KEGGID	Term	Gene
4920	Adipocytokine signaling pathway	CPT1A, RXRA, PRKAG2
3320	PPAR signaling pathway	CPT1A, RXRA
3440	Homologous recombination	NBN

symbol	refSeq	chrom	strand
ABCA17P	NR_003574	chr16	+
ABCA3	NM_001089	chr16	-
ABHD11	NR_026912	chr7	-
AHRR	NM_020731, NM_001242412	chr5	+
ALDOA	NM_000034, NM_184043	chr16	+
AP4E1	NM_007347	chr15	+
ATG16L2	NM_033388	chr11	+
ATP6AP2	NM_005765	chrX	+
C21orf128	NR_027243	chr21	-
C9orf91	NM_153045	chr9	+
CAP2	NM_006366	chr6	+
CASP7	NM_033340, NM_001227	chr10	+
COL5A1	NM_000093	chr9	+
CORO7	NM_024535, NM_001201472, NM_0012	chr16	-
CORO7-PAM1	NM_001201479	chr16	-
CPT1A	NM_001031847, NM_001876	chr11	-

CXXC5	NM_016463	chr5	+
CYP1B1	NM_000104	chr2	-
DFNB31	NM_001173425	chr9	-
DMRT2	NM_006557	chr9	+
DNMT1	NM_001130823, NM_001379	chr19	-
DNTTIP2	NM_014597	chr1	-
DOK7	NM_173660	chr4	+
ESR1	NM_001122742, NM_001122741, NM_0	chr6	+
EXOC3	NM_007277	chr5	+
FAM178B	NM_016490	chr2	-
FAM3B	NM_058186, NM_206964	chr21	+
FAM63A	NM_001163258, NM_018379, NM_0011	chr1	-
FMN1	NM_001103184	chr15	-
FOXA1	NM_004496	chr14	-
FREM2	NM_207361	chr13	+
GCLM	NM_002061	chr1	-
GEM	NM_005261	chr8	-
GRHL2	NM_024915	chr8	+
HOOK3	NM_032410	chr8	+
IL20	NM_018724	chr1	+
INHA	NM_002191	chr2	+
INPP4B	NM_001101669, NM_003866	chr4	-
KAT6B	NM_012330	chr10	+
KIAA0196	NM_014846	chr8	-
KRT13	NM_153490	chr17	-
LOC1001307	NR_027032	chr12	+
LOC1001314	NR_024594	chr20	+
LOC1001327	NR_027642	chr15	+
LOC1005061	NR_038955	chr9	+
LOC402160	NM_001193282	chr4	+
LOC730091	NR_038387	chr3	-
MESP1	NM_018670	chr15	-
MIR4322	NR_036206	chr19	+
MIRLET7F2	NR_029484	chrX	-

MTL5	NM_001039656	chr11	-
MX2	NM_002463	chr21	+
MYO18A	NM_078471, NM_203318	chr17	-
N4BP3	NM_015111	chr5	+
NBN	NM_002485	chr8	-
NCOA3	NM_006534	chr20	+
NSMCE2	NM_173685	chr8	+
OBSL1	NM_015311, NM_001173431, NM_0011	chr2	-
PADI1	NM_013358	chr1	+
PADI3	NM_016233	chr1	+
PGLYRP2	NM_052890	chr19	-
PRKAG2	NM_016203, NM_001040633	chr7	-
PTGES	NM_004878	chr9	-
RMND5B	NM_022762	chr5	+
RNF170	NM_001160224, NM_030954, NR_0276	chr8	-
RXRA	NM_002957	chr9	+
SAMD15	NM_001010860	chr14	+
SEMA3F	NM_004186	chr3	+
SEPTIN	NM_001113491, NM_001113492	chr17	+
SLC1A5	NM_005628, NM_001145145, NM_0011	chr19	-
SLC45A4	NM_001080431	chr8	-
SLC9A3R1	NM_004252	chr17	+
SMAD7	NM_001190821	chr18	-
STARD10	NM_006645	chr11	-
STRN4	NM_013403	chr19	-
SULT1A1	NM_001055, NM_177536, NM_177529,	chr16	-
TBCD	NM_005993	chr17	+
TIAF1	NM_004740	chr17	-
TMED8	NM_213601	chr14	-
TMEM104	NM_017728	chr17	+
UMODL1	NM_001199527, NM_001199528, NM_0	chr21	+
USP38	NM_032557	chr4	+
VASN	NM_138440	chr16	+
WDR74	NM_018093	chr11	-

ZFYVE28	NM_001172657	chr4	-
ZMYND8	NM_012408, NM_183048, NM_183047	chr20	-
ZNF669	NM_024804	chr1	-
ZNF706	NM_001042510	chr8	-
ZNF750	NM_024702	chr17	-

txStart-txEnd	entrezId
2330923-2416701	650655
2265879-2330748	21
72788362-72791126	83451
357290-491405	57491
29971911-29989242, 29983100-29989242	226
48988237-49085389	23431
72203098-72218328	89849
40325159-40350832	10159
42395312-42401713	150147
116413526-116448524	203197
17501714-17666002	10486
115428924-115480654, 115429415-115480654	840
136673472-136876509	1289
4344543-4406963	79585
4330252-4406963	100529144
68278663-68365975, 68278926-68365975	1374

139008484-139042864	51523
38148249-38156827	1545
116204180-116307557	25861
1040345-1047554	10655
10105021-10166755	1786
94107601-94117350	30836
3434830-3466007	285489
152053323-152466101, 152168500-152466101, 152170146-152466101, 152170506-152466101	2099
496333-520409	11336
96905345-96927597	51252
41610530-41651524	54097
149235924-149247478, 149235924-149245897, 149235924-149246009	55793
30845038-31147377	342184
37128941-37134240	3169
38159172-38359267	341640
94125177-94147600	2730
95330660-95343723	2669
102573843-102751128	79977
42871189-43004839	84376
205105776-205109191	50604
220145197-220148679	3623
143168631-143987054	8821
76256384-76462645	23522
126105684-126173243	9897
36910758-36915391	3860
56406289-56408406	100130776
45380652-45382905	100131496
49023617-49026054	100132724
131290759-131315786	100506190
2390498-2434488	402160
157947825-158017545	730091
88094101-88095544	55897
10202088-10202161	100422925
53600877-53600960	406889

68260175-68275564	9633
41655819-41702739	4600
24424653-24531533	399687
177473161-177485713	23138
91014739-91066075	4683
45564007-45719028	8202
126173264-126448549	286053
220123693-220144512, 220128115-220144512, 220134681-220144512	23363
17404207-17445088	29943
17448179-17483314	51702
15440456-15451315	114770
150884133-151205249, 150884133-151142890	51422
131540435-131555165	9536
177490633-177508085	64777
42823936-42871023, 42827594-42871023	81790
136358136-136472252	6256
76913514-76927340	161394
50167851-50201512	6405
72789086-73008273, 72795567-73008273	10801
51969979-51983682, 51969979-51979974, 51969979-51982385	6510
142290051-142307855	57210
70256357-70277094	9368
44700220-44731079	4092
72143421-72182398	10809
51914607-51941560	29888
28524408-28528866, 28524408-28542408, 28524408-28528150	6817
78303228-78494351	6904
24424664-24426753	9220
76877866-76913149	283578
70284216-70347517	54868
42356136-42436174, 42364494-42436174	89766
144325519-144362591	84640
4361849-4373530	114990
62356958-62364204	54663

2301777-2390168	57732
45271787-45418881	23613
245329886-245334297	79862
102278441-102287136	51123
78380598-78391220	79755

geneName	keggPathway
ATP-binding cassette, sub-family A (ABC1), member 17, pseudogene	NA
ATP-binding cassette, sub-family A (ABC1), member 3	NA
abhydrolase domain containing 11	NA
aryl-hydrocarbon receptor repressor	NA
aldolase A, fructose-bisphosphate	NA
adaptor-related protein complex 4, epsilon 1 subunit	NA
ATG16 autophagy related 16-like 2 (S. cerevisiae)	NA
ATPase, H+ transporting, lysosomal accessory protein 2	NA
chromosome 21 open reading frame 128	NA
chromosome 9 open reading frame 91	NA
CAP, adenylate cyclase-associated protein, 2 (yeast)	NA
caspase 7, apoptosis-related cysteine peptidase	NA
collagen, type V, alpha 1	NA
coronin 7	NA
CORO7-PAM16 readthrough	NA
carnitine palmitoyltransferase 1A (liver)	4920;3320

CXXC finger protein 5	NA
cytochrome P450, family 1, subfamily B, polypeptide 1	NA
deafness, autosomal recessive 31	NA
doublesex and mab-3 related transcription factor 2	NA
DNA (cytosine-5-)-methyltransferase 1	NA
deoxynucleotidyltransferase, terminal, interacting protein 2	NA
docking protein 7	NA
estrogen receptor 1	NA
exocyst complex component 3	NA
family with sequence similarity 178, member B	NA
family with sequence similarity 3, member B	NA
family with sequence similarity 63, member A	NA
formin 1	NA
forkhead box A1	NA
FRAS1 related extracellular matrix protein 2	NA
glutamate-cysteine ligase, modifier subunit	NA
GTP binding protein overexpressed in skeletal muscle	NA
grainyhead-like 2 (Drosophila)	NA
hook homolog 3 (Drosophila)	NA
interleukin 20	NA
inhibin, alpha	NA
inositol polyphosphate-4-phosphatase, type II, 105kDa	NA
MYST histone acetyltransferase (monocytic leukemia) 4	NA
KIAA0196	NA
keratin 13	NA
hypothetical LOC100130776	NA
hypothetical LOC100131496	NA
DDB1 and CUL4 associated factor 13 pseudogene	NA
hypothetical LOC100506190	NA
hypothetical protein LOC402160	NA
hypothetical LOC730091	NA
mesoderm posterior 1 homolog (mouse)	NA
microRNA 4322	NA
microRNA let-7f-2	NA

metallothionein-like 5, testis-specific (tesmin)	NA
myxovirus (influenza virus) resistance 2 (mouse)	NA
myosin XVIIIA	NA
NEDD4 binding protein 3	NA
nibrin	03440
nuclear receptor coactivator 3	NA
non-SMC element 2, MMS21 homolog (S. cerevisiae)	NA
obscurin-like 1	NA
peptidyl arginine deiminase, type I	NA
peptidyl arginine deiminase, type III	NA
peptidoglycan recognition protein 2	NA
protein kinase, AMP-activated, gamma 2 non-catalytic subunit	04920
prostaglandin E synthase	NA
required for meiotic nuclear division 5 homolog B (S. cerevisiae)	NA
ring finger protein 170	NA
retinoid X receptor, alpha	3320;4920
sterile alpha motif domain containing 15	NA
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	NA
septin 9	NA
solute carrier family 1 (neutral amino acid transporter), member 5	NA
solute carrier family 45, member 4	NA
solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	NA
SMAD family member 7	NA
StAR-related lipid transfer (START) domain containing 10	NA
striatin, calmodulin binding protein 4	NA
sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	NA
tubulin folding cofactor D	NA
TGFB1-induced anti-apoptotic factor 1	NA
transmembrane emp24 protein transport domain containing 8	NA
transmembrane protein 104	NA
uromodulin-like 1	NA
ubiquitin specific peptidase 38	NA
vasorin	NA
WD repeat domain 74	NA

zinc finger, FYVE domain containing 28	NA
zinc finger, MYND-type containing 8	NA
zinc finger protein 669	NA
zinc finger protein 706	NA
zinc finger protein 750	NA