Table 2. Identification of *Abcc6* as the candidate gene for *Dyscalc1* using *cis*-eQTL analysis

Symbol	Description	B6.apoE-/- vs. C3H.apoE-/-		*cis*-eQTL lod score	
		P(Wilcoxon)	*P*(*t* test)	BxH.apoE-/-	BxD
*Nucb1**	Nucleobindin 1	2.22E-05	<0.0001	3.9	NS
Tulp2	Tubby-like protein 2	NS	NS	NS	NS
Myd116	Myeloid differentiation primary response gene 116	0.0125	0.0102	NS	NS
*Plekha4**	Pleckstrin domain-containing protein family A member 4	8.71E-09	<0.0001	8.7†	n/a
Dhrs10	Dehydrogenase/reductase (SDR family) member 10	NS	0.0201	2.3	n/a
Bcat2	Branched-chain amino acid aminotransferase	n/a	n/a	n/a	n/a
*Fgf21**	Fibroblast growth factor-21	1.31E-07	<0.0001	6.8†	NS
Fut1	Fucosyltransferase 1	NS	NS	NS	NS
Izumo1	Izumo sperm-egg fusion 1	NS	NS	NS	NS
Rasip1	Ras-interacting protein 1	0.0155	0.012	3.0	NS
5430432N15Rik*	Riken cDNA 5430432N15 gene	7.80E-10	<0.0001	17.6†	NS
*Fut2**	Fucosyltransferase 2	8.03E-05	<0.0001	NS	2.8
Sec1	Secretory blood group 1	NS	NS	NS	NS
Ensmusg59749	NP_665806 peptide	n/a	n/a	n/a	n/a
*Car11**	Carbonic anhydrase 11	2.88E-23	<0.0001	56.5†	NS
Dbp	D site albumin promoter binding protein	NS	NS	NS	NS
*Sphk2**	Sphingosine kinase 2	1.37E-17	<0.0001	NS	18.5†
Ensmusg59070	n/a	n/a	n/a	n/a	n/a
4930403C10Rik	Riken cDNA 4930403C10 gene	NS	NS	NS	NS
Spaca4	Sperm acrosome associated 4	NS	NS	NS	NS
Sult2b1	Sulfotransferase family, cytosolic, 2B, member 1	NS	NS	4.5†	NS
Lmtk3	Lemur tyrosine kinase 3	NS	NS	NS	NS
Pscd2	Pleckstrin homology, Sec7 and coiled-coil domain 2	NS	0.031	NS	NS
*Kcnj14**	Potassium inwardly-rectifying channel J14	1.96E-14	<0.0001	21.6†	n/a
Grwd1	Glutamate-rich WD repeat containing 1	NS	NS	NS	n/a
Grin2d	Glutamate receptor, ionotropic, NMDA2D (epsilon 4)	NS	NS	NS	NS
Kdelr1	KDEL endoplasmic reticulum protein retention receptor 1	NS	0.0454	2.1	NS
Syngr4	Synaptogyrin 4	NS	NS	NS	NS
2310076021Rik*	Riken cDNA 2310076021 gene	1.75E-15	<0.0001	33.4†	NS
Emp3	Epithelial membrane protein-3	NS	NS	NS	2.7
BC013491	cDNA sequence BC013491	NS	NS	NS	n/a
Abcc6*	**ATP-binding cassette, subfamily C, member 6**	**5.57E-26**	**<0.0001**	**65.2†**	**6.1†**
Nomo1	Nodal modulator 1	NS	NS	NS	n/a
Kcnj11	ATP-sensitive inward rectifier potassium channel 11	NS	NS	NS	NS
Abcc8	ATP-binding cassette, subfamily C, member 8	NS	NS	NS	NS
Ush1c	Harmonin (Usher syndrome 1C protein homolog)	NS	NS	NS	NS
Q8CB92	n/a	n/a	n/a	n/a	n/a
Otog	Otogelin	NS	NS	NS	NS

Genes are listed in order of chromosomal location on Chromosome 7. Using the BxH cross generated on an apoE null background (BxH.apoE-/-), we compared F_2 mice with B6 homozygous genotype (B6.apoE-/-, N = 71) and C3H homozygous genotype (C3H.apoE-/-, N = 79) at the *Abcc6* locus, 12 and 15 genes showed significantly ($P < 0.05$) differential expression using nonparametric Wilcoxon test and Student's *t* test, respectively. After Bonferroni correction, 10 genes remained significant for both analyses, as indicated (*). Significant *P* values for the two analyses are shown. Logarithm of the odds (lod) scores for genes showing a *cis*-eQTL lod score of > 2.0 are shown. Lod scores > 4.3 (†) are considered significant for each cross. NS, not significant; n/a, not represented on the microarray chip.