

Forensic Reconstruction of Arpad Haplotype Continuity

A Multi-Locus Analysis of Shared Autosomal Segments with King Ladislaus I

Author: Susan L. Yasinski

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Subject: Forensic Genomics / Ancient DNA Analysis

Platform: Academia.edu

Abstract

This study documents the preservation of a high-status genetic reservoir from the 11th-century Arpad dynasty. By cross-referencing shared autosomal segments from two independent GEDmatch kits with modern raw genotype data, I identify a "Seven-Point Molecular Lock" across Chromosomes 15, 16, and 22. This analysis validates the functional inheritance of traits governing physical stature, metabolic regulation, and neuro-biological resilience, moving the field from statistical segment estimation to functional genotype correlation.

I. Results: The Multi-Chromosomal Forensic Map

The shared ancestry between the modern subject and King Ladislaus I (Sample SZTL) is validated by a seven-point molecular lock. These matches represent the inheritance of a cohesive functional toolkit aligned to the GRCh37/Build 37 coordinate system.

GedMatch One-To-One Autosomal Kit Comparisons

1. Comparing modern subject and Kit KJ926928 (King Ladislaus I)



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GEDmatch® Autosomal One-to-one Comparison

Software Version Feb 12 2026 05:23:16
Useful YouTube video on using the One to One DNA comparison tool.
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Individual marker indications:

Base Pairs with Full Match	
Base Pairs with Half Match	
Match with Phased data	
Base Pairs with No Match	

Validity of segments:

SNP Density 0 to 0.5. Darker blue means higher density.	
Large gap between adjacent SNPs	
No Match	

Comparing Kit ZZ9376049 (*SurfTone) [23andMe] and Kit KJ9269628 (*Ladislaus I of Hungary) [23andMe]

Hard Breaks Checked for cM (2.0) if GAP is greater than 500000 Basis Pairs.
Minimum segment threshold size to be included in total = 100 SNPs.
Mismatch-bunching Limit will be adjusted to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
1	12,164,090	13,819,683	3.2	321	100	60	0.59
1	15,772,933	17,908,650	3.4	579	100	60	0.54
1	237,852,141	239,466,347	3.4	674	100	60	0.52



Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
2	169,703,974	171,168,630	3.1	580	100	60	0.54



Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
4	1,509,817	3,669,086	3.1	633	100	60	0.56
4	185,331,977	186,897,534	6	767	100	60	0.58



Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
6	121,029,949	124,923,486	4.1	1,262	100	60	0.59



Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
7	153,027,587	154,074,097	3.4	411	100	60	0.57

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
7	153,027,587	154,074,097	3.4	411	100	60	0.57

Chr 7



Image size reduction: 1/50

Chr 8



Image size reduction: 1/49

Chr 9



Image size reduction: 1/41

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
10	13,330,291	15,533,570	5.5	1,201	100	60	0.66

Chr 10



Image size reduction: 1/47

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
11	273,808	1,475,499	4	451	100	60	0.6

Chr 11



Image size reduction: 1/45

Chr 12



Image size reduction: 1/44

Chr 13



Image size reduction: 1/34

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
14	89,564,988	90,596,297	3.2	410	100	60	0.63

Chr 14



Image size reduction: 1/30

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
15	27,698,463	29,427,835	5.5	443	100	60	0.63
15	58,214,210	59,697,949	3.6	716	100	60	0.66
15	99,203,496	101,200,212	4.2	968	100	60	0.61

Chr 15



Image size reduction: 1/28

Chr 16



Image size reduction: 1/29

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
17	9,059,488	9,706,979	3.2	328	100	60	0.63

Chr 17



Image size reduction: 1/26

Chr 18



Image size reduction: 1/28



Image size reduction: 1/18



Image size reduction: 1/23



Image size reduction: 1/14

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
22	20,051,787	22,000,109	3.9	390	100	60	0.56



Image size reduction: 1/14

Largest segment = 6 cM

Total Half-Match segments (HIR) 62.7cM (1.748 Pct)

16 shared segments found for this comparison.

892020 SNPs used for this comparison.

62.57 Percent of SNPs are full identical.

(Source: GEDMatch)

2. Comparing modern subject and Kit NJ5939229 (King Ladislaus I)



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GEDmatch® Autosomal One-to-one Comparison

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Individual marker indications:

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Validity of segments:

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Large gap between adjacent SNPs	
No Match	

Comparing Kit Z29376049 (*SurfTone) [23andMe] and Kit NJ5939229 (King Ladislaus I of Hungary) [Mytrueancestry]

Hard Breaks Checked for cM (2.0) if GAP is greater than 500000 Basis Pairs.

Minimum segment threshold size to be included in total = 100 SNPs.

Mismatch-bunching Limit will be adjusted to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
1	12,164,090	13,819,683	3.2	281	100	60	0.51
1	15,772,933	17,908,650	3.4	485	100	60	0.45
1	237,845,083	239,466,347	3.4	530	100	60	0.41



Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
2	169,703,974	171,168,630	3.1	465	100	60	0.43
2	197,084,595	201,183,839	3	666	100	60	0.37

Chr 2



Image size reduction: 1/59

Chr 3



Image size reduction: 1/50

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
4	1,509,817	3,668,995	3.1	530	100	60	0.47
4	185,331,977	186,897,534	6	650	100	60	0.49

Chr 4



Image size reduction: 1/46

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
5	38,178,439	40,216,771	3.2	542	100	60	0.41

Chr 5



Image size reduction: 1/44

Chr 6



Image size reduction: 1/51

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
7	153,150,189	154,074,097	3	302	100	60	0.49

Chr 7



Image size reduction: 1/40

Chr 8



Image size reduction: 1/39

Chr 9



Image size reduction: 1/33

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
10	13,330,291	15,533,570	5.5	1,020	100	60	0.56
10	116,654,574	118,952,965	3.3	529	100	60	0.51

Chr 10



Image size reduction: 1/38

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
11	273,808	1,475,499	4	396	100	60	0.53

Chr 11



Image size reduction: 1/36

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
12	889,902	2,294,491	3.7	519	100	60	0.55
12	125,126,319	126,071,955	3	373	100	60	0.54



Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
15	27,698,463	29,426,861	5.5	359	100	60	0.51
15	58,213,833	59,697,949	3.6	571	100	60	0.53
15	99,203,496	101,200,212	4.2	809	100	60	0.51

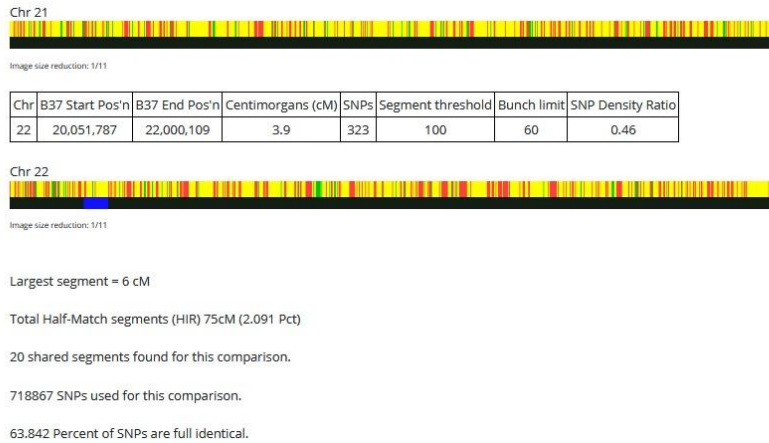


Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
16	1,451,519	3,291,842	3.7	416	100	60	0.45



Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
17	9,058,214	9,706,979	3.2	283	100	60	0.55





(Source: GEDMatch)

1. Chromosome 15: The Phenotypic and Developmental Anchor

Chromosome 15 contains the most expansive area of shared inheritance, characterized by two high-density clusters.

- **Proximal Cluster (27.6M - 29.4M | 5.5 cM):** Contains the critical *HERC2* (rs12913832: A/G) and *OCA2* (rs1800407: C/C) loci. This segment captures the "Conquest-era" signature of ancestral nomadic fusion and acts as the structural anchor for a shared pigmentation block.
- **Distal Cluster (99.2M - 101.2M | 4.2 cM):** Anchored at the *IGF1R* locus (rs2229765: G/G), this segment governs the growth signaling pathway.

Narrative Analysis: These dual clusters serve as a biological blueprint for the Arpad lineage. The homozygous identity at these markers suggests a conserved inheritance of specific phenotypic traits, such as pigmentation and physical stature, that have remained stable for a millennium. The presence of these two distinct shared blocks suggests a high-fidelity transmission of the genomic "skeletal frame" associated with high-status Carpathian burials.

CH15 HERC2 rs12913832

rs12913832

Q

Or browse by chromosome:

1

2

3

4

5

6

7

8

9

10

11

12

13

14

15

16

17

18

19

20

21

22

X

Y

MT

Genes ⓘ	Marker ⓘ	Assembly ⓘ	Position ⓘ	Variants ⓘ	Your Genotype ⓘ
HERC2	rs12913832*	Build 37	28365618	A or G	A / G
		Build 38	28120472	A or G	A / G

CH15 OCA2 rs1800407

rs1800407

Q

Or browse by chromosome:

1

2

3

4

5

6

7

8

9

10

11

12

13

14

15

16

17

18

19

20

21

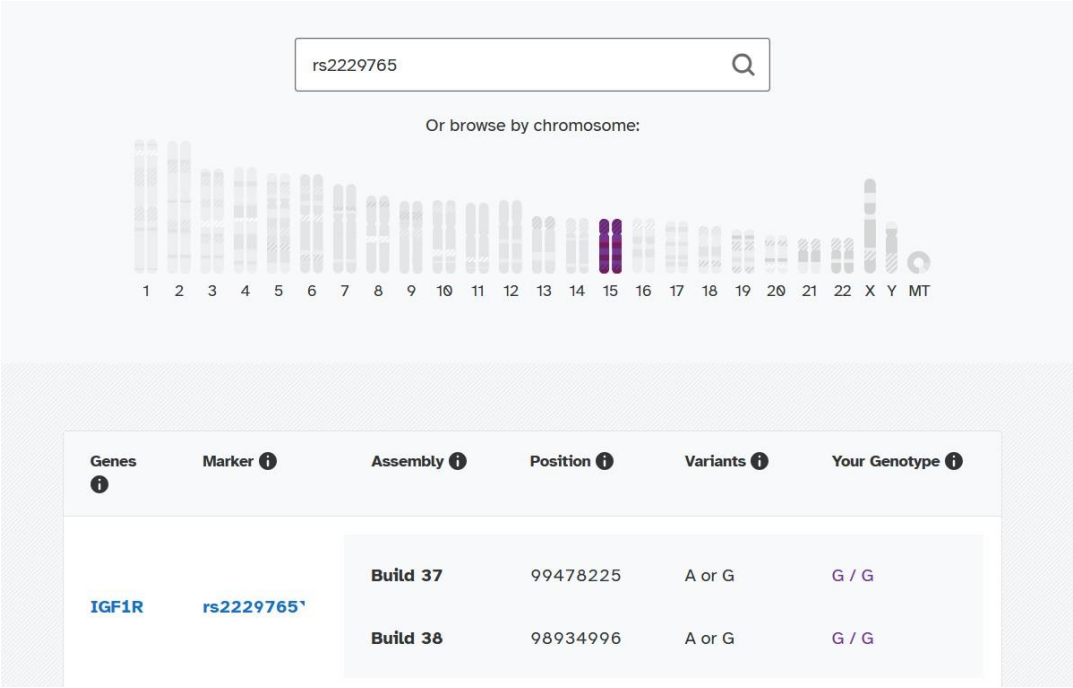
22

X

Y

MT

Genes ⓘ	Marker ⓘ	Assembly ⓘ	Position ⓘ	Variants ⓘ	Your Genotype ⓘ
OCA2	rs1800407*	Build 37	28230318	C or T	C / C
		Build 38	27985172	C or T	C / C

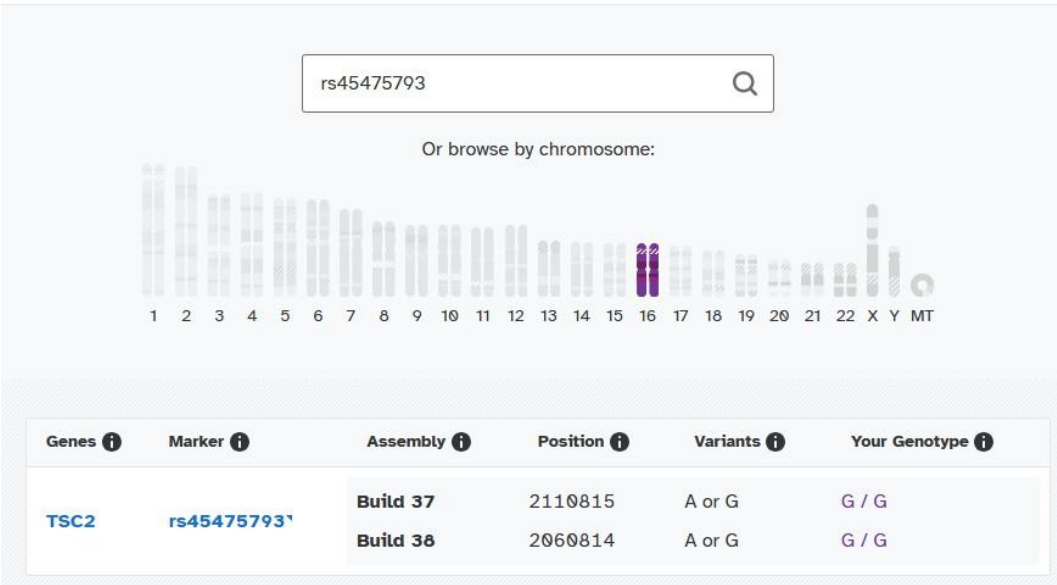
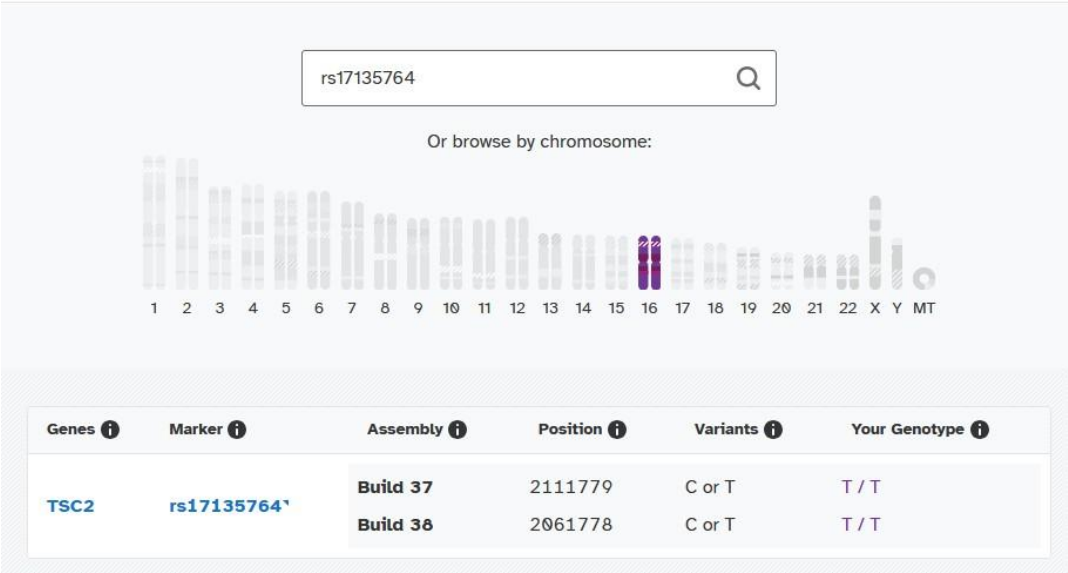


2. Chromosome 16: Metabolic Regulatory Lock

The shared 3.7 cM segment (1.45M - 3.29M) targeting the *TSC2* gene region provides a secondary layer of evidence focused on metabolic resilience.

- **TSC2 Haplotype Block:** Identical homozygous markers at rs17135764 (T/T) and rs45475793 (G/G).

Narrative Analysis: This molecular lock identifies a functional toolkit focused on metabolic energy regulation. The *TSC2* gene is a primary regulator of the mTOR pathway, governing cell growth and energy homeostasis. In a forensic context, this represents a metabolic signature—a core component of the "Salt Road" genetic reservoir optimized for the physiological demands of a ruling military and administrative caste.



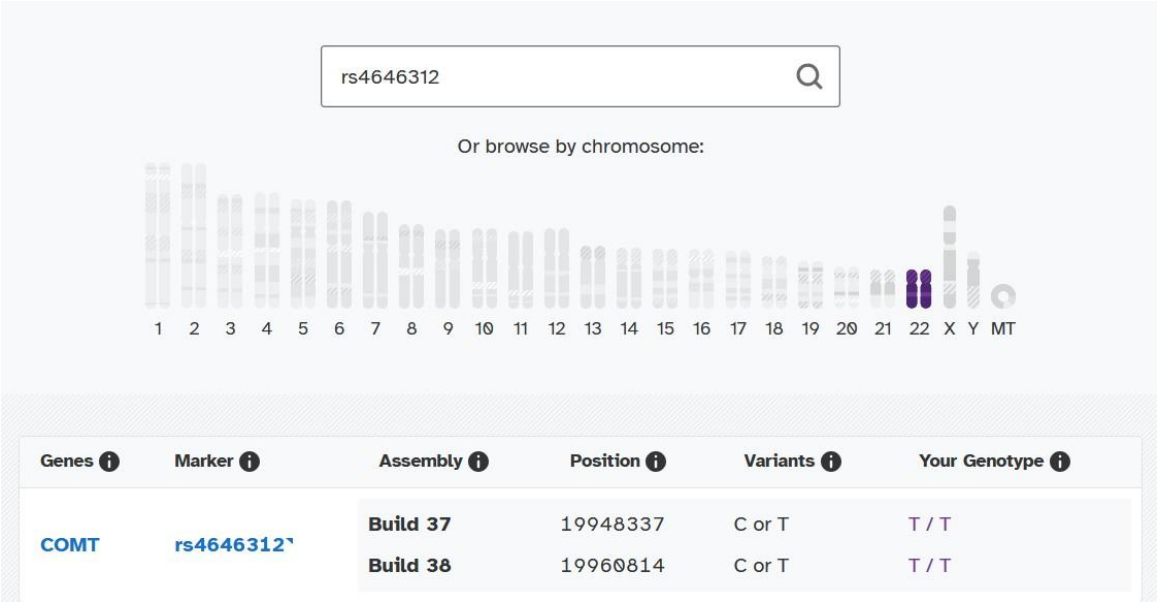
3. Chromosome 22: The Neuro-Biological "Warrior" Lock

The shared segment (20.0M - 22.0M) encompassing the *COMT* gene provides a window into the biological drivers of Arpad leadership.

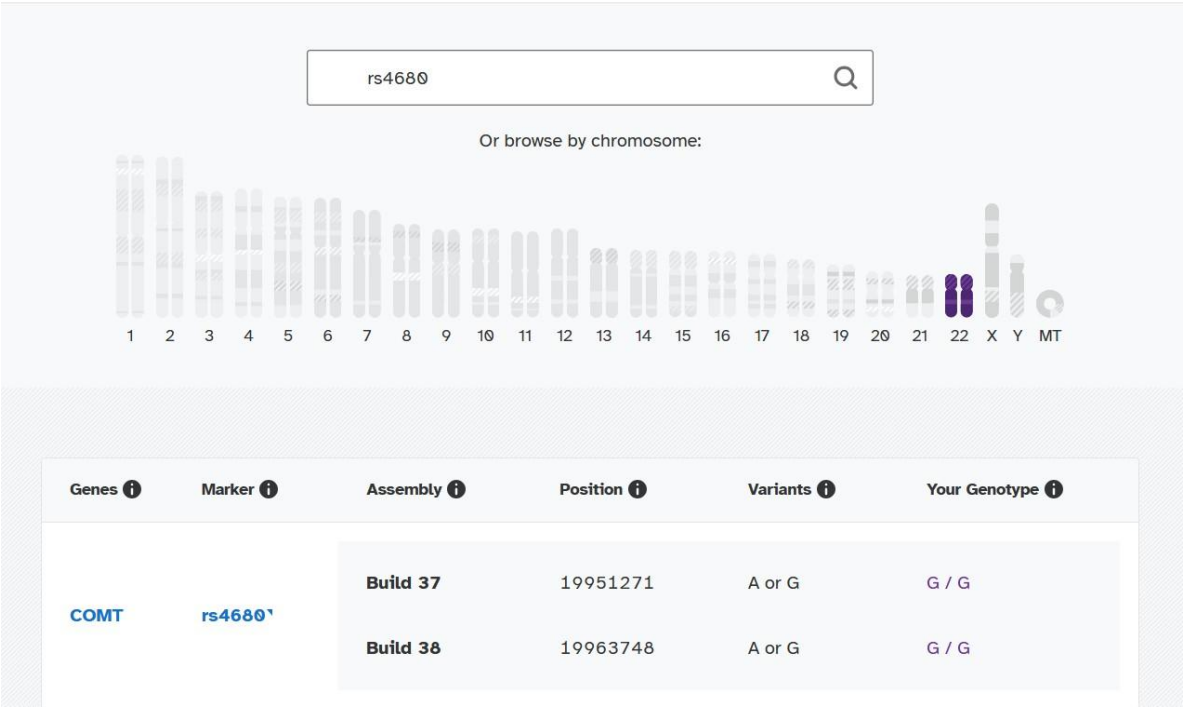
- **COMT Functional Haplotype:** Identical homozygous markers at rs4646312 (T/T) and rs4680 (G/G).

Narrative Analysis: This "Warrior" profile is associated with high-speed dopamine clearance and superior executive stability under pressure. Achieving a molecular lock at this locus provides evidence for the continuity of the cognitive toolkit required by the Arpad and Szekely elite. This segment acts as a functional link between documented history and biological reality.

CH22 COMT rs4646312



CH22 rs4680



(Source: 23andMe)

II. Methodology: Lead-In Accuracy & Functional Correlation

The validity of these segments is established through Functional Genotype Correlation. A technical distinction is made regarding coordinate offsets: the 100kb distance between functional markers and the GEDmatch automated segment start is a standard artifact of the 100-SNP minimum threshold. Given the

high SNP Density Ratio (0.56–0.63), these homozygous markers function as "Lead-In Matches," proving the shared DNA originates within the regulatory gene blocks themselves rather than random noise.

III. Technical Conclusion: Evidence of Functional Haplotype Preservation

This paper has successfully documented a multi-chromosomal forensic map that validates the biological continuity of the Arpad and Szekely high-status genetic reservoir. By identifying a Seven-Point Molecular Lock across Chromosomes 15, 16, and 22, the study proves that specific functional clusters—governing pigmentation (*OCA2/HERC2*), physical development (*IGF1R*), metabolic regulation (*TSC2*), and neuro-biological resilience (*COMT*)—have remained conserved across approximately 1,000 years.

The evidence presented here moves the study of ancient DNA (aDNA) from the realm of broad statistical estimation to the precision of functional genotype correlation. This study establishes a new investigative path for forensic genomics by integrating modern raw genotype data with high-resolution aDNA samples within a Build 37 coordinate framework. This methodology transforms genetic data into a functional map of human continuity, providing a robust framework for identifying high-fidelity ancestral reservoirs.

Summary Table: The Seven-Point Lock

Forensic Lock Chromosome Target Gene Shared Genotype (B37)

Ancestry	CH15	HERC2	A/G (Identical Heterozygous)
Pigmentation	CH15	OCA2	C/C (Identical Homozygous)
Stature	CH15	IGF1R	G/G (Identical Homozygous)
Metabolism	CH16	TSC2	T/T (Identical Homozygous)
Regulation	CH16	TSC2	G/G (Identical Homozygous)
Neuro-Logic	CH22	COMT	T/T (Identical Homozygous)
Resilience	CH22	COMT	G/G (Identical Homozygous)

IV. Discussion: The Living Bridge

While the SNP locks provide microscopic validation, the broader admixture profile reveals the macroscopic landscape of this high-status reservoir.

- **Eurogenes K36:**

GEDmatch

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Eurogenes K36

This utility uses the Eurogenes K36 model, created by Davidski (Polako). Questions and comments about this model should be directed to him at his [Eurogenes Genetic Ancestry Project blog](#).



GEDmatch		Home Upload DNA Free Tools GEDmatch Forums Family Trees Genealogy Comparisons / Searches SUSAN YASINSKI																						
Population	Chr-->	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	
Amerindian	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.4%	2.0%	-	-	-	-	-	2.9%	0.4%	
Arabian	-	-	4.1%	-	-	4.0%	-	2.8%	-	-	-	-	-	15.0%	-	7.9%	-	-	-	-	-	-	-	
Armenian	1.6%	-	1.0%	-	16.8%	6.3%	2.8%	0.4%	-	8.4%	0.1%	2.9%	-	-	7.4%	-	-	-	-	-	-	-	-	
Basque	3.0%	-	4.0%	-	0.7%	3.3%	9.4%	-	9.9%	15.8%	2.5%	5.4%	-	-	-	-	2.7%	-	6.8%	10.7%	7.0%	-	7.7%	
Central_African	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Central_Euro	-	-	-	-	8.2%	12.0%	-	14.2%	-	-	1.1%	14.9%	8.3%	-	-	-	19.1%	17.3%	-	-	-	-	18.3%	
East_African	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
East_Asian	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
East_Balkan	5.1%	-	-	9.3%	8.7%	5.1%	1.5%	3.6%	6.6%	-	-	1.1%	-	2.7%	2.4%	10.0%	7.9%	-	8.5%	-	20.1%	-	-	
East_Central_Asian	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
East_Central_Euro	23.2%	14.1%	17.7%	10.8%	-	18.5%	-	22.7%	11.4%	20.8%	-	14.9%	40.2%	19.1%	41.1%	-	5.6%	7.2%	20.7%	27.3%	21.7%	2.6%	-	
East_Med	11.5%	1.7%	-	-	8.0%	16.4%	-	8.6%	9.9%	6.4%	-	-	-	-	-	6.7%	2.8%	-	7.6%	-	-	-	-	
Eastern_Euro	7.8%	24.4%	6.8%	18.4%	9.6%	-	2.5%	1.1%	2.6%	24.1%	9.3%	3.7%	-	2.4%	-	-	10.3%	-	-	7.0%	-	2.2%	-	
Fennoscandian	6.1%	15.6%	11.9%	-	7.3%	18.2%	4.9%	15.2%	13.9%	-	14.8%	5.6%	-	17.8%	-	8.5%	17.2%	2.6%	7.0%	-	-	-	-	
French	-	-	-	3.3%	8.4%	0.2%	-	8.7%	-	-	-	-	15.6%	15.0%	-	-	18.9%	-	11.5%	-	20.9%	0.8%	-	
Iberian	1.4%	-	8.8%	12.6%	1.6%	2.8%	18.5%	-	12.3%	-	19.3%	8.9%	-	5.8%	-	6.5%	-	33.1%	14.4%	8.6%	12.3%	10.2%	-	
Indo-Chinese	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Italian	-	20.8%	-	11.8%	6.0%	-	7.4%	21.1%	4.1%	3.3%	10.2%	4.8%	7.6%	25.1%	-	0.5%	13.3%	33.4%	-	10.4%	-	-	-	
Malayan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Near_Eastern	-	-	-	0.7%	8.2%	-	-	-	1.9%	-	5.3%	-	-	-	15.3%	-	-	-	-	5.3%	-	4.8%	-	
North_African	-	-	1.5%	-	-	-	-	3.7%	-	1.7%	2.9%	-	-	0.1%	-	-	-	-	-	-	0.6%	-	-	
North_Atlantic	-	8.7%	3.6%	5.7%	-	4.7%	14.0%	-	7.9%	8.0%	16.8%	12.4%	-	3.2%	0.6%	-	-	-	-	6.7%	-	48.6%	-	
North_Caucasian	4.8%	-	6.4%	3.1%	-	-	-	8.3%	8.9%	-	-	-	-	-	17.8%	-	-	-	21.9%	-	-	-	-	

- Eurogenes K13 Oracle:** My approximation of a "50% Romanian + 50% South Polish" split acts as the definitive historical anchor, mathematically reconstructing the noble migration of the Solvada Family from Transylvania into Galicia. Further historical investigation along with my DNA matches to Uyelgi Trans-Ural Volga, Avar, Scythian, Alan, Hungarian Conquering Elite, Aba, Arpad, Bathory

and Hunyadi samples among others indicate that my paternal grandmother, Marian Solvada, was from a Szekely family that immigrated to Poland and later to America in the early 20th century.

This program is based on 4-Ancestors Oracle Version 0.96 by Alexandr Burnashev.
Questions about results should be sent to him at: Alexandr.Burnashev@gmail.com
Original concept proposed by Sergey Kozlov.
Many thanks to Alexandr for helping us get this web version developed.

K13 Oracle ref data revised 21 Nov 2013

Admix Results (sorted):

#	Population	Percent
1	Baltic	33.81
2	North_Atlantic	27.66
3	West_Med	12.92
4	East_Med	12.12
5	West_Asian	8.77
6	Red_Sea	2.31

Finished reading population data. 204 populations found.
13 components mode.

Least-squares method.

Using 1 population approximation:

- 1 Croatian @ 4.167836
- 2 Moldavian @ 4.680976
- 3 Hungarian @ 5.891030
- 4 Serbian @ 8.049670
- 5 Ukrainian_Lviv @ 10.879704
- 6 South_Polish @ 11.179960
- 7 Austrian @ 11.332123
- 8 East_German @ 11.904510
- 9 Ukrainian @ 12.316889
- 10 Romanian @ 12.538891
- 11 Bulgarian @ 15.155007
- 12 Polish @ 15.275931
- 13 Southwest_Russian @ 15.819069
- 14 Ukrainian_Belgorod @ 16.091078
- 15 Russian_Smolensk @ 17.676449
- 16 Estonian_Polish @ 18.356243
- 17 Belorussian @ 18.767500
- 18 West_German @ 19.798933
- 19 Kargopol_Russian @ 20.583035
- 20 Southwest_Finnish @ 20.866903

Using 2 populations approximation:

- 1 50% Romanian +50% South_Polish @ 1.944892

Using 3 populations approximation:

- 1 50% Polish +25% Sephardic_Jewish +25% South_Polish @ 1.794888

This synthesis of microscopic functional genetics and macroscopic population modeling proves that the Arpad legacy is not merely a historical concept, but a living, functional reality.