Supplementary Table 1. Genotyping and imputation methods by study

	FHS	GARP	RS1	RS3	TUK
Genotyping					
Platform	Affymetrix	Illumina	Illumina	Illumina	Illumina
Chip	500K or 100K or 10 K	Human660W quad	Human Hap550	Human Hap550	Human Hap300 or Human Hap610Q
Call rate	>0.97	> 0.95	> 0.975	> 0.975	>0.90
MAF	> 0.05	> 0.0025	> 0.01	> 0.01	>0.01
HWE p-value	$> 10^{-6}$	$> 10^{-6}$	$> 10^{-6}$	$> 10^{-6}$	$> 10^{-4}$
Imputation					
Variants included for imputation	534,982	462,361	512,349	514,073	314,075
Imputation software	MACH vs1	IMPUTE	MACH	MACH	IMPUTE vs 2
Genome build	HapMap Phase II release 22	Hapmap Phase II release 21	Hapmap Phase II release 22	Hapmap Phase II release 22	Hapmap Phase II release 36
Total number of SNPs available	2,543,887	1,830,498	2,543,887	2,543,887	3,044,064

Legend to Supplementary Table 1

FHS represents Framingham Heart Study; GARP, Genetics of OsteoArthrosis and Progression study; RS1, Rotterdam study cohort 1; RS3:, Rotterdam study cohort 3; TUK, TwinsUK: BMI, body mass index; MAF, Minor Allele Frequency; HWE, Hardy-Weinberg equilibrium

Supplementary Table 2. Results of the GWA meta-analysis adjusted for age and sex, showing those SNPs having $p<10^{-5}$.

				MAF					Imputation Quality*					Eff			
SNP	Chr	gene	N	RS1	RS3	TUK	FHS	GARP	RS1	RS3	TUK	FHS	GARP	All	BETA	SE	P
rs926849	6	PARK2	3939	0.31	0.32	NA	0.31	0.23	0.98	0.99	NA	0.9	95.04	C	-0.12	0.023	9.50E-08
rs17034687	3	NA	4429	0.09	0.1	0.05	0.08	NA	0.92	0.93	0.88	0.82	NA	C	0.19	0.037	3.67E-07
rs2187689	6	NA	4457	0.08	0.07	0.06	0.09	NA	0.98	0.99	0.95	0.93	NA	C	0.19	0.039	6.63E-07
rs7767277	6	NA	4457	0.08	0.07	0.06	0.09	NA	0.98	0.99	0.95	0.93	NA	A	0.19	0.039	6.64E-07
rs9488238	6	NA	4464	0.04	0.03	0.02	0.03	NA	0.87	0.88	0.87	0.97	NA	A	-0.28	0.058	7.30E-07
rs3019449	6	PARK2	4636	0.32	0.32	0.31	0.31	0.28	0.98	0.98	0.98	0.99	97.18	A	-0.11	0.022	7.42E-07
rs9301951	13	GPC6	4397	0.04	0.04	0.03	0.05	NA	0.96	0.97	0.74	0.78	NA	C	-0.25	0.051	1.35E-06
rs11136566	8	CSMD1	4610	0.39	0.39	0.36	0.39	0.46	0.99	0.98	0.97	0.96	97.39	A	-0.1	0.021	2.24E-06
rs7744666	6	NA	4466	0.1	0.09	0.06	0.1	NA	0.99	1	0.97	0.96	NA	C	0.16	0.035	3.07E-06
rs11969002	6	NA	4466	0.1	0.09	0.06	0.1	NA	0.99	1	0.97	0.96	NA	A	0.16	0.035	3.07E-06
rs365962	16	NA	4608	0.44	0.44	0.48	0.47	0.42	0.99	0.99	0.96	0.69	98.61	C	-0.1	0.020	3.10E-06
rs387953	16	NA	4683	0.46	0.45	0.48	0.46	0.43	1	0.99	1	0.67	99.99	G	-0.09	0.020	3.37E-06
rs737631	6	PARK2	4303	0.28	0.29	0.23	0.28	NA	0.92	0.91	0.89	0.83	NA	A	-0.11	0.023	3.57E-06
rs4802666	19	MYH14	4094	0.27	0.27	0.18	0.27	NA	0.7	0.74	0.76	0.64	NA	A	-0.13	0.027	3.76E-06
rs1154053	8	NA	4639	0.17	0.17	0.18	0.16	0.2	0.99	1	0.96	0.89	96.17	C	-0.12	0.026	4.68E-06
rs1205863	6	NA	3939	0.06	0.06	NA	0.06	0.07	0.99	1	NA	0.99	98.23	G	0.21	0.045	4.77E-06
rs3749982	6	NA	4458	0.1	0.09	0.06	0.1	NA	0.99	1	0.96	0.96	NA	A	0.16	0.035	4.97E-06
rs6457690	6	NA	4464	0.1	0.09	0.07	0.11	NA	0.98	1	0.96	0.97	NA	A	0.16	0.035	5.93E-06
rs1029296	6	NA	4464	0.1	0.09	0.07	0.11	NA	0.98	1	0.96	0.97	NA	C	0.16	0.035	5.93E-06
rs4875102	8	NA	4608	0.26	0.26	0.27	0.25	0.29	0.99	0.99	0.95	0.91	97.65	A	-0.1	0.023	6.24E-06
rs7234567	18	NA	4682	0.26	0.26	0.22	0.22	0.29	1	1	1	0.89	97.67	A	-0.1	0.023	6.34E-06

SNP	Chr	Gene	position												Eff All	beta	SE	p
rs6936004	6	NA	4462	0.1	0.09	0.07	0.11	NA	0.98	1	0.96	0.97	NA	C	0.16	0.035	6.52E-06
rs1884158	6	PARK2	4491	0.31	0.32	0.31	0.31	NA	0.98	0.99	0.99	0.91	NA	C	-0.1	0.022	6.54E-06
rs1981483	16	PIGQ	3939	0.42	0.43	NA	0.42	0.47	0.99	0.98	NA	0.44	99.64	A	0.1	0.022	6.79E-06
rs10890236	1	NA	4683	0.09	0.09	0.09	0.09	0.09	1	1	1	0.93	100	C	0.16	0.035	7.07E-06
rs1029295	6	NA	3747	0.1	0.09	NA	0.11	NA	0.98	1	NA	0.97	NA	C	0.16	0.037	7.08E-06
rs763014	16	RAB40C	3939	0.42	0.43	NA	0.43	0.47	0.98	0.99	NA	0.42	99.4	C	0.1	0.022	7.28E-06
rs10046257	6	NA	4461	0.1	0.09	0.08	0.11	NA	0.98	1	0.96	0.97	NA	A	0.15	0.034	8.21E-06
rs7204439	16	RAB40C	3939	0.42	0.43	NA	0.43	0.47	0.97	0.98	NA	0.43	97.37	C	0.1	0.022	8.23E-06
rs9469300	6	NA	4482	0.1	0.09	0.07	0.1	NA	0.99	1	0.92	0.96	NA	A	0.15	0.035	8.73E-06
rs7205409	16	RAB40C	4590	0.42	0.43	0.45	0.43	0.47	0.99	0.99	0.96	0.44	99.33	C	0.09	0.021	8.78E-06
rs10998466	10	NA	4446	0.01	0.01	0.01	0.02	NA	0.75	0.97	0.73	0.51	NA	A	-0.47	0.107	9.70E-06

Legend to Supplementary Table 2

Studies contributing data are denoted RS1: Rotterdam study cohort 1; RS3: Rotterdam study cohort 3; TUK: TwinsUK: BMI: body mass index; FHS: Framingham Heart Study; GARP: Genetics of OsteoArthrosis and Progression study;

SNP single nucleotide polymorphism; Chr chromosome; position, SNP location in base pairs; MAF minor allele frequency;

*R^2 from MACH for RS1, RS3, FHS and GARP; Information score from IMPUTE for TUK

Eff All, effect allele; beta, effect size; SE, standard error of beta; p, p value

Supplementary Figure 1. Quantile-quantile plot of meta-analysis adjusted GWA results

Legend to Supplementary Figure 1

The plots show GWA meta-analysis quantile-quantile plot of observed against expected results, adjusted for age and sex

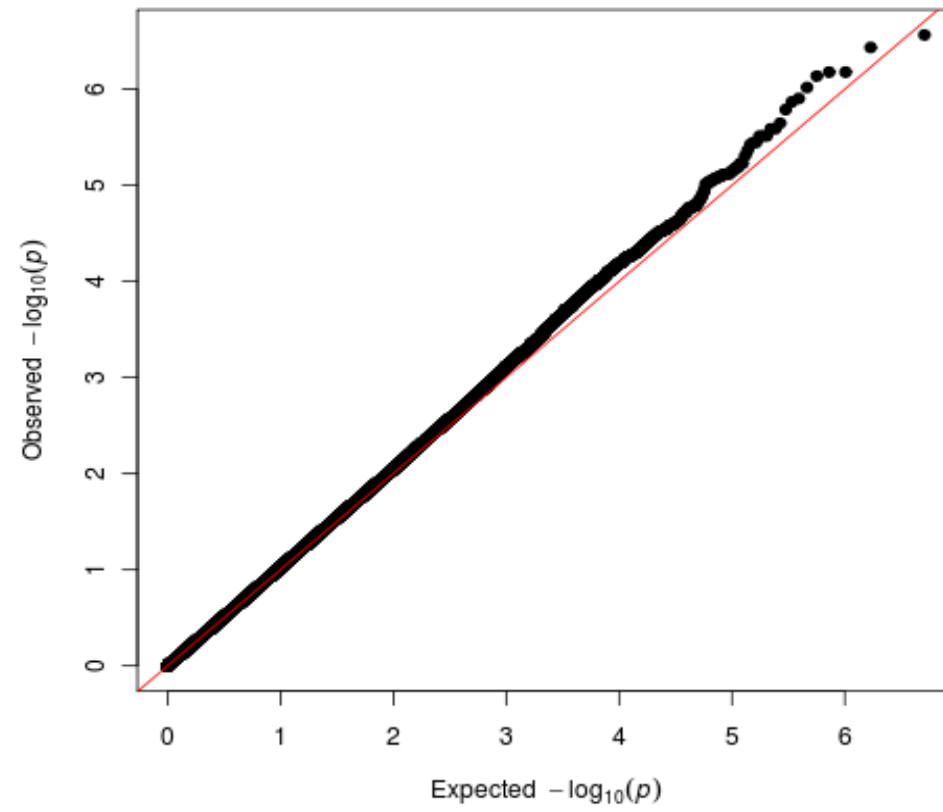**Supplementary Figure 2. Manhatten plot for meta-analysis of adjusted GWA results**
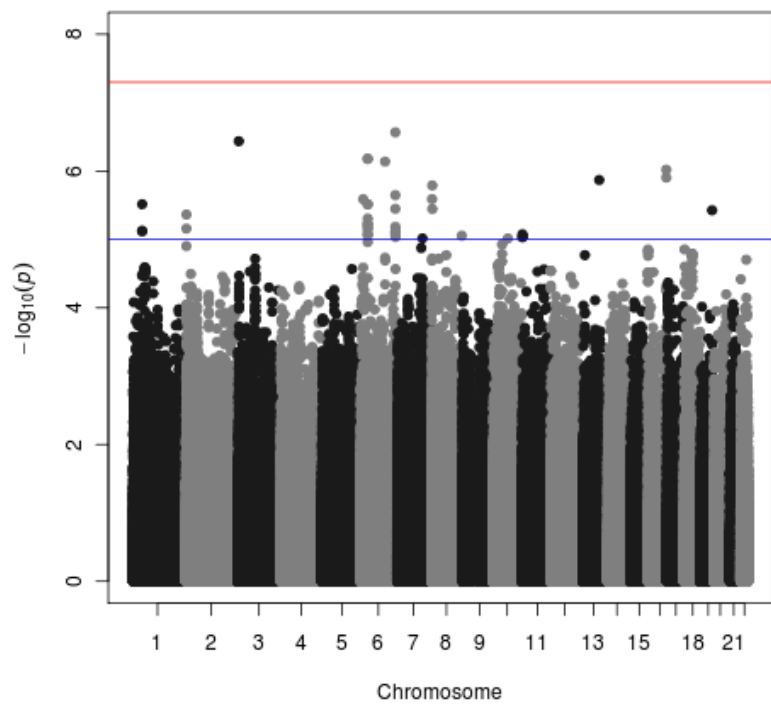
Legend to Supplementary Figure 2

Plot shows combined results for the 5 studies included in the meta-analysis, adjusted for age and sex. The blue and red horizontal lines mark the levels of suggestive and likely significance, respectively

Supplementary Figure 3. Regional plot of association results and recombination rates for the class II MHC region unadjusted for age and sex

Legend to Supplementary Figure 3

$-\log_{10} P$ values (y axis) of the SNPs are shown according to their chromosomal positions (x axis) with lead SNP shown as a purple diamond. The colour intensity of each symbol depicting a SNP reflects the extent of LD with the rs926849, coloured red ($r^2 > 0.8$) through to blue ($r^2 < 0.2$). Genetic recombination rates (cM/Mb), estimated using HapMap CEU samples, are shown with a light blue line. Physical positions are based on build 36 (NCBI) of the human genome. Also shown are the relative positions of genes mapping to the region of association. Genes have been redrawn to show the relative positions, and therefore, the maps are not to physical scale.