

Supplementary Materials and Methods

mRNA expression data

We used six high-throughput gene expression datasets, including five from human lymphoblastoid cell lines and one from primary leukocytes (Table 1). The first dataset is taken from (Wang et al. 2009). The expression data and relevant annotation files were retrieved from Gene Expression Omnibus with accession number GSE14794. We followed the mRNA expression determination procedures of (Wang et al. 2009) to identify the genes that are expressed in samples. We used quantile normalization to normalize the expression of probes of both mRNAs and miRNAs.

The second dataset is comprised of expression profiles of ~22,300 genes from leukocyte samples of 194 healthy Arab and Amazigh individuals from a city and two villages in southern Morocco (Idaghdour et al. 2010). The raw expression data were downloaded from Gene Expression Omnibus with accession number GSE17065. The annotation information of Human HT-12 Beadchip ([HumanHT-12_V3_o_R2_11283641-A.bgx](http://www.switchto.com)) used in that study was downloaded from <http://www.switchto.com>. The expression profiles were normalized with quantile normalization methods, and the top 22,300 probes with highest expression levels were used in this analysis. The analysis is restricted to autosomal genes.

The third to sixth datasets are the expression profiles of mRNAs from lymphoblastoid samples of four populations in the HapMap project –YRI (Yoruba in Ibadan), CEU (CEPH Utah), CHB (Han Chinese in Beijing), and JPT (Japanese in Tokyo). The normalized data were downloaded from <http://www.sanger.ac.uk/humgen/genevar/>. In the original studies (Stranger et al. 2005; Stranger et al. 2007a; Stranger et al. 2007b), the authors chose the 18,000 most variable genes from each population and then they selected the intersection from the four populations, resulting in a collection of 14,000 genes. Here we used a slightly different approach. Specifically, we download the data of CHB_180_gene_profile.txt (45 individuals, each 4 replicates), JPT_180_gene_profile.txt (45 individuals, each 4 replicates), CEUc_120_gene_profile.txt (30 individuals, each 4 replicates), YRIc_120_gene_profile.txt (30 individuals, each 4 replicates) from <http://www.sanger.ac.uk/humgen/genevar/>. In each population, we only selected probes that have expression evidence (Detection P -value > 0.05) in at least 50% of the samples. In total, 14,695 probes were considered to be expressed in this dataset. The annotation file for this platform (human-6 V1) was downloaded from <http://www.compbio.group.cam.ac.uk/Resources/Annotation/>. For the CEU and YRI populations, we only used the data from unrelated children in our analysis. The detailed information about the six populations is summarized in Table 1.

The gene expression in human, chimpanzee, and macaque were extracted from Blekhman et al. (2010). This dataset identified a large number of genes that are

differentially expressed among three primate species, specifically, 3,335 genes between human and chimpanzee, 6,030 genes between human and macaque, 5,549 genes between chimpanzee and macaque that are differentially expressed in liver. There are 1,391 genes under stabilizing selection during primate evolution, and 887 and 896 genes that are under directional selection in the human and chimpanzee lineages respectively (Blekhman et al. 2010).

Coefficient of variation in expression (CV)

In each of the six datasets, for each gene, we defined the variability of its expression levels across the individuals using the standard formula for the coefficient of

variation: $CV = \frac{\text{s.d. of expression levels across individuals}}{\text{mean of expression levels across individuals}} \times 100$, which is a reliable

means to measure variation of gene expression levels. This metric has been used in previous studies (Kaern et al. 2005; Zhang and Su 2008). We also use the same procedure to calculate the CV of miRNAs in the 90 European-American males that are determined by Wang et al. (2009).

miRNA expression

The miRNA expression data in the 90 European-American males were taken from Wang et al. (2009). We used the miRNA microarray results for two levels of information: (1) expression variation in miRNAs across human individuals, and (2) the expression profiles of miRNAs in the lymphoblastoid cells. The reproducibility of miRNA microarrays were justified by Sokilde et al. (2011). The authors compared the expression levels of microRNAs in the NCI60 cell lines between the LNA-enhanced miRCURY Dx 9.2 microarray platform (Sokilde et al. 2011) and pin-spotted microRNA microarray (Blower et al. 2007; Gaur et al. 2007; Liu et al. 2010). Sokilde et al. (2011) found the correlation of the microRNA levels determined in the four studies ranges from 0.5 to 0.7. Considering the variables in cell culture, RNA library construction, assay technologies and data processing in these studies, the authors conclude the reproducibility of microRNA microarrays are high, even across different technology platforms. Since miRNA expression data are only available in the dataset by Wang et al. 2009, we conservatively assume the same set of miRNAs in dataset 1 (Wang et al. 2009) are also expressed in the other five datasets because all the six datasets are based on the human blood samples. Among the 366 putative miRNAs that are expressed as determined by the microarray hybridization platform (Wang et al. 2009), we extracted the probe sequences from the annotation file of the miRNA microarray and used the program BLAT to map the probe sequences on the miRNA sequences that were deposited in miRBase V14 and V15 (<http://www.mirbase.org/>). In total, 274 of the 366 miRNAs have probe sequences that can be perfectly mapped on the miRNA precursors and on 287 mature miRNA sequences with up to 2 nt offsets.

There are 72 miRNAs expressed in the human liver by deep sequencing from (Landgraf et al. 2007). The miRNA lists were extracted from <http://www.microna.org>.

miRNA target prediction

To investigate the effect of miRNA regulating effects on the target genes, it is a prerequisite to accurately and reliably identify the target genes. We used state-of-the-art *in silico* miRNA target prediction algorithms, including canonical TargetScan based on conservation criteria (referred to TSs) (Lewis et al. 2005; Grimson et al. 2007; Friedman et al. 2009), Pictar (Krek et al. 2005), miRanda (John et al. 2004), and PITatop (Kertesz et al. 2007). The pre-computed results by TargetScan conservation were downloaded from TargetScan V5.1 (<http://www.targetscan.org>). The PITatop target predictions were downloaded from http://genie.weizmann.ac.il/pubs/miro7/catalogs/PITA-Sites_hg18_o_o_TOP.tab.gz; the Pictar prediction results were downloaded from UCSC genome browser (genome.usc.edu); and the miRanda predictions were downloaded from http://cbio.mskcc.org/microna_data/human_predictions-Sept2008.txt.gz. These miRNA target prediction algorithms rely heavily on conservation of the pairing between seed (position 2-8 of a mature miRNA) and target binding sites (Bartel 2009).

TargetScan based on context score (referred to as TSt) (Grimson et al. 2007) can accurately and efficiently predict conserved and non-conserved target genes without conservation information. The TargetScan context scores were calculated following (Grimson et al. 2007). The seed and mature sequences of miRNAs were downloaded from miRBase V15. The 3'UTR sequences were obtained from three sources: (1) extracted from TargetScan V5.1; (2) from RefSeq database based on the transcript annotations (<ftp://ftp.ncbi.nih.gov/refseq/H-Sapiens/>); and (3) from the Ensembl database (www.ensembl.org, version 57).

Experimentally verified miRNA targets

The experimentally verified target genes of the co-expressed miRNAs were parsed from TarBase (Papadopoulos et al. 2009) and miR2Disease (Jiang et al. 2009). The second source of experiment-based target identification was parsed based on the high-throughput sequencing of miRNAs and mRNA targets with the PAR-CLIP method by the Tuschl lab (Hafner et al. 2010). For the top 100 highly expressed miRNAs in the HEK293 cell line, we identified the bona-fide target genes with the following criteria: 1) the pairing probability between a mRNA and a miRNA is smaller than 0.0001 (from Table S7 of Hafner et al. 2010), 2) the miRNA target sites are located in the 3' UTRs and have Context Scores < -0.3 (based on this study). The experiment-based miRNA targets of the co-expressed miRNAs in the lymphoblastoid cells were pooled in the analysis as “known targets.”

High-Confidence miRNA targets

We considered genes predicted to be targets of the co-expressed miRNAs by TargetScan with conservation (aggregate PCT > 0.8) or context score (<-0.4 and percentile > 85), or by Pictar, or experimentally verified targets as High-Confidence miRNA targets because the former three methods have low false discovery rates (Baek et al. 2008). When we combine the miRNA target determination methods together, genes not targeted by co-expressed miRNAs as determined in the 4 methods and also not predicted by miRanda and PITAtop were considered as non-targets.

Gene annotation and probe mapping

We downloaded all the human RefSeq sequences and annotations from ftp://ftp.ncbi.nih.gov/refseq/H-Sapiens/mRNA_Prot/human.rna.fna.gz. More than 98% of the accession numbers beginning with NM_ used in TargetScan V5.1 are included in this dataset. The annotation of the RefSeq sequences were downloaded from wget ftp://ftp.ncbi.nih.gov/refseq/H-Sapiens/mRNA_Prot/human.rna.gbff.gz. Intron, exon, CDS and 5' UTR and 3' UTR positions were extracted from the protein-coding sequences based on the annotations. The genomic location of RefSeq transcripts on NCBI 36 (hg18 of UCSC Genome Browser) were downloaded from genome.ucsc.edu. For each of the six datasets in Table 1, the probe sequences from the microarray annotation files were used to map the transcripts to the RefSeq sequences. Based on the probe sequences matching, the miRNA target prediction results were mapped back to each probe.

Gene Ontology (GO) enrichment analysis

Rather than focusing on target genes of specific miRNAs, we conducted GO enrichment analysis on the most variable High-Confidence target genes of co-expressed miRNAs at a global level. In dataset I, there are 10,472 ensemble genes (11,019 microarray probes) with expression levels above threshold. There are 7,886 genes (8,377 probes) determined High-Confidence miRNA target genes, and the top 829 target genes (853 probes) with highest CVs are subjected to GO enrichment tests. The 10,472 genes are used as backgrounds for the analysis. In dataset II, there are 12,446 ensemble genes (15,803 microarray probes) with expression levels above the threshold. There are 9,171 genes (11,923 probes) determined High-Confidence miRNA target genes, and the top 1,085 target genes (1,180 probes) with highest CVs are subjected to GO enrichment tests. The 12,446 genes are used as background for the analysis in dataset II. The analysis was performed with GO FAT category on the website of DAVID bioinformatics resources with default settings (Huang et al. 2008). The Benjamini and Hochberg method was used for multiple test correction.

Genotype data from HapMap3 and the 1000 Genomes Projects

Phase3 release of HapMap data were downloaded from ftp://ftp.ncbi.nlm.nih.gov/hapmap/genotypes/latest_phaseIII_ncbi_b36/hapmap_format/polymorphic/. SNPs were mapped on the miRNAs, RefSeq or Ensembl genes based on the genomic

location coordinates. In the HapMap Phase 3 release, there are 1,634,652 non-redundant SNPs determined in the CEU, JPT, CHB, and YRI populations.

The October 2011 Integrated Variant Set release of the 1000 Human Genome Project was downloaded from <http://ftp-trace.ncbi.nih.gov/1000genomes/ftp/release/20110521>. SNPs, small indels (2-52 nts) and large indels (> 100 bp, referred to as structural variants in the release) in this datasets were determined from 1092 human individuals. The size of the large indels varied from 104 nts to 887,000 nts, with a median size of 2,546 nts. The genetic variants were mapped on miRNAs, RefSeq and Ensemble transcripts based on the genomic location coordinates.

Association study

We employed a compressed mixed linear model implemented in the GAPIT package (Zhang et al. 2010) to conduct the genome-wide association studies between genetic variants and expression levels of mRNAs. Since genotypic and expression data in the CEU population are from trio families, to exclude the dependence between the data points, we only include the unrelated CEU parents and YRI parents data from each trio family into our analysis. Among the samples with expression levels quantified by Stranger et al. (2007b), there are 196 unrelated samples genotyped in the HapMap 3 Project, including 43 CHB, 42 JPT, 56 CEU parents, and 55 YRI parents. Among the 1,092 samples that are sequenced in 1000 Genomes Project Phase 1, 149 un-related samples have mRNA expression data measured by Stranger et al. (2007b), including samples from 32 CEU parents, 41 CHB, 39 JPT and 37 YRI parents. To increase the statistical powers of association tests, we pooled samples from different populations into the analysis.

The association tests were performed in two steps. First, the population parameters, including the kinship between samples and Principal Components of genetic variance were estimated with genome-wide SNPs. The association tests between the *cis*-elements and expression levels of the host genes were performed based on the genome-wide population parameters. For SNPs from the HapMap 3 project and the 1000 Genomes project, the association tests were conducted separately. For small indels and large indels sequenced in the 1000 Genomes project, the association tests were performed based on the genome-wide population parameters estimated from SNPs. For each type of genetic variant, results of the association tests across genes were pooled together and the Benjamini-Hochberg method was used to correct for multiple tests.

We only considered genetic variants that are located inside 3' UTRs, introns, and 100 kb up- and down-stream regions of genes that are expressed in lymphoblastoid cell lines. The analysis was restricted to autosomal protein-coding genes that are annotated in the RefSeq database. We noticed SNPs or indels that located in the probes of the microarrays are significantly associated with host gene expression

levels. To exclude the possible bias caused by probe hybridization, we removed all the variants inside the probe matching regions in the analysis.

Population differentiation analysis

Genes that are differentially expressed between populations were detected with the LIMMA package (Diboun et al. 2006). For analysis between Asian (CHB + JPT) and CEU populations, we obtained consistent results when we use CEU parents or CEU children expression data. In the TEXT we present results based on CEU children data. For genes differentially expressed between YRI and Asian populations, samples from the YRI parents are used. All the statistical tests were performed with the open source statistics package R (www.r-project.org).

Factors affecting expression variation in miRNA target genes.

We found that variation in miRNA expression and mutations in miRNA target sites are associated with elevated inter-individual expression variation in miRNA target genes. We also identified several other factors affecting the observed patterns.

1 Gene annotations. For each of the three microarray platforms used in this study (Table 1 in TEXT), the majority of the probes with expression levels above the thresholds are mapped on the curated protein-coding genes in the RefSeq database (accessions beginning with "NM_"). There are 2,500 - 5,300 expressed probes, however, that are either not mapped on RefSeq transcripts or mapped on non-curated transcripts (accessions beginning with NR_, XM_, or XR in the RefSeq database). In each of the 6 datasets, the CVs of the non-NM transcripts are 20-30% lower than those of the NM_ transcripts (Figure S9). When we restricted our analysis to the curated RefSeq coding transcripts, the differences in CVs between miRNA targets and non-targets are attenuated but are still significant (Table S9, Figure S10; results in Figures 3,4,5D,S10 and Tables 3,4,5,6,7 are all based on curated RefSeq genes).

2 Abundance of target genes. For each gene, the CV is normalized by the mean expression level across individuals. However, we observed weak but significant correlations between CV and expression levels (Pearson correlation coefficient $r = -0.082$ and 0.10 for dataset I and II respectively, $P < 10^{-16}$ for both cases). To quantify this correlation, we rank the genes with increasing expression

levels and use a sliding window (a window size of 1,000 genes and a step size of 200 genes) to calculate the median CV for the High-Confidence miRNA targets and non-targets (Figure S11A and S11B for dataset I and II respectively). A salient feature is that in both cases, lowly expressed genes have higher CV values if they are repressed by co-expressed miRNAs; while contrasting patterns were observed for highly expressed genes – the miRNA targets have significantly lower CV values than the non-targets (Figure S11A,B). However, the impact of gene expression level on the CV is attenuated if we restrict our analysis to the curated protein-coding genes in the RefSeq datasets (Figure S11C,D).

Between European and east Asian populations, the difference in divergence ratios between miRNA targets and non-targets is mainly contributed by the lowly expressed genes. In Figure S12A (for all the transcripts expressed) and Figure S12B (for the curated RefSeq transcripts that are expressed), we ranked the genes with increasing expression levels and used a sliding window method (window size of 1000 genes and step size of 200 genes) to calculate the proportion of the targets and non-targets in that window that are differentially expressed between European vs. Asian populations (FDR cutoff of 0.001). For the genes in the lowest 50% of the distribution of expression levels, the proportion of miRNA targets is higher than non-targets in all the 33 windows (Figure S12A). Restricting the analysis to RefSeq transcripts, 21 out of 26 windows have elevated representation of miRNA targets (Figure S12B). Thus the canalization effects of miRNAs are mainly acting on the highly expressed genes.

3 Expression patterns of miRNAs. Expression of miRNAs was quantified only in lymphoblastoid cells from an European-American population (dataset I, Wang *et al.* 2009) but not in other populations (Table 1). In this study, we conjectured the same sets of miRNAs were expressed in samples from all six populations (Table 1). It was reported that ~100 miRNAs were expressed at different levels in lymphoblastoid cells of European and African populations (Huang *et al.* 2011b), however, even among these most differentially expressed miRNAs, we found at least 70% of them are overlapping with miRNAs expressed in Dataset 1. We also found that 203 miRNAs

expressed in Dataset 1 are also detected in lymphoblastoid cells in a separate study (Skalsky et al. 2012); and for the top 50 most abundantly expressed miRNAs in Dataset 1, at least 90% of them are expressed in other lymphoblastoid cell lines (Skalsky et al. 2012). Thus the expression patterns of miRNAs in terms of “present” and “absent” are highly conserved in lymphoblastoid cells from various sources.

In addition, we believe our analysis takes into account most effects of miRNA regulation for the following reasons: (1) Highly expressed miRNAs are less variable across human individuals. For the top 100 highly expressed miRNAs in dataset I, we found a strong negative correlation between CV and mean expression levels (Spearman's rank correlation coefficient is -0.73, $P = 10^{-19}$, Figure S13A). (2) Highly expressed miRNAs have more conserved target genes. We ranked miRNAs by decreased expression levels and binned every 10 miRNAs into one group (Supplementary Materials and Methods). Our observation is that the number of conserved targets significantly decreases with the decrease in miRNA expression levels (Spearman's rank correlation rho is -0.73, $P = 3 \times 10^{-5}$, Figure S13B). The top 50 highly expressed miRNAs targeted more than 80% (1,710 out of 2,068) of the conserved targets of the 283 co-expressed miRNAs (TargetScan PCT > 0.8). Thus our analysis essentially accounted for the majority of the regulatory impacts on the conserved miRNA target genes. For example, in dataset I, the conserved targets of the top 50 miRNAs have significantly higher CV than the remaining curated RefSeq transcripts ($P = 0.024$, KS test, Figure S14A). In dataset II, there are in total 2,893 highly conserved target transcripts for the 283 miRNAs, and 82% (2,377) of them are targeted by the top 50 highly expressed miRNAs. These 2,377 highly conserved miRNA target transcripts also have higher CVs than the remaining curated RefSeq transcripts ($P = 0.019$, Figure S14B).

4 Gene Ontology. Previous analysis has indicated that genes significantly correlated with specific miRNAs were over-represented in Gene Ontology (GO) categories such as DNA replication or cell cycle regulation (Wang et al. 2009). Here we ask whether expression variation of miRNA target genes is associated with

specific biological processes. For the top 10% of the High-Confidence miRNA target genes with highest CVs, we used the DAVID tool (Huang et al. 2008) for gene ontology enrichment analysis (Materials and Methods). In dataset I (Wang et al. 2009), the High-Confidence target genes with highest CVs are significantly enriched in 45 biological process GO terms, and in dataset II (Idaghdour et al. 2009), the top 10% of the High-Confidence miRNA target genes with highest CVs are significantly enriched in 47 GO terms (Table S10). There are 13 significant GO categories that overlap between datasets I and II, including immune response, cell motion or adhesion, which either reflect the expression variation in human populations or possibly are due to the transfection of Epstein-Barr Virus in the cell samples (Table S11). Although the non-overlapping GO categories between dataset I and II might be caused by population-specific biological features, they are also likely attributable to bias in microarray probe selection or gene sampling in the analysis.

Figure legends

Figure S1. Expression variation (CV) of mRNA probes in the 90 European-American males (dataset I, Wang et al. 2009). **S1A**, Distribution of CV for the ~14,000 mRNA probes with expression detected. **S1B**, CV for mRNA probes correlated with miRNAs. For transcripts that are exclusively negatively correlated (neg), exclusively positively correlated (pos), negatively and positively correlated (negpos) with miRNAs, the CV is significantly greater than for transcripts not correlated with miRNAs (non). The median CV for non, neg, pos, negpos class is 2.13, 2.54, 2.91, and 3.03 respectively, with standard deviation of 1.62, 1.75, 1.93 and 2.09 respectively (a microarray probe is treated as an individual transcript in this analysis).

Figure S2. The CV comparison between probes on transcripts of miRNA targets and non-targets. **S2A**, dataset II in the Arab and Amazigh populations; **S2B-E** are the CV comparisons between miRNA targets and non-targets in the YRI, CEU, CHB and JPT populations (dataset III-VI) respectively. TSs, TargetScan with conservation ($PCT > 0.8$); TSt, context score (< -0.4 and percentile > 85); Verified, experimentally verified targets taken from TarBase, miR2Disease and Hafner et al. (2010). The other three miRNA target determination methods are Pictar, PITatop and miRanda. All the microarray probes with expression levels above thresholds are used in the comparisons.

Figure S3. The magnitude of miRNA regulation effect is positively associated with gene expression variability. In each plot, the x-axis is the number of target sites. **S3A** (upper panel) are the number of the putative miRNA target sites predicted by TSt (context score < -0.3) and the median CV for the transcripts in dataset III to VI (Table 1). The number of distinct miRNA target sites that are harbored in a mRNA 3' UTR varies from 0 to 14 (a small number of mRNAs have >14 sites and are binned into 14). **S3B** (lower panel) are the number of conserved miRNA interacting sites (based on TSs $PCT > 0.8$) and the median CV of the transcripts. The number of conserved target sites located in one transcript is generally smaller than the sites predicted by context score - it varies from 0 to 5 (a small number of mRNAs have >5 sites and are binned into 5). Only microarray probes that are mapped on the curated RefSeq coding transcripts are used in the analysis.

Figure S4. The genetic variants (SNPs and Indels) in miRNA loci in the 1,092 human individuals (2,184 chromosomes) that are sequenced in the 1000 Genomes Project. There are 594 genetic variants (540 SNPs and 54 Indels) identified in miRNA loci in the global human populations. The spectra of minor alleles of SNPs are presented in Figure S4A and the spectra of minor alleles of indels (insertions and deletions) are presented in Figure S4B. Figure S4C is the spectra of minor alleles of variants (SNPs + Indels) in mature miRNAs; 65.1% (110 out of 169) of the genetic variants have minor allele frequency $< 0.5\%$. Figure S4D is the spectra of minor alleles of variants (SNPs + Indels) in miRNA precursors outside mature miRNAs; 58.7% (250 out of 426) of variants have minor allele frequency $< 0.5\%$. For the 149 human individuals used in the genome-wide association studies, there are 322 genetic variants (269 SNPs + 53 Indels) located inside miRNA loci (Figure S4E). 94 of these variants are located in the miRNAs that are expressed in the lymphoblastoid cells (Figure S4F).

Figure S5. The distribution of the coefficients of variation in expression (CV) of the 287 miRNAs in the 90 European-American males (Wang et al. 2009). The variability varies from 0.19 to 9.35, with a mean of 2.98, a median of 2.75 and a standard deviation of 1.64.

Figure S6. Minor allele frequency of the genetic variants that are identified in the 149 individuals that are sequenced by 1000 Genomes Project and have expression data quantified by Stranger et al. (2007). The spectra of minor alleles were plotted for 13.4 million SNPs (Figure S6A), 3.6 million small indels (2-51 nts in size, Figure S6B) and 3,247 large indels (> 100 nts, also termed as structural variants, Figure S6C). The cutoff of minor allele frequency is 5% for SNPs (S6A) and small indels (S6B), and 1% for large indels (S6C) in the association tests. In the GWAS analysis, for each expressed mRNA probe, the number of cis-variants used in the association tests were plot (Figure S6D: SNPs; S6E: small indels; S6F: large indels). In Figure S6D, genes having more than 1000 SNPs in were binned into one category in the plotting.

Figure S7. Spectra of minor alleles of genetic variants in the genome-wide association tests in the 1000 Genomes data. Among the 149 human individuals that are sequenced in the 1000 Genomes Project and have mRNA expression data quantified in Stranger et al. (2007), there are 20,699 SNPs in 3' UTR, 904,058 SNPs in Introns and 1,958,747 SNPs in 100kb up- and down-stream of genes that are expressed (minor allele frequency > 0.05). At an FDR of 0.05, spectra of minor alleles of SNPs that are associated with host gene expression levels (left panels) and all the tested SNPs (right panels) are presented. The x-axis is minor allele frequency of variants and the y-axis is the number of variants that have the corresponding MAF.

Figure S8. The cooperative effects of multiple miRNA targeting can also be observed in the target genes that are differentially expressed in the CEU vs. CHB+JPT populations. **S8A**, the number of distinct target sites with TSt score < -0.3 is significantly positively correlated with the proportion of genes that are differentially expressed between the CEU vs. CHB+JPT populations at an FDR cutoff of 0.001 (Pearson correlation coefficient $r = 0.63$, $P = 0.01$). **S8B**, a significant negative correlation is observed between the number of conserved miRNA target sites and the proportion of differentially expressed transcripts ($r = -0.94$, $P = 0.02$), which suggest that the impact of miRNA targeting on gene expression differentiation is mainly contributed by the non-conserved miRNA:mRNA pairing. x-axis is the number of target sites (conserved + non-conserved for **S8A** and conserved for **S8B**) harbored in a 3' UTR and the y-axis is the proportion of genes that are differentially expressed in CEU vs. CHB+JPT populations.

Figure S9. Transcripts mapped on curated protein coding genes in RefSeq database have higher expression variability (CV) than the remaining expressed transcripts that are not curated by the RefSeq database in each of the six datasets. The x-axis is the six datasets as described in Table 1 and the y-axis is the boxplot of CV values of the microarray probes. The white boxplots are the probes mapped on curated RefSeq coding transcripts and the grey boxplots are the remaining probes that are expressed in each dataset.

Figure S10. The expression variability (CV) of RefSeq transcripts targeted by co-expressed miRNAs is significantly higher than the RefSeq transcripts that are not targeted by miRNA

across six human datasets. High-Confidence miRNA targets: Only targets determined by TSs ($PCT > 0.8$), TSt (< -0.4 and percentile > 85), Pictar, or experimentally verified targets of the 287 coexpressed miRNAs. Non-targets: transcripts that are not targeted by the 287 coexpressed miRNAs with any of the miRNA target determination methods (including the 4 aforementioned methods, PITA and miRanda algorithms). Boxplots of CV for targets (grey) and non-target transcripts (white) are presented. For each microarray platform, only microarray probes that are mapped on the curated RefSeq coding transcripts are used in the analysis.

Figure S11. The impact of gene expression levels on CV. **S11A** and **S11B** are results for dataset I and II. In each figure, we ranked the genes with increasing expression levels and used a sliding window method (window size of 1,000 genes and step size of 200 genes) to calculate the median CV for the high confidence miRNA targets and non-targets in each window. Note that the top 40% lowly expressed genes have higher CV values if they are repressed by miRNAs; while the top 40% highly expressed genes have significantly lower CV values if they are miRNA targets. The impacts of gene expression levels on the CV vanish if we restrict our analysis to the curated RefSeq coding transcripts (Figure **S11C** for dataset I and **S11D** for dataset II). High confidence miRNA targets were considered as miRNA targets, while genes not targeted by co-expressed miRNAs in all the six methods were considered non-targets.

Figure S12. The difference in divergence ratios between miRNA targets and non-targets is mainly contributed by the lowly expressed genes. In **S12A** (all expressed transcripts) and **S12B** (all expressed RefSeq transcripts), we ranked the genes with increasing expression levels and used a sliding window method (window size of 1000 genes and step size of 200 genes) to calculate the proportion of the targets and non-targets in that window that are differentially expressed between CEU vs. CHB+JPT populations (FDR cutoff of 0.001).

Figure S13. The regulating effects of miRNAs that are expressed at various levels. In **S13A** and **S13B**, miRNAs are ranked by expression levels on the x-axis. **S13A**, CV of the top 100 highly expressed miRNAs are significantly negatively correlated with expression levels in the European-American males (data generated from Wang *et al* 2009). **S13B**, Number of conserved miRNA target genes significantly decrease with corresponding decrease in expression levels of miRNAs; every dot is 10 miRNAs that are grouped with decreasing expression levels (x-axis) and y-axis is the number of conserved targets of the 10 miRNAs.

Figure S14. The conserved targets of the top 50 miRNAs have significantly higher CV than the remaining curated RefSeq transcripts in both dataset I (**S14A**) and II (**S14B**). The y-axis is the boxplots of CV for the conserved targets of the top 50 highly expressed miRNAs and the remaining expressed transcripts. Dataset I: $P = 0.024$, KS test, Figure S12A; Dataset II: $P = 0.019$, KS test, Figure S12B.

Supplementary Figures

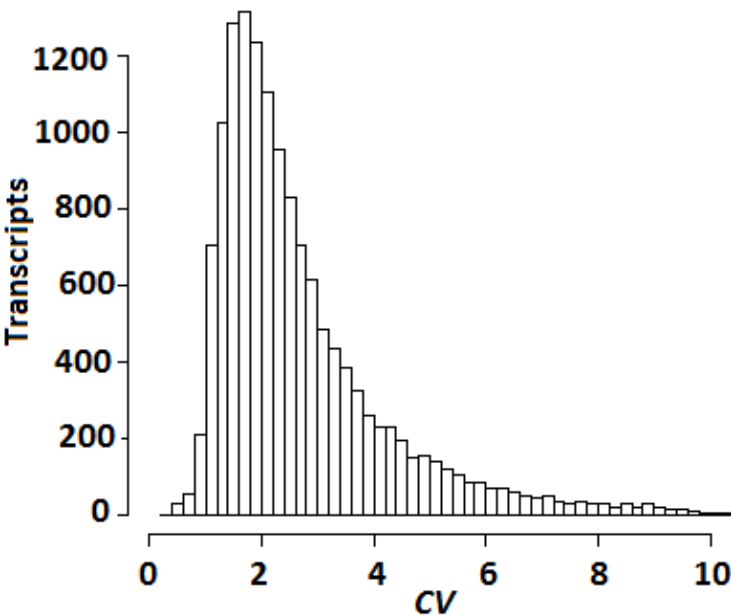


Figure S1A

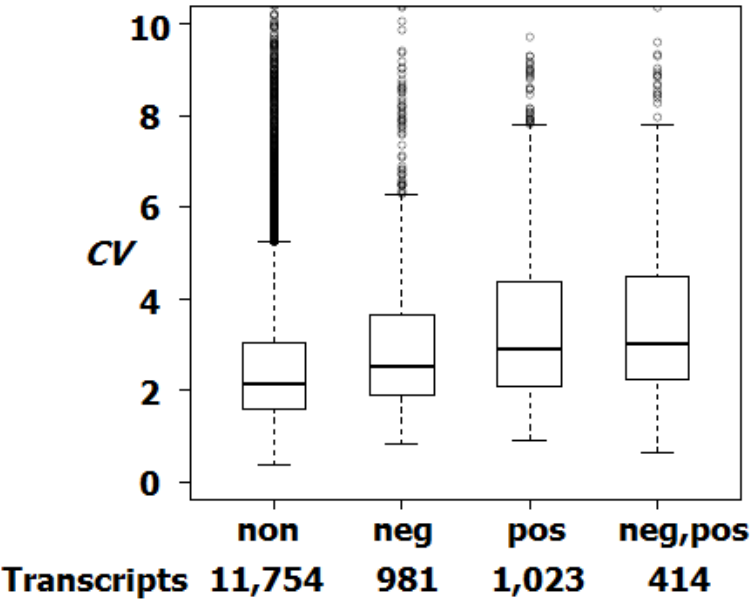


Figure S1B

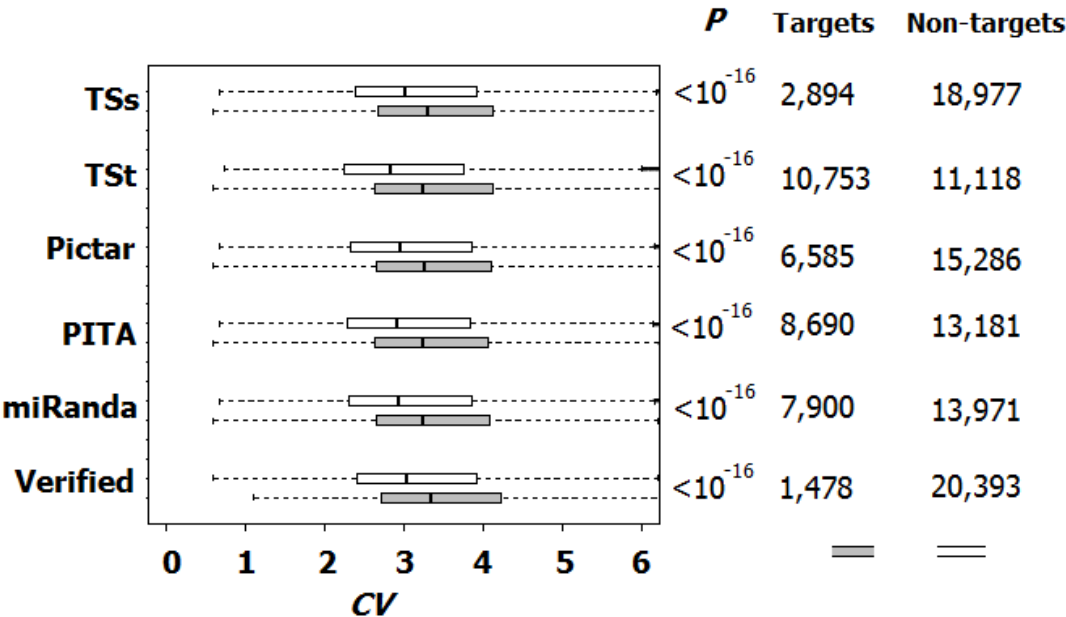


Figure S2A

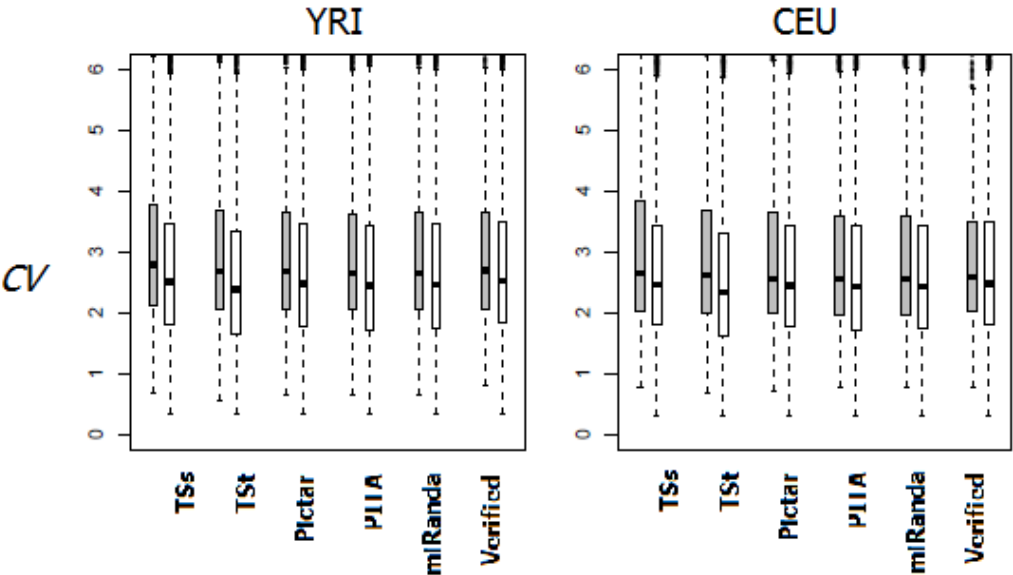


Figure S2B

Figure S2C

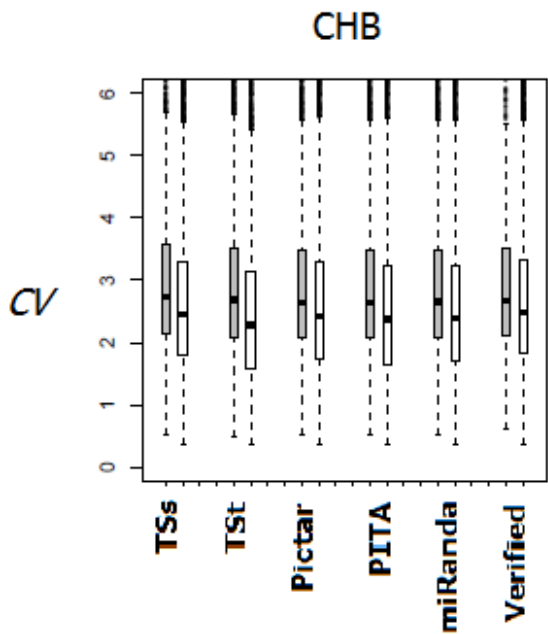


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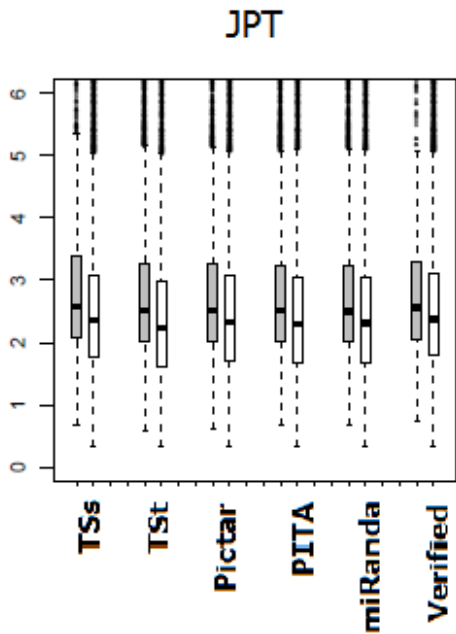


Figure S2E

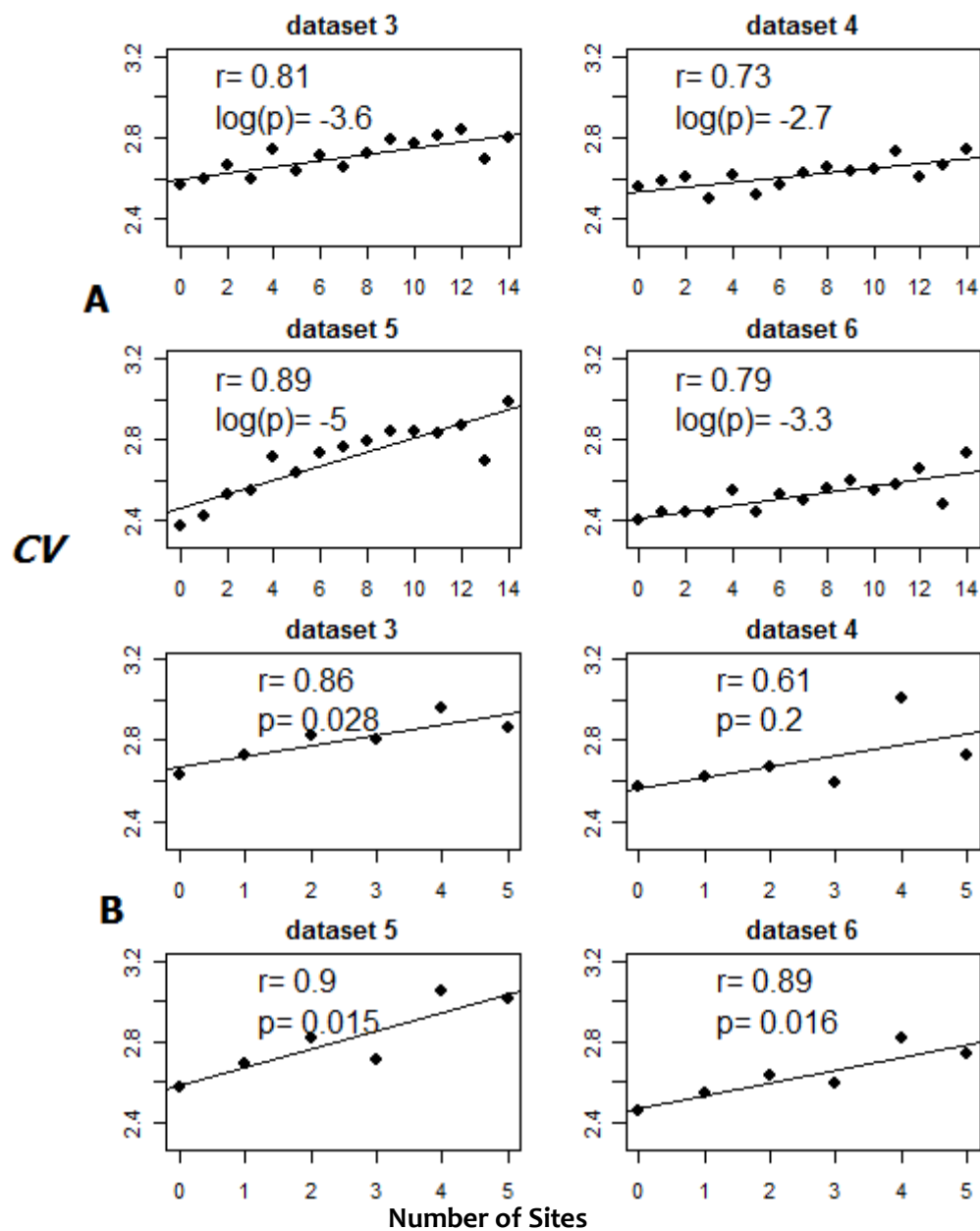


Figure S3

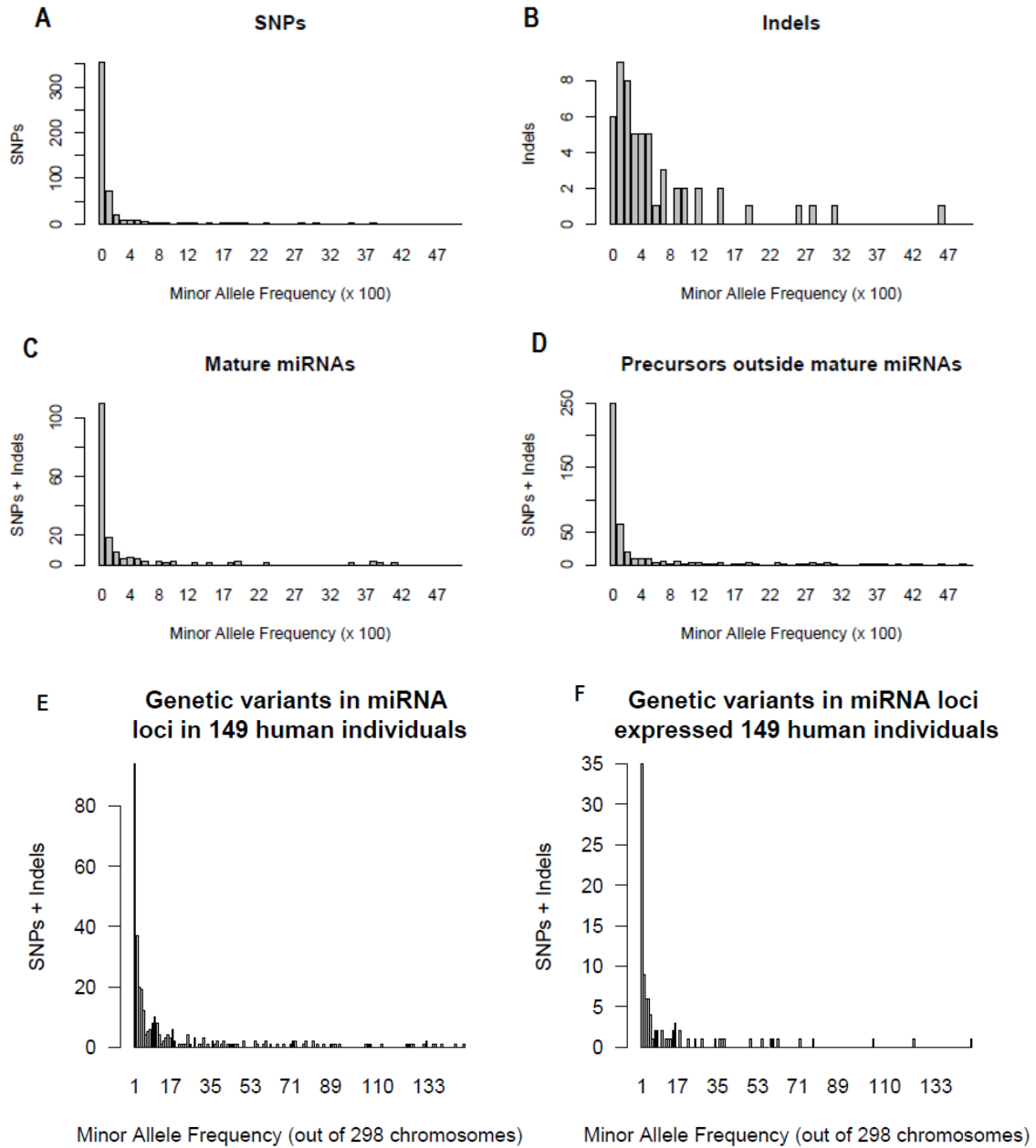


Figure S4

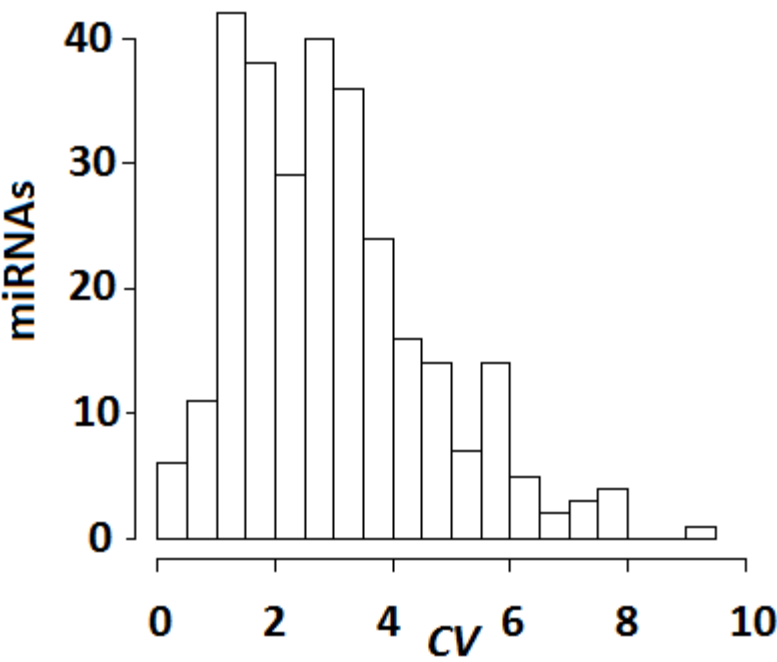


Figure S5

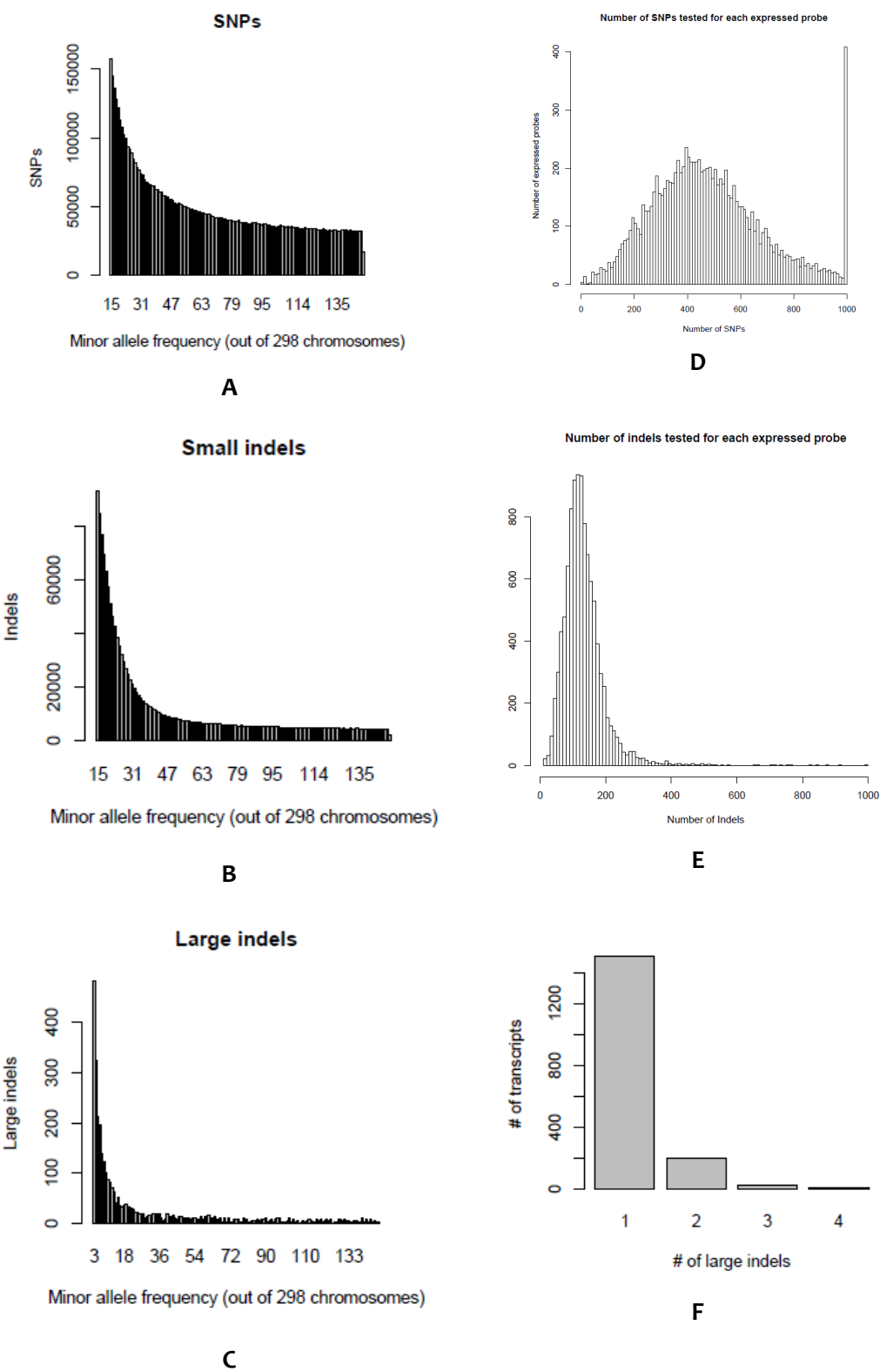


Figure S6

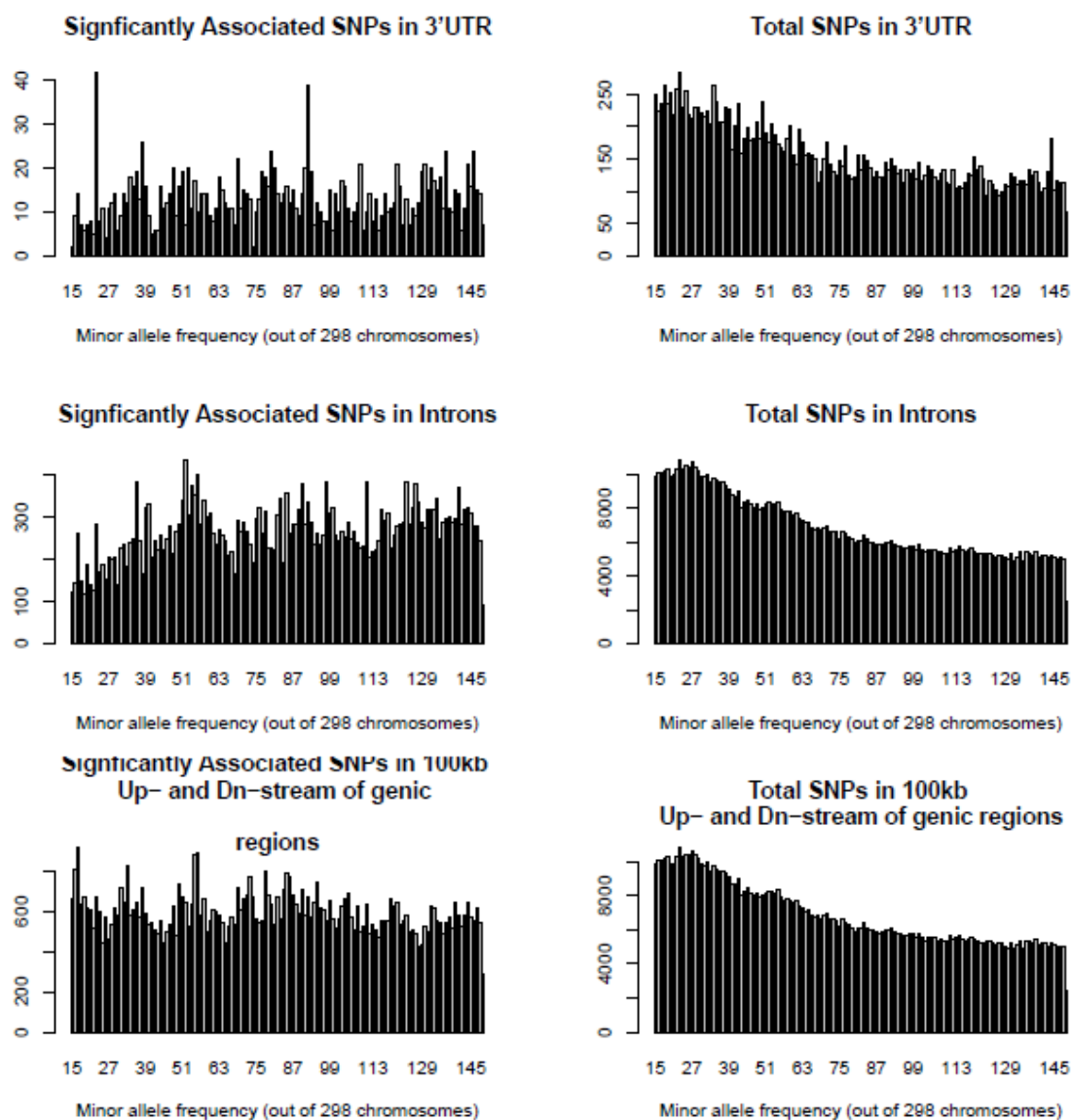


Figure S7

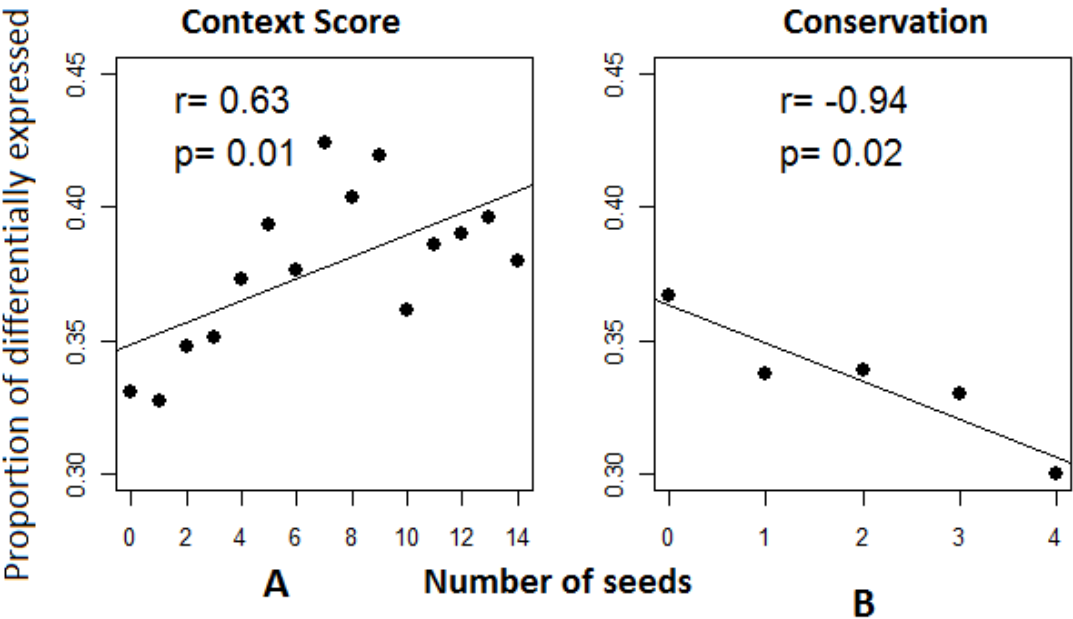


Figure S8

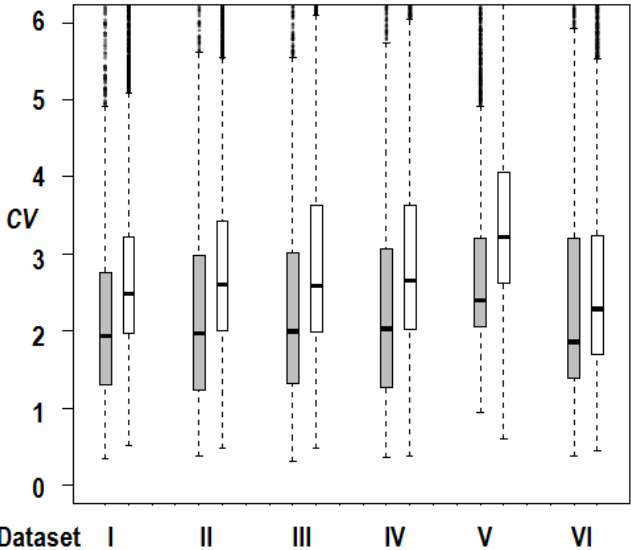


Figure S9

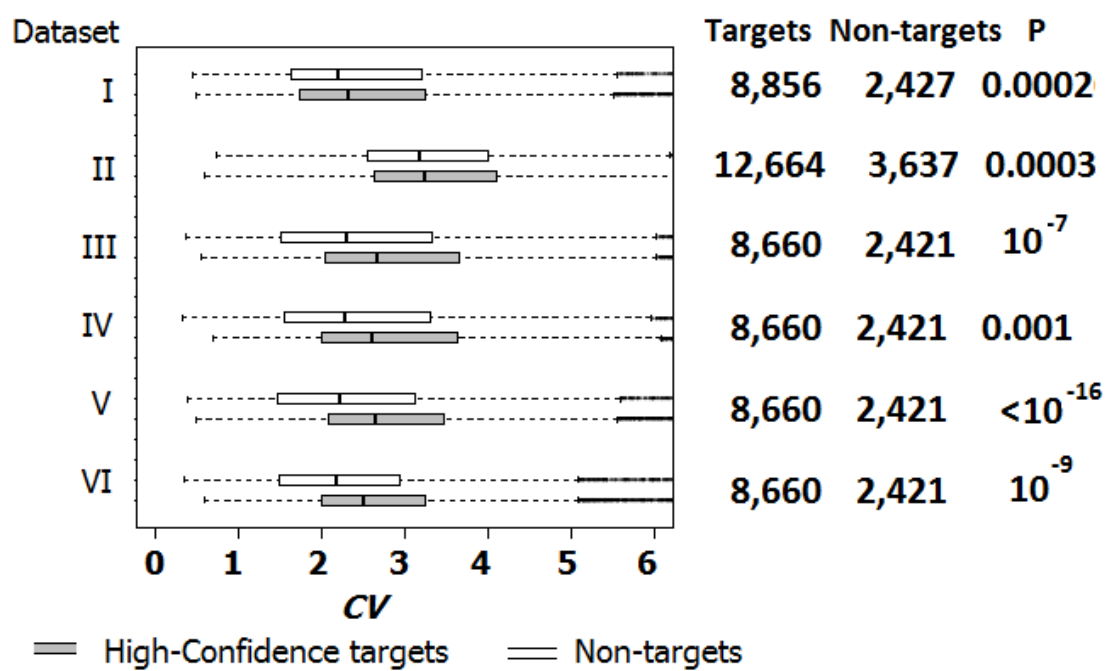


Figure S10

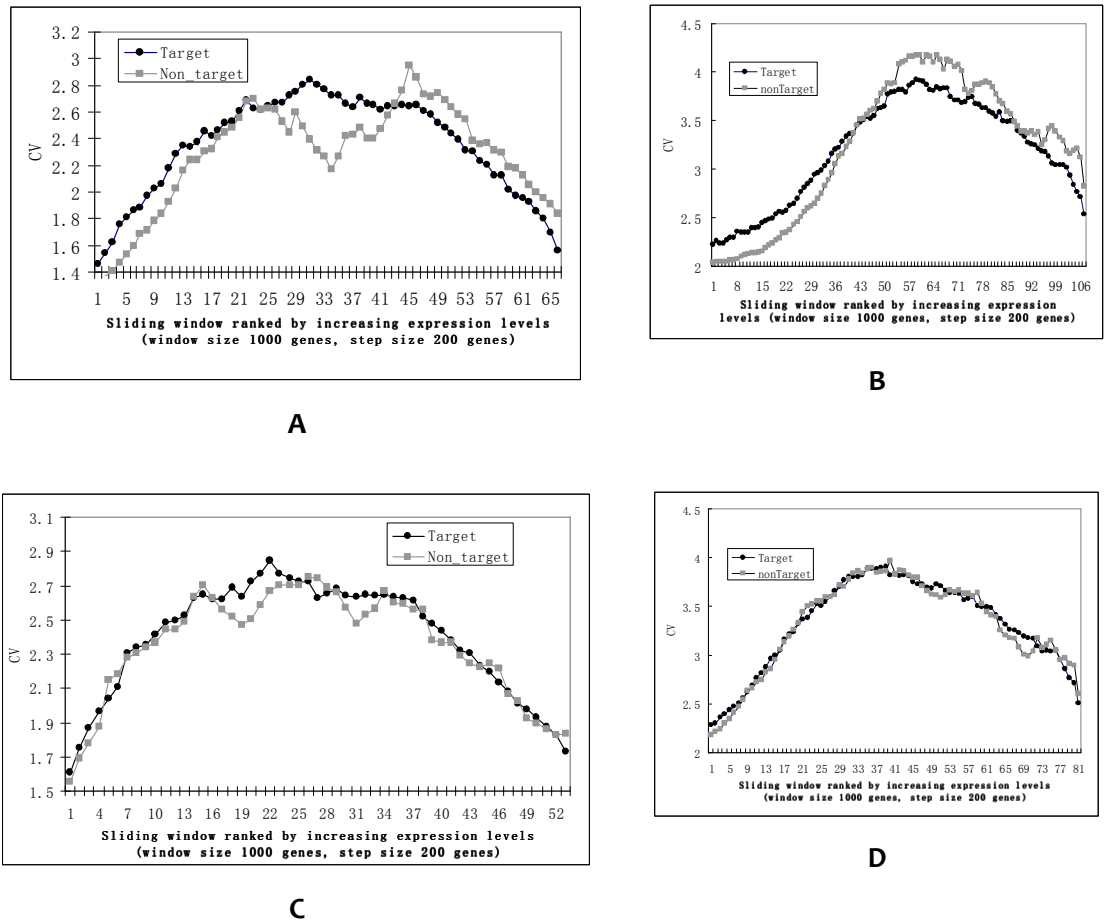


Figure S11

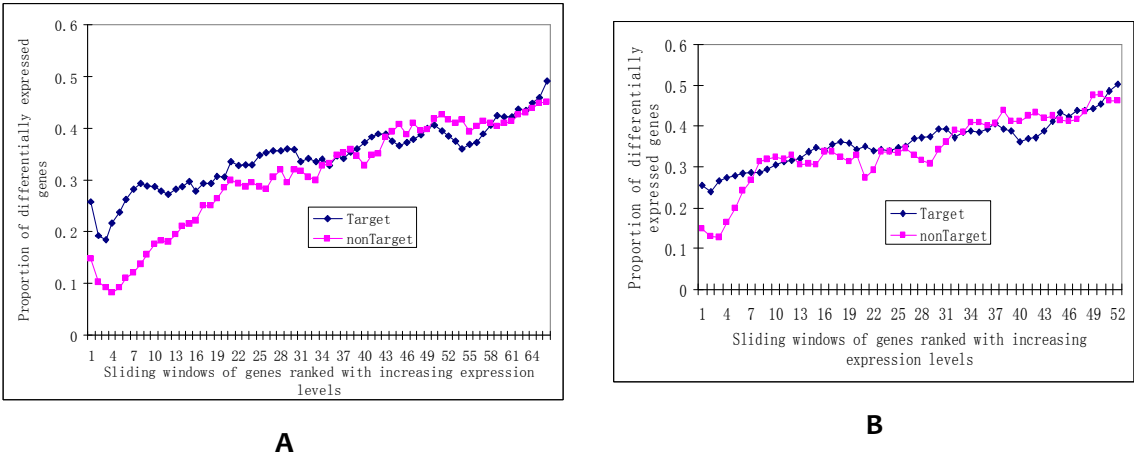


Figure S12

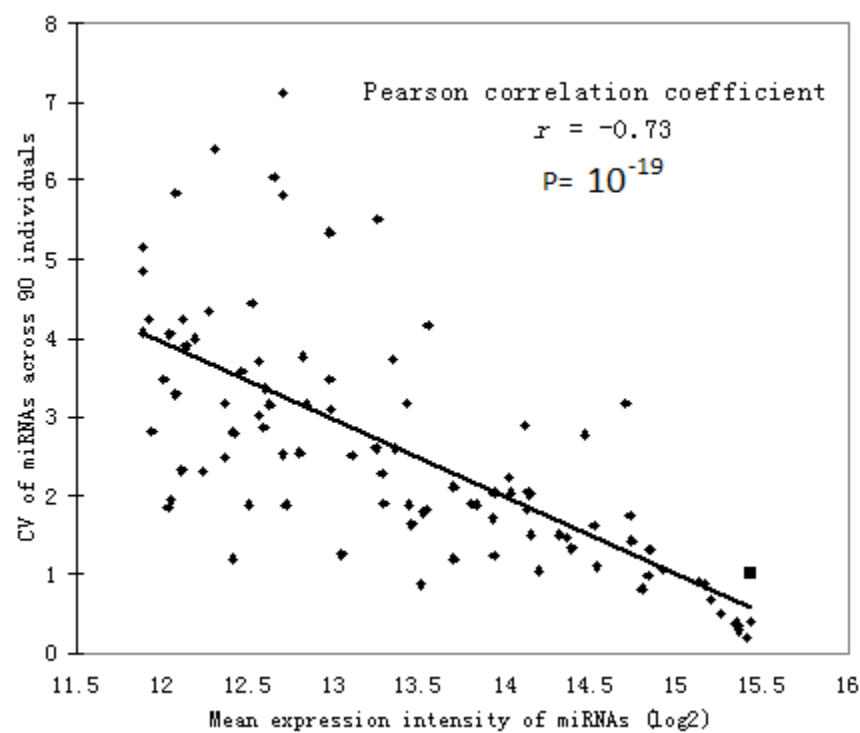


Figure S13A

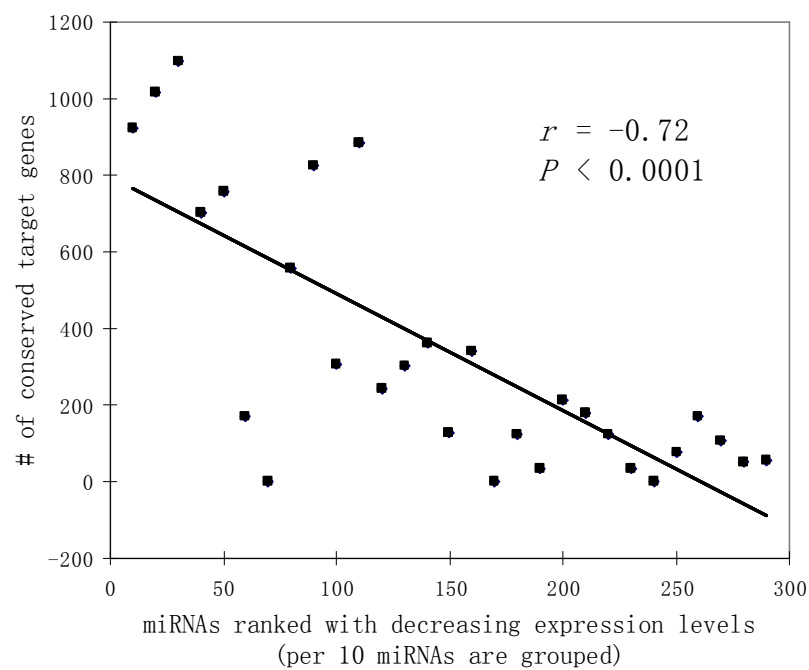


Figure S13B

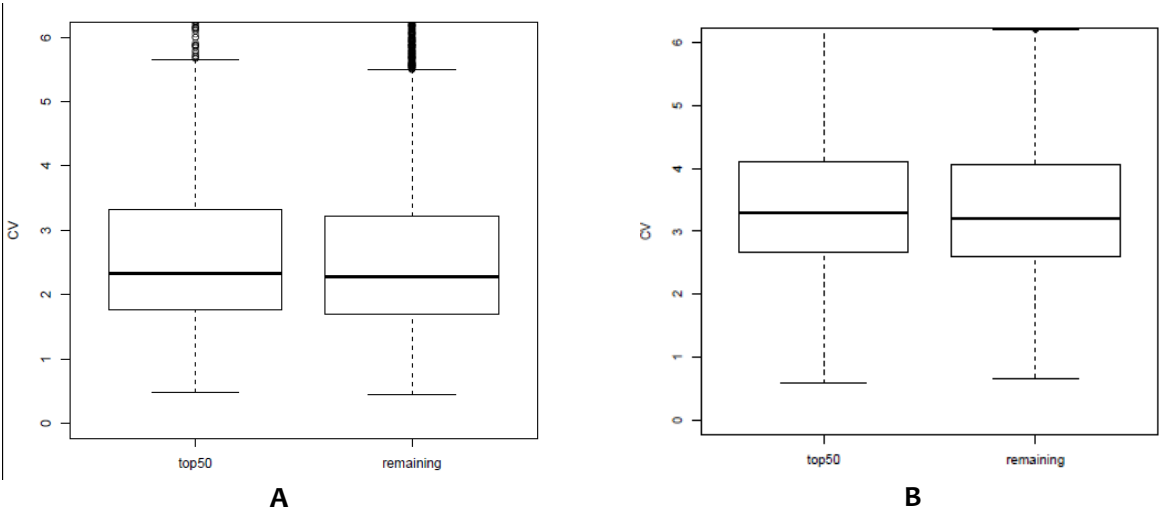


Figure S14

Supplementary Tables

Table S1 The SNPs located in miRNA loci in HapMap 3 Project

SNP-ID	Genotype	Chr	Position	Location in miRNA locus	miRNA locus	miRNA Expressed?	Disease association	Reference (PubMed ID)
rs2910164	C/G	5	159844996	seed	hsa-mir-146a	YES	predisposes to papillary thyroid carcinoma.	18474871
rs6971711	C/T	7	73243535	mature	hsa-mir-590	YES		
rs11014002	C/T	10	24604659	precursor	hsa-mir-603	YES		
rs11231898	A/G	11	64415412	precursor	hsa-mir-194-2	YES		
rs6505162	A/C	17	25468309	precursor	hsa-mir-423	YES	esophageal cancer	19138993
rs895819	C/T	19	13808292	precursor	hsa-mir-27a	YES	Breast cancer	19921425
rs9589207	A/G	13	90801590	precursor	hsa-mir-92a-1	YES		
rs11614913	C/T	12	52671866	mature	hsa-mir-196a	NO	survival in individuals with NSCLC	18634034
rs4919510	C/G	10	102724768	mature	hsa-mir-608	NO		
rs1077020	C/T	4	1957991	precursor	hsa-mir-943	NO		
rs11259096	C/T	10	14518624	precursor	hsa-mir-1265	NO		
rs11844707	A/G	14	100580366	precursor	hsa-mir-1185-2	NO		
rs17091403	C/T	10	115923895	precursor	hsa-mir-2110	NO		
rs17759989	A/G	17	58375343	precursor	hsa-mir-633	NO		
rs2043556	C/T	10	52729412	precursor	hsa-mir-605	NO		
rs2292832	C/T	2	241044176	precursor	hsa-mir-149	NO	Lung Cancer in Chinese	19293314
rs4822739	C/G	22	25281185	precursor	hsa-mir-548j	NO		
rs5965660	G/T	X	144883994	precursor	hsa-mir-888	NO		
rs5965990	A/G	X	144917048	precursor	hsa-mir-891a	NO		
rs6122014	A/G	20	60561960	precursor	hsa-mir-1-1	NO		
rs7911488	A/G	10	105144079	precursor	hsa-mir-1307	NO		

“miRNA expressed” means whether this miRNA is expressed in lymphoblastoid cells. “mature” means SNPs is located in mature miRNA; “precursor” means the SNP is located in the miRNA precursors outside mature miRNA region.

Table S2 Genetic variants (SNPs + Indels) in miRNA loci in the 1000 Human Genomes Project

Variant ID	Variant Type	MAF in global populations	Chr	Start	End	miRNA locus	Location in miRNA entire loci
rs72563729	SNP	0.0100	1	1102563	1102563	hsa-mir-200b	precursor
chr1_1104406	INDEL	0.0037	1	1104406	1104406	hsa-mir-429	precursor
rs183812340	SNP	0.0005	1	1104412	1104412	hsa-mir-429	precursor
rs187195064	SNP	0.0046	1	3477292	3477292	hsa-mir-551a	seed
rs72631823	SNP	0.0005	1	9211782	9211782	hsa-mir-34a	precursor
rs147869275	SNP	0.0100	1	19223571	19223571	hsa-mir-1290	precursor
rs75705742	SNP	0.0142	1	19223639	19223639	hsa-mir-1290	precursor
rs184377285	SNP	0.0005	1	35135204	35135204	hsa-mir-552	precursor
rs76067517	SNP	0.0037	1	35135270	35135270	hsa-mir-552	precursor
rs189946363	SNP	0.0005	1	35135274	35135274	hsa-mir-552	precursor
rs112439044	SNP	0.0046	1	41220077	41220077	hsa-mir-30e	precursor
rs147113488	SNP	0.0100	1	68649258	68649258	hsa-mir-1262	precursor
rs138343697	SNP	0.0014	1	68649290	68649290	hsa-mir-1262	precursor
rs190622705	SNP	0.0014	1	100746814	100746814	hsa-mir-553	seed
rs142872331	SNP	0.0005	1	110141578	110141578	hsa-mir-197	mature
rs115372145	SNP	0.0124	1	117637325	117637325	hsa-mir-942	precursor
rs79661940	SNP	0.0201	1	151518284	151518284	hsa-mir-554	precursor
rs184748971	SNP	0.0005	1	151518318	151518318	hsa-mir-554	precursor
rs189668852	SNP	0.0005	1	151518322	151518322	hsa-mir-554	precursor
rs149994627	SNP	0.0005	1	151518341	151518341	hsa-mir-554	precursor
chr1_154166214	INDEL	0.0023	1	154166214	154166214	hsa-mir-190b	precursor
chr1_156905968	INDEL	0.0005	1	156905968	156905969	hsa-mir-765	precursor
rs189709980	SNP	0.0009	1	167967904	167967904	hsa-mir-1255b	seed
rs79639536	SNP	0.0200	1	167967958	167967958	hsa-mir-1255b-2	precursor
rs142690749	SNP	0.0005	1	167967963	167967963	hsa-mir-1255b-2	precursor
rs78825966	SNP	0.0600	1	168344829	168344829	hsa-mir-557	seed
rs191927458	SNP	0.0005	1	171070937	171070937	hsa-mir-1295	precursor
rs147011290	SNP	0.0023	1	172113756	172113756	hsa-mir-199a-2	precursor
rs181176070	SNP	0.0014	1	176998548	176998548	hsa-mir-488	mature
rs186200318	SNP	0.0005	1	176998565	176998565	hsa-mir-488	seed
rs116338160	SNP	0.0100	1	201777751	201777751	hsa-mir-1231	mature
chr1_201777752	SNP	0.0100	1	201777752	201777752	hsa-mir-1231	mature
rs139405984	SNP	0.0018	1	205417483	205417483	hsa-mir-135b	precursor
rs149492792	SNP	0.0009	1	209605539	209605539	hsa-mir-205	precursor
rs189877545	SNP	0.0009	1	220291206	220291206	hsa-mir-215	precursor
rs72631834	SNP	0.0014	1	220291292	220291292	hsa-mir-215	precursor
rs145979015	SNP	0.0009	1	220291302	220291302	hsa-mir-215	precursor
rs113256801	SNP	0.0027	1	220373943	220373943	hsa-mir-664	mature
rs192140250	SNP	0.0005	1	236016347	236016347	hsa-mir-1537	precursor
rs114803590	SNP	0.0119	2	47604856	47604856	hsa-mir-559	precursor
rs58450758	SNP	0.2001	2	47604866	47604866	hsa-mir-559	precursor
rs188620729	SNP	0.0005	2	47604884	47604884	hsa-mir-559	seed
rs146825879	SNP	0.0009	2	47604893	47604893	hsa-mir-559	precursor
rs41291173	SNP	0.0100	2	56210140	56210140	hsa-mir-217	precursor
rs140509279	SNP	0.0009	2	56210168	56210168	hsa-mir-217	mature
rs150436368	SNP	0.0200	2	56210207	56210207	hsa-mir-217	precursor
rs41291179	SNP	0.0700	2	56216090	56216090	hsa-mir-216a	precursor
chr2_56227884	INDEL	0.0100	2	56227884	56227885	hsa-mir-216b	precursor
chr2_56227887	INDEL	0.0500	2	56227887	56227887	hsa-mir-216b	precursor
rs113580833	SNP	0.0041	2	70480051	70480051	hsa-mir-1285-2	precursor
rs111851523	SNP	0.0041	2	70480062	70480062	hsa-mir-1285-2	precursor
rs117812383	SNP	0.0005	2	136422988	136422988	hsa-mir-128-1	precursor
rs79402775	SNP	0.0500	2	176032376	176032376	hsa-mir-933	mature
rs139770589	SNP	0.0037	2	176032384	176032384	hsa-mir-933	seed
rs182717619	SNP	0.0005	2	176032408	176032408	hsa-mir-933	precursor
rs146754630	SNP	0.0124	2	180725568	180725568	hsa-mir-1258	precursor
rs184508542	SNP	0.0005	2	189162305	189162305	hsa-mir-561	precursor
rs113906492	SNP	0.0100	2	189842822	189842822	hsa-mir-1245	precursor
rs116237969	SNP	0.0243	2	208134114	208134114	hsa-mir-1302-4	precursor

rs188612260	SNP	0.0009	2	219267407	219267407	hsa-mir-26b	precursor
rs71428439	SNP	0.1410	2	241395500	241395500	hsa-mir-149	precursor
rs2292832	SNP	0.4200	2	241395503	241395503	hsa-mir-149	precursor
rs189766364	SNP	0.0005	3	10436194	10436194	hsa-mir-885-3p	mature
rs145590767	SNP	0.0023	3	15915306	15915306	hsa-mir-563	precursor
rs190898565	SNP	0.0005	3	38010938	38010938	hsa-mir-26a-1	precursor
rs182070256	SNP	0.0009	3	38010964	38010964	hsa-mir-26a-1	mature
rs114636202	SNP	0.0200	3	44903385	44903385	hsa-mir-564	precursor
rs2292181	SNP	0.0632	3	44903434	44903434	hsa-mir-564	precursor
rs181697923	SNP	0.0005	3	47891069	47891069	hsa-mir-1226	mature
rs141645399	SNP	0.0009	3	47891117	47891117	hsa-mir-1226	mature
rs187238646	SNP	0.0018	3	50210836	50210836	hsa-mir-566	precursor
rs146499813	SNP	0.0005	3	111831684	111831684	hsa-mir-567	mature
rs149509568	SNP	0.0014	3	114035388	114035388	hsa-mir-568	mature
rs142303836	SNP	0.0005	3	120114558	120114558	hsa-mir-198	mature
rs189554431	SNP	0.0014	3	125509250	125509250	hsa-mir-548i-1	precursor
rs146020563	SNP	0.0005	3	160122421	160122421	hsa-mir-15b	precursor
rs192595529	SNP	0.0005	3	160122434	160122434	hsa-mir-15b	seed
rs182926610	SNP	0.0005	3	164059159	164059159	hsa-mir-720	seed
rs73037390	SNP	0.0124	3	170824453	170824453	hsa-mir-569	precursor
rs116867000	SNP	0.0023	3	170824459	170824459	hsa-mir-569	precursor
rs148241223	SNP	0.0037	3	183959219	183959219	hsa-mir-1224	precursor
rs73063489	SNP	0.0018	3	186504532	186504532	hsa-mir-1248	precursor
rs78547906	SNP	0.0018	3	188406636	188406636	hsa-mir-28-3p	mature
rs75715827	SNP	0.0417	3	189547735	189547735	hsa-mir-944	precursor
rs186331124	SNP	0.0005	3	189547761	189547761	hsa-mir-944	precursor
rs77473380	SNP	0.0041	3	189547778	189547778	hsa-mir-944	mature
rs190786647	SNP	0.0009	3	189547779	189547779	hsa-mir-944	mature
rs9860655	SNP	0.0600	3	195426305	195426305	hsa-mir-570	precursor
chr3_195426368	INDEL	0.0137	3	195426368	195426368	hsa-mir-570	precursor
rs140463854	SNP	0.0005	3	197401371	197401371	hsa-mir-922	mature
rs182056447	SNP	0.0009	3	197401372	197401372	hsa-mir-922	mature
rs114814977	SNP	0.0200	3	197401415	197401415	hsa-mir-922	precursor
rs150407249	SNP	0.0005	3	197401442	197401442	hsa-mir-922	precursor
rs148718934	SNP	0.0005	4	343998	343998	hsa-mir-571	precursor
chr4_1988119	SNP	0.0014	4	1988119	1988119	hsa-mir-943	precursor
rs186568343	SNP	0.0009	4	1988144	1988144	hsa-mir-943	seed
chr4_1988170	SNP	0.0005	4	1988170	1988170	hsa-mir-943	precursor
chr4_1988184	INDEL	0.2802	4	1988184	1988184	hsa-mir-943	precursor
rs1077020	SNP	0.2605	4	1988193	1988193	hsa-mir-943	precursor
rs183460242	SNP	0.0005	4	8007066	8007066	hsa-mir-95	precursor
rs188573591	SNP	0.0005	4	8007104	8007104	hsa-mir-95	precursor
rs111482845	INDEL	0.3141	4	9557815	9557821	hsa-mir-548i-2	precursor
rs140817192	SNP	0.0046	4	9557851	9557851	hsa-mir-548i-2	precursor
rs111766467	SNP	0.0009	4	9557857	9557857	hsa-mir-548i-2	precursor
rs113384898	SNP	0.0009	4	9557888	9557888	hsa-mir-548i	mature
rs192259662	SNP	0.0005	4	24521871	24521871	hsa-mir-573	precursor
rs113789096	SNP	0.0018	4	36428006	36428006	hsa-mir-1255b-1	precursor
rs139535532	SNP	0.0014	4	36428046	36428046	hsa-mir-1255b	seed
rs6841938	SNP	0.0916	4	36428048	36428048	hsa-mir-1255b	mature
rs147472159	INDEL	0.0400	4	38869679	38869681	hsa-mir-574-5p	seed
rs73239138	SNP	0.3842	4	67142620	67142620	hsa-mir-1269	mature
rs149186367	SNP	0.0046	4	83674520	83674520	hsa-mir-575	seed
rs28664200	SNP	0.3500	4	102251501	102251501	hsa-mir-1255a	precursor
rs192307370	SNP	0.0018	4	102251532	102251532	hsa-mir-1255a	mature
rs185489298	SNP	0.0018	4	110409867	110409867	hsa-mir-576	precursor
rs77639117	SNP	0.0500	4	110409933	110409933	hsa-mir-576	precursor
rs150161032	SNP	0.0005	4	113569088	113569088	hsa-mir-367r	seed
rs138673224	SNP	0.0027	4	113569207	113569207	hsa-mir-302d	mature
chr4_113569539	INDEL	0.0200	4	113569539	113569543	hsa-mir-302c	seed
rs190807868	SNP	0.0014	4	113569680	113569680	hsa-mir-302b	precursor
rs183105707	SNP	0.0005	4	113569692	113569692	hsa-mir-302b	mature
rs114318553	SNP	0.0046	4	113569695	113569695	hsa-mir-302b	mature
rs148339577	SNP	0.0037	4	114028104	114028104	hsa-mir-1243	precursor
rs189506651	SNP	0.0014	4	115577996	115577996	hsa-mir-577	precursor
rs34115976	SNP	0.1200	4	115577997	115577997	hsa-mir-577	precursor

rs183399490	SNP	0.0005	4	117220909	117220909	hsa-mir-1973	seed
rs143042626	SNP	0.0009	4	166321867	166321867	hsa-mir-1979	mature
rs190183451	SNP	0.0100	4	183090511	183090511	hsa-mir-1305	mature
chr5_15935334	INDEL	0.0527	5	15935334	15935335	hsa-mir-887	precursor
rs115089112	SNP	0.0124	5	36148057	36148057	hsa-mir-580	precursor
rs184653784	SNP	0.0005	5	36148078	36148078	hsa-mir-580	precursor
rs116535054	SNP	0.0100	5	41475761	41475761	hsa-mir-1274a	mature
rs318039	SNP	0.2807	5	41475766	41475766	hsa-mir-1274a	precursor
rs149830925	SNP	0.0005	5	53247340	53247340	hsa-mir-581	precursor
rs144949536	SNP	0.0032	5	54466362	54466362	hsa-mir-449a	precursor
rs112310158	SNP	0.0100	5	54466378	54466378	hsa-mir-449a	precursor
rs10061133	SNP	0.1300	5	54466544	54466544	hsa-mir-449b	mature
rs184340760	SNP	0.0100	5	95414909	95414909	hsa-mir-583	precursor
rs141552882	SNP	0.0009	5	100152234	100152234	hsa-mir-548p	precursor
rs75310044	SNP	0.0018	5	132763335	132763335	hsa-mir-1289-2	precursor
rs115216563	SNP	0.0247	5	132763351	132763351	hsa-mir-1289-2	precursor
rs112928293	SNP	0.0005	5	132763362	132763362	hsa-mir-1289-2	precursor
rs190323149	SNP	0.0005	5	148810267	148810267	hsa-mir-145	seed
rs189565536	SNP	0.0005	5	153726728	153726728	hsa-mir-1294	mature
rs114020978	SNP	0.0100	5	153726756	153726756	hsa-mir-1294	precursor
rs13186787	SNP	0.0124	5	153726769	153726769	hsa-mir-1294	precursor
rs142414368	SNP	0.0018	5	154065347	154065347	hsa-mir-1303	precursor
rs77055126	SNP	0.0311	5	154065348	154065348	hsa-mir-1303	precursor
chr5_154065369	INDEL	0.0900	5	154065369	154065369	hsa-mir-1303	precursor
chr5_154065381	INDEL	0.4611	5	154065381	154065383	hsa-mir-1303	precursor
rs33982250	INDEL	0.2600	5	154065382	154065383	hsa-mir-1303	precursor
rs2910164	SNP	0.3814	5	159912418	159912418	hsa-mir-146a	seed
rs140638702	SNP	0.0014	5	168195174	168195174	hsa-mir-218-2	mature
rs115473017	SNP	0.0100	5	168690611	168690611	hsa-mir-585	precursor
rs62376934	SNP	0.2000	5	168690612	168690612	hsa-mir-585	precursor
rs62376935	SNP	0.1000	5	168690635	168690635	hsa-mir-585	seed
rs140379047	SNP	0.0100	5	168690664	168690664	hsa-mir-585	precursor
rs184601084	SNP	0.0005	5	168690697	168690697	hsa-mir-585	precursor
rs2291418	SNP	0.0300	5	179225324	179225324	hsa-mir-1229	precursor
rs12197631	SNP	0.1100	6	18572056	18572056	hsa-mir-548a-1	precursor
chr6_18572087	INDEL	0.0200	6	18572087	18572087	hsa-mir-548a-1	mature
rs185147690	SNP	0.0018	6	31924631	31924631	hsa-mir-1236	seed
rs76156362	SNP	0.0100	6	33967787	33967787	hsa-mir-1275	precursor
rs73735310	SNP	0.0100	6	45165473	45165473	hsa-mir-586	mature
rs149150037	SNP	0.0005	6	72113270	72113270	hsa-mir-30a	mature
rs190842689	SNP	0.0005	6	72113306	72113306	hsa-mir-30a	mature
rs117428639	SNP	0.0100	6	98472445	98472445	hsa-mir-2113	precursor
rs142927919	SNP	0.0023	6	98472446	98472446	hsa-mir-2113	precursor
rs188182113	SNP	0.0014	6	119390263	119390263	hsa-mir-548b-5p	mature
rs143896961	SNP	0.0009	6	166922862	166922862	hsa-mir-1913	mature
rs188302425	SNP	0.0005	6	166922916	166922916	hsa-mir-1913	precursor
rs72631820	SNP	0.0100	7	1062599	1062599	hsa-mir-339-3p	mature
rs145196722	SNP	0.0014	7	1062626	1062626	hsa-mir-339-5p	mature
rs187080847	SNP	0.0014	7	30329444	30329444	hsa-mir-550	mature
chr7_30329453	INDEL	0.0311	7	30329453	30329456	hsa-mir-550-1	precursor
rs180826747	SNP	0.0005	7	36958995	36958995	hsa-mir-1200	precursor
rs189727189	SNP	0.0018	7	73605546	73605546	hsa-mir-590	seed
rs192756765	SNP	0.0005	7	73605551	73605551	hsa-mir-590	mature
rs147169000	SNP	0.0014	7	73605578	73605578	hsa-mir-590	precursor
rs6971711	SNP	0.0300	7	73605599	73605599	hsa-mir-590	mature
rs189095137	SNP	0.0009	7	95849010	95849010	hsa-mir-591	precursor
chr7_95849054	INDEL	0.0311	7	95849054	95849054	hsa-mir-591	precursor
rs72631824	SNP	0.0046	7	99691429	99691429	hsa-mir-93	precursor
rs72631827	SNP	0.0027	7	99691652	99691652	hsa-mir-106b	precursor
rs181862774	SNP	0.0014	7	102046217	102046217	hsa-mir-5480	precursor
rs141762298	SNP	0.0009	7	102046219	102046219	hsa-mir-5480	precursor
rs117420576	SNP	0.0018	7	102046237	102046237	hsa-mir-5480	precursor
rs145823581	SNP	0.0005	7	102046276	102046276	hsa-mir-5480	precursor
rs185456116	SNP	0.0009	7	102046296	102046296	hsa-mir-5480	precursor
rs139323492	SNP	0.0005	7	126698143	126698143	hsa-mir-592	precursor
rs181133328	SNP	0.0005	7	126698158	126698158	hsa-mir-592	precursor

rs73721294	SNP	0.0200	7	127721934	127721934	hsa-mir-593	seed
rs184901939	SNP	0.0005	7	127721971	127721971	hsa-mir-593	precursor
rs76481776	SNP	0.0500	7	129410227	129410227	hsa-mir-182	precursor
rs77586312	SNP	0.0023	7	129410228	129410228	hsa-mir-182	precursor
rs80041074	SNP	0.0023	7	129410239	129410239	hsa-mir-182	precursor
rs41274239	SNP	0.0023	7	129414574	129414574	hsa-mir-96	precursor
rs72631833	SNP	0.0046	7	129414804	129414804	hsa-mir-183	precursor
rs114864936	SNP	0.0100	7	147075120	147075120	hsa-mir-548f-4	precursor
rs193186885	SNP	0.0005	7	147075204	147075204	hsa-mir-548f-4	precursor
rs148185602	SNP	0.0014	7	148638597	148638597	hsa-mir-1975	precursor
chr7_150935577	SNP	0.0005	7	150935577	150935577	hsa-mir-671	seed
rs117344178	SNP	0.0100	7	158325411	158325411	hsa-mir-595	precursor
rs114151270	SNP	0.0101	7	158325415	158325415	hsa-mir-595	precursor
rs4909237	SNP	0.1841	7	158325503	158325503	hsa-mir-595	precursor
rs116450906	SNP	0.0105	8	1765409	1765409	hsa-mir-596	precursor
rs61388742	SNP	0.0800	8	1765425	1765425	hsa-mir-596	mature
rs112056940	SNP	0.0100	8	9599212	9599212	hsa-mir-597	mature
rs146125159	SNP	0.0005	8	9599255	9599255	hsa-mir-597	precursor
rs79397096	SNP	0.0100	8	9599276	9599276	hsa-mir-597	precursor
rs59878596	SNP	0.0600	8	10682894	10682894	hsa-mir-1322	mature
rs189895541	SNP	0.0023	8	10682898	10682898	hsa-mir-1322	seed
rs112004155	SNP	0.0100	8	10682905	10682905	hsa-mir-1322	precursor
rs182042712	SNP	0.0005	8	14710983	14710983	hsa-mir-383	precursor
rs184836993	SNP	0.0005	8	14710999	14710999	hsa-mir-383	mature
rs73235381	SNP	0.0400	8	26906402	26906402	hsa-mir-548h-4	precursor
rs150141473	INDEL	0.1506	8	26906433	26906438	hsa-mir-548h-4	precursor
rs184537764	SNP	0.0400	8	26906437	26906437	hsa-mir-548h-4	precursor
rs115507344	SNP	0.0014	8	26906471	26906471	hsa-mir-548h-4	precursor
chr8_41517959	INDEL	0.0147	8	41517959	41517959	hsa-mir-486	precursor
rs150478047	SNP	0.0005	8	41518025	41518025	hsa-mir-486	precursor
rs72631829	SNP	0.0014	8	65291808	65291808	hsa-mir-124-2	precursor
rs186714401	SNP	0.0005	8	100548917	100548917	hsa-mir-599	precursor
rs184062845	SNP	0.0009	8	101036259	101036259	hsa-mir-1273	precursor
rs139528851	INDEL	0.0700	8	105496635	105496645	hsa-mir-548a-3	precursor
rs150167306	SNP	0.0014	8	105496675	105496675	hsa-mir-548a-3	precursor
rs10505168	SNP	0.3700	8	113655752	113655752	hsa-mir-2053	precursor
rs2114358	SNP	0.3000	8	129021179	129021179	hsa-mir-1206	precursor
rs191866221	SNP	0.0014	8	129061422	129061422	hsa-mir-1207	mature
rs148236411	SNP	0.0005	8	129061462	129061462	hsa-mir-1207	mature
rs56863230	SNP	0.0200	8	129162366	129162366	hsa-mir-1208	precursor
rs2648841	SNP	0.1928	8	129162433	129162433	hsa-mir-1208	precursor
rs149074929	SNP	0.0018	8	141742750	141742750	hsa-mir-151	precursor
chr8_142867668	INDEL	0.0100	8	142867668	142867671	hsa-mir-1302-7	precursor
chr8_144895168	SNP	0.0005	8	144895168	144895168	hsa-mir-937	precursor
chr8_144895170	SNP	0.0005	8	144895170	144895170	hsa-mir-937	precursor
chr8_144895179	SNP	0.0005	8	144895179	144895179	hsa-mir-937	precursor
rs149434817	SNP	0.0009	8	145619365	145619365	hsa-mir-939	precursor
rs141140965	SNP	0.3800	8	145625538	145625538	hsa-mir-1234	precursor
rs138231885	SNP	0.0005	9	4850301	4850301	hsa-mir-101-2	precursor
rs140761798	SNP	0.0009	9	20716104	20716104	hsa-mir-491	precursor
rs192552111	SNP	0.0009	9	97847807	97847807	hsa-mir-27b	mature
rs181496497	SNP	0.0005	9	97848343	97848343	hsa-mir-24-1	precursor
rs192895122	SNP	0.0005	9	100125949	100125949	hsa-mir-1302-8	precursor
rs181306653	SNP	0.0005	9	125873826	125873826	hsa-mir-600	precursor
rs147291680	SNP	0.0027	9	125873916	125873916	hsa-mir-600	precursor
rs184395895	SNP	0.0005	9	126164871	126164871	hsa-mir-601	precursor
rs146892675	SNP	0.0100	9	131007001	131007001	hsa-mir-199b	precursor
rs72631835	SNP	0.0005	9	131007109	131007109	hsa-mir-199b	precursor
rs116636751	SNP	0.0027	9	140732963	140732963	hsa-mir-602	precursor
rs149384303	SNP	0.0009	10	14478576	14478576	hsa-mir-1265	precursor
rs11259096	SNP	0.0900	10	14478618	14478618	hsa-mir-1265	precursor
rs11014002	SNP	0.0900	10	24564653	24564653	hsa-mir-603	precursor
rs186844507	SNP	0.0014	10	29833959	29833959	hsa-mir-604	seed
rs2368393	SNP	0.3031	10	29833998	29833998	hsa-mir-604	precursor
rs2368392	SNP	0.3000	10	29834003	29834003	hsa-mir-604	precursor
rs12416605	SNP	0.1529	10	29891260	29891260	hsa-mir-938	seed

rs113212828	SNP	0.0037	10	53059349	53059349	hsa-mir-605	seed
rs2043556	SNP	0.2800	10	53059406	53059406	hsa-mir-605	precursor
rs138812323	SNP	0.0005	10	70519093	70519093	hsa-mir-1254	seed
rs192456466	SNP	0.0023	10	98588440	98588440	hsa-mir-607	precursor
chr10_100154978	SNP	0.0009	10	100154978	100154978	hsa-mir-1287	precursor
chr10_100155033	SNP	0.0005	10	100155033	100155033	hsa-mir-1287	mature
rs4919510	SNP	0.3500	10	102734778	102734778	hsa-mir-608	mature
rs76149940	SNP	0.0101	10	104196269	104196269	hsa-mir-146b	precursor
rs147668271	SNP	0.0005	10	105154013	105154013	hsa-mir-1307	precursor
rs7911488	SNP	0.2700	10	105154089	105154089	hsa-mir-1307	precursor
rs149841873	SNP	0.0009	10	105807855	105807855	hsa-mir-936	precursor
rs145823228	SNP	0.0005	10	105807858	105807858	hsa-mir-936	precursor
rs140657237	SNP	0.0100	10	105807909	105807909	hsa-mir-936	mature
rs189063749	SNP	0.0005	10	105807912	105807912	hsa-mir-936	mature
rs79924817	SNP	0.0100	10	105807928	105807928	hsa-mir-936	seed
rs74154754	SNP	0.0100	10	105978581	105978581	hsa-mir-609	precursor
rs75407574	SNP	0.0100	10	115933876	115933876	hsa-mir-2110	precursor
rs17091403	SNP	0.0500	10	115933905	115933905	hsa-mir-2110	precursor
rs192664871	SNP	0.0005	10	115933913	115933913	hsa-mir-2110	mature
rs114530801	SNP	0.0005	10	115933922	115933922	hsa-mir-2110	mature
rs142676430	SNP	0.0005	10	135061109	135061109	hsa-mir-202	precursor
rs12355840	SNP	0.2900	10	135061112	135061112	hsa-mir-202	precursor
chr11_568128	INDEL	0.0400	11	568128	568130	hsa-mir-210	seed
rs143234363	SNP	0.0018	11	7256057	7256057	hsa-mir-302e	precursor
rs189052513	SNP	0.0005	11	43602984	43602984	hsa-mir-129-2	precursor
rs187944546	SNP	0.0005	11	61559981	61559981	hsa-mir-611	mature
rs144890118	SNP	0.0014	11	61560031	61560031	hsa-mir-611	precursor
rs174561	SNP	0.3100	11	61582708	61582708	hsa-mir-1908	precursor
chr11_64136102	SNP	0.0014	11	64136102	64136102	hsa-mir-1237	precursor
chr11_64136103	SNP	0.0009	11	64136103	64136103	hsa-mir-1237	precursor
rs139493589	SNP	0.0005	11	64658623	64658623	hsa-mir-192	precursor
rs188630835	SNP	0.0014	11	64658640	64658640	hsa-mir-192	mature
rs11231898	SNP	0.0133	11	64658836	64658836	hsa-mir-194-2	precursor
rs550894	SNP	0.1749	11	65211940	65211940	hsa-mir-612	precursor
rs12803915	SNP	0.1700	11	65211979	65211979	hsa-mir-612	precursor
rs191249039	SNP	0.0005	11	70130159	70130159	hsa-mir-548k	precursor
rs72561778	SNP	0.0023	11	75046227	75046227	hsa-mir-326	precursor
rs139601788	SNP	0.0041	11	90602296	90602296	hsa-mir-1261	precursor
rs2155248	SNP	0.1100	11	93466866	93466866	hsa-mir-1304	precursor
rs79759099	SNP	0.0200	11	93466909	93466909	hsa-mir-1304	seed
rs79462725	SNP	0.0229	11	93466919	93466919	hsa-mir-1304	precursor
rs186423401	SNP	0.0005	11	94199691	94199691	hsa-mir-548l	precursor
rs191135297	SNP	0.0005	11	94199696	94199696	hsa-mir-548l	precursor
rs11020790	SNP	0.0412	11	94199710	94199710	hsa-mir-548l	precursor
rs148377174	SNP	0.0005	11	94199711	94199711	hsa-mir-548l	mature
rs13447640	SNP	0.0403	11	94199721	94199721	hsa-mir-548l	mature
rs143312616	SNP	0.0014	11	94199735	94199735	hsa-mir-548l	precursor
rs147268651	SNP	0.0023	12	12917608	12917608	hsa-mir-613	precursor
rs138509294	INDEL	0.0302	12	24365357	24365362	hsa-mir-920	precursor
rs189740304	SNP	0.0023	12	50627935	50627935	hsa-mir-1293	precursor
rs113699072	SNP	0.0400	12	50627942	50627942	hsa-mir-1293	precursor
rs185070757	SNP	0.0005	12	54385558	54385558	hsa-mir-196a	mature
rs11614913	SNP	0.3900	12	54385599	54385599	hsa-mir-196a	mature
rs185315720	SNP	0.0005	12	54731000	54731000	hsa-mir-148b	precursor
chr12_57588322	SNP	0.0005	12	57588322	57588322	hsa-mir-1228	precursor
rs139262076	SNP	0.0037	12	57588323	57588323	hsa-mir-1228	precursor
chr12_57588336	SNP	0.0005	12	57588336	57588336	hsa-mir-1228	precursor
rs17120527	SNP	0.0600	12	65016300	65016300	hsa-mir-548c	precursor
rs115256251	SNP	0.0041	12	79813049	79813049	hsa-mir-1252	mature
rs145551269	SNP	0.0005	12	81329527	81329527	hsa-mir-618	precursor
rs2682818	SNP	0.2317	12	81329536	81329536	hsa-mir-618	precursor
chr12_95228198	INDEL	0.1003	12	95228198	95228202	hsa-mir-492	precursor
rs2289030	SNP	0.1200	12	95228286	95228286	hsa-mir-492	precursor
rs189214156	SNP	0.0005	12	109230729	109230729	hsa-mir-619	precursor
rs191263402	SNP	0.0018	12	113132857	113132857	hsa-mir-1302-1	precursor
rs74647838	SNP	0.0300	12	113132901	113132901	hsa-mir-1302	seed

rs139328587	SNP	0.0005	12	116586405	116586405	hsa-mir-620	precursor
chr12_116586409	INDEL	0.0746	12	116586409	116586415	hsa-mir-620	precursor
chr12_116586412	INDEL	0.1534	12	116586412	116586414	hsa-mir-620	precursor
chr12_116586433	INDEL	0.1900	12	116586433	116586437	hsa-mir-620	precursor
rs7311975	SNP	0.1300	12	120151493	120151493	hsa-mir-1178	precursor
rs74614893	SNP	0.0105	12	120151501	120151501	hsa-mir-1178	precursor
rs141225976	SNP	0.0005	12	120151527	120151527	hsa-mir-1178	precursor
rs181368210	SNP	0.0018	13	41302007	41302007	hsa-mir-320d-1	precursor
rs188415420	SNP	0.0005	13	41384931	41384931	hsa-mir-621	precursor
rs138641855	SNP	0.0014	13	41384940	41384940	hsa-mir-621	precursor
rs181274589	SNP	0.0014	13	41384997	41384997	hsa-mir-621	precursor
rs72631826	SNP	0.0100	13	50623143	50623143	hsa-mir-16-1	precursor
rs111371406	SNP	0.0032	13	90883517	90883517	hsa-mir-622	precursor
rs185831554	SNP	0.0005	13	92003356	92003356	hsa-mir-20a	precursor
chr13_92003469	INDEL	0.0545	13	92003469	92003470	hsa-mir-19b-1	mature
rs9589207	SNP	0.0211	13	92003589	92003589	hsa-mir-92a-1	mature
rs192917405	SNP	0.0005	13	100008451	100008451	hsa-mir-623	precursor
rs73251987	SNP	0.0100	14	31483883	31483883	hsa-mir-624	mature
rs144194694	SNP	0.0037	14	64561812	64561812	hsa-mir-548h	mature
rs28909969	INDEL	0.0300	14	77732622	77732623	hsa-mir-1260	precursor
chr14_100575996	INDEL	0.0900	14	100575996	100575998	hsa-mir-342	precursor
rs72631832	SNP	0.0114	14	100774203	100774203	hsa-mir-345	precursor
rs76090066	SNP	0.0014	14	101347355	101347355	hsa-mir-431	precursor
rs138412993	SNP	0.0027	14	101347448	101347448	hsa-mir-431	precursor
rs189881142	SNP	0.0005	14	101351048	101351048	hsa-mir-136	precursor
rs147448304	SNP	0.0005	14	101351088	101351088	hsa-mir-136	seed
rs115827677	SNP	0.0005	14	101488430	101488430	hsa-mir-379	precursor
rs182581788	SNP	0.0005	14	101488431	101488431	hsa-mir-379	precursor
rs11906529	SNP	0.0200	14	101489703	101489703	hsa-mir-411	precursor
rs150717115	SNP	0.0014	14	101489745	101489745	hsa-mir-411	precursor
rs141611518	SNP	0.0005	14	101491923	101491923	hsa-mir-1197	precursor
rs185946570	SNP	0.0005	14	101491965	101491965	hsa-mir-1197	mature
rs149411304	SNP	0.0005	14	101500098	101500098	hsa-mir-495	precursor
rs144777170	SNP	0.0018	14	101500133	101500133	hsa-mir-495	precursor
chr14_101506581	INDEL	0.0400	14	101506581	101506582	hsa-mir-654	mature
rs12894467	SNP	0.4300	14	101507727	101507727	hsa-mir-300	precursor
rs11844707	SNP	0.0500	14	101510613	101510613	hsa-mir-1185-2	precursor
rs145135208	SNP	0.0200	14	101512836	101512836	hsa-mir-487b	precursor
rs143972054	SNP	0.0009	14	101518827	101518827	hsa-mir-487a	precursor
rs192719529	SNP	0.0005	14	101520657	101520657	hsa-mir-382	seed
rs141238795	SNP	0.0005	14	101521608	101521608	hsa-mir-668	precursor
rs56103835	SNP	0.3040	14	101522556	101522556	hsa-mir-453	precursor
rs181310917	SNP	0.0005	14	101522578	101522578	hsa-mir-323b	mature
rs117380662	SNP	0.0041	14	101522582	101522582	hsa-mir-323b	mature
rs75330474	SNP	0.0300	14	101522589	101522589	hsa-mir-323b	mature
chr14_101522601	INDEL	0.0500	14	101522601	101522601	hsa-mir-453	precursor
rs41286570	SNP	0.0009	14	101526127	101526127	hsa-mir-154	mature
rs142661498	SNP	0.0009	14	101526951	101526951	hsa-mir-496	precursor
rs189230072	SNP	0.0005	14	101526957	101526957	hsa-mir-496	precursor
rs189165474	SNP	0.0005	14	101528401	101528401	hsa-mir-377	mature
rs138633099	SNP	0.0009	14	101530873	101530873	hsa-mir-541	precursor
rs115831106	SNP	0.0027	14	101531806	101531806	hsa-mir-412	precursor
rs61992671	SNP	0.2349	14	101531854	101531854	hsa-mir-412	mature
rs139967426	SNP	0.0023	14	101531857	101531857	hsa-mir-412	mature
rs58834075	SNP	0.0737	14	101533093	101533093	hsa-mir-656	precursor
rs185468172	SNP	0.0005	14	101533123	101533123	hsa-mir-656	mature
rs190189102	SNP	0.0005	14	101533133	101533133	hsa-mir-656	precursor
rs28599926	SNP	0.1946	15	22513271	22513271	hsa-mir-1268	seed
rs140017415	SNP	0.0023	15	31357238	31357238	hsa-mir-211	precursor
rs187960998	SNP	0.0005	15	31357301	31357301	hsa-mir-211	mature
rs141424579	SNP	0.0005	15	31357325	31357325	hsa-mir-211	precursor
rs2620381	SNP	0.0800	15	42491848	42491848	hsa-mir-627	seed
chr15_53230584	INDEL	0.0100	15	53230584	53230587	hsa-mir-1300	precursor
rs146591219	SNP	0.0005	15	63116226	63116226	hsa-mir-190	precursor
rs114965408	SNP	0.0014	15	65054668	65054668	hsa-mir-1272	precursor
rs111899904	SNP	0.0100	15	70371772	70371772	hsa-mir-629	mature

rs78212770	SNP	0.0540	15	70371777	70371777	hsa-mir-629	mature
rs139334001	INDEL	0.0746	15	72879653	72879653	hsa-mir-630	precursor
rs142273017	INDEL	0.0517	15	75645965	75645967	hsa-mir-631	precursor
rs145763978	SNP	0.0009	15	79502141	79502141	hsa-mir-184	precursor
rs41280052	SNP	0.0100	15	79502168	79502168	hsa-mir-184	precursor
rs141006148	SNP	0.0005	15	81134346	81134346	hsa-mir-549	mature
rs141312113	SNP	0.0009	15	89155064	89155064	hsa-mir-7-2	precursor
rs41276930	SNP	0.0041	15	89155073	89155073	hsa-mir-7-2	precursor
rs147579757	SNP	0.0014	15	89155121	89155121	hsa-mir-7-2	precursor
rs186890720	SNP	0.0005	15	89155162	89155162	hsa-mir-7-2	precursor
rs137952851	SNP	0.0100	16	820192	820192	hsa-mir-662	precursor
rs74656628	SNP	0.1122	16	820215	820215	hsa-mir-662	precursor
rs9745376	SNP	0.0500	16	820249	820249	hsa-mir-662	seed
chr16_2140240	SNP	0.0014	16	2140240	2140240	hsa-mir-1225	precursor
chr16_2140262	INDEL	0.0200	16	2140262	2140262	hsa-mir-1225	precursor
chr16_2140267	SNP	0.0005	16	2140267	2140267	hsa-mir-1225	mature
rs149527765	SNP	0.0005	16	2321809	2321809	hsa-mir-940	seed
rs138584205	SNP	0.0027	16	11400324	11400324	hsa-mir-548h-2	precursor
rs149601213	SNP	0.0005	16	11400356	11400356	hsa-mir-548h	mature
rs139365823	SNP	0.0009	16	56892431	56892431	hsa-mir-138-2	precursor
rs188892061	SNP	0.0014	16	67236292	67236292	hsa-mir-328	precursor
rs191393746	SNP	0.0133	16	69599735	69599735	hsa-mir-1538	precursor
rs57629257	SNP	0.1909	16	70064261	70064261	hsa-mir-1972	precursor
rs141946713	SNP	0.0005	16	70064324	70064324	hsa-mir-1972	precursor
rs183226620	SNP	0.0009	16	85775275	85775275	hsa-mir-1910	mature
rs7217038	SNP	0.0100	17	2651377	2651377	hsa-mir-1253	precursor
rs139010443	SNP	0.0009	17	2651398	2651398	hsa-mir-1253	precursor
rs77498226	SNP	0.0041	17	2651405	2651405	hsa-mir-1253	precursor
rs140470503	SNP	0.0046	17	13446846	13446846	hsa-mir-548h-3	precursor
rs189427199	SNP	0.0005	17	13446849	13446849	hsa-mir-548h-3	precursor
rs9913045	SNP	0.4103	17	13446924	13446924	hsa-mir-548h	mature
rs6505162	SNP	0.4900	17	28444183	28444183	hsa-mir-423	precursor
chr17_46114544	INDEL	0.0200	17	46114544	46114545	hsa-mir-152	mature
rs117091718	SNP	0.0100	17	46233806	46233806	hsa-mir-1203	precursor
rs186449583	SNP	0.0005	17	46709859	46709859	hsa-mir-196a-1	precursor
rs190478598	SNP	0.0009	17	46709899	46709899	hsa-mir-196a	mature
rs17759989	SNP	0.0243	17	61021611	61021611	hsa-mir-633	precursor
rs181392999	SNP	0.0005	17	61021625	61021625	hsa-mir-633	precursor
chr17_65467630	INDEL	0.0234	17	65467630	65467632	hsa-mir-548d-3p	mature
rs149172942	SNP	0.0005	17	65467665	65467665	hsa-mir-548d-5p	mature
rs77279010	SNP	0.0243	17	66420592	66420592	hsa-mir-635	precursor
rs192867879	SNP	0.0005	17	66420605	66420605	hsa-mir-635	precursor
rs146763174	SNP	0.0023	17	79099125	79099125	hsa-mir-657	precursor
rs148953276	INDEL	0.0600	17	79107017	79107018	hsa-mir-1250	precursor
rs182673735	SNP	0.0005	18	19405676	19405676	hsa-mir-133a	mature
rs114964240	SNP	0.0037	18	33484783	33484783	hsa-mir-187	precursor
rs41274312	SNP	0.0100	18	33484792	33484792	hsa-mir-187	precursor
rs41292412	SNP	0.0046	18	56118358	56118358	hsa-mir-122	seed
chr19_1816176	SNP	0.0032	19	1816176	1816176	hsa-mir-1909	mature
rs139405773	SNP	0.0009	19	2234080	2234080	hsa-mir-1227	mature
rs74807305	SNP	0.0005	19	2234086	2234086	hsa-mir-1227	precursor
rs190788838	SNP	0.0005	19	2234093	2234093	hsa-mir-1227	precursor
chr19_2234134	SNP	0.0014	19	2234134	2234134	hsa-mir-1227	precursor
rs149472696	SNP	0.0100	19	3961431	3961431	hsa-mir-637	mature
rs146575140	SNP	0.0027	19	4770747	4770747	hsa-mir-7-3	precursor
rs143415955	SNP	0.0005	19	6496006	6496006	hsa-mir-220b	precursor
chr19_10514157	SNP	0.0005	19	10514157	10514157	hsa-mir-1181	precursor
chr19_10662835	SNP	0.0014	19	10662835	10662835	hsa-mir-1238	precursor
chr19_10662844	SNP	0.0005	19	10662844	10662844	hsa-mir-1238	precursor
chr19_10662866	SNP	0.0005	19	10662866	10662866	hsa-mir-1238	seed
rs183664554	SNP	0.0100	19	10928119	10928119	hsa-mir-199b	seed
rs895819	SNP	0.3600	19	13947292	13947292	hsa-mir-27a	precursor
rs11671784	SNP	0.0101	19	13947296	13947296	hsa-mir-27a	precursor
rs114121047	SNP	0.0200	19	14640378	14640378	hsa-mir-639	precursor
rs142882191	SNP	0.0005	19	14640449	14640449	hsa-mir-639	precursor
rs147213560	SNP	0.0009	19	40788477	40788477	hsa-mir-641	precursor

rs78902025	SNP	0.0005	19	46178206	46178206	hsa-mir-642	seed
rs185689285	SNP	0.0009	19	46522255	46522255	hsa-mir-769	precursor
rs190748158	SNP	0.0018	19	46522298	46522298	hsa-mir-769	precursor
rs190452290	SNP	0.0009	19	52195904	52195904	hsa-mir-99b	precursor
rs143525573	SNP	0.0005	19	52196574	52196574	hsa-mir-125a	mature
rs181061154	SNP	0.0009	19	54170006	54170006	hsa-mir-512-2	precursor
chr19_54175283	INDEL	0.0114	19	54175283	54175284	hsa-mir-1323	precursor
rs186827259	SNP	0.0005	19	54175294	54175294	hsa-mir-1323	precursor
rs189977895	SNP	0.0005	19	54177532	54177532	hsa-mir-498	precursor
rs188152320	SNP	0.0009	19	54182261	54182261	hsa-mir-515-2	precursor
rs184037684	SNP	0.0005	19	54185457	54185457	hsa-mir-52of	precursor
rs75598818	SNP	0.0527	19	54185492	54185492	hsa-mir-52of	precursor
rs57111412	SNP	0.2300	19	54191743	54191743	hsa-mir-1283-1	precursor
rs142752420	SNP	0.0009	19	54191790	54191790	hsa-mir-1283-1	precursor
rs190453265	SNP	0.0005	19	54200843	54200843	hsa-mir-525-3p	seed
rs191624794	SNP	0.0014	19	54201692	54201692	hsa-mir-523	seed
rs150048439	SNP	0.0100	19	54204489	54204489	hsa-mir-520b	precursor
rs147743520	SNP	0.0009	19	54204496	54204496	hsa-mir-520b	precursor
rs151188894	SNP	0.0023	19	54210736	54210736	hsa-mir-518d-5p	mature
chr19_54210777	INDEL	0.0100	19	54210777	54210777	hsa-mir-520c-3p	mature
rs188936188	SNP	0.0005	19	54215584	54215584	hsa-mir-517b	mature
rs116796400	SNP	0.0027	19	54216670	54216670	hsa-mir-519d	mature
rs13382089	SNP	0.0100	19	54219854	54219854	hsa-mir-521-2	precursor
rs182126774	SNP	0.0005	19	54225437	54225437	hsa-mir-520g	precursor
rs186377499	SNP	0.0005	19	54225463	54225463	hsa-mir-520g	precursor
rs112328520	SNP	0.0444	19	54225501	54225501	hsa-mir-520g	precursor
chr19_54228741	INDEL	0.1200	19	54228741	54228741	hsa-mir-516b-2	precursor
chr19_54228770	INDEL	0.1236	19	54228770	54228772	hsa-mir-516b-2	precursor
rs141891128	INDEL	0.0400	19	54228773	54228775	hsa-mir-516b-2	precursor
rs141873214	SNP	0.0046	19	54234260	54234260	hsa-mir-518a-1	precursor
rs190044154	SNP	0.0009	19	54234265	54234265	hsa-mir-518a-1	precursor
chr19_54234270	INDEL	0.0200	19	54234270	54234270	hsa-mir-518a-1	precursor
rs116220629	SNP	0.0200	19	54238182	54238182	hsa-mir-518d	precursor
rs73602910	SNP	0.0027	19	54238189	54238189	hsa-mir-518d	seed
rs151129856	SNP	0.0005	19	54238203	54238203	hsa-mir-518d	mature
rs74704964	SNP	0.0200	19	54238208	54238208	hsa-mir-518d	precursor
rs183522542	SNP	0.0009	19	54240142	54240142	hsa-mir-516b-1	precursor
rs78861479	SNP	0.0229	19	54240174	54240174	hsa-mir-516a	mature
rs151073675	SNP	0.0133	19	54240184	54240184	hsa-mir-516b-1	precursor
rs188224089	SNP	0.0009	19	54242630	54242630	hsa-mir-518a-2	precursor
rs182664281	SNP	0.0005	19	54244647	54244647	hsa-mir-517c	precursor
rs148716001	SNP	0.0101	19	54245768	54245768	hsa-mir-520h	precursor
rs56013413	SNP	0.0820	19	54245788	54245788	hsa-mir-520h	precursor
rs111745142	INDEL	0.0234	19	54245839	54245839	hsa-mir-520h	mature
rs146976572	SNP	0.0005	19	54254494	54254494	hsa-mir-519a	mature
rs191444009	SNP	0.0005	19	54255679	54255679	hsa-mir-519a	mature
rs186554893	SNP	0.0005	19	54257304	54257304	hsa-mir-527	mature
chr19_54260030	INDEL	0.0403	19	54260030	54260032	hsa-mir-516a	mature
rs71363366	SNP	0.0119	19	54261549	54261549	hsa-mir-1283-2	precursor
rs115975528	SNP	0.0100	19	54264394	54264394	hsa-mir-516a-2	precursor
rs191772135	SNP	0.0018	19	54264468	54264468	hsa-mir-516a-2	precursor
rs137963341	SNP	0.0005	19	54265617	54265617	hsa-mir-519a-2	precursor
rs142071806	SNP	0.0014	19	54265626	54265626	hsa-mir-519a-2	precursor
rs140633075	INDEL	0.0300	19	54291989	54291993	hsa-mir-373	precursor
rs182623921	SNP	0.0005	19	54292016	54292016	hsa-mir-373	mature
rs114607347	SNP	0.0100	19	58024394	58024394	hsa-mir-1274b	precursor
chr20_2633462	SNP	0.0023	20	2633462	2633462	hsa-mir-1292	precursor
rs73576045	SNP	0.0100	20	2633466	2633466	hsa-mir-1292	precursor
rs183843457	SNP	0.0100	20	26188906	26188906	hsa-mir-663	precursor
rs181082862	SNP	0.0005	20	33054160	33054160	hsa-mir-644	precursor
rs186999403	SNP	0.0005	20	33054163	33054163	hsa-mir-644	precursor
rs191742048	SNP	0.0014	20	33054223	33054223	hsa-mir-644	precursor
rs140486571	SNP	0.0023	20	33578202	33578202	hsa-mir-499	precursor
rs3746444	SNP	0.1809	20	33578251	33578251	hsa-mir-499	seed
rs150018420	SNP	0.0014	20	33578255	33578255	hsa-mir-499	seed
rs7267163	SNP	0.0440	20	33578276	33578276	hsa-mir-499	precursor

rs139884309	SNP	0.0018	20	34041842	34041842	hsa-mir-1289-1	precursor
chr20_34041882	INDEL	0.0200	20	34041882	34041882	hsa-mir-1289-1	precursor
rs116993790	SNP	0.0032	20	47896907	47896907	hsa-mir-1259	precursor
rs117258475	SNP	0.0046	20	57392686	57392686	hsa-mir-296	mature
rs6513496	SNP	0.2400	20	58883534	58883534	hsa-mir-646	precursor
rs6513497	SNP	0.1900	20	58883605	58883605	hsa-mir-646	mature
rs140605296	SNP	0.0009	20	60528670	60528670	hsa-mir-1257	precursor
rs6122014	SNP	0.0100	20	61151515	61151515	hsa-mir-1-1	precursor
rs2427556	SNP	0.4048	20	62550824	62550824	hsa-mir-941-1	precursor
rs73147065	SNP	0.2335	20	62574006	62574006	hsa-mir-647	precursor
rs191451021	SNP	0.0041	20	62574016	62574016	hsa-mir-647	precursor
rs140021681	SNP	0.0005	21	26946325	26946325	hsa-mir-155	precursor
rs184815008	SNP	0.0005	21	37093089	37093089	hsa-mir-802	precursor
rs183799425	SNP	0.0005	22	21388510	21388510	hsa-mir-649	precursor
rs72631822	SNP	0.0037	22	22007634	22007634	hsa-mir-130b	precursor
rs140403670	SNP	0.0005	22	22007661	22007661	hsa-mir-130b	mature
rs5996397	SNP	0.1500	22	23165340	23165340	hsa-mir-650	precursor
rs4822739	SNP	0.1300	22	26951185	26951185	hsa-mir-548j	precursor
rs12161068	SNP	0.0300	22	26951215	26951215	hsa-mir-548j	precursor
chr22_38240283	SNP	0.0005	22	38240283	38240283	hsa-mir-658	precursor
rs182859563	SNP	0.0100	22	38240289	38240289	hsa-mir-658	precursor
rs141002682	SNP	0.0300	22	38240368	38240368	hsa-mir-658	precursor
rs77809319	SNP	0.0009	22	42296995	42296995	hsa-mir-33a	seed
rs144909301	SNP	0.0078	X	8095011	8095011	hsa-mir-651	precursor
rs7051072	SNP	0.0408	X	22080290	22080290	hsa-mir-1308	precursor
rs60180387	SNP	0.0234	X	32659592	32659592	hsa-mir-548f-5	precursor
rs187612279	SNP	0.0005	X	45606472	45606472	hsa-mir-222	precursor
rs191727254	SNP	0.0005	X	45606504	45606504	hsa-mir-222	precursor
rs456615	SNP	0.0485	X	49767832	49767832	hsa-mir-532	precursor
rs456617	SNP	0.0005	X	49767835	49767835	hsa-mir-532	precursor
rs190537859	SNP	0.0005	X	49767838	49767838	hsa-mir-532	precursor
rs191840972	SNP	0.0005	X	49768168	49768168	hsa-mir-188	seed
rs191321849	SNP	0.0032	X	49773087	49773087	hsa-mir-500	precursor
rs149912461	SNP	0.0087	X	49774381	49774381	hsa-mir-501	seed
rs112489955	SNP	0.0078	X	49774389	49774389	hsa-mir-501	mature
rs180785970	SNP	0.0005	X	49777907	49777907	hsa-mir-660	precursor
rs145760241	SNP	0.0082	X	63005918	63005918	hsa-mir-1468	precursor
rs184629807	SNP	0.0014	X	76225837	76225837	hsa-mir-325	precursor
rs72632467	SNP	0.0884	X	83480764	83480764	hsa-mir-548i-4	precursor
rs184631864	SNP	0.0041	X	109298558	109298558	hsa-mir-652	precursor
rs144963985	SNP	0.0009	X	113886051	113886051	hsa-mir-1912	precursor
chrX_113886091	INDEL	0.0046	X	113886091	113886091	hsa-mir-1912	precursor
rs188834116	SNP	0.0018	X	117520360	117520360	hsa-mir-1277	precursor
rs72631819	SNP	0.0101	X	122695978	122695978	hsa-mir-220a	precursor
rs72631817	SNP	0.0330	X	122696014	122696014	hsa-mir-220a	mature
rs182728148	SNP	0.0005	X	122696027	122696027	hsa-mir-220a	seed
chrX_122696050	INDEL	0.0037	X	122696050	122696050	hsa-mir-220a	precursor
rs186327902	SNP	0.0046	X	122696055	122696055	hsa-mir-220a	precursor
rs193073651	SNP	0.0005	X	133303758	133303758	hsa-mir-19b-2	mature
rs181664033	SNP	0.0014	X	133674399	133674399	hsa-mir-450a-1	precursor
rs185256782	SNP	0.0005	X	133674576	133674576	hsa-mir-450a-2	precursor
rs141784874	SNP	0.0023	X	133674612	133674612	hsa-mir-450a	seed
rs73558572	SNP	0.0279	X	135633045	135633045	hsa-mir-934	precursor
rs143213653	SNP	0.0005	X	139006339	139006339	hsa-mir-505	seed
rs138166791	SNP	0.0046	X	145075804	145075804	hsa-mir-890	precursor
rs5965660	SNP	0.1113	X	145076302	145076302	hsa-mir-888	precursor
rs143634721	SNP	0.0147	X	145076355	145076355	hsa-mir-888	mature
rs183818844	SNP	0.0005	X	145078244	145078244	hsa-mir-892a	precursor
rs146806052	SNP	0.0105	X	145078733	145078733	hsa-mir-892b	mature
rs143246735	SNP	0.0032	X	145082615	145082615	hsa-mir-891b	precursor
rs188075884	SNP	0.0009	X	145109328	145109328	hsa-mir-891a	precursor
rs5965990	SNP	0.0142	X	145109356	145109356	hsa-mir-891a	precursor
rs184216167	SNP	0.0005	X	146271266	146271266	hsa-mir-513c	precursor
rs145416750	SNP	0.0060	X	146271303	146271303	hsa-mir-513c	precursor
rs138509628	SNP	0.0032	X	146280644	146280644	hsa-mir-513b	precursor
rs193181398	SNP	0.0009	X	146307414	146307414	hsa-mir-513a-2	precursor

rs190684797	SNP	0.0005	X	146312560	146312560	hsa-mir-507	precursor
rs36092315	INDEL	0.1012	X	146340338	146340339	hsa-mir-509	mature
chrX_146342085	INDEL	0.0105	X	146342085	146342085	hsa-mir-509	seed
rs148964961	SNP	0.0037	X	146360813	146360813	hsa-mir-514-1	precursor
rs183412647	SNP	0.0005	X	146360826	146360826	hsa-mir-514-1	precursor
rs188519172	SNP	0.0027	X	151127092	151127092	hsa-mir-224	precursor
chrX_151128172	INDEL	0.0023	X	151128172	151128172	hsa-mir-452	precursor

In case a variant does not have an official Id, it was named with “chr_position”. For the location of the variants in a miRNA locus, “seed” means the variant is located in seed region (position 2-8) of a mature miRNA; “Mature” means this variant is located in mature miRNA outside seed region; “Hairpin” means this variant is located in the miRNA precursor but outside the mature miRNA, and “miRNA locus” means the indel spans the entire miRNA locus.

Table S3 Experimentally verified miRNA target genes that are significantly negatively correlated with the expression levels of miRNAs in the 90 European-American males in Wang et al. (2009)

target	miRNA	Spearman Correlation Coefficient	Pvalue	Qvalue
ENSG00000103021	hsa-miR-92a	-0.27573	8.53E-03	4.07E-02
ENSG00000133858	hsa-miR-92a	-0.39923	9.71E-05	1.32E-03
ENSG00000128590	hsa-miR-92a	-0.29784	4.36E-03	2.45E-02
ENSG00000090615	hsa-miR-92a	-0.42647	2.77E-05	4.97E-04
ENSG00000175265	hsa-miR-92a	-0.31359	2.61E-03	1.66E-02
ENSG00000112339	hsa-miR-92a	-0.47384	2.39E-06	7.24E-05
ENSG00000159110	hsa-miR-92a	-0.32379	1.85E-03	1.28E-02
ENSG00000159110	hsa-miR-92a	-0.4041	7.82E-05	1.11E-03
ENSG00000138448	hsa-miR-92a	-0.36652	3.81E-04	3.79E-03
ENSG00000138688	hsa-miR-92a	-0.42188	3.45E-05	5.90E-04
ENSG00000197535	hsa-miR-92a	-0.28526	6.43E-03	3.29E-02
ENSG00000157212	hsa-miR-92a	-0.3076	3.19E-03	1.93E-02
ENSG00000108187	hsa-miR-92a	-0.42871	2.49E-05	4.57E-04
ENSG00000112941	hsa-miR-92a	-0.307	3.25E-03	1.96E-02
ENSG00000125503	hsa-miR-92a	-0.32697	1.66E-03	1.17E-02
ENSG00000132424	hsa-miR-92a	-0.40571	7.27E-05	1.05E-03
ENSG00000159082	hsa-miR-92a	-0.40468	7.62E-05	1.09E-03
ENSG00000164305	hsa-let-7a	-0.56736	5.52E-09	5.58E-07
ENSG00000164045	hsa-let-7a	-0.30569	3.39E-03	2.02E-02
ENSG00000105810	hsa-let-7a	-0.33198	1.39E-03	1.03E-02
ENSG00000174842	hsa-let-7a	-0.59424	6.64E-10	9.78E-08
ENSG00000056345	hsa-let-7a	-0.26624	1.12E-02	4.99E-02
ENSG00000057657	hsa-let-7a	-0.40282	8.28E-05	1.16E-03
ENSG00000057657	hsa-let-7a	-0.3827	1.97E-04	2.28E-03
ENSG00000163104	hsa-let-7a	-0.51447	2.14E-07	1.06E-05
ENSG00000166575	hsa-let-7a	-0.36206	4.54E-04	4.34E-03
ENSG00000147854	hsa-let-7a	-0.30023	4.04E-03	2.31E-02
ENSG00000174842	hsa-let-7c	-0.45741	5.83E-06	1.46E-04
ENSG00000163104	hsa-let-7c	-0.44834	9.36E-06	2.13E-04
ENSG00000174842	hsa-let-7e	-0.55191	1.72E-08	1.40E-06
ENSG00000163104	hsa-let-7e	-0.44726	9.89E-06	2.22E-04
ENSG00000174842	hsa-let-7f	-0.47825	1.87E-06	5.95E-05
ENSG00000163104	hsa-let-7f	-0.34425	8.93E-04	7.30E-03
ENSG00000033050	hsa-miR-16	-0.26755	1.08E-02	4.86E-02
ENSG00000196177	hsa-miR-16	-0.29216	5.20E-03	2.80E-02
ENSG00000164305	hsa-miR-16	-0.27732	8.14E-03	3.93E-02
ENSG00000105173	hsa-miR-16	-0.36427	4.16E-04	4.06E-03
ENSG00000106993	hsa-miR-16	-0.36691	3.75E-04	3.75E-03
ENSG00000135164	hsa-miR-16	-0.29135	5.34E-03	2.86E-02
ENSG00000130119	hsa-miR-16	-0.28427	6.62E-03	3.36E-02
ENSG00000170445	hsa-miR-16	-0.35419	6.15E-04	5.48E-03
ENSG00000134265	hsa-miR-16	-0.38114	2.10E-04	2.40E-03
ENSG00000134250	hsa-miR-16	-0.28945	5.66E-03	2.98E-02
ENSG00000213240	hsa-miR-16	-0.28945	5.66E-03	2.98E-02
ENSG00000113643	hsa-miR-16	-0.28859	5.81E-03	3.04E-02

ENSG00000138018	hsa-miR-16	-0.33976	1.05E-03	8.28E-03
ENSG00000159140	hsa-miR-16	-0.38796	1.58E-04	1.92E-03
ENSG00000182934	hsa-miR-16	-0.35198	6.69E-04	5.84E-03
ENSG00000144867	hsa-miR-16	-0.38417	1.85E-04	2.17E-03
ENSG00000110344	hsa-miR-16	-0.31117	2.83E-03	1.77E-02
ENSG00000173545	hsa-miR-16	-0.2811	7.28E-03	3.61E-02
ENSG00000138071	hsa-miR-181a	-0.34189	9.74E-04	7.80E-03
ENSG00000176697	hsa-miR-181a	-0.34491	8.71E-04	7.16E-03
ENSG00000179218	hsa-miR-181a	-0.38916	1.50E-04	1.84E-03
ENSG00000125107	hsa-miR-181a	-0.4564	6.15E-06	1.53E-04
ENSG00000215301	hsa-miR-181a	-0.40551	7.34E-05	1.06E-03
ENSG00000138246	hsa-miR-181a	-0.51049	2.74E-07	1.30E-05
ENSG00000151577	hsa-miR-181a	-0.38251	1.99E-04	2.29E-03
ENSG00000132475	hsa-miR-181a	-0.37297	2.94E-04	3.10E-03
ENSG00000119862	hsa-miR-181a	-0.33815	1.12E-03	8.66E-03
ENSG00000177425	hsa-miR-181a	-0.29438	4.86E-03	2.66E-02
ENSG00000114166	hsa-miR-181a	-0.39778	1.03E-04	1.38E-03
ENSG00000181690	hsa-miR-181a	-0.30314	3.68E-03	2.16E-02
ENSG00000181690	hsa-miR-181a	-0.42141	3.53E-05	6.00E-04
ENSG00000132424	hsa-miR-181a	-0.32456	1.80E-03	1.25E-02
ENSG00000064313	hsa-miR-181a	-0.49215	8.36E-07	3.14E-05
ENSG00000181896	hsa-miR-181a	-0.34545	8.54E-04	7.05E-03
ENSG00000114166	hsa-miR-181b	-0.35444	6.09E-04	5.44E-03
ENSG00000181690	hsa-miR-181b	-0.28455	6.56E-03	3.34E-02
ENSG00000181690	hsa-miR-181b	-0.3508	6.99E-04	6.05E-03
ENSG00000215301	hsa-miR-181c	-0.38872	1.53E-04	1.87E-03
ENSG00000132475	hsa-miR-181c	-0.29193	5.24E-03	2.82E-02
ENSG00000087095	hsa-miR-181c	-0.3053	3.43E-03	2.04E-02
ENSG00000132424	hsa-miR-181c	-0.35376	6.25E-04	5.55E-03
ENSG00000181896	hsa-miR-181c	-0.33087	1.45E-03	1.06E-02
ENSG00000105810	hsa-miR-195	-0.43463	1.87E-05	3.65E-04
ENSG00000174574	hsa-miR-27b	-0.32245	1.94E-03	1.32E-02
ENSG00000109670	hsa-miR-27b	-0.49702	6.26E-07	2.50E-05
ENSG00000109670	hsa-miR-27b	-0.36122	4.69E-04	4.45E-03
ENSG00000109670	hsa-miR-27b	-0.27243	9.39E-03	4.37E-02
ENSG00000143815	hsa-miR-27b	-0.47674	2.03E-06	6.37E-05
ENSG00000066933	hsa-miR-27b	-0.29688	4.49E-03	2.51E-02
ENSG00000115137	hsa-miR-27b	-0.49546	6.87E-07	2.69E-05
ENSG00000048405	hsa-miR-27b	-0.44304	1.23E-05	2.63E-04
ENSG00000159322	hsa-miR-30a	-0.46265	4.41E-06	1.17E-04
ENSG00000174437	hsa-miR-30a	-0.33344	1.32E-03	9.86E-03
ENSG00000145734	hsa-miR-30a	-0.4213	3.55E-05	6.03E-04
ENSG00000126581	hsa-miR-30a	-0.36114	4.71E-04	4.46E-03
ENSG00000124541	hsa-miR-30a	-0.4919	8.49E-07	3.18E-05
ENSG00000153922	hsa-miR-30a	-0.2774	8.12E-03	3.92E-02
ENSG00000143924	hsa-miR-30a	-0.34436	8.89E-04	7.27E-03
ENSG00000141429	hsa-miR-30a	-0.2969	4.49E-03	2.51E-02
ENSG00000111727	hsa-miR-30a	-0.54883	2.14E-08	1.67E-06
ENSG00000099783	hsa-miR-30a	-0.29272	5.11E-03	2.77E-02
ENSG00000006652	hsa-miR-30a	-0.41075	5.79E-05	8.83E-04

ENSG00000140941	hsa-miR-30a	-0.42267	3.32E-05	5.73E-04
ENSG00000168906	hsa-miR-30a	-0.51866	1.63E-07	8.57E-06
ENSG00000108256	hsa-miR-30a	-0.35196	6.69E-04	5.85E-03
ENSG00000163939	hsa-miR-30a	-0.4359	1.75E-05	3.47E-04
ENSG00000131779	hsa-miR-30a	-0.31435	2.55E-03	1.63E-02
ENSG0000013375	hsa-miR-30a	-0.31812	2.25E-03	1.48E-02
ENSG00000187024	hsa-miR-30a	-0.29117	5.36E-03	2.87E-02
ENSG00000119318	hsa-miR-30a	-0.37726	2.47E-04	2.71E-03
ENSG00000166562	hsa-miR-30a	-0.30535	3.43E-03	2.04E-02
ENSG00000111371	hsa-miR-30a	-0.28417	6.64E-03	3.37E-02
ENSG00000134294	hsa-miR-30a	-0.30076	3.97E-03	2.28E-02
ENSG00000033867	hsa-miR-30a	-0.29389	4.93E-03	2.69E-02
ENSG00000103064	hsa-miR-30a	-0.5162	1.91E-07	9.73E-06
ENSG00000065526	hsa-miR-30a	-0.32581	1.73E-03	1.21E-02
ENSG00000115808	hsa-miR-30a	-0.27027	9.99E-03	4.58E-02
ENSG00000008952	hsa-miR-30a	-0.34254	9.51E-04	7.66E-03
ENSG00000143183	hsa-miR-30a	-0.28105	7.29E-03	3.62E-02
ENSG00000086598	hsa-miR-30a	-0.37859	2.34E-04	2.60E-03
ENSG00000166557	hsa-miR-30a	-0.28925	5.69E-03	3.00E-02
ENSG00000166471	hsa-miR-30a	-0.41628	4.49E-05	7.24E-04
ENSG00000103978	hsa-miR-30a	-0.5022	4.58E-07	1.95E-05
ENSG00000151239	hsa-miR-30a	-0.28494	6.49E-03	3.31E-02
ENSG00000117143	hsa-miR-30a	-0.42024	3.73E-05	6.27E-04
ENSG00000028203	hsa-miR-30a	-0.42498	2.98E-05	5.26E-04
ENSG00000198862	hsa-miR-30a	-0.49307	7.92E-07	3.01E-05
ENSG00000144827	hsa-miR-30b	-0.30044	4.01E-03	2.30E-02
ENSG00000145734	hsa-miR-30b	-0.33664	1.18E-03	9.03E-03
ENSG00000143924	hsa-miR-30b	-0.41499	4.77E-05	7.58E-04
ENSG00000111727	hsa-miR-30b	-0.44347	1.20E-05	2.58E-04
ENSG00000013375	hsa-miR-30b	-0.26962	1.02E-02	4.65E-02
ENSG00000065526	hsa-miR-30b	-0.29022	5.52E-03	2.93E-02
ENSG00000145734	hsa-miR-30c	-0.52984	7.87E-08	4.77E-06
ENSG00000144354	hsa-miR-30c	-0.3352	1.24E-03	9.40E-03
ENSG00000008300	hsa-miR-30c	-0.27025	9.99E-03	4.58E-02
ENSG00000113552	hsa-miR-30c	-0.2799	7.54E-03	3.71E-02
ENSG00000111727	hsa-miR-30c	-0.46997	2.96E-06	8.58E-05
ENSG00000013375	hsa-miR-30c	-0.4103	5.91E-05	8.97E-04
ENSG00000065526	hsa-miR-30c	-0.45018	8.51E-06	1.97E-04
ENSG00000144827	hsa-miR-30d	-0.28233	7.02E-03	3.51E-02
ENSG00000145734	hsa-miR-30d	-0.39009	1.44E-04	1.79E-03
ENSG00000144354	hsa-miR-30d	-0.33077	1.45E-03	1.06E-02
ENSG00000143924	hsa-miR-30d	-0.30113	3.92E-03	2.26E-02
ENSG00000111727	hsa-miR-30d	-0.58055	2.00E-09	2.44E-07
ENSG00000013375	hsa-miR-30d	-0.42291	3.29E-05	5.68E-04
ENSG00000065526	hsa-miR-30d	-0.3646	4.11E-04	4.02E-03

Table S4 miRNAs that have High-Confidence target genes with CV significantly different from the remaining RefSeq genes in dataset I and II.

Dataset	miRNA	Background		Targets		P	Q
		Genes	CV	Genes	CV		
I	miR-25	11327	2.27	388	2.50	0.000055	0.0036
I	miR-30b	10915	2.27	800	2.43	0.000297	0.0100
I	miR-30c	10915	2.27	800	2.43	0.000297	0.0100
I	miR-30d	10913	2.27	802	2.42	0.000309	0.0100
I	miR-32	11243	2.27	472	2.48	0.000087	0.0045
I	miR-363	11461	2.28	254	2.59	0.000004	0.0005
I	miR-92a	11461	2.28	254	2.59	0.000004	0.0005
I	miR-92b	11462	2.28	253	2.59	0.000006	0.0005
II	hsa-let-7e	16084	3.22	866	3.32	0.003337	0.0427
II	miR-106a	16414	3.22	536	3.44	0.000102	0.0021
II	miR-106b	16030	3.21	920	3.40	0.000001	0.0001
II	miR-130a	16226	3.22	724	3.33	0.002455	0.0392
II	miR-130b	16249	3.22	701	3.36	0.001508	0.0290
II	miR-142-5p	16347	3.21	603	3.44	0.000020	0.0006
II	miR-17	16414	3.22	536	3.44	0.000102	0.0021
II	miR-20a	16031	3.21	919	3.40	0.000001	0.0001
II	miR-20b	16040	3.21	910	3.40	0.000003	0.0001
II	miR-25	16398	3.21	552	3.44	0.000030	0.0008
II	miR-32	16280	3.21	670	3.43	0.000000	0.0000
II	miR-34b*	16883	3.22	67	3.85	0.003770	0.0461
II	miR-363	16595	3.22	355	3.46	0.000016	0.0005
II	miR-372	16152	3.21	798	3.41	0.000032	0.0008
II	miR-377	16687	3.22	263	3.50	0.002655	0.0392
II	miR-532-5p	16872	3.22	78	3.74	0.002539	0.0392
II	miR-545	16670	3.22	280	3.44	0.003004	0.0404
II	miR-550*	16875	3.22	75	3.82	0.002768	0.0392
II	miR-580	16773	3.22	177	3.43	0.002707	0.0392
II	miR-92a	16595	3.22	355	3.46	0.000016	0.0005
II	miR-92b	16596	3.21	354	3.46	0.000012	0.0005
II	miR-93	16041	3.21	909	3.42	0.000002	0.0001

KS test was used in each comparison. Benjamini-Hochberg method was used to correct multiple tests.

Table S5. The SNPs in 3' UTRs that are significantly associated with host gene expression levels
(Based on genotypes in the 1000 Genomes Project, FDR cutoff 0.001).

SNP	Chr	Pos	Q_value	Probe	Gene	miRNA that targets the gene	SNP in miRNA:target pairing region	Context Score < -0.3
rs4294600	12	39947308	0.000231137	GI_21536379_S	NM_005164	hsa-miR-668	seed	YES
rs9272976	6	32611341	5.72E-16	GI_18426974_S	NM_002122	hsa-miR-659	seed	YES
rs1058007	20	7962128	0.000663339	hmm9596_S	NM_021156	hsa-miR-627	flank	YES
rs40940	7	108202894	8.22E-10	GI_32698887_S	NM_182529	hsa-miR-624*	flank	YES
rs40939	7	108202792	2.11E-09	GI_32698887_S	NM_182529	hsa-miR-618	flank	YES
rs3757138	6	26376103	1.26E-12	GI_34932495_S	NM_007047	hsa-miR-610	flank	YES
rs73033012	6	167453683	8.34E-10	GI_36287109_A	NM_007045	hsa-miR-582-5p	seed	YES
rs4632936	6	3268242	4.05E-10	GI_41147302_S	NM_001128592	hsa-miR-576-5p	flank	YES
rs3758741	11	33106616	1.62E-09	GI_4557494_S	NM_001326	hsa-miR-544	seed	YES
rs1048726	6	32611012	5.07E-16	GI_18426974_S	NM_002122	hsa-miR-516b*	seed	YES
rs1065585	16	1878597	6.12E-09	GI_13654273_S	NM_031208	hsa-miR-516b*	flank	YES
rs9272932	6	32611003	2.26E-06	GI_18426974_S	NM_002122	hsa-miR-516b*	flank	YES
rs1130165	2	3502398	4.09E-07	GI_8922761_S	NM_018269	hsa-miR-500*	flank	YES
rs56137123	19	21133129	3.89E-09	GI_4508038_S	NM_003429	hsa-miR-499-5p	flank	YES
rs9272948	6	32611107	3.28E-16	GI_18426974_S	NM_002122	hsa-miR-494	flank	YES
rs36216730	6	32611094	0.00056631	GI_18426974_S	NM_002122	hsa-miR-494	flank	YES
rs10515	19	9523724	8.10E-08	GI_37622342_A	NM_198058	hsa-miR-485-3p	seed	YES
rs1130319	2	3502055	4.09E-07	GI_8922761_S	NM_018269	hsa-miR-421	flank	YES
rs9332	5	7900712	1.96E-06	GI_4505278_A	NM_024010	hsa-miR-361-5p	seed	YES
rs26429	5	102366053	4.97E-05	GI_21070979_A	NM_001177306	hsa-miR-33b	flank	YES
rs9508	1	28564279	3.20E-09	GI_30260191_I	NM_178191	hsa-miR-330-3p	flank	YES
rs760273	17	3564068	6.01E-10	GI_4826681_S	NM_001031681	hsa-miR-326	flank	YES
rs3826496	17	3564073	6.01E-10	GI_4826681_S	NM_001031681	hsa-miR-326	flank	YES
rs2657880	12	56863770	4.35E-07	GI_37542981_S	NM_207344	hsa-miR-3157	seed	YES
rs1037495	2	39209426	0.000388435	GI_15529995_S	NM_005633	hsa-miR-302d	flank	YES
rs8605	4	89617387	0.000172479	GI_24371267_S	NM_153757	hsa-miR-26b	flank	YES
rs11654	17	15881151	2.05E-12	Hs.379903_S	NM_001042698	hsa-miR-24	flank	YES
rs6942	2	190636411	1.14E-15	GI_31377759_S	NM_016467	hsa-miR-23b	flank	YES
rs1065587	16	1878740	6.12E-09	GI_13654273_S	NM_031208	hsa-miR-23b	seed	YES
rs73021542	19	21133309	2.26E-08	GI_4508038_S	NM_003429	hsa-miR-200a*	seed	YES
rs1130127	2	3502625	4.09E-07	GI_8922761_S	NM_018269	hsa-miR-200a*	flank	YES
rs368500	17	10616910	8.65E-08	GI_42661099_S	NM_001004313	hsa-miR-199b-3p	flank	YES
rs859	15	81601322	0.00059986	GI_27262654_A	NM_004513	hsa-miR-18a*	flank	YES
rs1045284	8	124453979	2.99E-06	GI_8922280_S	NM_018024	hsa-miR-185	flank	YES
rs1065584	16	1878521	6.12E-09	GI_13654273_S	NM_031208	hsa-miR-17*	flank	YES
rs9272974	6	32611315	2.78E-16	GI_18426974_S	NM_002122	hsa-miR-129-5p	flank	YES
rs9272975	6	32611321	2.37E-05	GI_18426974_S	NM_002122	hsa-miR-129-5p	flank	YES
rs1056438	1	53679878	3.56E-05	GI_8923540_S	NM_017887	hsa-miR-129-5p	flank	YES
rs524492	6	44796596	0.000565102	GI_4507308_A	NM_181356	hsa-miR-129-5p	flank	YES
rs2279326	5	10657134	6.06E-10	Hs.26039_S	NM_001164440	hsa-miR-9*	flank	
rs11346	13	43683020	0.000935327	GI_7019452_S	NM_013238	hsa-miR-9*	flank	
rs10858893	12	89913323	7.55E-07	GI_34452724_S	NM_003774	hsa-miR-95	seed	
rs2153914	10	97631051	5.36E-08	GI_45580699_S	NM_001098175	hsa-miR-9	flank	
rs6602129	10	16555332	8.80E-07	GI_20070185_S	NM_001001484	hsa-miR-889	flank	

rs67124903	18	20877295	7.30E-07	GI_40254998_S	NM_032933	hsa-miR-769-5p	flank
rs678859	9	33461567	4.09E-06	GI_39777589_A	NM_139235	hsa-miR-769-3p	flank
rs11539046	3	40503809	1.03E-09	GI_16753224_S	NM_003973	hsa-miR-766	seed
rs71357807	19	48712219	5.78E-08	GI_7662403_S	NM_014959	hsa-miR-766	flank
rs35829872	19	21608311	0.000944522	GI_40255231_S	NM_001076678	hsa-miR-766	seed
rs188394004	6	32485448	3.90E-13	GI_26665892_S	NM_002125	hsa-miR-7	flank
rs6796	7	6502367	8.60E-06	GI_8051609_S	NM_006854	hsa-miR-7	flank
rs6680	16	72146570	1.68E-05	GI_41406095_S	NM_014003	hsa-miR-7	seed
rs1128109	17	3566209	5.91E-05	GI_4826681_S	NM_001031681	hsa-miR-675	flank
rs1128098	17	3566213	5.91E-05	GI_4826681_S	NM_001031681	hsa-miR-675	seed
rs1054169	7	12273496	1.13E-05	GI_40254892_S	NM_018374	hsa-miR-671-5p	flank
rs1042861	17	73571030	8.95E-05	GI_4758679_S	NM_001031803	hsa-miR-671-3p	seed
rs4715300	6	52271204	0.000225394	GI_19115959_S	NM_133367	hsa-miR-671-3p	seed
rs13353	2	86437898	7.67E-06	GI_22035593_A	NM_016622	hsa-miR-668	flank
rs4727833	7	116147908	5.80E-05	GI_38176291_A	NM_198212	hsa-miR-668	flank
rs35147679	1	113068577	0.000218188	GI_38201636_A	NM_138727	hsa-miR-668	flank
rs1130804	1	33789588	3.76E-09	GI_37595529_A	NM_198040	hsa-miR-665	flank
rs7107522	11	703175	0.000954012	GI_28372560_S	NM_001042463	hsa-miR-665	flank
rs214504	6	18223566	0.000567725	hmm14450_S	NM_153042	hsa-miR-663	flank
rs1980817	14	67852171	1.21E-10	GI_34147492_S	NM_004094	hsa-miR-659	flank
rs7018	20	25278261	0.000407381	GI_34577123_S	NM_002862	hsa-miR-657	flank
rs2350630	22	45736767	8.43E-14	GI_8923587_S	NM_017911	hsa-miR-647	seed
rs2298213	1	1139202	0.000436667	GI_23238193_A	NM_004195	hsa-miR-647	flank
rs284855	10	104574422	0.000441208	GI_41152103_S	NM_017787	hsa-miR-647	seed
rs1130698	11	838542	0.00070152	GI_34328913_I	NM_004357	hsa-miR-647	flank
rs10736094	10	97630523	5.36E-08	GI_45580699_S	NM_001098175	hsa-miR-646	seed
rs1060435	11	68855595	0.000168895	GI_20589957_S	NM_139075	hsa-miR-646	flank
rs8984	14	65399306	8.18E-17	GI_21553312_S	NM_145165	hsa-miR-643	flank
rs3188491	1	101338482	0.000359751	GI_14149608_S	NM_001033025	hsa-miR-643	flank
rs1042288	11	110333608	0.000154009	GI_36054077_S	NM_004109	hsa-miR-641	flank
rs2020000	19	1038222	4.11E-06	GI_41327728_S	NM_201277	hsa-miR-625	flank
rs2226163	10	97628994	4.95E-07	GI_45580699_S	NM_001098175	hsa-miR-617	seed
rs56052963	2	231268342	2.11E-05	GI_20149710_S	NM_138402	hsa-miR-610	seed
rs9901637	17	8076802	3.86E-07	GI_34101277_A	NM_183065	hsa-miR-609	flank
rs3822410	5	10654769	3.56E-09	Hs.26039_S	NM_001164440	hsa-miR-603	flank
rs2280503	12	51138687	7.04E-12	GI_39930390_S	NM_173602	hsa-miR-596	flank
rs2594072	12	10005778	4.42E-09	GI_37577106_S	NM_005127	hsa-miR-596	flank
rs2539933	12	10005780	3.77E-08	GI_37577106_S	NM_005127	hsa-miR-596	flank
rs10131175	14	67852731	1.21E-10	GI_34147492_S	NM_004094	hsa-miR-591	flank
rs569	11	118894287	6.08E-07	GI_7706666_S	NM_016146	hsa-miR-591	flank
rs1805672	12	9163177	3.38E-06	GI_21361293_S	NM_005810	hsa-miR-584	seed
rs8007	3	119361250	3.98E-06	GI_22209003_S	NM_022135	hsa-miR-583	flank
rs12265362	10	16554373	0.00018666	GI_20070185_S	NM_001001484	hsa-miR-583	flank
rs9281	14	65399291	8.18E-17	GI_21553312_S	NM_145165	hsa-miR-582-5p	flank
rs12335	9	136197834	0.000276761	GI_39812452_S	NM_006753	hsa-miR-582-5p	flank
rs3667	6	32610934	2.96E-09	GI_18426974_S	NM_002122	hsa-miR-580	seed
rs1052990	7	116148370	1.77E-07	GI_38176291_A	NM_198212	hsa-miR-580	flank
rs8943	14	65399263	8.18E-17	GI_21553312_S	NM_145165	hsa-miR-579	flank
rs840389	5	34018684	2.98E-07	GI_13569918_I	NM_181435	hsa-miR-579	seed
rs1045270	8	124453799	2.99E-06	GI_8922280_S	NM_018024	hsa-miR-579	flank

rs1124836	2	85833046	1.10E-05	hmm28069_S	NM_001013649	hsa-miR-579	flank
rs1127968	14	65399255	9.75E-07	GI_21553312_S	NM_145165	hsa-miR-576-5p	flank
rs243607	21	19161515	0.000453632	GI_40254881_S	NM_017447	hsa-miR-576-5p	flank
rs4560	7	6063283	7.61E-08	GI_11125767_S	NM_001134335	hsa-miR-570	seed
rs1061810	11	43877934	2.22E-06	GI_7705854_S	NM_016142	hsa-miR-570	seed
rs284856	10	104574329	0.000683291	GI_41152103_S	NM_017787	hsa-miR-570	seed
rs12124	2	86253508	1.47E-08	GI_7661685_S	NM_015425	hsa-miR-569	seed
rs1055794	12	110290073	1.34E-05	GI_20357594_S	NM_016433	hsa-miR-569	flank
rs78450791	3	169712558	0.000913744	GI_23308546_S	NM_003262	hsa-miR-569	flank
rs3171741	22	21242247	4.17E-08	GI_18765736_S	NM_004782	hsa-miR-550*	flank
rs7075357	10	16554254	8.63E-15	GI_20070185_S	NM_001001484	hsa-miR-548d-3p	flank
rs5752201	22	21244229	4.17E-08	GI_18765736_S	NM_004782	hsa-miR-548d-3p	flank
rs7809	4	8368433	3.52E-07	GI_4501870_S	NM_003501	hsa-miR-548d-3p	flank
rs3848639	19	1037932	2.21E-06	GI_41327728_S	NM_201277	hsa-miR-548d-3p	flank
rs540	16	420907	6.35E-06	GI_10864068_S	NM_021259	hsa-miR-548d-3p	flank
rs2298746	11	74553834	1.22E-15	hmm1412_S	NM_182969	hsa-miR-548c-3p	flank
rs1142429	6	32610908	7.62E-06	GI_18426974_S	NM_002122	hsa-miR-548c-3p	flank
rs6927416	6	89873055	9.29E-06	GI_37551403_S	NM_001010853	hsa-miR-548c-3p	flank
rs1468804	7	12275508	1.42E-05	GI_40254892_S	NM_018374	hsa-miR-548c-3p	seed
rs11676089	2	231268085	2.11E-05	GI_20149710_S	NM_138402	hsa-miR-548c-3p	flank
rs60052574	12	393501	6.74E-05	GI_4826967_S	NM_001042603	hsa-miR-548c-3p	seed
rs12816400	12	122716447	0.000103334	GI_42544226_S	NM_022916	hsa-miR-548c-3p	seed
rs6052005	20	417612	0.000819792	GI_21389446_S	NM_144628	hsa-miR-548c-3p	flank
rs2279325	5	10657194	3.52E-10	Hs.26039_S	NM_001164440	hsa-miR-548a-3p	seed
rs4350264	10	70242946	2.21E-06	GI_31652216_S	NM_152707	hsa-miR-548a-3p	flank
rs10425594	19	39889691	0.000177429	GI_37552078_S	NM_017592	hsa-miR-548a-3p	flank
rs1130902	4	183812046	5.67E-10	GI_4503276_S	NM_001012732	hsa-miR-545	flank
rs1044218	21	34821570	4.25E-05	GI_40538810_S	NM_006134	hsa-miR-545	flank
rs11540417	16	85812631	5.26E-05	GI_34147520_S	NM_006067	hsa-miR-544	flank
rs77015062	6	32610825	2.13E-10	GI_18426974_S	NM_002122	hsa-miR-539	seed
rs2289405	2	190636039	7.64E-09	GI_31377759_S	NM_016467	hsa-miR-539	flank
rs2034	6	11200856	2.51E-05	GI_33667052_I	NM_182966	hsa-miR-539	flank
rs9533394	13	43682841	0.000130293	GI_7019452_S	NM_013238	hsa-miR-539	flank
rs10277	5	179264731	3.20E-09	GI_19923742_S	NM_003900	hsa-miR-522	flank
rs1058033	22	45583606	0.000112476	GI_24497446_A	NM_007172	hsa-miR-519e	flank
rs2279324	5	10657209	3.52E-10	Hs.26039_S	NM_001164440	hsa-miR-518e*	flank
rs77780351	4	25371679	8.79E-05	GI_42657116_S	NM_024936	hsa-miR-518e*	flank
rs243609	21	19161689	0.000634118	GI_40254881_S	NM_017447	hsa-miR-518e*	flank
rs3180067	6	52269547	0.000190212	GI_19115959_S	NM_133367	hsa-miR-518c*	flank
rs10954214	7	128589633	1.17E-12	GI_38683858_A	NM_032643	hsa-miR-516a-3p	flank
rs2005606	19	42093112	2.94E-10	GI_16117774_S	NM_001098506	hsa-miR-516a-3p	seed
rs12534379	7	129771117	1.71E-08	GI_44917618_S	NM_014997	hsa-miR-512-5p	seed
rs6007600	22	45737481	7.28E-05	GI_8923587_S	NM_017911	hsa-miR-512-5p	flank
rs112931520	6	32610769	1.19E-10	GI_18426974_S	NM_002122	hsa-miR-512-3p	flank
rs1048643	6	32610781	2.39E-05	GI_18426974_S	NM_002122	hsa-miR-512-3p	seed
rs1935815	10	97631492	7.01E-05	GI_45580699_S	NM_001098175	hsa-miR-512-3p	flank
rs6775	16	5135380	0.000274295	GI_42476336_I	NM_201400	hsa-miR-507	flank
rs840387	5	34019048	2.98E-07	GI_13569918_I	NM_181435	hsa-miR-505	seed
rs1056831	1	111786012	0.000916156	GI_11993934_S	NM_004000	hsa-miR-505	seed
rs3739677	9	33461881	7.04E-05	GI_39777589_A	NM_139235	hsa-miR-499-5p	flank

rs2056445	13	31905872	1.53E-09	GI_34996530_S	NM_194318	hsa-miR-495	seed
rs1062935	17	78939857	5.07E-08	GI_22094986_S	NM_020761	hsa-miR-495	flank
rs3735172	7	150028958	0.000725669	GI_19923960_S	NM_138434	hsa-miR-491-5p	flank
rs73413716	12	122215128	1.59E-05	GI_37543220_S	NM_001080825	hsa-miR-485-5p	seed
rs13830	20	3204231	0.00027613	GI_31657143_A	NM_181493	hsa-miR-485-5p	flank
rs2694555	19	47885524	0.000747434	GI_38158021_A	NM_014681	hsa-miR-485-5p	seed
rs1064993	6	32611181	3.96E-08	GI_18426974_S	NM_002122	hsa-miR-484	flank
rs9542	4	183812351	2.16E-06	GI_4503276_S	NM_001012732	hsa-miR-484	flank
rs2756367	6	89320589	1.03E-05	GI_4506562_S	NM_003800	hsa-miR-484	seed
rs1064991	6	32611176	0.000172485	GI_18426974_S	NM_002122	hsa-miR-484	flank
rs382745	16	89603586	2.34E-10	GI_40806172_I	NM_199367	hsa-miR-454*	seed
rs6429599	1	46827871	2.98E-11	hmm8232_S	NM_199044	hsa-miR-4323	seed
rs12214031	6	26376628	0.000733668	GI_34932495_S	NM_007047	hsa-miR-4323	flank
rs58184950	7	50470256	4.63E-11	GI_31657112_S	NM_006060	hsa-miR-432	seed
rs1130161	6	32610994	2.30E-08	GI_18426974_S	NM_002122	hsa-miR-432	flank
rs1130162	6	32610997	2.64E-08	GI_18426974_S	NM_002122	hsa-miR-432	flank
rs9954334	18	20876486	6.57E-07	GI_40254998_S	NM_032933	hsa-miR-431	seed
rs11681358	2	231268211	2.11E-05	GI_20149710_S	NM_138402	hsa-miR-431	flank
rs1132922	20	3855427	1.07E-05	GI_42734342_S	NM_020746	hsa-miR-425	seed
rs1133724	20	18465004	1.09E-07	GI_33598951_S	NM_006466	hsa-miR-421	flank
rs5867	20	18465001	1.09E-07	GI_33598951_S	NM_006466	hsa-miR-421	flank
rs1042949	7	12272116	1.13E-05	GI_40254892_S	NM_018374	hsa-miR-421	flank
rs2146837	9	123941033	0.000121052	GI_19923482_S	NM_016322	hsa-miR-421	flank
rs4057	13	31906291	1.53E-09	GI_34996530_S	NM_194318	hsa-miR-381	flank
rs10810186	9	14617069	0.000283198	GI_31341670_S	NM_178566	hsa-miR-381	flank
rs10518716	15	67494823	4.69E-07	GI_20070334_S	NM_024666	hsa-miR-380*	seed
rs1143034	16	1878067	6.12E-09	GI_13654273_S	NM_031208	hsa-miR-378*	flank
rs6546	5	34020030	2.73E-07	GI_13569918_I	NM_181435	hsa-miR-378*	flank
rs1132216	12	7247395	0.000163982	GI_7706082_S	NM_016546	hsa-miR-378	flank
rs7543	6	151422936	4.79E-07	GI_40018634_S	NM_015440	hsa-miR-377	flank
rs6933844	6	52271707	0.000190212	GI_19115959_S	NM_133367	hsa-miR-376b	flank
rs1971784	19	48712896	6.11E-08	GI_7662403_S	NM_014959	hsa-miR-374a	seed
rs1044744	22	45737310	7.28E-05	GI_8923587_S	NM_017911	hsa-miR-374a	seed
rs1065047	6	32611260	3.38E-07	GI_18426974_S	NM_002122	hsa-miR-363*	seed
rs3822008	4	84526767	1.00E-06	GI_40255053_S	NM_032717	hsa-miR-363*	flank
rs1137360	17	79640219	1.05E-05	GI_42661280_S	NM_199287	hsa-miR-363*	flank
rs12248905	10	129895483	0.000599009	GI_19923216_S	NM_002417	hsa-miR-363*	seed
rs3746662	20	3847325	0.000148492	GI_42734342_S	NM_020746	hsa-miR-34b*	seed
rs7020	20	25278600	0.000407381	GI_34577123_S	NM_002862	hsa-miR-34b*	seed
rs17618778	19	21608110	0.000519622	GI_40255231_S	NM_001076678	hsa-miR-34b*	flank
rs1065044	6	32611243	5.42E-07	GI_18426974_S	NM_002122	hsa-miR-34a	flank
rs1065045	6	32611255	7.72E-06	GI_18426974_S	NM_002122	hsa-miR-34a	seed
rs1055338	10	16555464	4.35E-07	GI_20070185_S	NM_001001484	hsa-miR-342-3p	seed
rs3746215	19	58153596	0.000293358	GI_38569444_S	NM_198855	hsa-miR-342-3p	flank
rs3087659	10	16554723	1.55E-14	GI_20070185_S	NM_001001484	hsa-miR-33a	flank
rs15797	12	122215626	1.18E-05	GI_37543220_S	NM_001080825	hsa-miR-33a	flank
rs11681234	2	231267957	2.11E-05	GI_20149710_S	NM_138402	hsa-miR-33a	flank
rs2839531	21	43892641	0.000331797	GI_18254455_S	NM_080860	hsa-miR-33a	flank
rs73033013	6	167453718	8.34E-10	GI_36287109_A	NM_007045	hsa-miR-339-5p	flank
rs840386	5	34020277	3.53E-06	GI_13569918_I	NM_181435	hsa-miR-339-5p	flank

rs13547	18	44634756	0.000240591	GI_34222341_S	NM_032124	hsa-miR-339-5p	flank
rs6986329	8	146280802	0.000305956	GI_12751496_S	NM_023080	hsa-miR-339-5p	flank
rs11672297	19	18686810	4.06E-13	GI_15451941_S	NM_001033930	hsa-miR-338-3p	flank
rs880530	16	66545106	3.00E-05	GI_33636700_S	NM_004614	hsa-miR-338-3p	seed
rs9804386	10	99375040	0.000170423	GI_31341691_S	NM_001098831	hsa-miR-338-3p	flank
rs12603821	17	62006432	8.24E-06	GI_11038675_A	NM_001039933	hsa-miR-335	flank
rs1051688	17	62006433	8.24E-06	GI_11038675_A	NM_001039933	hsa-miR-335	flank
rs284854	10	104574562	1.51E-05	GI_41152103_S	NM_017787	hsa-miR-335	flank
rs1005900	8	21964561	6.95E-06	GI_40254968_S	NM_024815	hsa-miR-331-3p	flank
rs3819001	1	1138913	0.000436667	GI_23238193_A	NM_148901	hsa-miR-331-3p	seed
rs6674384	1	114455907	1.86E-09	GI_24431998_S	NM_022836	hsa-miR-330-3p	flank
rs40942	7	108203050	1.30E-07	GI_32698887_S	NM_182529	hsa-miR-330-3p	flank
rs12276	19	58154092	0.000293358	GI_38569444_S	NM_198855	hsa-miR-330-3p	flank
rs9547190	13	36876703	0.000732895	GI_40806197_S	NM_001142295	hsa-miR-330-3p	flank
rs3826493	17	3564235	6.01E-10	GI_4826681_S	NM_001031681	hsa-miR-326	flank
rs79249112	17	33458724	6.97E-09	GI_20070287_S	NM_001014445	hsa-miR-324-5p	seed
rs6762	11	838722	5.58E-05	GI_34328913_I	NM_004357	hsa-miR-324-3p	flank
rs11672119	19	43979348	0.000276414	GI_27485260_S	NM_198850	hsa-miR-324-3p	flank
rs60092940	12	42706537	7.11E-07	GI_21314766_S	NM_033114	hsa-miR-320a	seed
rs12445303	16	81115573	0.000127417	GI_31542839_S	NM_004483	hsa-miR-320a	flank
rs1617350	8	110542337	2.76E-15	GI_31377831_S	NM_177531	hsa-miR-3157	flank
rs1971783	19	48712958	6.11E-08	GI_7662403_S	NM_014959	hsa-miR-31	flank
rs4556	14	75476071	0.0006426	GI_7657057_S	NM_014239	hsa-miR-31	flank
rs707947	6	32611068	3.15E-07	GI_18426974_S	NM_002122	hsa-miR-30a*	flank
rs3864928	12	89915549	7.55E-07	GI_34452724_S	NM_003774	hsa-miR-29a	seed
rs3211567	16	89629736	1.01E-05	GI_15431296_A	NM_000977	hsa-miR-29a	flank
rs73236629	4	38825449	1.68E-05	GI_20143970_S	NM_006068	hsa-miR-296-5p	flank
rs2534712	12	6572549	7.35E-05	GI_40549443_I	NM_014231	hsa-miR-296-5p	seed
rs13842	12	6572561	7.35E-05	GI_40549443_I	NM_014231	hsa-miR-296-5p	flank
rs73236628	4	38825443	0.000100722	GI_20143970_S	NM_006068	hsa-miR-296-5p	flank
rs699245	1	183521283	0.000174268	GI_42476073_A	NM_201568	hsa-miR-296-5p	seed
rs6745	14	65401695	8.18E-17	GI_21553312_S	NM_145165	hsa-miR-26a	flank
rs6498540	16	15130594	4.53E-06	GI_37541419_S	NM_015027	hsa-miR-26a	flank
rs61435333	17	15620647	0.00099619	GI_10190685_S	NM_020652	hsa-miR-26a	flank
rs13125773	4	44701256	2.35E-05	GI_11345459_S	NM_021927	hsa-miR-25	flank
rs28564677	18	59712554	4.92E-05	GI_34328903_A	NM_012327	hsa-miR-25	flank
rs56251216	2	231268201	2.11E-05	GI_20149710_S	NM_138402	hsa-miR-24	seed
rs7426	17	5288983	7.21E-05	GI_31377797_S	NM_004703	hsa-miR-24	flank
rs56080558	19	21608319	0.000820476	GI_40255231_S	NM_001076678	hsa-miR-23a	flank
rs12618	19	58153756	9.89E-05	GI_38569444_S	NM_198855	hsa-miR-223	flank
rs66823108	6	26377939	1.50E-08	GI_34932495_S	NM_007047	hsa-miR-221	flank
rs394128	16	337871	6.67E-11	GI_31083143_A	NM_181050	hsa-miR-214	flank
rs2871647	17	76137477	1.87E-09	GI_31377553_S	NM_152468	hsa-miR-214	flank
rs12949741	17	79640563	1.70E-05	GI_42661280_S	NM_199287	hsa-miR-214	flank
rs1128154	3	121350616	0.000406414	GI_37059786_S	NM_005335	hsa-miR-214	seed
rs284858	10	104573936	0.000412515	GI_41152103_S	NM_017787	hsa-miR-214	seed
rs1057745	19	39888390	5.35E-08	GI_37552078_S	NM_017592	hsa-miR-204	seed
rs1130333	2	3502035	4.09E-07	GI_8922761_S	NM_018269	hsa-miR-200b	flank
rs8177953	16	81116383	0.000127417	GI_31542839_S	NM_004483	hsa-miR-200b	flank
rs3765824	1	241796443	0.00067941	GI_4502810_S	NM_001821	hsa-miR-200b	seed

rs9359842	6	89872499	3.36E-06	GI_37551403_S	NM_001010853	hsa-miR-200a*	flank
rs1130158	6	32610972	5.44E-16	GI_18426974_S	NM_002122	hsa-miR-196b	flank
rs1055091	2	190635143	1.14E-15	GI_31377759_S	NM_016467	hsa-miR-196b	flank
rs1130156	6	32610968	1.48E-08	GI_18426974_S	NM_002122	hsa-miR-196b	flank
rs1142447	6	32610960	1.84E-06	GI_18426974_S	NM_002122	hsa-miR-196b	flank
rs7222136	17	46199592	2.56E-08	GI_23111027_I	NM_152244	hsa-miR-194	flank
rs79584669	17	33458935	6.97E-09	GI_20070287_S	NM_001014445	hsa-miR-193a-3p	flank
rs10425018	19	18687175	2.99E-13	GI_15451941_S	NM_001033930	hsa-miR-192	flank
rs9715769	4	38774489	2.74E-06	GI_13569929_S	NM_001017388	hsa-miR-192	flank
rs3778911	7	66276153	3.05E-09	GI_7657495_S	NM_014504	hsa-miR-190	flank
rs617655	17	10616766	8.65E-08	GI_42661099_S	NM_001004313	hsa-miR-190	flank
rs1045291	8	124454007	2.99E-06	GI_8922280_S	NM_018024	hsa-miR-18a*	flank
rs26431	5	102365794	0.00085445	GI_21070979_A	NM_001177306	hsa-miR-18a*	seed
rs56324594	2	227868854	0.000878311	GI_15890083_S	NM_000092	hsa-miR-18a*	seed
rs4559	12	57489648	2.80E-10	GI_23397677_S	NM_003153	hsa-miR-18a	flank
rs1978	6	26377573	1.50E-08	GI_34932495_S	NM_007047	hsa-miR-18a	flank
rs12120771	1	118065919	8.79E-08	GI_40254840_S	NM_006699	hsa-miR-18a	flank
rs4807907	19	1377173	0.000699426	GI_31652258_S	NM_032853	hsa-miR-18a	flank
rs9894790	17	8076778	1.22E-06	GI_34101277_A	NM_183065	hsa-miR-186	flank
rs1142422	6	32610897	2.48E-05	GI_18426974_S	NM_002122	hsa-miR-186	seed
rs2126852	4	76406846	0.000816876	GI_24308060_S	NM_001008925	hsa-miR-186	flank
rs11203205	21	43892775	6.28E-07	GI_18254455_S	NM_080860	hsa-miR-185	flank
rs2279327	5	10656785	1.43E-09	Hs.26039_S	NM_001164440	hsa-miR-182*	flank
rs10954213	7	128589427	9.92E-15	GI_38683858_A	NM_032643	hsa-miR-181a	seed
rs34210004	17	41370337	0.000177975	GI_21450795_S	NM_145041	hsa-miR-181a	flank
rs1137789	4	1381798	0.000465914	GI_22042949_S	NM_020894	hsa-miR-181a	seed
rs12608925	19	18687533	1.46E-14	GI_15451941_S	NM_001033930	hsa-miR-17*	flank
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rs1134381	17	79648366	4.00E-05	GI_29739147_S	NM_001040025	hsa-miR-150	flank
rs71314346	3	9427498	0.000537942	GI_14149689_S	NM_015453	hsa-miR-150	flank
rs10146885	14	65401819	3.88E-16	GI_21553312_S	NM_145165	hsa-miR-146a	flank
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rs2150820	6	89872976	1.74E-06	GI_37551403_S	NM_001010853	hsa-miR-143	flank
rs3798733	6	11201135	3.10E-05	GI_33667052_I	NM_182966	hsa-miR-143	flank
rs9804387	10	99375141	0.000170423	GI_31341691_S	NM_001098831	hsa-miR-143	seed
rs1979	6	26377591	1.50E-08	GI_34932495_S	NM_007047	hsa-miR-142-5p	flank
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rs2077976	17	6931769	0.000589874	GI_38327514_S	NM_181844
rs8400	17	18112845	0.000615923	GI_40353209_S	NM_017758
rs74333807	13	75859286	0.000622788	GI_42660198_S	NM_014832
rs16910556	9	124102350	0.000634413	GI_38016910_I	NM_004099
rs7320	10	127525072	0.000637695	GI_20336299_S	NM_018180
rs7584	22	39414699	0.000643966	GI_22907038_S	NM_014508
rs57866552	22	46689229	0.000651212	GI_8923627_S	NM_017931
rs75198900	1	40961738	0.000670313	GI_38348299_S	NM_198494
rs1052204	12	122215856	0.000672833	GI_37543220_S	NM_001080825
rs7317988	13	36877685	0.00067753	GI_40806197_S	NM_001142295

rs2721138	8	145750138	0.000699853	GI_7661859_S	NM_014665
rs9071	8	145750506	0.000699853	GI_7661859_S	NM_014665
rs12964	12	6572191	0.000715341	GI_40549443_I	NM_014231
rs1054144	13	36877894	0.000732895	GI_40806197_S	NM_001142295
rs75499917	11	124564614	0.00074796	GI_15718773_S	NM_017425
rs2076016	20	7962707	0.0007503	hmm9596_S	NM_021156
rs73208237	3	196745959	0.000761325	GI_16933548_I	NM_033316
rs1141561	19	1038862	0.000761434	GI_41327728_S	NM_201277
rs1570513	9	7076586	0.000774813	Hs.201493_S	NM_001146695
rs1048165	2	70131964	0.000781806	GI_24307918_S	NM_006857
rs3802481	9	14618668	0.00080638	GI_31341670_S	NM_178566
rs387142	17	10617314	0.000812274	GI_42661099_S	NM_001004313
rs3746793	20	418199	0.000819792	GI_21389446_S	NM_144628
rs842254	3	16300625	0.000820066	GI_45592951_S	NM_206831
rs10087	3	16301148	0.000820066	GI_45592951_S	NM_206831
rs10364	6	32780572	0.000828218	GI_18641377_S	NM_002120
rs41266072	1	174979635	0.000840391	GI_7656951_S	NM_001007214
rs28577270	14	35498443	0.000852234	GI_20149548_S	NM_003136
rs11540758	14	35498485	0.000852234	GI_20149548_S	NM_003136
rs3862142	15	44064806	0.000874605	GI_13376767_S	NM_025165
rs2788	15	44064886	0.000874605	GI_13376767_S	NM_025165
rs251859	19	39918729	0.000885804	GI_45237196_S	NM_022835
rs1206072	6	97243010	0.000903672	GI_13540556_S	NM_030784
rs213843	6	97244612	0.000903672	GI_13540556_S	NM_030784
rs496471	2	224741803	0.000903716	GI_30795191_I	NM_020830
rs682250	2	224741911	0.000903716	GI_30795191_I	NM_020830
rs584358	2	224742738	0.000903716	GI_30795191_I	NM_020830
rs678746	2	224741993	0.000928126	GI_30795191_I	NM_020830
rs45535532	11	110334690	0.000987279	GI_36054077_S	NM_004109
rs13740	16	3534892	0.000992425	GI_13376260_S	NM_001083600
rs2240075	16	3535540	0.000992425	GI_13376260_S	NM_001083600
rs1061172	6	32611216	0.000997764	GI_18426974_S	NM_002122

We first predict the target genes of miRNAs solely based on perfect “seed” pairing (column 8). If a SNP is located in the 3’ UTR regions that are perfectly matching position 2-8 of a miRNA, the location is labeled as “seed”; if the SNP is located in 3’ UTR regions that is 1-13 bp upstream the seed pairing regions, the location is labeled as “flank” (column 8). In case a miRNA target site is predicted by Context Score (< -0.3), it is labeled in column 9.

Table S6 miRNAs that have targets significantly enriched in stabilization selection or directional selection during primate evolution.

miRNA	Surrounding backgrounds			High-Confidence target			Q	
	Significant	Tested	%	Significant	Tested	%		
Stabilizing selection								
miR-23a	1220	15453	7.89	98	819	11.97	0.0039	
miR-23b	1220	15451	7.90	98	821	11.94	0.0039	
miR-194	1271	15937	7.98	47	335	14.03	0.0061	
Directional selection in human								
miR-103	789	15605	5.06	52	667	7.80	0.0491	
miR-107	789	15600	5.06	52	672	7.74	0.0491	
miR-25	804	15839	5.08	37	433	8.55	0.0491	
miR-92a	820	16064	5.10	21	208	10.10	0.0491	
miR-26a	778	15610	4.98	63	662	9.52	0.0001	
miR-26b	777	15604	4.98	64	668	9.58	0.0001	
miR-15a	789	15595	5.06	52	677	7.68	0.0491	

For each miRNA, the proportion (%) of High-Confidence target genes under Stabilizing or directional selection (*significant*), out of the total number High-Confidence targets of that miRNA (*tested*) was calculated. All the transcripts that are not High-Confidence target of that miRNA were treated as surrounding background. Hypergeometric tests were used to determine the significance of miRNA target enrichments. Benjamini and Hochberg FDR (Q value) was used for multiple test correction. According to Blekhman *et al.* (2010), the genes under Stabilizing selection are genes with little variation in gene expression among individuals and species; and the genes under directional selection in human are genes having little variation in expression levels within and between chimpanzee and rhesus macaque individuals and a significantly different expression level in humans.

Table S7 SNPs located in 3' UTRs and miRNA target sites that are associated with human diseases

SNP	Gene	seed Pairing?	miRNA seed (MiRNA)	Phenotype	Reference
rs10046 rs1042026	CYP19A1 ADH1B	YES	CUUGGAG(miR-432)	Osteoporosis, Postmenopausal overall effect	Riancho, J. A. et al. 2005 Nasim Mavaddat , et al. Cancer epidemiology, biomarkers & prevention 2009 18(1):255-9
rs13181	ERCC2			Lung cancer	R P Young , et al. Postgraduate medical journal 2009 85(1008):515-24
rs1599796	CD80	YES	GUCUUAC(miR-550*) AUCUUAC(miR-200a*)	Celiac disease	G Trynka , et al. Gut 2009 58(8):1078-83
rs17154615 rs17799872 rs2165047 rs2297660 rs2317676	DLD ADCY3 DLG5 LRP8 ITGB3			Alzheimer's disease Alcohol dependence Crohn's disease Birth weight fetal growth Lung cancer	Brown, A. M. et al. 2004 Edenberg ,et al. Alcohol Clin Exp Res 2010 de Ridder, L. et al. 2007 Wang, L. et al. 2006 R P Young , et al. Postgraduate medical journal 2009 85(1008):515-24
rs3264	MPDZ			Alcohol Withdrawal Seizures Alcoholism Disease Models, Animal	Victor M Karpyak , et al. Alcoholism, clinical and experimental research 2009 33(4):712-21
rs3746544 rs4252041	SNAP25 IL1RN	YES	AAGACAU(miR-641)	ADHD Attention-Deficit Hyperactivity Disorder Type 2 Diabetes related glucose homeostasis traits	Ian R Gizer , et al. Human genetics 2009 126(1):51-90 Kari Luotola , et al. The Journal of clinical endocrinology and metabolism 2009 94(11):4575-83
rs4564 rs4986910	DLD CYP3A4			Alzheimer's disease Breast cancer	Brown, A. M. et al. 2004 Alice J Sigurdson , et al. Breast cancer research and treatment 2009 118(1):177-84
rs4986938	ESR2	YES	UCAGCCA(miR-3157)	Dementia, Vascular	Rivka Dresner-Pollak , et al. Genetic testing and molecular biomarkers 2009 13(3):339-42
rs5275 rs564398 rs6822	PTGS2 CDKN2B NDUFA8			Skin cancer, Non-melanoma, Diabetes Type 2 Aging/ Telomere Length	Vogel, U. et al. 2007 Hana Lango , et al. Diabetes 2008 57(11):3129-35 John M Starr , et al. Mechanisms of ageing and development 2008 129(12):745-51
rs686	DRD1	YES	AGCCCCA(miR-4323)	ADHD Attention-Deficit Hyperactivity Disorder	Robert D Oades , et al. Behavioral and brain functions 2008 4():48
rs7079 rs722651	AGT MPDZ	YES	UAUGGUU(miR-584)	Hypertension Alcohol Withdrawal Seizures Alcoholism Disease Models, Animal	Su, X. et al. 2007 Victor M Karpyak , et al. Alcoholism, clinical and experimental research 2009 33(4):712-21

Table S8 SNPs located in 3' UTRs that show signature of positive selection as detected by Grossman et al. (2010)

SNP	Chr	Pos	P value	Q_value	Probe	Gene	miRNA	SNP in miRNA:target pairing region
rs12952556	17	18231797	1.47E-06	0.000216621	GI_22547188-A	NM_148918		
rs7276320	21	44269588	0.000278	0.015880311	GI_40217837-A	NM_018669		
rs421533	19	40579468	0.000456	0.023037357	GI_37551919-S	NM_001010880	hsa-miR-376b	flank
rs13035	12	21623122	0.00067	0.030687788	GI_13376278-S	NM_024854	hsa-miR-190	flank
rs1507086	4	41956413	0.002541	0.080722764	GI_8922490-S	NM_018126		
rs3740487	10	102750783	0.002855	0.087444441	GI_39725941-S	NM_001163812		
rs1046011	1	65898996	0.029987	0.34750948	GI_41327153-S	NM_017526		
rs7281655	21	44269743	0.038678	0.3911471	GI_40217837-A	NM_018669		
rs311694	5	109756009	0.060092	0.471814198	GI_37550164-S	NM_001039763		
rs427461	19	40579842	0.060302	0.472399005	GI_37551919-S	NM_001010880		
rs3317	5	112212151	0.095881	0.563597503	GI_33667050-S	NM_005669		
rs7549683	1	94353449	0.122819	0.613055	GI_4504010-S	NM_002061		
rs6060539	20	34239382	0.131464	0.62648109	GI_33469953-A	NM_006047		
rs17731	10	3821561	0.140906	0.640639831	GI_37655156-S	NM_001300	hsa-miR-767-5p	flank
rs1009119	3	56763228	0.145214	0.646540535	GI_9506400-S	NM_019555	hsa-miR-1537	seed
rs6978	3	56761715	0.145214	0.646540535	GI_9506400-S	NM_019555		
rs1044040	2	25042625	0.149371	0.652403057	GI_13236564-S	NM_024322		
rs1043003	10	3820787	0.161035	0.667813266	GI_37655156-S	NM_001300	hsa-miR-532-5p	flank
rs1044040	2	25042625	0.175569	0.685387419	GI_10947058-S	NM_004036		
rs10359	20	34099789	0.208812	0.720607092	GI_21735547-S	NM_007186		
rs8031507	15	55651011	0.212007	0.723756315	GI_31621295-I	NM_004748		
rs13013	10	75562161	0.222033	0.732676039	GI_31377809-S	NM_003635	hsa-miR-518c*	flank
rs1051085	2	182794534	0.24115	0.74921705	GI_34222128-S	NM_006751	hsa-miR-429	seed
rs2919051	2	122095640	0.290682	0.786336853	GI_31563536-S	NM_001142273	hsa-miR-30a*	flank
rs11732	15	55647786	0.310713	0.7995662	GI_31621295-I	NM_004748	hsa-miR-568	flank
rs13232194	7	102742554	0.327354	0.809566605	GI_42476173-S	NM_198990		
rs246400	5	64885885	0.360875	0.827874854	GI_44955890-I	NM_001656		
rs13756	4	42113241	0.363828	0.829448491	Hs.120591-S	NM_207406		
rs8961	7	151254175	0.375646	0.835763276	GI_33186924-S	NM_001040633	hsa-miR-7	flank
rs2304176	19	38794895	0.473844	0.878412478	GI_24308363-S	NM_033557		
rs2073731	22	19437938	0.484136	0.882418935	GI_34222257-S	NM_001035247		
rs17754	4	39289308	0.50789	0.890764922	GI_32528305-S	NM_002913		
rs7460	8	141668860	0.523508	0.895909849	GI_27886592-A	NM_005607	hsa-miR-539	flank
rs1057807	4	39289473	0.583142	0.915021815	GI_32528305-S	NM_002913	hsa-miR-579	flank
rs1050088	3	49570882	0.58862	0.916666816	GI_4758115-S	NM_004393		
rs2546115	5	112214093	0.5922	0.917750714	GI_33667050-S	NM_005669	hsa-miR-493*	flank
rs1060681	14	70836753	0.592456	0.917826259	GI_8922963-S	NM_018373		
rs2073730	22	19437946	0.597094	0.919223122	GI_34222257-S	NM_001035247		
rs927302	10	102722916	0.597964	0.919431809	GI_27532981-I	NM_018121		
rs9228	15	52484589	0.697482	0.946010613	GI_9055283-S	NM_018728		
rs13858	15	72433144	0.780429	0.964478655	GI_33942065-S	NM_145204	hsa-miR-7	flank
rs10482	1	227175119	0.847783	0.977198912	GI_34147521-S	NM_020247		
rs11732	15	55647786	0.868666	0.980791152	GI_22538447-S	NM_004855		
rs2229714	1	26900708	0.880648	0.982681723	GI_20149546-S	NM_001006665	hsa-miR-29a	flank
rs13035	12	21623122	0.965211	0.995473087	GI_14591901-A	NM_002907		
rs4861163	4	42117173	0.989309	0.998591623	Hs.120591-S	NM_207406	hsa-miR-181a	flank

Table S9 miRNA target genes have higher expression variability if only curated RefSeq transcripts are considered in analysis. (For each dataset, the median variability is presented)

Dataset	TargetScan conservation (PCT > 0.8)					TargetScan context score (<-0.4 and percentile > 85)				
	Non-target		Targets		P	Non-target		Targets		P
	# of genes	CV	# of genes	CV		# of genes	CV	# of genes	CV	
I	9,647	2.27	2,068	2.33	0.002	4,240	2.17	7,475	2.34	10^{-10}
II	14,056	3.21	2,894	3.29	0.003	6,197	3.19	10,753	3.25	0.0001
III	9,508	2.63	2,022	2.80	10^{-7}	4,221	2.58	7,309	2.69	10^{-6}
IV	9,508	2.57	2,022	2.65	0.006	4,221	2.53	7,309	2.62	10^{-4}
V	9,508	2.57	2,022	2.72	10^{-11}	4,221	2.43	7,309	2.69	$< 10^{-16}$
VI	9,508	2.46	2,022	2.59	10^{-7}	4,221	2.42	7,309	2.52	10^{-7}

Table S10 Gene Ontology categories that are enriched in the top 10% High-Confidence Target genes with highest CV that are significant in either dataset I (Wang et al. 2009) or II (Idaghdour et al. 2009).

GO ID	GO Name	Fold Enrichment	Q value	Dataset
GO:0007267	cell-cell signaling	2.5	8.68E-06	I
GO:0030182	neuron differentiation	2.7	3.22E-05	I
GO:0000904	cell morphogenesis involved in differentiation	3.5	1.13E-04	I
GO:0031175	neuron projection development	3.2	1.60E-04	I
GO:0016477	cell migration	2.8	2.89E-04	I
GO:0043062	extracellular structure organization	4.2	3.89E-04	I
GO:0007409	Axonogenesis	3.6	4.12E-04	I
GO:0048812	neuron projection morphogenesis	3.4	6.45E-04	I
GO:0048667	cell morphogenesis involved in neuron differentiation	3.4	8.05E-04	I
GO:0048870	cell motility	2.6	8.26E-04	I
GO:0051674	localization of cell	2.6	8.26E-04	I
GO:0030030	cell projection organization	2.4	0.002	I
GO:0000902	cell morphogenesis	2.4	0.002	I
GO:0032989	cellular component morphogenesis	2.3	0.003	I
GO:0048666	neuron development	2.5	0.003	I
GO:0007411	axon guidance	4.5	0.004	I
GO:0030198	extracellular matrix organization	4.9	0.004	I
GO:0007186	G-protein coupled receptor protein signaling pathway	2.1	0.005	I
GO:0048858	cell projection morphogenesis	2.7	0.006	I
GO:0006875	cellular metal ion homeostasis	2.8	0.009	I
GO:0055065	metal ion homeostasis	2.7	0.013	I
GO:0007626	locomotory behavior	2.5	0.014	I
GO:0001764	neuron migration	4.5	0.019	I
GO:0043067	regulation of programmed cell death	1.6	0.019	I
GO:0010941	regulation of cell death	1.6	0.021	I
GO:0032990	cell part morphogenesis	2.5	0.021	I
GO:0042981	regulation of apoptosis	1.5	0.025	I
GO:0050877	neurological system process	1.7	0.032	I
GO:0070482	response to oxygen levels	2.8	0.034	I
GO:0006874	cellular calcium ion homeostasis	2.7	0.035	I
GO:0002526	acute inflammatory response	3.9	0.046	I
GO:0055074	calcium ion homeostasis	2.6	0.048	I
GO:0007610	Behavior	1.9	0.049	I
GO:0001775	cell activation	2.0	0.004	II
GO:0010033	response to organic substance	1.6	0.004	II
GO:0006576	biogenic amine metabolic process	3.5	0.005	II
GO:0009967	positive regulation of signal transduction	2.0	0.005	II
GO:0009617	response to bacterium	2.4	0.006	II
GO:0010647	positive regulation of cell communication	2.0	0.006	II
GO:0018958	phenol metabolic process	6.0	0.006	II
GO:0048514	blood vessel morphogenesis	2.4	0.007	II
GO:0007243	protein kinase cascade	1.8	0.007	II
GO:0045321	leukocyte activation	2.0	0.009	II
GO:0006575	cellular amino acid derivative metabolic process	2.5	0.010	II
GO:0042325	regulation of phosphorylation	1.7	0.011	II

GO:0001525	Angiogenesis	2.5	0.014	II
GO:0002684	positive regulation of immune system process	2.0	0.014	II
GO:0034097	response to cytokine stimulus	2.8	0.015	II
GO:0002237	response to molecule of bacterial origin	2.8	0.015	II
GO:0010740	positive regulation of protein kinase cascade	2.2	0.019	II
GO:0043408	regulation of MAPKKK cascade	2.6	0.019	II
GO:0010627	regulation of protein kinase cascade	2.0	0.020	II
GO:0006584	catecholamine metabolic process	5.7	0.021	II
GO:0009620	response to fungus	5.7	0.021	II
GO:0009712	catechol metabolic process	5.7	0.021	II
GO:0034311	diol metabolic process	5.7	0.021	II
GO:0019220	regulation of phosphate metabolic process	1.7	0.021	II
GO:0051174	regulation of phosphorus metabolic process	1.7	0.021	II
GO:0043066	negative regulation of apoptosis	1.8	0.025	II
GO:0043410	positive regulation of MAPKKK cascade	3.6	0.027	II
GO:0030097	Hemopoiesis	2.0	0.029	II
GO:0043069	negative regulation of programmed cell death	1.7	0.031	II
GO:0060548	negative regulation of cell death	1.7	0.033	II
GO:0006468	protein amino acid phosphorylation	1.5	0.036	II
GO:0048729	tissue morphogenesis	2.3	0.037	II
GO:0016337	cell-cell adhesion	2.1	0.037	II
GO:0007242	intracellular signaling cascade	1.4	0.039	II
GO:0048534	hemopoietic or lymphoid organ development	1.9	0.048	II

Table S11 Gene Ontology categories enriched in the top 10% High-Confidence Target genes with highest CVs (categories are significant in both dataset I and II)

GO ID	GO Name	Dataset I (Wang et al. 2009)		Dataset II (Idaghdour et al. 2009)	
		Enrichment Score	Benjamini Q value	Enrichment Score	Benjamini Q value
GO:0006955	immune response	2.4	1.71E-08	2.2	3.29E-11
GO:0006928	cell motion	2.9	2.58E-08	1.9	0.004
GO:0022610	biological adhesion	2.6	7.48E-08	1.8	0.003
GO:0007155	cell adhesion	2.6	8.56E-08	1.8	0.003
GO:0007166	cell surface receptor linked signal transduction	1.8	1.48E-05	1.5	5.83E-04
GO:0009611	response to wounding	2.3	1.15E-04	2.1	3.38E-06
GO:0006952	defense response	2.1	4.43E-04	2.2	5.72E-09
GO:0006954	inflammatory response	2.4	0.003	2.3	4.43E-05
GO:0006935	Chemotaxis	2.9	0.013	2.3	0.027
GO:0042330	Taxis	2.9	0.013	2.3	0.027
GO:0051094	positive regulation of developmental process	2.1	0.045	1.9	0.040
GO:0001568	blood vessel development	2.3	0.046	2.3	0.006
GO:0001944	vasculature development	2.3	0.048	2.2	0.007