The contribution of the functional *IL6R* polymorphism rs2228145, eQTLs and other genome-wide SNPs to the heritability of plasma sIL-6R levels

Jenny van Dongen,[1,2,*] Rick Jansen,[3,4] Dirk Smit,[1,4] Jouke-Jan Hottenga,[1,2] Hamdi Mbarek,[1,2] Gonneke Willemsen,[1,2] Cornelis Kluft,[5] David L. Duffy,[6] Melanie C. Matheson,[7] Guy B. Marks,[8] Jennie Hui,[9,10,11,12] Peter Le Souëf,[13] Patrick Danoy,[14] Svetlana Baltic,[15] Dale R. Nyholt,[6] Mark Jenkins,[7] Catherine Hayden,[13] John Beilby,[9,11,12] Faang Cheah,[15] Pamela A. Madden,[16] Andrew C. Heath,[16] John L. Hopper,[7] Bill Musk,[10,12,17,18] Stephen R. Leeder,[19] Eugene H Walters,[20] Nicholas G. Martin,[6] Alan James,[12,18,21] Graham Jones,[22] Michael J. Abramson,[23] Colin F. Robertson,[24] Shyamali C. Dharmage,[7] Matthew A. Brown,[14] Grant W. Montgomery,[6] Philip J. Thompson,[15] Brenda W.J. Penninx,[2,3,4] Manuel A. Ferreira,[6] Dorret I. Boomsma,[1,2,4,25] Eco J. C. de Geus,[1,2,25]

[1] Department of Biological Psychology, Van der Boechorststraat 1, 1081 BT, VU University Amsterdam, Amsterdam, The Netherlands

[2] EMGO institute for Health and Care Research, VU University Medical Center, Van der Boechorststraat 7, 1081BT, Amsterdam, The Netherlands

[3] Department of Psychiatry, VU University Medical Center, A.J. Ernststraat 1187, 1081HL, Amsterdam, The Netherlands

[4] Neuroscience Campus Amsterdam, De Boelelaan 1085, 1081HV, Amsterdam, The Netherlands

[5] Good Biomarker Sciences, Zernikedreef 8, 2333CL, Leiden, The Netherlands

[6] Queensland Institute of Medical Research, Royal Brisbane Hospital, Locked Bag 2000, Herston QLD 4029, Australia

[7] Centre for Molecular, Environmental, Genetic and Analytic Epidemiology, University of Melbourne, Melbourne, Australia.

[8] Woolcock Institute of Medical Research, University of Sydney, Sydney, Australia.

[9] PathWest Laboratory Medicine of Western Australia (WA), Nedlands, Australia.

[10] School of Population Health, The University of WA, Nedlands, Australia.

[11] School of Pathology and Laboratory Medicine, The University of WA, Nedlands, Australia.

[12] Busselton Population Medical Research Foundation, Sir Charles Gairdner Hospital, Perth, Australia.

[13] School of Paediatrics and Child Health, Princess Margaret Hospital for Children, Perth, Australia.

[14] University of Queensland Diamantina Institute, Princess Alexandra Hospital, Brisbane, Australia.

[15] Lung Institute of WA and Centre for Asthma, Allergy and Respiratory Research, University of WA, Perth, Australia.

[16] Washington University School of Medicine, St Louis, United States

[17] Department of Respiratory Medicine, Sir Charles Gairdner Hospital, Perth, Australia

[18] School of Medicine and Pharmacology, University of WA, Nedlands, Australia

[19] Australian Health Policy Institute, University of Sydney, Sydney, Australia

[20] School of Medicine, University of Tasmania

[21] Department of Pulmonary Physiology, West Australian Sleep Disorders Research Institute, Nedlands, Australia

[22] School of Science and Health, University of Western Sydney, Penrith, Australia

[23] Department of Epidemiology& Preventive Medicine, Monash University, Melbourne, Australia.

[24] Respiratory Medicine, Murdoch Children's Research Institute, Melbourne, Australia

[25] These authors contributed equally to the manuscript

* Corresponding author, Department of Biological Psychology, VU University Amsterdam, Van der

Boechorststraat 1, 1081BT, Amsterdam, The Netherlands, T: +31-(0)20-598 3570, F: +31-(0)20-598 8832,

j.van.dongen@vu.nl

Supplementary Figures

Figure S1: Variance of sIL-6R level explained by genome-wide SNPs in unrelated individuals.

Estimates are expressed as a proportion of the total variance of sIL-6R level (V_A/V_P). Error bars represent standard errors. *IL6R*= All SNPs in the *IL6R* gene +/- 10 MB on chromosome 1 (1q21.3). 1 rest= All other SNPs on chromosome 1.

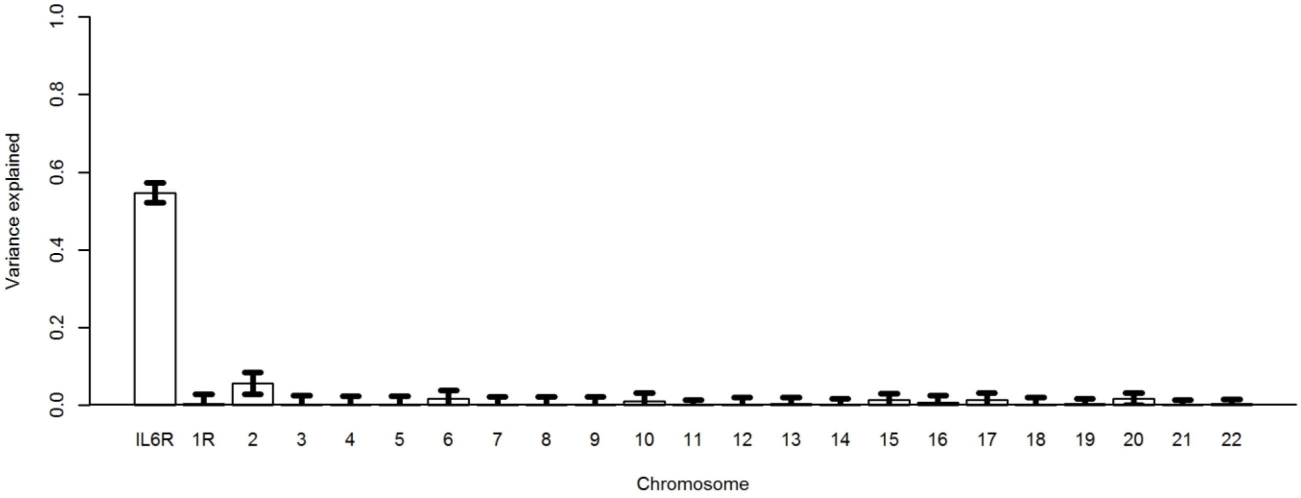
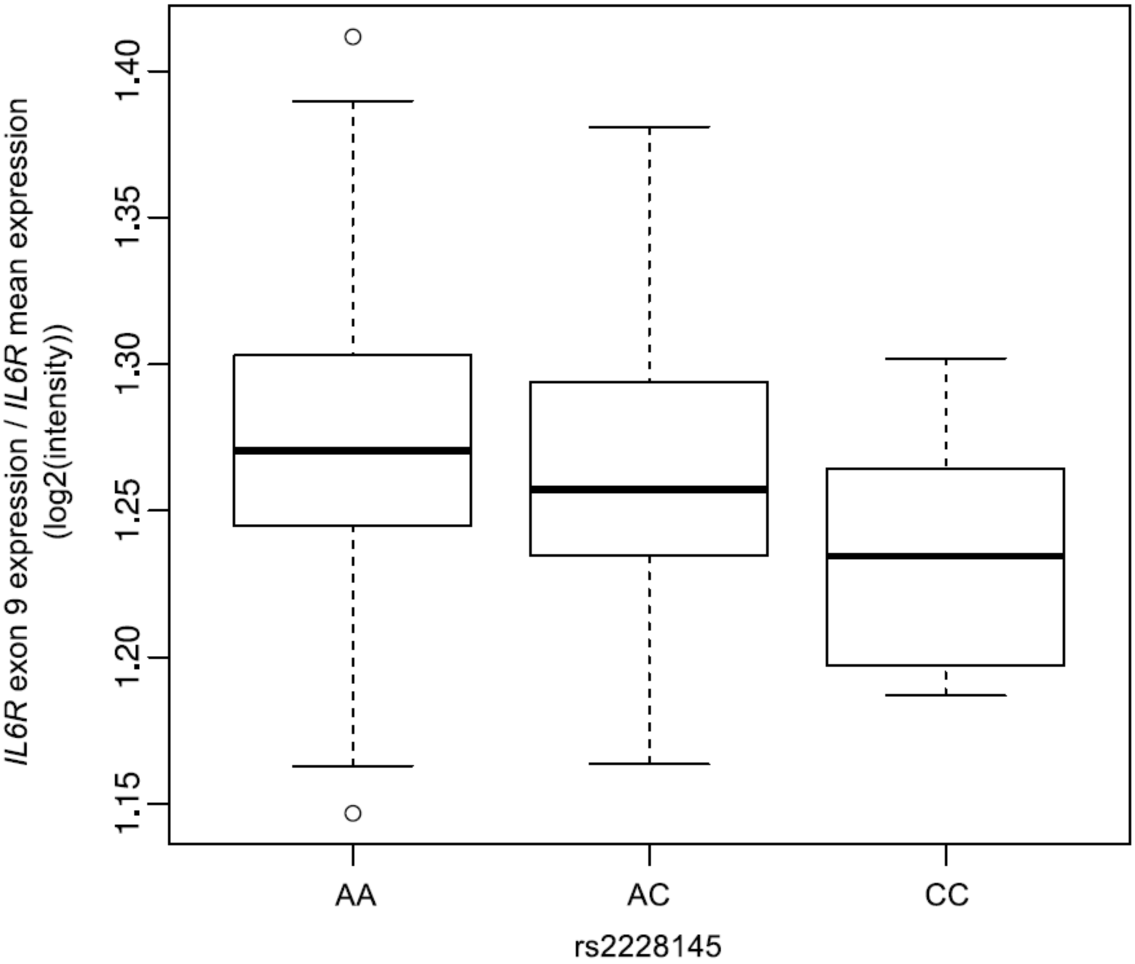


Figure S2: Association between rs2228145 genotype and the ratio of *IL6R* exon 9 expression over mean *IL6R* expression*.* Boxplots of the relative transcript abundance (transcripts containing exon 9/ mean expression of all *IL6R* transcripts) in lymphoblastoid cell lines from HAPMAP (GEO accession nr = GSE9703, N=162) are displayed for each rs2228145 genotype (P < 0.01).



Supplementary Tables

Table S1: Characteristics of subjects included in the analyses.

Analysis	**N subjects**	**Mean age (SD), min-max**	**% Male**	**Cohort**
Heritability analysis and biometrical model (MZ and DZ twins, siblings, and parents)	4980	42.7 (14.3), 18-89	36.2	NTR
GWA and GCTA (unrelated + related Ss)	4846	44.2 (14.4), 18-90	38.7	NTR
GCTA (unrelated Ss)	2875	46.5 (14.4), 18-89	38.8	NTR
Combined linkage and association analysis (Nuclear families)	1254	48.3 (15.7), 18-89	44.4	NTR
eQTL analysis (unrelated + related Ss)	4467	38.4 (13.0), 25-51	34.4	NTR + NESDA
Correlation between sIL-6R level and *IL6R* expression (unrelated + related Ss)	2727	37.5 (12.0), 18-79	34.5	NTR

Table S2: GWA results and information for all 680 SNPs reaching genome-wide significance in the GWAS of sIL-6R level.

SNP[A]	Chr	Position[B]	A1[C]	A2[D]	Frequency A1[E]	Info[F]	Beta[G]	SE[H]	*P* value
rs11265611	1	154395125	G	A	0.42	0.894	-9748.6	236.8	< 1 E-176
rs4133213	1	154395212	C	A	0.58	0.893	-11519.4	219.2	< 1 E-176
rs6689306	1	154395946	A	G	0.45	0.937	-9896.3	226.5	< 1 E-176
rs12118721	1	154397416	T	C	0.45	0.961	-9916.3	222.9	< 1 E-176
rs12118770	1	154397589	T	C	0.44	0.959	-9827.9	223.7	< 1 E-176
rs12117832	1	154397610	A	G	0.45	0.959	-9890.3	222.6	< 1 E-176
rs10908836	1	154397932	C	T	0.46	0.913	-9625.9	230.7	< 1 E-176
rs35109459	1	154397933	G	A	0.47	0.917	-9778.4	228.7	< 1 E-176
rs10908838	1	154397984	T	G	0.44	0.963	-9822.9	223.4	< 1 E-176
rs6687726	1	154400320	A	G	0.45	0.969	-9890.7	222.1	< 1 E-176
rs6427658	1	154400799	T	C	0.45	0.965	-9877.7	221.5	< 1 E-176
rs6694817	1	154401972	T	C	0.44	0.965	-9923.9	221.6	< 1 E-176
rs7549250	1	154404336	C	T	0.45	0.970	-10068.0	219.3	< 1 E-176
rs7549338	1	154404380	C	G	0.44	0.970	-9995.9	219.8	< 1 E-176
rs56383622	1	154405024	A	G	0.60	0.969	-12091.3	204.4	< 1 E-176
rs4845619	1	154405058	T	G	0.45	0.970	-10088.9	219.2	< 1 E-176
rs59632925	1	154406540	T	G	0.44	0.970	-10014.3	219.7	< 1 E-176
rs4845620	1	154406656	A	G	0.61	0.969	-12111.3	203.9	< 1 E-176
rs7521458	1	154407713	T	C	0.61	0.969	-12123.6	203.6	< 1 E-176
rs4845371	1	154408340	T	C	0.44	0.969	-10034.3	219.6	< 1 E-176
rs6667434	1	154409100	A	G	0.44	0.969	-10040.3	219.6	< 1 E-176
rs4845621	1	154409730	G	A	0.61	0.970	-12152.8	203.3	< 1 E-176
rs4845622	1	154411419	A	C	0.61	0.970	-12171.5	203.1	< 1 E-176
rs4393147	1	154414037	C	T	0.60	0.973	-12194.9	202.5	< 1 E-176
rs4453032	1	154414086	A	G	0.60	0.973	-12195.2	202.5	< 1 E-176
rs6664201	1	154414296	C	T	0.60	0.973	-12196.2	202.5	< 1 E-176
rs4845372	1	154415396	C	A	0.60	0.974	-12019.9	204.0	< 1 E-176
rs12753254	1	154416935	G	A	0.61	0.977	-12294.5	199.9	< 1 E-176
rs12730036	1	154416969	C	T	0.61	0.977	-12296.6	199.8	< 1 E-176
rs11265612	1	154417044	A	G	0.44	0.975	-10170.5	217.6	< 1 E-176
rs4845373	1	154417829	C	T	0.61	0.979	-12291.5	200.7	< 1 E-176
rs6683206	1	154418088	T	C	0.44	0.969	-10228.0	218.1	< 1 E-176
rs11265613	1	154418415	T	C	0.61	0.983	-12322.0	198.5	< 1 E-176
rs4576655	1	154418749	C	T	0.60	0.989	-12163.1	199.6	< 1 E-176

rs6686750	1	154419843	A	G	0.45	0.990	-10227.6	215.8	< 1 E-176
rs12730935	1	154419892	G	A	0.61	0.985	-12393.1	198.6	< 1 E-176
rs61812598	1	154420087	G	A	0.61	0.993	-12357.8	197.2	< 1 E-176
rs7512646	1	154420402	G	C	0.60	0.991	-12186.8	198.9	< 1 E-176
rs7529229	1	154420778	T	C	0.60	0.991	-12189.7	198.8	< 1 E-176
rs12404927	1	154421438	T	C	0.48	0.931	-10032.6	229.5	< 1 E-176
rs12129500	1	154423764	T	C	0.45	0.992	-10227.7	215.7	< 1 E-176
rs7536152	1	154423909	A	G	0.45	0.992	-10228.0	215.6	< 1 E-176
rs7526131	1	154425135	G	A	0.45	0.993	-10228.4	215.6	< 1 E-176
rs12126142	1	154425456	G	A	0.61	0.997	-12361.6	196.6	< 1 E-176
rs6689393	1	154426097	A	G	0.45	0.993	-10229.8	215.7	< 1 E-176
rs12133641	1	154428283	A	G	0.61	0.993	-12381.4	196.2	< 1 E-176
rs6694258	1	154428505	C	A	0.45	0.991	-10267.7	214.6	< 1 E-176
rs6690230	1	154432877	C	G	0.40	0.990	-6873.5	232.7	2.58E-176
rs6695045	1	154432957	A	G	0.40	0.990	-6872.5	232.7	2.96E-176
rs12044132	1	154462360	C	T	0.85	0.853	-10008.7	341.2	3.70E-174
rs55676222	1	154435289	A	T	0.89	0.637	-13456.9	485.4	5.24E-157
rs10752641	1	154432042	G	C	0.24	0.973	-6740.6	248.2	3.75E-151
rs6698040	1	154432948	T	C	0.24	0.990	-6658.3	247.1	5.34E-149
rs7537291	1	154433407	G	A	0.24	0.990	-6650.5	247.1	1.11E-148
rs7546068	1	154433415	C	T	0.24	0.990	-6650.4	247.1	1.13E-148
rs7537316	1	154433466	G	A	0.24	0.990	-6649.5	247.1	1.23E-148
rs12023772	1	154483868	G	A	0.85	0.920	-8936.2	332.4	2.12E-148
rs72698169	1	154486799	A	C	0.85	0.920	-8930.3	332.3	2.66E-148
rs7546552	1	154433905	C	A	0.24	0.992	-6635.3	247.0	3.76E-148
rs7546555	1	154433911	C	T	0.24	0.992	-6635.2	247.1	3.83E-148
rs6427672	1	154435346	C	T	0.24	0.992	-6629.8	247.3	1.14E-147
rs6687597	1	154434936	G	A	0.24	0.992	-6618.1	247.5	5.38E-147
rs11265621	1	154442960	G	A	0.37	0.991	-6427.1	240.4	6.34E-147
rs10908839	1	154430798	C	G	0.24	0.986	-6641.6	248.8	1.73E-146
rs4509570	1	154436384	G	C	0.24	0.994	-6585.7	247.4	8.69E-146
rs4341355	1	154436404	C	G	0.24	0.994	-6585.8	247.4	9.25E-146
rs4638123	1	154505704	C	T	0.37	0.997	-6418.6	241.2	1.20E-145
rs12407048	1	154505270	C	T	0.37	0.997	-6418.6	241.2	1.20E-145
rs12037271	1	154507888	G	A	0.37	0.996	-6418.8	241.2	1.22E-145
rs4478801	1	154464572	G	A	0.37	0.994	-6413.3	241.0	1.27E-145
rs6698971	1	154475331	C	A	0.37	0.995	-6424.3	241.5	1.55E-145
rs11265632	1	154514067	G	A	0.37	0.995	-6413.2	241.1	1.74E-145

rs11265628	1	154496489	C	T	0.37	0.997	-6412.6	241.2	2.07E-145
rs10908843	1	154494480	C	G	0.37	0.997	-6412.5	241.2	2.09E-145
rs12136771	1	154511502	T	C	0.37	0.994	-6419.6	241.5	2.11E-145
rs10908845	1	154500898	C	T	0.37	0.996	-6412.9	241.4	3.43E-145
rs10908847	1	154504954	G	A	0.37	0.995	-6418.7	241.7	4.36E-145
rs4845647	1	154514331	C	A	0.37	0.995	-6407.6	241.3	4.90E-145
rs4845642	1	154498028	G	A	0.37	0.996	-6410.8	241.5	5.48E-145
rs4345797	1	154495675	C	T	0.37	0.997	-6406.9	241.4	5.76E-145
rs10908842	1	154492702	G	A	0.37	0.998	-6390.6	241.2	1.82E-144
rs6700296	1	154473660	T	C	0.37	0.998	-6388.9	241.2	1.85E-144
rs4845638	1	154490269	T	A	0.37	0.998	-6389.9	241.2	1.95E-144
rs12128408	1	154488533	A	G	0.37	0.998	-6389.8	241.2	1.97E-144
rs12740969	1	154487060	T	G	0.37	0.998	-6389.7	241.2	1.99E-144
rs12118018	1	154477440	G	A	0.37	0.999	-6388.7	241.2	2.00E-144
rs4845637	1	154490178	A	G	0.37	0.998	-6390.8	241.3	2.00E-144
rs10908841	1	154487763	C	T	0.37	0.998	-6389.5	241.2	2.10E-144
rs6664608	1	154479670	C	T	0.37	0.999	-6388.3	241.2	2.23E-144
rs4382717	1	154518610	C	T	0.37	0.989	-6410.5	242.1	2.40E-144
rs6689965	1	154470606	T	A	0.37	0.999	-6386.6	241.2	2.43E-144
rs6686276	1	154466188	C	A	0.37	0.998	-6385.8	241.2	2.66E-144
rs6684921	1	154464945	A	C	0.37	0.997	-6388.3	241.4	3.51E-144
rs12753680	1	154474900	G	A	0.37	0.998	-6385.9	241.3	3.98E-144
rs4845639	1	154490352	C	T	0.37	0.998	-6383.3	241.4	5.47E-144
rs7519499	1	154487926	G	A	0.37	0.998	-6383.1	241.4	5.56E-144
rs7518694	1	154484788	C	G	0.37	0.998	-6382.9	241.4	5.69E-144
rs9660786	1	154484017	A	T	0.37	0.998	-6382.8	241.4	5.72E-144
rs12119111	1	154478600	G	A	0.37	0.998	-6382.0	241.4	6.35E-144
rs6658175	1	154475330	T	A	0.37	0.997	-6377.4	241.6	1.65E-143
rs12753666	1	154474875	G	A	0.38	0.986	-6404.8	243.1	5.49E-143
rs9616	1	154555733	A	T	0.71	0.978	-7349.6	282.2	6.01E-140
rs11265616	1	154419980	T	C	0.60	0.702	-7757.1	301.5	7.72E-137
rs55668699	1	154435293	T	A	0.76	0.955	6435.5	253.5	1.80E-133
rs78664422	1	154499246	G	A	0.84	0.944	6973.1	286.3	1.13E-123
rs4072391	1	154438880	T	C	0.20	0.983	-6376.1	262.8	9.85E-123
rs112231452	1	154504900	G	A	0.79	0.988	6356.5	262.1	1.25E-122
rs61275241	1	154504887	T	G	0.79	0.988	6332.1	262.2	1.16E-121
rs60255122	1	154504702	A	G	0.79	0.988	6332.1	262.2	1.16E-121
rs60760897	1	154504849	C	T	0.79	0.988	6330.6	262.3	1.49E-121

rs61698846	1	154504854	C	T	0.79	0.988	6330.6	262.3	1.49E-121
rs61403567	1	154504927	T	C	0.79	0.988	6339.2	263.1	3.75E-121
rs77994623	1	154505106	C	T	0.84	0.933	6922.3	287.4	4.36E-121
rs60498985	1	154504172	C	T	0.79	0.995	6296.4	261.4	4.53E-121
rs7526293	1	154444209	T	C	0.21	0.990	-6278.9	261.2	1.25E-120
rs6669229	1	154444591	A	G	0.21	0.990	-6277.4	261.3	1.46E-120
rs58348886	1	154446198	T	C	0.79	0.990	6280.2	261.6	2.25E-120
rs59741504	1	154504601	T	C	0.79	0.991	6311.6	263.0	2.70E-120
rs12405637	1	154501285	C	T	0.79	0.995	6284.0	262.4	7.39E-120
rs57783436	1	154511709	A	G	0.79	0.995	6283.0	262.5	9.98E-120
rs73023346	1	154512077	C	T	0.79	0.995	6283.1	262.5	1.00E-119
rs12408461	1	154512710	T	C	0.79	0.994	6283.2	262.5	1.01E-119
rs73023348	1	154513418	G	A	0.79	0.994	6283.5	262.5	1.02E-119
rs73023349	1	154513440	T	C	0.79	0.994	6283.5	262.5	1.02E-119
rs72999415	1	154513712	C	T	0.79	0.994	6283.5	262.5	1.03E-119
rs72999419	1	154514092	T	C	0.79	0.994	6283.7	262.5	1.04E-119
rs41313910	1	154514203	C	G	0.79	0.994	6283.7	262.5	1.04E-119
rs72999422	1	154514942	G	A	0.79	0.994	6283.9	262.5	1.05E-119
rs58881140	1	154515193	C	T	0.79	0.994	6283.9	262.5	1.07E-119
rs6672087	1	154516122	A	C	0.79	0.994	6284.2	262.6	1.09E-119
rs6681207	1	154517217	T	C	0.79	0.993	6284.5	262.6	1.20E-119
rs112394421	1	154512008	T	C	0.79	0.995	6281.7	262.5	1.22E-119
rs3811449	1	154517504	G	A	0.79	0.993	6284.6	262.6	1.25E-119
rs41308419	1	154507197	T	C	0.79	0.996	6276.6	262.3	1.28E-119
rs60368585	1	154509340	T	C	0.79	0.995	6277.3	262.4	1.29E-119
rs111742980	1	154508764	T	A	0.79	0.995	6277.1	262.3	1.29E-119
rs73023339	1	154510852	C	T	0.79	0.995	6277.6	262.4	1.31E-119
rs112236096	1	154510790	C	T	0.79	0.995	6277.6	262.4	1.31E-119
rs59084843	1	154518286	A	G	0.79	0.993	6284.8	262.7	1.41E-119
rs61559765	1	154518349	T	C	0.79	0.993	6284.8	262.7	1.42E-119
rs60092776	1	154518496	A	G	0.79	0.992	6284.8	262.7	1.46E-119
rs60931472	1	154518642	T	C	0.79	0.992	6284.9	262.8	1.50E-119
rs112585956	1	154507767	T	C	0.79	0.996	6275.3	262.4	1.63E-119
rs4633282	1	154507899	T	C	0.79	0.996	6275.3	262.4	1.63E-119
rs73023331	1	154508210	G	A	0.79	0.996	6275.4	262.4	1.63E-119
rs4639752	1	154508974	T	A	0.79	0.996	6275.7	262.4	1.63E-119
rs112674677	1	154508792	C	T	0.79	0.996	6275.6	262.4	1.63E-119
rs113915076	1	154508812	G	A	0.79	0.996	6275.6	262.4	1.63E-119

rs7551873	1	154505857	C	T	0.79	0.995	6274.9	262.4	1.63E-119
rs58710275	1	154505010	C	T	0.79	0.996	6274.6	262.4	1.63E-119
rs111600849	1	154487489	G	A	0.79	0.997	6240.5	262.0	1.27E-118
rs11490956	1	154487258	G	T	0.79	0.997	6239.2	261.9	1.30E-118
rs41269915	1	154521584	T	A	0.79	0.986	6269.8	263.3	1.35E-118
rs77184252	1	154492533	A	G	0.79	0.997	6234.2	261.9	1.90E-118
rs4390168	1	154509096	A	G	0.79	0.992	6255.6	262.8	1.94E-118
rs12403537	1	154487726	G	A	0.79	0.997	6233.2	261.9	2.05E-118
rs73020246	1	154485640	A	G	0.79	0.997	6233.0	261.9	2.07E-118
rs73020234	1	154482767	C	A	0.79	0.997	6232.7	261.9	2.11E-118
rs73020232	1	154482669	C	T	0.79	0.997	6232.7	261.9	2.12E-118
rs59838898	1	154466301	C	T	0.79	0.997	6222.7	261.9	4.25E-118
rs73018293	1	154465577	C	T	0.79	0.997	6222.7	261.9	4.26E-118
rs12406822	1	154499484	C	T	0.79	0.983	6286.5	265.5	2.40E-117
rs59239860	1	154492107	G	T	0.80	0.994	6233.4	265.1	8.67E-116
rs6675472	1	154445503	T	C	0.22	0.972	-5986.3	264.6	8.64E-108
rs4291493	1	154436920	T	C	0.27	0.919	-5772.3	259.5	2.27E-104
rs35717427	1	154391882	G	A	0.86	0.685	-8971.6	429.1	5.53E-93
rs11579998	1	154580834	C	T	0.93	0.650	-11125.0	616.9	2.18E-70
rs11264224	1	154568086	A	C	0.80	0.802	-6930.6	384.4	2.25E-70
rs57569414	1	154380419	C	A	0.86	0.786	-7433.4	420.5	8.69E-68
rs3738030	1	154575315	A	C	0.87	0.965	5418.8	313.7	6.35E-65
rs7525477	1	154394297	G	A	0.53	0.708	5242.3	309.8	1.99E-62
rs10908421	1	154635885	G	T	0.71	0.912	-4865.2	297.1	1.05E-58
rs4601580	1	154394417	T	A	0.48	0.736	-5037.2	307.9	1.45E-58
rs11264237	1	154636276	G	A	0.71	0.955	-4654.5	293.6	3.40E-55
rs55873271	1	154610952	C	T	0.79	0.971	4327.6	273.6	5.49E-55
rs12132326	1	154376896	G	A	0.96	0.656	-11470.7	739.5	5.52E-53
rs59618219	1	154589931	C	T	0.79	0.995	4220.8	272.9	1.05E-52
rs41269913	1	154461480	C	T	0.97	0.612	-13738.6	888.3	1.07E-52
rs56020456	1	154591882	G	T	0.79	0.994	4216.1	272.9	1.38E-52
rs58655370	1	154580458	C	A	0.79	0.990	4207.2	272.6	1.76E-52
rs11264227	1	154596551	C	T	0.79	0.990	4209.9	273.2	2.44E-52
rs61811397	1	154606846	G	A	0.79	0.984	4217.1	273.9	3.01E-52
rs12739228	1	154426190	G	A	0.95	0.894	7822.9	509.1	4.68E-52
rs56019122	1	154596051	C	T	0.79	0.992	4198.0	273.3	5.28E-52
rs61811390	1	154592832	A	C	0.79	0.998	4187.5	273.2	8.44E-52
rs56064112	1	154602271	A	G	0.79	0.991	4197.7	274.0	9.06E-52

rs2335230	1	154589628	A	C	0.79	0.979	4207.0	275.2	1.53E-51
rs79438587	1	154342517	C	T	0.84	0.685	-6238.8	408.4	1.79E-51
rs12059682	1	154579585	T	C	0.79	0.995	4153.0	272.3	2.58E-51
rs59711031	1	154599500	G	C	0.79	0.993	4175.2	274.0	3.06E-51
rs3766926	1	154564417	T	C	0.79	0.994	4124.5	272.0	9.46E-51
rs17655362	1	154565914	G	A	0.79	0.995	4118.1	272.0	1.26E-50
rs9427106	1	154603322	T	C	0.54	0.973	-3974.1	265.4	1.39E-49
rs79778789	1	154409434	A	G	0.96	0.506	-14297.8	968.2	2.71E-48
rs9426831	1	154609657	A	T	0.54	0.983	-3891.2	263.8	3.30E-48
rs12403159	1	154421521	G	C	0.96	0.378	-19001.0	1289.3	4.15E-48
rs11264230	1	154608418	G	T	0.54	0.983	-3885.4	263.8	4.52E-48
rs66980031	1	154481153	C	G	0.96	0.868	7709.4	527.4	2.20E-47
rs113580743	1	154420333	G	A	0.95	0.640	8600.5	596.4	3.54E-46
rs9427109	1	154609009	A	G	0.56	0.932	-3904.4	273.2	2.14E-45
rs9427110	1	154616804	G	A	0.55	0.964	-3833.4	268.3	2.24E-45
rs9427092	1	154553722	T	C	0.80	0.937	4113.8	294.1	1.31E-43
rs9426829	1	154592201	T	C	0.51	0.988	-3630.9	259.9	1.68E-43
rs35504625	1	154599778	C	G	0.51	0.989	-3574.1	260.0	3.43E-42
rs7531982	1	154596122	A	T	0.51	0.992	-3568.6	259.7	3.46E-42
rs9426828	1	154591489	G	A	0.51	0.995	-3560.3	259.4	4.30E-42
rs9426827	1	154589965	T	C	0.51	0.995	-3560.0	259.3	4.34E-42
rs12125166	1	154582129	C	T	0.51	0.992	-3562.3	259.6	4.66E-42
rs9427102	1	154586957	A	G	0.51	0.994	-3556.4	259.3	5.11E-42
rs9427104	1	154589232	C	T	0.51	0.995	-3556.8	259.4	5.18E-42
rs9426826	1	154585480	C	G	0.51	0.995	-3555.7	259.3	5.34E-42
rs9427100	1	154583762	G	A	0.51	0.995	-3555.0	259.3	5.56E-42
rs61811388	1	154581231	G	C	0.51	0.994	-3553.2	259.4	6.41E-42
rs6702549	1	154583102	T	C	0.51	0.995	-3550.2	259.3	7.13E-42
rs6702449	1	154583210	A	C	0.51	0.995	-3550.2	259.4	7.18E-42
rs6699729	1	154582896	A	T	0.51	0.995	-3550.1	259.4	7.23E-42
rs11802588	1	154580895	C	G	0.51	0.993	-3550.1	259.5	8.18E-42
rs3766922	1	154577055	T	G	0.51	0.989	-3551.1	259.9	1.01E-41
rs6703672	1	154474557	T	C	0.20	0.902	-3891.2	287.0	4.08E-41
rs11580535	1	154364317	G	T	0.86	0.968	-5340.8	397.0	1.57E-40
rs72633650	1	154360838	T	C	0.86	0.969	-5339.5	396.9	1.59E-40
rs11264239	1	154653052	G	A	0.94	0.850	-8296.0	621.0	5.37E-40
	1	154353503	T	C	0.92	0.723	-7451.9	558.2	6.09E-40
	1	154430647	C	T	0.97	0.680	10346.0	782.2	3.00E-39

rs9427094	1	154557685	C	T	0.50	0.990	-3428.7	260.9	8.60E-39
rs10908419	1	154567699	G	A	0.50	0.995	-3394.3	260.6	3.88E-38
rs116710125	1	154502312	C	T	0.95	0.810	6463.0	497.2	5.35E-38
rs11264223	1	154565519	G	A	0.50	0.995	-3378.5	260.4	7.49E-38
rs77993403	1	154316996	G	A	0.96	0.697	-9378.5	729.3	3.12E-37
rs66654715	1	154376820	G	C	0.96	0.776	7326.8	571.7	5.31E-37
rs12122449	1	154283908	C	T	0.86	0.789	-5446.7	432.0	6.94E-36
rs9427103	1	154587817	A	G	0.80	0.980	3755.1	298.6	1.07E-35
rs11580217	1	154353499	T	C	0.91	0.750	-6712.8	538.3	3.76E-35
rs75456865	1	154478114	A	T	0.96	0.838	6376.5	511.8	4.28E-35
rs60517797	1	154642224	T	C	0.90	0.862	5033.9	409.8	3.55E-34
rs116059394	1	154483655	A	G	0.95	0.702	6876.6	568.4	3.31E-33
rs78042851	1	154627572	A	C	0.97	0.490	-12080.3	1011.0	1.90E-32
rs76289529	1	154516404	C	T	0.98	0.638	-13735.3	1153.8	3.17E-32
rs116306348	1	154653601	A	T	0.96	0.883	5926.5	498.1	3.38E-32
rs11265623	1	154454674	C	G	0.03	0.331	16001.3	1347.4	4.44E-32
rs77801962	1	154566932	T	C	0.97	0.489	-12434.9	1064.4	4.10E-31
rs4845626	1	154423485	G	T	0.84	0.985	3427.2	295.1	8.89E-31
rs114660934	1	154413904	G	A	0.96	0.774	6651.6	573.0	9.60E-31
	1	154509061	G	A	0.97	0.649	8678.9	750.3	1.52E-30
rs116141616	1	154416069	G	A	0.98	0.641	11083.8	958.5	1.60E-30
rs114879247	1	154434836	T	C	0.96	0.807	6463.7	560.6	2.34E-30
rs34450945	1	154289348	C	T	0.96	0.768	7042.2	611.4	2.66E-30
rs116323753	1	154586202	G	C	0.97	0.493	-12144.5	1056.2	3.34E-30
	1	154392851	G	A	0.98	0.605	-13591.7	1185.7	4.96E-30
rs112559935	1	154336175	G	T	0.96	0.599	8056.8	705.8	8.54E-30
rs6427720	1	154501756	G	A	0.17	0.980	-3346.6	293.4	9.57E-30
rs9427116	1	154631123	T	C	0.48	0.974	-2987.3	263.2	1.74E-29
rs10796931	1	154652119	G	A	0.48	0.944	-2994.4	264.1	2.00E-29
rs7554871	1	154650598	G	A	0.53	0.943	2991.1	264.3	2.55E-29
	1	154353507	T	C	0.95	0.625	-8057.0	712.9	2.98E-29
rs10908423	1	154644546	G	A	0.48	0.968	-2945.1	262.0	5.79E-29
rs9427117	1	154632231	C	G	0.48	0.983	-2935.8	261.6	7.30E-29
rs6426877	1	154651044	C	G	0.53	0.939	2972.0	264.9	7.64E-29
	1	154628059	G	A	0.97	0.492	-12081.3	1081.0	1.20E-28
rs9330261	1	154634998	T	A	0.48	0.986	-2911.4	260.7	1.33E-28
rs79925547	1	154443014	C	T	0.99	0.722	-11248.9	1009.8	1.79E-28
	1	154415848	C	G	0.98	0.753	8072.8	725.3	1.98E-28

rs10159236	1	154431405	C	A	0.84	0.983	3296.8	296.4	2.14E-28
rs12748485	1	154560471	C	T	0.96	0.748	7362.1	662.2	2.28E-28
rs6688149	1	154637946	C	G	0.47	0.987	-2898.1	260.9	2.51E-28
rs79480105	1	154445104	G	A	0.96	0.790	6367.1	573.4	2.66E-28
rs6703211	1	154637950	T	C	0.47	0.987	-2896.8	260.9	2.67E-28
rs61812599	1	154421554	G	A	0.84	0.988	3302.2	298.3	3.83E-28
rs111301013	1	154419584	C	A	0.84	0.988	3301.0	298.5	4.28E-28
rs7523890	1	154622234	T	C	0.84	0.969	3440.0	311.4	4.91E-28
	1	154353511	T	C	0.95	0.594	-8400.1	760.7	5.17E-28
rs55800510	1	154417187	C	T	0.84	0.976	3293.9	298.4	5.36E-28
rs4308966	1	154432622	T	C	0.84	0.994	3262.9	295.6	5.38E-28
rs4845374	1	154426947	T	A	0.84	0.992	3281.1	297.3	5.60E-28
rs11804305	1	154424497	C	T	0.84	0.992	3279.4	297.8	7.18E-28
rs11265634	1	154522248	A	G	0.17	0.984	-3229.3	293.3	7.40E-28
rs80033405	1	154416572	A	C	0.99	0.701	-11265.3	1024.0	8.06E-28
rs60682501	1	154351304	A	G	0.86	0.972	-4378.7	398.7	9.76E-28
rs116088025	1	154354350	C	T	0.86	0.972	-4381.2	399.1	1.04E-27
rs11579718	1	154353358	A	G	0.86	0.972	-4371.2	398.9	1.29E-27
rs7547072	1	154639255	C	T	0.48	0.950	-2922.1	266.7	1.30E-27
rs61812596	1	154414691	C	T	0.84	0.976	3265.0	298.2	1.43E-27
rs1889313	1	154351717	C	A	0.86	0.972	-4363.5	398.8	1.54E-27
rs60412881	1	154351323	T	C	0.86	0.972	-4362.3	398.8	1.58E-27
rs60767732	1	154351277	G	T	0.86	0.972	-4362.2	398.8	1.58E-27
rs57100877	1	154351247	C	G	0.86	0.972	-4362.0	398.8	1.59E-27
rs9803896	1	154347450	G	A	0.86	0.971	-4331.1	396.3	1.78E-27
rs11582433	1	154349605	C	T	0.86	0.972	-4356.2	398.7	1.82E-27
rs61812626	1	154436436	G	A	0.84	0.984	3245.8	297.1	1.86E-27
rs11264233	1	154625632	G	A	0.49	0.963	-2934.9	268.7	1.89E-27
rs59356432	1	154349159	A	G	0.86	0.972	-4354.6	398.7	1.89E-27
rs56264602	1	154349121	G	A	0.86	0.972	-4354.5	398.7	1.90E-27
rs9803950	1	154348513	G	C	0.86	0.972	-4347.0	398.1	1.94E-27
rs4345796	1	154436750	C	T	0.84	0.985	3227.5	296.5	2.82E-27
rs79753070	1	154652279	G	A	0.98	0.600	-12335.1	1133.9	3.02E-27
rs9427113	1	154626477	A	G	0.49	0.980	-2898.8	266.7	3.30E-27
rs41310893	1	154514267	C	T	0.96	0.781	6286.9	579.5	4.20E-27
rs61812594	1	154411628	A	G	0.84	0.974	3228.9	298.8	6.63E-27
rs61812593	1	154410490	T	C	0.84	0.973	3227.5	299.0	7.49E-27
rs61812592	1	154410482	G	A	0.84	0.973	3227.4	299.0	7.52E-27

rs61811421	1	154653951	C	T	0.78	0.866	3255.4	302.4	1.03E-26
rs12024175	1	154643443	G	A	0.48	0.958	-2847.7	264.6	1.03E-26
rs113325045	1	154413242	G	A	0.97	0.662	7827.7	727.8	1.12E-26
rs9427115	1	154627852	G	A	0.49	0.964	-2879.3	268.1	1.35E-26
rs79219014	1	154415675	G	T	0.97	0.566	-9849.7	917.5	1.39E-26
rs57502626	1	154408916	T	A	0.84	0.973	3214.6	299.6	1.49E-26
rs55826755	1	154409520	C	G	0.84	0.973	3211.7	299.5	1.55E-26
	1	154345962	C	A	0.86	0.973	-4259.7	399.3	2.79E-26
rs56047170	1	154528053	G	A	0.84	0.972	3162.4	298.2	5.40E-26
rs6689710	1	154470356	T	C	0.16	0.998	-3132.4	296.0	6.82E-26
rs56807273	1	154340230	C	T	0.86	0.974	-4222.4	399.2	7.23E-26
rs6662503	1	154477069	T	A	0.16	0.999	-3126.6	296.2	9.01E-26
rs6696177	1	154477263	G	A	0.16	0.999	-3126.9	296.2	9.06E-26
rs12124333	1	154478292	T	A	0.16	0.999	-3126.3	296.2	9.34E-26
rs7526247	1	154485039	T	C	0.16	0.999	-3128.0	296.4	9.42E-26
rs4288587	1	154492357	A	T	0.16	1.000	-3125.7	296.3	9.85E-26
rs4518898	1	154492432	T	C	0.16	1.000	-3125.7	296.3	9.86E-26
rs6687112	1	154497146	C	T	0.16	0.998	-3129.1	296.7	1.00E-25
rs6427716	1	154497329	C	A	0.16	0.998	-3125.1	296.6	1.10E-25
rs4845640	1	154497802	C	T	0.16	0.998	-3124.6	296.6	1.15E-25
rs4845641	1	154497930	C	G	0.16	0.998	-3124.6	296.6	1.15E-25
rs4845643	1	154498239	T	C	0.16	0.998	-3124.6	296.6	1.16E-25
rs6697103	1	154499926	C	T	0.16	0.998	-3124.6	296.6	1.16E-25
rs6697115	1	154499947	C	T	0.16	0.998	-3124.6	296.6	1.16E-25
rs6656395	1	154500016	T	C	0.16	0.998	-3124.6	296.6	1.16E-25
rs4131514	1	154500089	A	G	0.16	0.998	-3124.6	296.6	1.16E-25
rs4585969	1	154498957	C	T	0.16	0.998	-3124.5	296.6	1.16E-25
rs10908844	1	154500857	G	A	0.16	0.998	-3124.5	296.6	1.16E-25
rs4307560	1	154499345	G	A	0.16	0.998	-3124.5	296.6	1.16E-25
rs6701586	1	154499611	A	T	0.16	0.998	-3124.5	296.6	1.16E-25
rs12129484	1	154501204	C	A	0.16	0.998	-3124.5	296.6	1.16E-25
rs6427722	1	154502123	G	C	0.16	0.998	-3124.5	296.6	1.16E-25
rs6427724	1	154502499	T	A	0.16	0.998	-3124.5	296.6	1.16E-25
rs10752643	1	154503601	G	A	0.16	0.998	-3124.4	296.6	1.16E-25
rs4269769	1	154494082	G	C	0.16	0.999	-3124.1	296.6	1.17E-25
rs6670375	1	154494947	G	A	0.16	0.999	-3124.1	296.6	1.17E-25
rs4575077	1	154495011	C	A	0.16	0.999	-3124.1	296.6	1.17E-25
rs11265629	1	154498574	G	A	0.16	0.998	-3123.4	296.6	1.20E-25

rs10908846	1	154501364	C	A	0.16	0.998	-3123.4	296.6	1.20E-25
rs6691727	1	154497005	A	G	0.16	0.999	-3123.2	296.7	1.23E-25
rs11265627	1	154496286	C	A	0.16	0.998	-3122.2	296.6	1.26E-25
rs111885536	1	154461260	G	A	0.84	0.994	3126.2	297.1	1.28E-25
rs113624284	1	154339299	A	G	0.86	0.975	-4196.2	398.8	1.29E-25
rs14021	1	154452204	T	C	0.84	0.998	3116.5	296.2	1.30E-25
rs7550664	1	154528709	A	C	0.84	0.973	3139.7	298.5	1.36E-25
rs16836054	1	154462195	G	A	0.84	0.999	3113.4	296.1	1.38E-25
rs76518735	1	154454309	A	C	0.98	0.670	8211.9	781.0	1.40E-25
	1	154455249	T	C	0.98	0.670	8211.8	781.0	1.41E-25
rs12118074	1	154477585	G	A	0.16	0.999	-3113.9	296.2	1.42E-25
rs4845634	1	154464160	G	A	0.84	0.999	3113.0	296.1	1.43E-25
rs61812631	1	154467816	A	T	0.84	0.999	3112.8	296.1	1.44E-25
rs56233546	1	154471371	A	G	0.84	1.000	3112.7	296.2	1.46E-25
rs7513603	1	154481158	T	C	0.16	0.999	-3111.0	296.2	1.58E-25
rs4292956	1	154548946	C	T	0.93	0.945	4751.9	453.5	2.06E-25
rs72698167	1	154480157	G	A	0.84	1.000	3104.2	296.3	2.11E-25
rs45490696	1	154548992	C	T	0.93	0.940	4782.8	456.6	2.14E-25
rs6427729	1	154518874	G	A	0.16	0.995	-3109.1	296.9	2.21E-25
rs9427415	1	154508437	A	T	0.84	0.995	3107.0	297.0	2.42E-25
rs4845644	1	154501576	A	G	0.84	0.998	3103.5	296.7	2.46E-25
rs61812654	1	154502517	G	A	0.84	0.998	3103.5	296.7	2.46E-25
rs9427076	1	154503022	C	T	0.84	0.998	3103.0	296.7	2.50E-25
rs12135008	1	154384293	G	A	0.96	0.612	-8308.8	794.5	2.52E-25
rs4845648	1	154514338	A	T	0.84	0.997	3097.3	296.9	3.24E-25
rs61811362	1	154512495	G	A	0.84	0.997	3097.0	296.8	3.26E-25
rs12048091	1	154395077	A	G	0.84	0.910	3243.4	312.1	4.88E-25
rs67860750	1	154538917	G	C	0.85	0.712	-4805.5	463.1	5.78E-25
rs7553602	1	154529421	A	T	0.84	0.982	3080.5	297.0	6.10E-25
rs6680410	1	154550724	C	T	0.93	0.952	4679.1	451.6	6.88E-25
rs112095222	1	154627851	C	T	0.89	0.921	3981.7	384.6	7.41E-25
	1	154450510	A	C	0.98	0.669	8119.7	784.4	7.53E-25
rs10752605	1	154627213	A	G	0.11	0.926	-3953.9	382.3	8.20E-25
rs9427082	1	154523562	G	T	0.84	0.990	3068.3	297.2	1.01E-24
rs7539745	1	154526414	C	G	0.16	0.988	-3063.6	297.2	1.16E-24
rs41302545	1	154525999	C	T	0.84	0.989	3063.4	297.3	1.23E-24
	1	154450365	T	A	0.99	0.686	9532.3	927.5	1.59E-24
rs6664039	1	154337238	A	G	0.86	0.985	-4075.6	397.0	1.78E-24

rs72633647	1	154335609	T	A	0.86	0.988	-4050.4	396.5	2.96E-24
rs76093405	1	154411768	G	A	0.98	0.745	8061.6	790.8	3.72E-24
rs72633646	1	154334683	G	A	0.86	0.985	-4020.4	396.2	5.93E-24
rs77710113	1	154618623	T	C	0.94	0.859	5241.5	516.6	6.02E-24
	1	154412524	G	A	0.98	0.743	8065.8	795.9	6.74E-24
rs12023358	1	154399649	C	T	0.84	0.966	3098.0	305.9	7.34E-24
	1	154394484	G	A	0.98	0.607	-10548.2	1048.0	1.36E-23
rs11590203	1	154333569	G	T	0.86	0.981	-3989.9	396.9	1.53E-23
rs12048950	1	154394966	T	C	0.84	0.914	3138.0	314.1	2.84E-23
	1	154419517	T	A	0.98	0.575	-9871.0	989.2	3.19E-23
rs73001418	1	154585594	T	A	0.93	0.961	4507.2	452.2	3.60E-23
rs73001420	1	154586759	C	G	0.93	0.961	4506.6	452.3	3.67E-23
rs6686467	1	154329095	G	A	0.86	0.985	-3930.0	394.7	3.95E-23
rs72633645	1	154328434	C	T	0.86	0.985	-3931.5	394.9	3.97E-23
rs6698881	1	154332672	T	A	0.86	0.989	-3910.6	392.8	4.01E-23
rs61300392	1	154575685	A	T	0.93	0.973	4492.9	452.2	4.86E-23
rs12404936	1	154421530	T	C	0.98	0.337	-23260.1	2342.0	5.04E-23
rs72999485	1	154559360	G	C	0.93	0.972	4479.0	451.9	6.15E-23
rs78062588	1	154566225	T	C	0.94	0.864	5136.9	518.7	6.63E-23
rs115800464	1	154569895	G	C	0.94	0.864	5136.8	518.7	6.63E-23
rs12047973	1	154394766	A	G	0.84	0.912	3108.1	315.0	9.67E-23
rs113936582	1	154327737	C	G	0.86	0.973	-3925.4	400.2	1.67E-22
rs116805289	1	154510155	A	C	0.98	0.755	7740.3	790.7	2.03E-22
rs45478197	1	154422733	C	T	0.91	0.928	3634.5	371.4	2.07E-22
rs115617158	1	154405495	G	A	0.98	0.744	8056.2	827.2	3.30E-22
rs11576151	1	154327420	C	T	0.86	0.980	-3875.1	400.2	5.70E-22
rs116247632	1	154476522	C	T	0.98	0.612	-8942.5	926.9	7.93E-22
	1	154519249	G	A	0.98	0.612	-8934.8	927.2	8.85E-22
rs79794939	1	154390932	C	T	0.93	0.745	4987.8	524.2	2.79E-21
	1	154301261	C	A	0.86	0.903	-3945.9	415.6	3.42E-21
rs34693607	1	154661369	C	G	0.77	0.760	-3261.0	343.6	3.51E-21
rs78739139	1	154675520	G	A	0.95	0.519	-7919.4	835.7	4.03E-21
rs11264247	1	154685607	G	A	0.95	0.909	-5966.8	631.7	5.40E-21
rs4845645	1	154502909	T	A	0.18	0.922	-2828.3	301.2	8.99E-21
rs35221765	1	154345344	G	A	0.74	0.977	2713.8	289.8	1.14E-20
rs34055426	1	154345519	G	A	0.74	0.976	2714.0	290.2	1.27E-20
rs4521987	1	154388668	T	C	0.14	0.834	-3542.7	379.0	1.34E-20
rs56100876	1	154496473	G	A	0.98	0.520	-11811.6	1264.0	1.37E-20

rs4845653	1	154551368	G	A	0.85	0.887	3153.8	337.6	1.41E-20
rs75631461	1	154498153	T	C	0.98	0.520	-11798.9	1263.8	1.49E-20
	1	154608755	C	T	0.97	0.740	6976.4	747.7	1.58E-20
rs4307559	1	154499123	G	C	0.17	0.953	-2865.9	307.6	1.79E-20
rs115880387	1	154585644	A	G	0.99	0.549	-14698.5	1579.7	2.00E-20
rs114292408	1	153641058	T	C	0.99	0.607	11437.5	1230.1	2.12E-20
rs113721028	1	154293096	G	A	0.95	0.634	5890.0	634.0	2.27E-20
rs111923597	1	154293099	G	C	0.95	0.634	5889.9	634.0	2.28E-20
rs4556348	1	154394296	C	T	0.87	0.761	3464.5	376.3	4.92E-20
	1	154534480	C	T	0.98	0.710	7860.8	853.9	4.96E-20
rs11264245	1	154682776	C	T	0.95	0.956	-5776.0	627.9	5.25E-20
rs56048555	1	154630668	C	T	0.89	0.921	3608.6	393.0	6.15E-20
rs17699328	1	154322473	A	G	0.88	0.992	-3883.9	423.3	6.61E-20
rs12134719	1	154687229	A	C	0.95	0.951	-5769.8	630.1	7.76E-20
rs35013837	1	154480123	C	T	0.85	0.761	-4117.4	450.2	8.61E-20
rs2010828	1	154314225	C	T	0.88	0.997	-3869.9	424.0	1.01E-19
rs56258967	1	154334023	C	T	0.99	0.434	-15877.4	1739.8	1.03E-19
rs6427575	1	154305560	C	T	0.88	0.995	-3867.3	424.5	1.18E-19
rs6691345	1	154302826	C	T	0.88	0.992	-3859.1	424.5	1.41E-19
rs115513320	1	154668908	G	T	0.99	0.700	-9373.6	1032.6	1.59E-19
rs2297607	1	154320942	A	G	0.75	0.952	2644.1	291.5	1.67E-19
rs58892549	1	154688488	T	C	0.95	0.929	-5715.9	630.3	1.73E-19
rs11265539	1	154290852	C	G	0.88	0.970	-3864.9	428.3	2.57E-19
rs6427568	1	154290535	G	A	0.88	0.968	-3864.3	429.3	3.17E-19
rs41310887	1	154321623	G	A	0.95	0.591	6276.5	697.9	3.38E-19
rs1194583	1	154320196	T	C	0.12	0.965	3794.1	422.7	4.00E-19
rs6673495	1	154289966	G	A	0.88	0.963	-3860.9	431.1	4.69E-19
rs6687971	1	154334253	G	C	0.74	0.971	2603.7	291.9	6.44E-19
rs6687939	1	154334176	G	A	0.74	0.971	2602.3	291.9	6.79E-19
rs3103309	1	154270877	C	T	0.65	0.777	-2870.8	324.4	1.22E-18
rs4845657	1	154630335	T	C	0.81	0.967	2650.5	304.3	4.08E-18
	1	154206013	C	A	0.97	0.632	-8870.2	1028.9	8.91E-18
rs72696248	1	154212541	G	A	0.97	0.632	-8869.7	1029.0	8.99E-18
rs6426875	1	154650870	T	C	0.03	0.767	-6098.6	709.1	1.06E-17
rs55675282	1	154167180	A	C	0.97	0.631	-8796.2	1025.8	1.32E-17
rs1931299	1	154283831	G	T	0.74	0.935	2525.6	295.2	1.55E-17
rs1931298	1	154283896	C	T	0.88	0.933	-3731.5	440.9	3.39E-17
rs733228	1	154639618	T	C	0.81	0.969	2590.7	306.2	3.52E-17

rs2335251	1	154634568	T	C	0.04	0.329	10199.1	1207.3	3.88E-17
rs11578646	1	154282917	C	A	0.88	0.930	-3726.1	441.1	3.90E-17
rs115306743	1	154463784	A	C	0.98	0.721	7285.6	862.7	3.98E-17
	1	154431123	T	A	0.93	0.824	3598.6	426.8	4.46E-17
rs11588248	1	154390575	A	G	0.83	0.782	3155.6	375.2	5.29E-17
	1	154454553	A	G	0.98	0.369	-17337.6	2065.3	6.08E-17
rs116037345	1	154404454	C	T	0.97	0.890	4985.5	597.5	9.29E-17
rs56120520	1	154650381	C	T	0.81	0.952	2586.0	310.3	1.02E-16
rs61811419	1	154643702	A	G	0.81	0.972	2556.6	306.8	1.02E-16
rs11800830	1	154274638	A	G	0.88	0.922	-3693.2	443.6	1.08E-16
rs56128567	1	154274672	C	T	0.88	0.919	-3687.3	443.9	1.27E-16
	1	154428309	G	T	0.99	0.710	7981.3	964.2	1.61E-16
rs111829145	1	154545240	C	T	0.99	0.682	7791.9	941.4	1.63E-16
rs72698115	1	154379369	A	C	0.89	0.935	3301.1	400.1	2.02E-16
rs35387092	1	154288680	T	C	0.75	0.956	2433.7	295.4	2.24E-16
rs56293184	1	154288351	C	T	0.75	0.955	2431.6	295.6	2.45E-16
rs6427561	1	154287733	T	A	0.75	0.953	2426.0	295.8	3.02E-16
rs4845658	1	154643382	G	A	0.82	0.944	2590.1	315.8	3.03E-16
rs6427560	1	154287687	A	G	0.75	0.953	2425.7	295.8	3.05E-16
rs34569656	1	154670136	A	G	0.94	0.787	4011.2	489.4	3.14E-16
rs35800693	1	154284894	A	G	0.75	0.951	2418.3	295.6	3.56E-16
rs3916566	1	154282146	C	T	0.75	0.943	2430.4	297.3	3.74E-16
rs56367957	1	154283217	A	G	0.75	0.950	2415.9	295.6	3.83E-16
rs7547298	1	154281680	G	A	0.75	0.950	2414.4	295.7	4.11E-16
rs115870735	1	154472809	T	C	0.99	0.711	8094.4	992.5	4.39E-16
rs35362987	1	154279756	G	A	0.75	0.948	2411.1	296.2	5.03E-16
rs61578738	1	154278943	T	C	0.75	0.947	2411.3	296.4	5.21E-16
rs12753821	1	154628799	C	T	0.94	0.845	3850.7	473.4	5.23E-16
rs34640592	1	154276010	G	A	0.75	0.944	2416.2	297.1	5.29E-16
rs2297606	1	154321084	G	T	0.72	0.927	2356.5	290.3	5.98E-16
rs73026617	1	154369981	C	T	0.89	0.991	3126.4	387.2	8.45E-16
rs113057497	1	154367754	C	T	0.89	0.993	3119.7	386.5	8.68E-16
rs111810442	1	154369683	C	G	0.89	0.991	3124.2	387.1	8.69E-16
	1	154416805	C	T	0.99	0.533	9284.7	1152.9	1.01E-15
rs12033701	1	154365886	C	T	0.89	0.994	3113.9	386.9	1.04E-15
rs7547455	1	154371753	T	C	0.73	0.929	2362.1	293.7	1.10E-15
rs9651053	1	154359411	G	A	0.89	0.996	3108.9	386.6	1.11E-15
rs72696301	1	154355501	G	C	0.89	0.994	3105.0	386.2	1.12E-15

rs9651036	1	154360492	C	A	0.89	0.995	3108.9	386.7	1.12E-15
rs9651055	1	154360684	A	G	0.89	0.995	3108.9	386.7	1.12E-15
rs111920902	1	154361226	C	T	0.89	0.995	3108.8	386.7	1.12E-15
rs12026876	1	154361788	G	A	0.89	0.995	3108.8	386.7	1.13E-15
	1	154363137	A	T	0.89	0.995	3108.0	386.7	1.15E-15
	1	154650925	C	T	0.82	0.926	2558.0	318.6	1.23E-15
	1	154431128	G	A	0.93	0.827	3565.4	445.0	1.41E-15
rs2135694	1	154651725	C	T	0.82	0.924	2553.3	318.8	1.45E-15
rs35735180	1	154325411	G	T	0.82	0.967	2605.9	325.6	1.51E-15
rs2335254	1	154652093	G	T	0.82	0.923	2554.1	319.2	1.52E-15
	1	154367898	C	T	0.89	0.980	3124.9	391.5	1.80E-15
rs77302258	1	154396203	A	G	0.91	0.898	3273.7	411.0	2.03E-15
rs112203594	1	154553430	C	A	0.98	0.643	7310.4	918.1	2.08E-15
	1	154335324	C	T	0.98	0.705	-9698.4	1227.3	3.37E-15
rs12075836	1	154371487	C	T	0.86	0.927	2881.1	365.8	4.15E-15
	1	154331320	C	T	0.98	0.700	-9663.9	1228.2	4.40E-15
rs111908494	1	154368095	A	G	0.90	0.963	3167.3	402.8	4.62E-15
rs61386354	1	154685551	G	A	0.97	0.458	8214.5	1045.6	4.84E-15
	1	154328261	C	T	0.98	0.699	-9658.2	1230.2	5.06E-15
rs113639721	1	154368098	T	C	0.89	0.978	3106.3	396.9	6.09E-15
	1	154532599	A	T	0.89	0.765	3126.8	401.1	7.85E-15
rs6427721	1	154501770	A	G	0.18	0.907	-2394.2	307.7	8.77E-15
	1	154536197	A	G	0.98	0.642	7580.3	977.5	1.07E-14
rs115697580	1	154517689	G	A	0.98	0.780	5697.6	736.3	1.22E-14
	1	154368224	C	T	0.89	0.971	3067.3	396.8	1.30E-14
	1	154368223	G	A	0.97	0.667	-6262.1	810.3	1.32E-14
rs78038982	1	154539156	G	T	0.98	0.642	7538.7	976.1	1.37E-14
	1	154479486	G	A	0.98	0.644	7513.1	973.2	1.41E-14
	1	154499328	G	A	0.98	0.657	-9007.7	1171.6	1.80E-14
	1	154469825	T	C	0.98	0.657	-9009.7	1172.3	1.83E-14
rs6688376	1	154326366	C	T	0.70	0.959	2211.3	287.9	1.91E-14
	1	154645937	T	C	0.98	0.702	7658.0	999.3	2.18E-14
rs41304075	1	154507190	T	C	0.98	0.666	-8979.1	1175.9	2.69E-14
	1	154418200	C	T	0.99	0.459	11666.9	1532.0	3.14E-14
	1	154333027	G	T	0.98	0.877	6145.5	812.7	4.74E-14
rs1626035	1	154311144	C	T	0.27	0.999	-2121.3	280.7	4.89E-14
rs1352333	1	154310677	C	A	0.27	0.999	-2121.0	280.7	4.94E-14
rs11809740	1	154319689	G	A	0.73	0.998	2123.0	281.0	5.03E-14

rs2481064	1	154309474	G	A	0.27	0.999	-2119.4	280.7	5.18E-14
rs2483711	1	154309444	T	A	0.27	0.999	-2119.3	280.7	5.19E-14
rs111237020	1	153842032	C	T	0.96	0.553	-6446.3	854.6	5.45E-14
rs1760796	1	154307664	A	G	0.27	0.999	-2117.6	280.7	5.45E-14
rs2274988	1	154316434	C	T	0.73	0.993	2121.8	281.4	5.54E-14
rs2988721	1	154308641	A	C	0.27	0.997	-2118.6	280.9	5.55E-14
rs2483710	1	154306180	G	A	0.27	0.997	-2118.0	280.9	5.58E-14
	1	154637113	G	A	0.98	0.660	-8326.1	1104.9	5.78E-14
rs115178836	1	154011624	C	A	0.99	0.538	8417.0	1117.4	5.90E-14
rs35463210	1	154313764	C	A	0.73	0.999	2116.0	281.0	6.00E-14
rs12131108	1	154657905	C	A	0.60	0.868	2058.6	274.3	7.28E-14
rs115200978	1	154374850	C	T	0.98	0.608	-10185.2	1360.2	8.29E-14
	1	154510957	T	C	0.98	0.365	-14964.3	2014.4	1.29E-13
rs115224285	1	154411473	C	T	0.98	0.522	9485.5	1278.2	1.37E-13
rs28654266	1	153942593	C	T	0.98	0.573	6918.5	938.0	1.92E-13
rs77490383	1	153899248	G	T	0.98	0.686	6495.3	884.8	2.48E-13
	1	154307776	C	T	0.98	0.880	6104.0	831.9	2.54E-13
rs11802757	1	154658849	G	C	0.60	0.871	1996.6	273.3	3.20E-13
	1	154433897	G	A	0.97	0.799	5351.8	733.3	3.40E-13
rs12090237	1	154389741	G	A	0.99	0.492	-10025.5	1374.2	3.46E-13
rs6426880	1	154655042	G	A	0.10	0.922	3381.4	464.2	3.76E-13
rs3887104	1	154376671	C	T	0.83	0.857	2629.8	361.2	3.87E-13
rs12138773	1	153843489	C	A	0.97	0.751	-6063.6	836.5	4.87E-13
rs72698126	1	154388686	A	G	0.99	0.495	-9938.7	1373.1	5.27E-13
rs1027809	1	154656371	C	G	0.10	0.915	3371.2	466.2	5.53E-13
	1	153870483	A	C	0.97	0.747	-6093.1	842.7	5.56E-13
rs72698128	1	154391819	G	A	0.99	0.510	-10025.0	1386.5	5.57E-13
rs114492020	1	154044615	A	G	0.98	0.676	5749.4	796.0	5.90E-13
rs6701860	1	154653632	A	G	0.10	0.924	3341.2	465.6	8.24E-13
rs72698123	1	154387025	T	C	0.99	0.498	-9793.7	1369.9	1.00E-12
rs11265607	1	154357678	A	G	0.71	0.997	-2094.9	293.2	1.04E-12
rs6427631	1	154370020	T	C	0.71	0.984	-2104.6	294.7	1.06E-12
rs6670683	1	154623950	A	G	0.04	0.309	8156.4	1147.9	1.38E-12
rs2481065	1	154311911	G	A	0.12	0.998	-2651.2	373.3	1.40E-12
rs1209264	1	154305010	A	G	0.12	0.997	-2649.6	373.3	1.45E-12
rs11265609	1	154364328	C	T	0.71	0.998	-2078.8	292.9	1.47E-12
rs9724691	1	154365235	T	A	0.71	0.998	-2075.2	292.9	1.61E-12
rs10908426	1	154657909	C	T	0.10	0.929	3290.6	466.3	1.95E-12

rs55886061	1	154383261	C	T	0.99	0.502	-9610.4	1364.6	2.16E-12
	1	154320191	C	T	0.88	0.997	2632.1	374.0	2.22E-12
rs1205591	1	154298374	T	G	0.12	0.992	-2631.9	374.0	2.24E-12
rs7411976	1	154382443	A	C	0.99	0.502	-9593.6	1364.1	2.31E-12
rs114821176	1	154004498	G	A	0.98	0.833	5901.4	839.8	2.41E-12
rs9662562	1	154364762	A	T	0.71	0.996	-2059.1	293.2	2.50E-12
rs61806853	1	154154587	T	C	0.95	0.786	-4601.0	655.6	2.56E-12
rs72698116	1	154380934	A	G	0.99	0.502	-9558.4	1362.7	2.64E-12
	1	154362445	C	T	0.72	0.982	-2079.3	296.8	2.77E-12
rs1395566	1	154658966	A	G	0.10	0.930	3259.9	465.9	2.96E-12
rs72698118	1	154381781	T	C	0.99	0.498	-9521.7	1360.8	2.98E-12
rs6672010	1	154292161	C	T	0.70	0.992	1989.4	285.1	3.40E-12
rs12727865	1	154303705	C	T	0.70	0.999	1984.4	284.8	3.64E-12
rs58548028	1	154347784	G	A	0.89	0.965	2751.1	394.9	3.69E-12
rs12077870	1	154305190	G	C	0.70	0.998	1982.2	284.8	3.86E-12
rs6702754	1	154303976	T	C	0.70	0.997	1981.0	284.8	4.01E-12
rs10737169	1	154653704	T	C	0.10	0.912	3286.7	472.6	4.02E-12
rs6685323	1	154295592	C	T	0.70	0.998	1975.1	284.3	4.21E-12
rs116828691	1	154080990	T	C	0.97	0.748	-6608.1	951.2	4.22E-12
rs3890153	1	154295089	C	G	0.70	0.999	1972.3	284.3	4.51E-12
rs12748146	1	154292982	T	A	0.70	0.998	1968.5	284.2	4.86E-12
rs6668968	1	154293675	G	A	0.70	0.998	1968.5	284.2	4.89E-12
	1	154075227	C	A	0.97	0.784	4924.3	711.0	4.92E-12
rs35950207	1	154291958	C	T	0.70	0.999	1965.7	283.9	4.94E-12
	1	154303783	G	A	0.98	0.846	5234.6	760.2	6.49E-12
	1	154445362	G	T	0.99	0.591	8179.2	1188.9	6.78E-12
	1	154475027	C	T	0.99	0.401	-10883.0	1595.5	1.02E-11
rs115188583	1	153849029	T	C	0.99	0.657	6958.0	1027.1	1.40E-11
rs11265606	1	154356459	C	T	0.71	0.985	-1986.1	293.5	1.48E-11
	1	154064138	G	A	0.89	0.857	2765.1	409.2	1.57E-11
rs2633438	1	154308508	G	A	0.28	0.982	-1890.1	280.2	1.70E-11
	1	154252188	A	G	0.99	0.732	-10114.6	1503.4	1.92E-11
	1	153389207	G	A	0.98	0.440	7330.4	1089.7	1.94E-11
rs114980362	1	154209281	C	T	0.98	0.864	5345.8	795.8	2.06E-11
rs114779784	1	154239549	G	C	0.98	0.695	5514.2	822.0	2.20E-11
rs6676680	1	154662203	G	A	0.60	0.828	1890.3	282.8	2.59E-11
rs36046176	1	154355875	A	G	0.92	0.867	3240.3	488.5	3.64E-11
	1	153962327	C	T	0.99	0.396	-13519.7	2048.6	4.57E-11

rs2230324	1	153954646	C	T	0.96	0.833	-4408.1	673.1	6.42E-11
rs41264642	1	153392663	G	A	0.98	0.440	7029.7	1075.9	7.08E-11
rs76401668	1	154610358	G	A	0.98	0.656	6181.9	949.6	8.26E-11
	1	153768598	G	A	0.98	0.869	5170.5	798.0	1.02E-10
rs12130660	1	154088258	T	C	0.95	0.812	-4282.6	662.3	1.11E-10
rs12135246	1	154618028	A	G	0.97	0.336	8098.6	1253.6	1.15E-10
rs115165870	1	154303228	G	A	0.97	0.854	4319.7	671.4	1.37E-10
rs10908840	1	154459477	C	T	0.52	0.953	-1763.2	274.1	1.39E-10
rs116039813	1	154185514	G	T	0.97	0.727	4905.2	764.0	1.49E-10
rs114639817	1	154186137	G	T	0.97	0.727	4904.8	764.0	1.50E-10
rs114772434	1	154182928	C	G	0.97	0.727	4905.2	764.1	1.50E-10
rs114003180	1	153820352	T	C	0.98	0.863	5221.9	814.3	1.57E-10
	1	154317077	G	A	0.99	0.649	6392.2	1003.5	2.07E-10
rs10797084	1	154264736	C	T	0.69	0.866	-1929.6	303.7	2.28E-10
	1	154011426	A	C	0.99	0.849	6189.6	975.2	2.40E-10
	1	154697624	C	G	0.97	0.495	5532.7	876.2	2.95E-10
	1	153985235	A	C	0.99	0.862	6119.5	971.6	3.28E-10
	1	153962470	A	G	0.99	0.865	6101.4	971.0	3.60E-10
rs114166921	1	154211108	G	A	0.99	0.720	-9853.8	1568.3	3.62E-10
	5	61040597	C	T	0.99	0.613	6938.6	1107.0	3.98E-10
rs12069266	1	154664175	G	T	0.60	0.858	1730.4	276.9	4.51E-10
rs75940909	1	153932075	G	A	0.99	0.875	6053.7	969.6	4.65E-10
rs6427641	1	154380486	G	A	0.45	0.850	1775.3	284.8	4.99E-10
	1	154072601	G	A	0.97	0.785	4279.2	686.7	5.01E-10
rs10908804	1	154262857	A	C	0.69	0.885	-1860.4	299.3	5.58E-10
rs111412860	1	154462988	T	A	0.96	0.331	-7693.3	1242.7	6.48E-10
	1	153885456	C	T	0.99	0.880	5970.4	967.0	7.20E-10
	1	153872026	G	A	0.99	0.869	6358.0	1035.4	8.89E-10
	1	154100908	C	T	0.99	0.770	6655.5	1089.2	1.07E-09
	1	154301378	T	C	0.88	0.490	3115.6	510.6	1.13E-09
rs78740769	1	153789150	C	A	0.96	0.539	-5519.3	908.2	1.32E-09
	1	153874665	G	A	0.99	0.868	6080.7	1002.8	1.43E-09
rs1979575	1	154318172	A	G	0.85	0.999	2160.6	357.9	1.68E-09
rs11580594	1	154291386	C	T	0.85	0.986	2167.2	359.4	1.76E-09
rs76789167	1	153805095	T	C	0.99	0.853	5890.5	977.7	1.82E-09
rs11580613	1	154291559	C	T	0.85	0.991	2154.2	359.3	2.17E-09
rs9660850	1	154317281	G	A	0.85	0.991	2141.2	358.4	2.48E-09
	1	153872788	A	C	0.99	0.741	-8821.5	1483.9	2.96E-09

rs116612897	1	154663267	G	A	0.98	0.683	5595.9	943.0	3.17E-09
	1	154006203	T	C	0.98	0.743	4767.5	808.0	3.87E-09
rs61812595	1	154411852	G	A	0.94	0.843	2886.9	492.5	4.88E-09
rs7547947	1	154651751	A	T	0.71	0.914	1804.5	308.0	4.97E-09
	1	154540865	G	T	0.98	0.543	4949.8	845.4	5.09E-09
	1	153850697	T	C	0.99	0.840	6613.1	1130.5	5.25E-09
	1	153828359	A	G	0.99	0.840	6612.2	1130.5	5.28E-09
rs1552483	1	154324898	G	A	0.15	0.980	-2078.2	356.4	5.88E-09
rs56211693	1	154355008	C	T	0.70	0.992	-1697.6	292.1	6.58E-09
rs41313936	1	153617749	C	T	0.98	0.558	5170.0	892.0	7.22E-09
	1	154351995	G	A	0.93	0.858	3034.8	524.7	7.74E-09
rs11580178	1	154353262	T	A	0.70	0.992	-1690.6	292.6	8.05E-09
rs76697909	1	153451003	C	T	0.99	0.450	7019.6	1215.4	8.16E-09
rs1889315	1	154351960	T	C	0.70	0.991	-1688.0	292.7	8.56E-09
rs34437053	1	154351199	G	A	0.70	0.991	-1686.1	292.7	8.96E-09
	1	153454043	G	A	0.99	0.449	7007.5	1217.2	9.10E-09
	1	153965150	C	G	0.99	0.710	6617.7	1149.6	9.13E-09
rs10908834	1	154349381	C	T	0.30	0.989	1678.3	292.6	1.03E-08
rs114603881	1	154293923	T	G	0.96	0.802	3522.3	615.2	1.10E-08
rs55874907	1	153903129	C	T	0.95	0.839	-3744.2	654.4	1.12E-08
rs1889314	1	154351880	G	A	0.30	0.990	1670.7	292.6	1.19E-08
rs112505856	1	154107960	C	T	0.96	0.495	-5734.3	1005.9	1.27E-08
rs116038461	1	153412147	G	A	0.98	0.455	6808.1	1195.8	1.32E-08
rs41308403	1	154294560	C	T	0.92	0.935	2612.1	459.0	1.34E-08
rs115891382	1	154277834	T	C	0.96	0.804	3513.0	617.4	1.35E-08
rs79438264	1	154611891	C	T	0.97	0.619	-5075.4	894.9	1.50E-08
rs4845387	1	154645691	G	A	0.30	0.932	-1727.5	305.0	1.56E-08
rs391831	8	90685350	G	A	0.08	0.574	-3089.2	547.2	1.75E-08
	1	154643536	C	T	0.29	0.946	-1712.1	303.6	1.80E-08
	1	153743937	T	C	0.98	0.885	4499.9	798.8	1.87E-08
	1	153737991	T	C	0.98	0.885	4488.6	796.8	1.87E-08
	1	153880288	T	C	0.99	0.725	-8730.0	1550.4	1.90E-08
rs116072155	1	153831877	G	A	0.99	0.725	-8730.2	1550.5	1.90E-08
rs2280781	1	154540468	C	T	0.92	0.929	2408.2	429.4	2.17E-08
	1	154257452	C	T	0.99	0.747	-8268.1	1494.8	3.35E-08
rs113191295	1	153912623	G	A	0.95	0.593	-4468.4	809.0	3.50E-08
rs71503474	8	90685351	A	C	0.09	0.562	-2976.2	540.6	3.87E-08
	20	429758	G	A	0.99	0.380	7743.4	1409.9	4.18E-08

[A] rsnumber is given where available
[B] Base pair position build 37/hg19
[C] Allele 1 (effect allele)
[D] Allele 2
[E] Frequency of allele 1
[F] Info= Imputation quality metric from SNPtest
[G] Beta for the effect on sIL-6R levels associated with allele 1.
[H] SE = Standard error of the beta estimate

Table S3: SNP information and Conditional GWAS results of all 293 SNPs reaching genome wide significance in the GWAS of sIL-6R level after correction for the effect of rs2228145.

SNP[A]	Chr	Position[B]	A1[C]	A2[D]	Frequency A1[E]	Info[F]	Beta[G]	SE[H]	*P* value
rs6694258	1	154428505	C	A	0.45	0.991	-3458.1	244.1	1.43E-44
rs6689393	1	154426097	A	G	0.45	0.993	-3420.2	244.7	1.85E-43
rs7526131	1	154425135	G	A	0.45	0.993	-3409.1	244.6	3.23E-43
rs7536152	1	154423909	A	G	0.45	0.992	-3404.6	244.6	4.15E-43
rs12129500	1	154423764	T	C	0.45	0.992	-3402.3	244.7	4.74E-43
rs6686750	1	154419843	A	G	0.45	0.990	-3387.8	245.0	1.35E-42
rs11265612	1	154417044	A	G	0.44	0.975	-3334.0	244.1	1.30E-41
rs12404927	1	154421438	T	C	0.48	0.931	-3176.9	232.9	1.61E-41
rs6683206	1	154418088	T	C	0.44	0.969	-3321.0	245.7	8.15E-41
rs7549250	1	154404336	C	T	0.45	0.970	-3270.3	243.9	3.45E-40
rs6667434	1	154409100	A	G	0.44	0.969	-3246.5	242.4	4.20E-40
rs4845371	1	154408340	T	C	0.44	0.969	-3241.7	242.3	4.74E-40
rs4845619	1	154405058	T	G	0.45	0.970	-3277.8	245.2	5.64E-40
rs59632925	1	154406540	T	G	0.44	0.970	-3222.6	241.8	9.19E-40
rs7549338	1	154404380	C	G	0.44	0.970	-3208.6	241.3	1.43E-39
rs6694817	1	154401972	T	C	0.45	0.965	-3155.8	238.8	4.12E-39
rs6427658	1	154400799	T	C	0.45	0.965	-3123.7	238.0	1.24E-38
rs6687726	1	154400320	A	G	0.45	0.969	-3147.8	242.1	5.87E-38
rs12117832	1	154397610	A	G	0.45	0.959	-3093.0	238.4	8.35E-38
rs12118721	1	154397416	T	C	0.45	0.961	-3150.0	242.8	8.54E-38
rs10908838	1	154397984	T	G	0.44	0.963	-3091.4	239.3	1.71E-37
rs12118770	1	154397589	T	C	0.44	0.959	-3071.4	238.8	3.52E-37
rs6689306	1	154395946	A	G	0.45	0.937	-3090.6	241.9	1.03E-36
rs10908836	1	154397932	C	T	0.46	0.913	-2956.2	231.5	1.09E-36
rs35109459	1	154397933	G	A	0.47	0.917	-3002.4	236.9	3.64E-36
rs4308966	1	154432622	T	C	0.84	0.994	-3047.7	242.6	1.41E-35
rs4345796	1	154436750	C	T	0.84	0.985	-3057.8	243.7	1.65E-35
rs61812626	1	154436436	G	A	0.84	0.984	-3061.8	244.1	1.81E-35
rs4845374	1	154426947	T	A	0.84	0.992	-3047.7	243.8	3.01E-35
rs10159236	1	154431405	C	A	0.84	0.983	-3037.9	243.5	4.00E-35
rs11804305	1	154424497	C	T	0.84	0.992	-3048.6	244.4	4.13E-35
rs61812599	1	154421554	G	A	0.84	0.988	-3032.3	246.3	2.93E-34
rs61811362	1	154512495	G	A	0.84	0.997	-2976.0	242.9	5.74E-34
rs4845648	1	154514338	A	T	0.84	0.997	-2974.6	242.9	6.18E-34

rs9427076	1	154503022	C	T	0.84	0.998	-2966.6	242.7	8.15E-34
rs4845644	1	154501576	A	G	0.84	0.998	-2965.7	242.7	8.45E-34
rs61812654	1	154502517	G	A	0.84	0.998	-2965.7	242.7	8.48E-34
rs14021	1	154452204	T	C	0.84	0.998	-2966.1	242.8	9.19E-34
rs6427729	1	154518874	G	A	0.16	0.995	2968.3	243.0	9.21E-34
rs9427415	1	154508437	A	T	0.84	0.995	-2967.4	243.1	9.80E-34
rs11265627	1	154496286	C	A	0.16	0.998	2961.6	242.6	1.01E-33
rs72698167	1	154480157	G	A	0.84	1.000	-2963.9	242.8	1.01E-33
rs6691727	1	154497005	A	G	0.16	0.999	2961.4	242.6	1.04E-33
rs6670375	1	154494947	G	A	0.16	0.999	2960.5	242.6	1.06E-33
rs4575077	1	154495011	C	A	0.16	0.999	2960.5	242.6	1.06E-33
rs4269769	1	154494082	G	C	0.16	0.999	2960.4	242.6	1.06E-33
rs56233546	1	154471371	A	G	0.84	1.000	-2960.5	242.7	1.13E-33
rs4845634	1	154464160	G	A	0.84	0.999	-2960.0	242.7	1.13E-33
rs16836054	1	154462195	G	A	0.84	0.999	-2959.4	242.6	1.13E-33
rs61812631	1	154467816	A	T	0.84	0.999	-2960.2	242.7	1.13E-33
rs7513603	1	154481158	T	C	0.16	0.999	2961.0	242.8	1.16E-33
rs111885536	1	154461260	G	A	0.84	0.994	-2969.8	243.5	1.18E-33
rs12118074	1	154477585	G	A	0.16	0.999	2960.9	242.8	1.18E-33
rs6687112	1	154497146	C	T	0.16	0.998	2957.3	242.7	1.34E-33
rs9427082	1	154523562	G	T	0.84	0.990	-2960.8	243.1	1.41E-33
rs4845640	1	154497802	C	T	0.16	0.998	2955.0	242.7	1.43E-33
rs4845641	1	154497930	C	G	0.16	0.998	2955.0	242.7	1.43E-33
rs4845643	1	154498239	T	C	0.16	0.998	2955.0	242.7	1.43E-33
rs4585969	1	154498957	C	T	0.16	0.998	2954.9	242.7	1.43E-33
rs4307560	1	154499345	G	A	0.16	0.998	2954.9	242.7	1.43E-33
rs11265629	1	154498574	G	A	0.16	0.998	2954.9	242.7	1.43E-33
rs6701586	1	154499611	A	T	0.16	0.998	2954.9	242.7	1.43E-33
rs6697103	1	154499926	C	T	0.16	0.998	2954.9	242.7	1.44E-33
rs6697115	1	154499947	C	T	0.16	0.998	2954.8	242.7	1.44E-33
rs6656395	1	154500016	T	C	0.16	0.998	2954.8	242.7	1.44E-33
rs4131514	1	154500089	A	G	0.16	0.998	2954.8	242.7	1.44E-33
rs10908844	1	154500857	G	A	0.16	0.998	2954.8	242.7	1.44E-33
rs12129484	1	154501204	C	A	0.16	0.998	2954.8	242.7	1.44E-33
rs10908846	1	154501364	C	A	0.16	0.998	2954.7	242.7	1.44E-33
rs6427722	1	154502123	G	C	0.16	0.998	2954.7	242.7	1.45E-33
rs6427724	1	154502499	T	A	0.16	0.998	2954.7	242.7	1.45E-33
rs10752643	1	154503601	G	A	0.16	0.998	2954.7	242.7	1.45E-33

rs4518898	1	154492432	T	C	0.16	1.000	2952.2	242.8	1.74E-33
rs4288587	1	154492357	A	T	0.16	1.000	2952.2	242.8	1.75E-33
rs6662503	1	154477069	T	A	0.16	0.999	2952.2	242.8	1.76E-33
rs6696177	1	154477263	G	A	0.16	0.999	2952.4	242.8	1.77E-33
rs6689710	1	154470356	T	C	0.16	0.998	2949.9	242.6	1.80E-33
rs12124333	1	154478292	T	A	0.16	0.999	2952.1	242.8	1.80E-33
rs7526247	1	154485039	T	C	0.16	0.999	2951.0	242.8	1.93E-33
rs41302545	1	154525999	C	T	0.84	0.989	-2955.6	243.3	2.04E-33
rs4845626	1	154423485	G	T	0.84	0.985	-2966.7	244.2	2.06E-33
rs6427716	1	154497329	C	A	0.16	0.998	2945.3	242.6	2.21E-33
rs7539745	1	154526414	C	G	0.16	0.988	2952.2	243.3	2.45E-33
rs111301013	1	154419584	C	A	0.84	0.988	-3013.3	248.7	3.03E-33
rs7553602	1	154529421	A	T	0.84	0.982	-2927.2	243.5	9.01E-33
rs7550664	1	154528709	A	C	0.84	0.973	-2937.6	245.0	1.28E-32
rs56047170	1	154528053	G	A	0.84	0.972	-2933.7	245.0	1.53E-32
rs4307559	1	154499123	G	C	0.17	0.953	3041.1	254.1	1.68E-32
rs12047973	1	154394766	A	G	0.84	0.912	-3133.2	262.8	2.85E-32
rs12048950	1	154394966	T	C	0.84	0.914	-3118.9	262.4	4.30E-32
rs55800510	1	154417187	C	T	0.84	0.976	-3005.1	253.2	5.31E-32
rs6427720	1	154501756	G	A	0.17	0.980	2861.2	241.7	7.39E-32
rs12048091	1	154395077	A	G	0.84	0.910	-3087.7	260.9	7.80E-32
rs61812592	1	154410482	G	A	0.84	0.973	-3001.8	254.1	1.03E-31
rs61812593	1	154410490	T	C	0.84	0.973	-3001.7	254.1	1.03E-31
rs12023358	1	154399649	C	T	0.84	0.966	-3036.1	257.3	1.16E-31
rs4845645	1	154502909	T	A	0.18	0.922	2847.6	241.3	1.19E-31
rs57502626	1	154408916	T	A	0.84	0.973	-3001.5	254.4	1.21E-31
rs61812594	1	154411628	A	G	0.84	0.974	-2998.0	254.2	1.28E-31
rs55826755	1	154409520	C	G	0.84	0.973	-2999.6	254.5	1.37E-31
rs61812596	1	154414691	C	T	0.84	0.976	-2990.4	253.9	1.48E-31
rs11265634	1	154522248	A	G	0.17	0.984	2835.5	240.9	1.62E-31
rs11265611	1	154395125	G	A	0.42	0.894	-2789.6	242.4	3.22E-30
rs6427721	1	154501770	A	G	0.18	0.907	2868.2	249.3	3.30E-30
rs6703672	1	154474557	T	C	0.20	0.902	2591.9	235.9	1.03E-27
rs4556348	1	154394296	C	T	0.87	0.761	-3240.3	316.1	2.22E-24
rs11265616	1	154419980	T	C	0.60	0.702	-2426.7	237.7	3.42E-24
rs12128984	1	154498406	G	A	0.23	0.772	2415.0	239.2	1.03E-23
rs10465961	1	154487354	T	A	0.26	0.729	2381.1	236.2	1.23E-23
rs6690230	1	154432877	C	G	0.40	0.990	1900.7	209.2	1.56E-19

rs6695045	1	154432957	A	G	0.40	0.990	1900.4	209.3	1.59E-19
	1	154431123	T	A	0.93	0.824	-3080.9	343.7	4.57E-19
rs45478197	1	154422733	C	T	0.91	0.928	-2594.7	306.1	3.12E-17
rs11265621	1	154442960	G	A	0.37	0.991	1777.8	210.2	3.68E-17
	1	154431128	G	A	0.93	0.827	-3023.8	357.5	3.70E-17
rs4478801	1	154464572	G	A	0.37	0.994	1770.2	210.5	5.46E-17
rs6658175	1	154475330	T	A	0.37	0.997	1757.8	210.7	9.62E-17
rs6684921	1	154464945	A	C	0.37	0.997	1758.6	211.0	1.05E-16
rs12119111	1	154478600	G	A	0.37	0.998	1753.8	210.6	1.09E-16
rs12133641	1	154428283	A	G	0.61	0.993	-13784.0	1656.1	1.13E-16
rs9660786	1	154484017	A	T	0.37	0.998	1751.3	210.6	1.19E-16
rs7518694	1	154484788	C	G	0.37	0.998	1751.2	210.6	1.19E-16
rs7519499	1	154487926	G	A	0.37	0.998	1751.1	210.6	1.20E-16
rs4845639	1	154490352	C	T	0.37	0.998	1751.0	210.6	1.20E-16
rs6686276	1	154466188	C	A	0.37	0.998	1752.8	210.9	1.24E-16
rs6700296	1	154473660	T	C	0.37	0.998	1752.7	210.9	1.25E-16
rs6689965	1	154470606	T	A	0.37	0.999	1752.3	210.9	1.26E-16
rs12753680	1	154474900	G	A	0.37	0.998	1751.5	210.9	1.31E-16
rs12118018	1	154477440	G	A	0.37	0.999	1750.3	210.8	1.33E-16
rs6664608	1	154479670	C	T	0.37	0.999	1749.1	210.7	1.35E-16
rs4845637	1	154490178	A	G	0.37	0.998	1748.9	210.8	1.40E-16
rs10908841	1	154487763	C	T	0.37	0.998	1748.4	210.7	1.40E-16
rs12740969	1	154487060	T	G	0.37	0.998	1748.0	210.7	1.42E-16
rs12128408	1	154488533	A	G	0.37	0.998	1747.9	210.7	1.42E-16
rs4845638	1	154490269	T	A	0.37	0.998	1747.9	210.7	1.43E-16
rs10908842	1	154492702	G	A	0.37	0.998	1747.6	210.7	1.45E-16
rs6698971	1	154475331	C	A	0.37	0.995	1754.1	211.6	1.48E-16
rs4345797	1	154495675	C	T	0.37	0.997	1730.8	211.5	3.54E-16
rs10908843	1	154494480	C	G	0.37	0.997	1728.2	211.6	4.06E-16
rs11265628	1	154496489	C	T	0.37	0.997	1728.0	211.6	4.10E-16
rs4845647	1	154514331	C	A	0.37	0.995	1719.8	212.3	7.00E-16
rs12136771	1	154511502	T	C	0.37	0.994	1720.9	212.5	7.27E-16
rs10908847	1	154504954	G	A	0.37	0.995	1723.3	213.0	7.57E-16
rs11265632	1	154514067	G	A	0.37	0.995	1717.0	212.4	8.05E-16
rs4845642	1	154498028	G	A	0.37	0.996	1715.0	212.1	8.06E-16
rs10908845	1	154500898	C	T	0.37	0.996	1714.4	212.2	8.38E-16
rs4382717	1	154518610	C	T	0.37	0.989	1712.5	212.4	9.50E-16
rs12407048	1	154505270	C	T	0.37	0.997	1710.7	212.4	1.01E-15

rs4638123	1	154505704	C	T	0.37	0.997	1710.6	212.4	1.02E-15
rs12037271	1	154507888	G	A	0.37	0.996	1710.6	212.4	1.02E-15
rs6688376	1	154326366	C	T	0.70	0.959	1516.3	189.5	1.55E-15
rs77302258	1	154396203	A	G	0.91	0.898	-2581.9	325.6	2.77E-15
rs55908418	1	154513387	A	C	0.94	0.926	-3002.6	378.8	2.82E-15
rs12753666	1	154474875	G	A	0.37	0.986	1666.1	210.9	3.54E-15
rs72698182	1	154533863	G	C	0.93	0.905	-2967.3	376.5	4.06E-15
rs12083537	1	154381103	A	G	0.79	0.850	1843.7	234.9	5.25E-15
rs1386821	1	154382049	T	G	0.80	0.804	1919.9	247.8	1.16E-14
rs61812598	1	154420087	G	A	0.61	0.993	-13155.7	1704.3	1.44E-14
rs1889312	1	154326473	G	A	0.57	0.978	1364.8	177.7	1.96E-14
rs61812595	1	154411852	G	A	0.94	0.843	-3156.7	422.4	9.38E-14
rs61811370	1	154537502	T	A	0.93	0.988	-2580.9	355.0	4.23E-13
rs61811371	1	154537505	T	C	0.93	0.988	-2580.7	355.0	4.25E-13
rs4845378	1	154544651	G	T	0.93	0.951	-2599.6	360.0	6.06E-13
rs77994623	1	154505106	C	T	0.84	0.933	1665.2	230.7	6.19E-13
rs78664422	1	154499246	G	A	0.84	0.944	1659.1	230.0	6.35E-13
rs6662003	1	154343588	C	T	0.86	0.921	1848.4	257.0	7.47E-13
rs12077265	1	154359915	T	G	0.84	0.955	1728.7	241.3	9.23E-13
rs61804489	1	154354643	C	T	0.85	0.979	1718.2	240.2	9.86E-13
rs61804488	1	154354370	A	G	0.85	0.979	1717.8	240.2	1.00E-12
rs61812565	1	154363305	C	T	0.85	0.972	1726.5	241.5	1.01E-12
rs68138282	1	154363441	C	T	0.85	0.972	1726.4	241.5	1.01E-12
rs112527081	1	154354257	G	A	0.85	0.979	1717.6	240.2	1.01E-12
rs36029470	1	154352194	T	C	0.84	0.974	1719.3	240.5	1.02E-12
rs34065906	1	154354129	G	A	0.85	0.979	1717.3	240.2	1.03E-12
rs34146123	1	154353846	C	A	0.85	0.979	1716.7	240.2	1.05E-12
rs35595831	1	154353743	C	T	0.85	0.979	1716.3	240.2	1.06E-12
rs35629421	1	154352252	C	A	0.85	0.980	1714.4	240.3	1.13E-12
rs35091500	1	154352310	G	A	0.85	0.980	1714.3	240.3	1.13E-12
rs35112510	1	154352165	T	C	0.85	0.980	1714.3	240.3	1.13E-12
rs4304577	1	154352133	T	C	0.85	0.980	1714.3	240.3	1.13E-12
rs1889316	1	154352017	C	T	0.85	0.980	1714.0	240.3	1.14E-12
rs16865579	1	154351073	T	C	0.85	0.980	1713.4	240.3	1.17E-12
rs3811451	1	154350589	T	C	0.85	0.980	1713.2	240.3	1.18E-12
rs61803414	1	154350238	C	G	0.85	0.980	1712.9	240.3	1.19E-12
rs6690468	1	154349639	T	A	0.85	0.980	1712.3	240.3	1.21E-12
rs34749203	1	154352641	C	T	0.85	0.977	1717.8	241.2	1.25E-12

rs6661998	1	154343576	C	T	0.88	0.848	2025.5	284.8	1.32E-12
rs2280781	1	154540468	C	T	0.92	0.929	-2504.5	352.5	1.41E-12
rs28410194	1	154348336	C	T	0.85	0.980	1701.6	240.2	1.61E-12
rs28530583	1	154348332	C	G	0.85	0.980	1701.5	240.2	1.61E-12
rs61811372	1	154543215	T	C	0.93	0.971	-2527.3	357.2	1.73E-12
rs61803412	1	154348199	A	G	0.85	0.980	1698.8	240.2	1.75E-12
rs71586008	1	154343577	A	G	0.87	0.855	1985.0	282.7	2.53E-12
rs4622059	1	154347662	C	T	0.85	0.981	1687.1	240.6	2.71E-12
rs4526605	1	154347467	C	T	0.84	0.982	1684.4	240.4	2.84E-12
rs9728024	1	154346161	C	T	0.85	0.966	1700.2	243.6	3.42E-12
rs9727988	1	154345857	C	T	0.84	0.942	1684.3	242.4	4.22E-12
rs4406622	1	154346416	A	G	0.84	0.982	1673.3	241.5	4.83E-12
rs6663105	1	154346950	G	C	0.84	0.982	1672.7	241.4	4.84E-12
rs12072348	1	154547292	A	C	0.91	0.855	-2340.7	337.8	4.86E-12
rs6662855	1	154346669	G	A	0.84	0.982	1672.3	241.4	4.92E-12
rs7530868	1	154345567	T	C	0.84	0.982	1671.7	241.4	5.02E-12
rs7530735	1	154345371	T	C	0.84	0.982	1671.5	241.4	5.04E-12
rs7523399	1	154345275	C	G	0.84	0.982	1671.4	241.4	5.05E-12
rs7511806	1	154344897	G	A	0.84	0.982	1671.2	241.4	5.09E-12
rs12066892	1	154344275	C	T	0.84	0.982	1670.6	241.4	5.17E-12
rs6701309	1	154343935	G	C	0.84	0.982	1670.5	241.4	5.19E-12
rs6667225	1	154343941	A	C	0.84	0.982	1670.5	241.4	5.19E-12
rs7518394	1	154342022	T	A	0.85	0.983	1669.6	241.4	5.32E-12
rs12058332	1	154341406	G	A	0.85	0.983	1669.1	241.4	5.40E-12
rs7552370	1	154340321	C	T	0.84	0.983	1668.4	241.4	5.50E-12
rs12063437	1	154340084	G	A	0.85	0.984	1667.0	241.4	5.72E-12
rs68031662	1	154339892	C	T	0.85	0.984	1665.6	241.4	5.92E-12
rs6662976	1	154338499	C	T	0.85	0.973	1665.5	242.7	7.70E-12
rs6672627	1	154346967	C	A	0.84	0.982	1658.3	241.6	7.72E-12
rs12068128	1	154338155	T	A	0.85	0.989	1651.5	241.1	8.39E-12
rs12749618	1	154337824	C	T	0.84	0.987	1649.4	241.1	8.87E-12
	1	154532599	A	T	0.89	0.765	-2175.8	318.0	8.91E-12
rs12739228	1	154426190	G	A	0.95	0.894	2705.9	396.3	9.84E-12
rs6427741	1	154535817	A	C	0.92	0.872	-2572.2	377.3	1.05E-11
rs12730935	1	154419892	G	A	0.61	0.985	-10941.5	1608.1	1.16E-11
rs1948143	1	154334264	G	C	0.84	0.988	1631.0	240.4	1.32E-11
rs10908840	1	154459477	C	T	0.52	0.953	1239.5	183.9	1.79E-11
rs11265594	1	154328508	G	A	0.85	0.997	1623.8	241.4	1.95E-11

rs4414034	1	154331186	A	G	0.84	0.977	1601.3	243.3	5.25E-11
rs3811452	1	154321802	C	T	0.85	0.996	1598.2	243.5	5.87E-11
rs34968830	1	154313689	G	A	0.85	0.999	1571.9	243.6	1.22E-10
rs66980031	1	154481153	C	G	0.95	0.868	2637.6	410.1	1.39E-10
rs35229198	1	154330289	C	T	0.85	0.978	1583.4	246.2	1.40E-10
rs6686621	1	154293925	T	A	0.85	0.992	1566.2	244.1	1.55E-10
rs6702754	1	154303976	T	C	0.70	0.997	1251.3	195.4	1.67E-10
rs4601580	1	154394417	T	A	0.48	0.736	-1511.5	236.2	1.72E-10
rs9787014	1	154308680	G	A	0.85	0.997	1558.2	243.5	1.73E-10
rs749966	1	154314408	C	T	0.85	0.997	1559.7	243.8	1.76E-10
rs6672010	1	154292161	C	T	0.70	0.992	1252.9	195.9	1.78E-10
rs6685323	1	154295592	C	T	0.70	0.998	1246.9	195.2	1.85E-10
rs12727865	1	154303705	C	T	0.70	0.999	1247.5	195.3	1.85E-10
rs35950207	1	154291958	C	T	0.70	0.999	1246.5	195.2	1.87E-10
rs3890153	1	154295089	C	G	0.70	0.999	1245.4	195.2	1.96E-10
rs12748146	1	154292982	T	A	0.70	0.998	1246.0	195.3	1.96E-10
rs12077870	1	154305190	G	C	0.70	0.998	1241.3	194.7	2.01E-10
rs6668968	1	154293675	G	A	0.70	0.998	1244.4	195.2	2.04E-10
rs34880256	1	154308089	C	T	0.85	0.998	1548.1	243.7	2.33E-10
rs12726220	1	154171550	A	G	0.96	0.813	2974.7	472.0	3.23E-10
	1	154540865	G	T	0.98	0.543	-4207.9	676.2	5.36E-10
	1	154430647	C	T	0.97	0.680	3732.3	607.2	8.64E-10
rs12730036	1	154416969	C	T	0.61	0.977	-6971.3	1134.6	8.76E-10
rs11265613	1	154418415	T	C	0.61	0.983	-8293.4	1352.3	9.41E-10
rs12753254	1	154416935	G	A	0.61	0.977	-6933.7	1130.6	9.41E-10
rs66654715	1	154376820	G	C	0.96	0.776	2774.4	454.2	1.09E-09
rs34450945	1	154289348	C	T	0.96	0.768	2759.7	469.8	4.56E-09
rs72700210	1	154665602	T	A	0.93	0.813	-2189.5	373.1	4.72E-09
rs72698179	1	154522394	C	A	0.98	0.663	-3800.1	652.8	6.27E-09
rs7529229	1	154420778	T	C	0.60	0.991	-5952.6	1032.7	8.76E-09
rs7512646	1	154420402	G	C	0.60	0.991	-5915.2	1028.5	9.46E-09
rs55997241	1	154671128	G	A	0.93	0.753	-2335.4	409.9	1.29E-08
rs4576655	1	154418749	C	T	0.60	0.989	-5555.9	977.3	1.39E-08
rs12729561	1	154321663	C	T	0.86	0.978	1482.1	260.7	1.39E-08
rs10218433	1	154330183	T	C	0.71	0.982	1174.8	207.7	1.64E-08
rs12143987	1	154330725	C	G	0.30	0.992	-1162.5	206.2	1.84E-08
rs67881926	1	153831229	C	G	0.94	0.885	2258.1	400.6	1.84E-08
rs1889314	1	154351880	G	A	0.30	0.990	-1175.7	208.7	1.89E-08

rs10908834	1	154349381	C	T	0.30	0.989	-1174.1	208.9	2.02E-08
rs12759389	1	153773326	G	C	0.94	0.887	2247.5	400.6	2.15E-08
rs1073907	1	154332520	C	T	0.70	0.995	1155.3	206.0	2.17E-08
rs11577266	1	154333216	A	G	0.70	0.994	1156.2	206.2	2.18E-08
rs12719998	1	154335417	A	G	0.70	0.993	1157.2	206.4	2.21E-08
rs34845300	1	153755335	C	A	0.94	0.852	2118.3	378.1	2.24E-08
rs34437053	1	154351199	G	A	0.70	0.991	1168.9	208.8	2.30E-08
rs11265593	1	154328464	T	C	0.70	0.991	1157.6	206.8	2.30E-08
rs7555891	1	154329595	A	G	0.70	0.991	1156.5	206.6	2.32E-08
rs1889315	1	154351960	T	C	0.70	0.991	1168.0	208.8	2.34E-08
rs11580178	1	154353262	T	A	0.70	0.992	1167.4	208.7	2.37E-08
rs11576193	1	154330749	T	G	0.70	0.993	1152.6	206.3	2.46E-08
rs6696089	1	154332870	A	G	0.70	0.990	1157.4	207.5	2.56E-08
rs2072661	1	154548880	G	A	0.76	0.883	1219.1	218.7	2.64E-08
rs12738097	1	154335378	C	T	0.71	0.995	1151.3	207.0	2.85E-08
rs6698143	1	154337209	G	T	0.71	0.993	1152.1	207.3	2.92E-08
rs56023096	1	154291416	C	T	0.86	0.973	1450.3	261.1	2.94E-08
rs6657938	1	154336126	A	G	0.71	0.995	1150.4	207.1	2.94E-08
rs56211693	1	154355008	C	T	0.70	0.992	1157.0	208.4	2.98E-08
rs6698130	1	154337177	G	A	0.71	0.993	1151.2	207.4	3.00E-08
rs12118634	1	154335146	C	T	0.30	0.972	-1139.4	205.4	3.08E-08
rs12061599	1	154344135	G	T	0.71	0.989	1152.9	208.3	3.32E-08
rs6661909	1	154343486	C	T	0.71	0.989	1152.4	208.3	3.33E-08
rs35982711	1	154339919	C	A	0.71	0.989	1152.6	208.3	3.34E-08
rs7525436	1	154345089	A	G	0.71	0.989	1152.2	208.3	3.35E-08
rs9728585	1	154346077	A	C	0.71	0.989	1152.0	208.3	3.35E-08
rs113445115	1	154122787	T	C	0.92	0.807	-2051.5	370.9	3.37E-08
rs6659828	1	154341479	A	G	0.71	0.989	1151.7	208.3	3.39E-08
rs2229857	1	154573967	T	C	0.29	0.977	-1109.9	200.9	3.48E-08
rs7544062	1	154554022	C	T	0.29	0.987	-1106.0	200.3	3.58E-08
rs11576181	1	154330659	T	G	0.71	0.984	1140.7	206.8	3.67E-08

[A] rsnumber is given where available
[B] Base pair position build 37/hg19
[C] Allele 1 (effect allele)
[D] Allele 2
[E] Frequency of allele 1
[F] Info= Imputation quality metric from SNPtest
[G] Beta for the effect on sIL-6R levels associated with allele 1.
[H] SE = Standard error of the beta estimate

Table S4: Location (Build 37/hg19) and sequence of expression probes targeting *IL6R* transcripts (Affymetrix U219 array).

Probe ID	**Sequence**	**Chr**	**Start**	**End**	**Location**
11736509_x_at;545;104	GGTTACCCAGTTAGCTCTCAAGTTA	1	154439782	154439807	3'-end
11736509_x_at;40;550	GATTTTAGACCCTATTGCTGCTTGA	1	154440035	154440060	3'-end
11736509_x_at;410;418	TCATTGCTGGGCTTGTCTGTAGATT	1	154440014	154440039	3'-end
11736509_x_at;308;15	AAATCAGCCGTGTAACCATGGACCC	1	154439837	154439862	3'-end
11736509_x_at;553;369	ACTTCAGCTGACTTTTCTGTCCGAG	1	154439733	154439758	3'-end
11736509_x_at;372;285	CCATGTTTTGTTTACGGTTTTCCAG	1	154439953	154439978	3'-end
11736509_x_at;495;603	GTTCCTTGAGTTGATTCAGCTCTGC	1	154439660	154439685	3'-end
11736509_x_at;61;280	ACTGTCTTCAGTAAGCCGTGATTTT	1	154439990	154440015	3'-end
11736509_x_at;551;225	GCTCTCAAGTTATCAGGGTATTCCA	1	154439795	154439820	3'-end
11736510_a_at;390;362	ACGGAGCCCTTATGACATCAGCAAT	1	154437807	154437832	3'-end
11736510_a_at;323;134	CAGGAGTCCTCCAGCTGAGAACGAG	1	154420604	154420629	Exon 7
11736510_a_at;609;718	AAGACAAGCATGCATCCGCCGTACT	1	154437649	154437674	3'-end
11736510_a_at;58;615	GGGTCTGACAATACCTCGAGCCACA	1	154437760	154437785	3'-end
11736510_a_at;46;386	AGACTACTTCTTCCCCAGATAGCTG	1	154437834	154437859	3'-end
11736510_a_at;484;717	GATTCTGCAAATGCGACAAGCCTCC	1	154422428	154422453	Exon 8
11736510_a_at;659;168	GCCACAACCGACCAGATGCCAGGGA	1	154437779	154437804	3'-end
11736510_a_at;201;497	TCCAGCTGAGAACGAGGTGTCCACC	1	154420613	154420638	Exon 7
11736510_a_at;435;552	TCAGCAATACAGACTACTTCTTCCC	1	154437824	154437849	3'-end
11741958_a_at;264;163	TACAGACTACGGTTTGAGCTCAGAT	1	154407569	154407594	Exon 5
11741958_a_at;582;132	CAGGAGTCCTCCAGCTGAGAACGAG	1	154420604	154420629	Exon 7
11741958_a_at;610;718	AAGACAAGCATGCATCCGCCGTACT	1	154437649	154437674	3'-end
11741958_a_at;483;717	GATTCTGCAAATGCGACAAGCCTCC	1	154422428	154422453	Exon 8
11741958_a_at;235;610	ACTGTGTCATCCACGACGCCTGGAG	1	154408463	154408488	Exon 6
11741958_a_at;202;497	TCCAGCTGAGAACGAGGTGTCCACC	1	154420613	154420638	Exon 7
11741958_a_at;705;156	CAGCTGGTCCCGGAGAGGCCTCGAC	1	154437682	154437707	3'-end
11741958_a_at;314;329	TACGGTTTGAGCTCAGATATCGGGC	1	154407576	154407601	Exon 5
11741959_x_at;505;200	CTGCTGACTGTTTTCTCTTGAGAGG	1	154438903	154438928	3'-end
11741959_x_at;361;694	AATATCCAATATTCGCTGTGTCAGC	1	154438932	154438957	3'-end
11741959_x_at;586;417	TTTACTGCAGCTTTGTTTGTTGTCA	1	154438780	154438805	3'-end
11741959_x_at;735;334	TGTGGTAGAGTGTGCCTGAAGTCCC	1	154439183	154439208	3'-end
11741959_x_at;109;540	TGTTGTCAGCTGAACCTGGGTAACT	1	154438797	154438822	3'-end
11741959_x_at;260;360	AGCACCATAACTTTGTTTAGCCCAA	1	154438986	154439011	3'-end
11741959_x_at;218;13	ATCAAAACGGTTTTACTGCAGCTTT	1	154438769	154438794	3'-end
11741959_x_at;267;582	CGCTGTGTCAGCATAGAAGTAACTT	1	154438945	154438970	3'-end

11741959_x_at;548;21	TCTCTTGAGAGGGTGGAATATCCAA	1	154438916	154438941	3'-end
11741959_x_at;7;323	GCTTTGTTTGTTGTCAGCTGAACCT	1	154438789	154438814	3'-end

Table S5: SNP information and eQTL *P*-values for all 341 significant eQTL associations.

Probe Name[A]	**SNP**	**SNP Chr**	**SNP position**[B]	**Alleles**		**MAF**	**Info**[C]	**eQTL *P*-value**
582_132	rs7512646	1	154420402	G	C	0.40	0.991	2.84E-22
582_132	rs4845372	1	154415396	C	A	0.40	0.974	2.93E-22
582_132	rs7529229	1	154420778	T	C	0.40	0.991	3.41E-22
582_132	rs4576655	1	154418749	C	T	0.40	0.989	5.14E-22
323_134	rs4845372	1	154415396	C	A	0.40	0.974	6.44E-22
582_132	rs4845623	1	154415777	A	G	0.40	0.973	7.29E-22
582_132	rs4537545	1	154418879	C	T	0.39	0.976	1.30E-21
323_134	rs4845623	1	154415777	A	G	0.40	0.973	1.37E-21
323_134	rs7529229	1	154420778	T	C	0.40	0.991	2.62E-21
323_134	rs7512646	1	154420402	G	C	0.40	0.991	2.77E-21
323_134	rs4576655	1	154418749	C	T	0.40	0.989	4.29E-21
323_134	rs12753254	1	154416935	G	A	0.39	0.977	1.78E-20
323_134	rs12730036	1	154416969	C	T	0.39	0.977	1.78E-20
323_134	rs4537545	1	154418879	C	T	0.39	0.976	1.78E-20
323_134	rs6664201	1	154414296	C	T	0.39	0.973	1.90E-20
323_134	rs4845373	1	154417829	C	T	0.39	0.979	5.24E-20
323_134	rs4393147	1	154414037	C	T	0.39	0.973	5.81E-20
323_134	rs4453032	1	154414086	A	G	0.39	0.973	5.81E-20
323_134	rs11265613	1	154418415	T	C	0.39	0.983	6.31E-20
323_134	rs61812598	1	154420087	G	A	0.39	0.993	1.05E-19
582_132	rs12730935	1	154419892	G	A	0.38	0.985	1.10E-19
323_134	rs12133641	1	154428283	A	G	0.39	0.993	1.11E-19
323_134	rs12730935	1	154419892	G	A	0.38	0.985	1.14E-19
582_132	rs4393147	1	154414037	C	T	0.39	0.973	1.27E-19
582_132	rs4453032	1	154414086	A	G	0.39	0.973	1.27E-19
582_132	rs12753254	1	154416935	G	A	0.39	0.977	1.29E-19
582_132	rs12730036	1	154416969	C	T	0.39	0.977	1.29E-19
582_132	rs61812598	1	154420087	G	A	0.39	0.993	1.31E-19
582_132	rs6664201	1	154414296	C	T	0.39	0.973	1.40E-19
323_134	rs12126142	1	154425456	G	A	0.39	0.997	1.54E-19
323_134	rs4129267	1	154426264	C	T	0.38	0.995	1.59E-19
323_134	rs4845622	1	154411419	A	C	0.39	0.970	1.88E-19
582_132	rs11265613	1	154418415	T	C	0.39	0.983	1.89E-19
582_132	rs12133641	1	154428283	A	G	0.39	0.993	2.02E-19
323_134	rs2228145	1	154426970	A	C	0.39	0.967	2.25E-19

582_132	rs12126142	1	154425456	G	A	0.39	0.997	2.53E-19
582_132	rs4845373	1	154417829	C	T	0.39	0.979	2.77E-19
582_132	rs4845622	1	154411419	A	C	0.39	0.970	2.98E-19
582_132	rs2228145	1	154426970	A	C	0.39	0.967	3.14E-19
582_132	rs4129267	1	154426264	C	T	0.38	0.995	5.85E-19
323_134	rs4845621	1	154409730	G	A	0.39	0.970	1.21E-18
323_134	rs4845620	1	154406656	A	G	0.39	0.969	1.87E-18
323_134	rs56383622	1	154405024	A	G	0.39	0.969	2.27E-18
323_134	rs7521458	1	154407713	T	C	0.39	0.969	2.40E-18
582_132	rs4845621	1	154409730	G	A	0.39	0.970	2.48E-18
323_134	rs7518199	1	154407419	A	C	0.39	0.968	2.77E-18
582_132	rs7518199	1	154407419	A	C	0.39	0.968	5.36E-18
582_132	rs7521458	1	154407713	T	C	0.39	0.969	8.57E-18
202_497	rs4845372	1	154415396	C	A	0.40	0.974	1.19E-17
202_497	rs4845623	1	154415777	A	G	0.40	0.973	1.58E-17
582_132	rs4845620	1	154406656	A	G	0.39	0.969	1.77E-17
582_132	rs56383622	1	154405024	A	G	0.39	0.969	2.54E-17
323_134	rs6684439	1	154395839	C	T	0.39	0.926	2.79E-17
202_497	rs7529229	1	154420778	T	C	0.40	0.991	3.92E-17
202_497	rs7512646	1	154420402	G	C	0.40	0.991	4.06E-17
202_497	rs4576655	1	154418749	C	T	0.40	0.989	6.39E-17
202_497	rs6664201	1	154414296	C	T	0.39	0.973	1.40E-16
202_497	rs12753254	1	154416935	G	A	0.39	0.977	1.56E-16
202_497	rs12730036	1	154416969	C	T	0.39	0.977	1.56E-16
202_497	rs12730935	1	154419892	G	A	0.38	0.985	1.70E-16
202_497	rs11265613	1	154418415	T	C	0.39	0.983	1.89E-16
202_497	rs4393147	1	154414037	C	T	0.39	0.973	2.06E-16
202_497	rs4453032	1	154414086	A	G	0.39	0.973	2.06E-16
202_497	rs4845373	1	154417829	C	T	0.39	0.979	2.41E-16
202_497	rs4845620	1	154406656	A	G	0.39	0.969	2.42E-16
202_497	rs56383622	1	154405024	A	G	0.39	0.969	2.45E-16
202_497	rs7521458	1	154407713	T	C	0.39	0.969	3.29E-16
202_497	rs7518199	1	154407419	A	C	0.39	0.968	3.32E-16
202_497	rs61812598	1	154420087	G	A	0.39	0.993	4.08E-16
323_134	rs11265612	1	154417044	A	G	0.44	0.975	4.77E-16
202_497	rs4537545	1	154418879	C	T	0.39	0.976	4.90E-16
202_497	rs4845622	1	154411419	A	C	0.39	0.970	5.17E-16
202_497	rs4845621	1	154409730	G	A	0.39	0.970	5.82E-16

323_134	rs6683206	1	154418088	T	C	0.44	0.969	6.75E-16
323_134	rs4133213	1	154395212	C	A	0.42	0.893	1.33E-15
323_134	rs6686750	1	154419843	A	G	0.45	0.990	1.34E-15
202_497	rs4129267	1	154426264	C	T	0.38	0.995	1.39E-15
202_497	rs12133641	1	154428283	A	G	0.39	0.993	1.39E-15
323_134	rs12129500	1	154423764	T	C	0.45	0.992	1.64E-15
323_134	rs7536152	1	154423909	A	G	0.45	0.992	1.64E-15
202_497	rs12126142	1	154425456	G	A	0.39	0.997	1.64E-15
582_132	rs6684439	1	154395839	C	T	0.39	0.926	1.64E-15
323_134	rs7526131	1	154425135	G	A	0.45	0.993	1.67E-15
582_132	rs4133213	1	154395212	C	A	0.42	0.893	1.70E-15
323_134	rs6694258	1	154428505	C	A	0.45	0.991	1.70E-15
323_134	rs4845625	1	154422067	T	C	0.45	0.991	1.82E-15
323_134	rs6689393	1	154426097	A	G	0.45	0.993	2.61E-15
582_132	rs6686750	1	154419843	A	G	0.45	0.990	2.75E-15
582_132	rs4845625	1	154422067	T	C	0.45	0.991	2.80E-15
202_497	rs2228145	1	154426970	A	C	0.39	0.967	2.98E-15
582_132	rs11265612	1	154417044	A	G	0.44	0.975	4.12E-15
582_132	rs6694258	1	154428505	C	A	0.45	0.991	4.32E-15
582_132	rs6689393	1	154426097	A	G	0.45	0.993	4.34E-15
582_132	rs7526131	1	154425135	G	A	0.45	0.993	4.49E-15
582_132	rs12129500	1	154423764	T	C	0.45	0.992	4.89E-15
582_132	rs7536152	1	154423909	A	G	0.45	0.992	4.89E-15
582_132	rs6683206	1	154418088	T	C	0.44	0.969	5.91E-15
202_497	rs6684439	1	154395839	C	T	0.39	0.926	1.06E-14
202_497	rs4133213	1	154395212	C	A	0.42	0.893	2.55E-14
323_134	rs7549338	1	154404380	C	G	0.44	0.970	2.81E-14
323_134	rs59632925	1	154406540	T	G	0.44	0.970	3.15E-14
323_134	rs7553796	1	154404406	A	C	0.44	0.969	5.24E-14
323_134	rs4845371	1	154408340	T	C	0.44	0.969	6.95E-14
323_134	rs6667434	1	154409100	A	G	0.44	0.969	1.06E-13
582_132	rs7549338	1	154404380	C	G	0.44	0.970	1.26E-13
582_132	rs6667434	1	154409100	A	G	0.44	0.969	1.56E-13
323_134	rs10908838	1	154397984	T	G	0.44	0.963	1.57E-13
582_132	rs7553796	1	154404406	A	C	0.44	0.969	1.65E-13
323_134	rs6694817	1	154401972	T	C	0.44	0.965	1.71E-13
582_132	rs59632925	1	154406540	T	G	0.44	0.970	1.72E-13
582_132	rs4845371	1	154408340	T	C	0.44	0.969	1.83E-13

323_134	rs6689306	1	154395946	A	G	0.44	0.937	2.03E-13
323_134	rs6427658	1	154400799	T	C	0.45	0.965	2.11E-13
323_134	rs12118770	1	154397589	T	C	0.44	0.959	2.69E-13
201_497	rs4845623	1	154415777	A	G	0.40	0.973	3.35E-13
323_134	rs7549250	1	154404336	C	T	0.45	0.970	4.83E-13
323_134	rs4553185	1	154410955	C	T	0.45	0.966	5.71E-13
201_497	rs4845372	1	154415396	C	A	0.40	0.974	5.77E-13
323_134	rs4845619	1	154405058	T	G	0.45	0.970	6.12E-13
323_134	rs12404927	1	154421438	T	C	0.48	0.931	6.59E-13
323_134	rs10908836	1	154397932	C	T	0.46	0.913	7.31E-13
582_132	rs6694817	1	154401972	T	C	0.44	0.965	1.48E-12
201_497	rs7529229	1	154420778	T	C	0.40	0.991	1.55E-12
201_497	rs7512646	1	154420402	G	C	0.40	0.991	1.88E-12
323_134	rs12118721	1	154397416	T	C	0.45	0.961	2.79E-12
323_134	rs6687726	1	154400320	A	G	0.45	0.969	2.79E-12
582_132	rs12404927	1	154421438	T	C	0.48	0.931	3.04E-12
323_134	rs4845618	1	154400015	G	T	0.45	0.964	3.32E-12
323_134	rs12117832	1	154397610	A	G	0.45	0.959	3.51E-12
582_132	rs6427658	1	154400799	T	C	0.45	0.965	3.57E-12
201_497	rs4537545	1	154418879	C	T	0.39	0.976	3.84E-12
201_497	rs4576655	1	154418749	C	T	0.40	0.989	4.57E-12
582_132	rs10908838	1	154397984	T	G	0.44	0.963	5.16E-12
582_132	rs12118770	1	154397589	T	C	0.44	0.959	5.74E-12
582_132	rs6689306	1	154395946	A	G	0.44	0.937	6.49E-12
582_132	rs10908836	1	154397932	C	T	0.46	0.913	7.59E-12
582_132	rs4553185	1	154410955	C	T	0.45	0.966	9.04E-12
582_132	rs7549250	1	154404336	C	T	0.45	0.970	1.09E-11
323_134	rs35109459	1	154397933	G	A	0.47	0.917	1.11E-11
308_15	rs4072391	1	154438880	T	C	0.21	0.983	1.32E-11
201_497	rs6664201	1	154414296	C	T	0.39	0.973	1.48E-11
308_15	rs60255122	1	154504702	A	G	0.21	0.988	1.80E-11
308_15	rs60760897	1	154504849	C	T	0.21	0.988	1.80E-11
308_15	rs61698846	1	154504854	C	T	0.21	0.988	1.80E-11
308_15	rs61275241	1	154504887	T	G	0.21	0.988	1.80E-11
201_497	rs12753254	1	154416935	G	A	0.39	0.977	1.87E-11
201_497	rs12730036	1	154416969	C	T	0.39	0.977	1.87E-11
308_15	rs59239860	1	154492107	G	T	0.21	0.994	2.03E-11
308_15	rs112231452	1	154504900	G	A	0.21	0.988	2.03E-11

201_497	rs4393147	1	154414037	C	T	0.39	0.973	2.04E-11
201_497	rs4453032	1	154414086	A	G	0.39	0.973	2.04E-11
308_15	rs61403567	1	154504927	T	C	0.21	0.988	2.11E-11
582_132	rs4845619	1	154405058	T	G	0.45	0.970	2.12E-11
308_15	rs59741504	1	154504601	T	C	0.21	0.991	2.13E-11
308_15	rs2229238	1	154437896	T	C	0.21	0.993	2.26E-11
201_497	rs11265613	1	154418415	T	C	0.39	0.983	2.33E-11
201_497	rs4845373	1	154417829	C	T	0.39	0.979	2.39E-11
308_15	rs11490956	1	154487258	G	T	0.21	0.997	2.50E-11
308_15	rs111600849	1	154487489	G	A	0.21	0.997	2.50E-11
308_15	rs60498985	1	154504172	C	T	0.21	0.995	2.51E-11
308_15	rs4379670	1	154439865	T	A	0.21	0.986	2.71E-11
308_15	rs12405637	1	154501285	C	T	0.21	0.995	2.75E-11
308_15	rs7514452	1	154438084	C	T	0.21	0.993	2.76E-11
308_15	rs73020232	1	154482669	C	T	0.21	0.997	2.80E-11
308_15	rs73020234	1	154482767	C	A	0.21	0.997	2.80E-11
308_15	rs73020246	1	154485640	A	G	0.21	0.997	2.80E-11
308_15	rs12403537	1	154487726	G	A	0.21	0.997	2.80E-11
308_15	rs77184252	1	154492533	A	G	0.21	0.997	2.80E-11
308_15	rs58348886	1	154446198	T	C	0.21	0.990	2.86E-11
201_497	rs4845622	1	154411419	A	C	0.39	0.970	3.03E-11
308_15	rs58710275	1	154505010	C	T	0.21	0.996	3.07E-11
308_15	rs7551873	1	154505857	C	T	0.21	0.995	3.07E-11
308_15	rs41308419	1	154507197	T	C	0.21	0.996	3.07E-11
308_15	rs112585956	1	154507767	T	C	0.21	0.996	3.07E-11
308_15	rs4633282	1	154507899	T	C	0.21	0.996	3.07E-11
308_15	rs73023331	1	154508210	G	A	0.21	0.996	3.07E-11
308_15	rs111742980	1	154508764	T	A	0.21	0.995	3.07E-11
308_15	rs112674677	1	154508792	C	T	0.21	0.996	3.07E-11
308_15	rs113915076	1	154508812	G	A	0.21	0.996	3.07E-11
308_15	rs4639752	1	154508974	T	A	0.21	0.996	3.07E-11
308_15	rs60368585	1	154509340	T	C	0.21	0.995	3.07E-11
308_15	rs112236096	1	154510790	C	T	0.21	0.995	3.07E-11
308_15	rs73023339	1	154510852	C	T	0.21	0.995	3.07E-11
308_15	rs6674171	1	154491683	A	G	0.21	0.997	3.34E-11
308_15	rs73018293	1	154465577	C	T	0.21	0.997	3.51E-11
308_15	rs59838898	1	154466301	C	T	0.21	0.997	3.51E-11
201_497	rs4129267	1	154426264	C	T	0.38	0.995	3.58E-11

308_15	rs4390168	1	154509096	A	G	0.21	0.992	3.64E-11
308_15	rs10047079	1	154468135	T	C	0.21	0.997	4.19E-11
201_497	rs12730935	1	154419892	G	A	0.38	0.985	4.41E-11
308_15	rs7556449	1	154505886	A	G	0.21	0.996	4.43E-11
308_15	rs12406822	1	154499484	C	T	0.21	0.983	4.48E-11
308_15	rs7526293	1	154444209	T	C	0.21	0.990	4.61E-11
308_15	rs6669229	1	154444591	A	G	0.21	0.990	5.03E-11
201_497	rs61812598	1	154420087	G	A	0.39	0.993	5.49E-11
308_15	rs6675472	1	154445503	T	C	0.22	0.972	5.53E-11
308_15	rs41269915	1	154521584	T	A	0.21	0.986	5.70E-11
308_15	rs57783436	1	154511709	A	G	0.21	0.995	6.30E-11
308_15	rs112394421	1	154512008	T	C	0.21	0.995	6.30E-11
308_15	rs73023346	1	154512077	C	T	0.21	0.995	6.30E-11
308_15	rs12408461	1	154512710	T	C	0.21	0.994	6.30E-11
308_15	rs73023348	1	154513418	G	A	0.21	0.994	6.30E-11
308_15	rs73023349	1	154513440	T	C	0.21	0.994	6.30E-11
308_15	rs72999415	1	154513712	C	T	0.21	0.994	6.30E-11
308_15	rs72999419	1	154514092	T	C	0.21	0.994	6.30E-11
308_15	rs41313910	1	154514203	C	G	0.21	0.994	6.30E-11
308_15	rs72999422	1	154514942	G	A	0.21	0.994	6.30E-11
308_15	rs58881140	1	154515193	C	T	0.21	0.994	6.30E-11
308_15	rs6672087	1	154516122	A	C	0.21	0.994	6.30E-11
308_15	rs6681207	1	154517217	T	C	0.21	0.993	6.30E-11
308_15	rs3811449	1	154517504	G	A	0.21	0.993	6.30E-11
308_15	rs59084843	1	154518286	A	G	0.21	0.993	6.30E-11
308_15	rs61559765	1	154518349	T	C	0.21	0.993	6.30E-11
308_15	rs60092776	1	154518496	A	G	0.21	0.992	6.30E-11
308_15	rs60931472	1	154518642	T	C	0.21	0.992	6.30E-11
201_497	rs12133641	1	154428283	A	G	0.39	0.993	6.65E-11
201_497	rs7518199	1	154407419	A	C	0.39	0.968	7.25E-11
201_497	rs7521458	1	154407713	T	C	0.39	0.969	7.70E-11
201_497	rs4845621	1	154409730	G	A	0.39	0.970	8.80E-11
308_15	rs3811448	1	154516578	G	A	0.21	0.994	9.09E-11
201_497	rs4845620	1	154406656	A	G	0.39	0.969	9.11E-11
201_497	rs56383622	1	154405024	A	G	0.39	0.969	9.97E-11
201_497	rs12126142	1	154425456	G	A	0.39	0.997	1.18E-10
308_15	rs4291493	1	154436920	T	C	0.27	0.919	1.18E-10
323_134	rs11265611	1	154395125	G	A	0.42	0.894	1.41E-10

201_497	rs2228145	1	154426970	A	C	0.39	0.967	1.77E-10
202_497	rs6683206	1	154418088	T	C	0.44	0.969	2.45E-10
202_497	rs11265612	1	154417044	A	G	0.44	0.975	3.03E-10
582_132	rs4845618	1	154400015	G	T	0.45	0.964	3.24E-10
308_15	rs7537291	1	154433407	G	A	0.25	0.990	3.80E-10
308_15	rs7546068	1	154433415	C	T	0.25	0.990	3.80E-10
308_15	rs7537316	1	154433466	G	A	0.25	0.990	3.80E-10
308_15	rs7546552	1	154433905	C	A	0.25	0.992	3.80E-10
308_15	rs7546555	1	154433911	C	T	0.25	0.992	3.80E-10
308_15	rs6687597	1	154434936	G	A	0.25	0.992	3.80E-10
308_15	rs4509570	1	154436384	G	C	0.25	0.994	3.80E-10
308_15	rs4341355	1	154436404	C	G	0.25	0.994	3.80E-10
308_15	rs6698040	1	154432948	T	C	0.25	0.990	4.04E-10
308_15	rs6427672	1	154435346	C	T	0.25	0.992	4.15E-10
308_15	rs4240872	1	154436195	C	T	0.25	0.971	4.22E-10
582_132	rs12117832	1	154397610	A	G	0.45	0.959	4.25E-10
202_497	rs6686750	1	154419843	A	G	0.45	0.990	4.26E-10
582_132	rs12118721	1	154397416	T	C	0.45	0.961	4.38E-10
582_132	rs6687726	1	154400320	A	G	0.45	0.969	4.38E-10
202_497	rs4845625	1	154422067	T	C	0.45	0.991	4.53E-10
308_15	rs10752641	1	154432042	G	C	0.25	0.973	4.60E-10
308_15	rs10908839	1	154430798	C	G	0.24	0.986	5.77E-10
202_497	rs7549338	1	154404380	C	G	0.44	0.970	6.61E-10
582_132	rs11265611	1	154395125	G	A	0.42	0.894	6.66E-10
582_132	rs35109459	1	154397933	G	A	0.47	0.917	6.88E-10
202_497	rs7553796	1	154404406	A	C	0.44	0.969	7.50E-10
202_497	rs6694258	1	154428505	C	A	0.45	0.991	7.96E-10
201_497	rs6684439	1	154395839	C	T	0.39	0.926	8.22E-10
202_497	rs7526131	1	154425135	G	A	0.45	0.993	8.52E-10
202_497	rs12129500	1	154423764	T	C	0.45	0.992	8.54E-10
202_497	rs7536152	1	154423909	A	G	0.45	0.992	8.54E-10
202_497	rs59632925	1	154406540	T	G	0.44	0.970	8.64E-10
202_497	rs4845371	1	154408340	T	C	0.44	0.969	9.26E-10
202_497	rs6689393	1	154426097	A	G	0.45	0.993	1.03E-09
201_497	rs4133213	1	154395212	C	A	0.42	0.893	1.27E-09
308_15	rs55668699	1	154435293	T	A	0.25	0.955	1.29E-09
202_497	rs6427658	1	154400799	T	C	0.45	0.965	1.69E-09
582_132	rs6690230	1	154432877	C	G	0.41	0.990	2.03E-09

582_132	rs6695045	1	154432957	A	G	0.41	0.990	2.03E-09
202_497	rs6694817	1	154401972	T	C	0.44	0.965	2.35E-09
202_497	rs6667434	1	154409100	A	G	0.44	0.969	2.50E-09
202_497	rs6689306	1	154395946	A	G	0.44	0.937	3.10E-09
202_497	rs7549250	1	154404336	C	T	0.45	0.970	3.61E-09
202_497	rs10908838	1	154397984	T	G	0.44	0.963	3.86E-09
202_497	rs12118770	1	154397589	T	C	0.44	0.959	4.31E-09
202_497	rs10908836	1	154397932	C	T	0.46	0.913	4.70E-09
202_497	rs4845619	1	154405058	T	G	0.45	0.970	4.94E-09
582_132	rs10908839	1	154430798	C	G	0.24	0.986	9.75E-09
202_497	rs4553185	1	154410955	C	T	0.45	0.966	1.67E-08
582_132	rs4845647	1	154514331	C	A	0.37	0.995	1.77E-08
202_497	rs12404927	1	154421438	T	C	0.48	0.931	2.20E-08
202_497	rs4845618	1	154400015	G	T	0.45	0.964	2.64E-08
582_132	rs11265632	1	154514067	G	A	0.37	0.995	2.67E-08
582_132	rs4345797	1	154495675	C	T	0.37	0.997	2.69E-08
582_132	rs4845642	1	154498028	G	A	0.37	0.996	2.69E-08
582_132	rs10908845	1	154500898	C	T	0.37	0.996	2.69E-08
582_132	rs11265621	1	154442960	G	A	0.37	0.991	2.80E-08
582_132	rs12119111	1	154478600	G	A	0.37	0.998	2.92E-08
582_132	rs9660786	1	154484017	A	T	0.37	0.998	2.92E-08
582_132	rs7518694	1	154484788	C	G	0.37	0.998	2.92E-08
582_132	rs7519499	1	154487926	G	A	0.37	0.998	2.92E-08
582_132	rs4845639	1	154490352	C	T	0.37	0.998	2.92E-08
582_132	rs4382717	1	154518610	C	T	0.37	0.989	2.95E-08
582_132	rs6698971	1	154475331	C	A	0.37	0.995	3.02E-08
582_132	rs4584384	1	154495697	T	C	0.38	0.996	3.04E-08
582_132	rs6658175	1	154475330	T	A	0.37	0.997	3.30E-08
202_497	rs35109459	1	154397933	G	A	0.47	0.917	3.39E-08
202_497	rs12118721	1	154397416	T	C	0.45	0.961	3.44E-08
202_497	rs6687726	1	154400320	A	G	0.45	0.969	3.44E-08
582_132	rs10908841	1	154487763	C	T	0.37	0.998	3.57E-08
582_132	rs4845637	1	154490178	A	G	0.37	0.998	3.57E-08
582_132	rs5018567	1	154480318	T	C	0.37	0.997	3.68E-08
582_132	rs10908843	1	154494480	C	G	0.38	0.997	4.03E-08
582_132	rs11265628	1	154496489	C	T	0.38	0.997	4.03E-08
582_132	rs12407048	1	154505270	C	T	0.38	0.997	4.03E-08
582_132	rs4638123	1	154505704	C	T	0.38	0.997	4.03E-08

582_132	rs12037271	1	154507888	G	A	0.38	0.996	4.03E-08
202_497	rs12117832	1	154397610	A	G	0.45	0.959	4.08E-08
582_132	rs6700296	1	154473660	T	C	0.37	0.998	4.23E-08
582_132	rs12118018	1	154477440	G	A	0.37	0.999	4.36E-08
582_132	rs6664608	1	154479670	C	T	0.37	0.999	4.36E-08
582_132	rs12740969	1	154487060	T	G	0.37	0.998	4.36E-08
582_132	rs12128408	1	154488533	A	G	0.37	0.998	4.36E-08
582_132	rs4845638	1	154490269	T	A	0.37	0.998	4.36E-08
582_132	rs10908842	1	154492702	G	A	0.37	0.998	4.36E-08
582_132	rs6684921	1	154464945	A	C	0.37	0.997	4.51E-08
582_132	rs6686276	1	154466188	C	A	0.37	0.998	4.51E-08
582_132	rs6689965	1	154470606	T	A	0.37	0.999	4.51E-08
582_132	rs12753680	1	154474900	G	A	0.38	0.998	4.51E-08
582_132	rs7514452	1	154438084	C	T	0.21	0.993	4.64E-08
582_132	rs10908847	1	154504954	G	A	0.37	0.995	4.80E-08
582_132	rs4478801	1	154464572	G	A	0.37	0.994	4.87E-08
582_132	rs12136771	1	154511502	T	C	0.37	0.994	5.02E-08
582_132	rs11265622	1	154451420	A	G	0.37	0.998	5.49E-08
582_132	rs12568083	1	154455949	T	C	0.37	0.998	5.49E-08
308_15	rs6686750	1	154419843	A	G	0.45	0.990	6.23E-08
308_15	rs6427658	1	154400799	T	C	0.45	0.965	6.52E-08
308_15	rs12129500	1	154423764	T	C	0.45	0.992	6.56E-08
308_15	rs7536152	1	154423909	A	G	0.45	0.992	6.56E-08
582_132	rs2229238	1	154437896	T	C	0.21	0.993	6.63E-08
308_15	rs6694258	1	154428505	C	A	0.45	0.991	6.95E-08
308_15	rs6689393	1	154426097	A	G	0.45	0.993	6.99E-08
308_15	rs7526131	1	154425135	G	A	0.45	0.993	7.09E-08
202_497	rs4382717	1	154518610	C	T	0.37	0.989	7.25E-08
202_497	rs12753666	1	154474875	G	A	0.38	0.986	7.75E-08
582_132	rs4379670	1	154439865	T	A	0.21	0.986	8.10E-08
308_15	rs6694817	1	154401972	T	C	0.44	0.965	8.32E-08
308_15	rs12118770	1	154397589	T	C	0.44	0.959	8.87E-08
202_497	rs4845647	1	154514331	C	A	0.37	0.995	8.94E-08
202_497	rs6698971	1	154475331	C	A	0.37	0.995	9.16E-08
202_497	rs5018567	1	154480318	T	C	0.37	0.997	9.51E-08
308_15	rs4845625	1	154422067	T	C	0.45	0.991	9.69E-08
202_497	rs11265621	1	154442960	G	A	0.37	0.991	9.82E-08
308_15	rs6683206	1	154418088	T	C	0.44	0.969	9.84E-08

202_497	rs11265611	1	154395125	G	A	0.42	0.894	9.86E-08
308_15	rs10908838	1	154397984	T	G	0.44	0.963	9.95E-08

[A] For complete Affymetrix probe IDs and further information on probes, see Table S5.

[B] Base pair position build 37/hg19.

[C] Info= Imputation quality metric from SNPtest

Table S6: Correlations between sIL-6R level and *IL6R* expression level for all expression probes.

IL6R probe[A]	Probe location	r / P value	Total sample (N=2727)	Total sample, correction for rs2228145 (N=2727)	Genotype AA (N=991)	Genotype AC (N=1278)	Genotype CC (N=458)
545_104	3'-end	r	-0.008	-0.011	0.040	-0.020	-0.008
		P value	0.672	0.567	0.204	0.474	0.872
40_550	3'-end	r	-0.028	-0.019	0.022	0.007	-0.100
		P value	0.139	0.317	0.497	0.799	0.033
410_418	3'-end	r	-0.011	-0.008	0.026	-0.016	-0.075
		P value	0.563	0.668	0.421	0.570	0.111
308_15	3'-end	r	-0.055	-0.003	0.031	-0.043	-0.088
		P value	0.004	0.894	0.335	0.124	0.059
553_369	3'-end	r	-0.023	-0.026	0.011	-0.018	-0.032
		P value	0.234	0.172	0.741	0.514	0.495
372_285	3'-end	r	-0.040	-0.026	0.032	0.024	-0.109
		P value	0.036	0.176	0.319	0.383	0.019
495_603	3'-end	r	-0.057	-0.001	0.026	-0.072	-0.060
		P value	0.003	0.979	0.422	0.010	0.202
61_280	3'-end	r	-0.029	0.008	-0.033	-0.025	-0.074
		P value	0.133	0.681	0.300	0.367	0.113
551_225	3'-end	r	-0.017	0.017	0.041	-0.015	-0.028
		P value	0.386	0.369	0.199	0.596	0.556
390_362	3'-end	r	0.009	0.008	0.047	0.009	-0.012
		P value	0.645	0.680	0.139	0.738	0.802
323_134	Exon 7	r	-0.086	0.001	0.032	0.015	-0.023
		P value	7.48 x 10^{-6}	0.955	0.312	0.601	0.618
609_718	3'-end	r	-0.010	0.022	-0.004	0.013	-0.082
		P value	0.598	0.247	0.892	0.648	0.079
58_615	3'-end	r	-0.017	-0.011	0.012	0.010	-0.029
		P value	0.366	0.549	0.713	0.722	0.535
46_386	3'-end	r	0.021	0.014	0.050	0.036	0.001
		P value	0.270	0.449	0.118	0.199	0.981
484_717	Exon 8	r	-0.004	0.012	-0.018	0.018	-0.084
		P value	0.820	0.532	0.569	0.525	0.073
659_168	3'-end	r	-0.018	0.012	0.033	0.029	-0.010
		P value	0.345	0.541	0.298	0.297	0.826
201_497	Exon 7	r	-.054	0.011	0.047	0.009	0.002
		P value	0.005	0.577	0.136	0.755	0.974
435_552	3'-end	r	0.016	0.014	-0.004	0.041	-0.003

		P value	0.392	0.454	0.911	0.144	0.948
264_163	Exon 5	r	0.014	-0.004	0.060	0.009	-0.002
		P value	0.473	0.852	0.060	0.751	0.961
582_132	Exon 7	r	-0.092	0.019	0.024	0.005	-0.063
		P value	1.42×10^{-6}	0.314	0.449	0.857	0.178
610_718	3'-end	r	-0.029	0.003	0.008	-0.011	-0.004
		P value	0.133	0.884	0.803	0.694	0.925
483_717	Exon 8	r	0.019	0.006	0.029	0.023	-0.074
		P value	0.317	0.753	0.364	0.407	0.114
235_610	Exon 6	r	-0.010	0.021	0.056	-0.001	-0.052
		P value	0.585	0.276	0.080	0.970	0.263
202_497	Exon 7	r	-0.071	0.005	0.072	-0.016	-0.017
		P value	1.94×10^{-4}	0.791	0.023	0.569	0.724
705_156	3'-end	r	0.017	-0.016	0.021	0.059	-0.020
		P value	0.361	0.418	0.503	0.036	0.673
314_329	Exon 5	r	-0.006	-0.010	0.037	0.005	-0.024
		P value	0.735	0.602	0.249	0.870	0.606
505_200	3'-end	r	-0.014	0.003	0.013	-0.007	-0.106
		P value	0.463	0.880	0.674	0.800	0.023
361_694	3'-end	r	0.001	-0.011	0.038	-0.011	-0.102
		P value	0.947	0.553	0.237	0.691	0.030
586_417	3'-end	r	-0.006	0.017	-0.014	0.026	-0.012
		P value	0.754	0.381	0.669	0.354	0.798
735_334	3'-end	r	-0.027	-0.003	0.021	0.003	-0.135
		P value	0.152	0.875	0.516	0.921	0.004
109_540	3'-end	r	0.016	0.013	0.030	0.022	0.029
		P value	0.412	0.499	0.351	0.435	0.539
260_360	3'-end	r	0.003	-0.022	0.066	-0.014	-0.077
		P value	0.892	0.260	0.038	0.625	0.101
218_13	3'-end	r	0.003	-0.028	0.003	0.037	0.002
		P value	0.865	0.149	0.913	0.188	0.968
267_582	3'-end	r	-0.020	0.001	0.044	-0.033	-0.127
		P value	0.302	0.972	0.169	0.243	0.006
548_21	3'-end	r	0.001	-0.002	0.022	-0.003	-0.037
		P value	0.969	0.903	0.497	0.924	0.429
7_323	3'-end	r	-0.013	0.003	-0.007	0.027	-0.025
		P value	0.498	0.890	0.833	0.326	0.599

[A] For complete Affymetrix probe IDs and further information on probes, see Table S5.

r= Pearson correlation between residualized expression level (corrected for technical covariates, age and sex). The last column only is based on levels that were additionally corrected for rs2228145 genotype) and residualized sIL-6R level (corrected for age and sex). P values are two-tailed.

Table S7: SNP information and conditional eQTL *P* values for all 80 significant eQTL associations after correction for the effect of rs2228145.

Probe Name[A]	SNP	SNP Chr	SNP position[B]	Alleles		MAF	Info[C]	eQTL *P* value
308_15	rs60255122	1	154504702	A	G	0.21	0.988	1.89E-09
308_15	rs60760897	1	154504849	C	T	0.21	0.988	1.89E-09
308_15	rs61698846	1	154504854	C	T	0.21	0.988	1.89E-09
308_15	rs61275241	1	154504887	T	G	0.21	0.988	1.89E-09
308_15	rs4072391	1	154438880	T	C	0.21	0.983	2.10E-09
308_15	rs112231452	1	154504900	G	A	0.21	0.988	2.14E-09
308_15	rs61403567	1	154504927	T	C	0.21	0.988	2.17E-09
308_15	rs59741504	1	154504601	T	C	0.21	0.991	2.20E-09
308_15	rs11490956	1	154487258	G	T	0.21	0.997	2.52E-09
308_15	rs111600849	1	154487489	G	A	0.21	0.997	2.52E-09
308_15	rs60498985	1	154504172	C	T	0.21	0.995	2.54E-09
308_15	rs73020232	1	154482669	C	T	0.21	0.997	2.75E-09
308_15	rs73020234	1	154482767	C	A	0.21	0.997	2.75E-09
308_15	rs73020246	1	154485640	A	G	0.21	0.997	2.75E-09
308_15	rs12403537	1	154487726	G	A	0.21	0.997	2.75E-09
308_15	rs77184252	1	154492533	A	G	0.21	0.997	2.75E-09
308_15	rs12405637	1	154501285	C	T	0.21	0.995	2.78E-09
308_15	rs58348886	1	154446198	T	C	0.21	0.990	2.91E-09
308_15	rs58710275	1	154505010	C	T	0.21	0.996	3.04E-09
308_15	rs7551873	1	154505857	C	T	0.21	0.995	3.04E-09
308_15	rs41308419	1	154507197	T	C	0.21	0.996	3.04E-09
308_15	rs112585956	1	154507767	T	C	0.21	0.996	3.04E-09
308_15	rs4633282	1	154507899	T	C	0.21	0.996	3.04E-09
308_15	rs73023331	1	154508210	G	A	0.21	0.996	3.04E-09
308_15	rs111742980	1	154508764	T	A	0.21	0.995	3.04E-09
308_15	rs112674677	1	154508792	C	T	0.21	0.996	3.04E-09
308_15	rs113915076	1	154508812	G	A	0.21	0.996	3.04E-09
308_15	rs4639752	1	154508974	T	A	0.21	0.996	3.04E-09
308_15	rs60368585	1	154509340	T	C	0.21	0.995	3.04E-09
308_15	rs112236096	1	154510790	C	T	0.21	0.995	3.04E-09
308_15	rs73023339	1	154510852	C	T	0.21	0.995	3.04E-09
308_15	rs59239860	1	154492107	G	T	0.21	0.994	3.08E-09
308_15	rs6674171	1	154491683	A	G	0.21	0.997	3.24E-09
308_15	rs73018293	1	154465577	C	T	0.21	0.997	3.39E-09

308_15	rs59838898	1	154466301	C	T	0.21	0.997	3.39E-09
308_15	rs4390168	1	154509096	A	G	0.21	0.992	3.57E-09
308_15	rs2229238	1	154437896	T	C	0.21	0.993	3.76E-09
308_15	rs10047079	1	154468135	T	C	0.21	0.997	3.99E-09
308_15	rs12406822	1	154499484	C	T	0.21	0.983	4.18E-09
308_15	rs7556449	1	154505886	A	G	0.21	0.996	4.23E-09
308_15	rs4379670	1	154439865	T	A	0.21	0.986	4.39E-09
308_15	rs7514452	1	154438084	C	T	0.21	0.993	4.47E-09
308_15	rs7526293	1	154444209	T	C	0.21	0.990	4.55E-09
308_15	rs6675472	1	154445503	T	C	0.22	0.972	4.62E-09
308_15	rs6669229	1	154444591	A	G	0.21	0.990	4.89E-09
308_15	rs41269915	1	154521584	T	A	0.21	0.986	5.22E-09
308_15	rs57783436	1	154511709	A	G	0.21	0.995	5.76E-09
308_15	rs112394421	1	154512008	T	C	0.21	0.995	5.76E-09
308_15	rs73023346	1	154512077	C	T	0.21	0.995	5.76E-09
308_15	rs12408461	1	154512710	T	C	0.21	0.994	5.76E-09
308_15	rs73023348	1	154513418	G	A	0.21	0.994	5.76E-09
308_15	rs73023349	1	154513440	T	C	0.21	0.994	5.76E-09
308_15	rs72999415	1	154513712	C	T	0.21	0.994	5.76E-09
308_15	rs72999419	1	154514092	T	C	0.21	0.994	5.76E-09
308_15	rs41313910	1	154514203	C	G	0.21	0.994	5.76E-09
308_15	rs72999422	1	154514942	G	A	0.21	0.994	5.76E-09
308_15	rs58881140	1	154515193	C	T	0.21	0.994	5.76E-09
308_15	rs6672087	1	154516122	A	C	0.21	0.994	5.76E-09
308_15	rs6681207	1	154517217	T	C	0.21	0.993	5.76E-09
308_15	rs3811449	1	154517504	G	A	0.21	0.993	5.76E-09
308_15	rs59084843	1	154518286	A	G	0.21	0.993	5.76E-09
308_15	rs61559765	1	154518349	T	C	0.21	0.993	5.76E-09
308_15	rs60092776	1	154518496	A	G	0.21	0.992	5.76E-09
308_15	rs60931472	1	154518642	T	C	0.21	0.992	5.76E-09
308_15	rs3811448	1	154516578	G	A	0.21	0.994	8.02E-09
308_15	rs4291493	1	154436920	T	C	0.27	0.919	1.24E-08
308_15	rs7537291	1	154433407	G	A	0.25	0.990	5.23E-08
308_15	rs7546068	1	154433415	C	T	0.25	0.990	5.23E-08
308_15	rs7537316	1	154433466	G	A	0.25	0.990	5.23E-08
308_15	rs7546552	1	154433905	C	A	0.25	0.992	5.23E-08
308_15	rs7546555	1	154433911	C	T	0.25	0.992	5.23E-08
308_15	rs6687597	1	154434936	G	A	0.25	0.992	5.23E-08

308_15	rs4509570	1	154436384	G	C	0.25	0.994	5.23E-08
308_15	rs4341355	1	154436404	C	G	0.25	0.994	5.23E-08
308_15	rs4240872	1	154436195	C	T	0.25	0.971	5.53E-08
308_15	rs6698040	1	154432948	T	C	0.25	0.990	5.53E-08
308_15	rs6427672	1	154435346	C	T	0.25	0.992	5.63E-08
308_15	rs10752641	1	154432042	G	C	0.25	0.973	6.45E-08
308_15	rs10908839	1	154430798	C	G	0.24	0.986	1.07E-07
308_15	rs55668699	1	154435293	T	A	0.25	0.955	1.66E-07

[A] For complete Affymetrix probe IDs and further information on probes, see Table S5.

[B] Base pair position build 37/hg19.

[C] Info= Imputation quality metric from SNPtest

Table S8: Results for the association with asthma for rs60760897 and SNPs in LD in the Australian Asthma Genetics consortium.

SNP	r^2 with rs60760897	Position[A]	A1[B]	A2[C]	MAF	*P*	OR A1[D]	SE[E]
rs60760897	1	154504849	T	C	0.191	0.495	0.96	0.054
rs61275241	1	154504887	G	T	0.190	0.566	0.97	0.055
rs61403567	1	154504927	C	T	0.191	0.514	0.97	0.054
rs61698846	1	154504854	T	C	0.189	0.515	0.97	0.055
rs10047079	0.9787	154468135	C	T	0.191	0.415	0.96	0.054
rs11490956	0.9787	154487258	T	G	0.191	0.400	0.96	0.054
rs12405637	0.9787	154501285	T	C	0.191	0.495	0.96	0.054
rs41308419	0.9787	154507197	C	T	0.189	0.505	0.96	0.055
rs4633282	0.9787	154507899	C	T	0.191	0.511	0.96	0.054
rs4639752	0.9787	154508974	A	T	0.191	0.511	0.96	0.054
rs59838898	0.9787	154466301	T	C	0.191	0.415	0.96	0.054
rs60368585	0.9787	154509340	C	T	0.191	0.511	0.96	0.054
rs6674171	0.9787	154491683	G	A	0.191	0.429	0.96	0.054
rs7551873	0.9787	154505857	T	C	0.191	0.495	0.96	0.054
rs7556449	0.9787	154505886	G	A	0.191	0.496	0.96	0.054
rs4390168	0.9718	154509096	G	A	0.191	0.511	0.96	0.054
rs59741504	0.9652	154504601	C	T	0.191	0.514	0.97	0.054
rs12408461	0.9644	154512710	C	T	0.187	0.604	0.97	0.055
rs3811448	0.9644	154516578	A	G	0.190	0.492	0.96	0.054
rs3811449	0.9644	154517504	A	G	0.190	0.511	0.96	0.054
rs41313910	0.9644	154514203	G	C	0.191	0.510	0.96	0.054
rs57783436	0.9644	154511709	G	A	0.191	0.493	0.96	0.054
rs58881140	0.9644	154515193	T	C	0.190	0.510	0.96	0.054
rs61559765	0.9644	154518349	C	T	0.190	0.511	0.96	0.054
rs6672087	0.9644	154516122	C	A	0.190	0.511	0.96	0.054
rs6681207	0.9644	154517217	C	T	0.190	0.511	0.96	0.054
rs58348886	0.9642	154446198	C	T	0.191	0.383	0.95	0.054
rs6669229	0.9572	154444591	A	G	0.190	0.363	0.95	0.055
rs7526293	0.9572	154444209	T	C	0.191	0.401	0.96	0.054
rs41269915	0.9503	154521584	A	T	0.190	0.511	0.96	0.054
rs59239860	0.9223	154492107	T	G	0.191	0.400	0.96	0.054
rs4379670	0.8945	154439865	T	A	0.185	0.506	0.96	0.055
rs2229238	0.8874	154437896	T	C	0.179	0.602	0.97	0.056
rs4072391	0.8874	154438880	T	C	0.179	0.611	0.97	0.056

rs7514452	0.8803	154438084	C	T	0.180	0.514	0.96	0.056
rs10752641	0.7052	154432042	G	C	0.216	0.241	0.94	0.052
rs35699331	0.7052	154432904	T	C	0.222	0.122	0.92	0.052
rs6698040	0.7052	154432948	T	C	0.216	0.217	0.94	0.052
rs7537316	0.7052	154433466	G	A	0.217	0.246	0.94	0.052
rs7546068	0.7052	154433415	C	T	0.217	0.240	0.94	0.052
rs4240872	0.7029	154436195	C	T	0.220	0.266	0.94	0.052
rs4341355	0.7029	154436404	C	G	0.219	0.273	0.94	0.052
rs4509570	0.7029	154436384	G	C	0.219	0.273	0.94	0.052
rs7537291	0.7008	154433407	G	A	0.217	0.240	0.94	0.052
rs10908839	0.6589	154430798	C	G	0.214	0.267	0.94	0.052
rs55668699	0.5989	154435293	A	T	0.215	0.386	0.96	0.052
rs12128408	0.4703	154488533	A	G	0.357	0.165	0.94	0.045
rs11265622	0.4693	154451420	A	G	0.357	0.153	0.94	0.045
rs10908843	0.4669	154494480	C	G	0.357	0.210	0.95	0.045
rs12753680	0.4663	154474900	G	A	0.357	0.165	0.94	0.045
rs10908841	0.4605	154487763	C	T	0.357	0.165	0.94	0.045
rs10908842	0.4605	154492702	G	A	0.357	0.165	0.94	0.045
rs10908847	0.4605	154504954	G	A	0.357	0.226	0.95	0.045
rs11265628	0.4605	154496489	C	T	0.357	0.210	0.95	0.045
rs12037271	0.4605	154507888	G	A	0.357	0.226	0.95	0.045
rs12118018	0.4605	154477440	G	A	0.357	0.165	0.94	0.045
rs12119111	0.4605	154478600	G	A	0.357	0.165	0.94	0.045
rs12407048	0.4605	154505270	C	T	0.352	0.173	0.94	0.045
rs12568083	0.4605	154455949	T	C	0.357	0.153	0.94	0.045
rs12740969	0.4605	154487060	T	G	0.357	0.165	0.94	0.045
rs4345797	0.4605	154495675	C	T	0.357	0.210	0.95	0.045
rs4478801	0.4605	154464572	G	A	0.357	0.154	0.94	0.045
rs4584384	0.4605	154495697	T	C	0.357	0.229	0.95	0.045
rs4638123	0.4605	154505704	C	T	0.357	0.226	0.95	0.045
rs4845638	0.4605	154490269	T	A	0.357	0.165	0.94	0.045
rs4845639	0.4605	154490352	C	T	0.357	0.165	0.94	0.045
rs4845642	0.4605	154498028	G	A	0.357	0.226	0.95	0.045
rs5018567	0.4605	154480318	T	C	0.357	0.193	0.94	0.045
rs6664608	0.4605	154479670	C	T	0.357	0.165	0.94	0.045
rs6684921	0.4605	154464945	A	C	0.358	0.159	0.94	0.045
rs6686276	0.4605	154466188	C	A	0.357	0.165	0.94	0.045
rs6700296	0.4605	154473660	T	C	0.358	0.160	0.94	0.045

rs7518694	0.4605	154484788	C	G	0.356	0.216	0.95	0.045
rs7519499	0.4605	154487926	G	A	0.357	0.165	0.94	0.045
rs9660786	0.4605	154484017	A	T	0.357	0.165	0.94	0.045
rs6658175	0.4593	154475330	T	A	0.357	0.165	0.94	0.045
rs11265632	0.4483	154514067	G	A	0.357	0.226	0.95	0.045
rs12136771	0.4483	154511502	T	C	0.358	0.226	0.95	0.045
rs4845647	0.4483	154514331	C	A	0.357	0.226	0.95	0.045
rs10908845	0.4474	154500898	C	T	0.357	0.226	0.95	0.045
rs12753666	0.4448	154474875	G	A	0.356	0.172	0.94	0.045
rs11265621	0.4437	154442960	G	A	0.357	0.159	0.94	0.045
rs6690230	0.3532	154432877	C	G	0.383	0.165	0.94	0.044
rs6695045	0.3532	154432957	A	G	0.383	0.165	0.94	0.044
rs11265611	0.3095	154395125	G	A	0.411	0.184	0.94	0.044
rs4845625	0.3019	154422067	T	C	0.415	0.156	0.94	0.043
rs6689393	0.3019	154426097	A	G	0.413	0.173	0.94	0.043
rs4553185	0.3015	154410955	C	T	0.414	0.107	0.93	0.043
rs4845619	0.3015	154405058	T	G	0.414	0.124	0.94	0.043
rs7549250	0.3015	154404336	C	T	0.414	0.123	0.94	0.043

The Australian Asthma Genetics Consortium (AAGC) cohorts and methods are described in(Ferreira et al. 2011).

[A] Base pair position build 37/hg19

[B] Allele 1 (effect allele)

[C] Allele 2

[D] Odds ratio associated with allele 1

[E] SE = Standard error of the odds ratio

Table S9: Results for the association with asthma for SNPs in LD with rs60760897 in the GABRIEL consortium.

SNP	**r^2 with rs60760897**	**Position^A**	**A1^B**	**A2^C**	**OR A1^D**	**SE^E**	***P***
rs7556449	0.979	154505886	G	A	1.01	0.025	0.722
rs3811448	0.964	154516578	G	A	0.99	0.025	0.738
rs7514452	0.880	154438084	T	C	1.00	0.025	0.999
rs4240872	0.703	154436195	T	C	1.00	0.024	0.942
rs4584384	0.460	154495697	T	C	0.95	0.021	0.015
rs4478801	0.460	154464572	G	A	0.95	0.021	0.014
rs4553185	0.302	154410955	T	C	1.04	0.020	0.076

For a description of the GABRIEL consortium cohorts and methods, see(Moffatt et al. 2010).

[A] Base pair position build 37/hg19

[B] Allele 1 (effect allele)

[C] Allele 2

[D] Odds ratio associated with allele 1

[E] SE = Standard error of the odds ratio

Supplementary Note

Subjects

The twin family and biometrical model analyses were based on data from 4980 individuals from 2360 NTR families, including 3083 twins, 236 of their non-twin brothers (up to two per family), 453 non-twin sisters (up to 2 per family), 657 of their mothers and 551 fathers (non-biological siblings, non-biological parents, spouses of twins and other types of family members were excluded). The GWAS of sIL-6R was performed on data from 4846 NTR participants (including all types of familial relations except for MZ twin pairs). The eQTL analysis included subjects with genome-wide SNP and expression data from the NTR (N=2977) and from the Netherlands Study of Depression and Anxiety (NESDA(Penninx et al. 2008), N=1966). Correlations between sIL-6R level and *IL6R* expression were examined in a subset of NTR subjects with data on sIL-6R, expression data and genome-wide SNP data (N=2727). The combined analysis of linkage and association was performed using data from 355 nuclear families from the NTR (total N subjects=1254), consisting of two parents and one child (213 families), two children (98 families), three children (43 families) or five children (1 family). The GCTA analysis of variance explained by chromosome-wide SNPs was performed on data from NTR participants including all types of familial relations except for MZ twin pairs (N=4846, same subjects as included in GWAS), and on data from a subset of unrelated NTR subjects (N=2875). Individuals using anti-inflammatory medication or medication influencing the HPA (Hypothalamic-Pituitary-Adrenal)-axis (NTR: N = 426/4.8%, NESDA: N=538/26%), or with a sIL-6R level > 100.000 pg/mL (N=6/0.07% of NTR subjects) at the time of blood sampling were excluded from all analyses. Individuals of non-Dutch origin identified based on genotype data(Abdellaoui et al. 2013) (N= 455, 3.8 % of the entire sample of 12,133 genotyped individuals from NTR and NESDA), were excluded from all SNP-based analyses (GWA, GCTA , eQTL and combined linkage and association analysis) to rule out potential effects of population stratification. Characteristics of the subjects included in each analysis are described in Table S1.

sIL-6R level

sIL-6R levels were measured in pg/mL. For the extended twin-family model and linkage analyses, sIL-6R level (pg/mL) was divided by 10.000 (corresponding to 10^{-8} g/mL) while retaining all decimals to meet the computational demands of the software used. For practical reasons, the variance due to rs2228145 and biometrical model estimates (Table 2) are also displayed in 10^{-8} g/mL. The original sIL-6R values in pg/mL were used as input for all other analyses.

Medication use

Following the ATC-coding system, anti-inflammatory medication was defined as all L-class (antineoplastic and immunomodulating) medication and M01 class medication (anti-inflammatory and antirheumatic medication). Medication influencing the HPA-axis was defined as medication in class H01 (pituitary and hypothalamic hormones and analogues) and class H02 (corticosteroids for systemic use).
Following the ATC-coding system, anti-inflammatory medication was defined as all L-class (antineoplastic and immunomodulating) medication and M01 class medication (anti-inflammatory and antirheumatic medication). Medication influencing the HPA-axis was defined as medication in class H01 (pituitary and hypothalamic hormones and analogues) and class H02 (corticosteroids for systemic use).

Pre-imputation QC

Quality control was done within and between chip platforms. For each platform the individual SNP markers were lifted over to build 37 (HG19) of the Human reference genome, using the LiftOver tool (“http://genome.sph.umich.edu/wiki/LiftOver”). SNPs that were not mapped at all, SNPs that had ambiguous locations, and SNPs that did not have matching - or strand opposite alleles were removed. Subsequently, the data were strand aligned with the 1000 Genomes phase I Interim release ALL panel of 23 November 2010 (sequence) and June 2011 (haplotypes) prepared by J. Marchini & B. Howie for IMPUTEv2.1 (https://mathgen.stats.ox.ac.uk/impute/data_download_1000G_phase1_interim.html). SNPs from each platform were removed if they still had mismatching alleles with this imputation reference set, if the allele frequencies differed more than 0.20 with the reference set, if the MAF was < 1%, if the HWE p-value was < 0.00001 or if the call rate was <95%. All samples were excluded from the data if their expected sex did not match their genotyped sex, if the genotype missing rate was above 10% or if the Plink F inbreeding value was either > 0.10 or < -0.10 (heterozygosity). After these steps the data of the individual chips were merged into a single dataset using the Plink 1.07 software.

Within the merged set IBD was calculated between all possible individual pairs and compared to the expected family structure of the NTR and NESDA studies. Samples were removed if the data did not match the expected IBD sharing, or if potentially consistent with biographic data, corrections were made to the family structure. DNA samples that were typed on multiple platforms were tested if the overlapping SNPs had a concordance rate above 99.0% and if not, all data of these samples were removed. On the merged data, the HWE and MAF SNP filters were re-applied, as well as the reference allele frequency difference <0.20 checks. As a final prior step to imputation SNPs with C/G and A/T allele combinations were removed if the MAF was between 0.35 and 0.50 to avoid wrong strand alignment for these SNPs.

Imputation

Genome wide SNP imputation was done with the IMPUTE 2.1.2 program for the autosomal genome using the above phase I integrated reference panel. A total number of 10,726 unique samples (for MZ twin pairs data imputation was done including one twin) were imputed in batches of around 500 individuals for 5 million base blocks, a 250 kb buffer and the NE parameter set to 20.000. Monomorphic SNPs present in the 500 individual subsets were removed. To avoid issues having SNPs from different platforms partly imputed and partly genotyped we re-imputed all genotyped SNPs. After imputation of these SNPs, we generally find a high concordance between re-imputed SNPs and the original genotype (0.9868), if the SNP info or R2 is above 30%.

Post-imputation QC

After imputation, additional QC included evaluation of the SNP platforms effect, the Mendelian error rate in families and filters for HWE, imputation quality and MAF. First we tested the effect of having different platforms imputed, and we removed SNPs showing platform effects. This was done, defining an individual with a specific platform as a case and the remaining individuals as controls. Allelic association was then calculated and SNPs were removed if the specific platform allele frequencies were significantly different from the remaining platforms with $p < 0.00001$. Subsequently, HWE was calculated on the SNPTEST allele probability counts for the full sample and SNPs were removed if the p-value < 0.000001. The Mendelian error rate was calculated on the best guess genotypes in families (trios and sib-pairs with parents) using first Gtool and then Plink 1.07. SNPs were removed if the Mendelian error rate was above 2%. SNPs were subsequently filtered from the dataset if the imputation quality R2 < 0.30 (mean is 0.85) and if the MAF in the total sample was less than 0.004. Finally, all SNPs were removed that were by then known to show problems in the reference sequence data of the phase I Interim set (159k).

Statistical analysis

Analyses of genotype data

All analyses were performed on imputed data from autosomal SNPs. The heritability analysis in twin families, biometrical model, GCTA analyses, linkage analyses and eQTL analyses were performed using best guess genotypes, and the GWAS was performed on genotype dosage data (using only SNPs with no missing data). SNPs with a mendelian error rate > 2 % were removed during post-imputation QC. For linkage analysis, all mendelian errors were removed from the data to meet software demands, using the option --me 1 1 --set-me-missing in PLINK(Purcell et al. 2007), which sets both parental and offspring genotype to missing when a mendelian error is encountered (rather than removing the entire family or SNP). In all analyses of genome-wide SNP data (GWA, eQTL, combined linkage and association, and GCTA analyses), covariates for 6 principle components (PCs) were included: 3 PCs to correct for population structure within the Dutch population, 1 PC for effects of the plate and source of DNA (blood vs buccal) and 2 PCs reflecting the effects of genotype array(Abdellaoui et al. 2013).

Observed variance due to rs2228145 genotype

The confidence interval around the observed variance due to rs2228145 genotype (V_{SNP}, Table 2) was estimated as follows: Confidence interval (CI) lower value = V_{SNP} *((N-1) /lower critical value)= 0.71 * ((4980-1)/ 5176.472= 0.68, and upper value= V_{SNP} *((N-1) /upper critical value)= 0.71 * ((4980-1)/ 4785.317=0.74, where lower critical value corresponds to (1- alpha)/2 from a chi-squared distribution with df =N-1=4979, and upper critical value corresponds to alpha/2, from a chi-squared distribution with df =N-1=4979.

Heritability of sIL-6R level based on twin family data

Models were fitted in Mx using raw-data maximum likelihood(Neale et al. 2006). We used the model described by Neale *et al*(Neale et al. 1994), for mono- and dizygotic twins, siblings and parents. For each model, Mx computes a goodness-of-fit statistic based on minus twice the logarithm of the likelihood (-2LL). Comparison of sub-models was done by means of likelihood-ratio tests; the ratio of likelihoods of sub-models follows a X^2 distribution with degrees of freedom (df) equal to the difference in the number of parameters of the two models. If a more restricted model fits the data significantly worse, the more general model is preferred.

In a so-called saturated model, familial correlations of sIL-6R level were estimated while taking age and sex effects on sIL-6R level into account. Next, the covariance structure among family members was modeled as a function of additive genetic variance (variance due to A, or V_A), non-additive genetic variance (variance due to D, or V_D), sibling-shared environment environmental variance (variance due to C, or V_C) and unique environmental variance (variance due to E, or V_E)(Distel et al. 2009; Falconer 1960). MZ twins derive from a single fertilized egg cell (zygote) and therefore share (nearly) 100% of their genetic material. DZ twins (who are derived from two zygotes) and non-twin sibling pairs share on average 50% of their segregating genetic material. Parents and offspring always share half of their segregating genetic material. Siblings and both types of twins share 100% of V_C. V_E comprises all variation that is not shared among family members. Thus, familial correlations in sIL-6R level may be represented as:

$r= a^2 + d^2 + c^2$ for MZ twins, $r= \frac{1}{2} a^2 + \frac{1}{4} d^2 + c^2$ for DZ twins and non-twin sib pairs, and $r= \frac{1}{2} a^2$ for Parent-offspring;

Where a^2= proportion of the variance due to additive genetic effects ($V_A / V_{P,}$ also called narrow-sense heritability or h^2), d^2= proportion of the variance due to non-additive genetic effects (V_D / V_P), c^2= proportion of the variance due to sibling-shared environment (V_C / V_P), and V_P=Total (phenotypic) variance of sIL-6R level = $V_A + V_D + V_C + V_{E.}$ We additionally fitted models that incorporated assortative mating (results not shown), which gave highly similar estimates of variance components.

Variance explained by chromosome-wide SNPs

The variance of sIL-6R level that can be explained by all imputed SNPs was estimated using GCTA (Genome-wide Complex Trait Analysis(Yang et al. 2011a; Yang et al. 2011b)). GCTA uses the genotype data to estimate the fraction of total DNA that two individuals share, which is summarized in a genetic relationship matrix (GRM). Next, a linear model is fitted in which the measure of genetic relatedness is used to predict phenotypic similarity of individuals, giving an estimate of the variance explained by all SNPs. The analyses in GCTA were performed using unrelated subjects only (excluding individuals from pairs with an estimated genetic relatedness > 0.025 (corresponding to third or fourth cousins) (1) and with inclusion of close relatives (including DZ twins, siblings and parent-offspring pairs) (2). An advantage compared to traditional methods of estimating heritability (e.g. the twin-family model) is that the SNP-based method in GCTA allows to assess the contribution of specific genomic regions (e.g. chromosomes) to the total heritability and does not require assumptions about IBD-sharing among family members.

GRMs were estimated separately for each chromosome (and for chromosome 1 separately for the *IL6R* gene +/-10MB vs all other SNPs), and GRMs for all chromosomes were fitted simultaneously in the regression model to estimate the variance attributable to each chromosome. SNPs with a MAF lower than 0.001 were excluded. To estimate the variance explained by the *IL6R* region after taking out the effect of rs2228145, a regression model was fitted that included the GRM for the *IL6R* region plus a covariate for rs2228145 (with genotype coded as 0, 1, 2 – corresponding to the number of minor alleles).

References

Abdellaoui A, Hottenga JJ, Knijff PD, Nivard MG, Xiao X, Scheet P, Brooks A, Ehli EA, Hu Y, Davies GE, Hudziak JJ, Sullivan PF, van BT, Willemsen G, de Geus EJ, Penninx BW, Boomsma DI (2013) Population structure, migration, and diversifying selection in the Netherlands. Eur.J.Hum.Genet.:doi: 10.1038/ejhg.2013.48

Distel MA, Rebollo-Mesa I, Willemsen G, Derom CA, Trull TJ, Martin NG, Boomsma DI (2009) Familial resemblance of borderline personality disorder features: genetic or cultural transmission? PLoS One 4(4):e5334

Falconer DS (1960) Introduction to quantitative genetics, Ronald Press Co, New York

Ferreira MA, Matheson MC, Duffy DL, Marks GB, Hui J, Le SP, Danoy P, Baltic S, Nyholt DR, Jenkins M, Hayden C, Willemsen G, Ang W, Kuokkanen M, Beilby J, Cheah F, de Geus EJ, Ramasamy A, Vedantam S, Salomaa V, Madden PA, Heath AC, Hopper JL, Visscher PM, Musk B, Leeder SR, Jarvelin MR, Pennell C, Boomsma DI, Hirschhorn JN, Walters H, Martin NG, James A, Jones G, Abramson MJ, Robertson CF, Dharmage SC, Brown MA, Montgomery GW, Thompson PJ (2011) Identification of IL6R and chromosome 11q13.5 as risk loci for asthma. Lancet 378(9795):1006-1014

Moffatt MF, Gut IG, Demenais F, Strachan DP, Bouzigon E, Heath S, von ME, Farrall M, Lathrop M, Cookson WO (2010) A large-scale, consortium-based genomewide association study of asthma. N.Engl.J.Med. 363(13):1211-1221

Neale MC, Boker SM, Xie G, Maes HH (2006) Mx: Statistical Modeling., Department of Psychiatry, Virginia Commonwealth University, Richmond, VA

Neale MC, Walters EE, Eaves LJ, Maes HH, Kendler KS (1994) Multivariate genetic analysis of twin-family data on fears: Mx models. Behav.Genet 24(2):119-139

Penninx BW, Beekman AT, Smit JH, Zitman FG, Nolen WA, Spinhoven P, Cuijpers P, De Jong PJ, Van Marwijk HW, Assendelft WJ, Van Der MK, Verhaak P, Wensing M, De GR, Hoogendijk WJ, Ormel J, van DR (2008) The Netherlands Study of Depression and Anxiety (NESDA): rationale, objectives and methods. Int.J.Methods Psychiatr.Res. 17(3):121-140

Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ, Sham PC (2007) PLINK: a tool set for whole-genome association and population-based linkage analyses. Am.J.Hum.Genet. 81(3):559-575

Yang J, Lee SH, Goddard ME, Visscher PM (2011a) GCTA: a tool for genome-wide complex trait analysis. Am.J.Hum.Genet. 88(1):76-82

Yang J, Manolio TA, Pasquale LR, Boerwinkle E, Caporaso N, Cunningham JM, de AM, Feenstra B, Feingold E, Hayes MG, Hill WG, Landi MT, Alonso A, Lettre G, Lin P, Ling H, Lowe W, Mathias RA, Melbye M, Pugh E, Cornelis MC, Weir BS, Goddard ME, Visscher PM (2011b) Genome partitioning of genetic variation for complex traits using common SNPs. Nat.Genet. 43(6):519-525