Revised 12 April 2007

www.sciencemag.org/cgi/content/full/316/5821/112/DC1

Supporting Online Material for

A Single *IGF1* Allele Is a Major Determinant of Small Size in Dogs

Nathan B. Sutter, Carlos D. Bustamante, Kevin Chase, Melissa M. Gray, Keyan Zhao,
Lan Zhu, Badri Padhukasahasram, Eric Karlins, Sean Davis, Paul G. Jones,
Pascale Quignon, Gary S. Johnson, Heidi G. Parker, Neale Fretwell, Dana S. Mosher,
Dennis F. Lawler, Ebenezer Satyaraj, Magnus Nordborg, K. Gordon Lark,
Robert K. Wayne, Elaine A. Ostrander*

*To whom correspondence should be addressed. E-mail: eostrand@mail.nih.gov

Published 6 April, *Science* **316**, 112 (2007)
DOI: 10.1126/science.1137045

This PDF file includes:

Materials and Methods
Figs. S1 to S9
Tables S1 to S6
References

Revised 12 April 2007:

In the fig. S1 legend, the labels for two genotypes in the histogram were reversed. The solid line with closed triangles represents I/I, and the gray line with closed circles represents B/B.
In the fig. S7 legend, a Fig. 2 reference has been changed to a Fig. 3A reference.

Supporting Online Material

Materials and Methods
Figures S1 – S9
Tables S1 – S6
References

Materials and methods

Sample and Data Collection

Whole blood was collected from purebred dogs with written consent from dog owners. Wild canid genomic DNA samples were also typed (*1*). This process was reviewed and approved by the animal care and use committees at the National Human Genome Research Institute, University of Utah, and the University of Missouri. Genomic DNA was extracted from blood by a standard phenol-chloroform protocol. Portuguese water dog samples were whole genome amplified (repli-G kit, Qiagen) prior to SNPlex genotyping but un-amplified DNA was used for sequence based marker discovery.

SNPs and insertion/deletion polymorphisms (Table. S4) were discovered by sequencing PCR amplicons (Table. S3) from dog genomic DNA. Sequencing reactions (Applied Biosystems) were bi-directional from exonuclease/shrimp alkaline phosphatase cleaned PCR amplicons by standard methods. Sequence data were collected on an ABI 3730xl and aligned and genotyped using phred/phrap and consed. SNP genotyping utilized the SNPlex platform (Applied Biosystems) following the manufacturer's protocol with 40-200 ng genomic DNA (small and giant breeds) or 80-200 ng whole genome amplified genomic DNA (Portuguese water dog) from each sample.

Serum levels of *IGF1* in Portuguese water dogs were measured by ELISA following standard methods.

Mixed model for Portuguese water dog fine-mapping

A mixed model was applied for fine mapping within the Portuguese water dog population since the shared ancestry within the breed could lead to spurious associations. To reduce the affect of this cryptic relatedness between dogs, we applied the mixed model analysis of Yu et al (*2*) using:

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\alpha} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

where **Y** is the vector of the skeletal size trait; **α** is a vector of fixed effect, the SNP effect we are testing; **u** is a vector of random effect reflecting the polygenetic background; and **X** and **Z** are known incidence matrices relating the observations to fixed and random effects, respectively. The essential idea is that relatedness is incorporated into the model. The variance in the model can be expressed as:

$$Var\begin{bmatrix} \mathbf{u} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{K}\sigma_u^2 & 0 \\ 0 & \mathbf{I}\sigma_e^2 \end{bmatrix}$$

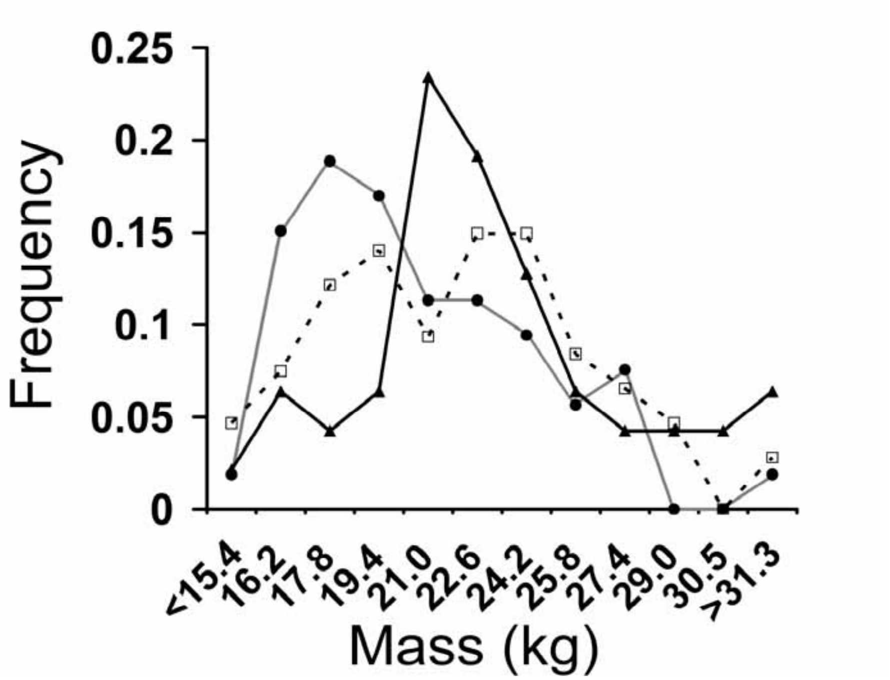
where **K** is the consanguinity matrix estimated from the known pedigree, which reflects the genetic background correlations between individuals.

Mann-Whitney U test for association

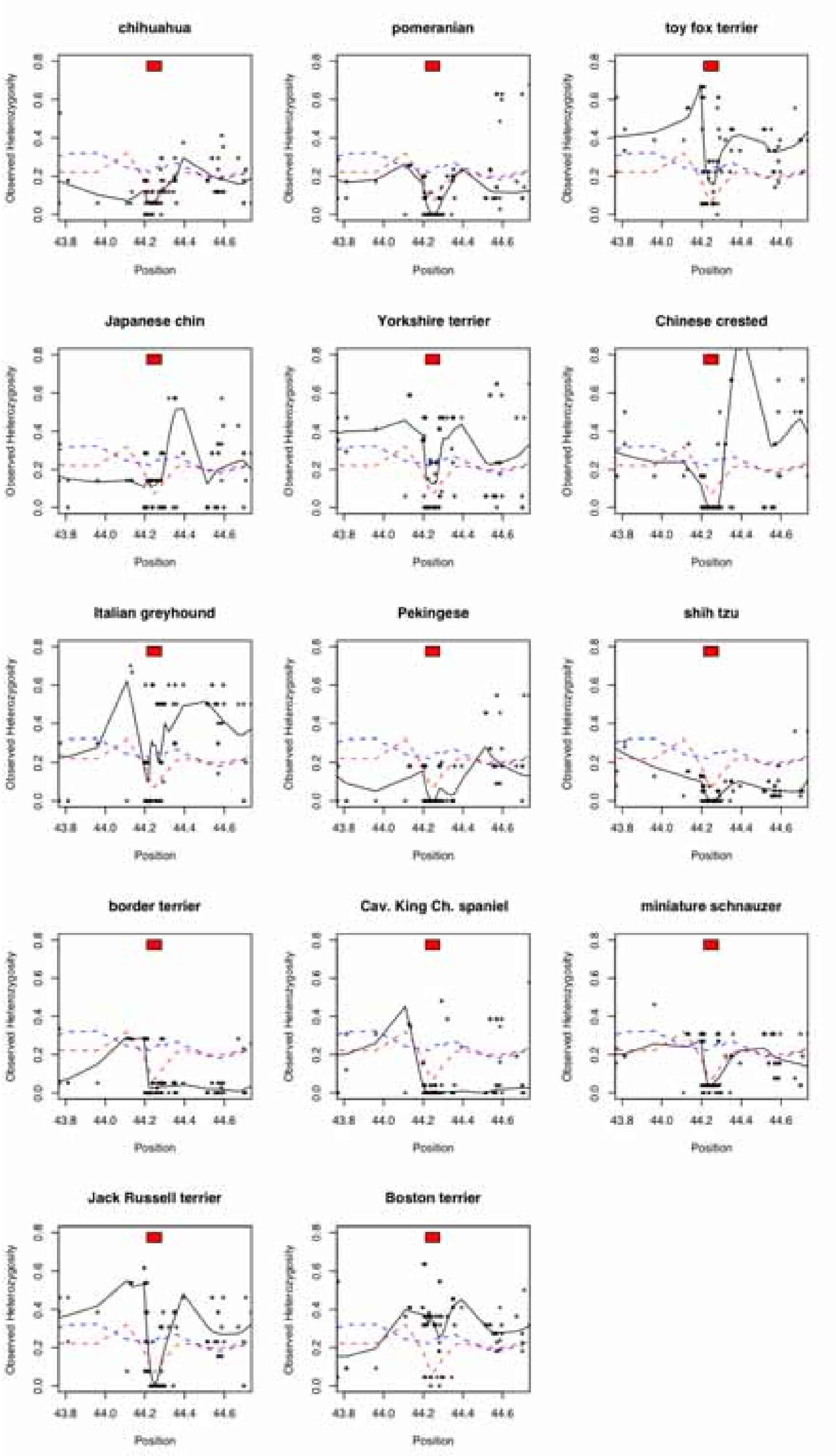
When testing for association across structured populations such as dog breeds, there is a large inflation of nominal p-values in Fisher's exact test that is caused by the relatedness between samples within populations (see Fig. S6). Because dogs from different breeds are only very distantly related, a reasonable strategy is to only remove cryptic relatedness within breeds by collapsing the information obtained from dogs within the same breed into an allele frequency distribution. For each breed, we first calculated the relative frequency of the minor allele at a marker and then conducted a Mann-Whitney U test comparing the frequency in small dog breeds with the frequency in giant dog breeds. The test rejects the null hypothesis of no association if there is a large difference in the median allele frequency across small breeds as compared to the median frequency in large breeds.

Estimation of the ancestral recombination graph

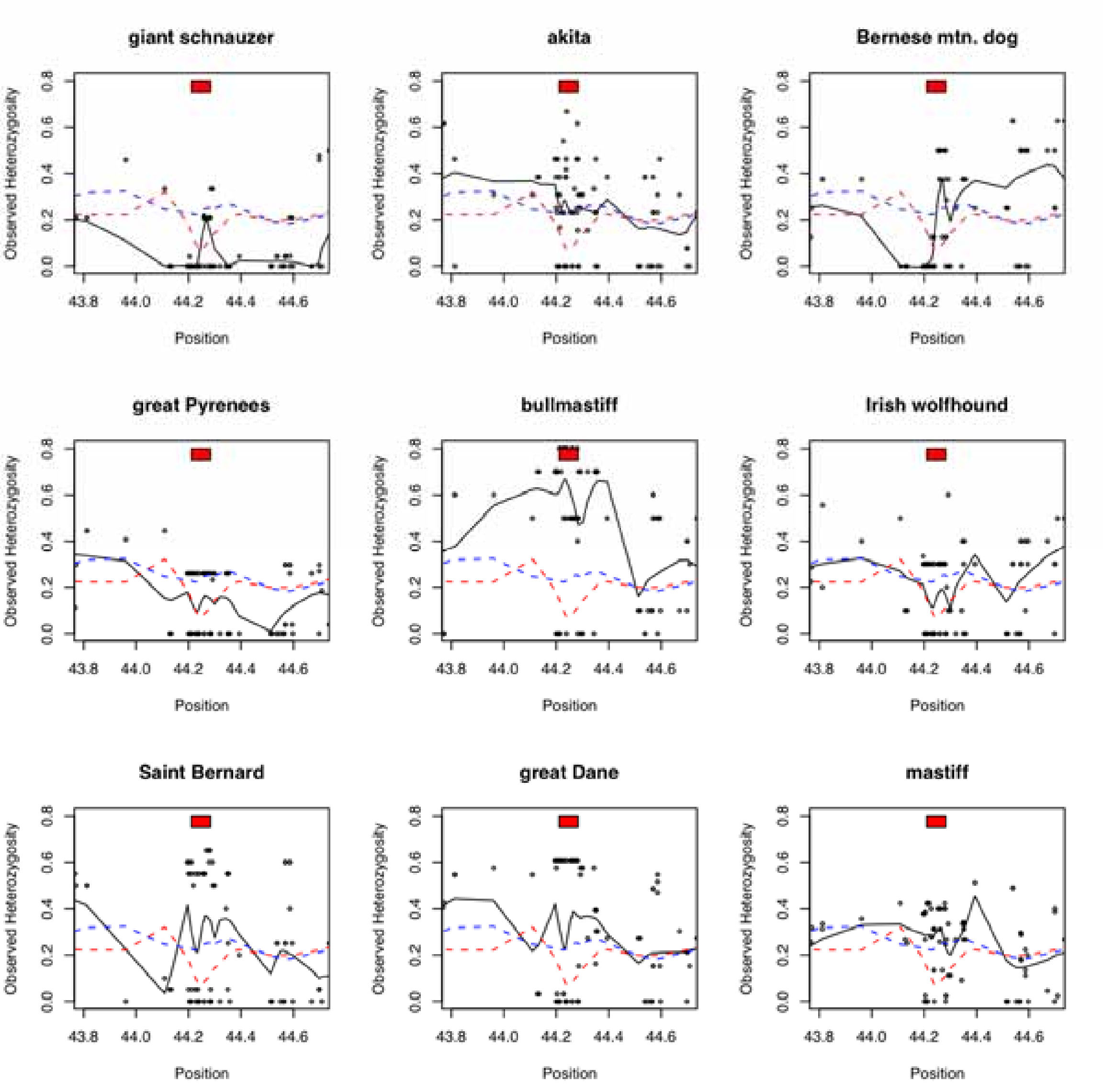
An ancestral recombination graph was reconstructed for a 1.2 Mb interval (chr15:43.7-44.9 Mb) that includes the *IGF1*core region from 1052 sequences of all small and giant dog breeds and is rooted with data from the golden jackal (*Canis aureus*) using the software SHRUB (*3*) [http://www.cs.ucdavis.edu/~yssong/lu.html]. Given a set of sequences and the ancestral sequence, SHRUB uses efficient branch and bound methods to compute the minimum number of recombination events necessary to explain the data and generates ARGs consistent with the data.



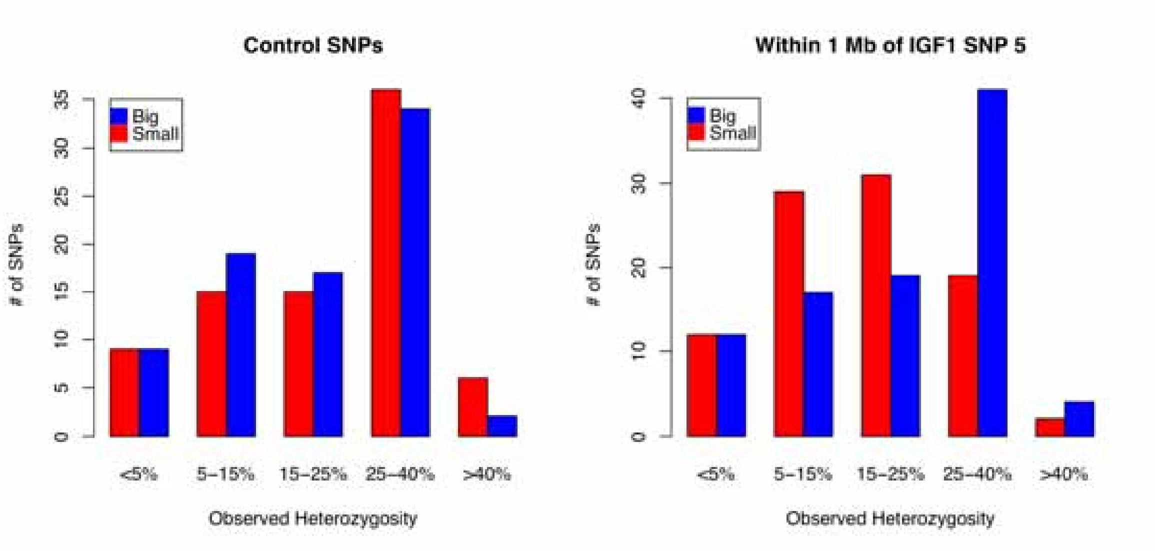
Supplementary Figure S1. Portuguese water dog *IGF1* haplotypes and mass. Haplotypes were inferred for 20 markers spanning the *IGF1* gene (cfa15:44,212,792-44,278,140, Canfam1). Out of the 720 chromosomes with successful inference, 96% carry one of just two haplotypes, "B" and "I", identical to haplotypes inferred for small and giant dogs, respectively (see Fig. 3). Data are graphed as a histogram for each genotype: I/I (closed triangle, solid line), B/I, (open square, dashed line) and B/B (closed circle, grayed line).



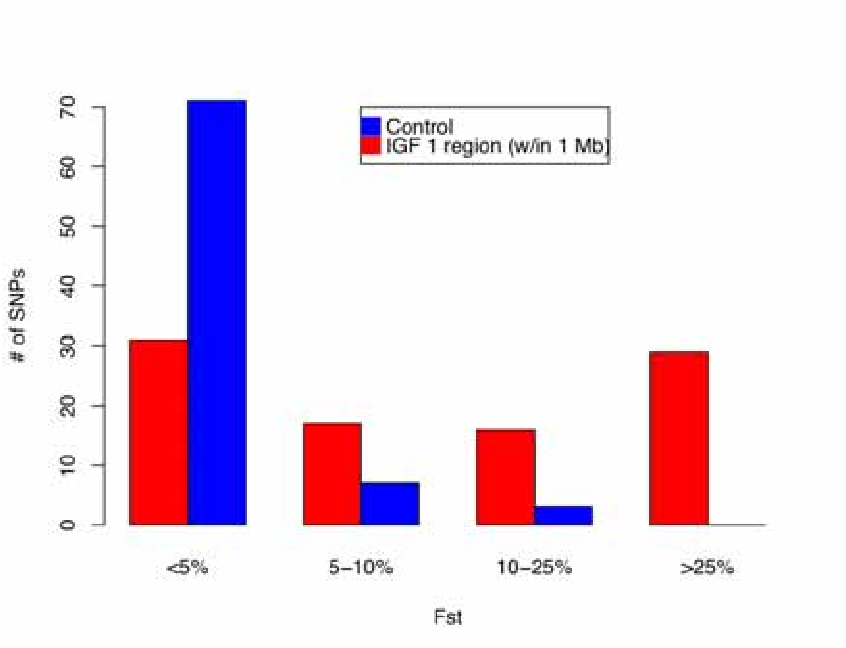
Supplementary Figure S2. Observed heterozygosity for markers spanning *IGF1* in individual small dog breeds. The x-axis indicates marker position on canine chromosome 15 and the red box indicates the position of *IGF1*. Only breeds with data from at least 10 chromosomes are shown.



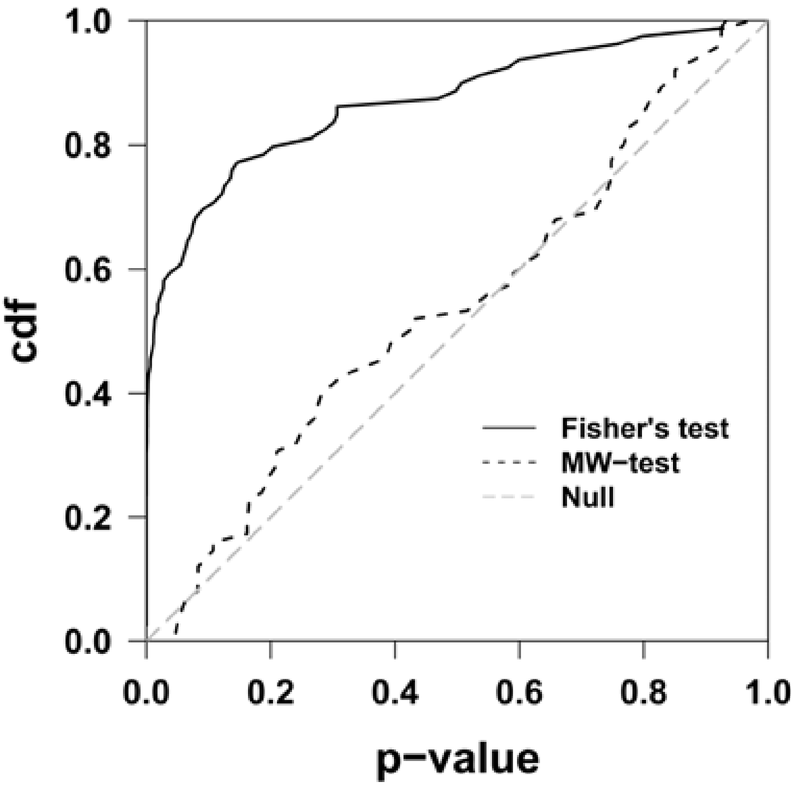
Supplementary Figure S3. Observed heterozygosity for markers spanning *IGF1* in individual giant dog breeds. The X-axis indicates marker position on canine chromosome 15 and the red box indicates the position of *IGF1*. Only breeds with data from at least 10 chromosomes are shown.



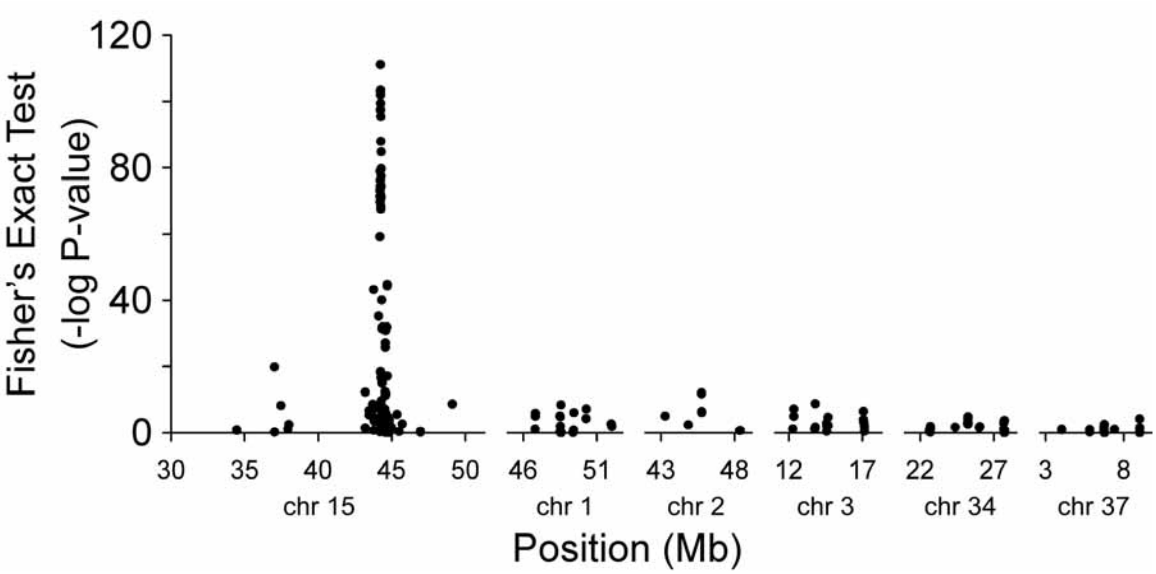
Supplementary Figure S4. Distribution of observed heterozygosity for 83 genomic control SNPs and SNPs at the *IGF1* locus.



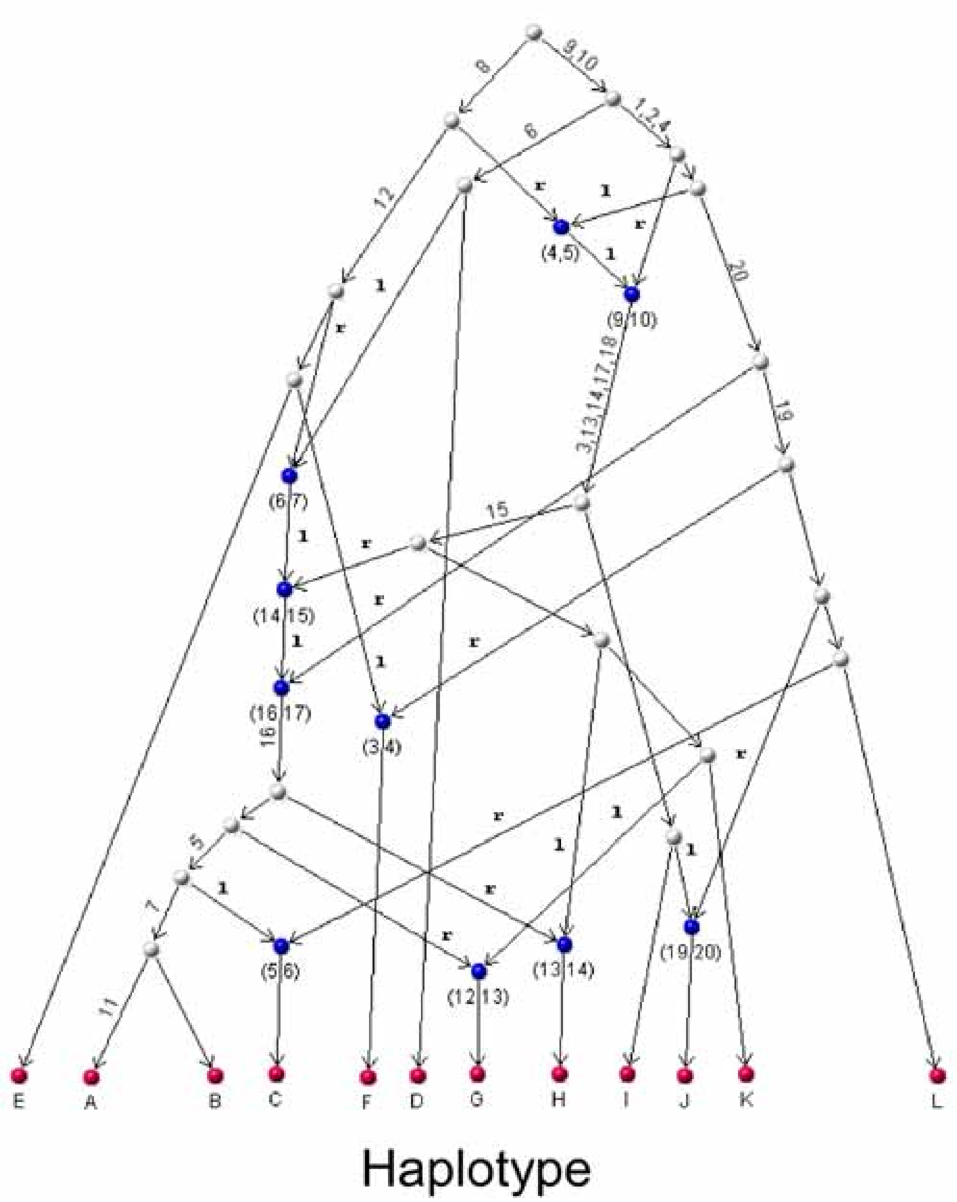
Supplementary Figure S5. Distribution of Fst between small and giant breeds for 83 genomic control SNPs (blue) and SNPs in the *IGF1* locus (red).



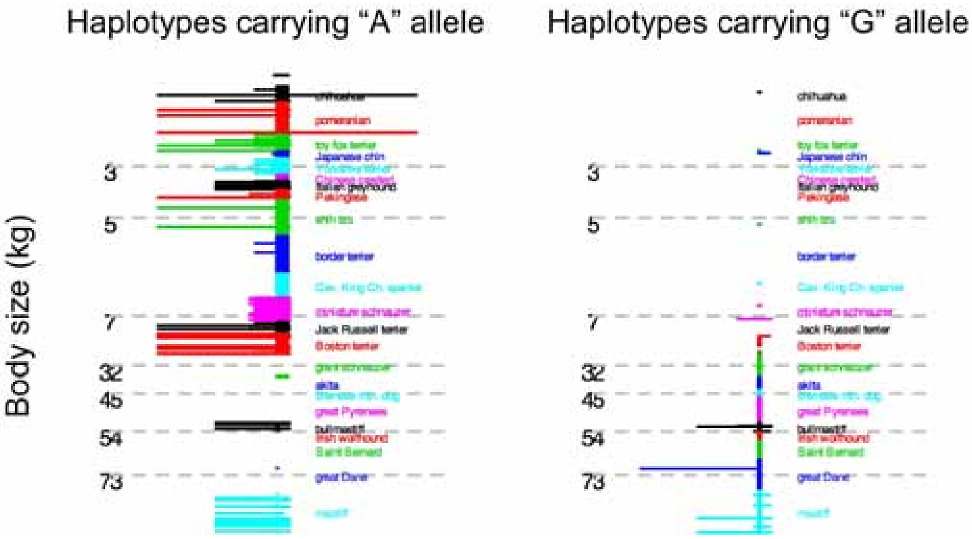
Supplementary Figure S6. Cumulative distribution function for Fisher's exact test and Mann-Whitney U statistic calculated from 83 genomic control SNPs genotyped in small and giant dogs.



Supplementary Figure S7. Fisher's exact test p-values for tests of association between individual SNPs and body size (small vs. giant) for 116 SNPs on chromosome 15 and 83 SNPs on five control chromosomes. Only breeds with data for at least ten chromosomes were included (14 small and 9 giant breeds). Note that, unlike p-values in Fig. 3A, these p-values clearly reflect confounding by population structure (see Material and Methods).



Supplementary Figure S8. An ancestral recombination graph that is consistent with the 12 haplotypes shown in Fig. 3B for the interval chr15:44,212,792 – 44,278,140. Red dots denote the 12 haplotypes, white dots denote coalescent events and blue dots indicate recombination vertices. The numbers in parentheses below recombination vertices denote breakpoint intervals, given as SNP positions reading from left to right in Fig 3b. Numbers along the edges in the graph indicate mutations. Recombination branches are labeled "l" or "r" to denote material to the left or right of recombination breakpoints.



Supplementary Figure S9. Haplotype sharing among 952 dog chromosomes from 22 breeds. We display the longest region containing SNP 5 (chr15:44,228,468) in both 5’ and 3’ directions until a recombination breakpoint is inferred from an ancestral recombination graph. Haplotypes carrying the SNP 5 “A” allele are shown in the left hand column and those carrying the “G” allele in the right hand column. Within each column the rows are individual chromosomes colored to indicate the breed from which they were sampled. Chromosomes are sorted according to the size of the breed from which they were sampled with small breeds at the top and giant breeds at the bottom. An empty row position indicates chromosomes in a breed that do not carry the given SNP 5 allele. For example, the empty rows at the top of the right hand column illustrate the rarity of the SNP 5 “G” allele in the small breeds. Non-recombined intervals with the SNP 5 “A” allele, regardless of whether they occur in small or giant dogs, are much longer on average (median length = 51.4 kb) than non-recombined intervals with the “G” allele (median = 9.9 kb; $p < 10^{-16}$, Mann-Whitney U test).

Supplementary Table S1. SNP genotypes from wild canids for *IGF1* SNP "5" (chr 15:44,228,468 CanFam1). Entries within the table are the count of chromosomes for each species and, for *Canis lupus*, each population.

Species	common name	population	**G**	**A**
Canis lupus	grey wolf			
		Alaska	46	0
		China	4	0
		Croatia	6	0
		India	10	0
		Isle Royale	18	0
		Israel	68	0
		Italy	24	0
		Mexico	4	0
		Minnesota	52	0
		N. Canada	36	0
		NW Territory	56	0
		Quebec	2	0
		Spain	40	0
		Yellowstone	28	0
		wolf total	394	0
C. rufus	red wolf		6	0
C. latrans	coyote		24	0
C. aureus	golden jackal		32	0
Urocyon cinereoargenteus	gray fox		28	0
U. littoralis	island fox		24	0

Supplementary Table S2. Haplotype inference for six tagging SNPs spanning 50 kb within the *IGF1* gene in a sample of 3231 dogs from 143 breeds. Haplotypes are shown vertically with genome position in the Canfam1 assembly to the left. These haplotypes match the more highly resolved haplotypes from Fig. 3b as indicated by letters shown at the bottom of eight of these haplotypes. Major haplotype groups from Fig. 3b (e.g. ‘B’, ‘C’, ‘F’ and ‘I’) are all resolved from one another. Marker ancestral states are inferred from golden jackal genotyping and are colored white. Derived alleles are colored gray. Entries within the table are the count of chromosomes for each breed. PHASE inference and chromosome counting follows the method for Fig. 3.

Position:	44212792	T	C	C	C	C	C	C	C	C	T	T	T	C	T
	44226324	G	G	G	G	G	G	G	G	G	A	A	A	A	G
	44226684	C	C	C	C	C	C	C	T	T	T	T	T	T	T
	44228468	A	A	A	A	G	G	G	G	G	G	G	G	G	G
	44237388	G	G	A	G	A	G	G	A	G	A	G	G	G	A
	44260949	A	A	G	G	G	A	G	G	G	G	A	G	G	G
	Fig. 3 Haplotype(s) tagged:		**AB**	**C**		**D**		**E**	**F**			**GH**	**IJK**		**L**
Size (kg)	**Breed**														
2	Toy Fox Terrier		35	1									2		
2	Maltese		51	1											
2	Pomeranian		54	2											
2	Chihuahua		65	1											
3	Manchester Terrier Toy		34												
3	Japanese Chin		41										3		
3	Yorkshire Terrier		42	6											
3	Chinese Crested		56												
4	Affenpinscher		22												
4	Italian Greyhound		29	11											
4	Papillon		46										2		
4	Poodle Toy		49	1											
4	Brussels Griffon		50												
4	Pekingese		49										5		
5	Silky Terrier		25	1											
5	Havanese		29										5		
5	Shih Tzu		36												
5	Australian Terrier		40												
5	Miniature Pinscher		44	2											
5	Norfolk Terrier		13						35						
5	Bichon Frise		38	1									15		
5	Norwich Terrier		51						3						

5	Tibetan Spaniel		56												
6	Lhasa Apso		30	1					2				11		
6	Cavalier King Charles Spaniel		50										2		
6	Border Terrier		56												
7	Schipperke		36						2						
7	American Eskimo Dog		32	9					3						
7	Poodle Miniature		44												
7	Miniature Schnauzer	1	43	1	1							1	1	1	
7	Jack Russell Terrier		52												
7	Cairn Terrier		40						10				4		
7	Pug		56												
7	Shetland Sheepdog		23						20				15		
7	Dachshund		156	9			1		2				50		
8	Cesky Terrier		10												
8	Lakeland Terrier		16												
8	Manchester Terrier		32												
8	Fox Terrier Wire	2	23		3							3	5	2	
8	Fox Terrier Smooth		45	1											
8	Boston Terrier		42		1								7		
8	West Highland White Terrier		28										22		
9	Welsh Terrier		42										4		
9	Scottish Terrier		45										13		
9	Bedlington Terrier		64												
10	Dandie Dinmont Terrier		10												
10	Pembroke Welsh Corgi		10	1					34				3		
10	Beagle		46	4									2		
10	Whippet		2						26				34		
10	American Cocker Spaniel		63	7					1						
11	Sealyham Terrier		14												
11	Basenji		38												
11	Japanese Shiba Inu		26	3					6	3					
11	French Bulldog		42												
11	Tibetan Terrier		51	7					7						
12	Cardigan Welsh Corgi		2						10				28		
12	Irish Terrier		42												
14	English Cocker Spaniel		22	23									3		
15	Staffordshire Bull Terrier		34										2		
15	Australian Cattle Dog		21						8				14		
16	Basset Griffon Vendeen Petit		16						6				18		
16	Glen of Imaal Terrier		30										10		
16	American Water Spaniel		5	1					6				32		
17	Brittany		13	7									20		
17	Schnauzer Standard		27	7									6		
17	Kerry Blue Terrier		48										2		
17	Border Collie		22	3					19				6		
18	Keeshond		18	3									3		
18	Soft Coated Wheaten Terrier		38												
18	Sussex Spaniel		42												

20	Field Spaniel		8										4		
20	Welsh Springer Spaniel		9	25											
20	Nova Scotia Duck Tolling Retriever		38										2		
22	Ibizan Hound		11						4				25		
23	Pharaoh Hound												29		
23	Saluki								42				6		
23	Portuguese Water Dog		13										36		
23	English Springer Spaniel		26	8	1				2				15		
23	Norwegian Elkhound		9	1					7				35		
23	Bearded Collie								68				8		
24	Bulldog		24										8		
24	Chinese Shar Pei		8		1		1		2	13		1	11		
24	English Bulldog		33	1									6		
24	Siberian Husky								29	3			16		
24	Hungarian Viszla		18									1	31		
25	Wirehaired Pointing Griffon												12		
25	Irish Water Spaniel												26		
25	Poodle Standard		14										18		
25	Australian Shepherd Dog	2	15						6				11		
25	Samoyed		2						30				14		
25	Dalmatian	1	12	27									16		
26	Bassett Hound		2	1	1							1	33	1	
26	Airedale Terrier		34										6		2
27	American Staffordshire Terrier		29										5		
28	Irish Red and White Setter		1	4									13		
28	Belgian Malinois		3						2				17		
28	Weimaraner		7						1				21		
28	Afghan Hound		1		1	1	1	13	7	2	3		7		
28	German Shorthaired Pointer		6	7								1	40		
29	Boxer												40		
29	Pointer												42		
29	Bull Terrier		39										5		
29	German Wirehaired Pointer		16								3		26		
29	Belgian Sheepdog												48		
29	Flat Coated Retriever			5								19	32		
29	Old English Sheepdog			4					4				48		
30	Greyhound								20				12		
30	Labrador Retriever		14	9					9			3	39		
31	English Setter		22										16		
31	Gordon Setter			4									39	1	
31	Collie								72				8		
32	Giant Schnauzer											10	28		
32	Belgian Tervuren												44		
32	Clumber Spaniel		1	16									33		
32	Irish Setter			2									50		
32	Italian Spinone		6						13				33		
32	Golden Retriever		4	1	1							17	31		
33	Chesapeake Bay Retreiver		7	9					12				4		8

33	Curly Coated Retriever		11						2				35		
34	Briard												42		
34	Rhodesian Ridgeback		6		1				9			1	28		8
35	Dobermann Pinscher								26				28		
37	German Shepherd Dog								4			2	46		
38	Bouvier Des Flanders												62		
39	Komondor								13				5		
40	Alaskan Malamute								48				10		
41	Scottish Deerhound			4					14				16		
41	Borzoi								35				23		
44	Akita					27		11	5	1			2	1	
45	Bloodhound								3				3	38	
45	Rottweiler		48						2						
45	Bernese Mountain Dog		3									25	30		
50	Black Russian Terrier		7										9		
50	Pyrenean Mountain Dog								5				47		
52	Chow Chow		7			21	2	2	6	10			2		
54	Leonberger								7				13		
54	Irish Wolfhound								2				20		
54	Bullmastiff		15						1				25		15
59	Saint Bernard								13				31		
60	Greater Swiss Mountain Dog												43		1
64	Newfoundland								15				41		
73	Great Dane								24				20		
82	Mastiff		8						4				36		

Supplementary Table S3. Amplicons sequenced for marker discovery. Start and end positions are given for the Canfam1 dog genome assembly.

ID	chr	start	end	strand	forward_primer	reverse_primer
SQ_5055	15	44209944	44210739	+	ATCTTTTGGGTGTGCTATTTGACT	AAATTAAAAGCTAAAGGCCCATCT
SQ_5058	15	44278583	44279400	+	TGTGGATAAGAAAGGATTTGTGAA	TGACTGAGTCTGTTTCTCCAAAAG
SQ_5059	15	44279555	44280363	+	CTCCTGATTCTTGTTAACACAACG	GTGGAGGTTCTCTCTCATCCTAGA
SQ_5060	15	44280436	44281237	+	CCCCAAAAGAAAACAATAACAAAC	GTAGGTAAAGGTGTCCTGCCTAGA
SQ_5061	15	44281219	44282019	+	GCAGGACACCTTTACCTACTGAAT	CTGTATATACGGAAAGCGGAAACT
SQ_5062	15	44282104	44282905	+	CTCTAACTTTGACTCCCTGAGCAT	TTGCTAAATCTCACTGTCACTGCT
SQ_5063	15	44282902	44283698	+	GCAAACAGAAGAGGGATTTAGAGA	TGTTCAAGCTATGCAGAAAAACAT
SQ_5064	15	44283587	44284397	+	CCTTTCTCTCCTAGGCTTCCTATC	GTTGGGCACATAGTAGACATTCAC
SQ_5065	15	44284500	44285297	+	GCACAATGAAAGGGAATAAAAGAC	GATTGTGACATAAAAACTGGGACA
SQ_5067	15	44207925	44208725	+	GCATCTAAATCCACAGAACACATC	TATTCCTACTCCTTGGGCAATCTA
SQ_5068	15	44203964	44204769	+	TCTTAAGGAATGACACACCAACAT	GGCCTACTGCATCCTAAAAGTAAA
SQ_5069	15	44204669	44205466	+	GTGACTTGGAACTTTGAGGTTTTT	GATTCTTTGTTTTCGGTTTGTTTT
SQ_5070	15	44205443	44206251	+	AAAACAAACCGAAAACAAAGAATC	TTTTTGTGCTCTGCTCTAAAACTG
SQ_5071	15	44206202	44206811	+	AAAAATTTTCTCCACTTGCTGAAT	TCAATGTTTGTGTAGATGAAACCA
SQ_5072	15	44202415	44203222	+	AGTTCTTTCTAAGGGAGGAGAGGA	TCACTGTACCCAGCAGTGAGTTAT
SQ_5073	15	44194696	44195503	+	ACTGTTCAGAAGGCAATAGGTGTT	CAATATAGTTCCATGTGCTTTTGG
SQ_5074	15	44195373	44196175	+	CAAGAGTGTCTTCAAGTGGGTTTA	AGAAATATCCCTAATGTGGCAAAC
SQ_5075	15	44190721	44191507	+	GTGAATTAGTGTGTTGCATGTCTG	GTAGGGTGATGGGTGATGACTT
SQ_5076	15	44182396	44183198	+	TTTTCAGTTAATCCCTTGGACTGT	GTAAAATACGTGGGCATTTCATCT
SQ_5077	15	44183040	44183843	+	GGAAATCTCCCACTTCATGTAATC	TGGACAAGAACTTTGTACATCCTG
SQ_5078	15	44183881	44184683	+	CTCCTCCTTGGACTCAACTGTTAT	ACATGGTTTAGGTGCTTTTCAAAC
SQ_5079	15	44180832	44181617	+	AGGCAAAATGAAACAAAAGAAAAT	GACTATGTTTTGGGGGTTATTTGT
SQ_5080	15	44179584	44180385	+	AGGTGTAACAACCAACAAGGGTAT	AAGCACTTCTAAGTCCACCATAGG
SQ_5081	15	44176228	44177022	+	TATGCTGGAGGTATGAGAAGTTCA	GGTGAAATTGGAGGAGACTCTAAG
SQ_5082	15	44172863	44173660	+	ATGAGTTGCTTGTGTCTCTCAAAG	TGACAGGAGAGATATCGGTAATGA
SQ_5083	15	44167058	44167852	+	TTGTAGTTGCTTGCTTCTTTCTTG	CCTTTTTCCTGTCTCTGGACTAAA
SQ_5085	15	44163979	44164784	+	TAAAATCCCTTCAGACATTGAACA	ATTTTTACTGGTCTCACCCATGAT
SQ_5087	15	44158293	44159086	+	CGGTCCTATAATTTGGTATTGAGG	TGCCACAGTGATTTTAGACTTTGT
SQ_5088	15	44159118	44159896	+	AATTATTTTTGCCAAGTGTTAGGC	CATGCTTTAGATATGTTGGCAATC
SQ_5089	15	44157006	44157805	+	AGCTCATGTCTTTGGTCAGATGTA	TGCTTTTAAATCCTGAAAAACTCC
SQ_5090	15	44153555	44154358	+	TGCAAAGTACATATTGGGCTAAAA	ATTATACCAAGGTGCCACGTAATC
SQ_5091	15	44147798	44148593	+	GCACAAAGAGATCATCTGCTCTAA	CAGAGTTCAAGGATATGTTCATGG
SQ_5092	15	44136451	44137251	+	AGGCTATACCCAAGAAGGAAGAAT	CATGACACAAGCCATAGAAAAATC
SQ_5093	15	44137224	44138021	+	ATTGGATTTTTCTATGGCTTGTGT	AAGGAACTGAGTGAAGAGGGATAA
SQ_5094	15	44137998	44138796	+	TTATCCCTCTTCACTCAGTTCCTT	TTTATCCTCTCTCAAGCTTTTTGC
SQ_5110	15	43476298	43477079	-	GCATTCATTCATGGATTTGTTCTT	CCATTATGTTGGGAGCAGTTTCTA
SQ_5111	15	43470933	43471630	-	TTTTAAAAAGTAATTCTTGGGCCTTT	ATTTAGGCAGAACATCCAGTCAAG
SQ_5112	15	43463432	43464227	-	TCAGGGTCTTTTGTTACTTGAAGC	CCCATTTCAAAGCTGAAGATACTG
SQ_5113	15	43461498	43462287	-	TGTGAGATGCTGAAAGTGTTCTGT	CACTTAATGCAAAGAGGAAGTGGT
SQ_5114	15	43459745	43460545	-	GATTGGTGGGTAGTGTAAGCTTTG	GGAAGACCATGACTTACCAGAAAA
SQ_5115	15	43454946	43455745	-	AGGATGTTAAGTGGGACTTTTCCT	CCTTCAACTGTGCTATGTCAAATG
SQ5258F	15	44212309	44212886	+	GGTTGTGGGAAGAAGTTTGGTA	ATCTGGGATTAATTTGGCTTGA
SQ5259F	15	44224603	44225116	+	TCTCCTCCAGTTTCCTTTCTTG	AAGCACCACAGTAGCAGCATAA
SQ5260F	15	44226141	44226769	+	TACAATGTGGAGTGACCAGAGG	GGGTGTAGACGAGATCCTTGAC
SQ5261F	15	44239248	44239802	+	GGGCTGTTGGTCTAGAAACATT	AGGTAGCATGTTTGGGCATAGT
SQ5262F	15	44263742	44264259	+	CCCTATCCAAAGATCTCCCTCT	TCCTTAAGATCTTGCCAGCTTC

SQ5263F	15	44278791	44278940	+	GTAGGATTTAGGCATGAAATTGG	TCTTTTGCAAGTTTTGAGTCCA
SQ5264F	15	44281218	44281817	+	GGCAGGACACCTTTACCTACTG	TCAAGTTTCCATTCTCAGCAAA
SQ5265F	15	44286696	44287216	+	AAGGAGCTCTGTCATTCCTCAG	AACACGCAGCTTATTGATTTCC
SQ5266F	15	44346657	44347193	+	TGTACAGACTGAGGCTTCCAGA	TGAAGACTCCACAAAGGGATTT
SQ5267F	15	44349138	44349650	+	GCTCCTCAGGGTTTTACATTCA	GCCTCATTCAGCCTCATTATCT
SQ5268F	15	44350515	44351164	+	AGGCAGTCCTGAAACTTGGATA	TACAGCCTCAGGTTCCTTCTGT
SQ5270F	15	43767606	43768292	+	GTTTGATAGCATCTGGGGACTC	CAACTCTGGCCTTTCTCTCCTA
SQ5271F	15	43770961	43771602	+	CAAACAGCCACTAAACAAGCTG	GCACCTAACTGGGATGATAACC
SQ5272F	15	43780580	43781279	+	GTCTCTGCCTTTTTCTGATGCT	AAATAGAATGGTGGGAAGCTGA
SQ5274F	15	43790148	43790847	+	CACAGTTCAGTCCGATGTCACT	AGCTCCTGGAGAGAGAGAGTCA
SQ5275F	15	43799921	43800569	+	CGGAGAGCTCTTATTTTTGCAC	CATGGCCTTTCTAACGCTTC
SQ5277F	15	43806257	43806890	+	GCCCAAGACATCTGATTTAAGG	GTCCTCTTTCTCCCCATTTTCT
SQ5278F	15	43813427	43814075	+	GACTAGAAGGGGTGTCTTGGAA	ATTTGGCCAACTGGTTTATTTG
SQ5280F	15	43842369	43842985	+	GCCCCTTGGCCTTATAACTAAC	CCCCAGCATCTAGACTATCACC
SQ5281F	15	43850762	43851400	+	ATGTGAAACAGCCTCAAGGATT	TGAGGGAGGAGTTTCTCAATGT
SQ5282F	15	43890060	43890687	+	TTTTTGCTCAGTGCAGACAGAT	CAGCACCCCTAATACTTCCTTG
SQ5284F	15	44057335	44058030	+	GGCAGTGTGGAATAAAAAGGAC	TGGGCTAATTCCAGTAAAGCAT
SQ5285F	15	44072590	44073221	+	TCCACTCTCTCTCCCAGAAAAG	ATGGTATCCAAGGAGGATAGGG
SQ5286F	15	37945959	37946566	+	CTGTTTGGATTTGAGCTGTCTG	ATAAGCTCACTGTCGGATCACA
SQ5287F	15	37955025	37955678	+	GCTGTCAGCCTCCGTTATTAGT	CATCTTTTACAAGCCCCTGAAC
SQ5288F	15	37959419	37960041	+	CAACCAAGGTAATTGTGTGTGG	CCAGCTTTCATCCCTTTGATAC
SQ5289F	15	37965413	37966100	+	TAAAGTCTGGTAGGCCCAAAAA	CTCCGTCTTTCACTCTTGCTTT
SQ5290F	15	37973516	37974121	+	CAACTTTTCAGAGGCCAGTTCT	ACCTACTGTCCACCTGCTAAGG
SQ5291F	15	38002925	38003533	+	GCTGCTGCATCGACTAGTAAAA	AGCTGTGGAGACTGGAAGAGTC
SQ5292F	15	38024901	38025584	+	TGAGAATAAAGGATGGGCAGTT	GCACAAATGTACGCTAAGCAAG
SQ5293F	15	38062267	38062870	+	TCTCATGCCAAAAGAGGTACAA	ATCCCTTCTGTGATTCCAAATG
SQ5294F	15	38072358	38073032	+	GGCATGCCATCTAGCTTTATTC	TTGTTTCCAAGAACTGCAGAAA
SQ5295F	15	38111081	38111757	+	GTTTCTGATCACAGCAACCAAA	GCATAATGTCACCAGGTCTGAA
SQ5296F	15	37028870	37029519	+	CAAGAGGAACTTGGATGAAACC	CATTTGCATCAAAAGGAGATGA
SQ5297F	15	37032497	37033185	+	GAGGAACTTCTGAAGCCAGAGA	TAAGTGAATGTGCTGCCACTCT
SQ5298F	15	37067861	37068496	+	ATGACCGACTCCTTGTCAGTTT	CAAATGGTTTCACCTTTCTTCC
SQ5299F	15	37101098	37101769	+	TGATAGATTGCGATTGTTCCAC	CATCTAATAGTGCAGCCCAGGT
SQ5300F	15	37284853	37285523	+	AGAATGGAATGGAACTGTTGCT	TTCAGCTTGTGCAGTAGTGCTT
SQ5301F	15	37334257	37334946	+	CCCACGTTTATTCCCATGTTAC	ATCCGGGTAGTAAAGCTCATCA
SQ5302F	15	37465569	37466198	+	CAAACAGTAGGCATCTGAACCA	CCTCAGGAGGTGTTTGATCTTT
SQ5303F	15	37618677	37619368	+	AGAGGAAATCCGAAGGAAAAAC	GAATCCTTGTCCATGGTTGACT
SQ5304F	15	37654230	37654925	+	GTAATGCAAATCAAGCAACCAA	TTTCTCTCCTTCAGAGCTGCTT
SQ5305F	15	37698079	37698776	+	TGTTCCTTTTCCAAGGAATGTT	ATGAGTAATGGCCAAAAGCAGT
SQ5306F	15	44568197	44568879	+	CCAGGCTTATCTAGCATCCAAC	GTTTCAAACCCAAGCCATTTAG
SQ5307F	15	44569341	44570015	+	TTTCCTCCAAGGTGCTTTTCTA	GTTGCAGCTTCAAAGGAAAACT
SQ5308F	15	44585145	44585808	+	AATTTCCCCCTTCAAACTAACC	AACTCCAGACCCTGTGGAAGTA
SQ5309F	15	44586071	44586673	+	GCAAAAATGGACCTAAAGCAAG	CCCTTGCAATGACTTATGCTTC
SQ5310F	15	44596731	44597398	+	GCTGAAGTTCAAGTGCACACA	TGCTGTAGGACATTTTGCATCT
SQ5311F	15	44601228	44601891	+	TCTGAGTGAGGGATCTGTGAGA	TCTCCAGGTAAGCCATTTGTTT
SQ5312F	15	44605591	44606289	+	CCCTTCTGCTTTGTAGACTCGT	TGTTGGCAGTACATCAGAAACC
SQ5313F	15	44612763	44613394	+	GCCAGCTGTGAGTTAGGCTATT	TTTCTACCTGCCCATTTCTCAT
SQ5314F	15	44698337	44698968	+	CTAAGGTTTGGTCCACTTCCAG	ATTTGTCCCTATTCTCCCCACT
SQ5315F	15	44704943	44705572	+	TGCTCTTCCTTCACTTTTAGGC	TTTTTCCCCTTAATTACGCTCA
SQ5316F	15	44708081	44708761	+	TTCCGGAAAATGAGGATGATAC	GCTTCCTGCCATTAACCTACAC
SQ5317F	15	44732884	44733577	+	AGGTATTTGCCAGGGTGTTCTA	GAACAAAGTAACAGTGCCCACA

SQ5318F	15	44776844	44777487	+	TTGTCAGGATGTAACCCATCAG	GGTCTAAAATGCTCTGGTTTGG
SQ5319F	15	44782215	44782853	+	AAAGCCTGTGAGAAATGATGGT	CCAGATTAATATCACCGCATCA
SQ5320F	15	44782215	44782853	+	AAAGCCTGTGAGAAATGATGGT	CCAGATTAATATCACCGCATCA
SQ5321F	15	44810322	44810974	+	ATTTTCTGCCGTGGTATGAAGT	AGCAGTTTTATCCGTTGCTCTC
SQ5322F	15	44834614	44835215	+	TAGGAGCACCATAGTCCACAGA	TGGATACAACCCTTTGAGTGTG
SQ5324F	15	44835364	44835970	+	TCAGAGCAATGGGGTTTTATCT	TCTGGATACACAATGCAGAACC
SQ5325F	15	44923352	44924023	+	ACCCCAGGAAAATAAAGATGGT	ATTTCTTTCCAAGGGTCTCTCC
SQ5326F	15	44934676	44935360	+	ACTGCCACAGATCTACCTCCAT	TTCCCTTGTGTTGCCTTTTATT
SQ5327F	15	44942372	44943012	+	CATGGGAAACTGGTTTGAAAAT	GAGGATCCAGGCTAGAAATGTG
SQ5328F	15	44949172	44949848	+	AGCTGAAACTGTCTAGGGCAAG	AACTGAAAGTAGCGGTTTGCTC
SQ5329F	15	44954416	44955088	+	CAATTGTTACCAGGCAGAGTCA	GGAGTTTGGATTTGGAGTGTTC
SQ5330F	15	45010358	45011024	+	ATGCAGCAAAATGAAAACATTG	GCATTTCATCATGCTTTGTGAT
SQ5331F	15	45050399	45051008	+	TGAATGGGCATTTCTCTTCTTT	ACTTCAAGTGGTCCCACACTTT
SQ5332F	15	45065234	45065852	+	ACTTTCCCCCACCCTCTAAATA	TGGCCACAGAAAATGTAACTTG
SQ5334F	15	45165425	45166091	+	CTGGACATCCTCCTCTGACTTC	GGACATGACAGAGACCTGAGTG
SQ5335F	15	45187154	45187756	+	CTGGAGGCAACCATTTACTTTC	TTTCCCCAGTGCTCCTATTCTA
SQ5336F	15	45337604	45338259	+	TACAGGGCCTCTTACACCAAGT	TTGTGTGGCCTCTTACTTCTCA
SQ5337F	15	45339000	45339618	+	GGATCAGGTCGTTTACTTCCAG	GGTTGGGAGAACAAAATCAGAC
SQ5338F	15	45716536	45717136	+	TGGAGGGAGTAGGGACATGATA	CTGCAACATCCCTTCCTCTTT
SQ5339F	15	45717859	45718547	+	TGACCCCTGGAGTAGGGTACTT	ATTGGGTCAGCCACAATATCTC
SQ5340F	15	45719292	45719985	+	CCTGGAGAAGAGGGTATGTCAC	GCAGGACAGGACTCGATATCTT
SQ5342F	15	46501085	46501751	+	CATGTCACGTTTTTCACCAGTT	TCCAAGTCTCCCAAACCTAAAA
SQ5343F	15	46514686	46515334	+	CAATCCAAATTCTCCTCCAAAG	CCTATGCCTGTGTATGAGGACA
SQ5346F	15	46940291	46940933	+	CTCCTGGGTTCATGGTAATGTT	AAATTCTGCCATCAGGAAGTGT
SQ5347F	15	46952441	46953088	+	CCCCAGTTCTTCATAGGAGATG	AACTGGATTGAATTGCGTTTCT
SQ5350F	15	46998455	46999067	+	TCATCTTCAACCCTCTTGACCT	TAGGAGGATCAGGCATGAATTT
SQ5499F	15	44282413	44283018	+	CCTGCAGAAGTGGAGGATTT	TTTGCCAGAAGAGGGAGAGA
SQ5500F	15	44281919	44282527	+	ACATGAAACCCCAAGTCCAA	TGCAATTCTGTGGGATCTGA
SQ5501F	15	44277687	44278288	+	AGGGCAGAGCACAATGATTT	CAGGGGAGTCCTCAGTGCTA
SQ5502F	15	44226112	44226715	-	AAATCCCCAGTGCACAAGTT	GATCGTCCAGAGGAGTGGAA
SQ5503F	15	44210193	44210779	+	CCATGCATTTGTGGCTCTT	CCTCAGGGGCACATAAAAGT
SQ5504F	15	44283643	44283832	-	CATCCAGTTGAGGGATTTGAA	CACCTGAGGGGCAAACTATT
SQ5505F	15	25184230	25184954	+	ATGCAAGGGCAAGAGAAAAA	GGGCTAGAGCTTGAGAACCTT
SQ5506F	15	29997805	29998408	+	TGCCCAGATGATTTTGAGTT	TGCTAAACAACTGTGTGTGGA
SQ5507F	15	35584200	35584787	+	TGGGTTAAATGTGGGGTTTG	TGGTTTTGCCACAAAAGGAT
SQ5508F	15	36501317	36501944	+	GGTTTTGAAGCACACATAGCC	CCCATCCCCTCCCTACTAGA
SQ5509F	15	47546976	47547624	+	TTTTAGGGGGACATTTTCCTG	GACAAAAGGAAGGGGAAAGC
SQ5510F	15	47995467	47996110	+	TCCAAGGATGGGTTCCTAAA	TTTCAGAAGGCCTTGCACTT
SQ5511F	15	50036040	50036690	+	ATAGGAGGAACGCACTGAGG	TGGTCTCACACCTGAAACCTT
SQ5512F	15	52993336	52994108	+	TGCACCATATTGCTTAAACCAG	TCTGGGCTGGAGAGTTTCAT
SQ5513F	15	59941967	59942550	+	CAAATTTAGCAGAGTGCAGCAT	AAAACAGCGGGAGTCAAGC
SQ5514F	15	59947570	59948101	+	TTGCCGTTAGAAAGGCAGAT	TCAAGAAAGGAGGCAAAGTTC
SQ5515F	15	26022374	26022930	+	TCTTATCCAGTTGGCATTCCC	GCGTGCACACAATATTAACGAT
SQ5516F	15	27184047	27184707	+	TCCCTGAGACTTAACACCTGGA	CTGTCTCCAACCTACTGATGGG
SQ5517F	15	28010859	28011412	+	CCAATAAAATATATCTGAGGCCAGC	CCAAGCCAGTACACTTGACAAA
SQ5519F	15	31046295	31046857	+	CAACAAAGGAGACAGGAGATGC	AAGATCCATAGGGATTTCAGTGTT
SQ5520F	15	32008341	32008925	+	TCGTCATAAGCCAAACATCACA	AGACTGGGGTGGGATAACATCT
SQ5522F	15	34074156	34074708	+	CCAAACATCAAATTTCCCGTAA	ATAGTCTCACTCCTGCGTCCTG
SQ5523F	15	34467459	34468009	+	CATCTGTTGCTTCCAAAAAGACA	GAAAAATTGTGCTTGGCAGTGT
SQ5524F	15	34986364	34986964	+	TGCAGACATGCAGATTTTTGAC	AATAAAGGGATTTGCCTCTCCA

SQ5525F	15	35999731	36000280	+	TTATAGTGGCCCCTGAGGAAAT	AGGATTTTGTGCCTGCAAAGTA
SQ5526F	15	38481727	38482276	+	CCAGAAGGCACATGTTTCTTAGTA	ACATCACATAAATCATATTGCCCC
SQ5527F	15	39000249	39000967	+	AAGGGAAATCCAGGCTGTTAAG	CTATTCGTCCTGTCCCACCAC
SQ5528F	15	39508096	39508668	+	GTGCAGAAGCTTCAGATGGAGT	TCTGACCAGCAAGTCAGTGGTA
SQ5529F	15	39993919	39994629	+	TGATCCTAAAGCATGTTTCCGT	TGCCCAACCTTTTCTCTCATAA
SQ5530F	15	40593041	40593596	+	ACTGTTCAGTCAGGGGGACTTT	GACAAGGACTCGGAAGAACAGA
SQ5532F	15	41489683	41490236	+	ATGGAGATCACTTCCAGAAGCA	TCTAGCTCAGGGAAAACAGTGC
SQ5533F	15	42118571	42119128	+	AGCCCATGCATACCCTTTTAGT	AAACACAGCATGGTTACTGCCT
SQ5534F	15	42448417	42448969	+	CGGTGGCTTAAAGGAGGGT	AGCACAGTGCCTGTCTTGCTAT
SQ5535F	15	42942792	42943436	+	ATGTTCTCCACTGCCACAATCT	CCCCCATATCAAAGCAGTTACA
SQ5536F	15	43117066	43117693	+	GGGAAAGGCTCCTGTGTTAAGT	AGGCTATTTACTGCAATGGGGT
SQ5537F	15	43199545	43200127	+	TCCTTCTTTTTCTCAAGGTCCC	GGAACCAGGGCTTAAGTCATTC
SQ5538F	15	43303070	43303656	+	TGGGCCTAAAATTGTAGAAAACAA	TTGATTTGCAGGTGAGTCTTCA
SQ5539F	15	49120093	49120679	+	TCTTTTCAAAACACATATTTGCCA	TGTGGATCCTCAGGGTAATCAT
SQ5541F	15	52007173	52007735	+	TGAATGTGATGCTAACATGAAAATACT	AAGCAGACACAAAATCCATAGCA
SQ5542F	15	54013030	54013592	+	CCACTTGTACAAAAACATTGCAT	AAAACCACAGTGTGAAGATTGC
SQ5543F	15	55016069	55016717	+	GGGATGTTCATTTCCAATTTCA	AAAGTTCTGATCGCTTGCTCAC
SQ5566F	15	44115047	44115722	+	GAGCTGGATGTCATACCTTTCG	GGCAGACATAGGAGGGAGACTT
SQ5567F	15	44134228	44134729	+	GTCAGCCCATAGAGCTTTTCCT	GAGAGAGAGAGAGATGGGCTCC
SQ5568F	15	44166989	44167543	+	TTCTGCTTCATCTTTCTCCTGC	TGCAATCCTACTCACAGCTTCA
SQ5569F	15	44212301	44213076	+	TGAGAAAAGGTTGTGGGAAGAA	CCAGAGGATCTCTGTGCTCACT
SQ5570F	15	44228123	44228764	+	ACTAGTTTGGCTGCTTCACTGC	AGCAGCCATTACCTGTGGTAGA
SQ5571F	15	44231845	44232434	+	CCTAGGCTTTGACTCCACAATG	AACTGGCTATTTCCCTCTTTGC
SQ5572F	15	44237010	44237609	+	CATTCTGGAGATCAGGGTTCTG	ACCATTCAGCTTCAGTTTGCAT
SQ5573F	15	44244615	44245259	+	GGGAGCAAGGAGAGGAAAGTTA	CTCTTGTTTCCTTGGGGAGACT
SQ5574F	15	44253111	44253836	+	TCCCTCACTGAATTTCATGCTT	AGGCTTCATTCAAGGCTAAACC
SQ5575F	15	44260853	44261500	+	TTCCCAGCATATTTGTGCTCTT	ATTTTCCTGAGCTTTCCTCCTG
SQ5576F	15	44269651	44270298	+	CCCAAGTTGACATTGGAGAGAG	AGGGTTTCCAAGCCAAAAATTA
SQ5577F	15	44273047	44273825	+	AATGGTGTAGCTCAAACCCAGA	TTATTGATTGCCACAACCTTCC
SQ5578F	15	44275709	44276478	+	CTTCTCTTGGGCAAAAAGGATT	TGGGTGGGTACGTTTCAAATAG
SQ5579F	15	44293604	44294168	+	GAAAGAGCAAGCAAAAGCGATA	TCAGTAAGGGCTACAGGGACAA
SQ5580F	15	44310890	44311649	+	ACTTCCATCTTTCCGTAGCCTC	GAAAACATACCTTCCCACACCA
SQ5581F	15	44280718	44281321	+	TCCAGATGTCTGGGCTACAA	AGCAATGCCGTTACTTCTCC
SQ5582F	15	44281416	44282010	+	CAACCCCTTTTATGGTCGTC	CGGAAAGCGGAAACTTTCTA
SQ5583F	15	44277923	44279921	+	GGGTGGGCTTGTACTTACTGAA	AAGATCAGTTCGGAGTTTGCTC
SQ5617F	15	44280829	44282719	+	GCAGGTCAGGGTGGGTATTA	CAGCAGTCTTCCAACCCAAT
SQ5650F	15	44101407	44101964	+	TGTTCATCATGTATTTTTTTTTTTTCTG	ACAAATAGCTGAATACCAAGAGG
SQ5651F	15	44102775	44103425	+	TTTTGTGTTGTTTTTGTGACTGG	GTGTCATTGTGGAAGGGTGAAG
SQ5652F	15	44103142	44103815	+	GCATAGATACTTGGCTGGTTCTT	TCACTAAATGGGTTATTCACTGTACC
SQ5653F	15	44104588	44105267	+	TTAATCACATGCTCATACAGAAATAG	TGACAATGCAACTGGGTAAGAA
SQ5654F	15	44108646	44109303	+	CTTTGCGGAGAACAGAAATATG	GTCAGGCAATGGGTTAAAGAAC
SQ5655F	15	44111842	44112532	+	AATATTTGTGATTTCTTTTGGTGAC	CTCCATTAACATGAAAAAAAAAAAAACT
SQ5656F	15	44116223	44116892	+	CTCACAGATCCCTTTTTTTTTTTTTAAG	GTTACCATTTTGCCTTTTTTTTTTTTAG
SQ5657F	15	44117720	44118419	+	GCAAACACAAACCATGACAAAC	GGAGTAGAGAAAAAGGGGATTTTA
SQ5658F	15	44125676	44126358	+	TCTTGGTATAAACAGGGAAAATAAGC	CCAGGAGACCATTTCAACATCT
SQ5659F	15	44126961	44127659	+	GCACAGAGGCTATTATTTTAACAGG	AAAATGAAAAAAAAAAAAACCCAAC
SQ5660F	15	44127632	44128331	+	CTCGTTGGGTTTTTTTTTTTTTCAT	AGTGCTTTACATGTGTTATTTCACTTA
SQ5661F	15	44136408	44137057	+	TCTGGGACATCTGCTGGTTCTA	TCCTTAGATAACTTCATTTTTCCTTGT
SQ5662F	15	44136731	44137383	+	CATGTAGCATGACAAAAGAAAGAAA	CAAGCATGTAGGAAAAAAAAAAAAACA
SQ5663F	15	44138324	44139016	+	TTCCCAGTAAACAATAGGCAGAA	TTTCATTGGCTCATTCACACTC

SQ5664F	15	44156989	44157609	+	AACTTGCATTCACATTCAGCTC	TTTCTCCCTCCAATTAACCGTAT
SQ5665F	15	44158391	44159064	+	CTGACTACTTTTTGGGGGTGTC	GTGCAAATCTACCCTAAGCAACT
SQ5666F	15	44158819	44159518	+	TCAAGCCCAGACAGATAGAGAA	ACAATAGGAGCTGCAAGGTGTT
SQ5667F	15	44160918	44161616	+	CTTCTTTCCTTCATGTGCTCTG	TAAAATGTTTCCTTGGGCAGGT
SQ5668F	15	44164030	44164724	+	TTGTTACTAGGAGATGTTCACAAAT	ACTCTACCTTACTTGACCCCAAA
SQ5669F	15	44164548	44165246	+	GTTCCCAGTTCTTTCAGCATCT	GGGCCACACTTATTTTCACAT
SQ5670F	15	44164971	44165667	+	AGTTTTCTGCATTTTGCCTTTG	TCTTTTAGAGCACCACATTCACTT
SQ5671F	15	44167362	44168058	+	ACATTTGCCAGTCCTCTCTCTG	TGCTCAGGTTCTCTCTCCTTTC
SQ5672F	15	44169630	44170299	+	GCATAGTGTGGAGCCCTATATGT	AACCATTGTCTAATTTCCCAGTGT
SQ5673F	15	44170101	44170788	+	AGGGTCACAATTCCCTGTATGA	TTGAAATCATGCTACAAAACCTG
SQ5674F	15	44172661	44173337	+	AGGCATATGTATGTTTATTGTCTGTAA	AAAAAAAAAAAAAAGAACCAGGCATC
SQ5676F	15	44178129	44178818	+	GAATAACCATCAGGGCAACCT	TCAGACATACATTAAGAGGAGAAGTCA
SQ5677F	15	44179428	44180120	+	TGTTTTCTATAAGGGAGGCATCA	TTAAAAAGGGCAAGGCAGAC
SQ5678F	15	44179919	44180603	+	TTTTGCTGCGTCAGGGATA	GAATAACCTCTCTTACTTCACAAGAAT
SQ5679F	15	44180309	44181008	+	CGGTATTGGGCATAGATGTGTT	TGAACATGGAAGAAATGCTGAA
SQ5680F	15	44182135	44182827	+	TTCAAGAAATGTTTACCTAGCTCCT	ACACCTAAGAGTTGACTGGATTTTT
SQ5681F	15	44182597	44183291	+	CTTCCCTCCTCTTTTTGCTTTA	AATGTTTGTGCCAATTTCTGGT
SQ5682F	15	44183092	44183651	+	GAATTTGTCACTTTGTCACCTAGC	GGCCCTGGTTGGAATAAAGAT
SQ5683F	15	44183393	44184073	+	TGTCTGGTCCCTTGAATTTGT	ACACACACACACATACCACTGC
SQ5684F	15	44183870	44184560	+	CATCTCCTTGCCTCCTCCTT	AGCCATATTGGTTTTTCTGAGC
SQ5685F	15	44194765	44195456	+	ACGGGAGACGTTTGAATATAGG	TGATCTCTGTCCACAAGCTGAA
SQ5686F	15	44195270	44195880	+	TGCATTCCTAATCTTGTCTACTTGTC	TTGTCCAAAGGTTGTTTTATGG
SQ5687F	15	44195662	44196361	+	ATAAACCCCAGAGAGCATGAAT	ACGAATTTTTCAGCCACTTTTC
SQ5688F	15	44196143	44196726	+	AGGGACTCTGTTTGCCACATTA	TTTTTCTGACATTGACCAAGTGAT
SQ5689F	15	44199697	44200316	+	TCCTTTCTAGGCCACATTTTGTA	AGGACTCTCTGTACCCATAAACATC
SQ5690F	15	44203079	44203778	+	AGTGCTGAGAGACCACATTCTT	ACAGTGCTCATCCTGCCAAAT
SQ5691F	15	44203859	44204558	+	TCTCCATTCTGTTGTATGATTAGTTTT	GACTCTGAAACCTCGAACTGTCT
SQ5694F	15	44206649	44207334	+	CTTAAAGAAACAATAGCACCACA	CCCCAAATAACGTAACAGTGTC
SQ5695F	15	44209077	44209768	+	CAGTTTCCTAGCTGTACCATGAA	ACAGTTCCTTAAAATGATGAGTTAGTG
SQ5696F	15	44209538	44210230	+	AGCTCCAGGCTTCTTTTGTTTT	ATCTTAATCCCTGCCTCTCAAG
SQ5697F	15	44209947	44210599	+	TTTTGGGTGTGCTATTTGACTG	TGTTGCTGTTTCTCCCTTACTTT
SQ5698F	15	44210264	44210937	+	CATTATTGATAAAGGATCAACAGCA	TTTTTTTTTTTTCTCTTTTTTCTCC
SQ5699F	15	44212992	44213670	+	TCTTATCCTTTTCCCCAACAGA	AACCAACCTGAGCAAGCTAGAG
SQ5700F	15	44213551	44214223	+	GATTTTTGAAAGGAAAACAGTAGTGAG	AAAAAAAAACTGATGCAAATAATATCAC
SQ5702F	15	44217725	44218424	+	TGGGCAGCTTGTTCAGTTAG	TCTTGTGCCATTTTCTGTCTTG
SQ5703F	15	44218187	44218873	+	GTATGACACATCTGGGCACAAC	AAGAGGTCAAGCGATCAAAGAC
SQ5704F	15	44218661	44219357	+	CCACACTCACACCATAGCATAAA	TTGAAGTGCCAGAAAGAAGTTG
SQ5705F	15	44220714	44221398	+	GACTCTTTTTTTTTTTTTTTGCCTCT	TGCTTAAAATGGTTCTTGGCATA
SQ5706F	15	44223633	44224325	+	TCTGACCTAGATTCGTGTCTGTG	CCCTCCCTGCTAAAAAAAAAAAAATA
SQ5707F	15	44224308	44224992	+	TTTTTTTAGCAGGGAGGGGAAT	GGGAGGGGTCAGAGATGAGT
SQ5708F	15	44226173	44226872	+	TGAAGTGAGGACGGTGTCTTT	CCTGAGCATAAAAACTAGGCAGAT
SQ5709F	15	44227910	44228593	+	CACTGATCCAGAAGAATCCAACT	CAAAGAACCATGTAAGCCTATTTGT
SQ5710F	15	44228302	44229001	+	CTTTGGGTGGGGTCTACTTTCT	TGCATGAAATGGAAATGCTAAA
SQ5713F	15	44233526	44234216	+	AAACGTGTCAAGGAGTCTAGTGA	ACGGTAATGTTTCTGCTCTGAAT
SQ5714F	15	44233942	44234624	+	TTCTCAGCTACTAAATCCCCACA	CGACACTGGTATGTCTCCTGTC
SQ5715F	15	44235687	44236386	+	TGAGAAAGACTATGACGGAAATTG	ATCACACACAACGCAACTGG
SQ5716F	15	44236164	44236854	+	CCCATAAGGAGAGGCACTGG	CCCTATTTTCCTCCATCAAATTC
SQ5717F	15	44237806	44238505	+	TCTTTGGACAAGATAGCAAACTCA	AGGCAGATGTTGAGGGAAATAA
SQ5719F	15	44239394	44240078	+	AGTCTTGGTCTTCACATATCTTCTCA	GGCCTCCATTGTTCTAAATGTC
SQ5720F	15	44240732	44241364	+	TTCTAGTTCTCCAGATGCACACA	TCAATTTCATTTTTCCTGGTTTT

SQ5721F	15	44241116	44241815	+	AAGGGAAGACCAAAGGACTAAAA	TCAAGGCTATCCCAGTCATCAG
SQ5722F	15	44241547	44242246	+	GGAATACCGAGTTCTTGTCCA	CTCATGTTGGATTTCTTCTACCA
SQ5723F	15	44242772	44243459	+	CCCCTAATTCATAATACAGTTCATAA	TCTGGGGTTTTTAAAGTATAAGAGG
SQ5725F	15	44245004	44245639	+	TAGCACACCCAGTCTCAAGAAA	CCACAGGAAGTGGATAGACATT
SQ5726F	15	44246527	44247187	+	AATGGGCTCCAGTTGACAGA	CATAGAATGGGGGTGCTTAGTG
SQ5727F	15	44246929	44247628	+	ACAAGGGTAAACAGACGAGTGC	GAGGAGATGGTATAGAATAAGGAGTCA
SQ5728F	15	44247335	44248014	+	AGAGGCCAGTTCTTGTCCTGAT	TGAGCATCATCCAATTATATCACA
SQ5729F	15	44249205	44249903	+	TGATAAACAGAGTGAAGTGGAAATG	GAGAATGGATATTGGGCAAAAG
SQ5730F	15	44255137	44255834	+	GGATACATTCACCTGTGGGAGA	TGCTCAATTAACATACCCTGAGTT
SQ5731F	15	44256686	44257383	+	GAAACTTCCCATTAAGCACAGC	CACACTCCCAGCCAAAATTC
SQ5732F	15	44257119	44257807	+	GGAAGTAAAGTCAGGCCGTTAG	GGGTGCCAACACATAAAGAAAT
SQ5733F	15	44257593	44258292	+	TCTCAGTAGTTGAATGCACAGC	ACTCCTTGTCCTCTGCTCATGT
SQ5734F	15	44258000	44258696	+	ACTCTCACCTACAGCCTTTTTCTT	CACCTTCTCGGGATCTCTTCTT
SQ5735F	15	44258458	44259157	+	TTGATTGCTAAAGACCCACAAT	TGCTAGAATTACAAGGGCAAAA
SQ5736F	15	44258944	44259530	+	TCTCTTTGGTGTTCCATGTTTC	TGTTAGGTATCAGAATGGGCTCT
SQ5737F	15	44260806	44261502	+	TGGATACCTTTGAATGCAGTGT	TTATTTTCCTGAGCTTTCCTCCT
SQ5738F	15	44261292	44261954	+	ATAAAACAGCCCTCACCTTTGA	CCATCCCACCCATGAAATTA
SQ5739F	15	44261755	44262422	+	TGCCAGTTTGTGAGCTTTGTT	GGCTTCATGGTTCTCCTCAAAT
SQ5740F	15	44264051	44264750	+	CAATAGCAAACCTAATGGAACTAATC	CTTCACACAGAGAGTAGCCTTGTT
SQ5741F	15	44264917	44265544	+	CTTTGTTCCTTATTATTGCCATTGT	TCCTATGGATTCAAGCATTTCA
SQ5742F	15	44265359	44266057	+	GAATCAGCAGAAAAGAAGGAATCT	AGCTACCCAAAACAAAGGATATTG
SQ5744F	15	44267061	44267745	+	TAAGTGCCCAACACTGATGC	AAAAAAAAAAGAAAGAAAAGTATGTTGG
SQ5745F	15	44269110	44269795	+	CATGCCACTTGGTCTCATAAAG	AATTCCTTGCCTATTCCTTATACATT
SQ5746F	15	44269547	44270241	+	GCCGTCATAGAAATCTCCAGAA	TGCTAAAACCCCTGTGATGATA
SQ5747F	15	44269990	44270661	+	GCATTGGAATCAGAAAACAGAA	TGCAGTAAGTTGTACGCCTATTT
SQ5748F	15	44270365	44271058	+	GGTTGCATAATTTCTTTGTGTCC	AGCAGCCTTCCTTCCTGTTT
SQ5749F	15	44272769	44273466	+	AGTGGTCTTTTGATTGCGTAGA	CACTTTGCTTTGCTTTGTTTTG
SQ5750F	15	44273445	44274105	+	CAAAACAAAGCAAAGCAAAGTG	TTGAGAACAACCAAAAGAAAGAAA
SQ5751F	15	44273830	44274524	+	GAAATTCCATGCAAAGTTTCAC	TAATTAATGCAGCTTCCCCAGA
SQ5752F	15	44274350	44275001	+	TATCTAGCTCTTTCCCGATGTG	AAAGCAGTCTTCCTCACCTCTAC
SQ5753F	15	44274711	44275400	+	ACGTTAAGAAAACTCCCCTTGTT	TTTGATCACTGAACTGACAAGC
SQ5755F	15	44276691	44277383	+	ATCAGCCTCTCCCTTCCTATCT	TGTCCTCTATGCAAATCAACCTT
SQ5757F	15	44280720	44281385	+	CAGATGTCTGGGCTACAATG	TTGGAAAAATGTCTCCGAATG
SQ5758F	15	44281487	44282136	+	CACGGTACAGGTCGTATGTGTT	TCTGCACTTATGCTCAGGGAGT
SQ5759F	15	44281836	44282521	+	AAACGAGAAGTTGGCATGAAC	TCTGTGGGATCTGAAAAATTAGC
SQ5760F	15	44282334	44283006	+	GAAAGTTCATATCCACGCTCTA	GGGAGAGAGAGAGAAGGCAAAT
SQ5761F	15	44282717	44283405	+	CTGATTTTTCCCATTGCTTCTG	CGGTGCTGTCTTTCAACCTACT
SQ5762F	15	44283207	44283902	+	ACGGAGAAACACACATCTGCTA	TCTCAATGGCAAAGGCAAGTAT
SQ5764F	15	44285103	44285693	+	AGTGTGCATGGATTGCCTGT	TTCCTCATCCCCTGAGACTACT
SQ5765F	15	44285465	44286164	+	GAGCAGGGCAATAATTCCTAGA	TTTTTAAGAAAGGTGTCAGAAGTC
SQ5767F	15	44291976	44292675	+	TCAGGATGGATTAGGGACAGTT	TGGGTTTCATGTTTTGTCTATTTC
SQ5768F	15	44292127	44292813	+	GCTCTTTTCCTGGCTAATGAA	AAAAAAAAAAAGCAAATTTATCACC
SQ5769F	15	44299670	44300345	+	TCAGAAAGGAGACTACAGCCAGAG	AGCTGAGATAGAGTGGAGGAACTG
SQ5770F	15	44303438	44304136	+	TGCTCATGGACAAGTACAAATG	CTTAGCTGGCCCTTGGATATAA
SQ5771F	15	44306547	44307244	+	CCATGCAGTAGGCAATCAATAA	TTGCTGTGTTTTAAGTTTTGAGGT
SQ5772F	15	44319606	44320303	+	GGACAAGAATTTATACGCAACCTT	CTTAGGATCACTTACTCTCTCACTTCA
SQ5773F	15	44322640	44323337	+	AGTGGGGATGTGTGCCACT	CCCCTTTGGAAAAAAAAAAAAAGT
SQ5774F	15	44323401	44324099	+	AAAAAGGGACAGCCAGGTAG	CTATTCCTCTCAGGTCCATCTCA
SQ5775F	15	44323860	44324543	+	CATCTGGGCTGTGATGGAT	CATGTTGTCCCACCTGTCACT
SQ5776F	15	44327923	44328622	+	AAGTCAGTGGCGGTGATTATTT	CAAGGAGCCGATTCATTTTT

SQ5777F	15	44343049	44343748	+	CATGGAGCGACTGCACTTT	ATTAGCAAAGCCAGCCAGAA
SQ5778F	15	44343509	44344133	+	CACTATCATCCCTCTCTGTTGC	AAGACCATGTGAGCATACCAGT
SQ5779F	15	44346728	44347421	+	ATTATGACCCTGCCTTCCTGAC	CCGCCCATGTAAAGTAGTTG
SQ5780F	15	44348348	44349047	+	TAGAGACATACTGGGGGAGATG	AGAATTTTGATGCGCTAACACT
SQ5781F	15	44348776	44349472	+	TGGGTTGTAGTTTGTGATTTTGA	GTGCTCTTTCCCATGTCCACTA
SQ5782F	15	44351519	44352198	+	ATCCAACTTCCTTATCCCCACT	TGTCTTAGTTTGTGACTCCCTCCT
SQ5784F	15	44354830	44355527	+	GGACTGGCTGGAGATGTTTC	AAAAAAAAAAAAAAACCAAATGAGC
SQ5785F	15	44356841	44357480	+	TTTCTTCACATTGGACCCTACA	AAAAATTAAGTCTGCGACCAAAA
SQ5786F	15	44357300	44357994	+	CCCTTTGTGGTATTTGGCTATG	TGAATGAAGGAGAGAGGGAAGA
SQ5787F	15	44357997	44358695	+	AGGGCAATTAAGGCAATGTTT	ACAGGTCTTCATAAAAGCAAAGTG
SQ5788F	15	44363153	44363710	+	AGCTTGGAGGATTTTTCTGACT	AGCTTGATGCCAAACACAGAT
SQ5789F	15	44363535	44364230	+	CAAGTAGATTTTCCTGGGGGATA	AAATGTGTGTGGGCTTGG
SQ5790F	15	44365529	44366222	+	AAGACCTGTGAAACCTAAATAAATGAA	TGCAGTGAAACCACTTACAAGA
SQ5791F	15	44373895	44374594	+	GTTTCCTCATCTCTCCATCTCA	AGTCTACTGTCAATGTGTGCATAAAC
SQ5792F	15	44378458	44379154	+	TTTCTCTCCCCCGCTTATTT	TCGTCTTTCAGGCCAAGTTAAT
SQ5793F	15	44378946	44379637	+	CAGGTGAGATCAGTGTGCAAAT	GTTCTCCTCATCCAAAAACAAAA
SQ5794F	15	44380319	44381012	+	GAAGAATCTGATCATCTTAGACTCAA	TTTTACAACCTCATGAATTTATTGT
SQ5795F	15	44385931	44386581	+	AGGAATGATATGCAGGCTTGA	GCTTCAGGAGAGAAGGGCTA
SQ5796F	15	44386359	44386994	+	TGTTTTGAAAGTCAGCTGGAGA	TCTGTATACTTTGGGGCTATGGA
SQ5797F	15	44392637	44393299	+	AAAGGCACCAGACCCAGATAAC	TGACCATTCTTGTAATGACTAACATC
SQ5798F	15	44393016	44393693	+	TGGAGTTTGATAGAAAGGGATACTT	CGAGGTATAGAGAAATGAATTGACC
SQ5994F	15	44207528	44208012	+	TCCATCAATCCTGGGTCATT	CAGACAAAGGTAAAAGAAACTGG
SQ5996F	15	44234536	44235309	+	CCATTTTCTGGTCACATCGTT	TGCTGGCTAAAAGTGAATGG
SQ5997F	15	44241277	44242055	+	CTGAAGGAAACATGGGGTGT	GTTGGGAAAATGTGCCAGTC
SQ5998F	15	44268781	44269593	+	TACTCATGGCTTTCCCATCC	TGACGAGTTGTTGGATCAGC
SQ5999F	15	44279309	44280007	+	AAGCGGGCACTGTAAGGAG	AAGAAGGGAGGGACAGAGAAA
SQ6000F	15	44280733	44281534	+	TACAATGAAAATGCCCAGCA	TTTACAAGCAGCGAAGTCCA
SQ6002F	15	44289726	44290425	+	CCCTCCCTCACTAAAATTAAGC	GATAGCACCTATCAATGATGTTTTT
SQ6003F	15	44355593	44356160	+	ATGAGGAAGAGGGCACAATG	GCAAATGGTAACTTCCTTGGAC
SQ6014F	15	44226864	44227512	+	ATGCTCAGGATGGCTCAAGT	GGGACTCATGATGTGCCTCT
SQ6015F	15	44227362	44228100	+	GTGTAATGGGCCTTCCTCCT	GGTCTGATCTTCCCAACCAG
SQ6016F	15	44228859	44229505	+	TGGGGTAGTAAAGGTGGTTCC	TCCCAATGAAGTACAATTAGTCCA
SQ6017F	15	44229255	44230112	+	AGCTGTGCTTTTTCAGTCCA	CAATGTGCAACACAGGGTTT
SQ6018F	15	44230096	44230824	+	CCCTGTGTTGCACATTGTCT	AAAAATCCCCATTTTTCTCAAA
SQ6019F	15	44230718	44231568	+	CATTTGTTGCTATGGGCTGA	TTTATGCCTCTTGGAGAACTCA
SQ6020F	15	44232265	44233123	+	AAATGCAATTGGGATGCTGT	GCTCCTATTTCACTCAACTTTCC
SQ6021F	15	44232815	44233690	+	TGGGCCACCCTGTCTAATAA	GATCCTTCTGCCAAAAAGCA
SQ6022F	15	44234404	44235102	+	TTTGCTGGACAGAAATGTCG	GTCACGGTGTCTCTTGTGGA
SQ6023F	15	44234911	44235734	+	GCAGGTATCCCCTTCCTCTC	CAAGTTGGAGCCAGACTCATC
SQ6024F	15	44236810	44237088	+	AAGGAAAGCAGGGATCAGTGT	CTCAATTCCCAGTGCCACA
SQ6025F	15	44237589	44237972	+	TGCAAACTGAAGCTGAATGG	AACCACACCTCTCTTTCTCCTT
SQ6026F	15	44238408	44239249	+	ACGTGAGGACCAATGTGTCA	CCCCTTTTTCCCATCATTCT
SQ6027F	15	44225012	44225768	+	ACATTGTGAGGCAGTGGTCA	TTCACATTCAATGGCAAACTT
SQ6028F	15	44225414	44226163	+	TCTCCTTACCCACCCTTCCT	CCCTCTGGTCACTCCACATT
SQ6047F	15	44218028	44219023	+	CTTATGCTGGGGTCCTGAAA	TCCCAGTGAGAGACCAAGAGA
SQ6048F	15	44286692	44287381	+	TGGGAAGGAGCTCTGTCATT	AAACCAACAGCTCCGCTTT
SQ6231F	15	44208537	44209235	+	TTTTGCCTCTCAACTAGCAACTC	ATGCCATCTACCTACCTCATGG

Supplementary Table S4. SNP and insertion/deletion variations discovered from sequencing within *IGF1* and flanking loci. For insertion/deletion variations, alleles are given as, e.g. 'AAA/***', where asterisks indicate the number of bases deleted (or, not inserted) at the position.

Genome position (Canfam1)	Left flank	Mutation	Right flank
34467609	AAAAATATGG	C/T	CCATTATTTC
34467705	ACCACCCCTT	C/T	AGGATTCCCC
34467742	TTAAACAGTC	A/G	GTTGGCTATG
34467769	GACTTTTCAT	C/T	TACTAAAGCA
37029157	AATGACAGGA	C/T	GTATCTCCAA
37029408	GAGAAATATT	A/T	TCCTCTAGAC
37032637	TAATATGAAA	C/T	GAATAAAACT
37334423	GTTTCAGTCC	A/G	CAGATGTGTT
37334731	GCAAATCCTA	C/T	CCATACACTG
37466132	AAGGATAACC	G/T	TGTGGGATTA
37946398	TGAAACAATA	C/T	CCAGCCCATG
37946458	TGTCCATCCA	T/G	CCTTTTGAAA
38003377	ATCATCTCGG	C/T	CAACTGTTTA
38062418	ATATATTTTT	C/T	GCATCAGCAG
38062483	CTTGATGTGT	C/*	CTTTTATTTA
38072501	TAAAATACAG	ACC/***	CCACCCAAGC
39508148	ACCCCGGGTC	A/G	TGTGTTTGAC
39508338	TTGAGGTGAC	C/T	GAGAAGTTCA
39508364	GACCCCATTC	A/G	GATTCTGGTC
39508396	GTTGACCCTC	A/G	AGGGCATCCG
39508458	ACACGCTGTG	C/T	GACTTGTACG
39508482	CTCTGACCAT	C/T	ACGCAGGCAG
39508484	CTGACCATCA	C/T	GCAGGCAGTC
39508511	ATCAACACCC	A/G	AAGGAAGGTG
39508546	GAAGATGCAC	A/G	CCCAAGACTT
39508568	ACCGTGTCTG	C/T	CATACACGGA
39508574	ACCGTGTCTG	C/T	CATACACGGA
43199781	AATCACATGG	C/T	TGATAGTAGG
43199823	ATTTAATCTC	C/T	GAAAAAATAG
43199924	ATTGTGCTTC	A/G	GGATAATTAG
43200020	ATGTCCTCTC	A/G	GAAGATACTT
43200053	TTTGGAAAAC	C/T	TGAGTTCCTC
43200091	GTATCCATGT	A/G	TTCTGTTAGA
43463997	TAAGCACACT	C/T	ATCCAGGATT
43471190	AATAGTGGTC	C/T	TGGTTCCAGC
43471401	CACTTTCTTT	C/T	GTAATATTAG
43471508	CTTTGATCAC	C/T	ATCTTTTTTC
43471534	AATGATAATT	A/G	CTTCATTGTT
43767762	GGAGGAGAGC	A/C	GTGCGGCAGC

43767876	TCTCAGTCCC	C/G	CCTGGCGTTG
43768131	CCCAAGGTGG	G/T	CCTAAAATGG
43771302	AGTTCTGCAT	C/G	CTGGTTGCTT
43771473	GAAGACCAAA	C/T	TGGCGTCATA
44103304	GACTCAGTGg	TGTG/****	gtgtgtgtgt
44105030	attgttttac	TAT/***	attaagaatg
44105067	tcattgttgc	C/T	gtaatgtagg
44108838	AAGGAAcctt	A/G	tcttttggtc
44111904	ttgatttatt	A/G	cctctattta
44111958	gaagaagaaa	AAAGA/*****	gatacaattt
44112009	caaattctac	C/T	cttggatcca
44116630	CTGATAGCCA	G/T	TGACATTATA
44126223	GGAAAAAAAA	A/T	TTAATTTTTA
44127769	CACCAAACAG	A/G	AAGATTTTGT
44128080	accagaggct	G/T	cattaaatgT
44134426	TCGAATATAT	C/T	TTTGTCCATA
44136626	TGAACTTTTT	A/T	AAATGTTTCT
44137099	GTTAACTCAG	G/T	TTCATAGTGA
44165333	TAATTTTTTA	A/G	TATGCTGTAT
44169713	taccagattt	C/T	cttgccaacc
44170285	TACACTGGGA	A/T	ATTAGACAAT
44170352	CTTACCCATT	A/G	GGCTTATGAC
44173049	AACTACCCCC	A/G	AAATCTCCCT
44173114	TTTTCCCCCC	C/*	AACATTTTCT
44178275	TTAAAAAAAA	A/*	TCCCAGAAAT
44180886	AGTAAATTAT	C/T	AGGCTTTGAT
44184120	AAAATATACC	C/T	TGCATGTGGT
44194828	GCATTGGATG	AA/**	TCAAATGTGT
44195931	GATTTTCTGG	G/T	ATAGTATCTG
44195963	TGTAGATACT	A/G	CATTTTCAAA
44196459	GTACTATATG	C/G	AGACAGCCTG
44196571	TAAAAAAAAA	A/*	GGATTAGTGA
44199850	CCATCACCGG	G/T	TGAAGGAAAG
44200160	atttatagat	A/G	atgctggcat
44202877	CAAGTACAAG	A/G	CTCCTGAGCA
44203214	TCACTGCTGG	A/G	TACAGTGAGT
44204084	CATACATTTT	C/T	CCAAATATGC
44204307	TTCAGTGTCT	A/G	TATGTGTATT
44209414	CTCTAGACTC	A/G	CCAATCGAAT
44209812	TGCCTAAAAA	C/T	GATTGGCCTC
44210239	ATATATATAT	A/T	TTTTTTTCTT
44212591	CTTTTCTGTT	C/T	GATATGCAAT
44212736	GCCTTCTTTT	C/T	GCTTTAACAG
44212792	TAATGATGCT	C/T	ACACTTGGAA
44213544	TAGTATGCAA	A/C	TAGACAGATT
44213697	CCAAGGGAAA	TGTTGACCAACTCATAATAGGGAATAA/***************************	GTTGACCAAC
44218314	AACACTATGA	C/T	AAGTTAAAGT

44223950	agcacaaccc	C/T	aagcagacaa
44225914	tgcaggatgc	A/G	gaaagaattg
44226324	TGGGCATGTC	A/G	GTGTGGCGCT
44226684	CTGCCCCACA	C/T	GCCTTAGCAC
44228468	TTCGCCAGCC	A/G	GGCCCTGGCA
44231095	AAATGAGATA	G/T	AATGAATTGT
44231412	attctgtTAC	A/G	AGTAAAGAAA
44232955	tgggagcctg	A/C	ttcaccctcc
44234755	taaaatggac	A/G	tatgtaaaag
44235098	AAGAGACACC	A/G	TGACAATGGA
44236627	GGTATCGAGG	A/G	CTCATTCTAA
44236768	CCTCTTTTTC	A/G	GGTTTAATTT
44237388	GCTTCAGACA	A/G	GCCATCACCT
44237485	ACCCCCCCCC	C/*	TTTTGGAAAA
44237985	GTTGTGGCTT	A/G	TCTCCAAGAT
44238540	TCTAAGTATG	A/G	GAAGGTTGCA
44239577	ACAAATTACC	C/T	TGGACTTCTC
44241425	GTTTCTTCTC	C/T	AGGGTGGGGA
44241708	atggagcacc	TAAC/****	atgttctaga
44244799	AAAATGATCT	C/T	CATTCACTAA
44245140	TGCATTTTTT	T/*	GTAGGAGACC
44249286	AGGCTCCTTT	C/T	AGTGTGCTGC
44249353	CTTTTGTCTT	A/G	TTTGACACCA
44249558	TCTTAGaatg	ATA/***	taataataat
44253397	CAAATGGACT	C/*	CAATAGCTCT
44253636	TCAAGTTCTA	C/T	ATGCTGTTTA
44258017	CCTACAGCCT	C/T	TTTCTTAATG
44258630	ttaaaaaGTA	GT/**	tgtgtgtgtg
44259236	TTAGCTAACC	C/T	AATTGCAACT
44260949	TGACAAAGTC	A/G	AGCATACTAA
44261639	GTGGTGAAGA	A/T	TCTGGTGCCA
44261848	aaattgtgga	C/G	tttggattca
44263980	AGTGGTTTTA	A/G	TTTACCCTTC
44264050	CTTTTAGATT	c/T	CAATAGCAAA
44265060	TCAGAACCAG	A/C	CAGAAGTAAG
44265948	ACTCAAAATA	C/T	GTAGGAAAAT
44267458	CTGAACACTG	C/T	ATTTTGAAGC
44269183	CCAAAATCTA	C/T	AGTATCCTTA
44270404	CTGCTGATCA	A/C	ATATTGCAAA
44274799	CAAATTTCAA	A/G	TGCAGATCAG
44274840	AAAAAGAAAA	CAA/***	AACACTATTA
44277163	AGGCAATGTG	C/T	TGATTTATGT
44277903	ACCGAGTGGC	G/*	GGGGGTGGGG
44278140	CCTCCTTGGT	C/T	CTCACGAGGC
44278880	AATATCAAAT	C/T	CACATATGTG
44278905	GATTGCCCTC	C/T	GTGAACAGGG
44278906	ATTGCCCTCC	G/C	TGAACAGGGC
44279290	CTATCCAAAG	A/G	GCCTTGGAGT
44280625	aagaaTTCAG	A/G	ACAATCCCTC
44281297	CAGGTACTGG	G/T	GGGGGGAGAA

44281298	AGGTACTGGG	G/T	GGGGGAGAAG
44281633	ATTTGACTAA	G/T	AAAGTCCTAG
44281852	GAAGTTGGCA	C/T	GAACGGCAGC
44282040	TTAAATTATC	C/T	AAATATCTTG
44282162	AGCTCCAGAG	A/T	TCATATTTAA
44282216	TATGTGGCTT	A/G	CCTTATAATA
44283403	AAAGACAGCA	C/T	CGGGGTGACC
44283574	GAAAAAATAA	T/*	TTTTTTTTCT
44284186	GTTGTCCTGT	A/G	GCCAGAAAAC
44285600	TTAGGAGAAA	A/T	AGAAAGGAGA
44285618	AGATGTATCT	A/G	TTACTAGACA
44285658	CTAAGCCCAG	A/G	AAAAGTCCGG
44292077	GAATTTTGGC	C/T	TTTTACTCCC
44292534	GTGGATTTTT	C/T	AGATAAAGCA
44300004	tatatttcac	A/G	aaaaacaggg
44300179	tcttcttggt	C/T	attccccttt
44311482	TGTGCTGCCC	C/*	ATTGGGAGGA
44319631	CGCAACCTTT	A/T	CTCCCTCCCA
44320055	TTTCCTAACA	GTCA/****	TCAGAGAGAG
44320180	TACTCACAGC	A/G	CAGTCACTTC
44320227	aaaacaaaaa	CAAAA/*****	aaaacaaaaa
44322763	ACttaaaaaa	A/C	aataaaaaat
44324053	AAATTGTCTG	C/*	TTTTGTCATG
44324462	cctctccatc	A/*	cgttggtgta
44343089	ATCACCTGCC	A/G	AGGCATAAAA
44343382	TGGATGGTAA	A/G	GATGCTCTGT
44344029	CTGGGGCTGC	A/T	TGGACCTTCA
44346926	GTTATTGAAA	A/G	AATGCACCTT
44346948	AAAATTGTTG	C/T	GCTCTTCACA
44347221	TTCACAACCA	C/T	TTTtaaagca
44348436	TGCTCATCTT	C/T	CAACCTCACA
44349012	GTGTGTTCCC	C/T	CCCTTGGTCA
44349028	GGTCAGTAAG	C/T	GTTAGCGCAT
44349040	TTAGCGCATC	A/G	AAATTCTTAG
44349100	AAATAACTGT	A/G	TTACTGGTCC
44349363	TTCCTTCACC	A/G	TTTAGGATTC
44349505	TACTCAGGAG	C/T	TAGGGTGGTG
44349542	GTGGTTTGGA	C/G	GCTTGGTTCT
44350759	GTTTGCTAAA	c/T	TGCTAAGACA
44353046	AACTTTGGAA	C/T	AGTCTTCATT
44356907	ACATGGTGTA	A/C	CAAGGACTGG
44356919	AAGGACTGGG	A/T	AATTCTTTTC
44357667	agcattacaa	C/T	caccaccaca
44357909	TGTTTTTGTC	C/T	tcctctcccc
44357923	tctcccctcg	C/T	ctgtgttcct
44358189	CACACCTTCT	SINEC_CF/220*	TCCTTTGATG
44374108	ATTCTGTatg	450bp INDEL	acacagtcaa
44374301	agaaggacaa	A/C	cattttatgg
44379120	GGTTTTTGAG	T/*	TTTTTTACTT
44386327	AAAAACAAAA	C/*	AAAACAAAAA

44392908	TTACGGTTTT	C/T	GTTGTGAATA
44393461	GTGGGAGACT	A/G	AGGTGGCTCT
44393668	gacttcgggc	A/G	ggtcaattca
44568224	CCAACCTCCC	A/G	GTAGATTATC
44568247	TCAACTCTTT	G/T	AACATTATTC
44568300	TCTTGTTTCA	G/A	CCCTAATTCT
44568391	CACTTCACAC	T/A	GTGTTTGGCT
44568606	GTTGACCATC	C/T	AGTTACATAA
44568721	AACATTATGC	C/T	TCTATGTTGA
44569513	TTTGAAGAAG	A/G	ACTTTTTAAT
44569631	TTTTAATATT	A/C	TCTCAACTGG
44569764	TTTCCAGTCA	A/G	CTCTTTAGGG
44569821	TCGGAACTTT	************/TTCTCTAGGATGA	TCTCTAGGAT
44586165	AAAGCCACTT	C/T	CTCCCTGTCA
44586326	CCTTTGTGGG	C/T	GCCTGGCTCT
44586452	GAGGCTGCCC	T/G	GCACAGGCGG
44586461	CGGCACAGGC	T/G	GCGAGGCCTG
44586496	AGCTGTCCGC	T/G	GTCCTGGCGG
44586505	CGGTCCTGGC	G/C	GATGTGGATG
44597038	GGATTTTGTG	C/T	ATGTGGTGGG
44605999	TGGTTGAATC	C/T	AGAGTTGGCT
44698414	GGGCTTCTAT	G/T	GTTTGGGAGG
44698423	TTGTTTGGGA	G/*	GAAAAAGAGA
44698644	TCTTTTGTTC	A/G	AAACTGGTGA
44698699	CTTTGGCAGT	G/A	ACACAGTCCC
44708219	TGGTGCCGGC	GGCTTGGTACCAAGACCAACAAAAACTATGCCTCGGTGG/42*(identical 42 bases to right)	GCTTGGTACC
44708388	CTAGGACTCG	TTTTA/*****	TTTATATCTT
44708483	TGAATATCCT	C/T	AACCCTATTT
44782831	CCTTCCACCC	C/T	agttttgaga
44810434	ATTGCATAAA	T/C	GGGACATGAC
44810520	TATATACATC	T/C	TTTGAGTAGA
44834860	CCTTGTTATA	G/A	GGTGTAAATG
44834869	AGGGTGTAAA	T/G	GAGGGGAGAA
44834881	AGGGGAGAAA	A/T	AGTAACTTTT
44835487	TCTTTTAGTC	C/T	TTAAAAAATT
44835614	CTGAAAAATC	T/C	TAAGAGGCTG
44835660	CCAGGAAGAT	A/G	AGAGGAATAT
44835743	CCCACCCATT	CAGGTGTTTACTT/*************	AGGTGTTTAC
45010866	TTGTTTTCAG	C/T	CATTTTCATC
45187369	TGTGTCCACA	A/C	GGGGTCACTG
45187610	GTCCAGGCAC	C/G	GACTGCCTGA
45187620	GGACTGCCTG	A/G	CTACACGTTA
45337787	ACATGGAGCC	A/G	CTGAGCCCAT
45338141	CAAGCCTCGC	A/G	GCCACTCAGG

45339308	GGTCCCGGGA	A/G	ATAACCCACA
45716651	GCCAACTGCA	A/G	TCTGGTCCCA
45716732	GCCGACCCCT	A/T	CAGGGGTCCT
45716834	CCCTGGGAGA	C/T	GACCAGATGT
45716855	CGGCCTCTCC	C/T	AACCGTGGTC
45716856	GGCCTCTCCC	A/G	ACCGTGGTCC
45716895	ATGGCAGACC	A/C	CTCCATAGGT
45717030	ACTAGGGTCC	T/C	GGGAGAGGAT
45717115	CTGGGGTCCC	A/G	AAAGAGGAAG
45719374	ACCTGTGTCC	C/T	GGGGACAGGA
46501108	TCACCAGTTT	A/G	GATAATTCCT
46501114	GTTTGGATAA	C/T	TCCTCAGACT
46501616	CCACCGTTGT	C/G	ACAACTGATG
46952832	AACTGGCTGA	C/T	TAGGATATAT
46952945	TTTCTGATTG	C/T	GTGTGTAGGA
49120291	ATCTGTTTCA	C/T	TCATGAGGTG
49120349	GAATATTTAC	G/T	TCAGTAAATA
49120484	CCTGTTCTGT	A/G	TTATTTTCTT

Supplementary Table S5. Insertion of a SINEC_Cf within an *IGF1* intron was genotyped in 23 dogs from 13 breeds using bi-directional sequencing by standard methods. "SS" = homozygous SINEC_Cf insertion, "WW" = homozygous non-insertion. "SW" = heterozygous for insertion. The SINEC_Cf is inserted at chr15:44,228,010 (canFam1) between SNP 4 and SNP 5 (Fig. 3) and has a characteristic 12 bp duplication of the insertion site flanking it. SINEC_Cf insertion is perfectly correlated with haplotypes B and C.

Dog No.	Breed	SINEC_Cf genotype	*IGF1* SNP haplotype
1	Cav. King Charles spaniel	SS	BB
2	Chihuahua	SS	BB
3	Italian greyhound	SS	BB
4	Japanese chin	SS	BB
5	mastiff	SS	BB
6	mastiff	SS	BB
7	miniature schnauzer	SS	BB
8	pomeranian	SS	BB
9	rottweiler	SS	BB
10	shih tzu	SS	BB
11	toy fox terrier	SS	BB
12	Italian greyhound	SS	CC
13	Saint Bernard	WW	FF
14	great dane	WW	FF
15	great dane	WW	FI
16	Saint Bernard	WW	II
17	Cav. King Charles spaniel	WW	II
18	mastiff	WW	II
19	mastiff	WW	II
20	miniature schnauzer	WW	II
21	shih tzu	WW	II
22	bullmastiff	SW	BI
23	bullmastiff	SW	BI

Supplementary Table S6. Genotypes for an *IGF1* promoter CA_n microsatellite at chr15:44,283,699 - 44,283,736 (Canfam1). Alleles are named as the length of the PCR amplicon in base pairs. Table entries are counts of chromosomes from dogs within all 14 small breeds, all nine giant breeds, and the Portuguese water dog breed.

	Multiple Breeds		
Allele	Small	Giant	Portuguese water dog
203	-	1	-
207	16	214	397
209	83	85	23
211	328	12	389
213	8	24	-
215	28	54	9
217	2	-	-
219	89	-	-

References

S1. R. K. Wayne *et al.*, *J Hered* **80**, 447-54 (Nov-Dec, 1989).
S2. J. Yu *et al.*, *Nat Genet* **38**, 203-8 (Feb, 2006).
S3. Y. S. Song, Y. Wu, D. Gusfield, *Bioinformatics* **21 Suppl 1**, i413-22 (Jun, 2005).