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Supplementary table 1: Pairwise F_{ST} estimates (below diagonal) and associated *p*-values (above diagonal) for 10 populations at the *MAOA* locus

Population	**Afrikaner**	**Hispanic/ Latino**[a]	**American white/ non-Hispanic**[a]	**New Zealand, European origin**[b]	**German, European origin**[c]	**German, European origin**[d]	**Italian**[c]	**Chinese**[e]	**Asian/ Pacific Islander**[a]	**African American**[a]
Afrikaner		0.74	0.22	0.21	0.15	0.08	0.00	0.00	0.00	0.00
Hispanic/Latino	-0.006		0.38	0.32	0.23	0.10	0.07	0.00	0.00	0.00
American white/non-Hispanic	0.001	-0.001		0.45	0.36	0.15	0.01	0.00	0.00	0.00
New Zealand, European origin	0.003	0.002	0.000		0.62	0.34	0.05	0.00	0.00	0.00
German, European origin	0.006	0.006	-0.001	-0.003		0.97	0.47	0.00	0.00	0.00
German, European origin	0.009	0.008	0.001	0.000	-0.005		0.35	0.00	0.00	0.00
Italian	**0.023**	0.024	**0.011**	**0.006**	-0.003	0.000		0.00	0.00	0.01
Chinese	**0.135**	**0.137**	**0.105**	**0.093**	**0.070**	**0.072**	**0.043**		0.50	0.59
Asian/Pacific Islander	**0.173**	**0.179**	**0.138**	**0.124**	**0.098**	**0.099**	**0.065**	-0.005		0.90
African American	**0.167**	**0.173**	**0.136**	**0.122**	**0.094**	**0.097**	**0.063**	-0.004	-0.011	

Sources: [a]*Sabol et al.*[16]; [b]*Caspi et al.*[18]; [c]*Deckert et al.*[44]; [d]*Kuepper et al.*[13]; [e]*Lu et al.*[45]

F_{ST} *values in boldface are significant at* $p<0.05$ *level. Data were taken from the papers indicated and summarised in Table 1.*

Supplementary table 2: Gene diversity, equivalent to expected heterozygosity, and its standard deviation as calculated by Arlequin[42]

Population	Expected heterozygosity	SD
Afrikaner[a]	0.8609	0.0083
Israeli 1[b]	0.8323	0.0097
American[c]	0.8387	0.0082
British[d]	0.8396	0.0053
Israeli 2[e]	0.8253	0.0023

Sources: [a]this study; [b]Avinum et al.[30]; [c]Kim et al.[32];. [d]Morley et al.[37]; [e]Yirmiya et al.[33] Data were taken from the papers indicated and summarised in Table 2.

Supplementary table 3: Pairwise F_{ST} estimates (below diagonal) and associated *p*-values (above diagonal) for four populations at the *AVPR1A* RS3 locus before the allele length correction of Table 2

Population	Afrikaner[a]	Israeli 1[b]	American[c]	British[d]
Afrikaner		0.000	0.000	0.000
Israeli 1	0.036		0.036	0.000
American	0.037	0.005		0.000
British	0.027	0.071	0.069	

Sources: [a]this study; [b]Avinum et al.[30]; [c]Kim et al.[32]; [d]Morley et al.[37] Data were taken from the papers indicated and summarised in Table 2.

Supplementary table 4: Pairwise F_{ST} estimates (below diagonal) and *p*-values (above diagonal) for five populations at the *AVPR1A* RS3 locus after the allele length correction of Table 2

Population	Afrikaner[a]	Israeli 1[b]	American[c]	British[d]	Israeli 2[e]
Afrikaner		0.045	0.135	0.117	0.000
Israeli 1	0.004		0.018	0.000	0.775
American	0.001	0.005		0.793	0.000
British	0.001	0.004	-0.001		0.000
Israeli 2	0.005	-0.001	0.005	0.004	

Sources: [a]this study; [b]Avinum et al.[30]; [c]Kim et al.[32]; [d]Morley et al.[37]; [e]Yirmiya et al.[33] Data were taken from the papers indicated and summarised in Table 2.