

## Gene Name

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*Abca1*  
*Acadsb*  
*Amotl1*  
*Btd*  
*Cd300lg*  
*Cped1*  
*Cpne5*  
*Ctse*  
*Cyb561a3*  
*D3ZGN7\_RAT*  
*Dntt*  
*Ephb2*  
*Fgf12*  
*Folr1*  
*Gcom1*  
*Ifitm3*  
*Kansl1l*  
*Kif7*  
*Lzts2*  
*Maff*  
*Man1c1*  
*Mcoln2*  
*Mcoln3*  
*Mgmt*  
*Mmp11*  
*Myo1d*  
*Myo5b*  
*Pithd1*  
*Plekhh2*  
*RGD1309870*  
*Rhbdl3*  
*Rin2*  
*Rnaset2*  
*Rnpep*  
*Scd1*  
*Sept1*  
*She*  
*Slc38a1*  
*Slc4a5*  
*Smtn*

*Ston2*

*Svep1*

*Thrb*

*Tmem82*

*Trem1*

*U1*

*Ydjc*

## Gene Description

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ATP-binding cassette, subfamily A (ABC1), member 1  
acyl-CoA dehydrogenase, short/branched chain  
angiomin-like 1  
biotinidase  
Cd300 molecule-like family member G  
cadherin-like and PC-esterase domain containing 1  
copine V  
cathepsin E  
cytochrome b561 family, member A3  
Uncharacterized protein  
DNA nucleotidylexotransferase  
Eph receptor B2  
fibroblast growth factor 12  
folate receptor 1 (adult)  
GRINL1A complex locus protein 1  
interferon induced transmembrane protein 3  
KAT8 regulatory NSL complex subunit 1-like  
kinesin family member 7  
leucine zipper, putative tumor suppressor 2  
v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F  
mannosidase, alpha, class 1C, member 1  
mucolipin 2  
mucolipin 3  
O-6-methylguanine-DNA methyltransferase  
matrix metalloproteinase 11  
myosin ID  
myosin Vb  
PITH (C-terminal proteasome-interacting domain of thioredoxin-like) domain containing 1  
pleckstrin homology domain containing, family H (with MyTH4 domain) member 2  
hypothetical LOC289778  
rhomboid, veinlet-like 3 (Drosophila)  
Ras and Rab interactor 2  
ribonuclease T2  
arginyl aminopeptidase (aminopeptidase B)  
stearoyl-Coenzyme A desaturase 1  
septin 1  
Src homology 2 domain containing E  
solute carrier family 38, member 1  
solute carrier family 4, sodium bicarbonate cotransporter, member 5  
smoothelin

stonin 2

sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1

thyroid hormone receptor beta

transmembrane protein 82

triggering receptor expressed on myeloid cells-like 1

U1 spliceosomal RNA

YdjC homolog (bacterial)

/KY and LEW rat strains that are also di

<b>Ensembl Gene ID</b>	<b>CHR</b>
ENSRNOG00000018126	chr5
ENSRNOG00000020624	chr1
ENSRNOG00000008990	chr8
ENSRNOG00000019656	chr16
ENSRNOG00000020837	chr10
ENSRNOG00000021840	chr4
ENSRNOG00000000522	chr20
ENSRNOG00000006963	chr13
ENSRNOG00000020702	chr1
ENSRNOG00000027841	chr4
ENSRNOG00000013615	chr1
ENSRNOG00000012531	chr5
ENSRNOG00000001931	chr11
ENSRNOG00000019902	chr1
ENSRNOG00000017202	chr8
ENSRNOG00000015078	chr1
ENSRNOG00000028149	chr9
ENSRNOG00000026857	chr1
ENSRNOG00000014969	chr1
ENSRNOG00000012886	chr7
ENSRNOG00000017087	chr5
ENSRNOG00000015089	chr2
ENSRNOG00000015024	chr2
ENSRNOG00000016038	chr1
ENSRNOG00000028344	chr20
ENSRNOG00000003276	chr10
ENSRNOG00000014104	chr18
ENSRNOG00000010873	chr5
ENSRNOG00000005124	chr6
ENSRNOG000000037621	chr14
ENSRNOG00000005515	chr10
ENSRNOG00000010131	chr3
ENSRNOG00000013190	chr1
ENSRNOG00000006720	chr13
ENSRNOG00000013552	chr1
ENSRNOG00000017804	chr1
ENSRNOG00000020797	chr2
ENSRNOG00000005291	chr7
ENSRNOG00000010378	chr4
ENSRNOG00000019451	chr14

ENSRNOG00000004458	chr6
ENSRNOG000000033110	chr5
ENSRNOG000000006649	chr15
ENSRNOG000000011970	chr5
ENSRNOG000000040109	chr9
ENSRNOG000000035334	chr2
ENSRNOG00000001861	chr11

fferentially expressed between the two strains in the same tissue.

### DMR Gene overlap

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70555077-70555215  
190990317-190990437  
11391719-11392350  
7121594-7121762  
91104033-91104084/91104084-91104178/91103844-91104033/91104033-91104041  
48334740-48334986  
7471342-7471507/7471342-7471507  
44601546-44601743  
213078596-213079072/213078596-213079072  
157369967-157369979  
246217613-246217908  
155446650-155447336/155447682-155447726/155578344-155578692  
74423528-74423536  
159315263-159315432/159315263-159315300  
75999078-75999242  
201199522-201199807/201199807-201200184/201199716-201199807  
65578002-65578018/65578002-65578018  
135484912-135485255  
250085410-250085533  
117335736-117336128  
153336351-153336935/153345531-153346146  
244382399-244382456/244382223-244382399  
244285393-244285537/244286406-244286792  
196783603-196784043  
13130833-13131181  
68789450-68789566/68789190-68789566  
71444981-71445138  
154761710-154762122  
7949640-7949973  
92374023-92374031  
68549388-68549672  
134342611-134342621/134416266-134416684  
47244465-47244525  
48283546-48283871  
249471145-249471156/249470979-249471145  
186478917-186479089  
182060749-182061173  
135296975-135297088  
117447942-117448201  
84172871-84173275/84173275-84173369/84173369-84173390

115280790-115281128

76087419-76087478/76088075-76088118/76087478-76088075/76203959-76203980

9324042-9324638

160519056-160519285

8052189-8052235/8052044-8052189

244285393-244285537

85848019-85848083/85847836-85848019/85847836-85848164/85848019-85848083



Average methylation difference	Gene feature	log <sub>2</sub> fold change (diff. expression)
-0.55	intron	0.77
-0.65	intron	1.13
-0.40	intron	-2.56
-0.49	intron	0.81
-0.43/-0.43/-0.43/-0.43	exon/intron/upstream/5' UTR	3.42
0.38	intron	-2.27
-0.41/-0.41	downstream/intron	-1.95
-0.34	intron	-1.05
-0.37/-0.37	exon/3' UTR	-1.03
0.38	intron	-1.23
-0.42	intron	4.31
0.35/0.36/0.40	intron/intron/intron	-5.29
0.35	intron	3.21
-0.40/-0.40	exon/3' UTR	-1.58
0.48	intron	-2.78
-0.39/-0.39/-0.39	exon/upstream/5' UTR	3.62
0.38/0.38	end/intron	1.30
-0.35	exon	1.37
0.35	intron	-0.97
0.35	intron	-2.66
-0.43/-0.46	intron/intron	1.04
-0.49/-0.489	exon/intron	-1.22
-0.35/0.40	intron/intron	-2.63
0.38	intron	1.06
-0.34	intron	-1.81
0.39/0.39	downstream/intron	-2.94
-0.44	intron	-3.46
0.36	intron	0.82
0.43	intron	-5.27
0.37	intron	-4.04
-0.38	intron	6.22
0.43/0.40	intron/intron	0.96
0.40	exon	0.80
0.44	intron	-0.86
0.36/0.36	exon/intron	-1.68
-0.34	up	-2.01
-0.41	intron	2.18
-0.42	intron	1.75
0.43	intron	-1.37
0.49/0.49/0.49	exon/intron/exon	-2.02

-0.38	intron	-1.62
-0.45/-0.45/-0.45/0.34	exon/exon/intron/upstream	1.37
-0.39	intron	1.20
-0.40	up	-3.02
-0.37/-0.37	exon/intron	1.90
-0.35	up	-8.45
0.41/0.41/0.41/0.41	exon/intron/upstream/5' UTR	-1.91

**adjusted p-value  
(diff. expression)**

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0.014  
0.002  
0.001  
0.038  
0.011  
2.74E-04  
0.049  
0.005  
0.011  
0.029  
1.25E-15  
8.28E-05  
0.032  
0.002  
0.007  
1.71E-08  
0.008  
5.80E-06  
0.007  
5.90E-12  
0.006  
0.002  
2.42E-19  
0.034  
0.040  
6.45E-24  
5.37E-05  
0.030  
6.75E-09  
1.41E-05  
1.08E-40  
0.028  
0.029  
0.049  
0.027  
0.001  
0.012  
2.60E-08  
1.86E-04  
8.91E-06

0.012  
0.015  
0.032  
1.87E-04  
0.002  
0.008  
5.69E-09

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