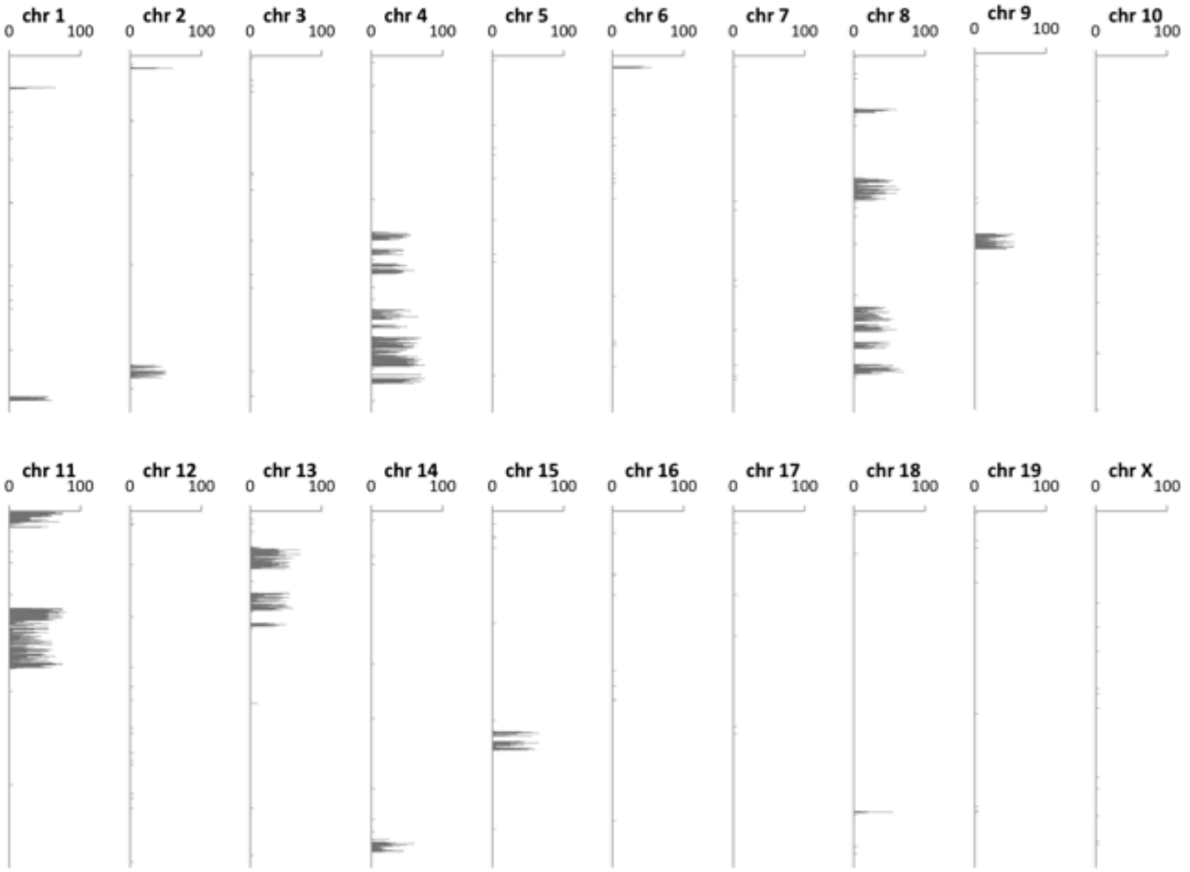
Table S1: Survey of Mouse Phenome Database CGD-MDA1 SNP set for B6 vs B10 polymorphisms

	NCBI build 38							
Chr	**congenic start**	**congenic stop**	**Polymorphic SNPs**	**Total SNPs**	**congenic size (Mb)**	**B6.B10 congenic strain name (chr/Mb format)**	**latest generation tested**	**Informative SSLP markers within congenic interval**
1	21,641,028	22,367,196	49	178	0.7	B6.B10-1/21-22;8/114-117	N4F7	D1Dcr8, D8Dcr46, 47, 48
1	187,056,961	188,938,319	169	511	1.9	B6.B10-1/187-188	N8F7	D1Dcr19
2	9,318,530	9,822,955	45	109	0.5	B6.B10-2/9-10	N7F6	D2Dcr45
2	159,389,745	164,247,427	265	1265	4.9	B6.B10-2/159-164	N3F14	D2Dcr115
4	85,424,026	101,139,995	523	3663	15.7	B6.B10-4/85-101	N11F2	D4Dcr10, D4Dcr14
4	115,888,824	142,973,945	1462	6496	27.1	B6.B10-4/117-143	N11F6	D4Dcr25, 26, 27, 28, 29
6	7,955,563	8,458,659	57	148	0.5	B6.B10-6/8-9	N11F4	D6Dcr2, D6Dcr3
8	22,713,943	24,112,792	94	339	1.4	B6.B10-8/22-109	N4F10	D8Dcr5, 17, 20, 32, 33, 34, 37
8	48,448,184	57,943,948	421	1750	9.5			
8	94,374,289	108,954,590	553	3268	14.6	B6.B10-8/94-109	N4F15	D8Dcr32, 33, 34, 37
8	114,544,756	117,251,376	250	738	2.7	B6.B10-1/22;8/114-117	N4F7	D1Dcr8, D8Dcr46, 47, 48
9	65,711,109	69,135,679	331	1175	3.4	B6.B10-9/65-69	N11F5	D9Dcr2, 3, 6, 7, 8
11	3,105,931	8,644,832	388	1103	5.5	B6.B10-11/3-57	N4F8	D11Dcr1, 7, 12, 34
11	37,580,981	56,653,819	1399	4159	19.1			
13	16,316,718	22,293,617	490	1545	6.0	B6.B10-13/16-41	N11F5	D13Dcr1, 3, 5
13	31,070,618	36,685,498	351	1260	5.6			
13	39,889,868	40,771,645	63	231	0.9			
14	115,702,035	119,622,245	154	797	3.9	B6.B10-14/115-120	N11F9	D14Dcr7, D14Dcr9
15	67,989,428	72,421,994	272	1204	4.4	B6.B10-15/68-73	N11F4	D15Dcr4
18	77,379,821	77,672,891	24	77	0.3	B6.B10-18/77-78	N11F3	D18Dcr3

Table S2: SSLP markers polymorphic between B6 And B10

Chr	MGI Name	Alias	UCSCPosition(NCBI38/mm10)	B6 Size (bp)	B10 vs B6	Forward Primer	Reverse Primer	MIT Markers Colocated
1	D1Dcr8	D1Dcr22.118	chr1:22,133,369-22,133,467	99	B6>>B10	CATCTTAACACTCGCAAAAACACA	TTTATATACCGCATTGGAGAAAAGTACTT	
1	D1Dcr19	D1Dcr190.120	chr1:188,419,328-188,419,425	98	B6>>B10	GCACTTGAAATTCTTTCTAGTGTTTTACA	GAAAGATCCAGTAAGTAGATAGGTGTGTGT	
2	D2Dcr131	D2Dcr9.520v2	chr2:9,602,710-9,602,826	117	B6>B10	TATGTACATATATCCACAATAACAGGCATGTA	TTCTTTTTAAGAAACATGATTTGTAGGGTAT	
2	D2Dcr113	D2Dcr159.121	chr2:159,430,118-159,430,237	120	B10>>B6	TGAGGAAGATACCAAATGTCAACCT	TGACTTGTATGTGGTATGACAGATGC	D2Mit287
2	D2Dcr124	D2Dcr162.143	chr2:162,452,335-162,452,432	98	B6>>B10	CAGATTCTCTCTGGCCACACATT	ATGGGAGGTATGAGAAAGGCTGT	
2	D2Dcr115	D2Dcr162.885	chr2:163,194,446-163,194,547	102	B10>>B6	TTTTTGCAACTTTGTTAAGAATTCCA	GAAAACACCCTCCCACCCTT	D2Mit226
4	D4Dcr10	D4Dcr87.274	chr4:87,803,407-87,803,508	102	B6>B10	TTGTCAGCATCTACTTCCTAACCATCT	TCAAACCTGACGGCAGTGAGT	
4	D4Dcr14	D4Dcr99.535	chr4:100,037,690-100,037,789	100	B6>>B10	TTCAGGCATAACACACACTATCAATTT	GACACGCAGCCAGTGAATGTA	
4	D4Dcr17	D4Dcr116.293	chr4:116,796,039-116,796,142	104	B6>>B10	GTTTGCTAGGTGCACATCTACACA	ATTACAAACATGAGCCGGCATA	
4	D4Dcr25	D4Dcr127.617	chr4:128,115,255-128,115,350	97	B10>>B6	AGACTCCACTTTCTGTCATGTGTAGAA	TCATCCCCGTGAACTTCCAT	D4Mit16
4	D4Dcr26	D4Dcr128.357	chr4:128,855,509-128,855,604	96	B10>B6	TGTCTAAAACATGCAAGCACACA	CAAAACACAGCATCAGGGTATTTATT	
4	D4Dcr27	D4Dcr132.699	chr4:133,427,364-133,427,461	98	B6>>B10	GCCTCAGGCACCTAAGTACATGT	GATTCTCTCCGGCTCACACCT	
4	D4Dcr28	D4Dcr133.058	chr4:133,785,938-133,786,036	99	B6>>B10	CTGCATGAAAGAAACCCCAAA	CACCCAACAACCACCATCAAAT	D4Mit71
4	D4Dcr29	D4Dcr135.633	chr4:136,361,089-136,361,191	103	B6>>B10	CCTCTGCTGACCTCCACATGT	TGTGTGCATTTGCTACTTGTGTGT	D4Mit69
6	D6Dcr2	D6Dcr8.203	chr6:8,253,036-8,253,139	104	B10>>B6	AGGGAAAATTGAGTATGGTTAGCAA	ACAGCTTACCTATCTCAAGCATATAATTGAGT	
6	D6Dcr3	D6Dcr8.237	chr6:8,287,720-8,287,815	96	B6>>B10	ACATGTGCACCTGTGTGTATATGAA	GAGCCTGATGTCATACTAATATTTCTGTGT	
8	D8Dcr5	D8Dcr24.267	chr8:22,802,019-22,802,114	96	B10>>B6	AGCCCCATCTCTGTGGTTTTAA	TGTGTAACTTACTGAAAGCCAGGAA	
8	D8Dcr17	D8Dcr52.336	chr8:50,837,361-50,837,458	98	B10>>B6	CTTTGACTGCATTGACATTCTCCTAT	CAAGTAAAATAAGCATAATGCACACACA	D8Mit205
8	D8Dcr20	D8Dcr56.096	chr8:54,597,803-54,597,898	96	B10>>B6	TTTCCAAATCACCTGTTCCTTGT	TGTACCTTGTACGTATGCGTGTGT	
8	D8Dcr32	D8Dcr104.407	chr8:101,518,319-101,518,431	113	B6>>B10	CCCTGAACAAACTCATACACAAACA	ACAGGAAAGACAGTTACTTCACACATGT	
8	D8Dcr33	D8Dcr104.626	chr8:101,737,509-101,737,607	99	B10>B6	AACAAACCAACCAACATTCATCATA	GCAAATAAGAAATCAACATAATAAATCAGTGT	
8	D8Dcr34	D8Dcr104.710	chr8:101,820,922-101,821,026	105	B10>>B6	CCCTCATTACTACCAAATGAAGGAAT	AATTAGAAAGCACAAGGTTAGCTCTGT	
8	D8Dcr37	D8Dcr105.511	chr8:102,622,642-102,622,737	96	B6>>B10	AACAGTGATTGTCAGTAGTCCTTAGAGCT	TGAATAGAATTGCCAGAATCCTTGT	
8	D8Dcr46	D8Dcr118.408	chr8:115,522,531-115,522,626	96	B10>>B6	CCTTGCAGGGAGAAGCTGAATA	AAGCTAGAAGGTGGCATGCG	
8	D8Dcr47	D8Dcr118.613	chr8:115,727,709-115,727,808	100	B10>>B6	GGAAGGACTGAACCAAATACAAAACTT	TCACCAGTTGCTTCTATTACCGC	
8	D8Dcr48	D8Dcr118.630	chr8:115,744,354-115,744,449	96	B10>B6	AATGCAAGAACATGCCCCAA	GACTGGAGGCCTGTCAACAACT	
9	D9Dcr2	D9Dcr65.375	chr9:65,577,857-65,577,972	116	B6>>B10	CATAGGCAAGTGGTTCACAGAAAT	GTAAAGGGGTTAAGAATGTGAAGTTTTATA	D9Mit336
9	D9Dcr3	D9Dcr65.784	chr9:65,986,191-65,986,295	105	B6>>B10	CATGACTCTGAATAGATAAGCATTTTATCA	ATCAAAAATATTCTTAAGGGCTCTGTGT	
9	D9Dcr6	D9Dcr67.328	chr9:67,529,227-67,529,322	96	B6>>B10	TGCTCTCTGATCTTAACACGTATGCTA	TTGGCATGAAACAACAGAACAATA	
9	D9Dcr7	D9Dcr67.793	chr9:67,993,744-67,993,852	109	B10>>B6	CTCAGGCTTACCCACCATTCA	TGCCAACTGTGTATGTTTTCTTAAGA	D9Mit260
9	D9Dcr8	D9Dcr68.628	chr9:68,828,916-68,829,019	104	B10>>B6	ATACCTGATGCCCTCCTCTGACTT	ATCTGAGTATCATGGAGACTGTAGGAGT	
11	D11Dcr1	D11Dcr3.215	chr11:3,315,493-3,315,591	99	B10>B6	GGAAAAGCTCTGGCCTCTGA	TTTTCCGTAACCCTTAACATTGTGT	
11	D11Dcr34	D11Dcr8.331	chr11:8,431,175-8,431,272	98	B6>>B10	CAGACACAGCAGTACACAGGTGC	ACCCCAGACTGTATGTGCATTGT	
11	D11Dcr7	D11Dcr39.441	chr11:39,598,310-39,598,413	104	B10>>B6	GCATCCCTGACATTGTGTGAA	GGCTAGAGAAAAAAGGCACAGAAT	
11	D11Dcr12	D11Dcr55.733	chr11:55,889,987-55,890,090	104	B10>>B6	GATGCTCTAGTCTCATTGAGAATGTTAATTTA	GTAAATCTCCCCAAAGTAATTTTGTGA	
13	D13Dcr5	D13Dcr20.347	chr13:20,255,418-20,255,513	96	B6>>B10	AGGAAAATATGTGTCATTCAGTCAAGTCT	GGGTGATGAGTGATCTGCACAG	
13	D13Dcr1	D13Dcr20.438	chr13:20,431,332-20,431,458	127	B10>>B6	GAAGAACATCTTTTGCAGAGAACACA	TAGAGTCACTGTCACCTGGAAGCTATT	
13	D13Dcr3	D13Dcr36.683	chr13:36,676,310-36,676,405	96	B10>>B6	AGTGAAATGTTTTGTGTGTGACACA	CCTCCACATTTCATAACTATACATTTTGT	
14	D14Dcr7	D14Dcr116.408	chr14:117,525,375-117,525,476	102	B10>>B6	TCTACCACAAGGCTTCCTTGTCA	AACTGGTGAAATTAAAGCCTAAGTGTGT	
14	D14Dcr9	D14Dcr117.317	chr14:118,434,159-118,434,263	105	B6>>B10	AATCTTCCTGCTATACCTGCTGTGT	GCTCAGTCTTTCAAATGCACAAGTT	
15	D15Dcr4	D15Dcr70.887	chr15:71,057,532-71,057,629	100	B10>>B6	GCATCCCATGCTGCTATCAA	CAGGCTATGTTCTCAGATAGGATTCATT	
18	D18Dcr3	D18Dcr77.728	chr18:77,524,014-77,524,113	100	B10>B6	AGCAGGCCCTCAGGAAGACT	CGAGATGCTTACAGCCACCAA	

Figure S1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