

Identification of Prioritized SNPs Involved in Human Reproductive Behavior

Genetic Epidemiology and Bioinformatics

Life Science & Technology, Biomedical Sciences

Bachelor Research Project

Author: Daniils Zilkins (S3757722) Contributor: Andrei Guriencu (S3959872) Coordinator: Ilja Nolte Supervisor: Ahmad Vaez May/July, 2022

Abstract

Background

In previously conducted studies, 371 specific germline substitution mutations, also known as SNPs, that are linked to human reproductive behavior have been identified through the GWAS analysis. Applied GWAS method was based on the linkage disequilibrium (LD), which is the association network that arises between DNA variants within the human genome.

Research Aim & Question

Aim of this study is to identify functional SNPs through the post-GWAS analysis, and create a list of prioritized genes underlying the GWAS signals. This list of genes could be the foundation for future laboratory studies and that may result in a therapeutic applications and implementation of knowledge on the most relevant SNPs with a possible pathogenic effect on human reproductive behavior. The following research question is set to be answered – What are the most significant genes that are involved in human reproductive behavior, particularly in the context of AFB and AFS phenotypic traits?

Methods

Post-GWAS analysis consisted of two phases. The goal of the first In-Silico Sequencing Phase was to identify all of the SNPs linked to the 371 gSNPs. Aim of the second eQTL phase was to analyze whether the associated missense SNPs, identified in the previous phase, impact expression levels in adjacent genes.

Results

Two lists, each contains the five most significant SNPs and their correspondent gene associations were created. In-Silico phase list is composed of five missense gSNPs with the highest CADD score and LD value closest to 1. The eQTL analysis phase list consists of five most significant associations of previously identified missense SNPs with the ciseQTLs and associated genes, with the highest Z-score.

Conclusion

The study was concluded with the two lists, each consisting of five prioritized genes, that though further bibliography analysis, indeed were found to be potential triggers of various disorders. Four of five genes from the first phase were linked to reproductive behavioral traits, as well as to different pathologies, of which some potentially affecting reproduction. Although, further research is needed in order to confirm and test whether there is a certain connection between the increased disease risk and single nucleotide polymorphisms within the GWAS-associated gene, which are involved in human reproductive behavior.

Introduction

The method of finding associations between genetic variants across the genome and expressed phenotypes in a studied population is known as GWAS analysis. Its core objective is to gain a better understanding of the disease biology so that more effective prevention and treatment strategies could be designed. The GWAS method is based on the linkage disequilibrium (LD), an association network that occurs between DNA variants in human genome, which arises as a result of prior evolutionary changes, such as population size constraints, mutations, recombination rate, as well as natural selection. (Visscher P. M. et al., 2017) Systemic biases produced by marginal sources of error can magnify the number of false-positive and falsenegative associations, therefore precise genotyping is crucial for feasibility through any large-scale GWAS study. (Anderson C. A. et al., 2017)

Since the objective of GWAS is the study of genetic variation and their associations with complex traits and diseases, it worth mentioning the most prevalent genetic variation occurring within the human genome, known as single nucleotide polymorphisms. SNPs are germline substitution mutations of a single nucleotide at a particular location within the genome. SNP array-based GWAS studies as research method have limitations due to required high significance threshold as a result of multiple testing correction, although these could easily be compensated by increased sampling size. (Kim S. et al., 2007)

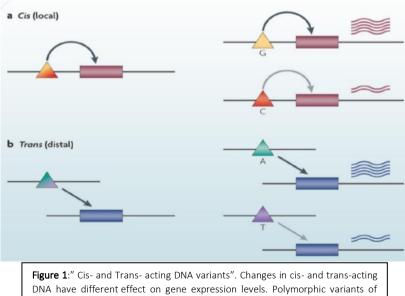
In previously conducted studies, GWAS techniques have been used to identify specific SNPs, which are associated with the human reproductive behavior. 371 SNPs have been found to have an associated with the two particular reproductive behavioral parameters – the age at first sexual intercourse or AFS, and the age of the first child birth or AFB. One of the most important is the one associated with the elevated levels of C-Reactive Protein, a protein involved in variety of diseases in humans. For example, the CRP related genes with their linked genetic pathways and heritability may be associated to the specific genetic variants, relevant for reproductive human behaviors. (Vaez A. et al., 2015)

When one amino acid is replaced by another, a missense SNP, which is the type of nonsynonymous mutation (nsSNPs), occurs leading to a mutant protein with structural and functional impairments. This faulty protein could later cause onset of an illness. Finding SNPs that are pathogenic or associated to a specific phenotype's expression in individuals is one of the most challenging tasks for the research. (Dakal T. C. et al., 2017) Pleiotropy arises if a certain SNP linked to

changes in the expression of the target genes. The nonsynonymous missense SNPs commonly associated with not only with the pleiotropic effect on gene expression, but also as likely deleterious, thereby harmful. These SNPs are often analyzed through the expression quantitative trait loci (eQTL). (Gratten J. et al., 2016)

Many human gene expression levels are influenced by common DNA variants. The previously mentioned eQTLs are the genetic variants which govern that genetic regulation (see Figure 1). The subsequent difference in gene expression amongst individuals has been established as a determinant for phenotypic variation and vulnerability towards the onset of the complex genetic disorders. (Majewski J. et al., 2011) There are two mechanisms of action for DNA genetic variants on a given gene within the human genome. Cis- acting DNA variants modulate the gene expression levels at adjacent gene sites, while the transacting variants modulate the gene expression levels at the distal gene sites. (Cheung et al., 2009) (Xu Z. et al., 2017) Figure 1 shows the visual representation of the variant activity modes. Both the cis- and trans- acting variants are may have a profound genomic effect, however I am considering only significant cis-acting eQTLs since they interact in a more direct manner.

Since the link between these 371 SNPs and their biological-medical associations are still not wellestablished, the main goal of this study is to identify novel genes associated with the human reproductive behavior through in-silico sequencing and eQTL post-GWAS analyses. (Vaez A. et al., 2015)



DNA have different effect on gene expression levels. Polymorphic variants of regulators that operate in cis (a) or trans (b) (also known as local and distal regulators, respectively) to the target genes cause changes in target gene expression. Cis-acting variants are located near by the target genes, whilst transacting variants are found much farther away, sometimes on another chromosome.

The following research question is set to be answered – What are the most significant genes that are involved in human reproductive behavior, particularly in the context of AFB and AFS phenotypic traits?

To find and fully establish the link between the pathology and heritability of gene involved in a human reproductive behavior, one approach is to identify what are the functional SNPs (missense, pleiotropic and eQTLs) among the original 371 GWAS SNPs (gSNPs) as well as SNPs in linkage disequilibrium (LD) with these gSNPs. Identification of functional SNPs will allow us to create a list of prioritized genes underlying the GWAS signals. This list of genes could be the foundation for future laboratory studies and that may result in a therapeutic applications and implementation of knowledge on the most relevant SNPs with a possible pathogenic effect on human reproductive behavior.

Methods

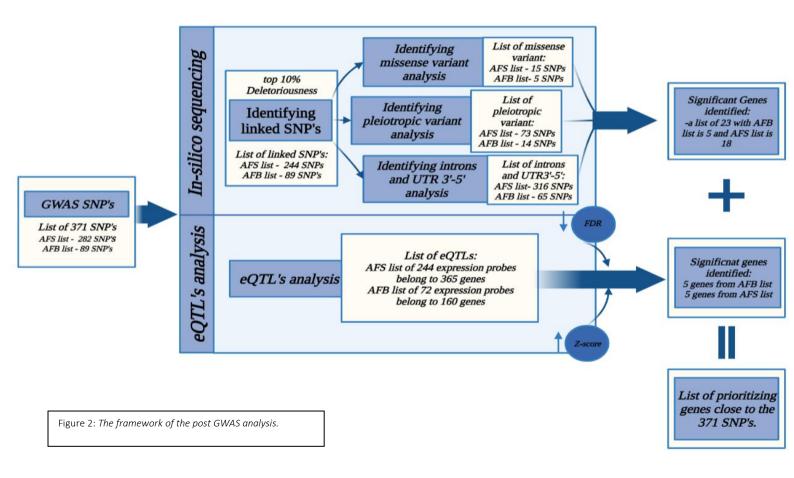
For this project, the open-source software R was used for the post GWAS analysis of the 371 gSNPs.

Open-source software is software that has been published freely or is publicly shared and is accessible to everyone (Corbly J. E. et al., 2014). Due to these advancements in the software industry, open-source software provides a unique outlook to big data analysis for the studies conducted by academics from public institutions to scientific research with R programming (Thorbergsson H. et al., 2007).

R is a data processing, analysis, and visualization programming language (Krotov V. et al., 2017). The most significant aspects of R and R-Studio, which is a graphical user interface developed explicitly for R using the webserver or an app (Rstudio.com, 2011), are similar to those of other computation languages. R studio allows statistical assessment and in-/out-put instructions. The R environment includes features such as graphical utilities for data retrieval, manipulation, and storage, among many others. This computer software is especially well-suited for data analysis (Krotov V. et al., 2017) since it assists in handling a large set of instructions simultaneously, stores all data and progress, and allows analysts to effortlessly fix minor errors (Zumel N. et al., 2016).

To analyze the 371 SNPs, R-studio required an additional package known as SNPannotator used only in the first phase of the experiment.

The SNPannotator package can be found in the CRAN repository, which is a list of installable packages in the R-studio environment. An advantage of using R-studio is that it provides access to all transcripts, with no functional or practical bias. Therefore, genes could be analyzed in a broader context and compared to components of a homologous gene ensemble or genes involved in similar physiological pathways (Aubourg & Rouzé, 2001).



This package requires data from the Ensembl server, which is a website that provides genomic information, containing genetic variants, multi-species alignments, orthologous and paralogous gene descriptions, and substantial polymorphism and regulatory data (Flicek et al., 2009). This server is essential to this study, as it provides useful insights into variation between the sample and the reference genome, facilitating the discovery of conserved regions (Crosswell & Thornton, 2014).

From the Ensemble server, two datasets were used to process of 371 SNPs which are:

- Gene_Names_Ensembl_104_GRCh8
- homo_sapiens.GRCh38.Regulatory_Build.reg ulatory_features.20210107

The first Gene Names dataset has a table of 57623 items and 6 columns related to SNP rs numbers, chromosomes, start-end locations, gene type, and gene name. Aside from the gene names of rs SNPs, the second dataset homo sapiens comprises of a table with 600908 elements and 5 columns, which are similar to the first dataset.

The study took a bioinformatics-based strategy, with two separate phases, each with several steps, as mentioned subsequently (*Figure 2*).

Phase 1: In-silico sequencing analysis

Identifying Linked Variants

The experiment began with a list of 371 SNPs acquired from a previous study (with 89 from AFB and 282 from AFS). The goal of this phase was to identify all of the SNPs linked to the 371 GWAS SNPs (gSNP's), which are SNP's found in the GWAS Catalog. The software SNPannotator uses rs numbers of the SNP's input to analyze the data, the list utilized in this study was filtered for SNPs lacking an rs number and the final number of AFB associated gSNPs were 72. The analyses also made use of data from the 1000 Genomes Project Full Phase 1 November 2010 release (using alignments from August 2010), which included European ancestry. After that, the r2 between each gSNP and all neighboring SNPs was determined as a marker of linkage disequilibrium (LD). LD is a single gene non-random alleles association at different loci. In the following stage of the study, only SNPs with high $(r_{2}>0.80)$ LD with the matching gSNP were utilized (Figure. 2).

Identifying Linked Nonsynonymous SNPs

All SNPs in LD with any of the gSNPs were evaluated using the SNPannotator package and then sorted sequentially BASED ON. More essential arguments include LDlist, which is a variable that, if set to TRUE, finds and adds variants with high LD to the output, and caad, which is an expression that, if set to TRUE, adds CADD scores to variant details. The Combined Annotation-Dependent Depletion (CADD) is a common measurement of variant deleteriousness that can efficiently highlight responsible mutations in genetic analyses, particularly those that are high drivers of severe Mendelian syndromes (Rentzsch et al., 2018).

The second stage was to generate three separate tables based on the type of variations (missense, introns and phenotypes) using the information from the previously created table. The remaining types were left out of the analysis.

The final step was to filter the tables using the CADD scores for deleteriousness, which is a measure of the negative effect of SNPs, to the top 10% of deleteriousness. This final step was taken to improve the analysis of the most relevant SNPs.

In Silico Pleiotropy Analysis

To broaden our understanding of the potential functions of the SNPs discovered in the preceding steps, the study filters the results identified in the previously generated table for age at first birth (AFB) and age of first intercourse (AFS). These parameters (AFS, AFB) were taken into account due to their significance in human reproductive behaviour. The final step in the research was to search on the University of California Santa Cruz (UCSC) Genome Project website for genes that are close to the SNPs reported in the three tables found in the Data Supplement (*Tables 1,2,3*). The genes discovered will be useful in establishing patterns between SNPs and determining the activities of genes relevant to human reproductive behaviour.

Phase 2: eQTLs analysis

Expression-Quantitative-Trait-Locus, also known as eQTL analysis is carried out in order to see whether the associated SNPs, previously identified by the post GWAS analysis.

There are two mechanisms of action for DNA genetic variants on a given gene. *Cis*- acting DNA variants modulate the gene expression levels at adjacent gene sites, while the *Trans*- acting variants modulate the gene expression levels at the distal gene. (Cheung et al., 2009). The research is going to focus on the expression levels in an adjacent gene, hence in a cis- manner. The list of 10,507,664 significant cis-eQTLs was downloaded from the eQTLGen portal, which contains data on 31,684 individuals' levels of gene expression in blood.

The cis-eQTL list was compared with the AFS and AFB lists of 371 SNPs to determine which gSNPs influencing

expression of nearby genes. Then, the top 5 linked SNPs of the highest significance were chosen. On the basis of having the lowest False Discovery Rate, FDR, and the highest absolute Z-score, the top 5 SNPs were chosen. Z- score is determined by subtraction of the total average gene frequency out of each raw expression of the gene. Then, this result is divided by the standard deviation (SD) from all counts obtained throughout all samples. (E. Khabirova, 2017)

To sum up, these top five SNPs are the most likely to alter expression of nearby genes.

Results

Phase 1: Post-GWAS In-Silico Sequencing Analysis

The GWAS analysis on human reproductive behavior originally identified 282 SNPs related to the age of first sexual intercourse (AFS) and 89 SNPs related to the age of first child birth (AFB) (Mills M et al. 2021). Since there are two characteristics, the original dataset was split into two sets and this part of the project is focused on the SNPs associated with AFS.

Composed table of linked SNPs (SNPAnnotator dataset) with dataset of 282 gSNPs, originally consisted of 19,471 outputs, with the linkage disequilibrium (LD) threshold value of $r^2 = 0.5$. To narrow down the large dataset, the LD threshold was changed to $r^2 = 0.8$. Changing the r^2 decreased the sample data to 7,525 outputs, with already computed CADD scores.

Data was further processed via applying the deleteriousness level of below 10%, which filtered out 244 AFS associated probes. The 244 AFS gSNP dataset was further sorted out based on the types of SNP, with only missense and intronic being considered.

First, two tables, one with 15 missense and the other one with 316 intronic and 5'-3'-UTR SNPs were composed. Secondly, a table listing all of the pleiotropic associations of linked gSNPs from the 244 dataset was made, which contained 73 phenotypic associations. The pleiotropic table included some overlap with both the missense and intronic tables. Proceeding that, the SNPs rs-id numbers of linked gSNPs were used to find the associated genes and their names on the UCSC genome Browser. Finally, the five gSNPs with the highest CADD score and LD value closest to 1 were chosen to compose a top 5 missense gSNPs table, represented by the figure 3.

Phase 2: Post-GWAS eQTL Analysis

For the eQTL analysis, the large population dataset from the eQTLGen portal was downloaded and compared with the list of 244 linked gSNPs. **Figure 3**: "Diagram of top 5 gSNPs from In-Silico Sequencing", the highest CADD score, also shows for each variant allele. Outer circle shows chromosome locations highlighted with different colors. Then there are gene names, then rsids of SNPs in LD with gSNPs within the blue circle, CADD score and respective alleles are on peach colored circle. In the central yellow cercle three are phenotypic associations of these five prioritized genes.

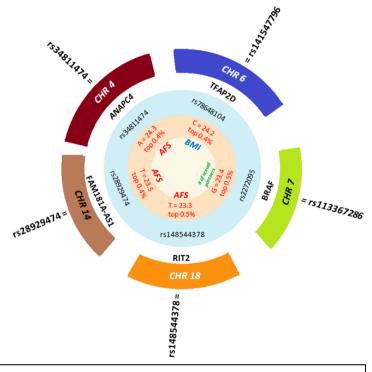
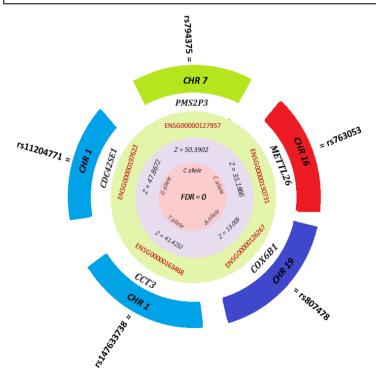


Figure 4:" Diagram of top 5 most significant gSNPs for eQTL". Outer circle shows chromosome locations highlighted with different colors. Then there are gene names, then gene-ids within the green circle, Z-scores are on purple circle. In the central pink cercle three is alleles for different variants and the FDR value is zero for all five gene associations.



The auxiliary code in R studio (see Appendix) produced a list of 365 gene association based on the 244 gSNP probes. Then, the missense, pleiotropic and intronic gSNPs tables were made, similar to those in Phase 1. The top 5 eQTLs of the missense table were chosen based on the highest Z-score and with a zero or close to zero score of False Discovery Rate (FDR). The table, shown by the figure 4 was composed.

Discussion

In the present study, the post-GWAS analysis of 282 gSNPs, that have been found to be associated with the AFS reproductive behavior traits was conducted. In the first phase of the study, in-silico sequencing found 244 association between gSNPs and SNPs in linkage disequilibrium (LD) with them and then evaluating the top 10% deleterious SNPs. This dataset was used to create missense and intronic SNP lists, however, only the missense table was considered for selection of the top five significant gene associations, since the missense SNPs are known to possess detrimental deleterious character. In the second phase, the eQTL analysis, which was aimed at finding associations between 371 linked-gSNPs and the most significant ciseOTLs. Resulting list of 365 eOTLs was processed based on the highest z-score and zero FDR. Moreover, similar to phase one, the list of five most significant gSNPs was evaluated further.

In the following paragraphs each of five gSNP-gene associations from the first phase of the study will be discussed in terms of gene function, potential deleterious effect as well as its phenotypic associations.

Phase 1: In Silico Sequencing Analysis of most significant missense gSNPs

Reproductive Behavior – Gene Associations

As a result of In-Silico Sequencing Analysis, all five identified gSNPs have a CADD score of above twenty, implying that all of these polymorphisms are predicted to have the most deleterious impact on the gene expression of their target genes. Moreover, each of the five gSNPs has been linked to one or more phenotypic associations. Four gSNPs have been linked to reproductive behavior characteristics such as the main subject of this study - Age of First Sexual Intercourse (AFS) and the Number of Sexual Partners (NSP). One of the gSNPs has been linked to changes in BMI and other related health risks. Four reproductive behaviorassociated gSNPs were linked to ANAPC4, BRAF, FAM181A-AS1, and RIT2 genes, with each of them having several various phenotypic associations. Nevertheless, the BRAF gene has only been linked to the NSP.

Based on the bibliography assessment, autism spectrum disorders (ASD), schizophrenia, and PD, at least to some degree, could all be leading to a lack of individual reproductive success. A large-scale study performed on schizophrenia suffering patients showed that these patients are roughly twice as prone to partake in significantly riskier and most frequently unprotected sexual intercourse. The study also depicted those schizophrenic individuals have a 60 % higher likelihood of contracting STDs. (Cournos F. et al., 2013)

During the following year, the first quantitative analysis of reproductive stoppage in households affected by ASD had has conducted, in order to identify the potential hereditary risk factors. Since the release of the research results, there has been substantial progress in genetic screening of ASD risk-posing genetic variants. When assessing birth rates for ASD-affected families were contrasted with the unaffected ASD group. It shows that the number of births in ASD-affected families is about 0.668 times smaller than that of the control group. (Hoffmann T. J. et al., 2014) Considering the presented arguments, there is a foundation aiding the conclusion, that neurological disorders can affect the success of human reproductive behavior. For instance, individual reproductive success is reduced due to abnormal or hostile behavior, which was caused by an individual unstable cognitive state.

Bibliography-Aided Results Analysis

Upon further assessment of the gSNPs rs-ids and their associated genes throughout the literature and via the GeneCards database, the presence of at least three of the five gSNPs were confirmed as possible risk factors for variety of disorders.

TFAP2D

One of the gSNPs tied to the TFAP2D gene, with an rsid of rs141547796, has been linked to being potentially a risk factor for developing abnormalities in expression various phenotypic traits such as body mass index (BMI), systolic blood pressure, and even cognitive function, as well as educational achievement and an increased chance of developing ADHD (attention deficit & hyperactivity disorder). Since there was no precise match in bibliography for the rs141547796 gSNP linked to a TFAP2D gene, it was examined separately in light of CADD score-derived phenotypic associations from its post-GWAS in-silico sequencing analysis phase of the study.

One of the key phenotypic associations of this particular gSNP is its impact on the expression of the gene, responsible for the determination of BMI. The research conducted in 2013 by J.N. Painter et al. found that missense SNPs in the TFAP2D gene are linked to an onset of metabolic syndrome and an overall elevated BMI, which is consistent with my In-silico sequencing analysis results, as well as the CADD-score prediction of gSNP-gene phenotypic associations. Given that a

high BMI is often tied to an increased risk of endometrial cancer, a form of uterus cancer, the gSNP (rs141547796) within the TFAP2D gene may well be associated with this particular type of cancer. Thus, further research into this gSNP is required. (Painter J.N. et al., 2013) Both link to the development of female reproductive system conditions, and the association with the increased risk of oncology development related to mutations within the TFAP2D gene, as well as a high CADD score of 24. This indicates high deleterious effect of rs141547796 gSNP, thus, it may be concluded that this association fits well within the context of this study. As a suggestion for future research, this particular missense SNP within the TFAP2D gene could be explored as a potential genomic biomarker for the detection and early-stage treatment of female endometrial cancer.

RIT2

Protein product RIT2 is a member of the Ras protein superfamily of small GTPases, which is involved in a number of key cellular functions such as survival and cell differentiation. (Wennerberg K. et al., 2005) RIT2 gene has recently been found as a novel Parkinson's disease (PD) associated gene, as well as a candidate gene for other neurological and developmental disorders such as schizophrenia and autism. (Daneshmandpour Y. et al., 2018) Previously conducted research

Furthermore, merely this year, a new study on axial impairment following deep brain stimulation in Parkinson's disease identified a RIT2 gene SNP variant with the rs-id of rs148544378, with a CADD score of 31, which illustrates the highly deleterious character of this particular variant. (Visanji N. P. et al., 2022) This study supports the results of my post-GWAS analysis of linked-gSNPs, since the RIT2 gene gSNP variant has an identical rs-id. The phenotypic analysis identified this gSNP variant to be associated with AFS and NSP reproductive behavior traits. Associations for this gSNP include quite an unorthodox phenotypic characteristic measurement "Leisure sedentary behavior: television watching". The link between this variant being a potential risk factor for the onset of PD and simultaneously being involved in human reproductive behavior makes it an important matter of focus from the perspective of future clinical research.

ANAPC4

Another, yet even more significant variant gSNP with an rs-id rs34811474, was found to be associated with the anaphase-promoting complex subunit 4. ANAPC4 is an E3 ubiquitin ligase that regulates mitosis and mediates the G1 phase of the cell cycle as part of the anaphase-promoting complex/cyclosome (APC/C). Previous research on the ANAPC4 gene found that its SNP variants may be clinically implicated as biomarkers of the early-stage development of oral squamous cell carcinoma. (Diniz M.G. et al., 2015) In 2019, a study aimed at the identification of novel therapeutic targets for osteoarthritis through the GWAS analysis using the UK Biobank archive, with over 95% posterior probability, identified three causal nonsynonymous missense SNP variants. One of these three missense SNPs, with an rs-id rs34811474, was linked to an ANAPC4 gene. (Tachmazidou I. et al., 2019) Analysis of the phenotypic associations identified gSNP (rs34811474) variant that possess a highly pleiotropic effect, since it is associated not only with AFS along with BMI, but additionally, it has been linked to several cognitive performance traits, as well as a variety of chronic conditions. Furthermore, this gSNP variant has the highest CADD score of 24.3, pointing at the significance of its highly deleterious character. A summarized amount of data strongly suggests that gSNP (rs34811474) variant of the ANAPC4 gene has to be considered to be of prime importance from the perspective of future research, as well as potential clinical implementation, especially considering this variant's potential in the diagnostics of oral squamous cell carcinoma.

BRAF

B-Raf proto-oncogene, serine/threonine kinase is a member of the RAF family of protein kinases, which are key players in the MAPK signaling pathway that governs cellular proliferation and differentiation. (Ciampi R. et al., 2005) From 50% to 70% of all human cancer melanomas are caused by the gain-of-function mutation within the BRAF oncogene region. (Garnett M. J. et al., 2004). Post-GWAS In-Silico Sequencing only states a single phenotypic association found for this missense gSNP. Nevertheless, single missense phenotypic association, being a number of sexual partners (NSP), which is an important reproductive behavior determinant. Additionally, there have been records of a variety of disorders linked to deleterious **SNP** within this such oncogene, as cardiofaciocutaneous. Leopard, Noonan and syndromes, as well as posing as onset risk factors of both colorectal and lung cancers. BRAF gene has a CADD score of C = 23, which signifies the very deleterious character of this gSNP, the rs-id is rs113367286, within the BRAF proto-oncogene region.

FAM181A-AS1

FAM181A Antisense RNA-1, abbreviated as FAM181A-AS1, is the RNA gene, part of the Long noncoding RNA class. There are a few types of cancer associated with missense SNPs within the FAM181A-AS1 gene. Since the missense SNP disrupts normal FAM181A-AS1 gene function, it then loses control over the cell cycle. This frequently promotes the growth and division of thyroid cancer cells. During the de novo thyroid cancer pathway research, the gene mutation could also be used to a benefit, since the missense SNP variant within a gene could serve as a diagnostic marker. (Tian J. et al., 2020)

The phenotypic analysis states that this particular gene possesses a very strong pleiotropic character since there are over 35 various phenotypic associations. Among these associations, are the AFS, as well as determinants of various sex hormones like testosterone, or a variety of physical trait associations, such as BMI/Free-Fat-Mass and blood pressure, or the important association with determinants of breast size. Obviously, there are quite a few associations with a health risk, especially for the lifestyle and addictions association like alcohol consumption and smoking. Lastly, it is worth pointing out that there are a few associations, that were not mentioned here, and some of these associations are various blood nutrient content and internal organs with separate liver-disruptions health. three associations.

GeneCards database identified a single association of the FAM181A-AS1 missense SNP variant, being the increased glioma susceptibility. The majority of potentially harmful FAM181A-AS1 variant is stored within the testis. Although, the testis is directly linked to human reproductive behavior, possibly even playing a role in reproduction success and long-term survival. (Dessen P., 2014)

According to Liu Z. Q. et al. research done merely last year, the missense SNP within the FAM181A-AS1 gene will most likely lead to loss of control over the expression, thereby it was proposed that downregulated FAM181A Antisense RNA-1 influences the development of BRCA mutations in elderly people. With age, BRCA loses its heterozygous character and becomes as well susceptible to transformation into breast cancer in the elderly. (Liu Z. Q. et al., 2021)

Phase 2: eQTL Analysis Interpretation

In the following section, I will be discussing the outcomes of the eQTL analysis, specifically on three out of the five most significant gene associations since these have the highest Z-score. Notably, the 3 most significant genes, CDC42SE1, PMS2P3, and COX6B1, were all linked to an increased risk of cancer onset.

CDC42 is a GTPase protein encoded by the CDC42SE1 gene. This protein's main function is to increase cell adhesion and spreading, which in turn promotes ECM

and cell actin cytoskeleton remodeling. (Price L. S. et al., 1998) The CDC42SE1 gene promotes carcinogenesis when it is downregulated, making it an effective diagnostic biomarker for skin cancer treatment. (Kalailingam P. et al., 2019)

The PMS2P3 gene is a product of the PMS2 gene, which has been attributed to the development of breast cancer and is tied to a poor prognosis. (Wang X. et al., 2022) Out of the five most significant linkages, this gene had the highest Z-score of 50.4, indicating that the rs794375 gSNP was the most important for this gene and could be considered for the future clinical-based research.

The human respiratory chain is comprised with several subunits, features cytochrome c oxidase, encoded by the COX6B1 gene. It was found that a mutation in the Cox6B1 gene can cause COX deficiency and a reduction in the protein's overall regulatory function. As a consequence, the COX6B1 gene has been associated with the increased risk of colorectal cancer. (Lascorz J. et al., 2012)

Conclusion

Since the main aim of this study was to find a link between pathology and the heritability of genes involved in human reproductive behavior, it was possible to conclude that the majority of the genes were indeed found to be triggers of various disorders. Although, further research is needed in order to confirm and test whether there is a certain connection between the increased disease risk and single nucleotide polymorphisms within the GWAS-associated gene, which are involved in human reproductive behavior.

Critic of the Study & Future Outlook

Gene enrichment analysis is be done, in order to compose a complete picture of the genome-wide interactions of the key identified genes. However, this most important part of the study, which would also be the third and concluding part of this research was not performed, due to time limitations. Therefore, the future outlook of this research would be a completion of the gene enrichment analysis phase and identification of the most significant interactions and pathways, of genes involved with human reproductive behavior, specifically in the context of the AFS and AFB phenotypical traits.

References

Visscher, P. M., Wray, N. R., Zhang, Q., Sklar, P., McCarthy, M. I., Brown, M. A., & Yang, J. (2017). 10 Years of GWAS Discovery: Biology, Function, and Translation. The American Journal of Human Genetics, 101(1), 5–22. <u>https://doi.org/10.1016/j.ajhg.2017.06.005</u>

Anderson, C. A. et al. Data quality control in genetic case-control association studies. Nat. Protoc. 5, 1564–1573 (2010).

Xu, Z., Wu, C., Wei, P., & Pan, W. (2017). A powerful framework for integrating eQTL and GWAS summary data. Genetics, 207(3), 893-902.

Majewski, J., & Pastinen, T. (2011). The study of eQTL variations by RNA-seq: from SNPs to phenotypes. Trends in Genetics, 27(2), 72-79.

Vaez, A., Jansen, R., Prins, B. P., Hottenga, J. J., De Geus, E. J., Boomsma, D. I., Penninx, B. W., Nolte, I. M., Snieder, H., & Alizadeh, B. Z. (2015). In Silico Post Genome-Wide Association Studies Analysis of C-Reactive Protein Loci Suggests an Important Role for Interferons. Circulation: Cardiovascular Genetics, 8(3), 487–497. <u>https://doi.org/10.1161/circgenetics.114.000714</u>

Kim, S., & Misra, A. (2007). SNP Genotyping: Technologies and Biomedical Applications. Annual Review of Biomedical Engineering, 9(1), 289–320. <u>https://doi.org/10.1146/annurev.bioeng.9.060906.152037</u>

Dakal, T. C., Kala, D., Dhiman, G., Yadav, V., Krokhotin, A., & Dokholyan, N. V. (2017). Predicting the functional consequences of non-synonymous single nucleotide polymorphisms in IL8 gene. Scientific reports, 7(1), 6525. <u>https://doi.org/10.1038/s41598-017-06575-4</u>

Gratten, J., & Visscher, P. M. (2016). Genetic pleiotropy in complex traits and diseases: implications for genomic medicine. Genome medicine, 8(1), 78. https://doi.org/10.1186/s13073-016-0332-x

Krotov, Vlad. (2017). A Quick Introduction to R and RStudio. 10.13140/RG.2.2.10401.92009. https://www.researchgate.net/publication/32111041 A Quick Introduction to R and RStudio

Rstudio.com. (2011). RStudio, new open-source IDE for R. Available at: https://www.rstudio.com/blog/rstudio-new-open-source-ide-for-r/

Efdal Kaya, Muge Agca, Fatih Adiguzel & Mehmet Cetin (2019) Spatial data analysis with R programming for environment, Human and Ecological Risk Assessment: An International Journal, 25:6, 1521-1530, DOI: <u>10.1080/10807039.2018.1470896</u>

Thorbergsson, Helgi & Björgvinsson, Tryggvi & Valfells, Ársæll. (2007). Economic benefits of free and open source software in electronic governance. 183-186. 10.1145/1328057.1328095.

Corbly, James Edward (25 September 2014). "The Free Software Alternative: Freeware, Open Source Software, and Libraries". *Information Technology and Libraries*. **33** (3): 65. doi:10.6017/ital.v33i3.5105. ISSN 2163-5226\

Flicek, P., Aken, B. L., Ballester, B., Beal, K., Bragin, E., Brent, S., Chen, Y., Clapham, P., Coates, G., Fairley, S., Fitzgerald, S., Fernandez-Banet, J., Gordon, L., Gräf, S., Haider, S., Hammond, M., Howe, K., Jenkinson, A., Johnson, N., Kähäri, A., ... Searle, S. M. (2010). Ensembl's 10th year. *Nucleic acids research*, *38*(Database issue), D557–D562. <u>https://doi.org/10.1093/nar/gkp972</u>

Nina Zumel, (March 2016), Preparing data for analysis using R, Win-Vector LLC-Microsoft, 2, <u>https://info.microsoft.com/rs/157-GQE-382/images/EN-CNTNT-Whitepaper-Data-Prep-Using-</u> R.pdf#:~:text=One%20of%20the%20advantages%20of%20data%20analysis%20in,run%20summary%28%29%20on%20our%20data%20and%20g

et%20this%3A1

Aubourg, S., & Rouzé, P. (2001). Genome annotation. *Plant Physiology and Biochemistry*, 39(3-4), 181–193. <u>https://doi.org/10.1016/s0981-9428(01)01242-6</u>

Ani, A., Kamali, Z., & Vaez, A. (2022, April 27). SNPannotator: Investigating the Functional Characteristics of Selected SNPs and Their Vicinity Genomic Region. R-Packages. <u>https://cloud.r-project.org/web/packages/SNPannotator/index.html</u>

L.C. Crosswell, J.M. Thornton, 6.12 - EBI and ELIXIR, Anders Brahme, Comprehensive Biomedical Physics, Elsevier, 2014, Pages 175-190,ISBN 9780444536334, https://doi.org/10.1016/B978-0-444-53632-7.01123-0. (http://www.sciencedirect.com/science/article/pii/B9780444536327011230)

Cheung, V. G., & Spielman, R. S. (2009). Genetics of human gene expression: mapping DNA variants that influence gene expression. *Nature reviews. Genetics*, *10*(9), 595–604. <u>https://doi.org/10.1038/nrg2630</u>

Rentzsch, P., Witten, D., Cooper, G.M., Shendure, J. and Kircher, M. (2018). CADD: predicting the deleteriousness of variants throughout the human genome. *Nucleic Acids Research*, [online] 47(D1), pp.D886–D894. doi:10.1093/nar/gky1016.

E. Khabirova. (2017). Review of RNA-seq normalization methods. Software Solutions for Life Science Data Management and Integration. <u>https://genestack.com/news/blog/review-of-rna-seq-normalisation-</u> methods/#:%7E:text=Z%2Dscore%3A%20calculated%20by%20subtracting,measured%20counts%20across%20all%20samples.

Diniz M.G. de Fatima Correia Silva I. de Souza E.T.A. *et al* Association between cell cycle gene transcription and tumor size in oral

Diniz, M.G., de Fatima Correia Silva, J., de Souza, F.T.A. *et al*. Association between cell cycle gene transcription and tumor size in oral squamous cell carcinoma. *Tumor Biol.* 36, 9717–9722 (2015). <u>https://doi.org/10.1007/s13277-015-3735-1</u>

Painter, J. N., Macgregor, S., Tomlinson, I., Nyholt, D. R., Zondervan, K., Thompson, D., Dunning, A., Easton, D., Montgomery, G. W., & Spurdle, A. B. (2013). Abstract 3182: A GWAS-based cross-disease approach suggests genes predisposing to risk of endometriosis and endometrial cancer. *Molecular and Cellular Biology*. <u>https://doi.org/10.1158/1538-7445.am2013-3182</u>

Ciampi, R., & Nikiforov, Y. E. (2005). Alterations of the <I>BRAF</I> Gene in Thyroid Tumors. *Endocrine Pathology*, *16*(3), 163–172. https://doi.org/10.1385/ep:16:3:163

Daneshmandpour, Y., Darvish, H. & Emamalizadeh, B. *RIT2*: responsible and susceptible gene for neurological and psychiatric disorders. *Mol Genet Genomics* **293**, 785–792 (2018). <u>https://doi.org/10.1007/s00438-018-1451-4</u>

Tian, J., & Luo, B. (2022). Identification of Three Prognosis-Related Differentially Expressed IncRNAs Driven by Copy Number Variation in Thyroid Cancer. *Journal of Immunology Research*, 2022, 1–18. https://doi.org/10.1155/2022/9203796

Diniz, M.G., de Fatima Correia Silva, J., de Souza, F.T.A. *et al.* Association between cell cycle gene transcription and tumor size in oral squamous cell carcinoma. *Tumor Biol.* **36**, 9717–9722 (2015). <u>https://doi.org/10.1007/s13277-015-3735-1</u>

Warren, H., Evangelou, E., Cabrera, C. *et al.* Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nat Genet* **49**, 403–415 (2017). <u>https://doi.org/10.1038/ng.3768</u>

Tachmazidou, I., Hatzikotoulas, K., Southam, L. *et al.* Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. *Nat Genet* **51**, 230–236 (2019). <u>https://doi.org/10.1038/s41588-018-0327-1</u>

Visanji, N. P., Ghani, M., Yu, E., Kakhki, E. G., Sato, C., Moreno, D., Naranian, T., Poon, Y. Y., Abdollahi, M., Naghibzadeh, M., Rajalingam, R., Lozano, A. M., Kalia, S. K., Hodaie, M., Cohn, M., Statucka, M., Boutet, A., Elias, G. J., Germann, J., Fasano, A. (2022). Axial Impairment Following Deep Brain Stimulation in Parkinson's Disease: A Surgicogenomic Approach. *Journal of Parkinson's Disease*, *12*(1), 117–128. <u>https://doi.org/10.3233/jpd-212730</u>

Wennerberg, K., Rossman, K. L., & Der, C. J. (2005). The Ras superfamily at a glance. *Journal of Cell Science*, 118(5), 843–846. https://doi.org/10.1242/jcs.01660

Liu, Z. Q., Zhang, G. T., Jiang, L., Li, C. Q., Chen, Q. T., & Luo, D. Q. (2021). Construction and Comparison of ceRNA Regulatory Network for Different Age Female Breast Cancer. *Frontiers in Genetics*, *12*. <u>https://doi.org/10.3389/fgene.2021.603544</u>

Price, L. S., Leng, J., Schwartz, M. A., & Bokoch, G. M. (1998). Activation of Rac and Cdc42 by Integrins Mediates Cell Spreading. *Molecular Biology* of the Cell, 9(7), 1863–1871. <u>https://doi.org/10.1091/mbc.9.7.1863</u>

Kalailingam, P., Tan, H. B., Pan, J. Y., Tan, S. H., & Thanabalu, T. (2019). Overexpression of CDC42SE1 in A431 Cells Reduced Cell Proliferation by Inhibiting the Akt Pathway. *Cells*, 8(2), 117. https://doi.org/10.3390/cells8020117

Wang, X., Chen, H., Kapoor, P. M., Su, Y. R., Bolla, M. K., Dennis, J., Dunning, A. M., Lush, M., Wang, Q., Michailidou, K., Pharoah, P. D., Hopper, J. L., Southey, M. C., Koutros, S., Freeman, L. E. B., Stone, J., Rennert, G., Shibli, R., Murphy, R. A., . . . Lindström, S. (2022). A Genome-Wide Gene-Based Gene-Environment Interaction Study of Breast Cancer in More than 90,000 Women. *Cancer Research Communications*, 2(4), 211–219. https://doi.org/10.1158/2767-9764.crc-21-0119

Massa, V., Fernandez-Vizarra, E., Alshahwan, S., Bakhsh, E., Goffrini, P., Ferrero, I., Mereghetti, P., D'Adamo, P., Gasparini, P., & Zeviani, M. (2008). Severe infantile encephalomyopathy caused by a mutation in COX6B1, a nucleus-encoded subunit of cytochrome c oxidase. *American journal of human genetics*, *82*(6), 1281–1289. <u>https://doi.org/10.1016/j.ajhg.2008.05.002</u>

Cournos F., Coomaraswamy S., Guido J.R., Meyer-Bahlburg H.F.; Sexual activity and risk of HIV infection among patients with schizophrenia. Am J. Psychiatry. 2013. <u>https://doi.org/10.1176/ajp.151.2.228</u>

Hoffmann, T. J., Windham, G. C., Anderson, M., Croen, L. A., Grether, J. K., & Risch, N. (2014). Evidence of Reproductive Stoppage in Families with Autism Spectrum Disorder. *JAMA Psychiatry*, *71*(8), 943. <u>https://doi.org/10.1001/jamapsychiatry.2014.420</u>

Bronner, G., Hassin-Baer, S., & Gurevich, T. (2017). Sexual Preoccupation Behavior in Parkinson's Disease. *Journal of Parkinson's Disease*, 7(1), 175–182. <u>https://doi.org/10.3233/jpd-160926</u>

Dhomen, N., Reis-Filho, J. S., Da Rocha Dias, S., Hayward, R., Savage, K., Delmas, V., Larue, L., Pritchard, C., & Marais, R. (2009). Oncogenic Braf Induces Melanocyte Senescence and Melanoma in Mice. *Cancer Cell*, 15(4), 294–303. <u>https://doi.org/10.1016/j.ccr.2009.02.022</u>

Garnett, M. J., & Marais, R. (2004). Guilty as charged: B-RAF is a human oncogene. Cancer cell, 6(4), 313-319.

Liu, F., Ma, D., Chen, W., Chen, X., Qian, Y., Zhao, Y., Hu, T., Yin, R., Zhu, Y., Zhang, Y., Zhang, Y., & Zhao, W. (2019). Gold Nanoparticles Suppressed Proliferation, Migration, and Invasion in Papillary Thyroid Carcinoma Cells via Downregulation of CCT3. *Journal of Nanomaterials*, 2019, 1–12. https://doi.org/10.1155/2019/1687340

Lascorz, J., Bevier, M., Schönfels, W. V., Kalthoff, H., Aselmann, H., Beckmann, J., Egberts, J., Buch, S., Becker, T., Schreiber, S., Hampe, J., Hemminki, K., Försti, A., & Schafmayer, C. (2012). Polymorphisms in the mitochondrial oxidative phosphorylation chain genes as prognostic markers for colorectal cancer. *BMC Medical Genetics*, 13(1). <u>https://doi.org/10.1186/1471-2350-13-31</u>

Dessen Ρ., FAM181A-AS1 (FAM181A antisense RNA. Atlas Genet Cytogenet Oncol Haematol 2014-11-01 Online version: http://atlasgeneticsoncology.org/gene/63085/

GeneCards the human gene database. https://www.genecards.org Safran M, Rosen N, Twik M, BarShir R, Iny Stein T, Dahary D, Fishilevich S, and Lancet D. The GeneCards Suite Chapter, Practical Guide to Life Science Databases (2022) pp 27-56 [PDF]

Supplements

Scripts

Scripts used for Phase 1 post-GWAS In-Silico sequencing analysis:

setwd("C:/Users/Daniil/Desktop/B.R.P.35.#2 ")

install.packages("SNPannotator")

load the library library(SNPannotator)

select server for GRCh38 or GRCh37 # server <- "https://grch37.rest.ensembl.org" ### GRCh37</pre> server <- "https://rest.ensembl.org" ### GRCh38

select database population for LD calculation # db <-"1000GENOMES:phase_3:ALL" ### all samples in 1000G study db <- "1000GENOMES:phase_3:EUR" ### European super population in 1000G study

create a vector from variant rs numberss

create a vector from variant rs numberss
rslist=c('rs1962545', 'rs803679', 'rs7533341', 'rs1392816', 'rs111991969', 'rs7525548', 'rs77214504', 'rs140681455', 'rs141655075', 'rs1156981', 'rs10922907', 'rs1931262', 'rs1146566'
, 'rs2274568', 'rs79764489', 'rs11204771', 'rs113142203', 'rs1763738', 'rs11240331', 'rs10157166', 'rs6586405', 'rs1320330', 'rs2091377', 'rs2014149', 'rs138850767', 'rs12463727'
, 'rs4952343', 'rs35508442', 'rs985919', 'rs1516172', 'rs9789483', 'rs6719762', 'rs359243', 'rs7059844', 'rs6253389', 'rs76536952', 'rs875097', 'rs104654949', 'rs1226414'
, 'rs1205366', 'rs11678980', 'rs10165889', 'rs13387970', 'rs13009323', 'rs7575189', 'rs56306056', 'rs14772578', 'rs762533392', 'rs76536952', 'rs875097', 'rs14456303', 'rs2278480', 'rs67723420', 'rs562462868', 'rs2188151', 'rs2612029', 'rs186723454', 'rs6764919', 'rs6445264', 'rs7618715', 'rs4334682'
, 'rs2317603', 'rs12714592', 'rs112523595', 'rs6797231', 'rs12714702', 'rs369789482', 'rs57945129', 'rs705240', 'rs56339241', 'rs7767462343', 'rs2613396', 'rs3401377'
, 'rs3080996', 'rs561029885', 'rs2191032', 'rs11729080', 'rs809955', 'rs435383', 'rs12517438', 'rs8185308', 'rs731301503', 'rs12653396', 'rs3407370', 'rs2406374'
, 'rs35080996', 'rs561029885', 'rs2198310', 'rs4868800', 'rs11955405', 'rs435383', 'rs12517438', 'rs8185308', 'rs7381195', 'rs71301503', 'rs12653396', 'rs3407370', 'rs2406374'
, 'rs35080996', 'rs510029885', 'rs2284582', 'rs12204714', 'rs59498508', 'rs785195', 'rs765066200', 'rs138310', 'rs3851551', 'rs10233473', 'rs1201263', 'rs794375'
, 'rs1092812', 'rs13307225', 'rs2694934', 'rs7783012', 'rs11772444', 'rs6966888', 'rs113367286', 'rs1991651', 'rs7083127', 'rs282172', 'rs7824756'
, 'rs1092812', 'rs77352006', 'rs988640', 'rs11255003', 'rs11772444', 'rs6966888', 'rs113367286', 'rs1981651', 'rs7083026', 'rs12854512', 'rs10746578'
, 'rs1092812', 'rs77352006', 'rs988640', 'rs11255003', 'rs11772444', 'rs6966888', 'rs113367286', 'rs1089955', 'rs7828172', 'rs7824756'
, 'rs1092812', 'rs77352066', 'rs11386786', 'rs10746578', 'rs1074 , 'rs139362447', 'rs34902169', 'rs12147463', 'rs3007104', 'rs12878359', 'rs551086366', 'rs10134692', 'rs282929474', 'rs76509', 'rs783544', 'rs702', 'rs101403', 'rs763053', 'rs9923553' , 'rs2870488', 'rs4985127', 'rs7188873', 'rs12448731', 'rs76513770', 'rs12446652', 'rs200005647', 'rs11866420', 'rs410520', 'rs3853548', 'rs28406364', 'rs6504551', 'rs7503604', 'rs4800204 , 'rs2870488', 'rs56393977', 'rs148544378', 'rs34155040', 'rs9964201', 'rs776081653', 'rs7236339', 'rs10853981', 'rs4804512', 'rs807478', 'rs117831144', 'rs2145108', 'rs6058613' , 'rs35852264', 'rs1609598', 'rs4809346', 'rs375909440', 'rs7473421', 'rs62599791', 'rs146852038', 'rs6637831', 'rs961522', 'rs7608187', 'rs34481141', 'rs7024334', 'rs11038866' , 'rs76702070', 'rs590648', 'rs11392435', 'rs1435757')

run the pipeline

the result will be returned as a data frame and also saved as an excel filers2174752

fetch information for the rslist, add cadd score and regulatory type output <- annotate(rslist,server,db, 'sampleOutput.xlsx', LDlist = FALSE, cadd = TRUE qeneNames.file = 'Gene_Names_Ensembl_104_GRCh38 (1).rds' regulatoryType.file = 'homo_sapiens.GRCh38.Regulatory_Build.regulatory_features.20210107.rds'

Script for the Phase 2 eQTL analysis:

setwd("C:/Users/Daniil/Desktop/B.R.P.35.#2 ")

install.packages("SNPannotator")

load the library library(SNPannotator)

select database population for LD calculation # db <- "1000GENOMES:phase_3:ALL" ### all samples in 1000G study # db <- "1000GENOMES:phase_3:ALL" ### all samples in 1000G study db <- "1000GENOMES:phase_3:EUR" ### European super population in 1000G study

create a vector from variant rs numberss

create a vector from variant rs numberss
rslist=c('rs1962545', 'rs803679', 'rs7533341', 'rs11991969', 'rs7525548', 'rs77214504', 'rs140681455', 'rs141655075', 'rs1156981', 'rs10922907', 'rs1931262', 'rs1146566'
,'rs2274568', 'rs79764489', 'rs1204771', 'rs113142203', 'rs147633738', 'rs1120331', 'rs10157166', 'rs5586405', 'rs120330', 'rs2091377', 'rs2014149', 'rs138850614', 'rs1204771', 'rs11342203', 'rs759243', 'rs759959844', 'rs582180269', 'rs1168802', 'rs1688051', 'rs1049649', 'rs1226414'
,'rs12692596', 'rs11678980', 'rs10165889', 'rs13387970', 'rs13009323', 'rs7575189', 'rs56306056', 'rs147725178', 'rs76253389', 'rs67536952', 'rs875097', 'rs6748341', 'rs909849'
,'rs2084572', 'rs550942', 'rs114456333', 'rs278480', 'rs5772420', 'rs57945229', 'rs105807344', 'rs67642343', 'rs767462343', 'rs7077211', 'rs1274702', 'rs1237631060'
,'rs1671317', 'rs993700', 'rs10516875', 'rs11729080', 'rs455338', 'rs12517438', 'rs8185308', 'rs7381195', 'rs71301503', 'rs12653396', 'rs34073570', 'rs2640374', 'rs5208096'
,'rs51029885', 'rs283822', 'rs12204714', 'rs1209458', 'rs2783106', 'rs3781195', 'rs71301503', 'rs12653396', 'rs34073570', 'rs1406874', 'rs37080986', 'rs7381058', 'rs283882', 'rs12204714', 'rs50945808', 'rs1237743', 'rs1201637', 'rs1201637', 'rs120474', 'rs53080996'
,'rs51029885', 'rs2845882', 'rs12204714', 'rs120474', 'rs1204588', 'rs1237438', 'rs1815514', 'rs1023473', 'rs1270163', 'rs370005844', 'rs1925686', 'rs2397678'
,'rs1307225', 'rs2694934', 'rs7783102', 'rs11767444', 'rs69698888', 'rs113367286', 'rs1991651', 'rs708955', 'rs7828172', 'rs724756', 'rs10925864', 'rs191651', 'rs709170', 'rs18658', 'rs749435', 'rs11206714', 'rs1886202', 'rs1886202', 'rs198698', 'rs113367286', 'rs1991651', 'rs709170', 'rs1865745', 'rs10926865', 'rs740614', 'rs1148242', 'rs1047286922', 'rs789611', 'rs7023473', 'rs1229407', 'rs7801456', 'rs7408144', 'rs1148242', 'rs1084022', 'rs780611', 'rs70970457', 'rs1388644', 'rs138658', 'rs2186774', 'rs38081447', 'rs12847463', 'rs198678', 'rs31980955', 'rs733296', 'rs1398611', 'rs7090707', 'rs1

for (snp in rslist) { first <- snp==rslist[1]</pre>

write.table(cis.eQTLs.txt[cis.eQTLs.txt\$SNP == snp,], "eQTLS.txt", col.names=first, row.names=F, quote=F, sep="\t", append=!first)

Tables

Supplementary table 1: Missense gSNPs for In-Silico Phase 1. Following table consists of list of rs-ids of GWAS SNPs, as well as rs-ids of the SNPs in a LD with these qSNPs, chromosomes and positions within these chromosomes, CADD score, showing also an allele prediction, deleteriousness level and associations with linked SNP. All of these SNPs are missense ones. rs-ids and candidate gene names are highlighted in yellow. Blue color indicates chosen top five missense SNPs with the highest CADD score. Deleteriousness up to top 10%.

gSNP	Linked_SNP	chr	Pos_37	LD	gene	Associations	cadd	Deleteriousness
rs11204771	rs4971007	1	151135661	0,8168	LYSMD1		G = 20.1	top 1.0%
rs147633738	rs11548200	1	156320865	0,980451	LYSMD1	Household income, red cell distribution width, Walking pace	C = 22.5	top 0.6%
rs875097	rs55760516	2	219489386	0,980451	PLCD4	ματε	G = 21.5	top 0.7%
rs12714702	rs9813894	3	88139270	0,949671	CGGBP1/ZNF654		A = 11.97	top 6.4%
rs12714702	rs7653652	3	88140191	0,949671	CGGBP1/ZNF654		C = 17.41	top 1.8%
24011474			25407236			AFB, AFS, BMI, Body size at age 10, Cognitive aspects of educational attainment, Cognitive performance, Heel bone mineral density, Height, Highest math class taken, Intelligence, Leisure sedentary behavior television watching, Lung function, Male-pattern baldness, Menarche age at onset, Multisite chronic pain, Osteoarthritis, predicted visceral adipose tissue, Snoring, Urate levels, Verbal-numerical reasoning,		
rs34811474	rs34811474	4	25407216	1	ANAPC4	White blood cell count Attention deficit	A = 24.3	top 0.4%
rs141547796	rs78648104	6	50715296	0,886266	TFAP2D	hyperactivity disorder, BMI, Cognitive performance, Cystatin C levels, educational attainment, Systolic blood pressure	C = 24.2	top 0.4%
rs794375	rs6947307	7	75494199	0,968015	RHBDD2	-,	T = 19.7	top 1.1%
rs113367286	rs2272095	7	140459051	0,896095	BRAF	NSP	G = 23.4	top 0.5%

						AFS, Cognitive performance		
						Highest math class taken,		
						Hypogonadotropic		
						hypogonadism 19 with or		
						without anosmia, Self-		
rs2279574	rs2279574	12	89351700	1	DUSP6	reported math ability	A = 22.9	top 0.5%
						AFS, Alanine		
						aminotransferase levels,		
						Alanine transaminase levels, Alanine transaminase levels		
						in high alcohol intake,		
						Alcohol consumption		
						(drinks per week), Alcohol		
						consumption drinks per		
						week, ALPHA-1-		
						ANTITRYPSIN DEFICIENCY,		
						Antineutrophil cytoplasmic		
						antibody-associated		
						vasculitis, Appendicular lean		
						mass, Aspartate aminotransferase levels,		
						Aspartate aminotransferase		
						to alanine aminotransferase		
						ratio, Aspartate		
						transaminase levels in high		
						alcohol intake, Bioavailable		
						testosterone levels, Bitter		
						alcoholic beverage		
						consumption, Blood protein levels, Brain morphology		
						MOS Test, Breast size, C-		
						reactive protein levels,		
						Calcium levels, Chronic		
						obstructive pulmonary		
						disease, Cirrhosis (alcohol		
						related), Cirrhosis multi-		
						trait analysis, Cystatin C		
						levels, Direct bilirubin levels, Fat-free mass,		
						FRAXE, Gallstone disease,		
						Gamma glutamyl		
						transferase levels, Glucagon		
						levels in response to oral		
						glucose tolerance test		
						(fasting), Heel bone mineral		
						density, Height, Hip		
						circumference adjusted for BMI, Inborn genetic		
						diseases, Insulin-like growth		
						factor 1 levels, Liver enzyme		
						levels (alanine		
						transaminase), Liver		
						enzyme levels (alkaline		
						phosphatase), Liver enzyme		
						levels (gamma-glutamyl		
						transferase), Low density lipoprotein cholesterol		
						levels, Metabolite levels		
						(small molecules and		
						protein measures),		
						Osteoprotegerin levels, PI Z,		
						PI Z(AUGSBURG), PI Z(TUN),		
						Post bronchodilator FEV1,		
						Post bronchodilator		
						FEV1/FVC ratio, Post bronchodilator FEV1/FVC		
						ratio in smoking, Post		
						bronchodilator percent		
						predicted FEV1 in smoking,		
						Problematic alcohol use		
						MTAG, Serum albumin		
						level, Serum alkaline		
						phosphatase levels, Serum alpha-fetoprotein levels,		
						Serum total protein level,		
						Sex hormone-binding		
						globulin levels, Sex		
rs28929474	rs28929474	14	94378610	1	FAM181A-AS1	hormone-binding globulin	T = 23.5	top 0.4%

						levels adjusted for BMI, Systolic blood pressure, Testosterone levels, TNF- related apoptosis-inducing ligand levels, Total testosterone levels, Urea levels		
rs763053	rs1139897	16	670986	0,802361	RAB40C	Age of smoking initiation (MTAG), Smoking initiation (ever regular vs never regular), Smoking initiation (ever regular vs never regular) (MTAG)	A = 16.32	top 2.3%
rs148544378	rs148544378	18	42743602	1	RIT2	AFS, Leisure sedentary behavior television watching, NSP	T = 23.3	top 0.5%
rs807478	rs231591	19	35733804	0,873839	KMT2B		G = 11.41	top 7.2%
rs11038866	rs1317826	11	46366318	0,949319	DGKZ		G = 11.06	top 7.8%

Supplementary table 2: Phenotypes table of gSNPs for In-Silico Phase 1. Following table consists of list of rs-ids of GWAS SNPs, as well as rs-ids of the SNPs in a LD with these gSNPs, chromosomes and positions within these chromosomes, CADD score, showing also an allele prediction, deleteriousness level and associations with linked SNP, and most importantly the phenotypic associations. All of these SNPs are of different type, as listed in a table. rs-ids and candidate gene names are highlighted in yellow. Deleteriousness up to top 10%.

acND	Linked CND								
gSNP	Linked_SNP	Chr	Pos_37	LD	Gene	Туре	Associations	cadd	Deleteriousness
rs7525548	rs12041912	1	74538026	0,995998	LRRIQ3	intron_variant	Body Mass Index	A = 10.16	top 9.6%
rs7525548	rs3895907	1	74540343	0,988036	LRRIQ3	intron_variant	Body Mass Index	G = 12.09	top 6.2%
							Body Mass Index, Smoking		
							initiation, Smoking initiation (ever regular vs		
rs7525548	rs1514175	1	74525960	0,892618	LRRIQ3	intron_variant	never regular)	G = 18.15	top 1.5%
rs7525548	**284F24F	1	7452002	0.861000	LRRIQ3	intron variant	Dody Mass Index	T - 12 22	top 5 8%
187323348	rs3845345	1	74536983	0,861009	LINIQS	intron_variant	Body Mass Index	T = 12.33	top 5.8%
rs7525548	rs6703637	1	74532111	0,845463	LRRIQ3	intron_variant	Body Mass Index	A = 12.06	top 6.2%
							Age at first sexual		
							intercourse, Body shape index, Hip circumference		
							adjusted for BMI, Leisure		
							sedentary behavior		
							computer use, Leisure sedentary behavior		
							television watching, mean		
							corpuscular volume, mean		
							spheric corpuscular volume, Waist-hip index,		
							Waist-to-hip ratio adjusted		
rs140681455	rs140681455	1	77979081	1	AK5	5_prime_UTR_variant	for BMI	GACCGG = 20.6	top 0.9%
1.11.055.075	444655075	4	0700010	4			Age at first sexual	T 10 C2	
rs141655075	rs141655075	1	87328913	1	SELENOF	5_prime_UTR_variant	intercourse Educational attainment,	T = 19.63	top 1.1%
							Number of sexual		
							partners, Smoking status		
rs10922907	rs12042107	1	90730619	0,996032		intergenic_variant	(ever vs never smokers) Household income MTAG,	C = 22.2	top 0.6%
							Red cell distribution width,		
rs147633738	rs11548200	1	156320865	0,980451	ССТ3	missense_variant	Walking pace	C = 22.5	top 0.6%
							Educational attainment		
							(MTAG), Educational attainment (years of		
rs6586405	rs1329125	1	234605134	0,99095	TARBP1	3_prime_UTR_variant	education)	T = 16.17	top 2.4%
rs1320330	rs11127491	2	646145	0,93788		intergenic_variant	Body Mass Index	C = 12.34	top 5.8%
rs12463727					 OTOF			T = 17.65	
	rs1631026	2	26730982	0,972412		3_prime_UTR_variant	Adult body size		top 1.7%
rs12463727	rs1731259	2	26730714	0,972412	OTOF	3_prime_UTR_variant	Body Mass Index	G = 10.72	top 8.5%
rs35508442	rs12998046	2	44653786	0,942716	САМКМТ	intron_variant	Chronotype	A = 10.81	top 8.3%
rs62180269	rs62180269	2	63093389	1	EHBP1	intergenic variant	Age at first sexual intercourse	C = 14.18	top 3.8%
					CHOP 1				
rs10496949	rs2381473	2	143394233	0,99189		intron_variant	Trauma exposure Age at first sexual	A = 13.83	top 4.1%
							intercourse, Cognitive		
							aspects of educational		
							attainment, Cognitive		
							performance, Cognitive performance (MTAG),		
							Cognitive traits MTAG,		
11670000	11670000	2	4 6 4 2 4 4 7 5 2		555.464		Educational attainment	4 42 62	. 5.49/
rs11678980	rs11678980	2	161244750	1	RBMS1	non_coding_transcript_exon_variant	(MTAG), Educational	A = 12.69	top 5.4%

		I	Í	1		1	attainment (years of		1
							education), Highest math		
							class taken, Highest math		
							class taken (MTAG), Self- reported math ability, Self-		
							reported math ability		
							(MTAG), Smoking initiation		
							(ever regular vs never		
							regular), Smoking initiation (ever regular vs never		
							regular) (MTAG), Verbal-		
							numerical reasoning		
							Estimated glomerular		
rs875097	rs1050816	2	219493476	0,890128	PLCD4	3_prime_UTR_variant	filtration rate	T = 15.1	top 3.1%
rs114456303	rs114456303	3	24631667	1	THRB-AS1	intron_variant	Age at first sexual intercourse	A = 13.71	top 4.3%
							Age at first sexual		
rs2278480	rs2278480	3	25594252	1	RARB	intron_variant	intercourse	C = 14.2	top 3.8%
rs186723454	rs186723454	3	E4122E71	1		E primo LITP variant	Age at first sexual intercourse	C = 19 1	top 1 5%
15180723434	15180723434	3	54122571	1	<u> </u>	5_prime_UTR_variant	Age at first sexual	G = 18.1	top 1.5%
							intercourse, Body Mass		
rs6445264	rs6445264	3	62368750	1		intron_variant	Index	A = 16.48	top 2.2%
							Smoking status, Smoking status (ever vs never		
rs112523595	rs34495106	3	85601986	0,995741	CADM2	intron_variant	status (ever vs never smokers)	G = 19.62	top 1.1%
		_		-,			Smoking initiation (ever		
rs57945129	rs62264764	3	117920728	1		intron_variant	regular vs never regular)	A = 14.02	top 4.0%
mE (2022.14	F02054252	2	100170057	0.004200	DNALCCO		Core binding factor acute	C 15 15	tor 2.10/
rs56392241	rs3851353	3	132170357	0,894299	DNAJC13	intron_variant	myeloid leukemia Adult body size, Age at	G = 15.15	top 3.1%
							first sexual intercourse,		
							Body Mass Index, Body		
							size at age 10, Cognitive		
							aspects of educational attainment, Cognitive		
							performance, Cognitive		
							performance (MTAG),		
							Educational attainment		
							(MTAG), Educational attainment (years of		
							education), General		
							cognitive ability, Heel bone		
							mineral density, Height, Highest math class taken		
							(MTAG), Intelligence,		
							Intelligence (MTAG),		
							Leisure sedentary behavior		
							television watching, Lung function (FVC), Male-		
							pattern baldness,		
							Menarche age at onset,		
							Multisite chronic pain,		
							Osteoarthritis, Predicted visceral adipose tissue,		
							Self-reported math ability		
							(MTAG), Snoring, Urate		
							levels, Verbal-numerical		
							reasoning, Waist circumference adjusted for		
							body mass index, White		
rs34811474	rs34811474	4	25407216	1	ANAPC4	missense_variant	blood cell count	A = 24.3	top 0.4%
							Age of smoking initiation (MTAG), Educational		
							attainment (MTAG),		
							Lifetime smoking index,		
							Smoking cessation		
							(MTAG), Smoking initiation (ever regular vs never		
							regular) (MTAG), Smoking		
							status, Smoking status		
rs11729080	rs72678864	4	111500989	0,984627		intergenic_variant	(ever vs never smokers)	A = 20.3	top 0.9%
							Age at first sexual intercourse, Attention		
							deficit hyperactivity		
							disorder or caudate		
							nucleus volume		
							(pleiotropy), Body Mass Index, Educational		
							attainment (MTAG),		
							Educational attainment		
							(years of education),		
							Highest math class taken (MTAG), Noncognitive		
							aspects of educational		
rs12653396	rs12653396	5	88551455	1	MEF2C-AS1	intron_variant	attainment	A = 19.09	top 1.2%
rs11055420	rs11055420	5	167002201	1	PANK3	intron variant	Age at first sexual	G = 10 70	top 5 3%
rs11955430	rs11955430	Э	167993291	1	PAINK3	intron_variant	intercourse	G = 12.73	top 5.3%

		l					Body Mass Index, HDL		
rs245753	rs7730898	5	171032671	0,802441		intron_variant	cholesterol	A = 16.63	top 2.2%
							Age at first sexual intercourse, Aging traits		
							health span, parental		
							lifespan or longevity		
							multivariate analysis,		
							Balding type 1, Basal cell		
							carcinoma, Black vs. blond hair color, Black vs. red		
							hair color, cutaneous		
							squamous cell carcinoma,		
							Eye color, Eye color		
							(brightness), Eye color		
							traits, Facial pigmentation, Feeling nervous, Freckling,		
							Hair color, Hair greying,		
							Hair morphology traits,		
							Keratinocyte cancer		
							MTAG, Low tan response,		
							Lymphocyte counts, Male puberty timing age at		
							voice breaking MTAG,		
							Male puberty timing early		
							vs. average onset facial		
							hair, Male puberty timing		
							late vs. average onset facial hair, Male-pattern		
							baldness, Monobrow,		
							Neuroblastoma, Nevus		
							count, Non-melanoma skin		
							cancer, Progressive		
							supranuclear palsy, Rosacea symptom		
							severity, Skin aging		
							(microtopography		
							measurement), Skin color		
							saturation, Skin pigmentation, Skin		
							pigmentation traits, Skin,		
							hair and eye pigmentation		
							(multivariate analysis),		
							Skin/hair/eye		
							pigmentation, variation in, 8, Smoking cessation,		
							Smoking cessation,		
							(MTAG), Squamous cell		
							carcinoma, Sunburns,		
							Tanning, Vitiligo, White		
rs12203592	rs12203592	6	396321	1	IRF4	intron_variant	blood cell count, Youthful appearance self-reported	T = 14.22	top 3.8%
1312203352	1312203352	0	550521	1	111 4	intron_variant	Cognitive performance	1 - 14.22	top 5.676
							(MTAG), Educational		
							attainment (MTAG),		
							Educational attainment		
							(years of education), Highest math class taken		
rs767943	rs767943	6	23446463	1	_	intron_variant	(MTAG)	A = 17.68	top 1.7%
							Educational attainment		
rs767943	rs2022330	6	23446327	0,800427		intron_variant	(years of education)	G = 10.47	top 9.0%
							Attention deficit		
							hyperactivity disorder MTAG, Body Mass Index,		
							Cognitive performance		
							(MTAG), Cystatin C levels,		
							educational attainment		
							(MTAG), Educational attainment (years of		
							education), Systolic blood		
rs141547796	rs78648104	6	50715296	0,886266	TFAP2D	missense_variant	pressure	C = 24.2	top 0.4%
rs1925686	rs2031522	6	87111783	0,991515		intergenic_variant	Atrial fibrillation	G = 12.6	top 5.5%
				,		<u>-</u> ant	Age at first sexual		p = 1270
							intercourse, educational		
							attainment (MTAG),		
							Smoking initiation (ever regular vs never regular)		
							(MTAG), Sporadic		
rs72990858	rs72990858	6	104699909	1		intergenic_variant	neuroblastoma	A = 21.9	top 0.6%
	4000/	_	45404455		00000		Age at first sexual	T 17.6	
rs12204714	rs12204714	6	151914204	1	CCDC170	intron_variant	intercourse	T = 17.63	top 1.7%
rs12204714	rs6557171	6	151913458	0,889834	CCDC170	intron_variant	Educational attainment (years of education)	C = 12.45	top 5.7%
rs12701263	rs1045530	7	32868523	0,880174	AVL9/DPY19L1P2	3_prime_UTR_variant	Mean corpuscular volume	G = 14.78 AATTTCATAATTTCAT	top 3.3%
rs7783012	rs71149745	7	114416441	0,909981		intron variant	Age at first birth	AATTICATAATTICAT = 16.66	top 2.2%
		,	11/10441	0,000001	_		Cognitive ability, years of	10.00	10p 2.270
							educational attainment or		
rs6966898	rs4732129	7	135540408	0,813515	_	intergenic_variant	schizophrenia pleiotropy	C = 13.78	top 4.2%

rs113367286	rs2272095	7	140459051	0,896095	BRAF	missense variant	Number of sexual partners	G = 23.4	top 0.5%
13113307280	132272035	/	140433031	0,890093	DIAI	missense_variant	Adult body size, Age of	0 - 23.4	100 0.5%
							smoking initiation (MTAG),		
							Body size at age 10, Smoking initiation (ever		
							regular vs never regular)		
rs7828172	rs4739558	8	38479746	1		intergenic_variant	(MTAG)	G = 14.41	top 3.6%
							Body Mass Index, Triglyceride levels, Waist-		
rs7828172	rs36061954	8	38472132	0,978997		regulatory_region_variant	hip ratio	T = 18.83	top 1.3%
							Craniosynostosis syndrome,		
							HYPOGONADOTROPIC		
							HYPOGONADISM 2 WITH		
							OR WITHOUT ANOSMIA, OSTEOGLOPHONIC		
							DYSPLASIA,		
rs7828172	rs3213849	8	38468528	0,879855		5 prime UTR variant	TRIGONOCEPHALY 1, Waist-hip ratio	A = 16.36	top 2.3%
15/8281/2	155215649	0	56406526	0,879833		5_prime_ork_variant	Electrocardiogram	A - 10.50	top 2.3%
		_					morphology amplitude at		
<u>rs7828172</u>	rs62505473	8	38466247	0,852217		intron_variant	temporal datapoints Achromatopsia 3, ClinVar:	G = 12.24	top 6.0%
							phenotype not specified,		
rs11382985	rs6471482	8	86667075	0,983457		stop gained	Heart failure, STARGARDT DISEASE 1	C = 18.82	top 1.3%
1511582985	150471482	0	80007075	0,983437		stop_gained	No syndromic cleft lip with	C = 18.82	top 1.5%
rs72674824	rs957448	8	94529074	0,809655	LINC00535	synonymous_variant	cleft palate	G = 11.65	top 6.8%
rs12554512	rs7029201	9	23358083	0,979807		intron variant	Educational attainment (vears of education)	A = 13.4	top 4.6%
1312334312	13/029201	9	2000000	0,01001		intron_vandht	Educational attainment	A = 13.4	top 4.070
rs9886840	rs10818604	9	121846330	0,971053		intron_variant	(years of education)	A = 11.16	top 7.7%
							Age at first sexual intercourse, Childhood		
							maltreatment, Cognitive		
							performance (MTAG),		
							Intelligence, Lifetime smoking index, Smoking		
rs3896224	rs3896224	10	104708095	1	CCNM2	intron_variant	status, Trauma exposure	G = 18.61	top 1.4%
							Cognitive performance (MTAG), General cognitive		
rs1866710	rs2099744	11	12844599	0,985212	TEAD1	intron_variant	ability	A = 14.42	top 3.6%
rs59957074	rs4759073	12	54259474	0,995815		5_prime_UTR_variant	Adult body size	A = 18.19	top 1.5%
							Heel bone mineral density,		
							Smoking status, Smoking status (ever vs never		
rs7955865	rs772921	12	56009793	0,912063	_	intron_variant	status (ever vs never smokers)	T = 15.14	top 3.1%
							Age at first sexual		
							intercourse, Cognitive performance (MTAG),		
							Highest math class taken,		
							Highest math class taken (MTAG),		
							Hypogonadotropic		
							hypogonadism 19 with or		
							without anosmia, Self- reported math ability		
rs2279574	rs2279574	12	89351700	1		missense_variant	(MTAG)	A = 22.9	top 0.5%
rs7987501	rs2165985	13	53402639	0,920861		intron_variant	Body Height	C = 15.22	top 3.0%
		4.0	100000000				Lobe attachment (rater-		
rs10646652	rs10612751	13	106993685	0,925872		intergenic_variant	scored or self-reported) Age at first sexual	TG = 12.18	top 6.1%
							intercourse, Alanine		
							aminotransferase levels, Alanine transaminase		
							levels, Alanine		
							transaminase levels in high		
							alcohol intake, Alcohol consumption (drinks per		
							week) (MTAG), Alcohol		
							consumption drinks per week, ALPHA-1-		
							ANTITRYPSIN DEFICIENCY,		
							Antineutrophil cytoplasmic antibody-associated		
							vasculitis, Appendicular		
							lean mass, Aspartate		
							aminotransferase levels, Aspartate		
							aminotransferase to		
							alanine aminotransferase ratio, Aspartate		
							transaminase levels in high		
							alcohol intake, Bioavailable testosterone levels, Bitter		
							alcoholic beverage		
rs28929474	rs28929474	14	94378610	1	FAM181A-AS1	missense_variant	consumption, Blood	T = 23.5	top 0.4%

	I	1	1	1		1	I		
							protein levels, Brain morphology MOSTest,		
							Breast size, C-reactive		
							protein levels, Calcium		
							levels, Chronic obstructive		
							pulmonary disease, Cirrhosis (alcohol related),		
							Cirrhosis multi-trait		
							analysis, ClinVar:		
							phenotype not specified,		
							Cystatin C levels, Direct bilirubin levels, Fat-free		
							mass, FRAXE, Gallstone		
							disease, Gamma glutamyl		
							transferase levels,		
							Glucagon levels in response to oral glucose		
							tolerance test (fasting),		
							Heel bone mineral density,		
							Height, Hip circumference		
							adjusted for BMI, Inborn genetic diseases, Insulin-		
							like growth factor 1 levels,		
							Liver enzyme levels		
							(alanine transaminase),		
							Liver enzyme levels (alkaline phosphatase),		
							Liver enzyme levels		
							, (gamma-glutamyl		
							transferase), Low density		
							lipoprotein cholesterol		
							levels, Metabolite levels (small molecules and		
							protein measures),		
							Osteoprotegerin levels, PI		
							Z, PI Z(AUGSBURG), PI		
							Z(TUN), Post bronchodilator FEV1, Post		
							bronchodilator FEV1/FVC		
							ratio, Post bronchodilator		
							FEV1/FVC ratio in smoking,		
							Post bronchodilator percent predicted FEV1 in		
							smoking, Problematic		
							alcohol use MTAG, Serum		
							albumin level, Serum		
							alkaline phosphatase levels, Serum alpha-		
							fetoprotein levels, Serum		
							total protein level, Sex		
							hormone-binding globulin		
							levels, Sex hormone- binding globulin levels		
							adjusted for BMI, Systolic		
							blood pressure,		
							Testosterone levels, TNF-		
							related apoptosis-inducing		
							ligand levels, Total testosterone levels, Urea		
							levels		
							Age at first sexual		
rs783544	rs783544	15	82571543	1	SAXO2	5_prime_UTR_variant	intercourse	C = 16.52	top 2.2%
		1					Age at first sexual intercourse, anorexia		
		1					nervosa, attention-		
							deficit/hyperactivity		
							disorder, autism spectrum		
							disorder, bipolar disorder, major depression,		
		1					obsessive-compulsive		
		1					disorder, schizophrenia, or		
							Tourette syndrome		
							pleiotropy, Autism spectrum disorder or		
		1					schizophrenia, Bipolar		
		1					disorder MTAG, Childhood		
		1					maltreatment, Cognitive		
							ability, years of educational attainment or		
							schizophrenia pleiotropy,		
		1					Feeling hurt, General risk		
							tolerance (MTAG),		
							INSOMNIA, Neuropsychiatric		
							disorders, Number of		
							sexual partners,		
							Schizophrenia,		
rs4702	rs4702	15	90883330	1	_	3_prime_UTR_variant	Schizophrenia MTAG	A = 12.84	top 5.2%

			l			l	Age of smoking initiation		1
							(MTAG), Smoking initiation		
							(ever regular vs never		
							regular), Smoking initiation		
							(ever regular vs never		
rs763053	rs1139897	16	670986	0,802361	RAB40C	missense variant	regular) (MTAG)	A = 16.32	top 2.3%
				-,			Smoking initiation (ever		
							regular vs never regular)		
rs9923553	rs7189389	16	5758519	0,863752		intron variant	(MTAG)	G = 16.7	top 2.1%
				,			Age at first sexual		
							intercourse, Body Mass		
							Index, Risk-taking		
							tendency (4-domain		
							principal component		
rs76513770	rs76513770	16	72471635	1	AC004158.3	intron_variant	model)	C = 17.96	top 1.6%
							Atopic asthma, Atopic		
							dermatitis, Brain		
							morphology MOSTest,		
							Cancer, Coronary Artery		
							Disease, Diastolic blood		
							pressure, Height, Systolic		
rs28406364	rs16948048	17	49363104	0,928621	UTP18	intron_variant	blood pressure	G = 10.66	top 8.6%
							Asthma, Asthma		
							(moderate or severe),		
							Cortical surface area		
rs28406364	rs112502960	17	49361940	0,908263	UTP18	5_prime_UTR_variant	MOSTest	A = 14.7	top 3.4%
							Allergic disease (asthma,		
							hay fever or eczema),		
							Eosinophil counts,		
							Eosinophil percentage of		
rs28406364	rs9889262	17	49320708	0,904211	MBTD1	intron_variant	granulocytes, Respiratory diseases	A = 16.09	top 2.5%
1526400504	139009202	17	49320708	0,904211	IVIDIDI	Introl1_vallallt	Height, Thyroid stimulating	A - 10.09	top 2.5%
rs28406364	rs35587648	17	49340816	0,899785	UTP18	intron variant	hormone levels	A = 11.47	top 7.1%
1320400304	1355507040	17	45540010	0,055705	01110	intron_vanant	Age at first sexual	A - 11.47	1007.170
rs4800204	rs4800204	18	25067306	1	RP11-739N10.1	intron variant	intercourse	T = 15.85	top 2.6%
191000204	.54000204	10	23007300	-		intron_vananc	Educational attainment	1 10.00	top 2.070
rs4800204	rs8089996	18	25068541	0,983761	RP11-739N10.1	intron variant	(years of education)	A = 17.9	top 1.6%
				, –			Age at first sexual		
							intercourse, Leisure		
							sedentary behaviour		
							, television watching,		
rs148544378	rs148544378	18	42743602	1	-	missense_variant	Number of sexual partners	T = 23.3	top 0.5%
							Age at first sexual		
rs146852038	rs146852038	Х	129984833	1	ENOX2	intron_variant	intercourse	A = 18.66	top 1.4%
							ClinVar: phenotype not		
rs11038866	rs1317826	11	46366318	0,949319	DGKZ	missense_variant	specified	G = 11.06	top 7.8%
re11202425	m1102027	17	111570054	0.000010		regulatory resident versions.	Moint him with	A - 12 70	top (20/
rs11392435	rs1163627	13	111573354	0,858012	_	regulatory_region_variant	Waist-hip ratio	A = 13.78	top 4.2%

Supplementary table 3: In-Silico Phase Intronic gSNP list. Following table consists of list of rs-ids of GWAS SNPs, as well as rsids of the SNPs in a LD with these gSNPs, chromosomes and positions within these chromosomes, CADD score, showing also an allele prediction, deleteriousness level and associations with linked SNP. All of these SNPs are all intronic. rs-ids with no found candidate gene names are highlighted in black in the "Gene" column. Deleteriousness up to top 10%.

								Deleteriousne
gSNP	Linked_SNP	ch	Pos_37	LD	Gene	Туре	cadd	SS
rs11252359			8550267					
5	rs12638798	3	0	0,90848	CADM2	intron_variant	C = 21	top 0.8%
			1080907					
rs1991651	rs11250078	8	1	0,88665	PINX1	intron_variant	A = 21	top 0.8%
			1,18E+0	0,94468				
rs57945129	rs62264768	3	8	4	RP11-384F7.2	intron_variant	C = 20.3	top 0.9%
				0,85578				
rs809955	rs769657	4	1,4E+08	6	MAML3	intron_variant	G = 20.3	top 0.9%
			4457948	0,85086				
rs35508442	rs4952715	2	1	2		intron_variant	T = 19.92	top 1.0%
			4461811	0,83776				
rs35508442	rs934777	2	9	5		intron_variant	C = 19.83	top 1.0%
			1,06E+0	0,82046				
rs7024334	rs12555670	9	8	2		intron_variant	C = 20.2	top 1.0%
			6091664	0,90663				
rs6764919	rs13097786	3	3	1		intron_variant	C = 19.46	top 1.1%
rs11252359			8560198	0,99574				
5	rs34495106	3	6	1		intron_variant	G = 19.62	top 1.1%
rs11252359			8554728	0,98723				
5	rs1463205	3	2	8		intron_variant	A = 19.68	top 1.1%

Solution rests 27247 3 One 1 One 3 Intron variant A = 19.72 Itep 1.1% rs10114692 rs986651 4 0 8 intron variant G = 19.6 top 1.1% rs9923553 rs57105172 6 574005172 2 3029268 intron variant I = 19.87 top 1.1% rs2101203 rs272761 0 5 3029268 jiit 10.2% jiit 11.2% jiit 10.2% jiit 10.2% jiit 10.2% jiit 10.2% jiit 11.2% jiit 10.2% jiit 10.2%	rs11252359	I	I	8543351	0,94605				1 1
ist 1 947165 0.97893 rs9923553 rs57105172 6 740082 8 intron_variant T = 19.67 top 1.1% rs9923553 rs57105172 6 5740082 8 intron_variant T = 19.67 top 1.1% rs2145108 rs7272551 0 5 3 intron_variant T = 19.67 top 1.1% rs2145108 rs7272551 0 5 3 intron_variant T = 19.67 top 1.1% rs11252135 rs2029130 2 7 8 5 intron_variant A = 19.22 top 1.2% rs11752335 rs12653396 5 5 1 intron_variant A = 19.22 top 1.2% rs1263394 rs1263394 5 5 1 intron_variant A = 19.22 top 1.2% rs1263794 1 6 1 1 6 19.2% rs1263795 rs624029 3 8 6 intron_variant A = 19.39 top 1.2%		rs35827242	3		,		intron variant	A = 19.72	top 1.1%
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$				9347165	0,97983				
re992353 rs7105112 6 574062	rs10134692	rs996661	4	0			intron_variant	G = 19.6	top 1.1%
rs722559 2 302598 0.92703 intron_variant I = 19.62 top 1.1% rs11252359 rs2029130 3 7 8 intron_variant A = 19.22 top 1.2% rs11252359 rs2029130 3 7 8 intron_variant A = 19.22 top 1.2% rs11252359 rs17456840 8555685 0.98723 intron_variant A = 19.22 top 1.2% rs1255336 rs1725536 5 1 intron_variant A = 19.22 top 1.2% rs1757537 rs10479693 5 6 1 intron_variant A = 19.22 top 1.2% rs1757357 rs10479693 5 6 1 intron_variant A = 19.22 top 1.2% rs1455757 rs10479693 8 6 intron_variant A = 19.32 top 1.2% rs1455757 rs202112 8 1 intron_variant T = 19.32 top 1.2% rs1455757 rs2021212 8 1 1 intron_variant T = 19.32			_						
rr2145108 rr277551 0 5 3 0 1 <th1< th=""> 1 1</th1<>	rs9923553	rs57105172					intron_variant	T = 19.67	top 1.1%
rs11252393 rs2029130 3 7 8 intron_variant A - 19.20 top 1.2% rs11252339 rs2029130 3 7 8 intron_variant A - 19.20 top 1.2% rs11252339 rs1455820 3 9 8 intron_variant A = 19.16 top 1.2% rs1265336 rs1265336 5 1 intron_variant A = 19.06 top 1.2% rs1265336 rs1265336 5 1 intron_variant A = 19.00 top 1.2% rs1265336 rs1265336 5 1 intron_variant A = 19.00 top 1.2% rs1265337 rs47342018 4 1 intron_variant A = 19.00 top 1.2% rs1265338 rs26548359 4 1 intron_variant A = 19.22 top 1.2% rs1265337 rs4050590 3 8 6 intron_variant A = 19.20 top 1.3% rs1265326 rs1265339 9 8 1 intron_variant T = 19.32 top 1.3%	rc21/15108	rs7272651			-		intron variant	T – 19 62	top 1 1%
5 rs20210 3 7 8 intron_variant A = 19.22 top 1.2% rs11252359 - 8553878 0,88723 - intron_variant A = 19.16 top 1.2% rs11252359 - 8555688 0,98723 - intron_variant A = 19.16 top 1.2% rs11252359 - 8855485 - - intron_variant A = 19.22 top 1.2% rs1252359 rs10754267 8 6 -	-	137272031	0					1 - 19.02	top 1.176
S rs17456820 3 9 8 intron_variant A = 19.66 top 1.2% rs1252359 - 855685 0,98723 intron_variant G = 19.28 top 1.2% rs1265396 rs6549039 3 3 8 intron_variant G = 19.28 top 1.2% rs1265396 rs1754227 rs1047596 5 8 6 intron_variant A = 19.09 top 1.2% rs37242018 - 924002 - - intron_variant A = 19.29 top 1.2% rs173538144 - 924002 - - - top 1.2% rs1743577 rs624339 4 0 -		rs2029130	3		-		intron_variant	A = 19.22	top 1.2%
rs11252359 rs6549039 3 3 3 1 1 1 10p1.2% rs12653396 rs12653396 rs12653396 5 5 1 1 1 10p1.2% rs27242018 8 4 1 0.99084 1 10ren_variant A = 19.28 1op 1.2% rs12653396 rs12653396 7 8 4 1 100776 1op 1.2% rs13742018 9 8 6 1 1ntron_variant C = 19.31 top 1.2% rs138814 1 3027367 1 1ntron_variant C = 19.31 top 1.2% rs1435757 rs652580 3 9 8 6 intron_variant T = 19.32 top 1.2% rs1253738 rs652580 9 8 1 intron_variant T = 18.87 top 1.3% rs1263203 rs1265239 1 1,71140 1 intron_variant T = 18.87 top 1.3% rs1265239 7 7 7452594 0 8 1 intron_variant C = 18.34 top 1.3% rs1265230 rs1265230 1,05464 1 intron_variant C = 18.45 top 1.4% rs1265234 rs14685203 rs1	rs11252359			8553378	0,98723				
5 rs6549039 3 3 8 intron_variant G = 19.28 top 1.2% rs12653396 5 5 1 intron_variant A = 19.09 top 1.2% rs245753 rs10475963 5 8 6 intron_variant A = 19.09 top 1.2% rs13742018 - 9240602 - intron_variant A = 19.29 top 1.2% rs137388144 1 3027367 - intron_variant A = 19.39 top 1.2% rs1453757 rs8007136 5 8 6 intron_variant T = 19.32 top 1.2% rs145575 rs800259 3 9 8 1 intron_variant T = 18.32 top 1.3% rs1252575 rs21114 5 8 1 intron_variant T = 18.39 top 1.3% rs245753 rs3062024 1 1,05F+0 intron_variant A = 18.9 top 1.3% rs12894024 rs3896224 1 1,05F+0 intron_variant A = 18.6 top		rs17456820	3				intron_variant	A = 19.16	top 1.2%
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$		ma CE 40020	2		-		interne servicent	C 10.20	ton 1 20/
	5	156549039	3		ð		Intron_variant	G = 19.28	top 1.2%
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	rs12653396	rs12653396	5		1		intron variant	A = 19.09	top 1.2%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$				1,71E+0	0,99084				
1 1 302 1 10 <td>rs245753</td> <td>rs10475963</td> <td>5</td> <td>8</td> <td>6</td> <td></td> <td>intron_variant</td> <td>A = 19.22</td> <td>top 1.2%</td>	rs245753	rs10475963	5	8	6		intron_variant	A = 19.22	top 1.2%
			_						
7 rs76548359 4 0 1 475758 0.88631 intron_variant A = 19.39 top 1.2% rs1435757 rs8027136 5 8 6 intron_variant T = 19.32 top 1.2% rs11252359 rs450559 3 9 9 intron_variant T = 19.32 top 1.3% rs2125753 rs212114 5 8 1 intron_variant T = 18.96 top 1.3% rs245753 rs1366206 5 8 1 intron_variant A = 18.89 top 1.3% rs12894023 rs1680203 4 1 7 intron_variant A = 18.89 top 1.3% rs12894023 rs1685204 5 8 1 intron_variant A = 18.89 top 1.3% rs12894024 rs3896224 6 1 7 a A = 18.69 top 1.4% rs14685203 rs1468520 7 8 1 BCORL1 intron_variant A = 18.66 top 1.5% rs5255444 rs5141		rs4734227		-	1		intron_variant	C = 19.31	top 1.2%
$\begin{array}{c c c c c c c c c c c c c c c c c c c $		rs765/18359			1		intron variant	Λ - 10 30	top 1.2%
rs1325757 rs8027136 5 8 6 intron_variant T = 19.32 top 1.2% rs11252359 - rs450259 3 9 8 intron_variant T = 18.96 top 1.3% rs245753 rs21114 5 8 1 intron_variant T = 18.96 top 1.3% rs245753 rs1366206 5 8 1 intron_variant A = 18.89 top 1.3% rs12894029 rs8008023 4 1 7 intron_variant A = 18.89 top 1.3% rs12894029 rs389624 4 1 7 intron_variant G = 18.94 top 1.3% rs14685203 rs14685203 8 1 BCORL1 intron_variant G = 18.95 top 1.4% rs14685203 rs1514175 1 0 8 1 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 </td <td>/</td> <td>1370348333</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>A - 15.55</td> <td>top 1.276</td>	/	1370348333						A - 15.55	top 1.276
5 rs4502590 3 9 8 intron_variant $T = 18.96$ top 1.3% rs245753 rs212114 5 8 1 intron_variant $T = 18.87$ top 1.3% rs245753 rs1366206 5 8 1 intron_variant $T = 18.87$ top 1.3% rs245753 rs1366206 5 8 1 intron_variant $T = 18.87$ top 1.3% rs12689029 rs8008023 4 1 7 intron_variant $A = 18.94$ top 1.3% rs389624 rs389624 0 8 1 intron_variant $G = 18.94$ top 1.3% rs14685203 rs14685203 rs14685203 734685206 8 9 8 7 1 90.0 8 rs5752548 rs1514175 1 0 8.92.6 9 9 9 9 rs3502402 rs6442680 3 1 3 TE1D5 intron_variant A = 18.16 100,1.5% rs752540	rs1435757	rs8027136	_		-		intron_variant	T = 19.32	top 1.2%
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	rs11252359			8554732	0,98723				
rs245753 rs2121124 5 8 1 rs245753 rs2121124 5 8 1 rs245753 rs166026 5 8 1 rs245753 rs1608023 4 11 7713991 0,99027 rs12894029 rs808023 4 11 7 intron_variant 6=18.94 top 1.3% rs3896224 rs3896224 0 8 1 intron_variant 6=18.61 top 1.4% rs14685203 rs14685203 rs14685203 rs14685203 rs14685203 rs14685203 rs14685203 rs14685203 1 BCORL1 intron_variant A=18.66 top 1.4% rs555548 rs1514175 1 0 8 1 BCORL1 intron_variant A=18.66 top 1.5% rs555542 rs6442680 3 1 0 8 T top 1.5% rs555542 rs6442680 3 1 3 TBC1D5 intron_variant C=18.32 top 1.5% rs705240 rs69777 3 8 5 ENS60000243266 intron_variant	5	rs4502590	3		8		intron_variant	T = 18.96	top 1.3%
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	245752	2424424	F	-				- 10.07	1 20/
rs245753rs136206fs81127.139910.99027intron_variantA=18.89top 1.3%rs12894029rs80080234176.38.940.51.861.05.87 <t< td=""><td>rs245753</td><td>rs2121124</td><td>5</td><td></td><td>1</td><td></td><td>intron_variant</td><td>1 = 18.87</td><td>top 1.3%</td></t<>	rs245753	rs2121124	5		1		intron_variant	1 = 18.87	top 1.3%
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	rs245753	rs1366206	5	-	1		intron variant	A = 18 89	top 1 3%
rs12894029rs8008023417intron_variantG = 18.94top 1.3%rs3896224rs389622411,05E+0rs3896224rs3896224081 <td>152 157 55</td> <td>191900200</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>10.05</td> <td></td>	152 157 55	191900200						10.05	
rs3896224 rs3896224 0 8 1 intron_variant $G = 18.61$ top 1.4% rs14685203 rs14685203 rs14685203 rs14685203 rs14685203 rs14685203 rs14685203 rs1458506 0.89261 intron_variant $A = 18.66$ top 1.4% rs7525548 rs1514175 1 0 8 intron_variant $G = 18.15$ top 1.5% rs35508442 rs495310 2 7 2 CAMMKMT intron_variant $A = 18.16$ top 1.5% rs2084572 rs6442680 3 1 3 TBC1D5 intron_variant $A = 18.16$ top 1.5% rs705240 rs697377 3 8 5 ENS60000243276 intron_variant $A = 18.32$ top 1.5% rs7651370 rs61377 1 6 4 HSD17B12 intron_variant $A = 18.33$ top 1.5% rs76513770 rs6 5 1 72 intron_variant $A = 17.9$ top 1.6% rs76513770 rs689996	rs12894029	rs8008023	4	1			intron_variant	G = 18.94	top 1.3%
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$			1	1,05E+0					
88X1,3E+081BCORL1intron_variantA = 18.66top 1.4%rs7525548rs1514175108intron_variantA = 18.66top 1.5%rs7525548rs1514175108intron_variantA = 18.16top 1.5%rs3550842rs495310272CAMKMTintron_variantA = 18.16top 1.5%rs55084572rs6442680313TBC1D5intron_variantA = 18.16top 1.5%rs705240rs697377385ENSG0000243276intron_variantA = 18.12top 1.5%rs755240rs697377380,9924intron_variantA = 18.13top 1.5%rs7551370rs61377064HSD17B12intron_variantA = 18.33top 1.5%rs75513770rs7551377065172intron_variantA = 18.33top 1.5%rs75513770rs7551377065172intron_variantA = 17.96top 1.6%rs7533341rs827641274ZNF521intron_variantC = 17.59top 1.7%rs7533341rs82764274RP11-444A22.1intron_variantC = 17.65top 1.7%rs7533341rs8276430,8669FBC1D5intron_variantA = 17.2top 1.7%rs7533341rs82764530,8669FBC1D5intron_variantA = 17.82top 1.7%rs7533341			0	8	1		intron_variant	G = 18.61	top 1.4%
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$			v	1 25,09	1		intron variant	A - 19 CC	top 1 4%
rs7525548rs1514175108intron_variantG = 18.15top 1.5%rs35508442rs4953110272CAMKMTintron_variantA = 18.16top 1.5%rs2085752rs6442680313TBC1D5intron_variantC = 18.32top 1.5%rs705240rs697377385ENSG0000243276intron_variantA = 18.12top 1.5%rs705240rs697377385ENSG0000243276intron_variantA = 18.12top 1.5%rs705240rs697377380,97924intron_variantA = 18.12top 1.5%rs705240rs697377380,97924intron_variantA = 18.13top 1.5%rs705240rs697377380,97924intron_variantA = 18.12top 1.5%rs705240rs697377364HSD17B12intron_variantA = 18.33top 1.5%rs753370rs765137065172intron_variantA = 18.34top 1.5%rs7651370rs765137065172intron_variantA = 18.29top 1.6%rs4800244rs88089968112506451intron_variantA = 17.99top 1.6%rs4800244rs8808996115DAB1intron_variantA = 17.99top 1.7%rs4800244rs882764115DAB1intron_variantC = 17.65top 1.7%rs5273	0	0	^			BCORLI		A = 18.00	top 1.470
rs35508442rs4953110272CAMKMTintron_variantA = 18.16top 1.5%rs2084572rs6442680313TBC1D5intron_variantC = 18.32top 1.5%rs2084572rs6442680313TBC1D5intron_variantC = 18.32top 1.5%rs705240rs697377385ENSG000243276intron_variantA = 18.12top 1.5%rs705240rs697377385ENSG000243276intron_variantA = 18.33top 1.5%rs3480422rs1103765164HSD17B12intron_variantA = 18.33top 1.5%rs76513770rs765137765172intron_variantA = 18.33top 1.5%rs76513770rs785137765172intron_variantA = 18.33top 1.5%rs76513770rs808996811ZNF521intron_variantA = 17.9top 1.6%rs7533341rs852764115DAB1intron_variantA = 17.9top 1.7%rs671776rs2419405274RP11-444A22.1intron_variantA = 17.82top 1.7%rs2084572rs981352320,86669TBC1D5intron_variantA = 17.82top 1.7%rs1252359rs2875908338CADM2intron_variantA = 17.63top 1.7%rs1252359rs2875908338CADM2intron_variant	rs7525548	rs1514175	1		,		intron_variant	G = 18.15	top 1.5%
rs2084572rs64426803113737040,95246intron_variantC = 18.32top 1.5%rs2084572rs6442680313TBC1D5intron_variantC = 18.32top 1.5%rs705240rs697377385ENSG0000243276intron_variantA = 18.12top 1.5%rs34804222rs11037653164HSD17B12intron_variantA = 18.33top 1.5%rs7651377065172intron_variantC = 17.96top 1.6%rs76513770rs7651377065172intron_variantC = 17.96top 1.6%rs4800204rs808996811ZNF521intron_variantA = 17.9top 1.6%rs7533341rs852764115DAB1intron_variantC = 17.59top 1.7%rs6719762rs2419405274RP11-444A22.1intron_variantC = 17.65top 1.7%rs11252359320,86669TBC1D5intron_variantA = 17.82top 1.7%rs112523593338CADM2intron_variantC = 17.63top 1.7%rs112523593338CADM2intron_variantC = 17.63top 1.7%rs112523593338CADM2intron_variantC = 17.63top 1.7%				4457947	0,85086				
rs2084572 rs6442680 3 1 3 TBC1D5 intron_variant C = 18.32 top 1.5% rs705240 rs697377 3 8 5 ENSG0000243276 intron_variant A = 18.12 top 1.5% rs705240 rs697377 3 8 5 ENSG0000243276 intron_variant A = 18.12 top 1.5% rs3480422 rs1037653 1 6 4 HSD17B12 intron_variant A = 18.33 top 1.5% rs76513770 rs76513770 6 5 1 72 intron_variant C = 17.96 top 1.6% rs76513770 rs76513776 6 5 1 72 intron_variant C = 17.96 top 1.6% rs76513770 rs76513776 1 2506854 0,98376 intron_variant C = 17.96 top 1.6% rs4800204 rs8089969 8 1 1 Z 506854 A = 17.9 top 1.6% rs75753341 rs852764 1 1 S 992404 NP1444422.1	rs35508442	rs4953110	2			CAMKMT	intron_variant	A = 18.16	top 1.5%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0004570	6449699	-			70.0105			1 50(
rs705240 rs697377 3 8 5 ENSG0000243276 intron_variant A = 18.12 top 1.5% rs34804222 rs11037653 1 6 4 HSD17B12 intron_variant A = 18.33 top 1.5% rs34804222 rs11037653 1 6 4 HSD17B12 intron_variant A = 18.33 top 1.5% rs75513770 6 5 1 72 intron_variant C = 17.96 top 1.6% rs76513770 6 5 1 72 intron_variant C = 17.96 top 1.6% rs4800204 rs8089996 8 1 1 ZNF521 intron_variant A = 17.9 top 1.6% rs4800204 rs8089996 8 1 1 ZNF521 intron_variant A = 17.9 top 1.6% rs7533341 rs852764 1 1 5 DA81 intron_variant C = 17.65 top 1.7% rs6719762 rs2419405 2 7 4 RP11-444A22.1 intron_variant A = 17.82 top 1.7% rs2084572 rs981352 3	rs2084572	rs6442680	3			IBCID2	intron_variant	C = 18.32	top 1.5%
rs34804222rs1037653143803810,97924HSD17B12intron_variantA = 18.33top 1.5%rs34804222rs11037653164HSD17B12intron_variantA = 18.33top 1.5%rs76513770rs7651377065172intron_variantC = 17.96top 1.6%rs4800204rs808999681125068540,98376rs4800204rs8058996811ZNF521intron_variantA = 17.9top 1.6%rs7533341rs852764115DAB1intron_variantC = 17.59top 1.7%rs6719762rs2419405274RP11-444A22.1intron_variantC = 17.65top 1.7%rs2084572rs9813532320,86669TBC1D5intron_variantA = 17.82top 1.7%rs112523595rs2875908338CADM2intron_variantC = 17.63top 1.7%s2344646ss38CADM2intron_variantC = 17.63top 1.7%	rs705240	rs697377	З		-	ENSG00000243276	intron variant	A = 18 12	top 1 5%
rs34804222rs11037653164HSD17B12intron_variantA = 18.33top 1.5%rs76513770672intron_variantC = 17.96top 1.6%rs7651377065172intron_variantC = 17.96top 1.6%rs4800204rs8089996811ZNF521intron_variantA = 17.9top 1.6%rs4800204rs852764111ZNF521intron_variantA = 17.9top 1.6%rs7533341rs852764115DAB1intron_variantC = 17.59top 1.7%rs6719762rs2419405274RP11-444A22.1intron_variantC = 17.65top 1.7%rs1252359rs9813532320,8669TBC1D5intron_variantA = 17.82top 1.7%rs11252359rs2875908338CADM2intron_variantC = 17.63top 1.7%rs12845449.8744111111111rs2084572rs2813532320,8669TBC1D5intron_variantA = 17.82top 1.7%rs11252359s338CADM2intron_variantC = 17.63top 1.7%rs112523593338CADM2intron_variantC = 17.63top 1.7%								10,11	
rs76513770rs7651377065172intron_variantC = 17.96top 1.6%rs4800204rs8089906811ZNF521intron_variantA = 17.9top 1.6%rs4800204rs8089906811ZNF521intron_variantA = 17.9top 1.6%rs7533341rs852764115DAB1intron_variantC = 17.59top 1.7%rs6719762rs2419405274RP11-444A22.1intron_variantC = 17.65top 1.7%rs2084572rs9813532320,86669TBC1D5intron_variantA = 17.82top 1.7%rs1125235985548540,98723srs2875908338CADM2intron_variantC = 17.63top 1.7%srs1125235985548540,98723intron_variantC = 17.63top 1.7%ssrs2875908338CADM2intron_variantC = 17.63top 1.7%	rs34804222	rs11037653	1			HSD17B12	intron_variant	A = 18.33	top 1.5%
rs4800204 rs8089996 1 2506854 0,98376 intron_variant A = 17.9 top 1.6% rs4800204 rs8089996 8 1 1 ZNF521 intron_variant A = 17.9 top 1.6% rs7533341 rs852764 1 1 5 DAB1 intron_variant C = 17.59 top 1.7% rs6719762 rs2419405 2 7 4 RP11-444A22.1 intron_variant C = 17.65 top 1.7% rs2084572 rs9813532 3 2 0,86669 TBC1D5 intron_variant A = 17.82 top 1.7% rs11252359 . . 8554854 0,98723 . A = 17.63 top 1.7% 5 rs2875908 3 3 8 CADM2 intron_variant C = 17.63 top 1.7%									
rs4800204 rs8089996 8 1 1 ZNF521 intron_variant A = 17.9 top 1.6% rs7533341 rs852764 1 1 5 DAB1 intron_variant C = 17.59 top 1.7% rs6719762 rs2419405 2 7 4 RP11-444A22.1 intron_variant C = 17.65 top 1.7% rs2084572 rs9813532 3 2 0,8669 TBC1D5 intron_variant A = 17.82 top 1.7% rs11252359 3 3 3 8 CADM2 intron_variant C = 17.63 top 1.7% rs11252359 1 2 3 3 8 CADM2 intron_variant C = 17.63 top 1.7% rs11252359 1 2 3 3 8 CADM2 intron_variant C = 17.63 top 1.7% rs11252359 1 2 344646 8 6 1	rs76513770	rs76513770				72	intron_variant	C = 17.96	top 1.6%
rs7533341 rs852764 1 1 5 DAB1 intron_variant C = 17.59 top 1.7% rs6719762 rs2419405 2 7 4 RP11-444A22.1 intron_variant C = 17.65 top 1.7% rs2084572 rs9813532 3 2 0,86669 TBC1D5 intron_variant A = 17.82 top 1.7% rs11252359 5 rs2875908 3 3 8 CADM2 intron_variant C = 17.63 top 1.7%	rs/1200204	rcSUSOUUC			-	7NE501	intron variant	Δ = 17 Ω	top 1 6%
rs7533341 rs852764 1 1 5 DAB1 intron_variant C = 17.59 top 1.7% rs6719762 rs2419405 2 7 4 RP11-444A22.1 intron_variant C = 17.65 top 1.7% rs2084572 rs9813532 3 2 0,8669 TBC1D5 intron_variant A = 17.82 top 1.7% rs11252359 rs2875908 3 3 0,98723 CADM2 intron_variant C = 17.63 top 1.7% f 2344646 0.98723 CADM2 intron_variant C = 17.63 top 1.7%	134000204	130003330	0			LINFJZI		A = 17.9	toh 1.0%
rs6719762 rs2419405 2 5992404 0,91816 rs1742421 intron_variant C = 17.65 top 1.7% rs2084572 rs9813532 3 2 0,86669 TBC1D5 intron_variant A = 17.82 top 1.7% rs11252359 3 2 0,86669 TBC1D5 intron_variant A = 17.82 top 1.7% rs1252359 5 rs2875908 3 3 8 CADM2 intron_variant C = 17.63 top 1.7%	rs7533341	rs852764	1			DAB1	intron variant	C = 17.59	top 1.7%
rs2084572 rs9813532 3 2 0,86669 TBC1D5 intron_variant A = 17.82 top 1.7% rs11252359 s 8554854 0,98723 s top 1.7% top 1.7% 5 rs2875908 3 3 8 CADM2 intron_variant C = 17.63 top 1.7%				5992404					
rs2084572 rs9813532 3 2 0,86669 TBC1D5 intron_variant A = 17.82 top 1.7% rs11252359 5 8554854 0,98723 -	rs6719762	rs2419405	2		4	RP11-444A22.1	intron_variant	C = 17.65	top 1.7%
rs11252359 s 8554854 0,98723 5 rs2875908 3 3 8 CADM2 intron_variant C = 17.63 top 1.7% 2344646 2344646 6 6 6 6 6 6	2004575	0010555	_		0.00000	700105			
5 rs2875908 3 3 8 CADM2 intron_variant C = 17.63 top 1.7% 2344646	-	rs9813532	3			IBCID5	intron_variant	A = 17.82	top 1./%
2344646		rs2875908	ч		-	CADM2	intron variant	C = 17 63	top 1 7%
		132073500					vanant	C - 11.00	cop 1.770
	rs767943	rs767943	6		1		intron_variant	<u>A = 17.68</u>	top 1.7%

		I	1,52E+0			I		
rs12204714	rs12204714	6	8	1	ESR1	intron_variant	T = 17.63	top 1.7%
		1	4724437	0,95193				
rs34155040	rs10502880	8	5	1	SKOR2	intron_variant	C = 17.81	top 1.7%
rs70959844	rs6747099	2	6055036 3	0,80229 4	BCL11A	intron variant	C = 17.24	top 1.9%
1370333011	1307 17055	2	1723293		DCLIIA	vuluit	C = 17.24	100 1.570
rs2084572	rs2733502	3	0	0,98396	TBC1D5	intron_variant	T = 17.16	top 1.9%
rs11252359	17450560		8556021	0,98723	0.1 5 1.42			1.00(
5 rs11252359	rs17459563	3	5 8553508	8 0,98723	CADM2	intron_variant	A = 17.27	top 1.9%
5	rs76034006	3	5	8	CADM2	intron variant	AA = 17.17	top 1.9%
		1	4758451					
rs1435757	rs11633288	5	3	0,98813	SEMA6D	intron_variant	T = 17.23	top 1.9%
rs2274568	rs11102050	1	1,1E+08	0,88338 9		intron variant	C 17.04	top 2.0%
132274308	1311102030	1	2,05E+0	9 0,93546		intron_variant	C = 17.04	τορ 2.078
rs11240331	rs4950976	1	8	8	NFASC	intron_variant	G = 17.03	top 2.0%
rs11252359			8554855	0,98302			AATAATAATAA =	
5	rs3086190	3	0	1	CADM2	intron_variant	16.99	top 2.0%
rs2910032	rs1438946	5	1,53E+0 8	0,82172 2	LINC01470	intron variant	C = 16.93	top 2.0%
132310032	101100010		1735382	0,99197		vuluite	0 10.55	000 2.070
rs2084572	rs13318609	3	8	7	TBC1D5	intron_variant	C = 16.72	top 2.1%
rs11252359	62250745	2	8546684	0,98723	CADNAD			2.404
5 rs11252359	rs62250715	3	6 8555229	8	CADM2	intron_variant	A = 16.69	top 2.1%
5	rs12492753	3	0	0,90446	CADM2	intron variant	A = 16.84	top 2.1%
		1	8936416	0,99197				·
rs2279574	rs10506971	2	0	7		intron_variant	A = 16.85	top 2.1%
rs9923553	rs7189389	1 6	5758519	0,86375 2	RBFOX1	intron variant	G = 16.7	top 2.1%
139923555	13/109209	0	4457959	0,85086	NBI OX1	Intron_vanant	G - 10.7	top 2.176
rs35508442	rs4952716	2	2	2	CAMKMT	intron_variant	C = 16.55	top 2.2%
			6236875					/
rs6445264	rs6445264	3	0 1,71E+0	1 0,97725	PTPRG-AS1	intron_variant	A = 16.48	top 2.2%
rs245753	rs13180996	5	1,71E+0 8	2	RANBP17	intron variant	G = 16.5	top 2.2%
			1,71E+0	0,80244				•
rs245753	rs7730898	5	8	1	RANBP17	intron_variant	A = 16.63	top 2.2%
rs7783012	rs71149745	7	1,14E+0 8	0,90998 1	FOXP2/AC073626.2	intron variant	AATTTCATAATTTC	top 2.2%
137783012	13/1149/43	/	0 1,14E+0	0,90998	FUXF2/AC073020.2	Intron_vanant	AT = 16.66	top 2.276
rs7783012	rs7785701	7	8	, 1	FOXP2	intron_variant	G = 16.5	top 2.2%
rs11252359			8559126	0,99147				
5 rs11252359	rs68001049	3	8 8553892	8 0,98723	CADM2	intron_variant	G = 16.32	top 2.3%
5	rs34467301	3	8553892 0	0,98723	CADM2	intron variant	C = 16.37	top 2.3%
rs11252359		-	8544760	0,94605				1
5	rs2033526	3	8	3	CADM2	intron_variant	C = 16.32	top 2.3%
rc7C71217	rc7CEE100	л	6210691 7			intron veriant	0 100	top 2 20/
rs7671317	rs7655188	4	7 7773253	0,98651	ADGRL3	intron_variant	C = 16.3	top 2.3%
rs11688027	rs78876578	2	2	0,88534	LRRTM4	intron_variant	C = 16.11	top 2.4%
rs11252359			8552002	0,98723				
5	rs17515586	3	2	8	CADM2	intron_variant	G = 16.28	top 2.4%
rs2406374	rs34644687	5	1,08E+0 8	1	FBXL17	intron variant	A = 16 24	top 2.4%
rs875097	rs2385539	2	° 2,2E+08	0,80049	I DALT /	intron_variant	A = 16.24 C = 16.06	top 2.4%
1507 5077	132303333	<u>ک</u>	1723368	0,80049			C - 10.00	100 2.370
rs2084572	rs2060628	3	1	8	TBC1D5	intron_variant	C = 16.09	top 2.5%
			L -				5 10.05	10 P 210/0

rs89955 r.76987.1 4 L.4.4-0.8 2 NOCT Intron variant I = 1-3:90 top 2.5% rs280036 rs989502 7 8 1 MBTD1 Intron variant A = 16.00 top 2.5% rs2145108 rv409702 0 6 3 BC1.211 Intron variant C = 15.99 top 2.5% rs4800204 8 6 1 RP11-739110.1 Intron variant T = 18.85 top 2.5% rs45508442 rs489307 3 4 6 FHI Intron variant G = 15.75 top 2.7% rs17023019 3 2 4 6 FHI Intron variant G = 15.75 top 2.7% rs17023019 3 2 9 Stop 2.7% Intron variant C = 15.73 top 2.7% rs17023010 3 2 9.99848 CADM2 Intron variant C = 15.24 top 2.7% rs705540 rs6728714 2 5 3 Stop 2.7% Intron variant C = 15.23					0,86052		1		
index index <th< td=""><td>rs809955</td><td>rs769671</td><td>4</td><td>1,4E+08</td><td>,</td><td>NOCT</td><td>intron_variant</td><td>T = 15.99</td><td>top 2.5%</td></th<>	rs809955	rs769671	4	1,4E+08	,	NOCT	intron_variant	T = 15.99	top 2.5%
2145108 74097052 0			_		-				
introl introl variant c = 15.99 top 2.5% rs4800204 is 6 1 RP11.739N10.1 intron_variant T = 15.85 top 2.5% rs55508427 rs493307 2 445997 0.8180 ntron_variant G = 15.75 top 2.5% rs6756419 rs6804218 3 609.95% - intron_variant C = 15.75 top 2.7% rs17125239 - 8 503.816 0.97949 -	rs28406364	rs9889262				MBTD1	intron_variant	A = 16.09	top 2.5%
rx4800204 1 250070 r ref re	rs2145108	rs4097052			-	BCI 21 1	intron variant	C = 15 99	top 2.5%
rx3550842 rx4953107 2 4 8 PRFPI intron_variant 6 = 15.75 rx5676419 rs6804218 3 4 6 FHIT intron_variant 6 = 15.75 top 2.7% rs7676419 rs6804218 3 2 0.90848 CADM2 intron_variant 6 = 15.75 top 2.7% rs70817 rs7023019 3 2 0.90848 CADM2 intron_variant 6 = 15.75 top 2.7% rs705280 rs705220 3 8 1 intron_variant 6 = 15.75 top 2.7% rs705240 rs20724452 6 308742 0.93422 intron_variant 6 = 15.59 top 2.8% rs705240 rs274452 6 308763 0.89742 intron_variant 6 = 15.91 top 2.8% rs125339 5 3 8 1 iststop 2.8% intron_variant 6 = 15.91 top 2.8% rs1125339 1 9.8724 3 8 8 intron_variant 6 = 15.44 top		101007002						6 15.55	cop 21070
rs3558442 rs495107 2 4 8 PREPL intron_variant G=15.75 top 2.7% rs6764919 rs6804218 3 4 0.9857 intron_variant C=15.69 top 2.7% rs1125239 - 8556512 - intron_variant G=15.65 top 2.7% rs1125239 - 5 0.90848 CADM2 intron_variant G=15.65 top 2.7% rs705241 1 9 NRXN1 intron_variant G=15.73 top 2.7% rs755241 2 1 9 NRXN1 intron_variant G=15.73 top 2.7% rs757520 rs705275 3 8 1 intron_variant C=15.23 top 2.8% rs705240 rs757452 2 5 4 NRXN1 intron_variant G=15.59 top 2.8% rs1252349 rs524450 3 8 0.8723 intron_variant G=15.54 top 2.8% rs1252349 rs524470 3 8 CADM2	rs4800204	rs4800204	8			RP11-739N10.1	intron_variant	T = 15.85	top 2.6%
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$									
rsf560410 rs6804218 3 4 6 FHI intron variant C = 15.69 top 2.7% rs1125235 rs17023019 3 2 0,00848 CADM2 intron variant G = 15.66 top 2.7% rs6708107 rs6728741 2 1 9 NRXN1 intron variant C = 15.73 top 2.7% rs5508442 rs11451478 2 3 PREPL intron variant C = 15.73 top 2.7% rs550847 rs11451478 2 3 PREPL intron variant C = 15.73 top 2.8% rs7505240 rs2 3 8 1 GSF11 intron variant C = 15.52 top 2.8% rs722440 rs2 5 4 NRXN1 intron variant C = 15.51 top 2.8% rs1252580 3 8 8 GAD24 intron variant C = 15.51 top 2.8% rs1252591 rs5254612 1 438040 098312 intron variant C = 15.31 top 2.9% <t< td=""><td>rs35508442</td><td>rs4953107</td><td>2</td><td></td><td></td><td>PREPL</td><td>intron_variant</td><td>G = 15.75</td><td>top 2.7%</td></t<>	rs35508442	rs4953107	2			PREPL	intron_variant	G = 15.75	top 2.7%
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	rs6764919	rs6804218	2		,	FHIT	intron variant	C = 15.69	ton 2.7%
5 rs17023019 3 2 9,90849 CADM2 intron_variant G = 15.65 top 2.7% rs7608187 rs6728711 2 1 9 NRXN1 intron_variant C = 15.73 top 2.7% rs550842 rs11541747 2 2 3 PREPL intron_variant C = 15.73 top 2.7% rs550842 rs11541747 2 2 3 PREPL intron_variant C = 15.52 top 2.7% rs750750 rs757575 3 S308752 0.89364 intron_variant C = 15.52 top 2.8% rs222440 rs2744452 6 S308752 0.89373 intron_variant C = 15.52 top 2.8% rs75781512 1 S538940 0.89723 intron_variant C = 15.52 top 2.8% rs1152526 783789162 3 8 C ADM2 intron_variant C = 15.24 top 2.8% rs1152529 rs6245780 3 8 8 C ADM2 intron_variant C = 15.24 top 2.9% rs1152529 rs6245780 3 8 8 C ADM2 intron_variant C = 15.24 top 2.9% rs1152529 rs6245780 3 9.98129 intron_variant <t< td=""><td></td><td>130004210</td><td>5</td><td></td><td>0</td><td></td><td>Intron_variant</td><td>C = 15.05</td><td>100 2.770</td></t<>		130004210	5		0		Intron_variant	C = 15.05	100 2.770
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $		rs17023019	3		0,90848	CADM2	intron_variant	G = 15.65	top 2.7%
$\begin{array}{c c c c c c c c c c c c c c c c c c c $				5034816	-				
rs35508442 rs11451478 2 2 2 9 PREPL intron_araint 15.54 top 2.8% rs705240 rs705252 3 8 1 iGSF11 intron_araint C = 15.52 top 2.8% rs22240 rs704525 6 3 6 intron_araint C = 15.59 top 2.8% rs705205 7 5038768 0.98730 C = 15.51 top 2.8% rs11252355 7 5 74 NRXN1 intron_araint C = 15.51 top 2.8% rs11252355 7 1 151539 0.98723 recommon and and and and and and and and and an	rs7608187	rs6728741	2			NRXN1	intron_variant	C = 15.73	top 2.7%
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	rc2EE09442	rc114E1470	2				intron variant		top 2.8%
rs705240 rs70522 3 8 1 IGSF11 intron_variant C = 15.20 top 2.8% rs222440 rs274452 6 3 6 intron_variant C = 15.50 top 2.8% rs7508187 rs757452 2 5 4 intron_variant C = 15.51 top 2.8% rs11252387 rs7574512 75578951 3 8 4 NRXN1 intron_variant C = 15.51 top 2.9% rs11252387 rs3578916 3 8 8 CADM2 intron_variant C = 15.32 top 2.9% rs11587107 1 915339 0,98132 intron_variant G = 15.44 top 2.9% rs1158142 1 4380040 0,9837 intron_variant G = 15.26 top 2.9% rs11314220 rs4545645 1 5 3 HSD17B12 intron_variant G = 15.26 top 3.0% rs11314220 rs4545645 2 0,8537 intron_variant G = 15.26 top 3.0% rs113158104 </td <td>1555506442</td> <td>1511451478</td> <td>2</td> <td></td> <td></td> <td>PNEPL</td> <td>IIILIOII_VallallL</td> <td>15.54</td> <td>τυμ 2.8%</td>	1555506442	1511451478	2			PNEPL	IIILIOII_VallallL	15.54	τυμ 2.8%
stress stres stres stres <td>rs705240</td> <td>rs705225</td> <td>3</td> <td>-</td> <td>-</td> <td>IGSF11</td> <td>intron_variant</td> <td>C = 15.52</td> <td>top 2.8%</td>	rs705240	rs705225	3	-	-	IGSF11	intron_variant	C = 15.52	top 2.8%
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $				5308752	0,89346				
rs7608187 rs7574552 2 5 6 4 NRXN1 intron_variant C = 15.51 top 2.8% rs1223379 - rs3578916 3 3 8 CADM2 intron_variant AAAA = 15.35 top 2.9% rs5794519 rs62264780 3 8 8 intron_variant C = 15.32 top 2.9% rs61856678 rs11597197 0 9 3 intron_variant G = 15.44 top 2.9% rs64854627 1 5 3 3 HSD17B12 intron_variant A = 15.33 top 2.9% rs4480422 rs6485465 1 5 3 HSD17B12 intron_variant A = 15.33 top 2.9% rs11314220 - 1 5 6 UBR3 intron_variant A = 15.33 top 3.0% rs113009323 rs28780764 2 8 5 UBR3 intron_variant C = 15.23 top 3.0% rs113009323 rs28780765 4 1,44±08 6 NOCT <td>rs222440</td> <td>rs2744452</td> <td>6</td> <td></td> <td></td> <td></td> <td>intron_variant</td> <td>G = 15.59</td> <td>top 2.8%</td>	rs222440	rs2744452	6				intron_variant	G = 15.59	top 2.8%
rs11252359 rs rs 8553891 0,98723 cADM2 intron_variant AAAA = 15.35 top 2.9% rs57945129 rs527845129 rs62264780 3 8 8 intron_variant C = 15.32 top 2.9% rs61856678 rs11597177 0 9 3 intron_variant C = 15.32 top 2.9% rs61856678 rs11597177 0 9 3 intron_variant C = 15.42 top 2.9% rs61856678 rs11597107 0 9 3 intron_variant C = 15.32 top 2.9% rs11341202 rs11581644 1 8 0,812 DENND48 intron_variant G = 15.46 top 3.0% rs11309323 rs28780764 2 8 0,812 DENND48 intron_variant C = 15.23 top 3.0% rs11309323 rs28780764 2 8 0,8204 intron_variant C = 15.24 top 3.0% rs11252359 rs769675 4 1,424-08 6 NOCT intron_variant			2		,			0 15 51	tau 2.00/
5 rs35789162 3 3 8 CADM2 intron_variant AAAA = 15.35 top 2.9% rs5794512 rs6226780 3 8 8 rs67 rs17879179 0 9 3 intron_variant C = 15.32 top 2.9% rs6186978 rs11591797 0 9 3 intron_variant C = 15.32 top 2.9% rs6186407 1 4380404 098337 intron_variant A = 15.33 top 2.9% rs1181420 1 1 808040 098337 intron_variant G = 15.44 top 2.9% rs1181420 1 1 8 0,912 intron_variant G = 15.46 top 2.9% rs1181420 1 1 8 0,9337 intron_variant G = 15.26 top 3.0% rs1181420 1 1 8 0,812 Intron_variant G = 15.26 top 3.0% rs11818140 1 8 0,812 Intron_variant G = 15.26 top 3.0% rs1181420 1 856026 0 Intron_variant G = 15.26 top 3.0% rs118140 8 0 0 Intron_variant G = 15.26 top 3.0% rs1181414 1		rs/5/4552	2			NKXN1	Intron_variant	C = 15.51	top 2.8%
$\begin{array}{c c c c c c c c c c c c c c c c c c c $		rs35789162	3		-	CADM2	intron variant	AAAA = 15.35	top 2.9%
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $			-						
rs61856978rs11597197093intron_variantG = 15.44top 2.9%rs34804222rs648568153HSD17B12intron_variantA = 15.33top 2.9%rs1314222rs648568153HSD17B12intron_variantA = 15.33top 2.9%rs11581644180,812DENND4Bintron_variantG = 15.26top 3.0%rs13009323rs2878076285UBR3intron_variantC = 15.23top 3.0%rs112523598556020,98723intron_variantT = 15.17top 3.0%rs80955rs7785243328CADM2intron_variantT = 15.17top 3.0%rs80955rs756967541,4E4086NOCTintron_variantC = 15.22top 3.0%rs7783012rs1253005781intron_variantC = 15.16top 3.0%rs7785013rs125585391intron_variantC = 15.22top 3.0%rs7782434rs1295012391intron_variantC = 15.26top 3.0%rs7782434rs129502391intron_variantC = 15.26top 3.0%rs7898750rs62793760391intron_variantAcACA = 15.07top 3.0%rs7895751rs62793760398CADM2intron_variantAcACA = 15.05top 3.1%rs7895754rs62793760398 <td>rs57945129</td> <td>rs62264780</td> <td>3</td> <td>8</td> <td></td> <td></td> <td>intron_variant</td> <td>C = 15.32</td> <td>top 2.9%</td>	rs57945129	rs62264780	3	8			intron_variant	C = 15.32	top 2.9%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$			_						
rs34804222rs6485465153HSD17B12intron_variantA = 15.33top 2.9%rs113142201,54E+0	rs61856978	rs11597197					intron_variant	G = 15.44	top 2.9%
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	rs34804222	rs6485465				HSD17B12	intron variant	Λ - 15 33	ton 2.9%
3 rs11581644 1 8 0,812 DENND4B intron_variant G = 15.26 top 3.0% rs1300323 rs2878076 2 0 0.93998 intron_variant C = 15.23 top 3.0% rs11252359 rs7785248 3 2 8 CADM2 intron_variant T = 15.17 top 3.0% rs80955 rs7785248 3 2 8 CADM2 intron_variant T = 15.17 top 3.0% rs80955 rs7785248 4 1.4E+08 6 NOCT intron_variant C = 15.2 top 3.0% rs80955 rs725300 7 8 1 intron_variant C = 15.2 top 3.0% rs7783012 rs1253805 7 8 1 intron_variant C = 15.2 top 3.0% rs7783012 rs1253805 7 8 1 intron_variant C = 15.2 top 3.0% rs7892750 rs216598 3 9 1 intron_variant A = 15.17 top 3.0% rs7125238 rs3295012 9 8 2 intron_variant A = 15.15<		130-03-03	-		5	HIJDITUIZ	Intron_valiant	A - 13.55	100 2.570
rs13009323rs28780764285UBR3intron_variantC = 15.23top 3.0%rs11252359rs7785243328CADM2intron_variantT = 15.17top 3.0%rs80955rs7785243328CADM2intron_variantT = 15.17top 3.0%rs80955rs76967541,4E+086NOCTintron_variantC = 15.22top 3.0%rs80955rs76967541,4E+086NOCTintron_variantC = 15.22top 3.0%rs7783012rs12533005781intron_variantC = 15.26top 3.0%rs7785701rs1253595391intron_variantC = 15.26top 3.0%rs7785701rs1329501982intron_variantC = 15.26top 3.0%rs11252369rs1329501398CADM2intron_variantA = 15.17top 3.0%rs11252369rs62793760398CADM2intron_variantAcACA = 15.05top 3.1%rs1252369rs62793760398CADM2intron_variantAcACA = 15.05top 3.1%rs6567244f9SAB494fibl 3.0%fibl 3.0%fibl 3.0%fibl 3.0%fibl 3.0%fibl 3.0%fibl 3.0%rs6767137rs7855208499AADGRL3intron_variantC = 15.15top 3.1%rs7874574fs1518816163HSD17B12intron_variant <td></td> <td>rs11581644</td> <td>1</td> <td></td> <td>0,812</td> <td>DENND4B</td> <td>intron_variant</td> <td>G = 15.26</td> <td>top 3.0%</td>		rs11581644	1		0,812	DENND4B	intron_variant	G = 15.26	top 3.0%
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$									
5rs77852438328CADM2intron_variantT=15.17top 3.0%rs809955rs76967541.4E+086NOCTintron_variantC=15.22top 3.0%rs809955rs78967541.4E+086NOCTintron_variantC=15.22top 3.0%rs7783012rs1253305781intron_variantC=15.22top 3.0%rs7895701rs2165985391intron_variantC=15.22top 3.0%rs7895701rs2165985391intron_variantC=15.22top 3.0%rs7895701rs2165985391intron_variantA=15.17top 3.0%rs7802434rs13295012982intron_variantA=15.17top 3.0%rs12523611.06E+00.82046intron_variantA=15.17top 3.0%rs1252365182intron_variantA=15.17top 3.0%rs5639241rs385135389DNAIC13intron_variantAEACAC = 15.15top 3.1%rs5639241rs385135440.98651ADGR13intron_variantC=15.15top 3.1%rs7671317rs765208440.98651ADGR13intron_variantC=15.15top 3.1%rs78480422rs151816163HSD17B12intron_variantC=15.14top 3.1%rs76751569rs7729218333intron_variant<		rs28780764	2			UBR3	intron_variant	C = 15.23	top 3.0%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$		rs77852438	2		,		intron variant	T – 15 17	ton 3.0%
rs809955rs76967541,4E+086NOCTintron_variantC = 15.22top 3.0%rs7783012rs12533005781intron_variantC = 15.16top 3.0%rs7783012rs1253305781intron_variantC = 15.16top 3.0%rs7783012rs2165985391intron_variantC = 15.22top 3.0%rs7987501rs216598391intron_variantC = 15.22top 3.0%rs7024334rs13295012982intron_variantA = 15.17top 3.0%rs125259982intron_variantA = 15.17top 3.0%rs125259241rs3295012398CADM2intron_variantAcACA = 15.05top 3.0%rs56392241rs3851353389DNAJC13intron_variantG = 15.15top 3.1%rs7671317rs765528440,98651AADGRL3intron_variantC = 15.15top 3.1%rs3840422rs1518816163HSD17B12intron_variantC = 15.15top 3.1%rs76751367rs7292115609790,91267intron_variantT = 15.14top 3.1%rs76751569rs72921199LINC02291intron_variantT = 15.14top 3.1%rs76751569rs8019512429LINC02291intron_variantA = 15.12top 3.1%		1377032430	5	۷		CADIVIZ		1 - 15.17	100 3.070
rs7783012 rs12533005 7 8 1 intron_variant C = 15.16 top 3.0% rs7987501 rs2165985 3 9 1 intron_variant C = 15.22 top 3.0% rs7987501 rs2165985 3 9 1 intron_variant C = 15.22 top 3.0% rs7024334 rs13295012 9 8 2 intron_variant A = 15.17 top 3.0% rs11252359 9 8 2 intron_variant A = 15.17 top 3.0% rs1252359 13 9 8 2 intron_variant A = 15.17 top 3.0% rs1252359 rs62793760 3 9 8 CADM2 intron_variant ACACA = 15.05 top 3.1% rs5385135 3 9 8 CADM2 intron_variant G = 15.15 top 3.1% rs56392241 rs3851353 3 8 9 DNAJC13 intron_variant G = 15.15 top 3.1% rs7671317 rs7655208 4 4 0,98651 ADGRL3 intron_variant C = 15.07 top 3.1% <td>rs809955</td> <td>rs769675</td> <td>4</td> <td>1,4E+08</td> <td>-</td> <td>NOCT</td> <td>intron_variant</td> <td>C = 15.22</td> <td>top 3.0%</td>	rs809955	rs769675	4	1,4E+08	-	NOCT	intron_variant	C = 15.22	top 3.0%
rs7987501153402630,92086rs7987501rs2165985391rs7024334rs13295012982rs1125235985591410,912875rs62793760398CADM2intron_variantA = 15.17top 3.0%rs56392241rs3851353389DNAJC13intron_variantG = 15.15top 3.1%rs7671317rs7655208440,98651ADGRL3rs784804222rs1518816163HSD17B12rs7955865rs772921233HSD17B12intron_variantrs7671306198109160,93315intron_variantC = 15.12rs767515069rs8019512429LINC02291intron_variantA = 15.12rs76715069rs8019512429LINC02291intron_variantA = 15.12rs76715069rs8019512429LINC02291intron_variantA = 15.12rs76715069rs8019512429LINC02291intron_variantA = 15.12rs76715069rs8019512429LINC02291intron_variantA = 15.12top 3.1%					0,90998				
rs7987501rs2165985391intron_variantC = 15.22top 3.0%rs7024334rs13295012982intron_variantA = 15.17top 3.0%rs11252359-85591410,91287intron_variantA = 15.17top 3.0%rs1252359-85591410,91287intron_variantACACA = 15.05top 3.1%rs12523591,32E400,89429intron_variantACACA = 15.05top 3.1%rs56392241rs3851353389DNAJC13intron_variantG = 15.15top 3.1%rs7671317rs7655208440,98651ADGRL3intron_variantC = 15.15top 3.1%rs38404222rs1518816163HSD17B12intron_variantC = 15.07top 3.1%rs7955865rs772921233rs7671307rs80195124Q0,93315intron_variantT = 15.14top 3.1%rs7671308rs8019512429LINC02291intron_variantA = 15.12top 3.1%	rs7783012	rs12533005					intron_variant	C = 15.16	top 3.0%
rs7024334rs13295012982intron_variantA = 15.17top 3.0%rs1125235985591410,91287intron_variantA = 15.17top 3.1%5rs62793760398CADM2intron_variantACACA = 15.05top 3.1%rs56392241rs3851353398ONAJC13intron_variantG = 15.15top 3.1%rs7671317rs7655208440,98651ADGRL3intron_variantC = 15.15top 3.1%rs7671317rs7655208440,98651ADGRL3intron_variantC = 15.15top 3.1%rs7671317rs7655208440,98651ADGRL3intron_variantC = 15.15top 3.1%rs784804222rs1518816163HSD17B12intron_variantC = 15.07top 3.1%rs7955865rs77292123331top 3.1%intron_variantT = 15.14top 3.1%rs76715069rs8019512429LINC02291intron_variantA = 15.12top 3.1%	rc7097501	F021CE08E			-		intron variant	C 15 22	top 2.0%
rs7024334rs13295012982intron_variantA = 15.17top 3.0%rs11252359-85591410,91287intron_variantACACA = 15.05top 3.1%5rs62793760398CADM2intron_variantACACA = 15.05top 3.1%rs56392241rs3851353389DNAJC13intron_variantG = 15.15top 3.1%rs7671317rs765520846210693rs7671317rs765520840,98651ADGRL3intron_variantC = 15.15top 3.1%rs7671317rs765520840,98651ADGRL3intron_variantC = 15.15top 3.1%rs7671317rs765520816210693rs785865rs77291190,9837rs7955865rs772921233rs76715069rs8019512429LINC02291intron_variantA = 15.12top 3.1%rs76715069rs8019512429LINC02291intron_variantA = 15.12top 3.1%	15/98/501	152103983	5				IIILIOII_Vallall	C = 15.22	τομ 5.0%
rs11252359 5rs62793760385591410,91287 8intron_variantACACA = 15.05top 3.1%5rs62793760398CADM2intron_variantACACA = 15.05top 3.1%rs56392241rs3851353389DNAJC13intron_variantG = 15.15top 3.1%rs76571317rs7655208440,98651ADGRL3intron_variantC = 15.15top 3.1%rs34804222rs1518816163HSD17B12intron_variantC = 15.07top 3.1%rs7955865rs7729212333410,93315intron_variantT = 15.14top 3.1%rs76715069rs8019512429LINC02291intron_variantA = 15.12top 3.1%	rs7024334	rs13295012	9				intron_variant	A = 15.17	top 3.0%
rs56392241 rs3851353 3 1,32E+0 0,89429 DNAJC13 intron_variant G = 15.15 top 3.1% rs7671317 rs7655208 4 4 0,98651 ADGRL3 intron_variant C = 15.15 top 3.1% rs7671317 rs7655208 4 4 0,98651 ADGRL3 intron_variant C = 15.15 top 3.1% rs34804222 rs1518816 1 6 3 HSD17B12 intron_variant C = 15.07 top 3.1% rs7955865 rs772921 2 3 3 4 0,93315 intron_variant T = 15.14 top 3.1% rs76715069 rs8019512 4 2 9 LINC02291 intron_variant A = 15.12 top 3.1%	rs11252359			8559141	0,91287				
rs56392241 rs3851353 3 8 9 DNAJC13 intron_variant G = 15.15 top 3.1% rs7671317 rs7655208 4 4 0,98651 ADGRL3 intron_variant C = 15.15 top 3.1% rs7671317 rs7655208 4 4 0,98651 ADGRL3 intron_variant C = 15.15 top 3.1% rs34804222 rs1518816 1 4380359 0,98337 intron_variant C = 15.07 top 3.1% rs75755865 rs772921 2 3 A HSD17B12 intron_variant C = 15.07 top 3.1% rs75755865 rs772921 2 3 3 HSD17B12 intron_variant T = 15.14 top 3.1% rs76715069 rs8019512 4 0,93315 Intron_variant A = 15.12 top 3.1% rs76715069 rs8019512 4 2 9 LINC02291 intron_variant A = 15.12 top 3.1%	5	rs62793760	3			CADM2	intron_variant	ACACA = 15.05	top 3.1%
rs7671317 rs7655208 4 6210693 ADGRL3 intron_variant C = 15.15 top 3.1% rs34804222 rs1518816 1 4380359 0,98337 intron_variant C = 15.07 top 3.1% rs34804222 rs1518816 1 6 3 HSD17B12 intron_variant C = 15.07 top 3.1% rs7955865 rs772921 2 3 3 intron_variant T = 15.14 top 3.1% rs76715069 rs8019512 4 2 9 LINC02291 intron_variant A = 15.12 top 3.1%	F65000044	m2051252	2				intro	0 15 15	tor 2 10/
rs7671317 rs7655208 4 4 0,98651 ADGRL3 intron_variant C = 15.15 top 3.1% rs34804222 rs1518816 1 4380359 0,98337 intron_variant C = 15.07 top 3.1% rs34804222 rs1518816 1 6 3 HSD17B12 intron_variant C = 15.07 top 3.1% rs7955865 rs772921 2 3 0,91206 intron_variant T = 15.14 top 3.1% rs7955865 rs772921 2 3 3 intron_variant T = 15.14 top 3.1% rs76715069 rs8019512 4 2 9 LINC02291 intron_variant A = 15.12 top 3.1% rs76715069 rs8019512 4 2 9 LINC02291 intron_variant A = 15.12 top 3.1%	1556392241	183821323	5		9	UNAJC13	intron_variant	G = 15.15	lop 3.1%
rs34804222 rs1518816 1 4380359 0,98337 HSD17B12 intron_variant C = 15.07 top 3.1% rs7955865 rs772921 2 3 3 intron_variant T = 15.14 top 3.1% rs76715069 rs8019512 4 2 9 LINC02291 intron_variant A = 15.12 top 3.1% rs76715069 rs8019512 4 2 9 LINC02291 intron_variant A = 15.12 top 3.1%	rs7671317	rs7655208	4		0,98651	ADGRL3	intron variant	C = 15.15	top 3.1%
rs34804222 rs1518816 1 6 3 HSD17B12 intron_variant C = 15.07 top 3.1% rs7955865 rs772921 2 3 -									1 1-
rs7955865 rs772921 2 3 3 intron_variant T = 15.14 top 3.1% rs76715069 rs8019512 4 9810916 0,93315 intron_variant A = 15.12 top 3.1% rs76715069 rs8019512 4 2 9 LINC02291 intron_variant A = 15.12 top 3.1%	rs34804222	rs1518816	1	6	3	HSD17B12	intron_variant	C = 15.07	top 3.1%
rs76715069 rs8019512 1 9810916 0,93315 LINC02291 intron_variant A = 15.12 top 3.1% 6323932 0,89338									
rs76715069 rs8019512 4 2 9 LINC02291 intron_variant A = 15.12 top 3.1% 6323932 0,89338 </td <td>rs/955865</td> <td>rs/72921</td> <td></td> <td></td> <td></td> <td></td> <td>Intron_variant</td> <td>T = 15.14</td> <td>top 3.1%</td>	rs/955865	rs/72921					Intron_variant	T = 15.14	top 3.1%
6323932 0,89338	rs76715069	rs8019512					intron variant	Δ = 15 10	top 3.1%
	1370713003	130013312	-					Λ = 13.1Z	COP 3.170
	rs62180269	rs17432775	2			EHBP1	intron_variant	T = 15	top 3.2%

I	I	l	1,56E+0	0,89614				
rs1226414	rs12997268	2	8	4		intron variant	G = 14.9	top 3.2%
rs11252359			8556024	0,98302				
5	rs72615727	3	8	1	CADM2	intron_variant	C = 14.94	top 3.2%
			1,18E+0					
rs57945129	rs6778926	3	8	0,81597		intron_variant	G = 14.83	top 3.3%
rs245753	rs10076357	5	1,71E+0 8	0,99543 2	FGF18	intron variant	C - 14 9F	top 2.29/
15245755	1210070227	5	ہ 5375556	Ζ	FGF10	intron_variant	C = 14.85	top 3.3%
rs2612029	rs7373253	3	7	0,8899	CACNA1D	intron variant	C = 14.64	top 3.4%
			1,71E+0	0,99542				'
rs245753	rs3849709	5	8	4		intron_variant	T = 14.71	top 3.4%
			4465408	0,95071				
rs35508442	rs12712920	2	1	3	CAMKMT	intron_variant	G = 14.56	top 3.5%
rs809955	rs797090	4	1,4E+08	0,98680 7	NOCT	intron variant	C = 14.4	top 3.6%
18803333	13737030	4	1284459	, 0,98521	NOCT		G = 14.4	τορ 3.0%
rs1866710	rs2099744	1	9	2	TEAD1	intron_variant	A = 14.42	top 3.6%
			4461219					
rs35508442	rs5830797	2	3	0,83345	CAMKMT	intron_variant	TT = 14.3	top 3.7%
			8729746	0,99149				
rs1925686	rs6938885	6	1	8		intron_variant	G = 14.32	top 3.7%
rs7987501	rs4883678	1 3	5336849 7	0,87418 4		intron variant	A = 14.37	top 3.7%
137587501	134003070	1	, 7556658	0,98045		Intron_variant	A - 14.37	100 3.770
rs12446652	rs8192516	6	7	1	RP11-77K12.7/CHST5	intron_variant	C = 14.3	top 3.7%
			4464473	0,82890				
rs35508442	rs13400118	2	5	4	CAMKMT	intron_variant	C = 14.2	top 3.8%
10000000	2222247	_	1,71E+0	0,93998	11222			
rs13009323	rs28892917	2	8 2559425	5	UBR3	intron_variant	C = 14.23	top 3.8%
rs2278480	rs2278480	3	2559425	1	RARB	intron variant	C = 14.2	top 3.8%
rs11252359	152270100		8555898	0,98723			0 14.2	100 3.070
5	rs724304	3	9	8	CADM2	intron_variant	C = 14.23	top 3.8%
rs12203592	rs12203592	6	396321	1	IRF4	intron_variant	T = 14.22	top 3.8%
			8729266	0,99575				
rs1925686	rs9444491	6	7	1		intron_variant	G = 14.22	top 3.8%
		0	9675948	0,81864	CO - "f27 AC1			t
rs10955084	rs2319923	8	0 1,22E+0	7 0,97948	C8orf37-AS1	intron_variant	G = 14.2	top 3.8%
rs9886840	rs10760192	9	8	8		intron_variant	T = 14.18	top 3.8%
		1		0,86984				
rs9923553	rs12051184	6	5741333	3		intron_variant	G = 14.16	top 3.8%
			7544184	0,91324				
rs794375	rs236607	7	3	9	CCL24	intron_variant	C = 14.05	top 3.9%
rs7987501	rs1017539	1 3	5346753 1	0,87949 7		intron variant	A = 14 10	top 3.9%
13/38/301	131017333	5	1,06E+0	, 0,82046			A = 14.12	top 3.9%
rs7024334	rs16925382	9	8	2		intron_variant	G = 14.08	top 3.9%
rs11252359			8550181	0,98723				
5	rs62250750	3	9	8	CADM2	intron_variant	C = 13.94	top 4.0%
			1,18E+0	4		inter i i		t., 1.001
rs57945129	rs62264764	3	8 5026731	1 0,86298		intron_variant	A = 14.02	top 4.0%
rs7824756	rs4873442	8	5026731 7	0,86298 4		intron variant	A = 14.02	top 4.0%
137027730	131073772	1	, 9620199	4 0,84941		ind on_variant	··· 17.02	.op 1.070
rs61856978	rs10882743	0	2	7	TBC1D12	intron_variant	A = 13.98	top 4.0%
			1,43E+0					
rs10496949	rs2381473	2	8	0,99189		intron_variant	A = 13.83	top 4.1%
ra2004572	ro1440001	2	1724532 Г	0,98800		intron	C 12.55	top 4 10/
rs2084572	rs1449881	3	5	2	TBC1D5	intron_variant	G = 13.86	top 4.1%

rs11252359			8543344	0,94605				
5	rs7609594	3	5	3	CADM2	intron_variant	A = 13.91	top 4.1%
			1,32E+0	0,89429				
rs56392241	rs1010899	3	8 5337333	9 0,86638	DNAJC13	intron_variant	A = 13.91	top 4.1%
rs7987501	rs2197304	3	0	5		intron variant	A = 13.82	top 4.1%
			5783581	0,94512				
rs7533341	rs852786	1	9	5	DAB1	intron_variant	C = 13.76	top 4.2%
rs11772444	rs14797782 8	7	1,34E+0 8	0,94859 5	EXOC4	intron variant	TTAGTTT = 13.73	top 4.2%
1311/72444	0	1	4724316	0,95193	LXOC4	Intron_variant	TIAGTIT - 13.73	100 4.278
rs34155040	rs17785603	8	3	1		intron_variant	A = 13.75	top 4.2%
rs11445630	rs11445630		2463166					
3	3 rs13812952	3	7 2857733	1 0,83507		intron_variant	A = 13.71	top 4.3%
rs702	6	4	0	4		intron variant	AAAAA = 13.7	top 4.3%
			2857739	0,83507				·
rs702	rs2458628	4	8	4		intron_variant	T = 13.67	top 4.3%
rs1435757	rs5812402	1 5	4756691 4	0,88250 1	SEMA6D	intron_variant	- 12 67	top 4.3%
131433737	133012402	5	4 1734984	0,91140	SLIVIAOD	Intron_variant	- = 13.67	100 4.576
rs2084572	rs1867772	3	7	1	TBC1D5	intron_variant	A = 13.54	top 4.4%
0004570	2525542	2	1726590	0,90829	700105			
rs2084572	rs2596649	3	3 1,22E+0	8 0,84047	TBC1D5	intron_variant	A = 13.52	top 4.4%
rs9886840	rs7046409	9	8	2		intron variant	T = 13.61	top 4.4%
			5308751	0,86837				
rs222440	rs2744451	6	9	4		intron_variant	T = 13.43	top 4.5%
rs34804222	rs10838157	1 1	4372401 4	0,93389 6	HSD17B12	intron variant	G = 13.44	top 4.5%
1334004222	1310030137	1	5339021	0,88573	113017012	Intron_variant	0 - 13.44	100 4.370
rs7987501	rs9536408	3	1	2		intron_variant	T = 13.46	top 4.5%
rs13009323	rc12C2407	2	1,71E+0 8	0,82017 7		intron variant	C 12.11	top 4 69/
1813009323	rs1362487	2	8 2335808	,97980	UBR3	intron_variant	C = 13.41	top 4.6%
rs12554512	rs7029201	9	3	7		intron_variant	A = 13.4	top 4.6%
rs11314220			1,54E+0	0,81642				
3	rs12043350	1	8	9	GATAD2B	intron_variant	T = 13.25	top 4.7%
rs37590944 0	rs9984518	2 1	3921124 0	0,91508 5	KCNJ6	intron variant	C = 13.29	top 4.7%
	100001010	-	4464199	0,81432			0 10.20	
rs35508442	rs734016	2	7	6	CAMKMT	intron_variant	C = 13.15	top 4.8%
rs12714702	rs4374552	3	8813573 3	0,94967 1	CGGBP1	intron variant	A - 12 17	top 4.8%
1312/14/02	154574552	5	1,71E+0	1	CGGBF1	Intron_variant	A = 13.17	top 4.876
rs245753	rs10041523	5	8	1		intron_variant	C = 13.2	top 4.8%
	40-04-04	_		0,86731				
rs7785195	rs12700808	7	3344512	3 0,99149	SDK1	intron_variant	G = 13.21	top 4.8%
rs1925686	rs9450630	6	8718944 2	0,99149 8		intron variant	A = 13.14	top 4.9%
		1	9339485	0,91066				
rs10134692	rs1910517	4	7	7	CHGA	intron_variant	G = 13.14	top 4.9%
rs35508442	rs4953111	2	4458026 7	0,83253 5	PREPL	intron variant	A = 13	top 5.0%
1355500442		2	, 1,06E+0	0,82570			CI – A	top 3.070
rs590414	rs539238	1	8	3	KBTBD3	intron_variant	G = 12.89	top 5.1%
		~	1,85E+0	0,99305				
rs34481141	rs13396624	2	8 4459310	9 0,83617		intron_variant	G = 12.92	top 5.1%
rs35508442	rs62132285	2	2	8	CAMKMT	intron_variant	G = 12.81	top 5.2%
			1	ı				

rs1516172 rs1878135 2 7 4 1735073 0,99197	intron_variant	G = 12.86	+ E 20/
1/320/3 0,9919/			top 5.2%
rs2084572 rs5846958 3 1 7 TBC1D5	intron_variant	G = 12.88	top 5.2%
rs2084572 rs2733509 3 3 2 TBC1D5	intron_variant	G = 12.86	top 5.2%
1,08E+0 0,85580	ind on_variant	0 - 12.00	100 3.270
rs2406374 rs12656108 5 8 7 FBXL17	intron_variant	G = 12.8	top 5.2%
1 6790689 0,81600			
rs6504551 rs12947658 7 0 1	intron_variant	G = 12.87	top 5.2%
rs2084572 rs2470577 3 9 1 TBC1D5	intron_variant	G = 12.79	top 5.3%
rs11955430 rs11955430 5 8 1 PANK3	intron variant	G = 12.73	top 5.3%
2,19E+0 0,81251	Intron_vanant	0 - 12.75	top 5.576
rs875097 rs2010528 2 8 1 PLCD4	intron_variant	G = 12.67	top 5.4%
1,68E+0 0,87386	_		
rs11955430 rs1345735 5 8 7 PANK3	intron_variant	C = 12.69	top 5.4%
1,14E+0			5 404
rs7783012 rs10249234 7 8 1 9450891 0,81373	intron_variant	A = 12.65	top 5.4%
rs72674824 rs12678305 8 1 7 LINC00535	intron variant	C = 12.71	top 5.4%
1 1286668	vuluite	0 12.71	
rs1866710 rs11022519 1 9 0,97544 TEAD1	intron_variant	C = 12.68	top 5.4%
rs11314220 1,54E+0 0,81642			
3 rs11590099 1 8 9 GATAD2B	intron_variant	T = 12.54	top 5.6%
1,71E+0 0,99084	introp verient		ton 5 (0)
rs245753 rs7735245 5 8 6 1,52E+0 0,88983	intron_variant	C = 12.53	top 5.6%
rs12204714 rs6557171 6 8 4 CCDC170	intron variant	C = 12.45	top 5.7%
1 4755186 0,88642			
rs1435757 rs28505872 5 2 5 SEMA6D	intron_variant	C = 12.42	top 5.7%
7453698 0,86100			
rs7525548 rs3845345 1 3 9 LRRIQ3	intron_variant	T = 12.33	top 5.8%
rs1226414 rs1226422 2 8 9	intron_variant	G = 12.31	top 5.9%
1 4726704 0,91545	Introll_vallant	0 - 12.51	top 5.576
rs34155040 rs4534948 8 8 9	intron_variant	A = 12.32	top 5.9%
2566190 0,84201			
rs2278480 rs59134881 3 9 2 TOP2B	intron_variant	C = 12.21	top 6.0%
rs7828172 rs62505473 8 7 7	intron variant	C 12.24	top 6.0%
rs7828172 rs62505473 8 7 7 1,85E+0	intron_variant	G = 12.24	τομ 6.0%
rs34481141 rs13422256 2 8 1	intron_variant	T = 12.24	top 6.0%
5781856 0,94927			
rs7533341 rs852759 1 4 6 DAB1	intron_variant	G = 12.14	top 6.1%
1740694			
rs2084572 rs9824952 3 5 0,86669 TBC1D5	intron_variant	A = 12.13	top 6.1%
rs222440 rs222449 6 4 7	intron variant	T = 10 1E	top 6.1%
7454034 0,98803		T = 12.15	100 0.170
rs7525548 rs3895907 1 3 6 LRRIQ3	intron_variant	G = 12.09	top 6.2%
7453211 0,84546			
rs7525548 rs6703637 1 1 3 LRRIQ3	intron_variant	A = 12.06	top 6.2%
1,71E+0 0,99542	interes and the	0 10 55	to:: (20/
rs245753 rs4868049 5 8 4 8719719 0,99575	intron_variant	C = 12.08	top 6.2%
rs1925686 rs6940325 6 8 1	intron variant	G = 12.06	top 6.2%
8812703 0,98553			
rs12714702 rs6551273 3 9 5 CGGBP1	intron_variant	T = 11.93	top 6.4%

			9455230	0,81373				
rs72674824	rs12679345	8	5	7	LINC00535	intron_variant	G = 11.95	top 6.4%
rs9886840	rs7027567	9	1,22E+0 8	0,83967 1		intron variant	C = 11.96	top 6.4%
133000010	13/02/30/	5	1,85E+0	-			0 11.50	top 0.170
rs34481141	rs10206254	2	8	1		intron_variant	A = 11.94	top 6.4%
rs11252359 5	rs4856273	3	8554911 0	0,98297 6	CADM2	intron variant	A = 11.9	top 6.5%
	101000270		8666413	0,99171	0,101112			
rs11382985	rs6471476	8	0	2		intron_variant	C = 11.82	top 6.6%
rs11252359 5	rs11127899	3	8554541 2	0,98723 8	CADM2	intron variant	G = 11.77	top 6.7%
			8810941	0,94967	0,101112			
rs12714702	rs7650707	3	6	1	CGGBP1	intron_variant	C = 11.72	top 6.7%
rs1925686	rs1188817	6	8734600 1	0,83345 4		intron variant	G = 11.73	top 6.7%
		1	9336032			_		1
rs10134692	rs8003519	4	6	0,89216		intron_variant	G = 11.75	top 6.7%
rs7533341	rs706409	1	5781649 4	0,94927 6	DAB1	intron_variant	G = 11.68	top 6.8%
			4459857	0,83541				
rs35508442	rs17032420	2	4	6	CAMKMT	intron_variant	A = 11.61	top 6.9%
rs18672345 4	rs73083946	3	5413012 8	0,95190 7		intron variant	T = 11.63	top 6.9%
			6211504	0,91614				
rs7671317	rs13151071	4	6	8	ADGRL3	intron_variant	G = 11.57	top 7.0%
rs7671317	rs10003184	4	6208612 5	0,88653 5	ADGRL3	intron variant	A = 11.54	top 7.0%
			1,71E+0	0,99542	, is chief			
rs245753	rs10042357	5	8	4		intron_variant	A = 11.54	top 7.0%
rs245753	rs4362957	5	1,71E+0 8	0,99542 4		intron variant	G = 11.48	top 7.1%
		1	9339226	0,91066			0 1110	
rs10134692	rs1503958	4	4	7	CHGA	intron_variant	T = 11.47	top 7.1%
rs28406364	rs35587648	1 7	4934081 6	0,89978 5	UTP18	intron_variant	A = 11.47	top 7.1%
		1	4688927	0,94302				
rs3007104	rs2933223	4	1	4	LINC00871	intron_variant	C = 11.44	top 7.2%
rs37590944 0	rs9979936	2 1	3928046 3	1	KCNJ6	intron variant	G = 11.42	top 7.2%
			6094468					
rs6764919	rs7356063	3	5	0,82632 0,99543	FHIT	intron_variant	A = 11.39	top 7.3%
rs245753	rs10475962	5	1,71E+0 8	0,99543	FGF1	intron variant	G = 11.37	top 7.3%
		1	4651299	0,93571				·
rs11038866	rs3802890	1	6 2,25E+0	3 0,95171	AMBRA1	intron_variant	G = 11.31	top 7.4%
rs6748341	rs60714794	2	2,25E+0 8	0,95171 3		intron_variant	AAAAAAAAA = 11.23	top 7.5%
		1	1,34E+0	0,81337				·
rs11428242 rs11314220	rs61909696	1	8 1,54E+0	7 0,81642	GLB1L2	intron_variant	C = 11.23	top 7.5%
3	rs71697078	1	1,54E+0 8	0,81642 9	DENND4B	intron_variant	AATTAATTA = 11.18	top 7.6%
			4463730	0,82810	_			
rs35508442	rs10204480	2	2 1,71E+0	6 0,93998	САМКМТ	intron_variant	G = 11.21	top 7.6%
rs13009323	rs7594247	2	1,71E+0 8	0,93998 5	UBR3	intron_variant	T = 11.2	top 7.6%
			1725426	0,90410				
rs2084572	rs2348005	3	4	5 0,94605	TBC1D5	intron_variant	C = 11.22	top 7.6%
rs11252359 5	rs1865252	3	8543959 0	0,94605 3	CADM2	intron variant	G = 11.22	top 7.6%
L		i	1	ı				1

1		1		0,98524				
rs9923553	rs13335882	6	5775964	7		intron_variant	T = 11.17	top 7.6%
7000055	****	4	1 45 - 00	0,86052	NOCT	intern contract	A 1114	to:: 7 70/
rs809955	rs769673	4	1,4E+08 1,22E+0	2 0,97105	NOCT	intron_variant	A = 11.14	top 7.7%
rs9886840	rs10818604	9	8	3		intron_variant	A = 11.16	top 7.7%
		1	5308079	0,84441				
rs9964201	rs12957045	8	0 4459456	6 0,83175	TCF4	intron_variant	G = 11.13	top 7.7%
rs35508442	rs79542623	2	4459450	0,85175	CAMKMT	intron_variant	C = 11.09	top 7.8%
			1,56E+0	0,88802		_		· · · ·
rs1226414	rs13002285	2	8	2		intron_variant	T = 11.06	top 7.8%
rs2084572	rs13093375	3	1739410 6	0,94837 8	TBC1D5	intron variant	G = 11.05	top 7.9%
132001372	1313033373	5	3569808	0,92231	100105	Intron_variant	6 11.05	top 7.570
rs67723420	rs13097782	3	3	1	ARPP21	intron_variant	T = 11.05	top 7.9%
	rs37531296	2	7779512	0,98729		internet and in the		tan 0.10/
rs11688027	5	2	7 1721826	9 0,98403		intron_variant	C = 10.9	top 8.1%
rs2084572	rs1597393	3	5	9	TBC1D5	intron_variant	C = 10.91	top 8.1%
			6213731	0,89405				
rs7671317	rs10013024	4	8	1	ADGRL3	intron_variant	A = 10.89	top 8.1%
rs34804222	rs10838173	1 1	4379916 9	0,98337 3	HSD17B12	intron variant	G = 10.89	top 8.1%
	10100001/0	1	5336357	0,87801	110017012		0 10.05	
rs7987501	rs1342669	3	0	1		intron_variant	C = 10.86	top 8.2%
rs76702070	rs77664243	1 1	8558116 0	0,97573 1	CCDC83	intron variant	T - 10.90	top 8 2%
15/0/020/0	1577004245	1	5778026	0,91131	CCDC85	intron_variant	T = 10.86	top 8.2%
rs7533341	rs1323828	1	8	4	DAB1	intron_variant	A = 10.82	top 8.3%
		_	4465378	0,94271				
rs35508442	rs12998046	2	6 1,19E+0	6 0,89687	САМКМТ	intron_variant	A = 10.81	top 8.3%
rs705240	rs798581	3	1,19E+0 8	0,89687	IGSF11	intron variant	C = 10.83	top 8.3%
			5026734			_		
rs7824756	rs4873443	8	1	0,85348		intron_variant	T = 10.8	top 8.3%
rs10955084	rs4735438	8	9681768 9	0,96473 5	C8orf37-AS1	intron variant	T = 10.82	top 8.3%
1310555004	134733430	0	1,68E+0	0,95063	C001137-A31	Intron_variant	1 - 10.82	100 0.570
rs11955430	rs12522181	5	8	4	PANK3	intron_variant	G = 10.78	top 8.4%
***245752	m21C121C	F	1,71E+0	0,97263		intern conicet		tan 0,404
rs245753	rs2161216	5	8 2335566	9 0,97980		intron_variant	A = 10.74	top 8.4%
rs12554512	rs4977836	9	6	7		intron_variant	A = 10.74	top 8.4%
		1	4724599	0,95193				
rs34155040	rs57971954	8	8	1 0,82113		intron_variant	GGAG = 10.78	top 8.4%
rs35508442	rs6726493	2	4456822 5	0,82113	PREPL	intron variant	C = 10.72	top 8.5%
			6089894	0,98093				
rs6764919	rs6763967	3	4	8	FHIT	intron_variant	A = 10.73	top 8.5%
rs11252359 5	rs59417256	3	8557133 1	0,98723 8	CADM2	intron variant	G = 10.71	top 8.5%
	1333417230	2	1,18E+0	8 0,93812	CADIVIZ		0 = 10.71	τομ 6.3%
rs57945129	rs1456196	3	8	8		intron_variant	A = 10.69	top 8.5%
E COOCE LE	1017000	_	1,32E+0	0,89429				
rs56392241	rs1847832	3	8 1,06E+0	9	DNAJC13	intron_variant	C = 10.73	top 8.5%
rs7024334	rs12685887	9	1,00E+0 8	0,80259		intron_variant	G = 10.71	top 8.5%
			1,56E+0	0,89614				
rs1226414	rs2695440	2	8	4		intron_variant	G = 10.64	top 8.6%

$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	I		1722933	l		1		
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	rs2084572	rs2596673	3		0,98396	TBC1D5	intron_variant	G = 10.64	top 8.6%
sila first sic 474 (a) 8385 rs12 first rs16 first rs12 first			1	4936310	0,92862				
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	rs28406364	rs16948048	7			UTP18	intron_variant	G = 10.66	top 8.6%
intron_variant T = 10.59 top 8.7% rs341521 rs341530 3 4 intron_variant T = 10.55 top 8.7% rs341521 rs341530 3 4 intron_variant T = 10.55 top 8.8% rs1275339 rs56073108 3 8 CADM2 intron_variant G = 10.5 top 8.9% rs127234702 rs59073108 3 7 intron_variant G = 10.5 top 8.9% rs127234702 rs5907310 2.944632 0.99670 intron_variant T = 10.53 top 8.9% rs767943 rs202330 6 7 intron_variant G = 10.47 top 9.0% rs782195 rs416733 7 333229 0.86274 intron_variant G = 10.41 top 9.0% rs2021501 8 0.93171 intron_variant G = 10.41 top 9.0% rs2021501 8 0.94967 intron_variant G = 10.41 top 9.1% rs2021520 3 1 1 10.2454 TENM2 int	rc1E16172	rc1606072	2		-		intron variant	T 10.0	top 9.70/
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	151516172	121000972	2				Intron_variant	1 = 10.6	lop 8.7%
1 598031 0,92772 intron_variant T = 10.55 top 8.9% rs111252359 rs59073108 3 9 8 CADM2 intron_variant G = 10.5 top 8.9% rs1172174702 rs959048 3 7 1 intron_variant G = 10.5 top 8.9% rs7608187 rs111250 0.038700 0.08970 intron_variant G = 10.47 top 9.9% rs765195 rs416731 7 3332320 0.8072 intron_variant G = 10.47 top 9.0% rs7765195 rs4416731 7 3332320 0.8072 intron_variant G = 10.47 top 9.0% rs7263195 rs4416731 7 3332320 0.8072 intron_variant G = 10.47 top 9.0% rs204572 0 3 1 1 TBC1D5 intron_variant C = 10.42 top 9.1% rs4868800 rs883222 5 8 4 TEND2 intron_variant I = 10.41 top 9.1% rs12714702 rs9447019	rs2084572	rs283911	3		-	TBC1D5	intron variant	T = 10.59	top 8.7%
rs11252359 rs5907310 3 9 8 CADM2 intron_variant 6 = 10.5 top 8.9% rs12714702 rs959048 3 7 1 intron_variant C = 10.5 top 8.9% rs760817 rs1112501 2 2 4 NRXN1 intron_variant T = 10.53 top 8.9% rs767943 rs202212 2344632 0.8042 intron_variant G = 10.47 top 9.0% rs7785195 rs441673 7 3332329 0.86274 intron_variant G = 10.47 top 9.0% rs20125930 1734447 0.91140 intron_variant C = 10.42 top 9.0% rs204572 0 3 1 1 TBC1D5 intron_variant C = 10.42 top 9.1% rs1224752 0 3 2 1 intron_variant C = 10.41 top 9.1% rs204572 0 3 2 1 intron_variant C = 10.42 top 9.1% rs12214702 rs8402943 0.94724 <t< td=""><td></td><td></td><td>1</td><td>5980531</td><td>0,92772</td><td></td><td>_</td><td></td><td>·</td></t<>			1	5980531	0,92772		_		·
5 rs59073108 3 9 8 CAOM2 intron_variant G = 10.5 top 8.9% rs12714702 rs959048 3 7 1 intron_variant C = 10.5 top 8.9% rs7608187 rs11125301 2 2 4 NRXN1 intron_variant C = 10.5 top 8.9% rs767943 rs202330 6 7 7 intron_variant G = 10.47 top 9.0% rs7785195 rs4416733 7 3332329 0.86274 intron_variant G = 10.47 top 9.0% rs7824756 rs34020561 8 2 9 intron_variant G = 10.47 top 9.0% rs2045930 1 1734447 0,91140 intron_variant G = 10.41 top 9.0% rs12714702 rs8467019 3 2 1 intron_variant G = 10.41 top 9.1% rs1274702 rs4402954 3 3 9 intron_variant T = 10.41 top 9.1% rs12634572 rs23915 3	-	rs341530	3				intron_variant	T = 10.55	top 8.8%
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$,				
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	5	rs590/3108	3			CADM2	intron_variant	G = 10.5	top 8.9%
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	rs12714702	rs959048	З		-		intron variant	C = 10 5	ton 8.9%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1012/11/02	15555616			-			0 10.5	
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	rs7608187	rs11125301	2		-	NRXN1	intron_variant	T = 10.53	top 8.9%
$\begin{array}{cccccccccccccccccccccccccccccccccccc$					-				
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	rs767943	rs2022330	6		7		intron_variant	G = 10.47	top 9.0%
Ins7824756 rs3204575 rs2019530 rs2019530 a 1234447 0.91140 0.91140 intron_variant A = 10.44 top 9.0% rs2048572 0 3 1 1 TBC1D5 intron_variant C = 10.42 top 9.1% rs12714702 rs9847019 3 2 1 intron_variant G = 10.41 top 9.1% rs4868800 rs883322 5 8 4 TENM2 intron_variant T = 10.41 top 9.1% rs12714702 rs9847019 3 3 9 intron_variant T = 10.41 top 9.1% rs1252359 8 4 TENM2 intron_variant A = 10.36 top 9.2% rs1252359 3 7 8 CADM2 intron_variant A = 10.27 top 9.4% rs2084572 rs7386148 0 7 8 CADM2 intron_variant A = 10.21 top 9.5% rs7987501 rs7356148 0 0 9 1 1.34E+0 0.80360 rs1.34E+0 0.	rs7785195	rs4416733	7		,		intron_variant	G = 10.47	top 9.0%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	rc7071750	rc2/100001	0		-		intron variant	A 10 44	top 0.0%
rs2084572 0 3 1 1 TBC1D5 intron_variant C = 10.42 top 9.1% rs12714702 rs9847019 3 2 1 intron_variant G = 10.41 top 9.1% rs4868800 rs883322 5 8 4 TENM2 intron_variant T = 10.41 top 9.1% rs12714702 rs4402954 3 3 9 intron_variant T = 10.41 top 9.2% rs1225239 - 8535553 0,98723 . top 9.2% top 9.2% rs2084572 rs283915 3 6 4 TBC1D5 intron_variant C = 10.23 top 9.4% rs2084572 rs283915 3 6 4 TBC1D5 intron_variant C = 10.23 top 9.5% rs73987501 rs7336148 3 0 7 intron_variant A = 10.16 top 9.5% rs1772444 rs254264 7 8 5 intron_variant A = 10.16 top 9.6% rs10992812 rs3	15/824/50		ð				Intron_variant	A = 10.44	top 9.0%
rs12714702 rs8877884 0,94967 intron_variant G = 10.41 top 9.1% rs4868800 rs883322 5 8 4 intron_variant G = 10.41 top 9.1% rs4868800 rs883322 5 8 4 intron_variant T = 0.41 top 9.1% rs12714702 rs4002954 3 3 9 intron_variant T = 10.41 top 9.2% rs1252359 8 4 TENM2 intron_variant A = 10.36 top 9.2% rs2084572 rs283915 3 6 4 TBC1D5 intron_variant C = 10.23 top 9.5% rs7987501 rs736148 3 0 7 intron_variant A = 10.21 top 9.5% rs7255548 rs12041912 1 6 8 IRRIQ3 intron_variant A = 10.16 top 9.6% rs11772444 rs2542264 7 8 5 intron_variant A = 10.19 top 9.6% rs11034692 rs7467480 9 2 9 </td <td>rs2084572</td> <td></td> <td>3</td> <td></td> <td>,</td> <td>TBC1D5</td> <td>intron variant</td> <td>C = 10.42</td> <td>top 9.1%</td>	rs2084572		3		,	TBC1D5	intron variant	C = 10.42	top 9.1%
$\begin{array}{c c c c c c c c c c c c c c c c c c c $				8807884	0,94967		_		·
rs888800 rs883322 5 8 4 TENM2 intron_variant T = 10.41 top 9.1% rs12714702 rs4402954 3 3 9 intron_variant A = 10.36 top 9.2% rs1252359 8 553553 0,98794 intron_variant TTTT = 10.27 top 9.2% rs2084572 rs283915 3 6 4 TBC1D5 intron_variant C = 10.23 top 9.5% rs7987501 rs736148 3 0 7 intron_variant A = 10.21 top 9.5% rs7987501 rs736148 3 0 7 intron_variant A = 10.21 top 9.5% rs1772444 rs2542264 7 8 5 intron_variant A = 10.16 top 9.6% rs103292812 rs375354 9 1 8 5 intron_variant A = 10.19 top 9.6% rs1034692 rs474548 0.91671 intron_variant A = 10.19 top 9.6% rs105992812 rs3705354 9	rs12714702	rs9847019	3				intron_variant	G = 10.41	top 9.1%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$									
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	rs4868800	rs883322	5			TENM2	intron_variant	T = 10.41	top 9.1%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	rs1271/702	rs/102951	З				intron variant	A - 10 36	ton 9.2%
5 rs74384786 3 7 8 CADM2 intron_variant TTTT = 10.27 top 9.4% rs2084572 rs23915 3 6 4 TBC1D5 intron_variant C = 10.23 top 9.5% rs7987501 rs7336148 3 0 7 intron_variant A = 10.21 top 9.5% rs7987501 rs7336148 3 0 7 intron_variant A = 10.21 top 9.5% rs7525548 rs12041912 1 6 8 LRRIQ3 intron_variant A = 10.16 top 9.6% rs11772444 rs2542264 7 8 5 intron_variant G = 10.16 top 9.6% rs11772444 rs2542264 7 8 5 intron_variant G = 10.16 top 9.6% rs11772444 rs2542264 7 8 5 intron_variant G = 10.16 top 9.6% rs1175244 rs2542264 7 8 5 intron_variant T = 10.18 top 9.6% rs11034692		134402334	5				Intron_variant	A = 10.50	100 5.270
rs2084572 rs283915 3 6 4 TBC1D5 intron_variant C = 10.23 top 9.5% rs7987501 rs7336148 3 0 7 intron_variant A = 10.21 top 9.5% rs7525548 rs12041912 1 6 8 LRRIQ3 intron_variant A = 10.21 top 9.6% rs1772444 rs254226 7 8 5 intron_variant A = 10.16 top 9.6% rs11772444 rs254264 7 8 5 intron_variant A = 10.16 top 9.6% rs1175244 rs254264 9 2.9 intron_variant A = 10.19 top 9.6% rs1175244 rs375035 9 1 8 SYK intron_variant A = 10.19 top 9.6% rs10992812 rs3750364 9 1 8 SYK intron_variant T = 10.18 top 9.6% rs10134692 rs57184074 4 2 2 ITPK1 intron_variant C = 10.17 top 9.6%		rs74384786	3		-	CADM2	intron_variant	TTTTT = 10.27	top 9.4%
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$				1728827	0,98794				
rs7987501rs7336148307intron_variantA = 10.21top 9.5%rs7525548rs12041912168LRRIQ3intron_variantA = 10.16top 9.6%rs1772444rs2542264785intron_variantG = 10.16top 9.6%rs11772444rs254264785intron_variantG = 10.16top 9.6%rs11772444rs254264785intron_variantA = 10.19top 9.6%rs11772444rs254264785intron_variantA = 10.19top 9.6%rs11772444rs254264785intron_variantA = 10.19top 9.6%rs1175245rs7467480929intron_variantA = 10.19top 9.6%rs1092812rs37503549182SYKintron_variantT = 10.18top 9.6%rs10134692rs57184074422ITPK1intron_variantT = 10.18top 9.6%rs1125235918533880,9872311top 9.6%1top 9.6%rs1388507622331770,94202intron_variantC = 10.17top 9.6%rs1388507622331770,94202intron_variantC = 10.07top 9.8%rs13885076199LINC02291intron_variantC = 10.07top 9.8%rs27647518265intron_variantC = 10.07top 9.8%rs2674457126	rs2084572	rs283915	1			TBC1D5	intron_variant	C = 10.23	top 9.5%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	rc7087501	rc722C149			-		intron variant	4 10 01	top 0 5%
rs7525548 rs12041912 1 6 8 LRR\Q3 intron_variant A = 10.16 top 9.6% rs11772444 rs2542264 7 8 5 intron_variant G = 10.16 top 9.6% rs11772444 rs2542264 7 8 5 intron_variant G = 10.16 top 9.6% rs12554512 rs7467480 9 2 9 intron_variant A = 10.19 top 9.6% rs10992812 rs3750354 9 1 8 SYK intron_variant T = 10.18 top 9.6% rs10134692 rs57184074 4 2 2 ITPK1 intron_variant T = 10.18 top 9.6% rs10134692 rs57184074 4 2 2 ITPK1 intron_variant T = 10.18 top 9.6% rs10134692 rs51402128 2 5 4 NRXN1 intron_variant T = 10.12 top 9.6% rs10134692 rs62252513 3 7 8 CADM2 intron_variant T = 10.12<	15/98/501	157336148	3				Intron_variant	A = 10.21	top 9.5%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	rs7525548	rs12041912	1		-	LRRIQ3	intron variant	A = 10.16	top 9.6%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$					0,80360		_		·
rs12554512 rs7467480 9 2 9 1 intron_variant A = 10.19 top 9.6% rs10992812 rs3750354 9 1 8 SYK intron_variant T = 10.18 top 9.6% rs10992812 rs3750354 9 1 8 SYK intron_variant T = 10.18 top 9.6% rs10134692 rs57184074 4 2 2 ITPK1 intron_variant T = 10.18 top 9.6% rs10134692 rs57184074 4 2 2 ITPK1 intron_variant T = 10.18 top 9.6% rs1252359 rs1402128 2 5 4 NRXN1 intron_variant C = 10.17 top 9.6% rs1252359 rs62252513 3 7 8 CADM2 intron_variant T = 10.12 top 9.7% rs13885076 rs67446571 2 6 5 intron_variant G = 10.07 top 9.8% rs76715069 rs79504488 9 9 LLNC02291 intron_variant C = 10.07 top 9.8% rs2084572 rs2733500 3 <t< td=""><td>rs11772444</td><td>rs2542264</td><td>7</td><td></td><td></td><td></td><td>intron_variant</td><td>G = 10.16</td><td>top 9.6%</td></t<>	rs11772444	rs2542264	7				intron_variant	G = 10.16	top 9.6%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	12554542	7467400							
rs10992812 rs3750354 9 1 8 SYK intron_variant T = 10.18 top 9.6% rs10134692 rs57184074 4 2 2 ITPK1 intron_variant T = 10.18 top 9.6% rs10134692 rs57184074 4 2 2 ITPK1 intron_variant T = 10.18 top 9.6% rs7608187 rs1402128 2 5 4 NRXN1 intron_variant C = 10.17 top 9.6% rs11252359 . . 8553838 0,98723 .<	rs12554512	rs/46/480	9				Intron_variant	A = 10.19	top 9.6%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	rs10992812	rs3750354	9			SYK	intron variant	T = 10.18	top 9.6%
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$. 10110	
rs7608187 rs1402128 2 5 4 NRXN1 intron_variant C = 10.17 top 9.6% rs11252359 rs62252513 3 7 8 CADM2 intron_variant T = 10.12 top 9.7% rs13885076 7 8 CADM2 intron_variant T = 10.12 top 9.7% rs13885076 2 233177 0,94202 intron_variant G = 10.07 top 9.8% 7 rs67446571 2 6 5 intron_variant G = 10.07 top 9.8% rs76715069 rs79504488 4 9 9 LINC02291 intron_variant C = 10.07 top 9.8% rs2084572 rs2733500 3 7 0,98396 TBC1D5 intron_variant A = 10.05 top 9.9% rs6764919 rs9826649 3 1 4 FHIT intron_variant C = 10.04 top 9.9% rs11252359 1 4 FHIT intron_variant C = 10.04 top 9.9%	rs10134692	rs57184074	4	2	2	ITPK1	intron_variant	T = 10.18	top 9.6%
rs11252359 8 8553838 0,98723 intron_variant T = 10.12 top 9.7% rs13885076 2233177 0,94202 intron_variant T = 10.12 top 9.7% rs13885076 2233177 0,94202 intron_variant G = 10.07 top 9.8% rs76715069 rs79504488 4 9 9 LINC02291 intron_variant C = 10.07 top 9.8% rs2084572 rs2733500 3 7 0,98396 TBC1D5 intron_variant A = 10.05 top 9.9% rs6764919 rs9826649 3 1 4 FHIT intron_variant C = 10.04 top 9.9% rs11252359 5 8557854 0,99147 5					,				
5 rs62252513 3 7 8 CADM2 intron_variant T = 10.12 top 9.7% rs13885076 . . 2233177 0,94202 . <td>-</td> <td>rs1402128</td> <td>2</td> <td></td> <td></td> <td>NRXN1</td> <td>intron_variant</td> <td>C = 10.17</td> <td>top 9.6%</td>	-	rs1402128	2			NRXN1	intron_variant	C = 10.17	top 9.6%
rs13885076 2233177 0,94202 intron_variant G = 10.07 top 9.8% 7 rs67446571 2 6 5 intron_variant G = 10.07 top 9.8% rs76715069 rs79504488 4 9 9 LINC02291 intron_variant C = 10.07 top 9.8% rs2084572 rs2733500 3 7 0,98396 TBC1D5 intron_variant A = 10.05 top 9.9% rs6764919 rs9826649 3 1 4 FHIT intron_variant C = 10.04 top 9.9% rs11252359 5 8557854 0,99147 5 5 5 5 5 5		rs62252512	2		-		intron variant	T = 10 12	ton 9.7%
7 rs67446571 2 6 5 intron_variant G = 10.07 top 9.8% rs76715069 rs79504488 4 9 9 LINC02291 intron_variant C = 10.07 top 9.8% rs2084572 rs2733500 3 7 0,98396 TBC1D5 intron_variant A = 10.05 top 9.9% rs6764919 rs9826649 3 1 4 FHIT intron_variant C = 10.04 top 9.9% rs11252359 - - - - - - -		1302232313					incion_variant	1 - 10.12	lop 5.770
rs76715069 rs79504488 4 9 9 LINC02291 intron_variant C = 10.07 top 9.8% rs2084572 rs2733500 3 7 0,98396 TBC1D5 intron_variant A = 10.05 top 9.9% rs6764919 rs9826649 3 1 4 FHIT intron_variant C = 10.04 top 9.9% rs11252359 - - - - - - -		rs67446571	2				intron_variant	<u>G = 10.</u> 07	top 9.8%
rs2084572 rs2733500 3 7 0,98396 TBC1D5 intron_variant A = 10.05 top 9.9% rs6764919 rs9826649 3 1 4 FHIT intron_variant C = 10.04 top 9.9% rs11252359 8557854 0,99147			1		0,93315				
rs2084572 rs2733500 3 7 0,98396 TBC1D5 intron_variant A = 10.05 top 9.9% rs6764919 rs9826649 3 1 4 FHIT intron_variant C = 10.04 top 9.9% rs11252359 - 8557854 0,99147 -	rs76715069	rs79504488	4		9	LINC02291	intron_variant	C = 10.07	top 9.8%
rs6764919 rs9826649 3 1 4 FHIT intron_variant C = 10.04 top 9.9% rs11252359 8557854 0,99147 0 <t< td=""><td>rc2004572</td><td>rc2722500</td><td>2</td><td></td><td>0.00200</td><td></td><td>intron united</td><td>A 10.05</td><td>top 0.0%</td></t<>	rc2004572	rc2722500	2		0.00200		intron united	A 10.05	top 0.0%
rs6764919 rs9826649 3 1 4 FHIT intron_variant C = 10.04 top 9.9% rs11252359 8557854 0,99147 <t< td=""><td>152084572</td><td>152/33500</td><td>5</td><td></td><td></td><td>IRCID2</td><td>intron_variant</td><td>A = 10.05</td><td>rob a'aw</td></t<>	152084572	152/33500	5			IRCID2	intron_variant	A = 10.05	rob a'aw
rs11252359 8557854 0,99147	rs6764919	rs9826649	3		-	FHIT	intron variant	C = 10.04	top 9.9%
			-					- 10.01	I
	5	rs62250500	3	1	8	CADM2	intron_variant	T = 10.05	top 9.9%

Supplementary table 4: eQTL Phase list of top 5 most significant gSNPs.

Values for this table were chosen based on the highest Z-score. The False Discovery Rate (FDR) is zero in all five cases.

gSNP	Alleles	Gene	Z-score
rs11204771	G	CDC42SE1	47.8672
rs794375	С	PMS2P3	50.3902
rs763053	С	METTL26	35.1866
rs807478	А	COX6B1	41.4232
rs147633738	Т	CCT3	13.009

Supplementary table 5: In-Silico Phase list of top 5 most significant gSNPs.

Table shows rs-ids, candidate gene names, values were chosen based on the highest CADD score, shown for each variant allele.

gSNP	Linked_SNP	Chr	Pos_37	LD	gene	cadd	Deleteriousness
rs34811474	rs34811474	4	25407216	1	ANAPC4	A = 24.3	top 0.4%
rs141547796	rs78648104	6	50715296	0,886266	TFAP2D	C = 24.2	top 0.4%
rs113367286	rs2272095	7	140459051	0,896095	BRAF	G = 23.4	top 0.5%
rs28929474	rs28929474	14	94378610	1	FAM181A-AS1	T = 23.5	top 0.4%
rs148544378	rs148544378	18	42743602	1	RIT2	T = 23.3	top 0.5%

Supplementary table 6: eQTL Phase table of most significant missense gSNPs from eQTL analysis.

Table shows rs-ids of missense variants, their corresponding allele, predicted candidate gene name and the Z-score. The yellow color represents the failure in fining and establishing association between eQTLs and gSNP variants.

gSNP	Alleles	Gene	Z-score
rs11204771	G	CDC42SE1	47.8672
rs147633738	Т	CCT3	13.009
rs875097			
rs12714702	А	C3orf38	-14.209
rs12714702	А	C3orf38	-14.209
rs34811474	А	ANAPC4	-35.412
rs141547796			
rs794375	С	PMS2P3	50.3902
rs113367286	Т	SLC37A3	-7.3043
rs2279574	С	RP11-981P6.1	7.9902
rs28929474	Т	SERPINA1	10.0133
rs763053	С	C16orf13	35.1866
rs148544378			
rs807478	А	COX6B1	41.4232
rs11038866	G	MADD	9.3395