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ARIC. The ARIC study is a prospective population-based study of atherosclerosis and cardiovascular disease that included 15792 participants (27% AfA) aged 45-64 years at baseline visit from four US communities (1). In this study, 955 T2D subjects diagnosed at any of the baseline or follow up visits and 414 subjects with normal glucose tolerance (NGT) in all visits were included. All subjects were self-reported AfA recruited from two communities (Jackson, MS and Forsyth, NC).

CARDIA. The CARDIA study is a prospective multi-center investigation of the natural history and etiology of cardiovascular disease that included 5115 participants (52% AfA) aged 18-30 years at baseline visit from four US communities (Birmingham, AL; Chicago, IL; Minneapolis, MN and Oakland, CA) (2). Follow-up examinations occurred at years 2, 5, 7, 10, 15 and 20. In this study, 94 T2D subjects diagnosed at any visits and 654 subjects with NGT in all visits were included. All subjects were self-reported AfA.

CFS. The CFS study is a prospective family-based study originally designed to study the risk factors for sleep apnea that included 2534 subjects (46% AfA) from 352 families in the Cleveland, Ohio metropolitan area examined for up to four visits in 16 years (3). The mean family size was 4.4±3.5 subjects per family in all AfA participants. In this study, 81 T2D and 98 NGT related subjects at the fourth visit who were AfA were included. The respective mean family size was 2.5±1.9 subjects per family, and 30% of families are singletons.

JHS. The JHS is a prospective population-based study to examine the risk factors of cardiovascular diseases among 5301 AfA from two cohorts of unrelated (aged 35-84 years) and nested family-based (aged ≥21 years) subjects in the Jackson, Mississippi metropolitan area (4). The mean family size was 1.4±1.5 subjects per family. In this study, 333 T2D and 1450 NGT subjects at baseline visit who were not enrolled in the ARIC study were included. The respective mean family size was 1.3±1.4 subjects per family, and 88% of families are singletons. Family relationship was not accounted during association analysis due to the low degree of relatedness.

MESA. The MESA is a prospective community-based study of the characteristics of subclinical cardiovascular disease and included 6,814 individuals (28% AfA) free from known cardiovascular disease between 45–84 years old at baseline (5). Subjects were recruited from six field centers (Wake Forest School of Medicine, Columbia University, Johns Hopkins University, University of Minnesota, Northwestern University and University of California - Los Angeles). Data from up to the fourth visit are available for analyses. In this study, 411 T2D subjects diagnosed at any visits and 793 subjects with NGT in all visits who were self-reported AfA were included.

WFSM. The WFSM is a cross-sectional case-control study designed to examine the genetics of T2D and end-stage renal disease (ESRD) in AfA (6; 7). In this study, the cases included 932 subjects with both T2D and ESRD recruited from dialysis facilities. In addition, cases had at least one of the following inclusion criteria: a) T2D diagnosed at least 5 years before initiating renal replacement therapy, b) background or greater diabetic retinopathy and/or c) ≥100 mg/dl proteinuria on urinalysis in the absence of other causes of nephropathy. The controls included 856 AfA subjects without a current diagnosis of diabetes or renal disease recruited from the community and internal medicine clinics. All subjects were recruited in North Carolina, South Carolina, Georgia, Tennessee or Virginia.

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Supplementary Table 1. Selection of T2D-associated index SNPs and power to detect previously reported effect size in this study

Reported loci	Index SNP[†]	Chr	Position	RA/ NRA[‡]	Flanking Region (bp)[§]		Length (kb)	Population	OR for T2D	References	N_{eff}	Power
NOTCH2-ADAM30	rs10923931	1	120319482	T/G	120055542	120500700	445.158	European	1.10	(8)	6700	0.79
PROX1	rs340874*	1	212225879	C/T	212075919	212356406	280.487	European	1.07	(9)	6701	0.36
GCKR	rs780094*	2	27594741	C/T	27304471	28067415	762.944	European	1.06	(9)	6694	0.27
THADA	rs7578597	2	43586327	T/C	43202889	43804094	601.205	European	1.14	(8)	6701	0.91
BCL11A	rs243021	2	60438323	A/G	60299636	60563915	264.279	European	1.08	(10)	6701	0.64
RBMS1-ITGB6	rs7593730	2	160879700	C/T	160688143	161152308	464.165	European	1.09	(11)	6701	0.71
IRS1	rs7578326	2	226728897	A/G	226506229	226989927	483.698	European	1.10	(10)	6701	0.81
PPARG	rs1801282	3	12368125	C/G	12142084	12488339	346.255	European	1.12	(8)	6531	0.14
ADAMTS9	rs4607103	3	64686944	C/T	64573853	64804932	231.079	European	1.08	(8)	6701	0.55
ADCY5	rs11708067*	3	124548468	A/G	124347118	124713944	366.826	European	1.12	(9)	6698	0.63
IGF2BP2	rs4402960	3	186994381	T/G	186855759	187131377	275.618	European	1.17	(8)	6701	1
WFS1-PPP2R2C	rs4689388	4	6320957	A/G	6215869	6475686	259.817	European	1.13	(12)	6701	0.89
ZBED3	rs4457053	5	76460705	G/A	76360705	76590315	229.61	European	1.07	(10)		-
CDKAL1	rs10440833	6	20796100	A/T	20543949	20933219	389.27	European	1.25	(10)	6701	1
DGKB-TMEM195	rs2191349*	7	15030834	T/G	14883467	15132137	248.67	European	1.06	(9)	6701	0.41
JAZF1	rs864745	7	28147081	T/C	28004718	28322765	318.047	European	1.09	(8)	6701	0.61
GCK	rs4607517*	7	44202193	A/G	44090246	44315353	225.107	European	1.07	(9)	6701	0.25
KLF14	rs972283	7	130117394	G/A	129975084	130218730	243.646	European	1.06	(10)	6701	0.24
TP53INP1	rs896854	8	96029687	T/C	95764264	96275026	510.762	European	1.05	(10)	6701	0.28
SLC30A8	rs3802177	8	118254206	G/A	118153964	118389451	235.487	European	1.15	(10)	6701	0.59
PTPRD	rs17584499	9	8869118	T/C	8769118	8969118	200	East Asian	1.61	(13)	5234	1
CDKN2A-CDKN2B	rs10811661	9	22124094	T/C	22017613	22226489	208.876	European	1.19	(10)	6698	0.65
CHCHD9	rs13292136	9	81141948	C/T	80971650	81297538	325.888	European	1.08	(10)	6701	0.25
CDC123-CAMK1D	rs10906115	10	12355003	A/G	-	-	-	East Asian	1.17	(14)	6648	0.98

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CDC123-CAMK1D	rs12779790	10	12368016	G/A	12179950	12468016	288.066	European	1.10	(8)	6701	0.53
HHEX-IDE	rs5015480	10	94455539	C/T	94092885	94582696	489.811	European	1.18	(10)	6696	1
TCF7L2	rs7903146	10	114748339	T/C	114638487	114903037	264.55	European	1.40	(10)	6701	1
KCNQ1	rs231362	11	2648047	G/A	2548047	2915016	366.969	European	1.07	(10)	6701	0.38
KCNQ1	rs2237892	11	2796327	C/T	-	-	-	East Asian	1.40	(15)	6701	1
KCNJ11	rs5215	11	17365206	C/T	16958130	17478436	520.306	European	1.09	(8)	6693	0.35
CENTD2	rs1552224	11	72110746	A/C	71942053	72629111	687.058	European	1.14	(10)	6531	0.23
MTNR1B	rs1387153	11	92313476	T/C	92207378	92464969	257.591	European	1.08	(10)	6701	0.64
HMGA2	rs1531343	12	64461161	C/G	64351738	64680062	328.324	European	1.08	(10)	6700	0.64
TSPAN8-LGR5	rs7961581	12	69949369	C/T	69775513	70052453	276.94	European	1.08	(8)	6701	0.49
HNF1A	rs7957197	12	119945069	T/A	119581507	120163407	581.9	European	1.05	(10)	6701	0.18
SPRY2	rs1359790	13	79615157	G/A	79466875	79742662	275.787	East Asian	1.20	(14)	6688	0.85
C2CD4A-C2CD4B	rs7172432	15	60183681	A/G	60070025	60373586	303.561	East Asian	1.10	(16)	6701	0.78
C2CD4B	rs11071657*	15	60221254	A/G	-	-	-	European	1.03	(9)	6701	0.10
ZFAND6	rs11634397	15	78219277	G/A	78032561	78319277	286.716	European	1.05	(10)	6701	0.32
PRC1	rs8042680	15	89322341	A/C	89151445	89467866	316.421	European	1.06	(10)	6636	0.25
FTO	rs8050136	16	52373776	A/C	52255409	52502988	247.579	European	1.15	(8)	6700	0.99
SRR	rs391300	17	2163008	C/T	1930631	2284211	353.58	East Asian	1.26	(13)	6701	1
HNF1B	rs4430796	17	33172153	G/A	33070413	33280426	210.013	European	1.14	(10)		-

† The independent index SNP for each locus was selected from the study showing the lowest *p* value ($P<5\times10^{-8}$) for T2D risk in the catalog of published GWAS at National Human Genome Research Institute for T2DM and related glucose homeostasis traits. SNPs in asterisk were initially identified to be associated with fasting glucose (22). Index SNPs for *PPARG* ($P= 2\times10^{-4}$) and *HNF1B* ($P= 2\times10^{-6}$) were included due to strong candidacy and consistent replication despite not reaching genome-wide significance.

‡ risk allele (RA) and non-risk allele (NRA) as reported in the references. Alleles were indexed to the forward strand of NCBI Build 36.

§ flanking region was defined as the boundary of the farthest SNPs that show LD at $r^2 \geq 0.3$ with the index SNP at the reported populations and further extended by 100kb.

ℑ *ZBED3* rs4457053 and *HNF1B* rs4430796 failed quality control in this study and power were not reported

T2D: type 2 diabetes; N_{eff}: effective sample size

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Supplementary Table 2. Univariate and conditional analyses of index and best SNPs for association with T2D in African Americans.

Reported	**Univariate Analysis**						**Conditional Analysis**			
Loci	**Best SNP***			**Index SNP†**			**Best SNP‡**		**Index SNP§**	
		OR (95% CI)	***P***		**OR (95% CI)**	***P***	**OR (95% CI)**	***P***	**OR (95% CI)**	***P***
KLF14	rs13234269	1.26(1.14-1.40)	1.55E-05	rs972283	1.24(1.09-1.41)	8.12E-04	1.26(1.1-1.44)	7.53E-04	1.04(0.89-1.22)	0.620
HMGA2	rs12049974	1.24(1.14-1.35)	1.73E-06	rs1531343	0.91(0.84-0.99)	0.022	1.35(1.18-1.53)	5.07E-06	1.14(1-1.29)	0.051
NOTCH2-ADAM30	rs12075171	1.34(1.15-1.55)	1.25E-04	rs10923931	1.05(0.96-1.14)	0.256	1.33(1.14-1.54)	2.08E-04	1.02(0.94-1.12)	0.584
KCNQ1	rs231361	1.17(1.07-1.28)	6.64E-04	rs231362	1.07(0.95-1.20)	0.251	1.13(1.02-1.25)	0.018	1.03(0.9-1.17)	0.661
KCNQ1	rs231361	1.17(1.07-1.28)	6.64E-04	rs2237892	1.25(1.09-1.43)	1.80E-03	1.15(1.05-1.27)	2.99E-03	1.21(1.04-1.41)	0.012

* meta-analysis of associations of the best SNP adjusted for age, gender, study center, PC1 and corrected for study-specific inflation factor
† meta-analysis of associations of the index SNP adjusted for age, gender, study center, PC1 and corrected for study-specific inflation factor
‡ meta-analysis of associations of the best SNP adjusted for age, gender, study center, PC1, index SNP and corrected for study-specific inflation factor
§ meta-analysis of associations of the index SNP adjusted for age, gender, study center, PC1, best SNP and corrected for study-specific inflation factor

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Supplementary Table 3. Allele frequency, fixation index (F_{ST}) and Integration Haplotype Scores (iHS) of index SNPs in African Americans and HapMap CEU, JPT+CHB (ASN) and YRI populations

Reported Loci	Index SNP	RA/NRA*	RAF in CEU (ASN)†	RAF in AfA	RAF |CEU (ASN)† - AfA|	F_{ST} in CEU (ASN)† vs YRI‡	iHS in CEU (ASN)†,§	iHS in YRI§
NOTCH2-ADAM30	rs10923931	T/G	0.09	0.33	0.24	0.105	**2.25**	-1.63
PROX1	rs340874	C/T	0.56	0.17	0.40	0.207	-0.06	-0.09
GCKR	rs780094	C/T	0.61	0.82	0.22	0.095	-0.39	0.14
THADA	rs7578597	T/C	0.88	0.73	0.15	0.071	-1.00	1.17
BCL11A	rs243021	A/G	0.48	0.39	0.09	0.005	0.13	0.58
RBMS1-ITGB6	rs7593730	C/T	0.83	0.62	0.21	0.059	-1.03	-0.93
IRS1	rs7578326	A/G	0.65	0.57	0.08	0.004	0.27	1.20
PPARG	rs1801282	C/G	0.90	0.98	0.08	-	-0.57	
ADAMTS9	rs4607103	C/T	0.81	0.71	0.10	0.01	0.54	0.89
ADCY5	rs11708067	A/G	0.77	0.85	0.08	0.035	-0.36	-0.79
IGF2BP2	rs4402960	T/G	0.30	0.52	0.22	0.068	1.64	-0.31
WFS1-PPP2R2C	rs4689388	A/G	0.67	0.71	0.04	0.001	1.68	0.79
ZBED3	rs4457053	G/A	0.26	-	-	-	0.28	-
CDKAL1	rs10440833	A/T	0.25	0.22	0.03	-		-
DGKB-TMEM195	rs2191349	T/G	0.47	0.60	0.13	0.016	-0.13	-0.07
JAZF1	rs864745	T/C	0.49	0.74	0.26	0.063	-1.56	0.02
GCK	rs4607517	A/G	0.20	0.10	0.10	0.045	-0.26	-0.20
KLF14	rs972283	G/A	0.55	0.85	0.30	0.192	-0.87	1.15
TP53INP1	rs896854	T/C	0.44	0.69	0.25	0.102	-0.47	-0.81
SLC30A8	rs3802177	G/A	0.76	0.91	0.15	0.07	-1.86	-0.59
PTPRD	rs17584499	T/C	(0.09)	0.06	(0.03)	(0.034)	(-0.73)	-
CDKN2A-CDKN2B	rs10811661	T/C	0.80	0.93	0.13	-	0.33	-
CHCHD9	rs13292136	C/T	0.93	0.91	0.03	0.002	-1.04	-1.14
CDC123-	rs10906115	A/G	(0.65)	0.69	(0.04)	(0.001)	(0.62)	-0.34

CAMK1D								
CDC123-CAMK1D	rs12779790	G/A	0.23	0.13	0.10	-	-	-
HHEX-IDE	rs5015480	C/T	0.58	0.62	0.04	0	0.48	-0.04
TCF7L2	rs7903146	T/C	0.28	0.31	0.03	0.002	0.09	-0.27
KCNQ1	rs231362	G/A	0.52	0.79	0.27	0.142	1.22	-0.59
KCNQ1	rs2237892	C/T	(0.64)	0.89	(0.25)	(0.095)	(-0.62)	-0.66
KCNJ11	rs5215	C/T	0.40	0.09	0.30	0.243	-0.44	-
CENTD2	rs1552224	A/C	0.87	0.97	0.10	-	-	-
MTNR1B	rs1387153	T/C	0.27	0.38	0.11	0.022	0.37	-0.09
HMGA2	rs1531343	C/G	0.12	0.38	0.27	0.166	**2.33**	1.39
TSPAN8-LGR5	rs7961581	C/T	0.25	0.20	0.05	0.004	-0.52	0.91
HNF1A	rs7957197	T/A	0.85	0.86	0.01	0.001	-1.42	0.31
SPRY2	rs1359790	G/A	(0.69)	0.89	(0.20)	(0.061)	(-0.60)	1.45
C2CD4A-C2CD4B	rs7172432	A/G	(0.55)	0.31	(0.24)	(0.114)	(-1.11)	-1.34
C2CD4B	rs11071657	A/G	0.59	0.86	0.27	0.171	1.07	-1.65
ZFAND6	rs11634397	G/A	0.64	0.44	0.21	-	0.02	-
PRC1	rs8042680	A/C	0.26	0.84	0.58	**0.597**	-1.39	-
FTO	rs8050136	A/C	0.46	0.43	0.03	0	**2.06**	1.12
SRR	rs391300	C/T	(0.78)	0.49	(0.29)	(0.097)	(1.75)	0.14
HNF1B	rs4430796	G/A	0.51	-	-	0.006	0.85	0.48

***** risk allele (RA) and non-risk allele (NRA) as reported previously in European or East Asian populations. Alleles were indexed to the forward strand of NCBI Build 36.

† risk allele frequency, F_{ST} and iHS were shown for HapMap CEU population in loci reported in Europeans, and for HapMap JPT+CHB (ASN) populations in loci reported in East Asians

‡ F_{ST} above top 5 percentile for pairwise population comparison are bolded

§ iHS >2 or <-2 represented suggestive evidence of recent positive selection are bolded

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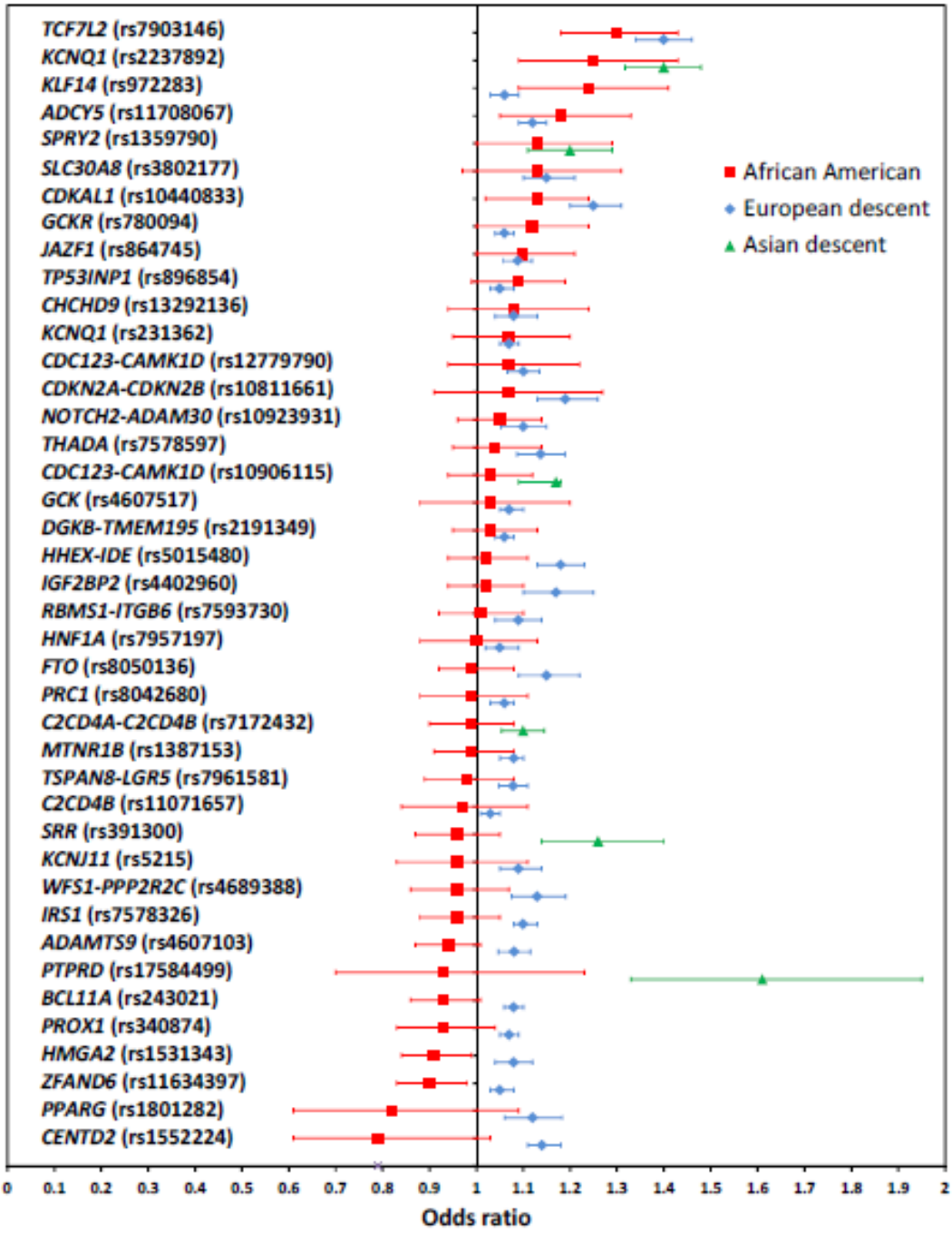
Supplementary Figure 1. Odds ratio (95% CI) of index SNPs in African Americans (this study), individuals of European descent (17;18;22;28;29), and Asian descent (19;20;21;30) sorted in descending effect size in African Americans.



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