

## Correction

**Correction: Association of the FCRL3 gene with rheumatoid arthritis: a further example of population specificity?**

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Following publication of our article [1] we have noticed the following error in nomenclature:

All four polymorphisms studied were referred to as FCRL3-169\*C/T.

**Table 1**

**Genotype frequencies of Fc receptor-like 3 (FCRL3) single nucleotide polymorphisms in rheumatoid arthritis cases, in controls and in subgroups**

Single nucleotide polymorphism	Controls	Cases	Two-copy shared epitope alleles <sup>b</sup>		Rheumatoid factor-positive <sup>a, c</sup>
			Controls	Cases	
FCRL3-169*C/T (fcl3_3, rs7528684)					
T/T	595 (28.7)	324 (30.4)	45 (36.9)	71 (32.0)	324 (30.4)
C/T	1055 (50.9)	524 (49.2)	52 (42.6)	103 (46.4)	524 (49.2)
C/C	423 (20.4)	217 (20.4)	25 (20.5)	48 (21.6)	217 (20.4)
P value	0.57		0.69		0.57
FCRL3-110*C/T (fcl3_4, rs11264799)					
1/1	258 (53.3)	404 (53.1)	13 (50.0)	132 (52.6)	404 (53.1)
1/2	190 (39.3)	296 (38.9)	10 (38.5)	95 (37.8)	296 (38.9)
2/2	36 (7.4)	61 (8.0)	3 (11.5)	24 (9.6)	61 (8.0)
P value	0.93		0.94		0.93
FCRL3+358*C/G (fcl3_5, rs945635)					
1/1	123 (27.9)	209 (28.4)	9 (36.0)	64 (27.3)	209 (28.4)
1/2	200 (45.3)	362 (49.3)	12 (48.0)	116 (49.6)	362 (49.3)
2/2	118 (26.8)	164 (22.3)	4 (16.0)	54 (23.1)	164 (22.3)
P value	0.46		0.57		0.46
FCRL3+1370*A/G (fcl3_6, rs3761959)					
1/1	124 (26.3)	209 (27.8)	8 (30.8)	65 (27.1)	209 (27.8)
1/2	220 (46.7)	370 (49.3)	12 (46.1)	120 (50.0)	370 (49.3)
2/2	127 (27.0)	172 (22.9)	6 (23.1)	55 (22.9)	172 (22.9)
P value	0.28		0.91		0.28

Data presented as n (%). <sup>a</sup>Comparison group = all controls. <sup>b</sup>Subgroup stratified by two copies of shared epitope alleles. <sup>c</sup>Subgroup stratified by the presence of rheumatoid factor (measured cumulatively).

FCRL3-169\*C/T (fcl3\_3, rs7528684) is correctly named.

FCRL3-169\*C/T (fcl3\_4, rs11264799) should be FCRL3-110\*C/T (fcl3\_4, rs11264799).

FCRL3-169\*C/T (fcl3\_5, rs945635) should be FCRL3+358\*C/G (fcl3\_5, rs945635).

FCRL3-169\*C/T (fcl3\_6, rs3761959) should be FCRL3+1370\*A/G (fcl3\_6, rs3761959).

Thus, Table 1 should appear as shown above.

Within 'Patients and methods', the paragraph 'Polymorphisms selected' should read as follows:

Four SNPs – FCRL3-169\*C/T (fcl3\_3, rs7528684), FCRL3-110\*C/T (fcl3\_4, rs11264799), FCRL3+358\*C/G (fcl3\_5, rs945635) and FCRL3+1370\*A/G (fcl3\_6, rs3761959) – were initially selected for investigation because they had all been associated with RA in the Japanese population on single-point analysis, because the SNPs formed a haplotype associated with RA and because the most probable disease causal SNP (FCRL3-169\*C/T (fcl3\_3, rs7528684)) was included [7].

The second paragraph of 'Results' should read as follows:

No deviation from Hardy–Weinberg expectations was observed for any of the SNPs in either cases or controls. Interim analysis after genotyping a subset of the total cohort revealed that extensive linkage disequilibrium was present across the four SNPs tested. Indeed, the  $D'$  value between all the SNPs was 0.98 while the correlation between SNPs FCRL3-169\*C/T (fcl3\_3, rs7528684), FCRL3+358\*C/G fcl3\_5 (rs945635) and FCRL3+1370\*A/G fcl3\_6 (rs3761959) was also 0.98 in this sample. The correlation between these SNPs and FCRL3-110\*C/T fcl3\_4 (rs11264799) was 0.6 or greater, reflecting the difference in allele frequency of this SNP compared with the others. Hence, genotyping of all four SNPs was unnecessary and, in the remaining samples, only the putative disease causal polymorphism was genotyped.

The above changes in no way affect the conclusions of the study.

## Competing interests

The authors declare that they have no competing interests.

## Reference

1. Eyre S, Bowes J, Potter C, Worthington J, Barton A: **Association of the FCRL3 gene with rheumatoid arthritis: a further example of population specificity?** *Arthritis Research & Therapy* 2006, **8**:R117.