Logic and Justification

1. Top 1000 DEGs:
   1. The **adjusted p value(q)** column was sorted from largest to smallest.
   2. The rows corresponding to q=NA were removed.
   3. The **adjusted p value(q)** column was given a threshold of **q<0.05**.
   4. The top 1000 rows were extracted to another csv file.
   5. The top 1000 DEGs are hereby obtained according to log2foldchange, p-value and adjusted p value

1. Top 20 significant upregulated and downregulated genes:
   1. The **adjusted p value(q)** column was sorted from largest to smallest.
   2. The rows corresponding to q=NA were removed.
   3. The **adjusted p value(q)** column was given a threshold of **q<0.05**
   4. **Log2foldchange** column was sorted from largest to lowest.
   5. **Top 20 rows** will be the top 20 significant upregulated genes.
   6. **Last 20 rows** will be the top 20 significant downregulated genes.
2. Function of genes:
   1. The function of the significant upregulated and downregulated genes was identified using [pantherdb.org](http://pantherdb.org/) and attached as excel sheets respectively.