

SUPPLEMENTARY DATA

Supplementary Table 1. Meta-analysis results for SNPs associated with IL-1RA in the discovery cohorts.

MarkerName	Chr	Position (HG18)	Gene	Minor (Coded) Allele	Major Allele	Mean MAF	Discovery			
							N	Effect	SE	P
rs4251961	2	113590938	<i>IL1RN</i>	C	T	0.32	9092	-0.078	0.006	2.19E-34
rs6759676	2	113552819	closest <i>IL1F10</i>	C	T	0.44	9131	0.063	0.006	6.12E-27
rs10186133	2	113553415	closest <i>IL1F10</i>	G	T	0.42	9126	0.060	0.006	4.52E-24
rs315949	2	113609245	closest <i>IL1RN</i>	A	G	0.37	5306	-0.070	0.008	2.80E-19
rs6731551	2	113561024	closest <i>IL1F10</i>	C	T	0.47	9133	-0.052	0.006	1.20E-18
rs10199363	2	113557262	closest <i>IL1F10</i>	G	A	0.18	9134	0.065	0.008	1.31E-16
rs315921	2	113588522	closest <i>IL1RN</i>	A	G	0.17	9096	0.065	0.008	4.89E-16
rs6761276	2	113548783	<i>IL1F10</i>	T	C	0.43	5310	0.061	0.008	1.13E-15
rs315920	2	113589489	closest <i>IL1RN</i>	T	C	0.19	9095	0.059	0.008	1.26E-14
rs10176274	2	113557046	closest <i>IL1F10</i>	G	C	0.34	3209	-0.085	0.012	6.37E-13
rs10188292	2	113556914	closest <i>IL1F10</i>	T	A	0.34	3209	-0.085	0.012	6.37E-13
rs6743171	2	113556529	closest <i>IL1F10</i>	C	G	0.34	3209	-0.085	0.012	6.37E-13
rs13398728	2	113558977	closest <i>IL1F10</i>	C	T	0.34	3209	-0.085	0.012	6.37E-13
rs13410964	2	113559754	closest <i>IL1F10</i>	A	G	0.34	3209	-0.085	0.012	6.37E-13
rs6722922	2	113557986	closest <i>IL1F10</i>	T	C	0.34	3209	-0.085	0.012	6.37E-13
rs6750559	2	113558003	closest <i>IL1F10</i>	A	G	0.34	3209	-0.085	0.012	6.37E-13
rs4496335	2	113560946	closest <i>IL1F10</i>	T	C	0.34	3209	-0.085	0.012	6.37E-13
rs6741180	2	113560855	closest <i>IL1F10</i>	A	G	0.34	3209	-0.085	0.012	6.37E-13
rs12328766	2	113563209	closest <i>IL1F10</i>	G	A	0.34	3209	-0.085	0.012	6.38E-13
rs12329129	2	113563478	closest <i>IL1F10</i>	A	G	0.34	3209	-0.085	0.012	6.38E-13
rs12328368	2	113563615	closest <i>IL1F10</i>	G	C	0.34	3209	-0.085	0.012	6.38E-13
rs6730516	2	113565432	closest <i>IL1RN</i>	T	C	0.34	3209	-0.085	0.012	6.44E-13
rs1446510	2	113567988	closest <i>IL1RN</i>	T	C	0.34	3209	-0.085	0.012	6.47E-13
rs1446509	2	113567630	closest <i>IL1RN</i>	T	A	0.34	3209	-0.085	0.012	6.47E-13
rs6738239	2	113567263	closest <i>IL1RN</i>	A	C	0.34	3209	-0.085	0.012	6.47E-13
rs13409360	2	113554573	closest <i>IL1F10</i>	A	G	0.34	3209	-0.084	0.012	7.78E-13
rs6734238	2	113557501	closest <i>IL1F10</i>	G	A	0.34	3209	-0.084	0.012	1.06E-12

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rs6743376	2	113548804	<i>IL1F10</i>	C	A	0.37	5303	0.056	0.008	2.28E-12
rs315943	2	113610809	closest <i>IL1RN</i>	G	A	0.34	3209	-0.082	0.012	2.46E-12
rs13409371	2	113554616	closest <i>IL1F10</i>	A	G	0.40	3209	-0.083	0.012	3.83E-12
rs4145013	2	113547159	<i>IL1F10</i>	G	A	0.35	5306	0.055	0.008	5.91E-12
rs7574159	2	113576232	<i>IL1RN</i>	A	G	0.33	3209	-0.082	0.012	1.24E-11
rs17207494	2	113580481	<i>IL1RN</i>	C	A	0.33	3209	-0.082	0.012	1.34E-11
rs10171849	2	113582305	<i>IL1RN</i>	C	A	0.33	3209	-0.082	0.012	1.35E-11
rs13382561	2	113580007	<i>IL1RN</i>	G	A	0.33	3209	-0.082	0.012	1.37E-11
rs13424580	2	113569035	closest <i>IL1RN</i>	A	G	0.33	3209	-0.081	0.012	1.37E-11
rs6746979	2	113570591	closest <i>IL1RN</i>	A	T	0.33	3209	-0.081	0.012	1.38E-11
rs7574427	2	113576509	<i>IL1RN</i>	A	G	0.33	3209	-0.082	0.012	1.39E-11
rs11885498	2	113616648	closest <i>IL1RN</i>	G	A	0.36	3209	-0.078	0.012	2.53E-11
rs2902452	2	113611987	closest <i>IL1RN</i>	A	C	0.36	3209	-0.078	0.012	2.80E-11
rs6754298	2	113612684	closest <i>IL1RN</i>	A	T	0.36	3209	-0.078	0.012	2.85E-11
rs1374281	2	113615260	closest <i>IL1RN</i>	G	C	0.36	3209	-0.078	0.012	2.86E-11
rs895496	2	113615496	closest <i>IL1RN</i>	T	C	0.36	3209	-0.078	0.012	2.93E-11
rs1530551	2	113534037	<i>IL36RN</i>	T	C	0.38	5307	0.050	0.008	1.08E-10
rs380092	2	113605371	<i>IL1RN</i>	T	A	0.36	5308	0.052	0.008	1.13E-10
rs2472188	2	113537285	<i>IL36RN</i>	C	G	0.38	5304	0.049	0.008	1.89E-10
rs11123167	2	113623340	closest <i>IL1RN</i>	C	G	0.36	3209	-0.074	0.012	2.82E-10
rs3827763	2	113547760	<i>IL1F10</i>	A	G	0.30	5310	0.052	0.008	6.99E-10
rs1867828	2	113485091	closest <i>IL1F10</i>	A	G	0.26	5310	-0.052	0.009	2.27E-09
rs3811050	2	113546644	<i>IL1F10</i>	T	C	0.18	5310	-0.062	0.011	3.22E-09
rs315952	2	113606775	<i>IL1RN</i>	C	T	0.35	5300	0.047	0.008	4.62E-09
rs11678375	2	113552162	closest <i>IL1F10</i>	T	C	0.43	3209	0.060	0.011	2.58E-08
rs13386602	2	113551291	closest <i>IL1F10</i>	A	C	0.43	3209	0.060	0.011	2.61E-08
rs12469822	2	113547034	<i>IL1F10</i>	G	A	0.44	3209	0.060	0.011	3.22E-08

Variants that passed the discovery *P* value threshold of 5.0×10^{-8} are shown. The two most significantly associated independent SNPs from the discovery meta-analysis (marked in bold) were then taken forward for replication.

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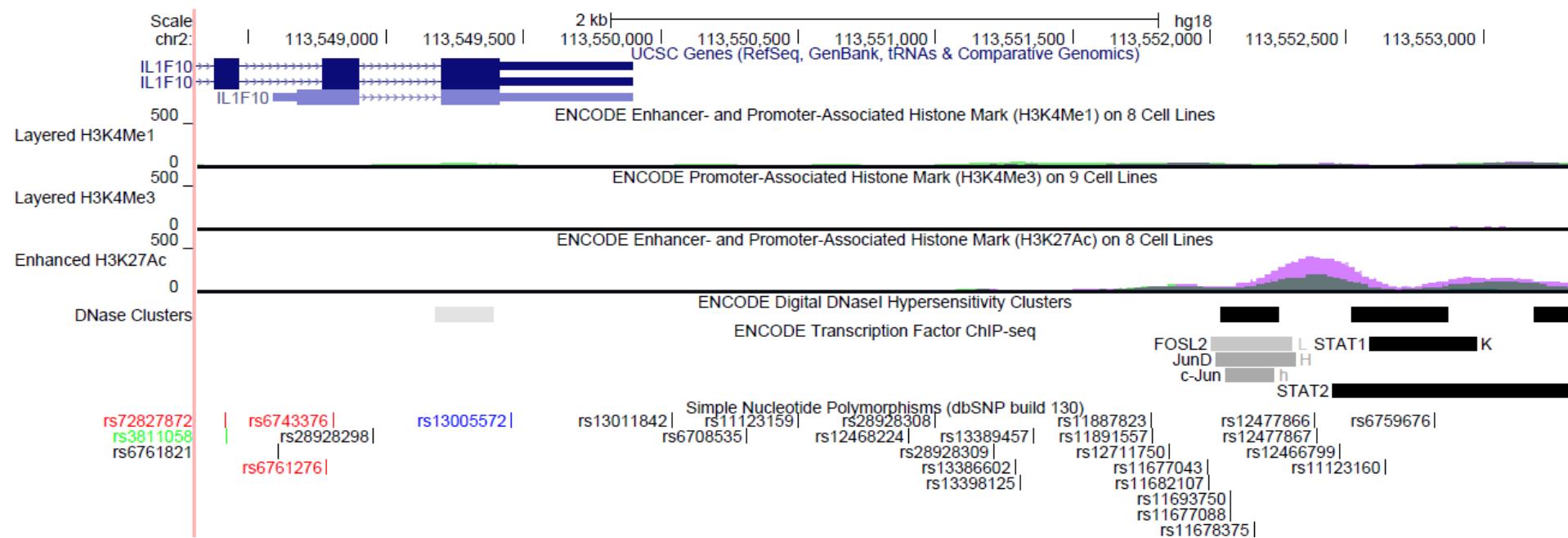
Supplementary Table 2. Replication and combined meta-analysis results for the SNPs independently associated with circulating IL-1RA levels with YFS included in analyses.

Marker name	Chr	Position (HG18)	Gene	Minor (coded) allele	Major allele	Mean MAF	Replication				I^2 (%)	Meta-analysis model
							N	Effect	SE	P		
rs4251961	2	113590938	<i>IL1RN</i>	C	T	0.32	6802	-0.064	0.027	0.016	90.74	RE
rs6759676	2	113552819	closest <i>IL1F10</i>	C	T	0.44	6802	0.073	0.034	0.031	94.94	RE

Marker name	Chr	Position (HG18)	Gene	Minor (coded) allele	Major allele	Mean MAF	Combined				I^2 (%)	Meta-analysis model
							N	Effect	SE	P		
rs4251961	2	113590938	<i>IL1RN</i>	C	T	0.32	15894	-0.077	0.012	9.46E-11	79.72	RE
rs6759676	2	113552819	closest <i>IL1F10</i>	C	T	0.44	15933	0.068	0.013	9.14E-08	84.69	RE

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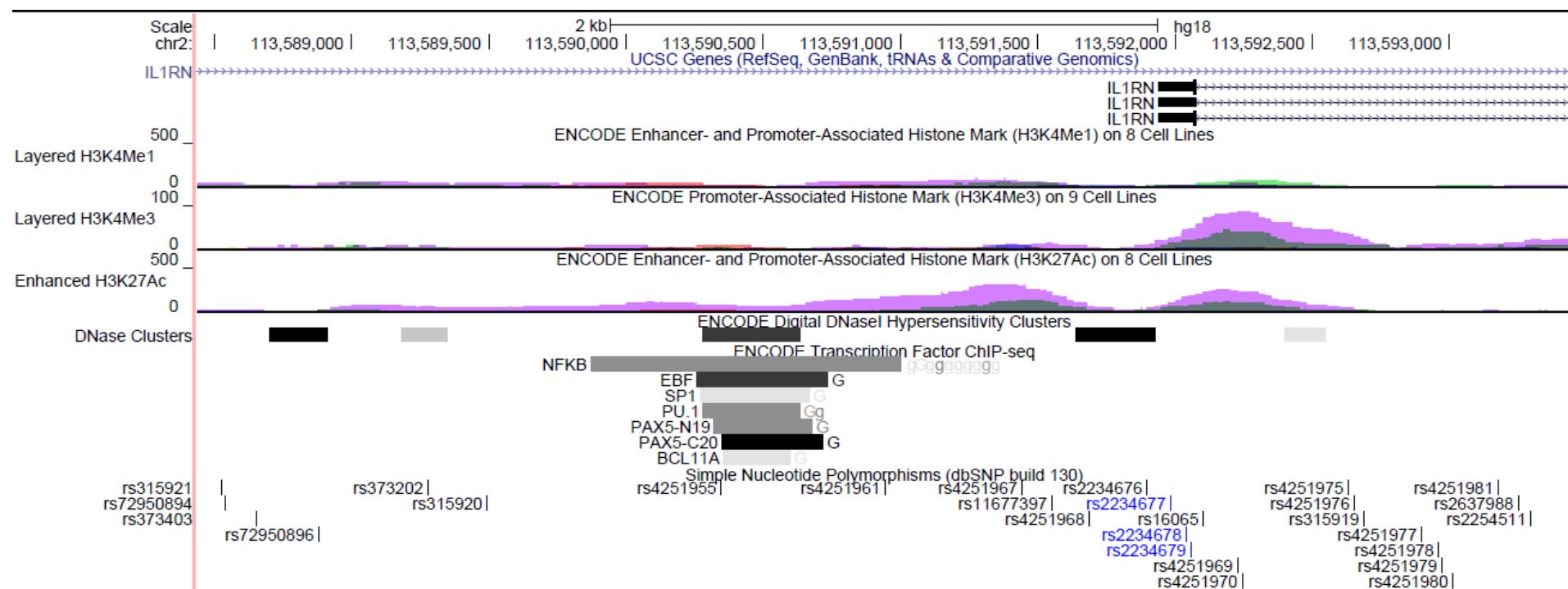
Supplementary Figure 1. In silico functional analysis for rs6759676.



A snapshot of the UCSC Genome Browser shows that rs6759676 falls within a region enriched for H3K27Ac histone acetylation (often found near active regulatory elements) in epidermal keratinocytes cells (pink peak) and human mammary epithelial cells (grey peak); within a DNase hypersensitive region (characteristic of open chromatin regions) in multiple cell lines; and also within STAT transcription factor binding sites.

SUPPLEMENTARY DATA

Supplementary Figure 2. In silico functional analysis for rs4251961.

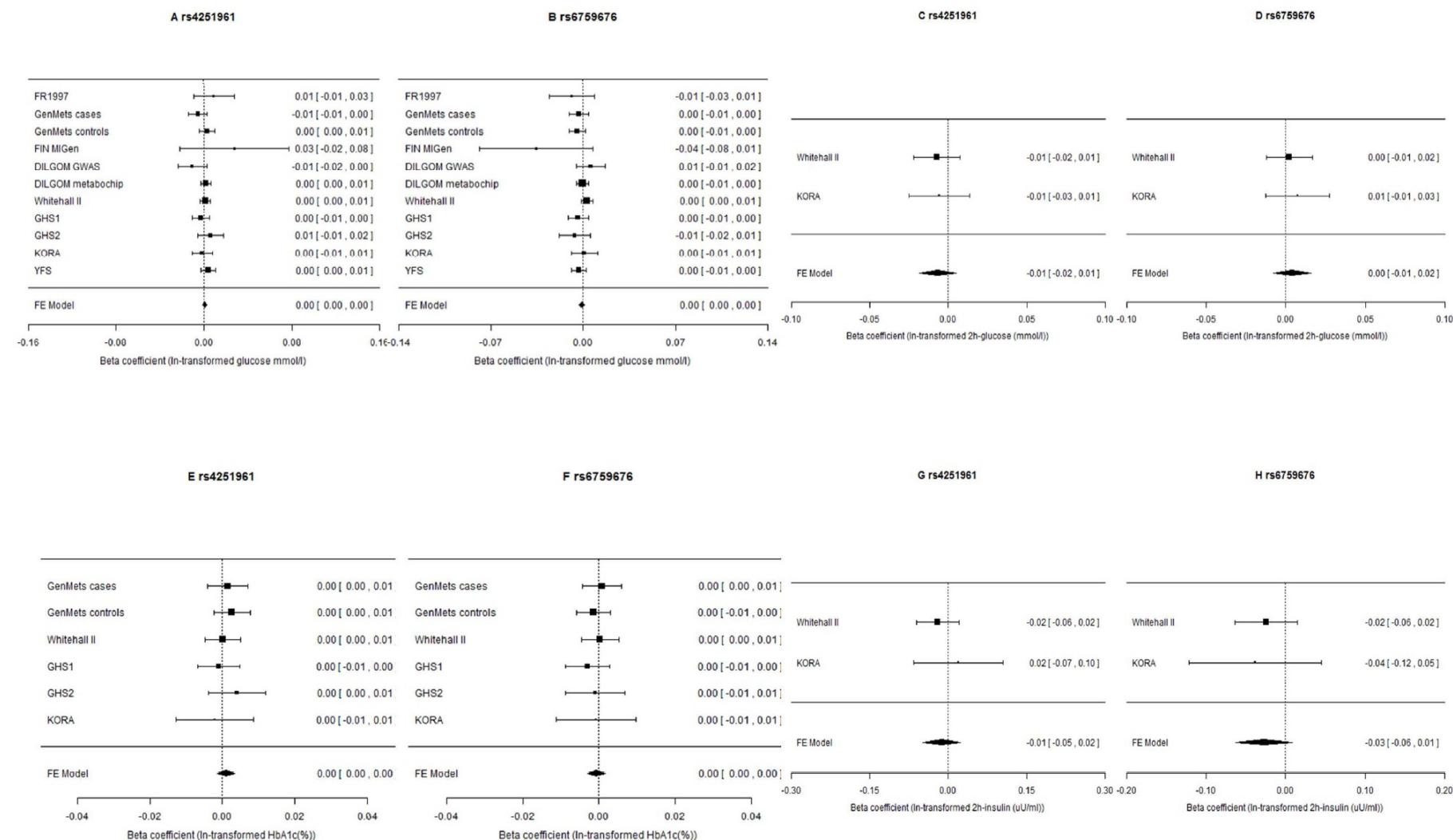


A snapshot of the UCSC Genome Browser shows that rs4251961 falls within a region enriched for the H3K27Ac histone acetylation mark (often found near active regulatory elements) in epidermal keratinocytes cells (pink peak) and human mammary epithelial cells (grey peak) (Supplementary Figure 2), upstream of the IL1RN gene. It is very close to regions enriched for transcription factor binding and DNase hypersensitivity, indicative of open chromatin.

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Supplementary Figure 3. Association of rs4251961 and rs6759676 with circulating fasting glucose, 2-hr glucose, HbA1c and 2-hr insulin in individual studies included in the discovery and replication analysis.

A, B: fasting glucose; C, D: 2-hr glucose; E, F: HbA1c; G, H: 2-hr insulin.
All analyses were adjusted for age, sex, BMI, waist-to-hip ratio and smoking.



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Supplementary Figure 4. Association of rs4251961 and rs6759676 with circulating IL-1RA levels in individual discovery and replication studies while YFS is included in the replication analysis.

All analyses were adjusted for age, sex, BMI, waist-to-hip ratio and smoking.

