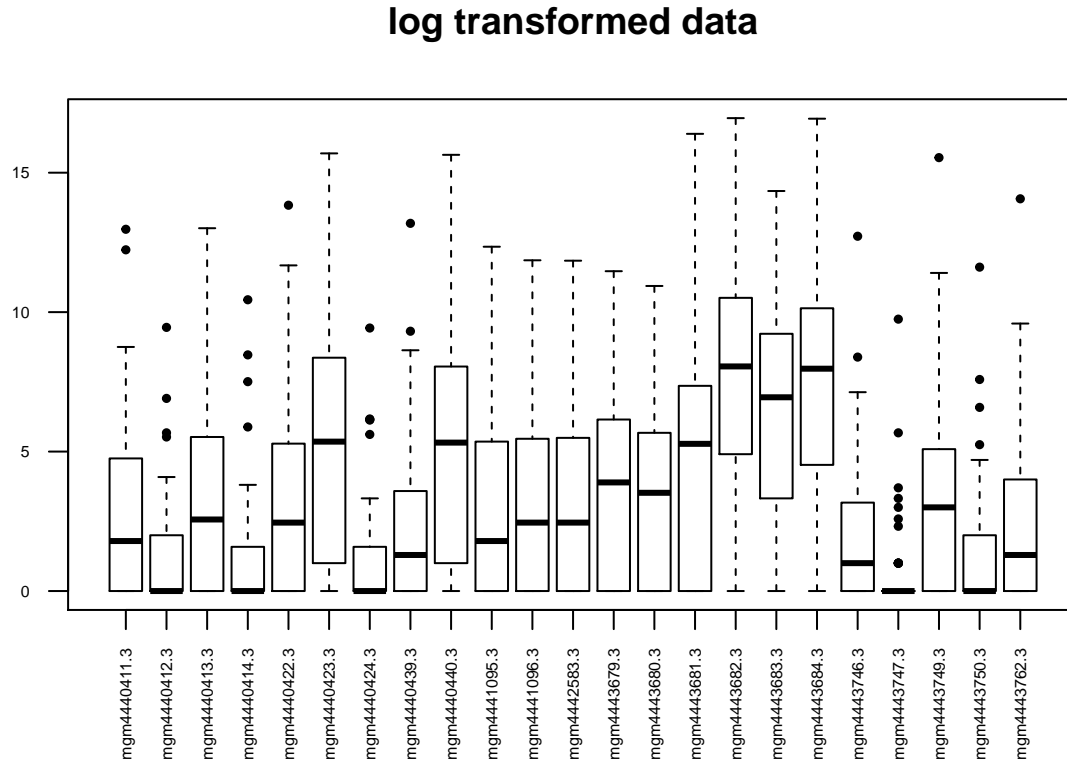


Boxplots of Annotation Distributions

Simple use of the `boxplot.biom()` function is as follows:

```
options(width=120)
xx2t <- transform (xx2, t_Log)
boxplot (xx2t, main="log transformed data", notch=FALSE)
```



It's easy to involve metadata in the plot:

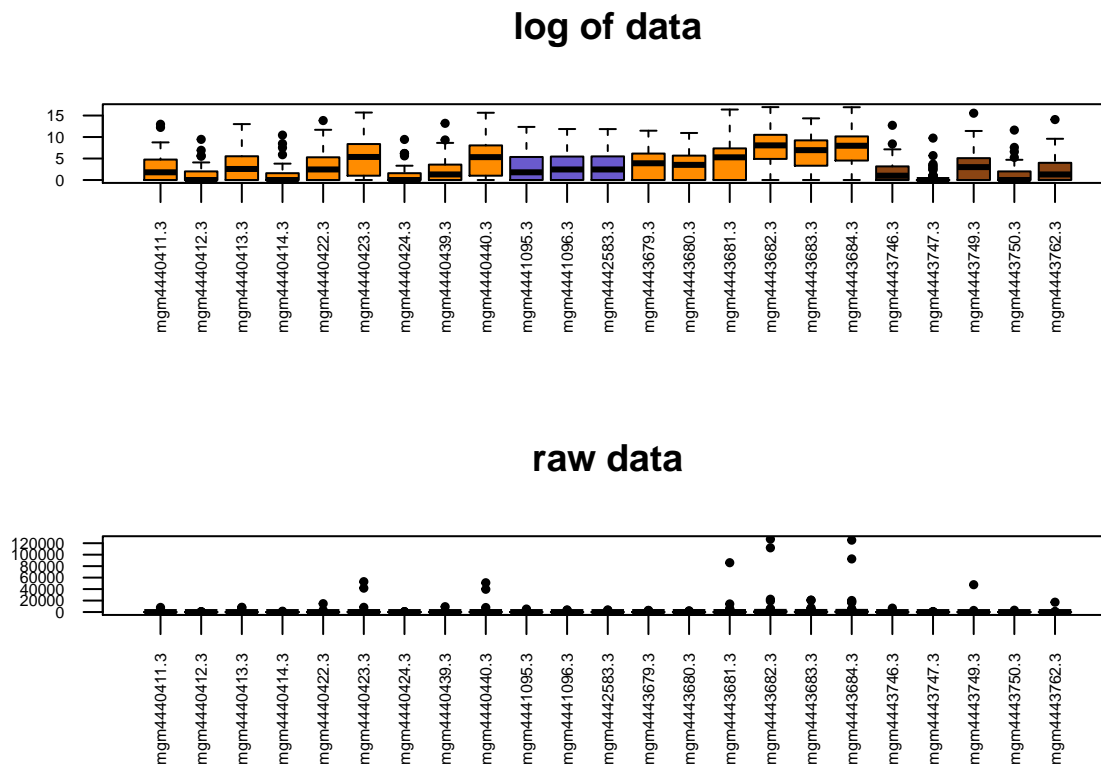
```
columns (xx2t, "material")
```

```
##          sample.data.material
## mgm4440411.3      freshwater
## mgm4440412.3      freshwater
## mgm4440413.3      freshwater
## mgm4440414.3      freshwater
## mgm4440422.3      freshwater
## mgm4440423.3      freshwater
## mgm4440424.3      freshwater
## mgm4440439.3      freshwater
## mgm4440440.3      freshwater
## mgm4441095.3      hot spring
## mgm4441096.3      hot spring
## mgm4442583.3      hot spring
## mgm4443679.3      freshwater
## mgm4443680.3      freshwater
## mgm4443681.3      freshwater
## mgm4443682.3      freshwater
```

```
## mgm4443683.3      freshwater
## mgm4443684.3      freshwater
## mgm4443746.3 hot spring ; microbial mat
## mgm4443747.3 hot spring ; microbial mat
## mgm4443749.3 hot spring ; microbial mat
## mgm4443750.3 hot spring ; microbial mat
## mgm4443762.3 hot spring ; microbial mat
```

And this plot also shows raw and normalized counts against each other:

```
boxplot (xx2t, xx2, x.main="log of data", y.main="raw data", map=c(col="material"), notch=FALSE,
        col=c("freshwater"="darkorange", "hot spring"="slateblue", "hot spring ; microbial mat"="chocolate4"))
```



This plot labels the boxes by metadata:

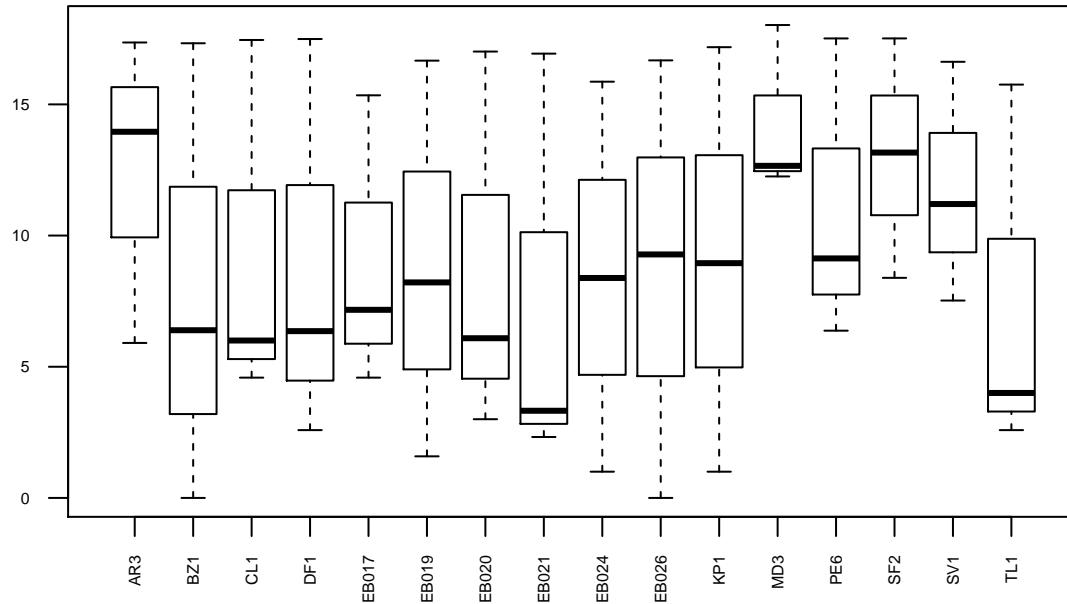
```
columns (xx4, "sample_name")
```

##	env_package.data.sample_name	library.data.sample_name	sample.data.sample_name
## mgm4575333.3	AR3	AR3	AR3
## mgm4575334.3	BZ1	BZ1	BZ1
## mgm4575335.3	CL1	CL1	CL1
## mgm4575336.3	DF1	DF1	DF1
## mgm4575337.3	EB017	EB017	EB017
## mgm4575338.3	EB019	EB019	EB019
## mgm4575339.3	EB020	EB020	EB020
## mgm4575340.3	EB021	EB021	EB021
## mgm4575341.3	EB024	EB024	EB024
## mgm4575342.3	EB026	EB026	EB026
## mgm4575343.3	KP1	KP1	KP1

```
## mgm4575344.3          MD3          MD3          MD3
## mgm4575345.3          PE6          PE6          PE6
## mgm4575346.3          SF2          SF2          SF2
## mgm4575347.3          SV1          SV1          SV1
## mgm4575348.3          TL1          TL1          TL1
```

```
boxplot (transform (xx4, t_Log), names="$$sample.data.sample_name", notch=FALSE)
```

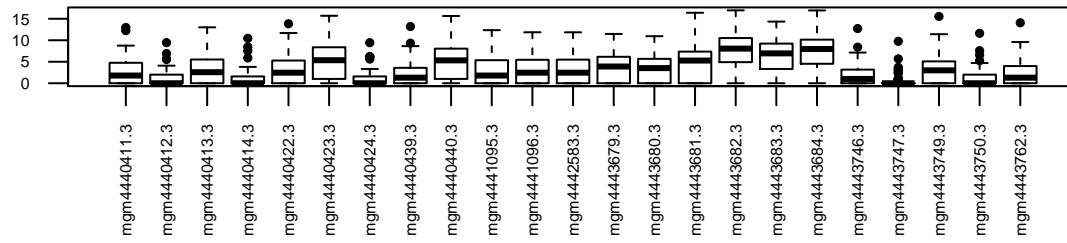
```
## Warning: is.na() applied to non-(list or vector) of type 'NULL'
```



And here, two different normalizations are plotted against each other:

```
xx2tt <- transform (xx2, t_Threshold=list(entry.min=5), t_Log)
boxplot (xx2t, xx2tt, notch=FALSE, x.main="log transformation", y.main="low counts removed, then log tr
```

log transformation



low counts removed, then log transformation

