

SUPPLEMENTARY MATERIALS

Supplementary Tables

Supplementary Table 1: 56 loci associated with clinical melanoma used to calculate the PRS.

rsID	Effect allele	Odds ratio
rs7412746	C	0.9262
rs76798800	G	0.9048
rs2695237	T	1.1134
rs1800440	T	1.0943
rs10931936	T	1.0856
rs149617956	G	0.3503
rs3950296	C	1.0763
rs2301293	C	0.8933
rs466502	A	0.8586
<i>rs16891982*</i>	<i>C*</i>	<i>0.4617*</i>
rs11747245	A	1.0703
rs32578	G	1.0973
rs6914598	T	0.9028
rs16886790	T	1.1094
rs117132860	G	0.6918
rs1894765	C	0.9136
rs4731207	G	0.924
rs10090648	G	0.9037
rs13263376	G	0.9244
rs520015	C	1.0637
rs10960710	G	0.9344
rs871024	C	1.192
rs2811711	T	1.1256
rs55797833	T	1.6087
rs3217986	T	0.8405
rs72652478	C	1.2513
rs10739221	T	1.1108
rs1339759	C	1.0983
rs7902587	C	0.8521
rs4617548	A	0.9382
rs660963	A	1.0981
rs1126809	G	0.8251
rs1801516	G	1.1715
rs1861183	A	0.9293

rs4763456	T	0.9201
rs2300560	C	1.0711
rs112761681	A	0.9027
rs1278768	G	0.9364
rs141514981	C	0.8252
rs12913832	A	0.8817
rs150962800	C	0.8016
rs62034139	G	0.9065
rs12597188	G	0.9234
rs2911423	C	1.0745
rs116927526	C	0.6017
rs11649196	G	0.9101
rs11538871	C	0.7204
rs1805007	C	0.58
rs1805009	G	0.6553
rs78378222	T	0.7301
rs77733715	A	0.659
rs6059655	A	1.441
rs143190905	G	1.1404
rs35640778	G	1.3691
rs443099	G	0.8806
rs132941	T	1.1083

* Variant did not pass imputation quality control and was not included in subsequent analysis.

Supplementary Table 2. Participants distribution of melanoma events by polygenic risk score (PRS) group

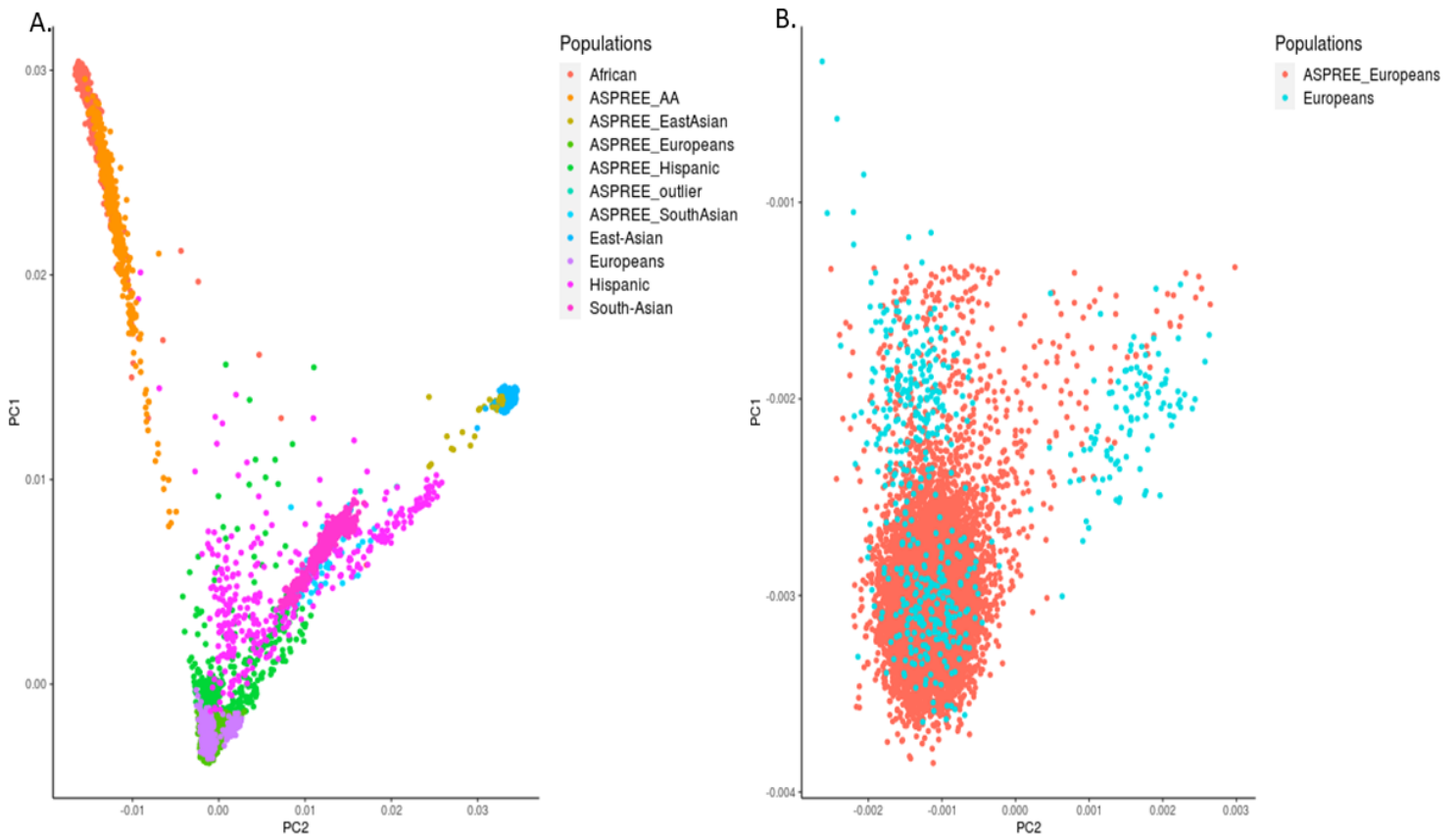
Participants	No. of events in each PRS group		
	Low	Medium	High
Incident melanoma	12	57	29
Incident melanoma + prevalent melanoma	2	7	13
Incident melanoma - male	5	38	18
Incident melanoma - female	7	19	11
Prevalent melanoma - male	33	151	77
Prevalent melanoma - female	19	141	107

Supplementary Table 3: Logistic Regression model for prevalent melanoma at enrolment stratified by sex.

	Male Participants		Female Participants	
	OR ^a (95% CI)	<i>P</i>	OR ^a (95% CI)	<i>P</i>
OR (per SD)	1.39 (1.23;1.57)	<0.001	1.72 (1.53;1.94)	<0.001
Family History	2.25 (1.19;3.91)	0.007	2.42 (1.49;3.76)	<0.001

^aOdds ratio (OR) as Continuous Variable (per standard deviation). CI = confidence interval.

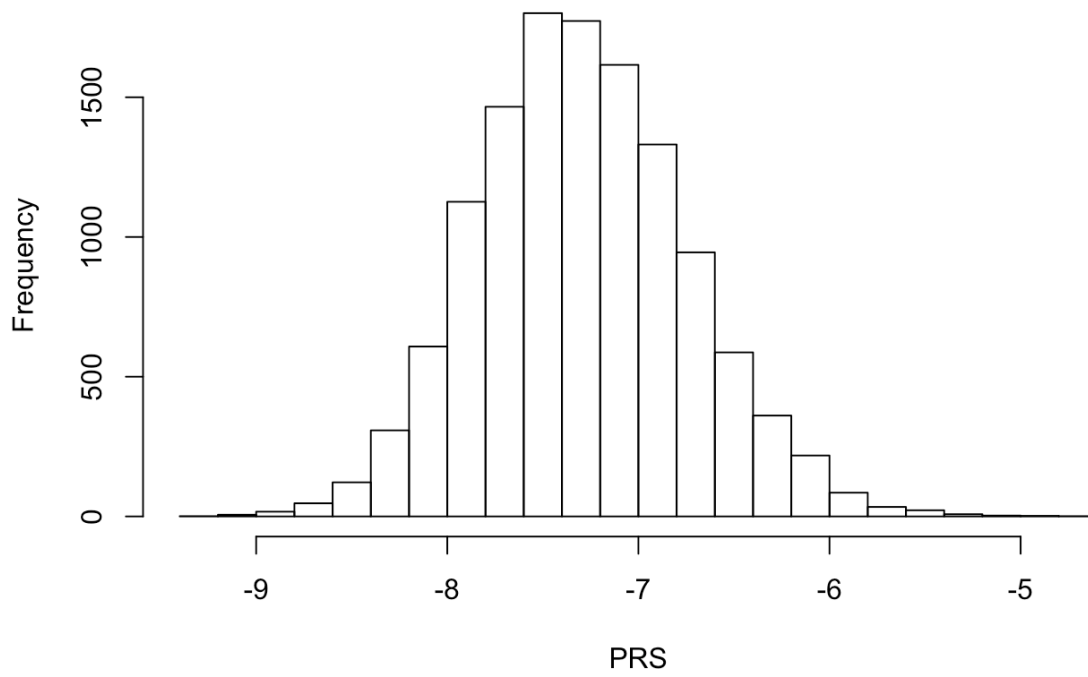
Supplementary Figures



Supplementary Figure 1: Principal component (PC) analysis of the ASPREE cohort compared with the 1,000 Genome Project.

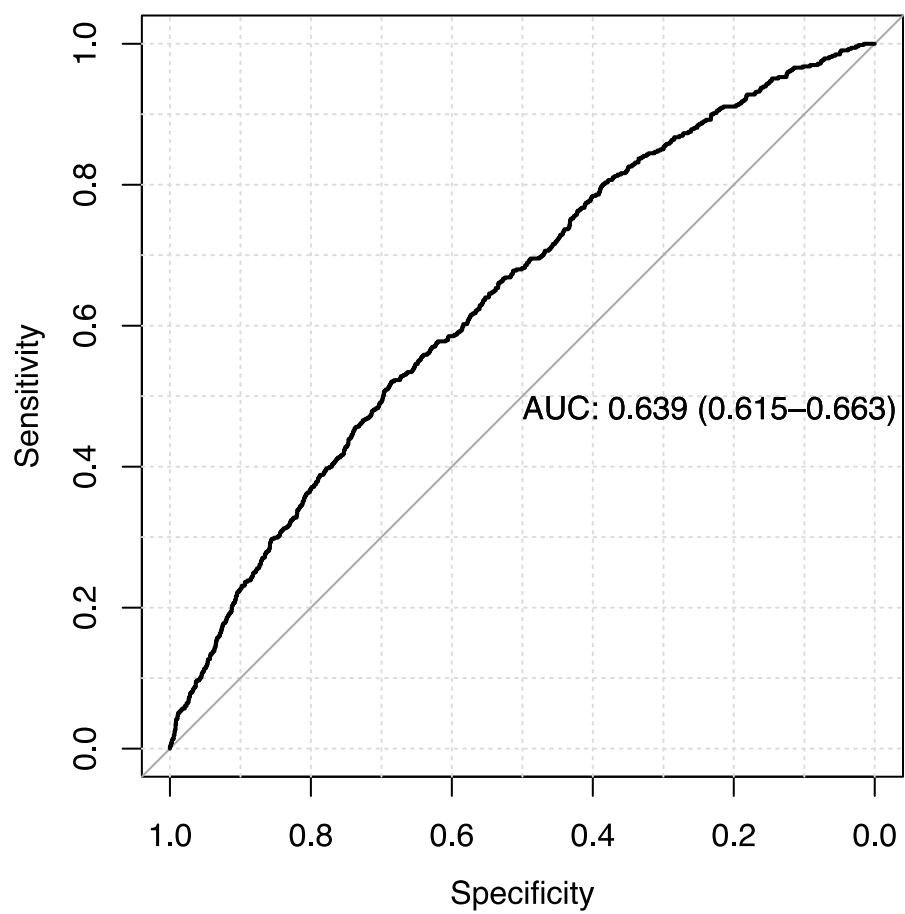
A) PC plot of all genotyped ASPREE participants mapped against the 1,000 Genome population groups (Europeans, South Asians, East Asians, African American and Hispanics). (ASPREE_AA = ASPREE participants of African American descent). **B)** PC plot of European ASPREE genotyped participants included in the PRS study mapped against the 1,000 Genome European population.

Distribution of PRS for Melanoma



Supplementary Figure 2: Distribution of the Polygenic Risk Score in the ASPREE study population

PRS = polygenic risk score.



Supplementary Figure 3: ROC curve for Prevalent Melanoma

Area under the curve and the 95% confidence interval are shown.