Association between long-term air pollution exposure and DNA methylation: the REGICOR study.

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ABSTRACT

Introduction: Limited evidence suggests that epigenetic mechanisms may partially mediate the adverse effects of air pollution on health. Our aims were to identify new genomic loci showing differential DNA methylation associated with long-term exposure to air pollution and to replicate loci previously identified in other studies.

Methods: A two-stage epigenome-wide association study was designed: 630 individuals from the REGICOR study were included in the discovery and 454 participants of the EPIC-Italy study in the validation stage. DNA methylation was assessed using the Infinium HumanMethylation450 BeadChip. NOX, NO₂, PM₁₀, PM_{2.5}, PM_{coarse}, traffic intensity and traffic load exposure were measured according to the ESCAPE protocol. A systematic review was undertaken to identify those cytosine-phosphate-guanine (CpGs) associated with air pollution in previous studies and we screened for them in the discovery study.

Results: In the discovery stage of the epigenome-wide association study, 81 unique CpGs were associated with air pollution (p-value <10⁻⁵) but none of them were validated in the replication sample. Furthermore, we identified 15 CpGs in the systematic review showing differential methylation with a p-value fulfilling the Bonferroni criteria and 1673 CpGs fulfilling the false discovery rate criteria, all of which were related to PM_{2.5} or NO₂. None of them was replicated in the discovery study, in which the top hits were located in an intergenic region on chromosome 1 (cg10893043, p-value=6.79·10⁻⁵) and in the *LRRC45* and *PXK* genes (cg05088605, p-value=2.15·10⁻⁰⁴; cg16560256, p-value= 2.23·10⁻⁰⁴).

Conclusions: Neither new genomic loci associated with long-term air pollution were identified, nor previously identified loci were replicated. Continued efforts to test this potential association are warranted.

Keywords: Air pollution, DNA methylation, Epigenome-wide association study.

LIST OF ABBREVIATIONS

WHO: World Health Organization.

REGICOR: REgistre Gironí del COR.

EPIC-Italy: The Italy center of European Prospective Investigation into Cancer and Nutrition.

450K: Infinium Human Methylation450 BeadChip.

CpG: Cytosine-phosphate-guanine.

PM₁₀: Particulate matter with an aerodynamic diameter of <10µm.

PM_{2.5}: Particulate matter with an aerodynamic diameter of <2.5µm.

PM_{coarse}: The difference between PM₁₀ and PM_{2.5}.

NO_x: Nitrogen oxides.

NO₂: Nitrogen dioxide

LUR: Land use regression.

FDR: False Discovery Rate.

1. INTRODUCTION

Exposure to air pollution remains a global threat with more than 90% of the world's population now exceeding the exposure limits proposed for particulate matter by the World Health Organization (WHO) (WHO, 2018). At the same time, a growing body of evidence consistently supports the adverse health effects of air pollution, which the same WHO report estimates to be related with 3 million premature deaths worldwide each year. However, the mechanisms by which air pollution induces these deleterious effects are not completely understood.

Epigenetics encompasses mechanisms that regulate gene expression without changing the DNA sequence, and may contribute to the relation between air pollution and health. The most studied epigenetic mechanism is DNA methylation, which is heritable but can also be modified by life-style and environmental factors. Recently, several studies have analyzed the association between air pollution and DNA methylation using a genome-wide approach, and have reported numerous loci showing differential methylation related to this exposure (Breton et al., 2016; Chi et al., 2016; de F.C. Lichtenfels et al., 2018; Goodrich et al., 2016; Gruzieva et al., 2017; Jiang et al., 2014; Panni et al., 2016; Plusquin et al., 2017; Zhong et al., 2017).

The aims of this study were both to identify new genomic loci showing differential methylation associated with long-term exposure to air pollution in a population-based study in Spain and to replicate loci previously reported in other studies.

2. METHODS

2.1. Identification of new genomic loci showing differential methylation related to long-term air pollution exposure (Aim 1)

2.1.1. Study design and population

We designed a cross-sectional epigenome-wide association study in two stages. We used the REGICOR (REgistre Gironí del COR) cohort as the discovery study and the Italy center of the European Prospective Investigation into Cancer and Nutrition (EPIC-Italy) as the replication study, followed by a meta-analysis of the results observed in both studies (REGICOR + EPIC-Italy).

As previously described (Grau et al., 2007), the REGICOR discovery sample included 648 participants randomly selected from the second wave of the REGICOR study in 2008-2013. The initial survey, performed during 2003-2005, included participants aged between 35 and 79 years, not institutionalized, and residing in Girona province (Catalonia, Spain) (Grau et al., 2007).

The EPIC-Italy replication study included 47,749 individuals in a multicenter prospective cohort recruited during 1993-1998 (Beulens et al., 2010; Palli et al., 2003). The samples selected for the present study were from two case-control studies on breast cancer (van Veldhoven et al., 2015) and colorectal cancer in Varese and Turin.

2.1.2. HumanMethylation450 BeadChip

DNA was extracted using standardized methods from peripheral blood (Puregen TM; Gentra Systems) and buffy coats (QIAGEN QIAasympyony DNA Midi Kit) in the REGICOR and EPIC-Italy studies, respectively. DNA was bisulphite-converted and the epigenome-wide methylation profiles were obtained using the Infinium HumanMethylation450 BeadChip (Illumina) (450K) to assess methylation on 485,577 cytosine-phosphate-guanine (CpGs) throughout the genome, following the Illumina Infinium HD Methylation protocol (Bibikova et al., 2011; Sandoval et al., 2011). The REGICOR samples were processed in two centers of the Spanish National Genotyping Center: the Center for Genomic Regulation in Barcelona (n=188 samples) and the Centro Nacional de Investigaciones Oncológicas in Madrid (n=460

samples). All the processed batches contained two duplicate samples used as an internal quality control. The EPIC-Italy samples were analyzed at the Human Genetics Foundation in Turin. The same well-defined pipeline was used in both studies to assess the quality control of the methylation data (Sayols-Baixeras et al., 2016).

We used the M-value as the main DNA methylation measurement (Equation 1). An M-value=0 indicates that the CpG is half methylated, a positive M-value that the CpG is more methylated than unmethylated, and a negative M-value the inverse result. We standardized the M-value by batch (Equation 2) to reduce the batch effect and other potential technical sources of variation.

Equation 1: $M_{value} = \log_2 \left(\frac{M_i + \alpha}{U_i + \alpha} \right)$
 Mi= intensity of methylated probes.
 Ui= intensity of unmethylated probes.
 $\alpha = 1$.

Equation 2: $Z = \frac{(X - \bar{X})}{\sqrt{\frac{\sum (X - \bar{X})^2}{(n-1)}}}$
 X= M-value for a specific individual.
 $\bar{X}$ = mean of M-value for a specific batch.
 n= sample size.

2.1.3. Air pollution exposure

Both the REGICOR data and the Turin component of EPIC-Italy contained particulate matter exposure [aerodynamic diameter of <10 μ m (PM₁₀), <2.5 μ m (PM_{2.5}), and PM_{coarse} (the difference between PM₁₀ and PM_{2.5})], nitrogen oxides (NO_x) and nitrogen dioxide (NO₂) measurements. For the Varese component of EPIC-Italy, only NO_x and NO₂ were available.

Both studies used the ESCAPE protocol to assess long-term exposure to air pollution (Beelen et al., 2013; Eeftens et al., 2012). As previously described, address histories for the past 10 years were collected by questionnaire, and each address was geocoded at the front-door level (Rivera et al., 2013). Using land use regression (LUR) models, 10-year weighted average exposure to NO_x and to nitrogen dioxide NO₂ for each participant were estimated (Basagaña

et al., 2013). The model's coefficient of determination for NO₂ was 0.63 for REGICOR and 70% for Turin, and for NO_x was 66% and 72%, respectively (Rivera et al., 2013).

PM₁₀, PM_{2.5} and PM_{coarse} were also assessed using LUR models. The R² of the models for REGICOR and Turin was 71% and 69% for PM₁₀, 51% and 59% for PM_{2.5}, and 71% and 58% for PM_{coarse}, respectively (Eeftens et al., 2012).

We also used traffic proximity markers as surrogates of air pollution exposure in independent analyses. For each address, we calculated the traffic intensity at the nearest street and the traffic load (sum of traffic intensity multiplied by length of road segment) for all segments in a 100 meters buffer and derived 10-year average values for each participant.

2.1.4. Other covariates

REGICOR's trained team of nurses collected relevant sociodemographic, lifestyle, and cardiovascular risk factors using standardized and validated questionnaires (Baena-Díez et al., 2010; WHO, 2000). Smoking exposure was grouped in four categories: current smoker (smoked ≥ 1 cigarette/day at the time of the visit, on average, or gave up smoking within the year of the visit); former smoker, 1-5 years (gave up smoking up to 5 years before the visit); former smokers >5 years; and never smokers. The EPIC-Italy study collected the same variables, as well as the participating center and patient's diagnostic status.

We estimated cell concentration using Houseman algorithm by means of *minfi* R package (Aryee et al., 2014; Houseman et al., 2012). In both cohorts, we also calculated surrogate variables to control for potential residual confounding, using the *sva* R package (Leek et al., 2014). These variables are directly constructed from high-throughput data, and identify and remove potential and non-measured sources of variation due to technical and biological confounders.

2.1.5. Statistical analysis

We assessed the association between air pollution and DNA methylation using robust linear regression model to reduce the effect of outliers. We used the differing air pollution exposures as independent variables and DNA methylation as the dependent variable. The models were adjusted for age, sex, smoking exposure, and cell composition (Model 1). Moreover, a second model adjusted for surrogate variables was also fitted (Model 2).

In the REGICOR discovery study, we selected for validation those CpGs with a p-value of the association below an arbitrary threshold ($p\text{-value} < 10^{-5}$) for each specific exposure, as previously described (Sayols-Baixeras et al., 2015; Jovanova et al., 2018). The results were replicated in the EPIC-Italy study using the same method and models, including also disease status and study center as additional covariates. The results for each CpG were then meta-analyzed using a random effects model. We applied Bonferroni criteria ($0.05/427,948$ CpGs; $p\text{-value} < 1.17 \cdot 10^{-07}$) and false discovery rate (FDR), using the Benjamini-Hochberg procedure, to assess the statistical significance of the associations of interest.

2.2. Replication of previously published CpGs associated with air pollution (Aim 2)

We performed a systematic review to identify relevant epigenome-wide association studies indexed in Pubmed (<https://www.ncbi.nlm.nih.gov/pubmed/>) from its inception to March 2019. We used the following search terms strategy: (methylation* [Title/Abstract]) AND (epigenome-wide [Title/Abstract] OR genome-wide [Title/Abstract] OR 450K [Title/Abstract] OR 450 [Title/Abstract] OR HumanMethylation450 [Title/Abstract]) AND ("Air pollution" [Title/Abstract]). The articles identified were manually screened by 1 reviewer (SS-B), focusing first on the title and abstract and then on the complete manuscripts to assess their appropriateness for inclusion in the review. The same author extracted the CpGs that were significantly associated with air pollution and replicated in at least one

external population or experimental studies. In case of doubts the article was evaluated by a second reviewer (RE) to achieve a consensus. The identified CpGs were then screened in the selected REGICOR cohort.

2.2.1. Statistical analysis

The same analysis strategy and methodology described above was followed for the replication. We selected as distinctive the CpGs reported as statistically significant in the original studies, based on both Bonferroni corrected p-values and false discovery rate (FDR) p-values < 0.05. We considered as replicated those CpGs that fulfilled both the Bonferroni criteria according to the number of CpGs previously discovered and the FDR p-value.

3. RESULTS

3.1. Identification of new genomic loci showing differential methylation related to air pollution (Aim 1)

3.1.1. Discovery Stage

After applying the quality control of the 450K array, we excluded 3 individuals and 57,629 CpG probes. Moreover, we removed those individuals without information on air pollution exposure (n=15). Finally, 630 individuals and 427,948 probes were included in the analysis.

The main sociodemographic and clinical characteristics and the air pollution exposures of the study participants are shown in Table 1. The Manhattan plots and q-q plots of the associations between air pollution exposures and DNA methylation are shown in Supplementary Figure 1. We identified 81 unique CpGs associated with air pollution exposures with a p-value < 10^{-5} . In model 1, 6 CpGs were associated with PM₁₀, 0 related to PM_{2.5}, 5 to PM_{coarse}, 2 to NO_x, 4 to NO₂, and 2 to traffic at the nearest street (Supplementary Table 1). In model 2, 7 CpGs were

associated with PM₁₀, 18 related to PM_{2.5}, 6 to PM_{coarse}, 28 to NO_x, 32 to NO₂, and 9 to traffic at the nearest street (Supplementary Table 2).

3.1.2. Validation Stage and Meta-analysis

After applying a similar quality control of the 450K array, we included all 81 CpGs selected for replication and we excluded 5 individuals. Moreover, we removed those individuals without information on confounder variables (n=15) and air pollution exposure (n=61). Finally, 454 individuals were included in the analysis of NO traits (Turin and Varese) and 297 in the analysis of PM traits (Turin). The main characteristics and air pollution exposures of the EPIC-Italy participants are shown in Table 1. The associations between air pollution and the selected CpGs in this analysis are shown in Supplementary Table 1 and 2.

The results of the meta-analysis of the REGICOR and the EPIC-Italy studies are shown in Supplementary Table 1 and 2. None of the selected CpGs was validated in the joint analysis.

3.1.3. Statistical power

The regression coefficient values (effect size) that we could detect as statistically significant in the meta-analysis, accepting an alpha risk of $1.17 \cdot 10^{-07}$ in a two-sided test and with an 80% power, are shown in Supplementary Table 1 and 2.

3.2. Replication of the previously published CpGs associated with air pollution (Aim 2)

We initially identified 31 manuscripts (Abraham et al., 2018; Anto et al., 2017; Breton et al., 2016; Chi et al., 2016; Christensen and Marsit, 2011; Commodore et al., 2019; de F.C. Lichtenfels et al., 2018; Gao et al., 2019; Goodrich et al., 2016; Gref et al., 2017; Gruzieva et al., 2017; Holloway et al., 2012; Hong and Wang, 2014; Janssen et al., 2013; Jeong et al.,

2019; Jiang et al., 2017, 2014; Ladd-Acosta et al., 2019; Lee et al., 2019; Li et al., 2018; Mostafavi et al., 2017; Nwanaji-Enwerem et al., 2018; Panni et al., 2016; Plusquin et al., 2017; Shukla et al., 2019; Sominen et al., 2016; van Dongen et al., 2018; Wang et al., 2012; Zhang et al., 2017, 2018; Zhong et al., 2017) based on the search terms and after reading the full manuscripts we selected 17 studies (Abraham et al., 2018; Breton et al., 2016; Chi et al., 2016; Commodore et al., 2019; de F.C. Lichtenfels et al., 2018; Gao et al., 2019; Goodrich et al., 2016; Gruzieva et al., 2017; Jiang et al., 2014; Ladd-Acosta et al., 2019; Lee et al., 2019; Li et al., 2018; Mostafavi et al., 2018; Panni et al., 2016; Plusquin et al., 2017; Zhang et al., 2018; Zhong et al., 2017). Finally, we selected CpGs from two manuscripts. A total of 15 CpGs showing differential methylation in relation to PM_{2.5} from two manuscripts after correcting for Bonferroni criteria (Li et al., 2018; Panni et al., 2016). Three of these CpGs could not be analyzed in the REGICOR study as they did not pass the quality control, and none of the others was replicated (Supplementary Table 3).

In a secondary analysis, we included 1,673 CpGs from three manuscripts (Gruzieva et al., 2017; Li et al., 2018; Panni et al., 2016) fulfilling a FDR $p\text{-value} < 0.05$. Among all the selected FDR results, 195 CpGs could not be analyzed in our study as they did not pass the quality control and 14 because they weren't available in the 450k array. We did not replicate any of the 1,464 CpGs analyzed (Table 2 and Supplementary Table 3). In the REGICOR study, the top hits were located in an intergenic region on chromosome 1 (cg10893043, $p\text{-value} = 6.79 \cdot 10^{-5}$) and in the *LRRC45* and *PXK* genes (cg05088605, $p\text{-value} = 2.15 \cdot 10^{-04}$; cg16560256, $p\text{-value} = 2.23 \cdot 10^{-04}$) for PM_{2.5}.

4. DISCUSSION

This population-based and cross-sectional study did not identify new loci or replicate loci previously identified as showing differential methylation related to long-term exposure to air pollution.

The lack of positive results in our study should be interpreted with caution and some methodological issues must be considered. First, our study is underpowered to detect small effect size associations. The statistical power of our study was estimated (Supplementary Table 1 and 2) and is similar to previous studies. Second, we defined strict criteria to consider an association as statistically significant based on the Bonferroni or the false discovery rate multiple comparisons correction. Third, the exposure to air pollution and its variability is lower than that observed in other studies, limiting our capability to identify real associations. Fourth, the exposure assessment was estimated using land use regression models. Although this methodology is commonly used and we followed the ESCAPE protocol (Beelen et al., 2013; Eeftens et al., 2012), using validated exposure estimations (Basagaña et al., 2013), some exposure misclassification could still be present, reducing the power to detect the association of interest in our study. Fifth, the replication was carried in a case-control study that may have a different methylation pattern. Sixth, we estimated long-term exposure to air pollution whereas other studies have analyzed the association between short-term exposure and DNA methylation, thus, comparison may be limited given that response patterns may indeed vary across time domains. Gruzieva et al analyzed gestational NO₂ exposure and DNA methylation at birth (cord blood), 4 years and 8 years of age (Gruzieva et al., 2017). Li et al designed a crossover experimental studies to assess the effect of 9 days of controlled exposure to high and low PM exposure (Li et al., 2018). However, in studies that analyzed several time exposures, the longer the exposure the higher the number of loci showing differential methylation (Panni et al., 2016). Seventh, the great heterogeneity between the three studies and ours in terms of sample size, age of the participants (children, young individuals, and

adult population), design (experimental vs observational), and air pollution exposure of interest (PM, NO₂) could also explain the poor replication of previous findings. Eighth, we have also to consider the cross-sectional design of our study that limits the analysis of changes in air pollution exposure and changes in DNA methylation over time. Finally, we could not adjust for potential relevant variables such as indoor air pollution and second-hand smoking.

Despite these limitations that should be considered, we would highlight some of the results observed in this study. In the discovery effort, we identified 7 CpGs associated with PM₁₀, 18 related to PM_{2.5}, 6 with PM_{coarse}, 28 with NO_x, 32 with NO₂, and 9 related to traffic at the nearest street in the REGICOR study. However, none of them were validated in the EPIC-Italy study. In our effort to replicate previous findings, we identified one locus located in an intergenic region on chromosome 1 (cg10893043, p-value=6.79·10⁻⁵) as potentially associated with PM_{2.5}. The cg10893043 is close to the *CDKN2C* gene. The protein encoded by this gene is a member of the INK4 family of cyclin-dependent kinase inhibitors and regulates cell growth by controlling cell-cycle G1 progression (Cánepa et al., 2007). Some studies have shown that the expression of this gene inhibits the growth of human cells in animal models and have suggested a potential role in tumorigenesis (van Veelen et al., 2009). Among the strengths of our study, we would mention the standardized methodology following the ESCAPE protocol that was consistently used to assess air pollution exposure. This methodology was validated in our population and was used to assess long-term air pollution exposure. Moreover, we applied a commonly used methodology to assess DNA methylation at the genome-wide level and a standardized methodology with both a discovery and an independent validation population.

5. CONCLUSIONS

The results of our study are negative as we did not identify any new genomic loci associated with long-term air pollution and we did not replicate any previously identified loci. However, these negative results should be interpreted with caution. New joint efforts, increasing the statistical power of the analysis and the variability of the exposure to air pollution, and considering both short- and long-term exposure, are warranted to assess the potential association between air pollution and DNA methylation.

DECLARATIONS

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Ethics approval and consent to participate

All participants in both studies (REGICOR and EPIC-Italy) signed an informed consent; the studies were approved by the local ethic committees (PSMAR CEIC- 2012/4729/I) and followed national legislation and the Declaration of Helsinki criteria.

Availability of data and material

The datasets used and/or analyzed during the current study are available from the corresponding author [RE] on request.

Competing interests

The authors declare that they have no competing interests.

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Table 1: Main characteristics of the participants included in the discovery and validation studies.

	REGICOR N=630	EPIC-Italy N=454
Age, years*	63.3 (11.7)	54.2 (7.1)
Sex, female, n (%)	323 (51.3)	323 (71)
PM10, µg/m3†	29.9 [27.5; 32.7]	46.91 [38.24; 53.23]
PMcoarse, µg/m3†	14.1 [13.3; 15.7]	16.75 [10.88; 20.65]
PM2.5, µg/m3†	15.0 [13.5; 15.9]	30.95 [26.74; 32.73]
PM2.5abs, µg/m3†	2.40 [1.90; 2.91]	3.38 [2.34; 3.64]
NoX, µg/m3†	61.7 [42.5; 72.8]	92.83 [34.46; 131.00]
NO2, µg/m3†	36.9 [24.3; 42.6]	50.00 [22.26; 67.92]
Traffic near, m†	1725 [862; 7000]	4029 [0; 45012]
Total Cholesterol, mg/dL*	209 (36.6)	357 (136.2)
LDL Cholesterol, mg/dL*	135 (32.4)	-
HDL Cholesterol, mg/dL*	53.1 (12.4)	-
Triglycerides, mg/dL†	89.0 [67.0;121]	-
SBP, mmHg*	131 (18.2)	135.8 (19.4)
DBP, mmHg*	76.0 (9.93)	84.3 (10.7)
Hypertension, n (%)	297 (47.3)	119 (26.2)
Diabetes, n (%)	62 (9.89)	7 (1.54)
Smoking status, n (%)		
Current smokers	105 (16.7)	234 (51.5)
Former 1-5 years	30 (4.76)	-
Former >5 years	159 (25.2)	-
Former	-	111 (24.4)
Never smokers	336 (53.3)	109 (24.0)
Cholesterol Treatment, n (%)	151 (24.0)	-
Diabetes Treatment, n (%)	43 (6.86)	-
Blood pressure treatment, n (%)	196 (31.3)	-
Breast cancer cases, n (%)	-	82 (18.1)
Colorectal cancer cases, n (%)	-	133 (29.3)
Controls, n (%)	-	239 (52.6)

PM10: Particulate matter aerodynamic diameter of <10µm; PMcoarse: Particulate matter difference between PM10 and PM2.5; PM2.5: Particulate matter aerodynamic diameter of <2.5µm; PM2.5abs: Absorbance of PM2.5; NoX: Nitrogen oxides; NO2: Nitrogen dioxide; SBP: Systolic blood pressure; DBP: Diastolic blood pressure.

*Mean (Standard Deviation); † Median (Interquartile range)

Table 2: Top hits of the replication of previously published CpGs associated with NO₂ (Nitrogen dioxide) and PM_{2.5} (Particulate matter aerodynamic diameter of <2.5µm) exposures.

CpG	Chr.	Pos.	Gene	Coef.	SE	P value	FDR
cg24172570	7	27561178	<i>HIBADH</i>	4.92E-04	1.91E-03	7.97E-01	9.30E-01
cg08973675	10	101380289	<i>SLC25A28</i>	-7.67E-04	2.74E-03	7.80E-01	9.30E-01
cg12283362	19	5709149	<i>LONPI</i>	-1.88E-04	2.15E-03	9.30E-01	9.30E-01
CpG	Chr.	Pos.	Gene	Coef.	SE	P value	FDR
cg10893043	1	51442760	<i>Intergenic</i>	4.30E-02	1.08E-02	6.79E-05	1.12E-01
cg05088605	17	79987813	<i>LRRC45</i>	-4.15E-02	1.12E-02	2.15E-04	1.23E-01
cg16560256	3	58328580	<i>PXK</i>	-4.39E-02	1.19E-02	2.23E-04	1.23E-01

Chr.: Chromosome; Pos.: Position; Coef.: Coefficient; SE: Standard error; FDR: False

Discovery Rate.

Supplementary Table 1: Results of the main epigenome-wide association study using model 1 (adjusted for age, sex, smoking exposure, and cell composition).

NO ₂																													
CpG	CHR	Position	Gene	REGICOR			EPIC-Italy			Random Meta-analysis				Heterogeneity		Power													
				Coef	SE	Pval	Coef	SE	Pval	Coef	SE	Pval	FDR	I ²	Pval														
cg10943458	3	120627085	STXBP5L	-9,42E-03	2,10E-03	7,22E-06	-1,10E-03	5,64E-04	5,16E-02	-2,92E-03	2,16E-02	8,92E-01	9,47E-01	0,932	1,29E-04	0,133													
cg25500080	5	140346199	PCDHAC2;	-8,06E-03	1,73E-03	3,22E-06	1,94E-04	3,78E-04	6,08E-01	-1,36E-03	1,82E-02	9,40E-01	9,47E-01	0,954	3,19E-06	0,112													
			PCDHA7;																										
			PCDHA12;																										
			PCDHA6;																										
			PCDHA10;																										
			PCDHA4;																										
			PCDHA11;																										
			PCDHA8;																										
cg18236477	13	26043066	ATP8A2	-1,05E-02	2,35E-03	7,20E-06	5,82E-05	2,31E-04	8,01E-01	-1,06E-03	1,59E-02	9,47E-01	9,47E-01	0,95	7,10E-06	0,098													
			PPP1R14A														-8,22E-03	1,86E-03	9,37E-06	1,78E-04	3,94E-04	6,51E-01	-1,37E-03	1,87E-02	9,41E-01	9,47E-01	0,949	9,50E-06	0,115
cg02571816	19	38747378																											
NO _x																													
CpG	CHR	Position	Gene	REGICOR			EPIC-Italy			Random Meta-analysis				Heterogeneity		Power													
				Coef	SE	Pval	Coef	SE	Pval	Coef	SE	Pval	FDR	I ²	Pval														
cg10943458	3	120627085	STXBP5L	-4,75E-03	1,05E-03	6,46E-06	-7,17E-04	2,57E-04	5,20E-03	-1,52E-03	1,45E-02	9,17E-01	9,51E-01	0,928	1,98E-04	0,089													
			PCDHAC2;	-4,08E-03	8,07E-04	4,25E-07	1,25E-05	1,85E-04	9,46E-01	-7,73E-04	1,25E-02	9,51E-01	9,51E-01	0,959	7,65E-07	0,077													
			PCDHA7;																										
			PCDHA12;																										
			PCDHA6;																										
			PCDHA10;																										
			PCDHA4;																										
			PCDHA11;																										
			PCDHA8;																										
			PCDHA1;	-4,08E-03	8,07E-04	4,25E-07	1,25E-05	1,85E-04	9,46E-01	-7,73E-04	1,25E-02	9,51E-01	9,51E-01	0,959	7,65E-07	0,077													
			PCDHA9;																										
			PCDHA13;																										
			PCDHA5;																										
			PCDHA6;																										
			PCDHA1;																										
			PCDHA3;																										
PM10																													
CpG	CHR	Position	Gene	REGICOR			EPIC-Italy			Random Meta-analysis				Heterogeneity		Power													
				Coef	SE	Pval	Coef	SE	Pval	Coef	SE	Pval	FDR	I ²	Pval														
cg19241927	1	56333494	NA	3,88E-02	8,46E-03	4,34E-06	4,29E-03	2,43E-03	7,77E-02	1,29E-02	4,74E-02	7,85E-01	8,89E-01	0,935	8,59E-05	0,291													
cg09504320	1	157164796	NA	-3,55E-02	7,58E-03	2,82E-06	-6,89E-04	1,35E-03	6,11E-01	-7,35E-03	3,95E-02	8,52E-01	8,89E-01	0,951	6,16E-06	0,243													
cg07745624	4	21950952	KCNIP4	-3,17E-02	6,98E-03	5,38E-06	4,19E-04	1,00E-03	6,76E-01	-4,94E-03	3,53E-02	8,89E-01	8,89E-01	0,952	5,05E-06	0,217													
cg11538641	6	100902258	SIM1	-3,35E-02	7,47E-03	7,12E-06	-2,57E-04	1,47E-03	8,61E-01	-6,91E-03	4,00E-02	8,63E-01	8,89E-01	0,948	1,23E-05	0,246													
cg04671329	10	105614985	SH3PXD2A	-4,20E-02	9,00E-03	3,00E-06	-5,73E-04	1,26E-03	6,50E-01	-7,82E-03	4,14E-02	8,50E-01	8,89E-01	0,952	5,06E-06	0,254													
cg05664472	11	2444788	TRPM5	3,73E-02	8,17E-03	4,95E-06	1,18E-03	1,16E-03	3,10E-01	7,27E-03	3,85E-02	8,50E-01	8,89E-01	0,948	1,20E-05	0,236													
PM2.5																													
CpG	CHR	Position	Gene	REGICOR			EPIC-Italy			Random Meta-analysis				Heterogeneity		Power													
				Coef	SE	Pval	Coef	SE	Pval	Coef	SE	Pval	FDR	I ²	Pval														
No CpG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-													
PMcoarse																													
CpG	CHR	Position	Gene	REGICOR			EPIC-Italy			Random Meta-analysis				Heterogeneity		Power													
				Coef	SE	Pval	Coef	SE	Pval	Coef	SE	Pval	FDR	I ²	Pval														
cg13176979	6	79944654	HMGNC3	4,99E-02	1,60E-02	1,78E-03	-4,09E-04	1,13E-03	7,17E-01	5,47E-03	4,47E-02	9,03E-01	9,03E-01	0,899	1,67E-03	0,274													
cg15356660	7	23456368	IGF2BP3	-6,61E-02	1,80E-02	2,37E-04	-2,00E-03	2,48E-03	4,19E-01	-1,35E-02	5,98E-02	8,21E-01	9,03E-01	0,92	4,13E-04	0,367													
cg08224212	11	34196093	ABTB2	-5,50E-02	1,74E-02	1,61E-03	2,34E-04	1,12E-03	8,34E-01	-6,22E-03	4,69E-02	8,94E-01	9,03E-01	0,9	1,57E-03	0,288													
cg22460206	19	37861707	ZNF527	6,35E-02	1,76E-02	3,14E-04	-3,18E-03	3,73E-03	3,94E-01	1,20E-02	6,69E-02	8,58E-01	9,03E-01	0,927	2,14E-04	0,411													
cg18394527	20	43594843	STK4	4,38E-02	1,54E-02	4,45E-03	-1,01E-04	1,71E-03	9,53E-01	5,87E-03	4,70E-02	9,01E-01	9,03E-01	0,875	4,60E-03	0,289													
Trafnear																													
CpG	CHR	Position	Gene	REGICOR			EPIC-Italy			Random Meta-analysis				Heterogeneity		Power													
				Coef	SE	Pval	Coef	SE	Pval	Coef	SE	Pval	FDR	I ²	Pval														
cg21920221	5	171612889	STK10	-2,13E-05	4,68E-06	5,45E-06	-7,26E-07	9,83E-07	4,60E-01	-4,30E-06	9,01E-04	9,96E-01	9,97E-01	0,946	1,73E-05	0,006													
cg02414034	17	5185283	RABEP1	-2,47E-05	5,10E-06	1,28E-06	4,80E-07	7,92E-07	5,78E-01	-2,94E-06	8,28E-04	9,97E-01	9,97E-01	0,958	1,11E-06	0,005													
CHR: Chromosome; Coef: Coefficient; Comp.: Comparison; SE: Standard Error; Pval: P value; FDR: False Discovery Rate; NA: Not available.																													

CHR: Chromosome; Coef: Coefficient; Comp.: Comparison; SE: Standard Error; Pval: P value; FDR: False Discovery Rate; NA: Not available.

Supplementary Table 2: Results of the main epigenome-wide association study using model 2 (adjusted for age, sex, smoking exposure, cell composition, and surrogate variables).

NO ₂																
CpG	CHR	Position	Gene	REGICOR			EPIC-Italy			Random Meta-analysis				Heterogeneity		Power
				Coef	SE	Pval	Coef	SE	Pval	Coef	SE	Pval	FDR	I ²	Pval	
cg0430911	1	3691439	OSCP1	-4.33E-03	8.96E-04	1.38E-06	1.65E-04	1.01E-04	1.02E-01	-3.24E-04	9.93E-03	9.74E-01	9.74E-01	0.96	6.33E-07	0.061
cg22228439	1	46766431	LRR41	-3.81E-03	8.61E-04	9.81E-06	8.39E-05	1.02E-04	4.11E-01	-3.51E-04	9.85E-03	9.72E-01	9.74E-01	0.95	7.21E-06	0.06
cg25076881	1	159409836	OR10J1	6.76E-03	1.34E-03	4.15E-07	-3.42E-04	1.58E-04	3.02E-02	4.97E-04	1.27E-02	9.69E-01	9.74E-01	0.964	1.28E-07	0.078
cg2291058	1	207277466	C4BP4	-3.94E-03	7.86E-04	5.46E-07	3.11E-05	1.52E-04	8.38E-01	-6.35E-04	1.15E-02	9.56E-01	9.74E-01	0.959	7.17E-07	0.071
cg02477458	1	226112258	PYCR2	7.85E-03	1.75E-03	7.57E-06	4.79E-07	2.13E-04	9.98E-01	9.40E-04	1.46E-02	9.49E-01	9.74E-01	0.949	8.83E-06	0.09
cg1890989	2	26388502	NA	7.15E-03	1.57E-03	5.42E-06	-9.04E-05	2.38E-04	7.04E-01	9.33E-04	1.50E-02	9.50E-01	9.74E-01	0.952	5.28E-06	0.092
cg02012974	3	66492992	LRIG1	-3.77E-03	8.37E-04	6.76E-06	6.27E-06	1.35E-04	9.63E-01	-5.38E-04	1.10E-02	9.61E-01	9.74E-01	0.95	8.55E-06	0.068
cg10943458	3	120627085	STXBPL5L	-9.29E-03	2.09E-03	8.87E-06	-1.10E-03	5.64E-04	5.16E-02	-2.89E-03	2.16E-02	8.93E-01	9.74E-01	0.93	1.55E-04	0.132
cg22777326	4	13546316	NKX3-2	-8.96E-03	1.92E-03	3.07E-06	-1.25E-04	2.15E-04	5.60E-01	-1.13E-03	1.49E-02	9.40E-01	9.74E-01	0.952	4.82E-06	0.092
cg04747180	4	39116218	KLHL5	-3.75E-03	7.69E-04	1.05E-06	1.06E-05	1.35E-04	9.38E-01	-5.72E-04	1.10E-02	9.58E-01	9.74E-01	0.957	1.43E-06	0.067
cg11193767	4	83930905	LINS4	-4.37E-03	8.53E-04	2.98E-07	-1.40E-04	1.12E-04	2.13E-01	-6.60E-04	1.03E-02	9.49E-01	9.74E-01	0.959	8.75E-07	0.063
cg25500080	5	140346199	V4: PCDHA11;	-8.19E-03	1.63E-03	4.96E-07	1.94E-04	3.78E-04	6.08E-01	-1.47E-03	1.82E-02	9.36E-01	9.74E-01	0.96	5.34E-07	0.112
cg05783854	5	140346403	V4: PCDHA11;	-7.93E-03	1.76E-03	6.37E-06	2.35E-04	2.72E-04	3.88E-01	-9.51E-04	1.61E-02	9.53E-01	9.74E-01	0.953	4.38E-06	0.099
cg01323964	7	65219171	ORA22; CC76	-5.01E-03	9.92E-04	4.47E-07	2.25E-04	1.82E-04	2.17E-01	-6.27E-04	1.28E-02	9.61E-01	9.74E-01	0.963	2.13E-07	0.079
cg04598292	7	158495856	NCAPG2	-8.82E-03	1.26E-03	3.69E-06	-1.70E-04	2.12E-04	4.22E-01	-1.03E-03	1.39E-02	9.41E-01	9.74E-01	0.949	9.40E-06	0.085
cg02469095	8	9960921	OSR2	-7.67E-03	1.73E-03	9.54E-06	-2.45E-04	3.55E-04	4.89E-01	-1.57E-03	1.77E-02	9.29E-01	9.74E-01	0.943	2.69E-05	0.109
cg13787987	10	50970591	OGDHL	-8.99E-03	1.89E-03	5.70E-06	-2.74E-04	3.08E-04	3.74E-01	-1.52E-03	1.70E-02	9.29E-01	9.74E-01	0.947	1.45E-05	0.104
cg23815853	12	48147034	RAPGEF3	-3.85E-03	8.53E-04	6.55E-06	1.14E-04	1.56E-04	4.65E-01	-5.18E-04	1.17E-02	9.65E-01	9.74E-01	0.952	4.98E-06	0.072
cg01183510	12	66582582	IRAK3	-4.00E-03	8.77E-04	5.06E-06	2.49E-04	1.55E-04	1.08E-01	-4.13E-04	1.17E-02	9.72E-01	9.74E-01	0.956	1.82E-06	0.072
cg04682193	12	121867725	KDM2B	-3.94E-03	8.83E-04	7.92E-06	1.37E-04	1.36E-04	3.16E-01	-4.31E-04	1.11E-02	9.69E-01	9.74E-01	0.952	4.92E-06	0.068
cg18236477	13	26043066	PTRAA2	-9.93E-03	1.94E-03	3.19E-07	5.82E-05	2.31E-04	8.01E-01	-1.17E-03	1.56E-02	9.40E-01	9.74E-01	0.962	3.29E-07	0.096
cg04118119	13	47371987	ESD	-4.50E-03	9.34E-04	1.42E-06	1.45E-04	1.38E-04	2.93E-01	-4.86E-04	1.13E-02	9.66E-01	9.74E-01	0.959	8.49E-07	0.07
cg01945427	14	90729278	PSMC1	7.68E-03	1.67E-03	4.42E-06	4.48E-06	3.63E-04	9.90E-01	1.44E-03	1.78E-02	9.36E-01	9.74E-01	0.95	7.34E-06	0.109
cg01741756	14	94780400	SERPINA5	5.96E-03	1.34E-03	9.24E-06	-1.72E-04	1.66E-04	3.00E-01	5.58E-04	1.27E-02	9.65E-01	9.74E-01	0.951	5.96E-06	0.078
cg11357013	15	73588054	NEO1	-4.32E-03	8.86E-04	1.11E-06	2.92E-04	1.40E-04	3.73E-02	-3.70E-04	1.14E-02	9.74E-01	9.74E-01	0.962	2.86E-07	0.077
cg08576185	16	2055684	ZNF598	-6.21E-03	1.27E-03	1.07E-06	4.30E-05	1.60E-04	7.89E-01	-7.19E-04	1.25E-02	9.54E-01	9.74E-01	0.958	1.09E-06	0.077
cg08154963	17	33426885	RAD51L3	-3.81E-03	8.28E-04	4.19E-06	7.22E-06	1.12E-04	9.49E-01	-4.70E-04	1.02E-02	9.63E-01	9.74E-01	0.952	4.91E-06	0.063
cg20938699	17	35296966	LHX1	-9.77E-03	2.19E-03	8.20E-06	-2.39E-04	3.63E-04	5.11E-01	-1.71E-03	1.85E-02	9.27E-01	9.74E-01	0.946	1.77E-05	0.114
cg25730408	18	46061606	NA	-5.76E-03	1.29E-03	7.60E-06	-1.58E-04	1.60E-04	3.26E-01	-8.23E-04	1.24E-02	9.47E-01	9.74E-01	0.946	1.56E-05	0.076
cg00775818	19	2431171	LMNB2	-4.28E-03	9.38E-04	4.98E-06	2.21E-04	1.44E-04	1.26E-01	-4.09E-04	1.15E-02	9.72E-01	9.74E-01	0.956	2.08E-06	0.071
cg16452651	21	35016873	ITSN1	-4.22E-03	7.42E-04	1.30E-08	1.46E-04	1.37E-04	2.85E-01	-5.65E-04	1.11E-02	9.59E-01	9.74E-01	0.97	7.24E-09	0.068
cg23312431	21	45773997	TRPM2	-4.20E-03	8.85E-04	2.10E-06	2.20E-04	1.24E-04	7.54E-02	-3.53E-04	1.08E-02	9.74E-01	9.74E-01	0.959	7.64E-07	0.066

NO _x																
CpG	CHR	Position	Gene	REGICOR			EPIC-Italy			Random Meta-analysis				Heterogeneity		Power
				Coef	SE	Pval	Coef	SE	Pval	Coef	SE	Pval	FDR	I ²	Pval	
cg0430911	1	3691439	OSCP1	-2.27E-03	4.65E-04	1.01E-06	9.34E-05	4.08E-05	2.21E-02	-1.08E-04	6.31E-03	9.86E-01	9.86E-01	0.961	3.95E-07	0.039
cg25076881	1	159409836	OR10J1	3.07E-03	6.78E-04	5.67E-06	-1.61E-04	8.10E-05	4.71E-02	2.01E-04	8.74E-03	9.82E-01	9.86E-01	0.956	2.12E-06	0.054
cg2291058	1	207277466	C4BP4	-1.95E-03	3.98E-04	9.19E-07	3.10E-05	6.68E-05	6.43E-01	-2.60E-04	7.66E-03	9.73E-01	9.86E-01	0.959	8.78E-07	0.047
cg02012974	3	66492992	LRIG1	-1.91E-03	4.31E-04	9.17E-06	-1.47E-05	6.60E-05	8.23E-01	-2.71E-04	7.65E-03	9.72E-01	9.86E-01	0.947	1.35E-05	0.047
cg27317909	3	77087684	NA	-3.90E-03	8.63E-04	6.24E-06	4.97E-05	1.10E-04	6.51E-01	-4.19E-04	1.02E-02	9.67E-01	9.86E-01	0.951	5.65E-06	0.062
cg22777326	4	13546316	NKX3-2	-4.40E-03	9.82E-04	7.24E-06	-7.67E-05	1.02E-04	4.51E-01	-5.12E-04	9.98E-03	9.59E-01	9.86E-01	0.948	1.16E-05	0.061
cg04747180	4	39116218	KLHL5	-1.85E-03	3.88E-04	1.75E-06	3.47E-05	6.28E-05	5.80E-01	-2.34E-04	7.44E-03	9.75E-01	9.86E-01	0.957	1.53E-06	0.046
cg11193767	4	83930905	LINS4	-2.20E-03	4.32E-04	3.48E-07	-4.81E-05	5.39E-05	3.72E-01	-2.94E-04	7.05E-03	9.67E-01	9.86E-01	0.959	7.59E-07	0.043
cg24539910	4	164253470	NPY1R	-4.17E-03	9.32E-04	7.76E-06	-9.24E-05	1.37E-04	5.01E-01	-6.38E-04	1.12E-02	9.55E-01	9.86E-01	0.947	1.52E-05	0.069
cg25500080	5	140346199	V4: PCDHA11;	-4.02E-03	7.73E-04	2.00E-07	1.25E-05	1.85E-04	9.46E-01	-7.88E-04	1.24E-02	9.50E-01	9.86E-01	0.961	3.94E-07	0.076
cg05783854	5	140346403	V4: PCDHA11;	-4.05E-03	8.89E-04	5.34E-06	8.47E-05	1.26E-04	5.01E-01	-4.52E-04	1.08E-02	9.67E-01	9.86E-01	0.953	4.22E-06	0.066
cg26560110	6	28603161	NA	-3.69E-03	8.19E-04	6.59E-06	5.84E-05	1.42E-04	6.81E-01	-5.14E-04	1.12E-02	9.63E-01	9.86E-01	0.951	6.47E-06	0.069
cg05314350	6	28874702	TRIM27	-2.20E-03	4.85E-04	5.56E-06	4.63E-05	8.61E-05	5.91E-01	-3.00E-04	8.66E-03	9.72E-01	9.86E-01	0.952	4.95E-06	0.053
cg05860220	6	99632147	NA	-3.45E-03	7.70E-04	7.62E-06	-7.11E-05	1.19E-04	5.49E-01	4.15E-04	1.04E-02	9.68E-01	9.86E-01	0.951	6.34E-06	0.064
cg01323964	7	65219171	ORA22; CC76	-2.52E-03	4.88E-04	2.43E-07	5.39E-05	8.03E-05	5.02E-01	-3.20E-04	8.45E-03	9.70E-01	9.86E-01	0.963	1.95E-07	0.052
cg04598292	7	158495856	NCAPG2	-2.98E-03	6.50E-04	4.50E-06	-9.92E-05	9.79E-05	3.11E-01	-4.88E-04						

Supplementary Table 3: Replication results of the previously published CpGs associated with NO₂ and PM_{2.5} exposures.

NO2							
CpG	Chromosome	Position	Gene	Coef	SE	Pvalue	FDR
cg24172570	7	27561178	<i>HIBADH</i>	4,92E-04	1,91E-03	7,97E-01	9,30E-01
cg08973675	10	101380289	<i>SLC25A28</i>	-7,67E-04	2,74E-03	7,80E-01	9,30E-01
cg12283362	19	5709149	<i>LONP1</i>	-1,88E-04	2,15E-03	9,30E-01	9,30E-01
PM25							
CpG	Chromosome	Position	Gene	Coef	SE	Pvalue	FDR
cg10490668	1	987502	<i>AGRN</i>	-1,37E-03	1,65E-02	9,34E-01	9,94E-01
cg15207999	1	1021210	<i>C1orf159</i>	1,16E-02	1,80E-02	5,19E-01	9,70E-01
cg05655247	1	1065028	NA	3,33E-03	1,25E-02	7,90E-01	9,90E-01
cg03058163	1	1153338	<i>SDF4</i>	-1,44E-03	1,02E-02	8,88E-01	9,94E-01
cg22225577	1	1221823	<i>SCNN1D</i>	-3,76E-03	1,71E-02	8,25E-01	9,94E-01
cg15901950	1	1256513	<i>CPSF3L</i>	-5,33E-03	1,54E-02	7,30E-01	9,82E-01
cg16174225	1	1268469	<i>TAS1R3</i>	-1,49E-02	1,80E-02	4,09E-01	9,70E-01
cg15633699	1	1356728	<i>LOC441869</i>	1,09E-02	1,26E-02	3,83E-01	9,70E-01
cg04871460	1	1991521	<i>PRKCZ</i>	-8,63E-03	9,79E-03	3,78E-01	9,70E-01
cg25976434	1	2008510	<i>PRKCZ</i>	-1,91E-02	1,22E-02	1,16E-01	9,39E-01
cg02361803	1	2014371	<i>PRKCZ</i>	1,33E-02	1,91E-02	4,85E-01	9,70E-01
cg20975074	1	2066430	<i>PRKCZ</i>	4,66E-03	1,19E-02	6,95E-01	9,82E-01
cg19870743	1	2097158	<i>PRKCZ</i>	1,45E-02	1,35E-02	2,82E-01	9,70E-01
cg03395993	1	2109923	<i>PRKCZ</i>	8,19E-03	1,39E-02	5,55E-01	9,70E-01
cg18934822	1	2191402	<i>SKI</i>	1,28E-02	2,02E-02	5,25E-01	9,70E-01
cg04619852	1	2234433	<i>SKI</i>	-5,40E-03	1,21E-02	6,56E-01	9,82E-01
cg15644634	1	2757162	NA	1,34E-03	1,60E-02	9,34E-01	9,94E-01
cg16115688	1	2819993	NA	2,11E-02	1,15E-02	6,69E-02	9,19E-01
cg05348888	1	2937278	<i>ACTRT2</i>	-1,62E-04	1,16E-02	9,89E-01	9,97E-01
cg25008795	1	2992414	<i>PRDM16</i>	-1,54E-02	1,62E-02	3,41E-01	9,70E-01
cg21107944	1	3001100	<i>PRDM16</i>	-1,77E-02	1,35E-02	1,90E-01	9,47E-01
cg24335751	1	3182620	<i>PRDM16</i>	-1,79E-02	1,35E-02	1,84E-01	9,47E-01
cg00329272	1	3191481	<i>PRDM16</i>	2,10E-02	1,11E-02	5,71E-02	9,19E-01
cg26000536	1	3276535	<i>PRDM16</i>	1,45E-02	1,37E-02	2,91E-01	9,70E-01
cg01065697	1	3320738	<i>PRDM16</i>	1,07E-03	1,16E-02	9,26E-01	9,94E-01
cg21821103	1	3563485	<i>WDR8</i>	-9,63E-03	1,31E-02	4,62E-01	9,70E-01
cg23953592	1	4219116	NA	1,72E-03	1,33E-02	8,97E-01	9,94E-01
cg16176837	1	5919155	NA	-8,87E-03	1,18E-02	4,52E-01	9,70E-01
cg09976670	1	5934941	<i>NPHP4</i>	-1,42E-02	1,40E-02	3,11E-01	9,70E-01
cg16361915	1	6132185	<i>KCNAB2</i>	-2,24E-02	1,24E-02	7,22E-02	9,19E-01
cg00087511	1	9069875	<i>SLC2A7</i>	1,59E-03	1,36E-02	9,07E-01	9,94E-01
cg24305710	1	9669053	<i>TMEM201</i>	-2,52E-02	1,40E-02	7,11E-02	9,19E-01
cg02787675	1	9686058	NA	-1,41E-02	1,26E-02	2,63E-01	9,70E-01
cg24551579	1	9884600	<i>CLSTN1</i>	-9,86E-03	1,32E-02	4,54E-01	9,70E-01
cg14037769	1	9895799	NA	-1,50E-02	1,16E-02	1,97E-01	9,56E-01
cg06816087	1	9927360	<i>CTNNBIP1</i>	-6,44E-03	1,19E-02	5,88E-01	9,71E-01
cg18760055	1	10788219	<i>CASZ1</i>	-1,31E-02	1,31E-02	3,14E-01	9,70E-01
cg26258588	1	11589971	<i>PTCHD2</i>	1,29E-02	1,53E-02	3,99E-01	9,70E-01

cg12126344	1	12207564	NA	-2,76E-02	1,83E-02	1,32E-01	9,39E-01
cg23097499	1	12225569	<i>TNFRSF1B</i>	-1,97E-02	1,22E-02	1,05E-01	9,39E-01
cg23280013	1	15250209	<i>KIAA1026</i>	4,33E-03	1,68E-02	7,97E-01	9,91E-01
cg26228591	1	16054846	<i>PLEKHM2</i>	-5,35E-03	1,27E-02	6,75E-01	9,82E-01
cg19916794	1	16061408	<i>SLC25A34</i>	-8,00E-03	1,20E-02	5,05E-01	9,70E-01
cg26059919	1	16265848	<i>SPEN</i>	-1,68E-02	1,58E-02	2,87E-01	9,70E-01
cg12695612	1	17308092	<i>MFAP2</i>	8,86E-04	1,33E-02	9,47E-01	9,94E-01
cg18681905	1	17331886	<i>ATP13A2</i>	-9,40E-03	1,38E-02	4,97E-01	9,70E-01
cg18028575	1	17332003	<i>ATP13A2</i>	-3,63E-02	1,41E-02	9,93E-03	8,22E-01
cg22626525	1	20008900	<i>TMCO4</i>	-1,14E-02	1,20E-02	3,43E-01	9,70E-01
cg27230749	1	20123989	<i>TMCO4</i>	-1,23E-02	1,18E-02	2,95E-01	9,70E-01
cg27298252	1	24645380	<i>GRHL3</i>	-1,06E-02	1,44E-02	4,60E-01	9,70E-01
cg01519464	1	24861818	<i>RCAN3</i>	-5,08E-03	9,55E-03	5,95E-01	9,72E-01
cg07191152	1	25061987	NA	-5,07E-03	1,08E-02	6,40E-01	9,80E-01
cg06640822	1	25291472	<i>RUNX3</i>	4,47E-03	7,51E-03	5,52E-01	9,70E-01
cg13235717	1	27188505	<i>SFN</i>	2,72E-03	1,08E-02	8,01E-01	9,92E-01
cg23922819	1	27335739	<i>FAM46B</i>	9,94E-03	1,19E-02	4,02E-01	9,70E-01
cg20816789	1	27462916	<i>SLC9A1</i>	-5,56E-03	9,88E-03	5,74E-01	9,70E-01
cg06361006	1	27689976	<i>MAP3K6</i>	5,17E-03	1,44E-02	7,19E-01	9,82E-01
cg22226904	1	27819060	NA	1,14E-02	1,53E-02	4,56E-01	9,70E-01
cg13443661	1	27875065	<i>AHDC1</i>	8,04E-03	1,24E-02	5,18E-01	9,70E-01
cg17110920	1	27893925	<i>AHDC1</i>	-2,03E-02	1,44E-02	1,57E-01	9,47E-01
cg18133072	1	28287782	<i>XKR8</i>	1,43E-03	1,98E-02	9,42E-01	9,94E-01
cg13844287	1	28476989	<i>PTAFR</i>	-2,64E-03	1,46E-02	8,57E-01	9,94E-01
cg12640482	1	28905573	<i>SNHG12; SNORD99</i>	-1,88E-02	1,37E-02	1,68E-01	9,47E-01
cg08878713	1	31325813	NA	-7,11E-03	1,16E-02	5,41E-01	9,70E-01
cg07478791	1	31886160	<i>SERINC2</i>	-1,76E-02	1,80E-02	3,28E-01	9,70E-01
cg00973823	1	32226349	<i>BAI2</i>	2,62E-02	1,80E-02	1,45E-01	9,39E-01
cg14975122	1	32761824	<i>HDAC1</i>	-2,31E-02	1,22E-02	5,79E-02	9,19E-01
cg16286249	1	33625400	<i>TRIM62</i>	-1,77E-02	1,32E-02	1,79E-01	9,47E-01
cg04486873	1	34644252	<i>C1orf94</i>	1,18E-02	1,88E-02	5,31E-01	9,70E-01
cg23276912	1	35326118	<i>C1orf212</i>	1,72E-02	9,69E-03	7,64E-02	9,19E-01
cg22402261	1	36026611	<i>NCDN</i>	-3,14E-02	1,45E-02	2,97E-02	9,19E-01
cg18755829	1	38512230	<i>POU3F1</i>	-6,35E-04	1,41E-02	9,64E-01	9,94E-01
cg09019648	1	39574285	<i>MACF1</i>	-4,44E-03	1,41E-02	7,53E-01	9,82E-01
cg15616998	1	40435396	<i>MFSD2A</i>	-1,96E-03	1,26E-02	8,76E-01	9,94E-01
cg19234495	1	43748663	<i>C1orf210</i>	-4,15E-03	8,71E-03	6,34E-01	9,78E-01
cg20942219	1	44141161	<i>KDM4A</i>	-3,35E-02	1,25E-02	7,25E-03	7,50E-01
cg26023051	1	45103896	<i>RNF220</i>	1,25E-02	1,58E-02	4,29E-01	9,70E-01
cg11251215	1	45103933	<i>RNF220</i>	-6,35E-03	1,40E-02	6,49E-01	9,81E-01
cg04079251	1	45120632	<i>TMEM53</i>	2,59E-03	1,26E-02	8,38E-01	9,94E-01
cg10893043	1	51442760	NA	4,30E-02	1,08E-02	6,79E-05	1,12E-01
cg16365663	1	51705878	<i>RNF11</i>	-2,68E-02	1,11E-02	1,61E-02	8,28E-01
cg06806477	1	54002750	<i>GLIS1</i>	1,01E-02	1,45E-02	4,87E-01	9,70E-01
cg04863508	1	54519587	<i>C1orf83; TMEM59</i>	2,42E-02	2,00E-02	2,26E-01	9,59E-01
cg11386376	1	55106106	<i>C1orf175</i>	1,89E-02	1,08E-02	7,99E-02	9,19E-01

cg13548810	1	55349365	<i>DHCR24</i>	-2,70E-02	1,44E-02	6,10E-02	9,19E-01
cg07826946	1	62120090	NA	-1,68E-02	1,40E-02	2,32E-01	9,70E-01
cg20611882	1	68696709	<i>GPR177</i>	-2,90E-03	1,31E-02	8,25E-01	9,94E-01
cg05725004	1	76082568	NA	-1,69E-02	1,30E-02	1,96E-01	9,55E-01
cg18172358	1	76734569	<i>ST6GALNAC3</i>	-7,78E-03	8,99E-03	3,87E-01	9,70E-01
cg10435609	1	78805320	<i>MGC27382</i>	4,89E-03	1,50E-02	7,44E-01	9,82E-01
cg09414863	1	85049548	NA	-1,14E-02	1,23E-02	3,54E-01	9,70E-01
cg21155367	1	90229095	NA	-1,51E-02	1,30E-02	2,46E-01	9,70E-01
cg10399789	1	92945668	<i>GFII</i>	1,63E-03	1,35E-02	9,04E-01	9,94E-01
cg19366591	1	92951355	<i>GFII</i>	-9,00E-04	1,40E-02	9,49E-01	9,94E-01
cg26282150	1	110091625	<i>GNAI3</i>	3,88E-02	2,11E-02	6,66E-02	9,19E-01
cg15831200	1	110765724	<i>KCNC4</i>	-1,11E-02	1,89E-02	5,58E-01	9,70E-01
cg01440333	1	111770111	<i>CHI3L2</i>	-9,44E-04	9,74E-03	9,23E-01	9,94E-01
cg03845435	1	112015443	<i>C1orf162</i>	2,91E-02	1,42E-02	3,99E-02	9,19E-01
cg09185179	1	112297970	<i>C1orf183; DDX20</i>	1,68E-02	1,20E-02	1,63E-01	9,47E-01
cg10883612	1	113063235	<i>WNT2B</i>	3,54E-02	1,45E-02	1,45E-02	8,28E-01
cg01101364	1	114544915	NA	-1,71E-02	1,50E-02	2,55E-01	9,70E-01
cg00967809	1	115829419	<i>NGF</i>	1,04E-02	1,28E-02	4,16E-01	9,70E-01
cg02614187	1	117664089	<i>TRIM45</i>	-2,33E-03	2,01E-02	9,08E-01	9,94E-01
cg07318158	1	149915753	<i>OTUD7B</i>	-8,83E-03	1,04E-02	3,95E-01	9,70E-01
cg13841804	1	150207467	<i>ANP32E</i>	-1,63E-02	1,87E-02	3,83E-01	9,70E-01
cg16559275	1	150522121	<i>ADAMTSL4</i>	-1,21E-02	2,00E-02	5,47E-01	9,70E-01
cg27630771	1	150533123	<i>ADAMTSL4</i>	5,96E-03	1,26E-02	6,37E-01	9,80E-01
cg12588301	1	152487335	<i>CRCT1</i>	6,07E-03	9,83E-03	5,37E-01	9,70E-01
cg13283942	1	153606541	<i>S100A13; C1orf77</i>	8,85E-03	1,52E-02	5,61E-01	9,70E-01
cg18821316	1	153931119	<i>CRTC2</i>	-1,18E-02	1,48E-02	4,26E-01	9,70E-01
cg22128197	1	154529357	<i>UBE2Q1</i>	2,57E-04	1,26E-02	9,84E-01	9,95E-01
cg01178854	1	154913744	NA	-2,15E-02	1,23E-02	7,96E-02	9,19E-01
cg10594506	1	155166889	<i>THBS3</i>	-4,09E-03	1,27E-02	7,47E-01	9,82E-01
cg15447017	1	156095882	<i>LMNA</i>	1,59E-03	1,60E-02	9,21E-01	9,94E-01
cg21396539	1	156164025	<i>SLC25A44</i>	-1,63E-02	2,01E-02	4,17E-01	9,70E-01
cg07794409	1	156473988	NA	7,90E-03	1,52E-02	6,03E-01	9,72E-01
cg22451632	1	157075626	NA	4,07E-03	1,20E-02	7,34E-01	9,82E-01
cg20985269	1	158576809	<i>OR10Z1</i>	2,13E-02	1,03E-02	3,98E-02	9,19E-01
cg09905199	1	159158497	<i>CADM3</i>	1,30E-02	1,10E-02	2,38E-01	9,70E-01
cg08853487	1	160171148	<i>CASQ1</i>	1,29E-02	1,06E-02	2,23E-01	9,59E-01
cg27582585	1	161069839	<i>KLHDC9</i>	-1,69E-02	1,19E-02	1,55E-01	9,47E-01
cg17166812	1	161169574	<i>NDUFS2; ADAMTS4</i>	-1,13E-02	7,70E-03	1,43E-01	9,39E-01
cg12154153	1	168195108	<i>SFT2D2</i>	2,91E-02	1,64E-02	7,60E-02	9,19E-01
cg20310385	1	171639856	NA	-1,43E-02	1,13E-02	2,03E-01	9,59E-01
cg12525949	1	173639916	<i>ANKRD45</i>	7,53E-03	1,64E-02	6,46E-01	9,81E-01
cg09554701	1	180323123	<i>ACBD6</i>	-1,68E-02	1,83E-02	3,59E-01	9,70E-01
cg22430700	1	180511495	NA	2,90E-03	1,33E-02	8,28E-01	9,94E-01
cg25604316	1	181104570	NA	-2,91E-03	1,34E-02	8,29E-01	9,94E-01
cg07168274	1	181382080	NA	4,57E-03	1,46E-02	7,54E-01	9,82E-01
cg24351427	1	185670109	NA	2,36E-03	1,36E-02	8,63E-01	9,94E-01

cg21851672	1	200007863	<i>NR5A2</i>	6,14E-03	1,27E-02	6,29E-01	9,75E-01
cg19899385	1	200422671	NA	-1,39E-03	1,47E-02	9,25E-01	9,94E-01
cg10210094	1	201374614	<i>TNNI1</i>	-1,40E-03	1,30E-02	9,14E-01	9,94E-01
cg25468907	1	201380680	<i>TNNI1</i>	1,47E-02	1,31E-02	2,63E-01	9,70E-01
cg01828733	1	201708932	<i>NAV1</i>	1,90E-03	1,29E-02	8,83E-01	9,94E-01
cg16545821	1	204118840	<i>ETNK2</i>	2,55E-03	1,96E-02	8,96E-01	9,94E-01
cg09828420	1	204308523	<i>PLEKHA6</i>	1,86E-03	1,22E-02	8,79E-01	9,94E-01
cg13946929	1	205477308	<i>CDK18</i>	-1,72E-02	1,11E-02	1,23E-01	9,39E-01
cg06437052	1	205897159	<i>SLC26A9</i>	2,32E-03	1,04E-02	8,23E-01	9,94E-01
cg17744604	1	206946166	<i>IL10</i>	-1,21E-02	7,43E-03	1,03E-01	9,39E-01
cg27179367	1	208347965	<i>PLXNA2</i>	1,77E-02	1,10E-02	1,08E-01	9,39E-01
cg20695760	1	212591689	NA	6,98E-03	1,02E-02	4,96E-01	9,70E-01
cg04108127	1	222885781	<i>AIDA; C1orf58</i>	1,81E-02	1,86E-02	3,30E-01	9,70E-01
cg09988837	1	224811939	<i>CNIH3</i>	-1,02E-02	1,47E-02	4,88E-01	9,70E-01
cg11526665	1	224896204	<i>CNIH3</i>	-4,66E-03	1,09E-02	6,68E-01	9,82E-01
cg12433423	1	225659296	NA	2,31E-03	1,19E-02	8,46E-01	9,94E-01
cg10836509	1	226299603	NA	3,94E-04	1,23E-02	9,75E-01	9,94E-01
cg00279700	1	226734755	NA	-4,00E-03	1,75E-02	8,19E-01	9,94E-01
cg20452738	1	226828650	<i>ITPKB</i>	-7,93E-04	1,08E-02	9,42E-01	9,94E-01
cg20775370	1	228473933	<i>OBSCN</i>	1,11E-02	1,39E-02	4,27E-01	9,70E-01
cg04212081	1	230000928	NA	5,49E-03	1,39E-02	6,92E-01	9,82E-01
cg27224809	1	230458334	<i>PGBD5</i>	1,65E-02	1,01E-02	1,03E-01	9,39E-01
cg02298525	1	233596023	NA	5,60E-03	9,93E-03	5,73E-01	9,70E-01
cg09861476	1	234617742	NA	-1,97E-02	1,28E-02	1,24E-01	9,39E-01
cg01514015	1	236318427	<i>GPR137B</i>	-1,19E-03	1,43E-02	9,33E-01	9,94E-01
cg14778267	1	240506799	<i>FMN2</i>	2,20E-02	1,49E-02	1,38E-01	9,39E-01
cg22673688	1	246148901	<i>SMYD3</i>	6,20E-03	1,21E-02	6,09E-01	9,72E-01
cg27468270	2	642539	NA	1,97E-02	1,27E-02	1,20E-01	9,39E-01
cg11985116	2	1567042	NA	3,30E-02	1,28E-02	9,86E-03	8,22E-01
cg20570797	2	1712800	<i>PXDN</i>	-2,24E-02	1,39E-02	1,08E-01	9,39E-01
cg03205046	2	1805302	<i>MYT1L</i>	1,34E-02	1,74E-02	4,42E-01	9,70E-01
cg03758732	2	2030712	<i>MYT1L</i>	-3,58E-03	1,22E-02	7,69E-01	9,84E-01
cg13585492	2	3187884	NA	-5,31E-03	1,70E-02	7,54E-01	9,82E-01
cg10071113	2	3328376	<i>TSSC1</i>	-2,88E-03	1,48E-02	8,46E-01	9,94E-01
cg25841802	2	3393367	<i>TTC15</i>	1,27E-02	1,68E-02	4,49E-01	9,70E-01
cg00680277	2	3465103	<i>TTC15</i>	-7,06E-03	1,30E-02	5,86E-01	9,70E-01
cg26744308	2	7909341	NA	-1,27E-02	1,26E-02	3,16E-01	9,70E-01
cg05696950	2	8715754	NA	-7,43E-03	1,33E-02	5,75E-01	9,70E-01
cg14984257	2	8822600	<i>ID2</i>	-1,53E-02	1,31E-02	2,45E-01	9,70E-01
cg17731409	2	9397282	<i>ASAP2</i>	-4,95E-04	1,26E-02	9,69E-01	9,94E-01
cg25819429	2	10310255	<i>C2orf48</i>	-8,60E-03	1,77E-02	6,27E-01	9,75E-01
cg26236235	2	10584541	<i>ODC1</i>	1,05E-02	1,18E-02	3,71E-01	9,70E-01
cg12343591	2	16031275	NA	6,74E-03	1,12E-02	5,47E-01	9,70E-01
cg04511411	2	16408214	NA	-6,27E-03	1,14E-02	5,84E-01	9,70E-01
cg21646084	2	16802843	<i>FAM49A</i>	4,40E-03	1,31E-02	7,37E-01	9,82E-01
cg11046593	2	17997660	<i>MSGN1</i>	1,99E-05	1,19E-02	9,99E-01	9,99E-01

cg13611499	2	19547417	NA	-6,56E-03	1,35E-02	6,27E-01	9,75E-01
cg17125688	2	20646181	<i>RHOB</i>	-4,58E-04	1,89E-02	9,81E-01	9,94E-01
cg03960488	2	23864195	<i>KLHL29</i>	1,84E-03	1,06E-02	8,62E-01	9,94E-01
cg07490699	2	23918679	<i>KLHL29</i>	-9,82E-03	1,36E-02	4,71E-01	9,70E-01
cg23924222	2	24658294	NA	-1,34E-02	1,62E-02	4,08E-01	9,70E-01
cg26752663	2	25142016	<i>ADCY3</i>	1,16E-02	8,89E-03	1,91E-01	9,47E-01
cg03766400	2	25467168	<i>DNMT3A</i>	-3,65E-03	1,17E-02	7,55E-01	9,83E-01
cg10616515	2	25470908	<i>DNMT3A</i>	-1,91E-02	1,16E-02	1,01E-01	9,39E-01
cg02607972	2	25964061	<i>ASXL2</i>	-1,61E-02	9,87E-03	1,03E-01	9,39E-01
cg10324116	2	29276263	NA	-1,44E-02	1,37E-02	2,94E-01	9,70E-01
cg27580905	2	39335085	<i>SOS1</i>	3,94E-03	1,22E-02	7,47E-01	9,82E-01
cg13787029	2	42721631	<i>KCNG3</i>	1,57E-02	1,85E-02	3,97E-01	9,70E-01
cg24304789	2	43451423	<i>ZFP36L2</i>	9,57E-03	1,35E-02	4,77E-01	9,70E-01
cg22385702	2	45175881	NA	1,62E-02	1,25E-02	1,93E-01	9,51E-01
cg13261971	2	45231226	NA	-2,29E-02	1,72E-02	1,83E-01	9,47E-01
cg22013055	2	47054833	<i>LOC100134259</i>	1,34E-03	9,39E-03	8,86E-01	9,94E-01
cg09044294	2	50234533	<i>NRXN1</i>	-3,83E-04	1,31E-02	9,77E-01	9,94E-01
cg23851515	2	51057218	<i>NRXN1</i>	2,01E-02	1,50E-02	1,81E-01	9,47E-01
cg03455255	2	54483193	<i>TSPYL6; ACYP2</i>	-1,15E-02	1,85E-02	5,36E-01	9,70E-01
cg08981537	2	54858444	<i>SPTBN1</i>	-7,72E-03	1,42E-02	5,86E-01	9,70E-01
cg14411804	2	56420171	<i>CCDC85A</i>	5,26E-03	1,36E-02	6,98E-01	9,82E-01
cg00774457	2	58479214	NA	-2,22E-02	1,62E-02	1,70E-01	9,47E-01
cg27159979	2	60763331	<i>BCL11A</i>	6,03E-03	8,50E-03	4,77E-01	9,70E-01
cg14957430	2	64995219	NA	8,78E-03	1,70E-02	6,07E-01	9,72E-01
cg10954469	2	71115370	NA	1,92E-04	1,39E-02	9,89E-01	9,97E-01
cg06122697	2	72363781	<i>CYP26B1</i>	7,92E-04	1,03E-02	9,39E-01	9,94E-01
cg02352181	2	74058083	<i>STAMBP</i>	-8,42E-03	1,12E-02	4,53E-01	9,70E-01
cg24691835	2	74119781	<i>ACTG2</i>	7,76E-03	1,16E-02	5,02E-01	9,70E-01
cg09591830	2	74975236	NA	3,57E-03	1,06E-02	7,38E-01	9,82E-01
cg10063845	2	80363347	<i>CTNNA2</i>	2,07E-03	1,29E-02	8,72E-01	9,94E-01
cg03271080	2	86255119	<i>POLR1A</i>	-8,74E-03	1,23E-02	4,79E-01	9,70E-01
cg25939861	2	87020937	<i>CD8A</i>	1,85E-02	1,11E-02	9,60E-02	9,39E-01
cg05778739	2	96676295	<i>LOC729234</i>	2,01E-02	1,30E-02	1,23E-01	9,39E-01
cg22939866	2	97361264	<i>FER1L5</i>	5,23E-03	1,50E-02	7,28E-01	9,82E-01
cg27051778	2	101594321	<i>NPAS2</i>	2,28E-03	1,34E-02	8,66E-01	9,94E-01
cg08023416	2	102803787	<i>IL1RL2</i>	1,35E-02	1,84E-02	4,63E-01	9,70E-01
cg06596991	2	105483826	NA	-5,92E-04	1,20E-02	9,61E-01	9,94E-01
cg23427406	2	107872344	NA	-2,27E-02	1,31E-02	8,38E-02	9,39E-01
cg17787988	2	113954732	<i>PSD4; LOC440839</i>	-9,23E-03	1,38E-02	5,03E-01	9,70E-01
cg24409539	2	114034595	<i>PAX8; LOC440839</i>	7,13E-03	1,51E-02	6,36E-01	9,80E-01
cg00826615	2	121330875	NA	-1,51E-02	1,23E-02	2,20E-01	9,59E-01
cg04223863	2	121678052	<i>GLI2</i>	-5,41E-03	1,26E-02	6,68E-01	9,82E-01
cg21905068	2	124439823	NA	-1,20E-02	1,40E-02	3,92E-01	9,70E-01
cg22924840	2	127646404	NA	1,05E-02	1,02E-02	3,05E-01	9,70E-01
cg22196977	2	128263013	<i>IWS1</i>	-1,43E-02	1,38E-02	3,00E-01	9,70E-01
cg11416620	2	129072147	<i>HS6ST1</i>	-5,64E-03	1,36E-02	6,79E-01	9,82E-01

cg27614215	2	129251945	NA	-4,56E-03	1,56E-02	7,70E-01	9,84E-01
cg07144318	2	129301519	NA	9,26E-03	1,81E-02	6,10E-01	9,72E-01
cg01787445	2	130344243	NA	-3,67E-03	1,22E-02	7,63E-01	9,84E-01
cg20496134	2	130945155	<i>FAM128B</i>	-1,58E-02	1,12E-02	1,57E-01	9,47E-01
cg03147598	2	131104160	<i>IMP4</i>	-6,14E-03	1,14E-02	5,91E-01	9,72E-01
cg21372107	2	134900674	NA	-1,08E-02	1,29E-02	4,03E-01	9,70E-01
cg27618483	2	155433424	NA	-3,06E-03	1,49E-02	8,37E-01	9,94E-01
cg13392885	2	161593271	NA	1,91E-02	1,33E-02	1,52E-01	9,39E-01
cg12341429	2	161887154	NA	-9,75E-03	1,38E-02	4,81E-01	9,70E-01
cg12520549	2	162280741	<i>TBR1</i>	-1,84E-03	1,40E-02	8,95E-01	9,94E-01
cg05624376	2	169939876	<i>DHRS9</i>	-1,44E-02	6,97E-03	3,90E-02	9,19E-01
cg23497644	2	170654835	<i>SSB</i>	3,95E-03	1,70E-02	8,16E-01	9,94E-01
cg07321354	2	173078588	NA	6,37E-03	1,66E-02	7,01E-01	9,82E-01
cg16233311	2	175199259	<i>SP9</i>	-1,11E-02	1,36E-02	4,14E-01	9,70E-01
cg11248896	2	177003747	NA	8,04E-03	1,46E-02	5,83E-01	9,70E-01
cg10039988	2	177355604	NA	-7,34E-03	1,25E-02	5,58E-01	9,70E-01
cg17516156	2	191207820	<i>INPP1</i>	-1,56E-02	1,04E-02	1,34E-01	9,39E-01
cg02894966	2	192700717	<i>SDPR</i>	1,16E-03	1,48E-02	9,37E-01	9,94E-01
cg14813485	2	196460621	NA	1,44E-02	1,08E-02	1,82E-01	9,47E-01
cg02489219	2	197676272	<i>C2orf66</i>	7,34E-03	9,22E-03	4,26E-01	9,70E-01
cg05247767	2	201526925	<i>AOX1</i>	9,65E-03	1,43E-02	5,01E-01	9,70E-01
cg21210220	2	202948038	NA	1,09E-02	1,29E-02	4,01E-01	9,70E-01
cg24588278	2	203134514	<i>NOP58</i>	1,33E-02	1,28E-02	3,00E-01	9,70E-01
cg13651908	2	204570033	<i>CD28</i>	6,96E-05	7,64E-03	9,93E-01	9,98E-01
cg10258063	2	217363243	<i>RPL37A</i>	-2,81E-03	1,76E-02	8,73E-01	9,94E-01
cg26429381	2	217639206	NA	4,93E-03	1,13E-02	6,63E-01	9,82E-01
cg16964117	2	219145237	<i>TMBIM1; PNKD</i>	-2,32E-02	1,14E-02	4,14E-02	9,19E-01
cg13835894	2	219148914	<i>PNKD; TMBIM1</i>	-1,22E-02	1,44E-02	3,94E-01	9,70E-01
cg17130789	2	219256187	<i>SLC11A1</i>	-2,11E-03	1,23E-02	8,64E-01	9,94E-01
cg13859511	2	219749205	<i>WNT10A</i>	-2,31E-02	1,43E-02	1,06E-01	9,39E-01
cg12007362	2	220039014	<i>C2orf24</i>	-2,07E-02	1,37E-02	1,31E-01	9,39E-01
cg26784162	2	220089128	<i>ATG9A</i>	-7,25E-03	1,44E-02	6,14E-01	9,72E-01
cg26512226	2	220282165	<i>DES</i>	-1,54E-03	1,20E-02	8,98E-01	9,94E-01
cg17037231	2	220387027	<i>ACCN4</i>	4,32E-03	1,04E-02	6,77E-01	9,82E-01
cg13000039	2	220428227	<i>OBSL1</i>	-8,39E-03	1,26E-02	5,07E-01	9,70E-01
cg04447708	2	220432872	<i>OBSL1</i>	1,94E-03	1,33E-02	8,84E-01	9,94E-01
cg12045030	2	220865785	NA	1,34E-02	1,06E-02	2,06E-01	9,59E-01
cg10015830	2	228727869	NA	1,88E-03	1,31E-02	8,85E-01	9,94E-01
cg12565502	2	228881689	<i>SPHKAP</i>	5,73E-03	1,40E-02	6,81E-01	9,82E-01
cg26870961	2	231740356	<i>ITM2C</i>	-1,12E-02	1,62E-02	4,91E-01	9,70E-01
cg08210297	2	233320854	<i>ALPI</i>	-7,80E-03	1,11E-02	4,82E-01	9,70E-01
cg12834730	2	234159346	<i>ATG16LI</i>	-2,11E-02	1,30E-02	1,05E-01	9,39E-01
cg00978848	2	235680305	NA	-9,54E-03	8,31E-03	2,51E-01	9,70E-01
cg23337031	2	236416064	<i>AGAP1</i>	1,67E-03	1,60E-02	9,17E-01	9,94E-01
cg23551605	2	236442942	<i>AGAP1</i>	-8,36E-03	1,17E-02	4,75E-01	9,70E-01
cg09042437	2	236643760	<i>AGAP1</i>	-6,07E-04	1,88E-02	9,74E-01	9,94E-01

cg06747919	2	236716372	<i>AGAP1</i>	-6,48E-03	1,25E-02	6,04E-01	9,72E-01
cg02878739	2	236840858	<i>AGAP1</i>	-4,76E-03	1,02E-02	6,41E-01	9,81E-01
cg04787916	2	237755762	NA	-1,52E-02	1,18E-02	1,98E-01	9,56E-01
cg05223158	2	238271966	<i>COL6A3</i>	-1,68E-03	1,16E-02	8,86E-01	9,94E-01
cg21911868	2	239034264	<i>ESPNL</i>	-1,20E-02	1,60E-02	4,53E-01	9,70E-01
cg02558267	2	239976138	<i>HDAC4</i>	-6,11E-03	1,23E-02	6,21E-01	9,73E-01
cg23076987	2	239990233	<i>HDAC4</i>	-8,07E-03	1,27E-02	5,26E-01	9,70E-01
cg11924452	2	241185198	NA	-8,96E-03	1,87E-02	6,32E-01	9,78E-01
cg08485186	2	241397486	<i>PP14571; GPC1</i>	-1,19E-02	1,17E-02	3,10E-01	9,70E-01
cg24958325	2	241498221	<i>ANKMY1; DUSP28</i>	1,55E-02	1,18E-02	1,91E-01	9,47E-01
cg24090192	2	241718825	<i>KIF1A</i>	1,40E-02	1,44E-02	3,32E-01	9,70E-01
cg04398322	2	241991130	<i>SNED1</i>	-8,76E-03	1,06E-02	4,10E-01	9,70E-01
cg21663667	2	242169936	<i>HDLBP</i>	6,05E-03	1,33E-02	6,48E-01	9,81E-01
cg20801783	2	242693230	<i>D2HGDH</i>	-7,04E-03	1,41E-02	6,17E-01	9,72E-01
cg25991761	2	242927449	NA	4,35E-03	1,63E-02	7,89E-01	9,90E-01
cg17998076	3	3386094	NA	-1,43E-02	1,58E-02	3,66E-01	9,70E-01
cg23479065	3	3843811	<i>LRRN1</i>	-1,41E-02	1,41E-02	3,20E-01	9,70E-01
cg03107436	3	10400456	<i>ATP2B2</i>	-1,34E-02	1,19E-02	2,59E-01	9,70E-01
cg12179658	3	11178652	<i>HRH1</i>	-2,51E-03	1,00E-02	8,02E-01	9,93E-01
cg07963181	3	11195902	<i>HRH1</i>	4,90E-03	1,67E-02	7,70E-01	9,84E-01
cg05361415	3	11610138	<i>VGLL4</i>	2,71E-03	1,43E-02	8,49E-01	9,94E-01
cg02217386	3	12856862	<i>CAND2</i>	-1,38E-02	1,43E-02	3,33E-01	9,70E-01
cg13537146	3	12926674	NA	-7,01E-03	1,25E-02	5,75E-01	9,70E-01
cg20957164	3	12965323	<i>IQSEC1</i>	-8,17E-03	1,16E-02	4,83E-01	9,70E-01
cg09361614	3	12994821	<i>IQSEC1</i>	5,71E-03	1,70E-02	7,36E-01	9,82E-01
cg09538633	3	13834894	NA	-1,79E-03	1,58E-02	9,10E-01	9,94E-01
cg01374266	3	13895994	<i>WNT7A</i>	-1,18E-02	1,19E-02	3,23E-01	9,70E-01
cg19148404	3	14443444	<i>SLC6A6</i>	1,29E-02	1,61E-02	4,23E-01	9,70E-01
cg21068907	3	14861931	<i>FGD5</i>	-3,53E-03	1,84E-02	8,48E-01	9,94E-01
cg15605530	3	17069926	<i>PLCL2</i>	1,17E-02	1,20E-02	3,32E-01	9,70E-01
cg16154073	3	32433121	<i>CMTM7</i>	2,62E-02	1,80E-02	1,45E-01	9,39E-01
cg20685600	3	33067603	<i>GLB1</i>	4,83E-04	1,31E-02	9,71E-01	9,94E-01
cg19879491	3	42803396	<i>CCDC13</i>	-2,00E-02	1,36E-02	1,43E-01	9,39E-01
cg05553879	3	43404068	NA	2,35E-03	1,34E-02	8,60E-01	9,94E-01
cg07997066	3	44154910	<i>MIR138-1</i>	-1,81E-02	1,25E-02	1,50E-01	9,39E-01
cg03655706	3	44496780	<i>ZNF445</i>	5,45E-03	1,19E-02	6,48E-01	9,81E-01
cg05670596	3	46448496	<i>CCRL2</i>	5,25E-03	1,33E-02	6,94E-01	9,82E-01
cg04078416	3	47017981	<i>CCDC12</i>	7,61E-03	1,69E-02	6,52E-01	9,82E-01
cg06086785	3	47889040	<i>DHX30</i>	-2,92E-02	1,24E-02	1,85E-02	8,28E-01
cg13741103	3	48080464	<i>MAP4</i>	5,67E-03	1,30E-02	6,63E-01	9,82E-01
cg15622805	3	48249410	NA	1,88E-03	1,12E-02	8,66E-01	9,94E-01
cg01458495	3	48310544	<i>ZNF589</i>	6,92E-03	9,26E-03	4,55E-01	9,70E-01
cg22533419	3	48311815	<i>ZNF589</i>	-2,50E-02	1,35E-02	6,37E-02	9,19E-01
cg04484520	3	48697594	<i>CELSR3</i>	-9,66E-03	1,32E-02	4,64E-01	9,70E-01
cg01833222	3	49162453	<i>LAMB2</i>	-1,47E-02	1,26E-02	2,44E-01	9,70E-01
cg00987743	3	49581113	NA	1,49E-02	1,67E-02	3,73E-01	9,70E-01

cg02047221	3	49686805	<i>BSN</i>	3,96E-03	1,03E-02	7,01E-01	9,82E-01
cg24679124	3	49694978	<i>BSN</i>	1,14E-03	1,13E-02	9,20E-01	9,94E-01
cg22229016	3	50304279	<i>SEMA3B</i>	-1,07E-02	1,42E-02	4,50E-01	9,70E-01
cg27230510	3	50404023	<i>CACNA2D2</i>	-2,84E-02	1,39E-02	4,11E-02	9,19E-01
cg10144104	3	50518896	<i>CACNA2D2</i>	-1,09E-02	1,67E-02	5,14E-01	9,70E-01
cg21368729	3	51971929	<i>RRP9</i>	2,13E-02	1,32E-02	1,05E-01	9,39E-01
cg07598930	3	52233294	<i>ALAS1</i>	-1,87E-02	9,88E-03	5,88E-02	9,19E-01
cg25188828	3	52526356	<i>NISCH</i>	-4,01E-03	1,34E-02	7,64E-01	9,84E-01
cg27565382	3	53032988	<i>SFMBT1</i>	1,04E-02	1,44E-02	4,69E-01	9,70E-01
cg06270249	3	55809537	<i>ERC2</i>	-1,22E-02	1,33E-02	3,59E-01	9,70E-01
cg16560256	3	58328580	<i>PXK</i>	-4,39E-02	1,19E-02	2,23E-04	1,23E-01
cg26386826	3	58555510	<i>FAM107A</i>	-5,80E-03	1,16E-02	6,16E-01	9,72E-01
cg25008571	3	62189112	<i>PTPRG</i>	-1,29E-02	1,15E-02	2,63E-01	9,70E-01
cg18858064	3	65463611	<i>MAGI1</i>	3,98E-03	1,36E-02	7,70E-01	9,84E-01
cg03296801	3	73487900	<i>PDZRN3</i>	-1,16E-02	2,18E-02	5,92E-01	9,72E-01
cg12226735	3	98610584	<i>DCBLD2</i>	-1,80E-03	9,71E-03	8,53E-01	9,94E-01
cg14579314	3	99944324	NA	2,01E-02	1,31E-02	1,26E-01	9,39E-01
cg09821685	3	109034944	<i>DPPA2</i>	7,81E-03	1,42E-02	5,81E-01	9,70E-01
cg23670794	3	111313065	<i>ZBED2; CD96</i>	8,75E-03	1,32E-02	5,06E-01	9,70E-01
cg06479057	3	112358468	<i>CCDC80</i>	-2,55E-03	1,82E-02	8,89E-01	9,94E-01
cg09246203	3	114018592	<i>TIGIT</i>	2,07E-02	1,49E-02	1,64E-01	9,47E-01
cg12024811	3	123979446	<i>KALRN</i>	1,32E-02	9,66E-03	1,72E-01	9,47E-01
cg19918027	3	123987645	<i>KALRN</i>	2,67E-02	1,49E-02	7,42E-02	9,19E-01
cg14688451	3	124303035	<i>KALRN</i>	3,24E-03	1,19E-02	7,85E-01	9,90E-01
cg15100992	3	125736070	<i>SLC41A3</i>	-1,21E-02	1,47E-02	4,13E-01	9,70E-01
cg24303306	3	126261837	<i>CHST13</i>	1,24E-02	1,32E-02	3,46E-01	9,70E-01
cg18482576	3	127350189	<i>PODXL2</i>	4,64E-03	1,01E-02	6,45E-01	9,81E-01
cg09089421	3	127803668	<i>RUVBL1</i>	-1,71E-02	1,33E-02	1,98E-01	9,56E-01
cg12190305	3	127815173	<i>RUVBL1</i>	5,09E-03	1,16E-02	6,61E-01	9,82E-01
cg24377070	3	128182041	<i>DNAJB8</i>	-1,87E-02	1,29E-02	1,45E-01	9,39E-01
cg02727530	3	128712175	<i>KIAA1257</i>	-1,25E-02	1,47E-02	3,94E-01	9,70E-01
cg07562926	3	133668017	<i>SLCO2A1</i>	-1,15E-02	1,04E-02	2,69E-01	9,70E-01
cg12632315	3	134069894	NA	1,58E-03	1,17E-02	8,92E-01	9,94E-01
cg26869578	3	137482539	<i>SOX14</i>	-3,04E-02	1,29E-02	1,84E-02	8,28E-01
cg10602180	3	137729133	<i>CLDN18</i>	7,15E-04	1,78E-02	9,68E-01	9,94E-01
cg16171849	3	139254260	<i>RBP1</i>	-5,17E-03	1,03E-02	6,17E-01	9,72E-01
cg14497255	3	143127934	<i>SLC9A9</i>	2,97E-03	1,79E-02	8,68E-01	9,94E-01
cg27235955	3	154848194	<i>MME</i>	-7,29E-03	1,13E-02	5,17E-01	9,70E-01
cg09452751	3	155572485	<i>SLC33A1</i>	2,39E-02	1,76E-02	1,76E-01	9,47E-01
cg21770060	3	159583545	<i>SCHIP1</i>	7,23E-03	1,30E-02	5,77E-01	9,70E-01
cg14778576	3	160477458	<i>PPM1L</i>	-4,80E-03	1,64E-02	7,70E-01	9,84E-01
cg14141843	3	183889395	<i>DVL3</i>	-1,81E-02	1,20E-02	1,32E-01	9,39E-01
cg24643062	3	183948943	<i>VWA5B2</i>	-6,32E-03	1,53E-02	6,79E-01	9,82E-01
cg20766467	3	184097946	<i>CHRD</i>	-1,47E-02	1,88E-02	4,35E-01	9,70E-01
cg13748287	3	184290594	<i>EPHB3</i>	5,73E-03	1,39E-02	6,79E-01	9,82E-01
cg15975443	3	192551962	<i>C3orf59</i>	-2,55E-03	1,20E-02	8,32E-01	9,94E-01

cg01012330	3	192634059	<i>C3orf59</i>	-1,49E-02	1,34E-02	2,64E-01	9,70E-01
cg14163776	3	195164580	<i>ACAP2</i>	8,85E-03	1,39E-02	5,25E-01	9,70E-01
cg15932961	3	195869691	NA	1,01E-02	1,42E-02	4,77E-01	9,70E-01
cg23052855	3	195929389	<i>ZDHHC19</i>	-2,91E-02	1,87E-02	1,19E-01	9,39E-01
cg00477017	3	196731150	<i>MF12</i>	-1,44E-03	1,34E-02	9,14E-01	9,94E-01
cg13334788	3	197232612	NA	-3,36E-02	2,01E-02	9,48E-02	9,39E-01
cg23464319	4	733598	<i>PCGF3</i>	-1,18E-02	1,42E-02	4,05E-01	9,70E-01
cg21790314	4	955469	<i>DGKQ</i>	-1,44E-02	1,19E-02	2,25E-01	9,59E-01
cg23620889	4	957642	<i>DGKQ</i>	1,27E-02	2,01E-02	5,28E-01	9,70E-01
cg00070460	4	1227676	<i>CTBP1</i>	-1,31E-02	1,21E-02	2,77E-01	9,70E-01
cg14919643	4	1367748	<i>KIAA1530</i>	-3,31E-03	1,70E-02	8,46E-01	9,94E-01
cg10164264	4	1373477	<i>KIAA1530</i>	2,12E-02	2,04E-02	2,98E-01	9,70E-01
cg14296331	4	1949947	<i>WHSC1</i>	-1,38E-02	1,51E-02	3,60E-01	9,70E-01
cg18274320	4	2306547	<i>ZFYVE28</i>	-5,97E-03	1,50E-02	6,90E-01	9,82E-01
cg27509213	4	3499546	NA	-8,52E-03	1,42E-02	5,47E-01	9,70E-01
cg19633353	4	3530501	<i>LRPAP1</i>	2,87E-03	1,89E-02	8,79E-01	9,94E-01
cg26958924	4	6296934	<i>WFS1</i>	-2,10E-02	1,14E-02	6,39E-02	9,19E-01
cg02500960	4	8122233	<i>ABLIM2</i>	3,14E-02	1,71E-02	6,60E-02	9,19E-01
cg25107528	4	8607947	<i>CPZ</i>	-8,23E-03	1,17E-02	4,84E-01	9,70E-01
cg16147221	4	10020634	<i>SLC2A9</i>	-1,74E-02	1,78E-02	3,28E-01	9,70E-01
cg25206536	4	11369007	<i>MIR572</i>	4,90E-03	1,78E-02	7,83E-01	9,90E-01
cg21329975	4	15471214	<i>CC2D2A</i>	8,97E-03	1,40E-02	5,22E-01	9,70E-01
cg22949170	4	39773308	<i>UBE2K</i>	4,91E-03	1,55E-02	7,51E-01	9,82E-01
cg25117091	4	40518143	<i>RBM47</i>	-1,73E-02	1,35E-02	2,01E-01	9,59E-01
cg07657463	4	40753247	<i>NSUN7</i>	1,08E-02	1,52E-02	4,78E-01	9,70E-01
cg04495313	4	42348136	NA	-1,32E-02	1,22E-02	2,78E-01	9,70E-01
cg26656258	4	54969688	NA	-1,54E-02	1,24E-02	2,15E-01	9,59E-01
cg10923036	4	57931299	<i>IGFBP7</i>	-1,75E-03	9,78E-03	8,58E-01	9,94E-01
cg03093825	4	76648888	<i>USO1</i>	1,69E-02	1,52E-02	2,67E-01	9,70E-01
cg24782087	4	77870838	<i>SEPT11</i>	4,14E-03	1,80E-02	8,18E-01	9,94E-01
cg17903782	4	81345395	<i>C4orf22</i>	4,92E-03	1,34E-02	7,13E-01	9,82E-01
cg03064914	4	88655139	NA	1,75E-02	9,98E-03	7,96E-02	9,19E-01
cg01471384	4	107957265	<i>DKK2</i>	1,26E-02	1,33E-02	3,47E-01	9,70E-01
cg03500398	4	109827459	<i>COL25A1</i>	-1,90E-02	1,20E-02	1,14E-01	9,39E-01
cg18197092	4	117626456	NA	1,23E-03	1,31E-02	9,25E-01	9,94E-01
cg24920271	4	125571982	NA	1,14E-02	1,32E-02	3,88E-01	9,70E-01
cg06057952	4	152682178	<i>PET112L</i>	5,93E-03	1,55E-02	7,02E-01	9,82E-01
cg24284882	4	154418379	<i>KIAA0922</i>	2,42E-02	1,57E-02	1,24E-01	9,39E-01
cg25570522	4	154443833	<i>KIAA0922</i>	1,78E-02	8,29E-03	3,15E-02	9,19E-01
cg21746884	4	165928617	NA	6,46E-03	1,72E-02	7,07E-01	9,82E-01
cg04828587	4	174251028	NA	1,05E-02	1,76E-02	5,52E-01	9,70E-01
cg10509254	4	174452133	<i>NBLA00301; HAND2</i>	-2,29E-02	1,07E-02	3,18E-02	9,19E-01
cg02521102	4	175750583	<i>GLRA3</i>	-1,80E-02	1,58E-02	2,53E-01	9,70E-01
cg01590753	4	177714373	<i>VEGFC</i>	-9,43E-03	1,80E-02	6,01E-01	9,72E-01
cg05854261	4	184297631	NA	-1,92E-02	2,08E-02	3,57E-01	9,70E-01
cg06908241	4	184335095	NA	-1,77E-02	9,89E-03	7,42E-02	9,19E-01

cg08276984	4	184366236	<i>CDKN2AIP</i>	1,50E-02	1,44E-02	3,00E-01	9,70E-01
cg01826897	4	186131639	<i>SNX25</i>	2,42E-03	1,33E-02	8,56E-01	9,94E-01
cg04945735	4	186456009	<i>PDLIM3</i>	-4,37E-03	1,28E-02	7,32E-01	9,82E-01
cg08027433	5	90070	NA	-2,23E-04	1,27E-02	9,86E-01	9,96E-01
cg20653695	5	139859	<i>PLEKHG4B</i>	-1,11E-03	1,34E-02	9,34E-01	9,94E-01
cg12507879	5	488078	<i>SLC9A3</i>	-9,98E-03	1,52E-02	5,10E-01	9,70E-01
cg07262320	5	621696	<i>CEP72</i>	4,74E-04	1,38E-02	9,73E-01	9,94E-01
cg06973176	5	1067634	<i>SLC12A7</i>	-1,39E-02	1,25E-02	2,69E-01	9,70E-01
cg08293408	5	1077731	<i>SLC12A7</i>	-9,47E-03	1,16E-02	4,14E-01	9,70E-01
cg25388971	5	1085895	<i>SLC12A7</i>	-4,18E-02	1,82E-02	2,19E-02	8,51E-01
cg06812019	5	1143331	NA	3,12E-02	1,68E-02	6,27E-02	9,19E-01
cg20655458	5	1143404	NA	-4,86E-03	1,42E-02	7,32E-01	9,82E-01
cg15927295	5	1270057	<i>TERT</i>	3,45E-03	1,50E-02	8,18E-01	9,94E-01
cg26221342	5	1272400	<i>TERT</i>	1,41E-02	1,35E-02	2,96E-01	9,70E-01
cg17229371	5	1485470	<i>LPCAT1</i>	1,04E-02	9,88E-03	2,94E-01	9,70E-01
cg12389685	5	1779542	NA	-1,19E-03	1,78E-02	9,47E-01	9,94E-01
cg05990988	5	4223068	NA	-8,02E-03	1,28E-02	5,32E-01	9,70E-01
cg16002929	5	9344131	<i>SEMA5A</i>	2,07E-02	1,30E-02	1,11E-01	9,39E-01
cg06758827	5	14492774	<i>TRIO</i>	2,43E-02	1,05E-02	2,03E-02	8,51E-01
cg10984165	5	28809121	NA	-1,77E-04	1,55E-02	9,91E-01	9,98E-01
cg26404463	5	32317417	NA	-4,02E-03	1,07E-02	7,07E-01	9,82E-01
cg15996282	5	36152109	<i>LMBRD2; SKP2</i>	-1,18E-02	1,67E-02	4,81E-01	9,70E-01
cg21077636	5	37209182	<i>C5orf42</i>	-2,36E-03	1,95E-02	9,03E-01	9,94E-01
cg06795635	5	49962609	<i>PARP8</i>	-1,89E-02	1,68E-02	2,61E-01	9,70E-01
cg15473084	5	50265600	NA	-1,43E-02	1,30E-02	2,72E-01	9,70E-01
cg05247112	5	64399044	NA	3,14E-02	1,68E-02	6,20E-02	9,19E-01
cg22685009	5	71597700	<i>MRPS27</i>	2,01E-02	1,22E-02	9,86E-02	9,39E-01
cg26922546	5	72678459	NA	8,75E-03	1,64E-02	5,94E-01	9,72E-01
cg17680767	5	73623208	NA	1,08E-02	1,36E-02	4,27E-01	9,70E-01
cg16666329	5	76932526	<i>OTP</i>	5,38E-03	1,18E-02	6,49E-01	9,81E-01
cg04175399	5	80383034	<i>RASGRF2</i>	-4,60E-03	1,68E-02	7,85E-01	9,90E-01
cg09496599	5	80383224	<i>RASGRF2</i>	2,42E-03	1,52E-02	8,74E-01	9,94E-01
cg25347127	5	81654031	NA	1,92E-02	1,19E-02	1,05E-01	9,39E-01
cg16600634	5	92907881	<i>FLJ42709</i>	-1,23E-02	1,10E-02	2,61E-01	9,70E-01
cg15112442	5	99382144	NA	-1,51E-03	1,53E-02	9,22E-01	9,94E-01
cg08666956	5	107040942	NA	-4,87E-03	1,88E-02	7,95E-01	9,91E-01
cg16110711	5	112042851	<i>APC</i>	7,62E-03	1,88E-02	6,84E-01	9,82E-01
cg26881360	5	112622133	<i>MCC</i>	2,25E-03	1,34E-02	8,67E-01	9,94E-01
cg27581816	5	112849405	<i>YTHDC2</i>	1,50E-02	1,97E-02	4,47E-01	9,70E-01
cg22043118	5	114915630	<i>TMED7-TICAM2; TI</i>	-1,53E-02	1,07E-02	1,54E-01	9,47E-01
cg07644368	5	115152785	<i>CDO1</i>	1,45E-02	1,80E-02	4,21E-01	9,70E-01
cg00557236	5	115782227	<i>SEMA6A</i>	1,07E-02	1,65E-02	5,18E-01	9,70E-01
cg24780284	5	120444080	NA	3,21E-02	1,80E-02	7,42E-02	9,19E-01
cg05569742	5	122429414	<i>PRDM6</i>	3,19E-02	1,31E-02	1,48E-02	8,28E-01
cg11359771	5	131558794	<i>P4HA2</i>	1,54E-03	1,11E-02	8,90E-01	9,94E-01
cg26074851	5	133512410	<i>SKP1</i>	-1,03E-02	1,63E-02	5,29E-01	9,70E-01

cg25916993	5	134880580	NA	-1,21E-02	1,51E-02	4,25E-01	9,70E-01
cg21583694	5	135365401	<i>TGFB1</i>	-1,90E-02	1,38E-02	1,69E-01	9,47E-01
cg06999346	5	136837077	NA	4,37E-03	1,24E-02	7,25E-01	9,82E-01
cg25443836	5	137419610	<i>WNT8A</i>	-7,47E-03	1,07E-02	4,86E-01	9,70E-01
cg02304580	5	139124312	NA	-7,05E-03	1,27E-02	5,78E-01	9,70E-01
cg05687498	5	139523278	NA	1,25E-02	9,92E-03	2,06E-01	9,59E-01
cg01860693	5	139557145	<i>C5orf32</i>	1,66E-02	1,48E-02	2,64E-01	9,70E-01
cg26488999	5	141235690	<i>PCDH1</i>	2,38E-03	1,41E-02	8,66E-01	9,94E-01
cg18116174	5	142311682	<i>ARHGAP26</i>	-1,14E-02	1,28E-02	3,74E-01	9,70E-01
cg09714615	5	148033068	<i>HTR4</i>	2,23E-02	1,44E-02	1,21E-01	9,39E-01
cg24808105	5	148339194	NA	-1,04E-02	1,26E-02	4,08E-01	9,70E-01
cg01410292	5	148754026	<i>IL17B</i>	-1,88E-02	1,36E-02	1,66E-01	9,47E-01
cg07289335	5	158937447	NA	1,81E-02	1,32E-02	1,72E-01	9,47E-01
cg21050416	5	159411100	NA	4,74E-03	9,25E-03	6,09E-01	9,72E-01
cg17752270	5	169706238	<i>LCP2</i>	-2,11E-03	1,14E-02	8,53E-01	9,94E-01
cg16572224	5	171788937	<i>SH3PXD2B</i>	9,38E-03	1,53E-02	5,39E-01	9,70E-01
cg17924225	5	172030564	NA	3,36E-03	1,11E-02	7,62E-01	9,84E-01
cg26326382	5	176003200	<i>PCDH24</i>	1,03E-02	1,28E-02	4,25E-01	9,70E-01
cg23994191	5	176310098	<i>HK3</i>	1,28E-02	1,63E-02	4,33E-01	9,70E-01
cg11274816	5	176863257	<i>GRK6</i>	-1,69E-02	1,26E-02	1,80E-01	9,47E-01
cg16426715	5	176868293	<i>GRK6</i>	-2,30E-02	1,15E-02	4,56E-02	9,19E-01
cg13676583	5	176938866	<i>DDX41; DOK3</i>	-1,14E-02	9,25E-03	2,18E-01	9,59E-01
cg01050965	5	177650821	<i>AGXT2L2</i>	-1,17E-02	1,11E-02	2,95E-01	9,70E-01
cg22020813	5	177805003	<i>COL23A1</i>	-4,13E-03	1,18E-02	7,27E-01	9,82E-01
cg16604066	5	178680976	<i>ADAMTS2</i>	9,00E-03	1,32E-02	4,97E-01	9,70E-01
cg01791000	5	178687780	<i>ADAMTS2</i>	4,65E-03	1,19E-02	6,96E-01	9,82E-01
cg24795093	5	179290715	<i>TBC1D9B</i>	-1,65E-02	1,17E-02	1,61E-01	9,47E-01
cg12984014	5	179755324	<i>GFPT2</i>	4,02E-03	1,48E-02	7,86E-01	9,90E-01
cg22203607	5	180536151	NA	1,79E-02	1,69E-02	2,91E-01	9,70E-01
cg17808866	6	503857	<i>EXOC2</i>	-2,41E-02	1,71E-02	1,59E-01	9,47E-01
cg16929012	6	3140784	<i>BPHL</i>	-5,41E-03	1,53E-02	7,23E-01	9,82E-01
cg23801012	6	3227981	<i>TUBB2B</i>	-1,88E-02	1,55E-02	2,27E-01	9,59E-01
cg06288253	6	3269952	<i>SLC22A23</i>	5,95E-03	1,58E-02	7,07E-01	9,82E-01
cg11903854	6	3292969	<i>SLC22A23</i>	-3,55E-03	1,31E-02	7,85E-01	9,90E-01
cg24102242	6	3327319	<i>SLC22A23</i>	2,87E-03	1,06E-02	7,87E-01	9,90E-01
cg00702872	6	3524580	NA	2,38E-03	1,14E-02	8,34E-01	9,94E-01
cg02647297	6	3867369	NA	-3,51E-02	1,23E-02	4,38E-03	5,58E-01
cg11229160	6	5510800	<i>FARS2</i>	-4,65E-02	2,09E-02	2,59E-02	8,94E-01
cg00244352	6	15495498	<i>JARID2</i>	-3,41E-03	1,37E-02	8,04E-01	9,93E-01
cg23567726	6	15513677	<i>JARID2</i>	3,49E-03	1,35E-02	7,96E-01	9,91E-01
cg04611912	6	15538569	<i>DTNBP1</i>	4,37E-03	1,15E-02	7,05E-01	9,82E-01
cg04899492	6	24126312	<i>NRSN1</i>	-6,66E-04	1,44E-02	9,63E-01	9,94E-01
cg04870110	6	27596156	NA	2,12E-02	1,82E-02	2,46E-01	9,70E-01
cg00412749	6	28603173	NA	-1,20E-02	1,09E-02	2,72E-01	9,70E-01
cg20675150	6	28876197	<i>TRIM27</i>	1,43E-03	1,91E-02	9,40E-01	9,94E-01
cg24876969	6	28971902	<i>ZNF311</i>	-1,21E-02	1,33E-02	3,62E-01	9,70E-01

cg20642417	6	29577082	<i>GABBR1</i>	-1,01E-03	1,15E-02	9,30E-01	9,94E-01
cg03810301	6	29590017	<i>GABBR1</i>	5,69E-03	1,17E-02	6,27E-01	9,75E-01
cg17569438	6	29768230	NA	3,61E-03	1,71E-02	8,33E-01	9,94E-01
cg01452581	6	30131915	<i>TRIM15</i>	-1,52E-03	1,19E-02	8,98E-01	9,94E-01
cg19606484	6	30132679	<i>TRIM15</i>	-6,01E-03	1,19E-02	6,14E-01	9,72E-01
cg25367940	6	30163370	<i>TRIM26</i>	-3,47E-03	1,56E-02	8,24E-01	9,94E-01
cg25746489	6	30173974	<i>TRIM26</i>	-2,08E-03	1,24E-02	8,67E-01	9,94E-01
cg18804722	6	30431770	NA	1,01E-02	1,47E-02	4,92E-01	9,70E-01
cg24372586	6	30520094	<i>GNL1</i>	4,38E-03	1,38E-02	7,52E-01	9,82E-01
cg11320544	6	30526487	<i>PRR3; GNL1</i>	-8,90E-03	1,73E-02	6,07E-01	9,72E-01
cg23068345	6	30582738	<i>PPP1R10</i>	1,33E-02	1,35E-02	3,24E-01	9,70E-01
cg00682802	6	30682855	<i>MDC1</i>	1,49E-02	1,75E-02	3,97E-01	9,70E-01
cg09761550	6	30879552	<i>GTF2H4</i>	-1,64E-02	1,19E-02	1,67E-01	9,47E-01
cg19014295	6	30884928	<i>VAR52</i>	-1,24E-02	1,16E-02	2,84E-01	9,70E-01
cg14425114	6	30926197	NA	7,93E-03	1,25E-02	5,25E-01	9,70E-01
cg27092297	6	31116343	<i>CCHCR1</i>	9,33E-03	1,24E-02	4,51E-01	9,70E-01
cg10995925	6	31539601	<i>LTA</i>	1,60E-02	9,84E-03	1,04E-01	9,39E-01
cg27490128	6	31560441	<i>NCR3</i>	4,64E-03	1,29E-02	7,18E-01	9,82E-01
cg09802546	6	31645540	<i>LY6G5C</i>	-1,26E-02	1,21E-02	2,98E-01	9,70E-01
cg06151074	6	31669888	<i>BAT5</i>	4,50E-03	1,38E-02	7,45E-01	9,82E-01
cg20794828	6	31688229	<i>LY6G6C</i>	1,40E-02	1,63E-02	3,90E-01	9,70E-01
cg10914115	6	31704828	<i>CLIC1</i>	-5,30E-03	1,05E-02	6,13E-01	9,72E-01
cg13214149	6	31740978	<i>C6orf27</i>	-1,05E-02	1,30E-02	4,21E-01	9,70E-01
cg24143221	6	31780526	<i>HSPA1L</i>	1,76E-02	1,08E-02	1,02E-01	9,39E-01
cg10012878	6	31827858	<i>NEU1</i>	-4,90E-03	1,35E-02	7,17E-01	9,82E-01
cg20498033	6	31833291	<i>SLC44A4</i>	-1,65E-03	1,44E-02	9,09E-01	9,94E-01
cg04637007	6	31856010	<i>EHMT2</i>	-6,67E-03	1,43E-02	6,40E-01	9,80E-01
cg21786114	6	31866072	<i>EHMT2</i>	1,31E-02	1,48E-02	3,78E-01	9,70E-01
cg05227556	6	32037290	<i>TNXB</i>	-2,25E-03	1,10E-02	8,37E-01	9,94E-01
cg03822479	6	32037913	<i>TNXB</i>	-9,39E-03	1,33E-02	4,82E-01	9,70E-01
cg08753391	6	32049622	<i>TNXB</i>	-8,26E-03	1,01E-02	4,14E-01	9,70E-01
cg10463626	6	32054094	<i>TNXB</i>	6,47E-03	1,26E-02	6,08E-01	9,72E-01
cg23636802	6	32054441	<i>TNXB</i>	2,56E-03	9,50E-03	7,87E-01	9,90E-01
cg08952475	6	32085171	<i>ATF6B</i>	-2,22E-02	1,33E-02	9,49E-02	9,39E-01
cg14226867	6	32131056	<i>EGFL8; PPT2</i>	-9,64E-03	1,33E-02	4,68E-01	9,70E-01
cg16689962	6	32144119	<i>AGPAT1</i>	3,01E-02	1,45E-02	3,75E-02	9,19E-01
cg02525705	6	32145146	<i>RNF5P1; RNF5; AG</i>	-1,86E-02	1,95E-02	3,39E-01	9,70E-01
cg22696073	6	32939982	<i>BRD2</i>	2,45E-02	1,93E-02	2,04E-01	9,59E-01
cg22748722	6	33135868	<i>COL11A2</i>	-2,78E-03	1,32E-02	8,33E-01	9,94E-01
cg00505762	6	33156926	<i>COL11A2</i>	2,20E-03	1,50E-02	8,83E-01	9,94E-01
cg25472257	6	33163566	<i>RXRΒ</i>	-1,88E-02	1,74E-02	2,80E-01	9,70E-01
cg10673265	6	33169975	<i>SLC39A7</i>	3,60E-04	1,16E-02	9,75E-01	9,94E-01
cg08255724	6	33558900	<i>C6orf227</i>	-6,45E-04	1,16E-02	9,56E-01	9,94E-01
cg15153228	6	33562509	<i>C6orf227</i>	-4,58E-03	1,36E-02	7,37E-01	9,82E-01
cg00364051	6	33647861	<i>ITPR3</i>	2,66E-03	1,50E-02	8,59E-01	9,94E-01
cg22147917	6	33656031	<i>ITPR3</i>	-3,76E-02	1,18E-02	1,40E-03	3,15E-01

cg04103326	6	34489623	<i>PACSIM1</i>	7,28E-04	1,20E-02	9,52E-01	9,94E-01
cg18401376	6	35141132	NA	-1,78E-02	9,60E-03	6,31E-02	9,19E-01
cg25145023	6	35348742	<i>PPARD</i>	3,73E-03	1,13E-02	7,41E-01	9,82E-01
cg22184996	6	35773505	<i>LHFPL5</i>	-7,26E-03	1,29E-02	5,73E-01	9,70E-01
cg17055833	6	36936560	<i>MTCH1</i>	1,51E-02	1,12E-02	1,77E-01	9,47E-01
cg12228717	6	37516306	NA	-1,59E-02	1,19E-02	1,81E-01	9,47E-01
cg05897803	6	39290478	<i>KCNK16</i>	-1,64E-03	1,23E-02	8,94E-01	9,94E-01
cg23317857	6	41696297	<i>TFEB</i>	1,73E-02	1,23E-02	1,58E-01	9,47E-01
cg23678165	6	41704577	<i>TFEB; PGC</i>	-2,07E-02	1,25E-02	9,82E-02	9,39E-01
cg09804858	6	42397121	<i>TRERF1</i>	-3,53E-03	1,51E-02	8,15E-01	9,94E-01
cg12691866	6	43211491	<i>TTBK1</i>	4,03E-03	1,66E-02	8,08E-01	9,93E-01
cg11806084	6	43265339	<i>SLC22A7</i>	1,44E-03	1,71E-02	9,33E-01	9,94E-01
cg11553755	6	43458554	<i>TJAP1</i>	-1,34E-02	1,38E-02	3,34E-01	9,70E-01
cg06526189	6	43603987	<i>MAD2L1BP</i>	1,56E-03	1,16E-02	8,93E-01	9,94E-01
cg00904122	6	43612346	<i>RSPH9</i>	-7,55E-03	1,39E-02	5,86E-01	9,70E-01
cg01172073	6	43857911	<i>LOC100132354</i>	-6,88E-04	9,41E-03	9,42E-01	9,94E-01
cg14155184	6	44120425	<i>TMEM63B</i>	1,02E-02	1,60E-02	5,26E-01	9,70E-01
cg24641186	6	50804147	<i>TFAP2B</i>	-1,11E-02	1,14E-02	3,30E-01	9,70E-01
cg03142905	6	53728998	<i>LRRC1</i>	-5,64E-03	1,25E-02	6,53E-01	9,82E-01
cg10172319	6	56983365	<i>ZNF451</i>	2,44E-03	1,95E-02	9,00E-01	9,94E-01
cg26545913	6	66819090	NA	6,31E-03	1,43E-02	6,58E-01	9,82E-01
cg06598631	6	88300029	<i>RARS2; ORC3L</i>	2,15E-02	1,17E-02	6,70E-02	9,19E-01
cg18018027	6	99275335	NA	-4,70E-03	1,56E-02	7,63E-01	9,84E-01
cg03016906	6	99275391	NA	2,32E-03	1,21E-02	8,47E-01	9,94E-01
cg14762454	6	99791204	<i>C6orf168</i>	-1,87E-03	1,31E-02	8,86E-01	9,94E-01
cg04859726	6	100894513	<i>SIMI</i>	-6,46E-03	1,05E-02	5,40E-01	9,70E-01
cg23796329	6	107423930	<i>BEND3</i>	1,43E-02	1,34E-02	2,85E-01	9,70E-01
cg26330809	6	112620506	NA	-8,77E-03	1,08E-02	4,17E-01	9,70E-01
cg27423027	6	131147800	<i>LOC285733</i>	1,89E-02	1,30E-02	1,47E-01	9,39E-01
cg24826784	6	131952764	NA	-5,04E-03	1,47E-02	7,32E-01	9,82E-01
cg25380151	6	135259247	<i>ALDH8A1</i>	6,23E-03	1,26E-02	6,21E-01	9,73E-01
cg16364191	6	138745647	<i>NHSL1</i>	-1,29E-02	1,83E-02	4,82E-01	9,70E-01
cg23160829	6	145219031	NA	-2,21E-03	1,42E-02	8,76E-01	9,94E-01
cg01163931	6	149305804	<i>UST</i>	5,59E-03	1,22E-02	6,48E-01	9,81E-01
cg14081861	6	151288153	<i>MTHFD1L</i>	9,22E-03	9,76E-03	3,45E-01	9,70E-01
cg17264670	6	153452732	<i>RGS17</i>	-2,18E-02	1,33E-02	1,03E-01	9,39E-01
cg02843277	6	155569443	<i>TIAM2</i>	5,63E-03	1,24E-02	6,50E-01	9,81E-01
cg17415033	6	157009149	NA	1,19E-02	1,34E-02	3,77E-01	9,70E-01
cg07487751	6	157982145	<i>ZDHHC14</i>	1,81E-03	1,47E-02	9,02E-01	9,94E-01
cg05787951	6	166100605	NA	8,02E-03	1,14E-02	4,82E-01	9,70E-01
cg13386903	6	167250429	<i>RPS6KA2</i>	-7,84E-03	1,30E-02	5,47E-01	9,70E-01
cg27312458	6	169277149	NA	-7,64E-03	1,31E-02	5,60E-01	9,70E-01
cg10308611	6	169567348	NA	-1,22E-02	1,72E-02	4,80E-01	9,70E-01
cg12035402	6	170559277	NA	1,08E-02	1,64E-02	5,12E-01	9,70E-01
cg15984460	6	170744215	NA	6,96E-03	1,62E-02	6,67E-01	9,82E-01
cg23884358	7	184010	NA	6,91E-03	1,70E-02	6,84E-01	9,82E-01

cg22891003	7	537740	<i>PDGFA</i>	-1,34E-04	1,45E-02	9,93E-01	9,98E-01
cg13832457	7	590072	<i>PRKAR1B</i>	-5,80E-03	1,05E-02	5,82E-01	9,70E-01
cg04179654	7	594082	<i>PRKAR1B</i>	-6,00E-03	1,58E-02	7,04E-01	9,82E-01
cg15899297	7	734968	<i>PRKAR1B</i>	-6,02E-03	1,55E-02	6,98E-01	9,82E-01
cg20109936	7	818309	<i>HEATR2</i>	-7,45E-03	1,23E-02	5,46E-01	9,70E-01
cg16285946	7	906799	<i>UNC84A</i>	-1,67E-02	1,47E-02	2,55E-01	9,70E-01
cg18664915	7	1043861	<i>C7orf50</i>	-1,10E-02	1,09E-02	3,12E-01	9,70E-01
cg17893108	7	1057944	<i>C7orf50</i>	8,89E-03	1,05E-02	3,97E-01	9,70E-01
cg17581870	7	1062965	<i>MIR339; C7orf50</i>	3,84E-04	1,69E-02	9,82E-01	9,94E-01
cg19765378	7	1148301	<i>C7orf50</i>	-1,28E-03	1,47E-02	9,31E-01	9,94E-01
cg02471897	7	1281200	NA	-7,92E-03	1,64E-02	6,30E-01	9,76E-01
cg09754845	7	1408818	NA	-9,59E-03	1,58E-02	5,44E-01	9,70E-01
cg24172278	7	1526831	<i>INTS1</i>	-2,66E-02	1,45E-02	6,76E-02	9,19E-01
cg21593345	7	1602273	NA	1,11E-02	1,03E-02	2,78E-01	9,70E-01
cg07803377	7	1641886	NA	-3,28E-02	1,22E-02	7,05E-03	7,50E-01
cg20824189	7	1704082	NA	-1,08E-02	1,70E-02	5,26E-01	9,70E-01
cg03994184	7	1714969	NA	-1,75E-02	1,44E-02	2,25E-01	9,59E-01
cg12677853	7	1865923	<i>MAD1L1</i>	1,24E-02	1,92E-02	5,18E-01	9,70E-01
cg13700912	7	1968348	<i>MAD1L1</i>	-4,49E-03	1,35E-02	7,39E-01	9,82E-01
cg25300390	7	1976351	<i>MAD1L1</i>	-1,74E-02	1,26E-02	1,68E-01	9,47E-01
cg25573368	7	1993468	<i>MAD1L1</i>	-9,14E-03	1,43E-02	5,23E-01	9,70E-01
cg22500280	7	2007588	<i>MAD1L1</i>	-1,36E-02	1,44E-02	3,43E-01	9,70E-01
cg20943353	7	2020583	<i>MAD1L1</i>	-4,26E-03	1,25E-02	7,33E-01	9,82E-01
cg17373904	7	2091006	<i>MAD1L1</i>	-2,06E-02	1,48E-02	1,66E-01	9,47E-01
cg02568153	7	2184201	<i>MAD1L1</i>	-4,91E-03	1,56E-02	7,53E-01	9,82E-01
cg14397500	7	2214759	<i>MAD1L1</i>	-1,27E-02	1,20E-02	2,91E-01	9,70E-01
cg03358113	7	2253070	<i>MAD1L1</i>	-2,18E-02	1,51E-02	1,48E-01	9,39E-01
cg22966391	7	2416675	<i>EIF3B</i>	-9,05E-03	1,11E-02	4,14E-01	9,70E-01
cg20870668	7	2608671	<i>IQCE</i>	-1,58E-02	1,28E-02	2,15E-01	9,59E-01
cg23873200	7	2626189	<i>IQCE</i>	-1,59E-02	1,31E-02	2,26E-01	9,59E-01
cg12904298	7	2698123	<i>TTYH3</i>	-1,01E-02	1,19E-02	3,96E-01	9,70E-01
cg26603629	7	2752217	<i>AMZ1</i>	-9,60E-03	1,07E-02	3,71E-01	9,70E-01
cg15638239	7	3025736	<i>CARD11</i>	3,60E-03	1,36E-02	7,91E-01	9,90E-01
cg20780013	7	4302246	<i>SDK1</i>	8,79E-03	1,28E-02	4,93E-01	9,70E-01
cg10007182	7	4743146	<i>FOXK1</i>	-1,98E-02	1,26E-02	1,17E-01	9,39E-01
cg02843503	7	6865989	<i>C7orf28B</i>	3,38E-02	1,57E-02	3,18E-02	9,19E-01
cg23976336	7	8254711	<i>ICA1</i>	-2,10E-02	1,35E-02	1,20E-01	9,39E-01
cg23074799	7	18126459	NA	-9,48E-03	1,63E-02	5,61E-01	9,70E-01
cg20052718	7	19156902	<i>TWIST1</i>	5,98E-04	1,38E-02	9,66E-01	9,94E-01
cg12593515	7	22233159	<i>RAPGEF5</i>	-5,41E-04	1,67E-02	9,74E-01	9,94E-01
cg17102984	7	23749885	<i>STK31</i>	-3,77E-04	1,18E-02	9,75E-01	9,94E-01
cg21778348	7	27194614	<i>HOXA7</i>	-1,26E-02	1,75E-02	4,70E-01	9,70E-01
cg19081450	7	30965448	NA	7,04E-04	1,15E-02	9,51E-01	9,94E-01
cg25820223	7	41925404	NA	-3,13E-03	1,44E-02	8,28E-01	9,94E-01
cg09838336	7	43733719	<i>C7orf44</i>	-4,33E-03	1,22E-02	7,23E-01	9,82E-01
cg19146577	7	44171808	NA	7,93E-04	1,43E-02	9,56E-01	9,94E-01

cg23339363	7	44261644	<i>CAMK2B</i>	-1,14E-02	1,15E-02	3,21E-01	9,70E-01
cg25592353	7	45139780	<i>TBRG4</i>	-1,76E-02	1,33E-02	1,87E-01	9,47E-01
cg02897457	7	45144268	<i>TBRG4; SNORA5A</i>	-1,74E-02	1,39E-02	2,10E-01	9,59E-01
cg04018023	7	47616088	NA	-1,38E-02	1,17E-02	2,38E-01	9,70E-01
cg26050906	7	50800202	<i>GRB10</i>	9,30E-04	1,03E-02	9,28E-01	9,94E-01
cg16182302	7	55553545	<i>VOPPI</i>	-6,87E-03	1,36E-02	6,13E-01	9,72E-01
cg17162319	7	57927783	NA	3,41E-03	1,40E-02	8,07E-01	9,93E-01
cg27429258	7	73093795	NA	-9,41E-03	1,29E-02	4,67E-01	9,70E-01
cg20991937	7	73790421	<i>CLIP2</i>	1,07E-02	1,84E-02	5,63E-01	9,70E-01
cg09346547	7	75189280	<i>HIP1</i>	-2,82E-02	1,36E-02	3,88E-02	9,19E-01
cg02435538	7	75507337	<i>RHBDD2</i>	1,14E-02	1,24E-02	3,55E-01	9,70E-01
cg27154660	7	75599137	<i>POR</i>	-1,94E-02	1,23E-02	1,14E-01	9,39E-01
cg13422359	7	75959073	<i>YWHAG</i>	8,39E-03	1,42E-02	5,55E-01	9,70E-01
cg05879075	7	76030355	<i>ZP3; SRCRB4D</i>	-3,27E-04	1,01E-02	9,74E-01	9,94E-01
cg17304553	7	76623419	<i>PMS2L11</i>	-1,38E-02	1,31E-02	2,94E-01	9,70E-01
cg06765022	7	76628673	<i>PMS2L11</i>	1,64E-02	1,53E-02	2,85E-01	9,70E-01
cg06857316	7	97846357	<i>TECPR1</i>	-2,04E-02	1,20E-02	8,93E-02	9,39E-01
cg21768835	7	97857938	<i>TECPR1</i>	5,47E-03	1,59E-02	7,31E-01	9,82E-01
cg13878520	7	98254487	<i>NPTX2</i>	-2,06E-02	1,11E-02	6,46E-02	9,19E-01
cg10154880	7	98603502	<i>TRRAP</i>	4,78E-04	9,43E-03	9,60E-01	9,94E-01
cg07213487	7	98603561	<i>TRRAP</i>	7,01E-03	1,10E-02	5,22E-01	9,70E-01
cg22940022	7	99691200	<i>MCM7; MIR25</i>	-1,49E-02	1,20E-02	2,14E-01	9,59E-01
cg12981876	7	100279795	<i>GIGYF1</i>	7,03E-03	1,35E-02	6,04E-01	9,72E-01
cg11693986	7	100805303	NA	-1,23E-02	1,23E-02	3,17E-01	9,70E-01
cg14859317	7	100853623	<i>PLOD3</i>	1,15E-02	2,22E-02	6,03E-01	9,72E-01
cg10720966	7	101863862	<i>CUX1</i>	-2,39E-02	1,39E-02	8,58E-02	9,39E-01
cg01338378	7	102036355	<i>PRKRIP1</i>	-5,17E-03	1,25E-02	6,80E-01	9,82E-01
cg20102246	7	102036757	<i>PRKRIP1</i>	-1,46E-02	1,74E-02	4,04E-01	9,70E-01
cg09490124	7	105128488	<i>PUS7</i>	1,29E-02	1,40E-02	3,56E-01	9,70E-01
cg25011530	7	105162470	<i>PUS7</i>	1,95E-02	1,76E-02	2,68E-01	9,70E-01
cg22811478	7	111505623	<i>DOCK4</i>	-1,20E-02	1,28E-02	3,49E-01	9,70E-01
cg14107644	7	123673390	<i>TMEM229A</i>	-2,15E-02	1,49E-02	1,50E-01	9,39E-01
cg11694513	7	127720696	<i>SDN1; MIR593</i>	-2,16E-02	1,18E-02	6,74E-02	9,19E-01
cg00670111	7	128500474	NA	-6,32E-03	8,80E-03	4,73E-01	9,70E-01
cg23537419	7	128533587	<i>KCP</i>	-8,31E-03	1,08E-02	4,43E-01	9,70E-01
cg08751971	7	128587827	<i>IRF5</i>	-1,46E-02	1,48E-02	3,26E-01	9,70E-01
cg09388414	7	129414651	<i>MIR96</i>	-6,31E-03	1,02E-02	5,36E-01	9,70E-01
cg16811875	7	132192823	<i>PLXNA4</i>	-9,51E-03	1,38E-02	4,90E-01	9,70E-01
cg16690859	7	132332297	<i>PLXNA4</i>	-2,21E-02	1,22E-02	7,08E-02	9,19E-01
cg07718324	7	133995578	<i>SLC35B4</i>	-2,35E-03	1,70E-02	8,90E-01	9,94E-01
cg04915064	7	137983235	NA	-1,14E-02	1,64E-02	4,87E-01	9,70E-01
cg26407309	7	139479119	<i>TBXAS1; HIPK2</i>	-2,12E-03	1,16E-02	8,55E-01	9,94E-01
cg25009327	7	148820504	<i>ZNF425</i>	-1,44E-02	1,63E-02	3,77E-01	9,70E-01
cg00643862	7	150865186	<i>GBX1</i>	-2,15E-03	1,49E-02	8,85E-01	9,94E-01
cg15977893	7	151475761	<i>PRKAG2</i>	-1,80E-02	1,38E-02	1,91E-01	9,47E-01
cg26407811	7	151565595	<i>PRKAG2</i>	-1,50E-02	1,28E-02	2,42E-01	9,70E-01

cg27570732	7	155738650	NA	1,36E-02	1,86E-02	4,64E-01	9,70E-01
cg07134031	7	157073436	NA	2,59E-02	1,66E-02	1,19E-01	9,39E-01
cg00461149	7	157452656	<i>PTPRN2</i>	-1,55E-02	1,15E-02	1,76E-01	9,47E-01
cg21587319	7	157633985	<i>PTPRN2</i>	-5,68E-03	1,34E-02	6,72E-01	9,82E-01
cg16486501	7	157639351	<i>PTPRN2</i>	8,40E-04	1,11E-02	9,40E-01	9,94E-01
cg09042009	7	157641737	<i>PTPRN2</i>	-2,60E-03	1,12E-02	8,16E-01	9,94E-01
cg13409070	7	158114558	<i>PTPRN2</i>	-4,39E-03	1,75E-02	8,03E-01	9,93E-01
cg09512004	7	158802917	<i>LOC154822</i>	-1,99E-03	1,20E-02	8,69E-01	9,94E-01
cg10765397	8	1283671	NA	9,71E-03	1,16E-02	4,01E-01	9,70E-01
cg11966432	8	1617616	<i>DLGAP2</i>	1,23E-02	1,38E-02	3,73E-01	9,70E-01
cg09529783	8	1958930	NA	1,59E-02	1,07E-02	1,39E-01	9,39E-01
cg18050997	8	8176225	<i>PRAGMIN</i>	-1,30E-02	1,27E-02	3,04E-01	9,70E-01
cg17371580	8	9182401	NA	-1,19E-03	1,17E-02	9,19E-01	9,94E-01
cg20744156	8	9476731	<i>TNKS</i>	-1,17E-02	1,46E-02	4,26E-01	9,70E-01
cg10147394	8	11350297	<i>BLK</i>	1,63E-02	1,22E-02	1,80E-01	9,47E-01
cg16015276	8	11550445	NA	-1,29E-02	1,40E-02	3,58E-01	9,70E-01
cg22320962	8	11560299	<i>GATA4</i>	4,92E-03	1,44E-02	7,33E-01	9,82E-01
cg03654169	8	11710911	<i>CTSB</i>	1,16E-02	1,47E-02	4,29E-01	9,70E-01
cg06933322	8	12654008	<i>LOC340357</i>	1,88E-02	1,81E-02	3,00E-01	9,70E-01
cg12741231	8	19321936	<i>CSGALNACT1</i>	7,57E-03	1,34E-02	5,72E-01	9,70E-01
cg22272100	8	22069313	<i>BMP1</i>	1,77E-02	1,32E-02	1,82E-01	9,47E-01
cg18025275	8	22498768	<i>BIN3; FLJ14107</i>	4,27E-03	1,31E-02	7,45E-01	9,82E-01
cg26718357	8	22554232	NA	-2,96E-02	1,23E-02	1,56E-02	8,28E-01
cg00742963	8	22721575	<i>PEBP4</i>	-1,98E-03	1,27E-02	8,76E-01	9,94E-01
cg19879483	8	26025686	NA	-5,40E-03	1,18E-02	6,49E-01	9,81E-01
cg24468765	8	37176193	NA	1,62E-02	1,10E-02	1,39E-01	9,39E-01
cg09576978	8	41554080	<i>ANK1</i>	-5,52E-03	1,08E-02	6,08E-01	9,72E-01
cg26248082	8	42356127	<i>SLC20A2</i>	2,15E-03	1,70E-02	8,99E-01	9,94E-01
cg26393356	8	49466210	NA	-3,10E-03	1,05E-02	7,68E-01	9,84E-01
cg16318412	8	49745160	NA	-2,78E-03	1,04E-02	7,90E-01	9,90E-01
cg22862746	8	53477545	<i>FAM150A</i>	-1,90E-02	1,43E-02	1,84E-01	9,47E-01
cg19963313	8	59571604	<i>NSMAF</i>	1,70E-02	1,29E-02	1,89E-01	9,47E-01
cg27135989	8	61088342	NA	1,02E-02	1,41E-02	4,68E-01	9,70E-01
cg10757989	8	61621248	<i>CHD7</i>	-1,23E-02	2,00E-02	5,39E-01	9,70E-01
cg19783015	8	61936333	NA	-9,53E-04	1,06E-02	9,29E-01	9,94E-01
cg12897502	8	67425316	<i>C8orf46</i>	-7,31E-03	1,23E-02	5,52E-01	9,70E-01
cg03347018	8	72756882	<i>MSC</i>	-6,88E-03	1,75E-02	6,95E-01	9,82E-01
cg06592178	8	74197678	NA	-2,45E-02	1,44E-02	8,90E-02	9,39E-01
cg05525416	8	81983499	<i>PAG1</i>	7,77E-03	1,12E-02	4,87E-01	9,70E-01
cg04904932	8	87073162	<i>PSKH2</i>	3,79E-03	1,05E-02	7,18E-01	9,82E-01
cg10419556	8	98273126	NA	-3,00E-03	1,23E-02	8,07E-01	9,93E-01
cg13170640	8	98471635	NA	1,05E-02	9,85E-03	2,86E-01	9,70E-01
cg25605550	8	101256880	NA	-1,61E-02	1,18E-02	1,72E-01	9,47E-01
cg14603085	8	101485532	NA	-1,59E-02	1,38E-02	2,51E-01	9,70E-01
cg00402617	8	101962843	<i>YWHAZ</i>	-4,33E-04	1,68E-02	9,79E-01	9,94E-01
cg20402658	8	102702514	<i>NCALD</i>	1,09E-03	1,36E-02	9,36E-01	9,94E-01

cg20611272	8	103548145	NA	1,59E-02	6,31E-03	1,16E-02	8,28E-01
cg25021532	8	107782513	<i>ABRA</i>	1,12E-02	1,77E-02	5,27E-01	9,70E-01
cg01823440	8	120870729	NA	1,64E-02	1,23E-02	1,82E-01	9,47E-01
cg20364222	8	125259763	NA	-4,11E-03	1,02E-02	6,87E-01	9,82E-01
cg15235922	8	125678187	<i>MTSSI</i>	1,06E-02	1,11E-02	3,40E-01	9,70E-01
cg23409608	8	128878013	<i>PVT1</i>	-1,47E-02	9,90E-03	1,36E-01	9,39E-01
cg21473775	8	131423145	NA	6,15E-03	1,03E-02	5,51E-01	9,70E-01
cg13157158	8	133911007	<i>TG</i>	2,25E-03	1,11E-02	8,40E-01	9,94E-01
cg06772221	8	134062192	<i>SLA; TG</i>	-7,84E-04	1,13E-02	9,45E-01	9,94E-01
cg01668008	8	134701487	NA	1,87E-02	1,25E-02	1,36E-01	9,39E-01
cg02225004	8	140970377	<i>TRAPPC9</i>	-1,92E-02	1,32E-02	1,46E-01	9,39E-01
cg08626916	8	141111080	<i>TRAPPC9</i>	-8,42E-03	1,36E-02	5,36E-01	9,70E-01
cg24388061	8	141249678	<i>TRAPPC9</i>	1,01E-03	1,30E-02	9,38E-01	9,94E-01
cg14301764	8	141636542	<i>EIF2C2</i>	-1,19E-02	1,34E-02	3,74E-01	9,70E-01
cg10064585	8	142186995	<i>DENND3</i>	8,89E-03	1,38E-02	5,19E-01	9,70E-01
cg07437919	8	142234483	<i>SLC45A4</i>	-4,41E-03	1,44E-02	7,60E-01	9,84E-01
cg00131691	8	142295774	NA	9,07E-03	1,59E-02	5,70E-01	9,70E-01
cg10982692	8	142367177	<i>GPR20</i>	-1,19E-02	1,19E-02	3,17E-01	9,70E-01
cg23278359	8	142439128	<i>PTP4A3</i>	-2,96E-02	1,17E-02	1,15E-02	8,28E-01
cg10796400	8	143129203	NA	-2,71E-02	1,23E-02	2,82E-02	9,19E-01
cg24823764	8	143192949	NA	-1,66E-02	1,45E-02	2,51E-01	9,70E-01
cg02860255	8	143405663	<i>TSNARE1</i>	9,60E-03	1,41E-02	4,95E-01	9,70E-01
cg23641319	8	143862739	NA	-3,58E-05	1,33E-02	9,98E-01	9,99E-01
cg21600380	8	143887648	NA	-2,35E-02	1,02E-02	2,12E-02	8,51E-01
cg04517258	8	144094955	<i>LOC100133669</i>	-1,68E-02	1,34E-02	2,11E-01	9,59E-01
cg00598766	8	144099719	<i>LY6E; LOC1001336</i>	2,24E-02	1,87E-02	2,32E-01	9,70E-01
cg01121892	8	144294486	<i>GPIHBP1</i>	-1,81E-02	1,22E-02	1,37E-01	9,39E-01
cg01779882	8	144408866	<i>TOP1MT</i>	-1,28E-02	1,41E-02	3,64E-01	9,70E-01
cg26387966	8	144503421	NA	1,29E-02	1,93E-02	5,04E-01	9,70E-01
cg05716567	8	144620690	<i>ZC3H3</i>	-1,82E-02	1,20E-02	1,28E-01	9,39E-01
cg04146982	8	144943809	<i>EPPK1</i>	-1,72E-02	1,12E-02	1,25E-01	9,39E-01
cg00128812	8	145019377	<i>PLEC1; MIR661</i>	-2,83E-02	1,28E-02	2,71E-02	9,16E-01
cg26403198	8	145581686	<i>FBXL6; GPR172A</i>	-9,06E-03	1,33E-02	4,97E-01	9,70E-01
cg03492874	8	145649623	<i>VPS28</i>	-4,98E-03	1,86E-02	7,89E-01	9,90E-01
cg25765796	8	145770921	<i>KIAA1688</i>	2,06E-02	1,36E-02	1,32E-01	9,39E-01
cg22094607	8	145822053	<i>KIAA1688</i>	6,81E-03	1,58E-02	6,67E-01	9,82E-01
cg00998132	8	145844626	NA	1,56E-02	1,25E-02	2,14E-01	9,59E-01
cg14312921	9	1979255	NA	1,39E-02	1,21E-02	2,51E-01	9,70E-01
cg21186778	9	4855519	<i>RCL1</i>	-9,45E-05	1,31E-02	9,94E-01	9,98E-01
cg14323977	9	35160337	NA	-3,98E-03	1,39E-02	7,75E-01	9,88E-01
cg15518883	9	35650561	<i>SIT1</i>	3,57E-03	7,58E-03	6,38E-01	9,80E-01
cg14068176	9	35833117	<i>TMEM8B</i>	5,71E-03	1,58E-02	7,18E-01	9,82E-01
cg13415773	9	38091405	NA	-1,53E-02	1,13E-02	1,76E-01	9,47E-01
cg14184130	9	38437270	NA	2,74E-03	1,08E-02	8,00E-01	9,92E-01
cg13580827	9	72081155	<i>APBA1</i>	7,08E-03	9,97E-03	4,78E-01	9,70E-01
cg21217093	9	81871809	NA	-1,50E-02	1,56E-02	3,36E-01	9,70E-01

cg13803727	9	89445247	NA	-4,97E-03	1,01E-02	6,21E-01	9,73E-01
cg13912573	9	92293297	<i>LOC100129066</i>	-4,14E-03	9,38E-03	6,59E-01	9,82E-01
cg13439189	9	93926553	NA	-2,20E-04	9,41E-03	9,81E-01	9,94E-01
cg05385163	9	96717349	<i>BARX1</i>	-6,71E-03	1,41E-02	6,33E-01	9,78E-01
cg21175995	9	100212503	<i>TDRD7</i>	1,19E-02	1,65E-02	4,73E-01	9,70E-01
cg14172375	9	112540087	<i>PALM2</i>	6,19E-03	1,21E-02	6,10E-01	9,72E-01
cg14074944	9	117820838	<i>TNC</i>	9,91E-03	1,27E-02	4,37E-01	9,70E-01
cg13418964	9	124753187	<i>TTLL11</i>	-1,54E-02	1,58E-02	3,30E-01	9,70E-01
cg14584535	9	125797187	<i>GPR21; RABGAP1</i>	-1,20E-02	6,70E-03	7,29E-02	9,19E-01
cg13543915	9	134293793	NA	-5,07E-03	1,12E-02	6,49E-01	9,81E-01
cg01944288	9	135036217	<i>NTNG2</i>	-1,38E-02	6,53E-03	3,45E-02	9,19E-01
cg25020204	9	136500234	<i>DBH</i>	1,44E-02	1,25E-02	2,49E-01	9,70E-01
cg14581063	9	137015854	<i>WDR5</i>	4,02E-03	1,72E-02	8,15E-01	9,94E-01
cg14462321	9	137232372	<i>RXRA</i>	-1,38E-02	1,32E-02	2,98E-01	9,70E-01
cg05328939	9	137731025	<i>COL5A1</i>	-8,07E-03	1,33E-02	5,44E-01	9,70E-01
cg05517900	9	139127931	<i>QSOX2</i>	5,70E-03	1,41E-02	6,86E-01	9,82E-01
cg14186779	9	139243399	<i>GPSM1</i>	-7,74E-03	9,73E-03	4,26E-01	9,70E-01
cg14108380	9	139299357	<i>SDCCAG3</i>	3,11E-03	1,44E-02	8,29E-01	9,94E-01
cg14031679	9	139466195	NA	-2,84E-02	1,36E-02	3,64E-02	9,19E-01
cg21157923	9	139637747	<i>LCN10</i>	-2,75E-03	1,29E-02	8,31E-01	9,94E-01
cg16536450	9	139658896	<i>LCN15</i>	-1,20E-02	2,02E-02	5,52E-01	9,70E-01
cg13710542	9	140261971	<i>EXD3</i>	-1,57E-02	1,19E-02	1,89E-01	9,47E-01
cg12149666	9	140375580	<i>PNPLA7</i>	-1,45E-02	1,27E-02	2,54E-01	9,70E-01
cg23889654	10	860862	<i>LARP4B</i>	8,55E-03	1,50E-02	5,69E-01	9,70E-01
cg22671939	10	1000300	NA	-1,96E-02	1,39E-02	1,59E-01	9,47E-01
cg10435021	10	1383845	<i>ADARB2</i>	-5,81E-03	1,30E-02	6,54E-01	9,82E-01
cg17405812	10	1708500	<i>ADARB2</i>	1,14E-02	1,24E-02	3,57E-01	9,70E-01
cg22851864	10	5688470	<i>ASB13</i>	-1,42E-02	1,74E-02	4,13E-01	9,70E-01
cg18184053	10	5882739	NA	-3,04E-03	1,11E-02	7,84E-01	9,90E-01
cg12664173	10	6220910	<i>PFKFB3</i>	4,94E-03	1,81E-02	7,84E-01	9,90E-01
cg20619600	10	8056766	NA	-1,87E-02	1,76E-02	2,88E-01	9,70E-01
cg15043723	10	8106006	<i>GATA3</i>	-2,81E-02	1,24E-02	2,36E-02	8,77E-01
cg26394636	10	11934469	NA	-7,57E-03	1,32E-02	5,68E-01	9,70E-01
cg25844612	10	13510336	<i>BEND7</i>	-8,64E-03	1,08E-02	4,25E-01	9,70E-01
cg17436460	10	17028480	<i>CUBN</i>	-1,35E-02	1,51E-02	3,71E-01	9,70E-01
cg02165095	10	17428870	<i>ST8SIA6</i>	-1,76E-02	1,93E-02	3,60E-01	9,70E-01
cg13307451	10	22541442	NA	1,15E-02	1,35E-02	3,97E-01	9,70E-01
cg13590166	10	28749464	NA	1,30E-03	1,55E-02	9,33E-01	9,94E-01
cg06338697	10	34587539	<i>PARD3</i>	1,41E-02	1,65E-02	3,93E-01	9,70E-01
cg26795540	10	35082070	<i>PARD3</i>	-4,03E-03	1,01E-02	6,89E-01	9,82E-01
cg27432596	10	35703937	<i>CCNY</i>	-1,09E-02	1,08E-02	3,14E-01	9,70E-01
cg07024656	10	42970618	<i>LOC84856</i>	-1,93E-02	1,22E-02	1,14E-01	9,39E-01
cg00441573	10	43428471	NA	8,17E-03	1,18E-02	4,89E-01	9,70E-01
cg11200635	10	43573195	<i>RET</i>	2,46E-03	1,59E-02	8,77E-01	9,94E-01
cg07262450	10	44500868	NA	-8,86E-03	1,52E-02	5,60E-01	9,70E-01
cg12877354	10	45873196	<i>ALOX5</i>	-1,34E-02	1,24E-02	2,78E-01	9,70E-01

cg10690063	10	45934973	<i>ALOX5</i>	-7,29E-03	1,31E-02	5,79E-01	9,70E-01
cg10195962	10	47656369	NA	1,04E-02	1,69E-02	5,38E-01	9,70E-01
cg00350920	10	48416463	<i>GDF2</i>	-1,76E-02	1,28E-02	1,70E-01	9,47E-01
cg16181642	10	48491692	NA	6,37E-05	1,15E-02	9,96E-01	9,99E-01
cg25921502	10	50363896	<i>C10orf128</i>	-1,24E-02	1,27E-02	3,31E-01	9,70E-01
cg06325088	10	50506748	<i>C10orf71</i>	6,20E-03	1,16E-02	5,94E-01	9,72E-01
cg07113562	10	52834093	<i>PRKG1</i>	1,15E-02	1,55E-02	4,56E-01	9,70E-01
cg19531732	10	71583676	<i>COL13A1</i>	-9,95E-03	1,04E-02	3,39E-01	9,70E-01
cg13908507	10	71876389	<i>AIFM2</i>	-1,33E-02	1,25E-02	2,88E-01	9,70E-01
cg25256493	10	72297852	<i>KIAA1274</i>	-2,61E-02	1,24E-02	3,59E-02	9,19E-01
cg05824757	10	72574568	<i>SGPL1</i>	-7,62E-03	1,23E-02	5,37E-01	9,70E-01
cg26005973	10	72643678	<i>PCBD1</i>	-9,25E-03	1,11E-02	4,03E-01	9,70E-01
cg02581163	10	73063873	NA	1,59E-04	1,08E-02	9,88E-01	9,97E-01
cg23432673	10	75549286	<i>KIAA0913</i>	-2,28E-02	1,28E-02	7,39E-02	9,19E-01
cg03299991	10	79273865	<i>KCNMA1</i>	-3,02E-03	1,24E-02	8,08E-01	9,93E-01
cg04951051	10	79601860	<i>DLG5</i>	6,63E-04	1,93E-02	9,73E-01	9,94E-01
cg03455990	10	80052820	NA	9,85E-03	1,11E-02	3,75E-01	9,70E-01
cg08354614	10	80673607	NA	-1,48E-03	1,11E-02	8,94E-01	9,94E-01
cg19215199	10	81005284	<i>ZMIZ1</i>	-7,25E-03	1,33E-02	5,85E-01	9,70E-01
cg02795981	10	81045119	<i>ZMIZ1</i>	2,42E-02	1,08E-02	2,48E-02	8,77E-01
cg03481488	10	81091172	NA	-2,33E-03	1,19E-02	8,45E-01	9,94E-01
cg26185061	10	81744786	NA	4,60E-03	8,69E-03	5,96E-01	9,72E-01
cg03730709	10	81954663	<i>ANXA11</i>	4,90E-03	1,40E-02	7,26E-01	9,82E-01
cg12575674	10	82362642	<i>SH2D4B</i>	3,10E-03	9,48E-03	7,44E-01	9,82E-01
cg18165251	10	85961024	<i>PCDH21</i>	-2,76E-03	1,35E-02	8,38E-01	9,94E-01
cg16232721	10	86003563	<i>RGR</i>	-4,46E-03	1,23E-02	7,17E-01	9,82E-01
cg14861584	10	89970534	NA	1,49E-02	1,48E-02	3,13E-01	9,70E-01
cg15433798	10	92913556	<i>NUDT9P1</i>	-3,22E-02	1,90E-02	8,94E-02	9,39E-01
cg27220117	10	95218729	<i>MYOF</i>	-3,62E-03	8,92E-03	6,85E-01	9,82E-01
cg20540372	10	98031961	<i>BLNK</i>	1,71E-02	1,26E-02	1,75E-01	9,47E-01
cg22756156	10	99477573	<i>MARVELD1; LOC100</i>	-1,99E-03	1,34E-02	8,82E-01	9,94E-01
cg14108015	10	99539219	NA	-1,01E-02	1,15E-02	3,78E-01	9,70E-01
cg03236397	10	100992429	<i>HPSE2</i>	-2,63E-03	1,46E-02	8,57E-01	9,94E-01
cg19842683	10	102795320	<i>SFXN3</i>	-1,51E-02	1,49E-02	3,10E-01	9,70E-01
cg02721701	10	104597307	<i>CYP17A1</i>	1,24E-02	1,38E-02	3,68E-01	9,70E-01
cg12264333	10	105209552	<i>CALHM2</i>	-7,47E-03	1,15E-02	5,18E-01	9,70E-01
cg04762698	10	105362388	<i>SH3PXD2A</i>	7,74E-03	1,78E-02	6,63E-01	9,82E-01
cg11385165	10	105388937	<i>SH3PXD2A</i>	-1,39E-02	1,18E-02	2,38E-01	9,70E-01
cg20289746	10	106075738	<i>ITPRIP</i>	-1,55E-02	1,18E-02	1,86E-01	9,47E-01
cg27020161	10	108318417	NA	3,61E-03	1,21E-02	7,65E-01	9,84E-01
cg24480227	10	114489426	<i>VTI1A</i>	7,01E-04	1,46E-02	9,62E-01	9,94E-01
cg15018122	10	114804865	<i>TCF7L2</i>	-1,17E-02	1,09E-02	2,84E-01	9,70E-01
cg17897352	10	121011644	<i>GRK5</i>	1,75E-03	1,63E-02	9,14E-01	9,94E-01
cg18430255	10	121028978	<i>GRK5</i>	1,01E-02	7,70E-03	1,91E-01	9,47E-01
cg10837142	10	121765342	NA	5,21E-03	1,56E-02	7,39E-01	9,82E-01
cg16595750	10	123338597	<i>FGFR2</i>	-6,31E-03	1,15E-02	5,83E-01	9,70E-01

cg23262973	10	123966834	<i>TACC2</i>	7,67E-04	8,70E-03	9,30E-01	9,94E-01
cg03205140	10	124133802	<i>PLEKHA1</i>	6,31E-03	1,75E-02	7,18E-01	9,82E-01
cg05426956	10	124246168	<i>HTRA1</i>	5,79E-03	8,38E-03	4,89E-01	9,70E-01
cg12164321	10	125651085	<i>CPXM2</i>	-1,08E-02	1,39E-02	4,37E-01	9,70E-01
cg10502884	10	125852315	NA	-6,08E-03	1,49E-02	6,83E-01	9,82E-01
cg16214693	10	126278299	<i>LHPP</i>	-9,59E-03	1,06E-02	3,66E-01	9,70E-01
cg18593374	10	126302546	<i>LHPP</i>	1,77E-03	9,86E-03	8,57E-01	9,94E-01
cg10402121	10	126487101	NA	-3,91E-03	1,27E-02	7,59E-01	9,84E-01
cg05964557	10	130295781	NA	-6,93E-03	1,79E-02	6,99E-01	9,82E-01
cg12881520	10	130844399	NA	-2,76E-03	1,43E-02	8,47E-01	9,94E-01
cg18862686	10	131479347	<i>MGMT</i>	-3,63E-03	1,42E-02	7,98E-01	9,91E-01
cg23239690	10	131505815	<i>MGMT</i>	-1,28E-02	1,38E-02	3,53E-01	9,70E-01
cg15553532	10	131591484	NA	-1,20E-02	1,27E-02	3,44E-01	9,70E-01
cg08975834	10	133036065	<i>TCERGIL</i>	3,97E-03	1,31E-02	7,62E-01	9,84E-01
cg26256560	10	133039159	<i>TCERGIL</i>	1,01E-02	1,18E-02	3,91E-01	9,70E-01
cg25352281	10	133768054	<i>PPP2R2D</i>	4,14E-03	1,54E-02	7,87E-01	9,90E-01
cg10206933	10	133786713	<i>BNIP3</i>	7,42E-03	6,69E-03	2,67E-01	9,70E-01
cg16014906	10	134095321	<i>STK32C</i>	1,34E-02	1,24E-02	2,82E-01	9,70E-01
cg24950817	10	134119275	<i>STK32C</i>	4,13E-03	1,49E-02	7,81E-01	9,90E-01
cg07402396	10	134360977	<i>INPP5A</i>	-2,50E-02	1,22E-02	4,07E-02	9,19E-01
cg00875476	10	134521848	<i>INPP5A</i>	-7,60E-03	1,07E-02	4,77E-01	9,70E-01
cg00483825	10	134751640	<i>C10orf93</i>	-5,85E-03	1,20E-02	6,26E-01	9,75E-01
cg19100464	10	134861410	NA	8,77E-03	1,31E-02	5,02E-01	9,70E-01
cg13457427	10	134955698	NA	4,69E-03	1,65E-02	7,77E-01	9,90E-01
cg23400579	10	135061015	<i>MIR202</i>	-8,27E-03	1,39E-02	5,51E-01	9,70E-01
cg08735411	10	135168096	NA	-2,33E-02	1,16E-02	4,48E-02	9,19E-01
cg06916873	10	135182790	<i>ECHS1</i>	1,30E-02	1,31E-02	3,18E-01	9,70E-01
cg06005177	10	135190664	NA	-5,20E-03	1,32E-02	6,93E-01	9,82E-01
cg23250185	10	135191257	<i>PAOX</i>	-9,05E-03	1,27E-02	4,77E-01	9,70E-01
cg00282877	10	135265980	<i>LOC619207</i>	2,31E-02	1,58E-02	1,44E-01	9,39E-01
cg09216143	10	135270030	<i>LOC619207</i>	-3,42E-02	1,80E-02	5,77E-02	9,19E-01
cg15883382	10	135333805	NA	2,36E-02	1,84E-02	2,01E-01	9,59E-01
cg26203336	11	303166	NA	-1,81E-02	1,31E-02	1,65E-01	9,47E-01
cg25868831	11	368588	<i>B4GALNT4</i>	-2,83E-03	2,07E-02	8,91E-01	9,94E-01
cg11004323	11	490558	<i>PTDSS2</i>	7,39E-03	1,32E-02	5,76E-01	9,70E-01
cg01655721	11	498864	<i>RNH1</i>	1,88E-03	1,75E-02	9,14E-01	9,94E-01
cg02877433	11	660680	<i>DEAF1</i>	9,76E-03	1,15E-02	3,98E-01	9,70E-01
cg00330825	11	811545	<i>RPLP2; SNORA52</i>	-6,35E-03	1,09E-02	5,59E-01	9,70E-01
cg19216994	11	811557	<i>RPLP2; SNORA52</i>	-1,01E-02	1,09E-02	3,53E-01	9,70E-01
cg11650874	11	907967	<i>CHID1</i>	-3,02E-02	1,58E-02	5,63E-02	9,19E-01
cg14504636	11	1001163	<i>AP2A2</i>	-1,93E-02	1,32E-02	1,44E-01	9,39E-01
cg01369233	11	1316833	<i>TOLLIP</i>	-2,26E-02	1,34E-02	9,14E-02	9,39E-01
cg16723180	11	1503195	<i>HCCA2</i>	-2,64E-02	1,43E-02	6,55E-02	9,19E-01
cg25918267	11	1524715	<i>HCCA2</i>	-3,05E-02	1,29E-02	1,83E-02	8,28E-01
cg19432283	11	1526031	<i>HCCA2</i>	-1,30E-02	1,07E-02	2,22E-01	9,59E-01
cg15708618	11	1994117	NA	-5,72E-03	1,03E-02	5,78E-01	9,70E-01

cg22025454	11	2002928	NA	-6,34E-03	1,24E-02	6,10E-01	9,72E-01
cg06495763	11	2925470	<i>SLC22A18</i>	-1,02E-02	1,23E-02	4,09E-01	9,70E-01
cg02390725	11	2925768	<i>SLC22A18</i>	-1,23E-02	1,26E-02	3,30E-01	9,70E-01
cg22366698	11	3400543	<i>ZNF195</i>	1,24E-02	1,66E-02	4,53E-01	9,70E-01
cg07179688	11	3950928	<i>STIM1</i>	3,59E-03	1,35E-02	7,90E-01	9,90E-01
cg22160073	11	5653405	<i>TRIM34</i>	9,15E-03	1,08E-02	3,99E-01	9,70E-01
cg25541544	11	6261598	<i>CNGA4</i>	5,99E-03	1,06E-02	5,73E-01	9,70E-01
cg14240790	11	6378691	NA	1,06E-02	1,08E-02	3,27E-01	9,70E-01
cg08350126	11	6463476	<i>HPX</i>	-1,88E-03	1,30E-02	8,85E-01	9,94E-01
cg04456892	11	6898245	<i>OR10A4</i>	-9,33E-04	1,33E-02	9,44E-01	9,94E-01
cg06324635	11	8787892	<i>ST5</i>	-1,10E-03	9,63E-03	9,09E-01	9,94E-01
cg22997252	11	11643842	<i>GALNTL4</i>	2,36E-02	1,89E-02	2,12E-01	9,59E-01
cg13997645	11	15136475	<i>INSC</i>	-9,67E-03	1,35E-02	4,72E-01	9,70E-01
cg03771731	11	20643929	<i>SLC6A5</i>	-9,20E-03	1,36E-02	4,99E-01	9,70E-01
cg27218154	11	36469878	<i>PRR5L</i>	-1,10E-02	1,41E-02	4,37E-01	9,70E-01
cg01476222	11	36522143	<i>TRAF6</i>	1,47E-02	1,21E-02	2,26E-01	9,59E-01
cg24819471	11	45107960	NA	-1,43E-02	1,65E-02	3,86E-01	9,70E-01
cg05068461	11	45392805	NA	-4,04E-03	1,86E-02	8,29E-01	9,94E-01
cg14904638	11	46726595	<i>ZNF408</i>	-1,40E-02	1,38E-02	3,10E-01	9,70E-01
cg27186519	11	46732376	NA	4,43E-04	1,30E-02	9,73E-01	9,94E-01
cg13527922	11	46741299	<i>F2</i>	-5,25E-03	1,61E-02	7,45E-01	9,82E-01
cg12841566	11	47296317	<i>MADD</i>	-1,03E-02	1,41E-02	4,66E-01	9,70E-01
cg24194730	11	47436603	<i>SLC39A13</i>	-6,66E-04	1,39E-02	9,62E-01	9,94E-01
cg13309027	11	47870224	<i>NUP160</i>	1,86E-02	2,09E-02	3,73E-01	9,70E-01
cg10951214	11	48069893	<i>PTPRJ</i>	-2,04E-02	1,41E-02	1,48E-01	9,39E-01
cg02147041	11	57308142	<i>SMTNL1</i>	-2,24E-02	1,45E-02	1,23E-01	9,39E-01
cg02526508	11	58494370	<i>GLYAT</i>	1,18E-02	1,41E-02	4,04E-01	9,70E-01
cg14329059	11	58940964	<i>DTX4</i>	-7,61E-03	1,72E-02	6,59E-01	9,82E-01
cg25967612	11	59482691	<i>OR10V1</i>	2,65E-03	1,18E-02	8,21E-01	9,94E-01
cg04017555	11	61062704	<i>VWCE</i>	-2,46E-02	1,56E-02	1,15E-01	9,39E-01
cg20242427	11	61115736	<i>DAK</i>	-5,78E-03	6,88E-03	4,01E-01	9,70E-01
cg23111641	11	61117715	<i>CYBASC3</i>	-1,89E-02	1,43E-02	1,84E-01	9,47E-01
cg07607813	11	61488195	<i>DAGLA</i>	-4,91E-03	1,15E-02	6,69E-01	9,82E-01
cg01455069	11	62382430	<i>ROM1</i>	-1,05E-02	1,34E-02	4,33E-01	9,70E-01
cg03347015	11	62490152	<i>HNRNPUL2</i>	-1,88E-02	1,42E-02	1,84E-01	9,47E-01
cg14288399	11	64110785	<i>CCDC88B</i>	-1,79E-03	1,83E-02	9,22E-01	9,94E-01
cg16389348	11	64337279	<i>SLC22A11</i>	1,60E-03	1,24E-02	8,97E-01	9,94E-01
cg03663788	11	64514658	<i>PYGM</i>	1,47E-05	1,27E-02	9,99E-01	9,99E-01
cg07019638	11	64635774	<i>EHD1</i>	4,52E-03	1,07E-02	6,72E-01	9,82E-01
cg20668450	11	64812208	<i>SAC3D1</i>	-9,35E-03	1,35E-02	4,90E-01	9,70E-01
cg11824257	11	65168547	<i>FRMD8</i>	4,73E-03	1,40E-02	7,36E-01	9,82E-01
cg14690315	11	65268175	<i>MALAT1</i>	5,33E-03	1,50E-02	7,22E-01	9,82E-01
cg13179915	11	65362949	<i>KCNK7</i>	-1,34E-02	1,24E-02	2,81E-01	9,70E-01
cg10093679	11	65482056	<i>KAT5</i>	-1,67E-02	1,83E-02	3,60E-01	9,70E-01
cg04519387	11	65556438	<i>OVOL1</i>	2,64E-02	1,86E-02	1,56E-01	9,47E-01
cg01415344	11	65733956	<i>SART1</i>	-5,93E-03	1,67E-02	7,22E-01	9,82E-01

cg22719871	11	66105148	<i>BRMS1; RIN1</i>	-1,85E-02	1,37E-02	1,76E-01	9,47E-01
cg18145189	11	66137134	<i>SLC29A2</i>	-4,26E-03	1,36E-02	7,54E-01	9,82E-01
cg22110770	11	66360551	<i>CCDC87; CCS</i>	-2,62E-02	1,68E-02	1,19E-01	9,39E-01
cg26070604	11	66452967	<i>SPTBN2</i>	-5,97E-03	1,30E-02	6,46E-01	9,81E-01
cg21628794	11	66631894	<i>PC</i>	-2,03E-02	1,84E-02	2,71E-01	9,70E-01
cg04917258	11	66647170	<i>PC</i>	-1,53E-02	1,03E-02	1,38E-01	9,39E-01
cg04420547	11	66676295	<i>PC</i>	-2,96E-02	1,58E-02	6,16E-02	9,19E-01
cg04784101	11	66824465	<i>RHOD</i>	-1,08E-02	2,13E-02	6,13E-01	9,72E-01
cg12128589	11	67202122	<i>RPS6KB2</i>	-6,37E-03	1,13E-02	5,73E-01	9,70E-01
cg05750788	11	67210225	<i>CORO1B</i>	-1,34E-02	1,10E-02	2,21E-01	9,59E-01
cg26754560	11	67379955	<i>NDUFV1</i>	-1,52E-02	1,32E-02	2,51E-01	9,70E-01
cg18192917	11	67401533	<i>TBX10</i>	-2,68E-02	1,31E-02	4,02E-02	9,19E-01
cg24563501	11	67442408	<i>ALDH3B2</i>	-5,23E-03	9,02E-03	5,62E-01	9,70E-01
cg16087630	11	67890322	<i>CHKA</i>	1,19E-02	1,21E-02	3,25E-01	9,70E-01
cg10477989	11	68039601	<i>C11orf24</i>	6,58E-03	1,87E-02	7,24E-01	9,82E-01
cg10486439	11	68919970	NA	-7,60E-03	1,31E-02	5,62E-01	9,70E-01
cg26123414	11	69490316	<i>ORAOV1</i>	5,12E-03	1,21E-02	6,73E-01	9,82E-01
cg09530156	11	69867139	NA	-1,03E-02	1,37E-02	4,51E-01	9,70E-01
cg10548355	11	70129868	<i>PPFIA1; MIR548K</i>	1,09E-03	1,39E-02	9,37E-01	9,94E-01
cg19227606	11	71202329	<i>NADSYN1</i>	4,09E-04	1,30E-02	9,75E-01	9,94E-01
cg14817211	11	71239055	<i>KRTAP5-7</i>	-1,87E-02	1,49E-02	2,08E-01	9,59E-01
cg27219654	11	72136711	<i>CLPB</i>	-5,09E-03	1,38E-02	7,11E-01	9,82E-01
cg23149454	11	72380070	<i>PDE2A</i>	3,44E-03	8,36E-03	6,81E-01	9,82E-01
cg17472796	11	72406685	<i>ARAP1</i>	1,78E-03	1,52E-02	9,07E-01	9,94E-01
cg23249399	11	72437871	<i>ARAP1</i>	-1,86E-02	1,51E-02	2,17E-01	9,59E-01
cg07091552	11	73721170	<i>UCP3</i>	3,33E-03	1,36E-02	8,07E-01	9,93E-01
cg04240079	11	74300279	NA	-9,58E-03	1,64E-02	5,60E-01	9,70E-01
cg03522035	11	76370510	<i>LRRC32</i>	-9,02E-03	1,15E-02	4,34E-01	9,70E-01
cg01233306	11	78369375	<i>ODZ4</i>	2,44E-03	1,33E-02	8,55E-01	9,94E-01
cg20759345	11	86745909	NA	-2,16E-03	1,39E-02	8,77E-01	9,94E-01
cg10096321	11	113934294	<i>ZBTB16</i>	-1,75E-02	1,37E-02	2,00E-01	9,59E-01
cg11966524	11	115631762	NA	-1,08E-02	1,08E-02	3,17E-01	9,70E-01
cg18283361	11	116692155	<i>APOA4</i>	2,80E-02	1,59E-02	7,92E-02	9,19E-01
cg22064610	11	117282521	<i>CEP164</i>	-1,97E-02	1,36E-02	1,46E-01	9,39E-01
cg12220703	11	117389445	<i>DSCAML1</i>	4,28E-03	1,67E-02	7,98E-01	9,91E-01
cg19314882	11	117391953	<i>DSCAML1</i>	-1,50E-02	1,34E-02	2,63E-01	9,70E-01
cg26925644	11	118476517	<i>PHLDB1</i>	1,40E-02	1,24E-02	2,60E-01	9,70E-01
cg03203114	11	118505622	<i>PHLDB1</i>	-1,94E-02	1,70E-02	2,55E-01	9,70E-01
cg16235962	11	118754507	<i>CXCR5</i>	7,27E-03	9,98E-03	4,66E-01	9,70E-01
cg16280667	11	118754593	<i>CXCR5</i>	-4,46E-03	8,63E-03	6,05E-01	9,72E-01
cg26785702	11	118846877	<i>FOXRI</i>	4,47E-03	9,13E-03	6,25E-01	9,75E-01
cg25387593	11	118927868	<i>HYOU1</i>	3,15E-02	1,76E-02	7,30E-02	9,19E-01
cg04919489	11	120283690	<i>ARHGEF12</i>	1,04E-02	1,15E-02	3,67E-01	9,70E-01
cg08441314	11	121446689	<i>SORLI</i>	-1,06E-02	1,59E-02	5,04E-01	9,70E-01
cg03111502	11	124609885	<i>NRGN</i>	1,34E-02	1,22E-02	2,74E-01	9,70E-01
cg13812731	11	124615143	<i>NRGN</i>	-7,23E-03	1,23E-02	5,55E-01	9,70E-01

cg08750439	11	128321880	NA	-3,24E-02	1,28E-02	1,12E-02	8,28E-01
cg03707169	11	128647051	<i>FLII</i>	-1,44E-03	1,72E-02	9,33E-01	9,94E-01
cg25892168	11	130059549	<i>STI4</i>	2,52E-03	1,49E-02	8,66E-01	9,94E-01
cg24321787	11	130343533	<i>ADAMTS15</i>	-3,53E-04	1,32E-02	9,79E-01	9,94E-01
cg01596901	11	131241286	<i>NTM</i>	-8,65E-03	1,34E-02	5,18E-01	9,70E-01
cg17253407	11	133917375	NA	1,19E-02	1,20E-02	3,24E-01	9,70E-01
cg10279055	11	134117051	<i>VPS26B</i>	-7,84E-03	1,78E-02	6,59E-01	9,82E-01
cg21104351	11	134152202	<i>GLB1L3</i>	-1,57E-02	1,23E-02	2,00E-01	9,59E-01
cg06644638	11	134213772	<i>GLB1L2</i>	2,68E-02	1,15E-02	1,94E-02	8,45E-01
cg07125269	12	1928481	<i>LRTM2; CACNA2D4</i>	-7,35E-03	1,14E-02	5,18E-01	9,70E-01
cg01398181	12	2279968	<i>CACNA1C</i>	2,05E-02	1,36E-02	1,34E-01	9,39E-01
cg20490175	12	2797745	<i>CACNA1C</i>	-3,20E-03	1,18E-02	7,86E-01	9,90E-01
cg24952640	12	3108225	<i>TEAD4</i>	-1,88E-02	1,01E-02	6,33E-02	9,19E-01
cg20792062	12	5153288	<i>KCNA5</i>	-1,38E-04	1,23E-02	9,91E-01	9,98E-01
cg01909705	12	6337308	<i>CD9</i>	-4,45E-03	1,41E-02	7,52E-01	9,82E-01
cg16617510	12	6438317	<i>TNFRSF1A</i>	1,67E-02	1,38E-02	2,28E-01	9,61E-01
cg02149069	12	6649733	<i>IFFO1</i>	-4,58E-03	1,36E-02	7,36E-01	9,82E-01
cg00808175	12	6949119	<i>GNB3</i>	7,08E-03	1,01E-02	4,84E-01	9,70E-01
cg24860716	12	7066938	<i>PTPN6</i>	-1,22E-02	1,45E-02	4,01E-01	9,70E-01
cg11211965	12	7076545	<i>SCARNA12; PHB2</i>	-1,36E-02	1,22E-02	2,64E-01	9,70E-01
cg11729019	12	7188330	<i>C1R</i>	-6,59E-03	1,50E-02	6,60E-01	9,82E-01
cg00774435	12	7249439	<i>C1RL</i>	-9,71E-03	1,46E-02	5,05E-01	9,70E-01
cg27634295	12	8043600	NA	-1,18E-03	1,36E-02	9,31E-01	9,94E-01
cg05418042	12	16063771	<i>DERA</i>	-9,17E-03	1,50E-02	5,40E-01	9,70E-01
cg16064364	12	19088662	NA	8,75E-03	1,59E-02	5,82E-01	9,70E-01
cg16095464	12	24228975	<i>SOX5</i>	-4,97E-03	1,65E-02	7,63E-01	9,84E-01
cg22349126	12	25348261	<i>LYRM5; CASC1</i>	1,54E-02	1,64E-02	3,47E-01	9,70E-01
cg26462457	12	25535797	NA	1,12E-02	1,33E-02	4,00E-01	9,70E-01
cg09486764	12	26288294	NA	-1,55E-02	1,03E-02	1,35E-01	9,39E-01
cg05606767	12	27917375	<i>LOC100133893</i>	-1,88E-02	1,81E-02	2,98E-01	9,70E-01
cg14690649	12	31884655	NA	9,94E-03	1,59E-02	5,32E-01	9,70E-01
cg26257969	12	48722474	<i>H1FNT</i>	-1,29E-02	1,43E-02	3,65E-01	9,70E-01
cg07218487	12	49418559	<i>MLL2</i>	-1,37E-02	1,26E-02	2,78E-01	9,70E-01
cg15921228	12	52240368	NA	-4,38E-03	1,13E-02	6,99E-01	9,82E-01
cg26335971	12	52341795	NA	-1,31E-02	1,21E-02	2,76E-01	9,70E-01
cg15889548	12	52641212	<i>KRT7</i>	5,68E-03	1,08E-02	6,00E-01	9,72E-01
cg05178192	12	52750508	NA	-1,58E-02	1,26E-02	2,10E-01	9,59E-01
cg23020795	12	52788318	<i>KRT82</i>	-2,77E-03	1,34E-02	8,37E-01	9,94E-01
cg00713401	12	52800087	<i>KRT82</i>	-1,14E-02	1,20E-02	3,39E-01	9,70E-01
cg01658663	12	53440247	<i>TENC1</i>	-6,58E-03	1,13E-02	5,61E-01	9,70E-01
cg09631652	12	53451981	<i>TENC1</i>	4,08E-04	1,78E-02	9,82E-01	9,94E-01
cg27409154	12	53490412	<i>IGFBP6</i>	1,22E-03	1,15E-02	9,15E-01	9,94E-01
cg25278343	12	53589908	<i>ITGB7</i>	-6,62E-04	1,34E-02	9,61E-01	9,94E-01
cg10961753	12	54332530	<i>HOXC13</i>	1,76E-03	1,79E-02	9,21E-01	9,94E-01
cg00344358	12	56135693	<i>GDF11</i>	-2,41E-02	1,20E-02	4,41E-02	9,19E-01
cg23689080	12	56159704	<i>SARNP</i>	-1,91E-02	1,16E-02	1,00E-01	9,39E-01

cg13544195	12	57571021	<i>LRP1</i>	5,26E-03	1,78E-02	7,67E-01	9,84E-01
cg25966682	12	57577597	<i>LRP1</i>	-5,37E-03	1,09E-02	6,22E-01	9,73E-01
cg26676360	12	57578696	<i>LRP1</i>	-4,51E-03	1,07E-02	6,74E-01	9,82E-01
cg04688889	12	57581972	<i>LRP1</i>	8,81E-03	1,25E-02	4,81E-01	9,70E-01
cg25664021	12	57595357	<i>LRP1</i>	-1,52E-02	1,29E-02	2,38E-01	9,70E-01
cg09840824	12	57600427	<i>LRP1</i>	-8,61E-03	1,06E-02	4,16E-01	9,70E-01
cg15389589	12	57600444	<i>LRP1</i>	2,70E-02	1,87E-02	1,49E-01	9,39E-01
cg02364642	12	58005758	<i>GEFT</i>	3,14E-04	1,13E-02	9,78E-01	9,94E-01
cg17385414	12	58950898	NA	2,83E-03	1,44E-02	8,45E-01	9,94E-01
cg10942227	12	67160208	NA	-2,08E-02	1,18E-02	7,71E-02	9,19E-01
cg07817608	12	76219528	NA	-3,92E-03	1,11E-02	7,24E-01	9,82E-01
cg24981283	12	79188000	NA	-3,41E-02	1,71E-02	4,67E-02	9,19E-01
cg22199628	12	80327755	<i>PPP1R12A</i>	-6,39E-03	1,48E-02	6,65E-01	9,82E-01
cg03742132	12	81227142	<i>LIN7A; MIR617</i>	6,03E-03	1,09E-02	5,80E-01	9,70E-01
cg26383838	12	93096819	<i>C12orf74</i>	-2,30E-03	1,57E-02	8,83E-01	9,94E-01
cg23347790	12	94670294	<i>PLXNC1</i>	-1,20E-02	1,43E-02	4,01E-01	9,70E-01
cg17109042	12	99139387	<i>ANKS1B</i>	-8,84E-03	1,78E-02	6,20E-01	9,73E-01
cg13494887	12	105605477	<i>APPL2</i>	-3,18E-02	1,10E-02	4,01E-03	5,53E-01
cg18526332	12	110146053	NA	-1,06E-02	1,88E-02	5,73E-01	9,70E-01
cg13484329	12	110342823	<i>TCHP</i>	-1,90E-02	1,24E-02	1,25E-01	9,39E-01
cg07066635	12	110434276	<i>GIT2</i>	1,50E-02	1,75E-02	3,92E-01	9,70E-01
cg01831767	12	111874281	<i>SH2B3</i>	-4,86E-04	1,21E-02	9,68E-01	9,94E-01
cg07668671	12	113305756	<i>RPH3A</i>	6,63E-03	1,05E-02	5,27E-01	9,70E-01
cg19516733	12	113830907	<i>SDS</i>	-9,70E-03	1,45E-02	5,05E-01	9,70E-01
cg22585562	12	117465849	<i>FBXW8</i>	-1,59E-02	1,30E-02	2,21E-01	9,59E-01
cg20285745	12	117798627	<i>NOS1</i>	6,71E-03	1,39E-02	6,29E-01	9,75E-01
cg11510131	12	120679618	<i>PXN</i>	9,86E-04	1,31E-02	9,40E-01	9,94E-01
cg20092046	12	121476596	<i>OASL</i>	5,55E-03	1,37E-02	6,85E-01	9,82E-01
cg08630639	12	121666925	<i>P2RX4</i>	6,95E-03	1,38E-02	6,15E-01	9,72E-01
cg12800105	12	121972412	<i>KDM2B</i>	5,94E-03	1,26E-02	6,38E-01	9,80E-01
cg25142228	12	122246256	<i>SETD1B</i>	-1,26E-03	1,44E-02	9,30E-01	9,94E-01
cg07949141	12	123451874	<i>ABCB9</i>	-4,79E-03	9,53E-03	6,15E-01	9,72E-01
cg07989629	12	124782528	<i>FAM101A</i>	1,49E-02	1,29E-02	2,49E-01	9,70E-01
cg07222420	12	124807302	NA	-9,13E-03	1,41E-02	5,18E-01	9,70E-01
cg20121920	12	124833935	<i>NCOR2</i>	-2,05E-02	1,83E-02	2,64E-01	9,70E-01
cg12157156	12	124880173	<i>NCOR2</i>	-1,70E-02	1,47E-02	2,47E-01	9,70E-01
cg22611259	12	124979893	<i>NCOR2</i>	-5,72E-03	1,55E-02	7,13E-01	9,82E-01
cg25449924	12	125020192	<i>NCOR2</i>	-1,21E-02	1,23E-02	3,27E-01	9,70E-01
cg25696906	12	131927876	NA	-6,42E-03	1,23E-02	6,03E-01	9,72E-01
cg01525916	12	132915958	NA	-1,12E-02	1,58E-02	4,80E-01	9,70E-01
cg24283804	12	133219305	<i>POLE</i>	-1,23E-02	1,34E-02	3,57E-01	9,70E-01
cg26243330	12	133307652	<i>ANKLE2</i>	-9,16E-03	1,15E-02	4,26E-01	9,70E-01
cg04900436	12	133312085	<i>ANKLE2</i>	-2,05E-02	1,39E-02	1,41E-01	9,39E-01
cg17461234	12	133373022	<i>GOLGA3</i>	1,45E-02	1,11E-02	1,93E-01	9,51E-01
cg05614952	12	133384565	<i>GOLGA3</i>	-5,17E-03	1,29E-02	6,89E-01	9,82E-01
cg03960313	13	24152357	<i>TNFRSF19</i>	3,46E-03	1,63E-02	8,32E-01	9,94E-01

cg22942528	13	25468426	<i>CENPJ</i>	-1,55E-02	1,49E-02	2,98E-01	9,70E-01
cg26226408	13	41055261	<i>LOC646982</i>	5,00E-03	1,16E-02	6,66E-01	9,82E-01
cg00692833	13	42795206	<i>DGKH</i>	-2,42E-02	1,45E-02	9,65E-02	9,39E-01
cg17015467	13	45885356	NA	1,72E-02	1,54E-02	2,66E-01	9,70E-01
cg22355224	13	49168127	NA	-1,25E-02	1,17E-02	2,85E-01	9,70E-01
cg10795666	13	49794635	<i>MLNR</i>	-8,02E-03	1,43E-02	5,75E-01	9,70E-01
cg21028785	13	51946399	<i>INTS6</i>	2,79E-04	1,18E-02	9,81E-01	9,94E-01
cg13080336	13	55628454	NA	7,44E-03	1,37E-02	5,88E-01	9,71E-01
cg01729717	13	84456486	<i>SLITRK1</i>	-2,61E-02	1,79E-02	1,46E-01	9,39E-01
cg22122715	13	96086023	<i>CLDN10</i>	-2,22E-03	1,50E-02	8,82E-01	9,94E-01
cg03440508	13	98084247	NA	-2,85E-02	1,65E-02	8,42E-02	9,39E-01
cg21099575	13	99092226	<i>FARPI</i>	-1,25E-03	1,42E-02	9,30E-01	9,94E-01
cg13936797	13	99180389	<i>STK24</i>	8,38E-03	1,35E-02	5,35E-01	9,70E-01
cg19635644	13	100007277	<i>UBAC2; MIR623</i>	-2,67E-03	1,19E-02	8,22E-01	9,94E-01
cg12127863	13	100252695	NA	1,31E-02	1,90E-02	4,92E-01	9,70E-01
cg11997806	13	100278363	<i>CLYBL</i>	-2,06E-02	1,14E-02	6,92E-02	9,19E-01
cg03313945	13	100622158	<i>ZIC5</i>	-1,24E-02	1,29E-02	3,38E-01	9,70E-01
cg13776095	13	101185965	<i>A2LD1</i>	-8,34E-04	1,28E-02	9,48E-01	9,94E-01
cg26739849	13	111165419	NA	1,46E-02	1,26E-02	2,47E-01	9,70E-01
cg04210544	13	111806530	<i>ARHGEF7</i>	-8,76E-03	1,24E-02	4,79E-01	9,70E-01
cg14352298	13	112236639	NA	2,29E-03	1,16E-02	8,44E-01	9,94E-01
cg22216757	13	112321270	NA	-2,70E-03	1,33E-02	8,39E-01	9,94E-01
cg23552509	13	112338216	NA	-1,26E-03	1,86E-02	9,46E-01	9,94E-01
cg12230889	13	113512466	<i>ATP11A</i>	-1,20E-02	1,63E-02	4,62E-01	9,70E-01
cg07828606	13	113565674	NA	-1,68E-02	1,41E-02	2,34E-01	9,70E-01
cg15914766	13	113660495	<i>MCF2L</i>	-1,27E-02	1,35E-02	3,49E-01	9,70E-01
cg03049340	13	114085732	<i>ADPRHL1</i>	3,08E-03	1,32E-02	8,15E-01	9,94E-01
cg22923006	13	114150139	<i>TMCO3</i>	-6,77E-03	1,51E-02	6,54E-01	9,82E-01
cg24926364	13	114748575	<i>RASA3</i>	-1,82E-02	1,22E-02	1,38E-01	9,39E-01
cg18995031	13	114780876	<i>RASA3</i>	-1,42E-02	1,89E-02	4,50E-01	9,70E-01
cg21236457	13	114790112	<i>RASA3</i>	3,57E-03	1,29E-02	7,81E-01	9,90E-01
cg13121938	13	114871497	<i>RASA3</i>	2,41E-05	1,18E-02	9,98E-01	9,99E-01
cg08380284	14	21852549	<i>SUPT16H</i>	3,33E-03	1,22E-02	7,84E-01	9,90E-01
cg19818298	14	21905552	<i>CHD8</i>	-2,00E-02	1,66E-02	2,27E-01	9,59E-01
cg21537049	14	22464528	NA	2,56E-02	1,32E-02	5,21E-02	9,19E-01
cg20976833	14	22953113	NA	2,82E-02	1,58E-02	7,37E-02	9,19E-01
cg02867735	14	22975384	NA	6,74E-03	9,28E-03	4,68E-01	9,70E-01
cg23198262	14	22978073	NA	1,10E-02	8,36E-03	1,89E-01	9,47E-01
cg01797899	14	22978195	NA	1,15E-03	7,41E-03	8,77E-01	9,94E-01
cg06771839	14	22981235	NA	3,88E-03	8,97E-03	6,65E-01	9,82E-01
cg26083141	14	23878455	<i>MYH6</i>	-7,03E-03	1,26E-02	5,75E-01	9,70E-01
cg04399988	14	24018055	NA	-3,30E-03	1,26E-02	7,94E-01	9,91E-01
cg04882359	14	24032626	<i>APIG2</i>	1,15E-02	1,26E-02	3,60E-01	9,70E-01
cg16000077	14	24777803	<i>LTBR2; CIDEB</i>	-1,29E-03	1,34E-02	9,23E-01	9,94E-01
cg10039281	14	24880346	<i>NYNRIN</i>	-1,71E-02	1,19E-02	1,50E-01	9,39E-01
cg04389921	14	26226996	NA	7,49E-04	1,33E-02	9,55E-01	9,94E-01

cg09400092	14	38677295	<i>SSTR1</i>	-2,19E-03	1,73E-02	8,99E-01	9,94E-01
cg18195228	14	50474181	<i>C14orf182</i>	2,26E-03	1,32E-02	8,64E-01	9,94E-01
cg04706229	14	50550589	<i>C14orf183</i>	1,29E-03	9,13E-03	8,88E-01	9,94E-01
cg26350222	14	55093382	<i>SAMD4A</i>	7,55E-04	1,64E-02	9,63E-01	9,94E-01
cg09274864	14	55226964	<i>SAMD4A</i>	-1,08E-02	1,02E-02	2,90E-01	9,70E-01
cg21042179	14	58329331	NA	-7,62E-04	1,12E-02	9,46E-01	9,94E-01
cg18695670	14	61123667	NA	-1,30E-02	1,55E-02	4,02E-01	9,70E-01
cg14286928	14	67826449	<i>EIF2S1; ATP6VID</i>	2,01E-02	1,05E-02	5,43E-02	9,19E-01
cg22792862	14	67827087	<i>EIF2S1; ATP6VID</i>	-1,98E-02	1,93E-02	3,03E-01	9,70E-01
cg21104155	14	68040530	<i>PLEKHH1</i>	-1,09E-02	1,60E-02	4,97E-01	9,70E-01
cg25126812	14	69445989	<i>ACTN1</i>	1,18E-02	1,20E-02	3,26E-01	9,70E-01
cg08255017	14	74727001	<i>VSX2</i>	-1,02E-02	1,50E-02	4,97E-01	9,70E-01
cg09945147	14	88625382	NA	9,66E-03	9,94E-03	3,31E-01	9,70E-01
cg17856915	14	89882896	<i>FOXN3</i>	3,46E-02	1,07E-02	1,21E-03	3,15E-01
cg13784460	14	90096812	NA	-2,14E-02	1,01E-02	3,37E-02	9,19E-01
cg25946790	14	90187489	NA	-1,16E-02	1,04E-02	2,69E-01	9,70E-01
cg09943560	14	91581064	<i>C14orf159</i>	2,22E-02	1,23E-02	7,01E-02	9,19E-01
cg09208864	14	91805692	<i>CCDC88C</i>	1,12E-02	1,43E-02	4,33E-01	9,70E-01
cg15491094	14	95948132	NA	-7,84E-03	1,41E-02	5,78E-01	9,70E-01
cg00995457	14	100057570	<i>CCDC85C</i>	-3,08E-04	1,30E-02	9,81E-01	9,94E-01
cg26055840	14	100118833	<i>HHIPL1</i>	-2,11E-02	1,09E-02	5,34E-02	9,19E-01
cg19971102	14	100135277	<i>HHIPL1</i>	9,54E-03	1,49E-02	5,22E-01	9,70E-01
cg14187585	14	101235871	NA	1,66E-03	1,19E-02	8,89E-01	9,94E-01
cg12197579	14	101287676	NA	4,59E-03	9,89E-03	6,43E-01	9,81E-01
cg04304932	14	101292128	<i>MEG3</i>	-3,13E-03	1,82E-02	8,63E-01	9,94E-01
cg13662173	14	101348161	<i>MIR127; MIR433;</i>	-7,73E-03	1,49E-02	6,03E-01	9,72E-01
cg11120364	14	101528579	NA	2,65E-03	1,44E-02	8,54E-01	9,94E-01
cg02180737	14	101530856	<i>MIR412; MIR410;</i>	-1,94E-02	1,27E-02	1,25E-01	9,39E-01
cg10548805	14	101538070	NA	-6,91E-03	9,74E-03	4,78E-01	9,70E-01
cg08221136	14	102422608	NA	-4,62E-03	1,21E-02	7,02E-01	9,82E-01
cg02147905	14	102814857	<i>CINP</i>	8,62E-03	1,36E-02	5,25E-01	9,70E-01
cg01812401	14	102979275	NA	9,10E-03	1,37E-02	5,05E-01	9,70E-01
cg04528445	14	103545835	NA	3,68E-03	8,67E-03	6,72E-01	9,82E-01
cg09380688	14	103566349	<i>C14orf73</i>	-5,79E-03	1,45E-02	6,89E-01	9,82E-01
cg19000871	14	103996768	<i>TRMT61A</i>	-2,72E-02	1,43E-02	5,68E-02	9,19E-01
cg09922085	14	104175768	<i>XRCC3</i>	-3,06E-02	1,41E-02	3,01E-02	9,19E-01
cg19828748	14	104175847	<i>XRCC3</i>	8,28E-03	1,32E-02	5,32E-01	9,70E-01
cg09333325	14	104611819	<i>KIF26A</i>	-1,88E-03	1,34E-02	8,89E-01	9,94E-01
cg04731084	14	104636633	<i>KIF26A</i>	3,19E-03	1,30E-02	8,06E-01	9,93E-01
cg14879065	14	104662468	NA	-1,58E-03	1,77E-02	9,29E-01	9,94E-01
cg21083556	14	105193326	<i>ADSSL1</i>	-5,78E-03	1,30E-02	6,57E-01	9,82E-01
cg15925940	14	105330630	<i>KIAA0284</i>	-3,05E-02	1,97E-02	1,21E-01	9,39E-01
cg27017580	14	105717038	<i>BRF1; BTBD6</i>	4,06E-03	1,22E-02	7,40E-01	9,82E-01
cg01318265	14	105884721	<i>MTA1</i>	-1,99E-02	1,32E-02	1,32E-01	9,39E-01
cg17324588	14	106743777	NA	-2,39E-02	1,91E-02	2,11E-01	9,59E-01
cg12910936	15	25473120	<i>SNORD115-15; SNO</i>	-4,55E-03	1,34E-02	7,34E-01	9,82E-01

cg26478036	15	25961967	<i>ATP10A</i>	-2,23E-02	1,77E-02	2,06E-01	9,59E-01
cg20119871	15	25972400	<i>ATP10A</i>	-8,38E-03	1,23E-02	4,95E-01	9,70E-01
cg02393591	15	28244615	<i>OCA2</i>	3,91E-03	1,39E-02	7,78E-01	9,90E-01
cg26216730	15	28271914	<i>OCA2</i>	-1,39E-02	1,52E-02	3,60E-01	9,70E-01
cg23885965	15	32149178	NA	-4,73E-03	1,23E-02	7,01E-01	9,82E-01
cg18735114	15	37110774	<i>CSNK1A1P</i>	1,32E-03	1,32E-02	9,20E-01	9,94E-01
cg11448015	15	40374034	NA	1,33E-03	1,22E-02	9,13E-01	9,94E-01
cg04658699	15	40538101	<i>PAK6</i>	-3,65E-03	1,10E-02	7,40E-01	9,82E-01
cg17940694	15	40657813	<i>DISP2</i>	-1,08E-02	1,06E-02	3,08E-01	9,70E-01
cg03350493	15	41837400	<i>RPAP1</i>	3,82E-03	1,14E-02	7,37E-01	9,82E-01
cg09225537	15	41952491	<i>MGA</i>	1,40E-02	1,80E-02	4,39E-01	9,70E-01
cg20935245	15	42234343	<i>EHD4</i>	-1,07E-02	1,37E-02	4,35E-01	9,70E-01
cg15441230	15	44069583	<i>ELL3</i>	-1,88E-03	1,92E-02	9,22E-01	9,94E-01
cg02556940	15	44092166	<i>SERINC4; C15orf6</i>	1,34E-02	1,30E-02	3,05E-01	9,70E-01
cg16381449	15	44281505	<i>FRMD5</i>	-2,29E-02	1,28E-02	7,35E-02	9,19E-01
cg02723856	15	53086726	NA	-2,50E-03	1,35E-02	8,54E-01	9,94E-01
cg09481404	15	53087316	NA	2,33E-02	1,52E-02	1,26E-01	9,39E-01
cg18017853	15	55563294	<i>RAB27A</i>	-1,62E-02	1,09E-02	1,38E-01	9,39E-01
cg05964373	15	56657478	<i>TEX9</i>	6,20E-03	1,96E-02	7,52E-01	9,82E-01
cg04885315	15	57731648	<i>CGNL1</i>	1,02E-02	1,45E-02	4,83E-01	9,70E-01
cg16455476	15	60771540	<i>NARG2</i>	2,17E-02	9,66E-03	2,49E-02	8,77E-01
cg19252691	15	62545331	NA	-4,05E-03	1,35E-02	7,64E-01	9,84E-01
cg25007414	15	63250281	NA	-7,52E-04	1,27E-02	9,53E-01	9,94E-01
cg09985793	15	65629756	<i>IGDCC3</i>	6,26E-03	1,14E-02	5,82E-01	9,70E-01
cg06650067	15	66084924	<i>DENND4A</i>	-1,30E-02	1,76E-02	4,59E-01	9,70E-01
cg01710852	15	67457967	<i>SMAD3</i>	-1,97E-02	1,25E-02	1,14E-01	9,39E-01
cg16674047	15	68867577	NA	1,27E-02	1,39E-02	3,63E-01	9,70E-01
cg26945392	15	71087092	NA	1,30E-02	1,48E-02	3,80E-01	9,70E-01
cg26787096	15	72094989	NA	-1,60E-02	1,92E-02	4,04E-01	9,70E-01
cg05897699	15	75146514	<i>SCAMP2</i>	-7,37E-04	1,09E-02	9,46E-01	9,94E-01
cg09353345	15	78918560	<i>CHRNA4</i>	-1,68E-03	1,20E-02	8,89E-01	9,94E-01
cg26166433	15	78937416	NA	-1,99E-02	1,24E-02	1,08E-01	9,39E-01
cg09175993	15	81214816	<i>KIAA1199</i>	-2,05E-02	1,43E-02	1,52E-01	9,39E-01
cg25135706	15	86301987	NA	3,99E-04	1,44E-02	9,78E-01	9,94E-01
cg02311794	15	86302971	<i>KLHL25</i>	-6,14E-03	1,54E-02	6,90E-01	9,82E-01
cg13845952	15	89047486	NA	-1,84E-02	1,40E-02	1,89E-01	9,47E-01
cg17941015	15	89903704	NA	-2,13E-02	1,19E-02	7,40E-02	9,19E-01
cg21029612	15	89921258	<i>LOC254559</i>	1,38E-02	1,44E-02	3,36E-01	9,70E-01
cg26742275	15	99971423	NA	1,46E-02	1,13E-02	1,95E-01	9,53E-01
cg19945554	15	100913842	NA	9,20E-03	1,71E-02	5,91E-01	9,72E-01
cg10010898	16	339598	<i>AXIN1</i>	8,04E-03	1,27E-02	5,25E-01	9,70E-01
cg27331759	16	347891	<i>AXIN1</i>	1,05E-03	1,86E-02	9,55E-01	9,94E-01
cg06779421	16	464516	NA	-3,68E-02	1,18E-02	1,73E-03	3,15E-01
cg17524151	16	475494	<i>RAB11FIP3</i>	3,19E-03	1,42E-02	8,23E-01	9,94E-01
cg02143778	16	575420	NA	-1,74E-02	9,69E-03	7,22E-02	9,19E-01
cg03216729	16	603845	<i>SOLH</i>	-1,54E-03	1,59E-02	9,23E-01	9,94E-01

cg06219301	16	671340	<i>RAB40C</i>	-1,53E-02	1,30E-02	2,41E-01	9,70E-01
cg27313492	16	679543	<i>WFIKKNI</i>	-1,84E-02	1,24E-02	1,38E-01	9,39E-01
cg03855706	16	770778	<i>FAM173A</i>	1,33E-02	1,79E-02	4,57E-01	9,70E-01
cg08145839	16	922126	<i>LMF1</i>	-1,85E-02	1,46E-02	2,05E-01	9,59E-01
cg01115732	16	1005903	<i>LMF1</i>	1,08E-02	1,22E-02	3,76E-01	9,70E-01
cg05696436	16	1373786	<i>UBE2I</i>	3,54E-03	1,11E-02	7,51E-01	9,82E-01
cg03424469	16	1552183	<i>TELO2</i>	-2,27E-02	1,46E-02	1,20E-01	9,39E-01
cg00209206	16	1574816	<i>IFT140</i>	-2,69E-02	1,46E-02	6,41E-02	9,19E-01
cg05337607	16	1723984	<i>CRAMP1L</i>	1,38E-02	2,01E-02	4,92E-01	9,70E-01
cg07264815	16	1795240	<i>MAPK8IP3</i>	-3,89E-03	9,94E-03	6,96E-01	9,82E-01
cg02492708	16	2005062	<i>RPL3L</i>	-1,02E-02	1,21E-02	3,98E-01	9,70E-01
cg00358155	16	2025688	<i>TBL3</i>	-2,93E-02	1,63E-02	7,27E-02	9,19E-01
cg16353272	16	2124240	<i>TSC2</i>	-1,19E-03	2,03E-02	9,53E-01	9,94E-01
cg27107485	16	2295352	<i>DCI</i>	-1,93E-02	1,41E-02	1,71E-01	9,47E-01
cg05654361	16	2338111	<i>ABCA3</i>	-3,33E-02	1,21E-02	5,85E-03	6,92E-01
cg08011223	16	2661622	<i>LOC652276</i>	-2,86E-02	1,34E-02	3,32E-02	9,19E-01
cg06377256	16	2769484	<i>PRSS27</i>	-6,00E-04	1,14E-02	9,58E-01	9,94E-01
cg05958351	16	2804731	<i>SRRM2</i>	-9,01E-03	1,17E-02	4,40E-01	9,70E-01
cg06402590	16	2820155	<i>SRRM2</i>	-2,48E-02	1,28E-02	5,26E-02	9,19E-01
cg04245634	16	3140535	<i>ZSCAN10</i>	-1,61E-02	1,57E-02	3,04E-01	9,70E-01
cg27638742	16	3143250	<i>ZSCAN10</i>	-8,51E-03	1,40E-02	5,43E-01	9,70E-01
cg05215277	16	3439780	<i>ZNF434</i>	1,08E-02	1,27E-02	3,93E-01	9,70E-01
cg24062157	16	3724848	<i>TRAP1</i>	-4,04E-02	1,34E-02	2,55E-03	3,84E-01
cg09740815	16	3777892	<i>CREBBP</i>	1,17E-03	1,49E-02	9,38E-01	9,94E-01
cg01782904	16	4453563	<i>CORO7</i>	-4,15E-03	1,59E-02	7,94E-01	9,91E-01
cg09450828	16	4785164	<i>C16orf71; ANKS3</i>	-1,15E-02	1,44E-02	4,23E-01	9,70E-01
cg16613029	16	9052762	<i>USP7</i>	6,05E-03	1,11E-02	5,84E-01	9,70E-01
cg03935060	16	10272021	<i>GRIN2A</i>	5,63E-03	1,44E-02	6,95E-01	9,82E-01
cg04010868	16	11876381	<i>ZC3H7A</i>	-1,78E-02	9,83E-03	7,05E-02	9,19E-01
cg26521448	16	11876426	<i>ZC3H7A</i>	-1,76E-02	1,20E-02	1,44E-01	9,39E-01
cg10457079	16	12298857	<i>SNX29</i>	3,98E-03	1,27E-02	7,54E-01	9,82E-01
cg09632876	16	12484175	<i>SNX29</i>	-3,29E-02	1,64E-02	4,47E-02	9,19E-01
cg05426160	16	15942420	<i>MYH11</i>	-8,20E-03	1,39E-02	5,55E-01	9,70E-01
cg27565277	16	17228474	<i>XYLT1</i>	8,86E-03	9,59E-03	3,56E-01	9,70E-01
cg03625515	16	18157108	NA	5,42E-03	9,89E-03	5,83E-01	9,70E-01
cg08248577	16	19727447	<i>IQCK; C16orf88</i>	1,25E-02	1,13E-02	2,69E-01	9,70E-01
cg02944637	16	19733345	<i>IQCK</i>	-1,37E-02	1,16E-02	2,35E-01	9,70E-01
cg04695882	16	20756332	NA	-1,03E-02	7,11E-03	1,47E-01	9,39E-01
cg09591886	16	22333264	<i>POLR3E</i>	-5,21E-03	1,41E-02	7,11E-01	9,82E-01
cg05997801	16	27472247	<i>GTF3C1</i>	-1,95E-02	1,33E-02	1,44E-01	9,39E-01
cg07647796	16	28884330	<i>SH2B1</i>	-6,55E-03	1,25E-02	6,00E-01	9,72E-01
cg00474657	16	28989308	<i>SPNS1</i>	-1,51E-02	9,96E-03	1,29E-01	9,39E-01
cg04891924	16	29856011	<i>MVP</i>	3,04E-02	2,08E-02	1,43E-01	9,39E-01
cg10238917	16	30942621	<i>FBXL19</i>	-9,21E-03	1,73E-02	5,94E-01	9,72E-01
cg05106869	16	31142991	<i>PRSS8</i>	-1,22E-02	1,45E-02	3,99E-01	9,70E-01
cg01015003	16	31157126	<i>PRSS36</i>	-2,70E-03	1,21E-02	8,23E-01	9,94E-01

cg09971653	16	48559770	NA	-3,28E-03	9,07E-03	7,17E-01	9,82E-01
cg09132790	16	49533226	<i>ZNF423</i>	1,43E-02	1,62E-02	3,78E-01	9,70E-01
cg00160027	16	49583602	<i>ZNF423</i>	-2,14E-02	1,30E-02	1,01E-01	9,39E-01
cg05544500	16	54324346	NA	-3,40E-03	1,53E-02	8,24E-01	9,94E-01
cg06847237	16	55094729	NA	2,91E-03	1,31E-02	8,24E-01	9,94E-01
cg26719862	16	55902037	<i>CES7</i>	-1,11E-02	1,49E-02	4,57E-01	9,70E-01
cg13156121	16	58010114	<i>TEPP</i>	-6,18E-03	1,25E-02	6,22E-01	9,73E-01
cg03000116	16	65611369	<i>LOC283867</i>	1,62E-02	1,29E-02	2,12E-01	9,59E-01
cg01633417	16	67437389	<i>ZDHHC1</i>	6,76E-03	1,21E-02	5,76E-01	9,70E-01
cg07125278	16	67683757	<i>RLTPR</i>	-1,36E-02	1,22E-02	2,66E-01	9,70E-01
cg07073135	16	67688696	<i>RLTPR</i>	-8,91E-03	1,25E-02	4,76E-01	9,70E-01
cg06378129	16	67998246	<i>SLC12A4</i>	1,68E-02	1,17E-02	1,50E-01	9,39E-01
cg01162920	16	68362700	<i>PRMT7</i>	1,49E-02	1,17E-02	2,04E-01	9,59E-01
cg06993715	16	69345386	<i>VPS4A</i>	-1,20E-02	1,79E-02	5,02E-01	9,70E-01
cg07905627	16	69368764	<i>COG8</i>	-2,54E-02	1,28E-02	4,74E-02	9,19E-01
cg07459409	16	70698831	<i>MTSS1L</i>	-3,55E-02	1,97E-02	7,10E-02	9,19E-01
cg04961620	16	70720083	<i>MTSS1L</i>	2,62E-03	1,33E-02	8,43E-01	9,94E-01
cg08282578	16	70733234	<i>VAC14</i>	-3,31E-02	1,40E-02	1,82E-02	8,28E-01
cg00507823	16	71894108	<i>ZNF821; ATXN1L</i>	3,34E-03	1,22E-02	7,84E-01	9,90E-01
cg08011959	16	77233235	<i>SYCE1L; MON1B</i>	-9,91E-03	1,19E-02	4,07E-01	9,70E-01
cg02578846	16	77233353	<i>SYCE1L; MON1B</i>	-1,22E-02	1,74E-02	4,82E-01	9,70E-01
cg06460189	16	81740096	<i>CMIP</i>	-2,10E-02	1,24E-02	9,04E-02	9,39E-01
cg03279631	16	84553297	NA	-5,54E-03	1,20E-02	6,45E-01	9,81E-01
cg02484335	16	84623830	<i>COTL1</i>	1,12E-02	1,73E-02	5,17E-01	9,70E-01
cg06080014	16	84822990	NA	-1,97E-02	1,32E-02	1,37E-01	9,39E-01
cg02480489	16	85024131	<i>ZDHHC7</i>	-3,34E-02	1,94E-02	8,58E-02	9,39E-01
cg09175137	16	85143959	<i>FAM92B</i>	-1,23E-02	1,13E-02	2,76E-01	9,70E-01
cg27090678	16	85514649	NA	3,69E-03	1,05E-02	7,25E-01	9,82E-01
cg00206468	16	85990019	NA	6,66E-03	1,06E-02	5,28E-01	9,70E-01
cg05142023	16	86570343	<i>MTHFSD</i>	-1,57E-02	1,20E-02	1,91E-01	9,47E-01
cg09825080	16	86940337	NA	-2,48E-02	1,54E-02	1,08E-01	9,39E-01
cg08419921	16	87110129	NA	-3,01E-03	1,59E-02	8,50E-01	9,94E-01
cg01007838	16	87247486	NA	-1,64E-03	1,24E-02	8,95E-01	9,94E-01
cg05196076	16	87404139	<i>FBXO31</i>	-9,95E-03	1,38E-02	4,72E-01	9,70E-01
cg04302704	16	87701668	<i>JPH3</i>	3,37E-03	1,17E-02	7,73E-01	9,86E-01
cg04481596	16	87864591	<i>SLC7A5</i>	-1,85E-02	2,06E-02	3,70E-01	9,70E-01
cg09385650	16	88018033	<i>BANP</i>	-2,92E-03	1,32E-02	8,25E-01	9,94E-01
cg02956639	16	88110295	<i>BANP</i>	3,64E-04	1,28E-02	9,77E-01	9,94E-01
cg05377041	16	88473713	NA	1,92E-03	1,81E-02	9,15E-01	9,94E-01
cg06030362	16	88537692	<i>ZFPM1</i>	-1,75E-03	2,03E-02	9,31E-01	9,94E-01
cg07906473	16	88573286	<i>ZFPM1</i>	-9,09E-03	1,20E-02	4,49E-01	9,70E-01
cg27631965	16	88575243	<i>ZFPM1</i>	-1,56E-02	1,55E-02	3,14E-01	9,70E-01
cg07099810	16	88575557	<i>ZFPM1</i>	-6,97E-03	1,23E-02	5,72E-01	9,70E-01
cg05067156	16	88591451	<i>ZFPM1</i>	-5,42E-03	9,94E-03	5,85E-01	9,70E-01
cg04801098	16	88690990	<i>ZC3H18</i>	-8,66E-03	1,68E-02	6,05E-01	9,72E-01
cg10246531	16	88717628	<i>CYBA</i>	2,23E-02	1,76E-02	2,04E-01	9,59E-01

cg03040848	16	88993053	<i>CBFA2T3</i>	1,72E-03	1,10E-02	8,76E-01	9,94E-01
cg08843248	16	89009929	<i>CBFA2T3</i>	4,08E-03	1,06E-02	7,01E-01	9,82E-01
cg01197871	16	89323411	NA	-1,22E-02	1,74E-02	4,84E-01	9,70E-01
cg26608982	16	89560068	NA	-4,10E-03	1,08E-02	7,05E-01	9,82E-01
cg06111441	16	89649705	<i>CPNE7</i>	-2,20E-02	1,11E-02	4,83E-02	9,19E-01
cg10350251	16	89727194	<i>C16orf55</i>	3,57E-03	1,45E-02	8,05E-01	9,93E-01
cg03147900	16	89762721	<i>CDK10</i>	-1,73E-02	1,40E-02	2,17E-01	9,59E-01
cg05966394	16	89764007	<i>SPATA2L</i>	-7,78E-03	1,24E-02	5,30E-01	9,70E-01
cg26983744	16	89913833	<i>SPIRE2</i>	-3,15E-02	1,51E-02	3,77E-02	9,19E-01
cg27529240	16	89960078	<i>TCF25</i>	-1,01E-02	1,37E-02	4,62E-01	9,70E-01
cg01973164	16	89972593	<i>TCF25</i>	-1,73E-02	1,49E-02	2,45E-01	9,70E-01
cg04022811	16	90097752	<i>C16orf3; GAS8</i>	-1,49E-02	1,20E-02	2,16E-01	9,59E-01
cg04970064	17	266066	NA	1,13E-03	1,43E-02	9,37E-01	9,94E-01
cg25433496	17	293505	<i>FAM101B</i>	-5,09E-04	1,56E-02	9,74E-01	9,94E-01
cg24101979	17	709725	<i>NXN</i>	-4,50E-03	1,03E-02	6,63E-01	9,82E-01
cg26003785	17	839754	<i>NXN</i>	-1,34E-02	1,55E-02	3,85E-01	9,70E-01
cg26283240	17	851933	<i>NXN</i>	-9,40E-03	1,39E-02	4,97E-01	9,70E-01
cg00634573	17	953069	<i>ABR</i>	-1,55E-02	1,37E-02	2,58E-01	9,70E-01
cg20612875	17	1094308	NA	-2,37E-03	1,40E-02	8,66E-01	9,94E-01
cg08676455	17	1374948	<i>MYO1C</i>	-2,33E-02	1,32E-02	7,78E-02	9,19E-01
cg04423431	17	1578460	<i>PRPF8</i>	4,48E-03	1,40E-02	7,50E-01	9,82E-01
cg06809823	17	1837787	NA	1,20E-02	1,74E-02	4,91E-01	9,70E-01
cg14311597	17	2652531	<i>MIR1253</i>	-5,54E-04	1,29E-02	9,66E-01	9,94E-01
cg13415865	17	2831573	<i>RAP1GAP2</i>	-5,98E-03	1,22E-02	6,24E-01	9,75E-01
cg17745562	17	3539728	<i>CTNS; SHPK</i>	-1,65E-02	1,65E-02	3,16E-01	9,70E-01
cg20777461	17	3782904	<i>CAMKK1</i>	-4,03E-03	1,06E-02	7,03E-01	9,82E-01
cg18323018	17	4856222	<i>ENO3</i>	-2,18E-02	1,44E-02	1,32E-01	9,39E-01
cg24995783	17	4984094	<i>ZFP3</i>	-5,34E-03	1,25E-02	6,68E-01	9,82E-01
cg14897188	17	6917185	<i>RNASEK; C17orf49</i>	3,70E-03	8,84E-03	6,75E-01	9,82E-01
cg11816229	17	7017968	<i>ASGR2</i>	-1,28E-02	1,48E-02	3,87E-01	9,70E-01
cg25575464	17	7232771	<i>NEURL4</i>	-9,00E-03	1,65E-02	5,86E-01	9,70E-01
cg27486151	17	7367439	<i>ZBTB4</i>	-3,16E-02	1,28E-02	1,33E-02	8,28E-01
cg20616186	17	7468154	<i>SENP3</i>	-1,64E-03	1,53E-02	9,14E-01	9,94E-01
cg13749033	17	7480826	<i>EIF4A1; SNORA67</i>	1,75E-02	1,14E-02	1,25E-01	9,39E-01
cg22129111	17	8009699	<i>ALOXE3</i>	3,98E-03	1,04E-02	7,02E-01	9,82E-01
cg20643039	17	8791596	<i>PIK3R5</i>	-6,42E-03	1,57E-02	6,83E-01	9,82E-01
cg24089133	17	9479954	<i>WDR16; STX8</i>	-1,01E-02	1,57E-02	5,21E-01	9,70E-01
cg13898605	17	9675212	<i>DHRS7C</i>	-1,01E-02	1,87E-02	5,89E-01	9,71E-01
cg26135975	17	10635580	NA	6,28E-03	1,15E-02	5,84E-01	9,70E-01
cg18121946	17	12697550	<i>RICH2</i>	7,61E-03	9,75E-03	4,35E-01	9,70E-01
cg13553400	17	14248369	<i>HS3ST3B1</i>	2,01E-03	1,31E-02	8,78E-01	9,94E-01
cg07935357	17	17469733	<i>PEMT</i>	-3,67E-03	1,07E-02	7,32E-01	9,82E-01
cg10171253	17	17699911	<i>RAI1</i>	-2,32E-02	1,46E-02	1,13E-01	9,39E-01
cg21275283	17	18011513	<i>MYO15A</i>	-2,67E-02	1,25E-02	3,23E-02	9,19E-01
cg11433608	17	19246574	<i>B9D1</i>	-8,48E-03	1,37E-02	5,37E-01	9,70E-01
cg00797477	17	19264814	<i>B9D1</i>	-1,77E-02	1,46E-02	2,26E-01	9,59E-01

cg24126880	17	19624390	NA	3,31E-03	1,01E-02	7,44E-01	9,82E-01
cg13763516	17	20947094	<i>USP22</i>	2,70E-02	1,30E-02	3,79E-02	9,19E-01
cg22436527	17	26832833	NA	8,50E-03	1,27E-02	5,03E-01	9,70E-01
cg01799602	17	26894979	<i>PIGS</i>	6,69E-03	1,35E-02	6,20E-01	9,73E-01
cg20657324	17	27905480	<i>GIT1</i>	-1,07E-02	1,28E-02	4,01E-01	9,70E-01
cg25705266	17	30049574	NA	1,84E-02	1,57E-02	2,43E-01	9,70E-01
cg09324608	17	30823087	<i>MYO1D</i>	-7,40E-05	1,55E-02	9,96E-01	9,99E-01
cg12188903	17	33211323	NA	-1,29E-02	1,26E-02	3,06E-01	9,70E-01
cg02380585	17	33776683	<i>SLFN13</i>	-4,89E-03	7,11E-03	4,92E-01	9,70E-01
cg19874450	17	34900926	<i>GGNBP2</i>	1,86E-03	1,92E-02	9,23E-01	9,94E-01
cg08245425	17	34957834	<i>MRM1</i>	-7,57E-03	1,29E-02	5,57E-01	9,70E-01
cg00651005	17	36499258	<i>GPR179</i>	-3,05E-03	1,18E-02	7,96E-01	9,91E-01
cg01485645	17	36862199	<i>MLLT6</i>	1,27E-02	1,37E-02	3,53E-01	9,70E-01
cg17215234	17	36908932	<i>PSMB3</i>	-9,28E-03	1,32E-02	4,83E-01	9,70E-01
cg04848235	17	36927361	<i>PIP4K2B</i>	-4,26E-03	1,26E-02	7,35E-01	9,82E-01
cg12658374	17	37323563	<i>ARL5C</i>	2,78E-03	1,28E-02	8,28E-01	9,94E-01
cg27255115	17	38603555	<i>IGFBP4</i>	8,38E-03	1,43E-02	5,58E-01	9,70E-01
cg07479709	17	38711505	<i>CCR7</i>	-1,31E-02	1,12E-02	2,40E-01	9,70E-01
cg26750927	17	39977959	<i>FKBP10</i>	8,36E-05	9,26E-03	9,93E-01	9,98E-01
cg09746031	17	40336180	<i>HCRT</i>	6,80E-03	1,69E-02	6,88E-01	9,82E-01
cg24950402	17	40443790	<i>STAT5A</i>	1,11E-02	1,53E-02	4,69E-01	9,70E-01
cg02294870	17	41479663	NA	3,57E-03	8,96E-03	6,91E-01	9,82E-01
cg08498539	17	42013514	NA	1,58E-02	1,82E-02	3,86E-01	9,70E-01
cg11514301	17	42267990	<i>TMUB2</i>	-1,77E-02	1,31E-02	1,76E-01	9,47E-01
cg12837296	17	42426483	<i>GRN</i>	-7,52E-03	9,41E-03	4,24E-01	9,70E-01
cg08126815	17	42476617	<i>GPATCH8</i>	-1,27E-02	1,59E-02	4,25E-01	9,70E-01
cg11068337	17	43224582	<i>HEXIM1</i>	-5,71E-04	1,51E-02	9,70E-01	9,94E-01
cg03782381	17	43450670	NA	-1,25E-02	1,31E-02	3,40E-01	9,70E-01
cg22311200	17	46695514	NA	4,12E-03	1,99E-02	8,36E-01	9,94E-01
cg11769332	17	48046663	<i>DLX4</i>	-8,99E-03	1,39E-02	5,19E-01	9,70E-01
cg26768556	17	48179239	<i>PDK2</i>	-1,11E-03	1,15E-02	9,23E-01	9,94E-01
cg26501664	17	48247390	<i>SGCA</i>	-1,57E-02	1,15E-02	1,74E-01	9,47E-01
cg07081054	17	52978409	<i>TOM1L1</i>	-8,42E-03	1,32E-02	5,24E-01	9,70E-01
cg20318252	17	55594714	<i>MSI2</i>	-1,45E-02	9,53E-03	1,29E-01	9,39E-01
cg10325253	17	58166296	<i>LOC645638</i>	-1,40E-02	1,48E-02	3,42E-01	9,70E-01
cg19826045	17	61561602	<i>ACE</i>	-9,75E-03	1,13E-02	3,88E-01	9,70E-01
cg21796427	17	61562170	<i>ACE</i>	-1,69E-02	1,77E-02	3,38E-01	9,70E-01
cg01442319	17	62017288	<i>SCN4A</i>	1,54E-02	1,35E-02	2,55E-01	9,70E-01
cg23011419	17	63545705	<i>AXIN2</i>	-5,08E-03	1,52E-02	7,39E-01	9,82E-01
cg17255712	17	70116185	<i>SOX9</i>	7,20E-03	1,13E-02	5,24E-01	9,70E-01
cg23835923	17	70710154	<i>SLC39A11</i>	1,38E-02	1,33E-02	3,00E-01	9,70E-01
cg19038490	17	71733130	NA	-3,41E-03	1,18E-02	7,72E-01	9,86E-01
cg15325704	17	72207518	<i>MGC16275</i>	-1,14E-02	1,45E-02	4,30E-01	9,70E-01
cg01483627	17	72368401	<i>GPR142</i>	-1,38E-03	1,19E-02	9,07E-01	9,94E-01
cg00439658	17	72848669	<i>GRIN2C</i>	5,21E-03	1,34E-02	6,99E-01	9,82E-01
cg22247041	17	73004677	NA	-6,20E-03	9,92E-03	5,32E-01	9,70E-01

cg20863668	17	73518382	<i>TSEN54</i>	-2,06E-02	1,16E-02	7,50E-02	9,19E-01
cg13194822	17	73911116	<i>FBF1</i>	-1,84E-05	1,16E-02	9,99E-01	9,99E-01
cg14343334	17	74387045	<i>UBE2O</i>	1,08E-02	1,50E-02	4,72E-01	9,70E-01
cg14608550	17	75398014	<i>SEPT9;</i>	3,44E-03	1,35E-02	7,98E-01	9,91E-01
cg02397064	17	75462916	<i>SEPT9;</i>	5,37E-03	1,61E-02	7,38E-01	9,82E-01
cg17053854	17	75463180	<i>SEPT9;</i>	9,00E-04	1,65E-02	9,57E-01	9,94E-01
cg08757611	17	76250500	NA	9,30E-03	1,66E-02	5,76E-01	9,70E-01
cg24677192	17	76430314	<i>DNAH17</i>	1,25E-02	1,31E-02	3,41E-01	9,70E-01
cg24200401	17	76573401	<i>DNAH17</i>	-3,19E-03	1,08E-02	7,68E-01	9,84E-01
cg12871285	17	76713379	<i>CYTH1</i>	-3,84E-03	1,79E-02	8,30E-01	9,94E-01
cg23898320	17	76818733	<i>USP36</i>	-1,42E-02	9,70E-03	1,44E-01	9,39E-01
cg12780873	17	77454278	<i>HRNBP3</i>	2,01E-02	1,36E-02	1,40E-01	9,39E-01
cg00025795	17	77983156	<i>TBC1D16</i>	-1,10E-02	1,32E-02	4,03E-01	9,70E-01
cg07724971	17	78035629	<i>CCDC40</i>	-9,60E-03	1,14E-02	4,00E-01	9,70E-01
cg05022061	17	78156060	<i>CARD14</i>	-4,32E-03	1,32E-02	7,44E-01	9,82E-01
cg22161784	17	78337534	<i>RNF213; LOC10029</i>	-4,67E-03	1,33E-02	7,26E-01	9,82E-01
cg20656830	17	78439562	NA	-4,01E-03	1,34E-02	7,65E-01	9,84E-01
cg24239992	17	78483800	NA	-1,45E-02	1,40E-02	3,02E-01	9,70E-01
cg25705936	17	78795864	<i>RPTOR</i>	-5,75E-03	1,56E-02	7,12E-01	9,82E-01
cg02910299	17	78796166	<i>RPTOR</i>	-2,14E-02	1,74E-02	2,19E-01	9,59E-01
cg21550504	17	78800321	<i>RPTOR</i>	-6,51E-03	1,13E-02	5,66E-01	9,70E-01
cg21289763	17	78868835	<i>RPTOR</i>	-1,79E-02	1,34E-02	1,81E-01	9,47E-01
cg18612040	17	78904485	<i>RPTOR</i>	1,23E-02	1,91E-02	5,21E-01	9,70E-01
cg19776366	17	79032662	<i>BAIAP2</i>	-1,35E-02	1,18E-02	2,52E-01	9,70E-01
cg24171594	17	79080659	<i>BAIAP2</i>	-1,21E-03	1,73E-02	9,44E-01	9,94E-01
cg26998842	17	79108218	<i>AATK; MIR1250</i>	-7,94E-03	1,65E-02	6,29E-01	9,75E-01
cg00591333	17	79109910	<i>AATK</i>	-3,50E-02	1,35E-02	9,57E-03	8,22E-01
cg11031372	17	79173614	<i>AZII</i>	-2,15E-02	1,29E-02	9,64E-02	9,39E-01
cg16985966	17	79177523	<i>AZII</i>	-1,37E-02	1,31E-02	2,97E-01	9,70E-01
cg14621907	17	79251255	<i>SLC38A10</i>	-1,58E-02	1,16E-02	1,71E-01	9,47E-01
cg05088605	17	79987813	<i>LRRC45</i>	-4,15E-02	1,12E-02	2,15E-04	1,23E-01
cg19122948	17	80207982	<i>CSNK1D</i>	-1,96E-02	1,23E-02	1,11E-01	9,39E-01
cg01038738	17	80275965	<i>CD7</i>	4,39E-03	2,24E-02	8,45E-01	9,94E-01
cg23565607	17	80395310	<i>HEXDC</i>	7,24E-03	1,41E-02	6,09E-01	9,72E-01
cg05996835	17	80436418	<i>NARF</i>	1,10E-02	1,60E-02	4,91E-01	9,70E-01
cg19218102	17	80559059	<i>FOXK2</i>	-6,87E-03	1,24E-02	5,78E-01	9,70E-01
cg25901400	17	80625811	<i>RAB40B</i>	9,76E-03	1,20E-02	4,16E-01	9,70E-01
cg01469594	17	80706786	<i>FN3K</i>	-5,68E-03	1,48E-02	7,01E-01	9,82E-01
cg25912699	17	81034122	NA	-1,60E-03	1,13E-02	8,88E-01	9,94E-01
cg07392482	18	10524910	<i>NAPG</i>	-9,71E-03	1,10E-02	3,79E-01	9,70E-01
cg18038361	18	29170604	<i>TTR</i>	-2,91E-03	1,29E-02	8,21E-01	9,94E-01
cg18515624	18	30049316	<i>FAM59A</i>	7,46E-03	1,28E-02	5,59E-01	9,70E-01
cg14477514	18	35124846	<i>BRUNOL4</i>	-1,58E-02	8,49E-03	6,29E-02	9,19E-01
cg19860752	18	37332566	<i>LOC647946</i>	7,87E-03	1,20E-02	5,11E-01	9,70E-01
cg13103051	18	44260790	<i>ST8SIA5</i>	-6,53E-03	1,04E-02	5,28E-01	9,70E-01
cg21444002	18	46388932	<i>KIAA0427</i>	1,44E-03	1,55E-02	9,26E-01	9,94E-01

cg07661480	18	46447737	<i>SMAD7</i>	-2,83E-02	1,93E-02	1,42E-01	9,39E-01
cg21585100	18	55922747	<i>NEDD4L</i>	8,56E-03	2,04E-02	6,75E-01	9,82E-01
cg16978268	18	60646671	<i>PHLPP1</i>	-4,89E-03	9,42E-03	6,04E-01	9,72E-01
cg23319171	18	74804128	<i>MBP</i>	-1,13E-03	1,19E-02	9,24E-01	9,94E-01
cg06554192	18	75691425	NA	-4,60E-03	1,03E-02	6,56E-01	9,82E-01
cg15784814	18	77171832	<i>NFATC1</i>	-7,90E-03	1,22E-02	5,19E-01	9,70E-01
cg06937978	18	77193759	<i>NFATC1</i>	-6,49E-03	1,27E-02	6,08E-01	9,72E-01
cg25332265	18	77194663	<i>NFATC1</i>	-7,74E-03	1,80E-02	6,67E-01	9,82E-01
cg13226362	18	77466175	<i>CTDP1</i>	1,33E-03	1,21E-02	9,13E-01	9,94E-01
cg24752582	18	77675387	<i>PQLC1</i>	1,17E-02	1,97E-02	5,53E-01	9,70E-01
cg15297799	18	77794239	<i>C18orf22</i>	2,20E-02	2,35E-02	3,50E-01	9,70E-01
cg06551168	19	308524	<i>MIER2</i>	-7,55E-03	1,12E-02	5,00E-01	9,70E-01
cg11570697	19	649464	<i>RNF126</i>	-4,18E-03	1,40E-02	7,66E-01	9,84E-01
cg25651627	19	653639	<i>RNF126</i>	-1,04E-03	1,52E-02	9,46E-01	9,94E-01
cg19628469	19	856107	<i>ELANE</i>	-5,24E-03	1,74E-02	7,64E-01	9,84E-01
cg01390135	19	868220	<i>MED16</i>	-1,14E-02	1,51E-02	4,51E-01	9,70E-01
cg19548313	19	1065712	<i>HMHA1</i>	-7,75E-03	1,16E-02	5,04E-01	9,70E-01
cg03095527	19	1230768	<i>C19orf26</i>	-1,10E-02	1,47E-02	4,55E-01	9,70E-01
cg26242446	19	1299677	<i>EFNA2</i>	-7,63E-03	1,41E-02	5,89E-01	9,71E-01
cg23408615	19	1552315	NA	-4,23E-02	1,34E-02	1,68E-03	3,15E-01
cg15974216	19	1599248	<i>UOCR</i>	-7,87E-03	1,46E-02	5,90E-01	9,72E-01
cg20118823	19	1612208	<i>TCF3</i>	-8,29E-03	1,22E-02	4,98E-01	9,70E-01
cg05889881	19	1626684	<i>TCF3</i>	-1,40E-02	1,32E-02	2,90E-01	9,70E-01
cg08430680	19	1650452	<i>TCF3</i>	8,56E-03	1,14E-02	4,54E-01	9,70E-01
cg15562859	19	1853618	<i>KLF16</i>	1,98E-02	1,66E-02	2,33E-01	9,70E-01
cg01471710	19	1953866	<i>C19orf34; CSNK1G</i>	1,01E-02	1,59E-02	5,25E-01	9,70E-01
cg05610244	19	1985686	<i>BTBD2</i>	-7,42E-03	1,24E-02	5,51E-01	9,70E-01
cg18179735	19	2038539	<i>MKNK2</i>	-1,24E-02	1,25E-02	3,24E-01	9,70E-01
cg10696539	19	2321980	<i>LSM7</i>	-1,84E-03	1,51E-02	9,03E-01	9,94E-01
cg14240723	19	2363170	NA	-3,75E-03	1,39E-02	7,87E-01	9,90E-01
cg05255884	19	2444318	<i>LMNB2</i>	3,19E-03	1,48E-02	8,29E-01	9,94E-01
cg24723883	19	2608495	<i>GNG7</i>	-3,42E-03	8,38E-03	6,83E-01	9,82E-01
cg15468423	19	2700763	<i>GNG7</i>	-1,22E-02	1,21E-02	3,13E-01	9,70E-01
cg00510948	19	2730590	NA	1,77E-02	1,34E-02	1,88E-01	9,47E-01
cg05299479	19	2813428	<i>THOP1</i>	-6,90E-03	1,23E-02	5,76E-01	9,70E-01
cg11552585	19	3196206	<i>NCLN</i>	-9,58E-03	1,82E-02	6,00E-01	9,72E-01
cg15541401	19	3490856	<i>DOHH</i>	-1,50E-02	1,76E-02	3,96E-01	9,70E-01
cg01608045	19	3532665	<i>FZR1</i>	-6,75E-03	1,09E-02	5,34E-01	9,70E-01
cg21756367	19	3762740	<i>MRPL54; APBA3</i>	1,50E-03	1,76E-02	9,32E-01	9,94E-01
cg18748062	19	3966842	<i>DAPK3</i>	-2,19E-02	1,77E-02	2,15E-01	9,59E-01
cg17715482	19	3979910	<i>EEF2</i>	3,54E-03	1,72E-02	8,37E-01	9,94E-01
cg00253971	19	4038851	NA	-1,84E-02	1,33E-02	1,66E-01	9,47E-01
cg10633491	19	4066815	<i>ZBTB7A</i>	-2,11E-02	1,73E-02	2,21E-01	9,59E-01
cg08468472	19	4101947	<i>MAP2K2</i>	2,16E-02	1,45E-02	1,38E-01	9,39E-01
cg00966686	19	4103040	<i>MAP2K2</i>	-8,13E-04	1,25E-02	9,48E-01	9,94E-01
cg14791922	19	5144160	<i>KDM4B</i>	1,23E-02	1,48E-02	4,05E-01	9,70E-01

cg08462941	19	5288631	<i>PTPRS</i>	1,14E-02	1,11E-02	3,07E-01	9,70E-01
cg26242866	19	5711310	<i>LONP1</i>	3,10E-03	1,20E-02	7,97E-01	9,91E-01
cg11233468	19	5831171	<i>FUT6</i>	4,71E-03	1,08E-02	6,63E-01	9,82E-01
cg02305651	19	5997013	<i>RFX2</i>	-3,59E-03	1,22E-02	7,68E-01	9,84E-01
cg11846064	19	5997274	<i>RFX2</i>	1,42E-02	1,13E-02	2,10E-01	9,59E-01
cg14039368	19	7543466	<i>PEX11G</i>	-2,89E-02	1,18E-02	1,39E-02	8,28E-01
cg15882797	19	7615191	<i>PNPLA6</i>	-1,04E-02	1,40E-02	4,56E-01	9,70E-01
cg25871543	19	7686181	<i>XAB2</i>	-2,87E-02	1,44E-02	4,56E-02	9,19E-01
cg12002047	19	7767279	<i>FCER2</i>	1,60E-02	1,09E-02	1,41E-01	9,39E-01
cg24115835	19	8491580	<i>MARCH2;</i>	-1,81E-02	1,26E-02	1,52E-01	9,39E-01
cg23188331	19	8661264	<i>ADAMTS10</i>	-1,52E-02	1,41E-02	2,81E-01	9,70E-01
cg27503117	19	10434962	<i>RAVER1</i>	4,55E-03	1,79E-02	7,99E-01	9,91E-01
cg14567332	19	10790551	<i>ILF3</i>	-2,31E-02	1,68E-02	1,70E-01	9,47E-01
cg02660440	19	10928233	<i>MIR199A1; DNMT2</i>	-5,49E-03	1,78E-02	7,57E-01	9,84E-01
cg15506281	19	11283688	<i>KANK2</i>	-9,50E-03	1,45E-02	5,13E-01	9,70E-01
cg25713411	19	11289087	<i>KANK2</i>	-1,77E-03	1,73E-02	9,19E-01	9,94E-01
cg07801378	19	11562021	NA	-1,99E-02	1,14E-02	8,15E-02	9,31E-01
cg22565389	19	11660848	<i>CNN1</i>	-3,67E-03	1,42E-02	7,96E-01	9,91E-01
cg02874942	19	11689649	<i>ACP5</i>	-7,06E-04	1,57E-02	9,64E-01	9,94E-01
cg25603587	19	12076549	<i>ZNF763</i>	-4,89E-03	1,14E-02	6,68E-01	9,82E-01
cg26839807	19	12444741	<i>ZNF563</i>	-2,64E-03	1,12E-02	8,14E-01	9,94E-01
cg19515390	19	12784100	<i>MORG1</i>	2,01E-02	1,44E-02	1,62E-01	9,47E-01
cg03126177	19	12982076	<i>MAST1</i>	-5,97E-03	1,30E-02	6,46E-01	9,81E-01
cg05360665	19	13868773	<i>CCDC130</i>	-2,29E-03	1,28E-02	8,59E-01	9,94E-01
cg15205568	19	15292616	<i>NOTCH3</i>	-5,73E-03	1,88E-02	7,60E-01	9,84E-01
cg27261412	19	15550742	<i>WIZ</i>	5,06E-03	1,25E-02	6,84E-01	9,82E-01
cg22270364	19	16178426	<i>TPM4</i>	-2,34E-02	1,57E-02	1,35E-01	9,39E-01
cg15820397	19	17622945	<i>PGLS</i>	-6,16E-03	1,84E-02	7,38E-01	9,82E-01
cg25775386	19	17932001	<i>INSL3</i>	-1,67E-02	1,59E-02	2,95E-01	9,70E-01
cg26848184	19	18278032	<i>PIK3R2</i>	-1,40E-02	1,46E-02	3,40E-01	9,70E-01
cg07727295	19	18553995	<i>ELL</i>	-2,29E-04	1,20E-02	9,85E-01	9,96E-01
cg07015183	19	18830695	<i>CRTC1</i>	-8,38E-03	1,28E-02	5,11E-01	9,70E-01
cg12289801	19	19106904	<i>SFRS14</i>	2,22E-03	1,17E-02	8,49E-01	9,94E-01
cg15995070	19	19253185	NA	8,46E-04	1,25E-02	9,46E-01	9,94E-01
cg10836101	19	30020886	<i>VSTM2B</i>	-4,84E-03	1,52E-02	7,50E-01	9,82E-01
cg25586175	19	30169446	NA	2,24E-02	1,83E-02	2,20E-01	9,59E-01
cg11339587	19	30298341	NA	-2,13E-02	1,19E-02	7,39E-02	9,19E-01
cg03049846	19	33712790	<i>SLC7A10</i>	1,80E-02	1,11E-02	1,04E-01	9,39E-01
cg16896911	19	33895690	<i>PEPD</i>	-8,55E-04	1,40E-02	9,51E-01	9,94E-01
cg06642503	19	35597415	<i>LOC100128675</i>	-4,84E-03	1,07E-02	6,50E-01	9,81E-01
cg06721806	19	35942172	<i>FFAR2</i>	1,05E-02	1,12E-02	3,45E-01	9,70E-01
cg24346223	19	36279422	<i>SNX26</i>	-3,14E-02	1,20E-02	8,66E-03	8,22E-01
cg04361053	19	38686253	<i>SIPA1L3</i>	2,00E-03	1,36E-02	8,83E-01	9,94E-01
cg27653370	19	39663876	<i>PAK4</i>	-1,44E-02	1,11E-02	1,95E-01	9,53E-01
cg25455352	19	39834947	<i>SAMD4B</i>	-1,29E-02	1,06E-02	2,22E-01	9,59E-01
cg12576859	19	40321086	<i>DYRK1B</i>	-7,37E-03	1,48E-02	6,18E-01	9,73E-01

cg18376335	19	40854523	<i>C19orf47; PLD3</i>	3,08E-03	1,44E-02	8,31E-01	9,94E-01
cg27170720	19	40889902	<i>HIPK4</i>	-8,28E-03	1,21E-02	4,94E-01	9,70E-01
cg18536042	19	40899779	<i>PRX</i>	-8,48E-04	1,36E-02	9,50E-01	9,94E-01
cg00540558	19	40930735	<i>SERTAD1</i>	2,36E-02	1,21E-02	5,14E-02	9,19E-01
cg20525355	19	41190250	<i>NUMBL</i>	1,37E-02	1,29E-02	2,88E-01	9,70E-01
cg24083702	19	41281104	<i>MIA</i>	6,71E-03	1,33E-02	6,15E-01	9,72E-01
cg21500909	19	41870640	<i>TMEM91; B9D2</i>	-1,82E-02	7,95E-03	2,17E-02	8,51E-01
cg26920057	19	41889874	<i>TMEM91</i>	-3,77E-03	1,79E-02	8,33E-01	9,94E-01
cg05503433	19	42409117	<i>ARHGEF1</i>	-2,02E-02	1,06E-02	5,68E-02	9,19E-01
cg08304525	19	45895397	<i>PPP1R13L</i>	-2,40E-02	1,24E-02	5,32E-02	9,19E-01
cg23195373	19	45954891	NA	-5,53E-03	1,50E-02	7,13E-01	9,82E-01
cg12067547	19	46385115	NA	-6,02E-03	1,27E-02	6,36E-01	9,80E-01
cg25920686	19	46455981	<i>NOVA2</i>	7,61E-03	2,03E-02	7,07E-01	9,82E-01
cg03067574	19	47767875	<i>CCDC9</i>	-2,68E-02	1,79E-02	1,35E-01	9,39E-01
cg26018431	19	48800072	<i>CCDC114</i>	-1,88E-03	1,34E-02	8,89E-01	9,94E-01
cg05015176	19	49403253	<i>TULP2; NUCB1</i>	-3,35E-02	1,41E-02	1,75E-02	8,28E-01
cg14547801	19	49643015	<i>PPFIA3</i>	4,38E-04	1,86E-02	9,81E-01	9,94E-01
cg01483653	19	50015511	<i>FCGRT</i>	1,62E-03	1,75E-02	9,26E-01	9,94E-01
cg14067541	19	50202524	<i>CPT1C</i>	-1,08E-04	1,33E-02	9,94E-01	9,98E-01
cg19545560	19	51688987	NA	-1,11E-02	9,48E-03	2,42E-01	9,70E-01
cg15985184	19	51830311	<i>IGLON5</i>	9,75E-03	1,71E-02	5,68E-01	9,70E-01
cg19510663	19	55824316	<i>TMEM150B</i>	-4,50E-02	1,34E-02	7,45E-04	2,47E-01
cg06161930	19	56633191	<i>ZNF787</i>	-1,15E-02	1,37E-02	4,01E-01	9,70E-01
cg02449608	19	58486600	<i>C19orf18</i>	1,25E-02	1,02E-02	2,23E-01	9,59E-01
cg16107172	19	59023222	<i>SLC27A5</i>	-3,73E-03	1,15E-02	7,45E-01	9,82E-01
cg26621911	19	59063026	<i>CHMP2A</i>	1,17E-02	1,41E-02	4,06E-01	9,70E-01
cg22192692	20	2451760	<i>SNRPB</i>	1,11E-02	1,09E-02	3,10E-01	9,70E-01
cg11149768	20	4129361	<i>SMOX</i>	1,86E-02	1,58E-02	2,37E-01	9,70E-01
cg22042908	20	4802684	<i>RASSF2</i>	1,67E-02	1,40E-02	2,32E-01	9,70E-01
cg09119967	20	9494838	<i>C20orf103</i>	2,25E-02	1,55E-02	1,45E-01	9,39E-01
cg06821919	20	16710653	<i>SNRPB2</i>	1,93E-02	1,79E-02	2,80E-01	9,70E-01
cg17428560	20	31153746	NA	3,49E-03	1,41E-02	8,04E-01	9,93E-01
cg04027612	20	34022351	<i>GDF5</i>	-5,43E-03	1,23E-02	6,60E-01	9,82E-01
cg03001863	20	36037325	NA	2,50E-02	1,09E-02	2,21E-02	8,51E-01
cg17820025	20	36152813	<i>BLCAP</i>	-2,59E-02	1,08E-02	1,64E-02	8,28E-01
cg16206836	20	36157266	<i>BLCAP</i>	-4,73E-03	1,26E-02	7,08E-01	9,82E-01
cg02849754	20	40627977	NA	1,57E-03	2,00E-02	9,37E-01	9,94E-01
cg26238800	20	45142206	<i>ZNF334</i>	-1,28E-02	1,61E-02	4,28E-01	9,70E-01
cg04898124	20	46410405	<i>SULF2</i>	-7,20E-04	1,01E-02	9,43E-01	9,94E-01
cg01798385	20	47284667	<i>PREX1</i>	-1,36E-02	1,10E-02	2,15E-01	9,59E-01
cg03199996	20	49211573	<i>FAM65C</i>	-1,90E-03	8,21E-03	8,17E-01	9,94E-01
cg24442435	20	55983730	<i>RBM38</i>	-2,29E-02	1,30E-02	7,81E-02	9,19E-01
cg23987549	20	56285728	<i>PMEPA1</i>	-2,65E-03	2,06E-02	8,97E-01	9,94E-01
cg14728235	20	57415177	<i>GNASAS; GNAS</i>	-1,62E-02	1,85E-02	3,83E-01	9,70E-01
cg08093619	20	60449051	<i>CDH4</i>	-2,45E-02	1,24E-02	4,81E-02	9,19E-01
cg27500575	20	60739596	<i>SS18L1</i>	-4,88E-03	1,30E-02	7,08E-01	9,82E-01

cg11284582	20	62270540	NA	5,75E-03	1,20E-02	6,33E-01	9,78E-01
cg10842070	20	62549359	<i>MIR941-1; DNAJC5</i>	-6,97E-03	1,57E-02	6,57E-01	9,82E-01
cg27205487	21	17961996	<i>C21orf34; MIR125</i>	-1,02E-02	1,37E-02	4,57E-01	9,70E-01
cg12349676	21	34350934	NA	-2,79E-02	2,09E-02	1,82E-01	9,47E-01
cg26703511	21	44817420	NA	1,30E-02	1,29E-02	3,12E-01	9,70E-01
cg03566291	21	44831040	NA	3,17E-02	1,59E-02	4,70E-02	9,19E-01
cg00929871	21	44905245	NA	-3,61E-03	1,15E-02	7,54E-01	9,82E-01
cg08406714	21	45223723	<i>RRP1</i>	4,92E-03	1,36E-02	7,17E-01	9,82E-01
cg16087633	21	45702039	NA	-8,58E-03	1,18E-02	4,67E-01	9,70E-01
cg04285033	21	46143498	NA	-1,72E-02	1,72E-02	3,15E-01	9,70E-01
cg05190098	21	46192069	<i>UBE2G2</i>	-1,10E-02	1,36E-02	4,18E-01	9,70E-01
cg05732300	21	46708497	<i>LOC642852; POFUT</i>	-9,96E-03	1,45E-02	4,93E-01	9,70E-01
cg01145544	21	46889296	<i>COL18A1</i>	-1,24E-02	1,29E-02	3,35E-01	9,70E-01
cg08247297	21	46917541	<i>COL18A1</i>	-2,32E-02	1,14E-02	4,08E-02	9,19E-01
cg14581803	21	47576844	<i>FTCD</i>	6,02E-04	1,48E-02	9,68E-01	9,94E-01
cg03816851	22	18324769	<i>MICAL3</i>	-1,75E-03	1,15E-02	8,80E-01	9,94E-01
cg25476775	22	19644037	NA	-1,71E-02	1,26E-02	1,76E-01	9,47E-01
cg00592411	22	19787329	<i>GNB1L</i>	2,16E-02	1,50E-02	1,51E-01	9,39E-01
cg18943949	22	19842501	<i>GNB1L; C22orf29</i>	1,96E-02	1,82E-02	2,80E-01	9,70E-01
cg06045576	22	19948957	<i>COMT</i>	-1,53E-02	1,32E-02	2,48E-01	9,70E-01
cg25161283	22	20103922	<i>TRMT2A; RANBP1</i>	5,88E-04	1,32E-02	9,64E-01	9,94E-01
cg03328201	22	22007633	<i>MIR130B</i>	-8,56E-03	1,68E-02	6,11E-01	9,72E-01
cg17609330	22	23503927	<i>RAB36</i>	-7,23E-03	1,37E-02	5,98E-01	9,72E-01
cg21889604	22	23607606	<i>BCR</i>	-5,53E-03	1,36E-02	6,85E-01	9,82E-01
cg06935052	22	24176449	<i>SMARCB1</i>	6,57E-03	1,23E-02	5,94E-01	9,72E-01
cg22510462	22	24185121	NA	-9,25E-03	1,01E-02	3,60E-01	9,70E-01
cg21021469	22	24615800	<i>GGT5</i>	-7,53E-03	1,19E-02	5,26E-01	9,70E-01
cg27381549	22	24824483	<i>ADORA2A</i>	4,04E-03	9,47E-03	6,70E-01	9,82E-01
cg26253663	22	25799504	NA	-1,93E-02	8,16E-03	1,78E-02	8,28E-01
cg11665583	22	26893201	<i>TFPI1</i>	-3,61E-02	1,16E-02	1,90E-03	3,15E-01
cg20680669	22	28189870	<i>MNI</i>	-1,39E-02	1,71E-02	4,18E-01	9,70E-01
cg06004017	22	28191222	<i>MNI</i>	-1,97E-02	1,34E-02	1,43E-01	9,39E-01
cg26532826	22	31003127	<i>TCN2</i>	-1,10E-02	1,17E-02	3,46E-01	9,70E-01
cg22281206	22	31522176	<i>INPP5J</i>	5,57E-03	1,33E-02	6,74E-01	9,82E-01
cg25791279	22	32026902	<i>PISD</i>	-4,71E-04	1,29E-02	9,71E-01	9,94E-01
cg21732245	22	34313250	<i>LARGE</i>	-5,79E-04	1,13E-02	9,59E-01	9,94E-01
cg20146967	22	35822357	NA	2,07E-03	1,26E-02	8,69E-01	9,94E-01
cg23441210	22	36899848	<i>FOXRED2</i>	-1,55E-02	1,56E-02	3,18E-01	9,70E-01
cg09984479	22	38635620	<i>TMEM184B</i>	-1,47E-02	1,25E-02	2,41E-01	9,70E-01
cg07431064	22	39529217	<i>CBX7</i>	1,14E-02	1,99E-02	5,66E-01	9,70E-01
cg22089929	22	39773861	<i>SYNGR1</i>	-2,09E-02	1,17E-02	7,44E-02	9,19E-01
cg10576267	22	41641887	<i>RANGAP1</i>	9,35E-03	1,71E-02	5,84E-01	9,70E-01
cg02233213	22	42296877	<i>MIR33A; SREBF2</i>	-5,47E-03	1,17E-02	6,39E-01	9,80E-01
cg09569869	22	42469756	<i>FAM109B</i>	-2,91E-02	1,30E-02	2,47E-02	8,77E-01
cg21425232	22	42947198	NA	1,91E-02	1,47E-02	1,94E-01	9,53E-01
cg01021975	22	43570314	<i>TTLL12</i>	-2,40E-02	1,00E-02	1,64E-02	8,28E-01

cg26112317	22	45132994	<i>PRR5-ARHGAP8;PRR</i>	-2,18E-02	1,63E-02	1,82E-01	9,47E-01
cg13166171	22	45133951	<i>PRR5-ARHGAP8</i>	-6,60E-03	1,18E-02	5,74E-01	9,70E-01
cg09137533	22	46469091	NA	1,05E-02	1,18E-02	3,74E-01	9,70E-01
cg14572705	22	47066434	<i>GRAMD4</i>	-1,67E-02	1,79E-02	3,49E-01	9,70E-01
cg02895639	22	48970993	<i>FAM19A5</i>	2,06E-02	1,69E-02	2,22E-01	9,59E-01
cg06937832	22	49141793	<i>FAM19A5</i>	-2,76E-03	1,81E-02	8,79E-01	9,94E-01
cg20200388	22	50869841	<i>SAPS2</i>	8,34E-04	1,08E-02	9,39E-01	9,94E-01
cg11953250	22	51065435	<i>ARSA</i>	-4,29E-02	1,20E-02	3,64E-04	1,51E-01

Coef: Coefficient; SE: Standard Error; FDR: False Discovery Rate; NA: Not available.