Supplementary Table 9. Genetic correlation between RA subsets*

Denmark-Iceland-Finland (15,976 cases & 554,675 controls)	Norway-Sweden-UK (15,337 cases & 440,702 controls)	rg	se	*P*
RA overall	RA overall	0.99	0.06	*1.1E-55*
Seropositive RA	Seropositive RA	1.03	0.08	*7.6E-39*
Seronegative RA	Seronegative RA	1.09	0.53	*0.038*
RA overall	Seropositive RA	0.91	0.07	*1.3E-35*
Seropositive RA	RA overall	1.05	0.07	*1.7E-54*
	META	**0.98**	**0.049**	***6.5E-88***
RA overall	Seronegative RA	1.39	0.61	*0.022*
Seronegative RA	RA overall	0.93	0.12	*1.1E-14*
	META	**0.95**	**0.12**	***1.0E-15***
Seropositive RA	Seronegative RA	1.34	0.57	*0.019*
Seronegative RA	Seropositive RA	0.85	0.13	*5.1E-11*
	META	**0.87**	**0.13**	***4.5E-12***

*The study population was divided into two groups of similar size, and the correlation of subsets made between the two. We estimated the genetic correlation between RA subtypes using cross-trait LD score regression. In this analysis, we used results for about 1.2 million well imputed variants, and for LD information we used precomputed LD scores for European populations. To avoid bias due to overlapping samples, we calculated the genetic correlation between a meta-analysis of Danish, Icelandic and Finnish datasets and a meta-analysis of Norwegian, Swedish and UK datasets for the different RA subtypes. The results of the two analyses were subsequently meta-analysed.