SLY Archaeogenetic Master Dossier (v8.1 Consolidated)

Subject: SLY (BXWEAO_scaled | GEDmatch ZZ9376049 | Female XX, b. 1954) • Primary Royal Reference: King Saint Ladislaus I (SZTL, d. 1095 AD)

Binder Overview & Key Headline Metrics: 8,666 Audited Markers (100% IBS ≥ 1) • **57.4 cM** across 15 Non-Pileup ROH Cores (62.7–75.0 cM Full HIR) • **110.17 Mb + 37 PAR1** Unrecombined 1888 Székely Paternal X • **#1 Báthory (0.0162) & #3 Aba (0.0190)** G25 Distances out of 2,760 Ancient Populations.

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Page 3 — Quick-Reference Sheet 2: Unrecombined 1888 Székely Paternal X Connection
Explains non-recombining paternal X inheritance (1888 Grandmother → 1927 Father `TVIPUB` → SLY) with a physical map of Chromosome 23 showing 100% concordance across `110.17 Mb` (`MAOA` → `EDA2R x3` → `G6PD`) plus all `37/37` markers in `PAR1`.

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Assembly & Controls: GRCh37 (hg19) Forward (+) Strand • Paternal Control: `TVIPUB_scaled` (b. 1927) • Maternal Control: `ILAWCS_scaled`.

Your DNA Link to King Saint Ladislaus I's Maternal Line

Byzantine I14843 (550 AD) & Merovingian Rhineland/Bavaria (600 AD) → King Saint Ladislaus I (SZTL) → SLY

30-Second Summary: "My DNA matches King Saint Ladislaus I (sample SZTL) on the exact same chromosome spots where both of us match ancient people from his mother's family homelands—Byzantine Turkey (550 AD) and the German Rhineland/Bavaria (600 AD). Parental testing confirms these segments are on **my mother's side (ILAWCS)**, forming a direct genetic bridge to King Ladislaus I through his maternal lineage."

Key Shared Chromosome Hubs (Where History & DNA Meet)

Chr	Who Stacks Together on You	Overlap Location (GRCh37)	SNPs	Plain-English Meaning
Chr 16	**King Ladislaus I** + **Bavaria Alh_117**	31.17 – 46.74 Mb (15.57 Mb)	**380** / **121**	Bavarian ancestor covers 100% of Ladislaus's 90.95 cM block on you.
Chr 19	**Byzantine I14843 → 4 Merovingians → Core**	19.41 – 49.21 Mb (29.80 Mb)	**113–309**	Unbroken 7-step chain leading straight to your exact APOE–FUT2 match.
Chr 11	**King Ladislaus I** + **Rhineland IND005**	47.98 – 51.58 Mb (3.60 Mb)	**415** / **149**	Rhineland ancestor locks onto the exact start of your Ladislaus hub.
Chr 20	**King Ladislaus I** + **Rhineland IND003 & 005**	25.49 – 29.52 Mb (4.04 Mb)	**110–169**	Two Rhineland ancestors stack directly over Ladislaus's segment.
Chr 2	**Rhineland IND003 & 005** + **Bavaria Alh_117**	88.75 – 95.70 Mb (6.95 Mb)	**122–133**	Three Merovingian individuals lock together on your maternal side.

1. Why His Mother's Side?

King Ladislaus I descended maternally from **Byzantine Princess Theophanu** and **Rhineland nobility** (Richeza of Lotharingia)—the exact regions of I14843 and IND003/005/012/014.

2. Why Maternal on SLY?

Trio G25 controls (mother **ILAWCS** vs. father **TVIPUB**) place your Rhineland/Bavarian blocks on your mother's side, meeting paternal Székely blocks at APOE & FUT2.

3. Solid Marker Counts

Ancient DNA matches require 50–100 SNPs to be reliable. Every hub here clears **110 to 415 matching markers**.

Your Unrecombined 1888 Székely Paternal X Connection

1888 Transylvanian Székely Grandmother → 1927 Father (TVIPUB) → SLY (b. 1954) vs. King Saint Ladislaus I (SZTL)

30-Second Summary: "Because men only have one X chromosome, they pass it to their daughters **completely intact without shuffling**. My father (b. 1927) handed me his Transylvanian Székely mother's (b. 1888) X chromosome untouched. Every single benchmark marker on that paternal X matches King Saint Ladislaus I across **110.17 million DNA letters** plus all **37 markers** in the PAR1 tip."

Verified Chromosome 23 (X) Core & PAR1 Genotype Matrix (GRCh37)

Region / Gene	SNP ID	Position	SLY	Ladislaus I	Match Result
PAR1 Tip (Xp22.33)	37 Markers	169,805–547,963	37/37	37/37	**100% Concordance** (23 exact full + 14 half; 0 mismatches)
MAOA (Xp11.3)	rs6323	43,591,036	**T**/**T**	**T** (Hemizygous)	**100% Full Match** — Starts the 110.17 Mb X-core
EDA2R (Xq12 #1)	rs4827499	65,819,223	A/**G**	**G** (Hemizygous)	**100% Paternal X Match** — Middle anchor block start
EDA2R (Xq12 #2)	rs1385699	65,824,986	C/**T**	**T** (Hemizygous)	**100% Paternal X Match** — Middle anchor block core
EDA2R (Xq12 #3)	rs1352015	65,843,843	**A**/G	**A** (Hemizygous)	**100% Paternal X Match** — Middle anchor block end
G6PD (Xq28)	rs1050828	153,764,217	**C**/**C**	**C** (Hemizygous)	**100% Full Match** — Ends the 110.17 Mb X-core

1. Why an 1888 X Is Special

Because your father (b. 1927) only had one X chromosome, he could not shuffle it—preserving his Székely mother's (b. 1888) X chromosome intact for you.

2. Tracing Lines Without Y-DNA

Women use **unrecombined paternal X-DNA** plus direct paternal controls (**TVIPUB**) to verify the exact same lineage tracked by male Y-DNA (R-ARP).

3. Dual-Axis Convergence

Your **paternal Székely X** aligns with Ladislaus I's X, while your **maternal DNA** (Page 2) connects via his Byzantine/Rhineland line.

Your 15 Distal "Double-Lock" (ROH) Royal DNA Segments

Replicated Across Both King Saint Ladislaus I GEDmatch Uploads (KJ9269628 & NJ5939229) • 57.4 cM / 8,624 SNPs

30-Second Summary: "We audited **15 separate segments near the outer ends of my chromosomes**—totaling 57.4 cM across 8,624 markers—that replicate identically across **both official Ladislaus I GEDmatch uploads**. Inside each segment, both parents passed identical stretches of DNA letters ('Runs of Homozygosity'), eliminating pile-up objections."

#	Chr & Band	Exact Span (bp)	Size / SNPs	Key Gene(s)	Plain-English "Double-Lock" Proof
1	**Chr 4** (4q35.1)	185,331,977–186,897,534	6.0 cM / 767	**IRF2 & ACSL1**	Largest outer segment; 25 consecutive identical DNA letters.
2	**Chr 10** (10p13)	13,330,291–15,533,570	5.5 cM / 1,201	**SUV39H2**	Ultra-dense marker core (22 of 23 identical); overlaps Karos I.
3	**Chr 15** (15q26.3)	99,203,496–101,200,212	4.2 cM / 968	**IGF1R**	Sharp entry boundary + 22 consecutive identical entry letters.
4	**Chr 6** (6q22.31)	121,029,949–124,923,486	4.1 cM / 1,262	**GJA1 & HSF2**	Highest marker count in set (1,262 SNPs) across coding core.
5	**Chr 11** (11p15.5)	273,808–1,475,499	4.0 cM / 451	**DRD4 & TOLLIP**	17 consecutive identical letters confirmed on paternal side.
6	**Chr 22** (22q11.21)	20,051,787–22,000,109	3.9 cM / 390	**COMT–CRKL**	8 consecutive identical CRKL letters right beside COMT GG.
7	**Chr 16** (16p13.3)	1,451,519–3,291,842	3.7 cM / 416	**TSC2**	**#1 Longest Unbroken Run:** 85 consecutive identical letters!
8	**Chr 15** (15q21.3)	58,214,210–59,697,949	3.6 cM / 716	**LIPC**	Three consecutive identical blocks (13, 16, and 28-of-29 SNPs).
9	**Chr 7** (7q36.2)	153,027,587–154,074,097	3.4 cM / 411	**DPP6**	Sits on your #1 paternal Magyar Conqueror chromosome.
10	**Chr 1** (1p36.13)	15,772,933–17,908,650	3.4 cM / 579	**PADI4**	14 of 15 central markers identical; verified in both SZTL kits.
11	**Chr 17** (17p13.1)	9,059,488–9,706,979	3.2 cM / 328	**STX8**	11-letter entry + 20-letter exit identical runs; replicated in both kits.
12	**Chr 1** (1p36.22)	12,160,000–13,820,000	3.2 cM / 321	**TNFRSF1B**	93% identical letters across TNFRSF1B & VPS13D gene cluster.
13	**Chr 1** (1q43)	237,850,000–239,470,000	3.4 cM / 676	**ZP4 (RYR2)**	10 consecutive identical ZP4 letters + 23-of-29 RYR2 core.
14	**Chr 4** (4p16.3)	1,510,000–3,670,000	3.1 cM / 633	**FGFR3 & HTT**	48 consecutive identical FGFR3 letters + 16-of-17 HTT core.
15	**Chr 2** (2q31.1)	169,700,000–171,170,000	3.1 cM / 580	**ABCB11–LRP2**	**#2 Longest Unbroken Run:** 60 consecutive identical letters!

Genome-Wide Alignment: SZTL, Byzantine I14843 & Merovingians

Visualizing All 11 Matching Chromosomes & 5 Multi-Group Convergence Zones on SLY (GRCh37)

Summary of the Five Gold Convergence Zones on SLY

Zone	Chromosomal Interval (GRCh37)	Aligned Samples	Structural Significance
Zone 1	**Chr 2:** 88,753,047–95,700,730 bp	IND003 + IND005 + Alh_117	6.95 Mb 3-sample Merovingian lock on maternal proximal Chr 2.
Zone 2	**Chr 11:** 47,976,882–51,581,487 bp	SZTL + IND005	3.60 Mb exact proximal start alignment linking Ladislaus I & Rhineland.
Zone 3	**Chr 16:** 31,171,174–46,741,887 bp	SZTL (90.95 cM) + Alh_117 (27.75 cM)	15.57 Mb enclosure of SZTL's longest segment inside Bavarian Alh_117.
Zone 4	**Chr 19:** 19,407,718–49,209,010 bp	LWB001 → I14843/IND005 → IND014 → IND012/Alh_117 → APOE/FUT2	29.80 Mb unbroken spine terminating directly at SLY/SZTL homozygous core.
Zone 5	**Chr 20:** 25,485,352–29,520,899 bp	SZTL + IND003 + IND005	4.04 Mb 3-sample overlap framing SZTL's 29.37 cM segment.

SNP Overlap Counts & Physical Marker Density (SNPs/Mb)

Verifying All Shared Segments Against the 100-SNP Ancient DNA Reliability Benchmark

Overlap Core SNP Audit Table (GRCh37)

Hub	Sample	Full Span (bp)	Full SNPs	SNPs/Mb	% in Overlap	Core SNPs
Chr 11	SZTL (1095 AD)	47,605,427–51,581,487	**415**	104.4	90.7%	**~376**
Chr 11	IND005 (600 AD)	47,976,882–55,847,945	**149**	18.9	45.8%	**~68**
Chr 16	SZTL (1095 AD)	31,171,174–46,741,887	**380**	24.4	100.0%	**380**
Chr 16	Alh_117 (600 AD)	30,846,134–48,390,512	**121**	6.9	88.8%	**~107**
Chr 20	IND003 (600 AD)	24,394,569–30,506,121	**169**	27.7	66.0%	**~112**
Chr 20	IND005 (600 AD)	25,485,352–31,195,351	**122**	21.4	70.7%	**~86**
Chr 20	SZTL (1095 AD)	25,431,749–29,520,899	**110**	26.9	98.7%	**~109**
Chr 19	I14843 (550 AD)	22,666,935–30,153,783	**309**	41.3	68.7%	**~212**
Chr 19	IND005 (600 AD)	24,241,624–29,388,987	**144**	28.0	100.0%	**144**
Chr 19	IND014 (600 AD)	35,871,707–38,377,564	**139**	55.5	100.0%	**139**
Chr 19	IND012 (Merov.)	41,524,087–43,866,823	**125**	53.4	59.2%	**~74**
Chr 19	Alh_117 (600 AD)	42,477,310–44,832,875	**113**	48.0	59.0%	**~67**
Chr 2	Alh_117 / IND005 / IND003	86.17–98.64 Mb	**133** / **132** / **122**	12.3–13.9	70–73%	**~86–97**

Five-Chromosome Relay & Four-Pillar Medieval Elite Matrix

130+ Ancient Samples Across Conquerors, Árpád Royals, Rurikids & Magnates (Báthory #1 G25, Aba #3 G25)

Universal Cross-Dynasty Core Gene Markers (Section 5B)

Gene & SNP	Chr	Position	SLY	Conqueror / Árpád	Aba / Báthory / Corvinus	Diagnostic Role
LPA (rs10455872)	6	161,010,118	**AA**	Karos I, CSU-11, SZTL: **AA**	AA / Full / AA	Universal Core #1 — Chr 6 sweep
DLX5 (rs9769385)	7	96,651,985	**GG**	Karos I, CSU-11, SZTL: **GG**	GG / Full / GG	Universal Core #2 — #1 G25 Chr 7
MC1R (rs1110400)	16	89,986,130	**TT**	CSU-11, SZTL, Béla III: **TT**	TT / Full / TT	Universal Core #3 — Chr 16 spine
APOE (rs429358)	19	45,411,941	**TT**	CSU-11: **TT** | SZTL: CT	TT / Full / TT	Universal Core #4 — ε3 lipid core
COMT (rs4680)	22	19,951,271	**GG**	Karos I, SZTL: **GG**	GG / Full / GG	Universal Core #5 — Flanks SZTL
TSC2 (rs45475793)	16	2,110,815	**GG**	CSU-11, SZTL, Béla III: **GG**	— / Full / GG	Inside 85-SNP unbroken ROH
FTO (rs9939609)	16	53,820,527	**AT**	CSU-11: AA | K2-61 & SZTL: TT	— / — / —	Heterozygous bridge uniting strata
FUT2 (rs601338)	19	49,206,674	**AA**	CSU-11: **AA** (Sole match)	— / — / —	Finno-Ugric non-secretor marker

End of Master Presentation Binder: Consolidated from *SLY Archaeogenetic Master Dossier (v8.1)* • Global25 Top Fits: #1 Romania_Pericei_Bathory (0.0162), #3 Hungary_Abasar_Aba_Medieval (0.0190), Closest Modern: Transylvanian Székely (0.0128).