Supplementary Figure Legend:

Supplementary Figure 1: STRUCTURE analysis with 18 AIMs illustrating no significant population substructure in the Bt20 cohort. The values of K indicate the number of hypothetical ancestral populations. The clustering at K = 2 distinctly separated the African ((1) South African and (2) YRI) from the Non-African ((3) CHB and (4) CEU) populations. Higher order clustering (K=3 to K=4) was found to resolve the Bt20 cohort from all other populations, indicating that these 18 SNPs have the power to detect major differences in population structure. Population designations: (1) South African cohort; (2) HapMap YRI; (3) HapMap CHB; (4) HapMap CEU.

Supplementary Figure 2: LD across *LEP* in a South African black population. The top section of the figure illustrates the gene and represents the location of the SNPs in *LEP* that were genotyped in this study. The lower section of the figure shows the output of Haploview – each square (with D' values depicted within the box) represents a pair-wise LD relationship between two SNPs.

Supplementary Tables:

Supplementary table 1: Summary of SNP information genotyped in candidate genes

Gene	SNP	Genomic location *	Chrom	RefSNP Alleles **	Ancestral allele **	BMI assoc SNP	TagSNP	AIM
FTO	rs9939973	53800568	16	A/G	G	x		
	rs9940128	53800754		A/G	G	x		
	rs1421085	53800954		C/T	T	x		
	rs1121980	53809247		C/T	T	x		
	rs17817449	53813367		G/T	G	x		
	rs8050136	53816275		A/C	A	x		
	rs9939609	53820527		A/T	A	x		
LEP	rs1349419	127877213	7	A/G	A	x		
	rs12535708	127878098		A/C	C	x		
	rs11770725	127878267		C/T	T	x		
	rs12535747	127878335		A/C	C	x		
	rs2167270	127881349		A/G	G		x	
	rs2278815	127881851		A/G	G		x	
	rs2122627	127883323		C/T	C		x	
	rs4236625	127883695		A/T	T		x	
	rs12706832	127887139		A/G	A		x	
	rs10244329	127888689		A/T	T		x	
	rs7791621	127889696		A/C	A		x	
	rs7795794	127890151		A/G	C		x	
	rs10954173	127891440		A/G	G		x	
	rs3828942	127894305		A/G	G		x	
	rs17151919	127894592		A/G	G		x	
	rs17151922	127895216		G/T	G		x	
	rs6966536	127896059		A/G	A		x	
	rs10954174	127896536		A/G	G		x	

	rs11761556	127897069		A/C	A		x	
LEPR	rs1137100	66036441	1	A/G	A	x		
	rs1137101	66058513		A/G	A	x		
MC4R	rs17782313	57851097	18	C/T	T	x		
	rs12970134	57884750		A/G	G	x		
NPY2R	rs2880416	156124543	4	C/G	C		x	
	rs2342676	156124704		A/G	A	x		
	rs12649641	156125333		A/C	A		x	
	rs11099992	156125510		A/G	A		x	
	rs33977152	156128589		A/G	G		x	
	rs12507396	156129044		A/T	A		x	
	rs6857530	156129154		A/G	A		x	
	rs10461238	156132216		C/G	G	x		
	rs2342674	156135250		A/G	G		x	
	rs1047214	156135676		C/T	T	x		
	rs2880415	156136027		A/G	A		x	
POMC	rs6713532	25384833	2	C/T	C		x	
	rs7565427	25385638		A/G	G		x	
	rs7565877	25386064		A/G	A		x	
Ancestry informative markers	rs723854	192511012	1	C/G	G			x
	rs1876482	17362568	2	C/T	C			x
	rs952718	215888624	2	A/C	A			x
	rs1344870	21307401	3	A/C	A			x
	rs720096	179551071	4	C/G	C			x
	rs1363448	140783596	5	C/T	T			x
	rs217538	108483470	6	C/G	C			x
	rs65264	28545611	7	C/T	T			x
	rs679047	12883664	9	A/T	T			x
	rs2077559	36014850	9	C/T	T			x
	rs714857	15974389	11	C/T	T			x
	rs953386	110943692	13	A/G	A			x
	rs722869	97277005	14	C/G	C			x

	rs735612	34076642	15	G/T	G			x
	rs2089740	36310531	15	G/T	G			x
	rs1823718	74147244	15	C/T	T			x
	rs1858465	51142920	17	A/T	A			x
	rs2112527	9603751	19	A/G	G			x

* Chromosomal location of SNPs obtained from NCBI genome build 37.1 (hg19).

** RefSNP allele and ancestral alleles according to NCBI dbSNP Build 134.

Supplementary table 2: Allele- and genotype frequencies of AIMs in the South African cohort

				Frequency				
		RefSNP alleles*		Genotype			Allele	
SNP	**n**	**A**	**B**	**AA**	**AB**	**BB**	**A**	**B**
rs723854	974	C	G	0.05	0.31	0.65	0.20	0.80
rs1876482	983	T	C	0.00	0.00	1.00	0.00	1.00
rs952718	973	A	C	0.49	0.42	0.09	0.70	0.30
rs1344870	977	A	C	0.90	0.10	0.00	0.95	0.05
rs720096	970	C	G	0.64	0.32	0.05	0.79	0.21
rs1363448	981	T	C	1.00	0.00	0.00	1.00	0.00
rs217538	984	C	G	0.00	0.03	0.97	0.02	0.98
rs65264	982	T	C	0.64	0.33	0.03	0.80	0.20
rs679047	978	A	T	0.08	0.43	0.50	0.29	0.71
rs2077559	972	T	C	0.44	0.45	0.10	0.67	0.33
rs953386	988	A	G	0.21	0.50	0.30	0.46	0.54
rs722869	986	C	G	0.79	0.20	0.01	0.89	0.11
rs735612	979	T	G	0.21	0.51	0.28	0.47	0.53
rs2089740	970	T	G	0.11	0.46	0.42	0.35	0.65
rs1823718	972	T	C	0.62	0.35	0.03	0.79	0.21
rs1858465	972	A	T	0.02	0.26	0.72	0.15	0.85
rs2112527	984	A	G	0.43	0.47	0.11	0.66	0.34

* RefSNP allele and ancestral alleles according to NCBI dbSNP Build 134.

Supplementary table 3: Allele frequencies of AIMs in the South African cohort (SAB) and three HapMap populations

			Allele Frequencies							
	RefSNP alleles*		YRI		CEU		CHB		SAB	
SNP ID	**A**	**B**	**A**	**B**	**A**	**B**	**A**	**B**	**A**	**B**
rs723854	C	G	0.19	0.81	0.62	0.38	0.62	0.38	0.20	0.80
rs1876482	T	C	0.00	1.00	0.03	0.98	0.70	0.30	0.00	1.00
rs952718	A	C	0.74	0.26	0.11	0.89	0.04	0.96	0.70	0.30
rs1344870	A	C	0.95	0.05	0.98	0.02	0.73	0.27	0.95	0.05
rs720096	C	G	0.04	0.96	0.53	0.48	0.01	0.99	0.79	0.21
rs1363448	T	C	0.86	0.14	0.42	0.58	0.35	0.65	1.00	0.00
rs217538	C	G	0.97	0.03	0.68	0.32	0.41	0.59	0.02	0.98
rs65264	T	C	0.87	0.13	0.67	0.33	0.42	0.58	0.80	0.20
rs679047	A	T	0.22	0.78	0.08	0.92	0.09	0.91	0.29	0.71
rs2077559	T	C	0.77	0.23	0.88	0.12	0.73	0.27	0.67	0.33
rs953386	A	G	0.46	0.54	0.15	0.85	0.09	0.91	0.46	0.54
rs722869	C	G	0.93	0.07	0.88	0.12	0.14	0.86	0.89	0.11
rs735612	T	G	0.42	0.58	0.61	0.39	0.98	0.02	0.47	0.53
rs2089740	T	G	0.29	0.71	0.06	0.94	0.32	0.69	0.35	0.65
rs1823718	T	C	0.77	0.23	0.54	0.46	0.99	0.01	0.79	0.21
rs1858465	A	T	0.90	0.10	0.18	0.82	0.34	0.66	0.15	0.85
rs2112527	A	G	0.55	0.45	0.93	0.07	0.97	0.03	0.66	0.34

* RefSNP allele and ancestral alleles according to NCBI dbSNP Build 134

YRI – HapMap Yoruba from Nigeria; CEU – HapMap Utah residents with European ancestry ; CHB – HapMap Han Chinese population; SAB – South African black population (Bt20).