SUPPLEMENTAL MATERIAL

Supplementary Table 1. Coefficient of variation of the studied 4 serum biomarkers

Serum Biomarkers, CV*	**African Americans**	**Whites**
Fractalkine (pg/mL)	0.36	0.39
P-selectin (ng/mL)	0.33	0.34
Platelet factor 4 (ng/mL)	0.45	0.44
TNFα (pg/mL)	1.13	1.08

* Coefficient of variation is defined as the ratio of the standard deviation to the mean

Supplementary Table 2. Association of rs1429637 and rs1435520 SNPs with serum PF4 levels under different genetic models

				African Americans					Whites					Combined				
				PF4 levels		95% CI			PF4 levels		95% CI			PF4 levels		95% CI		
SNP	Position	Model	Genotypes	Mean	SE	Lower	Upper	P	Mean	SE	Lower	Upper	P	Mean	SE	Lower	Upper	P
rs1429637	75,052,310	Dominant																
			CC	9.72	0.01	-	-	0.06	9.82	0.02	-	-	0.011	9.76	0.01	-	-	0.0016
			CT-TT	9.62	0.04	-0.2	0		9.68	0.04	-0.22	-0.03		9.66	0.03	-0.18	-0.04	
		Recessive																
			CC-CT	9.71	0.01	-	-	0.0039	9.8	0.02	-	-	0.613	9.75	0.01			0.02
			TT	8.83	0.41	-1.44	-0.28		9.67	0.26	-0.76	0.45		9.25	0.32	-0.91	-0.08	
rs1435520	75,064,281	Dominant																
			AA	9.71	0.01	-	-	0.045	9.82	0.02	-	-	0.0084	9.75	0.01	-	-	0.0009
			AC-CC	9.58	0.07	-0.28	0		9.67	0.05	-0.24	-0.04		9.64	0.04	-0.22	-0.06	
		Recessive																
			AA-AC	9.71	0.01	-	-	0.0023	9.8	0.02	-	-	0.613	9.75	0.01	-	-	0.03
			CC	8.41	0	-2.1	-0.46		9.67	0.26	-0.76	0.45		9.25	0.45	-1	-0.04	

Supplementary Table 3. Conditional analysis of rs183028 in the PF4 region

			African Americans			**Whites**			**Combined**
SNPs	**Position**	**Coded/ Noncoded Allele**	**Coded Allele Freq**	**Rsq***	**rs183028 Conditional P-value¶**	**Coded Allele Freq**	**Rsq***	**rs183028 Conditional P-value¶**	**rs183028 Conditional P-value¶**
rs1429637	**75,052,310**	**T/C**	**0.036**	**1**	**0.034**	**0.060**	**1**	**0.02**	**0.002**
rs351997	75,052,923	T/C	0.087	1	0.622	0.090	1	0.57	0.82
rs6813952	75,063,296	C/A	0.073	1	0.109	0.059	1	0.03	0.07
rs1435520	**75,064,281**	**C/A**	**0.019**	**1**	**0.025**	**0.053**	**1**	**0.02**	**0.001**
rs352004	75,065,434	T/C	0.253	1	0.918	0.008	1	0.10	0.93
rs352007	75,066,156	G/C	0.440	0.97	0.781	0.092	0.95	0.99	0.44
rs394408	75,068,216	T/C	0.407	0.98	0.220	0.091	0.98	0.72	0.32
rs447206	75,068,787	A/G	0.060	0.99	0.301	0.088	0.99	0.67	0.17
rs168449	75,069,487	T/C	0.407	0.98	0.690	0.091	0.99	0.81	0.72
rs191601	75,069,569	C/T	0.406	0.98	0.690	0.091	0.99	0.75	0.34
rs193263	75,069,687	T/A	0.406	0.98	0.690	0.091	0.99	0.76	0.34
rs442155	75,070,096	G/A	0.060	1	0.301	0.088	1	0.70	0.17
rs377579	75,070,524	T/C	0.412	0.99	0.800	0.091	0.99	0.99	0.69
rs352009	75,070,557	G/A	0.406	0.98	0.820	0.091	0.99	0.72	0.41
rs183028	**75,070,782**	**A/G**	**0.412**	**1**	**-**	**0.091**	**1**	**-**	**-**
rs352010	75,074,095	A/G	0.409	0.97	0.800	0.094	0.96	0.97	0.73
rs552582	75,074,722	A/G	0.497	0.95	0.254	0.100	0.96	0.76	0.58
rs2457996	75,075,399	C/T	0.409	0.97	0.119	0.091	0.99	0.96	0.78
rs187080	75,075,527	T/C	0.416	0.97	0.302	0.093	0.98	0.39	0.73
rs426901	75,076,379	G/A	0.455	0.96	0.260	0.098	0.98	0.28	0.11
rs409336	75,076,522	C/A	0.538	1	0.167	0.104	1	0.53	0.33
rs416046	75,076,546	A/G	0.053	0.84	0.357	0.072	0.81	0.59	0.16
rs440676	75,076,834	C/A	0.424	0.96	0.290	0.095	0.98	0.35	0.15
rs450373	75,076,915	G/A	0.424	0.96	0.290	0.095	0.98	0.35	0.14
rs2564594	75,077,164	T/A	0.424	0.96	0.290	0.095	0.98	0.34	0.14
rs420389	75,077,352	G/C	0.424	0.96	0.290	0.095	0.98	0.34	0.13
rs2437285	75,079,102	T/C	0.412	1	0.336	0.102	1	0.44	0.61
rs352047	75,080,954	C/G	0.427	0.98	0.060	0.098	0.98	0.10	0.10
rs425535	75,082,861	T/C	0.416	0.98	0.070	0.099	0.99	0.10	0.10
rs352046	75,083,414	G/C	0.425	0.99	0.070	0.100	0.99	0.10	0.10

Positions are in reference to NCBI build 36.3

*Squared correlation between imputed and true genotypes. Directly genotyped SNPs are marked as 1

¶ Uncorrected conditional P-values

Significant SNP and the P-values for their association are highlighted in bold

Supplementary Table 4. Association analysis of *PF4* variants with serum TNFα levels

			African Americans							**Caucasians**					**Combined**			
SNP	**Position**	**Coded/ Noncoded Allele**	**Coded Allele Freq**	**Rsq***	**β†**	**SE**	**P**	**Pc**	**rs8180167 Conditional P¶**	**Coded Allele Freq**	**Rsq***	**β†**	**SE**	**P**	**β‡**	**SE**	**P**	**Pc**
rs10017182	75,050,352	G/A	0.799	0.940	0.015	0.007	0.025	0.18	0.83	0.183	0.966	0.003	0.006	0.61	0.010	0.005	0.03	0.18
rs8180167	**75,052,237**	**A/T**	**0.752**	**0.987**	**0.016**	**0.006**	**0.008**	**0.048**	**-**	**0.180**	**0.982**	**0.003**	**0.006**	**0.66**	**0.011**	**0.004**	**0.01**	**0.07**
rs1429637	75,052,310	C/T	0.964	1	-0.010	0.017	0.531	0.99	0.64	0.940	1	-0.015	0.008	0.14	-0.013	0.008	0.15	0.55
rs1595008	75,053,322	C/A	0.798	0.949	0.015	0.007	0.024	0.19	0.87	0.179	0.962	0.003	0.006	0.61	0.010	0.005	0.03	0.19
rs1595009	75,053,520	C/T	0.812	0.878	0.016	0.007	0.025	0.19	0.86	0.230	0.717	0.003	0.006	0.64	0.010	0.005	0.04	0.19
rs2175498	75,054,231	A/G	0.800	0.954	0.015	0.007	0.025	0.19	0.86	0.180	0.975	0.003	0.006	0.63	0.010	0.005	0.03	0.19
rs4694659	75,056,016	C/A	0.800	0.954	0.015	0.007	0.025	0.19	0.86	0.179	0.973	0.003	0.006	0.65	0.010	0.005	0.04	0.19
rs4694180	75,056,266	T/C	0.800	0.954	0.015	0.007	0.025	0.19	0.86	0.179	0.973	0.003	0.006	0.65	0.010	0.005	0.04	0.19
rs6446973	75,057,336	A/T	0.800	0.954	0.015	0.007	0.026	0.19	0.87	0.179	0.973	0.003	0.006	0.65	0.009	0.005	0.04	0.19
rs6820253	75,057,935	C/T	0.582	0.974	-0.011	0.005	0.044	0.29	0.37	0.901	0.982	0.006	0.008	0.41	-0.007	0.004	0.13	0.57
rs4694660	75,059,309	T/A	0.800	0.955	0.015	0.007	0.026	0.19	0.87	0.179	0.973	0.003	0.006	0.66	0.009	0.005	0.04	0.20
rs4694661	75,059,477	A/T	0.800	0.955	0.015	0.007	0.026	0.19	0.87	0.179	0.973	0.003	0.006	0.66	0.009	0.005	0.04	0.20
rs1594230	75,060,249	C/T	0.582	0.976	-0.011	0.005	0.043	0.29	0.37	0.901	0.985	0.006	0.008	0.41	-0.007	0.004	0.13	0.57
rs1594229	75,060,428	C/G	0.582	0.977	-0.011	0.005	0.043	0.29	0.37	0.901	0.985	0.006	0.008	0.41	-0.007	0.004	0.13	0.57
rs6810940	75,061,053	C/T	0.801	0.957	0.015	0.007	0.026	0.19	0.88	0.178	0.974	0.003	0.006	0.67	0.009	0.005	0.04	0.20
rs1836663	75,061,436	T/C	0.582	0.979	-0.011	0.005	0.042	0.25	0.36	0.901	0.987	0.006	0.008	0.41	-0.007	0.004	0.13	0.51
rs2472655	75,061,882	T/C	0.582	0.979	-0.011	0.005	0.042	0.25	0.36	0.901	0.988	0.006	0.008	0.41	-0.007	0.004	0.13	0.51
rs1156554	75,063,996	C/T	0.584	0.970	-0.012	0.005	0.032	0.20	0.34	0.901	0.996	0.006	0.008	0.40	-0.007	0.005	0.10	0.44
rs1156553	75,064,018	T/G	0.591	0.995	-0.012	0.005	0.033	0.20	0.33	0.901	0.997	0.006	0.008	0.40	-0.007	0.005	0.11	0.44
rs1435520	75,064,281	A/C	0.981	1	-0.004	0.033	0.866	0.99	0.96	0.947	1	-0.017	0.008	0.10	-0.014	0.010	0.19	0.63
rs168449	75,069,487	T/C	0.407	0.980	0.001	0.006	0.816	0.99	0.55	0.091	0.988	-0.015	0.007	0.08	-0.003	0.005	0.51	0.99
rs183028	75,070,782	A/G	0.412	1	0.002	0.006	0.780	0.99	0.60	0.091	1	-0.015	0.007	0.08	-0.003	0.005	0.54	0.99
rs2472649	75,076,572	A/G	0.819	1	0.012	0.006	0.064	0.31	0.78	0.165	1	-0.008	0.006	0.21	0.004	0.005	0.40	0.92
rs12512838	75,078,267	C/T	0.817	0.928	0.012	0.007	0.078	0.36	0.70	0.201	0.772	-0.008	0.006	0.21	0.004	0.005	0.44	0.94

Positions are in reference to NCBI build 36.3

*Squared correlation between imputed and true genotypes. Directly genotyped SNPs are marked as 1

†Effect size of the coded allele based on the multivariate linear regression adjusted for age and sex (using allele dosages)

‡Effect size of the coded allele based on the multivariate linear regression adjusted for age, sex and race (using allele dosages)

Corrected P-values (Pc) were generated by gene-wide multiple correction (maximum likelihood genotypes) using 5000 permutations

¶ Uncorrected conditional P-values

Most significant SNP and the P-values for their association are highlighted in bold

Supplementary Table 5. Association of *CX3CR1* previously reported SNPs with serum fractalkine levels

Chr	SNP	Position	Coded/ Noncoded Allele	African Americans				Caucasians				Combined		
				Coded Allele Freq	**β†**	**SE**	**P**	**Coded Allele Freq**	**β†**	**SE**	**P**	**β‡**	**SE**	**P**
3	**rs3732378 (Thr280Met)**	**39,282,166**	**A/G**	**0.028**	**0.04**	**0.05**	**0.43**	**0.18**	**0.05**	**0.02**	**0.05**	**0.04**	**0.02**	**0.04**
3	rs3732379 (Val249Ile)	39,282,260	T/C	0.119	0.006	0.02	0.81	0.287	0.003	0.02	0.89	0.004	0.02	0.78

Positions are in reference to NCBI build 36.3

†Effect size of the coded allele based on the multivariate linear regression adjusted for age and sex

‡Effect size of the coded allele based on the multivariate linear regression adjusted for age, sex and race

Marginal significant SNP and the P-values for the association are highlighted in bold

Supplementary Figure 1. Linkage disequilibrium (LD) pattern of SNPs associated with serum TNFα level in African Americans