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## Research

# Derived variants at six genes explain nearly half of size reduction in dog breeds

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Selective breeding of dogs by humans has generated extraordinary diversity in body size. A number of multibreed analyses have been undertaken to identify the genetic basis of this diversity. We analyzed four loci discovered in a previous genome-wide association study that used 60,968 SNPs to identify size-associated genomic intervals, which were too large to assign causative roles to genes. First, we performed fine-mapping to define critical intervals that included the candidate genes *GHR*, *HMG2*, *SMAD2*, and *STC2*, identifying five highly associated markers at the four loci. We hypothesize that three of the variants are likely to be causative. We then genotyped each marker, together with previously reported size-associated variants in the *IGF1* and *IGFIR* genes, on a panel of 500 domestic dogs from 93 breeds, and identified the ancestral allele by genotyping the same markers on 30 wild canids. We observed that the derived alleles at all markers correlated with reduced body size, and smaller dogs are more likely to carry derived alleles at multiple markers. However, breeds are not generally fixed at all markers; multiple combinations of genotypes are found within most breeds. Finally, we show that 46%–52.5% of the variance in body size of dog breeds can be explained by seven markers in proximity to exceptional candidate genes. Among breeds with standard weights <41 kg (90 lb), the genotypes accounted for 64.3% of variance in weight. This work advances our understanding of mammalian growth by describing genetic contributions to canine size determination in non-giant dog breeds.

[Supplemental material is available for this article.]

Domestic dogs exhibit the greatest diversity in body size of any land mammal. Mastiffs can be 50 times heavier than Chihuahuas, and Great Danes five times taller than Pekingese. Dog breeds are all descended from the gray wolf (Wayne 1993; Lindblad-Toh et al. 2005) and are the product of artificial selection that began between 15,000 and 100,000 yr ago (Vilà et al. 1997; Sablin and Khlopachev 2002; Savolainen et al. 2002; Germonpré et al. 2009; Pang et al. 2009; Ovodov et al. 2011). However, the majority of the modern dog breeds were developed within the past 300 yr (American Kennel Club 1998; Parker et al. 2004). More than 400 breeds now exist worldwide, including 175 that are recognized in the United States by the American Kennel Club (AKC; [www.akc.org](http://www.akc.org)).

Modern domestic dog breeds are codified by standards, which apply persistent selective pressure on fixed phenotypes that are often breed defining, such as coat color, skull shape, leg length, and body size. This pressure reduces phenotypic and genetic heterogeneity within breeds, yet enormous phenotypic diversity exists across breeds (Parker et al. 2004, 2007; vonHoldt et al. 2010). These factors, along with the genetic isolation of breeds, have established domestic dog breeds as an excellent genetic system for the study of complex traits, including skeletal

size and shape variation (Chase et al. 2002; Shearin and Ostrander 2010).

Loci determining size have strong signatures of selection (Akey et al. 2010; Boyko et al. 2010; Vaysse et al. 2011). The first association studies of canine body size found an influential locus in spite of sparse marker density (Chase et al. 2002; Jones et al. 2008). Chase et al. (2002) used genotypes at ~500 microsatellites to analyze the genetic basis for canid morphological variation in Portuguese water dogs, a breed with significant variation in skeletal size (Chase et al. 2002), and identified multiple quantitative trait loci (QTLs) related to canine body size. A locus on canine chromosome 15 (CFA15) was observed to be highly associated with measures of skeletal size. Further investigation by our collaborative group led to the identification of a single haplotype composed of 20 single-nucleotide polymorphisms (SNPs) that was shared among all small breeds (<9 kg [20 lb]), but was nearly absent from giant breeds (>30 kg [66 lb]) (Sutter et al. 2007). The haplotype spans the insulin-like growth factor 1 (*IGF1*) gene, which is known to regulate skeletal size in both mice and humans (Baker et al. 1993; Woods et al. 1996).

A subsequent study by Jones et al. (2008) extended these findings and pioneered the use of breed-defined phenotypes (“stereotypes”) to identify associated markers, a method which is

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also used in the present study. Jones et al. (2008) tested the association of genotypes in 2801 dogs representing 147 breeds at 1536 SNPs with several breed stereotypes including weight, limb length, and height. They identified several new body size loci as well as replicating findings from previous studies (Chase et al. 2002, 2005), thus further supporting the use of breed standard measures, rather than individual measurements on each dog, in genetic studies of canine morphology.

Subsequent studies performed by our collaborative group on a much larger data set of 915 dogs from 80 breeds genotyped using 60,968 SNPs (the “CanMap project”) highlighted a number of phenotype-associated loci (Boyko et al. 2010). Among these were loci important in body size, some of which had been previously identified (Chase et al. 2002, 2005; Jones et al. 2008). Associations at four of the size-associated loci were replicated in data released by a subsequent study of 509 dogs from 46 breeds genotyped with 170,000 SNPs (Vaysse et al. 2011). Finally, the CanMap data set was used by Hoopes et al. (2012) to identify a new dog body size locus on CFA3 at the insulin-like growth factor 1 receptor gene (*IGF1*).

Here we describe the combinatorial effects of genetic variation at six loci on determining body size in dog breeds. At four autosomal loci previously found to be associated with canine body size (Boyko et al. 2010), the critical intervals resulting from our fine-mapping revealed excellent candidate genes, including growth hormone receptor (*GHR*), high mobility group AT-hook 2 (*HMG2*), stanniocalcin 2 (*STC2*), and SMAD family member 2 (*SMAD2*). We genotyped the most highly associated marker(s) at each locus, together with highly associated markers from the *IGF1* and *IGF1R* genes in a large set of dogs representing the entire range of canine body size. The resulting analysis shows that approximately half of the variance of the weights of dog breeds can be explained by polymorphisms at just these six loci.

## Results

We fine-mapped four body size QTLs identified in a previous genome-wide association study (GWAS) (Boyko et al. 2010). Initial critical intervals were selected based on association scores in the CanMap study at the following positions in CanFam3.1 coordinates: CFA10 (8,454,499,  $P = 7.06 \times 10^{-09}$ ), CFA4 (39,200,720,  $P = 9.10 \times 10^{-09}$  and 67,026,055,  $P = 2.58 \times 10^{-07}$ ), and CFA7 (43,865,905,  $P = 1.05 \times 10^{-06}$ ).

Standard breed weight (SBW) was used as a surrogate for body size, as has been done previously (Boyko et al. 2010). Specifically, when a weight was specified as part of an AKC breed standard, that value was used as the SBW for each dog of the breed in the data set. For breeds with no specified weight, values from other authorities were used (Methods; Supplemental Table 1). Where a range or different weights for male and female were given, an average was used. Since the phenotypic basis of this study is the standard weights of AKC breeds, which are specified and widely referred to in lb units, results are reported in lb as well as kg.

### Fine-mapping the size loci

Fine-mapping of the four autosomal loci validated the scan associations and revealed critical intervals that include the excellent candidate genes *GHR*, *HMG2*, *STC2*, and *SMAD2* (see Supplemental Results, Supplemental Figs. 1–3, and Supplemental Tables 2–5 for details on the fine-mapping experiments). The most highly associated variants at each locus were two nonsynonymous SNPs in *GHR*, one SNP in the 5′ UTR of *HMG2*, one SNP 20-kb down-

stream from *STC2*, and one deletion 24-kb downstream from *SMAD2* (Fig. 1A–D; Table 1). Here we refer to each variant by the name of the proximal gene. The two nonsynonymous SNPs in *GHR* are termed *GHR*(1) and *GHR*(2).

### Frequency of derived alleles at size-associated markers in 500 dogs

In order to determine the effective contributions of variants in or around *IGF1*, *IGF1R*, *GHR*, *HMG2*, *SMAD2*, and *STC2* on body size, the allele frequencies of tagging markers for each locus were determined from a large, physically diverse set of dogs representing 93 breeds.

We added previously described and highly associated markers at *IGF1* (Sutter et al. 2007; Gray et al. 2010) and *IGF1R* (Hoopes et al. 2012) to the panel of size-associated markers identified by fine-mapping, for a total of seven markers (Table 1). Of note, a SNP (CFA15:41,221,438) and a SINE insertion (CFA15:41,220,980) in intron 2 of *IGF1* were genotyped on DNA from 500 dogs and found to be in complete LD, which is consistent with previous reports (Sutter et al. 2007; Gray et al. 2010). Consequently, all future references to the *IGF1* variant refer to the SNP, but the conclusions apply to the SINE element as well. The *IGF1R* SNP marker (CFA3:41,849,479) codes for a missense mutation, as we described previously (Hoopes et al. 2012).

We genotyped DNA from 500 dogs, representing 93 AKC-recognized breeds, at each of the seven markers (genotyping results are in Supplemental Table 6). Breeds span the entire range of canine weights. All dogs are unrelated at the grandparent level, and at least two males and two females were genotyped from each breed.

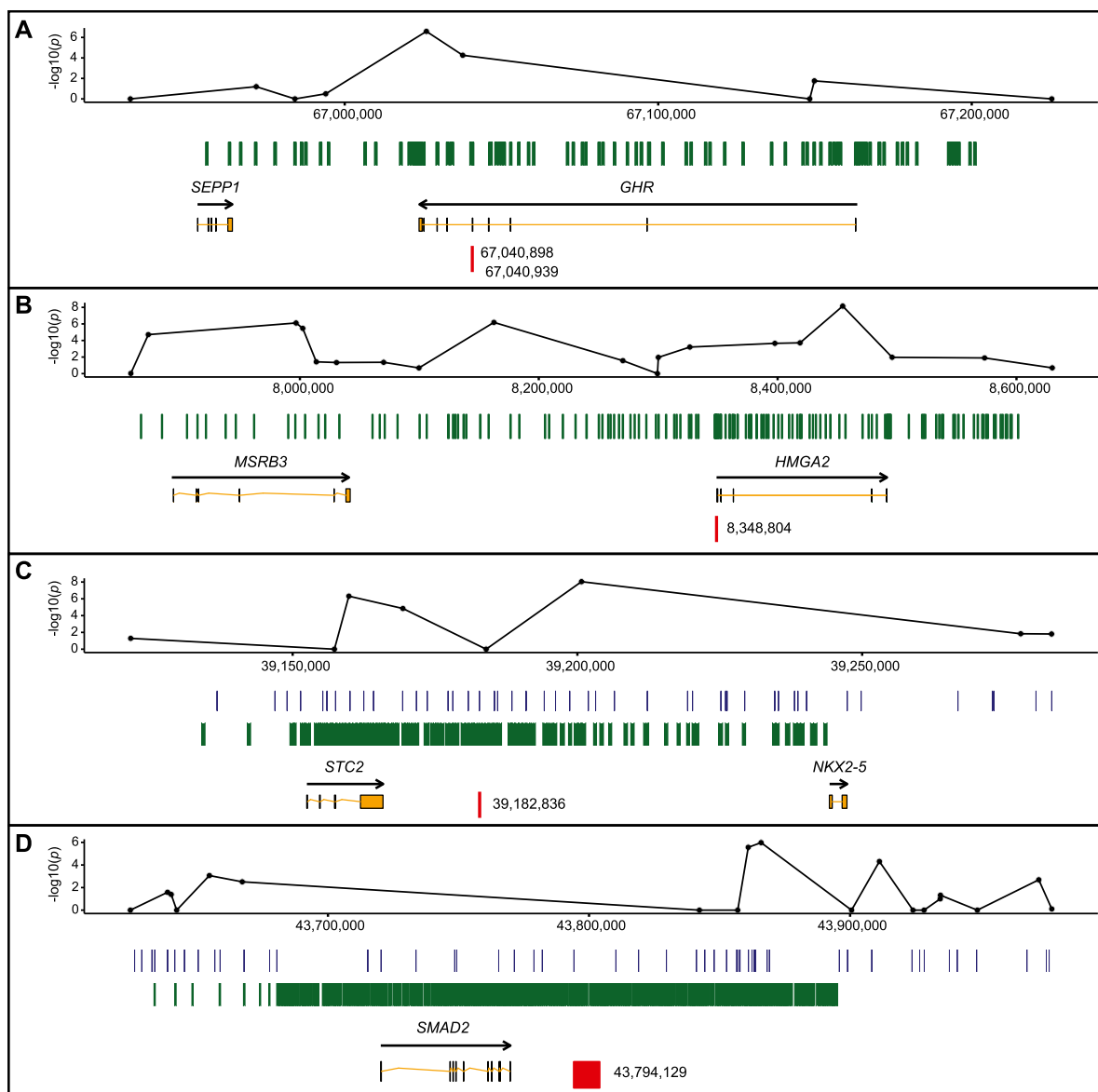
To determine the ancestral allele for each marker, we genotyped a set of wild canids, including 26 geographically diverse gray wolves, two red wolves, and two coyotes. The genotypes in the red wolves and coyotes were all homozygous, defining the ancestral alleles (Table 1; Supplemental Table 7). In gray wolves, the ancestral alleles greatly predominated (Supplemental Table 7).

The SBWs of dogs with different genotypes were compared (Fig. 2). To ensure that no single breed was overrepresented, we randomly selected only two males and two females from each breed for this analysis.

Genotypes at each marker corresponded to differences in size. Reflecting the similarity of size between larger dogs and gray wolves, the ancestral alleles of each variant were always those more commonly found in larger dogs. For each variant, SBWs of dogs homozygous for the derived allele (D/D) were significantly less than SBWs of dogs homozygous for the ancestral allele (A/A). Moreover, SBWs of D/D dogs were also significantly less than the SBWs of heterozygotes (A/D) at four of seven markers (Fig. 2).

When comparing across loci, we observed similar trends. At all loci except *IGF1*, the mean SBW of the D/D dogs was 4–7 kg (8–15 lb). For most pairs of loci, the SBWs of dogs homozygous for the derived allele at one locus had a distribution similar to the SBWs of dogs homozygous for the derived allele at each of the other loci (boxplots) (Fig. 2A). However, dogs that were homozygous for the derived allele at *IGF1* had a greater size range and a higher mean SBW (9.8 kg [21.6 lb]) than D/D dogs at any other locus (Fig. 2B).

The relationship of D/D and A/D dogs was more complicated at *HMG2*, *IGF1R*, and *GHR*(2), in part because fewer heterozygotes were observed. *HMG2* was the most extreme, with only 16 A/D dogs and 87 D/D dogs (Fig. 2B). This ratio (16:87) was smaller than that observed at any other locus. By comparison, the small number of heterozygotes at *IGF1R* and *GHR*(2) was due in part to the low



**Figure 1.** Fine-mapping of four loci associated with canine body size. (A–D) Regional plots of the four fine-mapped loci: CFA4:67 Mb (A), CFA10:8 Mb (B), CFA4:39 Mb (C), and CFA7:43 Mb (D). Each plot includes the following tracks, from *top* to *bottom*:  $P$ -values of the genotyped SNPs in the CanMap data set (Boyko et al. 2010) (with coordinates updated to CanFam 3.1 genome assembly); the regions of the genome covered during fine-mapping (green and blue; amplicons for marker discovery and SNP positions for SNPlex, respectively); genes (orange; see Methods for identifiers); and the most highly associated marker(s) identified in each region (red).

frequencies of the derived alleles (7.5% and 7.3%, respectively), which were found almost exclusively in the smallest breeds. Dogs with the D/D genotype at *IGF1R* or *GHR*(2) had a breed mean weight of 4–4.5 kg (9–10 lb), which was consistent with our previously reported findings (Hoopes et al. 2012). The frequency of genotypes did not differ between male and female dogs at any of the loci (no  $P$ -value <0.6).

#### Allelic trends among dogs of similar weights

A step-like pattern was apparent in the allele frequencies found in 5-lb bins (2.3 kg) (Fig. 3). Overall, as body size decreased the derived allele frequency increased, as did the number of markers with derived alleles. Considering each variant separately (Fig. 3, columns),

in most cases allele frequencies changed gradually across body sizes, as represented by the gradient from yellow to red. By comparison, the incidence of the *HMGA2* derived allele dropped abruptly in dogs with an SBW of 4.5–9.1 kg (10–20 lb).

While most derived alleles are observed in smaller breeds, the *IGF1* derived allele is observed surprisingly frequently in several larger breeds. Notably, nine of the 10 Rottweilers (the only breed in the data set between 45.4 and 47.6 kg [100 and 105 lb]) were homozygous D/D at *IGF1*.

More typically, all dogs  $\geq 40.8$  kg (90 lb) were either homozygous for ancestral alleles at all markers or carried derived alleles at only one marker, usually *IGF1*. Among dogs <11.3 kg (25 lb), 90% carried derived alleles at three or more markers, and 98% carried the derived allele at *IGF1*.

**Table 1.** Size-associated markers

CFA	Position	Type	Ancestral allele (A)	Derived allele (D)	Closest gene	Distance to gene and effect on gene	Marker name	Mean SBW of D/D dogs (in kg)	Mean SBW of D/D dogs (in lb)
4	39,182,836	SNP	T	A	<i>STC2</i>	20 kb downstream from the protein-coding region of <i>STC2</i>	<i>STC2</i>	6.2 (±6)	13.8 (±12)
4	67,040,898	SNP	G	A	<i>GHR</i>	exon5/E191K	<i>GHR(1)</i>	6.6 (±5)	14.6 (±11)
4	67,040,939	SNP	C	T	<i>GHR</i>	exon5/P177L	<i>GHR(2)</i>	3.9 (±2)	8.6 (±4)
7	43,794,129	Structural variation	-	9.9 kb deletion	<i>SMAD2</i>	24 kb downstream from the protein-coding region of <i>SMAD2</i>	<i>SMAD2</i>	5.5 (±3)	12.1 (±7)
10	8,348,804	SNP	G	A	<i>HMGA2</i>	5' UTR	<i>HMGA2</i>	4.7 (±2)	10.3 (±5)
3	41,849,479	SNP	G	A	<i>IGF1R</i> <sup>a</sup>	exon2/R204H	<i>IGF1R</i>	4.6 (±4)	10.1 (±9)
15	41,221,438	SNP	G	A	<i>IGF1</i> <sup>b</sup>	Intron 2	<i>IGF1</i>	9.8 (±9)	21.6 (±20)
15	41,220,980	SINE insertion	-	207 bp SINE insertion	<i>IGF1</i> <sup>b</sup>	Intron 2	<i>IGF1</i> SINE	9.8 (±9)	21.6 (±20)

The mean SBWs (±SD) of dogs were calculated for the dogs selected in Figure 2. Newly mapped markers are in the first five rows. (*STC2*) stannocalcin 2; (*GHR*) growth hormone receptor; (*SMAD2*) SMAD family member 2; (*HMGA2*) high mobility group AT-hook 2; (*IGF1R*) insulin-like growth factor 1 receptor; (*IGF1*) insulin-like growth factor 1.

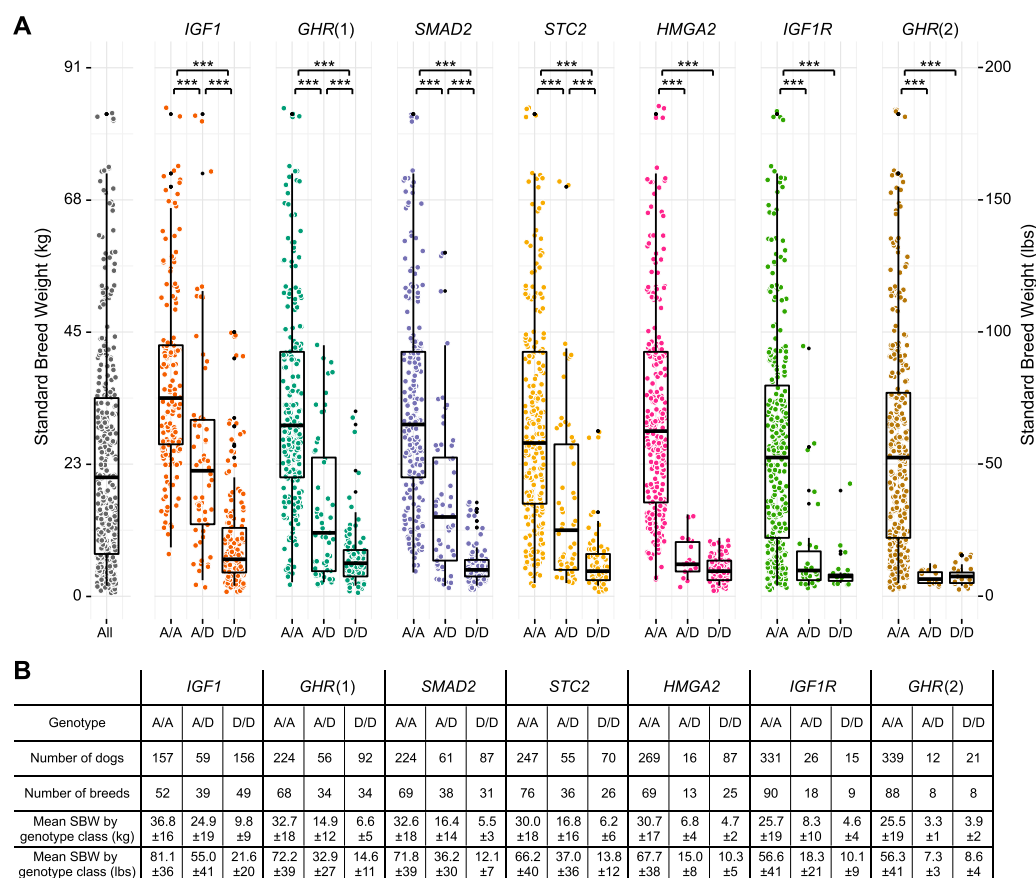
<sup>a</sup>Hoopes et al. (2012).

<sup>b</sup>Sutter et al. (2007).

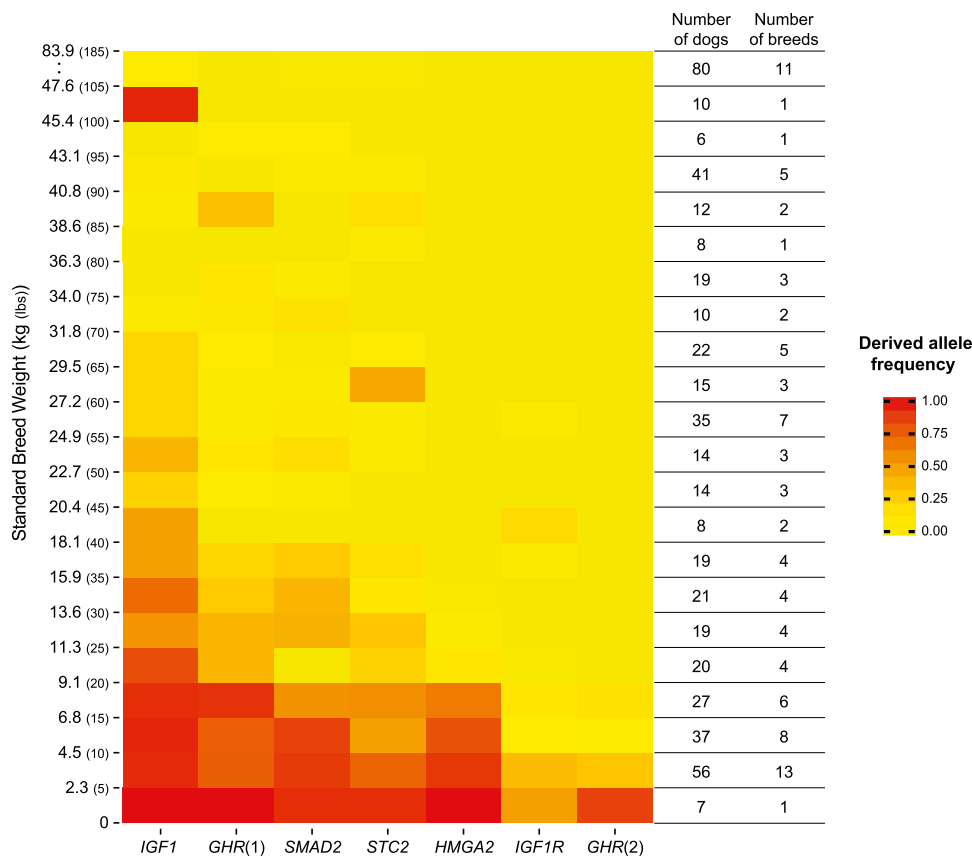
### Combinations of genotypes

Many allelic combinations were observed when all seven markers were considered. To define the combination present in a given dog,

we recorded the markers at which the dog carried the derived allele (A/D or D/D). While 128 possible combinations exist, only 39 were observed in this data set (Fig. 4A). Thirteen combinations were common, as defined by their presence in 10 or more dogs. In the



**Figure 2.** Body size is tightly regulated in dogs homozygous for the derived alleles. (A) The standard breed weight (SBW) of each dog (y-axis) is plotted by genotype at each marker (x-axis). The SBWs of dogs homozygous for the derived allele (D/D) at the *IGF1* marker are significantly smaller than dogs that are heterozygous (A/D) or homozygous for the ancestral allele (A/A), as determined by Kolmogorov-Smirnov and Mann-Whitney-Wilcoxon tests. (\*\*\*)  $P < 0.001$ . The distribution of SBWs for a given genotype/marker combination is generally less for homozygous D/D dogs than for other genotypes (the median and first and third quartiles are indicated by the boxplots). Statistics for each genotype/marker combination are summarized in B. SBWs of genotype classes are reported as mean ± SD. Two females and two males were randomly selected from each breed for this analysis. The SBWs of all selected dogs are plotted in the *leftmost* column. Points were randomly scattered on the x-axis within each column to facilitate visualization.



**Figure 3.** Derived allele frequencies increase at multiple loci as body weight decreases. The frequency of the derived allele in 5-lb weight classes is represented on a color scale. The smallest dogs (*bottom row*) are consistently red at all markers except *IGF1R*, while the largest dogs rarely carry a derived allele, as observed in weight classes of 90–95 (40.8–43.1 kg), 95–100 (43.1–45.4 kg), and above 105 (47.6 kg). The high frequency of the *IGF1* derived allele in the 100–105 class represents the only breed we tested in the class, Rottweilers. Dogs with an SBW above 105 lb are collapsed in a single category due to the lack of genotype variation in the group at these markers. This analysis includes all 500 dogs genotyped.

most frequent combination, both alleles at every marker were ancestral. This combination was observed most frequently in large breeds (Fig. 4B), but was also noted infrequently in breeds with an SBW as low as 15.9 kg (35 lb) (Supplemental Table 1). Combinations were generally not breed-specific. Of the 31 combinations that occur more than once, only two are limited to a single breed. Rare combinations of alleles were also identified. For instance, eight combinations were found in only one dog each, suggesting that other low-frequency combinations exist in the population at large.

There is one set of combinations that is unlikely to exist in any dog. Of four possible haplotypes at the two nonsynonymous *GHR* markers (GC, GT, AC, and AT), only three were observed. The missing haplotype contains the allele associated with large dogs at *GHR(1)* and the allele associated with tiny dogs at a marker 41 bases away, *GHR(2)*. In essence, we found haplotypes corresponding to “large + not tiny” (GC), “small + not tiny” (AC), and “small + tiny” (AT), but never “large + tiny” (GT). Since the *GHR(2)* marker T allele occurs at very low frequency and the two markers are in close proximity, we believe the GT haplotype is unlikely to exist in the general population. This suggests that selection of the *GHR(2)* derived variant occurred among dogs that were already carriers of the *GHR(1)* derived allele.

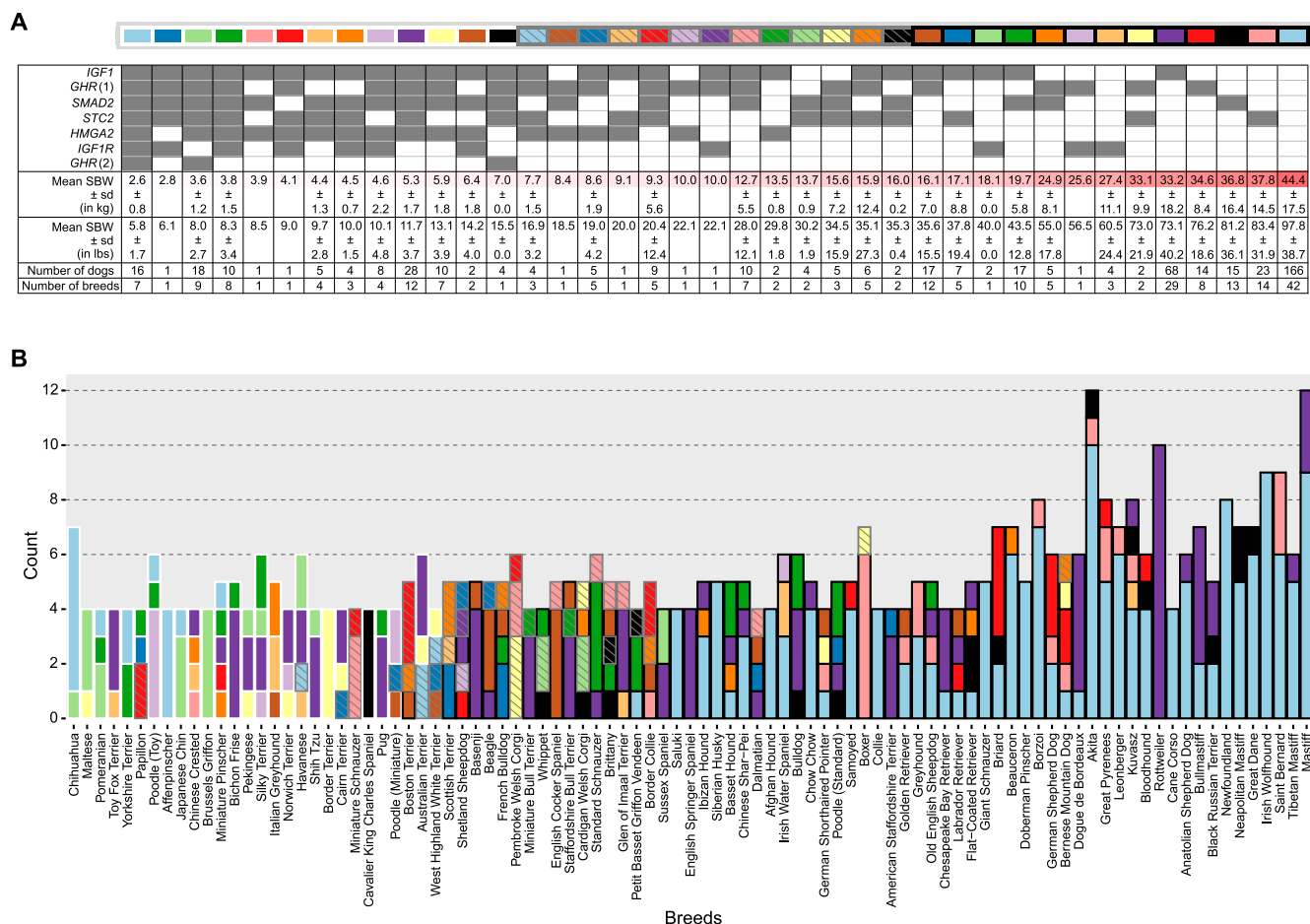
In one of the few widely observed combinations, a derived allele was present only at the *IGF1* locus. Dogs presenting this

combination belonged to two broad categories of breeds. The first group contained breeds with SBWs <31.8 kg (70 lb) and included Basenjis, English Springer Spaniels, and American Staffordshire Terriers (with SBWs of 10.2, 20.4, and 29.0 kg, respectively [22.5, 45, and 64 lb]). The second were breeds with SBWs  $\geq$ 40.8 kg (90 lb) and included Mastiffs and related breeds such as Tibetan Mastiffs, Bullmastiffs, Dogues de Bordeaux, Rottweilers, and Black Russian Terriers (Fig. 4).

The mean SBW of dogs with a given combination was calculated (Fig. 4). As expected, the combination with the lowest mean SBW had derived alleles at all markers, and the heaviest combination had no derived alleles. In some cases, breeds that vary substantially in size shared the same combination, such as Papillons, Boston Terriers, and Border Collies (2.8, 7.9, and 17.9 kg, respectively [6.1, 17.5, and 39.5 lb]). Nevertheless, the standard deviation of SBWs for dogs sharing a combination was generally lower than that observed for weight groups defined by genotypes at a single marker (Fig. 2), indicating that combinations of genotypes explain body size differences better than any single genotype.

### Unifying model

Since derived allele frequencies among the seven profiled markers clearly corresponded to progressive diminution, we sought to quantify how well alleles at these markers accounted for differ-



**Figure 4.** Multiple combinations of genotypes are observed in most breeds. We assessed combinations of genotypes in individual dogs (A). The presence of a derived allele (whether heterozygous or homozygous) is indicated by a filled square. The first column represents the combination with derived genotypes at each marker; the mean weight of dogs with this combination is less than the mean weight of any other combination. The percent standard deviations for a given combination are typically smaller than the percent standard deviations of dogs sharing only a genotype at a single marker (which are reported in Fig. 2). The combinations observed in each breed are uniquely identified by the pairing of fill and outline color in B. Breeds are sorted by SBW. This analysis includes all 500 dogs genotyped.

ences in body size. We used breed-averaged allele frequencies to calculate the proportion of phenotypic variance that these seven markers explained in a linear model. In order to determine which components should be present in the model, we first tested the mode of inheritance for each marker. We found that both *HMGA2* ( $P = 0.0094$ ) and *GHR(2)* ( $P = 0.0366$ ) have a significant dominance component, consistent with the log of the mean SBW of heterozygotes deviating from the mean of the homozygotes (Supplemental Fig. S4).

The resulting model related the log-transformed SBW to the allele frequencies at each of the seven size-associated markers and the breed-average of the dominance component for *HMGA2* and *GHR(2)*. Derived allele frequencies at each marker accounted for 86.0% of SBW variance for the 93 breeds, as measured by the adjusted R-squared (Fig. 5A). The terms corresponding to all markers except *GHR(2)* were significant by ANOVA ( $P < 0.05$ ).

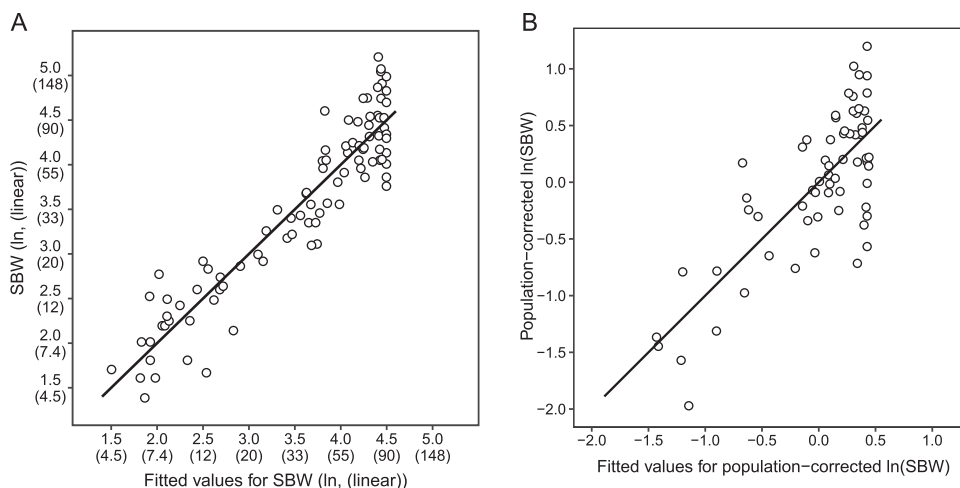
Because dog breeds do not represent a randomly mating population, we investigated the role of population structure in the explanatory power of the allele frequencies. In order to use them to correct for population structure, we calculated breed-averaged principal components (PCs) from genome-wide SNP profiles for

each of the 65 breeds that were present in both our data set and the CanMap data set (Boyko et al. 2010). We then compared the SBW variance explained with and without terms representing PCs, using only PCs that are significantly predictive of SBW and the 65 breeds that have PCs. Genotypes alone account for 85.8% of variance; PCs alone, 44.2%; and PCs and genotypes together, 90.0%. These variances are not additive, but rather they indicate the upper limit that each could contribute in our model. Taken together, our uncorrected and population-corrected models show that genotypes at these seven loci account for between 45.8% and 85.8% of SBW variance.

As an alternate approach to accounting for population structure, corrected SBW (cSBW) values were determined by taking the residuals of a linear regression of SBW on PCs. Allele frequencies would then explain 52.5% of the variance in the resulting cSBWs (Fig. 5B). The two numbers, 46% and 52.5%, bracket a conservative estimate of the variance of SBW explained by genotypes at these markers.

The seven markers are less informative in large and giant dog breeds. Allele frequencies accounted for 64.3% of cSBW variance in dogs with SBWs <40.8 kg (90 lb), but only 8.4% of cSBW among





**Figure 5.** Allele frequencies at size markers explain 86% of size variation before correction for population structure (A) and 52.5% after (B). (A) A linear model was generated to assess the power of breed-averaged allele frequencies to explain variance in standard breed weights (SBWs). SBWs in lb (in parentheses) were transformed by natural log to approximate a normal distribution as was done in previous studies (Boyko et al. 2010). The black line indicates perfect equality of the fitted values with the SBWs. The cluster of breeds with a fitted weight of 90 lb (40.8 kg) reflects the lack of informativeness of these loci for large breeds. Small amounts of scatter ( $\leq 0.05$ ) were added to plotted values to reduce overplotting ( $n = 93$ ). (B) A correction for population structure was performed by regressing the SBW on breed-averaged, genome-wide principal components (PCs). More than half (52.5%) of the variance in the residuals of this regression, the corrected SBWs (cSBWs), was explained by allele frequencies at the seven size markers. Since PCs were calculated from the CanMap data set, cSBWs could only be calculated for the 65 breeds that were present in both our data set and the CanMap data set.

dogs with SBW  $\geq 40.8$  kg. This is reflected in the cluster of fitted values around 90 lb in Figure 5, A and B. These points represent breeds that were homozygous for the ancestral allele at all markers and reflect the lack of relevance of these markers to differences in size among large and giant breeds.

The genotype-phenotype relationships were subjected to further analysis. We found no significant interactions between markers (Supplemental Results). We also found that the model is unlikely to be overfitting the data, since 42.1% of cSBW variance in a test set could be accounted for using coefficients calculated by a training set. The comparable number in the full 65-breed cSBW data set is 52.5%. The applicability of our findings to individuals was also assessed. Tests with 124 individually weighed dogs showed that 74.4% of the variance of their uncorrected weight could be accounted for using individual allele frequencies with coefficients derived from calculations based on uncorrected SBW, in which 86% of SBW variance was explained with allele frequencies averaged by breeds. The cross-validation and the model's ability to explain size variance in individuals underscore the substantial nature of the effects we describe.

## Discussion

We have identified the source of approximately half of size variation in domestic dog breeds by genotyping DNA from 500 dogs at seven markers, five of which we identified by fine-mapping, and two of which we identified previously (Sutter et al. 2007; Hoopes et al. 2012). The dog breeds we analyzed were selected to represent the full range of canine body size, and by analyzing the relationship of the standard breed weight with genotype, the underlying pattern was revealed: For each variant, the derived allele corresponds to reduced body size relative to the ancestral gray wolf, and the presence of derived alleles at multiple variants further reduces body size. In a linear model, allele frequencies account for  $\sim 86\%$  of variance in SBW without correction and, conservatively, 46%–52.5% after correcting for population structure, a degree of ex-

planatory power rarely seen in genetic studies. This strong statistical relationship of genotypes with phenotype is compelling evidence of functional effects by variants in LD with these markers, if not the markers themselves.

Modern dog breeds are defined by rigorous standards, which describe the ideal representatives of the breed. For genetic studies of these strongly selected traits, the fixed phenotype can be used as a proxy for the individual's genetically determined phenotype, as we (Sutter et al. 2007, 2008; Jones et al. 2008; Boyko et al. 2010) and others (Vaysse et al. 2011) have done previously, and as we have done here. By leveraging AKC breed standards and averaged measurements from registered dogs, we can reduce the effect of environment, thus targeting genes underlying strongly selected traits, which often reflect the defining features of a breed. In this study, the approach resulted in the identification of variants under strong selection by breeders that correspond to major differences in overall breed body size. By virtue of our study design, intrabreed body size variation is discounted and genes that contribute exclusively to it will not be identified. Indeed, given that the participants in our study are mostly show animals that compete for breed standard conformation titles, we expect the genetic contribution of intrabreed size variants to be minor compared with those that are the major contributors to interbreed size differences.

The starting point of this study was our earlier multibreed GWAS, which used breed standard weight to identify QTLs associated with dog body size variation (Boyko et al. 2010), a study which found that six size-associated SNP chip markers explained 72% of variance of SBWs without correction for population structure. Our fine-mapping experiments were designed to identify the most highly associated and diagnostic variants. Each variant is potentially causal, with compelling cases for three of the variants: the two protein-altering SNPs in *GHR* and the SNP in the 5' UTR of *HMG2*. The *SMAD2* variant is a large deletion (9.9 kb) that appears to be in complete LD with a neighboring 5.7-kb deletion. Although the deletions are more than 15 kb from the gene, they could potentially affect transcription efficiency, as predicted by the loss of

a transcription factor binding site cluster (Supplemental Fig. 3). The *STC2* SNP is the least likely to be the causal variant, as it only affects a single base and is 20 kb from the gene. However, it is highly associated and therefore remains an excellent marker. There are no better-associated markers in the exons of the studied genes, yet the possibility remains that there are better-associated markers within the extensive range of regulatory effect. As high-throughput sequencing is applied to more dog genomes, further information about the potentially functional role of regions far from genes will be available.

Several of the genes reported in this study are known to be involved in size regulation in other organisms. *IGF1*, *IGF1R*, and *GHR* participate in the GH/IGF1 pathway, which is required for normal stature in humans. Mutations in the GH/IGF1 pathway genes have been associated with human growth disorders (Walenkamp and Wit 2006; Rosenfeld et al. 2007; David et al. 2011). The interdependence of these three proteins—GHR, IGF1, and IGF1R—is well documented (David et al. 2011), but we see no strong evidence for statistical interactions in the effects of the variants studied here.

*GHR* is an attractive candidate for canine size regulation because it is implicated in human body size (Amselem et al. 1989; Ayling et al. 1997) and affects IGF1 signal transduction (David et al. 2011). Human studies suggest a mechanism by which the *GHR* variants identified here could cause reduced body size. The *GHR* SNPs selected in this study are located in the extracellular domain of the canine GH receptor. In the syntenic human exon, three disease-associated SNPs have been reported <25 amino acids away. These SNPs affect growth hormone binding and are believed to cause a human growth hormone insensitivity disorder termed Laron Syndrome (Wojcik et al. 1998).

*HMG2* has been associated with height determination in multiple human GWAS (Weedon et al. 2007, 2008; Gudbjartsson et al. 2008; Lettre et al. 2008; Sanna et al. 2008; Soranzo et al. 2009; N'Diaye et al. 2011; Carty et al. 2012). *HMG2* is a transcription factor expressed during embryonic and fetal development (Rogalla et al. 1996; Gattas et al. 1999). *Hmg2* knockout mice have a pygmy phenotype, characterized by reduced birth weight and growth retardation (Benson and Chada 1994; Zhou et al. 1995).

Neither *STC2* nor *SMAD2* have been implicated in size determination in humans. However, *STC2*, a secreted glycoprotein hormone inhibits growth in mice independently of the GH/IGF1 pathway (Gagliardi et al. 2005; Chang et al. 2008). Although no *SMAD2*-mediated size phenotype has been reported, it is a transcription factor known to transduce signals from members of the transforming growth factor beta (TGF-beta) superfamily (Moustakas and Heldin 2009; Wu and Hill 2009). An appealing possibility is that the deletion identified proximal to *SMAD2* is acting in *cis* to alter this gene's expression in developmental processes such as myogenesis, chondrogenesis, or osteogenesis (Sartori et al. 2009; Song et al. 2009; Chen et al. 2012).

While it is not surprising that genes with a conserved role in mammalian size determination might have variants in both humans and dogs, both the population structure and the study methods complicate comparisons. GWAS in humans have identified 180 loci significantly associated with height (Gudbjartsson et al. 2008; Lettre et al. 2008; Sanna et al. 2008; Weedon et al. 2008; Soranzo et al. 2009; Kim et al. 2010; Lango Allen et al. 2010; N'Diaye et al. 2011; Carty et al. 2012). However, even together, these loci account for only ~10% of the adult human height variation (Lango Allen et al. 2010), although the heritability of height is ~80% (Silventoinen 2003; Visscher et al. 2006; Perola et al. 2007). Unlike our approach, which uses SBWs, human studies

have focused on individual measurements of subpopulations, enabling partitioning of variance attributable to environment and capturing intra-group variation. However, methodological approaches are unlikely to explain the entire difference in study results (six genes explaining ~50% of SBW in dogs vs. 180 loci explaining ~10% of individual height in humans). Dogs are under intense artificial selection and have a much greater range of sizes than humans. The relative subtlety of height regulation in humans may be more typical of species subjected to many thousands of generations of natural selection, such as wolves. We hypothesize that the variants of large effect in dogs that we have found are superimposed on a subtler size-regulation system inherited from wolves.

In addition to explaining ~65% of variance in dogs <40.8 kg (90 lb), this study defines two substantial types of body size variation that remain to be explained: 35% of body size variation in dogs <40.8 kg, and ~90% of the body size variation among dogs weighing ≥40.8 kg. Some of the unexplained variation in dogs <40.8 kg is evident in breeds like Shih Tzu and Pugs. Shih Tzu weigh 20% less than Pugs, but most individuals belonging to either breed have identical genotypes at the seven size variants studied here. To investigate size determination on a finer scale, individual dog weights and perhaps measurements will be necessary. Individual weights and measurements may also permit the elucidation of epistatic relationships, which have been observed in other domesticated species (Carlborg et al. 2006).

Although typically found in small dogs, we found the *IGF1* derived allele in Rottweilers, consistent with previous reports (Sutter et al. 2007), and in other large mastiff-related breeds (Fig. 4). We offer two explanatory hypotheses. First, it is possible that neither of the two *IGF1* variants genotyped in this study (a SNP and a SINE insertion) are causal; rather they tag the ancestral haplotype on which the causal variant first emerged. Thus, some very large breeds could carry the tagging variants and yet lack the causal variant. Alternatively, epistasis of a yet-unidentified locus may reduce the effects of the *IGF1* small allele in some large dog breeds.

The genotypes of dogs from breeds with an SBW ≥40.8 kg (90 lb), represented by 18 breeds in our study, allow us to distinguish them from small and medium dogs, but not from each other (Fig. 5A). The genotypes at the seven size markers account for <9% of differences among dogs over 40.8 kg. Clearly, other loci that contribute to large body size in dogs remain to be found, and further analysis of these giant breeds is warranted.

Size determination in large and giant dogs probably shares features of size determination observed in small and medium-sized dogs. Several size-associated intervals on the X chromosome have been identified, but not studied further (Boyko et al. 2010; Vaysse et al. 2011). In a predictive model that considered breeds of all sizes, adding the locus at 104 Mb on the X chromosome to a model with only the *IGF1* locus increased the amount of variance explained from 47.6% to 57.8%, without correction for population structure (Boyko et al. 2010). However, our ongoing efforts indicate that fine-mapping the chromosome X loci is extremely challenging, as LD on this chromosome extends over megabases (M Rimbault, unpubl.) and includes dozens of genes.

Size determination could also be more wolf-like in large dogs than in small dogs. Compared with small dogs, the sizes of large dogs overlap more with the sizes of wolves. Wolves vary substantially in size, with the weights of adult male wolves in Yellowstone National Park alone ranging from 38 to 66 kg (85 to 145 lb) (MacNulty et al. 2009). Size determination in wolves may be more similar to height determination in humans than to an artificially

selected group like domestic dogs and result from the collective effects of many variants of small effect (Lango Allen et al. 2010).

In this study, we identified markers at loci that define the major size ranges in domestic dogs and show how combinations of alleles produce the extensive range of dog sizes present in modern breeds. It remains to be seen how size is regulated on a finer scale, within breeds, between sexes, and among giant dogs. Some of these studies will require individual measurements and perhaps larger numbers to compensate for noise due to environmental effects. It will also be valuable to extend our existing findings by identifying the functional consequences of size-determining variants. It is our hope that these studies can shed light on growth-related health issues in dogs and humans.

## Methods

All coordinates refer to the CanFam3.1 dog genome assembly (Sept. 2011). Unless otherwise noted, analysis was performed using the software program R (R Development Core Team 2012), and figures were generated with R base graphics and the plotting package ggplot2 (Wickham 2009). The genes and identification numbers in Figure 1 are: *SEPP1* (NM\_001115118), *GHR* (NM\_001003123), *NKX2-5* (NM\_001010959), *STC2* (ENSCAFG00000031727), *SMAD2* (ENSCAFG00000017567), *MSRB3* (ENSCAFG00000029740), and *HMG2* (BLAT results of KC529658).

### Sample collection and DNA extraction

Blood samples were collected from dogs belonging to AKC-registered breeds at AKC-sanctioned dog shows, specialty events, breed clubs, and veterinary clinics. Samples were collected as whole blood into ACD or EDTA anticoagulant tubes after obtaining written consent from dog owners. Genomic DNA was isolated from whole blood using a standard proteinase-K/phenol:chloroform extraction protocol (Maniatis et al. 1982). All procedures were reviewed and approved by the NHGRI Animal Care and Use Committee at the National Institutes of Health.

### Phenotype assignment

Standard breed weights were obtained from several publications. If the AKC specified a weight for a breed, it was used (American Kennel Club 1998). If separate values were listed for males and females, those values were averaged. When the AKC did not specify a weight or if only an upper or lower limit was specified, we used data from *The Encyclopedia of the Dog* (Fogle 1995). If no weight was specified, we utilized data from *Atlas of Dog Breeds of the World* (Wilcox and Walkowicz 1995). We also considered weights recorded in our NHGRI database of individual dogs. These owner-reported weights were collected at AKC-sanctioned dog shows, breed specialty events, and breed club meetings. If there were more than six adult dog weights listed for a breed in our database, we removed the maximum and minimum weights listed and compared the mean of the remaining weights with the published breed standard weight. If the weights differed by >20%, we used the mean breed weight from our database. A list of the breeds and of the standard breed weight used in this study can be found in Supplemental Table 1. Because the phenotype of interest is size, we treated the three varieties of poodles as separate breeds.

### Genotyping of the highly associated markers

The highly size-associated markers (Table 1) were genotyped on an additional set of samples consisting of 500 dogs, termed the vali-

ation set, from 93 AKC-recognized breeds representing the full range of canine body size (Supplemental Table 6). Dogs were unrelated to one another at the grandparent level. Forty-one percent of the 500 dogs had also been included in the CanMap data set (Boyko et al. 2010). The validation set was not fully independent from this study's discovery set either: 13 dogs, six small and seven large, were used for both marker discovery and validation experiments. Wild canids, including 26 geographically diverse gray wolves from North America, Europe, and Asia (10 females and 16 males), two coyotes (one female and one male), and two red wolves (two males) were also genotyped (Supplemental Table 7).

Three hundred and eighty-four dogs were genotyped at the following markers using a GoldenGate genotyping assay (Illumina): *IGF1*, *IGF1R*, *GHR*(1), and *STC2*. GoldenGate genotypes at one position, *GHR*(1), were all validated by Sanger sequencing with 100% concordance. The remaining dogs and variants were genotyped by PCR and Sanger sequencing (see Supplemental Methods for reaction conditions). The SINE insertion in intron two of *IGF1* was genotyped by PCR amplification, and PCR products were analyzed after migration on 1% agarose gels to determine the presence or absence of the insertion. To genotype the 9.9-kb deletion downstream from the *SMAD2* gene on CFA7, PCR products from two different primer pairs were analyzed on 1% agarose gels to determine the absence or the presence of the deletion. A list of the primers and PCR conditions are given in Supplemental Table 8.

### Model

In all models, we used the natural log of weight in lb to approximate a normal distribution, as was done previously (Boyko et al. 2010). Twenty principal components were calculated on the CanMap data set using SmartPCA from the Eigensoft package (Patterson et al. 2006; Price et al. 2006). We used a pruned data set that excludes individuals with >10% missing genotype data, SNPs in high LD as defined by pairwise genotypic  $r^2 > 0.8$  within sliding windows of 50 SNPs, and SNPs that were within 2 Mb of the most strongly size-associated markers at each of the six loci. Outliers of more than six  $\sum$  were excluded, as were breeds with fewer than four dogs remaining after individual outliers were excluded. The breed average of each PC was calculated. Ninety-three breeds were represented in the pool of dogs genotyped at all seven markers; PC values were available for 65 of those breeds (Supplemental Table 9). The PCs predictive of SBW (PC2, PC4, PC6, PC10, PC11, and PC18 at  $P < 0.05$ ) were used for subsequent corrections for population structure.

Significant dominance components were identified by applying a nested ANOVA to each marker with and without a partial dominance term. PCs that were significant for weight were included in both equations.

For the purposes of testing our model on individual dogs, we used individual measurements from dogs in our own database. For each dog, we calculated the mean and standard deviation of the other dogs in the breed. If a dog's Z-score relative to those numbers exceeded 1.5, the dog was excluded.

### Data access

The sequence containing the first exon of canine *HMG2* has been submitted to the National Center for Biotechnology Information (NCBI) GenBank (<http://www.ncbi.nlm.nih.gov/genbank>) under accession number KC529659. The mRNA sequence of *HMG2* has been submitted to NCBI GenBank under accession number KC529658.

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