

# Interactions between earliest *Linearbandkeramik* farmers and central European hunter gatherers at the dawn of European Neolithization

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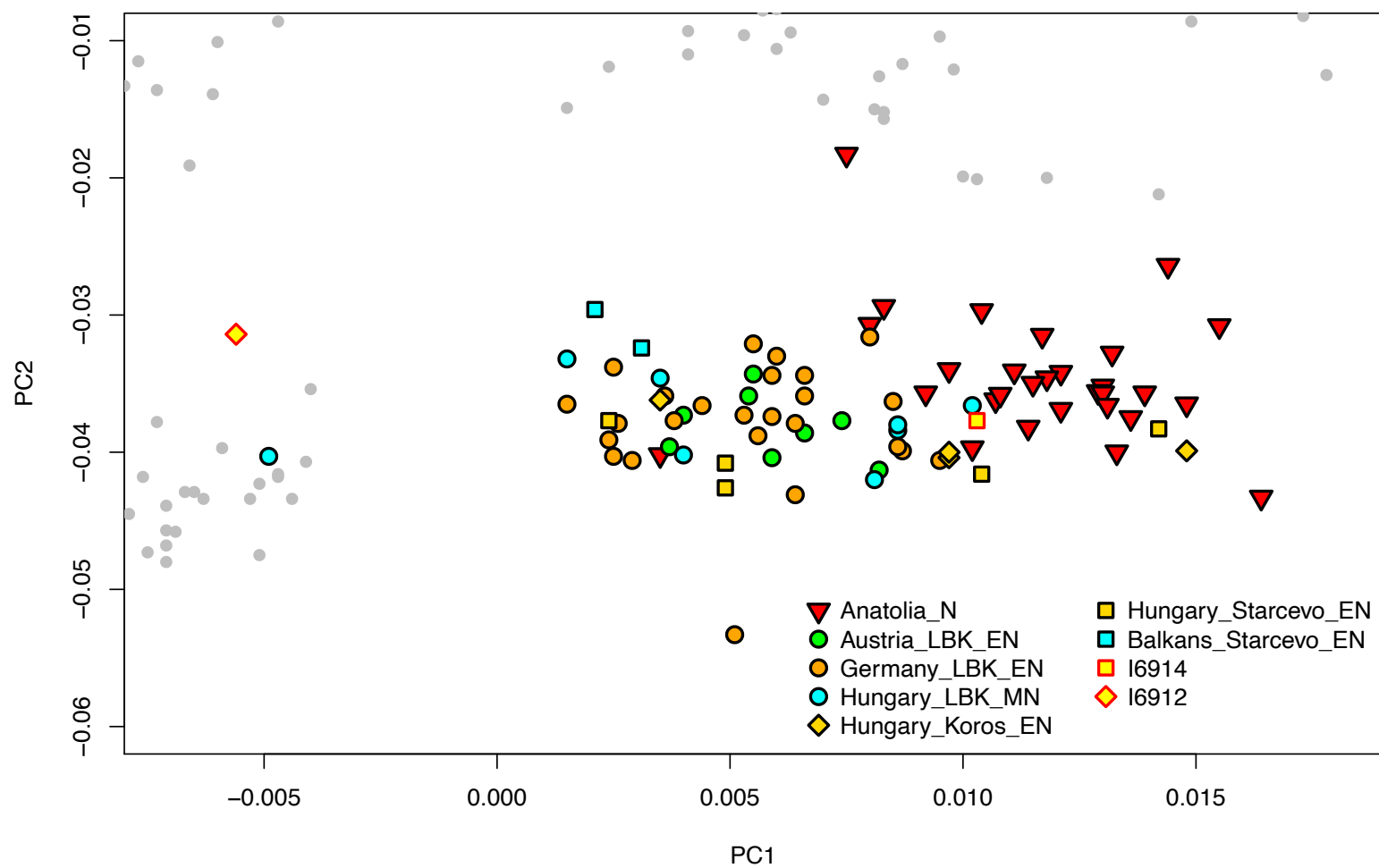
## Supplementary Information

### **Supplementary Figure S1.**

A zoomed-in PCA plot from Figure 1, showing the position of Individuals 1 (I6912) and 3 (I6914) relative to Anatolian and European Neolithic farmers. .... 2

**Supplementary Table S1.** Library-level metrics for Brunn Wolfholz site 2 genetic data. .... 3

**Supplementary Figure S1.** A zoomed-in PCA plot from Figure 1, showing the position of Individuals 1 (I6912) and 3 (I6914) relative to Anatolian and European Neolithic farmers.



**Supplementary Table S1.** Library-level metrics for Brunn Wolfholz site 2 genetic data.

Library ID	S6912.E1.L3	S6912.E1.L2	S6912.E1.L3	S6912.E1.L5	S6912.E1.L6	S6913.E1.L1	S6914.E1.L1	S6915.E1.L1
Lab Ind. ID	I6912	I6912	I6912	I6912	I6912	I6913	I6914	I6915
Skeletal Code/Element	Ind. #1, left lower first or second molar (permanent tooth no. 36 or 37)					Ind. #2, left or right lower second molar (permanent mandibular molar no. 37 or 47)	Ind. #3, right lower second molar (permanent mandibular molar no. 47)	Ind. #4, left lower second molar (permanent mandibular molar no. 37)
Powder Extracted (mg)	69	69	69	69	69	73	82	76
Library protocol	Double-stranded	Double-stranded	Single-stranded	Double-stranded	Single-stranded	Double-stranded	Double-stranded	Double-stranded
UDG Treatment	partial	minus	minus	partial	partial	partial	partial	partial
uL Extract Used	10	10	10	10	10	10	10	10
mg Equivalent Powder Used	7.7	7.7	7.7	7.7	7.7	8.1	9.1	8.4
mtDNA Raw Sequences	1540475	4895353	5569976	4363797	5222170	1763868	1574760	1628891
mtDNA Sequences Passing Filters	1328578	4280940	4539284	3394382	4031310	1557034	1443480	1320302

<b>mtDNA Sequences Aligning</b>	344350	33525	61320	28964	61225	393193	46072	2623
<b>mtDNA Sequences Aligning PostDedup</b>	19275	17161	36981	13126	35607	58380	18405	346
<b>mtDNA Coverage</b>	54.4	55.5	127.3	39.7	111.8	187.0	48.7	0.9
<b>mtDNA Median [Mean] Seq Length</b>	45	[53.6]	[57.1]	[50.1]	[52.0]	50	43	43
<b>mtDNA Damage Last Base</b>	0.13	0.45	0.47	0.13	0.14	0.08	0.14	0.11
<b>mtDNA Consensus Match</b>	1.000	0.984	0.955	0.998	0.976	1.000	0.961	0.918
<b>mtDNA Consensus Match 95CI</b>	[0.997,1.000]	[0.963,0.994]	[0.932,0.973]	[0.990,1.000]	[0.962,0.986]	[0.998,1.000]	[0.951,0.968]	[0.838,0.967]
<b>mtDNA Haplogroup</b>	J1	J1	J1c8	J1	J1c	U5a1	K1b1a	..
<b>Nuclear Raw Reads</b>	4142974	4895353	5569976	4363797	5222170	4716548	11664837	5602849
<b>Nuclear Sequences Merged with Barcode</b>	3456700	4280940	4539284	3394382	4031310	4092020	10590010	4933624

<b>Nuclear Target Sequences Passing QC PreDedup</b>	76508	13533	26209	10776	32522	52727	2709080	10521
<b>Nuclear Target Sequences Passing QC PostDedup</b>	5222	4751	12941	3298	15246	7699	642592	1219
<b>Nuclear Unique SNPS Hit</b>	4830	3866	10888	3351	15488	7223	429000	..
<b>Nuclear Coverage at Targeted Positions</b>	0.004	0.004	0.011	0.003	0.013	0.006	0.497	..
<b>Nuclear Median [Mean] Seq Length</b>	43	[58.8]	[64.7]	[55.9]	[62.4]	39	44	37
<b>Nuclear Damage Last Base</b>	0.03	0.32	0.32	0.09	0.08	0.03	0.10	0.01
<b>Nuclear X Hits</b>	103	77	303	56	333	150	9551	..
<b>Nuclear Y Hits</b>	73	40	142	25	135	107	7109	..
<b>Nuclear Sex</b>	M	M	M	M	M	M	M	..
<b>Nuclear ANGSD SNPs</b>	1	0	0	1	4	0	345	0
<b>Nuclear ANGSD X-contam Mean</b>							0.0044	

**Nuclear ANGSD  
X-contam Z-  
score**

0.8999