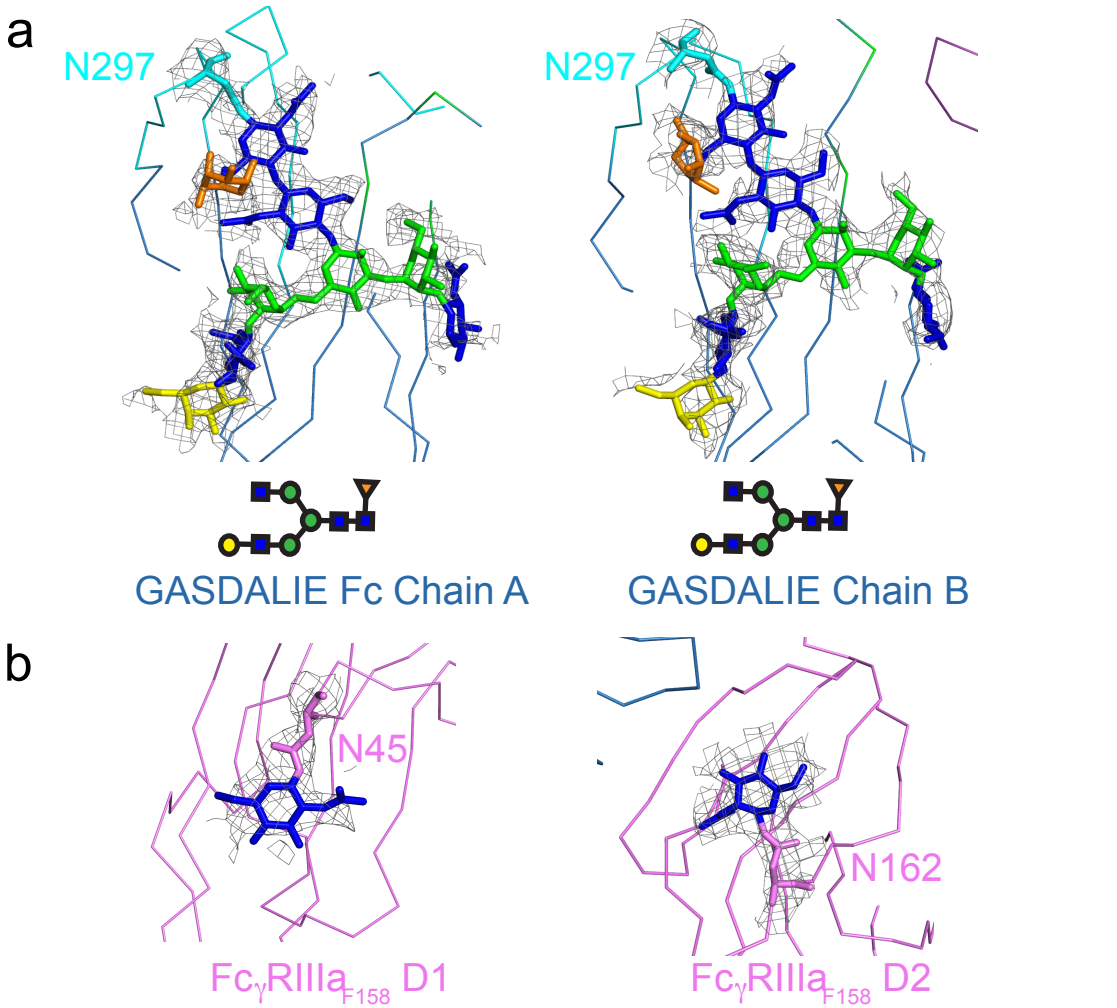

Ahmed et al. Supplementary Figure 1

Supplementary Figure 1. $2F_o$-F_c electron density contoured at 0.7σ from annealed omit maps. (a) Asn297-linked *N*-glycans on FcγRIIIa-bound GASDALIE Fc. (b) Asn45- and Asn162-linked *N*-glycans on $Fc\gamma RIIIa_{F158}$ (c) G236/S239D/A330L/I332E mutations in the FcγRIIIa-bound GASDALIE Fc. (d) Unbound GASDALIE Fc. Ordered glycan residues in panels A and B are shown as colored sticks (fucose, orange; GlcNAc, blue; mannose, green; galactose, yellow) with schematic versions of the ordered portions of the Fc *N*-glycans on each chain shown in panel a (fucose, orange triangle; GlcNAc, blue squares; mannose, green circles; galactose, yellow circle).

Supplementary Table 1. Data collection and refinement statistics

	GASDALIE Fc:FcγRIIIa$_{F158}$	GASDALIE Fc
Data Collection		
Space group	$P2_12_1\ 2_1$	$P2_12_1\ 2_1$
Cell dimensions		
a, b, c (Å)	74.38, 94.50, 108.67	49.32, 79.13, 137.62
α, β, γ (°)	90.0, 90.0, 90.0	90.0, 90.0, 90.0
Resolution (Å)	71.31 - 3.13 (3.24 - 3.12)	46.43 - 2.39 (2.47 -2.38)
R_{merge}	0.11 (1.26)	0.14 (0.58)
Completeness (%)	100.00 (100.00)	100.00 (100.00)
Redundancy	2.0 (2.0)	1.9 (1.9)
I/σI	7.52 (0.61)	6.62 (1.41)
$CC_{1/2}$(%)	99.9 (79.5)	99.2 (88.5)
Refinement		
Resolution (Å)	3.13	2.39
No. reflections	28106	31591
R_{work}/R_{free}	.270/.296	.241/.258
No. atoms		
Protein	4507	3291
Ligand/ion	248	210
Water	0	93
Average B factor	35.00	58.10
rmsd		
Bond lengths (Å)	0.015	0.012
Bond angles (°)	1.46	1.25

Statistics for the highest-resolution shell are shown in parentheses.