

SUPPLEMENTAL MATERIAL

Supplemental Tables:

Table S1. Candidate genes selected for genotyping

Gene		
Abbreviation	Gene Name	Location
<i>ACE</i>	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	17q23
<i>ACTN3</i>	actinin, alpha 3	3p22
<i>ADIPOR1</i>	adiponectin receptor 1	1q32
<i>ADRA2A</i>	adrenergic, alpha-2A-, receptor	10q24-q26
<i>ADRB1</i>	adrenergic, beta-1-, receptor	10q24-q26
<i>AGT</i>	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	1q42-q43
<i>AMPD1</i>	adenosine monophosphate deaminase 1 (isoform M)	1p13
<i>ANG</i>	angiogenin, ribonuclease, RNase A family, 5	14q11.1-q11.2
<i>ATP1A2</i>	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 (+) polypeptide	1q21-q23
<i>BDKRB2</i>	bradykinin receptor, beta 2	14q32.1-q32.2
<i>CKM</i>	creatine kinase, muscle	19q13.2-q13.3
<i>EDN1</i>	endothelin 1	6p24.1
<i>GNB3</i>	guanine nucleotide binding protein (G protein), beta polypeptide 3	12p13
<i>HIF1A</i>	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	14q21-q24
<i>NOS3</i>	nitric oxide synthase 3 (endothelial cell)	7q36
<i>PPARGCIA</i>	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	4p15.1
<i>TTN</i>	titin	2q31

Table S2. Genotypes associated with greater baseline exercise test duration (A) or lesser decrease in exercise test duration over 20 years (B) used in multiple regression analyses.

A. Model: Baseline duration

		High-treadmill duration genotype(s)	
Blacks			
<i>ATPIA2</i>	rs9660705	C/C	C/T
<i>HIF1A</i>	rs1957755	G/G	A/G
<i>NOS3</i>	rs3918196	A/A	A/G
<i>PPARGCIA</i>	rs7657517	T/T	G/T
<i>PPARGCIA</i>	rs2932971	C/C	C/T
Whites			
		High-treadmill duration genotype(s)	
<i>HIF1A</i>	rs1957757	T/T	
<i>PPARGCIA</i>	rs3774909	G/G	A/G

B. Model: Change in duration over 20 years

		Low-treadmill duration decrease genotype(s)	
Whites			
<i>AGT</i>	rs5051	T/T	
<i>AMPD1</i>	rs2010899	G/G	
<i>ANG</i>	rs1010458	C/C	C/T
<i>PPARGCIA</i>	rs4452416	T/T	

For each treadmill time model (baseline duration or decrease in duration), the sum of high/low-treadmill duration genotypes possessed across all remaining SNPs was used in multiple regression analyses as an index of genetic exercise test duration predisposition.

Table S3. Baseline (a) and year 20 (b) characteristics.

A.	Blacks (n=1835) mean (SD)	Whites (n=1948) mean (SD)	
Baseline variables	or %	or %	p value*
% female	56.6	52.7	0.016
Age, yrs	24.3 (3.8)	25.4 (3.4)	<0.0001
Weight, kg	72.6 (17.2)	69.5 (14.4)	<0.0001
BMI, kg/m ²	25.2 (5.5)	23.6 (3.9)	<0.0001
Exercise duration, min	9.0 (2.8)	10.7 (2.6)	<0.0001
% Current smoker	38.1	32.9	0.003
% Hypertensive	11.4	8.6	0.0038
% Diabetic	0.8	0.5	0.1688

B.	Blacks (n=1035) mean (SD)	Whites (n=1300) mean (SD)	
Year 20 Variables	or %	or %	p value*
% female	58.1	52.7	0.009
Age, yrs	44.3 (3.7)	45.5 (3.4)	<0.0001
Weight, kg	88.8 (20.5)	81.0 (18.8)	<0.0001
ΔWeight, kg	17.7 (13.5)	12.2 (10.9)	<0.0001
BMI, kg/m ²	30.7 (6.7)	27.4 (5.7)	<0.0001
ΔBMI, kg/m ²	5.9 (4.7)	4.1 (4.0)	<0.0001
Exercise duration, min	6.1 (2.3)	8.1 (2.5)	<0.0001
ΔExercise duration, min	-3.0 (2.1)	-2.8 (2.0)	0.0337
% Current smoker	20	12.7	<0.0001
% Hypertensive	35.7	16.9	<0.0001
% Diabetic	9.2	5.5	0.0005

Δ refers to change in the variable, value at year 20 minus baseline value (negative sign represents decrease).

*p value for difference between ethnic groups.

Table S4a. SNP physical map locations, minor allele frequencies (MAF), Hardy-Weinberg equilibrium (HWE) test statistics, and pairwise linkage disequilibrium (LD) estimates (r^2 below median, D' above median) among all included SNPs in the *ACE*, *ACTN3*, *ADIPOR1*, *ADRA2*, *ADRB1*, *AGT*, *AMPD1*, *ANG*, *ATPIA2*, *CKM*, *EDN1*, *GNB3*, *HIF1A*, and *NOS3* loci in black participants of the CARDIA Fitness Study.

<i>ACE</i>	MAP	Minor Allele	MAF	HWE	rs4303	rs4316	rs4318	rs4351	rs4357	rs4461142	rs4267385	rs8066276	rs8066114	rs4611524	rs4968591
rs4303	58,911,555	T	0.0883	0.7703		0.984	0.812	0.924	0.032	0.956	0.922	0.62	0.539	0.17	0.899
rs4316	58,916,041	T	0.3949	0.6412	0.034		0.987	0.97	0.875	0.833	0.381	0.22	0.379	0.296	0.398
rs4318	58,916,105	G	0.1689	0.3496	0.329	0.067		0.983	0.008	0.993	0.831	0.592	0.437	0.042	0.88
rs4351	58,923,464	G	0.4718	0.5292	0.039	0.71	0.086		0.984	0.809	0.405	0.269	0.408	0.388	0.484
rs4357	58,925,362	T	0.2484	0.6805	0	0.138	0	0.134		0.974	0.663	0.594	0.456	0.419	0.757
rs4461142	58,931,780	T	0.1675	0.5712	0.02	0.257	0.043	0.319	0.064		0.334	0.574	0.461	0.562	0.627
rs4267385	58,937,488	C	0.2185	0.9291	0.019	0.092	0.03	0.078	0.03	0.026		0.825	0.995	0.884	0.995
rs8066276	58,942,997	C	0.3548	0.7231	0.016	0.034	0.029	0.068	0.045	0.171	0.307		0.998	0.837	0.997
rs8066114	58,943,572	G	0.2918	0.5723	0.007	0.058	0.009	0.089	0.015	0.193	0.254	0.571		0.914	0.984
rs4611524	58,945,384	C	0.4797	0.7105	0.001	0.079	0	0.127	0.028	0.131	0.444	0.558	0.379		0.999
rs4968591	58,951,850	C	0.1599	0.0025	0.014	0.048	0.028	0.094	0.031	0.326	0.188	0.423	0.722	0.337	

<i>ACTN3</i>	MAP	Minor Allele	MAF	HWE	rs544021	rs1791690	rs12223171	rs677488	rs509556	rs2275998	rs1815739	rs618838	rs540874	rs11227532
rs544021	66,072,237	C	0.4189	0.3025		0.987	0.939	0.798	0.689	0.762	0.761	0.765	0.963	
rs1791690	66,074,399	G	0.3841	0.1324	0.904		0.985	0.818	0.788	0.617	0.785	0.783	0.789	1
rs12223171	66,079,967	T	0.0851	0.3794	0.037	0.044		1	1	0.995	1	1	0.996	
rs677488	66,081,338	G	0.2671	0.5461	0.376	0.417	0.026		0.998	0.473	0.999	0.997	0.988	1
rs509556	66,082,938	G	0.1707	0.0505	0.283	0.312	0.021	0.81		0.901	0.982	0.996	0.958	1
rs2275998	66,083,157	T	0.2919	0.1993	0.143	0.126	0.14	0.041	0.119		1	1	0.831	0.982
rs1815739	66,084,671	T	0.177	0.1405	0.272	0.301	0.02	0.789	0.935	0.143		0.986	0.998	1
rs618838	66,085,295	T	0.1691	0.1542	0.273	0.301	0.02	0.784	0.958	0.142	0.971		0.995	1
rs540874	66,086,308	T	0.2167	0.3953	0.301	0.337	0.022	0.851	0.857	0.109	0.904	0.897		1
rs11227532	66,087,344	G	0.067	0.3916	0.031	0.037	0.748	0.02	0.017	0.108	0.016	0.016	0.018	

<i>ADIPOR1</i>	MAP	Minor Allele	MAF	HWE	rs2275736	rs1342387	rs7518457	rs12733285	rs10494839	rs10753929	rs1539355
rs2275736	201,178,108	A	0.1921	0.2692		0.996	0.998	1	1	1	0.845
rs1342387	201,180,979	A	0.4798	0.2008	0.225		0.884	0.95	0.965	0.988	0.646
rs7518457	201,182,159	G	0.0545	0.0002	0.014	0.05		0.943	1	1	1
rs12733285	201,188,663	T	0.2011	0.4466	0.061	0.249	0.201		1	1	1
rs10494839	201,188,817	C	0.1548	0.695	0.044	0.158	0.011	0.046		1	1
rs10753929	201,189,801	T	0.1862	0.1513	0.057	0.241	0.013	0.059	0.042		1
rs1539355	201,190,703	G	0.4467	0.607	0.213	0.313	0.046	0.203	0.227	0.188	

<i>ADRA2</i>	MAP	Minor Allele	MAF	HWE
rs11195419	112,829,358	A	0.274	0.9958

<i>ADRB1</i>	MAP	Minor Allele	MAF	HWE	rs1801252	rs1801253
rs1801252	115,794,026	G	0.2322	0.2217		0.97
rs1801253	115,795,046	G	0.4069	0.0096	0.107	

<i>AGT</i>	MAP	Minor Allele	MAF	HWE	rs7079	rs11568045	rs2493129	rs2493131	rs2493132	rs3789671	rs2478545	rs2478544	rs2478543	rs2478539	rs11122577	rs3889728	rs3789679	rs5051
rs7079	228,904,954	A	0.098	0.2197		1	1	0.98	0.977	0.986	0.93	0.916	0.923	0.943	0.731	0.796	0.964	0.874
rs11568045	228,906,106	C	0.1654	0.941	0.025		0.849	0.042	0.47	0.193	0.746	0.766	0.854	0.871	0.48	0.526	0.563	0.903
rs2493129	228,907,565	A	0.079	0.4148	0.018	0.004		0.942	0.983	0.852	0.864	0.907	0.944	0.979	0.999	0.845	0.792	0.969
rs2493131	228,910,128	T	0.0892	0.7245	0.018	0.001	0.834		0.995	0.968	0.848	0.875	0.912	0.981	0.998	1	0.903	0.953
rs2493132	228,910,180	C	0.4967	0.0162	0.179	0.03	0.089	0.096		0.337	0.839	0.812	0.95	0.933	0.891	0.918	0.716	0.94
rs3789671	228,910,423	T	0.3739	0.2024	0.107	0.009	0.017	0.023	0.029		0.625	0.574	0.987	0.957	0.983	0.02	0.564	0.982
rs2478545	228,910,744	T	0.46	0.2312	0.126	0.096	0.09	0.091	0.544	0.076		0.987	1	0.936	0.986	0.478	0.365	0.955
rs2478544	228,910,819	C	0.4291	0.1317	0.104	0.12	0.119	0.116	0.43	0.055	0.824		1	0.934	0.553	0.241	0.343	0.982
rs2478543	228,910,933	A	0.1817	0.0146	0.39	0.04	0.035	0.034	0.374	0.235	0.321	0.271		0.973	0.976	0.981	0.991	0.955
rs2478539	228,911,395	C	0.2023	0.0211	0.386	0.044	0.039	0.041	0.379	0.232	0.297	0.249	0.897		0.875	0.926	1	0.975
rs11122577	228,914,179	T	0.0885	0.1036	0.022	0.003	0.009	0.009	0.171	0.053	0.277	0.103	0.085	0.072		0.996	0.941	0.865
rs3889728	228,915,454	A	0.1479	0.0114	0.045	0.006	0.011	0.016	0.321	0	0.112	0.033	0.149	0.141	0.571		0.266	0.917
rs3789679	228,916,317	A	0.1525	0.134	0.035	0.209	0.005	0.007	0.104	0.11	0.035	0.037	0.082	0.087	0.016	0.037		0.982
rs5051	228,916,495	C	0.1646	0.0215	0.36	0.044	0.036	0.036	0.358	0.229	0.286	0.255	0.89	0.881	0.065	0.129	0.08	

<i>AMPD1</i>	MAP	Minor Allele	MAF	HWE	rs6679869	rs11102831	rs2268697	rs2268699	rs12354159	rs2336363	rs12038990	rs2010899
rs6679869	115,019,250	C	0.1463	0.9338		0.999	0.848	0.761	0.921	0.726	0.558	0.904
rs11102831	115,019,342	T	0.1379	0.5793	0.012		0.891	0.885	0.968	0.997	0.999	0.852
rs2268697	115,029,016	A	0.4997	0.7845	0.091	0.045		1	1	0.943	0.979	0.773
rs2268699	115,029,419	A	0.4709	0.9831	0.078	0.047	0.939		0.972	0.944	0.974	0.775
rs12354159	115,030,802	G	0.0992	0.779	0.007	0.662	0.041	0.04		0.795	0.895	0.954
rs2336363	115,034,091	A	0.1179	0.4609	0.435	0.009	0.09	0.096	0.004		0.832	0.908
rs12038990	115,036,155	T	0.0562	0.3669	0.167	0.006	0.065	0.068	0.004	0.457		1
rs2010899	115,036,533	G	0.2692	0.718	0.074	0.092	0.27	0.287	0.083	0.06	0.049	

<i>ANG</i>	MAP	Minor Allele	MAF	HWE	rs9322855	rs11851044	rs8004382	rs4470055	rs1010458	rs12895066	rs17114699	rs12100929	rs11156631
rs9322855	20,223,139	A	0.4987	0.5835		0.997	0.96	0.722	0.982	0.409	0.171	0.155	0.987
rs11851044	20,224,335	C	0.1085	0.9072	0.145		1	0.944	0.999	0.902	0.931	0.924	0.912
rs8004382	20,225,233	A	0.3942	0.7763	0.657	0.102		0.982	0.982	0.751	0.612	0.641	0.987
rs4470055	20,226,031	A	0.4544	0.1891	0.324	0.065	0.417		0.987	0.501	0.565	0.514	0.988
rs1010458	20,226,312	T	0.1287	0.272	0.202	0.025	0.141	0.334		0.945	0.994	0.993	1
rs12895066	20,228,417	A	0.3129	0.7839	0.075	0.045	0.183	0.188	0.403		0.288	0.12	0.995
rs17114699	20,228,750	T	0.4044	0.3849	0.011	0.039	0.101	0.199	0.063	0.012		0.978	0.985
rs12100929	20,228,881	G	0.4079	0.1439	0.01	0.042	0.122	0.176	0.067	0.002	0.885		1
rs11156631	20,229,446	A	0.0896	0.2381	0.04	0.005	0.035	0.082	0.008	0.11	0.127	0.125	

Table S4a continued

<i>ATPIA2</i>	MAP	Minor Allele	MAF	HWE	rs1016732	rs7532556	rs2854247	rs2854248	rs1023420	rs1321655	rs11265329	rs16831388	rs9660705	rs6695366	rs12072167	rs6686067	rs10797059	rs1046995
rs1016732	158,353,592	A	0.1112	0.1934		1	1	0.989	0.992	0.994	0.946	0.949	0.999	0.84	0.999	0.773	0.587	0.897
rs7532556	158,357,083	G	0.05	0.7048	0.004		1	1	0.995	0.14	1	0.987	0.016	0.061	0.015	0.095	0.22	0.335
rs2854247	158,359,069	C	0.1483	0.8775	0.013	0.313		1	0.9	1	1	0.905	0.009	0.476	0.551	0.231	0.057	0.106
rs2854248	158,360,551	A	0.4713	0.0608	0.228	0.014	0.046		0.981	1	0.931	0.488	0.499	0.851	0.011	0.836	0.576	0.175
rs1023420	158,360,967	C	0.2701	0.7514	0.564	0.007	0.018	0.389		0.778	0.995	0.969	0.593	0.88	0.236	0.877	0.583	0.409
rs1321655	158,361,082	A	0.0568	0.652	0.004	0	0.364	0.016	0.005		1	0.864	0.006	0.945	0.583	0.726	0.594	0.036
rs11265329	158,362,070	T	0.0698	0.0473	0.039	0.007	0.022	0.167	0.076	0.008		0.969	1	0.97	1	0.975	1	0.467
rs16831388	158,362,249	G	0.1577	0.0857	0.027	0.005	0.013	0.031	0.048	0.004	0.05		0.699	0.898	0.805	0.886	0.378	0.518
rs9660705	158,363,434	T	0.064	0.4308	0.005	0	0	0.011	0.039	0	0.009	0.003		0.999	0.255	0.971	0.586	0.819
rs695366	158,364,290	G	0.0817	0.2668	0.643	0.001	0.003	0.152	0.407	0.004	0.037	0.022	0.004		1	0.934	0.755	0.968
rs12072167	158,367,868	C	0.0679	0.3069	0.005	0	0.129	0	0.007	0.292	0.009	0.004	0.064	0.005		0.993	0.632	0.845
rs686067	158,368,684	C	0.0845	0.1189	0.405	0.007	0.002	0.001	0.121	0.336	0.002	0.032	0.017	0.003	0.004		0.992	0.975
rs10797059	158,368,880	A	0.2609	0.9191	0.224	0.005	0.001	0.116	0.296	0.002	0.066	0.007	0.044	0.336	0.003	0.486		0.772
rs1046995	158,379,365	C	0.2368	0.4571	0.037	0.001	0	0.006	0.013	0	0.018	0.177	0.006	0.04	0.007	0.033	0.042	

<i>CKM</i>	MAP	Minor Allele	MAF	HWE	rs4884	rs7260463	rs432979	rs344816
rs4884	50,501,875	T	0.19	0.8508		0.838	0.689	0.426
rs7260463	50,506,700	T	0.4885	0.0438	0.159		0.207	0.718
rs432979	50,513,531	G	0.312	0.472	0.037	0.007		0.797
rs344816	50,517,466	A	0.1584	0.895	0.108	0.195	0.084	

<i>EDN1</i>	MAP	Minor Allele	MAF	HWE	rs1800542	rs9296343	rs5369	rs1794849	rs10478723	rs6912834	rs2071943	rs1629862	rs1630736	rs5370
rs1800542	12,400,514	A	0.2564	0.1196		0.992	0.999	0.998	0.995	1	0.985	1	1	1
rs9296343	12,401,519	G	0.1965	0.8432	0.764		0.998	1	0.997	1	0.98	0.999	1	1
rs5369	12,402,244	A	0.138	0.9446	0.025	0.019		0.995	0.983	1	1	0.996	1	1
rs1794849	12,402,848	C	0.3738	0.6187	0.214	0.164	0.177		0.999	0.993	0.998	0.988	0.989	0.918
rs10478723	12,403,447	A	0.3913	0.5993	0.635	0.493	0.038	0.34		1	0.992	1	0.978	0.826
rs6912834	12,403,521	G	0.0927	0.5072	0.02	0.015	0.017	0.141	0.031		1	0.999	1	1
rs2071943	12,403,800	A	0.1727	0.3624	0.039	0.029	0.035	0.191	0.062	0.028		1	0.981	0.996
rs1629862	12,403,862	A	0.1122	0.2824	0.022	0.016	0.887	0.156	0.034	0.015	0.032		1	1
rs1630736	12,403,973	T	0.1051	0.0002	0.069	0.053	0.06	0.32	0.105	0.047	0.096	0.054		0.982
rs5370	12,404,241	T	0.1869	0.1615	0.042	0.032	0.037	0.169	0.045	0.029	0.951	0.033	0.101	

<i>GNB3</i>	MAP	Minor Allele	MAF	HWE	rs2301339	rs5446
rs2301339	6,824,885	G	0.2675	0.0002		0.975
rs5446	6,826,723	T	0.4284	0.8292	0.518	

<i>HIF1A</i>	MAP	Minor Allele	MAF	HWE	rs12435848	rs10129270	rs10138032	rs4899056	rs1957755	rs17099141	rs1957757	rs12885226	rs966824	rs2301113
rs12435848	61,246,644	G	0.2589	0.3312		0.999	0.996	0.94	1	1	0.999	1	1	0.968
rs10129270	61,251,707	A	0.3749	0.7261	0.307		0.932	0.993	0.035	0.997	0.994	0.12	0.091	0.996
rs10138032	61,253,935	G	0.2877	0.8487	0.184	0.525		0.948	0.051	0.944	0.942	0.054	0.134	0.995
rs4899056	61,259,284	C	0.2721	0.8748	0.675	0.399	0.22		1	0.992	0.997	0.997	0.995	0.965
rs1957755	61,260,089	A	0.0682	0.2401	0.04	0	0.001	0.053		0.833	1	0.991	0.99	1
rs17099141	61,263,992	A	0.0565	0.9656	0.044	0.01	0.006	0.056	0.001		1	0.545	1	1
rs1957757	61,266,701	C	0.3371	0.1691	0.655	0.464	0.25	0.857	0.061	0.066		0.964	0.997	0.997
rs12885226	61,268,676	T	0.19	0.1073	0.119	0	0.002	0.158	0.318	0.001	0.169		0.975	1
rs966824	61,270,271	T	0.2788	0.1433	0.21	0.006	0.001	0.275	0.185	0.207	0.319	0.54		0.994
rs2301113	61,276,301	A	0.1969	0.5468	0.788	0.256	0.155	0.596	0.034	0.036	0.551	0.101	0.175	

<i>NOS3</i>	MAP	Minor Allele	MAF	HWE	rs1799983	rs3918186	rs3918187	rs3918188	rs3918196	rs1808593	rs3918211
rs1799983	150,327,044	T	0.108	0.4116		0.982	0.947	0.897	0.208	0.365	0.951
rs3918186	150,333,365	T	0.196	0.5306	0.042		0.487	0.893	0.922	0.255	0.078
rs3918187	150,333,524	G	0.0818	0.0744	0.01	0.002		1	0.999	0.097	0.275
rs3918188	150,333,714	A	0.3797	0.0089	0.129	0.074	0.026		0.743	0.492	0.711
rs3918196	150,336,775	A	0.0501	0.0708	0.01	0.008	0.003	0.02		0.264	0.999
rs1808593	150,339,235	G	0.2177	0.9493	0.121	0.003	0.001	0.042	0.001		0.266
rs3918211	150,341,840	C	0.1581	0.6099	0.021	0.003	0.038	0.026	0.005	0.021	

Table S5a. SNP physical map locations, minor allele frequencies (MAF), Hardy-Weinberg equilibrium (HWE) test statistics, and pairwise linkage disequilibrium (LD) estimates (r^2 below median, D' above median) among all included SNPs in the *ACE*, *ACTN3*, *ADIPOR1*, *ADRA2*, *ADRB1*, *AGT*, *AMPD1*, *ANG*, *ATPIA2*, *CKM*, *EDN1*, *GNB3*, *HIF1A*, and *NOS3* loci in white participants of the CARDIA Fitness Study.

<i>ACE</i>	MAP	Minor Allele	MAF	HWE ChiSq	rs4316	rs4351	rs4461142	rs4267385	rs8066276	rs8066114	rs4611524	rs4968591
rs4316	58,916,041	T	0.4693	0.759		0.97	0.833	0.381	0.22	0.379	0.296	0.398
rs4351	58,923,464	A	0.4791	0.5295	0.71		0.809	0.405	0.269	0.408	0.388	0.484
rs4461142	58,931,780	T	0.4751	0.7475	0.257	0.319		0.334	0.574	0.461	0.562	0.627
rs4267385	58,937,488	C	0.4252	0.9446	0.092	0.078	0.026		0.825	0.995	0.884	0.995
rs8066276	58,942,997	T	0.3955	0.2241	0.034	0.068	0.171	0.307		0.998	0.837	0.997
rs8066114	58,943,572	G	0.3981	0.877	0.058	0.089	0.193	0.254	0.571		0.914	0.984
rs4968591	58,945,384	C	0.3999	0.3677	0.079	0.127	0.131	0.444	0.558	0.379		0.999
rs4611524	58,951,850	T	0.4037	0.6018	0.048	0.094	0.326	0.188	0.423	0.722	0.337	

<i>ACTN3</i>	MAP	Minor Allele	MAF	HWE ChiSq	rs544021	rs1791690	rs677488	rs509556	rs2275998	rs1815739	rs618838	rs540874
rs544021	66,072,237	G	0.4232	0.6571		0.987	0.798	0.768	0.689	0.762	0.761	0.765
rs1791690	66,074,399	A	0.4141	0.0625	0.904		0.818	0.788	0.617	0.785	0.783	0.789
rs677488	66,081,338	G	0.4697	0.4513	0.376	0.417		0.998	0.473	0.999	0.997	0.988
rs509556	66,082,938	T	0.4678	0.6311	0.283	0.312	0.81		0.901	0.982	0.996	0.958
rs2275998	66,083,157	G	0.1776	0.27	0.143	0.126	0.041	0.119		1	1	0.831
rs1815739	66,084,671	T	0.4477	0.2591	0.272	0.301	0.789	0.935	0.143		0.986	0.998
rs618838	66,085,295	T	0.4552	0.2986	0.273	0.301	0.784	0.958	0.142	0.971		0.995
rs540874	66,086,308	T	0.4539	0.258	0.301	0.337	0.851	0.857	0.109	0.904	0.897	

<i>ADIPOR1</i>	MAP	Minor Allele	MAF	HWE ChiSq	rs1342387	rs12733285	rs10494839	rs10753929	rs1539355
rs1342387	201,180,979	A	0.4575	0.5474		0.98	0.997	0.993	0.998
rs12733285	201,188,663	T	0.3179	0.6257	0.527		1	1	1
rs10494839	201,188,817	C	0.2985	0.6981	0.363	0.198		1	0.999
rs10753929	201,189,801	T	0.1131	0.8208	0.152	0.06	0.055		1
rs1539355	201,190,703	G	0.3049	0.4061	0.372	0.205	0.958	0.057	

<i>ADRA2</i>	MAP	Minor Allele	MAF	HWE ChiSq	rs11195419
rs11195419	112,829,358	A	0.1055	0.8116	

<i>ADRB1</i>	MAP	Minor Allele	MAF	HWE ChiSq	rs1801252	rs1801253
rs1801252	115,794,026	G	0.1324	0.1641		0.97
rs1801253	115,795,046	G	0.2769	0.2126	0.107	

<i>AGT</i>	MAP	Minor Allele	MAF	HWE ChiSq	rs7079	rs2493132	rs3789671	rs2478545	rs2478544	rs2478543	rs2478539	rs11122577	rs3889728	rs3789679	rs5051
rs7079	228,904,954	A	0.3388	0.4336		0.963	0.985	0.849	0.781	0.896	0.901	0.827	0.872	0.922	0.854
rs2493132	228,910,180	C	0.2979	0.7545	0.201		0.198	0.935	0.901	0.979	0.972	0.921	0.939	0.97	0.932
rs3789671	228,910,423	T	0.1874	0.0323	0.114	0.021		0.984	1	0.984	0.982	0.947	0.227	0.973	0.976
rs2478545	228,910,744	T	0.219	0.7862	0.104	0.578	0.062		0.964	1	0.979	0.983	0.682	1	0.928
rs2478544	228,910,819	C	0.1762	0.9813	0.068	0.408	0.049	0.711		1	0.974	0.613	0.57	1	0.965
rs2478543	228,910,933	G	0.4174	0.1328	0.296	0.567	0.314	0.392	0.301		0.995	0.984	0.991	0.991	0.965
rs2478539	228,911,395	A	0.4156	0.0849	0.295	0.567	0.317	0.38	0.288	0.977		0.992	0.996	1	0.968
rs11122577	228,914,179	T	0.154	0.3281	0.064	0.368	0.039	0.637	0.324	0.247	0.253		1	1	0.911
rs3889728	228,915,454	A	0.2454	0.4154	0.127	0.687	0.036	0.401	0.215	0.447	0.458	0.567		0.941	0.948
rs3789679	228,916,317	A	0.0817	0.4314	0.037	0.194	0.358	0.025	0.019	0.119	0.122	0.016	0.233		0.976
rs5051	228,916,495	T	0.4136	0.0606	0.264	0.522	0.315	0.342	0.283	0.916	0.935	0.213	0.415	0.12	

<i>AMPD1</i>	MAP	Minor Allele	MAF	HWE ChiSq	rs6679869	rs761755	rs2268697	rs2268699	rs2336363	rs12038990	rs2010899	rs17602729
rs6679869	115,019,250	C	0.1307	0.8005		1	0.935	0.934	0.742	0.752	0.895	0.938
rs761755	115,023,957	C	0.1388	0.5656	0.025		0.99	0.99	0.027	0.03	0.709	0.81
rs2268697	115,029,016	A	0.3854	0.2401	0.082	0.099		1	0.958	0.985	0.737	0.989
rs2268699	115,029,419	C	0.3834	0.5755	0.082	0.099	0.996		0.958	0.985	0.734	0.989
rs2336363	115,034,091	A	0.1052	0.1502	0.451	0.001	0.069	0.07		0.976	0.969	1
rs12038990	115,036,155	T	0.0971	0.8038	0.421	0.001	0.066	0.066	0.855		1	1
rs2010899	115,036,533	G	0.4554	0.0891	0.101	0.096	0.287	0.283	0.092	0.09		1
rs17602729	115,037,580	A	0.1216	0.119	0.019	0.573	0.086	0.086	0.016	0.015	0.166	

<i>ANG</i>	MAP	Minor Allele	MAF	HWE ChiSq	rs11851044	rs8004382	rs4470055	rs1010458	rs17114699	rs12100929
rs11851044	20,224,335	C	0.123	0.3771		1	0.944	0.999	0.931	0.924
rs8004382	20,225,233	A	0.4813	0.0461	0.102		0.982	0.982	0.612	0.641
rs4470055	20,226,031	A	0.262	0.6716	0.065	0.417		0.987	0.565	0.514
rs1010458	20,226,312	T	0.1858	0.1141	0.025	0.141	0.334		0.994	0.993
rs17114699	20,228,750	T	0.1138	0.5289	0.039	0.101	0.199	0.063		0.978
rs12100929	20,228,881	G	0.1287	0.0149	0.042	0.122	0.176	0.067	0.885	

Table S5a continued

<i>ATPIA2</i>	MAP	Minor Allele	MAF	HWE											
				ChiSq	rs1016732	rs2854248	rs1023420	rs11265329	rs16831388	rs2295623	rs6695366	rs6686067	rs10797059	rs12410866	rs1046995
rs1016732	158,353,592	A	0.1579	0.209		0.991	0.992	0.98	0.961	1	0.978	0.925	0.935	1	0.965
rs2854248	158,360,551	A	0.3398	0.1484	0.355		0.985	0.917	0.973	0.99	0.939	0.938	0.937	1	0.322
rs1023420	158,360,967	C	0.1634	0.1445	0.946	0.364		0.991	0.96	1	0.979	0.971	0.968	1	0.967
rs11265329	158,362,070	T	0.3566	0.842	0.1	0.244	0.107		0.982	0.971	0.991	0.987	1	0.807	0.435
rs16831388	158,362,249	G	0.1618	0.1246	0.033	0.093	0.034	0.109		0.941	0.927	0.945	0.945	0.766	0.674
rs2295623	158,363,939	A	0.1067	0.8888	0.023	0.227	0.023	0.063	0.02		1	1	1	1	0.348
rs6695366	158,364,290	G	0.1663	0.0955	0.907	0.338	0.941	0.109	0.033	0.024		0.997	1	1	0.969
rs6686067	158,368,684	C	0.1236	0.2305	0.653	0.24	0.692	0.077	0.024	0.017	0.718		0.995	0.936	0.978
rs10797059	158,368,880	A	0.1243	0.2124	0.663	0.24	0.691	0.079	0.024	0.017	0.719	0.99		1	0.957
rs12410866	158,375,427	T	0.1176	0.1156	0.025	0.069	0.026	0.048	0.016	0.016	0.027	0.017	0.019		0.972
rs1046995	158,379,365	C	0.2182	0.4044	0.05	0.015	0.051	0.029	0.317	0.051	0.053	0.038	0.037	0.036	

<i>CKM</i>	MAP	Minor Allele	MAF	HWE				
				ChiSq	rs4884	rs7260463	rs432979	rs344816
rs4884	50,501,875	T	0.2899	0.8247		0.838	0.689	0.426
rs7260463	50,506,700	T	0.3425	0.3093	0.159		0.207	0.718
rs432979	50,513,531	G	0.0848	0.6938	0.037	0.007		0.797
rs344816	50,517,466	T	0.4738	0.8493	0.108	0.195	0.084	

<i>EDN1</i>	MAP	Minor Allele	MAF	HWE							
				ChiSq	rs5369	rs1794849	rs6912834	rs2071943	rs1629862	rs1630736	rs5370
rs5369	12,402,244	A	0.1163	0.7751		0.995	1	1	0.996	1	1
rs1794849	12,402,848	T	0.2648	0.6896	0.177		0.993	0.998	0.988	0.989	0.918
rs6912834	12,403,521	G	0.1138	0.2623	0.017	0.141		1	0.999	1	1
rs2071943	12,403,800	A	0.2121	0.1551	0.035	0.191	0.028		1	0.981	0.996
rs1629862	12,403,862	A	0.1115	0.6564	0.887	0.156	0.015	0.032		1	1
rs1630736	12,403,973	T	0.4623	0.0185	0.06	0.32	0.047	0.096	0.054		0.982
rs5370	12,404,241	T	0.2135	0.5089	0.037	0.169	0.029	0.951	0.033	0.101	

<i>GNB3</i>	MAP	Minor Allele	MAF	HWE		
				ChiSq	rs2301339	rs5446
rs2301339	6,824,885	A	0.305	0.0136		0.975
rs5446	6,826,723	T	0.2959	0.0083	0.518	

<i>H1F1A</i>	MAP	Minor Allele	MAF	HWE						
				ChiSq	rs12435848	rs10129270	rs4899056	rs1957757	rs2301113	rs11549465
rs12435848	61,246,644	A	0.2132	0.0206		0.999	0.94	0.999	0.968	0.981
rs10129270	61,251,707	A	0.0634	0.0649	0.307		0.993	0.994	0.996	0.921
rs4899056	61,259,284	T	0.0983	0.1318	0.675	0.399		0.997	0.965	1
rs1957757	61,266,701	T	0.0906	0.2217	0.655	0.464	0.857		0.997	1
rs2301113	61,276,301	C	0.2394	0.2001	0.788	0.256	0.596	0.551		1
rs11549465	61,277,310	T	0.1116	0.4923	0.089	0.019	0.055	0.048	0.076	

<i>NOS3</i>	MAP	Minor Allele	MAF	HWE						
				ChiSq	rs1799983	rs3918227	rs3918186	rs3918188	rs3918196	rs1808593
rs1799983	150,327,044	T	0.3106	0.0304		0.97	0.982	0.897	0.208	0.365
rs3918227	150,331,879	A	0.0926	0.0818	0.206		0.999	1	0.999	0.876
rs3918186	150,333,365	T	0.0803	0.3933	0.042	0.009		0.893	0.922	0.255
rs3918188	150,333,714	A	0.3669	0.5875	0.129	0.035	0.074		0.743	0.492
rs3918196	150,336,775	A	0.0656	0.8656	0.01	0.004	0.008	0.02		0.264
rs1808593	150,339,235	G	0.2313	0.3711	0.121	0.013	0.003	0.042	0.001	

Table S6. Significance level for associations between SNPs and baseline treadmill time and decrease in treadmill time over 20 years by ethnic group in participants of CARDIA.

Blacks			Whites		
	p value			p value	
Locus	Baseline treadmill time	Decrease in treadmill time	Locus	Baseline treadmill time	Decrease in treadmill time
<i>ADIPOR1</i>			<i>ADIPOR1</i>		
rs2275736	0.622	0.4184	rs1342387	0.9092	0.3457
rs1342387	0.5719	0.241	rs12733285	0.8838	0.4394
rs7518457	0.4605	0.7449	rs10494839	0.6614	0.4928
rs12733285	0.1109	0.6789	rs10753929	0.4056	0.0698
rs10494839	0.7422	0.9043	rs1539355	0.7642	0.6085
rs10753929	0.7556	0.7894			
rs1539355	0.5768	0.6122			
<i>AGT</i>			<i>AGT</i>		
rs7079	0.7147	0.8356	rs7079	0.0726	0.8687
rs11568045	0.0454	0.7383	rs2493132	0.4828	0.1966
rs2493129	0.9122	0.1019	rs3789671	0.3175	0.3397
rs2493131	0.4347	0.129	rs2478545	0.8869	0.4651
rs2493132	0.6859	0.553	rs2478544	0.4193	0.723
rs3789671	0.7516	0.7941	rs2478543	0.5821	0.0405#
rs2478545	0.2098	0.3998	rs2478539	0.8111	0.0322#
rs2478544	0.119	0.7024	rs11122577	0.4481	0.442
rs2478543	0.3972	0.8107	rs3889728	0.1154	0.1791
rs2478539	0.9202	0.9155	rs3789679	0.6918	0.9029
rs11122577	0.7876	0.287	rs5051	0.7816	0.0229#
rs3889728	0.6896	0.4371			
rs3789679	0.0678	0.9501	#SNPs in strong LD ($r>0.9$), thus results from only rs5051 used		
rs5051	0.416	0.6099			
<i>AMPD1</i>			<i>AMPD1</i>		
rs6679869	0.6598	0.6277	rs6679869	0.9804	0.1403
rs11102831	0.2287	0.6452	rs761755	0.701	0.467
rs2268697	0.6156	0.7114	rs2268697	0.986	0.3987
rs2268699	0.9625	0.6032	rs2268699	0.9631	0.2111
rs12354159	0.4641	0.5631	rs2336363	0.777	0.2685
rs2336363	0.4425	0.2314	rs12038990	0.7541	0.3189
rs12038990	0.6495	0.1784	rs2010899	0.5367	0.0323
rs2010899	0.9017	0.4016	rs17602729	0.8871	0.1208

Table S6 cont'd

Blacks			Whites		
	p value			p value	
Locus	Baseline treadmill time	Decrease in treadmill time	Locus	Baseline treadmill time	Decrease in treadmill time
<i>ATPIA2</i>			<i>ATPIA2</i>		
rs1016732	0.6862	0.0003	rs1016732	0.8545	0.4515
rs7532556	0.3405	0.1463	rs2854248	0.8167	0.5487
rs2854247	0.2303	0.4902	rs1023420	0.5666	0.6826
rs2854248	0.0715	0.0015	rs11265329	0.0541	0.0642
rs1023420	0.7522	0.4077	rs16831388	0.2006	0.859
rs1321655	0.6493	0.9312	rs2295623	0.172	0.6982
rs11265329	0.109	0.3092	rs6695366	0.842	0.5827
rs16831388	0.1343	0.8968	rs6686067	0.7353	0.2305
rs9660705	0.0148	0.2982	rs10797059	0.4938	0.2187
rs6695366	0.5446	0.7714	rs12410866	0.7042	0.5423
rs12072167	0.8772	0.5524	rs1046995	0.2478	0.5521
rs6686067	0.7559	0.9646			
rs10797059	0.726	0.9567			
rs1046995	0.1073	0.9182			
<i>TTN</i>			<i>TTN</i>		
rs10515939	0.8246	0.5799	rs3829748	0.3829	0.8491
rs3829748	0.8921	0.3014	rs12464787	0.9502	0.9622
rs11897366	0.2455	0.3291	rs2288571	0.7022	0.993
rs11887722	0.194	0.6563	rs4894030	0.2285	0.8978
rs6732060	0.0146	0.2029	rs1017323	0.9881	0.9348
rs10164753	0.2494	0.1636	rs12614435	0.9257	0.7137
rs12464787	0.5303	0.7512	rs6723526	0.6153	0.1812
rs2288571	0.1639	0.2743	rs2562845	0.7356	0.9247
rs4894030	0.2043	0.323	rs2562848	0.9466	0.6118
rs10497518	0.7664	0.9936	rs12998857	0.9959	0.7409
rs12614435	0.9242	0.9866	rs2303828	0.7825	0.8175
rs7590037	0.4513	0.1696	rs2042995	0.9167	0.8646
rs1469473	0.0963	0.327	rs2742345	0.8506	0.4423
rs2562845	0.9428	0.111	rs16866465	0.8296	0.5341
rs2562848	0.0732	0.8582	rs2562830	0.6425	0.1638
rs12998857	0.2504	0.0317	rs17076	0.4593	0.4608
rs12998857*	---	0.0388	rs2742347	0.7185	0.6729
rs4894034	0.955	0.3805	rs3754953	0.8078	0.762
rs2303828	0.7026	0.0676	rs7604033	0.7167	0.8406
rs2042995	0.0695	0.9769	rs2627038	0.2627	0.8824
rs2366753	0.0147	0.3149	rs2291313	0.9805	0.2495
rs2742345	0.4284	0.7581	rs4471922	0.8025	0.4657

Table S6 cont'd

Blacks			Whites		
	p value			p value	
Locus	Baseline treadmill time	Decrease in treadmill time	Locus	Baseline treadmill time	Decrease in treadmill time
<i>TTN cont'd</i>			<i>TTN cont'd</i>		
rs4893852	0.11	0.8904	rs2291306	0.3832	0.4985
rs10183361	0.0659	0.9436	rs10497520	0.849	0.2798
rs16866465	0.5149	0.3307	rs2054708	0.963	0.8551
rs2562831	0.1043	0.6716	rs3769863	0.8161	0.7658
rs2562830	0.1291	0.3246	rs6715901	0.5308	0.7306
rs16866473	0.0886	0.2099	rs10497521	0.9526	0.8759
rs17076	0.2493	0.9329	rs10184892	0.582	0.3139
rs2742347	0.6068	0.5377	rs3769858	0.9184	0.6374
rs16866479	0.4712	0.7281			
rs10803917	0.9252	0.3075			
rs3754953	0.2412	0.8359			
rs7604033	0.509	0.3427			
rs2627038	0.0222	0.9715			
rs2291313	0.3445	0.8222			
rs4471922	0.2751	0.6433			
rs1905520	0.5856	0.2295			
rs2291306	0.4479	0.5913			
rs3816781	0.4377	0.045			
rs719201	0.2482	0.3487			
rs10497520	0.1836	0.472			
rs2054708	0.698	0.8639			
rs3769863	0.7528	0.1681			
rs6715901	0.1018	0.5926			
rs16866534	0.311	0.1971			
rs10184892	0.9616	0.7796			
rs3754949	0.9678	0.7859			
rs3769858	0.17	0.4696			
<i>PPARGCIA</i>			<i>PPARGCIA</i>		
rs3821952	0.781	0.7872	rs768695	0.6247	0.0003
rs768695	0.2768	0.1917	rs7682765	0.207	0.1792
rs2932965	0.4587	0.1611	rs2932965	0.1016	0.0501
rs3774921	0.1665	0.4226	rs3774921	0.1179	0.0442
rs3736265	0.9163	0.78	rs3736265	0.2942	0.2843
rs3755862	0.7788	0.6678	rs3755862	0.212	0.6472
rs2970849	0.1388	0.6441	rs2970849	0.0834	0.6266
rs2932970	0.6085	0.1018	rs2932970	0.0636	0.6193
rs2932971	0.0198	0.6424	rs2932971	0.1774	0.7501

Table S6 cont'd

Blacks			Whites		
	p value			p value	
Locus	Baseline treadmill time	Decrease in treadmill time	Locus	Baseline treadmill time	Decrease in treadmill time
<i>PPARGCIA</i> cont'd			<i>PPARGCIA</i> cont'd		
rs2970851	0.2441	0.7319	rs2970851	0.291	0.8671
rs2932977	0.8668	0.1884	rs2932977	0.0046	0.1248
rs2290604	0.6606	0.8195	rs3774909	0.0244	0.3719
rs16874209	0.5419	0.7028	rs2290604	0.452	0.8305
rs4697046	0.6129	0.9443	rs4697046	0.0106	0.8683
rs6448226	0.5141	0.9605	rs6448226	0.0211	0.4522
rs6838835	0.2595	0.6447	rs7665116	0.0233	0.7285
rs7665116	0.664	0.3955	rs12374310	0.7346	0.3892
rs12374310	0.1958	0.0514	rs12374408	0.2559	0.4211
rs12374408	0.4664	0.041	rs10002477	0.9312	0.7191
rs10002477	0.1732	0.0946	rs10002521	0.3786	0.5576
rs10002521	0.8462	0.0225	rs7657517	0.156	0.0071
rs10002521*	---	0.0271	rs4452416	0.4575	0.0134
rs7657517	0.0363	0.8949	rs4235308	0.7732	0.0924
rs6828403	0.1542	0.5243	rs10212638	0.4292	0.9995
rs4452416	0.663	0.1924	rs7677000	0.2945	0.0067
rs4235308	0.4184	0.1134	rs13106578	0.8309	0.7263
rs10212638	0.47	0.2766	rs6838600	0.5578	0.7822
rs7677000	0.9704	0.4325	rs4361373	0.7996	0.1852
rs13106578	0.2636	0.14	rs16874271	0.1881	0.8038
rs6838600	0.2431	0.1587	rs17637318	0.6686	0.3501
rs4361373	0.885	0.4664	rs7674429	0.0996	0.6768
rs16874271	0.8013	0.7687	rs4469064	0.4483	0.9134
rs17637318	0.8932	0.5107	rs16874283	0.0992	0.5838
rs7674429	0.4117	0.1521	rs2970871	0.4277	0.2946
rs4469064	0.7911	0.9869			
rs16874283	0.9624	0.8775			
rs2970875	0.5271	0.6491			
rs2970871	0.1548	0.9372			
rs16874290	0.6949	0.3096			

Table S6 cont'd

Blacks			Whites		
	p value			p value	
Locus	Baseline treadmill time	Decrease in treadmill time	Locus	Baseline treadmill time	Decrease in treadmill time
<i>EDN1</i>			<i>EDN1</i>		
rs1800542	0.6344	0.3238	rs5369	0.2986	0.1083
rs9296343	0.8011	0.1125	rs1794849	0.3598	0.9048
rs5369	0.5468	0.9894	rs6912834	0.9504	0.7763
rs1794849	0.3948	0.1537	rs2071943	0.3916	0.5022
rs10478723	0.5427	0.9457	rs1629862	0.5121	0.1032
rs6912834	0.678	0.047	rs1630736	0.0089	0.5147
rs6912834*	---	0.039	rs5370	0.3205	0.6416
rs2071943	0.0843	0.8863			
rs1629862	0.3087	0.8707			
rs1630736	0.6429	0.2381			
rs5370	0.0772	0.9669			
<i>NOS3</i>			<i>NOS3</i>		
rs1799983	0.0015	0.2389	rs1799983	0.5988	0.2207
rs3918186	0.2437	0.2208	rs3918227	0.339	0.739
rs3918187	0.3682	0.4772	rs3918186	0.58	0.8486
rs3918188	0.5574	0.1798	rs3918188	0.9171	0.3889
rs3918196	0.0068	0.157	rs3918196	0.8483	0.8222
rs3918196*	0.0039	---	rs1808593	0.3241	0.0518
rs1808593	0.2884	0.1864			
rs3918211	0.3896	0.5633			
<i>ADRA2</i>			<i>ADRA2</i>		
rs11195419	0.491	0.9806	rs11195419	0.8287	0.6397
<i>ADRB1</i>			<i>ADRB1</i>		
rs1801252	0.1012	0.1352	rs1801252	0.3847	0.4358
rs1801253	0.3356	0.044	rs1801253	0.6528	0.7059

Table S6 cont'd

Blacks			Whites		
	p value			p value	
Locus	Baseline treadmill time	Decrease in treadmill time	Locus	Baseline treadmill time	Decrease in treadmill time
ACTN3			ACTN3		
rs544021	0.1702	0.7946	rs544021	0.3596	0.6045
rs1791690	0.5448	0.7805	rs1791690	0.3395	0.5091
rs12223171	0.8378	0.7338	rs677488	0.5717	0.7933
rs677488	0.4705	0.9676	rs509556	0.5827	0.7385
rs509556	0.1247	0.411	rs2275998	0.5264	0.9891
rs2275998	0.0275	0.3654	rs1815739	0.457	0.6409
rs1815739	0.1621	0.6174	rs618838	0.6835	0.7652
rs618838	0.0936	0.5627	rs540874	0.3531	0.5244
rs540874	0.062	0.5174			
rs11227532	0.9915	0.974			
GNB3			GNB3		
rs2301339	0.1335	0.0026	rs2301339	0.343	0.3327
rs5446	0.4389	0.4476	rs5446	0.2545	0.3959
ANG			ANG		
rs9322855	0.92	0.3667	rs11851044	0.714	0.0825
rs11851044	0.3713	0.9708	rs8004382	0.2041	0.4437
rs8004382	0.4391	0.7027	rs4470055	0.971	0.0037
rs4470055	0.5117	0.5948	rs1010458	0.9242	0.0245
rs1010458	0.7602	0.7536	rs17114699	0.3292	0.4201
rs12895066	0.7909	0.8327	rs12100929	0.6293	0.9893
rs17114699	0.9529	0.4362			
rs12100929	0.8481	0.5526			
rs11156631	0.9146	0.5255			
BDKRB2			BDKRB2		
rs1959053	0.8889	0.7394	rs1959053	0.311	0.7019
rs12433275	0.1723	0.4391	rs12433275	0.2149	0.9598
rs8016905	0.6339	0.1828	rs8016905	0.6548	0.7976
rs4900312	0.9861	0.1392	rs4900312	0.4681	0.1887
rs4905462	0.883	0.2243	rs4905462	0.5396	0.1624
rs945040	0.496	0.9167	rs945040	0.5124	0.0882
rs945039	0.9332	0.3438	rs945039	0.2659	0.8997
rs10132462	0.6387	0.9848	rs4905466	0.5026	0.2715
rs4905466	0.583	0.1711	rs11847625	0.3307	0.0873
rs11847625	0.441	0.6487	rs8013400	0.0738	0.2953
rs8013400	0.1171	0.2833	rs8012552	0.6804	0.1894

Table S6 cont'd

Blacks			Whites		
	p value			p value	
Locus	Baseline treadmill time	Decrease in treadmill time	Locus	Baseline treadmill time	Decrease in treadmill time
<i>BDKRB2</i> cont'd			<i>BDKRB2</i> cont'd		
rs8012552	0.3612	0.5599	rs4900318	0.7275	0.0636
rs4900318	0.5018	0.266	rs6575578	0.6554	0.8454
rs6575578	0.2667	0.8254	rs4905470	0.7145	0.3301
rs4905470	0.7557	0.7136	rs7149163	0.645	0.3479
rs7149163	0.4365	0.0524	rs4905474	0.9033	0.6943
rs4905474	0.9331	0.8463	rs10130005	0.7564	0.6658
rs10130005	0.24	0.2488	rs2069571	0.6909	0.3671
rs2069571	0.3293	0.5916	rs2069575	0.3047	0.311
rs2069575	0.5003	0.8716	rs1046248	0.256	0.5102
rs1046248	0.3941	0.3819	rs1800515	0.5383	0.7231
rs2242966	0.5735	0.845	rs2069591	0.7005	0.6803
<i>HIF1A</i>			<i>HIF1A</i>		
rs12435848	0.8435	0.9624	rs12435848	0.1356	0.8748
rs10129270	0.4279	0.8676	rs10129270	0.0999	0.8733
rs10138032	0.6205	0.3494	rs4899056	0.3625	0.8325
rs4899056	0.505	0.9573	rs1957757	0.0065	0.8895
rs1957755	0.0228	0.3041	rs2301113	0.3413	0.4923
rs17099141	0.1201	0.0506	rs11549465	0.6433	0.5233
rs1957757	0.5457	0.9718			
rs12885226	0.3554	0.8073			
rs966824	0.8969	0.5311			
rs2301113	0.811	0.7564			
<i>ACE</i>			<i>ACE</i>		
rs4303	0.8825	0.3009	rs4316	0.2682	0.3583
rs4316	0.0483	0.9546	rs4351	0.2933	0.457
rs4318	0.1704	0.6847	rs4461142	0.1983	0.4423
rs4351	0.0846	0.9864	rs4267385	0.2714	0.4279
rs4357	0.5191	0.7994	rs8066276	0.9137	0.7065
rs4461142	0.3506	0.7088	rs8066114	0.3889	0.7027
rs4267385	0.2661	0.7673	rs4968591	0.3582	0.7598
rs8066276	0.6732	0.4265	rs4611524	0.718	0.3825
rs8066114	0.2452	0.484			
rs4968591	0.5987	0.3649			
rs4611524	0.6391	0.3816			

Table S6 cont'd

Blacks			Whites		
	p value			p value	
Locus	Baseline treadmill time	Decrease in treadmill time	Locus	Baseline treadmill time	Decrease in treadmill time
<i>CKM</i>			<i>CKM</i>		
rs4884	0.6249	0.1565	rs4884	0.1193	0.5524
rs7260463	0.4837	0.5092	rs7260463	0.6239	0.1761
rs432979	0.3257	0.89	rs432979	0.9008	0.7729
rs344816	0.1126	0.3809	rs344816	0.0443	0.694

*genotypes grouped by minor allele carrier status for analyses

Table S7. Stepwise regression results for predictors of decrease in exercise test duration over 20 years in Blacks.

Variable	β	partial r^2	p-value
Baseline duration, min	-0.66	0.3051	<0.0001
Δ Weight, kg	-0.05	0.0874	<0.0001
Baseline BMI, kg/m ²	-0.08	0.0224	<0.0001
Sex (M/F)	-1.24	0.0282	<0.0001
Smoking at year 20 (N/Y)	-0.86	0.0244	<0.0001
Baseline Age, yrs	-0.06	0.009	<0.0001
Diabetes (N/Y)	-0.46	0.0039	0.0056

Model r^2 0.4804

β is the estimated regression coefficient (β coefficient) for each variable in the model.

Table S8. Description of gene loci where predictor SNPs from CARDIA are located, as well as description of the SNPs themselves.

Gene	Chr	Name	Proposed Mechanism of action*	Predictor SNP(s) in CARDIA†		SNP	
				MAP‡	Location	SNP notes	
<i>AGT</i>	1	angiotensinogen (serpin peptidase inhibitor, clade A, member 8) adenosine monophosphate deaminase	Blood pressure and Fat metabolism	rs5051	230,849,872	5'UTR	tags rs2148582 in blacks
<i>AMPD1</i>	1	1 (isoform M) angiogenin, ribonuclease, RNase A	Skeletal muscle function	rs2010899	115,235,010	intron 2 intron 1;	tags rs9724640, rs6667218, rs7516111
<i>ANG</i>	14	family, 5 ATPase, Na+/K+ transporting, alpha 2	Blood pressure	rs1010458	21,156,472	5' near	
<i>ATPIA2</i>	1	(+) polypeptide hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	Skeletal muscle function	rs9660705	160,096,810	intron 7	
<i>HIF1A</i>	14		Hypoxia	rs1957755 rs1957757	62,190,336 62,196,948	intron 4 intron 6	tags rs8005745, rs2301108, rs2246350, rs2284999, rs7143164 in whites
<i>NOS3</i>	7	nitric oxide synthase 3 (endothelial cell) peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	Blood pressure	rs3918196	150,705,842	intron 17	tags rs1799983 in blacks. SNP rs1799983 induces Asp298Glu and is assoc. with BP and fitness
<i>PPARGCIA</i>	4		Fat metabolism	rs2932971	23,818,884	intron 7	tags rs2932966, rs2932971, rs1472095, rs2932970, rs2970852, rs2932976, rs2970851, rs2932975 in whites tags rs2970852, rs2932975, rs2932966, rs2932971 in blacks
				rs7657517 rs3774909 rs4452416	23,857,451 23,828,708 23,863,873	intron 2 intron 5 intron 2	rs6850464, rs7677000, rs7657517, rs10002590 in whites tags rs2305681 in whites and blacks tags rs12640088, rs4452416, rs10213440 in whites

*See below for a more detailed description of proposed gene function(s).

†SNPs made up the multimarker constructs in the regression models, which were significantly associated with baseline duration in blacks and decrease in duration in whites.

‡MAP location based on MAP to Genome Build 37.1

Gene:	Function(s):
<i>ATPIA2</i>	THE Na ⁺ /K ⁺ -ATPase (NKA) is a transmembrane protein that sets and maintains the electrochemical gradient by extruding three Na ⁺ in exchange for two K ⁺ , which underlies numerous Na ⁺ -coupled transport processes. An important physiological role proposed for NKA is the regulation of blood pressure via modulation of vascular smooth muscle contractility
<i>NOS3</i>	Physical exercise stimulates <i>NOS3</i> activity and increases nitric oxide release through the augmentation of sheer stress and thereby is considered generally to lower blood pressure.
<i>PPARGCIA</i>	The protein encoded by the <i>PPARGCIA</i> gene coactivates multiple transcription factors involved in the regulation of oxidative stress, mitochondrial biogenesis, and lipid and glucose oxidation. Exposure to cold, exercise and fasting have all been shown to influence <i>PPARGCIA</i> transcription rates, raising the possibility that the gene interacts with energy balance behaviours to influence cardiovascular and metabolic health.
<i>AMPD1</i>	During intense exercise causing AMP accumulation, the enzyme adenosine monophosphate deaminase (AMPD) is activated in skeletal muscle. AMP accumulation also activates AMP-activated protein kinase, which enhances fat oxidation and glucose transport. By converting AMP to IMP, AMPD displaces the equilibrium of the myokinase reaction toward ATP production. The AMPD reaction is also the major contributor to the production of ammonia, a biochemical indicator of the intensity of exercise. Moreover, AMPD is the initial reaction of the purine nucleotide cycle (PNC), which plays a central role in the salvage of adenine nucleotides and in determining energy charge. Thus AMPD might be an important regulator of muscle energy metabolism during exercise. The skeletal muscle-specific isoform (M) of AMPD is encoded by the <i>AMPD1</i> gene, located on the short arm of chromosome 1. This isoform accounts for more than 95% of the total AMPD in muscle. It is mainly located in type II muscle fibers particularly at the neuromuscular junction, but also in capillaries.
<i>AGT</i>	<i>AGT</i> is mainly synthesized by the liver and secreted into the blood stream as a precursor of the vasoactive peptide AngII. <i>AGT</i> is also expressed in other tissues where it is known to play a local role, and white adipose tissue (WAT) is considered to be a major extrahepatic synthesis site of <i>AGT</i> . A role for <i>AGT</i> in adipose tissue development is suggested from several observations: <i>AGT</i> expression and secretion increase with differentiation and are significant in adipocytes compared with preadipocytes; WAT and isolated adipocytes contain the components of the RAS, which gives rise to AngII from <i>AGT</i> ; and AngII increases lipogenesis and triglyceride accumulation in 3T3-L1 preadipocytes and human adipocytes, consistent with the observation that rats treated with an oral AngII antagonist exhibit a decrease in adipocyte size
<i>ANG</i>	<i>ANG</i> is a very effective inducer of neovascularization and has a high degree of homology with the primary sequence of the RNase A superfamily. The development of vascular networks, angiogenesis, is a key factor that influences individual variability in peripheral resistance and blood pressure.
<i>HIF1A</i>	<i>HIF1A</i> is a transcription factor that regulates several genes in response to hypoxia, and these genes are involved in angiogenesis, erythropoiesis, and metabolism making <i>HIF1A</i> a candidate gene in establishing maximal oxygen consumption (VO ₂ max) before and after aerobic exercise training

Supplemental Figures:

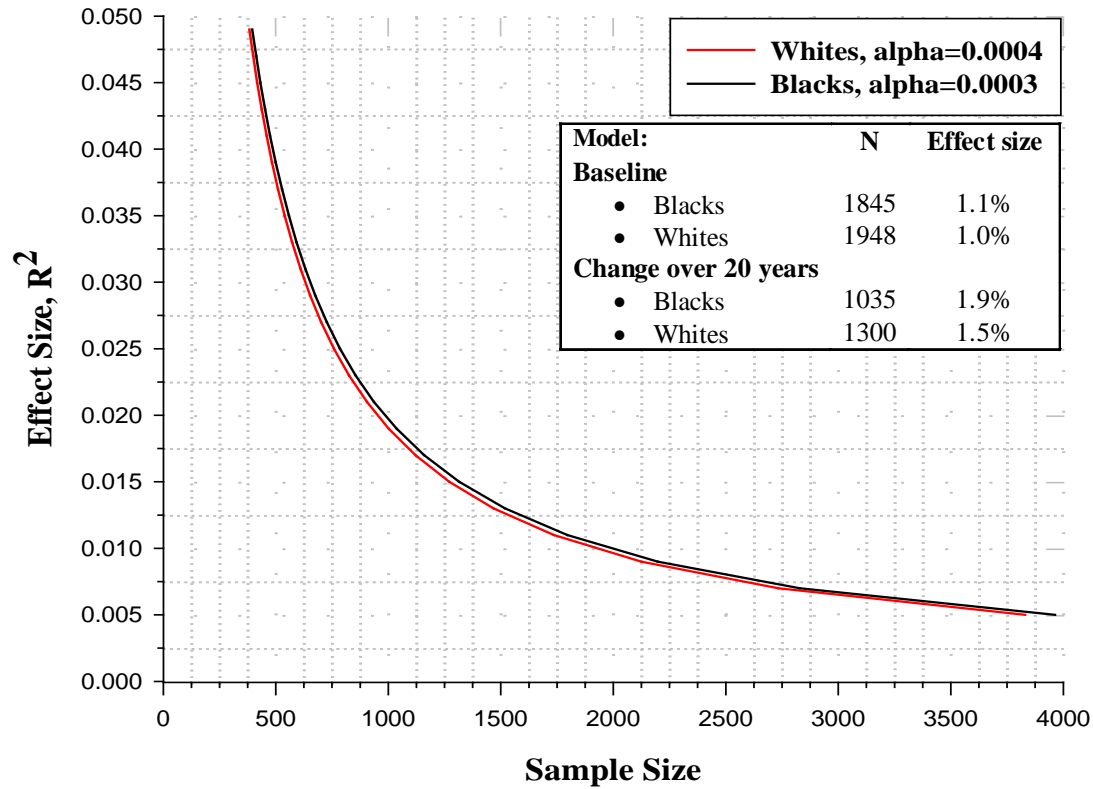


Figure S1. Relationship between genotype effect size and total sample size to obtain 80% power under additive genetic model.

We had 80% power to detect effect sizes of 1.0% in whites and 1.1% in blacks in the baseline models and of 1.5% in whites and 1.9% in blacks for the change over 20 years models, under an additive genetic model when alpha level is equal to the multiple testing corrected values of 0.0003 in blacks and 0.0004 in whites.