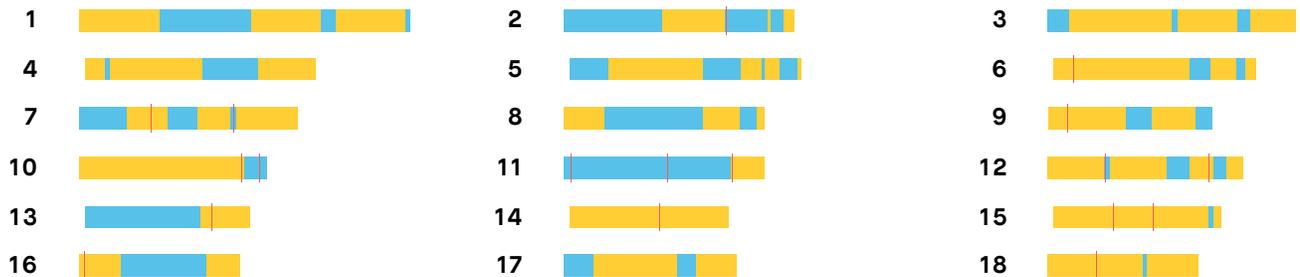




Advanced results

Inbreeding by Chromosome *BETA* ?

We analyzed the areas of inbreeding across your dog's genome. Below is a graphical representation of your dog's inbreeding, displayed chromosome by chromosome. Any inbred areas appear in blue, while outbred areas appear in yellow.



STR TRACKS: [Show](#) [Hide](#)

Traits report *BETA* ?

[Hide descriptions](#)

Coat Color

A number of genetic loci are known to affect coat color in dogs, and they all interact. In some cases, other genetic effects may also influence color and pattern.

E Locus (Mask/Grizzle/Red)

? **EE**

CHROMOSOME 5

Controls the characteristic melanistic mask seen in the German Shepherd and Pug as well as the grizzled "widow's peak" of the Afghan and Borzoi. Melanistic mask (E^m) is dominant to grizzle (E^g) which is dominant to black (E) and red (e). The E

Locus is dominant to and will mask the effects of K Locus and A Locus. Dogs that are ee will be a shade of red or cream regardless of their genotype at K and A. The shade of red, which can range from a deep copper like the Irish Setter to the near-white of some Golden Retrievers, is dependent on other genetic factors including the Intensity (I) Locus, which has yet to be genetically mapped.

Want to help us map I Locus? If you haven't already, complete your ee pup's Embark profile with a photo! Remember, a picture is worth a thousand words!

Citations: Schmutz et al 2003 (<http://www.ncbi.nlm.nih.gov/pubmed/12692165>) , Dreger and Schmutz 2010 (<http://www.ncbi.nlm.nih.gov/pubmed/20525767>) ,

More information: <http://www.doggenetics.co.uk/masks.html>
(<http://www.doggenetics.co.uk/masks.html>)

K Locus (Dominant Black)

K^Bk^Y

CHROMOSOME 16

Causes a dominant black coat. Dogs with a dominant K^B allele have black coats regardless of their genotype at the A locus; the coat color of dogs homozygous for the recessive k^Y allele are controlled by A locus. Alleles: K^B > k^Y

Citations: Candille et al 2007 (<http://www.ncbi.nlm.nih.gov/pubmed/17947548>)

More information: <http://www.doggenetics.co.uk/black.htm>
(<http://www.doggenetics.co.uk/black.htm>)

A Locus (Agouti)

? aa

CHROMOSOME 24

Determines whether hair pigment is produced in a banded red and black pattern or solid black. Fawn or sable (a^Y) is dominant to wolf sable (a^W) which is dominant to black-and-tan (a^t), which is in turn dominant to recessive black (a).

Citations: Berryere et al 2005 (<http://www.ncbi.nlm.nih.gov/pubmed/15965787>) , Dreger and Schmutz 2011 (<http://www.ncbi.nlm.nih.gov/pubmed/21846741>) ,

More information: <http://www.doggenetics.co.uk/tan.html>
(<http://www.doggenetics.co.uk/tan.html>)

D Locus (Dilute)

DD

CHROMOSOME 25

Lightens a black coat to blue and a red coat to buff. A dilute phenotype requires two copies of the recessive d allele.

Citations: Drogemuller et al 2007 (<http://www.ncbi.nlm.nih.gov/pubmed/17519392>)

More information: <http://www.doggenetics.co.uk/dilutes.html>
(<http://www.doggenetics.co.uk/dilutes.html>)

B Locus (Brown/Chocolate/Liver)

BB

CHROMOSOME 11

Lightens a black coat to brown, chocolate or liver. The brown phenotype requires two copies of the recessive b allele. Red or cream dogs that carry two b alleles remain red or cream but have brown noses and footpads.

Citations: Schmutz et al 2002 (<http://www.ncbi.nlm.nih.gov/pubmed/12140685>)

More information: <http://www.doggenetics.co.uk/liver.html>
(<http://www.doggenetics.co.uk/liver.html>)

Other Coat Traits

Furnishings, shedding and curls are all genetic! And they all interact, too. In fact, the combination of these genetic loci explain the coat phenotypes of 90% of AKC registered dog breeds.

For more information on the genetics of coat types you can refer to
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2897713/figure/F3/>
(<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2897713/figure/F3/>)

Some other Embark dogs with this Coat Traits genotype:

Lila
(/dog/lila)

Indiana
(/dog/indiana)

Gracie
(/dog/gracie13)

Buzz Pawldrin
(/dog/buzzpawldrin)





Furnishings / Improper Coat (RSP02)

II

CHROMOSOME 13

Confers the distinguished moustache, beard, and eyebrows characteristic of breeds like the Schnauzer, Scottish Terrier, and Wire Haired Dachshund; only one copy of the dominant F allele is required for furnishings. The FI genotype is furnished but is an improper coat carrier. A dog with two I alleles has improper coat. The mutation is a 167-bp insertion which we measure indirectly using linked markers highly correlated with the insertion.

Citations: Cadieu et al 2010 (<http://www.ncbi.nlm.nih.gov/pubmed/19713490>)

Long Haircoat (FGF5)

TT

CHROMOSOME 32

Confers a long, silky haircoat as observed in the Yorkshire Terrier and the Long Haired Whippet. The "T" allele is associated with longer hair.

Citations: Housley & Venta 2006 (<http://www.ncbi.nlm.nih.gov/pubmed/16879338>), Cadieu et al 2010 (<https://www.ncbi.nlm.nih.gov/pubmed/19713490>)

Shedding (MC5R)

CT

CHROMOSOME 1

Affects shedding propensity in non-wire-haired dogs. Dogs with the ancestral C allele, like many Labradors and German Shepherd Dogs, are heavy or seasonal shedders, while those with one or more T allele, including many Boxers, Shih Tzus and Chihuahuas, tend to be low shedders. Dogs with furnished/wire-haired coats tend to be low shedders regardless of their MC5R genotype.

Citations: Hayward et al 2016

(<http://www.nature.com/ncomms/2016/160122/ncomms10460/full/ncomms10460.html>)

Curly Coat (KRT71)

CC

CHROMOSOME 27

Causes the curly coat characteristic of Poodles and Bichons Frises. Dogs need at least one copy of the "T" allele to have a curly coat.

Citations: Cadieu et al 2010 (<http://www.ncbi.nlm.nih.gov/pubmed/19713490>)

Other Body Features

Brachycephaly (BMP3)

CC

CHROMOSOME 32

Affects skull size and shape. Many brachycephalic or "smushed face" breeds such as the English Bulldog, Pug, and Pekingese have two copies of the derived A allele. Mesocephalic (Staffordshire Terrier, Labrador) and dolichocephalic (Whippet, Collie) dogs have one, or more commonly two, copies of the ancestral C allele. At least five different genes affect snout length in dogs, with BMP3 being the only one with a known causal mutation. For example, the skull shape of some breeds, including the dolichocephalic Scottish Terrier or the brachycephalic Japanese Chin, appear to be caused by other genes.

Citations: Schoenbeck et al 2012

(<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3410846/>)

Natural Bobtail (T)

CC

CHROMOSOME 1

Whereas most dogs have two C alleles and a long tail, dogs with one G allele are likely to have a bobtail, which is an unusually short or absent tail. This mutation causes natural bobtail in many breeds including the Pembroke Welsh Corgi, the Australian Shepherd, and the Brittany Spaniel. Dogs with GG genotypes have not been observed, suggesting that the GG genotype results in embryonic lethality.

Please note that this mutation does not explain every natural bobtail! While certain lineages of Boston Terrier, English Bulldog, Rottweiler, Miniature Schnauzer, Cavalier King Charles Spaniel, and Parson Russell Terrier, and Dobermans are born with a natural bobtail, these breeds do not have this mutation. This suggests that other unknown genetic mutations can also lead to a natural bobtail. If your dog does **not** have a CG genotype but was born with a bobtail, please email us at howdy@embarkvet.com!

Citations: Haworth et al 2001 (<https://www.ncbi.nlm.nih.gov/pubmed/11252170>) , Hytonen et al 2009 (<https://www.ncbi.nlm.nih.gov/pubmed/18854372>)

Hind Dewclaws (LMBR1)

TT

CHROMOSOME 16

Common in certain breeds, hind dewclaws are extra, nonfunctional digits located midway between your dog's paw and hock. Dogs with at least one copy of the T allele have about a 50% of chance of having hind dewclaws.

Citations: Park et al 2008
(<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2516088/>)

Body Size

Body size is a complex trait that is affected by both genetic and environmental variation. Our genetic analysis includes genes that, together, explain over 80% of the variation in dog body size. It does not account for runting or stunting; nor does it account for the interactions between various genes both known and unknown.

Some other Embark dogs with this Body Size genotype:

Fionna

(/dog/fionna)



(/dog/fionna)

Woody

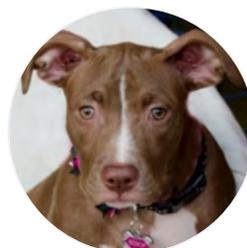
(/dog/woody3)



(/dog/woody3)

Beebop

(/dog/beebop)



(/dog/beebop)

Mocha

(/dog/mocha5)



(/dog/mocha5)

IGF1

II

CHROMOSOME 15

The "I" allele is associated with smaller size.

Citations: Sutter et al 2007

(<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2789551/>)

IGF1R

GG

CHROMOSOME 3

The "A" allele is associated with smaller size.

Citations: Hoopes et al 2012

(<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3511640/>)

STC2

TA

CHROMOSOME 4

The "A" allele is associated with smaller size.

Citations: Rimbault et al 2013

(<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3847769/>)

GHR (E195K)

GG

CHROMOSOME 4

The "A" allele is associated with smaller size.

Citations: Rimbault et al 2013

(<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3847769/>)

GHR (P177L)

CC

CHROMOSOME 4

The "T" allele is associated with smaller size.

Citations: Rimbault et al 2013

(<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3847769/>)

Performance

Altitude Adaptation (EPAS1)

GG

CHROMOSOME 10

Confers hypoxia tolerance. Dogs with at least one A allele are more tolerant of high altitude environments. This mutation was originally identified in breeds from high altitude areas such as the Tibetan Mastiff.

Citations: Gou et al 2014

(<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4120084/>)

Genetic Diversity

Inbreeding is a measure of how closely related your dog's parents were. The higher the inbreeding coefficient, the more closely related the parents. In general, higher inbreeding coefficients are associated with increased incidence of genetically inherited conditions.

Diversity of the maternal and paternal haplotypes in the Major Histocompatibility Complex (MHC) region of the genome has been found in some studies to be associated with the incidence of certain autoimmune diseases. Dogs that have less diversity in the MHC region haplotypes—i.e. the Dog Leukocyte Antigen (DLA) inherited from the mother is similar to the DLA inherited from the father—are considered less immunologically diverse. A High Diversity result means the dog has two highly dissimilar haplotypes. A Low Diversity result means the dog has two similar but not identical haplotypes. A No Diversity result means the dog has inherited identical haplotypes from both parents.

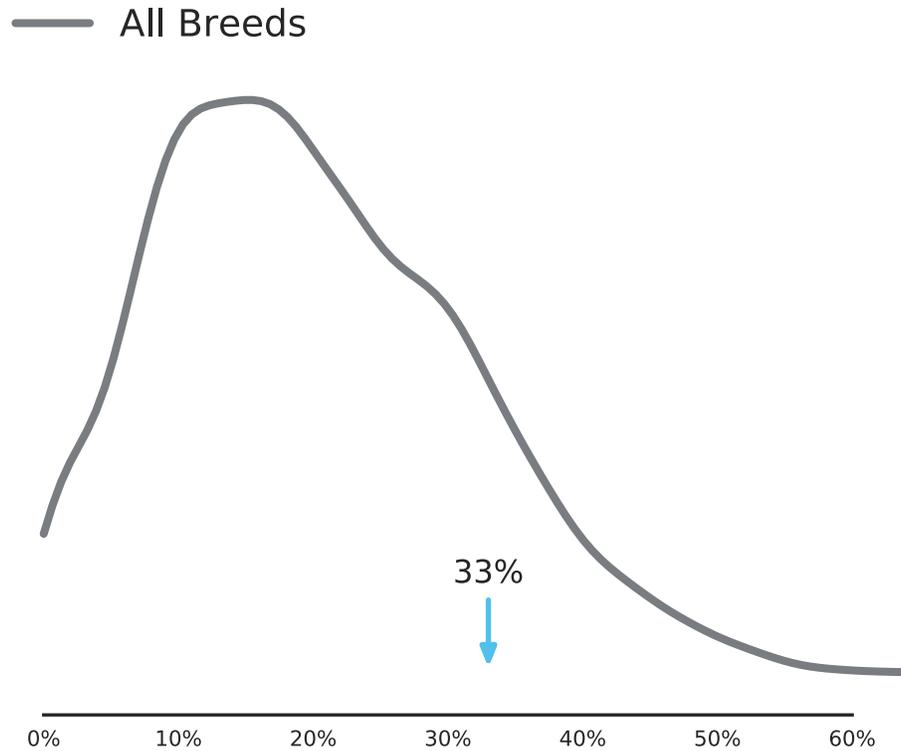
Inbreeding Coefficient

33%

Measures the proportion of the genome where the genes on the mother's side are identical by descent to those on the father's side.

This chart shows how common various inbreeding levels are in different groups of dogs. At the left are dogs with 0% inbreeding, i.e. completely outbred. As you look

right, the amount of inbreeding increases. The height of the line shows how many dogs have that amount of inbreeding. The arrow shows where Sante Yfke fan Bûten Út fits into this picture.

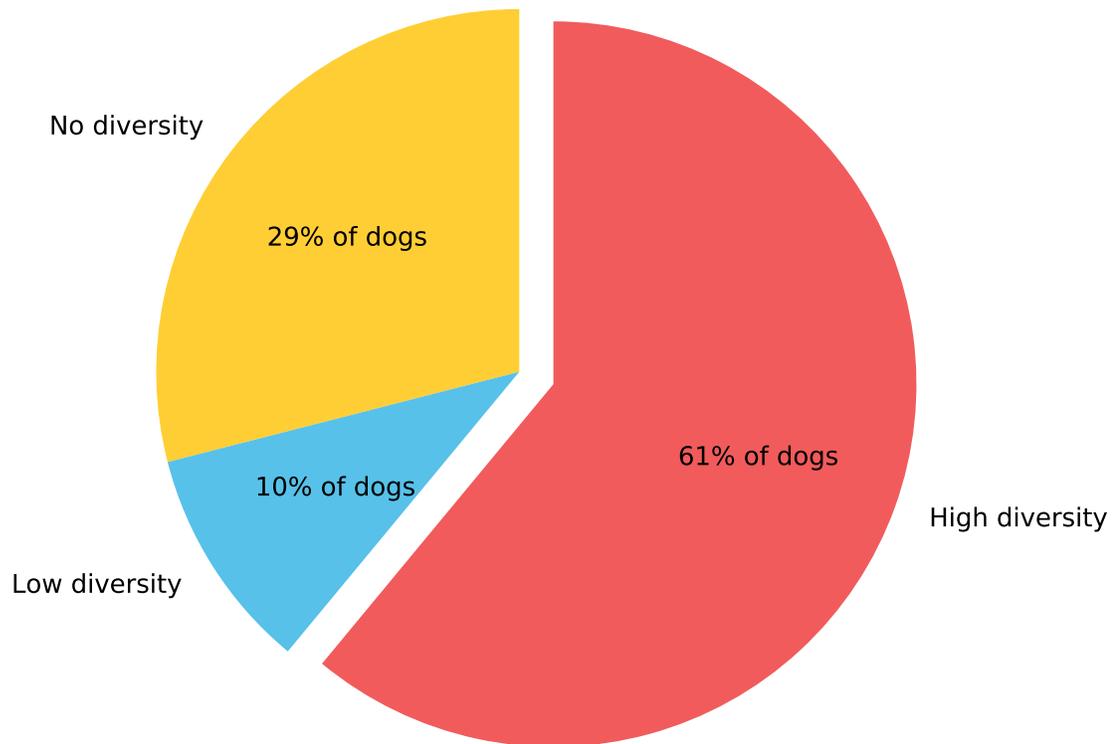


MHC Class II - DLA DRB1 High Diversity

CHROMOSOME 12

A Dog Leukocyte Antigen (DLA) gene, DRB1 encodes a major histocompatibility complex (MHC) protein involved in the immune response. Some studies have shown associations between certain DRB1 haplotypes and autoimmune diseases such as Cushing's disease, but these findings have yet to be scientifically validated.

How common is this amount of diversity in purebreds?



Citations: Angles et al 2005 (<https://www.ncbi.nlm.nih.gov/pubmed/16101828>)

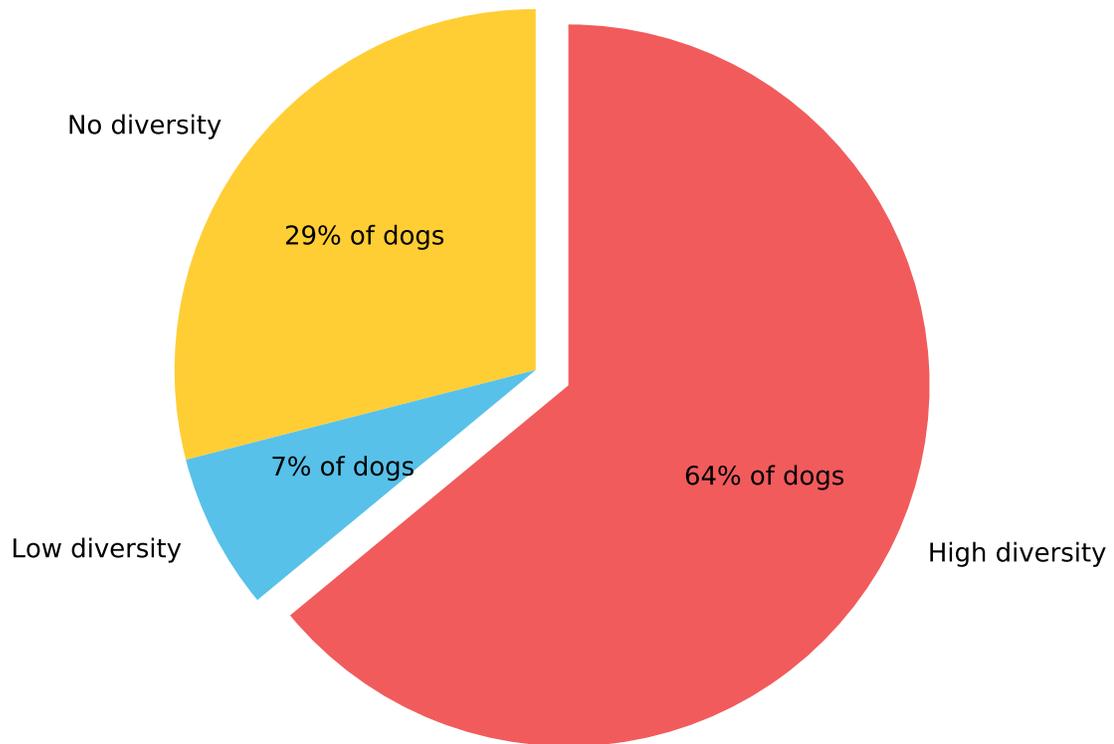
MHC Class II - DLA DQA1 and DQB1

High Diversity

CHROMOSOME 12

DQA1 and DQB1 are two tightly linked DLA genes that code for MHC proteins involved in the immune response. A number of studies have shown correlations of DQA-DQB1 haplotypes and certain autoimmune diseases; however, these have not yet been scientifically validated.

How common is this amount of diversity in purebreds?



Citations: Angles et al 2005 (<https://www.ncbi.nlm.nih.gov/pubmed/16101829>)

Raw Data *BETA*

Click here (</members/results/raw-data>) to download the raw genetic data and results for Sante Yfke fan Bûten Út.

From time to time, Embark updates our genotyping technology to add additional genetic markers. The technology in use at the time of genotyping may impact which genetic markers are included in your raw data or the results we can provide.

Technology used to genotype Sante Yfke fan Bûten Út: Generation 2 microarray