Supplemental information

# Corroborating written history with ancient

DNA: The case of the Well-man

described in an Old Norse *saga*

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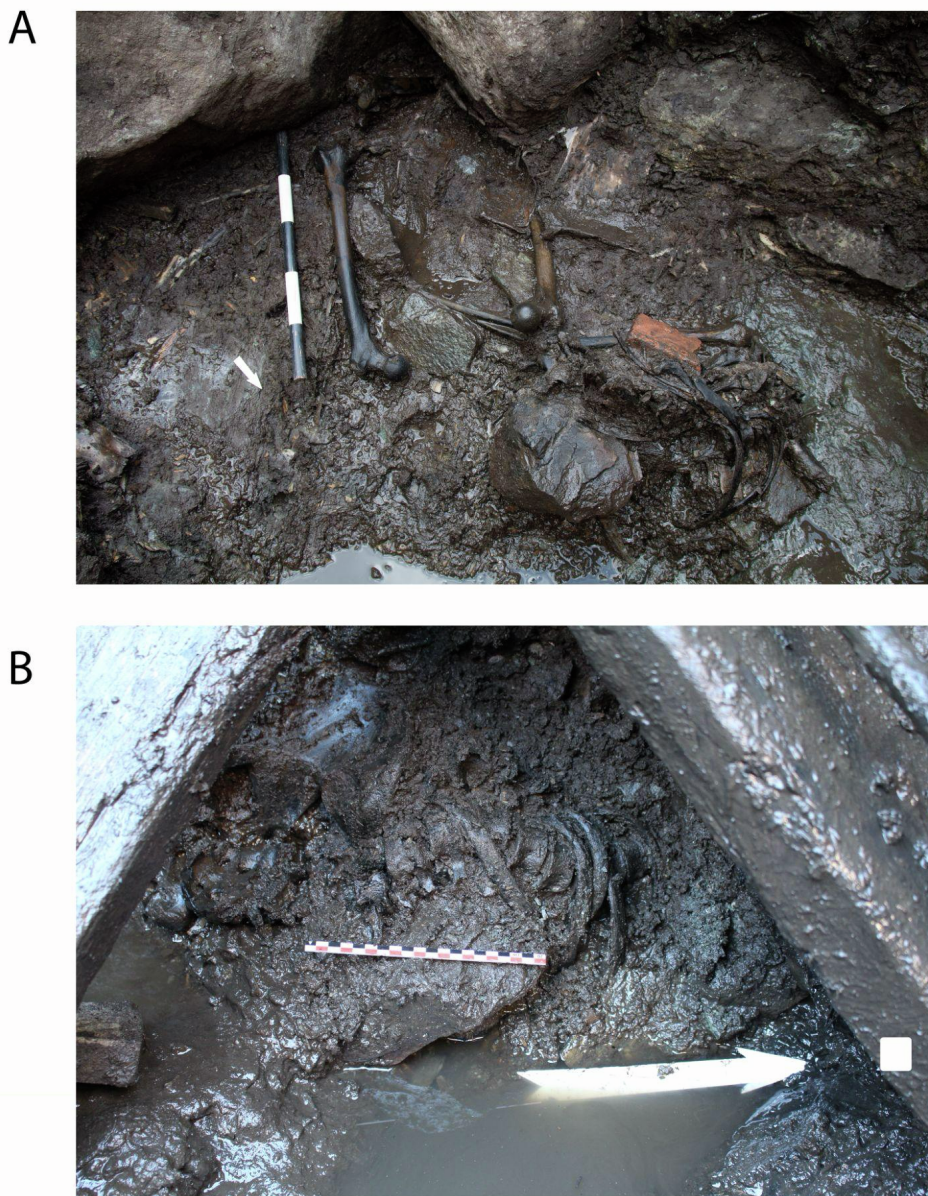
Figure S1. Photographs of the Well-man skeletal remains during excavation, Related to Figure 1. (A) Excavation in 2016. Image courtesy of NIKU. (B) Excavation in 2014. Image courtesy of NIKU.
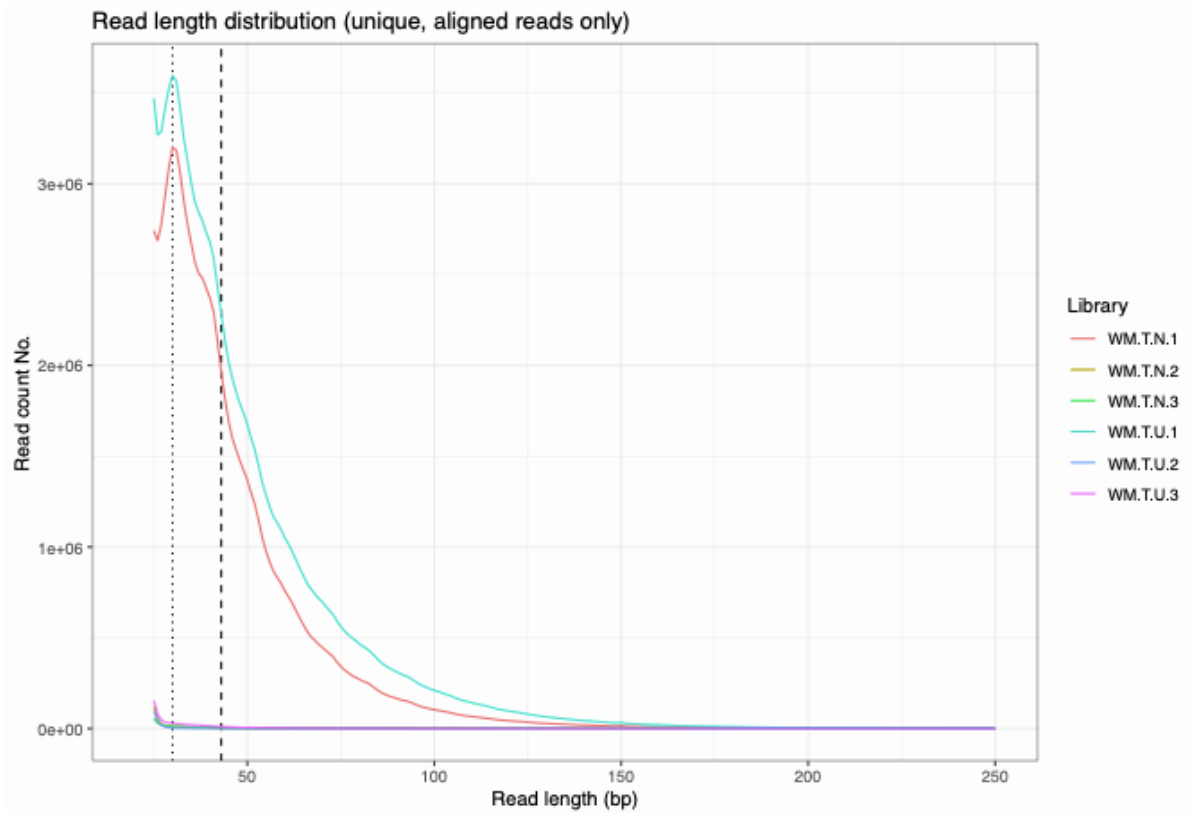
Figure S2. Distributions of read length for six libraries built on the Well-man DNA extracts, Related to Figure 1. The dotted line indicates the mode of all libraries. The dashed line indicates the mean of all libraries.
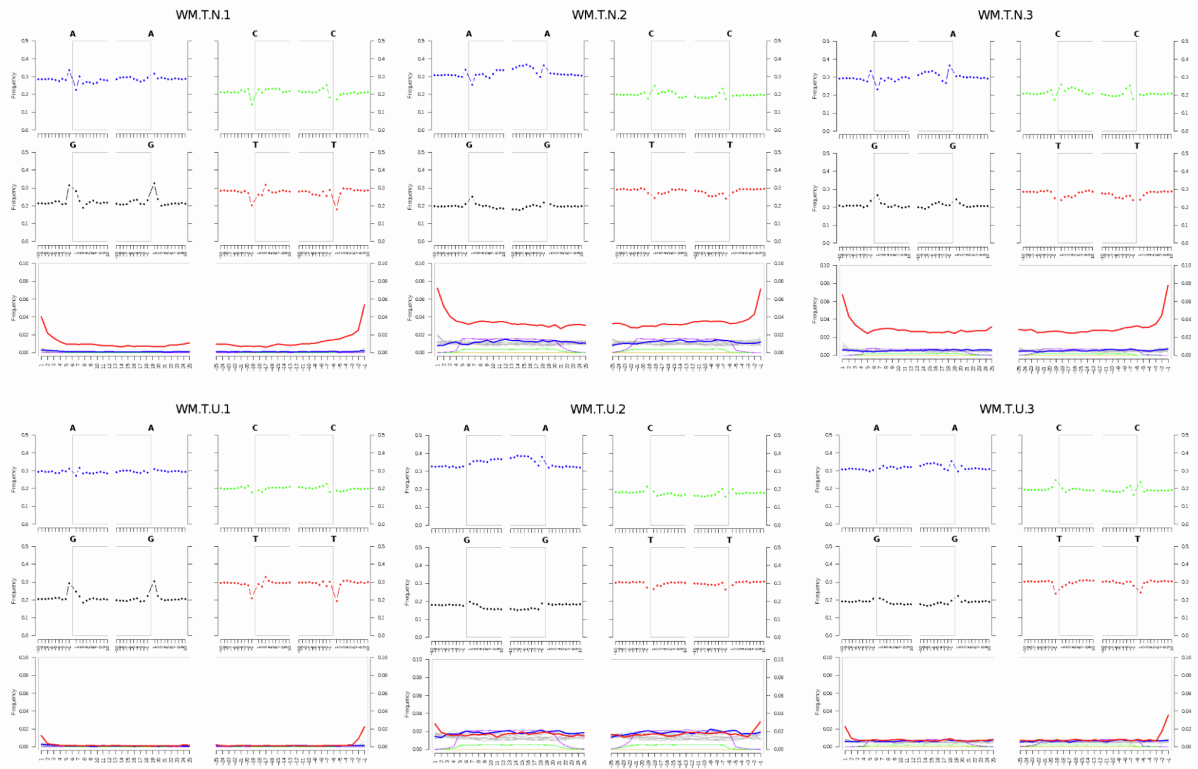
Figure S3. MapDamage results for the six Well-man libraries, Related to Figure 1. Top row: DNA extracts not USER-treated (samples WM.T.N.1, WM.T.N.2, and WM.T.N.3). Bottom row: USER-treated DNA extracts (samples WM.T.U.1, WM.T.U.2, and WM.T.U.3).
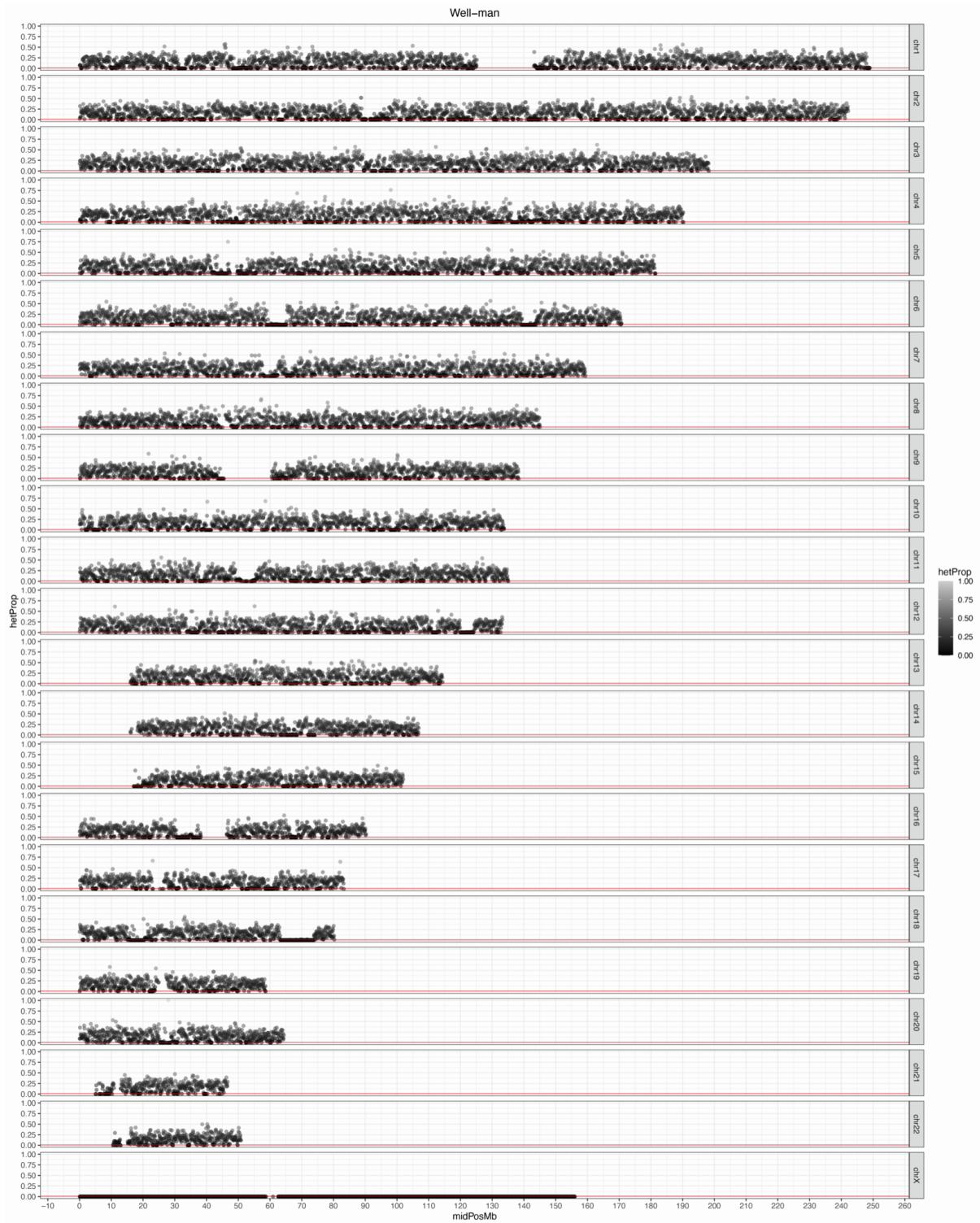
Figure S4. Chromosome-specific distributions of heterozygosity for the Well-man sample, Related to Figure 2.

Table S1. Data generation and mapping statistics, Related to Figure 1. Total read pairs: total number of 150-bp read pairs. Mapped reads: number of reads mapped to the human reference genome. Unique reads: number of reads uniquely mapped to the human reference genome. Mean read length: average fragment length of unique reads. Endog. content: proportion of uniquely mapped reads to total reads. Depth MT: final sequencing depth of mitochondrial genome after read filtering. Depth NR: final sequencing depth of autosomes. Y-chrom. hap.: Y-chromosome haplogroup. MT hap: mitochondrial genome haplogroup. Library NTC = library no-template control.

Sample ID	Total read pairs	Mapped reads	Unique reads	Mean read length (bp)	Library clonality (%)	Endog. content (%)	Mean depth MT (x)	Mean depth AU (x)	9 Y-chrom. hap.	10 MT hap.
Well-man	5,860,146,617	262,100,736	204,791,462	47.9	21.9	3.49	1278.7	3.18	I1a1a2a1	H2a2a1
Extraction Blank	2,064,161	428	100	109.8	76.6	0.02	0.0	0.00	-	-
Library NTC	11,066,006	6,235	3,076	74.8	50.7	0.06	0.0	0.00	-	-

Table S2. Estimates of contamination in each of the six Well-man libraries, Related to Figure 1. MT: mitochondrial genome.

Library type	Test type	ContamMix			ANGSD			
		Reads in MT	Better match	Contamination estimate (%)	Method1		Method2	
WM.T.N.1	MT	26,856	867	3.2	-	-	-	-
WM.T.N.2	MT	6,473	140	2.2	-	-	-	-
WM.T.N.3	MT	4,292	87	2.0	-	-	-	-
WM.T.U.1	MT	28,305	99	0.3	-	-	-	-
WM.T.U.2	MT	4,268	7	0.2	-	-	-	-
WM.T.U.3	MT	12,420	16	0.1	-	-	-	-
all libraries	X-chrom	-	-	-	0.00831%	p-val=0.6226	0.00663%	p-val=0.8815

Table S3. Well-man sex determination based on statistical analysis of reads mapping to the X and Y chromosomes, Related to Figure 1.

Reads mapped to X	Reads mapped to Y	Total X+Y reads	Ry	SE	95% CI	NGS sex (male / female)
5,379,644	601,184	5,980,828	0.100519	0.000123	0.000241	male

Table S5. Provenance and information on sex, contamination, and haplogroup for 24 ancient Norwegian specimens analysed in this study, Related to Figure 4.

Sample ID	Burial region	Lat	Lon	Age	Sample type	Depth (X)	Sex	Contam. mtDNA (%)	Y hap.	mtDNA hap.	Publication
SK312	Trondheim	63.4	10.4	1100-1175 CE	Tooth	0.46	F	1.45	N/A	U5a2d1	Gopalakrishnan et al. (2022)
SK340	Trondheim	63.4	10.4	1100-1175 CE	Tooth	1.09	F	1.35	N/A	T2e1	Gopalakrishnan et al. (2022)
SK356	Trondheim	63.4	10.4	1175-1275 CE	Tooth	7.15	F	0	N/A	H10a1	Gopalakrishnan et al. (2022)
VK387	Oppland	60.31	10.43	900-1100 CE	Petrous	1.20	F	1.56	N/A	U5a1a1	Margaryan et al. 2020
VK388	Nordland	68.34	15.66	700-1500 CE	Tooth	1.01	M	0.2	I1	J1c5	Margaryan et al. 2020
VK389	Telemark	59.22	9.61	900-1000 CE	Petrous	1.29	M	0.82	R1b1a1b1a1a1c2b2a1b1a4b	T2b	Margaryan et al. 2020
VK392	Telemark	59.58	7.92	700-1000 CE	Tooth	1.14	F	1.92	N/A	H1g1	Margaryan et al. 2020
VK393	Hedmark	60.84	11	900-1000 CE	Tooth	1.25	F	1.04	N/A	U8a1a	Margaryan et al. 2020
VK394	Hedmark		11.34	900-1000 CE	Petrous	0.95	M	0.61	R1a1a1b1a3	H13a1a1a	Margaryan et al. 2020
VK414	Oppland	61.88	8.4	900-1100 CE	Petrous	1.32	M	1.35	R1a1a1b1a3a2a	H6a1a	Margaryan et al. 2020
VK415	Oppland	60.29	10.63	700-1100 CE	Petrous	1.31	F	0.18	N/A	H6a1a	Margaryan et al. 2020
VK417	Oppland	60.36	10.57	600-1100 CE	Petrous	1.25	F	0.55	N/A	H7b	Margaryan et al. 2020
VK419	Nordland	67.29	14.42	600-1000 CE	Petrous	1.25	M	1.82	N1a1a1a1a1a1a	U5b1b1g1	Margaryan et al. 2020
VK420	Hedmark	60.8	11.1	700-1100 CE	Petrous	1.52	M	0.62	I1	I4a	Margaryan et al. 2020
VK514	Nordland	67.91	15.13	600-1000 CE	Tooth	1.11	M	1.3	R1a1a1b1a3a1	K2b1a1	Margaryan et al. 2020
VK516	Sor-Trondelag	63.7	9.75	900-1000 CE	Tooth	1.44	M	0.87	R1a1a1b1a3a2	H6a1a	Margaryan et al. 2020
VK519	Nordland	67.93	14.96	600-1000 CE	Tooth	0.24	M	0.3	I1	HV0a1	Margaryan et al. 2020
VK520	Troms	69.65	18.13	900-1000 CE	Tooth	1.84	F	0.67	N/A	U5b2a1a2	Margaryan et al. 2020
VK523	Sor-Trondelag	63.83	9.7	500-1100 CE	Petrous	1.15	F	0.86	N/A	I1a1	Margaryan et al. 2020

VK524	Nordland	66.26	12.73	900-1000 CE	Tooth	1.49	M	0.45	I1a2a1a1d1a	HV0a1	Margaryan et al. 2020
VK529	Nordland	67.64	14.79	700-900 CE	Tooth	2.02	M	1.11	I1a1b1a4a2	H7	Margaryan et al. 2020
VK547	Nordland	68.55	16.4	800-1100 CE	Tooth	5.39	M	0.74	I1a1b1a4a2	V	Margaryan et al. 2020
VK548	Nord-Trondelag	63.44	11.22	900-1000 CE	Tooth	3.80	F	0.47	N/A	A12a	Margaryan et al. 2020
Well-man	Trondheim	63.25	10.21	1154-1285 CE	Tooth	3.40	M	1.34	I1a1a2a1	H2a2a1	This study

Table S6. Heterozygosity proportions and related statistics in the autosomes of ancient Norwegian individuals, Related to Figure 4. Hom GT cnt: number of homozygous genotypes. Het GT cnt: number of homozygous genotypes. Miss GT cnt: number of missing genotypes. Het prop: proportion of genotypes in heterozygous state. Frag cnt: number of autosomal chromosome regions in contiguous homozygous state. Frag len pos sum: total length of autosomal chromosome regions in contiguous homozygous state (bp). Frag len cM sum: total length of autosomal chromosome regions in contiguous homozygous state (cM). Hom IBD prop: inbreeding coefficient (proportion of autosomal genome identical by descent).

Sample	Hom GT cnt	Het GT cnt	Missing GT cnt	Het prop	Frag cnt	Frag len pos sum	Frag len cM sum	Hom IBD prop
SK312	10,438,873	2,034,685	0	0.1631200	1	1,812,200	1.371	0.000389
SK340	10,410,684	2,062,874	0	0.1653800	2	4,043,691	6.413	0.00182
VK519	10,406,730	2,066,828	0	0.1656970	2	4,074,100	3.232	0.000917
VK420	10,444,151	2,029,407	0	0.1626970	3	4,316,013	5.894	0.001673
VK415	10,424,151	2,049,407	0	0.1643000	3	5,802,075	7.602	0.002157
VK419	10,428,162	2,045,396	0	0.1639790	3	6,074,603	6.27	0.001779
VK524	10,420,793	2,052,765	0	0.1645690	5	7,826,070	7.252	0.002058
VK514	10,430,987	2,042,571	0	0.1637520	3	8,211,893	5.652	0.001604
SK356	10,432,951	2,040,607	0	0.1635950	2	8,256,441	2.627	0.000746
VK388	10,428,130	2,045,428	0	0.1639810	5	9,048,710	8.437	0.002395
VK394	10,420,098	2,053,460	0	0.1646250	3	9,371,627	5.19	0.001473
VK547	10,406,135	2,067,423	0	0.1657440	4	9,780,076	13.357	0.003791
VK548	10,429,889	2,043,669	0	0.1638400	6	11,722,002	13.698	0.003888
VK387	10,412,174	2,061,384	0	0.1652600	6	11,970,757	13.379	0.003797
VK414	10,423,959	2,049,599	0	0.1643160	7	13,523,934	18.027	0.005116
VK520	10,425,717	2,047,841	0	0.1641750	5	14,002,723	13.101	0.003718
VK389	10,408,052	2,065,506	0	0.1655910	6	17,949,501	9.986	0.002834
VK516	10,445,104	2,028,454	0	0.1626200	9	18,230,084	27.7	0.007862
VK529	10,422,114	2,051,444	0	0.1644630	6	18,639,719	9.394	0.002666
VK393	10,428,235	2,045,323	0	0.1639730	9	19,103,449	22.262	0.006318
Well-man	10,420,846	2,052,712	0	0.1645650	10	29,563,116	40.223	0.011416
VK392	10,449,351	2,024,207	0	0.1622800	10	31,431,160	29.791	0.008455
VK417	10,456,171	2,017,387	0	0.1617330	15	57,554,666	70.963	0.02014
VK523	10,483,493	1,990,065	0	0.1595430	18	61,872,880	68.996	0.019582

Table S7. HIrisPlex pigmentation phenotype allele dosages for the Well-man, Related to Figure 4.

Variant	Allele dosage in Well-man		Variant	Allele dosage in Well-man
rs312262906_A	0		Full_AUC_BlueEye	0.93897364
rs11547464_A	0		Full_AUC_IntermediateEye	0.73608861
rs885479_T	0		Full_AUC_BrownEye	0.94607779
rs1805008_T	1		Numb_missingSNPs_Eye	0
rs1805005_T	0		AUC_Loss_BlueEye	0
rs1805006_A	0		AUC_Loss_IntermediateEye	0
rs1805007_T	0		AUC_Loss_BrownEye	0
rs1805009_C	0		PBlondHair	0.38480042
rs201326893_A	NA		PBrownHair	0.41050149
rs2228479_A	0		PRedHair	0.16092068
rs1110400_C	0		PBlackHair	0.04377742
rs28777_C	0		Full_AUC_BlondHair	0.81328159
rs16891982_C	0		Full_AUC_BrownHair	0.74106545
rs12821256_G	0		Full_AUC_RedHair	0.92893302
rs4959270_A	1		Full_AUC_BlackHair	0.85924813
rs12203592_T	1		Numb_missingSNPs_Hair	1
rs1042602_T	0		Name_missingSNPs_Hair	rs201326893_A
rs1800407_A	0		AUC_Loss_BlondHair	0.00140796
rs2402130_G	0		AUC_Loss_BrownHair	0.00042713
rs12913832_T	0		AUC_Loss_RedHair	0.00332208
rs2378249_C	1		AUC_Loss_BlackHair	3.63E-05
rs12896399_T	1		PLightHair	8.69E-01
rs1393350_T	0		PDarkHair	0.13086645
rs683_G	1		Full_AUC_HairShade	0.90544361
rs3114908_T	0		Numb_missingSNPs_HairShade	0
rs1800414_C	0		AUC_Loss_HairShade	0
rs10756819_G	2		PVeryPaleSkin	9.19E-08
rs2238289_C	0		PPaleSkin	1.62E-09
rs17128291_C	1		PIntermediateSkin	1.00E+00
rs6497292_C	0		PDarkSkin	1.49E-19
rs1129038_G	0		PDarktoBlackSkin	7.62E-13
rs1667394_C	1		Full_AUC_Very PaleSkin	8.30E-01
rs1126809_A	0		Full_AUC_PaleSkin	0.76279635
rs1470608_A	0		Full_AUC_IntermediateSkin	0.78330427
rs1426654_G	1		Full_AUC_DarkSkin	0.9806167
rs6119471_C	2		Full_AUC_DarktoBlackSkin	0.99347337
rs1545397_T	0		Numb_missingSNPs_Skin	0
rs6059655_T	1		AUC_Loss_VeryPaleSkin	0
rs12441727_A	0		AUC_Loss_PaleSkin	0
rs3212355_A	0		AUC_Loss_IntermediateSkin	0
rs8051733_C	1		AUC_Loss_DarkSkin	0
PBlueEye	0.92584671		AUC_Loss_DarktoBlackSkin	0
PIntermediateEye	0.05707147			
PBrownEye	0.01708183			