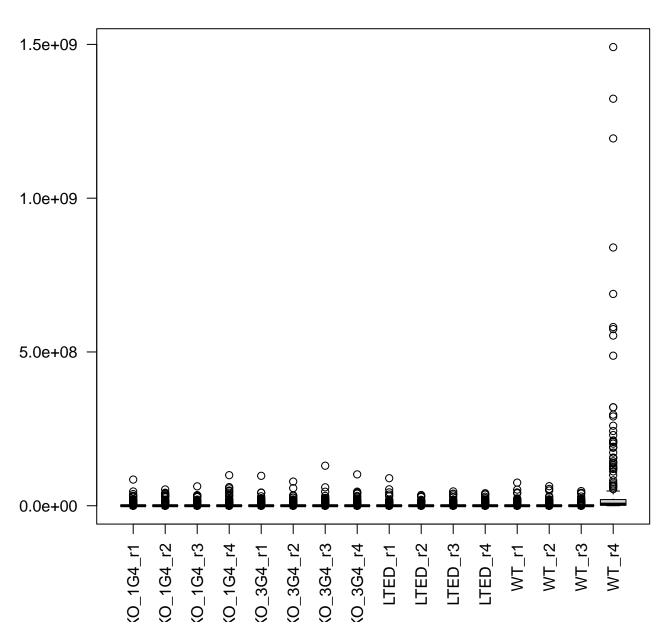
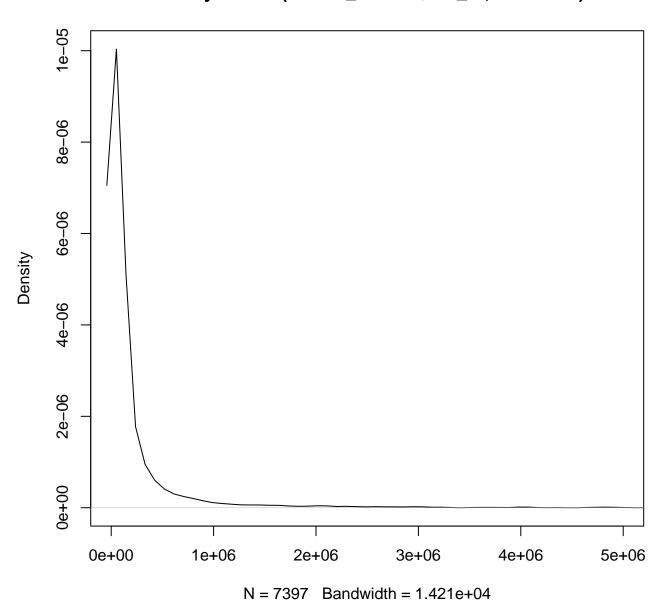
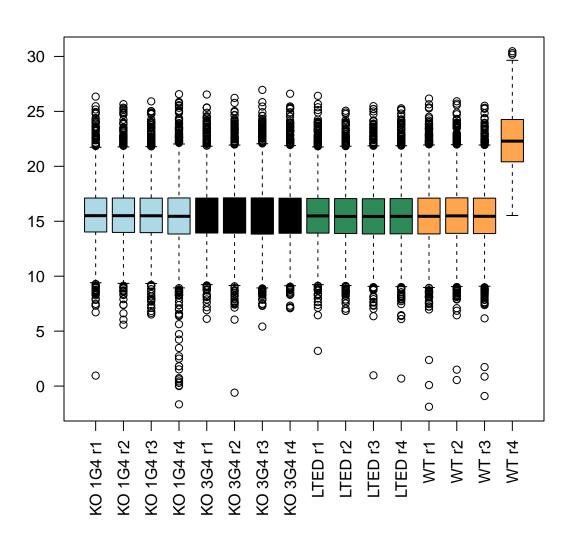
#### **Boxplot of the MS DATA**



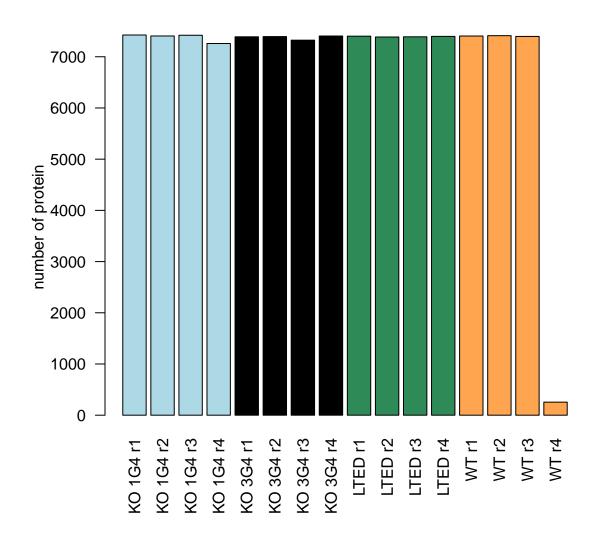
## density.default(x = dia\_results\$WT\_r3, na.rm = T)



### **Boxplot of the MS DATA**



### **Number of Protein Groups Identified**



# **Scree Plot**

