

ГЕНОМИКА ПСОВ(ЫХ)



Новосибирск, 2014

Подотряд Псообразные - *Caniformia*
Семейство Псовые - *Canidae* ,
Род Волки - *Lupus*



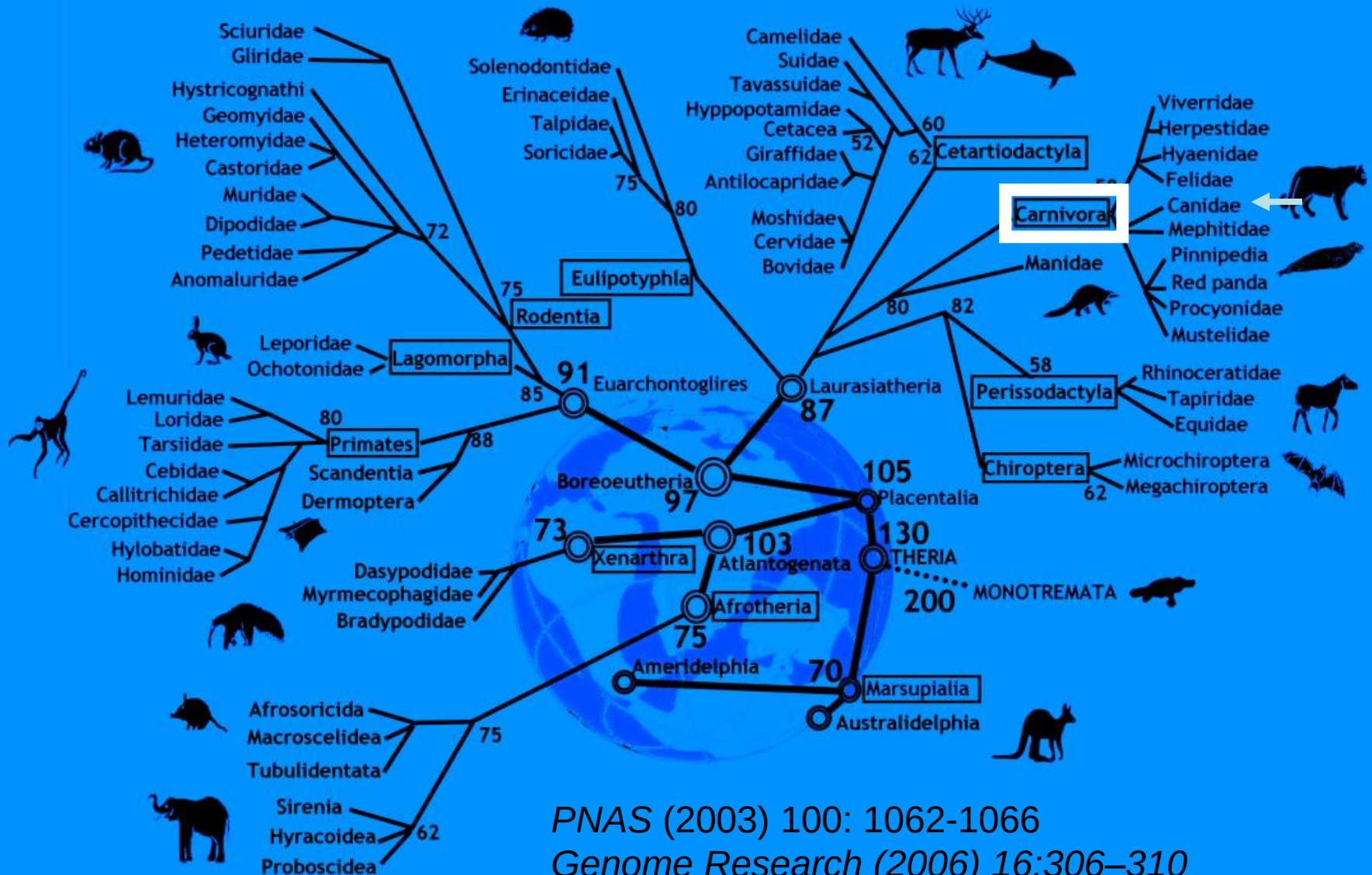
Вид Серый Волк – *Canis lupus*



Соба́ка домашняя
- *Canis lupus familiaris*

MAMMALIA

5 000-5 500 видов
(Около 20 000 видов,
включая вымершие)



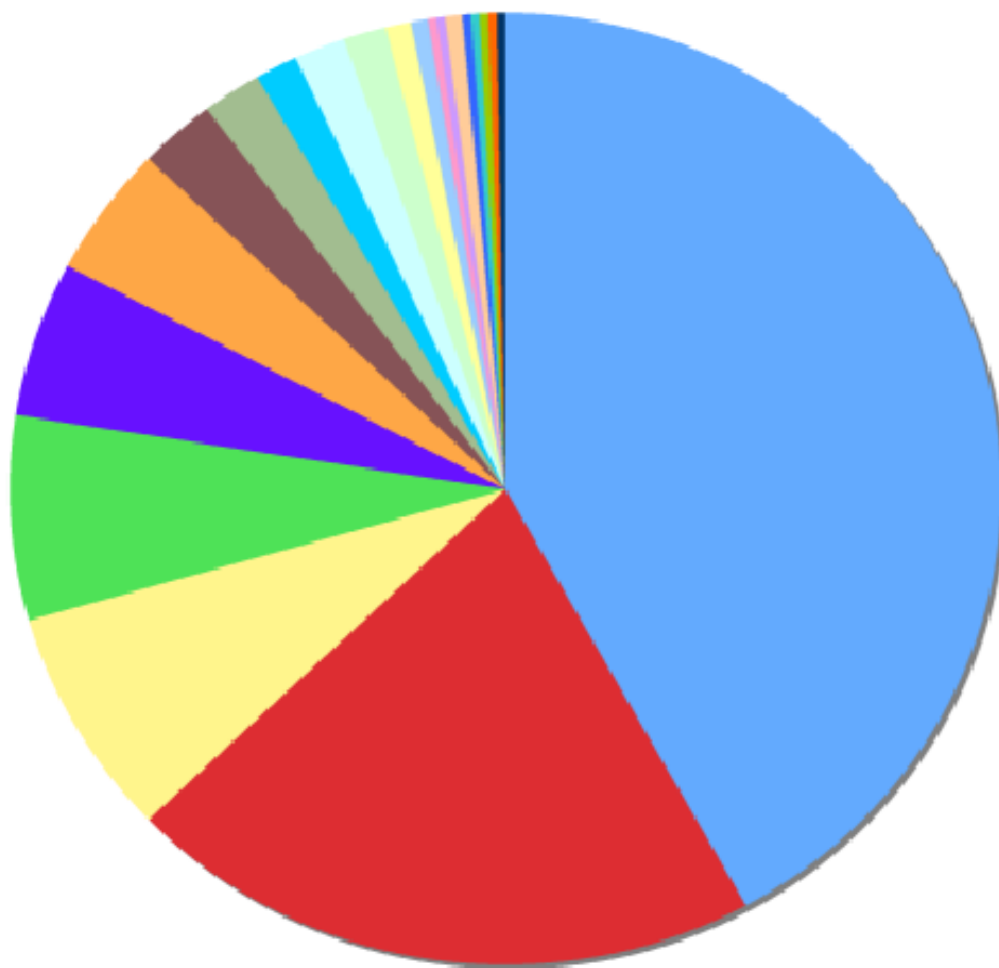
PNAS (2003) 100: 1062-1066

Genome Research (2006) 16:306-310

Nature Rev. Genetics, (2007)8: 950-962

Distribution of Extant and Recently Extinct Mammal Species across Orders

(based on Wilson and Reeder, 2005: 5,416 spp. total)



Rodentia	Грызуны Mammal Species of the World (2005) 2277 видов
Chiroptera	Рукокрылые
Soricomorpha	Землеройкообразные
Primates	Приматы (более 400 видов)
Carnivora	<u>Хищные 11 семейств около 270 видов</u>
Artiodactyla	Парнокопытные ок. 220 видов
Diprotodontia	Двурезцовые сумчатые ок.120 видов
Lagomorpha	Зайцеобразные около
Didelphimorphia	Сумчатые
Cetacea	Китообразные (около 30 видов)
Dasyuromorphia	Хищные сумчатые
Afrosoricida	Афросорициды
Erinaceomorpha	Ежеобразные (23 вида)
Cingulata	Броненосцы
Paramylemorpha	Бандикуты (Сумчатые барсуки)
Scandentia	Тупайи (20 видов)
Perissodactyla	Непарнокопытные (17 видов)
Macroscelidea	Прыгунчиковые
Pilosa	Неполнозубые
Pholidota	Панголины (Ящеры, 8 видов)
Paucituberculata	Ценолесты (6 видов)
Monotremata	Однопроходные (Яйцекладущие)
Sirenia	Сирены (5 видов)
Hyracoidea	Домановые (4 вида)
Proboscidea	Хоботные
Dermoptera	Шерстокрылы (Кагуаны, 2 вида)
Notoryctemorphia	Сумчатые кроты (2 вида)
Microbiotheria	Соневидные опоссумы
Tubulidentata	Трубказубые

Canids have a much longer rostrum



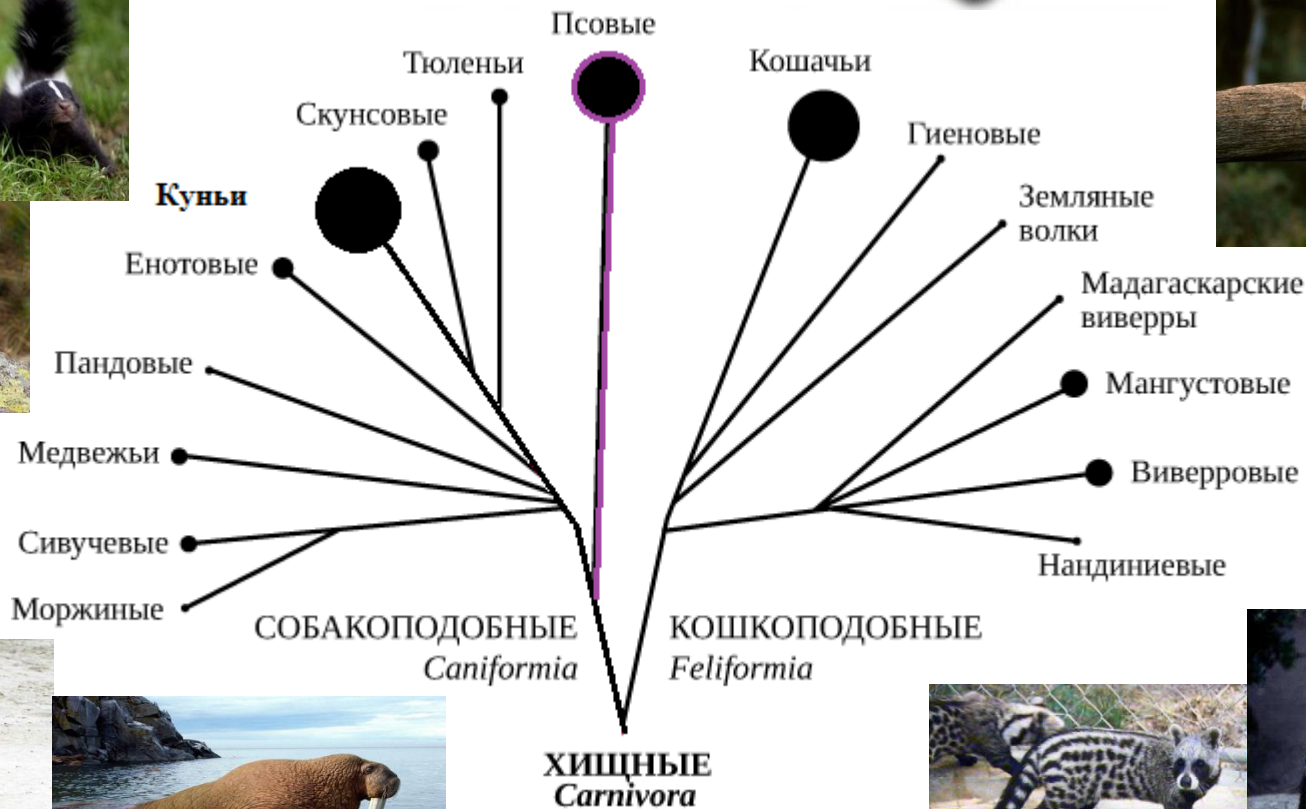
Canids



Carnivore Skulls



Felids



Род Малые лисицы
(*Atelocynus*)

Род Серые лисицы (*Urocyon*)

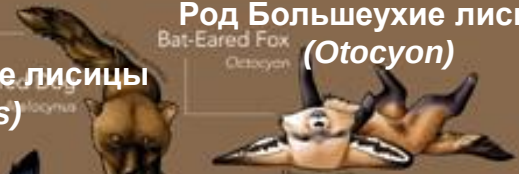


Род Красные волки (*Cuon*)



Род Лисицы (*Vulpes*)

Род Большеухие лисицы
(*Otocyon*)



Род Майконги (*Cerdosyon*)



Род Кустарниковые собаки
(*Speothos*)



Род Гиеновидные собаки
(*Lycaon*)



Род Гривистые волки
(*Chrysocyon*)



Род Волки (*Canis*)



Род Енотовидные собаки
(*Nyctereutes*)



Род Южноамериканские лисицы
(*Lycalopex*)

FAMILY CANIDAE

Coyote, Fox, Jackal, Wild Dog, and Wolf Species of the World

Род Волки (*Canis*)



- Койот (*Canis latrans*)

- Шакал (*Canis aureus*)

- Волк (*Canis lupus*)

Классификация собак в Европе и России (2013 год, МКФ, 339 пород собак):

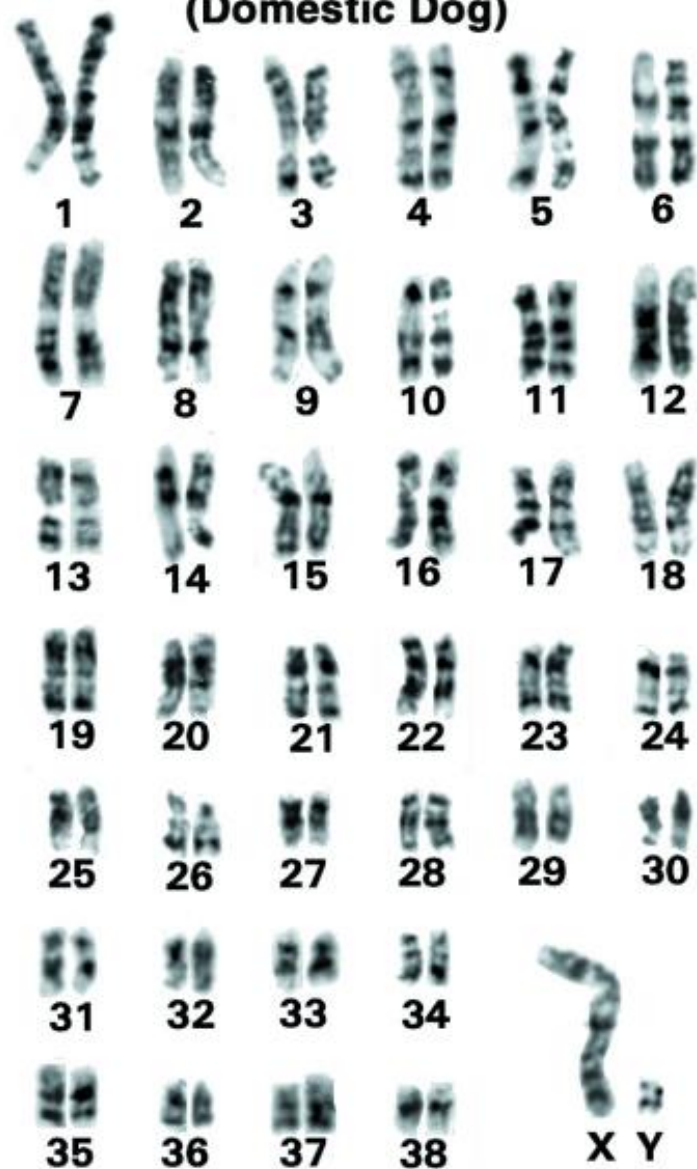


1. Пастушьи
2. Сторожевые и охранные собаки;
3. Терьеры;
4. Таксы;



1. Лайки, шпицы и другие примитивные породы;
2. Гончие и собаки, работающие по кровавому следу;
3. Собаки, работающие со стойкой (легавые);
4. Собаки, поднимающие дичь, апортирующие её и работающие на воде (спаниели и ретриверы)
5. Комнатно-декоративные собаки и собаки-компаньоны;
6. Борзые;

Canis familiaris (Domestic Dog)



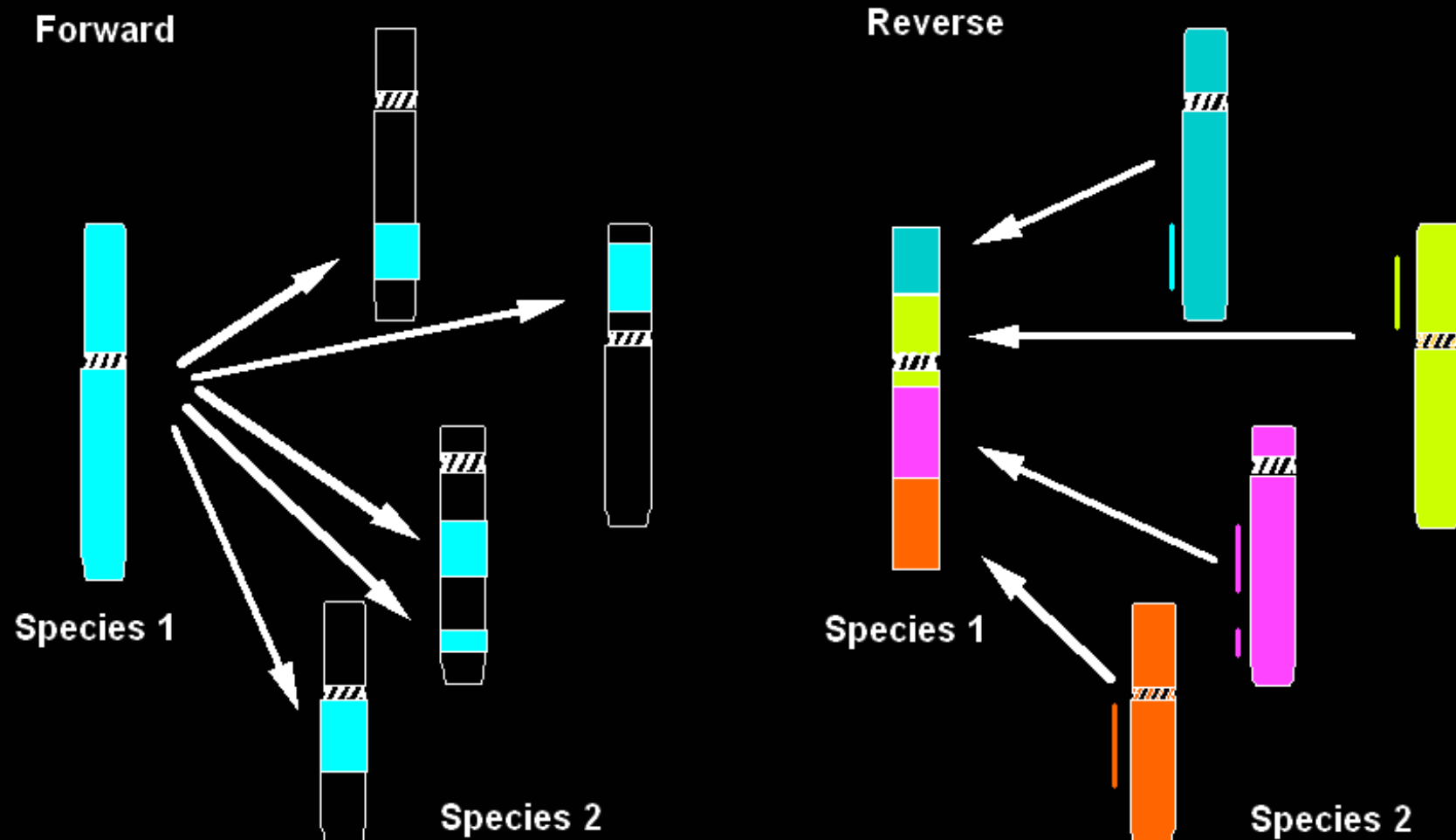
2n=78

A. Graphodatsky, V. Beklemisheva and F. Yang (unpublished)

Contributed by A. Graphodatsky



Reciprocal Chromosome Painting



Reciprocal chromosome painting allows the identification of segment-to-segment homologies of two species.

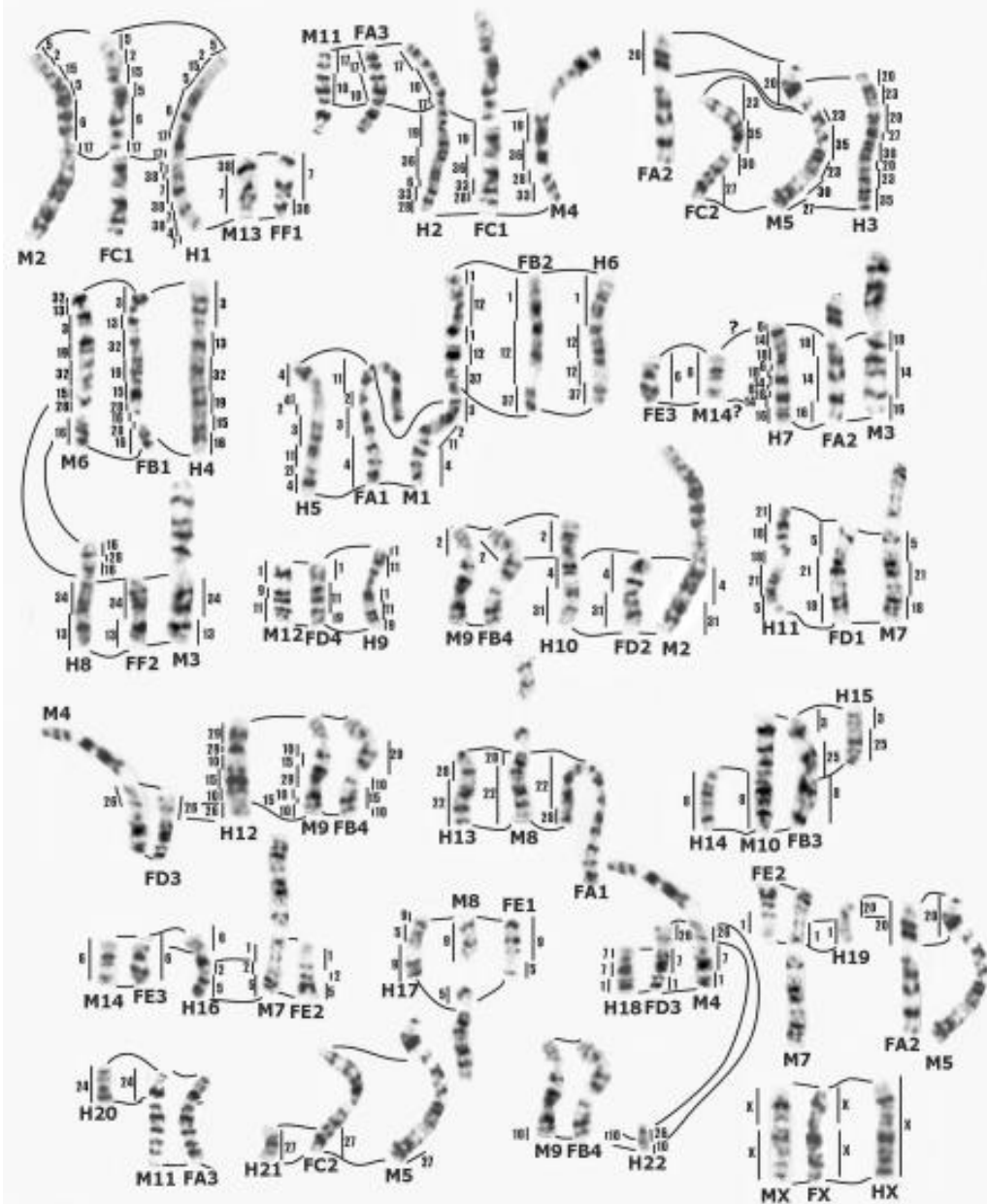
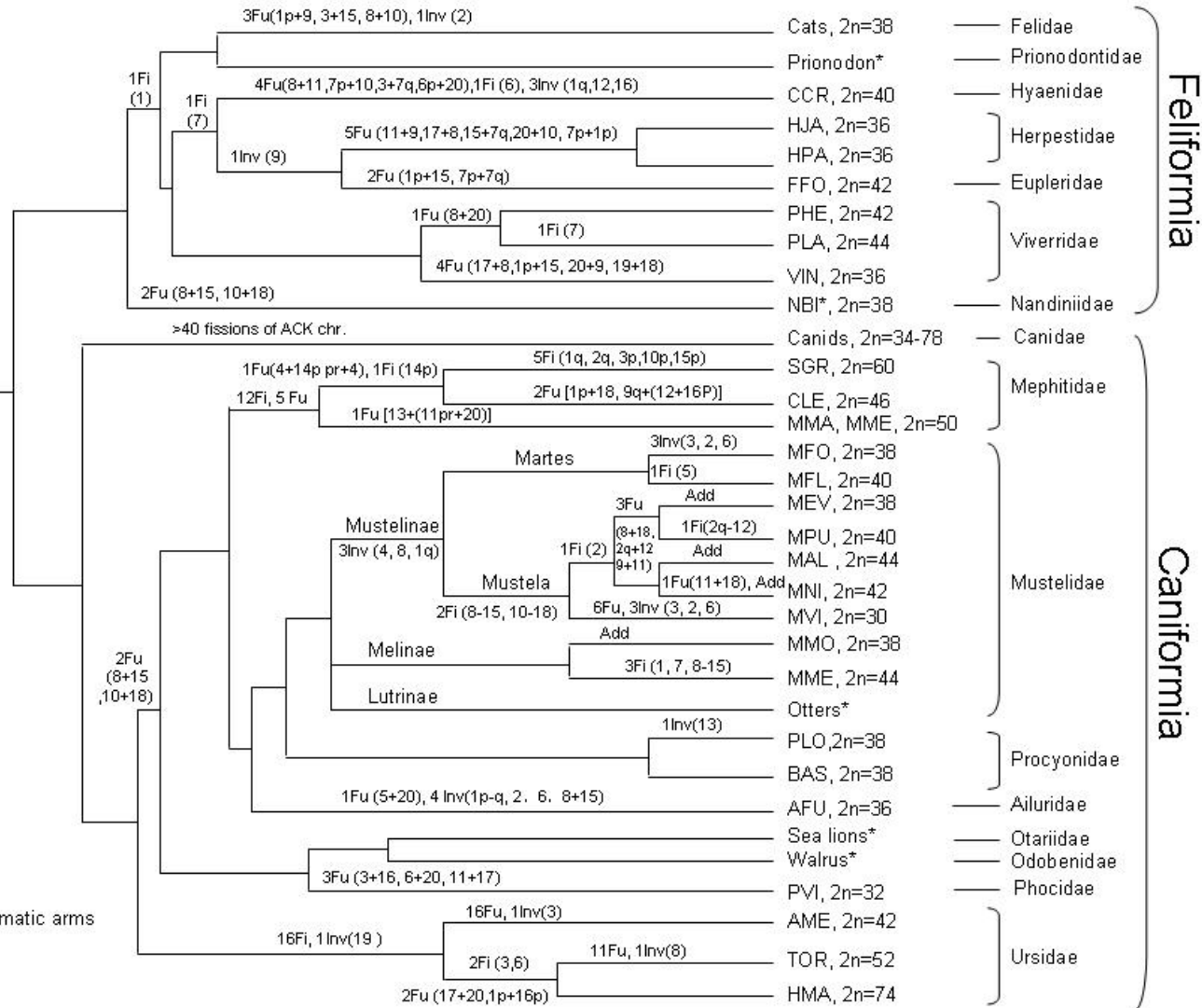


Figure 7

**Ancestral
Carnivora
Karyotype
ACK, 2n=42**

1(A2p+C2), 2
(B1), 3(A1q),
4(B2), 5(B3),
6(B4), 7(A3),
8(C1q), 9(A2q),
10(C1p), 11(D2),
12(D1), 13(D3),
14(D4), 15(A1p),
16(E1), 17(F1),
18(F2), 19(E2),
20(E3), X

Fi, fission
Fu, fussion
Inv, inversion
Add, additional heterochromatic arms

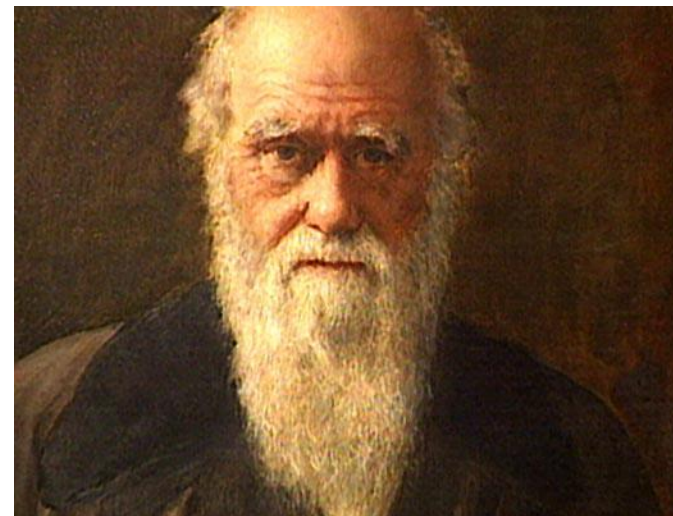


Nie et al, Hidden intrachromosomal rearrangements in carnivores revealed by dog chromosome-specific probes. **Heredity**, 2011



Кóнрад Захариас Лóренц

лауреат Нобелевской премии по физиологии и медицине 1973, совместно с Карлом фон Фришем и Николасом Тинбергеном).

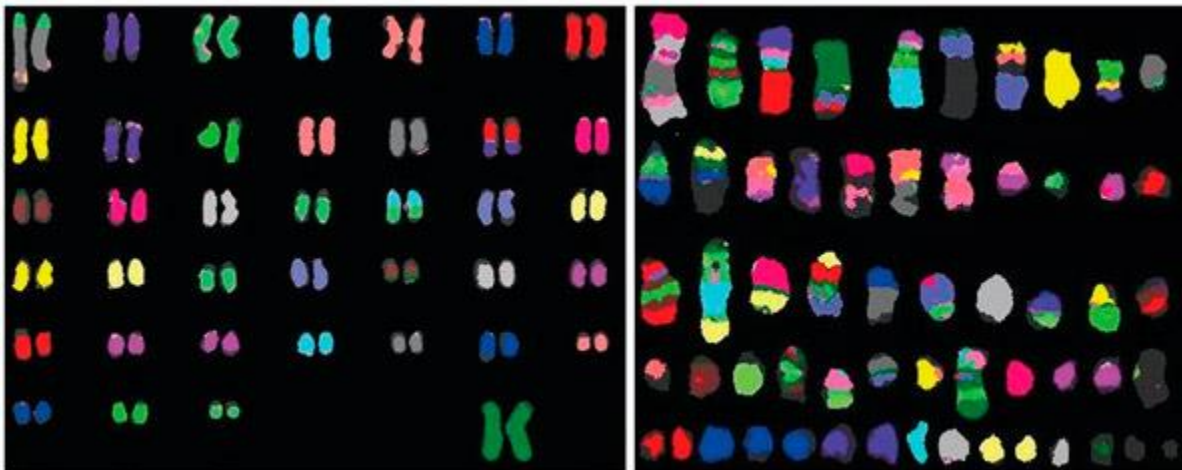


Чарлз Рóберт Дáрвин (12 февраля 1809 — 19 апреля 1882) — английский натуралист и путешественника, автор «Происхождение видов»

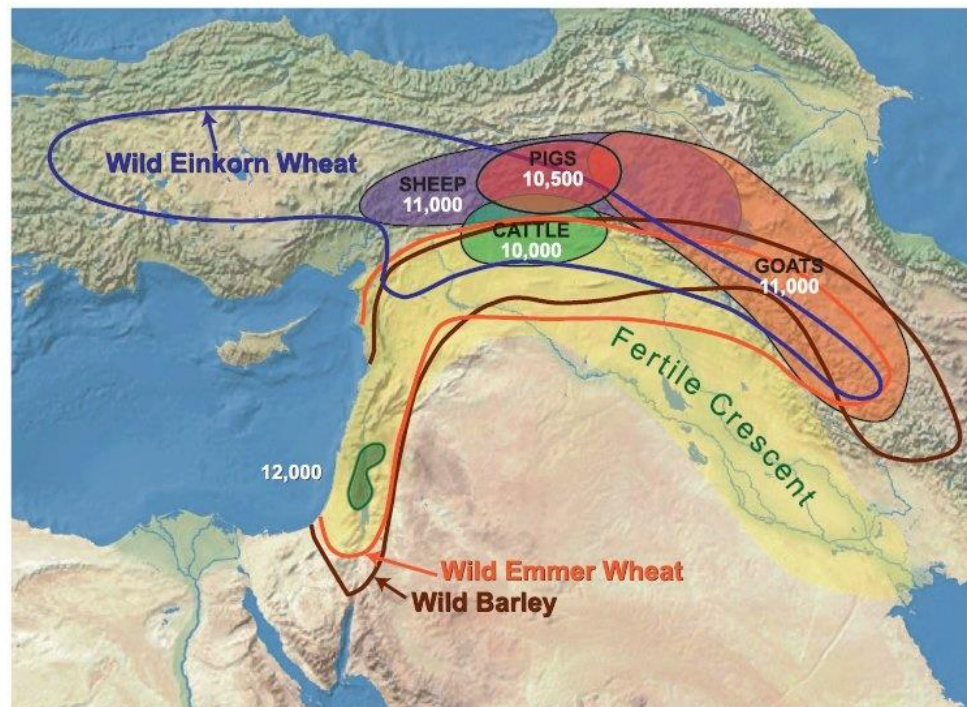
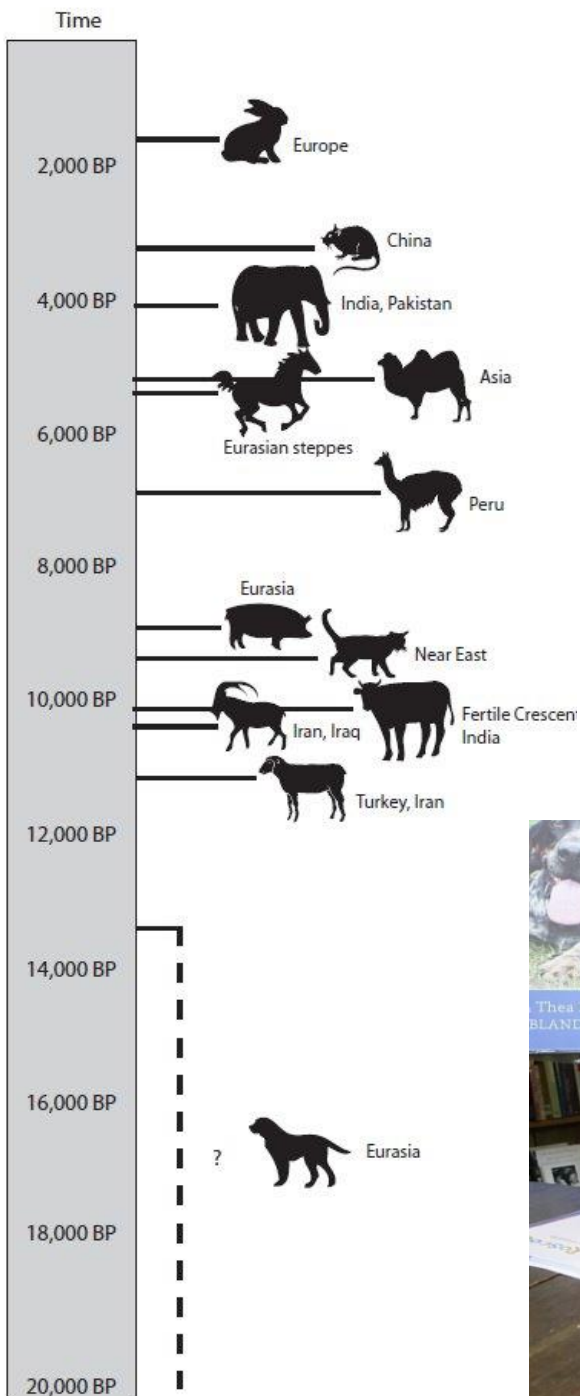
Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage

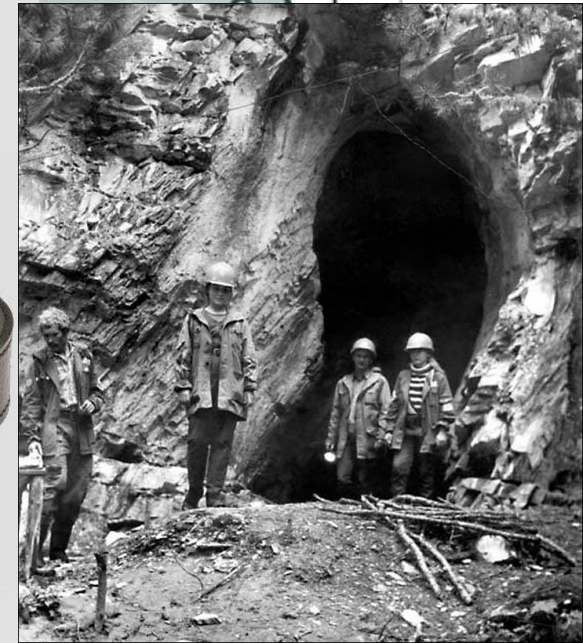
Elizabeth P. Murchison,^{1,2,*†} David C. Wedge,^{1*} Ludmil B. Alexandrov,¹ Beiyuan Fu,¹ Inigo Martincorena,¹ Zemin Ning,¹ Jose M. C. Tubio,¹ Emma I. Werner,¹ Jan Allen,³ Andriago Barboza De Nardi,⁴ Edward M. Donelan,³ Gabriele Marino,⁵ Ariberto Fassati,⁶ Peter J. Campbell,¹ Fengtang Yang,¹ Austin Burt,⁷ Robin A. Weiss,⁶ Michael R. Stratton^{1†}

Canine transmissible venereal tumor (CTVT) is the oldest known somatic cell lineage. It is a transmissible cancer that propagates naturally in dogs. We sequenced the genomes of two CTVT tumors and found that CTVT has acquired 1.9 million somatic substitution mutations and bears evidence of exposure to ultraviolet light. CTVT is remarkably stable and lacks subclonal heterogeneity despite thousands of rearrangements, copy-number changes, and retrotransposon insertions. More than 10,000 genes carry nonsynonymous variants, and 646 genes have been lost. CTVT first arose in a dog with low genomic heterozygosity that may have lived about 11,000 years ago. The cancer spawned by this individual dispersed across continents about 500 years ago.



Метафазные хромосомы нормальной собаки (слева) и ТВС (справа): определение кариотипа методом флуоресцентной гибридизации. Хорошо видна массовая реорганизация хромосом ТВС по сравнению с собачьими, хотя остается много аналогичных участков. Рисунок из обсуждаемой статьи в Science





Ancient DNA Analysis Affirms the Canid from Altai as a Primitive Dog

Anna S. Druzhkova^{1,3}, Olaf Thalmann^{2,3}, Vladimir A. Trifonov^{1*}, Jennifer A. Leonard³, Nadezhda V. Vorobieva¹, Nikolai D. Ovodov⁴, Alexander S. Graphodatsky¹, Robert K. Wayne⁵

1 Department of Genomic Diversity and Evolution, Institute of Molecular and Cellular Biology, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia, **2** Division of Genetics and Physiology, Department of Biology, University of Turku, Turku, Finland, **3** Conservation and Evolutionary Genetics Group, Estación Biológica de Doñana (Consejo Superior de Investigaciones Científicas), Seville, Spain, **4** Institute of Archaeology and Ethnography, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia, **5** Department of Ecology and Evolutionary Biology, University of California, Los Angeles, California, United States of America

Первобытная Собака
Была приручена человеком
34 тыс. лет назад



...remains controversial, with genetic data indicating a separation between modern dogs and wolves. However, only a few dog-like fossils are found prior to the Last Glacial Maximum, and it is unclear if dog domestication predates the beginning of agriculture about 10,000 years ago. In order to establish the relationship of one of the oldest dogs, we have isolated ancient DNA from a 34,000-year-old Pleistocene dog from Altai and analysed 413 nucleotides of the mitochondrial genome. The unique haplotype of the Altai dog is more closely related to modern dogs than to contemporary wolves. Further genetic analyses of ancient canids are required to clarify the relationship between modern dogs and wolves.

Trifonov VA, Leonard JA, Vorobieva NV, et al. (2013) Ancient DNA Analysis Affirms the Canid from Altai as a Primitive Dog. *PLOS ONE* 8(11): e7754. doi:10.1371/journal.pone.0057754



Г Е Н Е Т И К А
СОБАКИ

DNA extraction

library preparation

WGA amplification

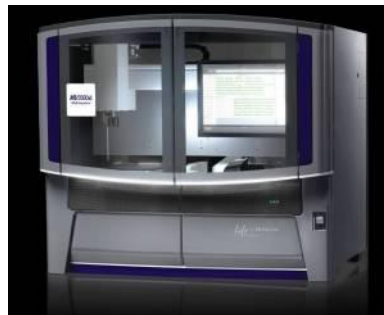
PCR amplification

gel extraction

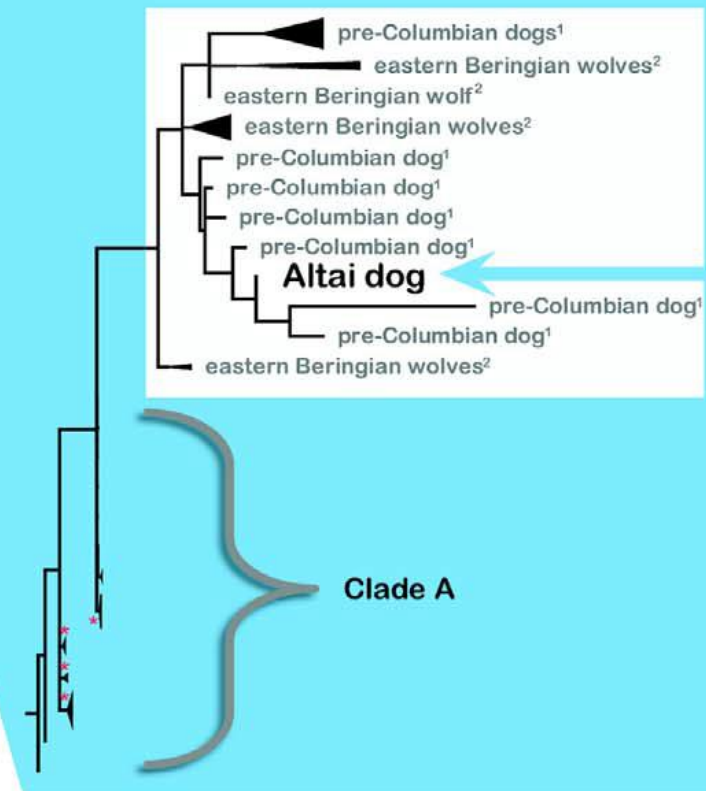
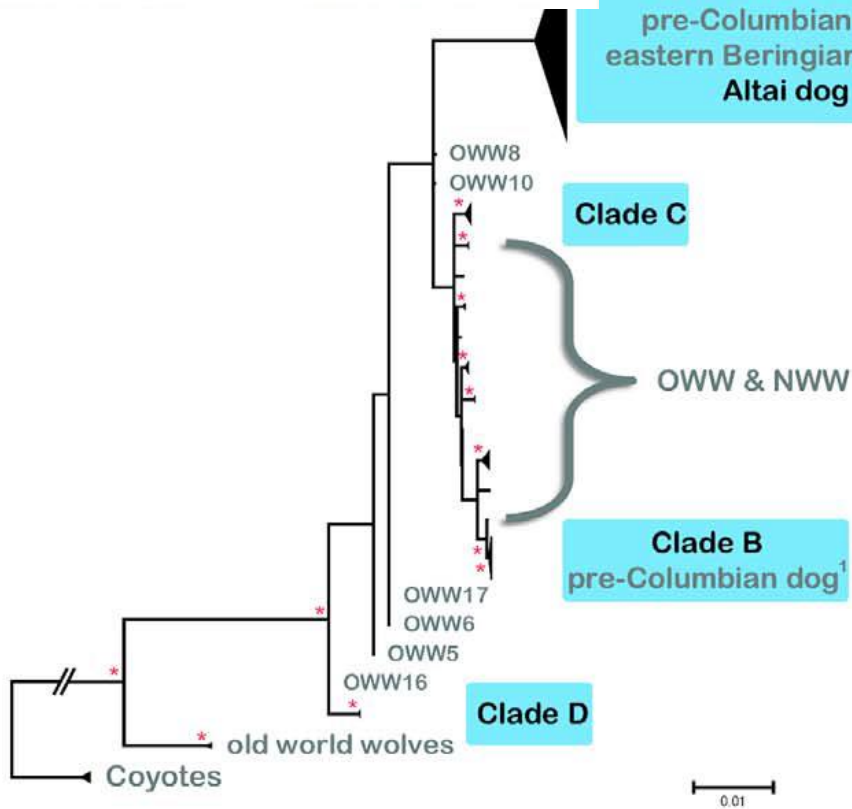
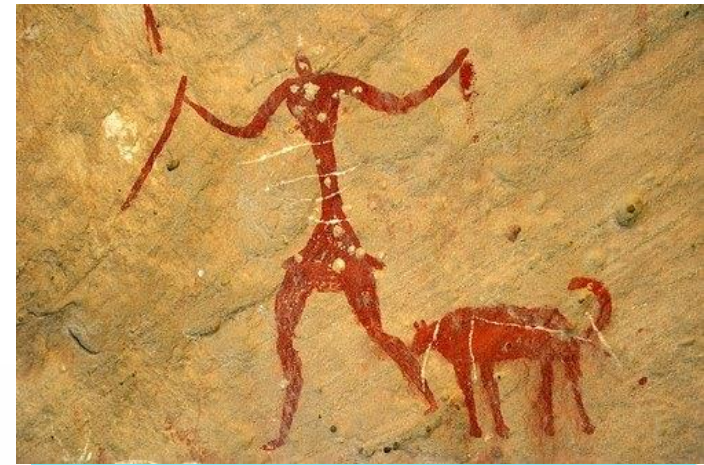
cloning

sequencing on the MiSeq & SOLID platform

Sengler sequencing



DATA ANALYSIS





AAAS

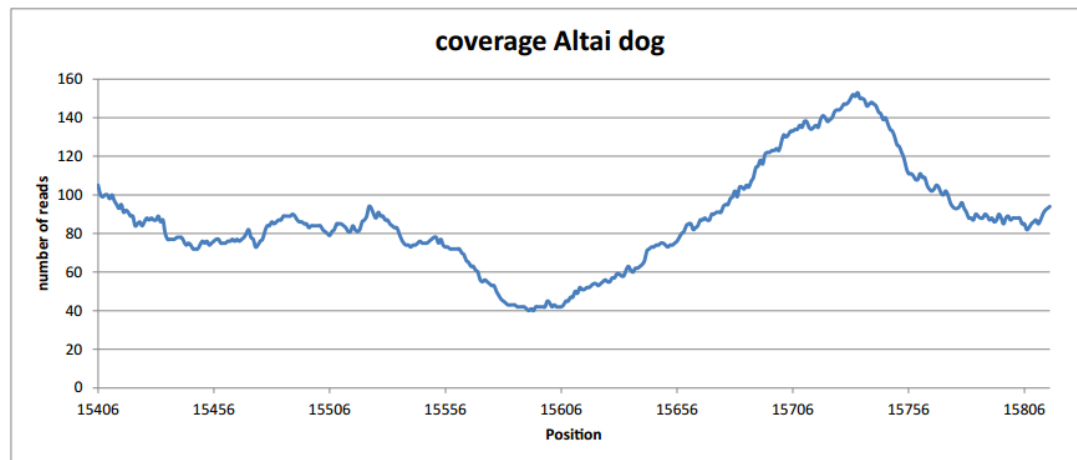
monitors, such as
effective ther-
apies. GS-1101
tested in phase
ment of chronic
inical trials.gov).
S patients with
be considered

Complete Mitochondrial Genomes of Ancient Canids Suggest a European Origin of Domestic Dogs

O. Thalmann,^{1*} B. Shapiro,² P. Cui,³ V. J. Schuenemann,⁴ S. K. Sawyer,³ D. L. Greenfield,⁵ M. B. Germonpré,⁶ M. V. Sablin,⁷ F. López-Giráldez,⁸ X. Domingo-Roura,^{9†} H. Napierala,¹⁰ H-P. Uerpmann,⁴ D. M. Loponte,¹¹ A. A. Acosta,¹¹ L. Giemsch,^{12,13} R. W. Schmitz,¹² B. Worthington,¹⁴ J. E. Buikstra,¹⁵ A. Druzhkova,¹⁶ A. S. Graphodatsky,¹⁶ N. D. Ovodov,¹⁷ N. Wahlberg,¹ A. H. Freedman,⁵ R. M. Schweizer,⁵ K.-P. Koepfli,¹⁸ J. A. Leonard,¹⁹ M. Meyer,³ J. Krause,⁴ S. Pääbo,³ R. E. Green,²⁰ R. K. Wayne^{5*}

The geographic and temporal origins of the domestic dog remain controversial, as genetic data suggest a domestication process in East Asia beginning 15,000 years ago, whereas the oldest doglike fossils are found in Europe and Siberia and date to >30,000 years ago. We analyzed the mitochondrial genomes of 18 prehistoric canids from Eurasia and the New World, along with a comprehensive panel of modern dogs and wolves. The mitochondrial genomes of all modern dogs are phylogenetically most closely related to either ancient or modern canids of Europe. Molecular dating suggests an onset of domestication there 18,800 to 32,100 years ago. These findings imply that domestic dogs are the culmination of a process that initiated with European hunter-gatherers and the canids with whom they interacted.

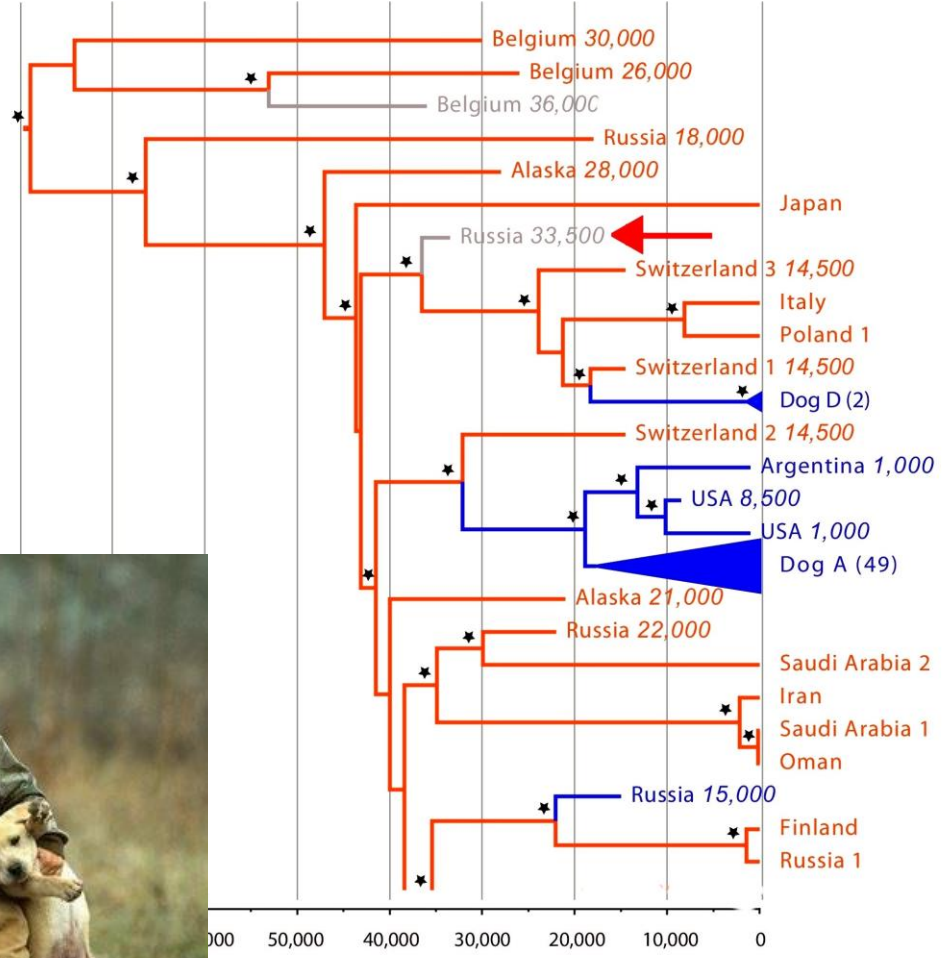
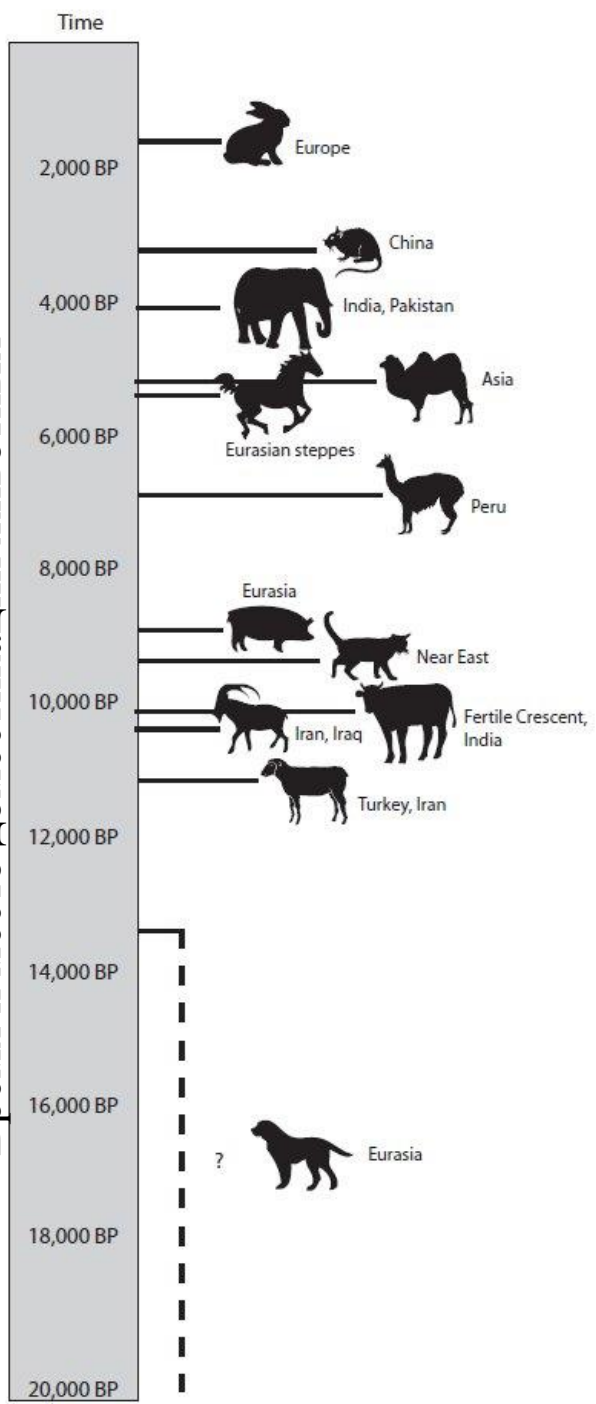
A)



tribution that can be heavily influenced by human dispersal. The extensive phenotypic variation among dog breeds hinders a simple inference of dog origins based on the presence of traits shared between dogs and any specific population of the

ER 2013

Время и место domestikации животных



Институт молекулярной и клеточной биологии
Институт археологии и этнографии СО РАН

Jamthund (Swedish Elkhound)



Norwegian Elkhound is one of the ancient Northern Spitz-type breed of dog and is the National Dog of Norway.

Dog Genome Assembled

Canine Genome Now Available to Research Community Worldwide



BETHESDA, Md., Wed., July 14, 2004 - The first draft of the dog genome sequence has been deposited into free public databases for use by biomedical and veterinary researchers around the globe, the National Human Genome Research Institute (NHGRI), one of the National Institutes of Health (NIH), announced today.

A team led by Kerstin Lindblad-Toh, Ph.D., of the Broad Institute of MIT and Harvard, Cambridge, Mass., and Agencourt Bioscience Corp., Beverly, Mass., successfully assembled the genome of the domestic dog (*Canis familiaris*). The breed of dog sequenced was the boxer, which was chosen after analyses of 60 dog breeds found it was one of the breeds with the least amount of variation in its genome and therefore likely to provide the most reliable reference genome sequence.

The initial assembly is based on seven-fold coverage of the dog genome. Researchers can access the sequence data through the following public databases: GenBank (www.ncbi.nih.gov/Genbank) at NIH's National Center for Biotechnology Information (NCBI); EMBL Bank (www.ebi.ac.uk/index.html) at the European Molecular Biology Laboratory's Nucleotide Sequence Database; and the DNA Data Bank of Japan (www.ddbj.nih.ac.jp). The data can also be viewed through the UCSC

OPEN ACCESS Freely available online

PLOS GENETICS

Genome Sequencing Highlights the Dynamic Early History of Dogs

Adam H. Freedman¹, Ilan Gronau², Rena M. Schweizer¹, Diego Ortega-Del Vecchyo¹, Eunjung Han¹, Pedro M. Silva³, Marco Galaverni⁴, Zhenxin Fan⁵, Peter Marx⁶, Belen Lorente-Galdos⁷, Holly Beale⁸, Oscar Ramirez⁷, Farhad Hormozdiani⁹, Can Alkan¹⁰, Carles Vilà¹¹, Kevin Squire¹², Eli Geffen¹³, Josip Kusak¹⁴, Adam R. Boyko¹⁵, Heidi G. Parker⁸, Clarence Lee¹⁶, Vasisht Tadigotla¹⁶, Adam Siepel², Carlos D. Bustamante¹⁷, Timothy T. Harkins¹⁶, Stanley F. Nelson¹², Elaine A. Ostrander⁸, Tomas Marques-Bonet^{7,18}, Robert K. Wayne^{1*}, John Novembre^{1a*}

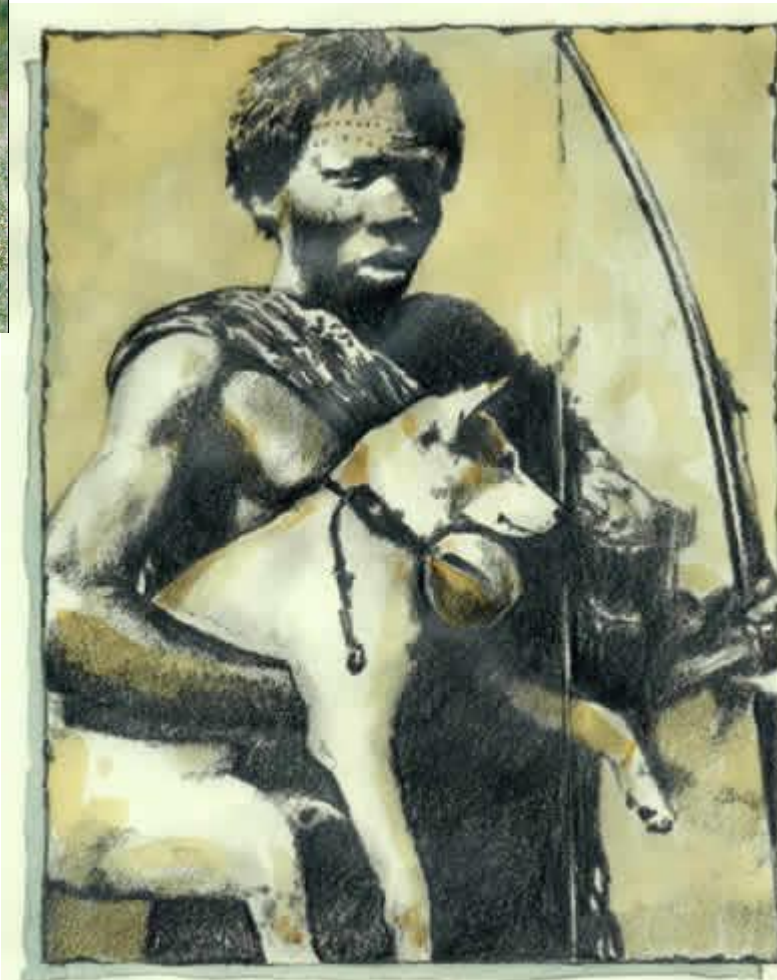
¹ Department of Ecology and Evolutionary Biology, University of California, Los Angeles, Los Angeles, California, United States of America, ² Department of Biological



Figure 1. Geographic distribution of sampled lineages.
doi:10.1371/journal.pgen.1004016.g001



Басенджи (лесная собака из Конго, конго-терьер, ньям-ньям-терьер, собака Занде)



Обыкновенный шакал (*Canis aureus*)



Аравийский волк (*Canis lupus arabis*)



Динго (*Canis lupus dingo*)

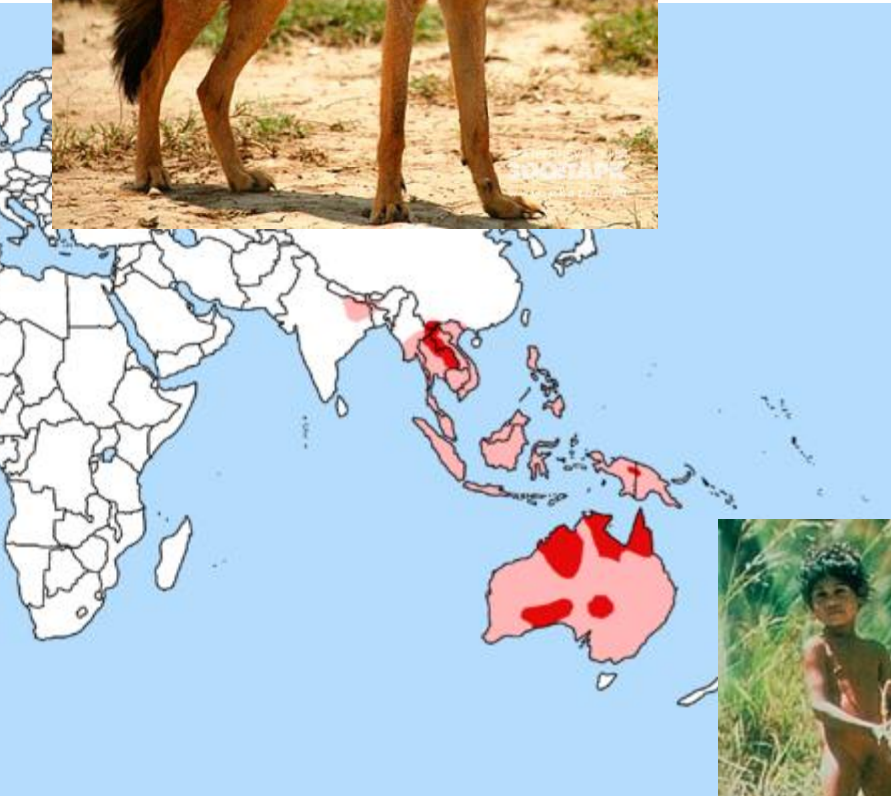




Figure 1. Geographic distribution of sampled lineages.
doi:10.1371/journal.pgen.1004016.g001

Genome Sequencing Highlights Early History of Dogs

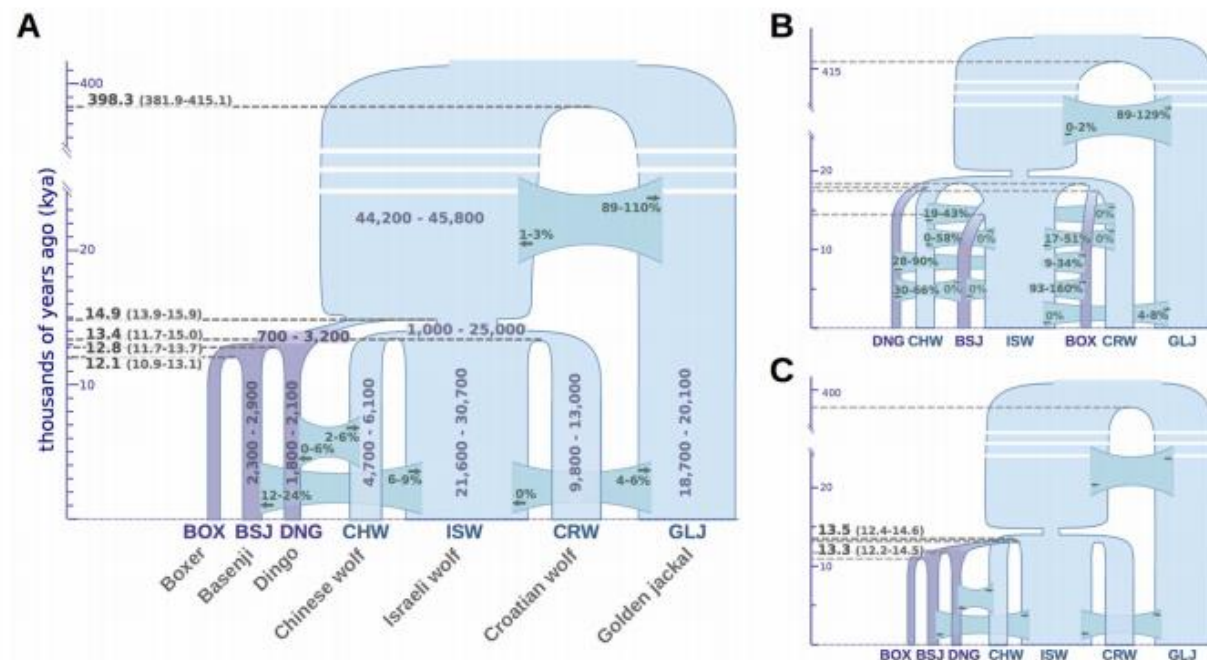


Figure 5. Demographic model of domestication. Divergence times, effective population sizes (N_e), and post-divergence gene flow inferred by G-PhoCS in joint analysis of the Boxer reference genome, and the sequenced genomes of two basal dog breeds, three wolves, and a golden jackal. The width of each population branch is proportional to inferred population size, and stated ranges of parameter estimates indicate 95% Bayesian credible intervals. Horizontal gray dashed lines indicate timing of lineage divergences, with associated means in bold, and 95% credible intervals in parentheses. Migration bands are shown in green with associated values indicating estimates of total migration rates, which equal the probability that a lineage will migrate through the band during the time period when the two populations co-occur. Panels show parameter estimates for (A) the population tree best supported by genome-wide sequence divergence (Fig. 4A) (B) a regional domestication model, and (C) a single wolf lineage origin model in which dogs diverged most recently from the Israeli wolf lineage (similar star-like divergences are found assuming alternative choices for the single wolf ancestor). Estimated divergence times and effective population sizes are calibrated assuming an average mutation rate of 1×10^{-8} substitutions per generation and an average generation time of three years. See Text S9 and Table S12 for details.
doi:10.1371/journal.pgen.1004016.g005

Изучение копийности гена амилазы AMY2B

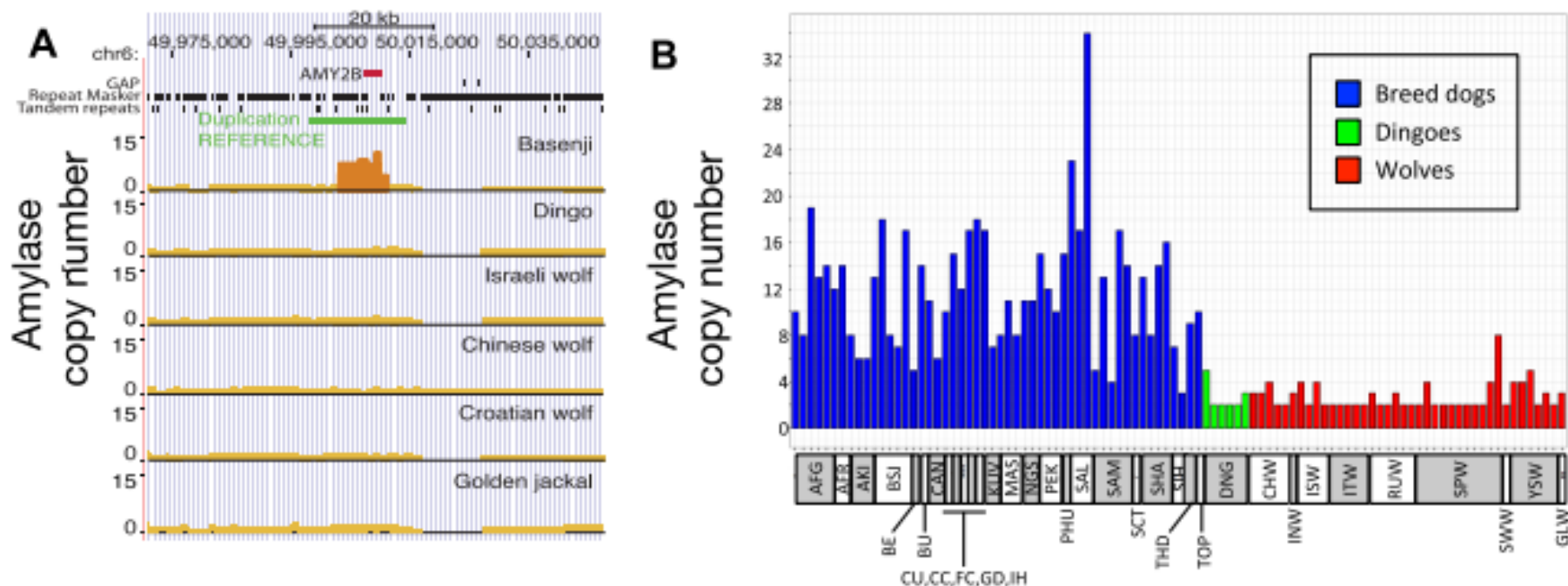


Figure 6. Copy number variation at amylase (*AMY2B*) locus. (A) Copy number variation (CNV) at *AMY2B* estimated from whole genome sequence data, showing presence of elevated copy number in Basenji but not in other lineages. Results are based on SOLiD data, except for the Chinese wolf (see Text S6 for supporting results and Text S10 for CNV analyses in an additional 12 dog breeds). (B) qPCR results on CNV state in an expanded set of wolf and dog lineages. Abbreviations for lineages are: AFG, Afghan Hound; AFR, Africanis; AKI, Akita; BSJ, Basenji; BE, Beagle; BU, Bulldog; CAN, Cane Corso; CUV, Cuvac; MAS, Mastiff; NGS, New Guinea Singing Dog; PEK, Pekinese; PHU, Phu Quoc; SAL, Saluki; SAM, Samoyed; SCT, Scottish Terrier; SHA, Shar Pei; SHI, Siberian Husky; THD, Thai Dog; TOP, Toy Poodle; DNG, Dingo; CHW, Chinese wolf; INW, Indian wolf; ISW, Israeli wolf; ITW, Italian wolf; RUW, Russian wolf; SPW, Spanish wolf; YSW, Yellowstone wolf; GLW, Great Lakes wolf.

doi:10.1371/journal.pgen.1004016.g006

