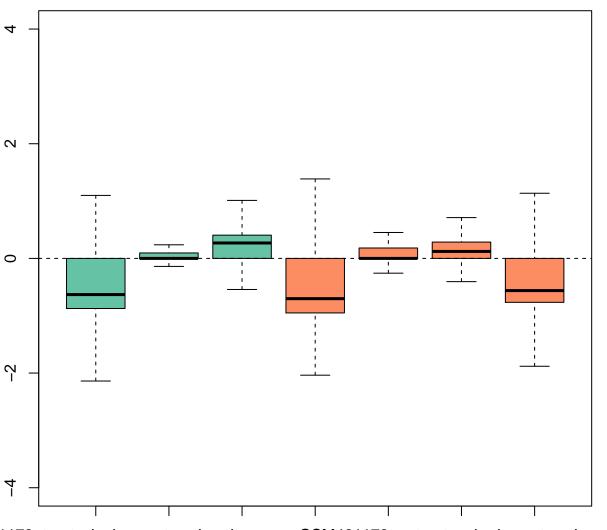
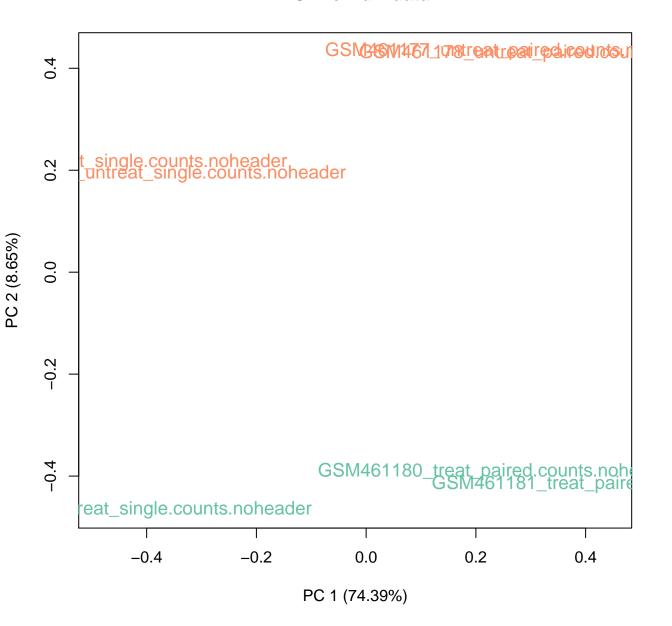
#### **RLE for raw data**



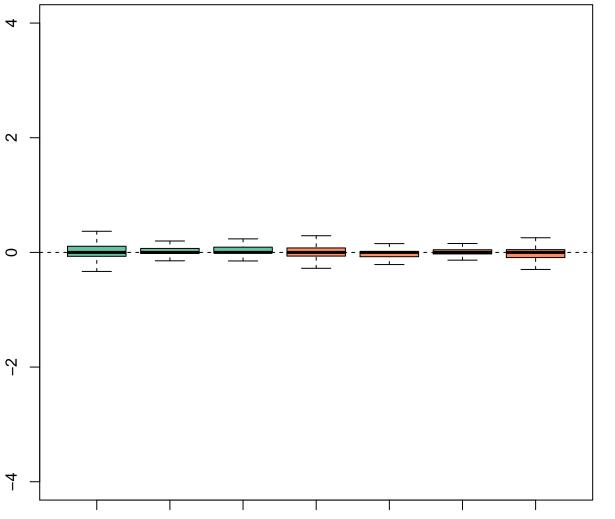
SM461179\_treat\_single.counts.noheader

 $GSM461178\_untreat\_paired.counts.noheader$ 

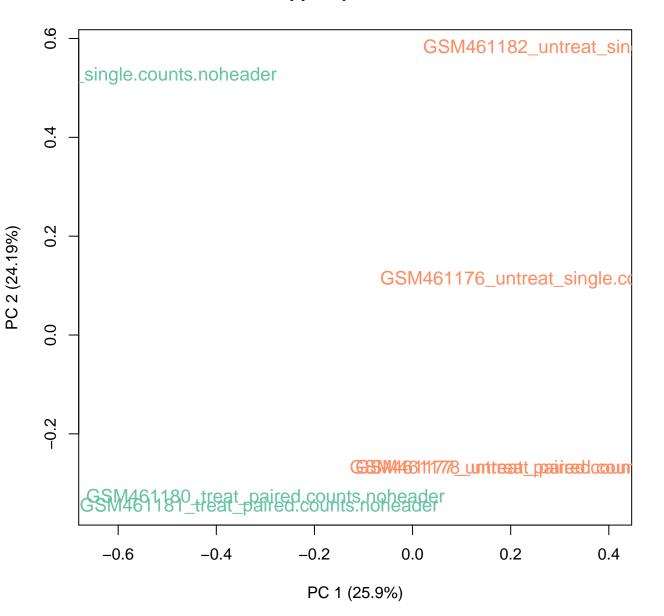
#### PCA for raw data



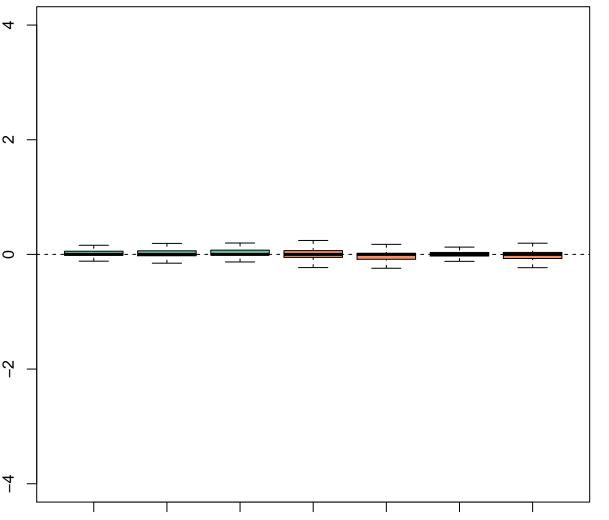
# RLE for upper quartile normalized



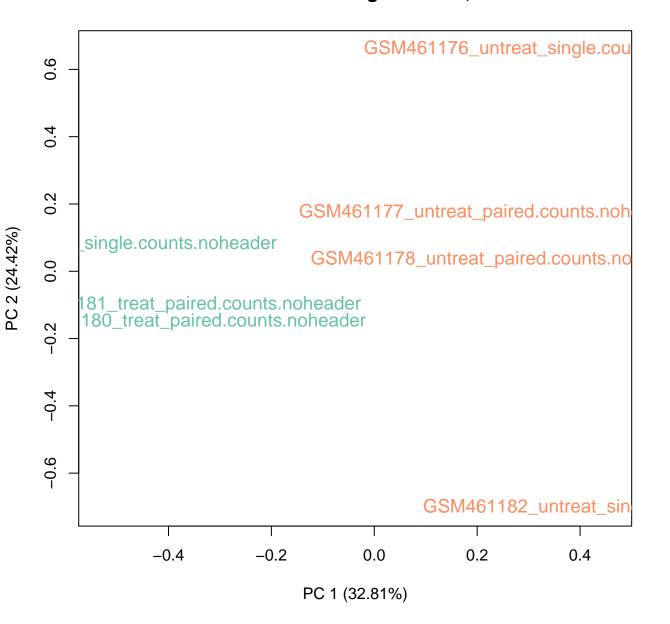
## PCA for upper quartile normalized



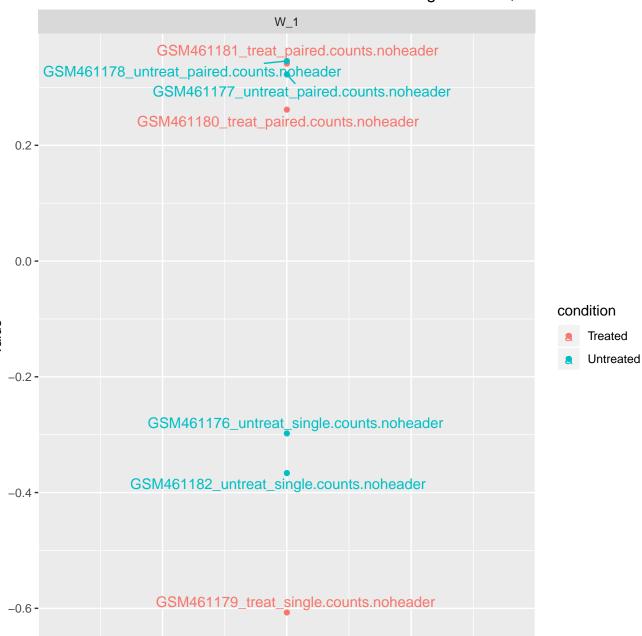
## RLE for RUVr using residuals, k=1



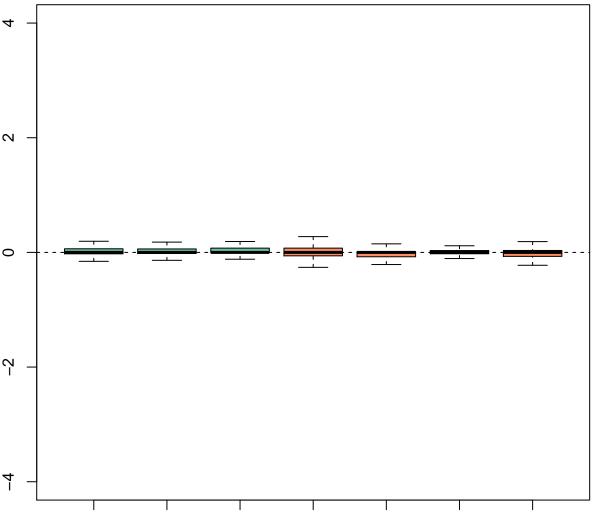
### PCA for RUVr using residuals, k=1



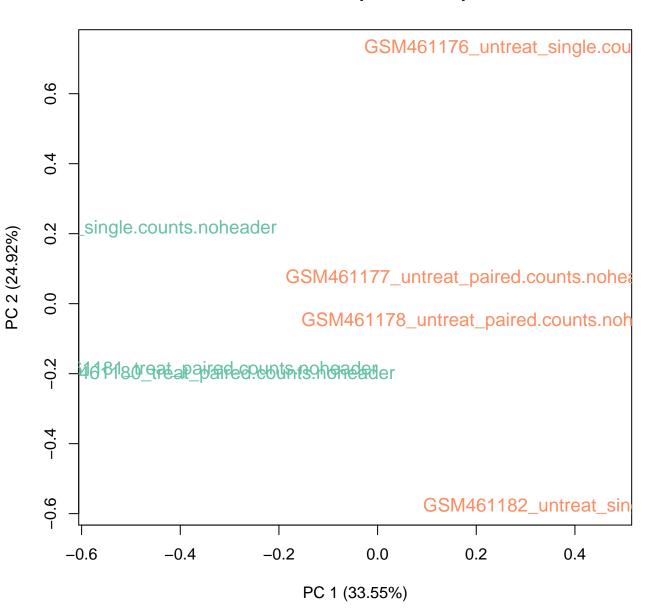
#### Factors of unwanted variation for method: RUVr using residuals, k=1



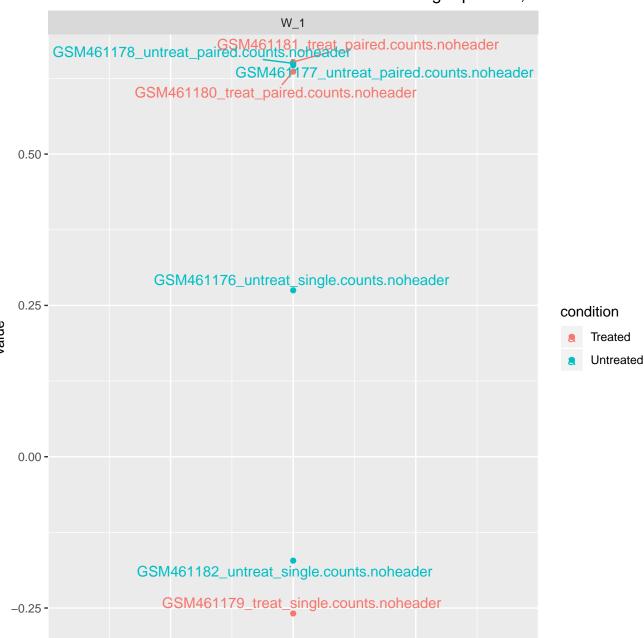
## RLE for RUVs with replicate samples, k=1



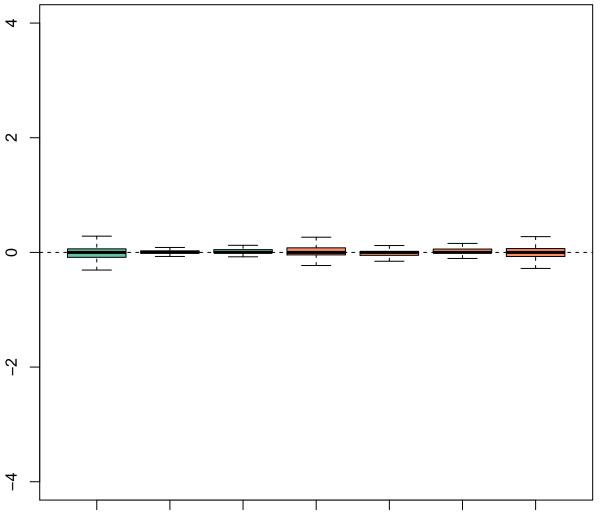
#### PCA for RUVs with replicate samples, k=1



Factors of unwanted variation for method: RUVs using replicates, k=1



## RLE for RUVg with empirical control genes, k=1



### PCA for RUVg with empirical control genes, k=1

