Supporting Information

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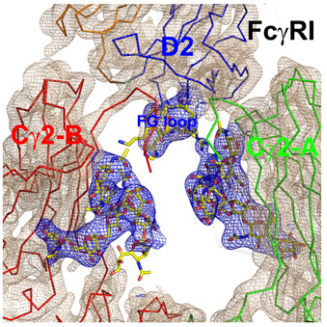

Fig. S1. Portion of the 2Fo-Fc electron density map (1σ) of the FcγRI and Fc complex, with glycan densities shown in blue.

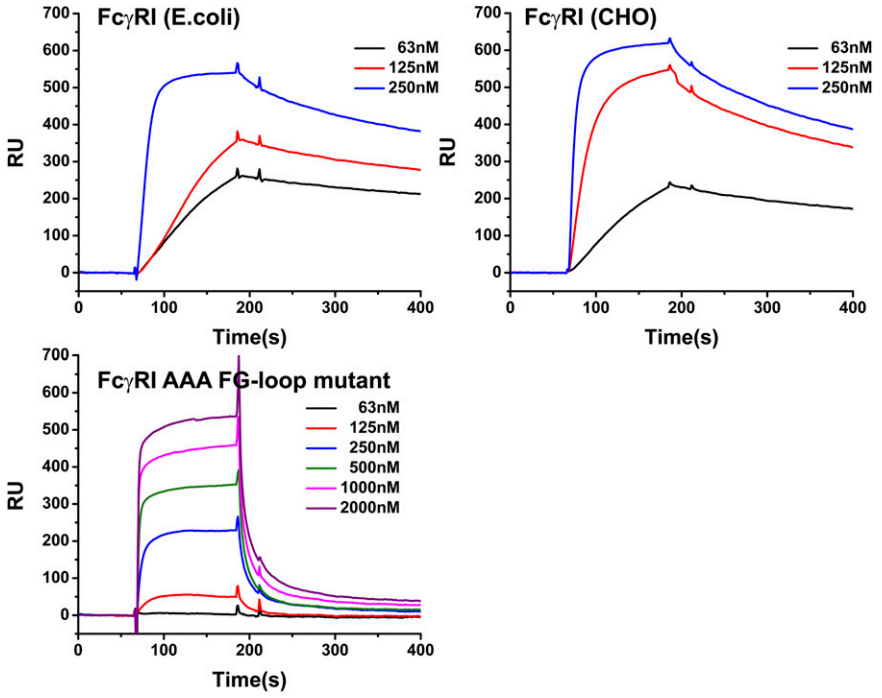

Fig. S2. Solution IgG_4 binding sensorgrams for serial dilutions of the WT and FG loop AAA mutant FcγRI receptors.

Table S1. X-ray crystallographic data collection and refinement statistics

Variable	Value
Data collection	
Space group	P1
Unit cell dimension, Å	a = 59.9, b = 68.0, c = 125.0; α= 89.9, β = 112.3, γ = 90.0
Resolution range, Å	50.0–3.50 (3.56–3.50)
Unique reflections	20,950 (813)*
Average redundancy	5.0 (1.5)*
R_{merge}, %[†]	13.5 (65.0)*
I/σ(I)	22.1 (1.0)*
Completeness (%)	91.5 (68.8)*
Refinement statistics	
Refinement resolution, Å	40.6–3.50
R_{cryst}, %[‡]	24.5 (31.7)[¶]
R_{free}, %	29.6 (34.6)[¶]
Protein atoms	10,947
Ligands	16× NAG, 12× MAN, 4× FUC, 2× GAL, 1× SIA
rmsd from ideal values	
Bond length, Å	0.006
Bond angle, °	1.72
Mean B-factor, Å^2	183.0
Wilson plot B-factor, Å^2	127.4
Ramachandran statistics	
Most favored region, %	94.5
Additionally allowed, %	5.5

*Values for the highest-resolution shell in data collection (3.56–3.50 Å).

[†]$R_{merge} = \sum_h \sum_i |I_i(hkl) - \langle I(hkl)\rangle| / \sum_h \sum_i I_i(hkl)$.

[‡]$R_{cryst} = \sum ||Fo| - |Fc|| / \sum |Fo|$ calculated from working dataset. R_{free} is calculated from 5.18% of the data randomly chosen to be excluded from refinement.

[¶]Values for the highest-resolution shell in structure refinement (3.67–3.50 Å).