU.3 removed.

```
> plotBCV(d)
```

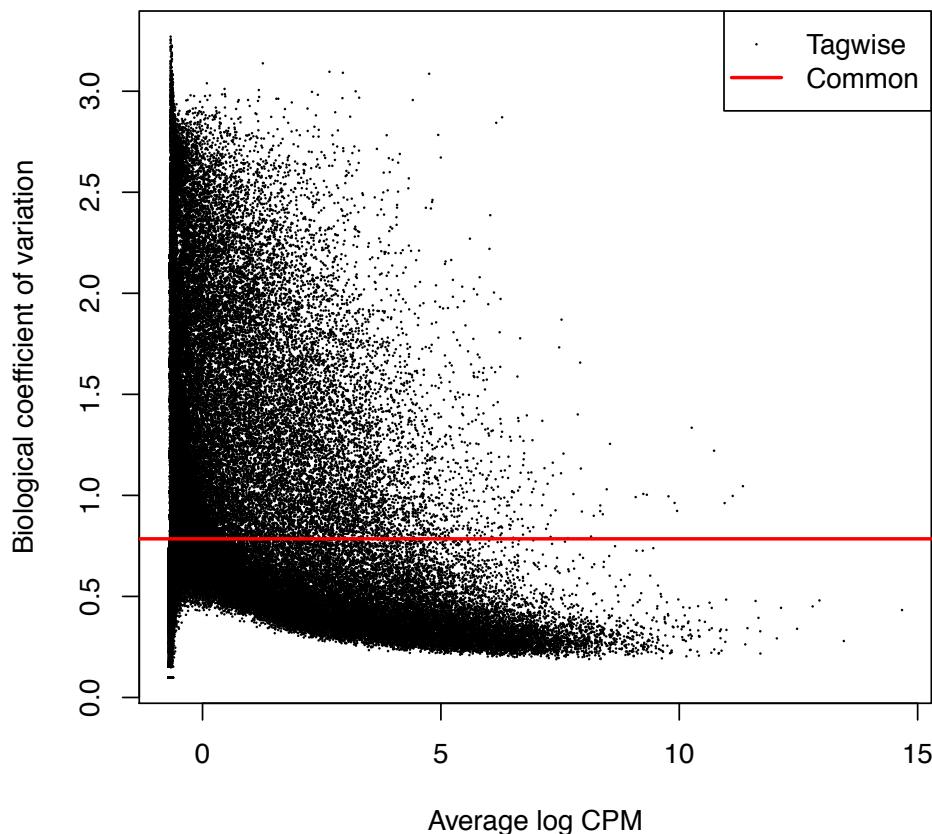


Figure 12: MDS plot NU.3 removed.

```
> ##### Create pairwise significance tests #####
>
> for (i in 1:(length(myVec)-1)){
+   for (j in (i+1):length(myVec)){
+
+     # Test for differential expression
+     de = exactTest(d, pair=c(myVec[i],myVec[j]))
+
+     #This automatically sorts by ascending p-value, and creates an FDR column (by dividing p-value by the number of comparisons)
+     tt = topTags(de, n=nrow(d))
+     head(tt$table)
+
+     # Inspect the depth-adjusted reads per million for some of the top differentially expressed genes (DE)
+     nc = cpm(d, normalized.lib.sizes=TRUE)
+     rn = rownames(tt$table)
+     # Sorted in order of lowest FDR from DE comparison
+     head(nc[rn,order(listcond)],5)
+
+ }
```

```
+ # Create a graphical summary, such as an M (log-fold change) versus A (log-average expression) plot
+ deg = rn[tt$table$FDR < .05]
+ dev.off()
+ jpeg(file = paste(getwd(), "/", myVec[i], "_", myVec[j], "_PlotSmear.jpg", sep=""), height = 700, width = 600)
+ print(plotSmear(d, de.tags=deg))
+ dev.off()
+
+ # Would save file
+ write.csv(tt$table, file=paste(getwd(), "/", "TopTags_", myVec[i], "_", myVec[j], ".csv", sep=""))
+ }
+ }
```