Gene Expression Array Processing Pipeline v1 (Illumina HT12v4)

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Microarry pre-processing for Illumina BeadArray data.

1. Load the following R Libraries:-

```
> library(lumi)
> library(annotate)
> library(lumiHumanAll.db)
> library(affy)
> library(cluster)
> library(impute)
> library(WGCNA)
> library(gplots)
> library(limma)
> library(vsn)
> library(MBCB)
> library(lumiHumanIDMapping)
> library(scatterplot3d)
> library(relaimpo)
> source("./sjnewhouse_misc_R.R")
>
>
```

Email Dr Stephen J Newhouse; stephen.newhouse@kcl.ac.uk for source code sjnewhouse_misc_R.R. This contains a number of fucntion required for running the pipeline. It Will be on git soon.

2. Reading Sample Table Final Report generated in Genomestudio

3. Reading Sample phenotype file

4. Reading Sample batch or technical information file