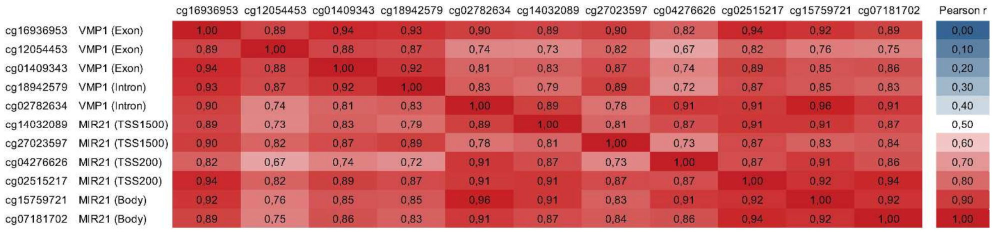
Supplementary Figure 1



		cg16936953	cg12054453	cg01409343	cg18942579	cg02782634	cg14032089	cg27023597	cg04276626	cg02515217	cg15759721	cg07181702
cg16936953	VMP1 (Exon)	1,00	0,89	0,94	0,93	0,90	0,89	0,90	0,82	0,94	0,92	0,89
cg12054453	VMP1 (Exon)	0,89	1,00	0,88	0,87	0,74	0,73	0,82	0,67	0,82	0,76	0,75
cg01409343	VMP1 (Exon)	0,94	0,88	1,00	0,92	0,81	0,83	0,87	0,74	0,89	0,85	0,86
cg18942579	VMP1 (Intron)	0,93	0,87	0,92	1,00	0,83	0,79	0,89	0,72	0,87	0,85	0,83
cg02782634	VMP1 (Intron)	0,90	0,74	0,81	0,83	1,00	0,89	0,78	0,91	0,91	0,96	0,91
cg14032089	MIR21 (TSS1500)	0,89	0,73	0,83	0,79	0,89	1,00	0,81	0,87	0,91	0,91	0,87
cg27023597	MIR21 (TSS1500)	0,90	0,82	0,87	0,89	0,78	0,81	1,00	0,73	0,87	0,83	0,84
cg04276626	MIR21 (TSS200)	0,82	0,67	0,74	0,72	0,91	0,87	0,73	1,00	0,87	0,91	0,86
cg02515217	MIR21 (TSS200)	0,94	0,82	0,89	0,87	0,91	0,91	0,87	0,87	1,00	0,92	0,94
cg15759721	MIR21 (Body)	0,92	0,76	0,85	0,85	0,96	0,91	0,83	0,91	0,92	1,00	0,92
cg07181702	MIR21 (Body)	0,89	0,75	0,86	0,83	0,91	0,87	0,84	0,86	0,94	0,92	1,00

Pearson r
0,00
0,10
0,20
0,30
0,40
0,50
0,60
0,70
0,80
0,90
1,00

Supplementary Figure 1: Correlation between DNA methylation levels at 11 CpGs in the region.
Analysis was performed on β-values from RR-MS, SP-MS and HC (n=32) using the Pearson correlation test and Pearson's r is displayed.

Supplementary Figure 1: Correlation between DNA methylation levels at 11 CpGs in the region.

154x64mm (600 x 600 DPI)

Supplementary Methods

Samples

Multiple Sclerosis cohorts

A discovery cohort comprised RR-MS, SP-MS and matched healthy controls (HC) recruited at the local Neurology clinic at the Karolinska University Hospital in Stockholm, Sweden. Detailed patient demographics are provided in Table 1. An independent cohort comprising RR-MS, SP-MS, inflammatory neurological disease controls (INDC) and HC was recruited at the same clinic and used for validation. Detailed patient demographics are provided in Table S1. All patients had given informed consent and the study was approved by the ethical review board of Stockholm (2009/2107-31/2 and 2010/879-31/1).

The GOLDN cohort

The Genetics of Lipid Lowering Drugs and Diet Network (GOLDN) study, aimed at investigating genetic and epigenetic determinants of response to interventions targeting blood lipid levels, recruited families with at least two siblings from the National Heart, Lung, and Blood Institute Family Heart Study sites at Minneapolis and Salt Lake City. The study obtained epigenome-wide DNA methylation data on CD4+ T-cells using the Illumina Infinium 450K Human Methylation Beadchip as described in previous publications[1-3]. Genotyping of GOLDN participants was performed using the Affymetrix Genome-Wide Human 6.0 array[4]. After all quality control procedures were performed, 717 out of 994 participants had both genetic and epigenetic data and were included in this analysis. The Institutional Review Board (IRB) approved the GOLDN study (E160405007).

Preparation of CD4+ T cells

For the discovery cohort peripheral blood mononuclear cells (PBMCs) were isolated and collected in sodium heparin tubes using a standard Ficoll (GE Healthcare) procedure. Cells were separated using density gradient centrifugation, collected from the interphase, washed twice in Dulbecco's phosphate buffered saline and prepared for cell sorting. Sorting of the $CD4^+$ T cell population was performed by adding fluorochrome-conjugated antibodies against human CD4 (Becton Dickinson) and CD3 (BD Bioscience) using a MoFlo high-speed cell sorter (Beckman Coulter).

For the validation cohort PBMCs were isolated from peripheral blood using sodium citrate-containing cell preparation tubes (BD Vacutainer™ CPT™ Tube, Becton Dickinson), Sorting of the CD4+ T cell population was performed by adding microbeads against human CD4 using an autoMACS® cell separator (Miltenyi Biotec).

Directly after sorting, cell pellets were frozen and kept at -80C° until DNA/RNA extraction.

DNA extraction

Extraction of genomic DNA was carried out using a Gen Elute Mammalian Genomic DNA Miniprep kit (Sigma-Aldrich). The amount and quality of DNA was accessed by NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies).

DNA methylation analysis

DNA methylation was profiled using the Infinium HumanMethylation450 BeadChip (Illumina) arrays at the bioinformatics and expression analysis core facility (BEA) at Karolinska Institutet. Methylation data was individually analyzed in R using the Minfi and ChAMP package, probes containing SNPs within 2 bp of the CpG were removed, and type 1 and type 2 probes were normalized using quantile normalization and BMIQ[5]. The sex of the patients was confirmed using the GetSex function from the Minfi package and the cell type was confirmed using the cell type deconvolution method from Minfi based on the Houseman algorithm[6]. Significant cofounders were identified using PCA. Batch effects were corrected using ComBat from the SVA package[7]. Differentially methylated positions (DMPs) were determined by using the limma package[8] applying a linear modeling that included MS status, age and sex as co-variates. Differences were calculated between HC and RR-MS and RR-MS and SP-MS. Additionally any significant differences between all three groups were identified using the moderated F-statistic test included in eBayes[9].

Meta-analysis

Meta-analysis on the 11 CpG probes was performed by combining the outcomes of the analyses between RR-MS and HC using β-values from the cohorts from Sweden (n=24), Norway (n=30) and Australia (n=40). Comparison of RR-MS with HC was performed on β-values and corrected for age in the Norwegian and Australian cohort (comprising females only), and age and sex in the Swedish cohort. Due to the strong impact of age on the methylation in the *MIR21* region only individuals with available age information and age-matched HC where retained for analysis. Similar data were obtained with all individuals (data not shown). We used two different meta-analysis methodologies: (1) the "summation of p value" method for combining p-values[10], and (2) the effect-size based meta-analysis using a fixed effect model (estimated by restricted maximum-likelihood) since there was no evidence of significant heterogeneity[11]. Similar outcome to "summation of p value" was obtained using the Fisher's test for combining p-values (data not shown). To conduct the meta-analysis we used the R packages metaphor and metap.

Pyrosequencing

A representative CpG within miR21 locus exhibiting significant DNA methylation differences in the Illumina 450K array (cg07181702) was selected for pyrosequencing validation. Primers were designed using PyroMark Design software (Qiagen) (Fwd: GAA ATG TTT GGG TTT TTT TGG TTT G, Rev: ACC CAT CCA CTA ATA TTA CCA TAA AAT TCA, sequencing: ATT CAA CAA TCA ACA TCA AT). Genomic DNA (200 ng) was bisulfite-converted using an EpiTect Bisulfite Kit (Qiagen), bisulfite-converted DNA was eluted in 20 µl of elution buffer and ~15 ng was applied as a template in the PCR performed with the PyroMarks PCR kit (Qiagen) using 5'-biotinylated forward primer. The entire PCR product, 4 pmol of the sequencing primer, and streptavidin sepharose high-performance beads (GR Healthcare), were used for pyrosequencing on the PSQ 96 system and PyroMark Gold 96 reagent kit (Qiagen). The PyroMark CpG software 1.0.11 (Qiagen) served for data analysis.

RNA extraction

For subsequent qPCR analysis total RNA from the discovery and independent sample cohort was isolated using standard TRIzol protocol (Invitrogen) and Allprep Total RNA/DNA Kit (Qiagen), respectively, according to manufacturer´s recommendations. RNA concentration and purity were determined by measurement of A260/A280 ratios with a NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies). For subsequent transcriptome analysis RNA, was extracted using the miRNeasy Kit (Qiagen) according to manufacturer´s recommendations. The RNA integrity was determined using Bioanalyzer (Agilent Technologies). All samples had an RNA integrity number (RIN) above 8. All RNA samples obtained from the different preparations were immediately frozen and stored at −80°C until further use.

Quantitative real-time PCR analysis

Expression levels of miR-21 were determined by quantitative real-time PCR (qRT-PCR) using TaqMan MicroRNA Assay Kit specific for mature miR-21 (No: 000397, Applied Biosystems) following the manufacturer's protocol. Expression levels were quantified by the CFX384 Real-Time PCR Detection System and analyzed using CFX manager software (Bio-Rad). Relative quantification of miRNA was quantified using the $2^{-\Delta\Delta CT}$ method and normalized against RNU48 for each sample. For *VMP1* expression detection cDNA was converted from RNA using the Bio-Rad iScript cDNA sythesis Kit (Bio-Rad). *VMP1* expression was accessed by qPCR (fwd 5'-GGT GCT GAA CCA AGA TGA-3'; rev 5'-GCA CTG TGT TGG CGT ACA G-3') using CFX384 Real-Time detection system and analyzed by CFX manager software (Bio-Rad). Cycling conditions were as follows 95C° for 2 min followed by 40 repeats at 95 C° for 20 s, 58C° for 20 s and 72C° for 30 s. *VMP1* expression was normalized to beta actin reference gene (fwd 5'-GAC TTC GAG CAA GAG ATG G-3' rev 5'-GCA CTG TGT TGG CGT ACA G-3') for every sample and quantified using the $2^{-\Delta\Delta CT}$ method. Statistical analysis between the groups was performed using Student's t-test (for two groups) and ANOVA with Bonferroni correction for selected groups (for more than two groups), and correlation between expression and methylation levels was assessed using Pearson's correlation test in GraphPad Prism 5 (GraphPad).

Genotyping

Allelic discrimination of rs8070345 (in the *VMP1* locus) was performed using a predesigned TaqMan SNP Genotyping Assay (Cat. No: 4351379, Applied Biosystems) according to the manufacturer's protocol. PCR amplification was done in a CFX384 Real-Time PCR Detection System (Bio-Rad) and results were read on a QuantStudio ™ 7 Flex system (Applied Biosystems).

Association and correlation analysis

In the GOLDN cohort we used the *lmekin* function of the R *kinship* package to fit linear mixed effects models with the methylation β-value at each of the interrogated CpG sites as the outcome and the following predictors: SNP, age, sex, study site (Utah vs. Minnesota), current smoking (yes vs. no), body mass index, 4 principal components capturing T-cell purity[3] (as fixed effects), and family (as a random effect). We additionally fit linear regression models with the methylation β-value at each CpG site as the outcome and the non-genetic predictors, namely age, smoking, and BMI, and the T-cell purity principal components.

In the Multiple Sclerosis cohort we fit linear regression model with the methylation β-value at each of the interrogated CpG sites as the outcome and the following predictors: SNP, age and sex. We additionally fit linear regression model with the methylation β-value at each of the interrogated CpG sites as the outcome and the following predictors: age, sex, Multiple Sclerosis Severity Score (MSSS) and lymphocyte count. All analyses were done in Rcmd.

Transcriptome analysis

Total RNA (500ng) with RIN above 8.0, was subjected to the Illumina TruSeq Stranded mRNA Library Preparation Protocol with Dual Indexes (Cat. No: RS-122-2013, Illumina). Libraries were quantified using the Kapa Library Quantification Kit (Cat. No: KK4824, Illumina). Sequencing was carried out on the Illumina HiSeq 2500 to generate 75bp Paired End Data with an average of 10M reads above Q30. The sequence reads were mapped to hg19 reference with Tophat2[12] and HTSeq[13] was used to quantify counts-per-gene. The expression data from CD4$^+$ cells (34 samples) were normalized with Conditional Quantile Normalization (CQN) method[14] followed by batch reduction by ComBat[7]. Differential expression analysis was conducted using limma tool[8] in order to identify differences between disease types.

Target gene enrichment analysis

Genes identified as miR-21 targets in Jurkat T cells by RIP-Chip (Czepiel *et al.*, ISBN 978-90-367-6788-0) and genes predicted and experimentally validated to be miR-21 targets by TarBase7.0[15] were selected for further investigation. Deviation of up- and down-regulated miR-21 target genes from the expected ratio of up-and down-regulated genes in RNAseq analysis (for p-values of 0.1, 0.05 and 0.01) was calculated for both lists of miR-21 target genes using a Chi-squared test. Enrichment of up- and down-regulated targets among differentially expressed targets in RNAseq analysis (for p-values of 0.1, 0.05 and 0.01) was calculated for both lists of miR-21 target genes using the Fisher's exact test in GraphPad Prism 5 (GraphPad Software, San Diego, CA, USA). Similar results were obtained when predicted miR-21 target genes were based on being predicted by a minimum of the two of the following tools: miR-21 targets in Jurkat cells, miRTar, TarBase7.0, TargetScan7.1 and microT-CDS.

Ingenuity Pathways Analysis

Two list of genes, 1) differentially expressed genes between RR-MS and HC ($p<0.05$) and 2) TarBase7.0-predicted miR-21 target genes up-regulated in RR-MS compared to HC ($p<0.05$) from RNAseq analysis were uploaded to the Ingenuity Pathways Analysis platform (Qiagen). The first list was used to assess significant up-stream regulators that can explain observed gene expression changes estimated by the overlap p-value, which is calculated using Fisher's exact test and significance is generally attributed to $p<0.01$. The activation z-score is used to infer the activation states of predicted upstream regulators and $z<-2$ and $z>2$ indicate significantly inhibited and activated upstream regulators, respectively. The second list of genes was used to infer biological functions that might be affected by miR-21. Right-tailed Fisher's exact test was used to calculate a p-value determining the probability that each biological function assigned to that data set is due to chance alone. Benjamini-Hochberg correction for multiple testing was used to calculate significant p-values.

References

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Cohort	**Status**	**Gender**	**Age**	**EDSS**	**MSSS**
discovery	RR-MS remissior	F	37	3	2.91
discovery	RR-MS remissior	F	40	0	0.67
discovery	RR-MS remissior	M	44	1.5	
discovery	RR-MS remissior	M	40	0.5	2.44
discovery	RR-MS remissior	F	26	1	5.87
discovery	RR-MS remissior	F	29	2	5.87
discovery	RR-MS remissior	M	34	2	4.3
discovery	RR-MS remissior	F	35	1	1.13
discovery	RR-MS remissior	F	46	5	3.44
discovery	RR-MS remissior	F	37	1.5	3.34
discovery	RR-MS remissior	M	29	1	0.88
discovery	RR-MS remissior	M	32	3	3.05
discovery	RR-MS remissior	F	57	2.5	4.13
discovery	RR-MS remissior	F	41	2	0.71
discovery	SP-MS	M	45	4	2.82
discovery	SP-MS	M	50	6.5	5.99
discovery	SP-MS	M	56	6.5	5.99
discovery	SP-MS	F	62	7	7.97
discovery	SP-MS	F	63	5	
discovery	SP-MS	F	56	8	8.75
discovery	SP-MS	F	35	5	7.32
discovery	SP-MS	F	60	5	5.82
discovery	SP-MS	M	44	6	5.43
discovery	SP-MS	F	53	6	6.01
discovery	SP-MS	F	53	6.5	5.61
discovery	SP-MS	F	50	3.5	4.55
discovery	HC	F	60		
discovery	HC	F	44		
discovery	HC	M	31		
discovery	HC	F	35		
discovery	HC	M	31		
discovery	HC	F	48		
discovery	HC	F	28		
discovery	HC	M	30		
discovery	HC	F	30		
discovery	HC	F	28		
discovery	HC	F	27		
discovery	HC	F	32		
discovery	HC	F	62		
discovery	HC	M	44		
discovery	HC	M	54		
Summarized discovery cohort 450K; mean (range):					
RR-MS		9F (75%) / 3M (25%)	38 (26-57)	2,0 (0-5,0)	2,9 (0,7-5,9)
SP-MS		4F (50%) / 4F (50%)	50 (35-63)	5,2 (3,5-6,5)	5,4 (2,8-7,3)

HC		8F (67%) / 4M (33%)	42 (28-62)	N/A	N/A
Summarized discovery cohort RNA-seq, mean (range):					
RR-MS		6F (54%) / 5M (46%)	36 (26-46)	1,8 (0-5,0)	3,1 (0,7-5,9)
SP-MS		7F (64%) / 4M (36%)	52 (35-63)	6,0 (4,0-8,0)	6,2 (2,8-8,8)
HC		7F (58%) / 5M (42%)	40 (27-62)	N/A	N/A
validation	CIS - RR-MS	F	41		
validation	CIS - RR-MS	F	50		
validation	RR-MS relapse	F	54		
validation	RR-MS relapse	F	38		
validation	RR-MS remissior	F	36		
validation	RR-MS remissior	F	33		
validation	RR-MS remissior	M	48		
validation	RR-MS remissior	F	34		
validation	RR-MS remissior	F	52		
validation	RR-MS remissior	F	31		
validation	RR-MS remissior	F	27		
validation	RR-MS remissior	F	73		
validation	RR-MS remissior	M	23		
validation	RR-MS remissior	M	37		
validation	RR-MS remissior	M	52		
validation	RR-MS remissior	M	36		
validation	RR-MS remissior	M	45		
validation	RR-MS remissior	F	29		
validation	RR-MS remissior	F	32		
validation	RR-MS remissior	F	29		
validation	RR-MS remissior	M	34		
validation	RR-MS remissior	F	40		
validation	RR-MS remissior	F	34		
validation	RR-MS remissior	F	27		
validation	RR-MS remissior	M	28		
validation	RR-MS remissior	F	31		
validation	RR-MS remissior	F	50		
validation	RR-MS remissior	F	35		
validation	RR-MS remissior	F	31		
validation	RR-MS remissior	F	24		
validation	SP-MS	F	54		
validation	SP-MS	M	47		
validation	SP-MS	M	57		
validation	SP-MS	F	41		
validation	SP-MS	F	51		
validation	SP-MS	F	65		
validation	SP-MS	F	36		
validation	SP-MS	F	51		
validation	SP-MS	F	52		
validation	SP-MS	F	59		

validation	SP-MS	M	59		
validation	HC	F	22		
validation	HC	F	23		
validation	HC	M	35		
validation	HC	M	28		
validation	HC	F	33		
validation	HC	M	35		
validation	HC	M	23		
validation	HC	M	21		
validation	HC	F	22		
validation	HC	F	34		
validation	HC	M	30		
validation	HC	M	40		
validation	INDC	F	47		
validation	INDC	M	53		
validation	INDC	F	32		
validation	INDC	F	64		
validation	INDC	F	40		
validation	INDC	M	51		
validation	INDC	F	68		
validation	INDC	F	53		
validation	INDC	F	74		
Summarized validation Cohort					
RR-MS patients		22F (73%) / 8M (27%)	38 (23-73)		
SP-MS patients		8F (73%) / 3M (27%)	52 (36-65)		
HC		5F (42%) / 7M (58%)	29 (21-40)		
INDC		7F (78%) / 2M (22%)	54 (32-74)		

Lymphocytes	Treatment at sampling	Treatment prior to sampling	450K	RNAseq
1.7	never Tx		X	X
1.8	never Tx		X	X
1.8	never Tx		X	X
	never Tx			X
2.4	never Tx		X	X
1.7	never Tx		X	X
	never Tx			X
2.2	no Tx	Fingolimod	X	X
1.6	IVIg		X	X
2.7	study drug		X	
1.6	no Tx	IFN	X	X
2.7	no Tx	IFN	X	X
1.9	no Tx	study drug	X	
1.6	never Tx		X	
2.3	no Tx	IFN	X	X
2.0	no Tx	study drug	X	X
2.2	never Tx		X	X
	no Tx	IFN		X
2.3	never Tx		X	X
	no Tx	Copaxone, IFN		X
1.8	no Tx	IFN, Copaxone	X	X
1.5	no Tx	IFN, Mitoxantrone	X	X
2.0	no Tx	IFN, study drug	X	X
1.3	no Tx	IFN, Mitoxantrone		X
2.3	no Tx	IFN, study drug		X
1.4	no Tx	IFN	X	
			X	X
			X	
			X	X
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			X	
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			X	X
			X	X
			X	X
			X	X
2,0 (1,6-2,7) 1,9 (1,4-2,3)				

N/A

1,9 (1,6-2,7)
2,0 (1,3-2,3)
N/A

	never Tx			
	never Tx			
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miR-21qPCR
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Supplementary Table 2: Differential expression in CD4+ T cells of predicted miR-21 target genes betw

in Jurkat T cells by RIP-Chip and genes predicted and experimentally validated to be miR-21 targets by

Jurkat target ID	Gene Name	Description	logFC	AveExpr	P.Value	TarBase7.0 target ID
ENSG00000180667	**YOD1**	YOD1 deubiqui	0.30	5.09	3.28E-04	ENSG00000164284
ENSG00000100354	TNRC6B	trinucleotide re	0.13	6.71	4.99E-03	ENSG00000180667
ENSG00000146676	**PURB**	purine rich eler	0.17	5.75	9.29E-03	ENSG00000113369
ENSG00000145715	RASA1	RAS p21 protei	0.17	6.59	1.23E-02	ENSG00000143753
ENSG00000110987	**BCL7A**	BCL tumor supp	0.63	2.13	2.20E-02	ENSG00000180979
ENSG00000197579	**TOPORS**	TOP1 binding a	0.12	5.20	3.33E-02	ENSG00000150753
ENSG00000152518	ZFP36L2	ZFP36 ring fing	0.18	11.05	3.64E-02	ENSG00000253719
ENSG00000131023	**LATS1**	large tumor sup	-0.07	5.87	3.88E-02	ENSG00000131381
ENSG00000124209	**RAB22A**	RAB22A, memb	0.11	4.57	4.50E-02	ENSG00000141582
ENSG00000138336	**TET1**	tet methylcytos	-0.26	1.57	4.81E-02	ENSG00000146676
ENSG00000076641	**PAG1**	phosphoprotei	0.18	8.28	7.03E-02	ENSG00000119844
ENSG00000165244	**ZNF367**	zinc finger prot	0.16	3.85	7.29E-02	ENSG00000118402
ENSG00000152520	PAN3	PAN3 poly(A) s	0.09	7.10	7.60E-02	ENSG00000164466
ENSG00000166225	**FRS2**	fibroblast grow	0.08	4.97	9.50E-02	ENSG00000163629
ENSG00000171316	CHD7	chromodomain	0.14	5.57	1.10E-01	ENSG00000104643
ENSG00000107679	PLEKHA1	pleckstrin hom	-0.12	5.70	1.25E-01	ENSG00000145907
ENSG00000171132	PRKCE	protein kinase	0.12	2.63	1.31E-01	ENSG00000196776
ENSG00000110848	CD69	CD69 molecule	-0.19	10.25	1.42E-01	ENSG00000110987
ENSG00000155640	-	-	0.16	4.26	1.46E-01	ENSG00000070214
ENSG00000174010	**KLHL15**	kelch like famil	0.12	4.55	1.48E-01	ENSG00000173698
ENSG00000134698	**AGO4**	argonaute 4, RI	0.17	5.75	1.65E-01	ENSG00000109787
ENSG00000152601	MBNL1	muscleblind lik	-0.06	9.23	1.86E-01	ENSG00000119778
ENSG00000197323	**TRIM33**	tripartite motif	0.04	6.56	1.95E-01	ENSG00000185658
ENSG00000138593	SECISBP2L	SECIS binding p	0.05	6.04	1.96E-01	ENSG00000158079
ENSG00000162599	NFIA	nuclear factor I	0.13	1.27	2.43E-01	ENSG00000096060
ENSG00000177189	**RPS6KA3**	ribosomal prot	0.06	7.43	2.83E-01	ENSG00000119899
ENSG00000188895	MSL1	male specific le	0.07	7.40	2.87E-01	ENSG00000196459
ENSG00000118922	KLF12	Kruppel like fac	0.05	7.01	2.98E-01	ENSG00000100664
ENSG00000181690	**PLAG1**	PLAG1 zinc fing	0.14	4.53	2.99E-01	ENSG00000143013
ENSG00000162378	**ZYG11B**	zyg-11 family m	0.05	5.21	3.05E-01	ENSG00000164190
ENSG00000204217	**BMPR2**	bone morphog	0.06	4.33	3.20E-01	ENSG00000048471
ENSG00000081014	AP4E1	adaptor relate	-0.04	4.62	3.29E-01	ENSG00000197579
ENSG00000185009	**AP3M1**	adaptor relate	-0.04	5.67	3.68E-01	ENSG00000127337
ENSG00000107864	**CPEB3**	cytoplasmic po	0.07	2.84	3.74E-01	ENSG00000196262
ENSG00000150593	**PDCD4**	programmed c	0.05	8.46	3.90E-01	ENSG00000092871
ENSG00000143756	FBXO28	F-box protein 2	0.04	5.30	3.91E-01	ENSG00000131023
ENSG00000182568	**SATB1**	SATB homeobo	0.09	7.64	4.06E-01	ENSG00000144909
ENSG00000119866	**BCL11A**	B-cell CLL/lymp	-0.35	-0.92	4.47E-01	ENSG00000066933
ENSG00000173281	**PPP1R3B**	protein phosph	0.09	3.82	4.58E-01	ENSG00000118971
ENSG00000171940	**ZNF217**	zinc finger prot	0.03	6.68	5.29E-01	ENSG00000169564

ENSG00000157933	**SKI**	SKI proto-onco	0.05	7.14	5.44E-01
ENSG00000143878	**RHOB**	ras homolog fa	-0.19	5.49	5.62E-01
ENSG00000102908	NFAT5	nuclear factor	-0.03	5.84	5.65E-01
ENSG00000163939	**PBRM1**	polybromo 1 [S	-0.02	5.89	5.65E-01
ENSG00000165572	**KBTBD6**	kelch repeat an	-0.05	2.93	5.77E-01
ENSG00000155744	**FAM126B**	family with seq	0.03	4.63	6.01E-01
ENSG00000196937	**FAM3C**	family with seq	0.04	4.85	6.18E-01
ENSG00000123124	WWP1	WW domain co	0.03	6.97	6.71E-01
ENSG00000101972	**STAG2**	stromal antiger	0.01	6.93	6.78E-01
ENSG00000204116	CHIC1	cysteine rich hy	0.02	5.46	6.97E-01
ENSG00000095015	**MAP3K1**	mitogen-activa	0.03	8.20	7.24E-01
ENSG00000112739	PRPF4B	pre-mRNA proc	-0.01	7.52	7.66E-01
ENSG00000157741	UBN2	ubinuclein 2 [S	-0.02	5.00	7.75E-01
ENSG00000113300	**CNOT6**	CCR4-NOT tran	0.02	5.64	7.85E-01
ENSG00000128923	**FAM63B**	family with seq	0.02	4.99	8.39E-01
ENSG00000105810	CDK6	cyclin depende	0.02	5.82	8.84E-01
ENSG00000138081	**FBXO11**	F-box protein 1	0.00	6.64	8.93E-01
ENSG00000178177	LCORL	ligand depende	0.01	2.93	9.10E-01
ENSG00000148730	**EIF4EBP2**	eukaryotic tran	0.00	7.12	9.40E-01
ENSG00000103064	SLC7A6	solute carrier f	0.01	8.52	9.45E-01
ENSG00000115020	PIKFYVE	phosphoinositi	0.00	6.42	9.73E-01
ENSG00000145675	PIK3R1	phosphoinositi	0.00	7.40	9.80E-01
ENSG00000123472	ATPAF1	ATP synthase n	0.00	5.17	9.89E-01
ENSG00000172575	**RASGRP1**	RAS guanyl rele	0.00	8.41	9.99E-01

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een RR-MS and HC. Genes identified as miR-21 targets

TarBase7.0 were selected for investigation.

Gene Name	Description	logFC	AveExpr	P.Value
GRPEL2	GrpE like 2, mi	0.44	5.87	6.63E-05
YOD1	YOD1 deubiqu	0.30	5.09	3.28E-04
ARRDC3	arrestin domai	0.44	8.17	7.68E-04
DEGS1	delta 4-desatu	0.21	6.40	2.74E-03
LRRC57	leucine rich re	0.33	5.02	4.09E-03
CCT5	chaperonin co	-0.17	6.06	4.97E-03
ATXN7L3B	ataxin 7 like 3	0.17	8.07	5.66E-03
RBSN	rabenosyn, RA	0.13	5.61	7.10E-03
CBX4	chromobox 4 [	0.22	6.52	9.03E-03
PURB	purine rich ele	0.17	5.75	9.29E-03
AFTPH	aftiphilin [Sour	-0.14	6.05	1.24E-02
ELOVL4	ELOVL fatty ac	0.61	2.44	1.48E-02
SFXN1	sideroflexin 1 [	0.14	6.23	1.49E-02
PTPN13	protein tyrosir	0.67	3.10	1.55E-02
MTMR9	myotubularin	0.09	4.85	1.65E-02
G3BP1	G3BP stress gr	0.09	6.92	1.88E-02
CD47	CD47 molecule	0.09	8.47	1.95E-02
BCL7A	BCL tumor sup	0.63	2.13	2.20E-02
SLC44A1	solute carrier f	-0.13	3.78	2.27E-02
ADGRG2	adhesion G pro	-1.00	-1.29	2.30E-02
KLF3	Kruppel like fa	0.17	7.88	2.33E-02
ATAD2B	ATPase family,	-0.12	4.38	2.36E-02
BRWD1	bromodomain	0.10	6.29	2.41E-02
PTPDC1	protein tyrosir	-0.19	3.27	2.52E-02
FKBP5	FK506 binding	0.31	6.88	2.56E-02
SLC17A5	solute carrier f	0.14	4.31	2.74E-02
TRAPPC2	trafficking prot	0.11	5.06	3.06E-02
EIF5	eukaryotic trar	0.13	7.55	3.10E-02
LMO4	LIM domain or	0.33	4.30	3.20E-02
NIPBL	NIPBL, cohesin	-0.07	6.49	3.25E-02
SNX29	sorting nexin 2	0.12	4.84	3.29E-02
TOPORS	TOP1 binding a	0.12	5.20	3.33E-02
YEATS4	YEATS domain	-0.25	5.66	3.42E-02
PPIA	peptidylprolyl	0.11	8.48	3.71E-02
RFFL	ring finger and	0.11	5.60	3.76E-02
LATS1	large tumor su	-0.07	5.87	3.88E-02
OSBPL11	oxysterol bindi	-0.17	4.79	4.23E-02
MYO9A	myosin IXA [Sc	-0.09	4.35	4.30E-02
CCND2	cyclin D2 [Sour	0.13	7.23	4.31E-02
PCBP1	poly(rC) bindir	-0.14	9.08	4.32E-02

KMT2D	lysine methyltı	-0.08	6.96	4.38E-02
IL1B	interleukin 1 b	-1.38	0.88	4.39E-02
SPCS3	signal peptidas	0.10	7.47	4.41E-02
RAB22A	RAB22A, mem	0.11	4.57	4.50E-02
TET1	tet methylcyto	-0.26	1.57	4.81E-02
HNRNPU	heterogeneou:	-0.10	8.12	4.94E-02
PRPF39	pre-mRNA pro	-0.08	6.85	5.31E-02
GAB1	GRB2 associate	-0.83	-1.43	5.55E-02
MDN1	midasin AAA A	-0.12	6.59	5.75E-02
ANXA1	annexin A1 [Sc	-0.29	8.85	5.78E-02
CENPQ	centromere pr	-0.25	3.52	6.30E-02
FAM217B	family with sec	0.12	5.04	6.53E-02
ATP5G3	ATP synthase,	0.10	4.69	6.92E-02
RSF1	remodeling an	0.07	5.37	6.93E-02
PAG1	phosphoprotei	0.18	8.28	7.03E-02
MAP3K2	mitogen-activa	0.06	6.44	7.07E-02
ZNF367	zinc finger pro	0.16	3.85	7.29E-02
BNIP2	BCL2 interactir	0.07	6.14	7.31E-02
GATAD2B	GATA zinc fing	0.06	6.47	7.94E-02
CDS1	CDP-diacylglyc	-0.27	0.83	8.08E-02
FAM46C	family with sec	-0.44	6.75	8.49E-02
ADAM22	ADAM metallo	-0.23	1.73	8.58E-02
HDAC2	histone deacet	-0.13	4.32	8.59E-02
SESN1	sestrin 1 [Sour	0.25	6.65	8.70E-02
FICD	FIC domain cor	0.21	2.08	9.01E-02
IQGAP1	IQ motif conta	-0.13	6.82	9.03E-02
UBE2W	ubiquitin conju	0.08	4.35	9.23E-02
FRS2	fibroblast grov	0.08	4.97	9.50E-02
KLF7	Kruppel like fa	0.16	6.27	9.58E-02
RP2	retinitis pigme	-0.15	3.81	9.83E-02
SNTB2	syntrophin bet	0.19	4.62	1.03E-01
SEC63	SEC63 homolo	0.06	5.69	1.03E-01
RIC1	RIC1 homolog,	0.07	5.43	1.04E-01
KBTBD7	kelch repeat aı	0.29	2.02	1.08E-01
FOXK1	forkhead box k	0.12	5.91	1.13E-01
PWP1	PWP1 homolo;	-0.07	6.17	1.14E-01
BDH2	3-hydroxybuty	0.17	4.17	1.16E-01
LYRM7	LYR motif cont	-0.10	5.42	1.17E-01
SLK	STE20 like kina	-0.08	6.04	1.24E-01
ZRANB1	zinc finger RAN	0.06	5.57	1.25E-01
BAG4	BCL2 associate	0.11	4.01	1.27E-01
SMG1	SMG1, nonsen	-0.08	7.37	1.36E-01
LRRC8B	leucine rich re|	0.14	4.83	1.36E-01
RGS1	regulator of G-	-0.45	8.05	1.37E-01

GAPVD1	GTPase activat	0.07	5.09	1.37E-01
CMBL	carboxymethy	-0.37	0.54	1.40E-01
SLC5A3	solute carrier f	-0.16	5.06	1.40E-01
KIAA1551	KIAA1551 [Sou	-0.13	8.85	1.40E-01
APAF1	apoptotic pept	-0.08	5.15	1.43E-01
PGRMC1	progesterone r	0.08	5.17	1.45E-01
-	-	0.16	4.26	1.46E-01
FAM160B1	family with sec	0.18	5.76	1.46E-01
KLHL15	kelch like fami	0.12	4.55	1.48E-01
RBMS1	RNA binding m	0.10	6.79	1.48E-01
SKP2	S-phase kinase	-0.12	4.79	1.55E-01
NAA25	N(alpha)-acety	0.08	5.08	1.58E-01
CERK	ceramide kinas	0.09	7.87	1.59E-01
AGO4	argonaute 4, R	0.17	5.75	1.65E-01
AGGF1	angiogenic fac	-0.06	5.64	1.65E-01
DDX1	DEAD/H-box h	-0.06	6.10	1.66E-01
NT5E	5'-nucleotidase	-0.43	2.73	1.71E-01
EPHA4	EPH receptor A	0.24	5.25	1.74E-01
HS3ST3B1	heparan sulfat	0.11	5.43	1.76E-01
KLF9	Kruppel like fa	0.18	7.60	1.81E-01
TC2N	tandem C2 dor	-0.11	8.46	1.82E-01
HIPK3	homeodomain	-0.08	6.58	1.84E-01
PKD2	polycystin 2, tr	0.18	4.94	1.86E-01
CEP97	centrosomal p	0.07	4.48	1.90E-01
REST	RE1 silencing t	0.05	6.04	1.92E-01
PHF6	PHD finger pro	-0.07	4.94	1.93E-01
DCTN4	dynactin subur	0.06	5.33	1.95E-01
TRIM33	tripartite motif	0.04	6.56	1.95E-01
FNIP2	folliculin intera	-0.07	3.32	1.97E-01
STK38L	serine/threoni	-0.06	4.69	1.99E-01
SMAD7	SMAD family n	-0.28	4.63	2.08E-01
RAB11A	RAB11A, mem	-0.05	5.76	2.12E-01
GID4	GID complex su	-0.14	4.12	2.13E-01
NBEA	neurobeachin	0.23	2.11	2.16E-01
MEGF9	multiple EGF li	0.11	5.54	2.18E-01
GNAQ	G protein subu	0.05	6.60	2.18E-01
ARCN1	archain 1 [Sou	-0.08	7.02	2.20E-01
RMND5B	required for m	-0.06	4.33	2.22E-01
FKTN	fukutin [Source	0.08	5.14	2.26E-01
PTAR1	protein prenyl	0.05	6.78	2.32E-01
ADNP	activity depend	0.05	6.66	2.35E-01
HGSNAT	heparan-alpha	0.07	5.52	2.38E-01
PCBP2	poly(rC) bindin	0.05	6.83	2.43E-01
DERL1	derlin 1 [Sourc	-0.07	5.60	2.47E-01

MAPRE1	microtubule as	-0.05	7.41	2.50E-01
RBM12B	RNA binding m	-0.08	4.97	2.53E-01
OLA1	Obg-like ATPas	0.06	5.00	2.54E-01
IREB2	iron responsive	0.05	5.96	2.57E-01
TANC1	tetratricopepti	0.29	-0.39	2.57E-01
POLR3B	RNA polymera	-0.10	3.60	2.61E-01
MAPK1	mitogen-activa	-0.06	6.48	2.62E-01
SMARCD1	SWI/SNF relate	0.04	6.43	2.66E-01
SLC26A2	solute carrier f	0.05	4.32	2.67E-01
ITFG1	integrin alpha	0.06	3.57	2.67E-01
MOAP1	modulator of a	0.09	7.87	2.68E-01
TSPAN31	tetraspanin 31	-0.10	4.22	2.70E-01
ZNF10	zinc finger pro	-0.07	4.06	2.71E-01
TGFBI	transforming g	-0.33	1.53	2.73E-01
RPS6KA3	ribosomal prot	0.06	7.43	2.83E-01
MFSD14A	major facilitato	0.05	6.70	2.84E-01
SLC16A10	solute carrier f	0.16	4.08	2.86E-01
NCEH1	neutral cholest	-0.14	2.41	2.91E-01
CHD9	chromodomain	0.08	4.59	2.92E-01
ZNF354C	zinc finger pro	0.06	4.99	2.95E-01
ROCK2	Rho associated	-0.05	4.86	2.95E-01
NRIP1	nuclear recept	0.08	5.14	2.97E-01
BRMS1L	breast cancer r	-0.07	3.53	2.98E-01
AFDN	afadin, adhere	0.24	3.44	2.99E-01
PLAG1	PLAG1 zinc fing	0.14	4.53	2.99E-01
LSM3	LSM3 homolog	0.07	5.10	3.00E-01
PELI1	pellino E3 ubic	0.11	7.00	3.02E-01
MIB1	mindbomb E3	0.07	5.54	3.04E-01
ZYG11B	zyg-11 family m	0.05	5.21	3.05E-01
CRKL	CRK like proto-	-0.07	6.49	3.07E-01
KLHL42	kelch like fami	-0.08	5.27	3.10E-01
MSI2	musashi RNA b	0.05	5.89	3.17E-01
EHD1	EH domain con	-0.07	6.61	3.19E-01
BMPR2	bone morphog	0.06	4.33	3.20E-01
TBCEL	tubulin folding	0.07	4.51	3.23E-01
IPO11	importin 11 [So	0.05	3.32	3.26E-01
DPP8	dipeptidyl pep	0.03	5.74	3.29E-01
GLCCI1	glucocorticoid	0.08	5.73	3.32E-01
PKNOX1	PBX/knotted 1	-0.05	3.79	3.37E-01
SMC1A	structural main	-0.10	6.25	3.37E-01
CCAR1	cell division cy	0.04	7.30	3.45E-01
APPL1	adaptor protei	-0.04	5.21	3.54E-01
CLCN5	chloride voltag	-0.10	1.88	3.60E-01
HAX1	HCLS1 associat	-0.06	6.87	3.63E-01

RRAGC	Ras related GT	-0.07	4.65	3.65E-01
AP3M1	adaptor relate	-0.04	5.67	3.68E-01
RAB27B	RAB27B, mem	0.17	2.88	3.69E-01
CPEB3	cytoplasmic pc	0.07	2.84	3.74E-01
ACAT1	acetyl-CoA ace	-0.08	3.93	3.75E-01
MEF2A	myocyte enhar	0.06	5.71	3.79E-01
KPNA4	karyopherin su	-0.04	5.45	3.82E-01
SGCB	sarcoglycan be	-0.08	3.39	3.83E-01
MIA3	MIA family me	-0.04	5.87	3.85E-01
DNM1L	dynamin 1 like	0.03	5.96	3.90E-01
PDCD4	programmed c	0.05	8.46	3.90E-01
GPD1L	glycerol-3-pho	-0.07	5.84	3.95E-01
LONRF2	LON peptidase	-0.28	-0.67	3.97E-01
CLTC	clathrin heavy	-0.03	5.84	3.98E-01
MED21	mediator comp	0.06	5.65	3.99E-01
SAMD4A	sterile alpha m	-0.20	-0.19	4.00E-01
SPPL2A	signal peptide	0.06	5.57	4.02E-01
SATB1	SATB homeobo	0.09	7.64	4.06E-01
TXNL4A	thioredoxin lik	0.05	5.67	4.08E-01
ATP11B	ATPase phosph	-0.03	7.06	4.10E-01
RNF6	ring finger pro	0.04	5.79	4.12E-01
FANCI	Fanconi anemi	-0.07	3.36	4.16E-01
SUZ12	SUZ12 polycon	-0.04	6.13	4.19E-01
PAFAH1B1	platelet activat	0.03	7.22	4.20E-01
PDZD8	PDZ domain cc	-0.08	5.11	4.24E-01
VPS13A	vacuolar prote	-0.05	6.20	4.26E-01
RERE	arginine-glutar	0.05	6.56	4.32E-01
PM20D2	peptidase M20	-0.04	5.20	4.33E-01
USP13	ubiquitin speci	-0.06	3.82	4.35E-01
TGFBR2	transforming g	0.06	8.68	4.35E-01
GRSF1	G-rich RNA sec	0.04	5.80	4.36E-01
CCNI	cyclin I [Source	0.04	9.14	4.37E-01
TMED4	transmembrar	0.03	7.80	4.37E-01
ZADH2	zinc binding al	0.06	5.30	4.37E-01
BCL11A	B-cell CLL/lymp	-0.35	-0.92	4.47E-01
ARHGEF12	Rho guanine n	0.17	2.66	4.49E-01
SNX30	sorting nexin f	-0.06	4.81	4.50E-01
QSER1	glutamine and	0.05	4.39	4.53E-01
PPP1R3B	protein phospl	0.09	3.82	4.58E-01
FAM208B	family with sec	-0.03	6.22	4.69E-01
AP3B1	adaptor relate	-0.04	4.91	4.71E-01
STAT3	signal transduc	-0.03	6.67	4.79E-01
RASEF	RAS and EF-ha	-0.21	0.50	4.80E-01
FASLG	Fas ligand [Sou	-0.26	1.02	4.81E-01

RTN4	reticulon 4 [So	0.04	6.20	4.90E-01
UBA6	ubiquitin like r	-0.03	5.57	4.93E-01
CCNG1	cyclin G1 [Sour	-0.03	7.42	4.98E-01
JAG1	jagged 1 [Sour	-0.33	-0.72	4.99E-01
CYBRD1	cytochrome b	-0.25	-0.14	5.01E-01
KAT6A	lysine acetyltra	-0.02	7.15	5.07E-01
GLG1	golgi glycoprot	0.02	7.47	5.11E-01
CDK2AP1	cyclin depende	0.15	1.66	5.14E-01
SOWAHC	sosondowah a	0.18	1.61	5.16E-01
TRIM2	tripartite moti	0.11	2.37	5.19E-01
E2F3	E2F transcripti	0.05	5.22	5.21E-01
BTG2	BTG anti-prolif	-0.07	10.18	5.21E-01
ABI2	abl interactor	-0.04	5.52	5.24E-01
TOR1AIP2	torsin 1A inter	0.03	3.96	5.28E-01
ZNF217	zinc finger pro	0.03	6.68	5.29E-01
SNAP29	synaptosome	-0.04	5.41	5.35E-01
TSNAX	translin associ	0.02	5.44	5.36E-01
PJA2	praja ring finge	0.03	6.98	5.41E-01
SKI	SKI proto-onco	0.05	7.14	5.44E-01
PPP1R37	protein phospl	-0.04	3.62	5.53E-01
JADE1	jade family PH	-0.03	5.90	5.60E-01
RHOB	ras homolog fa	-0.19	5.49	5.62E-01
DUSP16	dual specificity	0.06	6.63	5.64E-01
LTV1	LTV1 ribosome	0.03	6.53	5.65E-01
ATL3	atlastin GTPas	0.03	5.11	5.65E-01
PBRM1	polybromo 1 [	-0.02	5.89	5.65E-01
NUBPL	nucleotide bin	0.04	2.87	5.70E-01
RPRD2	regulation of n	-0.02	6.12	5.70E-01
NCOA2	nuclear recept	0.03	5.86	5.75E-01
KBTBD6	kelch repeat ar	-0.05	2.93	5.77E-01
PTP4A2	protein tyrosir	0.03	8.12	5.77E-01
MALT1	MALT1 paraca	-0.02	7.30	5.77E-01
GPD2	glycerol-3-pho	0.04	4.12	5.83E-01
TMEM30A	transmembrar	0.02	7.15	5.85E-01
TNPO1	transportin 1 [	-0.02	6.04	5.86E-01
WEE1	WEE1 G2 chec	-0.09	2.26	5.90E-01
TESK2	testis-specific	0.05	3.95	5.91E-01
SREK1	splicing regula	0.02	6.57	5.92E-01
PANK3	pantothenate	0.02	6.15	5.95E-01
ARMCX3	armadillo repe	-0.03	5.47	5.96E-01
EIF1AX	eukaryotic trar	-0.08	6.96	5.99E-01
CUX1	cut like homec	0.03	4.27	5.99E-01
FAM126B	family with sec	0.03	4.63	6.01E-01
PFKFB2	6-phosphofruc	-0.07	1.95	6.02E-01

PAPD7	poly(A) RNA p	0.03	6.88	6.06E-01
UGCG	UDP-glucose c	0.05	6.21	6.09E-01
AGPAT5	1-acylglycerol-	0.03	4.39	6.14E-01
DDX3X	DEAD-box heli	-0.07	9.08	6.16E-01
FAM3C	family with se	0.04	4.85	6.18E-01
CAPN2	calpain 2 [Sou	-0.04	7.66	6.19E-01
TMED10	transmembran	-0.03	7.44	6.22E-01
ZBTB38	zinc finger and	-0.05	5.16	6.25E-01
ZFYVE16	zinc finger FYV	-0.02	4.16	6.28E-01
DCUN1D3	defective in cu	-0.04	3.16	6.29E-01
GOLGA4	golgin A4 [Sou	0.03	5.91	6.32E-01
FBXO46	F-box protein	-0.05	5.26	6.35E-01
HBP1	HMG-box tran	0.03	6.72	6.41E-01
ESYT2	extended syna	0.03	8.09	6.42E-01
KLHL8	kelch like fami	-0.03	4.04	6.50E-01
CCSER2	coiled-coil seri	0.04	6.74	6.53E-01
EPM2A	epilepsy, prog	0.05	3.67	6.56E-01
ARL1	ADP ribosylati	0.02	5.09	6.59E-01
SNN	stannin [Sourc	0.06	6.03	6.63E-01
ZSWIM6	zinc finger SW	0.03	5.09	6.64E-01
RAB6A	RAB6A, memb	-0.02	6.18	6.65E-01
MCAM	melanoma cell	-0.13	0.02	6.66E-01
MED28	mediator com	-0.02	6.64	6.66E-01
RBM27	RNA binding m	-0.02	5.91	6.67E-01
RMND5A	required for m	0.02	5.69	6.75E-01
AZIN1	antizyme inhib	0.02	6.37	6.76E-01
TNFRSF10B	TNF receptor s	-0.03	6.27	6.77E-01
STAG2	stromal antige	0.01	6.93	6.78E-01
SOS2	SOS Ras/Rho g	0.02	5.66	6.79E-01
USP15	ubiquitin speci	0.02	7.12	6.87E-01
PURA	purine rich ele	-0.03	5.03	6.99E-01
ZNF462	zinc finger pro	0.16	-0.06	7.08E-01
TBK1	TANK binding	-0.05	4.73	7.11E-01
RECK	reversion indu	-0.02	4.99	7.16E-01
HNRNPA2B1	heterogeneou	0.01	9.69	7.17E-01
LMNB1	lamin B1 [Sou	0.03	5.03	7.17E-01
RAB11FIP2	RAB11 family i	0.02	5.72	7.17E-01
ATXN10	ataxin 10 [Sou	0.02	5.80	7.22E-01
MAP3K1	mitogen-activ	0.03	8.20	7.24E-01
SOCS5	suppressor of	-0.02	4.54	7.31E-01
CCDC93	coiled-coil do	0.01	6.25	7.34E-01
HMGB3	high mobility	0.11	0.70	7.37E-01
STRN	striatin [Sourc	0.01	5.74	7.54E-01
MRPL49	mitochondrial	0.02	5.86	7.57E-01

CSTB	cystatin B [Sou	0.03	5.96	7.57E-01
YY1	YY1 transcripti	0.01	7.09	7.59E-01
MYH9	myosin heavy	-0.02	9.63	7.59E-01
SCD	stearoyl-CoA d	0.11	1.11	7.69E-01
PGK1	phosphoglycer	0.01	7.52	7.74E-01
RYBP	RING1 and YY1	-0.02	5.95	7.81E-01
CNOT6	CCR4-NOT trar	0.02	5.64	7.85E-01
DOCK8	dedicator of cy	-0.03	7.03	7.87E-01
VPS36	vacuolar prote	0.01	6.53	7.87E-01
CD44	CD44 molecule	0.01	8.30	7.91E-01
SOCS6	suppressor of	0.07	1.04	7.91E-01
FAM53C	family with sec	-0.02	4.73	7.97E-01
COPS4	COP9 signalos	-0.01	4.95	7.98E-01
CSNK2A1	casein kinase 2	-0.01	6.15	7.99E-01
MARCH6	membrane ass	0.01	7.97	8.01E-01
NPTN	neuroplastin [S	0.02	5.93	8.03E-01
KLHL9	kelch like fami	0.02	5.32	8.03E-01
IGF1R	insulin like gro	0.04	5.68	8.13E-01
FNDC3B	fibronectin typ	0.02	3.71	8.15E-01
CBFB	core-binding fa	-0.01	6.92	8.16E-01
SLC31A1	solute carrier f	0.03	2.77	8.16E-01
ZNF493	zinc finger pro	0.02	4.63	8.19E-01
DDI2	DNA damage i	0.01	5.28	8.21E-01
KRIT1	KRIT1, ankyrin	-0.01	5.68	8.22E-01
FOXN2	forkhead box N	0.02	6.48	8.26E-01
FAM20B	family with sec	0.01	5.32	8.27E-01
MED13	mediator comp	0.01	6.02	8.31E-01
ZNF148	zinc finger pro	0.01	5.56	8.32E-01
SPIN1	spindlin 1 [Sou	-0.01	5.84	8.34E-01
KANSL1L	KAT8 regulator	-0.03	3.22	8.38E-01
FAM63B	family with sec	0.02	4.99	8.39E-01
MARCKSL1	MARCKS like 1	-0.02	6.60	8.45E-01
CBX5	chromobox 5 [	0.01	6.29	8.47E-01
ABAT	4-aminobutyra	0.01	3.40	8.48E-01
PGM3	phosphogluco	0.01	4.44	8.49E-01
CLNS1A	chloride nucle	0.01	6.16	8.49E-01
PTK2	protein tyrosir	0.03	2.26	8.49E-01
NUFIP2	NUFIP2, FMR1	-0.01	7.11	8.64E-01
ALPP	alkaline phosp	-0.05	0.81	8.68E-01
EFR3A	EFR3 homolog	0.01	6.14	8.70E-01
RAB1A	RAB1A, memb	-0.01	6.55	8.73E-01
WDR3	WD repeat dor	-0.01	5.29	8.73E-01
TAF5	TATA-box bind	-0.02	4.19	8.75E-01
IRF2BPL	interferon regu	-0.02	5.08	8.79E-01

CD164	CD164 molecu	-0.01	7.54	8.80E-01
MTPN	myotrophin [S	-0.01	7.32	8.82E-01
PRKAB2	protein kinase	0.01	5.80	8.84E-01
RC3H2	ring finger and	0.01	6.01	8.86E-01
PITHD1	PITH domain c	-0.01	6.57	8.87E-01
SUB1	SUB1 homolog	-0.01	6.56	8.89E-01
MRPS10	mitochondrial	-0.01	5.78	8.91E-01
FBXO11	F-box protein	0.00	6.64	8.93E-01
SEMA5A	semaphorin 5	-0.04	1.13	8.98E-01
LYRM2	LYR motif cont	-0.01	3.78	9.01E-01
SERAC1	serine active si	-0.01	2.92	9.08E-01
CLIC2	chloride intrac	-0.03	0.90	9.22E-01
USP1	ubiquitin speci	0.01	6.53	9.27E-01
USP47	ubiquitin speci	0.00	6.01	9.27E-01
KLF5	Kruppel like fa	-0.02	2.89	9.34E-01
EFHD2	EF-hand doma	-0.02	6.91	9.37E-01
EIF4EBP2	eukaryotic tra	0.00	7.12	9.40E-01
BEX3	brain expresse	0.01	5.63	9.49E-01
UHRF1BP1L	UHRF1 binding	0.00	4.33	9.52E-01
DDHD2	DDHD domain	0.00	5.68	9.52E-01
WHSC1L1	Wolf-Hirschho	0.00	6.89	9.57E-01
OSBPL3	oxysterol bindi	0.00	5.73	9.61E-01
MXD1	MAX dimeriza	0.00	4.36	9.68E-01
SUSD6	sushi domain	0.00	6.55	9.70E-01
LPGAT1	lysophosphati	0.00	5.45	9.76E-01
LARP4	La ribonucleo	0.00	4.77	9.79E-01
ARMC8	armadillo repe	0.00	5.17	9.83E-01
ZBTB34	zinc finger and	0.00	3.83	9.84E-01
PIK3C2A	phosphatidyli	0.00	5.43	9.95E-01
RNF11	ring finger pro	0.00	6.45	9.96E-01
RUFY3	RUN and FYVE	0.00	4.73	9.96E-01
TSPAN2	tetraspanin 2 [	0.00	4.10	9.99E-01
RASGRP1	RAS guanyl rel	0.00	8.41	9.99E-01
HK2	hexokinase 2 [	0.00	3.94	1.00E+00
GPRC5A	G protein-cou	-		
LIMCH1	LIM and calpo	-		
HOXA9	homeobox A9	-		
TNS1	tensin 1 [Sour	-		
TGFB2	transforming g	-		
JADE3	jade family PH	-		
JPH1	junctophilin 1	-		
COL12A1	collagen type	-		
LIFR	leukemia inhib	-		
PEX5L	peroxisomal bi	-		

DLX2	distal-less hom	-
PRRX1	paired related	-
PCDH17	protocadherin	-
PTGFR	prostaglandin	-
KIAA1549	KIAA1549 [Sou	-
CALD1	caldesmon 1 [	-
SOX9	SRY-box 9 [Sou	-
HRK	harakiri, BCL2	-
PRRG4	proline rich an	-
LAMC1	laminin subuni	-
IL10	interleukin 10	-
ARHGAP24	Rho GTPase ac	-
OSR1	odd-skipped re	-
THRB	thyroid hormo	-
TMEM56	transmembrar	-
DDAH1	dimethylargini	-
ENAH	enabled homo	-
IGF2BP1	insulin like gro	-
PLPP3	phospholipid p	-
PRKAA2	protein kinase	-
NIPAL1	NIPA like doma	-
PRICKLE2	prickle planar	-
EDIL3	EGF like repea	-
TNFRSF11B	TNF receptor s	-
ALDH1A1	aldehyde dehy	-
ST5	suppression of	-
CXCL10	C-X-C motif ch	-
ANO5	anoctamin 5 [	-
GNG12	G protein subu	-
OLR1	oxidized low d	-
B3GNT5	UDP-GlcNAc:b	-
SKIDA1	SKI/DACH dom	-
SOX2	SRY-box 2 [Sou	-
PAPPA	pappalysin 1 [	-
MARC1	mitochondrial	-
SAMD5	sterile alpha m	-
SERPINB5	serpin family B	-
TOMM6	translocase of	-
RAB6C	RAB6C, memb	-
GTF2I	general transc	-
ZNF595	zinc finger pro	-