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Supplemental Information

circCELSR1 (hsa_circ_0063809) Contributes to Paclitaxel Resistance of Ovarian Cancer Cells by Regulating FOXR2 Expression via miR-1252

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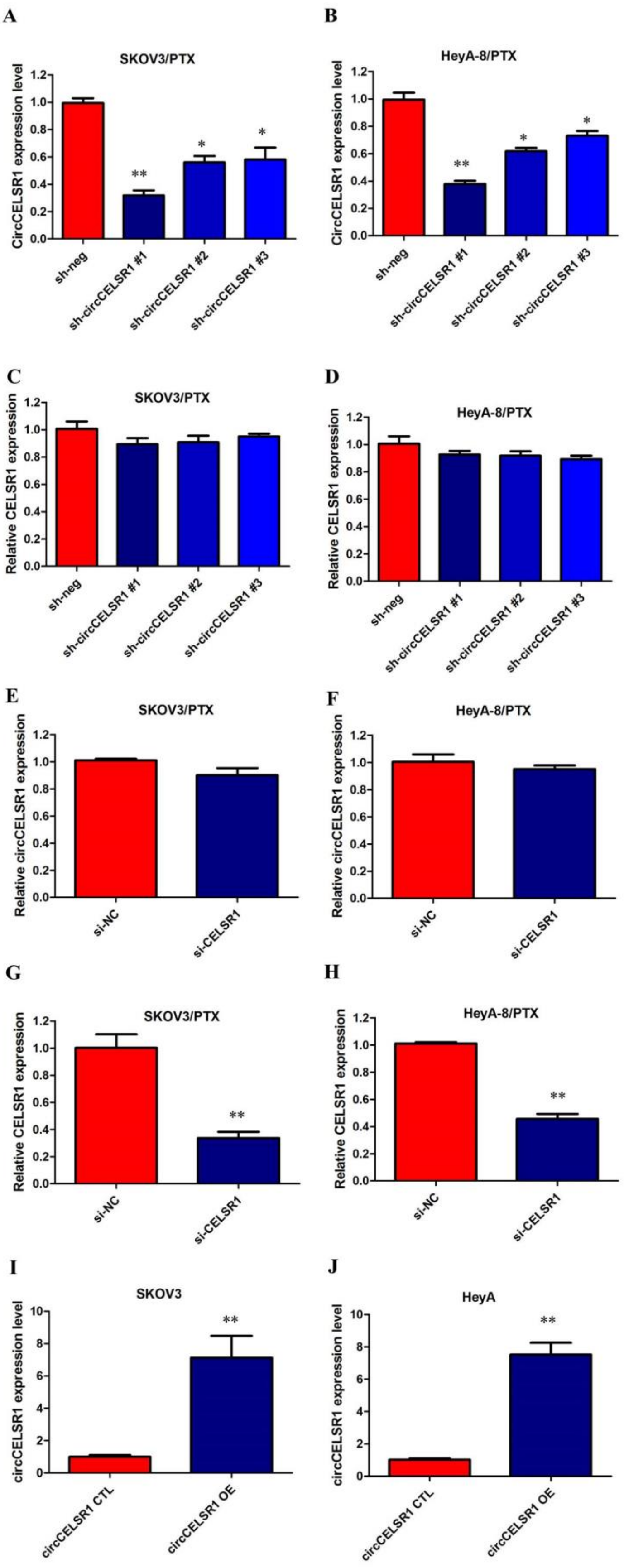

Figure S1 (A) The qRT-PCR analysis confirmed that circCELSR1 expression level was significantly downregulated in SKOV3/PTX cells by sh-circCELSR1; (B) The qRT-PCR analysis confirmed that circCELSR1 expression level was significantly downregulated in HeyA-8/PTX cells by sh-circCELSR1; (C) The qRT-PCR assay indicated the expression level of CELSR1 in SKOV3/PTX cells treated with sh-circCELSR1; (D) The qRT-PCR assay indicated the expression level of CELSR1 in HeyA-8/PTX cells treated with sh-circCELSR1; (E) The qRT-PCR assay indicated the expression level of circCELSR1 in SKOV3/PTX cells treated with si-CELSR1; (F) The qRT-PCR assay indicated the expression level of circCELSR1 in HeyA-8/PTX cells treated with si-CELSR1; (G) The qRT-PCR assay indicated the expression level of CELSR1 in SKOV3/PTX cells treated with si-CELSR1; (H) The qRT-PCR assay indicated the expression level of CELSR1 in HeyA-8/PTX cells treated with si-CELSR1; (I) The qRT-PCR assay indicated the relative abundance of circCELSR1 in SKOV3 cells infected with circCELSR1 overexpressing adenovirus (circCELSR1 OE) or control GFP adenovirus (circCELSR1 CTL); (J) The qRT-PCR assay indicated the relative abundance of circCELSR1 in HeyA-8 cells infected with circCELSR1 overexpressing adenovirus (circCELSR1 OE) or control GFP adenovirus (circCELSR1 CTL); All tests were at least performed three times. Data were expressed as mean ± SD. ***P < 0.001;**P < 0.01;

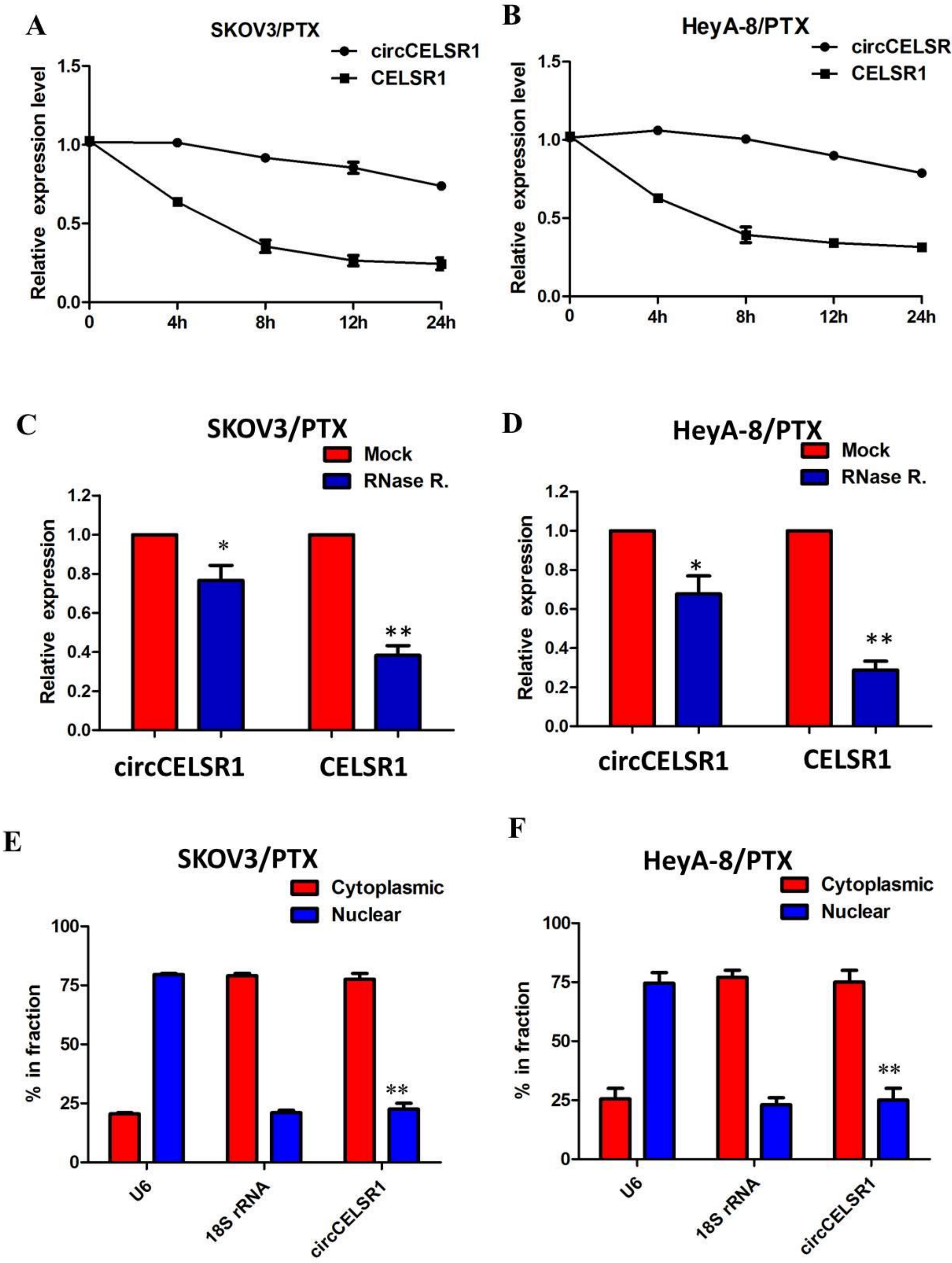

Figure S2 (A) The qRT-PCR for the abundance of circCELSR1 and CELSR1 in SKOV3/PTX cells treated with Actinomycin D at the indicated time point; (B) The qRT-PCR for the abundance of circCELSR1 and CELSR1 in HeyA-8/PTX cells treated with Actinomycin D at the indicated time point; (C) circCELSR1 was resistant to RNase R digestion in SKOV3/PTX cells. (D) circCELSR1 was resistant to RNase R digestion in HeyA-8/PTX cells. (E) Levels of circCELSR1 in the nuclear and cytoplasmic fractions of SKOV3/PTX cells; (F) Levels of circCELSR1 in the nuclear and cytoplasmic fractions of HeyA-8/PTX cells. Data are the means ± SD of three experiments, $*P<0.05$, $**P<0.01$;

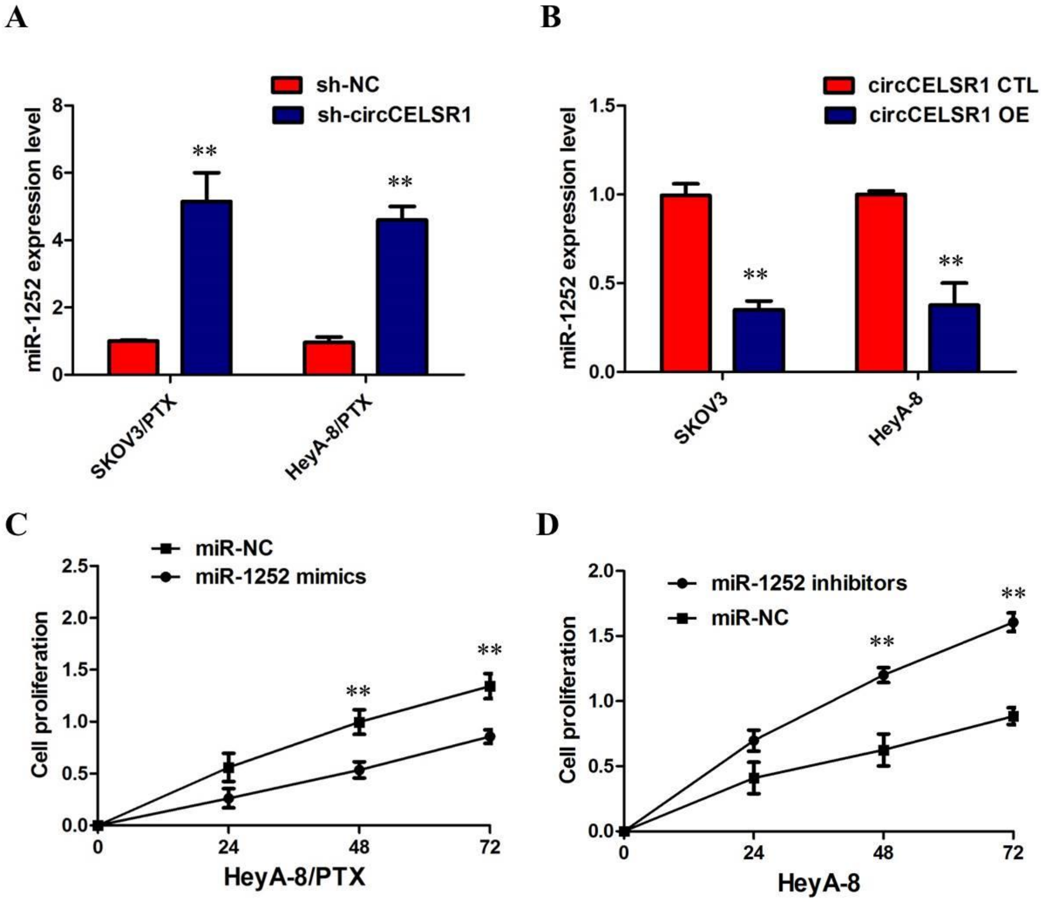

Figure S3 (A) Inhibition of circCELSR1 increased the expression level of miR-1252 in SKOV3/PTX and HeyA-8/PTX cells; (B) Overexpression of circCELSR1 decreased the expression level of miR-1252 in SKOV3 and HeyA-8 cells; (C) CCK-8 assay showed that miR-1252 overexpression could dramatically inhibit the proliferation of HeyA-8/PTX cells; (D) CCK-8 assay showed that inhibition of miR-1252 could dramatically promote the proliferation of HeyA-8 cells; All tests were at least performed three times. Data were expressed as mean ± SD. ***$P < 0.001$;**$P < 0.01$;

CircRNA Mirbase ID	TargetScan CircRNA (Top) - miRNA (Bottom) pairing
hsa_circ_0063809 (5' ... 3') hsa-miR-1203 (3' ... 5')	CGGCACGGCACAGCUGCUCCGGC ||| ||||||| CUCGACGUAGGACCGAGGCCC
hsa_circ_0063809 (5' ... 3') hsa-miR-1204 (3' ... 5')	GCCUACCAGCUGCUGGGCCACGU ||||||| UAUUACCUCUGGUCCGGUGCU
hsa_circ_0063809 (5' ... 3') hsa-miR-1205 (3' ... 5')	GGACGGCGCCAGGGCCCUGCAGC ||||||| GAGUUUCGUUUGGGACGUCU
hsa_circ_0063809 (5' ... 3') hsa-miR-1227 (3' ... 5')	GGCUACUUCAGCAACGUGGCACG ||||||| GACCCCUUUUCCCACCGUGC

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miRNA predictions

Site Type	CircRNA Start	CircRNA End	3' pairing	local AU	position	TA	SPS	context + score
7mer-m8	303	309	-0.016	0.091	-0.029	-0.066	-0.101	-0.241
7mer-m8	136	142	0.003	0.074	-0.043	-0.057	-0.099	-0.242
7mer-m8	48	54	0.003	0.129	-0.055	0.028	-0.064	-0.079
7mer-m8	334	340	0.012	0.086	-0.034	0.001	-0.071	-0.126

7mer-1a	143	149	0.008	0.072	-0.034	0.026	-0.017	-0.019
7mer-m8	96	102	0.003	0.106	-0.048	0.012	0.018	-0.029
7mer-m8	271	277	0.012	0.133	-0.025	0	-0.038	-0.038
7mer-m8	119	125	0.021	0.076	-0.045	-0.06	-0.068	-0.196
7mer-m8	434	440	0.003	0.081	-0.048	0.016	-0.069	-0.137

7mer-m8	163	169	0.021	0.111	-0.039	0.02	-0.064	-0.071
8mer-1a	460	467	0.003	0.101	-0.096	-0.012	0.014	-0.237
7mer-m8	261	267	0.003	0.134	-0.025	0.023	-0.069	-0.054
7mer-1a	424	430	0.001	0.035	-0.038	0.031	0.082	0.037
7mer-m8	320	326	0.021	0.115	-0.032	-0.009	0.012	-0.013

7mer-1a	37	43	0.001	0.067	-0.046	-0.055	-0.127	-0.234
7mer-m8	107	113	0.012	0.085	-0.047	-0.089	0.014	-0.145
7mer-1a	181	187	0.001	0.059	-0.03	-0.002	-0.104	-0.15
7mer-m8	105	111	0.012	0.099	-0.047	-0.004	0.029	-0.031
7mer-m8	128	134	0.012	0.125	-0.044	0.011	-0.047	-0.063

7mer-m8	299	305	0.003	0.144	-0.029	0.011	-0.047	-0.038
7mer-m8	181	187	0.021	0.11	-0.036	0.01	-0.084	-0.099
7mer-1a	260	266	-0.009	0.085	-0.022	-0.05	-0.079	-0.149
7mer-m8	135	141	0.003	0.051	-0.043	0.004	-0.119	-0.224
7mer-m8	235	241	-0.016	0.161	-0.029	0.033	-0.066	-0.037

7mer-m8	483	489	0.012	0.048	-0.055	0.031	-0.069	-0.153
7mer-1a	265	271	0.001	0.073	-0.021	0.011	-0.052	-0.062
7mer-m8	113	119	0.003	0.107	-0.046	-0.087	-0.067	-0.21

context + score percentile
75
78
71
78

76
81
46
83
80

64
97
68
83
70

82
68
73
74
58

48
62
63
89
63

88
65
73

Target gene	Representative transcript
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LTF	ENST00000231751.4
DDX53	ENST00000327968.5
PTPRF	ENST00000372414.3
NKX2-1	ENST00000354822.5
FZD8	ENST00000374694.1
QSOX1	ENST00000367602.3
MRPL22	ENST00000523037.1
GATSL2	ENST00000426327.3
CARD11	ENST00000396946.4
EMC1	ENST00000477853.1
ABCA6	ENST00000284425.2
TCP10L	ENST00000300258.3
EPS8	ENST00000543523.1
HBS1L	ENST00000367837.5
GNRHR	ENST00000420975.2
USP15	ENST00000353364.3
INSIG1	ENST00000342407.5
TCP1	ENST00000321394.7
NUDCD3	ENST00000355451.7
ZNF141	ENST00000240499.7
RANGAP1	ENST00000405486.1
TIMD4	ENST00000274532.2
TIMELESS	ENST00000229201.4
HPS4	ENST00000398145.2
SEC23B	ENST00000336714.3
RAB43	ENST00000476465.1
NDNF	ENST00000379692.4
WDR13	ENST00000218056.5
LLPH	ENST00000266604.2
LHPP	ENST00000368839.1
SLC25A4	ENST00000281456.6
C12orf79	ENST00000549802.1
LRP8	ENST00000306052.6
ADAM7	ENST00000175238.6
FAM229B	ENST00000368656.2
NUP93	ENST00000542526.1
ARGFX	ENST00000334384.3
DNAJC15	ENST00000379221.2
EIF2A	ENST00000460851.1

RNF126	ENST00000292363.5
CRHR2	ENST00000506074.2
SOBP	ENST00000317357.5
FUS	ENST00000254108.7
TCF3	ENST00000262965.5
TMEM39A	ENST00000319172.5
MFSD12	ENST00000398558.4
SHMT1	ENST00000316694.3
WDR75	ENST00000314761.4
LRRC34	ENST00000446859.1
SMTNL2	ENST00000338859.4
LRRC2	ENST00000395905.3
EBF4	ENST00000380648.4
GPR183	ENST00000376414.4
ANKS4B	ENST00000311620.5
GGACT	ENST00000376250.2
LMCD1	ENST00000157600.3
CRMP1	ENST00000324989.7
SF3A1	ENST00000215793.8
TIMM50	ENST00000599794.1
KIAA1715	ENST00000272748.4
NRG3	ENST00000372142.2
MARCH6	ENST00000274140.5
AQP1	ENST00000509504.1
ANKFY1	ENST00000341657.4
CELF3	ENST00000290585.4
IL10RA	ENST00000227752.3
FGB	ENST00000302068.4
VCAM1	ENST00000347652.2
KLF2	ENST00000248071.5
POLD4	ENST00000312419.3
COPS8	ENST00000354371.2
FAM208A	ENST00000493960.2
RPS6KL1	ENST00000555647.1
CYFIP1	ENST00000313077.7
CLDN11	ENST00000064724.3
LRRC40	ENST00000370952.3
SPATA6L	ENST00000381890.5
DLGAP3	ENST00000373347.1
FAM213A	ENST00000372187.5
C9orf156	ENST00000375119.3
ZNF334	ENST00000457685.2
NQO2	ENST00000338130.2
ARHGAP12	ENST00000311380.4
C16orf45	ENST00000300006.4
RWDD1	ENST00000466444.2
DNAJB4	ENST00000370763.5
RPS24	ENST00000435275.1
PXK	ENST00000463280.1
LRRC49	ENST00000260382.5
CLEC4C	ENST00000542353.1
GUCY1A3	ENST00000296518.7
CPED1	ENST00000310396.5
SOX17	ENST00000297316.4

PCNXL2	ENST00000258229.9
RNLS	ENST00000331772.4
CPVL	ENST00000265394.5
HSD11B1	ENST00000367028.2
CCRN4L	ENST00000280614.2
IFIT1	ENST00000371804.3
C11orf54	ENST00000528288.1
KIAA1551	ENST00000312561.4
DDRGK1	ENST00000354488.3
ZNF140	ENST00000355557.2
FAM120AOS	ENST00000423591.1
C8A	ENST00000361249.3
BLVRA	ENST00000402924.1
GLTSCR2	ENST00000246802.5
FAM127C	ENST00000391440.1
CHST2	ENST00000309575.3
MYH9	ENST00000216181.5
GPR56	ENST00000388812.4
PANK2	ENST00000497424.1
SOCS5	ENST00000306503.5
UQCR11	ENST00000589880.1
CFL2	ENST00000341223.3
ST20-MTHFS	ENST00000479961.1
MYO1F	ENST00000338257.8
PRMT7	ENST00000339507.5
MRPL39	ENST00000352957.4
HNRNPA0	ENST00000314940.4
INTS6	ENST00000311234.4
TNFAIP8L3	ENST00000327536.5
PRPF4	ENST00000374199.4
CACNA1C	ENST00000399655.1
CYB5D2	ENST00000301391.3
CYP20A1	ENST00000356079.4
SCN1A	ENST00000423058.2
BET1	ENST00000222547.3
CD1D	ENST00000368171.3
GPR35	ENST00000319838.5
FHL2	ENST00000409177.1
N6AMT1	ENST00000303775.5
BLOC1S2	ENST00000441611.1
MSRB2	ENST00000376510.3
PLCL1	ENST00000428675.1
PRDX2	ENST00000301522.2
FGG	ENST00000404648.3
MTHFS	ENST00000258874.3
CYB5A	ENST00000299438.9
SLA	ENST00000338087.5
GPC5	ENST00000377067.3
CHRFAM7A	ENST00000397827.3
APOBEC3F	ENST00000308521.5
PCK1	ENST00000319441.4
GPI	ENST00000415930.3
LOXL2	ENST00000389131.3
PPDPF	ENST00000370179.3

CACNA1B	ENST00000277551.2
PIK3AP1	ENST00000339364.5
GPR125	ENST00000334304.5
GPR25	ENST00000304244.2
C18orf32	ENST00000579820.1
ACE	ENST00000290866.4
PPP2R1A	ENST00000322088.6
TCEANC2	ENST00000234827.1
AKAP11	ENST00000025301.2
SYCP2L	ENST00000283141.6
BID	ENST00000317361.7
KCNQ5	ENST00000370398.1
RIT1	ENST00000368323.3
TMEM257	ENST00000408967.2
ACKR4	ENST00000249887.2
RNF41	ENST00000345093.4

Gene name	3P-seq tags + 5
POU class 2 associating factor 1	19
LIM domain containing preferred translocation	1894
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransfe	196
cytochrome P450, family 3, subfamily A, polype	5
cysteine-serine-rich nuclear protein 3	24
chromosome 9 open reading frame 152	5
lysophosphatidic acid receptor 6	5
serine palmitoyltransferase, small subunit B	15
calcium/calmodulin-dependent protein kinase IV	73
Alport syndrome, mental retardation, midface h	5
sterile alpha motif domain containing 12	57
XK, Kell blood group complex subunit-related f	5
potassium inwardly-rectifying channel, subfami	5
pleckstrin homology domain containing, family	7
atypical chemokine receptor 2	5
protein tyrosine phosphatase, receptor type, T	5
ribosomal protein L7a	4327
glutathione S-transferase omega 1	377
CD209 molecule	5
EH-domain containing 2	2072
eukaryotic translation initiation factor 4E bi	690
adiponectin, C1Q and collagen domain containin	5
guanine nucleotide binding protein (G protein)	3695
ferritin, heavy polypeptide 1	15624
EF-hand calcium binding domain 6	23
D-amino acid oxidase activator	5
progesterone receptor membrane component 2	2089
AP2 associated kinase 1	27
GSG1-like	5
myotubularin related protein 1	489
Cbl proto-oncogene, E3 ubiquitin protein ligas	309
zinc finger protein 544	173
family with sequence similarity 83, member F	5
chromosome 1 open reading frame 143	5
proline rich 4 (lacrimal)	29
poly (ADP-ribose) polymerase family, member 11	75
signal sequence receptor, delta	6838
vacuolar protein sorting 13 homolog B (yeast)	262
phosphatidylinositol-specific phospholipase C,	81
phosphotriesterase related	217
decapping mRNA 1B	715
SRY (sex determining region Y)-box 4	2736
tyrosine 3-monooxygenase/tryptophan 5-monooxyg	473
tropomyosin 4	332
myeloproliferative leukemia virus oncogene	0
dimethylarginine dimethylaminohydrolase 1	46
heme binding protein 1	2855
transmembrane protein 14E	5
RUN and SH3 domain containing 1	909
rhotekin 2	192
paraneoplastic Ma antigen 2	362
protein phosphatase 1, regulatory (inhibitor)	17
growth regulation by estrogen in breast cancer	30

SIX homeobox 2	75
opioid binding protein/cell adhesion molecule-	5
sorting nexin family member 27	46
solute carrier family 39, member 9	824
chromosome 10 open reading frame 40	5
Protein LOC388813	5
	5
Berardinelli-Seip congenital lipodystrophy 2 (	169
PQ loop repeat containing 3	26
sprouty homolog 3 (Drosophila)	5
Sec23 homolog A (S. cerevisiae)	413
cyclic nucleotide gated channel alpha 3	5
glutaredoxin (thioltransferase)	79
selectin L	5
chromosome 11 open reading frame 87	5
discs, large (Drosophila) homolog-associated p	1064
cystatin A (stefin A)	5
adenylate kinase 4	116
v-rel avian reticuloendotheliosis viral oncoge	116
tyrosine aminotransferase	5
potassium intermediate/small conductance calci	5
ubiquilin 2	70
fibrinogen-like 2	189
sterile alpha motif domain containing 13	253
dual specificity phosphatase 10	70
CD4 molecule	5
protein tyrosine phosphatase type IVA, member	5740
mitochondrial ribosomal protein S6	3816
NAD(P) dependent steroid dehydrogenase-like	5261
doublecortin	5
neuroblastoma 1, DAN family BMP antagonist	852
5-hydroxytryptamine (serotonin) receptor 2C, G	5
N-acylsphingosine amidohydrolase (non-lysosoma	5
hydroxy-delta-5-steroid dehydrogenase, 3 beta-	5
MINOS1-NBL1 readthrough	852
synaptophysin-like 2	69
A kinase (PRKA) anchor protein 5	75
small proline-rich protein 1A	5
ring finger protein 125, E3 ubiquitin protein	214
G protein-coupled receptor 111	5
insulin-like growth factor binding protein 4	4053
one cut homeobox 2	847
heart and neural crest derivatives expressed 1	5
Sad1 and UNC84 domain containing 1	376
keratin associated protein 3-3	5
mitogen-activated protein kinase kinase kinase	44
endoplasmic reticulum protein 27	5
transmembrane protein 178B	129
Fc fragment of IgA, receptor for	5
protein kinase, cAMP-dependent, regulatory, ty	583
membrane-spanning 4-domains, subfamily A, memb	5
gamma-aminobutyric acid (GABA) A receptor, bet	5
hydroxy-delta-5-steroid dehydrogenase, 3 beta-	5
glutamate receptor, ionotropic, N-methyl D-asp	5

protein phosphatase 1, regulatory subunit 12B	18
uncoupling protein 2 (mitochondrial, proton ca	32
BTB (POZ) domain containing 19	61
tRNA aspartic acid methyltransferase 1	248
trichohyalin-like 1	5
eukaryotic translation initiation factor 4H	5
sulfotransferase family, cytosolic, 1C, member	97
brain and acute leukemia, cytoplasmic	137
neurensin 1	5
KIAA1737	57
oleoyl-ACP hydrolase	5
interleukin 2 receptor, gamma	10
basic leucine zipper transcription factor, ATF	212
tripartite motif containing 58	68
GRB2-binding adaptor protein, transmembrane	5
small integral membrane protein 11	108
tetra-peptide repeat homeobox 1	5
diacylglycerol kinase, eta	46
neuronal differentiation 4	5
kinase suppressor of ras 2	22
R-spondin 4	5
zinc finger, matrin-type 1	5
heat shock 105kDa/110kDa protein 1	4109
transmembrane and ubiquitin-like domain contai	1043
clathrin, light chain A	167
ubiquitin-conjugating enzyme E2G 2	681
WW domain containing adaptor with coiled-coil	322
CD1a molecule	5
transferrin receptor	296
CD3d molecule, delta (CD3-TCR complex)	8
PHD finger protein 6	630
zinc finger protein 391	63
basigin	6876
CDNA FLJ26875 fis, clone PRS08969; Uncharacter	22
cell division cycle 16	279
trafficking protein particle complex 3-like	5
Uncharacterized protein	5
apolipoprotein L, 6	5
chromosome 6 open reading frame 164	5
neuroblastoma breakpoint family, member 8	5
pyruvate dehydrogenase kinase, isozyme 3	659
ring finger protein 150	518
nuclear cap binding protein subunit 2, 20kDa	4301
sprouty homolog 1, antagonist of FGF signaling	150
zinc finger protein 25	11
BTG family, member 2	758
transketolase-like 1	6
peroxisomal, testis specific 1	5
integrin, alpha V	2407
chromosome 11 open reading frame 82	579
forkhead box F1	836
Uncharacterized protein	5
zinc finger and BTB domain containing 37	213
StAR-related lipid transfer (START) domain con	767

MMS22-like, DNA repair protein	102
GS homeobox 1	5
estrogen-related receptor gamma	5
zinc finger protein 280D	173
SGT1, suppressor of G2 allele of SKP1 (S. cere	430
TSPY-like 4	5
coronin, actin binding protein, 2B	751
interleukin 26	5
glutamate-cysteine ligase, modifier subunit	809
integrin, beta-like 1 (with EGF-like repeat do	106
meiosis/spermiogenesis associated 1	16
palmitoyl-protein thioesterase 1	1961
serpin peptidase inhibitor, clade B (ovalbumin	285
family with sequence similarity 195, member B	164
heparan sulfate 6-O-sulfotransferase 3	598
CDNA FLJ27256 fis, clone SYN09689; Uncharacter	24
E2F transcription factor 7	308
poly (ADP-ribose) polymerase 2	2959
keratin associated protein 9-6	5
zinc finger protein 33A	39
kelch repeat and BTB (POZ) domain containing 4	7
paralemmin 2	35
transmembrane (C-terminal) protease, serine 12	5
archain 1	1139
ring finger protein 181	329
kynurenine 3-monooxygenase (kynurenine 3-hydro	5
ubinuclein 2	238
leupaxin	1533
ZFP3 zinc finger protein	29
FYVE, RhoGEF and PH domain containing 6	21
estrogen receptor binding site associated, ant	238
aminomethyltransferase	63
beaded filament structural protein 2, phakinin	8
inter-alpha-trypsin inhibitor heavy chain fami	5
nuclear factor, erythroid 2	11
villin 1	390
TAF6 RNA polymerase II, TATA box binding prote	8012
BCL2-associated athanogene 6	1221
solute carrier family 22, member 15	25
bestrophin 2	5
carbonic anhydrase X	5
apolipoprotein L domain containing 1	27
arrestin domain containing 4	10
solute carrier family 4, sodium bicarbonate co	17
transmembrane protein 33	1470
Down syndrome critical region gene 3	494
lysine (K)-specific demethylase 5A	118
Ras suppressor protein 1	10596
C1q and tumor necrosis factor related protein	5
zinc finger, BED-type containing 3	399
	5
coiled-coil domain containing 60	5
elongator acetyltransferase complex subunit 4	282
Transcription factor SOX-7; Uncharacterized pr	47

CDC42 effector protein (Rho GTPase binding) 2	449
late endosomal/lysosomal adaptor, MAPK and MTO	1317
cytochrome b5 reductase 4	329
optic atrophy 3 (autosomal recessive, with cho	137
transmembrane protein 138	1694
rotatin	288
	5
proline rich 15-like	159
protein phosphatase 1, regulatory subunit 8	1066
APEX nuclease (multifunctional DNA repair enzy	15798
TELO2 interacting protein 2	188
T-cell acute lymphocytic leukemia 2	21
Rac/Cdc42 guanine nucleotide exchange factor (	15
zinc finger protein 660	5
integrin, alpha E (antigen CD103, human mucosa	683
sterol carrier protein 2	3640
inturned planar cell polarity protein	105
LMBR1 domain containing 2	211
centrosomal protein 250kDa	25
sorting nexin 6	254
small integral membrane protein 3	3180
paternally expressed 10	8778
zinc finger protein 236	60
myelin oligodendrocyte glycoprotein	5
protein phosphatase 4, catalytic subunit	59
chloride intracellular channel 6	16
sialic acid acetylesterase	22
late cornified envelope 1D	5
fibroblast growth factor 12	150
vesicle-associated membrane protein 2 (synapto	1840
leucine rich repeat containing 16A	718
ribosomal RNA adenine dimethylase domain conta	367
small integral membrane protein 19	265
branched chain amino-acid transaminase 1, cyto	1346
guanine nucleotide binding protein (G protein)	199
B-cell CLL/lymphoma 11B (zinc finger protein)	73
docking protein 6	8
pleckstrin homology-like domain, family A, mem	82
chromosome 8 open reading frame 48	22
glutathione S-transferase mu 5	5
	12
transmembrane channel-like 2	5
CD160 molecule	5
polypyrimidine tract binding protein 1	7007
solute carrier family 10, member 7	77
Zic family member 4	5
osteoclast stimulatory transmembrane protein	5
karyopherin alpha 4 (importin alpha 3)	111
kelch-like family member 17	46
chromosome 15 open reading frame 41	48
Homo sapiens glycosyltransferase 54 domain-con	5
syntrophin, beta 2 (dystrophin-associated prot	254
spastic paraplegia 21 (autosomal recessive, Ma	227
glial cells missing homolog 1 (Drosophila)	5

glycophorin A (MNS blood group)	5
midnolin	621
peroxisomal biogenesis factor 2	662
regulator of G-protein signaling 20	77
transporter 2, ATP-binding cassette, sub-famil	466
tocopherol (alpha) transfer protein-like	265
pim-1 oncogene	2041
cardiotrophin 1	25
RAB27B, member RAS oncogene family	5
clock circadian regulator	86
zinc finger protein 627	105
family with sequence similarity 3, member C	15
cell division cycle 14A	123
Sel1 repeat containing 1	321
zinc finger protein 345	24
MOB kinase activator 3B	52
zinc finger protein 30	99
zinc finger protein 772	22
Rho guanine nucleotide exchange factor (GEF) 2	156
ADP-ribosylation factor-like 8B	664
v-akt murine thymoma viral oncogene homolog 3	168
cyclin K	1777
Mdm4 p53 binding protein homolog (mouse)	443
zinc finger protein 440	12
zinc finger protein 154	5
transmembrane channel-like 3	5
corneodesmosin	5
tripartite motif containing 67	41
	5
additional sex combs like 3 (Drosophila)	65
fibroblast growth factor 16	5
p21 protein (Cdc42/Rac)-activated kinase 3	8
WNK lysine deficient protein kinase 3	55
adenosine deaminase	116
discs, large homolog 1 (Drosophila)	813
retinol dehydrogenase 11 (all-trans/9-cis/11-c	1177
DEAH (Asp-Glu-Ala-His) box polypeptide 16	879
Uncharacterized protein	5
myeloid-associated differentiation marker	3436
Uncharacterized protein	937
cerebellin 3 precursor	30
RAB2B, member RAS oncogene family	171
family with sequence similarity 222, member B	100
UDP-Gal:betaGlcNAc beta 1,3-galactosyltransfer	5
T-cell acute lymphocytic leukemia 1	5
olfactory receptor, family 52, subfamily B, me	5
family with sequence similarity 73, member B	651
calcium/calmodulin-dependent protein kinase I	3500
elastin microfibril interfacer 3	12
zinc finger protein 444	1792
PHD finger protein 2	151
cystatin B (stefin B)	203
chemokine (C-X-C motif) ligand 12	719
growth hormone receptor	102

CDNA FLJ20147 fis, clone COL07954; HCG1781466;	253
integrin, alpha 2 (CD49B, alpha 2 subunit of V	50
ATPase, Ca++ transporting, plasma membrane 1	699
beta-gamma crystallin domain containing 3	46
zinc finger with KRAB and SCAN domains 8	281
high mobility group 20A	391
follistatin-like 1	6788
serine-rich single-pass membrane protein 1	5
oxoglutarate (alpha-ketoglutarate) receptor 1	7
cullin-associated and neddylation-dissociated	1568
chorionic somatomammotropin hormone 2	5
potassium channel tetramerization domain conta	693
mucin 3A, cell surface associated	20
histone cluster 1, H2bf	16
dynactin 3 (p22)	1816
caspase recruitment domain family, member 16	18
chromosome 15 open reading frame 26	5
transmembrane emp24 domain trafficking protein	3025
chromosome 5 open reading frame 64	5
late cornified envelope 1B	5
C2 calcium-dependent domain containing 3	605
peptidase inhibitor 3, skin-derived	26
profilin 2	2184
NADH dehydrogenase (ubiquinone) 1 alpha subcom	28
serine/threonine kinase 24	486
lymphocyte antigen 9	5
chromosome 20 open reading frame 141	5
fragile histidine triad	141
zinc finger, CCHC domain containing 17	100
tektin 1	5
N-acylsphingosine amidohydrolase (non-lysosoma	5
hydroxyprostaglandin dehydrogenase 15-(NAD)	140
KIAA1549	508
sulfotransferase family, cytosolic, 1B, member	5
fructosamine 3 kinase related protein	486
regulator of G-protein signaling 7	8
abhydrolase domain containing 10	929
angiopoietin-like 7	5
chromosome 20 open reading frame 85	5
lysozyme-like 2	5
pepsinogen 4, group I (pepsinogen A)	5
BRCA1 associated RING domain 1	162
stathmin-like 4	5
interferon-induced protein with tetratricopept	9
sentan, cilia apical structure protein	5
transmembrane protein 254	61
interferon regulatory factor 2 binding protein	30
RAD50 interactor 1	26
prostate and testis expressed 3	5
lysozyme-like 1	5
family with sequence similarity 13, member B	220
CWC27 spliceosome-associated protein homolog (	94
smoothened, frizzled family receptor	142
transmembrane protein 155	5

pepsinogen 3, group I (pepsinogen A)	5
uroplakin 2	5
DnaJ (Hsp40) homolog, subfamily C, member 19	223
signal transducer and activator of transcripti	326
oxidoreductase-like domain containing 1	1608
tripartite motif containing 22	163
testis-specific serine kinase 6	5
solute carrier family 44, member 3	13
praja ring finger 2, E3 ubiquitin protein liga	220
ER degradation enhancer, mannosidase alpha-lik	948
TSPY-like 1	2195
G patch domain containing 2-like	96
coiled-coil domain containing 112	370
LIM and senescent cell antigen-like domains 1	68
keratin associated protein 9-7	5
chromosome 2 open reading frame 76	11
zinc finger protein 704	124
regulator of G-protein signaling 5	56
keratin 37	5
SSU72 RNA polymerase II CTD phosphatase homolo	262
ARP3 actin-related protein 3 homolog B (yeast)	660
acyl-CoA synthetase medium-chain family member	5
solute carrier family 7 (amino acid transporte	15
histone cluster 2, H2be	256
V-set and immunoglobulin domain containing 1	5
ArfGAP with SH3 domain, ankyrin repeat and PH	196
keratin 78	5
hydroxycarboxylic acid receptor 1	38
RING1 and YY1 binding protein	342
mitotic spindle organizing protein 2B	44
MICAL C-terminal like	62
prefoldin subunit 4	4331
signal-regulatory protein gamma	5
claudin 9	5
trans-golgi network vesicle protein 23 homolog	5
acireductone dioxygenase 1	5881
arrestin, beta 2	158
aldehyde dehydrogenase 1 family, member A2	401
translocation associated membrane protein 2	2774
SPRY domain containing 4	1999
interleukin 17A	5
PDZ domain containing ring finger 4	5
protein prenyltransferase alpha subunit repeat	161
isoleucyl-tRNA synthetase	65
TMEM56-RWDD3 protein	49
S100 calcium binding protein A7A	5
nuclear assembly factor 1 ribonucleoprotein	1208
caseinolytic mitochondrial matrix peptidase ch	251
late cornified envelope 1E	5
ligand dependent nuclear receptor corepressor-	194
solute carrier family 39, member 11	544
kelch domain containing 10	347
neurotrophic tyrosine kinase, receptor, type 2	48
chromosome 3 open reading frame 55	7

testis expressed 30	231
HMG box domain containing 4	966
retinol binding protein 5, cellular	256
olfactory receptor, family 51, subfamily E, me	5
forkhead box P1	264
solute carrier family 16 (monocarboxylate tran	26
hypoxia inducible factor 3, alpha subunit	5
fatty acid amide hydrolase 2	65
WD repeat domain 26	1229
chromosome 9 open reading frame 142	1840
Uncharacterized protein	5
late cornified envelope 4A	5
transmembrane protein 59-like	33
zinc finger, DHHC-type containing 23	10
cholecystokinin A receptor	5
galactokinase 2	626
family with sequence similarity 71, member F1	5
myelin protein zero-like 1	3146
Ral GTPase activating protein, beta subunit (n	1120
plasmalemma vesicle associated protein	5
defensin, beta 110 locus	5
COX assembly mitochondrial protein 2 homolog (	87
Rap guanine nucleotide exchange factor (GEF) 1	335
RCAN family member 3	395
ADAM metallopeptidase domain 32	5
lymphocyte antigen 6 complex, locus D	5
transmembrane protein 260	44
wingless-type MMTV integration site family, me	13
retinol binding protein 3, interstitial	5
phosphodiesterase 3B, cGMP-inhibited	258
ribosomal modification protein rimK-like famil	164
coiled-coil domain containing 66	38
chemokine (C-X-C motif) ligand 17	8
solute carrier family 26 (anion exchanger), me	5
interferon regulatory factor 6	28
akirin 1	798
transportin 1	2041
proline-rich coiled-coil 2B	97
microfibrillar-associated protein 3-like	69
carboxypeptidase N, polypeptide 2	8
receptor accessory protein 1	49
inosine triphosphatase (nucleoside triphosphat	187
thymic stromal lymphopoietin	62
sidekick cell adhesion molecule 1	60
tripartite motif containing 4	694
glycolipid transfer protein	5
glutathione S-transferase mu 4	767
cyclin H	250
coiled-coil domain containing 149	187
serine/threonine kinase 35	263
serpin peptidase inhibitor, clade B (ovalbumin	5
small muscle protein, X-linked	19
microphthalmia-associated transcription factor	593
prostaglandin E synthase 3 (cytosolic)-like	139

aquaporin 2 (collecting duct)	5
adaptor-related protein complex 3, sigma 1 sub	24
vacuolar protein sorting 26 homolog A (S. pomb	127
transmembrane protein 194A	43
islet cell autoantigen 1,69kDa-like	82
zinc finger protein 654	456
RPA3 antisense RNA 1	22
mannosidase, alpha, class 1A, member 2	603
spindle and kinetochore associated complex sub	414
arginase 2	6
dynein, light chain, Tctex-type 3	27
SRSF protein kinase 1	114
ADP-ribosylation factor interacting protein 1	275
mitotic spindle organizing protein 2A	25
adaptor-related protein complex 1, sigma 3 sub	130
mannosidase, beta A, lysosomal-like	2819
potassium voltage-gated channel, KQT-like subf	5
argonaute RISC catalytic component 1	402
malectin	12084
ArfGAP with SH3 domain, ankyrin repeat and PH	185
oxysterol binding protein	101
aarF domain containing kinase 1	215
forkhead box L2	20
MAP3K7 C-terminal like	87
programmed cell death 1 ligand 2	64
MTERF domain containing 2	704
secretory carrier membrane protein 4	223
homeobox A10	1910
PHD finger protein 21B	8
DnaJ (Hsp40) homolog, subfamily C, member 4	67
secretagogin, EF-hand calcium binding protein	590
fibrinogen alpha chain	1401
RecQ mediated genome instability 2	17
UBX domain protein 10	5
	3180
gamma-aminobutyric acid (GABA) A receptor, alp	5
olfactory receptor, family 12, subfamily D, me	5
complement component 5a receptor 2	5
chromosome 12 open reading frame 36	5
SMAD family member 4	403
heat shock protein, alpha-crystallin-related,	121
unc-5 homolog C (C. elegans)	60
keratin associated protein 2-1	5
protocadherin 9	102
syntaxin 16	756
COMM domain containing 9	1146
chromosome 14 open reading frame 1	4423
prolyl 4-hydroxylase, alpha polypeptide II	1077
chemokine (C motif) receptor 1	5
tripartite motif containing 52	43
vacuolar protein sorting 52 homolog (S. cerevi	124
annexin A13	5
family with sequence similarity 107, member A	12
Homo sapiens coiled-coil domain-containing pro	5

nudix (nucleoside diphosphate linked moiety X)	17
protein tyrosine phosphatase, receptor type, C	7
leucine, glutamate and lysine rich 1	7
DENN/MADD domain containing 1B	6
carboxypeptidase A4	1319
forkhead box J2	9
sema domain, seven thrombospondin repeats (typ	98
exonuclease 5	237
tripartite motif containing 5	435
WAP four-disulfide core domain 1	196
cyclin-dependent kinase 17	475
aquaporin 4	10
nucleotide-binding oligomerization domain cont	8
5-hydroxytryptamine (serotonin) receptor 3E, i	5
dermatopontin	5
SH3 domain containing 19	245
proline synthetase co-transcribed homolog (bac	414
UDP-glucose ceramide glucosyltransferase	1200
pleckstrin homology domain containing, family	5
ankyrin repeat and SOCS box containing 11	5
claudin 8	5
chromosome 6 open reading frame 136	307
IKAROS family zinc finger 5 (Pegasus)	83
DIRAS family, GTP-binding RAS-like 2	5
peroxisomal biogenesis factor 11 beta	766
6-phosphofructo-2-kinase/fructose-2,6-biphosph	83
INTS3 and NABP interacting protein	423
disrupted in schizophrenia 1	132
GATA binding protein 3	136
insulin-like growth factor 2 mRNA binding prot	460
nicastrin	578
taste receptor, type 2, member 5	16
retinoblastoma binding protein 8	88
aspartate beta-hydroxylase domain containing 2	102
potassium voltage-gated channel, Isk-related f	5
abl-interactor 1	317
zinc finger, DHHC-type containing 15	5
coiled-coil domain containing 115	329
E2F transcription factor 3	91
phosphodiesterase 4B, cAMP-specific	127
acrosomal vesicle protein 1	5
aryl hydrocarbon receptor nuclear translocator	283
family with sequence similarity 71, member E1	89
Purkinje cell protein 4 like 1	23
RBM14-RBM4 readthrough	151
sperm-tail PG-rich repeat containing 1	24
keratin 31	5
phosphoglycerate kinase 2	5
nuclear factor I/B	1149
protein-L-isoaspartate (D-aspartate) O-methylt	476
immunoglobulin superfamily, DCC subclass, memb	12
small integral membrane protein 9	5
proteolipid protein 1	5
HGF activator	15

RNA binding motif protein 4	151
neuro-oncological ventral antigen 2	7
ubiquinol-cytochrome c reductase complex assem	500
RAB30, member RAS oncogene family	274
progestin and adipoQ receptor family member IX	233
tumor necrosis factor (ligand) superfamily, me	30
family with sequence similarity 60, member A	58
small proline-rich protein 4	5
S100 calcium binding protein A11	433
GC-rich sequence DNA-binding factor 2	88
solute carrier family 25, member 30	92
spermatogenesis associated 3	5
alcohol dehydrogenase 1A (class I), alpha poly	5
transmembrane emp24 protein transport domain c	3117
cyclin-dependent kinase 3	109
chromosome 20 open reading frame 26	5
RIC3 acetylcholine receptor chaperone	5
transmembrane 4 L six family member 4	348
inositol 1,4,5-trisphosphate receptor interact	893
cancer/testis antigen 62	5
midline 2	194
ataxin 7-like 1	67
COMM domain containing 2	833
methylcrotonoyl-CoA carboxylase 2 (beta)	1590
killer cell immunoglobulin-like receptor, two	5
ubiquitin-conjugating enzyme E2G 1	5620
zinc finger protein 552	9
killer cell immunoglobulin-like receptor, two	5
KIAA1671	549
keratin associated protein 5-2	5
HERV-H LTR-associating 3	5
family with sequence similarity 13, member C	343
serpin peptidase inhibitor, clade I (pancpin),	5
casein kappa	5
synapsin III	5
DnaJ (Hsp40) homolog, subfamily C, member 27	41
CAP-GLY domain containing linker protein famil	490
kinesin heavy chain member 2A	905
coiled-coil-helix-coiled-coil-helix domain con	8
oligodendrocyte lineage transcription factor 2	15
TMPRSS11B N-terminal like	5
solute carrier family 22 (organic cation/carni	0
keratin associated protein 9-9	5
thioredoxin-related transmembrane protein 2	1344
polymerase (RNA) III (DNA directed) polypeptid	216
protein phosphatase 1, regulatory subunit 3C	416
ring finger protein 165	18
intraflagellar transport 46 homolog (Chlamydom	214
homeobox A1	157
NAD(P)H dehydrogenase, quinone 1	4421
dermatan sulfate epimerase-like	26
H2B histone family, member M	5
E2F-associated phosphoprotein	2883
enamelin	5

distal-less homeobox 6	76
antioxidant 1 copper chaperone	43
cytochrome b561 family, member D1	105
signal recognition particle 54kDa	1789
insulinoma-associated 2	5
G protein-coupled receptor 39	151
sepiapterin reductase (7,8-dihydrobiopterin:NA	554
diencephalon/mesencephalon homeobox 1	31
NudC domain containing 2	308
HECT and RLD domain containing E3 ubiquitin pr	18
vestigial like 3 (Drosophila)	187
PBX/knotted 1 homeobox 2	46
Fc receptor-like 1	5
sulfotransferase family, cytosolic, 1C, member	16
triple QxxK/R motif containing	210
F-box protein 3	813
purine nucleoside phosphorylase	50
arginine and glutamate rich 1	9450
KIAA1147	73
B-cell acute lymphoblastic leukemia expressed	5
v-myc avian myelocytomatosis viral oncogene ho	22906
coiled-coil domain containing 39	5
NAD kinase	173
cytochrome P450, family 4, subfamily F, polype	121
ATP-binding cassette, sub-family B (MDR/TAP),	5
methylmalonyl CoA epimerase	34
histone cluster 1, H2bk	57
major intrinsic protein of lens fiber	5
ADP-ribosylarginine hydrolase	5
inositol hexakisphosphate kinase 3	8
ADP-ribosylation factor GTPase activating prot	6000
solute carrier organic anion transporter famil	1614
SprT-like N-terminal domain	1128
FK506 binding protein 8, 38kDa	118
exostosin-like glycosyltransferase 2	204
solute carrier family 25, member 46	391
SPRY domain containing 3	353
chromosome 14 open reading frame 2	1228
synaptotagmin XV	5
echinoderm microtubule associated protein like	62
Uncharacterized protein	5
RNA binding motif protein 22	4854
nuclear GTPase, germinal center associated	10
cytochrome P450, family 2, subfamily B, polype	5
RAR-related orphan receptor A	102
TM2 domain containing 2	1085
lin-7 homolog C (C. elegans)	1701
voltage-dependent anion channel 1	106
ring finger protein 121	610
toll-interleukin 1 receptor (TIR) domain conta	82
G protein-coupled receptor 27	781
placenta-specific 9	7
loricrin	5
inositol-trisphosphate 3-kinase B	5

protein tyrosine phosphatase, receptor type, H	21
ankyrin repeat domain 65	5
arylacetamide deacetylase	5
RNA binding motif protein, X-linked-like 2	5
SH2B adaptor protein 3	89
family with sequence similarity 76, member A	173
family with sequence similarity 89, member A	368
ATP-binding cassette, sub-family D (ALD), memb	53
ring finger and CHY zinc finger domain contain	821
interleukin 2 receptor, alpha	5
par-6 family cell polarity regulator beta	277
GPRIN family member 3	213
remodeling and spacing factor 1	216
membrane metallo-endopeptidase	37
RAB GTPase activating protein 1-like	364
homeobox B5	55
family with sequence similarity 187, member A	31
muscleblind-like splicing regulator 1	135
gamma-aminobutyric acid (GABA) A receptor, gam	5
gap junction protein, beta 1, 32kDa	96
HSPA (heat shock 70kDa) binding protein, cytop	368
ER lipid raft associated 1	86
solute carrier family 39 (zinc transporter), m	2413
sortilin-related VPS10 domain containing recep	88
plexin A2	8
paired box 7	7
OTU domain containing 6A	5
C-type lectin domain family 6, member A	5
retinoblastoma binding protein 4	486
zinc finger protein 561	156
von Hippel-Lindau tumor suppressor, E3 ubiquit	2386
SEC22 vesicle trafficking protein homolog A (S	294
T-cell leukemia/lymphoma 1B	5
aquaporin 8	7
ELAV like neuron-specific RNA binding protein	5
peptidylprolyl isomerase A (cyclophilin A)-lik	5
mitochondrial ribosomal protein L13	1730
cytochrome c oxidase assembly homolog 10 (yeas	72
peptidylprolyl isomerase A (cyclophilin A)-lik	5
olfactory receptor, family 52, subfamily L, me	5
protein kinase, DNA-activated, catalytic polyp	707
chemokine (C-C motif) ligand 22	5
eukaryotic elongation factor-2 kinase	115
transmembrane protein 218	553
peptidylprolyl isomerase A (cyclophilin A)-lik	5
peptidylprolyl isomerase A (cyclophilin A)-lik	5
peptidylprolyl isomerase A (cyclophilin A)-lik	5
calcium channel, voltage-dependent, gamma subu	5
long intergenic non-protein coding RNA 923	5
sperm associated antigen 6	23
hippocampus abundant transcript-like 2	111
phosphoribosyl pyrophosphate synthetase 1	2966
TBC1 domain family, member 5	400
HOP homeobox	55

ubiquitin-conjugating enzyme E2B	3421
acetyl-CoA acyltransferase 2	189
SLIT and NTRK-like family, member 5	429
Myb/SANT-like DNA-binding domain containing 4	304
calpain 9	5
interleukin 6 (interferon, beta 2)	472
interleukin-1 receptor-associated kinase 3	13
tyrosine 3-monooxygenase/tryptophan 5-monooxyg	7321
enhancer of rudimentary homolog (Drosophila)	843
alcohol dehydrogenase 6 (class V)	17
transmembrane protein 154	5
dopamine receptor D4	20
PAN2 poly(A) specific ribonuclease subunit hom	310
olfactory receptor, family 10, subfamily AD, m	5
complement component 9	5
secretory carrier membrane protein 5	127
THO complex 3	29
EWS RNA-binding protein 1	8833
zinc finger protein 259	265
Esophagus cancer-related gene-2 interaction su	30
Uncharacterized protein	5
transcription factor AP-2 gamma (activating en	22
TNF receptor-associated factor 3	833
solute carrier family 6 (neurotransmitter tran	83
carbohydrate (N-acetylgalactosamine 4-0) sulfo	20
WAP four-disulfide core domain 9	5
HIRA interacting protein 3	4526
CD68 molecule	267
transmembrane protein 167B	42
dual specificity phosphatase 9	3766
secreted protein, acidic, cysteine-rich (osteo	2467
zinc finger protein 460	164
ring finger protein 139	237
bone morphogenetic protein 8b	88
zinc finger, CCHC domain containing 8	297
PR domain containing 7	5
myeloid leukemia factor 2	623
regulator of microtubule dynamics 2	7
chemokine (C-X-C motif) ligand 9	5
basic helix-loop-helix family, member e40	1571
chromosome 9 open reading frame 85	57
cat eye syndrome chromosome region, candidate	5
suppressor APC domain containing 1	12
Fc fragment of IgG, low affinity IIIa, recepto	5
chloride intracellular channel 4	226
protein kinase, cAMP-dependent, regulatory, ty	1257
PR domain containing 1, with ZNF domain	48
chromosome 2 open reading frame 49	161
transient receptor potential cation channel, s	242
granulysin	5
THAP domain containing, apoptosis associated p	109
CD101 molecule	5
NDRG family member 3	960
clavesin 2	19

LY6/PLAUR domain containing 6	261
CDC42 small effector 2	1057
cystatin S	5
mbt domain containing 1	113
chromosome 10 open reading frame 82	5
chromosome 12 open reading frame 68	5
v-erb-b2 avian erythroblastic leukemia viral o	27
DDB1- and CUL4-associated factor 8	1924
GABA(A) receptor-associated protein	10137
cytidine deaminase	302
zinc finger protein 423	170
cyclin-dependent kinase 15	7
protein phosphatase 1, regulatory (inhibitor)	8
NME1-NME2 readthrough	191
T-box 3	71
cyclin T2	381
F-box protein 47	5
chromosome 11 open reading frame 72	5
megalencephalic leukoencephalopathy with subco	5
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialy	5
aprataxin and PNKP like factor	57
RAD51 recombinase	838
zinc finger protein 770	52
prostaglandin E synthase	248
Mdm1 nuclear protein homolog (mouse)	146
UDP glycosyltransferase 3 family, polypeptide	5
Fas-activated serine/threonine kinase	645
GINS complex subunit 1 (Psf1 homolog)	56
annexin A5	9387
ring finger protein 144A	124
calmegin	288
caspase 14, apoptosis-related cysteine peptida	5
zinc finger protein 676	5
Selenoprotein M	1505
nuclear receptor subfamily 4, group A, member	244
prostate and testis expressed 1	5
kelch repeat and BTB (POZ) domain containing 7	362
fission 1 (mitochondrial outer membrane) homol	11997
2’-deoxynucleoside 5’-phosphate N-hydrolase 1	101
dishevelled associated activator of morphogene	167
keratin associated protein 8-1	5
cystatin D	5
neurogenin 2	5
NFKB activating protein	422
phosphoribosyl pyrophosphate synthetase 2	739
LSM1 homolog, U6 small nuclear RNA associated	920
tropomyosin 1 (alpha)	21798
WAS protein family, member 2	311
homeobox D3	23
melanoma antigen family E, 2	5
mature T-cell proliferation 1	18
solute carrier family 28 (concentrative nucleo	14
F-box protein 28	461
PWWP domain containing 2A	272

kinectin 1 (kinesin receptor)	469
lymphocyte antigen 6 complex, locus G6C	5
ZFP69 zinc finger protein B	176
pleckstrin homology domain containing, family	529
transmembrane protein 200B	152
von Willebrand factor A domain containing 9	4511
zinc finger protein 436	73
phosphoglucomutase 2-like 1	183
HCG2028865; Uncharacterized protein	5
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialy	9
parvin, alpha	1912
chromosome 7 open reading frame 41	235
arachidonate 15-lipoxygenase	5
cytoplasmic polyadenylation element binding pr	48
Uncharacterized protein	5
nicolin 1	244
integral membrane protein 2C	67220
MEF2BNB-MEF2B readthrough	35
cystatin SN	5
SMAD family member 1	240
endoplasmic reticulum metallopeptidase 1	53
Sp8 transcription factor	95
phospholipid scramblase 2	5
chromosome 10 open reading frame 71	5
caspase 1, apoptosis-related cysteine peptidas	5
upstream transcription factor 1	5
retinoblastoma binding protein 9	102
major facilitator superfamily domain containin	257
StAR-related lipid transfer (START) domain con	17
zinc finger protein 264	412
LIM domain containing 2	90
serine/threonine kinase 32A	8
chromosome 14 open reading frame 39	5
CDK5 regulatory subunit associated protein 1-l	541
septin 6	1854
nucleolar and spindle associated protein 1	686
mirror-image polydactyly 1	45
olfactory receptor, family 9, subfamily Q, mem	5
ring finger protein 187	13589
KIAA0040	15
B and T lymphocyte associated	5
peptidylprolyl isomerase A (cyclophilin A)	878
methyltransferase like 15	17
coproporphyrinogen oxidase	377
pre-mRNA processing factor 6	689
PTC7 protein phosphatase homolog (S. cerevisia	817
notch 3	45
macrophage erythroblast attacher	5906
PHD finger protein 14	112
UDP-glucose pyrophosphorylase 2	4271
prolactin receptor	95
katanin p80 subunit B-like 1	105
X-prolyl aminopeptidase (aminopeptidase P) 1,	38
family with sequence similarity 92, member B	5

mannosidase, alpha, class 2A, member 1	1521
POU class 2 homeobox 1	83
zinc finger CCCH-type, antiviral 1-like	98
cytochrome P450, family 2, subfamily J, polype	22
Uncharacterized protein	5
glyoxalase domain containing 5	5
adenylate cyclase 1 (brain)	76
ADP-ribosylation factor-like 11	5
cysteine-rich hydrophobic domain 1	16
HCG1643653; Uncharacterized protein	5
stearoyl-CoA desaturase (delta-9-desaturase)	9726
long intergenic non-protein coding RNA 346	26
abhydrolase domain containing 2	210
ISY1-RAB43 readthrough	5
guanine nucleotide binding protein (G protein)	5
glycine receptor, beta	118
acyl-CoA synthetase long-chain family member 6	7
chronic lymphocytic leukemia up-regulated 1	5
casein kinase 1, epsilon	3032
solute carrier family 2 (facilitated glucose t	5
sal-like 3 (Drosophila)	64
motile sperm domain containing 2	76
relaxin 1	5
zinc finger protein 641	87
wingless-type MMTV integration site family, me	25
solute carrier family 2 (facilitated glucose t	47
butyrophilin, subfamily 3, member A2	5
neugrin, neurite outgrowth associated	1754
NIPA-like domain containing 4	17
NK3 homeobox 1	240
zinc finger protein 235	69
coiled-coil domain containing 126	846
neurogranin (protein kinase C substrate, RC3)	60
coiled-coil domain containing 121	5
SWT1 RNA endoribonuclease homolog (S. cerevisi	104
leucine-rich repeat, immunoglobulin-like and t	5
Uncharacterized protein	5
chromogranin A (parathyroid secretory protein	7
v-maf avian musculoaponeurotic fibrosarcoma on	608
aconitase 1, soluble	738
insulin-like growth factor 1 (somatomedin C)	19
ribosomal protein L32	2274
phosphodiesterase 6A, cGMP-specific, rod, alph	5
annexin A7	1433
transcription factor CP2	1274
melanoma antigen family A, 8	5
myotubularin related protein 11	16
sec1 family domain containing 1	41
V-set and immunoglobulin domain containing 10	355
centriole, cilia and spindle-associated protei	1210
interferon, alpha-inducible protein 6	141
solute carrier family 3 (amino acid transporte	1100
NEDD4 binding protein 2-like 1	92
interaction protein for cytohesin exchange fac	16

glycine-N-acyltransferase-like 2	23
MYST/Esa1-associated factor 6	440
ecto-NOX disulfide-thiol exchanger 2	215
ubiquitin specific peptidase 7 (herpes virus-a	656
ankyrin repeat domain 44	187
maelstrom spermatogenic transposon silencer	9
diffuse panbronchiolitis critical region 1	5
TNFAIP3 interacting protein 1	334
chemokine (C-C motif) ligand 1	6
aprataxin	310
replication initiator 1	2836
cysteine-serine-rich nuclear protein 2	104
family with sequence similarity 217, member B	175
ankyrin repeat domain 45	10
sorting nexin 13	100
lysophosphatidylcholine acyltransferase 1	298
fatty acyl CoA reductase 1	814
	5
signal peptidase complex subunit 2 homolog (S.	28
thioredoxin-related transmembrane protein 4	466
dickkopf WNT signaling pathway inhibitor 2	5
chromosome 4 open reading frame 26	5
zinc finger, DHHC-type containing 22	32
lin-28 homolog B (C. elegans)	118
vacuole membrane protein 1	2505
chemokine (C-C motif) receptor 3	5
high mobility group AT-hook 1	2024
RERG/RAS-like	17
ER degradation enhancer, mannosidase alpha-lik	535
keratin associated protein 5-7	5
ornithine aminotransferase	5
pleckstrin homology domain containing, family	3303
failed axon connections homolog (Drosophila)	95
zinc finger, RAN-binding domain containing 1	724
sclerostin domain containing 1	5
ubiquitin-conjugating enzyme E2N	321
glutathione peroxidase 6 (olfactory)	5
2,3-bisphosphoglycerate mutase	1028
chromosome X open reading frame 48	5
D-amino-acid oxidase	26
protein phosphatase, Mg2+/Mn2+ dependent, 1N (	79
calsyntenin 2	119
tripartite motif containing 66	33
collagen, type XV, alpha 1	371
cyclin M3	934
CD84 molecule	5
mitogen-activated protein kinase kinase kinase	226
solute carrier family 6 (neurotransmitter tran	5
trafficking protein particle complex 4	649
C-type lectin domain family 1, member B	5
mediator complex subunit 17	197
MYC binding protein	85
ELK4, ETS-domain protein (SRF accessory protei	39
TIA1 cytotoxic granule-associated RNA binding	1370

ubiquitin-conjugating enzyme E2R 2	2442
cadherin 7, type 2	42
Rho GTPase activating protein 11A	410
TSR2, 20S rRNA accumulation, homolog (S. cerev	233
shisa family member 6	5
proline rich 23A	5
eukaryotic translation initiation factor 4E bi	121
chromosome 2 open reading frame 42	13
carbonic anhydrase XIII	42
solute carrier family 9, subfamily A (NHE3, ca	2939
pecanex-like 4 (Drosophila)	268
v-myb avian myeloblastosis viral oncogene homo	39
chromosome X open reading frame 24	60
transmembrane protein 38A	158
phosphodiesterase 4C, cAMP-specific	5
solute carrier family 1 (glutamate/neutral ami	380
striatin, calmodulin binding protein	476
leucine rich repeat containing 41	1532
RAR-related orphan receptor C	42
transmembrane protein 215	5
exocyst complex component 6B	106
annexin A8	5
annexin A8-like 2	5
R3H domain containing-like	5
annexin A8-like 1	5
methyltransferase like 21B	51
attractin	39
POM121 transmembrane nucleoporin C	5
nephronophthisis 3 (adolescent)	44
receptor accessory protein 4	78
nudix (nucleoside diphosphate linked moiety X)	190
upper zone of growth plate and cartilage matri	5
major histocompatibility complex, class I, A	276
WW domain binding protein 1-like	5
long intergenic non-protein coding RNA 908	5
forkhead box R2	5
DEXH (Asp-Glu-X-His) box polypeptide 58	5
heterogeneous nuclear ribonucleoprotein A2/B1	25319
retinoblastoma binding protein 7	270
sprouty homolog 4 (Drosophila)	110
KIAA2018	23
RNA-binding region (RNP1, RRM) containing 3	419
relaxin 2	20
aspartoacylase	5
G protein-coupled receptor 12	5
flap structure-specific endonuclease 1	31
zinc finger, C4H2 domain containing	432
chromosome 12 open reading frame 77	5
matrilin 2	371
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosamin	5
hephaestin	44
FERM domain containing 6	508
interleukin 12 receptor, beta 2	5
heterogeneous nuclear ribonucleoprotein A1	2079

RAB3D, member RAS oncogene family	111
Scm-like with four mbt domains 1	116
cyclin F	1432
egl-9 family hypoxia-inducible factor 3	71
vaccinia related kinase 2	25
mitochondrially encoded NADH dehydrogenase 5	675
nescient helix loop helix 1	5
nuclear casein kinase and cyclin-dependent kin	1692
glutamine--fructose-6-phosphate transaminase 1	1313
serum/glucocorticoid regulated kinase 1	369
interferon-induced protein 44-like	11
Uncharacterized protein	5
B-cell CLL/lymphoma 7A	96
mitogen-activated protein kinase 1	630
cytochrome P450, family 7, subfamily B, polype	53
protein phosphatase, Mg2+/Mn2+ dependent, 1E	178
leukocyte receptor tyrosine kinase	5
ubiquilin 4	5
mohawk homeobox	165
melanoma antigen family D, 1	8092
family with sequence similarity 155, member A	118
v-myc avian myelocytomatosis viral oncogene ne	73
HCG20425, isoform CRA_a; Uncharacterized prote	283
regulator of G-protein signaling 21	5
methyltransferase like 6	20
synaptotagmin XI	750
IKAROS family zinc finger 4 (Eos)	329
crystallin, zeta (quinone reductase)-like 1	340
platelet-derived growth factor beta polypeptid	5
interleukin 6 signal transducer (gp130, oncost	213
interferon regulatory factor 2	420
family with sequence similarity 65, member B	7
chromosome 5 open reading frame 51	124
PHD finger protein 1	19
anaplastic lymphoma receptor tyrosine kinase	5
solute carrier family 15 (oligopeptide transpo	5
activating transcription factor 7 interacting	667
xenotropic and polytropic retrovirus receptor	544
myosin, heavy chain 10, non-muscle	134
itchy E3 ubiquitin protein ligase	769
popeye domain containing 2	7
armadillo repeat containing 8	398
tumor necrosis factor	5
oxysterol binding protein-like 11	101
protein kinase C, beta	81
golgi SNAP receptor complex member 2	1099
CUB domain containing protein 1	137
hedgehog interacting protein	65
3-ketodihydrosphingosine reductase	322
leukocyte immunoglobulin-like receptor, subfam	5
TBP-like 1	69
LanC lantibiotic synthetase component C-like 1	3395
maestro heat-like repeat family member 2A	13
zinc finger protein 608	22

claudin 4	64
kallikrein-related peptidase 5	5
HCG1997999; cDNA FLJ33996 fis, clone DFNES2008	44
signal transducer and activator of transcripti	33
Uncharacterized protein	5
PCI domain containing 2	508
chromosome 7 open reading frame 72	5
solute carrier family 32 (GABA vesicular trans	5
keratin 4	5
ankyrin repeat domain 17	1334
TatD DNase domain containing 2	894
ADP-ribosylation factor-like 15	119
HECT domain containing E3 ubiquitin protein li	1514
	5
S100 calcium binding protein A4	943
splicing factor 1	17473
TBC1 domain family, member 28	5
ATP-binding cassette, sub-family B (MDR/TAP),	5
lens epithelial protein	5
phospholipase D1, phosphatidylcholine-specific	128
zinc finger and BTB domain containing 8 opposi	74
ash2 (absent, small, or homeotic)-like (Drosop	140
HIG1 hypoxia inducible domain family, member 1	254
ring finger protein 169	204
trafficking protein particle complex 6B	69
N-acylethanolamine acid amidase	115
calneuron 1	5
cortactin binding protein 2	29
male-specific lethal 2 homolog (Drosophila)	175
POZ (BTB) and AT hook containing zinc finger 1	165
chemokine (C-X3-C motif) receptor 1	17
ribonuclease, RNase A family, 13 (non-active)	5
nebulette	181
ankyrin repeat domain 13A	1644
IQ motif containing J	5
fibroblast growth factor 13	17
prepronociceptin	13
host cell factor C1 regulator 1 (XPO1 dependen	2156
prospero homeobox 1	131
chromosome 10 open reading frame 25	29
eukaryotic translation initiation factor 1	415
ALX homeobox 4	52
ets variant 3	37
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosamin	57
coiled-coil domain containing 176	61
family with sequence similarity 227, member B	44
myozenin 3	8
excision repair cross-complementing rodent rep	36
keratin associated protein 5-4	5
zinc finger and BTB domain containing 16	73
5’-nucleotidase domain containing 3	235
ribonuclease, RNase A family, 1 (pancreatic)	5
polymerase (RNA) III (DNA directed) polypeptid	47
cannabinoid receptor interacting protein 1	29

ninjurin 2	11
Uncharacterized protein; cDNA FLJ46300 fis, cl	5
BCL2-like 2	1380
myelin protein zero-like 3	59
wingless-type MMTV integration site family, me	2080
Ras association (RalGDS/AF-6) domain family me	515
adaptor-related protein complex 3, mu 1 subuni	601
programmed cell death 5	158
tumor necrosis factor, alpha-induced protein 8	5
LIM domain and actin binding 1	780
destrin (actin depolymerizing factor)	10116
xylosylprotein beta 1,4-galactosyltransferase,	2968
neurexin 2	5
solute carrier family 2 (facilitated glucose t	14
cofilin 1 (non-muscle)	341
acyl-CoA thioesterase 4	5
chromosome 16 open reading frame 47	8
yippee-like 5 (Drosophila)	307
arginine decarboxylase	15
BCL2/adenovirus E1B 19kD interacting protein 1	13
Wolf-Hirschhorn syndrome candidate 1-like 1	481
DDB1 and CUL4 associated factor 12-like 2	20
transmembrane protein 165	2603
protein O-glucosyltransferase 1	262
chymotrypsin C (caldecrin)	5
family with sequence similarity 118, member B	788
establishment of sister chromatid cohesion N-a	94
butyrophilin, subfamily 3, member A1	5
thyroid peroxidase	5
RAB7A, member RAS oncogene family	7894
olfactomedin-like 2B	5
delta(4)-desaturase, sphingolipid 2	5
growth factor independent 1 transcription repr	154
tetratricopeptide repeat domain 26	211
VAMP (vesicle-associated membrane protein)-ass	391
nuclear receptor subfamily 1, group I, member	5
CD302 molecule	860
vestigial like 2 (Drosophila)	5
nonhomologous end-joining factor 1	33
muskelin 1, intracellular mediator containing	477
Rho guanine nucleotide exchange factor (GEF) 1	815
Sep (O-phosphoserine) tRNA:Sec (selenocysteine	279
developmental pluripotency associated 4	5
RecQ mediated genome instability 1	409
Rho GTPase activating protein 19	1051
protein phosphatase, Mg2+/Mn2+ dependent, 1L	59
dynactin associated protein	5
extracellular matrix protein 1	575
mitochondrial elongation factor 1	2319
multiple C2 domains, transmembrane 2	59
family with sequence similarity 126, member B	132
endothelin receptor type A	35
CSRP2 binding protein	408
male-specific lethal 1 homolog (Drosophila)	4715

coiled-coil domain containing 155	5
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosamin	5
collagen, type XXII, alpha 1	5
family with sequence similarity 46, member B	18
holocytochrome c synthase	1615
fyn-related kinase	37
chromosome 17 open reading frame 51	464
potassium voltage-gated channel, subfamily H (	157
phosphatidylserine synthase 1	91
deiodinase, iodothyronine, type I	5
neurensin 2	101
ankyrin repeat domain 13C	369
lin-54 homolog (C. elegans)	228
sparc/osteonectin, cwcv and kazal-like domains	935
translocase of inner mitochondrial membrane 10	290
transmembrane 9 superfamily member 2	5046
V-set and transmembrane domain containing 2A	5
G protein-coupled receptor 151	5
chromosome 9 open reading frame 170	5
olfactory receptor, family 2, subfamily H, mem	5
solute carrier family 2 (facilitated glucose t	5
retinol dehydrogenase 12 (all-trans/9-cis/11-c	20
mesencephalic astrocyte-derived neurotrophic f	1895
mitogen-activated protein kinase kinase kinase	187
methyltransferase like 7B	58
sodium leak channel, non-selective	5
succinate dehydrogenase complex assembly facto	545
Vpr (HIV-1) binding protein	102
tectonic family member 3	1900
coiled-coil domain containing 141	5
coiled-coil domain containing 94	127
SRY (sex determining region Y)-box 9	2595
LRP2 binding protein	5
leucine-rich repeats and immunoglobulin-like d	241
carbonic anhydrase XII	42
MAX dimerization protein 4	1173
CD207 molecule, langerin	5
neuroblastoma breakpoint family, member 6	5
R-spondin 3	118
ankyrin repeat and death domain containing 1B	18
G protein-coupled receptor 61	5
ankyrin repeat and SOCS box containing 6	725
urotensin 2B	13
SEC62 homolog (S. cerevisiae)	746
tetratricopeptide repeat domain 30B	63
ubiquitin family domain containing 1	6826
Dexi homolog (mouse)	1646
ectonucleoside triphosphate diphosphohydrolase	136
caspase recruitment domain family, member 8	159
acidic (leucine-rich) nuclear phosphoprotein 3	1003
tripartite motif containing 14	44
RAD21 homolog (S. pombe)	5
leukocyte receptor cluster (LRC) member 8	244
GA binding protein transcription factor, alpha	8

dopamine receptor D2	5
neuropeptide Y receptor Y2	5
dynamin 3	59
melanoma antigen family D, 4	5
UDP-Gal:betaGlcNAc beta 1,3-galactosyltransfer	5
syndecan binding protein (syntenin)	1071
cytochrome P450, family 2, subfamily A, polype	5
casein kinase 2, alpha 1 polypeptide	1927
melanoma antigen family D, 4B	5
spermatogenesis associated 19	5
sema domain, transmembrane domain (TM), and cy	106
dehydrodolichyl diphosphate synthase	325
zinc finger protein 384	8
leucine zipper protein 2	33
Fas (TNFRSF6)-associated via death domain	79
potassium voltage-gated channel, Shal-related	23
serine incorporator 3	1218
chromosome 5 open reading frame 24	2668
solute carrier family 16, member 14	34
DnaJ (Hsp40) homolog, subfamily A, member 3	3281
phosphoinositide-3-kinase, regulatory subunit	5
keratin associated protein 5-11	5
ubiquitin specific peptidase 28	85
cytochrome b561 family, member D2	6
transmembrane protein 253	25
mab-21-like 2 (C. elegans)	63
spermine synthase	14
steroid-5-alpha-reductase, alpha polypeptide 1	2684
CD47 molecule	520
tumor necrosis factor receptor superfamily, me	93
solute carrier family 13 (sodium-dependent cit	4848
zinc finger protein 805	58
chromosome 1 open reading frame 61	5
butyrophilin, subfamily 1, member A1	5
lymphocyte transmembrane adaptor 1	5
zinc finger E-box binding homeobox 1	59
ADP-ribosylation factor interacting protein 2	798
chromosome 9 open reading frame 91	151
nudE neurodevelopment protein 1-like 1	396
protein tyrosine phosphatase-like (proline ins	1275
RAP2B, member of RAS oncogene family	594
scinderin	23
SEC14-like 1 (S. cerevisiae)	1399
NME/NM23 nucleoside diphosphate kinase 2	191
dynein, light chain, roadblock-type 1	970
QKI, KH domain containing, RNA binding	323
pleckstrin homology domain containing, family	1358
DAZ associated protein 2	4265
calcium/calmodulin-dependent protein kinase ki	1157
BCL2-like 11 (apoptosis facilitator)	105
formin binding protein 1-like	219
glutamate decarboxylase 2 (pancreatic islets a	5
radixin	44
zinc finger protein 8	24

SIX homeobox 3	15
feline leukemia virus subgroup C cellular rece	29
doublesex and mab-3 related transcription fact	21
transmembrane protein with metallophosphoester	22
neuronal pentraxin I	1876
CD109 molecule	1272
heart and neural crest derivatives expressed 2	30
transmembrane protein 200A	1609
chromosome 18 open reading frame 21	410
homeobox C10	152
unc-5 homolog D (C. elegans)	37
solute carrier family 31 (copper transporter),	171
frizzled family receptor 3	192
ezrin	3757
BTB (POZ) domain containing 9	65
STT3B, subunit of the oligosaccharyltransferas	4458
tubulin tyrosine ligase-like family, member 7	93
RAB33B, member RAS oncogene family	270
neurocalcin delta	49
chromosome 21 open reading frame 49	5
cutaneous T-cell lymphoma-associated antigen 1	5
keratin associated protein 4-12	31
chromosome 12 open reading frame 40	5
galactose mutarotase (aldose 1-epimerase)	963
Uncharacterized protein	9
erythrocyte membrane protein band 4.1-like 2	353
transmembrane protein 106B	615
mitochondrial calcium uniporter	2421
nuclear factor of activated T-cells 5, tonicit	128
regulatory factor X, 3 (influences HLA class I	37
shisa family member 9	5
asparaginase homolog (S. cerevisiae)	5
solute carrier family 17 (vesicular glutamate	5
dynein assembly factor with WDR repeat domains	82
sprouty-related, EVH1 domain containing 2	53
CUGBP, Elav-like family member 2	45
sorting nexin 18	174
sterol O-acyltransferase 2	823
non-SMC condensin I complex, subunit H	217
secretory carrier membrane protein 2	101
glypican 2	52
presenilin enhancer gamma secretase subunit	322
zinc finger protein 41	86
RAB31, member RAS oncogene family	726
golgin A1	334
histone cluster 1, H2bd	236
caspase 2, apoptosis-related cysteine peptidas	274
Hepatoma-derived growth factor-related protein	2577
ELOVL fatty acid elongase 7	52
protein-L-isoaspartate (D-aspartate) O-methylt	136
SLAM family member 6	5
guanine nucleotide binding protein (G protein)	50
family with sequence similarity 83, member A	22
thymocyte selection associated family member 2	41

F-box and WD repeat domain containing 11	81
major histocompatibility complex, class I, G	5
gap junction protein, beta 6, 30kDa	5
leucine-rich repeat kinase 2	37
acyl-CoA dehydrogenase family, member 8	329
HRAS-like suppressor family, member 5	5
signaling threshold regulating transmembrane a	7
lysosomal-associated membrane protein 3	11
ATPase, class II, type 9A	1511
BCL2/adenovirus E1B 19kDa interacting protein	203
guanylate binding protein 4	5
transmembrane protein 100	86
fibulin 7	44
LOC644617 protein; Uncharacterized protein	430
interleukin-1 receptor-associated kinase 4	223
MANSC domain containing 1	185
hook microtubule-tethering protein 3	403
desumoylating isopeptidase 2	147
guanylate binding protein family, member 6	5
solute carrier family 1 (glial high affinity g	5
colony stimulating factor 2 receptor, beta, lo	5
	5
ankyrin repeat and BTB (POZ) domain containing	180
polymerase (DNA-directed), delta 3, accessory	371
family with sequence similarity 98, member A	89
protein kinase C, iota	103
Lix1 homolog (mouse)-like	695
pyruvate dehyrogenase phosphatase catalytic su	102
cell division cycle 20B	5
calreticulin	17017
SYS1 Golgi-localized integral membrane protein	384
pleckstrin homology domain containing, family	767
sphingosine-1-phosphate receptor 1	251
GRB2-associated binding protein 2	627
mastermind-like 2 (Drosophila)	104
chromosome 14 open reading frame 23	5
solute carrier family 2 (facilitated glucose t	17
sodium channel, voltage-gated, type IV, beta s	13
mitogen-activated protein kinase 10	5
chromosome 1 open reading frame 158	5
deleted in azoospermia 3	5
cannabinoid receptor 1 (brain)	40
cyclin-dependent kinase 6	1116
tripartite motif containing 8	525
SLP adaptor and CSK interacting membrane prote	5
Iron/zinc purple acid phosphatase-like protein	5
aldo-keto reductase family 1, member E2	5
hepatocyte nuclear factor 4, gamma	5
plasmolipin	22
MOB kinase activator 1B	54
seryl-tRNA synthetase 2, mitochondrial	700
solute carrier family 22 (organic anion/urate	5
otogelin-like	5
otopetrin 2	5

upstream binding protein 1 (LBP-1a)	1418
zinc finger protein 585B	46
syntaxin 7	1395
astrotactin 2	39
sorting nexin 19	1157
coagulation factor VIII, procoagulant componen	16
collagen, type XXV, alpha 1	270
ribosomal protein S9	54
bromodomain adjacent to zinc finger domain, 2B	25
synuclein, beta	5
pyrimidinergic receptor P2Y, G-protein coupled	5
testis expressed 35	5
programmed cell death 7	64
zinc finger protein, Y-linked	5
WD repeat domain 70	23
coiled-coil domain containing 88A	141
homeobox A3	57
zinc finger CCCH-type, antiviral 1	45
nuclear receptor subfamily 6, group A, member	1082
histone cluster 1, H2bn	29
claspin	92
glycerol kinase 5 (putative)	73
retinol dehydrogenase 16 (all-trans)	13
zinc finger protein 441	5
deleted in azoospermia 4	5
regulator of chromosome condensation 1	1156
chromosome 19 open reading frame 66	567
mitochondrial inner membrane organizing system	287
UDP-N-acetyl-alpha-D-galactosamine:polypeptide	114
integrin, alpha L (antigen CD11A (p180), lymph	340
ATP-binding cassette, sub-family A (ABC1), mem	5
N-acetyltransferase 16 (GCN5-related, putative	5
fatty acid binding protein 7, brain	5
NADH dehydrogenase (ubiquinone) complex I, ass	68
pre-mRNA processing factor 4B	602
family with sequence similarity 169, member B	5
septin 3	241
tumor protein D52-like 3	5
Fc receptor-like 6	5
melanoma associated antigen (mutated) 1-like 1	50
transmembrane protein 62	9
angiomotin like 1	712
protein tyrosine phosphatase, non-receptor typ	301
proline-rich coiled-coil 1	2351
zinc finger CCCH-type containing 12C	150
PILR alpha associated neural protein	8
antagonist of mitotic exit network 1 homolog (	125
grainyhead-like 2 (Drosophila)	5
lactate dehydrogenase A	375
NLR family member X1	36
sodium channel, voltage gated, type VIII, alph	44
C-type lectin domain family 4, member D	5
coronin, actin binding protein, 1C	1970
recoverin	5

La ribonucleoprotein domain family, member 4	35
FERM domain containing 5	161
mitogen-activated protein kinase kinase kinase	634
bone morphogenetic protein 7	83
zinc binding alcohol dehydrogenase domain cont	207
zinc finger protein 709	90
mannosidase, endo-alpha-like	381
	51
potassium channel, subfamily K, member 13	11
tachykinin receptor 2	5
cytosolic iron-sulfur protein assembly 1	1143
Zic family member 2	1173
sodium channel, voltage-gated, type III, beta	10
CD72 molecule	7
zinc finger and BTB domain containing 41	33
coiled-coil domain containing 50	961
polycomb group ring finger 5	176
deleted in colorectal carcinoma	5
matrix metallopeptidase 16 (membrane-inserted)	12
zinc fingers and homeoboxes 1	88
sodium channel, non-voltage-gated 1, beta subu	5
fibrillin 1	798
pellino E3 ubiquitin protein ligase family mem	257
trafficking protein, kinesin binding 2	353
potassium voltage-gated channel, subfamily G,	0
glutathione S-transferase mu 1	5
CD83 molecule	414
hematopoietic cell-specific Lyn substrate 1	6
synaptotagmin IV	11
chromosome 1 open reading frame 213	49
NECAP endocytosis associated 1	13
collagen, type V, alpha 2	4327
family with sequence similarity 69, member A	171
collagen, type IV, alpha 3 (Goodpasture antige	286
Serine--tRNA ligase, mitochondrial	700
tumor necrosis factor (ligand) superfamily, me	85
ATPase, H+ transporting, lysosomal accessory p	2095
matrix-remodelling associated 7	421
leucine rich repeat neuronal 4	5
phosphatidylserine decarboxylase	61
deleted in azoospermia 2	5
ubiquitin specific peptidase 51	26
inhibitor of CDK, cyclin A1 interacting protei	6
phosphate cytidylyltransferase 1, choline, bet	5
prickle homolog 2 (Drosophila)	20
platelet-activating factor acetylhydrolase 2,	287
glutamyl aminopeptidase (aminopeptidase A)	10
aldehyde dehydrogenase 9 family, member A1	4094
transmembrane 9 superfamily protein member 4	3096
solute carrier family 6 (neurotransmitter tran	280
cellular repressor of E1A-stimulated genes 1	318
phosphatidylinositol-4,5-bisphosphate 3-kinase	5
myeloma overexpressed	14
coilin	5

tetratricopeptide repeat domain 18	7
myocyte enhancer factor 2B	35
CD300 molecule-like family member g	5
membrane-associated ring finger (C3HC4) 8, E3	48
polymerase (RNA) III (DNA directed) polypeptid	67
dysferlin	47
pyroglutamylated RFamide peptide receptor	0
zinc finger protein 852	26
sorting nexin 17	479
Kruppel-like factor 15	7
isopentenyl-diphosphate delta isomerase 1	827
hyperpolarization activated cyclic nucleotide-	41
suppressor of defective silencing 3 homolog (S	224
ERO1-like (S. cerevisiae)	1333
mediator complex subunit 8	745
complement component 5a receptor 1	5
KN motif and ankyrin repeat domains 2	1735
cystinosin, lysosomal cystine transporter	308
leukocyte immunoglobulin-like receptor, subfam	5
tafazzin	1269
Ca++-dependent secretion activator	5
family with sequence similarity 133, member A	14
nicotinamide nucleotide adenylyltransferase 2	18
family with sequence similarity 180, member A	51
DnaJ (Hsp40) homolog, subfamily A, member 1	789
histone deacetylase 9	13
cAMP responsive element binding protein 5	54
transmembrane BAX inhibitor motif containing 1	2201
G protein-coupled receptor 135	40
phosphoinositide-3-kinase, regulatory subunit	335
protein phosphatase 1, regulatory subunit 12A	276
jumonji domain containing 8	164
ADP-ribosylation factor-like 2	7073
vesicle-associated membrane protein 1 (synapto	8
protein tyrosine phosphatase, non-receptor typ	52
NK1 homeobox 2	5
spermatogenesis and oogenesis specific basic h	15
F-box protein 21	1035
glyceraldehyde-3-phosphate dehydrogenase, sper	5
phosphatidylinositol-4-phosphate 3-kinase, cat	5
sortilin-related VPS10 domain containing recep	85
RAB, member of RAS oncogene family-like 3	165
coiled-coil domain containing 103	72
sirtuin 1	220
FGFR1 oncogene partner 2	104
membrane magnesium transporter 1	113
ADAM-like, decysin 1	5
cholinergic receptor, nicotinic, beta 1 (muscl	56
mitochondrial ribosomal protein S11	1452
coiled-coil domain containing 140	5
proline rich membrane anchor 1	5
hair growth associated	248
centrosomal protein 290kDa	10
tripartite motif containing 27	492

transmembrane protease, serine 3	5
T-box 5	68
docking protein 5	5
Rho guanine nucleotide exchange factor (GEF) 7	361
CXXC finger protein 4	121
chromosome 19 open reading frame 10	1263
chaperonin containing TCP1, subunit 4 (delta)	153
muscleblind-like splicing regulator 3	593
ribosomal protein S6 kinase, 70kDa, polypeptid	16
monoamine oxidase B	32
family with sequence similarity 178, member A	130
zinc finger protein 260	165
hyperpolarization activated cyclic nucleotide-	19
URGCP-MRPS24 readthrough	110
ubiquitin specific peptidase 39	6197
guanylate cyclase 2C (heat stable enterotoxin	5
copine III	756
APEX nuclease (apurinic/apyrimidinic endonucle	972
polymerase (RNA) I polypeptide D, 16kDa	2372
solute carrier family 16 (monocarboxylate tran	707
mitochondrial ribosomal protein L50	56
chromosome 12 open reading frame 61	5
receptor-interacting serine-threonine kinase 3	5
prostaglandin E synthase 3 (cytosolic)	93
tripartite motif containing 44	4203
potassium inwardly-rectifying channel, subfami	5
protein kinase, X-linked	12
mindbomb E3 ubiquitin protein ligase 1	897
signal-regulatory protein beta 1	5
exportin 7	647
Uncharacterized protein	21
zinc finger and SCAN domain containing 32	8
KIAA1456	24
KIAA1217	320
NECAP endocytosis associated 2	1011
stannin	663
solute carrier family 7, member 14	5
RUN and FYVE domain containing 2	15
solute carrier family 6 (proline IMINO transpo	5
fibroblast growth factor 7	5
NFAT activating protein with ITAM motif 1	7
protease, serine, 8	5
zinc finger protein 302	13
leucine rich repeat containing 8 family, membe	71
heat shock 27kDa protein family, member 7 (car	5
lipoprotein lipase	7658
PR domain containing 6	69
von Willebrand factor C domain containing prot	5
Rap guanine nucleotide exchange factor (GEF) 6	38
DBF4 homolog B (S. cerevisiae)	34
paired box 1	5
immediate early response 5-like	24
G1 to S phase transition 2	97
polymerase (RNA) III (DNA directed) polypeptid	678

FYN binding protein	5
calcium/calmodulin-dependent protein kinase II	938
surfactant protein A1	5
breast carcinoma amplified sequence 3	339
uncharacterized protein LOC100127983	579
protease, serine, 16 (thymus)	77
striatin, calmodulin binding protein 3	697
phosphatidylinositol-5-phosphate 4-kinase, typ	148
transmembrane protein 40	5
Protein LOC400655	5
pleckstrin 2	44
bone morphogenetic protein receptor, type II (	287
XK, Kell blood group complex subunit-related,	11
IKAROS family zinc finger 3 (Aiolos)	7
pleiomorphic adenoma gene 1	58
ganglioside induced differentiation associated	37
CXXC finger protein 5	1285
UDP-N-acetyl-alpha-D-galactosamine:polypeptide	83
STEAP family member 4	23
ADAM metallopeptidase domain 28	5
SWI/SNF-related, matrix-associated actin-depen	371
NLR family, CARD domain containing 3	5
retrotransposon gag domain containing 1	5
chromosome 14 open reading frame 159	5
Leucine-rich repeat-containing protein LOC4008	5
topoisomerase (DNA) III alpha	427
myocardial zonula adherens protein	10
chromosome 15 open reading frame 54	5
prenylcysteine oxidase 1	407
vimentin-type intermediate filament associated	28
zinc finger protein 488	61
UBA-like domain containing 2	506
malic enzyme 1, NADP(+)-dependent, cytosolic	586
cell division cycle 7	416
metaxin 3	304
axin interactor, dorsalization associated	48
protein tyrosine phosphatase, receptor type, B	42
heat shock 70kDa protein 9 (mortalin)	573
coiled-coil domain containing 92	105
ankyrin repeat domain 36	5
potassium voltage-gated channel, Shab-related	5
proline-rich transmembrane protein 2	33
choroideremia-like (Rab escort protein 2)	140
cyclin-dependent kinase-like 4	5
SAM and SH3 domain containing 3	5
estrogen receptor 2 (ER beta)	5
major facilitator superfamily domain containin	5122
caspase 9, apoptosis-related cysteine peptidas	390
GRIP and coiled-coil domain containing 1	26
transforming growth factor, beta receptor asso	435
chromosome 17 open reading frame 80	740
synaptotagmin binding, cytoplasmic RNA interac	4864
SIX homeobox 1	1264
Rho guanine nucleotide exchange factor (GEF) 1	326

glutamate receptor, ionotropic, AMPA 4	7
zinc finger and BTB domain containing 12	18
	185
somatostatin receptor 1	28
HCG2018282; Uncharacterized protein	5
carnitine palmitoyltransferase 1A (liver)	869
leprecan-like 1	875
plexin A4	9
carbohydrate (chondroitin 4) sulfotransferase	686
coiled-coil domain containing 113	29
calmodulin-lysine N-methyltransferase	18
testis expressed 22	9
phosphatidylinositol binding clathrin assembly	1173
heat shock protein 70kDa family, member 13	2175
MDS1 and EVI1 complex locus	138
protein arginine methyltransferase 6	270
BEN domain containing 4	187
transmembrane protein 140	858
trypsin domain containing 1	35
gem (nuclear organelle) associated protein 8	9
chromosome 7 open reading frame 31	40
enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydro	150
ribosomal protein S6 kinase, 52kDa, polypeptid	57
carbohydrate sulfotransferase 10	33
surfactant protein A2	5
	5
grainyhead-like 3 (Drosophila)	15
proline and serine rich 1	145
kallikrein-related peptidase 7	5
breast carcinoma amplified sequence 4	492
lysophospholipase I	57
leucine rich adaptor protein 1-like	266
solute carrier family 25 (mitochondrial carrie	206
K(lysine) acetyltransferase 7	48
Cell growth-inhibiting protein 7; HCG1784586;	9
POM121 transmembrane nucleoporin-like 2	0
interleukin 9 receptor	5
activation-induced cytidine deaminase	5
solute carrier family 10 (sodium/bile acid cot	5
A kinase (PRKA) anchor protein 1	843
zinc finger with KRAB and SCAN domains 1	1314
nanos homolog 2 (Drosophila)	5
family with sequence similarity 19 (chemokine	5
leucine rich repeat containing 66	5
son of sevenless homolog 2 (Drosophila)	70
chromosome 7 open reading frame 73	847
zinc finger protein 507	378
carcinoembryonic antigen-related cell adhesion	5
basonuclin 2	770
sel-1 suppressor of lin-12-like (C. elegans)	1271
family with sequence similarity 109, member A	780
DCN1, defective in cullin neddylation 1, domai	53
cornichon family AMPA receptor auxiliary prote	1348
zinc finger protein 280B	7

ERO1-like beta (S. cerevisiae)	478
histone cluster 1, H3h	256
HCG2000720; Hypothetical gene supported by AK0	5
WBP2 N-terminal like	5
orthopedia homeobox	9
kallikrein-related peptidase 12	5
schlafen-like 1	5
synaptic Ras GTPase activating protein 1	15
STAM binding protein	1274
ALG10B, alpha-1,2-glucosyltransferase	471
solute carrier family 25, member 45	67
deleted in azoospermia 1	5
LY75-CD302 readthrough	855
lymphocyte antigen 75	855
EP300 interacting inhibitor of differentiation	156
achaete-scute complex homolog 4 (Drosophila)	5
v-maf avian musculoaponeurotic fibrosarcoma on	5
mediator complex subunit 18	1766
short coiled-coil protein	922
lengsin, lens protein with glutamine synthetas	21
family with sequence similarity 220, member A	15
protein kinase, cAMP-dependent, catalytic, bet	344
Uncharacterized protein	5
zinc finger protein 865	75
TOX high mobility group box family member 4	309
ring finger protein 141	345
RNA binding motif protein 28	297
bone morphogenetic protein receptor, type IA	125
proteasome (prosome, macropain) activator subu	3605
KIAA0825	34
membrane protein, palmitoylated 7 (MAGUK p55 s	50
SWI/SNF related, matrix associated, actin depe	952
internexin neuronal intermediate filament prot	46
transmembrane protein 135	963
angiopoietin-like 2	39
syntrophin, gamma 1	5
ankyrin repeat domain 16	82
toll-like receptor 5	5
bromodomain containing 2	695
clarin 1	5
pseudouridylate synthase 7 homolog (S. cerevis	67
SPHK1 interactor, AKAP domain containing	5
transmembrane and coiled-coil domains 1	4447
solute carrier family 17 (vesicular glutamate	12
multiple inositol-polyphosphate phosphatase 1	1079
protein tyrosine phosphatase type IVA, member	5
carbohydrate (N-acetylgalactosamine 4-0) sulfo	1143
ubiquitin related modifier 1	345
zinc finger, FYVE domain containing 27	565
phosphatase and actin regulator 4	85
inositol polyphosphate-4-phosphatase, type II,	43
family with sequence similarity 49, member A	38
general transcription factor IIH, polypeptide	121
carcinoembryonic antigen-related cell adhesion	11

transmembrane protein 119	5
G protein-coupled receptor 85	21
forkhead box O4	48
collagen, type IX, alpha 1	9
methionyl-tRNA synthetase 2, mitochondrial	391
protein phosphatase 1, regulatory subunit 18	265
RNA polymerase II associated protein 2	222
zinc finger, NFX1-type containing 1	41
synaptic vesicle glycoprotein 2C	30
Uncharacterized protein	22
F11 receptor	2844
glucosamine (UDP-N-acetyl)-2-epimerase/N-acety	22
apoptosis, caspase activation inhibitor	230
zinc finger and BTB domain containing 26	83
coiled-coil-helix-coiled-coil-helix domain con	97
LON peptidase N-terminal domain and ring finge	36
N-acetyltransferase 14 (GCN5-related, putative	392
chromosome 2 open reading frame 50	5
protein phosphatase 3, regulatory subunit B, b	5
transmembrane protein 87B	219
chromosome 11 open reading frame 88	5
G protein-coupled receptor 153	39
acyl-CoA wax alcohol acyltransferase 1	5
chromosome 6 open reading frame 201	5
ADP-ribosylation factor 6	31
serine racemase	95
anaphase promoting complex subunit 7	819
zyg-11 family member A, cell cycle regulator	331
paired related homeobox 1	57
ubiquitin protein ligase E3 component n-recogn	468
myosin phosphatase Rho interacting protein	521
p21 protein (Cdc42/Rac)-activated kinase 1	374
poliovirus receptor-related 3	361
mediator complex subunit 28	1483
protein phosphatase 1, regulatory subunit 3A	5
chloride channel accessory 2	5
WW domain binding protein 2	362
SWI/SNF related, matrix associated, actin depe	158
synaptosomal-associated protein, 91kDa	68
tenascin R	5
Uncharacterized protein; cDNA FLJ43210 fis, cl	7
trophoblast glycoprotein-like	8
dihydropyrimidinase-like 2	3087
molybdenum cofactor synthesis 1	179
fibrous sheath interacting protein 1	10
chemokine (C-C motif) receptor 9	5
jumonji C domain containing histone demethylas	470
thrombospondin 1	46844
potassium channel tetramerization domain conta	36
family with sequence similarity 213, member B	409
transient receptor potential cation channel, s	11
solute carrier family 31 (copper transporter),	110
prostaglandin D2 synthase 21kDa (brain)	13
zinc finger and SCAN domain containing 9	121

neuroblastoma breakpoint family, member 4	5
transmembrane protein 30A	1221
nuclear receptor subfamily 2, group F, member	4428
transcription factor AP-4 (activating enhancer	13
zinc finger protein 580	154
peptidyl arginine deiminase, type II	11
nuclear receptor coactivator 1	200
mago-nashi homolog B (Drosophila)	63
H1 histone family, member 0	234
transmembrane protein 127	296
methionine sulfoxide reductase B3	83
zinc finger and BTB domain containing 46	71
transmembrane 4 L six family member 1	1401
phosphoprotein associated with glycosphingolip	53
chromosome X open reading frame 36	5
HNF1 homeobox B	25
estrogen receptor 1	5
GTP binding protein 2	388
INO80 complex subunit D	5
RUN domain containing 3A	11
zinc finger protein 160	68
signal sequence receptor, gamma (translocon-as	6034
chromosome 18 open reading frame 25	688
mitochondrial ribosomal protein L17	1447
ATPase, H+ transporting, lysosomal 70kDa, V1 s	180
hydroxyacyl-CoA dehydrogenase	1894
dihydroxyacetone kinase 2 homolog (S. cerevisi	242
zinc finger E-box binding homeobox 2	33
synaptosomal-associated protein, 23kDa	99
PH domain and leucine rich repeat protein phos	172
PRAME family member 18	0
catenin (cadherin-associated protein), alpha 3	5
potassium channel, subfamily K, member 12	5
PRAME family member 19	5
tetratricopeptide repeat domain 31	132
PITPNM family member 3	5
TGF-beta activated kinase 1/MAP3K7 binding pro	201
slit homolog 2 (Drosophila)	579
CD38 molecule	23
TEA domain family member 1 (SV40 transcription	740
tetratricopeptide repeat domain 33	676
KIAA1462	360
dual specificity phosphatase 28	84
cell cycle associated protein 1	650
APC membrane recruitment protein 2	7
Uncharacterized protein; cDNA FLJ34594 fis, cl	5
PRAME family member 22	0
5-hydroxytryptamine (serotonin) receptor 1F, G	5
D4, zinc and double PHD fingers family 2	1164
OTU domain containing 4	18
PRAME family member 3	5
protein phosphatase 2, regulatory subunit B, g	115
complement component 7	5
solute carrier family 26 (anion exchanger), me	748

transcription factor EC	5
carnosine dipeptidase 1 (metallopeptidase M20	5
SUMO1 activating enzyme subunit 1	87
B-cell receptor-associated protein 29	326
serpin peptidase inhibitor, clade B (ovalbumin	295
myelin protein zero-like 2	260
glycerol-3-phosphate dehydrogenase 2 (mitochon	196
protein kinase, AMP-activated, beta 1 non-cata	99
trinucleotide repeat containing 6B	69
claudin 2	19
arylacetamide deacetylase-like 4	5
low density lipoprotein receptor adaptor prote	111
cyclin-dependent kinase 20	25
CGRP receptor component	1776
nephronectin	518
KxDL motif containing 1	117
chromobox homolog 5	360
four and a half LIM domains 1	239
speckle-type POZ protein	883
dystroglycan 1 (dystrophin-associated glycopro	241
exportin 1 (CRM1 homolog, yeast)	404
THAP domain containing 11	1536
solute carrier family 24 (sodium/potassium/cal	5
Uncharacterized protein	5
spindlin family, member 2A	5
adrenoceptor beta 2, surface	50
ubinuclein 1	586
WAS/WASL interacting protein family, member 2	214
early B-cell factor 3	101
CKLF-like MARVEL transmembrane domain containi	169
CD300 molecule-like family member b	5
interferon-induced protein with tetratricopept	160
CD96 molecule	5
cyclin Y	672
neuroblastoma breakpoint family, member 14	10
zinc finger protein 485	36
abhydrolase domain containing 17C	406
homeobox A5	63
ribonuclease, RNase A family, 11 (non-active)	5
RAP2A, member of RAS oncogene family	721
sialic acid binding Ig-like lectin 10	5
ankyrin repeat domain 27 (VPS9 domain)	349
cytoplasmic FMR1 interacting protein 2	303
gap junction protein, alpha 5, 40kDa	5
	5
galactosidase, beta 1-like 2	38
chromosome 20 open reading frame 96	257
ubiquitin specific peptidase 14 (tRNA-guanine	561
transmembrane protein 173	676
DEAH (Asp-Glu-Ala-His) box polypeptide 33	724
GrpE-like 2, mitochondrial (E. coli)	79
serine/threonine kinase 32B	196
neurobeachin-like 1	42
progestin and adipoQ receptor family member IV	703

opioid receptor, kappa 1	5
Uncharacterized protein; cDNA FLJ26048 fis, cl	5
KIAA0907	48
G protein-coupled receptor 83	33
ectodysplasin A	9
myosin, heavy chain 7B, cardiac muscle, beta	5
glutathione S-transferase, C-terminal domain c	411
bleomycin hydrolase	1511
CD300c molecule	5
protein kinase, AMP-activated, beta 2 non-cata	363
chromosome 3 open reading frame 36	8
vomeronasal 1 receptor 1	12
MAM domain containing 2	365
keratin 80	617
serine palmitoyltransferase, long chain base s	2578
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransfe	2265
plexin domain containing 1	9
desmocollin 3	390
Mitogen-activated protein kinase kinase kinase	405
sal-like 1 (Drosophila)	95
mitogen-activated protein kinase kinase kinase	144
glutamine-fructose-6-phosphate transaminase 2	70
APC membrane recruitment protein 1	11
S100 calcium binding protein A14	5
peptidase domain containing associated with mu	40
SET and MYND domain containing 1	5
keratin 35	5
neuron navigator 1	702
myotubularin related protein 10	30
purine-rich element binding protein G	29
cytochrome b5 domain containing 1	546
spindlin family, member 3	12
myosin ID	16
solute carrier family 25 (mitochondrial iron t	49
chromosome 21 open reading frame 62	5
target of myb1 (chicken)	309
FRAS1 related extracellular matrix 1	25
MAS-related GPR, member X2	5
thymocyte expressed, positive selection associ	5
chromosome 11 open reading frame 68	1192
chromosome 17 open reading frame 58	48
pregnancy up-regulated non-ubiquitously expres	5
Rac GTPase activating protein 1	19
microfibrillar associated protein 5	216
lines homolog (Drosophila)	18
NME/NM23 nucleoside diphosphate kinase 1	25174
dCTP pyrophosphatase 1	820
regulatory factor X, 4 (influences HLA class I	5
5-hydroxytryptamine (serotonin) receptor 2A, G	5
absent in melanoma 1	35
serine/arginine repetitive matrix 1	7
solute carrier family 35 (UDP-xylose/UDP-N-ace	899
phosphorylase kinase, alpha 1 (muscle)	277
PR domain containing 5	22

CREB3 regulatory factor	24
family with sequence similarity 174, member B	16
histone cluster 1, H2bj	383
ectonucleotide pyrophosphatase/phosphodiestera	5
SH3 and cysteine rich domain	172
UTP14, U3 small nucleolar ribonucleoprotein, h	174
engulfment and cell motility 2	22
G protein-coupled receptor 97	8
family with sequence similarity 110, member C	29
cancer susceptibility candidate 5	144
immediate early response 5	11212
general transcription factor IIA, 1, 19/37kDa	88
regulator of calcineurin 2	32
zinc finger CCCH-type containing 7A	1071
ATPase, Ca++ transporting, plasma membrane 3	5
glutamate dehydrogenase 2	22
TAF12 RNA polymerase II, TATA box binding prot	183
SFT2 domain containing 2	97
BRO1 domain and CAAX motif containing	149
sialic acid binding Ig-like lectin 14	5
dual serine/threonine and tyrosine protein kin	256
sorting nexin 29	266
piggyBac transposable element derived 4	136
basonuclin 1	6
zinc finger protein 80	5
2’-5’-oligoadenylate synthetase 2, 69/71kDa	5
pleckstrin homology domain containing, family	1172
NUAK family, SNF1-like kinase, 1	489
polymerase (RNA) III (DNA directed) polypeptid	96
unc-13 homolog A (C. elegans)	5
C1q and tumor necrosis factor related protein	5
chromosome 9 open reading frame 62	5
matrix-remodelling associated 5	5
hepatic leukemia factor	15
tripartite motif containing 32	285
twist basic helix-loop-helix transcription fac	190
spondin 2, extracellular matrix protein	1611
casein kinase 1, gamma 1	149
diacylglycerol kinase, alpha 80kDa	186
progestin and adipoQ receptor family member VI	106
tuftelin 1	599
torsin A interacting protein 1	3069
Folliculin-interacting protein 1	38
EFR3 homolog A (S. cerevisiae)	372
zinc finger protein 584	282
karyopherin alpha 6 (importin alpha 7)	272
trans-golgi network protein 2	1914
centrosomal protein 97kDa	290
SEC31 homolog B (S. cerevisiae)	43
adaptor-related protein complex 1, mu 2 subuni	26
SMYD family member 5	344
transmembrane protein 105	5
DDB1 and CUL4 associated factor 10	433
neurogenin 3	5

vasoactive intestinal peptide	5
septin 9	7738
paternally expressed 3	5
potassium large conductance calcium-activated	5
RAR-related orphan receptor B	5
tumor necrosis factor (ligand) superfamily, me	5
solute carrier family 35 (GDP-fucose transport	910
annexin A4	2119
LIM homeobox 4	13
small nuclear RNA activating complex, polypept	2406
S-phase response (cyclin related)	202
Uncharacterized protein	7
cysteine-rich secretory protein LCCL domain co	397
FEZ family zinc finger 2	5
FCF1 rRNA-processing protein	119
TAF5-like RNA polymerase II, p300/CBP-associat	5
discoidin domain receptor tyrosine kinase 1	195
microtubule-associated protein 7	444
gap junction protein, alpha 9, 59kDa	85
SEC16 homolog A (S. cerevisiae)	814
neuropilin (NRP) and tolloid (TLL)-like 1	5
RAB22A, member RAS oncogene family	484
enolase-phosphatase 1	615
leishmanolysin-like (metallopeptidase M8 famil	18
zinc finger protein 740	2137
allograft inflammatory factor 1-like	487
tubulin folding cofactor E-like	89
serine/arginine-rich splicing factor 6	1914
von Willebrand factor C domain containing 2	5
alpha-2-glycoprotein 1, zinc-binding	11
family with sequence similarity 27, member E1	5
PAX interacting (with transcription-activation	19
ring finger protein 26	1208
XK, Kell blood group complex subunit-related f	7
Uncharacterized protein	5
mitochondrial calcium uptake family, member 3	9
SAM domain and HD domain 1	448
tubulin, beta 6 class V	5820
latrophilin 2	407
EGF containing fibulin-like extracellular matr	992
Fli-1 proto-oncogene, ETS transcription factor	116
epithelial mitogen	26
myeloid cell leukemia sequence 1 (BCL2-related	374
potassium inwardly-rectifying channel, subfami	9
CWC25 spliceosome-associated protein homolog (	300
DDB1 and CUL4 associated factor 4-like 1	5
zinc finger protein 878	17
interferon regulatory factor 2 binding protein	2145
peptidase inhibitor 15	12
RUN and FYVE domain containing 1	187
pleckstrin homology domain containing, family	125
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 2	289
sarcalumenin	5
SLX4 interacting protein	0

lysyl oxidase-like 3	235
D-dopachrome tautomerase-like	7
microcephalin 1	167
phosphatidylinositol glycan anchor biosynthesi	1071
NIPA-like domain containing 3	775
VMA21 vacuolar H+-ATPase homolog (S. cerevisia	2162
cell death-inducing p53 target 1	1857
leucine-rich repeats and calponin homology (CH	381
membrane protein, palmitoylated 2 (MAGUK p55 s	78
glucosamine-phosphate N-acetyltransferase 1	429
OTU domain containing 5	957
sprouty-related, EVH1 domain containing 1	547
adaptor-related protein complex 3, beta 1 subu	180
solute carrier family 7 (anionic amino acid tr	61
T-cell leukemia translocation altered	204
Uncharacterized protein	5
interleukin 1 receptor accessory protein	313
Uncharacterized protein	5
ubiquitin-conjugating enzyme E2, J2	3002
eyes absent homolog 3 (Drosophila)	50
leukocyte immunoglobulin-like receptor, subfam	5
LIM domain binding 1	61
3'(2'), 5'-bisphosphate nucleotidase 1	201
nuclear factor, erythroid 2-like 3	36
CUGBP, Elav-like family member 1	153
signal recognition particle receptor (docking	2980
glucosamine-6-phosphate deaminase 1	1130
transcription factor 12	101
biogenesis of lysosomal organelles complex-1,	182
adherens junctions associated protein 1	5
kinesin family member 4B	5
mex-3 RNA binding family member C	5
BCL2-like 1	7726
teneurin transmembrane protein 1	5
mitogen-activated protein kinase kinase 1	8
family with sequence similarity 27, member E2	5
archaelysin family metallopeptidase 1	5
glycerol kinase	38
CTD (carboxy-terminal domain, RNA polymerase I	1299
transmembrane protein 231	243
polymerase (DNA directed), theta	51
ninein (GSK3B interacting protein)	594
TSPY-like 5	20
zinc finger CCCH-type containing 6	10
coiled-coil domain containing 180	10
family with sequence similarity 167, member A	85
A kinase (PRKA) anchor protein 17A	5
Rho GTPase activating protein 22	10
fibroblast growth factor 5	1478
NEDD4 binding protein 2-like 2	74
phosphodiesterase 5A, cGMP-specific	69
sema domain, immunoglobulin domain (Ig), trans	32
adaptor protein, phosphotyrosine interaction,	908
inhibin, beta C	5

zinc finger protein 202	704
prostaglandin F2 receptor inhibitor	591
glutaminase	1927
monooxygenase, DBH-like 1	168
cadherin 6, type 2, K-cadherin (fetal kidney)	213
tetratricopeptide repeat domain 9	39
synaptotagmin I	13
wingless-type MMTV integration site family, me	5
neuroblastoma breakpoint family, member 3	5
proline rich Gla (G-carboxyglutamic acid) 3 (t	5
Uncharacterized protein; cDNA FLJ42623 fis, cl	5
synaptosomal-associated protein, 25kDa	54
myosin VC	39
ras homolog family member U	3519
proteasomal ATPase-associated factor 1	22
carcinoembryonic antigen-related cell adhesion	925
phosphatase and tensin homolog	118
chromosome 3 open reading frame 72	11
latrophilin 3	93
S100 calcium binding protein Z	20
MEF2 activating motif and SAP domain containin	100
chromobox homolog 7	5
homeobox D11	124
zinc finger protein 578	0
zinc finger protein 438	15
solute carrier family 18 (vesicular acetylchol	5
zinc finger protein 619	17
family with sequence similarity 27, member E3	5
prolyl 4-hydroxylase, beta polypeptide	17931
serine/threonine kinase 4	276
FRAS1 related extracellular matrix protein 2	33
cyclin T1	86
protein phosphatase 1, regulatory subunit 10	893
phytanoyl-CoA 2-hydroxylase interacting protei	14
dynein, axonemal, heavy chain 10 opposite stra	89
zinc finger and SCAN domain containing 25	230
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum p	5077
CaM kinase-like vesicle-associated	47
solute carrier family 6 (neurotransmitter tran	5
solute carrier family 22 (organic cation/carni	37
gamma-glutamyltransferase 7	16
Bardet-Biedl syndrome 10	186
adenosine A2a receptor	337
ring finger protein 185	97
transmembrane protease, serine 2	11
phytanoyl-CoA 2-hydroxylase interacting protei	26
stromal interaction molecule 1	1672
histocompatibility (minor) 13	4848
serine incorporator 5	175
bromodomain and WD repeat domain containing 3	506
Rieske (Fe-S) domain containing	15
death effector domain containing	239
KIAA0408	95
zinc finger protein 662	11

chromosome 1 open reading frame 85	4649
cytoplasmic polyadenylation element binding pr	472
solute carrier organic anion transporter famil	19
HID1 domain containing	5
trimethyllysine hydroxylase, epsilon	5
ARHGAP19-SLIT1 readthrough (NMD candidate)	15
5-hydroxytryptamine (serotonin) receptor 4, G	5
NIPA-like domain containing 1	137
solute carrier family 25, member 42	1088
zinc finger protein 562	130
tensin 4	40
heparan sulfate (glucosamine) 3-O-sulfotransfe	148
synaptotagmin VII	192
zinc finger protein 207	839
family with sequence similarity 64, member A	392
insulin receptor	577
apoptotic peptidase activating factor 1	23
NHL repeat containing 3	49
chromosome 2 open reading frame 88	156
signal recognition particle 19kDa	243
ribosomal protein L22	1455
SEH1-like (S. cerevisiae)	632
post-GPI attachment to proteins 1	106
transmembrane protein 37	2076
transmembrane protein 43	2575
replication protein A1, 70kDa	2834
hepatoma-derived growth factor	10112
transferrin receptor 2	330
family with sequence similarity 153, member C	5
methenyltetrahydrofolate synthetase domain con	149
metastasis associated in colon cancer 1	5
contactin 1	40
Rho GTPase activating protein 27	5
mitogen-activated protein kinase 4	77
alkylglycerone phosphate synthase	1610
tumor necrosis factor receptor superfamily, me	39
RNA binding motif, single stranded interacting	56
zinc finger protein 275	465
tyrosine 3-monooxygenase/tryptophan 5-monooxyg	184
KIAA0226	89
CD164 molecule, sialomucin	2038
erythrocyte membrane protein band 4.1 like 5	108
zinc finger and BTB domain containing 33	65
kinesin light chain 2	11832
trinucleotide repeat containing 6A	267
thrombospondin, type I, domain containing 7A	5
retina and anterior neural fold homeobox	5
sorting nexin 22	5
transient receptor potential cation channel, s	5
chromosome 20 open reading frame 194	1083
angiopoietin 1	21
syndecan 4	1252
translation machinery associated 16 homolog (S	34
DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	729

histone cluster 1, H2ak	26
fatty acid desaturase 6	12
CD300 molecule-like family member d	5
zinc finger protein 525	30
protocadherin 11 Y-linked	0
abhydrolase domain containing 14B	189
Ellis van Creveld syndrome	165
protein tyrosine phosphatase, non-receptor typ	5
copine V	13
ubiquitin specific peptidase 35	21
ATP-binding cassette, sub-family A (ABC1), mem	7
keratin 83	5
inhibitor of growth family, member 4	548
tectorin alpha	19
chromosome 7 open reading frame 65	5
small glutamine-rich tetratricopeptide repeat	205
chloride channel, voltage-sensitive 2	44
transmembrane protein 246	367
regulator of G-protein signaling 17	11
leucine rich repeat containing 58	940
naked cuticle homolog 1 (Drosophila)	26
WD repeat domain 36	282
killer cell lectin-like receptor subfamily C,	25
intracisternal A particle-promoted polypeptide	216
diaphanous-related formin 2	91
golgi-associated, gamma adaptin ear containing	645
synaptojanin 2 binding protein	329
death domain containing 1	5
calcium and integrin binding family member 2	119
C-type lectin domain family 1, member A	5
G protein-coupled receptor 114	5
transmembrane protein 214	1344
cholinergic receptor, nicotinic, alpha 4 (neur	5
activin A receptor type II-like 1	68
centromere protein O	298
echinoderm microtubule associated protein like	60
ORM1-like 1 (S. cerevisiae)	998
ATM interactor	129
CCR4-NOT transcription complex, subunit 8	319
latent transforming growth factor beta binding	5324
fms-related tyrosine kinase 1	7
leucine rich repeat transmembrane neuronal 2	5
sushi domain containing 5	23
coagulation factor XIII, A1 polypeptide	5
Smad nuclear interacting protein 1	355
phospholipase B1	5
suppressor of cytokine signaling 3	5
zinc finger protein 774	27
nucleoredoxin-like 2	198
Rho/Rac guanine nucleotide exchange factor (GE	313
signal recognition particle 72kDa	185
mannosidase, endo-alpha	41
CREB/ATF bZIP transcription factor	1115
phosphatidylinositol glycan anchor biosynthesi	179

guanine nucleotide binding protein (G protein)	513
zinc finger, DHHC-type containing 18	268
ATPase, Cu++ transporting, alpha polypeptide	141
RAS p21 protein activator 4	5
Uncharacterized protein	5
yippee-like 2 (Drosophila)	62
	75
p21 protein (Cdc42/Rac)-activated kinase 2	145
kallikrein-related peptidase 9	5
chemokine (C-X-C motif) receptor 5	5
phorbol-12-myristate-13-acetate-induced protei	12503
ralA binding protein 1	134
immunoglobulin superfamily, member 3	141
pentatricopeptide repeat domain 3	2308
solute carrier family 38, member 1	1967
GRB2 associated, regulator of MAPK1	536
zinc finger and BTB domain containing 25	149
kelch-like family member 14	66
transmembrane and coiled-coil domain family 1	97
sorting nexin 10	9
tumor protein p53 inducible nuclear protein 2	12
polymerase (DNA directed), gamma	16
transcription factor-like 5 (basic helix-loop-	183
solute carrier family 34 (type II sodium/phosp	5
FERM and PDZ domain containing 3	0
Rap guanine nucleotide exchange factor (GEF)-l	20
family with sequence similarity 91, member A1	731
VANGL planar cell polarity protein 2	560
ectonucleoside triphosphate diphosphohydrolase	15
nucleoporin 155kDa	814
ring finger protein 157	163
protein phosphatase, Mg2+/Mn2+ dependent, 1A	412
fibroblast growth factor 11	10
dual specificity phosphatase 16	444
autophagy related 5	1078
NK6 homeobox 1	9
TBC/LysM-associated domain containing 2	5
splA/ryanodine receptor domain and SOCS box co	827
major histocompatibility complex, class I, E	1858
aryl hydrocarbon receptor interacting protein-	5
LIM homeobox 9	40
ubiquitin specific peptidase 26	5
Kruppel-like factor 6	4644
cytohesin 1	553
ring finger protein 208	30
tropomodulin 2 (neuronal)	117
integrin, beta 8	17
deoxycytidine kinase	200
cylindromatosis (turban tumor syndrome)	696
protein tyrosine phosphatase-like A domain con	17
DNA cross-link repair 1B	687
NAD kinase 2, mitochondrial	1039
zinc finger protein 703	1557
sterile alpha motif domain containing 4A	449

neuroblastoma breakpoint family, member 10	5
transmembrane protein 236	5
ATPase, Ca++ transporting, cardiac muscle, fas	12
Uncharacterized protein; cDNA FLJ52611	5
solute carrier family 5 (sodium/monocarboxylat	8
U2AF homology motif (UHM) kinase 1	48
Rho guanine nucleotide exchange factor (GEF) 4	189
	5
enhancer of zeste homolog 1 (Drosophila)	70
glutathione peroxidase 8 (putative)	2107
NCK-associated protein 5	51
family with sequence similarity 222, member A	23
phosphatidylinositol glycan anchor biosynthesi	211
N-acylsphingosine amidohydrolase (acid ceramid	445
interferon regulatory factor 2 binding protein	8690
Yip1 domain family, member 3	616
Ras association (RalGDS/AF-6) domain family me	461
signal peptide peptidase like 3	799
GIPC PDZ domain containing family, member 2	16
phosphodiesterase 1B, calmodulin-dependent	6
potassium voltage-gated channel, shaker-relate	5
cholinergic receptor, nicotinic, alpha 10 (neu	5
transcriptional regulating factor 1	52
filamin binding LIM protein 1	581
sperm antigen with calponin homology and coile	3720
fermitin family member 1	245
Uncharacterized protein	5
chemokine (C-X-C motif) receptor 2	5
NADPH oxidase, EF-hand calcium binding domain	5
family with sequence similarity 110, member D	5
claudin 18	5
far upstream element (FUSE) binding protein 1	2021
carbohydrate (N-acetylglucosamine 6-O) sulfotr	406
stonin 2	40
EPH receptor A7	213
adenylate cyclase 7	238
N-deacetylase/N-sulfotransferase (heparan gluc	12
synaptotagmin XIII	5
zinc finger and SCAN domain containing 22	45
chromosome 14 open reading frame 180	5
G protein regulated inducer of neurite outgrow	5
zinc finger CCCH-type containing 11A	71
leukocyte immunoglobulin-like receptor, subfam	5
sterile alpha motif domain containing 4B	46
ring finger protein 38	348
hormonally up-regulated Neu-associated kinase	85
potassium channel tetramerization domain conta	3328
plexin domain containing 2	506
sushi-repeat containing protein, X-linked 2	69
CTD (carboxy-terminal domain, RNA polymerase I	372
thyroid hormone receptor interactor 12	145
protein tyrosine phosphatase, non-receptor typ	104
zinc metallopeptidase STE24	513
RAB3A interacting protein (rabin3)-like 1	157

pleckstrin and Sec7 domain containing 3	133
kinesin family member 21A	37
serpin peptidase inhibitor, clade B (ovalbumin	154
xylosyltransferase I	159
fucosyltransferase 9 (alpha (1,3) fucosyltrans	5
iodotyrosine deiodinase	5
sideroflexin 3	154
keratin 74	5
POU class 4 homeobox 2	5
Ras protein-specific guanine nucleotide-releas	140
chromosome 5 open reading frame 42	45
protein phosphatase 2, regulatory subunit B',	23
Uncharacterized protein	10
RAB5B, member RAS oncogene family	14
mitogen-activated protein kinase 8	227
CCR4-NOT transcription complex, subunit 2	1189
tripartite motif containing 41	494
interleukin 7 receptor	293
MAK16 homolog (S. cerevisiae)	97
podoplanin	264
par-3 family cell polarity regulator beta	38
polybromo 1	689
oligodendrocyte transcription factor 1	34
calcium channel, voltage-dependent, beta 1 sub	81
family with sequence similarity 124A	5
shisa family member 2	30
cadherin 24, type 2	44
tRNA methyltransferase 10 homolog A (S. cerevi	89
potassium voltage-gated channel, shaker-relate	5
T-box 15	14
suppressor of Ty 5 homolog (S. cerevisiae)	390
SIX homeobox 6	5
chromosome 3 open reading frame 58	118
AKT1 substrate 1 (proline-rich)	754
BMP2 inducible kinase	164
cytochrome b5 reductase 3	542
trichoplein, keratin filament binding	140
centromere protein C	45
OTU domain containing 7B	299
pogo transposable element with KRAB domain	377
Uncharacterized protein	145
PHD finger protein 21A	301
arrestin domain containing 3	1313
synaptotagmin V	5
hippocampus abundant transcript-like 1	767
histamine receptor H2	5
nitrogen permease regulator-like 3 (S. cerevis	129
F-box protein 40	5
golgin A8 family, member A	2264
ELKS/RAB6-interacting/CAST family member 2	11
serpin peptidase inhibitor, clade F (alpha-2 a	2334
transmembrane anterior posterior transformatio	105
insulin-like growth factor 2 receptor	46
vinculin	189

serine/threonine kinase 10	655
zinc finger protein 398	305
chromosome 4 open reading frame 33	18
UBX domain protein 2B	157
kelch repeat and BTB (POZ) domain containing 1	5
calsyntenin 3	5
potassium inwardly-rectifying channel, subfami	53
SCY1-like 3 (S. cerevisiae)	124
FGFR1 oncogene partner	552
DDB1 and CUL4 associated factor 7	3289
capping protein (actin filament) muscle Z-line	1159
activin A receptor, type IC	27
uroplakin 1A	5
mitogen-activated protein kinase 13	499
cyclin I family, member 2	5
kinesin family member 5A	5
coiled-coil-helix-coiled-coil-helix domain con	1577
matrix metallopeptidase 15 (membrane-inserted)	605
cryptochrome 2 (photolyase-like)	63
tropomyosin 3	669
CCDC169-SOHLH2 readthrough	15
UBX domain protein 7	95
solute carrier family 30 (zinc transporter), m	19
FSHD region gene 1 family, member B	94
vasohibin 2	70
nidogen 2 (osteonidogen)	4292
BTB and CNC homology 1, basic leucine zipper t	273
F-box protein 32	500
G protein-coupled receptor 64	175
sorting nexin 11	20
non-POU domain containing, octamer-binding	177
zinc finger protein 549	7
zinc finger protein 776	1447
Protein FAM47E	503
neuroblastoma breakpoint family, member 9	5
paraneoplastic Ma antigen family-like 1	313
myelin protein zero	17
Uncharacterized protein	5
synaptotagmin XIV	16
activating transcription factor 2	123
heparanase	37
dynein, light chain, LC8-type 2	1162
myosin VA (heavy chain 12, myoxin)	573
ets variant 6	44
MDM2 oncogene, E3 ubiquitin protein ligase	455
SRC kinase signaling inhibitor 1	5
DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	817
chromosome 9 open reading frame 72	25
armadillo repeat containing, X-linked 6	5
neuroblastoma breakpoint family, member 16	5
KIAA0087	5
chromosome 2 open reading frame 48	32
neuroblastoma breakpoint family, member 15	5
adaptor-related protein complex 3, beta 2 subu	15

sorting nexin family member 21	343
delta/notch-like EGF repeat containing	143
reticulon 4 interacting protein 1	19
RAN binding protein 10	140
family with sequence similarity 124B	5
24-dehydrocholesterol reductase	7645
SKI family transcriptional corepressor 1	22
thyroid hormone receptor interactor 11	13
F-box protein 22	1310
nuclear receptor coactivator 3	282
ring finger protein 4	33
syntaxin 2	216
unc-5 homolog A (C. elegans)	7
peroxisomal biogenesis factor 5-like	5
secretin receptor	7
apelin	48
glutamate receptor, metabotropic 1	5
SEC14-like 3 (S. cerevisiae)	5
transmembrane protein 151B	5
transmembrane protein 143	160
CDK2-associated, cullin domain 1	213
ring finger protein 114	1488
tetratricopeptide repeat domain 37	296
CAP-GLY domain containing linker protein 1	17
ISY1 splicing factor homolog (S. cerevisiae)	897
N-ethylmaleimide-sensitive factor	86
transmembrane BAX inhibitor motif containing 6	4043
adenylate kinase 3	323
bone morphogenetic protein 8a	13
tribbles pseudokinase 1	313
chromosome 22 open reading frame 26	5
glypican 6	410
cysteine-rich, DPF motif domain containing 1	169
golgi membrane protein 1	4212
sorting nexin 12	849
synuclein, alpha interacting protein	236
aryl-hydrocarbon receptor nuclear translocator	39
desmocollin 1	7
RNA binding motif protein 14	3993
eukaryotic translation initiation factor 2B, s	901
ADAM metallopeptidase with thrombospondin type	5
spastin	239
ring finger protein 217	92
RNA binding motif protein 20	7
serine palmitoyltransferase, long chain base s	95
LIM domain 7	4663
phosphate cytidylyltransferase 1, choline, alp	731
testis expressed 15	58
transmembrane protein 38B	755
guanine nucleotide binding protein (G protein)	565
kinesin family member 26B	25
RAB6A, member RAS oncogene family	9
kelch-like family member 6	5
purine-rich element binding protein B	497

LIM homeobox transcription factor 1, beta	8
collagen, type IV, alpha 4	133
homeobox containing 1	27
SET domain, bifurcated 2	70
protein phosphatase 4, regulatory subunit 1-li	27
biotinidase	183
Uncharacterized protein	110
coiled-coil domain containing 89	11
homeobox D4	214
LIM and SH3 protein 1	552
low density lipoprotein receptor-related prote	270
transducin (beta)-like 2	990
heparan sulfate (glucosamine) 3-O-sulfotransfe	5
threonine synthase-like 1 (S. cerevisiae)	140
solute carrier family 6 (neutral amino acid tr	5
neurobeachin	5
gamma-aminobutyric acid (GABA) A receptor, alp	55
neuropeptide FF receptor 1	5
phosphoinositide-3-kinase, regulatory subunit	1484
synaptotagmin II	5
ferredoxin-fold anticodon binding domain conta	60
fibronectin type III domain containing 3B	509
lin-7 homolog A (C. elegans)	86
calnexin	17053
ribosomal RNA processing 15 homolog (S. cerevi	243
charged multivesicular body protein 1B	3248
contactin associated protein-like 2	29
TMEM256-PLSCR3 readthrough (NMD candidate)	976
kin of IRRE like (Drosophila)	493
vacuolar protein sorting 4 homolog B (S. cerev	180
ventral anterior homeobox 1	8
protein arginine methyltransferase 2	584
calmodulin regulated spectrin-associated prote	966
Ras association (RalGDS/AF-6) domain family (N	147
seizure threshold 2 homolog (mouse)	123
shroom family member 3	2841
YTH domain family, member 1	748
abhydrolase domain containing 4	102
fibronectin leucine rich transmembrane protein	11
tetraspanin 5	107
dihydrolipoamide branched chain transacylase E	117
leucine-rich alpha-2-glycoprotein 1	1511
epithelial splicing regulatory protein 1	74
kallikrein-related peptidase 10	5
dymeclin	547
sideroflexin 1	1018
calcium binding protein 39-like	12
trinucleotide repeat containing 6C	248
mediator complex subunit 14	1038
G protein-coupled receptor 20	34
T cell receptor associated transmembrane adapt	5
zinc finger protein 620	78
zinc fingers and homeoboxes 3	131
zinc finger protein 529	120

TBC1 domain family, member 20	761
cingulin	17
nucleoporin 210kDa	246
ribonuclease L (2',5'-oligoisoadenylate synthe	86
tumor necrosis factor receptor superfamily, me	243
translocase of outer mitochondrial membrane 40	13
prohibitin	759
cytochrome P450, family 2, subfamily W, polype	5
TIMP metallopeptidase inhibitor 2	3147
golgin A7 family, member B	5
somatomedin B and thrombospondin, type 1 domai	8
runt-related transcription factor 1; transloca	9
zinc finger protein 586	137
caprin family member 2	17
chromosome 1 open reading frame 226	369
zinc finger protein 75a	145
Down syndrome cell adhesion molecule	5
zinc finger protein 256	18
ubiquitin-conjugating enzyme E2I	291
killer cell lectin-like receptor subfamily C,	9
carbamoyl-phosphate synthase 1, mitochondrial	11682
ribosomal RNA processing 7 homolog A (S. cerev	522
UDP-N-acetyl-alpha-D-galactosamine:polypeptide	49
phosphatidylinositol transfer protein, alpha	366
ripply transcriptional repressor 3	16
protein phosphatase 1, regulatory subunit 3E	77
family with sequence similarity 3, member A	260
chromosome 12 open reading frame 60	11
protein tyrosine phosphatase, receptor type, G	696
zinc finger and BTB domain containing 44	236
tet methylcytosine dioxygenase 3	1437
C-type lectin domain family 2, member D	11
gigaxonin	185
wingless-type MMTV integration site family, me	40
empty spiracles homeobox 2	54
transmembrane protein 132B	5
heparan sulfate 6-O-sulfotransferase 2	4566
PHD finger protein 8	85
family with sequence similarity 153, member A	5
PHD finger protein 15	387
RNA binding motif protein 44	5
B-cell CLL/lymphoma 9	70
G protein-coupled receptor, family C, group 5,	84
short stature homeobox 2	66
oculocerebrorenal syndrome of Lowe	818
G protein-coupled receptor 37 like 1	5
serine/threonine/tyrosine kinase 1	13
forkhead box C1	1301
solute carrier family 16, member 4	19
solute carrier family 15 (oligopeptide transpo	588
zinc finger protein 687	1250
DEAD (Asp-Glu-Ala-Asp) box polypeptide 19B	690
LSM12 homolog (S. cerevisiae)	20
thioredoxin-related transmembrane protein 3	348

nucleoredoxin	811
G patch domain containing 8	337
poly(A) binding protein interacting protein 2B	42
TraB domain containing 2A	94
chloride channel, voltage-sensitive 4	182
KIAA1024-like	5
alcohol dehydrogenase 1B (class I), beta polyp	5
potassium voltage-gated channel, shaker-relate	35
aryl hydrocarbon receptor nuclear translocator	456
anoctamin 3	5
chemokine (C-C motif) receptor 5 (gene/pseudog	5
tudor domain containing 1	5
mitochondrial fission factor	129
epilepsy, progressive myoclonus type 2A, Lafor	197
nuclear factor of activated T-cells, cytoplasm	105
cyclin-dependent kinase-like 2 (CDC2-related k	7
arginine vasopressin receptor 1A	9
chromosome 11 open reading frame 74	57
translocase of inner mitochondrial membrane 13	5135
family with sequence similarity 96, member A	191
RAB23, member RAS oncogene family	32
reticulon 3	85
tetratricopeptide repeat domain 13	3928
ubiquitin protein ligase E3B	916
purinergic receptor P2Y, G-protein coupled, 1	58
signal-induced proliferation-associated 1 like	1578
core-binding factor, runt domain, alpha subuni	107
tripartite motif containing 71, E3 ubiquitin p	67
sema domain, immunoglobulin domain (Ig), trans	30
transmembrane protein 30B	10
RB-associated KRAB zinc finger	99
helicase-like transcription factor	127
spermatogenesis associated 13	900
JAZF zinc finger 1	869
APOBEC1 complementation factor	80
RAB15, member RAS oncogene family	23
inositol monophosphatase domain containing 1	1488
chromosome 2 open reading frame 72	3885
leucine-rich repeats and death domain containi	9
ARP2 actin-related protein 2 homolog (yeast)	71
transmembrane protein 19	1378
mucin 1, cell surface associated	388
Cdc42 guanine nucleotide exchange factor (GEF)	13
phosphatase and actin regulator 3	84
WD repeat domain 31	23
regulator of G-protein signaling 7 binding pro	5
butyrophilin, subfamily 3, member A3	16
tumor protein p53 regulated apoptosis inducing	5
	8
enolase superfamily member 1	95
speckle-type POZ protein-like	216
melanoma cell adhesion molecule	398
arsenic (+3 oxidation state) methyltransferase	379
progesterone receptor	8

chromosome 11 open reading frame 58	1782
zinc finger protein 148	230
neuronal calcium sensor 1	1083
sterile alpha motif domain containing 8	100
chromodomain protein, Y-like	24
oxidative stress responsive 1	1790
mediator complex subunit 9	256
fukutin	153
zinc finger, CCHC domain containing 16	5
zinc finger protein 320	10
sorting nexin 20	5
TBC1 domain family, member 22B	127
amylo-alpha-1, 6-glucosidase, 4-alpha-glucanot	48
inhibitor of kappa light polypeptide gene enha	334
aarF domain containing kinase 2	294
chromosome 21 open reading frame 90	26
USP6 N-terminal like	183
protein-O-mannosyltransferase 1	2617
CTD (carboxy-terminal domain, RNA polymerase I	457
elongation factor RNA polymerase II	250
homeodomain interacting protein kinase 2	48
crumbs homolog 1 (Drosophila)	115
regulatory associated protein of MTOR, complex	190
coatomer protein complex, subunit alpha	803
SWAP switching B-cell complex 70kDa subunit	492
transmembrane protein 45B	67
leucine zipper protein 1	434
sialic acid binding Ig-like lectin 11	5
polymeric immunoglobulin receptor	13
dual oxidase maturation factor 1	5
homeobox C12	5
hydroxy-delta-5-steroid dehydrogenase, 3 beta-	173
regulator of G-protein signaling 16	7
DDHD domain containing 2	961
PHD finger protein 13	1207
adrenomedullin 2	129
caldesmon 1	1013
frizzled family receptor 2	807
signal peptide, CUB domain, EGF-like 3	47
ATPase, H+ transporting, lysosomal 13kDa, V1 s	8219
chloride channel, voltage-sensitive 5	154
schlafen family member 5	195
SOGA family member 3	95
ciliary neurotrophic factor	46
RAB GTPase activating protein 1	514
B-cell CLL/lymphoma 9-like	91
egl-9 family hypoxia-inducible factor 1	505
VENT homeobox	5
tumor protein p53 inducible protein 11	90
TAF4b RNA polymerase II, TATA box binding prot	52
solute carrier family 39 (zinc transporter), m	845
fibroblast growth factor receptor 2	75
stromal antigen 2	216
chromosome 15 open reading frame 38	325

calcium activated nucleotidase 1	538
poly (ADP-ribose) polymerase family, member 14	502
cytidine monophosphate (UMP-CMP) kinase 2, mit	13
Sec61 alpha 2 subunit (S. cerevisiae)	105
osteosarcoma amplified 9, endoplasmic reticulu	1038
ribosomal protein S6 kinase, 90kDa, polypeptid	156
centrosomal protein 350kDa	705
SRY (sex determining region Y)-box 5	43
KAT8 regulatory NSL complex subunit 1	5
G protein-coupled receptor 180	161
alcohol dehydrogenase, iron containing, 1	33
EGF-like, fibronectin type III and laminin G d	123
DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11	175
coronin 6	48
membrane protein, palmitoylated 6 (MAGUK p55 s	389
CAP-GLY domain containing linker protein 3	9
proprotein convertase subtilisin/kexin type 7	92
keratin 38	5
phospholipase C, delta 1	21
actin binding LIM protein 1	1321
polycystin (PKD) family receptor for egg jelly	5
paired box 8	11
RAD54-like 2 (S. cerevisiae)	215
glutamyl-tRNA synthetase 2, mitochondrial	394
solute carrier family 7 (amino acid transporte	155
uncharacterized serine/threonine-protein kinas	17
family with sequence similarity 134, member C	397
zinc finger CCCH-type containing 13	229
ADNP homeobox 2	808
zinc finger protein 142	252
lipase, member H	18
OTU domain containing 6B	18
major facilitator superfamily domain containin	395
tetratricopeptide repeat domain 14	99
hexamethylene bis-acetamide inducible 1	179
cytochrome c oxidase assembly factor 1 homolog	244
zinc finger protein 317	433
ADP-ribosylation factor-like 5B	368
cell adhesion associated, oncogene regulated	173
zinc finger protein 510	40
IKAROS family zinc finger 1 (Ikaros)	11
hypoxia inducible factor 1, alpha subunit inhi	1545
chromosome 17 open reading frame 103	54
kinesin family member 21B	12
adrenoceptor beta 3	5
calpain 6	5
zinc finger protein 621	39
v-myb avian myeloblastosis viral oncogene homo	53
laminin, beta 4	5
casein kinase 1, gamma 2	5
inhibitor of kappa light polypeptide gene enha	5
chromosome 18 open reading frame 63	5
zinc finger protein 534	5
mitochondrial antiviral signaling protein	211

heme binding protein 2	252
ankyrin repeat domain 52	2913
F-box and leucine-rich repeat protein 20	455
wings apart-like homolog (Drosophila)	185
OTU domain containing 3	438
potassium channel tetramerization domain conta	404
solute carrier family 35 (GDP-fucose transport	856
chromatin target of PRMT1	2499
UDP glycosyltransferase 3 family, polypeptide	90
v-maf avian musculoaponeurotic fibrosarcoma on	333
zinc finger protein 501	24
neurolysin (metallopeptidase M3 family)	885
sorcin	278
maestro heat-like repeat family member 6	24
Crm, cramped-like (Drosophila)	731
zinc finger protein 678	89
ALG6, alpha-1,3-glucosyltransferase	140
coiled-coil domain containing 3	16
zinc finger, FYVE domain containing 1	5
CDP-diacylglycerol synthase (phosphatidate cyt	720
GATA binding protein 4	5
family with sequence similarity 131, member B	5
eukaryotic translation initiation factor 4 gam	61971
zinc finger protein 512	189
MAU2 sister chromatid cohesion factor	5234
adaptor-related protein complex 5, beta 1 subu	22
retinoblastoma-like 1 (p107)	88
ELOVL fatty acid elongase 2	99
cytohesin 3	248
insulin-like growth factor binding protein 5	10709
C2 calcium-dependent domain containing 4B	14
chromosome 1 open reading frame 116	17
ubiquitin specific peptidase 31	214
KIAA0355	538
HECT domain containing E3 ubiquitin protein li	45
LSM11, U7 small nuclear RNA associated	1458
FOS-like antigen 2	2255
solute carrier family 16, member 2 (thyroid ho	22
zinc finger protein 268	156
Uncharacterized protein	15
kinesin family member 24	84
kelch-like family member 18	74
RNA binding motif protein 41	41
mediator complex subunit 1	87
ATPase, class VI, type 11A	731
ybeY metallopeptidase (putative)	40
peroxidasin homolog (Drosophila)	872
translational activator of mitochondrially enc	755
mediator complex subunit 22	43
family with sequence similarity 84, member B	45
chromosome 1 open reading frame 95	28
REST corepressor 1	403
BRI3 binding protein	820
ST6 beta-galactosamide alpha-2,6-sialyltranfer	549

alanine and arginine rich domain containing pr	7
AT rich interactive domain 4A (RBP1-like)	33
chromosome 17 open reading frame 102	5
chromosome 19 open reading frame 54	18
chemokine (C-X-C motif) receptor 6	5
eukaryotic translation initiation factor 4E fa	475
testis specific, 10	8
transmembrane protein 108	31
transformation/transcription domain-associated	351
missing oocyte, meiosis regulator, homolog (Dr	77
zinc finger protein 611	7
regulating synaptic membrane exocytosis 2	8
apolipoprotein O-like	109
RAD9 homolog A (S. pombe)	38
CD22 molecule	13
ribosomal protein L12	30
zinc finger and BTB domain containing 21	802
TAF4 RNA polymerase II, TATA box binding prote	61
digestive organ expansion factor homolog (zebr	493
insulin-degrading enzyme	446
Fas (TNFRSF6) associated factor 1	428
diablo, IAP-binding mitochondrial protein	1700
chromosome 2 open reading frame 54	13
zinc finger protein 526	256
erythrocyte membrane protein band 4.2	5
solute carrier family 25, member 34	5
G patch domain containing 11	113
zinc finger protein 804B	0
chromosome 14 open reading frame 177	5
neuroblastoma breakpoint family, member 12	5
NYN domain and retroviral integrase containing	1928
bassoon presynaptic cytomatrix protein	31
amine oxidase, copper containing 3	59
chromosome 6 open reading frame 141	28
GATA zinc finger domain containing 2A	986
syntaxin binding protein 4	62
LIM domains containing 1	1092
discs, large (Drosophila) homolog-associated p	1188
Usher syndrome 2A (autosomal recessive, mild)	5
proline rich 20D	5
zinc finger protein 300	107
solute carrier family 6 (amino acid transporte	5
lymphocyte antigen 6 complex, locus G5B	200
proline rich 20A	5
proline rich 20C	5
zyg-11 family member B, cell cycle regulator	975
proline rich 20E	5
GRAM domain containing 1C	12
phosphodiesterase 4A, cAMP-specific	48
protocadherin 17	477
inducible T-cell co-stimulator	5
proline rich 20B	5
intermediate filament family orphan 2	139
PAP associated domain containing 7	3195

NEDD4 binding protein 1	105
ubiquitin-like modifier activating enzyme 6	169
olfactomedin 4	5
INO80 complex subunit	279
podocalyxin-like	2928
chromosome 12 open reading frame 66	98
tubulin, beta 4A class IVa	8
Lipid phosphate phosphatase-related protein ty	5
synaptotagmin-like 5	37
androgen receptor	57
neuroblastoma breakpoint family, member 11	5
protein tyrosine phosphatase, receptor type, f	5
tousled-like kinase 1	200
forkhead box K1	368
family with sequence similarity 212, member B	211
zinc finger, FYVE domain containing 16	388
abhydrolase domain containing 17A	202
DnaJ (Hsp40) homolog, subfamily C, member 10	709
mediator complex subunit 13-like	73
membrane-spanning 4-domains, subfamily A, memb	5
immunoglobulin superfamily containing leucine-	6
solute carrier family 4 (sodium bicarbonate co	6
family with sequence similarity 216, member B	5
arachidonate lipoxygenase 3	5
alpha-kinase 3	16
myocyte enhancer factor 2A	654
transmembrane protein 245	1320
coagulation factor IX	5
ataxin 7-like 3	43
lipocalin 10	10
saccharopine dehydrogenase (putative)	1752
family with sequence similarity 199, X-linked	856
Src homology 2 domain containing E	9
vitamin K epoxide reductase complex, subunit 1	2291
SERTA domain containing 1	603
phosphofurin acidic cluster sorting protein 1	87
distal-less homeobox 2	653
tumor necrosis factor (ligand) superfamily, me	29
cholinergic receptor, nicotinic, beta 4 (neuro	5
KIAA0247	161
endothelin receptor type B	5
neuroblastoma breakpoint family, member 1	21
serine active site containing 1	129
solute carrier family 9, subfamily A (NHE7, ca	147
mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-	223
aldehyde dehydrogenase 3 family, member A2	940
DET1 and DDB1 associated 1	76
guanylate cyclase 1, soluble, alpha 2	24
solute carrier family 7, member 6 opposite str	751
family with sequence similarity 129, member A	213
chromosome 22 open reading frame 39	360
KH-type splicing regulatory protein	4469
dopachrome tautomerase	5
tenascin XB	5

RNA binding motif protein 48	220
mesenchyme homeobox 1	5
dpy-19-like 1 (C. elegans)	80
phosphatidylinositol glycan anchor biosynthesi	1203
leucine rich repeat containing 3	176
family with sequence similarity 169, member A	90
zinc finger protein 35	71
chromosome 19 open reading frame 25	498
dimethylglycine dehydrogenase	17
cleavage stimulation factor, 3' pre-RNA, subun	658
TIMP metallopeptidase inhibitor 4	38
RNA guanylyltransferase and 5'-phosphatase	1384
cell division cycle 25C	125
protocadherin gamma subfamily A, 11	145
protocadherin gamma subfamily B, 6	145
retinoid X receptor, beta	46
protein tyrosine phosphatase, receptor type, S	322
KAT8 regulatory NSL complex subunit 1-like	5
HCG1811579; Uncharacterized protein	25
protocadherin gamma subfamily B, 7	145
protocadherin gamma subfamily A, 4	145
zona pellucida-like domain containing 1	5
pim-2 oncogene	77
hydroxycarboxylic acid receptor 2	5
tau tubulin kinase 2	18
cancer susceptibility candidate 3	493
protocadherin gamma subfamily B, 2	145
interleukin 17D	130
solute carrier organic anion transporter famil	5
glycerophosphodiester phosphodiesterase domain	8
CAP-GLY domain containing linker protein 2	2111
protocadherin gamma subfamily A, 1	145
protocadherin gamma subfamily B, 3	145
mediator complex subunit 13	561
protocadherin gamma subfamily B, 4	145
protocadherin gamma subfamily A, 5	145
protocadherin gamma subfamily B, 1	145
toll interacting protein	1536
mannan-binding lectin serine peptidase 1 (C4/C	838
mediator complex subunit 20	32
PCF11 cleavage and polyadenylation factor subu	218
F-box protein 42	854
Uncharacterized protein	32
cyclin-dependent kinase 5, regulatory subunit	335
SKI-like oncogene	210
solute carrier family 8 (sodium/calcium exchan	61
peroxisome proliferator-activated receptor gam	12
lysine (K)-specific methyltransferase 2A	1092
neurofibromin 2 (merlin)	828
protocadherin gamma subfamily A, 3	145
TNF receptor-associated factor 1	5
protocadherin gamma subfamily C, 3	145
	164
protocadherin gamma subfamily A, 12	145

protocadherin gamma subfamily A, 6	145
Ras and Rab interactor 2	539
platelet-derived growth factor receptor, alpha	39
cyclic nucleotide gated channel beta 3	5
coiled-coil domain containing 85A	46
metastasis associated 1 family, member 2	1168
multivesicular body subunit 12B	29
ubiquitin protein ligase E3C	1332
protocadherin gamma subfamily A, 9	145
poly (ADP-ribose) polymerase family, member 16	97
protocadherin gamma subfamily A, 7	145
protocadherin gamma subfamily A, 2	145
transcriptional adaptor 3	135
protocadherin gamma subfamily A, 8	145
leucine-rich repeat LGI family, member 3	5
protein associated with topoisomerase II homol	703
solute carrier family 35 (UDP-N-acetylglucosam	191
dipeptidyl-peptidase 8	1293
Cbl proto-oncogene B, E3 ubiquitin protein lig	469
signal peptide, CUB domain, EGF-like 2	57
GINS complex subunit 4 (Sld5 homolog)	500
tetratricopeptide repeat domain 9C	475
major histocompatibility complex, class II, DO	5
splA/ryanodine receptor domain and SOCS box co	572
RNA binding motif protein 23	1540
endosulfine alpha	167
protein phosphatase 1, regulatory subunit 7	119
T-cell leukemia homeobox 2	5
protocadherin gamma subfamily A, 10	145
Ral GEF with PH domain and SH3 binding motif 2	201
microfibrillar-associated protein 2	10
junctophilin 3	318
retrotransposon gag domain containing 4	34
protocadherin gamma subfamily C, 4	145
protocadherin gamma subfamily C, 5	145
ectonucleoside triphosphate diphosphohydrolase	5
coxsackie virus and adenovirus receptor	56
F-box and WD repeat domain containing 8	169
striatin interacting protein 1	114
dynactin 5 (p25)	764
sal-like 4 (Drosophila)	155
	5
major histocompatibility complex, class II, DP	5
chromosome 9 open reading frame 66	13
taxilin alpha	564
endonuclease domain containing 1	100
dual specificity phosphatase 2	41
actin filament associated protein 1-like 1	10
calmin (calponin-like, transmembrane)	53
methylmalonic aciduria (cobalamin deficiency)	38
AF4/FMR2 family, member 2	8
vesicle transport through interaction with t-S	376
calcium binding and coiled-coil domain 2	1160
chromodomain helicase DNA binding protein 4	145

YKT6 v-SNARE homolog (S. cerevisiae)	2409
hydroxycarboxylic acid receptor 3	5
tumor suppressor candidate 5	5
cell division cycle associated 7-like	292
solute carrier family 26 (anion exchanger), me	18
anoctamin 1, calcium activated chloride channe	78
interferon, epsilon	65
ribosomal protein S17-like	5
ribosomal protein S17	5
golgi-associated, gamma adaptin ear containing	325
SRR1 domain containing	1069
dihydropyrimidinase-like 3	5209
anthrax toxin receptor 2	51
zinc finger protein 28	9
ZFP37 zinc finger protein	24
discs, large homolog 3 (Drosophila)	185
T-box 18	54
cytochrome c oxidase subunit VIb polypeptide 1	1779
SLIT-ROBO Rho GTPase activating protein 1	64
fibulin 5	146
zinc finger, MYM-type 2	172
pentatricopeptide repeat domain 2	377
shroom family member 4	5
aquaporin 7	10
synaptic vesicle glycoprotein 2B	7
APH1A gamma secretase subunit	475
elongation factor Tu GTP binding domain contai	3704
alkaline ceramidase 1	5
unc-80 homolog (C. elegans)	5
biphenyl hydrolase-like (serine hydrolase)	618
zinc finger protein 467	11
TNFRSF1A-associated via death domain	117
armadillo repeat containing 5	376
proline/arginine-rich end leucine-rich repeat	5
adaptor-related protein complex 2, mu 1 subuni	10753
troponin I type 1 (skeletal, slow)	5
uveal autoantigen with coiled-coil domains and	82
ectonucleoside triphosphate diphosphohydrolase	105
drebrin-like	1802
septin 11	515
small integral membrane protein 13	199
family with sequence similarity 111, member B	39
chemokine (C-X3-C motif) ligand 1	218
protein phosphatase 3, regulatory subunit B, a	117
interleukin-1 receptor-associated kinase 1 bin	30
kelch-like family member 7	90
suppressor of fused homolog (Drosophila)	247
carboxylesterase 2	24
GEN1 Holliday junction 5’ flap endonuclease	161
vesicle-associated membrane protein 7	5
importin 9	3549
CCR4-NOT transcription complex, subunit 6	300
integrin, alpha 9	9
dishevelled associated activator of morphogene	5

nuclear mitotic apparatus protein 1	7
pipecolic acid oxidase	30
serine/arginine repetitive matrix 4	22
H2A histone family, member V	9640
hexose-6-phosphate dehydrogenase (glucose 1-de	467
DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	141
chromosome 17 open reading frame 72	5
tetratricopeptide repeat domain 39A	174
SET binding protein 1	77
Yip1 domain family, member 4	3482
KIAA1958	117
LON peptidase N-terminal domain and ring finge	36
nucleolar protein 12	536
family with sequence similarity 196, member B	174
GTPase activating protein (SH3 domain) binding	688
collagen, type IX, alpha 2	189
protein kinase, cGMP-dependent, type I	12
myocardin	62
zinc finger protein 609	103
seizure related 6 homolog (mouse)-like	5
cullin-associated and neddylation-dissociated	92
Uncharacterized protein; cDNA FLJ45856 fis, cl	7
geranylgeranyl diphosphate synthase 1	184
gamma-aminobutyric acid (GABA) A receptor, eps	6
cAMP-regulated phosphoprotein, 19kDa	1316
transportin 2	1620
ring finger protein 115	757
transforming growth factor beta regulator 1	275
pleckstrin homology-like domain, family B, mem	126
poly (ADP-ribose) polymerase family, member 8	80
prickle homolog 1 (Drosophila)	146
chloride channel CLIC-like 1	849
neuron navigator 2	337
v-rel avian reticuloendotheliosis viral oncoge	1707
centlein, centrosomal protein	42
NDC1 transmembrane nucleoporin	371
zinc finger homeobox 3	57
NLR family, pyrin domain containing 10	21
proline and serine-rich protein 2	61
chromosome 14 open reading frame 119	6513
transmembrane and tetratricopeptide repeat con	406
methyltransferase like 20	47
wingless-type MMTV integration site family mem	5
leucine rich repeat containing 38	5
anoctamin 5	12
transmembrane protein 86A	5
BCL2 binding component 3	87
metallothionein 1A	19
serine/arginine-rich splicing factor 10	1920
p53 and DNA-damage regulated 1	116
zinc finger, DHHC-type containing 20	1486
formin-like 3	132
lectin, galactoside-binding, soluble, 3 bindin	238
Sp2 transcription factor	779

ATP-binding cassette, sub-family F (GCN20), me	48
dynamin 1-like	399
protein kinase D3	203
ring finger protein 40, E3 ubiquitin protein l	773
RPGRIP1-like	55
histone deacetylase 4	48
chromosome 11 open reading frame 48	29
kinesin family member 5C	19
short stature homeobox	5
CMT1A duplicated region transcript 4	109
eukaryotic translation initiation factor 4B	37
methyl-CpG binding domain protein 3	393
transcription factor 4	394
BCL2-associated transcription factor 1	1732
vacuolar protein sorting 53 homolog (S. cerevi	1332
pre-B-cell leukemia homeobox 1	18
glutamate-rich WD repeat containing 1	2673
Bet1 golgi vesicular membrane trafficking prot	702
Zinc finger protein 268	156
peroxisomal biogenesis factor 26	157
transmembrane protein 65	769
queuine tRNA-ribosyltransferase domain contain	123
torsin family 1, member B (torsin B)	222
Mab-21 domain containing 2	48
EGF domain-specific O-linked N-acetylglucosami	302
protein tyrosine kinase 6	27
suppressor of cancer cell invasion	74
ring finger protein 220	474
PR domain containing 15	328
hedgehog acyltransferase	583
adenosine deaminase, tRNA-specific 2	303
zinc finger and BTB domain containing 39	7
spermatogenesis associated 18	19
KIAA1257	5
zinc finger and BTB domain containing 43	396
lysine (K)-specific demethylase 8	62
transient receptor potential cation channel, s	21
CUB domain containing protein 2	5
pleckstrin homology domain containing, family	45
phosphatidylinositol glycan anchor biosynthesi	152
F-box protein 48	13
GATA zinc finger domain containing 2B	48
neuregulin 2	9
family with sequence similarity 102, member A	85
utrophin	87
BTB (POZ) domain containing 7	590
zinc finger, DHHC-type containing 3	426
homeobox A13	328
growth factor receptor-bound protein 10	1382
sorting nexin 8	303
CD28 molecule	5
proteasome (prosome, macropain) assembly chape	31
deltex 3-like (Drosophila)	319
fidgetin	10

nucleoporin 35kDa	210
serine incorporator 2	624
baculoviral IAP repeat containing 3	9
sema domain, transmembrane domain (TM), and cy	179
solute carrier family 34 (type II sodium/phosp	5
chromosome 10 open reading frame 105	5
KIAA1045	42
single-strand-selective monofunctional uracil-	242
PAN3 poly(A) specific ribonuclease subunit hom	361
developmental pluripotency associated 3	11
nuclear export mediator factor	18
zinc finger, DHHC-type containing 2	171
zinc finger and BTB domain containing 8B	18
zinc finger protein 451	190
coiled-coil domain containing 80	570
forkhead box B1	31
ADAM metallopeptidase with thrombospondin type	68
adenosylmethionine decarboxylase 1	725
zinc finger and BTB domain containing 6	55
ubiquitin specific peptidase 37	14
solute carrier family 46 (folate transporter),	580
Ras association (RalGDS/AF-6) domain family me	27
BAI1-associated protein 3	10
cap methyltransferase 1	109
RAD23 homolog B (S. cerevisiae)	1012
PRELI domain containing 2	63
family with sequence similarity 122A	1277
phospholipid scramblase 1	220
synapse defective 1, Rho GTPase, homolog 2 (C.	72
nuclear factor I/C (CCAAT-binding transcriptio	26
zinc finger protein 516	311
branched chain keto acid dehydrogenase E1, bet	143
F-box protein 46	197
keratin associated protein 4-9	10
dual specificity phosphatase 3	836
myelin basic protein	96
family with sequence similarity 63, member B	41
piezo-type mechanosensitive ion channel compon	158
Uncharacterized protein	5
cytoplasmic polyadenylation element binding pr	367
sema domain, immunoglobulin domain (Ig), short	85
inhibitor of DNA binding 4, dominant negative	3400
membrane bound O-acyltransferase domain contai	1145
cAMP responsive element binding protein 1	295
calcium channel, voltage-dependent, T type, al	11
F-box and leucine-rich repeat protein 4	321
neutral cholesterol ester hydrolase 1	1779
pogo transposable element with ZNF domain	170
ubiquitin protein ligase E3 component n-recogn	728
SERTA domain containing 4	296
Kruppel-like factor 8	8
activating signal cointegrator 1 complex subun	293
shroom family member 2	121
protein kinase C, alpha	726

zinc finger protein 532	5
microtubule-associated protein 1B	259
tachykinin receptor 1	5
signal-regulatory protein beta 2	5
tetraspanin 1	16
KIAA1009	7
hippocalcin like 4	5
dpy-19-like 3 (C. elegans)	146
UHRF1 binding protein 1	360
2-oxoglutarate and iron-dependent oxygenase do	2120
SIX homeobox 5	47
limbic system-associated membrane protein	19
tetraspanin 2	43
gap junction protein, gamma 1, 45kDa	195
zinc finger protein 845	67
chondroitin sulfate synthase 3	221
POU class 2 homeobox 2	5
ankyrin repeat domain 42	224
ELMO/CED-12 domain containing 3	31
poly (ADP-ribose) polymerase family, member 9	456
myopalladin	73
KIAA1199	660
ankyrin repeat domain 10	37
BCL6 corepressor-like 1	209
adenosine monophosphate deaminase 3	5
complement component 2	52
nuclear RNA export factor 1	1017
GRB2-associated binding protein family, member	5
DEP domain containing 5	221
tubby bipartite transcription factor	743
nipsnap homolog 3B (C. elegans)	26
RNA binding motif (RNP1, RRM) protein 3	1325
integrin, alpha 6	1328
GDP-D-glucose phosphorylase 1	65
inhibitor of growth family, member 5	529
solute carrier family 25, member 44	760
family with sequence similarity 168, member B	122
chromobox homolog 6	215
ATP synthase mitochondrial F1 complex assembly	1637
mitochondrial ribosomal protein L19	816
SMAD family member 5	225
decapping enzyme, scavenger	320
regulation of nuclear pre-mRNA domain containi	280
immunity-related GTPase family, Q	62
solute carrier family 30 (zinc transporter), m	711
SDA1 domain containing 1	91
zinc finger protein 285	31
cyclin-dependent kinase 19	51
zinc finger protein 287	14
aryl hydrocarbon receptor nuclear translocator	574
DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	472
ceramide synthase 3	5
SID1 transmembrane family, member 1	5
shisa family member 7	5

zinc finger protein 831	5
regulating synaptic membrane exocytosis 1	45
BEN domain containing 3	13
WD repeat domain 52	5
phosphatidylinositol-3,4,5-trisphosphate-depen	14
Scm-like with four mbt domains 2	107
PDZ domain containing 2	5
5-hydroxytryptamine (serotonin) receptor 7, ad	12
piccolo presynaptic cytomatrix protein	22
leucine zipper, putative tumor suppressor 1	33
DIP2 disco-interacting protein 2 homolog B (Dr	1613
TRAF family member-associated NFKB activator	176
biogenesis of lysosomal organelles complex-1,	2383
AT rich interactive domain 3A (BRIGHT-like)	320
potassium large conductance calcium-activated	8
platelet-activating factor acetylhydrolase 1b,	180
eukaryotic translation initiation factor 2, su	575
formin 1	25
collagen beta(1-O)galactosyltransferase 1	427
zinc finger protein 605	147
homeobox and leucine zipper encoding	100
homeodomain interacting protein kinase 1	930
Rho GTPase activating protein 39	14
proline-rich transmembrane protein 4	5
phosphoinositide-interacting regulator of tran	5
lysine (K)-specific demethylase 5C	422
sidekick cell adhesion molecule 2	8
DENN/MADD domain containing 4B	167
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galact	28
GEM interacting protein	9
zinc finger protein 652	33
alcohol dehydrogenase 5 (class III), chi polyp	217
deiodinase, iodothyronine, type II	98
leucine zipper transcription factor-like 1	593
angel homolog 1 (Drosophila)	299
ras responsive element binding protein 1	340
glutamate-ammonia ligase	1073
HECT, C2 and WW domain containing E3 ubiquitin	28
natural killer-tumor recognition sequence	798
NACC family member 2, BEN and BTB (POZ) domain	172
RAB5C, member RAS oncogene family	96
phosphoinositide kinase, FYVE finger containin	107
transcriptional adaptor 2A	278
nucleus accumbens associated 1, BEN and BTB (P	337
ELK3, ETS-domain protein (SRF accessory protei	2719
poliovirus receptor-related 1 (herpesvirus ent	50
CDNA FLJ27243 fis, clone SYN08134; Uncharacter	5
vav 2 guanine nucleotide exchange factor	477
additional sex combs like 2 (Drosophila)	139
melanocortin 2 receptor (adrenocorticotropic h	5
neuronal PAS domain protein 3	9
kinesin family member C3	65
pumilio RNA-binding family member 2	1047
gamma-glutamyl carboxylase	254

N(alpha)-acetyltransferase 50, NatE catalytic	260
Ras homolog enriched in brain	14
checkpoint kinase 1	338
ATP-binding cassette, sub-family A (ABC1), mem	159
ariadne RBR E3 ubiquitin protein ligase 2	938
guanylate binding protein 2, interferon-induci	1309
phosphatidylinositol-5-phosphate 4-kinase, typ	457
homeobox B6	12
wingless-type MMTV integration site family, me	28
patched domain containing 4	19
two pore segment channel 2	629
double homeobox A	5
dual specificity phosphatase 7	68
DnaJ (Hsp40) homolog, subfamily C, member 28	24
transient receptor potential cation channel, s	18
aldo-keto reductase family 1, member C2	5
homeobox C13	63
spectrin, beta, non-erythrocytic 5	7
coiled-coil domain containing 120	170
paired box 5	5
dipeptidyl-peptidase 10 (non-functional)	5
KIAA1524	498
collagen, type III, alpha 1	215
transducer of ERBB2, 2	71
HemK methyltransferase family member 1	99
EDAR-associated death domain	76
PRP40 pre-mRNA processing factor 40 homolog A	459
chromosome 12 open reading frame 23	602
sarcospan	25
cancer susceptibility candidate 10	116
insulin receptor substrate 1	804
abl-interactor 2	877
A kinase (PRKA) anchor protein 13	53
tripartite motif containing 46	69
ribonucleoprotein, PTB-binding 1	362
ubiquitin-conjugating enzyme E2Z	3688
period circadian clock 3	16
mutated in colorectal cancers	115
kelch repeat and BTB (POZ) domain containing 8	22
radical S-adenosyl methionine domain containin	463
arylacetamide deacetylase-like 3	5
serine/threonine kinase 36	218
U2 small nuclear RNA auxiliary factor 2	1093
peptidylprolyl isomerase (cyclophilin)-like 2	1911
phosphodiesterase 11A	7
thyrotrophic embryonic factor	60
mitogen-activated protein kinase-activated pro	155
metallophosphoesterase domain containing 1	51
molybdenum cofactor sulfurase	627
tumor protein p53 inducible nuclear protein 1	39
chromosome 3 open reading frame 70	19
nicalin	442
WD repeat domain 59	24
mediator complex subunit 29	2453

chromosome 20 open reading frame 144	10
sorting nexin family member 30	33
pleckstrin and Sec7 domain containing 4	72
signal transducer and activator of transcripti	478
hairy/enhancer-of-split related with YRPW moti	37
Kv channel interacting protein 2	5
formin-like 2	31
Uncharacterized protein	200
nuclear fragile X mental retardation protein i	440
tensin 1	591
sodium channel, voltage-gated, type II, alpha	7
chromodomain protein, Y-like 2	239
family with sequence similarity 110, member B	60
ATPase, H+ transporting, lysosomal 42kDa, V1 s	951
methionine adenosyltransferase II, alpha	8
secretogranin III	15
proprotein convertase subtilisin/kexin type 1	83
phosphodiesterase 4D interacting protein	36
TBC1 domain family, member 30	153
aspartylglucosaminidase	601
lysine (K)-specific methyltransferase 2D	78
leucine zipper and CTNNBIP1 domain containing	508
c-abl oncogene 2, non-receptor tyrosine kinase	892
zinc finger, BED-type containing 1	5
solute carrier family 6 (neurotransmitter tran	5
excision repair cross-complementing rodent rep	93
cytochrome c-1	2640
FLYWCH-type zinc finger 1	97
heparan sulfate (glucosamine) 3-O-sulfotransfe	1489
carbonic anhydrase VII	5
N-ethylmaleimide-sensitive factor attachment p	82
DCN1, defective in cullin neddylation 1, domai	267
Src-like-adaptor 2	5
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialy	5
activin A receptor, type IIB	21
zinc finger and BTB domain containing 7A	37
TEA domain family member 2	589
presenilin 1	1340
tankyrase, TRF1-interacting ankyrin-related AD	943
NHL repeat containing 2	368
TGFB1-induced anti-apoptotic factor 1	152
Rho GTPase activating protein 17	1337
5-hydroxytryptamine (serotonin) receptor 1D, G	99
golgi transport 1B	848
myeloid/lymphoid or mixed-lineage leukemia (tr	24
family with sequence similarity 78, member A	7
chromosome 17 open reading frame 85	718
SRY (sex determining region Y)-box 6	22
purinergic receptor P2X, ligand-gated ion chan	260
zinc finger, BED-type containing 4	2276
zinc finger protein 70	99
NLR family, pyrin domain containing 5	5
phenylalanyl-tRNA synthetase, alpha subunit	1994
testis development related protein	235

synaptogyrin 1	101
transmembrane protein 55A	151
ectodysplasin A2 receptor	64
lysophosphatidylglycerol acyltransferase 1	135
E74-like factor 4 (ets domain transcription fa	69
synaptic vesicle glycoprotein 2A	10
TBC1 domain family, member 10C	5
angiomotin	515
fin bud initiation factor homolog (zebrafish)	135
zinc finger protein 484	22
transcription factor AP-2 beta (activating enh	23
histamine N-methyltransferase	530
heparan-alpha-glucosaminide N-acetyltransferas	865
tubulin, beta 4B class IVb	101
ceramide synthase 6	1932
GRB2-associated binding protein 1	26
arylsulfatase B	86
carboxypeptidase M	125
ATPase, class V, type 10D	440
ankyrin 2, neuronal	133
G protein-coupled receptor 75	35
epiregulin	5
argonaute RISC catalytic component 4	96
tripartite motif containing 26	102
family with sequence similarity 117, member A	185
HAUS augmin-like complex, subunit 6	24
Rho GTPase activating protein 32	13
protein tyrosine phosphatase, receptor type, f	21
sal-like 2 (Drosophila)	233
annexin A11	2285
interleukin 17 receptor D	108
regulator of G-protein signaling 10	457
bobby sox homolog (Drosophila)	141
adaptor-related protein complex 5, mu 1 subuni	198
transcription elongation factor B (SIII), poly	637
EFR3 homolog B (S. cerevisiae)	14
HCG1787533; Uncharacterized protein	14
aminoacyl tRNA synthetase complex-interacting	740
adaptor-related protein complex 5, sigma 1 sub	492
kelch-like family member 38	13
zinc and ring finger 1, E3 ubiquitin protein l	519
solute carrier family 12 (potassium/chloride t	5
ATPase, Na+/K+ transporting, beta 2 polypeptid	34
transmembrane protein 255A	113
zinc finger CCCH-type containing 12B	29
mitogen-activated protein kinase kinase 6	235
cytochrome P450, family 27, subfamily B, polyp	11
YTH domain family, member 3	444
MLX, MAX dimerization protein	771
glucoside xylosyltransferase 2	207
GINS complex subunit 2 (Psf2 homolog)	136
F-box protein 41	175
methyltransferase like 2B	22
glucosamine-6-phosphate deaminase 2	117

zinc finger protein 799	17
microtubule-associated protein 9	45
ankyrin repeat domain 40	409
mutL homolog 3	152
tudor domain containing 6	65
nuclear transport factor 2	222
chromosome 6 open reading frame 89	1972
sterile alpha and TIR motif containing 1	130
Sjogren syndrome nuclear autoantigen 1	160
zinc finger, CCHC domain containing 24	359
fibrosin-like 1	778
potassium channel tetramerization domain conta	2483
RasGEF domain family, member 1A	10
chromosome 3 open reading frame 14	67
SAR1 homolog B (S. cerevisiae)	1404
kelch repeat and BTB (POZ) domain containing 1	173
tau tubulin kinase 1	7
mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-a	9
TBC1 domain family, member 2B	5
kinesin family member 3C	177
zinc finger protein 862	7
discs, large (Drosophila) homolog-associated p	5
glycosylphosphatidylinositol specific phosphol	51
TRAF-interacting protein with forkhead-associa	5
hypoxia up-regulated 1	29
chromosome 8 open reading frame 86	5
prostaglandin E receptor 3 (subtype EP3)	14
transmembrane protein 151A	163
attractin-like 1	26
ArfGAP with FG repeats 2	3985
period circadian clock 2	106
catsper channel auxiliary subunit gamma	5
meningioma (disrupted in balanced translocatio	15
	5
C2 calcium-dependent domain containing 2	106
one cut homeobox 3	5
unc-5 homolog B (C. elegans)	90
ribosomal protein S14	2353
cytochrome P450, family 4, subfamily F, polype	5
calcium homeostasis modulator 1	5
Fas apoptotic inhibitory molecule 2	5
synaptotagmin IX	5
zinc finger, FYVE domain containing 26	104
potassium voltage-gated channel, Shaw-related	5
solute carrier family 25 (pyrimidine nucleotid	264
Ras association (RalGDS/AF-6) domain family (N	9
F-box and WD repeat domain containing 2	227
coiled-coil domain containing 47	1484
lysine (K)-specific demethylase 5B	187
v-erb-b2 avian erythroblastic leukemia viral o	511
ubiquitin specific peptidase 10	66
GID complex subunit 4	79
ELKS/RAB6-interacting/CAST family member 1	159
cleavage and polyadenylation specific factor 4	7

choline dehydrogenase	249
DnaJ (Hsp40) homolog, subfamily C, member 5	1089
influenza virus NS1A binding protein	2215
ring finger protein 8, E3 ubiquitin protein li	301
formin binding protein 1	165
dystrophin	211
cell adhesion molecule 3	5
TVP23C-CDRT4 readthrough	109
family with sequence similarity 179, member B	12
Uncharacterized protein	5
zinc finger protein 331	553
chromosome 10 open reading frame 126	5
actin filament associated protein 1	1966
tetratricopeptide repeat domain 7A	400
tuberous sclerosis 1	838
importin 11	202
Myb-like, SWIRM and MPN domains 1	38
Sin3A-associated protein, 30kDa	43
TGF-beta activated kinase 1/MAP3K7 binding pro	577
protein phosphatase 2, regulatory subunit B'',	32
inner centromere protein antigens 135/155kDa	1299
dual specificity phosphatase 22	1330
family with sequence similarity 172, member A	257
murine retrovirus integration site 1 homolog	26
bromodomain and PHD finger containing, 3	7032
single-minded homolog 1 (Drosophila)	104
lactation elevated 1	42
DEAH (Asp-Glu-Ala-His) box polypeptide 36	108
coiled-coil domain containing 6	193
ArfGAP with GTPase domain, ankyrin repeat and	109
transducin (beta)-like 1X-linked	125
zinc finger and BTB domain containing 8A	287
notch 2	734
inducible T-cell co-stimulator ligand	47
RAD18 homolog (S. cerevisiae)	211
zinc finger protein 426	70
epidermal growth factor receptor	632
vasoactive intestinal peptide receptor 2	35
transmembrane protein 81	17
zinc finger protein 730	8
mesoderm induction early response 1, family me	137
immunoglobulin-like domain containing receptor	7
integrin, alpha M (complement component 3 rece	10
two pore segment channel 1	401
MACRO domain containing 2	5
carbohydrate (N-acetylgalactosamine 4-sulfate	59
golgin A3	944
Fanconi anemia, complementation group C	408
coatomer protein complex, subunit zeta 1	2623
F-box protein 30	224
stanniocalcin 1	2932
chromodomain helicase DNA binding protein 9	447
protein tyrosine phosphatase, receptor type, E	44
EF-hand calcium binding domain 11	25

pyruvate dehydrogenase phosphatase regulatory	69
anoctamin 10	330
zinc finger protein 24	1796
GRAM domain containing 3	232
PDZ domain containing 4	7
zinc finger protein 346	5
tweety family member 1	5
Sec61 alpha 1 subunit (S. cerevisiae)	2966
arylsulfatase G	73
SRY (sex determining region Y)-box 1	5
glutamate receptor, ionotropic, AMPA 1	5
androgen-induced 1	1226
MYC induced nuclear antigen	209
colony stimulating factor 3 receptor (granuloc	49
TWIST neighbor	133
chromosome 4 open reading frame 46	128
spermatogenesis associated 5	168
phospholipase C, gamma 1	69
MAP/microtubule affinity-regulating kinase 4	192
zinc finger and BTB domain containing 40	124
glycerophosphocholine phosphodiesterase GDE1 h	155
janus kinase and microtubule interacting prote	26
F-box and leucine-rich repeat protein 7	16
deleted in lymphocytic leukemia 1 (non-protein	22
potassium voltage-gated channel, delayed-recti	5
family with sequence similarity 109, member B	78
tetraspanin 9	1410
retinol binding protein 2, cellular	46
Rho GTPase activating protein 44	22
UDP-N-acetyl-alpha-D-galactosamine:polypeptide	953
nuclear receptor binding SET domain protein 1	685
dual specificity phosphatase 4	245
TBC1 domain containing kinase	20
selectin P ligand	20
G protein-coupled receptor 156	12
growth arrest-specific 7	186
nucleobindin 2	71
A kinase (PRKA) anchor protein 6	5
porcupine homolog (Drosophila)	35
glutamate receptor, metabotropic 5	5
RNA binding motif protein 5	150
bestrophin 3	5
G protein-coupled receptor 176	2683
Rho GTPase activating protein 33	8
RPTOR independent companion of MTOR, complex 2	441
B lymphoid tyrosine kinase	5
neurexin 3	14
transmembrane protein, adipocyte asscociated 1	44
aryl-hydrocarbon receptor repressor	1049
Rho guanine nucleotide exchange factor (GEF) 5	200
TBC1 domain family, member 19	77
PRKC, apoptosis, WT1, regulator	1872
RAP1A, member of RAS oncogene family	382
solute carrier family 22, member 23	353

MRE11 meiotic recombination 11 homolog A (S. c	199
telomerase-associated protein 1	39
TAF9B RNA polymerase II, TATA box binding prot	19
dynein, axonemal, light intermediate chain 1	56
teashirt zinc finger homeobox 2	351
pleckstrin homology domain containing, family	144
NK3 homeobox 2	36
phosphatidylinositol 3-kinase, catalytic subun	286
SET domain containing 5	48
origin recognition complex, subunit 4	1180
BCL2/adenovirus E1B 19kDa interacting protein	1255
isoprenoid synthase domain containing	12
C2 calcium-dependent domain containing 4C	70
phosphodiesterase 8A	183
oligodendrocytic myelin paranodal and inner lo	5
zinc finger protein 701	15
ring finger and SPRY domain containing 1	735
frizzled family receptor 1	391
sparc/osteonectin, cwcv and kazal-like domains	31
ArfGAP with coiled-coil, ankyrin repeat and PH	253
Werner syndrome, RecQ helicase-like	560
ClpB caseinolytic peptidase B homolog (E. coli	476
SWI/SNF related, matrix associated, actin depe	298
1-acylglycerol-3-phosphate O-acyltransferase 4	142
zinc finger protein 626	24
malate dehydrogenase 1B, NAD (soluble)	20
musashi RNA-binding protein 2	283
arylsulfatase family, member I	19
enhancer of yellow 2 homolog (Drosophila)	1814
solute carrier family 20 (phosphate transporte	205
F-box and leucine-rich repeat protein 19	75
putative homeodomain transcription factor 2	1730
katanin p60 subunit A-like 1	335
ankyrin repeat domain 33B	9
Ras-related GTP binding D	644
arginine-glutamic acid dipeptide (RE) repeats	199
WW and C2 domain containing 1	43
tubulin tyrosine ligase	442
anterior gradient 2	13
Nedd4 family interacting protein 2	1747
mitochondrial poly(A) polymerase	137
family with sequence similarity 110, member A	73
heparan sulfate (glucosamine) 3-O-sulfotransfe	9
huntingtin interacting protein 1	37
AT rich interactive domain 5B (MRF1-like)	397
basal cell adhesion molecule (Lutheran blood g	4647
KIAA0232	119
solute carrier family 35 (UDP-GlcA/UDP-GalNAc	186
plexin C1	47
collagen, type V, alpha 3	5
kelch repeat and BTB (POZ) domain containing 1	5
glutamate receptor, ionotropic, N-methyl-D-asp	5
SLIT and NTRK-like family, member 4	86
Rho family GTPase 2	26

	141
CXADR-like membrane protein	212
zwilch kinetochore protein	43
solute carrier family 25 (mitochondrial oxoadi	110
sema domain, immunoglobulin domain (Ig), short	54
HECT, C2 and WW domain containing E3 ubiquitin	11
STEAP family member 3, metalloreductase	160
leucyl/cystinyl aminopeptidase	28
amnion associated transmembrane protein	71
TATA box binding protein (TBP)-associated fact	73
zinc finger protein 155	13
PR domain containing 16	64
RAD51 paralog D	73
MARVEL domain containing 2	227
widely interspaced zinc finger motifs	1321
one cut homeobox 1	10
arrestin, beta 1	598
zinc finger protein 592	1128
RAD1 homolog (S. pombe)	584
transcription factor Dp-2 (E2F dimerization pa	128
myosin IE	198
mitochondrial ribosomal protein L4	3854
kringle containing transmembrane protein 1	606
kelch-like family member 29	414
sodium channel, voltage-gated, type IV, alpha	5
hyaluronan synthase 3	15
G protein-coupled receptor 116	5
gap junction protein, delta 3, 31.9kDa	0
ubiquitin specific peptidase 2	19
La ribonucleoprotein domain family, member 1	4979
transmembrane protein 181	924
poly(A)-specific ribonuclease	5
nuclear receptor binding protein 2	1011
unc-45 homolog B (C. elegans)	5
chromodomain helicase DNA binding protein 2	1237
proprotein convertase subtilisin/kexin type 2	9
zinc finger protein 646	5
microtubule-associated protein 4	3914
storkhead box 2	379
Rho-associated, coiled-coil containing protein	7
zinc finger and BTB domain containing 4	1039
zinc finger, DBF-type containing 2	102
chromodomain helicase DNA binding protein 6	85
tripartite motif containing 33	201
AHNAK nucleoprotein	682
fem-1 homolog a (C. elegans)	57
protein phosphatase 1, regulatory subunit 16B	16
scratch homolog 1, zinc finger protein (Drosop	5
like-glycosyltransferase	411
collagen, type VIII, alpha 2	15
platelet-activating factor receptor	5
mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-	1627
protein phosphatase 2, regulatory subunit B’,	13
membrane-associated ring finger (C3HC4) 9	328

dedicator of cytokinesis 5	504
ribosomal protein S6 kinase, 90kDa, polypeptid	1043
transmembrane protein 237	2209
protein serine kinase H1	699
zinc finger, matrin-type 3	459
synapse associated protein 1	2689
pantothenate kinase 3	522
hemochromatosis	563
microtubule associated serine/threonine kinase	317
required for meiotic nuclear division 5 homolo	959
regulating synaptic membrane exocytosis 3	24
ATPase, H+ transporting, lysosomal 31kDa, V1 s	2139
solute carrier family 16 (aromatic amino acid	233
RAB interacting factor	948
natural killer cell cytotoxicity receptor 3 li	214
mitochondrial ribosomal protein S16	3942
transcription factor CP2-like 1	36
peptidyl-tRNA hydrolase domain containing 1	1255
son of sevenless homolog 1 (Drosophila)	189
ADP-ribosylation factor-like 10	236
mitochondrial ribosome recycling factor	85
GRAM domain containing 2	5
N-acetyltransferase 9 (GCN5-related, putative)	36
COP9 signalosome subunit 7B	331
ataxin 2	7
cyclin-dependent kinase 16	2095
prion protein	1136
lysine-rich nucleolar protein 1	157
basic helix-loop-helix family, member a15	136
GDP-mannose pyrophosphorylase B	425
dynein, cytoplasmic 1, light intermediate chai	2144
TNF receptor-associated factor 6, E3 ubiquitin	91
kinesin family member 6	12
RAB11 family interacting protein 4 (class II)	169
acyl-CoA binding domain containing 5	77
early B-cell factor 1	42
cyclin D2	66
cell division cycle associated 2	215
N-myristoyltransferase 2	318
3-phosphoinositide dependent protein kinase-1	104
leukemia inhibitory factor receptor alpha	44
BTB and CNC homology 1, basic leucine zipper t	74
nucleolar protein 10	106
RAB3A interacting protein	73
autophagy related 2B	146
leucine rich repeat containing 8 family, membe	326
adenylate cyclase 2 (brain)	13
pregnancy-associated plasma protein A, pappaly	350
cullin 2	27
cyclin E2	76
tripartite motif containing 13	139
growth differentiation factor 11	847
DnaJ (Hsp40) homolog, subfamily C, member 18	253
sodium channel, voltage-gated, type II, beta s	5

SID1 transmembrane family, member 2	341
homeobox C8	5
SPOC domain containing 1	755
leucine-rich repeats and immunoglobulin-like d	348
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galact	41
cytosolic thiouridylase subunit 1	170
potassium channel, subfamily K, member 3	19
centromere protein I	379
tRNA-yW synthesizing protein 3 homolog (S. cer	140
tetratricopeptide repeat domain 39C	494
programmed cell death 11	1551
mitogen-activated protein kinase kinase kinase	1551
pituitary tumor-transforming 1 interacting pro	1170
small nuclear ribonucleoprotein D3 polypeptide	3251
solute carrier family 10 (sodium/bile acid cot	7
Uncharacterized protein	24
cytoplasmic linker associated protein 1	210
zinc finger protein 333	72
hydroxysteroid (17-beta) dehydrogenase 12	1422
guanine monphosphate synthase	867
inositol 1,4,5-trisphosphate receptor, type 2	334
ubiquitin specific peptidase 36	192
decapping mRNA 2	155
eukaryotic translation initiation factor 2-alp	1726
TBC1 domain family, member 16	556
helicase, lymphoid-specific	329
integrin, alpha 1	400
methyl CpG binding protein 2 (Rett syndrome)	1474
calcium/calmodulin-dependent protein kinase II	5
visual system homeobox 2	5
RNA binding protein, fox-1 homolog (C. elegans	262
E2F transcription factor 4, p107/p130-binding	1433
von Willebrand factor D and EGF domains	9
TXK tyrosine kinase	7
ring finger protein 152	57
stomatin (EPB72)-like 1	18
vacuolar protein sorting 39 homolog (S. cerevi	165
follistatin-like 4	60
arylsulfatase family, member K	298
leukocyte receptor cluster (LRC) member 1	14
transforming growth factor, beta receptor 1	249
ZFP82 zinc finger protein	42
zinc finger protein 566	310
laminin, gamma 1 (formerly LAMB2)	1082
solute carrier family 7 (amino acid transporte	1044
sprouty-related, EVH1 domain containing 3	42
ganglioside induced differentiation associated	28
cat eye syndrome chromosome region, candidate	46
interferon, lambda receptor 1	15
phosphodiesterase 7A	84
myosin IA	106
sortilin 1	2111
dynein, axonemal, heavy chain 10	11
protein arginine methyltransferase 10 (putativ	71

Rho GTPase activating protein 31	32
methylenetetrahydrofolate reductase (NAD(P)H)	207
ubiquitin specific peptidase 46	180
general transcription factor IIIC, polypeptide	1598
cell cycle progression 1	808
succinate dehydrogenase complex, subunit C, in	172
DnaJ (Hsp40) homolog, subfamily C, member 11	361
regulator of G-protein signaling 11	5
7-dehydrocholesterol reductase	3418
HCG1980662; Uncharacterized protein	60
nuclear factor of kappa light polypeptide gene	316
thioesterase superfamily member 4	262
pleckstrin homology domain containing, family	661
beta-site APP-cleaving enzyme 1	486
zinc finger, DHHC-type containing 14	253
chitobiase, di-N-acetyl-	33
Rho GTPase activating protein 23	289
B-cell CLL/lymphoma 2	55
platelet-activating factor acetylhydrolase 1b,	1570
zinc finger protein 597	159
epsin 2	1609
solute carrier family 6 (neurotransmitter tran	73
pyruvate dehydrogenase kinase, isozyme 1	637
kelch-like family member 11	16
aquarius intron-binding spliceosomal factor	314
protein tyrosine phosphatase, receptor type, f	167
hexosaminidase A (alpha polypeptide)	209
ribosomal RNA processing 8, methyltransferase,	423
X-ray radiation resistance associated 1	136
lysophospholipase II	21
chromosome 5 open reading frame 63	42
alanyl-tRNA synthetase 2, mitochondrial	262
chromosome 2 open reading frame 69	82
carbohydrate (N-acetylglucosamine 6-O) sulfotr	37
golgi SNAP receptor complex member 1	668
single-minded homolog 2 (Drosophila)	108
NIP7, nucleolar pre-rRNA processing protein	659
family with sequence similarity 46, member C	74
ankyrin repeat and EF-hand domain containing 1	25
ribosome production factor 2 homolog (S. cerev	869
spindle and kinetochore associated complex sub	199
chromosome 21 open reading frame 59	288
RAB3C, member RAS oncogene family	242
pseudopodium-enriched atypical kinase 1	209
methyltransferase like 16	8
sterol regulatory element binding transcriptio	1518
neuroligin 1	36
myocyte enhancer factor 2D	759
carbohydrate (keratan sulfate Gal-6) sulfotran	5
sideroflexin 2	547
cell division cycle 73	579
coiled-coil serine-rich protein 2	123
spleen tyrosine kinase	25
lymphatic vessel endothelial hyaluronan recept	5

Transmembrane 9 superfamily member 1	555
GDNF family receptor alpha 2	13
OTU domain, ubiquitin aldehyde binding 1	2977
transmembrane emp24 protein transport domain c	612
bromodomain PHD finger transcription factor	7
DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	174
ribosomal protein S28	375
proteasome (prosome, macropain) inhibitor subu	2709
xylulokinase homolog (H. influenzae)	119
NIMA-related kinase 9	733
SH3 and PX domains 2B	123
sorting nexin 9	210
regulation of nuclear pre-mRNA domain containi	333
transmembrane protein 186	287
KIAA1598	94
AF4/FMR2 family, member 1	28
ceramide synthase 4	1182
myoneurin	289
adaptor-related protein complex 1, gamma 1 sub	436
excision repair cross-complementing rodent rep	118
poly (ADP-ribose) polymerase 1	1264
transforming, acidic coiled-coil containing pr	186
zinc finger protein 614	55
zinc finger protein 519	40
RALY heterogeneous nuclear ribonucleoprotein	1489
family with sequence similarity 26, member E	32
thyroid hormone receptor, beta	55
helicase with zinc finger 2, transcriptional c	692
cold shock domain containing C2, RNA binding	31
phospholipase A2-activating protein	416
RIC8 guanine nucleotide exchange factor B	49
small nuclear RNA activating complex, polypept	211
glycoprotein 2 (zymogen granule membrane)	29
neural precursor cell expressed, developmental	617
centrosomal protein 85kDa-like	14
mitochondrial amidoxime reducing component 1	1613
ankyrin repeat and SOCS box containing 16	14
differentially expressed in FDCP 6 homolog (mo	35
SET domain containing 9	45
sodium/myo-inositol cotransporter	24
diacylglycerol kinase, epsilon 64kDa	470
IQ motif and Sec7 domain 1	415
La ribonucleoprotein domain family, member 4B	705
microtubule-associated protein 2	68
ORM1-like 3 (S. cerevisiae)	82
LanC lantibiotic synthetase component C-like 3	15
limb development membrane protein 1	1435
lysophosphatidic acid receptor 3	35
cyclin-dependent kinase 9	197
IQ motif and Sec7 domain 2	5
uridine-cytidine kinase 2	437
polymerase (RNA) III (DNA directed) polypeptid	490
endo-beta-N-acetylglucosaminidase	33
CUB and Sushi multiple domains 3	5

MLX interacting protein-like	58
sodium channel, voltage-gated, type VII, alpha	5
pleckstrin homology domain containing, family	279
zinc finger protein 445	370
Tax1 (human T-cell leukemia virus type I) bind	4402
aryl hydrocarbon receptor	25
bladder cancer associated protein	38
ubiquitin-conjugating enzyme E2Q family-like 1	10
pleckstrin homology domain containing, family	11
family with sequence similarity 49, member B	52
armadillo repeat containing, X-linked 3	353
protein kinase (cAMP-dependent, catalytic) inh	542
sema domain, immunoglobulin domain (Ig), short	162
zinc finger protein 347	33
neuronal growth regulator 1	28
dynein, axonemal, light chain 1	81
protein phosphatase 2, regulatory subunit A, b	341
Sp1 transcription factor	402
zinc finger with KRAB and SCAN domains 3	63
leucine zipper-EF-hand containing transmembran	198
chromosome 6 open reading frame 223	17
ST3 beta-galactoside alpha-2,3-sialyltransfera	102
syntaxin 11	13
potassium inwardly-rectifying channel, subfami	9
leucine-rich repeats and transmembrane domains	5
mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-	85
phosphatidylinositol-4,5-bisphosphate 3-kinase	5
large 60S subunit nuclear export GTPase 1	47
ADAM metallopeptidase domain 23	113
thioredoxin domain containing 5 (endoplasmic r	1190
RNA binding motif, single stranded interacting	451
KIAA0895-like	15
G patch domain containing 2	108
DDHD domain containing 1	103
Rho GTPase activating protein 42	36
ISL LIM homeobox 2	381
kinesin-associated protein 3	42
ankyrin repeat domain 34C	5
heparanase 2	12
glucosidase, beta, acid	27
calcium/calmodulin-dependent protein kinase ID	258
sex comb on midleg-like 4 (Drosophila)	10
cAMP responsive element binding protein 3-like	2872
arginine vasopressin-induced 1	4404
mitochondrial ribosomal protein S5	71
notch 2 N-terminal like	5
SH3 domain and tetratricopeptide repeats 2	31
v-yes-1 Yamaguchi sarcoma viral related oncoge	61
DEAD (Asp-Glu-Ala-Asp) box polypeptide 19A	148
solute carrier family 10 (sodium/bile acid cot	5
filaggrin family member 2	5
BRCA1 associated protein-1 (ubiquitin carboxy-	445
polyhomeotic homolog 2 (Drosophila)	11
zinc finger protein 416	17

selenocysteine lyase	232
kin of IRRE like 3 (Drosophila)	16
ADAM metallopeptidase with thrombospondin type	5
kelch-like family member 34	5
neuralized homolog 1B (Drosophila)	5
zinc finger, DHHC-type containing 5	1505
zinc finger RNA binding protein 2	5
cadherin, EGF LAG seven-pass G-type receptor 2	2475
phosphatidylinositol-4-phosphate 5-kinase, typ	13
ADAM metallopeptidase domain 8	9
LIM homeobox transcription factor 1, alpha	5
stathmin-like 3	17
SNF related kinase	153
family with sequence similarity 53, member B	27
frizzled family receptor 4	5
potassium voltage-gated channel, KQT-like subf	196
cholinergic receptor, nicotinic, beta 2 (neuro	16
neuroblastoma breakpoint family, member 20	5
solute carrier family 29 (equilibrative nucleo	678
chordin-like 1	5
guanine deaminase	5
RAB11 family interacting protein 1 (class I)	106
chromosome 15 open reading frame 62	8
low density lipoprotein receptor-related prote	939
WAS protein family, member 3	24
chromosome 1 open reading frame 172	190
zinc finger protein 664	736
immunoglobulin superfamily, DCC subclass, memb	464
chromosome 4 open reading frame 50	5
leucine zipper, down-regulated in cancer 1-lik	348
protein phosphatase 1, catalytic subunit, gamm	3739
acyl-CoA binding domain containing 4	10
solute carrier family 2 (facilitated glucose t	233
UDP-N-acetyl-alpha-D-galactosamine:polypeptide	2834
Nik related kinase	5
zinc finger protein 37A	11
bone morphogenetic protein/retinoic acid induc	5
flavin containing monooxygenase 2 (non-functio	5
myosin, heavy chain 11, smooth muscle	5
tumor necrosis factor, alpha-induced protein 2	442
deltex homolog 4 (Drosophila)	5
solute carrier family 39 (zinc transporter), m	1510
teneurin transmembrane protein 3	30
ankyrin and armadillo repeat containing	5
v-akt murine thymoma viral oncogene homolog 2	525
transmembrane protease, serine 4	5
fer (fps/fes related) tyrosine kinase	665
pyrroline-5-carboxylate reductase 1	157
anaphase promoting complex subunit 16	986
delta-like 4 (Drosophila)	605
kinesin family member 16B	113
synaptopodin	311
myelin transcription factor 1-like	5
SET domain containing 1B	703

promyelocytic leukemia	83
laminin, alpha 4	605
secreted frizzled-related protein 1	148
cystatin C	11
ATPase, Ca++ transporting, ubiquitous	40
WD and tetratricopeptide repeats 1	137
coiled-coil domain containing 64	7
diaphanous-related formin 1	399
cholinergic receptor, nicotinic, alpha 7 (neur	5
immunoglobulin mu binding protein 2	34
kelch-like family member 24	143
FERM, RhoGEF and pleckstrin domain protein 2	19
Rho GTPase activating protein 6	12
paralemmin	341
calcium channel, voltage-dependent, R type, al	5
nucleoporin 188kDa	3481
EPH receptor A8	5
THUMP domain containing 1	39
kinesin family member 1B	234
MAP/microtubule affinity-regulating kinase 2	845
mannose receptor, C type 2	74
zinc finger protein 787	191
heterogeneous nuclear ribonucleoprotein U-like	11882
Sp6 transcription factor	5
TLC domain containing 2	107
engulfment and cell motility 1	118
zinc finger protein 585A	77
solute carrier family 38, member 7	635
dystrophin related protein 2	5
potassium voltage-gated channel, Shaw-related	138
upstream binding transcription factor, RNA pol	1090
glycerol-3-phosphate dehydrogenase 1 (soluble)	5
KIAA1239	5
KIAA0513	5
calcium channel, voltage-dependent, T type, al	5
lipin 1	357
polyamine modulated factor 1 binding protein 1	5
G protein-coupled receptor 179	5
nitric oxide synthase 1 (neuronal) adaptor pro	5
Sad1 and UNC84 domain containing 2	501
FLT3-interacting zinc finger 1	136
zinc finger protein 707	106
cerebellar degeneration-related protein 2-like	28
guanine nucleotide binding protein (G protein)	1513
GATA binding protein 5	7
CUGBP, Elav-like family member 5	5
cat eye syndrome chromosome region, candidate	46
cut-like homeobox 2	15
potassium inwardly-rectifying channel, subfami	12
tenascin N	17
ferric-chelate reductase 1-like	11
synapsin I	17
calcium binding protein 7	12
filamin B, beta	467

IQ motif and Sec7 domain 3	5
CREB regulated transcription coactivator 3	612
hypermethylated in cancer 1	76
SH3 domain containing ring finger 2	53
potassium voltage-gated channel, KQT-like subf	46
kinase insert domain receptor (a type III rece	5
chemokine-like receptor 1	5
guanylyl cyclase domain containing 1	2990
interleukin 21 receptor	5
zinc finger protein 319	521
FH2 domain containing 1	53
tudor domain containing 10	14
oral cancer overexpressed 1	78
alkaline phosphatase, liver/bone/kidney	251
G protein-coupled receptor 63	5
matrix metallopeptidase 11 (stromelysin 3)	1719
spinster homolog 2 (Drosophila)	7
shadow of prion protein homolog (zebrafish)	5
taxilin beta	5
zinc finger protein 829	103
zinc finger protein 132	31
XK, Kell blood group complex subunit-related f	5
mahogunin ring finger 1, E3 ubiquitin protein	2337
forkhead box I2	5
phosphate cytidylyltransferase 2, ethanolamine	2340
ArfGAP with RhoGAP domain, ankyrin repeat and	253
glycogen synthase 1 (muscle)	100
protocadherin 7	95
N-sulfoglucosamine sulfohydrolase	109
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galact	178
chromosome 9 open reading frame 9	44
SH3-domain binding protein 4	783
UBA-like domain containing 1	41
chromosome 15 open reading frame 53	5
leucine rich repeat containing 15	12
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransfe	1000
autophagy related 16-like 2 (S. cerevisiae)	16
v-crk avian sarcoma virus CT10 oncogene homolo	2142
schlafen family member 11	402
ral guanine nucleotide dissociation stimulator	188
FAT atypical cadherin 3	30
solute carrier family 8 (sodium/calcium exchan	5
ADAM metallopeptidase domain 33	5
dihydrolipoamide S-succinyltransferase (E2 com	64
syntaphilin	13
bromodomain containing 4	849
activin A receptor, type IB	3319
zinc finger protein 512B	8
kelch-like family member 30	5
RGP1 retrograde golgi transport homolog (S. ce	203
kinesin family member 18B	172
IQ motif containing GTPase activating protein	7
ADAM metallopeptidase domain 19	981
DnaJ (Hsp40) homolog, subfamily B, member 2	2187

oxoglutarate (alpha-ketoglutarate) dehydrogena	672
potassium voltage-gated channel, shaker-relate	67
low density lipoprotein receptor-related prote	152
POU class 3 homeobox 1	9
NADH dehydrogenase (ubiquinone) 1 alpha subcom	32826
adenylate cyclase activating polypeptide 1 (pi	9
FAD-dependent oxidoreductase domain containing	200
nuclear pore associated protein 1	5
MAP-kinase activating death domain	282
regulating synaptic membrane exocytosis 4	30
hornerin	5
cut-like homeobox 1	1205
tetraspanin 11	27
calcium channel, voltage-dependent, L type, al	5
tectonin beta-propeller repeat containing 2	109
C1q and tumor necrosis factor related protein	74
neuron navigator 3	277
EPH receptor A10	11
solute carrier family 30, member 10	66
ankyrin repeat and sterile alpha motif domain	21
ecotropic viral integration site 5-like	15
leucine-rich repeats and calponin homology (CH	399
kinesin family member 3B	182
KIAA1024	5
transmembrane protein 198	80
death effector domain containing 2	32
chromosome 5 open reading frame 20	5
methionine adenosyltransferase I, alpha	19
zinc finger protein 81	10
RAB36, member RAS oncogene family	7
N-deacetylase/N-sulfotransferase (heparan gluc	13660
transcription factor 7 (T-cell specific, HMG-b	883
transglutaminase 2	731
N(alpha)-acetyltransferase 38, NatC auxiliary	458
E1A binding protein p400	1798
ATPase, class VI, type 11C	590
neuropilin 1	586
cleavage and polyadenylation specific factor 7	1283
Phosphatidylinositol 4-kinase type 2-alpha; Un	1489
aarF domain containing kinase 3	1106
AVL9 homolog (S. cerevisiase)	246
suppressor of Ty 16 homolog (S. cerevisiae)	528
mitochondrial calcium uniporter regulator 1	129
limb bud and heart development	1956
vitamin D (1,25- dihydroxyvitamin D3) receptor	416
PHD finger protein 12	307
NSFL1 (p97) cofactor (p47)	397
zinc finger and BTB domain containing 34	726
cyclin-dependent kinase 18	262
N-myc downstream regulated 1	2195
synaptotagmin-like 4	84
GLI family zinc finger 2	73
carboxypeptidase D	1766
transient receptor potential cation channel, s	68

microtubule associated monooxygenase, calponin	58
leukocyte immunoglobulin-like receptor, subfam	5
transmembrane protein 251	14
phosphoribosylformylglycinamidine synthase	901
adaptor-related protein complex 1, mu 1 subuni	416
glycerol-3-phosphate acyltransferase, mitochon	153
pleckstrin homology domain interacting protein	668
neural precursor cell expressed, developmental	289
polyhomeotic homolog 3 (Drosophila)	366
contactin 3 (plasmacytoma associated)	27
zinc finger, CCHC domain containing 14	64
metastasis associated 1 family, member 3	194
clathrin interactor 1	581
cysteinyl leukotriene receptor 2	5
UPF1 regulator of nonsense transcripts homolog	513
solute carrier family 7 (cationic amino acid t	338
tetratricopeptide repeat domain 28	227
family with sequence similarity 177, member A1	765
1-acylglycerol-3-phosphate O-acyltransferase 3	2443
damage-specific DNA binding protein 1, 127kDa	22506
kinesin family member 1C	149
collagen, type I, alpha 1	73360
zinc finger protein 469	139
CUB and Sushi multiple domains 2	5
solute carrier family 16 (monocarboxylate tran	73
ligand dependent nuclear receptor corepressor	94
EPH receptor A6	19
BCL2-associated athanogene 2	2237
EPM2A (laforin) interacting protein 1	218
transmembrane protein 139	17
transient receptor potential cation channel, s	13
citron (rho-interacting, serine/threonine kina	134
collagen, type IV, alpha 6	37
adrenergic, beta, receptor kinase 2	215
KIN, antigenic determinant of recA protein hom	443
translocase of inner mitochondrial membrane 8	147
growth differentiation factor 7	27
chromosome 14 open reading frame 37	25
PQ loop repeat containing 1	1060
peptidylprolyl isomerase (cyclophilin)-like 6	58
mucolipin 3	47
T-cell, immune regulator 1, ATPase, H+ transpo	2756
mitochondrial ribosomal protein S25	630
thrombospondin 2	372
fibrillin 2	167
bifunctional apoptosis regulator	376
solute carrier family 23 (ascorbic acid transp	121
selenoprotein N, 1	104
protein arginine methyltransferase 3	120
myotubularin related protein 7	33
tRNA methyltransferase 2 homolog B (S. cerevis	174
glycerate kinase	3833
F-box and leucine-rich repeat protein 18	92
mannosidase, alpha, class 2A, member 2	340

transmembrane and tetratricopeptide repeat con	379
fms-related tyrosine kinase 3	15
zinc finger protein 573	12
latrophilin 1	49
solute carrier family 30 (zinc transporter), m	204
peroxisomal biogenesis factor 19	1804
poly(A) polymerase gamma	49
ladinin 1	89
lemur tyrosine kinase 2	51
family with sequence similarity 211, member A	23
suppressor of cytokine signaling 4	336
solute carrier organic anion transporter famil	133
NADPH dependent diflavin oxidoreductase 1	1044
transport and golgi organization 6 homolog (Dr	143
nucleolar protein with MIF4G domain 1	842
chromosome 20 open reading frame 112	148
tumor protein p73	831
IBA57, iron-sulfur cluster assembly homolog (S	66
gamma-aminobutyric acid (GABA) A receptor, the	14
kazrin, periplakin interacting protein	34
aminopeptidase puromycin sensitive	2194
zinc finger protein 708	16
transmembrane protein 184B	1362
discoidin, CUB and LCCL domain containing 2	798
Rab interacting lysosomal protein-like 1	155
cytochrome c oxidase subunit VIIa polypeptide	289
SUMO/sentrin specific peptidase family member	80
EF-hand calcium binding domain 2	204
Rho GTPase activating protein 26	131
frizzled family receptor 5	122
solute carrier family 35, member F6	272
forkhead box D3	7
ethanolaminephosphotransferase 1 (CDP-ethanola	449
farnesyltransferase, CAAX box, beta	13
diphosphoinositol pentakisphosphate kinase 2	203
ubiquitin specific peptidase 49	44
SH3 and PX domains 2A	152
suppressor of Ty 3 homolog (S. cerevisiae)	175
splA/ryanodine receptor domain and SOCS box co	419
leukotriene B4 receptor	70
G protein-coupled receptor 107	1429
sperm autoantigenic protein 17	189
myotubularin related protein 12	156
gamma-aminobutyric acid (GABA) A receptor, bet	267
protocadherin 1	30
tumor necrosis factor, alpha-induced protein 8	603
related RAS viral (r-ras) oncogene homolog 2	57
coiled-coil domain containing 85C	86
chromosome 8 open reading frame 59	164
extracellular leucine-rich repeat and fibronec	22
hemopexin	307
RAB4A, member RAS oncogene family	850
myosin IXA	137
cystathionase (cystathionine gamma-lyase)	430

nucleolar protein 9	194
transcription elongation factor A (SII), 3	128
spectrin, beta, non-erythrocytic 2	910
amyloid beta (A4) precursor protein-binding, f	704
actin binding LIM protein family, member 3	9
solute carrier family 35, member E1	4273
protein tyrosine phosphatase, non-receptor typ	438
large tumor suppressor kinase 1	176
primase, DNA, polypeptide 1 (49kDa)	178
syntaxin 4	53
Ral GTPase activating protein, alpha subunit 2	24
lanosterol synthase (2,3-oxidosqualene-lanoste	564
NEDD4 binding protein 3	35
golgi-associated, gamma adaptin ear containing	14
BCL2-like 13 (apoptosis facilitator)	741
zinc finger, MYND-type containing 8	235
membrane-associated ring finger (C3HC4) 4, E3	68
GATA binding protein 6	691
aldehyde dehydrogenase 1 family, member L2	22
chromosome 4 open reading frame 19	51
eukaryotic translation initiation factor 2, su	3360
endogenous retrovirus group MER34, member 1	28
alpha-kinase 1	47
low density lipoprotein receptor class A domai	314
serpin peptidase inhibitor, clade E (nexin, pl	1508
nucleotide-binding oligomerization domain cont	31
chromosome 16 open reading frame 52	102
zinc finger protein 841	21
chromosome 2 open reading frame 82	72
methionyl aminopeptidase 1	887
zinc finger protein 589	20
active BCR-related	58
solute carrier family 33 (acetyl-CoA transport	145
TNF receptor-associated factor 5	250
nuclear receptor subfamily 1, group H, member	99
adenylate cyclase 9	166
spermatid maturation 1	7
prune homolog 2 (Drosophila)	121
F-box protein 11	359
WD repeat domain 7	365
cleavage and polyadenylation specific factor 6	5819
chemokine (C-C motif) receptor 6	35
fibronectin leucine rich transmembrane protein	73
SH3-domain binding protein 2	449
guanine nucleotide binding protein (G protein)	47
YOD1 deubiquitinase	55
phospholipase A2, group XVI	2547
protein phosphatase 1, regulatory subunit 3G	29
adenylate kinase 2	3125
tripartite motif containing 38	62
family with sequence similarity 19 (chemokine	14
cyclin-dependent kinase 13	32
ADAM metallopeptidase with thrombospondin type	466
sortilin-related receptor, L(DLR class) A repe	40

Zic family member 1	26
chromosome 1 open reading frame 50	1217
myosin XVIIIA	159
junctional adhesion molecule 2	41
ectopic P-granules autophagy protein 5 homolog	269
CNKSR family member 3	567
NHP2 non-histone chromosome protein 2-like 1 (	18476
superoxide dismutase 2, mitochondrial	993
SWIM-type zinc finger 7 associated protein 1	55
polymerase (DNA directed) iota	321
tubulin polymerization promoting protein	7
transmembrane protein 53	234
nuclear transcription factor, X-box binding 1	215
sushi domain containing 2	16
SWI/SNF related, matrix associated, actin depe	727
T-cell lymphoma invasion and metastasis 1	20
empty spiracles homeobox 1	35
N(alpha)-acetyltransferase 11, NatA catalytic	66
Rho guanine nucleotide exchange factor (GEF) 1	346
RNA (guanine-7-) methyltransferase	64
NOP9 nucleolar protein	353
vacuolar protein sorting 13 homolog A (S. cere	110
RAB8A, member RAS oncogene family	226
family with sequence similarity 168, member A	68
fibronectin 1	1064
ubiquitin specific peptidase 13 (isopeptidase	379
myelin expression factor 2	358
UDP-glucose 6-dehydrogenase	735
zinc finger protein 326	162
ankyrin repeat and SOCS box containing 1	408
negative regulator of ubiquitin-like proteins	85
solute carrier family 24 (sodium/potassium/cal	5
dopey family member 1	17
heat shock protein 90kDa beta (Grp94), member	42
versican	542
WD repeat domain 41	313
derlin 3	129
chromosome 9 open reading frame 64	126
solute carrier family 38, member 9	156
solute carrier family 22 (organic cation trans	86
small nuclear ribonucleoprotein polypeptide B	593
RNA binding motif protein, X-linked 2	139
OTU domain containing 7A	35
ATPase, aminophospholipid transporter, class I	22
coiled-coil domain containing 127	615
ubiquitin specific peptidase 30	76
glycosyltransferase-like domain containing 1	241
Hermansky-Pudlak syndrome 3	60
carbonic anhydrase VIII	197
selenium binding protein 1	173
calcium binding and coiled-coil domain 1	68
ALG10, alpha-1,2-glucosyltransferase	13
family with sequence similarity 120B	764
transmembrane channel-like 7	54

mucin 20, cell surface associated	11
insulin-like growth factor binding protein-lik	13
OTU domain, ubiquitin aldehyde binding 2	110
methyltransferase like 8	124
collagen and calcium binding EGF domains 1	54
WD repeat domain 3	1166
shroom family member 1	150
N-ethylmaleimide-sensitive factor attachment p	277
membrane-associated ring finger (C3HC4) 3, E3	77
NADH dehydrogenase (ubiquinone) Fe-S protein 1	1041
eyes absent homolog 4 (Drosophila)	242
signal-regulatory protein alpha	1235
cms1 ribosomal small subunit homolog (yeast)	423
transmembrane channel-like 8	13
tRNA-yW synthesizing protein 5	148
forkhead box L1	367
ADP-ribosylation factor guanine nucleotide-exc	111
non imprinted in Prader-Willi/Angelman syndrom	805
zinc finger protein 248	43
ATP-binding cassette, sub-family G (WHITE), me	20
slingshot protein phosphatase 3	159
X-prolyl aminopeptidase (aminopeptidase P) 3,	112
BCL2/adenovirus E1B 19kDa interacting protein	191
transportin 3	30
ATPase, class VI, type 11B	459
monoglyceride lipase	453
IWS1 homolog (S. cerevisiae)	343
NADH dehydrogenase (ubiquinone) 1 alpha subcom	2249
RE1-silencing transcription factor	31
G protein-coupled receptor, family C, group 5,	341
acid-sensing (proton-gated) ion channel 1	111
phosphatidylinositol glycan anchor biosynthesi	122
zinc finger protein 490	97
polymerase (RNA) I polypeptide A, 194kDa	675
runt-related transcription factor 1	182
mucolipin 2	39
late endosomal/lysosomal adaptor, MAPK and MTO	67
required for meiotic nuclear division 5 homolo	261
ribosomal modification protein rimK-like famil	100
ras homolog family member F (in filopodia)	399
charged multivesicular body protein 3	2466
RALBP1 associated Eps domain containing 2	36
synaptotagmin-like 3	16
solute carrier family 12 (potassium/chloride t	17
translocase of outer mitochondrial membrane 20	674
zyg-11 related, cell cycle regulator	336
TATA box binding protein (TBP)-associated fact	214
chromosome 19 open reading frame 40	129
karyopherin alpha 3 (importin alpha 4)	104
maestro	11
WD repeat and FYVE domain containing 2	85
2,4-dienoyl CoA reductase 1, mitochondrial	131
myristoylated alanine-rich protein kinase C su	188
polymerase (DNA directed), mu	45

latent transforming growth factor beta binding	1616
guanine nucleotide binding protein (G protein)	343
Myb/SANT-like DNA-binding domain containing 3	78
dicer 1, ribonuclease type III	25
enhancer of polycomb homolog 1 (Drosophila)	102
plexin A3	2992
potassium channel tetramerization domain conta	88
solute carrier family 30 (zinc transporter), m	5
TBC1 domain family, member 24	269
Usher syndrome 1G (autosomal recessive)	5
myosin, heavy chain 15	5
RNF103-CHMP3 readthrough	2466
interleukin 17 receptor E-like	5
cell division cycle 14B	2
RAB37, member RAS oncogene family	875
activating transcription factor 3	2704
dystonin	439
schlafen family member 13	11
coiled-coil domain containing 170	15
ADAM metallopeptidase with thrombospondin type	18
contactin 2 (axonal)	5
WEE1 homolog (S. pombe)	331
CUGBP, Elav-like family member 6	5
microtubule-associated protein tau	11
family with sequence similarity 189, member A1	12
septin 8	199
TBC1 domain family, member 10A	184
bromodomain adjacent to zinc finger domain, 1B	40
junctophilin 2	76
platelet-derived growth factor receptor, beta	320
mitogen-activated protein kinase binding prote	36
matrix metallopeptidase 14 (membrane-inserted)	276
RUN and FYVE domain containing 4	5
zinc finger protein 618	778
beta 1,3-galactosyltransferase-like	200
NMDA receptor synaptonuclear signaling and neu	507
zinc finger protein 324	82
VANGL planar cell polarity protein 1	721
tubulin, gamma complex associated protein 4	129
5’-nucleotidase domain containing 1	127
histone cluster 1, H2ah	22
endonuclease/exonuclease/phosphatase family do	39
Smith-Magenis syndrome chromosome region, cand	219
epithelial membrane protein 2	1725
homeobox D12	6
caspase 10, apoptosis-related cysteine peptida	55
X-ray repair complementing defective repair in	86
TBC1 domain family, member 8B (with GRAM domai	69
transcription termination factor, RNA polymera	837
pygopus homolog 1 (Drosophila)	104
cordon-bleu WH2 repeat protein-like 1	70
acid phosphatase-like 2	72
tankyrase, TRF1-interacting ankyrin-related AD	205
tRNA selenocysteine 1 associated protein 1	763

diacylglycerol kinase, iota	16
collagen, type V, alpha 1	3111
transmembrane protein 167A	1029
epithelial membrane protein 1	814
adenosine deaminase, RNA-specific, B2 (non-fun	9
DENN/MADD domain containing 5B	832
StAR-related lipid transfer (START) domain con	28
MHC class I polypeptide-related sequence A	742
developmentally regulated GTP binding protein	1478
nanos homolog 1 (Drosophila)	158
ubiquinol-cytochrome c reductase, Rieske iron-	59
frizzled-related protein	43
TRAF2 and NCK interacting kinase	106
fatty acid desaturase 1	1170
RAN binding protein 3	908
transmembrane emp24-like trafficking protein 1	1753
KIAA0368	57
CHURC1-FNTB readthrough	13
DnaJ (Hsp40) homolog, subfamily B, member 13	7
exocyst complex component 2	192
adenosine deaminase, RNA-specific, B1	860
solute carrier family 25 (mitochondrial iron t	145
adaptor-related protein complex 4, mu 1 subuni	163
syntaxin 17	510
ER membrane protein complex subunit 3	4423
centromere protein P	85
ST3 beta-galactoside alpha-2,3-sialyltransfera	59
protein phosphatase 5, catalytic subunit	973
solute carrier family 11 (proton-coupled dival	526
mitochondrial ribosomal protein S14	2140
ubiquinol-cytochrome c reductase binding prote	1173
polypyrimidine tract binding protein 2	70
cell division cycle 6	772
polymerase (DNA directed), epsilon, catalytic	238
thymidine kinase 2, mitochondrial	439
major facilitator superfamily domain containin	47
inositol hexakisphosphate kinase 1	406
raftlin family member 2	21
Ephrin-A3; Uncharacterized protein; cDNA FLJ57	9
calcineurin-like phosphoesterase domain contai	511
PET112 homolog (yeast)	1036
coiled-coil domain containing 153	46
bicaudal D homolog 2 (Drosophila)	38
G patch domain containing 4	715
oxysterol binding protein-like 8	141
cytochrome c oxidase assembly factor 5	72
FK506 binding protein 7	645
ATP-binding cassette, sub-family G (WHITE), me	197
inhibitor of growth family, member 2	193
ANKH inorganic pyrophosphate transport regulat	770
chromosome 8 open reading frame 46	6
adenosine deaminase-like	105
lectin, mannose-binding 2-like	355
ubiquitin-conjugating enzyme E2 variant 2	1770

antigen identified by monoclonal antibody Ki-6	468
trafficking protein particle complex 2-like	1619
PAP associated domain containing 5	152
chromosome 22 open reading frame 29	351
phosphatidylinositol transfer protein, cytopla	797
TraB domain containing 2B	244
RAS protein activator like 2	950
mitochondrial ribosomal protein L46	95
Rap guanine nucleotide exchange factor (GEF) 3	19
trophoblast glycoprotein	170
FERM domain containing 4A	192
ubiquitin protein ligase E3 component n-recogn	733
tumor suppressor candidate 2	611
EH-domain containing 1	335
roundabout, axon guidance receptor, homolog 2	22
Rho-associated, coiled-coil containing protein	142
SLIT-ROBO Rho GTPase activating protein 3	38
zinc finger protein 180	195
fibrinogen C domain containing 1	44
ATP/GTP binding protein-like 3	148
karyopherin (importin) beta 1	465
sterol O-acyltransferase 1	654
GLIS family zinc finger 3	47
DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	865
RAN binding protein 2	814
zinc finger protein 695	123
poly (ADP-ribose) glycohydrolase	445
nerve growth factor receptor (TNFRSF16) associ	114
ST3 beta-galactoside alpha-2,3-sialyltransfera	150
ubiquitin-conjugating enzyme E2A	618
pyruvate kinase, liver and RBC	112
anoctamin 7	79
small integral membrane protein 1	309
chromosome 6 open reading frame 211	65
phosphoribosyl pyrophosphate synthetase-associ	2649
pleckstrin homology domain containing, family	97
uridine monophosphate synthetase	374
BUB1 mitotic checkpoint serine/threonine kinas	515
zinc finger protein 827	17
mitochondrial ribosomal protein L30	246
chromosome 2 open reading frame 15	246
DnaJ (Hsp40) homolog, subfamily B, member 5	379
methyl-CpG binding domain protein 5	7
zinc finger, DHHC-type containing 24	304
suppressor of cytokine signaling 7	15
ligand of numb-protein X 1, E3 ubiquitin prote	156
steroid 5 alpha-reductase 3	402
Snf2-related CREBBP activator protein	643
RAB3 GTPase activating protein subunit 2 (non-	461
survival motor neuron domain containing 1	949
slit homolog 1 (Drosophila)	15
AT rich interactive domain 1B (SWI1-like)	220
solute carrier family 44 (choline transporter)	407
WD repeat and SOCS box containing 2	938

propionyl CoA carboxylase, beta polypeptide	379
solute carrier family 30 (zinc transporter), m	396
zinc finger protein 283	194
ESF1, nucleolar pre-rRNA processing protein, h	180
mitochondrial ribosomal protein S30	4883
zinc finger protein 622	145
family with sequence similarity 105, member A	2613
dual-specificity tyrosine-(Y)-phosphorylation	1091
MAD2 mitotic arrest deficient-like 1 (yeast)	3013
chromosome 15 open reading frame 40	133
lysophosphatidic acid receptor 2	45
TRAF-interacting protein with forkhead-associa	400
family with sequence similarity 227, member A	16
ATP-binding cassette, sub-family B (MDR/TAP),	161
splicing factor, suppressor of white-apricot h	134
Ca++-dependent secretion activator 2	100
THUMP domain containing 2	700
transmembrane 9 superfamily member 3	1030
family with sequence similarity 126, member A	241
guanine nucleotide binding protein (G protein)	92
tsukushi, small leucine rich proteoglycan	293
cleavage stimulation factor, 3’ pre-RNA, subun	3550
serine incorporator 1	2408
lipoyl(octanoyl) transferase 2 (putative)	198
galactosylceramidase	94
histone acetyltransferase 1	3017
chromodomain helicase DNA binding protein 1	35
homeobox B13	80
RAB3B, member RAS oncogene family	611
histone deacetylase 5	266
activating signal cointegrator 1 complex subun	159
plakophilin 4	373
UDP-Gal:betaGlcNAc beta 1,3-galactosyltransfer	35
golgi glycoprotein 1	2175
chromosome 11 open reading frame 1	18
UV radiation resistance associated	116
coiled-coil domain containing 93	395
collagen beta(1-O)galactosyltransferase 2	70
serum response factor binding protein 1	102
killer cell lectin-like receptor subfamily G,	18
testis expressed 2	127
tumor necrosis factor receptor superfamily, me	36
beta-transducin repeat containing E3 ubiquitin	96
argonaute RISC catalytic component 3	198
glutamate dehydrogenase 1	287
BRCA1/BRCA2-containing complex, subunit 3	14
activating transcription factor 6	382
tetraspanin 31	72
dual-specificity tyrosine-(Y)-phosphorylation	173
neuropeptide Y receptor Y4	10
zinc finger protein 223	180
TOX high mobility group box family member 3	59
DEAD (Asp-Glu-Ala-Asp) box helicase 6	11
ariadne RBR E3 ubiquitin protein ligase 1	671

CD248 molecule, endosialin	439
STAM binding protein-like 1	675
solute carrier family 27 (fatty acid transport	523
PERP, TP53 apoptosis effector	437
GDNF family receptor alpha 1	69
suppression of tumorigenicity 5	139
quinolinate phosphoribosyltransferase	1165
lipase, endothelial	40
opsin 3	208
leiomodin 1 (smooth muscle)	148
HHIP-like 1	29
pyridoxamine 5'-phosphate oxidase	583
inositol polyphosphate-4-phosphatase, type I,	387
EF-hand domain (C-terminal) containing 1	61
ubiquitin-conjugating enzyme E2D 3	2312
zinc finger protein 613	131
exonuclease 1	1028
family with sequence similarity 179, member A	21
transmembrane protein with EGF-like and two fo	179
nudix (nucleoside diphosphate linked moiety X)	325
kelch-like family member 4	58
HERPUD family member 2	30
Cdk5 and Abl enzyme substrate 1	341
prohibitin 2	120
general transcription factor IIA, 2, 12kDa	1068
cytochrome c oxidase assembly homolog 15 (yeas	984
5-azacytidine induced 2	530
nuclear factor I/X (CCAAT-binding transcriptio	24
heterogeneous nuclear ribonucleoprotein A3	329
PHD finger protein 5A	317
C7orf55-LUC7L2 readthrough	419
cytohesin 2	383
tubulin tyrosine ligase-like family, member 1	125
family with sequence similarity 149, member B1	33
leucine rich repeat containing 27	68
arginine/serine-rich coiled-coil 2	320
ADP-ribosylation factor-like 1	600
zinc finger and BTB domain containing 11	179
annexin A6	10462
cell adhesion molecule 1	676
tRNA methyltransferase 10 homolog C (S. cerevi	655
syndecan 3	34
cholinergic receptor, muscarinic 3	47
N-acetylglutamate synthase	562
EH-domain containing 4	515
CCR4-NOT transcription complex, subunit 6-like	23
zinc finger protein 639	614
syntaxin 3	564
SRY (sex determining region Y)-box 11	1100
potassium channel, subfamily K, member 1	410
NSL1, MIS12 kinetochore complex component	180
cytochrome P450, family 4, subfamily F, polype	1613
zinc finger, FYVE domain containing 9	32
ets variant 1	160

ALG14, UDP-N-acetylglucosaminyltransferase sub	572
pyridoxal (pyridoxine, vitamin B6) kinase	5653
proteasome (prosome, macropain) assembly chape	1452
ribosomal protein L13	46038
sorbin and SH3 domain containing 3	1126
Mitogen-activated protein kinase kinase kinase	734
transmembrane emp24 protein transport domain c	1571
v-ets avian erythroblastosis virus E26 oncogen	3965
tubulin polyglutamylase complex subunit 2	508
adenomatous polyposis coli	794
component of oligomeric golgi complex 6	122
atonal homolog 8 (Drosophila)	21
BMP and activin membrane-bound inhibitor	515
SH3-domain GRB2-like (endophilin) interacting	180
low density lipoprotein receptor-related prote	378
LUC7-like 2 (S. cerevisiae)	419
mediator complex subunit 6	776
RAB24, member RAS oncogene family	908
small nuclear ribonucleoprotein polypeptide G	163
Zinc finger protein 177	36
RAS p21 protein activator (GTPase activating p	1700
protein phosphatase, Mg2+/Mn2+ dependent, 1H	45
scavenger receptor class B, member 2	5609
polymerase (RNA) I polypeptide E, 53kDa	540
v-ets avian erythroblastosis virus E26 oncogen	184
ribonuclease T2	214
catenin, beta like 1	206
dynactin 6	745
hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA t	525
intraflagellar transport 57 homolog (Chlamydom	214
heat shock 70kDa protein 2	600
mutS homolog 5	661
centrosomal protein 72kDa	230
tetraspanin 14	239
CDP-diacylglycerol synthase (phosphatidate cyt	782
O-6-methylguanine-DNA methyltransferase	2473
coiled-coil domain containing 77	8
nucleoside-triphosphatase, cancer-related	2755
RNA binding motif protein 15B	1925
hypermethylated in cancer 2	28
deoxynucleotidyltransferase, terminal, interac	599
RAB6B, member RAS oncogene family	669
SH3-domain GRB2-like endophilin B1	3418
smu-1 suppressor of mec-8 and unc-52 homolog (	325
zinc finger, CCHC domain containing 11	97
torsin A interacting protein 2	569
EH-domain containing 3	206
centromere protein F, 350/400kDa	181
RAB40B, member RAS oncogene family	495
ceroid-lipofuscinosis, neuronal 8 (epilepsy, p	122
ankyrin repeat and sterile alpha motif domain	98
HAUS augmin-like complex, subunit 3	466
spire-type actin nucleation factor 1	103
eukaryotic translation initiation factor 2B, s	789

notchless homolog 1 (Drosophila)	526
vacuolar protein sorting 33 homolog A (S. cere	282
Rho GTPase activating protein 29	451
peptidase (mitochondrial processing) beta	653
KH and NYN domain containing	421
zinc finger and BTB domain containing 3	96
microtubule associated serine/threonine kinase	1084
translocase of outer mitochondrial membrane 40	14
peroxisome proliferator-activated receptor gam	861
calpain 2, (m/II) large subunit	1090
chondroitin sulfate synthase 1	200
KIAA0141	1078
calcium/calmodulin-dependent serine protein ki	892
RAB32, member RAS oncogene family	1894
CCHC-type zinc finger, nucleic acid binding pr	2257
mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-	831
mitogen-activated protein kinase-activated pro	573
lymphoid enhancer-binding factor 1	104
peptidylprolyl isomerase (cyclophilin)-like 4	1565
abhydrolase domain containing 5	884
protein inhibitor of activated STAT, 2	194
protocadherin beta 2	199
amyloid beta (A4) precursor-like protein 2	5552
tRNA methyltransferase 61 homolog A (S. cerevi	296
cartilage associated protein	3154
G protein-coupled receptor kinase 5	337
methyltransferase like 10	919
zinc finger CCCH-type containing 14	395
jumping translocation breakpoint	872
retinoic acid receptor, alpha	560
mesoderm development candidate 2	1433
heat shock factor binding protein 1	3000
eukaryotic translation initiation factor 1B	1106
zinc finger and BTB domain containing 17	136
transmembrane protein 220	143
solute carrier family 2 (facilitated glucose t	136
thyroid hormone receptor interactor 4	143
carbonic anhydrase VB, mitochondrial	245
RNA binding motif protein 18	963
COX20 cytochrome C oxidase assembly factor	693
TIA1 cytotoxic granule-associated RNA binding	1342
SET and MYND domain containing 2	1381
zinc finger protein 749	69
DNA-damage inducible 1 homolog 2 (S. cerevisia	357
glyoxylate reductase/hydroxypyruvate reductase	572
YTH domain containing 1	307
minichromosome maintenance complex component 1	838
cytochrome b5 reductase 1	545
lectin, mannose-binding, 1	2293
chromosome 4 open reading frame 32	325
metallothionein-like 5, testis-specific (tesmi	30
zinc finger and BTB domain containing 20	5
kelch-like family member 5	366
forkhead box N3	42

calcium regulated heat stable protein 1, 24kDa	113
chromosome 19 open reading frame 47	94
V-set and transmembrane domain containing 4	59
talin 2	371
FK506 binding protein 4, 59kDa	727
Rho GTPase activating protein 18	176
pannexin 1	576
ubiquitin-conjugating enzyme E2T (putative)	679
hairy/enhancer-of-split related with YRPW moti	70
general transcription factor IIF, polypeptide	1014
centromere protein M	68
myeloid/lymphoid or mixed-lineage leukemia (tr	385
zinc finger protein 446	44
chromosome 12 open reading frame 52	1319
spermatid perinuclear RNA binding protein	575
PQ loop repeat containing 2	94
tyrosyl-tRNA synthetase 2, mitochondrial	192
ubiquitin D	112
BTB (POZ) domain containing 1	84
zinc finger and SCAN domain containing 2	125
CCR4-NOT transcription complex, subunit 7	415
peptidase (mitochondrial processing) alpha	105
centrosomal protein 63kDa	191
rhomboid, veinlet-like 3 (Drosophila)	100
TRAF3 interacting protein 2	44
mitochondrial ribosomal protein L2	935
exonuclease 3'-5' domain containing 2	3135
methylenetetrahydrofolate dehydrogenase (NADP+	4677
ADP-ribosylation factor-like 3	1387
proteasome (prosome, macropain) subunit, beta	156
G protein-coupled receptor 124	72
hypoxia inducible factor 1, alpha subunit (bas	1955
hyaluronan synthase 2	398
MAGI family member, X-linked	118
zinc finger protein 736	36
T-cell leukemia homeobox 1	47
Opa interacting protein 5	178
thyroid hormone receptor interactor 13	3078
integrin, alpha 11	390
inverted formin, FH2 and WH2 domain containing	484
mesoderm posterior 1 homolog (mouse)	303
translocase of outer mitochondrial membrane 6	2735
signal-induced proliferation-associated 1 like	291
bromodomain containing 3	77
migration and invasion inhibitory protein	782
adenylosuccinate lyase	2319
cytoskeleton-associated protein 4	1923
AT rich interactive domain 2 (ARID, RFX-like)	891
nucleoporin like 2	1714
FAST kinase domains 2	579
prostaglandin-endoperoxide synthase 1 (prostag	399
aspartyl aminopeptidase	710
ankyrin repeat domain 9	766
very low density lipoprotein receptor	977

integrin, beta 5	3180
HCG1981372, isoform CRA_c; Uncharacterized pro	142
ribonuclease P/MRP 30kDa subunit	494
methionine sulfoxide reductase B1	2102
forkhead box E1 (thyroid transcription factor	497
Rho GTPase activating protein 20	85
phosphoglycerate kinase 1	7680
EBNA1 binding protein 2	930
forkhead box D1	423
shugoshin-like 1 (S. pombe)	766
ubiquitin specific peptidase 9, X-linked	2433
dishevelled segment polarity protein 3	373
msh homeobox 2	316
ring finger protein 214	271
VAMP (vesicle-associated membrane protein)-ass	2926
mediator complex subunit 16	3677
POU class 4 homeobox 1	61
ubiquitin specific peptidase 3	583
thymidylate synthetase	21261
coiled-coil domain containing 59	140
kinetochore-localized astrin/SPAG5 binding pro	1628
isoamyl acetate-hydrolyzing esterase 1 homolog	553
contactin associated protein-like 5	5
cyclin M2	517
acid phosphatase 6, lysophosphatidic	657
myocyte enhancer factor 2C	70
centrin, EF-hand protein, 3	498
p21 protein (Cdc42/Rac)-activated kinase 4	130
solute carrier family 43 (amino acid system L	68
vacuolar protein sorting 18 homolog (S. cerevi	295
WD repeat domain 37	107
Rtf1, Paf1/RNA polymerase II complex component	1869
squamous cell carcinoma antigen recognized by	469
methyltransferase like 22	553
tigger transposable element derived 6	155
BCL2-associated athanogene	8934
carboxymethylenebutenolidase homolog (Pseudomo	2602
phospholipase A2, group XIIA	214
vesicle (multivesicular body) trafficking 1	1424
ADP-ribosylation factor-like 14 effector prote	164
oligonucleotide/oligosaccharide-binding fold c	184
inhibitor of DNA binding 3, dominant negative	1295
signal sequence receptor, alpha	12917
pleckstrin homology domain containing, family	106
ribosomal RNA processing 1	1000
glutathione S-transferase mu 3 (brain)	1071
mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-	1470
COX assembly mitochondrial protein 1 homolog (	1203
serine/threonine kinase 16	1416
upregulator of cell proliferation	180
ankyrin repeat and LEM domain containing 2	504
fucosyltransferase 10 (alpha (1,3) fucosyltran	124
alpha-methylacyl-CoA racemase	308
presenilin associated, rhomboid-like	1214

mitochondrial ribosome-associated GTPase 2	509
WD repeat domain, phosphoinositide interacting	1038
aldo-keto reductase family 7, member A2 (aflat	1134
polymerase (RNA) II (DNA directed) polypeptide	223
cadherin 11, type 2, OB-cadherin (osteoblast)	448
ATP-binding cassette, sub-family G (WHITE), me	64
uroporphyrinogen III synthase	221
zinc finger, matrin-type 2	1926
N-acetyltransferase 10 (GCN5-related)	132
lon peptidase 2, peroxisomal	1004
HAUS augmin-like complex, subunit 8	827
cholinergic receptor, nicotinic, alpha 5 (neur	903
POU class 6 homeobox 1	135
progestin and adipoQ receptor family member II	217
peroxisomal biogenesis factor 7	661
synaptosomal-associated protein, 47kDa	7416
hexamethylene bis-acetamide inducible 2	306
transmembrane emp24 protein transport domain c	12499
ubiquitin-conjugating enzyme E2F (putative)	905
melanophilin	85
DNL-type zinc finger	373
glutamate receptor, ionotropic, delta 1	45
NADH dehydrogenase (ubiquinone) flavoprotein 3	1449
G patch domain and KOW motifs	420
gamma-aminobutyric acid (GABA) A receptor, bet	5
kinocilin	5
CSE1 chromosome segregation 1-like (yeast)	96
squamous cell carcinoma antigen recognized by	94
nudix (nucleoside diphosphate linked moiety X)	629
lamin B2	89
guanine nucleotide binding protein (G protein)	10881
chromosome 2 open reading frame 68	565
paired box 6	191
mitogen-activated protein kinase 14	1191
1-acylglycerol-3-phosphate O-acyltransferase 6	474
transmembrane protein 98	98
transcription factor 21	552
calmodulin-like 4	307
thioredoxin reductase 3	272
splicing factor 3b, subunit 3, 130kDa	2541
NCK-associated protein 1	700
dedicator of cytokinesis 7	66
DEAH (Asp-Glu-Ala-His) box polypeptide 34	469
phosphofurin acidic cluster sorting protein 2	234
thioredoxin-like 1	1779
mutS homolog 3	443
fat mass and obesity associated	240
chromosome 3 open reading frame 17	460
transcription elongation factor B (SIII), poly	3007
CD59 molecule, complement regulatory protein	19017
gem (nuclear organelle) associated protein 4	339
AHA1, activator of heat shock 90kDa protein AT	820
mortality factor 4 like 1	1137
inositol(myo)-1(or 4)-monophosphatase 1	309

outer dense fiber of sperm tails 2-like	149
calcium/calmodulin-dependent protein kinase II	6631
serpin peptidase inhibitor, clade A (alpha-1 a	203
diacylglycerol O-acyltransferase 1	3108
crooked neck pre-mRNA splicing factor 1	519
asparaginyl-tRNA synthetase	467
thioredoxin-related transmembrane protein 1	3176
mediator complex subunit 31	1743
dual specificity phosphatase 6	1056
transferrin	2533
F-box protein 33	306
H6 family homeobox 1	171
biorientation of chromosomes in cell division	1465
G-rich RNA sequence binding factor 1	4414
ATP/GTP binding protein-like 5	354
cAMP responsive element binding protein-like 2	218
solute carrier family 35, member E3	250
GTPase, IMAP family member 6	5
ATPase, Ca++ transporting, plasma membrane 2	170
transmembrane protein 67	219
neuropilin (NRP) and tolloid (TLL)-like 2	723
PAP associated domain containing 4	434
inositol 1,3,4,5,6-pentakisphosphate 2-kinase	211
IQ motif containing GTPase activating protein	588
isoleucyl-tRNA synthetase 2, mitochondrial	2978
brain and reproductive organ-expressed (TNFRSF	880
proline-rich nuclear receptor coactivator 1	413
phosphatidylserine synthase 2	1031
growth hormone secretagogue receptor	5
RFT1 homolog (S. cerevisiae)	392
transformer 2 beta homolog (Drosophila)	1868
enabled homolog (Drosophila)	415
ring finger protein 213	630
tripartite motif containing 11	727
cysteine and histidine-rich domain (CHORD) con	891
polycystic kidney and hepatic disease 1 (autos	5
ATP/GTP binding protein 1	187
RAN binding protein 6	117
heterogeneous nuclear ribonucleoprotein L-like	753
nibrin	342
staufen double-stranded RNA binding protein 2	306
	5
fragile site, folic acid type, rare, fra(10)(q	289
mitochondrial ribosomal protein S23	7140
olfactory receptor, family 7, subfamily A, mem	5
glycogen synthase kinase 3 beta	498
cathepsin V	601
tRNA 5-methylaminomethyl-2-thiouridylate methy	150
YLP motif containing 1	1542
N-acetylglucosamine-1-phosphate transferase, g	677
fucosyltransferase 4 (alpha (1,3) fucosyltrans	354
UDP-glucose glycoprotein glucosyltransferase 2	423
solute carrier family 35, member A5	168
G protein-coupled receptor 137C	110

DIP2 disco-interacting protein 2 homolog A (Dr	298
SMAD family member 6	660
FCH and double SH3 domains 1	364
exostosin glycosyltransferase 1	694
trophinin associated protein	270
dual-specificity tyrosine-(Y)-phosphorylation	448
lectin, galactoside-binding, soluble, 1	50186
integrin-binding sialoprotein	5
glutamate receptor, ionotropic, N-methyl D-asp	5
N-acetylated alpha-linked acidic dipeptidase 2	5
glucose-6-phosphatase, catalytic, 2	5
catenin (cadherin-associated protein), delta 1	743
germ cell associated 1	5
leucine rich repeat containing 6	5
G protein-coupled receptor 34	5
kelch-like family member 36	483
chromosome 9 open reading frame 3	1591
complement component 3	932
E2F transcription factor 1	479
transmembrane protein 233	5
chromosome 6 open reading frame 25	5
peptidylprolyl isomerase D	1544
interleukin 5 receptor, alpha	5
G protein-coupled receptor 137B	389
dual specificity phosphatase 1	37211
TRK-fused gene	2164
guanine nucleotide binding protein (G protein)	210
GRB2-related adaptor protein 2	5
Spi-C transcription factor (Spi-1/PU.1 related	5
ARP3 actin-related protein 3 homolog (yeast)	816
solute carrier family 2 (facilitated glucose t	13928
phosphofructokinase, muscle	7010
phytanoyl-CoA 2-hydroxylase	1932
schlafen family member 12-like	5
aldo-keto reductase family 1, member C4	5
myoglobin	5
Bartter syndrome, infantile, with sensorineura	5
delta-like 1 homolog (Drosophila)	1865
neuropeptide S receptor 1	5
TNFAIP3 interacting protein 3	5
cytochrome P450, family 2, subfamily C, polype	5
proline-rich protein HaeIII subfamily 2	5
PHD finger protein 19	490
ER membrane protein complex subunit 10	1981
RUN domain containing 1	927
cyclin B1	6970
trafficking protein particle complex 8	502
NCK interacting protein with SH3 domain	4158
SEC16 homolog B (S. cerevisiae)	251
C-reactive protein, pentraxin-related	5
ZFP62 zinc finger protein	170
caseinolytic mitochondrial matrix peptidase pr	4038
thyroglobulin	5
purinergic receptor P2Y, G-protein coupled, 10	5

olfactory receptor, family 2, subfamily A, mem	5
RNA terminal phosphate cyclase-like 1	203
dynein, axonemal, heavy chain 9	5
solute carrier family 2 (facilitated glucose t	5
cadherin 19, type 2	5
mannose-binding lectin (protein C) 2, soluble	5
chromosome 18 open reading frame 42	5
CD1c molecule	5
peptidylprolyl isomerase domain and WD repeat	1377
BTAF1 RNA polymerase II, B-TFIID transcription	917
mitochondrial ribosomal protein L12	2476
formyl peptide receptor 1	5
RAB18, member RAS oncogene family	1410
serpin peptidase inhibitor, clade A (alpha-1 a	5
alpha- and gamma-adaptin binding protein	2536
3-hydroxyanthranilate 3,4-dioxygenase	7
lipase maturation factor 1	155
wingless-type MMTV integration site family, me	5
goosecoid homeobox 2	5
glycine-N-acyltransferase	5
interleukin 1 receptor accessory protein-like	5
Uncharacterized protein; Zinc finger protein 7	5
proline, glutamate and leucine rich protein 1	266
LSM14A, SCD6 homolog A (S. cerevisiae)	362
leucine rich repeat containing 4C	5
methyltransferase like 24	5
podocan-like 1	9
mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-	5
ribosomal protein S23	832
adenosine A3 receptor	5
tripartite motif containing 55	5
cyclin Pas1/PHO80 domain containing 1	234
proprotein convertase subtilisin/kexin type 9	2345
BCL2-like 15	5
angiopoietin-like 1	5
TSC22 domain family, member 2	1062
ATH1, acid trehalase-like 1 (yeast)	314
zinc finger, MYM-type 4	280
general transcription factor IIIC, polypeptide	981
transforming growth factor, beta-induced, 68kD	6307
four and a half LIM domains 5	5
quinoid dihydropteridine reductase	4326
Sp3 transcription factor	285
THAP domain containing 7	769
gamma-aminobutyric acid (GABA) A receptor, rho	5
aquaporin 6, kidney specific	5
McKusick-Kaufman syndrome	543
Uncharacterized protein	1851
zinc finger protein 699	5
v-erb-b2 avian erythroblastic leukemia viral o	926
potassium voltage-gated channel, subfamily H (	5
protocadherin 11 X-linked	5
Kinesin light chain 1	499
tetraspanin 33	237

mutS homolog 2	1468
staphylococcal nuclease and tudor domain conta	7201
forkhead box K2	450
non-SMC element 1 homolog (S. cerevisiae)	1418
cerebellar degeneration-related protein 1, 34k	5
centromere protein H	1267
tumor protein p53 binding protein, 2	1531
enoyl CoA hydratase domain containing 3	315
G protein-coupled receptor 22	5
platelet factor 4	11
ZFP36 ring finger protein-like 2	317
muscular LMNA-interacting protein	8
epidermal growth factor	5
deoxyribonuclease I-like 3	5
intraflagellar transport 74 homolog (Chlamydom	246
ecotropic viral integration site 2A	5
collectin sub-family member 10 (C-type lectin)	5
MAM domain containing 4	377
family with sequence similarity 181, member B	5
cysteine-rich secretory protein 1	5
histone deacetylase 2	1701
bone morphogenetic protein 10	5
CD63 molecule	7483
ankyrin repeat and KH domain containing 1	247
angiopoietin 4	5
fibronectin type III domain containing 5	5
ankyrin repeat and SOCS box containing 15	5
metallothionein 1F	19
G protein-coupled receptor 78	5
seryl-tRNA synthetase	20549
C-type lectin domain family 17, member A	5
toll-like receptor 4	47
reticulocalbin 2, EF-hand calcium binding doma	4448
autophagy related 2A	3795
fatty acid amide hydrolase	19
cytohesin 1 interacting protein	8
tyrosinase-related protein 1	16
NLR family, pyrin domain containing 9	5
CD180 molecule	5
ets homologous factor	5
dihydrolipoamide dehydrogenase	1623
UDP-N-acetyl-alpha-D-galactosamine:polypeptide	5
collectin sub-family member 11	41
ADP-ribosylation-like factor 6 interacting pro	1454
neuroblastoma breakpoint family, member 24	5
leukocyte-associated immunoglobulin-like recep	5
5-aminoimidazole-4-carboxamide ribonucleotide	5791
SHC (Src homology 2 domain containing) transfo	18
myosin IG	5
HECT, UBA and WWE domain containing 1, E3 ubiq	741
DEAH (Asp-Glu-Ala-His) box helicase 30	252
transthyretin	12915
serine/arginine-rich splicing factor 7	16077
tubulin, gamma complex associated protein 2	1638

X-ray repair complementing defective repair in	14802
ArfGAP with GTPase domain, ankyrin repeat and	5
GTPase activating protein (SH3 domain) binding	4413
ectonucleotide pyrophosphatase/phosphodiestera	15
toll-like receptor 8	5
abhydrolase domain containing 16B	5
ATP-binding cassette, sub-family D (ALD), memb	5
capping protein (actin filament) muscle Z-line	545
apolipoprotein B	31
ficolin (collagen/fibrinogen domain containing	5
tripartite motif containing 72	8
solute carrier family 22 (organic cation trans	5
WD repeat domain 77	1214
bone marrow stromal cell antigen 1	44
zinc finger and BTB domain containing 38	1270
lactotransferrin	5
DEAD (Asp-Glu-Ala-Asp) box polypeptide 53	5
protein tyrosine phosphatase, receptor type, F	14842
NK2 homeobox 1	9
frizzled family receptor 8	791
quiescin Q6 sulfhydryl oxidase 1	9246
mitochondrial ribosomal protein L22	5309
GATS protein-like 2	5
caspase recruitment domain family, member 11	13
ER membrane protein complex subunit 1	5396
ATP-binding cassette, sub-family A (ABC1), mem	7
t-complex 10-like	5
epidermal growth factor receptor pathway subst	2643
HBS1-like (S. cerevisiae)	2367
gonadotropin-releasing hormone receptor	5
ubiquitin specific peptidase 15	286
insulin induced gene 1	1776
t-complex 1	15828
NudC domain containing 3	659
zinc finger protein 141	19
Ran GTPase activating protein 1	2648
T-cell immunoglobulin and mucin domain contain	10
timeless circadian clock	3085
Hermansky-Pudlak syndrome 4	719
Sec23 homolog B (S. cerevisiae)	1829
RAB43, member RAS oncogene family	5
neuron-derived neurotrophic factor	51
WD repeat domain 13	1128
LLP homolog, long-term synaptic facilitation (	88
phospholysine phosphohistidine inorganic pyrop	2365
solute carrier family 25 (mitochondrial carrie	1169
chromosome 12 open reading frame 79	5
low density lipoprotein receptor-related prote	16
ADAM metallopeptidase domain 7	5
family with sequence similarity 229, member B	237
nucleoporin 93kDa	1604
arginine-fifty homeobox	5
DnaJ (Hsp40) homolog, subfamily C, member 15	3290
eukaryotic translation initiation factor 2A, 6	3166

ring finger protein 126	658
corticotropin releasing hormone receptor 2	5
sine oculis binding protein homolog (Drosophil	22
fused in sarcoma	30612
transcription factor 3	1267
transmembrane protein 39A	1088
major facilitator superfamily domain containin	6
serine hydroxymethyltransferase 1 (soluble)	3432
WD repeat domain 75	174
leucine rich repeat containing 34	48
smoothelin-like 2	23
leucine rich repeat containing 2	5
early B-cell factor 4	1194
G protein-coupled receptor 183	112
ankyrin repeat and sterile alpha motif domain	40
gamma-glutamylamine cyclotransferase	164
LIM and cysteine-rich domains 1	1023
collapsin response mediator protein 1	252
splicing factor 3a, subunit 1, 120kDa	1091
translocase of inner mitochondrial membrane 50	2210
KIAA1715	858
neuregulin 3	27
membrane-associated ring finger (C3HC4) 6, E3	14086
Uncharacterized protein	5
ankyrin repeat and FYVE domain containing 1	969
CUGBP, Elav-like family member 3	5
interleukin 10 receptor, alpha	5
fibrinogen beta chain	1017
vascular cell adhesion molecule 1	33
Kruppel-like factor 2 (lung)	431
polymerase (DNA-directed), delta 4, accessory	6724
COP9 signalosome subunit 8	1979
family with sequence similarity 208, member A	60
ribosomal protein S6 kinase-like 1	9
cytoplasmic FMR1 interacting protein 1	40959
claudin 11	1116
leucine rich repeat containing 40	88
spermatogenesis associated 6-like	14
discs, large (Drosophila) homolog-associated p	8
family with sequence similarity 213, member A	482
chromosome 9 open reading frame 156	177
zinc finger protein 334	36
NAD(P)H dehydrogenase, quinone 2	62
Rho GTPase activating protein 12	190
chromosome 16 open reading frame 45	60
RWD domain containing 1	296
DnaJ (Hsp40) homolog, subfamily B, member 4	633
ribosomal protein S24	39029
PX domain containing serine/threonine kinase	220
leucine rich repeat containing 49	94
C-type lectin domain family 4, member C	5
guanylate cyclase 1, soluble, alpha 3	42
cadherin-like and PC-esterase domain containin	77
SRY (sex determining region Y)-box 17	65

pecanex-like 2 (Drosophila)	49
renalase, FAD-dependent amine oxidase	48
carboxypeptidase, vitellogenic-like	439
hydroxysteroid (11-beta) dehydrogenase 1	61
CCR4 carbon catabolite repression 4-like (S. c	101
interferon-induced protein with tetratricopept	72
chromosome 11 open reading frame 54	47
KIAA1551	15
DDRGK domain containing 1	3324
zinc finger protein 140	137
family with sequence similarity 120A opposite	258
complement component 8, alpha polypeptide	5
biliverdin reductase A	144
glioma tumor suppressor candidate region gene	18735
family with sequence similarity 127, member C	1251
carbohydrate (N-acetylglucosamine-6-O) sulfotr	154
myosin, heavy chain 9, non-muscle	1317
G protein-coupled receptor 56	44
pantothenate kinase 2	1244
suppressor of cytokine signaling 5	72
ubiquinol-cytochrome c reductase, complex III	34490
cofilin 2 (muscle)	902
ST20-MTHFS readthrough	1604
myosin IF	33
protein arginine methyltransferase 7	6277
mitochondrial ribosomal protein L39	470
heterogeneous nuclear ribonucleoprotein A0	22668
integrator complex subunit 6	433
tumor necrosis factor, alpha-induced protein 8	259
pre-mRNA processing factor 4	2735
calcium channel, voltage-dependent, L type, al	69
cytochrome b5 domain containing 2	668
cytochrome P450, family 20, subfamily A, polyp	170
sodium channel, voltage-gated, type I, alpha s	21
Bet1 golgi vesicular membrane trafficking prot	722
CD1d molecule	7
G protein-coupled receptor 35	71
four and a half LIM domains 2	3097
N-6 adenine-specific DNA methyltransferase 1 (	93
biogenesis of lysosomal organelles complex-1,	83
methionine sulfoxide reductase B2	6585
phospholipase C-like 1	31
peroxiredoxin 2	7500
fibrinogen gamma chain	488
5,10-methenyltetrahydrofolate synthetase (5-fo	1604
cytochrome b5 type A (microsomal)	549
Src-like-adaptor	5
glypican 5	65
CHRNA7 (cholinergic receptor, nicotinic, alpha	5
apolipoprotein B mRNA editing enzyme, catalyti	10
phosphoenolpyruvate carboxykinase 1 (soluble)	5
glucose-6-phosphate isomerase	8230
lysyl oxidase-like 2	701
pancreatic progenitor cell differentiation and	17979

calcium channel, voltage-dependent, N type, al	5
phosphoinositide-3-kinase adaptor protein 1	14
G protein-coupled receptor 125	1042
G protein-coupled receptor 25	5
chromosome 18 open reading frame 32	733
angiotensin I converting enzyme	12
protein phosphatase 2, regulatory subunit A, a	65937
transcription elongation factor A (SII) N-term	78
A kinase (PRKA) anchor protein 11	71
synaptonemal complex protein 2-like	140
BH3 interacting domain death agonist	187
potassium voltage-gated channel, KQT-like subf	50
Ras-like without CAAX 1	192
transmembrane protein 257	5
atypical chemokine receptor 4	5
ring finger protein 41	152

Total sites	8mer sites	7mer-m8 sites
18	0	18
10	2	7
6	1	2
4	2	0
4	2	1
6	0	6
2	2	0
2	2	0
5	2	1
8	1	7
4	2	2
5	1	2
5	4	0
2	0	1
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4	2	1
1	1	0
1	1	0
2	0	2
7	0	7
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4	0	3
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3	0	3
4	0	1
4	1	1
3	1	0
4	0	2
5	0	0
4	1	2
1	1	0
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2	1	0

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1	1	0
4	0	3
2	0	2
4	2	0
1	1	0
3	0	2
2	0	2
6	1	5
1	1	0
3	1	1
2	1	1
4	2	1
1	1	0
8	2	3

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2	0	2
6	0	4
3	1	2
2	0	1
3	0	2
2	0	1
4	0	3
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1	1	0
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1	1	0
3	1	2
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4	3	0
2	1	0
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1	1	0
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3	0	1
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2	0	1
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5	2	1
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3	0	2
2	0	1
7	1	4
2	1	1

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2	0	1
1	1	0
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3	0	2
1	0	1
1	1	0
3	0	2
1	0	1
1	1	0
4	0	3
2	1	1
3	0	3
2	0	1
5	2	3
1	1	0
1	0	0
4	1	3
2	1	1
3	2	1
2	0	0
3	1	2
1	1	0
3	0	1
3	0	0
3	1	1
2	0	2
4	0	3
2	1	1
2	1	1
1	0	0
3	0	1
1	1	0
1	1	0
1	1	0
1	1	0
3	2	1
1	1	0
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Representative miRNA	Cumulati\	Total cor	Aggregate PCT
hsa-miR-1252-5p	-2.01	-2.01	N/A
hsa-miR-1252-5p	-1.65	-1.65	N/A
hsa-miR-1252-5p	-1.09	-1.09	N/A
hsa-miR-1252-5p	-1.03	-1.03	N/A
hsa-miR-1252-5p	-1	-1	N/A
hsa-miR-1252-5p	-0.98	-0.98	N/A
hsa-miR-1252-5p	-0.93	-0.93	N/A
hsa-miR-1252-5p	-0.91	-0.91	N/A
hsa-miR-1252-5p	-0.88	-1.14	N/A
hsa-miR-1252-5p	-0.85	-0.85	N/A
hsa-miR-1252-5p	-0.8	-0.8	N/A
hsa-miR-1252-5p	-0.8	-0.8	N/A
hsa-miR-1252-5p	-0.79	-0.79	N/A
hsa-miR-1252-5p	-0.77	-0.77	N/A
hsa-miR-1252-5p	-0.77	-0.86	N/A
hsa-miR-1252-5p	-0.74	-0.74	N/A
hsa-miR-1252-5p	-0.73	-0.73	N/A
hsa-miR-1252-5p	-0.72	-0.91	N/A
hsa-miR-1252-5p	-0.71	-0.71	N/A
hsa-miR-1252-5p	-0.7	-0.72	N/A
hsa-miR-1252-5p	-0.69	-1.11	N/A
hsa-miR-1252-5p	-0.69	-0.69	N/A
hsa-miR-1252-5p	-0.69	-0.78	N/A
hsa-miR-1252-5p	-0.68	-0.68	N/A
hsa-miR-1252-5p	-0.68	-0.94	N/A
hsa-miR-1252-5p	-0.66	-0.66	N/A
hsa-miR-1252-5p	-0.66	-0.7	N/A
hsa-miR-1252-5p	-0.65	-1.43	N/A
hsa-miR-1252-5p	-0.65	-0.65	N/A
hsa-miR-1252-5p	-0.64	-0.64	N/A
hsa-miR-1252-5p	-0.64	-0.64	N/A
hsa-miR-1252-5p	-0.64	-0.65	N/A
hsa-miR-1252-5p	-0.63	-0.63	N/A
hsa-miR-1252-5p	-0.63	-0.63	N/A
hsa-miR-1252-5p	-0.63	-0.63	N/A
hsa-miR-1252-5p	-0.62	-0.62	N/A
hsa-miR-1252-5p	-0.62	-0.62	N/A
hsa-miR-1252-5p	-0.61	-0.61	N/A
hsa-miR-1252-5p	-0.61	-0.63	N/A
hsa-miR-1252-5p	-0.6	-0.64	N/A
hsa-miR-1252-5p	-0.6	-0.6	N/A
hsa-miR-1252-5p	-0.6	-0.69	N/A
hsa-miR-1252-5p	-0.59	-0.59	N/A
hsa-miR-1252-5p	-0.59	-0.65	N/A
hsa-miR-1252-5p	-0.59	-0.59	N/A
hsa-miR-1252-5p	-0.59	-0.59	N/A
hsa-miR-1252-5p	-0.58	-0.58	N/A
hsa-miR-1252-5p	-0.57	-0.57	N/A
hsa-miR-1252-5p	-0.57	-0.58	N/A
hsa-miR-1252-5p	-0.57	-0.64	N/A
hsa-miR-1252-5p	-0.57	-0.57	N/A
hsa-miR-1252-5p	-0.57	-0.61	N/A
hsa-miR-1252-5p	-0.57	-0.57	N/A

hsa-miR-1252-5p	-0.57	-0.57	N/A
hsa-miR-1252-5p	-0.56	-0.56	N/A
hsa-miR-1252-5p	-0.56	-0.56	N/A
hsa-miR-1252-5p	-0.56	-0.6	N/A
hsa-miR-1252-5p	-0.56	-0.56	N/A
hsa-miR-1252-5p	-0.55	-0.55	N/A
hsa-miR-1252-5p	-0.55	-0.55	N/A
hsa-miR-1252-5p	-0.55	-0.55	N/A
hsa-miR-1252-5p	-0.54	-0.58	N/A
hsa-miR-1252-5p	-0.54	-0.54	N/A
hsa-miR-1252-5p	-0.54	-0.59	N/A
hsa-miR-1252-5p	-0.54	-0.54	N/A
hsa-miR-1252-5p	-0.53	-0.53	N/A
hsa-miR-1252-5p	-0.53	-0.53	N/A
hsa-miR-1252-5p	-0.53	-0.53	N/A
hsa-miR-1252-5p	-0.53	-0.53	N/A
hsa-miR-1252-5p	-0.53	-0.53	N/A
hsa-miR-1252-5p	-0.53	-0.53	N/A
hsa-miR-1252-5p	-0.53	-0.53	N/A
hsa-miR-1252-5p	-0.53	-0.53	N/A
hsa-miR-1252-5p	-0.53	-0.53	N/A
hsa-miR-1252-5p	-0.53	-0.56	N/A
hsa-miR-1252-5p	-0.52	-0.52	N/A
hsa-miR-1252-5p	-0.52	-0.52	N/A
hsa-miR-1252-5p	-0.52	-0.52	N/A
hsa-miR-1252-5p	-0.52	-0.52	N/A
hsa-miR-1252-5p	-0.51	-0.52	N/A
hsa-miR-1252-5p	-0.51	-0.51	N/A
hsa-miR-1252-5p	-0.5	-0.52	N/A
hsa-miR-1252-5p	-0.5	-0.5	N/A
hsa-miR-1252-5p	-0.5	-0.51	N/A
hsa-miR-1252-5p	-0.5	-0.5	N/A
hsa-miR-1252-5p	-0.5	-0.71	N/A
hsa-miR-1252-5p	-0.5	-0.5	N/A
hsa-miR-1252-5p	-0.5	-0.51	N/A
hsa-miR-1252-5p	-0.5	-0.5	N/A
hsa-miR-1252-5p	-0.5	-0.51	N/A
hsa-miR-1252-5p	-0.49	-0.49	N/A
hsa-miR-1252-5p	-0.49	-0.49	N/A
hsa-miR-1252-5p	-0.49	-0.49	N/A
hsa-miR-1252-5p	-0.49	-0.49	N/A
hsa-miR-1252-5p	-0.49	-0.62	N/A
hsa-miR-1252-5p	-0.49	-0.49	N/A
hsa-miR-1252-5p	-0.49	-0.49	N/A
hsa-miR-1252-5p	-0.48	-0.48	N/A
hsa-miR-1252-5p	-0.48	-0.6	N/A
hsa-miR-1252-5p	-0.48	-0.48	N/A
hsa-miR-1252-5p	-0.48	-0.49	N/A
hsa-miR-1252-5p	-0.48	-0.48	N/A
hsa-miR-1252-5p	-0.48	-0.49	N/A
hsa-miR-1252-5p	-0.47	-0.47	N/A
hsa-miR-1252-5p	-0.47	-0.47	N/A
hsa-miR-1252-5p	-0.47	-0.47	N/A
hsa-miR-1252-5p	-0.47	-0.47	N/A

hsa-miR-1252-5p	-0.47	-0.49	N/A
hsa-miR-1252-5p	-0.47	-0.47	N/A
hsa-miR-1252-5p	-0.47	-0.51	N/A
hsa-miR-1252-5p	-0.47	-0.64	N/A
hsa-miR-1252-5p	-0.47	-0.47	N/A
hsa-miR-1252-5p	-0.47	-0.47	N/A
hsa-miR-1252-5p	-0.46	-0.49	N/A
hsa-miR-1252-5p	-0.46	-0.81	N/A
hsa-miR-1252-5p	-0.46	-0.78	N/A
hsa-miR-1252-5p	-0.46	-0.51	N/A
hsa-miR-1252-5p	-0.46	-0.46	N/A
hsa-miR-1252-5p	-0.46	-0.46	N/A
hsa-miR-1252-5p	-0.46	-0.46	N/A
hsa-miR-1252-5p	-0.46	-0.46	N/A
hsa-miR-1252-5p	-0.46	-0.46	N/A
hsa-miR-1252-5p	-0.46	-0.46	N/A
hsa-miR-1252-5p	-0.46	-0.46	N/A
hsa-miR-1252-5p	-0.46	-0.8	N/A
hsa-miR-1252-5p	-0.46	-0.46	N/A
hsa-miR-1252-5p	-0.45	-0.45	N/A
hsa-miR-1252-5p	-0.45	-0.45	N/A
hsa-miR-1252-5p	-0.45	-0.45	N/A
hsa-miR-1252-5p	-0.45	-0.45	N/A
hsa-miR-1252-5p	-0.45	-0.46	N/A
hsa-miR-1252-5p	-0.45	-0.45	N/A
hsa-miR-1252-5p	-0.45	-0.46	N/A
hsa-miR-1252-5p	-0.44	-0.57	N/A
hsa-miR-1252-5p	-0.44	-0.44	N/A
hsa-miR-1252-5p	-0.44	-0.44	N/A
hsa-miR-1252-5p	-0.44	-0.82	N/A
hsa-miR-1252-5p	-0.44	-0.44	N/A
hsa-miR-1252-5p	-0.44	-0.44	N/A
hsa-miR-1252-5p	-0.43	-0.46	N/A
hsa-miR-1252-5p	-0.43	-0.43	N/A
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hsa-miR-1252-5p	-0.43	-0.43	N/A
hsa-miR-1252-5p	-0.43	-0.43	N/A
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hsa-miR-1252-5p	-0.43	-0.76	N/A
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hsa-miR-1252-5p	-0.42	-0.42	N/A
hsa-miR-1252-5p	-0.42	-0.42	N/A
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hsa-miR-1252-5p	-0.42	-0.42	N/A
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hsa-miR-1252-5p	-0.42	-0.61	N/A

hsa-miR-1252-5p	-0.42	-0.78	N/A
hsa-miR-1252-5p	-0.42	-0.42	N/A
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hsa-miR-1252-5p	-0.41	-0.68	N/A
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hsa-miR-1252-5p	-0.4	-0.46	N/A
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hsa-miR-1252-5p	-0.4	-0.41	N/A
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hsa-miR-1252-5p	-0.39	-0.39	N/A
hsa-miR-1252-5p	-0.39	-0.42	N/A
hsa-miR-1252-5p	-0.39	-0.39	N/A
hsa-miR-1252-5p	-0.39	-0.39	N/A
hsa-miR-1252-5p	-0.39	-0.39	N/A
hsa-miR-1252-5p	-0.39	-0.39	N/A
hsa-miR-1252-5p	-0.39	-0.55	N/A
hsa-miR-1252-5p	-0.39	-0.83	N/A
hsa-miR-1252-5p	-0.39	-0.48	N/A
hsa-miR-1252-5p	-0.39	-0.61	N/A
hsa-miR-1252-5p	-0.39	-0.48	N/A
hsa-miR-1252-5p	-0.39	-0.39	N/A
hsa-miR-1252-5p	-0.38	-0.56	N/A
hsa-miR-1252-5p	-0.38	-0.38	N/A
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hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.38	-0.4	N/A

hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.38	-0.42	N/A
hsa-miR-1252-5p	-0.38	-0.44	N/A
hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.38	-0.53	N/A
hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.38	-0.51	N/A
hsa-miR-1252-5p	-0.38	-0.44	N/A
hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.38	-0.38	N/A
hsa-miR-1252-5p	-0.37	-0.61	N/A
hsa-miR-1252-5p	-0.37	-0.48	N/A
hsa-miR-1252-5p	-0.37	-0.37	N/A
hsa-miR-1252-5p	-0.37	-0.47	N/A
hsa-miR-1252-5p	-0.37	-0.37	N/A
hsa-miR-1252-5p	-0.37	-0.37	N/A
hsa-miR-1252-5p	-0.37	-0.4	N/A
hsa-miR-1252-5p	-0.37	-0.37	N/A
hsa-miR-1252-5p	-0.37	-0.37	N/A
hsa-miR-1252-5p	-0.37	-0.38	N/A
hsa-miR-1252-5p	-0.37	-0.37	N/A
hsa-miR-1252-5p	-0.37	-0.37	N/A
hsa-miR-1252-5p	-0.37	-0.6	N/A
hsa-miR-1252-5p	-0.37	-0.37	N/A
hsa-miR-1252-5p	-0.37	-0.37	N/A
hsa-miR-1252-5p	-0.36	-0.61	N/A
hsa-miR-1252-5p	-0.36	-0.41	N/A
hsa-miR-1252-5p	-0.36	-0.59	N/A
hsa-miR-1252-5p	-0.36	-0.46	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.52	N/A
hsa-miR-1252-5p	-0.36	-0.42	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.37	N/A
hsa-miR-1252-5p	-0.36	-0.45	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.51	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.47	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A

hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.56	N/A
hsa-miR-1252-5p	-0.36	-0.4	N/A
hsa-miR-1252-5p	-0.36	-0.49	N/A
hsa-miR-1252-5p	-0.36	-0.42	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.36	N/A
hsa-miR-1252-5p	-0.36	-0.4	N/A
hsa-miR-1252-5p	-0.35	-0.35	N/A
hsa-miR-1252-5p	-0.35	-0.35	N/A
hsa-miR-1252-5p	-0.35	-0.35	N/A
hsa-miR-1252-5p	-0.35	-0.39	N/A
hsa-miR-1252-5p	-0.35	-0.35	N/A
hsa-miR-1252-5p	-0.35	-0.65	N/A
hsa-miR-1252-5p	-0.35	-0.35	N/A
hsa-miR-1252-5p	-0.35	-0.52	N/A
hsa-miR-1252-5p	-0.35	-0.35	N/A
hsa-miR-1252-5p	-0.35	-0.47	N/A
hsa-miR-1252-5p	-0.35	-0.37	N/A
hsa-miR-1252-5p	-0.35	-0.47	N/A
hsa-miR-1252-5p	-0.35	-0.38	N/A
hsa-miR-1252-5p	-0.35	-0.35	N/A
hsa-miR-1252-5p	-0.35	-0.35	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.37	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.39	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.36	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.36	N/A
hsa-miR-1252-5p	-0.34	-0.46	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.36	N/A
hsa-miR-1252-5p	-0.34	-0.38	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
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hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
hsa-miR-1252-5p	-0.34	-0.34	N/A
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hsa-miR-1252-5p	-0.33	-0.35	N/A
hsa-miR-1252-5p	-0.33	-0.33	N/A
hsa-miR-1252-5p	-0.33	-0.44	N/A

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hsa-miR-1252-5p	-0.33	-0.33	N/A
hsa-miR-1252-5p	-0.33	-0.33	N/A
hsa-miR-1252-5p	-0.33	-0.34	N/A
hsa-miR-1252-5p	-0.33	-0.35	N/A
hsa-miR-1252-5p	-0.33	-0.33	N/A
hsa-miR-1252-5p	-0.33	-0.33	N/A
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hsa-miR-1252-5p	-0.33	-0.33	N/A
hsa-miR-1252-5p	-0.33	-0.33	N/A
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hsa-miR-1252-5p	-0.33	-0.33	N/A
hsa-miR-1252-5p	-0.33	-0.33	N/A
hsa-miR-1252-5p	-0.33	-0.33	N/A
hsa-miR-1252-5p	-0.33	-0.33	N/A
hsa-miR-1252-5p	-0.33	-0.33	N/A
hsa-miR-1252-5p	-0.33	-0.33	N/A
hsa-miR-1252-5p	-0.33	-0.33	N/A
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hsa-miR-1252-5p	-0.32	-0.62	N/A
hsa-miR-1252-5p	-0.32	-0.32	N/A
hsa-miR-1252-5p	-0.32	-0.32	N/A
hsa-miR-1252-5p	-0.32	-0.32	N/A
hsa-miR-1252-5p	-0.32	-0.32	N/A
hsa-miR-1252-5p	-0.32	-0.38	N/A
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hsa-miR-1252-5p	-0.32	-0.35	N/A
hsa-miR-1252-5p	-0.32	-0.32	N/A
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hsa-miR-1252-5p	-0.32	-0.41	N/A
hsa-miR-1252-5p	-0.32	-0.36	N/A
hsa-miR-1252-5p	-0.32	-0.32	N/A
hsa-miR-1252-5p	-0.32	-0.32	N/A
hsa-miR-1252-5p	-0.31	-0.39	N/A
hsa-miR-1252-5p	-0.31	-0.32	N/A
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hsa-miR-1252-5p	-0.31	-0.54	N/A
hsa-miR-1252-5p	-0.31	-0.33	N/A
hsa-miR-1252-5p	-0.31	-0.31	N/A
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hsa-miR-1252-5p	-0.31	-0.31	N/A
hsa-miR-1252-5p	-0.31	-0.31	N/A
hsa-miR-1252-5p	-0.31	-0.39	N/A
hsa-miR-1252-5p	-0.31	-0.33	N/A
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hsa-miR-1252-5p	-0.31	-0.36	N/A
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hsa-miR-1252-5p	-0.31	-0.43	N/A
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hsa-miR-1252-5p	-0.3	-0.35	N/A
hsa-miR-1252-5p	-0.3	-0.3	N/A
hsa-miR-1252-5p	-0.3	-0.36	N/A
hsa-miR-1252-5p	-0.3	-0.41	N/A
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hsa-miR-1252-5p	-0.3	-0.45	N/A
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hsa-miR-1252-5p	-0.3	-0.33	N/A
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hsa-miR-1252-5p	-0.3	-0.49	N/A
hsa-miR-1252-5p	-0.3	-0.3	N/A
hsa-miR-1252-5p	-0.3	-0.35	N/A
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hsa-miR-1252-5p	-0.29	-0.37	N/A
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hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.57	N/A
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hsa-miR-1252-5p	-0.27	-0.43	N/A
hsa-miR-1252-5p	-0.27	-0.3	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.31	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.3	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.36	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.32	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.27	-0.31	N/A
hsa-miR-1252-5p	-0.27	-0.27	N/A
hsa-miR-1252-5p	-0.26	-0.32	N/A
hsa-miR-1252-5p	-0.26	-0.27	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.37	N/A
hsa-miR-1252-5p	-0.26	-0.27	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.42	N/A

hsa-miR-1252-5p	-0.26	-0.27	N/A
hsa-miR-1252-5p	-0.26	-0.4	N/A
hsa-miR-1252-5p	-0.26	-0.3	N/A
hsa-miR-1252-5p	-0.26	-0.37	N/A
hsa-miR-1252-5p	-0.26	-0.28	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.44	N/A
hsa-miR-1252-5p	-0.26	-0.28	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.3	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.27	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.34	N/A
hsa-miR-1252-5p	-0.26	-0.27	N/A
hsa-miR-1252-5p	-0.26	-0.38	N/A
hsa-miR-1252-5p	-0.26	-0.3	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.27	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.26	-0.26	N/A
hsa-miR-1252-5p	-0.25	-0.28	N/A
hsa-miR-1252-5p	-0.25	-0.28	N/A
hsa-miR-1252-5p	-0.25	-0.34	N/A
hsa-miR-1252-5p	-0.25	-0.32	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
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hsa-miR-1252-5p	-0.25	-0.26	N/A
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hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.36	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A

hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.31	N/A
hsa-miR-1252-5p	-0.25	-0.3	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
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hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.26	N/A
hsa-miR-1252-5p	-0.25	-0.76	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
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hsa-miR-1252-5p	-0.25	-0.3	N/A
hsa-miR-1252-5p	-0.25	-1.08	N/A
hsa-miR-1252-5p	-0.25	-0.27	N/A
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hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.3	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
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hsa-miR-1252-5p	-0.25	-0.25	N/A
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hsa-miR-1252-5p	-0.25	-0.33	N/A
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hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.4	N/A
hsa-miR-1252-5p	-0.25	-0.38	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
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hsa-miR-1252-5p	-0.25	-0.26	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
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hsa-miR-1252-5p	-0.25	-0.3	N/A
hsa-miR-1252-5p	-0.25	-0.3	N/A
hsa-miR-1252-5p	-0.25	-0.25	N/A
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hsa-miR-1252-5p	-0.24	-0.24	N/A
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hsa-miR-1252-5p	-0.24	-0.26	N/A
hsa-miR-1252-5p	-0.24	-0.25	N/A
hsa-miR-1252-5p	-0.24	-0.39	N/A
hsa-miR-1252-5p	-0.24	-0.25	N/A
hsa-miR-1252-5p	-0.24	-0.64	N/A
hsa-miR-1252-5p	-0.24	-0.24	N/A
hsa-miR-1252-5p	-0.24	-0.25	N/A
hsa-miR-1252-5p	-0.24	-0.28	N/A
hsa-miR-1252-5p	-0.24	-0.28	N/A
hsa-miR-1252-5p	-0.24	-0.27	N/A
hsa-miR-1252-5p	-0.24	-0.25	N/A
hsa-miR-1252-5p	-0.24	-0.24	N/A
hsa-miR-1252-5p	-0.24	-0.24	N/A
hsa-miR-1252-5p	-0.24	-0.24	N/A
hsa-miR-1252-5p	-0.24	-0.24	N/A
hsa-miR-1252-5p	-0.24	-0.36	N/A
hsa-miR-1252-5p	-0.24	-0.28	N/A
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hsa-miR-1252-5p	-0.24	-0.24	N/A
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hsa-miR-1252-5p	-0.24	-0.29	N/A
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hsa-miR-1252-5p	-0.24	-0.26	N/A
hsa-miR-1252-5p	-0.24	-0.56	N/A
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hsa-miR-1252-5p	-0.24	-0.35	N/A
hsa-miR-1252-5p	-0.24	-0.25	N/A
hsa-miR-1252-5p	-0.24	-0.71	N/A
hsa-miR-1252-5p	-0.24	-0.25	N/A
hsa-miR-1252-5p	-0.24	-0.25	N/A

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hsa-miR-1252-5p	-0.24	-0.44	N/A
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hsa-miR-1252-5p	-0.24	-0.24	N/A
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hsa-miR-1252-5p	-0.24	-0.29	N/A
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hsa-miR-1252-5p	-0.23	-0.26	N/A

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hsa-miR-1252-5p	-0.23	-0.23	N/A
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hsa-miR-1252-5p	-0.23	-0.36	N/A
hsa-miR-1252-5p	-0.23	-0.3	N/A
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hsa-miR-1252-5p	-0.23	-0.28	N/A
hsa-miR-1252-5p	-0.23	-0.58	N/A
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hsa-miR-1252-5p	-0.22	-0.31	N/A
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hsa-miR-1252-5p	-0.22	-0.22	N/A
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hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.41	N/A
hsa-miR-1252-5p	-0.22	-0.24	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.28	N/A
hsa-miR-1252-5p	-0.22	-0.36	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.23	N/A
hsa-miR-1252-5p	-0.22	-0.29	N/A
hsa-miR-1252-5p	-0.22	-0.33	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.29	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.35	N/A
hsa-miR-1252-5p	-0.22	-0.4	N/A
hsa-miR-1252-5p	-0.22	-0.23	N/A
hsa-miR-1252-5p	-0.22	-0.29	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.23	N/A
hsa-miR-1252-5p	-0.22	-0.23	N/A
hsa-miR-1252-5p	-0.22	-0.27	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.35	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.27	N/A
hsa-miR-1252-5p	-0.22	-0.23	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.29	N/A
hsa-miR-1252-5p	-0.22	-0.56	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A

hsa-miR-1252-5p	-0.22	-0.23	N/A
hsa-miR-1252-5p	-0.22	-0.23	N/A
hsa-miR-1252-5p	-0.22	-0.24	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.22	-0.52	N/A
hsa-miR-1252-5p	-0.22	-0.24	N/A
hsa-miR-1252-5p	-0.22	-0.22	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.24	N/A
hsa-miR-1252-5p	-0.21	-0.27	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.36	N/A
hsa-miR-1252-5p	-0.21	-0.31	N/A
hsa-miR-1252-5p	-0.21	-0.29	N/A
hsa-miR-1252-5p	-0.21	-0.24	N/A
hsa-miR-1252-5p	-0.21	-0.22	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.23	N/A
hsa-miR-1252-5p	-0.21	-0.22	N/A
hsa-miR-1252-5p	-0.21	-0.7	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.37	N/A
hsa-miR-1252-5p	-0.21	-0.23	N/A
hsa-miR-1252-5p	-0.21	-0.22	N/A
hsa-miR-1252-5p	-0.21	-0.31	N/A
hsa-miR-1252-5p	-0.21	-0.22	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A

hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.26	N/A
hsa-miR-1252-5p	-0.21	-0.45	N/A
hsa-miR-1252-5p	-0.21	-0.35	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.64	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.27	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.3	N/A
hsa-miR-1252-5p	-0.21	-0.31	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.22	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.51	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.27	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.29	N/A
hsa-miR-1252-5p	-0.21	-0.24	N/A
hsa-miR-1252-5p	-0.21	-0.36	N/A
hsa-miR-1252-5p	-0.21	-0.43	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.22	N/A
hsa-miR-1252-5p	-0.21	-0.28	N/A
hsa-miR-1252-5p	-0.21	-0.25	N/A
hsa-miR-1252-5p	-0.21	-0.23	N/A
hsa-miR-1252-5p	-0.21	-0.22	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
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hsa-miR-1252-5p	-0.21	-0.61	N/A
hsa-miR-1252-5p	-0.21	-0.3	N/A
hsa-miR-1252-5p	-0.21	-0.24	N/A

hsa-miR-1252-5p	-0.21	-0.25	N/A
hsa-miR-1252-5p	-0.21	-0.24	N/A
hsa-miR-1252-5p	-0.21	-0.29	N/A
hsa-miR-1252-5p	-0.21	-0.21	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.21	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.33	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
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hsa-miR-1252-5p	-0.2	-0.38	N/A
hsa-miR-1252-5p	-0.2	-0.21	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.24	N/A
hsa-miR-1252-5p	-0.2	-0.42	N/A
hsa-miR-1252-5p	-0.2	-0.54	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.47	N/A
hsa-miR-1252-5p	-0.2	-0.23	N/A
hsa-miR-1252-5p	-0.2	-0.23	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
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hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
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hsa-miR-1252-5p	-0.2	-0.2	N/A
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hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.22	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A

hsa-miR-1252-5p	-0.2	-0.21	N/A
hsa-miR-1252-5p	-0.2	-0.39	N/A
hsa-miR-1252-5p	-0.2	-0.21	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
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hsa-miR-1252-5p	-0.2	-0.21	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.28	N/A
hsa-miR-1252-5p	-0.2	-0.4	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.23	N/A
hsa-miR-1252-5p	-0.2	-0.3	N/A
hsa-miR-1252-5p	-0.2	-0.22	N/A
hsa-miR-1252-5p	-0.2	-0.24	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
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hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.21	N/A
hsa-miR-1252-5p	-0.2	-0.23	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.3	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.22	N/A
hsa-miR-1252-5p	-0.2	-0.3	N/A
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hsa-miR-1252-5p	-0.2	-0.25	N/A
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hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.37	N/A
hsa-miR-1252-5p	-0.2	-0.26	N/A
hsa-miR-1252-5p	-0.2	-0.49	N/A
hsa-miR-1252-5p	-0.2	-0.22	N/A
hsa-miR-1252-5p	-0.2	-0.46	N/A
hsa-miR-1252-5p	-0.2	-0.25	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A

hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
hsa-miR-1252-5p	-0.2	-0.2	N/A
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hsa-miR-1252-5p	-0.19	-0.2	N/A
hsa-miR-1252-5p	-0.19	-0.25	N/A
hsa-miR-1252-5p	-0.19	-0.21	N/A
hsa-miR-1252-5p	-0.19	-0.2	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.33	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.24	N/A
hsa-miR-1252-5p	-0.19	-0.41	N/A
hsa-miR-1252-5p	-0.19	-0.22	N/A
hsa-miR-1252-5p	-0.19	-0.21	N/A
hsa-miR-1252-5p	-0.19	-0.29	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
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hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.27	N/A
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hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.2	N/A
hsa-miR-1252-5p	-0.19	-0.25	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.22	N/A
hsa-miR-1252-5p	-0.19	-0.22	N/A
hsa-miR-1252-5p	-0.19	-0.24	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.2	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A

hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.45	N/A
hsa-miR-1252-5p	-0.19	-0.2	N/A
hsa-miR-1252-5p	-0.19	-0.26	N/A
hsa-miR-1252-5p	-0.19	-0.2	N/A
hsa-miR-1252-5p	-0.19	-0.49	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.23	N/A
hsa-miR-1252-5p	-0.19	-0.23	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.21	N/A
hsa-miR-1252-5p	-0.19	-0.2	N/A
hsa-miR-1252-5p	-0.19	-0.21	N/A
hsa-miR-1252-5p	-0.19	-0.22	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.22	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.23	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.21	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.19	-0.3	N/A
hsa-miR-1252-5p	-0.19	-0.44	N/A
hsa-miR-1252-5p	-0.19	-0.36	N/A
hsa-miR-1252-5p	-0.19	-0.24	N/A
hsa-miR-1252-5p	-0.19	-0.2	N/A
hsa-miR-1252-5p	-0.19	-0.19	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.22	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.31	N/A
hsa-miR-1252-5p	-0.18	-0.24	N/A
hsa-miR-1252-5p	-0.18	-0.3	N/A
hsa-miR-1252-5p	-0.18	-0.19	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A

hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.31	N/A
hsa-miR-1252-5p	-0.18	-0.43	N/A
hsa-miR-1252-5p	-0.18	-0.2	N/A
hsa-miR-1252-5p	-0.18	-0.25	N/A
hsa-miR-1252-5p	-0.18	-0.32	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.3	N/A
hsa-miR-1252-5p	-0.18	-0.36	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.45	N/A
hsa-miR-1252-5p	-0.18	-0.28	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.23	N/A
hsa-miR-1252-5p	-0.18	-0.19	N/A
hsa-miR-1252-5p	-0.18	-0.24	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.38	N/A
hsa-miR-1252-5p	-0.18	-0.21	N/A
hsa-miR-1252-5p	-0.18	-0.2	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.21	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.25	N/A
hsa-miR-1252-5p	-0.18	-0.2	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.21	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.2	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.2	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.54	N/A
hsa-miR-1252-5p	-0.18	-0.24	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A

hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.2	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.31	N/A
hsa-miR-1252-5p	-0.18	-0.37	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.21	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.28	N/A
hsa-miR-1252-5p	-0.18	-0.35	N/A
hsa-miR-1252-5p	-0.18	-0.51	N/A
hsa-miR-1252-5p	-0.18	-0.26	N/A
hsa-miR-1252-5p	-0.18	-0.18	N/A
hsa-miR-1252-5p	-0.18	-0.62	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.26	N/A
hsa-miR-1252-5p	-0.17	-0.21	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.18	N/A
hsa-miR-1252-5p	-0.17	-0.18	N/A
hsa-miR-1252-5p	-0.17	-0.36	N/A
hsa-miR-1252-5p	-0.17	-0.33	N/A
hsa-miR-1252-5p	-0.17	-0.19	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.52	N/A
hsa-miR-1252-5p	-0.17	-0.18	N/A
hsa-miR-1252-5p	-0.17	-0.19	N/A
hsa-miR-1252-5p	-0.17	-0.18	N/A
hsa-miR-1252-5p	-0.17	-0.27	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.21	N/A

hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.23	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.2	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.22	N/A
hsa-miR-1252-5p	-0.17	-0.19	N/A
hsa-miR-1252-5p	-0.17	-0.21	N/A
hsa-miR-1252-5p	-0.17	-0.3	N/A
hsa-miR-1252-5p	-0.17	-0.21	N/A
hsa-miR-1252-5p	-0.17	-0.22	N/A
hsa-miR-1252-5p	-0.17	-0.2	N/A
hsa-miR-1252-5p	-0.17	-0.2	N/A
hsa-miR-1252-5p	-0.17	-0.18	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.22	N/A
hsa-miR-1252-5p	-0.17	-0.43	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.61	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.37	N/A
hsa-miR-1252-5p	-0.17	-0.26	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.19	N/A
hsa-miR-1252-5p	-0.17	-0.19	N/A
hsa-miR-1252-5p	-0.17	-0.25	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.34	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.45	N/A
hsa-miR-1252-5p	-0.17	-0.18	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A

hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.25	N/A
hsa-miR-1252-5p	-0.17	-0.22	N/A
hsa-miR-1252-5p	-0.17	-0.34	N/A
hsa-miR-1252-5p	-0.17	-0.19	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.18	N/A
hsa-miR-1252-5p	-0.17	-0.19	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.34	N/A
hsa-miR-1252-5p	-0.17	-0.2	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.19	N/A
hsa-miR-1252-5p	-0.17	-0.3	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.2	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.2	N/A
hsa-miR-1252-5p	-0.17	-0.39	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.2	N/A
hsa-miR-1252-5p	-0.17	-0.23	N/A
hsa-miR-1252-5p	-0.17	-0.59	N/A
hsa-miR-1252-5p	-0.17	-0.18	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.17	-0.17	N/A
hsa-miR-1252-5p	-0.16	-0.17	N/A
hsa-miR-1252-5p	-0.16	-0.18	N/A
hsa-miR-1252-5p	-0.16	-0.18	N/A
hsa-miR-1252-5p	-0.16	-0.17	N/A
hsa-miR-1252-5p	-0.16	-0.27	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A

hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.26	N/A
hsa-miR-1252-5p	-0.16	-1.08	N/A
hsa-miR-1252-5p	-0.16	-0.27	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.17	N/A
hsa-miR-1252-5p	-0.16	-0.17	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.22	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.24	N/A
hsa-miR-1252-5p	-0.16	-0.27	N/A
hsa-miR-1252-5p	-0.16	-0.22	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.35	N/A
hsa-miR-1252-5p	-0.16	-0.18	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.17	N/A
hsa-miR-1252-5p	-0.16	-0.2	N/A
hsa-miR-1252-5p	-0.16	-0.2	N/A
hsa-miR-1252-5p	-0.16	-0.22	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.36	N/A
hsa-miR-1252-5p	-0.16	-0.22	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.18	N/A
hsa-miR-1252-5p	-0.16	-0.18	N/A
hsa-miR-1252-5p	-0.16	-0.22	N/A
hsa-miR-1252-5p	-0.16	-0.21	N/A
hsa-miR-1252-5p	-0.16	-0.25	N/A
hsa-miR-1252-5p	-0.16	-0.27	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.21	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A

hsa-miR-1252-5p	-0.16	-0.21	N/A
hsa-miR-1252-5p	-0.16	-0.47	N/A
hsa-miR-1252-5p	-0.16	-0.17	N/A
hsa-miR-1252-5p	-0.16	-0.17	N/A
hsa-miR-1252-5p	-0.16	-0.25	N/A
hsa-miR-1252-5p	-0.16	-0.21	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.2	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.21	N/A
hsa-miR-1252-5p	-0.16	-0.31	N/A
hsa-miR-1252-5p	-0.16	-0.18	N/A
hsa-miR-1252-5p	-0.16	-0.23	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.23	N/A
hsa-miR-1252-5p	-0.16	-0.18	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.31	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.25	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.31	N/A
hsa-miR-1252-5p	-0.16	-0.22	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.21	N/A
hsa-miR-1252-5p	-0.16	-0.24	N/A
hsa-miR-1252-5p	-0.16	-0.16	N/A
hsa-miR-1252-5p	-0.16	-0.17	N/A
hsa-miR-1252-5p	-0.16	-0.17	N/A
hsa-miR-1252-5p	-0.16	-0.17	N/A
hsa-miR-1252-5p	-0.16	-0.24	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A

hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.2	N/A
hsa-miR-1252-5p	-0.15	-0.16	N/A
hsa-miR-1252-5p	-0.15	-0.2	N/A
hsa-miR-1252-5p	-0.15	-0.17	N/A
hsa-miR-1252-5p	-0.15	-0.19	N/A
hsa-miR-1252-5p	-0.15	-0.17	N/A
hsa-miR-1252-5p	-0.15	-0.2	N/A
hsa-miR-1252-5p	-0.15	-0.66	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.16	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.19	N/A
hsa-miR-1252-5p	-0.15	-0.43	N/A
hsa-miR-1252-5p	-0.15	-0.29	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.26	N/A
hsa-miR-1252-5p	-0.15	-0.2	N/A
hsa-miR-1252-5p	-0.15	-0.25	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.3	N/A
hsa-miR-1252-5p	-0.15	-0.28	N/A
hsa-miR-1252-5p	-0.15	-0.17	N/A
hsa-miR-1252-5p	-0.15	-0.22	N/A
hsa-miR-1252-5p	-0.15	-0.16	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A

hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.16	N/A
hsa-miR-1252-5p	-0.15	-0.22	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.18	N/A
hsa-miR-1252-5p	-0.15	-0.19	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.18	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.22	N/A
hsa-miR-1252-5p	-0.15	-0.23	N/A
hsa-miR-1252-5p	-0.15	-0.16	N/A
hsa-miR-1252-5p	-0.15	-0.19	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.25	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.17	N/A
hsa-miR-1252-5p	-0.15	-0.2	N/A
hsa-miR-1252-5p	-0.15	-0.25	N/A
hsa-miR-1252-5p	-0.15	-0.18	N/A
hsa-miR-1252-5p	-0.15	-0.19	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.16	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.18	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.18	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.17	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.29	N/A

hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.2	N/A
hsa-miR-1252-5p	-0.15	-0.66	N/A
hsa-miR-1252-5p	-0.15	-0.19	N/A
hsa-miR-1252-5p	-0.15	-0.18	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.26	N/A
hsa-miR-1252-5p	-0.15	-0.28	N/A
hsa-miR-1252-5p	-0.15	-0.25	N/A
hsa-miR-1252-5p	-0.15	-0.17	N/A
hsa-miR-1252-5p	-0.15	-0.29	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.17	N/A
hsa-miR-1252-5p	-0.15	-0.48	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.22	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.16	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.17	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.15	N/A
hsa-miR-1252-5p	-0.15	-0.33	N/A
hsa-miR-1252-5p	-0.15	-0.18	N/A
hsa-miR-1252-5p	-0.15	-0.28	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.33	N/A
hsa-miR-1252-5p	-0.14	-0.16	N/A
hsa-miR-1252-5p	-0.14	-0.16	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A

hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
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hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.16	N/A
hsa-miR-1252-5p	-0.14	-0.24	N/A
hsa-miR-1252-5p	-0.14	-0.16	N/A
hsa-miR-1252-5p	-0.14	-0.22	N/A
hsa-miR-1252-5p	-0.14	-0.2	N/A
hsa-miR-1252-5p	-0.14	-0.16	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.18	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.39	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.25	N/A
hsa-miR-1252-5p	-0.14	-0.17	N/A
hsa-miR-1252-5p	-0.14	-0.23	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
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hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.18	N/A
hsa-miR-1252-5p	-0.14	-0.34	N/A
hsa-miR-1252-5p	-0.14	-0.33	N/A
hsa-miR-1252-5p	-0.14	-0.18	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.31	N/A
hsa-miR-1252-5p	-0.14	-0.21	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.25	N/A
hsa-miR-1252-5p	-0.14	-0.16	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.24	N/A
hsa-miR-1252-5p	-0.14	-0.43	N/A
hsa-miR-1252-5p	-0.14	-0.19	N/A

hsa-miR-1252-5p	-0.14	-0.18	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.18	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.22	N/A
hsa-miR-1252-5p	-0.14	-0.22	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.2	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.37	N/A
hsa-miR-1252-5p	-0.14	-0.2	N/A
hsa-miR-1252-5p	-0.14	-0.56	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.23	N/A
hsa-miR-1252-5p	-0.14	-0.3	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.34	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.46	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.19	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.28	N/A
hsa-miR-1252-5p	-0.14	-0.18	N/A
hsa-miR-1252-5p	-0.14	-0.17	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A

hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.17	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.17	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.19	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.17	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.25	N/A
hsa-miR-1252-5p	-0.14	-0.18	N/A
hsa-miR-1252-5p	-0.14	-0.16	N/A
hsa-miR-1252-5p	-0.14	-0.21	N/A
hsa-miR-1252-5p	-0.14	-0.21	N/A
hsa-miR-1252-5p	-0.14	-0.42	N/A
hsa-miR-1252-5p	-0.14	-0.41	N/A
hsa-miR-1252-5p	-0.14	-0.25	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.42	N/A
hsa-miR-1252-5p	-0.14	-0.15	N/A
hsa-miR-1252-5p	-0.14	-0.19	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A

hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.4	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.14	-0.14	N/A
hsa-miR-1252-5p	-0.13	-0.14	N/A
hsa-miR-1252-5p	-0.13	-0.26	N/A
hsa-miR-1252-5p	-0.13	-0.16	N/A
hsa-miR-1252-5p	-0.13	-0.52	N/A
hsa-miR-1252-5p	-0.13	-0.15	N/A
hsa-miR-1252-5p	-0.13	-0.28	N/A
hsa-miR-1252-5p	-0.13	-0.33	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.14	N/A
hsa-miR-1252-5p	-0.13	-0.37	N/A
hsa-miR-1252-5p	-0.13	-0.14	N/A
hsa-miR-1252-5p	-0.13	-0.34	N/A
hsa-miR-1252-5p	-0.13	-0.17	N/A
hsa-miR-1252-5p	-0.13	-0.17	N/A
hsa-miR-1252-5p	-0.13	-0.18	N/A
hsa-miR-1252-5p	-0.13	-0.34	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
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hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.14	N/A
hsa-miR-1252-5p	-0.13	-0.4	N/A
hsa-miR-1252-5p	-0.13	-0.53	N/A
hsa-miR-1252-5p	-0.13	-0.14	N/A
hsa-miR-1252-5p	-0.13	-0.14	N/A
hsa-miR-1252-5p	-0.13	-0.16	N/A
hsa-miR-1252-5p	-0.13	-0.31	N/A
hsa-miR-1252-5p	-0.13	-0.23	N/A
hsa-miR-1252-5p	-0.13	-0.15	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.15	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A

hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.3	N/A
hsa-miR-1252-5p	-0.13	-0.34	N/A
hsa-miR-1252-5p	-0.13	-0.19	N/A
hsa-miR-1252-5p	-0.13	-0.14	N/A
hsa-miR-1252-5p	-0.13	-0.15	N/A
hsa-miR-1252-5p	-0.13	-0.17	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.33	N/A
hsa-miR-1252-5p	-0.13	-0.27	N/A
hsa-miR-1252-5p	-0.13	-0.17	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.17	N/A
hsa-miR-1252-5p	-0.13	-0.16	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
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hsa-miR-1252-5p	-0.13	-0.2	N/A
hsa-miR-1252-5p	-0.13	-0.16	N/A
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hsa-miR-1252-5p	-0.13	-0.21	N/A
hsa-miR-1252-5p	-0.13	-0.19	N/A
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hsa-miR-1252-5p	-0.13	-0.13	N/A
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hsa-miR-1252-5p	-0.13	-0.21	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.17	N/A
hsa-miR-1252-5p	-0.13	-0.31	N/A
hsa-miR-1252-5p	-0.13	-0.16	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A

hsa-miR-1252-5p	-0.13	-0.13	N/A
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hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.21	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.24	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.23	N/A
hsa-miR-1252-5p	-0.13	-0.2	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
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hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.24	N/A
hsa-miR-1252-5p	-0.13	-0.14	N/A
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hsa-miR-1252-5p	-0.13	-0.13	N/A
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hsa-miR-1252-5p	-0.13	-0.13	N/A
hsa-miR-1252-5p	-0.13	-0.16	N/A
hsa-miR-1252-5p	-0.13	-0.13	N/A
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hsa-miR-1252-5p	-0.13	-0.33	N/A
hsa-miR-1252-5p	-0.13	-0.44	N/A
hsa-miR-1252-5p	-0.13	-0.18	N/A
hsa-miR-1252-5p	-0.13	-0.49	N/A
hsa-miR-1252-5p	-0.13	-0.16	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
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hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.13	N/A
hsa-miR-1252-5p	-0.12	-0.31	N/A
hsa-miR-1252-5p	-0.12	-0.3	N/A

hsa-miR-1252-5p	-0.12	-0.15	N/A
hsa-miR-1252-5p	-0.12	-0.21	N/A
hsa-miR-1252-5p	-0.12	-0.69	N/A
hsa-miR-1252-5p	-0.12	-0.15	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
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hsa-miR-1252-5p	-0.12	-0.23	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
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hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.16	N/A
hsa-miR-1252-5p	-0.12	-0.25	N/A
hsa-miR-1252-5p	-0.12	-0.66	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.56	N/A
hsa-miR-1252-5p	-0.12	-0.13	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.13	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
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hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.13	N/A
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hsa-miR-1252-5p	-0.12	-0.26	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
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hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.13	N/A
hsa-miR-1252-5p	-0.12	-0.16	N/A
hsa-miR-1252-5p	-0.12	-0.15	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.13	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
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hsa-miR-1252-5p	-0.12	-0.12	N/A
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hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.19	N/A
hsa-miR-1252-5p	-0.12	-0.3	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.68	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.18	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.31	N/A
hsa-miR-1252-5p	-0.12	-0.37	N/A
hsa-miR-1252-5p	-0.12	-0.13	N/A
hsa-miR-1252-5p	-0.12	-0.15	N/A
hsa-miR-1252-5p	-0.12	-0.21	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.21	N/A
hsa-miR-1252-5p	-0.12	-0.17	N/A
hsa-miR-1252-5p	-0.12	-0.16	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.13	N/A
hsa-miR-1252-5p	-0.12	-0.18	N/A
hsa-miR-1252-5p	-0.12	-0.18	N/A
hsa-miR-1252-5p	-0.12	-0.29	N/A
hsa-miR-1252-5p	-0.12	-0.18	N/A
hsa-miR-1252-5p	-0.12	-0.23	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A

hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.15	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.17	N/A
hsa-miR-1252-5p	-0.12	-0.16	N/A
hsa-miR-1252-5p	-0.12	-0.13	N/A
hsa-miR-1252-5p	-0.12	-0.22	N/A
hsa-miR-1252-5p	-0.12	-0.19	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.22	N/A
hsa-miR-1252-5p	-0.12	-0.53	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.15	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.17	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.17	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.14	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.25	N/A
hsa-miR-1252-5p	-0.12	-0.13	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.12	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.27	N/A
hsa-miR-1252-5p	-0.11	-0.24	N/A
hsa-miR-1252-5p	-0.11	-0.22	N/A
hsa-miR-1252-5p	-0.11	-0.19	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.43	N/A

hsa-miR-1252-5p	-0.11	-0.18	N/A
hsa-miR-1252-5p	-0.11	-0.13	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.22	N/A
hsa-miR-1252-5p	-0.11	-0.22	N/A
hsa-miR-1252-5p	-0.11	-0.27	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.2	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.14	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.19	N/A
hsa-miR-1252-5p	-0.11	-0.18	N/A
hsa-miR-1252-5p	-0.11	-0.27	N/A
hsa-miR-1252-5p	-0.11	-0.52	N/A
hsa-miR-1252-5p	-0.11	-0.17	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.17	N/A
hsa-miR-1252-5p	-0.11	-0.13	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.2	N/A
hsa-miR-1252-5p	-0.11	-0.17	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.16	N/A
hsa-miR-1252-5p	-0.11	-0.3	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.17	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.49	N/A
hsa-miR-1252-5p	-0.11	-0.2	N/A
hsa-miR-1252-5p	-0.11	-0.4	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A

hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.13	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.13	N/A
hsa-miR-1252-5p	-0.11	-0.3	N/A
hsa-miR-1252-5p	-0.11	-0.18	N/A
hsa-miR-1252-5p	-0.11	-0.22	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.14	N/A
hsa-miR-1252-5p	-0.11	-0.13	N/A
hsa-miR-1252-5p	-0.11	-0.16	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.2	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.23	N/A
hsa-miR-1252-5p	-0.11	-0.18	N/A
hsa-miR-1252-5p	-0.11	-0.14	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.13	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.14	N/A
hsa-miR-1252-5p	-0.11	-0.21	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.23	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.22	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.13	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
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hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.16	N/A
hsa-miR-1252-5p	-0.11	-0.19	N/A
hsa-miR-1252-5p	-0.11	-0.2	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A

hsa-miR-1252-5p	-0.11	-0.16	N/A
hsa-miR-1252-5p	-0.11	-0.17	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
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hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.23	N/A
hsa-miR-1252-5p	-0.11	-0.19	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.14	N/A
hsa-miR-1252-5p	-0.11	-0.15	N/A
hsa-miR-1252-5p	-0.11	-0.14	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.15	N/A
hsa-miR-1252-5p	-0.11	-0.33	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.18	N/A
hsa-miR-1252-5p	-0.11	-0.15	N/A
hsa-miR-1252-5p	-0.11	-0.16	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.13	N/A
hsa-miR-1252-5p	-0.11	-0.14	N/A
hsa-miR-1252-5p	-0.11	-0.14	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.11	-0.14	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.23	N/A
hsa-miR-1252-5p	-0.11	-0.21	N/A

hsa-miR-1252-5p	-0.11	-0.16	N/A
hsa-miR-1252-5p	-0.11	-0.12	N/A
hsa-miR-1252-5p	-0.11	-0.11	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.21	N/A
hsa-miR-1252-5p	-0.1	-0.14	N/A
hsa-miR-1252-5p	-0.1	-0.15	N/A
hsa-miR-1252-5p	-0.1	-0.15	N/A
hsa-miR-1252-5p	-0.1	-0.15	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.15	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.27	N/A
hsa-miR-1252-5p	-0.1	-0.15	N/A
hsa-miR-1252-5p	-0.1	-0.11	N/A
hsa-miR-1252-5p	-0.1	-0.32	N/A
hsa-miR-1252-5p	-0.1	-0.15	N/A
hsa-miR-1252-5p	-0.1	-0.11	N/A
hsa-miR-1252-5p	-0.1	-0.26	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.14	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.14	N/A
hsa-miR-1252-5p	-0.1	-0.4	N/A
hsa-miR-1252-5p	-0.1	-0.11	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.23	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A

hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.22	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.41	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.18	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.22	N/A
hsa-miR-1252-5p	-0.1	-0.11	N/A
hsa-miR-1252-5p	-0.1	-0.11	N/A
hsa-miR-1252-5p	-0.1	-0.26	N/A
hsa-miR-1252-5p	-0.1	-0.23	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.22	N/A
hsa-miR-1252-5p	-0.1	-0.11	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.25	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.2	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.13	N/A
hsa-miR-1252-5p	-0.1	-0.11	N/A
hsa-miR-1252-5p	-0.1	-0.13	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.35	N/A
hsa-miR-1252-5p	-0.1	-0.24	N/A
hsa-miR-1252-5p	-0.1	-0.13	N/A
hsa-miR-1252-5p	-0.1	-0.15	N/A
hsa-miR-1252-5p	-0.1	-0.11	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A

hsa-miR-1252-5p	-0.1	-0.14	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.13	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.18	N/A
hsa-miR-1252-5p	-0.1	-0.53	N/A
hsa-miR-1252-5p	-0.1	-0.2	N/A
hsa-miR-1252-5p	-0.1	-0.3	N/A
hsa-miR-1252-5p	-0.1	-0.16	N/A
hsa-miR-1252-5p	-0.1	-0.26	N/A
hsa-miR-1252-5p	-0.1	-0.13	N/A
hsa-miR-1252-5p	-0.1	-0.11	N/A
hsa-miR-1252-5p	-0.1	-0.13	N/A
hsa-miR-1252-5p	-0.1	-0.18	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.13	N/A
hsa-miR-1252-5p	-0.1	-0.35	N/A
hsa-miR-1252-5p	-0.1	-0.2	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.22	N/A
hsa-miR-1252-5p	-0.1	-0.17	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.16	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.16	N/A

hsa-miR-1252-5p	-0.1	-0.14	N/A
hsa-miR-1252-5p	-0.1	-0.15	N/A
hsa-miR-1252-5p	-0.1	-0.39	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.29	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.28	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.28	N/A
hsa-miR-1252-5p	-0.1	-0.15	N/A
hsa-miR-1252-5p	-0.1	-0.22	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.12	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.1	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.35	N/A
hsa-miR-1252-5p	-0.09	-0.14	N/A
hsa-miR-1252-5p	-0.09	-0.11	N/A
hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.17	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.22	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.2	N/A
hsa-miR-1252-5p	-0.09	-0.15	N/A
hsa-miR-1252-5p	-0.09	-0.17	N/A
hsa-miR-1252-5p	-0.09	-0.67	N/A
hsa-miR-1252-5p	-0.09	-0.18	N/A
hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A

hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.38	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.11	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.35	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.13	N/A
hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.22	N/A
hsa-miR-1252-5p	-0.09	-0.15	N/A
hsa-miR-1252-5p	-0.09	-0.11	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.3	N/A
hsa-miR-1252-5p	-0.09	-0.11	N/A
hsa-miR-1252-5p	-0.09	-0.15	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.11	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.22	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.15	N/A
hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.15	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.15	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.18	N/A

hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.27	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.26	N/A
hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.12	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.17	N/A
hsa-miR-1252-5p	-0.09	-0.2	N/A
hsa-miR-1252-5p	-0.09	-0.11	N/A
hsa-miR-1252-5p	-0.09	-0.43	N/A
hsa-miR-1252-5p	-0.09	-0.2	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.14	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.13	N/A
hsa-miR-1252-5p	-0.09	-0.11	N/A
hsa-miR-1252-5p	-0.09	-0.11	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.2	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.22	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.11	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.22	N/A
hsa-miR-1252-5p	-0.09	-0.11	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.22	N/A
hsa-miR-1252-5p	-0.09	-0.29	N/A
hsa-miR-1252-5p	-0.09	-0.3	N/A
hsa-miR-1252-5p	-0.09	-0.14	N/A

hsa-miR-1252-5p	-0.09	-0.13	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.1	N/A
hsa-miR-1252-5p	-0.09	-0.16	N/A
hsa-miR-1252-5p	-0.09	-0.14	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.09	N/A
hsa-miR-1252-5p	-0.09	-0.21	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.1	N/A
hsa-miR-1252-5p	-0.08	-0.11	N/A
hsa-miR-1252-5p	-0.08	-0.19	N/A
hsa-miR-1252-5p	-0.08	-0.23	N/A
hsa-miR-1252-5p	-0.08	-0.12	N/A
hsa-miR-1252-5p	-0.08	-0.29	N/A
hsa-miR-1252-5p	-0.08	-0.17	N/A
hsa-miR-1252-5p	-0.08	-0.1	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.16	N/A
hsa-miR-1252-5p	-0.08	-0.14	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.12	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.13	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.18	N/A
hsa-miR-1252-5p	-0.08	-0.12	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.28	N/A
hsa-miR-1252-5p	-0.08	-0.13	N/A
hsa-miR-1252-5p	-0.08	-0.15	N/A

hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.45	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.1	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.2	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.41	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.18	N/A
hsa-miR-1252-5p	-0.08	-0.32	N/A
hsa-miR-1252-5p	-0.08	-0.12	N/A
hsa-miR-1252-5p	-0.08	-0.26	N/A
hsa-miR-1252-5p	-0.08	-0.2	N/A
hsa-miR-1252-5p	-0.08	-0.25	N/A
hsa-miR-1252-5p	-0.08	-0.19	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.11	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.12	N/A
hsa-miR-1252-5p	-0.08	-0.27	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.21	N/A
hsa-miR-1252-5p	-0.08	-0.42	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.2	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.14	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.22	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.13	N/A

hsa-miR-1252-5p	-0.08	-0.62	N/A
hsa-miR-1252-5p	-0.08	-0.12	N/A
hsa-miR-1252-5p	-0.08	-0.11	N/A
hsa-miR-1252-5p	-0.08	-0.17	N/A
hsa-miR-1252-5p	-0.08	-0.14	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.27	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.15	N/A
hsa-miR-1252-5p	-0.08	-0.2	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.12	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.11	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.13	N/A
hsa-miR-1252-5p	-0.08	-0.12	N/A
hsa-miR-1252-5p	-0.08	-0.38	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.13	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.14	N/A
hsa-miR-1252-5p	-0.08	-0.25	N/A
hsa-miR-1252-5p	-0.08	-0.18	N/A
hsa-miR-1252-5p	-0.08	-0.14	N/A
hsa-miR-1252-5p	-0.08	-0.23	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.11	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.12	N/A

hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.11	N/A
hsa-miR-1252-5p	-0.08	-0.18	N/A
hsa-miR-1252-5p	-0.08	-0.14	N/A
hsa-miR-1252-5p	-0.08	-0.15	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.24	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.42	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.14	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.12	N/A
hsa-miR-1252-5p	-0.08	-0.14	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.29	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.15	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.2	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.29	N/A
hsa-miR-1252-5p	-0.08	-0.1	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.24	N/A
hsa-miR-1252-5p	-0.08	-0.2	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.08	-0.16	N/A
hsa-miR-1252-5p	-0.08	-0.1	N/A
hsa-miR-1252-5p	-0.08	-0.09	N/A
hsa-miR-1252-5p	-0.08	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.16	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.13	N/A

hsa-miR-1252-5p	-0.07	-0.4	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.18	N/A
hsa-miR-1252-5p	-0.07	-0.09	N/A
hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.21	N/A
hsa-miR-1252-5p	-0.07	-0.09	N/A
hsa-miR-1252-5p	-0.07	-0.19	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.21	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.3	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.11	N/A
hsa-miR-1252-5p	-0.07	-0.23	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.17	N/A
hsa-miR-1252-5p	-0.07	-0.11	N/A
hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.17	N/A
hsa-miR-1252-5p	-0.07	-0.22	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.14	N/A
hsa-miR-1252-5p	-0.07	-0.12	N/A
hsa-miR-1252-5p	-0.07	-0.13	N/A
hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-1.03	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.11	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.15	N/A
hsa-miR-1252-5p	-0.07	-0.09	N/A
hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.71	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.33	N/A
hsa-miR-1252-5p	-0.07	-0.15	N/A
hsa-miR-1252-5p	-0.07	-0.2	N/A
hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.11	N/A

hsa-miR-1252-5p	-0.07	-0.31	N/A
hsa-miR-1252-5p	-0.07	-0.13	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.25	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.13	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.2	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.12	N/A
hsa-miR-1252-5p	-0.07	-0.13	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.17	N/A
hsa-miR-1252-5p	-0.07	-0.17	N/A
hsa-miR-1252-5p	-0.07	-0.19	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
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hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.15	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.17	N/A
hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A

hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.09	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.09	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.21	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.09	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.77	N/A
hsa-miR-1252-5p	-0.07	-0.13	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.08	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.41	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.14	N/A
hsa-miR-1252-5p	-0.07	-0.12	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.12	N/A
hsa-miR-1252-5p	-0.07	-0.14	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.15	N/A
hsa-miR-1252-5p	-0.07	-0.14	N/A
hsa-miR-1252-5p	-0.07	-0.42	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.36	N/A
hsa-miR-1252-5p	-0.07	-0.43	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.16	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A

hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.13	N/A
hsa-miR-1252-5p	-0.07	-0.14	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.51	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.09	N/A
hsa-miR-1252-5p	-0.07	-0.17	N/A
hsa-miR-1252-5p	-0.07	-0.14	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.29	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.1	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.07	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.26	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.31	N/A
hsa-miR-1252-5p	-0.06	-0.09	N/A
hsa-miR-1252-5p	-0.06	-0.13	N/A
hsa-miR-1252-5p	-0.06	-0.08	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.09	N/A
hsa-miR-1252-5p	-0.06	-0.31	N/A
hsa-miR-1252-5p	-0.06	-0.08	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.08	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A

hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
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hsa-miR-1252-5p	-0.06	-0.06	N/A
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hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.12	N/A
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hsa-miR-1252-5p	-0.06	-0.38	N/A
hsa-miR-1252-5p	-0.06	-0.08	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.24	N/A
hsa-miR-1252-5p	-0.06	-0.23	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
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hsa-miR-1252-5p	-0.06	-0.17	N/A
hsa-miR-1252-5p	-0.06	-0.25	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
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hsa-miR-1252-5p	-0.06	-0.08	N/A
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hsa-miR-1252-5p	-0.06	-0.17	N/A
hsa-miR-1252-5p	-0.06	-0.27	N/A
hsa-miR-1252-5p	-0.06	-0.09	N/A
hsa-miR-1252-5p	-0.06	-0.17	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.11	N/A
hsa-miR-1252-5p	-0.06	-0.18	N/A
hsa-miR-1252-5p	-0.06	-0.12	N/A
hsa-miR-1252-5p	-0.06	-0.36	N/A
hsa-miR-1252-5p	-0.06	-0.16	N/A
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hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.09	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A

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hsa-miR-1252-5p	-0.06	-0.09	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.16	N/A
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hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.25	N/A
hsa-miR-1252-5p	-0.06	-0.1	N/A
hsa-miR-1252-5p	-0.06	-0.18	N/A
hsa-miR-1252-5p	-0.06	-0.25	N/A
hsa-miR-1252-5p	-0.06	-0.36	N/A
hsa-miR-1252-5p	-0.06	-0.12	N/A
hsa-miR-1252-5p	-0.06	-0.13	N/A
hsa-miR-1252-5p	-0.06	-0.08	N/A
hsa-miR-1252-5p	-0.06	-0.17	N/A
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hsa-miR-1252-5p	-0.06	-0.15	N/A
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hsa-miR-1252-5p	-0.06	-0.21	N/A
hsa-miR-1252-5p	-0.06	-0.16	N/A
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hsa-miR-1252-5p	-0.06	-0.17	N/A
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hsa-miR-1252-5p	-0.06	-0.34	N/A
hsa-miR-1252-5p	-0.06	-0.09	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
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hsa-miR-1252-5p	-0.06	-0.17	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
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hsa-miR-1252-5p	-0.06	-0.06	N/A
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hsa-miR-1252-5p	-0.06	-0.21	N/A
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hsa-miR-1252-5p	-0.06	-0.2	N/A
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hsa-miR-1252-5p	-0.06	-0.08	N/A
hsa-miR-1252-5p	-0.06	-0.13	N/A
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hsa-miR-1252-5p	-0.06	-0.18	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
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hsa-miR-1252-5p	-0.06	-0.29	N/A
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hsa-miR-1252-5p	-0.06	-0.23	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.1	N/A

hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.29	N/A
hsa-miR-1252-5p	-0.06	-0.21	N/A
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hsa-miR-1252-5p	-0.06	-0.19	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
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hsa-miR-1252-5p	-0.06	-0.46	N/A
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hsa-miR-1252-5p	-0.06	-0.09	N/A
hsa-miR-1252-5p	-0.06	-0.31	N/A
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hsa-miR-1252-5p	-0.06	-0.12	N/A
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hsa-miR-1252-5p	-0.06	-0.06	N/A
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hsa-miR-1252-5p	-0.06	-0.07	N/A
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hsa-miR-1252-5p	-0.06	-0.56	N/A
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hsa-miR-1252-5p	-0.06	-0.14	N/A
hsa-miR-1252-5p	-0.06	-0.15	N/A
hsa-miR-1252-5p	-0.06	-0.09	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
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hsa-miR-1252-5p	-0.06	-0.23	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.07	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.15	N/A
hsa-miR-1252-5p	-0.06	-0.36	N/A
hsa-miR-1252-5p	-0.06	-0.06	N/A
hsa-miR-1252-5p	-0.06	-0.11	N/A

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hsa-miR-1252-5p	-0.05	-0.11	N/A
hsa-miR-1252-5p	-0.05	-0.2	N/A
hsa-miR-1252-5p	-0.05	-0.19	N/A
hsa-miR-1252-5p	-0.05	-0.11	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.16	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.32	N/A
hsa-miR-1252-5p	-0.05	-0.17	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.13	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.08	N/A
hsa-miR-1252-5p	-0.05	-0.14	N/A
hsa-miR-1252-5p	-0.05	-0.67	N/A
hsa-miR-1252-5p	-0.05	-0.32	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.1	N/A
hsa-miR-1252-5p	-0.05	-0.35	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.27	N/A
hsa-miR-1252-5p	-0.05	-0.17	N/A
hsa-miR-1252-5p	-0.05	-0.2	N/A
hsa-miR-1252-5p	-0.05	-0.12	N/A
hsa-miR-1252-5p	-0.05	-0.09	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.09	N/A
hsa-miR-1252-5p	-0.05	-0.14	N/A
hsa-miR-1252-5p	-0.05	-0.18	N/A
hsa-miR-1252-5p	-0.05	-0.34	N/A
hsa-miR-1252-5p	-0.05	-0.12	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A

hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.17	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.24	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.2	N/A
hsa-miR-1252-5p	-0.05	-0.16	N/A
hsa-miR-1252-5p	-0.05	-0.31	N/A
hsa-miR-1252-5p	-0.05	-0.1	N/A
hsa-miR-1252-5p	-0.05	-0.22	N/A
hsa-miR-1252-5p	-0.05	-0.1	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.23	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.24	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.18	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.21	N/A
hsa-miR-1252-5p	-0.05	-0.21	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.13	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.54	N/A
hsa-miR-1252-5p	-0.05	-0.08	N/A
hsa-miR-1252-5p	-0.05	-0.18	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.25	N/A
hsa-miR-1252-5p	-0.05	-0.22	N/A
hsa-miR-1252-5p	-0.05	-0.15	N/A
hsa-miR-1252-5p	-0.05	-0.09	N/A
hsa-miR-1252-5p	-0.05	-0.11	N/A
hsa-miR-1252-5p	-0.05	-0.17	N/A
hsa-miR-1252-5p	-0.05	-0.23	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A

hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.21	N/A
hsa-miR-1252-5p	-0.05	-0.28	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.14	N/A
hsa-miR-1252-5p	-0.05	-0.15	N/A
hsa-miR-1252-5p	-0.05	-0.21	N/A
hsa-miR-1252-5p	-0.05	-0.12	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.17	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.25	N/A
hsa-miR-1252-5p	-0.05	-0.24	N/A
hsa-miR-1252-5p	-0.05	-0.09	N/A
hsa-miR-1252-5p	-0.05	-0.11	N/A
hsa-miR-1252-5p	-0.05	-0.1	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.38	N/A
hsa-miR-1252-5p	-0.05	-0.1	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.18	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.12	N/A
hsa-miR-1252-5p	-0.05	-0.14	N/A

hsa-miR-1252-5p	-0.05	-0.95	N/A
hsa-miR-1252-5p	-0.05	-0.1	N/A
hsa-miR-1252-5p	-0.05	-0.34	N/A
hsa-miR-1252-5p	-0.05	-0.14	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.09	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.09	N/A
hsa-miR-1252-5p	-0.05	-0.31	N/A
hsa-miR-1252-5p	-0.05	-0.13	N/A
hsa-miR-1252-5p	-0.05	-0.08	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.2	N/A
hsa-miR-1252-5p	-0.05	-0.14	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.08	N/A
hsa-miR-1252-5p	-0.05	-0.12	N/A
hsa-miR-1252-5p	-0.05	-0.27	N/A
hsa-miR-1252-5p	-0.05	-0.13	N/A
hsa-miR-1252-5p	-0.05	-0.13	N/A
hsa-miR-1252-5p	-0.05	-0.17	N/A
hsa-miR-1252-5p	-0.05	-0.08	N/A
hsa-miR-1252-5p	-0.05	-0.36	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
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hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.19	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.12	N/A
hsa-miR-1252-5p	-0.05	-0.1	N/A
hsa-miR-1252-5p	-0.05	-0.06	N/A
hsa-miR-1252-5p	-0.05	-0.12	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.07	N/A
hsa-miR-1252-5p	-0.05	-0.22	N/A
hsa-miR-1252-5p	-0.05	-0.09	N/A

hsa-miR-1252-5p	-0.05	-0.09	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.27	N/A
hsa-miR-1252-5p	-0.05	-0.05	N/A
hsa-miR-1252-5p	-0.05	-0.13	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.35	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.24	N/A
hsa-miR-1252-5p	-0.04	-0.24	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.14	N/A
hsa-miR-1252-5p	-0.04	-0.09	N/A
hsa-miR-1252-5p	-0.04	-0.13	N/A
hsa-miR-1252-5p	-0.04	-0.19	N/A
hsa-miR-1252-5p	-0.04	-0.42	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.1	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.17	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.08	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.1	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.29	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.16	N/A
hsa-miR-1252-5p	-0.04	-0.08	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.15	N/A
hsa-miR-1252-5p	-0.04	-0.12	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.14	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.07	N/A

hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.14	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
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hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.17	N/A
hsa-miR-1252-5p	-0.04	-0.15	N/A
hsa-miR-1252-5p	-0.04	-0.21	N/A
hsa-miR-1252-5p	-0.04	-0.27	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.2	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.09	N/A
hsa-miR-1252-5p	-0.04	-0.17	N/A
hsa-miR-1252-5p	-0.04	-0.1	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
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hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.36	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.47	N/A
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hsa-miR-1252-5p	-0.04	-0.2	N/A
hsa-miR-1252-5p	-0.04	-0.35	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.44	N/A
hsa-miR-1252-5p	-0.04	-0.13	N/A
hsa-miR-1252-5p	-0.04	-0.55	N/A
hsa-miR-1252-5p	-0.04	-0.2	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.3	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
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hsa-miR-1252-5p	-0.04	-0.26	N/A
hsa-miR-1252-5p	-0.04	-0.08	N/A
hsa-miR-1252-5p	-0.04	-0.08	N/A
hsa-miR-1252-5p	-0.04	-0.15	N/A
hsa-miR-1252-5p	-0.04	-0.13	N/A
hsa-miR-1252-5p	-0.04	-0.1	N/A
hsa-miR-1252-5p	-0.04	-0.07	N/A
hsa-miR-1252-5p	-0.04	-0.19	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A

hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.18	N/A
hsa-miR-1252-5p	-0.04	-0.16	N/A
hsa-miR-1252-5p	-0.04	-0.3	N/A
hsa-miR-1252-5p	-0.04	-0.13	N/A
hsa-miR-1252-5p	-0.04	-0.07	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
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hsa-miR-1252-5p	-0.04	-0.11	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.17	N/A
hsa-miR-1252-5p	-0.04	-0.28	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
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hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.19	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.08	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.1	N/A
hsa-miR-1252-5p	-0.04	-0.5	N/A
hsa-miR-1252-5p	-0.04	-0.47	N/A
hsa-miR-1252-5p	-0.04	-0.16	N/A
hsa-miR-1252-5p	-0.04	-0.17	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.14	N/A
hsa-miR-1252-5p	-0.04	-0.38	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.18	N/A

hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.23	N/A
hsa-miR-1252-5p	-0.04	-0.31	N/A
hsa-miR-1252-5p	-0.04	-0.18	N/A
hsa-miR-1252-5p	-0.04	-0.23	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.09	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.27	N/A
hsa-miR-1252-5p	-0.04	-0.2	N/A
hsa-miR-1252-5p	-0.04	-0.29	N/A
hsa-miR-1252-5p	-0.04	-0.1	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.11	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.14	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.11	N/A
hsa-miR-1252-5p	-0.04	-0.12	N/A
hsa-miR-1252-5p	-0.04	-0.09	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.23	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.19	N/A
hsa-miR-1252-5p	-0.04	-0.4	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.18	N/A
hsa-miR-1252-5p	-0.04	-0.1	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.12	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.2	N/A
hsa-miR-1252-5p	-0.04	-0.07	N/A
hsa-miR-1252-5p	-0.04	-0.18	N/A
hsa-miR-1252-5p	-0.04	-0.07	N/A
hsa-miR-1252-5p	-0.04	-0.1	N/A
hsa-miR-1252-5p	-0.04	-0.19	N/A

hsa-miR-1252-5p	-0.04	-0.07	N/A
hsa-miR-1252-5p	-0.04	-0.05	N/A
hsa-miR-1252-5p	-0.04	-0.1	N/A
hsa-miR-1252-5p	-0.04	-0.16	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.14	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.17	N/A
hsa-miR-1252-5p	-0.04	-0.08	N/A
hsa-miR-1252-5p	-0.04	-0.32	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.16	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.06	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.14	N/A
hsa-miR-1252-5p	-0.04	-0.15	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.28	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.04	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.4	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.12	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.14	N/A
hsa-miR-1252-5p	-0.03	-0.18	N/A
hsa-miR-1252-5p	-0.03	-0.16	N/A
hsa-miR-1252-5p	-0.03	-0.25	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.2	N/A
hsa-miR-1252-5p	-0.03	-0.23	N/A
hsa-miR-1252-5p	-0.03	-0.14	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A

hsa-miR-1252-5p	-0.03	-0.1	N/A
hsa-miR-1252-5p	-0.03	-0.1	N/A
hsa-miR-1252-5p	-0.03	-0.14	N/A
hsa-miR-1252-5p	-0.03	-0.14	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.47	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.14	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.4	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.28	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
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hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.1	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.1	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.14	N/A
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hsa-miR-1252-5p	-0.03	-0.08	N/A
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hsa-miR-1252-5p	-0.03	-0.41	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.21	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.15	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.26	N/A
hsa-miR-1252-5p	-0.03	-0.09	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.21	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.25	N/A
hsa-miR-1252-5p	-0.03	-0.2	N/A
hsa-miR-1252-5p	-0.03	-0.14	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
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hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.14	N/A
hsa-miR-1252-5p	-0.03	-0.17	N/A

hsa-miR-1252-5p	-0.03	-0.2	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.29	N/A
hsa-miR-1252-5p	-0.03	-0.35	N/A
hsa-miR-1252-5p	-0.03	-0.15	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.18	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.17	N/A
hsa-miR-1252-5p	-0.03	-0.31	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
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hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
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hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.49	N/A

hsa-miR-1252-5p	-0.03	-0.14	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.22	N/A
hsa-miR-1252-5p	-0.03	-0.09	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.12	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.09	N/A
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hsa-miR-1252-5p	-0.03	-0.2	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.17	N/A
hsa-miR-1252-5p	-0.03	-0.09	N/A
hsa-miR-1252-5p	-0.03	-0.27	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.24	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.11	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.13	N/A
hsa-miR-1252-5p	-0.03	-0.25	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.11	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.13	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.1	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.1	N/A
hsa-miR-1252-5p	-0.03	-0.15	N/A
hsa-miR-1252-5p	-0.03	-0.53	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.12	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A

hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.12	N/A
hsa-miR-1252-5p	-0.03	-0.11	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.27	N/A
hsa-miR-1252-5p	-0.03	-0.12	N/A
hsa-miR-1252-5p	-0.03	-0.14	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.29	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.12	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.16	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.12	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.15	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.28	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.22	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.12	N/A
hsa-miR-1252-5p	-0.03	-0.19	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.07	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.15	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.09	N/A

hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.12	N/A
hsa-miR-1252-5p	-0.03	-0.11	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.2	N/A
hsa-miR-1252-5p	-0.03	-0.15	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.08	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.41	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.05	N/A
hsa-miR-1252-5p	-0.03	-0.24	N/A
hsa-miR-1252-5p	-0.03	-0.18	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.06	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.17	N/A
hsa-miR-1252-5p	-0.03	-0.21	N/A
hsa-miR-1252-5p	-0.03	-0.04	N/A
hsa-miR-1252-5p	-0.03	-0.31	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.2	N/A
hsa-miR-1252-5p	-0.03	-0.5	N/A
hsa-miR-1252-5p	-0.03	-0.39	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.22	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.03	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.31	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.23	N/A
hsa-miR-1252-5p	-0.02	-0.09	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.17	N/A
hsa-miR-1252-5p	-0.02	-0.22	N/A
hsa-miR-1252-5p	-0.02	-0.09	N/A
hsa-miR-1252-5p	-0.02	-0.39	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.19	N/A
hsa-miR-1252-5p	-0.02	-0.09	N/A
hsa-miR-1252-5p	-0.02	-0.23	N/A
hsa-miR-1252-5p	-0.02	-0.14	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A

hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.06	N/A
hsa-miR-1252-5p	-0.02	-0.07	N/A
hsa-miR-1252-5p	-0.02	-0.19	N/A
hsa-miR-1252-5p	-0.02	-0.11	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.11	N/A
hsa-miR-1252-5p	-0.02	-0.25	N/A
hsa-miR-1252-5p	-0.02	-0.14	N/A
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hsa-miR-1252-5p	-0.02	-0.12	N/A
hsa-miR-1252-5p	-0.02	-0.24	N/A
hsa-miR-1252-5p	-0.02	-0.2	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A
hsa-miR-1252-5p	-0.02	-0.06	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.12	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A
hsa-miR-1252-5p	-0.02	-0.13	N/A
hsa-miR-1252-5p	-0.02	-0.27	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
hsa-miR-1252-5p	-0.02	-0.07	N/A
hsa-miR-1252-5p	-0.02	-0.09	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.17	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
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hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.18	N/A
hsa-miR-1252-5p	-0.02	-0.38	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.09	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
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hsa-miR-1252-5p	-0.02	-0.07	N/A
hsa-miR-1252-5p	-0.02	-0.09	N/A
hsa-miR-1252-5p	-0.02	-0.16	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
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hsa-miR-1252-5p	-0.02	-0.34	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A

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hsa-miR-1252-5p	-0.02	-0.17	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.24	N/A
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hsa-miR-1252-5p	-0.02	-0.23	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.12	N/A
hsa-miR-1252-5p	-0.02	-0.23	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
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hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.29	N/A
hsa-miR-1252-5p	-0.02	-0.19	N/A
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hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
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hsa-miR-1252-5p	-0.02	-0.17	N/A
hsa-miR-1252-5p	-0.02	-0.07	N/A
hsa-miR-1252-5p	-0.02	-0.19	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.21	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
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hsa-miR-1252-5p	-0.02	-0.21	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.14	N/A
hsa-miR-1252-5p	-0.02	-0.19	N/A
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hsa-miR-1252-5p	-0.02	-0.07	N/A
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hsa-miR-1252-5p	-0.02	-0.08	N/A
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hsa-miR-1252-5p	-0.02	-0.05	N/A
hsa-miR-1252-5p	-0.02	-0.19	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
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hsa-miR-1252-5p	-0.02	-0.02	N/A
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hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
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hsa-miR-1252-5p	-0.02	-0.02	N/A
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hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.11	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A

hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A

hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.14	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
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hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.8	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A

hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.3	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.07	N/A
hsa-miR-1252-5p	-0.02	-0.11	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.11	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.18	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.25	N/A
hsa-miR-1252-5p	-0.02	-0.47	N/A
hsa-miR-1252-5p	-0.02	-0.06	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.21	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.07	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.16	N/A
hsa-miR-1252-5p	-0.02	-0.11	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.06	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.07	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.11	N/A
hsa-miR-1252-5p	-0.02	-0.17	N/A
hsa-miR-1252-5p	-0.02	-0.2	N/A
hsa-miR-1252-5p	-0.02	-0.11	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A

hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.06	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
hsa-miR-1252-5p	-0.02	-0.12	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.21	N/A
hsa-miR-1252-5p	-0.02	-0.14	N/A
hsa-miR-1252-5p	-0.02	-0.07	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.19	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A
hsa-miR-1252-5p	-0.02	-0.07	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.3	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.35	N/A
hsa-miR-1252-5p	-0.02	-0.18	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.17	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.2	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.24	N/A
hsa-miR-1252-5p	-0.02	-0.05	N/A
hsa-miR-1252-5p	-0.02	-0.3	N/A
hsa-miR-1252-5p	-0.02	-0.45	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.11	N/A

hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.09	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.46	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.31	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.11	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.09	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.02	-0.79	N/A
hsa-miR-1252-5p	-0.02	-0.03	N/A
hsa-miR-1252-5p	-0.02	-0.52	N/A
hsa-miR-1252-5p	-0.02	-0.12	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.15	N/A
hsa-miR-1252-5p	-0.02	-0.04	N/A
hsa-miR-1252-5p	-0.02	-0.08	N/A
hsa-miR-1252-5p	-0.02	-0.1	N/A
hsa-miR-1252-5p	-0.02	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.13	N/A
hsa-miR-1252-5p	-0.01	-0.32	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.13	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.23	N/A
hsa-miR-1252-5p	-0.01	-0.11	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.14	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-2.94	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.39	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A

hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.16	N/A
hsa-miR-1252-5p	-0.01	-0.09	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.24	N/A
hsa-miR-1252-5p	-0.01	-0.23	N/A
hsa-miR-1252-5p	-0.01	-0.99	N/A
hsa-miR-1252-5p	-0.01	-0.16	N/A
hsa-miR-1252-5p	-0.01	-0.46	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.15	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
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hsa-miR-1252-5p	-0.01	-0.03	N/A
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hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.09	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.11	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.15	N/A
hsa-miR-1252-5p	-0.01	-0.26	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.1	N/A
hsa-miR-1252-5p	-0.01	-0.11	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.14	N/A
hsa-miR-1252-5p	-0.01	-0.15	N/A
hsa-miR-1252-5p	-0.01	-0.23	N/A
hsa-miR-1252-5p	-0.01	-0.28	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.28	N/A
hsa-miR-1252-5p	-0.01	-0.15	N/A
hsa-miR-1252-5p	-0.01	-0.33	N/A
hsa-miR-1252-5p	-0.01	-0.22	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.2	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A

hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.12	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.14	N/A
hsa-miR-1252-5p	-0.01	-0.33	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.21	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.16	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.33	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.1	N/A
hsa-miR-1252-5p	-0.01	-0.29	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.44	N/A
hsa-miR-1252-5p	-0.01	-0.78	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-1.1	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.15	N/A
hsa-miR-1252-5p	-0.01	-0.1	N/A
hsa-miR-1252-5p	-0.01	-0.15	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.1	N/A
hsa-miR-1252-5p	-0.01	-0.09	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.17	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.24	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.26	N/A
hsa-miR-1252-5p	-0.01	-0.24	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A

hsa-miR-1252-5p	-0.01	-0.12	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.09	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.09	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
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hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
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hsa-miR-1252-5p	-0.01	-0.18	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
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hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.11	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.11	N/A
hsa-miR-1252-5p	-0.01	-0.14	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.1	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.14	N/A
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hsa-miR-1252-5p	-0.01	-0.25	N/A

hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.27	N/A
hsa-miR-1252-5p	-0.01	-0.23	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.22	N/A
hsa-miR-1252-5p	-0.01	-0.1	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.15	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.19	N/A
hsa-miR-1252-5p	-0.01	-0.09	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.18	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.09	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.15	N/A
hsa-miR-1252-5p	-0.01	-0.16	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.18	N/A
hsa-miR-1252-5p	-0.01	-0.24	N/A
hsa-miR-1252-5p	-0.01	-0.26	N/A
hsa-miR-1252-5p	-0.01	-0.36	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.12	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.09	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.2	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.27	N/A
hsa-miR-1252-5p	-0.01	-0.3	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.13	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.21	N/A
hsa-miR-1252-5p	-0.01	-0.48	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.18	N/A
hsa-miR-1252-5p	-0.01	-0.1	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A

hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.26	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.12	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.26	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.28	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.34	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.13	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.12	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
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hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
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hsa-miR-1252-5p	-0.01	-0.09	N/A
hsa-miR-1252-5p	-0.01	-0.11	N/A
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hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.12	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.26	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.1	N/A
hsa-miR-1252-5p	-0.01	-0.1	N/A
hsa-miR-1252-5p	-0.01	-0.13	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.23	N/A
hsa-miR-1252-5p	-0.01	-0.13	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.14	N/A
hsa-miR-1252-5p	-0.01	-0.09	N/A

hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.27	N/A
hsa-miR-1252-5p	-0.01	-0.2	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.18	N/A
hsa-miR-1252-5p	-0.01	-0.25	N/A
hsa-miR-1252-5p	-0.01	-0.11	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.13	N/A
hsa-miR-1252-5p	-0.01	-0.26	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.45	N/A
hsa-miR-1252-5p	-0.01	-0.17	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.25	N/A
hsa-miR-1252-5p	-0.01	-0.1	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.06	N/A
hsa-miR-1252-5p	-0.01	-0.25	N/A
hsa-miR-1252-5p	-0.01	-0.34	N/A
hsa-miR-1252-5p	-0.01	-0.11	N/A
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hsa-miR-1252-5p	-0.01	-0.28	N/A
hsa-miR-1252-5p	-0.01	-0.04	N/A
hsa-miR-1252-5p	-0.01	-0.09	N/A
hsa-miR-1252-5p	-0.01	-0.2	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.19	N/A
hsa-miR-1252-5p	-0.01	-0.12	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.05	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.2	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.15	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.09	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.12	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.12	N/A
hsa-miR-1252-5p	-0.01	-0.08	N/A
hsa-miR-1252-5p	-0.01	-0.01	N/A
hsa-miR-1252-5p	-0.01	-0.22	N/A

hsa-miR-1252-5p	-0.01	-0.03	N/A
hsa-miR-1252-5p	-0.01	-0.11	N/A
hsa-miR-1252-5p	-0.01	-0.12	N/A
hsa-miR-1252-5p	-0.01	-0.14	N/A
hsa-miR-1252-5p	-0.01	-0.07	N/A
hsa-miR-1252-5p	-0.01	-0.21	N/A
hsa-miR-1252-5p	-0.01	-0.4	N/A
hsa-miR-1252-5p	-0.01	-0.12	N/A
hsa-miR-1252-5p	-0.01	-0.22	N/A
hsa-miR-1252-5p	-0.01	-0.15	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	-0.01	-0.02	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.23	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.35	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.26	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.21	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.56	N/A
hsa-miR-1252-5p	0	-0.32	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.34	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.14	N/A

hsa-miR-1252-5p	0	-0.24	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.23	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.35	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.37	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.43	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.28	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.39	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.19	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.24	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.19	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.12	N/A

hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.42	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.23	N/A
hsa-miR-1252-5p	0	-0.26	N/A
hsa-miR-1252-5p	0	-0.28	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-1	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.29	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.24	N/A
hsa-miR-1252-5p	0	-0.25	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.53	N/A
hsa-miR-1252-5p	0	-0.51	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-2.99	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.02	N/A

hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.47	N/A
hsa-miR-1252-5p	0	-0.23	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.27	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.26	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.06	N/A

hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.19	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.3	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-1.13	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.23	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.7	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.44	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.38	N/A
hsa-miR-1252-5p	0	-0.24	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.28	N/A

hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.29	N/A
hsa-miR-1252-5p	0	-0.21	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.25	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.21	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.72	N/A
hsa-miR-1252-5p	0	-0.66	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.32	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.19	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.36	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.1	N/A

hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.36	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.26	N/A
hsa-miR-1252-5p	0	-0.3	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.47	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.28	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.19	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.43	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.23	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.43	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.36	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.21	N/A
hsa-miR-1252-5p	0	-0.34	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.08	N/A

hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.31	N/A
hsa-miR-1252-5p	0	-0.3	N/A
hsa-miR-1252-5p	0	-0.25	N/A
hsa-miR-1252-5p	0	-0.28	N/A
hsa-miR-1252-5p	0	-0.29	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.29	N/A
hsa-miR-1252-5p	0	-0.28	N/A
hsa-miR-1252-5p	0	-0.27	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.41	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.26	N/A
hsa-miR-1252-5p	0	-0.3	N/A
hsa-miR-1252-5p	0	-0.19	N/A
hsa-miR-1252-5p	0	-0.26	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.23	N/A
hsa-miR-1252-5p	0	-0.24	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.21	N/A
hsa-miR-1252-5p	0	-0.21	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.19	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.21	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.19	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.3	N/A
hsa-miR-1252-5p	0	-0.24	N/A
hsa-miR-1252-5p	0	-0.17	N/A

hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.25	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.23	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.19	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.27	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.23	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.01	N/A

hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.24	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.29	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.38	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.02	N/A

hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.24	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.17	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.56	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.24	N/A
hsa-miR-1252-5p	0	-0.26	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.28	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.5	N/A
hsa-miR-1252-5p	0	-0.18	N/A

hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.21	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.22	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.21	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.16	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.19	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.11	N/A

hsa-miR-1252-5p	0	-0.24	N/A
hsa-miR-1252-5p	0	-0.14	N/A
hsa-miR-1252-5p	0	-0.33	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.11	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.04	N/A
hsa-miR-1252-5p	0	-0.47	N/A
hsa-miR-1252-5p	0	-0.36	N/A
hsa-miR-1252-5p	0	-0.18	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.09	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.12	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.23	N/A
hsa-miR-1252-5p	0	-0.06	N/A
hsa-miR-1252-5p	0	-0.21	N/A
hsa-miR-1252-5p	0	-0.13	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.08	N/A
hsa-miR-1252-5p	0	-0.23	N/A
hsa-miR-1252-5p	0	-0.05	N/A
hsa-miR-1252-5p	0	-0.32	N/A
hsa-miR-1252-5p	0	-0.01	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.1	N/A
hsa-miR-1252-5p	0	-0.07	N/A

hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.07	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.02	N/A
hsa-miR-1252-5p	0	-0.2	N/A
hsa-miR-1252-5p	0	-0.03	N/A
hsa-miR-1252-5p	0	-0.15	N/A
hsa-miR-1252-5p	N/A	N/A	N/A
hsa-miR-1252-5p	N/A	N/A	N/A
hsa-miR-1252-5p	N/A	N/A	N/A
hsa-miR-1252-5p	N/A	N/A	N/A
hsa-miR-1252-5p	N/A	N/A	N/A
hsa-miR-1252-5p	N/A	N/A	N/A
hsa-miR-1252-5p	N/A	N/A	N/A
hsa-miR-1252-5p	N/A	N/A	N/A
hsa-miR-1252-5p	N/A	N/A	N/A