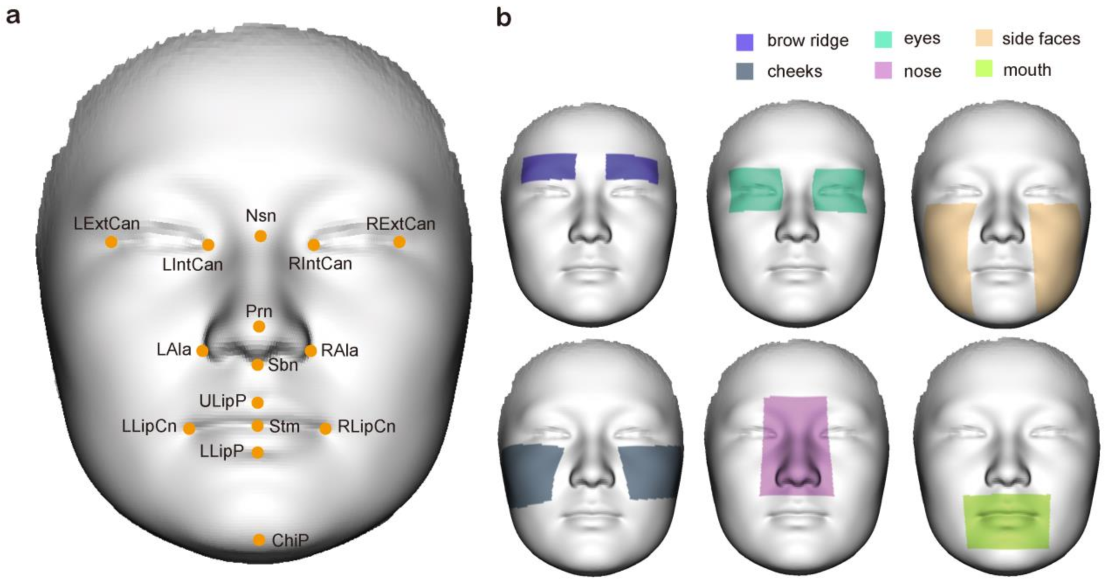
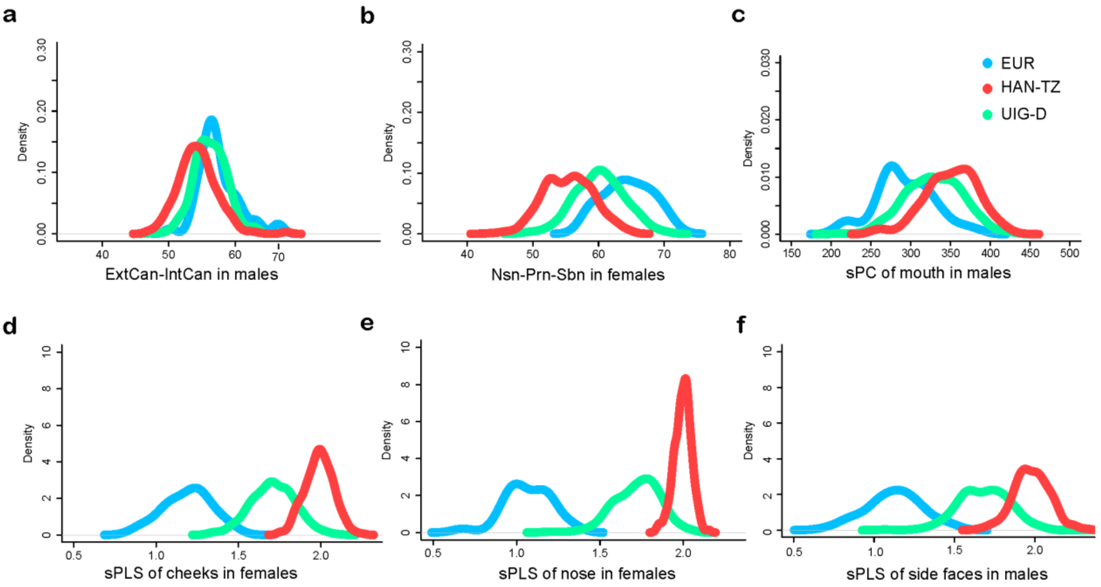
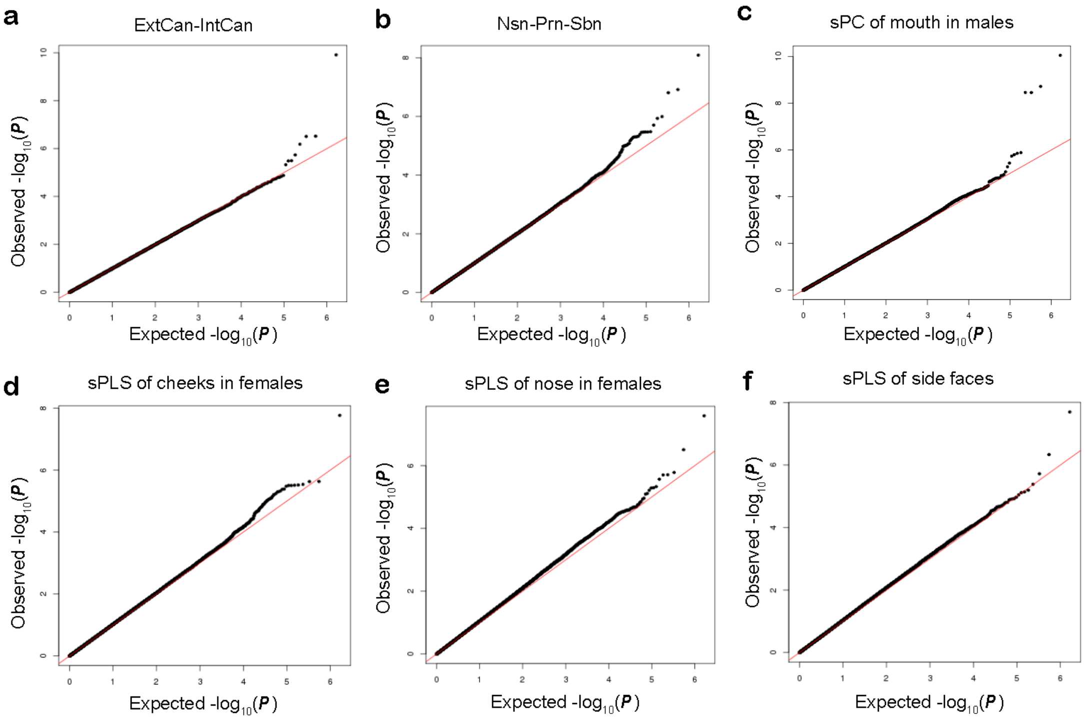


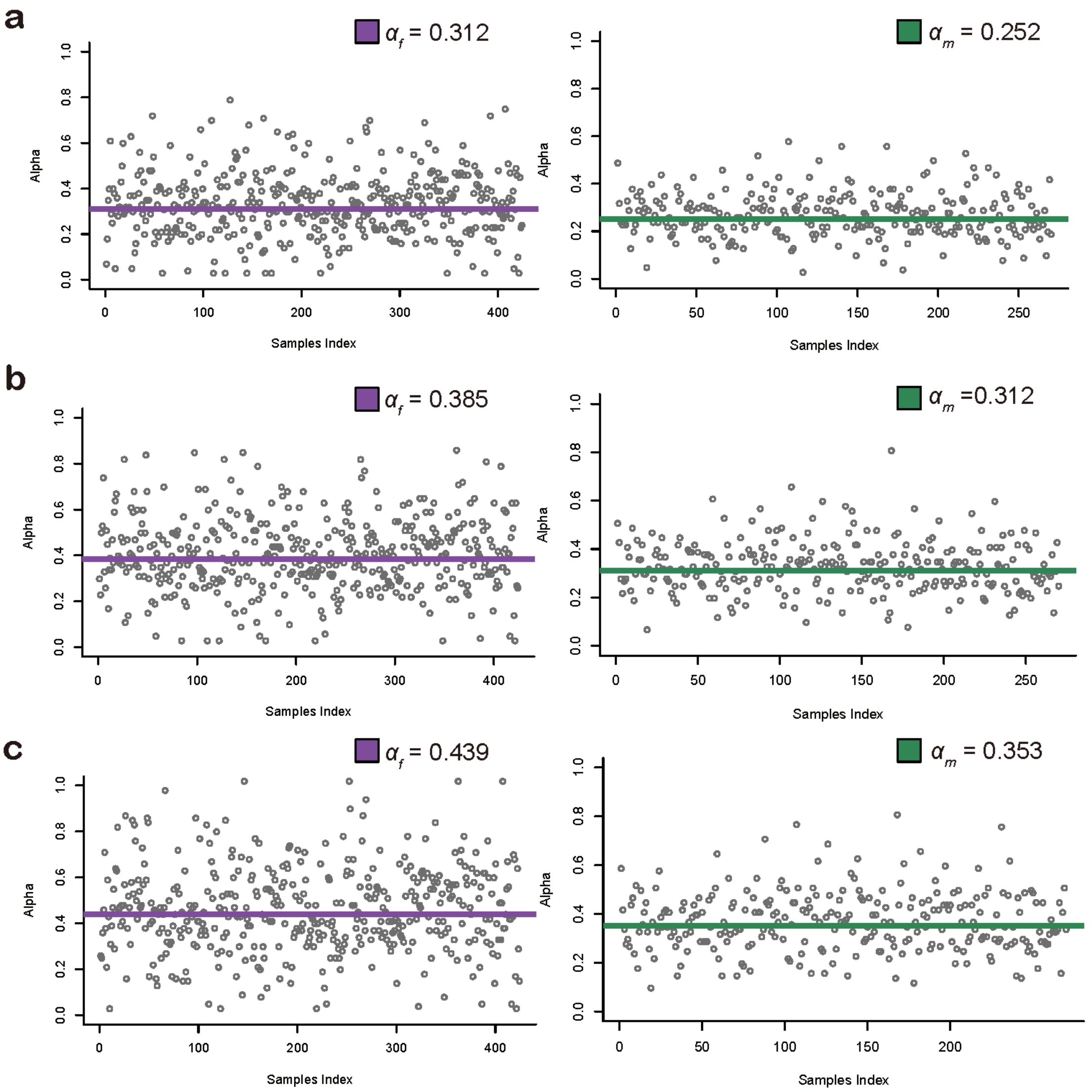
Supplementary Figure 1 | The 15 landmarks and facial features extracted from 3D images. (a) fifteen landmarks. (b) six facial features used to analysis.



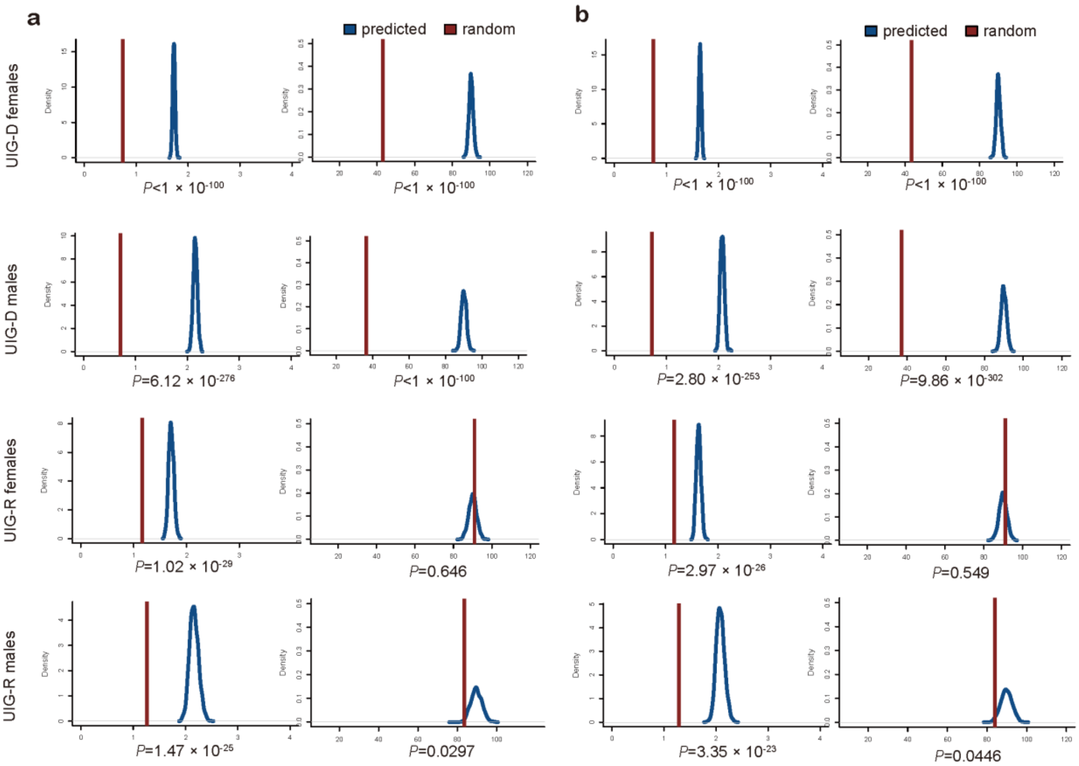
Supplementary Figure 2 | Few candidate phenotype examples show strong divergence between EUR and HAN-TZ with UIG-D covering in-between. (a) distance between ExtCan and IntCan in males, (b) distance of Nsn-Prn-Sbn in females, (c) sPC of mouth in males, (d) sPLS of cheek in females, (e) nasal sPLS in females, (f) sPLS of side faces in males.



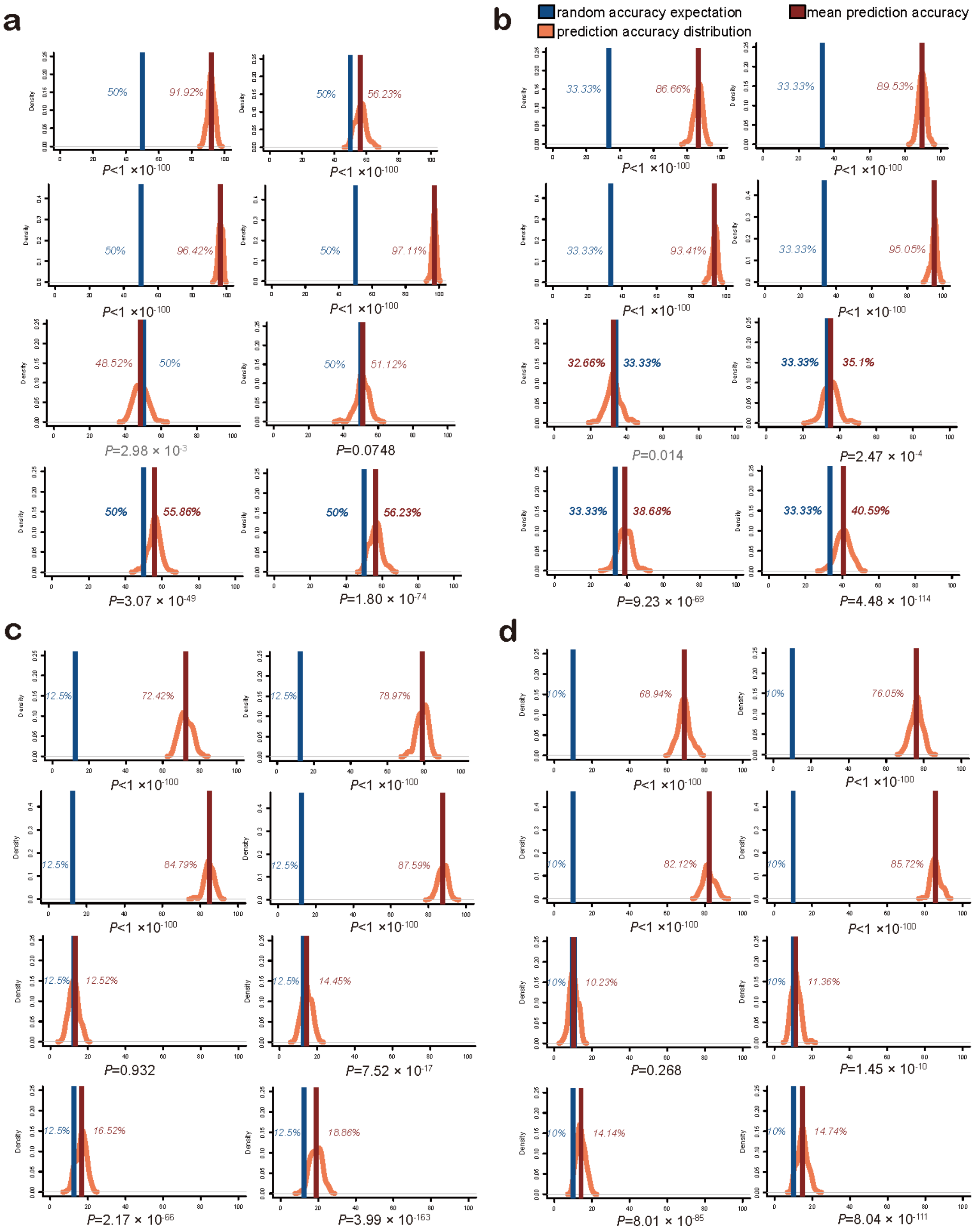
Supplementary Figure 3 | Q-Q plot of six genome-wide significant SNPs. (a) rs1868752, (b) rs118078182, (c) rs60159418, (d) rs17868256, (e) rs3920540, (f) rs61672954.



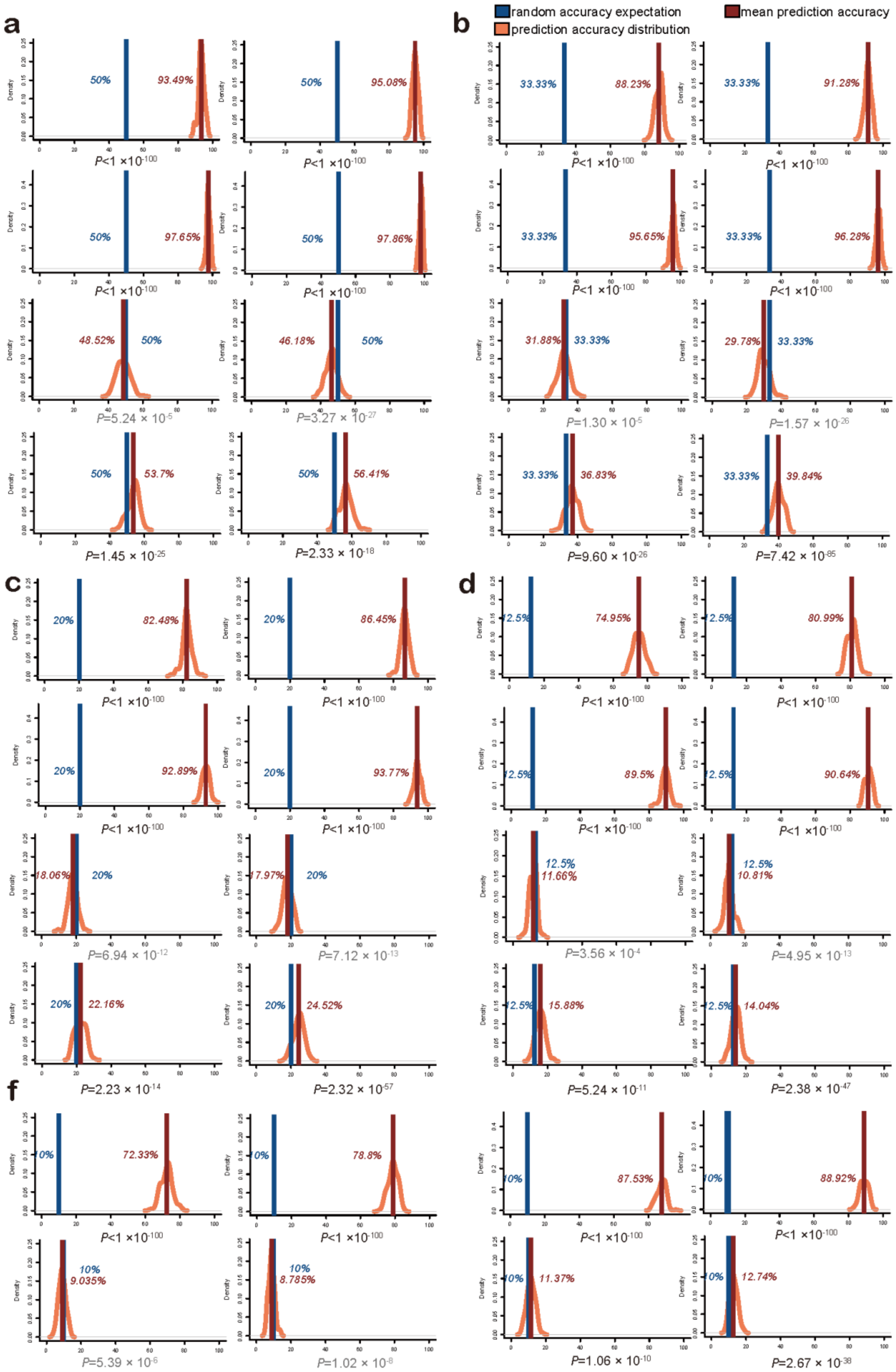
Supplementary Figure 4 | Global effect coefficient α_f and α_m from UIG-D females and UIG-D males. (a) for 277-top-SNP prediction model. (b) for 240-top-SNP prediction model after trimmed the potential LD by pairwise LD < 0.8. (c) for 209-top-SNP prediction model after trimmed the potential LD by inter-marker physical distance < 400kb. The global factor was averaged by all individual factor (female in plum, male in green).



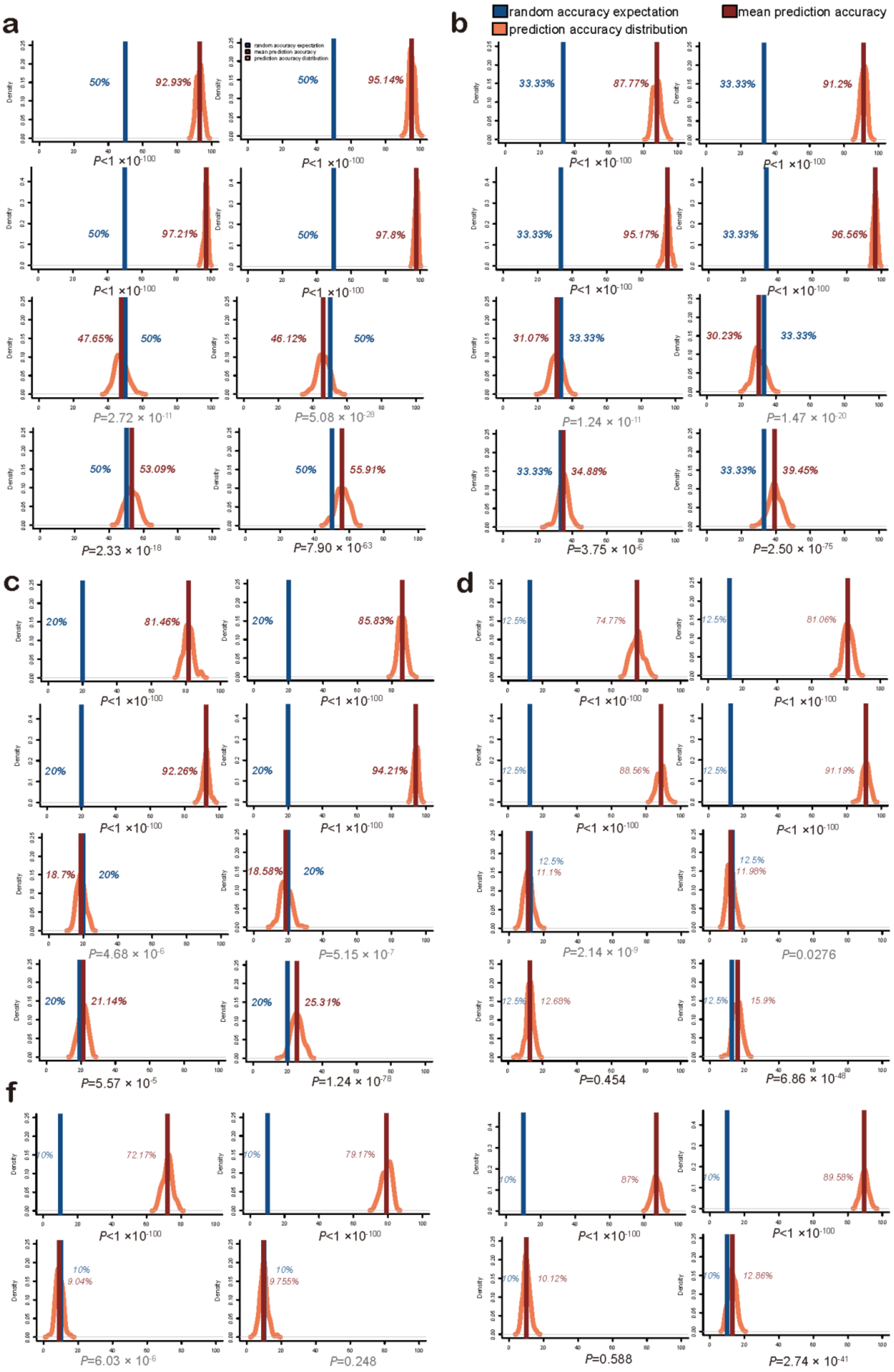
Supplementary Figure 5 | Test of prediction model using low LD SNPs face prediction model. (a) for 240-top-SNP prediction model after trimmed the potential LD by pairwise LD < 0.8, (b) for 209-top-SNP prediction model after trimmed the potential LD by inter-marker physical distance < 400kb. The average PSD (left column) and SSA (right column) determined for the cohorts (in red) were compared to the random distributions under null hypothesis (in blue).



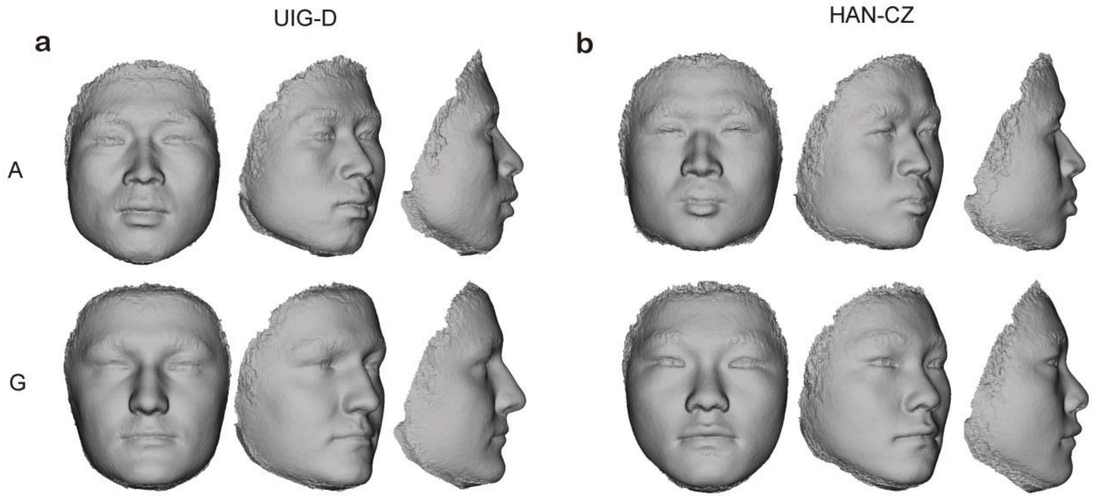
Supplementary Figure 6 | Evaluation of the face prediction in hypothetic forensic scenarios (2/3/8/10 candidates) using 277-SNP face prediction model. (a) N=2, (b) N=3, (c) N=8, (d) N=10. In each kind of scenario, the samples from top row to bottom are UIG-D females, UIG-D males, UIG-R females, UIG-R males. For each cohort, the accuracy rates are decided based on PSD (left column) and SSA (right column). *P* values in black indicate that the prediction perform significantly better than random draws.



Supplementary Figure 7 | Evaluation of the face prediction in hypothetic forensic scenarios (2/3/5/8/10 candidates) using 240-SNP face prediction model. (a) N=2, (b) N=3, (c) N=5, (d) N=8, (e) N=10. In each kind of scenario, the samples from top row to bottom are UIG-D females, UIG-D males, UIG-R females, UIG-R males. For each cohort, the accuracy rates are decided based on PSD (left column) and SSA (right column). *P* values in black indicate that the prediction perform significantly better than random draws.



Supplementary Figure 8 | Evaluation of the face prediction in hypothetic forensic scenarios (2/3/5/8/10 candidates) using 209-SNP face prediction model. (a) N=2, (b) N=3, (c) N=5, (d) N=8, (e) N=10. In each kind of scenario, the samples from top row to bottom are UIG-D females, UIG-D males, UIG-R females, UIG-R males. For each cohort, the accuracy rates are decided based on PSD (left column) and SSA (right column). *P* values in black indicate that the prediction perform significantly better than random draws.



Supplementary Figure 9 | Extrapolated faces of rs61672954 in discovery and independent cohorts. (a) in UIG-D males, (b) in HAN-CZ males. We showed the extreme faces based on residual faces with their allele labeled in front. The top extrapolated faces and alleles are corresponding to Han Chinese liked faces. The bottom extrapolations are European liked faces.

Supplementary Table 1 | Landmark-based phenotypes

Landmrk-based phenotypes	**P**	
	Female	**Male**
LAla-Prn-RAla	**2.70×10^{-11}**	**1.52×10^{-21}**
Nsn-Prn-Sbn	**2.43×10^{-15}**	**6.71×10^{-23}**
LIntCan-Nsn-RIntCan	**2.38×10^{-10}**	**5.27×10^{-27}**
height of Nsn to eyes	**1.22×10^{-21}**	**5.50×10^{-47}**
Sbn-ULipP	**3.28×10^{-8}**	**2.80×10^{-9}**
LLipCn-RLipCn	**0.00535**	**1.52×10^{-8}**
ULipP-Stm-LLipP	**0.0026**	**7.41×10^{-9}**
ExtCan-IntCan	**1.46×10^{-7}**	**2.58×10^{-10}**
LIntCan-RIntCan	**8.69×10^{-7}**	**4.31×10^{-9}**
Sbn-ULipP-ChiP	**0.00359**	**6.78×10^{-7}**

Supplementary Table 2 | Eurasian-specified phenotypes

		PCA based		PLS based	
Partial Features	**Gender[A]**	**ncomp.[B]**	**P[C]**	**ncomp.[B]**	**P[C]**
brow ridge	Female	2	**5.80×10^{-19}**	1:6	**6.41×10^{-23}**
	Male	2	**1.00×10^{-29}**	1:8	**2.78×10^{-49}**
eyes	Female	5	**1.69×10^{-16}**	1:8	**1.45×10^{-25}**
	Male	2	**8.62×10^{-17}**	1:11	**1.00×10^{-60}**
side faces	Female	1	**5.79×10^{-13}**	1:25	**6.48×10^{-27}**
	Male	2	**1.71×10^{-17}**	1:9	**1.94×10^{-47}**
cheeks	Female	1	**4.71×10^{-15}**	1:22	**1.10×10^{-27}**
	Male	2	**5.79×10^{-21}**	1:8	**4.03×10^{-43}**
nose	Female	2	**1.43×10^{-22}**	1:17	**2.94×10^{-29}**
	Male	2	**2.24×10^{-46}**	1:12	**6.09×10^{-57}**
mouth	Female	4	**3.41×10^{-11}**	1:20	**1.85×10^{-24}**
	Male	2	**8.73×10^{-18}**	1:15	**1.72×10^{-48}**

[A] sex specified test

[B] Number of components that used to distinguish Han Chinese and European features

[C] Student's test

Supplementary Table 3 | Inflation factor in GWAS

SNP	**P**	**Inflation factor**	**genome PC corrected P values**	**genome PC corrected Inflation factor**
rs1868752	$\mathbf{1.22 \times 10^{-10}}$	1	$\mathbf{1.02 \times 10^{-10}}$	1
rs118078182	$\mathbf{8.19 \times 10^{-9}}$	1.00961	$\mathbf{1.09 \times 10^{-8}}$	1.01032
rs60159418	$\mathbf{8.96 \times 10^{-11}}$	1.01437	$\mathbf{1.38 \times 10^{-9}}$	1
rs17868256	$\mathbf{7.22 \times 10^{-9}}$	1.03422	$\mathbf{1.20 \times 10^{-7}}$	1.0013
rs3920540	$\mathbf{3.31 \times 10^{-8}}$	1.06986	$\mathbf{2.28 \times 10^{-7}}$	1.00707
rs61672954	$\mathbf{2.00 \times 10^{-8}}$	1.03794	$\mathbf{1.04 \times 10^{-7}}$	1

Supplementary Table 4 | Previous candidate SNPs associated with Uyghur facial shape

							P	
SNP	**Chr.**	**BP**^{A}	**Gene**	**Discovered Trait**^{B}	**Studied Trait**	**Female**	**Male**	**Mixed**
rs4648379	1	3261516	PRDM16	LAla-Prn-RAla	LAla-Prn-RAla	0.7133	0.172	0.2357
					angle of LAla-Prn-Rala	0.2207	**0.02539**	**0.02028**
rs642961	1	209989270	IRF6	ULipP-Stm-LLipP	ULipP-Stm-LLipP	**0.05197**	0.778	0.2358
rs3827760	2	109513601	EDAR	Chin protrusion	angle of Sbn-ULipP-ChiP	**0.06131**	**0.09733**	**0.01238**
rs7559271	2	223068286	PAX3	Nasion	height of Nasion to eyes	**0.005811**	0.117	**0.001986**
rs17447439	3	189549423	TP63	EyeR-EyeL	LExtCan-RExtCan	0.7631	0.4777	0.9567
rs2045323	4	154831899	DCHS2	Columella inclination/Nose protrusion/Nose tip angle	height of Prn to Ala	**0.05813**	**0.04288**	0.815
rs6184	5	42719344	GHR	mandibular height (ear-Gn)	Ear-ChiP	**0.0915**	0.2674	0.5894
rs1852985	6	45329656	SUPT3H/RUNX2	Nose bridge breadth	LAla-RAla	0.6941	0.1894	0.244
rs7773292	6	132099761	ENPP1	upper and lower face height	Sbn-UlipP-ChiP	0.9239	0.9781	0.9585
rs17640804	7	42131390	GLI3	Nose wing breadth	LAla-RAla	0.1402	0.1242	**0.03421**
rs805722	10	105810400	COL17A1	EyeLR-Nsn	LIntCan-Nsn-RExtCan	0.4636	0.3311	0.9475
					angle of LIntCan-Nsn-RExtCan	**0.004021**	0.8374	**0.01856**
rs927833	20	22041577	PAX1	Nose wing breadth	LAla-RAla	0.4841	**0.007729**	**0.02703**

^{A}NCBI build 37

^{B}original measurements in previous studies