

Supplementary data S1: Metabolic characteristics of the subjects

	Control subjects n = 15	T2D matched control subjects n = 5	T2D patients n = 5
Sex (M/F)	6/10	2/3	2/3
Age (yr)	36 ± 3	51 ± 2	50 ± 3
BMI (kg/m ²)	22.6 ± 0.5	24.64 ± 1.09	30.78 ± 1.2 *
Fasting glucose (g/L)	0.87 ± 0.02	0.91 ± 0.04	1.4 ± 0.08 *
Fasting insulin (mU/L)	6.9 ± 0.5	6.2 ± 0.9	12.4 ± 2.5 *
NEFA (μM)	538 ± 50	527 ± 68	517 ± 37
Clamp Study:			
Glucose (g/L)	0.88 ± 0.02	0.92 ± 0.06	0.98 ± 0.04
Insulin (mU/L)	173 ± 8	172 ± 9	184 ± 7
Glucose disposal rate (mg/kg/min)	10.2 ± 0.6	11.2 ± 1.1	6.1 ± 1.1 *
NEFA (μM)	38 ± 3	39 ± 3	73 ± 15 *

*p < 0.05 when comparing type 2 diabetic patients (T2D) vs group of control subjects.

Supplementary data S2: Primer sequences used in this study for qRT-PCR, sequencing and ChIP assay.

Gene Names	Forward primers	Reverse primers
DiGeorge syndrome critical region gene 8 (DGCR8)	5'-CTGGAAATCCTCATCCCTGA-3'	5'-TCCCAGGAACCACTTCAAAC-3'
Nuclear RNase III (Drosha)	5'-GACAAACAGAAGCTGGCACA-3'	5'-TGCATTAGGCATTGGTGGTA-3'
Chromosome 20 open reading frame 166 (C20orf166)	5'-CACGTGGTCAGCTCCAAGT-3'	5'-AGCTGTTGCCCTTCACACAC-3'
Mindbomb homolog 1, (MIB1)	5'-ATGTGCTGTGGAGGGAAAAG-3'	5'-GACACACAGGGCACATTGTC-3'
Dcr-1 homolog (Drosophila) (DICER1)	5'-TGACTTGCTATGTGCGCTTG-3'	5'-TCTGGATCACATTTCCCATTT-3'
Eukaryotic translation initiation factor 2C, 2 (AGO2)	5'-CGTTTCTCCTCTGATGAGCTG-3'	5'-CTTCCTCAGCACTGTCATGTTC-3'
Eukaryotic translation initiation factor 2C, 3 (AGO3)	5'-CTTACCAGCTCTGCCACACTT-3'	5'-CTTCCTCAGCACTGTCATGTTC-3'
Eukaryotic translation initiation factor 2C, 1 (AGO1)	5'-ACTGCCCATTTGGCAACGAAC-3'	5'-CACAGACTCCAAGGGAACAG-3'
Eukaryotic translation initiation factor 2C, 4 (AGO4)	5'-ATGTGCTTGTGCCTCATCAA-3'	5'-GACCTTTGACTGTAGAGGA-3'
Exportin 5 (XPO5)	5'-GGAAGCCCTCAAGTTTTGTG-3'	5'-GCTCCATGACACTGTTCTTC-3'
adenosine deaminase, RNA-specific, B1, (ADARB1/ADAR2)	5'-TGTAAGCACGCGCTGTACTGT-3'	5'-GACTCGTGGTATGTGGTAGGCTTAG-3'
Adenosine deaminase, RNA-specific (ADAR1)	5'-GCCAGTTCAGAAGAACTATGC-3'	5'-AAGCTGTTAGTCAGAGTGTGAAG-3'
Hsa-pri-mir-1-1	5'-AAGGCTGTCCTGCTCACAC-3'	5'-TGTCTGGTGAGCACTTCCAC-3'
Hsa-pri-mir-133a2	5'-CGGGTGTGTGTGTCTGTGTA-3'	5'-TACTTGGAGCTGACCACGTG-3'
Hsa-pri-mir-1-2	5'-CACTGGATCTTCTTTTCCITTCA-3'	5'-TCCACCAAGAATATGGAACC-3'
Hsa-pri-mir-133a1	5'-AACCATTCTAGCTTTTCCAGGT-3'	5'-AGCGCAGGAAAACAGTAGGA-3'
MEF2C binding region (ChIP)	5'-GTGAAACAGGTATTTGGTTGC-3'	5'-GGCCTCTCCTTGTCTGATA-3'

Supplementary data S3: 192 miRNAs expressed in human muscle cells
 Results are expressed as fold changes (myotubes vs myoblasts, for each subject)

miRNA identifications are from <http://microrna.sanger.ac.uk/>

miRNA identifications	Subject 1	Subject 2	Subject 3	Mean	SEM
hsa-let-7a	1.05	1.75	0.72	1.17	0.3
hsa-let-7b	1.33	0.99	0.7	1.01	0.18
hsa-let-7c	1.67	1.40	0.86	1.31	0.23
hsa-let-7d	1.38	0.83	0.58	0.93	0.23
hsa-let-7e	1.61	2.11	1.20	1.64	0.26
hsa-let-7f	0.82	2.75	0.65	1.41	0.67
hsa-let-7g	1.36	1.73	0.67	1.25	0.31
hsa-miR-1	3.43	5.44	0.73	3.20	1.36
hsa-miR-100	0.64	0.55	0.80	0.67	0.07
hsa-miR-101	1.94	1.82	0.80	1.52	0.36
hsa-miR-103	0.72	1.54	0.56	0.94	0.30
hsa-miR-106b	0.64	0.61	0.49	0.58	0.04
hsa-miR-107	2.10	1.82	0.95	1.63	0.34
hsa-miR-10a	0.75	0.74	0.95	0.82	0.06
hsa-miR-10b	1.72	1.32	1.07	1.37	0.19
hsa-miR-125a	0.96	1.11	1.71	1.26	0.22
hsa-miR-125b	1.06	1.34	1.13	1.18	0.08
hsa-miR-126	0.79	0.45	0.94	0.72	0.14
hsa-miR-127	1.55	0.35	2.74	1.55	0.68
hsa-miR-128b	15.17	17.75	3.00	11.97	4.54
hsa-miR-130a	1.07	1.06	0.84	0.99	0.07
hsa-miR-130b	0.74	0.72	0.76	0.74	0.01
hsa-miR-132	3.00	1.44	1.47	1.97	0.51
hsa-miR-133a	4.71	7.43	1.29	4.48	1.77
hsa-miR-133b	2.20	1.72	1.06	1.66	0.33
hsa-miR-134	0.74	0.19	3.90	1.61	1.15
hsa-miR-135b	1.58	0.02	0.27	0.62	0.48
hsa-miR-137	0.58	0.56	0.44	0.53	0.04
hsa-miR-139	22.92	26.59	1.82	17.11	7.71
hsa-miR-140	1.23	0.79	1.91	1.31	0.32
hsa-miR-142-3p	0.71	0.24	0.71	0.55	0.15
hsa-miR-143	6.65	13.62	2.39	7.55	3.27
hsa-miR-145	3.06	24.91	5.33	11.10	6.93
hsa-miR-146b	1.04	1.06	2.23	1.44	0.39
hsa-miR-148a	1.85	1.06	1.13	1.35	0.25
hsa-miR-148b	0.77	0.96	0.44	0.72	0.15
hsa-miR-149	0.95	1.19	1.16	1.10	0.07
hsa-miR-151	0.73	1.03	1.45	1.07	0.20
hsa-miR-152	1.38	1.67	1.67	1.58	0.09
hsa-miR-155	0.34	0.15	0.47	0.32	0.09
hsa-miR-15a	0.74	0.82	0.74	0.77	0.02

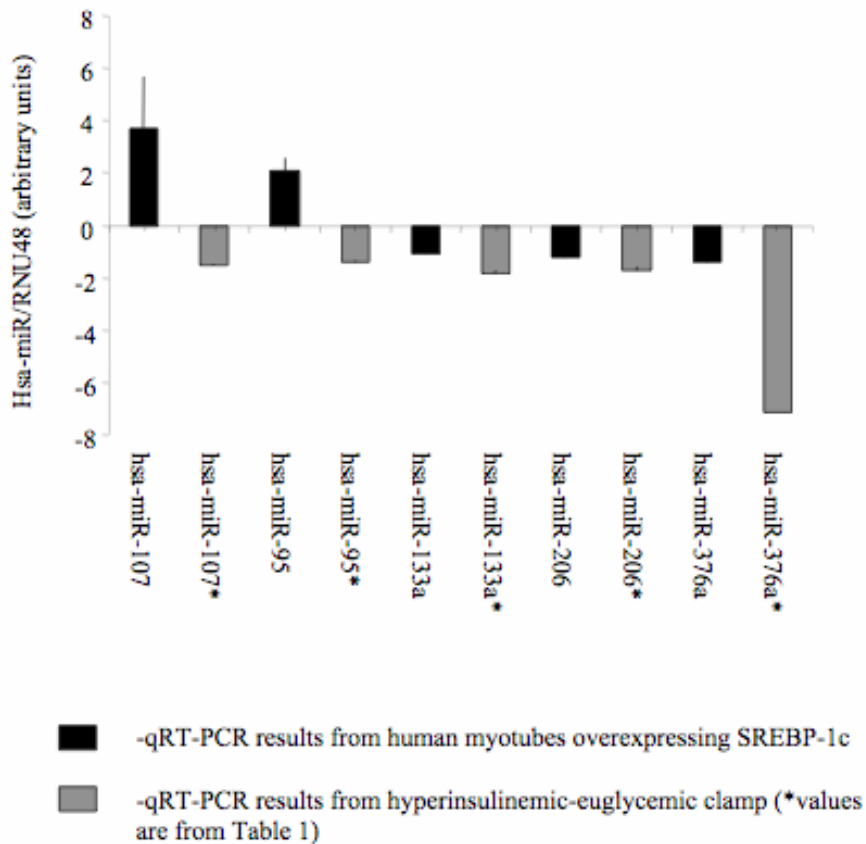
hsa-miR-15b	0.25	0.29	0.38	0.31	0.03
hsa-miR-16	0.47	0.35	0.92	0.58	0.17
hsa-miR-17-3p	22.58	0.35	10.18	11.03	6.43
hsa-miR-17-5p	1.10	0.70	0.62	0.81	0.14
hsa-miR-181b	1.28	1.57	1.09	1.31	0.13
hsa-miR-181c	1.54	1.52	1.18	1.41	0.11
hsa-miR-181d	1.27	1.66	1.29	1.41	0.12
hsa-miR-182	0.08	0.91	0.06	0.35	0.28
hsa-miR-184	1.91	36.70	3.55	14.06	11.33
hsa-miR-186	1.20	0.91	1.46	1.19	0.15
hsa-miR-189	0.56	1.97	1.43	1.32	0.40
hsa-miR-18a	0.68	0.73	0.44	0.61	0.09
hsa-miR-190	0.84	0.80	0.01	0.55	0.26
hsa-miR-191	0.78	0.74	1.16	0.89	0.13
hsa-miR-192	2.66	0.84	0.65	1.38	0.64
hsa-miR-193a	1.48	2.47	1.47	1.81	0.33
hsa-miR-193b	2.09	3.52	0.67	2.09	0.82
hsa-miR-194	1.75	1.09	1.04	1.29	0.23
hsa-miR-195	0.47	0.65	0.73	0.62	0.07
hsa-miR-196a	0.67	0.44	0.70	0.60	0.07
hsa-miR-196b	0.63	0.51	0.75	0.63	0.06
hsa-miR-197	0.76	0.84	1.02	0.87	0.07
hsa-miR-199a	1.13	0.77	0.99	0.96	0.10
hsa-miR-199b	0.61	0.39	1.03	0.68	0.18
hsa-miR-19a	0.68	0.41	0.39	0.49	0.09
hsa-miR-19b	0.85	0.49	0.44	0.60	0.12
hsa-miR-200b	11.32	0.05	11.87	7.74	3.85
hsa-miR-200c	1.57	0.12	0.18	0.62	0.47
hsa-miR-203	11.41	3.31	0.10	4.94	3.36
hsa-miR-204	0.68	0.33	0.24	0.42	0.13
hsa-miR-206	1.60	1.31	1.15	1.36	0.13
hsa-miR-208	11.37	13.36	11.67	12.13	0.61
hsa-miR-20a	0.70	0.53	0.36	0.53	0.09
hsa-miR-20b	0.70	0.54	0.37	0.53	0.09
hsa-miR-21	1.98	1.92	0.62	1.51	0.44
hsa-miR-210	0.69	0.56	1.57	0.94	0.31
hsa-miR-213	1.38	2.02	0.88	1.42	0.33
hsa-miR-214	0.93	0.25	0.64	0.61	0.19
hsa-miR-218	1.24	1.55	1.09	1.29	0.13
hsa-miR-22	1.60	1.73	1.53	1.62	0.05
hsa-miR-221	0.41	0.45	0.55	0.47	0.04
hsa-miR-222	0.25	0.28	0.82	0.45	0.18
hsa-miR-223	0.07	6.79	0.17	2.34	2.22
hsa-miR-224	1.44	0.68	1.76	1.29	0.32
hsa-miR-23a	1.53	1.45	1.43	1.47	0.02
hsa-miR-23b	2.09	1.53	1.16	1.59	0.26
hsa-miR-24	1.33	1.38	1.29	1.33	0.02

hsa-miR-25	0.63	1.16	0.50	0.77	0.20
hsa-miR-26a	1.71	1.95	1.44	1.70	0.14
hsa-miR-26b	0.91	0.76	0.63	0.77	0.08
hsa-miR-27a	1.15	1.16	1.23	1.18	0.02
hsa-miR-27b	1.73	1.16	0.75	1.21	0.28
hsa-miR-28	0.67	0.77	0.73	0.72	0.028
hsa-miR-296	1.04	1.13	0.81	1.00	0.09
hsa-miR-299-3p	0.30	0.09	23.93	8.11	7.91
hsa-miR-299-5p	0.68	0.75	0.64	0.69	0.03
hsa-miR-29a	0.57	0.45	0.73	0.59	0.07
hsa-miR-29c	1.09	0.71	0.73	0.84	0.12
hsa-miR-301	0.70	0.58	0.32	0.53	0.11
hsa-miR-30a-3p	1.64	1.40	1.29	1.44	0.10
hsa-miR-30a-5p	2.20	2.15	0.68	1.68	0.49
hsa-miR-30b	1.65	1.33	1.07	1.35	0.16
hsa-miR-30c	1.73	1.46	1.18	1.45	0.15
hsa-miR-30d	2.51	2.89	1.01	2.14	0.57
hsa-miR-30e-3p	1.33	1.02	1.12	1.16	0.09
hsa-miR-30e-5p	4.40	2.25	0.73	2.46	1.06
hsa-miR-31	0.50	0.32	1.37	0.73	0.32
hsa-miR-32	0.79	0.52	0.40	0.57	0.11
hsa-miR-320	0.91	1.00	1.47	1.13	0.17
hsa-miR-323	1.01	0.58	1.95	1.18	0.40
hsa-miR-324-3p	0.93	1.06	1.09	1.02	0.048
hsa-miR-324-5p	1.82	1.68	0.82	1.44	0.31
hsa-miR-328	0.77	0.71	1.06	0.85	0.10
hsa-miR-330	2.02	1.85	0.71	1.53	0.41
hsa-miR-331	1.44	1.61	1.42	1.49	0.06
hsa-miR-335	0.34	1.20	0.44	0.66	0.27
hsa-miR-339	0.23	0.54	1.37	0.71	0.34
hsa-miR-340	0.61	3.36	0.81	1.59	0.88
hsa-miR-342	0.90	0.75	1.15	0.93	0.11
hsa-miR-345	0.82	0.62	0.99	0.81	0.10
hsa-miR-34a	1.20	1.06	0.55	0.94	0.19
hsa-miR-34b	0.16	2.62	1.62	1.47	0.71
hsa-miR-34c	2.04	0.41	3.18	1.88	0.80
hsa-miR-361	1.64	1.50	1.47	1.53	0.05
hsa-miR-362	1.30	1.61	1.43	1.45	0.09
hsa-miR-365	1.11	1.63	1.04	1.26	0.18
hsa-miR-374	1.07	0.80	0.65	0.84	0.12
hsa-miR-376a	0.85	0.17	1.46	0.83	0.37

hsa-miR-378	2.98	28.62	0.90	10.83	8.91
hsa-miR-379	1.71	0.60	1.26	1.19	0.32
hsa-miR-381	0.68	0.12	11.58	4.13	3.72
hsa-miR-382	1.65	0.88	2.38	1.64	0.43
hsa-miR-409-5p	11.34	0.05	3.92	5.10	3.31
hsa-miR-410	0.69	0.34	4.67	1.90	1.38
hsa-miR-411	1.40	0.56	2.30	1.42	0.50
hsa-miR-422a	11.08	13.37	23.26	15.91	3.73
hsa-miR-423	0.62	0.75	0.76	0.71	0.04
hsa-miR-424	0.81	0.62	0.29	0.57	0.15
hsa-miR-425	0.43	0.74	2.13	1.10	0.52
hsa-miR-425-5p	0.64	0.51	0.58	0.58	0.03
hsa-miR-432	1.22	1.02	2.29	1.51	0.39
hsa-miR-433	1.37	0.52	0.52	0.80	0.28
hsa-miR-449	0.04	0.09	1.36	0.50	0.43
hsa-miR-449b	0.10	0.04	9.10	3.08	3.00
hsa-miR-450	1.48	0.75	0.31	0.84	0.33
hsa-miR-452	1.26	1.69	0.85	1.27	0.24
hsa-miR-484	1.28	0.89	1.37	1.18	0.14
hsa-miR-485-3p	1.01	0.14	1.86	1.00	0.49
hsa-miR-485-5p	0.88	0.05	189.75	63.56	63.09
hsa-miR-486	0.64	0.61	0.46	0.57	0.05
hsa-miR-487b	1.81	0.52	1.93	1.42	0.45
hsa-miR-491	2.95	2.39	2.48	2.61	0.17
hsa-miR-493	1.72	0.05	1.57	1.11	0.53
hsa-miR-494	0.08	0.11	10.93	3.71	3.61
hsa-miR-497	0.91	0.79	0.95	0.88	0.04
hsa-miR-500	1.68	1.78	0.63	1.36	0.36
hsa-miR-501	1.41	3.25	0.84	1.83	0.72
hsa-miR-502	5.09	2.23	0.35	2.56	1.37
hsa-miR-503	0.96	0.39	0.17	0.51	0.23
hsa-miR-504	11.32	3.95	3.13	6.13	2.60
hsa-miR-532	1.77	1.99	1.54	1.77	0.13
hsa-miR-542-5p	1.64	2.79	2.80	2.41	0.38
hsa-miR-545	8.22	7.88	0.43	5.51	2.54
hsa-miR-550	0.55	0.44	0.56	0.51	0.03
hsa-miR-565	0.59	1.31	0.30	0.73	0.29
hsa-miR-572	0.34	1.63	1.15	1.04	0.37
hsa-miR-575	5.54	0.09	0.08	1.90	1.81
hsa-miR-576	0.31	0.39	0.52	0.41	0.06
hsa-miR-589	11.03	0.13	0.02	3.73	3.65
hsa-miR-594	0.72	1.29	0.58	0.86	0.21
hsa-miR-597	0.51	3.52	0.42	1.49	1.01
hsa-miR-615	0.95	0.65	0.75	0.78	0.08

hsa-miR-616	0.04	2.02	2.23	1.43	0.69
hsa-miR-618	1.28	0.11	0.65	0.68	0.33
hsa-miR-627	0.80	1.66	3.30	1.92	0.73
hsa-miR-629	0.49	0.63	2.00	1.04	0.48
hsa-miR-630	2.27	6.81	0.20	3.09	1.95
hsa-miR-646	0.69	0.40	1.81	0.97	0.42
hsa-miR-650	0.87	0.38	1.92	1.06	0.45
hsa-miR-654	3.41	52.67	3.26	19.78	16.44
hsa-miR-656	3.64	0.50	2.10	2.08	0.90
hsa-miR-659	0.68	0.15	2.15	0.99	0.59
hsa-miR-660	2.30	2.55	1.28	2.04	0.38
hsa-miR-7	0.20	0.72	0.01	0.31	0.21
hsa-miR-9	22.87	0.41	0.95	8.08	7.39
hsa-miR-92	0.86	0.90	0.70	0.82	0.06
hsa-miR-93	0.66	0.51	0.48	0.55	0.05
hsa-miR-95	1.30	4.88	0.92	2.37	1.26
hsa-miR-98	0.94	2.12	0.57	1.21	0.46
hsa-miR-99a	0.47	0.47	1.16	0.70	0.22
hsa-miR-99b	0.69	0.98	1.74	1.14	0.31

Supplementary data S4



Supplementary data S5: Genes up-regulated by insulin during a 3h-hyperinsulinemic euglycemic clamp (n=6 subjects) and predicted as target of the 39 miRNAs down-regulated during hyperinsulinemia, in human skeletal muscle.

*We considered genes targeted by at least 6 different miRNAs which corresponded to percentile 95th of the distribution of predicted miRNA target sites in 3'UTR, for the 11,863 genes expressed in muscle, when using predictions from TargetScan 4.2 (conserved site across Human, Mouse, Rat and Dog)

Symbols	Name	Number of microRNA-mRNA pairs*	Mean fold change	LLID
ABHD2	Abhydrolase domain containing 2	12	1.6	11057
ABL1	V-abl Abelson murine leukemia viral oncogene homolog 1	6	1.23	25
ALPK3	Alpha-kinase 3	6	1.22	57538
AMOTL2	Angiomotin like 2	8	1.27	51421
APC	Adenomatosis polyposis coli	9	1.20	324
ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	6	1.22	23365
ATP2A2	ATPase, Ca ⁺⁺ transporting, cardiac muscle, slow twitch 2	8	1.35	488
C2orf55	Chromosome 2 open reading frame 55	6	1.20	343990
C5orf13	Chromosome 5 open reading frame 13	8	1.36	9315
CALM3	Calmodulin 3 (phosphorylase kinase, delta)	6	1.21	808
CDC37L1	Cell division cycle 37 homolog (S. cerevisiae)-like 1	7	1.30	55664
CDH13	Cadherin 13, H-cadherin (heart)	8	1.18	1012
CHD9	Chromodomain helicase DNA binding protein 9	11	1.33	80205
CPEB2	Cytoplasmic polyadenylation element binding protein 2	10	1.20	132864
CPEB3	Cytoplasmic polyadenylation element binding protein 3	15	1.21	22849
CPEB4	Cytoplasmic polyadenylation element binding protein 4	17	1.34	80315
DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4	6	1.20	23142
EBF3	Early B-cell factor 3	9	1.29	253738
EPHB2	EPH receptor B2	7	1.22	2048
G3BP2	GTPase activating protein (SH3 domain) binding protein 2	7	1.28	9908
GATA6	GATA binding protein 6	6	1.20	2627
HOXA11	Homeobox A11	6	1.22	3207
IGF1R	Insulin-like growth factor 1 receptor	7	1.20	3480
KCTD5	Potassium channel tetramerisation domain containing 5	8	1.20	54442
KIAA0241	KIAA0241	6	1.36	23080
KIF3A	Kinesin family member 3A	7	1.24	11127
KLF13	Kruppel-like factor 13	13	1.53	51621
KLF4	Kruppel-like factor 4 (gut)	8	3.90	9314
KPNA1	Karyopherin alpha 1 (importin alpha 5)	7	1.25	3836
LATS2	LATS, large tumor suppressor, homolog 2	7	1.20	26524
MAB21L1	Mab-21-like 1 (C. elegans)	8	1.20	4081
MAFG	V-maf musculoaponeurotic fibrosarcoma oncogene homolog G	7	1.36	4097
MARK3	MAP/microtubule affinity-regulating kinase 3	7	1.20	4140
MBNL2	Muscleblind-like 2	13	1.22	10150
MECP2	Methyl CpG binding protein 2	14	1.32	4204
MED13	Mediator complex subunit 13	7	1.21	9969
MEX3B	Mex-3 homolog B	11	1.23	84206
MIER3	Mesoderm induction early response 1, family member 3	17	1.20	166968

MTF1	Metal-regulatory transcription factor 1	6	1.43	4520
NAP1L5	Nucleosome assembly protein 1-like 5	8	1.32	266812
NARG1	NMDA receptor regulated 1	11	1.18	80155
NAV1	Neuron navigator 1	11	1.40	89796
NCOA1	Nuclear receptor coactivator 1	8	1.36	8648
NCOR2	Nuclear receptor co-repressor 2	8	1.40	9612
NEDD4	Neural precursor cell expressed, developmentally down-regulated 4	7	1.23	4734
NIPBL	Nipped-B homolog	8	1.18	25836
NOVA1	Neuro-oncological ventral antigen 1	13	1.26	4857
ORC2L	Origin recognition complex, subunit 2-like	7	1.21	4999
OTUD4	OTU domain containing 4	16	1.19	54726
PCGF3	Polycomb group ring finger 3	7	1.20	10336
PDCD10	Programmed cell death 10	9	1.32	11235
PDE4D	Phosphodiesterase 4D, cAMP-specific	7	1.37	5144
PDIK1L	PDLIM1 interacting kinase 1 like	6	1.20	149420
PHACTR2	Phosphatase and actin regulator 2	6	1.19	9749
PHF15	PHD finger protein 15	12	1.22	23338
PIK3R1	Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	6	1.70	5295
PNKD	Paroxysmal nonkinesigenic dyskinesia	6	1.21	25953
PRKCD	Protein kinase C, delta	6	1.33	5580
PTP4A1	Protein tyrosine phosphatase type IVA, member 1	10	1.24	7803
PTPN9	Protein tyrosine phosphatase, non-receptor type 9	6	1.23	5780
QKI	Quaking homolog, KH domain RNA binding	18	1.30	9444
RARB	Retinoic acid receptor, beta	12	1.55	5915
RNF19A	Ring finger protein 19A	6	1.22	25897
RNF38	Ring finger protein 38	7	1.20	152006
SBK1	SH3-binding domain kinase 1	7	1.18	388228
SIX4	SIX homeobox 4	11	1.24	51804
SLC25A25	Solute carrier family 25, member 25	8	1.30	114789
SOCS1	Suppressor of cytokine signaling 1	6	1.70	8651
SOX4	SRY (sex determining region Y)-box 4	7	1.30	6659
TDG	Thymine-DNA glycosylase	11	1.20	6996
TFDP1	Transcription factor Dp-1	6	1.28	7027
TGFBR1	Transforming growth factor, beta receptor I	7	1.30	7046
TMEM47	Transmembrane protein 47	6	1.20	83604
TNRC6A	Trinucleotide repeat containing 6A	10	1.31	27327
UBE2D2	Ubiquitin-conjugating enzyme E2D 2	6	1.19	7322
UBE2W	Ubiquitin-conjugating enzyme E2W	8	1.19	55284
UBE3C	Ubiquitin protein ligase E3C	6	1.26	9690
UNC5C	Unc-5 homolog C	7	1.19	8633
VAMP2	Vesicle-associated membrane protein 2	6	1.24	6844
WDR82	WD repeat domain 82	8	1.25	80335
ZBTB4	Zinc finger and BTB domain containing 4	8	1.28	57659
ZCCHC14	Zinc finger, CCHC domain containing 14	7	1.31	23174
ZNF644	Zinc finger protein 644	6	1.35	84146