

Skeleton	Place	Elevation	Geographical	Excavation	Dating	Coffin
Sk_1	Ptuj	232	46°25'07"N; 15°50'17"E	2011	16th	yes (wooden)
Sk_2	Ptuj	232	46°25'07"N; 15°50'17"E	2011	16th	yes (wooden)
Sk_3	Ptuj	232	46°25'07"N; 15°50'17"E	2011	16th	yes (wooden)
Sk_4	Koper	10	45°23'49"N; 13°43'48"E	2015	18th	yes (wooden)
Sk_5	Maribor	274	46°33'00"N; 15°38'00"E	2013	17th	yes (wooden)
Sk_6	Ponikva	194	46°15'27"N; 15°26'52"E	2012	18th	yes (wooden)
Sk_7	Ponikva	194	46°15'27"N; 15°26'52"E	2012	18th	yes (wooden)
Sk_12	Ptuj	232	46°25'07"N; 15°50'17"E	1984	3th	no
Sk_13	Ptuj	232	46°25'07"N; 15°50'17"E	1984	3th	no
Sk_16	Ljubljana	298	46°03'19"N; 14°30'29"E	2017	4th	no
Sk_17	Ljubljana	298	46°03'19"N; 14°30'29"E	2013	4th	no

Table S1 S1. Main data on the 11 ancient skeletons. Place: place of burial; Elevation: elevation at Geographical: geographical coordinates; Excavation: year of excavation; Dating: dating of the skeleton historical and archaeological records; Coffin: presence in coffin; Storage condition: storage conditions skeletons were discovered in non-disturbed individual graves and, after excavation, the bone remains were dried, and analyzed by a physical anthropologist. Based on the archaeological context and anthropological records, each grave was attributed to one individual. After anthropological analysis, the remains were placed in a museum storeroom under dark, dry, cold, and stable conditions until this study. These skeletons were dated according to anthropological records from the 3rd to 18th century AD.

Storage conditions
stone tomb
stone tomb
stone tomb
grave pit (sandy loam)
grave pit (sandy loam)
grave pit (clayey loam)
grave pit (clayey loam)
grave pit (sandy loam)
grave pit (sandy loam)
stone sarcophagus
clay loam

above sea level (in meters);
 as by century AD based on
 before excavation. All the
 were washed with water, air-
 al analyses, all the bones in
 cardboard box and kept in a
 ed in line with historical and

Sample	bone element	#	Auto	Deg	Y	IPC Shift	Auto/Deg
Sk_1	maxillary left incisive 1	141	0.2013	/	0.0117	-0.08	u-c
	maxillary right molar 3	144	0.0932	0.0021	0.0149	-0.15	44.04
	petrous	1D	0.0523	0.0003	0.0173	-0.05	179.51
	mandibular right molar 1	142	0.0231	0.0006	0.0041	-0.45	38.5
Sk_2	petrous	2D	0.0401	0.0005	0.0113	0.09	86.52
	metatarsal I.	125	0.0284	/	0.0018	-0.17	u-c
	maxillary right molar 1	147	0.0107	/	0.0021	-0.1	u-c
	tibia	129	0.0072	0.0002	0.0011	-0.41	38.25
Sk_3	proximal hand phalanx I.	37	0.0676	0.0052	0.0344	-0.03	12.99
	maxillary right canine	152	0.0179	0.0006	0.003	-0.7	30.02
	petrous	3D	0.0147	0.0005	0.0056	-0.36	30.24
	maxillary left molar 2	153	0.0143	/	0.0049	-0.18	u-c
	proximal foot phalanx I.	82	0.0116	0.0006	0.0031	0.1	19.12
Sk_4	proximal foot phalanx I.	97	0.0207	/	/	0.29	u-c
	metatarsal V.	98	0.015	/	/	-0.13	u-c
	cuneiforme lateralis	96	0.0132	/	/	0.12	u-c
	cuboid	95	0.0123	/	/	-0.06	u-c
Sk_5	navicularis	65	0.1582	0.0008	/	-0.27	190.78
	cuneiforme intermedialis	66	0.0891	0.0005	/	-0.2	178.2
	cuneiforme lateralis	68	0.0851	0.0003	/	0.03	283.67
	metatarsal V.	72	0.0773	0.0003	/	0.02	242.42
Sk_6	metatarsal II.	50	0.0819	0.0013	/	-0.12	65.41
	distal foot phalanx I.	59	0.0797	0.0009	/	-0.48	87.41
	navicularis	49	0.0688	0.0006	/	-0.18	107.64
	petrous	6D	0.0292	0.0006	/	-0.21	48.87
	talus	58	0.0208	0.0006	/	-0.81	36.36
Sk_7	proximal hand phalanx I.	138	0.1674	0.0035	/	0.06	48.24
	metatarsal IV	31	0.0875	0.0161	/	0.2	5.44
	metacarpal III	21	0.0822	0.0119	/	0.19	6.94
	metacarpal V	20	0.0583	0.0067	/	-0.03	8.69
	petrous	7D	0.0011	/	/	-0.29	u-c
	petrous	12D	0.0609	/	0.034	-0.04	u-c

Sk_12	maxillary right incizive 1	161	0.0121	/	0.0011	-0.38	u-c
	metacarpal I.	22	0.0034	/	0.0019	-0.32	u-c
	tibia	133	0.0028	0.0002	0.0004	-0.69	15.09
Sk_13	metacarpal I.	25	0.021	0.0005	0.0076	-0.27	42.00
	metacarpal IV.	23	0.0159	0.0006	0.0134	-0.47	26.03
	petrous	13D	0.0133	/	0.0055	-0.24	u-c
	metacarpal II.	24	0.0081	/	0.002	-0.4	u-c
Sk_16	petrous	194	0.0471	/	0.0037	0.14	u-c
	proximal foot phalanx I.	192	0.037	/	0.0045	0.18	u-c
	metatarsal I.	188	0.0286	/	0.0018	0.08	u-c
	cuneiforme lateralis	193	0.0284	/	0.0021	0.22	u-c
Sk_17	petrous	179	0.0097	/	0.0018	-0.96	u-c
	cuneiforme medialis	171	0.003	0.0003	0.0006	-0.83	8.58
	talus	176	0.0028	/	0.0009	-0.93	u-c
	tibia	180	0.0027	0.0004	0.0002	-0.92	6.48
WWII	petrous bone	279	0.3947	0.0479	0.2693	-0.55	8.24
	petrous bone	533	0.7704	0.0878	0.2942	-0.43	8.78
	petrous bone	536	0.0725	0.004	0.0284	-0.16	17.99
	petrous bone	537	0.078	0.0111	0.0323	-0.46	7.05
	petrous bone	538	0.1791	0.029	0.0810	-0.39	6.18
	petrous bone	783	1,386	0.0673	0.192	-0.12	20.59
	petrous bone	784	0.1143	0.001	0.0116	-0.27	118.5
	petrous bone	785	0.6317	0.0027	0.0253	0.14	236.64
	petrous bone	786	2,133	0.0202	0.0796	-0.44	105.44
	petrous bone	787	0.538	0.0155	0.0513	-0.24	34.77
	petrous bone	788	1.4424	0.0076	0.0824	-0.34	188.95
	petrous bone	789	1,254	0.0179	0.0945	-0.19	70.23
	petrous bone	790	0.3523	0.0019	0.0213	-0.28	190.28
	petrous bone	791	2.5601	0.0098	0.111	-0.63	262.31
	petrous bone	792	4.7677	0.0142	0.1605	-0.06	334.85
	petrous bone	793	1.1119	0.0063	0.0345	-0.27	177.03
petrous bone	794	4.1076	0.0382	0.1363	-0.65	107.58	

petrous bone	795	0.2421	0.0109	0.0381	0.14	22.25
petrous bone	796	1.7197	0.0941	0.3553	-0.98	18.28
petrous bone	797	2.0217	0.0269	0.098	-0.77	75.28
petrous bone	798	1.5764	0.0156	0.0902	-0.6	101.01
petrous bone	799	0.8835	0.0129	0.0698	-0.67	68.74
petrous bone	801	1.2054	0.0111	0.0739	-0.71	108.14
petrous bone	802	1.5382	0.0142	/	-0.7	108.34

Table S2. Quantification data of the 47 bone element types selected from the 11 ancient skeletons and the 24 WWII skulls obtained using the PowerQuant System (average values from duplicate tests). Raw data were obtained using the ABI 7500 Real-Time PCR System (Applied Biosystems, AB, Foster City, CA, USA), and the results were then converted using PowerQuant Analysis Tool software (www.promega.com/resources/tools/powerquantanalysis-tool). The imported data were then used to evaluate standard curves (acceptable r^2 and slope values), to determine quantities of Auto (Autosomal), Deg (Degradation), and Y targets in the samples, and to calculate the [Auto]/[Deg] ratio together with the IPC (Internal Positive Control) shift value. When the Deg probe gave no Cq, the degradation level was assumed to be as “un-calculable” (u-c in the Table).

SNP	Chromosomal position	Gene	Allelic variant	
			C	A
rs12821256	chr12:89328335	KITLG	0.088	0
rs1042602	chr11:88911696	TYR	0.648	0.352
rs12203592	chr6:396321	IRF4	0.860	0
rs16891982	chr5:33951693	SLC45A2	0.134	0
rs12913832	chr15:28365618	HERC2	0	0.366
rs683	chr9:12709305	TYRP1	0.394	0.606
rs1800407	chr15:28230318	OCA2	0.931	0
rs12896399	chr14:92773663	SLC2A4	0	0
rs4959270	chr6:457748	EXOC2	0.536	0.463
rs28777	chr5:33958959	SLC45A2	0.114	0.886
rs2378249	chr20:33218090	PIGU	0	0.841
rs1393350	chr11:89011046	TYR	0	0.239
rs2402130	chr14:92801203	SLC2A4	0	0.784
rs1805009	chr16:89986546	MC1R	0.014	0
rs796296176 (rs312262906)	chr16:89985750-1	MC1R		0.997
rs1110400	chr16:89986130	MC1R	0.009	0
rs11547464	chr16:89986091	MC1R	0	0.007
rs1805007	chr16:89986117	MC1R	0.934	0
rs1805008	chr16:89986144	MC1R	0.937	0
rs201326893	chr16:89986122	MC1R	0.998	0.002
rs885479	chr16:89986154	MC1R	0	0.066
rs1805005	chr16:89985844	MC1R	0	0
rs1805006	chr16:89985918	MC1R	0.991	0.009
rs2228479	chr16:89985940	MC1R	0	0.095

Table S3. List of the 24 SNP markers studied in this work. SNP: SNP identification code; C: C allele; A: A allele; τ : threshold value (in reads) adopted for locus call in this study. In agreement with ref. [9,27], all SNPs were amplified with different amounts of template.

ts (frequency)		Target (bp)	Threshold	
T	G		> 100 pg	< 100 pg
0.911	0	45	215	38
0	0	46	210	96
0.140	0	46	206	87
0	0.865	48	179	41
0	0.634	49	391	94
0	0	52	254	110
0.069	0	55	288	87
0.410	0.589	70	284	101
0	0	70	201	62
0	0	72	307	216
0	0.159	76	182	41
0	0.761	82	189	64
0	0.216	83	286	184
0	0.986	100	266	205
		102	291	159
0.991	0	112	248	172
0	0.993		249	172
0.066	0		249	173
0.063	0		249	172
0	0		249	172
0	0.934		246	172
0.130	0.870	114	308	233
0	0		318	238
0	0.915		320	236

Gene: gene nomenclature; Columns D-G report the allelic variants
 rget (bp): length (in base pairs) of the sequencing target; Threshold:
 different locus-to-locus thresholds values were applied for samples

sample	#	amount (ng)	cycles	Mapped Reads	On Target (%)	Mean Depth	Uniformity (%)	bacterial
Sk_1	141	1	25	282166	63.94	8600	94.44	
	144	1	25	476773	73.7	18389	100	
	1D	0.78	25	336052	82.39	13107	90.67	
	142	0.34	25	775937	93.94	40292	90.67	
Sk_2	2D	0.6	25	248015	71.57	8326	90.67	
	125	0.43	25	8073	0.31	1,295	91.35	A; T
	147	0.16	27	424085	96	21914	90.67	
	129	0.11	27	452393	11.32	2931	96.07	
Sk_3	37	1	25	646007	96.26	35119	100	
	152	0.27	27	414966	67.29	16714	81.01	
	3D	0.22	27	16906	86.98	767	84.94	
	153	0.21	27	460593	95.05	25258	90.67	
	82	0.17	27	4827	23.53	49.36	62.52	A
Sk_4	97	0.31	25	201098	81.1	9446	100	
	98	0.22	27	458778	68.27	19453	99.84	
	96	0.2	27	182052	82.08	7883	90.67	
	95	0.18	27	421558	96.25	21889	90.67	
Sk_5	65	1	25	306698	44.64	5197	100	
	66	1	25	265783	52.83	7273	100	
	68	1	25	217905	42.03	4076	100	
	72	1	25	170399	44.77	3418	97.49	
Sk_6	50	1	25	252554	92.1	14489	99.92	
	59	1	25	356583	55.39	8964	100	
	49	1	25	198944	76.55	8360	100	
	6D	0.44	25	425019	85.14	18115	100	
	58	0.31	25	250257	32.21	4557	84.45	
Sk_7	138	1	25	52822	53.41	1460	99.92	
	31	1	25	49012	0.04	0.313	95.59	
	21	1	25	20549	0.33	3.4	97.44	
	20	0.87	25	11660	0.38	1.97	99.81	
	7D	0.017	28	344696	6.01	1236	37.81	
	7D	0.017	28	320655	21.36	4096	73.32	

Sk_12	12D	0.92	25	767062	94.21	42070	100	
	161	0.18	27	81983	82.94	3485	82.41	
	22	0.05	28	192533	72.93	7476	74.39	
	133	0.04	28	242929	58.56	9576	80.11	
Sk_13	25	0.31	25	665035	97.55	34753	100	
	23	0.24	27	127531	37.03	2990	84.86	
	13D	0.2	27	176857	86.35	7512	66.28	
	24	0.12	27	150775	95.96	8384	91.65	
Sk_16	194	0.71	25	3312	1.63	2,764	97.78	A; T
	192	0.55	25	182894	97.19	9862	100	
	188	0.43	25	3569	3.28	6,528	93.78	A; T
	193	0.43	25	8410	0.24	1,029	89.61	A
Sk_17	179	0.146	27	280456	85.73	13637	81.01	
	171	0.045	28	182843	40.91	3948	68.58	
	176	0.042	28	214314	36.1	4572	72.97	
	180	0.04	28	137164	30.78	2575	69.97	
WWII	279	1	25	279164	96.29	15899	100	
	533	1	25	246356	96.08	13876	100	
	536	1	25	178172	96.21	9418	100	
	537	1	25	171037	97.67	9331	100	
	538	1	25	218952	95.2	12075	100	
	783	1	25	294965	95.54	16477	100	
	784	1	25	85720	54.46	2561	100	
	785	1	25	81120	68.1	3072	100	
	786	1	25	195575	92.99	10611	100	
	787	1	25	89410	76.83	4018	100	
	788	1	25	84475	88.49	4276	99.02	
	789	1	25	124136	71.67	4972	100	
	790	1	25	21209	92.23	1089	100	
	791	1	25	61551	87.76	3244	100	
	792	1	25	148007	84.41	6468	99.75	
	793	1	25	61223	64.08	2274	100	
794	1	25	108223	90.73	5601	100		

795	1	25	101076	65.99	3863	100	
796	1	25	216635	84.89	11216	100	
797	1	25	86924	88.88	4536	100	
798	1	25	102629	83.2	4809	100	
799	1	25	75589	81.63	3676	100	
801	1	25	36395	77.66	1714	100	
802	1	25	65404	69.46	2956	99.92	

Table S4. Main PCR parameters (amount of template DNA and number of cycles) and sequencing parameters (mapped reads, on target (%), mean depth, uniformity (%)) of the bone samples from the 11 ancient skeletons and the 24 WWII skulls. The eight samples that gave no reads above 20× of coverage are in **red characters**. The BAM file analysis of these eight libraries allowed the identification of similarity with *Arthrospira platensis* (A) and *Taylorella equigenitalis* (T) (see column I).

1

Chip well details	Ion 520 (Chip #9)		Ion 530 (Chip #10)	
Addressable Wells	12 530 194		37 849 615	
With ISPs	11 099 845	88.6%	33 677 542	89%
Live	11 054 518	99.6%	33 642 211	99.9%
Test Fragment	83 415	0.8%	626 690	1.9%
Library	10 971 103	99.2%	33 015 521	98.1%
Library ISP details				
Library ISPs	10 971 103		33 015 521	
Filtered: Polyclonal	2 864 742	26.1%	9 647 684	29.2%
Filtered: Low Quality	1 092 229	10.01%	3 248 970	9.8%
Filtered: Adapter Dimer	417 637	3.8%	2 819 910	8.5%
Final Library ISPs	6 596 495	60.1%	17 298 957	52.4%

Table S5. Chip well details (addressable wells, with ISPs, live, test fragment, and library) and library ISP de

Ion 530 (Chip #11)	
37 849 615	
34 986 632	92.4%
34 979 497	100%
658 848	1.9%
34 320 649	98.1%
34 320 649	
8 777 491	25.6%
2 437 387	7.1%
1 861 941	5.4%
21 243 830	61.9%

:tails (library ISPs, filtered polyclonal, filtered low quality, filtered adapter dimer, and final library ISPs) of I

lon chip 520 and two lon chips 530 run in this study.

		1 (n=4)	2 (n=4)	3 (n=5)	4 (n=4)	5 (n=4)	6 (n=5)	7 (n=6)	12 (n=4)
Mapped reads	average	467732	283142	308660	315872	240196	296671	133232	321127
	st. dev.	221244	204457	285317	144537	59008	91807	155487	304795
	CV %	47.3	72.2	92.4	45.8	24.6	30.9	116.7	94.9
	<i>median</i>	406413	336050	414966	311328	241844	252554	50917	217731
On target %	average	78.5	44.8	73.8	81.9	46.1	68.3	13.6	77.2
	st. dev.	12.8	46.3	30.4	11.4	4.7	24.4	21.2	15.1
	CV %	16.3	103.4	41.2	14.0	10.2	35.8	155.7	19.6
	<i>median</i>	78.0	41.4	87.0	81.6	44.7	76.6	3.2	77.9
Mean depth of coverage	average	20097	8293	15581	14668	4991	10897	1133	15652
	st. dev.	14045	9713	15308	7032	1689	5371	1596	17792
	CV %	69.9	117.1	98.2	47.9	33.8	49.3	140.9	113.7
	<i>median</i>	15748	5629	16714	14450	4637	8964	620	8526
Uniformity	average	93.9	92.2	83.8	95.3	99.4	96.9	84.0	84.2
	st. dev.	4.4	2.6	13.9	5.3	1.3	6.9	24.8	11.0
	CV %	4.7	2.8	16.6	5.6	1.3	7.2	29.5	13.1
	<i>median</i>	92.6	91.0	84.9	95.3	100.0	100.0	96.5	81.3

Table S6. Principal sequencing parameters (mapped reads, on target %, mean depth of coverage, and uniformity) of 11 ancient skeletons together with p-val

13 (n=4)	16 (n=4)	17 (n=4)	p-value
280050	49546	203694	0.214
257447	88929	60184	
91.9	179.5	29.5	
<i>163816</i>	<i>5990</i>	<i>198579</i>	
79.2	25.6	48.4	0.002
28.6	47.8	25.2	
36.1	186.6	52.2	
<i>91.2</i>	<i>2.5</i>	<i>38.5</i>	
13410	2468	6183	0.132
14424	4929	5039	
107.6	199.7	81.5	
<i>7948</i>	<i>5</i>	<i>4260</i>	
85.7	95.3	73.1	0.092
14.3	4.6	5.6	
16.7	4.8	7.6	
<i>88.3</i>	<i>95.8</i>	<i>71.5</i>	

ue of the ANOVA test. In brackets, the number of libraries built for each skeleton.

		eleven skeletons	WWII skulls
Mapped reads	average	259822	130581
	st. dev.	198285	76954
	CV %	76.3	58.9
	<i>median</i>	<i>230417</i>	<i>101852</i>
On target %	average	56.6	83.3
	st. dev.	33.9	12.2
	CV %	59.9	14.6
	<i>median</i>	<i>65.6</i>	<i>86.3</i>
Mean depth of coverage	average	10329	6584
	st. dev.	10617	4593
	CV %	102.8	69.7
	<i>median</i>	<i>7494</i>	<i>4672</i>
Uniformity	average	89.2	99.9
	st. dev.	13.1	0.2
	CV %	14.6	0.2
	<i>median</i>	<i>91.5</i>	<i>100</i>

Table S7. Principal sequencing parameters (mapped reads, on target %, mean depth and uniformity) of the 11 ancient skeletons and 24 WWII skulls. p-value: p-value since all WWII samples were sequenced in the Ion 520 chip, no comparison was made

p-value
*
3.8 E-6
*
3.9 E-7

0th of coverage,
 of the t -test. *:

allowed.

Marker	NN typing		Allelic imbalance	
	ancient skeletons	WWII	ancient skeletons	WWII
rs1042602	1		3	2
rs1110400	1			
rs11547464	2			
rs12203592	2			
rs12821256	2		1	1
rs12896399	1		5	1
rs12913832	2		5	4
rs1393350	2		1	1
rs16891982	2		1	1
rs1800407	1			
rs1805005	4		1	1
rs1805006	4			1
rs1805007	1		1	2
rs1805008	1			1
rs1805009	2			
rs201326893	2			
rs2228479	4		1	2
rs2378249	3		4	1
rs2402130	2		4	1
rs28777	1		2	
rs312262906	1			
rs4959270	5		6	2
rs683	5		6	1
rs885479	1			2

Table S8. List of the markers flagged by the Converge software in the two sets and WWII (Second World War) skulls). Values refer to number of observatio

Flagged Homozygotes	
ancient skeletons	WWII
1	
1	2
2	1
6	
4	1
1	2
3	2
5	2
2	1
6	3
1	3
3	1
3	2
2	1
1	1
3	
2	
1	
1	

of samples (ancient skeletons
ns.

list order	gene	marker	144	141	1D	142	CONSENSUS
17	TYR	rs1042602	AC	AC	AC	ACT	AC
11	MC1R	rs1110400	TT	TT	TT	TT	TT
2	MC1R	rs11547464	GG	GG	GG	GG	GG
16	IRF4	rs12203592	CT	CT	CT	CT	CT
14	KITLG	rs12821256	TT	TT	TT	TT	TT
22	LOC105370627	rs12896399	TT	TT	TT	TT[G]	TT
20	HERC2	rs12913832	GG	GG[A]	GG[A]	GG	GG
23	TYR	rs1393350	GG	GG	GG	GG	GG
13	SLC45A2	rs16891982	GG	GG	GG[A]	GG[C]	GG
18	OCA2	rs1800407	CC[T]	CC	CC[T]	CC	CC
5	MC1R	rs1805005	GG	GG[A]	GG	GG	GG
6	MC1R	rs1805006	CC	CC	CC	CC	CC
7	MC1R	rs1805007	CC	CC[T]	CC[T]	CC	CC
4	MC1R	rs1805008	CC	CC	CC	CC	CC
8	TUBB3	rs1805009	GG	GG	GG	GG	GG
9	MC1R	rs201326893	CC	CC	CC	CC[T]	CC
10	MC1R	rs2228479	GG	GG	GG	GG	GG
21	PIGU	rs2378249	AA	AA	AA	AA[G]	AA
19	SLC24A4	rs2402130	AA	AA	AA	AA	AA
12	SLC45A2	rs28777	AA	AA	AA	AA[C]	AA
1	MC1R	rs312262906	CC	CC	CC	CC	CC
15	LOC105374875	rs4959270	AA	AA	AA	AA	AA
24	TYRP1	rs683	AC	ACT	AC	AC	AC
3	MC1R	rs885479	GG	GG	GG	GG	GG

Table S9. Results of the genetic typing of skeleton 1.

The list order of SNP markers refers to the list order used in the HIrisPlex-S webtool (<https://hirisplex.erasmusmc.nl/>).

In case of three-allelic pattern, the dropped-in allele is in **bold red** characters.

Less-covered alleles are shown in **green bold characters** in the case of allelic imbalance (e.g., AC).

Flags alerting noising reads (1-10 % of the total) are shown in square brackets [].

Allelic drop-outs are shown in blue boxes.

NA= not available for phenotypic prediction.

list order	gene	marker	2D	129	147	CONSENSUS
17	TYR	rs1042602	CC	CC	CC	CC
11	MC1R	rs1110400	TT	TT	TT	TT
2	MC1R	rs11547464	GG	GG	GG	GG
16	IRF4	rs12203592	CC	CC	CC	CC
14	KITLG	rs12821256	TT	TT	TT	TT
22	LOC105370627	rs12896399	GT	GT	TT[G]	GT
20	HERC2	rs12913832	AA	AA	AA	AA
23	TYR	rs1393350	GG	GG	GG	GG
13	SLC45A2	rs16891982	GG	GG	GG	GG
18	OCA2	rs1800407	CC	CC	CC	CC
5	MC1R	rs1805005	GT	GT	GT	GT
6	MC1R	rs1805006	CT	CC	CC	CC
7	MC1R	rs1805007	CT	CC	CC	NA
4	MC1R	rs1805008	CC	CC	CC	CC
8	TUBB3	rs1805009	GG	GG	GG[A]	GG
9	MC1R	rs201326893	CC	CC	CC	CC
10	MC1R	rs2228479	GG	GG	GG	GG
21	PIGU	rs2378249	AA	AA	AA	AA
19	SLC24A4	rs2402130	AA	AA	AA[G]	AA
12	SLC45A2	rs28777	AA	AA	AA	AA
1	MC1R	rs312262906	CC	CC	CC	CC
15	LOC105374875	rs4959270	AC	AC	AC	AC
24	TYRP1	rs683	AC	AC	AC	AC
3	MC1R	rs885479	GG	GG	GG	GG

Table S9. Results of the genetic typing of skeleton 2.

The list order of SNP markers refers to the list order used in the HIrisPlex-S webtool (<https://hirisplex.erasmus.nl/>). In case of three-allelic pattern, the dropped-in allele is in **bold red** characters.

Less-covered alleles are shown in **green bold characters** in the case of allelic imbalance (e.g., **AC**).

Flags alerting noising reads (1-10 % of the total) are shown in square brackets [].

Allelic drop-outs are shown in blue boxes.

NA= not available for phenotypic prediction.

mc.nl/).

list order	gene	marker	37	3D	152	153	CONSENSUS
17	TYR	rs1042602	AC	AC	AC	AC	AC
11	MC1R	rs1110400	TT	NN	TT	TT	TT
2	MC1R	rs11547464	GG	NN	GG	GG	GG
16	IRF4	rs12203592	CC	CC	CC	CC	CC
14	KITLG	rs12821256	TT	NN	TT	TT	TT
22	LOC105370627	rs12896399	TT	TT	TT	TT[G]	TT
20	HERC2	rs12913832	AG	AG	AG	AG	AG
23	TYR	rs1393350	GG	GG	GG	GG	GG
13	SLC45A2	rs16891982	GG	GG	GG[A]	GG	GG
18	OCA2	rs1800407	CC	CC	CC	CC	CC
5	MC1R	rs1805005	GG	NN	GG	GG	GG
6	MC1R	rs1805006	CC	NN	CC	CC	CC
7	MC1R	rs1805007	CC	NN	CC[T]	CC	CC
4	MC1R	rs1805008	CC	NN	CC	CC	CC
8	TUBB3	rs1805009	GG	GG	GG	GG	GG
9	MC1R	rs201326893	CC	NN	CC	CC	CC
10	MC1R	rs2228479	GG	NN	GG	GG	GG
21	PIGU	rs2378249	AG	AG	AG	AG	AG
19	SLC24A4	rs2402130	AA	AA	AA	AA	AA
12	SLC45A2	rs28777	AA	AA	AA	AA	AA
1	MC1R	rs312262906	CC	CC	CC	CC	CC
15	LOC105374875	rs4959270	CC	NN	CC	CC	CC
24	TYRP1	rs683	AC	AC	AC	AC	AC
3	MC1R	rs885479	GG	NN	GG	GG	GG

Table S9. Results of the genetic typing of skeleton 3.

The list order of SNP markers refers to the list order used in the HIrisPlex-S webtool (<https://hirisplex.erasmusmc.nl/>).

In case of three-allelic pattern, the dropped-in allele is in **bold red** characters.

Less-covered alleles are shown in **green bold characters** in the case of allelic imbalance (e.g., **AC**).

Flags alerting noising reads (1-10 % of the total) are shown in square brackets [].

Allelic drop-outs are shown in blue boxes.

NA= not available for phenotypic prediction.

list order	gene	marker	97	98	96	95	CONSENSUS
17	TYR	rs1042602	AA	AA	AA	AA[C]	AA
11	MC1R	rs1110400	TT	TT	TT	TT	TT
2	MC1R	rs11547464	GG	GG	GG	GG	GG
16	IRF4	rs12203592	CC[T]	CC	CC	CC	CC
14	KITLG	rs12821256	TT	TT	TT	TT	TT
22	LOC105370627	rs12896399	GT A	GT	GT A	GT	GT
20	HERC2	rs12913832	AG	AG	AG	AG	AG
23	TYR	rs1393350	GG	GG	GG	GG	GG
13	SLC45A2	rs16891982	CG	CG	CG T	CG	CG
18	OCA2	rs1800407	CC	CC	CC	CC[T]	CC
5	MC1R	rs1805005	GT	GT	GG	GG	GT
6	MC1R	rs1805006	CC	CC	CC	CC	CC
7	MC1R	rs1805007	CC	CC	CC	CC	CC
4	MC1R	rs1805008	CC	CC	CC	CC	CC
8	TUBB3	rs1805009	GG	GG	GG	GG	GG
9	MC1R	rs201326893	CC	CC	CC	CC	CC
10	MC1R	rs2228479	GG	AG	AA	GG	AG
21	PIGU	rs2378249	AA	AA	AA	AG	NA
19	SLC24A4	rs2402130	AA	AA	AA	AA	AA
12	SLC45A2	rs28777	AC	AC	AC	AC	AC
1	MC1R	rs312262906	CC	CC	CC	CC	CC
15	LOC105374875	rs4959270	CC	CC	CC	CA	NA
24	TYRP1	rs683	AA	AA	AA	AA	AA
3	MC1R	rs885479	GG	GG	GG	GG	GG

Table S9. Results of the genetic typing of skeleton 4.

The list order of SNP markers refers to the list order used in the HIrisPlex-S webtool (<https://hirisplex.erasmusmc.nl/>).

In case of three-allelic pattern, the dropped-in allele is in **bold red** characters.

Less-covered alleles are shown in **green bold characters** in the case of allelic imbalance (e.g., **AC**).

Flags alerting noising reads (1-10 % of the total) are shown in square brackets [].

Allelic drop-outs are shown in blue boxes.

NA= not available for phenotypic prediction.

list order	gene	marker	65	66	68	72	CONSENSUS
17	TYR	rs1042602	CC	CC	CC	CC	CC
11	MC1R	rs1110400	TT	TT	TT	TT	TT
2	MC1R	rs11547464	GG	GG	GG	GG[A]	GG
16	IRF4	rs12203592	CC	CC	CC[T]	CC	CC
14	KITLG	rs12821256	TT	TT	TT	TT	TT
22	LOC105370627	rs12896399	GG	GG[A]	GG	GG[A]	GG
20	HERC2	rs12913832	GG	GG	GG	GG	GG
23	TYR	rs1393350	GG	GG[A]	GG	GG	GG
13	SLC45A2	rs16891982	GG	GG	GG	GG	GG
18	OCA2	rs1800407	CC[T]	CC	CC[T]	CC	CC
5	MC1R	rs1805005	GG	GG	GG	GG	GG
6	MC1R	rs1805006	CC	CC	CC	CC	CC
7	MC1R	rs1805007	CC	CC[T]	CC	CC	CC
4	MC1R	rs1805008	CC[T]	CC	CC	CC	CC
8	TUBB3	rs1805009	GG[A]	GG	GG	GG	GG
9	MC1R	rs201326893	CC	CC	CC	CC	CC
10	MC1R	rs2228479	GG	GG[A]	GG	GG	GG
21	PIGU	rs2378249	AA	AA	AA	AA	AA
19	SLC24A4	rs2402130	GG	GG	GG[A]	GG	GG
12	SLC45A2	rs28777	AA	AA	AA	AA	AA
1	MC1R	rs312262906	CC	CC	CC	CC	CC
15	LOC105374875	rs4959270	CC[A]	CC	CC	CC	CC
24	TYRP1	rs683	NN	NN	CC	CC[A]	CC
3	MC1R	rs885479	GG	GG	GG	GG	GG

Table S9. Results of the genetic typing of skeleton 5.

The list order of SNP markers refers to the list order used in the HIrisPlex-S webtool (<https://hirisplex.erasmusmc.nl/>).

In case of three-allelic pattern, the dropped-in allele is in **bold red** characters.

Less-covered alleles are shown in **green bold characters** in the case of allelic imbalance (e.g., AC).

Flags alerting noising reads (1-10 % of the total) are shown in square brackets [].

Allelic drop-outs are shown in blue boxes.

NA= not available for phenotypic prediction.

list order	gene	marker	59	49	6D	58	50	CONSENSUS
17	TYR	rs1042602	AC	AC	AC	AC	AA	AC
11	MC1R	rs1110400	TT	TT	TT	TT	TT	TT
2	MC1R	rs11547464	GG	GG	GG	GG	GG	GG
16	IRF4	rs12203592	CC	CC	CC	CC	CC	CC
14	KITLG	rs12821256	TT	TT	TT	TT	TC	NA
22	LOC105370627	rs12896399	GG	GG	GG	GG	GG	GG
20	HERC2	rs12913832	GG[A]	GG	GG	GG	AG	NA
23	TYR	rs1393350	AG	AG	AG	AG	GG	AG
13	SLC45A2	rs16891982	GG	GG	GG	GG	GG	GG
18	OCA2	rs1800407	CC	CC	CC	CC	CC	CC
5	MC1R	rs1805005	GT	GT	GT	GG	GT	GT
6	MC1R	rs1805006	CC	CC	CC	CC	CC	CC
7	MC1R	rs1805007	CC	CC	CC	CC	CC	CC
4	MC1R	rs1805008	CC	CC	CC	CC	CC	CC
8	TUBB3	rs1805009	GG[C]	GG	GG	GG	GG	GG
9	MC1R	rs201326893	CC	CC	CC	CC	CC	CC
10	MC1R	rs2228479	GG	GG	GG	GG	GG	GG
21	PIGU	rs2378249	AG	AG	AG	GG	AG	AG
19	SLC24A4	rs2402130	AA[G]	AA	AA	AA	GG	AG
12	SLC45A2	rs28777	AA	AA	AA	AA	AA	AA
1	MC1R	rs312262906	CC	CC	CC	CC	CC	CC
15	LOC105374875	rs4959270	ACT	AC	AC	AC	CC	AC
24	TYRP1	rs683	AC	AC	ACT	AC	AC	AC
3	MC1R	rs885479	GG	GG	GG	GG	GG	GG

Table S9. Results of the genetic typing of skeleton 6.

The list order of SNP markers refers to the list order used in the HIrisPlex-S webtool (<https://hirisplex.erasmusmc.nl/>).

In case of three-allelic pattern, the dropped-in allele is in **bold red** characters.

Less-covered alleles are shown in **green bold characters** in the case of allelic imbalance (e.g., AC).

Flags alerting noising reads (1-10 % of the total) are shown in square brackets [].

Allelic drop-outs are shown in blue boxes.

NA= not available for phenotypic prediction.

list order	gene	marker	138	7D_1	7D_2	CONSENSUS
17	TYR	rs1042602	CC	CC	CC	CC
11	MC1R	rs1110400	CT	TT	TT	NA
2	MC1R	rs11547464	AG	GG	GG	NA
16	IRF4	rs12203592	CC	NN	CC	CC
14	KITLG	rs12821256	CT	NN	CC	NA
22	LOC105370627	rs12896399	GT	NN	TT	NA
20	HERC2	rs12913832	GG	NN	NN	GG
23	TYR	rs1393350	AG	GG	GG	NA
13	SLC45A2	rs16891982	GG	NN	GG	GG
18	OCA2	rs1800407	CC	NN	CC	CC
5	MC1R	rs1805005	GG[A]	NN	NN	GG
6	MC1R	rs1805006	CC	NN	NN	CC
7	MC1R	rs1805007	CC	CC	CC	CC
4	MC1R	rs1805008	CC	CC	CC	CC
8	TUBB3	rs1805009	GG	GG	GG	GG
9	MC1R	rs201326893	CC	CC	CC	CC
10	MC1R	rs2228479	GG	NN	NN	GG
21	PIGU	rs2378249	AA	NN	AG	NA
19	SLC24A4	rs2402130	AG	NN	AA	NA
12	SLC45A2	rs28777	AA	NN	AA	AA
1	MC1R	rs312262906	CC	NN	CC	CC
15	LOC105374875	rs4959270	AC	AA	AA	NA
24	TYRP1	rs683	AC	AC	AC	AC
3	MC1R	rs885479	GG	GG	GG	GG

Table S9. Results of the genetic typing of skeleton 7.

The list order of SNP markers refers to the list order used in the HIrisPlex-S webtool (<https://hirisplex.erasmusmc.nl/>).

In case of three-allelic pattern, the dropped-in allele is in **bold red** characters.

Less-covered alleles are shown in **green bold characters** in the case of allelic imbalance (e.g., AC).

Flags alerting noising reads (1-10 % of the total) are shown in square brackets [].

Allelic drop-outs are shown in blue boxes.

NA= not available for phenotypic prediction.

list order	gene	marker	12D	161	22	133	CONSENSUS
17	TYR	rs1042602	AC	AC	CC	CC	AC
11	MC1R	rs1110400	TT	TT	TT	TT	TT
2	MC1R	rs11547464	GG	GG	GG	GG	GG
16	IRF4	rs12203592	NN	CC	CC	CC	CC
14	KITLG	rs12821256	TT	TT	TT	TT	TT
22	LOC105370627	rs12896399	GG[A]	GG	GT	GG	NA
20	HERC2	rs12913832	AG	AG	AG	GG	AG
23	TYR	rs1393350	GG	GG	GG	GG	GG
13	SLC45A2	rs16891982	GG	GG	GG	GG	GG
18	OCA2	rs1800407	CC	CC	CC	CC	CC
5	MC1R	rs1805005	GG	GG	NN	GG	GG
6	MC1R	rs1805006	CC	CC	NN	CC	CC
7	MC1R	rs1805007	CC[T]	CC	CC	CC	CC
4	MC1R	rs1805008	CC	CC	CC	CC	CC
8	TUBB3	rs1805009	GG	NN	GG	GG	GG
9	MC1R	rs201326893	CC	CC	CC	CC	CC
10	MC1R	rs2228479	GG[A]	GG	NN	GG	GG
21	PIGU	rs2378249	AA	AA	AA	AA	AA
19	SLC24A4	rs2402130	AA	AA	NN	AA	AA
12	SLC45A2	rs28777	AA	AA	AA	AA	AA
1	MC1R	rs312262906	CC	CC	CC	CC	CC
15	LOC105374875	rs4959270	AA	AA	NN	AA	AA
24	TYRP1	rs683	AA	AA	AA	NN	AA
3	MC1R	rs885479	GG	GG	GG	GG	GG

Table S9. Results of the genetic typing of skeleton 12.

The list order of SNP markers refers to the list order used in the HIrisPlex-S webtool (<https://hirisplex.erasmusmc.nl/>).

In case of three-allelic pattern, the dropped-in allele is in **bold red** characters.

Less-covered alleles are shown in **green bold characters** in the case of allelic imbalance (e.g., AC).

Flags alerting noising reads (1-10 % of the total) are shown in square brackets [].

Allelic drop-outs are shown in blue boxes.

NA= not available for phenotypic prediction.

list order	gene	marker	25	13D	23	24	CONSENSUS
17	TYR	rs1042602	AA	AA	AA	AA	AA
11	MC1R	rs1110400	TT	TT	TT	TT	TT
2	MC1R	rs11547464	GG	GG	NN	GG	GG
16	IRF4	rs12203592	CC	CC	CC	CC	CC
14	KITLG	rs12821256	TT	TT	TT	TT	TT
22	LOC105370627	rs12896399	GG	GG	GG	GG	GG
20	HERC2	rs12913832	AG	AG	AG	AG	AG
23	TYR	rs1393350	GG	GG	GG	GG	GG
13	SLC45A2	rs16891982	GG	GG	GG	GG	GG
18	OCA2	rs1800407	CC	CC	CC	CC	CC
5	MC1R	rs1805005	GG	GG	GG	GG	GG
6	MC1R	rs1805006	CC	CC	CC	CC	CC
7	MC1R	rs1805007	CC	CC	CC	CC	CC
4	MC1R	rs1805008	CC	CC	CC	CC	CC
8	TUBB3	rs1805009	GG	GG	GG	GG	GG
9	MC1R	rs201326893	CC[T]	CC	CC	CC	CC
10	MC1R	rs2228479	GG	GG	GG	GG	GG
21	PIGU	rs2378249	AA	AA	AA	AA	AA
19	SLC24A4	rs2402130	AG	AA	AA	AA	NA
12	SLC45A2	rs28777	AA	AA	AA	AA	AA
1	MC1R	rs312262906	CC	CC	CC	CC	CC
15	LOC105374875	rs4959270	AC	NN	NN	AC	AC
24	TYRP1	rs683	AC	AC	AC	AC	AC
3	MC1R	rs885479	GG	GG	GG	GG	GG

Table S9. Results of the genetic typing of skeleton 13.

The list order of SNP markers refers to the list order used in the HIrisPlex-S webtool (<https://hirisplex.erasmusmc.nl/>).

In case of three-allelic pattern, the dropped-in allele is in **bold red** characters.

Less-covered alleles are shown in **green bold characters** in the case of allelic imbalance (e.g., AC).

Flags alerting noising reads (1-10 % of the total) are shown in square brackets [].

Allelic drop-outs are shown in blue boxes.

NA= not available for phenotypic prediction.

list order	gene	marker	192
17	TYR	rs1042602	AA
11	MC1R	rs1110400	TT
2	MC1R	rs11547464	AG
16	IRF4	rs12203592	CC
14	KITLG	rs12821256	TT
22	LOC105370627	rs12896399	GG
20	HERC2	rs12913832	AA[G]
23	TYR	rs1393350	GG
13	SLC45A2	rs16891982	CC
18	OCA2	rs1800407	CC
5	MC1R	rs1805005	GT
6	MC1R	rs1805006	CC
7	MC1R	rs1805007	CC
4	MC1R	rs1805008	CC
8	TUBB3	rs1805009	GG
9	MC1R	rs201326893	CC[T]
10	MC1R	rs2228479	GG
21	PIGU	rs2378249	AA
19	SLC24A4	rs2402130	AG
12	SLC45A2	rs28777	AA[C]
1	MC1R	rs312262906	CC
15	LOC105374875	rs4959270	AC
24	TYRP1	rs683	AC
3	MC1R	rs885479	GG

Table S9. Results of the genetic typing of skeleton 16.

The list order of SNP markers refers to the list order used in the HIrisPlex-S webtool (<https://hirisplex>). In case of three-allelic pattern, the dropped-in allele is in **bold red** characters.

Less-covered alleles are shown in **green bold characters** in the case of allelic imbalance (e.g., **AC**). ^A

Flags alerting noising reads (1-10 % of the total) are shown in square brackets [].

Allelic drop-outs are shown in blue boxes.

NA= not available for phenotypic prediction.

.erasmusmc.nl/).

As stated in the text, the imbalanced loci were considered as **NA**.

list order	gene	marker	179	171	176	180	CONSENSUS
17	TYR	rs1042602	AC	AC	CTA	NN	AC
11	MC1R	rs1110400	TT	TT	TT	TT	TT
2	MC1R	rs11547464	GG	GG	GG	GG	GG
16	IRF4	rs12203592	CC	CC	CC	CC	CC
14	KITLG	rs12821256	TT	TT	TT	TT	TT
22	LOC105370627	rs12896399	GG	GG	GT	TT	GT
20	HERC2	rs12913832	AG	AA	AA	AA	NA
23	TYR	rs1393350	GG	AG	NN	NN	NA
13	SLC45A2	rs16891982	GG	GG	CG	NN	NA
18	OCA2	rs1800407	CC	CC	CC	CC	CC
5	MC1R	rs1805005	GG	GG	GG	GG	GG
6	MC1R	rs1805006	CC	CC	CC	CC	CC
7	MC1R	rs1805007	CC[A]	CC	CC	CC	CC
4	MC1R	rs1805008	CC	CC	CC	CC	CC
8	TUBB3	rs1805009	GG	NN	GG	GG	GG
9	MC1R	rs201326893	CC	CC	NN	CC	CC
10	MC1R	rs2228479	GG	GG	GG	AG	NA
21	PIGU	rs2378249	AA	AA	NN	NN	AA
19	SLC24A4	rs2402130	AA	AG	AG	AA	AG
12	SLC45A2	rs28777	AA	AA	AA	AA	AA
1	MC1R	rs312262906	CC	CC	CC	CC	CC
15	LOC105374875	rs4959270	AA	CC	CC	AA	AC
24	TYRP1	rs683	AA	NN	NN	AC	NA
3	MC1R	rs885479	GG	GG	GG	GG	GG

Table S9. Results of the genetic typing of skeleton 17.

The list order of SNP markers refers to the list order used in the HRisPlex-S webtool (<https://hirisplex.erasmusn.nl>). In case of three-allelic pattern, the dropped-in allele is in **bold red** characters.

Less-covered alleles are shown in **green bold characters** in the case of allelic imbalance (e.g., **AC**).

Flags alerting noising reads (1-10 % of the total) are shown in square brackets [].

Allelic drop-outs are shown in blue boxes.

NA= not available for phenotypic prediction.

ac.nl/).

marker	279	533	536	537	538	783	784
rs1042602	CC	AC	AC	AA	CC	CC	AC
rs1110400	TT	TT	TT	TT	CT	TT	TT
rs11547464	GG	GG	GG	GG	AG	GG	GG
rs12203592	CC	CC	CC	CC	CC	CC	CC
rs12821256	TT	TT	TT	CT	CT	TT	TT
rs12896399	TT	GG	GT	GG	GT	GT	GT
rs12913832	GG	AA	GG	AG	GG	AG	AG
rs1393350	GG	AG	AG	GG	AG	GG	GG
rs16891982	GG	GG	GG	GG	GG	GG	CG
rs1800407	CC	CC	CC	CC	CC	CC	CC
rs1805005	GG	GT	GG	GT	GG	GG	GG
rs1805006	CC	CC	CC	CC	CC	CC	CC
rs1805007	CC	CC	CC	CC	CC	CC	CC
rs1805008	CC	CC	CC	CC	CC	CC	CC
rs1805009	GG	GG	GG	GG	GG	GG	GG
rs201326893	CC	CC	CC	CC	CC	CC	CC
rs2228479	GG	AG	GG	GG	GG	GG	AG
rs2378249	AA	AA	AA	AG	AA	AA	AA
rs2402130	AA	AA	AA	GG	AG	AA	AA
rs28777	AA	AA	AA	AA	AA	AA	AC
rs312262906	CC	CC	CC	CC	CC	CC	CC
rs4959270	CC	AC	CC	CC	AC	AC	AC
rs683	AC	AA	AA	AC	AC	AC	AA
rs885479	GG	GG	GG	GG	GG	AG	GG

Table S10. Results of the genetic typing of the 24 WWII skulls using the HirisPlex

785	786	787	788	789	790	791	792	793
CC	CC	AC	AC	AC	AA	AC	AC	AC
TT	TT	TT	TT	TT	TT	TT	TT	TT
GG	GG	GG	GG	GG	GG	GG	GG	GG
CT	CC	CC	CC	CC	CC	CC	CC	CC
TT	TT	TT	TT	TT	TT	CT	TT	TT
GG	TT	TT	GG	GG	GG	GG	GT	GT
AG	GG	AG	GG	GG	AG	AG	AA	GG
GG	AA	GG	AG	GG	GG	AG	AG	GG
GG	GG	GG	GG	GG	GG	CG	GG	GG
CC	CC	CC	CT	CC	CC	CC	CC	CC
GG	GG	GG	GT	GG	GG	TT	GG	GG
CC	CC	CC	CC	CC	CC	CC	CC	CC
CC	CT	CC	CC	CC	CT	CC	CC	CC
CT	CC	CC	CC	CC	CT	CC	CC	CT
GG	GG	GG	GG	GG	GG	GG	GG	GG
CC	CC	CC	CC	CC	CC	CC	CC	CC
GG	GG	AG	GG	GG	AG	GG	GG	GG
AA	AA	AA	AA	AA	AG	AA	AA	AG
AG	AA	AA	GG	AG	AA	AG	AA	AA
AA	AA	AA	AA	AA	AA	AA	AA	AA
CC	CC	CC	CC	CC	CC	CC	AC	CC
AC	AA	AC	AC	AC	AC	AC	AC	CC
AC	AA	AC	AC	AC	AA	AA	AA	AA
GG	GG	GG	GG	GG	GG	GG	GG	AG

κ panel. Less-covered alleles (e.g., allelic imbalances) are shown in red characters.

794	795	796	797	798	799	801	802
AC	AC	CC	AC	AC	AA	AA	AC
TT	TT	TT	TT	TT	TT	TT	TT
GG	GG	GG	GG	GG	GG	GG	GG
CT	CC	CC	CC	CC	CC	CC	CC
TT	TT	CT	TT	CT	TT	TT	TT
GG	GT	GT	GG	TT	TT	TT	TT
GG	GG	GG	GG	AG	AG	GG	AG
AG	GG	AG	GG	AG	GG	GG	GG
GG	GG	GG	GG	GG	GG	GG	GG
CC	CC	CC	CC	CC	CC	CC	CC
GT	GT	GT	GG	GG	GT	GG	GT
CC	CC	CC	CC	CT	CC	CC	CC
CC	CC	CC	CC	CT	CC	CC	CC
CC	CC	CC	CC	CC	CC	CC	CC
GG	GG	GG	GG	GG	GG	GG	GG
CC	CC	CC	CC	CC	CC	CC	CC
GG	AG	GG	GG	GG	GG	GG	GG
AA	AA	AA	AG	AA	AG	AA	AA
AA	AG	AA	AA	AA	AA	AA	AA
AA	AA	AA	AA	AA	AA	AA	AA
CC	CC	CC	CC	CC	CC	CC	CC
AC	AC	AC	AA	AC	AA	CC	AC
CC	AA	CC	AC	AC	AA	AA	AC
GG	GG	GG	GG	AG	GG	GG	GG

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	Sample		eye			
			blue	interm.	brown	blond
ancient skeletons	sk_1	P- value	0.956	0.035	0.008	0.339
		<i>AUC loss</i>	0	0	0	0
	sk_2	P- value	0.001	0.017	0.982	0.107
		<i>AUC loss</i>	0	0	0	0.02
	sk_3	P- value	0.184	0.15	0.665	0.322
		<i>AUC loss</i>	0	0	0	0
	sk_4	P- value	0.026	0.063	0.912	0.103
		<i>AUC loss</i>	0	0	0	0.002
	sk_5	P- value	0.848	0.088	0.065	0.496
		<i>AUC loss</i>	0	0	0	0
	sk_6	P- value	0	0	0	0.391
		<i>AUC loss</i>	0.293	0.137	0.297	0.054
sk_7	P- value	0.914	0.055	0.031	0.691	
	<i>AUC loss</i>	0.016	0.041	0.009	0.011	
sk_12	P- value	0.101	0.131	0.769	0.438	
	<i>AUC loss</i>	0.01	0.027	0.006	0	
sk_13	P- value	0.05	0.114	0.836	0.327	
	<i>AUC loss</i>	0	0	0	0.001	
sk_16	P- value	0	0.002	0.998	0.012	
	<i>AUC loss</i>	0	0	0	0.005	
sk_17	P- value	0	0	0	0.46	
	<i>AUC loss</i>	0.325	0.15	0.337	0.06	
	279	P- value	0.949	0.035	0.016	0.667
		<i>AUC loss</i>	0	0	0	0
	533	P- value	0	0.016	0.983	0.122
		<i>AUC loss</i>	0	0	0	0
	536	P- value	0.932	0.046	0.021	0.69
		<i>AUC loss</i>	0	0	0	0
	537	P- value	0.05	0.114	0.836	0.171
		<i>AUC loss</i>	0	0	0	0.002
	538	P- value	0.932	0.046	0.021	0.701
		<i>AUC loss</i>	0	0	0	0
	783	P- value	0.099	0.134	0.767	0.291
		<i>AUC loss</i>	0	0	0	0
	784	P- value	0.012	0.05	0.938	0.13
		<i>AUC loss</i>	0	0	0	0
	785	P- value	0.084	0.188	0.727	0.169
		<i>AUC loss</i>	0	0	0	0.003
	786	P- value	0.97	0.023	0.007	0.683
		<i>AUC loss</i>	0	0	0	0
	787	P- value	0.184	0.15	0.665	0.379
		<i>AUC loss</i>	0	0	0	0.001
	788	P- value	0.934	0.054	0.012	0.62
		<i>AUC loss</i>	0	0	0	0.002

WWII skulls

789	P- value	0.848	0.088	0.065	0.618
	<i>AUC loss</i>	0	0	0	0
790	P- value	0.05	0.114	0.836	0.412
	<i>AUC loss</i>	0	0	0	0.021
791	P- value	0	0	0	0.466
	<i>AUC loss</i>	0.321	0.151	0.333	0.058
792	P- value	0.001	0.019	0.98	0
	<i>AUC loss</i>	0.002	0.006	0.002	0.001
793	P- value	0.903	0.06	0.037	0.627
	<i>AUC loss</i>	0.01	0.027	0.006	0.014
794	P- value	0.903	0.074	0.023	0.223
	<i>AUC loss</i>	0	0	0	0
795	P- value	0.911	0.057	0.032	0.606
	<i>AUC loss</i>	0	0	0	0
796	P- value	0.932	0.046	0.021	0.674
	<i>AUC loss</i>	0	0	0	0
797	P- value	0.848	0.088	0.065	0.689
	<i>AUC loss</i>	0	0	0	0
798	P- value	0	0	0	0
	<i>AUC loss</i>	0.293	0.137	0.297	0.074
799	P- value	0	0	0	0.514
	<i>AUC loss</i>	0.293	0.137	0.297	0.053
801	P- value	0.949	0.035	0.016	0.671
	<i>AUC loss</i>	0	0	0	0
802	P- value	0	0	0	0.47
	<i>AUC loss</i>	0.293	0.137	0.297	0.054
Accuracy thresholds		0.939	0.7361	0.9461	0.8133

Table S11. Phenotypic predictions for the 11 skeletons and the 24 skulls. The predictions affected shown in **bold characters**. The accuracy thresholds values are shown in the last line.

hair					phenotypic prediction	
brown	red	black	light	dark	eye	hair
0.581	0.006	0.075	0.82	0.18	blue	brown/dark-brown
<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.632	0.005	0.256	0.366	0.634	brown	dark-brown/black
0.015	0.088	0.011	0.007	0.007		
0.57	0.002	0.106	0.636	0.364	brown	dark-brown/black
<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.698	0.007	0.192	0.358	0.642	brown	dark-brown/black
0.002	0.007	<i>0</i>	0.001	0.001		
0.433	0.002	0.069	0.842	0.158	blue	dark-blond/brown
<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.547	0.015	0.047	0.87	0.13	<i>undetermined</i>	brown/dark-brown
0.039	0.002	0.052	0.079	0.079		
0.268	0.007	0.034	0.951	0.049	blue	blond/dark-blond
<i>0.011</i>	<i>0.022</i>	<i>0.006</i>	<i>0.007</i>	<i>0.007</i>		
0.472	0.003	0.087	0.839	0.161	brown	brown/dark-brown
<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.579	0.002	0.092	0.735	0.265	brown	dark-brown/black
0.002	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.605	0.002	0.381	0.999	0.001	brown	brown/dark-brown
0.003	0.003	0.001	0.004	0.004		
0.44	0.004	0.096	0.813	0.187	<i>undetermined</i>	dark-blond/brown
0.046	0.006	0.052	0.076	0.076		
0.285	0.002	0.046	0.933	0.067	blue	blond/dark-blond
<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.602	0.003	0.273	0.388	0.612	brown	dark-brown/black
<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.278	0.003	0.03	0.953	0.047	blue	blond/dark-blond
<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.763	0.006	0.059	0.582	0.418	brown	brown/dark-brown
0.002	<i>0</i>	0.004	0.004	0.004		
0.072	0.222	0.004	1	0	blue	blond
<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.457	0.001	0.251	0.647	0.353	brown	dark-brown/black
<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.619	0.001	0.25	0.319	0.681	brown	dark-brown/black
0.002	0.001	0.001	<i>0</i>	<i>0</i>		
0.621	0.036	0.175	0.517	0.483	brown	dark-brown/black
0.003	0.002	0.001	0.002	0.002		
0.148	0.164	0.005	0.996	0.004	blue	blond/dark-blond
<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.456	0.003	0.162	0.731	0.269	brown	dark-brown/black
<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>		
0.349	0.006	0.025	0.952	0.048	blue	blond/dark-blond
0.002	0.001	0.002	0.001	0.001		

0.343 <i>0</i>	0.004 <i>0</i>	0.035 <i>0</i>	0.937 <i>0</i>	0.063 <i>0</i>	blue	blond/dark-blond
0.345 <i>0.016</i>	0.214 <i>0.091</i>	0.028 <i>0.014</i>	0.909 <i>0.007</i>	0.091 <i>0.007</i>	brown	blond/dark-blond
0.497 <i>0.043</i>	0.02 <i>0.004</i>	0.017 <i>0.054</i>	0.963 <i>0.071</i>	0.037 <i>0.071</i>	<i>undetermined</i>	brown/dark-brown
0.689 <i>0.001</i>	0.311 <i>0.001</i>	0 <i>0.002</i>	0.342 <i>0.001</i>	0.658 <i>0.001</i>	brown	dark-brown/black
0.311 <i>0.016</i>	0.017 <i>0.066</i>	0.044 <i>0.004</i>	0.929 <i>0.002</i>	0.071 <i>0.002</i>	blue	blond/dark-blond
0.699 <i>0</i>	0.007 <i>0</i>	0.072 <i>0</i>	0.774 <i>0</i>	0.226 <i>0</i>	blue	dark-brown/black
0.339 <i>0</i>	0.021 <i>0</i>	0.034 <i>0</i>	0.959 <i>0</i>	0.041 <i>0</i>	blue	blond/dark-blond
0.304 <i>0</i>	0.005 <i>0</i>	0.017 <i>0</i>	0.981 <i>0</i>	0.019 <i>0</i>	blue	blond/dark-blond
0.281 <i>0</i>	0.01 <i>0</i>	0.021 <i>0</i>	0.959 <i>0</i>	0.041 <i>0</i>	blue	blond/dark-blond
0 <i>0.063</i>	0 <i>0.111</i>	0 <i>0.064</i>	0.96 0.081	0.04 0.081	<i>undetermined</i>	<i>undetermined</i>
0.437 <i>0.039</i>	0.021 <i>0.006</i>	0.028 <i>0.044</i>	0.944 <i>0.068</i>	0.056 <i>0.068</i>	<i>undetermined</i>	blond/dark-blond
0.302 <i>0</i>	0.003 <i>0</i>	0.024 <i>0</i>	0.957 <i>0</i>	0.043 <i>0</i>	blue	blond/dark-blond
0.466 <i>0.04</i>	0.007 <i>0.004</i>	0.057 <i>0.043</i>	0.89 <i>0.07</i>	0.11 <i>0.07</i>	<i>undetermined</i>	brown/dark-brown
0.7411	0.9289	0.8592	0.9054			

d by AUC loss are in **red characters**. The values above the accuracy thresholds are