SUPPLEMENTAL INFORMATION

Friedreich's Ataxia Induced Pluripotent Stem Cells Model Intergenerational GAA•TTC Triplet-Repeat Instability

Sherman Ku, Elisabetta Soragni, Erica Campau, Elizabeth A. Thomas, Gulsah Altun, Louise C. Laurent, Jeanne F. Loring, Marek Napierala, and Joel M. Gottesfeld

SUPPLEMENTAL DATA

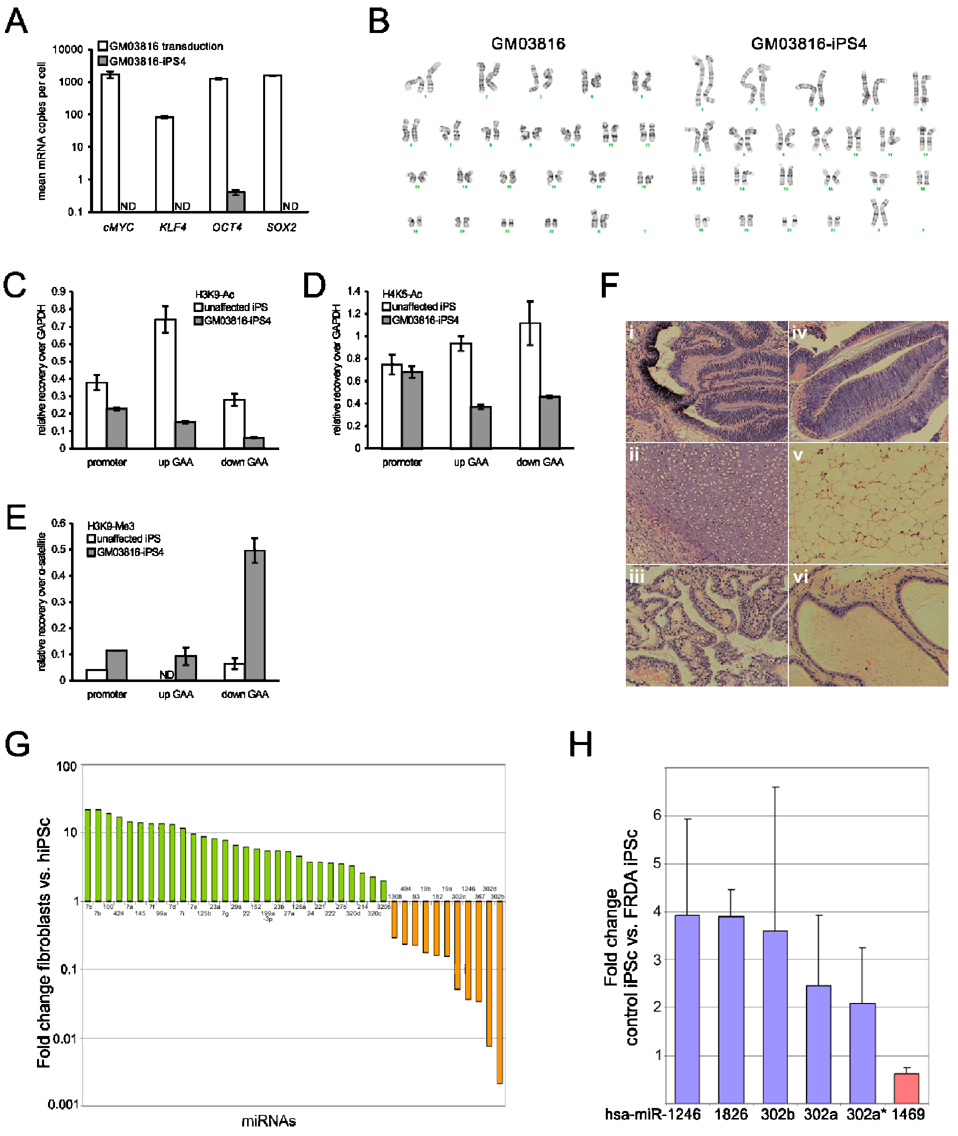


Figure S1. Molecular characterization of FRDA iPSCs (related to Figure 1).

(A) Absolute quantitative RT-PCR analysis of the expression levels of retrovirally expressed transcription factors used during reprogramming in GM03816-iPS4 compared to GM03816 fibroblasts at day 4 after transduction with the four reprogramming vectors. Quantitation of the levels of the retroviral encoded RNAs reveals no detectable presence of *cMYC*, *KLF4*, and *SOX2* transcripts and 0.3 – 0.5 transcripts of *OCT4* per cell, which is at or near the background level of detection in our assays. ND, not detected.

(B) Metaphase spread of FRDA donor fibroblasts GM03816 and FRDA iPSC line GM03816-iPS4.

(**C** – **E**) Quantitative ChIP data of H3K9 acetylation (**A**), H4K5 acetylation (**B**), and H3K9 tri-methylation (**C**) at the promoter of the *FXN* gene as well as regions directly upstream (up GAA) and downstream (down GAA) of the intronic GAA•TTC repeat expansion. Error bars = SEM of triplicate measurement; ND, not detected.

(F) Representative *in vivo* differentiation assay for assessing the pluripotency of FRDA iPSCs. Teratoma tissue sections were H&E stained and imaged by brightfield microscopy. Differentiated tissues were found representing ectoderm (neural tissue, panels i and iv), mesoderm (cartilage, panel ii; adipose tissue, panel v), and endoderm (gut epithelia, panel iii; thyroid-like gland, panel vi).

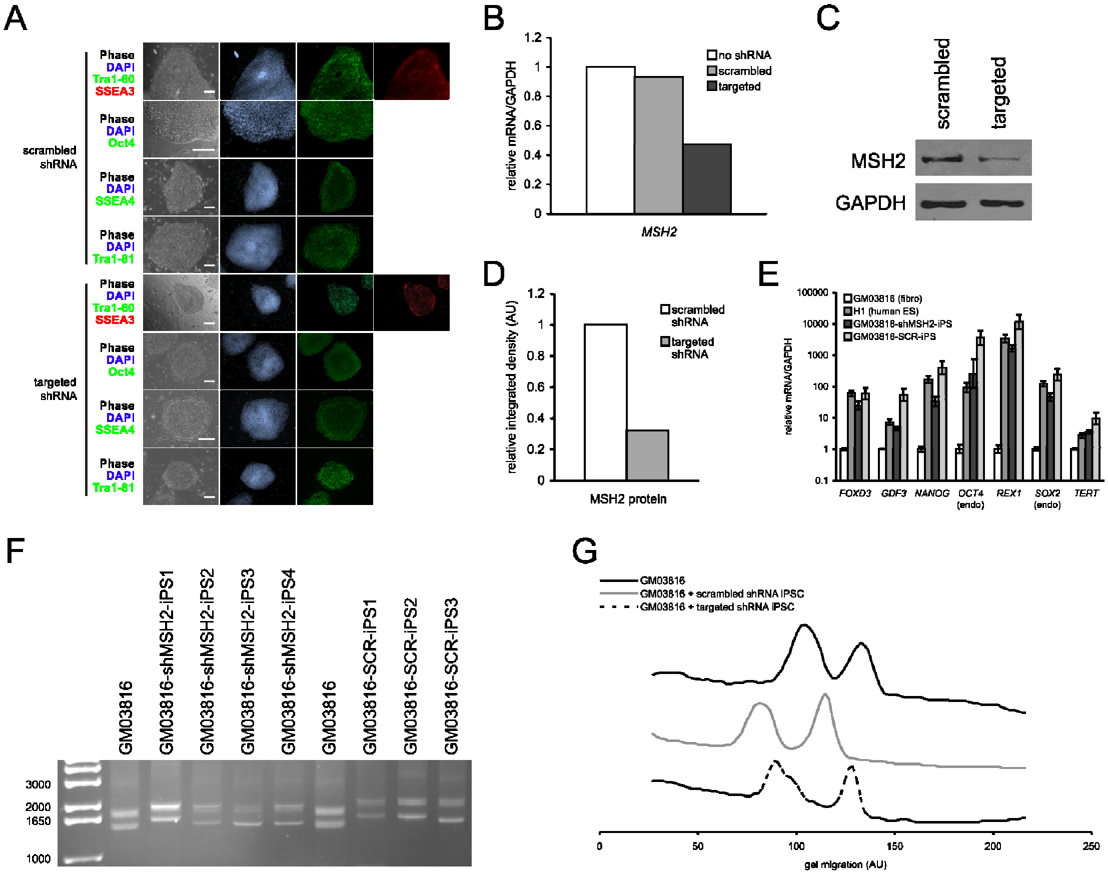
(G) Differentially expressed miRNAs as compared between GM03816-iPS4 and fibroblasts (FRDA and normal). Eleven miRNAs were upregulated, and 29 miRNAs were down-regulated. Green bars denote higher expression in fibroblasts, orange bars denote higher expression in GM03816-iPS4.

(H) Differentially expressed miRNAs as compared between the FRDA iPSC line GM03816-iPS4 and an unaffected iPSC line. Blue bars represent miRNAs with greater expression in unaffected iPSCs, and the red bar represents a miRNA with greater expression in GM03816-iPS4.

Table S1. Functional clustering of genes differentially expressed in FRDA iPSCs compared to unaffected pluripotent stem cells (related to Figure 1). The top significant annotation clusters are shown. The enrichment score for each group is based on the EASE scores (modified exact Fisher's p-value) for each term member. The p-values were determined by the Fisher Exact Probability Value for gene-enrichment analysis.
(Excel file attached as KuTableS1.xls)

Table S2. Significant enrichment of Gene Ontology terms (Biological Process) in FRDA iPSCs (related to Figure 1). Differentially expressed genes between database iPSCs and FRDA iPSCs are listed that meet a GO analysis significance criteria of $p < 0.05$.
(Excel file attached as KuTableS2.xls)

Table S3. Simple normalized data from miRNA expression analysis (related to Figure 1). Signal intensity data were LOWESS normalized to compensate for chip effects. Normalized data for all probes are listed.
(Excel file attached as KuTableS3.xls)



H

Summary of MSH2 shRNA silencing followed by reprogramming experiment				
		fibroblast	scrambled shRNA	targeted shRNA
PCR product length in kb (sample size)	large band	1.92 ± 0.03 (2)	2.26 ± 0.01 (3)	2.06 ± 0.05 (4)
	small band	1.58 ± 0.03 (2)	1.74 ± 0.06 (3)	1.64 ± 0.05 (4)
Appr. GAA repeats	large band	470 ± 10	585 ± 5	520 ± 20
	small band	360 ± 10	415 ± 20	380 ± 20
p value against scrambled shRNA	large band	0.0421	N/A	0.00567
	small band	0.0311	N/A	0.120

Figure S2. shRNA silencing of *MSH2* in FRDA iPSCs and fibroblasts (related to Figure 4). (**A**) Contrast enhanced immunostaining of pluripotency markers of GM03816-iPS4 FRDA iPSCs with stable *MSH2*-targeted shRNA and a scrambled shRNA control. Phase contrast (gray); nuclear staining (blue); pluripotency markers staining (green and red) is as denoted by the colored text labels. Tra1-60 and Tra1-81, surface markers; SSEA-3 and -4, stage-specific embryonic antigens; Oct4, transcription factor. Scale bars = 0.25 mm.

(B) *MSH2* mRNA levels of targeted and scrambled shRNA-expressing GM03816 FRDA fibroblasts.

(C) Western blot of MSH2 protein in GM03816 FRDA fibroblasts with scrambled shRNA and targeted shRNA. GAPDH, loading control.

(D) Densitometric analysis of MSH2 protein normalized to GAPDH of previous panel.

(E) Quantitative RT-PCR analysis of various pluripotency mRNAs in reprogrammed shRNA-expressing GM03816 FRDA fibroblasts, white bars; H1 hESCs, medium grey; reprogrammed GM03816 fibroblasts expressing *MSH2*-targeted shRNA (GM03816-shMSH2-IPS), dark grey; reprogrammed GM03816 fibroblasts expressing a scrambled shRNA control (GM03816-SCR-iPS), light grey. Error bars = SEM of duplicate measurements.

(F) PCR analysis of GAA•TTC repeat lengths of GM03816 FRDA fibroblasts and corresponding shRNA-expressing iPSC clones. Lanes are the following (left to right): GM03816 FRDA fibroblasts (GM03816), four *MSH2*-targeted shRNA-expressing iPSC clones (GM03816-shMSH2-iPS1 to 4), GM03816 FRDA fibroblasts, three scrambled shRNA-expressing iPSC clones (GM03816-SCR-iPS1 to 3).

(G) Signal intensity traces of ethidium-stained agarose gel from panel F. Higher migration represents smaller PCR bands (traces are from single samples and are not representative of pooled data). Traces of PCR products from GM03816 FRDA fibroblasts, solid black line; from reprogrammed GM03816 fibroblasts expressing a scrambled shRNA control, solid grey line; from reprogrammed GM03816 fibroblasts expressing *MSH2*-targeted shRNA, dashed black line.

(H) Summary of pooled repeat GAA•TTC repeat length data.

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Generation of viruses

Phoenix-amphotropic cells were transfected overnight with reprogramming retrovirus plasmids using the Fugene6 reagent (Roche) according to the manufacturer. After initial transfection, cells were incubated at 32℃ for 48 h, with virus-c ontaining supernatant collected every twelve hours. Plasmids used included the four described by Takahashi and colleagues (Takahashi et al., 2007) (pMXs-cMyc, pMXs-KLF4, pMXs-Oct4, pMXs-Sox2; obtained from Addgene). Additionally, a VSV-g plasmid was used, a generous gift from the laboratory of W. Balch. Lentiviral shRNA constructs were generated by cloning an *MSH2*-targeted oligonucleotide (5'-CCGGATGGAGAATCAGGTTGCAGTTTCATCACTTCAAGAGAGTGATGAAACTGCAACCTGATTCTCCATTTTTTG-3') into the vector pLKO.1-puro (Sigma-Aldrich) at AgeI and EcoRI sites downstream of the U6 promoter. A vector containing a scrambled sequence shRNA was obtained from Addgene (#1864). Lentiviral particles were then packaged by co-transfecting human 293 cells using Fugene6 reagent (Roche) with shRNA constructs along with psPAX2 and pMD2.G helper plasmids (both obtained from Addgene, #12260 and #12259, respectively) in hES media. Transfected cells were grown at 37℃ for a total of 60 h, with lentivirus-containing supernatant collected every 24 h for the last 48 h. Both retroviral- and lentiviral-containing supernatant were filtered through a 0.45 µm cellulose-acetate mesh to remove any contaminating cells or cell debris.

Immunocytochemistry

Primary antibodies Oct4, Tra1-60, Tra1-81, SSEA3, SSEA4, were obtained from Chemicon (MAB4305, MAB4360, MAB4381, MAB4303, and MAB4304) and were all used at 1:50 dilution except MAB4303 (used at 1:25). Fluorescent secondary antibodies were obtained from Santa Cruz Biotechnology (anti-mouse Texas Red conjugate, anti-mouse FITC conjugate, anti-rat

Texas Red conjugate, and anti-rat FITC conjugate). All secondary antibodies were used at 1:100 dilution.

Teratoma analysis

One million iPSCs were injected into the left testes capsules of immunocompromised mice (NOD.CB17-Prkdc^{scid}/J) as described (Gertow et al., 2007). Cells were allowed to grow and differentiated into teratomas for eight to twelve weeks, after which time animals were euthanized, and tumors were extracted. Subsequently, teratomas were fixed overnight in formalin, sectioned at a thickness of 3 µm and mounted onto slides, and stained with hematoxylin and eosin. All animal work was approved by the Institutional Animal Care and Use Committee at The Scripps Research Institute.

Karyotype analysis

Cultures were analyzed for karyotype through Cell Line Genetics.

PCR and quantitative RT-PCR

Quantitation of PCR band sizes was performed using an inverse power function directly correlating gel migration of a molecular weight ladder to its known sizes. PCR products from the *FXN* locus contain 499 bp of non-repeat sequences, so GAA•TTC repeat number estimations were adjusted accordingly. For *FXN* GAA•TTC repeat amplification, the primers GAA-104F and GAA-629R were used (Rindler et al., 2006) in 20 µL reactions cycled through the following conditions: 98℃ denaturation for 5 sec, 70℃ annealing for 15 sec, 72℃ extension for 90 sec for forty cycles with a five minute initial denaturation and a five minute final extension using the Phusion enzyme (New England Biolabs). For amplification of other GAA•TTC-containing loci, Phusion enzyme was used with the following primers: 2q36F (5’-AAAAGGGCAACATGAACTACTG-3’) and 2q36R (5’-ACTTTTGCCCAGAGATAACTC-3’);

4q31.1F (5’-AGCTTTGCTAGGAACCAATATG-3’) and 4q31.1R (5’-TGTCAGATAACTGAACTTGTAC-3’) (Clark et al., 2006). Cycling conditions consisted of a 98℃ denaturation for 5 sec, 64℃ annealing for 15 sec, 72℃ extension for 15 sec for 35 cycles with a 5 min initial denaturation and a 5 min final extension. Primers used for qRT-PCR are as follows: FXN-F (5’-CAGAGGAAACGCTGGGACTCT-3’) and FXN-R (5’-AGCCAGATTTGCTTGTTTGG-3’) (Herman et al., 2006). Pluripotent marker primer sequences are previously described (Huangfu et al., 2008; Park et al., 2008). Additionally, *MSH2*, *MSH3*, and *OGG1* levels were probed with the following primers: MSH2_RT02F (5’-GGAAAAGAAGATGCAGTCAACA-3’), MSH2_RT02R (5’-CAAACTGTGCACTGGAATCC-3’); MSH3_RT03F (5’-CACATGGGATTCTTGGTCAGT-3’), MSH3_RT03R (5’-GCTGCAATTCCTCTAGTTATTTGG-3’); OGG1_RT04F (5’-GCAGCTACGAGAGTCCTCATAT-3’), and OGG1_RT04R (5’-GCTTGTCTAGGGCCATCA-3’). All qRT-PCR signals were normalized to *GAPDH* (forward primer, 5’-GAGTCAACGGATTTGGTCGT-3’; reverse primer, 5’-GAGGTCAATGAAGGGGTCAT-3’). Reverse transcription was performed at 50℃ for 20 min, followed by PCR cycling at 95℃ for 30 sec, 55℃ for 30 sec, and 72℃ for 30 sec for 40 cycles.

Western analysis

Blocking, antibody incubation, and washes were performed in 5% milk in TBST (137 mM NaCl, 2.7 mM KCl, 25 mM Tris, 0.1% Tween-20). Washes after primary and secondary antibody incubation consisted of three 5 min washes. MSH2 and GAPDH antibodies were obtained from Abcam (ab52266 and ab9484, respectively) and were used at 1:4000 and 1:1000 dilutions, respectively. Ribosomal protein L13a antibody was obtained from Cell Signaling (2765S) and used at a 1:1000 dilution. Anti-mouse HRP secondary antibody was purchased from Santa Cruz Biotechnologies (sc-2005), and anti-rabbit HRP secondary antibody was purchased from Cell Signaling (7074). All secondary antibodies were used at a dilution of 1:1000.

Chromatin immunoprecipitation

ChIP was performed as described with some modifications (Herman et al., 2006). For histone tail modification immunoprecipitations, cells were crosslinked as described, and for MMR enzyme immunoprecipitations, cells were first crosslinked with 1.5 mM dithiobis-succinimidyl propionate (DSP) for 20 min followed by 4% formaldehyde crosslinking as described. For PCR detection, the following primers were used: -1254-F (5'-AGTACCTTCCCATCTTCTCTGC-3') and -1254-R (5'-GTGAATAGCCACAGCATTCC-3'); 11482-F (5'-TCCAAGTTCCATTGGCCAGAAAGG-3') and 11482-R (5'-AAGGCCACACCACTAAGTTCTTCC-3'); SATA-F (5'-CTGCACTACCTGAAGAGGAC-3') and SATA-R (5'-GATGGTTCAACACTCTTACA-3') (Jiang et al., 2004). All other primers used are previously described (Herman et al., 2006).

MicroRNA analysis

Total RNA including miRNA fraction was isolated using MiRNeasy Mini kit (Qiagen) according to manufacturer recommendations. Quality of RNA was determined using Nanodrop absorbance measurements and a 2100 Bioanalyzer (Agilent Technologies). All RNA samples used in microarray experiments demonstrated a RNA integrity number (RIN) of 10. MicroRNA microarray assays were performed using µParaflo microfluidic chips (miR human 14.0 array chips based on Sanger miRBase release 14; LC Sciences) starting with 2- 5 µg of total RNA sample. To allow direct comparison between different samples and avoid dye bias, all samples were labeled with the same dye (Cy3) and single chip hybridization was carried out for each sample. Raw data were normalized by the LOWESS method on the background-subtracted data. A Student's t-test was performed at a significance level of $\alpha < 0.01$ to analyze the statistical significance of the signal differences between the groups (human iPSC versus human fibroblasts and FRDA iPSC versus control iPSC). Because low signal intensity affects reliability of microarray results, only data sets harboring at least one sample with average signal intensity greater than 500 were considered. For selected miRNAs, validation of differential expression was conducted using TaqMan quantitative real-time PCR (Applied Biosystems) according to the manufacturer recommendations.

SUPPLEMENTAL REFERENCES

Clark, R.M., Bhaskar, S.S., Miyahara, M., Dalgliesh, G.L., and Bidichandani, S.I. (2006). Expansion of GAA trinucleotide repeats in mammals. Genomics *87*, 57-67.

Gertow, K., Przyborski, S., Loring, J.F., Auerbach, J.M., Epifano, O., Otonkoski, T., Damjanov, I., and Ahrlund-Richter, L. (2007). Isolation of human embryonic stem cell-derived teratomas for the assessment of pluripotency. Curr Protoc Stem Cell Biol *Chapter 1*, Unit1B.4.

Herman, D., Jenssen, K., Burnett, R., Soragni, E., Perlman, S.L., and Gottesfeld, J.M. (2006). Histone deacetylase inhibitors reverse gene silencing in Friedreich's ataxia. Nat Chem Biol *2*, 551--558.

Huangfu, D., Osafune, K., Maehr, R., Guo, W., Eijkelenboom, A., Chen, S., Muhlestein, W., and Melton, D.A. (2008). Induction of pluipotent stem cells from primary human fibroblasts with only Oct4 and Sox2. Nat Biotechnol *26*, 1269-1275.

Jiang, G., Yang, F., Sanchez, C., and Ehrlich, M. (2004). Histone modification in constitutive heterochromatin versus unexpressed euchromatin in human cells. Journal of cellular biochemistry *93*, 286-300.

Park, I.-H., Zhao, R., West, J.A., Yabuuchi, A., Huo, H., Ince, T.A., Lerou, P.H., Lensch, M.W., and Daley, G.Q. (2008). Reprogramming of human somatic cells to pluripotency with defined factors. Nature *451*, 141-146.

Rindler, P.M., Clark, R.M., Pollard, L.M., De Biase, I., and Bidichandani, S.I. (2006). Replication in mammalian cells recapitulates the locus-specific differences in somatic instability of genomic GAA triplet-repeats. Nucl Acids Res *34*, 6352-6361.

Takahashi, K., Okita, K., Nakagawa, M., and Yamanaka, S. (2007). Induction of pluripotent stem cells from fibroblast cultures, pp. -3089.

Table S1. Functional clustering of genes differentially expressed in FRDA iPS cells compared to normal pluripotent stem cells.

Annotation Cluster 1: **Enrichment Score: 15.002**

Annotation Category:	Annotation Term:	# genes:	% of total in category:	P-Value:	Fold Enrichment:	FDR:
GOTERM_CC	GO:0031974~membrane-enclosed lumen	372	16.424	1.17E-21	1.560	1.76E-18
GOTERM_CC	GO:0070013~intracellular organelle lumen	359	15.850	2.32E-21	1.571	3.48E-18
GOTERM_CC	GO:0043233~organelle lumen	362	15.982	1.96E-20	1.548	2.95E-17
GOTERM_CC	GO:0031981~nuclear lumen	288	12.715	1.20E-15	1.546	1.83E-12
GOTERM_CC	GO:0005654~nucleoplasm	177	7.815	4.46E-10	1.562	6.71E-07
GOTERM_CC	GO:0044451~nucleoplasm part	105	4.636	3.40E-05	1.473	0.050988291

Annotation Cluster 2: **Enrichment Score: 6.049**

Annotation Category:	Annotation Term:	# genes:	% of total in category:	P-Value:	Fold Enrichment:	FDR:
GOTERM_BP	GO:0006281~DNA repair	70	3.091	2.65E-07	1.859	4.92E-04
GOTERM_BP	GO:0006259~DNA metabolic process	108	4.768	3.75E-07	1.609	6.96E-04
GOTERM_BP	GO:0006974~response to DNA damage stimulus	85	3.753	4.67E-07	1.718	8.67E-04
SP_PIR_KEYWORDS	dna repair	47	2.075	1.28E-06	2.098	0.001932326
GOTERM_BP	GO:0033554~cellular response to stress	115	5.077	2.00E-06	1.532	0.003722577
SP_PIR_KEYWORDS	DNA damage	48	2.119	4.25E-06	1.996	0.00641003

Annotation Cluster 3: **Enrichment Score: 5.549**

Annotation Category:	Annotation Term:	# genes:	% of total in category:	P-Value:	Fold Enrichment:	FDR:
SP_PIR_KEYWORDS	mitochondrion	153	6.755	1.15E-08	1.568	1.73E-05
GOTERM_CC	GO:0005739~mitochondrion	201	8.874	2.81E-08	1.439	4.22E-05
SP_PIR_KEYWORDS	transit peptide	97	4.283	5.86E-08	1.737	8.84E-05
UP_SEQ_FEATURE	transit peptide:Mitochondrion	92	4.062	8.14E-07	1.670	0.001553832
GOTERM_CC	GO:0044429~mitochondrial part	114	5.033	8.29E-06	1.491	0.012458482
GOTERM_CC	GO:0005759~mitochondrial matrix	51	2.252	7.57E-05	1.749	0.113590451
GOTERM_CC	GO:0031980~mitochondrial lumen	51	2.252	7.57E-05	1.749	0.113590451
GOTERM_CC	GO:0005740~mitochondrial envelope	73	3.223	0.005522769	1.356	7.98269258

Annotation Cluster 4: **Enrichment Score: 4.901**

Annotation Category:	Annotation Term:	# genes:	% of total in category:	P-Value:	Fold Enrichment:	FDR:
SP_PIR_KEYWORDS	protein transport	105	4.636	5.08E-10	1.846	7.66E-07
GOTERM_BP	GO:0008104~protein localization	168	7.417	5.60E-07	1.436	0.001041072
GOTERM_BP	GO:0045184~establishment of protein localization	149	6.578	9.79E-07	1.461	0.001819088
GOTERM_BP	GO:0015031~protein transport	147	6.490	1.51E-06	1.455	0.002796457
GOTERM_BP	GO:0046907~intracellular transport	130	5.740	1.74E-06	1.492	0.003228339
SP_PIR_KEYWORDS	transport	238	10.508	7.46E-04	1.215	1.119761515
GOTERM_BP	GO:0034613~cellular protein localization	77	3.400	0.001427156	1.413	2.618574789
GOTERM_BP	GO:0070727~cellular macromolecule localization	77	3.400	0.001746088	1.402	3.194822092
GOTERM_BP	GO:0006886~intracellular protein transport	68	3.002	0.005692897	1.371	10.06410611

Annotation Cluster 5: **Enrichment Score: 4.806**

Annotation Category:	Annotation Term:	# genes:	% of total in category:	P-Value:	Fold Enrichment:	FDR:
SP_PIR_KEYWORDS	nucleotide-binding	274	12.097	6.41E-09	1.386	9.66E-06
SP_PIR_KEYWORDS	atp-binding	219	9.669	7.67E-08	1.408	1.16E-04
GOTERM_MF	GO:0000166~nucleotide binding	368	16.247	5.07E-07	1.253	8.40E-04
GOTERM_MF	GO:0032553~ribonucleotide binding	297	13.113	2.75E-05	1.236	0.045510595
GOTERM_MF	GO:0032559~adenyl ribonucleotide binding	247	10.905	3.73E-05	1.261	0.06166884
GOTERM_MF	GO:0005524~ATP binding	243	10.728	5.69E-05	1.257	0.09421836
GOTERM_MF	GO:0017076~purine nucleotide binding	304	13.422	9.87E-05	1.211	0.163363359
GOTERM_MF	GO:0030554~adenyl nucleotide binding	254	11.214	1.56E-04	1.231	0.258601975
GOTERM_MF	GO:0001882~nucleoside binding	258	11.391	2.08E-04	1.223	0.344093138
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	147	6.490	7.20E-04	1.295	1.365711199

Annotation Cluster 6: **Enrichment Score: 4.365**

Annotation Category:	Annotation Term:	# genes:	% of total in category:	P-Value:	Fold Enrichment:	FDR:
SP_PIR_KEYWORDS	rna-binding	120	5.298	4.31E-12	1.895	6.51E-09
SMART	SM00360:RRM	49	2.163	9.95E-06	1.908	0.013776677
INTERPRO	IPR000504:RNA recognition motif, RNP-1	49	2.163	2.66E-05	1.848	0.047158519
INTERPRO	IPR012677:Nucleotide-binding, alpha-beta plait	47	2.075	1.45E-04	1.755	0.257530744
UP_SEQ_FEATURE	domain:RRM 1	26	1.148	2.22E-04	2.182	0.422713381
UP_SEQ_FEATURE	domain:RRM	24	1.060	0.011336554	1.709	19.55490368
UP_SEQ_FEATURE	domain:RRM 3	10	0.442	0.128512484	1.695	92.75769121

Annotation Cluster 7: **Enrichment Score: 4.214**

Annotation Category:	Annotation Term:	# genes:	% of total in category:	P-Value:	Fold Enrichment:	FDR:
GOTERM_CC	GO:0030529~ribonucleoprotein complex	119	5.254	9.32E-11	1.799	1.40E-07
GOTERM_BP	GO:0006412~translation	81	3.576	3.81E-08	1.845	7.08E-05
SP_PIR_KEYWORDS	protein biosynthesis	48	2.119	3.10E-07	2.177	4.68E-04
SP_PIR_KEYWORDS	ribosomal protein	47	2.075	7.96E-07	2.132	0.001201458
GOTERM_CC	GO:0005840~ribosome	51	2.252	1.67E-05	1.847	0.025142551
GOTERM_MF	GO:0003735~structural constituent of ribosome	42	1.854	4.45E-05	1.910	0.073727362
SP_PIR_KEYWORDS	ribosome	22	0.971	6.48E-05	2.570	0.097741219
GOTERM_CC	GO:0033279~ribosomal subunit	33	1.457	1.29E-04	2.007	0.193780801
KEGG_PATHWAY	hsa03010:Ribosome	25	1.104	0.001050194	1.975	1.298561887
GOTERM_MF	GO:0005198~structural molecule activity	106	4.680	0.005522805	1.278	8.762266884
GOTERM_BP	GO:0006414~translational elongation	24	1.060	0.005927105	1.792	10.45688556
GOTERM_CC	GO:0044445~cytosolic part	31	1.369	0.010208737	1.588	14.28520693
GOTERM_CC	GO:0015935~small ribosomal subunit	16	0.706	0.012012764	1.977	16.60230564
GOTERM_CC	GO:0022626~cytosolic ribosome	18	0.795	0.026537729	1.730	33.23808574

Annotation Cluster 8: Enrichment Score: 4.076

Annotation Category:	Annotation Term:	# genes:	% of total in category:	P-Value:	Fold Enrichment:	FDR:
SP_PIR_KEYWORDS	er-golgi transport	27	1.192	1.60E-06	2.774	0.002407149
GOTERM_BP	GO:0048193~Golgi vesicle transport	34	1.501	1.62E-04	1.957	0.300731261
GOTERM_BP	GO:0006888~ER to Golgi vesicle-mediated transport	14	0.618	0.002274073	2.514	4.14169915

Annotation Cluster 9: Enrichment Score: 3.586

Annotation Category:	Annotation Term:	# genes:	% of total in category:	P-Value:	Fold Enrichment:	FDR:
GOTERM_CC	GO:0015630~microtubule cytoskeleton	108	4.768	4.44E-06	1.531	0.006663914
SP_PIR_KEYWORDS	cytoskeleton	109	4.812	4.29E-05	1.461	0.064765655
GOTERM_CC	GO:0005815~microtubule organizing center	55	2.428	9.68E-05	1.692	0.145329255
GOTERM_CC	GO:0005813~centrosome	50	2.208	1.06E-04	1.738	0.159772816
GOTERM_CC	GO:0005856~cytoskeleton	207	9.139	0.009044798	1.167	12.75849627
GOTERM_CC	GO:0044430~cytoskeletal part	145	6.402	0.017165084	1.186	22.9021064

Annotation Cluster 10: Enrichment Score: 3.437

Annotation Category:	Annotation Term:	# genes:	% of total in category:	P-Value:	Fold Enrichment:	FDR:
SP_PIR_KEYWORDS	nucleus	687	30.331	2.08E-22	1.368	3.13E-19
SP_PIR_KEYWORDS	Transcription	298	13.157	7.47E-05	1.227	0.112702515
SP_PIR_KEYWORDS	transcription regulation	286	12.627	4.02E-04	1.204	0.605171681
SP_PIR_KEYWORDS	dna-binding	246	10.861	0.028133356	1.123	34.98258999
GOTERM_BP_FAT	GO:0045449~regulation of transcription	375	16.556	0.032855487	1.087	46.24265609
GOTERM_MF_FAT	GO:0003677~DNA binding	334	14.746	0.032907704	1.095	42.53892619
GOTERM_BP_FAT	GO:0006350~transcription	303	13.377	0.055385129	1.087	65.30654029
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	216	9.536	0.086782677	1.092	77.75792027
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	257	11.347	0.124800473	1.069	91.59801713
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	249	10.993	0.166881688	1.059	96.63663159
GOTERM_MF_FAT	GO:0003700~transcription factor activity	120	5.298	0.812856895	0.940	100

Table S2. Significant Enrichment of Gene Ontology Terms (Biological Process) in FRDA iPS Cells.

Ontology Term:	# of genes	% of total in category	Fold Enrichment	p-value
GO:0007049~cell cycle	89	7.90	1.722	4.32E-07
GO:0043933~macromolecular complex subunit organization	78	6.93	1.649	1.24E-05
GO:0070271~protein complex biogenesis	60	5.33	1.784	1.55E-05
GO:0006461~protein complex assembly	60	5.33	1.784	1.55E-05
GO:0031397~negative regulation of protein ubiquitination	17	1.51	3.449	2.24E-05
GO:0031400~negative regulation of protein modification process	22	1.95	2.776	3.43E-05
GO:0065003~macromolecular complex assembly	71	6.31	1.603	8.03E-05
GO:0031396~regulation of protein ubiquitination	19	1.69	2.853	9.38E-05
GO:0022402~cell cycle process	62	5.51	1.648	1.16E-04
GO:0006281~DNA repair	37	3.29	1.956	1.42E-04
GO:0006259~DNA metabolic process	56	4.97	1.662	2.09E-04
GO:0051259~protein oligomerization	26	2.31	2.244	2.14E-04
GO:0016126~sterol biosynthetic process	10	0.89	4.290	3.59E-04
GO:0032269~negative regulation of cellular protein metabolic proces	26	2.31	2.169	3.64E-04
GO:0051444~negative regulation of ubiquitin-protein ligase activity	14	1.24	3.137	4.04E-04
GO:0051352~negative regulation of ligase activity	14	1.24	3.137	4.04E-04
GO:0006354~RNA elongation	12	1.07	3.533	4.32E-04
GO:0000278~mitotic cell cycle	43	3.82	1.745	4.72E-04
GO:0006974~response to DNA damage stimulus	43	3.82	1.731	5.57E-04
GO:0051248~negative regulation of protein metabolic process	26	2.31	2.088	6.48E-04
GO:0006368~RNA elongation from RNA polymerase II promoter	11	0.98	3.441	0.00104
GO:0051436~negative regulation of ubiquitin-protein ligase activity du	13	1.15	3.003	0.0010613
GO:0006695~cholesterol biosynthetic process	8	0.71	4.620	0.0012103
GO:0046394~carboxylic acid biosynthetic process	22	1.95	2.131	0.0014335
GO:0016053~organic acid biosynthetic process	22	1.95	2.131	0.0014335
GO:0008610~lipid biosynthetic process	37	3.29	1.720	0.0016089
GO:0051438~regulation of ubiquitin-protein ligase activity	14	1.24	2.695	0.0017841
GO:0006412~translation	37	3.29	1.678	0.0024638
GO:0051340~regulation of ligase activity	14	1.24	2.595	0.0025271
GO:0043542~endothelial cell migration	7	0.62	4.777	0.0025273
GO:0016192~vesicle-mediated transport	57	5.06	1.486	0.0026147
GO:0016125~sterol metabolic process	16	1.42	2.379	0.0026938
GO:0006631~fatty acid metabolic process	25	2.22	1.896	0.0031497
GO:0031145~anaphase-promoting complex-dependent proteasomal	12	1.07	2.772	0.0034676
GO:0008104~protein localization	80	7.10	1.362	0.003851
GO:0032268~regulation of cellular protein metabolic process	48	4.26	1.520	0.0038695

GO:0051260~protein homooligomerization	15	1.33	2.371	0.0039524
GO:0001101~response to acid	7	0.62	4.379	0.0040674
GO:0045184~establishment of protein localization	71	6.31	1.386	0.0043489
GO:0043534~blood vessel endothelial cell migration	5	0.44	6.825	0.0044002
GO:0032434~regulation of proteasomal ubiquitin-dependent protein	5	0.44	6.825	0.0044002
GO:0051726~regulation of cell cycle	36	3.20	1.633	0.0044286
GO:0007411~axon guidance	16	1.42	2.245	0.0047158
GO:0010605~negative regulation of macromolecule metabolic proces	68	6.04	1.391	0.0049039
GO:0015031~protein transport	70	6.22	1.379	0.0053541
GO:0034637~cellular carbohydrate biosynthetic process	12	1.07	2.611	0.0055498
GO:0006888~ER to Golgi vesicle-mediated transport	9	0.80	3.217	0.0057974
GO:0008652~cellular amino acid biosynthetic process	10	0.89	2.944	0.005946
GO:0016054~organic acid catabolic process	16	1.42	2.164	0.0066472
GO:0046395~carboxylic acid catabolic process	16	1.42	2.164	0.0066472
GO:0001568~blood vessel development	28	2.49	1.716	0.0067366
GO:0022403~cell cycle phase	42	3.73	1.523	0.0068625
GO:0007281~germ cell development	15	1.33	2.230	0.0068668
GO:0048514~blood vessel morphogenesis	25	2.22	1.779	0.0070162
GO:0007059~chromosome segregation	13	1.15	2.410	0.0070358
GO:0008203~cholesterol metabolic process	14	1.24	2.285	0.0076787
GO:0006352~transcription initiation	13	1.15	2.352	0.0085363
GO:0031330~negative regulation of cellular catabolic process	6	0.53	4.504	0.0086279
GO:0001944~vasculature development	28	2.49	1.675	0.0091997
GO:0031398~positive regulation of protein ubiquitination	13	1.15	2.324	0.0093747
GO:0016337~cell-cell adhesion	30	2.66	1.632	0.0097536
GO:0044271~nitrogen compound biosynthetic process	34	3.02	1.571	0.0100825
GO:0006694~steroid biosynthetic process	13	1.15	2.296	0.0102756
GO:0016051~carbohydrate biosynthetic process	15	1.33	2.105	0.0112841
GO:0006301~postreplication repair	4	0.36	7.507	0.0127603
GO:0009206~purine ribonucleoside triphosphate biosynthetic proces	14	1.24	2.145	0.0128355
GO:0006006~glucose metabolic process	19	1.69	1.865	0.0130287
GO:0000718~nucleotide-excision repair, DNA damage removal	6	0.53	4.095	0.0131243
GO:0009141~nucleoside triphosphate metabolic process	17	1.51	1.948	0.0133271
GO:0006007~glucose catabolic process	10	0.89	2.589	0.0137629
GO:0009145~purine nucleoside triphosphate biosynthetic process	14	1.24	2.123	0.0139067
GO:0009201~ribonucleoside triphosphate biosynthetic process	14	1.24	2.123	0.0139067
GO:0009063~cellular amino acid catabolic process	11	0.98	2.429	0.01395
GO:0006367~transcription initiation from RNA polymerase II promote	11	0.98	2.429	0.01395
GO:0006754~ATP biosynthetic process	13	1.15	2.193	0.0145649
GO:0051258~protein polymerization	9	0.80	2.758	0.0147162
GO:0019320~hexose catabolic process	11	0.98	2.394	0.0153737

GO:0006928~cell motion	45	4.00	1.422	0.0161083
GO:0046907~intracellular transport	59	5.24	1.348	0.0162339
GO:0006414~translational elongation	14	1.24	2.081	0.0162532
GO:0019318~hexose metabolic process	22	1.95	1.720	0.0168584
GO:0010498~proteasomal protein catabolic process	14	1.24	2.061	0.0175336
GO:0009142~nucleoside triphosphate biosynthetic process	14	1.24	2.061	0.0175336
GO:0043161~proteasomal ubiquitin-dependent protein catabolic proc	14	1.24	2.061	0.0175336
GO:0043086~negative regulation of catalytic activity	29	2.58	1.572	0.0177719
GO:0051270~regulation of cell motion	22	1.95	1.711	0.0177764
GO:0009309~amine biosynthetic process	12	1.07	2.224	0.0179549
GO:0046164~alcohol catabolic process	12	1.07	2.224	0.0179549
GO:0060284~regulation of cell development	23	2.04	1.685	0.0179551
GO:0046365~monosaccharide catabolic process	11	0.98	2.326	0.0185413
GO:0050678~regulation of epithelial cell proliferation	11	0.98	2.326	0.0185413
GO:0040008~regulation of growth	34	3.02	1.497	0.0192802
GO:0006090~pyruvate metabolic process	8	0.71	2.860	0.0196854
GO:0046034~ATP metabolic process	14	1.24	2.002	0.0218342
GO:0045669~positive regulation of osteoblast differentiation	6	0.53	3.603	0.0224605
GO:0031399~regulation of protein modification process	30	2.66	1.527	0.0225502
GO:0006366~transcription from RNA polymerase II promoter	25	2.22	1.604	0.0228482
GO:0005996~monosaccharide metabolic process	24	2.13	1.623	0.0229606
GO:0043200~response to amino acid stimulus	5	0.44	4.416	0.0230646
GO:0009205~purine ribonucleoside triphosphate metabolic process	15	1.33	1.925	0.0232245
GO:0044092~negative regulation of molecular function	33	2.93	1.483	0.0239168
GO:0000212~meiotic spindle organization	3	0.27	11.261	0.0242389
GO:0007346~regulation of mitotic cell cycle	18	1.60	1.778	0.0243404
GO:0033554~cellular response to stress	51	4.53	1.353	0.0245091
GO:0009199~ribonucleoside triphosphate metabolic process	15	1.33	1.909	0.0248012
GO:0044275~cellular carbohydrate catabolic process	12	1.07	2.120	0.0248907
GO:0000087~M phase of mitotic cell cycle	24	2.13	1.609	0.0251886
GO:0000079~regulation of cyclin-dependent protein kinase activity	9	0.80	2.502	0.0254039
GO:0042476~odontogenesis	9	0.80	2.502	0.0254039
GO:0009057~macromolecule catabolic process	67	5.95	1.288	0.0254582
GO:0048469~cell maturation	11	0.98	2.202	0.026274
GO:0009069~serine family amino acid metabolic process	6	0.53	3.465	0.0263299
GO:0033692~cellular polysaccharide biosynthetic process	6	0.53	3.465	0.0263299
GO:0030521~androgen receptor signaling pathway	7	0.62	2.919	0.0299099
GO:0042493~response to drug	23	2.04	1.599	0.0304321
GO:0009408~response to heat	9	0.80	2.413	0.0308989
GO:0048285~organelle fission	24	2.13	1.574	0.0314842
GO:0000279~M phase	32	2.84	1.460	0.0317405

GO:0009144~purine nucleoside triphosphate metabolic process	15	1.33	1.846	0.0319098
GO:0009310~amine catabolic process	11	0.98	2.117	0.0334198
GO:0044265~cellular macromolecule catabolic process	62	5.51	1.284	0.0336404
GO:0007098~centrosome cycle	5	0.44	3.951	0.033811
GO:0006096~glycolysis	8	0.71	2.556	0.0345132
GO:0009259~ribonucleotide metabolic process	17	1.51	1.736	0.0352636
GO:0051437~positive regulation of ubiquitin-protein ligase activity du	10	0.89	2.208	0.035458
GO:0009260~ribonucleotide biosynthetic process	15	1.33	1.816	0.035973
GO:0007067~mitosis	23	2.04	1.570	0.0363068
GO:0000280~nuclear division	23	2.04	1.570	0.0363068
GO:0006261~DNA-dependent DNA replication	9	0.80	2.330	0.0371569
GO:0070230~positive regulation of lymphocyte apoptosis	3	0.27	9.009	0.0386307
GO:0010629~negative regulation of gene expression	45	4.00	1.341	0.0387464
GO:0006417~regulation of translation	16	1.42	1.754	0.0388236
GO:0019439~aromatic compound catabolic process	5	0.44	3.754	0.0401068
GO:0009411~response to UV	9	0.80	2.290	0.0405835
GO:0009150~purine ribonucleotide metabolic process	16	1.42	1.741	0.0409987
GO:0051443~positive regulation of ubiquitin-protein ligase activity	10	0.89	2.145	0.0416528
GO:0032886~regulation of microtubule-based process	8	0.71	2.451	0.0420876
GO:0042475~odontogenesis of dentine-containing tooth	7	0.62	2.695	0.0423913
GO:0007265~Ras protein signal transduction	13	1.15	1.859	0.0459424
GO:0009152~purine ribonucleotide biosynthetic process	14	1.24	1.797	0.0470635
GO:0016481~negative regulation of transcription	41	3.64	1.341	0.0479339
GO:0031329~regulation of cellular catabolic process	9	0.80	2.215	0.0480517
GO:0008202~steroid metabolic process	21	1.87	1.561	0.0483438

Table S3. Simple normalized data from miRNA expression analysis.

No.	Reporter Name	FRDA_iPS_3816 Averaged Signal	FRDA_iPS_4078 Averaged Signal	Control_iPS_8333 A Averaged Signal
1	hsa-let-7a	217	158	400
2	hsa-let-7a*	35	6	22
3	hsa-let-7a-2*	36	10	44
4	hsa-let-7b	100	141	166
5	hsa-let-7b*	48	16	50
6	hsa-let-7c	136	120	265
7	hsa-let-7c*	33	48	23
8	hsa-let-7d	141	118	271
9	hsa-let-7d*	47	30	55
10	hsa-let-7e	92	103	170
11	hsa-let-7e*	34	8	20
12	hsa-let-7f	149	59	348
13	hsa-let-7f-1*	49	11	34
14	hsa-let-7f-2*	37	8	17
15	hsa-let-7g	62	43	144
16	hsa-let-7g*	47	22	25
17	hsa-let-7i	134	87	213
18	hsa-let-7i*	31	9	21
19	hsa-miR-1	20	17	21
20	hsa-miR-100	62	33	65
21	hsa-miR-100*	36	12	21
22	hsa-miR-101	251	30	160
23	hsa-miR-101*	69	21	28
24	hsa-miR-103	466	210	488
25	hsa-miR-103-2*	35	21	33
26	hsa-miR-103-as	45	12	34
27	hsa-miR-105	53	20	33
28	hsa-miR-105*	13	67	14
29	hsa-miR-106a	4,125	332	2,248
30	hsa-miR-106a*	62	8	33
31	hsa-miR-106b	358	67	376
32	hsa-miR-106b*	64	57	66
33	hsa-miR-107	416	132	450
34	hsa-miR-10a	50	47	76
35	hsa-miR-10a*	28	105	28
36	hsa-miR-10b	67	38	77
37	hsa-miR-10b*	34	232	28
38	hsa-miR-1178	42	130	28
39	hsa-miR-1179	29	43	31
40	hsa-miR-1180	46	113	74

41	hsa-miR-1181	90	233	65
42	hsa-miR-1182	19	288	39
43	hsa-miR-1183	33	146	71
44	hsa-miR-1184	15	38	32
45	hsa-miR-1185	36	47	28
46	hsa-miR-1197	41	44	38
47	hsa-miR-1200	16	14	27
48	hsa-miR-1201	48	19	63
49	hsa-miR-1202	14	171	45
50	hsa-miR-1203	11	81	44
51	hsa-miR-1204	11	37	25
52	hsa-miR-1205	8	39	19
53	hsa-miR-1206	13	26	30
54	hsa-miR-1207-3p	1	23	23
55	hsa-miR-1207-5p	50	705	88
56	hsa-miR-1208	222	502	129
57	hsa-miR-122	15	49	20
58	hsa-miR-122*	23	7	13
59	hsa-miR-1224-3p	99	12	45
60	hsa-miR-1224-5p	128	508	106
61	hsa-miR-1225-3p	39	48	29
62	hsa-miR-1225-5p	18	116	27
63	hsa-miR-1226	31	23	20
64	hsa-miR-1226*	21	86	17
65	hsa-miR-1227	117	32	119
66	hsa-miR-1228	81	55	88
67	hsa-miR-1228*	19	847	36
68	hsa-miR-1229	95	64	67
69	hsa-miR-1231	95	1,501	66
70	hsa-miR-1233	44	21	27
71	hsa-miR-1234	88	125	82
72	hsa-miR-1236	22	12	21
73	hsa-miR-1237	101	102	68
74	hsa-miR-1238	64	78	67
75	hsa-miR-124	38	89	71
76	hsa-miR-124*	18	49	25
77	hsa-miR-1243	24	71	16
78	hsa-miR-1244	18	79	46
79	hsa-miR-1245	22	41	17
80	hsa-miR-1246	1,881	422	4,061
81	hsa-miR-1247	59	22	36
82	hsa-miR-1248	32	13	22
83	hsa-miR-1249	185	107	116
84	hsa-miR-1250	18	54	16

85	hsa-miR-1251	12	23	23
86	hsa-miR-1252	21	27	30
87	hsa-miR-1253	34	31	18
88	hsa-miR-1254	20	126	25
89	hsa-miR-1255a	32	100	21
90	hsa-miR-1255b	14	88	17
91	hsa-miR-1256	16	16	17
92	hsa-miR-1257	24	70	27
93	hsa-miR-1258	17	51	20
94	hsa-miR-1259	31	23	27
95	hsa-miR-125a-3p	39	466	109
96	hsa-miR-125a-5p	241	23	326
97	hsa-miR-125b	740	173	708
98	hsa-miR-125b-1*	18	82	26
99	hsa-miR-125b-2*	43	161	53
100	hsa-miR-126	116	54	90
101	hsa-miR-126*	25	12	36
102	hsa-miR-1260	272	189	173
103	hsa-miR-1261	33	41	33
104	hsa-miR-1262	27	71	25
105	hsa-miR-1263	29	35	35
106	hsa-miR-1264	40	12	23
107	hsa-miR-1265	29	63	32
108	hsa-miR-1266	40	116	29
109	hsa-miR-1267	31	14	38
110	hsa-miR-1268	136	1,418	137
111	hsa-miR-1269	20	35	50
112	hsa-miR-1270	20	85	36
113	hsa-miR-1271	27	30	54
114	hsa-miR-1272	39	61	51
115	hsa-miR-1273	41	18	53
116	hsa-miR-127-3p	80	56	103
117	hsa-miR-1274a	93	20	79
118	hsa-miR-1274b	122	55	107
119	hsa-miR-1275	219	3,666	165
120	hsa-miR-127-5p	82	65	25
121	hsa-miR-1276	34	58	29
122	hsa-miR-1277	44	4	32
123	hsa-miR-1278	36	11	21
124	hsa-miR-1279	31	2	26
125	hsa-miR-128	107	6	137
126	hsa-miR-1280	2,005	2,400	1,140
127	hsa-miR-1281	92	99	101
128	hsa-miR-1282	13	6	29

129	hsa-miR-1283	29	9	37
130	hsa-miR-1284	120	13	44
131	hsa-miR-1285	26	94	57
132	hsa-miR-1286	22	73	32
133	hsa-miR-1287	16	59	35
134	hsa-miR-1288	33	49	34
135	hsa-miR-1289	37	47	33
136	hsa-miR-129*	52	54	37
137	hsa-miR-1290	91	91	167
138	hsa-miR-1291	35	76	33
139	hsa-miR-1292	59	198	57
140	hsa-miR-1293	31	81	32
141	hsa-miR-129-3p	71	59	37
142	hsa-miR-1294	27	56	37
143	hsa-miR-1295	14	63	60
144	hsa-miR-129-5p	57	146	53
145	hsa-miR-1296	38	50	41
146	hsa-miR-1297	28	65	27
147	hsa-miR-1298	36	41	28
148	hsa-miR-1299	34	81	24
149	hsa-miR-1301	15	116	41
150	hsa-miR-1302	23	24	32
151	hsa-miR-1303	25	97	45
152	hsa-miR-1304	33	47	21
153	hsa-miR-1305	76	89	58
154	hsa-miR-1306	35	58	48
155	hsa-miR-1307	105	192	84
156	hsa-miR-1308	884	304	972
157	hsa-miR-130a	354	176	208
158	hsa-miR-130a*	39	16	22
159	hsa-miR-130b	169	226	157
160	hsa-miR-130b*	67	23	88
161	hsa-miR-132	40	47	38
162	hsa-miR-132*	23	59	24
163	hsa-miR-1321	10	153	25
164	hsa-miR-1322	30	72	41
165	hsa-miR-1323	131	285	265
166	hsa-miR-1324	28	13	11
167	hsa-miR-133a	45	56	42
168	hsa-miR-133b	69	31	34
169	hsa-miR-134	43	235	388
170	hsa-miR-135a	52	16	77
171	hsa-miR-135a*	20	143	20
172	hsa-miR-135b	76	18	70

173	hsa-miR-135b*	21	84	32
174	hsa-miR-136	24	31	16
175	hsa-miR-136*	10	13	16
176	hsa-miR-137	19	19	23
177	hsa-miR-138	19	53	30
178	hsa-miR-138-1*	27	192	47
179	hsa-miR-138-2*	13	47	18
180	hsa-miR-139-3p	24	65	26
181	hsa-miR-139-5p	36	54	35
182	hsa-miR-140-3p	50	67	65
183	hsa-miR-140-5p	40	20	30
184	hsa-miR-141	40	48	16
185	hsa-miR-141*	19	29	11
186	hsa-miR-142-3p	24	26	10
187	hsa-miR-142-5p	35	8	22
188	hsa-miR-143	114	27	100
189	hsa-miR-143*	40	48	21
190	hsa-miR-144	13	15	31
191	hsa-miR-144*	19	10	19
192	hsa-miR-145	119	6	93
193	hsa-miR-145*	22	18	35
194	hsa-miR-1468	23	6	28
195	hsa-miR-1469	653	2,843	305
196	hsa-miR-146a	44	41	82
197	hsa-miR-146a*	14	2	23
198	hsa-miR-146b-3p	30	11	18
199	hsa-miR-146b-5p	47	23	74
200	hsa-miR-147	18	57	32
201	hsa-miR-1470	75	25	84
202	hsa-miR-1471	21	154	37
203	hsa-miR-147b	29	68	49
204	hsa-miR-148a	293	29	273
205	hsa-miR-148a*	40	33	47
206	hsa-miR-148b	87	17	94
207	hsa-miR-148b*	49	22	25
208	hsa-miR-149	59	21	64
209	hsa-miR-149*	278	7,706	172
210	hsa-miR-150	77	22	63
211	hsa-miR-150*	95	2,615	57
212	hsa-miR-151-3p	99	29	113
213	hsa-miR-151-5p	222	52	292
214	hsa-miR-152	55	55	79
215	hsa-miR-153	33	16	54
216	hsa-miR-1537	41	28	18

217	hsa-miR-1538	48	97	63
218	hsa-miR-1539	22	25	47
219	hsa-miR-154	35	9	28
220	hsa-miR-154*	35	20	24
221	hsa-miR-155	37	86	50
222	hsa-miR-155*	27	4	27
223	hsa-miR-15a	69	62	61
224	hsa-miR-15a*	21	19	35
225	hsa-miR-15b	347	44	581
226	hsa-miR-15b*	38	13	96
227	hsa-miR-16	1,110	224	868
228	hsa-miR-16-1*	19	46	27
229	hsa-miR-16-2*	57	7	73
230	hsa-miR-17	4,394	409	2,276
231	hsa-miR-17*	28	53	35
232	hsa-miR-181a	45	63	52
233	hsa-miR-181a*	57	225	75
234	hsa-miR-181a-2*	35	49	50
235	hsa-miR-181b	35	100	56
236	hsa-miR-181c	36	44	85
237	hsa-miR-181c*	38	120	392
238	hsa-miR-181d	36	77	56
239	hsa-miR-182	157	235	384
240	hsa-miR-182*	20	33	24
241	hsa-miR-1825	82	69	90
242	hsa-miR-1826	3,198	366	9,537
243	hsa-miR-1827	12	44	50
244	hsa-miR-183	70	35	181
245	hsa-miR-183*	27	77	55
246	hsa-miR-184	29	158	40
247	hsa-miR-185	44	70	61
248	hsa-miR-185*	24	12	34
249	hsa-miR-186	154	13	149
250	hsa-miR-186*	14	21	34
251	hsa-miR-187	50	56	69
252	hsa-miR-187*	29	122	52
253	hsa-miR-188-3p	7	40	35
254	hsa-miR-188-5p	31	204	62
255	hsa-miR-18a	422	70	410
256	hsa-miR-18a*	63	21	32
257	hsa-miR-18b	152	19	151
258	hsa-miR-18b*	61	14	43
259	hsa-miR-190	18	17	35
260	hsa-miR-1908	109	1,023	79

261	hsa-miR-1909	20	75	63
262	hsa-miR-1909*	26	79	51
263	hsa-miR-190b	16	17	39
264	hsa-miR-191	187	45	216
265	hsa-miR-191*	53	34	53
266	hsa-miR-1910	45	29	46
267	hsa-miR-1911	46	26	44
268	hsa-miR-1911*	17	18	30
269	hsa-miR-1912	18	51	34
270	hsa-miR-1913	120	102	97
271	hsa-miR-1914	91	42	59
272	hsa-miR-1914*	53	174	50
273	hsa-miR-1915	1,365	3,770	664
274	hsa-miR-1915*	23	44	42
275	hsa-miR-192	53	56	73
276	hsa-miR-192*	17	26	19
277	hsa-miR-193a-3p	32	16	36
278	hsa-miR-193a-5p	111	1,159	70
279	hsa-miR-193b	54	27	47
280	hsa-miR-193b*	20	447	26
281	hsa-miR-194	42	43	65
282	hsa-miR-194*	17	98	32
283	hsa-miR-195	89	82	70
284	hsa-miR-195*	49	144	60
285	hsa-miR-196a	35	55	30
286	hsa-miR-196a*	23	67	32
287	hsa-miR-196b	28	54	24
288	hsa-miR-196b*	31	18	28
289	hsa-miR-197	233	98	140
290	hsa-miR-1972	63	90	59
291	hsa-miR-1973	48	50	55
292	hsa-miR-1974	1,097	161	1,435
293	hsa-miR-1975	2,223	114	1,828
294	hsa-miR-1976	31	22	70
295	hsa-miR-1977	426	65	957
296	hsa-miR-1978	177	47	739
297	hsa-miR-1979	1,203	161	1,188
298	hsa-miR-198	14	232	47
299	hsa-miR-199a-3p	322	95	453
300	hsa-miR-199a-5p	51	50	62
301	hsa-miR-199b-5p	32	25	28
302	hsa-miR-19a	918	157	465
303	hsa-miR-19a*	41	56	52
304	hsa-miR-19b	3,043	544	1,273

305	hsa-miR-19b-1*	19	70	43
306	hsa-miR-19b-2*	20	65	34
307	hsa-miR-200a	53	51	49
308	hsa-miR-200a*	33	59	23
309	hsa-miR-200b	124	66	125
310	hsa-miR-200b*	31	99	32
311	hsa-miR-200c	303	109	624
312	hsa-miR-200c*	47	49	32
313	hsa-miR-202	34	479	25
314	hsa-miR-202*	27	4	13
315	hsa-miR-203	45	61	35
316	hsa-miR-204	100	27	107
317	hsa-miR-205	107	43	99
318	hsa-miR-205*	76	33	49
319	hsa-miR-2052	35	15	29
320	hsa-miR-2053	63	8	42
321	hsa-miR-2054	29	11	25
322	hsa-miR-206	26	65	62
323	hsa-miR-208a	32	60	19
324	hsa-miR-208b	31	55	15
325	hsa-miR-20a	4,656	430	2,491
326	hsa-miR-20a*	81	17	73
327	hsa-miR-20b	3,180	215	1,764
328	hsa-miR-20b*	93	62	31
329	hsa-miR-21	1,916	453	4,907
330	hsa-miR-21*	28	112	29
331	hsa-miR-210	42	77	55
332	hsa-miR-211	24	14	38
333	hsa-miR-2110	18	77	37
334	hsa-miR-2113	36	40	43
335	hsa-miR-2114	101	50	70
336	hsa-miR-2114*	14	133	34
337	hsa-miR-2115	45	61	47
338	hsa-miR-2115*	24	58	58
339	hsa-miR-2116	29	60	35
340	hsa-miR-2116*	29	36	37
341	hsa-miR-2117	30	40	29
342	hsa-miR-212	59	52	35
343	hsa-miR-214	211	158	311
344	hsa-miR-214*	15	25	24
345	hsa-miR-215	51	53	50
346	hsa-miR-216a	31	39	22
347	hsa-miR-216b	24	44	20
348	hsa-miR-217	45	42	22

349	hsa-miR-218	61	31	99
350	hsa-miR-218-1*	45	48	36
351	hsa-miR-218-2*	40	53	41
352	hsa-miR-219-1-3p	33	45	26
353	hsa-miR-219-2-3p	33	72	43
354	hsa-miR-219-5p	24	24	29
355	hsa-miR-22	80	81	72
356	hsa-miR-22*	27	44	32
357	hsa-miR-220a	44	19	27
358	hsa-miR-220b	38	18	17
359	hsa-miR-220c	21	59	22
360	hsa-miR-221	927	95	461
361	hsa-miR-221*	64	20	25
362	hsa-miR-222	1,052	139	528
363	hsa-miR-222*	56	26	25
364	hsa-miR-223	75	38	35
365	hsa-miR-223*	20	51	20
366	hsa-miR-224	35	19	43
367	hsa-miR-224*	31	47	19
368	hsa-miR-2276	36	151	26
369	hsa-miR-2277	33	33	36
370	hsa-miR-2278	23	56	34
371	hsa-miR-23a	438	109	565
372	hsa-miR-23a*	17	121	44
373	hsa-miR-23b	618	190	811
374	hsa-miR-23b*	18	27	29
375	hsa-miR-24	229	141	347
376	hsa-miR-24-1*	17	58	23
377	hsa-miR-24-2*	27	30	22
378	hsa-miR-25	735	94	931
379	hsa-miR-25*	21	81	28
380	hsa-miR-26a	1,128	199	1,775
381	hsa-miR-26a-1*	21	24	17
382	hsa-miR-26a-2*	33	12	28
383	hsa-miR-26b	224	55	463
384	hsa-miR-26b*	60	11	24
385	hsa-miR-27a	162	74	185
386	hsa-miR-27a*	50	42	34
387	hsa-miR-27b	198	94	247
388	hsa-miR-27b*	34	82	32
389	hsa-miR-28-3p	78	68	49
390	hsa-miR-28-5p	94	70	72
391	hsa-miR-296-3p	30	93	28
392	hsa-miR-296-5p	168	77	82

393	hsa-miR-297	22	88	44
394	hsa-miR-298	31	68	24
395	hsa-miR-299-3p	37	86	28
396	hsa-miR-299-5p	144	38	67
397	hsa-miR-29a	458	157	522
398	hsa-miR-29a*	31	33	37
399	hsa-miR-29b	74	70	59
400	hsa-miR-29b-1*	24	127	69
401	hsa-miR-29b-2*	31	80	26
402	hsa-miR-29c	73	31	73
403	hsa-miR-29c*	34	11	36
404	hsa-miR-300	73	49	39
405	hsa-miR-301a	114	28	64
406	hsa-miR-301b	32	35	26
407	hsa-miR-302a	3,646	281	4,782
408	hsa-miR-302a*	4,498	368	5,459
409	hsa-miR-302b	14,151	1,525	22,133
410	hsa-miR-302b*	298	50	181
411	hsa-miR-302c	1,287	141	1,102
412	hsa-miR-302c*	191	106	272
413	hsa-miR-302d	9,023	749	8,866
414	hsa-miR-302d*	156	62	180
415	hsa-miR-302e	61	29	61
416	hsa-miR-302f	39	27	29
417	hsa-miR-30a	114	56	86
418	hsa-miR-30a*	52	34	34
419	hsa-miR-30b	131	31	99
420	hsa-miR-30b*	25	82	42
421	hsa-miR-30c	210	43	215
422	hsa-miR-30c-1*	30	88	26
423	hsa-miR-30c-2*	24	65	22
424	hsa-miR-30d	98	42	93
425	hsa-miR-30d*	28	46	20
426	hsa-miR-30e	85	31	76
427	hsa-miR-30e*	50	22	124
428	hsa-miR-31	223	66	222
429	hsa-miR-31*	24	15	31
430	hsa-miR-32	33	21	20
431	hsa-miR-32*	29	38	79
432	hsa-miR-320a	201	2,387	182
433	hsa-miR-320b	149	363	162
434	hsa-miR-320c	162	223	174
435	hsa-miR-320d	103	105	133
436	hsa-miR-323-3p	35	40	24

437	hsa-miR-323-5p	20	63	39
438	hsa-miR-324-3p	27	67	55
439	hsa-miR-324-5p	41	62	59
440	hsa-miR-325	38	54	32
441	hsa-miR-326	29	37	35
442	hsa-miR-328	45	33	34
443	hsa-miR-329	39	19	21
444	hsa-miR-330-3p	40	53	39
445	hsa-miR-330-5p	14	65	30
446	hsa-miR-331-3p	82	34	70
447	hsa-miR-331-5p	22	48	33
448	hsa-miR-335	103	73	160
449	hsa-miR-335*	109	44	185
450	hsa-miR-337-3p	23	10	32
451	hsa-miR-337-5p	29	42	19
452	hsa-miR-338-3p	28	22	10
453	hsa-miR-338-5p	31	53	26
454	hsa-miR-339-3p	28	59	24
455	hsa-miR-339-5p	34	44	29
456	hsa-miR-33a	17	49	21
457	hsa-miR-33a*	41	24	24
458	hsa-miR-33b	29	39	23
459	hsa-miR-33b*	22	64	33
460	hsa-miR-340	127	32	119
461	hsa-miR-340*	51	23	59
462	hsa-miR-342-3p	123	52	99
463	hsa-miR-342-5p	27	59	18
464	hsa-miR-345	42	125	22
465	hsa-miR-346	42	17	31
466	hsa-miR-34a	62	34	61
467	hsa-miR-34a*	34	17	19
468	hsa-miR-34b	44	24	35
469	hsa-miR-34b*	31	31	12
470	hsa-miR-34c-3p	50	72	35
471	hsa-miR-34c-5p	39	75	48
472	hsa-miR-361-3p	19	53	20
473	hsa-miR-361-5p	72	116	161
474	hsa-miR-362-3p	62	19	22
475	hsa-miR-362-5p	48	83	42
476	hsa-miR-363	630	63	323
477	hsa-miR-363*	17	49	28
478	hsa-miR-365	121	72	90
479	hsa-miR-365*	32	208	30
480	hsa-miR-367	1,322	716	571

481	hsa-miR-367*	42	40	12
482	hsa-miR-369-3p	35	65	28
483	hsa-miR-369-5p	29	44	25
484	hsa-miR-370	13	86	26
485	hsa-miR-371-3p	49	71	91
486	hsa-miR-371-5p	131	3,264	139
487	hsa-miR-372	157	98	122
488	hsa-miR-373	120	141	208
489	hsa-miR-373*	166	9,726	92
490	hsa-miR-374a	360	63	211
491	hsa-miR-374a*	36	38	13
492	hsa-miR-374b	600	88	480
493	hsa-miR-374b*	49	17	40
494	hsa-miR-375	38	66	63
495	hsa-miR-376a	10	70	23
496	hsa-miR-376a*	32	30	27
497	hsa-miR-376b	34	29	26
498	hsa-miR-376c	21	25	26
499	hsa-miR-377	25	28	35
500	hsa-miR-377*	32	62	36
501	hsa-miR-378	69	72	74
502	hsa-miR-378*	29	21	28
503	hsa-miR-379	36	101	89
504	hsa-miR-379*	47	15	40
505	hsa-miR-380	24	21	30
506	hsa-miR-380*	41	42	48
507	hsa-miR-381	41	55	22
508	hsa-miR-382	43	84	57
509	hsa-miR-383	26	95	34
510	hsa-miR-384	31	14	26
511	hsa-miR-409-3p	41	49	55
512	hsa-miR-409-5p	50	38	30
513	hsa-miR-410	76	58	29
514	hsa-miR-411	36	42	29
515	hsa-miR-411*	79	19	54
516	hsa-miR-412	70	20	24
517	hsa-miR-421	227	252	190
518	hsa-miR-422a	106	193	68
519	hsa-miR-423-3p	61	46	34
520	hsa-miR-423-5p	80	242	102
521	hsa-miR-424	65	17	56
522	hsa-miR-424*	123	920	67
523	hsa-miR-425	205	28	106
524	hsa-miR-425*	44	40	34

525	hsa-miR-429	91	36	47
526	hsa-miR-431	34	43	30
527	hsa-miR-431*	22	84	31
528	hsa-miR-432	29	127	25
529	hsa-miR-432*	44	22	43
530	hsa-miR-433	52	61	38
531	hsa-miR-448	38	25	38
532	hsa-miR-449a	10	42	36
533	hsa-miR-449b	31	37	25
534	hsa-miR-449b*	61	23	38
535	hsa-miR-449c	40	44	22
536	hsa-miR-449c*	56	25	24
537	hsa-miR-450a	19	48	30
538	hsa-miR-450b-3p	24	20	26
539	hsa-miR-450b-5p	24	19	22
540	hsa-miR-451	32	24	29
541	hsa-miR-452	38	64	25
542	hsa-miR-452*	37	42	9
543	hsa-miR-453	8	41	26
544	hsa-miR-454	226	75	618
545	hsa-miR-454*	42	24	43
546	hsa-miR-455-3p	90	60	126
547	hsa-miR-455-5p	38	32	33
548	hsa-miR-483-3p	71	26	52
549	hsa-miR-483-5p	85	1,056	117
550	hsa-miR-484	97	81	73
551	hsa-miR-485-3p	106	50	80
552	hsa-miR-485-5p	22	79	16
553	hsa-miR-486-3p	36	77	29
554	hsa-miR-486-5p	50	31	33
555	hsa-miR-487a	35	48	17
556	hsa-miR-487b	54	53	31
557	hsa-miR-488	22	15	15
558	hsa-miR-488*	33	7	15
559	hsa-miR-489	87	57	73
560	hsa-miR-490-3p	46	31	27
561	hsa-miR-490-5p	35	120	32
562	hsa-miR-491-3p	45	13	24
563	hsa-miR-491-5p	36	49	35
564	hsa-miR-492	40	83	26
565	hsa-miR-493	33	75	32
566	hsa-miR-493*	35	40	50
567	hsa-miR-494	544	122	676
568	hsa-miR-495	42	20	22

569	hsa-miR-496	35	12	26
570	hsa-miR-497	31	60	19
571	hsa-miR-497*	23	52	19
572	hsa-miR-498	53	709	70
573	hsa-miR-499-3p	32	51	12
574	hsa-miR-499-5p	28	57	17
575	hsa-miR-500	26	74	27
576	hsa-miR-500*	39	106	34
577	hsa-miR-501-3p	26	90	38
578	hsa-miR-501-5p	35	59	35
579	hsa-miR-502-3p	17	73	28
580	hsa-miR-502-5p	29	44	27
581	hsa-miR-503	18	166	25
582	hsa-miR-504	33	47	29
583	hsa-miR-505	75	41	84
584	hsa-miR-505*	30	130	25
585	hsa-miR-506	38	60	25
586	hsa-miR-507	23	31	24
587	hsa-miR-508-3p	32	62	27
588	hsa-miR-508-5p	19	59	22
589	hsa-miR-509-3-5p	28	41	27
590	hsa-miR-509-3p	56	107	32
591	hsa-miR-509-5p	30	60	24
592	hsa-miR-510	52	69	35
593	hsa-miR-511	41	19	32
594	hsa-miR-512-3p	177	97	256
595	hsa-miR-512-5p	38	43	78
596	hsa-miR-513a-3p	45	19	28
597	hsa-miR-513a-5p	30	103	84
598	hsa-miR-513b	20	59	27
599	hsa-miR-513c	33	50	26
600	hsa-miR-514	30	37	44
601	hsa-miR-515-3p	80	72	63
602	hsa-miR-515-5p	87	16	111
603	hsa-miR-516a-3p	40	51	50
604	hsa-miR-516a-5p	26	58	50
605	hsa-miR-516b	83	80	63
606	hsa-miR-517*	35	62	63
607	hsa-miR-517a	157	51	268
608	hsa-miR-517b	137	53	251
609	hsa-miR-517c	101	44	91
610	hsa-miR-518a-3p	33	43	67
611	hsa-miR-518a-5p	32	65	35
612	hsa-miR-518b	74	39	68

613	hsa-miR-518c	35	33	33
614	hsa-miR-518c*	47	67	53
615	hsa-miR-518d-3p	43	18	56
616	hsa-miR-518d-5p	81	71	88
617	hsa-miR-518e	41	18	61
618	hsa-miR-518e*	33	46	56
619	hsa-miR-518f	62	20	51
620	hsa-miR-518f*	78	45	69
621	hsa-miR-519a	82	32	69
622	hsa-miR-519b-3p	65	32	56
623	hsa-miR-519c-3p	74	33	84
624	hsa-miR-519d	86	33	63
625	hsa-miR-519e	36	56	29
626	hsa-miR-519e*	54	68	60
627	hsa-miR-520a-3p	42	36	29
628	hsa-miR-520a-5p	40	36	38
629	hsa-miR-520b	67	65	62
630	hsa-miR-520c-3p	49	66	68
631	hsa-miR-520d-3p	66	113	88
632	hsa-miR-520d-5p	32	26	37
633	hsa-miR-520e	42	58	35
634	hsa-miR-520f	72	53	64
635	hsa-miR-520g	83	40	83
636	hsa-miR-520h	91	32	75
637	hsa-miR-521	31	27	31
638	hsa-miR-522	46	36	76
639	hsa-miR-523	33	52	30
640	hsa-miR-524-3p	48	51	80
641	hsa-miR-524-5p	48	50	65
642	hsa-miR-525-3p	29	42	29
643	hsa-miR-525-5p	21	30	72
644	hsa-miR-526b	29	45	61
645	hsa-miR-526b*	42	51	39
646	hsa-miR-532-3p	58	34	64
647	hsa-miR-532-5p	48	35	72
648	hsa-miR-539	29	36	36
649	hsa-miR-541	15	41	36
650	hsa-miR-541*	28	26	36
651	hsa-miR-542-3p	24	29	19
652	hsa-miR-542-5p	26	28	20
653	hsa-miR-543	20	19	12
654	hsa-miR-544	25	7	24
655	hsa-miR-545	30	18	21
656	hsa-miR-545*	16	16	9

657	hsa-miR-548a-3p	23	11	34
658	hsa-miR-548a-5p	29	18	23
659	hsa-miR-548b-3p	38	20	36
660	hsa-miR-548b-5p	19	27	42
661	hsa-miR-548c-3p	35	16	32
662	hsa-miR-548c-5p	30	43	40
663	hsa-miR-548d-3p	24	16	27
664	hsa-miR-548d-5p	20	22	25
665	hsa-miR-548e	34	25	30
666	hsa-miR-548f	43	32	50
667	hsa-miR-548g	42	32	31
668	hsa-miR-548h	34	34	48
669	hsa-miR-548i	31	67	29
670	hsa-miR-548j	46	106	42
671	hsa-miR-548k	48	79	32
672	hsa-miR-548l	27	91	53
673	hsa-miR-548m	34	103	59
674	hsa-miR-548n	17	78	29
675	hsa-miR-548o	29	48	26
676	hsa-miR-548p	33	74	49
677	hsa-miR-548q	332	1,109	146
678	hsa-miR-549	19	52	36
679	hsa-miR-550	34	109	47
680	hsa-miR-550*	62	61	40
681	hsa-miR-551a	74	60	55
682	hsa-miR-551b	36	48	67
683	hsa-miR-551b*	28	79	41
684	hsa-miR-552	24	40	30
685	hsa-miR-553	31	28	32
686	hsa-miR-554	23	49	46
687	hsa-miR-555	36	35	47
688	hsa-miR-556-3p	29	46	53
689	hsa-miR-556-5p	28	61	40
690	hsa-miR-557	52	141	52
691	hsa-miR-558	26	175	22
692	hsa-miR-559	38	74	28
693	hsa-miR-561	32	66	27
694	hsa-miR-562	40	68	26
695	hsa-miR-563	31	91	33
696	hsa-miR-564	97	217	181
697	hsa-miR-566	29	60	36
698	hsa-miR-567	61	85	32
699	hsa-miR-568	29	26	89
700	hsa-miR-569	23	40	25

701	hsa-miR-570	30	11	31
702	hsa-miR-571	37	52	35
703	hsa-miR-572	67	67	55
704	hsa-miR-573	35	22	27
705	hsa-miR-574-3p	150	146	168
706	hsa-miR-574-5p	221	163	588
707	hsa-miR-575	200	589	171
708	hsa-miR-576-3p	14	58	16
709	hsa-miR-576-5p	59	28	26
710	hsa-miR-577	14	20	21
711	hsa-miR-578	29	26	123
712	hsa-miR-579	42	26	15
713	hsa-miR-580	13	71	21
714	hsa-miR-581	30	21	19
715	hsa-miR-582-3p	29	46	26
716	hsa-miR-582-5p	42	24	20
717	hsa-miR-583	33	47	26
718	hsa-miR-584	35	112	32
719	hsa-miR-585	19	49	23
720	hsa-miR-586	35	20	16
721	hsa-miR-587	13	60	26
722	hsa-miR-588	12	80	27
723	hsa-miR-589	25	52	29
724	hsa-miR-589*	39	24	18
725	hsa-miR-590-3p	14	39	17
726	hsa-miR-590-5p	70	72	38
727	hsa-miR-591	25	20	14
728	hsa-miR-592	11	53	19
729	hsa-miR-593	17	48	20
730	hsa-miR-593*	41	60	790
731	hsa-miR-595	41	71	33
732	hsa-miR-596	121	95	67
733	hsa-miR-597	19	28	39
734	hsa-miR-598	44	18	72
735	hsa-miR-599	14	49	24
736	hsa-miR-600	33	21	33
737	hsa-miR-601	36	75	56
738	hsa-miR-602	61	131	44
739	hsa-miR-603	16	5	22
740	hsa-miR-604	27	126	35
741	hsa-miR-605	56	47	64
742	hsa-miR-606	25	21	27
743	hsa-miR-607	21	25	13
744	hsa-miR-608	33	164	32

745	hsa-miR-609	27	34	33
746	hsa-miR-610	10	63	18
747	hsa-miR-611	36	59	32
748	hsa-miR-612	84	216	111
749	hsa-miR-613	35	27	26
750	hsa-miR-614	38	53	48
751	hsa-miR-615-3p	37	60	33
752	hsa-miR-615-5p	31	50	55
753	hsa-miR-616	31	60	25
754	hsa-miR-616*	48	23	22
755	hsa-miR-617	32	54	40
756	hsa-miR-618	35	19	13
757	hsa-miR-619	70	57	25
758	hsa-miR-620	26	41	17
759	hsa-miR-621	36	45	24
760	hsa-miR-622	69	115	30
761	hsa-miR-623	80	288	30
762	hsa-miR-624	26	18	17
763	hsa-miR-624*	46	28	21
764	hsa-miR-625	29	131	18
765	hsa-miR-625*	134	87	83
766	hsa-miR-626	29	49	16
767	hsa-miR-627	34	66	22
768	hsa-miR-628-3p	29	120	55
769	hsa-miR-628-5p	44	53	22
770	hsa-miR-629	35	121	31
771	hsa-miR-629*	134	508	73
772	hsa-miR-630	41	191	45
773	hsa-miR-631	60	79	46
774	hsa-miR-632	36	74	29
775	hsa-miR-633	39	36	28
776	hsa-miR-634	98	58	57
777	hsa-miR-635	36	49	26
778	hsa-miR-636	49	99	45
779	hsa-miR-637	80	1,161	66
780	hsa-miR-638	1,700	14,970	910
781	hsa-miR-639	23	53	20
782	hsa-miR-640	58	43	29
783	hsa-miR-641	89	44	32
784	hsa-miR-642	93	39	27
785	hsa-miR-643	40	52	31
786	hsa-miR-644	34	58	27
787	hsa-miR-645	29	51	20
788	hsa-miR-646	21	68	24

789	hsa-miR-647	46	56	54
790	hsa-miR-648	32	105	431
791	hsa-miR-649	26	60	19
792	hsa-miR-650	66	242	122
793	hsa-miR-651	41	26	37
794	hsa-miR-652	12	60	39
795	hsa-miR-653	28	28	30
796	hsa-miR-654-3p	36	52	48
797	hsa-miR-654-5p	32	132	30
798	hsa-miR-655	44	19	23
799	hsa-miR-656	48	35	26
800	hsa-miR-657	95	28	60
801	hsa-miR-658	45	184	48
802	hsa-miR-659	24	109	32
803	hsa-miR-660	66	15	75
804	hsa-miR-661	36	30	46
805	hsa-miR-662	63	44	28
806	hsa-miR-663	355	2,651	241
807	hsa-miR-663b	31	60	36
808	hsa-miR-664	88	14	29
809	hsa-miR-664*	37	195	25
810	hsa-miR-665	36	86	55
811	hsa-miR-668	103	59	59
812	hsa-miR-670	31	62	20
813	hsa-miR-671-3p	46	83	37
814	hsa-miR-671-5p	95	1,609	72
815	hsa-miR-675	41	287	43
816	hsa-miR-675*	106	54	47
817	hsa-miR-7	121	88	292
818	hsa-miR-708	75	67	63
819	hsa-miR-708*	40	34	16
820	hsa-miR-7-1*	31	19	36
821	hsa-miR-711	24	154	31
822	hsa-miR-718	105	670	79
823	hsa-miR-7-2*	28	9	13
824	hsa-miR-720	379	308	237
825	hsa-miR-744	24	82	40
826	hsa-miR-744*	52	27	34
827	hsa-miR-758	36	28	21
828	hsa-miR-759	25	25	9
829	hsa-miR-760	28	241	23
830	hsa-miR-761	22	67	18
831	hsa-miR-762	948	7,530	540
832	hsa-miR-764	36	22	44

833	hsa-miR-765	32	171	70
834	hsa-miR-766	120	63	65
835	hsa-miR-767-3p	47	20	32
836	hsa-miR-767-5p	30	21	23
837	hsa-miR-769-3p	32	100	24
838	hsa-miR-769-5p	43	35	35
839	hsa-miR-770-5p	28	58	27
840	hsa-miR-802	35	18	14
841	hsa-miR-873	32	37	21
842	hsa-miR-874	123	904	156
843	hsa-miR-875-3p	10	41	15
844	hsa-miR-875-5p	38	30	22
845	hsa-miR-876-3p	12	47	12
846	hsa-miR-876-5p	17	29	13
847	hsa-miR-877	15	428	60
848	hsa-miR-877*	53	29	65
849	hsa-miR-885-3p	9	250	22
850	hsa-miR-885-5p	42	19	56
851	hsa-miR-886-3p	90	76	181
852	hsa-miR-886-5p	30	78	67
853	hsa-miR-887	29	82	41
854	hsa-miR-888	29	17	17
855	hsa-miR-888*	19	69	16
856	hsa-miR-889	13	42	5
857	hsa-miR-890	30	73	11
858	hsa-miR-891a	77	75	36
859	hsa-miR-891b	161	59	9
860	hsa-miR-892a	36	32	17
861	hsa-miR-892b	23	28	22
862	hsa-miR-9	49	12	147
863	hsa-miR-9*	97	56	87
864	hsa-miR-920	28	106	18
865	hsa-miR-921	21	110	24
866	hsa-miR-922	32	59	20
867	hsa-miR-924	27	54	30
868	hsa-miR-92a	1,387	156	1,453
869	hsa-miR-92a-1*	23	74	53
870	hsa-miR-92a-2*	25	108	23
871	hsa-miR-92b	1,000	128	1,059
872	hsa-miR-92b*	19	165	25
873	hsa-miR-93	692	227	471
874	hsa-miR-93*	47	56	61
875	hsa-miR-933	62	97	49
876	hsa-miR-934	33	93	19

877	hsa-miR-935	15	41	32
878	hsa-miR-936	53	305	77
879	hsa-miR-937	26	63	26
880	hsa-miR-938	41	40	19
881	hsa-miR-939	96	609	43
882	hsa-miR-940	171	234	143
883	hsa-miR-941	18	50	33
884	hsa-miR-942	26	35	16
885	hsa-miR-943	47	38	30
886	hsa-miR-944	38	63	11
887	hsa-miR-95	29	76	19
888	hsa-miR-96	52	17	31
889	hsa-miR-96*	21	72	18
890	hsa-miR-98	27	85	39
891	hsa-miR-99a	39	61	27
892	hsa-miR-99a*	28	74	19
893	hsa-miR-99b	174	46	187
894	hsa-miR-99b*	23	84	28

Control_iPS_8333 B Averaged Signal	HF_1893 Averaged Signal	HF_4078 Averaged Signal	HF_8399 Averaged Signal
170	1,264	4,966	4,156
28	6	21	53
23	9	45	67
103	1,094	4,267	2,998
57	44	85	128
68	1,206	4,722	3,751
27	26	30	52
117	862	2,669	2,923
72	32	50	73
66	520	982	1,627
32	15	32	43
69	817	2,780	2,864
40	20	47	69
27	10	27	50
61	181	572	1,036
29	16	45	46
64	265	1,960	2,177
31	18	54	33
26	7	30	43
41	295	966	1,635
34	13	55	56
58	40	78	132
18	16	23	34
151	99	177	248
27	93	58	56
33	30	48	59
24	38	68	67
27	44	32	26
976	79	178	253
69	9	39	55
132	71	124	154
72	56	79	53
93	87	153	234
79	52	99	762
99	47	32	99
93	51	188	818
100	79	58	66
46	13	59	42
78	30	40	40
70	61	59	60

165	104	85	61
86	155	84	57
58	71	66	54
65	28	57	50
59	53	99	36
72	52	61	51
76	20	40	31
79	26	38	36
80	106	75	59
92	83	54	32
62	16	26	31
41	25	34	28
68	34	45	41
31	26	29	48
371	488	103	75
212	183	143	96
74	27	39	47
26	3	17	39
51	32	76	66
644	263	114	102
43	31	77	52
48	96	73	42
28	38	57	48
36	64	55	35
76	68	134	84
57	72	128	71
305	928	57	46
102	55	88	74
954	1,191	96	79
69	40	53	44
222	135	119	74
60	23	43	32
129	95	140	81
98	92	107	66
56	74	55	52
66	60	33	53
36	26	28	24
69	53	36	44
30	30	26	26
2,254	94	94	51
103	37	56	78
59	15	20	48
208	115	139	91
70	66	27	29

59	27	32	55
49	42	20	31
51	50	58	55
63	98	57	50
26	68	28	40
27	84	18	32
28	20	35	59
32	42	93	64
28	53	24	56
45	40	29	55
101	288	113	47
51	188	785	1,240
217	2,228	5,394	4,582
32	36	25	50
90	320	44	64
73	33	172	71
31	24	12	36
603	358	208	270
56	65	43	37
66	70	28	38
27	55	57	52
37	16	48	48
33	69	58	43
46	100	44	33
33	24	26	27
589	514	374	230
28	69	77	36
31	47	55	34
34	36	61	46
39	70	45	33
53	63	35	61
36	77	270	298
122	95	96	52
260	171	113	131
4,138	1,773	257	171
64	92	85	44
35	72	70	55
88	22	57	73
27	21	69	32
23	17	51	33
71	44	91	100
3,573	1,757	941	542
87	103	227	112
26	35	165	32

78	28	61	40
99	43	68	42
115	104	57	46
94	63	75	35
79	49	52	50
68	68	87	47
135	61	82	58
72	59	73	45
407	48	68	28
61	87	58	22
129	254	81	45
89	84	82	35
76	48	66	48
63	40	63	36
77	58	80	24
106	125	71	56
77	69	54	43
86	33	60	28
105	49	62	53
119	66	50	50
96	84	56	46
66	29	51	42
99	76	47	50
87	44	42	52
73	60	48	50
69	67	65	46
191	147	110	85
546	126	253	219
167	117	96	138
22	57	64	58
107	121	93	94
28	24	42	58
30	24	173	178
27	41	62	54
121	89	51	30
38	60	62	44
124	220	44	44
23	19	36	31
75	69	67	55
73	67	45	44
91	141	107	87
30	16	29	30
77	124	70	25
43	20	35	27

45	70	83	39
47	20	36	31
44	18	49	34
44	48	60	142
49	69	70	118
59	248	39	53
48	72	31	43
35	54	48	25
31	51	57	49
36	61	95	174
35	27	48	59
68	28	44	22
56	16	21	27
60	12	24	52
47	6	25	21
67	76	538	1,100
35	51	45	51
30	9	23	32
39	7	136	32
45	146	1,113	1,565
30	23	56	206
26	16	21	25
2,006	1,765	395	194
41	42	35	32
24	14	14	34
33	31	25	20
30	27	150	68
72	36	60	40
76	66	88	63
95	74	37	24
21	47	34	47
96	39	73	203
54	25	32	56
38	33	55	136
32	27	72	55
67	37	73	55
4,481	8,127	215	150
65	53	86	67
784	1,778	53	54
34	35	79	146
82	64	306	349
37	92	360	548
55	17	50	62
21	21	47	30

39	230	82	51
53	55	59	54
54	15	39	77
46	26	57	70
72	42	87	121
22	7	29	64
48	68	134	342
23	40	63	24
140	62	301	428
40	17	32	59
208	393	1,257	1,380
34	71	31	35
30	15	44	104
1,067	79	152	251
78	56	68	43
74	67	143	154
137	114	124	53
37	84	66	65
63	71	117	156
71	63	84	61
82	87	62	30
81	79	94	70
742	96	67	21
69	23	500	18
93	73	116	54
1,574	1,383	2,023	1,003
61	77	54	31
86	42	67	29
77	72	52	25
100	115	59	36
99	74	85	98
56	25	45	24
101	50	89	120
59	19	36	74
30	42	57	45
227	178	77	57
25	54	41	20
80	150	134	114
72	57	64	61
25	31	58	46
56	27	50	54
47	30	74	56
27	29	27	36
1,716	839	80	109

31	96	63	54
56	113	71	49
51	13	25	31
92	66	138	283
92	80	94	85
20	47	55	48
23	29	62	36
26	39	37	26
20	42	38	27
124	103	140	96
71	48	90	70
93	98	71	42
5,196	1,566	519	282
27	34	43	26
67	41	77	49
38	27	274	55
72	61	36	41
398	513	262	260
41	52	73	55
109	223	73	89
47	27	50	32
37	97	61	23
105	123	260	336
38	434	74	50
15	53	47	162
18	36	23	37
32	50	72	49
16	14	50	18
157	78	180	157
77	73	86	32
57	49	39	29
820	397	1,172	864
589	119	846	539
76	53	50	58
82	95	309	223
59	66	125	98
663	744	2,267	2,254
126	175	58	61
106	636	1,706	1,638
78	109	178	165
26	63	96	114
809	34	95	147
36	14	45	44
1,475	86	415	349

28	12	69	36
29	19	47	41
24	21	39	35
46	39	47	47
57	17	32	32
52	49	44	30
91	27	36	42
33	18	82	35
112	222	55	33
28	4	21	32
56	21	65	49
69	10	83	65
56	48	67	63
49	19	66	46
45	13	62	41
50	13	47	56
40	15	25	33
30	41	59	51
35	73	32	47
36	63	69	25
1,188	67	198	264
64	17	56	29
927	71	119	192
58	68	69	25
343	1,612	6,400	5,493
46	76	48	49
75	83	109	150
42	11	57	33
51	48	81	39
52	20	54	61
53	40	76	63
42	78	67	33
60	26	70	31
55	46	38	24
43	26	68	31
52	23	58	35
19	63	47	36
36	28	59	55
118	164	724	672
36	11	46	36
53	43	46	39
47	36	47	31
50	37	459	62
51	353	71	32

55	54	80	105
67	36	77	41
47	34	66	54
54	30	62	37
60	44	47	59
52	16	30	36
81	219	533	702
56	65	122	207
26	7	56	51
47	27	41	31
54	41	33	18
189	1,097	1,714	1,852
46	12	61	97
211	1,098	2,021	2,139
51	50	51	61
72	22	68	33
54	16	59	23
67	52	366	319
28	43	30	34
54	84	69	25
26	29	55	29
60	38	53	21
130	1,413	3,506	2,900
61	68	85	111
166	1,518	2,987	2,751
65	32	47	43
86	218	1,124	925
49	31	30	50
43	26	66	75
276	39	196	281
60	80	49	21
224	467	1,856	1,633
47	4	21	19
45	0	22	18
124	173	473	714
20	5	21	20
70	235	759	944
60	63	56	44
100	262	573	860
34	64	66	78
28	54	68	77
56	64	88	145
56	65	76	37
166	94	133	77

57	49	53	42
41	59	58	32
44	48	69	40
87	61	111	172
114	1,722	1,852	2,713
46	49	59	107
72	258	101	259
54	48	117	159
36	51	28	48
67	473	103	291
21	13	28	34
51	70	27	38
56	27	50	68
35	32	29	34
980	26	32	35
1,070	52	36	39
8,735	14	25	35
92	26	64	35
698	42	57	25
78	81	37	38
2,447	55	31	35
65	69	33	53
74	26	41	51
63	20	34	53
72	60	125	206
37	52	69	94
125	61	168	247
45	54	59	31
110	90	127	197
135	111	59	41
30	79	63	42
54	83	107	192
21	57	63	29
47	201	81	122
23	38	77	97
40	136	1,324	707
16	60	79	66
43	20	23	31
39	39	20	50
801	988	461	391
199	240	534	524
201	218	551	546
83	140	415	514
29	74	62	40

27	71	77	23
49	115	76	66
32	81	61	61
29	42	29	22
26	30	43	55
62	51	78	42
27	33	58	79
54	57	69	52
27	59	40	41
51	53	51	65
30	68	65	53
66	54	37	41
60	40	57	50
35	23	83	156
32	54	47	57
43	18	22	25
51	32	44	52
24	66	65	26
42	76	85	60
47	50	27	31
26	35	27	33
51	48	38	45
37	48	70	50
41	18	34	74
46	8	19	29
54	65	109	119
25	66	73	44
64	81	68	49
28	62	64	62
42	61	89	129
42	44	54	54
26	40	31	57
46	35	54	32
46	41	31	44
53	53	63	40
42	40	54	35
46	63	106	144
20	16	57	34
28	51	51	63
98	45	69	57
37	53	38	21
66	92	129	303
82	312	57	48
2,443	37	53	39

42	24	66	53
45	41	69	70
22	47	66	56
18	84	52	56
31	50	64	32
1,227	2,140	102	52
74	72	71	38
73	80	71	58
815	6,620	139	74
68	58	71	87
18	14	37	34
87	67	101	145
14	12	33	47
23	37	70	46
17	56	56	142
20	16	31	60
24	35	54	46
22	67	127	262
17	48	55	71
26	55	56	48
46	58	38	33
26	21	20	21
33	51	90	133
33	20	42	79
53	22	27	56
28	27	27	19
56	35	38	37
57	61	114	110
33	65	25	22
25	8	17	26
60	51	89	90
29	44	36	31
23	28	34	69
63	53	37	97
111	24	38	97
45	24	30	25
85	113	45	29
88	88	40	25
82	34	84	51
169	126	151	160
66	107	1,103	1,377
135	1,036	178	165
75	26	104	109
53	62	39	38

29	23	25	22
36	45	39	23
25	51	25	20
24	73	63	57
28	31	32	15
27	36	38	33
66	25	27	20
64	39	19	18
29	32	31	24
33	47	63	47
41	66	35	27
44	28	79	28
36	23	46	88
42	18	14	11
33	12	23	23
29	11	24	10
29	44	54	66
32	26	20	6
31	37	24	14
81	44	105	123
33	36	37	25
68	72	126	191
65	29	35	72
71	38	68	53
925	584	97	61
122	81	77	86
79	26	75	78
64	52	31	23
73	52	32	24
72	52	644	35
71	78	38	111
40	66	46	86
18	17	12	27
24	7	16	18
77	88	67	38
17	29	30	40
57	63	30	31
18	5	22	22
43	68	36	53
74	117	35	23
52	57	47	28
49	44	79	184
504	126	93	107
60	29	36	132

25	20	9	22
35	39	28	71
25	29	19	27
250	469	92	98
28	32	22	29
17	15	17	24
26	42	24	17
36	65	22	42
32	91	20	21
46	28	21	21
19	57	11	18
71	33	19	26
81	124	52	80
53	13	11	15
61	28	30	61
68	89	14	8
65	27	58	45
58	15	14	26
27	17	24	30
22	85	39	30
24	70	37	7
23	53	33	29
15	71	31	19
37	84	31	23
43	47	25	33
67	61	33	25
25	62	20	20
28	42	19	8
150	73	29	8
65	36	28	15
52	43	61	26
31	43	30	17
20	21	14	35
49	15	13	45
28	17	27	28
24	26	18	17
38	24	29	36
23	28	18	19
42	22	31	27
52	23	14	25
61	23	22	27
23	12	28	22
52	47	22	25
63	22	36	35

17	22	27	25
60	70	18	24
34	9	13	27
44	68	34	23
19	26	39	15
56	73	25	27
49	20	25	19
77	57	22	24
59	24	32	20
66	19	20	24
56	15	54	22
65	37	34	31
43	33	25	27
77	63	16	20
30	34	39	27
31	35	21	7
42	47	22	34
55	51	40	22
39	42	33	22
38	113	24	18
47	24	60	22
39	32	31	31
71	32	32	27
36	33	23	23
32	25	23	11
37	47	27	10
42	35	31	9
28	45	36	18
41	46	19	18
49	28	21	8
43	32	16	6
42	46	21	19
56	42	35	25
49	43	45	30
38	39	31	30
33	35	15	57
31	74	16	17
22	46	45	22
29	25	40	90
31	28	18	18
26	23	20	19
15	17	13	15
24	16	13	13
17	4	12	20

18	16	10	14
24	17	9	35
41	17	16	24
25	23	7	26
19	2	15	24
30	18	19	36
20	2	13	36
25	13	20	32
23	24	10	28
29	24	12	40
15	28	12	22
117	52	30	80
24	34	6	29
33	46	23	27
31	53	11	28
24	30	10	27
126	23	43	128
25	22	6	22
20	19	21	20
57	35	11	27
426	393	245	129
21	22	9	24
62	83	20	28
47	48	19	29
57	13	21	38
15	11	3	25
55	79	18	15
21	38	11	12
15	89	17	24
20	53	25	23
19	49	19	55
30	27	20	30
29	33	25	21
63	171	30	36
28	287	35	46
22	73	16	20
21	21	22	27
16	36	15	34
23	45	53	19
106	155	102	40
21	30	18	32
24	48	12	24
18	35	15	27
14	46	17	14

49	16	8	23
69	57	11	25
92	67	42	33
67	47	19	17
583	372	179	227
142	91	159	133
419	238	96	70
56	51	50	18
50	14	21	24
27	18	14	17
47	21	16	7
54	37	13	19
33	23	20	12
43	14	20	25
54	23	17	13
56	18	18	23
66	33	24	32
87	52	37	29
76	26	23	7
71	16	162	17
78	21	22	29
46	29	19	22
26	35	26	22
35	24	15	20
39	12	8	23
70	35	24	36
37	41	28	14
55	24	9	21
53	37	24	27
47	34	25	27
52	39	34	31
74	60	70	73
67	32	45	27
32	9	18	51
72	40	14	22
37	30	22	14
77	80	30	50
171	138	46	69
44	20	4	7
76	99	25	18
87	30	81	58
49	26	17	14
54	21	16	9
68	123	34	34

32	25	28	25
59	49	24	15
65	77	35	54
1,724	296	34	67
39	38	17	15
95	46	26	18
70	64	29	44
40	59	32	25
37	54	13	52
61	33	16	14
65	49	23	43
53	31	16	14
59	19	16	24
50	23	9	18
32	18	17	27
65	108	29	28
85	116	31	27
19	10	12	18
38	25	16	28
59	164	20	17
138	81	96	79
22	23	23	24
30	33	26	15
38	61	9	16
34	20	15	22
33	92	14	21
310	430	86	61
92	75	34	22
62	61	34	29
56	26	35	22
38	13	14	16
79	69	49	46
43	42	13	15
78	54	52	34
323	1,837	74	60
18,465	8,947	824	541
37	38	15	15
43	36	14	17
32	47	17	37
54	34	27	25
39	49	20	29
28	46	20	20
30	47	23	24
25	51	32	30

28	74	65	47
37	74	36	32
24	22	17	27
111	205	38	37
56	44	7	29
25	57	20	19
19	33	10	10
50	74	85	136
80	110	18	33
34	51	17	31
34	18	14	29
45	47	42	51
201	161	33	35
90	58	42	33
65	10	37	70
72	30	35	34
51	20	42	53
3,060	3,102	183	206
42	56	57	31
39	17	35	56
76	87	25	22
83	90	63	27
37	26	92	57
26	18	28	25
68	51	63	40
474	567	106	69
224	231	57	44
121	49	82	66
92	47	92	113
82	52	67	100
56	18	37	27
30	10	33	34
162	124	31	28
147	206	114	67
27	34	21	22
627	251	601	324
37	101	35	33
59	17	51	42
27	23	40	54
23	43	22	38
65	92	63	44
54	50	22	30
12,373	5,862	363	249
40	10	51	38

234	127	34	53
81	48	110	80
55	40	49	54
28	24	23	18
69	115	32	32
49	36	29	53
28	35	22	19
14	9	14	21
63	29	558	22
515	329	74	35
26	27	22	24
21	13	37	43
23	11	19	29
29	16	14	27
88	242	67	29
90	47	45	55
152	247	21	29
51	22	57	30
107	91	122	89
33	32	58	58
40	49	42	20
43	4	14	15
58	41	30	22
34	22	16	36
25	16	21	19
43	36	40	77
42	13	20	32
15	7	22	53
39	12	25	27
21	5	25	77
13	20	19	32
20	66	27	23
78	82	42	30
16	38	19	24
23	25	7	30
352	62	210	331
26	44	33	32
41	103	18	22
270	56	200	221
43	91	57	32
376	70	94	138
30	33	54	54
84	90	60	57
32	48	58	34

15	25	46	19
243	250	82	63
21	55	46	24
17	28	706	23
418	318	93	76
248	194	248	120
31	70	22	19
29	16	25	17
31	30	37	25
19	33	15	34
25	12	16	20
21	16	33	33
18	34	26	32
28	122	117	288
12	146	291	973
16	29	26	22
32	78	199	370
16	55	54	40