Prenatal stress-induced programming of genome-wide promoter DNA methylation in 5-HTT deficient mice

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Supplementary methods and material

Methylated DNA immunoprecipitation followed by tiling array

Genomic DNA was extracted from the tissue using phenol/chloroform/isoamyl alcohol extraction. 300 µl 0.5%-SDS extraction buffer were added to the frozen tissue. The tissue was subsequently homogenized for 30 to 60 sec at 25 Hz at 4°C in the Tissue Lyser (Qiagen, Hilden, Germany) using a metallic bead. After adding 200 µl 0.5%-SDS extraction buffer and 50 µl 10- or 20mg/µl-proteinase K, samples were incubated at 55°C overnight. Following this, samples were incubated with 50 µl 10mg/µl-RNAse A with for 1 h at 37°C and then mixed with 700 µl of phenol/chloroform/isoamyl alcohol mixture (25:24:1). Phases were separated using MaXtract high density tubes (Qiagen) by centrifuging the samples at 14 000 rpm for 5 min at RT. The aqueous phase was then mixed with 700 µl phenol isoamyl alcohol (24:1) and phases were again separated by centrifuging the samples in MaXtract high density tubes as described above. DNA was precipitated with 50 µl sodium acetate and 1000 µl cold absolute ethanol (incubation 10 min at -20°C, centrifugation 20 min at 4°C, 14 000 rpm). The resulting pellet was washed with 500 µl cold 80%-ethanol using the same conditions as for the precipitation, dried at RT for 5 to 30 min and resuspended in 50 µl 1xTE. DNAs of 2-4 single animals were then pooled, creating 2-3 pools per group.

To gain fragments of 300 +/- 200 bp size, DNA was sheared using the BiorupterTM UCD-200 (Diagenode, Liège, Belgium). Conditions were 20 KHz, 30 sec ON alternated by 30 sec OFF, for 3 x 5 min at low power. Efficiency of the shearing was checked with the Bioanalyzer 2100 (Agilent, Santa Clara, California, USA).

Methyl DNA immunoprecipitation (MeDIP, Diagenode) using an antibody against 5-methylcytosine was performed as described in the Diagenode manual. IP samples were performed in duplicate, input sample once. 1000 ng of DNA were used for each IP and 100 ng for the input. DNA was then purified using IPure (Diagenode) according to the manufacturer's manual and the resulting IP DNA samples belonging together were pooled. Pooled IP DNA and input DNA was then amplified using two-step Whole Genome Amplification (GenomePlex Kit, Sigma, St. Louis, USA). Amplification, labeling, hybridization, and the actual tiling analysis were performed by the Interdisciplinary Centre for Clinical Research (IZKF) at the University of Wuerzburg. 7.5 µg DNA from the second amplification round were fragmented and labeled using the GeneChip 10K Xba Assay Kit (Affymetrix, Santa Clara, California, USA). The size of the obtained biotinylated cDNA fragments was checked with the Bioanalyzer (Agilent) and ranged between 25 and 250 bp (peak at 100 bp). Hybridization to GeneChip ® Mouse Promoter 1.0R Arrays and washing using the GeneChip® Expression Wash, Stain and Scan Kit (Affymetrix) was performed as described in the Affymetrix manuals. Arrays were scanned with the GeneChip® Scanner 3000 (Affymetrix). The promoter tiling array used in this study is comprised of over 4.6 million probes tiled to interrogate over 28,000 mouse promoter regions. Each promoter region covers approximately 6 kb upstream through 2.5 kb downstream of 5' transcription start sites. The probes are tiled at an average resolution of 35 bp, leaving a gap of approximately 10 bp between probes.

Evaluation of MeDIP-chip data

Affymetrix quality metrics and visual inspection of overall microarray signals confirmed high-quality readout from the hybridized samples. Genomic locations of microarray probes were adjusted to the *Mus musculus* NCBI assembly version 37.1 (MMv37 thereafter). Probe signals from corresponding MeDIP and input samples were subjected to within-sample pairwise loess normalization and calculation of MeDIP-input signal $\log_2$ ratios (SLRs). Quantile normalization was employed to ensure a common signal distribution between samples. To decrease the noise in the experiment readout, a sliding-window approach was applied to determine SLR medians in successive genomic regions of 300 bp width. The SLRs were then found to be free from biases introduced by varying probe GC content and particular probe sequence compositions (data not shown), thus confirming successful data normalization. A correspondence analysis further confirmed the absence of extreme outliers in samples and/or SLRs.

In each sample, genomic regions enriched by the MeDIP procedure were detected by the CMARRT algorithm.[1] Briefly, this does not apply a fixed threshold to all SLRs, but rather tests for increased signal content correcting for the signal autocorrelation in considered genomic regions, resulting in higher sensitivity and specificity of the detected enriched regions. For CMARRT modeling, the typical fragment length after DNA sonication was assumed to be 300 bp; enriched regions were required to cover at least five consecutive array probes and to display an enrichment statistic with a false discovery rate (FDR) less than 0.05. Of all detected regions, only those were retained in the analysis that were consistently found within each analysis group. With the present (=1) and absent (=0) calls for MeDIP enrichment, effect directions were determined as previously described.[2] Briefly, genotype (G) effect directions (d) were calculated by

$$G_d = \left(\left(\mathit{5\text{-}Htt+/\text{-}}\ \mathrm{C} + \mathit{5\text{-}Htt+/\text{-}}\ \mathrm{PS} \right) - \left(\mathit{5\text{-}Htt+/+}\ \mathrm{C} + \mathit{5\text{-}Htt+/+}\ \mathrm{PS} \right) \right) * 0.5,$$

environment (E) effect directions by

$$E_d = \left(\left(\mathit{5\text{-}Htt+/+}\ \mathrm{PS} + \mathit{5\text{-}Htt+/\text{-}}\ \mathrm{PS} \right) - \left(\mathit{5\text{-}Htt+/+}\ \mathrm{C} + \mathit{5\text{-}Htt+/\text{-}}\ \mathrm{C} \right) \right) * 0.5$$

and interaction (GxE) effect directions by

$$GxE_d = \left(\left(\mathit{5\text{-}Htt+/\text{-}}\ \mathrm{PS} - \mathit{5\text{-}Htt+/\text{-}}\ \mathrm{C} \right) - \left(\mathit{5\text{-}Htt+/+}\ \mathrm{PS} - \mathit{5\text{-}Htt+/+}\ \mathrm{C} \right) \right) * 0.5.$$

Effect directions for regions with inconclusive effect size (i.e. with absolute values less than 1) were set to zero. To obtain $\log_2$ fold changes (logFCs) quantifying the change of microarray signal for each effect described above, we first summarized data from probes localized inside the regions defined by CMARRT and of all samples of the same group to determine the median SLR per region and group. With these, we calculated “raw” logFCs (RlogFC) according to the aforementioned formulas. We observed that for a few regions, RlogFCs and effect (Eff) directions were not consistent (i.e. positive d_{Eff} and negative RlogFC or *vice versa*); therefore, RlogFCs were corrected according to the formula

$$logFC_{Eff} = RlogFC_{Eff} * \begin{cases} 1, if\ d_{Eff} * RlogFC_{Eff} > 0 \\ 0, if\ d_{Eff} * RlogFC_{Eff} < 0 \end{cases}$$

to obtain the logFC for each region and effect. Thus, whenever the RlogFC is not consistent with the effect direction, the logFC is set to zero; in turn, regions with non-zero logFC for the G, E or GxE effect display a conclusive effect direction which is concordant with the observed median signal change.

Preprocessing and analysis of Affymetrix tiling arrays was performed with R v2.15 along with the Bioconductor package Starr.[3] The package ChIPpeakAnno[4] was used for annotation of enriched regions.

Differentially methylated regions (DMRs)

No “cut off” value for the fold change (FC) was applied. A FC of 1 indicates no change whereas a FC of 2 indicates a double amount of methylation. For optimizing discrimination of DMRs associated with the same gene, a unique DMR identification number (ID) was assigned to each DMR. Sometimes, more than one gene was annotated to one DMR.

Functional Annotation Clustering

Functional Annotation Clustering is an enrichment analysis that clusters functionally similar annotations (terms) associated with user’s gene list into groups provided by DAVID[5, 6]. We performed Functional Annotation Clustering on our DMRs in order to gain insight into which annotation groups are enriched in our DMRs lists.

Validation of methylation data using Pyrosequencing and MeDIP-qPCR

The validity of the methylation data obtained from the promoter microarray was tested using Pyrosequencing® and MeDIP quantitative real-time PCR (MeDIP-qPCR). For Pyrosequencing, 400 ng of genomic DNA were treated with sodium bisulfite as described in the manufacturer's instruction using a standard PCR cycler (EZ DNA Methylation-Gold™ Kit by Zymo, Irvine, California, USA). The product was purified using Zymo-Spin™ IC Columns (Zymo Research). The desired PCR products were amplified using the HotStar Taq Plus DNA polymerase (Qiagen) and subsequently sequenced using the PyroMark Q96 MD™ Pyrosequencer (Biotage, Uppsala, Sweden) and PyroMark Gold Q96 CDT reagents (Qiagen). The PCR and the sequencing primers were designed with the PyroMark Assay Design 2.0 Software (Qiagen). The percentage of unconverted cytosines of single CpG sites was assessed using the Pyro Q-CpG™ Software (Qiagen).

For MeDIP-qPCR, the same MeDIP DNA as applied to the array was used for qPCR. qPCR was performed as described in the Diagenode MeDIP manual. qPCR was performed on the Bio-Rad CFX384 Real-Time PCR Detection System (in technical triplicates).

Statistics on pyrosequencing and MeDIP data were performed using IBM SPSS Statistics. Differences were considered significant when $p<0.05$.

Gene expression data and overlap with methylation data

In addition to focusing solely on differential DNA methylation, DMRs were also assessed in view of gene expression changes, the latter of which were previously examined in the same animals.[2] For this purpose, we identified genes that were both differentially methylated and differentially expressed in our *5-Htt* x PS paradigm. The expression array did not cover miRNAs, hence, no gene expression data from the expression array are available for miRNAs. Gene expression microarray results were validated using reverse transcription quantitative real-time PCR (RT-qPCR) as described in detail previously.[2] In brief, cDNA synthesis was performed using the iScript™ kit (Bio-Rad, Munich, Germany) according to the manufacturer's instructions. qPCR was performed on the Bio-Rad CFX384 Real-Time PCR Detection System (in technical triplicates). Mean efficiencies were calculated by LinReg.[7] Normalization and calculation of the relative expression was performed using qBase (Biogazelle, Zwijnaarde, Belgium).[8] *CCCTC-binding factor* (*Ctcf*), *guanosine diphosphate (GDP) dissociation inhibitor 2* (*Gdi2*) and *Smad nuclear interacting protein 1* (*Snip1*) were used for normalization. M-values were M<0.103.

Modulated Modularity Clustering (MMC)

We performed a Modulated Modularity Clustering (MMC)[9] with a subset of myelin-associated genes from the previously published gene expression array data[2] in order to identify clusters of myelin-associated genes that correlated in expression. The myelin-associated genes set was a compound category consisting of the gene ontologies GO:0004767, GO:0006684, GO:0006686, GO:0016230, GO:0016277, GO:0019911, GO:0022010, GO:0031641, GO:0031642, GO:0031643, GO:0032286, GO:0032288, GO:0032289, GO:0042552, GO:0043209, GO:0043217, GO:0043218, GO:0047157, GO:2000754 and GO:2000755.

Primer sequences:

RT-qPCR Primer	Mod.	Sequence	Product size (bp)	Genomic location in NCBIM37/mm9
<u>Gene expression</u>				
RT_Mbp_F		CTCCCTGCCCCAGAAGTC	95	
RT_Mbp_R		GAGGTGGTGTTCGAGGTGTC		
RT_Mbp_ex1/3_F		ACAGAGACACGGGCATCCT	90	
RT_Mbp_ex1/3_R		TGTGTGAGTCCTTGCCAGAG		
RT_Mbp_ex1/2_F		ACAGAGACACGGGCATCCT	89	
RT_Mbp_ex1/2_R		CCAGGGTACCTTGCCAGAG		
RT_Plp1_F		AGGCCAACATCAAGCTCATT	82	
RT_Plp1_R		CAAACACCAGGAGCCATACA		
RT_Mag_F		TTCTCAGGGGGAGACAACC	123	
RT_Mag_R		ACTCTCCTGGGGCTCTCAGT		
RT_Mog_F		CTGGCAGGACAGTTTCTTGA	113	
RT_Mog_R		AAAGAGGCCAATGGGAAATC		
RT_Sox10_F		ATGTCAGATGGGAACCCAGA	88	

RT_Sox10_R		CGGACTGCAGCTCTGTCTTT		
RT_Ctcf_F		ACACCCATGTGAAAAATCCTG	105	
RT_Ctcf_R		CAGAGCAAAGAAAATGTTGATGAG		
RT_Gdi2_F		GTCAGAATTGGTTGGTTCTGTTC	126	
RT_Gdi2_R		AGCTCTTGGATCACACAATCG		
RT_Snip1_F		CGTGGCTTCTACCAACAGG	129	
RT_Snip1_R		CAAAGCTAAAGAAAAAGACCAGATG		
Mbp MeDIP				
MeDIP Mbp forward		TGGCTAGTGCTTGTTCCTGA	119	chr18: 82694078-82694196
MeDIP Mbp reverse		GTGCATGTGTGAGGGTGACT		
Pyroseqencing Bisulfite-PCR Primer				
PP-Mbp-A-F		AGTATTTAGGGTAAGGTATGGTATAGA	250	chr18: 82693519-82693769
PP-Mbp-A-Rb	Biotin	ATTCAACCTCTAACATAACAAAATATCA		
PP-Mbp-B-F		GAGGTTGAATTTAGGAGTTGAATATATG	214	chr18: 82693760-82693972
PP-Mbp-B-Rb	Biotin	AAAAAAAATACTCACAAAAACCTCTTATA		
PP-Mbp-C-F		TTTGATTGAAGGTAGAATAATGTAGAAG	193	chr18: 82694026-82694219
PP-Mbp-C-Rb	Biotin	ACTCACCAACACCAATATAAATTATACA		
Pyrosequencing Sequencing Primer				
Seq-Mbp-A-CG3		GTATTGTGTTTAGGATGG		
Seq-Mbp-A-CG4		ATATTTATATATATAGAGGAGTAT		
Seq-Mbp-A-CG5-6		GGTATTAAAGGGAAGGTATAA		
Seq-Mbp-B-CG7		ATGTTTAAGTGATTGTTTTATTAT		
Seq-Mbp-B-CG8		GAGTTGTGGTATTAGTTTTAA		
Seq-Mbp-B-CG9		GATAGTAGTTTTTGTGTAATATTG		
Seq-Mbp-C-CG10		AGGTAGAATAATGTAGAAGTT		
Seq-Mbp-C-CG11-13		TTTTTGAGGTTTGGGAT		
Seq-Mbp-C-CG14-15		GTGGTATGAAGGTATTTTAG		

References

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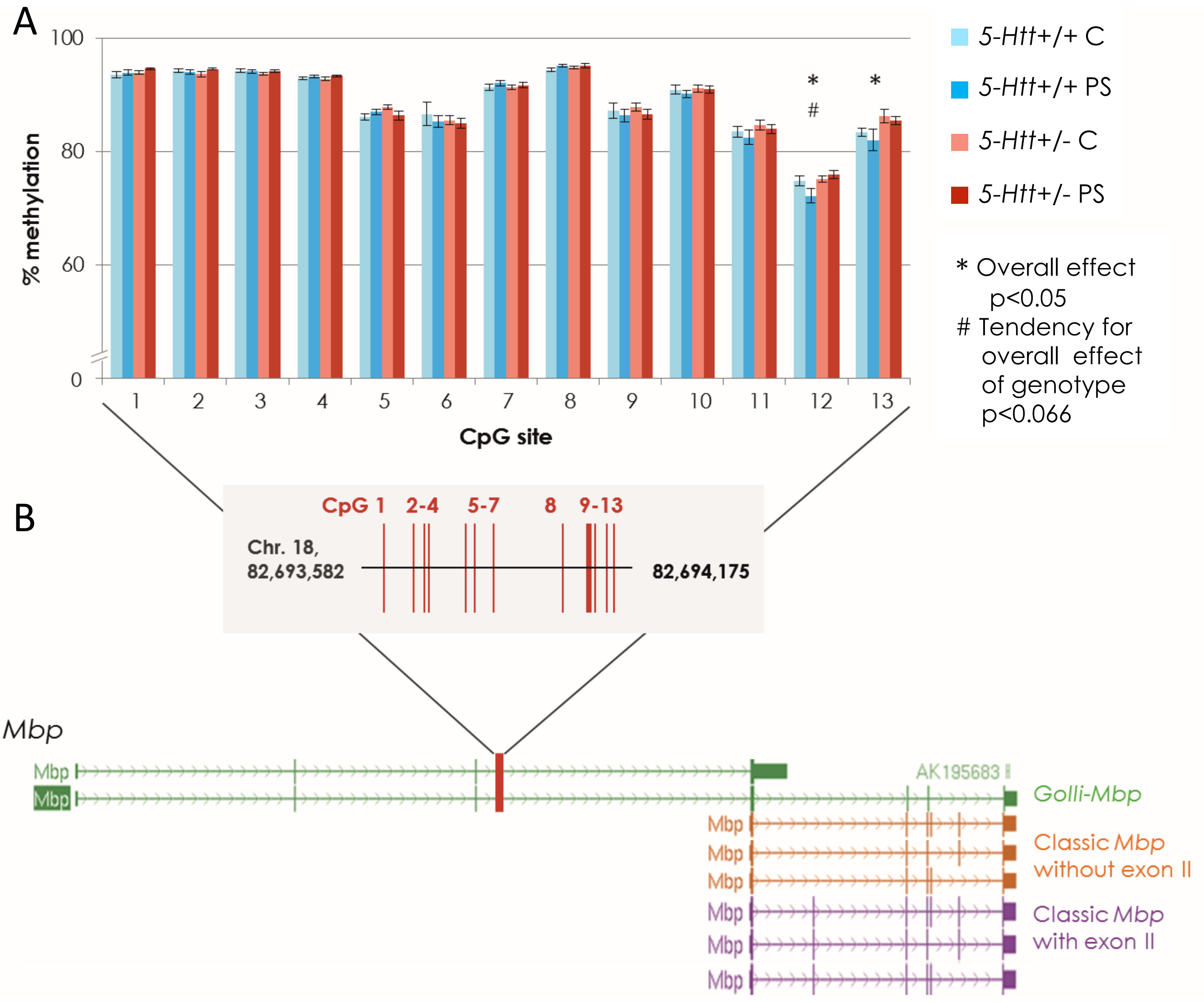
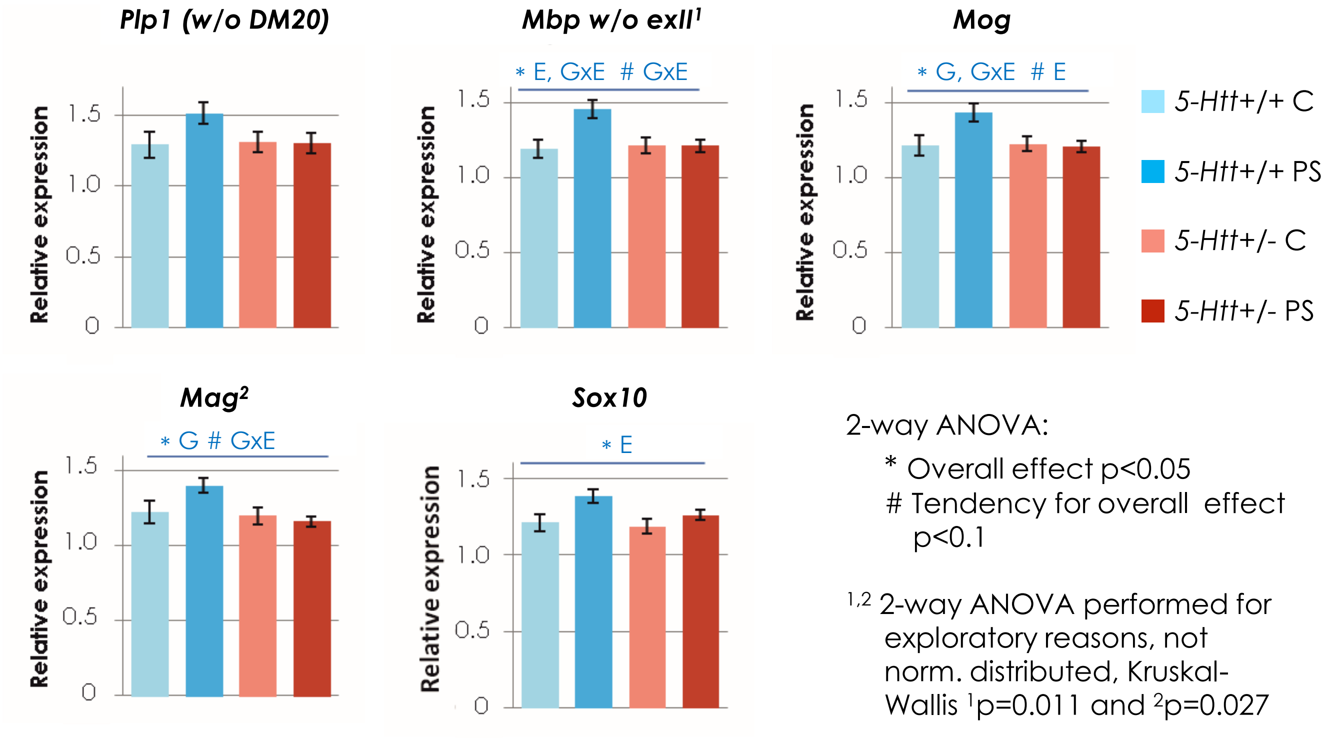
Supplementary Figures



Supplementary Figure 1. A) *Mbp* methylation rate obtained by pyrosequencing of bisulfite-treated DNA at the *Mbp* locus (chr. 18: 82 693 582 – 82 694 175) in the hippocampus of female *5-Htt+/-* or *5-Htt+/+* mice exposed to prenatal stress (PS) or not (control, C). Bars representing means, error bars representing SEM. *p<0.05 G-effect, #p=0.066 GxE-effect, two-way ANOVA. **B)** Scheme of the *Golli-Mbp* locus, modified from the USCS browser, and the location of the analyzed CpG sites 1 through 13.

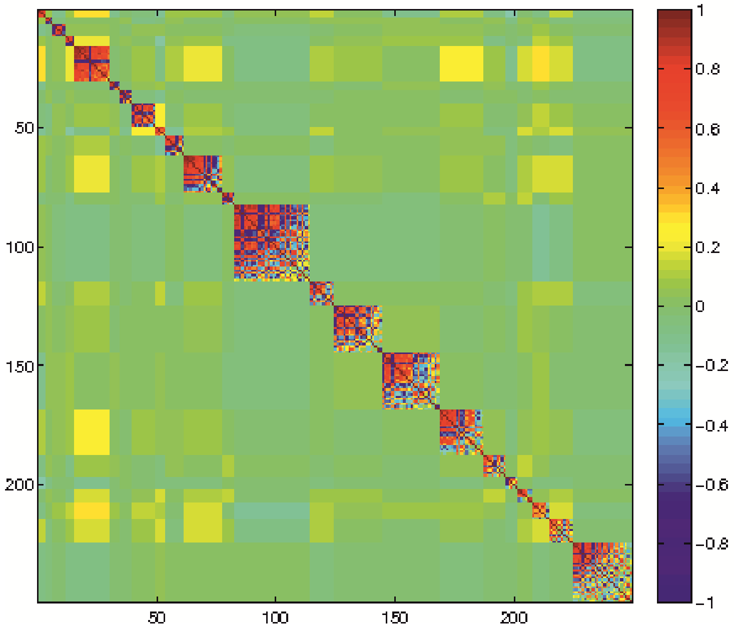


2-way ANOVA:

* Overall effect $p<0.05$
\# Tendency for overall effect $p<0.1$

[1,2] 2-way ANOVA performed for exploratory reasons, not norm. distributed, Kruskal-Wallis [1]p=0.011 and [2]p=0.027

Supplementary Figure 2. Expression of myelin-associated genes in the hippocampus of female *5-Htt+/-* or *5-Htt+/+* mice exposed to prenatal stress (PS) or not (control, C) obtained by RT-qPCR. Bars representing means, error bars representing SEM.



Supplementary Figure 3. Clusters of highly correlating genes identified using Modulatory Modularity Cluster (MMC) analysis on differentially expressed myelin-associated genes in the hippocampus of female *5-Htt+/-* and *5-Htt+/+* mice, exposed to prenatal stress or not (control). Dark red indicates a correlation of 1, violet-blue indicates a correlation of -1. See Supplementary Table 4 for details on the clusters.

Supplementary Tables

Supplementary Table 1

Differentially methylated regions in the hippocampus of female *5-Htt+/-* or *5-Htt+/+* mice exposed to prenatal stress (PS) or not (control, C), identified by applying enriched methylated DNA (MeDIP) to a promoter tiling array. FC = Fold change, Chr. = Chromosome, G = genotype (5-Htt), E = environment (PS), GxE = gene x environment interaction.

A) G-effects

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	**Chr.**	**start**	**end**	**width**	**C**	**PS**	**C**	**PS**	**effect dir.**	**logFC**	**ENSEMBL ID**	**symbol**	**gene name**	**next miRNA**
905	12	111082441	111082607	167	Yes	Yes	No	No	↓	-0.83	ENSMUSG00000065497	Mir410	microRNA 410	downstream mmu-mir-3072
715	11	104048702	104048948	247	Yes	Yes	No	No	↓	-0.42	ENSMUSG00000049506	4933407P14Rik	RIKEN cDNA 4933407P14 gene	downstream mmu-mir-3064
866	12	87088511	87088795	285	Yes	Yes	No	No	↓	-0.42	ENSMUSG00000034258	Mfsd7c	major facilitator superfamily domain containing 7C	downstream mmu-mir-3068
3459	6	145752604	145752976	373	Yes	Yes	No	No	↓	-0.40	ENSMUSG00000045110 // ENSMUSG00000030259	Rassf8 // Rassf8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8 // Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	downstream mmu-mir-680-1
2803	4	97188366	97188799	434	Yes	Yes	No	No	↓	-0.36	ENSMUSG00000084159	Gm12696	predicted gene 12696	downstream mmu-mir-872
2882	4	135054667	135055125	459	Yes	Yes	No	No	↓	-0.35	ENSMUSG00000028801	4930555I21Rik	RIKEN cDNA 4930555I21 gene	upstream mmu-mir-700
2066	19	44595070	44595399	330	Yes	Yes	No	No	↓	-0.35	ENSMUSG00000051984	Sec31b	Sec31 homolog B (S. cerevisiae)	downstream mmu-mir-5114
1830	18	14133191	14133387	197	Yes	Yes	No	No	↓	-0.33	ENSMUSG00000024420	Zfp521	zinc finger protein 521	downstream mmu-mir-1948
3754	8	26825162	26825534	373	Yes	Yes	No	No	↓	-0.33	ENSMUSG00000031570 // ENSMUSG00000054823	Ppapdc1b // Whsc1l1	phosphatidic acid phosphatase type 2 domain containing 1B // Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	upstream mmu-mir-3107
817	12	57474440	57474780	341	Yes	Yes	No	No	↓	-0.32	ENSMUSG00000021028 // ENSMUSG00000066491	Mbip // Gm6265	MAP3K12 binding inhibitory protein 1 // predicted pseudogene 6265	upstream mmu-mir-1892
2658	3	144760299	144760468	170	Yes	Yes	No	No	↓	-0.31	ENSMUSG00000036960	Clca5	chloride channel calcium activated 5	downstream mmu-mir-3963
3694	7	144142703	144143056	354	Yes	Yes	No	No	↓	-0.31	ENSMUSG00000054612	Mgmt	O-6-methylguanine-DNA methyltransferase	downstream mmu-mir-1962
3747	8	24774416	24774684	269	Yes	Yes	No	No	↓	-0.31	ENSMUSG00000037492	Zmat4	zinc finger, matrin type 4	upstream mmu-mir-3107
1832	18	14998503	14998709	207	Yes	Yes	No	No	↓	-0.30	ENSMUSG00000054321	Taf4b	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor	downstream mmu-mir-1948
978	13	47028519	47029667	1149	Yes	Yes	No	No	↓	-0.30	ENSMUSG00000021375	Kif13a	kinesin family member 13A	downstream mmu-let-7d
2743	4	43675169	43675597	429	Yes	Yes	No	No	↓	-0.30	ENSMUSG00000043770 // ENSMUSG00000043633	Gm12481 // 4930412F15Rik	predicted gene 12481 // RIKEN cDNA 4930412F15 gene	downstream mmu-mir-5106
2918	4	141799878	141800129	252	Yes	Yes	No	No	↓	-0.30	ENSMUSG00000040606	Kazn	kazrin, periplakin interacting protein	upstream mmu-mir-2139
3426	6	128393132	128393439	308	Yes	Yes	No	No	↓	-0.29	ENSMUSG00000059659	Gm10069	predicted gene 10069	upstream mmu-mir-680-1
2581	3	101089733	101090209	477	Yes	Yes	No	No	↓	-0.29	ENSMUSG00000027863	Cd2	CD2 antigen	downstream mmu-mir-190b
2994	5	41813062	41813495	434	Yes	Yes	No	No	↓	-0.28	ENSMUSG00000029128	Rab28	RAB28, member RAS oncogene family	downstream mmu-mir-3097
286	10	24285458	24285641	184	Yes	Yes	No	No	↓	-0.27	ENSMUSG00000081259	Gm6893	predicted gene 6893	downstream mmu-mir-5104
885	12	103945451	103945656	206	Yes	Yes	No	No	↓	-0.27	ENSMUSG00000057963	Itpk1	iNositol 1,3,4-triphosphate 5/6 kinase	upstream mmu-mir-1936
3958	9	30231240	30231969	730	Yes	Yes	No	No	↓	-0.26	ENSMUSG00000031993	Snx19	sorting nexin 19	upstream mmu-mir-1946b

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	Chr.	start	end	width	C	PS	C	PS	effect dir.	logFC	ENSEMBL ID	symbol	gene name	next miRNA
3683	7	140975216	140978199	2984	Yes	Yes	No	No	↓	-0.25	ENSMUSG00000030986 // ENSMUSG00000053111	Dhx32 // Fank1	DEAH (Asp-Glu-Ala-His) box polypeptide 32 // fibronectin type 3 and ankyrin repeat domains 1	upstream mmu-mir-1962
781	12	9030965	9031131	167	Yes	Yes	No	No	↓	-0.25	ENSMUSG00000066637 // ENSMUSG00000066643	Ttc32 // Wdr35	tetratricopeptide repeat domain 32 // WD repeat domain 35	upstream mmu-mir-3066
1266	14	77434538	77434857	320	Yes	Yes	No	No	↓	-0.25	ENSMUSG00000044350	9030625A04Rik	RIKEN cDNA 9030625A04 gene	downstream mmu-mir-1971
3938	9	15414614	15414891	278	Yes	Yes	No	No	↓	-0.25	ENSMUSG00000039977	Ccdc67	coiled-coil domain containing 67	downstream mmu-mir-1900
678	11	98046669	98047229	561	Yes	Yes	No	No	↓	-0.25	ENSMUSG00000083408 // ENSMUSG00000059399 // ENSMUSG00000018160	--- // --- // Med1	NA // NA // mediator complex subunit 1	upstream mmu-mir-5119
3110	5	106641725	106641886	162	Yes	Yes	No	No	↓	-0.24	ENSMUSG00000065942	---	NA	downstream mmu-mir-5619
4023	9	63445313	63445733	421	Yes	Yes	No	No	↓	-0.24	ENSMUSG00000037801	Iqch	IQ motif containing H	upstream mmu-mir-5133
3236	5	151251871	151252034	164	Yes	Yes	No	No	↓	-0.23	ENSMUSG00000075527 // ENSMUSG00000056602	--- // Fry	NA // furry homolog (Drosophila)	downstream mmu-mir-5105
953	13	30080878	30081078	201	Yes	Yes	No	No	↓	-0.23	ENSMUSG00000016477	E2f3	E2F transcription factor 3	upstream mmu-mir-1983
1377	15	68711062	68711326	265	Yes	Yes	No	No	↓	-0.23	ENSMUSG00000070713	Gm10282	predicted pseudogene 10282	upstream mmu-mir-30d
2247	2	76823368	76823897	530	Yes	Yes	No	No	↓	-0.22	ENSMUSG00000051747	Ttn	titin	downstream mmu-mir-10b
1663	17	9966375	9966701	327	Yes	Yes	No	No	↓	-0.22	ENSMUSG00000046173	Pabpc6	poly(A) binding protein, cytoplasmic 6	upstream mmu-mir-692-1
2900	4	138745073	138745267	195	Yes	Yes	No	No	↓	-0.22	ENSMUSG00000028745	Capzb	capping protein (actin filament) muscle Z-line, beta	downstream mmu-mir-2139
162	1	161971697	161972159	463	Yes	Yes	No	No	↓	-0.22	ENSMUSG00000050883	4930523C07Rik	RIKEN cDNA 4930523C07 gene	downstream mmu-mir-1927
1813	17	87847957	87848387	431	Yes	Yes	No	No	↓	-0.21	ENSMUSG00000036438	Calm2	calmodulin 2	upstream mmu-mir-1195
3415	6	124859259	124859495	237	Yes	Yes	No	No	↓	-0.21	ENSMUSG00000030124	Lag3	lymphocyte-activation gene 3	upstream mmu-mir-200c
1824	18	7581833	7582518	686	Yes	Yes	No	No	↓	-0.21	ENSMUSG00000062196 // ENSMUSG00000057440	--- // Mpp7	NA // membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	upstream mmu-mir-1893
2319	2	131635333	131635779	447	Yes	Yes	No	No	↓	-0.21	ENSMUSG00000081422	Gm14282	predicted gene 14282	downstream mmu-mir-103-2
706	11	102111877	102112086	210	Yes	Yes	No	No	↓	-0.21	ENSMUSG00000034773	BC030867	cDNA sequence BC030867	downstream mmu-mir-5119
3571	7	78493992	78494308	317	Yes	Yes	No	No	↓	-0.20	ENSMUSG00000070511	Gm10295	predicted gene 10295	downstream mmu-mir-211
3640	7	125885124	125885620	497	Yes	Yes	No	No	↓	-0.20	ENSMUSG00000030982	9030624J02Rik	RIKEN cDNA 9030624J02 gene	upstream mmu-mir-762
22	1	31233325	31233665	341	Yes	Yes	No	No	↓	-0.20	ENSMUSG00000050217	Lgsn	lengsin, lens protein with glutamine synthetase domain	downstream mmu-mir-5103
3537	7	52276223	52276502	280	Yes	Yes	No	No	↓	-0.20	ENSMUSG00000038387	Rras	Harvey rat sarcoma oncogene, subgroup R	upstream mmu-mir-150
2175	2	38568797	38569145	349	Yes	Yes	No	No	↓	-0.20	ENSMUSG00000026751	Nr5a1	nuclear receptor subfamily 5, group A, member 1	upstream mmu-mir-181a-2
550	11	50723606	50723859	254	Yes	Yes	No	No	↓	-0.20	ENSMUSG00000049321	Zfp2	zinc finger protein 2	upstream mmu-mir-804
3850	8	97050935	97051356	422	Yes	Yes	No	No	↓	-0.19	ENSMUSG00000074151	Nlrc5	NLR family, CARD domain containing 5	downstream mmu-mir-138-2
3976	9	37340926	37341162	237	Yes	Yes	No	No	↓	-0.19	ENSMUSG00000001946	Esam	endothelial cell-specific adhesion molecule	upstream mmu-mir-100
2012	19	29654132	29654407	276	Yes	Yes	No	No	↓	-0.19	ENSMUSG00000038658	C030046E11Rik	RIKEN cDNA C030046E11 gene	downstream mmu-mir-101b
3961	9	31082478	31082716	239	Yes	Yes	No	No	↓	-0.19	ENSMUSG00000042496	Prdm10	PR domain containing 10	upstream mmu-mir-1946b
3611	7	110700775	110701123	349	Yes	Yes	No	No	↓	-0.18	ENSMUSG00000078624	Olfr613	olfactory receptor 613	downstream mmu-mir-139
254	10	12809305	12809958	654	Yes	Yes	No	No	↓	-0.18	ENSMUSG00000019817	Plagl1	pleiomorphic adeNoma gene-like 1	downstream mmu-mir-5104

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	**Chr.**	**start**	**end**	**width**	**C**	**PS**	**C**	**PS**	**effect dir.**	**logFC**	**ENSEMBL ID**	**symbol**	**gene name**	**next miRNA**
375	10	85757313	85757484	172	Yes	Yes	No	No	↓	-0.18	ENSMUSG00000020044 // ENSMUSG00000059602	Timp3 // Syn3	tissue inhibitor of metalloproteinase 3 // synapsin III	downstream mmu-mir-3057
2265	2	98170120	98170838	719	Yes	Yes	No	No	↓	-0.18	ENSMUSG00000080802	Gm13804	predicted gene 13804	upstream mmu-mir-670
2688	3	153630863	153631205	343	Yes	Yes	No	No	↓	-0.18	ENSMUSG00000028360	Slc44a5	solute carrier family 44, member 5	upstream mmu-mir-3963
809	12	53060093	53060487	395	Yes	Yes	No	No	↓	-0.17	ENSMUSG00000035181	Heatr5a	HEAT repeat containing 5A	downstream mmu-mir-1892
3229	5	148673884	148674599	716	Yes	Yes	No	No	↓	-0.17	ENSMUSG00000029649	Pomp	proteasome maturation protein	downstream mmu-mir-5105
2211	2	70957388	70957814	427	Yes	Yes	No	No	↓	-0.17	ENSMUSG00000027015	Cybrd1	cytochrome b reductase 1	downstream mmu-mir-5115
4138	9	119246762	119247040	279	Yes	Yes	No	No	↓	-0.16	ENSMUSG00000032508	Myd88	myeloid differentiation primary response gene 88	downstream mmu-mir-26a-1
989	13	48360319	48360921	603	Yes	Yes	No	No	↓	-0.16	ENSMUSG00000021379	Id4	inhibitor of DNA binding 4	downstream mmu-let-7d
318	10	53018777	53019023	247	Yes	Yes	No	No	↓	-0.14	ENSMUSG00000038583 // ENSMUSG00000038594	Pln // Gm9766	phospholamban // predicted gene 9766	upstream mmu-mir-466j
3071	5	90316437	90316928	492	Yes	Yes	No	No	↓	-0.13	ENSMUSG00000043635	Adamts3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	upstream mmu-mir-3969
2122	19	59023959	59024160	202	Yes	Yes	No	No	↓	-0.13	ENSMUSG00000048029	ENo4	eNolase 4	upstream mmu-mir-3086
3631	7	122315033	122316086	1054	Yes	Yes	No	No	↓	-0.13	ENSMUSG00000046411	Gm6816	predicted gene 6816	upstream mmu-mir-762
94	1	93694882	93695159	278	Yes	Yes	No	No	↓	-0.12	ENSMUSG00000007805	Twist2	twist homolog 2 (Drosophila)	upstream mmu-mir-149
11	1	16610530	16610742	213	Yes	Yes	No	No	↓	-0.12	ENSMUSG00000025939	Ube2w	ubiquitin-conjugating enzyme E2W (putative)	upstream mmu-mir-206
811	12	53980545	53980725	181	Yes	Yes	No	No	↓	-0.12	ENSMUSG00000070192 // ENSMUSG00000061603	n-R5s58 // Akap6	nuclear encoded rRNA 5S 58 // A kinase (PRKA) anchor protein 6	downstream mmu-mir-1892
651	11	90106921	90107341	421	Yes	Yes	No	No	↓	-0.11	ENSMUSG00000003948	Mmd	moNocyte to macrophage differentiation-associated	downstream mmu-mir-378b
1453	15	94235922	94236235	314	Yes	Yes	No	No	↓	-0.11	ENSMUSG00000022449	Adamts20	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 20	upstream mmu-mir-1941
525	11	43288872	43289143	272	Yes	Yes	No	No	↓	-0.10	ENSMUSG00000046491	C1qtnf2	C1q and tumor necrosis factor related protein 2	upstream mmu-mir-146a
1787	17	78890955	78891668	714	Yes	Yes	No	No	↓	-0.10	ENSMUSG00000061062	Gm10093	predicted pseudogene 10093	upstream mmu-mir-1195
1489	15	98287084	98287440	357	Yes	Yes	No	No	↓	-0.10	ENSMUSG00000032987	Olfr281	olfactory receptor 281	upstream mmu-mir-1941
686	11	99352405	99352894	490	Yes	Yes	No	No	↓	-0.10	ENSMUSG00000006777	Krt23	keratin 23	downstream mmu-mir-5119
2176	2	38569234	38569481	248	Yes	Yes	No	No	↓	-0.09	ENSMUSG00000026751	Nr5a1	nuclear receptor subfamily 5, group A, member 1	upstream mmu-mir-181a-2
2728	4	34851386	34851594	209	Yes	Yes	No	No	↓	-0.09	ENSMUSG00000028298	Cga	glycoprotein hormones, alpha subunit	downstream mmu-mir-876
1719	17	37311836	37312086	251	Yes	Yes	No	No	↓	-0.08	ENSMUSG00000035186	Ubd	ubiquitin D	upstream mmu-mir-877
499	11	16136951	16137262	312	Yes	Yes	No	No	↓	-0.08	ENSMUSG00000082410	Gm12011	predicted gene 12011	downstream mmu-mir-1933
1136	14	21384184	21384553	370	Yes	Yes	No	No	↓	-0.08	ENSMUSG00000021816 // ENSMUSG00000034235	Ppp3cb // Usp54	protein phosphatase 3, catalytic subunit, beta isoform // ubiquitin specific peptidase 54	upstream mmu-mir-3075
1421	15	83079984	83080159	176	Yes	Yes	No	No	↓	-0.07	ENSMUSG00000047878	A4galt	alpha 1,4-galactosyltransferase	upstream mmu-mir-3080
4152	9	124040319	124040718	400	Yes	Yes	No	No	↓	-0.07	ENSMUSG00000079227	Ccr5	chemokine (C-C motif) receptor 5	downstream mmu-mir-138-1
3476	7	7247178	7247584	407	Yes	Yes	No	No	↓	-0.06	ENSMUSG00000000605	Clcn4-2	chloride channel 4-2	upstream mmu-mir-5620
1738	17	46576273	46576542	270	Yes	Yes	No	No	↓	-0.06	ENSMUSG00000067144	Slc22a7	solute carrier family 22 (organic anion transporter), member 7	downstream mmu-mir-693
909	12	112726883	112727245	363	Yes	Yes	No	No	↓	-0.06	ENSMUSG00000010529	Gm266	predicted gene 266	upstream mmu-mir-3073
2130	2	5056607	5056985	379	Yes	Yes	No	No	↓	-0.06	ENSMUSG00000026676	Ccdc3	coiled-coil domain containing 3	upstream mmu-mir-466m
593	11	66724684	66724991	308	Yes	Yes	No	No	↓	-0.05	ENSMUSG00000048070 // ENSMUSG00000072834	Pirt // Gm12298	phosphoiNositide-interacting regulator of transient receptor potential channels // predicted gene 12298	upstream mmu-mir-744

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	Chr.	start	end	width	C	PS	C	PS	effect dir.	logFC	ENSEMBL ID	symbol	gene name	next miRNA
1204	14	53070496	53070874	379	Yes	Yes	No	No	↓	-0.04	ENSMUSG00000035626	Olfr1509	olfactory receptor 1509	downstream mmu-mir-686
650	11	89896819	89897137	319	Yes	Yes	No	No	↓	-0.04	ENSMUSG00000069763	Tmem100	transmembrane protein 100	downstream mmu-mir-378b
2369	2	163369652	163369895	244	Yes	Yes	No	No	↓	-0.03	ENSMUSG00000046840	0610008F07Rik	RIKEN cDNA 0610008F07 gene	downstream mmu-mir-3474
1831	18	14133585	14133901	317	Yes	Yes	No	No	↓	-0.02	ENSMUSG00000024420	Zfp521	zinc finger protein 521	downstream mmu-mir-1948
2497	3	58456156	58456931	776	Yes	Yes	No	No	↓	-0.01	ENSMUSG00000070471	Fam194a	family with sequence similarity 194, member A	upstream mmu-mir-15b
2529	3	83645883	83646153	271	Yes	Yes	No	No	↓	-0.01	ENSMUSG00000027995	Tlr2	toll-like receptor 2	upstream mmu-mir-466k
3014	5	64268747	64268986	240	Yes	Yes	No	No	↓	-0.01	ENSMUSG00000060512	0610040J01Rik	RIKEN cDNA 0610040J01 gene	upstream mmu-mir-574
3050	5	75097307	75097823	517	Yes	Yes	No	No	↓	0.00	ENSMUSG00000029228	Lnx1	ligand of numb-protein X 1	upstream mmu-mir-5098
3539	7	52513997	52514293	297	Yes	Yes	No	No	↓	0.00	ENSMUSG00000030798	Cd37	CD37 antigen	upstream mmu-mir-5121
2402	2	169945208	169945407	200	No	No	Yes	Yes	↑	0.01	ENSMUSG00000052056	Zfp217	zinc finger protein 217	downstream mmu-mir-296
2608	3	120876377	120876657	281	No	No	Yes	Yes	↑	0.01	ENSMUSG00000028133	Rwdd3	RWD domain containing 3	downstream mmu-mir-760
3228	5	148633787	148633982	196	No	No	Yes	Yes	↑	0.01	ENSMUSG00000029649	Pomp	proteasome maturation protein	downstream mmu-mir-5105
3965	9	32130003	32130278	276	No	No	Yes	Yes	↑	0.02	ENSMUSG00000032034	Kcnj5	potassium inwardly-rectifying channel, subfamily J, member 5	upstream mmu-mir-100
1800	17	83612261	83612513	253	No	No	Yes	Yes	↑	0.02	ENSMUSG00000024247	Pkdcc	protein kinase domain containing, cytoplasmic	upstream mmu-mir-1195
2641	3	135146681	135146850	170	No	No	Yes	Yes	↑	0.03	ENSMUSG00000028164	Manba	manNosidase, beta A, lysosomal	upstream mmu-mir-1895
2898	4	138390529	138390886	358	No	No	Yes	Yes	↑	0.03	ENSMUSG00000058908 // ENSMUSG00000041193	Pla2g2a // Pla2g5	phospholipase A2, group IIA (platelets, syNovial fluid) // phospholipase A2, group V	downstream mmu-mir-2139
4060	9	85734696	85735012	317	No	No	Yes	Yes	↑	0.03	ENSMUSG00000035274	Tpbg	trophoblast glycoprotein	downstream mmu-mir-184
451	10	120749170	120749406	237	No	No	Yes	Yes	↑	0.03	ENSMUSG00000052302	Tbc1d30	TBC1 domain family, member 30	upstream mmu-mir-763
1182	14	47003300	47004526	1227	No	No	Yes	Yes	↑	0.03	ENSMUSG00000079261 // ENSMUSG00000021835	Gm15217 // Bmp4	predicted gene 15217 // bone morphogenetic protein 4	upstream mmu-mir-5131
556	11	53883752	53883994	243	No	No	Yes	Yes	↑	0.03	ENSMUSG00000020388	Pdlim4	PDZ and LIM domain 4	downstream mmu-mir-3061
3947	9	21989037	21989660	624	No	No	Yes	Yes	↑	0.04	ENSMUSG00000061167	Rpl15-ps3	ribosomal protein L15, pseudogene 3	upstream mmu-mir-1946b
2719	4	32843652	32844101	450	No	No	Yes	Yes	↑	0.04	ENSMUSG00000045854 // ENSMUSG00000058006	Lyrm2 // Mdn1	LYR motif containing 2 // midasin homolog (yeast)	downstream mmu-mir-876
1792	17	79330767	79331176	410	No	No	Yes	Yes	↑	0.04	ENSMUSG00000024081	Cebpz	CCAAT/enhancer binding protein zeta	upstream mmu-mir-1195
3104	5	104908083	104908330	248	No	No	Yes	Yes	↑	0.05	ENSMUSG00000034462	Pkd2	polycystic kidney disease 2	downstream mmu-mir-5619
3237	5	151319634	151319902	269	No	No	Yes	Yes	↑	0.05	ENSMUSG00000056586	Zar1l	zygote arrest 1-like	downstream mmu-mir-5105
480	11	3092744	3093013	270	No	No	Yes	Yes	↑	0.05	ENSMUSG00000023764	Sfi1	Sfi1 homolog, spindle assembly associated (yeast)	upstream mmu-mir-3060
3724	8	10807142	10807658	517	No	No	Yes	Yes	↑	0.06	ENSMUSG00000062458	Gm8623	predicted gene 8623	downstream mmu-mir-1968
2644	3	137796736	137797014	279	No	No	Yes	Yes	↑	0.06	ENSMUSG00000028158	Mttp	microsomal triglyceride transfer protein	upstream mmu-mir-1956
421	10	115028742	115029312	571	No	No	Yes	Yes	↑	0.07	ENSMUSG00000020140	Lgr5	leucine rich repeat containing G protein coupled receptor 5	downstream mmu-mir-763
2060	19	44065549	44066096	548	No	No	Yes	Yes	↑	0.07	ENSMUSG00000025196	Cpn1	carboxypeptidase N, polypeptide 1	upstream mmu-mir-5114
3852	8	98015206	98015695	490	No	No	Yes	Yes	↑	0.07	ENSMUSG00000046707	Csnk2a2	casein kinase 2, alpha prime polypeptide	upstream mmu-mir-1186b
4068	9	89945685	89946425	741	No	No	Yes	Yes	↑	0.07	ENSMUSG00000032359	Ctsh	cathepsin H	upstream mmu-mir-184
1111	13	114108131	114108794	664	No	No	Yes	Yes	↑	0.07	ENSMUSG00000021763	BC067074	cDNA sequence BC067074	downstream mmu-mir-449a
3049	5	74424926	74425458	533	No	No	Yes	Yes	↑	0.08	ENSMUSG00000054814	Usp46	ubiquitin specific peptidase 46	upstream mmu-mir-5098
2881	4	134959662	134960043	382	No	No	Yes	Yes	↑	0.09	ENSMUSG00000081136	Gm12990	predicted gene 12990	downstream mmu-mir-700
1643	16	92829018	92830155	1138	No	No	Yes	Yes	↑	0.09	ENSMUSG00000022952	Runx1	runt related transcription factor 1	upstream mmu-mir-802
2950	4	154845180	154845533	354	No	No	Yes	Yes	↑	0.10	ENSMUSG00000023153	Tmem52	transmembrane protein 52	downstream mmu-mir-429
2380	2	164414806	164415294	489	No	No	Yes	Yes	↑	0.10	ENSMUSG00000017733	Spinlw1	serine protease inhibitor-like, with Kunitz and WAP domains 1 (eppin)	downstream mmu-mir-3474

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	Chr.	start	end	width	C	PS	C	PS	effect dir.	logFC	ENSEMBL ID	symbol	gene name	next miRNA
3029	5	67993675	67994044	370	No	No	Yes	Yes	↑	0.10	ENSMUSG00000050010	Shisa3	shisa homolog 3 (XeNopus laevis)	downstream mmu-mir-574
462	10	124949359	124949886	528	No	No	Yes	Yes	↑	0.10	ENSMUSG00000020102	Slc16a7	solute carrier family 16 (moNocarboxylic acid transporters), member 7	upstream mmu-mir-26a-2
2875	4	133136543	133137352	810	No	No	Yes	Yes	↑	0.10	ENSMUSG00000028848 // ENSMUSG00000028850	Gpn2 // Gpatch3	GPN-loop GTPase 2 // G patch domain containing 3	downstream mmu-mir-5122
3343	6	87325328	87325644	317	No	No	Yes	Yes	↑	0.11	ENSMUSG00000030049	Gkn2	gastrokine 2	upstream mmu-mir-705
1116	13	115393466	115393678	213	No	No	Yes	Yes	↑	0.11	ENSMUSG00000051758	4930544M13Rik	RIKEN cDNA 4930544M13 gene	downstream mmu-mir-449a
1203	14	52996683	52996921	239	No	No	Yes	Yes	↑	0.11	ENSMUSG00000060640	---	NA	downstream mmu-mir-686
4099	9	107880954	107881122	169	No	No	Yes	Yes	↑	0.11	ENSMUSG00000032596	Uba7	ubiquitin-like modifier activating enzyme 7	upstream mmu-mir-191
2708	4	11057620	11058318	699	No	No	Yes	Yes	↑	0.11	ENSMUSG00000058164	---	NA	upstream mmu-mir-684-2
3212	5	143019222	143019509	288	No	No	Yes	Yes	↑	0.12	ENSMUSG00000029576	Radil	Ras association and DIL domains	upstream mmu-mir-339
1146	14	28023269	28023495	227	No	No	Yes	Yes	↑	0.12	ENSMUSG00000021895	Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	downstream mmu-mir-3075
1098	13	109100635	109100882	248	No	No	Yes	Yes	↑	0.12	ENSMUSG00000021697	Depdc1b	DEP domain containing 1B	upstream mmu-mir-582
1163	14	33821724	33822035	312	No	No	Yes	Yes	↑	0.12	ENSMUSG00000041673 // ENSMUSG00000051506	Lrrc18 // Wdfy4	leucine rich repeat containing 18 // WD repeat and FYVE domain containing 4	upstream mmu-mir-346
336	10	67012910	67013365	456	No	No	Yes	Yes	↑	0.13	ENSMUSG00000057134	Ado	2-amiNoethanethiol (cysteamine) dioxygenase	downstream mmu-mir-5108
527	11	43418691	43419752	1062	No	No	Yes	Yes	↑	0.13	ENSMUSG00000020405	Fabp6	fatty acid binding protein 6, ileal (gastrotropin)	upstream mmu-mir-146a
1161	14	33600582	33600925	344	No	No	Yes	Yes	↑	0.13	ENSMUSG00000041707	1810011H11Rik	RIKEN cDNA 1810011H11 gene	upstream mmu-mir-346
1392	15	76765122	76765559	438	No	No	Yes	Yes	↑	0.13	ENSMUSG00000054967	Zfp647	zinc finger protein 647	upstream mmu-mir-3079
1819	17	89024114	89024556	443	No	No	Yes	Yes	↑	0.13	ENSMUSG00000033855	Ston1	stonin 1	upstream mmu-mir-1195
2925	4	148506204	148506552	349	No	No	Yes	Yes	↑	0.13	ENSMUSG00000073705	Apitd1	apoptosis-inducing, TAF9-like domain 1	upstream mmu-mir-5616
1758	17	66768104	66768598	495	No	No	Yes	Yes	↑	0.13	ENSMUSG00000052105	1110012J17Rik	RIKEN cDNA 1110012J17 gene	downstream mmu-mir-5709
2269	2	103330312	103330597	286	No	No	Yes	Yes	↑	0.14	ENSMUSG00000027187	Cat	catalase	downstream mmu-mir-1902
41	1	52003151	52003381	231	No	No	Yes	Yes	↑	0.14	ENSMUSG00000065285	---	NA	upstream mmu-mir-5103
1282	14	104877036	104877211	176	No	No	Yes	Yes	↑	0.16	ENSMUSG00000048349 // ENSMUSG00000022120	Pou4f1 // Rnf219	POU domain, class 4, transcription factor 1 // ring finger protein 219	upstream mmu-mir-5130
3723	8	10560071	10560342	272	No	No	Yes	Yes	↑	0.16	ENSMUSG00000062458 // ENSMUSG00000039057	Gm8623 // Myo16	predicted gene 8623 // myosin XVI	downstream mmu-mir-1968
3576	7	86838583	86838862	280	No	No	Yes	Yes	↑	0.16	ENSMUSG00000050382 // ENSMUSG00000046591	Kif7 // 5730590G19Rik	kinesin family member 7 // RIKEN cDNA 5730590G19 gene	downstream mmu-mir-9-3
1053	13	91352863	91353176	314	No	No	Yes	Yes	↑	0.16	ENSMUSG00000021619	Atg10	autophagy-related 10 (yeast)	upstream mmu-mir-5624
2788	4	84529491	84529727	237	No	No	Yes	Yes	↑	0.16	ENSMUSG00000038070	Cntln	centlein, centrosomal protein	upstream mmu-mir-491
4003	9	53515949	53516155	207	No	No	Yes	Yes	↑	0.16	ENSMUSG00000055069	Rab39	RAB39, member RAS oncogene family	upstream mmu-mir-5710
2564	3	96957059	96957266	208	No	No	Yes	Yes	↑	0.16	ENSMUSG00000028093	Acp6	acid phosphatase 6, lysophosphatidic	downstream mmu-mir-190b
1532	16	17446806	17447033	228	No	No	Yes	Yes	↑	0.16	ENSMUSG00000006134	Crkl	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	upstream mmu-mir-301b
2592	3	102584291	102584599	309	No	No	Yes	Yes	↑	0.17	ENSMUSG00000027857	Tshb	thyroid stimulating hormone, beta subunit	downstream mmu-mir-190b
1123	13	119172747	119173041	295	No	No	Yes	Yes	↑	0.17	ENSMUSG00000021731	Mrps30	mitochondrial ribosomal protein S30	downstream mmu-mir-449a
1032	13	64467996	64468309	314	No	No	Yes	Yes	↑	0.18	ENSMUSG00000021477	Ctsl	cathepsin L	upstream mmu-mir-3074-1
2204	2	67956732	67956938	207	No	No	Yes	Yes	↑	0.18	ENSMUSG00000034780	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	downstream mmu-mir-5115

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	Chr.	start	end	width	C	PS	C	PS	effect dir.	logFC	ENSEMBL ID	symbol	gene name	next miRNA
3513	7	31349777	31350185	409	No	No	Yes	Yes	↑	0.18	ENSMUSG00000036826 // ENSMUSG00000078765	Tmem149 // U2af1l4	transmembrane protein 149 // U2 small nuclear RNA auxiliary factor 1-like 4	downstream mmu-mir-1964
454	10	121041099	121041382	284	No	No	Yes	Yes	↑	0.19	ENSMUSG00000020115 // ENSMUSG00000034667	Tbk1 // Xpot	TANK-binding kinase 1 // exportin, tRNA (nuclear export receptor for tRNAs)	upstream mmu-mir-763
230	1	191546433	191547188	756	No	No	Yes	Yes	↑	0.19	ENSMUSG00000026604	Ptpn14	protein tyrosine phosphatase, Non-receptor type 14	downstream mmu-mir-3473c
2652	3	141593558	141593900	343	No	No	Yes	Yes	↑	0.19	ENSMUSG00000080000 // ENSMUSG00000052430	--- // Bmpr1b	NA // bone morphogenetic protein receptor, type 1B	downstream mmu-mir-1956
377	10	86175833	86176109	277	No	No	Yes	Yes	↑	0.19	ENSMUSG00000044937	BC030307	cDNA sequence BC030307	downstream mmu-mir-135a-2
1486	15	98208788	98209102	315	No	No	Yes	Yes	↑	0.20	ENSMUSG00000056184	Olfr283	olfactory receptor 283	upstream mmu-mir-1941
89	1	92809681	92809996	316	No	No	Yes	Yes	↑	0.20	ENSMUSG00000026303	Mlph	melaNophilin	upstream mmu-mir-149
850	12	77486766	77486979	214	No	No	Yes	Yes	↑	0.20	ENSMUSG00000033454	Zbtb1	zinc finger and BTB domain containing 1	downstream mmu-mir-5135
2347	2	154078659	154079003	345	No	No	Yes	Yes	↑	0.20	ENSMUSG00000067998	Bpifb9a	BPI fold containing family B, member 9A	upstream mmu-mir-695
1799	17	81426032	81426276	245	No	No	Yes	Yes	↑	0.21	ENSMUSG00000024246	Thumpd2	THUMP domain containing 2	upstream mmu-mir-1195
275	10	21138856	21139464	609	No	No	Yes	Yes	↑	0.22	ENSMUSG00000037535	1700021A07Rik	RIKEN cDNA 1700021A07 gene	downstream mmu-mir-5104
581	11	61078258	61078515	258	No	No	Yes	Yes	↑	0.22	ENSMUSG00000010025	Aldh3a2	aldehyde dehydrogenase family 3, subfamily A2	downstream mmu-mir-5100
2385	2	165476902	165477422	521	No	No	Yes	Yes	↑	0.22	ENSMUSG00000081758 // ENSMUSG00000017897	Gm11460 // Eya2	predicted gene 11460 // eYes absent 2 homolog (Drosophila)	downstream mmu-mir-3474
3055	5	77021717	77022001	285	No	No	Yes	Yes	↑	0.22	ENSMUSG00000036403	Cep135	centrosomal protein 135	upstream mmu-mir-5098
3078	5	91315571	91316721	1151	No	No	Yes	Yes	↑	0.23	ENSMUSG00000029380	Cxcl1	chemokine (C-X-C motif) ligand 1	downstream mmu-mir-1961
1238	14	66698262	66698685	424	No	No	Yes	Yes	↑	0.23	ENSMUSG00000022039	Adam2	a disintegrin and metallopeptidase domain 2	downstream mmu-mir-3078
695	11	100219497	100219995	499	No	No	Yes	Yes	↑	0.23	ENSMUSG00000006930	Hap1	huntingtin-associated protein 1	downstream mmu-mir-5119
1009	13	55249814	55250054	241	No	No	Yes	Yes	↑	0.23	ENSMUSG00000005320	Fgfr4	fibroblast growth factor receptor 4	downstream mmu-mir-874
2053	19	42680733	42680970	238	No	No	Yes	Yes	↑	0.23	ENSMUSG00000025185	Loxl4	lysyl oxidase-like 4	upstream mmu-mir-3085
1220	14	57484938	57485648	711	No	No	Yes	Yes	↑	0.23	ENSMUSG00000021945	Zmym2	zinc finger, MYM-type 2	upstream mmu-mir-3077
4056	9	78254281	78254806	526	No	No	Yes	Yes	↑	0.23	ENSMUSG00000070291	Ddx43	DEAD (Asp-Glu-Ala-Asp) box polypeptide 43	upstream mmu-mir-5626
2021	19	32546110	32546481	372	No	No	Yes	Yes	↑	0.24	ENSMUSG00000062456	Rpl9-ps6	ribosomal protein L9, pseudogene 6	upstream mmu-mir-3970
1816	17	88407669	88408047	379	No	No	Yes	Yes	↑	0.24	ENSMUSG00000005370 // ENSMUSG00000005371	Msh6 // Fbxo11	mutS homolog 6 (E. coli) // F-box protein 11	upstream mmu-mir-1195
1895	18	58036113	58036461	349	No	No	Yes	Yes	↑	0.24	ENSMUSG00000024597	Slc12a2	solute carrier family 12, member 2	upstream mmu-mir-5107
2845	4	119202799	119203019	221	No	No	Yes	Yes	↑	0.24	ENSMUSG00000065240 // ENSMUSG00000062260	--- // ---	NA // NA	downstream mmu-mir-1957
922	13	3802066	3802383	318	No	No	Yes	Yes	↑	0.24	ENSMUSG00000063130	Calml3	calmodulin-like 3	upstream mmu-mir-466i
3494	7	28332101	28332288	188	No	No	Yes	Yes	↑	0.24	ENSMUSG00000003363	Pld3	phospholipase D family, member 3	downstream mmu-mir-1191
1371	15	63894542	63895059	518	No	No	Yes	Yes	↑	0.25	ENSMUSG00000022378	Fam49b	family with sequence similarity 49, member B	downstream mmu-mir-30b
3005	5	51948792	51948961	170	No	No	Yes	Yes	↑	0.25	ENSMUSG00000029167	Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	downstream mmu-mir-218-1
2571	3	97964249	97964719	471	No	No	Yes	Yes	↑	0.26	ENSMUSG00000043468	Adam30	a disintegrin and metallopeptidase domain 30	downstream mmu-mir-190b
1997	19	25107165	25107489	325	No	No	Yes	Yes	↑	0.26	ENSMUSG00000052085	Dock8	dedicator of cytokinesis 8	upstream mmu-mir-3084
2820	4	108536005	108536359	355	No	No	Yes	Yes	↑	0.27	ENSMUSG00000003411	Rab3b	RAB3B, member RAS oncogene family	upstream mmu-mir-761

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	**Chr.**	**start**	**end**	**width**	**C**	**PS**	**C**	**PS**	**effect dir.**	**logFC**	**ENSEMBL ID**	**symbol**	**gene name**	**next miRNA**
240	10	5733709	5733915	207	No	No	Yes	Yes	↑	0.27	ENSMUSG00000019768	Esr1	estrogen receptor 1 (alpha)	upstream mmu-mir-5104
3067	5	86986020	86986223	204	No	No	Yes	Yes	↑	0.27	ENSMUSG00000079451 // ENSMUSG00000048764	Tmprss11g // Tmprss11f	transmembrane protease, serine 11g // transmembrane protease, serine 11f	downstream mmu-mir-3969
1236	14	66625813	66626127	315	No	No	Yes	Yes	↑	0.27	ENSMUSG00000034450	Gulo	guloNolactone (L-) oxidase	downstream mmu-mir-3078
2759	4	53693414	53693700	287	No	No	Yes	Yes	↑	0.28	ENSMUSG00000078703	---	NA	downstream mmu-mir-32
1264	14	77430580	77430819	240	No	No	Yes	Yes	↑	0.28	ENSMUSG00000044350	9030625A04Rik	RIKEN cDNA 9030625A04 gene	downstream mmu-mir-1971
345	10	74323781	74323951	171	No	No	Yes	Yes	↑	0.29	ENSMUSG00000072407	Gm6419	predicted gene 6419	downstream mmu-mir-678
3033	5	72970136	72970575	440	No	No	Yes	Yes	↑	0.29	ENSMUSG00000063935	Zar1	zygote arrest 1	upstream mmu-mir-5098
3352	6	87617066	87617788	723	No	No	Yes	Yes	↑	0.30	ENSMUSG00000030051	Aplf	aprataxin and PNKP like factor	upstream mmu-mir-705
3727	8	11683366	11684307	942	No	No	Yes	Yes	↑	0.30	ENSMUSG00000031509	1700016D06Rik	RIKEN cDNA 1700016D06 gene	downstream mmu-mir-1968
2932	4	149331144	149332126	983	No	No	Yes	Yes	↑	0.30	ENSMUSG00000039911	Spsb1	splA/ryaNodine receptor domain and SOCS box containing 1	upstream mmu-mir-34a
3587	7	91561041	91561344	304	No	No	Yes	Yes	↑	0.30	ENSMUSG00000015709	Arnt2	aryl hydrocarbon receptor nuclear translocator 2	downstream mmu-mir-1839
822	12	66326292	66327082	791	No	No	Yes	Yes	↑	0.30	ENSMUSG00000035560	Wdr20b	WD repeat domain 20b	downstream mmu-mir-681
3941	9	20766078	20766307	230	No	No	Yes	Yes	↑	0.31	ENSMUSG00000004099	Dnmt1	DNA methyltransferase (cytosine-5) 1	downstream mmu-mir-1900
1861	18	37678974	37679310	337	No	No	Yes	Yes	↑	0.31	ENSMUSG00000073591	Pcdhb22	protocadherin beta 22	downstream mmu-mir-1949
3408	6	122800125	122800385	261	No	No	Yes	Yes	↑	0.31	ENSMUSG00000040552	C3ar1	complement component 3a receptor 1	downstream mmu-mir-141
1666	17	13106629	13106975	347	No	No	Yes	Yes	↑	0.31	ENSMUSG00000057388	Mrpl18	mitochondrial ribosomal protein L18	upstream mmu-mir-99b
98	1	109314463	109314750	288	No	No	Yes	Yes	↑	0.32	ENSMUSG00000067001	Serpinb7	serine (or cysteine) peptidase inhibitor, clade B, member 7	downstream mmu-mir-149
3271	6	34329666	34329904	239	No	No	Yes	Yes	↑	0.33	ENSMUSG00000081196 // ENSMUSG00000081991	Gm13858 // Gm13859	predicted gene 13858 // predicted gene 13859	upstream mmu-mir-490
2309	2	127946767	127947010	244	No	No	Yes	Yes	↑	0.33	ENSMUSG00000027381 // ENSMUSG00000027380	Bcl2l11 // Acoxl	BCL2-like 11 (apoptosis facilitator) // acyl-Coenzyme A oxidase-like	upstream mmu-mir-103-2
1035	13	67631796	67632037	242	No	No	Yes	Yes	↑	0.33	ENSMUSG00000071285	---	NA	upstream mmu-mir-466f-4
1276	14	96280847	96281169	323	No	No	Yes	Yes	↑	0.34	ENSMUSG00000034689	4921530L21Rik	RIKEN cDNA 4921530L21 gene	downstream mmu-mir-5130
835	12	73221642	73222696	1055	No	No	Yes	Yes	↑	0.34	ENSMUSG00000077094	---	NA	upstream mmu-mir-681
3939	9	15487157	15487512	356	No	No	Yes	Yes	↑	0.35	ENSMUSG00000043885	Slc36a4	solute carrier family 36 (proton/amiNo acid symporter), member 4	downstream mmu-mir-1900
2973	5	24608619	24609015	397	No	No	Yes	Yes	↑	0.35	ENSMUSG00000043833	2900005J15Rik	RIKEN cDNA 2900005J15 gene	downstream mmu-mir-671
2266	2	102029692	102029893	202	No	No	Yes	Yes	↑	0.35	ENSMUSG00000048058	Ldlrad3	low density lipoprotein receptor class A domain containing 3	downstream mmu-mir-1902
2559	3	96065100	96065415	316	No	No	Yes	Yes	↑	0.36	ENSMUSG00000068851	---	NA	downstream mmu-mir-190b
3438	6	136829507	136829785	279	No	No	Yes	Yes	↑	0.36	ENSMUSG00000030218	Mgp	matrix Gla protein	downstream mmu-mir-680-1
1518	15	101402117	101402431	315	No	No	Yes	Yes	↑	0.36	ENSMUSG00000022986	Krt75	keratin 75	downstream mmu-mir-1941
326	10	62069271	62069550	280	No	No	Yes	Yes	↑	0.36	ENSMUSG00000020075	Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	downstream mmu-mir-5108
1455	15	94378033	94378505	473	No	No	Yes	Yes	↑	0.39	ENSMUSG00000059883	Irak4	interleukin-1 receptor-associated kinase 4	upstream mmu-mir-1941
3268	6	31515562	31515798	237	No	No	Yes	Yes	↑	0.40	ENSMUSG00000025608	Podxl	podocalyxin-like	upstream mmu-mir-29b-1
2639	3	133897525	133897835	311	No	No	Yes	Yes	↑	0.41	ENSMUSG00000044365	Cxxc4	CXXC finger 4	downstream mmu-mir-1895
3116	5	108301808	108302471	664	No	No	Yes	Yes	↑	0.42	ENSMUSG00000011831	Evi5	ecotropic viral integration site 5	upstream mmu-mir-701
1742	17	47445342	47445549	208	No	No	Yes	Yes	↑	0.44	ENSMUSG00000034729 // ENSMUSG00000064043	Mrps10 // Trerf1	mitochondrial ribosomal protein S10 // transcriptional regulating factor 1	downstream mmu-mir-693
3171	5	124234434	124234853	420	No	No	Yes	Yes	↑	0.45	ENSMUSG00000029414	Kntc1	kinetochore associated 1	upstream mmu-mir-3965
348	10	75081881	75082202	322	No	No	Yes	Yes	↑	0.46	ENSMUSG00000006342	Susd2	sushi domain containing 2	downstream mmu-mir-678
2253	2	83562829	83563031	203	No	No	Yes	Yes	↑	0.46	ENSMUSG00000027087	Itgav	integrin alpha V	downstream mmu-mir-130a

					Enrichment meDNA									
					5-Htt+/+		**5-Htt+/-**							
reg. ID	**Chr.**	**start**	**end**	**width**	**C**	**PS**	**C**	**PS**	**effect dir.**	**logFC**	**ENSEMBL ID**	**symbol**	**gene name**	**next miRNA**
881	12	101125553	101126031	479	No	No	Yes	Yes	↑	0.48	ENSMUSG00000072886	---	NA	downstream mmu-mir-1190
2145	2	17957373	17957980	608	No	No	Yes	Yes	↑	0.49	ENSMUSG00000054057	A930004D18Rik	RIKEN cDNA A930004D18 gene	downstream mmu-mir-511
316	10	44181109	44181866	758	No	No	Yes	Yes	↑	0.49	ENSMUSG00000038151	Prdm1	PR domain containing 1, with ZNF domain	downstream mmu-mir-1929
2552	3	94408321	94408919	599	No	No	Yes	Yes	↑	0.55	ENSMUSG00000083323 // ENSMUSG00000062896	--- // Rpl31-ps11	NA // ribosomal protein L31, pseudogene 11	downstream mmu-mir-190b
2254	2	84513354	84513558	205	No	No	Yes	Yes	↑	0.55	ENSMUSG00000076437 // ENSMUSG00000050043	2700094K13Rik // Tmx2	RIKEN cDNA 2700094K13 gene // thioredoxin-related transmembrane protein 2	downstream mmu-mir-130a
1592	16	50435836	50436363	528	No	No	Yes	Yes	↑	0.66	ENSMUSG00000022641	Bbx	bobby sox homolog (Drosophila)	upstream mmu-mir-5118
1034	13	64986680	64986851	172	No	No	Yes	Yes	↑	0.72	ENSMUSG00000033063	Cntnap3	contactin associated protein-like 3	upstream mmu-mir-3074-1
2048	19	42104546	42104715	170	No	No	Yes	Yes	↑	0.73	ENSMUSG00000025172 // ENSMUSG00000025171	Ankrd2 // Ubtd1	ankyrin repeat domain 2 (stretch responsive muscle) // ubiquitin domain containing 1	downstream mmu-mir-3085

B) E-effects

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	**Chr.**	**start**	**end**	**width**	**C**	**PS**	**C**	**PS**	**effect dir.**	**logFC**	**ENSEMBL ID**	**symbol**	**gene name**	**next miRNA**
1812	17	87477480	87478570	1091	Yes	No	Yes	No	↓	-0.59	ENSMUSG00000071035	Gm5499	predicted pseudogene 5499	upstream mmu-mir-1195
3774	8	36033392	36033602	211	Yes	No	Yes	No	↓	-0.57	ENSMUSG00000031529	Tnks	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	downstream mmu-mir-383
3354	6	87960287	87960658	372	Yes	No	Yes	No	↓	-0.49	ENSMUSG00000044927 // ENSMUSG00000079477	H1fx // Rab7	H1 histone family, member X // RAB7, member RAS oncogene family	upstream mmu-mir-705
3726	8	11551940	11552376	437	Yes	No	Yes	No	↓	-0.48	ENSMUSG00000056228	Cars2	cysteinyl-tRNA synthetase 2 (mitochondrial)(putative)	downstream mmu-mir-1968
531	11	45534077	45534261	185	Yes	No	Yes	No	↓	-0.47	ENSMUSG00000077320		Small nucleolar RNA SNoRA17	upstream mmu-mir-146a
3215	5	143942968	143943209	242	Yes	No	Yes	No	↓	-0.44	ENSMUSG00000029586	4933411G11Rik	RIKEN cDNA 4933411G11Rik gene	upstream mmu-mir-5105
869	12	88074694	88075010	317	Yes	No	Yes	No	↓	-0.43	ENSMUSG00000059114	Gm6772	predicted gene 6772	downstream mmu-mir-3068
1176	14	35081410	35081865	456	Yes	No	Yes	No	↓	-0.37	ENSMUSG00000041471	Fam35a	family with sequence similarity 35, member A	upstream mmu-mir-346
794	12	25389222	25389739	518	Yes	No	Yes	No	↓	-0.35	ENSMUSG00000020649 // ENSMUSG00000066553	Rrm2 // Gm6969	ribonucleotide reductase M2 // predicted pseudogene 6969	downstream mmu-mir-3066
2102	19	56478325	56478881	557	Yes	No	Yes	No	↓	-0.35	ENSMUSG00000025076	Casp7	caspase 7	upstream mmu-mir-5623
635	11	85160714	85161044	331	Yes	No	Yes	No	↓	-0.35	ENSMUSG00000059439	Bcas3	breast carciNoma amplified sequence 3	upstream mmu-mir-1935
2172	2	34818037	34818578	542	Yes	No	Yes	No	↓	-0.33	ENSMUSG00000026875	Traf1	TNF receptor-associated factor 1	upstream mmu-mir-3960
3875	8	111477836	111478263	428	Yes	No	Yes	No	↓	-0.33	ENSMUSG00000038872	Zfhx3	zinc finger homeobox 3	downstream mmu-mir-3108
413	10	104626225	104626657	433	Yes	No	Yes	No	↓	-0.32	ENSMUSG00000077407 // ENSMUSG00000036019	// Tmtc2	Small nucleolar RNA SNoRA17 // transmembrane and tetratricopeptide repeat containing 2	downstream mmu-mir-3059
139	1	144990530	144990925	396	Yes	No	Yes	No	↓	-0.30	ENSMUSG00000078284	Cdc73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	downstream mmu-mir-181b-1
3634	7	123171580	123171989	410	Yes	No	Yes	No	↓	-0.30	ENSMUSG00000051910	Sox6	SRY-box containing gene 6	upstream mmu-mir-762
359	10	76632735	76633306	572	Yes	No	Yes	No	↓	-0.29	ENSMUSG00000001435	Col18a1	collagen, type XVIII, alpha 1	upstream mmu-mir-1930
2452	3	27923321	27923641	321	Yes	No	Yes	No	↓	-0.29	ENSMUSG00000027695	Pld1	phospholipase D1	upstream mmu-mir-466q
618	11	75399931	75400493	563	Yes	No	Yes	No	↓	-0.28	ENSMUSG00000017781	Pitpna	phosphatidyliNositol transfer protein, alpha	downstream mmu-mir-3971
2914	4	141569626	141569905	280	Yes	No	Yes	No	↓	-0.28	ENSMUSG00000051435	Fhad1	forkhead-associated (FHA) phosphopeptide binding domain 1	upstream mmu-mir-2139
2659	3	145538088	145538612	525	Yes	No	Yes	No	↓	-0.27	ENSMUSG00000028191 // ENSMUSG00000028194	Bcl10 // Ddah1	B cell leukemia/lymphoma 10 // dimethylarginine dimethylamiNohydrolase 1	downstream mmu-mir-3963
2432	2	180964456	180964941	486	Yes	No	Yes	No	↓	-0.25	ENSMUSG00000047841 // ENSMUSG00000027580	BC051628 // BC006779	cDNA sequence BC051628 // cDNA sequence BC006779	downstream mmu-mir-124-3
2749	4	44939851	44940124	274	Yes	No	Yes	No	↓	-0.25	ENSMUSG00000035637 // ENSMUSG00000035649	Grhpr // Zcchc7	glyoxylate reductase/hydroxypyruvate reductase // zinc finger, CCHC domain containing 7	upstream mmu-mir-5120
3316	6	67364538	67364983	446	Yes	No	Yes	No	↓	-0.25	ENSMUSG00000018341	Il12rb2	interleukin 12 receptor, beta 2	downstream mmu-mir-468
54	1	62684470	62684816	347	Yes	No	Yes	No	↓	-0.24	ENSMUSG00000046526 // ENSMUSG00000052062	--- // Pard3b	NA // par-3 partitioning defective 3 homolog B (C. elegans)	downstream mmu-mir-1928
3648	7	128123902	128124106	205	Yes	No	Yes	No	↓	-0.24	ENSMUSG00000030878	Cdr2	cerebellar degeneration-related 2	upstream mmu-mir-762
2444	3	17683961	17684158	198	Yes	No	Yes	No	↓	-0.23	ENSMUSG00000074674	Gm10742	predicted gene 10742	upstream mmu-mir-124-2

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	Chr.	start	end	width	C	PS	C	PS	effect dir.	logFC	ENSEMBL ID	symbol	gene name	next miRNA
3943	9	21192840	21193122	283	Yes	No	Yes	No	↓	-0.23	ENSMUSG00000032178	Ilf3	interleukin enhancer binding factor 3	downstream mmu-mir-199a-1
486	11	4164725	4165063	339	Yes	No	Yes	No	↓	-0.23	ENSMUSG00000034394	Lif	leukemia inhibitory factor	downstream mmu-mir-3060
2476	3	48412216	48412817	602	Yes	No	Yes	No	↓	-0.23	ENSMUSG00000037910	1700018B24Rik	RIKEN cDNA 1700018B24 gene	downstream mmu-mir-1897
995	13	50095635	50096127	493	Yes	No	Yes	No	↓	-0.22	ENSMUSG00000074908	---	NA	downstream mmu-mir-683-1
1650	16	98020737	98020899	163	Yes	No	Yes	No	↓	-0.22	ENSMUSG00000005251 // ENSMUSG00000014039	Ripk4 // Prdm15	receptor-interacting serine-threonine kinase 4 // PR domain containing 15	downstream mmu-mir-802
2911	4	141225826	141226072	247	Yes	No	Yes	No	↓	-0.22	ENSMUSG00000028917	Plekhm2	pleckstrin homology domain containing, family M (with RUN domain) member 2	upstream mmu-mir-2139
2225	2	76543768	76543971	204	Yes	No	Yes	No	↓	-0.22	ENSMUSG00000002733 // ENSMUSG00000051747	Plekha3 // Ttn	pleckstrin homology domain-containing, family A (phosphoiNositide binding specific) member 3 // titin	downstream mmu-mir-10b
2456	3	28774557	28775005	449	Yes	No	Yes	No	↓	-0.21	ENSMUSG00000074655	Gm1527	predicted gene 1527	downstream mmu-mir-466q
1213	14	56094004	56094170	167	Yes	No	Yes	No	↓	-0.20	ENSMUSG00000022210	Dhrs4	dehydrogenase/reductase (SDR family) member 4	upstream mmu-mir-208b
1044	13	69757968	69758351	384	Yes	No	Yes	No	↓	-0.19	ENSMUSG00000021595	Nsun2	NoL1/NoP2/Sun domain family member 2	upstream mmu-mir-466f-4
1090	13	103564348	103564628	281	Yes	No	Yes	No	↓	-0.19	ENSMUSG00000021624 // ENSMUSG00000034751	Cd180 // Mast4	CD180 antigen // microtubule associated serine/threonine kinase family member 4	upstream mmu-mir-582
1166	14	34730914	34731450	537	Yes	No	Yes	No	↓	-0.18	ENSMUSG00000021943	Gdf10	growth differentiation factor 10	upstream mmu-mir-346
1177	14	35417539	35417811	273	Yes	No	Yes	No	↓	-0.18	ENSMUSG00000021799	Opn4	opsin 4 (melaNopsin)	upstream mmu-mir-346
2210	2	69549549	69549768	220	Yes	No	Yes	No	↓	-0.16	ENSMUSG00000027086	Fastkd1	FAST kinase domains 1	downstream mmu-mir-5115
570	11	58600336	58600587	252	Yes	No	Yes	No	↓	-0.16	ENSMUSG00000059504	Olfr314	olfactory receptor 314	upstream mmu-mir-5100
2926	4	148848668	148849202	535	Yes	No	Yes	No	↓	-0.15	ENSMUSG00000028992	Nmnat1	nicotinamide nucleotide adenylyltransferase 1	upstream mmu-mir-5616
3317	6	71097883	71098064	182	Yes	No	Yes	No	↓	-0.14	ENSMUSG00000054474	Thnsl2	threonine synthase-like 2 (bacterial)	downstream mmu-mir-468
1209	14	55534627	55534907	281	Yes	No	Yes	No	↓	-0.14	ENSMUSG00000022199	Slc22a17	solute carrier family 22 (organic cation transporter), member 17	downstream mmu-mir-208a
665	11	95117001	95117197	197	Yes	No	Yes	No	↓	-0.13	ENSMUSG00000020872	Tac4	tachykinin 4	downstream mmu-mir-3063
3204	5	139787258	139787791	534	Yes	No	Yes	No	↓	-0.10	ENSMUSG00000056413	Adap1	ArfGAP with dual PH domains 1	downstream mmu-mir-339
3589	7	96658688	96659035	348	Yes	No	Yes	No	↓	-0.10	ENSMUSG00000030623 // ENSMUSG00000039405	1700019G06Rik // Prss23	RIKEN cDNA 1700019G06 gene // protease, serine, 23	upstream mmu-mir-708
3418	6	125446559	125446809	251	Yes	No	Yes	No	↓	-0.10	ENSMUSG00000030342	Cd9	CD9 antigen	downstream mmu-mir-3098
1572	16	36915463	36915709	247	Yes	No	Yes	No	↓	-0.09	ENSMUSG00000022831 // ENSMUSG00000034243	Hcls1 // Golgb1	hematopoietic cell specific Lyn substrate 1 // golgi autoantigen, golgin subfamily b, macrogolgin 1	downstream mmu-mir-1947
1225	14	58141531	58141774	244	Yes	No	Yes	No	↓	-0.08	ENSMUSG00000050222	Il17d	interleukin 17D	upstream mmu-mir-3077
2207	2	69386514	69386730	217	Yes	No	Yes	No	↓	-0.08	ENSMUSG00000027070	Lrp2	low density lipoprotein receptor-related protein 2	downstream mmu-mir-5115
2128	2	4878461	4878773	313	Yes	No	Yes	No	↓	-0.07	ENSMUSG00000082795	Gm13193	predicted gene 13193	upstream mmu-mir-466m
1426	15	83955189	83955587	399	Yes	No	Yes	No	↓	-0.05	ENSMUSG00000018868	Pnpla5	patatin-like phospholipase domain containing 5	downstream mmu-mir-1249
2806	4	101387961	101388267	307	Yes	No	Yes	No	↓	-0.05	ENSMUSG00000057722	Lepr	leptin receptor	upstream mmu-mir-101a
779	12	4749851	4750016	166	Yes	No	Yes	No	↓	-0.05	ENSMUSG00000079177	4930417G10Rik	RIKEN cDNA 4930417G10 gene	upstream mmu-mir-3066
1217	14	56467479	56467680	202	Yes	No	Yes	No	↓	-0.03	ENSMUSG00000075592	Nynrin	NYN domain and retroviral integrase containing	upstream mmu-mir-208b
1877	18	42419323	42419639	317	Yes	No	Yes	No	↓	-0.01	ENSMUSG00000024493	Lars	leucyl-tRNA synthetase	downstream mmu-mir-5097
770	11	120591735	120591982	248	Yes	No	Yes	No	↓	0.00	ENSMUSG00000025150	Cbr2	carbonyl reductase 2	upstream mmu-mir-338
3567	7	73909608	73910201	594	No	Yes	No	Yes	↑	0.00	ENSMUSG00000030510	Lass3	LAG1 homolog, ceramide synthase 3	downstream mmu-mir-211
2153	2	24776424	24777489	1066	No	Yes	No	Yes	↑	0.00	ENSMUSG00000036893	Ehmt1	euchromatic histone methyltransferase 1	upstream mmu-mir-3087
1037	13	67911042	67911446	405	No	Yes	No	Yes	↑	0.00	ENSMUSG00000030446	Zfp273	zinc finger protein 273	upstream mmu-mir-466f-4
2391	2	166885481	166885643	163	No	Yes	No	Yes	↑	0.01	ENSMUSG00000039501	Znfx1	zinc finger, NFX1-type containing 1	downstream mmu-mir-296

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	Chr.	start	end	width	C	PS	C	PS	effect dir.	logFC	ENSEMBL ID	symbol	gene name	next miRNA
808	12	52849737	52849976	240	No	Yes	No	Yes	↑	0.01	ENSMUSG00000020954 // ENSMUSG00000035247	Strn3 // Hectd1	striatin, calmodulin binding protein 3 // HECT domain containing 1	downstream mmu-mir-1892
382	10	87610930	87611132	203	No	Yes	No	Yes	↑	0.01	ENSMUSG00000035351	Nup37	nucleoporin 37	downstream mmu-mir-135a-2
3150	5	116376067	116376466	400	No	Yes	No	Yes	↑	0.02	ENSMUSG00000029516	Cit	citron	downstream mmu-mir-701
4088	9	104072319	104072594	276	No	Yes	No	Yes	↑	0.02	ENSMUSG00000032560	Dnajc13	DnaJ (Hsp40) homolog, subfamily C, member 13	upstream mmu-mir-2136
2044	19	41157150	41157501	352	No	Yes	No	Yes	↑	0.02	ENSMUSG00000050121 // ENSMUSG00000025013	Opalin // Tll2	oligodendrocytic myelin paraNodal and inner loop protein // tolloid-like 2	downstream mmu-mir-3085
1564	16	34685038	34685283	246	No	Yes	No	Yes	↑	0.02	ENSMUSG00000022833	Ccdc14	coiled-coil domain containing 14	downstream mmu-mir-1947
3488	7	25666274	25666504	231	No	Yes	No	Yes	↑	0.02	ENSMUSG00000040952	Rps19	ribosomal protein S19	downstream mmu-mir-3101
705	11	101613484	101613726	243	No	Yes	No	Yes	↑	0.02	ENSMUSG00000034931	Dhx8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	downstream mmu-mir-5119
1854	18	37502614	37502947	334	No	Yes	No	Yes	↑	0.02	ENSMUSG00000045062	Pcdhb7	protocadherin beta 7	downstream mmu-mir-1949
3492	7	26387031	26387393	363	No	Yes	No	Yes	↑	0.02	ENSMUSG00000074261	Gm7092	predicted gene 7092	downstream mmu-mir-3101
2998	5	44370699	44370911	213	No	Yes	No	Yes	↑	0.03	ENSMUSG00000048373	Fgfbp1	fibroblast growth factor binding protein 1	upstream mmu-mir-218-1
298	10	31133482	31133973	492	No	Yes	No	Yes	↑	0.03	ENSMUSG00000000296	Tpd52l1	tumor protein D52-like 1	upstream mmu-mir-3473b
3842	8	95261425	95261666	242	No	Yes	No	Yes	↑	0.03	ENSMUSG00000078967	Gm3272	predicted pseudogene 3272	upstream mmu-mir-138-2
3475	7	6683366	6683635	270	No	Yes	No	Yes	↑	0.03	ENSMUSG00000051527	Usp29	ubiquitin specific peptidase 29	upstream mmu-mir-3099
1716	17	36120733	36120966	234	No	Yes	No	Yes	↑	0.03	ENSMUSG00000038500 // ENSMUSG00000024429	Prr3 // Gnl1	proline-rich polypeptide 3 // guanine nucleotide binding protein-like 1	upstream mmu-mir-877
4008	9	57182026	57182403	378	No	Yes	No	Yes	↑	0.03	ENSMUSG00000066626	Gm5121	predicted gene 5121	downstream mmu-mir-5710
1573	16	36931815	36932065	251	No	Yes	No	Yes	↑	0.03	ENSMUSG00000022831 // ENSMUSG00000034243	Hcls1 // Golgb1	hematopoietic cell specific Lyn substrate 1 // golgi autoantigen, golgin subfamily b, macrogolgin 1	downstream mmu-mir-1947
2617	3	123143853	123144117	265	No	Yes	No	Yes	↑	0.03	ENSMUSG00000027978	Prss12	protease, serine, 12 neurotrypsin (motopsin)	upstream mmu-mir-760
2682	3	152336353	152336671	319	No	Yes	No	Yes	↑	0.03	ENSMUSG00000039058	Ak5	adenylate kinase 5	upstream mmu-mir-3963
2481	3	51497241	51497532	292	No	Yes	No	Yes	↑	0.04	ENSMUSG00000074603 // ENSMUSG00000061143	Gm10729 // Maml3	predicted gene 10729 // mastermind like 3 (Drosophila)	downstream mmu-mir-1897
2509	3	68492517	68492909	393	No	Yes	No	Yes	↑	0.04	ENSMUSG00000027776	Il12a	interleukin 12a	upstream mmu-mir-15b
1470	15	96849252	96849630	379	No	Yes	No	Yes	↑	0.04	ENSMUSG00000022464	Slc38a4	solute carrier family 38, member 4	upstream mmu-mir-1941
1309	14	122009137	122009513	377	No	Yes	No	Yes	↑	0.04	ENSMUSG00000025557 // ENSMUSG00000025558	Slc15a1 // Dock9	solute carrier family 15 (oligopeptide transporter), member 1 // dedicator of cytokinesis 9	downstream mmu-mir-92a-1
1987	19	21875988	21876273	286	No	Yes	No	Yes	↑	0.04	ENSMUSG00000024754	Tmem2	transmembrane protein 2	upstream mmu-mir-204
3686	7	142286142	142286654	513	No	Yes	No	Yes	↑	0.05	ENSMUSG00000047543 // ENSMUSG00000058325	--- // Dock1	NA // dedicator of cytokinesis 1	upstream mmu-mir-1962
3429	6	129803965	129804241	277	No	Yes	No	Yes	↑	0.05	ENSMUSG00000014543	Klra17	killer cell lectin-like receptor, subfamily A, member 17	downstream mmu-mir-680-1
1251	14	70921915	70922194	280	No	Yes	No	Yes	↑	0.05	ENSMUSG00000022097	Sftpc	surfactant associated protein C	downstream mmu-mir-320
2398	2	168580463	168580784	322	No	Yes	No	Yes	↑	0.05	ENSMUSG00000027547	Sall4	sal-like 4 (Drosophila)	downstream mmu-mir-296
1376	15	68023036	68023471	436	No	Yes	No	Yes	↑	0.05	ENSMUSG00000022335	Zfat	zinc finger and AT hook domain containing	downstream mmu-mir-30b
266	10	19430465	19430757	293	No	Yes	No	Yes	↑	0.05	ENSMUSG00000020007	Il20ra	interleukin 20 receptor, alpha	downstream mmu-mir-5104
1048	13	79092752	79093067	316	No	Yes	No	Yes	↑	0.05	ENSMUSG00000065339	---	NA	downstream mmu-mir-682
911	12	112948677	112948973	297	No	Yes	No	Yes	↑	0.05	ENSMUSG00000049792	Bag5	BCL2-associated athaNogene 5	upstream mmu-mir-3073
1079	13	99383774	99384423	650	No	Yes	No	Yes	↑	0.05	ENSMUSG00000074750	---	NA	downstream mmu-mir-1940

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	Chr.	start	end	width	C	PS	C	PS	effect dir.	logFC	ENSEMBL ID	symbol	gene name	next miRNA
666	11	95449473	95449949	477	No	Yes	No	Yes	↑	0.06	ENSMUSG00000000120	Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	downstream mmu-mir-3063
882	12	101127939	101128352	414	No	Yes	No	Yes	↑	0.06	ENSMUSG00000021177	Tdp1	tyrosyl-DNA phosphodiesterase 1	downstream mmu-mir-1190
1906	18	63108516	63109633	1118	No	Yes	No	Yes	↑	0.06	ENSMUSG00000071847	Apcdd1	adeNomatosis polyposis coli down-regulated 1	upstream mmu-mir-143
1580	16	43761565	43761948	384	No	Yes	No	Yes	↑	0.06	ENSMUSG00000022705	Drd3	dopamine receptor D3	downstream mmu-mir-568
3521	7	35445146	35445494	349	No	Yes	No	Yes	↑	0.06	ENSMUSG00000030499	Kctd15	potassium channel tetramerisation domain containing 15	downstream mmu-mir-1964
319	10	56216896	56217111	216	No	Yes	No	Yes	↑	0.06	ENSMUSG00000050953	Gja1	gap junction protein, alpha 1	upstream mmu-mir-466j
2522	3	82812246	82812531	286	No	Yes	No	Yes	↑	0.06	ENSMUSG00000033860	Fgg	fibriNogen gamma chain	upstream mmu-mir-466k
996	13	50559259	50559862	604	No	Yes	No	Yes	↑	0.06	ENSMUSG00000071909	Gm806	predicted gene 806	downstream mmu-mir-683-1
554	11	53450789	53451099	311	No	Yes	No	Yes	↑	0.06	ENSMUSG00000020383	Il13	interleukin 13	downstream mmu-mir-3061
1184	14	47013375	47013576	202	No	Yes	No	Yes	↑	0.07	ENSMUSG00000021835	Bmp4	bone morphogenetic protein 4	upstream mmu-mir-5131
2047	19	41899049	41899237	189	No	Yes	No	Yes	↑	0.07	ENSMUSG00000067199	Frat1	frequently rearranged in advanced T cell lymphomas	downstream mmu-mir-3085
241	10	5833726	5833961	236	No	Yes	No	Yes	↑	0.07	ENSMUSG00000019767	Gm221	predicted gene 221	upstream mmu-mir-5104
1884	18	48206052	48206319	268	No	Yes	No	Yes	↑	0.07	ENSMUSG00000059040	Gm5506	predicted gene 5506	downstream mmu-mir-5097
1659	17	8589782	8590059	278	No	Yes	No	Yes	↑	0.07	ENSMUSG00000058159	T2	brachyury 2	upstream mmu-mir-692-1
3297	6	48938474	48938862	389	No	Yes	No	Yes	↑	0.08	ENSMUSG00000039215	Svs1	seminal vesicle secretory protein 1	upstream mmu-mir-704
3107	5	105946140	105946378	239	No	Yes	No	Yes	↑	0.08	ENSMUSG00000054720	Lrrc8c	leucine rich repeat containing 8 family, member C	downstream mmu-mir-5619
1979	19	16034141	16034557	417	No	Yes	No	Yes	↑	0.08	ENSMUSG00000041491	Cep78	centrosomal protein 78	upstream mmu-mir-204
3379	6	101311897	101312124	228	No	Yes	No	Yes	↑	0.09	ENSMUSG00000035357	Pdzrn3	PDZ domain containing RING finger 3	upstream mmu-mir-705
3186	5	135826782	135827588	807	No	Yes	No	Yes	↑	0.09	ENSMUSG00000040013	Fkbp6	FK506 binding protein 6	downstream mmu-mir-721
258	10	14162696	14163007	312	No	Yes	No	Yes	↑	0.09	ENSMUSG00000071532 // ENSMUSG00000039116	Gm10335 // Gpr126	predicted gene 10335 // G protein-coupled receptor 126	downstream mmu-mir-5104
1675	17	24006224	24006528	305	No	Yes	No	Yes	↑	0.09	ENSMUSG00000024116	Prss21	protease, serine, 21	downstream mmu-mir-5125
3681	7	140893351	140893626	276	No	Yes	No	Yes	↑	0.09	ENSMUSG00000030979	Uros	uroporphyriNogen III synthase	upstream mmu-mir-1962
2771	4	59006179	59006341	163	No	Yes	No	Yes	↑	0.09	ENSMUSG00000028378	Ptgr1	prostaglandin reductase 1	upstream mmu-mir-3095
2181	2	52146535	52146897	363	No	Yes	No	Yes	↑	0.09	ENSMUSG00000026950	Neb	nebulin	upstream mmu-mir-5129
110	1	132835994	132836195	202	No	Yes	No	Yes	↑	0.09	ENSMUSG00000016524	Il19	interleukin 19	upstream mmu-mir-135b
1644	16	93865780	93866055	276	No	Yes	No	Yes	↑	0.10	ENSMUSG00000022945 // ENSMUSG00000039456	Chaf1b // Morc3	chromatin assembly factor 1, subunit B (p60) // microrchidia 3	downstream mmu-mir-802
1430	15	84278991	84279417	427	No	Yes	No	Yes	↑	0.10	ENSMUSG00000062760	1810041L15Rik	RIKEN cDNA 1810041L15 gene	downstream mmu-mir-1249
3158	5	118312626	118312968	343	No	Yes	No	Yes	↑	0.10	ENSMUSG00000029361	Nos1	nitric oxide synthase 1, neuronal	downstream mmu-mir-701
2780	4	69515070	69515539	470	No	Yes	No	Yes	↑	0.10	ENSMUSG00000080879 // ENSMUSG00000061015	--- // ---	NA // NA	downstream mmu-mir-455
2558	3	95999025	95999383	359	No	Yes	No	Yes	↑	0.10	ENSMUSG00000015943 // ENSMUSG00000038486	Bola1 // Sv2a	bolA-like 1 (E. coli) // synaptic vesicle glycoprotein 2 a	downstream mmu-mir-190b
3838	8	91573421	91573661	241	No	Yes	No	Yes	↑	0.10	ENSMUSG00000031665	Sall1	sal-like 1 (Drosophila)	upstream mmu-mir-3074-2
3974	9	37058270	37058666	397	No	Yes	No	Yes	↑	0.10	ENSMUSG00000066757 // ENSMUSG00000032122	--- // Slc37a2	NA // solute carrier family 37 (glycerol-3-phosphate transporter), member 2	upstream mmu-mir-100
2029	19	36808219	36808558	340	No	Yes	No	Yes	↑	0.10	ENSMUSG00000067279	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	downstream mmu-mir-1950
2256	2	86990202	86990477	276	No	Yes	No	Yes	↑	0.11	ENSMUSG00000075158	Olfr1111	olfactory receptor 1111	upstream mmu-mir-130a
3503	7	29418646	29419250	605	No	Yes	No	Yes	↑	0.11	ENSMUSG00000037469	C330005M16Rik	RIKEN cDNA C330005M16 gene	downstream mmu-mir-1963

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	**Chr.**	**start**	**end**	**width**	**C**	**PS**	**C**	**PS**	**effect dir.**	**logFC**	**ENSEMBL ID**	**symbol**	**gene name**	**next miRNA**
234	1	193732789	193733167	379	No	Yes	No	Yes	↑	0.11	ENSMUSG00000055833 // ENSMUSG00000037434	1700034H15Rik // Slc30a1	RIKEN cDNA 1700034H15 gene // solute carrier family 30 (zinc transporter), member 1	downstream mmu-mir-3473c
329	10	62407000	62407211	212	No	Yes	No	Yes	↑	0.11	ENSMUSG00000036875 // ENSMUSG00000071253	Dna2 // Slc25a16	DNA replication helicase 2 homolog (yeast) // solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16	downstream mmu-mir-5108
4121	9	115162948	115163232	285	No	Yes	No	Yes	↑	0.11	ENSMUSG00000032438 // ENSMUSG00000032437	--- // Stt3b	NA // STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	upstream mmu-mir-467h
1848	18	37135322	37135554	233	No	Yes	No	Yes	↑	0.11	ENSMUSG00000079714 // ENSMUSG00000007440	--- // Pcdha9	NA // protocadherin alpha subfamily C, 1	downstream mmu-mir-1949
2527	3	83075469	83075924	456	No	Yes	No	Yes	↑	0.11	ENSMUSG00000074517	Gm10710	predicted gene 10710	upstream mmu-mir-466k
411	10	99000422	99000988	567	No	Yes	No	Yes	↑	0.11	ENSMUSG00000044633	B530045E10Rik	RIKEN cDNA B530045E10 gene	downstream mmu-mir-3966
3442	6	137602579	137602746	168	No	Yes	No	Yes	↑	0.11	ENSMUSG00000015766	Eps8	epidermal growth factor receptor pathway substrate 8	downstream mmu-mir-680-1
1291	14	119030238	119030583	346	No	Yes	No	Yes	↑	0.11	ENSMUSG00000064644 // ENSMUSG00000032849	// Abcc4	U6 spliceosomal RNA // ATP-binding cassette, sub-family C (CFTR/MRP), member 4	downstream mmu-mir-92a-1
2007	19	26827128	26827469	342	No	Yes	No	Yes	↑	0.11	ENSMUSG00000074913 // ENSMUSG00000024921	Gm815 // Smarca2	predicted gene 815 // SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	upstream mmu-mir-3084
144	1	152604470	152604867	398	No	Yes	No	Yes	↑	0.11	ENSMUSG00000057399 // ENSMUSG00000066842	--- // Hmcn1	NA // hemicentin 1	upstream mmu-mir-488
1808	17	87155284	87155719	436	No	Yes	No	Yes	↑	0.12	ENSMUSG00000024140	Epas1	endothelial PAS domain protein 1	upstream mmu-mir-1195
1312	14	122575495	122575664	170	No	Yes	No	Yes	↑	0.12	ENSMUSG00000025545	Clybl	citrate lyase beta like	downstream mmu-mir-92a-1
2058	19	43986577	43986889	313	No	Yes	No	Yes	↑	0.12	ENSMUSG00000025195	Dnmbp	dynamin binding protein	upstream mmu-mir-5114
3144	5	115873837	115874905	1069	No	Yes	No	Yes	↑	0.12	ENSMUSG00000054256	Msi1	Musashi homolog 1(Drosophila)	downstream mmu-mir-701
2619	3	123282573	123282917	345	No	Yes	No	Yes	↑	0.12	ENSMUSG00000065113 // ENSMUSG00000027977	--- // Ndst3	NA // N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	upstream mmu-mir-760
1891	18	52854519	52855185	667	No	Yes	No	Yes	↑	0.12	ENSMUSG00000053624	Gykl1	glycerol kinase-like 1	upstream mmu-mir-5107
3807	8	58452572	58453004	433	No	Yes	No	Yes	↑	0.12	ENSMUSG00000038257	Glra3	glycine receptor, alpha 3 subunit	downstream mmu-mir-710
648	11	89862649	89862853	205	No	Yes	No	Yes	↑	0.12	ENSMUSG00000069765 // ENSMUSG00000020553	--- // Pctp	NA // phosphatidylcholine transfer protein	downstream mmu-mir-378b
3267	6	31346438	31346681	244	No	Yes	No	Yes	↑	0.12	ENSMUSG00000025609	Mkln1	muskelin 1, intracellular mediator containing kelch motifs	upstream mmu-mir-29b-1
14	1	20807895	20808068	174	No	Yes	No	Yes	↑	0.12	ENSMUSG00000041859	Mcm3	minichromosome maintenance deficient 3 (S. cerevisiae)	downstream mmu-mir-133b
643	11	87754336	87754505	170	No	Yes	No	Yes	↑	0.12	ENSMUSG00000044639	Gm11507	predicted gene 11507	downstream mmu-mir-142
1444	15	89205614	89205817	204	No	Yes	No	Yes	↑	0.12	ENSMUSG00000022615	Tymp	thymidine phosphorylase	downstream mmu-let-7b
3164	5	122803144	122803311	168	No	Yes	No	Yes	↑	0.12	ENSMUSG00000038569	Rad9b	RAD9 homolog B (S. cerevisiae)	downstream mmu-mir-701
971	13	41330037	41330823	787	No	Yes	No	Yes	↑	0.12	ENSMUSG00000021364	Elovl2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	downstream mmu-mir-5124
1507	15	100326264	100326870	607	No	Yes	No	Yes	↑	0.12	ENSMUSG00000044636	Csrnp2	cysteine-serine-rich nuclear protein 2	upstream mmu-mir-1941
1352	15	37100579	37100981	403	No	Yes	No	Yes	↑	0.13	ENSMUSG00000022286	Grhl2	grainyhead-like 2 (Drosophila)	upstream mmu-mir-875
3021	5	65614403	65614878	476	No	Yes	No	Yes	↑	0.13	ENSMUSG00000037890	Wdr19	WD repeat domain 19	downstream mmu-mir-574

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	Chr.	start	end	width	C	PS	C	PS	effect dir.	logFC	ENSEMBL ID	symbol	gene name	next miRNA
2846	4	119205358	119205848	491	No	Yes	No	Yes	↑	0.13	ENSMUSG00000065240 // ENSMUSG00000062260	--- // ---	NA // NA	downstream mmu-mir-1957
878	12	99923550	99923778	229	No	Yes	No	Yes	↑	0.13	ENSMUSG00000021009	Ptpn21	protein tyrosine phosphatase, Non-receptor type 21	downstream mmu-mir-1190
4078	9	99511591	99511868	278	No	Yes	No	Yes	↑	0.13	ENSMUSG00000037953	A4gnt	alpha-1,4-N-acetylglucosaminyltransferase	upstream mmu-mir-2136
2458	3	30645640	30645882	243	No	Yes	No	Yes	↑	0.13	ENSMUSG00000051860	Samd7	sterile alpha motif domain containing 7	downstream mmu-mir-551b
2873	4	132357714	132358054	341	No	Yes	No	Yes	↑	0.13	ENSMUSG00000081647	Gm13022	predicted gene 13022	upstream mmu-mir-5122
385	10	87964190	87964417	228	No	Yes	No	Yes	↑	0.13	ENSMUSG00000060002	Chpt1	choline phosphotransferase 1	downstream mmu-mir-135a-2
3374	6	99674161	99674602	442	No	Yes	No	Yes	↑	0.13	ENSMUSG00000030069	Prok2	prokineticin 2	upstream mmu-mir-705
2493	3	54863075	54863499	425	No	Yes	No	Yes	↑	0.14	ENSMUSG00000027793	Ccna1	cyclin A1	upstream mmu-mir-15b
566	11	58193871	58194338	468	No	Yes	No	Yes	↑	0.14	ENSMUSG00000013643	2210415F13Rik	RIKEN cDNA 2210415F13 gene	upstream mmu-mir-5100
704	11	101484122	101484320	199	No	Yes	No	Yes	↑	0.14	ENSMUSG00000065767		U2 spliceosomal RNA	downstream mmu-mir-5119
697	11	100566819	100567318	500	No	Yes	No	Yes	↑	0.14	ENSMUSG00000017830 // ENSMUSG00000020918	Dhx58 // Kat2a	DEXH (Asp-Glu-X-His) box polypeptide 58 // K(lysine) acetyltransferase 2A	downstream mmu-mir-5119
361	10	79110753	79111007	255	No	Yes	No	Yes	↑	0.14	ENSMUSG00000035963	Odf3l2	outer dense fiber of sperm tails 3-like 2	upstream mmu-mir-1982
1311	14	122229694	122230394	701	No	Yes	No	Yes	↑	0.14	ENSMUSG00000041765	Ubac2	ubiquitin associated domain containing 2	downstream mmu-mir-92a-1
4074	9	98502538	98503127	590	No	Yes	No	Yes	↑	0.14	ENSMUSG00000032459	Mrps22	mitochondrial ribosomal protein S22	upstream mmu-mir-2136
848	12	77142793	77143118	326	No	Yes	No	Yes	↑	0.14	ENSMUSG00000063450	Syne2	synaptic nuclear envelope 2	downstream mmu-mir-5101
3632	7	122316794	122317003	210	No	Yes	No	Yes	↑	0.15	ENSMUSG00000046411	Gm6816	predicted gene 6816	upstream mmu-mir-762
2027	19	36193238	36193603	366	No	Yes	No	Yes	↑	0.15	ENSMUSG00000024803	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	downstream mmu-mir-1950
3990	9	44189296	44189647	352	No	Yes	No	Yes	↑	0.15	ENSMUSG00000032115	Hyou1	hypoxia up-regulated 1	downstream mmu-mir-125b-1
4127	9	117261163	117261546	384	No	Yes	No	Yes	↑	0.15	ENSMUSG00000039607	Rbms3	RNA binding motif, single stranded interacting protein	upstream mmu-mir-26a-1
1881	18	46515779	46516173	395	No	Yes	No	Yes	↑	0.15	ENSMUSG00000080355	---	NA	downstream mmu-mir-5097
1422	15	83262952	83263203	252	No	Yes	No	Yes	↑	0.15	ENSMUSG00000049414 // ENSMUSG00000016664	Gm5417 // Pacsin2	predicted gene 5417 // protein kinase C and casein kinase substrate in neurons 2	upstream mmu-mir-3080
4024	9	64229192	64229640	449	No	Yes	No	Yes	↑	0.15	ENSMUSG00000036466	Megf11	multiple EGF-like-domains 11	upstream mmu-mir-5133
606	11	69290421	69290898	478	No	Yes	No	Yes	↑	0.15	ENSMUSG00000018476 // ENSMUSG00000005237	Kdm6b // Dnahc2	KDM1 lysine (K)-specific demethylase 6B // dynein, axonemal, heavy chain 2	downstream mmu-mir-467f
1319	15	6530516	6530757	242	No	Yes	No	Yes	↑	0.15	ENSMUSG00000022148	Fyb	FYN binding protein	upstream mmu-mir-1898
3573	7	82870878	82871179	302	No	Yes	No	Yes	↑	0.15	ENSMUSG00000076961 // ENSMUSG00000066406	// Akap13	// A kinase (PRKA) anchor protein 13	upstream mmu-mir-7a-2
1107	13	112601065	112601546	482	No	Yes	No	Yes	↑	0.16	ENSMUSG00000021754	Map3k1	mitogen-activated protein kinase kinase kinase 1	upstream mmu-mir-449c
898	12	109722642	109722991	350	No	Yes	No	Yes	↑	0.16	ENSMUSG00000082203 // ENSMUSG00000058070	Gm15636 // Eml1	predicted gene 15636 // echiNoderm microtubule associated protein like 1	upstream mmu-mir-342
4080	9	99617339	99617897	559	No	Yes	No	Yes	↑	0.16	ENSMUSG00000032473	Cldn18	claudin 18	upstream mmu-mir-2136
2395	2	167491630	167491871	242	No	Yes	No	Yes	↑	0.16	ENSMUSG00000019755	---	NA	downstream mmu-mir-296
1739	17	46793530	46793901	372	No	Yes	No	Yes	↑	0.16	ENSMUSG00000038545	Cul7	cullin 7	downstream mmu-mir-693
3584	7	89131205	89131697	493	No	Yes	No	Yes	↑	0.16	ENSMUSG00000052779 // ENSMUSG00000025105	4833418N17Rik // Bnc1	RIKEN cDNA 4833418N17 gene // basonuclin 1	downstream mmu-mir-1839
3031	5	72908087	72908363	277	No	Yes	No	Yes	↑	0.16	ENSMUSG00000005220 // ENSMUSG00000072889	Corin // Nfxl1	corin // nuclear transcription factor, X-box binding-like 1	upstream mmu-mir-5098

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	Chr.	start	end	width	C	PS	C	PS	effect dir.	logFC	ENSEMBL ID	symbol	gene name	next miRNA
2694	4	3948925	3949264	340	No	Yes	No	Yes	↑	0.17	ENSMUSG00000028236	Sdr16c5	short chain dehydrogenase/reductase family 16C, member 5	downstream mmu-mir-3471-2
2357	2	158357101	158357370	270	No	Yes	No	Yes	↑	0.17	ENSMUSG00000074625	Arhgap40	Rho GTPase activating protein 40	upstream mmu-mir-3474
1594	16	50593455	50593692	238	No	Yes	No	Yes	↑	0.17	ENSMUSG00000050685	Ccdc54	coiled-coil domain containing 54	upstream mmu-mir-5118
4073	9	97936180	97936420	241	No	Yes	No	Yes	↑	0.17	ENSMUSG00000032452	Clstn2	calsyntenin 2	upstream mmu-mir-2136
334	10	62919859	62920167	309	No	Yes	No	Yes	↑	0.17	ENSMUSG00000060843	Ctnna3	catenin (cadherin associated protein), alpha 3	downstream mmu-mir-5108
3312	6	64676526	64676756	231	No	Yes	No	Yes	↑	0.17	ENSMUSG00000073043	Atoh1	atonal homolog 1 (Drosophila)	upstream mmu-mir-196b
1558	16	33720634	33721023	390	No	Yes	No	Yes	↑	0.17	ENSMUSG00000075254 // ENSMUSG00000035500	Heg1 // ---	HEG homolog 1 (zebrafish) // NA	downstream mmu-mir-1947
446	10	120203054	120203709	656	No	Yes	No	Yes	↑	0.17	ENSMUSG00000044544	4921513I03Rik	RIKEN cDNA 4921513I03 gene	upstream mmu-mir-763
3036	5	73125441	73125606	166	No	Yes	No	Yes	↑	0.17	ENSMUSG00000054892	Txk	TXK tyrosine kinase	upstream mmu-mir-5098
3486	7	25607024	25607260	237	No	Yes	No	Yes	↑	0.17	ENSMUSG00000011350	Gm5893	predicted gene 5893	downstream mmu-mir-3101
1112	13	114137153	114137688	536	No	Yes	No	Yes	↑	0.18	ENSMUSG00000021763	BC067074	cDNA sequence BC067074	downstream mmu-mir-449a
3792	8	44710589	44711018	430	No	Yes	No	Yes	↑	0.18	ENSMUSG00000050190	Gm5346	predicted gene 5346	upstream mmu-mir-383
1362	15	56529643	56530037	395	No	Yes	No	Yes	↑	0.18	ENSMUSG00000022367	Has2	hyaluronan synthase 2	upstream mmu-mir-28c
788	12	14937154	14937432	279	No	Yes	No	Yes	↑	0.18	ENSMUSG00000064386		U6 spliceosomal RNA	upstream mmu-mir-3066
1502	15	99762022	99762403	382	No	Yes	No	Yes	↑	0.18	ENSMUSG00000045350	1700030F18Rik	RIKEN cDNA 1700030F18 gene	upstream mmu-mir-1941
1113	13	114409629	114410176	548	No	Yes	No	Yes	↑	0.18	ENSMUSG00000042364	Snx18	sorting nexin 18	downstream mmu-mir-449a
1725	17	43405594	43405872	279	No	Yes	No	Yes	↑	0.18	ENSMUSG00000041293	Gpr110	G protein-coupled receptor 110	upstream mmu-mir-693
2876	4	133803501	133803921	421	No	Yes	No	Yes	↑	0.18	ENSMUSG00000028840	Zfp593	zinc finger protein 593	downstream mmu-mir-5122
271	10	20602373	20602741	369	No	Yes	No	Yes	↑	0.19	ENSMUSG00000019986	Ahi1	Abelson helper integration site 1	downstream mmu-mir-5104
2076	19	47204376	47204624	249	No	Yes	No	Yes	↑	0.19	ENSMUSG00000033033 // ENSMUSG00000025047	Calhm2 // Pdcd11	calcium homeostasis modulator 2 // programmed cell death 11	downstream mmu-mir-146b
402	10	93657585	93657974	390	No	Yes	No	Yes	↑	0.19	ENSMUSG00000020022 // ENSMUSG00000005897	Ndufa12 // Nr2c1	NADH dehydrogenase (ubiquiNone) 1 alpha subcomplex, 12 // nuclear receptor subfamily 2, group C, member 1	upstream mmu-mir-331
1668	17	15461631	15462099	469	No	Yes	No	Yes	↑	0.19	ENSMUSG00000073453	---	NA	upstream mmu-mir-99b
2121	19	59015598	59015868	271	No	Yes	No	Yes	↑	0.19	ENSMUSG00000048029	ENo4	eNolase 4	upstream mmu-mir-3086
3128	5	111648319	111648886	568	No	Yes	No	Yes	↑	0.20	ENSMUSG00000072734 // ENSMUSG00000033209	--- // Ttc28	NA // tetratricopeptide repeat domain 28	downstream mmu-mir-701
161	1	160288942	160289246	305	No	Yes	No	Yes	↑	0.20	ENSMUSG00000004031	Fam5b	family with sequence similarity 5, member B	upstream mmu-mir-488
1375	15	68012383	68012847	465	No	Yes	No	Yes	↑	0.20	ENSMUSG00000022335	Zfat	zinc finger and AT hook domain containing	downstream mmu-mir-30b
1169	14	34899322	34899697	376	No	Yes	No	Yes	↑	0.20	ENSMUSG00000021950	Anxa8	annexin A8	upstream mmu-mir-346
2069	19	44618003	44618500	498	No	Yes	No	Yes	↑	0.20	ENSMUSG00000051984	Sec31b	Sec31 homolog B (S. cerevisiae)	downstream mmu-mir-5114
46	1	56693175	56693340	166	No	Yes	No	Yes	↑	0.20	ENSMUSG00000045336	Hsfy2	heat shock transcription factor, Y linked 2	downstream mmu-mir-1928
141	1	152270670	152270996	327	No	Yes	No	Yes	↑	0.20	ENSMUSG00000006010 // ENSMUSG00000006005	BC003331 // Tpr	cDNA sequence BC003331 // translocated promoter region	upstream mmu-mir-488
456	10	121044448	121044882	435	No	Yes	No	Yes	↑	0.21	ENSMUSG00000034667	Xpot	exportin, tRNA (nuclear export receptor for tRNAs)	upstream mmu-mir-763
801	12	36818451	36818624	174	No	Yes	No	Yes	↑	0.21	ENSMUSG00000059301	Gm5434	predicted gene 5434	upstream mmu-mir-5099
1538	16	21471098	21471306	209	No	Yes	No	Yes	↑	0.21	ENSMUSG00000033653	Vps8	vacuolar protein sorting 8 homolog (S. cerevisiae)	downstream mmu-mir-1224
3223	5	147764324	147764649	326	No	Yes	No	Yes	↑	0.21	ENSMUSG00000016503 // ENSMUSG00000016510	Gtf3a // Mtif3	general transcription factor III A // mitochondrial translational initiation factor 3	downstream mmu-mir-5105
2677	3	151097251	151097526	276	No	Yes	No	Yes	↑	0.21	ENSMUSG00000039167	Eltd1	EGF, latrophilin seven transmembrane domain containing 1	upstream mmu-mir-3963

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	**Chr.**	**start**	**end**	**width**	**C**	**PS**	**C**	**PS**	**effect dir.**	**logFC**	**ENSEMBL ID**	**symbol**	**gene name**	**next miRNA**
1841	18	34607244	34607481	238	No	Yes	No	Yes	↑	0.21	ENSMUSG00000014503 // ENSMUSG00000036501	Pkd2l2 // Fam13b	polycystic kidney disease 2-like 2 // family with sequence similarity 13, member B	upstream mmu-mir-1949
403	10	94411381	94412198	818	No	Yes	No	Yes	↑	0.21	ENSMUSG00000074785	Plxnc1	plexin C1	downstream mmu-mir-3058
3127	5	111606607	111606774	168	No	Yes	No	Yes	↑	0.21	ENSMUSG00000072734 // ENSMUSG00000033209	--- // Ttc28	NA // tetratricopeptide repeat domain 28	downstream mmu-mir-701
1344	15	27616554	27616952	399	No	Yes	No	Yes	↑	0.21	ENSMUSG00000056069	Fam105a	family with sequence similarity 105, member A	downstream mmu-mir-3964
2399	2	168808365	168808848	484	No	Yes	No	Yes	↑	0.22	ENSMUSG00000027551	Zfp64	zinc finger protein 64	downstream mmu-mir-296
3174	5	125255372	125256056	685	No	Yes	No	Yes	↑	0.22	ENSMUSG00000051869	---	NA	upstream mmu-mir-3965
2118	19	58744425	58744760	336	No	Yes	No	Yes	↑	0.22	ENSMUSG00000046008	Pnlip	pancreatic lipase	downstream mmu-mir-3086
2261	2	91288835	91289186	352	No	Yes	No	Yes	↑	0.22	ENSMUSG00000040591	1110051M20Rik	RIKEN cDNA 1110051M20 gene	upstream mmu-mir-1955
3066	5	86627049	86627217	169	No	Yes	No	Yes	↑	0.22	ENSMUSG00000029255	Gnrhr	gonadotropin releasing hormone receptor	downstream mmu-mir-3969
769	11	120481709	120482018	310	No	Yes	No	Yes	↑	0.22	ENSMUSG00000025137 // ENSMUSG00000025138	Pcyt2 // Sirt7	phosphate cytidylyltransferase 2, ethaNolamine // sirtuin 7 (silent mating type information regulation 2, homolog) 7 (S. cerevisiae)	upstream mmu-mir-338
1797	17	80743120	80743409	290	No	Yes	No	Yes	↑	0.23	ENSMUSG00000054901	Arhgef33	Rho guanine nucleotide exchange factor (GEF) 33	upstream mmu-mir-1195
949	13	26405315	26406249	935	No	Yes	No	Yes	↑	0.23	ENSMUSG00000084358	Gm11352	predicted gene 11352	upstream mmu-mir-1983
1428	15	84176876	84177219	344	No	Yes	No	Yes	↑	0.24	ENSMUSG00000022439	Parvg	parvin, gamma	downstream mmu-mir-1249
216	1	186630697	186631016	320	No	Yes	No	Yes	↑	0.24	ENSMUSG00000026621	Mosc1	MOCO sulphurase C-terminal domain containing 1	downstream mmu-mir-1981
1940	18	79055340	79055802	463	No	Yes	No	Yes	↑	0.24	ENSMUSG00000024548	Setbp1	SET binding protein 1	downstream mmu-mir-5127
3837	8	91572848	91573302	455	No	Yes	No	Yes	↑	0.24	ENSMUSG00000031665	Sall1	sal-like 1 (Drosophila)	upstream mmu-mir-3074-2
136	1	141373967	141374280	314	No	Yes	No	Yes	↑	0.24	ENSMUSG00000033952	Aspm	asp (abNormal spindle)-like, microcephaly associated (Drosophila)	downstream mmu-mir-181b-1
2442	3	14628742	14628985	244	No	Yes	No	Yes	↑	0.24	ENSMUSG00000027555	Car13	carbonic anhydrase 13	upstream mmu-mir-124-2
2913	4	141477891	141478291	401	No	Yes	No	Yes	↑	0.24	ENSMUSG00000040659 // ENSMUSG00000051435	Efhd2 // Fhad1	EF hand domain containing 2 // forkhead-associated (FHA) phosphopeptide binding domain 1	upstream mmu-mir-2139
739	11	113569751	113569968	218	No	Yes	No	Yes	↑	0.24	ENSMUSG00000018727	Cpsf4l	cleavage and polyadenylation specific factor 4-like	downstream mmu-mir-3968
2405	2	170286863	170287060	198	No	Yes	No	Yes	↑	0.24	ENSMUSG00000084067	Gm14269	predicted gene 14269	downstream mmu-mir-296
3086	5	93026098	93026452	355	No	Yes	No	Yes	↑	0.24	ENSMUSG00000047963	Stbd1	starch binding domain 1	downstream mmu-mir-1961
1471	15	96850052	96850679	628	No	Yes	No	Yes	↑	0.24	ENSMUSG00000022464	Slc38a4	solute carrier family 38, member 4	upstream mmu-mir-1941
2328	2	145756087	145756327	241	No	Yes	No	Yes	↑	0.25	ENSMUSG00000001767	Crnkl1	Crn, crooked neck-like 1 (Drosophila)	downstream mmu-mir-1953
4110	9	110701490	110701942	453	No	Yes	No	Yes	↑	0.25	ENSMUSG00000044664	Prss42	protease, serine, 42	downstream mmu-mir-128-2
2461	3	32380257	32380445	189	No	Yes	No	Yes	↑	0.25	ENSMUSG00000027667	Zfp639	zinc finger protein 639	upstream mmu-mir-1897
615	11	71849915	71850521	607	No	Yes	No	Yes	↑	0.25	ENSMUSG00000040554	Aipl1	aryl hydrocarbon receptor-interacting protein-like 1	downstream mmu-mir-195
2177	2	38849157	38849619	463	No	Yes	No	Yes	↑	0.26	ENSMUSG00000035295	Wdr38	WD repeat domain 38	downstream mmu-mir-181b-2
309	10	43164353	43164583	231	No	Yes	No	Yes	↑	0.26	ENSMUSG00000069885	---	NA	upstream mmu-mir-1929
2970	5	23758541	23758994	454	No	Yes	No	Yes	↑	0.26	ENSMUSG00000049380	---	NA	upstream mmu-mir-671
379	10	86298512	86298902	391	No	Yes	No	Yes	↑	0.26	ENSMUSG00000080679 // ENSMUSG00000054027	--- // Nt5dc3	NA // 5'-nucleotidase domain containing 3	downstream mmu-mir-135a-2
3091	5	100037981	100038156	176	No	Yes	No	Yes	↑	0.26	ENSMUSG00000029331 // ENSMUSG00000056908	4930522N08Rik // ---	RIKEN cDNA 4930522N08 gene // NA	upstream mmu-mir-703
3152	5	116457782	116458147	366	No	Yes	No	Yes	↑	0.26	ENSMUSG00000029513 // ENSMUSG00000029516	Prkab1 // Cit	protein kinase, AMP-activated, beta 1 Non-catalytic subunit // citron	downstream mmu-mir-701

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	**Chr.**	**start**	**end**	**width**	**C**	**PS**	**C**	**PS**	**effect dir.**	**logFC**	**ENSEMBL ID**	**symbol**	**gene name**	**next miRNA**
965	13	41091308	41091547	240	No	Yes	No	Yes	↑	0.26	ENSMUSG00000038683	Pak1ip1	PAK1 interacting protein 1	downstream mmu-mir-5124
458	10	122443012	122443256	245	No	Yes	No	Yes	↑	0.26	ENSMUSG00000065406 // ENSMUSG00000034602	Mirlet7i // Mon2	microRNA let7i // MON2 homolog (yeast)	upstream mmu-let-7i
1378	15	71140169	71140406	238	No	Yes	No	Yes	↑	0.27	ENSMUSG00000036800	Fam135b	family with sequence similarity 135, member B	downstream mmu-mir-151
1503	15	100131133	100131965	833	No	Yes	No	Yes	↑	0.27	ENSMUSG00000054619	Mettl7a1	methyltransferase like 7A1	upstream mmu-mir-1941
1187	14	47689339	47689594	256	No	Yes	No	Yes	↑	0.28	ENSMUSG00000072589 // ENSMUSG00000021838	Gm10371 // Samd4	predicted gene 10371 // sterile alpha motif domain containing 4	upstream mmu-mir-5131
1472	15	96855601	96855851	251	No	Yes	No	Yes	↑	0.28	ENSMUSG00000022464	Slc38a4	solute carrier family 38, member 4	upstream mmu-mir-1941
2089	19	51866739	51867081	343	No	Yes	No	Yes	↑	0.28	ENSMUSG00000035804	Ins1	insulin I	downstream mmu-mir-146b
795	12	31947546	31947788	243	No	Yes	No	Yes	↑	0.28	ENSMUSG00000002900	Lamb1	laminin B1	downstream mmu-mir-680-3
2976	5	30428904	30429154	251	No	Yes	No	Yes	↑	0.29	ENSMUSG00000044576	Fam59b	family with sequence similarity 59, member B	upstream mmu-mir-1960
1825	18	9909611	9910137	527	No	Yes	No	Yes	↑	0.29	ENSMUSG00000073635	---	NA	downstream mmu-mir-133a-1
3528	7	48745656	48746308	653	No	Yes	No	Yes	↑	0.29	ENSMUSG00000083500 // ENSMUSG00000074166 // ENSMUSG00000074160	Gm15470 // AW146154 // ---	predicted gene 15470 // expressed sequence AW146154	upstream mmu-mir-707
2517	3	79206063	79206308	246	No	Yes	No	Yes	↑	0.29	ENSMUSG00000061175	Fnip2	folliculin interacting protein 2	upstream mmu-mir-466k
1682	17	25995934	25996276	343	No	Yes	No	Yes	↑	0.30	ENSMUSG00000073434	Wdr90	WD repeat domain 90	upstream mmu-mir-3082
4001	9	50919228	50919520	293	No	Yes	No	Yes	↑	0.30	ENSMUSG00000032056	Btg4	B cell translocation gene 4	upstream mmu-mir-34b
2267	2	102295770	102296667	898	No	Yes	No	Yes	↑	0.30	ENSMUSG00000075012	Fjx1	four jointed box 1 (Drosophila)	downstream mmu-mir-1902
682	11	99146952	99147182	231	No	Yes	No	Yes	↑	0.30	ENSMUSG00000020913	Krt24	keratin 24	downstream mmu-mir-5119
2816	4	107381184	107381320	137	No	Yes	No	Yes	↑	0.30	ENSMUSG00000080460	---	NA	upstream mmu-mir-761
1178	14	37912666	37913077	412	No	Yes	No	Yes	↑	0.30	ENSMUSG00000021803	Cdhr1	cadherin-related family member 1	downstream mmu-mir-346
1404	15	79436710	79436978	269	No	Yes	No	Yes	↑	0.30	ENSMUSG00000022429	Dmc1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	upstream mmu-mir-1943
3598	7	107672495	107672817	323	No	Yes	No	Yes	↑	0.31	ENSMUSG00000030708	Dnajb13	DnaJ (Hsp40) related, subfamily B, member 13	downstream mmu-mir-3102
2314	2	129925284	129926709	1426	No	Yes	No	Yes	↑	0.31	ENSMUSG00000074804 // ENSMUSG00000081387	AU015228 // ---	expressed sequence AU015228 // NA	upstream mmu-mir-103-2
1023	13	59818518	59818830	313	No	Yes	No	Yes	↑	0.31	ENSMUSG00000043986	4932411G14Rik	RIKEN cDNA 4932411G14 gene	upstream mmu-mir-7a-1
707	11	102341776	102341987	212	No	Yes	No	Yes	↑	0.31	ENSMUSG00000050324 // ENSMUSG00000034621	--- // Gpatch8	NA // G patch domain containing 8	downstream mmu-mir-5119
265	10	18980753	18982015	1263	No	Yes	No	Yes	↑	0.32	ENSMUSG00000045591	Olig3	oligodendrocyte transcription factor 3	downstream mmu-mir-5104
3279	6	36474804	36475007	204	No	Yes	No	Yes	↑	0.32	ENSMUSG00000045613	Chrm2	cholinergic receptor, muscarinic 2, cardiac	downstream mmu-mir-490
1709	17	35021281	35021725	445	No	Yes	No	Yes	↑	0.33	ENSMUSG00000024372	---	NA	upstream mmu-mir-219-1
4151	9	123892333	123892750	418	No	Yes	No	Yes	↑	0.33	ENSMUSG00000064039	Ccr1l1	chemokine (C-C motif) receptor 1-like 1	downstream mmu-mir-138-1
1347	15	31378527	31378689	163	No	Yes	No	Yes	↑	0.34	ENSMUSG00000068964 // ENSMUSG00000022236	Gm6361 // Ropn1l	predicted gene 6361 // ropporin 1-like	upstream mmu-mir-3964
1653	17	4880676	4881955	1280	No	Yes	No	Yes	↑	0.34	ENSMUSG00000073473	---	NA	downstream mmu-mir-692-1
3523	7	36900763	36901209	447	No	Yes	No	Yes	↑	0.34	ENSMUSG00000066543	Gm10166	predicted pseudogene 10166	downstream mmu-mir-1964
338	10	67498813	67499010	198	No	Yes	No	Yes	↑	0.34	ENSMUSG00000037846	Rtkn2	rhotekin 2	downstream mmu-mir-5108
3397	6	118472562	118473155	594	No	Yes	No	Yes	↑	0.34	ENSMUSG00000007827	Ankrd26	ankyrin repeat domain 26	downstream mmu-mir-706
2696	4	5568113	5568422	310	No	Yes	No	Yes	↑	0.34	ENSMUSG00000049119	Fam110b	family with sequence similarity 110, member B	downstream mmu-mir-3471-2

					Enrichment meDNA									
					5-Htt+/+		5-Htt+/-							
reg. ID	Chr.	start	end	width	C	PS	C	PS	effect dir.	logFC	ENSEMBL ID	symbol	gene name	next miRNA
2593	3	102880788	102881130	343	No	Yes	No	Yes	↑	0.34	ENSMUSG00000070385	Ampd1	adeNosine moNophosphate deaminase 1	upstream mmu-mir-669n
1159	14	33480197	33480398	202	No	Yes	No	Yes	↑	0.35	ENSMUSG00000071540	3425401B19Rik	RIKEN cDNA 3425401B19 gene	downstream mmu-mir-3076
2436	3	9072303	9072844	542	No	Yes	No	Yes	↑	0.35	ENSMUSG00000056797	Gm4889	predicted gene 4889	upstream mmu-mir-124-2
1058	13	93345166	93345552	387	No	Yes	No	Yes	↑	0.35	ENSMUSG00000046957	Spz1	spermatogenic leucine zipper 1	upstream mmu-mir-5624
1685	17	28620956	28621127	172	No	Yes	No	Yes	↑	0.35	ENSMUSG00000024222	Fkbp5	FK506 binding protein 5	upstream mmu-mir-3083
2964	5	8792216	8792537	322	No	Yes	No	Yes	↑	0.36	ENSMUSG00000028970	Abcb1b	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	upstream mmu-mir-879
2670	3	146353374	146353549	176	No	Yes	No	Yes	↑	0.37	ENSMUSG00000048652	Samd13	sterile alpha motif domain containing 13	downstream mmu-mir-3963
337	10	67489441	67489693	253	No	Yes	No	Yes	↑	0.37	ENSMUSG00000037846	Rtkn2	rhotekin 2	downstream mmu-mir-5108
1826	18	13056787	13057336	550	No	Yes	No	Yes	↑	0.37	ENSMUSG00000080866 // ENSMUSG00000044252	Gm5687 // Osbpl1a	predicted gene 5687 // oxysterol binding protein-like 1A	downstream mmu-mir-1948
3854	8	99951047	99951637	591	No	Yes	No	Yes	↑	0.38	ENSMUSG00000081111	Gm5913	predicted gene 5913	downstream mmu-mir-1186b
192	1	173168306	173168720	415	No	Yes	No	Yes	↑	0.38	ENSMUSG00000058715 // ENSMUSG00000013593	Fcer1g // Ndufs2	Fc receptor, IgE, high affinity I, gamma polypeptide // NADH dehydrogenase (ubiquiNone) Fe-S protein 2	downstream mmu-mir-350
2784	4	83303475	83303838	364	No	Yes	No	Yes	↑	0.38	ENSMUSG00000080793 // ENSMUSG00000052407	Cbx3-ps3 // 4930473A06Rik	chromobox homolog 3 (Drosophila HP1 gamma), pseudogene 3 // RIKEN cDNA 4930473A06 gene	upstream mmu-mir-491
1335	15	12755943	12756295	353	No	Yes	No	Yes	↑	0.39	ENSMUSG00000022191	Drosha	drosha, ribonuclease type III	downstream mmu-mir-1898
2808	4	104549913	104550111	199	No	Yes	No	Yes	↑	0.39	ENSMUSG00000035031	C8a	complement component 8, alpha polypeptide	upstream mmu-mir-101a
2863	4	128291909	128292687	779	No	Yes	No	Yes	↑	0.39	ENSMUSG00000062545	Tlr12	toll-like receptor 12	downstream mmu-mir-692-2.1
259	10	14466914	14467435	522	No	Yes	No	Yes	↑	0.39	ENSMUSG00000059814	---	NA	downstream mmu-mir-5104
1495	15	99050982	99051487	506	No	Yes	No	Yes	↑	0.39	ENSMUSG00000037579	Kcnh3	potassium voltage-gated channel, subfamily H (eag-related), member 3	upstream mmu-mir-1941
212	1	184246716	184247109	394	No	Yes	No	Yes	↑	0.40	ENSMUSG00000047539	Fbxo28	F-box protein 28	downstream mmu-mir-1981
1011	13	55749228	55749440	213	No	Yes	No	Yes	↑	0.41	ENSMUSG00000021500	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	downstream mmu-mir-874
2031	19	37619145	37619409	265	No	Yes	No	Yes	↑	0.41	ENSMUSG00000053799	Exoc6	exocyst complex component 6	downstream mmu-mir-1950
913	12	113218228	113218501	274	No	Yes	No	Yes	↑	0.41	ENSMUSG00000021290	2010107E04Rik	RIKEN cDNA 2010107E04 gene	upstream mmu-mir-3073
2615	3	122815622	122815945	324	No	Yes	No	Yes	↑	0.43	ENSMUSG00000028116 // ENSMUSG00000050315	Myoz2 // Synpo2	myozenin 2 // synaptopodin 2	upstream mmu-mir-760
2902	4	139161007	139161329	323	No	Yes	No	Yes	↑	0.44	ENSMUSG00000028737 // ENSMUSG00000041025	Aldh4a1 // Iffo2	aldehyde dehydrogenase 4 family, member A1 // intermediate filament family orphan 2	downstream mmu-mir-2139
1731	17	44327479	44327718	240	No	Yes	No	Yes	↑	0.44	ENSMUSG00000023959	Clic5	chloride intracellular channel 5	upstream mmu-mir-693
3647	7	127981617	127981784	168	No	Yes	No	Yes	↑	0.47	ENSMUSG00000035064	Eef2k	eukaryotic elongation factor-2 kinase	upstream mmu-mir-762
3203	5	139628239	139628507	269	No	Yes	No	Yes	↑	0.48	ENSMUSG00000025857	Heatr2	HEAT repeat containing 2	downstream mmu-mir-339
3622	7	115413401	115413731	331	No	Yes	No	Yes	↑	0.50	ENSMUSG00000060549	---	NA	downstream mmu-mir-139
557	11	53915463	53915779	317	No	Yes	No	Yes	↑	0.50	ENSMUSG00000018906	P4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide	downstream mmu-mir-3061
1078	13	99259885	99260140	256	No	Yes	No	Yes	↑	0.50	ENSMUSG00000071222	---	NA	downstream mmu-mir-1940
3253	6	15672786	15673027	242	No	Yes	No	Yes	↑	0.51	ENSMUSG00000041390	Mdfic	MyoD family inhibitor domain containing	upstream mmu-mir-489
2278	2	111840721	111841251	531	No	Yes	No	Yes	↑	0.51	ENSMUSG00000081037	Gm13929	predicted gene 13929	upstream mmu-mir-1951
1429	15	84179604	84180261	658	No	Yes	No	Yes	↑	0.52	ENSMUSG00000022439	Parvg	parvin, gamma	downstream mmu-mir-1249

C) GxE effects

					Enrichment meDNA							
					5-Htt+/+		5-Htt+/-					
reg. ID	Chr.	start	end	width	C	PS	C	PS	ENSEMBL ID	symbol	gene name	next miRNA
12	16620450	16620622	173	790	No	Yes	Yes	No	ENSMUSG00000020593	Lpin1	lipin 1	upstream mmu-mir-3066
1	79921439	79921674	236	71	No	Yes	Yes	No	ENSMUSG00000067106	Gm5529	predicted pseudogene 5529	upstream mmu-mir-5126
5	24754488	24754761	274	2974	No	Yes	Yes	No	ENSMUSG00000054116 // ENSMUSG00000038072	E130116L18Rik // Galnt11	RIKEN cDNA E130116L18 gene // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11	downstream mmu-mir-671
10	68991227	68992000	774	343	No	Yes	Yes	No	ENSMUSG00000069601	Ank3	ankyrin 3, epithelial	downstream mmu-mir-678
2	172240549	172240961	413	2410	No	Yes	Yes	No	ENSMUSG00000074570	Cass4	Cas scaffolding protein family member 4	downstream mmu-mir-296
16	85555822	85556177	356	1616	No	Yes	Yes	No	ENSMUSG00000041134	Cyyr1	cysteine and tyrosine-rich protein 1	downstream mmu-mir-155
16	59553283	59553530	248	1600	No	Yes	Yes	No	ENSMUSG00000022723	Crybg3	beta-gamma crystallin domain containing 3	downstream mmu-mir-5118
9	114308807	114309002	196	4116	No	Yes	Yes	No	ENSMUSG00000079260	Glb1	galactosidase, beta 1	upstream mmu-mir-467h
16	18326679	18326871	193	1535	No	Yes	Yes	No	ENSMUSG00000065464 // ENSMUSG00000013539	Mir185 // D16H22S680E	microRNA 185 // DNA segment, Chr 16, human D22S680E, expressed	downstream mmu-mir-185
10	75229253	75229611	359	349	No	Yes	Yes	No	ENSMUSG00000020196	Cabin1	calcineurin binding protein 1	downstream mmu-mir-678
7	108938653	108939395	743	3601	No	Yes	Yes	No	ENSMUSG00000007946 // ENSMUSG00000001829	Phox2a // Clpb	paired-like homeobox 2a // ClpB caseiNolytic peptidase B homolog (E. coli)	downstream mmu-mir-139
8	49073362	49073530	169	3800	No	Yes	Yes	No	ENSMUSG00000031563	Wwc2	WW, C2 and coiled-coil domain containing 2	upstream mmu-mir-383
5	98756166	98756519	354	3087	No	Yes	Yes	No	ENSMUSG00000057816	1700007G11Rik	RIKEN cDNA 1700007G11 gene	downstream mmu-mir-703
12	73763288	73763668	381	837	No	Yes	Yes	No	ENSMUSG00000021094	Dhrs7	dehydrogenase/reductase (SDR family) member 7	upstream mmu-mir-681
12	76275174	76275331	158	843	No	Yes	Yes	No	ENSMUSG00000034402	Kcnh5	potassium voltage-gated channel, subfamily H (eag-related), member 5	upstream mmu-mir-5101
1	64660522	64661239	718	60	No	Yes	Yes	No	ENSMUSG00000025956	Mettl21a	methyltransferase like 21A	downstream mmu-mir-1928
6	96114742	96115018	277	3365	No	Yes	Yes	No	ENSMUSG00000072878 // ENSMUSG00000059187	1700123L14Rik // Fam19a1	RIKEN cDNA 1700123L14 gene // family with sequence similarity 19, member A1	upstream mmu-mir-705
11	117951073	117951265	193	757	No	Yes	Yes	No	ENSMUSG00000033987	Dnahc17	dynein, axonemal, heavy chain 17	upstream mmu-mir-1932
7	83552619	83553367	749	3574	No	Yes	Yes	No	ENSMUSG00000025754	Agbl1	ATP/GTP binding protein-like 1	upstream mmu-mir-7a-2
9	121018331	121018670	340	4147	No	Yes	Yes	No	ENSMUSG00000084706 // ENSMUSG00000040936	// Ulk4	7SK RNA // unc-51-like kinase 4 (C. elegans)	upstream mmu-mir-138-1
2	127514291	127514610	320	2308	No	Yes	Yes	No	ENSMUSG00000084006	Gm14245	predicted gene 14245	upstream mmu-mir-103-2
5	104276793	104277126	334	3100	No	Yes	Yes	No	ENSMUSG00000064629 // ENSMUSG00000029313	--- // Aff1	NA // AF4/FMR2 family, member 1	upstream mmu-mir-5619
7	31662811	31662985	175	3518	No	Yes	Yes	No	ENSMUSG00000030577	Cd22	CD22 antigen	downstream mmu-mir-1964
16	17113575	17113815	241	1530	No	Yes	Yes	No	ENSMUSG00000022771 // ENSMUSG00000049916	Ppil2 // 2610318N02Rik	peptidylprolyl isomerase (cyclophilin)-like 2 // RIKEN cDNA 2610318N02 gene	downstream mmu-mir-130b
12	87160119	87160359	241	867	No	Yes	Yes	No	ENSMUSG00000021252	0610007P14Rik	RIKEN cDNA 0610007P14 gene	downstream mmu-mir-3068
11	22523259	22523680	422	506	No	Yes	Yes	No	ENSMUSG00000083008	Gm12053	predicted gene 12053	upstream mmu-mir-1933
15	88586607	88586808	202	1437	No	Yes	Yes	No	ENSMUSG00000034333	Zbed4	zinc finger, BED domain containing 4	downstream mmu-let-7b
13	64374026	64374926	901	1031	No	Yes	Yes	No	ENSMUSG00000033102	Cdc14b	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	upstream mmu-mir-3074-1

					Enrichment meDNA							
					5-Htt+/+		5-Htt+/-					
reg. ID	**Chr.**	**start**	**end**	**width**	**C**	**PS**	**C**	**PS**	**ENSEMBL ID**	**symbol**	**gene name**	**next miRNA**
7	138758514	138758684	171	3672	No	Yes	Yes	No	ENSMUSG00000062758	Gm16477	predicted pseudogene 16477	downstream mmu-mir-5102
10	80635352	80635568	217	363	No	Yes	Yes	No	ENSMUSG00000034994	Eef2	eukaryotic translation elongation factor 2	upstream mmu-mir-5615-1
6	31998322	31998560	239	3269	No	Yes	Yes	No	ENSMUSG00000029766	1700012A03Rik	RIKEN cDNA 1700012A03 gene	upstream mmu-mir-29b-1
3	37614766	37615043	278	2469	No	Yes	Yes	No	ENSMUSG00000081549 // ENSMUSG00000058174	--- // Gm5148	NA // predicted gene 5148	downstream mmu-mir-1897
6	38063999	38064610	612	3282	No	Yes	Yes	No	ENSMUSG00000029829 // ENSMUSG00000038600	Tmem213 // Atp6v0a4	transmembrane protein 213 // ATPase, H+ transporting, lysosomal V0 subunit A4	downstream mmu-mir-490
19	38168221	38168446	226	2036	No	Yes	Yes	No	ENSMUSG00000054200	O3far1	omega-3 fatty acid receptor 1	downstream mmu-mir-1950
3	153507764	153508069	306	2687	No	Yes	Yes	No	ENSMUSG00000038997	Asb17	ankyrin repeat and SOCS box-containing 17	upstream mmu-mir-3963
5	66362494	66362774	281	3024	No	Yes	Yes	No	ENSMUSG00000029205	Chrna9	cholinergic receptor, nicotinic, alpha polypeptide 9	downstream mmu-mir-574
14	64125316	64125620	305	1232	No	Yes	Yes	No	ENSMUSG00000021953	Tdh	L-threonine dehydrogenase	upstream mmu-mir-598
14	54420660	54420948	289	1205	No	Yes	Yes	No	ENSMUSG00000076860	---	NA	downstream mmu-mir-686
12	106889441	106889717	277	891	No	Yes	Yes	No	ENSMUSG00000041341	Atg2b	ATG2 autophagy related 2 homolog B (S. cerevisiae)	upstream mmu-mir-3069
14	50939884	50940224	341	1194	No	Yes	Yes	No	ENSMUSG00000045306	Olfr734	olfactory receptor 734	downstream mmu-mir-686
8	87890113	87890452	340	3833	No	Yes	Yes	No	ENSMUSG00000031698	Mylk3	myosin light chain kinase 3	upstream mmu-mir-3074-2
5	103851411	103851650	240	3095	No	Yes	Yes	No	ENSMUSG00000034573	Ptpn13	protein tyrosine phosphatase, Non-receptor type 13	upstream mmu-mir-5619
5	77941031	77941489	459	3063	No	Yes	Yes	No	ENSMUSG00000047652	Pea15b	phosphoprotein enriched in astrocytes 15B	downstream mmu-mir-5098
8	86065508	86065826	319	3830	No	Yes	Yes	No	ENSMUSG00000047286	Olfr370	olfactory receptor 370	downstream mmu-mir-1199
9	120244802	120245088	287	4145	No	Yes	Yes	No	ENSMUSG00000083772 // ENSMUSG00000041794	Gm15566 // Myrip	predicted gene 15566 // myosin VIIA and Rab interacting protein	downstream mmu-mir-26a-1
4	138382101	138382425	325	2896	No	Yes	Yes	No	ENSMUSG00000058908 // ENSMUSG00000041193	Pla2g2a // Pla2g5	phospholipase A2, group IIA (platelets, syNovial fluid) // phospholipase A2, group V	downstream mmu-mir-2139
6	142523491	142523690	200	3446	No	Yes	Yes	No	ENSMUSG00000030247	Kcnj8	potassium inwardly-rectifying channel, subfamily J, member 8	downstream mmu-mir-680-1
6	38143282	38143563	282	3283	No	Yes	Yes	No	ENSMUSG00000063455	D630045J12Rik	RIKEN cDNA D630045J12 gene	downstream mmu-mir-490
8	119025770	119026177	408	3893	No	Yes	Yes	No	ENSMUSG00000034467	Dynlrb2	dynein light chain roadblock-type 2	upstream mmu-mir-3473d
2	52962557	52962757	201	2185	No	Yes	Yes	No	ENSMUSG00000061136 // ENSMUSG00000036053	Prpf40a // Fmnl2	PRP40 pre-mRNA processing factor 40 homolog A (yeast) // formin-like 2	upstream mmu-mir-5129
15	100256718	100257551	834	1506	No	Yes	Yes	No	ENSMUSG00000023030	Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	upstream mmu-mir-1941
7	74881586	74881908	323	3569	No	Yes	Yes	No	ENSMUSG00000070514 // ENSMUSG00000030554	--- // Synm	NA // synemin, intermediate filament protein	downstream mmu-mir-211
5	123745990	123746262	273	3166	No	Yes	Yes	No	ENSMUSG00000070519 // ENSMUSG00000029442	--- // Wdr66	NA // WD repeat domain 66	upstream mmu-mir-3965
7	54224905	54225077	173	3551	No	Yes	Yes	No	ENSMUSG00000043262	Uevld	UEV and lactate/malate dehyrogenase domains	upstream mmu-mir-5121
18	78340511	78340723	213	1939	No	Yes	Yes	No	ENSMUSG00000059336	Slc14a1	solute carrier family 14 (urea transporter), member 1	downstream mmu-mir-5127
11	94340542	94340847	306	659	No	Yes	Yes	No	ENSMUSG00000020866 // ENSMUSG00000020867	Cacna1g // Spata20	calcium channel, voltage-dependent, T type, alpha 1G subunit // spermatogenesis associated 20	downstream mmu-mir-3063
3	108645343	108645923	581	2604	No	Yes	Yes	No	ENSMUSG00000027882	Stxbp3a	syntaxin binding protein 3A	upstream mmu-mir-669n
18	50438458	50438693	236	1886	No	Yes	Yes	No	ENSMUSG00000035420	Fam170a	family with sequence similarity 170, member A	downstream mmu-mir-5097
11	55418779	55418960	182	562	No	Yes	Yes	No	ENSMUSG00000000263	Glra1	glycine receptor, alpha 1 subunit	downstream mmu-mir-3061

					Enrichment meDNA							
					5-Htt+/+		5-Htt+/-					
reg. ID	**Chr.**	**start**	**end**	**width**	**C**	**PS**	**C**	**PS**	**ENSEMBL ID**	**symbol**	**gene name**	**next miRNA**
1	153618252	153618453	202	147	No	Yes	Yes	No	ENSMUSG00000043019	Edem3	ER degradation enhancer, manNosidase alpha-like 3	upstream mmu-mir-488
9	115315905	115316202	298	4124	No	Yes	Yes	No	ENSMUSG00000080344	---	NA	downstream mmu-mir-467h
19	47770767	47771532	766	2080	No	Yes	Yes	No	ENSMUSG00000025064	Col17a1	collagen, type XVII, alpha 1	downstream mmu-mir-146b
5	66361850	66362047	198	3023	No	Yes	Yes	No	ENSMUSG00000029205	Chrna9	cholinergic receptor, nicotinic, alpha polypeptide 9	downstream mmu-mir-574
18	14005289	14005595	307	1827	No	Yes	Yes	No	ENSMUSG00000084481 // ENSMUSG00000024420	--- // Zfp521	NA // zinc finger protein 521	downstream mmu-mir-1948
7	127095816	127096230	415	3643	No	Yes	Yes	No	ENSMUSG00000052273	Dnahc3	dynein, axonemal, heavy chain 3	upstream mmu-mir-762
9	86467526	86467705	180	4062	No	Yes	Yes	No	ENSMUSG00000032417	Rwdd2a	RWD domain containing 2A	downstream mmu-mir-184
14	119284098	119284438	341	1302	No	Yes	Yes	No	ENSMUSG00000079997 // ENSMUSG00000042156	--- // Dzip1	NA // DAZ interacting protein 1	downstream mmu-mir-92a-1
10	116271669	116271994	326	427	No	Yes	Yes	No	ENSMUSG00000034057	Gm239	predicted gene 239	downstream mmu-mir-763
18	70691261	70691534	274	1927	No	Yes	Yes	No	ENSMUSG00000038425	Poli	polymerase (DNA directed), iota	upstream mmu-mir-694
15	97551697	97552038	342	1481	No	Yes	Yes	No	ENSMUSG00000022468	Endou	endonuclease, polyU-specific	upstream mmu-mir-1941
7	50221679	50222144	466	3530	No	Yes	Yes	No	ENSMUSG00000076190			upstream mmu-mir-707
9	61792905	61793223	319	4020	No	Yes	Yes	No	ENSMUSG00000032254	Kif23	kinesin family member 23	downstream mmu-mir-5133
12	88790172	88790412	241	871	No	Yes	Yes	No	ENSMUSG00000021041 // ENSMUSG00000021040	2700073G19Rik // 1810035L17Rik	RIKEN cDNA 2700073G19 gene // RIKEN cDNA 1810035L17 gene	upstream mmu-mir-3068
6	146975736	146976490	755	3465	No	Yes	Yes	No	ENSMUSG00000040121 // ENSMUSG00000016487	Rep15 // Ppfibp1	RAB15 effector protein // PTPRF interacting protein, binding protein 1 (liprin beta 1)	downstream mmu-mir-680-1
13	38127687	38128016	330	957	No	Yes	Yes	No	ENSMUSG00000044566	Cage1	cancer antigen 1	upstream mmu-mir-5124
13	64052638	64053017	380	1030	No	Yes	Yes	No	ENSMUSG00000021470	0610007P08Rik	RIKEN cDNA 0610007P08 gene	upstream mmu-mir-3074-1
14	55840766	55841028	263	1212	No	Yes	Yes	No	ENSMUSG00000022209	Dhrs2	dehydrogenase/reductase member 2	upstream mmu-mir-208b
7	144000575	144000977	403	3691	No	Yes	Yes	No	ENSMUSG00000054612	Mgmt	O-6-methylguanine-DNA methyltransferase	downstream mmu-mir-1962
6	108095158	108095361	204	3383	No	Yes	Yes	No	ENSMUSG00000030101	Sumf1	sulfatase modifying factor 1	downstream mmu-mir-706
2	13198165	13198478	314	2141	No	Yes	Yes	No	ENSMUSG00000026727 // ENSMUSG00000026726	Rsu1 // Cubn	Ras suppressor protein 1 // cubilin (intrinsic factor-cobalamin receptor)	upstream mmu-mir-511
16	92293942	92294259	318	1636	No	Yes	Yes	No	ENSMUSG00000039672	Kcne2	potassium voltage-gated channel, Isk-related subfamily, gene 2	upstream mmu-mir-802
6	90552774	90553063	290	3360	No	Yes	Yes	No	ENSMUSG00000030089	Slc41a3	solute carrier family 41, member 3	upstream mmu-mir-705
10	86979898	86980143	246	380	No	Yes	Yes	No	ENSMUSG00000020051	Pah	phenylalanine hydroxylase	downstream mmu-mir-135a-2
16	89571497	89571735	239	1625	No	Yes	Yes	No	ENSMUSG00000056706	Krtap7-1	keratin associated protein 7-1	upstream mmu-mir-802
17	34081730	34082180	451	1704	No	Yes	Yes	No	ENSMUSG00000024312	Wdr46	WD repeat domain 46	downstream mmu-mir-219-1
18	61013037	61013345	309	1896	No	Yes	Yes	No	ENSMUSG00000024613	Tcof1	Treacher Collins Franceschetti syndrome 1, homolog	downstream mmu-mir-5107
5	139051120	139051683	564	3202	No	Yes	Yes	No	ENSMUSG00000081142 // ENSMUSG00000058291	Gm15497 // Zfp68	predicted gene 15497 // zinc finger protein 68	upstream mmu-mir-106b
9	119473815	119474058	244	4141	No	Yes	Yes	No	ENSMUSG00000032511	Scn5a	sodium channel, voltage-gated, type V, alpha	downstream mmu-mir-26a-1
17	29659666	29660149	484	1689	No	Yes	Yes	No	ENSMUSG00000079580	Tmem217	transmembrane protein 217	upstream mmu-mir-3083
1	24034551	24034832	282	16	No	Yes	Yes	No	ENSMUSG00000026154 // ENSMUSG00000026153	1110058L19Rik // Fam135a	RIKEN cDNA 1110058L19 gene // family with sequence similarity 135, member A	downstream mmu-mir-30c-2
2	170110150	170110601	452	2404	No	Yes	Yes	No	ENSMUSG00000084013	Gm14270	predicted gene 14270	downstream mmu-mir-296
9	55128373	55128741	369	4006	No	Yes	Yes	No	ENSMUSG00000032311	Nrg4	neuregulin 4	downstream mmu-mir-5710

					Enrichment meDNA							
					5-Htt+/+		5-Htt+/-					
reg. ID	Chr.	start	end	width	C	PS	C	PS	ENSEMBL ID	symbol	gene name	next miRNA
17	32304227	32304848	622	1698	No	Yes	Yes	No	ENSMUSG00000038146	Notch3	Notch gene homolog 3 (Drosophila)	downstream mmu-mir-219-1
15	7088102	7088398	297	1320	No	Yes	Yes	No	ENSMUSG00000058898	---	NA	upstream mmu-mir-1898
13	56581605	56581947	343	1014	No	Yes	Yes	No	ENSMUSG00000021538	Il9	interleukin 9	downstream mmu-mir-874
13	62987190	62987786	597	1028	No	Yes	Yes	No	ENSMUSG00000069805 // ENSMUSG00000056199	Fbp1 // ---	fructose bisphosphatase 1 // NA	downstream mmu-mir-713
14	33670782	33671491	710	1162	No	Yes	Yes	No	ENSMUSG00000050666	E130203B14Rik	RIKEN cDNA E130203B14 gene	upstream mmu-mir-346
10	41775512	41775792	281	308	No	Yes	Yes	No	ENSMUSG00000051559	---	NA	downstream mmu-mir-3473b
13	38140859	38141140	282	958	No	Yes	Yes	No	ENSMUSG00000021428	Riok1	RIO kinase 1 (yeast)	upstream mmu-mir-5124
18	77189798	77190071	274	1934	No	Yes	Yes	No	ENSMUSG00000025421	Hdhd2	haloacid dehalogenase-like hydrolase domain containing 2	downstream mmu-mir-5127
17	85145116	85145421	306	1806	No	Yes	Yes	No	ENSMUSG00000024120	Lrpprc	leucine-rich PPR-motif containing	upstream mmu-mir-1195
6	73037138	73037377	240	3323	No	Yes	Yes	No	ENSMUSG00000077556 // ENSMUSG00000052861	--- // Dnahc6	NA // dynein, axonemal, heavy chain 6	downstream mmu-mir-468
5	103977519	103977875	357	3096	No	Yes	Yes	No	ENSMUSG00000084126 // ENSMUSG00000034573	Gm15844 // Ptpn13	predicted gene 15844 // protein tyrosine phosphatase, Non-receptor type 13	upstream mmu-mir-5619
1	88984850	88985091	242	77	No	Yes	Yes	No	ENSMUSG00000026246	Alppl2	alkaline phosphatase, placental-like 2	downstream mmu-mir-5126
8	60024215	60024508	294	3809	No	Yes	Yes	No	ENSMUSG00000077526 // ENSMUSG00000031608	// Galnt7	Small nucleolar RNA SNoRA65 // UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7	downstream mmu-mir-710
15	78691565	78691842	278	1400	No	Yes	Yes	No	ENSMUSG00000043501	Lgals2	lectin, galactose-binding, soluble 2	downstream mmu-mir-1943
8	111234049	111234594	546	3872	No	Yes	Yes	No	ENSMUSG00000038872	Zfhx3	zinc finger homeobox 3	upstream mmu-mir-3108
17	71372063	71372269	207	1770	No	Yes	Yes	No	ENSMUSG00000024049	Myom1	myomesin 1	upstream mmu-mir-1195
15	101325243	101325528	286	1515	No	Yes	Yes	No	ENSMUSG00000067613	5430421N21Rik	RIKEN cDNA 5430421N21 gene	downstream mmu-mir-1941
15	97838792	97839029	238	1484	No	Yes	Yes	No	ENSMUSG00000022483	Col2a1	collagen, type II, alpha 1	upstream mmu-mir-1941
9	110702212	110702842	631	4111	No	Yes	Yes	No	ENSMUSG00000044664	Prss42	protease, serine, 42	downstream mmu-mir-128-2
8	111237514	111237759	246	3874	No	Yes	Yes	No	ENSMUSG00000038872	Zfhx3	zinc finger homeobox 3	upstream mmu-mir-3108
3	148482292	148482575	284	2673	No	Yes	Yes	No	ENSMUSG00000028184	Lphn2	latrophilin 2	downstream mmu-mir-3963
7	112485391	112485820	430	3620	No	Yes	Yes	No	ENSMUSG00000043948	Olfr691	olfactory receptor 691	downstream mmu-mir-139
5	107693517	107693904	388	3112	No	Yes	Yes	No	ENSMUSG00000084218 // ENSMUSG00000029287	Gm8145 // Tgfbr3	predicted gene 8145 // transforming growth factor, beta receptor III	downstream mmu-mir-5619
10	118292685	118293005	321	440	No	Yes	Yes	No	ENSMUSG00000050709	4932442E05Rik	RIKEN cDNA 4932442E05 gene	downstream mmu-mir-763
19	5336127	5336455	329	1963	No	Yes	Yes	No	ENSMUSG00000038498	Catsper1	cation channel, sperm associated 1	upstream mmu-mir-194-2
8	32219619	32220083	465	3768	No	Yes	Yes	No	ENSMUSG00000039328	Rnf122	ring finger protein 122	upstream mmu-mir-1186
4	150371476	150371698	223	2938	No	Yes	Yes	No	ENSMUSG00000028963	Uts2	urotensin 2	downstream mmu-mir-34a
8	118235621	118236032	412	3892	No	Yes	Yes	No	ENSMUSG00000055435	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	upstream mmu-mir-3473d
13	47102005	47102256	252	979	No	Yes	Yes	No	ENSMUSG00000051606	2010001K21Rik	RIKEN cDNA 2010001K21 gene	downstream mmu-let-7d
2	13410986	13411223	238	2142	No	Yes	Yes	No	ENSMUSG00000026726	Cubn	cubilin (intrinsic factor-cobalamin receptor)	upstream mmu-mir-511
2	158610130	158610326	197	2360	No	Yes	Yes	No	ENSMUSG00000027655 // ENSMUSG00000027654	Dhx35 // Fam83d	DEAH (Asp-Glu-Ala-His) box polypeptide 35 // family with sequence similarity 83, member D	downstream mmu-mir-3474
19	28756535	28756817	283	2009	No	Yes	Yes	No	ENSMUSG00000052942	Glis3	GLIS family zinc finger 3	upstream mmu-mir-101b
1	187280556	187280819	264	222	No	Yes	Yes	No	ENSMUSG00000026614	Slc30a10	solute carrier family 30, member 10	downstream mmu-mir-215
7	107090832	107091162	331	3595	No	Yes	Yes	No	ENSMUSG00000058761	Rnf169	ring finger protein 169	downstream mmu-mir-326

					Enrichment meDNA							
					5-Htt+/+		5-Htt+/-					
reg. ID	Chr.	start	end	width	C	PS	C	PS	ENSEMBL ID	symbol	gene name	next miRNA
12	25270733	25271043	311	793	No	Yes	Yes	No	ENSMUSG00000020656	Grhl1	grainyhead-like 1 (Drosophila)	downstream mmu-mir-3066
2	181321734	181322397	664	2434	No	Yes	Yes	No	ENSMUSG00000000823	Znf512b	zinc finger protein 512B	downstream mmu-mir-124-3
16	22443504	22444077	574	1543	No	Yes	Yes	No	ENSMUSG00000013089	Etv5	ets variant gene 5	downstream mmu-mir-1224
19	7064270	7064466	197	1969	No	Yes	Yes	No	ENSMUSG00000024962 // ENSMUSG00000024963	Vegfb // Dnajc4	vascular endothelial growth factor B // DnaJ (Hsp40) homolog, subfamily C, member 4	upstream mmu-mir-5046
11	42964973	42965240	268	523	No	Yes	Yes	No	ENSMUSG00000055415	Atp10b	ATPase, class V, type 10B	downstream mmu-mir-146a
10	88896503	88896707	205	387	No	Yes	Yes	No	ENSMUSG00000074802	Gas2l3	growth arrest-specific 2 like 3	downstream mmu-mir-135a-2
6	126966774	126967045	272	3423	No	Yes	Yes	No	ENSMUSG00000000183	Fgf6	fibroblast growth factor 6	downstream mmu-mir-3098
17	80747899	80748257	359	1798	No	Yes	Yes	No	ENSMUSG00000054901	Arhgef33	Rho guanine nucleotide exchange factor (GEF) 33	upstream mmu-mir-1195
8	28128311	28128476	166	3759	No	Yes	Yes	No	ENSMUSG00000031483	Erlin2	ER lipid raft associated 2	upstream mmu-mir-3107
15	77791885	77792158	274	1395	No	Yes	Yes	No	ENSMUSG00000016552 // ENSMUSG00000016554	Foxred2 // Eif3d	FAD-dependent oxidoreductase domain containing 2 // eukaryotic translation initiation factor 3, subunit D	downstream mmu-mir-1943
13	12520880	12521218	339	935	No	Yes	Yes	No	ENSMUSG00000057554 // ENSMUSG00000050244	Lgals8 // Heatr1	lectin, galactose binding, soluble 8 // HEAT repeat containing 1	upstream mmu-mir-466i
11	59473695	59473903	209	574	Yes	No	No	Yes	ENSMUSG00000005417	Mprip	myosin phosphatase Rho interacting protein	upstream mmu-mir-5100
18	82693616	82694069	454	1947	Yes	No	No	Yes	ENSMUSG00000061684 // ENSMUSG00000041607	Rpl21-ps8 // Mbp	ribosomal protein L21, pseudogene 8 // myelin basic protein	upstream mmu-mir-5112
8	46036650	46037620	971	3795	Yes	No	No	Yes	ENSMUSG00000070047	Fat1	FAT tumor suppressor homolog 1 (Drosophila)	upstream mmu-mir-383
19	55811026	55811155	130	2097	Yes	No	No	Yes	ENSMUSG00000024985	Tcf7l2	transcription factor 7 like 2, T cell specific, HMG box	upstream mmu-mir-5623
3	138792237	138792755	519	2649	Yes	No	No	Yes	ENSMUSG00000028149	Rap1gds1	RAP1, GTP-GDP dissociation stimulator 1	downstream mmu-mir-1956
11	116218086	116218410	325	749	Yes	No	No	Yes	ENSMUSG00000034227 // ENSMUSG00000052949	Foxj1 // Rnf157	forkhead box J1 // ring finger protein 157	downstream mmu-mir-5621
4	155245936	155246284	349	2952	Yes	No	No	Yes	ENSMUSG00000029034	Cpsf3l	cleavage and polyadenylation specific factor 3-like	downstream mmu-mir-429
13	99955164	99955629	466	1083	Yes	No	No	Yes	ENSMUSG00000050919	Zfp366	zinc finger protein 366	downstream mmu-mir-1940
1	155697375	155697648	274	155	Yes	No	No	Yes	ENSMUSG00000045968	5830403L16Rik	RIKEN cDNA 5830403L16 gene	upstream mmu-mir-488
5	118691324	118691530	207	3160	Yes	No	No	Yes	ENSMUSG00000032850	Rnft2	ring finger protein, transmembrane 2	downstream mmu-mir-701
1	157130267	157130619	353	157	Yes	No	No	Yes	ENSMUSG00000033722 // ENSMUSG00000026469	BC034090 // Xpr1	cDNA sequence BC034090 // xeNotropic and polytropic retrovirus receptor 1	upstream mmu-mir-488
1	174058428	174058676	249	197	Yes	No	No	Yes	ENSMUSG00000003464	Pex19	peroxisomal biogenesis factor 19	downstream mmu-mir-350
11	50187982	50188294	313	548	Yes	No	No	Yes	ENSMUSG00000007850	Hnrnph1	heterogeneous nuclear ribonucleoprotein H1	upstream mmu-mir-804
1	122019584	122019852	269	104	Yes	No	No	Yes	ENSMUSG00000026388	3110009E18Rik	RIKEN cDNA 3110009E18 gene	upstream mmu-mir-128-1
1	64190793	64190970	178	59	Yes	No	No	Yes	ENSMUSG00000057599	---	NA	downstream mmu-mir-1928
9	72022276	72022772	497	4039	Yes	No	No	Yes	ENSMUSG00000058777	---	NA	upstream mmu-mir-5626
2	165475635	165476296	662	2384	Yes	No	No	Yes	ENSMUSG00000081758 // ENSMUSG00000017897	Gm11460 // Eya2	predicted gene 11460 // eYes absent 2 homolog (Drosophila)	downstream mmu-mir-3474
16	92467901	92468639	739	1640	Yes	No	No	Yes	ENSMUSG00000022951	Rcan1	regulator of calcineurin 1	upstream mmu-mir-802
2	76555309	76555697	389	2230	Yes	No	No	Yes	ENSMUSG00000002733 // ENSMUSG00000051747	Plekha3 // Ttn	pleckstrin homology domain-containing, family A (phosphoiNositide binding specific) member 3 // titin	downstream mmu-mir-10b

					Enrichment meDNA							
					5-Htt+/+		**5-Htt+/-**					
reg. ID	**Chr.**	**start**	**end**	**width**	**C**	**PS**	**C**	**PS**	**ENSEMBL ID**	**symbol**	**gene name**	**next miRNA**
4	117551930	117552343	414	2837	Yes	No	No	Yes	ENSMUSG00000078588 // ENSMUSG00000028541	Ccdc24 // B4galt2	coiled-coil domain containing 24 // UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	upstream mmu-mir-1957
16	48072535	48072881	347	1587	Yes	No	No	Yes	ENSMUSG00000078093	---	NA	upstream mmu-mir-3081
10	67604628	67604930	303	340	Yes	No	No	Yes	ENSMUSG00000019947	Arid5b	AT rich interactive domain 5B (MRF1-like)	downstream mmu-mir-5108
11	106932907	106933441	535	725	Yes	No	No	Yes	ENSMUSG00000078607 // ENSMUSG00000040481	1810010H24Rik // Bptf	RIKEN cDNA 1810010H24 gene // bromodomain PHD finger transcription factor	upstream mmu-mir-3064
7	108721935	108722423	489	3599	Yes	No	No	Yes	ENSMUSG00000030651	Art2b	ADP-ribosyltransferase 2b	downstream mmu-mir-139
6	86632793	86633003	211	3339	Yes	No	No	Yes	ENSMUSG00000001158	Snrnp27	small nuclear ribonucleoprotein 27 (U4/U6.U5)	upstream mmu-mir-705
8	107117522	107118207	686	3857	Yes	No	No	Yes	ENSMUSG00000048371	Pdp2	pyruvate dehyrogenase phosphatase catalytic subunit 2	downstream mmu-mir-328
5	107862010	107862425	416	3114	Yes	No	No	Yes	ENSMUSG00000033794	Lpcat2b	lysophosphatidylcholine acyltransferase 2B	downstream mmu-mir-5619
10	116410305	116410549	245	432	Yes	No	No	Yes	ENSMUSG00000069518	Gm10271	predicted gene 10271	downstream mmu-mir-763
6	55961773	55961974	202	3310	Yes	No	No	Yes	ENSMUSG00000002930	Ppp1r17	protein phosphatase 1, regulatory subunit 17	upstream mmu-mir-196b
7	69525724	69526023	300	3559	Yes	No	No	Yes	ENSMUSG00000056972	Magel2	melaNoma antigen, family L, 2	upstream mmu-mir-344i
5	4759623	4759898	276	2956	Yes	No	No	Yes	ENSMUSG00000044674	Fzd1	frizzled homolog 1 (Drosophila)	upstream mmu-mir-879
4	40642156	40642472	317	2734	Yes	No	No	Yes	ENSMUSG00000028411	Aptx	aprataxin	upstream mmu-mir-207
19	56470019	56470215	197	2101	Yes	No	No	Yes	ENSMUSG00000025076	Casp7	caspase 7	upstream mmu-mir-5623
7	143849226	143849653	428	3689	Yes	No	No	Yes	ENSMUSG00000054612	Mgmt	O-6-methylguanine-DNA methyltransferase	downstream mmu-mir-1962
9	77899102	77899339	238	4054	Yes	No	No	Yes	ENSMUSG00000023333	Gcm1	glial cells missing homolog 1 (Drosophila)	upstream mmu-mir-5626
13	53063137	53063349	213	999	Yes	No	No	Yes	ENSMUSG00000065771 // ENSMUSG00000056749	n-R5s54 // Nfil3	nuclear encoded rRNA 5S 54 // nuclear factor, interleukin 3, regulated	upstream mmu-mir-683-2
4	136445450	136445652	203	2892	Yes	No	No	Yes	ENSMUSG00000036896	C1qc	complement component 1, q subcomponent, C chain	upstream mmu-mir-700
13	100290146	100290309	164	1085	Yes	No	No	Yes	ENSMUSG00000052727	Mtap1b	microtubule-associated protein 1B	downstream mmu-mir-1940
14	33599914	33600496	583	1160	Yes	No	No	Yes	ENSMUSG00000041707	1810011H11Rik	RIKEN cDNA 1810011H11 gene	upstream mmu-mir-346
8	70220885	70221160	276	3815	Yes	No	No	Yes	ENSMUSG00000074285 // ENSMUSG00000030465	--- // Psd3	NA // pleckstrin and Sec7 domain containing 3	upstream mmu-mir-710
5	145939323	145939579	257	3219	Yes	No	No	Yes	ENSMUSG00000029625	Cpsf4	cleavage and polyadenylation specific factor 4	upstream mmu-mir-5105
6	5061769	5062105	337	3244	Yes	No	No	Yes	ENSMUSG00000002588 // ENSMUSG00000032827	Pon1 // Ppp1r9a	paraoxonase 1 // protein phosphatase 1, regulatory (inhibitor) subunit 9A	upstream mmu-mir-489
9	29772324	29772529	206	3957	Yes	No	No	Yes	ENSMUSG00000059974	Ntm	neurotrimin	upstream mmu-mir-1946b
16	88612382	88612658	277	1619	Yes	No	No	Yes	ENSMUSG00000050239	Krtap24-1	keratin associated protein 24-1	downstream mmu-mir-155
3	96958913	96959113	201	2565	Yes	No	No	Yes	ENSMUSG00000028093	Acp6	acid phosphatase 6, lysophosphatidic	downstream mmu-mir-190b
16	88562474	88562782	309	1618	Yes	No	No	Yes	ENSMUSG00000050520	Cldn8	claudin 8	downstream mmu-mir-155
7	134907704	134907966	263	3664	Yes	No	No	Yes	ENSMUSG00000043964 // ENSMUSG00000030811	Orai3 // Fbxl19	ORAI calcium release-activated calcium modulator 3 // F-box and leucine-rich repeat protein 19	downstream mmu-mir-762
9	67799114	67799383	270	4031	Yes	No	No	Yes	ENSMUSG00000035284	Vps13c	vacuolar protein sorting 13C (yeast)	upstream mmu-mir-190
3	87180840	87181224	385	2540	Yes	No	No	Yes	ENSMUSG00000059994	Fcrl1	Fc receptor-like 1	upstream mmu-mir-3093
6	122594236	122594653	418	3406	Yes	No	No	Yes	ENSMUSG00000046323	Dppa3	developmental pluripotency-associated 3	downstream mmu-mir-141
13	12265549	12265974	426	930	Yes	No	No	Yes	ENSMUSG00000071543	---	NA	upstream mmu-mir-466i
15	100498067	100498413	347	1508	Yes	No	No	Yes	ENSMUSG00000075411	---	NA	upstream mmu-mir-1941
2	29747152	29747467	316	2161	Yes	No	No	Yes	ENSMUSG00000026790	Odf2	outer dense fiber of sperm tails 2	upstream mmu-mir-219-2
3	54436844	54437123	280	2489	Yes	No	No	Yes	ENSMUSG00000027751	Fam48a	family with sequence similarity 48, member A	upstream mmu-mir-15b

reg. ID	Chr.	start	end	width	Enrichment meDNA				ENSEMBL ID	symbol	gene name	next miRNA
					5-Htt+/+		5-Htt+/-					
					C	PS	C	PS				
9	42212056	42212330	275	3987	Yes	No	No	Yes	ENSMUSG00000037705	Tecta	tectorin alpha	downstream mmu-mir-125b-1
17	24171843	24172081	239	1676	Yes	No	No	Yes	ENSMUSG00000050762	Prss27	protease, serine, 27	downstream mmu-mir-5134
17	87359293	87359731	439	1811	Yes	No	No	Yes	ENSMUSG00000024143	Rhoq	ras homolog gene family, member Q	upstream mmu-mir-1195
2	126374638	126374954	317	2303	Yes	No	No	Yes	ENSMUSG00000027359	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	downstream mmu-mir-147
6	136886442	136886658	217	3440	Yes	No	No	Yes	ENSMUSG00000030220	Arhgdib	Rho, GDP dissociation inhibitor (GDI) beta	downstream mmu-mir-680-1
17	29656335	29656796	462	1688	Yes	No	No	Yes	ENSMUSG00000024014	Pim1	proviral integration site 1	upstream mmu-mir-3083
19	34326627	34327071	445	2023	Yes	No	No	Yes	ENSMUSG00000035783	Acta2	actin, alpha 2, smooth muscle, aorta	downstream mmu-mir-107
17	45670186	45670390	205	1733	Yes	No	No	Yes	ENSMUSG00000023949	Tcte1	t-complex-associated testis expressed 1	upstream mmu-mir-693
7	30315563	30316083	521	3508	Yes	No	No	Yes	ENSMUSG00000074224	4932431P20Rik	RIKEN cDNA 4932431P20 gene	upstream mmu-mir-1964
13	22074876	22075224	349	941	Yes	No	No	Yes	ENSMUSG00000016982	Pom121l2	POM121 membrane glycoprotein-like 2 (rat)	upstream mmu-mir-1983
8	13055218	13055381	164	3730	Yes	No	No	Yes	ENSMUSG00000031445 // ENSMUSG00000031444	Proz // F10	protein Z, vitamin K-dependent plasma glycoprotein // coagulation factor X	downstream mmu-mir-1968
10	98590819	98591055	237	408	Yes	No	No	Yes	ENSMUSG00000055108 // ENSMUSG00000019952	Phxr2 // Poc1b	per-hexamer repeat gene 2 // POC1 centriolar protein homolog B (Chlamydomonas)	downstream mmu-mir-3966
16	35858088	35858439	352	1567	Yes	No	No	Yes	ENSMUSG00000034422	Parp14	poly (ADP-ribose) polymerase family, member 14	downstream mmu-mir-1947
15	73436045	73436479	435	1382	Yes	No	No	Yes	ENSMUSG00000036649 // ENSMUSG00000079020	--- // Slc45a4	NA // solute carrier family 45, member 4	upstream mmu-mir-151
6	137697901	137698137	237	3443	Yes	No	No	Yes	ENSMUSG00000030225 // ENSMUSG00000030224	Dera // Strap	2-deoxyribose-5-phosphate aldolase homolog (C. elegans) // serine/threonine kinase receptor associated protein	downstream mmu-mir-680-1
2	4574712	4574910	199	2124	Yes	No	No	Yes	ENSMUSG00000039449	Prpf18	PRP18 pre-mRNA processing factor 18 homolog (yeast)	upstream mmu-mir-466m
15	7346643	7346911	269	1321	Yes	No	No	Yes	ENSMUSG00000042961	Egflam	EGF-like, fibronectin type III and laminin G domains	upstream mmu-mir-1898
1	171386341	171386918	578	186	Yes	No	No	Yes	ENSMUSG00000058622	Gm5265	predicted pseudogene 5265	downstream mmu-mir-214
2	31283794	31284116	323	2167	Yes	No	No	Yes	ENSMUSG00000076441 // ENSMUSG00000055632	Ass1 // Hmcn2	arginiNosuccinate synthetase 1 // hemicentin 2	downstream mmu-mir-3089
5	3597766	3598151	386	2955	Yes	No	No	Yes	ENSMUSG00000040302 // ENSMUSG00000005907	C030048B08Rik // Pex1	RIKEN cDNA C030048B08 gene // peroxisomal biogenesis factor 1	upstream mmu-mir-879
13	93344528	93344898	371	1057	Yes	No	No	Yes	ENSMUSG00000046957	Spz1	spermatogenic leucine zipper 1	upstream mmu-mir-5624
14	26694148	26694447	300	1141	Yes	No	No	Yes	ENSMUSG00000052323 // ENSMUSG00000021866	--- // Anxa11	NA // annexin A11	downstream mmu-mir-3075
13	115756459	115756663	205	1119	Yes	No	No	Yes	ENSMUSG00000015533 // ENSMUSG00000042284	Itga2 // Itga1	integrin alpha 2 // integrin alpha 1	downstream mmu-mir-449a
8	113571557	113571907	351	3885	Yes	No	No	Yes	ENSMUSG00000080049 // ENSMUSG00000031960	--- // Aars	NA // alanyl-tRNA synthetase	upstream mmu-mir-3473d
7	28833208	28833515	308	3498	Yes	No	No	Yes	ENSMUSG00000030603	Psmc4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	downstream mmu-mir-1191
7	20380218	20380383	166	3481	Yes	No	No	Yes	ENSMUSG00000040525	Cblc	Casitas B-lineage lymphoma c	downstream mmu-mir-343
14	80984313	80984631	319	1273	Yes	No	No	Yes	ENSMUSG00000022026	Olfm4	olfactomedin 4	downstream mmu-mir-759

Supplementary Table 2

Enriched annotation term clusters of differentially methylated regions (DMRs) in the hippocampus of female *5-Htt+/-* and *5-Htt+/+* mice, exposed to prenatal stress (PS) or not (control, C). Clusters identified by Functional Annotation Clustering using DAVID. Score = enrichment score, FE = fold enrichment. Term with scores higher than 1.3 were considered enriched. G = genotype, E = environment, GxE = gene x environment interaction.

Cluster	Score	Category	Enrichment Term	# Genes	% Genes	p	FE
A) G-effects: 5-Htt+/+ vs 5-Htt+/-							
1	1,37	SP_PIR_KEYWORDS	ribosomal protein	8	2,87	0,01	3,67
		GOTERM_CC_FAT	GO:0005840~ribosome	8	2,87	0,01	3,52
		GOTERM_MF_FAT	GO:0003735~structural constituent of ribosome	7	2,51	0,01	3,83
		GOTERM_CC_FAT	GO:0030529~ribonucleoprotein complex	11	3,94	0,05	2,01
		GOTERM_BP_FAT	GO:0006412~translation	8	2,87	0,09	2,10
		GOTERM_MF_FAT	GO:0005198~structural molecule activity	10	3,58	0,09	1,83
		SP_PIR_KEYWORDS	ribonucleoprotein	6	2,15	0,23	1,83
		KEGG_PATHWAY	mmu03010:Ribosome	3	1,08	0,30	2,72
2	1,34	GOTERM_MF_FAT	GO:0043167~ion binding	61	21,86	0,02	1,28
		GOTERM_MF_FAT	GO:0043169~cation binding	60	21,51	0,02	1,27
		GOTERM_MF_FAT	GO:0046872~metal ion binding	59	21,15	0,03	1,26
		SP_PIR_KEYWORDS	zinc-finger	23	8,24	0,04	1,55
		GOTERM_MF_FAT	GO:0008270~zinc ion binding	34	12,19	0,06	1,33
		SP_PIR_KEYWORDS	metal-binding	42	15,05	0,08	1,27
		GOTERM_MF_FAT	GO:0046914~transition metal ion binding	40	14,34	0,08	1,27
		SP_PIR_KEYWORDS	zinc	30	10,75	0,12	1,29
B) E-effects: Controls vs Prenatal stress							
1	2,06	INTERPRO	IPR019775:WD40 repeat, conserved site	13	3,24	0,00	2,94
		SP_PIR_KEYWORDS	wd repeat	13	3,24	0,00	2,84
		UP_SEQ_FEATURE	repeat:WD 3	12	2,99	0,00	2,87
		UP_SEQ_FEATURE	repeat:WD 1	12	2,99	0,00	2,82
		UP_SEQ_FEATURE	repeat:WD 2	12	2,99	0,00	2,82
		INTERPRO	IPR017986:WD40 repeat, region	11	2,74	0,01	2,82
		UP_SEQ_FEATURE	repeat:WD 4	11	2,74	0,01	2,79
		UP_SEQ_FEATURE	repeat:WD 6	9	2,24	0,01	3,09
		UP_SEQ_FEATURE	repeat:WD 5	10	2,49	0,01	2,73
		INTERPRO	IPR019782:WD40 repeat 2	10	2,49	0,01	2,73
		INTERPRO	IPR001680:WD40 repeat	11	2,74	0,01	2,48
		INTERPRO	IPR019781:WD40 repeat, subgroup	10	2,49	0,02	2,49
		UP_SEQ_FEATURE	repeat:WD 7	7	1,75	0,02	3,12
		SMART	SM00320:WD40	11	2,74	0,04	2,07
		INTERPRO	IPR015943:WD40/YVTN repeat-like	10	2,49	0,08	1,92
2	1,77	SP_PIR_KEYWORDS	sh3 domain	10	2,49	0,01	2,81
		INTERPRO	IPR001452:Src homology-3 domain	10	2,49	0,01	2,77
		SMART	SM00326:SH3	10	2,49	0,03	2,31
		UP_SEQ_FEATURE	domain:SH3	8	2,00	0,03	2,71

3	1,72	GOTERM_CC_FAT	GO:0030017~sarcomere	6	1,50	0,01	4,38
		GOTERM_CC_FAT	GO:0031674~I band	5	1,25	0,01	5,51
		GOTERM_CC_FAT	GO:0044449~contractile fiber part	6	1,50	0,02	4,08
		GOTERM_CC_FAT	GO:0030016~myofibril	6	1,50	0,02	3,85
		GOTERM_CC_FAT	GO:0043292~contractile fiber	6	1,50	0,02	3,69
		GOTERM_CC_FAT	GO:0030018~Z disc	4	1,00	0,04	5,08
4	1,47	SP_PIR_KEYWORDS	tpr repeat	9	2,24	0,00	3,66
		INTERPRO	IPR011990:Tetratricopeptide-like helical	9	2,24	0,00	3,51
		UP_SEQ_FEATURE	repeat:TPR 3	8	2,00	0,01	3,75
		UP_SEQ_FEATURE	repeat:TPR 1	8	2,00	0,01	3,40
		UP_SEQ_FEATURE	repeat:TPR 2	8	2,00	0,01	3,40
		INTERPRO	IPR013026:Tetratricopeptide region	7	1,75	0,01	3,59
		UP_SEQ_FEATURE	repeat:TPR 5	5	1,25	0,02	4,53
		UP_SEQ_FEATURE	repeat:TPR 10	3	0,75	0,03	11,05
		UP_SEQ_FEATURE	repeat:TPR 9	3	0,75	0,06	7,53
		UP_SEQ_FEATURE	repeat:TPR 4	5	1,25	0,06	3,37
		UP_SEQ_FEATURE	repeat:TPR 6	4	1,00	0,08	4,02
		INTERPRO	IPR019734:Tetratricopeptide repeat	5	1,25	0,12	2,61
		UP_SEQ_FEATURE	repeat:TPR 8	3	0,75	0,15	4,36
		SMART	SM00028:TPR	5	1,25	0,19	2,18
		INTERPRO	IPR001440:Tetratricopeptide TPR-1	4	1,00	0,22	2,46
		UP_SEQ_FEATURE	repeat:TPR 7	3	0,75	0,22	3,38
5	1,31	INTERPRO	IPR001849:Pleckstrin homology	11	2,74	0,01	2,46
		SMART	SM00233:PH	11	2,74	0,04	2,06
		INTERPRO	IPR011993:Pleckstrin homology-type	10	2,49	0,06	2,02
		UP_SEQ_FEATURE	domain:PH	7	1,75	0,16	1,91
C) GxE-effects: 5-Htt x PS interaction							
1	2,14	GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	38	13,43	0,00	1,63
		GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	38	13,43	0,00	1,63
		GOTERM_CC_FAT	GO:0005856~cytoskeleton	25	8,83	0,00	1,83
		GOTERM_CC_FAT	GO:0044430~cytoskeletal part	18	6,36	0,01	1,91
		GOTERM_CC_FAT	GO:0015630~microtubule cytoskeleton	10	3,53	0,09	1,83
2	1,74	SP_PIR_KEYWORDS	hydroxylation	6	2,12	0,00	7,79
		INTERPRO	IPR008160:Collagen triple helix repeat	4	1,41	0,08	4,06
		SP_PIR_KEYWORDS	collagen	4	1,41	0,08	3,95
3	1,72	GOTERM_MF_FAT	GO:0030246~carbohydrate binding	11	3,89	0,01	2,81
		GOTERM_MF_FAT	GO:0005529~sugar binding	8	2,83	0,01	3,58
		SP_PIR_KEYWORDS	Lectin	7	2,47	0,02	3,48
		UP_SEQ_FEATURE	domain:Ricin B-type lectin	3	1,06	0,03	10,71
		INTERPRO	IPR000772:Ricin B lectin	3	1,06	0,04	8,81
		SMART	SM00458:RICIN	3	1,06	0,05	8,15
4	1,71	GOTERM_BP_FAT	GO:0030029~actin filament-based process	8	2,83	0,01	3,57

		GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	7	2,47	0,02	3,33
		GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	9	3,18	0,06	2,17
5	1,69	INTERPRO	IPR006209:EGF	8	2,83	0,00	5,14
		INTERPRO	IPR000152:EGF-type aspartate/asparagine hydroxylation conserved site	6	2,12	0,01	5,25
		INTERPRO	IPR000742:EGF-like, type 3	8	2,83	0,01	3,31
		INTERPRO	IPR006210:EGF-like	8	2,83	0,01	3,24
		SMART	SM00181:EGF	8	2,83	0,02	3,00
		SP_PIR_KEYWORDS	egf-like domain	8	2,83	0,02	2,99
		INTERPRO	IPR001881:EGF-like calcium-binding	5	1,77	0,02	4,52
		INTERPRO	IPR018097:EGF-like calcium-binding, conserved site	5	1,77	0,03	4,37
		SMART	SM00179:EGF_CA	5	1,77	0,03	4,18
		INTERPRO	IPR013032:EGF-like region, conserved site	9	3,18	0,04	2,39
		INTERPRO	IPR013091:EGF calcium-binding	4	1,41	0,05	4,77
		UP_SEQ_FEATURE	domain:EGF-like 2	4	1,41	0,08	3,98
		UP_SEQ_FEATURE	domain:EGF-like 1	4	1,41	0,15	2,96

Supplementary Table 3

Overview of the behavioral effects that we assessed in the same animals as used for the gene expression and DNA methylation study (published previously, Van den Hove & Jakob 2011, PLOS One[4]). FST = forced swim test, EZM = elevated zero maze, ORT = object recognition test, CORT = corticosterone levels. For details, see [4] in the references of the main text.

	G	**E**	**GxE**
FST, distance moved	=	↓	=
EZM, time spent in open arms	↑	=	=
EZM, distance moved	=	↓	=
ORT, 2h	=	↓	=
ORT, 3h	↑	=	=
CORT baseline	↓	=	=
CORT stress	=	=	=
CORT recovery	=	=	=
Adrenal weight	↑	=	=

Supplementary Table 4

Clusters of highly correlating genes identified using Modulatory Modularity Cluster (MMC) analysis on differentially expressed myelin-associated genes in the hippocampus of female *5-Htt+/-* and *5-Htt+/+* mice, exposed to prenatal stress (PS) or not (control, C). Avarage.Degree = avarage correlation of the cluster, Degree = correlation of single genes with the rest of the cluster. Clusters contaning *myelin basic protein (Mbp)* are highlighed in orange.

Module	Affy.ID	Entry.Index	Average.Degree	Degree	mgi.symbol
1	1440902_at	164	0.77156	0.81119	Ermn
1	1436578_at	147	0.77156	0.77972	Ermn
1	1456689_at	235	0.77156	0.72378	Rnf10
2	1426639_a_at	91	0.74126	0.83916	Tcf7l2
2	1418815_at	22	0.74126	0.69231	Cdh2
2	1450790_at	204	0.74126	0.69231	Tg
3	1443837_x_at	173	0.73846	0.80245	Bcl2
3	1421241_at	41	0.73846	0.74126	Ngfr
3	1419601_at	30	0.73846	0.73776	Kcnj10
3	1433886_at	130	0.73846	0.73601	Eif2b5
3	1438819_at	158	0.73846	0.67483	Nab1
4	1450180_a_at	198	0.73776	0.78555	Rara
4	1431781_at	123	0.73776	0.75291	Ypel1
4	1419415_a_at	27	0.73776	0.70629	Rarg
4	1450523_at	200	0.73776	0.70629	Cntn2
5	1451961_a_at	212	0.72734	0.83516	Mbp
5	1426960_a_at	94	0.72734	0.82168	Fa2h
5	1450088_a_at	195	0.72734	0.81269	Mobp
5	1460219_at	246	0.72734	0.76474	Mag
5	1421010_at	36	0.72734	0.75325	Mobp
5	1424567_at	67	0.72734	0.75325	Tspan2
5	1454722_at	224	0.72734	0.74525	Pten
5	1432558_a_at	126	0.72734	0.72478	Mal
5	1419064_a_at	25	0.72734	0.72378	Ugt8a
5	1425467_a_at	80	0.72734	0.70929	Plp1
5	1454078_a_at	220	0.72734	0.69081	Gal3st1
5	1417551_at	13	0.72734	0.68731	Cln3
5	1435166_at	139	0.72734	0.66234	Cntn2
5	1422833_at	55	0.72734	0.64136	Foxa2
5	1422068_at	46	0.72734	0.58442	Pou3f1
6	1421048_a_at	37	0.69231	0.79021	Ypel1
6	1460180_at	245	0.69231	0.73427	Hexb
6	1453977_at	218	0.69231	0.68065	Exoc4
6	1450177_at	197	0.69231	0.5641	Ngfr
7	1431782_s_at	124	0.68741	0.79895	Ypel1
7	1421678_at	42	0.68741	0.72028	Itpr2
7	1450748_at	202	0.68741	0.71154	Smpd3
7	1427693_at	103	0.68741	0.65035	Itpr2
7	1436727_x_at	149	0.68741	0.55594	Sptlc1

8	1422994_at	58	0.6819	0.77078	Pikfyve
8	1427206_at	95	0.6819	0.75758	Afg3l2
8	1447874_x_at	182	0.6819	0.7265	Smpd1
8	1448710_at	184	0.6819	0.70319	Cxcr4
8	1445360_at	177	0.6819	0.68765	Tgfb1
8	1434538_x_at	135	0.6819	0.65657	Eif2b2
8	1419416_a_at	28	0.6819	0.65579	Rarg
8	1416990_at	5	0.6819	0.64413	Rxrb
8	1427207_s_at	96	0.6819	0.64258	Afg3l2
8	1419132_at	26	0.6819	0.5742	Tlr2
9	1429530_a_at	111	0.65501	0.73427	Smpd4
9	1454773_at	225	0.65501	0.7296	Rxra
9	1443011_at	172	0.65501	0.59907	Prmt7
9	1422690_at	51	0.65501	0.55711	Sptlc1
10	1451718_at	210	0.62987	0.73726	Plp1
10	1437224_at	152	0.62987	0.6953	Rtn4
10	1439989_at	161	0.62987	0.69231	Tsc1
10	1426010_a_at	87	0.62987	0.68232	Epb4.1l3
10	1444117_at	174	0.62987	0.65734	Amigo1
10	1455989_at	229	0.62987	0.64735	Gjc2
10	1458408_at	240	0.62987	0.48651	Samd8
10	1430650_at	118	0.62987	0.44056	Zfp191
11	1435165_at	138	0.61993	0.76503	Cntn2
11	1417275_at	9	0.61993	0.74452	Mal
11	1419646_a_at	31	0.61993	0.72214	Mbp
11	1433785_at	129	0.61993	0.72121	Mobp
11	1439506_at	159	0.61993	0.68625	Myrf
11	1424568_at	68	0.61993	0.67086	Tspan2
11	1427420_at	99	0.61993	0.67086	Nkx6-2
11	1417133_at	8	0.61993	0.63263	Pmp22
11	1418663_at	19	0.61993	0.62005	Mpdz
11	1416999_at	6	0.61993	0.61585	Smpd2
11	1440770_at	163	0.61993	0.61352	Bcl2
11	1422686_s_at	50	0.61993	0.59347	Exoc4
11	1450655_at	201	0.61993	0.53613	Pten
11	1444418_at	176	0.61993	0.45082	Itpr2
11	1459020_at	241	0.61993	0.44942	Amigo1
11	1416635_at	4	0.61993	0.42611	Smpdl3a
12	1449244_at	190	0.61958	0.73951	Cdh2
12	1423259_at	62	0.61958	0.68706	Id4
12	1424838_at	71	0.61958	0.6486	Ncmap
12	1426576_at	90	0.61958	0.58392	Sgms1
12	1420653_at	34	0.61958	0.43881	Tgfb1
13	1438454_at	155	0.56794	0.71284	Pten
13	1418664_at	20	0.56794	0.71216	Mpdz
13	1455728_at	228	0.56794	0.6993	Pten
13	1448621_a_at	183	0.56794	0.68306	Smpd1
13	1419754_at	33	0.56794	0.67539	Myo5a
13	1426896_at	93	0.56794	0.66704	Zfp191
13	1421064_at	38	0.56794	0.66095	Mpp5

13	1417624_at	15	0.56794	0.65847	Nab1
13	1431320_a_at	122	0.56794	0.65509	Myo5a
13	1434954_at	137	0.56794	0.63321	Mpp5
13	1422847_a_at	56	0.56794	0.62711	Prkcd
13	1416531_at	3	0.56794	0.61606	Gsto1
13	1449940_a_at	192	0.56794	0.61155	Eif2b4
13	1452994_at	214	0.56794	0.60388	Pikfyve
13	1425460_at	79	0.56794	0.60072	Mtmr2
13	1442978_at	171	0.56794	0.59486	Mpdz
13	1457493_at	237	0.56794	0.59328	Pten
13	1460571_at	248	0.56794	0.58403	Dicer1
13	1440595_at	162	0.56794	0.58313	Epb4.1l3
13	1436205_at	144	0.56794	0.56801	Nfasc
13	1453182_a_at	215	0.56794	0.53643	Smpd4
13	1450113_at	196	0.56794	0.52109	Mpp5
13	1450928_at	206	0.56794	0.5062	Id4
13	1426895_at	92	0.56794	0.5035	Zfp191
13	1451248_at	209	0.56794	0.48928	Prmt7
13	1455993_at	230	0.56794	0.48139	Tenm4
13	1436051_at	142	0.56794	0.45883	Myo5a
13	1430371_x_at	115	0.56794	0.45319	Eif2ak3
13	1439650_at	160	0.56794	0.45048	Rtn4
13	1454903_at	226	0.56794	0.41642	Ngfr
13	1423260_at	63	0.56794	0.39477	Id4
13	1416412_at	2	0.56794	0.22242	Nsmaf
14	1425947_at	86	0.52044	0.65113	Ifng
14	1442253_at	169	0.52044	0.57187	Ercc2
14	1429428_at	110	0.52044	0.5641	Tcf7l2
14	1425229_a_at	75	0.52044	0.54545	Tcf7l2
14	1429427_s_at	109	0.52044	0.52991	Tcf7l2
14	1425796_a_at	84	0.52044	0.52525	Fgfr3
14	1424834_s_at	70	0.52044	0.47552	Itpr2
14	1459209_at	242	0.52044	0.46154	Rnf10
14	1453505_a_at	216	0.52044	0.45921	Eif2ak3
14	1450483_at	199	0.52044	0.42036	Gjc2
15	1418212_at	18	0.5078	0.65697	Omg
15	1437874_s_at	154	0.5078	0.63047	Hexb
15	1422042_at	44	0.5078	0.62275	Gjc3
15	1445523_at	178	0.5078	0.60397	Gjc3
15	1441964_at	167	0.5078	0.59919	Qk
15	1430497_at	116	0.5078	0.58557	Rxra
15	1419063_at	24	0.5078	0.5657	Ugt8a
15	1433571_at	128	0.5078	0.56496	Serinc5
15	1431101_a_at	121	0.5078	0.56386	Srd5a1
15	1421116_a_at	39	0.5078	0.5587	Rtn4
15	1457789_at	239	0.5078	0.55208	Cln3
15	1422684_a_at	48	0.5078	0.54693	Exoc4
15	1454257_at	221	0.5078	0.44755	Sptlc2
15	1422938_at	57	0.5078	0.4435	Bcl2
15	1427287_s_at	97	0.5078	0.43688	Itpr2

15	1422685_at	49	0.5078	0.42657	Exoc4
15	1456068_at	233	0.5078	0.40964	Nfasc
15	1435937_at	141	0.5078	0.34855	Sptlc2
15	1425468_at	81	0.5078	0.3191	Plp1
15	1417300_at	11	0.5078	0.2731	Smpdl3b
16	1422779_at	53	0.50296	0.66525	Smpd3
16	1421841_at	43	0.50296	0.62481	Fgfr3
16	1456010_x_at	231	0.50296	0.61204	Hes5
16	1425264_s_at	77	0.50296	0.61082	Mbp
16	1429735_at	113	0.50296	0.59775	Qk
16	1427682_a_at	101	0.50296	0.59137	Egr2
16	1455252_at	227	0.50296	0.5792	Tsc1
16	1417839_at	16	0.50296	0.57708	Cldn5
16	1449278_at	191	0.50296	0.55275	Eif2ak3
16	1449024_a_at	189	0.50296	0.55184	Hexa
16	1427683_at	102	0.50296	0.54454	Egr2
16	1423146_at	60	0.50296	0.49711	Hes5
16	1451888_a_at	211	0.50296	0.4959	Tenm4
16	1429318_a_at	108	0.50296	0.49438	Qk
16	1438699_at	157	0.50296	0.47826	Srd5a1
16	1437122_at	151	0.50296	0.47796	Bcl2
16	1446974_at	180	0.50296	0.46732	Pikfyve
16	1429736_at	114	0.50296	0.44208	Qk
16	1448781_at	186	0.50296	0.41745	Nab1
16	1442256_at	170	0.50296	0.41593	Prkcd
16	1441361_at	166	0.50296	0.37884	Mpdz
16	1457687_at	238	0.50296	0.34813	Bcl2
16	1423504_at	66	0.50296	0.33779	Jam3
16	1418782_at	21	0.50296	0.31256	Rxrg
17	1423102_a_at	59	0.50157	0.65812	Rnf10
17	1423221_at	61	0.50157	0.63015	Tubb4a
17	1449942_a_at	193	0.50157	0.62432	Ilk
17	1427481_a_at	100	0.50157	0.62393	Atp1a3
17	1417930_at	17	0.50157	0.59207	Nab2
17	1417456_at	12	0.50157	0.58042	Gnpat
17	1448807_at	187	0.50157	0.57187	Hrh3
17	1422553_at	47	0.50157	0.55556	Pten
17	1417558_at	14	0.50157	0.54429	Fyn
17	1430651_s_at	119	0.50157	0.51943	Zfp191
17	1429531_at	112	0.50157	0.50466	Smpd4
17	1447811_s_at	181	0.50157	0.49883	Amigo1
17	1454649_at	222	0.50157	0.48912	Srd5a1
17	1448945_at	188	0.50157	0.46698	Pllp
17	1423292_a_at	64	0.50157	0.39122	Prx
17	1453730_at	217	0.50157	0.38578	Samd8
17	1434402_at	133	0.50157	0.36092	Samd8
17	1425263_a_at	76	0.50157	0.33411	Mbp
17	1424833_at	69	0.50157	0.19814	Itpr2
18	1430533_a_at	117	0.49184	0.64248	Ctnnb1
18	1438665_at	156	0.49184	0.57692	Smpd3

18	1431062_a_at	120	0.49184	0.50524	Exoc4
18	1454003_at	219	0.49184	0.5	Afg3l2
18	1460727_at	249	0.49184	0.49738	Ercc2
18	1450762_s_at	203	0.49184	0.48077	Zfp191
18	1450008_a_at	194	0.49184	0.46241	Ctnnb1
18	1426096_at	88	0.49184	0.41259	Prmt7
18	1460038_at	244	0.49184	0.34878	Pou3f1
19	1422043_at	45	0.48881	0.62587	Tsc1
19	1421166_at	40	0.48881	0.5507	Atrn
19	1425851_a_at	85	0.48881	0.52622	Amigo1
19	1424919_at	73	0.48881	0.42832	Erbb2
19	1445908_at	179	0.48881	0.31294	Eif2b5
20	1436726_s_at	148	0.48298	0.62937	Sptlc1
20	1456036_x_at	232	0.48298	0.61259	Gsto1
20	1425459_at	78	0.48298	0.47413	Mtmr2
20	1426575_at	89	0.48298	0.4042	Sgms1
20	1419577_at	29	0.48298	0.39441	Fig4
20	1448765_at	185	0.48298	0.38322	Fyn
21	1422691_at	52	0.48252	0.58508	Sptlc1
21	1441308_at	165	0.48252	0.55594	Mobp
21	1423503_at	65	0.48252	0.54895	Jam3
21	1425061_at	74	0.48252	0.49068	Wasf3
21	1436263_at	145	0.48252	0.47902	Mobp
21	1456962_at	236	0.48252	0.47436	Cntn2
21	1428995_at	106	0.48252	0.24359	Smpd5
22	1436499_at	146	0.47226	0.59907	Sgms1
22	1437024_at	150	0.47226	0.56255	Smpd4
22	1434121_at	131	0.47226	0.55556	Lgi4
22	1451136_a_at	207	0.47226	0.48329	Eif2b2
22	1419722_at	32	0.47226	0.46387	Klk8
22	1428663_at	105	0.47226	0.44522	Sgms2
22	1424856_at	72	0.47226	0.43434	Atp1a3
22	1460243_at	247	0.47226	0.4289	Sptlc2
22	1437428_x_at	153	0.47226	0.40171	Eif2b2
22	1429029_at	107	0.47226	0.3481	Sgms2
23	1433532_a_at	127	0.4334	0.6014	Mbp
23	1420811_a_at	35	0.4334	0.5609	Ctnnb1
23	1456228_x_at	234	0.4334	0.5574	Mbp
23	1419062_at	23	0.4334	0.55274	Epb4.1l3
23	1425762_a_at	83	0.4334	0.55099	Rxra
23	1434530_at	134	0.4334	0.53001	Tenm4
23	1459357_at	243	0.4334	0.52069	Nfasc
23	1436201_x_at	143	0.4334	0.50262	Mbp
23	1416232_at	1	0.4334	0.49767	Olig2
23	1450803_at	205	0.4334	0.48164	Ntf3
23	1417073_a_at	7	0.4334	0.46941	Qk
23	1452649_at	213	0.4334	0.44435	Rtn4
23	1435214_at	140	0.4334	0.44231	Gjc2
23	1427941_at	104	0.4334	0.43269	Dicer1
23	1434197_at	132	0.4334	0.41725	Atrn

23	1451179_a_at	208	0.4334	0.40793	Qk
23	1434802_s_at	136	0.4334	0.39277	Ntf3
23	1422810_at	54	0.4334	0.36888	Zfp191
23	1427373_at	98	0.4334	0.35606	Amigo1
23	1432417_a_at	125	0.4334	0.32488	Tspan2
23	1454651_x_at	223	0.4334	0.32197	Mbp
23	1444243_at	175	0.4334	0.30828	Wasf3
23	1442079_at	168	0.4334	0.29516	Sgms1
23	1425597_a_at	82	0.4334	0.28497	Qk
23	1417297_at	10	0.4334	0.21212	Itpr3