## **Biological Sequence Analysis**

## Final Report

23.01.2022

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## **ABOUT RNA SEQUENCE**

Beta cells are cells that make insulin, a hormone that controls the level of glucose (a type of sugar) in the blood. Type 1 diabetes disease occurs when humans immune system destroys these cells mistakenly. However, type 2 diabetes was handling in this study. Saturated fatty acids cause beta-cell failure and causes type 2 diabetes if the individual has a genetic predisposition. In this study, the researchers used RNA sequencing to map the transcripts expressed for five palmitate-treated human islets. For type 2 diabetes analysis, the application of palmitate treatment to beta cells was followed for 48 hours. https://teaching.healthtech.dtu.dk/teaching/images/6/6d/1978.full.pdf.

#### WHY THIS PROJECT?

Diabetes, one of the most common chronic diseases of our time, is increasing day by day with the changing life habits. Although type 1 diabetes occurs at an early age due to genetic disorders, type 2 diabetes occurs due to reasons such as malnutrition and inactivity. Type 2 diabetes can be prevented with a conscious and healthy diet. In this project, I wanted to analyze the effect of fatty acids on beta cells that secrete insulin. Thus, I will be able to observe the effect of a bad diet on type 2 diabetes.

#### **DATA**

https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE53949 is url of my data. It has 10 samples and total size is 8.9 gb. For download the data, i used sra toolkit. I used sra toolkit with "prefix" command and list of samples like "SRR1105566". Original file format was sra. I converted datas from sra format to fastq format with "fastq-dump –split-files" command. I used –split-files command because at the first convert, fastqc quality scores were bad at the 50th position. Once i change the format of the files, they become human readable. Here is first entry if my SRR1105566\_1.fastq file:

@SRR1105566.1 1 length=51

+SRR1105566.1 1 length=51

B7CCCBCC@BCBBBB7ACBC=%9@BBBA=ABAA?BB?BABB<;%<<A;>@B

First line is a sequence identifier with information about the sequencing run and the cluster. Second line is the sequence. Third line is a separator. Fourth line calls quality scores.

When I changed the format of the files, their size increased about 4 times. This came as a surprise to me as I am working in a virtual machine, but I solved the problem by increasing the space I allocated to the disk.

## **FASTQC – MULTIQC**

I applied "fasqc" command to all fastq files to analysis. This tool used to provide an overview of basic quality control metrics for sequencing data. I installed this tool to my global environment with "sudo apt-get install fastqc" command.

MultiQC is a reporting tool that parses summary statistics from results and log files generated by fastqc and log files. I installed this tool with pip. Then i get a HTML formatted multiqc report from all fastqc reports before data cleaning.

### **CLEANING**

I had to trim the data because the data had adapter contents and quality scores were not good enough. For trimming i used flexbar tool. I used this command to clean data. flexbar -q TAIL -qf i1.8 --adapters trimrefs/illumina\_multiplex.fa --threads 4 --zip-output GZ --reads srrdata/sra/SRR1105572\_1.fastq --reads2 srrdata/sra/SRR1105572\_2.fastq --target trim2/SRR1105572. I used Quality-based trimming for getting better quality scores. I gave adapter sequences in a .fa formatted file with " --adapters" command. My adapters sequences are:

>Multiplexing\_Read\_1\_Sequencing\_Primer\_3\_to\_5

AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT

>Multiplexing\_Read\_2\_Sequencing\_Primer\_3\_to\_5

AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC

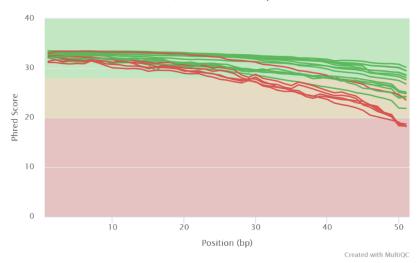
>Illumina Small RNA Adapter 2

TCGTATGCCGTCTTCTGCTTGT

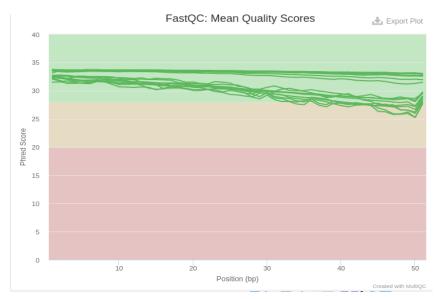
# Per Base Sequence Quality:

## Before:

FastQC: Mean Quality Scores



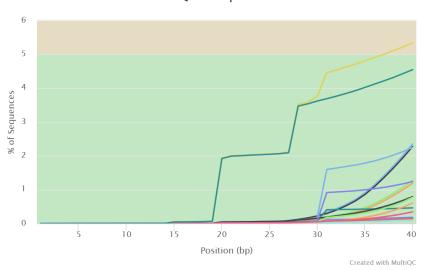
## After:



# **Adapter Content:**

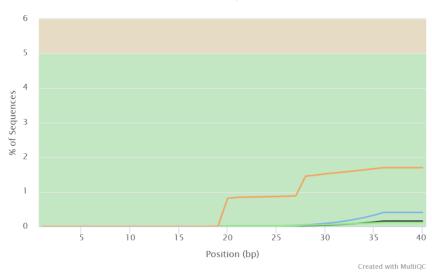
#### Before:

FastQC: Adapter Content



#### After:

FastQC: Adapter Content



# **Alignment**

### HISAT2

HISAT2 is an alignment program for mapping sequencing reads. With this tool, i mapped rna sequences with human genome. Here is a hisat2 command for one of my palmitate reads.

"hisat2 -p 8 --rg-id=SRR1105571 --rg SM:PALMITATE --rg LB:SRR1105571-PALMITATE --summary-file SRR1105571.out --rg PL:ILLUMINA -x refs/genome\_snp\_tran --dta --rna-strandness RF -1 trim2/SRR1105571\_1.fastq.gz -2 trim2/SRR1105571\_2.fastq.gz -S align/SRR1105571.sam"

I gave path to hisat2 index with -x option. I downloaded ENSEMBL indexed hg38 human genome and human genome gtf files with "wget --content-disposition <a href="https://cloud.biohpc.swmed.edu/index.php/s/grch38">https://cloud.biohpc.swmed.edu/index.php/s/grch38</a> snp tran/download" command.

Here is one of my hisat2 outputs:

```
6607142 reads; of these:
```

6607142 (100.00%) were paired; of these:

474976 (7.19%) aligned concordantly 0 times

5559599 (84.15%) aligned concordantly exactly 1 time

572567 (8.67%) aligned concordantly >1 times

----

474976 pairs aligned concordantly 0 times; of these:

31126 (6.55%) aligned discordantly 1 time

----

443850 pairs aligned 0 times concordantly or discordantly; of these:

887700 mates make up the pairs; of these:

516873 (58.23%) aligned 0 times

310939 (35.03%) aligned exactly 1 time

59888 (6.75%) aligned >1 times

96.09% overall alignment rate

Aligned concordantly exactly 1 time line told us quality of alignment. It should be bigger than 70%. This percentage is around 85 on all of my alignments.

For sam to bam convertion and sorting by aligned position "samtools sort -@ 8 -o SRR1105566.bam SRR1105566.sam" command used to each sam file. BAM files are smaller and more efficient for software to work with than SAM files, saving time and reducing costs of computation and storage.

For merging "control" bam files to a single file, i used picard tool.

java -Xmx2g -jar \$RNA\_HOME/student\_tools/picard.jar MergeSamFiles
OUTPUT=control.bam INPUT=SRR1105566.bam INPUT=SRR1105568.bam
INPUT=SRR1105570.bam INPUT=SRR1105572.bam INPUT=SRR1105574.bam

I also used this tool to create a single "palmitate" file. At the and i had 2 bam files: "control.bam" and "palmitate.bam"

I ran FastQC on my bam files and multiqc on FastQC reports. Result is below.

#### **General Statistics**

\$ Copy table	Configure Columns  III Plot Showing 10/10 rows and 4/6 columns.									
Sample Name	% Aligned	% Dups	% GC	M Seqs						
SRR1105566	96.6%	46.2%	53%	16.6						
SRR1105567	96.6%	35.8%	56%	18.5						
SRR1105568	98.0%	57.6%	50%	62.5						
SRR1105569	97.9%	58.2%	51%	63.7						
SRR1105570	98.7%	68.5%	50%	61.4						
SRR1105571	96.1%	60.4%	49%	70.7						
SRR1105572	97.1%	47.5%	51%	25.0						
SRR1105573	96.7%	60.7%	52%	44.4						
SRR1105574	98.0%	67.3%	51%	52.1						
SRR1105575	93.7%	43.1%	49%	9.8						

#### **Samtools**

I used "samtools flagstat control.bam" to get a basic summary of control sequence alignment. Output is below.

217585138 + 0 in total (QC-passed reads + QC-failed reads)

26531524 + 0 secondary

0 + 0 supplementary

0 + 0 duplicates

213737055 + 0 mapped (98.23% : N/A)

191053614 + 0 paired in sequencing

95526807 + 0 read1

95526807 + 0 read2

183026382 + 0 properly paired (95.80% : N/A)

184374410 + 0 with itself and mate mapped

2831121 + 0 singletons (1.48%: N/A)

579996 + 0 with mate mapped to a different chr

428366 + 0 with mate mapped to a different chr (mapQ>=5)

I used "samtools flagstat palmitate.bam" to get a basic summary of palmitate sequence alignment. Output is below.

207149089 + 0 in total (QC-passed reads + QC-failed reads)

```
30586231 + 0 secondary
```

0 + 0 supplementary

0 + 0 duplicates

201403711 + 0 mapped (97.23% : N/A)

176562858 + 0 paired in sequencing

88281429 + 0 read1

88281429 + 0 read2

163941890 + 0 properly paired (92.85% : N/A)

166490564 + 0 with itself and mate mapped

4326916 + 0 singletons (2.45%: N/A)

1463572 + 0 with mate mapped to a different chr

1225590 + 0 with mate mapped to a different chr (mapQ>=5)

## **Expression**

#### **Stringtie**

I used stringtie to generate expression estimates from the RNA-Seq alignments generated by HISAT2 in the previous module. Output transcripts is a gtf file. I used stringtie with the command below.

```
stringtie -p 8 -G ../../../refs/Homo_sapiens.GRCh38.99.gtf -e -B -o SRR1105566/transcripts.gtf -A SRR1105566/gene_abundances.tsv ../../../align/SRR1105566.bam
```

I created tidy expression matrix files for the StringTie results. With --expression\_metric option expression measures changed as coverage, FPKM (Fragments Per Kilobase Million), and TPM (Transcripts Per Kilobase Million) for gene and transcript level.

```
./stringtie_expression_matrix.pl --expression_metric=Coverage --
result_dirs='SRR1105566,SRR1105567,SRR1105568,SRR1105569,SRR1105570,SRR1105571,S
RR1105572,SRR1105573,SRR1105574,SRR1105575' --
transcript_matrix_file=transcript_coverage_all_samples.tsv --
gene_matrix_file=gene_coverage_all_samples.tsv
```

Here is a row from gene\_tpm\_all\_samples.tsv file:

```
Gene_ID SRR1105566 SRR1105567 SRR1105568 SRR1105569 SRR1105570 SRR1105571 SRR1105572 SRR1105573 SRR1105574 SRR1105575
```

ENSG00000000003	5.707782	5.069633	26.946156	22.382566	10.630384
10.464552	11.543087	3.830255	28.493668	8.769938	

Here is a row from gene\_fpkm\_all\_samples.tsv file:

Gene\_ID SRR1105566 SRR1105567 SRR1105568 SRR1105569 SRR1105570 SRR1105571 SRR1105572 SRR1105573 SRR1105574 SRR1105575

ENSG0000000003 2.941525 2.628471 13.866009 11.494489 5.975628 5.454505 5.786224 2.038644 14.692317 4.039905

#### **Htseq-count**

HTSeq is a Python package for analysis of high-throughput sequencing data. Given a file with aligned sequencing reads and a list of genomic features, htseq-count counts how many reads map to each feature. I ran htseq-count on alignments instead to produce raw counts instead of FPKM/TPM values for differential expression analysis. Htseq-count command for SRR1105566 is below.

htseq-count --format bam --order pos --mode intersection-strict --stranded reverse -minaqual 1 --type exon --idattr gene\_id ../../align/SRR1105566.bam ../../refs/Homo\_sapiens.GRCh38.99.gtf > SRR1105566\_gene.tsv

Default format is sam, i changed it to bam for using bam files. Previously i generated position sorted BAM files so i used 'pos' for '--order'. My data is stranded so i used –stranded reverse. I downloaded gtf file from <a href="http://ftp.ensembl.org/pub/release-99/gtf/homo\_sapiens/Homo\_sapiens.GRCh38.99.gtf.gz">http://ftp.ensembl.org/pub/release-99/gtf/homo\_sapiens/Homo\_sapiens.GRCh38.99.gtf.gz</a>.

I merged results files into a single matrix. The following joins the results for each replicate together, adds a header, reformats the result as a tsv file.

echo "GeneID SRR1105566 SRR1105567 SRR1105568 SRR1105569 SRR1105570 SRR1105571 SRR1105572 SRR1105573 SRR1105574 SRR1105575" > header.txt

rm -f gene read counts table all.tsv header.txt

3 rows of tsv file are below.

ENSG00000000419	48	47	145	159	182	302	75	101	129	38
ENSG00000000457	51	44	223	220	165	203	75	117	149	25
ENSG00000000460	32	10	73	67	73	90	34	53	57	5

# **Differantial Expression**

#### **Ballgown DE Analysis**

First i created a csv file with my 10 expression file name with ids, type and path columns. Then i started R code. I created a ballgown instance with 227818 transcripts and 10 samples. In this R code i created 4 tsv files with performing differential expression (DE) analysis. First

two is without filtering transcript and gene results, other two is filtered transcript and gene results. Difference of my code from tutorial code is at row 55 and 56.

sig\_transcripts = subset(results\_transcripts,
results\_transcripts\$pval<0.05&results\_transcripts\$fc>1.5)

sig\_genes = subset(results\_genes, results\_genes\$pval<0.05&results\_genes\$fc>1.5)

With the code above i gave threshold for fold change bigger than 1.5. I did this for getting more significant genes. After reading this article, I decided on thresholds: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2654802/.

Here is top 20 genes sorted by p value with fc>1.5 threshold with the following column name order "gene id, feature, fc, p value, q value, gene\_name".

grep -v feature control\_vs\_palmitate\_gene\_results\_sig.tsv | sort -k 4 | head -n 20

gene id	feature	fc	p value	q value	gene_name
ENSG00000198431	gene	1.814966770226	0.0002785718438100	0.9911893088703	TXNRD1
ENSG00000136244	gene	4.961289746239	0.0006801239964603	0.9911893088703	IL6
ENSG00000110090	gene	1.696156744485	0.0008358710099133	0.9911893088703	CPT1A
ENSG00000170345	gene	1.730196365263	0.0008630102641956	0.9911893088703	FOS
ENSG00000151726	gene	1.739518333235	0.0009241538100712	0.9911893088703	ACSL1
ENSG0000001084	gene	1.930508406247	0.0010598969505082	0.9911893088703	GCLC
ENSG00000151012	gene	2.334912435695	0.0010832061537988	0.9911893088703	SLC7A11
ENSG00000235899	gene	4.252019180605	0.0011630738380532	0.9911893088703	LINC01564
ENSG0000109321	gene	4.653830726109	0.0014333335336698	0.9995565730675	AREG
ENSG00000197279	gene	1.637989106056	0.0019461009583068	0.9995565730675	ZNF165
ENSG00000164038	gene	1.650919886095	0.0023834418788982	0.9995565730675	SLC9B2
ENSG00000130164	gene	1.923184772377	0.0024964250147260	0.9995565730675	LDLR
ENSG00000169429	gene	2.448638532707	0.0025130005508116	0.9995565730675	CXCL8
ENSG00000073756	gene	4.312707764786	0.0030235785734603	0.9995565730675	PTGS2
ENSG00000162772	gene	2.347403547334	0.0034588290866266	0.9995565730675	ATF3
ENSG00000095794	gene	1.830527618953	0.0045729542390642	0.9995565730675	CREM
ENSG00000270299	gene	4.301509699933	0.0049176994861062	0.9995565730675	AL121758.1
ENSG00000141526	gene	1.636865249945	0.0052033951802258	0.9995565730675	SLC16A3
ENSG00000113739	gene	1.794174294766	0.0054325352033646	0.9995565730675	STC2
ENSG00000167772	gene	4.317703930553	0.0060131644862807	0.9995565730675	ANGPTL4

#### **EdgeR Analysis**

In this part, first i create a mapping file to go from ENSG IDs (which htseq-count output) to Symbols:

perl -ne 'if ( $\= \$  /gene\_id\s\"(ENSG\S+)\"\;/) { \$id = \$1; \$name = undef; if ( $\= \$  /gene\_name\s\"(\S+)"\;/) { \$name = \$1; }; }; if (\$id && \$name) {print "\$id\t\$name\n";} if ( $\= \$  /gene\_id\s\"(ERCC\S+)\"/){print "\$1\t\$1\n";}' ../../refs/Homo\_sapiens.GRCh38.99.gtf | sort | uniq > ENSG\_ID2Name.txt

While using edgeR library, i used rawdata that i generated above using htseq-count. With R code new datas require at least 25% of samples to have count > 25. After necessary codes below, dimention (dim(rawdata)) reduced from 60676 10 to 14878 10. I used estimate dispersion, TMM normalization and differential expression test. Number of up/down significant genes at FDR = 0.05 significance level:

> summary(de <- decideTestsDGE(et, p=.05))

palmitate-control

Down 1

NotSig 14869

Up 8

DE genes.txt table:

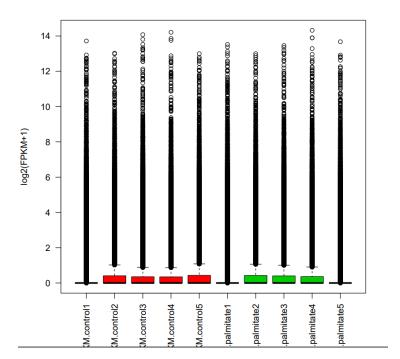
Gene	Gene_Name	Log10_Pvalue	Log_fold_change
ENSG00000167772	ANGPTL4	-6.273	2.023
ENSG00000109321	AREG	-7.176	2.453
ENSG00000136244	IL6	-7.803	2.545
ENSG00000147872	PLIN2	-15.093	2.491
ENSG00000162772	ATF3	-4.720	1.426
ENSG00000073756	PTGS2	-5.186	2.113
ENSG00000235899	LINC01564	-8.686	3.157
ENSG00000151012	SLC7A11	-7.432	1.781
ENSG00000261713	SSTR5-AS1	-4.927	-1.696

#### **DE Visualization**

#### 1)With Ballgown

In this section, graphics are plotted with Ballgown package.

https://github.com/griffithlab/rnaseq\_tutorial/blob/master/scripts/Tutorial\_Part2\_ballgown .R this R codes has guided me. In this code i used most significant gene from differential expression part. I changed gene stable id's to entrezgene id with biomart tool of ensembl.org Boxplot of FPKM Values:



Other plots can be viewed from this link:

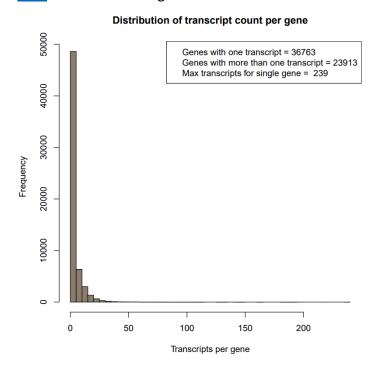
https://drive.google.com/file/d/1WmjaXJmd1v2n7CJQc-BLWElmNAoPUe3f/view?usp=sharing.

## 2) Without Ballgown

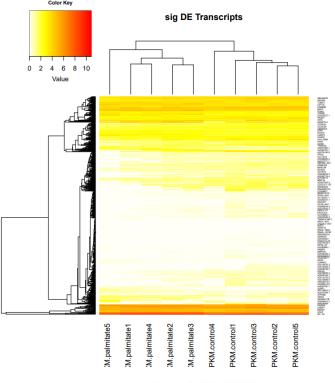
In this section, graphics are plotted without Ballgown package.

<a href="https://github.com/griffithlab/rnaseq">https://github.com/griffithlab/rnaseq</a> tutorial/blob/master/scripts/Tutorial Supplementary

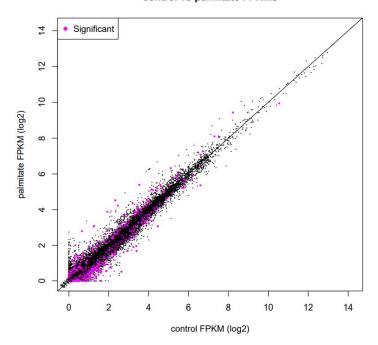
<a href="mailto:R.R.">R.R.</a> this R codes has guided me.



Heatmap shows the most significant DE transcripts:







Other plots can be viewed from this link:

https://drive.google.com/file/d/10nOjOJlSiTJaidkT3rbIvPKJP27oJyvA/view?usp=sharing.

# **Variation**

## Rnaseqmut

To variant detection from BAM files, i used rnaseqmut. I downloaded rnaseqmut from <a href="https://github.com/davidliwei/rnaseqmut">https://github.com/davidliwei/rnaseqmut</a>. For compilation and installation, i followed the

```
rundemo.sh. At first, i did cleaning:
#echo "###### cleaning ########"
#if [!-d results]; then
# mkdir results
#fi
#rm -rf results/.txt results/.vcf
Step 1 is de-novo mutation calling. $BAMFILELIST is BAM files produced in the previous
steps:
#for file in $BAMFILELIST; do
# filebase=`basename $file`
# CMD="rnasegmut $file > results/$filebase.1st.txt"
# echo "#### COMMAND LINE: $CMD"
# eval $CMD
#done
At Step 2, mutations merged in Step 1 into a candidate mutation list.
list ########"
CMD="merge1stfile results/*.1st.txt > results/ALLMUTLIST.txt"
echo "#### COMMAND LINE: $CMD"
eval $CMD
Step 3 is mutation calling from the merged lists.
for file in $BAMFILELIST; do
 filebase=`basename $file`
 CMD="rnaseqmut -l results/ALLMUTLIST.txt $file > results/$filebase.2nd.txt"
 echo "#### COMMAND LINE: $CMD"
 eval $CMD
done
Here are first lines of output from step 3 for one of my bam files.
BAM file:/home/batu/workspace/rnaseq/student_tools/align/SRR1105574.bam
Mut span:4
```

steps in the link. Then i ran rnaseqmut on the bam files and produced the vcf files with

Mutation list:results/ALLMUTLIST.txt Min read:1 Max mismatch:1 Reference genome: Reading 9232554 lines, 102 chromosomes. Switching to chromosome 1, length:248956422 Reading 9232554 lines, 1: 899158 records. At step 4, merged the second pass of mutations into a big table. My labels are: "control1,palmitate1,control2,palmitate2,control3,palmitate3,control4,palmitate4,control5, palmitate5" CMD="python3 ~/workspace/rnaseq/rnaseqmut/script/merge2ndvcf.py -I \$LABELS results/\*.2nd.txt > results/ALLMUT.txt" echo "#### COMMAND LINE: \$CMD" eval \$CMD At step 5, mutations filtered based on user-defined parameters. # defining the two normal samples as control groups CONTROLGROUP="0,2,4,6,8" # the following command keep mutations that occur in at least 1 non-control sample with at least 10 alternative read support. # By default, filtermut.py will only keep mutations that occur in at least 1 non-control sample (-t option) with 20% frequency (-f) and 10 alternative read support (-d), excluding those that also occur in control samples (-a) or does not have enough read coverage in control samples (-b) CMD="python3 ~/workspace/rnaseq/rnaseqmut/script/filtermut.py -d 10 -f 0.0 -b 0 -c \$CONTROLGROUP -I \$LABELS < results/ALLMUT.txt > results/ALLMUT FILTERED.vcf" echo "#### COMMAND LINE: \$CMD" eval \$CMD Output was:

Number of samples:10

1 1 14480

CONTROL group definition:0,2,4,6,8

TREATMENT group definition:1,3,5,7,9

100001 15 44715453

200001 20 44432751

300001 8 38757371

Found variations saved into nano/results/ALLMUT FILTERED.vcf

#### **Annovar**

Annovar is an efficient software tool to utilize update-to-date information to functionally annotate genetic variants detected from diverse genomes. For annovar, first i downloaded a few annotation databases into annovar directory.

perl annotate\_variation.pl -buildver hg38 -downdb -webfrom annovar refGene humandb/
perl annotate\_variation.pl -buildver hg38 -downdb cytoBand humandb/
perl annotate\_variation.pl -buildver hg38 -downdb genomicSuperDups humandb/
perl annotate\_variation.pl -buildver hg38 -downdb -webfrom annovar esp6500siv2\_all humandb/

perl annotate\_variation.pl -buildver hg38 -downdb -webfrom annovar 1000g2015aug humandb/

perl annotate\_variation.pl -buildver hg38 -downdb -webfrom annovar exac03 humandb/ perl annotate\_variation.pl -buildver hg38 -downdb -webfrom annovar avsnp150 humandb/ perl annotate\_variation.pl -buildver hg38 -downdb -webfrom annovar dbnsfp30a humandb/ perl annotate\_variation.pl -buildver hg38 -downdb -webfrom annovar clinvar\_20200316 humandb/

perl annotate\_variation.pl -buildver hg38 -downdb -webfrom annovar cosmic70 humandb/ Some of these databases downloaded as compressed file. We have to extract them for running. After the commands below, i get an tsv file as output.

perl table\_annovar.pl ../rnaseqmut/demo/results/ALLMUT\_FILTERED.filtercoladded.vcf humandb/ -buildver hg38 -out myanno -remove -protocol refGene,cytoBand,genomicSuperDups,esp6500siv2\_all,1000g2015aug\_all,1000g2015aug\_eu r,exac03,avsnp150,dbnsfp30a,cosmic70,clinvar\_20200316 -operation g,r,r,f,f,f,f,f,f,f,f - nastring . -vcfinput

cp myanno.hg38\_multianno.txt myanno.hg38\_multianno.tsv libreoffice myanno.hg38\_multianno.tsv

Chr	Start	End	Ref	Alt	Func.refG	Gene.refG	GeneDetail.refGene	E
MT	3432	3432	С	G	intergenic	NONE;NO	dist=NONE;dist=NONE	
MT	7767	7767	T	Α	intergenic	NONE;NO	dist=NONE;dist=NONE	
MT	14817	14817	С	С	intergenic	NONE;NO	dist=NONE;dist=NONE	
MT	16222	16222	С	T	intergenic	NONE;NO	dist=NONE;dist=NONE	
X	24064263	24064263	G	Α	exonic	EIF2S3		lr
X	55718363	55718363	Α	G	exonic	RRAGB		5
X	1,49E+08	1,49E+08	G	T	UTR3	IDS	NM_000202:c.*1470C>A;NM_001166550:c.*1470C>A	

When i examined variations, i saw that four of them are on the mitochondirial chromosome, three of them are on the X chromosome. "EIF2S3" and "RRAGB" are exonic.

## **Enrichment Analysis**

Gene set enrichment analysis (GSEA) is a method to identify classes of genes or proteins that are over-represented in a large set of genes or proteins, and may have an association with disease phenotypes. For enrichment analysis first i downloaded "c7.all.v7.1.entrez.gmt" and "c6.all.v7.1.entrez.gmt" files. Then i installed clusterProfiler, GSEABase and org.Hs.eg.db libraries with BiocManager. Then i ran following commands to get csv files.

```
filename <- "c7.all.v7.1.entrez.gmt"
gmtfile <- system.file(filename)</pre>
c6 <- read.gmt(gmtfile)
yourEntrezIdList<-
c(7296, 3569, 1374, 2353, 2180, 2729, 23657, 101927171, 374, 7718, 133308, 3949, 3576, 5743, 4676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3676, 3
,1390,9123,8614,51129) #ENTREZID of DE genes
ImmunSigEnrich <- enricher(yourEntrezIdList, TERM2GENE=c6, pvalueCutoff = 0.01)
ImmunSigEnrich <- setReadable(ImmunSigEnrich, OrgDb = org.Hs.eg.db, keyType =
"ENTREZID")
write.csv(ImmunSigEnrich,"MyImmunePathwayRelatedGenes.csv")
goEnrich<-enrichGO(gene= yourEntrezIdList,OrgDb= org.Hs.eg.db, ont=
"ALL",pAdjustMethod="BH",pvalueCutoff = 0.01,readable= TRUE)
write.csv(goEnrich,"MyGORelatedGenes.csv")
keggEnrich<-enrichKEGG(gene= yourEntrezIdList,organism= "hsa",pAdjustMethod="BH",
pvalueCutoff = 0.01)
write.csv(keggEnrich,"MyKEGGRelatedGenes.csv")
# Exit the R session
quit(save="no")
```

I used top 20 Differentialy expressed genes for EntrezIdList. I changed gene stable id's to entrezgene id with biomart tool of ensembl.org

Gene stable ID	NCBI gene (formerly Entrezgene) ID
ENSG00000001084	2729
ENSG00000073756	5743
ENSG00000095794	1390
ENSG00000109321	374
ENSG00000110090	1374
ENSG00000113739	8614
ENSG00000130164	3949
ENSG00000136244	3569
ENSG00000141526	9123
ENSG00000151012	23657
ENSG00000151726	2180
ENSG00000162772	467
ENSG00000164038	133308
ENSG00000167772	51129
ENSG00000169429	3576
ENSG00000170345	2353
ENSG00000197279	7718
ENSG00000198431	7296
ENSG00000235899	101927171

#### **KEGGRelatedGenes:**

Descriptions are IL-17 signaling pathway, Ferroptosis, PPAR signaling pathway, Kaposi sarcoma-associated herpesvirus infection, Pertussis, Lipid and atherosclerosis, Rheumatoid arthritis, Chagas disease and Toll-like receptor signaling pathway. When we examine geneID 3569, this gene encodes a cytokine that functions in inflammation and the maturation of B cells.

	ID	Descriptio	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04657	hsa04657	IL-17 signa	4/14	94/8112	1,55E-05	0,001874	0,001288	3569/2353	4
hsa04216	hsa04216	Ferroptosi	3/14	41/8112	4,2E-05	0,002539	0,001745	2180/2729	3
hsa03320	hsa03320	PPAR signa	3/14	75/8112	0,000257	0,006464	0,004442	1374/2180	3
hsa05167	hsa05167	Kaposi sar	4/14	194/8112	0,000263	0,006464	0,004442	3569/2353	4
hsa05133	hsa05133	Pertussis	3/14	76/8112	0,000267	0,006464	0,004442	3569/2353	3
hsa05417	hsa05417	Lipid and a	4/14	215/8112	0,00039	0,00786	0,005402	3569/2353	4
hsa05323	hsa05323	Rheumato	3/14	93/8112	0,000485	0,008376	0,005756	3569/2353	3
hsa05142	hsa05142	Chagas dis	3/14	102/8112	0,000635	0,00904	0,006213	3569/2353	3
hsa04620	hsa04620	Toll-like re	3/14	104/8112	0,000672	0,00904	0,006213	3569/2353	3

#### ImmunePathwayRelatedGenes:

The protein encoded by ACSL1 gene is an isozyme of the long-chain fatty-acid-coenzyme.

The LDLR gene provides instructions for making a protein called the low-density lipoprotein receptor.

STC2 gene encodes a secreted, homodimeric glycoprotein that is expressed in a wide variety of tissues and may have autocrine or paracrine functions.

	ID	Description	GeneRa	BgRatio	pvalue	p.adjus	qvalue	geneID	Cour
GSE13484_	GSE13484	GSE13484	4/18	198/169	5E-05	0,01	0,0082	ACSL1/LDLR/PTGS2/STC2	4

#### GORelatedGenes:

All 50 genes ontologies are Biological Process. These genes are mostly about palmitate operation like response to nutrient levels, response to fatty acid, response to oxidative stress, cellular response to chemical stress, peptide transport, response to nutrient...

G0:003161 BP G0:003161 response to nutrient levels 7/18 47/1872 1,596-07 0,000185 9,016-05 (PTIA/AC) 7 G0:007051 BP G0:007051 response to fatty acid 4/18 64/1872 3,576-07 0,000213 0,000104 (PTIA/AC) 4 G0:000691 BP G0:005061 response to oxidative stress 6/18 46/18722 2,575-06 0,0000994 0,000485 116/F05/G 6 G0:015001 BP G0:015001 regulation of neuroinflamman 3/18 44/18723 7,216-06 0,0000994 0,000485 116/F05/G 6 G0:015001 BP G0:015001 regulation of neuroinflamman 3/18 44/18723 7,216-06 0,001609 0,000784 116/F05/G 6 G0:015001 BP G0:015001 regulation of neuroinflamman 4/18 44/18723 1,056-05 0,001609 0,000784 116/F05/G 6 G0:190501 BP G0:09051 carboxylic acid transmembrane 4/18 149/18722 1,116-05 0,001609 0,000784 116/F05/G 4 G0:190501 BP G0:090319 response to corricosteroid 4/18 167/18722 1,116-05 0,001609 0,000784 CPTIA/AC 4 G0:190501 BP G0:000319 response to corricosteroid 4/18 167/18722 1,1691-05 0,001609 0,000784 CPTIA/AC 4 G0:0000751 BP G0:000051 response to corricosteroid 4/18 167/18722 1,1691-05 0,001609 0,000784 CPTIA/AC 4 G0:0000761 BP G0:0000761 response to corricosteroid 4/18 167/18722 1,691-05 0,001640 0,000164 116/F05/AC 4 G0:0000761 BP G0:0000761 response to toxic substance 4/18 462/18723 8,851-05 0,005684 0,00277 GCLC/SIC 2 G0:0000961 BP G0:0000761 response to toxic substance 4/18 264/18723 9,8381-05 0,007534 0,003671 F05/SIC/7 4 G0:0001581 BP G0:000167 response to toxic substance 4/18 264/18723 9,8381-05 0,007534 0,003671 F05/SIC/7 4 G0:0001681 BP G0:00017 neutrophil homeostasis 2/18 10/18723 0,000114 0,007534 0,003671 F05/SIC/7 4 G0:0001681 BP G0:00017 neutrophil homeostasis 2/18 10/18723 0,000114 0,007534 0,003671 GCLC/SIC 2 G0:1990201 BP G0:00017 neutrophil homeostasis 2/18 10/18723 0,000114 0,007534 0,003671 GCLC/SIC 2 G0:1990201 BP G0:000071 neutrophil homeostasis 2/18 10/18723 0,000114 0,007534 0,003671 GCLC/SIC 2 G0:1990201 BP G0:000067 regulation of microglial cell ac 2/18 13/18723 0,000114 0,007534 0,003671 GCLC/SIC 2 G0:1990201 BP G0:000067 regulation of microglial cell ac 2/18 13/18723 0,00		ONTOL	ID	Description	GeneRa	BgRatio	pvalue	p.adjust	qvalue	geneID	Coun
GO:00075: BP GO:000069 response to fatty acid	GO:003166			•	_	_		-		_	
GO:00069: BP GO:000691 response to oxidative stress				· ·	_	-	-	-		-	
G:0:01500 BP G:0:01500 regulation of neuroinflammate						-		-			
G:0:01500 BP G:0:01500 neuroinflammattory response fy18 d:4/18723 9,646-06 0,001609 0,000784 IL6/IDIR/I 3 G:0:005131 response to glucocorticoid 4/18 148/18722 1,05E-05 0,001609 0,000784 IL6/IDIR/I 3 G:0:19050 BP G:0:19050: carboxylic acid transmembrand 4/18 169/18722 1,10E-05 0,001609 0,000784 CPT1A/ACI 4 G:0:19038. BP G:0:19038 organic acid transmembrane fx4/18 169/18722 1,10E-05 0,001609 0,000784 CPT1A/ACI 4 G:0:19038 organic acid transmembrane fx4/18 167/18722 1,10E-05 0,001609 0,000784 CPT1A/ACI 4 G:0:000751 BP G:0:000751 response to roticosteroid 4/18 167/18722 1,19E-05 0,001609 0,000784 CPT1A/ACI 4 G:0:00055 BP G:0:00065 response to translotic stimuli 5/18 60:00057 BP G:0:00066 response to toxic substance 4/18 265/18722 8,88E-05 0,00584 0,00277 CPT1A/FCI 5 G:0:00076 BP G:0:00076 learning or memory 4/18 265/18722 8,88E-05 0,007534 0,003671 FOS/SLC7 4 G:0:00056 BP G:0:00066 response to toxic substance 4/18 265/18723 0,000101 0,007534 0,003671 FOS/SLC7 4 G:0:00056 BP G:0:00066 response to toxic substance 4/18 265/18723 0,000101 0,007534 0,003671 FOS/SLC7 4 G:0:00066 BP G:0:00066 response to toxic substance 4/18 265/18723 0,000110 0,007534 0,003671 FL6/FCTA 2 G:0:00066 BP G:0:00066 response to toxic substance 4/18 265/18723 0,000110 0,007534 0,003671 FL6/FCTA 2 G:0:00066 BP G:0:0:00067 response to toxic substance 4/18 266/18723 0,000110 0,007534 0,003671 FL6/FCTA 2 G:0:000171 response to transport 4/18 266/18723 0,000112 0,00758 0,003671 FL6/FCTA 2 G:0:000171 response to response 5/18 100/18723 0,000112 0,00758 0,003671 FL6/FCTA 2 G:0:000171 response 6/18 200017 response to response 5/18 100/18723 0,000112 0,00758 0,003697 FL6/FCTA 2 G:0:000171 response 6/18 200017 response 6/18				· ·	_	-		,			
GO:005131 PP GO:00513 response to glucocorticold 4/18					_	-		-			
GO:19050: RP GO:19050: carboxylic acid transmembrane 1/418					_	-	-	-			
GO:19038: P GO:19038: organic acid transmembrane t* 4/18 150/18722 1,11E-05 0,00169 0,000784 CPT1A/ACI 4 GO:000751 P GO:000319 (response to corticosteroid 4/18 167/18722 1,99E-05 0,002184 0,00169 (Lifs/FO/AL 4 GO:00065: P GO:000055: eysteine metabolic process 2/18 12/18723 1,99E-05 0,00231 0,001126 ACSL1/GCI 4 GO:00065: P GO:00004: response to variente 4/18 12/18723 1,99E-05 0,005684 0,00277 CPT1A/FCI 5 GO:00076: P GO:00094: response to variente 4/18 12/18723 5,88E-05 0,005684 0,00277 CPT1A/FCI 5 GO:00076: P GO:00094: response to toxic substance 4/18 262/18723 5,88E-05 0,005684 0,003671 FOS/SLC7 4 GO:00096: P GO:00096: peptide transport 4/18 264/18723 0,000101 0,007534 0,003671 FOS/SLC7 4 GO:00056: P GO:00066: peptide transport 4/18 264/18723 0,000101 0,007534 0,003671 FLG/CFT1A 4 GO:00066: P GO:00067: p GO:00066: p GO:00066: p GO:00066: p GO:00067: p GO:000					_	-					
GO:003191 RP GO:003191 response to corticosteroid 4/18 16/718721 1,995-05 0,002184 0,00217 GCIC/SICC 4 GO:000751 RP GO:000751 response to nutrient 4/18 12/18723 1,995-05 0,00584 0,00277 GCIC/SICC 2 GO:00094 RP GO:00094 response to xenobiotic stimuli 5/18 462/18722 5,885-05 0,005884 0,00277 GCIC/SICC 2 GO:00096 RP GO:00096 response to toxic substance 4/18 25/18722 8,885-05 0,00584 0,00277 GCIC/SICC 4 GO:00096 RP GO:00096 response to toxic substance 4/18 262/18722 9,838-05 0,005834 0,003671 TNNRD1/F 4 GO:00158 RP GO:00057 glutathione biosynthetic proce 4/18 264/18722 0,000101 0,007534 0,003671 GCIC/SICC 2 GO:00066 RP GO:00067 glutathione biosynthetic proce 4/18 16/18723 0,000101 0,007534 0,003671 GCIC/SICC 2 GO:00067 RP GO:00067 glutathione biosynthetic proce 4/18 16/18723 0,000114 0,007534 0,003671 GCIC/SICC 2 GO:00067 RP GO:00017 neutrophil homeostasis 2/18 16/18723 0,000114 0,007586 0,003697 CPT1A/ACC 3 GO:000171 RP GO:00017 neutrophil homeostasis 2/18 17/18723 0,000118 0,007586 0,003697 CPT1A/ACC 3 GO:001918 PP GO:00191 nonribosomal peptide biosynthetic 4/18 18/18723 0,000132 0,007676 0,003741 GCIC/SICC 2 GO:190201 RP GO:19039 RP GO:000588 (egnition of microglial cell ac 2/18 19/18723 0,000148 0,007981 0,003889 IGA/DLR 2 GO:000508 RP GO:000588 cognition of microglial cell ac 2/18 19/18723 0,000159 0,007891 0,003889 IGA/DLR 2 GO:000508 RP GO:000428 amide transport 4/18 301/1872 0,000159 0,007981 0,003889 IGA/DLR 2 GO:000508 RP GO:000588 cognition of microglial cell ac 2/18 201/1872 0,000159 0,007981 0,003889 IGA/DLR 3 GO:000508 RP GO:000598 rognitic and transport 4/18 301/1872 0,000159 0,007981 0,003889 IGA/DLR 3 GO:000508 RP GO:000508 cognition of small molecule n 4/18 301/1872 0,000159 0,003843 0,004163 CPT1A/ACC 3 GO:000508 RP GO:00058 corpain and transport 4/18 301/1872 0,000250 0,008543 0,004163 CPT1A/ACC 3 GO:000508 RP GO:00059 regulation of small molecule n 4/18 334/1872 0,000250 0,008543 0,004163 CPT1A/ACC 3 GO:000508 RP GO:00056 r					_	-	-				
GO:000751 BP						-		-			
GO:00056; IB GO:00065; cysteine metabolic process						-		-			
GO:00094 BP						-	-	-		-	
GO:00076 BP GO:00076: learning or memory 4/18 255/18723 8,85E-05 0,007534 0,003671 FOS/SLC7A 4 GO:00096: BP GO:00058: response to toxic substance 4/18 262/18723 9,83E-05 0,007534 0,003671 TNNRD1/F 4 GO:00067: BP GO:00067: glutathione biosynthetic proce 2/18 16/18723 0,000104 0,007534 0,003671 IRC/CPTIA 4 GO:00066: BP GO:00066: glutathione biosynthetic proce 2/18 16/18723 0,000104 0,007534 0,003671 GCLC/SLC: 2 GO:00066: BP GO:00066: triglyceride metabolic process 3/18 100/18723 0,000114 0,007586 0,003697 (PT1A/AC: 3 GO:00017: BP GO:00017: neutrophil homeostasis 2/18 18/18723 0,000112 0,007566 0,003671 IRC/SLC7A 2 GO:00191: BP GO:00191: nonribosomal peptide biosynt 2/18 18/18723 0,000132 0,007676 0,003741 GCLC/SLC: 2 GO:19020: BP GO:19020! fatty acid transmembrane tra 2/18 18/18723 0,000132 0,007676 0,003741 GCLC/SLC: 2 GO:19039: BP GO:19039: regulation of microglial cell ac 2/18 19/18723 0,000148 0,007881 0,003889 IRC/SLC7A 2 GO:00508: BP GO:00508: cognition 4/18 296/18722 0,000157 0,007981 0,003889 FOS/SLC7A 4 GO:000508: BP GO:00016: long-chain fatty acid metaboli 3/18 112/18723 0,000159 0,007981 0,003889 FOS/SLC7A 4 GO:000158: BP GO:000158: organic acid transport 4/18 303/18723 0,000168 0,007981 0,003889 IRC/FUPTIA 4 GO:00158: BP GO:00058: organic acid transport 4/18 303/18723 0,000112 0,007981 0,003889 IRC/FUPTIA 4 GO:00066: BP GO:00066: inclural lipid metabolic proces 3/18 129/18723 0,000122 0,007981 0,003889 IRC/SLC7A 2 GO:000714: BP GO:00066: acylglycerol metabolic proces 3/18 129/18723 0,000122 0,008543 0,004163 IRC/SLC7A 2 GO:00066: BP GO:00066: acylglycerol metabolic proces 3/18 129/18723 0,000124 0,008543 0,004163 IRC/SLC7A 2 GO:00066: BP GO:00066: acylglycerol metabolic proces 3/18 129/18723 0,000224 0,008543 0,004163 IRC/SLC7A 2 GO:00066: BP GO:00066: acylglycerol metabolic proces 3/18 139/18723 0,000245 0,008543 0,004163 IRC/SLC7A 2 GO:00066: BP GO:00066: acylglycerol metabolic proces 3/18 139/18723 0,000258 0,008543 0,004163 IRC/SLC7A 2 GO:00066: BP GO:00066: acylglycerol metabolic proces 3/18 139/						-					
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GO:00158:BP GO:00158: peptide transport 4/18 264/18723 0,000110 0,007534 0,003671 ILG/CPTIA 4 GO:00067: BP GO:00067: glutathione biosynthetic proces 3/18 100/18722 0,000114 0,007534 0,003671 GCLC/SLC: 2 GO:00017: BP GO:00017: neutrophil homeostasis 2/18 10/18723 0,000114 0,007586 0,003697 (PTIA/AC: 3 GO:00017: BP GO:00191: nonribosomal peptide biosynt 2/18 18/18723 0,000113 0,007566 0,003697 (ILG/SLC7A 2 GO:01918: BP GO:00191: nonribosomal peptide biosynt 2/18 18/18723 0,000113 0,007676 0,003741 GCLC/SLC: 2 GO:19020: BP GO:19020: fatty acid transmembrane trai 2/18 18/18723 0,000113 0,007676 0,003741 GCLC/SLC: 2 GO:19039: BP GO:19039: regulation of microglial cell ac 2/18 19/18723 0,000148 0,007981 0,003889 ILG/DLTR 2 GO:000508: BP GO:00058: cognition 4/18 296/18722 0,000157 0,007981 0,003889 ICF/LDLR 2 GO:00016: BP GO:00016: long-chain fatty acid metaboli 3/18 112/18722 0,000159 0,007981 0,003889 GPTIA/AC: 3 GO:00018: BP GO:00158: organic acid transport 4/18 301/18722 0,000159 0,007981 0,003889 GPTIA/AC: 3 GO:00018: BP GO:00059: inflammatory cell apoptotic pi 2/18 301/18722 0,000119 0,007981 0,003889 ILG/CPTIA 4 GO:00018: BP GO:00014: cellular response to external s 4/18 303/18722 0,000120 0,007981 0,003889 ILG/CPTIA 4 GO:00066: BP GO:00066: acylglycerol metabolic proces: 3/18 129/18723 0,000121 0,008543 0,004163 FOYIA/AC: 3 GO:00066: BP GO:00066: neutral lipid metabolic proces: 3/18 129/18723 0,000225 0,008543 0,004163 FOYIA/AC: 3 GO:00066: BP GO:00066: neutral lipid metabolic proces: 3/18 129/18723 0,000250 0,008543 0,004163 FOYIA/AC: 3 GO:00066: BP GO:00066: neutral lipid metabolic proces: 3/18 131/18723 0,000250 0,008543 0,004163 FOYIA/AC: 3 GO:00066: BP GO:00066: neutral lipid metabolic proces: 3/18 131/18723 0,000250 0,008543 0,004163 FOYIA/AC: 3 GO:00066: BP GO:00066: neutral lipid metabolic proces: 3/18 131/18723 0,000250 0,008543 0,004163 ILG/FOS/SI 4 GO:000466: BP GO:00048: regulation of small molecule n 4/18 337/18722 0,000250 0,008543 0,004163 ILG/FOS/SI 4 GO:000466: BP GO:000466: positive regulatio					_	-		-			
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GO:00069; BP GO:00069; inflammatory cell apoptotic pt 2/18	GO:001584	ВР	GO:00158	organic acid transport	4/18	303/18723	0,000172	0,007981	0,003889	CPT1A/AC	4
GO:00066: BP GO:00066: acylglycerol metabolic proces; 3/18 128/18722 0,000236 0,008543 0,004163 CPT1A/AC: 3 GO:00066: BP GO:00066: neutral lipid metabolic proces; 3/18 129/18723 0,000242 0,008543 0,004163 CPT1A/AC: 3 GO:00620: BP GO:00620: regulation of small molecule n 4/18 334/18723 0,00025 0,008543 0,004163 CPT1A/SC: 4 GO:00466: BP GO:00621: cellular response to organophosphoru 3/18 131/18723 0,00025 0,008543 0,004163 FOS/AREG: 3 GO:00621: BP GO:00621: cellular response to chemical: 4/18 337/18723 0,000258 0,008543 0,004163 ILG/FOS/SI: 4 GO:00481: BP GO:00481: astrocyte activation					2/18	21/18723	0,000181	0,008091	0,003943	IL6/SLC7A	2
GO:00066: BP GO:00066: neutral lipid metabolic proces; 3/18 129/18723 0,000242 0,008543 0,004163 CPT1A/AC: 3 GO:00620: BP GO:00620: regulation of small molecule n 4/18 334/18723 0,00025 0,008543 0,004163 CPT1A/SL: 4 GO:00466: BP GO:00466: response to organophosphoru 3/18 131/18723 0,000253 0,008543 0,004163 FOS/AREG 3 GO:00621: BP GO:00621: cellular response to chemical 4/18 337/18723 0,000258 0,008543 0,004163 IL6/FOS/SI 4 GO:00481: BP GO:00481: astrocyte activation 2/18 25/18723 0,000258 0,008543 0,004163 IL6/FOS/SI 4 GO:00485: response to steroid hormone 4/18 339/18723 0,000264 0,008543 0,004163 IL6/FOS/A 4 GO:00105: BP GO:00105: regulation of cellular ketone n 3/18 133/18723 0,000264 0,008543 0,004163 IL6/FOS/A 4 GO:00324: BP GO:00324: response to lipopolysaccharid 4/18 343/18723 0,000264 0,008543 0,004163 IL6/FOS/C 4 GO:00456: BP GO:00466: decidualization 2/18 26/18723 0,00026 0,008543 0,004163 IL6/FOS/C 4 GO:00466: BP GO:00466: decidualization 2/18 26/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00466: BP GO:00507: positive regulation of inflamm 3/18 142/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00507: BP GO:00507: positive regulation of acute in 2/18 28/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00105: BP GO:000507: positive regulation of acute in 2/18 28/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00105: BP GO:00105: positive regulation of acute in 2/18 28/18723 0,000325 0,008923 0,004348 IL6/EDLR/I 3 GO:00026: BP GO:00076: positive regulation of vascular 2/18 28/18723 0,000325 0,008923 0,004348 IL6/FTGS2 2 GO:00105: BP GO:00076: learning 3/18 144/18723 0,000325 0,008923 0,004348 IL6/FTGS2 2 GO:00105: BP GO:00076: learning 3/18 144/18723 0,000349 0,008923 0,004348 IL6/FCS/C 4 GO:00330: BP GO:00022: response to molecule of bacte 4/18 363/18723 0,000349 0,008923 0,004348 IL6/FCS/C 4 GO:00330: BP GO:00330: myeloid cell apoptotic proces; 2/18 29/18723 0,000362 0,008923 0,004348 IL6/FCS/C 4 GO:00442: BP GO:00442: sulfur compound biosynthetic 3/18 148/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:007149	ВР		1 1 1	_	320/18723	0,000212				
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GO:00621; BP GO:00621; cellular response to chemical (4/18 337/1872) 0,000258 0,008543 0,004163 IL6/FOS/SI 4 GO:00481 BP GO:00481 astrocyte activation 2/18 25/18723 0,000258 0,008543 0,004163 IL6/LDLR 2 GO:00485 BP GO:00485 response to steroid hormone 4/18 339/18723 0,000264 0,008543 0,004163 IL6/FOS/A 4 GO:00105 BP GO:00105 regulation of cellular ketone n 3/18 133/18723 0,000264 0,008543 0,004163 IL6/FOS/A 4 GO:00324 BP GO:00324 response to lipopolysaccharid 4/18 343/18723 0,000276 0,008543 0,004163 IL6/FOS/C 4 GO:00456 BP GO:00456 positive regulation of osteocle 2/18 26/18723 0,000276 0,008543 0,004163 IL6/FOS/C 4 GO:00466 BP GO:00466 decidualization 2/18 26/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00507 BP GO:00507 positive regulation of inflamm 3/18 142/18723 0,00028 0,008543 0,004163 PTGS2/STC 2 GO:00507 BP GO:00056 positive regulation of acute in 2/18 28/18723 0,000321 0,008923 0,004348 IL6/LDLR/I 3 GO:00026 BP GO:00105 positive regulation of vascular 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00705 BP GO:00705 response to interleukin-1 3/18 143/18723 0,000325 0,008923 0,004348 IL6/FTGS2 2 GO:00076 BP GO:00076 learning 3/18 144/18723 0,000349 0,008923 0,004348 IL6/FTGS/C 4 GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/FTGS/C 4 GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/FTGS/C 3 GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000362 0,008923 0,004348 FTDS/AREG 3 GO:00442 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CCPT1A/LDI 3 GO:00458 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CCPT1A/LDI 3	GO:004668	ВР				131/18723	0,000253	0,008543	0,004163	FOS/AREG	3
GO:00481 BP GO:00481 astrocyte activation 2/18 25/18723 0,000258 0,008543 0,004163 IL6/LDLR 2 GO:00485 BP GO:00485 response to steroid hormone 4/18 339/18723 0,000264 0,008543 0,004163 IL6/FOS/A 4 GO:00105 BP GO:00105 regulation of cellular ketone n 3/18 133/18723 0,000264 0,008543 0,004163 IL6/FOS/C 4 GO:00324 BP GO:00456 positive regulation of osteocle 2/18 26/18723 0,000276 0,008543 0,004163 IL6/FOS/C 4 GO:00456 BP GO:00456 positive regulation of osteocle 2/18 26/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00466 BP GO:00466 decidualization 2/18 26/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00466 BP GO:00507 positive regulation of inflamm 3/18 142/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00066 BP GO:000507 positive regulation of inflamm 3/18 142/18723 0,000321 0,008923 0,004348 IL6/LDLR/I 3 GO:00026 BP GO:00026 positive regulation of vascular 2/18 28/18723 0,000325 0,008923 0,004348 IL6/LDLR/I 3 GO:000705 BP GO:00105 positive regulation of vascular 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00705 BP GO:00705 response to interleukin-1 3/18 143/18723 0,000325 0,008923 0,004348 IL6/GCLC/ 3 GO:00076 BP GO:00076 Iearning 3/18 144/18723 0,000344 0,008923 0,004348 IL6/FOS/C 4 GO:00330 BP GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/SLC7A 2 GO:00140 BP GO:00422 sulfur compound biosynthetic 3/18 148/18723 0,000360 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:006219	ВР			_	337/18723	0,000258	0,008543	0,004163	IL6/FOS/SI	4
GO:00105 BP GO:00105 regulation of cellular ketone n 3/18 133/1872 0,000264 0,008543 0,004163 CPT1A/SLC 3 GO:00324 BP GO:00324 response to lipopolysaccharid 4/18 343/1872 0,000276 0,008543 0,004163 IL6/FOS/C: 4 GO:00456 BP GO:00456 positive regulation of osteocla 2/18 26/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00466 BP GO:00466 decidualization 2/18 26/18723 0,00028 0,008543 0,004163 PTGS2/STC 2 GO:00507 BP GO:00507 positive regulation of inflamm 3/18 142/1872 0,000321 0,008923 0,004348 IL6/LDLR/I 3 GO:00026 BP GO:00026 positive regulation of acute in 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00105 BP GO:00105 positive regulation of vascular 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00705 BP GO:00705 response to interleukin-1 3/18 143/18723 0,000325 0,008923 0,004348 IL6/GCLC/ 3 GO:00076 BP GO:00076 learning 3/18 144/1872 0,000327 0,008923 0,004348 IL6/GCLC/ 3 GO:00022 BP GO:000330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/FOS/C: 4 GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/FOS/C: 4 GO:00140 BP GO:00140 response to purine-containing 3/18 148/1872 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/1872 0,000369 0,008923 0,004348 CPT1A/LDI 3 GO:00458 BP GO:00458 positive regulation of lipid mei 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:004814	ВР				25/18723	0,000258	0,008543	0,004163	IL6/LDLR	2
GO:00324 BP GO:00324 response to lipopolysaccharid 4/18 343/18723 0,000276 0,008543 0,004163 IL6/FOS/C 4 GO:00456 BP GO:00456 positive regulation of osteocle 2/18 26/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00466 BP GO:00466 decidualization 2/18 26/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00507 BP GO:00507 positive regulation of inflamm 3/18 142/18723 0,000321 0,008923 0,004348 IL6/LDLR/I 3 GO:00026 BP GO:00026 positive regulation of acute in 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00105 BP GO:00105 positive regulation of vascular 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00705 BP GO:00705 response to interleukin-1 3/18 143/18723 0,000325 0,008923 0,004348 IL6/GCLC/ 3 GO:00076 BP GO:00076 learning 3/18 144/18723 0,000334 0,008923 0,004348 IL6/FOS/C 4 GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/FOS/C 4 GO:00140 BP GO:00140 response to purine-containing 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:004854	ВР	GO:00485	response to steroid hormone	4/18	339/18723	0,000264	0,008543	0,004163	IL6/FOS/A	4
GO:00456 BP GO:00456 positive regulation of osteocla 2/18 26/18723 0,00028 0,008543 0,004163 FOS/SLC9E 2 GO:00466 BP GO:00466 decidualization 2/18 26/18723 0,00028 0,008543 0,004163 PTGS2/STC 2 GO:00507 BP GO:00507 positive regulation of inflamm 3/18 142/18723 0,000321 0,008923 0,004348 IL6/LDLR/I 3 GO:00026 BP GO:00026 positive regulation of acute in 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00105 BP GO:00105 positive regulation of vascular 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00705 BP GO:00705 response to interleukin-1 3/18 143/18723 0,000327 0,008923 0,004348 IL6/GCLC/ 3 GO:00076 BP GO:00076 learning 3/18 144/18723 0,000344 0,008923 0,004348 FOS/SLC7# 3 GO:00022 BP GO:000330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/FOS/C 4 GO:00140 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:00105	BP	GO:00105	regulation of cellular ketone n	3/18	133/18723	0,000264	0,008543	0,004163	CPT1A/SLC	3
GO:00466 BP GO:00466 decidualization 2/18 26/18723 0,00028 0,008543 0,004163 PTGS2/STC 2 GO:00507 BP GO:00507 positive regulation of inflamm 3/18 142/18723 0,000321 0,008923 0,004348 IL6/LDLR/I 3 GO:00026 BP GO:00026 positive regulation of acute in 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00105 BP GO:00105 positive regulation of vascular 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00705 BP GO:00705 response to interleukin-1 3/18 143/18723 0,000325 0,008923 0,004348 IL6/GCLC/ 3 GO:00076 BP GO:00076 learning 3/18 144/18723 0,000334 0,008923 0,004348 FOS/SLC7/ 3 GO:00022 BP GO:00022 response to molecule of bacte 4/18 363/18723 0,000343 0,008923 0,004348 IL6/FOS/C 4 GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/SLC7/A 2 GO:00140 BP GO:00140 response to purine-containing 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000362 0,008923 0,004348 ACSL1/GC 3 GO:00458 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:003249	BP	GO:003249	response to lipopolysaccharid	4/18	343/18723	0,000276	0,008543	0,004163	IL6/FOS/C	4
GO:00507 BP GO:00507 positive regulation of inflamm 3/18 142/18723 0,000321 0,008923 0,004348 IL6/LDLR/I 3 GO:00026 BP GO:00026 positive regulation of acute in 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00105 BP GO:00105 positive regulation of vascular 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00705 BP GO:00705 response to interleukin-1 3/18 143/18723 0,000327 0,008923 0,004348 IL6/GCLC/ 3 GO:00076 BP GO:00076 learning 3/18 144/18723 0,000334 0,008923 0,004348 FOS/SLC74 3 GO:00022 BP GO:00022 response to molecule of bacte 4/18 363/18723 0,000343 0,008923 0,004348 IL6/FOS/C 4 GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/SLC7A 2 GO:00140 BP GO:00140 response to purine-containing 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:00456	BP	GO:00456	positive regulation of osteocla	2/18	26/18723	0,00028	0,008543	0,004163	FOS/SLC9E	2
GO:00507 BP GO:00507 positive regulation of inflamm 3/18 142/18723 0,000321 0,008923 0,004348 IL6/DLR/I 3 GO:00026 BP GO:00026 positive regulation of acute in 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00105 BP GO:00105 positive regulation of vascular 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00705 BP GO:00705 response to interleukin-1 3/18 143/18723 0,000327 0,008923 0,004348 IL6/GCLC/ 3 GO:00076 BP GO:00076 learning 3/18 144/18723 0,000334 0,008923 0,004348 FOS/SLC74 3 GO:00022 BP GO:00022 response to molecule of bacte 4/18 363/18723 0,000343 0,008923 0,004348 IL6/FOS/C 4 GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/SLC7A 2 GO:00140 BP GO:00140 response to purine-containing 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:004669	BP	GO:004669	decidualization	2/18	26/18723	0,00028	0,008543	0,004163	PTGS2/STC	2
GO:00105 BP GO:00105 positive regulation of vascular 2/18 28/18723 0,000325 0,008923 0,004348 IL6/PTGS2 2 GO:00705 BP GO:00705 response to interleukin-1 3/18 143/18723 0,000327 0,008923 0,004348 IL6/GCLC/ 3 GO:00076 BP GO:00076 learning 3/18 144/18723 0,000334 0,008923 0,004348 FOS/SLC74 3 GO:00022 BP GO:00022 response to molecule of bacte 4/18 363/18723 0,000343 0,008923 0,004348 IL6/FOS/C 4 GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/SLC7A 2 GO:00140 BP GO:00140 response to purine-containing 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000362 0,008923 0,004348 CPT1A/LDI 3 GO:00458 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:005072	BP	GO:005072	positive regulation of inflamm	3/18	142/18723	0,000321	0,008923	0,004348	IL6/LDLR/I	
GO:00705 BP GO:00705 response to interleukin-1 3/18 143/18723 0,000327 0,008923 0,004348 IL6/GCLC/ 3 GO:00076 BP GO:00076 learning 3/18 144/18723 0,000334 0,008923 0,004348 FOS/SLC74 3 GO:00022 BP GO:00022 response to molecule of bacte 4/18 363/18723 0,000343 0,008923 0,004348 IL6/FOS/C 4 GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/SLC7A 2 GO:00140 BP GO:00140 response to purine-containing 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000362 0,008923 0,004348 ACSL1/GCI 3 GO:00458 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:00026	BP	GO:00026	positive regulation of acute in	2/18	28/18723	0,000325	0,008923	0,004348	IL6/PTGS2	2
GO:00076 BP GO:00076 learning 3/18 144/18723 0,000334 0,008923 0,004348 FOS/SLC74 3 GO:00022 BP GO:00022 response to molecule of bacte 4/18 363/18723 0,000343 0,008923 0,004348 IL6/FOS/C 4 GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/SLC7A 2 GO:00140 BP GO:00140 response to purine-containing 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000362 0,008923 0,004348 ACSL1/GCI 3 GO:00458 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:00105	BP	GO:00105	positive regulation of vascular	2/18	28/18723	0,000325	0,008923	0,004348	IL6/PTGS2	2
GO:00022 BP GO:00022 response to molecule of bacte 4/18 363/18723 0,000343 0,008923 0,004348 IL6/FOS/C 4 GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/SLC7A 2 GO:00140 BP GO:00140 response to purine-containing 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000362 0,008923 0,004348 ACSL1/GCI 3 GO:00458 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:00705!	BP	GO:00705	response to interleukin-1	3/18	143/18723	0,000327	0,008923	0,004348	IL6/GCLC/	3
GO:00330 BP GO:00330 myeloid cell apoptotic process 2/18 29/18723 0,000349 0,008923 0,004348 IL6/SLC7A 2 GO:00140 BP GO:00140 response to purine-containing 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000362 0,008923 0,004348 ACSL1/GCI 3 GO:00458 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:00076	ВР	GO:00076	learning	3/18	144/18723	0,000334	0,008923	0,004348	FOS/SLC7A	
GO:00140 BP GO:00140 response to purine-containing 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000362 0,008923 0,004348 ACSL1/GC 3 GO:00458 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:000223	ВР	GO:00022	response to molecule of bacte	4/18	363/18723	0,000343	0,008923	0,004348	IL6/FOS/C	4
GO:00140 BP GO:00140 response to purine-containing 3/18 148/18723 0,000362 0,008923 0,004348 FOS/AREG 3 GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000362 0,008923 0,004348 ACSL1/GC 3 GO:00458 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:003302	ВР	GO:003302	myeloid cell apoptotic process	2/18				0,004348	IL6/SLC7A	
GO:00442 BP GO:00442 sulfur compound biosynthetic 3/18 148/18723 0,000362 0,008923 0,004348 ACSL1/GCI 3 GO:00458 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:00140				_	148/18723	0,000362	0,008923			
GO:00458 BP GO:00458 positive regulation of lipid me 3/18 149/18723 0,000369 0,008923 0,004348 CPT1A/LDI 3	GO:00442	ВР			_						
GO:00487 BP GO:00487 regulation of astrocyte differe 2/18 31/18723 0.000399 0.009452 0.004606 IL 6/LDLR 2	GO:004583	ВР	GO:004583	positive regulation of lipid me	3/18	149/18723	0,000369	0,008923	0,004348	CPT1A/LDI	
25.15.15.15.15.15.15.15.15.15.15.15.15.15	GO:00487	ВР	GO:00487	regulation of astrocyte differe	2/18	31/18723	0,000399	0,009452	0,004606	IL6/LDLR	2