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Introduction

Birnirk (1300 – 700 BP) are a proposed genetic intermediary population, descendant from Old Bering Sea (1950 – 950 BP) and ancestral to the Thule Inuit (1000 – 550 BP). Past and contemporary Inuit populations carry specific mitochondrial DNA (mtDNA) haplotypes, or named combinations of genetic variants, A2a, A2b1, and D4b1a2a1a, which represent distinct maternal lineages and provide information on ancestry and relatedness^{5,13,12,8,1,14,15}. Birnirk genetic analyses are limited to five individuals from the Paipelghak site on the Chukotka Peninsula carrying the A2a lineage¹³.

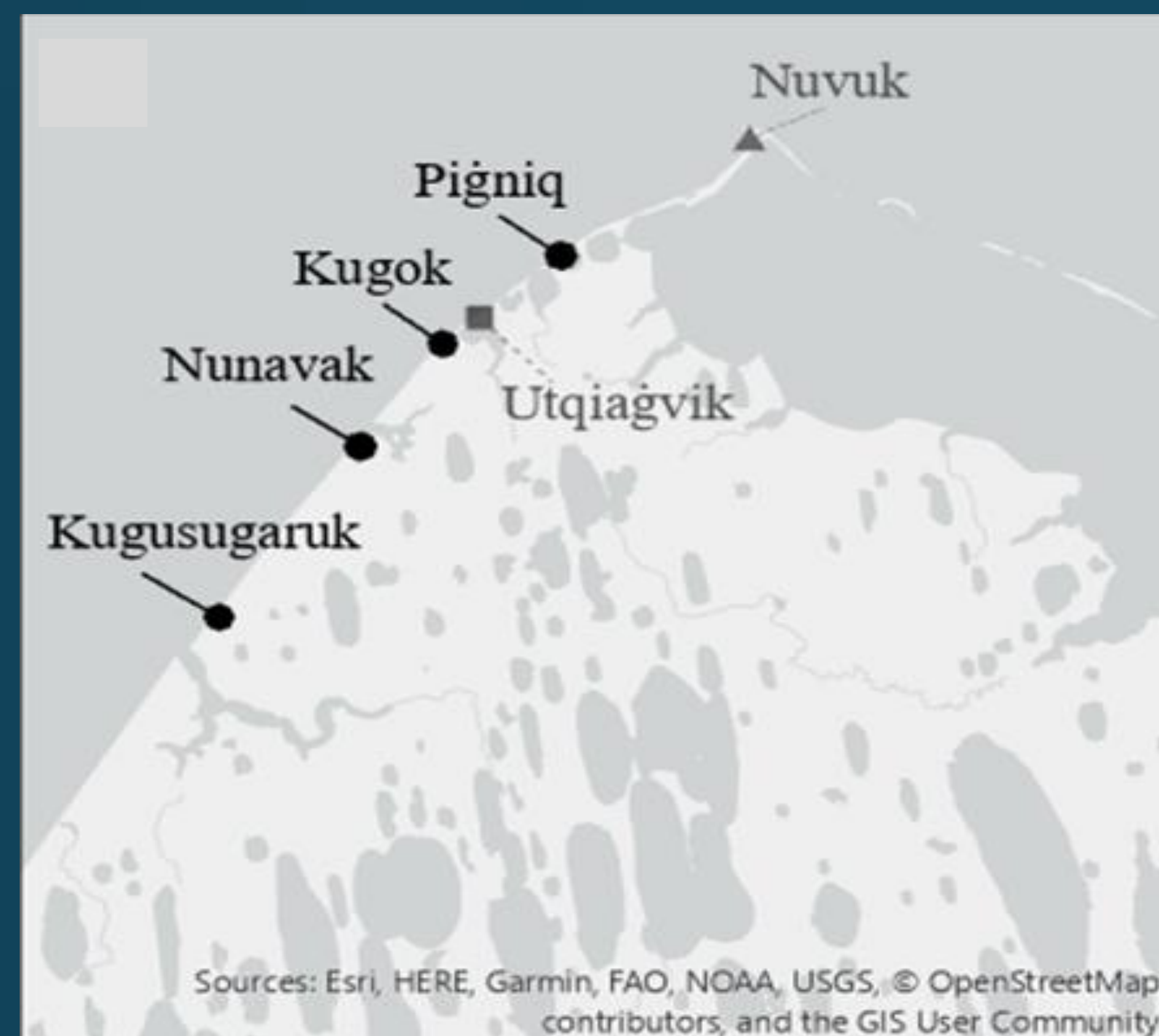


Figure 1. Sampled Birnirk sites on the Alaskan North Slope (black circles), Thule cemetery at Nuvuk (grey triangle), contemporary community of Utqiagvik, Alaska (grey square).

It is unclear if the A2a lineage represents the full extent of the Birnirk maternal gene pool, or if other Inuit lineages have yet to be documented in Birnirk populations. The Alaskan North Slope is a hypothesized location of archaeological transition from the Birnirk to Thule Inuit cultures and origin for the Thule Inuit migration across the North American Arctic^{13,7,10,4}. Four clearly associated Birnirk archaeological sites: Kugusugaruk, Nunavak, Kugok, and Pigniq (the Birnirk type site)² (Figure 1) present a unique opportunity to test for genetic continuity between Birnirk, Thule, and contemporary Inuit populations.

Permissions

Written permission was granted by the Native Village of Barrow and the Iñupiat History, Language and Culture department of the North Slope Borough to study the Birnirk collection curated at the Smithsonian National Museum of Natural History⁶.

Methods

Thirty-eight Birnirk individuals were selected for ancient DNA (aDNA) extraction. The first hypervariable region (HVR-1) of the mtDNA was sequenced^{6,9} to identify maternal haplotypes commonly found in Inuit populations.

Results

Lineages A2a, A2a1, A2a3, A2b1, and D4b1a2a1a were identified in 22 individuals from the North Slope Birnirk Inuit population (Table 1), demonstrating an expansion of maternal genetic diversity. Haplotype frequencies for the sampled population at each site is displayed in Figure 2.

Birnirk Inuit Haplotypes on the North Slope

HVR-1 SNPs:	16093	16111	16173	16192	16212	16223	16265	16261	16290	16311	16319	16362	Haplotype
rCRS:	T	C	C	C	A	C	A	C	C	T	G	T	
		T		T		T		T		A	C		A2a
		T		T		T		T		A	C		A2a1
		T		T		T		T	C	A	C		A2a3
		T		T		T	G	T		A	C		A2b1
	C		T			T				A	C		D4b1a2a1a

Table 1. Confirmed Birnirk Inuit Haplotypes found on the Alaskan North Slope.

Discussion

Identification of these maternal lineages (Table 1) supports Birnirk as an ancestral population to Thule Inuit and a continuation of genetic motifs through the Birnirk-Thule archaeological transition. Sequence diversity estimates across Inuit populations also suggest the observed maternal diversity from the North Slope was maintained through the eastward Thule migration and shift to contemporary Inuit culture.

Birnirk Inuit likely had a role in expanding the Inuit gene pool across the Bering Strait, prior to the Thule Inuit expansion. Clustering of Birnirk and past Inuit from the Chukotka Peninsula due to similarities in haplotype frequency variation (Figure 3) provides evidence for bi-directional maternal gene flow among these maritime people. Individuals across these localities may either be members of the same population that frequently traveled the Chukchi Sea, or shared a parent population.

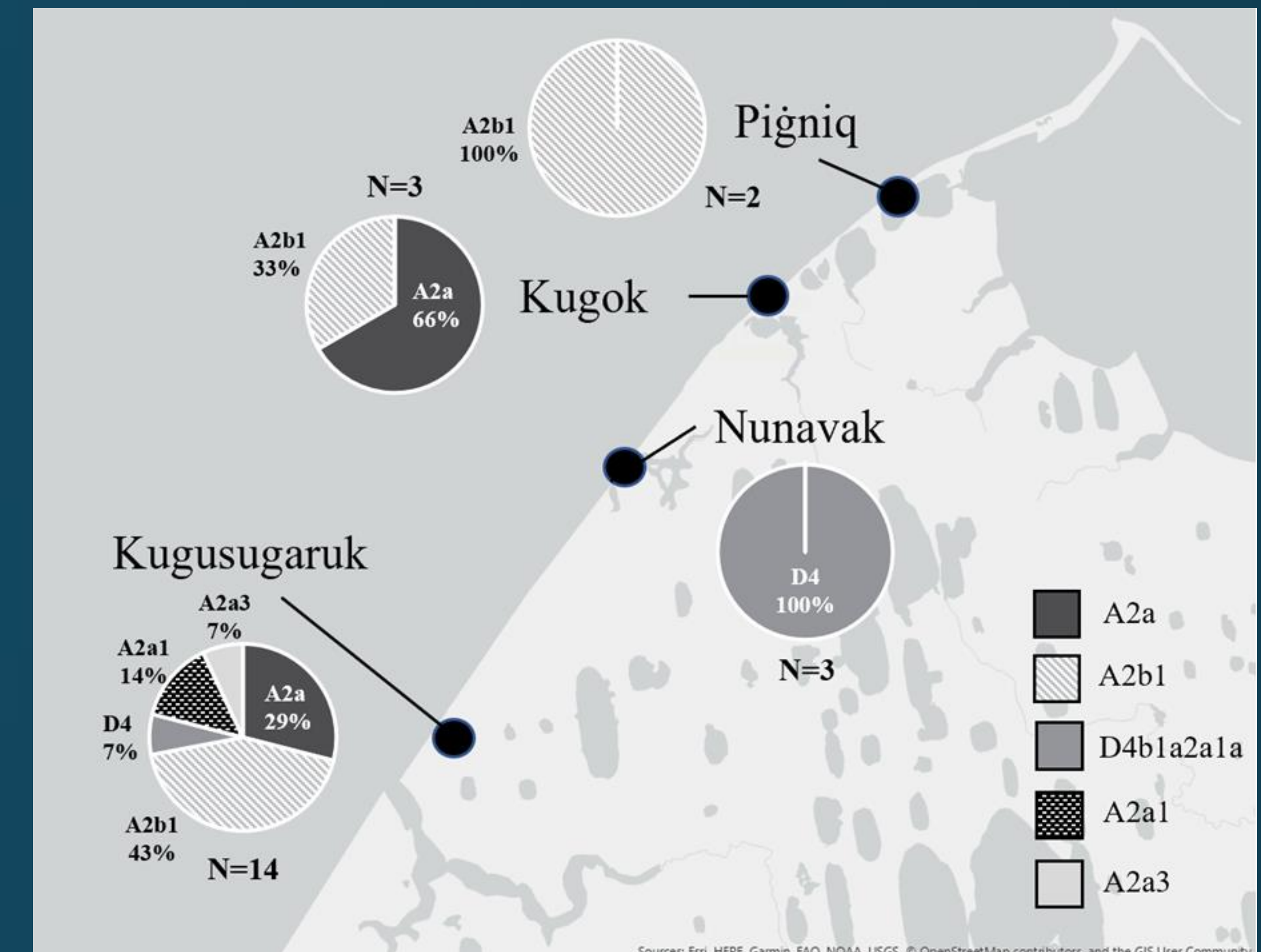


Figure 2. Haplotype frequencies for the sampled population were 27.3% A2a, 9.1% A2a1, 4.5% A2a3, 40.9% A2b1, and 18.2% D4b1a2a1a.

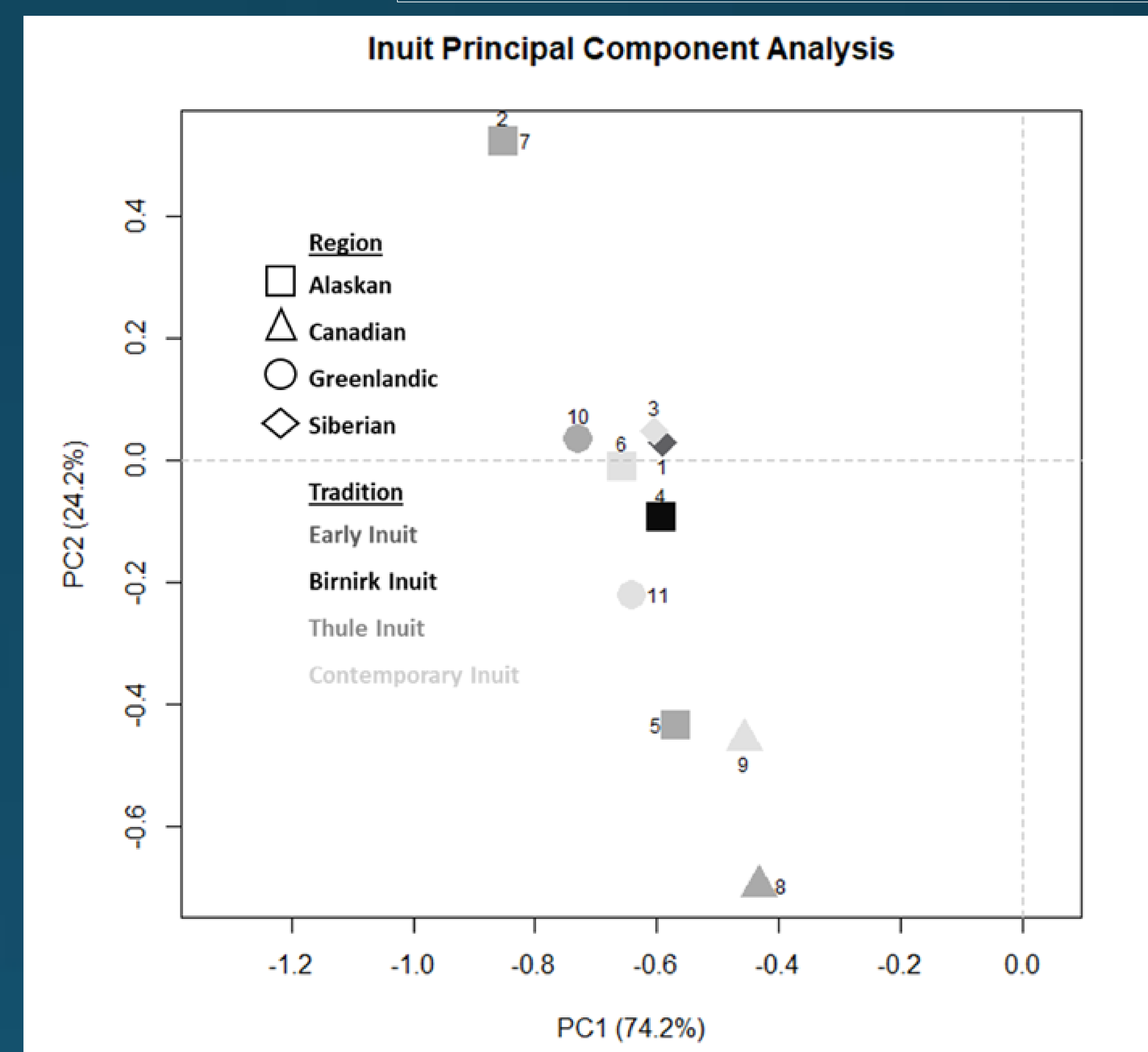


Figure 3. Principal Component Analysis. Uelen/Ekven Past Inuit (1), Paipelghak Birnirk Inuit (2), Siberian Contemporary Inuit (Sireniki, Chaplin, Naukan) (3), North Slope Birnirk Inuit (4) North Slope Thule Inuit (5), North Slope Contemporary Inuit (6), Nunalleq Thule Inuit (7), Canadian Thule Inuit (8), Canadian Contemporary Inuit (9), Greenlandic Thule Inuit (10), Greenlandic Contemporary Inuit (11).

Acknowledgements

We thank the Native Village of Utqiagvik and the Iñupiat History, Language and Culture department of the North Slope Borough for permission to sample from the collections stored at the Smithsonian National Museum of Natural History (NMNH). We appreciate NMNH Tribal Liaison, Dr. Eric Hollinger, and Collections Manager, Dr. David Hunt for their assistance. Thank you to Caroline Kisielinski for laboratory assistance, and Sarah Alden for assistance in R. We are also thankful for the National Science Foundation for funding support (Grant #1523160).

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