

# Supplementary Materials for

## MicroRNA-128 governs neuronal excitability and motor behavior in mice

**Authors:** *Chan Lek Tan[1#], Joshua L. Plotkin[2], Morten T. Venø[3], Melanie von Schimmelmann[1,4], Philip Feinberg[1,4], Silas Mann[1,4], Annie Handler[1], Jørgen Kjems[3], D. James Surmeier[2], Dónal O'Carroll[5,6], Paul Greengard[1], and Anne Schaefer[1,4*]*

correspondence to: anne.schaefer@mssm.edu

**This PDF file includes:**

Materials and Methods
Figures S1 to S10
Tables S1 to S4
Captions for Movies S1

**Other Supplementary Materials for this manuscript includes the following:**

Movie S1

## Materials and Methods

### Animals

Mice were housed at two to five animals per cage with a 12-hour light/dark cycle (lights on from 0700 to 1900 hours) at constant temperature (23 ºC) with *ad libitum* access to food and water. All animal protocols were approved by IACUC at The Rockefeller University, The Northwestern University, and Icahn School of Medicine at Mount Sinai.

### Generation of Mice

Generation of mice with a conditional deletion of *miR-128-1* and *miR-128-2*:

*Subcloning of targeting vectors:* A region of the *miR-128-1* or *miR-128-2* genomic locus containing the arms of homology was recombinogenically subcloned from a BAC clone (*mir128-1*: RP24-574G14, *miR128-2*: RP24-242F13, C57Bl/6J, CHORI, Oakland CA, USA) into pBlueScriptIIKS+ using amplicons that insert an AscI site and a XhoI site to flank the subcloned region.

PCR primers used for subcloning:

*mir-128-1*

5' ccttcatgttatgccctcatccctttatcacacaaatctgtgtagttttcggcgcgccattcgccctatagtgagtcg

5' aatcttctaaatttccatttgagcacctagttcatatgtaatttagattcctcgaggcttggcgtaatcatggtc

*mir-128-2*

5' cgaaaaatattttcatttattcttcgaaactttcatacattcatacaatgtggcgcgccattcgccctatagtgagtcg

5' tcaggcctgccagccttctgtctactgtttaatgactgacagccagtgaactcgaggcttggcgtaatcatggtc

*Modification of targeting vector for miR-128-1:*

pZeroloxP-FRT-neoR-FRT(-) was modified to replace the unique EcoRI site with a unique SmaI site. The following oligonucleotide fragments were annealed and inserted into the EcoRI site:

5' aattgcatcgcatgggtcacgacgagatcccgggc

5' aattgcccgggatctcgtcgtgacccatgcgatgc

The modified plasmid was digested with NsiI, and the fragment containing a single loxP site and the FRT-flanked *neo* gene was inserted into the unique NsiI site in the targeting vector and screened for proper orientation. For insertion of the second loxP site, the following oligonucleotide fragments were annealed and inserted into the unique SpeI site:
5' ctagaataacttcgtatagcatacattatacgaagttatgaattct
5' ctagagaattcataacttcgtataatgtatgctatacgaagttatt

*Modification of targeting vector for miR-128-2*
pZeroloxP-FRT-neoR-FRT(-) was modified by digesting the plasmid with SacI and ApaI and annealing and inserting the following oligonucleotide fragments:
5'ggaagttcctatactttctagagaataggaacttcggaataggaacttcagagctcatcgagcccgggtagacggccc
5'gtctacccgggctcgatgagctctgaagttcctattccgaagttcctattctctagaaagtataggaacttccagct
The plasmid was further digested with Acc65I and the following oligonucleotides were annealed and inserted:
5' gtacccccgggataacttcgtatagcatacattatacgaagttataagcttc
5' gtacgaagcttataacttcgtataatgtatgctatacgaagttatcccgggg

The modified plasmid was digested with SmaI and the fragment containing a single loxP site and the FRT-flanked *neo* gene was inserted into the unique SmaI site in the targeting vector and screened for proper orientation. For insertion of the second loxP site, the following oligonucleotides were annealed and inserted into the unique HindIII site:
5' agctaataacttcgtatagcatacattatacgaagttatggatcct
5' agctaggatccataacttcgtataatgtatgctatacgaagttatt

For both targeting vectors, the modified regions of homology were excised from pBluescript with XhoI and AscI digests and inserted into similarly digested pDTA-TK to produce the final targeting constructs. The targeting constructs were linearized with NotI, and E14 CY2.4 embryonic stem cells (homozygous C57Black/6JTyr-C-2J background with natural mutation in tyrosinase gene) were transfected and screened for successful recombination using a Southern probe. Positive clones were confirmed using an alternate Southern probe and by PCR sequencing of the modified region. Positive clones were used

to produce chimeric mice as described. Chimeras were crossed to C57BL6/J mice, and germline transmission was assessed by coat color, PCR and Southern blot analysis. Germline deletion of the FRT-flanked *neo* gene was accomplished by crossing mice carrying the targeted alleles with FLPe- transgenic mice (Jackson Laboratory). Germline deletion of *miR-128-1* and *miR-128-2* to generate *miR-128-1*$^{-/-}$ and *miR-128-2*$^{-/-}$ mice was achieved by crossing mice carrying floxed alleles to transgenic mice that express Cre-recombinase driven by the ubiquitously expressed *CMV* promoter (*CMV-cre* mice, Jackson Laboratory).

Postnatal, neuron-specific deletion in the mouse forebrain was achieved by breeding mice carrying floxed alleles (*miR-128-2*$^{fl/fl}$) to *Camk2a-cre* mice (*31*) to generate *Camk2a-cre; miR-128-2*$^{fl/fl}$ *mice*. *Drd1a-cre* (EY262) and *A2a-cre* (KG139) transgenic mice were obtained from Gensat (*32*) and crossed with *miR-128-2*$^{fl/fl}$ to generate *Drd1a*-cre; *miR-128-2*$^{fl/fl}$ and *A2a*-cre; *miR-128-2*$^{fl/fl}$ mice.

Routine genotyping of *miR-128-1* mice was performed using following primers:
5'-tctggaccaaatgaaccaaag
5'-ccgcaatgctgcctatattc
5'-gcctgaagaacgagatcagc
5'-gcagtcatgcaagcagctat

Wild type allele: 194bp
Null allele: 282bp
Floxed allele: 336bp

Routine genotyping of *miR-128-2* mice was performed using following primers:
5'-cgccttttagtttcccacag
5'-gaccacacagcaagcaggta
5'-aaagacgggaccattcacat
5'-tctctcgtgggatcattgttt

Wild type allele: 185bp
Null allele: 531bp
Floxed allele: 306bp

Generation of mice with a neuron-specific overexpression of *mir-128-2*.

The targeting vector for homologous recombination at the *ROSA26* locus was generously provided by K. Rajewsky (*30*). A 1kb region including miR-128-2 hairpin was amplified from genomic DNA with the following primers and cloned into the unique XhoI site in the targeting vector:
5' aaaggcgcgccacgtgACTAAAAGGCGCGAGGAGAT
5' aaaggcgcgccTACGCATTCCTGTACGGTTG

Modified targeting vector was linearized by NotI and used to generate chimeras as above. Successful germline transmission was assessed by coat color and confirmed by PCR and Southern analysis. Routine genotyping of *Rosa-miR-128* mice was performed using the following primers:
5'-gagttctctgctgcctcctg
5'-ggaaagtccctattggcgtta
5'-tgctgcataaaaccccagat

Wild type allele: 292 bp
*Rosa-miR-128* targeted allele: 408 bp

Postnatal, neuron-specific miR-128-2 overexpression in the mouse forebrain was achieved by breeding homozygous *Rosa-miR-128* mice to *Camk2a-cre* mice (*31*) to generate *Camk2a-cre; Rosa-miR-128* mice. *Rosa-miR-128* mice were bred to *Camk2a-cre; miR-128-2*$^{fl/fl}$ mice to generate *Camk2a-cre; miR-128-2*$^{fl/fl}$*; Rosa-miR-128* rescue mice.

Generation of mice with neuron-specific FLAG tagged-Ago2 expression:

Transgenic mice expressing a Cre-inducible FLAG-HA2-tagged Ago2 under the control

of the *ROSA26* promoter were generated as previously described (*9, 30*). The *STOP-eGFP-ROSA26TV* vector was a gift from K. Rajewsky, Harvard Medical School, Boston, MA. *Rosa-Stop$^{fl/fl}$-Flag-Ago2* mice were bred to *Camk2a-cre* transgenic mice (kindly provided by G. Schuetz, German Cancer Research Center, Heidelberg, Germany (*31*)) to generate *Camk2a-cre; Rosa-Stop$^{fl/fl}$-Flag-Ago2* mice.

**Camk2a-neuron specific RISC-associated RNA isolation and analysis**

*In vivo* Crosslinking and Immunoprecipitation (CLIP) procedure.

In three independent experiments (experiment 1-3), mice that express a Flag-tagged Ago2 protein specifically in Camk2+ neurons in the forebrain (*Camk2a-cre; Rosa-Stop$^{fl/fl}$-Flag-Ago2*) and control mice (*Rosa-Stop$^{fl/fl}$-Flag-Ago2*) were sacrificed at 8 to 14 weeks of age. Forebrains were excised, triturated to disrupt tissue, and UV-irradiated three times in a Stratalinker with 400mJ/cm$^2$. Immunoprecipitation was performed as described (*8*) with the following modifications to the protocol: After UV crosslinking the frozen lysates were sonicated to improve tissue homogenization. RNase digestion with RNase A was performed before IP (using one fourth the concentration of RNase A used by (*8*)), and after IP (using one twentieth the concentration of RNase A used by (*8*)). 30µl of magnetic beads pre-coupled to the M2 FLAG antibody (M8823, Sigma) were used for IP on half of one forebrain after pre-blocking the beads with 2% BSA, 1% t-RNAs and 1% salmon sperm for 1.5 hrs at 4$^o$ C. RNA was directly de-crosslinked from protein after extensive washing.

Illumina Sample Preparation and Sequencing.

The small RNA sample preparation kit, version 1.5 (Illumina), was used for library preparation with subtle modifications. Because low concentrations of RNA were purified from the CLIP procedure, as measured by Quant-iT RiboGreen RNA Assay (Invitrogen), the following modifications were made to the small RNA sample preparation kit (Illumina) to allow for low RNA input: Both the v1.5 sRNA 3' Adapter and the SRA 5' Adapter were diluted 10 times in nuclease-free water compared to the standard protocol before adapter ligation. The RT reaction was doubled (resulting in a final RT volume of 20 µl instead of the standard 10 µl), all of which was used for the downstream PCR

reaction. To allow for the larger volume of RT product, 10 µl less water was used in the PCR step, resulting in a final PCR volume of 50 µl. Instead of the 12 cycles of PCR directed in the standard protocol 15 cycles were performed to increase output.

RNA from four CLIP procedures were pooled for each library preparation, amounting to CLIP RNA from two mouse forebrains per library. At the end of the Illumina small RNA protocol, the products were purified from a gel at the size of 110 to 150 bp, containing adapter-linked RISC-associated mRNA target sites.

Prepared samples were amplified onto flow cells using the Illumina cluster station per manufacturer protocol and sequenced on the Illumina GAIIx platform for 76 cycles. Raw sequencing data was processed using the onboard SCS/RTA software.

Pre-processing of sequencing data

All sequence reads were trimmed by quality from both ends, removing any base with a quality score of less than 20. Next, reads were filtered to remove low quality reads, using a minimum average cutoff quality score of 20 over 90% of the read. Sequence reads were trimmed of any identifiable adapter sequence, and reads of at least 24 bases were used for mRNA target analysis. These reads were aligned to the current mouse genome (mm10) using bwa (Burrows-Wheeler Aligner) (*33*) with default settings for mismatch limits.

Aligned reads of three independent experiments:

| | |
|---|---|
| 1,826,496 | Control #1 |
| 2,889,818 | Flag-Ago2 #1 |
| | |
| 15,555,118 | Control #2 |
| 9,853,284 | Flag-Ago2 #2a |
| 8,634,607 | Flag-Ago2 #2b |
| | |
| 8,938,571 | Control #3 |
| 9,443,923 | Flag-Ago2 #3a |
| 7,405,866 | Flag-Ago2 #3b |

Detection of mRNA target sites clusters:

For the downstream analysis of mRNA targets, RISC-associated RNA reads were filtered and clustered to allow detection of mRNA target sites. Data processing is described below and shown as a flow chart in Fig. S5A. To reduce contributions of nonspecifically binding RNA species from cluster detection, any RISC-associated RNA read within 35 bp of 5 or more overlapping reads from the grouped control samples were discarded. Only reads occurring in at least two-filtered Flag-Ago2 samples were kept, and 30 nucleotides of genomic sequence was added to each end of the filtered reads. These reads were filtered to only retain clusters composed of minimum 10 overlapping reads. Filtering resulted in detection of 70,832 clusters. Genomic distribution of clusters was examined by use of Cis-regulatory Element Annotation System (CEAS) (*34*). Filtered clusters that specifically intersect with RefSeq 3'UTR plus 1 kilobase additional downstream genomic sequence (3'UTR+1kb) were used for MEME-ChIP analysis, 6mer analysis and genome-wide target site analysis.

MEME-ChIP analysis:

Enriched sequence motifs were detected by the motif discovery software, MEME-ChIP (*35*). The sequences of Ago2-CLIP clusters in the 3'UTR+1kb region of RefSeq genes (n=8794) were used as input for MEME-ChIP. A Markov background model was made from all 3'UTR+1kb regions in RefSeq and used with MEME-ChIP to allow detection of motifs enriched over the relevant background. Motifs were searched specifying that zero or one occurrence of a motif is present in each cluster sequence, the 'zoops' option. Otherwise, the default settings were used for the analysis.

6mer analysis:

The abundance of all possible 6mer sequences was found using the perl script countkmer.pl (by Marco Blanchette) on the sequences of Ago2-CLIP clusters in the 3'UTR+1kb region of RefSeq genes (n=8794). The same was done for all RefSeq 3'UTR+1kb genomic sequences to use as background (normalized to contain the same total number of 6mers as detected in clusters). The z-score and chi-square p-value were

calculated for all 6mer sequences enriched in clusters over RefSeq 3'UTR+1kb genomic sequences. The z-score was calculated for each 6mer by subtracting the abundance in RefSeq (background) from the abundance in clusters and subsequently dividing by the standard deviation of the background subtracted abundance of all 6mers. The value of the z-score conveys the distance from the mean for a given 6mer in units of standard deviation of the entire collection of 6mers.

Genome-wide target site analysis:

Bowtie (*36*) was used to map all occurrences of sequences complementary to the 6mer seed sequence of miR-128 in the mouse genome mm10, allowing no mismatches. Strand specific intersection was done with the filtered clusters in the 3'UTR+1kb RefSeq region, generating a genome-wide list with predicted miR-128 target sites.

**RNA Preparation**

Mice were anesthetized with $CO_2$, and the respective brain regions or peripheral organs were rapidly dissected and frozen in liquid nitrogen until further processing. RNA extraction from frozen samples was performed using the TRIzol/Chloroform technique according to manufacturer's instructions (Invitrogen Corporation, Carlsbad, CA). After extraction, RNA was precipitated overnight at -80C in isopropanol with 0.15M sodium acetate, washed twice with 70% ethanol, air-dried, and resuspended in RNase-free water.

**D1-neuron specific TRAP analysis**

Mice with D1-neuron specific loss of miR-128-2 (*Drd1a-cre; miR-128-2*$^{fl/fl}$) were crossed to mice carrying D1-MSN specific expression of eGFP-tagged ribosome protein L10 ((*11*), *D1-TRAP*). Polyribosome-associated mRNAs from 6 week old, age- and sex-matched *Drd1a-cre; Drd1a-TRAP; miR-128*$^{fl/fl}$ *and Drd1a-TRAP; miR-128*$^{fl/fl}$ mice (n=5/genotype) were obtained as previously described (*11*). eGFP-labeled ribosomes and associated mRNAs were immunoprecipitated using a mix of two monoclonal anti-GFP antibodies (50 μg of clones #19C8 and #19F7 for each IP, available at Sloan-Kettering Monoclonal Antibody Facility). Purified mRNA was amplified and processed for microarray and qPCR analysis using the Affymetrix two-cycle cDNA Synthesis kit

(Affymetrix, Santa Clara, CA) as previously described (*11*). Affymetrix Mouse Genome 430 2.0 arrays were used in all experiments. Information regarding the array design and features can be found at www.affymetrix.com. Mouse Genome 430 2.0 arrays were scanned using the GeneChip Scanner 3000 (Affymetrix, Santa Clara, CA) and globally scaled to 150 using the Affymetrix GeneChip Operating Software (GCOS v1.4). GeneChip files (.cel) were imported into GeneSpring software (Agilent Technologies, Santa Clara, CA) and processed with RMA algorithm, and expression values on each chip were normalized to median of all samples. D1-neuron specific ribosome-associated mRNAs from two independent experiments were analyzed. All probes with differential expression and p-value ≤0.05 using 2-way ANOVA (genotype) were considered significantly changed in the absence of miR-128-2.

Dataset from TRAP experiments were analyzed by SYLAMER algorithm to determine if miR-128 targets were more abundant among genes upregulated in the absence of miR-128 compared to genes downregulated in the absence of miR-128. Genes on the array were ranked from most upregulated to most downregulated genes in *Drd1a-cre; Drd1a-TRAP; miR-128$^{fl/fl}$* as compared to *Drd1a-TRAP; miR-128$^{fl/fl}$* mice according to fold-change t-statistic. The enrichment analysis was obtained by SYLAMER with Bonferroni-corrected p-value threshold of 0.05 (http://www.ebi.ac.uk/enright-srv/sylarray/).

**TaqMan Quantitative RT-PCR for miRNA and mRNA analysis**

Relative expression levels of mature miRNAs and mRNAs were measured by TaqMan assays using total extracted RNA from brain samples, according to manufacturer's protocol (Life Technologies, Carlsbad, CA). Purified RNA samples were assayed by qRT-PCR for relative gene expression using pre-designed TaqMan gene expression assays from Applied Biosystems (ABI) as recommended by the manufacture. The following pre-designed TaqMan gene expression assays from Applied Biosystems (ABI) were used: miR-128 (Assay ID 002216), sno135 (Assay ID 001230), miR-124a (Assay ID 001182), Fosb Mm00500401_m1, Fosl2 Mm00484442_m1, Arc Mm00479619_g1, JunB Mm04243546_s1, Darpp-32 Mm00454892_m1, Btg2 Mm00476162_m1, Gadd45g Mm01352550_g1, Dusp1 Mm00457274_g1, Nr4a1 Mm01300401_m1, Jun Mm00495062_s1, Actb Mm00607939_s1, Arpp-21 Mm00473630_m1 (exon spanning

probe detects exons that are common to all Arpp-21 isoforms), Arpp21 Mm00473645_m1 (exon spanning probe that specifically detects the long TARPP-isoform of Arpp-21). Cycle counts for miRNA quantification were normalized to snoRNA135 or miR-124a as indicated, and cycle counts for mRNA quantification were normalized to Actb or Gapdh. Relative expression (ΔCt) and quantification ($RQ=2^{-\Delta\Delta C}$) for each mRNA were calculated using RQ Manager Software and the ΔΔCt method as suggested. Calculation of standard deviation ($SD_{\Delta Ct}=(SD_{target}^2+SD_{ref}^2)^{1/2}$) and error bars ($RQ_1=2^{(-( \Delta\Delta Ct+SD_{\Delta\Delta Ct}))}$, and $RQ_2=2^{(-(\Delta\Delta Ct-SD_{\Delta\Delta Ct})))}$ was performed according to ABI technical literature Part Number 4371095 Rev B.

**Pathway analysis**

Bioinformatic network and pathway analyses of the 154 miR-128 target genes was performed using IPA (Ingenuity Systems, Redwood City, CA) and the Database for Annotation, Visualization and Integrated Discovery (DAVID) version 6.7 (david.abcc.ncifcrf.gov/).

**Protein Preparation and Expression Analysis**

Mice were anesthetized with $CO_2$ and the cortex, hippocampus, and striatum were rapidly dissected and frozen in liquid nitrogen until further processing. Samples were sonicated on ice in 1% SDS solution supplemented with protease inhibitor (Roche, Switzerland) and phosphatase inhibitor, and boiled for 10 minutes. Protein concentration was determined using BCA protein assay kit (ThermoFisherScientific, USA) according to the manufacturer's instructions. Protein samples were diluted in equal volume of 2X LDS sample buffer (Invitrogen) and supplemented with DTT to a final concentration of 200mM (Sigma). 25ug of protein samples were separated on 4-12% Bis-tris precast denaturing gels (Invitrogen), transferred onto PVDF membranes, and blocked with 5% milk in TBS- 0.1% Tween (TBST) solution for 1 hour at room temperature. Membranes were probed with primary antibodies diluted in 5% milk-TBST solution overnight at 4C. Membranes were then washed and probed with horseradish-peroxidase conjugated anti-mouse (GE) or anti-rabbit IgG secondary antibody (GE) for 1 hour at room temperature. Membranes were developed using enhanced chemiluminescence substrate (PerkinElmer,

USA) and exposed on BioMax film (Kodak, USA). Exposed films were scanned, and protein bands were quantified using ImageJ Software (NIH, USA). Protein quantities were normalized using beta-Actin, phosphoprotein levels were normalized to total non-phosphorylated protein levels, and all values plotted relative to control littermate sample. The following primary antibodies were used: total ERK1/2 (137F5), phosphoERK1/2 (Thr202/Tyr204), Arpp21 (mouse monoclonal 6A, gift. A. Nairn), beta-Actin (Abcam), PEA15a (H80) (Santa Cruz,), D4ertd22e (Atlas).

**ELISA Assay**

The ELISA quantification was performed using the PathScan MAP kinase Multi-Target Sandwich ELISA kit (Cell Signaling) according to manufacturer's instructions. Briefly, tissue samples were dissected and rapidly frozen in liquid nitrogen before further processing. Frozen samples were lysed in cell lysis buffer with brief sonication on ice. Cell lysate was centrifuged at 14,000 rpm for 10 min, and the supernatant was diluted 1:10 in sample diluent and used for incubation with antibody micro-wells according to the manufacturer's protocol. Standard curves were generated using dilutions of a mixture containing equal proportion of all control samples. Relative quantity of total or phosphorylated MAP kinase pathway proteins in *Drd1a-cre; miR-128-2*$^{fl/fl}$ and control striatum lysates were quantified based on the individual absorbance values at 450nm. The p-values were calculated using the Welch's test.

**Luciferase Reporter Assay**

Luciferase reporter assays were performed to measure the repression of RCS and TARPP mRNA expression by miR-128. MicroRNA 3'UTR target reporter plasmids that contain the full length sequences of the RCS and TARPP 3'UTR downstream of a firefly luciferase gene driven by a *SV40* promoter for expression in mammalian cells were purchased from GeneCopoeia, MD (pEZX-MT01). Control plasmids containing no 3'UTR inserts were used for comparison. Plasmids contain the Renilla luciferase gene to control for transfection and expression efficiency. The sequences of all plasmids were verified by sequencing and restriction enzyme digestion. Reporter or control plasmids were co-transfected with the Renilla luciferase plasmids into confluent Neuro2A cells

grown in 24-well culture plates with either no miRNA mimic, a miR-124a scrambled control mimic, or miR-128 mimics at the two indicated concentrations (Dharmacon, Thermo Fisher Scientific, USA). Cells were harvested and lysed 24 hour after transfection and cell lysates were assayed for firefly and Renilla luciferase activity using Dual-Luciferase Reporter Assay System (Promega, Wisconsin, USA) according to manufacturer's instructions. Firefly luciferase activity was normalized to Renilla luciferase activity for each cell culture well and plotted as activity relative to control transfections with no mimics added. At least 3 biological replicates were performed consisting of 3 technical replicates each.

**Electrophysiological Analysis**

Brain slice preparation:

Para-sagittal brain slices (275 μm) were obtained from 3-5 month old male and female *Drd1a-TRAP; Drd1a-cre; miR-128*$^{fl/fl}$ and *Drd1a-TRAP; miR-128*$^{fl/fl}$ littermate control mice following procedures approved by the Northwestern University Institutional Animal Care and Use Committee. The mice were anesthetized with a mixture of ketamine (50 mg $kg^{-1}$) and xylazine (4.5 mg $kg^{-1}$) and perfused transcardially with 5–10 ml ice-cold artificial cerebrospinal fluid (ACSF) containing (in mM): 124 NaCl, 3 KCl, 1 $CaCl_2$, 1.5 $MgCl_2$, 26 $NaHCO_3$, 1 $NaH_2PO_4$, and 16.66 glucose, continuously bubbled with carbogen (95% $O_2$ and 5% $CO_2$). The slices were then transferred to a holding chamber where they were incubated in ACSF containing (in mM) 2 $CaCl_2$, 1 $MgCl_2$, at 35ºC for 60 min, after which they were stored at room temperature until recording.

Electrophysiology:

Patch pipettes were pulled from thick-walled borosilicate glass on a Sutter P-97 puller. Pipette resistance was typically 3–5 MΩ when filled with recording solution. For studies involving bAP propagation, the internal recording solution contained (in mM): 135 $KMeSO_4$, 5 KCl, 10 HEPES, 2 ATP-$Mg^{2+}$, 0.5 GTP-$Na^{+}$, 5 phosphocreatine-tris; 5 phosphocreatine-$Na^{+}$, and 0.1 spermine. The pH was adjusted to 7.25 with NaOH and osmolarity to 270–280 mOsm $l^{-1}$. For $Ca^{2+}$ imaging experiments, the recording solution also contained 200 μM Fluo-4 pentapotassium salt and 50 μM Alexa Fluor 568 hydrazide

$Na^+$ salt (Invitrogen). For voltage clamp studies, the recording solution contained (in mM): 120 $CsMeSO_3$, 5 NaCl, 10 TEA-Cl (tetraethylammonium-Cl), 10 HEPES, 5 Qx-314, 4 ATP-Mg2, 0.3 GTP-Na, 0.2 Fluo 4 pentapotassium salt and 0.05 Alexa Fluor 568 hydrazide $Na^+$ salt (Invitrogen), pH 7.25, 270-280 $mOsm^{-1}$. Slices were transferred to a submersion-style recording chamber mounted on an Olympus BX51 upright, fixed-stage microscope and continuously perfused with carbogen-bubbled ACSF. Electrophysiological recordings were obtained with a Multiclamp 700B amplifier. Stimulation and display were obtained as previously described (Day et al., 2008) using the custom-written shareware package WinFluor (John Dempster, Strathclyde University, Glasgow, Scotland, UK), which automates and synchronizes the two-photon imaging and electrophysiological protocols. The amplifier bridge circuit was adjusted to compensate for serial resistance and continuously monitored during recordings.

2-photon laser scanning microscopy (2PLSM) and $Ca^{2+}$ imaging:

2PLSM and $Ca^{2+}$ imaging were performed as previously described (*37*). Striatonigral spiny projection neurons (SPNs) were identified by somatic eGFP two-photon excited fluorescence using an Ultima Laser Scanning Microscope system (Prairie Technologies). A DODT contrast detector system was used to provide a bright-field transmission image in registration with the fluorescent images. The green GFP signals (490–560 nm) were acquired using 810 nm excitation (Verdi/Mira laser). SPNs were patched using video microscopy with a Hitachi CCD camera and an Olympus 60X/0.9 NA lens. Alexa 568 fluorescence was used for visualization of cell bodies, dendrites, and spines. Following patch rupture, the internal solution was allowed to equilibrate for 15–20 minutes before imaging. High magnification maximum projection images of dendrites were acquired with 0.072 $\mu m^2$ pixels with 10 µm pixel dwell time. Approximately 20 images taken with 0.5 µm focal steps. Spine density was calculated from maximum projection images of dendritic segments ~100-120 µm from the soma, as previously described (*38*). Spines were manually counted and normalized to the length of the corresponding dendrite.

Single bAPs were generated by injecting somatic current pulses (2 nA, 2 ms). Dendritic changes in $Ca^{2+}$ were measured as $\Delta F/Fo$ via line scans, where Fo is the average green fluorescence before the bAP. Peak $\Delta F/Fo$ values were obtained from the average of 6

consecutive trials and calculated by a single exponential fit of the $Ca^{2+}$ transient decay. Green fluorescent line scan signals were acquired at 6 ms per line and 512 pixels per line with 0.08 μm pixels and 10 μs pixel dwell time. The laser-scanned images were acquired with 810 nm light pulsed at 90 MHz (~250 fs pulse duration). Power attenuation was achieved with two Pockels cells electro-optic modulators (models 350–80 and 350–50, Con Optics, Danbury, CT). The two cells were aligned in series to provide an enhanced modulation range for fine control of the excitation dose (0.1% steps over four decades). The line scan was started 200 ms before the stimulation protocol and continued 4 s after the stimulation to obtain the background fluorescence and to record the decay of the optical signal after stimulation. To reduce photo-damage and photo-bleaching, the laser was fully attenuated using the second Pockels cell at all times during the scan except for the period directly flanking the bAP burst. Dendritic line scans were acquired from proximal (~50 μm from soma) and distal (~100-120 μm from soma) dendritic regions for each cell. bAP attenuation was calculated by normalizing distal $Ca^{2+}$ transient peaks to the maximum proximal $Ca^{2+}$ transient per cell.

Glutamate uncaging was achieved using a Chameleon-XR laser system (Coherent Laser Group, Santa Clara, CA). 5 mM MNI-glutamate (Tocris, Cookson, Ellisville, MO) was superfused over the slice using a syringe pump and multi-barreled perfusion manifold (Cell MicroControls, Norfolk, VA). Glutamate was uncaged adjacent to individual spine heads using 1 ms pulses of 720 nm light typically 10-20 mW in power at the sample plane. Photolysis power was tuned via a third Pockels cell modulator (Con Optics, Danbury, CT) to achieve uncaged-EPSCs (uEPSCs) averaging 5-10 pA.

**Behavioral analysis**

For all behavioral experiments, experimenters were blinded to the genotypes of the animals. All behavior tests have been performed on 4- to 16-week-old mutants and their respective age- and sex-matched littermate controls. All behavior tests were conducted between 7 AM and 7 PM. Genotypes were decoded after data was processed and analyzed. Sample sizes of at least 5 animals were used for behavioral analyses. Subjects corresponding to data points that are more than 2 standard deviations from the sample mean were excluded from analyses. When possible, all littermate animals were included

in behavioral experiments as control groups. No randomization protocol was used. Animals were allocated to treatment groups to ensure uniform distribution of ages and sexes in each group. Where 2 conditions are compared, 2-tailed Welch's t-test was used. For comparisons involving multiple sample groups, either 1-way or 2-way ANOVA was used. When a factor had a significant effect, post-tests were performed for pairwise comparisons.

Open-Field Analysis:

Locomotion and exploratory behavior was measured using the open field (40 X 40 X 30 cm). Activity was quantified by the computer-operated Photobeam activity system (Accuscan Instruments, Columbia, OH). Mice were recorded for total distance moved in the whole arena and number of vertical episodes (rearing). Open field analysis was performed on 4 week old mice and their respective age and sex-matched littermate controls. To ensure that the experimental mice had no seizures at the time of the analysis, the mice used for the behavioral tests were kept under surveillance for 2 hours prior to the test, during the 1-hour motor test, and 4 hours after the test.

Drugs used:

Mice were injected intraperitoneally (i.p.) with the microliter volume equivalent of 10X body weight (g). D1-receptor agonist SKF 81297 (Taconic) was diluted from stock (10mg/ml in DMSO) with 0.9% saline to indicated concentration. MEK inhibitor SL327 (Taconic) was diluted from stock (diluted in DMSO) with 30% DMSO/Saline to indicated concentration. Cocaine (Sigma, C5776) was diluted in water to a 100mg/ml stock solution. Sodium valproate (Sigma, P4543) was prepared at a 0.26% w/v solution in drinking water for oral administration. Kainic acid (Sigma, K0250) was dissolved in saline just before use to 30mg/kg concentration for i.p. injections. Picrotoxin (Sigma, P1675) was prepared as a 25mg/ml stock solution in ethanol and further diluted in saline to inject at a 3mg/kg concentration for seizure induction.

Home Cage Seizure Monitoring:

Animals were housed in clear plexiglass chambers with pre-installed cameras

(Phenotyper, Noldus Information Technology), and provided with food and water *ad libitum*. Continuous 24-hour video recordings of mice were taken. Video recordings were manually scored for severity, duration and frequency of seizures. To constitute recorded tonic-clonic seizures, mice must cease all normal activity such as walking, sniffing or grooming, adopt a rigid posture with arched back and progress to repeated rearing and falling. A large majority of tonic-clonic seizure episodes progressed to a further stage with rapid running and bouncing behavior, although this was not required for inclusion as tonic-clonic seizure.

Chemically-induced seizures:

Mice were injected i.p. with kainic acid (30 mg/kg in saline) or picrotoxin (3 mg/kg in saline) and placed in chambers in isolation and observed for 60 min. after injection. All injected animals rapidly enter period of immobility (Stage 1). Animals were observed for the time of onset of tonic-clonic seizures characterized by repeated rearing and falling followed by running and bouncing, or constant limb movements if postural control is lost.

Survival curves:

Date of sacrifice or death in the home cage was recorded for mutants and cage mate controls, plotted as Kaplan-Meier survival curves, and compared using log-rank tests.

6-OHDA lesions:

Mice were anesthetized with ketamine/xylazine. Mice were stereotactically injected with 6-OHDA (3.5mg/ml in 0.02% ascorbic acid) 2X2ul in left striatum (ML=-2.1 AP=+1.0 DV=-3.4; ML=-2.3 AP=+0.3 DV=-3.4) and vehicle injection 2X2ul in right striatum (ML=+2.1 AP=+1.0 DV=-3.4; ML=+2.3 AP=+0.3 DV=-3.4). Mice were single housed for 3 weeks after surgery to allow for recovery before behavioral assays.

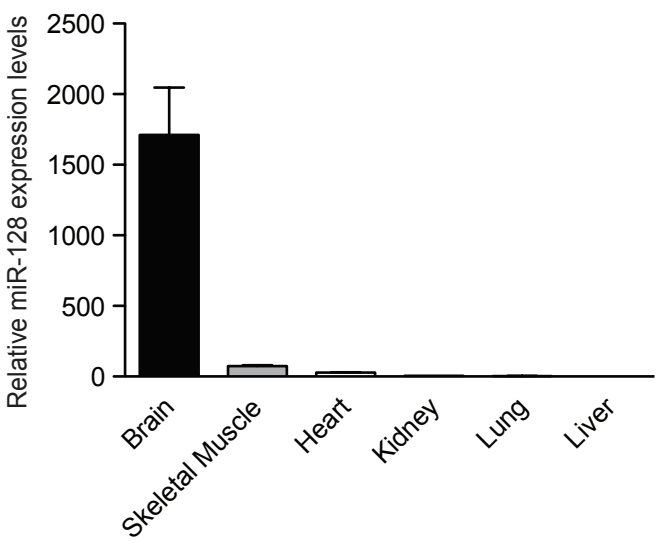
Rotational behavior:

Rotational behavior in lesioned mice was assayed by an experimenter blind to the genotypes for two consecutive 2-min intervals 5 min after i.p. injection of cocaine. Net contralateral rotations are given by total contralateral rotations minus ipsilateral rotations.

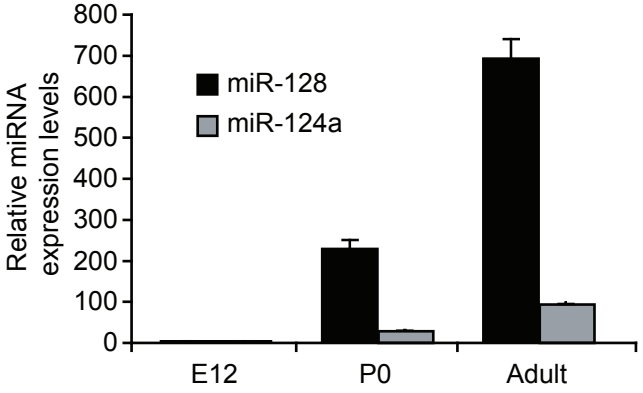
Data shows average of both readings. After 3 days, the same behavioral assay was recorded in response to SKF81297.

**Figure S1.**

**A**




**B**




**C**

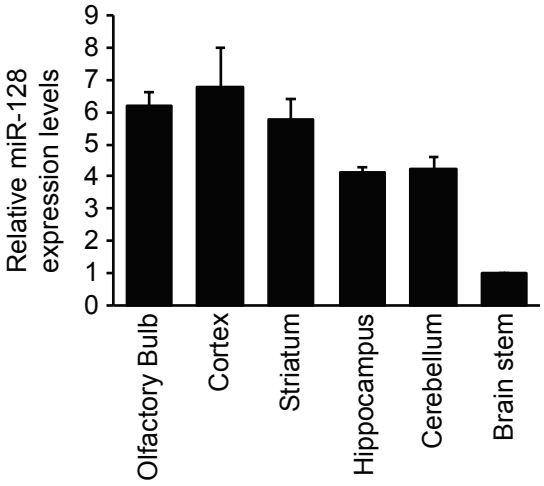


**Figure S1. miR-128 is highly expressed in the postnatal mouse brain.**

**(A) miR-128 is enriched in the mouse brain.** Expression levels of miR-128 were measured by qRT-PCR in RNA purified from the brain, skeletal muscle, heart, kidney, lung, and liver of 8-week old adult mice (n=3). The expression levels of miR-128 were normalized to snoRNA135 expression and displayed as fold increase over respective miRNA expression levels in the liver. 1-way ANOVA followed by Turkey's posttest, $p<0.01$ for brain vs. other organ comparisons. **(B) Postnatal brain development is accompanied by increase in miR-128 expression levels.** Expression levels of miR-128 and the neuron-enriched miR-124a were measured by qRT-PCR in the brain derived from mouse embryos at day 12 of embryonic development (E12), newborn mice (P0) or 8-week old adult mice (n=3 per age group). The expression levels of miRNAs were normalized to snoRNA135 expression and displayed as fold increase over respective miRNA expression levels in the E12 embryonic brain. **(C) miR-128 is expressed in different brain regions.** Expression of miR-128 in indicated brain regions in adult mice was quantified as in (A) and shown relative to mean miR-128 expression in the brain stem (n=3 per region). Error bars show s.e.m.

**Figure S2.**

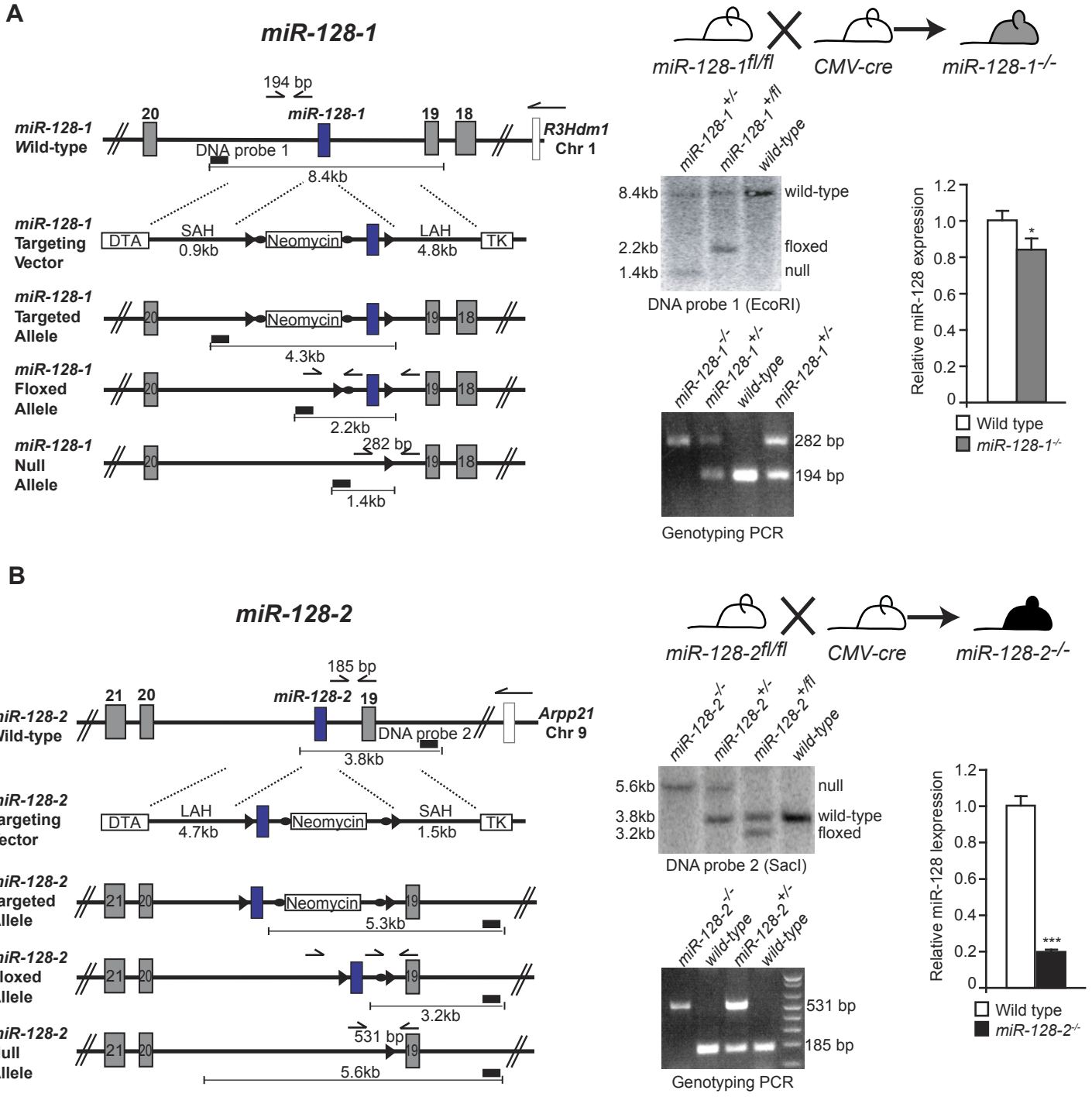

A
miR-128-1
194 bp
miR-128-1 Wild-type
20
miR-128-1
19
18
R3Hdm1 Chr 1
DNA probe 1
8.4kb
miR-128-1 Targeting Vector
DTA
SAH 0.9kb
Neomycin
LAH 4.8kb
TK
miR-128-1 Targeted Allele
4.3kb
miR-128-1 Floxed Allele
2.2kb
282 bp
miR-128-1 Null Allele
1.4kb
miR-128-1fl/fl
CMV-cre
miR-128-1-/-
miR-128-1+/-
miR-128-1+/fl
wild-type
8.4kb
2.2kb
1.4kb
wild-type
floxed
null
DNA probe 1 (EcoRI)
miR-128-1-/-
miR-128-1+/-
wild-type
miR-128-1+/-
282 bp
194 bp
Genotyping PCR
Relative miR-128 expression
1.2
1.0
0.8
0.6
0.4
0.2
0
*
Wild type
miR-128-1-/-
B
miR-128-2
185 bp
21
20
miR-128-2
19
miR-128-2 Wild-type
Arpp21 Chr 9
DNA probe 2
3.8kb
miR-128-2 Targeting Vector
DTA
LAH 4.7kb
Neomycin
SAH 1.5kb
TK
miR-128-2 Targeted Allele
5.3kb
miR-128-2 Floxed Allele
3.2kb
531 bp
miR-128-2 Null Allele
5.6kb
miR-128-2fl/fl
CMV-cre
miR-128-2-/-
miR-128-2-/-
miR-128-2+/-
miR-128-2+/fl
wild-type
5.6kb
3.8kb
3.2kb
null
wild-type
floxed
DNA probe 2 (SacI)
miR-128-2-/-
wild-type
miR-128-2+/-
wild-type
531 bp
185 bp
Genotyping PCR
Relative miR-128 lexpression
1.2
1.0
0.8
0.6
0.4
0.2
0
***
Wild type
miR-128-2-/-
C
Wild type
miR-128-1-/-
Distance (m)
160
140
120
100
80
60
40
20
0
ns
Rearing Episode Count
700
600
500
400
300
200
100
0
ns
Percent Survival
125
100
75
50
25
0
0
100
200
300
400
Days
Wild type
miR-128-1-/-
ns
D
Wild type
miR-128-2-/-
Rearing Episode Count
450
400
350
300
250
200
150
100
50
0
*
2

**Figure S2. *miR-128-1* and *miR-128-2* genes contribute differentially to miR-128 expression in the brain.**

**(A, B) Generation of the (A) *miR-128-1* and (B) *miR-128-2* loci for conditional gene inactivation in mice.** (**Left panels)** The strategy for gene modification and inactivation of *miR-128* genes are shown. The regions containing the miRNA hairpin in both of the miR-128 carrying genes were flanked with loxP sites in mouse ES cells followed by routine procedure for generation of *miR-128-1*$^{fl/fl}$ and *miR-128-2*$^{fl/fl}$ mice. MicroRNA hairpin, filled rectangle; exons, open rectangles; loxP sites, black triangles. Neomycin resistance gene flanked by FRT sequences (black circles) was removed from targeted loci by using FLT recombinase; DTA, diphtheria toxin gene; TK, thymidine kinase gene; LAH/SAH, long and short arm of homology. **(Right panels)** *miR-128-1* (*miR-128-1*$^{-/-}$) or *miR-128-2* (*miR-128-2*$^{-/-}$) deficient mice were generated by breeding *miR-128-1*$^{fl/fl}$ and *miR-128-2*$^{fl/fl}$ mice, respectively, to *CMV-cre* mice**.** Modified *miR-128-1* and *miR-128-2* alleles were identified by Southern blotting of the mouse tail DNA digested with EcoRI or SacI using the indicated DNA probes (black rectangles) or by PCR genotyping using primers as indicated in the scheme. The relative expression levels of miR-128 in the striatum of mice deficient for the *miR-128-1* **(** n=7 each**)** or miR-*128-2* (n=5 and 3) gene are shown. **(C) Inactivation of the *miR-128-1* gene does not affect motor activity or survival in mice.** The impact of *miR-128-1* deficiency on motor activity in mice was measured by using open field analysis. **(Left panel)** Total horizontal distance moved in meters and **(middle panel)** the number of vertical rearing episodes within 60 min in the open field are shown **(**n=7 and 9**)**. **(Right panel)** The life spans of mice deficient for *miR-128-1* **(**n=6**)** and their respective wild-type littermate controls (n= 22) are shown.
**(D) Inactivation of the *miR-128-2* gene increases exploration in mice.** The numbers of vertical rearing episodes **of** or *miR-128-2*$^{-/-}$ and littermate controls are shown **(**n=23 and 12**).**
Error bars show s.e.m., * $p \leq 0.05$, ** $p \leq 0.01$, Welch's t-test and log-rank test.

**Figure S3**

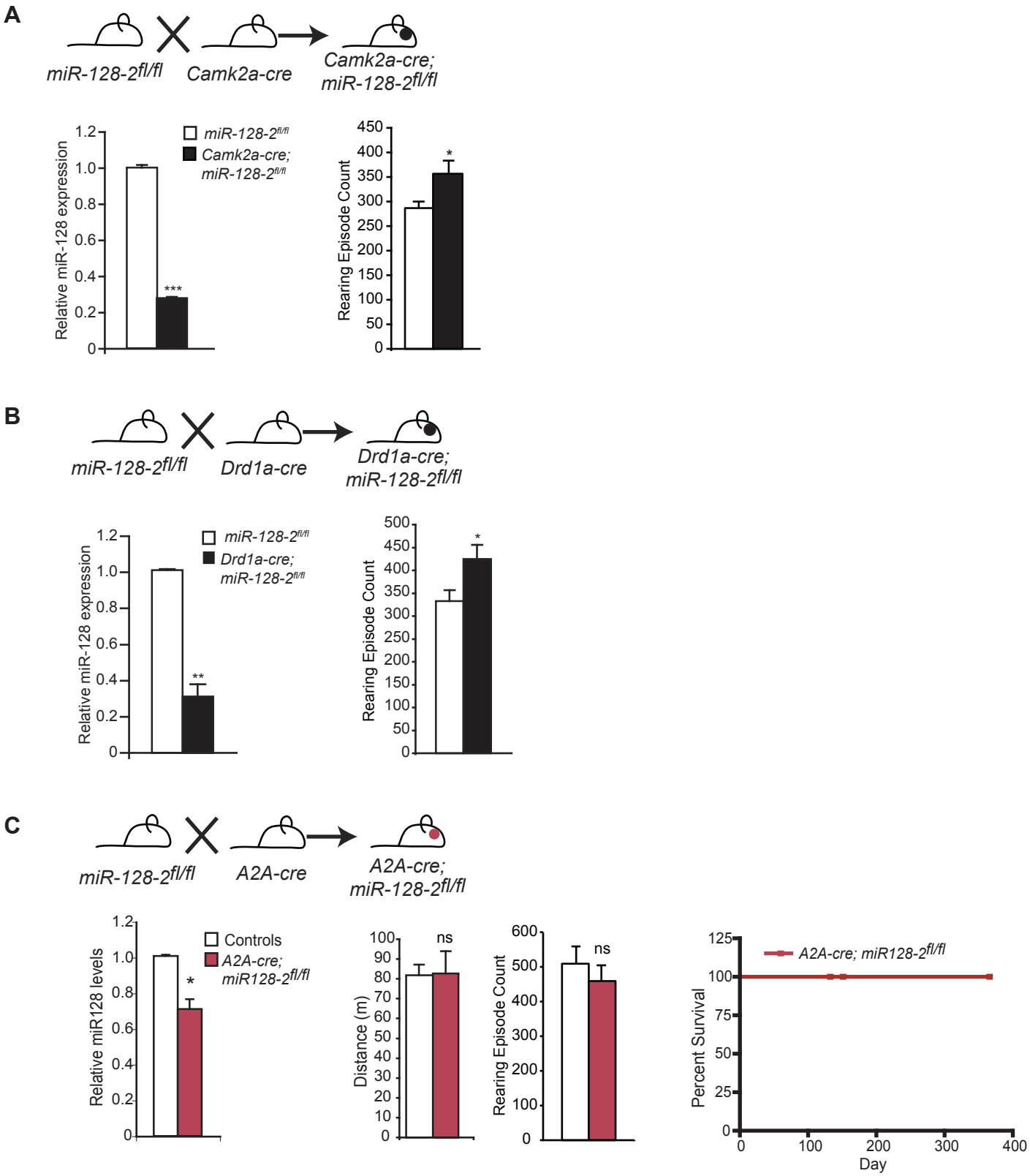

A
miR-128-2fl/fl
Camk2a-cre
Camk2a-cre; miR-128-2fl/fl
Relative miR-128 expression
miR-128-2fl/fl
Camk2a-cre; miR-128-2fl/fl
***
Rearing Episode Count
*
B
miR-128-2fl/fl
Drd1a-cre
Drd1a-cre; miR-128-2fl/fl
Relative miR-128 expression
miR-128-2fl/fl
Drd1a-cre; miR-128-2fl/fl
**
Rearing Episode Count
*
C
miR-128-2fl/fl
A2A-cre
A2A-cre; miR-128-2fl/fl
Relative miR128 levels
Controls
A2A-cre; miR128-2fl/fl
*
Distance (m)
ns
Rearing Episode Count
ns
Percent Survival
A2A-cre; miR128-2fl/fl
Day

**Figure S3. Increased explorative activity in mice with conditional inactivation in postnatal Camk2a- and D1-, but not D2-neurons in mice.**

**(A) miR-128 deficiency in postnatal Camk2a-neurons increases exploration.** miR-128 deficiency in postnatal Camk2a-neurons has been achieved by breeding *Camk2a-cre* with *miR-128-2*$^{fl/fl}$ mice. **(Left panel)** The bar graph shows the relative miR-128 expression levels in *Camk2a-cre*; *miR-128-2*$^{fl/fl}$ mice and control littermates (n=7 and 4). **(Right panel)** The number of vertical rearing episodes performed by *Camk2a-cre*; *miR-128-2*$^{fl/fl}$ mice and control littermates (n=21 and 8) are shown. **(B) miR-128 deficiency in D1-neurons increases exploration.** miR-128 deficiency in D1-neurons has been achieved by breeding *Drd1a-cre* with *miR-128-2*$^{fl/fl}$ mice. Relative striatal miR-128 expression levels (left, n=3 each), and vertical rearing episodes (right) of *Drd1a-cre; miR-128-2*$^{fl/fl}$ mice and control littermates (n=22 and 26) are shown**. (C) miR-128 deficiency in D2-neurons does not affect motor activity or survival in mice.** miR-128 deficiency in D2-neurons has been achieved by breeding *A2A-cre* with *miR-128-2*$^{fl/fl}$ mice. Striatal miR-128 expression levels (left, n=3 each), horizontal motor activity and vertical rearing episodes (middle, n=9 and 7), and survival span (right, n= 8 and 7) of *A2A-cre; miR-128-2*$^{fl/fl}$ mice and respective littermates (n=7) are shown.
Error bars show s.e.m., * $p \leq 0.05$, ** $p \leq 0.01$, Welch's t-test and log-rank test.

**Figure S4**

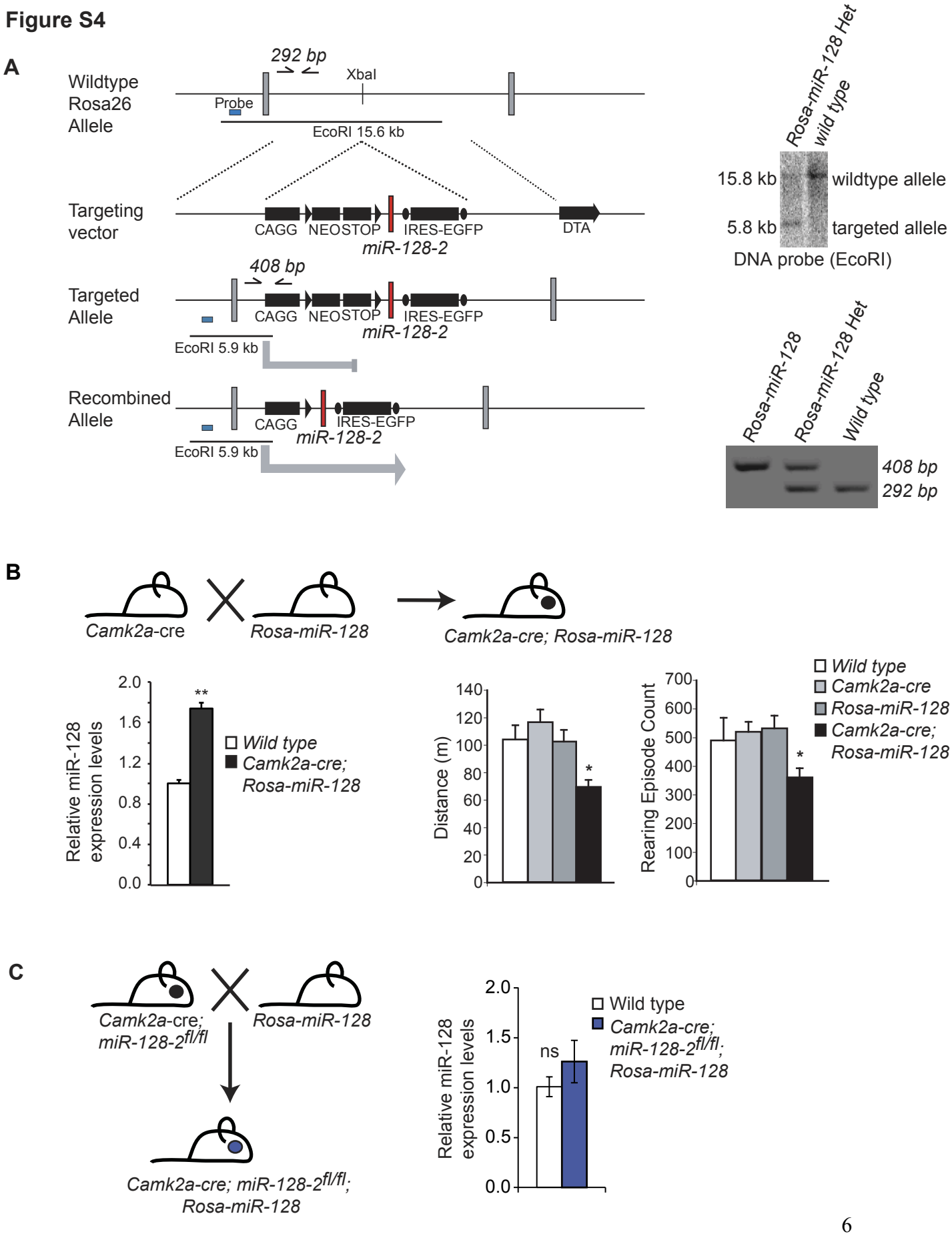

A
Wildtype Rosa26 Allele
292 bp
XbaI
Probe
EcoRI 15.6 kb
Targeting vector
CAGG NEOSTOP IRES-EGFP
DTA
miR-128-2
Targeted Allele
408 bp
CAGG NEOSTOP IRES-EGFP
miR-128-2
EcoRI 5.9 kb
Recombined Allele
CAGG IRES-EGFP
miR-128-2
EcoRI 5.9 kb
Rosa-miR-128 Het
wild type
15.8 kb
wildtype allele
5.8 kb
targeted allele
DNA probe (EcoRI)
Rosa-miR-128
Rosa-miR-128 Het
Wild type
408 bp
292 bp
B
Camk2a-cre
Rosa-miR-128
Camk2a-cre; Rosa-miR-128
Relative miR-128 expression levels
Wild type
Camk2a-cre; Rosa-miR-128
Distance (m)
Rearing Episode Count
Wild type
Camk2a-cre
Rosa-miR-128
Camk2a-cre; Rosa-miR-128
C
Camk2a-cre; miR-128-2fl/fl
Rosa-miR-128
Camk2a-cre; miR-128-2fl/fl; Rosa-miR-128
Relative miR-128 expression levels
ns
Wild type
Camk2a-cre; miR-128-2fl/fl; Rosa-miR-128

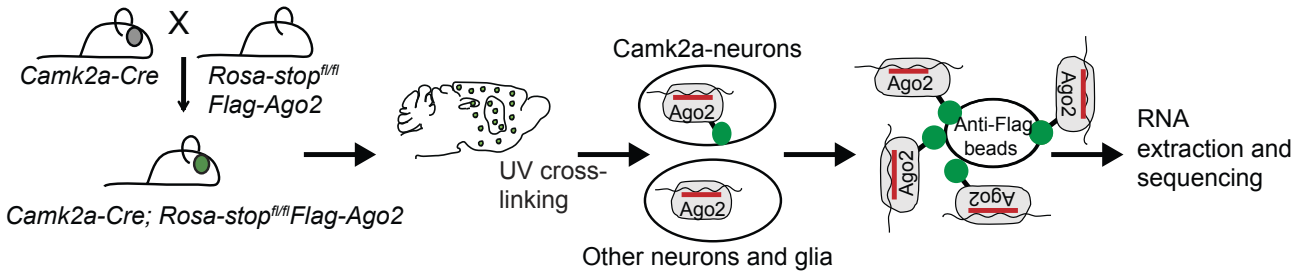
**Figure S4. Ectopic expression of miR-128 *in vivo* attenuates motor activity in wild-type mice and normalizes miR-128 expression levels in *Camk2a-cre; miR-128-2$^{fl/fl}$* mice.**

**(A) Targeting strategy for the generation of mice with conditional overexpression of *miR-128*.** The exogenous *miR-128-2* gene was inserted into the endogenous *Rosa26* gene locus in ES cells using a knock-in strategy as described previously (31). The *miR-128-2* gene **(red rectangle)** was separated from a strong CAGG promoter by a floxed-STOP-Neomycin cassette. Exons, grey rectangles. DTA, diphtheria toxin gene. The modified *ROSA-Stop$^{fl/fl}$-miR-128* allele (for simplification from now on called *Rosa-miR-128*) was confirmed by Southern blot analysis of the EcoRI digested DNA **(top right)** using the indicated DNA probe **(blue rectangle)** or by PCR genotyping **(bottom right,** primer locations as indicated in scheme**).** (**B) Reduced motor activity and exploration in mice with neuron-specific overexpression of miR-128.** (**Top)** Mice with postnatal neuron specific overexpression of miR-128 (*Camk2a-cre; Rosa-miR-128)* were generated by breeding *Camk2a-cre* with *Rosa-miR-128* mice. **(Left)** miR-128 expression levels in the striatum were measured by qRT-PCR (n=3 each) as described (Fig. S1) and are shown relative to mean miR-128 expression in the wild type striatum. Welch's t-test. **(Middle and right)** Total horizontal distance and rearing activity in an open-field over 60 minutes for *Camk2a-cre; Rosa-miR-128* mice (n=21) and littermate controls (wild type n=8, *Camk2a-cre* n=5, *Rosa-miR-128* n=17) are shown. 1-way ANOVA followed by Turkey's post test. **(C) Ectopic expression of miR-128 from the Rosa26 locus normalizes miR-128 expression levels in *Camk2a-cre; miR-128-2$^{fl/fl}$* mice. (Left)** Mice with postnatal neuron specific knock-out of *miR-128-2* and ectopic expression of *miR-128-2* from the Rosa26 locus (*Camk2a-cre; miR-128-2$^{fl/fl}$; Rosa-miR-128)* were generated by breeding *Camk2a-cre; miR-128-2$^{fl/fl}$* to *Rosa-miR-128* mice. **(Right)** miR-128 expression in the striatum of *Camk2a-cre; miR-128-2$^{fl/fl}$; Rosa-miR-128* mice (n=4) was measured by qRT-PCR and data are shown relative to mean expression in littermate controls (n=3). Welch's t-test.

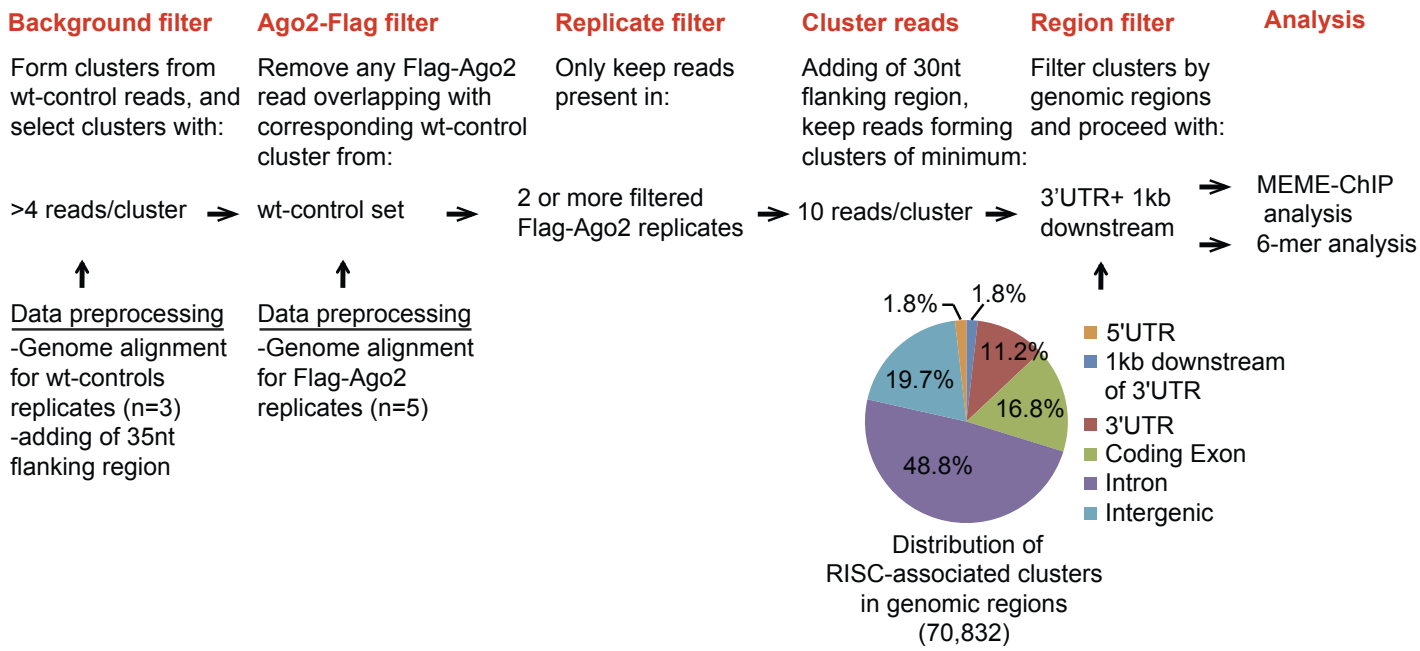
Error bars show s.e.m., * $p \leq 0.05$, ** $p \leq 0.01$.

## Figure S5

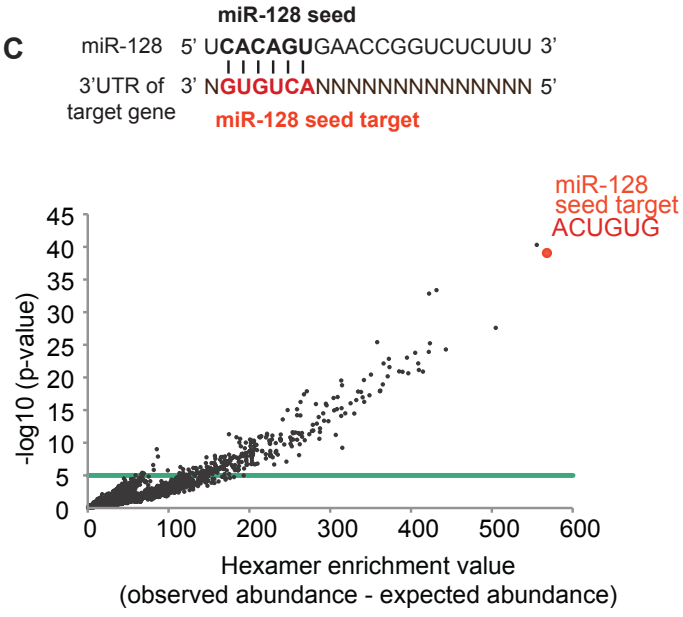
**A**

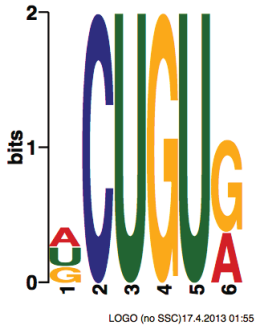



**B**




**C**



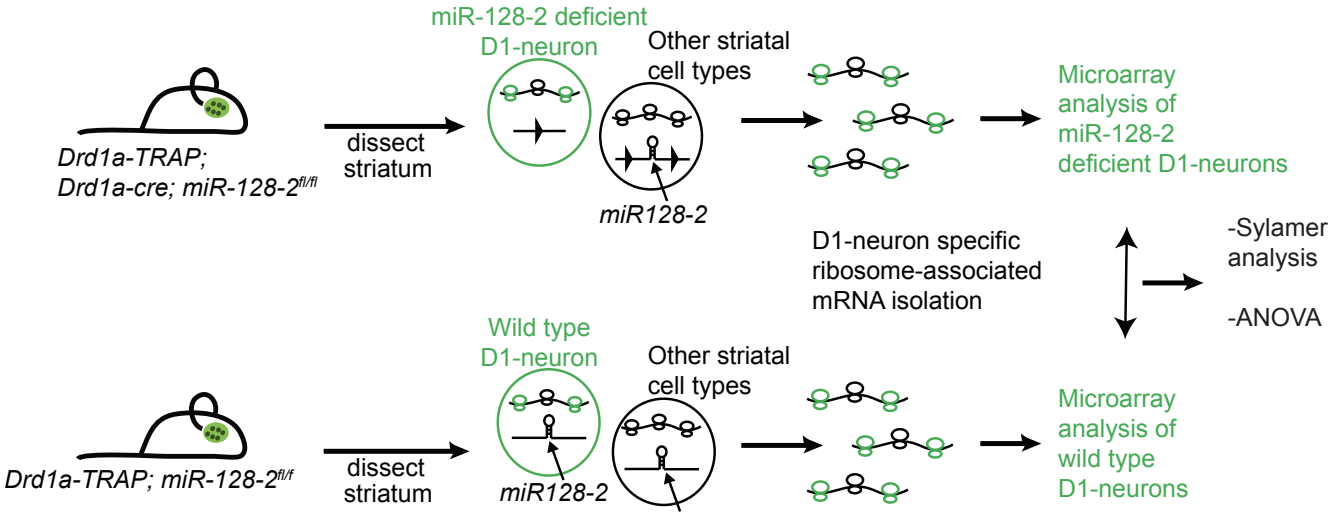

(E-value=2.2E-73)

**Figure S5. Strategy of neuron specific RISC-associated mRNA isolation and analysis.**

**(A) Identification of RISC-associated RNAs in Camk2a-neurons in mice.** The scheme outlines the experimental procedure for the isolation of Camk2a-neuron specific RISC-associated mRNAs from adult mice. The Cre-mediated expression of Flag-tagged Ago2 in Camk2a-neurons was achieved by breeding *Camk2a-cre* mice to *Rosa-Stop*$^{fl/fl}$*-Flag-Ago2* mice (8). The Flag-tagged Ago2 (green) was immunoprecipitated from lysates of Camk2a-neurons followed by isolation and sequencing of the RISC-associated RNAs as described in Material and Methods. **(B) Schematic overview for computational analysis of HITS-CLIP data from RISC-associated RNAs in neurons.** The flowchart displays the subsequent steps of data analysis as detailed in Supplementary Material and Methods. The Venn diagram displays the genomic distribution (Mouse Genome Reference Consortium, version mm10) of RISC-associated RNA clusters (70,832). **(C) Putative miR-128 targets are highly enriched among RISC-associated mRNAs in neurons. (Upper panel)** Scheme shows the miR-128 seed sequence (**bold black)** and the corresponding target seed sequence **(bold red)** within the 3'UTR of a potential miR-128 target gene. **(Lower panel, left)** Putative miR-128 targets are highly enriched among RISC-associated mRNAs in Camk2a-neurons. Scatter plot displays relative enrichment of all possible nucleotide hexamer sequences (4096) within the 3'UTR + 1 kb downstream sequence of RISC–associated mRNA clusters (8794). The hexamer alignment with the RefSeq annotated 3'UTR+1kb shows the highest degree of enrichment for the miR-128 seed target sequence **(red dot)**. X-axis shows the observed frequency of a hexamer that exceeds the normalized frequency of occurrences in the corresponding RefSeq region, y-axis shows –log10 (p-value) from chi-squared test, green line represents Bonferroni-corrected critical p-value: $0.05/(4^6)= 1.22\text{x}10^{-5}$. **(Middle)** Motif analysis of RISC-associated 3'UTR +1kb mRNAs clusters using MEME-Chip software identifies the miR-128 seed target sequence as the second highest enriched motif (E-value=2.2E-73).

**Figure S6**

**A**


miR-128-2 deficient D1-neuron
Other striatal cell types
Drd1a-TRAP; Drd1a-cre; miR-128-2fl/fl
dissect striatum
miR128-2
Microarray analysis of miR-128-2 deficient D1-neurons
D1-neuron specific ribosome-associated mRNA isolation
-Sylamer analysis
-ANOVA
Wild type D1-neuron
Other striatal cell types
Drd1a-TRAP; miR-128-2fl/f
dissect striatum
miR128-2
Microarray analysis of wild type D1-neurons

**B**

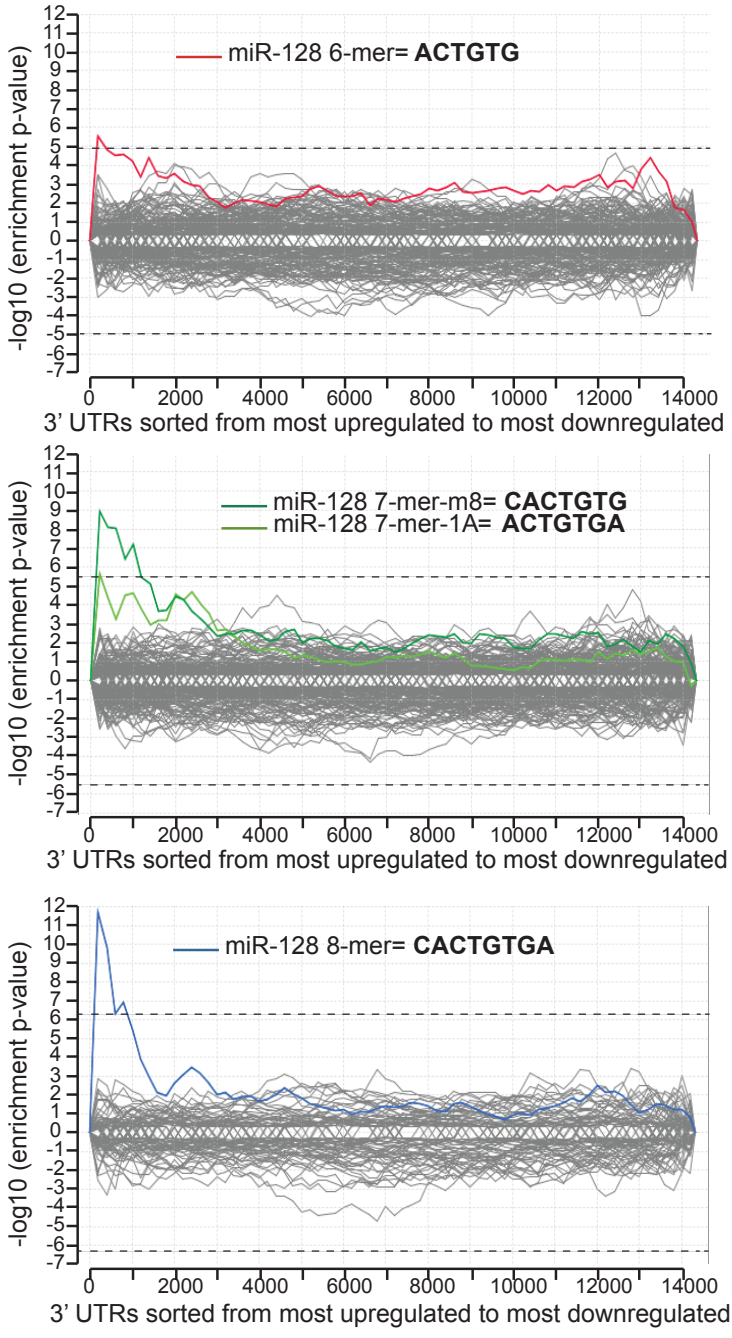

miR-128 6-mer= ACTGTG
-log10 (enrichment p-value)
3' UTRs sorted from most upregulated to most downregulated
miR-128 7-mer-m8= CACTGTG
miR-128 7-mer-1A= ACTGTGA
-log10 (enrichment p-value)
3' UTRs sorted from most upregulated to most downregulated
miR-128 8-mer= CACTGTGA
-log10 (enrichment p-value)
3' UTRs sorted from most upregulated to most downregulated

**Figure S6. Identification of primary miR-128 target genes in D1-neurons.**

**(A) The neuron-specific profiling of polyribosome-associated mRNAs in wild type and miR-128 deficient D1-neurons.** Polyribosome-associated mRNA transcripts were isolated from the striatum of control *Drd1a-TRAP; miR-128-2*$^{fl/fl}$ or mutant *Drd1a-TRAP; Drd1a-cre; miR-128-2*$^{fl/fl}$ mice (n=5/genotype) that express the eGFP-L10 protein in D1-neurons. The analysis of polyribosome-associated mRNAs has been performed as detailed in Supplementary Material and Methods. Differentially expressed genes between wild type and miR-128 deficient D1-neurons were identified by ANOVA. Green circles: D1-neurons; black circles: other cell types; green ribosomes: eGFP-tagged ribosome; black ribosomes: untagged ribosomes. **(B) 3'UTR's containing the miR-128 seed target sequence are significantly enriched among genes that are most up-regulated in miR-128 deficient D1-neurons**. Dataset from the D1-neuron TRAP experiments were analyzed using Sylamer algorithm to determine if potential miR-128 target genes were more abundant among 3'UTR's of mRNAs most upregulated in miR-128 deficient D1-neurons as compared to the rest. Sylamer enrichment landscapes show results for 6-nucleotide (top), 7-nucleotide (middle) and 8-nucleotide (bottom) sequences. The x-axes represent 3'UTRs ranked from the most upregulated (left) to the most downregulated (right) gene in miR-128 deficient D1-neurons. The y-axes show hypergeometric significance for each sequence at each leading bin (-log10 (P-value)). Horizontal dotted lines indicate Bonferroni-corrected p-value threshold of 0.05. The 4 colored lines indicate the sequences complementary to miR-128 seed. Among all tested 6-, 7- and 8-nucleotide sequences, only these four miR-128 seed target sequences show peak enrichment with p-values $\leq 0.05$.

**Figure S7**

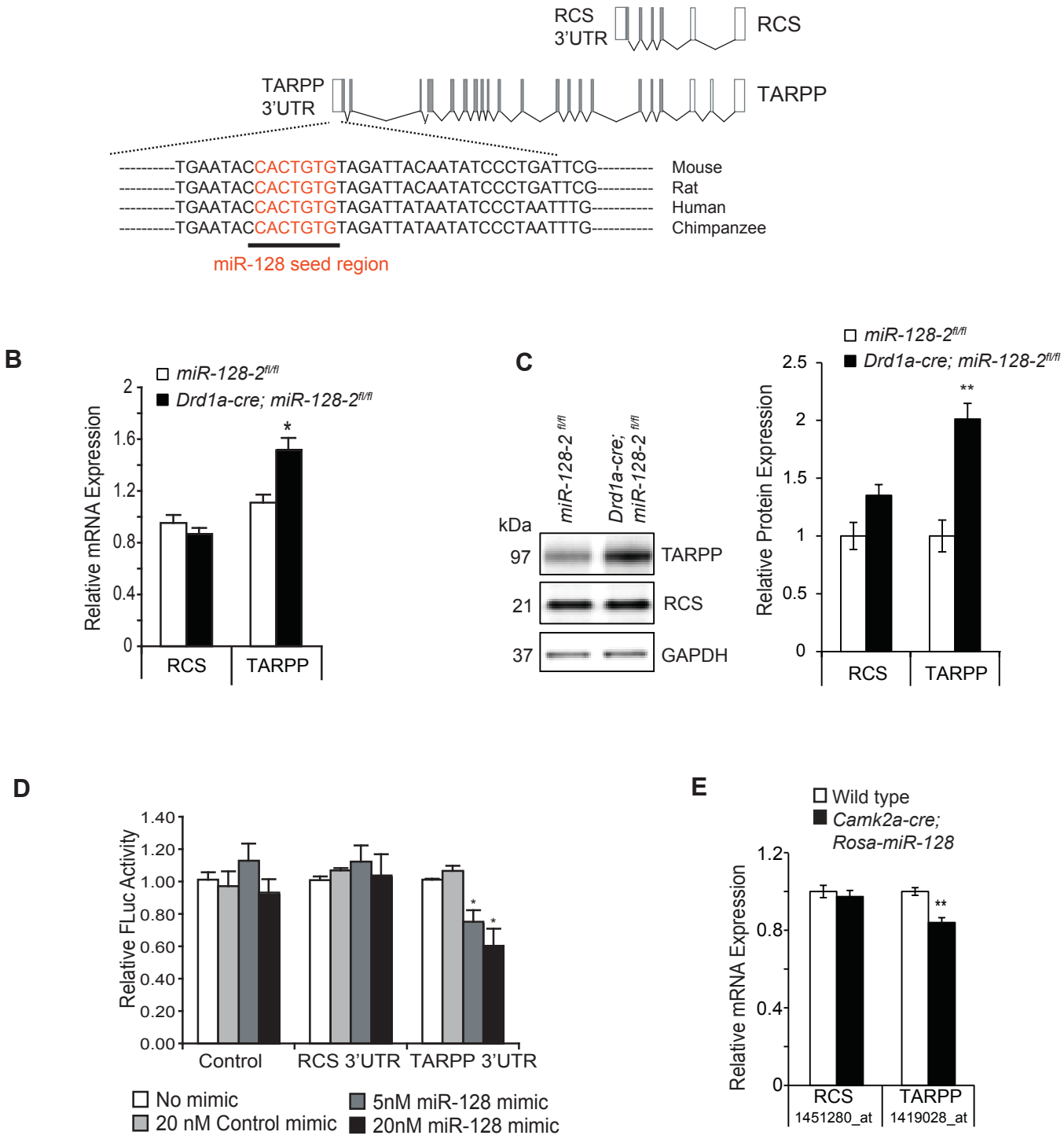

A
RCS 3'UTR
RCS
TARPP 3'UTR
TARPP
----------TGAATACCACTGTGTAGATTACAATATCCCTGATTCG---------- Mouse
----------TGAATACCACTGTGTAGATTACAATATCCCTGATTCG---------- Rat
----------TGAATACCACTGTGTAGATTATAATATCCCTAATTTG---------- Human
----------TGAATACCACTGTGTAGATTATAATATCCCTAATTTG---------- Chimpanzee
miR-128 seed region
B
miR-128-2fl/fl
Drd1a-cre; miR-128-2fl/fl
Relative mRNA Expression
RCS
TARPP
C
miR-128-2 fl/fl
Drd1a-cre; miR-128-2 fl/fl
kDa
97
21
37
TARPP
RCS
GAPDH
Relative Protein Expression
D
Relative FLuc Activity
Control
RCS 3'UTR
TARPP 3'UTR
No mimic
20 nM Control mimic
5nM miR-128 mimic
20nM miR-128 mimic
E
Wild type
Camk2a-cre; Rosa-miR-128
Relative mRNA Expression
RCS
1451280_at
TARPP
1419028_at

**Figure S7. miR-128 suppresses the expression of the TARPP-encoding long splice variant of the miR-128-2 host gene *Arpp21*.**

**(A) The TARPP-encoding mRNA splice variant of the *Arpp21* gene contains a miR-128 target seed sequence in the 3'UTR.** The scheme illustrates the two transcript isoforms of the *Arpp21* gene that encode the TARPP and RCS proteins. The 3'UTR of the long isoform TARPP contains a highly conserved miR-128 target seed sequence (shown in red). **(B, C) miR-128 deficiency leads to de-repression of TARPP. (B)** qRT-PCR quantification of RNA prepared from the striatum of *Drd1a-cre; miR-128-2*$^{fl/fl}$ mice and their littermate controls (n=3 each) show that only the long TARPP-encoding mRNA is upregulated in the absence of miR-128. **(C)** Expression levels of RCS (21 kDa) and TARPP (97 kDa) proteins in protein lysates from *Drd1a-cre; miR-128-2*$^{fl/fl}$ or littermate controls (n=3 each) were analyzed by Western blot. Bar graphs summarizes the mean protein expression levels as normalized to GAPDH. **(D, E) Specific suppression of TARPP in neurons overexpressing miR-128. (D)** The ability of miR-128 to target the 3'UTR of the TARPP and RCS mRNAs was analyzed using an *in-vitro* luciferase reporter assay. Plasmids expressing the firefly luciferase upstream of the RCS and TARPP specific 3'UTR sequence were transfected into N2A cells in the absence or presence of miR-128 mimics at the indicated concentrations. Firefly Luciferase activity was normalized to reporter Renilla Luciferase activity and visualized as activity relative to control transfections with no mimics added (n=3). **(E)** The level of mRNA expression of TARPP and RCS in the striatum of mice with a postnatal neuron specific overexpression of miR-128 and their littermate controls (n=4 each) were analyzed using Affymetrix microarray analysis. Mean normalized expression values corresponding to probes that are specific for the RCS and TARPP splice variant are shown.
Error bars show sem. * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, p-values calculated by Welch's t-test.

## Figure S8

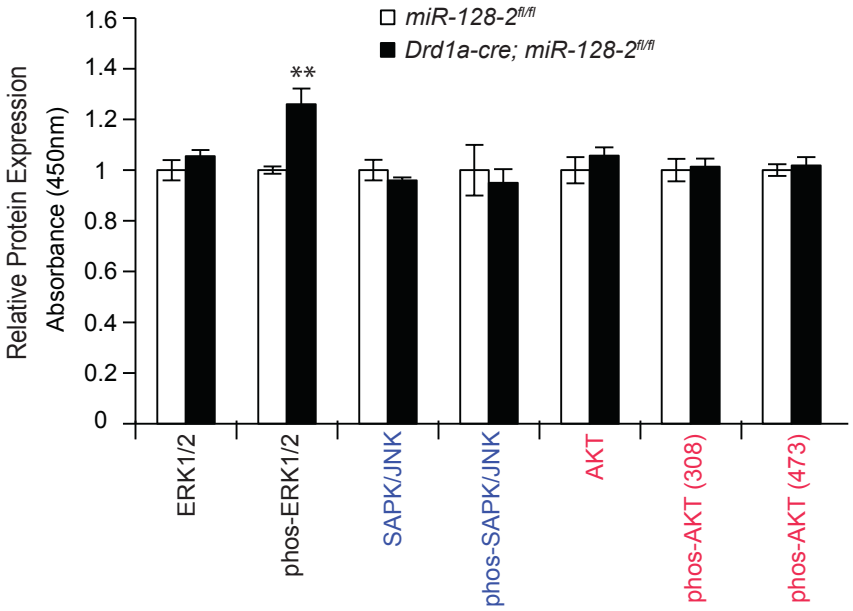
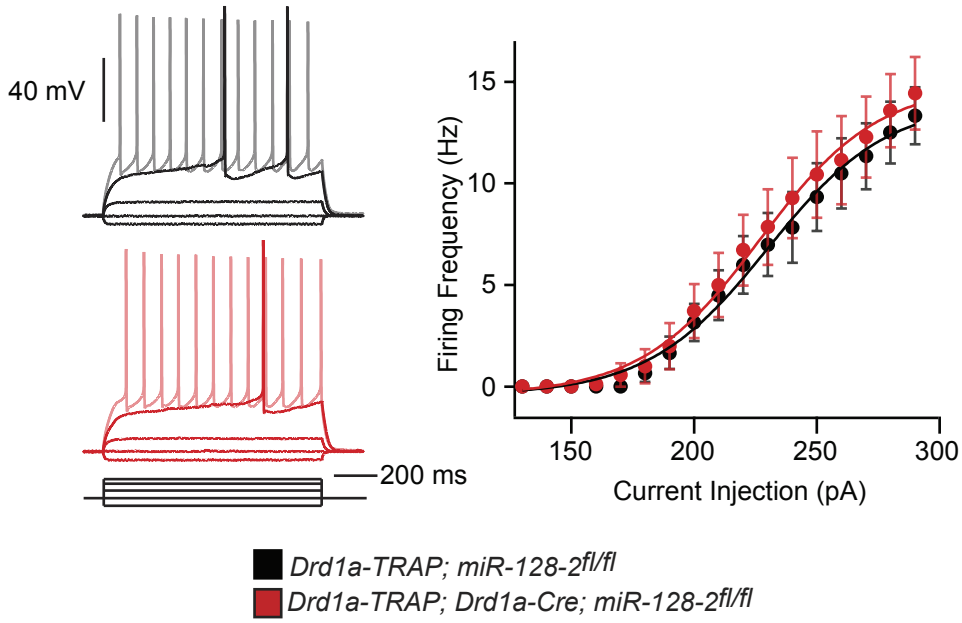



**Figure S8. Deficiency of miR-128 in D1-neurons leads to increase in ERK2 phosphorylation.**

Relative quantity of total or phosphorylated MAP kinase pathway proteins ERK1/2, SAPK/JNK, and AKT in striatal lysates from *Drd1a-cre; miR-128-2*$^{fl/fl}$ and littermate controls (n=4) were quantified by ELISA. Relative protein expression levels are based on absorbance values (450 nm) and displayed as bar graphs normalized to control values. Error bars show sem. ** $p \leq 0.01$, p-values calculated by Welch's t-test.

**Figure S9**

**A**


40 mV
200 ms
Firing Frequency (Hz)
15
10
5
0
150
200
250
300
Current Injection (pA)
Drd1a-TRAP; miR-128-2fl/fl
Drd1a-TRAP; Drd1a-Cre; miR-128-2fl/fl

**B**

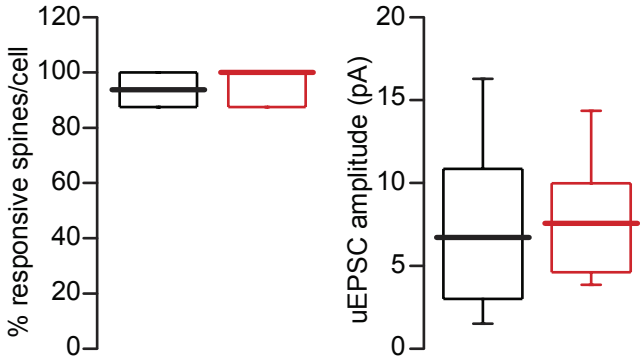
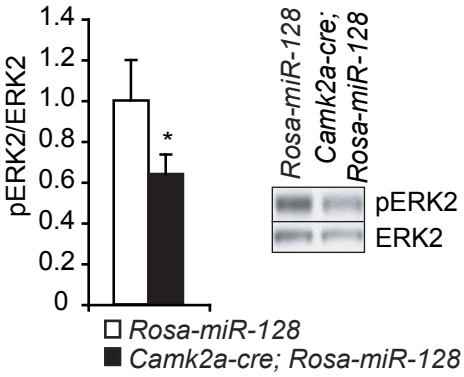

% responsive spines/cell
120
100
80
60
40
20
0
uEPSC amplitude (pA)
20
15
10
5
0

**Figure S9. miR-128 deficient striatal D1-neurons display D1-neuron characteristic somatic excitability.**

**(A, left)** Representative D1-neuron prototypic responses of control (*Drd1a-TRAP; miR-128-2*$^{fl/fl}$, **top, black**) and miR-128 deficient (*Drd1a-TRAP, Drd1a-cre; miR-128*$^{fl/fl}$, **bottom, red**) D1-neurons to somatic current injections. D1-neurons were identified by eGFP-L10 expression, voltage traces are in response to -100, -50, +100, +190 and +250 pA. **(A, right)** Frequency-current (F-I) plot showing D1-neuron characteristic average firing frequencies to somatic current injection. No difference was observed between wild-type **(black**, n=6) and mutant **(red**, n=7) D1-neurons. Mann-Whitney nonparametric test, $p>0.05$. (**B) miR-128 controls the number of functional spines in D1-neurons.** 2 photon uncaging of glutamate on successive neighboring spine heads revealed similar success rates for producing somatic EPSCs in control and miR-128 deficient D1 neurons **(n=5-6 cells, 40-48 spines per group, left)**, suggesting the increased spine density in **(Fig. 3B)** represents an increase in the number of spines with functional glutamate receptors. Glutamate uncaging-induced somatic EPSC amplitudes were similar in both groups **(right).**

**Figure S10**

**A**




**B**

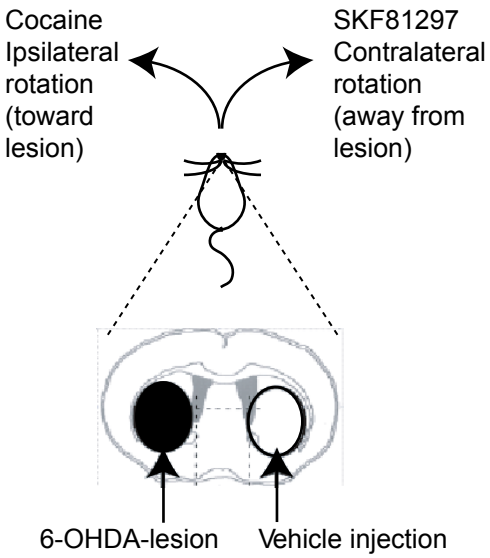


**Figure S10. Increased miR-128 expression in neurons suppresses ERK2 activation and protects against abnormal motor activity and seizures associated with chemically induced Parkinson's disease and seizures.**

**(A) miR-128 overexpression in Camk2a-neurons suppresses ERK2 phosphorylation in mice.** ERK2 phosphorylation levels in the striatum of transgenic *Camk2a-cre; Rosa-miR-128* mutant and control mice (n=4 each) were quantified by Western blotting, normalized to total ERK2 expression, and displayed relative to mean control levels. Representative blot is shown. Welch's t-test, * $p \leq 0.05$. **(B) miR-128 overexpression attenuates chemically triggered hyperresponsive motor behavior in mice.** The scheme shows the standard rotational responses of wild type mice with unilateral 6-OHDA-induced lesion. 6-OHDA and vehicle were injected into the left and right striatum, respectively, and rotational responses to either cocaine (which inhibits endogenous dopamine reuptake at dopaminergic terminals and thereby increases synaptic dopamine levels) or the Drd1-agonist SKF81297 (specific activation of the dopamine D1 receptor (Drd1)) are assayed after a 3-week recovery period. Cocaine injections induce ipsilateral (towards the lesioned side) rotations due to the stronger activation of the unlesioned contralateral striatum that still contains the functional dopaminergic terminals. Injections of the Drd1-agonist SKF81297 induce contralateral rotations (away from the lesioned side) due to the abnormal hypersensitivity of D1-neurons to Drd1 activation after dopamine depletion in the lesioned, ipsilateral striatum.

**Table S1.**

Overrepresented hexamers in RISC-associated 3'UTR clusters obtained from adult Camk2a-neurons.

**Table S2.**

Putative miR-128 RISC-associated target genes in adult Camk2a-neurons.

**Table S3.**

154 unique RISC-associated miR-128 target genes (189 microarray probes) that showed significantly ($p \leq 0.05$) increased ribosome-association in miR-128 deficient D1-neurons.

**Table S4.**

miR-128 targets in D1-neurons are enriched in ion channels, ion transporters, and signaling proteins.

**Movie S1. Tonic clonic seizure preceding miR-128-2$^{-/-}$ mouse death.**

Fatal tonic clonic seizure of a miR-128-2$^{-/-}$ mouse in Camera 1 (**Top Left**).

**Table S1. Overrepresented hexamers in RISC-associated 3'UTR clusters obtained from adult Camk2a-neurons.**

| 6mer sequence | # times in Ago2-CLIP cluster | # times in RefSeq background | Enrichment (observed-expected) | P-value | -log10(P-value) | z-score |
|---|---|---|---|---|---|---|
| **ACTGTG** | **1211** | **643** | **568** | **1.04E-39** | **38.98** | **6.02** |
| GGGCTG | 1136 | 581 | 555 | 5.94E-41 | 40.23 | 5.89 |
| CTGTGG | 1300 | 796 | 504 | 3.03E-28 | 27.52 | 5.35 |
| CTGTGA | 1143 | 700 | 443 | 6.16E-25 | 24.21 | 4.69 |
| GACTGT | 844 | 413 | 431 | 5.04E-34 | 33.30 | 4.57 |
| GAGGAG | 1020 | 597 | 423 | 7.00E-26 | 25.16 | 4.48 |
| GGACTG | 823 | 401 | 422 | 1.71E-33 | 32.77 | 4.47 |
| TGTGGG | 1060 | 638 | 422 | 1.44E-24 | 23.84 | 4.47 |
| GCTGTG | 1152 | 738 | 414 | 1.52E-21 | 20.82 | 4.39 |
| GGGAGG | 1115 | 706 | 409 | 8.53E-22 | 21.07 | 4.34 |
| GGAGGG | 1068 | 660 | 408 | 8.42E-23 | 22.07 | 4.33 |
| TGTGGA | 990 | 585 | 405 | 2.01E-24 | 23.70 | 4.29 |
| GGAAGG | 1073 | 677 | 396 | 2.73E-21 | 20.56 | 4.20 |
| GGAGGA | 971 | 576 | 395 | 1.11E-23 | 22.95 | 4.18 |
| AGGAGG | 1029 | 640 | 389 | 1.64E-21 | 20.79 | 4.13 |
| GGCTGG | 1006 | 621 | 385 | 1.40E-21 | 20.85 | 4.08 |
| GAGAGG | 926 | 553 | 373 | 3.12E-22 | 21.51 | 3.95 |
| GAGGGG | 880 | 508 | 372 | 1.68E-23 | 22.78 | 3.95 |
| GGGCAG | 970 | 599 | 371 | 8.04E-21 | 20.09 | 3.93 |
| AGACTG | 875 | 509 | 366 | 8.60E-23 | 22.07 | 3.88 |
| GGAGAG | 994 | 629 | 365 | 1.39E-19 | 18.86 | 3.87 |
| GGAAGA | 1023 | 661 | 362 | 1.22E-18 | 17.91 | 3.83 |
| TGGGGA | 1025 | 664 | 361 | 1.55E-18 | 17.81 | 3.83 |
| GGTGCT | 753 | 395 | 358 | 4.70E-26 | 25.33 | 3.79 |
| GAAGGG | 865 | 515 | 350 | 4.38E-21 | 20.36 | 3.71 |
| GAGAGA | 989 | 641 | 348 | 6.38E-18 | 17.20 | 3.69 |
| GGGAAG | 1007 | 665 | 342 | 6.51E-17 | 16.19 | 3.62 |
| GGCTGT | 856 | 515 | 341 | 2.99E-20 | 19.52 | 3.62 |
| GAGAAG | 961 | 621 | 340 | 1.32E-17 | 16.88 | 3.60 |
| GGGGAG | 913 | 575 | 338 | 2.00E-18 | 17.70 | 3.58 |
| GGACAG | 892 | 558 | 334 | 1.73E-18 | 17.76 | 3.54 |
| GAAGAG | 941 | 609 | 332 | 3.48E-17 | 16.46 | 3.52 |
| AGAGAG | 1044 | 715 | 329 | 3.99E-15 | 14.40 | 3.49 |
| GTGGGG | 929 | 604 | 325 | 1.08E-16 | 15.97 | 3.44 |
| GCTGGG | 978 | 660 | 318 | 3.72E-15 | 14.43 | 3.37 |
| TGTGTG | 1460 | 1145 | 315 | 7.11E-10 | 9.15 | 3.33 |
| CTGTAG | 764 | 450 | 314 | 1.88E-19 | 18.72 | 3.33 |
| GGCAGG | 909 | 595 | 314 | 6.08E-16 | 15.22 | 3.33 |
| TGTAGA | 736 | 423 | 313 | 3.49E-20 | 19.46 | 3.32 |
| GCAGAG | 974 | 661 | 313 | 9.37E-15 | 14.03 | 3.32 |
| AGGGCT | 806 | 497 | 309 | 1.19E-17 | 16.93 | 3.27 |
| GTGTGG | 886 | 578 | 308 | 8.42E-16 | 15.07 | 3.26 |
| AGGAAG | 1155 | 849 | 306 | 7.50E-12 | 11.13 | 3.25 |
| GTGCTG | 878 | 574 | 304 | 1.33E-15 | 14.87 | 3.23 |
| AGGGGA | 788 | 484 | 304 | 1.67E-17 | 16.78 | 3.22 |
| AGAGGA | 933 | 636 | 297 | 5.93E-14 | 13.23 | 3.15 |
| GTGGGA | 794 | 499 | 295 | 2.21E-16 | 15.66 | 3.13 |
| GTGGAG | 779 | 485 | 294 | 1.26E-16 | 15.90 | 3.12 |
| GAGCTG | 898 | 606 | 292 | 5.08E-14 | 13.29 | 3.10 |

| | | | | | | |
|---|---|---|---|---|---|---|
| AGAGGG | 830 | 539 | 291 | 3.73E-15 | 14.43 | 3.08 |
| TGGAGA | 945 | 658 | 287 | 7.56E-13 | 12.12 | 3.04 |
| CTGGAG | 985 | 698 | 287 | 2.69E-12 | 11.57 | 3.04 |
| TGCTGT | 1070 | 784 | 286 | 2.97E-11 | 10.53 | 3.03 |
| GGGAGA | 830 | 545 | 285 | 1.39E-14 | 13.86 | 3.03 |
| GAAGGA | 874 | 591 | 283 | 1.41E-13 | 12.85 | 3.00 |
| GGGGCT | 723 | 441 | 282 | 1.42E-16 | 15.85 | 2.99 |
| AGGGAG | 917 | 638 | 279 | 1.59E-12 | 11.80 | 2.95 |
| TGGAGG | 857 | 579 | 278 | 2.15E-13 | 12.67 | 2.95 |
| TGGGAG | 911 | 634 | 277 | 1.81E-12 | 11.74 | 2.94 |
| AGGAGA | 928 | 654 | 274 | 5.93E-12 | 11.23 | 2.90 |
| GGGGAC | 610 | 339 | 271 | 1.57E-18 | 17.81 | 2.87 |
| CTGGGG | 966 | 698 | 268 | 4.92E-11 | 10.31 | 2.84 |
| TGGTGC | 609 | 342 | 267 | 4.60E-18 | 17.34 | 2.83 |
| CACTGT | 901 | 636 | 265 | 1.43E-11 | 10.84 | 2.81 |
| GAGCAG | 859 | 594 | 265 | 3.84E-12 | 11.42 | 2.81 |
| GGGACT | 627 | 364 | 263 | 6.83E-17 | 16.17 | 2.79 |
| ACTGTA | 703 | 440 | 263 | 7.89E-15 | 14.10 | 2.78 |
| TGGGGG | 855 | 593 | 262 | 5.64E-12 | 11.25 | 2.78 |
| CTGGGA | 979 | 717 | 262 | 2.02E-10 | 9.70 | 2.78 |
| CTGCTG | 1165 | 904 | 261 | 9.43E-09 | 8.03 | 2.77 |
| GGAGAA | 834 | 574 | 260 | 3.94E-12 | 11.40 | 2.76 |
| GGTGGG | 898 | 639 | 259 | 4.16E-11 | 10.38 | 2.74 |
| GAACTG | 682 | 423 | 259 | 7.28E-15 | 14.14 | 2.74 |
| GACTGG | 646 | 387 | 259 | 8.78E-16 | 15.06 | 2.74 |
| TTGGGG | 806 | 549 | 257 | 3.22E-12 | 11.49 | 2.72 |
| AGAAGG | 864 | 610 | 254 | 3.82E-11 | 10.42 | 2.69 |
| GAGGGA | 797 | 543 | 254 | 4.21E-12 | 11.38 | 2.69 |
| GGCAGA | 784 | 531 | 253 | 2.94E-12 | 11.53 | 2.68 |
| TGGCTG | 940 | 688 | 252 | 4.17E-10 | 9.38 | 2.67 |
| GAGGAA | 850 | 599 | 251 | 4.03E-11 | 10.39 | 2.66 |
| GGAAAG | 894 | 644 | 250 | 1.68E-10 | 9.78 | 2.66 |
| TGTGAG | 818 | 568 | 250 | 1.82E-11 | 10.74 | 2.65 |
| AAGGGC | 599 | 352 | 247 | 1.18E-15 | 14.93 | 2.62 |
| CTGTGT | 1180 | 935 | 245 | 9.41E-08 | 7.03 | 2.60 |
| GGGTGG | 853 | 610 | 243 | 2.21E-10 | 9.66 | 2.57 |
| GACTGA | 624 | 383 | 241 | 3.20E-14 | 13.50 | 2.55 |
| TGGGCT | 782 | 544 | 238 | 5.80E-11 | 10.24 | 2.53 |
| AGAGAC | 722 | 484 | 238 | 6.58E-12 | 11.18 | 2.53 |
| TGAGAG | 765 | 527 | 238 | 3.41E-11 | 10.47 | 2.53 |
| TGTGGC | 758 | 520 | 238 | 2.99E-11 | 10.52 | 2.52 |
| AGGCAG | 945 | 710 | 235 | 7.93E-09 | 8.10 | 2.49 |
| TGGAAG | 873 | 640 | 233 | 2.14E-09 | 8.67 | 2.47 |
| GCAGGG | 770 | 538 | 232 | 1.35E-10 | 9.87 | 2.46 |
| CTGAGA | 890 | 658 | 232 | 3.64E-09 | 8.44 | 2.46 |
| TCTGTG | 1114 | 884 | 230 | 2.57E-07 | 6.59 | 2.44 |
| AGAAGA | 943 | 715 | 228 | 2.01E-08 | 7.70 | 2.42 |
| GTGGTG | 674 | 446 | 228 | 9.49E-12 | 11.02 | 2.42 |
| GCTGGA | 705 | 478 | 227 | 3.71E-11 | 10.43 | 2.41 |
| AGGCTG | 895 | 669 | 226 | 1.07E-08 | 7.97 | 2.40 |
| TGTGAA | 861 | 636 | 225 | 5.59E-09 | 8.25 | 2.39 |
| CAGGAG | 899 | 674 | 225 | 1.30E-08 | 7.89 | 2.39 |
| CTGGGC | 822 | 597 | 225 | 2.14E-09 | 8.67 | 2.39 |
| TGACTG | 736 | 511 | 225 | 1.80E-10 | 9.74 | 2.39 |

| | | | | | | |
|---|---|---|---|---|---|---|
| GCAGGA | 724 | 499 | 225 | 1.28E-10 | 9.89 | 2.38 |
| TTGTGG | 697 | 473 | 224 | 5.54E-11 | 10.26 | 2.38 |
| GAGACT | 625 | 404 | 221 | 5.05E-12 | 11.30 | 2.35 |
| GGGGGA | 635 | 414 | 221 | 8.18E-12 | 11.09 | 2.35 |
| GTGGAA | 647 | 427 | 220 | 1.83E-11 | 10.74 | 2.33 |
| GCTGCT | 900 | 680 | 220 | 3.10E-08 | 7.51 | 2.33 |
| AGCTGG | 830 | 610 | 220 | 6.81E-09 | 8.17 | 2.33 |
| TGAGGA | 760 | 544 | 216 | 2.41E-09 | 8.62 | 2.28 |
| TGGTGG | 753 | 538 | 215 | 2.09E-09 | 8.68 | 2.28 |
| TGGACT | 606 | 392 | 214 | 1.18E-11 | 10.93 | 2.27 |
| GGAGAC | 608 | 395 | 213 | 1.81E-11 | 10.74 | 2.26 |
| TGGGAC | 599 | 387 | 212 | 1.53E-11 | 10.82 | 2.25 |
| CAGAGG | 914 | 704 | 210 | 1.88E-07 | 6.73 | 2.22 |
| GGCTGC | 704 | 495 | 209 | 1.57E-09 | 8.80 | 2.22 |
| GGAGGC | 647 | 439 | 208 | 2.56E-10 | 9.59 | 2.21 |
| GGATGG | 636 | 429 | 207 | 2.31E-10 | 9.64 | 2.19 |
| TGGGAA | 901 | 695 | 206 | 2.44E-07 | 6.61 | 2.19 |
| AGGACT | 646 | 440 | 206 | 4.45E-10 | 9.35 | 2.18 |
| AGGGGC | 594 | 389 | 205 | 5.82E-11 | 10.24 | 2.18 |
| TGTTGG | 677 | 472 | 205 | 1.43E-09 | 8.85 | 2.17 |
| CTGGAC | 600 | 396 | 204 | 9.55E-11 | 10.02 | 2.17 |
| GGGGTG | 712 | 508 | 204 | 5.11E-09 | 8.29 | 2.16 |
| AAGGGA | 736 | 532 | 204 | 1.05E-08 | 7.98 | 2.16 |
| TGCTGC | 819 | 616 | 203 | 8.61E-08 | 7.06 | 2.15 |
| GGGGCA | 580 | 377 | 203 | 5.70E-11 | 10.24 | 2.15 |
| GAAAGG | 769 | 566 | 203 | 2.93E-08 | 7.53 | 2.15 |
| GGGGAA | 696 | 494 | 202 | 4.32E-09 | 8.36 | 2.15 |
| CTGAGG | 863 | 661 | 202 | 2.22E-07 | 6.65 | 2.14 |
| GGAGTG | 590 | 389 | 201 | 1.20E-10 | 9.92 | 2.14 |
| TGGGGC | 656 | 455 | 201 | 1.60E-09 | 8.80 | 2.13 |
| TGAAGG | 719 | 518 | 201 | 1.11E-08 | 7.96 | 2.13 |
| GAGTGG | 616 | 415 | 201 | 3.93E-10 | 9.41 | 2.13 |
| GAGGAC | 560 | 360 | 200 | 3.89E-11 | 10.41 | 2.12 |
| GGGACA | 660 | 461 | 199 | 2.80E-09 | 8.55 | 2.11 |
| CAGGGA | 828 | 631 | 197 | 2.40E-07 | 6.62 | 2.09 |
| AAGAGG | 699 | 502 | 197 | 1.42E-08 | 7.85 | 2.08 |
| CTGTGC | 827 | 631 | 196 | 2.82E-07 | 6.55 | 2.08 |
| TGGCAG | 764 | 568 | 196 | 8.12E-08 | 7.09 | 2.08 |
| CTGGTG | 737 | 541 | 196 | 4.37E-08 | 7.36 | 2.08 |
| AGGGGG | 556 | 361 | 195 | 1.14E-10 | 9.94 | 2.07 |
| GTGCCT | 651 | 456 | 195 | 4.65E-09 | 8.33 | 2.07 |
| AAGGGG | 596 | 402 | 194 | 8.32E-10 | 9.08 | 2.06 |
| TGCCTT | 878 | 685 | 193 | 1.04E-06 | 5.98 | 2.05 |
| GTGTGT | 1066 | 873 | 193 | 1.23E-05 | 4.91 | 2.04 |
| TGAGGG | 668 | 476 | 192 | 1.34E-08 | 7.87 | 2.04 |
| GGAGCT | 633 | 442 | 191 | 5.64E-09 | 8.25 | 2.03 |
| TGGATG | 633 | 443 | 190 | 6.78E-09 | 8.17 | 2.02 |
| GGCCTG | 734 | 544 | 190 | 1.05E-07 | 6.98 | 2.02 |
| GTTGGG | 552 | 363 | 189 | 4.19E-10 | 9.38 | 2.00 |
| GTAGAG | 495 | 307 | 188 | 2.99E-11 | 10.52 | 2.00 |
| GCACTG | 652 | 464 | 188 | 1.83E-08 | 7.74 | 1.99 |
| TGTAGG | 514 | 327 | 187 | 1.09E-10 | 9.96 | 1.98 |
| GCTGAG | 775 | 588 | 187 | 4.25E-07 | 6.37 | 1.98 |
| GTGGCT | 707 | 521 | 186 | 1.05E-07 | 6.98 | 1.98 |

| | | | | | | |
|---|---|---|---|---|---|---|
| TGCTGG | 837 | 651 | 186 | 1.39E-06 | 5.86 | 1.97 |
| GGCAGC | 657 | 471 | 186 | 3.06E-08 | 7.51 | 1.97 |
| AAGAGA | 848 | 662 | 186 | 1.77E-06 | 5.75 | 1.97 |
| GAAGAA | 858 | 672 | 186 | 2.10E-06 | 5.68 | 1.97 |
| GCCTGG | 814 | 630 | 184 | 1.26E-06 | 5.90 | 1.95 |
| GTGGAC | 464 | 280 | 184 | 1.71E-11 | 10.77 | 1.95 |
| GAGGTG | 627 | 444 | 183 | 2.09E-08 | 7.68 | 1.94 |
| AGCAGA | 819 | 637 | 182 | 1.91E-06 | 5.72 | 1.93 |
| CTGTTG | 722 | 540 | 182 | 3.14E-07 | 6.50 | 1.93 |
| AGAGAA | 993 | 812 | 181 | 2.14E-05 | 4.67 | 1.91 |
| AGGGAC | 595 | 415 | 180 | 1.38E-08 | 7.86 | 1.91 |
| CTGAGC | 754 | 574 | 180 | 7.91E-07 | 6.10 | 1.91 |
| GGAGCA | 605 | 426 | 179 | 2.45E-08 | 7.61 | 1.90 |
| TGGGTG | 724 | 545 | 179 | 5.02E-07 | 6.30 | 1.90 |
| ACTGAG | 695 | 517 | 178 | 3.26E-07 | 6.49 | 1.89 |
| GTGAGG | 619 | 443 | 176 | 6.29E-08 | 7.20 | 1.87 |
| GATGGA | 592 | 416 | 176 | 3.00E-08 | 7.52 | 1.87 |
| CCTGTG | 973 | 797 | 176 | 3.02E-05 | 4.52 | 1.86 |
| TCTGGG | 847 | 672 | 175 | 7.45E-06 | 5.13 | 1.85 |
| TGGACA | 629 | 455 | 174 | 1.15E-07 | 6.94 | 1.85 |
| GGTGGA | 544 | 370 | 174 | 7.85E-09 | 8.11 | 1.85 |
| GGATTG | 408 | 234 | 174 | 5.96E-12 | 11.22 | 1.85 |
| CAGGGG | 617 | 444 | 173 | 1.11E-07 | 6.96 | 1.83 |
| GGCTGA | 602 | 430 | 172 | 7.89E-08 | 7.10 | 1.83 |
| AGGAGC | 643 | 471 | 172 | 2.55E-07 | 6.59 | 1.82 |
| AAGGAG | 738 | 567 | 171 | 2.05E-06 | 5.69 | 1.82 |
| ACTGGG | 640 | 469 | 171 | 2.59E-07 | 6.59 | 1.82 |
| GACAGG | 629 | 458 | 171 | 2.12E-07 | 6.67 | 1.81 |
| CCTCTG | 972 | 802 | 170 | 5.32E-05 | 4.27 | 1.80 |
| GTGAGA | 584 | 414 | 170 | 7.25E-08 | 7.14 | 1.80 |
| CAGAGA | 917 | 747 | 170 | 3.09E-05 | 4.51 | 1.80 |
| GAGGCA | 623 | 454 | 169 | 2.40E-07 | 6.62 | 1.80 |
| GATGGG | 573 | 404 | 169 | 5.95E-08 | 7.23 | 1.80 |
| GAGGGC | 532 | 363 | 169 | 1.50E-08 | 7.82 | 1.80 |
| GAAAGA | 797 | 628 | 169 | 7.69E-06 | 5.11 | 1.79 |
| GCTGGC | 634 | 465 | 169 | 3.58E-07 | 6.45 | 1.79 |
| TTGGTG | 612 | 444 | 168 | 2.22E-07 | 6.65 | 1.78 |
| TGGAGC | 599 | 431 | 168 | 1.62E-07 | 6.79 | 1.78 |
| AGATGG | 684 | 516 | 168 | 1.28E-06 | 5.89 | 1.78 |
| AGAGGC | 660 | 492 | 168 | 7.98E-07 | 6.10 | 1.78 |
| AGGTGG | 673 | 506 | 167 | 1.10E-06 | 5.96 | 1.77 |
| GTAGAA | 518 | 352 | 166 | 1.79E-08 | 7.75 | 1.76 |
| TCTGAG | 840 | 674 | 166 | 2.02E-05 | 4.69 | 1.76 |
| GAAGGC | 574 | 409 | 165 | 1.30E-07 | 6.88 | 1.75 |
| GCTGTA | 510 | 346 | 164 | 1.91E-08 | 7.72 | 1.74 |
| AGGGTG | 626 | 462 | 164 | 6.50E-07 | 6.19 | 1.74 |
| AGGATG | 637 | 473 | 164 | 8.63E-07 | 6.06 | 1.74 |
| AGTGGG | 649 | 485 | 164 | 1.20E-06 | 5.92 | 1.73 |
| GTGGGC | 528 | 365 | 163 | 4.57E-08 | 7.34 | 1.73 |
| CAGCAG | 943 | 782 | 161 | 1.01E-04 | 3.99 | 1.71 |
| AGGGCA | 644 | 483 | 161 | 1.56E-06 | 5.81 | 1.71 |
| ACTGGA | 616 | 456 | 160 | 9.82E-07 | 6.01 | 1.70 |
| GACAGA | 688 | 528 | 160 | 4.52E-06 | 5.35 | 1.70 |
| GAGACA | 654 | 496 | 158 | 2.95E-06 | 5.53 | 1.68 |

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|---|---|---|---|---|---|---|
| GGGATG | 561 | 403 | 158 | 3.86E-07 | 6.41 | 1.67 |
| GAGACC | 485 | 328 | 157 | 3.34E-08 | 7.48 | 1.67 |
| GGGAGC | 552 | 395 | 157 | 3.16E-07 | 6.50 | 1.67 |
| TGTGAC | 634 | 477 | 157 | 2.40E-06 | 5.62 | 1.67 |
| GGGGGC | 457 | 300 | 157 | 1.18E-08 | 7.93 | 1.66 |
| GGTGTG | 641 | 484 | 157 | 2.90E-06 | 5.54 | 1.66 |
| GTGTGA | 632 | 476 | 156 | 2.58E-06 | 5.59 | 1.66 |
| GAGAAC | 521 | 365 | 156 | 1.48E-07 | 6.83 | 1.66 |
| CCTGGG | 946 | 790 | 156 | 1.76E-04 | 3.76 | 1.66 |
| CTGAAG | 806 | 650 | 156 | 4.24E-05 | 4.37 | 1.66 |
| ATGTGG | 618 | 462 | 156 | 2.05E-06 | 5.69 | 1.65 |
| GAATGT | 602 | 447 | 155 | 1.61E-06 | 5.79 | 1.65 |
| AGCAGG | 778 | 624 | 154 | 3.91E-05 | 4.41 | 1.63 |
| AACTGT | 663 | 509 | 154 | 6.99E-06 | 5.16 | 1.63 |
| AGTGGA | 582 | 428 | 154 | 1.37E-06 | 5.86 | 1.63 |
| GGTTGG | 501 | 348 | 153 | 1.58E-07 | 6.80 | 1.62 |
| CTCTGG | 893 | 740 | 153 | 1.59E-04 | 3.80 | 1.62 |
| GAGGCT | 630 | 478 | 152 | 4.94E-06 | 5.31 | 1.61 |
| GACCTG | 558 | 406 | 152 | 1.01E-06 | 5.99 | 1.61 |
| GAGAGC | 568 | 417 | 151 | 1.59E-06 | 5.80 | 1.60 |
| GACTTG | 535 | 385 | 150 | 7.58E-07 | 6.12 | 1.59 |
| GTGACT | 587 | 438 | 149 | 3.10E-06 | 5.51 | 1.58 |
| GGGCTC | 539 | 390 | 149 | 9.72E-07 | 6.01 | 1.58 |
| TGGGGT | 670 | 521 | 149 | 1.59E-05 | 4.80 | 1.58 |
| GCTGCA | 610 | 461 | 149 | 5.37E-06 | 5.27 | 1.58 |
| AGGGAA | 772 | 624 | 148 | 7.08E-05 | 4.15 | 1.57 |
| TTGGGA | 634 | 486 | 148 | 9.61E-06 | 5.02 | 1.57 |
| AGAAAG | 964 | 816 | 148 | 4.62E-04 | 3.34 | 1.57 |
| GAAGAC | 553 | 406 | 147 | 1.97E-06 | 5.70 | 1.56 |
| AAAGGG | 632 | 485 | 147 | 1.05E-05 | 4.98 | 1.56 |
| AGAACT | 654 | 507 | 147 | 1.58E-05 | 4.80 | 1.56 |
| TTTGGG | 732 | 585 | 147 | 5.07E-05 | 4.29 | 1.56 |
| AGTGTG | 751 | 604 | 147 | 6.49E-05 | 4.19 | 1.56 |
| GAGGGT | 507 | 360 | 147 | 6.03E-07 | 6.22 | 1.56 |
| AAGAAG | 781 | 634 | 147 | 9.37E-05 | 4.03 | 1.56 |
| GCCTTA | 414 | 268 | 146 | 2.01E-08 | 7.70 | 1.55 |
| GGGACC | 459 | 313 | 146 | 1.56E-07 | 6.81 | 1.55 |
| TGAAGA | 798 | 653 | 145 | 1.38E-04 | 3.86 | 1.54 |
| GGGCTT | 553 | 408 | 145 | 2.91E-06 | 5.54 | 1.54 |
| TGGGCA | 644 | 499 | 145 | 1.88E-05 | 4.73 | 1.53 |
| GTGGCA | 539 | 396 | 143 | 3.04E-06 | 5.52 | 1.51 |
| AGAGTG | 603 | 461 | 142 | 1.32E-05 | 4.88 | 1.51 |
| GGGTGT | 522 | 380 | 142 | 2.26E-06 | 5.65 | 1.51 |
| AGGACA | 701 | 559 | 142 | 6.33E-05 | 4.20 | 1.51 |
| GAGATG | 622 | 481 | 141 | 2.10E-05 | 4.68 | 1.50 |
| GAGTGT | 522 | 382 | 140 | 3.38E-06 | 5.47 | 1.48 |
| CCTGGA | 770 | 631 | 139 | 1.99E-04 | 3.70 | 1.48 |
| GGACCT | 460 | 321 | 139 | 6.46E-07 | 6.19 | 1.47 |
| CTGGCA | 632 | 493 | 139 | 3.39E-05 | 4.47 | 1.47 |
| CTTGGG | 691 | 552 | 139 | 8.29E-05 | 4.08 | 1.47 |
| GGTGAG | 552 | 413 | 139 | 8.19E-06 | 5.09 | 1.47 |
| ATGGAG | 611 | 473 | 138 | 2.97E-05 | 4.53 | 1.46 |
| TGAATG | 631 | 495 | 136 | 5.00E-05 | 4.30 | 1.44 |
| GCTCTG | 835 | 699 | 136 | 5.17E-04 | 3.29 | 1.44 |

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|---|---|---|---|---|---|---|
| CTCTGA | 799 | 663 | 136 | 3.82E-04 | 3.42 | 1.44 |
| GGACTT | 499 | 364 | 135 | 4.16E-06 | 5.38 | 1.43 |
| TGTGGT | 697 | 562 | 135 | 1.45E-04 | 3.84 | 1.43 |
| AGAGCA | 713 | 578 | 135 | 1.76E-04 | 3.75 | 1.43 |
| GGATGA | 454 | 320 | 134 | 1.38E-06 | 5.86 | 1.42 |
| CTGAAC | 498 | 364 | 134 | 5.26E-06 | 5.28 | 1.42 |
| GTTGGA | 435 | 302 | 133 | 8.83E-07 | 6.05 | 1.41 |
| TCTGGA | 716 | 583 | 133 | 2.18E-04 | 3.66 | 1.41 |
| AAGGAC | 535 | 403 | 132 | 1.60E-05 | 4.80 | 1.40 |
| ACAGGA | 698 | 566 | 132 | 2.11E-04 | 3.68 | 1.40 |
| TTGTAG | 496 | 365 | 131 | 8.31E-06 | 5.08 | 1.39 |
| CAGAGC | 772 | 642 | 130 | 5.20E-04 | 3.28 | 1.38 |
| TGAGTG | 620 | 490 | 130 | 9.13E-05 | 4.04 | 1.38 |
| GATTGT | 415 | 285 | 130 | 8.59E-07 | 6.07 | 1.38 |
| CTCTGT | 920 | 790 | 130 | 1.67E-03 | 2.78 | 1.38 |
| GGACCA | 465 | 336 | 129 | 4.99E-06 | 5.30 | 1.37 |
| CAGTGG | 703 | 574 | 129 | 3.05E-04 | 3.52 | 1.37 |
| TACTGT | 593 | 464 | 129 | 7.26E-05 | 4.14 | 1.37 |
| GAAGTG | 574 | 445 | 129 | 5.57E-05 | 4.25 | 1.36 |
| TCAGGG | 613 | 484 | 129 | 1.04E-04 | 3.98 | 1.36 |
| CAGAAG | 832 | 703 | 129 | 1.04E-03 | 2.98 | 1.36 |
| GTGAAG | 570 | 442 | 128 | 5.45E-05 | 4.26 | 1.36 |
| TGAGAA | 787 | 660 | 127 | 8.07E-04 | 3.09 | 1.35 |
| GTTTGG | 581 | 454 | 127 | 7.89E-05 | 4.10 | 1.35 |
| GTGGGT | 557 | 430 | 127 | 5.60E-05 | 4.25 | 1.34 |
| GGACTC | 442 | 316 | 126 | 4.36E-06 | 5.36 | 1.34 |
| GCAGCT | 648 | 522 | 126 | 2.19E-04 | 3.66 | 1.34 |
| GAAGCA | 651 | 525 | 126 | 2.33E-04 | 3.63 | 1.34 |
| GAGCCA | 613 | 487 | 126 | 1.43E-04 | 3.84 | 1.34 |
| CAGGGC | 664 | 538 | 126 | 2.86E-04 | 3.54 | 1.33 |
| ATGGGG | 508 | 382 | 126 | 2.50E-05 | 4.60 | 1.33 |
| CTGCAG | 901 | 775 | 126 | 2.15E-03 | 2.67 | 1.33 |
| ACTCTG | 678 | 553 | 125 | 3.49E-04 | 3.46 | 1.33 |
| TTTGGA | 698 | 573 | 125 | 4.65E-04 | 3.33 | 1.32 |
| GGAACT | 480 | 356 | 124 | 1.69E-05 | 4.77 | 1.32 |
| GGGGAT | 397 | 273 | 124 | 1.55E-06 | 5.81 | 1.32 |
| TTGGAG | 591 | 467 | 124 | 1.33E-04 | 3.88 | 1.32 |
| GATGTG | 542 | 418 | 124 | 6.36E-05 | 4.20 | 1.31 |
| GCTGGT | 520 | 397 | 123 | 5.18E-05 | 4.29 | 1.30 |
| GGCAAG | 472 | 350 | 122 | 2.05E-05 | 4.69 | 1.29 |
| GGGTTG | 440 | 318 | 122 | 9.44E-06 | 5.03 | 1.29 |
| TGGGAT | 539 | 417 | 122 | 8.38E-05 | 4.08 | 1.29 |
| GGAGGT | 488 | 367 | 121 | 3.23E-05 | 4.49 | 1.29 |
| CCTGGC | 715 | 594 | 121 | 8.07E-04 | 3.09 | 1.28 |
| GGGGGT | 463 | 342 | 121 | 2.05E-05 | 4.69 | 1.28 |
| AGAAGC | 657 | 536 | 121 | 4.84E-04 | 3.32 | 1.28 |
| GGGGCC | 446 | 326 | 120 | 1.46E-05 | 4.84 | 1.28 |
| ACTGTT | 640 | 520 | 120 | 4.07E-04 | 3.39 | 1.28 |
| CAAGGG | 502 | 382 | 120 | 5.73E-05 | 4.24 | 1.27 |
| CAGGAC | 576 | 456 | 120 | 1.97E-04 | 3.70 | 1.27 |
| GGTGGC | 506 | 387 | 119 | 6.33E-05 | 4.20 | 1.27 |
| GGGCCA | 503 | 384 | 119 | 6.19E-05 | 4.21 | 1.26 |
| AAGGAA | 903 | 784 | 119 | 3.76E-03 | 2.43 | 1.26 |
| CCAAGG | 603 | 484 | 119 | 3.14E-04 | 3.50 | 1.26 |

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|---|---|---|---|---|---|---|
| GGAATG | 513 | 394 | 119 | 8.23E-05 | 4.08 | 1.26 |
| GCAGCA | 622 | 503 | 119 | 4.07E-04 | 3.39 | 1.26 |
| AGAGCT | 681 | 563 | 118 | 7.82E-04 | 3.11 | 1.26 |
| GACTGC | 421 | 303 | 118 | 1.16E-05 | 4.93 | 1.25 |
| GTAGGG | 355 | 237 | 118 | 1.36E-06 | 5.87 | 1.25 |
| GTAGGA | 389 | 271 | 118 | 4.77E-06 | 5.32 | 1.25 |
| GATGAG | 467 | 350 | 117 | 3.98E-05 | 4.40 | 1.24 |
| AAGATG | 675 | 558 | 117 | 8.33E-04 | 3.08 | 1.24 |
| GTCTGT | 685 | 568 | 117 | 9.46E-04 | 3.02 | 1.24 |
| GCTGTT | 627 | 510 | 117 | 5.19E-04 | 3.28 | 1.24 |
| GCAGAC | 449 | 332 | 117 | 3.07E-05 | 4.51 | 1.24 |
| CTGGCC | 683 | 567 | 116 | 9.92E-04 | 3.00 | 1.23 |
| GGATGT | 459 | 343 | 116 | 4.35E-05 | 4.36 | 1.23 |
| GGAGCC | 553 | 437 | 116 | 2.35E-04 | 3.63 | 1.23 |
| GAAGAT | 528 | 413 | 115 | 1.67E-04 | 3.78 | 1.22 |
| TGGAAC | 452 | 337 | 115 | 4.08E-05 | 4.39 | 1.22 |
| TGGACC | 405 | 290 | 115 | 1.24E-05 | 4.91 | 1.22 |
| ACACTG | 694 | 579 | 115 | 1.28E-03 | 2.89 | 1.22 |
| GTAGAC | 320 | 206 | 114 | 6.33E-07 | 6.20 | 1.21 |
| GGTGGT | 479 | 365 | 114 | 8.98E-05 | 4.05 | 1.21 |
| TGAGCA | 614 | 501 | 113 | 6.77E-04 | 3.17 | 1.20 |
| AGCTGT | 739 | 626 | 113 | 2.17E-03 | 2.66 | 1.20 |
| GGGGGG | 636 | 523 | 113 | 8.86E-04 | 3.05 | 1.20 |
| TTGGAC | 365 | 252 | 113 | 5.33E-06 | 5.27 | 1.20 |
| AGAACC | 473 | 360 | 113 | 9.21E-05 | 4.04 | 1.20 |
| TGGTGA | 569 | 456 | 113 | 4.26E-04 | 3.37 | 1.20 |
| GCAGTG | 633 | 521 | 112 | 9.57E-04 | 3.02 | 1.19 |
| CAGCTG | 850 | 738 | 112 | 4.98E-03 | 2.30 | 1.19 |
| AGGACC | 466 | 354 | 112 | 9.36E-05 | 4.03 | 1.19 |
| AGCCAG | 790 | 678 | 112 | 3.51E-03 | 2.46 | 1.19 |
| GGGATT | 396 | 285 | 111 | 1.94E-05 | 4.71 | 1.18 |
| GAGAGT | 460 | 349 | 111 | 9.09E-05 | 4.04 | 1.18 |
| GAGGAT | 417 | 306 | 111 | 3.49E-05 | 4.46 | 1.18 |
| GCAAGG | 463 | 352 | 111 | 1.00E-04 | 4.00 | 1.18 |
| AAGGTG | 531 | 420 | 111 | 3.27E-04 | 3.49 | 1.17 |
| GGGTGA | 457 | 346 | 111 | 9.45E-05 | 4.02 | 1.17 |
| ACTGAA | 639 | 529 | 110 | 1.26E-03 | 2.90 | 1.17 |
| GAACTC | 405 | 296 | 109 | 3.54E-05 | 4.45 | 1.16 |
| GTGTAG | 395 | 286 | 109 | 2.82E-05 | 4.55 | 1.16 |
| AGGTGC | 414 | 306 | 108 | 5.74E-05 | 4.24 | 1.14 |
| GAGTTG | 440 | 332 | 108 | 1.03E-04 | 3.99 | 1.14 |
| GGGAAC | 428 | 321 | 107 | 8.54E-05 | 4.07 | 1.14 |
| CCAGAG | 797 | 690 | 107 | 5.39E-03 | 2.27 | 1.14 |
| GTTGGT | 424 | 317 | 107 | 8.25E-05 | 4.08 | 1.14 |
| ATGCTG | 636 | 529 | 107 | 1.70E-03 | 2.77 | 1.14 |
| GCCAGG | 674 | 567 | 107 | 2.42E-03 | 2.62 | 1.13 |
| ATGGGA | 538 | 431 | 107 | 6.15E-04 | 3.21 | 1.13 |
| GACCTC | 405 | 299 | 106 | 6.00E-05 | 4.22 | 1.13 |
| CAAGGA | 579 | 473 | 106 | 1.05E-03 | 2.98 | 1.13 |
| AACTGG | 494 | 388 | 106 | 3.62E-04 | 3.44 | 1.12 |
| AGCAGC | 690 | 584 | 106 | 3.04E-03 | 2.52 | 1.12 |
| ACAGAG | 751 | 645 | 106 | 4.68E-03 | 2.33 | 1.12 |
| TGAACT | 541 | 435 | 106 | 7.33E-04 | 3.13 | 1.12 |
| GTGGAT | 412 | 307 | 105 | 8.32E-05 | 4.08 | 1.12 |

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|---|---|---|---|---|---|---|
| TGTGCC | 590 | 485 | 105 | 1.33E-03 | 2.88 | 1.12 |
| GAGTGA | 470 | 366 | 104 | 3.08E-04 | 3.51 | 1.11 |
| GACAAG | 461 | 357 | 104 | 2.66E-04 | 3.58 | 1.11 |
| GCAGAA | 605 | 501 | 104 | 1.78E-03 | 2.75 | 1.10 |
| GCTGAA | 503 | 399 | 104 | 5.55E-04 | 3.26 | 1.10 |
| TGGAGT | 558 | 454 | 104 | 1.14E-03 | 2.94 | 1.10 |
| GCTTTG | 680 | 577 | 103 | 3.56E-03 | 2.45 | 1.10 |
| GGAACA | 513 | 410 | 103 | 6.74E-04 | 3.17 | 1.09 |
| TGAACC | 377 | 274 | 103 | 5.26E-05 | 4.28 | 1.09 |
| GTGGCC | 510 | 407 | 103 | 6.77E-04 | 3.17 | 1.09 |
| TGCAGG | 619 | 516 | 103 | 2.28E-03 | 2.64 | 1.09 |
| CCAGGG | 730 | 627 | 103 | 5.28E-03 | 2.28 | 1.09 |
| ACCTGT | 555 | 453 | 102 | 1.31E-03 | 2.88 | 1.08 |
| GGATGC | 403 | 301 | 102 | 1.22E-04 | 3.92 | 1.08 |
| GTGTTG | 513 | 412 | 101 | 8.84E-04 | 3.05 | 1.07 |
| ACTTGA | 529 | 428 | 101 | 1.09E-03 | 2.96 | 1.07 |
| ACCTGG | 568 | 467 | 101 | 1.69E-03 | 2.77 | 1.07 |
| TGTAGC | 427 | 326 | 101 | 2.50E-04 | 3.60 | 1.07 |
| AGGGGT | 447 | 347 | 100 | 3.66E-04 | 3.44 | 1.06 |
| GGTCTG | 505 | 405 | 100 | 8.80E-04 | 3.06 | 1.06 |
| GCAGGC | 519 | 419 | 100 | 1.06E-03 | 2.98 | 1.06 |
| GGAAGC | 586 | 486 | 100 | 2.19E-03 | 2.66 | 1.06 |
| CCTGAG | 741 | 641 | 100 | 7.37E-03 | 2.13 | 1.06 |
| GACTCT | 498 | 399 | 99 | 9.22E-04 | 3.04 | 1.05 |
| AGTAGA | 442 | 343 | 99 | 4.11E-04 | 3.39 | 1.05 |
| TGTCTG | 846 | 747 | 99 | 1.31E-02 | 1.88 | 1.05 |
| CGTGTG | 265 | 166 | 99 | 2.03E-06 | 5.69 | 1.05 |
| GTTGTG | 460 | 361 | 99 | 5.81E-04 | 3.24 | 1.05 |
| GGCCAG | 635 | 537 | 98 | 4.12E-03 | 2.39 | 1.04 |
| TGAGCC | 531 | 433 | 98 | 1.64E-03 | 2.79 | 1.04 |
| CTGGCT | 790 | 692 | 98 | 1.13E-02 | 1.95 | 1.03 |
| GGCAGT | 484 | 387 | 97 | 9.60E-04 | 3.02 | 1.03 |
| GAGGCC | 501 | 404 | 97 | 1.25E-03 | 2.90 | 1.03 |
| TGTTTG | 909 | 812 | 97 | 1.93E-02 | 1.71 | 1.03 |
| TGCAGA | 685 | 588 | 97 | 6.59E-03 | 2.18 | 1.03 |
| GGACAA | 413 | 316 | 97 | 3.41E-04 | 3.47 | 1.03 |
| GGGTGC | 373 | 277 | 96 | 1.59E-04 | 3.80 | 1.02 |
| TGTTGA | 539 | 443 | 96 | 2.16E-03 | 2.67 | 1.02 |
| TGAGAC | 473 | 378 | 95 | 1.06E-03 | 2.97 | 1.01 |
| GGGAGT | 424 | 329 | 95 | 5.24E-04 | 3.28 | 1.01 |
| AAGTGG | 519 | 424 | 95 | 1.99E-03 | 2.70 | 1.01 |
| TGATGG | 524 | 429 | 95 | 2.14E-03 | 2.67 | 1.00 |
| CCCTGG | 768 | 673 | 95 | 1.26E-02 | 1.90 | 1.00 |
| AGGGAT | 447 | 352 | 95 | 8.06E-04 | 3.09 | 1.00 |
| TGCTGA | 656 | 562 | 94 | 6.84E-03 | 2.16 | 1.00 |
| CTGCCC | 768 | 674 | 94 | 1.31E-02 | 1.88 | 1.00 |
| CTGTCC | 715 | 621 | 94 | 9.97E-03 | 2.00 | 1.00 |
| GGGGTC | 363 | 269 | 94 | 1.87E-04 | 3.73 | 1.00 |
| TTGCTG | 701 | 607 | 94 | 9.40E-03 | 2.03 | 1.00 |
| CTGTAC | 435 | 341 | 94 | 7.60E-04 | 3.12 | 0.99 |
| GAGCAA | 442 | 348 | 94 | 8.78E-04 | 3.06 | 0.99 |
| CTTGAA | 585 | 492 | 93 | 4.40E-03 | 2.36 | 0.99 |
| GAACCT | 404 | 311 | 93 | 4.83E-04 | 3.32 | 0.99 |
| CTGGAA | 737 | 644 | 93 | 1.23E-02 | 1.91 | 0.99 |

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|---|---|---|---|---|---|---|
| GGCACT | 412 | 319 | 93 | 6.12E-04 | 3.21 | 0.98 |
| ATGTAG | 433 | 341 | 92 | 8.82E-04 | 3.05 | 0.98 |
| GAACAG | 536 | 444 | 92 | 3.35E-03 | 2.47 | 0.97 |
| GTGAGC | 448 | 357 | 91 | 1.27E-03 | 2.90 | 0.97 |
| GGGAAA | 696 | 605 | 91 | 1.14E-02 | 1.94 | 0.97 |
| GTGAAC | 370 | 279 | 91 | 3.47E-04 | 3.46 | 0.97 |
| CTTTGG | 683 | 592 | 91 | 1.08E-02 | 1.97 | 0.96 |
| AGTGGC | 472 | 381 | 91 | 1.85E-03 | 2.73 | 0.96 |
| GATTGG | 314 | 223 | 91 | 9.20E-05 | 4.04 | 0.96 |
| GAGCTC | 440 | 350 | 90 | 1.28E-03 | 2.89 | 0.96 |
| GTCAGG | 477 | 387 | 90 | 2.12E-03 | 2.67 | 0.96 |
| AGAGGT | 507 | 417 | 90 | 2.98E-03 | 2.53 | 0.96 |
| GGACCC | 373 | 283 | 90 | 4.58E-04 | 3.34 | 0.95 |
| GAATGG | 461 | 371 | 90 | 1.88E-03 | 2.73 | 0.95 |
| GCCTGT | 600 | 510 | 90 | 7.11E-03 | 2.15 | 0.95 |
| GACAGC | 484 | 395 | 89 | 2.81E-03 | 2.55 | 0.94 |
| CAGGAA | 804 | 715 | 89 | 2.31E-02 | 1.64 | 0.94 |
| AGAATG | 625 | 537 | 88 | 9.51E-03 | 2.02 | 0.94 |
| AAGGCA | 602 | 514 | 88 | 8.16E-03 | 2.09 | 0.94 |
| GGTAGA | 372 | 284 | 88 | 5.68E-04 | 3.25 | 0.94 |
| ATGGAC | 370 | 282 | 88 | 5.47E-04 | 3.26 | 0.94 |
| AAGCTG | 667 | 579 | 88 | 1.25E-02 | 1.90 | 0.93 |
| TTGGAT | 441 | 353 | 88 | 1.83E-03 | 2.74 | 0.93 |
| TGCCTG | 792 | 705 | 87 | 2.44E-02 | 1.61 | 0.92 |
| GTTCTG | 626 | 539 | 87 | 1.09E-02 | 1.96 | 0.92 |
| TGGGCC | 479 | 392 | 87 | 3.36E-03 | 2.47 | 0.92 |
| GTACTG | 366 | 280 | 86 | 6.65E-04 | 3.18 | 0.92 |
| AGCTGC | 630 | 544 | 86 | 1.16E-02 | 1.93 | 0.92 |
| TGGACG | 160 | 74 | 86 | 1.55E-08 | 7.81 | 0.92 |
| CAGACT | 563 | 477 | 86 | 7.67E-03 | 2.12 | 0.91 |
| GACCCC | 346 | 260 | 86 | 4.80E-04 | 3.32 | 0.91 |
| GCTGCC | 619 | 533 | 86 | 1.14E-02 | 1.94 | 0.91 |
| GCTTGG | 494 | 408 | 86 | 4.26E-03 | 2.37 | 0.91 |
| AGGGCC | 464 | 378 | 86 | 3.12E-03 | 2.51 | 0.91 |
| GGTAGG | 357 | 271 | 86 | 6.25E-04 | 3.20 | 0.91 |
| AGCTGA | 606 | 520 | 86 | 1.08E-02 | 1.97 | 0.91 |
| AAGACT | 537 | 452 | 85 | 6.54E-03 | 2.18 | 0.91 |
| AGGAAC | 498 | 413 | 85 | 4.64E-03 | 2.33 | 0.91 |
| AGCCTG | 751 | 666 | 85 | 2.32E-02 | 1.63 | 0.91 |
| GGACGA | 140 | 55 | 85 | 1.16E-09 | 8.94 | 0.90 |
| AAGAAC | 528 | 444 | 84 | 6.73E-03 | 2.17 | 0.90 |
| CATGGG | 494 | 410 | 84 | 5.27E-03 | 2.28 | 0.89 |
| GTGATG | 473 | 390 | 83 | 4.53E-03 | 2.34 | 0.88 |
| AAAGAG | 679 | 596 | 83 | 2.07E-02 | 1.68 | 0.88 |
| GCCCTG | 692 | 610 | 82 | 2.24E-02 | 1.65 | 0.87 |
| GCCTGA | 485 | 403 | 82 | 5.86E-03 | 2.23 | 0.87 |
| GGTGAC | 403 | 321 | 82 | 2.31E-03 | 2.64 | 0.87 |
| TAGAAC | 365 | 283 | 82 | 1.29E-03 | 2.89 | 0.87 |
| GATGCT | 515 | 433 | 82 | 7.88E-03 | 2.10 | 0.87 |
| GACCAG | 446 | 364 | 82 | 4.08E-03 | 2.39 | 0.87 |
| TGGCAT | 485 | 403 | 82 | 6.15E-03 | 2.21 | 0.87 |
| CTCTGC | 803 | 721 | 82 | 3.65E-02 | 1.44 | 0.87 |
| TGGTGT | 580 | 498 | 82 | 1.30E-02 | 1.89 | 0.86 |
| CGAGGA | 185 | 104 | 81 | 1.72E-06 | 5.76 | 0.86 |

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|---|---|---|---|---|---|---|
| GTGCTT | 547 | 466 | 81 | 1.11E-02 | 1.96 | 0.86 |
| ATGGTG | 486 | 405 | 81 | 6.84E-03 | 2.16 | 0.86 |
| TGAGGC | 485 | 404 | 81 | 6.81E-03 | 2.17 | 0.86 |
| GGGACG | 164 | 83 | 81 | 3.04E-07 | 6.52 | 0.85 |
| AGAACA | 668 | 588 | 80 | 2.34E-02 | 1.63 | 0.85 |
| GTCTGG | 499 | 419 | 80 | 8.04E-03 | 2.09 | 0.85 |
| CCAGGA | 733 | 653 | 80 | 3.10E-02 | 1.51 | 0.85 |
| ACTTGG | 521 | 441 | 80 | 9.74E-03 | 2.01 | 0.85 |
| GGCTCT | 596 | 516 | 80 | 1.67E-02 | 1.78 | 0.85 |
| GATGGT | 394 | 314 | 80 | 2.74E-03 | 2.56 | 0.85 |
| GAGCCC | 470 | 390 | 80 | 6.71E-03 | 2.17 | 0.84 |
| TTGAGG | 467 | 388 | 79 | 6.58E-03 | 2.18 | 0.84 |
| AAAGGA | 775 | 696 | 79 | 3.86E-02 | 1.41 | 0.84 |
| GGCTTG | 474 | 395 | 79 | 7.24E-03 | 2.14 | 0.84 |
| CACTGG | 616 | 537 | 79 | 1.99E-02 | 1.70 | 0.84 |
| TAGAGA | 506 | 427 | 79 | 9.81E-03 | 2.01 | 0.84 |
| GAACCC | 335 | 256 | 79 | 1.21E-03 | 2.92 | 0.83 |
| AGTTGG | 429 | 350 | 79 | 4.86E-03 | 2.31 | 0.83 |
| AGGAAA | 931 | 853 | 78 | 6.31E-02 | 1.20 | 0.83 |
| TTCTGG | 725 | 647 | 78 | 3.42E-02 | 1.47 | 0.83 |
| CTGGAT | 488 | 410 | 78 | 8.89E-03 | 2.05 | 0.83 |
| GTGCTA | 339 | 261 | 78 | 1.43E-03 | 2.84 | 0.83 |
| GCAGCC | 558 | 480 | 78 | 1.56E-02 | 1.81 | 0.83 |
| GGAGAT | 427 | 349 | 78 | 5.22E-03 | 2.28 | 0.82 |
| AGAGCC | 583 | 505 | 78 | 1.84E-02 | 1.74 | 0.82 |
| GAAGGT | 446 | 368 | 78 | 6.46E-03 | 2.19 | 0.82 |
| CTGACC | 483 | 406 | 77 | 9.36E-03 | 2.03 | 0.82 |
| CTTGGA | 557 | 480 | 77 | 1.64E-02 | 1.79 | 0.82 |
| GGCGGG | 232 | 155 | 77 | 9.27E-05 | 4.03 | 0.82 |
| CCCTCC | 758 | 681 | 77 | 4.26E-02 | 1.37 | 0.82 |
| TTGAAG | 578 | 501 | 77 | 1.94E-02 | 1.71 | 0.81 |
| CACCTG | 603 | 526 | 77 | 2.27E-02 | 1.64 | 0.81 |
| CAGAAC | 529 | 453 | 76 | 1.48E-02 | 1.83 | 0.81 |
| GGGCAA | 352 | 276 | 76 | 2.32E-03 | 2.63 | 0.81 |
| GAAGCC | 532 | 456 | 76 | 1.54E-02 | 1.81 | 0.81 |
| GGTTTG | 504 | 428 | 76 | 1.28E-02 | 1.89 | 0.81 |
| GAACCA | 402 | 326 | 76 | 4.91E-03 | 2.31 | 0.80 |
| TGGATT | 477 | 401 | 76 | 1.06E-02 | 1.97 | 0.80 |
| GAACAA | 450 | 374 | 76 | 8.43E-03 | 2.07 | 0.80 |
| GGCATG | 397 | 321 | 76 | 4.82E-03 | 2.32 | 0.80 |
| GGAAGT | 511 | 435 | 76 | 1.41E-02 | 1.85 | 0.80 |
| TGCACT | 466 | 391 | 75 | 1.04E-02 | 1.98 | 0.80 |
| CGTGGA | 190 | 115 | 75 | 1.79E-05 | 4.75 | 0.79 |
| GCATGG | 421 | 346 | 75 | 6.90E-03 | 2.16 | 0.79 |
| TAGAGG | 399 | 324 | 75 | 5.42E-03 | 2.27 | 0.79 |
| AGTGAG | 563 | 488 | 75 | 2.13E-02 | 1.67 | 0.79 |
| GCCTTG | 542 | 467 | 75 | 1.88E-02 | 1.73 | 0.79 |
| GTAGGC | 257 | 183 | 74 | 3.82E-04 | 3.42 | 0.79 |
| CCTTGG | 621 | 547 | 74 | 2.94E-02 | 1.53 | 0.79 |
| GTAGAT | 313 | 239 | 74 | 1.53E-03 | 2.82 | 0.79 |
| GCTGTC | 525 | 451 | 74 | 1.73E-02 | 1.76 | 0.79 |
| TAGGAG | 393 | 319 | 74 | 5.48E-03 | 2.26 | 0.79 |
| GAGAAA | 808 | 734 | 74 | 5.94E-02 | 1.23 | 0.78 |
| GAATTG | 371 | 297 | 74 | 4.19E-03 | 2.38 | 0.78 |

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|---|---|---|---|---|---|---|
| GGTGCC | 367 | 293 | 74 | 4.03E-03 | 2.39 | 0.78 |
| AGTGAC | 468 | 394 | 74 | 1.20E-02 | 1.92 | 0.78 |
| GGGCCT | 481 | 407 | 74 | 1.34E-02 | 1.87 | 0.78 |
| GCCCCT | 503 | 429 | 74 | 1.58E-02 | 1.80 | 0.78 |
| TTGGGC | 370 | 297 | 73 | 4.42E-03 | 2.35 | 0.78 |
| AGATTG | 373 | 300 | 73 | 4.65E-03 | 2.33 | 0.78 |
| TAGGAC | 298 | 225 | 73 | 1.33E-03 | 2.87 | 0.78 |
| AGTGCC | 422 | 349 | 73 | 8.38E-03 | 2.08 | 0.78 |
| GACCAA | 341 | 268 | 73 | 3.02E-03 | 2.52 | 0.78 |
| GGTGCA | 334 | 261 | 73 | 2.80E-03 | 2.55 | 0.77 |
| GCACAG | 597 | 525 | 72 | 3.18E-02 | 1.50 | 0.76 |
| GGGTAG | 344 | 272 | 72 | 3.85E-03 | 2.41 | 0.76 |
| GACACT | 441 | 369 | 72 | 1.18E-02 | 1.93 | 0.76 |
| GCGGGG | 208 | 136 | 72 | 1.16E-04 | 3.93 | 0.76 |
| GAATGA | 461 | 390 | 71 | 1.47E-02 | 1.83 | 0.75 |
| GGCCCA | 431 | 360 | 71 | 1.16E-02 | 1.93 | 0.75 |
| CGGGGC | 198 | 127 | 71 | 8.51E-05 | 4.07 | 0.75 |
| CGTGGG | 207 | 136 | 71 | 1.31E-04 | 3.88 | 0.75 |
| GTAGTG | 305 | 234 | 71 | 2.35E-03 | 2.63 | 0.75 |
| GAGCCT | 543 | 473 | 70 | 2.81E-02 | 1.55 | 0.74 |
| GGACAT | 391 | 321 | 70 | 8.74E-03 | 2.06 | 0.74 |
| CGGCTG | 191 | 122 | 69 | 8.79E-05 | 4.06 | 0.74 |
| GAACAC | 406 | 337 | 69 | 1.11E-02 | 1.96 | 0.73 |
| GGGGTT | 396 | 327 | 69 | 1.02E-02 | 1.99 | 0.73 |
| GGACAC | 415 | 346 | 69 | 1.23E-02 | 1.91 | 0.73 |
| CGCAGA | 151 | 82 | 69 | 6.04E-06 | 5.22 | 0.73 |
| TGAAGC | 498 | 429 | 69 | 2.36E-02 | 1.63 | 0.73 |
| CTGCAC | 484 | 415 | 69 | 2.16E-02 | 1.67 | 0.73 |
| CAAGAG | 516 | 447 | 69 | 2.64E-02 | 1.58 | 0.73 |
| TGGTTG | 451 | 382 | 69 | 1.71E-02 | 1.77 | 0.73 |
| GGCATT | 385 | 316 | 69 | 9.40E-03 | 2.03 | 0.73 |
| GCTGCG | 177 | 109 | 68 | 5.47E-05 | 4.26 | 0.72 |
| GGCTCC | 501 | 433 | 68 | 2.57E-02 | 1.59 | 0.72 |
| GGGCCC | 372 | 304 | 68 | 8.82E-03 | 2.05 | 0.72 |
| TGAGCT | 568 | 500 | 68 | 3.83E-02 | 1.42 | 0.72 |
| GTGACA | 502 | 434 | 68 | 2.71E-02 | 1.57 | 0.72 |
| GACGTG | 156 | 89 | 67 | 1.77E-05 | 4.75 | 0.71 |
| TGAACG | 141 | 74 | 67 | 4.79E-06 | 5.32 | 0.71 |
| ACCTCT | 501 | 434 | 67 | 2.84E-02 | 1.55 | 0.71 |
| TGATTG | 389 | 322 | 67 | 1.21E-02 | 1.92 | 0.71 |
| GTGCAG | 497 | 430 | 67 | 2.81E-02 | 1.55 | 0.71 |
| GTGAAT | 415 | 348 | 67 | 1.56E-02 | 1.81 | 0.71 |
| TCACTG | 654 | 587 | 67 | 5.84E-02 | 1.23 | 0.71 |
| ACAGGG | 518 | 451 | 67 | 3.24E-02 | 1.49 | 0.71 |
| AGGACG | 157 | 91 | 66 | 2.38E-05 | 4.62 | 0.70 |
| ATTGGG | 319 | 253 | 66 | 5.64E-03 | 2.25 | 0.70 |
| TTGGAA | 635 | 569 | 66 | 5.68E-02 | 1.25 | 0.70 |
| GAGTGC | 325 | 259 | 66 | 6.27E-03 | 2.20 | 0.70 |
| GACGGG | 141 | 75 | 66 | 7.21E-06 | 5.14 | 0.70 |
| GCCAAG | 480 | 414 | 66 | 2.76E-02 | 1.56 | 0.70 |
| GTTGAG | 357 | 291 | 66 | 9.66E-03 | 2.01 | 0.70 |
| AACTGA | 515 | 449 | 66 | 3.41E-02 | 1.47 | 0.70 |
| GGTGAA | 375 | 310 | 65 | 1.24E-02 | 1.90 | 0.69 |
| CAGGCG | 168 | 103 | 65 | 7.34E-05 | 4.13 | 0.69 |

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|---|---|---|---|---|---|---|
| GGGCAC | 360 | 295 | 65 | 1.08E-02 | 1.97 | 0.69 |
| TCTCTG | 927 | 862 | 65 | 1.23E-01 | 0.91 | 0.69 |
| ATGAGA | 501 | 437 | 64 | 3.57E-02 | 1.45 | 0.68 |
| CTGCCT | 927 | 863 | 64 | 1.29E-01 | 0.89 | 0.68 |
| CGGGAG | 191 | 127 | 64 | 3.19E-04 | 3.50 | 0.68 |
| GGCGTG | 165 | 101 | 64 | 8.47E-05 | 4.07 | 0.68 |
| CTCGGA | 156 | 92 | 64 | 5.01E-05 | 4.30 | 0.68 |
| AAGAGC | 481 | 417 | 64 | 3.34E-02 | 1.48 | 0.68 |
| CCCCTC | 597 | 533 | 64 | 5.80E-02 | 1.24 | 0.68 |
| GTGAGT | 420 | 356 | 64 | 2.25E-02 | 1.65 | 0.67 |
| CGGGCT | 168 | 104 | 64 | 1.18E-04 | 3.93 | 0.67 |
| GGACGG | 146 | 82 | 64 | 2.62E-05 | 4.58 | 0.67 |
| CGGGCA | 157 | 94 | 63 | 6.53E-05 | 4.19 | 0.67 |
| GTGTCT | 621 | 558 | 63 | 6.76E-02 | 1.17 | 0.67 |
| AGACAG | 701 | 638 | 63 | 8.64E-02 | 1.06 | 0.67 |
| TGGGTT | 557 | 495 | 62 | 5.41E-02 | 1.27 | 0.66 |
| AGGAGT | 453 | 391 | 62 | 3.19E-02 | 1.50 | 0.66 |
| GGTCAG | 463 | 401 | 62 | 3.45E-02 | 1.46 | 0.66 |
| AGACCC | 403 | 341 | 62 | 2.32E-02 | 1.64 | 0.66 |
| CAGGTG | 577 | 515 | 62 | 6.13E-02 | 1.21 | 0.66 |
| GGGCAT | 344 | 282 | 62 | 1.36E-02 | 1.87 | 0.65 |
| ATGGGC | 340 | 278 | 62 | 1.32E-02 | 1.88 | 0.65 |
| AGGCGG | 165 | 103 | 62 | 1.72E-04 | 3.76 | 0.65 |
| TTGGGT | 479 | 417 | 62 | 3.99E-02 | 1.40 | 0.65 |
| AGACCA | 447 | 386 | 61 | 3.32E-02 | 1.48 | 0.65 |
| GATGGC | 369 | 308 | 61 | 1.82E-02 | 1.74 | 0.65 |
| TGCAGC | 520 | 459 | 61 | 4.97E-02 | 1.30 | 0.65 |
| GCCCAG | 652 | 591 | 61 | 8.18E-02 | 1.09 | 0.65 |
| CGAGAG | 149 | 88 | 61 | 6.84E-05 | 4.17 | 0.65 |
| TAGGGG | 287 | 226 | 61 | 6.96E-03 | 2.16 | 0.65 |
| AACCTG | 475 | 414 | 61 | 4.06E-02 | 1.39 | 0.65 |
| CCCAGG | 796 | 735 | 61 | 1.19E-01 | 0.93 | 0.65 |
| GAGCGG | 151 | 90 | 61 | 8.87E-05 | 4.05 | 0.65 |
| AGATGA | 549 | 488 | 61 | 5.89E-02 | 1.23 | 0.64 |
| CCTGCC | 783 | 722 | 61 | 1.17E-01 | 0.93 | 0.64 |
| ATTGTG | 466 | 405 | 61 | 3.96E-02 | 1.40 | 0.64 |
| TAAGGG | 313 | 252 | 61 | 1.09E-02 | 1.96 | 0.64 |
| ATTGGA | 348 | 288 | 60 | 1.64E-02 | 1.78 | 0.64 |
| CGGAGG | 176 | 116 | 60 | 4.06E-04 | 3.39 | 0.64 |
| ACGTGG | 182 | 122 | 60 | 5.47E-04 | 3.26 | 0.64 |
| GTGTGC | 532 | 472 | 60 | 5.73E-02 | 1.24 | 0.64 |
| GGGAAT | 385 | 325 | 60 | 2.41E-02 | 1.62 | 0.64 |
| TTGAAC | 367 | 307 | 60 | 2.10E-02 | 1.68 | 0.64 |
| ACTGAC | 399 | 339 | 60 | 2.76E-02 | 1.56 | 0.63 |
| TGGCCT | 649 | 589 | 60 | 8.93E-02 | 1.05 | 0.63 |
| GAGCAC | 380 | 321 | 59 | 2.48E-02 | 1.61 | 0.63 |
| CCCCTG | 566 | 507 | 59 | 6.98E-02 | 1.16 | 0.63 |
| ACCGTG | 171 | 112 | 59 | 4.21E-04 | 3.38 | 0.63 |
| AGACGG | 146 | 87 | 59 | 1.08E-04 | 3.97 | 0.63 |
| GGGTCT | 428 | 369 | 59 | 3.64E-02 | 1.44 | 0.63 |
| GACCGT | 119 | 60 | 59 | 1.15E-05 | 4.94 | 0.62 |
| CTGGGT | 636 | 577 | 59 | 9.24E-02 | 1.03 | 0.62 |
| GTGACC | 388 | 330 | 58 | 2.90E-02 | 1.54 | 0.62 |
| GGTTGT | 360 | 302 | 58 | 2.31E-02 | 1.64 | 0.62 |

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|---|---|---|---|---|---|---|
| AGACAC | 488 | 430 | 58 | 5.39E-02 | 1.27 | 0.62 |
| GGGGTA | 257 | 199 | 58 | 6.34E-03 | 2.20 | 0.62 |
| CCGAGG | 195 | 137 | 58 | 1.39E-03 | 2.86 | 0.62 |
| CCCCAG | 735 | 677 | 58 | 1.21E-01 | 0.92 | 0.62 |
| CGGAGA | 147 | 89 | 58 | 1.52E-04 | 3.82 | 0.62 |
| GATGAA | 441 | 383 | 58 | 4.27E-02 | 1.37 | 0.62 |
| AGCGGG | 154 | 96 | 58 | 2.37E-04 | 3.62 | 0.62 |
| GCAGAT | 404 | 346 | 58 | 3.39E-02 | 1.47 | 0.62 |
| GGAGCG | 150 | 92 | 58 | 1.94E-04 | 3.71 | 0.61 |
| AGAACG | 147 | 89 | 58 | 1.73E-04 | 3.76 | 0.61 |
| GGCCCC | 377 | 320 | 57 | 2.95E-02 | 1.53 | 0.61 |
| TGTGCT | 734 | 677 | 57 | 1.27E-01 | 0.90 | 0.61 |
| TGTACA | 540 | 483 | 57 | 7.45E-02 | 1.13 | 0.60 |
| GGCCAC | 426 | 369 | 57 | 4.31E-02 | 1.37 | 0.60 |
| CCGTGG | 207 | 150 | 57 | 2.56E-03 | 2.59 | 0.60 |
| GCAATA | 274 | 217 | 57 | 1.02E-02 | 1.99 | 0.60 |
| GGCTTT | 603 | 547 | 56 | 9.59E-02 | 1.02 | 0.60 |
| GAACGG | 125 | 69 | 56 | 5.04E-05 | 4.30 | 0.60 |
| GGCGGC | 154 | 98 | 56 | 3.85E-04 | 3.41 | 0.60 |
| AGGTTG | 382 | 326 | 56 | 3.50E-02 | 1.46 | 0.59 |
| CTGCCG | 186 | 130 | 56 | 1.60E-03 | 2.79 | 0.59 |
| AGGTAG | 369 | 313 | 56 | 3.18E-02 | 1.50 | 0.59 |
| GATTTG | 425 | 369 | 56 | 4.69E-02 | 1.33 | 0.59 |
| GGCGAG | 139 | 83 | 56 | 1.86E-04 | 3.73 | 0.59 |
| GGACGT | 121 | 65 | 56 | 4.55E-05 | 4.34 | 0.59 |
| TGGCCA | 583 | 527 | 56 | 9.52E-02 | 1.02 | 0.59 |
| CGGAGC | 155 | 99 | 56 | 4.94E-04 | 3.31 | 0.59 |
| GGAACC | 338 | 282 | 56 | 2.58E-02 | 1.59 | 0.59 |
| TCGGGG | 154 | 99 | 55 | 4.79E-04 | 3.32 | 0.59 |
| GAGTAG | 302 | 247 | 55 | 1.80E-02 | 1.74 | 0.59 |
| ACCAAG | 444 | 389 | 55 | 5.50E-02 | 1.26 | 0.59 |
| GGCCGG | 153 | 98 | 55 | 4.72E-04 | 3.33 | 0.59 |
| GACATG | 402 | 347 | 55 | 4.34E-02 | 1.36 | 0.59 |
| TAGGGC | 257 | 202 | 55 | 9.93E-03 | 2.00 | 0.59 |
| TGGCCC | 461 | 406 | 55 | 6.10E-02 | 1.21 | 0.58 |
| CCGGGC | 160 | 105 | 55 | 7.14E-04 | 3.15 | 0.58 |
| GAAGCT | 518 | 463 | 55 | 7.90E-02 | 1.10 | 0.58 |
| TCGGAG | 136 | 81 | 55 | 1.97E-04 | 3.70 | 0.58 |
| AGACGT | 142 | 87 | 55 | 3.00E-04 | 3.52 | 0.58 |
| GTTGAA | 378 | 324 | 54 | 3.99E-02 | 1.40 | 0.58 |
| CGGCAG | 160 | 106 | 54 | 8.59E-04 | 3.07 | 0.58 |
| CACTGA | 580 | 526 | 54 | 1.03E-01 | 0.99 | 0.58 |
| ACTGGC | 395 | 341 | 54 | 4.61E-02 | 1.34 | 0.57 |
| CGGGGT | 147 | 93 | 54 | 5.11E-04 | 3.29 | 0.57 |
| TGACCT | 498 | 444 | 54 | 7.94E-02 | 1.10 | 0.57 |
| CCGGGG | 169 | 115 | 54 | 1.47E-03 | 2.83 | 0.57 |
| AATGTG | 608 | 554 | 54 | 1.16E-01 | 0.94 | 0.57 |
| GTAGCA | 319 | 265 | 54 | 2.68E-02 | 1.57 | 0.57 |
| TGGGCG | 154 | 101 | 53 | 8.03E-04 | 3.10 | 0.57 |
| ACTGCA | 487 | 434 | 53 | 7.80E-02 | 1.11 | 0.57 |
| AACTTG | 473 | 420 | 53 | 7.43E-02 | 1.13 | 0.57 |
| CCACTG | 609 | 556 | 53 | 1.19E-01 | 0.92 | 0.56 |
| GAACGA | 111 | 58 | 53 | 4.33E-05 | 4.36 | 0.56 |
| CCGTGT | 194 | 141 | 53 | 3.71E-03 | 2.43 | 0.56 |

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|---|---|---|---|---|---|---|
| GGATTT | 459 | 406 | 53 | 7.11E-02 | 1.15 | 0.56 |
| AGCGAG | 152 | 99 | 53 | 8.12E-04 | 3.09 | 0.56 |
| AGGTGA | 483 | 430 | 53 | 8.06E-02 | 1.09 | 0.56 |
| GATTGA | 260 | 207 | 53 | 1.47E-02 | 1.83 | 0.56 |
| GTGACG | 123 | 70 | 53 | 1.56E-04 | 3.81 | 0.56 |
| CCTGAA | 548 | 496 | 52 | 1.04E-01 | 0.98 | 0.56 |
| CTCGGG | 189 | 137 | 52 | 3.81E-03 | 2.42 | 0.55 |
| TGAGCG | 138 | 86 | 52 | 5.10E-04 | 3.29 | 0.55 |
| TGGCCG | 148 | 96 | 52 | 8.87E-04 | 3.05 | 0.55 |
| AGCAAG | 545 | 493 | 52 | 1.07E-01 | 0.97 | 0.55 |
| GAGACG | 139 | 87 | 52 | 5.60E-04 | 3.25 | 0.55 |
| GGGTTT | 514 | 462 | 52 | 9.71E-02 | 1.01 | 0.55 |
| GCGTGG | 163 | 111 | 52 | 1.77E-03 | 2.75 | 0.55 |
| GGGCCG | 143 | 91 | 52 | 7.18E-04 | 3.14 | 0.55 |
| CTGAAT | 482 | 430 | 52 | 8.72E-02 | 1.06 | 0.55 |
| GCAAGA | 383 | 332 | 51 | 5.41E-02 | 1.27 | 0.55 |
| ACTGGT | 382 | 331 | 51 | 5.38E-02 | 1.27 | 0.55 |
| TGTGCG | 159 | 108 | 51 | 1.65E-03 | 2.78 | 0.54 |
| GGGCTA | 259 | 208 | 51 | 1.76E-02 | 1.75 | 0.54 |
| CGGATG | 125 | 74 | 51 | 2.80E-04 | 3.55 | 0.54 |
| CCCGGG | 194 | 143 | 51 | 5.36E-03 | 2.27 | 0.54 |
| TTGAGC | 346 | 295 | 51 | 4.35E-02 | 1.36 | 0.54 |
| TGGCGG | 143 | 92 | 51 | 8.75E-04 | 3.06 | 0.54 |
| ATGCAG | 487 | 436 | 51 | 9.39E-02 | 1.03 | 0.54 |
| TGTCGG | 117 | 66 | 51 | 1.78E-04 | 3.75 | 0.54 |
| GGCCAT | 367 | 316 | 51 | 5.23E-02 | 1.28 | 0.54 |
| GGAACG | 125 | 74 | 51 | 3.38E-04 | 3.47 | 0.54 |
| TGCACC | 316 | 266 | 50 | 3.66E-02 | 1.44 | 0.53 |
| CTGTAA | 525 | 475 | 50 | 1.11E-01 | 0.95 | 0.53 |
| GCGGAG | 142 | 92 | 50 | 1.00E-03 | 3.00 | 0.53 |
| AGGGCG | 147 | 97 | 50 | 1.28E-03 | 2.89 | 0.53 |
| GCAGGT | 427 | 377 | 50 | 7.62E-02 | 1.12 | 0.53 |
| ACCTGA | 441 | 391 | 50 | 8.24E-02 | 1.08 | 0.53 |
| TCTGCC | 658 | 608 | 50 | 1.59E-01 | 0.80 | 0.53 |
| CGGAAG | 154 | 104 | 50 | 1.86E-03 | 2.73 | 0.53 |
| CAGAGT | 581 | 531 | 50 | 1.34E-01 | 0.87 | 0.53 |
| ACGGAG | 142 | 92 | 50 | 1.19E-03 | 2.93 | 0.53 |
| CCCCGG | 167 | 118 | 49 | 3.34E-03 | 2.48 | 0.52 |
| TGAACA | 526 | 477 | 49 | 1.18E-01 | 0.93 | 0.52 |
| CGGTGG | 157 | 108 | 49 | 2.35E-03 | 2.63 | 0.52 |
| GTGGCG | 133 | 84 | 49 | 8.63E-04 | 3.06 | 0.52 |
| GTCCTG | 575 | 526 | 49 | 1.39E-01 | 0.86 | 0.52 |
| GTGCCC | 380 | 331 | 49 | 6.58E-02 | 1.18 | 0.52 |
| AGACCT | 458 | 409 | 49 | 9.59E-02 | 1.02 | 0.52 |
| GGGATA | 260 | 211 | 49 | 2.43E-02 | 1.61 | 0.52 |
| AACGGA | 119 | 70 | 49 | 4.20E-04 | 3.38 | 0.51 |
| AAGGCC | 420 | 372 | 48 | 8.48E-02 | 1.07 | 0.51 |
| CCTCCC | 770 | 722 | 48 | 2.09E-01 | 0.68 | 0.51 |
| CGGACA | 114 | 66 | 48 | 3.16E-04 | 3.50 | 0.51 |
| CCGGAG | 152 | 104 | 48 | 2.53E-03 | 2.60 | 0.51 |
| CTGCGG | 171 | 123 | 48 | 4.88E-03 | 2.31 | 0.51 |
| CGGGGA | 168 | 120 | 48 | 4.47E-03 | 2.35 | 0.51 |
| ACGCAG | 133 | 85 | 48 | 1.09E-03 | 2.96 | 0.51 |
| GATGCA | 349 | 301 | 48 | 5.86E-02 | 1.23 | 0.51 |

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|---|---|---|---|---|---|---|
| GCTGAC | 369 | 321 | 48 | 6.68E-02 | 1.18 | 0.51 |
| GGTGTT | 420 | 372 | 48 | 8.76E-02 | 1.06 | 0.51 |
| GCAGCG | 161 | 113 | 48 | 3.83E-03 | 2.42 | 0.51 |
| GCCGGA | 113 | 66 | 47 | 3.87E-04 | 3.41 | 0.50 |
| ACGGTG | 143 | 96 | 47 | 2.23E-03 | 2.65 | 0.50 |
| ACAAGG | 425 | 378 | 47 | 9.69E-02 | 1.01 | 0.50 |
| GCATGC | 332 | 285 | 47 | 5.95E-02 | 1.23 | 0.50 |
| CGCTGG | 164 | 117 | 47 | 5.29E-03 | 2.28 | 0.50 |
| TTAGGA | 418 | 371 | 47 | 9.68E-02 | 1.01 | 0.49 |
| GACGTT | 117 | 70 | 47 | 6.67E-04 | 3.18 | 0.49 |
| GCCGAG | 146 | 99 | 47 | 2.98E-03 | 2.53 | 0.49 |
| GTAGCT | 343 | 297 | 46 | 6.60E-02 | 1.18 | 0.49 |
| CCCTCT | 633 | 587 | 46 | 1.84E-01 | 0.74 | 0.49 |
| CGTAGA | 99 | 53 | 46 | 1.63E-04 | 3.79 | 0.49 |
| TCCCTC | 618 | 572 | 46 | 1.78E-01 | 0.75 | 0.49 |
| AGAGCG | 144 | 98 | 46 | 2.84E-03 | 2.55 | 0.49 |
| GACGAG | 108 | 62 | 46 | 3.71E-04 | 3.43 | 0.49 |
| AGCCGG | 150 | 104 | 46 | 3.61E-03 | 2.44 | 0.49 |
| GAGGCG | 147 | 101 | 46 | 3.31E-03 | 2.48 | 0.49 |
| GAAATG | 670 | 624 | 46 | 1.99E-01 | 0.70 | 0.49 |
| GAACCG | 106 | 60 | 46 | 3.51E-04 | 3.45 | 0.49 |
| CTGATG | 507 | 461 | 46 | 1.39E-01 | 0.86 | 0.49 |
| CGGGTG | 145 | 99 | 46 | 3.30E-03 | 2.48 | 0.49 |
| GACGAC | 90 | 44 | 46 | 7.40E-05 | 4.13 | 0.49 |
| CAGCGG | 160 | 114 | 46 | 5.61E-03 | 2.25 | 0.49 |
| GAACGT | 118 | 72 | 46 | 8.88E-04 | 3.05 | 0.49 |
| GACCAC | 302 | 256 | 46 | 5.24E-02 | 1.28 | 0.49 |
| CGGGGG | 148 | 102 | 46 | 3.82E-03 | 2.42 | 0.49 |
| TCTGTA | 608 | 562 | 46 | 1.81E-01 | 0.74 | 0.48 |
| GGCCAA | 331 | 285 | 46 | 6.54E-02 | 1.18 | 0.48 |
| TGCGTG | 162 | 116 | 46 | 6.12E-03 | 2.21 | 0.48 |
| GACCCT | 391 | 345 | 46 | 9.20E-02 | 1.04 | 0.48 |
| GACAGT | 453 | 407 | 46 | 1.20E-01 | 0.92 | 0.48 |
| GACGGC | 99 | 54 | 45 | 2.51E-04 | 3.60 | 0.48 |
| AGAAGT | 556 | 511 | 45 | 1.66E-01 | 0.78 | 0.48 |
| GCGAGG | 127 | 82 | 45 | 1.87E-03 | 2.73 | 0.48 |
| GGGCGG | 194 | 149 | 45 | 1.53E-02 | 1.81 | 0.48 |
| TGCCCC | 461 | 416 | 45 | 1.30E-01 | 0.89 | 0.48 |
| GACTCG | 118 | 73 | 45 | 1.19E-03 | 2.92 | 0.48 |
| TGACCG | 112 | 67 | 45 | 8.24E-04 | 3.08 | 0.47 |
| GCGTGT | 149 | 104 | 45 | 5.01E-03 | 2.30 | 0.47 |
| CGGGTT | 115 | 70 | 45 | 1.04E-03 | 2.98 | 0.47 |
| AATGGG | 392 | 347 | 45 | 1.01E-01 | 0.99 | 0.47 |
| AGAGAT | 512 | 467 | 45 | 1.55E-01 | 0.81 | 0.47 |
| GAGCGA | 114 | 69 | 45 | 1.01E-03 | 3.00 | 0.47 |
| GCCGTG | 160 | 116 | 44 | 7.36E-03 | 2.13 | 0.47 |
| GAATGC | 321 | 277 | 44 | 6.92E-02 | 1.16 | 0.47 |
| CGAGGG | 144 | 100 | 44 | 4.45E-03 | 2.35 | 0.47 |
| GATCGG | 80 | 36 | 44 | 3.70E-05 | 4.43 | 0.47 |
| TTGCAC | 324 | 280 | 44 | 7.12E-02 | 1.15 | 0.47 |
| CGGGAA | 148 | 104 | 44 | 5.61E-03 | 2.25 | 0.47 |
| AGGCCA | 552 | 508 | 44 | 1.77E-01 | 0.75 | 0.47 |
| GATTGC | 224 | 180 | 44 | 2.92E-02 | 1.53 | 0.46 |
| CTTTGA | 625 | 581 | 44 | 2.09E-01 | 0.68 | 0.46 |

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|---|---|---|---|---|---|---|
| AGGCCC | 412 | 368 | 44 | 1.19E-01 | 0.92 | 0.46 |
| GGAGTC | 352 | 309 | 43 | 9.06E-02 | 1.04 | 0.46 |
| GGCCGA | 107 | 64 | 43 | 8.69E-04 | 3.06 | 0.46 |
| GATGAC | 300 | 257 | 43 | 6.55E-02 | 1.18 | 0.46 |
| GAAGCG | 125 | 82 | 43 | 2.51E-03 | 2.60 | 0.46 |
| CGTGCT | 162 | 119 | 43 | 9.52E-03 | 2.02 | 0.46 |
| ACGGGA | 128 | 85 | 43 | 3.03E-03 | 2.52 | 0.46 |
| CGTGAG | 144 | 101 | 43 | 5.98E-03 | 2.22 | 0.46 |
| GCACCT | 350 | 307 | 43 | 9.34E-02 | 1.03 | 0.46 |
| TCTGAC | 446 | 403 | 43 | 1.40E-01 | 0.85 | 0.46 |
| GTACAG | 364 | 321 | 43 | 1.01E-01 | 1.00 | 0.46 |
| GATCTG | 369 | 326 | 43 | 1.05E-01 | 0.98 | 0.45 |
| GATGTA | 313 | 270 | 43 | 7.71E-02 | 1.11 | 0.45 |
| GGGCGT | 119 | 76 | 43 | 2.28E-03 | 2.64 | 0.45 |
| GCGCTG | 156 | 113 | 43 | 9.55E-03 | 2.02 | 0.45 |
| GCCGGG | 152 | 110 | 42 | 8.78E-03 | 2.06 | 0.45 |
| GCACGG | 130 | 88 | 42 | 4.15E-03 | 2.38 | 0.45 |
| CAGGAT | 457 | 415 | 42 | 1.52E-01 | 0.82 | 0.45 |
| ATACTG | 376 | 334 | 42 | 1.13E-01 | 0.95 | 0.45 |
| AAGCAG | 669 | 627 | 42 | 2.41E-01 | 0.62 | 0.45 |
| AAGACG | 129 | 87 | 42 | 4.14E-03 | 2.38 | 0.45 |
| TTTGTG | 796 | 754 | 42 | 2.85E-01 | 0.55 | 0.45 |
| CGGTGC | 127 | 85 | 42 | 3.82E-03 | 2.42 | 0.45 |
| GGACCG | 107 | 65 | 42 | 1.32E-03 | 2.88 | 0.45 |
| AGTCGG | 108 | 66 | 42 | 1.42E-03 | 2.85 | 0.45 |
| ATGAAC | 352 | 310 | 42 | 1.02E-01 | 0.99 | 0.45 |
| GTCGAG | 86 | 44 | 42 | 2.30E-04 | 3.64 | 0.45 |
| GTTGGC | 296 | 254 | 42 | 7.34E-02 | 1.13 | 0.45 |
| ACCTGC | 445 | 403 | 42 | 1.51E-01 | 0.82 | 0.44 |
| GAGCAT | 363 | 321 | 42 | 1.10E-01 | 0.96 | 0.44 |
| GCGAGA | 100 | 58 | 42 | 9.41E-04 | 3.03 | 0.44 |
| TGACGG | 106 | 64 | 42 | 1.44E-03 | 2.84 | 0.44 |
| TGTAGT | 406 | 364 | 42 | 1.34E-01 | 0.87 | 0.44 |
| CAGATG | 584 | 542 | 42 | 2.15E-01 | 0.67 | 0.44 |
| GCAAGC | 327 | 285 | 42 | 9.30E-02 | 1.03 | 0.44 |
| CCTCGG | 181 | 139 | 42 | 2.04E-02 | 1.69 | 0.44 |
| ACGGGG | 133 | 92 | 41 | 5.71E-03 | 2.24 | 0.44 |
| GGCATC | 315 | 274 | 41 | 8.79E-02 | 1.06 | 0.44 |
| TGGTAG | 351 | 310 | 41 | 1.08E-01 | 0.97 | 0.44 |
| AACGTG | 143 | 102 | 41 | 8.69E-03 | 2.06 | 0.44 |
| TGACAG | 562 | 521 | 41 | 2.12E-01 | 0.67 | 0.44 |
| TCCTGG | 760 | 719 | 41 | 2.86E-01 | 0.54 | 0.43 |
| AAGCGG | 110 | 69 | 41 | 2.27E-03 | 2.64 | 0.43 |
| AGACCG | 106 | 65 | 41 | 1.80E-03 | 2.74 | 0.43 |
| ACGGAC | 96 | 55 | 41 | 9.02E-04 | 3.04 | 0.43 |
| GACGGA | 104 | 63 | 41 | 1.61E-03 | 2.79 | 0.43 |
| TGTGCA | 604 | 563 | 41 | 2.33E-01 | 0.63 | 0.43 |
| ATGAAG | 552 | 511 | 41 | 2.13E-01 | 0.67 | 0.43 |
| CTGACG | 123 | 83 | 40 | 4.79E-03 | 2.32 | 0.43 |
| AAACTG | 619 | 579 | 40 | 2.43E-01 | 0.61 | 0.43 |
| TAGGGA | 363 | 323 | 40 | 1.24E-01 | 0.91 | 0.43 |
| GGCCGT | 117 | 77 | 40 | 3.78E-03 | 2.42 | 0.43 |
| GGACGC | 103 | 63 | 40 | 1.78E-03 | 2.75 | 0.43 |
| GACTCC | 351 | 311 | 40 | 1.19E-01 | 0.92 | 0.43 |

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|---|---|---|---|---|---|---|
| GCCTGC | 530 | 490 | 40 | 2.09E-01 | 0.68 | 0.42 |
| AGTGGT | 408 | 368 | 40 | 1.51E-01 | 0.82 | 0.42 |
| AGGCCT | 533 | 493 | 40 | 2.12E-01 | 0.67 | 0.42 |
| TCCGTG | 168 | 128 | 40 | 2.02E-02 | 1.69 | 0.42 |
| AGTCAG | 510 | 470 | 40 | 2.02E-01 | 0.69 | 0.42 |
| ACCGGG | 109 | 69 | 40 | 2.83E-03 | 2.55 | 0.42 |
| GGATAG | 248 | 208 | 40 | 6.26E-02 | 1.20 | 0.42 |
| GCGTGC | 122 | 82 | 40 | 5.41E-03 | 2.27 | 0.42 |
| GACCGA | 89 | 49 | 40 | 7.32E-04 | 3.14 | 0.42 |
| CGAAGA | 108 | 68 | 40 | 2.78E-03 | 2.56 | 0.42 |
| GTGTCG | 101 | 61 | 40 | 1.85E-03 | 2.73 | 0.42 |
| GCCGCC | 144 | 104 | 40 | 1.18E-02 | 1.93 | 0.42 |
| GAGAAT | 448 | 408 | 40 | 1.76E-01 | 0.75 | 0.42 |
| ACCAGG | 462 | 422 | 40 | 1.84E-01 | 0.74 | 0.42 |
| TGAGAT | 463 | 424 | 39 | 1.85E-01 | 0.73 | 0.42 |
| CCGGAA | 120 | 81 | 39 | 5.41E-03 | 2.27 | 0.42 |
| GCCAGC | 509 | 470 | 39 | 2.09E-01 | 0.68 | 0.42 |
| TGGCAC | 368 | 329 | 39 | 1.37E-01 | 0.86 | 0.42 |
| TCTGGC | 489 | 450 | 39 | 2.00E-01 | 0.70 | 0.42 |
| ACCCCG | 132 | 93 | 39 | 8.89E-03 | 2.05 | 0.42 |
| CTCCCT | 726 | 687 | 39 | 2.97E-01 | 0.53 | 0.42 |
| GCATTG | 336 | 297 | 39 | 1.19E-01 | 0.92 | 0.42 |
| CTTCGG | 124 | 85 | 39 | 6.81E-03 | 2.17 | 0.41 |
| TGGCGT | 124 | 85 | 39 | 6.81E-03 | 2.17 | 0.41 |
| GGGTAC | 206 | 167 | 39 | 4.32E-02 | 1.36 | 0.41 |
| GCACCG | 115 | 76 | 39 | 4.86E-03 | 2.31 | 0.41 |
| AGGGTC | 366 | 327 | 39 | 1.40E-01 | 0.85 | 0.41 |
| GGGCGA | 100 | 61 | 39 | 2.21E-03 | 2.66 | 0.41 |
| ACGAGA | 106 | 67 | 39 | 3.16E-03 | 2.50 | 0.41 |
| TGTCCC | 563 | 524 | 39 | 2.39E-01 | 0.62 | 0.41 |
| GCCTCT | 599 | 560 | 39 | 2.54E-01 | 0.59 | 0.41 |
| AATGGA | 487 | 448 | 39 | 2.06E-01 | 0.69 | 0.41 |
| AGCGGA | 106 | 67 | 39 | 3.34E-03 | 2.48 | 0.41 |
| TCGGGC | 108 | 69 | 39 | 3.77E-03 | 2.42 | 0.41 |
| CACCGT | 137 | 99 | 38 | 1.21E-02 | 1.92 | 0.41 |
| AGACTT | 525 | 487 | 38 | 2.26E-01 | 0.65 | 0.41 |
| CACGGA | 138 | 100 | 38 | 1.27E-02 | 1.89 | 0.41 |
| TCGAGG | 113 | 75 | 38 | 5.10E-03 | 2.29 | 0.41 |
| ATTGTA | 427 | 389 | 38 | 1.81E-01 | 0.74 | 0.41 |
| TTGATG | 426 | 388 | 38 | 1.80E-01 | 0.74 | 0.41 |
| CACCGG | 119 | 81 | 38 | 6.89E-03 | 2.16 | 0.40 |
| GGATCT | 313 | 275 | 38 | 1.15E-01 | 0.94 | 0.40 |
| TCGAGA | 96 | 58 | 38 | 2.11E-03 | 2.68 | 0.40 |
| TCGGAC | 79 | 41 | 38 | 4.99E-04 | 3.30 | 0.40 |
| TCGTGG | 133 | 95 | 38 | 1.16E-02 | 1.93 | 0.40 |
| CGTCTG | 148 | 110 | 38 | 1.78E-02 | 1.75 | 0.40 |
| CCGTGC | 147 | 109 | 38 | 1.74E-02 | 1.76 | 0.40 |
| AGGATT | 400 | 362 | 38 | 1.68E-01 | 0.77 | 0.40 |
| GTTGCT | 411 | 373 | 38 | 1.75E-01 | 0.76 | 0.40 |
| AAGCAC | 421 | 383 | 38 | 1.80E-01 | 0.74 | 0.40 |
| ACGGGC | 105 | 67 | 38 | 3.85E-03 | 2.41 | 0.40 |
| CCTCTC | 629 | 591 | 38 | 2.78E-01 | 0.56 | 0.40 |
| CGAGAA | 120 | 82 | 38 | 7.69E-03 | 2.11 | 0.40 |
| TGACGT | 128 | 90 | 38 | 1.04E-02 | 1.98 | 0.40 |

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| CCAGCC | 684 | 646 | 38 | 3.00E-01 | 0.52 | 0.40 |
| TAGACG | 85 | 47 | 38 | 1.03E-03 | 2.99 | 0.40 |
| GTGGTC | 333 | 295 | 38 | 1.33E-01 | 0.88 | 0.40 |
| GTGAAA | 478 | 440 | 38 | 2.14E-01 | 0.67 | 0.40 |
| CAGCGA | 128 | 90 | 38 | 1.10E-02 | 1.96 | 0.40 |
| ATCGGA | 80 | 42 | 38 | 6.84E-04 | 3.16 | 0.40 |
| TCGGAT | 85 | 48 | 37 | 1.12E-03 | 2.95 | 0.40 |
| GTCGGG | 107 | 70 | 37 | 4.79E-03 | 2.32 | 0.40 |
| CAGACG | 131 | 94 | 37 | 1.24E-02 | 1.91 | 0.40 |
| GCGGGA | 124 | 87 | 37 | 9.82E-03 | 2.01 | 0.40 |
| TTGTGA | 539 | 502 | 37 | 2.46E-01 | 0.61 | 0.40 |
| GGCACA | 412 | 375 | 37 | 1.83E-01 | 0.74 | 0.40 |
| TTCGGG | 110 | 73 | 37 | 5.76E-03 | 2.24 | 0.40 |
| GCCACT | 416 | 379 | 37 | 1.86E-01 | 0.73 | 0.40 |
| GCCTCG | 148 | 111 | 37 | 2.11E-02 | 1.68 | 0.39 |
| GAGCGC | 113 | 76 | 37 | 7.01E-03 | 2.15 | 0.39 |
| GACACG | 121 | 84 | 37 | 9.68E-03 | 2.01 | 0.39 |
| CTTCTG | 811 | 774 | 37 | 3.52E-01 | 0.45 | 0.39 |
| GTCGGA | 81 | 44 | 37 | 9.37E-04 | 3.03 | 0.39 |
| TGATGT | 507 | 470 | 37 | 2.37E-01 | 0.63 | 0.39 |
| CTCGAG | 122 | 85 | 37 | 1.02E-02 | 1.99 | 0.39 |
| CACGTG | 214 | 177 | 37 | 6.19E-02 | 1.21 | 0.39 |
| ACGGGT | 97 | 60 | 37 | 3.23E-03 | 2.49 | 0.39 |
| GTCAGA | 430 | 393 | 37 | 1.98E-01 | 0.70 | 0.39 |
| TCTCGG | 139 | 102 | 37 | 1.75E-02 | 1.76 | 0.39 |
| TGCATG | 486 | 449 | 37 | 2.28E-01 | 0.64 | 0.39 |
| TCGGGA | 124 | 87 | 37 | 1.13E-02 | 1.95 | 0.39 |
| TATGGG | 275 | 238 | 37 | 1.04E-01 | 0.98 | 0.39 |
| TGCGGA | 104 | 67 | 37 | 4.99E-03 | 2.30 | 0.39 |
| ACTCGC | 92 | 55 | 37 | 2.49E-03 | 2.60 | 0.39 |
| CTCGTG | 150 | 113 | 37 | 2.42E-02 | 1.62 | 0.39 |
| CAGACC | 404 | 367 | 37 | 1.88E-01 | 0.73 | 0.39 |
| ATGTGA | 522 | 485 | 37 | 2.50E-01 | 0.60 | 0.39 |
| ACGTGT | 169 | 133 | 36 | 3.59E-02 | 1.45 | 0.39 |
| GGTGTC | 344 | 308 | 36 | 1.54E-01 | 0.81 | 0.39 |
| TGCCCT | 609 | 573 | 36 | 2.91E-01 | 0.54 | 0.39 |
| ACCGAG | 125 | 89 | 36 | 1.30E-02 | 1.89 | 0.38 |
| TGTGTA | 637 | 601 | 36 | 3.03E-01 | 0.52 | 0.38 |
| CGCCTG | 153 | 117 | 36 | 2.75E-02 | 1.56 | 0.38 |
| CGTTGG | 104 | 68 | 36 | 5.86E-03 | 2.23 | 0.38 |
| CTGTCG | 124 | 88 | 36 | 1.32E-02 | 1.88 | 0.38 |
| GAGTCG | 97 | 61 | 36 | 4.16E-03 | 2.38 | 0.38 |
| ATGGCA | 420 | 384 | 36 | 2.06E-01 | 0.69 | 0.38 |
| CGTGGC | 155 | 119 | 36 | 3.09E-02 | 1.51 | 0.38 |
| CCCTCG | 142 | 106 | 36 | 2.37E-02 | 1.62 | 0.38 |
| CCCTGA | 529 | 493 | 36 | 2.65E-01 | 0.58 | 0.38 |
| ACGTTG | 110 | 74 | 36 | 8.81E-03 | 2.06 | 0.38 |
| ACTCGG | 128 | 93 | 35 | 1.68E-02 | 1.77 | 0.38 |
| ATGGGT | 342 | 307 | 35 | 1.64E-01 | 0.78 | 0.38 |
| CGAGTG | 119 | 84 | 35 | 1.30E-02 | 1.89 | 0.37 |
| AGCCGC | 127 | 92 | 35 | 1.70E-02 | 1.77 | 0.37 |
| TGATGA | 429 | 394 | 35 | 2.19E-01 | 0.66 | 0.37 |
| TGCCGG | 116 | 81 | 35 | 1.20E-02 | 1.92 | 0.37 |
| GACGAA | 80 | 45 | 35 | 1.62E-03 | 2.79 | 0.37 |

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| ACGGAA | 115 | 80 | 35 | 1.18E-02 | 1.93 | 0.37 |
| ACCGGA | 93 | 58 | 35 | 4.27E-03 | 2.37 | 0.37 |
| CTCGCA | 95 | 60 | 35 | 4.92E-03 | 2.31 | 0.37 |
| CAGTAG | 370 | 335 | 35 | 1.88E-01 | 0.73 | 0.37 |
| CGACTG | 99 | 64 | 35 | 6.17E-03 | 2.21 | 0.37 |
| AGGCCG | 130 | 95 | 35 | 1.99E-02 | 1.70 | 0.37 |
| TCAGGA | 576 | 541 | 35 | 2.96E-01 | 0.53 | 0.37 |
| AATCGG | 78 | 43 | 35 | 1.56E-03 | 2.81 | 0.37 |
| ACCCCT | 388 | 353 | 35 | 2.02E-01 | 0.70 | 0.37 |
| CGGAAA | 111 | 76 | 35 | 1.11E-02 | 1.96 | 0.37 |
| TAGAGC | 301 | 266 | 35 | 1.45E-01 | 0.84 | 0.37 |
| AGGTGT | 434 | 399 | 35 | 2.29E-01 | 0.64 | 0.37 |
| AACTCG | 100 | 65 | 35 | 7.09E-03 | 2.15 | 0.37 |
| GGGTCA | 350 | 315 | 35 | 1.80E-01 | 0.74 | 0.37 |
| ACTTTG | 564 | 529 | 35 | 2.96E-01 | 0.53 | 0.37 |
| AACGAA | 105 | 70 | 35 | 9.09E-03 | 2.04 | 0.37 |
| GTCTGC | 419 | 384 | 35 | 2.23E-01 | 0.65 | 0.37 |
| CGAGAC | 91 | 56 | 35 | 4.49E-03 | 2.35 | 0.37 |
| CCCTGC | 647 | 613 | 34 | 3.31E-01 | 0.48 | 0.37 |
| AGATGC | 426 | 392 | 34 | 2.29E-01 | 0.64 | 0.36 |
| AGTCTG | 528 | 494 | 34 | 2.83E-01 | 0.55 | 0.36 |
| GACCGG | 89 | 55 | 34 | 4.53E-03 | 2.34 | 0.36 |
| AACGGG | 101 | 67 | 34 | 8.60E-03 | 2.07 | 0.36 |
| GTTAGG | 260 | 226 | 34 | 1.24E-01 | 0.91 | 0.36 |
| CTGACT | 539 | 505 | 34 | 2.94E-01 | 0.53 | 0.36 |
| CGGTGA | 115 | 81 | 34 | 1.55E-02 | 1.81 | 0.36 |
| GGCGTC | 97 | 63 | 34 | 7.46E-03 | 2.13 | 0.36 |
| GCCAGA | 463 | 429 | 34 | 2.57E-01 | 0.59 | 0.36 |
| GTCTGA | 418 | 384 | 34 | 2.33E-01 | 0.63 | 0.36 |
| AAGGGT | 381 | 347 | 34 | 2.11E-01 | 0.68 | 0.36 |
| ACTGTC | 453 | 419 | 34 | 2.54E-01 | 0.59 | 0.36 |
| CCGGCC | 132 | 98 | 34 | 2.65E-02 | 1.58 | 0.36 |
| GGAGTT | 367 | 333 | 34 | 2.03E-01 | 0.69 | 0.36 |
| GCCCGG | 137 | 103 | 34 | 3.03E-02 | 1.52 | 0.36 |
| CGTAGG | 85 | 51 | 34 | 4.03E-03 | 2.39 | 0.36 |
| CGGCCA | 120 | 87 | 33 | 2.00E-02 | 1.70 | 0.35 |
| TTGAGA | 512 | 479 | 33 | 2.89E-01 | 0.54 | 0.35 |
| TAGGAT | 293 | 260 | 33 | 1.55E-01 | 0.81 | 0.35 |
| CCGCAG | 145 | 112 | 33 | 3.73E-02 | 1.43 | 0.35 |
| CCGCCT | 149 | 116 | 33 | 4.04E-02 | 1.39 | 0.35 |
| AGCACA | 566 | 533 | 33 | 3.14E-01 | 0.50 | 0.35 |
| TGTCGT | 117 | 84 | 33 | 1.90E-02 | 1.72 | 0.35 |
| CTCCTG | 798 | 765 | 33 | 4.01E-01 | 0.40 | 0.35 |
| CGACAG | 104 | 71 | 33 | 1.21E-02 | 1.92 | 0.35 |
| GCTCCC | 427 | 394 | 33 | 2.48E-01 | 0.61 | 0.35 |
| CGGACT | 91 | 58 | 33 | 6.67E-03 | 2.18 | 0.35 |
| TTCTGA | 729 | 696 | 33 | 3.83E-01 | 0.42 | 0.35 |
| AGGCAT | 387 | 354 | 33 | 2.27E-01 | 0.64 | 0.35 |
| AGGCGT | 106 | 73 | 33 | 1.41E-02 | 1.85 | 0.35 |
| GCGGTG | 125 | 92 | 33 | 2.58E-02 | 1.59 | 0.35 |
| GCAAAG | 451 | 418 | 33 | 2.66E-01 | 0.58 | 0.35 |
| AGCGGC | 114 | 81 | 33 | 1.90E-02 | 1.72 | 0.35 |
| CGACCT | 89 | 56 | 33 | 6.64E-03 | 2.18 | 0.35 |
| CGGAGT | 98 | 65 | 33 | 1.06E-02 | 1.97 | 0.35 |

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|---|---|---|---|---|---|---|
| ATCGTG | 101 | 68 | 33 | 1.21E-02 | 1.92 | 0.35 |
| CGAACT | 74 | 41 | 33 | 2.41E-03 | 2.62 | 0.35 |
| GCGCAG | 119 | 86 | 33 | 2.32E-02 | 1.63 | 0.34 |
| GGCGCA | 89 | 56 | 33 | 7.03E-03 | 2.15 | 0.34 |
| AGCGTG | 141 | 109 | 32 | 4.02E-02 | 1.40 | 0.34 |
| ACCCTG | 540 | 508 | 32 | 3.17E-01 | 0.50 | 0.34 |
| CGCTGC | 159 | 127 | 32 | 5.54E-02 | 1.26 | 0.34 |
| GGGATC | 235 | 203 | 32 | 1.23E-01 | 0.91 | 0.34 |
| CAGCCG | 155 | 123 | 32 | 5.30E-02 | 1.28 | 0.34 |
| CTGCGT | 138 | 106 | 32 | 3.92E-02 | 1.41 | 0.34 |
| GCGATG | 92 | 60 | 32 | 9.00E-03 | 2.05 | 0.34 |
| ACGTAG | 89 | 57 | 32 | 7.73E-03 | 2.11 | 0.34 |
| AGGCGA | 101 | 69 | 32 | 1.36E-02 | 1.87 | 0.34 |
| ATCAGG | 330 | 298 | 32 | 2.00E-01 | 0.70 | 0.34 |
| ACCGAC | 75 | 43 | 32 | 3.16E-03 | 2.50 | 0.34 |
| TTGTCG | 87 | 55 | 32 | 7.14E-03 | 2.15 | 0.34 |
| TCACGG | 122 | 90 | 32 | 2.80E-02 | 1.55 | 0.34 |
| GCTAGA | 270 | 238 | 32 | 1.57E-01 | 0.80 | 0.34 |
| AGGCAC | 379 | 347 | 32 | 2.36E-01 | 0.63 | 0.34 |
| GCGACT | 79 | 47 | 32 | 4.54E-03 | 2.34 | 0.34 |
| CAGTGA | 609 | 577 | 32 | 3.56E-01 | 0.45 | 0.34 |
| GTGGTA | 302 | 270 | 32 | 1.85E-01 | 0.73 | 0.34 |
| ATCGGG | 83 | 51 | 32 | 6.31E-03 | 2.20 | 0.34 |
| CCAGTG | 609 | 577 | 32 | 3.58E-01 | 0.45 | 0.34 |
| TGGAAA | 768 | 736 | 32 | 4.14E-01 | 0.38 | 0.34 |
| GAATCG | 79 | 47 | 32 | 4.89E-03 | 2.31 | 0.34 |
| AGCGGT | 97 | 65 | 32 | 1.31E-02 | 1.88 | 0.34 |
| GGGGCG | 159 | 127 | 32 | 6.26E-02 | 1.20 | 0.33 |
| GCCGGC | 113 | 81 | 32 | 2.39E-02 | 1.62 | 0.33 |
| CCAGCG | 153 | 122 | 31 | 5.74E-02 | 1.24 | 0.33 |
| TCGGTG | 121 | 90 | 31 | 3.04E-02 | 1.52 | 0.33 |
| GTGCGT | 110 | 79 | 31 | 2.23E-02 | 1.65 | 0.33 |
| TGCGGT | 104 | 73 | 31 | 1.83E-02 | 1.74 | 0.33 |
| GGTGTA | 238 | 207 | 31 | 1.37E-01 | 0.86 | 0.33 |
| GCGGAC | 73 | 42 | 31 | 3.48E-03 | 2.46 | 0.33 |
| CAGGCC | 525 | 494 | 31 | 3.28E-01 | 0.48 | 0.33 |
| TAGAAG | 444 | 413 | 31 | 2.87E-01 | 0.54 | 0.33 |
| GGCCCT | 431 | 400 | 31 | 2.79E-01 | 0.55 | 0.33 |
| CTGGCG | 129 | 98 | 31 | 3.84E-02 | 1.42 | 0.33 |
| CAAGGC | 414 | 383 | 31 | 2.70E-01 | 0.57 | 0.33 |
| TACGGG | 71 | 40 | 31 | 3.13E-03 | 2.50 | 0.33 |
| GCTCCT | 538 | 507 | 31 | 3.36E-01 | 0.47 | 0.33 |
| ACGCTG | 140 | 109 | 31 | 4.89E-02 | 1.31 | 0.33 |
| GGACTA | 206 | 175 | 31 | 1.12E-01 | 0.95 | 0.33 |
| AAGTAG | 377 | 346 | 31 | 2.49E-01 | 0.60 | 0.33 |
| CTCAGG | 637 | 606 | 31 | 3.81E-01 | 0.42 | 0.33 |
| ACCAGC | 395 | 364 | 31 | 2.63E-01 | 0.58 | 0.33 |
| CGGACC | 77 | 46 | 31 | 5.46E-03 | 2.26 | 0.33 |
| GCGGGC | 117 | 86 | 31 | 3.09E-02 | 1.51 | 0.33 |
| GAACGC | 81 | 50 | 31 | 7.27E-03 | 2.14 | 0.33 |
| CGCACT | 90 | 59 | 31 | 1.20E-02 | 1.92 | 0.33 |
| CTTGAG | 482 | 451 | 31 | 3.16E-01 | 0.50 | 0.32 |
| GTTTTG | 706 | 675 | 31 | 4.10E-01 | 0.39 | 0.32 |
| GACGTC | 88 | 57 | 31 | 1.13E-02 | 1.95 | 0.32 |

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|---|---|---|---|---|---|---|
| TGCGCT | 111 | 81 | 30 | 2.77E-02 | 1.56 | 0.32 |
| GTATTG | 281 | 251 | 30 | 1.87E-01 | 0.73 | 0.32 |
| GTAGCC | 255 | 225 | 30 | 1.65E-01 | 0.78 | 0.32 |
| TAGGAA | 492 | 462 | 30 | 3.25E-01 | 0.49 | 0.32 |
| CTTGTG | 555 | 525 | 30 | 3.55E-01 | 0.45 | 0.32 |
| AAACGG | 116 | 86 | 30 | 3.27E-02 | 1.48 | 0.32 |
| CTCCCC | 608 | 578 | 30 | 3.79E-01 | 0.42 | 0.32 |
| GACGCC | 89 | 59 | 30 | 1.28E-02 | 1.89 | 0.32 |
| ACTCGA | 84 | 54 | 30 | 1.02E-02 | 1.99 | 0.32 |
| TGACGA | 87 | 57 | 30 | 1.20E-02 | 1.92 | 0.32 |
| AGACGA | 100 | 70 | 30 | 2.12E-02 | 1.67 | 0.32 |
| TCGGAA | 99 | 69 | 30 | 2.05E-02 | 1.69 | 0.32 |
| CAGGCA | 593 | 563 | 30 | 3.78E-01 | 0.42 | 0.32 |
| GACGCA | 81 | 51 | 30 | 9.48E-03 | 2.02 | 0.32 |
| GCGAGC | 100 | 70 | 30 | 2.24E-02 | 1.65 | 0.32 |
| GGCGGA | 98 | 68 | 30 | 2.09E-02 | 1.68 | 0.32 |
| TCGGGT | 105 | 75 | 30 | 2.69E-02 | 1.57 | 0.32 |
| CGACTC | 82 | 52 | 30 | 1.06E-02 | 1.97 | 0.31 |
| TACCTC | 302 | 272 | 30 | 2.17E-01 | 0.66 | 0.31 |
| ATGGCG | 103 | 73 | 30 | 2.60E-02 | 1.58 | 0.31 |
| CGGTAG | 77 | 47 | 30 | 8.04E-03 | 2.09 | 0.31 |
| CGTGGT | 137 | 107 | 30 | 5.91E-02 | 1.23 | 0.31 |
| GGGTCC | 312 | 283 | 29 | 2.27E-01 | 0.64 | 0.31 |
| CCCAAG | 514 | 485 | 29 | 3.52E-01 | 0.45 | 0.31 |
| GCTTGA | 314 | 285 | 29 | 2.30E-01 | 0.64 | 0.31 |
| ATAGAG | 321 | 292 | 29 | 2.37E-01 | 0.62 | 0.31 |
| CGGGAC | 109 | 80 | 29 | 3.32E-02 | 1.48 | 0.31 |
| AGACTC | 393 | 364 | 29 | 2.90E-01 | 0.54 | 0.31 |
| AAGCCG | 117 | 88 | 29 | 4.24E-02 | 1.37 | 0.31 |
| CTGCGC | 123 | 94 | 29 | 4.85E-02 | 1.31 | 0.31 |
| AGCGAA | 84 | 55 | 29 | 1.37E-02 | 1.86 | 0.31 |
| CGCTGT | 147 | 118 | 29 | 7.47E-02 | 1.13 | 0.31 |
| AACGCA | 89 | 60 | 29 | 1.75E-02 | 1.76 | 0.31 |
| TGCCCG | 136 | 107 | 29 | 6.29E-02 | 1.20 | 0.31 |
| CGTGCC | 122 | 93 | 29 | 4.81E-02 | 1.32 | 0.31 |
| ACGAAG | 102 | 73 | 29 | 2.93E-02 | 1.53 | 0.31 |
| CGTGCA | 130 | 101 | 29 | 5.87E-02 | 1.23 | 0.30 |
| TCACCG | 110 | 81 | 29 | 3.76E-02 | 1.42 | 0.30 |
| TGGCTC | 522 | 493 | 29 | 3.68E-01 | 0.43 | 0.30 |
| GAGATC | 258 | 229 | 29 | 1.94E-01 | 0.71 | 0.30 |
| AACCGG | 81 | 52 | 29 | 1.31E-02 | 1.88 | 0.30 |
| GCGGCC | 111 | 82 | 29 | 3.99E-02 | 1.40 | 0.30 |
| GTGCCG | 101 | 72 | 29 | 3.01E-02 | 1.52 | 0.30 |
| TGTCGA | 75 | 46 | 29 | 9.55E-03 | 2.02 | 0.30 |
| TGTTGC | 392 | 363 | 29 | 2.99E-01 | 0.52 | 0.30 |
| CACGGG | 150 | 121 | 29 | 8.35E-02 | 1.08 | 0.30 |
| CCATGG | 496 | 468 | 28 | 3.59E-01 | 0.45 | 0.30 |
| CGCAGG | 125 | 97 | 28 | 5.60E-02 | 1.25 | 0.30 |
| GATGCG | 82 | 54 | 28 | 1.46E-02 | 1.83 | 0.30 |
| CGGCCT | 130 | 102 | 28 | 6.23E-02 | 1.21 | 0.30 |
| TCAGAG | 656 | 628 | 28 | 4.29E-01 | 0.37 | 0.30 |
| CAAGCC | 388 | 360 | 28 | 3.00E-01 | 0.52 | 0.30 |
| ACACCG | 106 | 78 | 28 | 3.74E-02 | 1.43 | 0.30 |
| ACCGTT | 91 | 63 | 28 | 2.30E-02 | 1.64 | 0.30 |

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|---|---|---|---|---|---|---|
| AGTGTA | 371 | 343 | 28 | 2.92E-01 | 0.53 | 0.30 |
| TGCCGC | 110 | 82 | 28 | 4.25E-02 | 1.37 | 0.30 |
| AAGGCT | 522 | 494 | 28 | 3.79E-01 | 0.42 | 0.30 |
| GAAAAG | 665 | 637 | 28 | 4.38E-01 | 0.36 | 0.30 |
| CCGTAG | 81 | 53 | 28 | 1.55E-02 | 1.81 | 0.30 |
| GCGGCT | 119 | 91 | 28 | 5.33E-02 | 1.27 | 0.30 |
| CGTGTC | 136 | 108 | 28 | 7.35E-02 | 1.13 | 0.30 |
| GTTAGA | 290 | 262 | 28 | 2.35E-01 | 0.63 | 0.30 |
| GTGGTT | 419 | 391 | 28 | 3.27E-01 | 0.49 | 0.30 |
| GCGGCA | 94 | 66 | 28 | 2.80E-02 | 1.55 | 0.29 |
| AATCGT | 80 | 52 | 28 | 1.60E-02 | 1.79 | 0.29 |
| CCAGCA | 621 | 593 | 28 | 4.27E-01 | 0.37 | 0.29 |
| TAGTGG | 278 | 250 | 28 | 2.29E-01 | 0.64 | 0.29 |
| AGTAGG | 295 | 267 | 28 | 2.46E-01 | 0.61 | 0.29 |
| GTTTGA | 423 | 395 | 28 | 3.36E-01 | 0.47 | 0.29 |
| TAGTGC | 217 | 190 | 27 | 1.73E-01 | 0.76 | 0.29 |
| ACAGAC | 456 | 429 | 27 | 3.56E-01 | 0.45 | 0.29 |
| TCGTGT | 130 | 103 | 27 | 7.22E-02 | 1.14 | 0.29 |
| CCCGTG | 172 | 145 | 27 | 1.24E-01 | 0.91 | 0.29 |
| ATTCTG | 578 | 551 | 27 | 4.17E-01 | 0.38 | 0.29 |
| GAGCTT | 398 | 371 | 27 | 3.26E-01 | 0.49 | 0.29 |
| GAGCCG | 132 | 105 | 27 | 7.85E-02 | 1.11 | 0.29 |
| CGAGCT | 106 | 79 | 27 | 4.64E-02 | 1.33 | 0.29 |
| CCCGCT | 129 | 102 | 27 | 7.57E-02 | 1.12 | 0.29 |
| ACGTGA | 125 | 98 | 27 | 7.12E-02 | 1.15 | 0.29 |
| CACTGC | 514 | 487 | 27 | 3.95E-01 | 0.40 | 0.29 |
| CGCATG | 93 | 66 | 27 | 3.29E-02 | 1.48 | 0.29 |
| CAAGCG | 89 | 62 | 27 | 2.90E-02 | 1.54 | 0.28 |
| GGTTGA | 260 | 233 | 27 | 2.28E-01 | 0.64 | 0.28 |
| GGATCG | 71 | 44 | 27 | 1.27E-02 | 1.90 | 0.28 |
| TCGTGA | 99 | 72 | 27 | 4.16E-02 | 1.38 | 0.28 |
| GAAGTA | 347 | 320 | 27 | 3.03E-01 | 0.52 | 0.28 |
| GCGGTA | 63 | 36 | 27 | 7.61E-03 | 2.12 | 0.28 |
| CGAGCA | 106 | 79 | 27 | 5.08E-02 | 1.29 | 0.28 |
| GCTCAG | 582 | 555 | 27 | 4.31E-01 | 0.37 | 0.28 |
| CCGGGA | 139 | 112 | 27 | 9.42E-02 | 1.03 | 0.28 |
| CGAAGG | 104 | 78 | 26 | 4.96E-02 | 1.30 | 0.28 |
| GAGGTA | 270 | 244 | 26 | 2.43E-01 | 0.61 | 0.28 |
| CCACCG | 130 | 104 | 26 | 8.39E-02 | 1.08 | 0.28 |
| GCTGAT | 322 | 296 | 26 | 2.89E-01 | 0.54 | 0.28 |
| GGTCGT | 71 | 45 | 26 | 1.46E-02 | 1.84 | 0.28 |
| TCGCAC | 68 | 42 | 26 | 1.23E-02 | 1.91 | 0.28 |
| CCTCGA | 99 | 73 | 26 | 4.55E-02 | 1.34 | 0.28 |
| ATGAGG | 386 | 360 | 26 | 3.37E-01 | 0.47 | 0.28 |
| ACGGCA | 94 | 68 | 26 | 3.95E-02 | 1.40 | 0.28 |
| CGATGC | 88 | 62 | 26 | 3.28E-02 | 1.48 | 0.28 |
| CTAGGG | 307 | 281 | 26 | 2.83E-01 | 0.55 | 0.28 |
| AGCATG | 450 | 424 | 26 | 3.79E-01 | 0.42 | 0.28 |
| GCCACC | 408 | 382 | 26 | 3.55E-01 | 0.45 | 0.28 |
| TCGGCT | 106 | 80 | 26 | 5.68E-02 | 1.25 | 0.28 |
| GTCCGG | 78 | 52 | 26 | 2.34E-02 | 1.63 | 0.27 |
| AGACGC | 97 | 71 | 26 | 4.64E-02 | 1.33 | 0.27 |
| GACGGT | 85 | 59 | 26 | 3.22E-02 | 1.49 | 0.27 |
| ACGACT | 76 | 50 | 26 | 2.21E-02 | 1.66 | 0.27 |

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|---|---|---|---|---|---|---|
| CGGGCC | 114 | 88 | 26 | 7.22E-02 | 1.14 | 0.27 |
| TGCGAA | 69 | 43 | 26 | 1.58E-02 | 1.80 | 0.27 |
| CCGCTG | 152 | 126 | 26 | 1.25E-01 | 0.90 | 0.27 |
| GTATGG | 244 | 218 | 26 | 2.35E-01 | 0.63 | 0.27 |
| GATAGG | 216 | 190 | 26 | 2.06E-01 | 0.69 | 0.27 |
| TCCCGG | 136 | 111 | 25 | 1.04E-01 | 0.98 | 0.27 |
| CGTGTT | 148 | 123 | 25 | 1.21E-01 | 0.92 | 0.27 |
| GACGAT | 69 | 44 | 25 | 1.65E-02 | 1.78 | 0.27 |
| CGAGGT | 95 | 70 | 25 | 4.76E-02 | 1.32 | 0.27 |
| CTCGTT | 107 | 82 | 25 | 6.43E-02 | 1.19 | 0.27 |
| CCTCGT | 125 | 100 | 25 | 9.11E-02 | 1.04 | 0.27 |
| TAGACT | 322 | 297 | 25 | 3.09E-01 | 0.51 | 0.27 |
| GAAAGC | 479 | 454 | 25 | 4.07E-01 | 0.39 | 0.27 |
| CCGGCA | 95 | 70 | 25 | 4.90E-02 | 1.31 | 0.27 |
| TGCCGT | 119 | 94 | 25 | 8.33E-02 | 1.08 | 0.27 |
| TTCCGT | 123 | 98 | 25 | 8.92E-02 | 1.05 | 0.27 |
| CACCAG | 495 | 470 | 25 | 4.16E-01 | 0.38 | 0.27 |
| GTTTAC | 307 | 282 | 25 | 2.98E-01 | 0.53 | 0.27 |
| CAGTCG | 88 | 63 | 25 | 4.02E-02 | 1.40 | 0.27 |
| GCGTGA | 87 | 62 | 25 | 4.01E-02 | 1.40 | 0.27 |
| GACTTA | 275 | 250 | 25 | 2.75E-01 | 0.56 | 0.27 |
| ACAGCG | 127 | 102 | 25 | 9.81E-02 | 1.01 | 0.27 |
| CGTTCT | 131 | 106 | 25 | 1.04E-01 | 0.98 | 0.27 |
| ACGTGC | 115 | 90 | 25 | 8.08E-02 | 1.09 | 0.27 |
| CCCGGA | 117 | 92 | 25 | 8.45E-02 | 1.07 | 0.26 |
| TCGAAC | 56 | 31 | 25 | 7.56E-03 | 2.12 | 0.26 |
| TGTACT | 402 | 377 | 25 | 3.72E-01 | 0.43 | 0.26 |
| ATGGAA | 554 | 529 | 25 | 4.49E-01 | 0.35 | 0.26 |
| CTGTAT | 483 | 458 | 25 | 4.17E-01 | 0.38 | 0.26 |
| CACGGC | 115 | 90 | 25 | 8.26E-02 | 1.08 | 0.26 |
| GCTAGG | 272 | 247 | 25 | 2.76E-01 | 0.56 | 0.26 |
| TCGCAG | 91 | 66 | 25 | 4.79E-02 | 1.32 | 0.26 |
| AACGCT | 95 | 70 | 25 | 5.41E-02 | 1.27 | 0.26 |
| CCTGCT | 730 | 705 | 25 | 5.13E-01 | 0.29 | 0.26 |
| ACGACA | 81 | 56 | 25 | 3.49E-02 | 1.46 | 0.26 |
| CACCGC | 109 | 84 | 25 | 7.57E-02 | 1.12 | 0.26 |
| CGCAGT | 93 | 68 | 25 | 5.20E-02 | 1.28 | 0.26 |
| AGGATC | 280 | 255 | 25 | 2.87E-01 | 0.54 | 0.26 |
| AATGCG | 67 | 42 | 25 | 1.85E-02 | 1.73 | 0.26 |
| ACCAGA | 441 | 416 | 25 | 4.00E-01 | 0.40 | 0.26 |
| CAGCGT | 144 | 119 | 25 | 1.29E-01 | 0.89 | 0.26 |
| ACGGCC | 89 | 64 | 25 | 4.78E-02 | 1.32 | 0.26 |
| GCGAAG | 81 | 57 | 24 | 3.69E-02 | 1.43 | 0.26 |
| TGCGAG | 84 | 60 | 24 | 4.12E-02 | 1.39 | 0.26 |
| CCCCCG | 129 | 105 | 24 | 1.10E-01 | 0.96 | 0.26 |
| TGTGAT | 507 | 483 | 24 | 4.38E-01 | 0.36 | 0.26 |
| ACGCTC | 87 | 63 | 24 | 4.60E-02 | 1.34 | 0.26 |
| CCGAGA | 119 | 95 | 24 | 9.49E-02 | 1.02 | 0.26 |
| CCGGTG | 112 | 88 | 24 | 8.41E-02 | 1.08 | 0.26 |
| AACCCG | 85 | 61 | 24 | 4.32E-02 | 1.36 | 0.26 |
| GGCTAG | 261 | 237 | 24 | 2.75E-01 | 0.56 | 0.26 |
| CAGGGT | 512 | 488 | 24 | 4.42E-01 | 0.35 | 0.26 |
| GTCGCA | 59 | 35 | 24 | 1.21E-02 | 1.92 | 0.26 |
| TACCCC | 232 | 208 | 24 | 2.47E-01 | 0.61 | 0.26 |

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|---|---|---|---|---|---|---|
| TGCGGG | 109 | 85 | 24 | 8.15E-02 | 1.09 | 0.26 |
| AGAGTT | 481 | 457 | 24 | 4.28E-01 | 0.37 | 0.26 |
| CACGGT | 121 | 97 | 24 | 1.01E-01 | 1.00 | 0.26 |
| ACGACC | 60 | 36 | 24 | 1.34E-02 | 1.87 | 0.26 |
| CGAACC | 60 | 36 | 24 | 1.34E-02 | 1.87 | 0.26 |
| TGGAAT | 480 | 456 | 24 | 4.31E-01 | 0.37 | 0.26 |
| TTCGGA | 84 | 60 | 24 | 4.47E-02 | 1.35 | 0.26 |
| CCCGGT | 97 | 73 | 24 | 6.55E-02 | 1.18 | 0.25 |
| GTTGAT | 280 | 256 | 24 | 3.00E-01 | 0.52 | 0.25 |
| CGGCGG | 67 | 43 | 24 | 2.24E-02 | 1.65 | 0.25 |
| GCAACA | 288 | 264 | 24 | 3.09E-01 | 0.51 | 0.25 |
| GTCGTG | 88 | 64 | 24 | 5.30E-02 | 1.28 | 0.25 |
| GGAATT | 377 | 353 | 24 | 3.78E-01 | 0.42 | 0.25 |
| CGGATT | 69 | 45 | 24 | 2.60E-02 | 1.59 | 0.25 |
| AACCAG | 421 | 397 | 24 | 4.06E-01 | 0.39 | 0.25 |
| ACCGAA | 79 | 55 | 24 | 4.04E-02 | 1.39 | 0.25 |
| GTAGGT | 249 | 225 | 24 | 2.76E-01 | 0.56 | 0.25 |
| ACGATG | 92 | 68 | 24 | 6.11E-02 | 1.21 | 0.25 |
| ACCTCA | 445 | 421 | 24 | 4.22E-01 | 0.37 | 0.25 |
| GATCGT | 67 | 43 | 24 | 2.46E-02 | 1.61 | 0.25 |
| CCGGCT | 124 | 100 | 24 | 1.15E-01 | 0.94 | 0.25 |
| TTAGGG | 306 | 282 | 24 | 3.31E-01 | 0.48 | 0.25 |
| ACACGG | 127 | 104 | 23 | 1.22E-01 | 0.91 | 0.25 |
| CCCTTG | 471 | 448 | 23 | 4.39E-01 | 0.36 | 0.25 |
| AACGAC | 66 | 43 | 23 | 2.47E-02 | 1.61 | 0.25 |
| CCTTAG | 354 | 331 | 23 | 3.71E-01 | 0.43 | 0.25 |
| CCGCCA | 113 | 90 | 23 | 1.01E-01 | 1.00 | 0.25 |
| TGTACG | 80 | 57 | 23 | 4.62E-02 | 1.34 | 0.25 |
| TCGGTC | 79 | 56 | 23 | 4.50E-02 | 1.35 | 0.25 |
| TGATCG | 67 | 44 | 23 | 2.75E-02 | 1.56 | 0.25 |
| GCACAA | 299 | 276 | 23 | 3.35E-01 | 0.48 | 0.25 |
| CCCAGC | 681 | 658 | 23 | 5.28E-01 | 0.28 | 0.24 |
| GCATCG | 84 | 61 | 23 | 5.55E-02 | 1.26 | 0.24 |
| GCCGCT | 114 | 91 | 23 | 1.08E-01 | 0.97 | 0.24 |
| CGGAAC | 75 | 52 | 23 | 4.09E-02 | 1.39 | 0.24 |
| CTAGGA | 351 | 328 | 23 | 3.79E-01 | 0.42 | 0.24 |
| ATGCGA | 61 | 38 | 23 | 2.12E-02 | 1.67 | 0.24 |
| GGCTCA | 407 | 384 | 23 | 4.15E-01 | 0.38 | 0.24 |
| GGTTGC | 226 | 203 | 23 | 2.69E-01 | 0.57 | 0.24 |
| CCCTGT | 593 | 570 | 23 | 5.03E-01 | 0.30 | 0.24 |
| TGCTAG | 315 | 292 | 23 | 3.54E-01 | 0.45 | 0.24 |
| GAGATT | 340 | 317 | 23 | 3.73E-01 | 0.43 | 0.24 |
| GACACC | 294 | 271 | 23 | 3.37E-01 | 0.47 | 0.24 |
| GAAACG | 115 | 92 | 23 | 1.13E-01 | 0.95 | 0.24 |
| ACGAGG | 102 | 79 | 23 | 9.02E-02 | 1.04 | 0.24 |
| CTCCTC | 646 | 623 | 23 | 5.23E-01 | 0.28 | 0.24 |
| ACTTCG | 79 | 56 | 23 | 5.16E-02 | 1.29 | 0.24 |
| GCATGA | 290 | 267 | 23 | 3.37E-01 | 0.47 | 0.24 |
| CACAGG | 630 | 607 | 23 | 5.20E-01 | 0.28 | 0.24 |
| GACTAG | 211 | 188 | 23 | 2.57E-01 | 0.59 | 0.24 |
| GACGCT | 94 | 71 | 23 | 7.85E-02 | 1.11 | 0.24 |
| TGTTAG | 380 | 357 | 23 | 4.06E-01 | 0.39 | 0.24 |
| CCGTGA | 123 | 100 | 23 | 1.32E-01 | 0.88 | 0.24 |
| CACTCG | 105 | 82 | 23 | 1.00E-01 | 1.00 | 0.24 |

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|---|---|---|---|---|---|---|
| CCCAGA | 650 | 627 | 23 | 5.29E-01 | 0.28 | 0.24 |
| GGCGAC | 70 | 48 | 22 | 3.80E-02 | 1.42 | 0.24 |
| AGATCG | 69 | 47 | 22 | 3.67E-02 | 1.44 | 0.24 |
| GGTAGC | 221 | 199 | 22 | 2.73E-01 | 0.56 | 0.24 |
| AGCCTT | 574 | 552 | 22 | 5.04E-01 | 0.30 | 0.24 |
| GCGAAC | 50 | 28 | 22 | 1.10E-02 | 1.96 | 0.24 |
| GCGTCC | 88 | 66 | 22 | 7.09E-02 | 1.15 | 0.24 |
| AACGAG | 86 | 64 | 22 | 6.83E-02 | 1.17 | 0.24 |
| CGGCAA | 67 | 45 | 22 | 3.51E-02 | 1.45 | 0.24 |
| GAGGTT | 335 | 313 | 22 | 3.83E-01 | 0.42 | 0.24 |
| GGCCTT | 450 | 428 | 22 | 4.54E-01 | 0.34 | 0.24 |
| TGCACG | 116 | 94 | 22 | 1.25E-01 | 0.90 | 0.24 |
| TGCGTT | 102 | 80 | 22 | 1.00E-01 | 1.00 | 0.23 |
| CGTGAA | 107 | 85 | 22 | 1.10E-01 | 0.96 | 0.23 |
| GGTGAT | 292 | 270 | 22 | 3.50E-01 | 0.46 | 0.23 |
| CGAATG | 80 | 58 | 22 | 6.02E-02 | 1.22 | 0.23 |
| CCTTGC | 447 | 425 | 22 | 4.55E-01 | 0.34 | 0.23 |
| CATGTG | 571 | 549 | 22 | 5.11E-01 | 0.29 | 0.23 |
| CCGACT | 86 | 64 | 22 | 7.25E-02 | 1.14 | 0.23 |
| GGTTTT | 667 | 645 | 22 | 5.44E-01 | 0.26 | 0.23 |
| CTGACA | 496 | 474 | 22 | 4.81E-01 | 0.32 | 0.23 |
| GTTCGG | 67 | 45 | 22 | 3.86E-02 | 1.41 | 0.23 |
| AGCGTC | 95 | 73 | 22 | 9.16E-02 | 1.04 | 0.23 |
| CCGAGT | 115 | 93 | 22 | 1.33E-01 | 0.88 | 0.23 |
| AAGACC | 342 | 320 | 22 | 4.02E-01 | 0.40 | 0.23 |
| AGGGTA | 285 | 263 | 22 | 3.57E-01 | 0.45 | 0.23 |
| CTACGA | 57 | 36 | 21 | 2.56E-02 | 1.59 | 0.23 |
| ATGCAA | 356 | 335 | 21 | 4.15E-01 | 0.38 | 0.23 |
| GGGTCG | 80 | 59 | 21 | 6.88E-02 | 1.16 | 0.23 |
| ACTGCG | 91 | 70 | 21 | 9.11E-02 | 1.04 | 0.23 |
| CGCCAT | 97 | 76 | 21 | 1.03E-01 | 0.99 | 0.23 |
| CCCGGC | 125 | 104 | 21 | 1.57E-01 | 0.80 | 0.23 |
| ACCTCG | 97 | 76 | 21 | 1.04E-01 | 0.98 | 0.23 |
| GCCGAC | 67 | 46 | 21 | 4.43E-02 | 1.35 | 0.23 |
| ACGCAC | 86 | 65 | 21 | 8.20E-02 | 1.09 | 0.23 |
| GCGGGT | 87 | 66 | 21 | 8.45E-02 | 1.07 | 0.23 |
| ACCGCC | 87 | 66 | 21 | 8.50E-02 | 1.07 | 0.23 |
| GAACTA | 253 | 232 | 21 | 3.35E-01 | 0.48 | 0.23 |
| CGTCCT | 124 | 103 | 21 | 1.58E-01 | 0.80 | 0.23 |
| GCCCCC | 325 | 304 | 21 | 3.97E-01 | 0.40 | 0.22 |
| TGGGTA | 353 | 332 | 21 | 4.18E-01 | 0.38 | 0.22 |
| ACCTCC | 389 | 368 | 21 | 4.41E-01 | 0.36 | 0.22 |
| ATCTGA | 423 | 402 | 21 | 4.61E-01 | 0.34 | 0.22 |
| CGTTTG | 127 | 106 | 21 | 1.66E-01 | 0.78 | 0.22 |
| GCGGCG | 69 | 48 | 21 | 5.04E-02 | 1.30 | 0.22 |
| AAAGCG | 99 | 78 | 21 | 1.12E-01 | 0.95 | 0.22 |
| GACCCA | 354 | 333 | 21 | 4.20E-01 | 0.38 | 0.22 |
| ACTGCC | 425 | 404 | 21 | 4.64E-01 | 0.33 | 0.22 |
| GTGTAC | 261 | 240 | 21 | 3.48E-01 | 0.46 | 0.22 |
| CAGCCA | 660 | 639 | 21 | 5.61E-01 | 0.25 | 0.22 |
| GATGAT | 293 | 272 | 21 | 3.78E-01 | 0.42 | 0.22 |
| CCAGAA | 605 | 584 | 21 | 5.44E-01 | 0.26 | 0.22 |
| AAAGGC | 467 | 446 | 21 | 4.90E-01 | 0.31 | 0.22 |
| TCGCTG | 125 | 104 | 21 | 1.69E-01 | 0.77 | 0.22 |

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| ATAGGA | 315 | 294 | 21 | 3.99E-01 | 0.40 | 0.22 |
| TCCGAG | 115 | 94 | 21 | 1.51E-01 | 0.82 | 0.22 |
| AAACGC | 87 | 66 | 21 | 9.34E-02 | 1.03 | 0.22 |
| GCAACG | 63 | 42 | 21 | 4.32E-02 | 1.36 | 0.22 |
| ATCTGG | 390 | 369 | 21 | 4.52E-01 | 0.35 | 0.22 |
| ATTTGG | 471 | 450 | 21 | 4.95E-01 | 0.31 | 0.22 |
| CCAGGC | 598 | 577 | 21 | 5.45E-01 | 0.26 | 0.22 |
| TGACCC | 351 | 330 | 21 | 4.28E-01 | 0.37 | 0.22 |
| AGCACG | 115 | 94 | 21 | 1.54E-01 | 0.81 | 0.22 |
| ACGGAT | 73 | 52 | 21 | 6.59E-02 | 1.18 | 0.22 |
| TACTCG | 65 | 44 | 21 | 4.91E-02 | 1.31 | 0.22 |
| AAGCGT | 90 | 69 | 21 | 1.04E-01 | 0.98 | 0.22 |
| TTGACG | 68 | 48 | 20 | 5.65E-02 | 1.25 | 0.22 |
| TCGTCC | 85 | 65 | 20 | 9.45E-02 | 1.02 | 0.22 |
| GCCTTC | 481 | 461 | 20 | 5.07E-01 | 0.30 | 0.22 |
| TCGTTC | 85 | 65 | 20 | 9.62E-02 | 1.02 | 0.22 |
| GCCAGT | 397 | 377 | 20 | 4.65E-01 | 0.33 | 0.22 |
| CATGGA | 467 | 447 | 20 | 5.01E-01 | 0.30 | 0.22 |
| TTGCGG | 70 | 50 | 20 | 6.40E-02 | 1.19 | 0.21 |
| TCGGCA | 78 | 58 | 20 | 8.23E-02 | 1.08 | 0.21 |
| CAGTGT | 702 | 682 | 20 | 5.87E-01 | 0.23 | 0.21 |
| TGCCGA | 86 | 66 | 20 | 1.01E-01 | 0.99 | 0.21 |
| TCCCCG | 149 | 129 | 20 | 2.26E-01 | 0.65 | 0.21 |
| GCGTTT | 104 | 84 | 20 | 1.41E-01 | 0.85 | 0.21 |
| ACGAAC | 62 | 42 | 20 | 4.84E-02 | 1.32 | 0.21 |
| GTGCAC | 309 | 289 | 20 | 4.11E-01 | 0.39 | 0.21 |
| GCGTCA | 73 | 53 | 20 | 7.36E-02 | 1.13 | 0.21 |
| GCCGGT | 78 | 58 | 20 | 8.52E-02 | 1.07 | 0.21 |
| GCGCCT | 102 | 82 | 20 | 1.40E-01 | 0.85 | 0.21 |
| GTCGGC | 66 | 46 | 20 | 5.87E-02 | 1.23 | 0.21 |
| GCATGT | 382 | 362 | 20 | 4.65E-01 | 0.33 | 0.21 |
| ACCGCT | 83 | 63 | 20 | 9.92E-02 | 1.00 | 0.21 |
| CCTGAC | 424 | 404 | 20 | 4.89E-01 | 0.31 | 0.21 |
| TTGCGA | 55 | 35 | 20 | 3.63E-02 | 1.44 | 0.21 |
| ATTGAG | 301 | 281 | 20 | 4.11E-01 | 0.39 | 0.21 |
| CACCGA | 95 | 75 | 20 | 1.28E-01 | 0.89 | 0.21 |
| TCCCTG | 743 | 723 | 20 | 6.05E-01 | 0.22 | 0.21 |
| CTCTCG | 120 | 100 | 20 | 1.83E-01 | 0.74 | 0.21 |
| CGTGAC | 100 | 80 | 20 | 1.41E-01 | 0.85 | 0.21 |
| GTCTCG | 87 | 67 | 20 | 1.14E-01 | 0.94 | 0.21 |
| TAGGCA | 297 | 277 | 20 | 4.14E-01 | 0.38 | 0.21 |
| GCGGAT | 60 | 40 | 20 | 5.14E-02 | 1.29 | 0.21 |
| TGACGC | 72 | 53 | 19 | 8.13E-02 | 1.09 | 0.21 |
| ACTGCT | 509 | 490 | 19 | 5.39E-01 | 0.27 | 0.21 |
| AAGCGA | 84 | 65 | 19 | 1.11E-01 | 0.95 | 0.21 |
| AAGTGC | 349 | 330 | 19 | 4.57E-01 | 0.34 | 0.21 |
| AAAACG | 129 | 110 | 19 | 2.10E-01 | 0.68 | 0.21 |
| CAAGTG | 436 | 417 | 19 | 5.09E-01 | 0.29 | 0.20 |
| GCTTGT | 403 | 384 | 19 | 4.92E-01 | 0.31 | 0.20 |
| TAGAGT | 328 | 309 | 19 | 4.46E-01 | 0.35 | 0.20 |
| CGTTAG | 70 | 51 | 19 | 8.00E-02 | 1.10 | 0.20 |
| CGATGG | 86 | 67 | 19 | 1.20E-01 | 0.92 | 0.20 |
| GGCCCG | 105 | 86 | 19 | 1.64E-01 | 0.78 | 0.20 |
| CGTCAG | 104 | 85 | 19 | 1.62E-01 | 0.79 | 0.20 |

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| TGGTCG | 71 | 52 | 19 | 8.30E-02 | 1.08 | 0.20 |
| GAGGTC | 299 | 280 | 19 | 4.26E-01 | 0.37 | 0.20 |
| AAATCG | 81 | 62 | 19 | 1.10E-01 | 0.96 | 0.20 |
| CGTCCA | 88 | 69 | 19 | 1.28E-01 | 0.89 | 0.20 |
| CTCGAA | 78 | 59 | 19 | 1.04E-01 | 0.98 | 0.20 |
| ATGCGG | 69 | 50 | 19 | 8.17E-02 | 1.09 | 0.20 |
| GCTCGG | 111 | 92 | 19 | 1.83E-01 | 0.74 | 0.20 |
| CCCGTT | 98 | 79 | 19 | 1.54E-01 | 0.81 | 0.20 |
| GCTTCG | 94 | 75 | 19 | 1.45E-01 | 0.84 | 0.20 |
| CCGTTG | 85 | 66 | 19 | 1.23E-01 | 0.91 | 0.20 |
| ACGAGC | 71 | 52 | 19 | 8.78E-02 | 1.06 | 0.20 |
| TTTGAG | 570 | 551 | 19 | 5.73E-01 | 0.24 | 0.20 |
| ACTCGT | 83 | 64 | 19 | 1.20E-01 | 0.92 | 0.20 |
| AGCCCT | 549 | 530 | 19 | 5.68E-01 | 0.25 | 0.20 |
| CCCCGA | 119 | 100 | 19 | 2.06E-01 | 0.69 | 0.20 |
| GGCGGT | 86 | 67 | 19 | 1.30E-01 | 0.89 | 0.20 |
| AACCGC | 64 | 45 | 19 | 7.44E-02 | 1.13 | 0.20 |
| ACGCCA | 88 | 69 | 19 | 1.38E-01 | 0.86 | 0.20 |
| GGGCGC | 98 | 79 | 19 | 1.63E-01 | 0.79 | 0.20 |
| CGCTCT | 120 | 101 | 19 | 2.12E-01 | 0.67 | 0.20 |
| CCCCGC | 157 | 138 | 19 | 2.80E-01 | 0.55 | 0.20 |
| TCCTCG | 130 | 112 | 18 | 2.34E-01 | 0.63 | 0.20 |
| TGTTCG | 83 | 65 | 18 | 1.30E-01 | 0.89 | 0.20 |
| TGCAAG | 362 | 344 | 18 | 4.89E-01 | 0.31 | 0.19 |
| AGCGCC | 104 | 86 | 18 | 1.83E-01 | 0.74 | 0.19 |
| ACAGTG | 625 | 607 | 18 | 6.02E-01 | 0.22 | 0.19 |
| GGTCCC | 317 | 299 | 18 | 4.61E-01 | 0.34 | 0.19 |
| ACACGA | 91 | 73 | 18 | 1.53E-01 | 0.82 | 0.19 |
| ATCACG | 76 | 58 | 18 | 1.14E-01 | 0.94 | 0.19 |
| TAGCTG | 394 | 376 | 18 | 5.10E-01 | 0.29 | 0.19 |
| GTCGTT | 73 | 55 | 18 | 1.06E-01 | 0.97 | 0.19 |
| TACGGA | 65 | 47 | 18 | 8.43E-02 | 1.07 | 0.19 |
| GCCCGT | 96 | 78 | 18 | 1.68E-01 | 0.77 | 0.19 |
| AACCGA | 77 | 59 | 18 | 1.20E-01 | 0.92 | 0.19 |
| TTACCG | 62 | 44 | 18 | 7.80E-02 | 1.11 | 0.19 |
| TCACGC | 80 | 62 | 18 | 1.28E-01 | 0.89 | 0.19 |
| TTGTTG | 535 | 517 | 18 | 5.76E-01 | 0.24 | 0.19 |
| CGCCTC | 125 | 107 | 18 | 2.36E-01 | 0.63 | 0.19 |
| GTGCAA | 264 | 246 | 18 | 4.25E-01 | 0.37 | 0.19 |
| GAGCGT | 88 | 70 | 18 | 1.52E-01 | 0.82 | 0.19 |
| GCTTCT | 602 | 584 | 18 | 6.02E-01 | 0.22 | 0.19 |
| GGCCGC | 101 | 83 | 18 | 1.85E-01 | 0.73 | 0.19 |
| GCGCAT | 66 | 48 | 18 | 9.28E-02 | 1.03 | 0.19 |
| AAGGCG | 96 | 78 | 18 | 1.74E-01 | 0.76 | 0.19 |
| GCGTCT | 98 | 80 | 18 | 1.80E-01 | 0.74 | 0.19 |
| CCGAAG | 100 | 82 | 18 | 1.86E-01 | 0.73 | 0.19 |
| CCGACA | 73 | 55 | 18 | 1.15E-01 | 0.94 | 0.19 |
| TAGGGT | 251 | 233 | 18 | 4.17E-01 | 0.38 | 0.19 |
| CCGGAT | 68 | 50 | 18 | 1.02E-01 | 0.99 | 0.19 |
| GCCGCA | 86 | 68 | 18 | 1.53E-01 | 0.82 | 0.19 |
| CGGCAT | 69 | 51 | 18 | 1.06E-01 | 0.97 | 0.19 |
| TGGCGA | 85 | 67 | 18 | 1.51E-01 | 0.82 | 0.19 |
| CGTAGC | 67 | 49 | 18 | 1.01E-01 | 0.99 | 0.19 |
| TCGAGC | 67 | 49 | 18 | 1.01E-01 | 0.99 | 0.19 |

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| CCTCGC | 110 | 92 | 18 | 2.14E-01 | 0.67 | 0.19 |
| TGCTTG | 532 | 514 | 18 | 5.85E-01 | 0.23 | 0.19 |
| GGCTAC | 212 | 194 | 18 | 3.83E-01 | 0.42 | 0.19 |
| TCGTAG | 64 | 46 | 18 | 9.40E-02 | 1.03 | 0.19 |
| CGCAGC | 120 | 102 | 18 | 2.38E-01 | 0.62 | 0.19 |
| ACCGTA | 61 | 43 | 18 | 8.54E-02 | 1.07 | 0.19 |
| CAAAGG | 518 | 500 | 18 | 5.83E-01 | 0.23 | 0.19 |
| TTAACG | 71 | 54 | 17 | 1.18E-01 | 0.93 | 0.18 |
| CGCCTT | 108 | 91 | 17 | 2.16E-01 | 0.66 | 0.18 |
| AACGCG | 31 | 14 | 17 | 9.09E-03 | 2.04 | 0.18 |
| TGAATC | 291 | 274 | 17 | 4.64E-01 | 0.33 | 0.18 |
| CGCACA | 104 | 87 | 17 | 2.08E-01 | 0.68 | 0.18 |
| CTTCCG | 129 | 112 | 17 | 2.62E-01 | 0.58 | 0.18 |
| GGCTCG | 93 | 76 | 17 | 1.81E-01 | 0.74 | 0.18 |
| GCCATG | 420 | 403 | 17 | 5.45E-01 | 0.26 | 0.18 |
| GACCCG | 85 | 68 | 17 | 1.60E-01 | 0.80 | 0.18 |
| TTGCCG | 81 | 64 | 17 | 1.49E-01 | 0.83 | 0.18 |
| TAAACG | 88 | 71 | 17 | 1.70E-01 | 0.77 | 0.18 |
| CGCGTG | 52 | 35 | 17 | 6.39E-02 | 1.19 | 0.18 |
| GTCCCC | 372 | 355 | 17 | 5.22E-01 | 0.28 | 0.18 |
| GTCAGC | 354 | 337 | 17 | 5.16E-01 | 0.29 | 0.18 |
| ACCGGC | 70 | 53 | 17 | 1.24E-01 | 0.91 | 0.18 |
| CGGAAT | 66 | 49 | 17 | 1.12E-01 | 0.95 | 0.18 |
| GTGCGG | 90 | 73 | 17 | 1.83E-01 | 0.74 | 0.18 |
| TCGCCT | 101 | 84 | 17 | 2.12E-01 | 0.67 | 0.18 |
| TCTCGT | 100 | 83 | 17 | 2.11E-01 | 0.68 | 0.18 |
| GCTCCG | 123 | 106 | 17 | 2.64E-01 | 0.58 | 0.18 |
| GCCGTC | 81 | 64 | 17 | 1.61E-01 | 0.79 | 0.18 |
| GATCAG | 266 | 249 | 17 | 4.57E-01 | 0.34 | 0.18 |
| TTCGAG | 76 | 59 | 17 | 1.47E-01 | 0.83 | 0.18 |
| CGCGCT | 48 | 31 | 17 | 5.81E-02 | 1.24 | 0.18 |
| CGGATC | 58 | 41 | 17 | 9.08E-02 | 1.04 | 0.18 |
| TCTGTC | 654 | 637 | 17 | 6.39E-01 | 0.19 | 0.18 |
| CTCCGT | 133 | 116 | 17 | 2.87E-01 | 0.54 | 0.18 |
| GCCACG | 126 | 109 | 17 | 2.73E-01 | 0.56 | 0.18 |
| ACGATT | 68 | 51 | 17 | 1.25E-01 | 0.90 | 0.18 |
| ATGACG | 80 | 63 | 17 | 1.62E-01 | 0.79 | 0.18 |
| CGTTGT | 95 | 78 | 17 | 2.04E-01 | 0.69 | 0.18 |
| GCGAGT | 69 | 52 | 17 | 1.29E-01 | 0.89 | 0.18 |
| GTAACG | 58 | 41 | 17 | 9.37E-02 | 1.03 | 0.18 |
| GCACTT | 363 | 346 | 17 | 5.31E-01 | 0.28 | 0.18 |
| CTCCGG | 121 | 104 | 17 | 2.67E-01 | 0.57 | 0.18 |
| ATTCGG | 68 | 51 | 17 | 1.27E-01 | 0.89 | 0.18 |
| ACCACG | 107 | 90 | 17 | 2.37E-01 | 0.63 | 0.18 |
| GCGGAA | 68 | 51 | 17 | 1.28E-01 | 0.89 | 0.18 |
| ATAACG | 60 | 43 | 17 | 1.02E-01 | 0.99 | 0.18 |
| TGGGTC | 377 | 360 | 17 | 5.41E-01 | 0.27 | 0.18 |
| AAGTCG | 73 | 56 | 17 | 1.46E-01 | 0.84 | 0.18 |
| TACGCA | 59 | 42 | 17 | 1.01E-01 | 0.99 | 0.17 |
| TAACGA | 59 | 43 | 16 | 1.02E-01 | 0.99 | 0.17 |
| AGCTCT | 591 | 575 | 16 | 6.30E-01 | 0.20 | 0.17 |
| AGTTGA | 356 | 340 | 16 | 5.34E-01 | 0.27 | 0.17 |
| GGAGTA | 225 | 209 | 16 | 4.31E-01 | 0.37 | 0.17 |
| TGACCA | 399 | 383 | 16 | 5.58E-01 | 0.25 | 0.17 |

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| CCTGCA | 559 | 543 | 16 | 6.23E-01 | 0.21 | 0.17 |
| CCACGC | 115 | 99 | 16 | 2.67E-01 | 0.57 | 0.17 |
| GCCCCG | 149 | 133 | 16 | 3.35E-01 | 0.48 | 0.17 |
| AGTGCT | 488 | 472 | 16 | 6.02E-01 | 0.22 | 0.17 |
| CCTGTC | 563 | 547 | 16 | 6.29E-01 | 0.20 | 0.17 |
| CTTTCG | 86 | 70 | 16 | 1.98E-01 | 0.70 | 0.17 |
| CTCCGA | 101 | 85 | 16 | 2.39E-01 | 0.62 | 0.17 |
| CGGCCG | 54 | 38 | 16 | 9.46E-02 | 1.02 | 0.17 |
| ACTACG | 51 | 35 | 16 | 8.49E-02 | 1.07 | 0.17 |
| CCACGG | 143 | 127 | 16 | 3.31E-01 | 0.48 | 0.17 |
| CCGGTC | 71 | 55 | 16 | 1.56E-01 | 0.81 | 0.17 |
| CTTGCG | 72 | 56 | 16 | 1.60E-01 | 0.79 | 0.17 |
| GTCACG | 93 | 77 | 16 | 2.24E-01 | 0.65 | 0.17 |
| TCGTCT | 98 | 82 | 16 | 2.37E-01 | 0.62 | 0.17 |
| CGAGCC | 95 | 79 | 16 | 2.30E-01 | 0.64 | 0.17 |
| CGGTCA | 77 | 61 | 16 | 1.79E-01 | 0.75 | 0.17 |
| AAGCGC | 75 | 59 | 16 | 1.74E-01 | 0.76 | 0.17 |
| GTCCCG | 97 | 81 | 16 | 2.38E-01 | 0.62 | 0.17 |
| CCGCTT | 90 | 74 | 16 | 2.22E-01 | 0.65 | 0.17 |
| CCGACG | 33 | 17 | 16 | 2.79E-02 | 1.55 | 0.17 |
| CTCACG | 114 | 98 | 16 | 2.84E-01 | 0.55 | 0.17 |
| TCCGGG | 110 | 94 | 16 | 2.77E-01 | 0.56 | 0.16 |
| ACGAAA | 77 | 61 | 16 | 1.87E-01 | 0.73 | 0.16 |
| CATCGG | 77 | 61 | 16 | 1.88E-01 | 0.73 | 0.16 |
| CGCTCA | 98 | 83 | 15 | 2.49E-01 | 0.60 | 0.16 |
| TTGCGT | 72 | 57 | 15 | 1.72E-01 | 0.76 | 0.16 |
| CGGTGT | 107 | 92 | 15 | 2.74E-01 | 0.56 | 0.16 |
| AGCGAC | 67 | 52 | 15 | 1.58E-01 | 0.80 | 0.16 |
| CGGTTT | 99 | 84 | 15 | 2.55E-01 | 0.59 | 0.16 |
| CCGGAC | 65 | 50 | 15 | 1.53E-01 | 0.82 | 0.16 |
| CACACG | 146 | 131 | 15 | 3.59E-01 | 0.44 | 0.16 |
| ATCGTC | 62 | 47 | 15 | 1.44E-01 | 0.84 | 0.16 |
| GCTAGT | 195 | 180 | 15 | 4.31E-01 | 0.37 | 0.16 |
| GCGCGC | 66 | 51 | 15 | 1.58E-01 | 0.80 | 0.16 |
| GGTCGC | 56 | 41 | 15 | 1.22E-01 | 0.91 | 0.16 |
| AGGAAT | 461 | 446 | 15 | 6.15E-01 | 0.21 | 0.16 |
| TGTCAG | 536 | 521 | 15 | 6.42E-01 | 0.19 | 0.16 |
| ATGTCG | 67 | 52 | 15 | 1.66E-01 | 0.78 | 0.16 |
| TTCTGT | 947 | 932 | 15 | 7.28E-01 | 0.14 | 0.16 |
| GAACTT | 406 | 391 | 15 | 5.94E-01 | 0.23 | 0.16 |
| CTGCAA | 383 | 368 | 15 | 5.83E-01 | 0.23 | 0.16 |
| ACTCCG | 83 | 68 | 15 | 2.22E-01 | 0.65 | 0.16 |
| ATCGCC | 62 | 47 | 15 | 1.50E-01 | 0.82 | 0.16 |
| TAACGC | 49 | 34 | 15 | 9.94E-02 | 1.00 | 0.16 |
| CGACAA | 55 | 40 | 15 | 1.25E-01 | 0.90 | 0.16 |
| TCTGAA | 655 | 640 | 15 | 6.79E-01 | 0.17 | 0.16 |
| AGCCCG | 119 | 104 | 15 | 3.19E-01 | 0.50 | 0.16 |
| TGCGTC | 74 | 59 | 15 | 1.97E-01 | 0.70 | 0.16 |
| GCCCGA | 83 | 68 | 15 | 2.27E-01 | 0.64 | 0.16 |
| TTCGGT | 82 | 67 | 15 | 2.24E-01 | 0.65 | 0.16 |
| TGCGAC | 50 | 35 | 15 | 1.09E-01 | 0.96 | 0.16 |
| GTCGTA | 46 | 31 | 15 | 9.24E-02 | 1.03 | 0.16 |
| TTTGCG | 70 | 55 | 15 | 1.87E-01 | 0.73 | 0.16 |
| AACGTT | 106 | 91 | 15 | 2.95E-01 | 0.53 | 0.16 |

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| GGAAAC | 439 | 424 | 15 | 6.17E-01 | 0.21 | 0.16 |
| TGCGCA | 87 | 72 | 15 | 2.48E-01 | 0.61 | 0.15 |
| GGCGTA | 45 | 30 | 15 | 9.32E-02 | 1.03 | 0.15 |
| CGGTCT | 82 | 67 | 15 | 2.33E-01 | 0.63 | 0.15 |
| GTCGCC | 69 | 54 | 15 | 1.90E-01 | 0.72 | 0.15 |
| ATCTCG | 69 | 54 | 15 | 1.90E-01 | 0.72 | 0.15 |
| CCGGGT | 98 | 83 | 15 | 2.80E-01 | 0.55 | 0.15 |
| AGTCGA | 56 | 41 | 15 | 1.41E-01 | 0.85 | 0.15 |
| ATGCGC | 63 | 48 | 15 | 1.70E-01 | 0.77 | 0.15 |
| GGCGAT | 60 | 46 | 14 | 1.58E-01 | 0.80 | 0.15 |
| CCTGCG | 130 | 116 | 14 | 3.56E-01 | 0.45 | 0.15 |
| GATCCG | 59 | 45 | 14 | 1.56E-01 | 0.81 | 0.15 |
| GCCCTC | 408 | 394 | 14 | 6.10E-01 | 0.21 | 0.15 |
| CCTTCG | 96 | 82 | 14 | 2.80E-01 | 0.55 | 0.15 |
| CTTCGT | 103 | 89 | 14 | 2.99E-01 | 0.52 | 0.15 |
| CCTGTA | 390 | 376 | 14 | 6.04E-01 | 0.22 | 0.15 |
| AGAGTC | 389 | 375 | 14 | 6.03E-01 | 0.22 | 0.15 |
| CCGAAC | 52 | 38 | 14 | 1.30E-01 | 0.89 | 0.15 |
| TTCGGC | 57 | 43 | 14 | 1.52E-01 | 0.82 | 0.15 |
| ACGGCT | 89 | 75 | 14 | 2.64E-01 | 0.58 | 0.15 |
| CTTAGG | 334 | 320 | 14 | 5.79E-01 | 0.24 | 0.15 |
| CGGACG | 32 | 18 | 14 | 4.48E-02 | 1.35 | 0.15 |
| CGAGGC | 114 | 100 | 14 | 3.33E-01 | 0.48 | 0.15 |
| CGTCCC | 101 | 87 | 14 | 3.02E-01 | 0.52 | 0.15 |
| CGTTTA | 86 | 72 | 14 | 2.60E-01 | 0.58 | 0.15 |
| CAAGAC | 322 | 308 | 14 | 5.74E-01 | 0.24 | 0.15 |
| TCGTCG | 30 | 16 | 14 | 3.82E-02 | 1.42 | 0.15 |
| ATTGCG | 46 | 32 | 14 | 1.12E-01 | 0.95 | 0.15 |
| ATCGGC | 49 | 35 | 14 | 1.26E-01 | 0.90 | 0.15 |
| AACCCT | 378 | 364 | 14 | 6.08E-01 | 0.22 | 0.15 |
| GTCCCT | 462 | 448 | 14 | 6.44E-01 | 0.19 | 0.15 |
| CATGCG | 80 | 66 | 14 | 2.55E-01 | 0.59 | 0.15 |
| TACCGA | 55 | 41 | 14 | 1.61E-01 | 0.79 | 0.15 |
| GTCGGT | 64 | 50 | 14 | 2.01E-01 | 0.70 | 0.15 |
| GGTCCG | 61 | 47 | 14 | 1.89E-01 | 0.72 | 0.14 |
| ATCGGT | 53 | 39 | 14 | 1.55E-01 | 0.81 | 0.14 |
| CGCGGA | 36 | 22 | 14 | 7.42E-02 | 1.13 | 0.14 |
| GGTTAG | 225 | 211 | 14 | 5.15E-01 | 0.29 | 0.14 |
| TGCAAT | 294 | 280 | 14 | 5.72E-01 | 0.24 | 0.14 |
| AGCGCA | 81 | 67 | 14 | 2.67E-01 | 0.57 | 0.14 |
| GTTGCG | 48 | 34 | 14 | 1.36E-01 | 0.87 | 0.14 |
| CGACCG | 29 | 16 | 13 | 4.30E-02 | 1.37 | 0.14 |
| ATAGGG | 198 | 185 | 13 | 4.91E-01 | 0.31 | 0.14 |
| TCCGGC | 74 | 61 | 13 | 2.46E-01 | 0.61 | 0.14 |
| TCCGGA | 82 | 69 | 13 | 2.75E-01 | 0.56 | 0.14 |
| AGGTCG | 64 | 51 | 13 | 2.12E-01 | 0.67 | 0.14 |
| AGCGCT | 107 | 94 | 13 | 3.45E-01 | 0.46 | 0.14 |
| ACCGGT | 55 | 42 | 13 | 1.78E-01 | 0.75 | 0.14 |
| CGTGAT | 80 | 67 | 13 | 2.74E-01 | 0.56 | 0.14 |
| GCGTTG | 72 | 59 | 13 | 2.47E-01 | 0.61 | 0.14 |
| TTTTGG | 592 | 579 | 13 | 7.01E-01 | 0.15 | 0.14 |
| AGCCGA | 91 | 78 | 13 | 3.12E-01 | 0.51 | 0.14 |
| CTCCCG | 142 | 129 | 13 | 4.26E-01 | 0.37 | 0.14 |
| GCGCTT | 82 | 69 | 13 | 2.86E-01 | 0.54 | 0.14 |

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| GATACT | 238 | 225 | 13 | 5.43E-01 | 0.26 | 0.14 |
| GTGCGA | 54 | 41 | 13 | 1.81E-01 | 0.74 | 0.14 |
| GCGACA | 59 | 46 | 13 | 2.03E-01 | 0.69 | 0.14 |
| AACGAT | 65 | 52 | 13 | 2.28E-01 | 0.64 | 0.14 |
| CGCAAC | 40 | 27 | 13 | 1.12E-01 | 0.95 | 0.14 |
| GTACGG | 48 | 35 | 13 | 1.54E-01 | 0.81 | 0.14 |
| TAGCGG | 49 | 36 | 13 | 1.61E-01 | 0.79 | 0.14 |
| TGCTCG | 98 | 85 | 13 | 3.40E-01 | 0.47 | 0.14 |
| CGCTAG | 52 | 39 | 13 | 1.77E-01 | 0.75 | 0.14 |
| GGCAAA | 356 | 343 | 13 | 6.26E-01 | 0.20 | 0.14 |
| AAGGAT | 400 | 387 | 13 | 6.46E-01 | 0.19 | 0.14 |
| CGGGCG | 54 | 41 | 13 | 1.88E-01 | 0.73 | 0.14 |
| CGCACC | 72 | 59 | 13 | 2.62E-01 | 0.58 | 0.14 |
| AGCTAG | 307 | 294 | 13 | 6.01E-01 | 0.22 | 0.14 |
| TGGCAA | 375 | 362 | 13 | 6.37E-01 | 0.20 | 0.14 |
| TCGTTT | 126 | 113 | 13 | 4.09E-01 | 0.39 | 0.14 |
| CGGGAT | 73 | 60 | 13 | 2.68E-01 | 0.57 | 0.14 |
| CAAACG | 88 | 75 | 13 | 3.20E-01 | 0.50 | 0.13 |
| CACGCA | 106 | 93 | 13 | 3.69E-01 | 0.43 | 0.13 |
| TGTATG | 484 | 471 | 13 | 6.82E-01 | 0.17 | 0.13 |
| GCATTC | 290 | 277 | 13 | 5.96E-01 | 0.22 | 0.13 |
| ATACGG | 51 | 38 | 13 | 1.82E-01 | 0.74 | 0.13 |
| AGCACC | 346 | 333 | 13 | 6.28E-01 | 0.20 | 0.13 |
| CGTCGC | 29 | 16 | 13 | 6.14E-02 | 1.21 | 0.13 |
| GCTCGT | 73 | 60 | 13 | 2.75E-01 | 0.56 | 0.13 |
| CGCTGA | 104 | 91 | 13 | 3.68E-01 | 0.43 | 0.13 |
| TCGCCG | 35 | 22 | 13 | 9.72E-02 | 1.01 | 0.13 |
| CTGTTA | 417 | 404 | 13 | 6.61E-01 | 0.18 | 0.13 |
| CGTTGC | 71 | 58 | 13 | 2.71E-01 | 0.57 | 0.13 |
| ACTTGC | 304 | 292 | 12 | 6.10E-01 | 0.22 | 0.13 |
| CGGTTG | 73 | 61 | 12 | 2.81E-01 | 0.55 | 0.13 |
| ACCGCG | 34 | 22 | 12 | 9.55E-02 | 1.02 | 0.13 |
| GGCAAC | 200 | 188 | 12 | 5.33E-01 | 0.27 | 0.13 |
| AGCAAC | 296 | 284 | 12 | 6.10E-01 | 0.21 | 0.13 |
| GTATGA | 248 | 236 | 12 | 5.77E-01 | 0.24 | 0.13 |
| CGTACT | 54 | 42 | 12 | 2.10E-01 | 0.68 | 0.13 |
| CGCCAA | 65 | 53 | 12 | 2.59E-01 | 0.59 | 0.13 |
| AGCCCC | 456 | 444 | 12 | 6.83E-01 | 0.17 | 0.13 |
| CTGATC | 275 | 263 | 12 | 5.98E-01 | 0.22 | 0.13 |
| TTGGCC | 343 | 331 | 12 | 6.38E-01 | 0.20 | 0.13 |
| ACGGTT | 78 | 66 | 12 | 3.08E-01 | 0.51 | 0.13 |
| CTCGTC | 82 | 70 | 12 | 3.23E-01 | 0.49 | 0.13 |
| CCGTCT | 114 | 102 | 12 | 4.09E-01 | 0.39 | 0.13 |
| GATAGA | 257 | 245 | 12 | 5.89E-01 | 0.23 | 0.13 |
| AACGTA | 68 | 56 | 12 | 2.77E-01 | 0.56 | 0.13 |
| TGCGGC | 83 | 71 | 12 | 3.31E-01 | 0.48 | 0.13 |
| CCGTTA | 57 | 45 | 12 | 2.32E-01 | 0.63 | 0.13 |
| CAACGA | 55 | 43 | 12 | 2.23E-01 | 0.65 | 0.13 |
| CGTATG | 61 | 49 | 12 | 2.50E-01 | 0.60 | 0.13 |
| AAACCG | 86 | 74 | 12 | 3.41E-01 | 0.47 | 0.13 |
| CTCGGT | 110 | 98 | 12 | 4.04E-01 | 0.39 | 0.13 |
| CGAGAT | 64 | 52 | 12 | 2.64E-01 | 0.58 | 0.13 |
| GACGTA | 52 | 40 | 12 | 2.11E-01 | 0.68 | 0.13 |
| CGCAAG | 62 | 50 | 12 | 2.57E-01 | 0.59 | 0.13 |

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|---|---|---|---|---|---|---|
| GTCGAA | 42 | 30 | 12 | 1.58E-01 | 0.80 | 0.13 |
| CGAACA | 62 | 50 | 12 | 2.60E-01 | 0.59 | 0.13 |
| GGATTC | 275 | 263 | 12 | 6.08E-01 | 0.22 | 0.13 |
| GTTACG | 49 | 37 | 12 | 2.02E-01 | 0.70 | 0.13 |
| ACCGCA | 74 | 62 | 12 | 3.10E-01 | 0.51 | 0.13 |
| AAGCCA | 598 | 586 | 12 | 7.31E-01 | 0.14 | 0.13 |
| CCTACG | 59 | 47 | 12 | 2.51E-01 | 0.60 | 0.13 |
| CGACGG | 29 | 17 | 12 | 8.21E-02 | 1.09 | 0.13 |
| TCTGCG | 108 | 96 | 12 | 4.09E-01 | 0.39 | 0.13 |
| ACGCGG | 34 | 22 | 12 | 1.16E-01 | 0.93 | 0.12 |
| CGTGTA | 95 | 83 | 12 | 3.78E-01 | 0.42 | 0.12 |
| ACGTCA | 90 | 78 | 12 | 3.66E-01 | 0.44 | 0.12 |
| AAACGA | 97 | 85 | 12 | 3.86E-01 | 0.41 | 0.12 |
| CGTTGA | 68 | 56 | 12 | 2.95E-01 | 0.53 | 0.12 |
| TTTCGG | 73 | 61 | 12 | 3.14E-01 | 0.50 | 0.12 |
| GCGAAT | 43 | 31 | 12 | 1.77E-01 | 0.75 | 0.12 |
| ACAGGC | 407 | 395 | 12 | 6.81E-01 | 0.17 | 0.12 |
| GTCGAC | 35 | 23 | 12 | 1.30E-01 | 0.89 | 0.12 |
| AGGCAA | 407 | 395 | 12 | 6.83E-01 | 0.17 | 0.12 |
| TCCGAC | 54 | 42 | 12 | 2.39E-01 | 0.62 | 0.12 |
| TGTCGC | 71 | 59 | 12 | 3.11E-01 | 0.51 | 0.12 |
| CCGTTC | 89 | 77 | 12 | 3.70E-01 | 0.43 | 0.12 |
| ACCCGT | 76 | 64 | 12 | 3.30E-01 | 0.48 | 0.12 |
| CGAACG | 23 | 11 | 12 | 4.92E-02 | 1.31 | 0.12 |
| CGGCTC | 109 | 97 | 12 | 4.23E-01 | 0.37 | 0.12 |
| GTTTCG | 62 | 50 | 12 | 2.78E-01 | 0.56 | 0.12 |
| CGTCTT | 106 | 94 | 12 | 4.16E-01 | 0.38 | 0.12 |
| GATTCG | 53 | 42 | 11 | 2.37E-01 | 0.63 | 0.12 |
| CGACTA | 37 | 26 | 11 | 1.46E-01 | 0.83 | 0.12 |
| AATTGG | 272 | 261 | 11 | 6.20E-01 | 0.21 | 0.12 |
| TAGTGT | 355 | 344 | 11 | 6.65E-01 | 0.18 | 0.12 |
| GGATTA | 202 | 191 | 11 | 5.65E-01 | 0.25 | 0.12 |
| CAGCCT | 715 | 704 | 11 | 7.62E-01 | 0.12 | 0.12 |
| GACCTT | 348 | 337 | 11 | 6.63E-01 | 0.18 | 0.12 |
| CTGTCA | 583 | 572 | 11 | 7.38E-01 | 0.13 | 0.12 |
| GCTAAG | 287 | 276 | 11 | 6.31E-01 | 0.20 | 0.12 |
| TTGACC | 254 | 243 | 11 | 6.11E-01 | 0.21 | 0.12 |
| CGCCAG | 102 | 91 | 11 | 4.15E-01 | 0.38 | 0.12 |
| GCCATC | 321 | 310 | 11 | 6.53E-01 | 0.18 | 0.12 |
| GCTACG | 51 | 40 | 11 | 2.36E-01 | 0.63 | 0.12 |
| CCGGTT | 69 | 58 | 11 | 3.17E-01 | 0.50 | 0.12 |
| GCACGT | 97 | 86 | 11 | 4.05E-01 | 0.39 | 0.12 |
| GTGCTC | 374 | 363 | 11 | 6.79E-01 | 0.17 | 0.12 |
| ACGCCT | 83 | 72 | 11 | 3.67E-01 | 0.43 | 0.12 |
| CCGATG | 76 | 65 | 11 | 3.45E-01 | 0.46 | 0.12 |
| GGATCC | 233 | 222 | 11 | 6.01E-01 | 0.22 | 0.12 |
| TGGTCC | 342 | 331 | 11 | 6.67E-01 | 0.18 | 0.12 |
| CCCGAT | 59 | 48 | 11 | 2.82E-01 | 0.55 | 0.12 |
| ACCCGG | 91 | 80 | 11 | 3.95E-01 | 0.40 | 0.12 |
| ACTCCC | 315 | 304 | 11 | 6.58E-01 | 0.18 | 0.12 |
| GCAGTA | 271 | 260 | 11 | 6.36E-01 | 0.20 | 0.12 |
| ACGCTA | 50 | 39 | 11 | 2.48E-01 | 0.61 | 0.12 |
| CCCCGT | 114 | 103 | 11 | 4.59E-01 | 0.34 | 0.12 |
| CAGGCT | 620 | 609 | 11 | 7.56E-01 | 0.12 | 0.12 |

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|---|---|---|---|---|---|---|
| CACGAC | 57 | 46 | 11 | 2.85E-01 | 0.55 | 0.12 |
| CCCGCA | 89 | 78 | 11 | 4.01E-01 | 0.40 | 0.12 |
| ACGCAA | 55 | 44 | 11 | 2.77E-01 | 0.56 | 0.11 |
| GTCGTC | 65 | 54 | 11 | 3.22E-01 | 0.49 | 0.11 |
| CGTCTC | 108 | 97 | 11 | 4.51E-01 | 0.35 | 0.11 |
| TTGGCT | 503 | 492 | 11 | 7.33E-01 | 0.13 | 0.11 |
| GCCCAA | 266 | 255 | 11 | 6.39E-01 | 0.19 | 0.11 |
| ACGTTT | 132 | 121 | 11 | 5.02E-01 | 0.30 | 0.11 |
| GGTATG | 215 | 204 | 11 | 6.02E-01 | 0.22 | 0.11 |
| CATCGC | 72 | 61 | 11 | 3.55E-01 | 0.45 | 0.11 |
| CGAGTA | 51 | 40 | 11 | 2.64E-01 | 0.58 | 0.11 |
| GCCGTA | 48 | 37 | 11 | 2.49E-01 | 0.60 | 0.11 |
| GCTATG | 270 | 259 | 11 | 6.44E-01 | 0.19 | 0.11 |
| GACGCG | 31 | 20 | 11 | 1.38E-01 | 0.86 | 0.11 |
| GAAGTC | 350 | 339 | 11 | 6.87E-01 | 0.16 | 0.11 |
| GCGACC | 50 | 39 | 11 | 2.64E-01 | 0.58 | 0.11 |
| ACAAGA | 435 | 425 | 10 | 7.22E-01 | 0.14 | 0.11 |
| CTTGGC | 454 | 444 | 10 | 7.28E-01 | 0.14 | 0.11 |
| AGCGTA | 53 | 43 | 10 | 2.87E-01 | 0.54 | 0.11 |
| TAGATC | 183 | 173 | 10 | 5.82E-01 | 0.23 | 0.11 |
| CTGCTA | 347 | 337 | 10 | 6.92E-01 | 0.16 | 0.11 |
| CTGCAT | 474 | 464 | 10 | 7.36E-01 | 0.13 | 0.11 |
| CGACCA | 56 | 46 | 10 | 3.06E-01 | 0.51 | 0.11 |
| CGGCTT | 99 | 89 | 10 | 4.52E-01 | 0.34 | 0.11 |
| CCAAGA | 476 | 466 | 10 | 7.37E-01 | 0.13 | 0.11 |
| CCAAGC | 379 | 369 | 10 | 7.08E-01 | 0.15 | 0.11 |
| TGTCCG | 90 | 80 | 10 | 4.33E-01 | 0.36 | 0.11 |
| CGGCCC | 96 | 86 | 10 | 4.48E-01 | 0.35 | 0.11 |
| TTCTCG | 99 | 89 | 10 | 4.60E-01 | 0.34 | 0.11 |
| CGAATC | 47 | 37 | 10 | 2.69E-01 | 0.57 | 0.11 |
| CTCGAC | 52 | 42 | 10 | 2.96E-01 | 0.53 | 0.11 |
| TCGAGT | 69 | 59 | 10 | 3.71E-01 | 0.43 | 0.11 |
| TACCGC | 44 | 34 | 10 | 2.54E-01 | 0.60 | 0.11 |
| CGCCAC | 85 | 75 | 10 | 4.26E-01 | 0.37 | 0.11 |
| ACGATC | 45 | 35 | 10 | 2.64E-01 | 0.58 | 0.11 |
| ATCGAA | 54 | 44 | 10 | 3.14E-01 | 0.50 | 0.11 |
| TCTCGA | 73 | 63 | 10 | 3.93E-01 | 0.41 | 0.11 |
| ACGCGT | 28 | 18 | 10 | 1.44E-01 | 0.84 | 0.11 |
| TTGCAG | 436 | 426 | 10 | 7.36E-01 | 0.13 | 0.11 |
| GATCGA | 44 | 34 | 10 | 2.62E-01 | 0.58 | 0.11 |
| TTACGG | 55 | 45 | 10 | 3.23E-01 | 0.49 | 0.10 |
| ACGAAT | 59 | 49 | 10 | 3.42E-01 | 0.47 | 0.10 |
| CCGCTC | 103 | 93 | 10 | 4.81E-01 | 0.32 | 0.10 |
| CACGCT | 105 | 95 | 10 | 4.86E-01 | 0.31 | 0.10 |
| CGGTCC | 75 | 65 | 10 | 4.10E-01 | 0.39 | 0.10 |
| GCGGTT | 63 | 53 | 10 | 3.67E-01 | 0.44 | 0.10 |
| CGCCTA | 49 | 39 | 10 | 3.00E-01 | 0.52 | 0.10 |
| AGATGT | 511 | 501 | 10 | 7.61E-01 | 0.12 | 0.10 |
| GCGTAC | 34 | 24 | 10 | 2.07E-01 | 0.68 | 0.10 |
| GAAACT | 460 | 450 | 10 | 7.50E-01 | 0.13 | 0.10 |
| AACACT | 459 | 449 | 10 | 7.50E-01 | 0.13 | 0.10 |
| GGCGCT | 99 | 89 | 10 | 4.85E-01 | 0.31 | 0.10 |
| ATACCG | 44 | 34 | 10 | 2.80E-01 | 0.55 | 0.10 |
| TAACCG | 49 | 39 | 10 | 3.10E-01 | 0.51 | 0.10 |

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| GTTGAC | 211 | 201 | 10 | 6.39E-01 | 0.19 | 0.10 |
| CGTACC | 44 | 34 | 10 | 2.82E-01 | 0.55 | 0.10 |
| CTTGTA | 382 | 372 | 10 | 7.29E-01 | 0.14 | 0.10 |
| CCCCTT | 458 | 448 | 10 | 7.52E-01 | 0.12 | 0.10 |
| GGTCGG | 68 | 59 | 9 | 3.99E-01 | 0.40 | 0.10 |
| CAATCG | 42 | 33 | 9 | 2.72E-01 | 0.57 | 0.10 |
| CCGTCA | 76 | 67 | 9 | 4.28E-01 | 0.37 | 0.10 |
| GGCACG | 86 | 77 | 9 | 4.59E-01 | 0.34 | 0.10 |
| ATGAGC | 304 | 295 | 9 | 7.00E-01 | 0.15 | 0.10 |
| CCGCAC | 77 | 68 | 9 | 4.34E-01 | 0.36 | 0.10 |
| CTACGG | 54 | 45 | 9 | 3.47E-01 | 0.46 | 0.10 |
| CCACGT | 132 | 123 | 9 | 5.59E-01 | 0.25 | 0.10 |
| TCGAAT | 52 | 43 | 9 | 3.39E-01 | 0.47 | 0.10 |
| CACGTC | 90 | 81 | 9 | 4.77E-01 | 0.32 | 0.10 |
| TAACGG | 52 | 43 | 9 | 3.45E-01 | 0.46 | 0.10 |
| CGTTTC | 115 | 106 | 9 | 5.36E-01 | 0.27 | 0.10 |
| TACGAG | 46 | 37 | 9 | 3.14E-01 | 0.50 | 0.10 |
| CTCGCT | 113 | 104 | 9 | 5.35E-01 | 0.27 | 0.10 |
| GACCAT | 272 | 263 | 9 | 6.93E-01 | 0.16 | 0.10 |
| CGAGTC | 76 | 67 | 9 | 4.46E-01 | 0.35 | 0.10 |
| CGTCAT | 75 | 66 | 9 | 4.44E-01 | 0.35 | 0.10 |
| GGCGTT | 71 | 62 | 9 | 4.32E-01 | 0.36 | 0.10 |
| CGACGA | 21 | 12 | 9 | 1.16E-01 | 0.94 | 0.10 |
| TTCGTC | 60 | 51 | 9 | 3.93E-01 | 0.41 | 0.10 |
| CGTCAC | 77 | 68 | 9 | 4.56E-01 | 0.34 | 0.10 |
| CGTGCG | 41 | 32 | 9 | 2.98E-01 | 0.53 | 0.09 |
| AGTCGT | 65 | 56 | 9 | 4.19E-01 | 0.38 | 0.09 |
| CGACTT | 68 | 59 | 9 | 4.33E-01 | 0.36 | 0.09 |
| TTCGTG | 96 | 87 | 9 | 5.15E-01 | 0.29 | 0.09 |
| CTACGC | 42 | 33 | 9 | 3.10E-01 | 0.51 | 0.09 |
| GCGTAG | 47 | 38 | 9 | 3.41E-01 | 0.47 | 0.09 |
| CCGGTA | 43 | 34 | 9 | 3.18E-01 | 0.50 | 0.09 |
| CGCTTT | 95 | 86 | 9 | 5.16E-01 | 0.29 | 0.09 |
| ATGTTG | 404 | 395 | 9 | 7.58E-01 | 0.12 | 0.09 |
| GCGTTA | 45 | 36 | 9 | 3.38E-01 | 0.47 | 0.09 |
| ACGCAT | 62 | 53 | 9 | 4.22E-01 | 0.38 | 0.09 |
| AGGCGC | 83 | 74 | 9 | 4.93E-01 | 0.31 | 0.09 |
| CTAGAG | 363 | 354 | 9 | 7.48E-01 | 0.13 | 0.09 |
| TACCGT | 62 | 53 | 9 | 4.27E-01 | 0.37 | 0.09 |
| GTACGA | 36 | 27 | 9 | 2.84E-01 | 0.55 | 0.09 |
| TGCGCG | 40 | 31 | 9 | 3.14E-01 | 0.50 | 0.09 |
| ACCGTC | 68 | 60 | 8 | 4.52E-01 | 0.34 | 0.09 |
| TAATCG | 43 | 35 | 8 | 3.37E-01 | 0.47 | 0.09 |
| AATACG | 58 | 50 | 8 | 4.18E-01 | 0.38 | 0.09 |
| ACACGT | 120 | 112 | 8 | 5.81E-01 | 0.24 | 0.09 |
| GCAGTC | 298 | 290 | 8 | 7.29E-01 | 0.14 | 0.09 |
| GCCGAA | 52 | 44 | 8 | 3.94E-01 | 0.40 | 0.09 |
| TCGTTG | 70 | 62 | 8 | 4.68E-01 | 0.33 | 0.09 |
| GACCGC | 57 | 49 | 8 | 4.18E-01 | 0.38 | 0.09 |
| CTTCGC | 68 | 60 | 8 | 4.63E-01 | 0.33 | 0.09 |
| TCGCCA | 77 | 69 | 8 | 4.94E-01 | 0.31 | 0.09 |
| CTTGGT | 461 | 453 | 8 | 7.85E-01 | 0.11 | 0.09 |
| CGACAC | 54 | 46 | 8 | 4.09E-01 | 0.39 | 0.09 |
| CCGAGC | 104 | 96 | 8 | 5.62E-01 | 0.25 | 0.09 |

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| GTACGT | 57 | 49 | 8 | 4.26E-01 | 0.37 | 0.09 |
| CGACGC | 23 | 15 | 8 | 1.85E-01 | 0.73 | 0.09 |
| ACGCGC | 30 | 22 | 8 | 2.60E-01 | 0.59 | 0.09 |
| CATACG | 54 | 46 | 8 | 4.19E-01 | 0.38 | 0.09 |
| CAACGC | 52 | 44 | 8 | 4.12E-01 | 0.38 | 0.09 |
| CGCTTG | 79 | 71 | 8 | 5.14E-01 | 0.29 | 0.08 |
| CGATGT | 72 | 64 | 8 | 4.93E-01 | 0.31 | 0.08 |
| TCAGGC | 385 | 377 | 8 | 7.72E-01 | 0.11 | 0.08 |
| AACGGT | 68 | 60 | 8 | 4.81E-01 | 0.32 | 0.08 |
| AACAGG | 421 | 413 | 8 | 7.83E-01 | 0.11 | 0.08 |
| CTTAGA | 390 | 382 | 8 | 7.76E-01 | 0.11 | 0.08 |
| TAGCCT | 332 | 324 | 8 | 7.58E-01 | 0.12 | 0.08 |
| AAAAGG | 578 | 570 | 8 | 8.17E-01 | 0.09 | 0.08 |
| GGTCGA | 39 | 31 | 8 | 3.48E-01 | 0.46 | 0.08 |
| CTCGCC | 102 | 94 | 8 | 5.75E-01 | 0.24 | 0.08 |
| GCACGA | 56 | 48 | 8 | 4.46E-01 | 0.35 | 0.08 |
| ATTCGC | 40 | 32 | 8 | 3.64E-01 | 0.44 | 0.08 |
| GACTAA | 208 | 200 | 8 | 7.03E-01 | 0.15 | 0.08 |
| CGATGA | 67 | 59 | 8 | 4.97E-01 | 0.30 | 0.08 |
| TCCGTA | 58 | 50 | 8 | 4.64E-01 | 0.33 | 0.08 |
| TGGCGC | 78 | 70 | 8 | 5.34E-01 | 0.27 | 0.08 |
| TCGAAG | 69 | 61 | 8 | 5.09E-01 | 0.29 | 0.08 |
| GTTCGA | 40 | 32 | 8 | 3.77E-01 | 0.42 | 0.08 |
| GTCCGA | 50 | 42 | 8 | 4.35E-01 | 0.36 | 0.08 |
| AACGGC | 57 | 50 | 7 | 4.69E-01 | 0.33 | 0.08 |
| ACGTCC | 66 | 59 | 7 | 5.04E-01 | 0.30 | 0.08 |
| ACGGCG | 27 | 20 | 7 | 2.75E-01 | 0.56 | 0.08 |
| GCGCAC | 66 | 59 | 7 | 5.06E-01 | 0.30 | 0.08 |
| TCGCGT | 21 | 14 | 7 | 2.07E-01 | 0.68 | 0.08 |
| CGGTAT | 44 | 37 | 7 | 4.10E-01 | 0.39 | 0.08 |
| CGAAGC | 81 | 74 | 7 | 5.54E-01 | 0.26 | 0.08 |
| CTGCGA | 75 | 68 | 7 | 5.43E-01 | 0.26 | 0.08 |
| AACACG | 94 | 87 | 7 | 5.89E-01 | 0.23 | 0.08 |
| TCGACG | 17 | 10 | 7 | 1.63E-01 | 0.79 | 0.08 |
| GTGTAA | 324 | 317 | 7 | 7.75E-01 | 0.11 | 0.08 |
| TGCGCC | 71 | 64 | 7 | 5.39E-01 | 0.27 | 0.08 |
| CTATGC | 216 | 209 | 7 | 7.30E-01 | 0.14 | 0.08 |
| CGATCG | 17 | 10 | 7 | 1.70E-01 | 0.77 | 0.08 |
| ATCGTA | 47 | 40 | 7 | 4.46E-01 | 0.35 | 0.08 |
| CGGGTA | 53 | 46 | 7 | 4.75E-01 | 0.32 | 0.08 |
| ATACGC | 39 | 32 | 7 | 3.99E-01 | 0.40 | 0.08 |
| CGCCGG | 39 | 32 | 7 | 3.99E-01 | 0.40 | 0.08 |
| GCGGTC | 53 | 46 | 7 | 4.77E-01 | 0.32 | 0.07 |
| AACCGT | 72 | 65 | 7 | 5.46E-01 | 0.26 | 0.07 |
| CACGCG | 38 | 31 | 7 | 3.95E-01 | 0.40 | 0.07 |
| CCGTAC | 43 | 36 | 7 | 4.27E-01 | 0.37 | 0.07 |
| GCGTAT | 43 | 36 | 7 | 4.30E-01 | 0.37 | 0.07 |
| TACGCT | 47 | 40 | 7 | 4.52E-01 | 0.34 | 0.07 |
| CGCATA | 40 | 33 | 7 | 4.12E-01 | 0.38 | 0.07 |
| GATCCC | 213 | 206 | 7 | 7.32E-01 | 0.14 | 0.07 |
| GTGCAT | 333 | 326 | 7 | 7.85E-01 | 0.10 | 0.07 |
| CGATCC | 49 | 42 | 7 | 4.64E-01 | 0.33 | 0.07 |
| GTGCCA | 368 | 361 | 7 | 7.96E-01 | 0.10 | 0.07 |
| GCCGCG | 46 | 39 | 7 | 4.50E-01 | 0.35 | 0.07 |

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|---|---|---|---|---|---|---|
| TAGCCG | 52 | 45 | 7 | 4.79E-01 | 0.32 | 0.07 |
| ATGACT | 379 | 372 | 7 | 7.99E-01 | 0.10 | 0.07 |
| CGTCGG | 26 | 19 | 7 | 2.99E-01 | 0.52 | 0.07 |
| CATTCG | 68 | 61 | 7 | 5.45E-01 | 0.26 | 0.07 |
| CCCTTC | 556 | 549 | 7 | 8.38E-01 | 0.08 | 0.07 |
| AGTGAA | 485 | 478 | 7 | 8.26E-01 | 0.08 | 0.07 |
| TAGGCG | 45 | 38 | 7 | 4.57E-01 | 0.34 | 0.07 |
| TTATCG | 44 | 37 | 7 | 4.51E-01 | 0.35 | 0.07 |
| GTGCGC | 76 | 69 | 7 | 5.73E-01 | 0.24 | 0.07 |
| CGTCGA | 17 | 10 | 7 | 1.94E-01 | 0.71 | 0.07 |
| ACCCGC | 66 | 59 | 7 | 5.45E-01 | 0.26 | 0.07 |
| CGATAG | 38 | 31 | 7 | 4.17E-01 | 0.38 | 0.07 |
| CCTCCT | 717 | 710 | 7 | 8.58E-01 | 0.07 | 0.07 |
| GCCCGC | 93 | 86 | 7 | 6.15E-01 | 0.21 | 0.07 |
| CCGACC | 67 | 60 | 7 | 5.50E-01 | 0.26 | 0.07 |
| GGTACC | 189 | 182 | 7 | 7.28E-01 | 0.14 | 0.07 |
| CGCTAC | 41 | 34 | 7 | 4.40E-01 | 0.36 | 0.07 |
| CGCGAC | 20 | 13 | 7 | 2.49E-01 | 0.60 | 0.07 |
| GCACCC | 262 | 255 | 7 | 7.70E-01 | 0.11 | 0.07 |
| CGTTAA | 56 | 49 | 7 | 5.20E-01 | 0.28 | 0.07 |
| ACTAGG | 222 | 215 | 7 | 7.52E-01 | 0.12 | 0.07 |
| CTACCG | 52 | 45 | 7 | 5.04E-01 | 0.30 | 0.07 |
| CCTTAC | 263 | 256 | 7 | 7.73E-01 | 0.11 | 0.07 |
| ACGCGA | 19 | 12 | 7 | 2.43E-01 | 0.61 | 0.07 |
| GATGTC | 313 | 306 | 7 | 7.93E-01 | 0.10 | 0.07 |
| GCGACG | 22 | 15 | 7 | 2.86E-01 | 0.54 | 0.07 |
| GCGCTC | 84 | 77 | 7 | 6.08E-01 | 0.22 | 0.07 |
| GAACAT | 376 | 369 | 7 | 8.12E-01 | 0.09 | 0.07 |
| TTCACG | 93 | 87 | 6 | 6.29E-01 | 0.20 | 0.07 |
| TAACTG | 361 | 355 | 6 | 8.09E-01 | 0.09 | 0.07 |
| CTGCCA | 608 | 602 | 6 | 8.53E-01 | 0.07 | 0.07 |
| CGGTAC | 43 | 37 | 6 | 4.70E-01 | 0.33 | 0.07 |
| CGTTCG | 20 | 14 | 6 | 2.68E-01 | 0.57 | 0.07 |
| AACGCC | 57 | 51 | 6 | 5.37E-01 | 0.27 | 0.07 |
| AAGAGT | 434 | 428 | 6 | 8.27E-01 | 0.08 | 0.07 |
| CGAAAA | 58 | 52 | 6 | 5.49E-01 | 0.26 | 0.07 |
| TTAGCG | 50 | 44 | 6 | 5.17E-01 | 0.29 | 0.07 |
| ATGCCG | 62 | 56 | 6 | 5.70E-01 | 0.24 | 0.07 |
| AAATGG | 548 | 542 | 6 | 8.52E-01 | 0.07 | 0.07 |
| TTCGCC | 51 | 45 | 6 | 5.31E-01 | 0.28 | 0.07 |
| AGCGAT | 63 | 57 | 6 | 5.75E-01 | 0.24 | 0.07 |
| CAAAGA | 556 | 550 | 6 | 8.54E-01 | 0.07 | 0.06 |
| TCACGT | 113 | 107 | 6 | 6.79E-01 | 0.17 | 0.06 |
| CGACGT | 20 | 14 | 6 | 2.94E-01 | 0.53 | 0.06 |
| CTCAGA | 654 | 648 | 6 | 8.66E-01 | 0.06 | 0.06 |
| TAGGTG | 269 | 263 | 6 | 7.91E-01 | 0.10 | 0.06 |
| CCTTCC | 741 | 735 | 6 | 8.74E-01 | 0.06 | 0.06 |
| TAACGT | 72 | 66 | 6 | 6.05E-01 | 0.22 | 0.06 |
| CCGCAT | 56 | 50 | 6 | 5.56E-01 | 0.25 | 0.06 |
| CGAGCG | 36 | 30 | 6 | 4.56E-01 | 0.34 | 0.06 |
| GGCTTC | 469 | 463 | 6 | 8.43E-01 | 0.07 | 0.06 |
| CGATAC | 32 | 26 | 6 | 4.28E-01 | 0.37 | 0.06 |
| TCAACG | 51 | 45 | 6 | 5.38E-01 | 0.27 | 0.06 |
| GCGCTA | 41 | 35 | 6 | 4.90E-01 | 0.31 | 0.06 |

| | | | | | | |
|---|---|---|---|---|---|---|
| CGCTAT | 39 | 33 | 6 | 4.82E-01 | 0.32 | 0.06 |
| CCTGGT | 482 | 476 | 6 | 8.48E-01 | 0.07 | 0.06 |
| CGCGGC | 43 | 37 | 6 | 5.08E-01 | 0.29 | 0.06 |
| ACGTCG | 20 | 14 | 6 | 3.12E-01 | 0.51 | 0.06 |
| CGAAAG | 69 | 63 | 6 | 6.08E-01 | 0.22 | 0.06 |
| CCCGAG | 144 | 138 | 6 | 7.28E-01 | 0.14 | 0.06 |
| CACGAG | 96 | 90 | 6 | 6.73E-01 | 0.17 | 0.06 |
| TCATCG | 70 | 64 | 6 | 6.19E-01 | 0.21 | 0.06 |
| CGCCCG | 44 | 38 | 6 | 5.26E-01 | 0.28 | 0.06 |
| GGGTTA | 213 | 207 | 6 | 7.81E-01 | 0.11 | 0.06 |
| CCACCT | 511 | 505 | 6 | 8.59E-01 | 0.07 | 0.06 |
| GCCTTT | 567 | 561 | 6 | 8.66E-01 | 0.06 | 0.06 |
| ACGACG | 21 | 15 | 6 | 3.47E-01 | 0.46 | 0.06 |
| TACTGC | 271 | 265 | 6 | 8.08E-01 | 0.09 | 0.06 |
| TCGTGC | 69 | 63 | 6 | 6.25E-01 | 0.20 | 0.06 |
| AATCGC | 43 | 37 | 6 | 5.31E-01 | 0.27 | 0.06 |
| TCGCAA | 38 | 32 | 6 | 5.08E-01 | 0.29 | 0.06 |
| AGTTCG | 49 | 43 | 6 | 5.64E-01 | 0.25 | 0.06 |
| ACACGC | 85 | 79 | 6 | 6.66E-01 | 0.18 | 0.06 |
| TGAGGT | 432 | 427 | 5 | 8.51E-01 | 0.07 | 0.06 |
| GAATCT | 335 | 330 | 5 | 8.31E-01 | 0.08 | 0.06 |
| AAACGT | 116 | 111 | 5 | 7.15E-01 | 0.15 | 0.06 |
| ATAGCG | 41 | 36 | 5 | 5.37E-01 | 0.27 | 0.06 |
| CCTTGA | 410 | 405 | 5 | 8.51E-01 | 0.07 | 0.06 |
| ATCCGA | 50 | 45 | 5 | 5.85E-01 | 0.23 | 0.06 |
| CACGAT | 62 | 57 | 5 | 6.26E-01 | 0.20 | 0.06 |
| AGCCCA | 508 | 503 | 5 | 8.68E-01 | 0.06 | 0.06 |
| ATCGAG | 58 | 53 | 5 | 6.18E-01 | 0.21 | 0.06 |
| CGACAT | 49 | 44 | 5 | 5.87E-01 | 0.23 | 0.06 |
| AAGTGA | 478 | 473 | 5 | 8.65E-01 | 0.06 | 0.06 |
| CGTAAG | 52 | 47 | 5 | 6.00E-01 | 0.22 | 0.06 |
| ATGTGC | 371 | 366 | 5 | 8.48E-01 | 0.07 | 0.06 |
| CGCTTA | 44 | 39 | 5 | 5.70E-01 | 0.24 | 0.05 |
| CGCCCA | 95 | 90 | 5 | 7.05E-01 | 0.15 | 0.05 |
| GACACA | 440 | 435 | 5 | 8.62E-01 | 0.06 | 0.05 |
| GCGCAA | 36 | 31 | 5 | 5.33E-01 | 0.27 | 0.05 |
| TCGGTA | 48 | 43 | 5 | 5.93E-01 | 0.23 | 0.05 |
| CGCGTT | 20 | 15 | 5 | 3.90E-01 | 0.41 | 0.05 |
| GGTGCG | 65 | 60 | 5 | 6.52E-01 | 0.19 | 0.05 |
| CGCCGC | 51 | 46 | 5 | 6.11E-01 | 0.21 | 0.05 |
| CCGCGG | 46 | 41 | 5 | 5.94E-01 | 0.23 | 0.05 |
| CCGTCC | 97 | 92 | 5 | 7.19E-01 | 0.14 | 0.05 |
| CCGTTT | 110 | 105 | 5 | 7.38E-01 | 0.13 | 0.05 |
| CGATTG | 45 | 40 | 5 | 5.98E-01 | 0.22 | 0.05 |
| ATCCGT | 64 | 59 | 5 | 6.61E-01 | 0.18 | 0.05 |
| CCGATC | 39 | 34 | 5 | 5.72E-01 | 0.24 | 0.05 |
| TACGAT | 42 | 37 | 5 | 5.88E-01 | 0.23 | 0.05 |
| TCGCTA | 41 | 36 | 5 | 5.86E-01 | 0.23 | 0.05 |
| CGCGAT | 15 | 10 | 5 | 3.41E-01 | 0.47 | 0.05 |
| ACAGCA | 580 | 575 | 5 | 8.89E-01 | 0.05 | 0.05 |
| CGGTCG | 19 | 14 | 5 | 4.12E-01 | 0.39 | 0.05 |
| TCTTCG | 83 | 78 | 5 | 7.09E-01 | 0.15 | 0.05 |
| TAGACC | 189 | 184 | 5 | 8.07E-01 | 0.09 | 0.05 |
| GCGTCG | 22 | 17 | 5 | 4.52E-01 | 0.34 | 0.05 |

| | | | | | | |
|---|---|---|---|---|---|---|
| TCCCGC | 91 | 86 | 5 | 7.24E-01 | 0.14 | 0.05 |
| TTCGCA | 50 | 45 | 5 | 6.31E-01 | 0.20 | 0.05 |
| GTATCG | 35 | 30 | 5 | 5.63E-01 | 0.25 | 0.05 |
| GCTCTC | 439 | 434 | 5 | 8.74E-01 | 0.06 | 0.05 |
| TCGCCC | 70 | 65 | 5 | 6.91E-01 | 0.16 | 0.05 |
| GCAAGT | 273 | 268 | 5 | 8.44E-01 | 0.07 | 0.05 |
| TAAGCG | 45 | 40 | 5 | 6.24E-01 | 0.20 | 0.05 |
| ACCCGA | 70 | 65 | 5 | 6.97E-01 | 0.16 | 0.05 |
| TTGCGC | 41 | 36 | 5 | 6.09E-01 | 0.22 | 0.05 |
| CCGTAT | 47 | 42 | 5 | 6.34E-01 | 0.20 | 0.05 |
| TCGACA | 47 | 43 | 4 | 6.37E-01 | 0.20 | 0.05 |
| CATGGC | 396 | 392 | 4 | 8.75E-01 | 0.06 | 0.05 |
| ATCGCT | 64 | 60 | 4 | 6.93E-01 | 0.16 | 0.05 |
| AGCGCG | 33 | 29 | 4 | 5.79E-01 | 0.24 | 0.05 |
| CTGAGT | 532 | 528 | 4 | 8.94E-01 | 0.05 | 0.05 |
| TCGACC | 37 | 33 | 4 | 6.02E-01 | 0.22 | 0.05 |
| CTGTTT | 815 | 811 | 4 | 9.15E-01 | 0.04 | 0.05 |
| TACGGT | 48 | 44 | 4 | 6.53E-01 | 0.19 | 0.05 |
| TCGCAT | 45 | 41 | 4 | 6.43E-01 | 0.19 | 0.05 |
| GGCATA | 184 | 180 | 4 | 8.23E-01 | 0.08 | 0.05 |
| ACAAGC | 311 | 307 | 4 | 8.64E-01 | 0.06 | 0.05 |
| AGACAA | 466 | 462 | 4 | 8.91E-01 | 0.05 | 0.04 |
| GGCGAA | 44 | 40 | 4 | 6.51E-01 | 0.19 | 0.04 |
| CGATCT | 48 | 44 | 4 | 6.72E-01 | 0.17 | 0.04 |
| CCGCGA | 22 | 18 | 4 | 5.20E-01 | 0.28 | 0.04 |
| CGAAGT | 58 | 54 | 4 | 7.04E-01 | 0.15 | 0.04 |
| CGGCGA | 23 | 19 | 4 | 5.37E-01 | 0.27 | 0.04 |
| GGGTAT | 194 | 190 | 4 | 8.42E-01 | 0.07 | 0.04 |
| TCAGCG | 96 | 92 | 4 | 7.76E-01 | 0.11 | 0.04 |
| CTGGTT | 462 | 458 | 4 | 8.99E-01 | 0.05 | 0.04 |
| CTGTTC | 534 | 530 | 4 | 9.08E-01 | 0.04 | 0.04 |
| AGTCGC | 51 | 47 | 4 | 7.06E-01 | 0.15 | 0.04 |
| CCGATA | 31 | 27 | 4 | 6.25E-01 | 0.20 | 0.04 |
| CCAAAG | 524 | 520 | 4 | 9.08E-01 | 0.04 | 0.04 |
| GTCGCG | 17 | 13 | 4 | 4.98E-01 | 0.30 | 0.04 |
| TTGGCG | 63 | 59 | 4 | 7.40E-01 | 0.13 | 0.04 |
| CCCGCG | 42 | 38 | 4 | 6.86E-01 | 0.16 | 0.04 |
| TACCGG | 37 | 33 | 4 | 6.72E-01 | 0.17 | 0.04 |
| GCGTAA | 31 | 27 | 4 | 6.45E-01 | 0.19 | 0.04 |
| ACGTCT | 88 | 84 | 4 | 7.89E-01 | 0.10 | 0.04 |
| TCGATC | 36 | 32 | 4 | 6.71E-01 | 0.17 | 0.04 |
| GATCGC | 35 | 31 | 4 | 6.66E-01 | 0.18 | 0.04 |
| TACGAA | 46 | 43 | 3 | 7.12E-01 | 0.15 | 0.04 |
| AAAGAC | 468 | 465 | 3 | 9.11E-01 | 0.04 | 0.04 |
| CCGCGT | 28 | 25 | 3 | 6.38E-01 | 0.19 | 0.04 |
| CGTACG | 14 | 11 | 3 | 4.93E-01 | 0.31 | 0.04 |
| TTCGCG | 14 | 11 | 3 | 4.97E-01 | 0.30 | 0.04 |
| TACTTG | 341 | 338 | 3 | 8.97E-01 | 0.05 | 0.04 |
| TCGACT | 43 | 40 | 3 | 7.12E-01 | 0.15 | 0.04 |
| CCGAAT | 54 | 51 | 3 | 7.44E-01 | 0.13 | 0.04 |
| CGAATT | 46 | 43 | 3 | 7.23E-01 | 0.14 | 0.04 |
| GGTACG | 36 | 33 | 3 | 6.89E-01 | 0.16 | 0.04 |
| TATCGG | 31 | 28 | 3 | 6.68E-01 | 0.18 | 0.03 |
| AGAGTA | 327 | 324 | 3 | 8.98E-01 | 0.05 | 0.03 |

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|---|---|---|---|---|---|---|
| TCCGAT | 49 | 46 | 3 | 7.41E-01 | 0.13 | 0.03 |
| CACGTA | 71 | 68 | 3 | 7.86E-01 | 0.10 | 0.03 |
| CGCGTA | 12 | 9 | 3 | 4.95E-01 | 0.31 | 0.03 |
| CGAAAC | 44 | 41 | 3 | 7.38E-01 | 0.13 | 0.03 |
| AGTGCG | 65 | 62 | 3 | 7.89E-01 | 0.10 | 0.03 |
| TTACGC | 32 | 29 | 3 | 6.99E-01 | 0.16 | 0.03 |
| ACTTGT | 429 | 426 | 3 | 9.18E-01 | 0.04 | 0.03 |
| CGCATC | 53 | 50 | 3 | 7.68E-01 | 0.11 | 0.03 |
| AATTCG | 44 | 41 | 3 | 7.47E-01 | 0.13 | 0.03 |
| CGCGAA | 14 | 11 | 3 | 5.60E-01 | 0.25 | 0.03 |
| ACTCAG | 486 | 483 | 3 | 9.26E-01 | 0.03 | 0.03 |
| CGTAAA | 51 | 48 | 3 | 7.72E-01 | 0.11 | 0.03 |
| CCGCTA | 38 | 35 | 3 | 7.39E-01 | 0.13 | 0.03 |
| CGGCAC | 63 | 60 | 3 | 7.98E-01 | 0.10 | 0.03 |
| CAAGAA | 531 | 528 | 3 | 9.31E-01 | 0.03 | 0.03 |
| TTCCGA | 72 | 69 | 3 | 8.15E-01 | 0.09 | 0.03 |
| GTTCCG | 59 | 56 | 3 | 7.98E-01 | 0.10 | 0.03 |
| CGCGCA | 30 | 27 | 3 | 7.21E-01 | 0.14 | 0.03 |
| CGCCGT | 26 | 23 | 3 | 7.07E-01 | 0.15 | 0.03 |
| ACCCCA | 471 | 468 | 3 | 9.32E-01 | 0.03 | 0.03 |
| GTTGCC | 250 | 247 | 3 | 9.08E-01 | 0.04 | 0.03 |
| CACGAA | 70 | 67 | 3 | 8.27E-01 | 0.08 | 0.03 |
| GACTCA | 323 | 320 | 3 | 9.20E-01 | 0.04 | 0.03 |
| GTAGCG | 42 | 39 | 3 | 7.80E-01 | 0.11 | 0.03 |
| GGCACC | 263 | 260 | 3 | 9.13E-01 | 0.04 | 0.03 |
| ACGCCC | 70 | 68 | 2 | 8.33E-01 | 0.08 | 0.03 |
| CGGATA | 33 | 31 | 2 | 7.60E-01 | 0.12 | 0.03 |
| CGTTAC | 43 | 41 | 2 | 7.91E-01 | 0.10 | 0.03 |
| CAACGG | 52 | 50 | 2 | 8.11E-01 | 0.09 | 0.03 |
| CATCGT | 82 | 80 | 2 | 8.51E-01 | 0.07 | 0.03 |
| CGGCGT | 24 | 22 | 2 | 7.27E-01 | 0.14 | 0.02 |
| TCGCGA | 11 | 9 | 2 | 5.95E-01 | 0.23 | 0.02 |
| ATTCCG | 55 | 53 | 2 | 8.26E-01 | 0.08 | 0.02 |
| ACCATG | 388 | 386 | 2 | 9.35E-01 | 0.03 | 0.02 |
| CCATCG | 77 | 75 | 2 | 8.54E-01 | 0.07 | 0.02 |
| TCCGCA | 63 | 61 | 2 | 8.39E-01 | 0.08 | 0.02 |
| AGCAGT | 500 | 498 | 2 | 9.44E-01 | 0.03 | 0.02 |
| CAACCG | 50 | 48 | 2 | 8.25E-01 | 0.08 | 0.02 |
| GGTAGT | 191 | 189 | 2 | 9.11E-01 | 0.04 | 0.02 |
| ACGAGT | 56 | 54 | 2 | 8.35E-01 | 0.08 | 0.02 |
| GGTACT | 200 | 198 | 2 | 9.15E-01 | 0.04 | 0.02 |
| TTGGCA | 392 | 390 | 2 | 9.40E-01 | 0.03 | 0.02 |
| TAGCGA | 40 | 38 | 2 | 8.15E-01 | 0.09 | 0.02 |
| GCGCCG | 36 | 34 | 2 | 8.07E-01 | 0.09 | 0.02 |
| CGGGTC | 71 | 69 | 2 | 8.64E-01 | 0.06 | 0.02 |
| CTGGTA | 300 | 298 | 2 | 9.35E-01 | 0.03 | 0.02 |
| GCGAAA | 36 | 34 | 2 | 8.17E-01 | 0.09 | 0.02 |
| TATCGA | 34 | 32 | 2 | 8.16E-01 | 0.09 | 0.02 |
| GCCTAC | 182 | 180 | 2 | 9.22E-01 | 0.04 | 0.02 |
| CTAGCG | 40 | 38 | 2 | 8.33E-01 | 0.08 | 0.02 |
| CCTCCG | 129 | 127 | 2 | 9.08E-01 | 0.04 | 0.02 |
| CCCGTC | 82 | 80 | 2 | 8.85E-01 | 0.05 | 0.02 |
| CGCACG | 30 | 28 | 2 | 8.13E-01 | 0.09 | 0.02 |
| TCCCGT | 100 | 98 | 2 | 8.98E-01 | 0.05 | 0.02 |

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|---|---|---|---|---|---|---|
| GTAACC | 168 | 166 | 2 | 9.22E-01 | 0.04 | 0.02 |
| ACGTTA | 63 | 61 | 2 | 8.73E-01 | 0.06 | 0.02 |
| TGCAAC | 199 | 197 | 2 | 9.30E-01 | 0.03 | 0.02 |
| GTAATC | 145 | 143 | 2 | 9.19E-01 | 0.04 | 0.02 |
| TGCGTA | 46 | 44 | 2 | 8.56E-01 | 0.07 | 0.02 |
| AGTACG | 38 | 36 | 2 | 8.46E-01 | 0.07 | 0.02 |
| CGGCTA | 40 | 38 | 2 | 8.52E-01 | 0.07 | 0.02 |
| CTCGAT | 52 | 50 | 2 | 8.70E-01 | 0.06 | 0.02 |
| CGCTCG | 30 | 28 | 2 | 8.31E-01 | 0.08 | 0.02 |
| TACCTG | 370 | 368 | 2 | 9.52E-01 | 0.02 | 0.02 |
| GTACCG | 40 | 38 | 2 | 8.55E-01 | 0.07 | 0.02 |
| CGTAAC | 35 | 33 | 2 | 8.47E-01 | 0.07 | 0.02 |
| GAGTCT | 393 | 391 | 2 | 9.57E-01 | 0.02 | 0.02 |
| AGCAAT | 335 | 333 | 2 | 9.53E-01 | 0.02 | 0.02 |
| GCCCAC | 345 | 343 | 2 | 9.54E-01 | 0.02 | 0.02 |
| CCCCCT | 390 | 389 | 1 | 9.58E-01 | 0.02 | 0.02 |
| TCGTAA | 43 | 42 | 1 | 8.73E-01 | 0.06 | 0.02 |
| ATGCGT | 60 | 59 | 1 | 8.94E-01 | 0.05 | 0.02 |
| CTACTG | 337 | 336 | 1 | 9.56E-01 | 0.02 | 0.02 |
| CCGCCG | 45 | 44 | 1 | 8.81E-01 | 0.05 | 0.01 |
| GACTTT | 468 | 467 | 1 | 9.63E-01 | 0.02 | 0.01 |
| GGCCTA | 192 | 191 | 1 | 9.43E-01 | 0.03 | 0.01 |
| CCCGAC | 67 | 66 | 1 | 9.04E-01 | 0.04 | 0.01 |
| GCCAAA | 342 | 341 | 1 | 9.58E-01 | 0.02 | 0.01 |
| CCCGAA | 69 | 68 | 1 | 9.09E-01 | 0.04 | 0.01 |
| CGCTCC | 98 | 97 | 1 | 9.27E-01 | 0.03 | 0.01 |
| CGTCGT | 21 | 20 | 1 | 8.41E-01 | 0.08 | 0.01 |
| ACGGTA | 48 | 47 | 1 | 8.98E-01 | 0.05 | 0.01 |
| GACAAT | 246 | 245 | 1 | 9.56E-01 | 0.02 | 0.01 |
| TCGGCG | 20 | 19 | 1 | 8.47E-01 | 0.07 | 0.01 |
| CGCGCG | 37 | 36 | 1 | 8.89E-01 | 0.05 | 0.01 |
| CCCGTA | 41 | 40 | 1 | 8.96E-01 | 0.05 | 0.01 |
| TACGTG | 76 | 75 | 1 | 9.25E-01 | 0.03 | 0.01 |
| ACATCG | 62 | 61 | 1 | 9.17E-01 | 0.04 | 0.01 |
| CCCGCC | 153 | 152 | 1 | 9.49E-01 | 0.02 | 0.01 |
| GGTACA | 231 | 230 | 1 | 9.59E-01 | 0.02 | 0.01 |
| GCGATT | 40 | 39 | 1 | 9.04E-01 | 0.04 | 0.01 |
| CCGTCG | 19 | 18 | 1 | 8.61E-01 | 0.06 | 0.01 |
| CAACGT | 60 | 59 | 1 | 9.24E-01 | 0.03 | 0.01 |
| ACCGAT | 39 | 38 | 1 | 9.06E-01 | 0.04 | 0.01 |
| GCTAGC | 198 | 197 | 1 | 9.59E-01 | 0.02 | 0.01 |
| TAGCGT | 49 | 48 | 1 | 9.18E-01 | 0.04 | 0.01 |
| TCTGCA | 586 | 585 | 1 | 9.77E-01 | 0.01 | 0.01 |
| TGGCTT | 667 | 666 | 1 | 9.78E-01 | 0.01 | 0.01 |
| CACCTC | 440 | 439 | 1 | 9.74E-01 | 0.01 | 0.01 |
| TGTGTC | 591 | 590 | 1 | 9.78E-01 | 0.01 | 0.01 |
| GCACTA | 172 | 171 | 1 | 9.60E-01 | 0.02 | 0.01 |
| CCCACG | 127 | 126 | 1 | 9.54E-01 | 0.02 | 0.01 |
| TCTCCG | 101 | 100 | 1 | 9.48E-01 | 0.02 | 0.01 |
| CGCATT | 44 | 43 | 1 | 9.24E-01 | 0.03 | 0.01 |
| CCAACG | 56 | 55 | 1 | 9.33E-01 | 0.03 | 0.01 |
| CTGTCT | 773 | 772 | 1 | 9.84E-01 | 0.01 | 0.01 |
| GATATG | 212 | 211 | 1 | 9.69E-01 | 0.01 | 0.01 |
| GTCCAG | 395 | 394 | 1 | 9.79E-01 | 0.01 | 0.01 |

| | | | | | | |
|---|---|---|---|---|---|---|
| CATCGA | 59 | 58 | 1 | 9.46E-01 | 0.02 | 0.01 |
| GCGCGA | 17 | 16 | 1 | 9.02E-01 | 0.04 | 0.01 |
| TCCTGC | 579 | 578 | 1 | 9.84E-01 | 0.01 | 0.01 |
| TCCGTC | 75 | 74 | 1 | 9.56E-01 | 0.02 | 0.01 |
| CGTCCG | 23 | 22 | 1 | 9.21E-01 | 0.04 | 0.01 |
| CGTTCA | 75 | 74 | 1 | 9.60E-01 | 0.02 | 0.01 |
| CCGCGC | 38 | 37 | 1 | 9.47E-01 | 0.02 | 0.01 |
| TCGATA | 32 | 31 | 1 | 9.45E-01 | 0.02 | 0.01 |
| TCGGCC | 67 | 66 | 1 | 9.63E-01 | 0.02 | 0.01 |
| AATCGA | 44 | 43 | 1 | 9.57E-01 | 0.02 | 0.01 |

**Table S2. Putative miR-128 RISC-associated target genes in adult Camk2a-neurons.**

| Gene name | # Reads in cluster | Genomic position | Strand | Targeting miR | Seed type |
|---|---|---|---|---|---|
| *Ogfrl1* | 17 | *1:23368497-23368505* | - | mmu-miR-128-3p | 8mer |
| *Pgap1* | 15 | *1:54474488-54474496* | - | mmu-miR-128-3p | 8mer |
| *Fam126b* | 81 | *1:58529358-58529366* | - | mmu-miR-128-3p | 8mer |
| *Plekhm3* | 12 | *1:64793596-64793604* | - | mmu-miR-128-3p | 8mer |
| *Plekhm3* | 12 | *1:64793635-64793643* | - | mmu-miR-128-3p | 8mer |
| *Unc80* | 32 | *1:66698909-66698917* | + | mmu-miR-128-3p | 8mer |
| *Irs1* | 10 | *1:82237388-82237396* | - | mmu-miR-128-3p | 8mer |
| *Nfasc* | 23 | *1:132567868-132567876* | - | mmu-miR-128-3p | 8mer |
| *7530420F21Rik* | 31 | *1:150076780-150076788* | - | mmu-miR-128-3p | 8mer |
| *Swt1* | 11 | *1:151368199-151368207* | - | mmu-miR-128-3p | 8mer |
| *Lamc1* | 11 | *1:153220197-153220205* | - | mmu-miR-128-3p | 8mer |
| *Rgs8* | 81 | *1:153694067-153694075* | + | mmu-miR-128-3p | 8mer |
| *Ildr2* | 13 | *1:166315229-166315237* | + | mmu-miR-128-3p | 8mer |
| *Kcnk2* | 15 | *1:189208581-189208589* | - | mmu-miR-128-3p | 8mer |
| *Tug1* | 12 | *11:3645366-3645374* | - | mmu-miR-128-3p | 8mer |
| *Pex13* | 28 | *11:23648703-23648711* | - | mmu-miR-128-3p | 8mer |
| *Erlec1* | 227 | *11:30929829-30929837* | - | mmu-miR-128-3p | 8mer |
| *Sec24a* | 14 | *11:51695032-51695040* | - | mmu-miR-128-3p | 8mer |
| *Ulk2* | 14 | *11:61775839-61775847* | - | mmu-miR-128-3p | 8mer |
| *Adora2b* | 14 | *11:62265795-62265803* | + | mmu-miR-128-3p | 8mer |
| *Dvl2* | 28 | *11:70009708-70009716* | + | mmu-miR-128-3p | 8mer |
| *1700071K01Rik* | 10 | *11:81572558-81572566* | - | mmu-miR-128-3p | 8mer |
| *Fbxl20* | 16 | *11:98085926-98085934* | - | mmu-miR-128-3p | 8mer |
| *Msl1* | 17 | *11:98807582-98807590* | + | mmu-miR-128-3p | 8mer |
| *Casc3* | 366 | *11:98833664-98833672* | + | mmu-miR-128-3p | 8mer |
| *Ccdc47* | 41 | *11:106200261-106200269* | - | mmu-miR-128-3p | 8mer |
| *H3f3b* | 14 | *11:116023028-116023036* | - | mmu-miR-128-3p | 8mer |
| *Kidins220* | 14 | *12:25060225-25060233* | + | mmu-miR-128-3p | 8mer |
| *Rgs6* | 22 | *12:83158068-83158076* | + | mmu-miR-128-3p | 8mer |
| *Dicer1* | 10 | *12:104690348-104690356* | - | mmu-miR-128-3p | 8mer |
| *Clmn* | 10 | *12:104766958-104766966* | - | mmu-miR-128-3p | 8mer |
| *Dlk1* | 22 | *12:109460801-109460809* | + | mmu-miR-128-3p | 8mer |
| *Tmem179* | 27 | *12:112500948-112500956* | - | mmu-miR-128-3p | 8mer |
| *Slc22a23* | 39 | *13:34179265-34179273* | - | mmu-miR-128-3p | 8mer |
| *Mtx3* | 22 | *13:92855392-92855400* | + | mmu-miR-128-3p | 8mer |
| *Pde8b* | 39 | *13:95026091-95026099* | - | mmu-miR-128-3p | 8mer |
| *Plk2* | 19 | *13:110400282-110400290* | + | mmu-miR-128-3p | 8mer |
| *Snx18* | 13 | *13:113593615-113593623* | - | mmu-miR-128-3p | 8mer |
| *Ercc6* | 17 | *14:32577321-32577329* | + | mmu-miR-128-3p | 8mer |
| *Nupl1* | 11 | *14:60218777-60218785* | - | mmu-miR-128-3p | 8mer |
| *Cct5* | 40 | *15:31590905-31590913* | - | mmu-miR-128-3p | 8mer |
| *Csdc2* | 11 | *15:81950592-81950600* | + | mmu-miR-128-3p | 8mer |
| *1700001L05Rik* | 33 | *15:83358847-83358855* | - | mmu-miR-128-3p | 8mer |
| *Nup50* | 21 | *15:84940284-84940292* | + | mmu-miR-128-3p | 8mer |
| *Nell2* | 17 | *15:95218498-95218506* | - | mmu-miR-128-3p | 8mer |
| *Tvp23a* | 51 | *16:10421373-10421381* | - | mmu-miR-128-3p | 8mer |
| *Ccdc50* | 29 | *16:27449454-27449462* | + | mmu-miR-128-3p | 8mer |
| *Tnk2* | 147 | *16:32683208-32683216* | + | mmu-miR-128-3p | 8mer |
| *Lrch3* | 21 | *16:33013539-33013547* | + | mmu-miR-128-3p | 8mer |
| *Itsn1* | 149 | *16:91918670-91918678* | + | mmu-miR-128-3p | 8mer |
| *Prr18* | 18 | *17:8342974-8342982* | + | mmu-miR-128-3p | 8mer |
| *Pde10a* | 73 | *17:8985876-8985884* | + | mmu-miR-128-3p | 8mer |
| *Pdpk1* | 68 | *17:24076069-24076077* | - | mmu-miR-128-3p | 8mer |
| *Mapk14* | 21 | *17:28746530-28746538* | + | mmu-miR-128-3p | 8mer |
| *Prr3* | 26 | *17:35978656-35978664* | - | mmu-miR-128-3p | 8mer |
| *Plcl2* | 18 | *17:50689553-50689561* | + | mmu-miR-128-3p | 8mer |
| *Myl12b* | 21 | *17:70974045-70974053* | - | mmu-miR-128-3p | 8mer |
| *Arhgap12* | 13 | *18:6025918-6025926* | - | mmu-miR-128-3p | 8mer |
| *Dtna* | 29 | *18:23653797-23653805* | + | mmu-miR-128-3p | 8mer |
| *Elp2* | 134 | *18:24638563-24638571* | + | mmu-miR-128-3p | 8mer |
| *Fads1* | 248 | *19:10196570-10196578* | + | mmu-miR-128-3p | 8mer |
| *Wbp1l* | 26 | *19:46657343-46657351* | + | mmu-miR-128-3p | 8mer |
| *Atrnl1* | 13 | *19:58133164-58133172* | + | mmu-miR-128-3p | 8mer |

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|---|---|---|---|---|---|
| *Bmi1* | 23 | *2:18684936-18684944* | + | mmu-miR-128-3p | 8mer |
| *Fam102a* | 17 | *2:32567617-32567625* | + | mmu-miR-128-3p | 8mer |
| *Slc39a13* | 92 | *2:91062739-91062747* | - | mmu-miR-128-3p | 8mer |
| *Madd* | 34 | *2:91137970-91137978* | - | mmu-miR-128-3p | 8mer |
| *Trim44* | 29 | *2:102303581-102303589* | - | mmu-miR-128-3p | 8mer |
| *Dut* | 16 | *2:125257564-125257572* | + | mmu-miR-128-3p | 8mer |
| *Dzank1* | 32 | *2:144470922-144470930* | - | mmu-miR-128-3p | 8mer |
| *Plagl2* | 15 | *2:153229052-153229060* | - | mmu-miR-128-3p | 8mer |
| *Pard6b* | 17 | *2:168100923-168100931* | + | mmu-miR-128-3p | 8mer |
| *Ppp1r3d* | 17 | *2:178413235-178413243* | - | mmu-miR-128-3p | 8mer |
| *Samd10* | 54 | *2:181596543-181596551* | - | mmu-miR-128-3p | 8mer |
| *Oprl1* | 11 | *2:181720096-181720104* | + | mmu-miR-128-3p | 8mer |
| *Zfp704* | 111 | *3:9432272-9432280* | - | mmu-miR-128-3p | 8mer |
| *Vangl1* | 10 | *3:102157258-102157266* | - | mmu-miR-128-3p | 8mer |
| *Slc6a17* | 20 | *3:107467878-107467886* | - | mmu-miR-128-3p | 8mer |
| *Csf1* | 23 | *3:107742361-107742369* | - | mmu-miR-128-3p | 8mer |
| *4933431E20Rik* | 25 | *3:107895527-107895535* | - | mmu-miR-128-3p | 8mer |
| *N28178* | 12 | *4:42942134-42942142* | + | mmu-miR-128-3p | 8mer |
| *E130308A19Rik* | 20 | *4:59753649-59753657* | + | mmu-miR-128-3p | 8mer |
| *6330416G13Rik* | 39 | *4:63585622-63585630* | + | mmu-miR-128-3p | 8mer |
| *Ak4* | 37 | *4:101466740-101466748* | + | mmu-miR-128-3p | 8mer |
| *Ppap2b* | 48 | *4:105231683-105231691* | + | mmu-miR-128-3p | 8mer |
| *Med8* | 15 | *4:118414920-118414928* | + | mmu-miR-128-3p | 8mer |
| *Stk40* | 24 | *4:126140285-126140293* | + | mmu-miR-128-3p | 8mer |
| *5730409E04Rik* | 23 | *4:126613703-126613711* | + | mmu-miR-128-3p | 8mer |
| *Szrd1* | 16 | *4:141115562-141115570* | - | mmu-miR-128-3p | 8mer |
| *Szrd1* | 16 | *4:141115590-141115598* | - | mmu-miR-128-3p | 8mer |
| *Szrd1* | 16 | *4:141115612-141115620* | - | mmu-miR-128-3p | 8mer |
| *Szrd1* | 16 | *4:141115636-141115644* | - | mmu-miR-128-3p | 8mer |
| *Tmem51* | 18 | *4:142031578-142031586* | - | mmu-miR-128-3p | 8mer |
| *Mthfr* | 86 | *4:148055973-148055981* | + | mmu-miR-128-3p | 8mer |
| *Fbxo2* | 18 | *4:148167191-148167199* | + | mmu-miR-128-3p | 8mer |
| *5930403L14Rik* | 27 | *4:154633291-154633299* | - | mmu-miR-128-3p | 8mer |
| *Adam22* | 17 | *5:8077056-8077064* | - | mmu-miR-128-3p | 8mer |
| *Xrcc2* | 75 | *5:25691175-25691183* | - | mmu-miR-128-3p | 8mer |
| *Lmbr1* | 13 | *5:29233062-29233070* | - | mmu-miR-128-3p | 8mer |
| *Sorcs2* | 25 | *5:36018257-36018265* | - | mmu-miR-128-3p | 8mer |
| *Stim2* | 24 | *5:54119455-54119463* | + | mmu-miR-128-3p | 8mer |
| *Limch1* | 28 | *5:67054253-67054261* | + | mmu-miR-128-3p | 8mer |
| *Bend4* | 31 | *5:67392837-67392845* | - | mmu-miR-128-3p | 8mer |
| *Guf1* | 25 | *5:69573848-69573856* | + | mmu-miR-128-3p | 8mer |
| *Rchy1* | 18 | *5:91957552-91957560* | - | mmu-miR-128-3p | 8mer |
| *Sparcl1* | 27 | *5:104078687-104078695* | - | mmu-miR-128-3p | 8mer |
| *Fbrsl1* | 13 | *5:110362665-110362673* | - | mmu-miR-128-3p | 8mer |
| *Med13l* | 86 | *5:118762944-118762952* | + | mmu-miR-128-3p | 8mer |
| *Abcb9* | 18 | *5:124062131-124062139* | - | mmu-miR-128-3p | 8mer |
| *Pitpnm2* | 23 | *5:124120220-124120228* | - | mmu-miR-128-3p | 8mer |
| *Sbno1* | 28 | *5:124371329-124371337* | - | mmu-miR-128-3p | 8mer |
| *Ccdc92* | 32 | *5:124835479-124835487* | - | mmu-miR-128-3p | 8mer |
| *Tmsb10* | 11 | *6:72957500-72957508* | - | mmu-miR-128-3p | 8mer |
| *Slc6a6* | 47 | *6:91757507-91757515* | + | mmu-miR-128-3p | 8mer |
| *Arl8b* | 97 | *6:108823215-108823223* | + | mmu-miR-128-3p | 8mer |
| *Wnk1* | 43 | *6:119925717-119925725* | - | mmu-miR-128-3p | 8mer |
| *Kcna1* | 13 | *6:126640031-126640039* | - | mmu-miR-128-3p | 8mer |
| *Cic* | 16 | *7:25294348-25294356* | + | mmu-miR-128-3p | 8mer |
| *Iglon5* | 48 | *7:43474292-43474300* | - | mmu-miR-128-3p | 8mer |
| *Siglech* | 12 | *7:55778178-55778186* | + | mmu-miR-128-3p | 8mer |
| *Apba2* | 128 | *7:64754441-64754449* | + | mmu-miR-128-3p | 8mer |
| *Trim66* | 15 | *7:109453347-109453355* | - | mmu-miR-128-3p | 8mer |
| *Ndufab1* | 27 | *7:122090943-122090951* | - | mmu-miR-128-3p | 8mer |
| *Prkcb* | 35 | *7:122632405-122632413* | + | mmu-miR-128-3p | 8mer |
| *Ypel3* | 62 | *7:126780258-126780266* | + | mmu-miR-128-3p | 8mer |
| *Map2k7* | 169 | *8:4246082-4246090* | + | mmu-miR-128-3p | 8mer |
| *Mcph1* | 57 | *8:18802349-18802357* | + | mmu-miR-128-3p | 8mer |
| *Car7* | 39 | *8:104550010-104550018* | + | mmu-miR-128-3p | 8mer |
| *Terf2* | 38 | *8:107075600-107075608* | - | mmu-miR-128-3p | 8mer |

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|---|---|---|---|---|---|
| *Elavl3* | 14 | *9:22017416-22017424* | - | mmu-miR-128-3p | 8mer |
| *Arhgap32* | 63 | *9:32263491-32263499* | + | mmu-miR-128-3p | 8mer |
| *Rab27a* | 20 | *9:73096052-73096060* | + | mmu-miR-128-3p | 8mer |
| *Nktr* | 11 | *9:121755037-121755045* | + | mmu-miR-128-3p | 8mer |
| *Pdha1* | 14 | *X:160122990-160122998* | - | mmu-miR-128-3p | 8mer |
| *3110035E14Rik* | 63 | *1:9625616-9625623* | + | mmu-miR-128-3p | 7mer-m8 |
| *Smap1* | 12 | *1:23845935-23845942* | - | mmu-miR-128-3p | 7mer-m8 |
| *Actr1b* | 37 | *1:36698521-36698528* | - | mmu-miR-128-3p | 7mer-m8 |
| *Actr1b* | 68 | *1:36699776-36699783* | - | mmu-miR-128-3p | 7mer-m8 |
| *Nrp2* | 77 | *1:62796562-62796569* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ino80d* | 23 | *1:63053467-63053474* | - | mmu-miR-128-3p | 7mer-m8 |
| *Unc80* | 67 | *1:66695833-66695840* | + | mmu-miR-128-3p | 7mer-m8 |
| *Agfg1* | 46 | *1:82895183-82895190* | + | mmu-miR-128-3p | 7mer-m8 |
| *Gpc1* | 40 | *1:92859147-92859154* | + | mmu-miR-128-3p | 7mer-m8 |
| *Gpc1* | 40 | *1:92859187-92859194* | + | mmu-miR-128-3p | 7mer-m8 |
| *Smg7* | 22 | *1:152837172-152837179* | - | mmu-miR-128-3p | 7mer-m8 |
| *Smg7* | 18 | *1:152838081-152838088* | - | mmu-miR-128-3p | 7mer-m8 |
| *Qsox1* | 27 | *1:155778253-155778260* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tor1aip2* | 19 | *1:156065553-156065560* | + | mmu-miR-128-3p | 7mer-m8 |
| *Atp1b1* | 133 | *1:164437502-164437509* | - | mmu-miR-128-3p | 7mer-m8 |
| *Uck2* | 15 | *1:167225255-167225262* | - | mmu-miR-128-3p | 7mer-m8 |
| *Pcp4l1* | 10 | *1:171173355-171173362* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ndufs2* | 11 | *1:171233983-171233990* | - | mmu-miR-128-3p | 7mer-m8 |
| *Cnih4* | 20 | *1:181167474-181167481* | + | mmu-miR-128-3p | 7mer-m8 |
| *Kctd3* | 26 | *1:188971628-188971635* | - | mmu-miR-128-3p | 7mer-m8 |
| *Angel2* | 15 | *1:190945918-190945925* | + | mmu-miR-128-3p | 7mer-m8 |
| *Tmem206* | 41 | *1:191350245-191350252* | + | mmu-miR-128-3p | 7mer-m8 |
| *Lpgat1* | 85 | *1:191779082-191779089* | + | mmu-miR-128-3p | 7mer-m8 |
| *Lpgat1* | 14 | *1:191782336-191782343* | + | mmu-miR-128-3p | 7mer-m8 |
| *Sf3a1* | 12 | *11:4182007-4182014* | + | mmu-miR-128-3p | 7mer-m8 |
| *Nf2* | 24 | *11:4767898-4767905* | - | mmu-miR-128-3p | 7mer-m8 |
| *Adcy1* | 16 | *11:7171520-7171527* | + | mmu-miR-128-3p | 7mer-m8 |
| *Adcy1* | 74 | *11:7173857-7173864* | + | mmu-miR-128-3p | 7mer-m8 |
| *Mgat4b* | 42 | *11:50234853-50234860* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ppp2ca* | 11 | *11:52122729-52122736* | + | mmu-miR-128-3p | 7mer-m8 |
| *9530068E07Rik* | 16 | *11:52408614-52408621* | + | mmu-miR-128-3p | 7mer-m8 |
| *Fxr2* | 45 | *11:69653093-69653100* | + | mmu-miR-128-3p | 7mer-m8 |
| *Mnt* | 17 | *11:74844108-74844115* | + | mmu-miR-128-3p | 7mer-m8 |
| *Pitpna* | 26 | *11:75626363-75626370* | + | mmu-miR-128-3p | 7mer-m8 |
| *Glod4* | 28 | *11:76221044-76221051* | - | mmu-miR-128-3p | 7mer-m8 |
| *Sez6* | 41 | *11:77978825-77978832* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ppm1e* | 31 | *11:87227707-87227714* | - | mmu-miR-128-3p | 7mer-m8 |
| *Zfp652* | 39 | *11:95764432-95764439* | + | mmu-miR-128-3p | 7mer-m8 |
| *Sp2* | 13 | *11:96953834-96953841* | - | mmu-miR-128-3p | 7mer-m8 |
| *Cwc25* | 20 | *11:97747131-97747138* | - | mmu-miR-128-3p | 7mer-m8 |
| *Pgap3* | 41 | *11:98389372-98389379* | - | mmu-miR-128-3p | 7mer-m8 |
| *Casc3* | 366 | *11:98833688-98833695* | + | mmu-miR-128-3p | 7mer-m8 |
| *Fam134c* | 21 | *11:101098135-101098142* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rundc3a* | 36 | *11:102401605-102401612* | + | mmu-miR-128-3p | 7mer-m8 |
| *Rundc3a* | 36 | *11:102401717-102401724* | + | mmu-miR-128-3p | 7mer-m8 |
| *Arf2* | 109 | *11:103984592-103984599* | + | mmu-miR-128-3p | 7mer-m8 |
| *Tanc2* | 436 | *11:105927963-105927970* | + | mmu-miR-128-3p | 7mer-m8 |
| *Dcaf7* | 37 | *11:106059121-106059128* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ern1* | 10 | *11:106397377-106397384* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tex2* | 54 | *11:106502851-106502858* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tex2* | 57 | *11:106503114-106503121* | - | mmu-miR-128-3p | 7mer-m8 |
| *Polg2* | 55 | *11:106781085-106781092* | - | mmu-miR-128-3p | 7mer-m8 |
| *Sox9* | 33 | *11:112786519-112786526* | + | mmu-miR-128-3p | 7mer-m8 |
| *H3f3b* | 14 | *11:116023221-116023228* | - | mmu-miR-128-3p | 7mer-m8 |
| *Nptx1* | 11 | *11:119540017-119540024* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ccdc71l* | 10 | *12:32382154-32382161* | + | mmu-miR-128-3p | 7mer-m8 |
| *Nrcam* | 14 | *12:44601625-44601632* | + | mmu-miR-128-3p | 7mer-m8 |
| *Sptssa* | 23 | *12:54645672-54645679* | - | mmu-miR-128-3p | 7mer-m8 |
| *Sgpp1* | 17 | *12:75715472-75715479* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rdh11* | 17 | *12:79175255-79175262* | - | mmu-miR-128-3p | 7mer-m8 |
| *Dcaf5* | 10 | *12:80337820-80337827* | - | mmu-miR-128-3p | 7mer-m8 |

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|---|---|---|---|---|---|
| *Calm1* | 101 | *12:100209638-100209645* | + | mmu-miR-128-3p | 7mer-m8 |
| *Itpk1* | 35 | *12:102570160-102570167* | - | mmu-miR-128-3p | 7mer-m8 |
| *D430019H16Rik* | 21 | *12:105491959-105491966* | + | mmu-miR-128-3p | 7mer-m8 |
| *Traf3* | 31 | *12:111266441-111266448* | + | mmu-miR-128-3p | 7mer-m8 |
| *Traf3* | 31 | *12:111266471-111266478* | + | mmu-miR-128-3p | 7mer-m8 |
| *Lyst* | 72 | *13:13778047-13778054* | + | mmu-miR-128-3p | 7mer-m8 |
| *Arid4b* | 10 | *13:14197990-14197997* | + | mmu-miR-128-3p | 7mer-m8 |
| *Gfod1* | 16 | *13:43196102-43196109* | - | mmu-miR-128-3p | 7mer-m8 |
| *Gfod1* | 15 | *13:43199793-43199800* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ptpdc1* | 22 | *13:48578059-48578066* | - | mmu-miR-128-3p | 7mer-m8 |
| *Phf2* | 22 | *13:48802958-48802965* | - | mmu-miR-128-3p | 7mer-m8 |
| *Diras2* | 34 | *13:52506151-52506158* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ddx46* | 22 | *13:55679395-55679402* | + | mmu-miR-128-3p | 7mer-m8 |
| *Smad5* | 11 | *13:56738800-56738807* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ntrk2* | 10 | *13:59130314-59130321* | + | mmu-miR-128-3p | 7mer-m8 |
| *Adcy2* | 159 | *13:68620520-68620527* | - | mmu-miR-128-3p | 7mer-m8 |
| *Thrb* | 19 | *14:18036361-18036368* | + | mmu-miR-128-3p | 7mer-m8 |
| *Samd8* | 30 | *14:21798177-21798184* | + | mmu-miR-128-3p | 7mer-m8 |
| *Serp2* | 22 | *14:76532915-76532922* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ctnnd2* | 12 | *15:31028061-31028068* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ankrd33b* | 18 | *15:31294385-31294392* | - | mmu-miR-128-3p | 7mer-m8 |
| *Mtdh* | 14 | *15:34141902-34141909* | + | mmu-miR-128-3p | 7mer-m8 |
| *Fbxo32* | 3041 | *15:58180264-58180271* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rbfox2* | 27 | *15:77081501-77081508* | - | mmu-miR-128-3p | 7mer-m8 |
| *Myh9* | 30 | *15:77761129-77761136* | - | mmu-miR-128-3p | 7mer-m8 |
| *Syngr1* | 44 | *15:80119512-80119519* | + | mmu-miR-128-3p | 7mer-m8 |
| *Cacna1i* | 19 | *15:80397477-80397484* | + | mmu-miR-128-3p | 7mer-m8 |
| *Xrcc6* | 43 | *15:82040046-82040053* | + | mmu-miR-128-3p | 7mer-m8 |
| *Sept3* | 39 | *15:82294273-82294280* | + | mmu-miR-128-3p | 7mer-m8 |
| *Nup50* | 23 | *15:84942041-84942048* | + | mmu-miR-128-3p | 7mer-m8 |
| *Tubgcp6* | 15 | *15:89100178-89100185* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ncaph2* | 11 | *15:89371692-89371699* | + | mmu-miR-128-3p | 7mer-m8 |
| *Lmbr1l* | 82 | *15:98904027-98904034* | - | mmu-miR-128-3p | 7mer-m8 |
| *Letmd1* | 11 | *15:100478931-100478938* | + | mmu-miR-128-3p | 7mer-m8 |
| *Sp1* | 10 | *15:102432504-102432511* | + | mmu-miR-128-3p | 7mer-m8 |
| *Sp1* | 14 | *15:102435737-102435744* | + | mmu-miR-128-3p | 7mer-m8 |
| *Pde1b* | 24 | *15:103528987-103528994* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ppp1r1a* | 17 | *15:103530439-103530446* | - | mmu-miR-128-3p | 7mer-m8 |
| *Glyr1* | 22 | *16:5014123-5014130* | - | mmu-miR-128-3p | 7mer-m8 |
| *Snn* | 94 | *16:11074509-11074516* | + | mmu-miR-128-3p | 7mer-m8 |
| *Mapk1* | 19 | *16:17046124-17046131* | + | mmu-miR-128-3p | 7mer-m8 |
| *2510009E07Rik* | 26 | *16:21649463-21649470* | - | mmu-miR-128-3p | 7mer-m8 |
| *2510009E07Rik* | 10 | *16:21653204-21653211* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ccdc50* | 358 | *16:27451794-27451801* | + | mmu-miR-128-3p | 7mer-m8 |
| *Lsg1* | 45 | *16:30561574-30561581* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ppp1r2* | 42 | *16:31253491-31253498* | - | mmu-miR-128-3p | 7mer-m8 |
| *Lrrc58* | 50 | *16:37882992-37882999* | + | mmu-miR-128-3p | 7mer-m8 |
| *Gm608* | 37 | *16:44222955-44222962* | + | mmu-miR-128-3p | 7mer-m8 |
| *Cpox* | 15 | *16:58678812-58678819* | + | mmu-miR-128-3p | 7mer-m8 |
| *Cpox* | 15 | *16:58678821-58678828* | + | mmu-miR-128-3p | 7mer-m8 |
| *Rcan1* | 44 | *16:92393344-92393351* | - | mmu-miR-128-3p | 7mer-m8 |
| *Pisd-ps2* | 25 | *17:3079599-3079606* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tulp4* | 10 | *17:6239696-6239703* | + | mmu-miR-128-3p | 7mer-m8 |
| *Srsf3* | 10 | *17:29041794-29041801* | + | mmu-miR-128-3p | 7mer-m8 |
| *Srsf3* | 10 | *17:29041802-29041809* | + | mmu-miR-128-3p | 7mer-m8 |
| *Mtch1* | 31 | *17:29332177-29332184* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tbc1d22b* | 58 | *17:29606379-29606386* | + | mmu-miR-128-3p | 7mer-m8 |
| *Tmem151b* | 60 | *17:45542031-45542038* | - | mmu-miR-128-3p | 7mer-m8 |
| *Med20* | 12 | *17:47623824-47623831* | + | mmu-miR-128-3p | 7mer-m8 |
| *Fem1a* | 13 | *17:56263557-56263564* | + | mmu-miR-128-3p | 7mer-m8 |
| *Soga2* | 10 | *17:66336532-66336539* | - | mmu-miR-128-3p | 7mer-m8 |
| *Sos1* | 19 | *17:80396697-80396704* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tmem178* | 24 | *17:81001481-81001488* | + | mmu-miR-128-3p | 7mer-m8 |
| *Kif5b* | 52 | *18:6203450-6203457* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rab18* | 20 | *18:6791112-6791119* | + | mmu-miR-128-3p | 7mer-m8 |
| *Syt4* | 2619 | *18:31439514-31439521* | - | mmu-miR-128-3p | 7mer-m8 |

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|---|---|---|---|---|---|
| *Paip2* | 37 | *18:35616347-35616354* | + | mmu-miR-128-3p | 7mer-m8 |
| *Fgf1* | 47 | *18:38841082-38841089* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ndst1* | 41 | *18:60687202-60687209* | - | mmu-miR-128-3p | 7mer-m8 |
| *St8sia3* | 29 | *18:64275798-64275805* | + | mmu-miR-128-3p | 7mer-m8 |
| *Onecut2* | 10 | *18:64388493-64388500* | + | mmu-miR-128-3p | 7mer-m8 |
| *Nedd4l* | 31 | *18:65215568-65215575* | + | mmu-miR-128-3p | 7mer-m8 |
| *Tcf4* | 15 | *18:69683400-69683407* | + | mmu-miR-128-3p | 7mer-m8 |
| *Tcf4* | 10 | *18:69684171-69684178* | + | mmu-miR-128-3p | 7mer-m8 |
| *Atp9b* | 23 | *18:80736093-80736100* | - | mmu-miR-128-3p | 7mer-m8 |
| *Zfp516* | 24 | *18:83001690-83001697* | + | mmu-miR-128-3p | 7mer-m8 |
| *Zfp516* | 11 | *18:83002517-83002524* | + | mmu-miR-128-3p | 7mer-m8 |
| *Cndp2* | 10 | *18:84667612-84667619* | - | mmu-miR-128-3p | 7mer-m8 |
| *Naa40* | 100 | *19:7227966-7227973* | - | mmu-miR-128-3p | 7mer-m8 |
| *Fads1* | 248 | *19:10196544-10196551* | + | mmu-miR-128-3p | 7mer-m8 |
| *Dagla* | 16 | *19:10246661-10246668* | - | mmu-miR-128-3p | 7mer-m8 |
| *Syt7* | 64 | *19:10451081-10451088* | + | mmu-miR-128-3p | 7mer-m8 |
| *Dtx4* | 47 | *19:12469031-12469038* | - | mmu-miR-128-3p | 7mer-m8 |
| *Trpm3* | 92 | *19:22990278-22990285* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ak3* | 10 | *19:29021780-29021787* | - | mmu-miR-128-3p | 7mer-m8 |
| *March5* | 38 | *19:37222449-37222456* | + | mmu-miR-128-3p | 7mer-m8 |
| *Slit1* | 38 | *19:41599511-41599518* | - | mmu-miR-128-3p | 7mer-m8 |
| *Golga7b* | 64 | *19:42269184-42269191* | + | mmu-miR-128-3p | 7mer-m8 |
| *Arl3* | 19 | *19:46530872-46530879* | - | mmu-miR-128-3p | 7mer-m8 |
| *Sh3pxd2a* | 15 | *19:47265824-47265831* | - | mmu-miR-128-3p | 7mer-m8 |
| *Cacul1* | 10 | *19:60527075-60527082* | - | mmu-miR-128-3p | 7mer-m8 |
| *Prpf18* | 21 | *2:4621713-4621720* | - | mmu-miR-128-3p | 7mer-m8 |
| *5031426D15Rik* | 16 | *2:6927244-6927251* | - | mmu-miR-128-3p | 7mer-m8 |
| *Nacc2* | 21 | *2:26058181-26058188* | - | mmu-miR-128-3p | 7mer-m8 |
| *Sdccag3* | 31 | *2:26383155-26383162* | - | mmu-miR-128-3p | 7mer-m8 |
| *Fnbp1* | 11 | *2:31028497-31028504* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rab14* | 39 | *2:35181312-35181319* | - | mmu-miR-128-3p | 7mer-m8 |
| *Dab2ip* | 30 | *2:35730791-35730798* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ttll11* | 15 | *2:35751523-35751530* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ttll11* | 15 | *2:35751537-35751544* | - | mmu-miR-128-3p | 7mer-m8 |
| *B3galt1* | 10 | *2:68119192-68119199* | + | mmu-miR-128-3p | 7mer-m8 |
| *Pdk1* | 19 | *2:71902933-71902940* | + | mmu-miR-128-3p | 7mer-m8 |
| *Sestd1* | 21 | *2:77180784-77180791* | - | mmu-miR-128-3p | 7mer-m8 |
| *Dnajc10* | 33 | *2:80353014-80353021* | + | mmu-miR-128-3p | 7mer-m8 |
| *Madd* | 34 | *2:91137862-91137869* | - | mmu-miR-128-3p | 7mer-m8 |
| *Madd* | 34 | *2:91137933-91137940* | - | mmu-miR-128-3p | 7mer-m8 |
| *Hipk3* | 30 | *2:104426705-104426712* | - | mmu-miR-128-3p | 7mer-m8 |
| *Vps39* | 14 | *2:120343177-120343184* | - | mmu-miR-128-3p | 7mer-m8 |
| *B2m* | 26 | *2:122153000-122153007* | + | mmu-miR-128-3p | 7mer-m8 |
| *Tmem87b* | 16 | *2:128852582-128852589* | + | mmu-miR-128-3p | 7mer-m8 |
| *Prnp* | 54 | *2:131938125-131938132* | + | mmu-miR-128-3p | 7mer-m8 |
| *Cds2* | 72 | *2:132310931-132310938* | + | mmu-miR-128-3p | 7mer-m8 |
| *Insm1* | 35 | *2:146224745-146224752* | + | mmu-miR-128-3p | 7mer-m8 |
| *Napb* | 15 | *2:148695067-148695074* | - | mmu-miR-128-3p | 7mer-m8 |
| *Acss1* | 12 | *2:150618613-150618620* | - | mmu-miR-128-3p | 7mer-m8 |
| *Pygb* | 34 | *2:150831594-150831601* | + | mmu-miR-128-3p | 7mer-m8 |
| *Epb4.1l1* | 23 | *2:156540701-156540708* | + | mmu-miR-128-3p | 7mer-m8 |
| *9830001H06Rik* | 14 | *2:157011152-157011159* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ralgapb* | 36 | *2:158496067-158496074* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ppp1r16b* | 57 | *2:158763552-158763559* | + | mmu-miR-128-3p | 7mer-m8 |
| *Chd6* | 20 | *2:160948946-160948953* | - | mmu-miR-128-3p | 7mer-m8 |
| *Sdc4* | 59 | *2:164424791-164424798* | - | mmu-miR-128-3p | 7mer-m8 |
| *Stx16* | 13 | *2:174097094-174097101* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ythdf1* | 29 | *2:180904780-180904787* | - | mmu-miR-128-3p | 7mer-m8 |
| *Arfrp1* | 12 | *2:181364085-181364092* | - | mmu-miR-128-3p | 7mer-m8 |
| *Slc7a14* | 24 | *3:31205498-31205505* | - | mmu-miR-128-3p | 7mer-m8 |
| *Zmat3* | 12 | *3:32340182-32340189* | - | mmu-miR-128-3p | 7mer-m8 |
| *Larp1b* | 25 | *3:40977943-40977950* | + | mmu-miR-128-3p | 7mer-m8 |
| *Slc7a11* | 20 | *3:50368055-50368062* | - | mmu-miR-128-3p | 7mer-m8 |
| *Naa15* | 11 | *3:51473314-51473321* | + | mmu-miR-128-3p | 7mer-m8 |
| *Setd7* | 23 | *3:51515933-51515940* | - | mmu-miR-128-3p | 7mer-m8 |
| *Setd7* | 255 | *3:51518367-51518374* | - | mmu-miR-128-3p | 7mer-m8 |

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|---|---|---|---|---|---|
| *Npy2r* | 15 | *3:82539975-82539982* | - | mmu-miR-128-3p | 7mer-m8 |
| *Cct3* | 14 | *3:88321617-88321624* | + | mmu-miR-128-3p | 7mer-m8 |
| *Syt11* | 18 | *3:88745929-88745936* | - | mmu-miR-128-3p | 7mer-m8 |
| *Pde4dip* | 21 | *3:97740393-97740400* | - | mmu-miR-128-3p | 7mer-m8 |
| *Hipk1* | 25 | *3:103742151-103742158* | - | mmu-miR-128-3p | 7mer-m8 |
| *St7l* | 12 | *3:104928523-104928530* | + | mmu-miR-128-3p | 7mer-m8 |
| *Wnt2b* | 17 | *3:104947024-104947031* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tmem64* | 10 | *4:15283973-15283980* | + | mmu-miR-128-3p | 7mer-m8 |
| *Mdn1* | 17 | *4:32774812-32774819* | + | mmu-miR-128-3p | 7mer-m8 |
| *Srsf12* | 40 | *4:33231487-33231494* | + | mmu-miR-128-3p | 7mer-m8 |
| *Rnf38* | 12 | *4:44129460-44129467* | - | mmu-miR-128-3p | 7mer-m8 |
| *Gabbr2* | 29 | *4:46664066-46664073* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tmem246* | 24 | *4:49585604-49585611* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rad23b* | 16 | *4:55391428-55391435* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ptpn3* | 24 | *4:57194184-57194191* | - | mmu-miR-128-3p | 7mer-m8 |
| *Akap2* | 19 | *4:57896023-57896030* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ugcg* | 32 | *4:59221248-59221255* | + | mmu-miR-128-3p | 7mer-m8 |
| *Rps6* | 116 | *4:86854414-86854421* | - | mmu-miR-128-3p | 7mer-m8 |
| *Focad* | 22 | *4:88410830-88410837* | + | mmu-miR-128-3p | 7mer-m8 |
| *Txndc12* | 18 | *4:108861555-108861562* | + | mmu-miR-128-3p | 7mer-m8 |
| *Elovl1* | 17 | *4:118432479-118432486* | + | mmu-miR-128-3p | 7mer-m8 |
| *Meaf6* | 15 | *4:125110506-125110513* | + | mmu-miR-128-3p | 7mer-m8 |
| *AU040320* | 11 | *4:126854037-126854044* | + | mmu-miR-128-3p | 7mer-m8 |
| *Syf2* | 21 | *4:134937454-134937461* | + | mmu-miR-128-3p | 7mer-m8 |
| *Iffo2* | 21 | *4:139617028-139617035* | + | mmu-miR-128-3p | 7mer-m8 |
| *Iffo2* | 21 | *4:139617051-139617058* | + | mmu-miR-128-3p | 7mer-m8 |
| *Aldh4a1* | 79 | *4:139649640-139649647* | + | mmu-miR-128-3p | 7mer-m8 |
| *Kif1b* | 34 | *4:149177191-149177198* | - | mmu-miR-128-3p | 7mer-m8 |
| *Kif1b* | 208 | *4:149180007-149180014* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rere* | 17 | *4:150619828-150619835* | + | mmu-miR-128-3p | 7mer-m8 |
| *Plch2* | 15 | *4:154983206-154983213* | - | mmu-miR-128-3p | 7mer-m8 |
| *Sdf4* | 22 | *4:156011151-156011158* | + | mmu-miR-128-3p | 7mer-m8 |
| *Adam22* | 10 | *5:8075020-8075027* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rbm33* | 42 | *5:28414970-28414977* | + | mmu-miR-128-3p | 7mer-m8 |
| *Rbm33* | 16 | *5:28418553-28418560* | + | mmu-miR-128-3p | 7mer-m8 |
| *Sgcb* | 22 | *5:73635099-73635106* | - | mmu-miR-128-3p | 7mer-m8 |
| *Clock* | 12 | *5:76216192-76216199* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rasgef1b* | 31 | *5:99218105-99218112* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ulk1* | 42 | *5:110784835-110784842* | - | mmu-miR-128-3p | 7mer-m8 |
| *Asphd2* | 26 | *5:112385640-112385647* | - | mmu-miR-128-3p | 7mer-m8 |
| *Adrbk2* | 13 | *5:112914937-112914944* | - | mmu-miR-128-3p | 7mer-m8 |
| *Svop* | 20 | *5:114028116-114028123* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rab35* | 47 | *5:115647112-115647119* | + | mmu-miR-128-3p | 7mer-m8 |
| *Rnft2* | 29 | *5:118190717-118190724* | - | mmu-miR-128-3p | 7mer-m8 |
| *Dtx1* | 39 | *5:120680230-120680237* | - | mmu-miR-128-3p | 7mer-m8 |
| *Bri3bp* | 45 | *5:125454882-125454889* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ywhag* | 44 | *5:135909577-135909584* | - | mmu-miR-128-3p | 7mer-m8 |
| *Plod3* | 41 | *5:136996291-136996298* | + | mmu-miR-128-3p | 7mer-m8 |
| *Mcm7* | 669 | *5:138165757-138165764* | - | mmu-miR-128-3p | 7mer-m8 |
| *BC037034* | 13 | *5:138260150-138260157* | - | mmu-miR-128-3p | 7mer-m8 |
| *Cpsf4* | 85 | *5:145181232-145181239* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ubl3* | 236 | *5:148505457-148505464* | - | mmu-miR-128-3p | 7mer-m8 |
| *Casd1* | 13 | *6:4642645-4642652* | + | mmu-miR-128-3p | 7mer-m8 |
| *Plxna4* | 65 | *6:32150087-32150094* | - | mmu-miR-128-3p | 7mer-m8 |
| *Slc37a3* | 25 | *6:39336686-39336693* | - | mmu-miR-128-3p | 7mer-m8 |
| *Wipf3* | 30 | *6:54502574-54502581* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ppm1k* | 23 | *6:57506703-57506710* | - | mmu-miR-128-3p | 7mer-m8 |
| *Sec61a1* | 84 | *6:88503664-88503671* | - | mmu-miR-128-3p | 7mer-m8 |
| *Iqsec1* | 22 | *6:90661733-90661740* | - | mmu-miR-128-3p | 7mer-m8 |
| *Prickle2* | 52 | *6:92373852-92373859* | - | mmu-miR-128-3p | 7mer-m8 |
| *Chl1* | 11 | *6:103731345-103731352* | + | mmu-miR-128-3p | 7mer-m8 |
| *Srgap3* | 31 | *6:112720805-112720812* | - | mmu-miR-128-3p | 7mer-m8 |
| *Atp2b2* | 30 | *6:113745187-113745194* | - | mmu-miR-128-3p | 7mer-m8 |
| *Cecr6* | 24 | *6:120489205-120489212* | - | mmu-miR-128-3p | 7mer-m8 |
| *Bcl2l13* | 32 | *6:120889868-120889875* | + | mmu-miR-128-3p | 7mer-m8 |
| *Slc2a3* | 19 | *6:122729896-122729903* | - | mmu-miR-128-3p | 7mer-m8 |

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|---|---|---|---|---|---|
| *Kcna1* | 15 | *6:126637221-126637228* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tspan9* | 49 | *6:127963503-127963510* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tspan9* | 49 | *6:127963775-127963782* | - | mmu-miR-128-3p | 7mer-m8 |
| *Crebl2* | 18 | *6:134857022-134857029* | + | mmu-miR-128-3p | 7mer-m8 |
| *Bhlhe41* | 41 | *6:145862236-145862243* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ccdc9* | 25 | *7:16275453-16275460* | - | mmu-miR-128-3p | 7mer-m8 |
| *Sptbn4* | 17 | *7:27357167-27357174* | - | mmu-miR-128-3p | 7mer-m8 |
| *Sptbn4* | 17 | *7:27357225-27357232* | - | mmu-miR-128-3p | 7mer-m8 |
| *Emc10* | 40 | *7:44490641-44490648* | - | mmu-miR-128-3p | 7mer-m8 |
| *Grin2d* | 20 | *7:45832418-45832425* | - | mmu-miR-128-3p | 7mer-m8 |
| *Nav2* | 54 | *7:49607627-49607634* | + | mmu-miR-128-3p | 7mer-m8 |
| *Synm* | 31 | *7:67730887-67730894* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tub* | 46 | *7:109032949-109032956* | + | mmu-miR-128-3p | 7mer-m8 |
| *Ampd3* | 13 | *7:110811126-110811133* | + | mmu-miR-128-3p | 7mer-m8 |
| *Coq7* | 10 | *7:118525128-118525135* | - | mmu-miR-128-3p | 7mer-m8 |
| *BC030336* | 44 | *7:120731456-120731463* | + | mmu-miR-128-3p | 7mer-m8 |
| *Tial1* | 23 | *7:128442175-128442182* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rnh1* | 68 | *7:141160385-141160392* | - | mmu-miR-128-3p | 7mer-m8 |
| *Kcnq1ot1* | 13 | *7:143290743-143290750* | - | mmu-miR-128-3p | 7mer-m8 |
| *Golga7* | 59 | *8:23241612-23241619* | - | mmu-miR-128-3p | 7mer-m8 |
| *Whsc1l1* | 48 | *8:25716972-25716979* | + | mmu-miR-128-3p | 7mer-m8 |
| *Erlin2* | 51 | *8:27037503-27037510* | + | mmu-miR-128-3p | 7mer-m8 |
| *Tmem59l* | 11 | *8:70484009-70484016* | - | mmu-miR-128-3p | 7mer-m8 |
| *Slc27a1* | 31 | *8:71586751-71586758* | + | mmu-miR-128-3p | 7mer-m8 |
| *Nacc1* | 57 | *8:84672431-84672438* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tnpo2* | 27 | *8:85055606-85055613* | + | mmu-miR-128-3p | 7mer-m8 |
| *Heatr3* | 16 | *8:88171705-88171712* | + | mmu-miR-128-3p | 7mer-m8 |
| *Gnao1* | 11 | *8:93961401-93961408* | + | mmu-miR-128-3p | 7mer-m8 |
| *Gnao1* | 28 | *8:93967920-93967927* | + | mmu-miR-128-3p | 7mer-m8 |
| *Cmtm4* | 11 | *8:104349096-104349103* | - | mmu-miR-128-3p | 7mer-m8 |
| *Smpd3* | 13 | *8:106253385-106253392* | - | mmu-miR-128-3p | 7mer-m8 |
| *Pdpr* | 27 | *8:111135460-111135467* | + | mmu-miR-128-3p | 7mer-m8 |
| *Hsdl1* | 21 | *8:119562082-119562089* | - | mmu-miR-128-3p | 7mer-m8 |
| *Fbxo31* | 14 | *8:121549807-121549814* | - | mmu-miR-128-3p | 7mer-m8 |
| *Slc7a5* | 19 | *8:121882482-121882489* | - | mmu-miR-128-3p | 7mer-m8 |
| *2310022B05Rik* | 22 | *8:124637511-124637518* | - | mmu-miR-128-3p | 7mer-m8 |
| *Slc35f3* | 39 | *8:126395595-126395602* | + | mmu-miR-128-3p | 7mer-m8 |
| *9230110C19Rik* | 12 | *9:8022372-8022379* | - | mmu-miR-128-3p | 7mer-m8 |
| *Fam76b* | 21 | *9:13844380-13844387* | + | mmu-miR-128-3p | 7mer-m8 |
| *Bbs9* | 13 | *9:22887952-22887959* | + | mmu-miR-128-3p | 7mer-m8 |
| *Aplp2* | 114 | *9:31149881-31149888* | - | mmu-miR-128-3p | 7mer-m8 |
| *Ddx6* | 67 | *9:44636683-44636690* | + | mmu-miR-128-3p | 7mer-m8 |
| *Mll1* | 20 | *9:44805694-44805701* | - | mmu-miR-128-3p | 7mer-m8 |
| *Mll1* | 20 | *9:44805711-44805718* | - | mmu-miR-128-3p | 7mer-m8 |
| *AI593442* | 51 | *9:52677510-52677517* | - | mmu-miR-128-3p | 7mer-m8 |
| *Cul5* | 41 | *9:53617295-53617302* | - | mmu-miR-128-3p | 7mer-m8 |
| *Tnfaip8l3* | 414 | *9:54024718-54024725* | - | mmu-miR-128-3p | 7mer-m8 |
| *Lingo1* | 39 | *9:56618429-56618436* | - | mmu-miR-128-3p | 7mer-m8 |
| *Parp6* | 13 | *9:59650291-59650298* | + | mmu-miR-128-3p | 7mer-m8 |
| *Myo9a* | 10 | *9:59928216-59928223* | + | mmu-miR-128-3p | 7mer-m8 |
| *Fem1b* | 24 | *9:62795626-62795633* | - | mmu-miR-128-3p | 7mer-m8 |
| *Polr2m* | 27 | *9:71478917-71478924* | - | mmu-miR-128-3p | 7mer-m8 |
| *Chst2* | 11 | *9:95401099-95401106* | - | mmu-miR-128-3p | 7mer-m8 |
| *Rab6b* | 42 | *9:103183285-103183292* | + | mmu-miR-128-3p | 7mer-m8 |
| *Rad54l2* | 124 | *9:106688621-106688628* | - | mmu-miR-128-3p | 7mer-m8 |
| *Myd88* | 36 | *9:119336424-119336431* | - | mmu-miR-128-3p | 7mer-m8 |
| *Prickle3* | 13 | *X:7668335-7668342* | + | mmu-miR-128-3p | 7mer-m8 |
| *Wdr13* | 26 | *X:8128968-8128975* | - | mmu-miR-128-3p | 7mer-m8 |
| *2900008C10Rik* | 17 | *X:12134820-12134827* | - | mmu-miR-128-3p | 7mer-m8 |
| *Prkx* | 270 | *X:77761786-77761793* | - | mmu-miR-128-3p | 7mer-m8 |
| *Pdk3* | 88 | *X:93764280-93764287* | - | mmu-miR-128-3p | 7mer-m8 |
| *C77370* | 10 | *X:104081313-104081320* | - | mmu-miR-128-3p | 7mer-m8 |
| *Drp2* | 41 | *X:134456508-134456515* | + | mmu-miR-128-3p | 7mer-m8 |
| *Iqsec2* | 132 | *X:152223874-152223881* | + | mmu-miR-128-3p | 7mer-m8 |
| *Paqr8* | 33 | *1:20935723-20935730* | + | mmu-miR-128-3p | 7mer-A1 |
| *Dst* | 19 | *1:34307667-34307674* | + | mmu-miR-128-3p | 7mer-A1 |

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|---|---|---|---|---|---|
| *2010300C02Rik* | 10 | *1:37612168-37612175* | - | mmu-miR-128-3p | 7mer-A1 |
| *Rnf149* | 15 | *1:39551474-39551481* | - | mmu-miR-128-3p | 7mer-A1 |
| *Nabp1* | 12 | *1:51471160-51471167* | - | mmu-miR-128-3p | 7mer-A1 |
| *Clk1* | 54 | *1:58417329-58417336* | - | mmu-miR-128-3p | 7mer-A1 |
| *Abi2* | 11 | *1:60479307-60479314* | + | mmu-miR-128-3p | 7mer-A1 |
| *Usp37* | 46 | *1:74437180-74437187* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ncl* | 44 | *1:86347033-86347040* | - | mmu-miR-128-3p | 7mer-A1 |
| *6430706D22Rik* | 15 | *1:88264296-88264303* | - | mmu-miR-128-3p | 7mer-A1 |
| *Capn10* | 19 | *1:92947862-92947869* | + | mmu-miR-128-3p | 7mer-A1 |
| *Ppip5k2* | 14 | *1:97705391-97705398* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ccnt2* | 16 | *1:127804415-127804422* | + | mmu-miR-128-3p | 7mer-A1 |
| *Slc41a1* | 10 | *1:131848484-131848491* | + | mmu-miR-128-3p | 7mer-A1 |
| *Cdk18* | 10 | *1:132113708-132113715* | - | mmu-miR-128-3p | 7mer-A1 |
| *Btg2* | 26 | *1:134076990-134076997* | - | mmu-miR-128-3p | 7mer-A1 |
| *Trove2* | 199 | *1:143757296-143757303* | - | mmu-miR-128-3p | 7mer-A1 |
| *1700025G04Rik* | 24 | *1:151886774-151886781* | - | mmu-miR-128-3p | 7mer-A1 |
| *Nmnat2* | 10 | *1:153117913-153117920* | + | mmu-miR-128-3p | 7mer-A1 |
| *Atf6* | 13 | *1:170707102-170707109* | - | mmu-miR-128-3p | 7mer-A1 |
| *Gm5069* | 10 | *1:180329929-180329936* | - | mmu-miR-128-3p | 7mer-A1 |
| *Camk1g* | 11 | *1:193346552-193346559* | - | mmu-miR-128-3p | 7mer-A1 |
| *Dusp18* | 30 | *11:3898461-3898468* | + | mmu-miR-128-3p | 7mer-A1 |
| *Cobl* | 10 | *11:12237223-12237230* | - | mmu-miR-128-3p | 7mer-A1 |
| *Cnrip1* | 31 | *11:17078686-17078693* | + | mmu-miR-128-3p | 7mer-A1 |
| *Ccdc104* | 19 | *11:29221770-29221777* | - | mmu-miR-128-3p | 7mer-A1 |
| *Gfpt2* | 36 | *11:49838045-49838052* | + | mmu-miR-128-3p | 7mer-A1 |
| *Rmnd5b* | 15 | *11:51624009-51624016* | - | mmu-miR-128-3p | 7mer-A1 |
| *Sowaha* | 83 | *11:53477583-53477590* | - | mmu-miR-128-3p | 7mer-A1 |
| *Sept8* | 17 | *11:53541967-53541974* | + | mmu-miR-128-3p | 7mer-A1 |
| *Map2k4* | 34 | *11:65690404-65690411* | - | mmu-miR-128-3p | 7mer-A1 |
| *Gas7* | 92 | *11:67684907-67684914* | + | mmu-miR-128-3p | 7mer-A1 |
| *Atp1b2* | 10 | *11:69600552-69600559* | - | mmu-miR-128-3p | 7mer-A1 |
| *Neurl4* | 27 | *11:69913645-69913652* | + | mmu-miR-128-3p | 7mer-A1 |
| *Supt6* | 19 | *11:78207142-78207149* | - | mmu-miR-128-3p | 7mer-A1 |
| *Sarm1* | 10 | *11:78471909-78471916* | - | mmu-miR-128-3p | 7mer-A1 |
| *Srsf1* | 12 | *11:88049849-88049856* | + | mmu-miR-128-3p | 7mer-A1 |
| *Ankrd40* | 20 | *11:94339724-94339731* | + | mmu-miR-128-3p | 7mer-A1 |
| *Kpnb1* | 34 | *11:97160011-97160018* | - | mmu-miR-128-3p | 7mer-A1 |
| *Npepps* | 40 | *11:97206849-97206856* | - | mmu-miR-128-3p | 7mer-A1 |
| *Lasp1* | 52 | *11:97838303-97838310* | + | mmu-miR-128-3p | 7mer-A1 |
| *Fam134c* | 21 | *11:101098100-101098107* | - | mmu-miR-128-3p | 7mer-A1 |
| *Mpp2* | 25 | *11:102058436-102058443* | - | mmu-miR-128-3p | 7mer-A1 |
| *Rundc3a* | 36 | *11:102401640-102401647* | + | mmu-miR-128-3p | 7mer-A1 |
| *Gosr2* | 36 | *11:103679135-103679142* | - | mmu-miR-128-3p | 7mer-A1 |
| *Tlk2* | 29 | *11:105281562-105281569* | + | mmu-miR-128-3p | 7mer-A1 |
| *Tanc2* | 27 | *11:105925177-105925184* | + | mmu-miR-128-3p | 7mer-A1 |
| *Dcaf7* | 60 | *11:106055958-106055965* | + | mmu-miR-128-3p | 7mer-A1 |
| *Dcaf7* | 29 | *11:106058347-106058354* | + | mmu-miR-128-3p | 7mer-A1 |
| *Amz2* | 77 | *11:109437393-109437400* | + | mmu-miR-128-3p | 7mer-A1 |
| *Slc39a11* | 328 | *11:113244884-113244891* | - | mmu-miR-128-3p | 7mer-A1 |
| *Grb2* | 32 | *11:115644067-115644074* | - | mmu-miR-128-3p | 7mer-A1 |
| *Mfsd11* | 121 | *11:116874043-116874050* | + | mmu-miR-128-3p | 7mer-A1 |
| *Fn3krp* | 18 | *11:121430531-121430538* | + | mmu-miR-128-3p | 7mer-A1 |
| *Dnajc27* | 19 | *12:4107215-4107222* | + | mmu-miR-128-3p | 7mer-A1 |
| *Itsn2* | 24 | *12:4713784-4713791* | + | mmu-miR-128-3p | 7mer-A1 |
| *Id2* | 31 | *12:25094378-25094385* | - | mmu-miR-128-3p | 7mer-A1 |
| *Sstr1* | 61 | *12:58213950-58213957* | + | mmu-miR-128-3p | 7mer-A1 |
| *Sgpp1* | 17 | *12:75715357-75715364* | - | mmu-miR-128-3p | 7mer-A1 |
| *0610007P14Rik* | 22 | *12:85815708-85815715* | - | mmu-miR-128-3p | 7mer-A1 |
| *Calm1* | 11 | *12:100209816-100209823* | + | mmu-miR-128-3p | 7mer-A1 |
| *Otub2* | 27 | *12:103404586-103404593* | + | mmu-miR-128-3p | 7mer-A1 |
| *Hsp90aa1* | 13 | *12:110691395-110691402* | - | mmu-miR-128-3p | 7mer-A1 |
| *Traf3* | 20 | *12:111265210-111265217* | + | mmu-miR-128-3p | 7mer-A1 |
| *Aldh5a1* | 37 | *13:24907742-24907749* | - | mmu-miR-128-3p | 7mer-A1 |
| *Tmem170b* | 29 | *13:41640583-41640590* | + | mmu-miR-128-3p | 7mer-A1 |
| *Rasgrf2* | 12 | *13:91883673-91883680* | - | mmu-miR-128-3p | 7mer-A1 |
| *Sgtb* | 19 | *13:104140345-104140352* | + | mmu-miR-128-3p | 7mer-A1 |

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| *Fam149b* | 13 | *14:20367949-20367956* | + | mmu-miR-128-3p | 7mer-A1 |
| *Kcnma1* | 15 | *14:23305789-23305796* | - | mmu-miR-128-3p | 7mer-A1 |
| *Zcchc24* | 41 | *14:25714962-25714969* | - | mmu-miR-128-3p | 7mer-A1 |
| *Dennd6a* | 13 | *14:26629587-26629594* | + | mmu-miR-128-3p | 7mer-A1 |
| *Arhgef3* | 11 | *14:27402963-27402970* | + | mmu-miR-128-3p | 7mer-A1 |
| *Cacna2d3* | 11 | *14:28905210-28905217* | - | mmu-miR-128-3p | 7mer-A1 |
| *Kpna3* | 41 | *14:61366157-61366164* | - | mmu-miR-128-3p | 7mer-A1 |
| *Dock9* | 38 | *14:121543365-121543372* | - | mmu-miR-128-3p | 7mer-A1 |
| *March6* | 13 | *15:31456791-31456798* | - | mmu-miR-128-3p | 7mer-A1 |
| *Sdc2* | 35 | *15:33034276-33034283* | + | mmu-miR-128-3p | 7mer-A1 |
| *Rnf139* | 26 | *15:58900246-58900253* | + | mmu-miR-128-3p | 7mer-A1 |
| *Rnf139* | 26 | *15:58900266-58900273* | + | mmu-miR-128-3p | 7mer-A1 |
| *Hsf1* | 18 | *15:76501050-76501057* | + | mmu-miR-128-3p | 7mer-A1 |
| *Cacng2* | 19 | *15:77993714-77993721* | - | mmu-miR-128-3p | 7mer-A1 |
| *Rbx1* | 36 | *15:81475620-81475627* | + | mmu-miR-128-3p | 7mer-A1 |
| *Chadl* | 24 | *15:81691531-81691538* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ldoc1l* | 23 | *15:84554913-84554920* | - | mmu-miR-128-3p | 7mer-A1 |
| *Mapk8ip2* | 75 | *15:89463180-89463187* | + | mmu-miR-128-3p | 7mer-A1 |
| *Shank3* | 24 | *15:89559645-89559652* | + | mmu-miR-128-3p | 7mer-A1 |
| *Arf3* | 98 | *15:98739053-98739060* | - | mmu-miR-128-3p | 7mer-A1 |
| *Tmbim6* | 18 | *15:99409961-99409968* | + | mmu-miR-128-3p | 7mer-A1 |
| *Zfp385a* | 57 | *15:103314222-103314229* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ccdc50* | 358 | *16:27451782-27451789* | + | mmu-miR-128-3p | 7mer-A1 |
| *Pcyt1a* | 43 | *16:32472323-32472330* | + | mmu-miR-128-3p | 7mer-A1 |
| *Kalrn* | 109 | *16:33970411-33970418* | - | mmu-miR-128-3p | 7mer-A1 |
| *Stxbp5l* | 29 | *16:37112982-37112989* | - | mmu-miR-128-3p | 7mer-A1 |
| *Atp6v1a* | 106 | *16:44087415-44087422* | - | mmu-miR-128-3p | 7mer-A1 |
| *Bbx* | 19 | *16:50196830-50196837* | - | mmu-miR-128-3p | 7mer-A1 |
| *Cadm2* | 11 | *16:66659461-66659468* | - | mmu-miR-128-3p | 7mer-A1 |
| *Rps6ka2* | 17 | *17:7303037-7303044* | + | mmu-miR-128-3p | 7mer-A1 |
| *Smoc2* | 17 | *17:14404406-14404413* | + | mmu-miR-128-3p | 7mer-A1 |
| *Neurl1b* | 19 | *17:26446149-26446156* | + | mmu-miR-128-3p | 7mer-A1 |
| *Adamts10* | 12 | *17:33553468-33553475* | + | mmu-miR-128-3p | 7mer-A1 |
| *Rcan2* | 88 | *17:44038680-44038687* | + | mmu-miR-128-3p | 7mer-A1 |
| *Sos1* | 19 | *17:80396747-80396754* | - | mmu-miR-128-3p | 7mer-A1 |
| *Zfp36l2* | 56 | *17:84184464-84184471* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ppm1b* | 44 | *17:85024643-85024650* | + | mmu-miR-128-3p | 7mer-A1 |
| *Crem* | 17 | *18:3267953-3267960* | - | mmu-miR-128-3p | 7mer-A1 |
| *Npc1* | 16 | *18:12190053-12190060* | - | mmu-miR-128-3p | 7mer-A1 |
| *Slc25a46* | 19 | *18:31581732-31581739* | - | mmu-miR-128-3p | 7mer-A1 |
| *Nrg2* | 22 | *18:36017473-36017480* | - | mmu-miR-128-3p | 7mer-A1 |
| *Onecut2* | 174 | *18:64388010-64388017* | + | mmu-miR-128-3p | 7mer-A1 |
| *Nedd4l* | 134 | *18:65217740-65217747* | + | mmu-miR-128-3p | 7mer-A1 |
| *Neto1* | 26 | *18:86500939-86500946* | + | mmu-miR-128-3p | 7mer-A1 |
| *AI846148* | 11 | *19:7356560-7356567* | - | mmu-miR-128-3p | 7mer-A1 |
| *Pla2g16* | 17 | *19:7587339-7587346* | + | mmu-miR-128-3p | 7mer-A1 |
| *Slc1a1* | 16 | *19:28912744-28912751* | + | mmu-miR-128-3p | 7mer-A1 |
| *Cpeb3* | 35 | *19:37022210-37022217* | - | mmu-miR-128-3p | 7mer-A1 |
| *March5* | 23 | *19:37221887-37221894* | + | mmu-miR-128-3p | 7mer-A1 |
| *Ccnj* | 10 | *19:40848377-40848384* | + | mmu-miR-128-3p | 7mer-A1 |
| *Fam171a1* | 12 | *2:3226871-3226878* | + | mmu-miR-128-3p | 7mer-A1 |
| *Prpf18* | 21 | *2:4621672-4621679* | - | mmu-miR-128-3p | 7mer-A1 |
| *Il15ra* | 10 | *2:11733204-11733211* | + | mmu-miR-128-3p | 7mer-A1 |
| *Thnsl1* | 35 | *2:21214205-21214212* | + | mmu-miR-128-3p | 7mer-A1 |
| *Nsmf* | 78 | *2:25062666-25062673* | + | mmu-miR-128-3p | 7mer-A1 |
| *Dnlz* | 31 | *2:26348441-26348448* | - | mmu-miR-128-3p | 7mer-A1 |
| *Cacfd1* | 17 | *2:27018971-27018978* | + | mmu-miR-128-3p | 7mer-A1 |
| *Rxra* | 11 | *2:27762799-27762806* | + | mmu-miR-128-3p | 7mer-A1 |
| *6530402F18Rik* | 11 | *2:29247774-29247781* | - | mmu-miR-128-3p | 7mer-A1 |
| *Fam78a* | 10 | *2:32066994-32067001* | - | mmu-miR-128-3p | 7mer-A1 |
| *Rabgap1* | 165 | *2:37565543-37565550* | + | mmu-miR-128-3p | 7mer-A1 |
| *Acvr1c* | 108 | *2:58269618-58269625* | - | mmu-miR-128-3p | 7mer-A1 |
| *Acp2* | 43 | *2:91211467-91211474* | + | mmu-miR-128-3p | 7mer-A1 |
| *Chst1* | 30 | *2:92615001-92615008* | + | mmu-miR-128-3p | 7mer-A1 |
| *Slc1a2* | 67 | *2:102782828-102782835* | + | mmu-miR-128-3p | 7mer-A1 |
| *Slc1a2* | 16 | *2:102787893-102787900* | + | mmu-miR-128-3p | 7mer-A1 |

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| *D430041D05Rik* | 45 | *2:104145702-104145709* | - | mmu-miR-128-3p | 7mer-A1 |
| *Pak6* | 28 | *2:118697144-118697151* | + | mmu-miR-128-3p | 7mer-A1 |
| *Slc30a4* | 31 | *2:122682949-122682956* | - | mmu-miR-128-3p | 7mer-A1 |
| *Prosapip1* | 27 | *2:130633203-130633210* | - | mmu-miR-128-3p | 7mer-A1 |
| *Tmx4* | 50 | *2:134594963-134594970* | - | mmu-miR-128-3p | 7mer-A1 |
| *Snap25* | 12 | *2:136781549-136781556* | + | mmu-miR-128-3p | 7mer-A1 |
| *Snap25* | 27 | *2:136782301-136782308* | + | mmu-miR-128-3p | 7mer-A1 |
| *Btbd3* | 24 | *2:138286673-138286680* | + | mmu-miR-128-3p | 7mer-A1 |
| *Flrt3* | 44 | *2:140659425-140659432* | - | mmu-miR-128-3p | 7mer-A1 |
| *Dzank1* | 65 | *2:144471679-144471686* | - | mmu-miR-128-3p | 7mer-A1 |
| *Epb4.1l1* | 23 | *2:156540756-156540763* | + | mmu-miR-128-3p | 7mer-A1 |
| *Epb4.1l1* | 23 | *2:156540859-156540866* | + | mmu-miR-128-3p | 7mer-A1 |
| *Zhx3* | 20 | *2:160771593-160771600* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ube2v1* | 11 | *2:167608806-167608813* | - | mmu-miR-128-3p | 7mer-A1 |
| *Bcas1* | 21 | *2:170347088-170347095* | - | mmu-miR-128-3p | 7mer-A1 |
| *Dclk1* | 10 | *3:55538320-55538327* | + | mmu-miR-128-3p | 7mer-A1 |
| *Ssr3* | 14 | *3:65381165-65381172* | - | mmu-miR-128-3p | 7mer-A1 |
| *1110032F04Rik* | 17 | *3:68870980-68870987* | + | mmu-miR-128-3p | 7mer-A1 |
| *Ppm1l* | 113 | *3:69556010-69556017* | + | mmu-miR-128-3p | 7mer-A1 |
| *Serpini1* | 12 | *3:75641199-75641206* | + | mmu-miR-128-3p | 7mer-A1 |
| *Hapln2* | 24 | *3:88021222-88021229* | - | mmu-miR-128-3p | 7mer-A1 |
| *Prune* | 10 | *3:95254650-95254657* | - | mmu-miR-128-3p | 7mer-A1 |
| *Dram2* | 22 | *3:106573757-106573764* | + | mmu-miR-128-3p | 7mer-A1 |
| *Fubp1* | 18 | *3:152236647-152236654* | + | mmu-miR-128-3p | 7mer-A1 |
| *2610301B20Rik* | 29 | *4:10898200-10898207* | + | mmu-miR-128-3p | 7mer-A1 |
| *Frrs1l* | 10 | *4:56962709-56962716* | - | mmu-miR-128-3p | 7mer-A1 |
| *Palm2* | 10 | *4:57710272-57710279* | + | mmu-miR-128-3p | 7mer-A1 |
| *Zkscan16* | 18 | *4:58959246-58959253* | + | mmu-miR-128-3p | 7mer-A1 |
| *Zdhhc21* | 50 | *4:82798986-82798993* | - | mmu-miR-128-3p | 7mer-A1 |
| *Zdhhc21* | 50 | *4:82799032-82799039* | - | mmu-miR-128-3p | 7mer-A1 |
| *E130102H24Rik* | 92 | *4:101346964-101346971* | - | mmu-miR-128-3p | 7mer-A1 |
| *Sgip1* | 10 | *4:102971227-102971234* | + | mmu-miR-128-3p | 7mer-A1 |
| *B4galt2* | 16 | *4:117877796-117877803* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ak2* | 12 | *4:129010824-129010831* | + | mmu-miR-128-3p | 7mer-A1 |
| *Nkain1* | 28 | *4:130531491-130531498* | - | mmu-miR-128-3p | 7mer-A1 |
| *Dnajc16* | 26 | *4:141762457-141762464* | - | mmu-miR-128-3p | 7mer-A1 |
| *Efhd2* | 40 | *4:141858742-141858749* | - | mmu-miR-128-3p | 7mer-A1 |
| *Camta1* | 118 | *4:151060070-151060077* | - | mmu-miR-128-3p | 7mer-A1 |
| *A330021E22Rik* | 11 | *5:5580884-5580891* | - | mmu-miR-128-3p | 7mer-A1 |
| *Cacna2d1* | 36 | *5:16371301-16371308* | + | mmu-miR-128-3p | 7mer-A1 |
| *Nat8l* | 39 | *5:34005735-34005742* | + | mmu-miR-128-3p | 7mer-A1 |
| *Add1* | 16 | *5:34631595-34631602* | + | mmu-miR-128-3p | 7mer-A1 |
| *Sgcb* | 24 | *5:73633851-73633858* | - | mmu-miR-128-3p | 7mer-A1 |
| *Clock* | 385 | *5:76213911-76213918* | - | mmu-miR-128-3p | 7mer-A1 |
| *Cox18* | 65 | *5:90222696-90222703* | - | mmu-miR-128-3p | 7mer-A1 |
| *Rchy1* | 33 | *5:91957890-91957897* | - | mmu-miR-128-3p | 7mer-A1 |
| *Prkg2* | 29 | *5:98931955-98931962* | - | mmu-miR-128-3p | 7mer-A1 |
| *Srrd* | 16 | *5:112337583-112337590* | - | mmu-miR-128-3p | 7mer-A1 |
| *Setd8* | 14 | *5:124462153-124462160* | + | mmu-miR-128-3p | 7mer-A1 |
| *Limk1* | 23 | *5:134656204-134656211* | - | mmu-miR-128-3p | 7mer-A1 |
| *Pom121* | 12 | *5:135376150-135376157* | - | mmu-miR-128-3p | 7mer-A1 |
| *Cox19* | 11 | *5:139337144-139337151* | - | mmu-miR-128-3p | 7mer-A1 |
| *Gna12* | 40 | *5:140760331-140760338* | - | mmu-miR-128-3p | 7mer-A1 |
| *Plxna4* | 11 | *6:32149954-32149961* | - | mmu-miR-128-3p | 7mer-A1 |
| *Plxna4* | 65 | *6:32150055-32150062* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ggct* | 24 | *6:54984761-54984768* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ppm1k* | 23 | *6:57506563-57506570* | - | mmu-miR-128-3p | 7mer-A1 |
| *Rmnd5a* | 22 | *6:71389257-71389264* | - | mmu-miR-128-3p | 7mer-A1 |
| *Tgoln1* | 22 | *6:72612030-72612037* | - | mmu-miR-128-3p | 7mer-A1 |
| *Tex261* | 20 | *6:83770546-83770553* | - | mmu-miR-128-3p | 7mer-A1 |
| *Rpn1* | 29 | *6:88103951-88103958* | + | mmu-miR-128-3p | 7mer-A1 |
| *Prickle2* | 15 | *6:92375029-92375036* | - | mmu-miR-128-3p | 7mer-A1 |
| *Setd5* | 23 | *6:113152793-113152800* | + | mmu-miR-128-3p | 7mer-A1 |
| *Slc6a1* | 14 | *6:114317164-114317171* | + | mmu-miR-128-3p | 7mer-A1 |
| *Slc6a1* | 14 | *6:114317173-114317180* | + | mmu-miR-128-3p | 7mer-A1 |
| *Hnrnpf* | 5730 | *6:117925525-117925532* | + | mmu-miR-128-3p | 7mer-A1 |

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|---|---|---|---|---|---|
| *Cecr6* | 102 | *6:120489944-120489951* | - | mmu-miR-128-3p | 7mer-A1 |
| *Itpr2* | 22 | *6:146108833-146108840* | - | mmu-miR-128-3p | 7mer-A1 |
| *Itpr2* | 22 | *6:146108906-146108913* | - | mmu-miR-128-3p | 7mer-A1 |
| *Gm4636* | 25 | *7:27988507-27988514* | - | mmu-miR-128-3p | 7mer-A1 |
| *Grin2d* | 20 | *7:45832217-45832224* | - | mmu-miR-128-3p | 7mer-A1 |
| *Grin2d* | 20 | *7:45832273-45832280* | - | mmu-miR-128-3p | 7mer-A1 |
| *Grin2d* | 20 | *7:45832322-45832329* | - | mmu-miR-128-3p | 7mer-A1 |
| *Grin2d* | 20 | *7:45832343-45832350* | - | mmu-miR-128-3p | 7mer-A1 |
| *Gabrb3* | 19 | *7:57826952-57826959* | + | mmu-miR-128-3p | 7mer-A1 |
| *Arrdc4* | 13 | *7:68738353-68738360* | - | mmu-miR-128-3p | 7mer-A1 |
| *Arrb1* | 61 | *7:99601647-99601654* | + | mmu-miR-128-3p | 7mer-A1 |
| *Wee1* | 145 | *7:110142153-110142160* | + | mmu-miR-128-3p | 7mer-A1 |
| *Prkcb* | 34 | *7:122631145-122631152* | + | mmu-miR-128-3p | 7mer-A1 |
| *Tnrc6a* | 775 | *7:123192971-123192978* | + | mmu-miR-128-3p | 7mer-A1 |
| *Gsg1l* | 38 | *7:125880348-125880355* | - | mmu-miR-128-3p | 7mer-A1 |
| *Sbk1* | 35 | *7:126294782-126294789* | + | mmu-miR-128-3p | 7mer-A1 |
| *Fank1* | 43 | *7:133880704-133880711* | + | mmu-miR-128-3p | 7mer-A1 |
| *Sprn* | 20 | *7:140151119-140151126* | - | mmu-miR-128-3p | 7mer-A1 |
| *Brsk2* | 20 | *7:142004199-142004206* | + | mmu-miR-128-3p | 7mer-A1 |
| *Zfp958* | 31 | *8:4630552-4630559* | + | mmu-miR-128-3p | 7mer-A1 |
| *Ankrd10* | 36 | *8:11615339-11615346* | - | mmu-miR-128-3p | 7mer-A1 |
| *Atp11a* | 28 | *8:12866075-12866082* | + | mmu-miR-128-3p | 7mer-A1 |
| *Zmat4* | 42 | *8:24060782-24060789* | + | mmu-miR-128-3p | 7mer-A1 |
| *Cnot7* | 12 | *8:40492842-40492849* | - | mmu-miR-128-3p | 7mer-A1 |
| *Galnt7* | 16 | *8:57525957-57525964* | - | mmu-miR-128-3p | 7mer-A1 |
| *Cbr4* | 10 | *8:61503225-61503232* | + | mmu-miR-128-3p | 7mer-A1 |
| *Mast3* | 12 | *8:70778352-70778359* | - | mmu-miR-128-3p | 7mer-A1 |
| *Cacna1a* | 21 | *8:84640181-84640188* | + | mmu-miR-128-3p | 7mer-A1 |
| *Neto2* | 20 | *8:85639294-85639301* | - | mmu-miR-128-3p | 7mer-A1 |
| *N4bp1* | 11 | *8:86841237-86841244* | - | mmu-miR-128-3p | 7mer-A1 |
| *Cyld* | 19 | *8:88749487-88749494* | + | mmu-miR-128-3p | 7mer-A1 |
| *Rpgrip1l* | 13 | *8:91219717-91219724* | - | mmu-miR-128-3p | 7mer-A1 |
| *Cbfb* | 19 | *8:105216049-105216056* | + | mmu-miR-128-3p | 7mer-A1 |
| *Ctcf* | 25 | *8:105681843-105681850* | + | mmu-miR-128-3p | 7mer-A1 |
| *Nfat5* | 45 | *8:107374456-107374463* | + | mmu-miR-128-3p | 7mer-A1 |
| *Phlpp2* | 57 | *8:109941464-109941471* | + | mmu-miR-128-3p | 7mer-A1 |
| *Cbfa2t3* | 11 | *8:122630143-122630150* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ankrd11* | 18 | *8:122896027-122896034* | - | mmu-miR-128-3p | 7mer-A1 |
| *Pgbd5* | 18 | *8:124369920-124369927* | - | mmu-miR-128-3p | 7mer-A1 |
| *Gucy1a2* | 525 | *9:3902759-3902766* | + | mmu-miR-128-3p | 7mer-A1 |
| *Arhgap42* | 35 | *9:8994903-8994910* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ubash3b* | 15 | *9:41014133-41014140* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ift46* | 20 | *9:44792718-44792725* | + | mmu-miR-128-3p | 7mer-A1 |
| *Scn2b* | 31 | *9:45129075-45129082* | + | mmu-miR-128-3p | 7mer-A1 |
| *Cadm1* | 37 | *9:47851139-47851146* | + | mmu-miR-128-3p | 7mer-A1 |
| *Exph5* | 35 | *9:53381106-53381113* | + | mmu-miR-128-3p | 7mer-A1 |
| *Slc35f2* | 13 | *9:53817445-53817452* | + | mmu-miR-128-3p | 7mer-A1 |
| *Dmxl2* | 11 | *9:54365940-54365947* | - | mmu-miR-128-3p | 7mer-A1 |
| *Sema7a* | 39 | *9:57962654-57962661* | + | mmu-miR-128-3p | 7mer-A1 |
| *Chst2* | 11 | *9:95401178-95401185* | - | mmu-miR-128-3p | 7mer-A1 |
| *Dbr1* | 18 | *9:99584035-99584042* | + | mmu-miR-128-3p | 7mer-A1 |
| *Stag1* | 37 | *9:100956615-100956622* | + | mmu-miR-128-3p | 7mer-A1 |
| *Rad54l2* | 124 | *9:106688717-106688724* | - | mmu-miR-128-3p | 7mer-A1 |
| *Rbm5* | 22 | *9:107740776-107740783* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ubp1* | 22 | *9:113975477-113975484* | + | mmu-miR-128-3p | 7mer-A1 |
| *Wdr13* | 18 | *X:8125611-8125618* | - | mmu-miR-128-3p | 7mer-A1 |
| *6720401G13Rik* | 13 | *X:50569885-50569892* | - | mmu-miR-128-3p | 7mer-A1 |
| *Vbp1* | 225 | *X:75534239-75534246* | + | mmu-miR-128-3p | 7mer-A1 |
| *Dlg3* | 59 | *X:100818117-100818124* | + | mmu-miR-128-3p | 7mer-A1 |
| *Zdhhc15* | 32 | *X:104540593-104540600* | - | mmu-miR-128-3p | 7mer-A1 |
| *Ngfrap1* | 75 | *X:136271692-136271699* | + | mmu-miR-128-3p | 7mer-A1 |
| *Txlng* | 12 | *X:162779114-162779121* | - | mmu-miR-128-3p | 7mer-A1 |
| *Lmbrd1* | 14 | *1:24762932-24762938* | + | mmu-miR-128-3p | 6mer |
| *Phf3* | 18 | *1:30803736-30803742* | - | mmu-miR-128-3p | 6mer |
| *Amer3* | 20 | *1:34590376-34590382* | + | mmu-miR-128-3p | 6mer |
| *Fam168b* | 14 | *1:34813597-34813603* | - | mmu-miR-128-3p | 6mer |

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|---|---|---|---|---|---|
| *Fam168b* | 89 | *1:34814145-34814151* | - | mmu-miR-128-3p | 6mer |
| *Plekhb2* | 39 | *1:34877446-34877452* | + | mmu-miR-128-3p | 6mer |
| *Kansl3* | 45 | *1:36336857-36336863* | - | mmu-miR-128-3p | 6mer |
| *Rnf149* | 16 | *1:39552024-39552030* | - | mmu-miR-128-3p | 6mer |
| *Creg2* | 35 | *1:39621883-39621889* | - | mmu-miR-128-3p | 6mer |
| *Pou3f3* | 18 | *1:42699056-42699062* | + | mmu-miR-128-3p | 6mer |
| *Nck2* | 19 | *1:43569910-43569916* | + | mmu-miR-128-3p | 6mer |
| *Gls* | 10 | *1:52165882-52165888* | - | mmu-miR-128-3p | 6mer |
| *Pgap1* | 15 | *1:54474404-54474410* | - | mmu-miR-128-3p | 6mer |
| *Pgap1* | 15 | *1:54474456-54474462* | - | mmu-miR-128-3p | 6mer |
| *Ino80d* | 12 | *1:63056931-63056937* | - | mmu-miR-128-3p | 6mer |
| *Map2* | 24 | *1:66441070-66441076* | + | mmu-miR-128-3p | 6mer |
| *Epha4* | 14 | *1:77367722-77367728* | - | mmu-miR-128-3p | 6mer |
| *Kif1a* | 16 | *1:93018085-93018091* | - | mmu-miR-128-3p | 6mer |
| *Arl8a* | 33 | *1:135155272-135155278* | + | mmu-miR-128-3p | 6mer |
| *Nav1* | 10 | *1:135439936-135439942* | - | mmu-miR-128-3p | 6mer |
| *Camsap2* | 24 | *1:136269629-136269635* | - | mmu-miR-128-3p | 6mer |
| *Rgs2* | 15 | *1:144001226-144001232* | - | mmu-miR-128-3p | 6mer |
| *Acbd6* | 12 | *1:155687305-155687311* | + | mmu-miR-128-3p | 6mer |
| *Astn1* | 67 | *1:158690906-158690912* | + | mmu-miR-128-3p | 6mer |
| *Vamp4* | 21 | *1:162598134-162598140* | + | mmu-miR-128-3p | 6mer |
| *Sft2d2* | 10 | *1:165176626-165176632* | - | mmu-miR-128-3p | 6mer |
| *Sft2d2* | 22 | *1:165177787-165177793* | - | mmu-miR-128-3p | 6mer |
| *Sft2d2* | 22 | *1:165177825-165177831* | - | mmu-miR-128-3p | 6mer |
| *Adamts4* | 19 | *1:171260905-171260911* | + | mmu-miR-128-3p | 6mer |
| *Pfdn2* | 17 | *1:171359006-171359012* | + | mmu-miR-128-3p | 6mer |
| *Pvrl4* | 19 | *1:171387261-171387267* | + | mmu-miR-128-3p | 6mer |
| *Pea15a* | 49 | *1:172197502-172197508* | - | mmu-miR-128-3p | 6mer |
| *Kcnj10* | 60 | *1:172371908-172371914* | + | mmu-miR-128-3p | 6mer |
| *Akt3* | 56 | *1:177021730-177021736* | - | mmu-miR-128-3p | 6mer |
| *Zbtb18* | 40 | *1:177449330-177449336* | + | mmu-miR-128-3p | 6mer |
| *Zbtb18* | 19 | *1:177450056-177450062* | + | mmu-miR-128-3p | 6mer |
| *Srp9* | 11 | *1:182131941-182131947* | + | mmu-miR-128-3p | 6mer |
| *Capn2* | 37 | *1:182467401-182467407* | - | mmu-miR-128-3p | 6mer |
| *Susd4* | 52 | *1:182895373-182895379* | + | mmu-miR-128-3p | 6mer |
| *Slc30a1* | 24 | *1:191911489-191911495* | + | mmu-miR-128-3p | 6mer |
| *Pik3ip1* | 10 | *11:3342820-3342826* | + | mmu-miR-128-3p | 6mer |
| *Tug1* | 34 | *11:3639866-3639872* | - | mmu-miR-128-3p | 6mer |
| *Tug1* | 69 | *11:3646960-3646966* | - | mmu-miR-128-3p | 6mer |
| *Sf3a1* | 12 | *11:4180541-4180547* | + | mmu-miR-128-3p | 6mer |
| *Adcy1* | 74 | *11:7173883-7173889* | + | mmu-miR-128-3p | 6mer |
| *Adcy1* | 74 | *11:7173934-7173940* | + | mmu-miR-128-3p | 6mer |
| *Adcy1* | 28 | *11:7177727-7177733* | + | mmu-miR-128-3p | 6mer |
| *Clint1* | 33 | *11:45909233-45909239* | + | mmu-miR-128-3p | 6mer |
| *Gfpt2* | 36 | *11:49838011-49838017* | + | mmu-miR-128-3p | 6mer |
| *Phf15* | 11 | *11:51814306-51814312* | - | mmu-miR-128-3p | 6mer |
| *Cdc42se2* | 12 | *11:54718817-54718823* | - | mmu-miR-128-3p | 6mer |
| *Slc36a1* | 11 | *11:55235771-55235777* | + | mmu-miR-128-3p | 6mer |
| *G3bp1* | 20 | *11:55500422-55500428* | + | mmu-miR-128-3p | 6mer |
| *Cnot8* | 23 | *11:58118325-58118331* | + | mmu-miR-128-3p | 6mer |
| *Zfp672* | 13 | *11:58315379-58315385* | - | mmu-miR-128-3p | 6mer |
| *Wnt9a* | 12 | *11:59333427-59333433* | + | mmu-miR-128-3p | 6mer |
| *Tom1l2* | 82 | *11:60228342-60228348* | - | mmu-miR-128-3p | 6mer |
| *Tom1l2* | 11 | *11:60229630-60229636* | - | mmu-miR-128-3p | 6mer |
| *Smcr8* | 14 | *11:60784514-60784520* | + | mmu-miR-128-3p | 6mer |
| *Ulk2* | 15 | *11:61777783-61777789* | - | mmu-miR-128-3p | 6mer |
| *Ankfy1* | 10 | *11:72768388-72768394* | + | mmu-miR-128-3p | 6mer |
| *Ctns* | 27 | *11:73184335-73184341* | - | mmu-miR-128-3p | 6mer |
| *Ywhae* | 34 | *11:75765221-75765227* | + | mmu-miR-128-3p | 6mer |
| *Glod4* | 28 | *11:76221052-76221058* | - | mmu-miR-128-3p | 6mer |
| *Sarm1* | 11 | *11:78471518-78471524* | - | mmu-miR-128-3p | 6mer |
| *Sarm1* | 10 | *11:78471871-78471877* | - | mmu-miR-128-3p | 6mer |
| *Poldip2* | 31 | *11:78522492-78522498* | + | mmu-miR-128-3p | 6mer |
| *Nlk* | 54 | *11:78568915-78568921* | - | mmu-miR-128-3p | 6mer |
| *Cdk5r1* | 12 | *11:80479508-80479514* | + | mmu-miR-128-3p | 6mer |
| *Cdk5r1* | 42 | *11:80480428-80480434* | + | mmu-miR-128-3p | 6mer |

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|---|---|---|---|---|---|
| *Cdk5r1* | 38 | *11:80481146-80481152* | + | mmu-miR-128-3p | 6mer |
| *Dusp14* | 12 | *11:84047964-84047970* | - | mmu-miR-128-3p | 6mer |
| *Appbp2* | 46 | *11:85190796-85190802* | - | mmu-miR-128-3p | 6mer |
| *Med13* | 29 | *11:86269669-86269675* | - | mmu-miR-128-3p | 6mer |
| *Spag9* | 45 | *11:94124832-94124838* | + | mmu-miR-128-3p | 6mer |
| *Mllt6* | 23 | *11:97685167-97685173* | + | mmu-miR-128-3p | 6mer |
| *Cwc25* | 20 | *11:97747118-97747124* | - | mmu-miR-128-3p | 6mer |
| *Ormdl3* | 15 | *11:98582425-98582431* | - | mmu-miR-128-3p | 6mer |
| *Thra* | 29 | *11:98765595-98765601* | + | mmu-miR-128-3p | 6mer |
| *Jup* | 21 | *11:100371408-100371414* | - | mmu-miR-128-3p | 6mer |
| *Atp6v0a1* | 105 | *11:101062611-101062617* | + | mmu-miR-128-3p | 6mer |
| *Becn1* | 53 | *11:101288319-101288325* | - | mmu-miR-128-3p | 6mer |
| *Ubtf* | 11 | *11:102305084-102305090* | - | mmu-miR-128-3p | 6mer |
| *Rundc3a* | 36 | *11:102401618-102401624* | + | mmu-miR-128-3p | 6mer |
| *Arhgap27* | 13 | *11:103332857-103332863* | - | mmu-miR-128-3p | 6mer |
| *Arf2* | 109 | *11:103984748-103984754* | + | mmu-miR-128-3p | 6mer |
| *Limd2* | 32 | *11:106158473-106158479* | - | mmu-miR-128-3p | 6mer |
| *Ccdc47* | 42 | *11:106199695-106199701* | - | mmu-miR-128-3p | 6mer |
| *Icam2* | 13 | *11:106377722-106377728* | - | mmu-miR-128-3p | 6mer |
| *Gna13* | 22 | *11:109397425-109397431* | + | mmu-miR-128-3p | 6mer |
| *Cdc42ep4* | 32 | *11:113727683-113727689* | - | mmu-miR-128-3p | 6mer |
| *Ttyh2* | 31 | *11:114719990-114719996* | + | mmu-miR-128-3p | 6mer |
| *Gga3* | 34 | *11:115585508-115585514* | - | mmu-miR-128-3p | 6mer |
| *Grb2* | 32 | *11:115644039-115644045* | - | mmu-miR-128-3p | 6mer |
| *Tnrc6c* | 12 | *11:117761665-117761671* | + | mmu-miR-128-3p | 6mer |
| *Tnrc6c* | 80 | *11:117762065-117762071* | + | mmu-miR-128-3p | 6mer |
| *Cyth1* | 12 | *11:118165449-118165455* | - | mmu-miR-128-3p | 6mer |
| *Cbx8* | 21 | *11:119038383-119038389* | - | mmu-miR-128-3p | 6mer |
| *Nploc4* | 10 | *11:120381211-120381217* | - | mmu-miR-128-3p | 6mer |
| *Alyref* | 16 | *11:120594769-120594775* | - | mmu-miR-128-3p | 6mer |
| *Gps1* | 10 | *11:120788849-120788855* | + | mmu-miR-128-3p | 6mer |
| *Csnk1d* | 12 | *11:120963921-120963927* | - | mmu-miR-128-3p | 6mer |
| *Rab10* | 10 | *12:3246435-3246441* | - | mmu-miR-128-3p | 6mer |
| *Klhl29* | 20 | *12:5080598-5080604* | - | mmu-miR-128-3p | 6mer |
| *Pum2* | 47 | *12:8749979-8749985* | + | mmu-miR-128-3p | 6mer |
| *Myt1l* | 21 | *12:29921255-29921261* | + | mmu-miR-128-3p | 6mer |
| *Nova1* | 16 | *12:46698044-46698050* | - | mmu-miR-128-3p | 6mer |
| *Clec14a* | 14 | *12:58267313-58267319* | - | mmu-miR-128-3p | 6mer |
| *Ppp2r5e* | 35 | *12:75453777-75453783* | - | mmu-miR-128-3p | 6mer |
| *Sgpp1* | 17 | *12:75715398-75715404* | - | mmu-miR-128-3p | 6mer |
| *Nek9* | 30 | *12:85300024-85300030* | - | mmu-miR-128-3p | 6mer |
| *Calm1* | 11 | *12:100209823-100209829* | + | mmu-miR-128-3p | 6mer |
| *Clmn* | 50 | *12:104771552-104771558* | - | mmu-miR-128-3p | 6mer |
| *Gm266* | 15 | *12:111484708-111484714* | - | mmu-miR-128-3p | 6mer |
| *Jag2* | 449 | *12:112908048-112908054* | - | mmu-miR-128-3p | 6mer |
| *Jag2* | 58 | *12:112908372-112908378* | - | mmu-miR-128-3p | 6mer |
| *Vipr2* | 17 | *12:116145160-116145166* | + | mmu-miR-128-3p | 6mer |
| *Rapgef5* | 31 | *12:117756479-117756485* | + | mmu-miR-128-3p | 6mer |
| *Zmynd11* | 34 | *13:9685123-9685129* | - | mmu-miR-128-3p | 6mer |
| *Chrm3* | 18 | *13:9876071-9876077* | - | mmu-miR-128-3p | 6mer |
| *Ero1lb* | 22 | *13:12608800-12608806* | + | mmu-miR-128-3p | 6mer |
| *Ero1lb* | 22 | *13:12608807-12608813* | + | mmu-miR-128-3p | 6mer |
| *Gng4* | 10 | *13:13826317-13826323* | + | mmu-miR-128-3p | 6mer |
| *BC005537* | 60 | *13:24812968-24812974* | + | mmu-miR-128-3p | 6mer |
| *Nrsn1* | 35 | *13:25252241-25252247* | - | mmu-miR-128-3p | 6mer |
| *Sox4* | 11 | *13:28950667-28950673* | - | mmu-miR-128-3p | 6mer |
| *Ssr1* | 65 | *13:37974476-37974482* | - | mmu-miR-128-3p | 6mer |
| *Ssr1* | 36 | *13:37979504-37979510* | - | mmu-miR-128-3p | 6mer |
| *Gcnt2* | 12 | *13:40960812-40960818* | + | mmu-miR-128-3p | 6mer |
| *Ccdc90a* | 11 | *13:43541522-43541528* | - | mmu-miR-128-3p | 6mer |
| *Nup153* | 25 | *13:46680211-46680217* | - | mmu-miR-128-3p | 6mer |
| *Bicd2* | 33 | *13:49386225-49386231* | + | mmu-miR-128-3p | 6mer |
| *Rnf44* | 17 | *13:54680080-54680086* | - | mmu-miR-128-3p | 6mer |
| *Nsd1* | 30 | *13:55317655-55317661* | + | mmu-miR-128-3p | 6mer |
| *Isca1* | 10 | *13:59756371-59756377* | - | mmu-miR-128-3p | 6mer |
| *Tppp* | 51 | *13:74032521-74032527* | + | mmu-miR-128-3p | 6mer |

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|---|---|---|---|---|---|
| *Arrdc3* | 47 | *13:80894063-80894069* | + | mmu-miR-128-3p | 6mer |
| *Edil3* | 20 | *13:89319884-89319890* | + | mmu-miR-128-3p | 6mer |
| *Rasgrf2* | 14 | *13:91881692-91881698* | - | mmu-miR-128-3p | 6mer |
| *Serinc5* | 23 | *13:92710709-92710715* | + | mmu-miR-128-3p | 6mer |
| *Mtx3* | 20 | *13:92854069-92854075* | + | mmu-miR-128-3p | 6mer |
| *Homer1* | 29 | *13:93404778-93404784* | + | mmu-miR-128-3p | 6mer |
| *Lhfpl2* | 11 | *13:94195131-94195137* | + | mmu-miR-128-3p | 6mer |
| *Wdr41* | 34 | *13:95023572-95023578* | + | mmu-miR-128-3p | 6mer |
| *Enc1* | 11 | *13:97252523-97252529* | + | mmu-miR-128-3p | 6mer |
| *Kif2a* | 21 | *13:106961559-106961565* | - | mmu-miR-128-3p | 6mer |
| *Il6st* | 25 | *13:112505633-112505639* | + | mmu-miR-128-3p | 6mer |
| *Ube2e2* | 14 | *14:18573635-18573641* | - | mmu-miR-128-3p | 6mer |
| *Gng2* | 25 | *14:19874843-19874849* | - | mmu-miR-128-3p | 6mer |
| *Fut11* | 22 | *14:20698398-20698404* | + | mmu-miR-128-3p | 6mer |
| *Zmiz1* | 46 | *14:25665243-25665249* | + | mmu-miR-128-3p | 6mer |
| *Anxa11* | 21 | *14:25886550-25886556* | + | mmu-miR-128-3p | 6mer |
| *Cacna2d3* | 11 | *14:28905139-28905145* | - | mmu-miR-128-3p | 6mer |
| *Cacna1d* | 15 | *14:30040106-30040112* | - | mmu-miR-128-3p | 6mer |
| *Sfmbt1* | 15 | *14:30818269-30818275* | + | mmu-miR-128-3p | 6mer |
| *Gpr137c* | 39 | *14:45280734-45280740* | + | mmu-miR-128-3p | 6mer |
| *Gmfb* | 16 | *14:46810996-46811002* | - | mmu-miR-128-3p | 6mer |
| *Naa30* | 29 | *14:49187671-49187677* | + | mmu-miR-128-3p | 6mer |
| *Jph4* | 567 | *14:55107155-55107161* | - | mmu-miR-128-3p | 6mer |
| *Zdhhc20* | 16 | *14:57835565-57835571* | - | mmu-miR-128-3p | 6mer |
| *Dleu2* | 297 | *14:61631900-61631906* | - | mmu-miR-128-3p | 6mer |
| *Dleu2* | 297 | *14:61632045-61632051* | - | mmu-miR-128-3p | 6mer |
| *Lrch1* | 55 | *14:74755202-74755208* | - | mmu-miR-128-3p | 6mer |
| *Slitrk1* | 17 | *14:108910983-108910989* | - | mmu-miR-128-3p | 6mer |
| *Hs6st3* | 15 | *14:119870750-119870756* | + | mmu-miR-128-3p | 6mer |
| *Myo10* | 20 | *15:25812558-25812564* | + | mmu-miR-128-3p | 6mer |
| *Sdc2* | 13 | *15:33034582-33034588* | + | mmu-miR-128-3p | 6mer |
| *Mtdh* | 35 | *15:34141057-34141063* | + | mmu-miR-128-3p | 6mer |
| *Mtdh* | 14 | *15:34141858-34141864* | + | mmu-miR-128-3p | 6mer |
| *Rims2* | 16 | *15:39684082-39684088* | + | mmu-miR-128-3p | 6mer |
| *Enpp2* | 89 | *15:54839192-54839198* | - | mmu-miR-128-3p | 6mer |
| *Ago2* | 37 | *15:73105587-73105593* | - | mmu-miR-128-3p | 6mer |
| *Nrbp2* | 49 | *15:76085680-76085686* | - | mmu-miR-128-3p | 6mer |
| *1110038F14Rik* | 14 | *15:76950621-76950627* | + | mmu-miR-128-3p | 6mer |
| *Elfn2* | 18 | *15:78671585-78671591* | - | mmu-miR-128-3p | 6mer |
| *Cbx7* | 13 | *15:79918291-79918297* | - | mmu-miR-128-3p | 6mer |
| *Pdgfb* | 15 | *15:79996988-79996994* | - | mmu-miR-128-3p | 6mer |
| *Syngr1* | 35 | *15:80117735-80117741* | + | mmu-miR-128-3p | 6mer |
| *Cacna1i* | 98 | *15:80397731-80397737* | + | mmu-miR-128-3p | 6mer |
| *Tnrc6b* | 13 | *15:80933053-80933059* | + | mmu-miR-128-3p | 6mer |
| *Tnrc6b* | 17 | *15:80936762-80936768* | + | mmu-miR-128-3p | 6mer |
| *Rbx1* | 36 | *15:81475673-81475679* | + | mmu-miR-128-3p | 6mer |
| *Rangap1* | 38 | *15:81705036-81705042* | - | mmu-miR-128-3p | 6mer |
| *Xrcc6* | 43 | *15:82040086-82040092* | + | mmu-miR-128-3p | 6mer |
| *Srebf2* | 14 | *15:82205237-82205243* | + | mmu-miR-128-3p | 6mer |
| *Tcf20* | 33 | *15:82808803-82808809* | - | mmu-miR-128-3p | 6mer |
| *Scube1* | 28 | *15:83606829-83606835* | - | mmu-miR-128-3p | 6mer |
| *Scube1* | 28 | *15:83606960-83606966* | - | mmu-miR-128-3p | 6mer |
| *Mpped1* | 27 | *15:83858083-83858089* | + | mmu-miR-128-3p | 6mer |
| *Phf21b* | 43 | *15:84786321-84786327* | - | mmu-miR-128-3p | 6mer |
| *Gramd4* | 36 | *15:86135542-86135548* | + | mmu-miR-128-3p | 6mer |
| *Kif21a* | 207 | *15:90933623-90933629* | - | mmu-miR-128-3p | 6mer |
| *Gxylt1* | 14 | *15:93244071-93244077* | - | mmu-miR-128-3p | 6mer |
| *Adcy6* | 13 | *15:98591945-98591951* | - | mmu-miR-128-3p | 6mer |
| *Adcy6* | 20 | *15:98592195-98592201* | - | mmu-miR-128-3p | 6mer |
| *Cacnb3* | 16 | *15:98643709-98643715* | + | mmu-miR-128-3p | 6mer |
| *Arf3* | 40 | *15:98737656-98737662* | - | mmu-miR-128-3p | 6mer |
| *Asic1* | 38 | *15:99700242-99700248* | + | mmu-miR-128-3p | 6mer |
| *Pou6f1* | 24 | *15:100577926-100577932* | - | mmu-miR-128-3p | 6mer |
| *Nudt16l1* | 66 | *16:4940906-4940912* | + | mmu-miR-128-3p | 6mer |
| *Mkl2* | 27 | *16:13417336-13417342* | + | mmu-miR-128-3p | 6mer |
| *Pdxdc1* | 16 | *16:13834103-13834109* | - | mmu-miR-128-3p | 6mer |

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|---|---|---|---|---|---|
| *Abcf3* | 12 | *16:20560533-20560539* | + | mmu-miR-128-3p | 6mer |
| *Ece2* | 90 | *16:20645261-20645267* | + | mmu-miR-128-3p | 6mer |
| *1700021K19Rik* | 370 | *16:32823550-32823556* | - | mmu-miR-128-3p | 6mer |
| *Heg1* | 39 | *16:33767993-33767999* | + | mmu-miR-128-3p | 6mer |
| *Kalrn* | 109 | *16:33970397-33970403* | - | mmu-miR-128-3p | 6mer |
| *Zbtb20* | 74 | *16:43619362-43619368* | + | mmu-miR-128-3p | 6mer |
| *Cd47* | 14 | *16:49911822-49911828* | + | mmu-miR-128-3p | 6mer |
| *Rcan1* | 44 | *16:92393390-92393396* | - | mmu-miR-128-3p | 6mer |
| *Wrb* | 24 | *16:96157853-96157859* | + | mmu-miR-128-3p | 6mer |
| *B3galt5* | 14 | *16:96319024-96319030* | + | mmu-miR-128-3p | 6mer |
| *Pisd-ps2* | 25 | *17:3079570-3079576* | - | mmu-miR-128-3p | 6mer |
| *Mas1* | 23 | *17:12841248-12841254* | - | mmu-miR-128-3p | 6mer |
| *Mrps34* | 27 | *17:24896134-24896140* | + | mmu-miR-128-3p | 6mer |
| *Cramp1l* | 52 | *17:24962771-24962777* | - | mmu-miR-128-3p | 6mer |
| *Pigq* | 22 | *17:25926606-25926612* | - | mmu-miR-128-3p | 6mer |
| *Slc29a1* | 41 | *17:45585550-45585556* | - | mmu-miR-128-3p | 6mer |
| *Gtpbp2* | 91 | *17:46168753-46168759* | + | mmu-miR-128-3p | 6mer |
| *Gtpbp2* | 91 | *17:46168828-46168834* | + | mmu-miR-128-3p | 6mer |
| *Gltscr1l* | 30 | *17:46799374-46799380* | - | mmu-miR-128-3p | 6mer |
| *Taf8* | 29 | *17:47489664-47489670* | - | mmu-miR-128-3p | 6mer |
| *Nfya* | 11 | *17:48388635-48388641* | - | mmu-miR-128-3p | 6mer |
| *Pja2* | 13 | *17:64281888-64281894* | - | mmu-miR-128-3p | 6mer |
| *Ankrd12* | 13 | *17:65970093-65970099* | - | mmu-miR-128-3p | 6mer |
| *Ehd3* | 10 | *17:73831596-73831602* | + | mmu-miR-128-3p | 6mer |
| *Sos1* | 19 | *17:80396684-80396690* | - | mmu-miR-128-3p | 6mer |
| *Srbd1* | 18 | *17:85984593-85984599* | - | mmu-miR-128-3p | 6mer |
| *Mcfd2* | 57 | *17:87255768-87255774* | - | mmu-miR-128-3p | 6mer |
| *Crem* | 17 | *18:3267979-3267985* | - | mmu-miR-128-3p | 6mer |
| *Kif5b* | 52 | *18:6203437-6203443* | - | mmu-miR-128-3p | 6mer |
| *Aqp4* | 16 | *18:15391942-15391948* | - | mmu-miR-128-3p | 6mer |
| *Iws1* | 27 | *18:32103678-32103684* | + | mmu-miR-128-3p | 6mer |
| *Dnajc18* | 31 | *18:35673686-35673692* | - | mmu-miR-128-3p | 6mer |
| *Pcdh1* | 42 | *18:38196793-38196799* | - | mmu-miR-128-3p | 6mer |
| *Mcc* | 31 | *18:44425576-44425582* | - | mmu-miR-128-3p | 6mer |
| *C330018D20Rik* | 29 | *18:56957285-56957291* | - | mmu-miR-128-3p | 6mer |
| *Ndst1* | 41 | *18:60687411-60687417* | - | mmu-miR-128-3p | 6mer |
| *St8sia3* | 13 | *18:64273561-64273567* | + | mmu-miR-128-3p | 6mer |
| *St8sia3* | 29 | *18:64275833-64275839* | + | mmu-miR-128-3p | 6mer |
| *Onecut2* | 15 | *18:64396218-64396224* | + | mmu-miR-128-3p | 6mer |
| *Gnal* | 56 | *18:67223603-67223609* | + | mmu-miR-128-3p | 6mer |
| *Rnf165* | 14 | *18:77458300-77458306* | - | mmu-miR-128-3p | 6mer |
| *Pitpnm1* | 15 | *19:4113800-4113806* | + | mmu-miR-128-3p | 6mer |
| *Pla2g16* | 17 | *19:7587278-7587284* | + | mmu-miR-128-3p | 6mer |
| *Hnrnpul2* | 37 | *19:8833251-8833257* | + | mmu-miR-128-3p | 6mer |
| *Hnrnpul2* | 11 | *19:8834031-8834037* | + | mmu-miR-128-3p | 6mer |
| *Vldlr* | 11 | *19:27252770-27252776* | + | mmu-miR-128-3p | 6mer |
| *Frat2* | 27 | *19:41847015-41847021* | - | mmu-miR-128-3p | 6mer |
| *Actr1a* | 28 | *19:46377692-46377698* | - | mmu-miR-128-3p | 6mer |
| *Nt5c2* | 27 | *19:46888217-46888223* | - | mmu-miR-128-3p | 6mer |
| *Sorcs1* | 17 | *19:50148055-50148061* | - | mmu-miR-128-3p | 6mer |
| *Add3* | 23 | *19:53245366-53245372* | + | mmu-miR-128-3p | 6mer |
| *Adra2a* | 34 | *19:54048853-54048859* | + | mmu-miR-128-3p | 6mer |
| *Vti1a* | 33 | *19:55626074-55626080* | + | mmu-miR-128-3p | 6mer |
| *Ablim1* | 10 | *19:57036808-57036814* | - | mmu-miR-128-3p | 6mer |
| *Ndor1* | 13 | *2:25246344-25246350* | - | mmu-miR-128-3p | 6mer |
| *Fbxw5* | 10 | *2:25505407-25505413* | + | mmu-miR-128-3p | 6mer |
| *Camsap1* | 14 | *2:25928407-25928413* | - | mmu-miR-128-3p | 6mer |
| *Sdccag3* | 31 | *2:26383122-26383128* | - | mmu-miR-128-3p | 6mer |
| *Wdr5* | 36 | *2:27534835-27534841* | + | mmu-miR-128-3p | 6mer |
| *Olfm1* | 43 | *2:28214507-28214513* | + | mmu-miR-128-3p | 6mer |
| *Gtf3c4* | 26 | *2:28825616-28825622* | - | mmu-miR-128-3p | 6mer |
| *Rapgef1* | 40 | *2:29739448-29739454* | + | mmu-miR-128-3p | 6mer |
| *Urm1* | 20 | *2:29844487-29844493* | + | mmu-miR-128-3p | 6mer |
| *Prrc2b* | 24 | *2:32230978-32230984* | + | mmu-miR-128-3p | 6mer |
| *Stxbp1* | 50 | *2:32788393-32788399* | - | mmu-miR-128-3p | 6mer |
| *Dab2ip* | 26 | *2:35728244-35728250* | + | mmu-miR-128-3p | 6mer |

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|---|---|---|---|---|---|
| *Lhx6* | 15 | *2:36082600-36082606* | - | mmu-miR-128-3p | 6mer |
| *Nr6a1* | 72 | *2:38727732-38727738* | - | mmu-miR-128-3p | 6mer |
| *Fmnl2* | 15 | *2:53132563-53132569* | + | mmu-miR-128-3p | 6mer |
| *Scn2a1* | 29 | *2:65766622-65766628* | + | mmu-miR-128-3p | 6mer |
| *Csrnp3* | 15 | *2:66023179-66023185* | + | mmu-miR-128-3p | 6mer |
| *Csrnp3* | 15 | *2:66023295-66023301* | + | mmu-miR-128-3p | 6mer |
| *Gad1* | 12 | *2:70601385-70601391* | + | mmu-miR-128-3p | 6mer |
| *Rapgef4* | 14 | *2:72256451-72256457* | + | mmu-miR-128-3p | 6mer |
| *Rapgef4* | 24 | *2:72256713-72256719* | + | mmu-miR-128-3p | 6mer |
| *Zdhhc5* | 22 | *2:84688464-84688470* | - | mmu-miR-128-3p | 6mer |
| *Ypel4* | 28 | *2:84738039-84738045* | + | mmu-miR-128-3p | 6mer |
| *Trim44* | 10 | *2:102304294-102304300* | - | mmu-miR-128-3p | 6mer |
| *Slc1a2* | 25 | *2:102784054-102784060* | + | mmu-miR-128-3p | 6mer |
| *Slc1a2* | 15 | *2:102789014-102789020* | + | mmu-miR-128-3p | 6mer |
| *Caprin1* | 17 | *2:103766147-103766153* | - | mmu-miR-128-3p | 6mer |
| *Fbxo3* | 55 | *2:104060467-104060473* | + | mmu-miR-128-3p | 6mer |
| *Fmn1* | 45 | *2:113710699-113710705* | + | mmu-miR-128-3p | 6mer |
| *Gpr176* | 23 | *2:118276318-118276324* | - | mmu-miR-128-3p | 6mer |
| *Ankrd63* | 456 | *2:118700855-118700861* | - | mmu-miR-128-3p | 6mer |
| *Ehd4* | 24 | *2:120090723-120090729* | - | mmu-miR-128-3p | 6mer |
| *Shf* | 17 | *2:122349163-122349169* | - | mmu-miR-128-3p | 6mer |
| *Ap4e1* | 14 | *2:127066861-127066867* | + | mmu-miR-128-3p | 6mer |
| *Sirpa* | 10 | *2:129630845-129630851* | + | mmu-miR-128-3p | 6mer |
| *Cds2* | 14 | *2:132306510-132306516* | + | mmu-miR-128-3p | 6mer |
| *Cds2* | 26 | *2:132308019-132308025* | + | mmu-miR-128-3p | 6mer |
| *Plcb1* | 33 | *2:135474732-135474738* | + | mmu-miR-128-3p | 6mer |
| *Btbd3* | 24 | *2:138286805-138286811* | + | mmu-miR-128-3p | 6mer |
| *Kif3b* | 21 | *2:153330544-153330550* | + | mmu-miR-128-3p | 6mer |
| *Ncoa6* | 29 | *2:155390842-155390848* | - | mmu-miR-128-3p | 6mer |
| *Epb4.1l1* | 23 | *2:156540811-156540817* | + | mmu-miR-128-3p | 6mer |
| *Epb4.1l1* | 16 | *2:156540973-156540979* | + | mmu-miR-128-3p | 6mer |
| *Dlgap4* | 47 | *2:156764120-156764126* | + | mmu-miR-128-3p | 6mer |
| *Nnat* | 17 | *2:157562066-157562072* | + | mmu-miR-128-3p | 6mer |
| *Snhg11* | 11 | *2:158384495-158384501* | + | mmu-miR-128-3p | 6mer |
| *Ralgapb* | 29 | *2:158497961-158497967* | + | mmu-miR-128-3p | 6mer |
| *Stk4* | 46 | *2:164152287-164152293* | + | mmu-miR-128-3p | 6mer |
| *Cdh22* | 16 | *2:165111839-165111845* | - | mmu-miR-128-3p | 6mer |
| *Slc35c2* | 32 | *2:165276845-165276851* | - | mmu-miR-128-3p | 6mer |
| *Kcnb1* | 141 | *2:167101098-167101104* | - | mmu-miR-128-3p | 6mer |
| *Kcnb1* | 56 | *2:167101550-167101556* | - | mmu-miR-128-3p | 6mer |
| *Kcnb1* | 30 | *2:167103624-167103630* | - | mmu-miR-128-3p | 6mer |
| *Zfp64* | 19 | *2:168925180-168925186* | - | mmu-miR-128-3p | 6mer |
| *Zfp64* | 19 | *2:168925211-168925217* | - | mmu-miR-128-3p | 6mer |
| *Zfp64* | 19 | *2:168925245-168925251* | - | mmu-miR-128-3p | 6mer |
| *Zfp64* | 19 | *2:168925276-168925282* | - | mmu-miR-128-3p | 6mer |
| *Pmepa1* | 24 | *2:173225698-173225704* | - | mmu-miR-128-3p | 6mer |
| *Stx16* | 13 | *2:174097047-174097053* | + | mmu-miR-128-3p | 6mer |
| *Gm14325* | 19 | *2:177830368-177830374* | - | mmu-miR-128-3p | 6mer |
| *Ppp1r3d* | 63 | *2:178412050-178412056* | - | mmu-miR-128-3p | 6mer |
| *Znf512b* | 36 | *2:181583123-181583129* | - | mmu-miR-128-3p | 6mer |
| *Oprl1* | 11 | *2:181720143-181720149* | + | mmu-miR-128-3p | 6mer |
| *Zfp704* | 111 | *3:9432294-9432300* | - | mmu-miR-128-3p | 6mer |
| *Zfp704* | 18 | *3:9432857-9432863* | - | mmu-miR-128-3p | 6mer |
| *Zmat3* | 61 | *3:32337794-32337800* | - | mmu-miR-128-3p | 6mer |
| *Mccc1* | 10 | *3:35959994-35960000* | - | mmu-miR-128-3p | 6mer |
| *Setd7* | 14 | *3:51515480-51515486* | - | mmu-miR-128-3p | 6mer |
| *Tsc22d2* | 36 | *3:58461340-58461346* | + | mmu-miR-128-3p | 6mer |
| *Mbnl1* | 30 | *3:60626953-60626959* | + | mmu-miR-128-3p | 6mer |
| *Kpna4* | 13 | *3:69073561-69073567* | - | mmu-miR-128-3p | 6mer |
| *Slitrk3* | 104 | *3:73048192-73048198* | - | mmu-miR-128-3p | 6mer |
| *Gria2* | 12 | *3:80688005-80688011* | - | mmu-miR-128-3p | 6mer |
| *Trim2* | 20 | *3:84161061-84161067* | - | mmu-miR-128-3p | 6mer |
| *Syt11* | 31 | *3:88744813-88744819* | - | mmu-miR-128-3p | 6mer |
| *Efna3* | 12 | *3:89314938-89314944* | - | mmu-miR-128-3p | 6mer |
| *Kcnn3* | 17 | *3:89669020-89669026* | + | mmu-miR-128-3p | 6mer |
| *Chrnb2* | 22 | *3:89753530-89753536* | - | mmu-miR-128-3p | 6mer |

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|---|---|---|---|---|---|
| *Chtop* | 10 | *3:90498576-90498582* | - | mmu-miR-128-3p | 6mer |
| *Sv2a* | 25 | *3:96194506-96194512* | + | mmu-miR-128-3p | 6mer |
| *Pde4dip* | 15 | *3:97690550-97690556* | - | mmu-miR-128-3p | 6mer |
| *Zfp697* | 20 | *3:98428940-98428946* | + | mmu-miR-128-3p | 6mer |
| *Man1a2* | 27 | *3:100563121-100563127* | - | mmu-miR-128-3p | 6mer |
| *Tspan2* | 25 | *3:102769367-102769373* | + | mmu-miR-128-3p | 6mer |
| *Bcas2* | 24 | *3:103178532-103178538* | + | mmu-miR-128-3p | 6mer |
| *Hipk1* | 61 | *3:103743263-103743269* | - | mmu-miR-128-3p | 6mer |
| *Cyb561d1* | 31 | *3:108198562-108198568* | - | mmu-miR-128-3p | 6mer |
| *Sort1* | 104 | *3:108357504-108357510* | + | mmu-miR-128-3p | 6mer |
| *Gpr88* | 21 | *3:116251091-116251097* | - | mmu-miR-128-3p | 6mer |
| *Agl* | 38 | *3:116743181-116743187* | - | mmu-miR-128-3p | 6mer |
| *D3Bwg0562e* | 61 | *3:117320692-117320698* | - | mmu-miR-128-3p | 6mer |
| *F3* | 19 | *3:121734306-121734312* | + | mmu-miR-128-3p | 6mer |
| *Ank2* | 25 | *3:126922022-126922028* | - | mmu-miR-128-3p | 6mer |
| *Col25a1* | 54 | *3:130596124-130596130* | + | mmu-miR-128-3p | 6mer |
| *H2afz* | 22 | *3:137866644-137866650* | + | mmu-miR-128-3p | 6mer |
| *Rap1gds1* | 44 | *3:138926036-138926042* | - | mmu-miR-128-3p | 6mer |
| *Hs2st1* | 34 | *3:144434443-144434449* | - | mmu-miR-128-3p | 6mer |
| *Necab1* | 24 | *4:14953602-14953608* | - | mmu-miR-128-3p | 6mer |
| *Faxc* | 15 | *4:21994470-21994476* | + | mmu-miR-128-3p | 6mer |
| *Aptx* | 10 | *4:40686050-40686056* | - | mmu-miR-128-3p | 6mer |
| *N28178* | 17 | *4:42941864-42941870* | + | mmu-miR-128-3p | 6mer |
| *Fam214b* | 12 | *4:43036432-43036438* | - | mmu-miR-128-3p | 6mer |
| *Gba2* | 13 | *4:43567173-43567179* | - | mmu-miR-128-3p | 6mer |
| *Rnf38* | 12 | *4:44129394-44129400* | - | mmu-miR-128-3p | 6mer |
| *Fbxo10* | 10 | *4:45035500-45035506* | - | mmu-miR-128-3p | 6mer |
| *Gabbr2* | 29 | *4:46664137-46664143* | - | mmu-miR-128-3p | 6mer |
| *Rad23b* | 80 | *4:55390826-55390832* | + | mmu-miR-128-3p | 6mer |
| *Lpar1* | 26 | *4:58436420-58436426* | - | mmu-miR-128-3p | 6mer |
| *Nfib* | 31 | *4:82290713-82290719* | - | mmu-miR-128-3p | 6mer |
| *Ttc39b* | 78 | *4:83222308-83222314* | - | mmu-miR-128-3p | 6mer |
| *Dab1* | 34 | *4:104741907-104741913* | + | mmu-miR-128-3p | 6mer |
| *Dhcr24* | 20 | *4:106588242-106588248* | + | mmu-miR-128-3p | 6mer |
| *Hectd3* | 13 | *4:117003542-117003548* | + | mmu-miR-128-3p | 6mer |
| *Atp6v0b* | 18 | *4:117884412-117884418* | - | mmu-miR-128-3p | 6mer |
| *AU022252* | 23 | *4:119226146-119226152* | - | mmu-miR-128-3p | 6mer |
| *1110065P20Rik* | 18 | *4:124849676-124849682* | - | mmu-miR-128-3p | 6mer |
| *Grik3* | 12 | *4:125712693-125712699* | + | mmu-miR-128-3p | 6mer |
| *Grik3* | 14 | *4:125714015-125714021* | + | mmu-miR-128-3p | 6mer |
| *Ago1* | 14 | *4:126438188-126438194* | - | mmu-miR-128-3p | 6mer |
| *Phc2* | 29 | *4:128752241-128752247* | + | mmu-miR-128-3p | 6mer |
| *Phc2* | 29 | *4:128752253-128752259* | + | mmu-miR-128-3p | 6mer |
| *Eya3* | 31 | *4:132723938-132723944* | + | mmu-miR-128-3p | 6mer |
| *Sfn* | 13 | *4:133600690-133600696* | - | mmu-miR-128-3p | 6mer |
| *Fbxo42* | 13 | *4:141202809-141202815* | + | mmu-miR-128-3p | 6mer |
| *Kif1b* | 50 | *4:149176390-149176396* | - | mmu-miR-128-3p | 6mer |
| *Per3* | 14 | *4:151005276-151005282* | - | mmu-miR-128-3p | 6mer |
| *Gpr153* | 53 | *4:152284885-152284891* | + | mmu-miR-128-3p | 6mer |
| *Lrrc47* | 57 | *4:154020439-154020445* | + | mmu-miR-128-3p | 6mer |
| *Ski* | 43 | *4:155155860-155155866* | - | mmu-miR-128-3p | 6mer |
| *Gnb1* | 45 | *4:155559043-155559049* | + | mmu-miR-128-3p | 6mer |
| *Gnb1* | 45 | *4:155559054-155559060* | + | mmu-miR-128-3p | 6mer |
| *Cacna2d1* | 21 | *5:16371738-16371744* | + | mmu-miR-128-3p | 6mer |
| *Gnai1* | 38 | *5:18265175-18265181* | - | mmu-miR-128-3p | 6mer |
| *Chpf2* | 16 | *5:24592943-24592949* | + | mmu-miR-128-3p | 6mer |
| *Pisd* | 79 | *5:32736551-32736557* | - | mmu-miR-128-3p | 6mer |
| *Whsc1* | 15 | *5:33876835-33876841* | + | mmu-miR-128-3p | 6mer |
| *Nat8l* | 55 | *5:34004730-34004736* | + | mmu-miR-128-3p | 6mer |
| *Cpeb2* | 10 | *5:43288690-43288696* | + | mmu-miR-128-3p | 6mer |
| *Lcorl* | 18 | *5:45733424-45733430* | - | mmu-miR-128-3p | 6mer |
| *Stim2* | 24 | *5:54119669-54119675* | + | mmu-miR-128-3p | 6mer |
| *Rfc1* | 14 | *5:65262129-65262135* | - | mmu-miR-128-3p | 6mer |
| *Dcun1d4* | 33 | *5:73559944-73559950* | + | mmu-miR-128-3p | 6mer |
| *Sgcb* | 14 | *5:73633940-73633946* | - | mmu-miR-128-3p | 6mer |
| *Usp46* | 14 | *5:74001412-74001418* | - | mmu-miR-128-3p | 6mer |

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|---|---|---|---|---|---|
| *Clock* | 385 | *5:76213895-76213901* | - | mmu-miR-128-3p | 6mer |
| *Mob1b* | 65 | *5:88756531-88756537* | + | mmu-miR-128-3p | 6mer |
| *Dck* | 16 | *5:88781933-88781939* | + | mmu-miR-128-3p | 6mer |
| *Slc4a4* | 102 | *5:89236708-89236714* | + | mmu-miR-128-3p | 6mer |
| *Rchy1* | 18 | *5:91957660-91957666* | - | mmu-miR-128-3p | 6mer |
| *Cdkl2* | 31 | *5:92007524-92007530* | - | mmu-miR-128-3p | 6mer |
| *Mapk10* | 101 | *5:102910163-102910169* | - | mmu-miR-128-3p | 6mer |
| *Sparcl1* | 27 | *5:104078714-104078720* | - | mmu-miR-128-3p | 6mer |
| *Evi5* | 40 | *5:107746795-107746801* | - | mmu-miR-128-3p | 6mer |
| *Evi5* | 40 | *5:107746843-107746849* | - | mmu-miR-128-3p | 6mer |
| *Pgam5* | 10 | *5:110259728-110259734* | - | mmu-miR-128-3p | 6mer |
| *Asphd2* | 26 | *5:112385683-112385689* | - | mmu-miR-128-3p | 6mer |
| *Asphd2* | 26 | *5:112385704-112385710* | - | mmu-miR-128-3p | 6mer |
| *Adrbk2* | 15 | *5:112911691-112911697* | - | mmu-miR-128-3p | 6mer |
| *2900026A02Rik* | 22 | *5:113089102-113089108* | - | mmu-miR-128-3p | 6mer |
| *Mmab* | 23 | *5:114431446-114431452* | - | mmu-miR-128-3p | 6mer |
| *Gltp* | 12 | *5:114669949-114669955* | - | mmu-miR-128-3p | 6mer |
| *Dtx1* | 39 | *5:120680160-120680166* | - | mmu-miR-128-3p | 6mer |
| *Ptpn11* | 34 | *5:121132038-121132044* | - | mmu-miR-128-3p | 6mer |
| *Ptpn11* | 17 | *5:121132719-121132725* | - | mmu-miR-128-3p | 6mer |
| *Atp2a2* | 84 | *5:122455931-122455937* | - | mmu-miR-128-3p | 6mer |
| *Vps33a* | 24 | *5:123530372-123530378* | - | mmu-miR-128-3p | 6mer |
| *Bri3bp* | 36 | *5:125455915-125455921* | + | mmu-miR-128-3p | 6mer |
| *Vkorc1l1* | 16 | *5:129983601-129983607* | + | mmu-miR-128-3p | 6mer |
| *Gatsl2* | 69 | *5:134139801-134139807* | + | mmu-miR-128-3p | 6mer |
| *Bcl7b* | 14 | *5:135181299-135181305* | + | mmu-miR-128-3p | 6mer |
| *Zfp12* | 39 | *5:143247381-143247387* | + | mmu-miR-128-3p | 6mer |
| *Daglb* | 51 | *5:143503490-143503496* | + | mmu-miR-128-3p | 6mer |
| *Cyth3* | 37 | *5:143709901-143709907* | + | mmu-miR-128-3p | 6mer |
| *Lmtk2* | 43 | *5:144187213-144187219* | + | mmu-miR-128-3p | 6mer |
| *Polr1d* | 10 | *5:147111059-147111065* | + | mmu-miR-128-3p | 6mer |
| *Tmem106b* | 53 | *6:13084255-13084261* | + | mmu-miR-128-3p | 6mer |
| *Tmem106b* | 53 | *6:13084466-13084472* | + | mmu-miR-128-3p | 6mer |
| *Klhdc10* | 66 | *6:30452898-30452904* | + | mmu-miR-128-3p | 6mer |
| *Klhdc10* | 11 | *6:30454213-30454219* | + | mmu-miR-128-3p | 6mer |
| *Mtpn* | 11 | *6:35509115-35509121* | - | mmu-miR-128-3p | 6mer |
| *Ubn2* | 12 | *6:38502835-38502841* | + | mmu-miR-128-3p | 6mer |
| *Hnrnpa2b1* | 16 | *6:51462438-51462444* | - | mmu-miR-128-3p | 6mer |
| *Ppm1k* | 23 | *6:57506776-57506782* | - | mmu-miR-128-3p | 6mer |
| *Rmnd5a* | 88 | *6:71391504-71391510* | - | mmu-miR-128-3p | 6mer |
| *Rmnd5a* | 88 | *6:71391511-71391517* | - | mmu-miR-128-3p | 6mer |
| *Reep1* | 13 | *6:71810050-71810056* | + | mmu-miR-128-3p | 6mer |
| *Tet3* | 35 | *6:83362775-83362781* | - | mmu-miR-128-3p | 6mer |
| *Rab11fip5* | 18 | *6:85336198-85336204* | - | mmu-miR-128-3p | 6mer |
| *Add2* | 88 | *6:86121562-86121568* | + | mmu-miR-128-3p | 6mer |
| *Add2* | 46 | *6:86124309-86124315* | + | mmu-miR-128-3p | 6mer |
| *Gmcl1* | 63 | *6:86692836-86692842* | - | mmu-miR-128-3p | 6mer |
| *Mgll* | 37 | *6:88826664-88826670* | + | mmu-miR-128-3p | 6mer |
| *Slc6a6* | 55 | *6:91756536-91756542* | + | mmu-miR-128-3p | 6mer |
| *Slc6a6* | 55 | *6:91756660-91756666* | + | mmu-miR-128-3p | 6mer |
| *Kbtbd8* | 26 | *6:95127060-95127066* | + | mmu-miR-128-3p | 6mer |
| *Arl8b* | 29 | *6:108823642-108823648* | + | mmu-miR-128-3p | 6mer |
| *Grm7* | 56 | *6:111566735-111566741* | + | mmu-miR-128-3p | 6mer |
| *Srgap3* | 10 | *6:112721547-112721553* | - | mmu-miR-128-3p | 6mer |
| *Lhfpl4* | 53 | *6:113169256-113169262* | - | mmu-miR-128-3p | 6mer |
| *Brk1* | 48 | *6:113616703-113616709* | + | mmu-miR-128-3p | 6mer |
| *Tatdn2* | 13 | *6:113710889-113710895* | + | mmu-miR-128-3p | 6mer |
| *Atp2b2* | 92 | *6:113747542-113747548* | - | mmu-miR-128-3p | 6mer |
| *Adipor2* | 16 | *6:119354374-119354380* | - | mmu-miR-128-3p | 6mer |
| *Wnk1* | 24 | *6:119924439-119924445* | - | mmu-miR-128-3p | 6mer |
| *Cecr6* | 24 | *6:120489111-120489117* | - | mmu-miR-128-3p | 6mer |
| *Cecr6* | 102 | *6:120489992-120489998* | - | mmu-miR-128-3p | 6mer |
| *Iqsec3* | 20 | *6:121372939-121372945* | - | mmu-miR-128-3p | 6mer |
| *Iqsec3* | 15 | *6:121375154-121375160* | - | mmu-miR-128-3p | 6mer |
| *Clstn3* | 34 | *6:124431285-124431291* | - | mmu-miR-128-3p | 6mer |
| *Ccnd2* | 35 | *6:127126445-127126451* | - | mmu-miR-128-3p | 6mer |

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|---|---|---|---|---|---|
| *Tspan9* | 49 | *6:127963872-127963878* | - | mmu-miR-128-3p | 6mer |
| *Crebl2* | 18 | *6:134856988-134856994* | + | mmu-miR-128-3p | 6mer |
| *Crebl2* | 37 | *6:134857513-134857519* | + | mmu-miR-128-3p | 6mer |
| *Pde3a* | 15 | *6:141499419-141499425* | + | mmu-miR-128-3p | 6mer |
| *Ccdc9* | 15 | *7:16274028-16274034* | - | mmu-miR-128-3p | 6mer |
| *Ap2s1* | 31 | *7:16749221-16749227* | + | mmu-miR-128-3p | 6mer |
| *Zfp180* | 12 | *7:24106358-24106364* | + | mmu-miR-128-3p | 6mer |
| *Grik5* | 25 | *7:25010135-25010141* | - | mmu-miR-128-3p | 6mer |
| *Gm5113* | 10 | *7:30179453-30179459* | + | mmu-miR-128-3p | 6mer |
| *Emc10* | 40 | *7:44490661-44490667* | - | mmu-miR-128-3p | 6mer |
| *Grin2d* | 20 | *7:45832234-45832240* | - | mmu-miR-128-3p | 6mer |
| *Luzp2* | 10 | *7:55266273-55266279* | + | mmu-miR-128-3p | 6mer |
| *C230091D08Rik* | 10 | *7:59307750-59307756* | - | mmu-miR-128-3p | 6mer |
| *Igf1r* | 20 | *7:68231831-68231837* | + | mmu-miR-128-3p | 6mer |
| *Arrdc4* | 13 | *7:68738282-68738288* | - | mmu-miR-128-3p | 6mer |
| *Sv2b* | 73 | *7:75117745-75117751* | - | mmu-miR-128-3p | 6mer |
| *Ap3s2* | 46 | *7:79879824-79879830* | - | mmu-miR-128-3p | 6mer |
| *Crtc3* | 51 | *7:80588678-80588684* | - | mmu-miR-128-3p | 6mer |
| *Crtc3* | 51 | *7:80588760-80588766* | - | mmu-miR-128-3p | 6mer |
| *Homer2* | 42 | *7:81603823-81603829* | - | mmu-miR-128-3p | 6mer |
| *Arnt2* | 16 | *7:84246408-84246414* | - | mmu-miR-128-3p | 6mer |
| *Fzd4* | 17 | *7:89409428-89409434* | + | mmu-miR-128-3p | 6mer |
| *Rab30* | 49 | *7:92836900-92836906* | + | mmu-miR-128-3p | 6mer |
| *Fam160a2* | 27 | *7:105371414-105371420* | - | mmu-miR-128-3p | 6mer |
| *Tpp1* | 11 | *7:105746460-105746466* | - | mmu-miR-128-3p | 6mer |
| *Olfml1* | 20 | *7:107590462-107590468* | + | mmu-miR-128-3p | 6mer |
| *Tub* | 46 | *7:109032957-109032963* | + | mmu-miR-128-3p | 6mer |
| *Rps15a* | 27 | *7:118105285-118105291* | - | mmu-miR-128-3p | 6mer |
| *Usp31* | 27 | *7:121642526-121642532* | - | mmu-miR-128-3p | 6mer |
| *Usp31* | 13 | *7:121648063-121648069* | - | mmu-miR-128-3p | 6mer |
| *Gga2* | 18 | *7:121988770-121988776* | - | mmu-miR-128-3p | 6mer |
| *Prkcb* | 27 | *7:122634169-122634175* | + | mmu-miR-128-3p | 6mer |
| *Tnrc6a* | 39 | *7:123194150-123194156* | + | mmu-miR-128-3p | 6mer |
| *Ate1* | 11 | *7:130391667-130391673* | - | mmu-miR-128-3p | 6mer |
| *Chst15* | 31 | *7:132236856-132236862* | - | mmu-miR-128-3p | 6mer |
| *Deaf1* | 88 | *7:141297448-141297454* | - | mmu-miR-128-3p | 6mer |
| *Dusp8* | 33 | *7:142081700-142081706* | - | mmu-miR-128-3p | 6mer |
| *Nap1l4* | 22 | *7:143513813-143513819* | - | mmu-miR-128-3p | 6mer |
| *Ctxn1* | 140 | *8:4258313-4258319* | - | mmu-miR-128-3p | 6mer |
| *Elavl1* | 46 | *8:4285688-4285694* | - | mmu-miR-128-3p | 6mer |
| *Arhgef7* | 11 | *8:11825421-11825427* | + | mmu-miR-128-3p | 6mer |
| *Atp11a* | 28 | *8:12865966-12865972* | + | mmu-miR-128-3p | 6mer |
| *Kbtbd11* | 13 | *8:15031451-15031457* | + | mmu-miR-128-3p | 6mer |
| *Vps36* | 186 | *8:22218717-22218723* | + | mmu-miR-128-3p | 6mer |
| *Ank1* | 108 | *8:23148598-23148604* | + | mmu-miR-128-3p | 6mer |
| *Tm2d2* | 53 | *8:25023190-25023196* | + | mmu-miR-128-3p | 6mer |
| *Hgsnat* | 27 | *8:25944829-25944835* | - | mmu-miR-128-3p | 6mer |
| *Erlin2* | 16 | *8:27036747-27036753* | + | mmu-miR-128-3p | 6mer |
| *Tnks* | 16 | *8:34829732-34829738* | - | mmu-miR-128-3p | 6mer |
| *Mfhas1* | 13 | *8:35678024-35678030* | + | mmu-miR-128-3p | 6mer |
| *Psd3* | 16 | *8:67689856-67689862* | - | mmu-miR-128-3p | 6mer |
| *Csgalnact1* | 27 | *8:68358255-68358261* | - | mmu-miR-128-3p | 6mer |
| *Nacc1* | 44 | *8:84671751-84671757* | - | mmu-miR-128-3p | 6mer |
| *N4bp1* | 11 | *8:86841258-86841264* | - | mmu-miR-128-3p | 6mer |
| *N4bp1* | 11 | *8:86841265-86841271* | - | mmu-miR-128-3p | 6mer |
| *Gnao1* | 15 | *8:93957682-93957688* | + | mmu-miR-128-3p | 6mer |
| *Gnao1* | 11 | *8:93961446-93961452* | + | mmu-miR-128-3p | 6mer |
| *D230025D16Rik* | 36 | *8:105251712-105251718* | + | mmu-miR-128-3p | 6mer |
| *Pskh1* | 12 | *8:105930523-105930529* | + | mmu-miR-128-3p | 6mer |
| *Pskh1* | 63 | *8:105931018-105931024* | + | mmu-miR-128-3p | 6mer |
| *Sntb2* | 27 | *8:107012198-107012204* | + | mmu-miR-128-3p | 6mer |
| *Sntb2* | 26 | *8:107013565-107013571* | + | mmu-miR-128-3p | 6mer |
| *Atxn1l* | 21 | *8:109730814-109730820* | - | mmu-miR-128-3p | 6mer |
| *Il34* | 34 | *8:110741929-110741935* | - | mmu-miR-128-3p | 6mer |
| *Cmip* | 29 | *8:117462078-117462084* | + | mmu-miR-128-3p | 6mer |
| *Emc8* | 28 | *8:120656765-120656771* | - | mmu-miR-128-3p | 6mer |

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|---|---|---|---|---|---|
| *Slc7a5* | 19 | *8:121882376-121882382* | - | mmu-miR-128-3p | 6mer |
| *Cbfa2t3* | 11 | *8:122630184-122630190* | - | mmu-miR-128-3p | 6mer |
| *Ankrd11* | 26 | *8:122900551-122900557* | - | mmu-miR-128-3p | 6mer |
| *Egln1* | 17 | *8:124910536-124910542* | - | mmu-miR-128-3p | 6mer |
| *Gria4* | 26 | *9:4420113-4420119* | - | mmu-miR-128-3p | 6mer |
| *Fat3* | 13 | *9:15914284-15914290* | - | mmu-miR-128-3p | 6mer |
| *Fat3* | 13 | *9:15914317-15914323* | - | mmu-miR-128-3p | 6mer |
| *Tmed1* | 35 | *9:21507994-21508000* | - | mmu-miR-128-3p | 6mer |
| *BC018242* | 17 | *9:21947612-21947618* | + | mmu-miR-128-3p | 6mer |
| *Arhgap32* | 18 | *9:32264211-32264217* | + | mmu-miR-128-3p | 6mer |
| *Ddx6* | 27 | *9:44638203-44638209* | + | mmu-miR-128-3p | 6mer |
| *Scn2b* | 43 | *9:45126667-45126673* | + | mmu-miR-128-3p | 6mer |
| *Scn2b* | 24 | *9:45127151-45127157* | + | mmu-miR-128-3p | 6mer |
| *Scn4b* | 29 | *9:45152163-45152169* | + | mmu-miR-128-3p | 6mer |
| *Pafah1b2* | 38 | *9:45968128-45968134* | - | mmu-miR-128-3p | 6mer |
| *Ptpn9* | 15 | *9:57061392-57061398* | + | mmu-miR-128-3p | 6mer |
| *Cln6* | 44 | *9:62851422-62851428* | + | mmu-miR-128-3p | 6mer |
| *Rab11a* | 12 | *9:64715569-64715575* | - | mmu-miR-128-3p | 6mer |
| *Tmod2* | 50 | *9:75571742-75571748* | - | mmu-miR-128-3p | 6mer |
| *Elovl5* | 10 | *9:77983036-77983042* | + | mmu-miR-128-3p | 6mer |
| *Snap91* | 13 | *9:86766060-86766066* | - | mmu-miR-128-3p | 6mer |
| *Chst2* | 11 | *9:95401144-95401150* | - | mmu-miR-128-3p | 6mer |
| *Slc25a36* | 15 | *9:97076329-97076335* | - | mmu-miR-128-3p | 6mer |
| *Rab6b* | 34 | *9:103181666-103181672* | + | mmu-miR-128-3p | 6mer |
| *Rab6b* | 22 | *9:103182814-103182820* | + | mmu-miR-128-3p | 6mer |
| *Rab6b* | 17 | *9:103185207-103185213* | + | mmu-miR-128-3p | 6mer |
| *Uba5* | 23 | *9:104047331-104047337* | - | mmu-miR-128-3p | 6mer |
| *Mon1a* | 15 | *9:107903087-107903093* | + | mmu-miR-128-3p | 6mer |
| *Map4* | 23 | *9:110003840-110003846* | + | mmu-miR-128-3p | 6mer |
| *Arpp21* | 47 | *9:112065802-112065808* | - | mmu-miR-128-3p | 6mer |
| *Arpp21* | 29 | *9:112182543-112182549* | - | mmu-miR-128-3p | 6mer |
| *Oxsr1* | 19 | *9:119304878-119304884* | - | mmu-miR-128-3p | 6mer |
| *Myrip* | 49 | *9:120472882-120472888* | + | mmu-miR-128-3p | 6mer |
| *Usp9x* | 10 | *X:13172279-13172285* | + | mmu-miR-128-3p | 6mer |
| *Sept6* | 76 | *X:36912918-36912924* | - | mmu-miR-128-3p | 6mer |
| *Fgf13* | 11 | *X:59063089-59063095* | - | mmu-miR-128-3p | 6mer |
| *Slitrk4* | 40 | *X:64270344-64270350* | - | mmu-miR-128-3p | 6mer |
| *Cd99l2* | 15 | *X:71420414-71420420* | - | mmu-miR-128-3p | 6mer |
| *Prrg3* | 29 | *X:71967655-71967661* | + | mmu-miR-128-3p | 6mer |
| *Prrg3* | 11 | *X:71968315-71968321* | + | mmu-miR-128-3p | 6mer |
| *Atp2b3* | 35 | *X:73571723-73571729* | + | mmu-miR-128-3p | 6mer |
| *Mecp2* | 20 | *X:74031328-74031334* | - | mmu-miR-128-3p | 6mer |
| *Rab39b* | 24 | *X:75571619-75571625* | - | mmu-miR-128-3p | 6mer |
| *Pls3* | 73 | *X:75786805-75786811* | - | mmu-miR-128-3p | 6mer |
| *Gpr165* | 46 | *X:96719750-96719756* | + | mmu-miR-128-3p | 6mer |
| *Slc16a2* | 43 | *X:103699373-103699379* | - | mmu-miR-128-3p | 6mer |
| *Drp2* | 20 | *X:134456256-134456262* | + | mmu-miR-128-3p | 6mer |
| *Pak3* | 40 | *X:143797716-143797722* | + | mmu-miR-128-3p | 6mer |
| *Gpm6b* | 19 | *X:166388293-166388299* | + | mmu-miR-128-3p | 6mer |
| *Frmpd4* | 166 | *X:167472239-167472245* | - | mmu-miR-128-3p | 6mer |

**Table S3. 154 RISC-associated miR-128 target genes that show increased ribosome-association in miR-128 deficient D1-neurons.**

| | **D1-neuron TRAP analysis** (mRNAs that show increase ribosome association in wild type versus miR-128-deficient D1-neurons) | | **RISC-associated 3'UTR mRNAs in adult neurons** | | | |
|---|---|---|---|---|---|---|
| **Gene Symbol** | ***p-value*** | **Fold Change** | **# Reads in Cluster** | **Gene Title** | **Entrez Gene** | **Probe Set ID** |
| *9530068E07Rik* | 3.2E-02 | 1.36 | 16 | RIKEN cDNA 9530068E07 gene | 213673 | 1427108_at |
| *Abcb9* | 1.1E-02 | 1.42 | 18 | ATP-binding cassette, sub-family B (MDR/TAP), member 9 | 56325 | 1416263_at |
| *Acvr1c* | 2.6E-02 | 1.26 | 108 | activin A receptor, type IC | 269275 | 1438309_at |
| *Acvr1c* | 2.7E-02 | 1.44 | 108 | activin A receptor, type IC | 269275 | 1443225_at |
| *Agl* | 4.5E-02 | 1.40 | 38 | amylo-1,6-glucosidase, 4-alpha-glucanotransferase | 77559 | 1431032_at |
| *AI593442* | 3.8E-03 | 1.22 | 51 | expressed sequence AI593442 | 330941 | 1434052_at |
| *Ak2* | 3.6E-03 | 1.36 | 12 | adenylate kinase 2 | 11637 | 1448450_at |
| *Ak3* | 5.8E-03 | 1.22 | 10 | adenylate kinase 3 | 56248 | 1423717_at |
| *Ankrd40* | 3.6E-02 | 1.31 | 20 | ankyrin repeat domain 40 | 71452 | 1453744_a_at |
| *Aplp2* | 2.5E-02 | 1.38 | 114 | amyloid beta (A4) precursor-like protein 2 | 11804 | 1421889_a_at |
| *Aplp2* | 4.5E-02 | 1.16 | 114 | amyloid beta (A4) precursor-like protein 2 | 11804 | 1421888_x_at |
| *Arfrp1* | 1.9E-02 | 1.14 | 12 | ADP-ribosylation factor related protein 1 | 76688 | 1425507_at |
| *Arfrp1* | 2.2E-02 | 1.24 | 12 | ADP-ribosylation factor related protein 1 | 76688 | 1425508_s_at |
| *Arpp21* | 1.0E-04 | 1.31 | 47 | cyclic AMP-regulated phosphoprotein, 21 | 74100 | 1419028_at |
| *Arrdc4* | 3.0E-03 | 1.40 | 13 | arrestin domain containing 4 | 66412 | 1426818_at |
| *Atp2a2* | 1.2E-02 | 1.16 | 84 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 | 11938 | 1452363_a_at |
| *AU022252* | 2.2E-02 | 1.24 | 23 | expressed sequence AU022252 | 230696 | 1438226_at |
| *B3galt1* | 3.9E-02 | 1.63 | 10 | UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 | 26877 | 1460509_at |
| *BC030336* | 4.2E-02 | 1.38 | 44 | cDNA sequence BC030336 | 233812 | 1434075_at |
| *Bmi1* | 2.0E-02 | 1.25 | 23 | Bmi1 polycomb ring finger oncogene | 12151 | 1448733_at |
| *Bmi1* | 3.4E-02 | 1.27 | 23 | Bmi1 polycomb ring finger oncogene | 12151 | 1417493_at |
| *Bri3bp* | 2.9E-02 | 1.29 | 45 | Bri3 binding protein | 76809 | 1438198_at |
| *Cacna2d3* | 6.4E-03 | 1.26 | 11 | calcium channel, voltage-dependent, alpha2/delta subunit 3 | 12294 | 1419225_at |
| *Cacng2* | 2.1E-02 | 1.22 | 19 | calcium channel, voltage-dependent, gamma subunit 2 | 12300 | 1440210_at |
| *Cacul1* | 1.9E-02 | 1.58 | 10 | RIKEN cDNA 2700078E11 gene | 78832 | 1424982_a_at |
| *Car7* | 2.6E-02 | 1.32 | 39 | carbonic anhydrase 7 | 12354 | 1443824_s_at |
| *Casd1* | 3.4E-02 | 1.09 | 13 | CAS1 domain containing 1 | 213819 | 1451980_at |
| *Ccdc47* | 4.0E-02 | 1.21 | 42 | coiled-coil domain containing 47 | 67163 | 1424636_at |
| *Cndp2* | 4.3E-05 | 1.46 | 10 | CNDP dipeptidase 2 (metallopeptidase M20 family) | 66054 | 1460177_at |
| *Cndp2* | 1.8E-02 | 1.20 | 10 | CNDP dipeptidase 2 (metallopeptidase M20 family) | 66054 | 1448263_a_at |
| *Cnot7* | 3.5E-02 | 1.38 | 12 | CCR4-NOT transcription complex, subunit 7 | 18983 | 1460665_a_at |

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|---|---|---|---|---|---|---|
| *Crem* | 5.1E-03 | 1.26 | 17 | cAMP responsive element modulator | 12916 | 1418322_at |
| *Csnk1d* | 4.1E-02 | 1.61 | 12 | casein kinase 1, delta | 104318 | 1449932_at |
| *Cwc25* | 3.6E-02 | 1.20 | 20 | CWC25 spliceosome-associated protein homolog (S. cerevisiae) | 67480 | 1428759_s_at |
| *D3Bwg0562e* | 4.5E-02 | 1.25 | 61 | DNA segment, Chr 3, Brigham & Women's Genetics 0562 expressed | 229791 | 1434685_at |
| *Dcaf5* | 3.8E-02 | 1.41 | 10 | DDB1 and CUL4 associated factor 5 | 320808 | 1455354_at |
| *Dnajc27* | 2.0E-02 | 1.35 | 19 | DnaJ (Hsp40) homolog, subfamily C, member 27 | 217378 | 1435117_a_at |
| *Egln1* | 2.4E-02 | 1.20 | 17 | EGL nine homolog 1 (C. elegans) | 112405 | 1423785_at |
| *Elfn2* | 1.4E-02 | 1.29 | 18 | leucine rich repeat and fibronectin type III, extracellular 2 | 207393 | 1456202_at |
| *Fads1* | 2.2E-03 | 1.33 | 248 | fatty acid desaturase 1 | 76267 | 1423680_at |
| *Fam102a* | 6.3E-03 | 1.30 | 17 | family with sequence similarity 102, member A | 98952 | 1426893_at |
| *Fam126b* | 2.7E-02 | 1.28 | 81 | family with sequence similarity 126, member B | 213056 | 1456320_at |
| *Fam168b* | 4.7E-02 | 1.09 | 89 | family with sequence similarity 168, member B | 214469 | 1434018_at |
| *Fam171a1* | 1.3E-02 | 1.33 | 12 | family with sequence similarity 171, member A1 | 269233 | 1438402_at |
| *Flrt3* | 2.6E-02 | 1.13 | 44 | fibronectin leucine rich transmembrane protein 3 | 71436 | 1429310_at |
| *Flrt3* | 4.2E-02 | 1.22 | 44 | fibronectin leucine rich transmembrane protein 3 | 71436 | 1453102_at |
| *Frrs1l* | 2.6E-02 | 1.39 | 10 | RIKEN cDNA 6430704M03 gene | 230235 | 1437640_at |
| *Fxr2* | 1.8E-02 | 1.18 | 45 | fragile X mental retardation, autosomal homolog 2 | 23879 | 1422522_at |
| *Gad1* | 3.0E-02 | 1.78 | 12 | glutamic acid decarboxylase 1 | 14415 | 1416562_at |
| *Gad1* | 3.2E-02 | 1.11 | 12 | glutamic acid decarboxylase 1 | 14415 | 1416561_at |
| *Gas7* | 2.3E-02 | 1.30 | 92 | growth arrest specific 7 | 14457 | 1417859_at |
| *Gpm6b* | 1.4E-02 | 1.12 | 19 | glycoprotein m6b | 14758 | 1423091_a_at |
| *Gpm6b* | 3.6E-02 | 1.37 | 19 | glycoprotein m6b | 14758 | 1425942_a_at |
| *Gpr176* | 4.7E-02 | 1.18 | 23 | G protein-coupled receptor 176 | 381413 | 1442116_at |
| *Gpr88* | 2.8E-02 | 1.17 | 21 | G-protein coupled receptor 88 | 64378 | 1423171_at |
| *Gps1* | 3.4E-02 | 1.22 | 10 | G protein pathway suppressor 1 | 209318 | 1415699_a_at |
| *Gsg1l* | 6.8E-03 | 1.36 | 38 | GSG1-like | 269994 | 1436013_at |
| *H3f3b* | 2.5E-04 | 1.34 | 14 | H3 histone, family 3B | 15081 | 1420376_a_at |
| *Hgsnat* | 2.1E-02 | 1.18 | 27 | Heparan-alpha-glucosaminide N-acetyltransferase | 52120 | 1436580_at |
| *Hs2st1* | 4.5E-02 | 1.24 | 34 | heparan sulfate 2-O-sulfotransferase 1 | 23908 | 1450729_at |
| *Iffo2* | 9.9E-03 | 1.18 | 21 | intermediate filament family orphan 2 | 212632 | 1435455_at |
| *Il34* | 4.5E-02 | 1.40 | 34 | interleukin 34 | 76527 | 1431920_a_at |
| *Insm1* | 1.4E-03 | 1.34 | 35 | insulinoma-associated 1 | 53626 | 1421399_at |
| *Insm1* | 2.9E-02 | 1.32 | 35 | insulinoma-associated 1 | 53626 | 1455865_at |
| *Kbtbd8* | 1.3E-02 | 1.24 | 26 | kelch repeat and BTB (POZ) domain containing 8 | 243574 | 1433902_at |
| *Kcnma1* | 3.7E-02 | 1.20 | 15 | potassium large conductance calcium-activated channel, subfamily M, alpha member 1 | 16531 | 1428948_at |
| *Kcnma1* | 4.3E-02 | 1.16 | 15 | potassium large conductance calcium-activated channel, subfamily M, alpha member 1 | 16531 | 1425987_a_at |
| *Kctd3* | 2.9E-02 | 1.32 | 26 | potassium channel tetramerisation domain containing 3 | 226823 | 1436811_at |
| *Kif1a* | 1.4E-02 | 1.40 | 16 | kinesin family member 1A | 16560 | 1450108_at |
| *Lhfpl2* | 4.9E-02 | 1.15 | 11 | lipoma HMGIC fusion partner-like 2 | 218454 | 1434129_s_at |
| *Lhfpl4* | 3.6E-02 | 1.21 | 53 | lipoma HMGIC fusion partner-like protein 4 | 269788 | 1436553_at |
| *Lmbr1* | 3.0E-02 | 2.29 | 13 | limb region 1 | 56873 | 1425605_a_at |
| *Lpgat1* | 7.6E-03 | 1.31 | 85 | lysophosphatidylglycerol acyltransferase 1 | 226856 | 1435327_at |

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|---|---|---|---|---|---|---|
| *Man1a2* | 1.1E-02 | 1.21 | 27 | mannosidase, alpha, class 1A, member 2 | 17156 | 1434395_at |
| *Man1a2* | 3.3E-02 | 1.19 | 27 | mannosidase, alpha, class 1A, member 2 | 17156 | 1420977_at |
| *Mapk14* | 3.3E-02 | 1.11 | 21 | mitogen-activated protein kinase 14 | 26416 | 1416703_at |
| *Meaf6* | 7.1E-04 | 1.44 | 15 | MYST/Esa1-associated factor 6 | 70088 | 1457977_at |
| *Msl1* | 3.6E-02 | 1.25 | 17 | male-specific lethal 1 homolog (Drosophila) | 74026 | 1428872_at |
| *Mtch1* | 1.9E-02 | 1.19 | 31 | mitochondrial carrier homolog 1 (C. elegans) | 56462 | 1460718_s_at |
| *Mtx3* | 5.2E-03 | 1.61 | 22 | metaxin 3 | 382793 | 1434806_at |
| *Mtx3* | 4.6E-02 | 1.15 | 22 | metaxin 3 | 382793 | 1434807_s_at |
| *Ndst1* | 4.4E-02 | 1.30 | 41 | N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 | 15531 | 1428367_at |
| *Ndufab1* | 1.4E-02 | 1.28 | 27 | NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 | 70316 | 1458678_at |
| *Neto1* | 4.7E-03 | 1.17 | 26 | neuropilin (NRP) and tolloid (TLL)-like 1 | 246317 | 1456283_at |
| *Neto2* | 1.9E-03 | 1.34 | 20 | neuropilin (NRP) and tolloid (TLL)-like 2 | 74513 | 1436309_at |
| *Nup50* | 4.5E-03 | 1.30 | 23 | nucleoporin 50 | 18141 | 1428328_at |
| *Obfc2a* | 2.2E-02 | 1.13 | 12 | oligonucleotide/oligosaccharide-binding fold containing 2A | 109019 | 1426806_at |
| *Oprl1* | 2.5E-02 | 1.16 | 11 | opioid receptor-like 1 | 18389 | 1426204_a_at |
| *Ormdl3* | 1.1E-02 | 1.50 | 15 | ORM1-like 3 (S. cerevisiae) | 66612 | 1419450_at |
| *Paip2* | 1.3E-02 | 1.14 | 37 | polyadenylate-binding protein-interacting protein 2 | 67869 | 1448493_at |
| *Pard6b* | 8.4E-03 | 1.38 | 17 | par-6 (partitioning defective 6) homolog beta (C. elegans) | 58220 | 1423174_a_at |
| *Pde10a* | 3.4E-02 | 1.11 | 73 | phosphodiesterase 10A | 23984 | 1439618_at |
| *Pde10a* | 3.9E-02 | 1.57 | 73 | phosphodiesterase 10A | 23984 | 1458499_at |
| *Pdgfb* | 2.7E-02 | 1.20 | 15 | platelet derived growth factor, B polypeptide | 18591 | 1450414_at |
| *Pea15a* | 9.9E-04 | 1.63 | 49 | phosphoprotein enriched in astrocytes 15A | 18611 | 1416407_at |
| *Pfdn2* | 1.4E-02 | 1.17 | 17 | prefoldin 2 | 18637 | 1421950_at |
| *Pigq* | 1.2E-02 | 1.26 | 22 | phosphatidylinositol glycan anchor biosynthesis, class Q | 14755 | 1415946_at |
| *Pmepa1* | 2.2E-03 | 1.17 | 24 | prostate transmembrane protein, androgen induced 1 | 65112 | 1422706_at |
| *Prkx* | 6.3E-04 | 1.59 | 270 | protein kinase, X-linked | 19108 | 1424286_at |
| *Prkx* | 2.0E-02 | 1.32 | 270 | protein kinase, X-linked | 19108 | 1451299_at |
| *Prr3* | 2.5E-02 | 1.19 | 26 | proline-rich polypeptide 3 | 75210 | 1424145_at |
| *Ptpn9* | 2.5E-03 | 1.38 | 15 | protein tyrosine phosphatase, non-receptor type 9 | 56294 | 1451037_at |
| *Pum2* | 1.5E-02 | 1.29 | 47 | pumilio 2 (Drosophila) | 80913 | 1418017_at |
| *Pygb* | 2.4E-02 | 1.20 | 34 | brain glycogen phosphorylase | 110078 | 1433504_at |
| *Rab14* | 3.7E-02 | 1.19 | 39 | RAB14, member RAS oncogene family | 68365 | 1415686_at |
| *Rab39b* | 9.9E-03 | 1.31 | 24 | RAB39B, member RAS oncogene family | 67790 | 1435014_at |
| *Rcan2* | 3.7E-02 | 1.09 | 88 | regulator of calcineurin 2 | 53901 | 1421425_a_at |
| *Rdh11* | 1.2E-03 | 1.61 | 17 | retinol dehydrogenase 11 | 17252 | 1449209_a_at |
| *Rgs2* | 7.5E-03 | 1.18 | 15 | regulator of G-protein signaling 2 | 19735 | 1419248_at |
| *Rgs6* | 3.0E-02 | 1.11 | 22 | regulator of G-protein signaling 6 | 50779 | 1452399_at |
| *Rgs8* | 5.1E-04 | 1.19 | 81 | regulator of G-protein signaling 8 | 67792 | 1453060_at |
| *Rmnd5a* | 1.6E-02 | 1.19 | 88 | required for meiotic nuclear division 5 homolog A (S. cerevisiae) | 68477 | 1426884_at |
| *Rmnd5a* | 2.7E-02 | 1.62 | 88 | required for meiotic nuclear division 5 homolog A (S. cerevisiae) | 68477 | 1431068_at |
| *Rnf149* | 3.7E-03 | 1.45 | 16 | ring finger protein 149 | 67702 | 1429321_at |
| *Rnh1* | 2.6E-04 | 1.60 | 68 | ribonuclease/angiogenin inhibitor 1 | 107702 | 1451201_s_at |

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|---|---|---|---|---|---|---|
| *Rpn1* | 4.7E-02 | 1.11 | 29 | ribophorin I | 103963 | 1438943_x_at |
| *Rps6* | 4.7E-02 | 1.19 | 116 | ribosomal protein S6 | 20104 | 1416142_at |
| *Samd10* | 6.8E-05 | 1.63 | 54 | sterile alpha motif domain containing 10 | 229011 | 1435756_at |
| *Samd8* | 9.8E-03 | 1.18 | 30 | sterile alpha motif domain containing 8 | 67630 | 1434402_at |
| *Scn2b* | 1.2E-02 | 1.17 | 43 | sodium channel, voltage-gated, type II, beta | 72821 | 1436134_at |
| *Scn2b* | 2.7E-02 | 1.60 | 43 | sodium channel, voltage-gated, type II, beta | 72821 | 1430648_at |
| *Scn4b* | 6.8E-03 | 1.14 | 29 | sodium channel, type IV, beta | 399548 | 1434008_at |
| *Sec61a1* | 7.7E-04 | 1.41 | 84 | Sec61 alpha 1 subunit (S. cerevisiae) | 53421 | 1448242_at |
| *Sec61a1* | 3.9E-02 | 1.35 | 84 | Sec61 alpha 1 subunit (S. cerevisiae) | 53421 | 1416189_a_at |
| *Sec61a1* | 4.1E-02 | 1.24 | 84 | Sec61 alpha 1 subunit (S. cerevisiae) | 53421 | 1434986_a_at |
| *Setd8* | 1.1E-02 | 1.21 | 14 | SET domain containing (lysine methyltransferase) 8 | 67956 | 1460687_at |
| *Sez6* | 9.4E-04 | 1.35 | 41 | seizure related gene 6 | 20370 | 1427674_a_at |
| *Sgcb* | 1.6E-06 | 1.98 | 24 | sarcoglycan, beta (dystrophin-associated glycoprotein) | 24051 | 1436678_at |
| *Sgcb* | 2.5E-05 | 1.77 | 24 | sarcoglycan, beta (dystrophin-associated glycoprotein) | 24051 | 1419668_at |
| *Sgpp1* | 2.0E-03 | 1.45 | 17 | sphingosine-1-phosphate phosphatase 1 | 81535 | 1420822_s_at |
| *Sgpp1* | 2.8E-02 | 1.43 | 17 | sphingosine-1-phosphate phosphatase 1 | 81535 | 1420821_at |
| *Sirpa* | 1.7E-02 | 1.15 | 10 | signal-regulatory protein alpha | 19261 | 1416985_at |
| *Sirpa* | 4.8E-02 | 1.40 | 10 | signal-regulatory protein alpha | 19261 | 1448534_at |
| *Slc1a1* | 4.6E-02 | 1.21 | 16 | solute carrier family 1 (high affinity glutamate transporter), member 1 | 20510 | 1425415_a_at |
| *Slc35f3* | 9.1E-04 | 1.37 | 39 | solute carrier family 35, member F3 | 210027 | 1456764_at |
| *Slc37a3* | 1.8E-02 | 1.28 | 25 | solute carrier family 37 (glycerol-3-phosphate transporter), member 3 | 72144 | 1453915_a_at |
| *Slc39a11* | 5.0E-06 | 1.58 | 328 | solute carrier family 39 (metal ion transporter), member 11 | 69806 | 1424905_a_at |
| *Slc39a13* | 4.3E-02 | 1.13 | 92 | solute carrier family 39 (metal ion transporter), member 13 | 68427 | 1423926_at |
| *Slc4a4* | 5.0E-02 | 1.23 | 102 | solute carrier family 4 (anion exchanger), member 4 | 54403 | 1452071_at |
| *Slc6a1* | 1.1E-02 | 1.27 | 14 | solute carrier family 6 (neurotransmitter transporter, GABA), member 1 | 232333 | 1452142_at |
| *Sos1* | 2.7E-02 | 1.17 | 19 | son of sevenless homolog 1 (Drosophila) | 20662 | 1434389_at |
| *Srsf13b* | 8.4E-03 | 1.39 | 40 | serine/arginine-rich splicing factor 13B | 272009 | 1437168_at |
| *Ssr3* | 1.8E-02 | 1.28 | 14 | signal sequence receptor, gamma | 67437 | 1415700_a_at |
| *Ssr3* | 2.1E-02 | 1.08 | 14 | signal sequence receptor, gamma | 67437 | 1447053_x_at |
| *St8sia3* | 8.9E-03 | 1.19 | 29 | ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3 | 20451 | 1440029_at |
| *St8sia3* | 3.6E-02 | 1.20 | 29 | ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3 | 20451 | 1451008_at |
| *Stim2* | 8.8E-03 | 1.20 | 24 | stromal interaction molecule 2 | 116873 | 1434219_at |
| *Stx16* | 2.9E-02 | 1.14 | 13 | syntaxin 16 | 228960 | 1429237_at |
| *Susd4* | 3.9E-02 | 1.11 | 52 | sushi domain containing 4 | 96935 | 1460593_at |
| *Svop* | 6.1E-03 | 1.25 | 20 | SV2 related protein | 68666 | 1452663_at |
| *Syt11* | 1.3E-02 | 1.44 | 31 | synaptotagmin XI | 229521 | 1449264_at |
| *Szrd1/D4Ertd22e* | 3.8E-04 | 1.68 | 16 | SUZ RNA binding domain containing 1 | 213491 | 1434482_at |
| *Szrd1/D4Ertd22e* | 2.3E-03 | 1.40 | 16 | SUZ RNA binding domain containing 1 | 213491 | 1454981_at |
| *Tex2* | 7.0E-03 | 1.23 | 57 | testis expressed gene 2 | 21763 | 1452213_at |
| *Tex261* | 1.4E-02 | 1.42 | 20 | testis expressed gene 261 | 21766 | 1452768_at |
| *Tgoln1* | 2.8E-02 | 1.18 | 22 | trans-golgi network protein | 22134 | 1423309_at |
| *Tial1* | 1.4E-02 | 1.09 | 23 | Tia1 cytotoxic granule-associated RNA binding protein-like 1 | 21843 | 1426352_s_at |

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|---|---|---|---|---|---|---|
| *Tm2d2* | 1.1E-02 | 1.24 | 53 | TM2 domain containing 2 | 69742 | 1433473_x_at |
| *Tm2d2* | 3.3E-02 | 1.22 | 53 | TM2 domain containing 2 | 69742 | 1439235_x_at |
| *Tm2d2* | 3.6E-02 | 1.31 | 53 | TM2 domain containing 2 | 69742 | 1451134_a_at |
| *Tmbim6* | 2.1E-03 | 1.16 | 18 | transmembrane BAX inhibitor motif containing 6 | 110213 | 1451586_at |
| *Tmem179* | 1.0E-02 | 1.35 | 27 | transmembrane protein 179 | 104885 | 1436754_at |
| *Tmem206* | 3.1E-02 | 1.21 | 41 | transmembrane protein 206 | 66950 | 1448552_s_at |
| *Tmem246* | 1.7E-03 | 1.22 | 24 | RIKEN cDNA 2810432L12 gene | 67063 | 1423679_at |
| *Tmem64* | 2.5E-03 | 1.48 | 10 | transmembrane protein 64 | 100201 | 1434307_at |
| *Tmem64* | 1.5E-02 | 1.34 | 10 | transmembrane protein 64 | 100201 | 1454709_at |
| *Tmem64* | 2.4E-02 | 1.30 | 10 | transmembrane protein 64 | 100201 | 1433735_a_at |
| *Tmem87b* | 1.6E-02 | 1.13 | 16 | transmembrane protein 87B | 72477 | 1429337_at |
| *Trim2* | 3.3E-02 | 1.31 | 20 | tripartite motif-containing 2 | 80890 | 1448551_a_at |
| *Trove2* | 1.8E-05 | 1.69 | 199 | TROVE domain family, member 2 | 20822 | 1423433_at |
| *Trove2* | 4.3E-04 | 1.37 | 199 | TROVE domain family, member 2 | 20822 | 1436533_at |
| *Trove2* | 1.1E-02 | 1.39 | 199 | TROVE domain family, member 2 | 20822 | 1436535_at |
| *Trove2* | 1.4E-02 | 1.40 | 199 | TROVE domain family, member 2 | 20822 | 1436534_at |
| *Ttll11* | 4.1E-02 | 1.14 | 15 | tubulin tyrosine ligase-like family, member 11 | 74410 | 1430064_at |
| *Tub* | 1.7E-02 | 1.25 | 46 | tubby candidate gene | 22141 | 1420925_at |
| *Tug1* | 9.7E-03 | 1.31 | 69 | taurine upregulated gene 1 | 544752 | 1415708_at |
| *Tug1* | 3.8E-02 | 1.84 | 69 | Taurine upregulated gene 1 | 544752 | 1456398_at |
| *Ube2e2* | 1.8E-02 | 1.15 | 14 | ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) | 218793 | 1424358_at |
| *Ugcg* | 3.0E-02 | 1.34 | 32 | UDP-glucose ceramide glucosyltransferase | 22234 | 1435133_at |
| *Usp9x* | 3.3E-02 | 1.46 | 10 | ubiquitin specific peptidase 9, X chromosome | 22284 | 1450038_s_at |
| *Usp9x* | 3.9E-02 | 1.55 | 10 | ubiquitin specific peptidase 9, X chromosome | 22284 | 1450037_at |
| *Wbp1l/D19Wsu162e* | 6.6E-03 | 1.62 | 26 | DNA segment, Chr 19, Wayne State University 162, expressed | 226178 | 1433717_at |
| *Wbp1l/D19Wsu162e* | 3.0E-02 | 1.34 | 26 | DNA segment, Chr 19, Wayne State University 162, expressed | 226178 | 1425529_s_at |
| *Whsc1* | 2.2E-02 | 1.19 | 15 | Wolf-Hirschhorn syndrome candidate 1 (human) | 107823 | 1455228_at |
| *Wrb* | 1.5E-02 | 1.31 | 24 | tryptophan rich basic protein | 71446 | 1460446_at |
| *Zdhhc21* | 4.0E-03 | 1.44 | 50 | zinc finger, DHHC domain containing 21 | 68268 | 1435104_at |
| *Zfp652* | 1.0E-02 | 1.41 | 39 | zinc finger protein 652 | 268469 | 1434720_at |
| *Zfp652* | 4.7E-02 | 1.15 | 39 | zinc finger protein 652 | 268469 | 1456520_at |
| *Zmat3* | 1.4E-02 | 1.12 | 61 | zinc finger matrin type 3 | 22401 | 1449353_at |

**Table S4. miR-128 targets in D1-neurons are enriched in ion channels, ion transporters, and signaling proteins.**

| Group | Gene Symbol | Gene Title | Entrez Gene | Anti-seizure drug |
|---|---|---|---|---|
| Ion channels and transporters | *Cacna2d3* | calcium channel, voltage-dependent, alpha2/delta subunit 3 | 12294 | Pregabalin |
| | *Cacng2* | calcium channel, voltage-dependent, gamma subunit 2 | 12300 | Pregabalin |
| | *Kcnma1* | potassium large conductance calcium-activated channel, subfamily M, alpha member 1 | 16531 | |
| | *Kctd3* | potassium channel tetramerisation domain containing 3 | 226823 | |
| | *Kcnma1* | potassium large conductance calcium-activated channel, subfamily M, alpha member 1 | 16531 | |
| | *Kctd3* | potassium channel tetramerisation domain containing 3 | 226823 | |
| | *Scn2b* | sodium channel, voltage-gated, type II, beta | 72821 | Riluzole |
| | *Scn4b* | sodium channel, type IV, beta | 399548 | Riluzole |
| | *Slc35f3* | solute carrier family 35, member F3 | 210027 | |
| | *Slc39a11* | solute carrier family 39 (metal ion transporter), member 11 | 69806 | |
| | *Slc39a13* | solute carrier family 39 (metal ion transporter), member 13 | 68427 | |
| | *Slc4a4* | solute carrier family 4 (anion exchanger), member 4 | 54403 | |
| | *Stim2* | stromal interaction molecule 2 | 116873 | |
| Glutamate and GABA signaling | *Gad1* | glutamic acid decarboxylase 1 | 14415 | |
| | *Gsg1l* | GSG1-like | 269994 | |
| | *Slc6a1* | solute carrier family 6 (neurotransmitter transporter, GABA), member 1 | 232333 | Tiagabin |
| | *Slc1a1* | solute carrier family 1 (high affinity glutamate transporter), member 1 | 20510 | Riluzole |
| | *Neto1* | neuropilin (NRP) and tolloid (TLL)-like 1 | 246317 | |
| | *Neto2* | neuropilin (NRP) and tolloid (TLL)-like 2 | 74513 | |
| G-protein coupled signaling transduction, | *Acvr1c* | activin A receptor, type IC | 269275 | |
| Mapk signaling pathway | *Arpp21* | cyclic AMP-regulated phosphoprotein, 21 | 74100 | |
| | *Arrdc4* | arrestin domain containing 4 | 66412 | |
| | *Crem* | cAMP responsive element modulator | 12916 | |
| | *Gpr176* | G protein-coupled receptor 176 | 381413 | |
| | *Gpr88* | G-protein coupled receptor 88 | 64378 | |
| | *Gps1* | G protein pathway suppressor 1 | 209318 | |
| | *Mapk14* | mitogen-activated protein kinase 14 | 26416 | |
| | *Ndst1* | N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 | 15531 | |
| | *Oprl1* | opioid receptor-like 1 | 18389 | |
| | *Pde10a* | phosphodiesterase 10A | 23984 | |
| | *Pdgfb* | platelet derived growth factor, B polypeptide | 18591 | |
| | *Pea15a* | phosphoprotein enriched in astrocytes 15A | 18611 | |
| | *Prkx* | protein kinase, X-linked | 19108 | |
| | *Rab14* | RAB14, member RAS oncogene family | 68365 | |
| | *Rab39b* | RAB39B, member RAS oncogene family | 67790 | |
| | *Rcan2* | regulator of calcineurin 2 | 53901 | |
| | *Rgs2* | regulator of G-protein signaling 2 | 19735 | |
| | *Rgs6* | regulator of G-protein signaling 6 | 50779 | |
| | *Rgs8* | regulator of G-protein signaling 8 | 67792 | |
| | *Sirpa* | signal-regulatory protein alpha | 19261 | |
| | *Sos1* | son of sevenless homolog 1 (Drosophila) | 20662 | |
| Other seizure or motor activity associated genes | *Car7* | carbonic anhydrase 7 | 12354 | Topiramad |
| | *Fxr2* | fragile X mental retardation, autosomal homolog 2 | 23879 | |
| | *Sez6* | seizure related gene 6 | 20370 | |