Supporting Information

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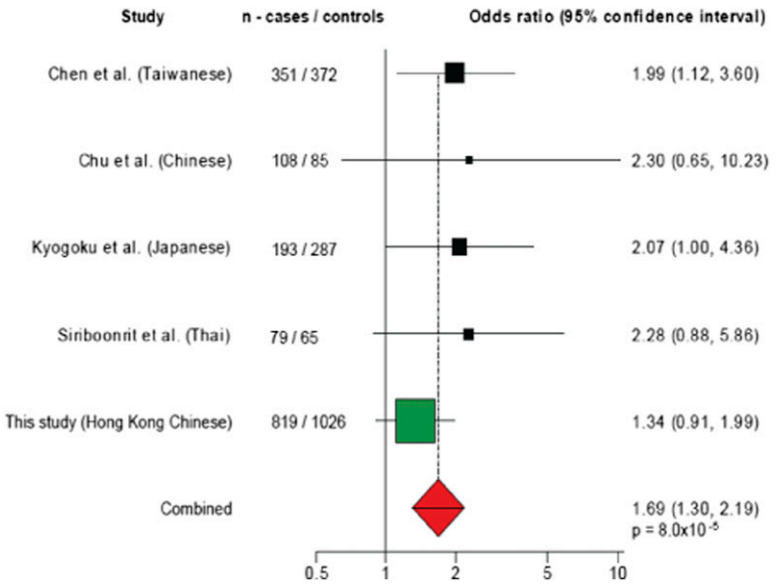

Fig. S1. Meta-analysis of association between FcγRIIb^{T232} homozygosity and systemic lupus erythematosus (SLE) in Asians. Meta-analysis performed using StatsDirect software (random effects model by DerSimonian and Laird shown in ref. 1).

1. DerSimonian R, Laird N (1986) Meta-analysis in clinical trials. *Control Clin Trials* 7:177–188.

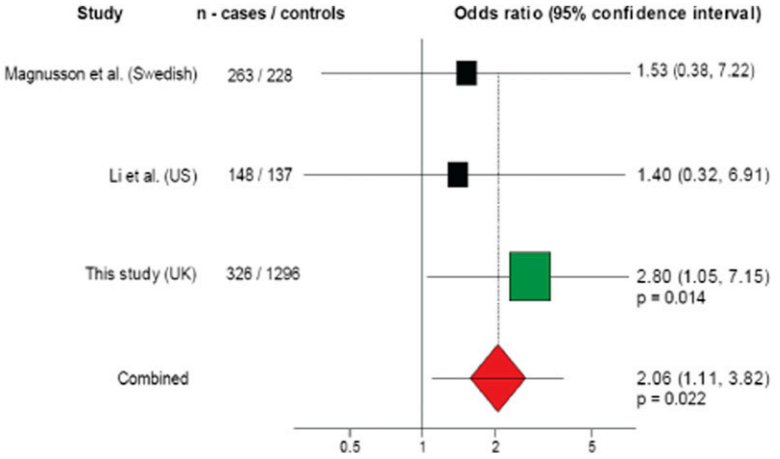

Fig. S2. Meta-analysis of association between FcγRIIb^{T232} homozygosity and SLE in Caucasians. Meta-analysis performed using StatsDirect software (random effects model by DerSimonian and Laird shown in ref. 1).

1. DerSimonian R, Laird N (1986) Meta-analysis in clinical trials. *Control Clin Trials* 7:177–188.

Table S1. Genotype and allele frequencies for FcγRIIb^{T232} in controls and SLE cohorts of Asian adults

	Taiwanese (1)					Thai (2)					Japanese (3)					Chinese (4)					Hong Kong Chinese				
	Controls		Cases			Controls		Cases			Controls		Cases			Controls		Cases			Controls*		Cases†		
Genotype	*n*	Freq	*n*	Freq	*P*	*n*	Freq	*n*	Freq	*P*	*n*	Freq	*n*	Freq	*P*	*n*	Freq	*n*	Freq	*P*	*n*	Freq	*n*	Freq	*P*
II	206	0.55	189	0.54		97	0.59	38	0.48		183	0.61	106	0.55		51	0.6	49	0.45		565	0.55	475	0.58	
TT	22	0.06	39	0.11	0.04‡	12	0.07	12	0.15	0.1‡	16	0.05	21	0.11	0.06‡	4	0.05	11	0.10	0.09‡	57	0.06	60	0.07	0.06‡
IT	144	0.39	123	0.35		56	0.34	29	0.37		104	0.34	66	0.34		30	0.35	48	0.44		404	0.39	284	0.35	
TT	22	0.06	39	0.11	0.02§	12	0.07	12	0.15	0.07§	16	0.05	21	0.11	0.02§	4	0.05	11	0.10	0.19§	57	0.06	60	0.07	0.12§
II and IT	350	0.94	312	0.89		153	0.93	67	0.85		287	0.95	172	0.89		81	0.95	97	0.90		969	0.94	759	0.93	

Freq, frequency.
*Controls are in Hardy–Weinberg equilibrium (HWE; $P = 0.38$).
†Cases are in HWE ($P = 0.16$).
‡P value calculated by χ^2 test using a 2 × 3 contingency table (df = 2).
§P value and odds ratio (OR) calculated by χ^2 test using a 2 × 2 contingency table (df = 1).

1. Chen JY, et al. (2006) Association of a transmembrane polymorphism of Fcgamma receptor IIb (FCGR2B) with systemic lupus erythematosus in Taiwanese patients. *Arthritis Rheum* 54: 3908–3917.
2. Siriboonrit U, et al. (2003) Association of Fcgamma receptor IIb and IIIb polymorphisms with susceptibility to systemic lupus erythematosus in Thais. *Tissue Antigens* 61:374–383.
3. Kyogoku C, et al. (2002) Fcgamma receptor gene polymorphisms in Japanese patients with systemic lupus erythematosus: Contribution of FCGR2B to genetic susceptibility. *Arthritis Rheum* 46:1242–1254.
4. Chu ZT, et al. (2004) Association of Fcgamma receptor IIb polymorphism with susceptibility to systemic lupus erythematosus in Chinese: A common susceptibility gene in the Asian populations. *Tissue Antigens* 63:21–27.

Table S2. Genotype and allele frequencies for FcγRIIb^{T232} in controls and SLE cohorts of Caucasian adults

	Sweden (1)					United States (2)					United Kingdom				
	Controls		Cases			Controls		Cases			Controls*		Cases†		
Genotype	*n*	Freq	*n*	Freq	*P*	*n*	Freq	*n*	Freq	*P*	*n*	Freq	*n*	Freq	*P*
II	171	0.75	189	0.72		106	0.77	112	0.76		1,051	0.81	269	0.83	
TT	4	0.02	7	0.03	0.65‡	4	0.03	6	0.04	0.86‡	13	0.01	9	0.03	0.02‡
IT	53	0.23	67	0.25		27	0.2	30	0.2		232	0.18	48	0.15	
TT	4	0.02	7	0.03	0.55§	4	0.03	6	0.04	0.75§	13	0.01	9	0.03	0.014§
II and IT	224	0.98	256	0.97		133	0.97	142	0.96		1,283	0.99	317	0.97	

Freq, frequency.
*Controls are in HWE ($P = 1.0$).
†Cases are not in HWE ($P = 0.003$).
‡P value calculated by χ^2 test using a 2 × 3 contingency table (df = 2).
§P value and odds ratio (OR) calculated by χ^2 test using a 2 × 2 contingency table (df = 1).

1. Magnusson V, et al. (2004) Polymorphisms of the Fc gamma receptor type IIB gene are not associated with systemic lupus erythematosus in the Swedish population. *Arthritis Rheum* 50: 1348–1350.
2. Li X, et al. (2003) A novel polymorphism in the Fcgamma receptor IIB (CD32B) transmembrane region alters receptor signaling. *Arthritis Rheum* 48:3242–3252.

Table S3. *FCGR2B* genotyping results for the mild malaria cohort: Incidence rates and unadjusted incidence rate ratios (IRR) for malaria

	n	Person weeks of observation	Malaria	Incidence	IRR	95% CI	*P* value
II	262	35,399	1,257	1.85	1		
IT	187	23,705	914	2.00	1.09	0.92–1.29	0.341
TT	24	3,323	99	1.55	0.84	0.57–1.23	0.372

All incidence rates are expressed as episodes per child per year. CI, confidence interval.

Table S4. *FCGR2B* genotyping results for the mild malaria cohort: IRRs adjusted for sickle cell, thalassaemia, season, ethnic group, and age

	n	Person weeks of observation	Malaria	Incidence	IRR	95% CI	*P* value
II	262	35,399	1,257	1.85	1		
IT	187	23,705	914	2.00	1.05	0.87–1.26	0.639
TT	24	3,323	99	1.55	0.92	0.61–1.37	0.668

All incidence rates are expressed as episodes per child per year. CI, confidence interval.

Table S5. *FCGR2B* genotyping results for the mild malaria cohort: Parasite densities during malaria infections

	n	Mean log parasitaemia	95% CI	*P* value
II	1,257	4.16	4.10–4.21	
IT	914	4.15	4.09–4.22	0.878
TT	99	4.24	4.05–4.43	0.438

All incidence rates are expressed as episodes per child per year. CI, confidence interval.

Table S6. *FCGR2B* genotyping results for the mild malaria cohort: Non-malaria fever detected by active surveillance (fever >37.5 °C in absence of malaria parasites)

	n	Patient weeks of observation	Nonmalaria fever	Incidence	IRR	95% CI	*P* value
II	262	35,399	710	1.04	1		
IT	187	23,705	479	1.05	1.01	0.85–1.19	1.19
TT	24	3,323	61	0.95	0.92	0.69–1.22	1.22

All incidence rates are expressed as episodes per child per year. CI, confidence interval.

Table S7. Distribution of genotype frequencies for FcγRIIb^{T232} in controls and bacteremia cohorts of Kenyan children from Kilifi District Hospital

	Bacterial control group 1**		Bacterial case group 1[†]			Control group 2[‡]		Bacterial case group 2[§]		
Genotype	*n*	Frequency	*n*	Frequency	*P* value	*n*	Frequency	*n*	Frequency	*P* value
II	270	0.490	436	0.504		875	0.513	445	0.469	
TT	42	0.076	48	0.045	0.155[¶‖]	125	0.073	64	0.068	0.049[¶‖]
IT	239	0.434	325	0.402		706	0.414	439	0.463	
TT	42	0.076	48	0.0593	0.219*	125	0.073	64	0.068	0.590*
IT and II	509	0.924	761	0.940	OR = 0.76 (0.50–1.17)	1,581	0.927	884	0.932	OR = 0.92 (0.68–1.26)

*P value and OR calculated by χ^2 test using a 2 × 2 contingency table (df = 1). Numbers in parentheses refer to 95% CIs.
[†]Bacterial case group 1 is in HWE (P = 0.47).
[‡]Control group 2 is in HWE (P = 0.56).
[§]Bacterial case group 2 is not in HWE (P = 0.006).
[¶]P value calculated by χ^2 test using a 2 × 3 contingency table (df = 2).
[‖]Genotype was not associated with a specific bacterium, Gram-stain positive or negative, HIV status of the child, or child survival of the infection (multiple logistic regression).
**Bacterial control group 1 is in HWE (P = 0.55).

Table S8. Multiple logistic regression of clinical features in severe malaria case group 1

Clinical parameters	*P* value
Blantyre coma scale	0.52
Prostration	0.88
Impaired consciousness	0.56
Deep breathing	0.12
Tachycardia	0.067
Mortality	0.35
White blood cell count	0.31
Red blood cell count	0.98
Hemoglobin	0.89
Mean corpuscular volume	0.88
Parasitemia	0.72