Human fetal Retinal Pigment Epithelium gene expression suggest ocular disease mechanisms

Introduction

The retinal pigment epithelium (RPE) is the pigmented layer of cells in the retina of the eye that serves vital roles in the visual mechanisms. Genetic variants that affect the RPE gene expression could lead to various ocular diseases. By examining genetics of gene expression of cultured human fetal RPE (fRPE) cells under two different metabolic conditions, these genetic variants could be elucidated.

Raw count data was compiled and analysed for Differentially Expressed Genes (DEGs). These analyses were processed with computational statistics based on a statistical model in the R programming language.

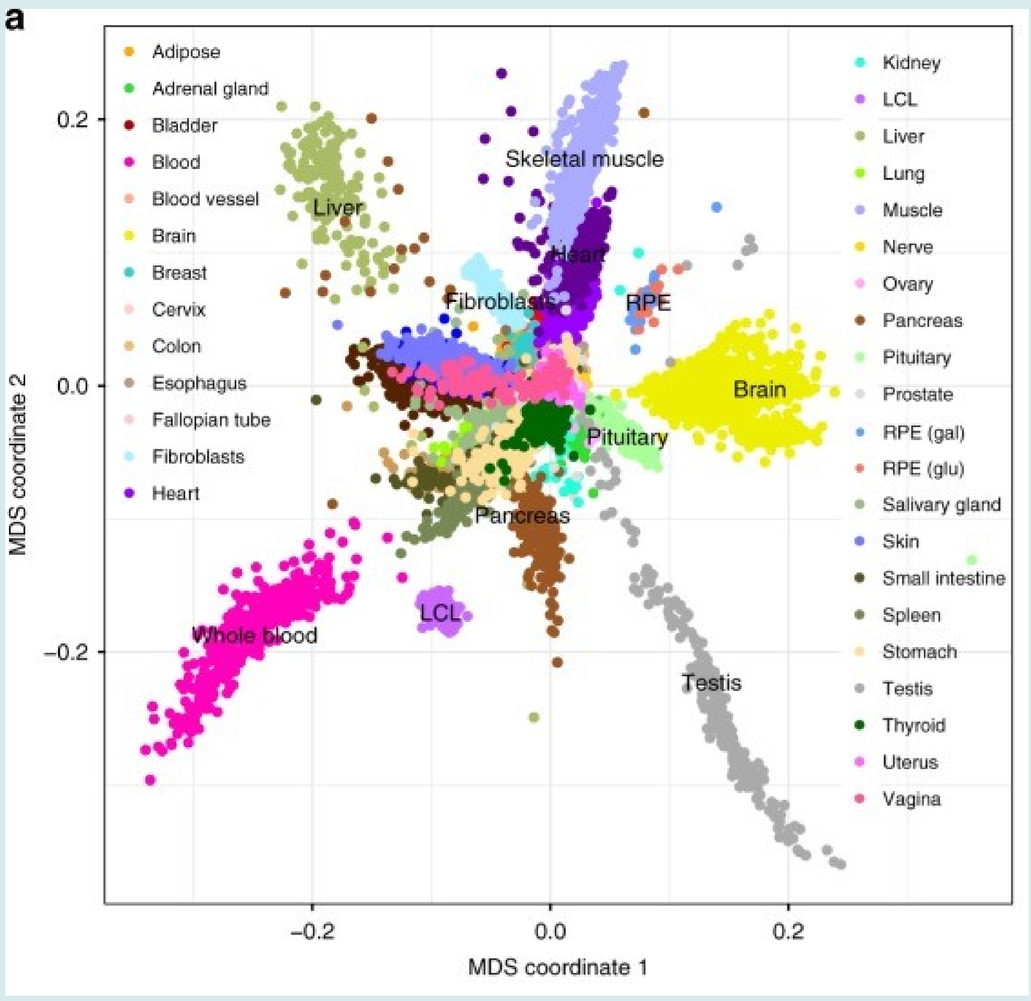


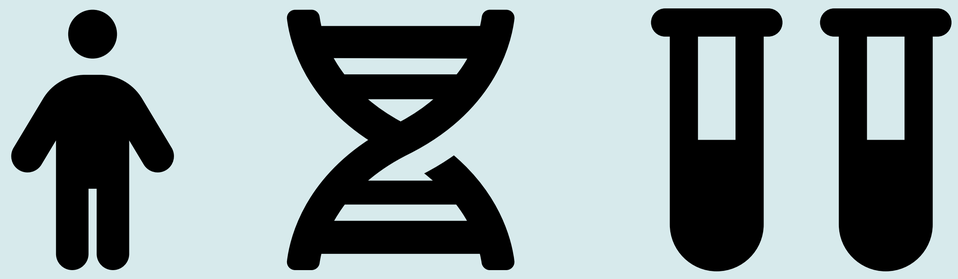
Figure 1: Multidimensional scaling against GTEx tissues. RPE between the brain, heart and skeletal muscle.
Source: Original paper (See References)

Hypothesis

- Eyes are special organs that catch light and convert it to electrical pulses for the brain to comprehend.
- The RPE is phagocytic and thus important for the renewal of visual cells.
- Mutations in the RPE can destroy optic cells and lead to variant ocular diseases and even blindness.
- The cells from the RPE tissue is similar to brain, heart and skeletal muscle tissues.

Final hypothesis: Most of the DEGs are genes expressing elements in the nervous system that impacts the growth of the body.

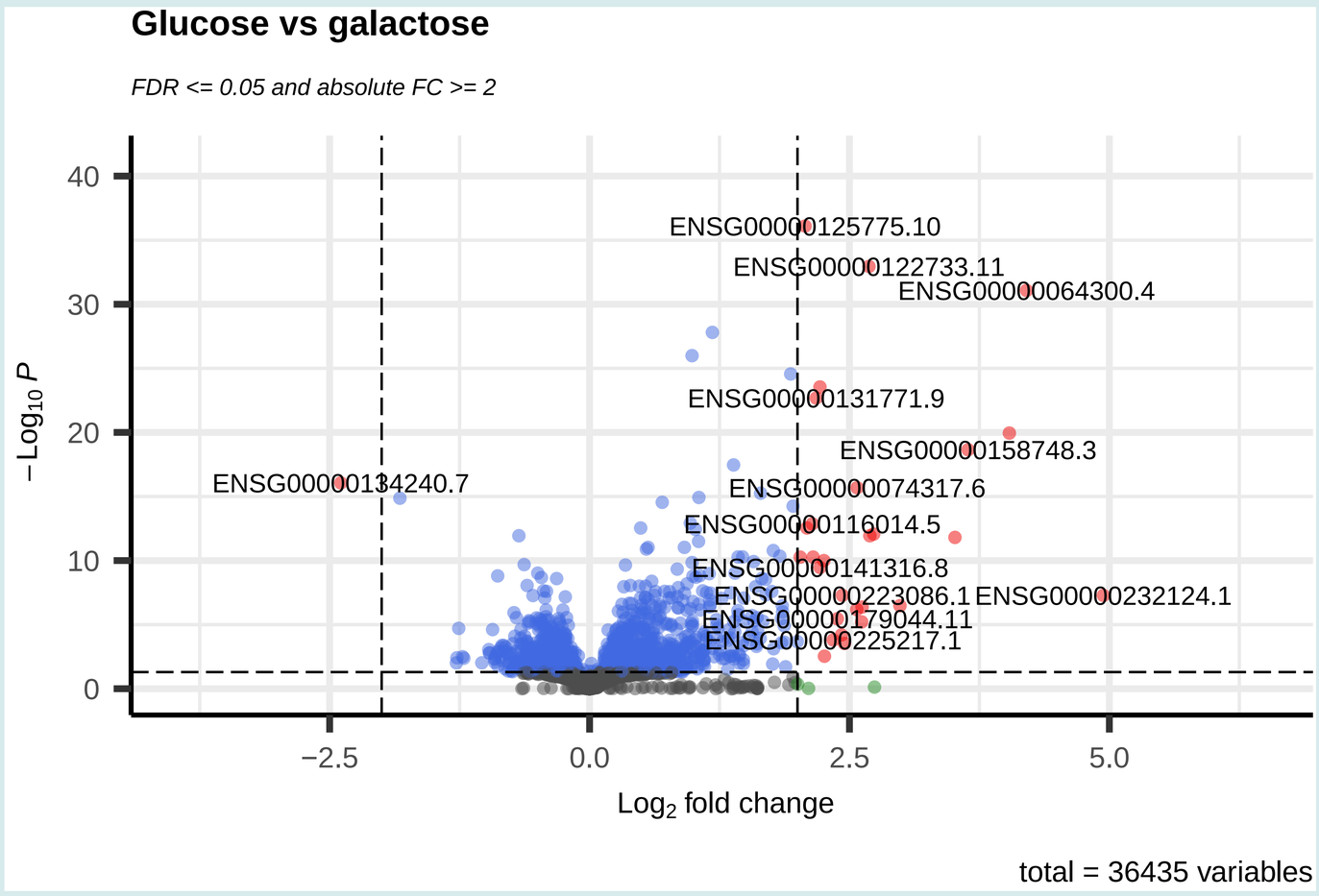
Materials and Methods



24 Homo sapiens	fRPE cell lines	48 glucose/galactose samples

The samples were obtained using high throughput sequencing to find the expression levels of the genes. The mapping of the genes was done using bcl2fastq2 from Illumina and aligned against the hg19 human reference genome using STAR (v2.4.2a) using GENCODE v19 annotation. Processing the expressions was done by using the R package DESeq2. Only samples with an average read count above 10 and with zero counts in less than 20% of the sample were used.

Results and conclusion



This volcano plot shows the differentially expressed genes with most significance. The genes have an Ensembl geneID, but this can be converted to gene symbols. The most remarkable gene is the one on the left side of the plot. This is the HMGCS2 gene, which codes for an enzyme that catalyzes the first step of ketogenesis and plays a crucial role in the fRPE ketogenesis. The other genes play a role in the nervous system or are lncRNAs.

Conclusion: Genes that are part of the nervous system are widely found in the DEGs.

Figure 2: Volcano plot to visualize the DEGs (red)
Source: Replicated project (See References)

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References
Original paper:
https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE129479
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6527609/
Replicated project:
https://github.com/cappuchinese/Gene-Expression-Analysis