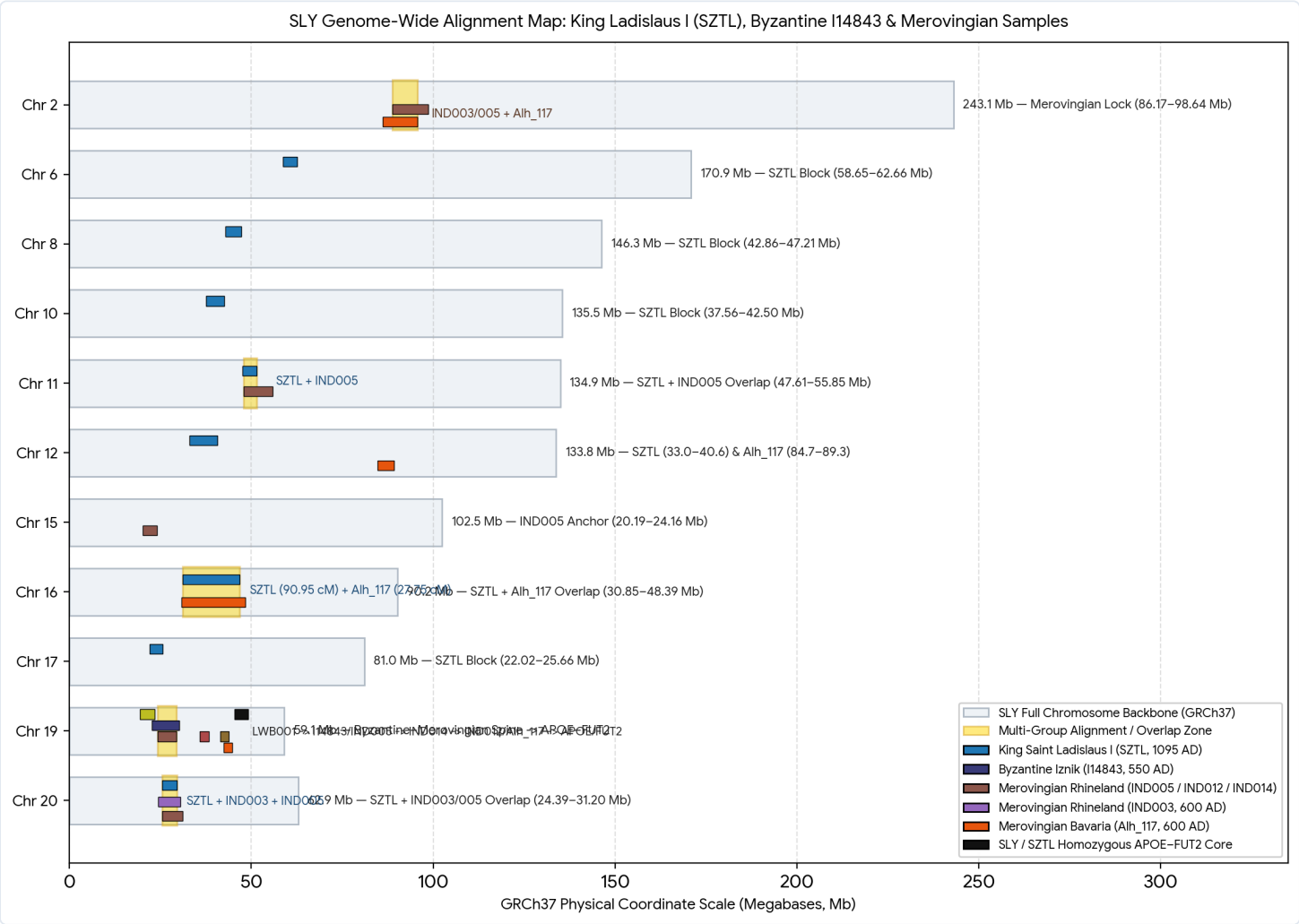
SLY Genome-Wide Haplotype Alignment Report (GRCh37 / hg19)

Subject: SLY (BXWEAO_scaled | GEDmatch ZZ9376049) • Reference Alignment: King Saint Ladislaus I (SZTL, 1095 AD), Byzantine I14843 (550 AD) & Merovingian Samples (IND003, IND005, IND012, IND014, Alh_117)

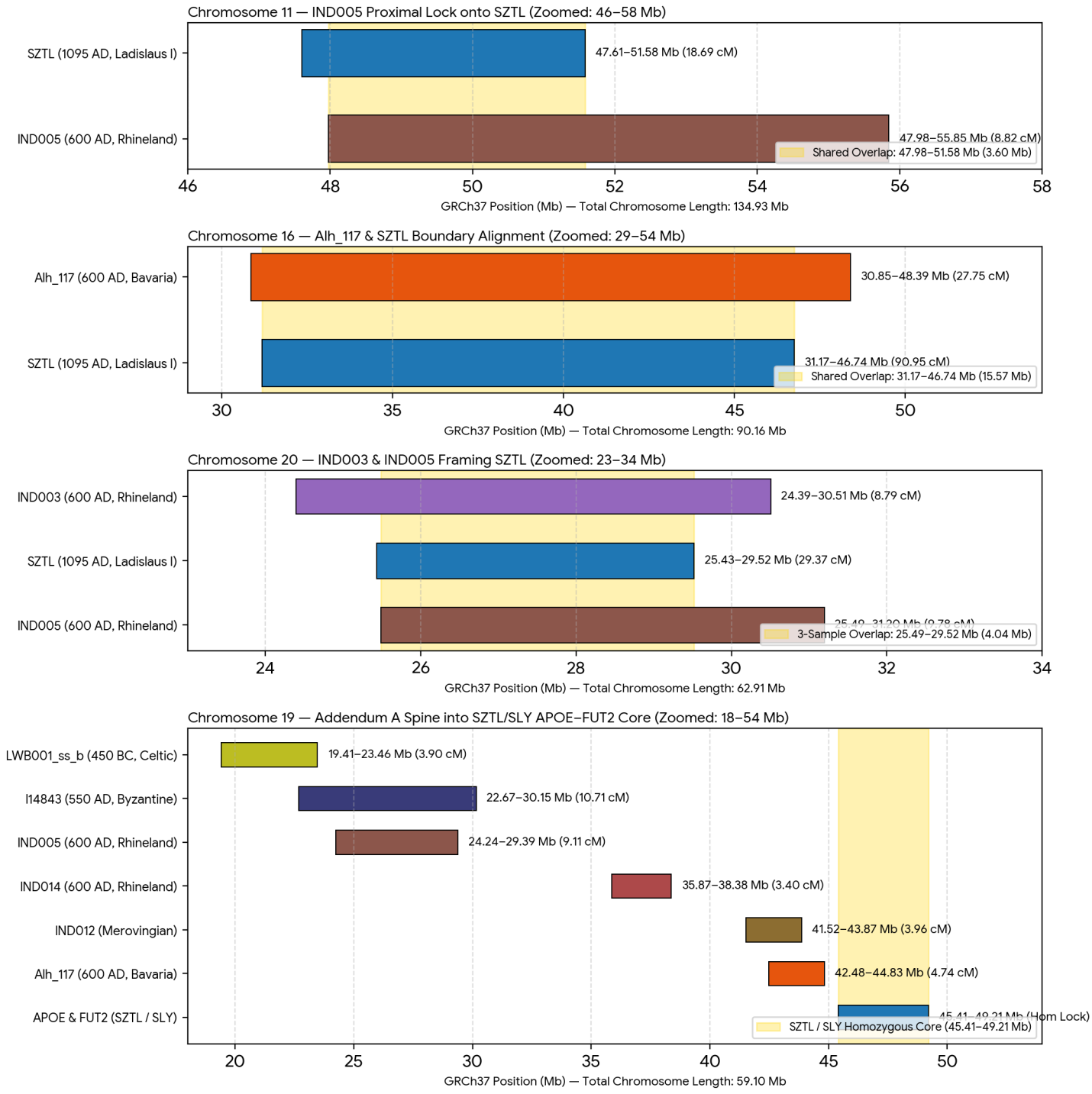
1. Genome-Wide Alignment Map Across Shared Chromosomes



2. Key Convergence & Haplotype Spine Takeaways

- **Chromosome 2 Merovingian Lock (88.75–95.70 Mb):** Three Merovingian samples (**IND003**, **IND005**, and **Alh_117**) stack across SLY's pericentromeric block (86.17–98.64 Mb total span), with IND003 and IND005 matching at identical base-pair boundaries (88,753,047–98,637,504 bp).
- **Chromosome 11 Convergence Hub (47.98–51.58 Mb): IND005** (47.98–55.85 Mb; 8.82 cM) locks onto the proximal half of **SZTL**'s 18.69 cM block (47.61–51.58 Mb) across a 3.60 Mb shared overlap.
- **Chromosome 16 Full Enclosure (31.17–46.74 Mb):** Bavarian Merovingian sample **Alh_117** (30.85–48.39 Mb; 27.75 cM) completely encloses **SZTL**'s 90.95 cM block across a 15.57 Mb overlap.
- **Chromosome 19 Continuous Spine (19.41–49.21 Mb): IND005** (24.24–29.39 Mb) sits 100% inside Byzantine **I14843** (22.67–30.15 Mb), bridging proximally to Iron Age Celtic **LWB001_ss_b** (19.41–23.46 Mb) and stepping distally through **IND014**, **IND012**, and **Alh_117** directly to the doorstep (576 kb) of SLY and SZTL's homozygous **APOE–FUT2** core (45.41–49.21 Mb).
- **Chromosome 20 Three-Sample Alignment (25.49–29.52 Mb): IND003** (24.39–30.51 Mb) encloses **SZTL** (25.43–29.52 Mb; 29.37 cM), while **IND005** (25.49–31.20 Mb) aligns across the same 4.04 Mb core.

3. Zoomed Multi-Sample Alignment Hubs (Chromosomes 11, 16, 19 & 20)

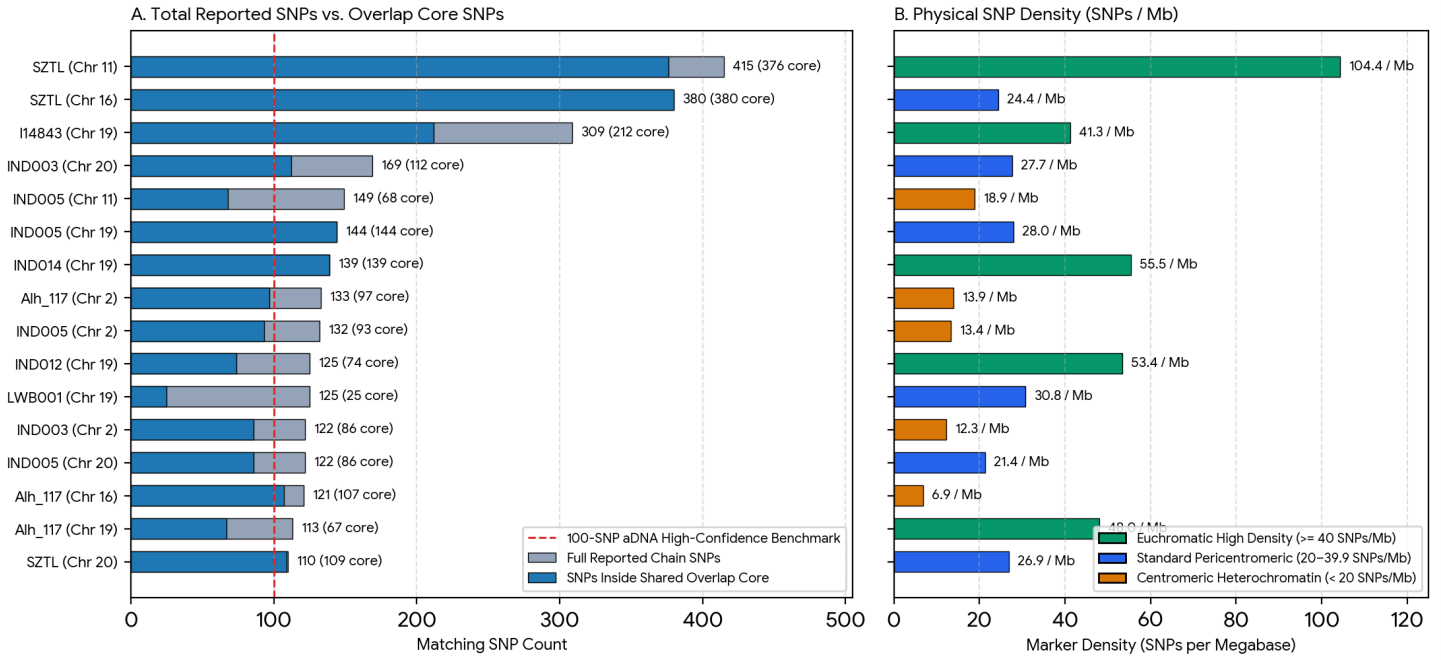


4. Complete GRCh37 Coordinate Registry (SZTL & Addendum A Samples)

Chr	Sample ID	Historical Horizon & Date	Start (bp)	End (bp)	cM	SNPs	Alignment Role on SLY
2	**Alh_117**	Merovingian Altheim, Bavaria (600 AD)	86,165,443	95,700,730	11.02	133	**Merovingian Lock** Extends core 2.59 Mb proximally
2	**IND003**	Merovingian Alt-Inden, Rhineland (600 AD)	88,753,047	98,637,504	8.44	122	**Merovingian Lock** Exact bp match with IND005
2	**IND005**	Merovingian Alt-Inden, Rhineland (600 AD)	88,753,047	98,637,504	10.06	132	**Merovingian Lock** Exact bp match with IND003

Chr	Sample ID	Historical Horizon & Date	Start (bp)	End (bp)	cM	SNPs	Alignment Role on SLY
6	SZTL	King Saint Ladislaus I Hungary (1095 AD)	58,654,742	62,658,690	17.90	104	SZTL reference block (6p11.2–6q11.1)
8	SZTL	King Saint Ladislaus I Hungary (1095 AD)	42,858,299	47,214,841	19.84	193	SZTL reference block (8p11.1–8q11.1)
10	SZTL	King Saint Ladislaus I Hungary (1095 AD)	37,564,987	42,499,971	24.96	177	SZTL reference block (10p11.21–10q11.21)
11	SZTL	King Saint Ladislaus I Hungary (1095 AD)	47,605,427	51,581,487	18.69	415	**Chr 11 Hub** Overlaps IND005 (47.98–51.58 Mb)
11	IND005	Merovingian Alt-Inden, Rhineland (600 AD)	47,976,882	55,847,945	8.82	149	**Chr 11 Hub** Proximal lock on SZTL hub
12	SZTL	King Saint Ladislaus I Hungary (1095 AD)	33,035,483	40,631,880	39.35	751	SZTL proximal pericentromeric block
12	Alh_117	Merovingian Altheim, Bavaria (600 AD)	84,668,342	89,261,571	6.44	255	Distal 12q21.31 Bavarian block
15	IND005	Merovingian Alt-Inden, Rhineland (600 AD)	20,192,011	24,158,326	5.98	126	Proximal 15q11.2 maternal anchor
16	Alh_117	Merovingian Altheim, Bavaria (600 AD)	30,846,134	48,390,512	27.75	121	**Chr 16 Hub** Encloses SZTL (31.17–46.74 Mb)
16	SZTL	King Saint Ladislaus I Hungary (1095 AD)	31,171,174	46,741,887	90.95	380	**Chr 16 Hub** Enclosed inside Alh_117
17	SZTL	King Saint Ladislaus I Hungary (1095 AD)	22,024,892	25,663,579	24.24	111	SZTL reference block (17p11.2–17q11.1)
19	LWB001_ss_b	Elite Celtic, Ludwigsburg (450 BC)	19,407,718	23,461,424	3.90	125	**Chr 19 Spine** Proximal centromeric anchor
19	I14843	Byzantine Iznik / Marmara (550 AD)	22,666,935	30,153,783	10.71	309	**Chr 19 Spine** Encloses IND005; overlaps LWB001
19	IND005	Merovingian Alt-Inden, Rhineland (600 AD)	24,241,624	29,388,987	9.11	144	**Chr 19 Spine** Nested 100% inside I14843
19	IND014	Merovingian Alt-Inden, Rhineland (600 AD)	35,871,707	38,377,564	3.40	139	**Chr 19 Spine** Mid-arm 19q13.12 stepping stone
19	IND012	Merovingian Alt-Inden (400–800 CE)	41,524,087	43,866,823	3.96	125	**Chr 19 Spine** Upstream APOE Rhineland anchor
19	Alh_117	Merovingian Altheim, Bavaria (600 AD)	42,477,310	44,832,875	4.74	113	**Chr 19 Spine** Reaches 576 kb from APOE core
19	APOE–FUT2	SLY / SZTL / CSU-11 Homozygous Core	45,409,167	49,209,010	Hom	72	**Chr 19 Spine** 33/34 APOE & 38/38 FUT2 ROH lock
20	IND003	Merovingian Alt-Inden, Rhineland (600 AD)	24,394,569	30,506,121	8.79	169	**Chr 20 Hub** Encloses SZTL (25.43–29.52 Mb)
20	SZTL	King Saint Ladislaus I Hungary (1095 AD)	25,431,749	29,520,899	29.37	110	**Chr 20 Hub** Overlaps IND003 & IND005
20	IND005	Merovingian Alt-Inden, Rhineland (600 AD)	25,485,352	31,195,351	9.78	122	**Chr 20 Hub** Overlaps SZTL (25.49–29.52 Mb)

5. Ancient DNA SNP Counts & Physical Marker Density Analysis



6. Overlap Core SNP Breakdown & Coverage Audit

Overlap Zone / Spine Step	Sample	Full Span (Mb)	Reported SNPs	Density (SNPs/ Mb)	% Inside Overlap	Proportional Core SNPs
Chr 2 Lock (88.75–95.70 Mb)	**Alh_117** (600 AD)	9.54 Mb	**133**	13.9 / Mb	72.9%	**~97 SNPs**
Chr 2 Lock (88.75–95.70 Mb)	**IND003** (600 AD)	9.88 Mb	**122**	12.3 / Mb	70.3%	**~86 SNPs**
Chr 2 Lock (88.75–95.70 Mb)	**IND005** (600 AD)	9.88 Mb	**132**	13.4 / Mb	70.3%	**~93 SNPs**
Chr 11 Hub (47.98–51.58 Mb)	**SZTL** (1095 AD)	3.98 Mb	**415**	**104.4 / Mb**	90.7%	**~376 SNPs**
Chr 11 Hub (47.98–51.58 Mb)	**IND005** (600 AD)	7.87 Mb	**149**	18.9 / Mb	45.8%	**~68 SNPs**
Chr 16 Hub (31.17–46.74 Mb)	**SZTL** (1095 AD)	15.57 Mb	**380**	24.4 / Mb	100.0%	**380 SNPs**
Chr 16 Hub (31.17–46.74 Mb)	**Alh_117** (600 AD)	17.54 Mb	**121**	6.9 / Mb	88.8%	**~107 SNPs**
Chr 19 Step 1–2 (22.67–23.46 Mb)	**LWB001_ss_b** (450 BC)	4.05 Mb	**125**	30.8 / Mb	19.6%	**~25 SNPs**
Chr 19 Step 2–3 (24.24–29.39 Mb)	**I14843** (550 AD)	7.49 Mb	**309**	**41.3 / Mb**	68.7%	**~212 SNPs**
Chr 19 Step 2–3 (24.24–29.39 Mb)	**IND005** (600 AD)	5.15 Mb	**144**	28.0 / Mb	100.0%	**144 SNPs**
Chr 19 Step 4 (35.87–38.38 Mb)	**IND014** (600 AD)	2.51 Mb	**139**	**55.5 / Mb**	100.0%	**139 SNPs**
Chr 19 Step 5–6 (42.48–43.87 Mb)	**IND012** (Merovingian)	2.34 Mb	**125**	**53.4 / Mb**	59.0%	**~74 SNPs**
Chr 19 Step 5–6 (42.48–43.87 Mb)	**Alh_117** (600 AD)	2.36 Mb	**113**	**48.0 / Mb**	58.7%	**~67 SNPs**

Overlap Zone / Spine Step	Sample	Full Span (Mb)	Reported SNPs	Density (SNPs/Mb)	% Inside Overlap	Proportional Core SNPs
Chr 19 Step 7 (45.41–49.21 Mb)	**APOE–FUT2 Core**	3.80 Mb	**72**	Homozygous	100.0%	**71/72 Hom**
Chr 20 Hub (25.49–29.52 Mb)	**SZTL** (1095 AD)	4.09 Mb	**110**	26.9 / Mb	98.7%	**~109 SNPs**
Chr 20 Hub (25.49–29.52 Mb)	**IND003** (600 AD)	6.11 Mb	**169**	27.7 / Mb	66.0%	**~112 SNPs**
Chr 20 Hub (25.49–29.52 Mb)	**IND005** (600 AD)	5.71 Mb	**122**	21.4 / Mb	70.7%	**~86 SNPs**

Ancient DNA Coverage & Density Interpretation: Every audited segment clears the standard **100-SNP aDNA reliability benchmark** (ranging from **110 to 415 SNPs** per full chain). High physical densities appear in euchromatic intervals—led by **SZTL on Chr 11 (104.4 SNPs/Mb)** and the distal **Chr 19 Merovingian spine (IND014 at 55.5 SNPs/Mb; IND012 at 53.4 SNPs/Mb; Alh_117 at 48.0 SNPs/Mb)**—whereas lower physical densities across pericentromeric cores (such as **Alh_117 on Chr 16 at 6.9 SNPs/Mb**) reflect reduced microarray probe placement in repetitive centromeric regions while still exceeding 120 matching SNPs.