Published in final edited form as:

Cell Syst. 2021 March 17; 12(3): 235–247.e9. doi:10.1016/j.cels.2020.12.002.

A platform for experimental precision medicine: The extended BXD mouse family

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Summary

The challenge of precision medicine is to model complex interactions among DNA variants, phenotypes, development, environments, and treatments. We address this challenge by expanding the BXD family of mice to 140 fully isogenic strains, creating a uniquely powerful model for precision medicine. This family segregates for 6 million common DNA variants—a level that exceeds many human populations. Because each member can be replicated, heritable traits can be

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Conceptualization, RWW, LL, JA; Methodology, DGA, DA, PP, JA, LL, RWW; Software DGA, DA, PP, AGC, LL, RWW; Formal Analysis, DGA, DA, EGW, RH, SS; Investigation; SR, CML, AV, CJB, JFI, MSM; Resources, CML, AV; Data Curation, DGA, DA, AGC, RWW; Writing – Original Draft DGA, DA, RH, RWW; Writing – Review & Editing, DGA, DA, PP, MKM, SR, EGW, RH, JH, LL, RWW; Visualization, DGA, DA, EGW; Supervision, JA, LL, RWW; Funding Acquisition, RWW, JA, CML.

Declaration of Interests

The authors declare no competing interests.

mapped with high power and precision. Current BXD phenomes are unsurpassed in coverage and include much omics data and thousands of quantitative traits. The BXDs can be extended by a single-generation cross to as many as 19,460 isogenic F1 progeny, and this extended BXD family is an effective platform for testing causal modeling and for predictive validation. The BXDs are a unique core resource for the field of experimental precision medicine.

Electronic Table of Contents blurb

Ashbrook et al., have expanded the BXD family to 140 strains, providing a new tool for translational precision and predictive biology, and extended the usefulness of the deep phenome of >100 omics datasets and >7500 classical phenotypes already available. They show increased precision and power by using new genotypes, updated models and more strains.

Keywords

Systems genetics; systems biology; gene mapping; complex trait; power calculation; personalized medicine; recombinant inbred strains; GXE

Introduction

The development of predictive, preventive, personalized, and participatory healthcare requires as prerequisites deep and coherent phenome data. These data must be matched to sophisticated causal models of complex interactions among sequence variants, phenotypes at many levels, and environmental exposures (Auffray et al., 2010; Hood and Friend, 2011; Williams, 2009). For most diseases it is not yet practical to predict risk and best treatment options for the simple reason that each human is unique (Schüssler-Fiorenza Rose et al., 2019). This *N-of-1* problem inhibits development and refinement of predictions. However, it is now possible to create optimized experimental platforms that fill this gap in the form of large and fully characterized families of isogenic rodents, such as the BXD.

The BXD family was started fifty years ago by crossing fully inbred female C57BL/6J (B6 or B) to male DBA/2J (D2 or D) mice. The first set of BXD recombinant inbred (RI) strains was used to map Mendelian traits (Taylor et al., 1973, 1999), but the BXDs are now used mainly to map complex traits including cancers, metabolic and cardiovascular disease (Grizzle et al., 2002; Koutnikova et al., 2009; Lee et al., 1995; McGinnis et al., 1993), brain structure (Belknap et al., 1992a; Rosen et al., 2009; Seecharan et al., 2003; Zhou and Williams, 1999), behavior, and pharmacology (Ashbrook et al., 2018a; Belknap et al., 1992b, 1993; Grisel et al., 1997; Jones et al., 2006; Knoll et al., 2018; Palmer et al., 2006; Phillips et al., 1998; Rodriguez et al., 1994; Weimar et al., 1982). We started a second wave of BXDs in the late 1990s (Peirce et al., 2004) using advanced intercross (AI) progeny (Darvasi, 1998) (Figure 1; Figure S1; Table S1). These AI-derived family members incorporate twice as many recombination junctions as do conventional BXDs (Broman, 2005; Crow, 2007; Haldane and Waddington, 1931; Williams et al., 2001) (Figure 1C)—an attribute that improves mapping precision about two-fold.

The BXDs are well suited for systems biology (Williams and Williams, 2017) thanks to a well-integrated phenome consisting of over 7500 classical phenotypes and over 100 omics data sets (Williams and Auwerx, 2015; Williams et al., 2001). This phenome extends back to Taylor's 1973 analysis of cadmium toxicity, through to recent studies of metabolism (Roy et al., 2020; Wang et al., 2013, 2016b; Williams et al., 2016, 2020; Wu et al., 2014), addiction (Dickson et al., 2016, 2019; Mulligan et al., 2013), behavior (Carhuatanta et al., 2014; Graybeal et al., 2014; Mulligan and Williams, 2015; Philip et al., 2010), infectious disease (Hayes et al., 2014; McKnite et al., 2012; Wang et al., 2020), epigenetics (Baker et al., 2019; Sandoval-Sierra et al., 2020), and even indirect genetic effects (Ashbrook et al., 2015a, 2017; Baud et al., 2017). The BXD have been used to test developmental and evolutionary hypotheses (Hager et al., 2012; Oren et al., 2015; Seecharan et al., 2003), to study GXE and consequences of treatments as a function of age, diet, and sex (Fleet et al., 2016; Philip et al., 2010; Roy et al., 2020; Sandoval-Sierra et al., 2020; Williams et al., 2016, 2020), gene pleiotropy (Wang et al., 2016a), and to test behavioral predictions based on differences in brain architecture (Yang et al., 2008).

Here we summarize the current status of this resource with a focus on genetic structure, and on the power and precision of mapping trait variance to loci and genes. We have almost doubled the size of the BXD family, from ~80 (Peirce et al., 2004) to 140 extant strains. Each of the 140 fully inbred and isogenic strains of mice is an immortal genometype that can be resampled at any stage, in both sexes, and under varied but controlled conditions to quantify gene-by-environmental interactions (GXE) and to test the accuracy and errors of genome-to-phenome prediction. Compared to progeny of conventional intercrosses, AIs, or heterogenous stock, the BXDs are advantageous when heritabilities of traits are low or when measurement errors are high because the genetic signal can be boosted by resampling many isogenic cases (Belknap, 1998; Crow, 2007). A further benefit is that each data set adds quadratically to the number of trait-to-trait associations, and even the oldest data becomes more powerful as genetic, genomic, and phenomic contexts are improved and enlarged. The BXD, like other replicable reference populations, are therefore well adapted to extensible multisystems analyses, to modeling, and to quantitative prediction (Andreux et al., 2012; Chesler et al., 2003; Jha et al., 2018b, 2018a; Li et al., 2018; Williams et al., 2016). We have therefore assembled deep companion resources, including full sequence for both parents (Baker et al., 2019; Keane et al., 2011; McKnite et al., 2012; Wang et al., 2016b; Wu et al., 2014). Access to data and statistical tools are available from open-source web services (GeneNetwork.org and Systems-Genetics.org) (Li et al., 2018; Sloan et al., 2016; Williams and Williams, 2017). High-density genetic maps are now combined with linear mixed model mapping to boost power and accuracy.

Results

The BXD family has been expanded to 140 inbred strains

We have approximately doubled the number of extant BXD strains, from ~35 (Taylor et al., 1999), to ~80 (Peirce et al., 2004), to 140 here. We started producing 108 new BXD strains between 2009 and 2013 (BXD104–BXD220). A total of 123 BXD lines are currently distributed by The Jackson Laboratory (JAX, Table S1). Seventeen additional strains are

available at UTHSC but will soon be donated to JAX. All strains are available under a standard material transfer agreement.

We have identified three sets of strains that have almost identical genomes. These are marked by the addition of “a” and “b” suffixes. For example, BXD65, BXD65a, and BXD65b are identical by descent across >90% of their genomes. Without correction, the inclusion of three BXD65 substrains will bias results. There is also more subtle kinship among BXD family members that results from drift, backcrossing, and unintended selection. Correcting for both types of kinship when mapping traits can be accomplished using linear mixed models during analyses, for example *Genome-wide Efficient Mixed Model Association* (GEMMA) (Zhou and Stephens, 2012) or R/qtl2 (Broman et al., 2003, 2019) discussed below.

Improved mapping using updated markers

Affymetrix and Illumina arrays have been used to genotype at more than 100,000 informative markers in 198 BXD strains (Morgan et al., 2015; Peirce et al., 2004; Shifman et al., 2006; Taylor et al., 1999; Zhang et al., 2012). Previously, a subset of 3,830 markers have been used for mapping, but here we have boosted marker numbers nearly two-fold to 7,324. This high-density marker set defines proximal and distal limits of chromosomal intervals that are non-recombinant. Markers are spaced at 0.63 Mb ± 1.0 SE, closely matching the expected asymptotic map resolution of ±1 Mb.

The increase in numbers of markers has significantly improved power and precision of linkage analysis (Figure 2, Figure S2) across all chromosomes (Figure S2). To quantify these improvements in mapping, we computed linkage for the entire BXD phenome—currently 7562 phenotypes—using three different genotype files: the original file from 2001 (Williams et al., 2001), the “classic” genotypes used from 2005 to about 2016, and the updated genotypes. Each of these stage roughly doubled the numbers of markers (from 1,578 to 3,811 to 7,324). We counted the number of traits associated with logarithm of the odds (LOD) linkage scores at three cut-offs: 2.2 (suggestive; a likelihood of one false positive per genome scan), 3.6 (significant; one false positives per 20 scans), and 5.4 (highly significant; one false positives per 100 scans) (Lander and Kruglyak, 1995) (Figure 2C). The largest boost in LOD is achieved for traits with linkage between 3.6 and 5.4 LOD—up 30% compared to older marker sets (Figure 2C and 2D).

We can further improve power and precision using linear mixed models

Compared to traditionally used Haley-Knott mapping (Haley and Knott, 1992), more recently developed algorithms can correct for variable kinship among genometypes and further improve mapping (Broman et al., 2003, 2019; Sul et al., 2016; Zhou and Stephens, 2012). We calculated linkage for 3300 phenotypes using both the Haley-Knott (H-K) method that does not correct for kinship or using linear mixed model (LMM) mapping that does correct for kinship (Broman et al., 2019). Genome-wide significance was estimated based on 5000 permutations and the improvement is substantial (Figure 3, Table S2). Using H-K, 638 phenotypes reach $p_{gw} < 0.05$ significance, whereas 763 reach the same criterion using the LMM, a 20% increase. To check that this was not due to phenotypes close to the

threshold, we counted the number of phenotypes with a peak LOD ≥ 1 above threshold: 196 for H-K and 262 for LMM, a 33% increase. Note that there is not a substantial average increase in LOD scores when using an LMM compared to H-K (a mean increase of 0.06 and a median of 0.07), nor is there a substantial change in the mean p_{gw} threshold (LMM 3.51 vs H-K 3.55; Table S2), demonstrating that LMM is not simply inflating all values.

Empirical mapping precision ranges from 0.25 to 5 Mb

We estimated the empirical precision of linkage maps using ~270,000 *cis*-acting expression QTLs (eQTLs) that have LOD scores greater than 3.0 and within 10 Mb of the mRNA transcription start site (Figure 4A). These criteria are conservative because an acceptance window of ±10 Mb will include a small number of regional *trans*-acting variants. However, this approach guards against overly optimistic estimates of precision. Mean precision for 17,805 eQTLs with LODs above 5.0 is about 1.0 Mb using only 60–80 BXD strains. The median precision is about 0.50 Mb. In other words, the offset between the location of a gene and the location of the marker with the highest LOD is generally less than 1 Mb using half the available strains. However, regional variation in precision is high (Figure 4A,B), and intervals with low precision have either few markers or low recombination rates— a problem that is currently being addressed by generating sequence-based infinite marker maps (Ashbrook et al., 2018b). There may also be regions that contain large structural variants—duplication, inversions, insertions—compared to the reference genome of C57BL/6J.

It is possible to achieve subcentimorgan mapping precision using only half of the full set of BXD strains (Figure 4)—a mean resolution of 500 Kb and a median resolution of 250 Kb for these Mendelian traits. Three factors contribute to this precision: 1. well-balanced distribution of only two haplotype across the genome (minor allele and haplotype frequencies close to 0.5). 2. the ability to boost the effective heritability of traits by resampling (Belknap, 1998); and 3. the high density of recombination junctions captured collectively within the BXD family (Figure 1C). Surprisingly, this level of map precision does not differ appreciably from that typical of the Collaborative Cross, the Diversity Outbred, or heterogeneous stock (HS), mainly because the minor haplotype frequencies (MHF) at loci are about four-fold higher in the BXDs than those typical of crosses made using many parental strains (MHFs of 0.05 to 0.10). In any case, precision much finer than this, while welcome, will often not be critical. The fuzzy functional boundaries of genes and the high density of sequence variants in linkage disequilibrium shifts the burden of proof from pure mapping to functional genomics, comparative analysis of human cohorts, complementary animal models, and direct pharmacological and genetic engineering (Smemo et al., 2014).

Mapping with the BXDs has high power

How many replicates and strains are needed to detect and resolve QTLs? To start with the conclusion—it is almost always better to study small numbers of as many strains as possible (Andreux et al., 2012; Belknap, 1998). Studying as few as 2–4 replicates of each of 100 or more strains may seem counterintuitive to those used to typing knockouts and their wildtype controls, but shallow comprehensive coverage is correct even for traits with low heritability. We have developed an R/shiny application (power.genenetwork.org) that provides guidance

on power and resampling for designs using the BXD. When heritability is low, the gain in power by increasing replicates is significant up to an *n* of 4–6 cases per genometype, but falls off rapidly at heritabilities above 0.5. At heritabilities above 0.5, power is high even using only two replicates (Figure 5). It may still make sense to add replicates for those strains that are in the tails of distributions because these extremes are both potential sampling errors but, if verified, are true research opportunities.

The effect sizes for loci in BXDs are usually high compared to those of outbred populations and humans. Two factors contribute to higher levels of genetic variance. First, nearly all loci in the BXDs are homozygous. The lack of heterozygotes increases the genetic variance two-fold compared to a matched intercross, and four times as much variance as in a backcross (Belknap, 1998). The drawback is obvious: we cannot detect dominance effects without adding at least a subset of heterozygous loci of the type we can generate easily with sets of F1 progeny and a diallel cross. The second contributor is replicability (Figure 5). When effect size is treated as the proportion of total variance explained by genometypes, this will increase as environmental “noise” is suppressed by replication (Belknap, 1998). To demonstrate this effect we collected all *cis*-eQTLs ($n = 6867$) for a brain gene expression data set—55,683 measurements across 129 individuals and 37 BXD strains (GeneNetwork.org ID GN381). We calculated the proportion of variance in expression explained by *cis*-eQTL markers using either each individual as a unit or each strain mean as a unit. The mean proportion of variance explained is greatly increased by the latter approach (Figure S3), and for variants with a smaller effect sizes ($z \leq 0.2$; $n = 800$) the improvement is 2.5-fold. The average proportion of explained variance is about 1.5-fold higher when using strain means than when using individual values. Across all *cis*-eQTLs, the effect size using individual as unit is 0.49, whereas using strain means is 0.66—a 56% increase.

Substrains and epochs allow rapid determination of causal variants

Although kinship and epoch structure of the BXDs have been framed as a problem that needs to be solved using linear mixed models, kinship can also provide unique opportunities. In some cases, substrain sets show substantial phenotypic differences and can be used to generate so-called *reduced complexity crosses* (Bryant et al., 2020). Due to the low genetic variation between substrain sets, causal variants can often be identified rapidly, and these sets can be used as models of disease (Chang et al., 2006; Cook et al., 2006; Rosen et al., 2013).

Each epoch of BXDs has been generated using unique B6 and D2 parents. Although nominally considered identical, these parents will have inherited small numbers of spontaneous mutations (Figure 1A). These *de novo* sequence variants that accumulated between epochs will lead to expression variation and differences in phenotypes, and due to their very small number, these variants are especially tractable. It becomes straightforward to define the quantitative trait nucleotides causing this higher order variation among epochs using reduced complexity crosses and coisogenic crosses (Heiker et al., 2014; Kirkpatrick and Bryant, 2014; Kumar et al., 2013; Mulligan et al., 2008). Well-defined epoch effect variants include *Gpnmb* in vision (Lu et al., 2011, 2019); *Gabra2* in CNS function (Figure 6;

(Hawkins et al., 2020; Mulligan et al., 2019); and *Taarl* in methamphetamine abuse (Reed et al., 2017; Shi et al., 2016; Stafford et al., 2019).

Discussion

Kinship and genetic drift

The expanded family of BXDs is a well powered resource for both forward and reverse genetic analyses of genome-to-phenome linkage. As this family has grown, relations among individual strains have become complex, requiring the use of linear mixed models (Arends et al., 2010; Sul et al., 2016; Zhou and Stephens, 2014) or nonparametric equivalents such as mixed random forests (Stephan et al., 2015) that account for kinship, epoch, and other cofactors. The family has kinship at several levels. First, there is random fixation and selection of alleles and haplotypes that occurs during inbreeding (Williams et al., 2001). Second, there is strong kinship among AI-derived strains, including BXD43 to BXD102 and BXD160 to BXD186 (Peirce et al., 2004), that has its origins mainly in the 8–14 generations of intercrossing that preceded inbreeding (Darvasi, 1998). Third, there are coisogenic pairs such as BXD29/TyJ and BXD29-*Tlr4*<*lps*-2J>/J (Rosen et al., 2013). One member of each pair has at least one highly penetrant spontaneous mutation. Other recombinant congenic strains result from breeding admixture, for example the two BXD48s and the three BXD73s. These small sibships are interesting and useful and have been used to quickly identify causal mutations for immune disfunction in *Tlr4* (Cook et al., 2006) and for retinal degeneration in *Cep290* (Chang et al., 2006). Finally, there is kinship that results from the epochs of BXD production.

Improved power and precision of mapping BXD phenotypes—a 50 year path of progress

The first set of BXDs were used to map traits to sparse linkage groups, not chromosomes, in the early 1970s (Taylor et al., 1973). While postmillennial mapping resources are obviously far better, there is still much room for improvement. We compared three sequential sets of markers used to map the BXDs—the original genotypes from 2001 (Williams et al., 2001), the set used from 2005 to 2016 (the “classic” set) (Shifman et al., 2006), and the new genotype file released here. This most recent set increases the yield of loci detected at genome-wide significance by about ~25%.

We highlight two key points. First, using the genetic resources we present in this manuscript, it is possible to map quantitative traits with modest LOD scores with good precision, even when using comparatively small numbers of strains (n = 25 to 50; e.g. (Chintalapudi et al., 2017; Houtkooper et al., 2013; Williams et al., 1998). Second, an effective way to transition from QTLs to causal genes and biological processes is to take advantage of complementary resources including other murine mapping resources, efficient *in vitro* and *in vivo* screens (Houtkooper et al., 2013; Williams and Auwerx, 2015), and human GWAS data (Ashbrook et al., 2014a, 2015b; Jha et al., 2018b, 2018a; Koutnikova et al., 2009). The brute-force way to improve precision and power is to just phenotype larger numbers of BXD strains. With 140 strains and nearly 20,000 easily made F1 hybrds, traits can be mapped with subcentimorgan precision.

Identification of causal variants is becoming easier thanks to improved genotypes (Rau et al., 2015; Shifman et al., 2006; Simecek et al., 2017; Williams et al., 2001), full genome sequence (Keane et al., 2011; Wang et al., 2016b), powerful omics resources (King et al., 2015; Williams et al., 2016, 2018; Wu et al., 2014), better Bayesian fine-mapping methods (Gonzales and Palmer, 2014; Mulligan et al., 2017; Wakefield, 2008; Wellcome Trust Case Control Consortium et al., 2012; Zhou and Stephens, 2014), and efficient molecular validation methods (Li et al., 2018). The BXD have been used to define specific genes and variants corresponding to well over 20 QTLs, including two tightly linked genes, *Iigp2* and *Irgb10,* for *Chlamydia* infectivity (Miyairi et al., 2007, 2012), *Fmn2* as a master controller of tRNA synthetases in neurons (Mozhui et al., 2008), *Ubp1* for blood pressure (Koutnikova et al., 2009), *Hc* for H5N1 influenza resistance (Boon et al., 2014), *Comt* as a master controller of neuropharmacological traits (Li et al., 2010), *Alpl* for hypophosphatasia (Andreux et al., 2012), *Mrps5* for longevity (Houtkooper et al., 2013), *Bckdhb* for maple syrup urine disease, *Dhtkd1* for diabetes (Wu et al., 2014), *Hp1bp3* for cognitive aging (Neuner et al., 2016), *Ahr* for locomotor activity (Williams et al., 2014), and *Gabra2* and *Taar1* for behavioral traits (Mulligan et al., 2019; Reed et al., 2017) .

The BXD family is the largest and the most deeply phenotyped mammalian genetic reference panel

Data sets for the BXD encompass multiple levels—from single molecules to complex behavioral repertoires, and to traits measured with environmental perturbations, including exposure to alcohol and drugs of abuse (Dickson et al., 2019; Mulligan et al., 2018; Théberge et al., 2019; Zhou et al., 2018) , infectious agents (Boon et al., 2014; Chella Krishnan et al., 2016; Russo et al., 2015), dietary modifications (Fleet et al., 2016; Jha et al., 2018b, 2018a; Jones and Jellen, 2017; Reyes Fernandez et al., 2016; Rodrigues et al., 2017), stress (Diessler et al., 2018; Jung et al., 2017) and even as a function of age (Sandoval-Sierra et al., 2020; Williams et al., 2020). This phenome is linked to over 500 publications, including state-of-the-art proteome, metabolome (Williams et al., 2018, 2020), epigenome (Baker et al., 2019; Sandoval-Sierra et al., 2019), and metagenome (Perez-Munoz et al., 2019) data sets available on GeneNetwork.org.

Genetic research is moving rapidly toward causal modeling of health and disease risk and toward the predicted efficacy of prevention and interventions (Hood and Flores, 2012). The size and depth of the BXD phenome makes it a strong foundation for this experimental precision medicine. The genetic architecture of traits can be dissected and causal relations among networks can be explored (Roy et al., 2020). The ability to resample genomes across a stable reference family enables the expansion of data in almost any direction. Improved phenotype ontologies and better access to FAIR data (Wilkinson et al., 2016) enables cross-species translation. This also enables more diverse researcher communities to engage in replicable trans-disciplinary studies of genome-phenome prediction.

Future Directions: Epistasis, pleiotropy, epigenetics, gene-by-environment interactions

Most work using the BXD family has had the simple goal of defining single gene variants and processes that contribute to heritable differences in disease risk. But we need to tackle a more important problem—the complex interplay among sets of variants, constellations of

phenotypes, and different treatments and environments (Ashbrook et al., 2014b; Mulligan and Williams, 2015; Williams and Auwerx, 2015; Williams et al., 2016). The BXDs are now sufficiently large to evaluate predictive models of biological processes of these more complex types (Li et al., 2008; Miyairi et al., 2012; Wang et al., 2016b) and to map epistatic interactions. But power to fit complex models can be greatly amplified by crossing BXD strains to generate a diallel cross of up to 19,460 F1 progeny. All isogenic BXD F1 lines are replicable and have entirely defined genomes. They have the advantage of being non-inbred and heterozygous. A subset of this massive diallel cross (DAX) can be generated efficiently from a central repository for cost-effective cell-based assays, and for matched *in vivo* predictive validation. Any part of this DAX can be used to study parent-of-origin and sex chromosome effects (Ashbrook and Hager, 2013). It is also practical to cross BXDs to other lines—for example to the humanized 5XFAD line used in Alzheimer's disease research by Kaczorowski and colleagues (Neuner et al., 2019a, 2019b). By crossing humanized or genetically engineered lines on a single genetic background to a diverse but defined subset of BXDs, variants that modify traits—such as memory loss in the 5XFAD model—can be mapped and can provide valuable information on disease process and outcomes. Kaczorowski and colleagues have also evaluated the efficacy of *reverse translation* from human to mouse (Neuner et al., 2019a). They generated a polygenic genetic risk score using 21 human genes that increase Alzheimer's risk and showed that allele dosage was significantly associated with cognitive outcomes in mice. This demonstrates that naturally occurring variation in these networks may have overlapping effects in mouse and humans.

In humans tens-of-thousands of variants have now been mapped to haplotype blocks of under 100 Kb (Huan et al., 2015; Schizophrenia Working Group of the Psychiatric Genomics Consortium, 2014; Wood et al., 2014). We need to revamp murine genetic resources to contribute more effectively, and in complementary ways, in an era flooded with GWAS hits. How are rodent resources best repositioned to help deliver on the still unmet and much more integrative promises of predictive genetics and personalized precision health care? The short answer is that we need large genetically complex resources with matched multiscalar and multisystems phenome data. We need resources that define and test progressively more sophisticated computational models as a function of genometype, stage, and exposure. We need replicable populations with the same intrinsic genetic complexity and admixture as humans but without the challenges of clinical research—high cost, marginal compliance and control, confidentiality, and of most importance, ethical constraints on designs and interventions. Rodent populations are ideally positioned to be replicable and extensible testbeds with which to define the power, accuracy, and limits of precision health care.

Conclusions

Systems genetics using rodent models has been revitalized over the last decade thanks to several resources, including the BXD family (Peirce et al., 2004), the Hybrid Mouse Diversity Panel (Bennett et al., 2015; Ghazalpour et al., 2012), and the Collaborative Cross (Churchill et al., 2004; Morgan and Welsh, 2015; Schughart and Williams, 2017; Valdar et al., 2006). The main limitation has been relatively modest mapping power and precision—a simple problem caused by small numbers of strains. With 140 strains now readily available,

and expandable to 19,460 isogenic F1s, the extended BXD family has overcome this problem. All phenome data is multiplicatively useful, and like a fine vintage, old data gets better with age.

STAR Methods

Lead Contact

Further information and requests for reagents may be directed to, and will be fulfilled by, the corresponding author David Ashbrook (dashbrook@UTHSC.edu).

Materials Availability

The BXD strains reported in this study are available from the JAX. JAX Stock No (RRIDs) can be found in the Key resources table and in Table S1.

Data and Software Availability

This paper analyzes existing, publicly available data. These data sets' accession numbers are provided in the Key Resource Table, and throughout the manuscript. Genotype files can be found at http://www.genenetwork.org/webqtl/main.py?FormID=sharinginfo&GN_AccessionId=600. GeneNetwork.org original code is publicly available at https://qithub.com/genenetwork/genenetwork2 and https://github.com/genenetwork/genenetwork1.

The scripts used to generate the figures reported in this paper are available in the BXDtools package (https://github.com/DannyArends/BXDtools) or using ggplot2 (version 3.3.2; https://cran.r-project.org/web/packages/ggplot2/index.html) and their use is described in the STAR Methods. Code for computing marker positions and visualization of recombinations is available in the BXDtools package (https://github.com/DannyArends/BXDtools).

Power estimates can be made using http://power.genenetwork.org/, and code is at https://github.com/Dashbrook/BXD_power_calculator_app.

The R/qtl2 software can be found here https://kbroman.org/qtl2/, and its use is described in the STAR Methods.

Experimental Model and Subject Details

Mice

Between 2009 and 2010 we initiated 74 BXD strains (BXD104 to BXD186). We initiated another 34 strains in 2013 (BXD187 to BXD220). We used both conventional F2 intercrosses ($n = 88$) and AI progeny ($n = 20$) to make the 108 new lines. BXD160 through BXD186 were derived from unique matings of AI progeny gifted us by Dr. Abraham Palmer at G8 and G9 late in 2010 (Figure 1, Figure S1, Table S1).

In cases of low reproductive fitness, we often attempted to rescue lines by outcrossing young male BXDs to C57BL/6J females followed by three or more sequential backcrosses (N3) to the RI male to produce progeny enriched for the BXD genome. In more recent cases, pairs

of at-risk strains were crossed to produce RIX progeny (Tsaih et al., 2005; Williams et al., 2001), which were then inbred by sibling mating. BXD221 to BXD228 are RIX-derived strains of this type (Figure S1, Table S1).

Unless otherwise specified, all animals used in this study were raised in a closed-barrier pathogen-free vivarium at the University of Tennessee Health Science Center. All BXD strains are available under a standard material transfer agreement; the most important limitation being that they cannot be sold or distributed without approval of the Jackson Laboratory or UTHSC. Availability information on all BXD lines can be found in Table S1.

Method details

Genetic map construction and genotype error correction

Individuals from each of the 198 BXD lines were genotyped in late 2011 and in late 2015 using the Neogen/GeneSeek MUGA or GigaMUGA arrays. These were combined with previous genotypes generated using Affymetrix and MUGA platforms. Unknown genotypes were imputed as B (C57**B**L/6J-like) or D (**D**BA/2J-like) or were called as H (heterozygous) if the genotype was uncertain.

The full data set contains 37,000 markers and was optimized for mapping efficiency by excluding markers showing identical strain distribution patterns. Markers that flank sites of recombination were retained. As a result, strain distribution patterns are often defined by proximal-distal marker pairs. Whenever possible, we verified and updated genotypes of the original BXD strains (BXD1 - BXD102) to reflect those of stock available from the Jackson Laboratory (Rau et al., 2015) and from Petr Simecek and Gary Churchill; http://cgd.jax.org/datasets/diversityarray.shtml).

Genotypes for all strains were smoothed and curated to remove highly implausible (double) recombination events, e.g. unsupported genotypes (singletons) that introduced two recombination events over less than 100 kb (Williams et al., 2001). In general, we imputed unknown or heterozygous genotypes on the basis of flanking markers. Undefined genotypes between recombinations were coded as heterozygous, and telomere genotypes were imputed using the closest flanking marker.

In the newer BXD strains many regions are still heterozygous. Generated genotypes using standard platforms still show regions of low marker density and a high frequency of recombinations. These regions of low marker density were filled with imputed genotypes using *cis*-eQTLs of genes in the problematic intervals. Microsatellites and *cis*-eQTL genotypes were generated by the Williams/Lu laboratory.

The assembled and error-checked genotype file includes 7,324 markers for 191 independent strains, and 7 substrains, has been available since January 2017 at http://www.genenetwork.org/genotypes/BXD.geno and is the default genetic map used when QTL mapping on GeneNetwork (http://www.genenetwork.org).

Genome-wide visualization of recombinations

For each chromosome we compute the number of observed recombinations per strain from the start of the chromosome (nRecS), ignoring the heterozygous and unknown genotypes. We then visualize this by plotting the number of recombinations for each BXD strain per chromosome using a color gradient. Strain numbers are used for the ordering on the X-axis, and horizontal lines are added to visually separate the different epochs and annotate the epochs on the X-axis.

Quantification and Statistical Analysis

Computing centimorgan positions

For each chromosome we compute the number of observed recombinations from one position to the next, ignoring the heterozygous and unknown genotypes (nRecP). We then compute the recombination fraction (R) by dividing the number of recombinations observed (nRecP) by the population size used to generate the genetic map. The recombination fractions (R) are then deflated using the formula:

$$r = R/(4 - 6R)$$

, which is the inverse of the formula R = 4r/(1+6r) for a recombinant inbred line by sibling mating. We then use the function imf.cf available in the R package R/qtl (Arends et al., 2010; Broman et al., 2003) to convert from centiMorgan using the Carter-Falconer map function (Rédei, 2008a). Positions obtained start at 0 on each chromosome, requiring all positions to be shifted so that the first marker on the map matches the known centiMorgan position of the first marker on the genetic map. The old genetic map and the mouse map converter (http://cgd.jax.org/mousemapconverter/) were used to obtain centiMorgan positions for the first marker on a chromosome, all position on a chromosome are shifted to align the genetic map to the known starting positions of the markers. Code for computing marker positions is available in the BXDtools package (https://github.com/DannyArends/BXDtools), and positions can be recomputed using different map functions when required (e.g. Haldane (Rédei, 2008b), Kosambi (Rédei, 2008c), Morgan (Rédei, 2008d)).

Comparing genotype files

Over the past four decades many genotype files have been used for QTL mapping of the BXDs. The first carefully vetted genome-wide map (which we call the ‘original’) was generated in 2001, and mainly made up of 1,578 microsatellite markers (Wang et al., 2003; Williams et al., 2001). The second ‘classic’ map was used between 2005–2016 and contained 3,811 SNPs from various array platforms (Shifman et al., 2006). The current third-generation file is based on 7,321 informative SNPs described above.

For the 2001 markers, Mouse Genome Informatics was used to update 1419 microsatellites to the current assembly. This left 159 orphaned markers without mm10 positions. We used the NCBI Probe database (www.ncbi.nlm.nih.gov/probe/) to search for these 159 markers, and extracted primer sequence for 107. We ran Primer-BLAST (www.ncbi.nlm.nih.gov/tools/primer-blast/index.cgi) to determine where in the mm10 genome they would amplify.

For the remaining 52 markers, we used BLAST to align the target sequence to identify the mm10 position. This left 11 markers which Primer-BLAST either predicted a different chromosome would be amplified, or which did not have any mm10 genomic targets.

These 'original' genotypes only exist for the first 36 BXD strains (BXD1–42), and so the remaining strains were imputed (BXD24a and BXD 43+), using the genotype at the microsatellite's position in the 'current' post-2017 genotyping file. To determine our power to detect QTLs, we ran mapping using QTL Reaper for the 7562 phenotypes collected for the BXD, and the number of phenotypes which had a LOD greater than three threshold values: 2.2, 3.6 and 5.4. These correspond to suggestive, significant, and highly significant LOD values. The larger the number of phenotypes above these thresholds, the greater our power to detect QTLs.

Precision and Resolution

To estimate the empirical precision of mapping across the genome we have extracted data from 40 large-scale genetic studies of gene expression of the BXD family. These studies used between 21 and 79 strains with variable numbers of within-strain replicates over 27 tissues. We defined eQTLs that map within ±20 Mb of the gene associated with the transcript's measurement as *cis*-acting expression QTLs (*cis*-eQTLs). Unlike a standard F2 intercross, this ±20 Mb window is roughly equivalent to a recombination distance of ±40 cM in the highly recombinant BXD family, and the statistical association between markers this far apart is generally quite low (r^2 less than 0.3).

Precision was estimated using the offset between the location of the gene (using the 5' end of the probe or probe set as a reference point), and the location of the SNP with the highest LOD score. Again, this is conservative, as the causal variant is unlikely to be exactly at the 5' end of the gene. There are often two or more neighboring SNPs with equally high LOD scores and we simply take the most proximal marker to compute offset. The light blue local regression (LOESS) smoother curve (Cleveland, 1979) was computed using a window with a size of 0.333% of the genome. Smoothing was carried out and data was plotted using the *ggplot2* R package.

QTL mapping

QTL mapping using GeneNetwork has been described in detail elsewhere (Mulligan et al., 2017). However, in brief, quantitative trait loci (QTLs) are segments of the genome affecting a particular phenotype (Falconer and Mackay, 1996). QTL mapping, identifying QTLs to explain the genetic basis of complex traits, relies on being able to make correlations between genetic markers and phenotypic traits in a population. Individuals are scored for their phenotype for a particular trait, and their genotype at a marker. If there is a difference in mean phenotype between those individuals with one genotype compared with the other than we can infer that there is a QTL linked to that marker. If there is no difference between the means we can conclude that the locus does not influence the phenotype in that population (Falconer and Mackay, 1996; Miles and Wayne, 2008).

Due to the very high density of markers, the mapping algorithm used to map BXD data sets has been modified and is a mixture of simple marker regression, linear interpolation, and

standard Haley-Knott interval mapping (Haley and Knott, 1992). When two adjacent markers have identical strain distribution patterns, they will have identical linkage statistics, as will the entire interval between these two markers (assuming complete and error-free haplotype data for all strains). On a physical map the LOD and the additive effect values will, therefore, be constant over this physical interval. Between neighboring markers that have different strain distribution patterns and that are separated by 1 cM or more, we use a conventional interval mapping method (Haley-Knott) combined with a Haldane estimate of genetic distance. When the interval is less than 1 cM, we simply interpolate linearly between markers based on a physical scale between those markers. The result of this mixture mapping algorithm is a linkage map of a trait that has an unusual profile that is particularly striking on a physical (Mb) scale, with many plateaus, abrupt linear transitions between plateaus, and a few regions with the standard graceful curves typical of interval maps.

Prior to the 2017 release of the genotypes described in this manuscript interval mapping in GeneNetwork relied on 3,795 informative SNP markers across all autosomes and the X chromosome (Wang et al., 2003). These markers were generated using the MUGA array in 2011, along with earlier generated genotypes on the Affymetrix and Illumina platforms (Shifman et al., 2006). As described above, loci are identified in GeneNetwork by the computation of a likelihood ratio statistic score (LRS), and significance was determined using at least 5,000 permutations of the phenotype data.

Updated QTL mapping methods, such as R/qtl (Broman et al., 2003, 2019), Multiple QTL mapping (Arends et al., 2010), GEMMA (Zhou and Stephens, 2012) and pyLMM (Sul et al., 2016), have been implemented on the GeneNetwork site (Sloan et al., 2016). The LMM based methods for kinship between BXD strains by computing a genetic kinship matrix given specific strains used in an analysis, allowing for precise kinship correction and improved QTL mapping performance when mapping any of the BXD phenotypes in the GeneNetwork database.

R/qtl2 (Broman et al., 2003, 2019) was also used to carry out QTL mapping, independently, in the R environment. The functions *scan1* and *scan1perm* were used to calculate linkage for all phenotypes, and permutation thresholds. For Haley-Knott mapping no kinship correction was used, and for LMM the *calc_kinship* function was used, with leave one chromosome out (LOCO).

Power calculation

Power calculations were carried out based on the method of Sen and colleagues (Sen et al., 2007) and implemented in the R program *qtlDesign* based on the H^2_{RIX} defined by Belknap (Belknap, 1998), which we renamed $H^2_{i\bar{x}}$ as it is applicable to any isogenic strain, not just recombinant inbreds. The *Detectable* function was used, to determine the power available with an RI design to detect a locus of a given effect size.

For calculation of the $H^2_{i\bar{x}}$, four variables need to be known: heritability (h^2), the number of within-strain replicates (biological replicates), the number of strains used, and the locus effect size (the proportion of total genetic variance explained by the locus). To calculate h^2,

the genomic variance (gen.var) was kept constant at 1, and the environmental variance (env.var) was varied to produce h^2 values ranging between 0 and 1. The number of biological replicates and the number of strains are self-explanatory, and were capped at 10 and 150 respectively, since >10 replicates produced a marginal increase in power, and because there are a maximum of 150 BXD lines.

The locus effect size is the amount of the variance which is due to genetics (gen.var) explained by a single QTL. That is, a value of 0.2 would mean that a QTL explains 20% of the genetic variance, and a value of 1.0 indicates a Mendelian locus (one QTL which explains all of the genetic variance).

The power given is the ability of the experiment to correctly detect a true positive QTL, given the other values above. The BXD power app can be found at http://power.genenetwork.org/ and uses the *Shiny* R package (https://CRAN.R-proiect.orq/packaqe=shiny).

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

Thanks to Dr. Abraham Palmer for providing B6D2 advanced intercross progeny (G8 and G9) to make BXD160 through BXD186. We thank Drs. Gerald McClearn and Lisa Tarantino for 60 eighth-generation (G8) AI progeny from Pennsylvania State University contributed to epoch 3. We thank Dr. Benjamin A. Taylor for initiating the BXD and for continued support and encouragement. We thank Dr. Saunak Sen for consultation on power calculations and qtlDesign. We thank members of the EPFL Center for Phenogenomics in particular Drs. Xavier Warot and Emilie Gesina for sharing data from their BXD colony, and Erik Soehnel from Scionics for assistance in obtaining the full breeding statistics.

The UTHSC Center for Integrative and Translational Genomics (CITG) has supported production of the BXD colony at UTHSC and will continue to support this colony for the duration of the grant. The CITG also provides generous support for computer hardware and programming associated with GeneNetwork, and our Galaxy and UCSC Genome Browser instances.

We thank the support of the UT Center for Integrative and Translational Genomics, and funds from the UT-ORNL Governor's Chair, NIDA grant P30DA044223, NIAAA U01 AA013499 and U01 AA016662 for the work at UTHSC. Work in the Auwerx lab on the BXDs is supported by the Ecole Polytechnique Fédérale de Lausanne, the ERC (AdG-787702), the SNSF (310030B-160318), the AgingX program of the Swiss Initiative for Systems Biology (RTD 2013/153), and the NIH (R01AG043930). The BXD Resource at the Jackson Laboratory is supported by NIH P40 OD011102 awarded to Dr. Cathleen M. Lutz.

The data sets generated and/or analyzed during the current study are available in the GeneNetwork repository, https://www.genenetwork.org/.

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Highlights

- There are now 140 fully inbred BXD strains available, with high-quality genotypes
- More strains, new genotypes, and new models have improved power and precision
- We have high power even for traits with low heritability or small effect sizes
- A phenome of >100 omics datasets and >7500 classic phenotypes is freely available

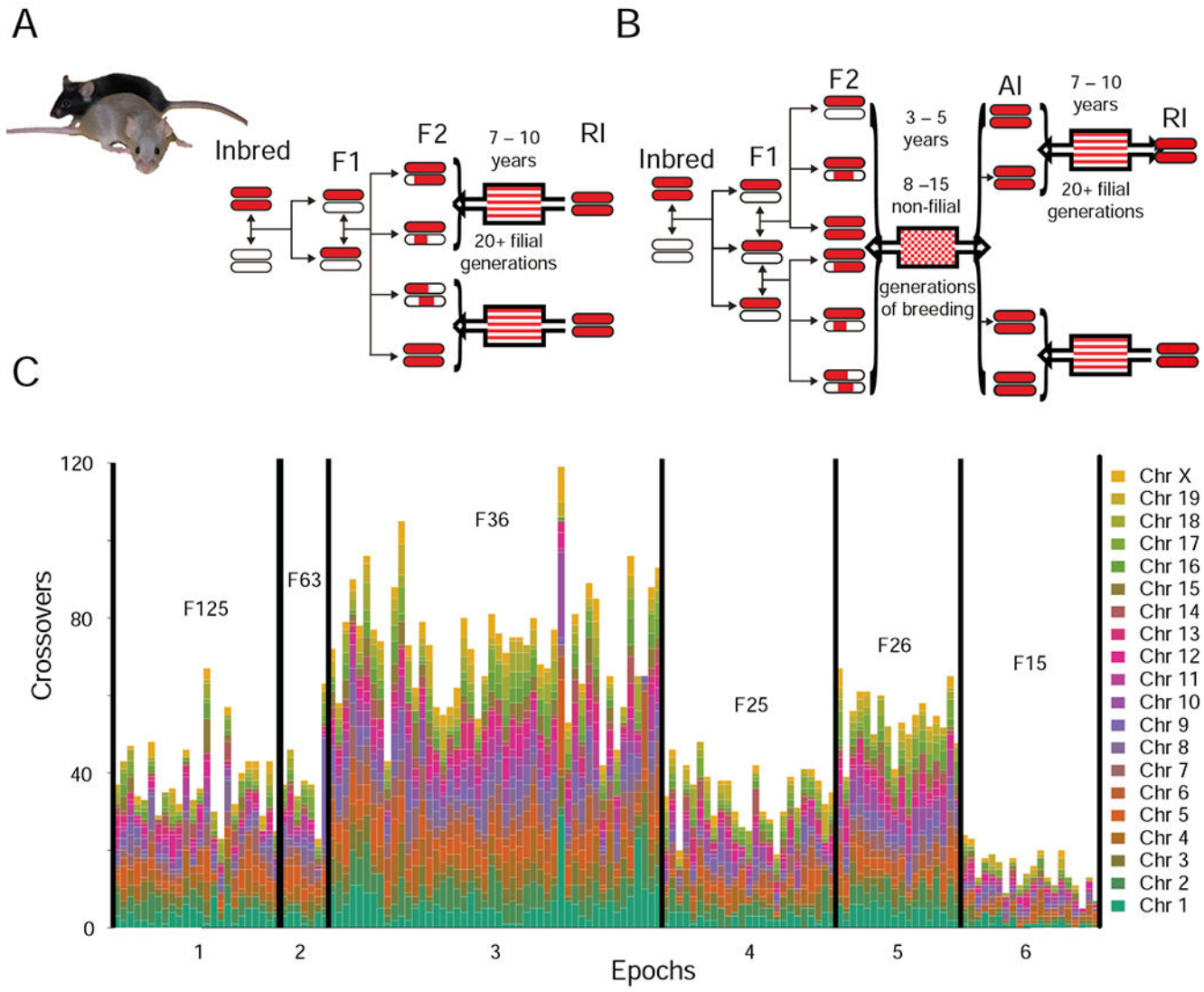

Figure 1: Production of the BXD family by standard F2 (A) or advanced intercross (B), and recombination differences (C).

Four epochs of the BXD were derived from F2 (**A**) (~75 strains; epochs 1,2,4,6 in **C**). Two epochs were derived from advanced intercross (**B**) (~65 strains; epochs 3, 5 in **C**). Red represents regions of the genome coming from C57BL/6J (B6), white represents regions from the DBA/2J (D2). Solid lines represent a single generation. Adapted from Peirce et al., 2004. **(C) Genome wide visualization of recombinations in the BXD.** Number of recombinations per strain (nRecS), ignoring heterozygous and unknown genotypes plotted using a color gradient. Strain numbers on the X-axis, horizontal lines separate the epochs, epochs are annotated on the X-axis. Mean number of inbreeding generations is shown for each epoch. Epoch 6 appears to have fewer recombinations due to a large number of heterozygous loci at genotyping. Details in Figure S1 and Table S1.

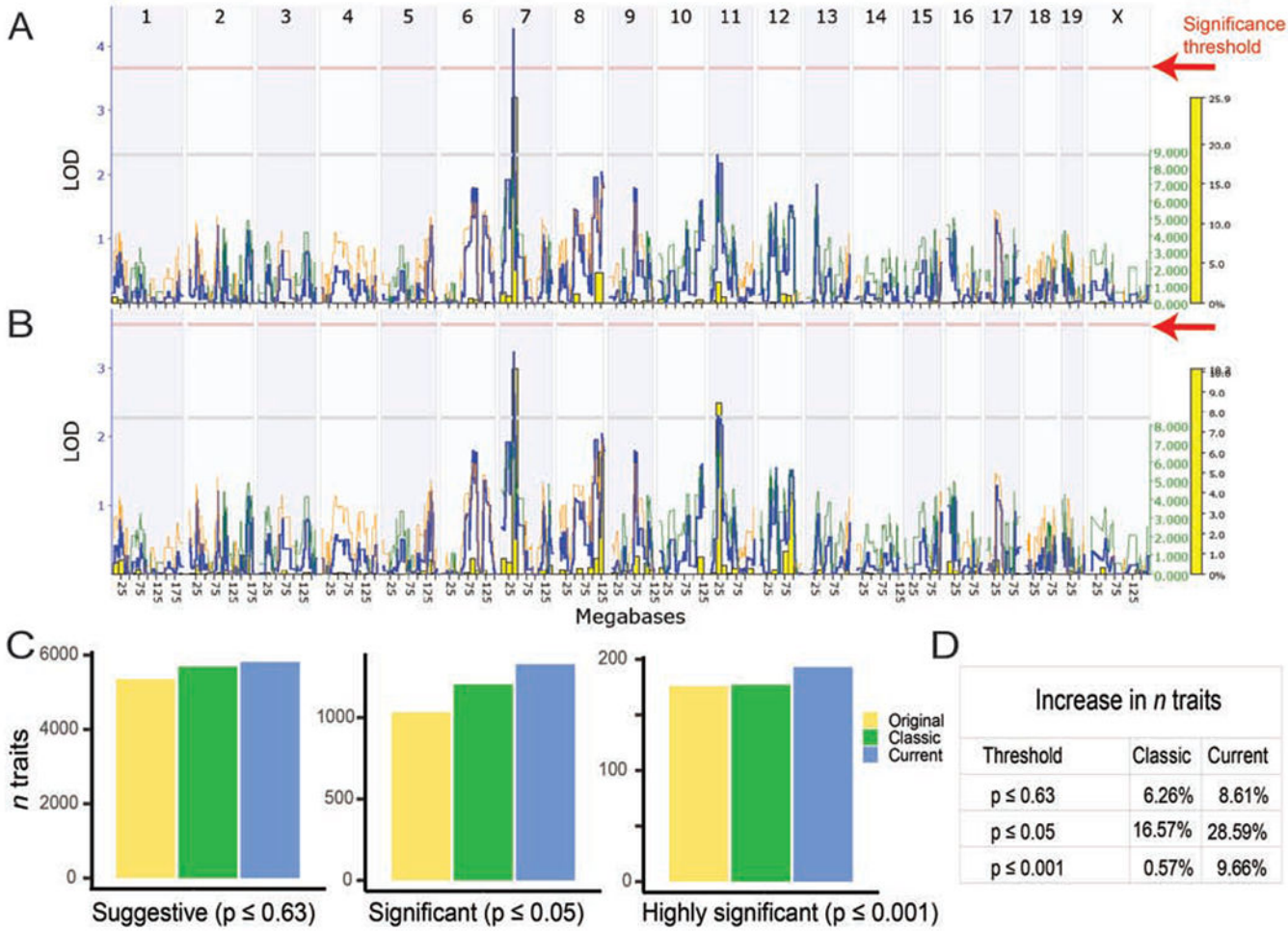

Figure 2: Improved, denser, genotypes increase linkage across chromosomes, decades of work, and number of strains.

Comparison of current **(A)** and classic **(B)** genotypes for BXD_10666, Cytotoxic T-cell (CTL) response (5 x 10^9 PFU AdLacZ iv), measured as interleukin 6 (IL-6) cytokine expression [pg/ml], published by Zhang et al., 2004, measured in 23 strains. A QTL on chromosome 7 is now significant (above the red p = 0.05 significance line) using the current genotypes **(A)**, compared to the classic genotypes **(B)**. Additional examples in Figure S2. **(C)** Bar chart showing the number of phenotypes with a peak LOD score over the suggestive (LOD ≥ 2.2; p ≤ 0.63), significant (LOD ≥ 3.6; p ≤ 0.05) and highly significant (LOD ≥ 5.4; p ≤ 0.001) thresholds, using original, classic or current marker maps. **(D)** Percentage increase in the number of traits passing the thresholds in the classic or current genotype map, compared to the original map.

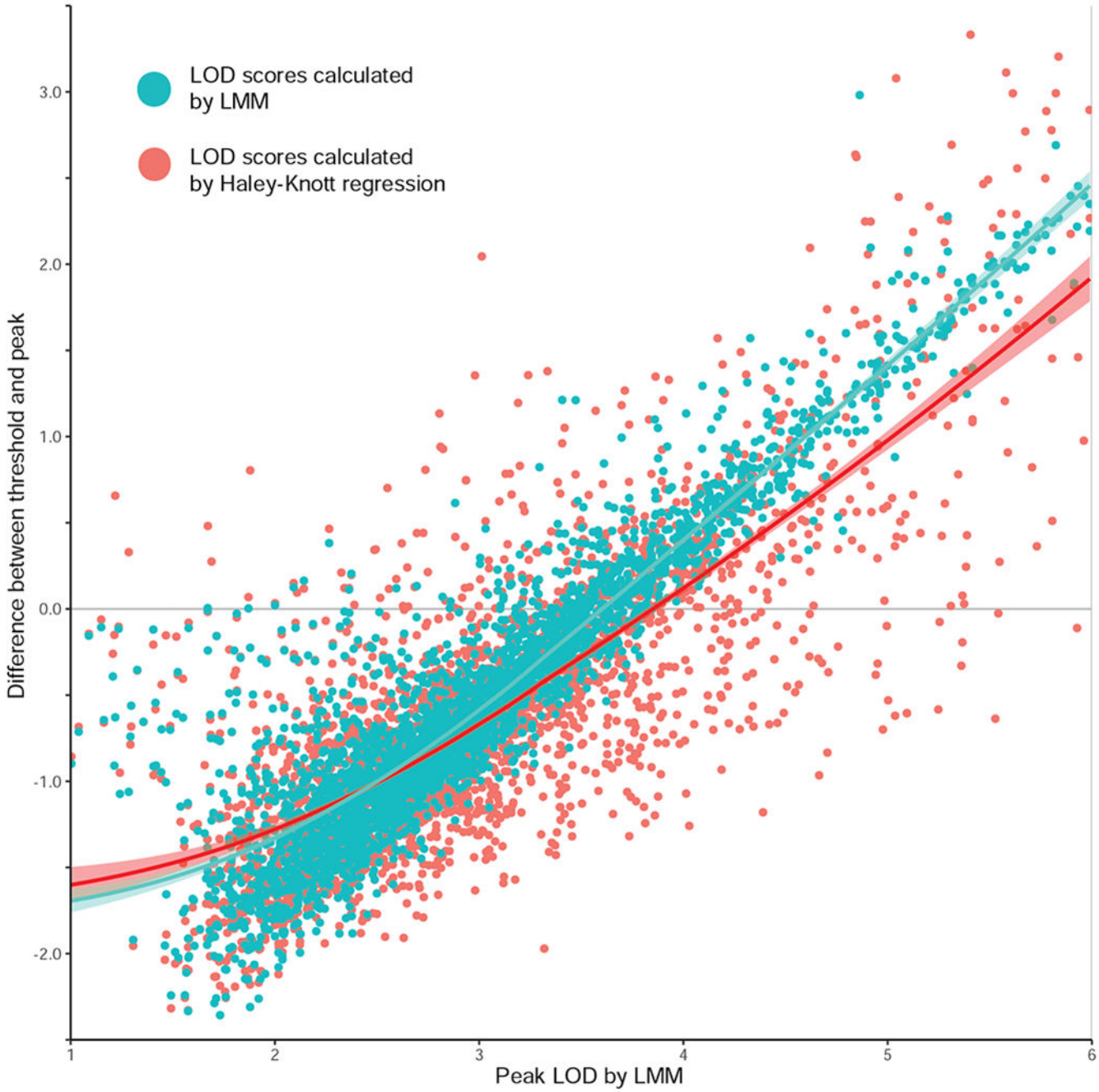

Figure 3: Improvement in mapping by using linear mixed models (LMMs) vs Haley-Knott regression (H-K).

Linkage measured in 3300 phenotypes from GeneNetwork, and mapped using Haley-Knott regression or an LMM in R/qtl2 (Broman et al., 2003, 2019). Y-axis is difference in LOD from the significance threshold (calculated by 5000 permutations) and the peak LOD. X-axis is the peak LOD, calculated by LMM, so that points can be directly compared. Each point represents a phenotype, LMM results plotted turquoise, Haley-Knott plotted red. A smoother was fitted in the same colors for comparison. Underlying data in Table S2.

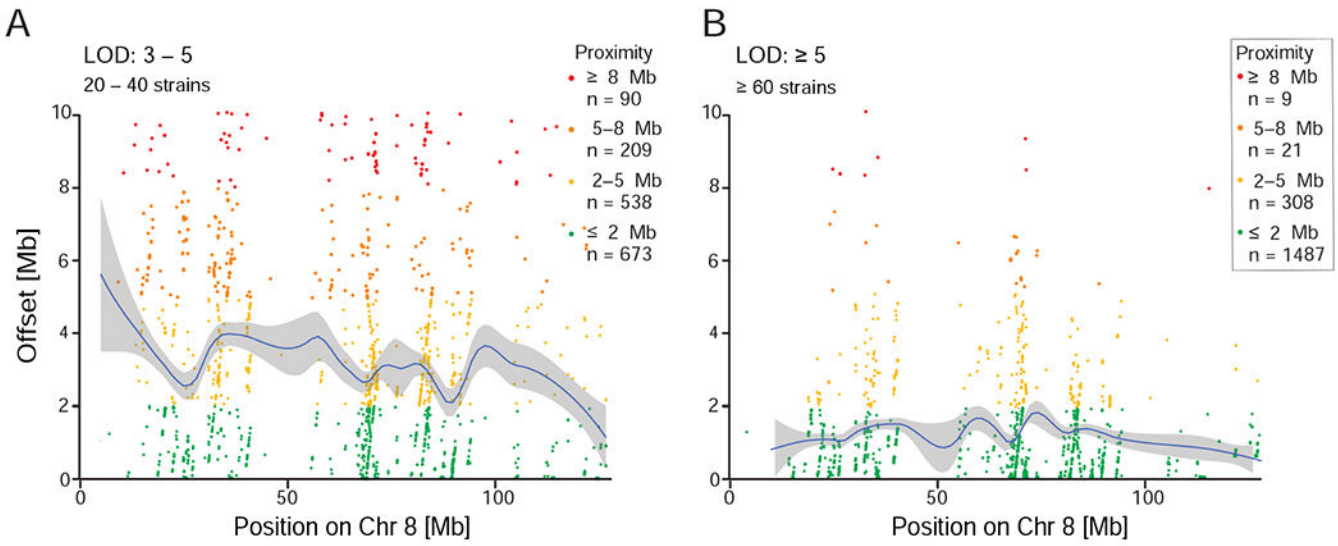

Figure 4: Empirical QTL mapping precision estimated using *cis*-eQTLs.

Each point shows the distance between a probe and an eQTL. **(A)** Precision achieved when mapping modest QTLs with LOD scores of 3-5 and using only 20-40 strains and 2-4 samples per strain. Number of replicates within each strain will affect the precision to a greater extent for QTLs with low heritability and modest LOD scores by increasing the effective heritability (see Belknap 1998). eQTL studies generally use only 1–4 replicates, so precision values are conservative. Mean offset across the genome is 4.67 Mb, median 2.72 Mb. **(B)** Precision achieved when mapping highly significant QTLs with LOD > 5, using 60–80 strains, with > 2 replicates. Mean offset is 1.38 Mb, median 0.76 Mb.

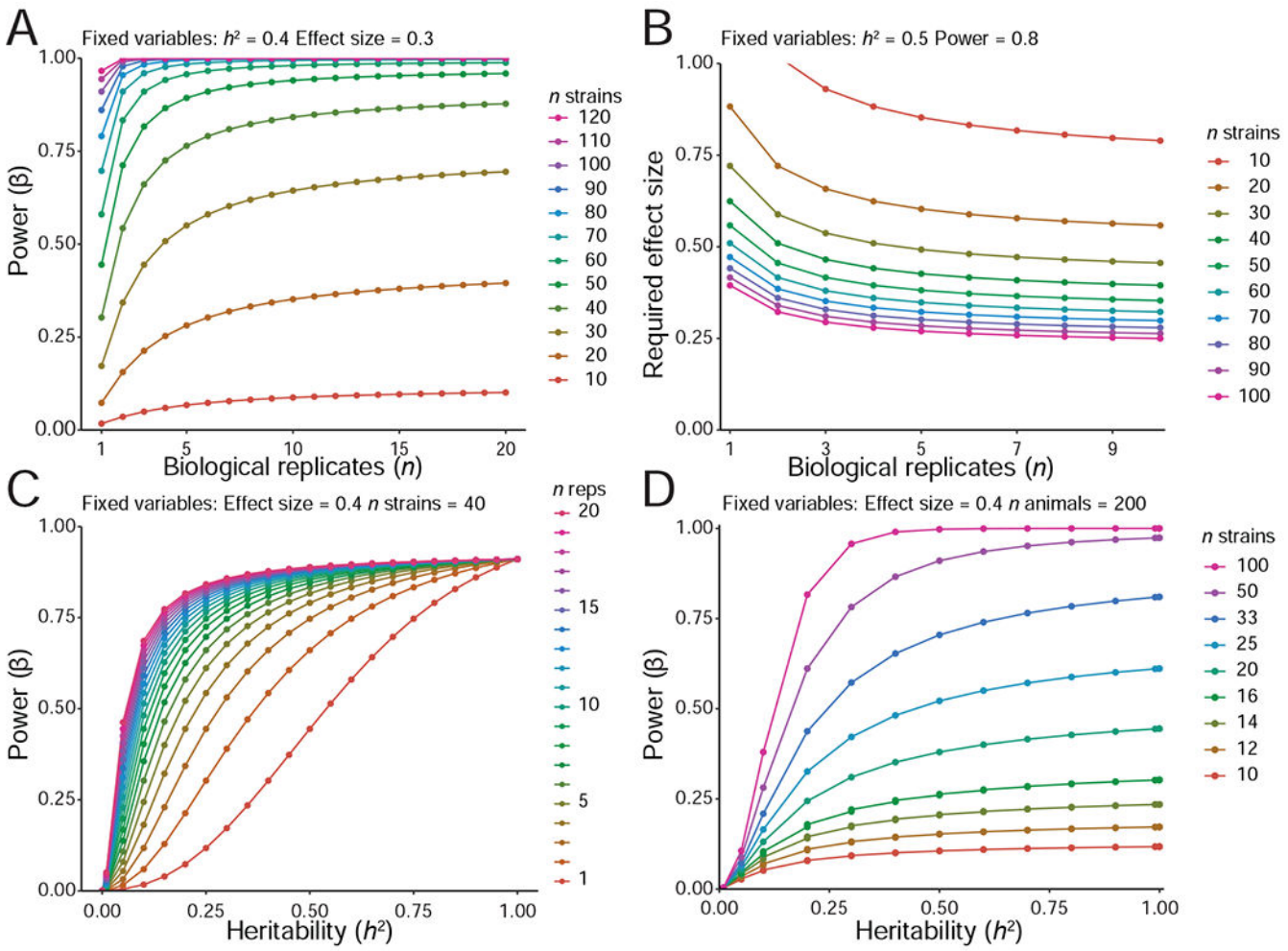

Figure 5: Relations between power, numbers of strains and replicates in BXD, generated using qtlDesign (Sen et al., 2007).

(**A)** Power to detect a given effect for *n* replicates and *n* strains. Locus effect size and heritability constant at 0.3 and 0.4 respectively. More replicates increase power but beyond four replicates gain in power is marginal. (**B)** Effect size detectable, given *n* replicates and strains. Heritability and power kept at 0.5 and 0.8. (**C)** Power to detect a given effect size, dependent upon heritability and *n* biological replicates. Locus effect size and *n* strains kept at 0.4 and 40. With very low h^2 there is no power, and with lower h^2 the gain in power is stronger with increasing number of replicates compared with high h^2. Beyond four replicates, the gain in power is marginal. (**D)** Power to detect a given effect size, dependent upon heritability, with a total of 200 animals. These range from 100 lines with 2 replicates to 10 lines with 20 replicates. In contrast to what one might assume, even for low levels of h^2, power always increases with more lines rather than more replicates. Effect size kept at 0.4. Empirical example of power in the BXD can be found in Figure S3.

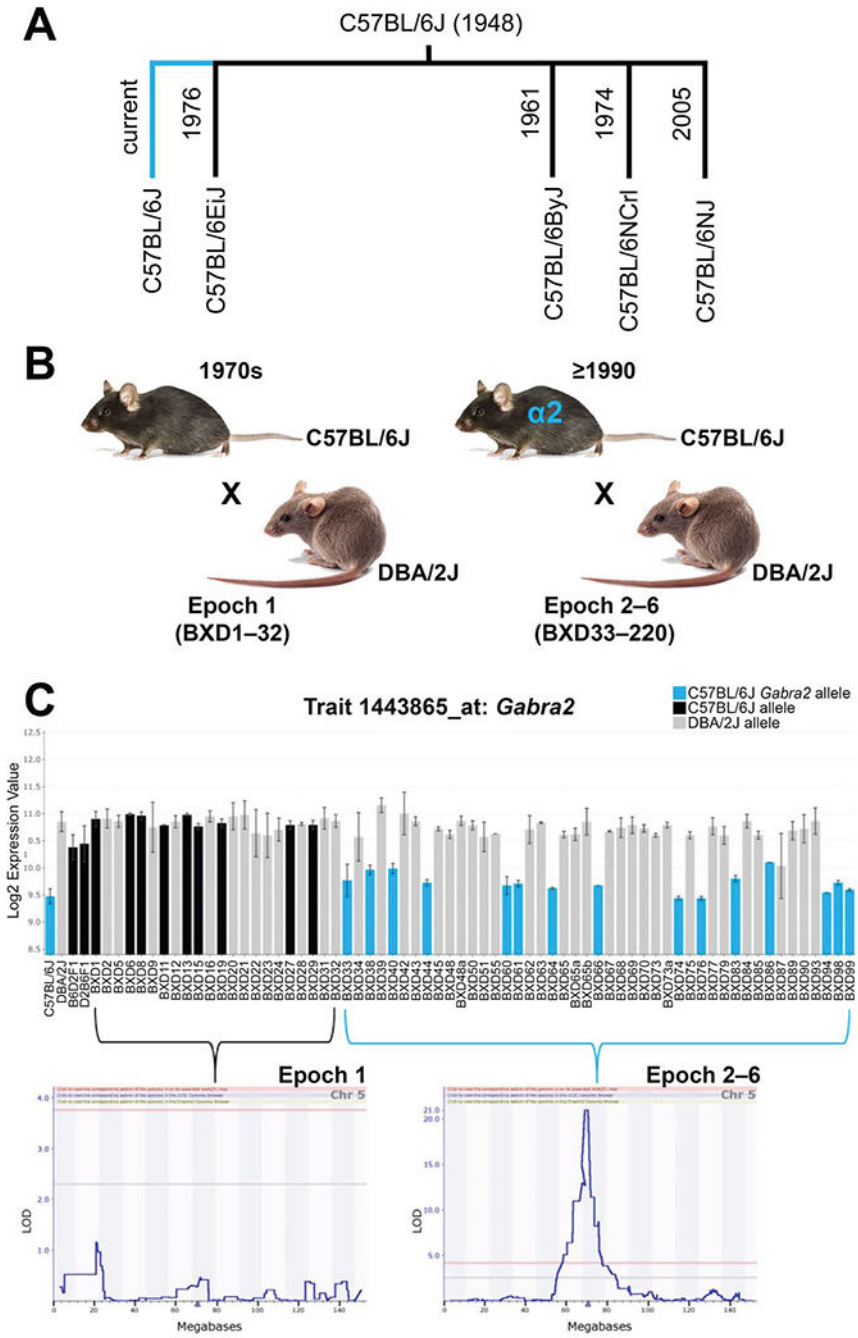

Figure 6: Impact of epoch-specific mutations in the BXD family.

(A) A private mutation (single nucleotide intronic deletion) in the Gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2 *(Gabra2)* gene occurred in the C57BL/6J lineage (turquoise line). The spontaneous mutation was fixed in Jackson Laboratory C57BL/6J foundation stock after separation of the C57BL/6EiJ substrain (1976), and **(B)** after the creation of the first BXD epoch (1970s). All BXD epochs (2–6) created after 1990 are derived from separate crosses between C57BL/6J and DBA/2J mice and segregate for the C57BL/6J *Gabra2* mutant allele (shown in turquoise). **(C)** Inheritance of the C57BL/6J

mutant allele (turquoise) results in a reduction of brain *Gabra2* expression levels relative to the ancestral C57BL/6J (black) or DBA/2J (gray) allele. Allele color coded based on *Gabra2* genotype at rs13478320. *Gabra2* mRNA expression values (trait 1443865) are shown for the hippocampus but are replicated in other brain regions and at the protein level. QTL mapping in epoch 1 or later epochs demonstrates how the absence or presence of segregating C57BL/6J mutant *Gabra2* alleles controls gene expression.

KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Deposited Data		
GeneNetwork	Genenetwork.org	RRID:SCR_002388
Experimental Models: Organisms/Strains		
Mouse: BXD1/TyJ	JAX	RRID:000036
Mouse: BXD2/TyJ	JAX	RRID:000075
Mouse: BXD3	JAX	
Mouse: BXD4	JAX	
Mouse: BXD5/TyJ	JAX	RRID:000037
Mouse: BXD6/TyJ	JAX	RRID:000007
Mouse: BXD7	JAX	
Mouse: BXD8/TyJ	JAX	RRID:000084
Mouse: BXD9/TyJ	JAX	RRID:000105
Mouse: BXD10	JAX	
Mouse: BXD11/TyJ	JAX	RRID:000012
Mouse: BXD12/TyJ	JAX	RRID:000045
Mouse: BXD13/TyJ	JAX	RRID:000040
Mouse: BXD14/TyJ	JAX	RRID:000329
Mouse: BXD15/TyJ	JAX	RRID:000095
Mouse: BXD16/TyJ	JAX	RRID:000013
Mouse: BXD17	JAX	
Mouse: BXD18/TyJ	JAX	RRID:000015
Mouse: BXD19/TyJ	JAX	RRID:000010
Mouse: BXD20/TyJ	JAX	RRID:000330
Mouse: BXD21/TyJ	JAX	RRID:000077
Mouse: BXD22/TyJ	JAX	RRID:000043
Mouse: BXD23/TyJ	JAX	RRID:000098
Mouse: BXD24/TyJ-Cep290rd16/J	JAX	RRID:000031 | rd16
Mouse: BXD24/TyJ	JAX	RRID:005243
Mouse: BXD25/TyJ	JAX	RRID:000081
Mouse: BXD26	JAX	
Mouse: BXD27/TyJ	JAX	RRID:000041
Mouse: BXD28/TyJ	JAX	RRID:000047
Mouse: BXD29/Ty	JAX	RRID:010981
Mouse: BXD29-Tlr4lps-2J/J	JAX	RRID:000029 | defective lipopolysaccharide response, 2J
Mouse: BXD30/TyJ	JAX	
Mouse: BXD31/TyJ	JAX	RRID:000083
Mouse: BXD32/TyJ	JAX	RRID:000078

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Mouse: BXD32/TyJ-Galctwi-5J/J	JAX	RRID:003613 | twitcher 5 Jackson
Mouse: BXD33/TyJ	JAX	RRID:003222
Mouse: BXD34/TyJ	JAX	RRID:003223
Mouse: BXD35/Ty	JAX	
Mouse: BXD36/TyJ	JAX	RRID:003225
Mouse: BXD37/Ty	JAX	
Mouse: BXD38/TyJ	JAX	RRID:003227
Mouse: BXD39/TyJ	JAX	RRID:003228
Mouse: BXD40/TyJ	JAX	RRID:003229
Mouse: BXD41/Ty	JAX	
Mouse: BXD42/TyJ	JAX	RRID:003230
Mouse: BXD43/RwwJ	JAX	RRID:007093
Mouse: BXD44/RwwJ	JAX	RRID:007094
Mouse: BXD45/RwwJ	JAX	RRID:007096
Mouse: BXD46	JAX	
Mouse: BXD47	JAX	
Mouse: BXD48/RwwJ	JAX	RRID:007097
Mouse: BXD48a/RwwJ	JAX	RRID:007139
Mouse: BXD49/RwwJ	JAX	RRID:007098
Mouse: BXD50/RwwJ	JAX	RRID:007099
Mouse: BXD51/RwwJ	JAX	RRID:007100
Mouse: BXD52	UTHSC	
Mouse: BXD53/2RwwJ	JAX	RRID:017749
Mouse: BXD54	UTHSC	
Mouse: BXD55/RwwJ	JAX	RRID:007103
Mouse: BXD56/RwwJ	JAX	RRID:007104
Mouse: BXD57	UTHSC	
Mouse: BXD58	UTHSC	
Mouse: BXD59	UTHSC	
Mouse: BXD60/RwwJ	JAX	RRID:007105
Mouse: BXD61/RwwJ	JAX	RRID:007106
Mouse: BXD62/RwwJ	JAX	RRID:007107
Mouse: BXD63/RwwJ	JAX	RRID:007108
Mouse: BXD64/RwwJ	JAX	RRID:007109
Mouse: BXD65/RwwJ	JAX	RRID:007110
Mouse: BXD65a/RwwJ	JAX	RRID:007140
Mouse: BXD65b/RwwJ	JAX	RRID:009677
Mouse: BXD66/RwwJ	JAX	RRID:007111
Mouse: BXD67/RwwJ	JAX	RRID:007112

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Mouse: BXD68/RwwJ	JAX	RRID:007113
Mouse: BXD69/RwwJ	JAX	RRID:007114
Mouse: BXD70/RwwJ	JAX	RRID:007115
Mouse: BXD71/RwwJ	JAX	RRID:007116
Mouse: BXD72	UTHSC	
Mouse: BXD73/RwwJ	JAX	RRID:007117
Mouse: BXD73a/RwwJ	JAX	RRID:007124
Mouse: BXD73b/RwwJ	JAX	RRID:007146
Mouse: BXD74/RwwJ	JAX	RRID:007118
Mouse: BXD75/RwwJ	JAX	RRID:007119
Mouse: BXD76	UTHSC	
Mouse: BXD77/RwwJ	JAX	RRID:007121
Mouse: BXD78/2RwwJ	JAX	RRID:024029
Mouse: BXD79/RwwJ	JAX	RRID:007123
Mouse: BXD80	UTHSC	
Mouse: BXD81/RwwJ	JAX	RRID:007125
Mouse: BXD82	UTHSC	
Mouse: BXD83/RwwJ	JAX	RRID:007126
Mouse: BXD84/RwwJ	JAX	RRID:007127
Mouse: BXD85/RwwJ	JAX	RRID:007128
Mouse: BXD86/RwwJ	JAX	RRID:007129
Mouse: BXD87/RwwJ	JAX	RRID:007130
Mouse: BXD88/2RwwJ	JAX	RRID:017750
Mouse: BXD89/RwwJ	UTHSC	
Mouse: BXD90/RwwJ	JAX	RRID:007133
Mouse: BXD91/2RwwJ	JAX	RRID:017751
Mouse: BXD92	UTHSC	
Mouse: BXD93	UTHSC	
Mouse: BXD94	UTHSC	
Mouse: BXD95/RwwJ	JAX	RRID:007138
Mouse: BXD96	UTHSC	
Mouse: BXD97	UTHSC	
Mouse: BXD98/RwwJ	JAX	RRID:007141
Mouse: BXD99/RwwJ	JAX	RRID:007142
Mouse: BXD100/RwwJ	JAX	RRID:007143
Mouse: BXD101/RwwJ	JAX	RRID:007144
Mouse: BXD102/RwwJ	JAX	RRID:007145
Mouse: BXD103	UTHSC	
Mouse: BXD104	UTHSC	

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Mouse: BXD105	UTHSC	
Mouse: BXD106	UTHSC	
Mouse: BXD107	UTHSC	
Mouse: BXD108	UTHSC	
Mouse: BXD109	UTHSC	
Mouse: BXD110	UTHSC	
Mouse: BXD111/RwwJ	JAX	RRID:030872
Mouse: BXD112	UTHSC	
Mouse: BXD113/RwwJ	JAX	RRID:024030
Mouse: BXD114		
Mouse: BXD115	UTHSC	
Mouse: BXD116	UTHSC	
Mouse: BXD117	UTHSC	
Mouse: BXD118	UTHSC	
Mouse: BXD119	UTHSC	
Mouse: BXD120	UTHSC	
Mouse: BXD121	UTHSC	
Mouse: BXD122/RwwJ	JAX	RRID:030873
Mouse: BXD122a	UTHSC	
Mouse: BXD123/RwwJ	JAX	RRID:025974
Mouse: BXD124/RwwJ	JAX	RRID:025975
Mouse: BXD125/RwwJ	JAX	RRID:024031
Mouse: BXD126	UTHSC	
Mouse: BXD127		
Mouse: BXD128/RwwJ	JAX	RRID:030874
Mouse: BXD128a/RwwJ	JAX	RRID:030875
Mouse: BXD129	UTHSC	
Mouse: BXD130	UTHSC	
Mouse: BXD131	UTHSC	
Mouse: BXD132	UTHSC	
Mouse: BXD133	UTHSC	
Mouse: BXD134	UTHSC	
Mouse: BXD135	UTHSC	
Mouse: BXD136	UTHSC	
Mouse: BXD137	UTHSC	
Mouse: BXD138	UTHSC	
Mouse: BXD139	UTHSC	
Mouse: BXD140	UTHSC	
Mouse: BXD141/RwwJ	JAX	RRID:029865

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Mouse: BXD142	UTHSC	
Mouse: BXD143	UTHSC	
Mouse: BXD144/RwwJ	JAX	RRID:025984
Mouse: BXD145	UTHSC	
Mouse: BXD146	UTHSC	
Mouse: BXD147	UTHSC	
Mouse: BXD148	UTHSC	
Mouse: BXD149	UTHSC	
Mouse: BXD150/RwwJ	JAX	RRID:029867
Mouse: BXD151/RwwJ	JAX	RRID:029868
Mouse: BXD152/RwwJ	JAX	RRID:029869
Mouse: BXD153	UTHSC	
Mouse: BXD154/RwwJ	JAX	RRID:025976
Mouse: BXD155	UTHSC	
Mouse: BXD156/RwwJ	JAX	RRID:029871
Mouse: BXD156a	UTHSC	
Mouse: BXD157/RwwJ	JAX	RRID:029872
Mouse: BXD158	UTHSC	
Mouse: BXD159	UTHSC	
Mouse: BXD160/RwwJ	JAX	RRID:029873
Mouse: BXD161/RwwJ	JAX	RRID:025985
Mouse: BXD162	UTHSC	
Mouse: BXD163	UTHSC	
Mouse: BXD164	UTHSC	
Mouse: BXD165	UTHSC	
Mouse: BXD166	UTHSC	
Mouse: BXD167	UTHSC	
Mouse: BXD168/RwwJ	JAX	RRID:029874
Mouse: BXD169/RwwJ	JAX	RRID:029876
Mouse: BXD170/RwwJ	JAX	RRID:029878
Mouse: BXD171/RwwJ	JAX	RRID:029879
Mouse: BXD172/RwwJ	JAX	RRID:029880
Mouse: BXD173	UTHSC	
Mouse: BXD174	UTHSC	
Mouse: BXD175	UTHSC	
Mouse: BXD176	UTHSC	
Mouse: BXD177/RwwJ	JAX	RRID:029881
Mouse: BXD178/RwwJ	JAX	RRID:029882
Mouse: BXD179	UTHSC	

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Mouse: BXD180/RwwJ	JAX	RRID:029883
Mouse: BXD181	UTHSC	
Mouse: BXD182	UTHSC	
Mouse: BXD183	UTHSC	
Mouse: BXD184/RwwJ	JAX	RRID:029884
Mouse: BXD185	UTHSC	
Mouse: BXD186/RwwJ	JAX	RRID:029885
Mouse: BXD187/RwwJ	JAX	RRID:031974
Mouse: BXD188	UTHSC	
Mouse: BXD189	UTHSC	
Mouse: BXD190/RwwJ	JAX	RRID:030876
Mouse: BXD191/RwwJ	JAX	RRID:030877
Mouse: BXD192	UTHSC	
Mouse: BXD193	UTHSC	
Mouse: BXD194/RwwJ	JAX	RRID:030878
Mouse: BXD195/RwwJ	JAX	RRID:030879
Mouse: BXD196	UTHSC	
Mouse: BXD197/RwwJ	JAX	RRID:030880
Mouse: BXD198	UTHSC	
Mouse: BXD199/RwwJ	JAX	RRID:030881
Mouse: BXD200	UTHSC	
Mouse: BXD201	UTHSC	
Mouse: BXD202/RwwJ	JAX	RRID:031975
Mouse: BXD203	UTHSC	
Mouse: BXD204	UTHSC	
Mouse: BXD205	UTHSC	
Mouse: BXD206	UTHSC	
Mouse: BXD207	UTHSC	
Mouse: BXD208	UTHSC	
Mouse: BXD209	UTHSC	
Mouse: BXD210/RwwJ	JAX	RRID:031976
Mouse: BXD211	UTHSC	
Mouse: BXD212	UTHSC	
Mouse: BXD213	UTHSC	
Mouse: BXD214/RwwJ	JAX	RRID:030882
Mouse: BXD215/RwwJ	JAX	RRID:031977
Mouse: BXD216/RwwJ	JAX	RRID:031978
Mouse: BXD217	UTHSC	
Mouse: BXD218	UTHSC	

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Mouse: BXD219	UTHSC	
Mouse: BXD220	UTHSC	
Mouse: BXD221	UTHSC	
Mouse: BXD222	UTHSC	
Mouse: BXD223	UTHSC	
Mouse: BXD224	UTHSC	
Mouse: BXD225	UTHSC	
Mouse: BXD226	UTHSC	
Mouse: BXD227	UTHSC	
Mouse: BXD228	UTHSC	
Software and Algorithms		
GeneNetwork	Genenetwork.org	RRID:SCR_002388
BXDtools		https://github.com/DannyArends/BXDtools
BXD power calculator app	http://power.genenetwork.org/; this paper	https://github.com/Dashbrook/BXD_power_calculator_app
R/qtl2	Broman et al., 2019	RRID:SCR_018181; https://kbroman.org/qtl2/