**Supplementary Table 1.** Linkage disequilibrium parameters D' and r2 for *IL1RN* single nucleotide polymorphisms (SNPs) rs419598, rs315952 and rs9005 for all three cohorts: New York University School of Medicine (NYU), Genetics of Generalized Osteoarthritis (GOGO) and Osteoarthritis Initiative (OAI).

	D' / r <sup>2</sup>			
SNP pair	NYU	GOGO	OAI	
rs419598 / rs315952	0.62 / 0.21	0.72 / 0.22	0.57 / 0.22	
rs419598 / rs9005	0.81 / 0.61	0.86 / 0.75	0.72 / 0.67	
rs35952 / rs9005	0.68 / 0.31	0.99 / 0.35	0.82 / 0.35	

## Supplementary Table 2: IL1RN haplotype TTG association with mJSW and radiographic severity in combined (NYU, GOGO, and OAI) cohorts.

Panel A. <i>IL1RN</i> SNP All Combined (n=1066)	mJSW: beta (± SE), p value, FDR
TTG-0 vs. TTG-1 haplotype	-0.35 (0.11), p=0.001, FDR=0.004
TTG-0 vs. TTG-2 haplotype	-0.45 (0.14), p=0.001, FDR=0.007
Panel B: <i>IL1RN</i> SNP All Combined (n=1066)	KL severity: OR (95% CI), p value, FDR
TTG-0 vs. TTG-1 haplotype	1.53 (1.12-2.08), p=0.008, FDR=0.017

In panel A, an association of medial joint space width (mJSW) in millimeters (mm) with IL1RN haplotypes were studied by comparing the indicated haplotype (TTG-0) with TTG-1 or TTG-2 using linear regression analysis. In panel B, Patients were classified by radiographic severity of knee OA by stratifying the KL scores to compare KL 1 or 2 versus KL 3 or 4. Odds ratios (OR) of KL vs. IL1RN haplotype also shows the association of Kellgren-Lawrence (KL) score with IL1RN haplotype.

Supplementary Table 3: Regression analysis of *IL1RN* haplotype (TTG) with radiographic medial joint space width (mJSW) in three cohorts of symptomatic knee OA patients.

	ALL (n=1022) Beta (SE); P=value		
mJSW (mm) (Baseline), TTG Haplotype (0 vs. 1/2)			
crude	-0.35 (0.11); 0.001		
adjusted for age, sex	-0.35 (0.10); 0.001		
adjusted for age, sex, BMI	-0.36 (0.10); 0.001		
mJSW (mm) (Baseline), TTG Haplotype (0 vs 2)			
crude	-0.45 (0.14); 0.001		
adjusted for age, sex	-0.40 (0.14); 0.004		
adjusted for age, sex, BMI	-0.40 (0.14); 0.003		

Medial joint space width (mJSW) in millimeters comparing the indicated haplotype (TTG-0) with TTG-1 or TTG-2. Haplotypes TTG-0 or TTG-1 or TTG-2, respectively, represent carriers of 0 or 1 or 2 copies of *IL1RN* haplotype produced using 3 *IL1RN* SNPs (rs419598, rs315952 and rs9005). Linear regression was performed unadjusted, adjusted for age and sex, as well as adjusted for age, sex, and body mass index (BMI) together.

Supplementary Table 4: Association of *IL1RN* haplotype (TTG) in male and female with radiographic signal knee medial joint space width (mJSW) in combined (NYU, GOGO, and OAI) cohorts of symptomatic knee OA patients.

	Beta (SE), p-value		
mJSW (mm) (Baseline), TTG Haplotype (0 vs 1/2) - Male	ALL (n=355)		
Crude	-0.48 (0.20), 0.018		
adjusted for age, sex	-0.54 (0.19), 0.006		
adjusted for age, sex, BMI	-0.50 (0.19), 0.009		
mJSW (mm) (Baseline), TTG Haplotype (0 vs 2) - Male	ALL (n=164)		
Crude	-0.58 (0.26), 0.027		
adjusted for age, sex	-0.51 (0.25), 0.042		
adjusted for age, sex, BMI	-0.49 (0.24), 0.047		
mJSW (mm) (Baseline), TTG Haplotype (0 vs 1/2) – Female	ALL (n=667)		
Crude	-0.28 (0.12), 0.021		
adjusted for age, sex	-0.27 (0.12), 0.025		
adjusted for age, sex, BMI	-0.28 (0.12), 0.023		
mJSW (mm) (Baseline), TTG Haplotype (0 vs 2) - Female	ALL (n=317)		
Crude	-0.38 (0.16), 0.018		
adjusted for age, sex	-0.34 (0.16), 0.033		
adjusted for age, sex, BMI	-0.34 (0.16), 0.034		
Medial joint space width (mJSW) in millimeters comparing the indicated haplotype (TTG-0)			

Medial joint space width (mJSW) in millimeters comparing the indicated haplotype (TTG-0) with TTG-1 or TTG-2. Haplotypes TTG-0 or TTG-1 or TTG-2, respectively, represent carriers of 0 or 1 or 2 copies of *IL1RN* haplotype produced using 3 *IL1RN* SNPs (rs419598, rs315952 and rs9005). A linear regression model was performed and adjusted for age and sex, as well as for age, sex, and body mass index (BMI) in the combined cohort.

Supplementary Table 5: Association of *IL1RN* haplotype (TTG) in Blacks with radiographic signal knee medial joint space width (mJSW) in combined (NYU and OAI) cohorts of symptomatic knee OA patients.

	Beta (SE), p-value
mJSW (mm) (Baseline), TTG Haplotype (0 vs 1/2)	ALL (n=82)
Crude	-0.48 (0.34), 0.165
adjusted for age, sex	-0.46 (0.34), 0.183
adjusted for age, sex, BMI	-0.44 (0.34), 0.201
mJSW (mm) (Baseline), TTG Haplotype (0 vs 2)	ALL (n=45)
Crude	-0.77 (0.44), 0.091
adjusted for age, sex	-0.79 (0.44), 0.080
adjusted for age, sex, BMI	-0.82 (0.45), 0.072

Medial joint space width (mJSW) in millimeters comparing the indicated haplotype (TTG-0) with TTG-1 or TTG-2. Haplotypes TTG-0 or TTG-1 or TTG-2, respectively, represent carriers of 0 or 1 or 2 copies of *IL1RN* haplotype produced using 3 *IL1RN* SNPs (rs419598, rs315952 and rs9005). A linear regression model was performed and adjusted for age and sex, as well as for age, sex, and body mass index (BMI), in the combined cohort.

Supplementary Table 6: Association of *IL1RN* haplotype (TTG) in Hispanic and non-Hispanic with baseline radiographic signal knee medial joint space width (mJSW) in combined (NYU and OAI) cohorts of symptomatic knee OA patients.

Hispanic	Beta (SE); P value
mJSW (mm), TTG Haplotype (0 vs 1/2)	ALL (n=347)
crude	-0.39 (0.24); 0.106
adjusted for age, sex	-0.33 (0.24); 0.160
adjusted for age, sex, BMI	-0.38 (0.24); 0.108
mJSW (mm), TTG Haplotype (0 vs 2)	ALL (n=122)
crude	-0.56 (0.29); 0.052
adjusted for age, sex	-0.37 (0.27); 0.176
adjusted for age, sex, BMI	-0.42 (0.27); 0.126
Non-Hispanic	Beta (SE); P value
mJSW (mm), TTG Haplotype (0 vs 1/2)	ALL (n=587)
	ALL (n=587) -0.33 (0.17); 0.057
mJSW (mm), TTG Haplotype (0 vs 1/2)	ALL (n=587) -0.33 (0.17); 0.057 -0.29 (0.17); 0.088
mJSW (mm), TTG Haplotype (0 vs 1/2) crude	ALL (n=587) -0.33 (0.17); 0.057
mJSW (mm), TTG Haplotype (0 vs 1/2) crude adjusted for age, sex adjusted for age, sex, BMI	ALL (n=587) -0.33 (0.17); 0.057 -0.29 (0.17); 0.088 -0.31 (0.17); 0.066
mJSW (mm), TTG Haplotype (0 vs 1/2) crude adjusted for age, sex adjusted for age, sex, BMI mJSW (mm), TTG Haplotype (0 vs 2)	ALL (n=587) -0.33 (0.17); 0.057 -0.29 (0.17); 0.088 -0.31 (0.17); 0.066
mJSW (mm), TTG Haplotype (0 vs 1/2) crude adjusted for age, sex adjusted for age, sex, BMI	ALL (n=587) -0.33 (0.17); 0.057 -0.29 (0.17); 0.088 -0.31 (0.17); 0.066  ALL (n=211) -0.63 (0.22); 0.005
mJSW (mm), TTG Haplotype (0 vs 1/2) crude adjusted for age, sex adjusted for age, sex, BMI mJSW (mm), TTG Haplotype (0 vs 2)	ALL (n=587) -0.33 (0.17); 0.057 -0.29 (0.17); 0.088 -0.31 (0.17); 0.066

Medial joint space width (mJSW) in millimeters comparing the indicated haplotype (TTG-0) with TTG-1 or TTG-2. Haplotypes TTG-0 or TTG-1 or TTG-2, respectively, represent carriers of 0 or 1 or 2 copies of *IL1RN* haplotype produced using 3 *IL1RN* SNPs (rs419598, rs315952 and rs9005). A linear regression model was performed and adjusted for age and sex, as well as for age, sex, and body mass index (BMI), in the combined cohort.

Supplementary Table 7: The IL1RN risk haplotype TTG (1 or 2) associated with decreased soluble IL-1Ra levels in chondrocytes

	Unstimulated, mean (±SD)		IL-1 induced, mean (±SD)			
	Extra- cellular (s)	Intra- cellular (ic)	Ratio (s vs. ic)	Extra- cellular (s)	Intra- cellular (ic)	Ratio (s vs. ic)
IL1RN haplotype						
TTG-1,2 (n=15)	5.05 (±8.1)	7.93 (±14.9)	1 : 1.2	6.19 (±7.1)	33.71 (±22.0)	1 : 5.4
TTG-0 (n=14)	1.46 (±2.2)	1.41 (±2.5)	1:1	10.36 (±11.9)	12.28 (±8.4)	1 : 1.2
P-value						
TTG-1, 2 vs. TTG-0	0.05	0.06	_	0.22	0.07	_
TTG-1,2 – Con vs. IL-1	_	_	_	0.62	0.04	_
TTG-0 – Con vs. IL-1	_	_	_	0.01	0.0005	_

We analyzed total cell lysate for extracellular and cell-associated IL-1Ra protein expression in primary chondrocytes by ELISA. Haplotypes TTG-0 or TTG-1 or TTG-2, respectively, represent carriers of 0 or 1 or 2 copies of *IL1RN* haplotype produced using 3 *IL1RN* SNPs (rs419598, rs315952 and rs9005). Chondrocytes with *IL1RN* TTG-1/2 haplotype produced significantly lower levels of soluble IL1Ra than TTG-0 carriers in both spontaneous conditions and following 24h IL-1 $\beta$  induction. The data represent mean (±SD), for n=15 individuals with TTG-1/2 and n=14 individuals with TTG-0. Mann Whitney U test was used to analyze difference between groups.