Volume 18

The Society News

The Society for the Perpetuation of Desert Bred Salukis

Winter 2022-2023

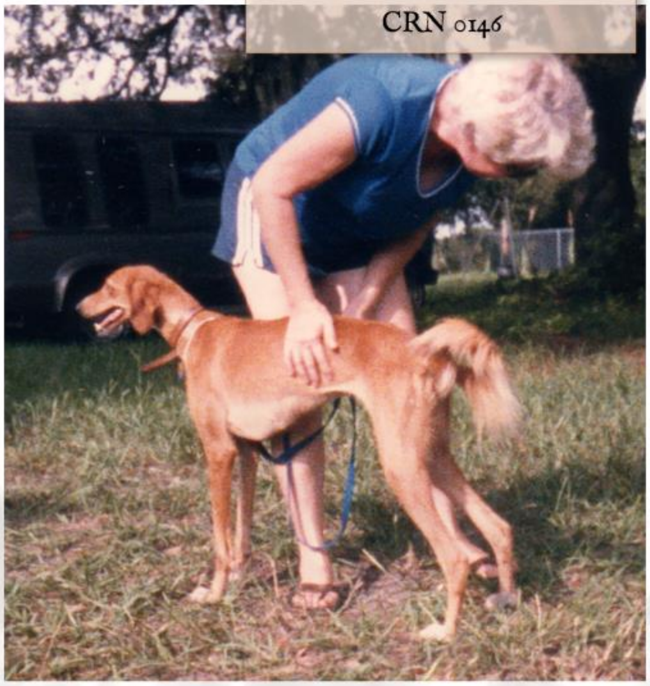
Society for the Perpetuation of Desert Bred Salukis

Menjad Mokhlisa

CRN 0421-002-1

Alia of El Baz

CRN 0146



El Baz Leila

CRN 0422-002-2

The Salukis

of

El Baz

El Baz Oma Omar

CRN 0451-005-2

El Baz Sahara Sue

CRN 0576-009-2

CONTENTS

President’s Message Pg 4

Secretary’s Report Pg 4

Treasurer’s Report Pg 6

Nominating Committee Report Pg 6

New Imports Pg 7

Registrar’s CRN Report Pg 8

New Litters Pg 10

Grey Wolf genomic History Reveals a dual ancestry of dogs Pg 12

Anders Bergstrom, Pontus Skoglund

Help to Turkey Pg 34

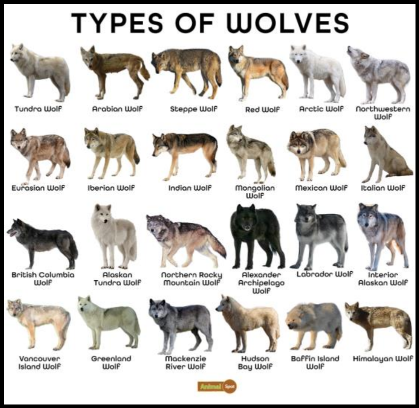
AKC Purebred Preservation Bank (PPB) *Jerold S. Bell DVM, Cummings School of Veterinary Medicine at Tufts University* Pg 38

Pictures from an Exhibition Pg 46

Sir Terence Clark

So You Want to Breed a Litter? Pg 53

Kokopelli Assisted Reproductive Services



Wolf Genomic History

Help in Turkey

Gertrude Bell

Litter Plans

President's Message

Mary Beth Rogers

We have opened a Desert Bred Salukis page on Facebook for our members and Supporters. Most of you are now on this Group. Please use it to share news, pictures, and anything else from our Salukis and their families. Help us stay in touch.

We continue to deal with the issues surrounding Registration and the Kazakh Tazy. SPDBS is now in contact with both the Parent Club SCOA and AKC about how we continue forward with the current registration irregularities. We should have news in the coming weeks on this topic.

We are still in the process of producing our archival recordings. These are the interviews we now have from Gertrude Hinsch, Sir Terence Clark, Chris Mason, Julia Holder, and Elizabeth Dawsari. If there is an interview you, as SPDBS members, would like to see done, please let the Secretary know. These interviews will be mounted on our website, accessible to all as Chai Talk, meetings over tea, shared with everyone.

We are seeing all our families that are or have transitioned into the AKC Studbook do quite well in the AKC show and Performance world. Congratulations to Stephanie and Brad Gamble on attaining Yamadan el Jabri for Tallahamra's AKC championship. A lovely achievement for this little typical grizzle smooth girl!

Both Carola Butler and Oksana Belova are doing quite well with their girls in the AKC world. Carola's Melik Baanu -Abi e Sheyda lacks only a major for her Championship and is doing well lure coursing. Ana's Melik Rataki Yaadegar e Bokan has one of her majors and went out to New Mexico and won a hunt! Her littermates have been VERY successful on the lure coursing fields.

MBIF,FC,UKC CH Rataki Yalda de Valle Compel SC,TKN,FCh won both the Pyramid Cup and the AKC Trial at the SCOA National, She joins MANY other SPDBS Salukis and Graduates on that Pyramid cup!! Brother Yaar-Jan, belonging to Susan and Bill Schroeder, also has his Field Championship and won the Open Stake at the Pyramid Cup as well as BOB ASFA ASA South Central Regional.

Paul Perez has imported a young male from the Kurdish region of Iraq. He has hunted once this season and won the hunt so next year should be an interesting one for *Kuhi of Iran.

Kathleen Tigan's Turkish boy * Kullah of Urfa not only survived the wet and the mud at this year's Grand Course, he won top honors adding GCW to his name! Turk finishes this season as the #1 Saluki and # 2 All Breed in NOFCA.

I have no doubt I have missed many successes this past year for which I apologize. If you have a brag please share! Sharing on the Desert Bred Saluki Group will let us all know of your success.

Secretary's Report

Only one motion was passed by the SPDBS Board of Directors in 2022. It reads as follows:

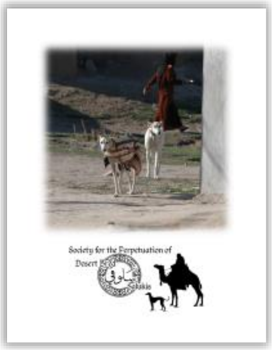
Motion to offer a SPDBS Supporter category. The SPDBS Supporter gains access to the SPDBS Facebook Group "Desert Bred Salukis" and the digital newsletter. This is not a membership and has no voting rights. Cost would be $10.00 annually, payable via PayPal. It requires agreement to support the Constitution and Bylaws as well as the mission of SPDBS. It will not confer Registration discounts. If approved Supporter benefits will be annual except for this initial period which will run through the next operating year to end December 31, 2023. Full memberships may be converted to SPDBS Supporters at the discretion of the Board by contacting the Secretary.

The motion passed unanimously with all board members voting.

Respectfully submitted by Lauri Domski, SPDBS Secretary

Society for the Perpetuation of
Desert Bred
Salukis

Volume 18



On the back cover:

Photograph from the collection of Mary Beth Rogers. Village scene from the Turkish/Syrian border taken in 2005.

On the front cover:

Afghanistan: late 15th century painting of a hunting scene from the Hast Bahist by Kamal al-Din Behzad.

Kamal ud-Din Behzad Herawi (c. 1450 - c. 1535), also known as Kamal al-din Bihzad or Kamaleddin Behzad, was a painter of Persian miniatures and head of the royal ateliers in Herat and Tabriz during the late Timurid and early Safavid periods. An orphan, he was raised by the prominent painter Mirak Naqqash, and was a protege of Mir Ali Shir Nava'i. His major patron in Herat was the Timurid sultan Husayn Bayqarah (ruled 1469 - 1506).

Behzad was instrumental in the development of the style that used geometry and architectural elements as the basis for the composition of his pieces and those of the painters under him in the ateliers he led.

This piece is housed today at Topkapi Palace, Istanbul, Turkey.

Our Advertisers

Stephanie and Brad Gamble	11
Kathleen Tigan	32/33
Marissa-Jo Wagenaar	36
Susan and Bill Schroeder	37
Lauri and Paul Domski	50
Carola Butler/Jan Isley	51
Joanne Klova/Danielle Rubin	59
Lorraine Trenholm	60/61
Mary Beth and George Rogers	62/IBC

Society for the Perpetuation of Desert Bred Salukis Statement of Revenue and Expenditures

For the Period Ending December 31, 2022

BEGINNING BALANCE DECEMBER 31, 2021	55,098.75
REVENUES:	
MEMBERSHIPS/SUBSCRIPTIONS	1,320.00
SUPPORTER FEE	110.00
CRITIQUES/CERTIFICATES/EXPORT PEDIGREE	260.00
HATS INCLUDING FEE FOR SHIPPING	435.00
NEWSLETTER	335.00
TOTAL REVENUES	2,460.00
EXPENSES:	
DIRECTOR & OFFICER INSURANCE	815.00
SPONSOR SHIP-THE BREED ARCHIVE	335.91
WEB SITE HOSTING/SERVICES	529.40
POD CAST EQUIPMENT	127.62
SOFTWARE/MEDIA SERVICES	612.16
PRINTING/POSTAGE/ SHIPPING	1,111.16
HATS	905.65
ADS	40.00
FLOWERS	107.35
PAYPAL FEES/BANK FEES	118.54
TOTAL EXPENSES	4,702.79
ENDING BALANCE AT DECEMBER 31, 2022	52,855.96

As there were no Nominations from the Floor, the Nominating Committee Slate is seated per our By-Laws.

The Society Board of Directors and Officers are as follows:

SPDBS Board of Directors

President/Registrar– Mary Beth Rogers
president@desertbred.org/spdbs.registrar@gmail.com
Vice–President– Elizabeth Dawsari
Treasurer- Ken Stahli
treasurer@desertbred.org
Secretary-Lauri Domski *secretary@desertbred.org*

Board of Directors

Oksana Belova	Paul Domski
Marsha Bradbury	Sue Nelson
Sir Terence Clark	Kathleen Tigan

New Imports

Miraj Little Sunshine Neshama Tova

Import from Israel, Generation 1

Bred by Keren Mintz

Owned by Amalia Gat, Brittany Gat, Ehud Gat

Whelped November 27, 2021

Kalibsuluaqi Naylli

Import United Kingdom, Generation 1

Bred by Christopher James Foster

Owned by Allison Meyer

Whelped May17, 2021

Murisa Marwa Ravan Bacht

Import from Germany, Generation 2

Bred by Martina Kissener, Heike Bräuer

Owned by Mary Beth Rogers

Whelped April 30, 2022

CRN 0807-017-1—CRN 0866-022-0

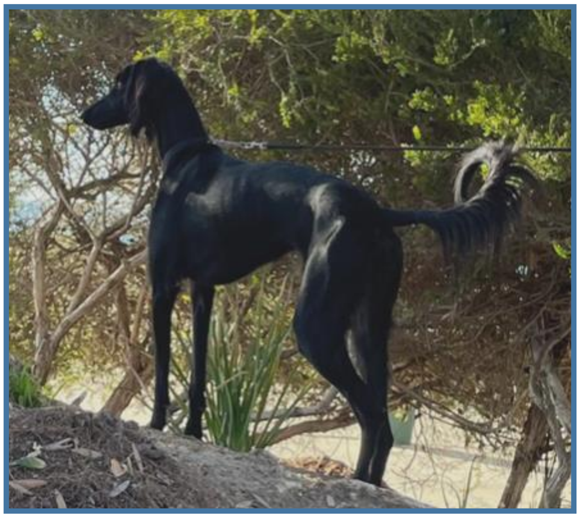
Rataki Xena
Bitch. CRN 0807-017-1
Red, white markings, Feathered
September 9, 2017
Whelped in Ignacio, CO
Breeder: Lorraine Trenholm
By Melik Khaliis
CRN 0719-013-1 x
*Aram de Diba of Boorchin
CRN 0641-011-0
Owner: Jeff Kauffman

Melik Boorchin Pazhal
Bitch. CRN 0848-020-1
Black and Tan,Feathered
November 3, 2020
Whelped in Milford VA
Breeder: Mary Beth/Mary-Wynn Rogers
By *Gare-Qush of Iran
CRN 0830-019-0 x
*Qushabee of Boorchin
CRN 0737-013-0
Owners: Josephine LeLoup/Daniela Bormacher

Melik Boorchin Parisa
Bitch. CRN 0849-020-1
Black, white markings, Feathered
November 3, 2020
Whelped in Milford VA
Breeder: Mary Beth/Mary-Wynn Rogers
By *Gare-Qush of Iran
CRN 0830-019-0 x
*Qushabee of Boorchin
CRN 0737-013-0
Owners: Paul and Adriana Perez/Mary Beth Rogers

CRN 0807-017-1—CRN 0866-022-0

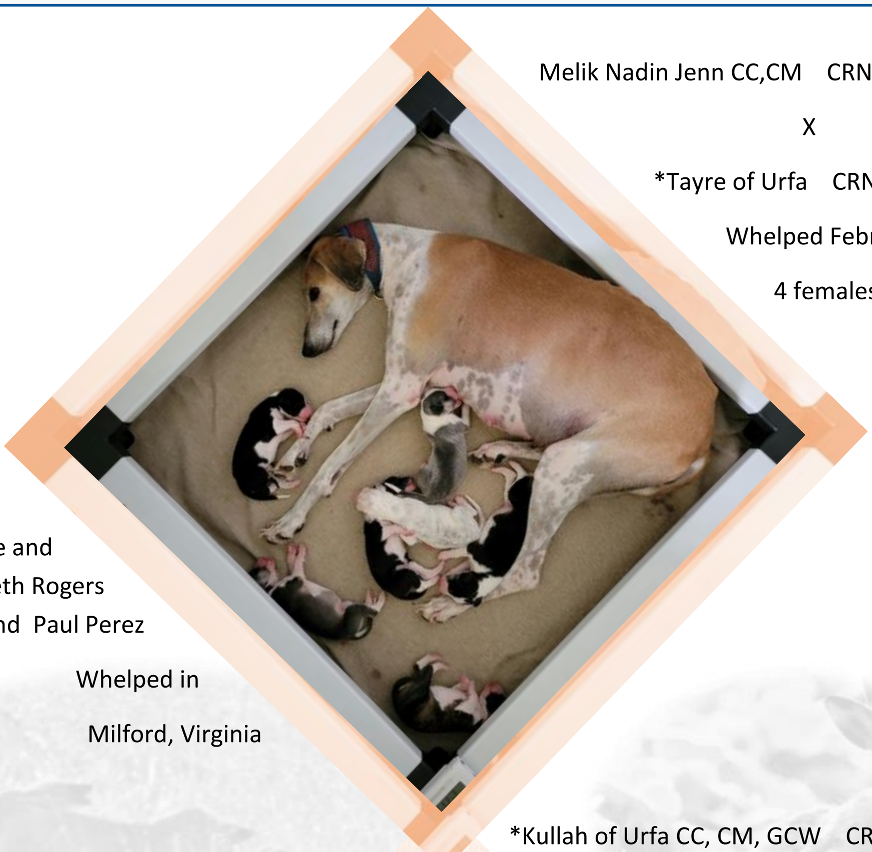
Melik Boorchin Parinaz
Bitch. CRN 0850-020-1
Black, white markings ,Feathered
November 3, 2020
Whelped in Milford VA
Breeder: Mary Beth/Mary-Wynn Rogers
By *Gare-Qush of Iran
CRN 0830-019-0 x
*Qushabee of Boorchin
CRN 0737-013-0
Owners: Verial Whitten/Barbara Nackerud



*Iti Be'Libi Tihii La'ad Ruah Midbar
Bitch. CRN 0854-021-2
Red grizzle, Irish marked
April 3, 2014
Whelped in Israel
Breeder: Micaela Okon
By Ben Hoor Silver Ruah Midbar
ISBR 95464 x
El Riyah Rami Suhayla
CRN 0583-009-3/ISBR 13569
Owner: Cassandra Kraham

*Kuhi of Iran
Dog. CRN 0866-022-0
Grey, Feathered
January 1, 2020
Whelped in Iran
Breeder: Unknown
By *Unknown x
Unknown
Owners:
Paul /Israel Perez and George/Mary Beth Rogers

New Litters



Melik Nadin Jenn CC,CM CRN 0773-015 –2

X

*Tayre of Urfa CRN 0813-018-0

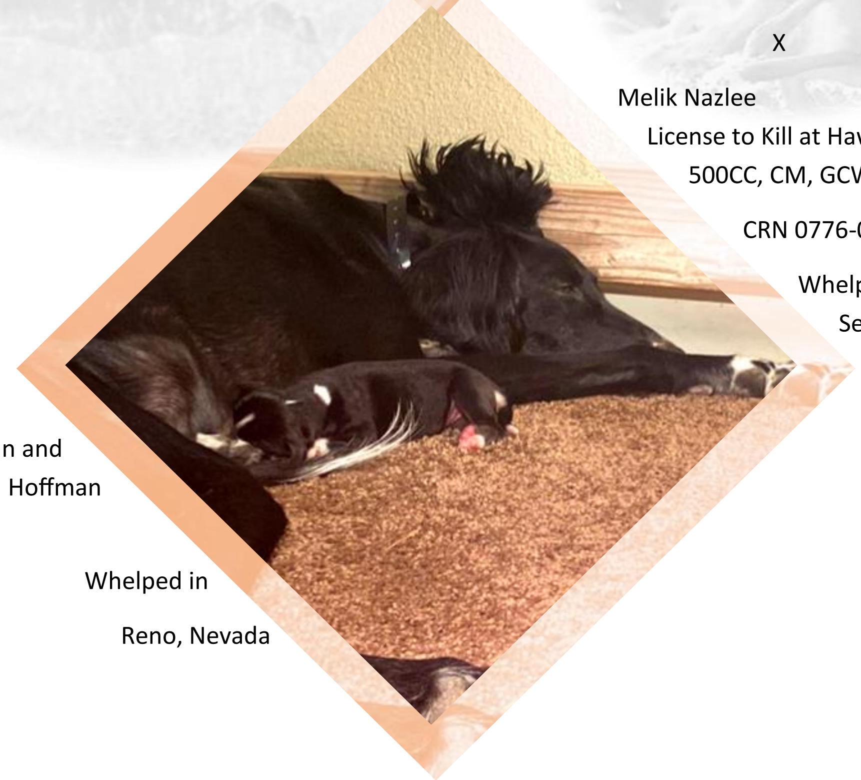
Whelped February 24, 2023

4 females, 3 males

Dr. George and
Mary Beth Rogers
and Paul Perez

Whelped in

Milford, Virginia



*Kullah of Urfa CC, CM, GCW CRN 0812-018-0

X

Melik Nazlee
License to Kill at HawksView
500CC, CM, GCW2

CRN 0776-015-2

Whelped
September 28, 2022

1 male

Kathleen Tigan and
Karen Hoffman

Whelped in

Reno, Nevada

Veni
Vidi
Vici


© Big Paw Prints 2013


Ginger Johnson Photography 2014

Haifa

Yamadan

Stephanie & Brad Gamble
Yamadan14@gmail.com

Grey wolf genomic history reveals a Dual ancestry of dogs

https://doi.org/10.1038/s41586-022-04824-9

Received: 27 August 2021

Accepted: 28 April 2022

Reprint from *Nature*

Supplementary information The online version contains supplementary material available at

https://doi.org/10.1038/s41586-022-04824-9.

Correspondence and requests for materials should be addressed to Anders Bergström or Pontus Skoglund.

Peer review information *Nature* thanks Kieren Mitchell, Claire Wade and the other, anonymous, reviewer(s) for their contribution to the peer review of this work. Peer reviewer reports are available.

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Anders Bergström[1,69], David W. G. Stanton[2,3,4,69], Ulrike H. Taron[5,69], Laurent Frantz[4,6],Mikkel-Holger S. Sinding[7,8,9,10], Erik Ersmark[2,3], Saskia Pfrengle[11,12], Molly Cassatt-Johnstone[13], Ophélie Lebrasseur[14], Linus Girdland-Flink[15,16], Daniel M. Fernandes[17,18], Morgane Ollivier[19], Leo Speidel[1,20], Shyam Gopalakrishnan[7], Michael V. Westbury[5,7], Jazmin Ramos-Madrigal[7], Tatiana R. Feuerborn[7,9,11], Ella Reiter[11], Joscha Gretzinger[11,21], Susanne C. Münzel[11],Pooja Swali[1], Nicholas J. Conard[22,23], Christian Carøe[7], James Haile[14], Anna Linderholm[3,14,24,25], Semyon Androsov[26], Ian Barnes[27], Chris Baumann[23,28], Norbert Benecke[29], Hervé Bocherens[23,30], Selina Brace[27], Ruth F. Carden[31], Dorothée G. Drucker[23], Sergey Fedorov[32], Mihály Gasparik[33], Mietje Germonpré[34], Semyon Grigoriev[32,70], Pam Groves[35], Stefan T. Hertwig[36,37], Varvara V. Ivanova[38], Luc Janssens[39], Richard P. Jennings[16], Aleksei K. Kasparov[40], Irina V. Kirillova[41], Islam Kurmaniyazov[42], Yaroslav V. Kuzmin[43], Pavel A. Kosintsev[44], Martina Lázničková-Galetová[45], Charlotte Leduc[46], Pavel Nikolskiy[47], Marc Nussbaumer[36], Cóilín O'Drisceoil[48], Ludovic Orlando[49], Alan Outram[50], Elena Y. Pavlova[51], Angela R. Perri[52,53], Małgorzata Pilot[54], Vladimir V. Pitulko[40], Valerii V. Plotnikov[55], Albert V. Protopopov[55], André Rehazek[36], Mikhail Sablin[56], Andaine Seguin-Orlando[49], Jan Storå[57], Christian Verjux[58], Victor F. Zaibert[59], Grant Zazula[60,61], Philippe Crombé[62], Anders J. Hansen[7], Eske Willerslev[7,63], Jennifer A. Leonard[64], Anders Götherström[3,57], Ron Pinhasi[17,68], Verena J. Schuenemann[11,12,17], Michael Hofreiter[5], M. Thomas P. Gilbert[7,65], Beth Shpiro[13,66], Greger Larson[14], Johannes Krause[67], Love Dalén[2,3] & Pontus Skoglund

The grey wolf (*Canis lupus*) was the first species to give rise to a domestic population, and they remained widespread throughout the last Ice Age when many other large mammal species went extinct. Little is known, however, about the history and possible extinction of past wolf populations or when and where the wolf progenitors of the present-day dog lineage (*Canis familiaris*) lived[1–8]. Here we analyzed 72 ancient wolf genomes spanning the last 100,000 years from Europe, Siberia and North America. We found that wolf populations were highly connected throughout the Late Pleistocene, with levels of differentiation an order of magnitude lower than they are today. This population connectivity allowed us to detect natural selection across the time series, including rapid fixation of mutations in the gene *IFT88* 40,000–30,000 years ago. We show that dogs are overall more closely related to ancient wolves from eastern Eurasia than to those from western Eurasia, suggesting a domestication process in the east. However, we also found that dogs in the Near East and Africa derive up to half of their ancestry from a distinct population related to modern southwest Eurasian wolves, reflecting either an independent domestication process or admixture from local wolves. None of the analyzed ancient wolf genomes is a direct match for either of these dog ancestries, meaning that the exact progenitor populations remain to be located.

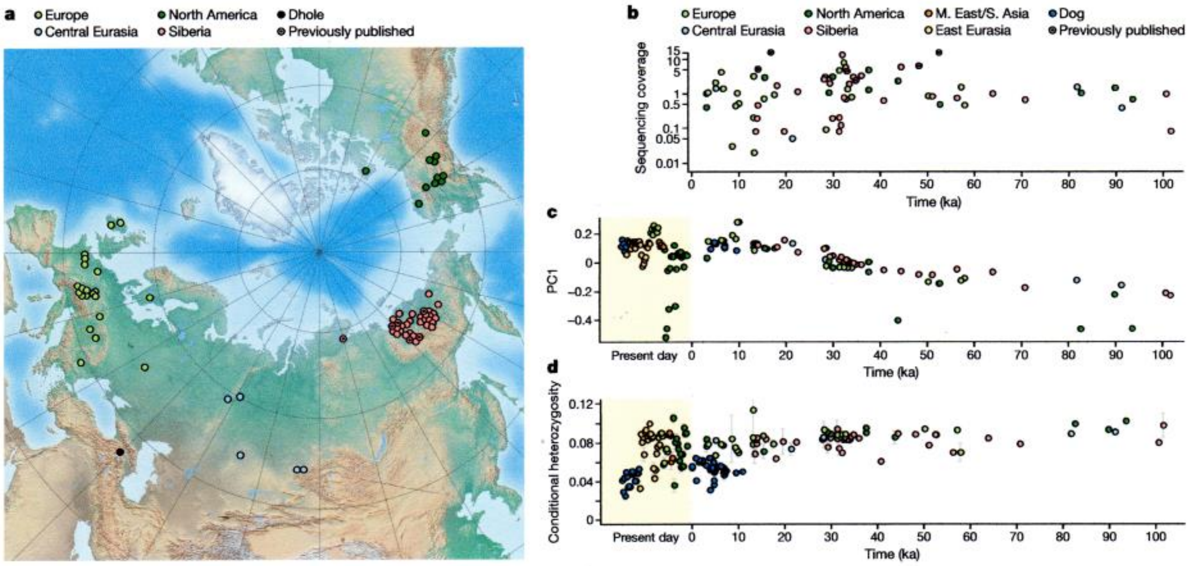

Fig. 1 | Seventy-two ancient wolf genomes. a, Sampling locations of ancient wolves and one ancient dhole analysed here, on a base map from Natural Earth (naturalearthdata.com). **b**, Ages and sequencing coverage of ancient wolves. **c**, PC1 from a PCA on outgroup f_3-statistics plotted against sample age. PCs were calculated from ancient wolves only, with present-day wolves and dogs projected onto the plot. **d**, Heterozygosity estimates from sampling of two reads at sites ascertained as heterozygous in a coyote. Bars denote 95% CIs from block jackknifing.

The grey wolf (*Canis lupus*) has been present across most of the northern hemisphere for the last few hundred thousand years and, unlike many other large mammals, did not go extinct in the Late Pleistocene. Studies of present-day genomes have found that current population structure formed mostly in the last ~30,000–20,000 years[9–11], or roughly since the Last Glacial Maximum (LGM; ~28–23 thousand years ago (ka)[12]). Siberian wolves predating the LGM have ancestries that are largely basal to present-day diversity, which has led to suggestions that many pre-LGM wolf lineages went extinct[13,14]. Among the central questions is thus to what extent the global wolf population was subject to extinction processes or responded to climate change with new adaptations. While it is clear that grey wolves gave rise to dogs, there is no consensus regarding when, where and how this happened[1–8]. Skeletal remains attributable to the present-day dog lineage appear archaeologically by 14 ka[15], and genetic estimates of when the ancestors of dogs and modern wolves diverged range from 40–14 ka[9,13,16]. However, genetic data from modern and ancient dogs coupled with modern wolves, to which previous studies were largely restricted, may not be able to resolve the origin of dogs. Genetic diversity within dogs is affected by their dynamic history and is unable to confidently pinpoint an origin. Relationships to modern wolves can likewise be affected by local extinction and gene flow since domestication[6,9]. Regions where early dogs have been found do not necessarily imply places of origin either, as the existence of earlier dogs elsewhere cannot be excluded. Instead, the origin of dogs could be resolved if wolf genetic diversity across space and time was exhaustively characterized and it could be determined which populations were closest to the ancestors of dogs.

Wolf genomes spanning 100,000 years

We sequenced 66 new ancient wolf genomes from Europe, Siberia and north-western North America to a median of 1× coverage (range, 0.02–13×) (Fig. 1a,b), incorporated five previously sequenced ancient wolf genomes[14,17] and increased coverage for one[13]. We also sequenced an ancient dhole genome from the Caucasus, contextually dated to >70 ka, to serve as an outgroup. Fractions of X-chromosome DNA showed that 69% of the wolves were male (95% confidence interval (CI), 57–80%; $P = 0.0013$, binomial test), mirroring male over-representation among ancient genomes from woolly mammoths[18], bison[19], brown bears[19] and domestic dogs[8]. For wolves without dates or with dates beyond the radiocarbon limit of ~50 ka, we estimated ages through mitochondrial tip dating[20] and obtained an average 95% CI of 21,573 years and an average prediction error of 5,133 years (Supplementary Figs. 1 and 2). We merged single-nucleotide polymorphism (SNP) genotypes called from these genomes with those from worldwide modern wolves (*n* = 68), modern (*n* = 369) and ancient (*n* = 33) dogs, and other canid species (Methods). The total dataset spans the last 100,000 years (Fig. 1b).

In a principal component analysis (PCA) on a matrix of shared genetic drift, the ancient wolves clustered strongly by age and not by geography (Pearson's rPC1,sample age = 0.85, P = 5 × 10−21) (Fig. 1c). Similarly, ancient wolves share more drift with modern wolves the younger they are (Extended Data Fig. 1a and Supplementary Fig. 3). Previous studies have suggested an LGM ancestry turnover[13,14,21], and, indeed, we found that all individuals younger than the LGM (that is, postdating 23 ka) were more similar to each other than to wolves predating ~28 ka (Extended Data Fig. 1b). However, the same pattern is also visible when contrasting affinities to younger versus older wolves at any point during the last 100,000 years (Supplementary Fig. 4). Using simulations, we confirmed that the observed temporal relationships are largely similar to what would be expected in a panmictic population (Supplementary Fig. 5). A long-standing process of ancestry homogenization due to connectivity thus seems to have driven Pleistocene wolf relationships. The changes during the LGM therefore represent not a shift in long-term population dynamics, but the most recent manifestation of this process.

...our results suggest that Siberia acted as a source and Europe as a sink for migration throughout the Late Pleistocene and show no evidence of gene flow in the other direction ...

Siberia as a source of global gene flow

We next tested for directionality in the gene flow that connected wolf ancestry over time. Analyses using f_4-statistics showed that all wolves postdating 23 ka are more similar to Siberian wolves than to European or Central Asian wolves from ~30 ka (Extended Data Fig. 1c and Supplementary Fig. 6). This suggests that Siberian-related ancestry expanded into Europe, in line with mitochondrial evidence[21]. The same dynamic of Siberian gene flow into Europe unfolded between 50 and 35 ka (Supplementary Fig. 6). We found that an admixture graph model with recurrent, unidirectional gene flow from Siberia into Europe could explain these relationships (Fig. 2a and Supplementary Fig. 8). Although we could not distinguish pulse-like from continuous gene flow, our results suggest that Siberia acted as a source and Europe as a sink for migration throughout the Late Pleistocene and show no evidence of gene flow in the other direction (Extended Data Fig. 1d and Supplementary Fig. 7).

While these results demonstrate pervasive gene flow, they also show that the ancestry replacements were incomplete and that minority fractions of deep European ancestry have persisted until the present day (Fig. 2a,b). Most analyzed modern Eurasian wolves probably retain local Pleistocene ancestry, as they are best modelled by qpAdm as having 10–40% ancestry that is more divergent than the oldest Siberian wolves in this study at ~100 ka (Supplementary Figs. 11 and 12). In addition to local grey wolf ancestry not represented among our ancient genomes, this may include African golden wolf-related ancestry in the Near East and South Asia[22] and ancestry of unknown canid origin in Tibet[23] (Supplementary Fig. 10). While all Eurasian wolves today share the majority of their ancestry within the last 25,000 years, the persistence of deep local ancestries provides evidence against widespread local extinction in Late Pleistocene Eurasia and suggests that the species as a whole, unlike many other megafauna, did not come close to extinction.

Many modern and ancient North American wolves show evidence of coyote (Canis latrans) admixture[24,25] (Extended Data Fig. 1e), which explains why some of them do not cluster with wolves of similar age in the PCA (Fig. 1c). On the basis of coalescence rates[26] between male X chromosomes, which have perfect haplotype phase, we estimated that wolves and coyotes began diverging ~700 ka (Supplementary Fig. 14), broadly in line with a fossil divergence of ~1 million years ago[27]. Our data show that coyote admixture has occurred at least since 100–80 ka, and two analysed Pleistocene wolves from the Yukon also carried coyote mitochondrial lineages. These findings imply

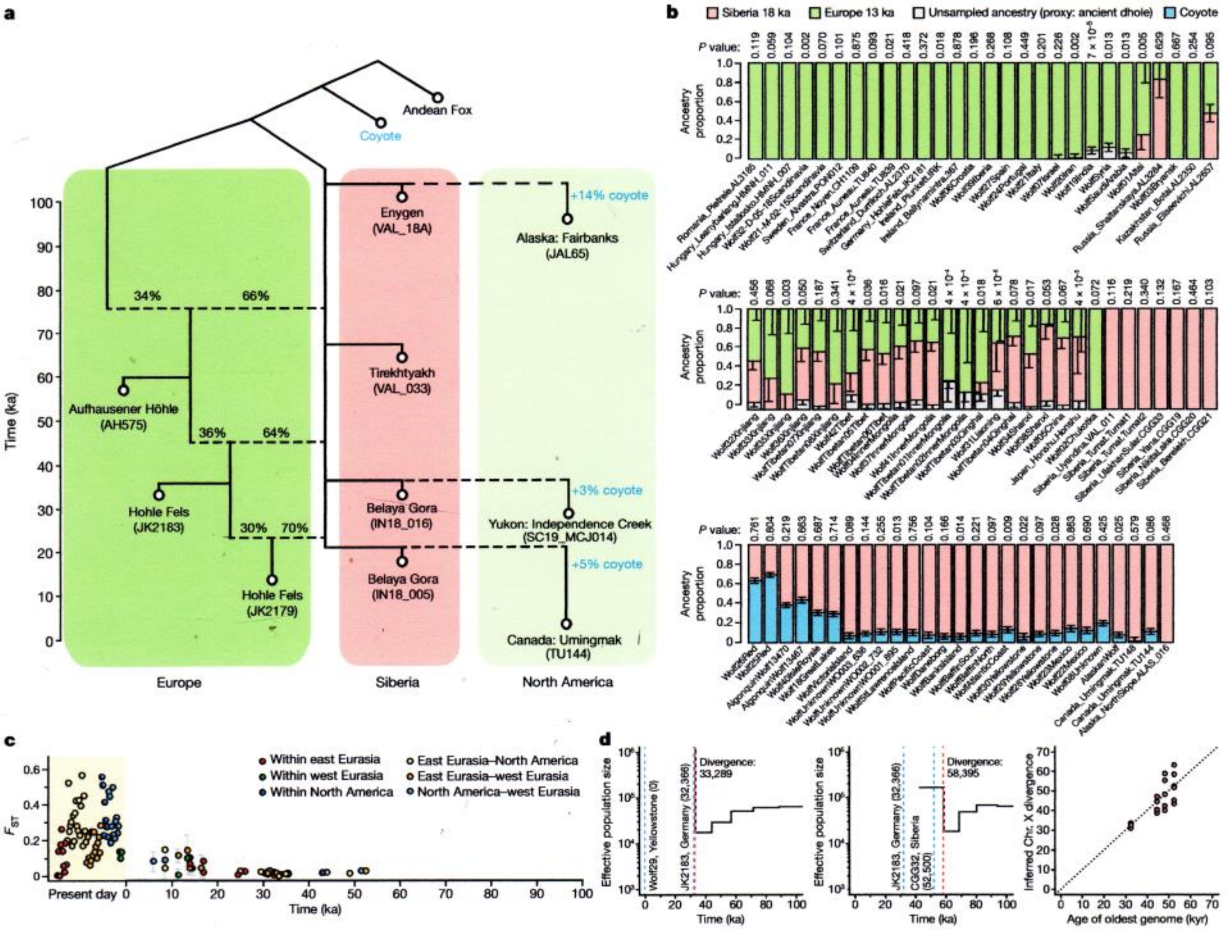

Fig. 2 | One hundred thousand years of wolf population history. **a,** Admixture graph fit by qpGraph to selected ancient wolves, with two outlier ($|Z| > 3$) f-statistics (worst = 3.16). **b**, Best-fitting qpAdm models for post-LGM and present-day wolves. An ancient dhole was used as the outgroup for Eurasian wolves to capture any unsampled divergent ancestry, while a coyote was used as the outgroup for North American wolves. Bars denote ±1 standard error estimated from a block jackknife. **c**, F_{ST} for pairs of sample groups with mean dates separated by ≤12,500 years. Bars denote ±1.96 standard errors **d**, MSMC2 results for pairs of male X chromosomes, with sample ages indicated by blue lines. A sharp upwards spike in the curve corresponds to population divergence, with estimated timings indicated by red lines. Example curves for two pairs of wolves (left and middle) and a summary of results for all pairs (right) are shown. kyr, thousand years.

that either the Pleistocene range of coyotes extended further north than currently thought or that admixture occurring further south propagated northwards through the wolf population. In our Eurasian wolves, no influx of coyote ancestry is observed over time (Extended Data Fig. 1e). We found a slight west–east gradient of increasing coyote affinity among Eurasian wolves, but this pattern probably reflects admixture into coyotes from North American wolves (which are related to wolves in eastern Siberia) (Supplementary Fig. 9).

After accounting for coyote admixture, we found that wolf ancestry in Alaska and the Yukon was highly connected to Siberia over time (Fig. 2a). This mirrors European wolf history, but, while some deep local European ancestry persists, no deep North American ancestry appears to persist to the present. The Bering land bridge probably allowed for an influx of Siberian wolves into Alaska intermittently between 70 and 11 ka[28,29], but we found no evidence of gene flow in the other direction. All present-day North American wolves can be modelled as having 10–20% coyote ancestry and the remaining ancestry from Siberian wolves younger than ~23 ka, with no contribution from earlier North American wolves (Fig. 2b). We found that red and Algonquin wolves similarly fit as shifted towards coyotes along this two-source admixture cline[11,25], but we cannot rule out greater complexity in their history. While genomic data alone cannot establish an absence of grey wolves at any particular time, our results are consistent with local extinction in North America,

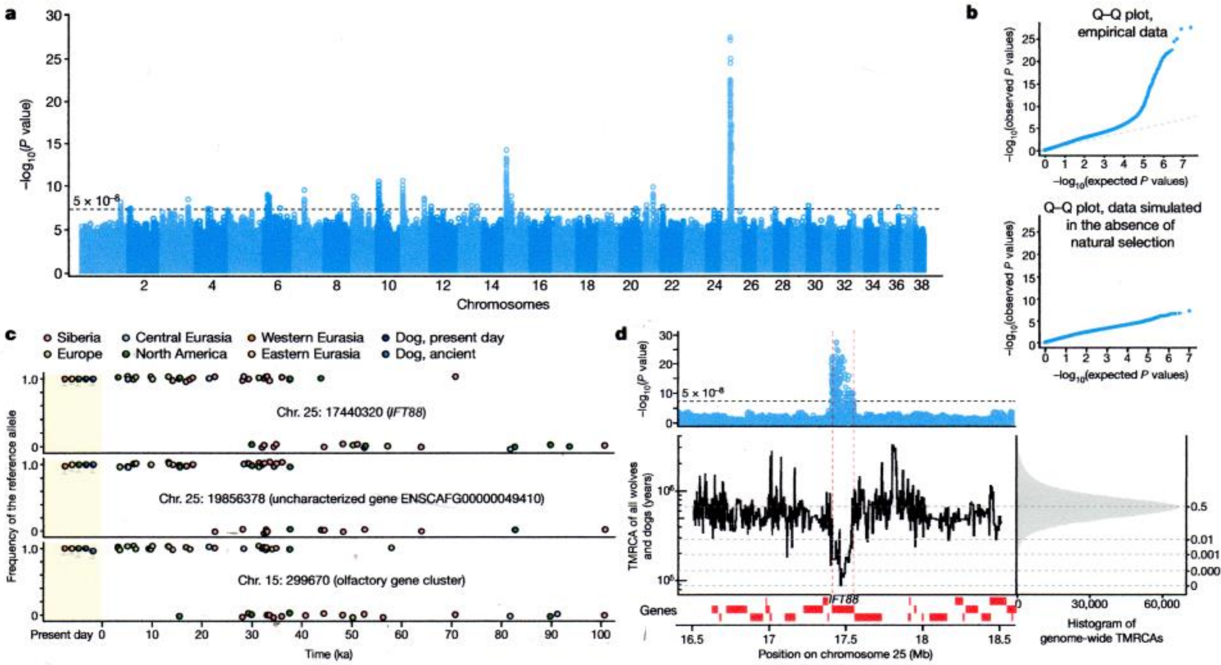

Fig. 3 | Natural selection in the ancient wolf time series. **a**, $-\log_{10}$ (P values) (two sided, not adjusted for multiple comparisons) from linear regression for association between allele frequency and sample age. **b**, Quantile–quantile plot comparing the P values in **a** to those expected under a uniform distribution (top) and likewise for results from a simulated neutrally evolving population (effective population size (N_e) = 50,000) (bottom). **c**, Allele observations in ancient wolves and frequencies in present-day populations for lead variants from the three strongest peaks. Bars denote 95% binomial CIs. **d**, Local P values (from **a**) and TMRCA inferred using Relate on modern wolves and dogs for the region surrounding *IFT88*. The genome-wide histogram (quantiles in grey lines) shows that this locus has the most recent TMRCA in the genome.

for example during the LGM when ice sheets covered the northern half of the continent[30], or, alternatively, an absence of grey wolves south of the ice sheets until after the ice retreated.

High connectivity in the Pleistocene

To understand how differentiated past wolf populations were, we calculated the proportion of genetic variation between rather than within (pairwise F_{ST}; ref.[31]) sets of wolves grouped in space and time. Before the LGM, differentiation even between distant regions was low ($F_{ST} < 3\%$) (Fig. 2c). Early European and North American populations were thus neither very different from each other nor from the Siberian-related wolves that over time replaced much of their ancestry. We also estimated X-chromosome coalescence rates[26], which suggested that any two Pleistocene wolves shared ancestry within ~10,000 years of the date of the older wolf (Fig. 2d and Supplementary Fig. 15). Pervasive gene flow thus prevented deep divergences among wolf populations in the Late Pleistocene.

In the last ~10,000 years (the Holocene), population dynamics were different from those in the Pleistocene, with no evidence for further Siberian gene flow into Europe; instead, European-related ancestry spread eastwards and contributed to modern wolves in China and Siberia (Fig. 2b). Higher levels of differentiation today (F_{ST} of ~10–60%) probably largely reflect population bottlenecks following habitat encroachment and persecution by humans in the last few centuries[32,33], although there is some evidence for increasing differentiation already during the last 20,000 years (Fig. 2c). MSMC2 estimates from present-day genomes suggest widespread effective population size declines in this period (Supplementary Fig. 13), but we found no concurrent decline in individual heterozygosity (Fig. 1d). Combined, this evidence suggests that an overall reduction in gene flow, as shown by the F_{ST} results, rather than a species-wide population decline[21] might have resulted in lower local effective population sizes.

Natural selection over 100,000 years

The strong connectivity observed among Late Pleistocene wolves raises the possibility of species-wide adaptation. Natural selection is typically inferred indirectly from present-day genetic variation, but our 100,000-year (~30,000 generations) dataset enables direct detection of selected alleles. Testing each variant for an association between allele frequency and time across 72 ancient and 68 modern wolves, and applying genomic control[34] to correct for allele frequency variance caused by genetic drift, we found 24 genomic regions with evidence for selection (Fig. 3a and Extended Data Table 1). We confirmed the robustness of our method to demographic history by applying it to data simulated in the absence of selection, finding no false positives (Fig. 3b and Supplementary Fig.17).

The geographical origin of the present-day dog lineage Canis familiaris has remained controversial.

The strongest signal was observed on chromosome 25, where variants closely overlapping the gene *IFT88* rose rapidly from close to 0% to 100% in frequency 40–30 ka and are still fixed in wolves and dogs today (Fig. 3c). Genealogical inference on modern wolves[35,36] further showed that *IFT88* had the youngest time to the most recent common ancestor (TMRCA) (~70,000 years) in the genome (Fig. 3d). Disruption of *IFT88* leads to craniofacial development defects in mice and to cleft lip and palate in humans[37]. If future fossil studies reveal rapid craniodental change in this time period, this could implicate the *IFT88* sweep as a driver, potentially in response to prey availability changes. But it is also possible that selection targeted unknown non-skeletal traits associated with *IFT88* variation. The second strongest signal in the genome was 2.5 Mb downstream of *IFT88*, where allele frequencies shifted in a similar timeframe 40–20 ka (Fig. 3c), but it is not clear whether this region could be involved in long-range regulation of *IFT88*.

Three regions with evidence for selection overlap olfactory receptor genes, with variants on chromosome 15 increasing in frequency from close to 0% to 100% 45–25 ka (Fig. 3c), suggesting that olfaction was a recurrent target of adaptation in wolves. Most of the detected selection episodes occurred before the divergence of dogs, and dogs share the selected alleles (Supplementary Fig. 18). However, variants in *YME1L1* increased in frequency from <5% to 50–70% in wolves from 20–0 ka but are not observed in dogs. A region on chromosome 10, where variation among dogs is associated with body size, drop ears and other traits38–40, was under recent selection in specific dog breeds[41], and we found that it was also selected in wolves in the last 20,000 years. Although it was not detected in our selection scan, the K^B deletion that underlies black fur[42] was identified in a 14,000-year-old wolf from Tumat, Siberia (Supplementary Fig. 19). This deletion probably introgressed into wolves from dogs in the Holocene[42], but our result also raises the possibility that its ultimate origin could have been in wild Pleistocene wolves.

Dog ancestry has eastern wolf affinities

We found that dogs share more genetic drift with wolves that lived after 28 ka than with those that lived before this time, which implies that the progenitors of dogs were genetically connected to other wolves at least until 28 ka (Fig. 1c and Extended Data Fig. 1b). A divergence around this time is also consistent with our MSMC2 analyses of X chromosomes (Supplementary Fig. 16). However, until the nature of the divergence process is better understood, it cannot be ruled out that domestication had started before this point.

The geographical origin of the present-day dog lineage Canis familiaris has remained controversial. Genetic studies have argued that wolves in East Asia[1,2], Central Asia[4], the Middle East[6], Europe[5], Siberia[16], or both eastern and western Eurasia independently[3], contributed ancestry to early dogs, whereas others have been consistent with a single, but geographically unknown, progenitor population[8,9]. Given our finding that part of wolf population structure is older than the likely time of dog domestication, we can expect dogs to be genetically closer to some ancient wolves than to others. To reduce the effects of gene flow since the emergence of dogs, we performed a PCA on wolves and dogs from the last 25,000 years, based on f_4-statistics quantifying their relationships only to wolves living before 28 ka (that is, before the LGM), and found that dogs showed relationship profiles similar to those of Siberian wolves from 23–13 ka (Fig. 4a, Extended Data Fig. 2 and Methods).

Direct f_4-tests also showed that dogs are closer to Siberian than to European wolves from this period (Fig. 4b and Extended Data Fig. 3). European wolves postdating 28 ka have an affinity to pre-LGM European wolves, reflecting the persistence of deep west Eurasian wolf ancestry (Fig. 2a). The absence of such western affinities in dogs suggests that they did not originate from the European wolf populations sampled here.

While the north-eastern Siberian wolves from 23–13 ka display the greatest overall affinity to dogs, we found that they were not the immediate ancestors of dogs. When a broad set of ancient wolves were tested as candidate sources using qpWave/qpAdm[43], all single-source models, including one using an 18,000-year-old Siberian wolf, were strongly rejected for all dogs studied ($P < 1 \times 10^{-6}$) (Methods and Fig. 4c). However, a model featuring the Siberian wolf and 10–20% ancestry from a component approximated by the outgroup dhole fit dogs such as the 9,500-year-old Siberian Zhokhov[17] individual ($P = 0.29$) (Fig. 4c). Although it uses an outgroup species, this two-source model does not necessarily imply admixture from two distinct populations or species. Instead, it could reflect dogs being derived from some local wolf ancestry that is unsampled and to some extent divergent from the available ancient wolves (Extended Data Fig. 4). Validating this interpretation, we found that recent European wolves, which have a small degree of deep, local European ancestry (Fig. 2a), obtain results very similar to those for dogs, requiring 10–20% unsampled ancestry, if only Siberian wolves were available as sources (Supplementary Fig. 11 and Supplementary Information). We therefore interpret the results for dogs as similarly reflecting some unsampled wolf ancestry that is not fully represented by the ancient Siberian wolves sampled here. This unsampled ancestry appears to have retained a partial degree of differentiation from the sampled ancient wolves since before 100 ka (Supplementary Fig. 12), and our results imply that it probably lived outside the regions of Europe, north-eastern Siberia and North America sampled here. .

...a model featuring the Siberian wolf and 10–20% ancestry from a component approximated by the outgroup dhole fit dogs such as the 9,500-year-old Siberian Zhokhov[17] individual...

The results obtained for the Zhokhov dog also applied to ancient dogs from Lake Baikal, North America and north-eastern Europe (a 10,900-year-old Karelian dog) and to modern New Guinea singing dogs. As a group, qpWave could fit these dogs as having originated from a single 'stream' of ancient wolf diversity, in an approach not requiring a proximate source (Extended Data Table 2). This result shows that ancient wolf genomes can circumvent the complexities of more recent processes, as the same models were rejected when modern wolves were used as sources instead (Extended Data Table 2), probably owing to gene flow from dogs into wolves[8].

Recent admixture and population changes thus complicate analyses of modern wolves. Even so, if wolf population structure has not been completely reshaped since the time of dog domestication, it is possible that part of the ancestry of the dog progenitors could still be represented and detectable among wolves today, even though the past geographical location of that ancestry would be unknown. We tested this in two ways. First, we projected dogs onto a PCA plot constructed using modern wolf genotypes, and found that they projected closer to wolves from China, Mongolia and the Altai than to wolves from Yakutia (Extended Data Fig. 5). Second, we extended our qpAdm analyses to modern wolf sources, and found that some Chinese wolves provided better fits than the 18,000-year-old Siberian wolf and could serve as single sources of Zhokhov dog ancestry without the need for an unsampled ancestry component (Extended Data Fig. 6). These results could be taken to support an eastern or central Eurasian dog origin outside of north-eastern Siberia, but we cannot draw firm geographical conclusions in the absence of ancient wolf genomes from these and other candidate regions.

A second source for western dog ancestry

We extended our analyses to a global set of ancient and modern dogs, to test for any ancestry contributions from additional, genetically distinct wolf progenitors. The strongest evidence for multiple progenitors would be if some dogs had different affinities to wolves that predate domestication, as such wolves cannot be affected by dog gene flow. Applying this rationale, we found that ancient Near Eastern and present-day African dogs, and to a lesser degree European dogs, are shifted towards western Eurasian wolves in the f_4-statistics PCA based on relationships to wolves that predate the LGM (Fig. 4a). This cline recapitulates the primary axis of population structure within dogs (between ancient Near Eastern and eastern Eurasian dogs[8]) (Fig. 4b), even when wolves from the last

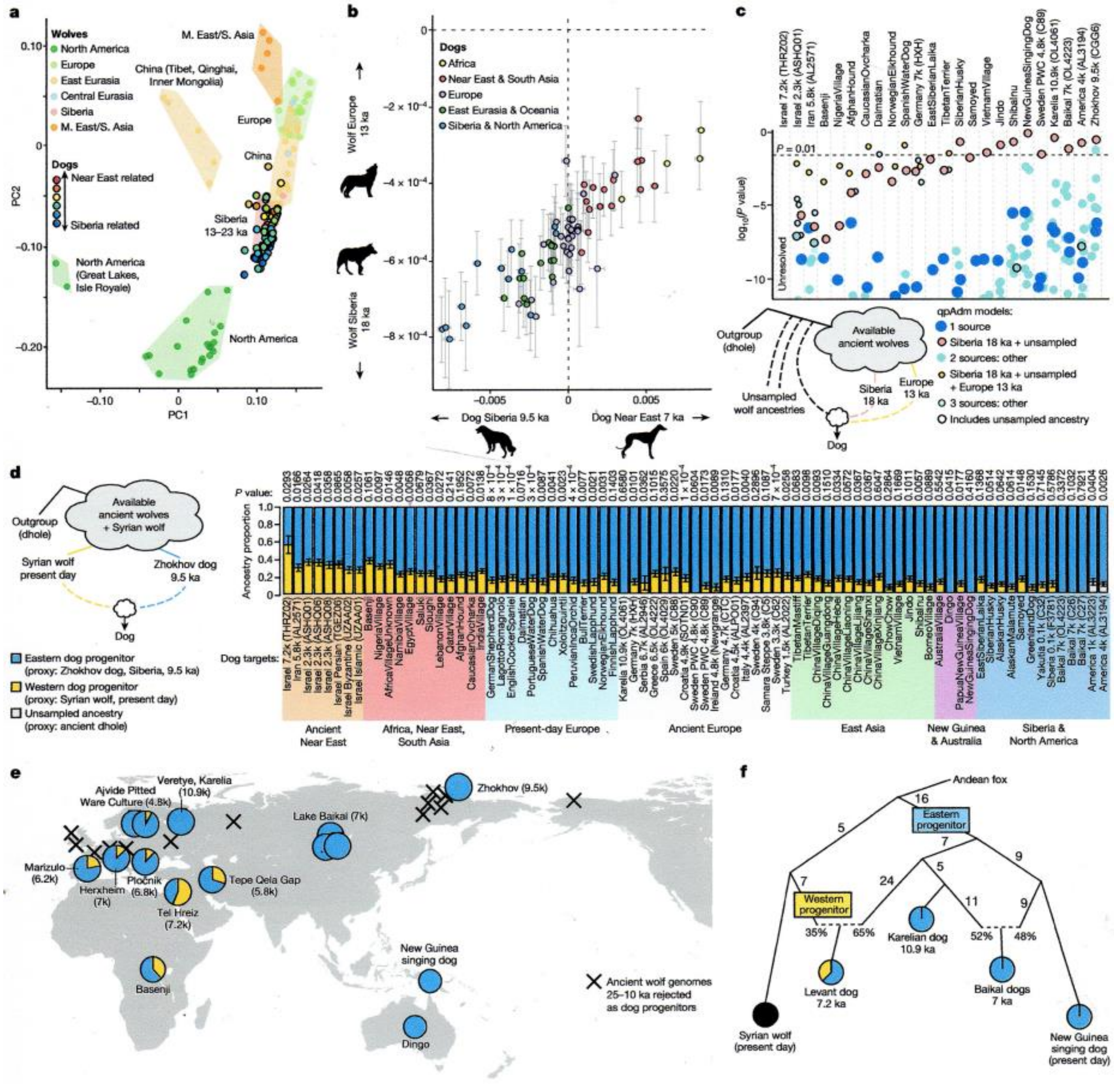

Fig. 4 | The ancestry of dogs. a, PCA on post-LGM and present-day wolves (X), based on f_4-statistics only of the form f_4(X,A;B,C), where A, B and C are any of 21 wolves predating 28 ka. Dogs are projected, and coloured by f_4(AndeanFox,X; Zhokhov dog 9.5 ka,Tel Hreiz dog 7.2 ka). **b**, For dogs (X), f_4(AndeanFox,X; Zhokhov dog 9.5 ka,Tel Hreiz dog 7.2 ka) horizontally against f_4(AndeanFox,X; Belaya Gora wolf 18 ka,Hohle Fels wolf 13 ka) vertically (Pearson's **r** = 0.86, $P = 3 \times 10^{-23}$). Bars denote ±1 standard error estimated from a block jackknife. Silhouettes from phylopic.org. **c**, $\log_{10}$(P values) for qpAdm models fit to dog targets, where a low P value means the model can be rejected. An ancient dhole was used to represent unsampled, divergent ancestry; models including this source have black outlines. Points are jittered horizontally to avoid overlap. **d**, qpAdm ancestry proportions for dogs, using the Zhokhov (9.5 ka) dog and a present-day Syrian wolf as proxies for eastern and western dog progenitor ancestry, respectively. Bars denote ±1 standard error estimated from a block jackknife. **e**, Map of early and relevant later dogs and their ancestry proportions as in **d**. Black crosses indicate the locations of wolves from 25–10 ka that can be rejected as dog progenitors. Base map from the mapdata R package. k, thousand years. **f**, Admixture graph model of major dog lineage relationships, fit by qpGraph with no outlier f-statistics. Edge lengths are in units of F_{ST} (×1,000).

28,000 years are excluded (Supplementary Fig. 20). The dog ancestry cline thus at least in part reflects wolf ancestry differences that predate the likely domestication timeframe. Testing the PCA observations explicitly, qpWave strongly rejected a single wolf progenitor when including Near Eastern dogs ($P < 10^{-4}$) (Extended Data Table 2). The best-fitting qpAdm models for these dogs instead involved a source related to ancient European wolves, in addition to the ancestry found in the Zhokhov dog (Fig. 4c).

To test whether the sampled ancient European wolves could be the actual source of this second component of dog ancestry, we tested qpAdm models featuring the Siberian Zhokhov dog as one source—representing the eastern-related dog ancestry—and an ancient European wolf as a second source. These models did not fit Near Eastern and African dogs unless a third, outgroup component was also included to represent unsampled, divergent ancestry (Supplementary Fig. 21), meaning that European wolves are not a match for the missing ancestry. Expanding to all post-LGM and present-day wolves, only present-day wolves from Syria, Israel, Iran and India achieved good fits (Extended Data Fig. 7). In line with a source from this part of the world, when projected onto present-day wolf structure, Near Eastern and African dogs are shifted towards Caucasian and Near Eastern rather than European wolves (Extended Data Fig. 5). Using a present-day Syrian wolf as a source, we estimated 56% (standard error, 10%) Near Eastern-related wolf ancestry in the earliest available dog (7.2 ka) from the Levant, 37% (standard error, 3.5%) in the African Basenji breed and 5–25% in Neolithic and later European dogs (Fig. 4d). While the evidence of dual ancestry is based on ancient wolves that predate domestication and are thus unaffected by potential later gene flow, these exact estimates could be inflated if there is dog admixture in the Syrian wolf.

Our results instead suggest that a balance of eastern and western wolf ancestries in central Asia (Fig. 2b) causes relative symmetry to the eastern and western dog ancestries.

Next, we exhaustively tested admixture graph models of dog relationships, allowing up to two admixture events among four dog populations and the Syrian wolf. We obtained results consistent with the qpAdm inferences, as a single graph featuring Syrian wolf admixture into early Near Eastern dogs fit the data (Fig. 4f), with a separate dog lineage giving rise to early Karelian and eastern dogs. In this graph, the Karelian dog is most closely related to the 'eastern' source that also contributed ancestry to the early Near Eastern dog.

The widespread ancestry asymmetries observed between wolves and dogs today have been interpreted as reflecting recent, local admixture[8,9]. Our finding that dogs have variable proportions of two distinct components of wolf ancestry may provide a unifying explanation for many of these asymmetries. For example, previous studies have explained an affinity between Pleistocene Siberian wolves and Arctic dogs by suggesting admixture in the latter[13,17]. The dual ancestry model can probably explain this asymmetry without such admixture, with the Arctic dogs instead having less of the western component (Supplementary Fig. 22). Conversely, higher levels of the western component in Near Eastern and African dogs probably explains at least part of their previously observed affinity to Near Eastern wolves[8,9,10]. An observation that wolves in Xinjiang, central Asia, display no asymmetries to different dogs was interpreted as suggesting that other asymmetries are primarily due to dog-to-wolf gene flow[8]. Our results instead suggest that a balance of eastern and western wolf ancestries in central Asia (Fig. 2b) causes relative symmetry to the eastern and western dog ancestries. The Xinjiang wolves are thus not evidence against the dual ancestry model.

Conclusion

We show that wolf populations were genetically connected throughout the Late Pleistocene, probably because of the high mobility of wolves in an open landscape[44]. The LGM did not necessarily correspond to an unprecedented time of change for the interconnected population of wolves, which might provide a clue to their perseverance when other northern Eurasian carnivores became extinct. Furthermore, the reason Pleistocene wolves appear basal to present-day diversity is not that they went extinct[13,14], but that continued gene flow homogenized later ancestry. Our finding that several selected alleles quickly reached fixation shows that adaptations spread to the whole population of Pleistocene wolves, a process that might have contributed to the survival of the species. At the same time, our results show that such rapid species-wide selective sweeps occurred only a few times over the last ~100,000 years.

Our results also provide insights into long-standing questions on the origin of dogs. First, dogs and present-day Eurasian wolves have been thought to be reciprocally monophyletic lineages[9]. We find that, overall, dogs are closer to eastern Eurasian wolves. Second, because no modern wolves are a good match for dog ancestry, the source population has been assumed to be extinct. Our results imply that this is not necessarily the case, as continued homogenization of wolf ancestry could have obscured earlier relationships to dogs. Third, it has been unclear whether more than one wolf population contributed to early and present-day dogs[3,7,8,9]. We find that an eastern Eurasian-related source, ‘eastern dog progenitor’, appears to have contributed ~100% of the ancestry of early dogs in Siberia, the Americas, East Asia and north-eastern Europe. On top of this, a western Eurasian-related source, ‘western dog progenitor’, contributed 20–60% of the ancestry of early Near Eastern and African dogs and 5–25% of the ancestry of Neolithic and later European dogs. The western ancestry subsequently spread worldwide with, for example, the prehistoric expansion of agriculture in western Eurasia[8] and the colonial era expansion of European dogs.

...we demonstrate that ancestry from at least two wolf populations is extant and ubiquitous in modern dogs, and is the major determinant of dog population structure today.

A previous study proposed that the earlier archaeological appearance of dogs in western and eastern Eurasia than in central Eurasia was due to independent domestication of western and eastern wolves, but that ancestry from the former was extinct or nearly extinct in present-day dogs[3]. Our results support the notion of two distinct ancestors of dogs but differ from this previous hypothesis. First, we demonstrate that ancestry from at least two wolf populations is extant and ubiquitous in modern dogs, and is the major determinant of dog population structure today. Second, we are able to reject Pleistocene European wolves related to those sampled here as a source for the C. familiaris lineage. Third, the previous study suggested that an Irish Neolithic dog had more ancestry from the western domestication than later dogs[3], whereas we find that this dog had less ancestry from the western progenitor identified here than present-day European dogs (Fig. 4d). The lack of genomes from the earliest dogs in Europe, however, means that future studies may reveal them to have arisen from an independent domestication process that did not contribute substantially to later populations[3,45,46]

Our results are consistent with two scenarios: (1) independent domestication of the eastern and western progenitors that later merged in the west or (2) single domestication of the eastern progenitor, followed by admixture from western wolves as dogs arrived into southwestern Eurasia. Our results cannot distinguish between these scenarios, but, in either case, the merging or admixture must have occurred before 7.2 ka, the age of the oldest available Near Eastern dog genome[8]. A single domestication of the western progenitor followed by admixture from eastern wolves does not seem compatible with our results, as it would require replacement of 100% of the ancestry of eastern dogs. If dogs of 100% western progenitor ancestry were discovered, for example, in the earliest Near Eastern[47] or European1[5] contexts, this would imply independent domestication. Alternatively, the first dogs in the west could be of eastern progenitor ancestry, similar to the Karelian dog from 10.9 ka, in line with a single domestication process. Additional ancient wolf genomes, including from outside the regions covered here, where DNA often preserves less well, will also be necessary to further identify the wolf progenitors of dogs.

Online content

Any methods, additional references, Nature Research reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at https://doi.org/10.1038/s41586-022-04824-9.

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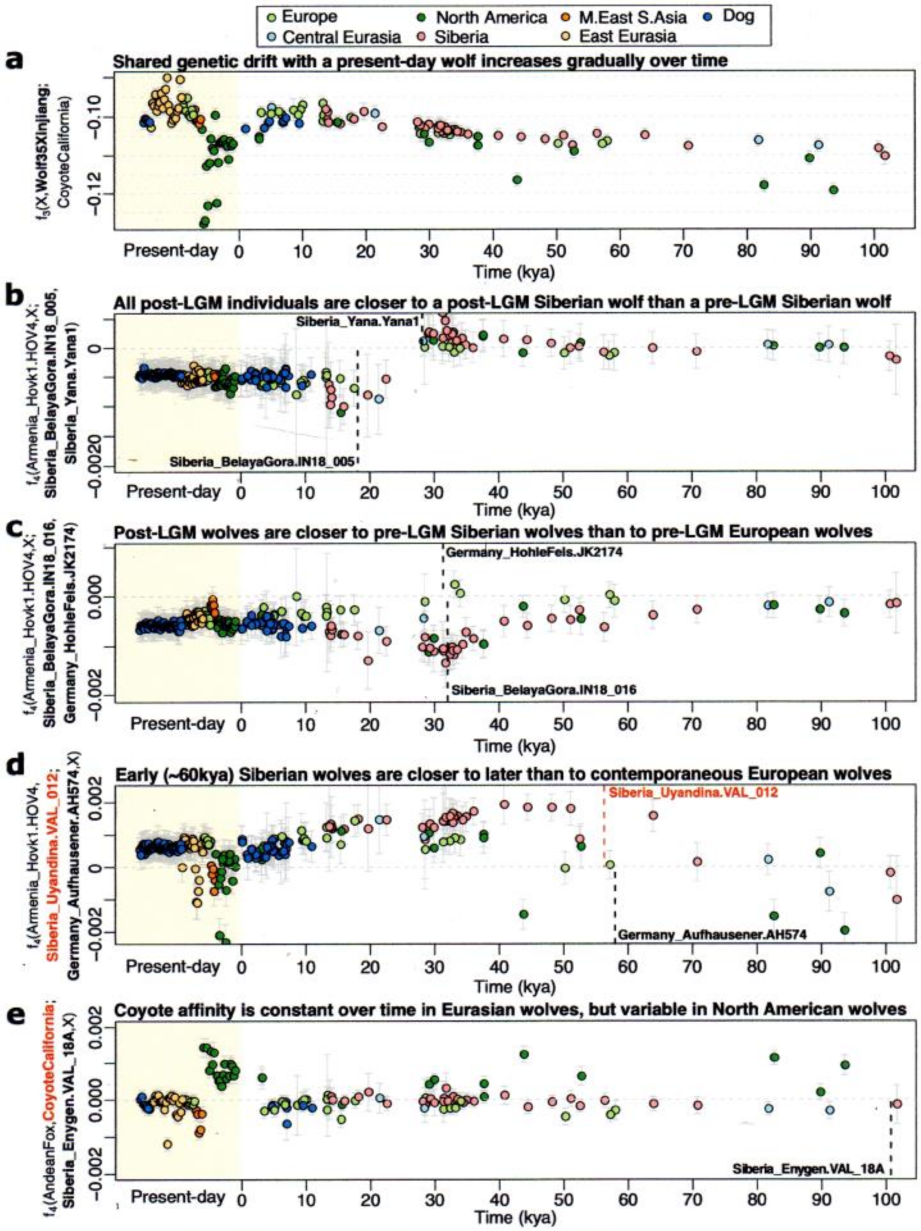
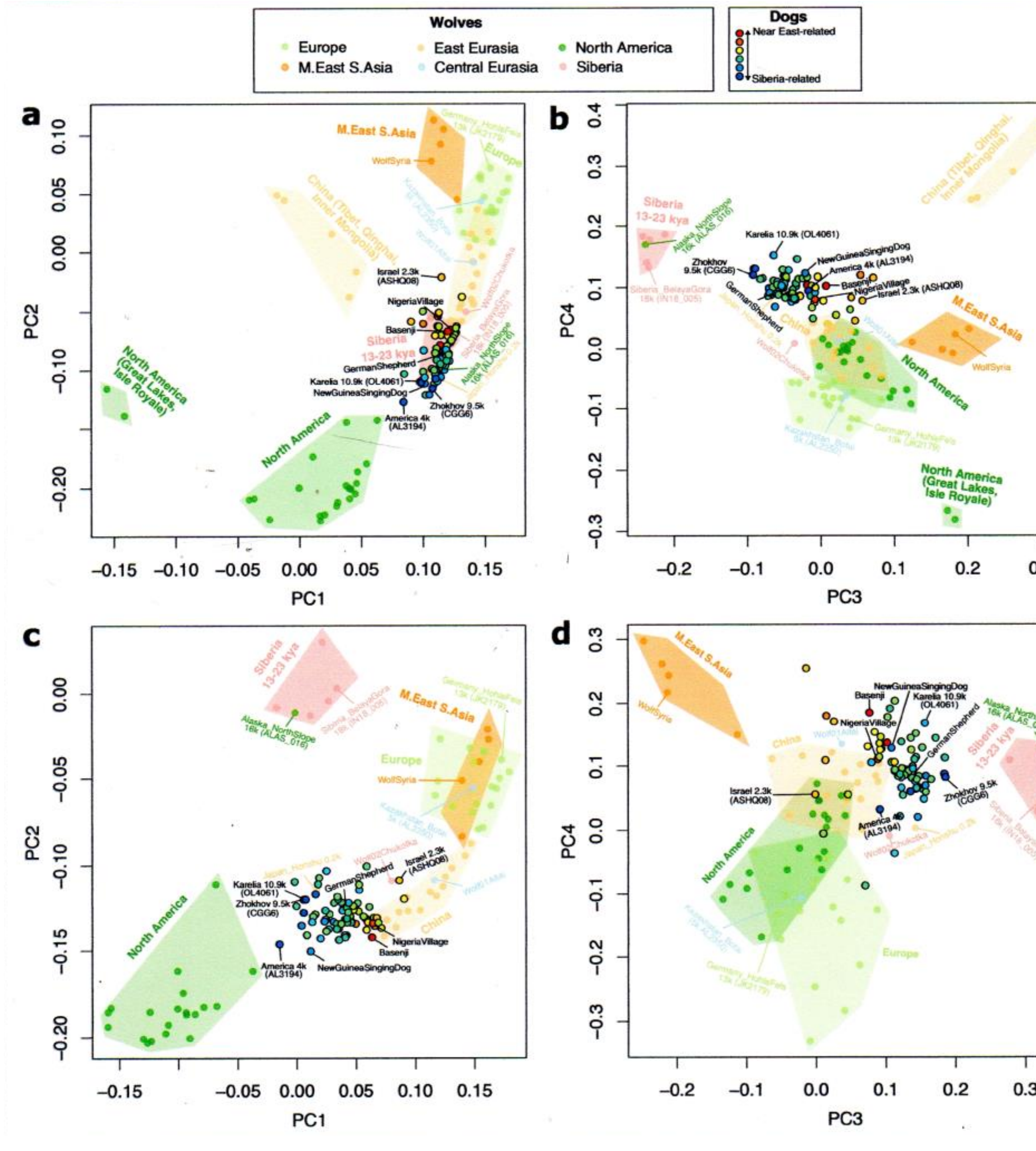
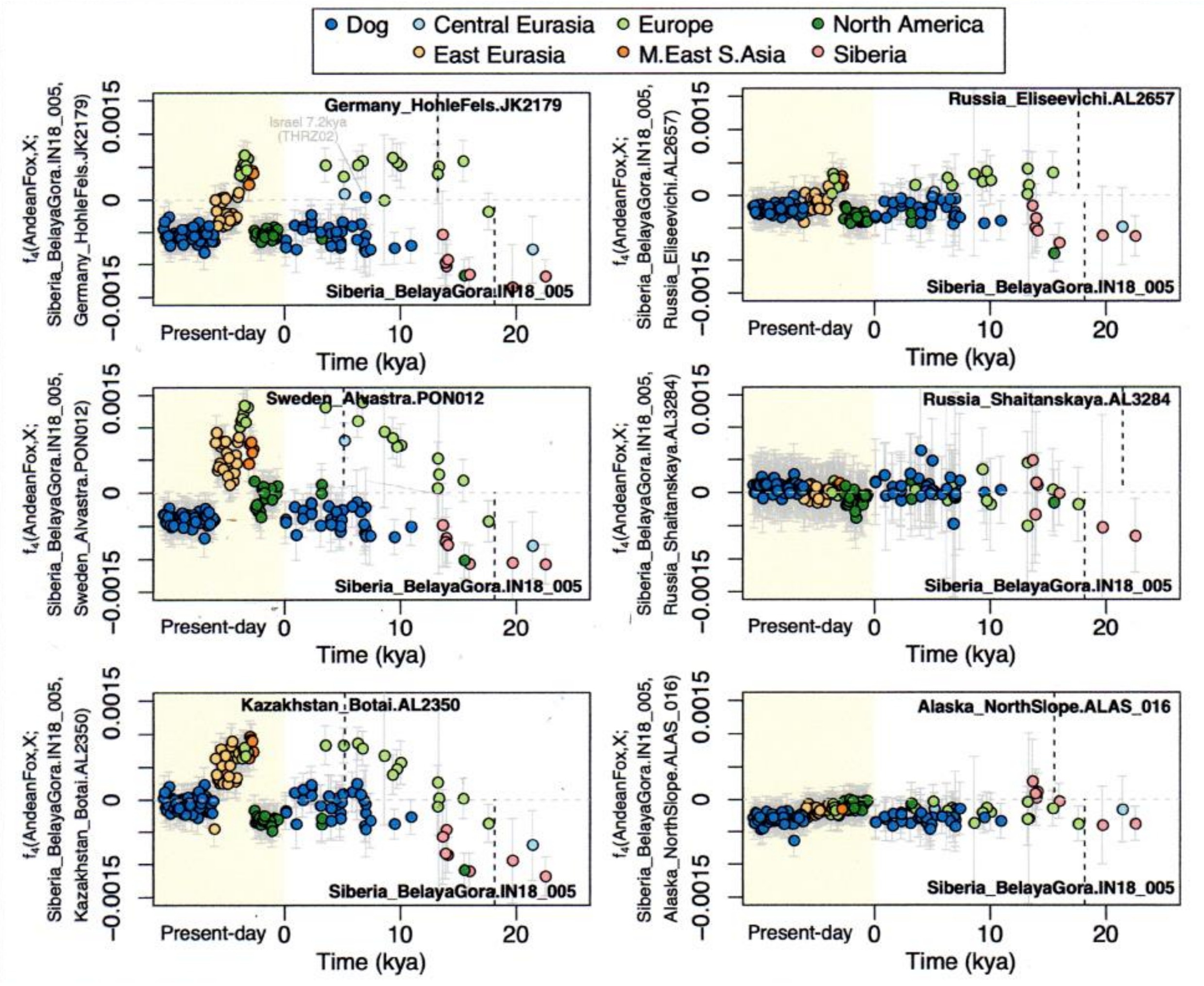


Extended Data Fig. 1 |*f*-statistics informing on wolf population history. Bars denote ±1.96 standard errors for f_3-statistics, and ±3 standard errors for f_4-statistics, estimated from a block jackknife. a) Outgroup f_3-statistics quantifying shared genetic drift with a present-day wolf (Fig. S3). b) f_4-statistics contrasting affinities to a pre-LGM and a post-LGM Siberian wolf (Fig. S4). c) f_4-statistics contrasting affinities to a Siberian and a European pre-LGM wolf (Fig. S6). d) f_4-statistics quantifying whether a ~60 ky old Siberian wolf is closer to a contemporaneous European wolf or other individuals (Fig. S7). e) f_4-statistics quantifying whether a coyote is closer to a ~100ky old Siberian wolf or later individuals.

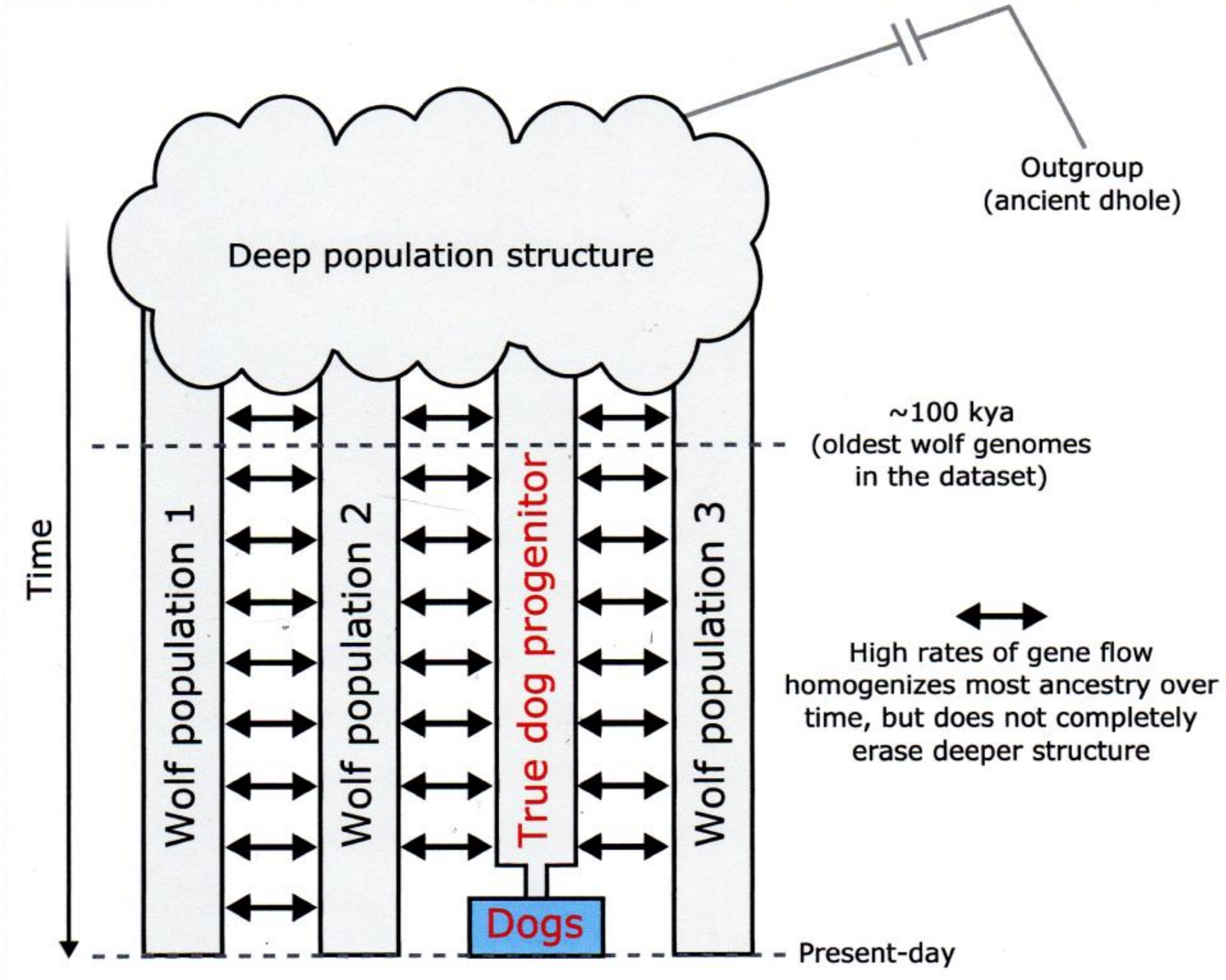


Extended Data Fig. 2 | Placing dogs into wolf diversity in a 'pre-LGM f_4 PCA'.

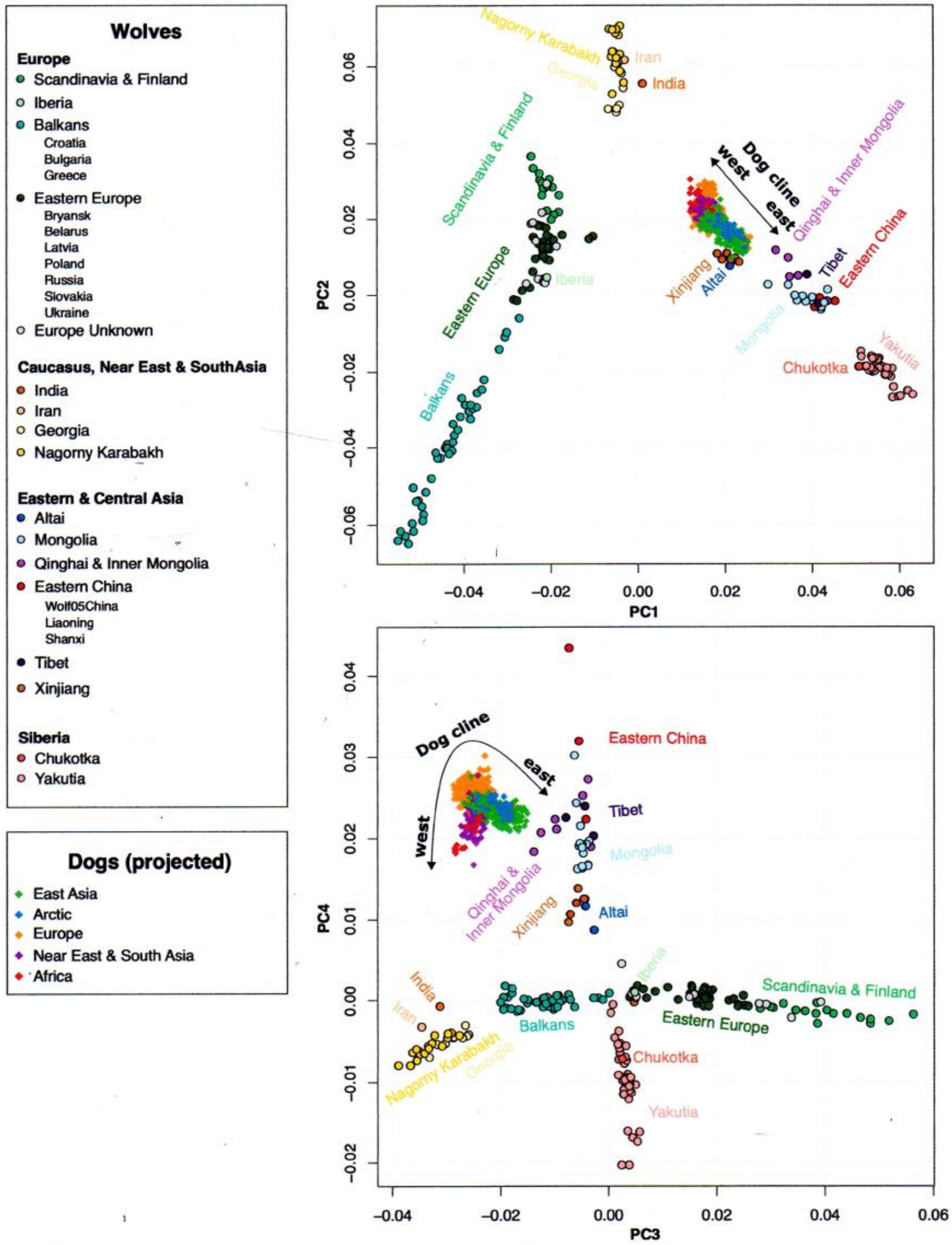
PCA on wolves that lived after 25 ka (including present-day), based on profiles of f_4-statistics only of the form $f_4(X,A;B,C)$, where A, B, and C are wolves that lived prior to 28 kya. Dogs are projected. Dogs are coloured according to the f_4-statistic $f_4(AndeanFox,X;Zhokhov\ dog\ 9.5ka,Tel\ Hreiz\ dog\ 7.2ka)$, with negative values going towards blue and positive values towards red. A few wolves (in colour) and dogs (in black) of particular interests are indicated with text labels. a) PC1 vs PC2 with the full set of wolves. b) PC3 vs PC4 with the full set of wolves. c) PC1 vs PC2 with western Chinese and North American outlier wolves removed. d) PC3 vs PC4 with western Chinese and North American outlier wolves removed.



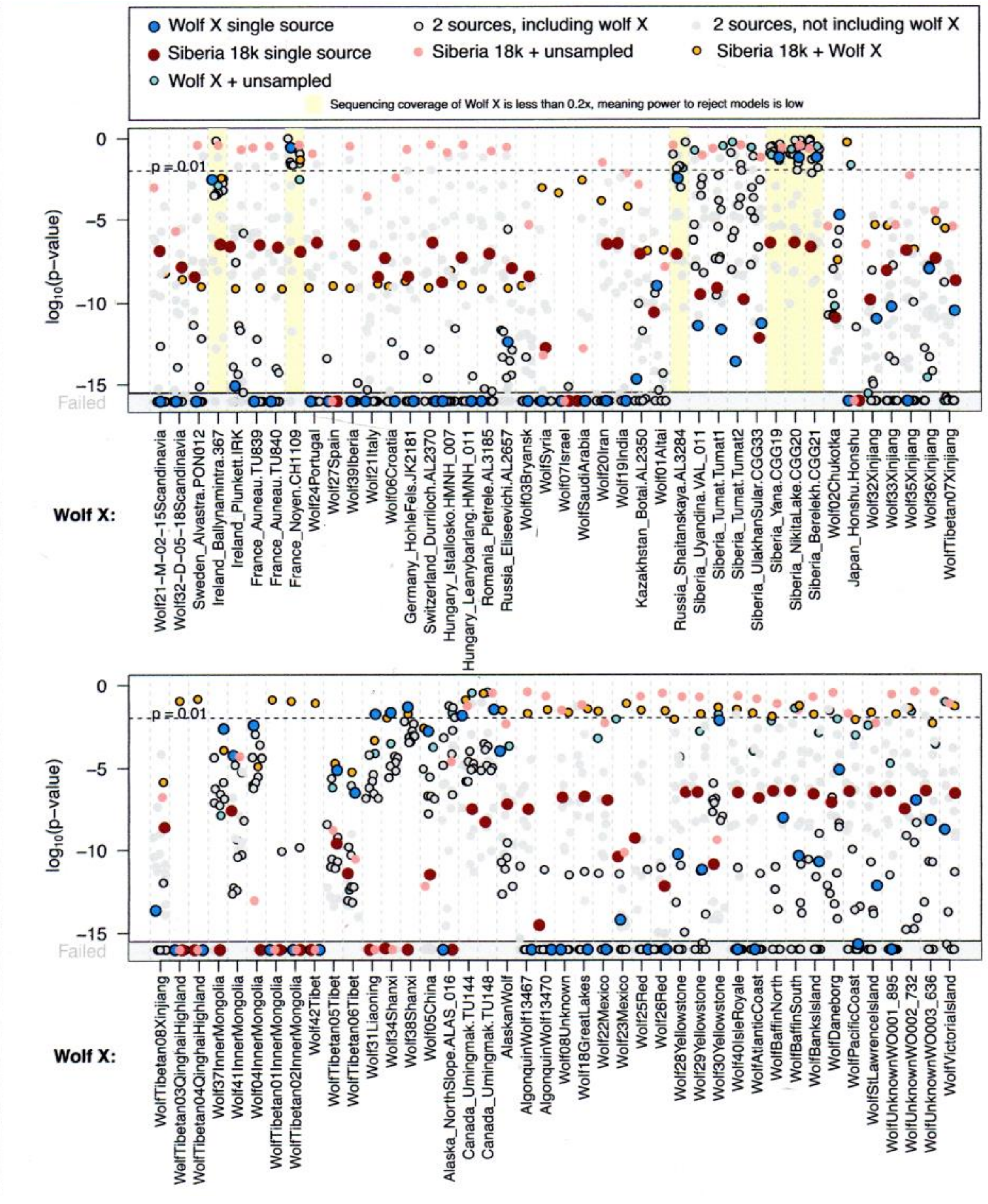
Extended Data Fig. 3 | Affinities of dogs to ancient wolves. a) f_4-statistics of the form f_4*(AndeanFox,X;wolf A,wolf B)*, quantifying for all individuals X whether they share more drift with wolf A or wolf B. The ages of A and B are indicated with dashed lines, with positive values indicating affinity to the upper individual and negative values indicating affinity to the lower individual. Bars denote ±3 standard errors estimated from a block jackknife.



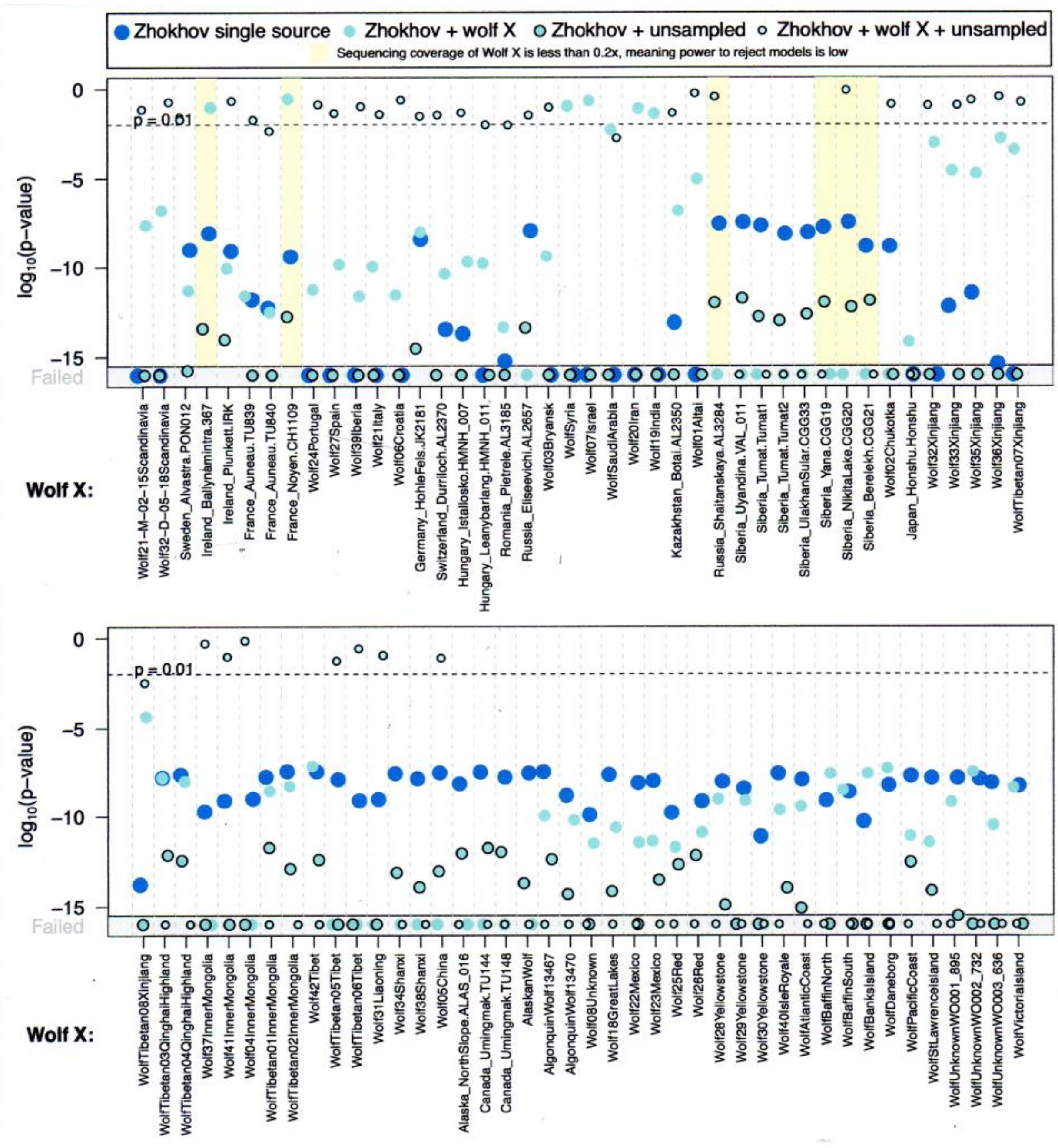
Extended Data Fig. 4 | A schematic model of how deep population structure could explain why dogs require ancestry from an outgroup population in qpAdm analyses. Under this model, there is deep population structure between different wolf populations, including the wolf population that becomes the progenitor of dogs. High rates of gene flow over time largely homogenises the ancestry of all populations, but it does not completely erase the deep structure. If the true dog progenitor population is not sampled, a single-source qpAdm model involving one of the sampled wolf populations will not fit dog ancestry, because dogs do not share all of the genetic drift that has occurred in the history of the sampled population. But if an outgroup population is included as a source in qpAdm, this can account for the 'missing' deep ancestry in dogs, and therefore result in a model that fits dog ancestry.



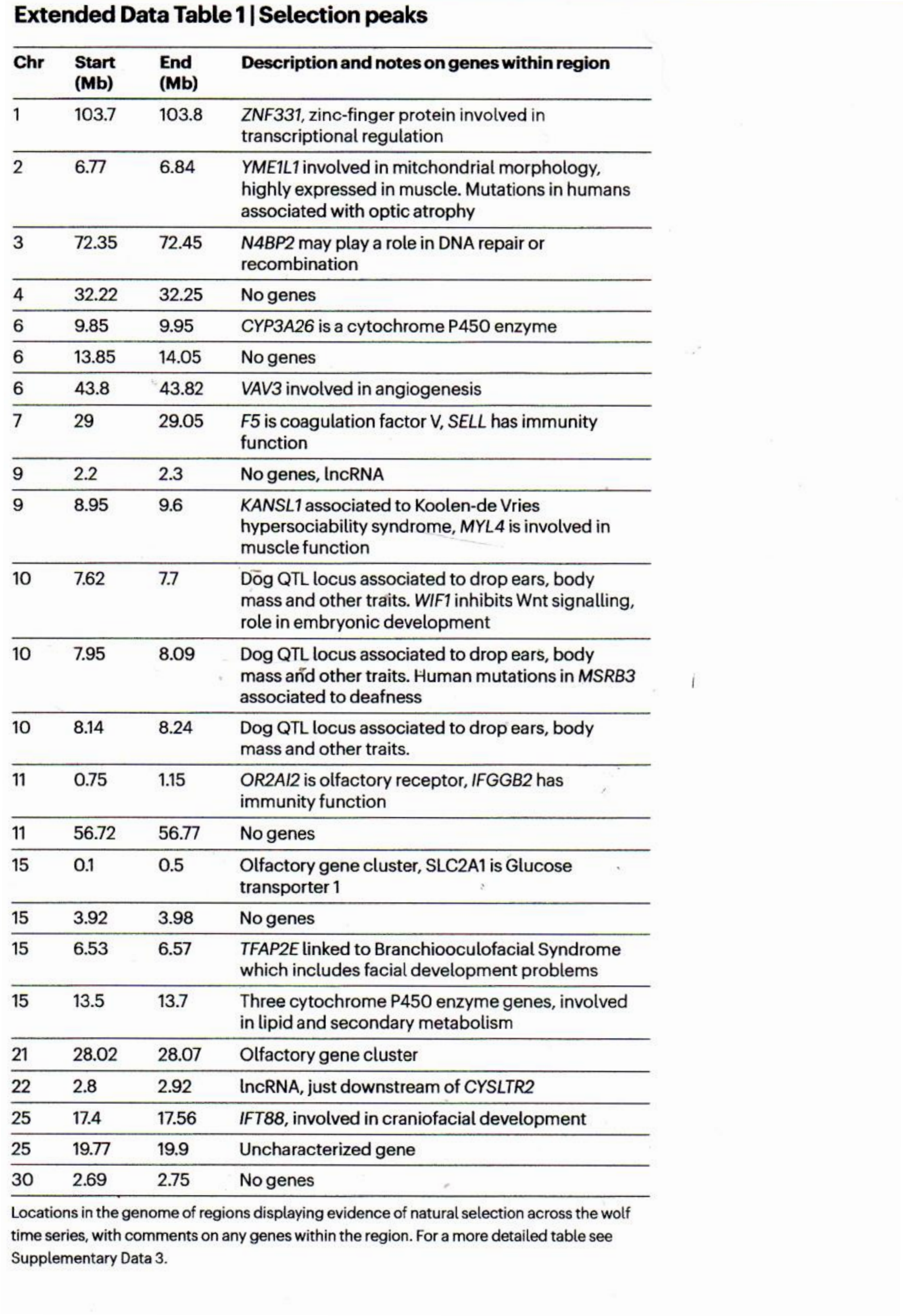
Extended Data Fig. 5 | Projecting dogs onto present-day wolf population structure. Principal components analyses performed only on modern wolves, with modern dogs projected.



Extended Data Fig. 6 | "Ocean plot" searching for the best available wolf match for the ancestry of eastern dogs. With the Siberian Zhokhov dog (9.5k BP) as the target, each candidate wolf X was added in turn into the rotating qpAdm analysis. When X is not part of the sources, it is placed in the reference list. Models placed within the gray space labelled "Failed" have p-values fall below the lower limit of the plot.



Extended Data Fig. 7 | "Ocean plot" searching for the best available wolf match for the west Eurasian wolf-related ancestry in western dogs. With the African Basenji dog as a target, all available post-LGM and present-day wolf genomes X are tested as sources combined with the 9.5k-year old Siberian Zhokhov dog, which is assumed to represent a baseline for the Eastern-related dog progenitor ancestry. When X is not part of the sources, it is placed in the reference list. If a target has a model with p > 0.01, models with a larger number of sources are not plotted. Only four individuals achieve good fits in the two-source model (Zhokhov + X): WolfSyria, Wolf07Israel, Wolf20Iran and Wolf19India. For other individuals, including ancient and present day European wolves, the two-source model can be rejected, and a three-source model with an unsampled ancestry component (Zhokhov + X + unsampled) is needed to fit the data.



Extended Data Table 1 | Selection peaks

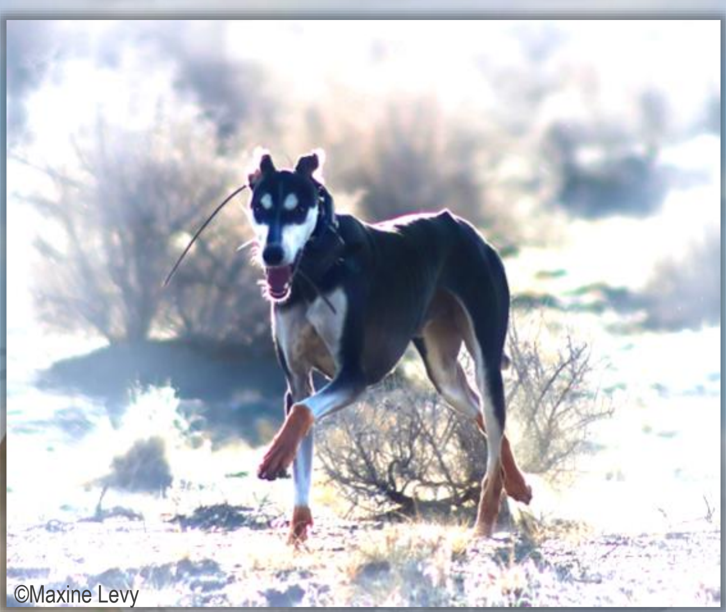
Chr	Start (Mb)	End (Mb)	Description and notes on genes within region
1	103.7	103.8	*ZNF331*, zinc-finger protein involved in transcriptional regulation
2	6.77	6.84	*YME1L1* involved in mitchondrial morphology, highly expressed in muscle. Mutations in humans associated with optic atrophy
3	72.35	72.45	*N4BP2* may play a role in DNA repair or recombination
4	32.22	32.25	No genes
6	9.85	9.95	*CYP3A26* is a cytochrome P450 enzyme
6	13.85	14.05	No genes
6	43.8	43.82	*VAV3* involved in angiogenesis
7	29	29.05	*F5* is coagulation factor V, *SELL* has immunity function
9	2.2	2.3	No genes, lncRNA
9	8.95	9.6	*KANSL1* associated to Koolen-de Vries hypersociability syndrome, *MYL4* is involved in muscle function
10	7.62	7.7	Dog QTL locus associated to drop ears, body mass and other traits. *WIF1* inhibits Wnt signalling, role in embryonic development
10	7.95	8.09	Dog QTL locus associated to drop ears, body mass and other traits. Human mutations in *MSRB3* associated to deafness
10	8.14	8.24	Dog QTL locus associated to drop ears, body mass and other traits.
11	0.75	1.15	*OR2AI2* is olfactory receptor, *IFGGB2* has immunity function
11	56.72	56.77	No genes
15	0.1	0.5	Olfactory gene cluster, SLC2A1 is Glucose transporter 1
15	3.92	3.98	No genes
15	6.53	6.57	*TFAP2E* linked to Branchiooculofacial Syndrome which includes facial development problems
15	13.5	13.7	Three cytochrome P450 enzyme genes, involved in lipid and secondary metabolism
21	28.02	28.07	Olfactory gene cluster
22	2.8	2.92	lncRNA, just downstream of *CYSLTR2*
25	17.4	17.56	*IFT88*, involved in craniofacial development
25	19.77	19.9	Uncharacterized gene
30	2.69	2.75	No genes

Locations in the genome of regions displaying evidence of natural selection across the wolf time series, with comments on any genes within the region. For a more detailed table see Supplementary Data 3.

Extended Data Table 2 | qpWave tests of dog cladality

Target sets	**Individuals**				
Eastern dogs	Karelia_Veretye.OL4061, Zhokhov.CGG6, PortauChoix.AL3194, Baikal.OL4223, NewGuineaSingingDog				
Southwestern dogs	Israel.THRZ02, Iran.AL2571, Israel.ASHQ01, Basenji				
Ancient reference sets	**Individuals**				
Ancient small (n=7)	Siberia_UlakhanSular.LOW008, Germany_Aufhausener.AH575, Germany_HohleFels.JK2183, Siberia_BungeToll.CGG29, Siberia_BelayaGora.IN18_016, Yukon_QuartzCreek.SC19.MCJ010, Altai_Razboinichya.AL2744				
Ancient large (n=25)	Germany_Aufhausener.AH574, Germany_Aufhausener.AH577, Siberia_Yana.CGG27, Siberia_Badyarikha.CGG34, Alaska_Fairbanks.JAL385, Alaska_Fairbanks.JAL48, Alaska_Fairbanks.JAL65, Alaska_Fairbanks.JAL69, Yukon_HunkerCreek.SC19.MCJ017, Germany_HohleFels.JK2174, Germany_HohleFels.JK2175, Germany_HohleFels.JK2183, Siberia_BungeToll.LOW003, Siberia_UlakhanSular.LOW008, Czechia_Predmosti.PDM100, Alaska_LillianCreek.ALAS_024, Siberia_Tirekhtyakh.VAL_033, Siberia_Badyarikha.VAL_008, Siberia_Ogorokha.VAL_050, Siberia_BelayaGora.IN18_016, Siberia_Tirekhtyakh.CGG32				
Target	**Reference set**	**p rank 0**	**p rank 1**	**p rank 2**	
Eastern dogs	Ancient small	0.3667	0.9566	0.9992	
Southwestern dogs	Ancient small	0.0229	0.8850	0.8474	
Eastern+Southwestern	Ancient small	6.1E-05	0.1900	0.7610	
Eastern dogs	Ancient large	0.0656	0.5352	0.8292	
Southwestern dogs	Ancient large	0.1622	0.8989	0.9525	
Eastern+Southwestern	Ancient large	9.2E-18	2.9E-04	0.0659	
Modern reference sets	**Individuals**				
Base modern	WolfSaudiArabia, WolfSyria, Wolf01Altai, Wolf02Chukotka, Wolf03Bryansk, Wolf04InnerMongolia, Wolf05China, Wolf06Croatia, Wolf07Israel, Wolf19India, Wolf20Iran, Wolf21Italy, Wolf24Portugal, Wolf27Spain, Wolf31Liaoning, Wolf32Xinjiang, Wolf33Xinjiang, Wolf34Shanxi, Wolf35Xinjiang, Wolf36Xinjiang, Wolf37InnerMongolia, Wolf38Shanxi, Wolf39Iberia, Wolf41InnerMongolia, Wolf42Tibet, WolfTibetan01InnerMongolia, WolfTibetan02InnerMongolia, WolfTibetan03QinghaiHighland, WolfTibetan04QinghaiHighland, WolfTibetan05Tibet, WolfTibetan06Tibet, WolfTibetan07Xinjiang, WolfTibetan08Xinjiang, Wolf21-M-02-15Scandinavia, Wolf32-D-05-18Scandinavia				
Target	**Reference set**	**p rank 0 (mean log across reps)**	**p rank 0: max**	**p rank 1 (mean log across reps)**	**p rank 1: max**
Eastern dogs	(Sample of n=7 from base) x100 reps	2.5E-11	0.0214	0.2643	0.9576
Southwestern dogs	(Sample of n=7 from base) x100 reps	0.0474	0.9247	0.3226	0.9990
Eastern+Southwestern	(Sample of n=7 from base) x100 reps	6.7E-77	1.2E-11	3.0E-05	0.4611
Eastern dogs	(Sample of n=25 from base) x100 reps	2.2E-46	1.1E-23	0.0033	0.3526
Southwestern dogs	(Sample of n=25 from base) x100 reps	7.1E-06	0.0525	0.0427	0.8939
Eastern+Southwestern	(Sample of n=25 from base) x100 reps	1.0E-100	1.0E-100	1.2E-54	1.0E-06

Two different dog target sets, and their union, are tested for cladality relative to reference sets consisting of ancient or modern wolves. From the modern wolves (bottom of table), for each target 100 different reference sets were constructed by randomly sampling either 7 or 25 individuals. The results across these 100 tests are summarised by displaying the mean (on a log-scale) and maximum p-values.



©Maxine Levy

Turk

Grand Course Winner

2023

Coming soon!!

BiBi!!!!!

©Maxine Levy

449 Points to date

3 Unassisted Kills, 5 Assisted Kills

CC, CM, GCW

Entered 19 hunts

Of those 19 hunts Turk took 1st Place 11 times

Earned 4 ASA Cup Trophies and
2 Perpetual Trophies

1st Place 2023 Grand Course Saluki Breed Hunt

2023 Grand Course Winner

2022/2023 NOFCA #1 Saluki and #2 All Breed
-- achieved by entering only 7 hunts,
1st place 5 times with 3 takes.

*Kullah of Urfa CC,CM,GCW

Kathleen and Jim Tigan, Reno NV


© Alicia Kittrell

Pete

Grand Course Winner

2017
& 2019

Melik Nazlee License to Kill at HawksView 500CC,CM,GCW2

LIFETIME: 22 hunts to date,

Placed 1st in 11 hunts
604 Lifetime points
4 Unassisted Kills, 6 Assisted Kills

2016 Pete won the ASA Ishtan Cup, ChristmasCup ,and Mia Cup – the first Saluki in ASA history to achieve this honor in a single year.

Novice year received 6 ASA Trophies

Two-time winner of the National Open Field Coursing Association's Grand Course.

Kathleen Tigan & Karen Hoffman, Reno NV

Help to Turkey :

As the Society News goes to bed, I reflect on the global situation. Conflict seems to be the order of the day combined with climate changes that are affecting all of us. The regions that are the homelands of our Salukis continue to cope with extreme drought, urbanization, loss of hunting. This does have an effect on the Salukis still able to live a tribal life.

Of grave concern is the pair of earthquakes that have decimated the South-east of Turkey. On February 6, a magnitude 7.8 earthquake occurred in southern Türkiye (Turkey) near the northern border of Syria. This quake was followed approximately nine hours later by a magnitude 7.5 earthquake located around 59 miles (95 kilometers) to the southwest. This area is the home of the Saluki.

The Society immediately reached out, as best we could, to find out what we might be able to do. We are running a small fund raiser (see our home page) and raised a bit over $4000.00 in 3 days. We transferred $3000.00 to Akin Tülübaş who rented a truck and procured 218 bags of dog kibble. This was taken to the Sanliurfa villages. The situation in Sanliurfa was not catastrophic which was great news. Akin then traveled up to Adiyaman to the north. This is the area both *Tek Kulak Tazi Var and *Pirzola are from. This area has been decimated. Akin reported "Today I went to Adıyaman and its districts villages in the evening. I couldn't believe my eyes. Everything was destroyed. Dogs. They collected them in places where they could feed them. We also bought things like biscuits and chocolate for the children. Tomorrow we will make a road trip over 1000 km. We will be more beneficial to at least 200 dogs. I think we did a good job, too. What we did in this difficult time was really effective. It was a help."

The Society is immeasurably grateful to Akin and his helpers for their assistance in getting help to the dogs and villagers in this disaster. I, personally, want to thank all of you who stepped up to help us provide this small amount of assistance. We will be regrouping and will most likely do this again as it will take a long time to recover in the region. Aftershocks, some quite sizable, are still occurring and still bringing down structures.

Since we sent this help in, Turkey has subsequently endured an extreme rain event that has resulted in flooding throughout the SanliUrfa area. Areas that were spared heavy earthquake damage have now been flooded with many of our Saluki villages having upwards of a foot of flood water inside homes.

At this writing we are not yet clear on the long term damage to both the peoples and the Salukis of the region.


COOL DOG

MBIF UKC Ch/FC Rataki Yalda de Valle Compel SC, TKN, VSWB, FCh


2022 BOB SCOA National Specialty AKC trial


©MyDogPhoto.com2022


BOB Pyramid Cup 2022


©Joe Stewart

American Saluki Association's Brahma II Cup

It was a very good year!

Bill and Susan
Schroeder

Ash-Shi'ra

Marissa Jo
Wagenaar

Compelling
Canines

Rataki Jaar-Jan at Ash-Shi'ra CGC, FCh

1st place Open, ASFA Pyramid Cup

ASFA ASA South Central Regional Trophy

AKC Purebred Preservation Bank (PPB)

Jerold S Bell DVM, Cummings School of Veterinary Medicine at Tufts University

The AKC Purebred Preservation Bank (PPB) was created by the AKC Board of Directors in August 2021. To understand the basis and need for a breed semen repository, there must be a realistic understanding of dog breed gene pools, genetic diversity, and genetic health.

The sustainability of dog breeds and purebred breeding has been a matter of consideration for some time. Can a breed continue to propagate over time with a closed gene pool and 1) Maintain adequate genetic diversity, 2) Not deteriorate in its health and quality?

Genetic Diversity

The sustainability of dog breeds and purebred breeding has been a matter of consideration for some time.

Pure breeds have closed gene pools. This means that all matings must be between AKC registered dogs from the same breed for the offspring to be AKC registered. Members of the breed from other countries and registries can be AKC registered if they conform to Foreign Registration eligibility (https://www.akc.org/rules/special-registry-services/). The issue with closed gene pools is that the genes of dogs not used for breeding are lost to the next generation. If entire lines of dogs cease to reproduce then that portion of the breed gene pool is lost. As only a small portion of the breed members are ever used for breeding, this represents a genetic bottleneck with each generation. This is why it is important that breed-wide selection of mates encompasses the breadth of genetic background of the breed gene pool, and the gene pool narrowing issue of the popular sire syndrome is avoided.

Small population breeds have concerns with genetic diversity because of low numbers of breedable dogs. Twelve AKC breeds registered fewer than 10 litters in 2021. Owners may also be reluctant to breed for fear of producing dogs affected with certain conditions such as hip dysplasia or epilepsy. For a breed to reproduce and sustain itself, breeders of small population breeds must select the best matings for quality and health and grow their populations. If breeders are not breeding, then the breed population will decline in numbers, in genetic diversity, quality, and health. Breeds with large populations had small populations many generations back. While all members of a breed originated from the same small background, population expansion creates many different “lines” of dogs that represent the breed’s genetic diversity and provides greater choices for selection.

Genes come on paired chromosomes – one from the sire and one from the dam. If a gene pair has two copies of the same gene this is called homozygosity. If a gene pair has two different variations of a gene it is called heterozygosity. Within a breed, there can be several variations of a gene available in each gene pair. Unless a gene variant is either desirable or deleterious then its homozygosity or heterozygosity has no effect on the quality or health of the dog. Molecular geneticists can measure the total percentage of homozygosity of all gene pairs, and this is a more accurate measurement than the pedigree-determined inbreeding coefficient. The percentage of heterozygosity is the opposite of the percentage of homozygosity; ex. 35% homozygosity equals 65% heterozygosity.

Any selection causes a loss of genetic diversity in what is being selected against. A loss of genetic diversity is not always detrimental to a breed unless its loss causes a decrease in health or quality. If a breed standard has certain requirements, or if breeders want to select against certain detrimental traits or disorders then you need breed-wide homozygosity at that gene location to reproduce the desired phenotype (what you see in the dog). It is homozygosity that allows a breed to breed true. Molecular genetic data shows that purebred dogs on average have higher homozygosity (44.87%) versus mixed- breed dogs (35.98%).[2] This indicates that it takes approximately 35.98% homozygosity to be a dog, but *on average* an additional 8.89% of homozygosity to be a purebred dog.

Breed-wide genetic diversity means maintaining dogs from different areas of the gene pool (different pedigree backgrounds) in the breeding population.

There is misunderstanding of the meaning of breed-wide genetic diversity, how it is measured, and how it can be maintained. Commercial genetic companies market "genetic diversity tests" for dogs based on the amount of heterozygosity or homozygosity. Homozygosity measurements do not reflect the genetic diversity of the breed, but only the average type of mating being performed. Linebreeding is mating two dogs together that are more related than the average in the breed and results in a higher homozygosity in the resultant litter. Outbreeding is mating two individuals together that are less related than the average of the breed, and results in higher heterozygosity in the resultant litter. If a handful of dogs are mated to the ones most related to each other, then that population of dogs will have higher homozygosity. If the same dogs are mated to the ones least related to each other then there will be lower homozygosity and higher heterozygosity. This has not changed the genetic diversity of the population – they are the same dogs and have the same gene frequencies within the breed. Breed-wide genetic diversity means maintaining dogs from different areas of the gene pool (different pedigree backgrounds) in the breeding population.

Some breeds have a higher average homozygosity but based on valid health surveys are relatively healthy. Some breeds have lower average homozygosity and have considerable issues with hereditary disease. Each breed has its own parameters. It is not the homozygosity or heterozygosity of a breed that determines health, it is the breed-wide accumulation of disease predisposing genes.

Genetic Disease

> *Genetic bottlenecks have been a significant factor in restricting breed diversity and possibly increasing the frequency of hereditary disease*

Disease predisposing genes that can cause impaired health or diminished ability to reproduce are a major concern in dog breeding. These are usually recessive genes or additive genes that may not be identifiable in the individual breeding dogs unless there is a valid genetic test available.

If breeds have issues with hereditary disease, then these must be actively selected against through genetic testing, or if valid genetic tests are not available, then selection against affected dogs and their close relatives. This is possible with genetic testing and screening databases such as the OFA – Canine Health Information Center (CHIC). The AKC *Bred with H.E.A.R.T. and AKC Breeder of Merit* program have adopted AKC Parent Club determined requirements for pre-breeding health screening.

It is selection against specific diseases and their associated liability genes that improves breed health, not an overall measurement of homozygosity. Commercial genetic testing companies that recommend lowering the average homozygosity of proposed matings through their genetic diversity tests are not differentiating the desirable homozygosity that creates and maintains breeds, from detrimental homozygosity of disease-associated genes. If breeders are not selecting for quality and health, then both will decline. Constant selection for quality AND health are required to obtain and maintain both in purebred breeds regardless of their population size or average homozygosity.

Is The Threat of Breed Extinction A Reality?

Genetic bottlenecks have been a significant factor in restricting breed diversity and possibly increasing the frequency of hereditary disease if liability genes are carried by the survivors of bottlenecks. Many breeds went through genetic bottlenecks during World War II and emerged with smaller and less diverse populations. Historically, some working breeds were abandoned by their breeders due losing the need for their function as technology advanced. Some breeds were replaced by similar but more popular breeds. The original breed sometimes contributed its genes through breeding to create the "new" breed that replaced it. However, this is less likely to occur today with closed studbooks.

The best way to preserve breed integrity and health is to utilize the existing gene pool diversity of the breed. This includes breed populations in other countries, or different breed varieties selected on working (hunting, herding, etc.) abilities. While these breed populations may diverge from each other and be based on different standards, they all derived from the original breed ancestors. They can be utilized to maintain overall breed diversity.

Crossbreeding (mating a purebred dog to another dog that is not of the same breed) can bring in new genes when disease-causing genes are "fixed" (homozygous) or at extremely high frequency in a breed gene pool. There are historical examples where at the request of the AKC Parent Club, stud books have been reopened and/or controlled crossbreedings have occurred. However, crossbreeding to other breeds to bring in new genes and genetic diversity, may also bring in deleterious and undesirable genes from the "other" dogs that are not present in the original breed. Therefore, breeding from within the breed's gene pool is the most desirable method to select for health and quality.

There are historical examples where at the request of the AKC Parent Club, stud books have been reopened

All of these are population-based issues: Are there enough numbers of breeding dogs to sustain the population? Is there enough variation in the breed gene pool to allow continued selection for quality and health? Is there enough availability of healthy dogs (and health-related genes) to provide for a healthy breed?

The Idea Behind a Purebred Preservation Bank

An excellent source of breed genetic material is in frozen semen. This preserves the dog's genetic diversity and chromosomal history of the breed and can be maintained for an almost unlimited duration. What if frozen semen were available from before the genetic bottlenecks in breeds with restricted genetic diversity or breed-wide inherited disease?

What if it were possible to add the conformation quality or health traits of a member of your breed from 50 or more years ago to today's gene pool? Preserving genetic material in the form of frozen semen of former and current quality dogs can have great value in future decades for maintaining and improving purebred dogs and can mitigate the risk of extinction due to genetic depletion. Encouraging and facilitating such banking is in the best interest of purebred dogs. A semen preservation bank is a hedge against breed deterioration, loss of genetic diversity, and population contraction, now or in the future.

Establishment of the AKC Purebred Preservation Bank

In 2017 the AKC approved a process allowing an AKC Parent Club to create a BREED REPRODUCTIVE BANK to own semen for use in AKC litters as a way to preserve genetic diversity in the breed. Since then, the Otterhound Club of America is the only breed that has fully established such an entity. The Akita Club of America is the only other club to formally request permission from the AKC Board to move forward their own reproductive bank. Other breed parent clubs have looked into initiating a breed reproductive bank, but have had difficulty navigating legal, procedural, financial, and political barriers. Due to these difficulties, AKC CEO Dennis Sprung suggested developing an AKC All-Breed Preservation Bank to benefit all Parent Clubs. An AKC breed preservation work group was established to explore the issues involved with establishing such a program, consisting of; Dr. Charles Garvin, Dr. Joellen Gregory, Dr. Marty Greer, Dr. Jerry Klein, Mark Dunn, Mary Beth O'Neill, and Ted Phillips. They contacted and surveyed the breed clubs, veterinary reproductive specialists, canine semen storage facilities, and legal counsel.

> *A semen preservation bank is a hedge against breed deterioration, loss of genetic diversity, and population contraction, now or in the future.*

In August 2021 the AKC Board approved the creation and funding of an AKC Purebred Preservation Bank as a separate 501c.3 organization. This is not a simple semen bank, and not designed to compete with current breeders. The PPB will not necessarily benefit todays breeds (with DNA from today's dogs), but for breeds 50 or 100 years in the future. It is to act as a safeguard against the depletion of breed genetic diversity and health, and for the long-term future of breeds.

The Mission of the AKC Purebred Preservation Bank is to ensure the long-term viability of purebred dogs. Through coordinating efforts with parent breed clubs, the AKCPPB will educate breeders, clubs, and the public about the importance of safeguarding frozen semen and protecting purebred dog breeds for future decades. This program is to assist parent breed clubs to preserve the genetic heritage of their breed.

In taking on this program, the AKCPPB will provide organization, infrastructure, funding and implementation of the program. This includes: legal, insurance, tax exempt administration, and initial funding. The breed Parent Club will provide crucial guidance on the use of semen for breed preservation, how it will be utilized, and selection criteria. The policies and procedures of the program are a work in progress, and basic and "ideal" guidelines are being worked out.

Practical Considerations for the PPB

Popular and prolific dogs from the past will not likely be good candidates if their contribution and that of their close relatives already is represented in the breed gene pool.

Possible criteria for acceptance of semen into the PPB includes: definitive identification of the source of the semen sample – ideally through DNA analysis, details of the dog's conformation, behavior, health test results, reproductive history, and the quality of the semen.

Over time, new diseases are emerging or being discovered, new knowledge about the genetics of existing diseases is being developed, and new genetic tests are being deployed. If breed-specific DNA testing has changed at the time of consideration of use of the semen, then DNA tests should ideally be run to determine the health status of the donor dog. While all genetic tests can be run on semen, it is advantageous to also have DNA stored in a DNA repository – such as the OFA CHIC DNA repository - so that future tests can be run without wasting valuable semen. Even if a dog in a semen bank tests positive for a disease liability gene, it can be bred to a normal-testing bitch and the offspring can be tested for normal individuals. Costs for updating health testing have not been worked out, but could be covered by the PPB, the Parent Club looking to utilize the semen, or a combination of both.

Possible criteria for distribution of semen from the PPB will also be determined with input from the breed Parent Club. "Ideal" guidelines being developed could include; 1) scientifically validated detrimental loss of genetic diversity causing low fertility or high frequency of genetic disease, and 2) DNA validation showing that semen in the PPB expands the breadth of the gene pool (represents unique lines that no longer exist in the breed).

Some possible criteria for selection of dams being considered for insemination with PPB semen could "ideally" include; dam has produced at least one litter (proven fertility), dam is up to date on all breed-specific health screening tests, dam has no disqualifying faults, and dam represents the quality of the current breed population.

The importance of a non-political process to equitably distribute semen at this point cannot be overemphasized. This program is about breed gene pool rescue. While the identity and reputation of dogs stored in the PPB is known, the process must determine the best means of widening the breed's gene pool. Popular and prolific dogs from the past will not likely be good candidates if their contribution and that of their close relatives already is represented in the breed gene pool. It is likely that by the time PPB semen is utilized the dog show reputation of specific dogs as well as their prior owners will be distant memories.

Semen Collection

How will the PPB semen be collected? A breeder can opt to donate the semen to the PPB. All owners must sign off ownership of the semen to the PPB. Semen can be bequeathed to the PPB. There can be a Parent Club semen collection event at a dog show or club event.

Hopefully, PPB will be used to; 1) maintain selective pressure for health and quality, 2) utilize the breadth of pedigree background of the breed, and 3) continue to expand the breed population.

After lengthy discussions with commercial semen storage centers, a large problem is abandoned semen after all legal contacts with the owners have been exhausted. These include when the owner dies or becomes incapacitated, or because bills for storage are no longer being paid. Large amounts of canine semen are currently destroyed in this process or donated to research centers. These semen samples can represent a large source of diversity to populate the PPB, but again, criteria for acceptance and usage must be worked out.

PPB Semen Storage

Contracts will be made by the AKCPPB and semen storage centers to ensure experienced, reliable, responsible management with risk mitigation procedures and strategies. These include proper identification of the semen samples and strategies for storage viability in the event of power outages or disasters.

Final Remarks

Most dog breeds have within their gene pool sufficient genetic diversity. Hopefully, PPB will be used to; 1) maintain selective pressure for health and quality, 2) utilize the breadth of pedigree background of the breed, and 3) continue to expand the breed population. However, its existence is a vital safety net if a breed finds itself in need of genetic rescue.

General References

1. Bell J. (2019) Understanding Breeds as Populations. Proceedings 2019 AKCCHF National Parent Club Canine Health Conference https://www.akcchf.org/educational-resources/library/AKCCHF-Understanding-Breeds-as-Populations-002.pdf

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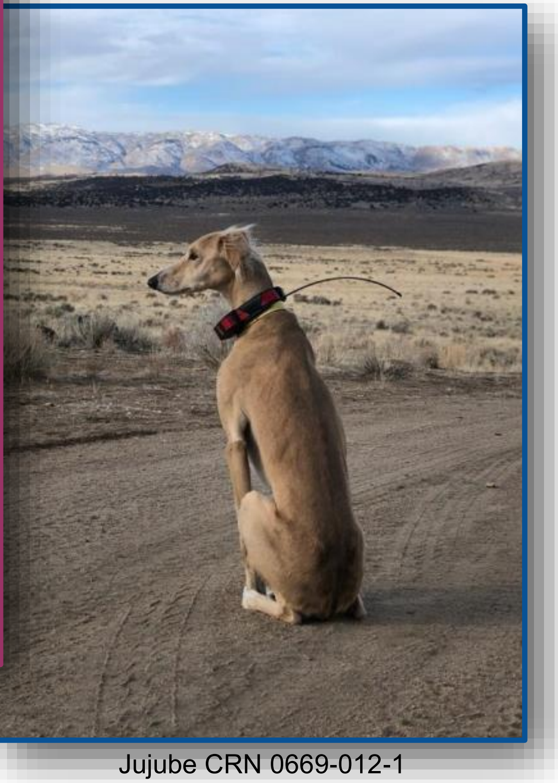
*Ghobad Import Iran CRN 0634-011-0



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Pictures From an Exhibition

By Sir Terence Clark

I was recently invited to attend at the Royal Geographical Society in London the inaugural UK showing of *Journey of a Lifetime*, a short film about the journey made by Princess Alice, Countess of Athlone across Arabia in 1938, which was the centrepiece of a discussion between two contemporary female explorers of Arabia, Dr Elisabeth Kendall, Arabist and Mistress of Girton College, Cambridge and Reem Philby, who had just completed an expedition across Arabia in the footsteps of her grandfather St John (Abdallah) Philby. The evening was rounded off by a tour of the accompanying *Early Women Explorers in Arabia Exhibition*, subtitled *Five extraordinary British women, with one destination and five different objectives.* These women were: the equestrian, Lady Anne Blunt, the diplomat and archaeologist, Gertrude Bell, the writer and explorer, Freya Stark, the Muslim, Lady Evelyn (Zaineb) Cobbold and Princess Alice; and the exhibition featured their photographs, paintings and maps, illustrating their journeys across Arabia.

SAND STORM IN THE WADY-ER-RAJEL. Vol. I., p. 80.

THE OASIS OF JÔF. [Vol. I., p. 120.

I already knew that both Gertrude Bell and Lady Anne Blunt were devotees of Salukis, so I was hoping their hounds might be reflected somewhere in the exhibition; and I was not disappointed. They appeared in two enlarged illustrations from Lady Anne's book *A Pilgrimage to Nejd*, published in 1881, describing her epic journey on horse or camel with her husband, Wilfred Scawen Blunt from Damascus in Syria down through Transjordan and across the vast Nefud desert of Arabia eventually to Baghdad, Mesopotamia, before continuing across western Persia down to the Persian Gulf. I recalled reading that early in the journey, they had acquired two Salukis, with which they hunted actively along the way. But there was something odd about the hounds' appearance in these illustrations, which aroused my curiosity: they gave the impression of Greyhounds rather than Salukis! So, as soon as I could, I delved into her book, which I had not read for many years, to see whether I might find some explanation.

Wilfred Scawen Blunt with Shiekhah

As soon as I opened the book, this impression was immediately reinforced by the frontispiece, showing Wilfred Scawen Blunt dressed as a Bedouin, complete with a falcon on his wrist and a very Greyhound-like hound at his side. Indeed, Lady Anne goes so far as to relate that in Syria they were given by some friendly Bedouin related to their guide "a pretty little fawn greyhound", called "Shiekhah" after a plant of that name; and in Transjordan their escort gave them his "very handsome greyhound… of the long-haired breed", a black and tan called Sayad .

Elsewhere in the book, I came across this hunting scene, which actually shows three hounds. However, Lady Anne mentions in the text that her two hounds were helped by "a sort of lurcher who attached himself to us. The servants call him "Merzug", which may be translated a "windfall" literally a gift from God, an unattractive animal but possessed of a nose".


RUN TO EARTH.

Prior to their journey across Arabia, the Blunts had already made another expedition in the region, which Lady Anne described graphically in *Bedouin Tribes of the Euphrates*, published in 1879. Here she mentions for the first time the appearance of Salukis among the Shammar tribe they met in northern Iraq, writing that they had "a great many dogs about the camp, and a few greyhounds, called by the Arabs *tazeh*". This is somewhat puzzling, as in my experience *"tazeh"* is not a term used by the Arabs in that area but by the Kurds and Turkomans there. However, she does go on to say that the hounds were also called "*slouguy*", which approximates to the word the Arabs in the area do indeed use to this day. So, it is clear that from an early stage of her introduction to the Middle East she was well aware of the Saluki as a distinct breed, yet throughout her writings she persistently refers to greyhounds, albeit with a small 'g'. She even underlines the distinction in one passage in *A Pilgrimage to Nejd* when she describes coursing with her two hounds after a hare which got up on stony ground "which would have broken every bone of an English greyhound, apparently without hurting themselves".


Sheikh Sukheil of the Zagrarit Shammar in Iraq , Gertrude Bell photograph 1911. From the Gertrude Bell Archive (https://gertrudebell.ncl.ac.uk/)

Lady Anne's usage of greyhound for her hounds is understandable, as at the time of the publication of her books such hounds had not started to be imported from the Middle East, and Saluki was not a term in current usage in England. It was after all adopted formally only after some debate in 1923 on the establishment in the UK of the Saluki or Gazelle Hound Club. Western travellers in the region found it convenient to use greyhound to describe what they encountered rather than the plethora of Arabic, Kurdish, Persian and Turkish words they heard or thought they heard which would have had little significance for their interlocutors back home. Even Gertrude Bell, great Middle East expert though she was, favoured the word greyhound when writing in a letter home to describe the arrival of her first hounds in Baghdad: “the two most beautiful Arab greyhounds…had walked ten days down the Euphrates with two tribesmen to conduct them, and came in half-starved. They are sitting beside me as I write, after wandering about the room for half an hour whining. They are very gentle and friendly and I hope they will soon get adjusted to living in a garden instead of a tent. They are perfectly lovely and of course of the finest Arab breed. We have named them Rishan and Najmah – the feathered (that’s because of his feathered tail) and the star…”.

Against that background, it becomes more explicable that the illustrator employed for *A Pilgrimage to Nejd* should have chosen the form of an English Greyhound as a model: photographs of Salukis had not yet made their appearance. It would of course have been open to Lady Anne to have questioned the model before publication, but it is quite likely that she did not see the illustrations before the printing stage. So, we shall never know what her hounds really looked like. Fortunately, photography had become commonplace later on and Gertrude Bell’s hounds were recorded pictorially for posterity, leaving no doubt that they were indeed Salukis and not Greyhounds.

Melik Palang e Sheyda LaaYudaani

Always in the points, Lemy only needs his kill credits for his titles.

Paul and Lauri Domski, New Mexico

Melik Bannu Abee e Sheyda Laa Yudaani CGC,TKN,SC

Our gratitude to Terence Wright for breeding this litter, to Mary Beth and George for sharing her with us and to Ron Bigford for piloting our Abi, knows no bounds, of course -neither does Abi! Our Grey Lady needs one major to finish her AKC Championship!

Carola Butler and
Jan Isley

Georgia

PUPPIES FROM PAST SPDBS LITTERS

SO YOU WANT TO BREED A LITTER

As we live with our treasured companions, often the decision to breed a litter is made. New puppies can be a joyous occasion. If you have not walked down the path of new lives, lost sleep, and puppy antics previously, it can be an intimidating prospect, even those who have had litters previously can find themselves in a place of "what is next".

The following is the Kokopelli Assisted Reproductive Services Handout on Pregnancy Management, Whelping Preparedness, and Neonatal Care. It is a great tool to go over and keep on hand whether you are having your first litter or a new litter.

What do you need on hand?

- Fast, digital, rectal thermometer
- System for keeping detailed notes
- Well-balanced, high calorie dog food (for bitch during last half of pregnancy and nursing)
- Whelping box, ideally with protective anti-roll shelf around perimeter
- Convective heating source (light or heating bulb)
- Area thermometer to track temperature of whelping box
- Kitchen-type gram/ounce scale

Radiographs-do I need one?

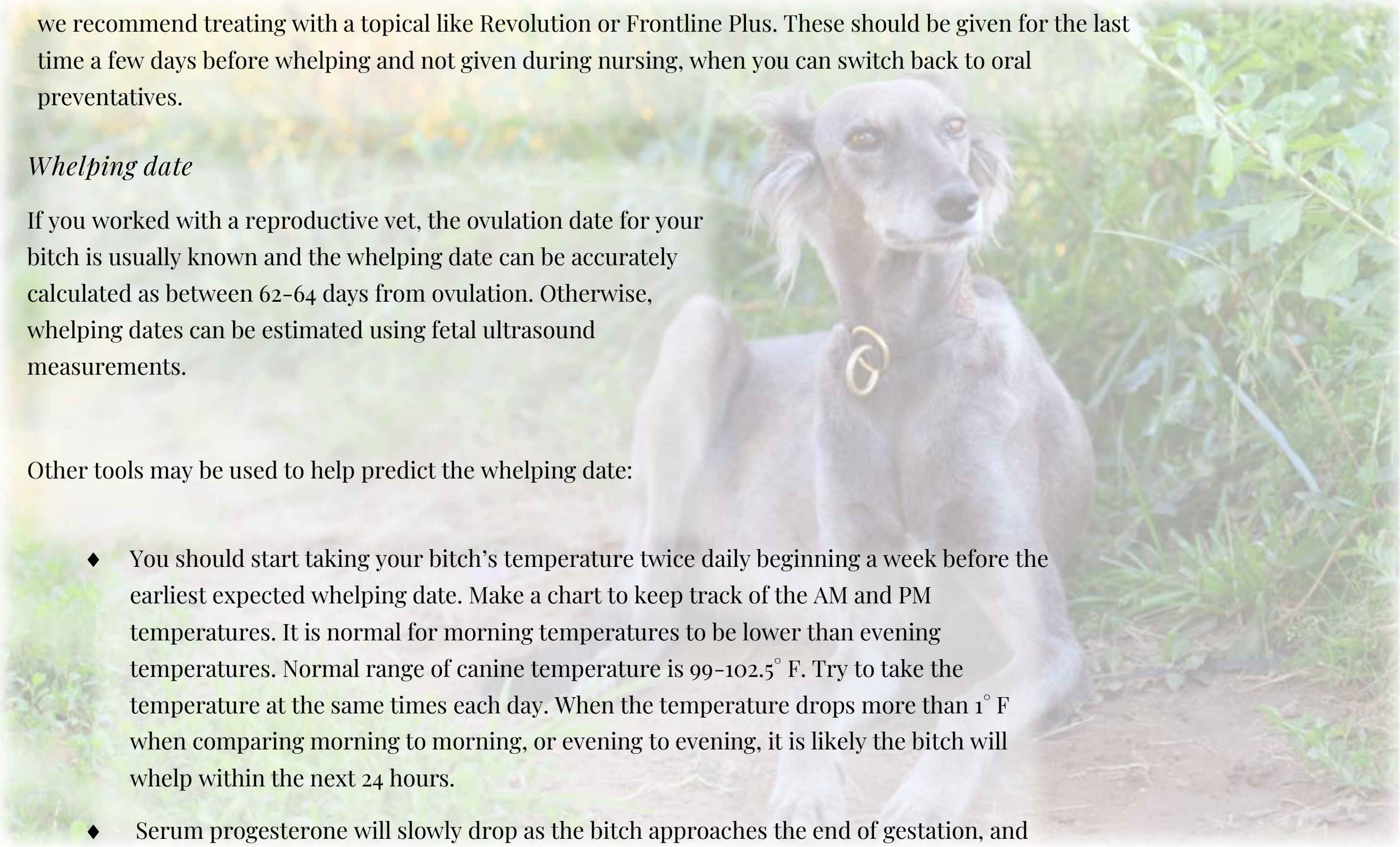
The power of this tool is in counting the fetuses and estimating size of the fetuses in relation to the maternal pelvis. This is useful information so that, once whelping occurs, you know when it is over. It is also useful to know, prior to allowing the bitch to whelp naturally, that the fetuses appear small enough to be able to fit through the pelvis without obstruction. For these reasons, radiographs should be taken just a few days prior to expected whelping. *(Editor's note: I have always x-rayed at 5 days before expected whelping.)*

Nutrition during pregnancy and nursing

You should maintain your bitch on her normal, maintenance diet during the first month of gestation (up until ultrasound diagnosis). If diagnosed pregnant, you should switch her over to a high-calorie diet. Do this by choosing a quality growth formula (puppy food or performance diet) and gradually switching her over the course of a week by mixing more and more of the new food into her regular food, while fazing the regular food out. Keep her on this high-calorie diet through the second month of pregnancy and while she is nursing her puppies. Once the puppies are weaned, switch her back onto her normal, maintenance diet the same way over the course of a week. Other supplements are not necessary, so long as you have chosen a well-balanced puppy food to feed her. Reliable brands include, but are not limited to, Hills Science Diet, Royal Canin, and Purina ProPlan. Be careful of trendy/boutique diets. (Avoid grain-free diets) If you have questions, consult with your general practice veterinarian. Most supplements are unnecessary and some can be dangerous.

Flea and Heartworm Prevention

Most heartworm medications are safe to give during pregnancy. You can ask us about the product you use. *None of the oral medications for prevention of fleas have been shown to be safe for pregnant or nursing dogs, and some have been correlated with adverse effects.* Fleas can be devastating for newborn puppies, so we recommend treating with a topical like Revolution or Frontline Plus. These should be given for the last time a few days before whelping and not given during nursing, when you can switch back to oral preventatives.



Whelping date

If you worked with a reproductive vet, the ovulation date for your bitch is usually known and the whelping date can be accurately calculated as between 62-64 days from ovulation. Otherwise, whelping dates can be estimated using fetal ultrasound measurements.

Other tools may be used to help predict the whelping date:

- You should start taking your bitch's temperature twice daily beginning a week before the earliest expected whelping date. Make a chart to keep track of the AM and PM temperatures. It is normal for morning temperatures to be lower than evening temperatures. Normal range of canine temperature is 99-102.5° F. Try to take the temperature at the same times each day. When the temperature drops more than 1° F when comparing morning to morning, or evening to evening, it is likely the bitch will whelp within the next 24 hours.
- Serum progesterone will slowly drop as the bitch approaches the end of gestation, and will abruptly drop to baseline (less than 2 ng/mL) the day she is ready to whelp. It is common for your reproductive vet to check the serum progesterone before proceeding with an elective c-section, but this tool can also be used to predict natural whelping.
- Ultrasound may be used to estimate gestational age and fetal maturity. This is done by looking at size and development of certain organs, like the intestines and kidneys, which mature very late in gestation. This tool is often used if ovulation dates, and therefore whelping dates, are uncertain. It is also used in high-risk pregnancy cases.

Whelping: What is normal? What is not?

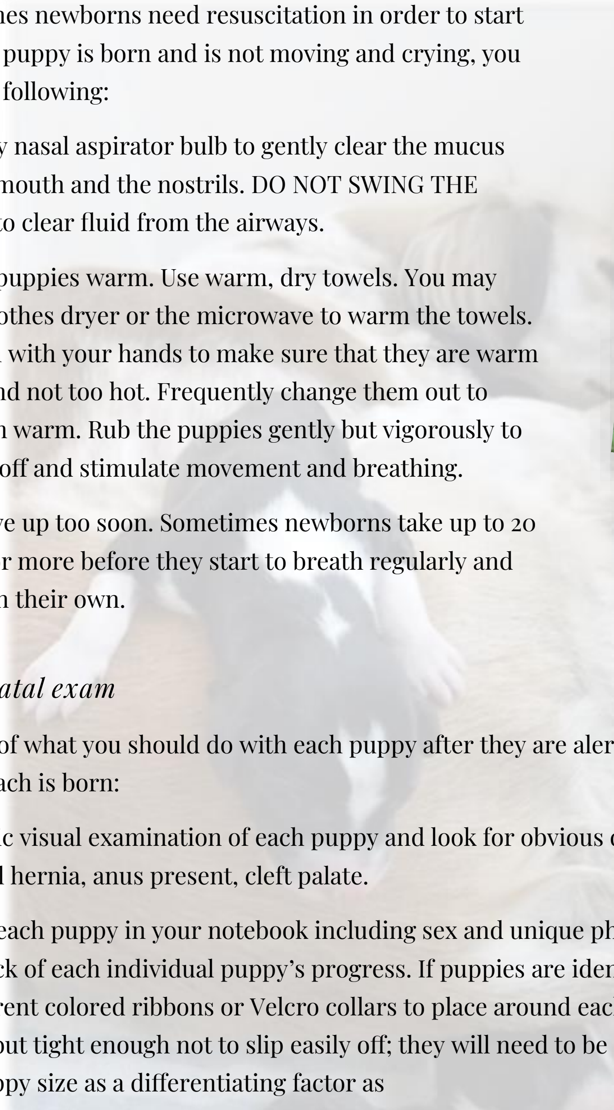
Whelping proceeds in three stages. The first stage is preparatory and includes behavioral cues, which may include any of the following: restlessness, seeking attention, seeking solitude, building a nest, gathering toys together, & loss of appetite. First-time mothers ("primiparous" bitches) are often more nervous and may show these behaviors for a longer period (up to 24 h before whelping) than experienced mothers ("multiparous" bitches).

The second stage is the birth of the fetuses. The third stage is the passage of the placentas. These two stages happen simultaneously in the bitch. Please consider the following important points while monitoring your bitch during natural whelping:

- Once visible abdominal contractions begin, she should give birth to a puppy within 15 minutes. Puppies are streamlined and pass easily through the birth canal. If the bitch is pushing for more than 15 minutes and no puppy is produced, it is stuck and you should seek immediate veterinary intervention.
- If the bitch has given birth to some puppies already, but not all of them, she may take a natural rest between puppies. As long as she is not having active abdominal contractions, it is normal for a bitch to rest for up to 2 hours between the birth of puppies. Less commonly, she may rest for up to 4 hours. It is important to err on the side of caution, however, and so if you know there are more puppies to be born (from your radiograph count), and it has been 2 hours since the last one was born, you should call your veterinarian and plan to bring her in for an immediate evaluation.
- Giving birth is not a difficult, arduous event for dogs, as it is for other species (like women…). Puppies are shaped like little torpedoes and pass very nicely through the bitch’s birth canal. If your bitch is crying in discomfort or pain, that is not a normal part of whelping. It indicates the puppy is stuck and you should take your bitch to the veterinarian immediately.
- Vaginal discharge during whelping is a mixture of dark green fluid (“uteroverdin” from the placenta), clear fluid (amniotic and allantoic fluids), and very little red blood. The smell of this discharge is relatively neutral. It does not stink. If the fluid has a foul odor, that is abnormal and indicates something likely has died sometime ago and you should have the bitch examined by your veterinarian.
- If there is more than just a little amount of red blood in the discharge, that may be abnormal and is worth having the bitch evaluated.
- Your bitch should be bright, alert, and attentive to the puppies throughout the whelping process. If she is lethargic and inattentive, this may be a sign of shock and she should be evaluated by a veterinarian.

Placentas will pass intermixed with the passage of puppies, and not always in order. This is normal. There is no published evidence to support claims that any added nutritional or immunological benefit is gained by letting the bitch eat the placentas. Some bitches will vomit them back up, creating a mess in the whelping area. While it is not a big deal if your bitch eats the placentas (and sometimes it’s impossible to prevent!), we don’t recommend actively feeding or encouraging the bitch to eat them.

Neonatal resuscitation



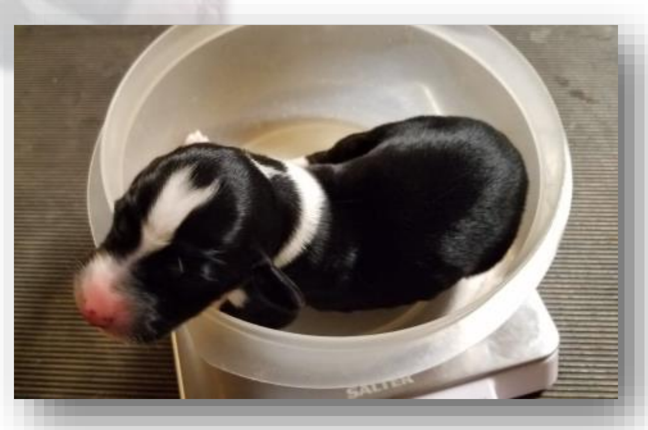
Puppies born at home should come out crying and the mother should be attentive and licking them. They should start seeking a nipple and begin suckling within the first hour after being born. Sometimes newborns need resuscitation in order to start breathing. If a puppy is born and is not moving and crying, you should try the following:

- Use a baby nasal aspirator bulb to gently clear the mucus from the mouth and the nostrils. DO NOT SWING THE PUPPIES to clear fluid from the airways.
- Keep the puppies warm. Use warm, dry towels. You may use the clothes dryer or the microwave to warm the towels. Test them with your hands to make sure that they are warm enough and not too hot. Frequently change them out to keep them warm. Rub the puppies gently but vigorously to dry them off and stimulate movement and breathing.
- Do not give up too soon. Sometimes newborns take up to 20 minutes or more before they start to breath regularly and actively on their own.

Initial neonatal exam

Here is a list of what you should do with each puppy after they are alert, moving, and crying, in the minutes to hours after each is born:

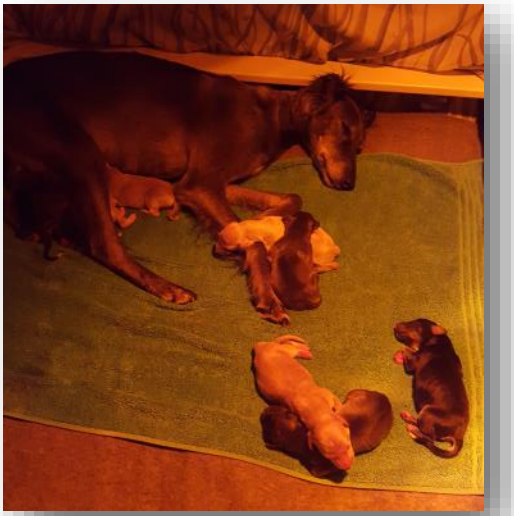
- Do a basic visual examination of each puppy and look for obvious defects including: open skull fontanels, umbilical hernia, anus present, cleft palate.
- Identify each puppy in your notebook including sex and unique physical characteristics that will allow you to keep track of each individual puppy's progress. If puppies are identical to each other or difficult to tell apart, get different colored ribbons or Velcro collars to place around each puppy's neck (obviously loose enough to be safe, but tight enough not to slip easily off; they will need to be adjusted as the puppies grow). Do not trust puppy size as a differentiating factor as that will change at different rates as the puppies grow.
- Using a gram scale, you will weigh each puppy twice daily and record his or her weight on a chart. Puppies may lose weight during the first 24-48 h, but afterwards should gain at least 10% of their original weight each day for the first few weeks of life. If a puppy fails to gain weight, this is often the first warning sign that something is wrong and you should give your vet a call.



Each puppy should start nursing very soon after birth. This is critical for a couple reasons. Puppies have very little fat reserves and need to eat on a regular basis or they will become hypoglycemic. As critical, puppies do not have a functional immune system at birth. Most of the immunity they acquire is through the first milk ("colostrum") from the dam. When they obtain this colostrum during the first hours of their life, their stomachs do not digest the important antibodies in the milk. Instead, their body absorbs them into their blood system and this forms the basis of protection against bacteria, viruses, and other disease-causing entities they are likely to encounter in their environment. After about 12 hours after whelping, their stomach and guts begin to change how they function and will no longer absorb these antibodies, but will instead just digest it all for nutrition. For this reason, it is critical that each puppy nurses actively during this time to get maximum benefit from the mother's colostrum. If this transfer of immunity does not happen, each puppy will almost certainly become very ill from disease-causing agents in the environment, which infections are often fatal. If a puppy does not nurse actively during this time, or if the dam is not producing milk, you need to contact us and we will discuss with you options we have for using serum to transfer these important antibodies to the puppies.

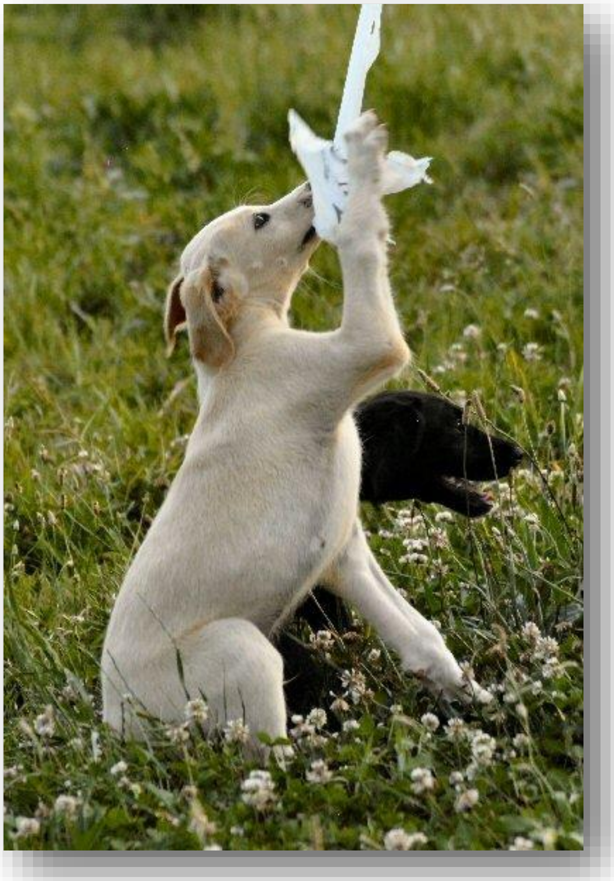
Neonatal care

The first two weeks of a puppy's life require different levels of care because many important survival traits are still developing. Puppies at this age are limited in mobility, sensory input, immune function, and ability to self-regulate body temperature. They have three things they need to do: eat, sleep, and stay warm. The whelping box should be kept very warm (85°-102° F) for the first 2 weeks. Newborn puppies are unable to internally regulate their body temperature. Instead, they are like little lizards, relying on environmental temperatures to keep warm. If they get too cold, they will not be able to digest food and their intestines will stop functioning, allowing milk to stagnate and ferment, causing them to get very sick. In addition, at lower temperatures their immune system will not fully function. One particularly dangerous virus, canine herpesvirus, thrives at lower body temperatures. Canine herpesvirus is one of the most common causes of "fading puppy syndrome." Your best defense against this virus is keeping the whelping box warm. The safest, most controllable method is to use a heating lamp that can be raised and lowered to obtain the desired temperature in the box. Try to have the center of the box around 100°-102° with the edges of the box being cooler. This will allow the puppies to move around and adjust accordingly.



Vaccinations

- *Combination vaccine (Distemper virus, parvovirus, adenovirus, parainfluenza virus) at 6-8 weeks old and then repeated 2 more times at 4 week intervals.*
- *Rabies virus given between 12-16 weeks old.*
- Canine influenza virus (depending on disease status in the area) with first dose given at 6-8 weeks old and a booster 2-4 weeks later.
- Bordetella bronchiseptica (only if puppy will be in at-risk environment, like groomers, dog parks, kennels, or boarding facility) given once intranasally as early as 3-4 weeks old. If given subcutaneously, start at 8 weeks old and give a booster 2-4 weeks later.
- Leptospira (only if puppy will be in at-risk environment wit access to water potentially contaminated with urine from other animals) with first does given at 8-9 weeks of age and a booster 2-4 weeks later.



Deworming

- Puppies should receive deworming medication at 2, 4, 6, and 8 weeks of age. Different drugs protect against different combinations of parasites. The following is one recommended protocol, but others appropriate protocols may be recommended by your veterinarian:
- Nemex2 (Pyrantel Pamoate) or Fenbendazole (Panacur®) given once a day for 3 days at 2, 4, 6, and 8 weeks of age.
- Starting at 12 weeks of age administer monthly heartworm preventatives that also protect against many internal parasites, such as milbemycin (Trifexis®, Interceptor®, or Sentinel®), moxidectin (Advantage®-Multi), or ivermectin/pyrantel (Tri-Heart Plus®).
- Trifexis® and Advantage®-Multi also protect against fleas.
- If tapeworms are noticed after 8 weeks of age, praziquantel (Droncit®) will need to be added.

Kokopelli is the premier theriogenology (reproductive medicine) practice serving Northern California from fully equipped facilities in Sacramento. It's led by founder Bruce Christensen, DVM, MS, DACT – the region's only board-certified theriogenologist serving canine and equine breeders and veterinarians – who is respected industry-wide for his deep knowledge and experience. The Society News is grateful to Kokopelli Assisted Reproductive Services for the use of their *Pregnancy Management, Whelping Preparedness, & Neonatal Care Handout.* For further information from Kokopelli they can be reached at repro@kokopellivet.net

2022 National Specialty
Best of Breed
and Select Bitch
4th Generation

Sabrina

NSBIS NSBIF MBIF

DC Tamarisk Diwan Takalluf of Skye
SC,FCh

2022 National Specialty Best of Breed
First saluki to win the National from
The Coursing Class
(Judge Mary Sanders Parker)

2018 SCOA National ASFA Lure Coursing
Trial Best of Breed

First saluki to win both the National
and the Pyramid Cup

Jovie

BIS MSBIS GCHS

Tamarisk Diwan Jovial Nairang e Skye TKN

Winner of 6 Specialty shows, first
SPDBS descent saluki to win an
All-Breed Best in Show,
National Specialty Best of Opposite Sex
(2018, Judge Frank Farrar)
National Specialty Award of Merit
(2021, Judge Deric Aube),
National Specialty Select Bitch
(2022, Judge Mary Sanders Parker)
Multiple Group Placer &
Supported Entry Winner
A TOP 10 SALUKI
2018, 2019, 2021, 2022

GCH Doubletimes Matrix Reloaded
BN CD JC

X

MSBIF MBIF BIE GCH DC
Tamarisk Cemal Desert Cerenade SC FCh

Thank you to my co-breeder and friend, Danielle Rubin, for her time and dedication in bringing these girls to the pinnacle of the breed.

I also want to thank our desert bred community, past and present, for their support, their commitment to the vision and their steadfast belief that anything is possible for our beloved desert bred and desert descent salukis.

Joanne Klova	Danielle Rubin
Tamarisk Salukis	Desert Skye Salukis

tamarisk74@charter.net
desertskyesalukis.com

Rataki Salukis

The Reed and Barton
Perpetual Trophy
For
Best of Opposite Sex Saluki
earned by Xyla for the
2021/22 NOFCA Coursing
Season

Rataki Xyla CC.CM
*Melik Khaliis x *Aram de Diba of Boorchin*

Rataki Salukis

Ignacio, Colorado

Lorraine Trenholm

rataki2@capecod.net

RUN!

NOFCA Best Opposite Sex
High Score Hound
Perpetual Trophy
earned by Xyla for
the 2021/22 NOFCA
Coursing Season

Rataki Yasmina de Valle

Melik Nadin Jenn CC, CM x Rataki Valle Voo

Yasmina has her NOFCA placements,
now on the hunt for the rest of her title qualifications.

Gare-Qush of Iran

Siring
Beauty
and
Performance

George and Mary Beth Rogers
Stanhope Farm
MelikSalukis.com

Our gratitude to all of you who show what Melik Salukis can achieve

Paschdou's
Daniela
Wilfried
Bormacher
Josiane
LeLoup

Shabaz
The
Perez
Family

Nox Infinita
Hanna
Arto
Ojanperä

Yuzak
Pirjo
Puttonen

Society for the Perpetuation of
Desert Bred
سلوقي
Salukis