Integrative Omics for Precision Medicine

This project was carried out by Felix Oluwasegun Ishabiyi from the transcriptomics team. The project aimed to ascertain that DNA methylation affects gene expression in asthma patients using an integrative omics approach. Integrative omics can be described as an approach to combining two or more omics data which includes major omics data types such as proteomics, genomics, transcriptomics, and metabolomics. Precision medicine is a term used in describing a medication that is tailored to a subgroup of patients depending on their genetic makeup.

Methods

1. The dataset used was obtained from Hackbio's GitHub page.
2. The Datasets were imported into R Studio and were read using the read.csv() function
3. Tidy verse and dyplr for the cleaning and manipulation of the dataset.
4. The DESeq2 library was installed, this library was used to carry out the differential expression analysis of our data.
5. The mean methylation score from the epigenomics methylation data set of the genes was calculated and the methylation score for the expressed gene was noted.
6. The gene annotation library was installed and loaded; this was done to get the respective gene symbols from the Ensembl IDs.
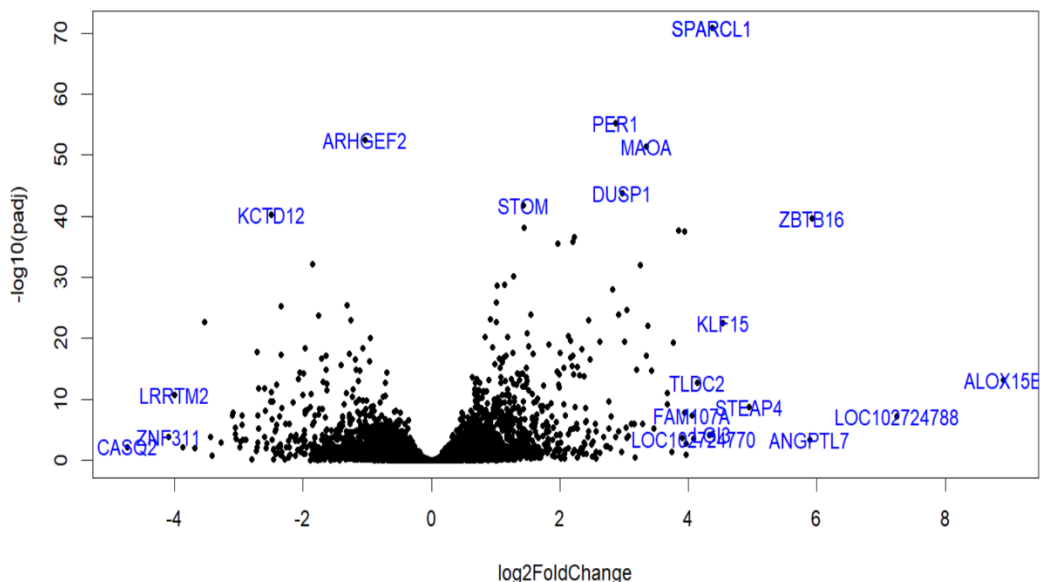7. The codes for this project can be found here

Results

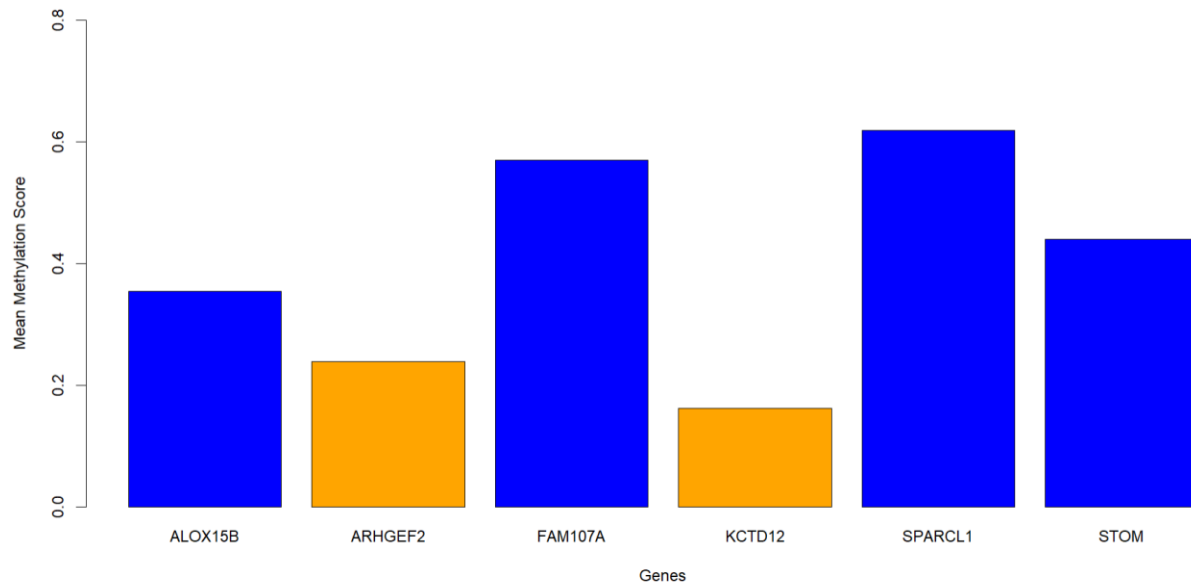Fig 1. The Differential Expression Analysis

Fig 2. The Mean Methylation Score Vs Genes Expressed.

Discussion

The differential expression analysis was illustrated using a scatterplot as indicated in Fig.1. The plot is made up of two types of gene expression, the upregulated genes, and the downregulated genes. An upregulated gene can be described as genes that are prominent and can further be transcribed due to a particular condition, while downregulated genes are genes that the transcription process of RNA is suppressed meaning, they cannot be translated into a protein. The Up-regulated genes observed in Fig 1 are SPARCL1, MAOA, PER1, KLF15, TLDC2, STEAP4, LOC102724788, LOC102724770, LG13, STOM, ALOX15B, FAM107A, DUSP, and ZBTB16. The downregulated genes are ARGHEF2, KCTD12, LRRTM2, ZNF311, and CASQ2. The downregulated genes are not expressed in asthmatic patients while the upregulated genes are very expressed in asthma patients.

To determine the methylation score for the genes, the mean methylation score was calculated from the epigenomics data. The epigenomics data were used to measure the DNA methylation of CpG dinucleotides. Fig 2 indicates that SPARCL1 has the highest methylation score of 0.61, and FAM107A has a methylation score of 0.569. while ARHGEF2 and KCTD12 have a methylation score of 0.238 and 0.167 respectively.

Conclusions

SPARCL1 is well expressed, and ARGHEF2 is well downregulated. The expressions of the genes are not dependent on the mean methylation score calculated from the epigenomics dataset given.