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Mapping genetic modifiers of survival in a mouse model of Dravet syndrome

Supplementary Data

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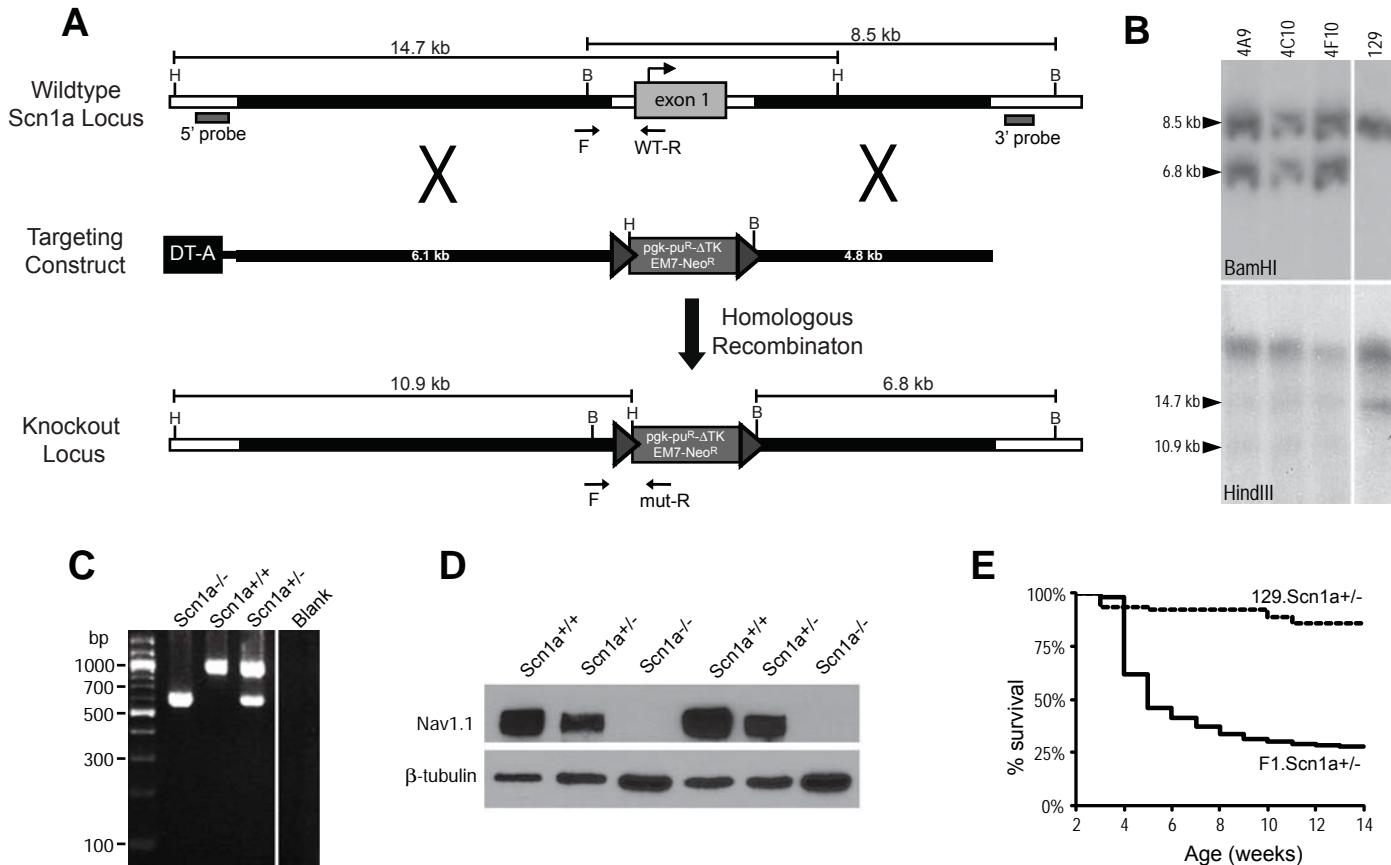


Figure S1. Generation and characterization of *Scn1a*^{+/−} null mice. (A) Exon 1 containing the translation start site was replaced by a selection cassette by homologous recombination in ES cells. The targeting vector contained the pGK-puR-Δtk-EM7-NeoR selection cassette flanked by lox sites (triangles), a 6.1 kb 5' homology arm and a 4.8 kb 3' homology arm. The diphtheria toxin cDNA (DT-A) cassette was located outside of the targeting arm for negative selection against random integrations. Arrows indicate primers for PCR genotyping of mice. Sizes of restriction fragments detected by Southern blot with 5' and 3' probes are indicated for the wild-type and recombinant locus. (B) Southern blot analysis of correctly targeted ES cell clones resulted in a predicted 10.9 kb fragment detected with the 5' probe in HindIII (H)-digested DNA and a predicted 6.8 kb fragment detected with the 3' probe in BamHI (B)-digested DNA. (C) Genotyping of offspring from intercrossing 129.Scn1a^{+/−} heterozygotes using multiplex PCR with primers F, WT-R and mut-R results in amplification of 983 bp product from the wild-type allele and a 622 bp product from the knockout allele. (D) Immunoblotting of brain membrane proteins (50 µg) with an Nav1.1 antibody (NeuroMab, clone K74/71) confirms the absence of Nav1.1 in *Scn1a*^{−/−} null homozygotes and reduction of Nav1.1 protein in *Scn1a*^{+/−} null heterozygotes compared to wildtype *Scn1a*^{+/+} mice. Immunoblotting for β-tubulin (Sigma, clone TUB2.1) serves as a loading control. Two representative biological replicates are shown. (E) Survival of F1.Scn1a^{+/−} mice (n=195) is significantly reduced compared to 129.Scn1a^{+/−} mice (n=63) (Log-Rank (Mantel-Cox) p<0.0001).

Supplementary Table S1. Single point marker analysis in 129-N2 early lethal progeny. All mapping progeny were obligate *Scn1a*^{+/−} heterozygotes and are expected to carry homozygous 129 alleles at the Scn1a locus on chromosome 2 (grey shading). Markers with a significant deviation from the expected Mendelian 1:1 ratio for a backcross are indicated by yellow shading ($p < 0.05$).

Chr	Marker	Pos (Mb)*	χ^2 value	p value
1	D1Mit211	25.5	0.000	1.000
1	D1Mit303	62.9	1.500	0.221
1	D1Mit424	160.8	0.667	0.414
1	D1Mit206	173.0	1.500	0.221
2	D2Mit1	3.9	0.000	1.000
2	D2Mit372	36.1	8.067	0.005
2	<i>Scn1a</i>	66.3	15.000	0.000
2	D2Mit206	106.9	11.267	0.001
2	D2Mit493	154.0	4.571	0.033
2	D2Mit148	178.8	0.286	0.593
3	D3Mit130	10.2	0.167	0.683
3	D3Mit278	72.0	0.222	0.637
3	D3Mit346	116.2	0.667	0.414
3	D3Mit44	148.1	0.167	0.683
4	D4Mit264	9.4	0.286	0.593
4	D4Mit178	67.2	0.529	0.467
4	D4Mit130	146.2	0.529	0.467
5	D5Mit346	4.9	5.261	0.022
5	D5Mit1	17.6	8.167	0.004
5	D5Mit349	25.0	10.667	0.001
5	D5Mit391	44.7	8.167	0.004
5	D5Mit197	64.6	3.522	0.061
5	D5Mit291	126.2	2.571	0.109
5	D5Mit286	150.2	0.000	1.000
6	D6Mit139	6.9	0.222	0.637
6	D6Mit268	34.7	0.000	1.000
6	D6Mit241	56.6	0.333	0.564
6	D6Mit102	93.5	0.222	0.637
6	D6Mit52	127.8	0.889	0.346
7	D7Mit152	4.7	2.571	0.109
7	D7Mit342	16.6	1.000	0.317
7	D7Mit145	51.4	0.000	1.000
7	D7Mit238	119.1	0.048	0.827
8	D8Mit155	5.0	0.286	0.593
8	D8Mit339	40.3	0.286	0.593
8	D8Mit242	101.8	1.087	0.297
8	D8Mit121	123.9	2.130	0.144
9	D9Mit1001	39.7	0.800	0.371
9	D9Mit1006	51.9	0.727	0.394
9	D9Mit182	101.5	0.059	0.808
10	D10Mit183a	22.4	1.800	0.180
10	D10Mit31	68.3	0.200	0.655
10	D10Mit266	115.0	0.727	0.394

Chr	Marker	Pos (Mb)*	χ^2 value	p value
11	D11Mit71	6.9	5.762	0.016
11	D11Mit2	12.3	6.000	0.014
11	D11Mit78	17.9	6.000	0.014
11	D11Mit188	45.3	2.667	0.102
11	D11Mit310	54.2	2.130	0.144
11	D11Mit48	118.1	2.130	0.144
12	D12Mit12	24.7	0.474	0.491
12	D12Mit201	72.3	0.391	0.532
12	D12Mit263	113.5	1.087	0.297
13	D13Mit64	45.1	1.087	0.297
13	D13Mit99	76.8	0.000	1.000
13	D13Mit77	116.9	0.043	0.835
14	D14Mit109	12.6	0.053	0.819
14	D14Mit268	54.9	0.800	0.371
14	D14Mit165	106.6	0.043	0.835
15	D15Mit252	22.6	0.800	0.371
15	D15Mit85	40.3	0.889	0.346
15	D15Mit242	90.4	2.130	0.144
16	D16Mit129	6.1	1.143	0.285
16	D16Mit64	57.5	0.182	0.670
16	D16Mit106	97.8	0.077	0.782
17	D17Mit19	4.8	0.600	0.439
17	D17Mit50	45.4	0.391	0.532
17	D17Mit180	51.4	1.087	0.297
18	D18Mit64	6.1	0.043	0.835
18	D18Mit60	32.5	0.000	1.000
18	D18Mit55	53.2	0.391	0.532
18	D18Mit40	63.7	0.474	0.491
19	D19Mit135	31.9	0.000	1.000
19	D19Mit10	47.2	0.200	0.655

*GRC m38 assembly

Supplementary Table S2. Number of genes with significant differences by RNA-seq in *Dsm* 1.5 LOD support intervals.

Category		<i>Dsm1</i> (Chr5:50.7-77.4 Mb)	<i>Dsm4</i> (Chr5:14.0-107.0 Mb)	<i>Dsm2</i> (Chr 7:16.6-70.8 Mb)	<i>Dsm3</i> (Chr 8:49.6-114.4 Mb)	<i>Dsm5</i> (Chr 11:6.9-57.1 Mb)
Expression or Regulation	Transcript	27	116	90	94	64
	Gene	5	19	19	15	12
	TSS	10	49	42	51	31
	Promoter	14	60	70	55	36
	Splicing	15	62	52	56	31
	TOTAL*	36	148	127	122	81
SNPs	Missense	14	61	111	105	10
	Stop Gained	-	-	3	-	-

*Total number of genes with a significant difference in any RNA-seq category. Genomic positions based on GRC m38 assembly.

Supplementary Table S3. Significant Differences in *Dsm* intervals by RNA-Seq. Significant differences are indicated by q-values (FDR-adjusted p-values); open boxes indicate no difference. Genes with a prior association with epilepsy or hyperexcitability are highlighted with yellow shading.

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
<i>Dsm4</i>	5	14.025276 - 14.256689	<i>Sema3e</i>	4.5E-02				1.7E-06
<i>Dsm4</i>	5	14.514918 - 14.863457	<i>Pclo</i>	1.0E-14				1.1E-05
<i>Dsm4</i>	5	15.934691 - 16.374511	<i>Cacna2d1</i>	1.1E-08		1.0E-14	4.4E-03	6.1E-11
<i>Dsm4</i>	5	17.574281 - 17.730268	<i>Sema3c</i>	1.3E-02		1.6E-02		
<i>Dsm4</i>	5	19.227046 - 20.704798	<i>Magi2</i>	5.2E-03				
<i>Dsm4</i>	5	20.758663 - 20.882124	<i>Phf2</i>	9.8E-03				
<i>Dsm4</i>	5	20.986645 - 21.055911	<i>Ptpn12</i>				5.0E-02	
<i>Dsm4</i>	5	21.737141 - 21.757152	<i>Pmpcb</i>	3.5E-02	1.5E-03			
<i>Dsm4</i>	5	21.884454 - 22.344702	<i>Reln</i>	4.5E-02				
<i>Dsm4</i>	5	23.434441 - 23.504235	<i>Mll5</i>	2.2E-05				
<i>Dsm4</i>	5	23.787711 - 23.820369	<i>Rint1</i>	2.7E-02		1.5E-03	2.1E-04	7.3E-06
<i>Dsm4</i>	5	23.915276 - 24.030690	<i>Fam126a</i>	4.9E-03		6.3E-03	2.8E-02	1.0E-14
<i>Dsm4</i>	5	24.319589 - 24.351604	<i>Kcnh2</i>	7.8E-03		1.0E-02		
<i>Dsm4</i>	5	24.393663 - 24.410054	<i>Abcb8</i>	4.3E-02		1.0E-02	8.0E-03	
<i>Dsm4</i>	5	24.423837 - 24.440950	<i>Slc4a2</i>	2.0E-02		5.0E-02	5.1E-03	1.7E-03
<i>Dsm4</i>	5	24.438440 - 24.445287	<i>Fastk</i>	4.3E-02	3.2E-02	3.0E-02		
<i>Dsm4</i>	5	24.452177 - 24.502047	<i>Agap3</i>				1.6E-02	
<i>Dsm4</i>	5	24.586741 - 24.594395	<i>Chpf2</i>	1.4E-03				3.9E-03
<i>Dsm4</i>	5	24.590818 - 24.602012	<i>Smarcd3</i>	3.1E-02				
<i>Dsm4</i>	5	24.802823 - 24.842624	<i>Rheb</i>	9.1E-03	4.2E-02			
<i>Dsm4</i>	5	24.862744 - 25.100642	<i>Prkag2</i>				4.9E-02	2.4E-03
<i>Dsm4</i>	5	24.985842 - 24.998168	<i>1500035N22Rik</i>	1.2E-02	2.7E-02	1.6E-02		
<i>Dsm4</i>	5	25.222882 - 25.265918	<i>Galnt11</i>	1.9E-02				
<i>Dsm4</i>	5	25.271798 - 25.498783	<i>Mll3</i>	5.6E-03				4.5E-02
<i>Dsm4</i>	5	25.759997 - 25.850342	<i>Actr3b</i>	2.1E-04				
<i>Dsm4</i>	5	26.817203 - 27.727505	<i>Dpp6</i>	2.5E-02				
<i>Dsm4</i>	5	28.071363 - 28.078662	<i>Insig1</i>	1.2E-02	2.7E-02	1.5E-02		
<i>Dsm4</i>	5	28.200819 - 28.245792	<i>Cnpy1</i>	4.9E-02				
<i>Dsm4</i>	5	29.195992 - 29.225524	<i>Rnf32</i>	3.4E-02				
<i>Dsm4</i>	5	30.118301 - 30.184593	<i>Hadha</i>					3.6E-02
<i>Dsm4</i>	5	30.232581 - 30.272012	<i>Ept1</i>	2.8E-02				
<i>Dsm4</i>	5	30.711564 - 30.799375	<i>Dpysl5</i>				2.9E-02	
<i>Dsm4</i>	5	30.814641 - 30.866106	<i>Mapre3</i>				3.8E-02	1.3E-02
<i>Dsm4</i>	5	30.869579 - 30.879191	<i>Tmem214</i>					1.2E-03
<i>Dsm4</i>	5	30.888694 - 30.906965	<i>Agbl5</i>	4.1E-02				1.4E-02
<i>Dsm4</i>	5	30.950066 - 30.955091	<i>Abhd1</i>	1.9E-08	3.8E-05	9.1E-09	1.0E-14	3.0E-05
<i>Dsm4</i>	5	30.950853 - 30.960330	<i>Preb</i>	2.1E-02			1.2E-04	2.5E-02
<i>Dsm4</i>	5	31.036036 - 31.048924	<i>Slc5a6</i>	5.0E-02		2.3E-03	7.1E-03	1.0E-14
<i>Dsm4</i>	5	31.048312 - 31.054633	<i>0610007C21Rik</i>	1.1E-02	5.2E-04	3.9E-03	1.0E-14	1.5E-02

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
<i>Dsm4</i>	5	31.054780 - 31.078479	<i>Cad</i>	4.1E-03		5.3E-03	1.5E-09	
<i>Dsm4</i>	5	31.140660 - 31.158153	<i>Gtf3c2,Mpv17</i>				2.5E-06	
<i>Dsm4</i>	5	31.140660 - 31.158153	<i>Mpv17</i>	2.2E-02				3.1E-02
<i>Dsm4</i>	5	31.151142 - 31.180144	<i>Gtf3c2</i>	4.7E-02				3.2E-02
<i>Dsm4</i>	5	31.187558 - 31.193430	<i>Eif2b4</i>	2.0E-04				
<i>Dsm4</i>	5	31.193227 - 31.198900	<i>Snx17</i>	3.3E-02		4.1E-02	1.9E-03	4.4E-05
<i>Dsm4</i>	5	31.624439 - 31.697627	<i>Rbks</i>	2.6E-02				
<i>Dsm4</i>	5	31.697684 - 32.084962	<i>Bre</i>	2.4E-03				
<i>Dsm4</i>	5	32.136472 - 32.157831	<i>Fosl2</i>	4.1E-02				
<i>Dsm4</i>	5	32.736301 - 32.785646	<i>Pisd</i>	4.5E-02		1.2E-02		3.3E-02
<i>Dsm4</i>	5	32.789218 - 32.854256	<i>C330019G07Rik</i>	3.0E-02	1.6E-04	3.9E-02	9.2E-03	5.7E-03
<i>Dsm4</i>	5	32.863701 - 32.994231	<i>Depdc5</i>	3.2E-02				
<i>Dsm4</i>	5	33.018816 - 33.027966	<i>Ywhah</i>	1.3E-02				
<i>Dsm4</i>	5	33.721724 - 33.737068	<i>Fgfr3</i>	3.3E-03		2.2E-02	6.7E-03	4.4E-02
<i>Dsm4</i>	5	33.759366 - 33.759536	<i>Gm10059</i>	1.0E-14	1.0E-14			
<i>Dsm4</i>	5	33.820725 - 33.897975	<i>Whsc1</i>	3.2E-02			4.8E-07	1.5E-03
<i>Dsm4</i>	5	34.194874 - 34.288449	<i>Zfyve28</i>	3.6E-02			2.2E-03	3.1E-02
<i>Dsm4</i>	5	34.573664 - 34.632308	<i>Add1</i>	1.4E-02			4.8E-04	1.1E-03
<i>Dsm4</i>	5	34.949445 - 35.039644	<i>Rgs12</i>	2.7E-02				1.3E-06
<i>Dsm4</i>	5	35.091490 - 35.105766	<i>Lrpap1</i>	1.9E-02		2.4E-02	3.9E-02	
<i>Dsm4</i>	5	35.757880 - 35.884973	<i>Ablim2</i>	1.4E-02		1.5E-02	8.2E-04	4.4E-03
<i>Dsm4</i>	5	36.490604 - 36.593276	<i>Tbc1d14</i>	3.7E-02		4.6E-02	0.0E+00	6.8E-04
<i>Dsm4</i>	5	36.868513 - 36.955078	<i>Ppp2r2c</i>				4.1E-03	
<i>Dsm4</i>	5	36.966104 - 36.988982	<i>Wfs1</i>		1.9E-02	4.7E-02		
<i>Dsm4</i>	5	37.242080 - 37.292132	<i>Crmp1</i>	3.4E-02		2.8E-02		
<i>Dsm4</i>	5	37.289098 - 37.336894	<i>Evc</i>				6.2E-03	1.1E-02
<i>Dsm4</i>	5	38.038742 - 38.137765	<i>Stx18</i>				1.7E-02	
<i>Dsm4</i>	5	38.260185 - 38.269622	<i>Tmem128</i>	1.5E-02			8.0E-03	
<i>Dsm4</i>	5	43.662379 - 43.740972	<i>Cc2d2a</i>	3.7E-02				
<i>Dsm4</i>	5	43.744616 - 43.821639	<i>Fbxl5</i>	2.5E-03		8.7E-08		
<i>Dsm4</i>	5	43.818886 - 43.843247	<i>Bst1</i>	4.8E-03		4.5E-03	5.2E-04	2.9E-03
<i>Dsm4</i>	5	43.993625 - 44.102032	<i>Prom1</i>	3.2E-02				
<i>Dsm4</i>	5	45.434032 - 45.450235	<i>Qdpr</i>	1.9E-03	7.2E-08	2.4E-03	4.2E-02	4.0E-02
<i>Dsm4</i>	5	45.669922 - 45.700544	<i>Ncapg</i>				8.0E-03	
<i>Dsm4</i>	5	45.697181 - 45.857615	<i>Lcorl</i>			2.6E-02		2.0E-02
<i>Dsm4</i>	5	47.983155 - 48.306282	<i>Slit2</i>	4.7E-04				
<i>Dsm1</i>	5	52.537864 - 52.566303	<i>Lgi2</i>	3.9E-03	9.4E-03	6.2E-03		9.2E-03
<i>Dsm1</i>	5	52.640087 - 52.669729	<i>Sept11</i>	4.7E-02				2.3E-03
<i>Dsm1</i>	5	52.834015 - 52.867797	<i>Anapc4</i>				2.2E-03	
<i>Dsm1</i>	5	53.267106 - 53.283510	<i>18J0013D10Rik</i>					3.8E-02
<i>Dsm1</i>	5	53.555779 - 53.657445	<i>Rbpj</i>	9.1E-04	4.8E-02	1.2E-03		
<i>Dsm1</i>	5	53.998417 - 54.121057	<i>Stim2</i>	5.1E-04				

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
<i>Dsm1</i>	5	57.718021 - 58.129351	<i>Pcdh7</i>				7.7E-03	
<i>Dsm1</i>	5	62.602445 - 62.766198	<i>Arap2</i>				1.1E-02	
<i>Dsm1</i>	5	64.159451 - 64.351486	<i>Tbc1d1</i>	3.1E-02				
<i>Dsm1</i>	5	65.107568 - 65.168188	<i>Klhl5</i>	4.8E-02				
<i>Dsm1</i>	5	65.199696 - 65.260415	<i>Wdr19</i>	3.4E-02		4.3E-02		
<i>Dsm1</i>	5	65.413202 - 65.435946	<i>Ugdh</i>	6.2E-04		8.1E-04	3.5E-04	
<i>Dsm1</i>	5	65.446844 - 65.537184	<i>1110003E01Rik</i>				3.2E-02	
<i>Dsm1</i>	5	65.537233 - 65.598988	<i>Ube2k</i>	3.0E-03		3.9E-03	1.1E-02	
<i>Dsm1</i>	5	66.298861 - 66.618828	<i>Apbb2</i>	2.8E-02				
<i>Dsm1</i>	5	66.745835 - 67.057159	<i>Limch1</i>	2.5E-02				
<i>Dsm1</i>	5	67.260565 - 67.291461	<i>Tmem33</i>	1.5E-03				1.2E-02
<i>Dsm1</i>	5	67.607883 - 67.623552	<i>Shisa3</i>					0.0E+00
<i>Dsm1</i>	5	67.618140 - 67.847432	<i>Atp8a1</i>				1.0E-14	2.2E-04
<i>Dsm1</i>	5	67.847066 - 67.909013	<i>Gm15477</i>					2.2E-02
<i>Dsm1</i>	5	69.556924 - 69.575972	<i>Guf1</i>	3.6E-02		4.5E-02	3.1E-02	3.5E-03
<i>Dsm1</i>	5	69.573108 - 69.592337	<i>Gnpda2</i>					4.1E-02
<i>Dsm1</i>	5	70.961057 - 71.095849	<i>Gabra2</i>	1.0E-14	1.0E-14	1.0E-14		
<i>Dsm1</i>	5	73.020322 - 73.256618	<i>Fryl</i>	2.5E-02		3.1E-02	4.5E-03	
<i>Dsm1</i>	5	73.292794 - 73.314077	<i>Ociad1</i>	2.7E-02				0.0E+00
<i>Dsm1</i>	5	73.481002 - 73.560794	<i>Dcun1d4</i>	4.8E-02			2.8E-02	3.0E-02
<i>Dsm1</i>	5	73.998463 - 74.068430	<i>Usp46</i>	4.2E-02				
<i>Dsm1</i>	5	74.204816 - 74.531747	<i>Scfd2</i>	1.6E-04				
<i>Dsm1</i>	5	74.535449 - 74.598790	<i>Fip111</i>	3.4E-02			3.1E-02	1.0E-14
<i>Dsm1</i>	5	74.592446 - 74.702911	<i>Lnx1</i>	3.9E-02		4.9E-02	7.1E-14	1.0E-14
<i>Dsm1</i>	5	75.932827 - 75.978458	<i>Kdr</i>	2.0E-02	4.4E-02	2.5E-02		
<i>Dsm1</i>	5	76.212177 - 76.304548	<i>Clock</i>	4.7E-02				
<i>Dsm1</i>	5	76.529311 - 76.570294	<i>Exoc1</i>	4.1E-03			2.6E-02	2.9E-02
<i>Dsm1</i>	5	76.928368 - 76.947758	<i>2310040G07Rik</i>	9.3E-04	1.7E-03			
<i>Dsm1</i>	5	76.951307 - 76.967509	<i>Paics</i>	3.3E-02				
<i>Dsm1</i>	5	76.974683 - 76.999937	<i>Srp72</i>	2.7E-02			3.7E-02	4.1E-03
<i>Dsm4</i>	5	81.020138 - 81.825133	<i>Lphn3</i>	4.6E-02				
<i>Dsm4</i>	5	84.057791 - 84.417382	<i>Epha5</i>	3.1E-02				
<i>Dsm4</i>	5	84.123313 - 84.123591	<i>Hmgm2-ps1</i>	3.5E-04	6.7E-04			
<i>Dsm4</i>	5	86.110720 - 86.172803	<i>Uba6</i>	3.6E-02		4.5E-02		2.1E-05
<i>Dsm4</i>	5	86.804221 - 86.836659	<i>Ythdc1</i>	4.3E-02				
<i>Dsm4</i>	5	88.583574 - 88.642671	<i>Rufy3</i>				3.2E-02	
<i>Dsm4</i>	5	88.659448 - 88.676171	<i>Grsf1</i>					4.4E-02
<i>Dsm4</i>	5	88.886818 - 89.239653	<i>Slc4a4</i>					1.7E-02
<i>Dsm4</i>	5	89.673841 - 89.883334	<i>Adamts3</i>	6.3E-06				
<i>Dsm4</i>	5	90.227190 - 90.366185	<i>Ankrd17</i>	4.3E-02				
<i>Dsm4</i>	5	92.006074 - 92.043042	<i>Cdkl2</i>	7.8E-03				
<i>Dsm4</i>	5	92.052146 - 92.083735	<i>G3bp2</i>	2.5E-13				

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
<i>Dsm4</i>	5	93.093457 - 93.174958	<i>Sepsecs</i>	2.2E-04				
<i>Dsm4</i>	5	93.267257 - 93.276231	<i>Ccng2</i>	2.4E-02			3.5E-07	7.4E-03
<i>Dsm4</i>	5	96.070333 - 96.164171	<i>Cnot6l</i>	9.6E-03		7.5E-03	4.4E-02	7.9E-06
<i>Dsm4</i>	5	97.082329 - 97.111596	<i>Paqr3</i>					7.5E-03
<i>Dsm4</i>	5	99.217426 - 99.252927	<i>Rasgef1b</i>	1.0E-02		1.3E-02	2.7E-05	
<i>Dsm4</i>	5	99.958426 - 99.978938	<i>Hnrrpd</i>	4.7E-02	7.6E-03	2.7E-03	3.5E-02	4.6E-05
<i>Dsm4</i>	5	100.033577 - 100.039664	<i>Hnrrpd</i>	2.3E-03		3.0E-03	4.4E-03	
<i>Dsm4</i>	5	100.077872 - 100.159808	<i>Tmem150c</i>	1.1E-02		1.5E-02	1.0E-14	
<i>Dsm4</i>	5	100.077962 - 100.095273	<i>5830403M04Rik</i>				1.0E-14	
<i>Dsm4</i>	5	100.361650 - 100.416234	<i>Sec31a</i>	1.2E-03				5.3E-03
<i>Dsm4</i>	5	100.518309 - 100.547803	<i>Cops4</i>	1.0E-02		1.3E-02	3.2E-03	
<i>Dsm4</i>	5	100.654723 - 100.675140	<i>Coq2</i>				1.7E-02	
<i>Dsm4</i>	5	100.762145 - 100.798598	<i>Helq</i>	4.3E-02		1.5E-02	4.5E-04	1.1E-02
<i>Dsm4</i>	5	102.907948 - 103.211334	<i>Mapk10</i>	3.7E-03		4.8E-03	6.6E-07	2.3E-09
<i>Dsm4</i>	5	103.692374 - 103.855322	<i>Affl</i>	3.7E-02		4.6E-02		
<i>Dsm4</i>	5	103.861973 - 103.911259	<i>Klhl8</i>	4.6E-02				
<i>Dsm4</i>	5	104.079111 - 104.114088	<i>Sparcl1</i>	1.0E-14	1.0E-14	1.0E-14		
<i>Dsm4</i>	5	104.435118 - 104.441050	<i>Spp1</i>	2.5E-02			9.0E-04	5.0E-02
<i>Dsm4</i>	5	104.525735 - 104.554211	<i>D930016D06Rik</i>	3.5E-02		4.4E-02		
<i>Dsm4</i>	5	105.519388 - 105.613018	<i>Lrrc8c</i>					2.6E-02
<i>Dsm4</i>	5	105.699969 - 105.832436	<i>Lrrc8d</i>	3.5E-02				
<i>Dsm4</i>	5	105.814773 - 105.818988	<i>Gm15817</i>	2.7E-02				
<i>Dsm4</i>	5	105.876565 - 105.915818	<i>Zfp326</i>	1.8E-02			8.8E-03	1.6E-02
<i>Dsm4</i>	5	106.500894 - 106.697287	<i>Zfp644</i>	2.3E-02				
<i>Dsm2</i>	7	16.098458 - 16.117975	<i>Napa</i>				1.0E-02	
<i>Dsm2</i>	7	16.119895 - 16.127516	<i>Kptn</i>	2.3E-02		9.3E-03		
<i>Dsm2</i>	7	16.274042 - 16.286795	<i>Ccdc9</i>	3.9E-04		5.1E-04	7.7E-08	
<i>Dsm2</i>	7	16.327053 - 16.387797	<i>Sae1</i>	3.1E-03	6.2E-03	4.2E-03		
<i>Dsm2</i>	7	16.738410 - 16.749294	<i>Ap2s1</i>				4.0E-02	
<i>Dsm2</i>	7	16.815889 - 16.840931	<i>Strn4</i>				4.5E-02	
<i>Dsm2</i>	7	16.915379 - 16.924114	<i>Calm3</i>	2.5E-03	4.9E-03	3.2E-03		
<i>Dsm2</i>	7	17.004640 - 17.027924	<i>Ppp5c</i>	2.9E-02		3.7E-02	2.6E-03	
<i>Dsm2</i>	7	17.074040 - 17.133450	<i>Psg16</i>	1.6E-02	9.6E-04	5.6E-03		3.6E-03
<i>Dsm2</i>	7	18.989554 - 18.992774	<i>Gm10676</i>	9.6E-03	2.0E-02			
<i>Dsm2</i>	7	19.076249 - 19.082776	<i>Dmwd</i>	2.4E-07			3.8E-03	
<i>Dsm2</i>	7	19.083849 - 19.093821	<i>Dmpk</i>	4.3E-02			1.9E-02	2.2E-03
<i>Dsm2</i>	7	19.344778 - 19.356524	<i>Ercc1</i>	3.9E-02				1.1E-04
<i>Dsm2</i>	7	19.382010 - 19.395694	<i>Ercc2</i>	4.0E-02				
<i>Dsm2</i>	7	19.386643 - 19.386717	<i>Ercc2,Mir343</i>		9.5E-04			
<i>Dsm2</i>	7	19.696109 - 19.699166	<i>Apoe</i>				3.5E-04	
<i>Dsm2</i>	7	19.701313 - 19.715438	<i>Tomm40</i>	1.5E-02				4.1E-02
<i>Dsm2</i>	7	24.399619 - 24.422778	<i>1500002O20Rik</i>				1.6E-02	

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
Dsm2	7	24.902912 - 24.926592	<i>Arhgef1</i>	6.5E-03		4.6E-03	9.1E-03	5.9E-08
Dsm2	7	24.978167 - 25.005957	<i>Atp1a3</i>	1.0E-14	3.8E-09	1.1E-10	2.1E-02	
Dsm2	7	25.267704 - 25.294159	<i>Cic</i>	2.7E-02		1.3E-02	8.5E-04	2.7E-03
Dsm2	7	25.306106 - 25.316195	<i>Tmem145</i>	1.3E-02		3.6E-02		
Dsm2	7	25.711106 - 25.719088	<i>Ccdc97</i>					3.2E-03
Dsm2	7	25.721498 - 25.754730	<i>Hnrnpull</i>					8.5E-03
Dsm2	7	25.757273 - 25.788705	<i>Axl</i>	2.7E-02				
Dsm2	7	27.153714 - 27.158668	<i>Cyp2t4</i>	7.1E-03	1.1E-04	9.1E-03	8.9E-03	
Dsm2	7	27.158658 - 27.166802	<i>Egln2</i>				3.1E-03	
Dsm2	7	27.168424 - 27.178896	<i>Mia1,Rab4b</i>				6.8E-11	
Dsm2	7	27.168424 - 27.178896	<i>Rab4b</i>	6.4E-05				3.1E-06
Dsm2	7	27.179742 - 27.181157	<i>Mia1</i>	5.9E-06				1.0E-14
Dsm2	7	27.187005 - 27.196271	<i>Snrpa</i>	7.4E-03				
Dsm2	7	27.233023 - 27.262252	<i>Adck4</i>	4.2E-02				
Dsm2	7	27.258433 - 27.282144	<i>Numbl</i>	3.3E-02				
Dsm2	7	27.305136 - 27.337692	<i>Ltbp4</i>	4.2E-02		1.3E-02	2.4E-03	1.3E-02
Dsm2	7	27.342133 - 27.356019	<i>Shkbp1</i>	2.1E-02				
Dsm2	7	27.356383 - 27.447686	<i>Shkbp1,Spnb4</i>		3.1E-02			
Dsm2	7	27.356383 - 27.447686	<i>Spnb4</i>	2.6E-02				
Dsm2	7	27.523267 - 27.531175	<i>Hipk4</i>			2.1E-02	2.1E-03	
Dsm2	7	27.591552 - 27.640826	<i>Akt2</i>	2.8E-02		1.6E-02	2.0E-02	8.0E-04
Dsm2	7	27.656375 - 27.674598	<i>Map3k10</i>				4.7E-02	
Dsm2	7	27.731389 - 27.753702	<i>Zfp60</i>				4.4E-02	
Dsm2	7	28.041707 - 28.050101	<i>Psmc4</i>	2.2E-02		2.9E-02	2.0E-04	
Dsm2	7	28.392951 - 28.399388	<i>Paf1</i>	2.5E-02		3.2E-02	2.0E-03	
Dsm2	7	28.758251 - 28.767512	<i>Nfkbib</i>	5.1E-04		6.7E-04	2.0E-04	
Dsm2	7	28.766735 - 28.788665	<i>Sirt2</i>	2.8E-02	4.4E-04	3.6E-02	2.2E-03	2.2E-02
Dsm2	7	28.808541 - 28.822266	<i>Hnrnpl</i>	5.0E-03				
Dsm2	7	29.303951 - 29.317588	<i>Dpf1</i>	4.6E-02				1.3E-02
Dsm2	7	29.859979 - 29.877292	<i>Zfp420</i>	4.1E-02			2.5E-02	3.2E-03
Dsm2	7	29.893333 - 29.906572	<i>Zfp27</i>	3.5E-02				7.1E-05
Dsm2	7	30.161274 - 30.169727	<i>Zfp146</i>	1.4E-02		1.7E-02		
Dsm2	7	30.186942 - 30.195164	<i>Capns1</i>				8.8E-03	
Dsm2	7	30.224131 - 30.232272	<i>Tcbc</i>	3.4E-02				
Dsm2	7	30.231948 - 30.233390	<i>Polr2i</i>	4.7E-02		8.5E-05	3.6E-02	1.1E-03
Dsm2	7	30.291672 - 30.308367	<i>Clip3</i>				2.6E-05	2.9E-02
Dsm2	7	30.308717 - 30.314304	<i>Alkbh6</i>	2.3E-02		2.9E-02	1.3E-04	
Dsm2	7	30.434981 - 30.445582	<i>Ap1p1</i>	1.0E-14	1.0E-14	1.0E-14		
Dsm2	7	30.522226 - 30.534180	<i>Arhgap33</i>	1.4E-02		1.8E-02	4.4E-03	
Dsm2	7	30.563301 - 30.567960	<i>U2af1l4</i>	4.6E-02		5.5E-04		1.0E-14
Dsm2	7	30.568858 - 30.588726	<i>Wbp7</i>	1.1E-02	3.8E-02	1.4E-02	7.8E-08	1.6E-02
Dsm2	7	30.640994 - 30.650317	<i>Haus5,Rbm42</i>				1.6E-10	

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
<i>Dsm2</i>	7	30.653711 - 30.664994	<i>Haus5</i>	3.5E-02		4.5E-02		1.3E-03
<i>Dsm2</i>	7	30.899183 - 30.914327	<i>Mag</i>	6.4E-03	3.2E-06	2.4E-06		7.1E-06
<i>Dsm2</i>	7	30.945252 - 30.956803	<i>Usf2</i>	2.7E-02			2.5E-02	2.2E-02
<i>Dsm2</i>	7	30.957409 - 30.983169	<i>Lsr</i>				3.0E-02	3.0E-04
<i>Dsm2</i>	7	30.973804 - 30.989720	<i>Fam187b</i>				1.4E-10	
<i>Dsm2</i>	7	31.042517 - 31.051462	<i>Fxyd7</i>	4.4E-02				1.0E-14
<i>Dsm2</i>	7	31.059342 - 31.070935	<i>Lgi4</i>	2.9E-02	2.3E-02	3.6E-02	1.0E-14	
<i>Dsm2</i>	7	31.068172 - 31.076704	<i>Fxyd3</i>				3.0E-03	3.8E-02
<i>Dsm2</i>	7	34.140689 - 34.169599	<i>Uba2</i>				1.3E-02	
<i>Dsm2</i>	7	34.202122 - 34.230289	<i>Gpi1</i>				1.1E-02	
<i>Dsm2</i>	7	35.186385 - 35.204898	<i>Slc7a10</i>	3.8E-02				2.0E-02
<i>Dsm2</i>	7	35.200027 - 35.215370	<i>Lrp3</i>	3.6E-03		3.2E-02		
<i>Dsm2</i>	7	35.685165 - 35.754454	<i>Dpy19l3</i>				6.5E-03	7.5E-03
<i>Dsm2</i>	7	43.296197 - 43.313294	<i>Zfp715</i>					2.7E-05
<i>Dsm2</i>	7	44.310253 - 44.358351	<i>Shank1</i>	2.3E-02	7.0E-03		2.9E-02	
<i>Dsm2</i>	7	44.360043 - 44.385820	<i>1700008O03Rik</i>	3.1E-02		3.9E-02	3.1E-06	
<i>Dsm2</i>	7	44.384102 - 44.400187	<i>Syt3</i>	4.2E-03			1.2E-03	2.4E-02
<i>Dsm2</i>	7	44.429018 - 44.463351	<i>Lrrc4b</i>				4.1E-02	
<i>Dsm2</i>	7	44.467980 - 44.471652	<i>Josd2</i>	2.7E-02		4.4E-02	5.0E-03	8.0E-03
<i>Dsm2</i>	7	44.489937 - 44.496529	<i>2310044H10Rik</i>	6.7E-04			1.1E-02	2.0E-05
<i>Dsm2</i>	7	44.549616 - 44.553951	<i>Nrlh2</i>	4.1E-02				
<i>Dsm2</i>	7	44.590664 - 44.604754	<i>Kcnc3</i>				1.0E-14	1.0E-14
<i>Dsm2</i>	7	44.605803 - 44.670843	<i>Myh14</i>	4.6E-02	2.7E-02	4.1E-02	2.1E-02	
<i>Dsm2</i>	7	44.812257 - 44.816658	<i>Atf5</i>	2.9E-03				
<i>Dsm2</i>	7	44.816370 - 44.840809	<i>Il4i1</i>	2.1E-04				
<i>Dsm2</i>	7	44.840901 - 44.849079	<i>Tbc1d17</i>	3.7E-02				4.5E-02
<i>Dsm2</i>	7	44.848991 - 44.855421	<i>Akt1s1</i>	2.6E-03		3.4E-03	3.5E-05	
<i>Dsm2</i>	7	44.863068 - 44.869788	<i>Ptov1</i>	2.3E-02		2.9E-02	1.7E-03	6.5E-04
<i>Dsm2</i>	7	44.879391 - 44.892397	<i>Med25</i>	2.1E-02				7.0E-06
<i>Dsm2</i>	7	44.896079 - 44.902631	<i>Fuz</i>	3.3E-02				4.3E-02
<i>Dsm2</i>	7	44.900373 - 44.929496	<i>Ap2a1</i>				1.1E-02	
<i>Dsm2</i>	7	44.975989 - 44.986492	<i>Prmt1</i>	1.6E-02			3.2E-02	5.6E-03
<i>Dsm2</i>	7	45.053613 - 45.062677	<i>Prrg2</i>	3.5E-02		4.4E-02	1.0E-06	1.4E-02
<i>Dsm2</i>	7	45.062429 - 45.078503	<i>Nosip</i>				2.8E-02	5.1E-04
<i>Dsm2</i>	7	45.125558 - 45.136231	<i>Rpl13a</i>	4.2E-02				
<i>Dsm2</i>	7	45.131188 - 45.136432	<i>Flt3l</i>	9.1E-03				
<i>Dsm2</i>	7	45.140684 - 45.154584	<i>Aldh16a1</i>	4.6E-02			1.8E-03	6.3E-03
<i>Dsm2</i>	7	45.303155 - 45.333780	<i>Trpm4</i>	4.1E-02				
<i>Dsm2</i>	7	45.339126 - 45.367019	<i>Ppfia3</i>	8.9E-03				
<i>Dsm2</i>	7	45.366163 - 45.367948	<i>Mtag2</i>	7.6E-05	1.1E-04			
<i>Dsm2</i>	7	45.418353 - 45.421854	<i>Lhb</i>	3.6E-02		2.8E-02	5.2E-04	1.0E-14
<i>Dsm2</i>	7	45.434844 - 45.456619	<i>Gys1</i>	1.0E-14		1.0E-14	2.4E-02	

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
Dsm2	7	45.457944 - 45.459884	Ftl1					5.3E-03
Dsm2	7	45.472956 - 45.488805	Dhdh				2.8E-02	
Dsm2	7	45.486262 - 45.523632	Tulp2					9.3E-03
Dsm2	7	45.492874 - 45.510406	Nucb1				3.5E-02	1.2E-02
Dsm2	7	45.699843 - 45.704682	Car11	2.5E-02	7.9E-03	3.1E-02	1.5E-02	
Dsm2	7	45.705088 - 45.710155	Dbp	3.5E-02	2.7E-02		1.2E-02	
Dsm2	7	45.715457 - 45.720835	Rpl18				4.8E-02	
Dsm2	7	45.783738 - 45.804144	Lmtk3	2.8E-03		5.1E-03	3.4E-02	
Dsm2	7	45.806637 - 45.814581	Cyth2	3.1E-02			1.0E-14	1.0E-14
Dsm2	7	46.098725 - 46.099897	Kcnj11	2.7E-02				
Dsm2	7	46.443168 - 46.639807	Sergef	3.4E-02				
Dsm2	7	46.796103 - 46.823800	Gtf2h1	1.1E-05				
Dsm2	7	46.841475 - 46.855627	Ldha				3.4E-03	
Dsm2	7	47.077798 - 47.133684	Ptpn5	4.7E-03		3.2E-02	3.0E-04	8.7E-03
Dsm2	7	49.246189 - 49.610087	Nav2	1.4E-06			4.5E-06	2.2E-06
Dsm2	7	49.778346 - 49.858265	Prmt3	4.1E-02				1.0E-06
Dsm2	7	49.974864 - 50.865255	Nell1	8.9E-03				
Dsm2	7	55.794148 - 55.831447	Tubgcp5	8.0E-03				
Dsm2	7	55.841745 - 55.930700	Cyfip1	1.9E-02				5.5E-04
Dsm2	7	55.931287 - 55.962476	Nipa2	4.5E-02			1.0E-14	4.7E-14
Dsm2	7	56.050155 - 56.231794	Herc2	4.1E-03		8.1E-04		
Dsm2	7	56.716465 - 57.387188	Gabrg3				2.2E-04	
Dsm2	7	57.590518 - 57.828802	Gabrb3	4.7E-02		2.7E-05	1.6E-02	7.4E-03
Dsm2	7	61.930913 - 61.982356	A330076H08Rik					2.7E-04
Dsm2	7	62.348277 - 62.349928	Ndn	2.7E-03	5.3E-03			
Dsm3	8	54.629055 - 54.887184	Wdr17	4.6E-02		1.5E-03	8.9E-03	3.8E-05
Dsm3	8	54.708987 - 54.710381	Gm15758					4.4E-02
Dsm3	8	54.954728 - 55.060877	Gpm6a	4.7E-09	7.1E-09	5.8E-09		
Dsm3	8	57.523828 - 57.653032	Galnt7	4.5E-02				
Dsm3	8	60.632827 - 60.676729	Mfap3l	3.2E-02				
Dsm3	8	60.890418 - 60.907580	2700029M09Rik	4.2E-02				
Dsm3	8	60.910389 - 60.983300	Clcn3	3.8E-03		4.1E-02	4.7E-10	2.8E-05
Dsm3	8	60.993195 - 61.131346	Nek1	1.3E-03				
Dsm3	8	62.951009 - 63.357103	Spock3	2.6E-02				
Dsm3	8	64.592558 - 64.693040	Cpe	1.0E-14	1.0E-14	1.0E-14		
Dsm3	8	65.617900 - 66.471637	March1	3.7E-03				
Dsm3	8	68.356781 - 68.735146	Csgalnact1	8.0E-03				
Dsm3	8	68.880491 - 68.907448	Lpl	2.0E-02	3.5E-03	8.9E-03		3.6E-02
Dsm3	8	69.037711 - 69.089235	Slc18a1				8.0E-05	9.4E-04
Dsm3	8	69.088646 - 69.113711	Atp6v1b2				9.4E-03	4.1E-03
Dsm3	8	69.610857 - 69.625548	Zfp868	4.2E-03		5.6E-03		4.6E-05
Dsm3	8	69.761326 - 69.791178	Zfp866	4.0E-03		7.1E-04	2.8E-08	1.9E-10

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
<i>Dsm3</i>	8	70.083529 - 70.090862	<i>Hapln4</i>	2.6E-03	5.1E-03	3.4E-03		
<i>Dsm3</i>	8	70.093085 - 70.120873	<i>Ncan</i>	1.8E-02	4.0E-02	2.4E-02		
<i>Dsm3</i>	8	70.172356 - 70.183681	<i>Tmem161a</i>					8.2E-03
<i>Dsm3</i>	8	70.184340 - 70.212305	<i>Slc25a42</i>	2.6E-02			5.0E-02	1.5E-02
<i>Dsm3</i>	8	70.220172 - 70.234466	<i>Armc6</i>	4.0E-02			1.8E-02	3.1E-03
<i>Dsm3</i>	8	70.234226 - 70.279915	<i>Sugp2</i>	1.7E-02		2.1E-02	1.0E-14	3.9E-02
<i>Dsm3</i>	8	70.282827 - 70.294361	<i>Homer3</i>	8.3E-03		1.1E-02	4.4E-03	
<i>Dsm3</i>	8	70.302518 - 70.312993	<i>Cope</i>	4.2E-02				
<i>Dsm3</i>	8	70.315787 - 70.331587	<i>Lass1</i>	5.2E-03		6.3E-03	2.0E-02	
<i>Dsm3</i>	8	70.382355 - 70.439579	<i>Crtc1</i>					4.2E-02
<i>Dsm3</i>	8	70.483876 - 70.487358	<i>Tmem59l</i>	1.6E-02	3.4E-02	2.0E-02		
<i>Dsm3</i>	8	70.508263 - 70.510801	<i>Uba52</i>	3.4E-02		2.5E-02		1.0E-14
<i>Dsm3</i>	8	70.508272 - 70.527956	<i>2810422J05Rik</i>	3.5E-02		1.6E-02	4.8E-03	6.8E-06
<i>Dsm3</i>	8	70.527724 - 70.535328	<i>Fkbp8</i>	3.0E-02		9.5E-05	1.0E-14	1.7E-03
<i>Dsm3</i>	8	70.597491 - 70.608314	<i>Ssbp4</i>	2.5E-03	5.0E-03	3.4E-03		
<i>Dsm3</i>	8	70.697739 - 70.700616	<i>Jund</i>	3.9E-02				
<i>Dsm3</i>	8	70.754679 - 70.758677	<i>Rab3a</i>	1.9E-03				7.5E-04
<i>Dsm3</i>	8	70.768176 - 70.776713	<i>Pik3r2</i>				1.8E-02	
<i>Dsm3</i>	8	70.778117 - 70.792433	<i>Mast3</i>	2.9E-02		3.7E-02		
<i>Dsm3</i>	8	71.248561 - 71.272934	<i>Haus8</i>	3.5E-02				1.6E-02
<i>Dsm3</i>	8	71.272714 - 71.360712	<i>Myo9b</i>	4.3E-02				
<i>Dsm3</i>	8	71.366848 - 71.369732	<i>Use1</i>	3.4E-02		1.0E-07	1.0E-14	2.1E-02
<i>Dsm3</i>	8	71.371298 - 71.379361	<i>Ocell</i>	3.4E-02			1.0E-14	1.0E-14
<i>Dsm3</i>	8	71.374123 - 71.381960	<i>Nr2f6</i>	4.3E-02		3.6E-02	1.4E-11	1.0E-14
<i>Dsm3</i>	8	71.469199 - 71.476098	<i>Dda1</i>	4.3E-02				4.3E-07
<i>Dsm3</i>	8	71.488103 - 71.499583	<i>Gtpbp3</i>	4.1E-02	3.9E-02	1.5E-02	1.1E-03	1.0E-14
<i>Dsm3</i>	8	71.497754 - 71.511769	<i>Plvap</i>	2.0E-03	3.9E-03	2.7E-03		
<i>Dsm3</i>	8	71.708387 - 71.725716	<i>Fcho1</i>	3.8E-02	3.9E-04	3.8E-02	3.0E-02	4.6E-02
<i>Dsm3</i>	8	72.341001 - 72.421474	<i>Eps15l1</i>	3.3E-02		4.2E-02		
<i>Dsm3</i>	8	72.480641 - 72.492614	<i>Slc35e1</i>	1.1E-03		1.4E-03	9.9E-03	
<i>Dsm3</i>	8	72.646711 - 72.714746	<i>Nwd1</i>				2.3E-03	3.4E-04
<i>Dsm3</i>	8	72.723288 - 72.758203	<i>Sin3b</i>					1.7E-06
<i>Dsm3</i>	8	75.033686 - 75.070121	<i>Tom1</i>	4.8E-02				
<i>Dsm3</i>	8	78.804865 - 78.821140	<i>Lsm6</i>					1.9E-07
<i>Dsm3</i>	8	79.028437 - 79.193766	<i>Zfp827</i>				4.7E-02	
<i>Dsm3</i>	8	81.342556 - 82.125036	<i>Inpp4b</i>	1.6E-02				
<i>Dsm3</i>	8	83.434493 - 83.458391	<i>Scoc</i>	1.5E-06	4.0E-02	2.0E-06	5.5E-11	
<i>Dsm3</i>	8	83.566671 - 83.571626	<i>Ndufb7</i>					4.6E-03
<i>Dsm3</i>	8	83.571700 - 83.594491	<i>Tecr</i>					4.4E-03
<i>Dsm3</i>	8	83.608175 - 83.611902	<i>Dnajb1</i>	5.6E-03		7.3E-03		
<i>Dsm3</i>	8	83.666833 - 83.672753	<i>Ptger1</i>	3.4E-02				5.2E-05
<i>Dsm3</i>	8	83.669762 - 83.699179	<i>Pkn1</i>	7.3E-03		9.5E-03	2.2E-02	

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
<i>Dsm3</i>	8	83.715177 - 83.726892	<i>Ddx39</i>	1.6E-02			1.6E-03	3.6E-02
<i>Dsm3</i>	8	83.723251 - 83.741326	<i>Cd97</i>	3.4E-02		3.0E-02	3.7E-07	3.7E-04
<i>Dsm3</i>	8	83.900105 - 83.941954	<i>Lphn1</i>	3.3E-02		4.1E-02	1.0E-14	1.0E-14
<i>Dsm3</i>	8	84.388440 - 84.640246	<i>Cacna1a</i>	1.5E-02				
<i>Dsm3</i>	8	84.686307 - 84.699808	<i>Trmt1</i>	1.7E-02				8.8E-03
<i>Dsm3</i>	8	84.699876 - 84.800344	<i>Nfix</i>				3.5E-04	
<i>Dsm3</i>	8	84.815405 - 84.822823	<i>Dand5</i>				8.5E-03	
<i>Dsm3</i>	8	84.834019 - 84.840665	<i>Rad23a</i>	1.8E-02				6.0E-03
<i>Dsm3</i>	8	84.841850 - 84.846934	<i>Calr</i>	4.1E-02			2.8E-02	
<i>Dsm3</i>	8	84.856989 - 84.869257	<i>Farsa</i>	1.4E-02				5.4E-09
<i>Dsm3</i>	8	84.872111 - 84.888221	<i>Syce2</i>	1.3E-02			7.1E-03	3.0E-06
<i>Dsm3</i>	8	84.886393 - 84.893921	<i>Gcdh</i>	5.1E-03				
<i>Dsm3</i>	8	84.908560 - 84.922915	<i>Dnase2a</i>				6.8E-03	
<i>Dsm3</i>	8	84.911903 - 84.937359	<i>Mast1</i>	4.8E-02			1.6E-02	1.0E-14
<i>Dsm3</i>	8	84.956610 - 84.969767	<i>Rnaseh2a</i>	3.3E-02		4.1E-02	5.9E-03	
<i>Dsm3</i>	8	84.969587 - 84.974834	<i>Prdx2</i>	4.8E-02		4.4E-03	1.0E-14	6.0E-04
<i>Dsm3</i>	8	85.036915 - 85.057583	<i>Tnpo2</i>	1.5E-02				
<i>Dsm3</i>	8	85.053160 - 85.060460	<i>A230103J11Rik</i>	4.1E-02				
<i>Dsm3</i>	8	85.060055 - 85.067124	<i>Fbxw9</i>	4.2E-02				
<i>Dsm3</i>	8	85.071757 - 85.075162	<i>Dhps</i>	1.4E-02		1.2E-02	3.8E-04	9.4E-04
<i>Dsm3</i>	8	85.075035 - 85.081306	<i>Wdr83</i>	2.7E-02		3.4E-02	1.6E-07	7.5E-03
<i>Dsm3</i>	8	85.080740 - 85.082339	<i>BC056474</i>	6.5E-03		8.4E-03	1.5E-13	
<i>Dsm3</i>	8	85.636588 - 85.690973	<i>Neto2</i>	1.5E-03		1.9E-03		
<i>Dsm3</i>	8	86.841139 - 86.885258	<i>N4bp1</i>	2.6E-02		3.6E-02	2.6E-02	
<i>Dsm3</i>	8	87.468854 - 87.472592	<i>Cbln1</i>				4.9E-02	
<i>Dsm3</i>	8	87.661810 - 87.7959595	<i>Zfp423</i>	4.5E-02				
<i>Dsm3</i>	8	88.118769 - 88.135110	<i>Tmem188</i>	4.4E-02				
<i>Dsm3</i>	8	88.137855 - 88.172027	<i>Heatr3</i>	1.6E-02				
<i>Dsm3</i>	8	88.199213 - 88.259722	<i>Papd5</i>	1.1E-02				
<i>Dsm3</i>	8	88.331039 - 88.362194	<i>Brd7</i>	1.4E-02		1.7E-02	1.1E-06	
<i>Dsm3</i>	8	88.697028 - 88.751945	<i>Cyld</i>	4.1E-03			4.3E-02	
<i>Dsm3</i>	8	90.828835 - 91.054508	<i>Chd9</i>	2.9E-06	4.5E-02			
<i>Dsm3</i>	8	91.070057 - 91.123844	<i>Rbl2</i>					1.0E-02
<i>Dsm3</i>	8	91.112041 - 91.134465	<i>Aktip</i>	4.0E-02		1.2E-02	1.3E-02	3.8E-02
<i>Dsm3</i>	8	91.313532 - 91.668439	<i>Fto</i>					2.0E-05
<i>Dsm3</i>	8	93.809966 - 93.969388	<i>Gnao1</i>				1.4E-10	1.0E-02
<i>Dsm3</i>	8	94.037198 - 94.067921	<i>Ogfodl1</i>	1.8E-02				
<i>Dsm3</i>	8	94.386438 - 94.395377	<i>Herpud1</i>				4.9E-02	
<i>Dsm3</i>	8	94.532990 - 94.570529	<i>Cpne2</i>	4.7E-02			7.5E-03	7.2E-03
<i>Dsm3</i>	8	94.674895 - 94.696242	<i>Pllp</i>	1.3E-02	2.9E-02	1.8E-02		
<i>Dsm3</i>	8	94.819818 - 94.838358	<i>Ciapin1</i>	3.4E-02				
<i>Dsm3</i>	8	94.838321 - 94.854895	<i>Coq9</i>	4.5E-02				

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
<i>Dsm3</i>	8	95.446096 - 95.488820	<i>Csnk2a2</i>					4.1E-02
<i>Dsm3</i>	8	95.676980 - 95.715119	<i>Ndrg4</i>	4.7E-02		2.6E-02	4.3E-05	
<i>Dsm3</i>	8	99.024471 - 99.416471	<i>Cdh8</i>	2.8E-02				
<i>Dsm3</i>	8	104.511028 - 104.534637	<i>Nae1</i>	2.1E-03		1.5E-04	3.5E-03	3.9E-02
<i>Dsm3</i>	8	104.534700 - 104.550343	<i>Car7</i>	6.5E-04		8.8E-04		
<i>Dsm3</i>	8	105.698159 - 105.701095	<i>Acd</i>	4.7E-03		8.5E-04		
<i>Dsm3</i>	8	105.880881 - 105.894908	<i>Edc4</i>					1.3E-02
<i>Dsm3</i>	8	105.893567 - 105.895023	<i>Edc4,Nrn1l</i>		2.1E-02		1.0E-14	
<i>Dsm3</i>	8	105.893567 - 105.895023	<i>Nrn1l</i>	1.9E-02		1.9E-06		1.2E-04
<i>Dsm3</i>	8	105.943590 - 105.966115	<i>Slc12a4</i>				4.7E-02	1.3E-03
<i>Dsm3</i>	8	106.210936 - 106.252794	<i>Prmt7</i>	1.0E-02		1.3E-02	1.3E-02	
<i>Dsm3</i>	8	106.572966 - 106.573461	<i>Gm10073</i>	1.8E-02	4.0E-02			
<i>Dsm3</i>	8	107.069400 - 107.096547	<i>Terf2</i>	1.5E-02		1.9E-02	1.1E-04	
<i>Dsm3</i>	8	107.293470 - 107.379517	<i>Nfat5</i>	4.1E-02		3.3E-02	1.0E-14	1.3E-03
<i>Dsm3</i>	8	110.142539 - 110.168206	<i>Calb2</i>					5.4E-04
<i>Dsm3</i>	8	110.721476 - 110.741400	<i>Mtss1l</i>	3.1E-02		3.8E-02	5.5E-03	
<i>Dsm3</i>	8	110.741829 - 110.805924	<i>Il34</i>					1.2E-02
<i>Dsm3</i>	8	110.846600 - 110.882227	<i>Cog4</i>	5.6E-06				
<i>Dsm3</i>	8	111.033144 - 111.057664	<i>Aars</i>				3.7E-02	4.3E-03
<i>Dsm3</i>	8	111.345135 - 111.393824	<i>Fa2h</i>	1.7E-02		2.1E-02		
<i>Dsm3</i>	8	111.710485 - 111.743849	<i>Bcar1</i>	3.3E-04		4.3E-04	1.1E-02	
<i>Dsm5</i>	11	7.063489 - 7.178506	<i>Adcy1</i>	8.9E-03	1.0E-14	1.1E-02		
<i>Dsm5</i>	11	11.930508 - 12.038683	<i>Grb10</i>	3.9E-02		4.8E-02	1.0E-14	1.0E-14
<i>Dsm5</i>	11	12.236608 - 12.464960	<i>Cobl</i>	6.5E-06		8.9E-06	6.1E-06	
<i>Dsm5</i>	11	16.971206 - 17.052381	<i>Plek</i>	4.9E-02			1.7E-02	
<i>Dsm5</i>	11	17.159263 - 17.200375	<i>Ppp3rl,Wdr92</i>				2.1E-03	
<i>Dsm5</i>	11	17.203198 - 17.211568	<i>Pno1</i>	8.9E-03		1.1E-02	4.2E-05	
<i>Dsm5</i>	11	17.257579 - 17.269176	<i>C1d</i>				4.9E-02	
<i>Dsm5</i>	11	20.062304 - 20.112913	<i>Actr2</i>					5.3E-03
<i>Dsm5</i>	11	20.201432 - 20.226856	<i>Rab1</i>	2.5E-03				
<i>Dsm5</i>	11	21.091291 - 21.150323	<i>Peli1</i>	5.7E-04				
<i>Dsm5</i>	11	21.239281 - 21.321136	<i>Vps54</i>	1.8E-02				
<i>Dsm5</i>	11	21.321138 - 21.371201	<i>Ugp2</i>	1.1E-02				
<i>Dsm5</i>	11	21.556787 - 21.572367	<i>Mdh1</i>	5.6E-03				
<i>Dsm5</i>	11	22.005828 - 22.342292	<i>Ehbpl</i>				1.1E-02	
<i>Dsm5</i>	11	22.834744 - 22.982382	<i>Commd1</i>	3.8E-03				
<i>Dsm5</i>	11	22.834747 - 22.860961	<i>B3gnt2</i>	4.4E-02				
<i>Dsm5</i>	11	23.306895 - 23.490560	<i>Usp34</i>	3.5E-02				
<i>Dsm5</i>	11	23.646479 - 23.665959	<i>Pex13</i>					3.4E-02
<i>Dsm5</i>	11	23.665674 - 23.732876	<i>Pus10</i>	6.6E-03		8.6E-03	1.0E-03	
<i>Dsm5</i>	11	24.078056 - 24.174123	<i>Bcl11a</i>				3.0E-02	2.7E-02
<i>Dsm5</i>	11	28.385685 - 28.584324	<i>Ccdc85a</i>	1.4E-02		7.0E-03	3.1E-03	3.9E-04

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
<i>Dsm5</i>	11	29.130744 - 29.161828	<i>Pnpt1</i>	3.6E-02		4.4E-02		1.8E-02
<i>Dsm5</i>	11	29.172890 - 29.220797	<i>Smek2</i>	1.1E-03		1.5E-03	4.8E-03	
<i>Dsm5</i>	11	29.221532 - 29.247409	<i>Ccdc104</i>	4.3E-02		3.9E-03	4.1E-02	4.9E-02
<i>Dsm5</i>	11	29.526408 - 29.545279	<i>Mtif2</i>	1.8E-02				4.1E-02
<i>Dsm5</i>	11	29.692947 - 29.744331	<i>Rtn4</i>	1.7E-02				
<i>Dsm5</i>	11	30.099395 - 30.268175	<i>Spnb2</i>				4.3E-02	
<i>Dsm5</i>	11	30.930774 - 30.954335	<i>Erlec1</i>					3.3E-02
<i>Dsm5</i>	11	31.872211 - 31.935634	<i>Cpeb4</i>	3.6E-02				2.8E-02
<i>Dsm5</i>	11	32.225628 - 32.267707	<i>Nprl3</i>	3.7E-02		3.4E-02	4.2E-02	8.4E-03
<i>Dsm5</i>	11	32.283511 - 32.284465	<i>Hba-a1</i>	1.1E-02	6.6E-03	1.4E-02	9.0E-03	
<i>Dsm5</i>	11	32.296489 - 32.297298	<i>Hba-a2</i>	8.9E-03	1.8E-02	1.2E-02		
<i>Dsm5</i>	11	32.642724 - 32.746816	<i>Fbxw11</i>	4.6E-02				
<i>Dsm5</i>	11	33.152287 - 33.163206	<i>Npm1</i>					6.5E-03
<i>Dsm5</i>	11	33.629339 - 33.993152	<i>Kcnip1</i>	3.8E-02	5.9E-09			
<i>Dsm5</i>	11	34.046920 - 34.092295	<i>Lcp2</i>	4.0E-05				
<i>Dsm5</i>	11	35.808381 - 35.834506	<i>Rars</i>	1.1E-04		1.5E-04	5.1E-07	
<i>Dsm5</i>	11	35.838400 - 35.980527	<i>Wwc1</i>	1.7E-02		2.2E-02	1.3E-06	
<i>Dsm5</i>	11	36.006656 - 37.235964	<i>Odz2</i>	4.7E-03				
<i>Dsm5</i>	11	40.679314 - 40.695203	<i>Mat2b</i>	2.3E-02				
<i>Dsm5</i>	11	40.748552 - 40.755311	<i>Ccng1</i>	3.3E-02		4.1E-02		
<i>Dsm5</i>	11	42.306437 - 42.321072	<i>Gabra6</i>	3.4E-03	1.5E-02	9.0E-03		7.2E-04
<i>Dsm5</i>	11	42.419757 - 42.629028	<i>Gabrb2</i>	1.4E-02				3.2E-04
<i>Dsm5</i>	11	43.729512 - 43.748008	<i>Ttc1</i>					2.7E-02
<i>Dsm5</i>	11	44.454571 - 44.470498	<i>Ublcp1</i>	1.8E-02	4.4E-02	2.3E-02	9.1E-05	
<i>Dsm5</i>	11	44.518964 - 44.565520	<i>Rnf145</i>	4.5E-02				
<i>Dsm5</i>	11	45.928269 - 45.944935	<i>Lsm11</i>					2.4E-02
<i>Dsm5</i>	11	46.055992 - 46.147343	<i>Adam19</i>	3.9E-02				2.4E-02
<i>Dsm5</i>	11	46.193850 - 46.312859	<i>Cyfip2</i>	1.8E-05				
<i>Dsm5</i>	11	48.800332 - 48.806434	<i>Gnb2l1</i>				4.4E-04	
<i>Dsm5</i>	11	48.806404 - 48.817353	<i>Trim41</i>	2.3E-02		2.6E-02	2.6E-02	
<i>Dsm5</i>	11	49.076587 - 49.096974	<i>Ifi47</i>	9.1E-03				
<i>Dsm5</i>	11	49.203292 - 49.218816	<i>Zfp62</i>	2.3E-02			3.7E-02	3.3E-02
<i>Dsm5</i>	11	49.244191 - 49.263030	<i>Mgat1</i>	1.4E-02			3.6E-02	2.4E-02
<i>Dsm5</i>	11	49.846751 - 49.886421	<i>Mapk9</i>				5.0E-02	
<i>Dsm5</i>	11	50.131396 - 50.172785	<i>Tbc1d9b</i>	2.1E-02			1.0E-02	4.6E-02
<i>Dsm5</i>	11	50.199366 - 50.210827	<i>Sqstm1</i>	3.7E-02		7.6E-05	1.8E-02	1.9E-02
<i>Dsm5</i>	11	50.210890 - 50.235103	<i>Mgat4b</i>	9.4E-03		1.2E-02	3.9E-05	
<i>Dsm5</i>	11	50.293961 - 50.325673	<i>Canx</i>	3.2E-02		3.8E-02	2.4E-02	
<i>Dsm5</i>	11	50.376990 - 50.386528	<i>Hnrnph1</i>	3.9E-02		4.9E-02		4.3E-03
<i>Dsm5</i>	11	50.811086 - 50.827724	<i>Zfp354c</i>					2.1E-02
<i>Dsm5</i>	11	51.253651 - 51.263046	<i>BC049762</i>	4.1E-02	2.5E-03	1.7E-03		1.1E-05
<i>Dsm5</i>	11	51.261730 - 51.281766	<i>Clk4</i>	2.5E-02				1.2E-02

Interval	Chr	Location (Mb)*	Gene	Transcript	Gene	TSS	Promoter	Splicing
<i>Dsm5</i>	11	51.584757 - 51.604489	<i>Agxt2l2</i>					4.5E-02
<i>Dsm5</i>	11	51.623671 - 51.635896	<i>Rmnd5b</i>	6.7E-07		8.5E-07	1.6E-02	
<i>Dsm5</i>	11	51.692264 - 51.763634	<i>Sec24a</i>	9.5E-03				
<i>Dsm5</i>	11	51.813455 - 51.857653	<i>Phf15</i>	1.6E-02	9.6E-03	4.8E-02		
<i>Dsm5</i>	11	52.004221 - 52.089784	<i>Cdkl3</i>	3.5E-02				
<i>Dsm5</i>	11	52.038850 - 52.039471	<i>Gm12205</i>	2.2E-08	1.6E-08			
<i>Dsm5</i>	11	52.231995 - 52.246858	<i>Skp1a</i>	9.6E-03				
<i>Dsm5</i>	11	53.259814 - 53.300457	<i>Hspa4</i>	4.6E-03	4.2E-02	6.1E-03	6.7E-09	
<i>Dsm5</i>	11	53.519257 - 53.549565	<i>Sept8</i>	1.4E-02		1.2E-02	2.4E-07	3.1E-02
<i>Dsm5</i>	11	53.567379 - 53.601967	<i>Kif3a</i>	2.0E-02		2.6E-02	9.0E-04	
<i>Dsm5</i>	11	53.602982 - 53.618669	<i>Il4</i>				4.5E-05	
<i>Dsm5</i>	11	53.983123 - 54.028090	<i>Slc22a4</i>				1.7E-02	
<i>Dsm5</i>	11	54.303798 - 54.364756	<i>Acsl6</i>	3.8E-02		1.5E-03	3.5E-02	2.2E-02
<i>Dsm5</i>	11	54.522847 - 54.699285	<i>Rapgef6</i>	7.1E-03			2.1E-05	1.0E-14
<i>Dsm5</i>	11	54.902453 - 54.910377	<i>Gpx3</i>	7.3E-03	2.2E-03	9.3E-03		
<i>Dsm5</i>	11	54.910785 - 54.962917	<i>Tnip1</i>	4.1E-03				
<i>Dsm5</i>	11	54.979108 - 55.033445	<i>Anxa6</i>	4.1E-12				4.2E-03
<i>Dsm5</i>	11	55.394500 - 55.420080	<i>Sparc</i>	2.1E-03	2.9E-04	2.8E-03	1.0E-14	7.2E-10

*GRC m38 assembly

Supplementary Table S4. Missense variants in *Dsm* intervals and the predicted impact on protein function.

Interval	Chr	Location (Mb)*	Gene	Amino acid change	Codon change	RS #	SIFT [†]
<i>Dsm4</i>	5	14521070	<i>Pclo</i>	D/E	gaT/gaA	novel	Tolerated
<i>Dsm4</i>	5	16120781	<i>Hgf</i>	R/H	cGc/cAc	rs45644218	Tolerated
<i>Dsm4</i>	5	19571437	<i>Magi2</i>	E/D	gaG/gaC	rs33653085	Tolerated
<i>Dsm4</i>	5	20692271	<i>Pion</i>	R/G	Aga/Gga	rs46927900	Tolerated
<i>Dsm4</i>	5	20881134	<i>Fgl2</i>	A/T	Gcc/Acc	rs33636152	Tolerated
<i>Dsm4</i>	5	21262249	<i>Pmpcb</i>	S/T	aGt/aCt	rs31979572	Tolerated
<i>Dsm4</i>	5	23003987	<i>Mll5</i>	M/L	Atg/Ctg	rs29723731	Tolerated
<i>Dsm4</i>	5	23293676	<i>Rint1</i>	D/E	gaT/gaG	rs32064947	Tolerated
<i>Dsm4</i>	5	23472208	<i>Fam126a</i>	I/V	Atc/Gtc	rs32047053	nd
<i>Dsm4</i>	5	23683839	<i>Nupl2</i>	V/I	Gta/Ata	rs29820223	Tolerated
<i>Dsm4</i>	5	23837846	<i>Kcnh2</i>	R/H	cGc/cAc	rs29526580	Tolerated
<i>Dsm4</i>	5	23909481	<i>Abcb8</i>	Q/R	cAa/cGa	rs33062222	nd
<i>Dsm4</i>	5	24002574	<i>Agap3</i>	T/A	Aca/Gca	rs50956984	Tolerated
<i>Dsm4</i>	5	24213641	<i>Nub1</i>	N/S	aAt/aGt	rs13462984	Tolerated
<i>Dsm4</i>	5	24414206	<i>Prkag2</i>	V/A	gTg/gCg	novel	Tolerated
<i>Dsm4</i>	5	24503481	<i>1500035N22Rik</i>	G/A	gGa/gCa	rs48167035	nd
<i>Dsm4</i>	5	24815889	<i>Mll3</i>	D/N	Gat/Aat	rs36787383	Tolerated
<i>Dsm4</i>	5	30686351	<i>Otof</i>	S/L	tCa/tTa	rs50888259	Tolerated
<i>Dsm4</i>	5	31236142	<i>Cgref1</i>	S/G	Agc/Ggc	rs48261697	Tolerated
<i>Dsm4</i>	5	31829984	<i>Slc4a1ap</i>	P/L	cCc/cTc	novel	Affect protein function
<i>Dsm4</i>	5	31950225	<i>Rbks</i>	M/L	Atg/Ttg	rs13466148	Affect protein function
<i>Dsm4</i>	5	33163358	<i>Prl14l</i>	A/T	Gct/Act	rs32525128	Tolerated
<i>Dsm4</i>	5	33163358	<i>Gm20671</i>	A/T	Gct/Act	rs32525128	Affect protein function
<i>Dsm4</i>	5	33289343	<i>Depdc5</i>	A/S	Gca/Tca	rs46971248	Tolerated
<i>Dsm4</i>	5	42199995	<i>Bod1l</i>	K/N	aaA/aaT	rs38590808	Tolerated
<i>Dsm1</i>	5	51854559	<i>Ppargc1a</i>	R/H	cGc/cAc	rs33152841	Tolerated
<i>Dsm1</i>	5	52759260	<i>Sod3</i>	N/D	Aat/Gat	rs38336994	Tolerated
<i>Dsm1</i>	5	52766635	<i>Ccdc149</i>	I/S	aTc/aGc	rs29686132	nd
<i>Dsm1</i>	5	53047499	<i>Sepsecs</i>	E/D	gaG/gaT	rs13478254	Tolerated
<i>Dsm1</i>	5	53507595	<i>Sell13</i>	R/L	cGg/cTg	novel	nd
<i>Dsm1</i>	5	64191768	<i>3110047P20Rik</i>	I/V	Atc/Gtc	rs47172680	Tolerated
<i>Dsm1</i>	5	64289838	<i>0610040J01Rik</i>	L/Q	cTg/cAg	rs13459170	Tolerated
<i>Dsm1</i>	5	64501811	<i>Pgm1</i>	C/S	Tgt/Agt	rs13460885	Tolerated
<i>Dsm1</i>	5	67655613	<i>Tmem33</i>	A/V	gCg/gTg	rs29520321	Tolerated
<i>Dsm1</i>	5	67715913	<i>Slc30a9</i>	V/A	gTa/gCa	rs29548855	Tolerated
<i>Dsm1</i>	5	73456565	<i>Fryl</i>	G/S	Ggt/Agt	rs33085471	Tolerated
<i>Dsm1</i>	5	73612295	<i>Fryl</i>	L/V	Ctc/Gtc	rs29683841	nd
<i>Dsm1</i>	5	76005459	<i>Kit</i>	A/T	Gct/Act	rs33129397	Tolerated
<i>Dsm1</i>	5	76576814	<i>Srd5a3</i>	S/G	Agt/Ggt	rs31545379	Tolerated
<i>Dsm4</i>	5	82223562	<i>Lphn3</i>	S/N	aGc/aAc	rs29679877	Tolerated
<i>Dsm4</i>	5	84510178	<i>Epha5</i>	S/A	Tcc/Gcc	rs47415520	Tolerated

Interval	Chr	Location (Mb)*	Gene	Amino acid change	Codon change	RS #	SIFT [†]
<i>Dsm4</i>	5	86445366	<i>Cenpc1</i>	R/Q	cGa/cAa	rs29680970	Tolerated
<i>Dsm4</i>	5	86547138	<i>Uba6</i>	N/K	aaC/aaG	rs31659821	Tolerated
<i>Dsm4</i>	5	88984370	<i>Utp3</i>	L/F	ttA/ttT	rs48286746	Tolerated
<i>Dsm4</i>	5	90150813	<i>Adamts3</i>	K/E	Aag/Gag	rs37094279	Tolerated
<i>Dsm4</i>	5	90646607	<i>Cox18</i>	Y/H	Tat/Cat	rs31692127	Tolerated
<i>Dsm4</i>	5	90673283	<i>Ankrd17</i>	P/L	cCt/cTt	novel	nd
<i>Dsm4</i>	5	92437113	<i>Cdkl2</i>	I/M	atA/atG	rs31762832	nd
<i>Dsm4</i>	5	92701496	<i>Naaa</i>	N/D	Aac/Gac	rs13469647	Tolerated
<i>Dsm4</i>	5	92717499	<i>Sdad1</i>	E/D	gaG/gaC	rs49130682	nd
<i>Dsm4</i>	5	92934327	<i>Scarb2</i>	R/K	aGa/aAa	rs33625832	Tolerated
<i>Dsm4</i>	5	93472539	<i>Sowahb</i>	G/E	gGa/gAa	novel	Tolerated
<i>Dsm4</i>	5	93616823	<i>Ccni</i>	A/T	Gct/Act	rs13460092	Tolerated
<i>Dsm4</i>	5	96693225	<i>Mrp11</i>	F/L	Ttt/Ctt	rs33633475	Affect protein function
<i>Dsm4</i>	5	97025853	<i>Fras1</i>	S/T	aGc/aCc	rs31848775	Tolerated
<i>Dsm4</i>	5	97241927	<i>Anxa3</i>	V/A	gTc/gCc	rs48568871	Tolerated
<i>Dsm4</i>	5	97516151	<i>Bmp2k</i>	T/A	Acg/Gcg	rs13478405	Tolerated
<i>Dsm4</i>	5	100488240	<i>Enoph1</i>	V/I	Gtc/Atc	rs13460000	Tolerated
<i>Dsm4</i>	5	103342229	<i>Mapk10</i>	A/V	gCg/gTg	rs36844177	Affect protein function
<i>Dsm4</i>	5	104315113	<i>Klhl8</i>	R/Q	cGg/cAg	rs32028849	Affect protein function
<i>Dsm4</i>	5	104521979	<i>Sparcl1</i>	D/E	gaC/gaA	rs33257002	Tolerated
<i>Dsm2</i>	7	17046685	<i>Npas1</i>	L/V	Ctg/Gtg	rs6295100	Tolerated
<i>Dsm2</i>	7	17617013	<i>Hif3a</i>	T/P	Act/Cct	rs49533089	nd
<i>Dsm2</i>	7	19677802	<i>Dmpk</i>	Y/*	taT/taG	rs46709471	nd
<i>Dsm2</i>	7	20099779	<i>Trappc6a</i>	L/R	cTg/cGg	rs13474030	Tolerated
<i>Dsm2</i>	7	38885640	<i>Ccne1</i>	H/Q	caT/caG	rs32379441	Tolerated
<i>Dsm2</i>	7	53088863	<i>Grin2d</i>	A/T	Gcc/Acc	novel	Tolerated
<i>Dsm2</i>	7	53171613	<i>Tmem143</i>	R/L	cGg/cTg	rs51175460	Tolerated
<i>Dsm2</i>	7	52113855	<i>Pnkp</i>	Q/H	caG/caT	novel	Tolerated
<i>Dsm2</i>	7	20345737	<i>Bcam</i>	V/A	gTg/gCg	rs31944997	Tolerated
<i>Dsm2</i>	7	20300394	<i>Tomm40</i>	E/D	gaA/gaC	rs32423207	Tolerated
<i>Dsm2</i>	7	20281675	<i>Apoe</i>	S/P	Tca/Cca	rs32422502	Tolerated
<i>Dsm2</i>	7	17613093	<i>Ppp5c</i>	T/A	Act/Gct	rs13469893	Tolerated
<i>Dsm2</i>	7	52997630	<i>Sult2b1</i>	G/E	gGa/gAa	rs46169639	nd
<i>Dsm2</i>	7	19938049	<i>Ercc1</i>	P/R	cCt/cGt	rs48117413	nd
<i>Dsm2</i>	7	28028384	<i>Adck4</i>	C/R	Tgc/Cgc	rs13460395	Tolerated
<i>Dsm2</i>	7	16784313	<i>Dhx34</i>	P/S	Ccc/Tcc	rs50034019	Tolerated
<i>Dsm2</i>	7	31359998	<i>Wbp7</i>	Q/R	cAa/cGa	rs3142532	Tolerated
<i>Dsm2</i>	7	52226749	<i>Cpt1c</i>	F/L	Ttc/Ctc	rs31199207	Tolerated
<i>Dsm2</i>	7	52312184	<i>Prrg2</i>	R/W	Cgg/Tgg	rs48233868	Tolerated
<i>Dsm2</i>	7	28439075	<i>Ttc9b</i>	P/S	Cct/Tct	rs51787077	Tolerated
<i>Dsm2</i>	7	51748639	<i>Emc10</i>	L/S	tTg/tCg	rs46532470	Tolerated
<i>Dsm2</i>	7	52108009	<i>Akt1s1</i>	Q/R	cAg/cGg	rs13459520	Tolerated

Interval	Chr	Location (Mb)*	Gene	Amino acid change	Codon change	RS #	SIFT [†]
<i>Dsm2</i>	7	30614703	<i>Zfp790</i>	H/R	cAt/cGt	rs36638155	Tolerated
<i>Dsm2</i>	7	52155551	<i>Fuz</i>	M/T	aTg/aCg	rs37767857	Tolerated
<i>Dsm2</i>	7	52339036	<i>Rcn3</i>	R/Q	cGa/cAa	rs31302575	Tolerated
<i>Dsm2</i>	7	37553935	<i>Tshz3</i>	I/T	aTc/aCc	rs32135386	Tolerated
<i>Dsm2</i>	7	19622040	<i>Sympk</i>	V/L	Gtg/Ctg	novel	Tolerated
<i>Dsm2</i>	7	66052942	<i>Atp10a</i>	E/D	gaG/gaT	rs33010602	Tolerated
<i>Dsm2</i>	7	17423076	<i>Strn4</i>	D/A	gAt/gCt	rs31961396	Tolerated
<i>Dsm2</i>	7	19978806	<i>Ercc2</i>	I/V	Att/Gtt	rs52046644	Tolerated
<i>Dsm2</i>	7	19846256	<i>Vasp</i>	A/T	Gca/Aca	novel	Tolerated
<i>Dsm2</i>	7	19678434	<i>Dmpk</i>	A/T	Gcc/Acc	novel	Tolerated
<i>Dsm2</i>	7	38752419	<i>C80913</i>	N/D	Aat/Gat	novel	Tolerated
<i>Dsm2</i>	7	39052484	<i>Pop4</i>	L/P	cTa/cCa	novel	nd
<i>Dsm2</i>	7	63386662	<i>Herc2</i>	G/D	gGt/gAt	rs50155421	Affect protein function
<i>Dsm2</i>	7	25045210	<i>Zfp108</i>	E/G	gAg/gGg	rs38414115	Tolerated
<i>Dsm2</i>	7	35971550	<i>Slc7a10</i>	H/R	cAc/cGc	novel	Tolerated
<i>Dsm2</i>	7	57053731	<i>Prmt3</i>	V/A	gTt/gCt	rs32892158	Tolerated
<i>Dsm2</i>	7	29937670	<i>Fam98c</i>	L/V	Ctc/Gtc	rs31011245	nd
<i>Dsm2</i>	7	29965339	<i>Psmd8</i>	N/S	aAc/aGc	rs13465857	Tolerated
<i>Dsm2</i>	7	51646184	<i>Syt3</i>	P/L	cCg/cTg	novel	Tolerated
<i>Dsm2</i>	7	53252134	<i>Abcc6</i>	K/R	aAa/aGa	rs32757904	Tolerated
<i>Dsm2</i>	7	53309894	<i>Nomo1</i>	A/S	Gcc/Tcc	rs48778509	Tolerated
<i>Dsm2</i>	7	53698651	<i>Sergef</i>	R/G	Aga/Gga	rs32795453	Tolerated
<i>Dsm2</i>	7	65067548	<i>Gabrb3</i>	R/*	Cga/Tga	rs8269312	Affect protein function
<i>Dsm2</i>	7	34990915	<i>Gpi1</i>	G/R	Ggg/Agg	novel	Affect protein function
<i>Dsm2</i>	7	31233216	<i>Kirrel2</i>	E/D	gaA/gaT	rs31589807	Tolerated
<i>Dsm2</i>	7	29480032	<i>Fbxo27</i>	R/C	Cgc/Tgc	rs31375778	Tolerated
<i>Dsm2</i>	7	52263187	<i>Scaf1</i>	R/H	cGt/cAt	rs32411905	Tolerated
<i>Dsm2</i>	7	51794017	<i>Pold1</i>	S/G	Agt/Ggt	rs3719256	Tolerated
<i>Dsm2</i>	7	51722089	<i>Aspdh</i>	A/V	gCt/gTt	rs30577492	nd
<i>Dsm2</i>	7	57167200	<i>Slc6a5</i>	T/A	Acg/Gcg	rs31048165	Tolerated
<i>Dsm2</i>	7	53173467	<i>Emp3</i>	T/I	aCt/aTt	rs47934871	Tolerated
<i>Dsm2</i>	7	28443354	<i>Map3k10</i>	L/M	Ctg/Atg	rs31866481	Tolerated
<i>Dsm2</i>	7	28090525	<i>Ltbp4</i>	V/I	Gtc/Atc	rs37849144	Tolerated
<i>Dsm2</i>	7	20491139	<i>Pvr</i>	S/A	Tca/Gca	rs6341533	Tolerated
<i>Dsm2</i>	7	26029737	<i>Erf</i>	L/P	cTa/cCa	novel	Tolerated
<i>Dsm2</i>	7	19441348	<i>Mill2</i>	Q/E	Cag/Gag	rs31011587	Tolerated
<i>Dsm2</i>	7	25316847	<i>Irgq</i>	P/L	cCg/cTg	rs31824681	Tolerated
<i>Dsm2</i>	7	17580300	<i>Ccdc8</i>	G/R	Ggg/Cgg	rs47531851	Tolerated
<i>Dsm2</i>	7	17545891	<i>Pnmai1</i>	L/F	ttA/ttT	rs32284680	Affect protein function
<i>Dsm2</i>	7	17435645	<i>Prkd2</i>	S/N	aGt/aAt	novel	Tolerated
<i>Dsm2</i>	7	16860667	<i>Ccdc9</i>	P/L	cCg/cTg	rs46238417	nd
<i>Dsm2</i>	7	31097313	<i>Alkbh6</i>	R/H	cGc/cAc	rs3143488	Tolerated

Interval	Chr	Location (Mb)*	Gene	Amino acid change	Codon change	RS #	SIFT [†]
<i>Dsm2</i>	7	52897754	<i>Mamstr</i>	T/P	Act/Cct	rs32122777	Tolerated
<i>Dsm2</i>	7	38264579	<i>Zfp536</i>	G/S	Ggc/Agc	rs32041433	Tolerated
<i>Dsm2</i>	7	52084270	<i>Nup62</i>	G/V	gGc/gTc	rs13475007	Tolerated
<i>Dsm2</i>	7	19591025	<i>Irf2bp1</i>	S/T	Tca/Aca	rs13461382	Tolerated
<i>Dsm2</i>	7	19807925	<i>Gpr4</i>	S/F	tCt/tTt	rs31773527	Tolerated
<i>Dsm2</i>	7	52891856	<i>Rasip1</i>	S/N	aGt/aAt	rs32519373	nd
<i>Dsm2</i>	7	30556399	<i>Zfp84</i>	V/M	Gtg/Atg	novel	Tolerated
<i>Dsm2</i>	7	26010142	<i>Zfp526</i>	T/M	aCg/aTg	rs31912321	Tolerated
<i>Dsm2</i>	7	52303204	<i>Prr12</i>	S/P	Tca/Cca	rs32068191	Tolerated
<i>Dsm2</i>	7	30577496	<i>Zfp30</i>	L/P	cTt/cCt	rs31994309	Tolerated
<i>Dsm2</i>	7	24925510	<i>Zfp235</i>	G/R	Gga/Aga	rs32277497	Tolerated
<i>Dsm2</i>	7	19942711	<i>Cd3eap</i>	F/L	ttC/ttA	novel	nd
<i>Dsm2</i>	7	17396056	<i>Fkrp</i>	N/S	aAc/aGc	rs31558982	Tolerated
<i>Dsm2</i>	7	30890057	<i>Zfp260</i>	R/K	aGa/aAa	rs31851232	Tolerated
<i>Dsm2</i>	7	19721002	<i>Fbxo46</i>	T/A	Acc/Gcc	rs32308077	Tolerated
<i>Dsm2</i>	7	25076783	<i>Zfp61</i>	T/S	Act/Tct	rs108114156	Tolerated
<i>Dsm2</i>	7	52713915	<i>Ftl1</i>	A/V	gCg/gTg	rs32426657	Tolerated
<i>Dsm2</i>	7	30620625	<i>Zfp940</i>	T/A	Aca/Gca	rs50868004	nd
<i>Dsm2</i>	7	51756796	<i>Fam71e1</i>	R/C	Cgt/Tgt	rs31759732	nd
<i>Dsm2</i>	7	20117187	<i>Ppp1r37</i>	P/S	Cca/Tca	rs46235837	Tolerated
<i>Dsm2</i>	7	56720197	<i>Nav2</i>	D/G	gAc/gGc	rs31226051	Tolerated
<i>Dsm2</i>	7	24907292	<i>Zfp112</i>	E/K	Gag/Aag	novel	Tolerated
<i>Dsm2</i>	7	53082982	<i>Grwd1</i>	G/S	Ggt/Agt	novel	Tolerated
<i>Dsm2</i>	7	30824171	<i>Zfp14</i>	G/E	gGa/gAa	rs31306390	Tolerated
<i>Dsm2</i>	7	25059792	<i>Zfp93</i>	T/K	aCa/aAa	rs50598724	Tolerated
<i>Dsm2</i>	7	28487585	<i>C030039L03Rik</i>	R/K	aGg/aAg	rs108764696	Tolerated
<i>Dsm2</i>	7	24886522	<i>Zfp180</i>	M/T	aTg/aCg	rs46156231	Tolerated
<i>Dsm2</i>	7	52968731	<i>Sphk2</i>	A/V	gCg/gTg	novel	Tolerated
<i>Dsm2</i>	7	17149475	<i>Grlf1</i>	K/R	aAg/aGg	rs32384591	Tolerated
<i>Dsm2</i>	7	30660543	<i>Zfp420</i>	E/K	Gaa/Aaa	rs49596855	Affect protein function
<i>Dsm2</i>	7	30841854	<i>Zfp82</i>	V/A	gTc/gCc	rs51511420	Tolerated
<i>Dsm2</i>	7	17018228	<i>Zc3h4</i>	R/Q	cGg/cAg	rs31143418	Tolerated
<i>Dsm2</i>	7	35533200	<i>Chst8</i>	R/Q	cGa/cAa	rs31398221	Affect protein function
<i>Dsm2</i>	7	20170652	<i>Clasrp</i>	G/D	gGc/gAc	novel	Tolerated
<i>Dsm2</i>	7	53049414	<i>Lmtk3</i>	D/G	gAc/gGc	rs50753342	Tolerated
<i>Dsm2</i>	7	36066391	<i>Gpatch1</i>	G/R	Gga/Aga	rs108098034	Affect protein function
<i>Dsm2</i>	7	35030779	<i>4931406P16Rik</i>	R/K	aGg/aAg	rs32485916	Tolerated
<i>Dsm2</i>	7	17676057	<i>Psg16</i>	F/Y	tTc/tAc	rs31886178	Tolerated
<i>Dsm2</i>	7	46790123	<i>Zfp619</i>	R/H	cGc/cAc	novel	Tolerated
<i>Dsm2</i>	7	24966120	<i>Zfp114</i>	A/S	Gca/Tca	rs36363112	Tolerated
<i>Dsm2</i>	7	28695930	<i>1700049G17Rik</i>	R/K	aGg/aAg	rs45819068	Tolerated
<i>Dsm2</i>	7	17531368	<i>Pnmal2</i>	D/E	gaT/gaA	novel	nd

Interval	Chr	Location (Mb)*	Gene	Amino acid change	Codon change	RS #	SIFT [†]
Dsm2	7	39006421	Plekhf1	D/E	gaT/gaG	novel	Tolerated
Dsm2	7	25088715	Zfp94	H/R	cAt/cGt	rs8276480	Affect protein function
Dsm2	7	25014557	Zfp109	C/R	Tgt/Cgt	rs36812494	Tolerated
Dsm2	7	19577440	Gm10676	R/*	Cga/Tga	rs31285526	nd
Dsm2	7	19476694	Ccdc61	A/T	Gcc/Acc	rs32198643	Tolerated
Dsm2	7	17470627	Dact3	V/I	Gta/Ata	novel	Tolerated
Dsm2	7	24984009	Zfp111	S/T	Tca/Aca	rs49700498	Tolerated
Dsm2	7	26014791	9130221H12Rik	L/P	cTc/cCc	rs31011588	nd
Dsm3	8	54603183	Aga	H/N	Cac/Aac	rs36265099	Tolerated
Dsm3	8	55750449	Wdr17	I/V	Atc/Gtc	rs31343316	Tolerated
Dsm3	8	59017427	BC088983	D/E	gaT/gaG	rs33607336	Tolerated
Dsm3	8	63485573	Nek1	R/S	agA/agT	novel	Affect protein function
Dsm3	8	63704973	Sh3rf1	G/V	gGc/gTc	rs33135970	Tolerated
Dsm3	8	71331435	Ints10	N/T	aAc/aCc	rs49601394	Tolerated
Dsm3	8	71423357	Lpl	D/N	Gat/Aat	rs48623874	Tolerated
Dsm3	8	71664583	Lzts1	I/M	atA/atG	rs46387265	Tolerated
Dsm3	8	71751909	Zfp930	K/T	aAa/aCa	rs33356689	Tolerated
Dsm3	8	71896186	Gm10033	C/Y	tGt/tAt	rs32839177	nd
Dsm3	8	71897538	Gm10311	N/K	aaC/aaA	rs33457667	nd
Dsm3	8	72136271	Zfp868	S/N	aGt/aAt	rs32562468	tolerated
Dsm3	8	72267147	Zfp963	S/N	aGt/aAt	rs33361474	Affect protein function
Dsm3	8	72340972	Gmip	A/V	gCa/gTa	rs32798929	Tolerated
Dsm3	8	72356662	Pbx4	T/S	Acc/Tcc	rs33520026	Tolerated
Dsm3	8	72414827	Yjefn3	R/C	Cgc/Tgc	rs48997630	Affect protein function
Dsm3	8	72588837	Sugp1	P/L	cCt/cTt	rs13471212	Tolerated
Dsm3	8	72601385	Tm6sf2	R/Q	cGg/cAg	rs33507109	Tolerated
Dsm3	8	72631376	Ncan	K/E	Aag/Gag	rs32944017	Tolerated
Dsm3	8	72775709	Sugp2	I/L	Att/Ctt	rs33248225	Tolerated
Dsm3	8	72816916	Homer3	S/A	Tcg/Gcg	rs33368143	Tolerated
Dsm3	8	72839765	Lass1	A/T	Gct/Act	rs32784207	Tolerated
Dsm3	8	72854735	Gdf1	S/C	Agt/Tgt	rs32650885	Affect protein function
Dsm3	8	73008269	Tmem59l	L/P	cTg/cCg	rs32740361	Tolerated
Dsm3	8	73030450	2810428I15Rik	Q/R	cAg/cGg	rs13466955	Tolerated
Dsm3	8	73043950	Kxd1	A/V	gCg/gTg	rs32856081	nd
Dsm3	8	73102993	Ell	Y/H	Tat/Cat	rs3654030	Tolerated
Dsm3	8	73289000	Ifi30	A/V	gCc/gTc	rs3689450	Tolerated
Dsm3	8	73294377	Pik3r2	I/V	Ata/Gta	rs33473198	Tolerated
Dsm3	8	73361103	Arrdc2	R/H	cGc/cAc	rs33374964	Tolerated
Dsm3	8	73392909	Ccdc124	A/V	gCc/gTc	rs32705818	Tolerated
Dsm3	8	73407779	Slc5a5	A/V	gCt/gTt	rs48608846	Tolerated
Dsm3	8	73437883	Mtap1s	Q/R	cAg/cGg	rs32782663	Tolerated
Dsm3	8	73781317	Haus8	G/V	gGa/gTa	rs49571184	Tolerated

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<i>Dsm3</i>	8	73862894	<i>Myo9b</i>	F/L	Ttc/Ctc	rs3662998	Tolerated
<i>Dsm3</i>	8	73890964	<i>Use1</i>	N/S	aAc/aGc	rs32955301	Tolerated
<i>Dsm3</i>	8	73895773	<i>Ocel1</i>	R/K	aGg/aAg	rs33439200	Tolerated
<i>Dsm3</i>	8	73902408	<i>Nr2f6</i>	V/L	Gtg/Ctg	rs16822094	nd
<i>Dsm3</i>	8	73909639	<i>Ushbp1</i>	L/R	cTg/cGg	rs48453311	Tolerated
<i>Dsm3</i>	8	73921694	<i>Babam1</i>	T/P	Acg/Ccg	rs32947475	Tolerated
<i>Dsm3</i>	8	74109902	<i>Slc27a1</i>	V/L	Gta/Cta	rs8262739	Tolerated
<i>Dsm3</i>	8	74122985	<i>Fam129c</i>	N/D	Aat/Gat	rs32985468	Tolerated
<i>Dsm3</i>	8	74142112	<i>Glt25d1</i>	T/P	Aca/Cca	rs32706986	Tolerated
<i>Dsm3</i>	8	74180183	<i>Unc13a</i>	D/E	gaT/gaG	rs108187400	Tolerated
<i>Dsm3</i>	8	74211147	<i>Jak3</i>	S/R	Agc/Cgc	rs33182445	Tolerated
<i>Dsm3</i>	8	74234961	<i>Fcho1</i>	A/T	Gcc/Acc	rs33190926	Tolerated
<i>Dsm3</i>	8	74414221	<i>Zfp709</i>	L/F	Ctc/Ttc	rs32828884	Tolerated
<i>Dsm3</i>	8	74433137	<i>Zfp882</i>	R/K	aGa/aAa	rs50630300	nd
<i>Dsm3</i>	8	74491837	<i>Zfp961</i>	S/R	agT/agG	rs50965195	Tolerated
<i>Dsm3</i>	8	74869897	<i>Eps15l1</i>	T/A	Acc/Gcc	rs49858650	Tolerated
<i>Dsm3</i>	8	74968867	<i>1700030K09Rik</i>	S/I	aGt/aTt	rs13479827	Tolerated
<i>Dsm3</i>	8	75008591	<i>Slc35e1</i>	T/I	aCc/aTc	rs51818739	Tolerated
<i>Dsm3</i>	8	75109914	<i>Tmem38a</i>	G/S	Ggc/Agc	rs13479828	Tolerated
<i>Dsm3</i>	8	75190542	<i>Nwd1</i>	S/N	aGc/aAc	rs108371156	Tolerated
<i>Dsm3</i>	8	83508407	<i>Usp38</i>	A/V	gCc/gTc	rs13461494	Tolerated
<i>Dsm3</i>	8	84368392	<i>Inpp4b</i>	L/P	cTg/cCg	rs33412198	nd
<i>Dsm3</i>	8	85388231	<i>Rnf150</i>	A/V	gCc/gTc	rs37159290	Tolerated
<i>Dsm3</i>	8	85689731	<i>Gm10645</i>	P/R	cCg/cGg	rs33302795	nd
<i>Dsm3</i>	8	85773343	<i>Tbc1d9</i>	G/D	gGc/gAc	rs46480564	Tolerated
<i>Dsm3</i>	8	85846636	<i>Elmod2</i>	Q/E	Cag/Gag	rs48577786	Tolerated
<i>Dsm3</i>	8	85934426	<i>Clgn</i>	R/K	aGg/aAg	rs16789437	Tolerated
<i>Dsm3</i>	8	85961937	<i>Scoc</i>	W/L	tGg/tTg	rs51827371	Tolerated
<i>Dsm3</i>	8	86248243	<i>Cd97</i>	S/A	Tcc/Gcc	rs13462843	Tolerated
<i>Dsm3</i>	8	86553434	<i>Palm3</i>	K/E	Aag/Gag	rs32994613	Tolerated
<i>Dsm3</i>	8	86590245	<i>C330011M18Rik</i>	L/M	Ttg/Atg	rs33393338	nd
<i>Dsm3</i>	8	86621618	<i>Dcaf15</i>	W/R	Tgg/Cgg	rs47675262	Affect protein function
<i>Dsm3</i>	8	86657762	<i>Cc2d1a</i>	P/S	Cct/Tct	rs33569206	Tolerated
<i>Dsm3</i>	8	86691126	<i>4930432K21Rik</i>	R/K	aGg/aAg	rs37326990	Tolerated
<i>Dsm3</i>	8	86750600	<i>Zswim4</i>	S/N	aGc/aAc	rs32556818	Tolerated
<i>Dsm3</i>	8	87186263	<i>Ier2</i>	G/S	Ggt/Agt	rs32599097	Tolerated
<i>Dsm3</i>	8	87213684	<i>Trmt1</i>	S/F	tCc/tTc	rs32652529	Tolerated
<i>Dsm3</i>	8	87226581	<i>Lyl1</i>	R/G	Aga/Gga	rs13460901	Tolerated
<i>Dsm3</i>	8	87356244	<i>Gadd45gip1</i>	G/S	Ggt/Agt	rs50271456	Tolerated
<i>Dsm3</i>	8	87391306	<i>Farsa</i>	G/D	gGc/gAc	rs32856242	Affect protein function
<i>Dsm3</i>	8	87416307	<i>Gcdh</i>	G/R	Gga/Cga	rs33533940	Tolerated
<i>Dsm3</i>	8	87476618	<i>Rtbdn</i>	V/E	gTg/gAg	rs45870120	Tolerated

Interval	Chr	Location (Mb)*	Gene	Amino acid change	Codon change	RS #	SIFT [†]
<i>Dsm3</i>	8	87515295	<i>Hook2</i>	N/D	Aac/Gac	rs32768427	Tolerated
<i>Dsm3</i>	8	87584174	<i>Fbxw9</i>	S/T	Tcg/Acg	rs51761769	Tolerated
<i>Dsm3</i>	8	87597303	<i>Dhps</i>	S/N	aGt/aAt	rs32601271	Tolerated
<i>Dsm3</i>	8	87614821	<i>Man2b1</i>	V/A	gTa/gCa	rs13466172	Tolerated
<i>Dsm3</i>	8	87633945	<i>Zfp791</i>	D/E	gaT/gaG	rs33372801	Tolerated
<i>Dsm3</i>	8	87826731	<i>Orc6</i>	V/M	Gtg/Atg	rs32970969	Tolerated
<i>Dsm3</i>	8	88077263	<i>Dnaja2</i>	K/R	aAg/aGg	rs13469334	Affect protein function
<i>Dsm3</i>	8	88250076	<i>Itfg1</i>	S/P	Tct/Cct	rs13465531	Tolerated
<i>Dsm3</i>	8	90663819	<i>Heatr3</i>	V/I	Gtt/Att	rs108308101	Tolerated
<i>Dsm3</i>	8	90833664	<i>Adcy7</i>	A/V	gCa/gTa	rs13479889	Tolerated
<i>Dsm3</i>	8	91115953	<i>Nkd1</i>	V/M	Gtg/Atg	rs33576350	Tolerated
<i>Dsm3</i>	8	91155703	<i>Snx20</i>	P/L	cCc/cTc	rs49016988	Tolerated
<i>Dsm3</i>	8	91556211	<i>Sall1</i>	A/E	gCa/gAa	rs33127605	Tolerated
<i>Dsm3</i>	8	93456791	<i>Chd9</i>	P/H	cCt/cAt	rs33410126	Tolerated
<i>Dsm3</i>	8	93611040	<i>Rbl2</i>	R/T	aGa/aCa	rs32687029	Tolerated
<i>Dsm3</i>	8	93636464	<i>Aktip</i>	F/S	tTc/tCc	rs50604922	nd
<i>Dsm3</i>	8	93784905	<i>Rpgrip1l</i>	Y/H	Tac/Cac	rs32896079	Tolerated
<i>Dsm3</i>	8	94009098	<i>Fto</i>	N/S	aAt/aGt	rs32686383	Tolerated
<i>Dsm3</i>	8	94322863	<i>Irx3</i>	I/T	aTc/aCc	rs13479918	Affect protein function
<i>Dsm3</i>	8	95379499	<i>Lpcat2</i>	T/R	aCg/aGg	rs50123544	Tolerated
<i>Dsm3</i>	8	96582159	<i>Ogfod1</i>	R/Q	cGa/cAa	rs32059856	Tolerated
<i>Dsm3</i>	8	97147084	<i>Rspryl</i>	T/A	Aca/Gca	rs32107374	Tolerated
<i>Dsm3</i>	8	97653100	<i>Kifc3</i>	N/K	aaT/aaA	rs36764080	Tolerated
<i>Dsm3</i>	8	97847605	<i>Zfp319</i>	V/I	Gtt/Att	rs32889436	nd
<i>Dsm3</i>	8	97869204	<i>AA960436</i>	V/I	Gtc/Atc	rs32783874	Tolerated
<i>Dsm3</i>	8	105174527	<i>Cdh11</i>	E/D	gaA/gaT	rs33464298	Tolerated
<i>Dsm3</i>	8	109572797	<i>Cog8</i>	M/V	Atg/Gtg	rs4227359	Tolerated
<i>Dsm3</i>	8	109600574	<i>Terf2</i>	K/E	Aag/Gag	rs47210744	Tolerated
<i>Dsm3</i>	8	111774838	<i>4922502B01Rik</i>	N/K	aaT/aaA	rs33402085	nd
<i>Dsm5</i>	11	7050842	<i>Adcy1</i>	T/M	aCg/aTg	rs26913279	Tolerated
<i>Dsm5</i>	11	8378426	<i>Tns3</i>	S/A	Tca/Gca	rs13480859	Tolerated
<i>Dsm5</i>	11	12153991	<i>Cobl</i>	H/Y	Cac/Tac	rs29456637	Affect protein function
<i>Dsm5</i>	11	17846044	<i>Etaa1</i>	G/D	gGc/gAc	rs29422803	Tolerated
<i>Dsm5</i>	11	21621166	<i>Wdpcp</i>	S/N	aGt/aAt	rs13480905	Tolerated
<i>Dsm5</i>	11	21956910	<i>Ehbp1</i>	D/E	gaT/gaG	rs26866453	Tolerated
<i>Dsm5</i>	11	42128461	<i>Gabra6</i>	Q/E	Caa/Gaa	rs50667464	Tolerated
<i>Dsm5</i>	11	54754327	<i>Tnip1</i>	G/R	Ggg/Cgg	rs51531280	Tolerated
<i>Dsm5</i>	11	54796819	<i>Anxa6</i>	K/I	aAa/aTa	rs13466153	Tolerated
<i>Dsm5</i>	11	55076001	<i>Fat2</i>	P/L	cCg/cTg	novel	Tolerated

*GRC m38 assembly; nd=not determined

[†]SIFT <<http://sift.bii.a-star.edu.sg/>>; Kumar P, Henikoff S, Ng PC (2009) Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. Nat Protoc 4, 1073-1081.