

Characterization of single nucleotide polymorphisms for a forward genetics approach using genetic crosses in C57BL/6 and BALB/c substrains of mice

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Abstract: Forward genetics is a powerful approach based on chromosomal mapping of phenotypes and has successfully led to the discovery of many mouse mutations in genes responsible for various phenotypes. Although crossing between genetically remote strains can produce F₂ and backcross mice for chromosomal mapping, the phenotypes are often affected by background effects from the partner strains in genetic crosses. Genetic crosses between substrains might be useful in genetic mapping to avoid genetic background effects. In this study, we investigated single nucleotide polymorphisms (SNPs) available for genetic mapping using substrains of C57BL/6 and BALB/c mice. In C57BL/6 mice, 114 SNP markers were developed and assigned to locations on all chromosomes for full utilization for genetic mapping using genetic crosses between the C57BL/6J and C57BL/6N substrains. Moreover, genetic differences were identified in the 114 SNP markers among the seven C57BL/6 substrains from five production breeders. In addition, 106 SNPs were detected on all chromosomes of BALB/cAJcl and BALB/cByJJcl substrains. These SNPs could be used for genotyping in BALB/cJ, BALB/cAJcl, BALB/cAnNCrIcrIj, and BALB/cCrSlc mice, and they are particularly useful for genetic mapping using crosses between BALB/cByJJcl and other BALB/c substrains. The SNPs characterized in this study can be utilized for genetic mapping to identify the causative mutations of the phenotypes induced by N-ethyl-N-nitrosourea mutagenesis and the SNPs responsible for phenotypic differences between the substrains of C57BL/6 and BALB/c mice.

Key words: BALB/c, C57BL/6, genotyping, single nucleotide polymorphism, substrain

Introduction

Mouse models are important tools for understanding the phenotypes of human diseases, genes responsible for diseases, and molecular mechanisms for the development of disease phenotypes. The approaches to developing mouse models include reverse genetics and forward genetics [1–4]. Reverse genetics is a powerful approach based on gene targeting and genome editing. This approach has successfully produced null mutations in almost all genes and mimics mutations associated with several human diseases. Although reverse genetics is a major approach in mouse genetics, forward genetics is a powerful approach based on chromosomal mapping of phenotypes and has led to the discovery of numerous mutations in genes responsible for various spontaneous phenotypes [4]. Moreover, the combination of forward genetics and large-scale N-ethyl-N-nitrosourea (ENU) mutagenesis studies has uncovered the functions of unknown genes and mutations [1, 5–7].

To identify genes associated with spontaneous and ENU-induced phenotypes using the classical forward genetic approach, researchers first produced experimental populations of chromosomal recombinants—F₂ and backcross (N₂) mice—by crossing between the mutant and wild-type mice. Wild-type mice must be chosen from other strains with different genetic backgrounds and mutants, and they are preferred over genetically diverse strains with mutants. This is because the mutations map to a chromosomal region via genotyping of the polymorphic markers, such as microsatellites and single nucleotide polymorphisms (SNPs), between both parental strains. Therefore, interspecific, intersubspecific, and interstrain genetic crosses have been used for classical chromosomal mapping of mutants of interest because of the availability of many polymorphic markers for genotyping in F₂ and N₂ mice from these genetic crosses [8].

However, partner strains that show highly similar phenotypes should be chosen to create a genetic cross in cases involving the mapping of causative mutations for mild phenotypes, which are easily affected by the genetic background of the partner strain. Crosses with similar phenotypic strains

are effective for the mapping of behavioral and sensorial traits. Since there are individual differences in these phenotypic traits, phenotypic noise caused by modifiers in the genetic background of the partner strain should be reduced. Substrains may be candidate partners for genetic crosses. Genetically different substrains have been established in most classical inbred strains [9–12]. Although there are far fewer genomic polymorphisms between substrains than between strains, previous studies have successfully identified the mutations associated with phenotypes via linkage and quantitative trait loci (QTL) analysis using intersubstrain genetic crosses [13–17].

To perform linkage and QTL analyses using intersubstrain genetic crosses, it is important to set up polymorphic markers between substrains of mice without large gaps on the chromosomes. Therefore, we investigated the SNPs that are available for immediate use in linkage and QTL analyses using substrains. In this study, we chose substrains of C57BL/6 and BALB/c mice as the research targets. These are very common inbred mice, and several substrains have been established. Moreover, there are potential mutants available as human disease models because several large-scale ENU mutagenesis studies have been carried out based on ENU-treated male mice from both strains [18–21]. Therefore, marker sets based on SNPs between substrains can be a useful tool for identifying new phenotypes associated with human diseases.

Materials and Methods

Mice and ethics statement

The C57BL/6 and BALB/c substrains used in this study were purchased from each their respective production breeders (Table 1). This study was reviewed and approved by the Institutional Animal Care and Use Committee of the RIKEN Tsukuba Branch and the Animal Care and Use Ethics Committee of the Tokyo Metropolitan Institute of Medical Science.

Preparation of PCR templates

All PCR templates were obtained from the pinna and/or tail samples of adult mice euthanized by carbon dioxide inhalation. The pinna (diameter: 2 mm) and tail (length: less than 2 mm) samples were incubated in 50 μ l of lysis buffer solution (50 mM Tris-HCl, pH 8.0; 20 mM EDTA, pH 8.0; 100 mM NaCl; and 1% sodium dodecyl sulfate) with 0.5 μ l of proteinase K solution (20 mg/ml) at 37°C overnight and then incubated at 95°C for 10 min. The solution samples were diluted with water (1:200) and used as PCR templates.

Validation of SNPs between C57BL/6J and C57BL/6N substrains

To prepare novel SNP markers, we selected SNPs between the C57BL/6J and C57BL/6N substrains, based on published data [16, 22–24]. For several SNPs, the flanking sequences including the SNPs were amplified by PCR using AmpliTaq Gold DNA Polymerase (Thermo Fisher Scientific, Waltham, MA, USA) or TaKaRa Ex Taq (Takara Bio, Inc., Kusatsu, Japan) and the primers listed in Supplementary Table 1 according to the manufacturer's protocol. The SNPs were validated via Sanger sequencing of the PCR products. The PCR products were purified using the ExoSAP-IT (Thermo Fisher Scientific) and sequenced using an Applied Biosystems 3130xl Genetic Analyzer and 3730xl DNA

Analyzer (Thermo Fisher Scientific) by the Genetic Analysis Division of Fasmac Co., Ltd. (Atsugi, Japan).

SNP genotyping

A set of validated SNPs was used to design TaqMan assays using a custom TaqMan SNP Genotyping Assay (Thermo Fisher Scientific; Supplementary Table 2). PCR template solutions (1 μ l) were dispensed into each well of 384-well plates and dried using a speed-vacuum drying system. The reaction mixtures for genotyping using TaqMan Genotyping Master Mix (Thermo Fisher Scientific) and the custom TaqMan assays were dispensed into 384-well plates and amplified via PCR following the manufacturer's instructions. The PCR products were analyzed using the TaqMan Genotyper software with an ABI PRISM 7900HT Sequence Detection System (Thermo Fisher Scientific) or QuantStudio 12K Flex Real-Time PCR System (Thermo Fisher Scientific) according to the manufacturer's instructions.

Detection of SNPs between BALB/cA and BALB/cByJ substrains

To obtain information on SNPs between BALB/cAJcl (BALB/cA) and BALB/cByJJcl (BALB/cByJ) mice, next-generation sequencing (NGS) technology was used. For sequencing, genomic DNA was extracted from the spleens of female BALB/cA and BALB/cByJ mice using a QIAamp DNA Mini Kit (QIAGEN, Hilden, Germany). Whole genome sequencing and listing of mutations were performed by Hokkaido System Science Co. Ltd. (Hokkaido, Japan). Paired-end reads of 150 bp were generated with HiSeq X with HiSeq X Ten Reagent Kit v2.5 (Illumina, San Diego, CA, USA) to achieve more than 30 \times genome coverage. The sequence reads were mapped on the reference genome sequence (mouse genome reference assembly, GRCm38.p6) and analyzed using Samtools/BCFtools version 1.2 [25] and SnpEff version 4.1g [26]. The quality of a given base call is measured as a Phred quality score, which indicates the probability that the base is correctly called. The scores generally range from 2 to 40,

with higher scores indicating greater confidence in the call. The candidate SNPs between BALB/cA and BALB/cByJ were confirmed via Sanger sequencing.

Results

Construction of marker sets for genetic mapping of genetic crosses between C57BL/6J and C57BL/6N substrains

We previously developed 101 primer and probe sets (Supplementary Table 2) for TaqMan assays and succeeded in linkage mapping of several phenotypes using these sets [14–17]. To place markers on chromosomal regions for linkage mapping at equal intervals without the absence of markers in the long-range chromosomal region, SNPs were screened from databases. Thirteen SNPs were identified as available for linkage mapping in genetic crosses between the C57BL/6J and C57BL/6N substrains via Sanger sequencing (Supplementary Tables 1 and 2). The locations of all markers for TaqMan assays are shown in Figure 1. The markers were assigned at 20.58 Mb intervals on the chromosomes on average in the case of choosing either one from the neighboring markers (*D2SNP38/D2SNP39*, *D3SNP39/D3SNP48*, *D4SNP38/D4SNP42*, *D12SNP38/D12SNP41*, *D17SNP34/D17SNP32*, and *D19SNP23/D19SNP26*) located within 10 Mb (Fig. 1 and Supplementary Tables 2). Although the SNP markers were absent in several long-range genomic regions (e.g., *D6SNP32–D6SNP33*, 50.18 Mb, and *DXSNP58–DXSNP52*, 48.43 Mb), we predicted that the marker sets for identifying the loci linked with phenotypes could be assigned to all chromosomes.

The marker sets were designed based on the SNPs between C57BL/6J mice from The Jackson Laboratory and C57BL/6NTac mice from Taconic Biosciences. C57BL/6J is the most commonly used substrain in biomedical research, and its genomic sequence was first published as a reference genome sequence by the Mouse Genome Sequencing Consortium (MGSC) [27, 28]. C57BL/6NTac was selected by the Knockout Mouse Project and the International Mouse Phenotyping Consortium as a background strain to produce genetically engineered mutants [29–31]. However, previous studies have reported that there are several SNPs at the intrasubstrain level in both C57BL/6J and C57BL/6N mice from each breeder [22, 32]. Therefore, we investigated SNPs in C57BL/6J and C57BL/6N mice purchased from

three major breeders (Table 1) in Japan using TaqMan assays. SNPs were detected in 25 markers, and SNPs in 13 markers were detected within the C57BL/6J substrains. The genotypes of 13 markers in C57BL/6JJmsSlc mice and 5 markers in C57BL/6JJcl mice were identical to those of all C57BL/6N mice (Fig. 1 and Table 2). In C57BL/6N mice, SNPs were detected in 12 markers and were identical to those of all C57BL/6J mice (Fig. 1 and Table 2). Twelve SNPs were detected in C57BL/6NCrSlc mice, and only one SNP was detected in C57BL/6NCrl mice. There were no SNPs in C57BL/6NTac and C57BL/6NJcl mice.

Identification of SNPs for genetic mapping of the genetic crosses between BALB/cA and BALB/cByJ substrains

Next, we performed NGS whole-genome sequencing to screen SNPs used for genetic mapping of the genetic crosses between the BALB/cA and BALB/cByJ substrains. In total, 912,105,404 and 636,697,536 reads of BALB/cA and BALB/cByJ mice, respectively, were mapped to the reference genome sequence. A large number of SNPs were detected in BALB/cA and BALB/cByJ mice via this analysis. However, the quality of the sequence data was low because the read coverage was poor in many genomic regions, including these SNPs. Therefore, candidate SNPs for genotyping between BALB/cA and BALB/cByJ mice were filtered according to several criteria that included read coverage, allele frequency, and genotype information (Supplementary Table 3). In addition, we selected SNPs that were assigned dbSNP IDs from the filtered SNPs to increase the reliability of SNPs because a large amount of SNP data generated using oligonucleotide arrays in BALB/cByJ mice have previously been reported [33]. Finally, 632 candidate SNPs were screened between BALB/cA and BALB/cByJ mice (Supplementary Table 3). To construct the marker sets for genetic mapping using F₂ and N₂ progeny between the BALB/c substrains, we used Sanger sequencing to validate SNPs selected based on the genomic locations. One hundred six SNPs were detected on all chromosomes in BALB/cA and BALB/cByJ mice (Supplementary Table 4). Figure 2 shows the locations of the 106 SNPs. Most of the

SNPs were assigned locations on all chromosomes, as planned. The average interval between the SNPs was 21.18 Mb when either SNP was chosen from the neighboring markers (*D10SNP302/D10SNP303*, *D16SNP304/D16SNP305*, *D18SNP301/D18SNP302*, *D19SNP301/D19SNP302*, *D19SNP302/D19SNP303*, and *DXSNP303/DXSNP304*) located within 10 Mb. However, we could not detect the SNPs in the long-range genomic region (~39.12 Mb) of the centromere on chromosome 1 because of difficulty of designing primer sets for Sanger sequencing to validate them. This was attributed to the presence of repetitive sequences and long stretches of a single nucleotide in the flanking sequence of all candidate SNPs. We also could not detect the SNPs on the proximal region (1–28.12 Mb) of chromosome 18 because there were no candidate SNPs in this region (Supplementary Table 3).

Regarding BALB/c substrains, the whole-genome sequence of BALB/cJ mice has been published by the Wellcome Trust Sanger Institute [23]. In addition, 106 SNPs were genotyped in BALB/cAnNCrJ (BALB/cAn) and BALB/cCrSlc (BALB/cCr) mice. Table 3 shows comparisons of the genotypes of the 106 SNPs among the five substrains. The genotypes of BALB/cJ and BALB/cA mice were identical at 90 SNPs. In contrast, the same genotypes were detected in only 16 positions in BALB/cJ and BALB/cByJ mice. The genotypes of the 106 SNPs matched exactly in BALB/cAn and BALB/cCr mice. The genotypes at 73, 57, and 49 SNPs of BALB/cAn and BALB/cCr were identical to those of BALB/cJ, BALB/cA, and BALB/cByJ, respectively.

Discussion

This study provides information on available SNP marker sets for genotyping of C57BL/6 and BALB/c substrains. As mentioned in the Introduction, a useful application of these marker sets is linkage and QTL analyses of the phenotypes produced by ENU mutagenesis. Large-scale ENU mutagenesis studies in mice have been powerful discovery platforms for identifying novel genes or gene functions associated with disease phenotypes [1, 5]. We also identified several genes and gene functions associated with several disease phenotypes, such as hair formation [34, 35], amelogenesis [36], development of single positive thymocytes [37], and abnormal behavior due to neurological disorders [38–40]. However, we could not identify the loci associated with several phenotypes by linkage and QTL analyses. In particular, the genetic mapping of several mild morphological and behavioral phenotypes, which were detected using a modified SHIRPA (SmithKline, Harwell, Imperial College, Royal Hospital, Phenotype Assessment) protocol, failed [20]. We have previously used interstrain genetic crosses between ENU-treated C57BL/6J and DBA/2J (or C3H/HeJ) mice for linkage and QTL analyses. We predicted that these mild phenotypes might be overlooked by the genetic background effects of DBA/2J and C3H/HeJ mice. In contrast, several studies have identified causative mutations associated with disease phenotypes using intersubstrain genetic crosses. Hossain et al. (2016) identified obesity-related genes based on genetic mapping of the N₂ progeny between ENU-treated C57BL/6J and C57BL/6N mice [14]. Funato et al. (2016) and Miyoshi et al. (2019) identified sleep-related genes by a forward genetics approach using the same intersubstrain cross [13, 15]. As it was assumed that target phenotypes in these studies are susceptible to genetic background effects, we predict that substrain crosses will become a key strategy for the successful identification of these causative genes.

In addition, we expect that the marker sets developed in the present study will be useful tools for identifying loci and mutated genes associated with phenotypic differences between substrains of C57BL/6 and BALB/c mice. Kirkpatrick et al. (2017) identified a robust difference in binge eating

between C57BL/6 substrains and a major genetic factor associated with the phenotype by QTL mapping using C57BL/6J × C57BL/6N-F₂ mice [41]. Kumar et al. (2013) confirmed that substrain differences in the locomotor response to cocaine in C57BL/6J and C57BL/6N mice were caused by an SNP [16]. Previous studies have reported several phenotypic differences among substrains of C57BL/6 and BALB/c mice [9, 11, 42, 43]. Although almost all causative genes and mutations are still unknown, they may be identified by linkage and QTL analyses using intersubstrain crosses and SNP markers in both substrains.

The phenotypic differences are estimated to be associated with approximately 10,000 SNPs between the C57BL/6J and C57BL/6N substrains [11, 23, 42]. In addition, Mekada et al. (2015) reported genetic differences among substrains of C57BL/6J and C57BL/6N mice produced by breeders [44]. We also detected several SNPs in both the C57BL/6J and C57BL/6N substrains from different breeders. Although we investigated only Japanese breeders, the genetic differences in mice from different breeders would probably be detected in mice from different breeders in other countries. Therefore, it is essential to pay attention to the genetic background of the mutant and control mice for the production of genetic crosses to perform linkage and QTL analyses using SNP markers between the C57BL/6J and C57BL/6N substrains.

In this study, we investigated and confirmed the SNPs between the BALB/cByJ and BALB/cA substrains purchased from CLEA Japan for linkage and QTL analyses, since this approach has been successful in discovering several phenotypic differences between these substrains. However, most reports have described phenotypic differences between BALB/cByJ and BALB/cJ substrains [45–48]. Although 90 markers within our marker sets are available for the genotyping of these substrains, SNP markers were absent in several long-range genomic regions (e.g., *D6SNP302–305*, *D9SNP302–304*, *D11SNP302–305*, and proximal and distal regions on chromosome 16; Fig. 2 and Table 3). Additional markers will need to be developed at several positions to perform detailed linkage and QTL analyses using genetic crosses between BALB/cByJ and BALB/cJ substrains. In addition, we screened the

genotypes of SNPs in BALB/cAn and BALB/cCr mice purchased from the Charles River Laboratories Japan and Japan SLC, respectively; however, the genotypes of these strains were the same for all SNPs. Our SNP markers might be used for linkage and QTL analyses to cross these mice (BALB/cAn and BALB/cCr) and BALB/cByJ mice. However, whole-genome genotyping is difficult for crosses between BALB/cA, BALB/cJ, BALB/cAn, and BALB/cCr mice using only our SNP markers because of the lack of polymorphisms in many chromosomal regions. Whole-genome sequencing of BALB/cAn and BALB/cCr mice can help screen the SNPs and compare them with those in other BALB/c substrains.

In the present study, we developed a genotyping system on 384-well plates using TaqMan assays. The approach can promptly distinguish the homozygous and heterozygous genotypes in progeny from the genetic crosses between C57BL/6 substrains, as shown in Supplementary Fig. 1. This genotyping system can provide researchers with the ability to identify the responsible and modifier genes via linkage and QTL analyses using genetic crosses between the C57BL/6 substrains. We are currently developing a similar high-throughput genotyping system for BALB/c substrains using the SNPs identified in the present study.

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Figure legends

Fig. 1. Chromosomal map of the 114 SNP markers for genotyping of genetic crosses between the C57BL/6J (C57BL/6J, C57BL/6Jcl, and C57BL/6JmsSlc) and C57BL/6N (C57BL/6NTac, C57BL/6NJcl, C57BL/6NCr1, and C57BL/6NCrSlc) substrains. The vertical gray lines and black diamonds indicate chromosomes and locations of SNP markers, respectively. The SNP markers common between C57BL/6J and C57BL/6N substrains are labeled in black. The intrasubstrain polymorphisms were detected in 25 markers, which are labeled in red, blue, green, and magenta.

Fig. 2. Chromosomal map of the 106 SNP markers for genotyping of genetic crosses between the BALB/c (BALB/cJ, BALB/cA, BALB/cByJ, BALB/cAn and BALB/cCr) substrains. The vertical gray lines and white diamonds indicate chromosomes and locations of SNP markers, respectively. The genotypes of the SNP markers are shown in different colors (black, red, and blue) for each marker name.

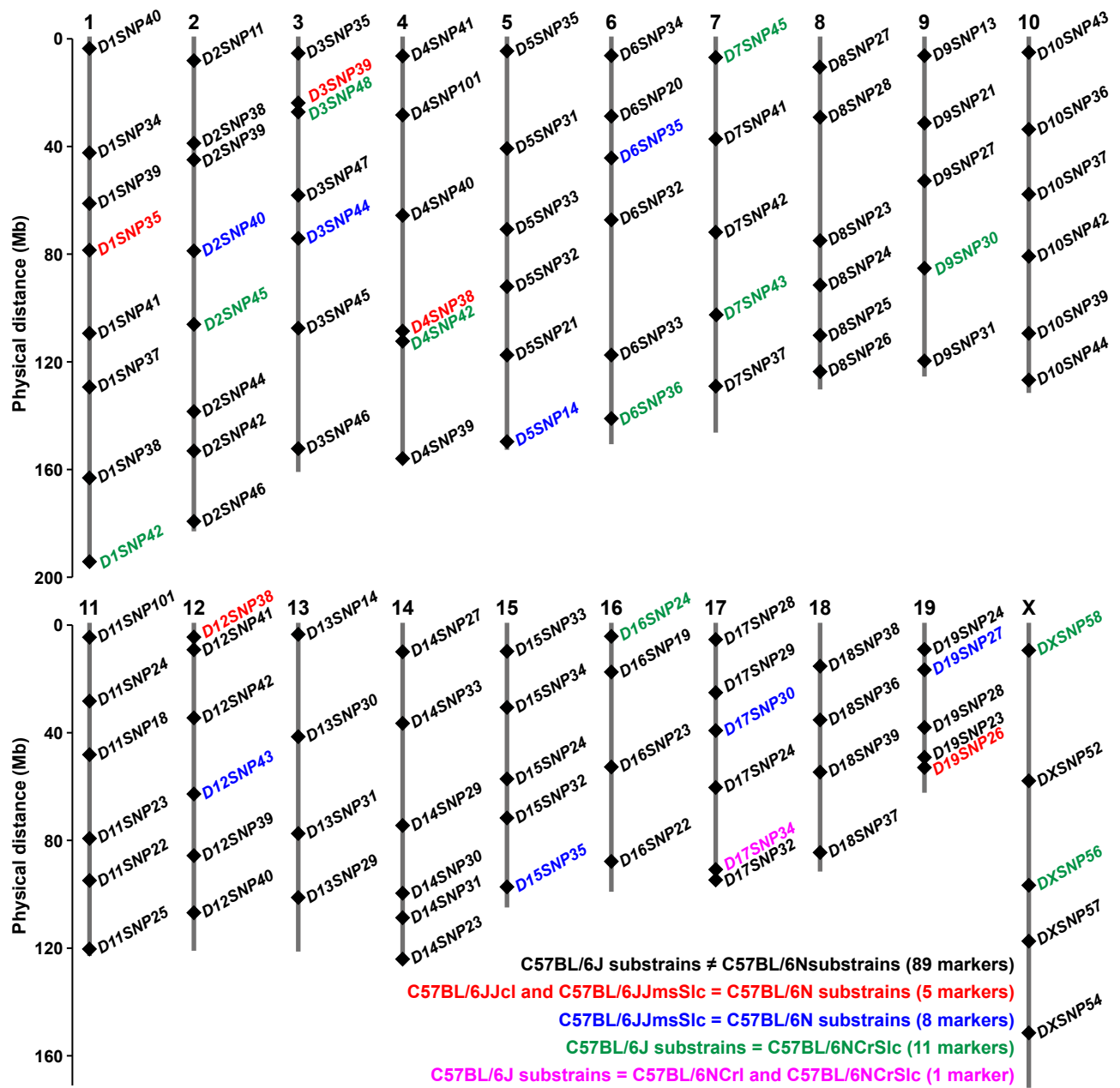


Table 1. C57BL/6 and BALB/c substrains used in this study

Strain	Substrain	Breeder
C57BL/6	C57BL/6J	The Jackson Laboratory via Charles River Laboratories Japan
	C57BL/6JJcl	CLEA Japan
	C57BL/6JJmsSlc	Japan SLC
	C57BL/6NTac	Taconic Biosciences via CLEA Japan
	C57BL/6NJcl	CLEA Japan
	C57BL/6NCrl	Charles River Laboratories Japan
	C57BL/6NCrSlc	Japan SLC
BALB/c	BALB/cAJcl	CLEA Japan
	BALB/cByJJcl	CLEA Japan
	BALB/cAnNCrCrIj	Charles River Laboratories Japan
	BALB/cCrSlc	Japan SLC

Table 2. SNPs among the C57BL/6 substrains within the markers developed in this study

SNP marker	Chr	dbSNP ID	C57BL/6J				C57BL/6N			
			Ref	J	JJcl	JJmsSlc	Ntac	NJcl	NCrl	NCrSlc
<i>D1SNP40</i>	1	rs32685032	A	A	A	A	T	T	T	T
<i>D1SNP34</i>	1	rs31362610	T	T	T	T	C	C	C	C
<i>D1SNP39</i>	1	rs13475886	T	T	T	T	C	C	C	C
<i>D1SNP35</i>	1	rs32481241	T	T	C	C	C	C	C	C
<i>D1SNP41</i>	1	rs30928757	T	T	T	T	C	C	C	C
<i>D1SNP37</i>	1	rs6327099	T	T	T	T	C	C	C	C
<i>D1SNP38</i>	1	rs6341208	A	A	A	A	T	T	T	T
<i>D1SNP42</i>	1	rs242712390	C	C	C	C	A	A	A	C
<i>D2SNP11</i>	2	rs13476337	A	A	A	A	T	T	T	T
<i>D2SNP38</i>	2	rs33064547	A	A	A	A	G	G	G	G
<i>D2SNP39</i>	2	rs33488914	A	A	A	A	G	G	G	G
<i>D2SNP40</i>	2	rs33162749	C	C	C	T	T	T	T	T
<i>D2SNP45</i>	2	rs227312316	G	G	G	G	A	A	A	G
<i>D2SNP44</i>	2	rs13476801	T	T	T	T	C	C	C	C
<i>D2SNP42</i>	2	rs29818510	C	C	C	C	G	G	G	G
<i>D2SNP46</i>	2	rs29673978	T	T	T	T	C	C	C	C
<i>D3SNP35</i>	3	rs13476956	C	C	C	C	T	T	T	T
<i>D3SNP39</i>	3	rs13477019	T	T	A	A	A	A	A	A
<i>D3SNP48</i>	3	rs237712466	T	T	T	T	G	G	G	T
<i>D3SNP47</i>	3	rs13477132	G	G	G	G	C	C	C	C
<i>D3SNP44</i>	3	rs31154737	A	A	A	T	T	T	T	T
<i>D3SNP45</i>	3	rs31321678	A	A	A	A	G	G	G	G
<i>D3SNP46</i>	3	rs31594267	A	A	A	A	C	C	C	C
<i>D4SNP41</i>	4	rs32143059	G	G	G	G	A	A	A	A
<i>D4SNP101</i>	4	rs13477622	T	T	T	T	C	C	C	C
<i>D4SNP40</i>	4	rs13477746	T	T	T	T	C	C	C	C
<i>D4SNP38</i>	4	rs3680956	A	A	G	G	G	G	G	G
<i>D4SNP42</i>	4	rs245725397	C	C	C	C	T	T	T	C
<i>D4SNP39</i>	4	rs6397070	T	T	T	T	C	C	C	C
<i>D5SNP35</i>	5	rs247844351	C	C	C	C	T	T	T	T
<i>D5SNP31</i>	5	rs33508711	C	C	C	C	T	T	T	T
<i>D5SNP33</i>	5	rs13478320	C	C	C	C	A	A	A	A
<i>D5SNP32</i>	5	rs33249065	A	A	A	A	G	G	G	G
<i>D5SNP21</i>	5	rs3662161	A	A	A	A	G	G	G	G
<i>D5SNP14</i>	5	rs33208334	T	T	T	C	C	C	C	C
<i>D6SNP34</i>	6	rs30450019	A	A	A	A	C	G	G	G
<i>D6SNP20</i>	6	rs30764547	T	T	T	T	A	A	A	A
<i>D6SNP35</i>	6	rs30892442	A	A	A	C	C	C	C	C
<i>D6SNP32</i>	6	rs6157367	T	T	T	T	A	A	A	A
<i>D6SNP33</i>	6	rs13478995	C	C	C	C	G	G	G	G
<i>D6SNP36</i>	6	rs235068709	G	G	G	G	T	T	T	G
<i>D7SNP45</i>	7	rs242748489	G	G	G	G	A	A	A	G
<i>D7SNP41</i>	7	rs31221380	A	A	A	A	C	C	C	C
<i>D7SNP42</i>	7	rs32060039	C	C	C	C	G	G	G	G
<i>D7SNP43</i>	7	rs243575509	C	C	C	C	T	T	T	C
<i>D7SNP37</i>	7	rs13479522	A	A	A	A	G	G	G	G
<i>D8SNP27</i>	8	rs13479605	C	C	C	C	A	A	A	A
<i>D8SNP28</i>	8	rs13479672	T	T	T	T	C	C	C	C
<i>D8SNP23</i>	8	rs32729089	T	T	T	T	A	A	A	A
<i>D8SNP24</i>	8	rs33601490	T	T	T	T	C	C	C	C
<i>D8SNP25</i>	8	rs33219858	T	T	T	T	C	C	C	C
<i>D8SNP26</i>	8	rs32577205	A	A	A	A	G	G	G	G
<i>D9SNP13</i>	9	rs33672596	A	A	A	A	G	G	G	G
<i>D9SNP21</i>	9	rs13480122	T	T	T	T	C	C	C	C
<i>D9SNP27</i>	9	rs29644859	T	T	T	T	G	G	G	G
<i>D9SNP30</i>	9	rs260373537	T	T	T	T	C	C	C	T
<i>D9SNP31</i>	9	rs30431245	T	T	T	T	C	C	C	C

SNPs with the reference genome sequence (genome assembly: GRCm38.p6) of C57BL/6J (Ref) are highlighted in gray. J, C57BL/6J; JJcl, C57BL/6JJcl; JJmsSlc, C57BL/6JJmsSlc; NTac, C57BL/6NTac; NJcl, C57BL/6NJcl; NCrl, C57BL/6NCrl; and NCrSlc, C57BL/6NCrSlc.

Table 2. (Continued)

SNP marker	Chr	dbSNP ID	C57BL/6J				C57BL/6N			
			Ref	J	JJcl	JJmsSlc	NTac	NJcl	NCrl	NCrSlc
<i>D10SNP43</i>	10	rs50477269	A	A	A	A	G	G	G	G
<i>D10SNP36</i>	10	rs13480575	T	T	T	T	C	C	C	C
<i>D10SNP37</i>	10	rs13480619	T	T	T	T	C	C	C	C
<i>D10SNP42</i>	10	rs13459122	A	A	A	A	T	T	T	T
<i>D10SNP39</i>	10	rs13480759	C	C	C	C	T	T	T	T
<i>D10SNP44</i>	10	rs236992510	G	G	G	G	A	A	A	A
<i>D11SNP101</i>	11	rs3659787	G	G	G	G	A	A	A	A
<i>D11SNP24</i>	11	rs259140591	C	C	C	C	T	T	T	T
<i>D11SNP18</i>	11	rs13481014	T	T	T	T	C	C	C	C
<i>D11SNP23</i>	11	rs13481117	G	G	G	G	T	T	T	T
<i>D11SNP22</i>	11	rs29411641	T	T	T	T	G	G	G	G
<i>D11SNP25</i>	11	rs49027247	T	T	T	T	C	C	C	C
<i>D12SNP38</i>	12	rs29158719	A	A	G	G	G	G	G	G
<i>D12SNP41</i>	12	rs29142759	A	A	A	A	G	G	G	G
<i>D12SNP42</i>	12	rs29487143	G	G	G	G	C	C	C	C
<i>D12SNP43</i>	12	rs29133146	A	A	A	C	C	C	C	C
<i>D12SNP39</i>	12	rs13481569	G	G	G	G	A	A	A	A
<i>D12SNP40</i>	12	rs13481634	A	A	A	A	C	C	C	C
<i>D13SNP14</i>	13	rs30039194	A	A	A	A	T	T	T	T
<i>D13SNP30</i>	13	rs3722313	T	T	T	T	C	C	C	C
<i>D13SNP31</i>	13	rs29802434	G	G	G	G	C	C	C	C
<i>D13SNP29</i>	13	rs3702296	A	A	A	A	G	G	G	G
<i>D14SNP27</i>	14	rs31187642	G	G	G	G	A	A	A	A
<i>D14SNP33</i>	14	rs31133670	A	A	A	A	G	G	G	G
<i>D14SNP29</i>	14	rs30264676	T	T	T	T	A	A	A	A
<i>D14SNP30</i>	14	rs31059846	A	A	A	A	G	G	G	G
<i>D14SNP31</i>	14	rs31273189	A	A	A	A	G	G	G	G
<i>D14SNP23</i>	14	rs31233932	C	C	C	C	T	T	T	T
<i>D15SNP33</i>	15	rs257670740	T	T	T	T	C	C	C	C
<i>D15SNP34</i>	15	rs261563123	C	C	C	C	T	T	T	T
<i>D15SNP24</i>	15	rs3702158	A	A	A	A	G	G	G	G
<i>D15SNP32</i>	15	rs31858887	T	T	T	T	C	C	C	C
<i>D15SNP35</i>	15	rs31921278	A	A	A	G	C	G	G	G
<i>D16SNP24</i>	16	rs219190959	C	C	C	C	T	T	T	C
<i>D16SNP19</i>	16	rs4165065	T	T	T	T	C	C	C	C
<i>D16SNP23</i>	16	rs4187179	T	T	T	T	C	C	C	C
<i>D16SNP22</i>	16	rs4214728	T	T	T	T	C	C	C	C
<i>D17SNP28</i>	17	rs4137196	T	T	T	T	C	C	C	C
<i>D17SNP29</i>	17	rs29512740	C	C	C	C	A	A	A	A
<i>D17SNP30</i>	17	rs33334258	G	G	G	A	A	A	A	A
<i>D17SNP24</i>	17	rs13483055	T	T	T	T	C	C	C	C
<i>D17SNP34</i>	17	rs229426697	C	C	C	C	T	T	C	C
<i>D17SNP32</i>	17	rs33132419	T	T	T	T	C	C	C	C
<i>D18SNP38</i>	18	rs13483221	C	C	C	C	T	T	T	T
<i>D18SNP36</i>	18	rs13483296	A	A	A	A	T	T	T	T
<i>D18SNP39</i>	18	rs13483369	A	A	A	A	C	C	C	C
<i>D18SNP37</i>	18	rs29690544	T	T	T	T	C	C	C	C
<i>D19SNP24</i>	19	rs31112038	G	G	G	G	C	C	C	C
<i>D19SNP27</i>	19	rs30709918	T	T	T	C	C	C	C	C
<i>D19SNP28</i>	19	rs30953636	G	G	G	G	T	T	T	T
<i>D19SNP23</i>	19	rs3724876	G	G	G	G	T	T	T	T
<i>D19SNP26</i>	19	rs30447436	C	C	T	T	T	T	T	T
<i>DXSNP58</i>	X	rs250603596	T	T	T	T	A	A	A	T
<i>DXSNP52</i>	X	rs6368704	A	A	A	A	G	G	G	G
<i>DXSNP56</i>	X	rs259126064	G	G	G	G	T	T	T	G
<i>DXSNP57</i>	X	rs213430510	A	A	A	A	T	T	T	T
<i>DXSNP54</i>	X	rs31266096	A	A	A	A	G	G	G	G

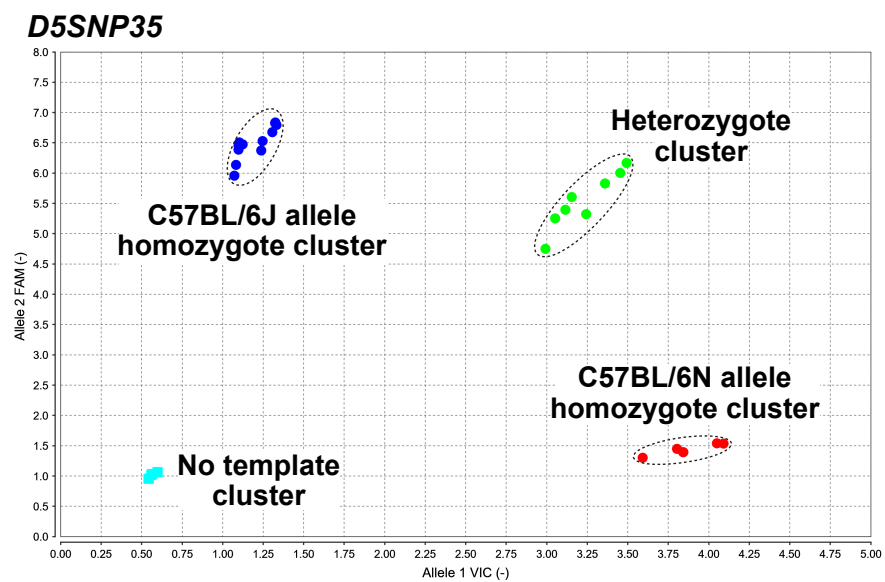
Table 3. SNPs among the BALB/c substrains within the markers developed in this study

Marker	Chr	dbSNP ID	cJ	cA	cByJ	cAn	cCr
<i>D1SNP301</i>	1	rs33109340	C	C	T	C	C
<i>D1SNP302</i>	1	rs33057227	C	C	T	C	C
<i>D1SNP303</i>	1	rs33365833	A	A	T	A	A
<i>D1SNP304</i>	1	rs31397868	G	G	A	G	G
<i>D1SNP305</i>	1	rs33202907	T	T	A	A	A
<i>D2SNP301</i>	2	rs243288053	G	A	G	G	G
<i>D2SNP302</i>	2	rs27169047	G	G	T	G	G
<i>D2SNP303</i>	2	rs27981830	G	G	A	G	G
<i>D2SNP304</i>	2	rs238060283	A	A	G	G	G
<i>D2SNP305</i>	2	rs27250976	C	C	T	T	T
<i>D2SNP306</i>	2	rs27622613	T	T	C	C	C
<i>D3SNP301</i>	3	rs46220062	C	C	T	T	T
<i>D3SNP302</i>	3	rs29938481	G	G	T	T	T
<i>D3SNP303</i>	3	rs36544985	A	A	G	G	G
<i>D3SNP304</i>	3	rs36506426	G	G	A	G	G
<i>D3SNP305</i>	3	rs221745548	G	G	A	A	A
<i>D3SNP306</i>	3	rs30857183	A	A	G	G	G
<i>D4SNP301</i>	4	rs231525592	C	C	T	C	C
<i>D4SNP302</i>	4	rs27767340	C	C	T	C	C
<i>D4SNP303</i>	4	rs3706082	T	T	C	T	T
<i>D4SNP304</i>	4	rs28126314	G	G	A	G	G
<i>D4SNP305</i>	4	rs27512361	C	C	T	T	T
<i>D4SNP306</i>	4	rs32877825	G	G	A	G	G
<i>D5SNP301</i>	5	rs31133755	C	C	A	C	C
<i>D5SNP302</i>	5	rs50896597	C	C	T	T	T
<i>D5SNP303</i>	5	rs52019376	G	G	A	A	A
<i>D5SNP304</i>	5	rs31892920	T	T	C	T	T
<i>D5SNP305</i>	5	rs32347776	G	G	A	A	A
<i>D6SNP301</i>	6	rs32502983	C	C	T	C	C
<i>D6SNP302</i>	6	rs36885644	G	G	T	G	G
<i>D6SNP303</i>	6	rs216689099	C	T	C	C	C
<i>D6SNP304</i>	6	rs230573527	C	T	C	C	C
<i>D6SNP305</i>	6	rs31952322	G	G	A	A	A
<i>D7SNP301</i>	7	rs32408583	A	A	C	C	C
<i>D7SNP302</i>	7	rs32445754	G	G	A	A	A
<i>D7SNP303</i>	7	rs33056660	A	A	C	C	C
<i>D7SNP304</i>	7	rs31482312	T	T	G	G	G
<i>D7SNP305</i>	7	rs51219759	A	A	T	A	A
<i>D8SNP301</i>	8	rs47376668	G	G	A	G	G
<i>D8SNP302</i>	8	rs30733023	C	C	T	C	C
<i>D8SNP303</i>	8	rs36881999	G	G	A	G	G
<i>D8SNP304</i>	8	rs38305200	G	G	A	G	G
<i>D8SNP305</i>	8	rs262469470	G	A	G	G	G
<i>D9SNP301</i>	9	rs51304512	T	T	C	T	T
<i>D9SNP302</i>	9	rs37879512	G	G	A	A	A
<i>D9SNP303</i>	9	rs38922776	A	G	A	A	A
<i>D9SNP304</i>	9	rs33134771	G	G	A	A	A
<i>D9SNP305</i>	9	rs50594159	C	C	T	C	C
<i>D10SNP301</i>	10	rs45892832	C	C	T	T	T
<i>D10SNP302</i>	10	rs33688332	C	C	A	A	A
<i>D10SNP303</i>	10	rs50315385	C	C	A	A	A
<i>D10SNP304</i>	10	rs46748961	C	C	T	C	C
<i>D10SNP305</i>	10	rs47483530	T	T	A	T	T
<i>D10SNP306</i>	10	rs233492562	A	A	G	A	A

Locations of SNPs are according to the mouse genome reference assembly (GRCm38.p6). SNPs with the genomic sequence (Mouse Genome Project: https://www.sanger.ac.uk/sanger/Mouse_SnpViewer/rel-1505) of BALB/cJ (cJ) are highlighted in gray. cA, BALB/cAJcl; cByJ, BALB/cByJJcl; cAn, BALB/cAnNCrIcrlj; and cCr, BALB/cCrSlc.

Table 3. (Continued)

Marker	Chr	dbSNP_ID	cJ	cA	cByJ	cAn	cCr
<i>D11SNP301</i>	11	rs26833083	G	G	A	A	A
<i>D11SNP302</i>	11	rs26912518	T	T	C	T	T
<i>D11SNP303</i>	11	rs220626677	G	A	G	G	G
<i>D11SNP304</i>	11	rs252587388	C	T	C	C	C
<i>D11SNP305</i>	11	rs27014504	C	C	T	T	T
<i>D12SNP301</i>	12	rs46528175	A	A	G	G	G
<i>D12SNP302</i>	12	rs231844185	A	G	A	A	A
<i>D12SNP303</i>	12	rs37803925	A	A	C	A	A
<i>D12SNP304</i>	12	rs51364971	C	C	T	C	C
<i>D12SNP305</i>	12	rs247716364	G	A	G	G	G
<i>D13SNP301</i>	13	rs33751539	C	A	C	C	C
<i>D13SNP302</i>	13	rs29965851	T	T	A	T	T
<i>D13SNP303</i>	13	rs30245925	C	C	T	C	C
<i>D13SNP304</i>	13	rs47717539	C	C	T	C	C
<i>D13SNP305</i>	13	rs38228777	G	G	C	G	G
<i>D14SNP301</i>	14	rs51648802	G	G	A	G	G
<i>D14SNP302</i>	14	rs50148147	T	T	C	T	T
<i>D14SNP303</i>	14	rs46892447	C	C	T	C	C
<i>D14SNP304</i>	14	rs32226962	A	A	G	A	A
<i>D14SNP305</i>	14	rs51211980	C	C	A	C	C
<i>D15SNP301</i>	15	rs48122948	G	G	C	G	G
<i>D15SNP302</i>	15	rs212086590	C	C	T	C	C
<i>D15SNP303</i>	15	rs220101808	C	T	C	C	C
<i>D15SNP304</i>	15	rs38263969	G	G	A	G	G
<i>D16SNP301</i>	16	rs49608214	A	G	A	A	A
<i>D16SNP302</i>	16	rs46364658	C	C	T	C	C
<i>D16SNP303</i>	16	rs50933320	C	C	T	C	C
<i>D16SNP304</i>	16	rs254664546	G	A	G	G	G
<i>D16SNP305</i>	16	rs227119859	A	T	A	A	A
<i>D17SNP301</i>	17	rs49061265	G	G	A	A	A
<i>D17SNP302</i>	17	rs45641253	C	C	A	C	C
<i>D17SNP303</i>	17	rs49487329	G	G	A	G	G
<i>D17SNP304</i>	17	rs47460807	G	G	A	A	A
<i>D18SNP301</i>	18	rs51512767	A	A	T	A	A
<i>D18SNP302</i>	18	rs221424480	C	T	C	C	C
<i>D18SNP303</i>	18	rs31785839	T	T	C	T	T
<i>D18SNP304</i>	18	rs39281136	C	C	T	C	C
<i>D18SNP305</i>	18	rs37625494	T	T	G	T	T
<i>D19SNP301</i>	19	rs36448887	G	G	A	A	A
<i>D19SNP302</i>	19	rs37039649	G	G	A	G	G
<i>D19SNP303</i>	19	rs38082986	G	G	A	G	G
<i>D19SNP304</i>	19	rs50157060	T	T	C	T	T
<i>D19SNP305</i>	19	rs36495646	A	A	G	G	G
<i>D19SNP306</i>	19	rs48624001	C	C	T	T	T
<i>DXSNP301</i>	X	rs33287577	T	T	A	T	T
<i>DXSNP302</i>	X	rs30035452	A	A	C	A	A
<i>DXSNP303</i>	X	rs29043150	T	T	C	C	C
<i>DXSNP304</i>	X	rs241499720	G	G	T	G	G
<i>DXSNP305</i>	X	rs8268104	C	C	A	A	A
<i>DXSNP306</i>	X	rs3718396	C	C	T	C	C
<i>DXSNP307</i>	X	rs29299426	G	G	A	G	G
<i>DXSNP308</i>	X	rs31827558	T	C	T	T	T



Supplementary Fig. 1. Representative allelic discrimination plots for SNPs of C57BL/6 substrains. Genotypes in a marker (*D5SNP35*) are determined by sequence-specific probes of the C57BL/6J allele (FAM dye, blue plots) and C57BL/6N allele (VIC dye, red plots).

Supplementary Table 1. PCR and sequencing primers used for the development of novel SNP markers for genotyping C57BL/6 substrains. Locations of SNPs are according to the mouse genome reference assembly (GRCm38.p6).

Marker	dbSNP ID	Chr	Location (bp)	Forward primer (Direct sequencing)	Reverse primer (Direct sequencing)
<i>D1SNP42</i>	rs242712390	1	194,246,275	GCCTCTTCAGGGATCCTTCT	TTCAAACCTCAAGGGCACCAT
<i>D2SNP45</i>	rs227312316	2	106,074,143	GGGTCAAAGTTTAACTCCAGCTC	CTTGCCCTTACCCCTCAACAA
<i>D3SNP48</i>	rs237712466	3	27,240,831	AGTACCCTGTGGAGTCACC	GTCAAATGGCAATGGCTTCT
<i>D4SNP42</i>	rs245725397	4	110,650,398	TGTGTGTGTGTTTCAGTTGCAG	GGATATGGGGGACTTTTGGT
<i>D6SNP36</i>	rs235068709	6	141,072,590	CCAACAGACTGCCTGGTGTA	GCCAAGCACCTTCTAACAGC
<i>D7SNP45</i>	rs242748489	7	6,976,737	TCAGGAGTCGTGCATCTGTC	TGGAGTTTGTGGGAAAGGAC
<i>D12SNP41</i>	rs29142759	12	7,453,718	CCACAGTGCTCAGACCTCCT	CTTGTTTGTTTCATGCGCTGT
<i>D16SNP24</i>	rs219190959	16	4,207,926	TACAGAACCCCCACCTTTTG	CTGCTCCCCCATCTTAAACA
<i>D17SNP34</i>	rs229426697	17	93,399,301	AATTGGCTTCTTGCTCCTT	TTCCTGTGCTGCTAGTGTG
<i>D19SNP23</i>	rs3724876	19	49,976,154	TGACTTTACTGCCCACTTTGG	CACCAGCATCCCGTTATCTT
<i>DXSNP58</i>	rs250603596	X	9,435,551	CAACAGCCAATTCAGTCCAA	GCCAGCACAGCTCTTTCTGT
<i>DXSNP56</i>	rs259126064	X	96,663,644	GATAACCAGAGTGGCTGCAC	CCCAATGGATGAATGGGATA
<i>DXSNP57</i>	rs213430510	X	117,408,768	TGTTTGGTTTTTCCTTTTGC	GCCATGGTTCTCAGTCTTCC

Supplementary Table 2. Primers and probes used for TaqMan assays in SNP genotyping among the C57BL/6 substrains. Locations of SNPs are according to the mouse genome reference assembly (GRCm38.p6). Intervals of proximal markers in each chromosome show the distance from proximal ends. Intervals of distal ends show the distance from distal markers in each chromosome.

Chr	Marker	Location (bp)	Interval (bp)	Forward primer (TaqMan)	Reverse primer (TaqMan)	FAM labeled probe	VIC labeled probe	Reference
1	<i>DISNP40</i>	3,607,559	3,607,559	CCCACACCCATAAATACTGACATAT	AGTCTAATTCATTCTCAGCCATTGGT	CAAGTGCTTGATGATATT	CAAGTGCTTGAGATATT	17
1	<i>DISNP34</i>	42,367,595	38,760,036	TGGCTTTCTCTATATACTTTCCGATGTG	GCAAACCTGCCCCATATGACTTAGT	TTGGTTGCAATAGTTAAAGT	TTGGTTGCAATAGCTAAAGT	16, 17
1	<i>DISNP39</i>	61,171,619	18,804,024	TGGAGGAGTCAGGAAGAGAAAAGG	CTGGCCAAGACAGAATTAAGGAGAA	TGAGATTGCGCCCCTG	TTGAGATTGTTGCCCTG	17
1	<i>DISNP35</i>	78,486,797	17,315,178	GCAATCAGAAACCAGTTCACAAGAAA	GATTGCCTTTCTGTTCAAGTTGTGT	CTTGTTACTTACTTTTTG	CTTGTTACTTGCTTTTTG	16, 17
1	<i>DISNP41</i>	109,423,026	30,936,229	ACCAGTAGCAATGAATGGATTAGTCTATA TCT	CTTGCATTCAAGGAATTGTTCAAGACA	TCCATTACTTTGGCTCATTA	TGTCCATTACTTTGGTTCATTA	17
1	<i>DISNP37</i>	129,386,361	19,963,335	AGTAGGGTTTTGTATTGGCTTAGTTTGT	GAGGTAGATGGATTGTGGTTTAGCT	CCCCAGAAAATCTCAA	CCCCAGAAGATCTCAA	16, 17
1	<i>DISNP38</i>	163,132,699	33,746,338	AACATGCTGACTCCTCGATTGTAAA	TGATCGTTCGATTGTTGAAATCCCTTT	CCTAATCCACTTGTCTTT	CCTAATCCACATGTCTTT	16, 17
1	<i>DISNP42</i>	194,246,275	31,113,576	CCAAATTCAGGAGTGATGCATTGAG	TCTATCTGCAAAGAACCTCTCATACCT	AAGTCTCCACTGTTTACAGAG	AGTCTCCACTGTTGACAGAG	This study
1	Distal end	195,471,971	1,225,696					
2	<i>D2SNP11</i>	8,069,855	8,069,855	CAGGATCCAAGCTTACTGACTCAT	GTGAAATTGATGACTCTCAAATGAAGGT	CCTTTGGAAGATATTTAGAC	CTTTGGAAGATAATTAGAC	17
2	<i>D2SNP38</i>	38,946,612	30,876,757	GCACACGCTATCAGTTAGAGTTCAG	GCTAAACTCCAAAGTGTGTCCAAAG	CACCCTATGTCCCCTCC	CACCCTATGTTCCCTCC	16
2	<i>D2SNP39</i>	45,143,008	6,196,396	GCAAGCGCATTGATGTTTTCATAGT	ACTCAGCTGGGAGACTTCTCT	TTGCGGGCCAACCT	CTTGCGGGCTAACT	16, 17
2	<i>D2SNP40</i>	78,799,176	33,656,168	TCTACTCTCCAGTTCAACAGTGGTA	GACACAGGCTTAACATGAGTATGGT	TAGGTGCAAAAATAATAAAA	TAGGTGCAAAAATGATAAAA	16, 17
2	<i>D2SNP45</i>	106,074,143	27,274,967	GCCTTAAAGTTTACAAAAAGCATGCCATA	CAAAACAAAAGATTACATATAGAAATATT GAGAACGAACT	TGGTATAGATCACTATCAATA A	TGGTATAGATCACTGTCAATA A	This study
2	<i>D2SNP44</i>	138,480,020	32,405,877	GAATGTGACATTATGTTTCATATTCATAATT AAATTTATTCCTTTT	CCTCAATCTACAGTCAGGCCAAATT	TTCTTCATCTCAATGAGCA	TTCTTCATCTCGATGAGCA	16, 17
2	<i>D2SNP42</i>	153,111,014	14,630,994	TGTTGAAAACCAATCCTTCCAGTCT	CTACATCGGGCTCTGCTATAATCTT	CACATTTGTTTATCGAGACAC	CACATTTGTTTATGGAGACAC	16
2	<i>D2SNP46</i>	179,262,364	26,151,350	GATCTTGCAATGTATGAGGGATGA	GCACTTAACAGTCTCAGCATTAGCT	CACATTGGCTTTGGG	AGCACATTGGCTTTAGG	17
2	Distal end	182,113,224	2,850,860					
3	<i>D3SNP35</i>	5,370,727	5,370,727	CAGATTCATCTTCTGCTAGACACA	TCCTAGATTACATATTTTCATAATTGATAA CTTCTGCAT	CAGAGGTTGACTACTCATATA	CAGAGGTTGACTACTCGTATA	16, 17
3	<i>D3SNP39</i>	23,824,920	18,454,193	ACTTGTTTAAAAATGTGCATGCAGTTCT	TCAGTGTTTAAACCAACTAATCAATATCC ATCAATA	CTAGTTGGATCTCTTACTGTT	CTAGTTGGATCTCTAACTGTT	16, 17
3	<i>D3SNP48</i>	27,240,831	3,415,911	GTCACCGAGCATGTGTAAACC	GCGGAAACTCACAAATCTTCATCTT	CCCTGCGGTCACAG	ATCCCTGCGTTCACAG	This study
3	<i>D3SNP47</i>	58,109,942	30,869,111	GCTGACCACTGAAGCATTAGCT	CTAGACTAGTCCAGGCCCTTCCA	ATGGTATAAATAGCCCC	CATGGTATAAATAGCCCC	17
3	<i>D3SNP44</i>	74,118,533	16,008,591	ATCCAAGCTCTGAATTGACCCATT	CTGGCCCTTTCACACATCTCA	CATTTGCGGATGACATA	ATCATTGCGGTTGACATA	16, 17
3	<i>D3SNP45</i>	107,470,377	33,351,844	CCTGCAAATTGTGCTCTGGAAA	GTGGTGGTCTTTGCCTCTGT	CTCACCCATTGTGACTG	CCTCACCCATTATGACTG	16, 17
3	<i>D3SNP46</i>	152,219,576	44,749,199	TCTTGCCCTCCGACCATGAAATG	TCAGCAGTTTTATCTTAGTCAGGTTTCAA	CCATATGACCCATTTAG	CCATATGACCAATTTAG	16, 17
3	Distal end	160,039,680	7,820,104					
4	<i>D4SNP41</i>	6,374,701	6,374,701	AGCTCATGTTGATATGAAAAATAAATTCT TAAAAAGGATT	ACATTTTATTAATAATCATTAGAGTTCTAT GTCTTGGGT	TGTATGTCAATTATTGCC	TGTATGTCAATTGTTGCC	17

Supplementary Table 2. (Continued)

Chr	Marker	Location (bp)	Interval (bp)	Forward primer (TaqMan)	Reverse primer (TaqMan)	FAM labeled probe	VIC labeled probe	Reference
4	<i>D4SNP101</i>	28,322,410	21,947,709	TGAAGGTCTCCATTGCCACATG	CAGTGAATATTCCTAATATAAGTGAAGCTGGT	CTACACAAGAAGACACAC	TCTACACAAGAAAACACAC	16, 17
4	<i>D4SNP40</i>	65,944,235	37,621,825	CCTTCTCCAATCCATTTCTCACTGT	AATCTGATAATATAGCTATTATAAAAAATGTAGTGTGCCA	AAGAACAATGCATTAAC	ATCAAGAACAATACATTAAC	16, 17
4	<i>D4SNP38</i>	109,874,495	43,930,260	AAGGCTGTATTTCAGCATCATCAT	TCTACTCTTACCTACCTCTAATCTTAAACATGTG	AGGTTACTGAAGTATGAGTTG	AGGTTACTGAAGTATAAGTTG	16, 17
4	<i>D4SNP42</i>	110,650,398	775,903	GAGCAGTCCATCTTGATATTGGAACA	AACGGAAAGCCAGTGTAACTAAA	TGAAAAGTCCAAAGTCCTTA	TGAAAAGTCCAAAGTCCTTA	This study
4	<i>D4SNP39</i>	155,910,817	45,260,419	AGTGTCCCTTGTCCTCAATGAAA	TCCAAGCTCTCTGTCCTTGAG	CAAGCAGCCTATCCCT	AAGCAGCCATCCCT	16, 17
4	Distal end	156,508,116	597,299					
5	<i>D5SNP35</i>	4,547,791	4,547,791	GCCGAATGGCATAGCAGAATT	CTGGATGGCGTCAGAGTTTCT	CCCAAAGACAGCAGGTT	CCCAAAGACGGCAGGTT	17
5	<i>D5SNP31</i>	40,761,789	36,213,998	GAATCTGTGATCGTACCTGTATCC	AAGAGAAAAAGGAGCCTTTGTGAGA	AGGAACCAAGGCAAGAG	CAGGAACCAAGGCGAGAG	16, 17
5	<i>D5SNP33</i>	70,742,061	29,980,272	GATACTGTTGTAGTCATTTACAGAAACCA	GATGTTTCTGGTCTTTGAGAGATGC	TGGAACAGACTCGTCCAT	CTGGAACAGACTAGTCCAT	16, 17
5	<i>D5SNP32</i>	92,081,078	21,339,017	ACCAAGGCACAAAAAACCAATTT	TGGCAGATGTGTGTTGATAGCT	ACAGGTTTGTCTTATC	ACACAGGTTTACTTTATC	16, 17
5	<i>D5SNP21</i>	117,459,347	25,378,269	ACCAAGGCATAGCATAGCATAGC	GTAAAAGCACCTGTATTGGGTTTGG	ATAGCGTCTAATTCATCGTT	ATAGCGTCTAATTCGTCGTT	16, 17
5	<i>D5SNP14</i>	149,626,021	32,166,674	AACATGGCCATAACCAACTGTACT	GGCTCTGCAGTAAGCACTTGTATA	ACTTCTCAACCATCCTAG	ACTTCTCAACCGTCCTAG	17
5	Distal end	151,834,684	2,208,663					
6	<i>D6SNP34</i>	6,233,941	6,233,941	AGGCAGCTGTAAATGCTAGCT	GCAAATCAGAAAGGTGGGAAAGAGA	TCAGTCTGGAACCCA	TCAGTCTGGAACCCA	17
6	<i>D6SNP20</i>	28,715,963	22,482,022	TGGTTCTGCAAGCTGAGATTGTATT	ACTCACATTATCAGCCCTCTAAGAGATT	CCCTAGCCTACTTGGTT	TCCCTAGCCTTCTTGGTT	17
6	<i>D6SNP35</i>	44,286,336	15,570,373	TGTTTCGACAATTCTGACTGAGCTC	AGTGTGCTATAACAACAAGACAATCGT	CAGGCCCCAATGTG	ACAGGCCACAATGTG	17
6	<i>D6SNP32</i>	67,287,180	23,000,844	CTACTCTTAAAGCAGTCCTGTCACT	TCTCTTACTTTTTTACTATGGATAAATGGCT	AAGTGAGATGTCTTTCAGGT	AAAGTGAGATGTCTATCAGGT	16, 17
6	<i>D6SNP33</i>	117,470,880	50,183,700	AGCAATCAGAGGAGGAAGAACCT	GCACCTCACATTTCTCTTCTACCA	CAGGCTGCCGTAGTC	CAGGCTGGCGTAGTC	16, 17
6	<i>D6SNP36</i>	141,072,590	23,601,710	GCGGTCTCACCATATTGTCCTA	CAGTTGTATGGCTGGAGATGCTT	CCAGCGTCTTTAGAGCA	CCAGCGTCTTGTAGAGCA	This study
6	Distal end	149,736,546	8,663,956					
7	<i>D7SNP45</i>	6,976,737	6,976,737	CCATCTTCCTCATGAAGAATATTAAGCTACA	CGGATCTCATGATGTGTCCCTTTTA	AGACGATCTTCATAGGCAG	AAGACGATCTTCGTAGGCAG	This study
7	<i>D7SNP41</i>	37,431,938	30,455,201	TCTGCCTCTCTTTCTCCTATTCCCT	CCCGTTTACTGAAAAGCACAATAT	AGGCTTTCCTCTTTTC	AGGCTTTCCTATTTC	16, 17
7	<i>D7SNP42</i>	71,816,909	34,384,971	GGAAGCGTGGGCTCCTC	TGCAATGCTTTTCTGGAGTAACTT	TTTGACACAGTCCCC	CTTTGACAGAGTCCCC	16, 17
7	<i>D7SNP43</i>	102,973,309	31,156,400	CTTTCAGCCCTTGAGGCAATG	TGCTCATCCTTCTCCTATGCA	CGCACCATATTGTC	CGCACCATTGTC	16
7	<i>D7SNP37</i>	129,035,694	26,062,385	CTGTCCCATCTGTTGAGAAGCA	GTAAGATGTGCACTCAGCATTGAC	CCGGACCAGTTGTT	CCGGACCAATTGTT	17
7	Distal end	145,441,459	16,405,765					
8	<i>D8SNP27</i>	10,521,755	10,521,755	GCATGTGCATGGGCTTTAATTAAGT	CTGACAGTCACTGGCTTCCCT	AGCAGATTAGACCTTGTTT	AGCAGATTAGACATTGTTT	17
8	<i>D8SNP28</i>	29,097,075	18,575,320	AATGATATGCACCACAGCACTCT	GCACTATTGCTAAGGGAAACGGATT	AGGAGGTACTGATTTAA	CAGGAGGTACTGGTTTAA	17
8	<i>D8SNP23</i>	74,953,357	45,856,282	CTACCCTATGTCAGGTGTTTTCATCA	GGGTGAGGTATTTGTGGTCTGTTA	ACTATGATGTTGACTAAAT	CATACTATGATGTAGACTAAAT	16, 17
8	<i>D8SNP24</i>	91,507,617	16,554,260	CTTGGTGCTATGGCTTTAAAAGGTT	CCTCAGATGTCTTACTCATAACAAGCT	ATGGGAGAACATCAAG	TCATGGGAGAACGTCAAG	16, 17

Supplementary Table 2. (Continued)

Chr	Marker	Location (bp)	Interval (bp)	Forward primer (TaqMan)	Reverse primer (TaqMan)	FAM labeled probe	VIC labeled probe	Reference
8	<i>D8SNP25</i>	110,098,371	18,590,754	TCAAGTGTGTAGGGTTGTGAAAAGA	CCCTAACTGTCCTCTGGATTTC	ACCACTCGAGACTCA	AACCACTCGGGACTCA	16
8	<i>D8SNP26</i>	123,630,996	13,532,625	GGAGGAGTCTCTAATTGCTTTTATGGT	GGGACTTTGTGATCACATCTAGCTT	ATCAGAGCGAGCACC	ATCAGAGCAAGCACC	16, 17
8	Distal end	129,401,213	5,770,217					
9	<i>D9SNP13</i>	6,238,770	6,238,770	GTGCACACATGAACCTGACAAA	GGCCCCCTAATTATCATTGATCATAACA	TCCTTCTGTTGTACTTAGT	CTTCTGTTGCACTTAGT	15, 17
9	<i>D9SNP21</i>	31,156,626	24,917,856	ACAAAGCAGAGAGAGGGCTGTAC	AGATCCCAGACCTCGGTGAG	TGCATGGCCACCC	ATGCATGGCTACCC	15, 17
9	<i>D9SNP27</i>	52,785,119	21,628,493	AGTGCTCTACAGTGCAAGAAATTGA	GTCTCTGACTCTTAAGAATGGCAAT	CAGCACAGATAATGGA	CAGCACAGAGAATGGA	15–17
9	<i>D9SNP30</i>	85,239,185	32,454,066	TCAAGGTTCTTCTGCCATAAAAAT	GAGGACTGAAATGGATTCTAACAGGAAA	CTGAGAAATGATGATCC	AATCTGAGAAATAATGATCC	15
9	<i>D9SNP31</i>	119,641,498	34,402,313	CAGGCTTGAGAGCAGTGGTATTTAT	GGCAGAAAAGGAAGTTAAGGAGAGA	TGGCTTCTCGTCAGTTC	TTGGCTTCTCATCAGTTC	17
9	Distal end	124,595,110	4,953,612					
10	<i>D10SNP37</i>	57,752,462	24,099,439	TTTGACAACAGGCTTCTACTCTTT	TGGGCTTGTCTAGTTTGAAAAGT	CCAGATGAGACAAAAC	CCAGATGAAAACAAAAC	14, 16, 17
10	<i>D10SNP42</i>	80,795,365	23,042,903	GGCAGCAACAATGTGTGAGATG	CTCTGTCTGTGATGACCTCTGT	CAATGCACCCCTTAAGT	CAATGCACCCATTAAGT	14, 16, 17
10	<i>D10SNP39</i>	109,378,627	28,583,262	GGTTTTCTGGCTTTTGTCTTCTGT	CGTGGAGGGATTAGAAGACACTT	AGGTTAAGGTAGTTAAACA	CAGGTTAAGGTAATTAACA	16, 17
10	<i>D10SNP44</i>	126,759,175	17,380,548	CCTCATCAACCACTCCAAGGT	CTCCTGAATTCTGCATCCAGTGA	TGCCAGTGATGTCACA	TGCCAGTGGTGCACA	17
10	Distal end	130,694,993	3,935,818					
11	<i>D11SNP101</i>	4,508,730	4,508,730	GCATGGTTCTAGCGCACGAA	CAACCCTGGTTGCACAAATGAG	CTTACTAAACAAACCC	CTTACTAAGCAAACCC	16, 17
11	<i>D11SNP24</i>	28,208,412	23,699,682	ACATAAGTGGTTTTCCAGAATTATTTTTT ATTTTCTT	AAGTGCTTCAGTATAAATAGATTTTTTTT TAAAT	CTTCAGACAAACCAGTACT	CTTCAGACAAGCCAGTACT	17
11	<i>D11SNP18</i>	48,117,382	19,908,970	TCTTACATGTTTTATAATCTCCAGTGCAT AATGT	GCGAGACAAGTATTTCTGATACTTATGT AT	CTATTTGAGGAAAACACC	TCTATTTGAGAAAACACC	16, 17
11	<i>D11SNP23</i>	79,252,230	31,134,848	AATCTTCCTTCTACCCACCCA	GAGGTCATGAGGTCAAGATTGTCT	CTATTGAGCTGAATCTG	ATTGAGCGGAATCTG	16, 17
11	<i>D11SNP22</i>	94,959,297	15,707,067	AGCAGCAGTGCACATAAAAATAAAAACA	GGGAATACCTGAGGGATAGTTGTCT	TGCTCAGAGTTATTTTTGT	TGCTCAGAGTTCTTTTTGT	16
11	<i>D11SNP25</i>	120,306,788	25,347,491	GGGAAGCCCATTGTAGAAGTATCAG	GGCTCCCAGGCAAGGT	TGCTCCTGGTGGGCG	CTGCTCCTAGTGGGCG	17
11	Distal end	122,082,543	1,775,755					
12	<i>D12SNP38</i>	5,961,128	5,961,128	AAACCACCAACCCAGTCAAGAT	GCTGCAAAGATGTAGGAGAACTGT	CAGAGCAAGTCTGTC	ACAGAGCAAATCTGTC	16, 17
12	<i>D12SNP41</i>	7,453,718	1,492,590	GTACATAAGTGCTTTTCTGGACT	CTTTGCAGGTAGAGTTCTAAGAACTATGA ATT	CTCCCCCAAGAAA	TCCTCCCTCAAGAAA	This study
12	<i>D12SNP42</i>	34,467,966	27,014,248	TGGTCTATGCTTCAGTGTATTGCA	ATTCATTTATTACATATGCAAAATGTTCA TCGT	CAGATGCTACCAACAAA	CAGATGCTAGCAACAAA	17
12	<i>D12SNP43</i>	62,767,534	28,299,568	GCTGTGGCTTGCTTAGGA	CCCCTACCGAAGATGCTT	ATCATCCACTACGAGTAAG	ATCATCCACTAAGAGTAAG	17
12	<i>D12SNP39</i>	85,645,337	22,877,803	TGGGTGCGCTGTTTCAGATT	GCTGGAATATTGAATGGCTTGGTTT	AGCTGTGAGGCCTACA	AAAAGCTGTGAGACCTACA	16, 17
12	<i>D12SNP40</i>	106,833,655	21,188,318	GCTGGACATGTTGCTTCTCACA	GAGCACCTGTCTCCAGCAT	CATGCCGTGATAAGA	CTCATGCAGTGATAAGA	16, 17
12	Distal end	120,129,022	13,295,367					
13	<i>D13SNP14</i>	3,428,651	3,428,651	TCGCAACCCAGCTCTTG	ACCAGTCTCTCAATCCAACATGTG	CAAAAGAAGACAACCTT	CAAAAGAAGTCAACCTT	17
13	<i>D13SNP30</i>	41,442,786	38,014,135	TGCCTGTCTGCCTTCTC	GGAGACAGGTGAAGAGTGAGGAA	TTGAGATCAGGCTAGGAAG	TTGAGATCAGGCTGGGAAG	16, 17
13	<i>D13SNP31</i>	77,411,106	35,968,320	TCAGCGATACCCCATGTTAAAATCA	GAAGACAAATACTGAGAGGCAAGAGT	TTTAACACCTGGAACAG	TTTAACACCTGGAACAG	17
13	<i>D13SNP29</i>	101,209,232	23,798,126	CCCATGTTATGGACTCAAGGAGTAG	TCTTTACGCCTGCTTCTCAATAAG	TGGCATCTTACCCTATTC	ATGGCATCTTACCCTATTC	16, 17

Supplementary Table 2. (Continued)

Chr	Marker	Location (bp)	Interval (bp)	Forward primer (TaqMan)	Reverse primer (TaqMan)	FAM labeled probe	VIC labeled probe	Reference
13	Distal end	120,421,639	19,212,407					
14	<i>DI4SNP27</i>	9,937,385	9,937,385	GGAAAGCAGGAAGCCAAGACA	TGTTAGAGCAGATGGGAGGTTACT	TTCACAACCGATGTTTT	AGTTCACAACCAATGTTTT	16, 17
14	<i>DI4SNP33</i>	36,479,449	26,542,064	ATTCTGAAGTATGACCCGTATTACAAC C	CAATTCTACATTTTATAGAGTAAAAAGAG AGAAAAATCTGG	AGTGTCAATCCCATCAAT	CAGTGTCAATTCATCAAT	15, 17
14	<i>DI4SNP29</i>	74,415,721	37,936,272	CTATGGCAAAAAGGGAAGTCAAAT	TTGTCACAACCTGTCTTCTTTCTGT	CAATATTGGAAAATTCTCA	CAATATTGGAAAATCTCA	15–17
14	<i>DI4SNP30</i>	99,624,996	25,209,275	TCACCGTGAGTGGGCATTC	TGCTTAAGACCTTTACCATGCATCTT	ACCCCGAAAAGCA	ACACCCCTGAAAAGCA	15–17
14	<i>DI4SNP31</i>	108,659,851	9,034,855	GCAAAGCCAAAAGTTTATACTGTGT	CTGCTTTTCAAATCTGGCAACAATCTATT	ATATTTGTCAAGCACATT	CATATTTGTCAAACACATT	16
14	<i>DI4SNP23</i>	124,108,797	15,448,946	GCGTCAATCTACTCATGGTAAGGATATT	TCAGTCTTCTCAGTCCCTAATGCTA	CGACAAAATTACATAAACT	ATCGACAAAATTACATGAACT	15, 17
14	Distal end	124,902,244	793,447					
15	<i>DI5SNP33</i>	9,757,093	9,757,093	AAAATAACCCTAGAATTAACCTCCTGTCT TCAG	CCTTGCTTCAAAGCATACTCTTCCA	AATATTTTAAACGAAATTC	CAGTAATATTTTAAATGAAAT TC	17
15	<i>DI5SNP34</i>	30,613,567	20,856,474	GGTCTGGGTGACTCTGTGAAAG	GGGAGTTTTTAGATCATTGACCTGTAGT	CTCAAACCTGTAGGTCCAC	CTCAAACCTGTGGGTCCAC	17
15	<i>DI5SNP24</i>	57,160,486	26,546,919	AGTCTTTGAGATGACTGGATACTGAGA	AGTAAACTTTGGAGCCCACTCATT	CAGTGTGAACAAAG	CCAGTGTAAACAAAG	16
15	<i>DI5SNP32</i>	71,632,551	14,472,065	TCATTTTATTGGCATCTGCCATTAGC	TCAGCGTGGGAGTGAATGATG	CTGAGTCATGGTATGCTTA	CTGAGTCATGGTGTGCTTA	16, 17
15	<i>DI5SNP35</i>	97,255,365	25,622,814	TGTGTTAGCACTACAGTTGTCATCA	GGAGTGGCTTTGAGATCATTAGACA	AGTGTGGGCCCA	AAGAGTGTAGGCCCA	17
15	Distal end	104,043,685	6,788,320					
16	<i>DI6SNP24</i>	4,207,926	4,207,926	GCTTTAACAGTATGCAACCATTGGT	GGGCTGCACTGGTAACTCTTC	AGAAAATGTGGTATAATTG	AGAAAATGTGGTATAATTG	This study
16	<i>DI6SNP19</i>	17,412,079	13,204,153	CTCCTACAAACACCCTGAATGCT	AGAAGTATATCAGAGATGTTTCATGAGATG GAA	CCATTTTATTTAAGGGACATG	CCATTTTATTTAAGGAACATG	16, 17
16	<i>DI6SNP23</i>	52,739,944	35,327,865	GTCTCCACGTCTGATGTCAAAGAG	GCTGAATGGTAGATTTACCAGCTGTA	CACATCTCCAAAACC	TTCACATCTTCAAACC	17
16	<i>DI6SNP22</i>	87,819,629	35,079,685	TGAAGCAGAAAGCAGTAACTTACCA	CTTTGTTTCCTTGACCACATTTTCTT	CCCTGAAAACCTCA	CCCTGAGAACTTCA	16, 17
16	Distal end	98,207,768	10,388,139					
17	<i>DI7SNP28</i>	5,332,903	5,332,903	GAATCTGATGCTGGCTGAATTGG	GTCCATGGCTGTTACTTCTAAGCA	ATACAGCCACAACGCA	CATACAGCCATAACGCA	16, 17
17	<i>DI7SNP29</i>	25,386,450	20,053,547	GGCAAGTACTGTAGCAAGCT	GGGAAAAGCCAAAAGAAGAGAACTGT	TGGACTCCTGCTTGATC	TGGACTCCTGATTGATC	16
17	<i>DI7SNP30</i>	39,170,355	13,783,905	CAGTGAATACTATTTCAGATATGAAAAGA AAAGT	CTTTAAGCCTGGATTACTACACTTTGG	AATTGGATGGACTTGAG	CAATTGGATGAACCTGAG	16, 17
17	<i>DI7SNP24</i>	60,319,945	21,149,590	TGCTTGTGGCAGAAAGATCTAATCA	TGAAACTTCTCTGGACCTCTCTT	CTGATAAGGTTCTGTTGCCT	CTGATAAGGTTCTGTTGCCT	16, 17
17	<i>DI7SNP34</i>	93,399,301	33,079,356	AAAATTTATGTAACAATAAGAGGCTAAT GTTTTGAATCT	TCTAGAGCTTTTAGGTGTGTTGTCAAG	CTGCTAATGTATAATTCT	TGCTAATGTGTAATTCT	This study
17	<i>DI7SNP32</i>	93,830,797	431,496	GACAGTGGGCTATAACAAGATAATAATTT CT	CCCATACTGATTGCCTCTGATGA	TGAATTGGGAATGGCAG	TTTTGAATTGGGAATGACAG	17
17	Distal end	94,987,271	1,156,474					
18	<i>DI8SNP38</i>	15,249,748	15,249,748	GCTGTCCAGTCAAGAGTCA	ACCAACCTGGATGAGTCACATTAG	TTGCCTCTGTGAGCTT	TGCCTCTGCGAGCTT	14, 16, 17
18	<i>DI8SNP36</i>	35,206,506	19,956,758	TGTACAGCTAATTTAGCTATTCTGCACAT	TGGTTGGTGCCAGTACTTAAAA	ATCAAAAAGGTAGAATAAA	ATCAAAAAGGTTGAATAAA	14, 16, 17
18	<i>DI8SNP39</i>	54,614,841	19,408,335	AGAAGCCCTGTCATGAAAATCACAT	GGGTGCCCCAAAATATTGTATGAAA	TGTGCGTATTCCG	CTGTGCTTATTCCG	14, 16, 17

Supplementary Table 2. (Continued)

Chr	Marker	Location (bp)	Interval (bp)	Forward primer (TaqMan)	Reverse primer (TaqMan)	FAM labeled probe	VIC labeled probe	Reference
18	<i>DI8SNP37</i>	84,516,845	29,902,004	ACCTTCAGGCAGTCCAGTACT	TCTCAGAGTTTCTCATCTTTAGGTGTACT	AAGACTTAGTCAACTCTCT	AAGACTTAGTCGACTCTCT	14, 16, 17
18	Distal end	90,702,639	6,185,794					
19	<i>DI9SNP24</i>	9,027,005	9,027,005	CCGGTGGGACCTTCATTTCTAAAA	CCTAAGATGCCGTCATATACAAAGTCA	CCCAACTCTCTCCTTTATA	CCCAACTCTCTGCTTTATA	17
19	<i>DI9SNP27</i>	16,602,218	7,575,213	GTTTACAAGTAACAGCAGGCAACAG	GTAAAACCTCCTGCATATCACTCTGA	TGTGGACAATAGAAGGAA	TGGACAATGGAAGGAA	16
19	<i>DI9SNP28</i>	38,005,411	21,403,193	GTTTGCAAAGCCAGATTTTCTCCTA	GGTTCAGCAGGGTCCTTTGT	TCTATCTAGGAGAAGGC	CTATCTCGGAGAAGGC	17
19	<i>DI9SNP23</i>	49,976,154	11,970,743	TCAGGCTTAGTTTTTTAATGTCAGGAGAT	CCTCAACGGAGCTTTGTCCTT	CACCAGAGCTGCCCTG	CCAGAGCGGCCCTG	This study
19	<i>DI9SNP26</i>	52,068,802	2,092,648	GGAGACTAAGCAGAGACTCTTTGAC	GCCCCAGAAGACAGAAATTATCAAATGTA AATAT	CTCCCAATGAGTTGTC	CTCCCAATGGGTTGTC	17
19	Distal end	61,431,566	9,362,764					
X	<i>DXSNP58</i>	9,435,551	9,435,551	TGATTCAGCATCAAAGCAAGCTTTAAT	TTGCAGCCATTGTATATGAACAGTCT	CTAGATCATCATCTCCC	CTCTAGATCATCTTCTCCC	This study
X	<i>DXSNP52</i>	57,867,627	48,432,076	GTTCAAAAATCTGTCAGCATCGATGT	CGGAAAAGGTTAGGTGGTCCTT	CTCCAGCATGACTGTAGT	ACTCCAGCATGATTGTAGT	16
X	<i>DXSNP56</i>	96,663,644	38,796,017	TGAATGTAGTGAGATGAAATGTCAAGGTT TA	CAGAGTTCTCAAATAAGATACAAAATTG GCT	ACTAAGGATGGTAACTAA	CTAAGGATGGTGAECTAA	This study
X	<i>DXSNP57</i>	117,408,768	20,745,124	CATTGTATTTGTTCCACTGGAGCAG	TCTGATGTTTGGGATATCTGATATGTAACC T	CCCCAAGAGTTTATG	CCCCAAGTGTTTATG	This study
X	<i>DXSNP54</i>	151,470,124	34,061,356	GCAAAAACCAGGAACCCATAGG	GTGATAGCTCTGAGTATTTAATGTGATAA ACTTGT	AGCTTATCTTTCAATCCCAT	CAGCTTATCTTTCAACCCCAT	16
X	Distal end	171,031,299	19,561,175					

Supplementary Table 3. The 632 candidate SNPs between the BALB/cA and BALB/cByJ based on the filtering criteria: dbSNP ID assignment; phred-scaled quality score (PQS) ≥ 50 ; filter, "PASS"; maximum (MAX) coverage ≥ 10 ; minimum (MIN) coverage ≥ 10 ; MAX phred-scaled genotyping quality (PGQ) ≥ 40 ; MAX Δ Allele (ALT) frequency (AF; ALT 1, 2, 3) ≥ 0.3 ; reference genotype, ref; homozygous genotype, hom; genotype information (Info), 0/0 or 1/1; and PGQ ≥ 50 .

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PQS	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX Δ AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGS
1	3934241	rs216213426	A	C	.	.	216	PASS	43	30	87	0.976744	hom	'1/1	84	ref	'0/0	87
1	4610250	rs31420912	C	G	.	.	216	PASS	51	36	127	1	ref	'0/0	127	hom	'1/1	104
1	8486066	rs52617967	T	C	.	.	216	PASS	47	41	127	1	ref	'0/0	127	hom	'1/1	119
1	10747979	rs31199787	G	T	.	.	216	PASS	59	33	127	1	hom	'1/1	127	ref	'0/0	95
1	21642952	rs224967830	T	A	.	.	216	PASS	34	29	77	0.936105	ref	'0/0	56	hom	'1/1	77
1	27280191	rs45737065	A	G	.	.	216	PASS	43	34	125	1	ref	'0/0	125	hom	'1/1	98
1	27593856	rs6244395	C	A	.	.	216	PASS	41	33	119	1	ref	'0/0	119	hom	'1/1	95
1	35428020	rs228529247	C	T	.	.	216	PASS	43	25	125	1	ref	'0/0	125	hom	'1/1	71
1	39118826	rs33109340	C	T	.	.	216	PASS	47	30	127	1	ref	'0/0	127	hom	'1/1	86
1	40947649	rs37999984	G	C	.	.	216	PASS	50	28	127	1	ref	'0/0	127	hom	'1/1	80
1	42918398	rs45634523	G	A	.	.	216	PASS	53	33	127	1	ref	'0/0	127	hom	'1/1	95
1	55489109	rs49529907	C	A	.	.	216	PASS	56	29	127	1	ref	'0/0	127	hom	'1/1	83
1	55568942	rs218559193	G	A	.	.	216	PASS	53	42	127	1	hom	'1/1	127	ref	'0/0	122
1	56810321	rs239662626	T	G	.	.	216	PASS	42	27	122	1	hom	'1/1	122	ref	'0/0	77
1	57614093	rs3679641	C	T	.	.	216	PASS	41	36	119	1	ref	'0/0	104	hom	'1/1	119
1	59724304	rs217251851	G	A	.	.	216	PASS	40	39	116	1	hom	'1/1	116	ref	'0/0	113
1	74954486	rs387540946	A	C	.	.	216	PASS	40	26	84	0.975	hom	'1/1	84	ref	'0/0	75
1	76453882	rs215581356	G	T	.	.	216	PASS	38	32	110	1	hom	'1/1	110	ref	'0/0	92
1	86164663	rs33057227	C	T	.	.	216	PASS	41	30	119	1	ref	'0/0	119	hom	'1/1	86
1	107779553	rs107984378	C	T	.	.	216	PASS	44	37	127	0.972973	hom	'1/1	127	ref	'0/0	66
1	109450170	rs32662396	G	T	.	.	216	PASS	34	26	98	1	hom	'1/1	98	ref	'0/0	74
1	109894986	rs225059761	A	G	.	.	216	PASS	40	28	116	1	hom	'1/1	116	ref	'0/0	80
1	110367737	rs257283321	G	A	.	.	216	PASS	52	29	127	1	ref	'0/0	127	hom	'1/1	83
1	117041233	rs30634895	C	T	.	.	216	PASS	37	19	107	1	ref	'0/0	107	hom	'1/1	53
1	119602808	rs32222488	G	A	.	.	216	PASS	39	27	78	0.974359	hom	'1/1	72	ref	'0/0	78
1	123476641	rs33365833	A	T	.	.	216	PASS	43	26	125	1	ref	'0/0	125	hom	'1/1	74
1	124585625	rs52538191	C	G	T	.	216	PASS	39	29	84	0.948718	hom	'1/1	80	ref	'0/0	84
1	125897741	rs30799741	C	T	.	.	216	PASS	50	21	127	1	ref	'0/0	127	hom	'1/1	59
1	130893444	rs243406748	G	A	.	.	216	PASS	58	30	127	1	ref	'0/0	127	hom	'1/1	86
1	140019081	rs36451137	C	T	.	.	216	PASS	64	39	127	1	ref	'0/0	127	hom	'1/1	113
1	146495202	rs31016032	T	C	.	.	216	PASS	48	28	127	1	ref	'0/0	127	hom	'1/1	80
1	147707934	rs244231370	C	T	G	.	216	PASS	40	35	110	0.975	hom	'1/1	110	ref	'0/0	101
1	148273764	rs31078414	C	A	.	.	216	PASS	49	31	127	1	ref	'0/0	127	hom	'1/1	89
1	152917257	rs31177800	C	T	.	.	216	PASS	64	27	127	1	ref	'0/0	127	hom	'1/1	77
1	153282827	rs51731256	C	T	.	.	216	PASS	50	20	127	1	ref	'0/0	127	hom	'1/1	56
1	160509342	rs250739905	A	G	.	.	216	PASS	40	25	116	1	ref	'0/0	116	hom	'1/1	71
1	160719997	rs52261250	T	C	.	.	216	PASS	39	33	113	1	ref	'0/0	113	hom	'1/1	95
1	165920441	rs31397868	G	A	.	.	216	PASS	38	34	110	1	ref	'0/0	110	hom	'1/1	98

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
1	175022752	rs108509603	G	A	.	.	216	PASS	34	20	74	0.970588	hom	'1/1	74	ref	'0/0	57
1	178569099	rs214582812	T	A	.	.	216	PASS	35	32	101	1	hom	'1/1	101	ref	'0/0	92
1	181336586	rs255915154	C	T	.	.	216	PASS	52	26	127	1	hom	'1/1	127	ref	'0/0	74
1	190879647	rs37250494	A	G	.	.	216	PASS	41	38	119	1	ref	'0/0	119	hom	'1/1	110
1	193479014	rs228463477	C	T	.	.	216	PASS	43	21	125	1	hom	'1/1	125	ref	'0/0	59
1	193818635	rs33202907	T	A	.	.	216	PASS	37	28	107	1	ref	'0/0	107	hom	'1/1	80
2	4556370	rs243288053	G	A	.	.	216	PASS	46	28	127	1	hom	'1/1	127	ref	'0/0	80
2	5621150	rs235168084	G	A	.	.	216	PASS	57	37	127	1	ref	'0/0	127	hom	'1/1	107
2	5837350	rs215722230	A	C	.	.	216	PASS	38	29	110	1	ref	'0/0	110	hom	'1/1	83
2	8312487	rs28274005	C	T	.	.	216	PASS	59	31	127	1	ref	'0/0	127	hom	'1/1	89
2	8649538	rs230758337	G	A	T	.	216	PASS	35	27	77	1	ref	'0/0	75	hom	'1/1	77
2	17984446	rs27173936	G	A	.	.	216	PASS	30	28	86	1	ref	'0/0	86	hom	'1/1	80
2	22067598	rs27119029	A	G	.	.	216	PASS	43	23	125	1	ref	'0/0	125	hom	'1/1	65
2	34982524	rs27169047	G	T	.	.	216	PASS	51	28	127	1	ref	'0/0	127	hom	'1/1	80
2	47826855	rs258611409	G	A	.	.	216	PASS	60	37	127	1	hom	'1/1	127	ref	'0/0	107
2	49506172	rs27901879	T	C	.	.	216	PASS	40	36	116	1	ref	'0/0	116	hom	'1/1	104
2	56143013	rs27888858	T	C	.	.	216	PASS	45	28	127	1	ref	'0/0	127	hom	'1/1	80
2	57195676	rs245939001	C	A	.	.	216	PASS	35	23	101	1	ref	'0/0	101	hom	'1/1	65
2	64174567	rs228117662	G	A	.	.	216	PASS	41	24	119	1	hom	'1/1	119	ref	'0/0	68
2	64912612	rs13475125	A	G	.	.	216	PASS	50	27	127	1	ref	'0/0	127	hom	'1/1	77
2	71919142	rs387807878	A	G	.	.	216	PASS	36	19	104	1	ref	'0/0	104	hom	'1/1	53
2	74655278	rs253836779	T	G	.	.	216	PASS	30	28	86	1	ref	'0/0	80	hom	'1/1	86
2	76807991	rs27981830	G	A	.	.	216	PASS	52	31	127	1	ref	'0/0	127	hom	'1/1	89
2	82475855	rs28009309	G	A	.	.	216	PASS	53	24	127	1	ref	'0/0	127	hom	'1/1	68
2	82911850	rs242122538	G	A	.	.	216	PASS	48	27	127	1	hom	'1/1	127	ref	'0/0	77
2	85405743	rs242140613	A	G	.	.	216	PASS	47	27	127	1	hom	'1/1	127	ref	'0/0	77
2	94070105	rs27393943	C	T	.	.	216	PASS	45	35	127	1	ref	'0/0	127	hom	'1/1	101
2	106287005	rs27400950	C	G	.	.	216	PASS	44	24	127	1	ref	'0/0	127	hom	'1/1	68
2	107752240	rs238060283	A	G	.	.	216	PASS	60	19	127	1	ref	'0/0	127	hom	'1/1	53
2	115219315	rs52234595	T	C	.	.	216	PASS	35	32	102	0.96875	hom	'1/1	102	ref	'0/0	70
2	124217491	rs108662151	A	G	.	.	216	PASS	39	21	81	0.974359	ref	'0/0	81	hom	'1/1	60
2	125641101	rs262242527	A	G	.	.	216	PASS	42	19	122	1	ref	'0/0	122	hom	'1/1	53
2	126468009	rs27438123	T	C	.	.	216	PASS	45	35	127	1	ref	'0/0	127	hom	'1/1	101
2	126520259	rs27437951	A	G	.	.	216	PASS	53	25	127	1	ref	'0/0	127	hom	'1/1	71
2	126595320	rs27421578	C	G	.	.	216	PASS	37	34	107	1	ref	'0/0	98	hom	'1/1	107
2	126618537	rs253650589	A	G	.	.	216	PASS	58	23	127	1	hom	'1/1	127	ref	'0/0	65
2	128009386	rs261663022	G	A	.	.	216	PASS	38	26	110	1	hom	'1/1	110	ref	'0/0	74
2	129173546	rs27433539	G	A	.	.	216	PASS	45	21	127	1	ref	'0/0	127	hom	'1/1	59
2	133211590	rs28288090	G	T	.	.	216	PASS	48	37	127	1	ref	'0/0	127	hom	'1/1	107
2	136498862	rs27257027	G	C	.	.	216	PASS	38	28	110	1	ref	'0/0	110	hom	'1/1	80
2	141282219	rs27205328	G	T	.	.	216	PASS	52	34	127	1	ref	'0/0	127	hom	'1/1	98

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
2	141495402	rs27250976	C	T	.	.	216	PASS	42	25	122	1	ref	'0/0	122	hom	'1/1	71
2	142718164	rs52440160	A	G	.	.	216	PASS	54	28	127	0.981481	hom	'1/1	127	ref	'0/0	81
2	148727175	rs229234635	G	A	.	.	216	PASS	34	21	60	0.970588	hom	'1/1	57	ref	'0/0	60
2	156571805	rs27305887	C	T	.	.	216	PASS	38	32	110	1	ref	'0/0	110	hom	'1/1	92
2	163325185	rs257071039	A	T	.	.	216	PASS	53	31	127	1	ref	'0/0	127	hom	'1/1	89
2	165656701	rs27298271	C	T	.	.	216	PASS	45	38	127	1	hom	'1/1	127	ref	'0/0	110
2	166878527	rs27295479	G	A	.	.	216	PASS	44	29	127	1	ref	'0/0	127	hom	'1/1	83
2	170602475	rs27632302	T	C	.	.	216	PASS	49	33	127	1	ref	'0/0	127	hom	'1/1	95
2	172908627	rs27622613	T	C	.	.	216	PASS	42	33	122	1	ref	'0/0	122	hom	'1/1	95
2	178864958	rs27684606	T	C	.	.	216	PASS	39	30	113	1	ref	'0/0	113	hom	'1/1	86
3	7170339	rs46220062	C	T	.	.	216	PASS	55	29	127	1	ref	'0/0	127	hom	'1/1	83
3	14725758	rs3700826	T	G	.	.	216	PASS	46	26	127	1	ref	'0/0	127	hom	'1/1	74
3	18788432	rs242792340	A	C	.	.	216	PASS	47	20	127	1	hom	'1/1	127	ref	'0/0	56
3	21142186	rs261798946	C	G	.	.	216	PASS	57	39	127	1	ref	'0/0	127	hom	'1/1	113
3	25659256	rs33785797	C	T	A	.	216	PASS	53	30	127	1	ref	'0/0	127	hom	'1/1	86
3	34236826	rs255953863	G	A	.	.	216	PASS	54	41	127	1	hom	'1/1	127	ref	'0/0	119
3	34676608	rs31527910	A	C	.	.	216	PASS	45	28	104	0.977778	hom	'1/1	104	ref	'0/0	81
3	39179320	rs387323566	A	T	.	.	216	PASS	38	24	110	1	hom	'1/1	110	ref	'0/0	68
3	39236366	rs29938481	G	T	.	.	216	PASS	49	36	127	1	ref	'0/0	127	hom	'1/1	104
3	39913654	rs29966920	C	T	.	.	216	PASS	60	34	127	1	ref	'0/0	127	hom	'1/1	98
3	40888838	rs52489829	T	C	.	.	216	PASS	49	22	127	1	ref	'0/0	127	hom	'1/1	62
3	40888843	rs52386779	G	C	.	.	216	PASS	49	24	127	1	ref	'0/0	127	hom	'1/1	68
3	42237806	rs45707176	G	A	.	.	216	PASS	43	22	125	1	ref	'0/0	125	hom	'1/1	62
3	49428983	rs46031517	A	C	.	.	216	PASS	42	31	122	1	ref	'0/0	122	hom	'1/1	89
3	52249689	rs262948879	T	A	.	.	216	PASS	36	28	81	0.972222	ref	'0/0	67	hom	'1/1	81
3	52609455	rs262198226	G	A	.	.	216	PASS	41	27	119	1	ref	'0/0	119	hom	'1/1	77
3	54045855	rs256274075	T	G	.	.	216	PASS	44	28	127	1	ref	'0/0	127	hom	'1/1	80
3	57198716	rs216678545	C	A	G	.	216	PASS	51	24	126	0.980392	hom	'1/1	126	ref	'0/0	68
3	62525570	rs36884448	C	T	.	.	216	PASS	55	42	127	1	ref	'0/0	127	hom	'1/1	122
3	65103756	rs36544985	A	G	.	.	216	PASS	47	32	127	1	ref	'0/0	127	hom	'1/1	92
3	67191402	rs36894992	G	T	.	.	216	PASS	50	34	127	1	ref	'0/0	127	hom	'1/1	98
3	72718425	rs36461472	A	G	.	.	216	PASS	58	37	127	1	ref	'0/0	127	hom	'1/1	107
3	75640494	rs223319787	T	G	.	.	216	PASS	53	31	123	0.981132	hom	'1/1	123	ref	'0/0	90
3	78914754	rs31209208	A	G	.	.	216	PASS	49	30	127	1	hom	'1/1	127	ref	'0/0	86
3	80066581	rs31285603	G	A	.	.	216	PASS	49	25	127	1	ref	'0/0	127	hom	'1/1	71
3	84949849	rs32729341	T	A	.	.	216	PASS	79	39	127	1	ref	'0/0	127	hom	'1/1	113
3	87004157	rs218636933	T	A	.	.	216	PASS	44	34	127	1	hom	'1/1	127	ref	'0/0	98
3	89749557	rs30204771	A	C	.	.	216	PASS	43	36	125	1	ref	'0/0	125	hom	'1/1	104
3	100874132	rs52151770	C	T	.	.	216	PASS	50	31	106	0.98	hom	'1/1	106	ref	'0/0	90
3	102126331	rs36506426	G	A	.	.	216	PASS	40	33	116	1	ref	'0/0	116	hom	'1/1	95
3	109018303	rs262408865	C	T	.	.	216	PASS	40	22	116	1	ref	'0/0	116	hom	'1/1	62

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
3	114574292	rs36695640	C	T	.	.	216	PASS	36	23	104	1	ref	'0/0	104	hom	'1/1	65
3	115092392	rs51954262	T	C	.	.	216	PASS	47	34	127	1	ref	'0/0	127	hom	'1/1	98
3	116393441	rs241901803	T	C	.	.	216	PASS	61	25	127	1	hom	'1/1	127	ref	'0/0	71
3	122795939	rs211697152	C	T	.	.	216	PASS	46	22	127	1	hom	'1/1	127	ref	'0/0	62
3	124143029	rs36274336	T	C	.	.	216	PASS	51	31	127	1	ref	'0/0	127	hom	'1/1	89
3	124357905	rs30286936	G	A	.	.	216	PASS	30	27	86	1	ref	'0/0	86	hom	'1/1	77
3	125266440	rs30380663	C	T	.	.	216	PASS	51	31	127	1	ref	'0/0	127	hom	'1/1	89
3	127224442	rs30576288	C	A	.	.	216	PASS	37	28	107	1	ref	'0/0	107	hom	'1/1	80
3	127525910	rs48491944	T	C	.	.	216	PASS	46	33	127	1	hom	'1/1	127	ref	'0/0	95
3	128705974	rs221745548	G	A	.	.	216	PASS	53	34	127	1	ref	'0/0	127	hom	'1/1	98
3	128852604	rs36822387	A	G	.	.	216	PASS	50	40	127	1	ref	'0/0	127	hom	'1/1	116
3	135526501	rs37667028	G	C	A	.	216	PASS	54	24	127	1	ref	'0/0	127	hom	'1/1	68
3	136749731	rs52487441	T	G	.	.	216	PASS	50	30	127	1	ref	'0/0	127	hom	'1/1	86
3	138642974	rs30922604	G	C	.	.	216	PASS	45	24	127	1	ref	'0/0	127	hom	'1/1	68
3	144209002	rs36927689	G	A	.	.	216	PASS	39	31	113	1	ref	'0/0	113	hom	'1/1	89
3	145072474	rs49049515	G	A	.	.	216	PASS	76	25	127	1	ref	'0/0	127	hom	'1/1	71
3	156119086	rs30857183	A	G	.	.	216	PASS	40	25	116	1	ref	'0/0	116	hom	'1/1	71
4	4281106	rs27671156	T	A	.	.	216	PASS	39	25	113	1	ref	'0/0	113	hom	'1/1	71
4	8496142	rs23152592	C	T	.	.	216	PASS	56	37	127	1	ref	'0/0	127	hom	'1/1	107
4	17009477	rs226052082	G	A	.	.	216	PASS	45	23	127	1	hom	'1/1	127	ref	'0/0	65
4	18542401	rs27663943	T	A	.	.	216	PASS	48	28	127	1	ref	'0/0	127	hom	'1/1	80
4	20687935	rs32396472	A	C	.	.	216	PASS	23	22	65	1	ref	'0/0	65	hom	'1/1	62
4	23107449	rs260525369	A	C	.	.	216	PASS	35	33	101	1	ref	'0/0	101	hom	'1/1	95
4	23377095	rs27733924	C	A	.	.	216	PASS	51	32	127	1	ref	'0/0	127	hom	'1/1	92
4	26470011	rs242182454	C	T	.	.	216	PASS	45	23	127	1	hom	'1/1	127	ref	'0/0	65
4	26947031	rs241053609	G	A	.	.	216	PASS	43	38	125	1	hom	'1/1	125	ref	'0/0	110
4	29672879	rs253500092	G	T	.	.	216	PASS	36	32	93	0.972222	hom	'1/1	67	ref	'0/0	93
4	31397731	rs255362649	A	T	.	.	216	PASS	49	33	127	1	ref	'0/0	127	hom	'1/1	95
4	39023568	rs27767340	C	T	.	.	216	PASS	56	29	127	1	ref	'0/0	127	hom	'1/1	83
4	40823067	rs107811703	T	G	.	.	216	PASS	49	31	127	1	ref	'0/0	127	hom	'1/1	89
4	51796685	rs52546101	G	T	.	.	216	PASS	43	27	125	1	hom	'1/1	125	ref	'0/0	77
4	51796693	rs52531930	G	T	.	.	216	PASS	39	28	113	1	hom	'1/1	113	ref	'0/0	80
4	58956799	rs27885209	G	A	.	.	216	PASS	56	28	127	1	ref	'0/0	127	hom	'1/1	80
4	65807248	rs3706082	T	C	.	.	216	PASS	37	34	99	0.972973	ref	'0/0	85	hom	'1/1	99
4	79728759	rs32161493	C	G	.	.	216	PASS	50	33	127	1	hom	'1/1	127	ref	'0/0	95
4	81623919	rs28104130	A	G	.	.	216	PASS	40	30	116	1	ref	'0/0	116	hom	'1/1	86
4	83554246	rs213671359	A	T	.	.	216	PASS	55	31	127	1	hom	'1/1	127	ref	'0/0	89
4	88047668	rs28097814	A	C	.	.	216	PASS	56	23	127	1	ref	'0/0	127	hom	'1/1	65
4	89786718	rs28126314	G	A	.	.	216	PASS	44	44	127	1	ref	'0/0	127	hom	'1/1	127
4	97572518	rs28111856	C	T	.	.	216	PASS	48	24	127	1	ref	'0/0	127	hom	'1/1	68
4	98970782	rs28306161	G	A	.	.	216	PASS	50	30	127	1	ref	'0/0	127	hom	'1/1	86

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
4	106328247	rs262379668	T	C	.	.	216	PASS	45	20	127	1	ref	'0/0	127	hom	'1/1	56
4	114423192	rs27512361	C	T	.	.	216	PASS	43	26	125	1	ref	'0/0	125	hom	'1/1	74
4	125871573	rs243249710	G	A	.	.	216	PASS	39	26	113	1	ref	'0/0	113	hom	'1/1	74
4	130547774	rs28334646	C	A	.	.	216	PASS	47	31	127	1	ref	'0/0	127	hom	'1/1	89
4	135004214	rs226602315	C	A	.	.	216	PASS	59	30	127	1	hom	'1/1	127	ref	'0/0	86
4	137543663	rs257687113	C	T	.	.	216	PASS	47	28	127	1	ref	'0/0	127	hom	'1/1	80
4	152532156	rs32877825	G	A	.	.	216	PASS	37	37	107	1	ref	'0/0	107	hom	'1/1	107
4	154762335	rs254787669	T	A	.	.	216	PASS	44	32	127	1	ref	'0/0	127	hom	'1/1	92
5	4484697	rs31133755	C	A	.	.	216	PASS	32	26	92	1	ref	'0/0	92	hom	'1/1	74
5	7566633	rs31314541	C	T	.	.	216	PASS	44	37	127	1	ref	'0/0	127	hom	'1/1	107
5	7738884	rs31291054	T	A	.	.	216	PASS	40	27	116	1	ref	'0/0	116	hom	'1/1	77
5	10210679	rs257538533	G	A	.	.	216	PASS	30	28	86	1	hom	'1/1	80	ref	'0/0	86
5	13168619	rs48011081	C	G	.	.	216	PASS	38	21	110	1	ref	'0/0	110	hom	'1/1	59
5	14873172	rs51824862	A	G	.	.	216	PASS	33	18	95	1	ref	'0/0	95	hom	'1/1	50
5	19981092	rs33715497	A	C	.	.	216	PASS	34	33	98	1	ref	'0/0	98	hom	'1/1	95
5	21003334	rs31879326	G	T	.	.	216	PASS	44	31	127	1	ref	'0/0	127	hom	'1/1	89
5	24672436	rs214930553	T	G	.	.	216	PASS	30	27	78	0.966667	ref	'0/0	59	hom	'1/1	78
5	41046168	rs52253128	C	T	.	.	216	PASS	43	25	84	0.953488	hom	'1/1	84	ref	'0/0	72
5	46735635	rs50896597	C	T	.	.	216	PASS	40	33	116	1	ref	'0/0	116	hom	'1/1	95
5	51801410	rs37618732	G	A	.	.	216	PASS	33	27	95	1	ref	'0/0	95	hom	'1/1	77
5	53319753	rs32937431	G	A	.	.	216	PASS	34	23	98	1	ref	'0/0	98	hom	'1/1	65
5	54678766	rs241396642	G	A	.	.	216	PASS	37	33	107	1	hom	'1/1	107	ref	'0/0	95
5	56613716	rs249159888	G	A	.	.	216	PASS	38	30	110	1	hom	'1/1	110	ref	'0/0	86
5	56650550	rs46019978	T	C	.	.	216	PASS	44	32	127	1	ref	'0/0	127	hom	'1/1	92
5	58933244	rs33006241	C	A	.	.	216	PASS	31	24	89	1	ref	'0/0	89	hom	'1/1	68
5	62170569	rs256975469	A	T	G	.	216	PASS	35	33	101	0.969697	hom	'1/1	79	ref	'0/0	101
5	72972653	rs259131922	C	T	.	.	216	PASS	31	22	89	1	ref	'0/0	62	hom	'1/1	89
5	73080631	rs33163841	G	A	.	.	216	PASS	44	32	127	1	hom	'1/1	127	ref	'0/0	92
5	74679783	rs52019376	G	A	.	.	216	PASS	35	28	101	1	ref	'0/0	101	hom	'1/1	80
5	75903780	rs38221987	C	T	.	.	216	PASS	40	36	116	1	ref	'0/0	104	hom	'1/1	116
5	78651801	rs31576711	G	T	.	.	216	PASS	41	41	119	1	ref	'0/0	119	hom	'1/1	119
5	79857660	rs37446657	T	G	.	.	216	PASS	44	40	117	0.977273	ref	'0/0	87	hom	'1/1	117
5	80002501	rs37076251	C	A	.	.	216	PASS	50	28	127	1	ref	'0/0	127	hom	'1/1	80
5	81396528	rs231430579	G	A	.	.	216	PASS	38	31	110	1	hom	'1/1	110	ref	'0/0	89
5	85602304	rs252428444	G	T	.	.	216	PASS	27	26	77	1	hom	'1/1	77	ref	'0/0	74
5	97815958	rs31892920	T	C	.	.	216	PASS	47	38	127	1	ref	'0/0	127	hom	'1/1	110
5	97930577	rs262764748	T	A	.	.	216	PASS	39	26	113	1	ref	'0/0	113	hom	'1/1	74
5	99956620	rs31960195	C	T	.	.	216	PASS	42	37	122	1	ref	'0/0	122	hom	'1/1	107
5	116413315	rs29566065	C	T	.	.	216	PASS	34	21	98	1	hom	'1/1	98	ref	'0/0	59
5	116836095	rs50427093	T	G	.	.	216	PASS	29	28	83	1	ref	'0/0	83	hom	'1/1	80
5	118220846	rs37121206	G	T	.	.	216	PASS	38	34	99	0.973684	ref	'0/0	83	hom	'1/1	99

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
5	120322918	rs33165131	A	C	.	.	216	PASS	24	20	68	1	ref	'0/0	56	hom	'1/1	68
5	130443486	rs33134263	T	G	.	.	216	PASS	46	22	63	0.956522	hom	'1/1	56	ref	'0/0	63
5	144206289	rs32347776	G	A	.	.	216	PASS	36	35	104	1	ref	'0/0	101	hom	'1/1	104
6	3288719	rs238942284	G	A	C	.	216	PASS	39	21	107	0.974359	hom	'1/1	107	ref	'0/0	59
6	4373056	rs32451704	T	C	.	.	216	PASS	43	26	125	1	ref	'0/0	125	hom	'1/1	74
6	5888237	rs32502983	C	T	.	.	216	PASS	50	26	127	1	ref	'0/0	127	hom	'1/1	74
6	15039937	rs37220474	A	G	.	.	216	PASS	52	36	127	1	ref	'0/0	127	hom	'1/1	104
6	17244414	rs33536930	C	T	.	.	216	PASS	45	26	127	1	ref	'0/0	127	hom	'1/1	74
6	20094435	rs252790903	A	C	.	.	216	PASS	45	35	127	0.971429	hom	'1/1	127	ref	'0/0	60
6	21020989	rs33655166	C	T	.	.	216	PASS	36	34	104	1	ref	'0/0	104	hom	'1/1	98
6	24603257	rs242540528	C	T	.	.	216	PASS	44	28	127	1	hom	'1/1	127	ref	'0/0	80
6	27483160	rs33791073	C	T	.	.	216	PASS	49	25	127	1	ref	'0/0	127	hom	'1/1	71
6	34962165	rs36885644	G	T	.	.	216	PASS	46	34	127	1	ref	'0/0	127	hom	'1/1	98
6	35348187	rs248174732	C	T	.	.	216	PASS	61	22	127	1	ref	'0/0	127	hom	'1/1	62
6	36439766	rs36844220	A	T	.	.	216	PASS	42	28	122	1	ref	'0/0	122	hom	'1/1	80
6	37620067	rs213520184	C	T	.	.	216	PASS	47	26	127	1	ref	'0/0	127	hom	'1/1	74
6	41218861	rs249866242	G	A	.	.	216	PASS	42	24	122	1	hom	'1/1	122	ref	'0/0	68
6	41819591	rs387861897	A	C	.	.	216	PASS	34	21	98	1	hom	'1/1	98	ref	'0/0	59
6	48740122	rs30269044	A	C	.	.	216	PASS	46	29	127	1	hom	'1/1	127	ref	'0/0	83
6	55786769	rs107654576	T	A	.	.	216	PASS	31	23	89	1	ref	'0/0	89	hom	'1/1	65
6	56356261	rs30243631	G	A	.	.	216	PASS	53	38	127	1	ref	'0/0	127	hom	'1/1	110
6	60965551	rs30413117	A	G	.	.	216	PASS	52	18	125	0.980769	hom	'1/1	125	ref	'0/0	51
6	63287902	rs237835376	C	T	.	.	216	PASS	34	26	98	1	hom	'1/1	98	ref	'0/0	74
6	66893429	rs216689099	C	T	.	.	216	PASS	47	30	127	1	hom	'1/1	127	ref	'0/0	86
6	72622883	rs213116451	C	T	.	.	216	PASS	26	25	74	1	hom	'1/1	71	ref	'0/0	74
6	81414880	rs52149393	T	A	.	.	216	PASS	37	18	75	0.972973	hom	'1/1	75	ref	'0/0	51
6	83132620	rs30996879	C	G	.	.	216	PASS	35	24	101	1	hom	'1/1	101	ref	'0/0	68
6	84045239	rs49989215	G	A	.	.	216	PASS	42	26	122	1	ref	'0/0	122	hom	'1/1	74
6	89176439	rs31000442	T	A	.	.	216	PASS	41	24	119	1	ref	'0/0	119	hom	'1/1	68
6	90780527	rs37775941	C	T	.	.	216	PASS	36	27	104	1	ref	'0/0	104	hom	'1/1	77
6	93057485	rs247874543	T	A	.	.	216	PASS	35	26	101	1	ref	'0/0	101	hom	'1/1	74
6	102060516	rs230573527	C	T	.	.	216	PASS	66	37	127	1	hom	'1/1	127	ref	'0/0	107
6	106062804	rs36823898	A	G	.	.	216	PASS	48	20	127	1	ref	'0/0	127	hom	'1/1	56
6	115356070	rs108539988	G	T	.	.	216	PASS	45	34	90	0.948366	hom	'1/1	90	ref	'0/0	66
6	124308891	rs31785819	C	T	.	.	216	PASS	64	30	127	1	ref	'0/0	127	hom	'1/1	86
6	125457107	rs52133628	C	T	.	.	216	PASS	38	29	110	1	hom	'1/1	110	ref	'0/0	83
6	137462482	rs31952322	G	A	.	.	216	PASS	42	30	122	1	ref	'0/0	122	hom	'1/1	86
6	138571450	rs52262963	A	G	.	.	216	PASS	32	19	92	1	ref	'0/0	92	hom	'1/1	53
6	139562423	rs238551637	G	A	.	.	216	PASS	33	24	95	1	hom	'1/1	95	ref	'0/0	68
6	141030475	rs233587596	T	G	.	.	216	PASS	28	25	80	1	hom	'1/1	71	ref	'0/0	80
7	12630989	rs245498099	G	A	.	.	216	PASS	35	22	101	1	ref	'0/0	101	hom	'1/1	62

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
7	18101721	rs32408583	A	C	.	.	216	PASS	40	21	116	1	ref	'0/0	116	hom	'1/1	59
7	21107457	rs33865477	G	A	.	.	216	PASS	42	28	122	1	hom	'1/1	122	ref	'0/0	80
7	36464009	rs32553424	C	G	.	.	216	PASS	46	28	127	1	ref	'0/0	127	hom	'1/1	80
7	37210542	rs238688779	T	C	.	.	216	PASS	27	23	77	1	ref	'0/0	77	hom	'1/1	65
7	37210546	rs248907111	T	C	.	.	216	PASS	26	22	74	1	ref	'0/0	74	hom	'1/1	62
7	50521428	rs38641728	G	A	.	.	216	PASS	42	40	122	1	ref	'0/0	122	hom	'1/1	116
7	51848464	rs32906845	C	A	.	.	216	PASS	43	32	125	1	ref	'0/0	125	hom	'1/1	92
7	53980915	rs256548283	G	C	.	.	216	PASS	31	31	89	1	hom	'1/1	89	ref	'0/0	89
7	57069689	rs253334041	A	G	T	.	216	PASS	40	34	99	0.95	hom	'1/1	73	ref	'0/0	99
7	57069706	rs211761599	C	T	.	.	216	PASS	38	34	111	0.970588	hom	'1/1	57	ref	'0/0	111
7	61911531	rs39143130	T	A	.	.	216	PASS	32	27	92	1	ref	'0/0	92	hom	'1/1	77
7	63058555	rs33056660	A	C	.	.	216	PASS	43	39	125	1	ref	'0/0	113	hom	'1/1	125
7	71358685	rs36406095	C	T	.	.	216	PASS	46	38	127	1	ref	'0/0	127	hom	'1/1	110
7	76188456	rs33162001	A	T	.	.	216	PASS	44	22	127	1	ref	'0/0	127	hom	'1/1	62
7	81751231	rs230038221	A	T	.	.	216	PASS	43	35	125	1	ref	'0/0	125	hom	'1/1	101
7	83903728	rs221791501	G	A	.	.	216	PASS	35	31	101	1	ref	'0/0	101	hom	'1/1	89
7	88649902	rs48087812	A	C	.	.	216	PASS	35	26	101	1	ref	'0/0	101	hom	'1/1	74
7	93007152	rs46961196	T	C	.	.	216	PASS	40	26	116	1	ref	'0/0	116	hom	'1/1	74
7	95489897	rs252262278	T	G	.	.	216	PASS	32	27	92	1	hom	'1/1	77	ref	'0/0	92
7	95833256	rs233356843	C	T	.	.	216	PASS	47	32	127	1	hom	'1/1	127	ref	'0/0	92
7	95928545	rs31482312	T	G	.	.	216	PASS	44	35	127	1	ref	'0/0	127	hom	'1/1	101
7	97597629	rs31340271	T	A	.	.	216	PASS	52	29	127	1	ref	'0/0	127	hom	'1/1	83
7	103647031	rs37083820	A	T	.	.	216	PASS	31	29	89	1	ref	'0/0	89	hom	'1/1	83
7	105776246	rs256050103	A	C	.	.	216	PASS	29	21	83	1	ref	'0/0	83	hom	'1/1	59
7	107346092	rs108528904	G	T	.	.	216	PASS	29	20	57	0.965517	hom	'1/1	51	ref	'0/0	57
7	110193737	rs228897811	G	A	.	.	216	PASS	39	27	113	1	hom	'1/1	113	ref	'0/0	77
7	128474626	rs51219759	A	T	.	.	216	PASS	31	29	89	1	ref	'0/0	83	hom	'1/1	89
7	141019152	rs45819623	T	G	.	.	216	PASS	29	27	78	0.965517	ref	'0/0	61	hom	'1/1	78
8	4539352	rs47376668	G	A	.	.	216	PASS	37	33	107	1	ref	'0/0	107	hom	'1/1	95
8	8694179	rs29735060	C	A	.	.	216	PASS	32	25	92	1	ref	'0/0	71	hom	'1/1	92
8	12728591	rs29842981	G	A	.	.	216	PASS	35	28	101	1	ref	'0/0	80	hom	'1/1	101
8	12731606	rs228235766	G	A	.	.	216	PASS	39	30	113	1	ref	'0/0	113	hom	'1/1	86
8	29005008	rs47616120	G	A	.	.	216	PASS	35	30	101	1	ref	'0/0	101	hom	'1/1	86
8	32320891	rs50671181	G	A	.	.	216	PASS	33	21	95	1	ref	'0/0	59	hom	'1/1	95
8	38986555	rs52199289	C	A	.	.	216	PASS	49	31	127	1	hom	'1/1	127	ref	'0/0	89
8	39267450	rs30687604	C	T	.	.	216	PASS	30	29	86	1	ref	'0/0	86	hom	'1/1	83
8	39797026	rs30733023	C	T	.	.	216	PASS	47	29	127	1	ref	'0/0	127	hom	'1/1	83
8	39932752	rs50446742	G	T	.	.	216	PASS	30	28	86	1	ref	'0/0	86	hom	'1/1	80
8	40364781	rs36336278	C	T	G	.	216	PASS	38	36	110	1	hom	'1/1	110	ref	'0/0	98
8	47723276	rs238094068	T	A	.	.	216	PASS	47	27	127	1	hom	'1/1	127	ref	'0/0	77
8	49265894	rs32557120	C	A	.	.	216	PASS	33	22	95	1	ref	'0/0	95	hom	'1/1	62

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
8	52576101	rs31292898	T	G	.	.	216	PASS	30	30	86	1	ref	'0/0	86	hom	'1/1	86
8	54565659	rs31327277	T	A	.	.	216	PASS	37	31	107	1	ref	'0/0	107	hom	'1/1	89
8	55650082	rs46950221	C	T	.	.	216	PASS	29	27	83	1	ref	'0/0	77	hom	'1/1	83
8	59747512	rs234312594	G	T	.	.	216	PASS	48	27	127	1	hom	'1/1	127	ref	'0/0	77
8	68481869	rs36881999	G	A	.	.	216	PASS	52	34	127	1	ref	'0/0	127	hom	'1/1	98
8	70244145	rs232118934	A	G	.	.	216	PASS	41	26	119	1	hom	'1/1	119	ref	'0/0	74
8	76803268	rs247952996	C	T	.	.	216	PASS	31	30	89	1	hom	'1/1	86	ref	'0/0	89
8	78754432	rs47192670	C	T	.	.	216	PASS	34	30	98	1	hom	'1/1	98	ref	'0/0	86
8	89321567	rs45771591	A	T	.	.	216	PASS	31	25	89	1	ref	'0/0	89	hom	'1/1	71
8	94157789	rs33218850	G	T	.	.	216	PASS	41	34	119	1	hom	'1/1	119	ref	'0/0	98
8	94315557	rs32081157	G	A	.	.	216	PASS	45	33	127	1	ref	'0/0	127	hom	'1/1	95
8	96895441	rs217340274	G	A	.	.	216	PASS	31	20	89	1	hom	'1/1	89	ref	'0/0	56
8	97012501	rs38305200	G	A	.	.	216	PASS	35	21	101	1	ref	'0/0	101	hom	'1/1	59
8	98905423	rs50884434	G	A	.	.	216	PASS	46	26	127	1	ref	'0/0	127	hom	'1/1	74
8	100541239	rs214367719	G	T	.	.	216	PASS	28	23	66	0.964286	hom	'1/1	50	ref	'0/0	66
8	101640360	rs32421909	T	A	.	.	216	PASS	36	26	104	1	ref	'0/0	104	hom	'1/1	74
8	107051774	rs245313288	G	A	.	.	216	PASS	34	26	98	1	hom	'1/1	98	ref	'0/0	74
8	107195596	rs223797069	G	A	.	.	216	PASS	24	20	68	1	ref	'0/0	56	hom	'1/1	68
8	114345300	rs249941267	C	T	.	.	216	PASS	39	36	113	1	hom	'1/1	104	ref	'0/0	113
8	114530719	rs31365082	T	A	.	.	216	PASS	36	25	104	1	ref	'0/0	71	hom	'1/1	104
8	117377305	rs36657749	C	G	.	.	216	PASS	40	31	116	1	ref	'0/0	89	hom	'1/1	116
8	118274086	rs46426133	T	C	.	.	216	PASS	34	29	98	1	ref	'0/0	98	hom	'1/1	83
8	120143430	rs246670445	G	A	.	.	216	PASS	35	35	101	1	hom	'1/1	101	ref	'0/0	101
8	124006304	rs213284076	T	A	.	.	216	PASS	58	24	127	1	ref	'0/0	127	hom	'1/1	68
8	128731434	rs262469470	G	A	.	.	216	PASS	42	33	122	1	hom	'1/1	122	ref	'0/0	95
9	7143163	rs51304512	T	C	.	.	216	PASS	43	36	125	1	ref	'0/0	125	hom	'1/1	104
9	8047702	rs257805953	T	A	.	.	216	PASS	31	30	89	1	hom	'1/1	86	ref	'0/0	89
9	8678079	rs37283858	T	C	.	.	216	PASS	33	33	95	1	ref	'0/0	95	hom	'1/1	95
9	10209999	rs49489102	T	A	.	.	216	PASS	44	29	127	1	ref	'0/0	127	hom	'1/1	83
9	14584976	rs50539755	C	G	.	.	216	PASS	41	27	119	1	ref	'0/0	119	hom	'1/1	77
9	19807567	rs386954952	C	G	.	.	216	PASS	44	36	127	0.972222	ref	'0/0	127	hom	'1/1	64
9	22283355	rs219572795	T	G	.	.	216	PASS	38	28	110	1	hom	'1/1	110	ref	'0/0	80
9	24560761	rs220888627	G	A	.	.	216	PASS	45	36	127	1	ref	'0/0	127	hom	'1/1	104
9	27209947	rs265928215	G	T	.	.	216	PASS	34	25	98	1	hom	'1/1	98	ref	'0/0	71
9	28064358	rs37879512	G	A	.	.	216	PASS	35	31	101	1	ref	'0/0	89	hom	'1/1	101
9	31511425	rs221256756	C	T	.	.	216	PASS	36	29	104	1	hom	'1/1	104	ref	'0/0	83
9	35034300	rs219552094	C	T	.	.	216	PASS	46	31	127	1	hom	'1/1	127	ref	'0/0	89
9	39771797	rs36581296	C	T	.	.	216	PASS	31	30	89	1	ref	'0/0	86	hom	'1/1	89
9	58658396	rs38922776	A	G	.	.	216	PASS	32	32	92	1	hom	'1/1	92	ref	'0/0	92
9	78382467	rs52005275	G	A	.	.	216	PASS	24	21	68	1	ref	'0/0	59	hom	'1/1	68
9	78812350	rs52353302	C	G	.	.	216	PASS	35	32	102	0.9375	ref	'0/0	65	hom	'1/1	102

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
9	83199142	rs33655058	G	A	.	.	216	PASS	30	30	86	1	hom	'1/1	86	ref	'0/0	86
9	85694463	rs260806757	A	C	.	.	216	PASS	40	37	116	1	ref	'0/0	116	hom	'1/1	107
9	93151921	rs37466321	C	T	.	.	216	PASS	37	27	107	1	ref	'0/0	107	hom	'1/1	77
9	93337289	rs234879714	G	A	.	.	216	PASS	39	27	113	1	hom	'1/1	77	ref	'0/0	113
9	95045718	rs36274038	C	G	.	.	216	PASS	50	23	127	1	ref	'0/0	127	hom	'1/1	65
9	97538326	rs33134771	G	A	.	.	216	PASS	39	36	113	1	ref	'0/0	113	hom	'1/1	104
9	102666841	rs245743812	G	A	.	.	216	PASS	36	27	104	1	ref	'0/0	104	hom	'1/1	77
9	106888870	rs3090276	C	T	.	.	216	PASS	36	28	104	1	ref	'0/0	104	hom	'1/1	80
9	107126333	rs46846782	G	C	.	.	216	PASS	36	30	104	1	ref	'0/0	104	hom	'1/1	86
9	110898311	rs239574196	G	A	.	.	216	PASS	36	36	104	1	hom	'1/1	104	ref	'0/0	104
9	111860605	rs217886659	G	A	.	.	216	PASS	38	30	110	1	ref	'0/0	110	hom	'1/1	86
9	112904916	rs52544799	T	G	.	.	216	PASS	38	21	110	1	ref	'0/0	110	hom	'1/1	59
9	118668402	rs50594159	C	T	.	.	216	PASS	37	30	107	1	ref	'0/0	107	hom	'1/1	86
9	124063484	rs238351190	A	T	.	.	216	PASS	38	38	111	0.973684	hom	'1/1	69	ref	'0/0	111
10	3819432	rs1315775	G	A	T	.	216	PASS	49	37	127	1	ref	'0/0	127	hom	'1/1	107
10	9210791	rs45892832	C	T	.	.	216	PASS	38	20	110	1	ref	'0/0	110	hom	'1/1	56
10	9877566	rs38110850	C	G	.	.	216	PASS	33	24	95	1	ref	'0/0	95	hom	'1/1	68
10	12751142	rs33564984	G	A	.	.	216	PASS	38	23	110	1	ref	'0/0	110	hom	'1/1	65
10	15095473	rs50097524	T	G	.	.	216	PASS	44	34	127	1	ref	'0/0	127	hom	'1/1	98
10	16164894	rs258201971	T	C	.	.	216	PASS	36	25	104	1	hom	'1/1	104	ref	'0/0	71
10	16460528	rs46218141	C	T	.	.	216	PASS	42	40	122	1	ref	'0/0	122	hom	'1/1	116
10	21089073	rs51998661	G	C	.	.	216	PASS	30	25	86	1	ref	'0/0	86	hom	'1/1	71
10	23070257	rs228396158	T	C	.	.	216	PASS	45	36	127	1	hom	'1/1	127	ref	'0/0	104
10	24502545	rs33688332	C	A	.	.	216	PASS	44	32	127	1	ref	'0/0	127	hom	'1/1	92
10	25416558	rs50315385	C	A	.	.	216	PASS	38	23	110	1	ref	'0/0	110	hom	'1/1	65
10	34212239	rs37418983	G	A	.	.	216	PASS	40	31	116	1	ref	'0/0	89	hom	'1/1	116
10	52250539	rs240783938	C	T	.	.	216	PASS	28	27	80	1	hom	'1/1	77	ref	'0/0	80
10	62235472	rs46748961	C	T	.	.	216	PASS	33	24	95	1	ref	'0/0	95	hom	'1/1	68
10	67376722	rs50369116	G	A	.	.	216	PASS	38	21	110	1	ref	'0/0	110	hom	'1/1	59
10	72220313	rs36839385	G	T	.	.	216	PASS	42	40	122	1	ref	'0/0	116	hom	'1/1	122
10	72375061	rs52109112	G	C	.	.	216	PASS	20	19	56	1	ref	'0/0	53	hom	'1/1	56
10	75952689	rs3165931	A	C	.	.	216	PASS	34	26	98	1	ref	'0/0	98	hom	'1/1	74
10	76999094	rs387046283	G	A	.	.	216	PASS	27	21	60	0.962963	ref	'0/0	50	hom	'1/1	60
10	80223571	rs243895528	G	T	.	.	216	PASS	42	24	122	1	hom	'1/1	122	ref	'0/0	68
10	84055908	rs46034478	C	T	.	.	216	PASS	29	21	83	1	ref	'0/0	83	hom	'1/1	59
10	84067952	rs46286019	G	T	.	.	216	PASS	35	26	101	1	ref	'0/0	74	hom	'1/1	101
10	86764013	rs245651895	C	T	.	.	216	PASS	37	33	107	1	ref	'0/0	107	hom	'1/1	95
10	88402761	rs213732726	C	A	.	.	216	PASS	42	42	122	1	ref	'0/0	122	hom	'1/1	122
10	94581490	rs259864177	T	A	G	.	216	PASS	45	27	78	0.933333	hom	'1/1	67	ref	'0/0	78
10	95829070	rs48840444	T	C	.	.	216	PASS	41	24	119	1	ref	'0/0	119	hom	'1/1	68
10	100538164	rs47483530	T	A	.	.	216	PASS	43	31	125	1	ref	'0/0	125	hom	'1/1	89

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
10	117184703	rs30920857	G	A	.	.	216	PASS	39	33	113	1	ref	'0/0	113	hom	'1/1	95
10	118900016	rs46363841	G	A	.	.	216	PASS	39	27	113	1	ref	'0/0	113	hom	'1/1	77
10	120961461	rs233492562	A	G	.	.	216	PASS	34	33	98	1	ref	'0/0	98	hom	'1/1	95
10	123892079	rs47400063	G	T	.	.	216	PASS	38	27	110	1	ref	'0/0	110	hom	'1/1	77
10	126337830	rs50489160	T	C	A	G	216	PASS	43	23	103	1	ref	'0/0	103	hom	'1/1	65
10	128178363	rs266246994	G	T	.	.	216	PASS	39	30	113	1	hom	'1/1	113	ref	'0/0	86
11	7837037	rs50412292	G	T	.	.	216	PASS	27	27	77	1	hom	'1/1	77	ref	'0/0	77
11	10446926	rs244197713	A	T	.	.	216	PASS	18	18	50	1	hom	'1/1	50	ref	'0/0	50
11	12807379	rs258946751	A	T	.	.	216	PASS	38	28	110	1	hom	'1/1	80	ref	'0/0	110
11	13743601	rs26833083	G	A	.	.	216	PASS	41	32	119	1	ref	'0/0	119	hom	'1/1	92
11	26301424	rs48929260	T	A	.	.	216	PASS	38	20	110	1	hom	'1/1	110	ref	'0/0	56
11	35661735	rs26912518	T	C	.	.	216	PASS	40	34	116	1	ref	'0/0	116	hom	'1/1	98
11	41829250	rs252479362	A	G	.	.	216	PASS	40	30	116	1	hom	'1/1	116	ref	'0/0	86
11	43681095	rs29433568	T	C	.	.	216	PASS	48	23	127	1	ref	'0/0	127	hom	'1/1	65
11	43974537	rs28184616	C	A	.	.	216	PASS	36	35	104	1	ref	'0/0	101	hom	'1/1	104
11	53569966	rs246684100	T	A	.	.	216	PASS	33	31	95	1	ref	'0/0	95	hom	'1/1	89
11	65312557	rs220626677	G	A	.	.	216	PASS	40	28	116	1	hom	'1/1	116	ref	'0/0	80
11	67042192	rs26937249	G	A	.	.	216	PASS	30	27	86	1	ref	'0/0	86	hom	'1/1	77
11	68525063	rs231300394	A	T	.	.	216	PASS	42	24	122	1	ref	'0/0	122	hom	'1/1	68
11	75621518	rs26901122	G	C	.	.	216	PASS	45	30	127	1	ref	'0/0	86	hom	'1/1	127
11	75971456	rs256807874	G	A	.	.	216	PASS	35	20	101	1	ref	'0/0	101	hom	'1/1	56
11	79168378	rs219511820	T	C	.	.	216	PASS	37	31	108	0.967742	ref	'0/0	67	hom	'1/1	108
11	79630725	rs28228682	G	A	.	.	216	PASS	32	25	92	1	ref	'0/0	92	hom	'1/1	71
11	84000380	rs219960376	G	A	.	.	216	PASS	34	26	98	1	ref	'0/0	98	hom	'1/1	74
11	92606217	rs252587388	C	T	.	.	216	PASS	42	38	122	1	hom	'1/1	122	ref	'0/0	110
11	96123497	rs29485410	C	G	.	.	216	PASS	30	29	86	1	ref	'0/0	86	hom	'1/1	83
11	97912759	rs29395731	T	C	.	.	216	PASS	37	30	107	1	ref	'0/0	107	hom	'1/1	86
11	104153227	rs238676928	C	T	.	.	216	PASS	42	29	122	1	hom	'1/1	122	ref	'0/0	83
11	106740655	rs387268848	A	G	.	.	216	PASS	35	18	101	1	ref	'0/0	101	hom	'1/1	50
11	107706333	rs27039723	G	A	.	.	216	PASS	36	35	104	1	ref	'0/0	101	hom	'1/1	104
11	108941461	rs253387530	A	T	.	.	216	PASS	32	22	92	1	ref	'0/0	92	hom	'1/1	62
11	113257856	rs27052405	C	T	.	.	216	PASS	45	37	127	1	ref	'0/0	127	hom	'1/1	107
11	121160359	rs27014504	C	T	.	.	216	PASS	44	35	127	1	ref	'0/0	127	hom	'1/1	101
12	10354244	rs52595370	A	G	.	.	216	PASS	41	20	119	1	ref	'0/0	119	hom	'1/1	56
12	11853935	rs46528175	A	G	.	.	216	PASS	31	28	89	1	ref	'0/0	80	hom	'1/1	89
12	12671094	rs47724108	G	A	.	.	216	PASS	35	28	101	1	ref	'0/0	101	hom	'1/1	80
12	34559495	rs220141110	G	A	.	.	216	PASS	39	30	97	0.974359	hom	'1/1	97	ref	'0/0	87
12	36074032	rs227207997	A	G	C	.	216	PASS	41	28	119	1	hom	'1/1	119	ref	'0/0	73
12	37027619	rs231844185	A	G	.	.	216	PASS	43	35	125	1	hom	'1/1	125	ref	'0/0	101
12	42455266	rs36483996	A	T	.	.	216	PASS	45	25	127	1	hom	'1/1	127	ref	'0/0	71
12	50761473	rs46932694	G	A	.	.	216	PASS	40	26	116	1	ref	'0/0	116	hom	'1/1	74

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
12	53100482	rs52450796	G	T	.	.	216	PASS	33	30	87	0.969697	hom	'1/1	87	ref	'0/0	54
12	63227700	rs49407974	A	C	.	.	216	PASS	27	26	77	1	ref	'0/0	77	hom	'1/1	74
12	67348149	rs387717100	G	C	.	.	216	PASS	39	24	113	1	ref	'0/0	113	hom	'1/1	68
12	67965792	rs48970875	G	A	.	.	216	PASS	41	35	119	1	ref	'0/0	119	hom	'1/1	101
12	68506399	rs37803925	A	C	.	.	216	PASS	48	23	127	1	ref	'0/0	127	hom	'1/1	65
12	74556530	rs222221505	G	A	.	.	216	PASS	36	32	104	1	hom	'1/1	92	ref	'0/0	104
12	82070543	rs217858050	C	G	.	.	216	PASS	43	26	125	1	ref	'0/0	125	hom	'1/1	74
12	82417244	rs46138386	G	A	.	.	216	PASS	28	21	80	1	ref	'0/0	80	hom	'1/1	59
12	92012865	rs51364971	C	T	.	.	216	PASS	39	28	113	1	ref	'0/0	113	hom	'1/1	80
12	96873048	rs217730163	C	T	.	.	216	PASS	35	32	101	1	ref	'0/0	92	hom	'1/1	101
12	97231894	rs48185879	A	T	.	.	216	PASS	44	42	127	1	ref	'0/0	122	hom	'1/1	127
12	103692308	rs256091453	G	A	.	.	216	PASS	38	32	110	1	hom	'1/1	110	ref	'0/0	92
12	107133347	rs47357454	A	C	.	.	216	PASS	32	19	92	1	ref	'0/0	92	hom	'1/1	53
12	108713594	rs256606757	C	G	.	.	216	PASS	31	22	89	1	ref	'0/0	89	hom	'1/1	62
12	117184038	rs46624656	A	G	.	.	216	PASS	36	22	104	1	ref	'0/0	104	hom	'1/1	62
12	118192234	rs247716364	G	A	.	.	216	PASS	54	38	127	1	hom	'1/1	127	ref	'0/0	110
13	3129814	rs228063905	C	G	.	.	216	PASS	30	20	86	1	hom	'1/1	56	ref	'0/0	86
13	3695139	rs33751539	C	A	.	.	216	PASS	39	33	113	1	hom	'1/1	113	ref	'0/0	95
13	4130880	rs247174880	T	A	.	.	216	PASS	45	31	127	1	hom	'1/1	127	ref	'0/0	89
13	7176600	rs221434430	A	T	.	.	216	PASS	59	30	127	1	hom	'1/1	127	ref	'0/0	86
13	9410008	rs220454449	G	T	.	.	216	PASS	42	32	122	1	ref	'0/0	122	hom	'1/1	92
13	12499856	rs242058966	G	C	.	.	216	PASS	33	26	95	1	hom	'1/1	95	ref	'0/0	74
13	23544520	rs248730029	T	C	.	.	216	PASS	42	37	122	1	hom	'1/1	122	ref	'0/0	107
13	23544598	rs239725425	A	G	.	.	216	PASS	30	29	86	1	hom	'1/1	86	ref	'0/0	83
13	24986028	rs29965851	T	A	.	.	216	PASS	42	32	122	1	ref	'0/0	122	hom	'1/1	92
13	26885215	rs264973936	C	T	.	.	216	PASS	51	37	127	1	ref	'0/0	127	hom	'1/1	107
13	29931480	rs238929889	C	T	.	.	216	PASS	49	32	127	1	hom	'1/1	127	ref	'0/0	92
13	30298620	rs29994255	G	A	.	.	216	PASS	30	27	86	1	ref	'0/0	86	hom	'1/1	77
13	31082160	rs29951681	G	A	.	.	216	PASS	40	34	116	1	ref	'0/0	116	hom	'1/1	98
13	32753433	rs29899219	C	T	.	.	216	PASS	46	31	127	1	ref	'0/0	127	hom	'1/1	89
13	38015953	rs256731445	C	T	.	.	216	PASS	46	37	127	1	ref	'0/0	107	hom	'1/1	127
13	47347952	rs3670873	T	C	.	.	216	PASS	40	38	116	1	ref	'0/0	116	hom	'1/1	110
13	55937833	rs37974622	G	A	.	.	216	PASS	38	34	110	1	ref	'0/0	110	hom	'1/1	98
13	57251342	rs3675448	A	T	.	.	216	PASS	48	28	127	1	ref	'0/0	127	hom	'1/1	80
13	59808311	rs30245925	C	T	.	.	216	PASS	51	30	127	1	ref	'0/0	127	hom	'1/1	86
13	68635207	rs241520077	T	C	.	.	216	PASS	25	18	71	1	ref	'0/0	71	hom	'1/1	50
13	73964396	rs50053913	G	A	.	.	216	PASS	39	38	113	1	ref	'0/0	110	hom	'1/1	113
13	79663216	rs46521972	A	G	.	.	216	PASS	34	34	98	1	ref	'0/0	98	hom	'1/1	98
13	81557548	rs47717539	C	T	.	.	216	PASS	37	35	107	1	ref	'0/0	107	hom	'1/1	101
13	81845203	rs108701696	C	T	.	.	216	PASS	40	31	116	1	ref	'0/0	116	hom	'1/1	89
13	82720342	rs29545181	C	T	.	.	216	PASS	22	19	62	1	ref	'0/0	62	hom	'1/1	53

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
13	94758861	rs6228868	G	A	.	.	216	PASS	46	37	127	1	hom	'1/1	127	ref	'0/0	107
13	96217840	rs30393973	G	A	.	.	216	PASS	48	32	127	1	ref	'0/0	127	hom	'1/1	92
13	98315679	rs247608036	T	A	.	.	216	PASS	38	32	110	1	ref	'0/0	110	hom	'1/1	92
13	98686419	rs49588229	T	C	.	.	216	PASS	36	32	104	1	hom	'1/1	104	ref	'0/0	92
13	99554222	rs46550497	T	C	.	.	216	PASS	38	25	110	1	ref	'0/0	110	hom	'1/1	71
13	100028363	rs264775280	C	T	.	.	216	PASS	32	23	92	1	hom	'1/1	92	ref	'0/0	65
13	113127661	rs38228777	G	C	.	.	216	PASS	47	31	127	1	ref	'0/0	89	hom	'1/1	127
13	116931059	rs52640134	T	A	.	.	216	PASS	43	32	93	0.976744	ref	'0/0	88	hom	'1/1	93
14	8335825	rs51648802	G	A	.	.	216	PASS	37	33	107	1	ref	'0/0	107	hom	'1/1	95
14	13403026	rs48403135	T	C	G	.	216	PASS	40	33	116	0.969697	ref	'0/0	116	hom	'1/1	74
14	20617086	rs239554725	A	C	.	.	216	PASS	26	25	74	1	ref	'0/0	71	hom	'1/1	74
14	25857244	rs47680887	A	G	.	.	216	PASS	46	42	127	1	ref	'0/0	122	hom	'1/1	127
14	31639398	rs386883218	G	T	.	.	216	PASS	30	23	86	1	hom	'1/1	86	ref	'0/0	65
14	36097291	rs242364690	C	A	.	.	216	PASS	24	21	68	1	hom	'1/1	68	ref	'0/0	59
14	43532850	rs108192464	T	G	.	.	105	PASS	32	20	92	1	hom	'1/1	56	ref	'0/0	92
14	43532864	rs108406047	C	G	.	.	104	PASS	33	21	95	1	hom	'1/1	59	ref	'0/0	95
14	43552527	rs51274449	C	A	.	.	216	PASS	31	28	89	1	hom	'1/1	80	ref	'0/0	89
14	43552528	rs47617963	C	A	.	.	216	PASS	31	29	84	0.935484	hom	'1/1	84	ref	'0/0	63
14	47914590	rs52606141	C	T	.	.	485	PASS	88	32	71	0.647727	hom	'1/1	56	hom	'1/1	71
14	47914596	rs52638251	T	C	.	.	485	PASS	89	37	68	0.655937	hom	'1/1	68	hom	'1/1	68
14	48130422	rs50148147	T	C	.	.	216	PASS	41	28	119	1	ref	'0/0	119	hom	'1/1	80
14	57516793	rs238514853	G	A	.	.	216	PASS	37	30	107	1	ref	'0/0	107	hom	'1/1	86
14	60411112	rs256056286	G	T	.	.	216	PASS	41	30	119	1	hom	'1/1	119	ref	'0/0	86
14	60647829	rs48443156	G	A	.	.	216	PASS	35	31	101	1	ref	'0/0	89	hom	'1/1	101
14	64022286	rs46892447	C	T	.	.	216	PASS	38	34	110	1	ref	'0/0	110	hom	'1/1	98
14	68609485	rs250593334	G	T	.	.	216	PASS	41	26	119	1	ref	'0/0	119	hom	'1/1	74
14	71470170	rs49372183	C	T	G	.	216	PASS	41	39	119	1	ref	'0/0	107	hom	'1/1	119
14	80821585	rs32226962	A	G	.	.	216	PASS	39	39	113	1	ref	'0/0	113	hom	'1/1	113
14	89765727	rs50770527	G	T	.	.	216	PASS	38	31	110	1	ref	'0/0	110	hom	'1/1	89
14	102753134	rs46012433	T	A	.	.	216	PASS	38	27	110	1	ref	'0/0	110	hom	'1/1	77
14	105646313	rs32462757	A	G	.	.	216	PASS	49	44	127	1	ref	'0/0	127	hom	'1/1	127
14	105704806	rs230001936	G	A	.	.	216	PASS	34	29	98	1	hom	'1/1	83	ref	'0/0	98
14	108719712	rs32526187	T	G	.	.	216	PASS	49	28	127	1	ref	'0/0	127	hom	'1/1	80
14	114639187	rs37323869	T	C	.	.	216	PASS	35	26	101	1	ref	'0/0	101	hom	'1/1	74
14	115379185	rs52573470	G	A	T	.	216	PASS	33	28	85	1	ref	'0/0	85	hom	'1/1	80
14	116111561	rs36535586	C	A	.	.	216	PASS	34	30	98	1	ref	'0/0	98	hom	'1/1	86
14	116765765	rs51211980	C	A	.	.	216	PASS	48	33	127	1	ref	'0/0	127	hom	'1/1	95
14	117785511	rs257863326	G	A	.	.	216	PASS	50	35	127	1	hom	'1/1	127	ref	'0/0	101
14	118423789	rs259356467	G	A	.	.	216	PASS	25	22	71	1	hom	'1/1	71	ref	'0/0	62
14	119708943	rs50743474	C	T	.	.	216	PASS	42	39	122	1	ref	'0/0	122	hom	'1/1	113
14	122408099	rs250760885	C	A	.	.	216	PASS	40	21	116	1	hom	'1/1	116	ref	'0/0	59

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
15	7190183	rs48122948	G	C	.	.	216	PASS	36	28	104	1	ref	'0/0	104	hom	'1/1	80
15	10026112	rs236638439	T	C	.	.	216	PASS	52	29	127	1	ref	'0/0	127	hom	'1/1	83
15	10516111	rs32273106	G	T	.	.	216	PASS	34	18	98	1	ref	'0/0	98	hom	'1/1	50
15	11069856	rs38439071	G	A	.	.	216	PASS	53	27	127	1	ref	'0/0	127	hom	'1/1	77
15	11414913	rs258125614	C	G	.	.	216	PASS	46	29	127	1	hom	'1/1	127	ref	'0/0	83
15	12501896	rs48384730	A	G	.	.	216	PASS	41	32	119	1	ref	'0/0	119	hom	'1/1	92
15	14006567	rs52674191	C	T	.	.	216	PASS	41	34	120	0.970588	ref	'0/0	120	hom	'1/1	66
15	18032782	rs49712433	G	C	.	.	216	PASS	44	27	127	1	ref	'0/0	127	hom	'1/1	77
15	25559323	rs217703620	C	A	.	.	216	PASS	44	26	127	1	hom	'1/1	127	ref	'0/0	74
15	28043699	rs13482496	A	C	T	.	216	PASS	30	29	60	0.89885	hom	'1/1	60	ref	'0/0	57
15	32323386	rs212086590	C	T	.	.	216	PASS	39	29	84	0.974359	ref	'0/0	72	hom	'1/1	84
15	34435619	rs49081993	A	G	.	.	216	PASS	59	32	127	1	ref	'0/0	127	hom	'1/1	92
15	59093635	rs37014273	G	A	.	.	216	PASS	49	31	127	1	ref	'0/0	127	hom	'1/1	89
15	59204839	rs220101808	C	T	.	.	216	PASS	36	30	104	1	hom	'1/1	104	ref	'0/0	86
15	64005893	rs46751988	C	T	.	.	216	PASS	48	39	127	1	ref	'0/0	127	hom	'1/1	113
15	70739799	rs237090736	T	G	.	.	216	PASS	43	20	84	0.976744	hom	'1/1	84	ref	'0/0	57
15	70805615	rs31366958	C	A	.	.	216	PASS	44	34	127	1	ref	'0/0	127	hom	'1/1	98
15	72172011	rs52423063	T	G	.	.	216	PASS	37	29	84	0.972973	hom	'1/1	70	ref	'0/0	84
15	73419059	rs31604589	A	G	C	.	216	PASS	59	31	91	0.949153	hom	'1/1	91	ref	'0/0	90
15	78507275	rs32007597	T	G	.	.	216	PASS	46	28	93	0.978261	hom	'1/1	93	ref	'0/0	81
15	81967993	rs231324156	C	T	.	.	216	PASS	41	23	119	1	ref	'0/0	119	hom	'1/1	65
15	86260798	rs47473718	T	C	.	.	216	PASS	44	25	127	1	ref	'0/0	127	hom	'1/1	71
15	86543747	rs31649049	T	C	.	.	216	PASS	38	24	110	1	hom	'1/1	110	ref	'0/0	68
15	88087198	rs37550565	C	T	.	.	216	PASS	39	36	113	1	ref	'0/0	113	hom	'1/1	104
15	91061394	rs214420689	C	T	.	.	216	PASS	53	29	127	1	hom	'1/1	127	ref	'0/0	83
15	92380149	rs32043533	C	G	.	.	216	PASS	50	34	127	1	ref	'0/0	127	hom	'1/1	98
15	93642519	rs38263969	G	A	.	.	216	PASS	64	28	127	1	ref	'0/0	127	hom	'1/1	80
15	96255426	rs46248036	C	T	A	.	216	PASS	36	29	98	1	ref	'0/0	98	hom	'1/1	83
16	13645760	rs49608214	A	G	.	.	216	PASS	43	30	125	1	hom	'1/1	125	ref	'0/0	86
16	19884827	rs51951853	G	A	.	.	216	PASS	38	22	110	1	hom	'1/1	110	ref	'0/0	62
16	27273066	rs46365721	A	G	.	.	216	PASS	46	38	127	1	ref	'0/0	127	hom	'1/1	110
16	35115316	rs233402455	A	C	.	.	216	PASS	35	21	101	1	hom	'1/1	101	ref	'0/0	59
16	35556433	rs46364658	C	T	.	.	216	PASS	45	30	127	1	ref	'0/0	127	hom	'1/1	86
16	42097379	rs45858550	T	A	.	.	216	PASS	31	30	89	1	ref	'0/0	89	hom	'1/1	86
16	43921141	rs4179366	C	A	.	.	216	PASS	41	39	114	0.97561	hom	'1/1	78	ref	'0/0	114
16	45673176	rs51592990	C	T	.	.	216	PASS	37	22	107	1	ref	'0/0	107	hom	'1/1	62
16	49656310	rs32804033	C	T	.	.	216	PASS	41	31	119	1	hom	'1/1	119	ref	'0/0	89
16	53282227	rs49448180	C	G	.	.	216	PASS	29	29	83	1	ref	'0/0	83	hom	'1/1	83
16	57620150	rs214808419	C	T	.	.	216	PASS	38	30	110	1	ref	'0/0	86	hom	'1/1	110
16	66087347	rs50933320	C	T	.	.	216	PASS	36	32	104	1	ref	'0/0	104	hom	'1/1	92
16	68688649	rs49745559	G	A	.	.	216	PASS	37	33	107	1	ref	'0/0	107	hom	'1/1	95

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
16	72792281	rs218420480	A	G	.	.	216	PASS	41	28	119	1	hom	'1/1	119	ref	'0/0	80
16	75889013	rs52329919	T	C	.	.	216	PASS	51	36	127	1	ref	'0/0	127	hom	'1/1	104
16	83959602	rs254664546	G	A	.	.	216	PASS	32	25	92	1	hom	'1/1	92	ref	'0/0	71
16	88590384	rs227119859	A	T	.	.	216	PASS	30	20	60	0.933333	hom	'1/1	60	ref	'0/0	57
16	92082063	rs259353807	A	T	.	.	216	PASS	36	33	104	1	hom	'1/1	104	ref	'0/0	95
17	9056643	rs49061265	G	A	.	.	216	PASS	43	30	125	1	ref	'0/0	125	hom	'1/1	86
17	10135313	rs33699267	C	T	.	.	216	PASS	48	23	127	1	ref	'0/0	127	hom	'1/1	65
17	11621478	rs46437325	G	A	.	.	216	PASS	48	33	127	1	ref	'0/0	127	hom	'1/1	95
17	19721915	rs108548807	G	A	.	.	216	PASS	53	33	127	1	hom	'1/1	127	ref	'0/0	95
17	23188749	rs33555086	G	T	.	.	216	PASS	24	23	68	1	hom	'1/1	68	ref	'0/0	65
17	31420638	rs33260077	A	T	.	.	216	PASS	32	29	92	1	hom	'1/1	92	ref	'0/0	83
17	42228319	rs219847693	T	C	.	.	216	PASS	46	34	127	1	hom	'1/1	127	ref	'0/0	98
17	44538706	rs45641253	C	A	.	.	216	PASS	47	28	127	1	ref	'0/0	127	hom	'1/1	80
17	44976738	rs108113117	T	G	.	.	216	PASS	54	36	127	0.972222	ref	'0/0	127	hom	'1/1	63
17	56566247	rs49680121	A	G	.	.	216	PASS	35	25	101	1	ref	'0/0	101	hom	'1/1	71
17	59446314	rs214810053	G	A	.	.	216	PASS	46	37	127	1	ref	'0/0	127	hom	'1/1	107
17	66564370	rs47756538	C	T	.	.	216	PASS	45	34	127	1	ref	'0/0	127	hom	'1/1	98
17	67094147	rs52268730	C	T	.	.	216	PASS	27	19	55	0.962963	ref	'0/0	55	hom	'1/1	54
17	67591109	rs48913588	C	T	.	.	216	PASS	55	23	127	1	ref	'0/0	127	hom	'1/1	65
17	67950470	rs48051517	C	G	.	.	216	PASS	52	32	127	1	ref	'0/0	127	hom	'1/1	92
17	69019613	rs261882790	T	C	.	.	216	PASS	58	28	127	1	hom	'1/1	127	ref	'0/0	80
17	70342725	rs108204495	T	C	.	.	216	PASS	42	19	122	1	ref	'0/0	122	hom	'1/1	53
17	73160648	rs49487329	G	A	.	.	216	PASS	48	38	127	1	ref	'0/0	127	hom	'1/1	110
17	74131993	rs49070013	A	G	.	.	216	PASS	45	30	127	1	ref	'0/0	127	hom	'1/1	86
17	75210479	rs51511802	A	G	.	.	216	PASS	48	26	127	1	ref	'0/0	127	hom	'1/1	74
17	78020032	rs6407946	G	A	.	.	216	PASS	50	39	114	0.98	hom	'1/1	106	ref	'0/0	114
17	78451429	rs47455721	G	A	.	.	216	PASS	55	30	127	1	ref	'0/0	127	hom	'1/1	86
17	79733867	rs262917772	C	T	.	.	216	PASS	37	22	107	1	hom	'1/1	107	ref	'0/0	62
17	84940572	rs48027427	C	T	.	.	216	PASS	45	34	127	1	ref	'0/0	127	hom	'1/1	98
17	88559741	rs107954045	C	T	.	.	216	PASS	37	32	107	1	hom	'1/1	107	ref	'0/0	92
17	93444664	rs47460807	G	A	.	.	216	PASS	68	29	127	1	ref	'0/0	127	hom	'1/1	83
18	18641575	rs30066083	T	A	.	.	216	PASS	52	30	127	1	hom	'1/1	127	ref	'0/0	86
18	26365873	rs231659997	T	G	.	.	216	PASS	48	30	127	1	ref	'0/0	127	hom	'1/1	86
18	28122298	rs51512767	A	T	.	.	216	PASS	44	36	127	1	ref	'0/0	127	hom	'1/1	104
18	30033468	rs221424480	C	T	.	.	216	PASS	39	26	113	1	hom	'1/1	113	ref	'0/0	74
18	36397012	rs217929804	C	T	.	.	216	PASS	37	26	107	1	ref	'0/0	107	hom	'1/1	74
18	36997793	rs31785839	T	C	.	.	216	PASS	49	42	127	1	ref	'0/0	127	hom	'1/1	122
18	41926761	rs29577484	C	T	G	.	216	PASS	36	33	95	0.972222	ref	'0/0	95	hom	'1/1	94
18	45924694	rs233382385	G	A	.	.	216	PASS	35	29	101	1	hom	'1/1	83	ref	'0/0	101
18	46996042	rs213994779	T	A	.	.	216	PASS	38	21	110	1	ref	'0/0	110	hom	'1/1	59
18	47707879	rs52077802	C	T	.	.	216	PASS	31	30	89	1	ref	'0/0	89	hom	'1/1	86

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
18	51216899	rs32064100	A	C	.	.	216	PASS	47	35	127	1	ref	'0/0	127	hom	'1/1	101
18	56780725	rs49288101	A	T	.	.	216	PASS	41	36	119	1	ref	'0/0	119	hom	'1/1	104
18	58340097	rs50022537	C	T	.	.	216	PASS	39	19	113	1	ref	'0/0	113	hom	'1/1	53
18	59385726	rs39281136	C	T	.	.	216	PASS	35	29	101	1	ref	'0/0	101	hom	'1/1	83
18	64460427	rs3656801	G	A	.	.	216	PASS	34	34	98	1	ref	'0/0	98	hom	'1/1	98
18	72865153	rs245979437	G	A	.	.	216	PASS	41	28	119	1	ref	'0/0	119	hom	'1/1	80
18	73293017	rs36513585	G	A	.	.	216	PASS	35	29	101	1	ref	'0/0	101	hom	'1/1	83
18	76592701	rs240414938	T	A	.	.	216	PASS	35	26	75	0.971429	hom	'1/1	74	ref	'0/0	75
18	79153526	rs48780231	C	T	.	.	216	PASS	41	33	119	1	ref	'0/0	119	hom	'1/1	95
18	80639140	rs36316588	C	T	.	.	216	PASS	35	24	101	1	ref	'0/0	68	hom	'1/1	101
18	80740351	rs36475616	T	C	.	.	216	PASS	47	34	127	1	ref	'0/0	127	hom	'1/1	98
18	81336492	rs30302013	T	G	.	.	216	PASS	54	25	127	1	ref	'0/0	127	hom	'1/1	71
18	81816685	rs49605357	G	A	.	.	216	PASS	42	32	122	1	ref	'0/0	122	hom	'1/1	92
18	88972013	rs37481649	T	A	.	.	216	PASS	32	28	92	1	ref	'0/0	92	hom	'1/1	80
18	89452136	rs37625494	T	G	.	.	216	PASS	38	27	110	1	ref	'0/0	110	hom	'1/1	77
19	5527218	rs36448887	G	A	.	.	216	PASS	46	34	127	1	ref	'0/0	127	hom	'1/1	98
19	13740321	rs37039649	G	A	.	.	216	PASS	36	31	104	1	ref	'0/0	89	hom	'1/1	104
19	15510092	rs38082986	G	A	.	.	216	PASS	39	29	113	1	ref	'0/0	113	hom	'1/1	83
19	15952552	rs37941728	C	T	.	.	216	PASS	39	39	113	1	ref	'0/0	113	hom	'1/1	113
19	23066782	rs36801652	A	T	.	.	216	PASS	33	24	95	1	ref	'0/0	95	hom	'1/1	68
19	23771912	rs237588533	A	C	.	.	216	PASS	30	19	86	1	ref	'0/0	86	hom	'1/1	53
19	25710853	rs36398811	A	G	.	.	216	PASS	51	38	127	1	ref	'0/0	127	hom	'1/1	110
19	26256902	rs241930050	G	T	.	.	216	PASS	44	35	127	1	hom	'1/1	101	ref	'0/0	127
19	29479336	rs36270423	C	T	.	.	216	PASS	42	31	122	1	ref	'0/0	122	hom	'1/1	89
19	31420825	rs242369407	C	G	.	.	216	PASS	40	20	116	1	ref	'0/0	116	hom	'1/1	56
19	32670321	rs50157060	T	C	.	.	216	PASS	43	25	125	1	ref	'0/0	125	hom	'1/1	71
19	32790171	rs387033292	T	C	.	.	216	PASS	33	20	68	0.969697	ref	'0/0	68	hom	'1/1	57
19	32790176	rs387357285	T	C	.	.	216	PASS	36	18	104	1	ref	'0/0	104	hom	'1/1	50
19	43084404	rs234619193	T	A	.	.	216	PASS	24	23	68	1	hom	'1/1	65	ref	'0/0	68
19	44139638	rs37451432	C	T	.	.	216	PASS	48	38	127	1	ref	'0/0	127	hom	'1/1	110
19	45443117	rs36495646	A	G	.	.	216	PASS	48	33	127	1	ref	'0/0	127	hom	'1/1	95
19	48414829	rs39191877	G	A	.	.	216	PASS	39	26	113	1	ref	'0/0	113	hom	'1/1	74
19	52180917	rs30317757	G	T	.	.	216	PASS	44	34	127	1	hom	'1/1	127	ref	'0/0	98
19	55966563	rs52222666	G	A	.	.	216	PASS	29	26	83	1	ref	'0/0	74	hom	'1/1	83
19	56830344	rs48624001	C	T	.	.	216	PASS	46	29	127	1	ref	'0/0	127	hom	'1/1	83
X	6183969	rs33287577	T	A	.	.	216	PASS	31	23	89	1	ref	'0/0	65	hom	'1/1	89
X	12894308	rs33650613	A	G	.	.	216	PASS	41	29	119	1	ref	'0/0	83	hom	'1/1	119
X	36087149	rs241896460	C	A	.	.	216	PASS	49	22	127	1	ref	'0/0	127	hom	'1/1	62
X	44778119	rs30035452	A	C	.	.	216	PASS	31	26	89	1	ref	'0/0	74	hom	'1/1	89
X	49381844	rs30219482	C	A	.	.	216	PASS	30	25	86	1	ref	'0/0	86	hom	'1/1	71
X	50053833	rs262394336	G	A	.	.	216	PASS	40	28	116	1	hom	'1/1	116	ref	'0/0	80

Supplementary Table 3. (Continued)

VCF information									Filtering		Additional filtering information		BALB/cA data			BALB/cByJ data		
Chr	Position	dbSNP_ID	Reference ALT	ALT 1	ALT 2	ALT 3	PGQ	Filter	MAX coverage	MIN coverage	MAX PGQ	MAX \angle AF (ALT 1, 2, 3)	Genotype	Genotype Info	PGQ	Genotype	Genotype Info	PGQ
X	50687650	rs232857079	A	C	.	.	216	PASS	33	30	95	1	ref	'0/0	95	hom	'1/1	86
X	56642959	rs31753589	G	A	.	.	216	PASS	47	27	127	1	ref	'0/0	127	hom	'1/1	77
X	57727688	rs31751875	T	C	.	.	216	PASS	34	32	98	1	ref	'0/0	98	hom	'1/1	92
X	58666776	rs31742615	C	A	.	.	216	PASS	34	27	98	1	ref	'0/0	98	hom	'1/1	77
X	70948771	rs29043150	T	C	.	.	216	PASS	42	30	100	0.97619	ref	'0/0	100	hom	'1/1	87
X	71601755	rs241499720	G	T	.	.	216	PASS	49	21	121	0.979592	ref	'0/0	121	hom	'1/1	60
X	90945156	rs255875402	G	T	.	.	216	PASS	37	23	107	1	hom	'1/1	107	ref	'0/0	65
X	95453076	rs216044861	C	A	.	.	216	PASS	28	21	80	1	ref	'0/0	80	hom	'1/1	59
X	98515983	rs31846526	G	A	.	.	216	PASS	36	26	104	1	ref	'0/0	104	hom	'1/1	74
X	104300680	rs8268104	C	A	.	.	216	PASS	39	34	113	1	ref	'0/0	113	hom	'1/1	98
X	116796513	rs230918346	C	G	T	.	216	PASS	42	31	116	0.97619	hom	'1/1	116	ref	'0/0	89
X	130017439	rs29114761	C	T	.	.	216	PASS	35	30	101	1	ref	'0/0	86	hom	'1/1	101
X	135959876	rs3718396	C	T	.	.	216	PASS	35	29	101	1	ref	'0/0	101	hom	'1/1	83
X	137423419	rs29262799	T	A	.	.	216	PASS	46	30	127	1	ref	'0/0	127	hom	'1/1	86
X	142163467	rs255507481	T	G	.	.	216	PASS	34	30	98	1	ref	'0/0	98	hom	'1/1	86
X	153590175	rs29289503	G	A	.	.	216	PASS	31	18	89	1	ref	'0/0	89	hom	'1/1	50
X	154862172	rs29299426	G	A	.	.	216	PASS	36	19	104	1	ref	'0/0	104	hom	'1/1	53
X	163213983	rs31387209	A	G	.	.	216	PASS	40	26	116	1	ref	'0/0	116	hom	'1/1	74
X	163676553	rs214215451	A	C	.	.	216	PASS	44	24	127	1	hom	'1/1	127	ref	'0/0	68
X	169982238	rs220525550	T	G	.	.	216	PASS	156	80	127	0.935897	hom	'1/1	127	ref	'0/0	127

Supplementary Table 4. Primers for detection of SNPs between BALB/cA and BALB/cByJ substrains

Chr	Marker	dbSNP_ID	Location (bp)	Interval (bp)	Forward primer	Reverse primer
1	<i>D1SNP301</i>	rs33109340	39,118,826	39,118,826	AGCTGGAAGAAACACCTGGA	CAGGCTCACACTTTGCACAT
1	<i>D1SNP302</i>	rs33057227	86,164,663	47,045,837	TGGTTCCAACACTGAAAAGGATGT T	CCCTTTTGTCTCCAGGTAGGTTTTG
1	<i>D1SNP303</i>	rs33365833	123,476,641	37,311,978	TCTTTTCACCCAGGAAGCTG	GGCATAACCAGCATGAGTGAA
1	<i>D1SNP304</i>	rs31397868	165,920,441	42,443,800	GAAATGCTTCCAAAATTTCAATGA ACAA	CTGAAGTCTGGGGAGGAATCCATT G
1	<i>D1SNP305</i>	rs33202907	193,818,635	27,898,194	TGTGAGCCATCCTATGTCCA	ATACAGGTGTCCCCACTCCA
1	Distal end	-	195,471,971	1,653,336	-	-
2	<i>D2SNP301</i>	rs243288053	4,556,370	4,556,370	TCTCTGACTGAGGCTGCTGA	ACACAACCTGGTTCCGAAGG
2	<i>D2SNP302</i>	rs27169047	34,982,524	30,426,154	GCCTATTTGCCACCACAGTT	ACCCTTACCACATCGAGAC
2	<i>D2SNP303</i>	rs27981830	76,807,991	41,825,467	AGGGAAAACCGGACTCACTT	TTTGGCACAGGAATGTGAAA
2	<i>D2SNP304</i>	rs238060283	107,752,240	30,944,249	CCTGACCAAGAAGTGGGATCAAA GG	TCCCTTTTCTGTAGGAATGCTTGG A
2	<i>D2SNP305</i>	rs27250976	141,495,402	33,743,162	TAGGCCAAATCCGTCTGTGT	GAAAATGCTGTTGGGCATT
2	<i>D2SNP306</i>	rs27622613	172,908,627	31,413,225	AGGCAAGCAGAGGTCACAAT	CATCTGCTTGTGGATGGATG
2	Distal end	-	182,113,224	9,204,597	-	-
3	<i>D3SNP301</i>	rs46220062	7,170,339	7,170,339	AGAGGCTGGTGGACTTGAGA	GGTTTATGAGCGGAAATGGA
3	<i>D3SNP302</i>	rs29938481	39,236,366	32,066,027	ACTTGGCTTTGACCCATCTTCCTG A	CAAAACTTCCAGCTGCATGGTCAA G
3	<i>D3SNP303</i>	rs36544985	65,103,756	25,867,390	AACAAAAGACACAGCACATATTT A	CCCTGCTGGCAATTAACACT
3	<i>D3SNP304</i>	rs36506426	102,126,331	37,022,575	CAGGTGAATGGATTGGCTTT	GGTGCTTGTGTGCTTTGGTA
3	<i>D3SNP305</i>	rs221745548	128,705,974	26,579,643	CACAAGCCAGAAAGGGAAAA	TGAGAACCACTCAGCACAGG
3	<i>D3SNP306</i>	rs30857183	156,119,086	27,413,112	GTGTTAAGTATCCCTGCCAGCTCC T	AAAAAGAGGATCATTTTTGGGGAC A
3	Distal end	-	160,039,680	3,920,594	-	-
4	<i>D4SNP301</i>	rs231525592	8,496,142	8,496,142	TACCCAGTTAGTGGAACTGCTTGG A	CATGTGGTGATGACTCCCAATCAT A
4	<i>D4SNP302</i>	rs27767340	39,023,568	30,527,426	TCAAGTTCCTCATCATCCTGCTTTC	AATTTGATTGCCATGGTGTTCAC
4	<i>D4SNP303</i>	rs3706082	65,807,248	26,783,680	CAAAGTGGGAACTCACACACAA GC	CTTGTAATGTGGGGAGGAGGCAAA A
4	<i>D4SNP304</i>	rs28126314	89,786,718	23,979,470	AACCCACATCTGATAAAGGGCTA A	TGAAAACCAAGTAGGGCAATAAG CA
4	<i>D4SNP305</i>	rs27512361	114,423,192	24,636,474	ATCCATAAGTGGGAGCTGTTTCA T	CCTGTCTGCAGCCTATGACTAGGA A
4	<i>D4SNP306</i>	rs32877825	152,532,156	38,108,964	GGAAGGGCTGGGAAAGTAGAAGG TG	CCTATAGAGAGGGGCTGCAGTGTG G
4	Distal end	-	156,508,116	3,975,960	-	-
5	<i>D5SNP301</i>	rs31133755	4,484,697	4,484,697	ATGGGTGTGTCACATCAGAAGGTT T	GAAGACAGACACAGACCTGCACA AA
5	<i>D5SNP302</i>	rs50896597	46,735,635	42,250,938	GCAGTGACATGCGTATCTGAAAAT G	CAACATTTAATTGGGGCTGCCTTA T
5	<i>D5SNP303</i>	rs52019376	74,679,783	27,944,148	GCCCTGGATTACAGACCAATA	CAGGGCATGGATTAGGGTTA
5	<i>D5SNP304</i>	rs31892920	97,815,958	23,136,175	TCAAATGGGCTAAATGTCACCTTC AC	GCTGGGCTGACTGGATGGATATTT T
5	<i>D5SNP305</i>	rs32347776	144,206,289	46,390,331	CCCTTTTCAGGAACACAAGCTCTG G	CCAAGCACTCCTTTGCCCTCTACA C
5	Distal end	-	151,834,684	7,628,395	-	-
6	<i>D6SNP301</i>	rs32502983	5,888,237	5,888,237	ACTCCTCATTCCCACTGAGATTTC C	GGGACAATGCTTTTCCATACACAA A
6	<i>D6SNP302</i>	rs36885644	34,962,165	29,073,928	GGATCAAACCCAGGACTTCA	GAAGAGTGGGCACAGAGACC

Supplementary Table 4. (Continued)

Chr	Marker	dbSNP_ID	Location (bp)	Interval (bp)	Forward primer	Reverse primer
6	<i>D6SNP303</i>	rs216689099	66,893,429	31,931,264	CTTCATGATAGGGGCTGCTG	TCCCTTCCCTTCTTGGTCTT
6	<i>D6SNP304</i>	rs230573527	102,060,516	35,167,087	TTCTCCCCACAGATTCAAACCTTT T	TCACCTCCAATTTCTGCATGCTTAT
6	<i>D6SNP305</i>	rs31952322	137,462,482	35,401,966	TGCTAAATCGAGTCCCTGCT	AGGAGCACACTCGCTCAGTT
6	Distal end	-	149,736,546	12,274,064	-	-
7	<i>D7SNP301</i>	rs32408583	18,101,721	18,101,721	TCTGTTTGGCTGCACAGAATCAAC A	TCCAAGGTGTCTACTTCCCTCCA A
7	<i>D7SNP302</i>	rs32445754	33,410,649	15,308,928	TTCTTGCTCCAGGTTTGCTT	CTTGCCATAAGTATCCCACTCA
7	<i>D7SNP303</i>	rs33056660	63,058,555	29,647,906	AACCACACAAGCATGCAAAC	TTGGTACTGCAAGCCTTCTC
7	<i>D7SNP304</i>	rs31482312	95,928,545	32,869,990	TTCATGACAGGTTGGATTACAGC A	TCGGGGAGACACTATTACATGAGG A
7	<i>D7SNP305</i>	rs51219759	128,474,626	32,546,081	GGTTGATGTCACTGGAAGAATGAC C	ACGAAGGACTTAGGGAGACAAGG TG
7	Distal end	-	145,441,459	16,966,833	-	-
8	<i>D8SNP301</i>	rs47376668	4,539,352	4,539,352	TTGTCTGCATCAGGTCAAGG	AGGAGGGAATTGGGAAAATG
8	<i>D8SNP302</i>	rs30733023	39,797,026	35,257,674	AGGGGGAGGGTATAGGAAGCTTTG G	CGTTTTATTGAATTTGCATCCAGTT GT
8	<i>D8SNP303</i>	rs36881999	68,481,869	28,684,843	CCATCTCTCCAAAGAGTTCAGAC A	ACAATAAAGTCCCCACAGCTGAAC A
8	<i>D8SNP304</i>	rs38305200	97,012,501	28,530,632	TTCCAGTCATTGACCCTTCC	TCCCTGTAICTCAGCACATTCA
8	<i>D8SNP305</i>	rs262469470	128,731,434	31,718,933	TCTGGCATTCTTTGTATTTGTTTT	CTCTGCCCATCAAGTCACAA
8	Distal end	-	129,401,213	669,779	-	-
9	<i>D9SNP301</i>	rs51304512	7,143,163	7,143,163	TGCACAGCTCTCAATGTCTC	AATGGCCACAGCAAGTGTTA
9	<i>D9SNP302</i>	rs37879512	28,064,358	20,921,195	AAGCCCTGATCTTGGTTTCA	TGGGGACCAAGACTTAAGAG
9	<i>D9SNP303</i>	rs38922776	58,658,396	30,594,038	TTGCTGCTACTGCTTCTGGA	TAGCAAGCCTGCCTTAGAGC
9	<i>D9SNP304</i>	rs33134771	97,538,326	38,879,930	ACTCAGCTCTGGCTTGAAAA	TTGTCTCAGGACCAGGCTTT
9	<i>D9SNP305</i>	rs50594159	118,668,402	21,130,076	CTTGTTGCTTGTCAAATGTCTG	TCATGACAACATGTTCCAGGGTCTG T
9	Distal end	-	124,595,110	5,926,708	-	-
10	<i>D10SNP301</i>	rs45892832	9,210,791	9,210,791	ACCAATTTCCCCAACCTTC	TGGGTCCTCTGCTATTTTG
10	<i>D10SNP302</i>	rs33688332	24,502,545	15,291,754	GGTATCCCTCCAAGAGATGCCTTC A	GGCTGGAGCTTGTTTCTCTGTGA T
10	<i>D10SNP303</i>	rs50315385	25,416,558	914,013	TCCACGTATGGTTGTCTCTGTTCA	ACCCGCTCCTTGTGTGTTA
10	<i>D10SNP304</i>	rs46748961	62,235,472	36,818,914	CTCAGGTCTCTGCATAGCC	GTGCCAGCCATTTCTGTAT
10	<i>D10SNP305</i>	rs47483530	100,538,164	38,302,692	GGGAGCCCAGAAGGTAAAAC	CCATTCAACTCTTCCCAAATG
10	<i>D10SNP306</i>	rs233492562	120,961,461	20,423,297	GACTTACAGGCTCGGGTGTTCCT G	ATTCCCAGTCTTGTCTGGCCCTTT
10	Distal end	-	130,694,993	9,733,532	-	-
11	<i>D11SNP301</i>	rs26833083	13,743,601	13,743,601	ATGCACTCTGTGAGCTCTTTGCTTT	TCCAATGGCTACCAACTACCTTTC A
11	<i>D11SNP302</i>	rs26912518	35,661,735	21,918,134	TTCAGATGTGGAATCTGCTTGTGA G	GTGGCTCAGTGGGTAAAGGTCTAC A
11	<i>D11SNP303</i>	rs220626677	65,312,557	29,650,822	TGCTGCTTTGTGTGTGTTCA	GTACATCATGGGGGATGGAG
11	<i>D11SNP304</i>	rs252587388	92,606,217	27,293,660	CCTTGGTGGCTGATTATGG	CAGACATTATGTCCCCTCA
11	<i>D11SNP305</i>	rs27014504	121,160,359	28,554,142	TCTCCACAGGACAAGTCC	ACGATGAAGGGAATGCTCAG
11	Distal end	-	122,082,543	922,184	-	-
12	<i>D12SNP301</i>	rs46528175	11,853,935	11,853,935	CAAGCAACTGTTCGTGAAAA	AGAGCTGAGCTGGAGATTCG

Supplementary Table 4. (Continued)

Chr	Marker	dbSNP_ID	Location (bp)	Interval (bp)	Forward primer	Reverse primer
12	<i>DI2SNP302</i>	rs231844185	37,027,619	25,173,684	TCATGTTTTGCTGACTCTTTGTCCA	CTTTCCTGGAAGTGGGGTAAAC T
12	<i>DI2SNP303</i>	rs37803925	68,506,399	31,478,780	GGCCCTATAAGAAGGCCTCA	CCAAACCCACTTTCATGGTC
12	<i>DI2SNP304</i>	rs51364971	92,012,865	23,506,466	GAATTTTGGCATGCTTCCAG	AGGGCAAAGTGTGGACTGAC
12	<i>DI2SNP305</i>	rs247716364	118,192,234	26,179,369	CCCAGCAATGTAGATGTGGA	GGGGCAAATGTCAAGAAGA
12	Distal end	-	120,129,022	1,936,788	-	-
13	<i>DI3SNP301</i>	rs33751539	3,695,139	3,695,139	TAGTGTGACATTCTGGAGGCAC A	ACAAAAATCTGGAGGGAAGGCTA CA
13	<i>DI3SNP302</i>	rs29965851	24,986,028	21,290,889	CTTCCACCTCCCAAGTGCTA	TGCTGGGTCCAGAGTTTAG
13	<i>DI3SNP303</i>	rs30245925	59,808,311	34,822,283	GCACATTAATGATATTAGTTAGGG GGTTGC	CTCAAACATAGCCACAGCACGGA AG
13	<i>DI3SNP304</i>	rs47717539	81,557,548	21,749,237	ACCCAGAAATCGGGTGAAATCAG T	CATGTGGTTTCTGGGAAATGAACT C
13	<i>DI3SNP305</i>	rs38228777	113,127,661	31,570,113	ATGCTTCTGGTGTCCATTCC	CCACTAGCACGTCACCTCTCG
13	Distal end	-	120,421,639	7,293,978	-	-
14	<i>DI4SNP301</i>	rs51648802	8,335,825	8,335,825	GTGTTTTGACAGCAGCCTCA	TGGGACTTCTTTTGGCCATC
14	<i>DI4SNP302</i>	rs50148147	48,130,422	39,794,597	TGAAACTACCATTGCTGCCTCTC A	GCTTATAGAACCTGCCGCTCTGCT G
14	<i>DI4SNP303</i>	rs46892447	64,022,286	15,891,864	GACACCGGCCAAGAAGATAA	TCACCAGAGTCAGCCTCCTT
14	<i>DI4SNP304</i>	rs32226962	80,821,585	16,799,299	CAGGACCAGACAACTTAGAACA ATGAGC	TGTGGAATTGAATGAACTGAACCA AA
14	<i>DI4SNP305</i>	rs51211980	116,765,765	35,944,180	AGCTAGGCCTTCCCAATTTC	TTGAGAAGCCTTTGGTCTCC
14	Distal end	-	124,902,244	8,136,479	-	-
15	<i>DI5SNP301</i>	rs48122948	7,190,183	7,190,183	GGCTGGTGCCTACATTTTGT	GAACGCTGAAGACGAAGACC
15	<i>DI5SNP302</i>	rs212086590	32,323,386	25,133,203	ACATGGCCACTAACCATCCCAAT A	CCCCCATACTCCTTTTCCATCAC T
15	<i>DI5SNP303</i>	rs220101808	59,204,839	26,881,453	AATAAGTGGGAGAATCAGTTCCTG	ACAGTCAGTGAGGGGCAGAC
15	<i>DI5SNP304</i>	rs38263969	93,642,519	34,437,680	GGAAAGCTGGTTGACACACA	TTAAAGACCCCAGCTTCCAA
15	Distal end	-	104,043,685	10,401,166	-	-
16	<i>DI6SNP301</i>	rs49608214	13,645,760	13,645,760	GGCAGAGAGATCCTTCCTTG	CTTTCCAACGTTGAGGCATT
16	<i>DI6SNP302</i>	rs46364658	35,556,433	21,910,673	GTGGCTGTCTGTATTCAGAGCAGA T	TTTTACAGCAGAGCATGAGGCTTT C
16	<i>DI6SNP303</i>	rs50933320	66,087,347	30,530,914	TTCCCTGTGCCTTTTAACTTGTA	TCTGAGAGTGTGTTGCATGGAGA G
16	<i>DI6SNP304</i>	rs254664546	83,959,602	17,872,255	TGCCATGTTGCAGTACTTGCCAT T	AGCGAAGATGTGAGACCAAGAAG CA
16	<i>DI6SNP305</i>	rs227119859	88,590,384	4,630,782	GAGCGTGCACCTGTTTGATTTCA G	TACTCTCAGTTCCCATCCACGCAC A
16	Distal end	-	98,207,768	9,617,384	-	-
17	<i>DI7SNP301</i>	rs49061265	9,056,643	9,056,643	TGCTTGCATTTCACTGGT	CACACAGAAAGCCAGCACAT
17	<i>DI7SNP302</i>	rs45641253	44,538,706	35,482,063	CAATGGTCTCTTCCCTGTC	GAAGAAGACATTGGGGACCA
17	<i>DI7SNP303</i>	rs49487329	73,160,648	28,621,942	TGGCTTATGCAGCAGAGTG	CACACAGCGCTTCGTTTCTA
17	<i>DI7SNP304</i>	rs47460807	93,444,664	20,284,016	ATAAACAGGACCAGCCATCAACA GA	TTGGGTTGAATTGTATCATCATAA AGC
17	Distal end	-	94,987,271	1,542,607	-	-
18	<i>DI8SNP301</i>	rs51512767	28,122,298	28,122,298	TTGGGAACTCAGCAAGTGAGAGA AGC	AAAGCCTCTGGGCTCCTTAGTT C
18	<i>DI8SNP302</i>	rs221424480	30,033,468	1,911,170	GGCCAGTTTTCTCCTTGATCACAG TG	AAGCCAGAGAGAGACTAGTGACC AGC
18	<i>DI8SNP303</i>	rs31785839	36,997,793	6,964,325	AATCCACAGAAGCAAACCAAGA TG	CCTCTGGGACAGAGTAGTGAAGCT G

Supplementary Table 4. (Continued)

Chr	Marker	dbSNP_ID	Location (bp)	Interval (bp)	Forward primer	Reverse primer
18	<i>D18SNP304</i>	rs39281136	59,385,726	22,387,933	GCGCTCTCTTTCCCTTTGTA	GGTCTCCTTCCCCTCAGTTC
18	<i>D18SNP305</i>	rs37625494	89,452,136	30,066,410	AGGCCAGCTTAAAGGCTCTACTCC T	CAGAAGAGGGCCTTAGACACAGA CA
18	Distal end	-	90,702,639	1,250,503	-	-
19	<i>D19SNP301</i>	rs36448887	5,527,218	5,527,218	AGCCTAAAGGCAGGTGACAACAG GA	ACTCTCATGCGCCTTGTGGTTTAC A
19	<i>D19SNP302</i>	rs37039649	13,740,321	8,213,103	TGCTGACCAAAACCTCCTGAACTG T	GGCCACTCTGGTCTTGTCACTACT TGA
19	<i>D19SNP303</i>	rs38082986	15,510,092	1,769,771	TGCTCCCAGGAATTGCTAAAACCTT CA	GGGTCCACAATGACTGGGAAAGA AA
19	<i>D19SNP304</i>	rs50157060	32,670,321	17,160,229	TTGCTGCCAACAGAATCCTA	ATGATGGCGCAGTTCTAACC
19	<i>D19SNP305</i>	rs36495646	45,443,117	12,772,796	TCGGAGAATGGACGATTAGAA	CTTTTCTGGACAGGCCAAAG
19	<i>D19SNP306</i>	rs48624001	56,830,344	11,387,227	GAAGGGGAGCTTTTTCTGCT	AAACCGCCTTCTCAATTCCT
19	Distal end	-	61,431,566	4,601,222	-	-
X	<i>DXSNP301</i>	rs33287577	6,183,969	6,183,969	TGCATGCCAAGCACTTTATTGACT A	ATCTGCCATGCAAACTCAATAGGA A
X	<i>DXSNP302</i>	rs30035452	44,778,119	38,594,150	CACTAAGCCCTCTTCTTTTGAA	CAAATGATGATTTTCCCAAT
X	<i>DXSNP303</i>	rs29043150	70,948,771	26,170,652	GTGGTCCCCAAAACATATGCTTGC T	AAGCTTACCCACATTGCTGGCAG T
X	<i>DXSNP304</i>	rs241499720	71,601,755	652,984	CCTGCCACCTACCTCTTCAGGTGT T	GCAGGCAGGAATCTCAGCTAGGA AA
X	<i>DXSNP305</i>	rs8268104	104,300,680	32,698,925	TTTCTTGGTGAGGAGTTGGGGAAG A	TGATGGTGAATGGACTGCTTTTTC A
X	<i>DXSNP306</i>	rs3718396	135,959,876	31,659,196	TCAAAGTCAAACCTGTGTTGGGAGC A	GTGACGATCCAGCCCTTGAACCT T
X	<i>DXSNP307</i>	rs29299426	154,862,172	18,902,296	ACAGACAGGTCCTAGGAGGCAAA AC	GTCTGGCCTTATTTTGAGTGCAAT G
X	<i>DXSNP308</i>	rs31827558	169,982,929	15,120,757	CCACCTATTCCGAATATCTCATAG GACC	TCTGGTGGAACCTCGAAAGGCCTTA GC
X	Distal end	-	171,031,299	1,048,370	-	-