Supporting Information for:

The weaker-binding Fc  $\gamma$  receptor IIIa F158 allotype retains sensitivity to N-glycan composition and exhibits a destabilized antibody-binding interface

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**Supplemental Table 1.** N162 glycan composition of CD16a expressed in HEK293F cells

									Mass	
				Calc	Obs	Intensity		PPM	error	
Allotype	Glycan	MS2	z	(M+zH)²⁺	(M+zH)²⁺	(arb)	RT	error	(Da)	Peptide
F	HexNAc(5)Hex(5)Fuc(1)	х	3	927.0392	927.0381	2500	9	1.230	0.00114	GSKNVSSE
F	HexNAc(5)Hex(4)Fuc(1)	х	3	873.0216	873.0211	5300	9	0.607	0.00053	GSKNVSSE
F	HexNAc(5)Hex(3)Fuc(1)	Х	3	819.0040	819.0026	2500	9	1.734	0.00142	GSKNVSSE
V	HexNAc(5)Hex(5)Fuc(1)	Х	3	960.0620	960.0625	103000	11	-0.479	0.00046	VGSKNVSSE
V	HexNAc(5)Hex(4)Fuc(1)	Х	3	906.0444	906.0444	377000	11	0.033	3E-05	VGSKNVSSE
V	HexNAc(5)Hex(3)Fuc(1)	Х	3	852.0268	852.0268	182000	11	0.023	2E-05	VGSKNVSSE
V	HexNAc(4)Hex(3)Fuc(1)	х	3	784.3337	784.3337	240000	10	0.000	0	VGSKNVSSE
V	HexNAc(2)Hex(5)	х	3	870.3758	870.3763	117000	15	-0.574	0.0005	CRGLVGSKNVSSE
V	HexNAc(6)Hex(3)Fuc(1)	Х	3	919.7200	919.7196	220000	10	0.381	0.00035	VGSKNVSSE
V	HexNAc(3)Hex(3)Fuc(1)	Х	2	1074.4572	1074.4572	150000	10	0.019	2E-05	VGSKNVSSE
V	HexNAc(4)Hex(5)Fuc(1)	Х	3	892.3689	892.3685	296000	10	0.471	0.00042	VGSKNVSSE
V	HexNAc(4)Hex(4)Fuc(1)	Х	3	838.3513	838.3509	215000	10	0.489	0.00041	VGSKNVSSE
V	HexNAc(5)Hex(6)Fuc(1)	х	3	1014.0797	1014.0799	100000	9	-0.247	0.00025	VGSKNVSSE

## Supplemental Table 2. CD16a affinities relative to the complex-type glycoform

	Complex-type	Man5	(1)GlcNAc	S164A
V158	1.0	3.4	13	1.1
F158	1.0	1.6	13	1.1



**Supplemental Figure 1**. SDS-PAGE of GFP-srCD16a fusions. The two different allotypes are expressed with four different glycosylation patterns. Distinct shifts in migration are observed between each type of glycosylated protein.



**Supplemental Figure 2.** Relative abundance of N162 glycans on the V158 and F158 allotypes as determined by glycoproteomics MS. The N162-containing glycopeptide for F158 provides less intense peaks by ESI-MS/MS as our lab previously noted (<u>Mol Cell</u> <u>Proteomics</u>. 2019 Nov;18(11):2178-2190; <u>Mol Cell Proteomics</u>. 2020 Feb;19(2):362-374). Possible N-glycan configurations are shown as cartoons below the chart.



**Supplemental Figure 3.** Representative surface plasmon resonance (SPR) sensorgrams of CD16a allotypes with either Man5 oligomannose N-glycans (A,E) or (1)GlcNAc N-glycans (C,G). Fits of the dissociation constants and associated errors from equilibrium binding measurements are also shown (B,D,F,H). Cartoons show the expected N-glycan at the N162 site.



**Supplemental Figure 4.** (**A**) Overlay of HSQC-TROSY spectra of CD16a V158 with (black) and without (green) the N162 glycan. Residues with large chemical shift perturbations are bolded. (**B**) Highlighted peaks showing differences between the V158, V158/S16A and F158 spectra.

Supplemental Figure 5. Assigned N162 glycopeptide MS2 spectra (following pages)



























5.000e+4

