Supplementary methods

CNV analysis

The paralogue ratio test (PRT) was used to determine CNVs at the *FCGR3* locus (including *FCGR3A* and *FCGR3B* genes). The same pair of fluorescently labeled primers amplified the test locus and a region within chromosome 18 known to have two copies (26). We amplified 10 ng of genomic DNA by 24 PCR cycles in order to obtain a non-saturated amount of product using standard conditions. PCR products were differentiated by length using an ABI 3100 Avant Genetic Analyzer (Applied Biosystems, Foster City, CA). Fragment analysis was carried out using Genescan software (Applied Biosystems, Foster City, CA). Peak area ratios between *FCGR3A*+*FCGR3B* (73 bp) and the reference region on chromosome 18 (83 bp) were used to estimate the total copy number (CN) of the *FCGR3* locus. Restriction enzyme digest variant ratio (REDVR) assay was used to distinguish between *FCGR3A* and *FCGR3B* genes using a single fluorescently labeled primer pair (26). Digestion products were separated by capillary electrophoresis on an ABI 3100 Avant Genetic Analyzer (Applied Biosystems Foster City, CA). Peak height ratios between *FCGR3A* (182 bp) and *FCGR3B* (134 bp) were used to estimate the CN of each gene. Mean values for the duplicates were taken. Internal controls for CN<2, CN=2, and CN>2 were run in each experiment.

FCGR3B CN was confirmed by duplex quantitative PCR using TaqMan CN assay for *FCGR3B* (Hs04211858_cn, Applied Biosystems) and normalizing with TaqMan Copy Number Reference Assay RNAse P (Part Number 4403326, Applied Biosystems Foster City, CA) on an ABI Prism 7000 Instrument (Applied Biosystems Foster City, CA). Quantitative PCR was carried out with 20 ng of DNA in triplicate following the manufacturer's instructions. Internal controls for CN<2, CN=2, and CN>2 were run in each experiment and CN calculations were performed using the delta-delta Ct method.

Supplementary Table 1. Association between SNPs within *HLA-DQA1* and *PLA2R1* genes and *FCGR3B* CNV with spontaneous remission

Gene (SNP)		n (Frequency)			OR (95% CI)	Genotypic P value
		G/G	A/G	A/A		
HLA-DQA1 (rs2187668)	SR	10 (43.5)	13 (56.5)	0 (0)	0.95 (0.35-2.61)	0.92[a]
	NSR	23 (41.8)	30 (54.5)	2 (3.6)		
PLA2R1 (rs4664308)	SR	2 (8.7)	7 (30.4)	14 (60.9)	1.36 (0.48-3.85)	0.57[a]
	NSR	5 (9.1)	18 (32.7)	32 (58.2)		
		CN <2	CN =2	CN >2		
CN *FCGR3B*	SR	1 (4.3)	22 (95.7)	0 (0)	4.84 (0.59-39.59)	0.17[b]
	NSR	7 (12.7)	45 (81.8)	3 (5.5)		

Abbreviations: SR, spontaneous remission; NSR, no spontaneous remission; CN, copy number; OR, odds ratio; 95% CI, 95% confidence interval.

[a]Genotype frequency difference test (X^2) under dominant model for *HLA-DQA1* and *PLA2R1.*

[b]Fisher's exact test considering CN =2 vs CN different from 2.