

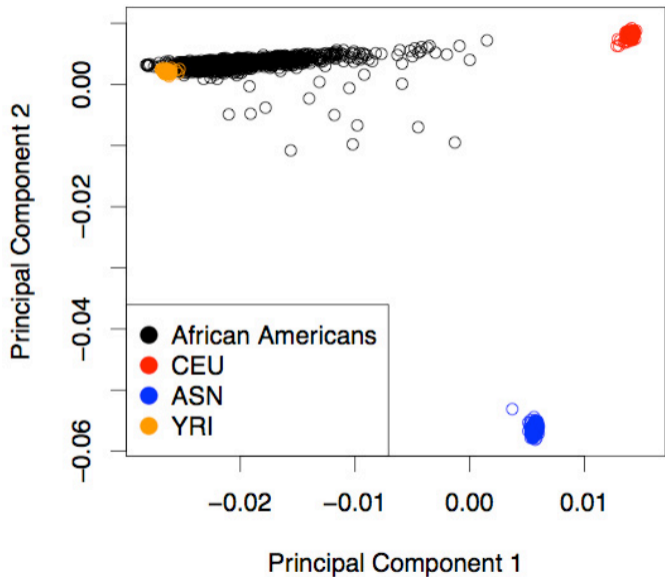
Table E1: Top signals of allelic association at SNPs within an ancestry association peak on 6q in African Americans correcting for global ancestry (global correction). None of the SNPs pass a bonferroni correction for 9,266 tests ($p < 5.4 \times 10^{-6}$). Included in the table are logistic regression p-values from local ancestry association testing, and allelic association testing corrected for local ancestry (local correction). Included are the reference allele frequencies (freq) in the HapMap CEU and YRI (release 28), indicating that all of the top SNPs are informative for European-African ancestry.

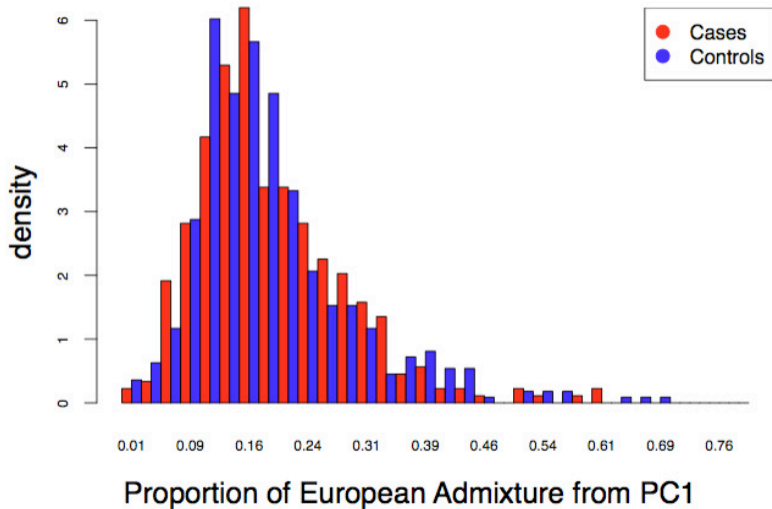
SNP	Position (hg18)	p-value local ancestry	p-value allelic, global correction	p-value allelic, local correction	freq CEU	freq YRI
rs10498989	95446907	6.30×10^{-4}	8.56×10^{-6}	1.46×10^{-3}	0.295	0.897
rs9345075	91799831	4.94×10^{-4}	1.61×10^{-5}	1.36×10^{-3}	0.902	0.367
rs9363229	95415689	6.30×10^{-4}	1.67×10^{-5}	2.29×10^{-3}	0.323	0.895
rs576231	100245282	9.18×10^{-4}	1.67×10^{-5}	4.38×10^{-4}	0.239	0.014
rs2207428	95209649	6.17×10^{-5}	4.20×10^{-5}	3.47×10^{-3}	0.332	0.003

Table E2: SNPs with association p-values < 0.01 among 257 genotyped SNPs within a 1Mb region centered on rs1361549 in stratified tests for African American subjects with one or more chromosomes of local European ancestry (Admixed) or two chromosomes of local African ancestry (African). Association p-values are also shown for the CSGA/SARP European Americans. SNPs are ordered based on position; p-values < 0.01 in any one of the stratified tests are shaded; the strongest signal of association is with rs1361549 (in bold). Estimates of LD with rs1361549 were calculated in African Americans with local European ancestry using Haploview (Figure E6 and S7).

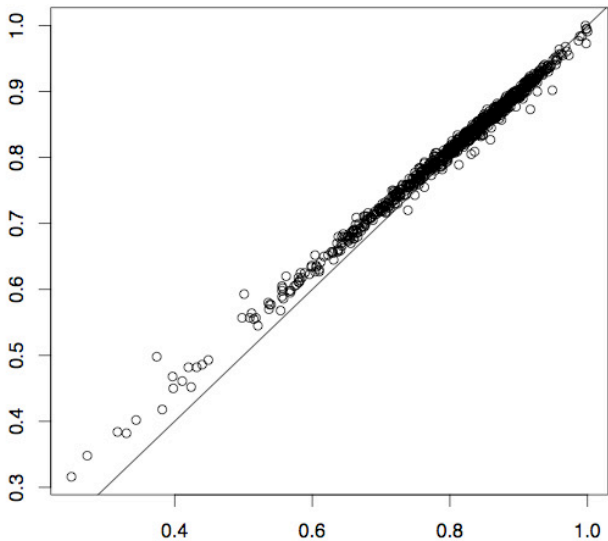
SNP	Position	P-value African	Coefficient African	P-value Admixed	Coefficient Admixed	P-value European Americans	Distance from rs136154 and LD (r^2)	eQTL candidates* (gene, p-value, population)
rs10455382	82077709	0.97	0.0049	9.4x10 ⁻⁵	-0.69	0.33	-266695 (0.24)	PRR15, CEU, 3e-05 SPSB1, YRI, 4e-05 ASB2, YRI, 8e-05
rs12055792	82079376	0.86	0.03	9.6x10 ⁻³	-0.58	0.51	-265028 (0.08)	IGF2BP3, CEU, 3e-05
rs4706889	82129155	0.88	-0.02	6.4x10 ⁻⁴	0.62	0.28	-215249 (0.32)	PRR15, CEU, 4e-05
rs1015916	82129430	0.38	-0.28	4.9 x10 ⁻³	-0.76	0.69	-214974 (0.05)	IGF2BP3, CEU, 5e-05
rs9341883	82148380	0.91	-0.015	4.8 x10 ⁻⁴	-0.62	0.91	-196024 (0.24)	NA
rs2323252	82155910	0.86	-0.024	3.5 x10 ⁻⁴	0.67	0.23	-188494 (0.33)	PRR15, CEU, 2e-05
rs11756740	82165844	0.48	-0.41	5.5 x10 ⁻³	-0.92	0.30	-178560 (0.033)	IGF2BP3, CEU, 0.0001
rs7741650	82185636	0.64	0.06	6.5 x10 ⁻³	-0.47	0.91	-158768 (0.22)	CNR2, YRI, 2e-05 GMIP, YRI, 0.0001
rs1343232	82187051	0.53	-0.09	3.5 x10 ⁻³	0.53	0.30	-157353 (0.32)	FCRLA, YRI, 2e-06 CNR2, YRI, 2e-05 PRR15, CEU, 0.0001
rs6940202	82190504	0.29	0.14	3.9 x10 ⁻³	-0.50	0.83	-153900 (0.26)	CNR2, YRI, 2e-05 FCRLA, YRI, 9e-05 VIPR1, YRI, 0.0001
rs2120533	82206201	0.38	-0.12	2.0 x10 ⁻³	0.56	0.31	-138203 (0.30)	NA
rs17438648	82216223	0.38	0.12	1.9 x10 ⁻³	-0.57	0.30	-128181 (0.30)	FCRLA, YRI, 1e-05 CNR2, YRI, 6e-05 PRR15, CEU, 0.0001
rs1361549	82344404	NA	NA	1.1 x10⁻⁵	-1.1	0.43	0 (1)	NA
rs2298053	82424008	1.4x10 ⁻³	1.6	0.32	-0.42	0.58	79604 (0.012)	NA
rs12664410	82428442	1.1x10 ⁻³	1.5	0.21	-0.52	0.58	84038 (0.013)	NA
rs1935420	82745959	0.60	0.20	6.9x10 ⁻³	1.4	0.82	401555 (0.034)	FGL2, CEU, 6e-05 TP53INP1, CEU, 0.0001

* From www.scandb.org (Gamazon, Zhang et al. 2010, Bioinformatics, 26(2):259-62)





Global African Ancestry



Mean Local African Ancestry

