

**Supplemental Table 1.** Primers for identifying the 129 region in each backcrossing generation

Marker	Location		Forward primer (5'-3')	Reverse primer (5'-3')
		(Mb)		
D1Mit386	102.3		CTCTTTTGTCTCTCTTTGTC	TGCCTTGAAGGCACAATGTA
D1Mit495	129.5		CCACCTTGCTCCAAAAGAAA	TCTGAGAGGCTGCCACAATA
rs4222719	158.3		TCTGTGCCCTATCATTCCCTA	GCCAACAACAAAATGGAGT
rs3711833	158.6		CTAACCTGGGAGCACACAAA	CTGTGGAGAGATGCCAAATG
D1Mit159	161.6		TCTGGGGCCACTATGAGATC	CACAATCAGAAAATATTATGA
D1Mit111	170.9		TTGCCTGACTCCAGTATTCTA	TTAGGTGTGTGAAAGACATTC
D1Mit206	174.9		TGAGGCACCTTTGTATTCAGC	CCAGATGTCTTTGAACATTCTC
D1Mit406	190.1		GAACTTGGAAACAAATATGA	TGCAAGAGAGTAAGTTTTACT
D1Mit291	186.6		TGCCCGTGATAACCCTATGT	TTGTGCACAAGCAGGAGC

**Supplemental Table 2.** QTL positional candidate genes

Mb	Gene	Mb	Gene	Mb	Gene	Mb	Gene
<b><u>Hdlq21 on Chr.3</u></b>							
127.68	<i>Alpk1</i>	127.80	<i>BC002199</i>	127.81	<i>NP_666076.2</i>	127.86	<i>5730508B09Rik</i>
127.78	<i>T2bp</i>						
<b><u>Hdlq52 on Chr5</u></b>							
8.05	<i>Sri</i>	11.06	<i>XR_002301.1</i>	12.39	<i>Sema3d</i>	21.32	<i>Slc26a5</i>
8.08	<i>Adam22</i>	11.19	<i>Speer1-ps1</i>	13.40	<i>Sema3a</i>	21.40	<i>Reln</i>
8.89	<i>Abcb4</i>	11.43	<i>EG623898</i>	14.03	<i>Sema3e</i>	22.00	<i>Orc5l</i>
9.27	<i>9330182L06Rik</i>	11.60	<i>NP_001033008.1</i>	14.52	<i>Pclo</i>	22.26	<i>Lhfpl3</i>
9.49	<i>Grm3</i>	11.61	<i>XR_002301.1</i>	15.45	<i>Cacna2d1</i>	22.95	<i>Mll5</i>
10.87	<i>EG623898</i>	11.93	<i>EG623898</i>	21.00	<i>Fbxl13</i>	23.02	<i>Srpk2</i>
<b><u>Hdlq44 on Chr.8</u></b>							
71.21	<i>Sh2d4a</i>	83.60	<i>Smarca5</i>	84.61	<i>Inpp4b</i>	86.18	<i>Ucp1</i>
71.29	<i>4732435N03Rik</i>	83.66	<i>Gab1</i>	85.23	<i>Il15</i>	86.20	<i>Elmod2</i>
71.72	<i>Ints10</i>	83.88	<i>Usp38</i>	85.65	<i>Zfp330</i>	86.24	<i>4933434I20Rik</i>
71.81	<i>Lpl</i>	83.91	<i>NP_776143.1</i>	85.75	<i>Rnf150</i>	86.28	<i>Clgn</i>
71.97	<i>Slc18a1</i>	84.20	<i>XR_003287.1</i>	86.06	<i>Tbc1d9</i>	86.32	<i>Scoc</i>
<b><u>Hdlq56 on Chr17</u></b>							
52.94	<i>Rab5a</i>	53.14	<i>Sgoll</i>	53.29	<i>Sult1c2</i>	53.75	<i>Slc5a7</i>
53.03	<i>Pcaf</i>	53.19	<i>4932415M13Rik</i>	53.43	<i>Sult1c1</i>		
<b><u>Hdlq57 on Chr18</u></b>							
12.12	<i>6030446N20Rik</i>	12.27	<i>Riok3</i>	12.31	<i>3110002H16Rik</i>		

**Supplemental Table 3.** SNPs for screening knockout mice made by stain 129 backcrossing into B6

QTL	Chr	Start SNP		End SNP	
		SNP ID	Position Mb <sup>a</sup>	SNP ID	Position Mb <sup>a</sup>
<i>Hdlq15</i>	1	rs3714825	170.0	rs3699295	175.8
<i>Hdlq21</i>	3	rs3708141	116.9	rs3089257	130.7
<i>Hdlq52</i>	5	rs31363472	7.0	rs6226708	33.7
<i>Hdlq1</i>	5	rs3678094	79.6	rs3705399	127.1
<i>Hdlq53</i>	6	rs4225658	5.4	rs13478673	26.9
<i>Hdlq44</i>	8	rs3089230	71.0	rs3706660	90.1
<i>Hdlq16</i>	8	rs3708282	94.1	rs6296597	122.5
<i>Hdlq17</i>	9	rs3704408	26.7	rs3653389	43.5
<i>Hdlq54</i>	9	rs3682798	60.2	rs3711701	97.2
	11	rs3712384	110.2	rs3023710	117.7
	13	rs3695486	4.1	rs3090002	53.2
<i>Hdlq55</i>	14	rs47145951	94.4	rs3665847	117.5
<i>Hdlq56</i>	17	rs13482973	37.7	rs4231722	86.7
<i>Hdlq57</i>	18	rs3718907	10.0	rs3693151	37.8
<i>Hdlq47</i>	18	rs3693151	37.8	rs3023468	63.6

<sup>a</sup> Mb is based on NCBI 36.