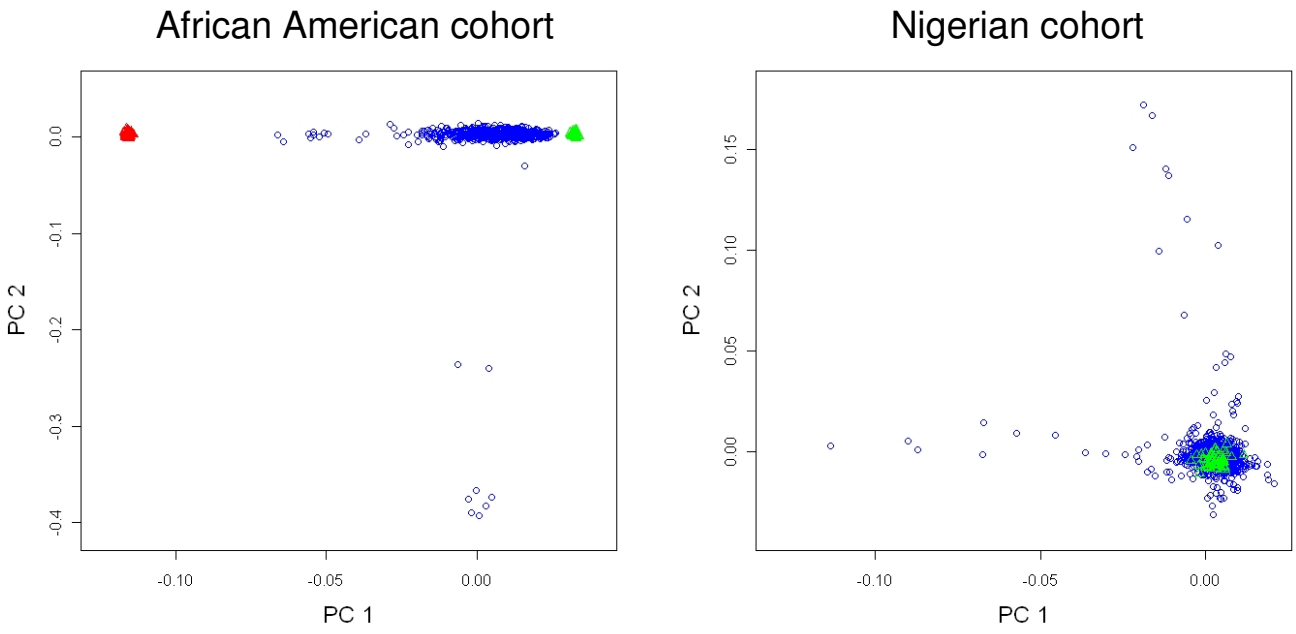
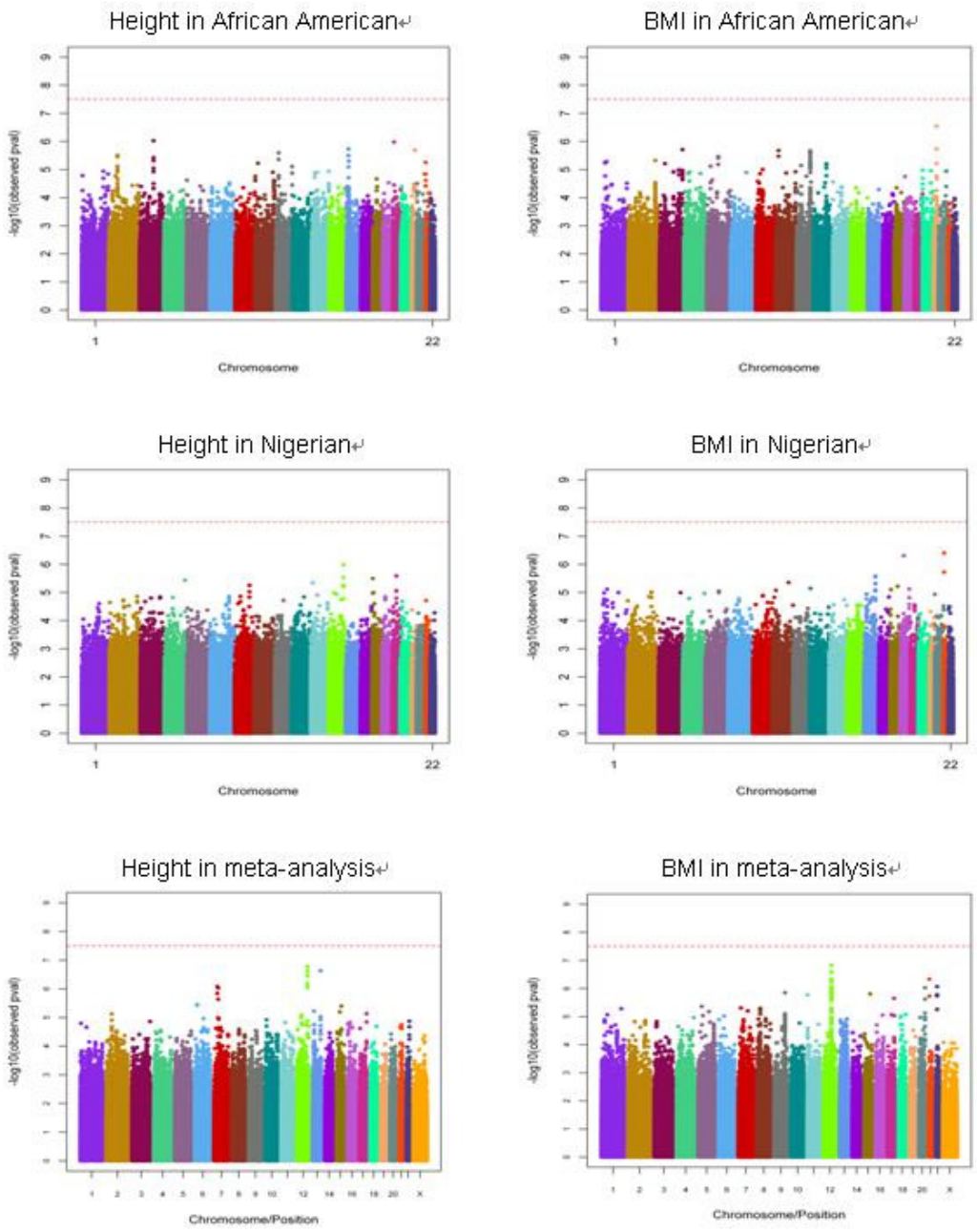
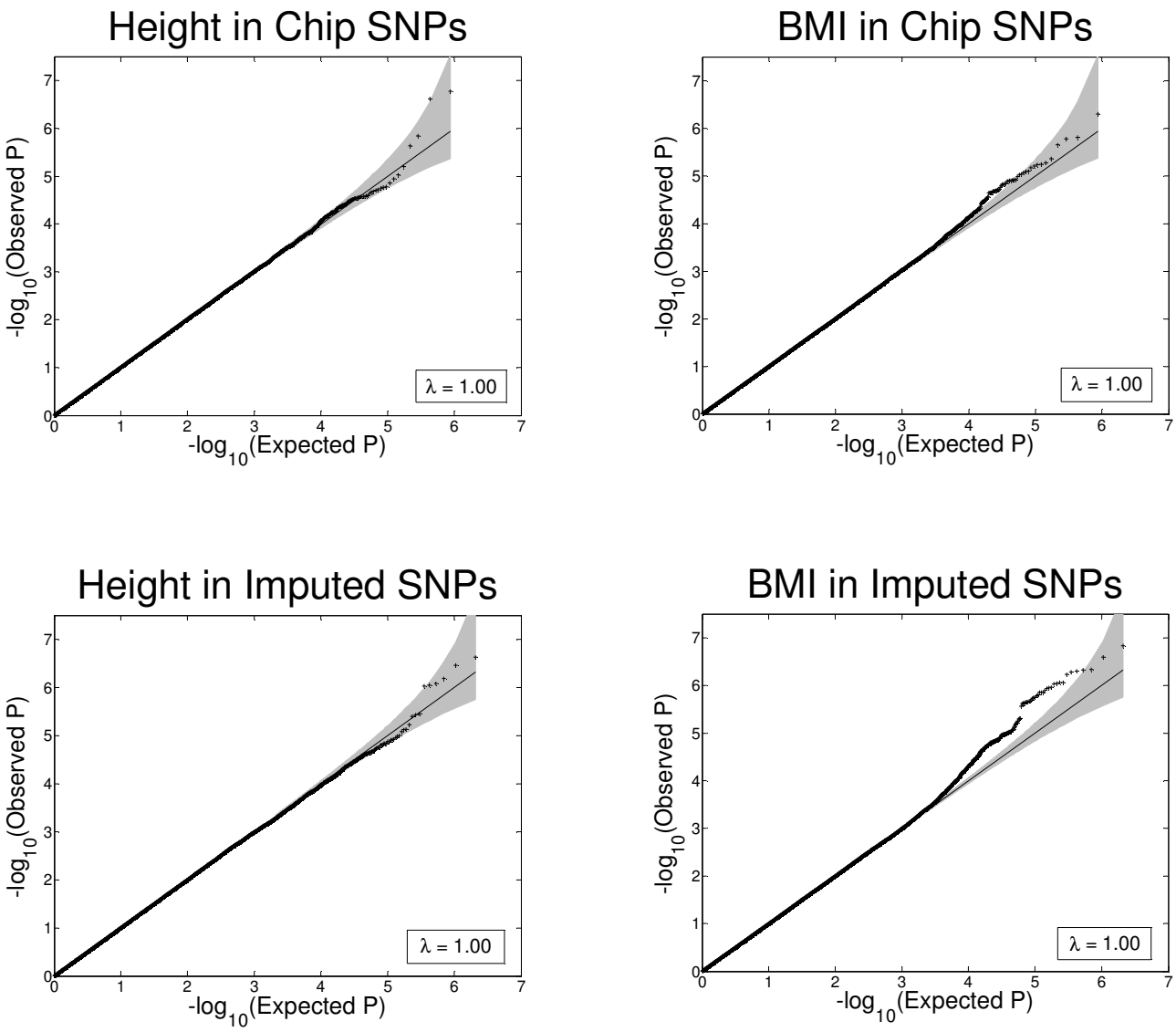


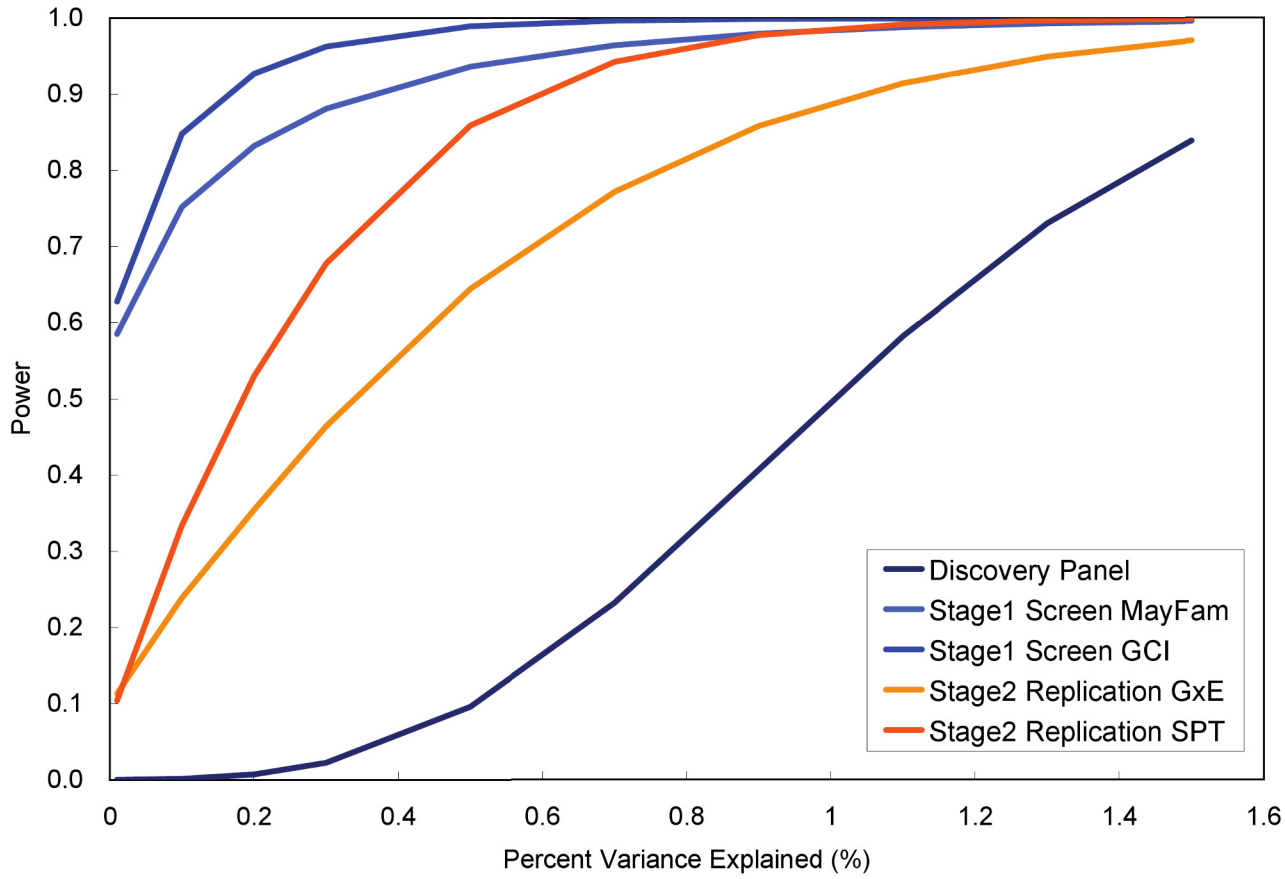
Supplemental Figure 1: Population stratification in African-American and Nigerian cohorts. HapMap inidividuals YRI (green) and CEU (red) were included as reference. African-Americans have a degree of admixture of African and European ancestry, while Nigerians were clustered as a single group.



Supplemental Figure 2: Manhattan plots of GWA results in the African-American, Nigerian, and meta-analysis for height (left) and BMI (right). The dotted line signifies genome-wide significance level at $P = 5 \times 10^{-8}$.

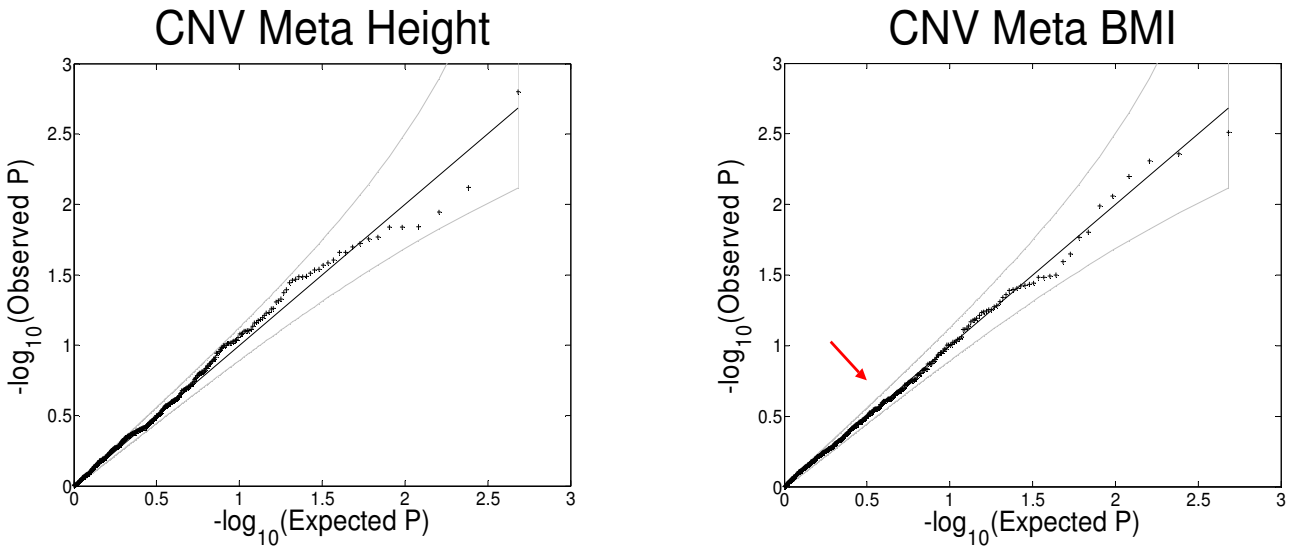


Supplemental Figure 3: QQ plots of GWA results for height and BMI using Chip SNPs only or Imputed SNPs only, after meta-analysis. The lambdas are 1.00 for both height and BMI in all cases.

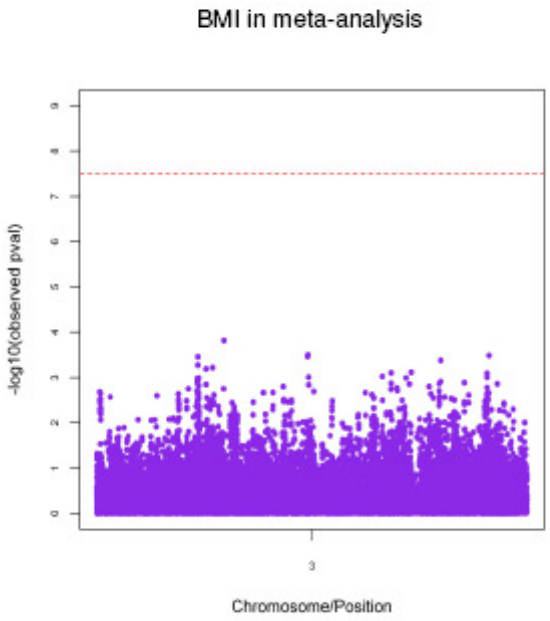


Supplemental Figure 4: Analysis of power in study design. The power was calculated over a range of effect sizes (percent variance explained) under the significance threshold (alpha) and effective sample size (N_e) in each phase of the study as described in **Methods**. Power for two-tailed alpha level at $1x10^{-5}$ was given for the GWA discovery panel; power for one-tailed alpha level were given for the rest of the panels (0.05 for GWA panel for follow-up of previously reported loci, and 0.5 for stage 1 screens and 0.05 for stage 2 replications). The number of individuals in each panel was used as the effective sample size in calculating power (1,931 for the discovery panel, 494 for GCI, 959 for GxE, and 1478 for SPT), with the exception of Maywood Family panel. Because of the significant component of sibships in the Maywood Family panel, we took the conservative estimate of the effective sample size by counting all siblings if genotypes from both parents were available, but only

one sibling per family if not. Therefore, an effective sample size of 465 was used to calculate power, rather than the 756 participants present in the panel. GCI African-American panels for BMI, height, and Jamaican GxE panel for BMI were analyzed as dichotomous traits, while the rest were analyzed as continuous traits. For stage 1 screen GCI and stage 2 replication GxE curves, the power were calculated based on the BMI analysis (as dichotomous trait), but the curves are similar to that for height.



Supplemental Figure 5: QQ plots for height (left) and BMI (right) in meta-analysis of common CNV associations in African-American and Nigerian cohorts. Red arrow indicates the common deletion in the *NEGR1* locus reported to be associated with BMI. The number of CNVs tested in meta-analysis is 482. The lambdas are 1.13 and 0.95 for height and BMI, respectively. Note that lambdas are likely unstable given the relatively few markers tested.



Supplemental Figure 6: Manhattan plots of GWA results in the 3q27 region after meta-analyzing the African-American and Nigerian cohorts. In total, we analyzed nearly 10,000 SNPs in this region, but none displayed compelling evidence of association to BMI, especially considering the number of SNPs we examined in this region. The SNP in 3q27 with the lowest combined *P* value is rs11927908 ($P = 1.5 \times 10^{-4}$), in the gene *SPATA16*.

Supplement Table 1: Stage 1 replication results in two independent cohorts of African-Americans for SNPs selected for having $P < 1x10^{-5}$ in GWA discovery phase of the study. All SNPs followed up were listed. Genes are within 50 kb upstream and downstream of the index SNP. A1 denotes reference allele with respect to which the effect or odds ratio (OR) is given. P* denotes one-tailed p-value. Notes column records if a SNP was genotyped in stage 1 due to its being in high LD ($r^2 > 0.8$) with a SNP targeted for follow-up to guard against failed genotyping (proxy), but do not represent independent signals. Note that for one of the top height associated SNP, rs4619 is a non-synonymous SNP in *IGFBP1* and near *IGFBP3*, which are potential biological candidates. As such, three additional SNPs in high LD with $P < 10^{-4}$ in the GWA panels were also genotyped in replication (rs1496496, rs1065780, and rs13223993), though they did not satisfy the two conditions described in **Methods** for criteria of follow up.

				Maywood Family		**GCI AA**		
Height								
Chr	SNP	Genes	A1	Effect	P*	Effect	P*	Notes
2	rs6746641		C	0.078	0.579	N/A		
6	rs734015	C6orf32	G	-0.092	0.600	1.08 (0.84-1.39)	0.282	
6	rs2817723	C6orf32	C	0.036	0.465	1.08 (0.83-1.41)	0.278	
7	rs6942726	ELMO1	C	0.022	0.520	0.94 (0.69-1.27)	0.335	
7	rs1065780	IGFBP1, IGFBP3	A	-0.510	0.917	0.98 (0.75-1.26)	0.576	proxy
7	rs4619	IGFBP1, IGFBP3	G	N/A		1.06 (0.82-1.37)	0.333	
7	rs1496496	IGFBP1, IGFBP3	G	-0.415	0.873	1.13 (0.88-1.46)	0.174	proxy
7	rs13223993	IGFBP1, IGFBP3	A	-0.264	0.766	1.03 (0.80-1.33)	0.404	proxy
12	rs6582380	GLT8D3	A	0.837	0.754	1.23 (0.53-2.88)	0.685	
12	rs11169806	BIN2, ELA1, GALNT6	A	0.232	0.267	0.90 (0.69-1.18)	0.773	
12	rs1463833		G	0.259	0.240	0.87 (0.67-1.13)	0.851	
12	rs1498759		T	N/A		0.93 (0.69-1.25)	0.688	
13	rs1359634		C	N/A		N/A		
13	rs323425		T	0.439	0.838	0.97 (0.71-1.32)	0.427	
15	rs10444801		G	-0.022	0.480	1.41(1.09-1.82)	0.996	
15	rs2994	THSD4	G	0.154	0.650	0.92 (0.70-1.21)	0.278	
17	rs12603456	TBCD, B3GNTL1	T	N/A		1.09 (0.83-1.42)	0.272	
BMI								
Chr	SNP	Genes	A1	Effect	P*	OR (95% CI)	P*	Notes

1	rs1395246	PGM1	C	0.070	0.271	0.78 (0.42-1.43)	0.791	
1	rs12063584	USH2A	G	-0.014	0.556	1.23 (0.74-2.04)	0.217	
5	rs16903085		C	0.049	0.379	0.69 (0.29-1.65)	0.799	
5	rs6892149	PARP8	C	0.046	0.732	0.66 (0.46-0.93)	0.009	
5	rs17136138		C	-0.204	0.951	0.77 (0.44-1.35)	0.820	
6	rs973089	DST	T	0.069	0.889	0.97 (0.73-1.29)	0.405	
7	rs739750	C7orf31, NPVF	A	0.062	0.170	1.13 (0.81-1.57)	0.245	
7	rs11772003	EMID2	G	-0.075	0.885	0.95 (0.70-1.30)	0.624	
8	rs7823476		A	N/A		0.96 (0.71-1.30)	0.611	
9	rs10981043	C9orf84	A	0.049	0.748	0.86 (0.58-1.26)	0.218	
11	rs4323851	BRSK2	G	N/A		0.86 (0.62-1.20)	0.811	
12	rs4370996	CCDC59, C12orf26	A	N/A		0.82 (0.55-1.21)	0.157	proxy
12	rs2401027	CCDC59, C12orf26	T	0.055	0.778	0.83 (0.57-1.21)	0.163	
15	rs6495634		T	0.033	0.629	1.01 (0.6-1.70)	0.515	
16	rs6564329	CNTNAP4	G	0.113	0.097	0.91 (0.55-1.51)	0.639	
17	rs492256	C17orf77, CD300E	T	-0.188	0.007	1.02 (0.67-1.56)	0.536	
18	rs7233501		A	-0.014	0.418	0.78 (0.55-1.10)	0.077	
20	rs3003172	OPRL1, NPBWR2, MYT1	G	-0.124	0.018	1.02 (0.75-1.37)	0.540	
21	rs415277		C	0.060	0.177	1.19 (0.84-1.67)	0.162	
21	rs451387		C	-0.069	0.828	1.02 (0.68-1.54)	0.459	
22	rs9608641		A	0.051	0.253	0.83 (0.56-1.23)	0.820	

Supplement Table 2: Stage 1 replication results in two independent cohorts of African-Americans for SNPs followed up for being a reported European association and showed $P < 0.05$ in the GWA discovery phase of this study. All SNPs genotyped were listed. Genes are within 50 kb upstreams and downstreams of the index SNP. A1 denotes reference allele with respect to which the effect or odds ratio (OR) is given. P* denotes one-tailed p-value. Notes column records if a SNP was genotyped in stage 1 due to its being in high LD ($r^2 > 0.8$) with a SNP targeted for follow-up to guard against failed genotyping (proxy), but do not represent independent signals, or was the exact SNP reported previously in literature (European hit).

				Maywood Family		**GCI AA**		
Height								
Chr	SNP	Genes	A1	Effect	P*	Effect	P*	Notes
2	rs10445823	CCDC108, IHH, NHEJ1	C	-0.877	0.008	0.97 (0.72-1.25)	0.402	
2	rs13398523	CCDC108, IHH, NHEJ1	T	-0.858	0.010	0.95 (0.74-1.22)	0.340	proxy
3	rs7619451	ANAPC13, CEP63	T	N/A		N/A		
3	rs11919350	ANAPC13, CEP63	C	-0.238	0.261	1.29 (1.00-1.68)	0.974	proxy
6	rs11964049	BMP6	T	-0.394	0.819	0.94 (0.70-1.27)	0.648	proxy
6	rs7769495	BMP6	G	-0.458	0.860	0.91 (0.69-1.21)	0.735	
6	rs12198986	BMP6	A	-0.515	0.863	1.07 (0.78-1.45)	0.344	European hit proxy
13	rs201762	DLEU7	G	-1.297	0.044	0.96 (0.58-1.60)	0.438	
18	rs4800455	CABLES1	A	0.422	0.877	0.89 (0.69-1.15)	0.190	
18	rs7506861	DYM	G	0.597	0.068	1.17 (0.86-1.59)	0.153	
BMI								
Chr	SNP	Genes	A1	Effect	P*	OR (95% CI)	P*	Notes
3	rs7635103	ETV5, DGKG	A	0.033	0.283	0.91 (0.69-1.21)	0.744	
18	rs1539952	MC4R	G	0.112	0.040	1.24 (0.89-1.74)	0.101	proxy
18	rs6567160	MC4R	C	0.134	0.024	1.14 (0.81-1.63)	0.227	

Supplemental Table 3: Genic rare CNV (frequency < 5%) burden analysis. Analysis conducted as described for Table 6, but restricting to only rare CNV segments within 20 kb of known genes (RefSeq gene list, hg18 coordinates, +/- 20kb around the largest transcript per gene).

Cohort	Group	Sample (N)	NSEG (N)	RATE	Total Span (Kb)	Avg Span (Kb)
African-Americans	Case	190	1,528	8.042	549.7	68.8
	Control	435	3,558	8.179	673.5	83.7
	Empirical *P*			0.654	0.0158	0.0116
Nigerians	Case	291	2,174	7.471	544.6	75.01
	Control	585	4,573	7.817	588.1	77.6
	Empirical *P*			0.350	0.316	0.542
Meta-analyzed *P*				0.315	0.020	0.036
Europeans /	Case	604	4,097	6.783	693.4	99.44
European-Americans	Control	1,204	8,042	6.679	623.6	93.65
	Empirical *P*			0.572	0.0326	0.192

Supplemental Table 4: Global rare CNV burden analysis stratified by sex. Analysis conducted as described for Table 6. Only analysis after combining the African-American and Nigerian cohorts are shown here.

Sex	Group	Sample (N)	NSEG (N)	RATE	Total Span (Kb)	Avg Span (Kb)
Male	Case	203	2,343	11.54	695.6	61.23
	Control	576	6,931	12.03	824.8	71.6
	Empirical *P*			0.330	0.0208	0.0198
Female	Case	278	3,211	11.55	723.8	65.1
	Control	444	5,377	12.11	855.2	72.05
	Empirical *P*			0.185	0.0109	0.0749
Meta-analyzed *P*				0.105	0.00060	0.0036