

# BIGverse

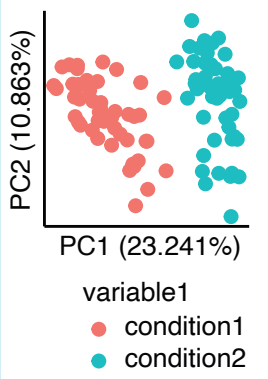
log2 normalized CPM

	lib1	lib2	...	libN
gene1				
gene2				
...				
geneN				

limma

plot\_pca( )

## BIGpicture



extract\_lmFit( )

kmFit( )  
kmFit\_eQTL( )

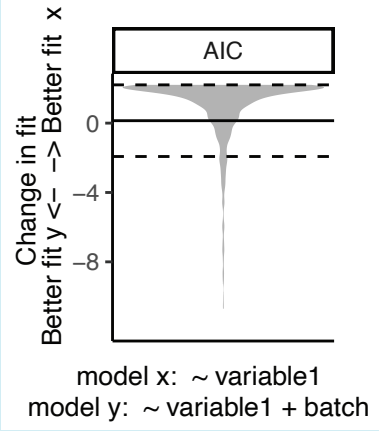
kimma

	FDR
	< 0.05
variable1	
...	
variableN	

summarize\_kmFit( )

```
list [ ]  
  lm           data.frame [ ]  
  lm.fit       data.frame [ ]  
  lm.contrast  data.frame [ ]  
  lm.error     data.frame [ ]  
  lme ...  
  lmerel ...
```

plot\_fit2( )



## SEARChways

BIGsea( )    BIGprofiler( )  
flexEnrich( )  
iterEnrich( )

plot\_gsea( )    map\_string( )  
+ plot\_string( )

plot\_venn\_genes( )

