

1 Title: Canine transmissible venereal tumor genome reveals ancient introgression from
2 coyotes to arctic sled dogs

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38 Dear Editor,

39 Ancient genome-sequencing studies have extensively refined our understanding of the
40 genetic histories and adaptive evolution of humans¹, as well as the domestic process
41 of livestock and crops². Recent studies about ancient and modern canids all indicate
42 that canids have intricate histories, and lots of canine populations disappeared during
43 evolution³⁻⁶. Thus, ancient genomes from canine fossils are in high demand to clarify
44 canine evolution and the processes leading to dog domestication. Canine transmissible
45 venereal tumor (CTVT), the oldest known somatic cell line, is a living fossil,
46 originating from cancer cells transmitted from a host to other canids during the mating
47 process⁷. Clonal origin analyses hints that the original dog infected with CTVT
48 (CTVT founder) came from an ancient sled dog or wolf population⁷⁻⁹. However, the
49 genetic composition of the CTVT founder is still not clear.

50

51 In order to explore this issue, we applied whole genome sequencing (WGS) to two
52 CTVT samples, their corresponding hosts, and 24 additional canids (Supplementary
53 Note). Combined with published WGS data of two CTVT samples and high quality
54 canine WGS data, we constructed a data set containing WGS data of four CTVT
55 samples a 169-individual reference panel composed of worldwide gray wolves (*Canis*
56 *lupus*), dogs (*Canis lupus familiaris*), coyotes (*Canis latrans*) and golden jackals
57 (*Canis aureus*) (Supplementary Note, Table S1).

58

59 We firstly developed a pipeline *transmissible tumor genotyper* to obtain the per-site

60 genotype for each tumor sample (Supplementary Note). All sites with the same
61 genotype among four CTVT samples were used for ascertainment. Next, we
62 successfully ascertained 18.9M biallelic single nucleotide polymorphisms (SNPs) for
63 the CTVT common genotype using 24.5M SNPs from the reference panel
64 (Supplementary Note). We denote these data Set A. SNPs from the CTVT data in set
65 A could be treated as the founder's germline polymorphisms because they showed a
66 typical germline mutation signature (Supplementary Note, Figure S5).

67

68 We utilized population phylogeny analysis, principal component analysis (PCA) and
69 outgroup f_3 (X, CTVT founder; Outgroup) statistical analysis to assess the genetic
70 relationship between the CTVT founder and modern samples in set A (Supplementary
71 Note). Our results reveal that the CTVT founder was more closely related to
72 present-day arctic sled dogs than to any other populations (Figure S6-8), in
73 accordance with very recent results^{7,8}. However, ADMIXTURE analysis showed that
74 the CTVT founder also possessed an ancestral component found predominantly in
75 non-dog populations, a result that we do not observe for any arctic sled dog
76 (Supplementary Note, Figure 1A). Moreover, the CTVT founder did not cluster
77 tightly with arctic sled dogs in the PCA analysis (Figure S7). These results imply that
78 the CTVT founder belonged to a previously unknown arctic dog population that is not
79 represented in the reference panel.

80

81 To further investigate whether the CTVT founder had introgression from a non-dog

82 population, we ascertained set A using the Andean fox (*Lycalopex culpaeus*) genome
83 (Supplementary Note), forming set B. Next, we tested every non-dog group in set B
84 as candidate introgressor using D statistics of the form $D(\text{CTVT founder, Pop2};$
85 Introgressor, Andean Fox), where Pop2 was tested using all other present-day groups
86 (Supplementary Note, Table S2). Only coyotes were found to be possible candidate
87 introgressors, showing significant ($Z > 4.2$) positive D statistics for all Pop2
88 populations except the New World wolves (Figure 1B). We then tested whether any
89 domesticated dog populations could act as the candidate introgressor for the CTVT
90 founder. Consistent with above results, we find that present-day arctic sled dogs
91 showed significant ($Z > 9.6$) positive $D(\text{CTVT founder, Pop2}; \text{Sled dog1, Andean Fox})$
92 statistics for all Pop2 populations (Figure 1C). D statistics suggest that the CTVT
93 founder was an arctic sled dog bearing gene flow from a population most closely
94 related to coyotes. We did not find strong evidence of coyote introgression into
95 present-day arctic sled dogs ($D(\text{Sled dog1, Pop2}; \text{Coyote, Andean Fox}) \sim 0$). Finally,
96 we used high frequency coyote private alleles to genotype the CTVT founder, in order
97 to manually check whether there was any evidence of continuous coyote-related
98 segments introgressed into the CTVT founder (Supplementary Note) and found one
99 segment longer than 3Mbps on chromosome 6, and several shorter segments on
100 chromosomes 6, 25 and 26. (Figure 1D). This finding helps us to reject the hypothesis
101 that our results were caused by somatic reverse mutations, rather than introgression.
102 29 protein coding genes are located within these segments in total. Among them, we
103 found four tumor-related genes^{10, 11} and a domestication gene¹² *AMY2B* (Figure 1D).

104 The presence of coyote genotypes at tumor-related genes may contribute to the
105 genetic susceptibility to CTVT tumorigenesis. The coyote genotypes at *AMY2B* may
106 lead to low adaptation on a diet rich in starch and the disappearance of the population
107 represented by the CTVT founder in agrarian age.

108

109 In conclusion, our detailed analyses reveal that the CTVT founder came from an
110 arctic sled dog population that possessed introgression from a population related to
111 coyotes, a result that was not known in previous studies. Considering the habitat of
112 coyotes in North America¹³, we propose two hypotheses: 1) The CTVT founder lived
113 in the arctic region of North America. 2) The CTVT founder lived in the arctic region
114 of the Far East, where arctic dogs possessing the introgressed segments migrated
115 through the Bering Strait in an unknown period. Hence, an ancient story of canine
116 admixture is hidden in the genome of a living fossil, the CTVT. To further test our
117 hypotheses of ancient admixture and to better understand the detailed evolutionary
118 history of dogs from the arctic region and Americas, it is crucial to acquire ancient
119 samples in these regions in future work.

120

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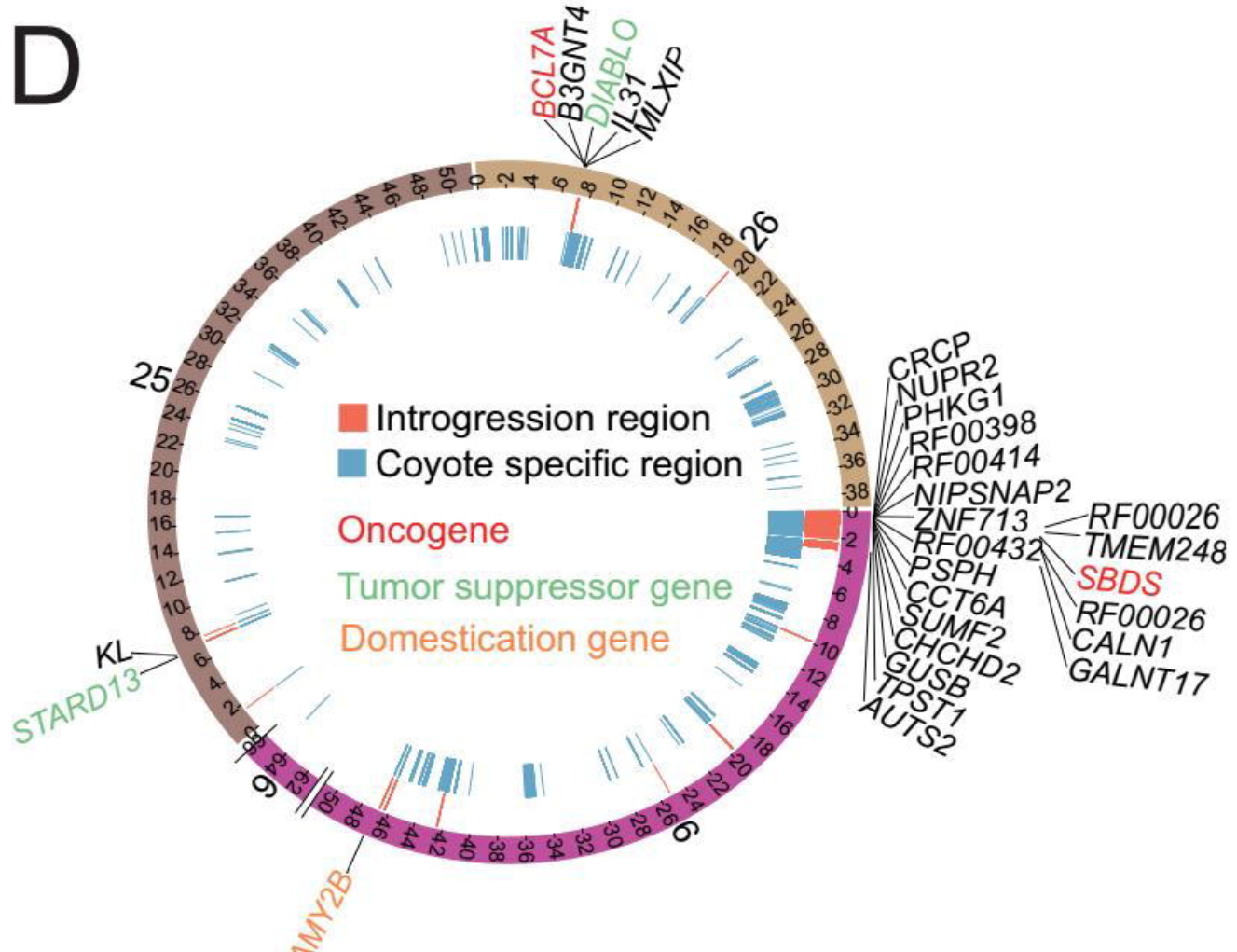
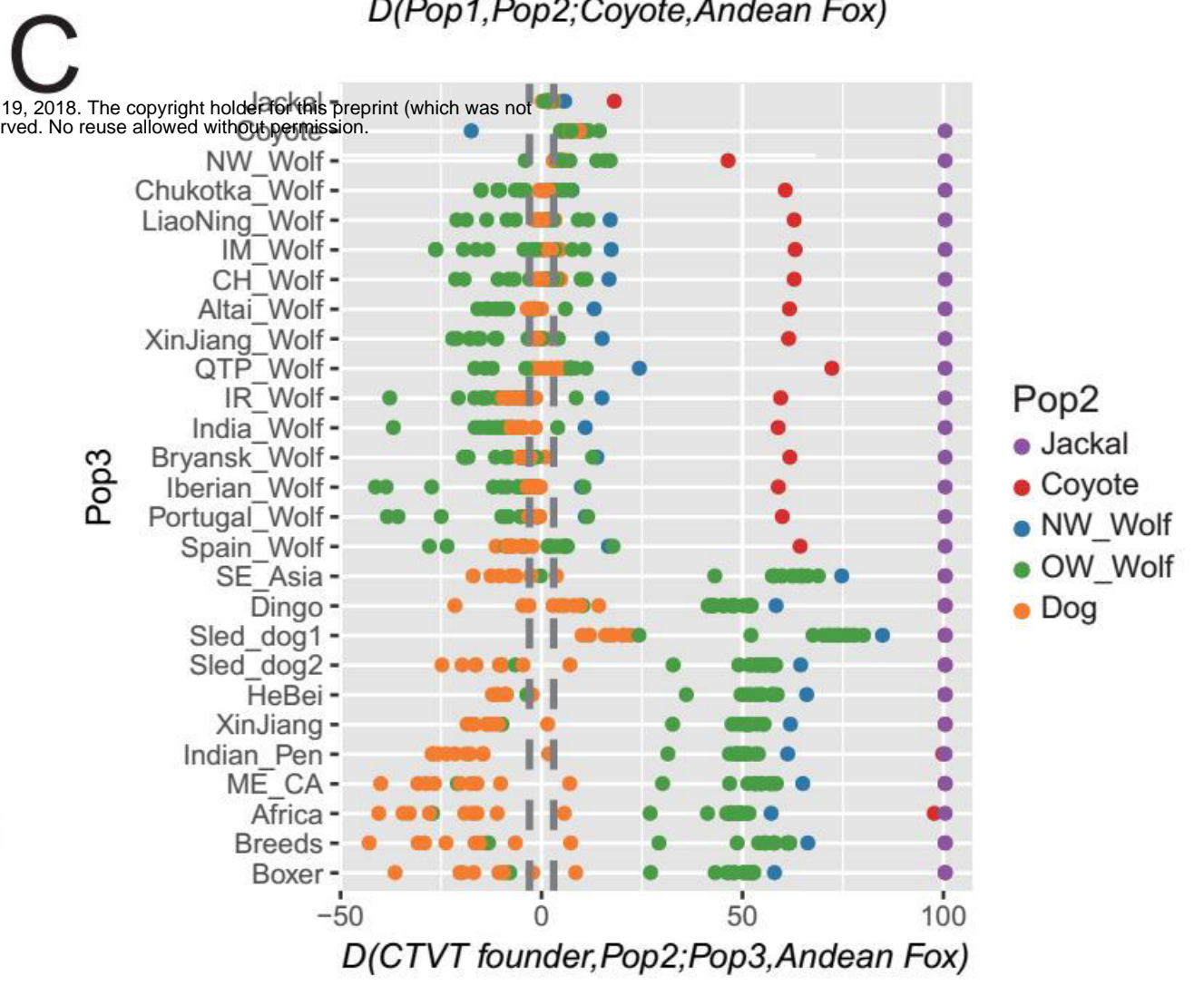
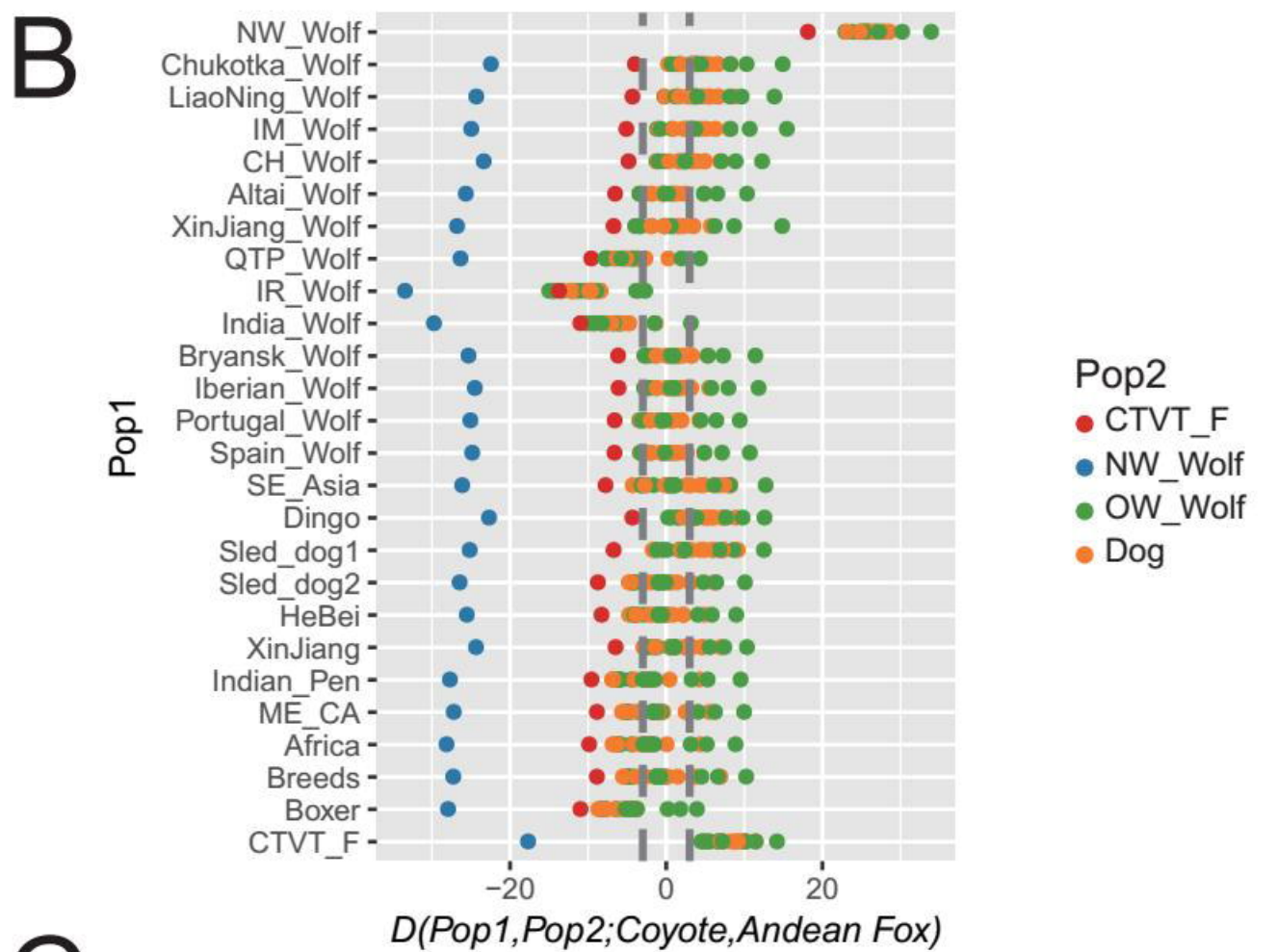
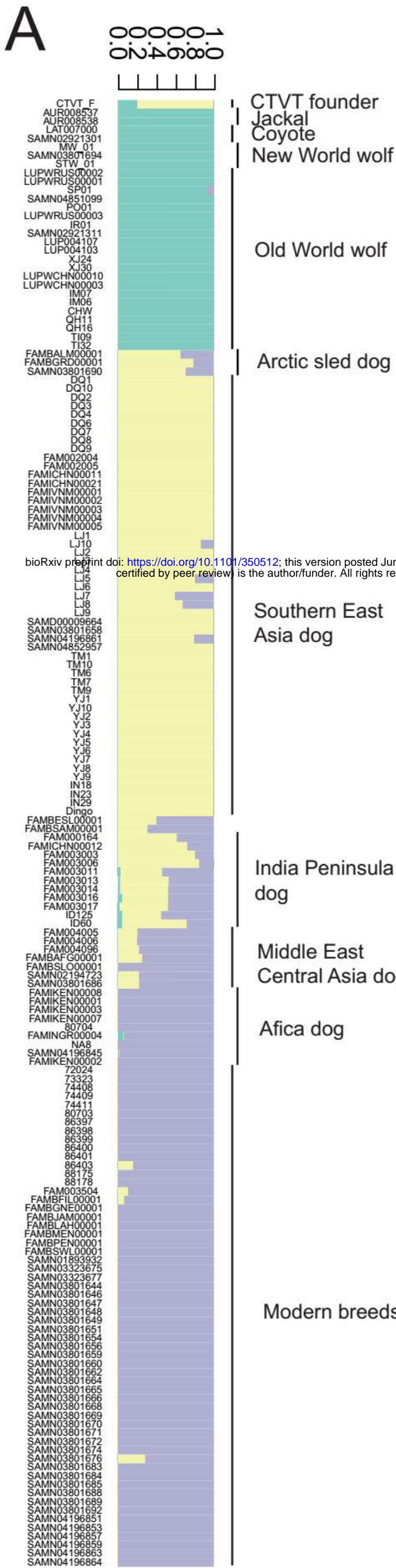
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168 **Figure Legends**

169 **Figure 1.** Analyses of introgression into the CTVT founder. **(A)** ADMIXTURE
170 analysis result (K=3) for jackal, coyote, gray wolf and dog populations with 163K
171 SNPs pruned by linkage disequilibrium. Colors indicate different ancestral
172 components. **(B)** $D(\text{Pop1}, \text{Pop2}; \text{Coyote}, \text{Andean Fox})$, with the Z-score given on the
173 x axis. When the CTVT founder is Pop2, $Z > 3$ for all Pop1 groups except the
174 New-World wolf which is a descendant of coyotes. **(C)** $D(\text{CTVT founder}, \text{Pop2}; \text{Pop3},$
175 $\text{Andean Fox})$, with the Z-score given on the x axis. When present-day arctic sled dogs
176 and coyotes are Pop3, $Z > 3$ scores for all Pop2 groups. **(D)** Introgressed segments (red
177 regions) traced by high frequency coyote private allele positions (blue regions), see
178 Supplementary Note. Genes within introgressed segments were labeled alongside
179 ideogram of chromosomes. Copy number loss regions on chromosome 6 were
180 truncated for clarity.



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