Supplementary Data for: Association of *FCGR2C* polymorphisms with HIV-1 vaccine protection in RV144

Supplemental Data included

1. Fc receptor sequencing

Figure S1. Fc receptor loci targeted for resequencing. The arrangements of the five *FCGR* genes on chromosome 1q23-24 and the *FCAR* gene on chromosome 19q13.42 are shown, with exon and intron structures depicted by boxes and lines respectively. The distances between the *FCGR* genes are not to scale and a single example of possible alternative splicing is represented. Coordinates within the reference human genome build are provided in supplementary Table S1. Arrows indicate the direction of transcription and beneath each gene the corresponding protein structures are depicted. Exon regions and the derivative protein domains targeted for resequencing are indicated in orange. The activating ITAM motifs and inhibitory ITIM motifs are indicated in green and red, respectively.

Table S1. **A.** Fc receptor amplicon primer sequences. **B.** Fc receptor amplification and sequencing reagents. **C.** Fc receptor thermal cycler conditions.

2. Supplemental results:

Table S2. **A.** Descriptives of the 148 *FCGR* SNP genotypes based on the 205 HIV uninfected vaccine recipients control subjects in the RV144 case-control study **B.** Tagging SNPs and SNPs captured in *FCGR*s **C.** Correlations of genotypes between the captured SNPs and tagging SNPs in *FCGR*s.

Table S3. **A.** Descriptives of 42 *FCAR* SNP-genotypes based on the 205 HIV uninfected vaccine recipient control subjects in the case-control study **B.** Tagging SNPs and SNPs captured in FcαR **C.** Correlation between the SNPs captured and the tagging SNPs in FcαR

Table S4. Association of twenty eight *FCR* SNPs genotypes with VE against any HIV-1 and CRF01_AE 169K HIV-1

Table S5. Assessment of *FCGR2C* 126C>T genotype modification of the correlation between IgG binding antibodies response to eleven V1V2 scaffold proteins (magnitude) at week 26 and risk of HIV-1 infection by 42 months among vaccine recipients. All HIV-1 infections and infections with CRF01_AE 169K HIV-1 were considered. Correlation was measured using the odds ratio (OR) of risk probability per 1-SD increase in immune response.

Table S6. Assessment of *FCGR2C* 126C>T genotype modification of the correlation between IgG3 binding antibodies response to eleven V1V2 scaffold proteins (magnitude) at week 26 and risk of HIV-1 infection by 42 months among vaccine recipients. All HIV-1 infections and infections with CRF01_AE 169K HIV-1 were considered. Correlation was measured using the odds ratio (OR) of risk probability per 1-SD increase in immune response.

Figure S2. Boxplots of the 8 “sensitivity immune response variables” and one secondary variable (IgA C1 peptide) at week 26 in vaccine recipients studied previously (1), cross-classified by *FCGR2C* 126C>T CC vs. CT/TT and by case-control status

Figure S3. Boxplots of IgG Abs to eleven V1V2-scaffold antigens studied previously (2) and IgG breadth score **(A)** and to two Env gp120 antigens (1) **(B)** at week 26 in vaccine recipients, cross-classified by *FCGR2C* 126C>T CC vs. CT/TT and by case-control status

Figure S4. Boxplots of IgG3 Abs to V1V2-scaffold antigens studied previously (3) and IgG3 breadth score (**A**) and to two Env gp120 antigens (1) (**B**) at week 26 in vaccine recipients, cross-classified by *FCGR2C* 126C>T CC vs. CT/TT and by case-control status

Figure S5. Heat map and hierarchical clustering tree of Spearman rank correlations of pairs of eleven IgG V1V2-scaffold antigens at week 26

Figure S6. Heat map and hierarchical clustering tree of Spearman rank correlations of pairs of eleven IgG3 V1V2-scaffold antigens at week 26

3. Methods

Hardy-Weinberg equilibrium (HWE) tests were used to assess the quality of the SNP genotyping. SNPs that failed the HWE test ($p<0.00001$) or that had a rare variant (minor allele frequency, MAF <5%) were excluded from the analyses. After failed and rare SNPs were filtered out, a subset of SNPs (called tagging SNPs) were selected to capture all SNPs at $r^2 \geq 0.8$, i.e. each of the remaining SNPs had at least 80% squared Pearson correlation with one of the tagging SNPs. This process was done using the data on the 205 HIV-1 uninfected vaccine recipient controls and Haploview Software (4)

<u>Fcγ Receptors</u>

A total of 148 SNPs in *FCGR*s were genotyped. Of these 148 SNPs, 42 passed the MAF threshold (≥5%) and 4 of these 42 failed the Hardy-Weinberg equilibrium test ($p<0.00001$). Therefore, 38 SNPs passed both filtering criteria. Table S2A shows descriptive statistics of all *FCGR*s SNPs genotypes based on the 205 controls data. Twenty-one tagging SNPs were identified to capture the 38 SNPs. Table S2B shows the tagging SNPs and the captured SNPs. Table S2C shows the correlations between the captured SNPs and the tagging SNPs.

Fcα Receptor

A total of 42 SNPs in *FCAR* were genotyped. Of the 42 SNPs, 17 passed the MAF threshold (MAF≥5%) and the HWE test ($p>0.00001$). Table S3A shows descriptive statistics of all *FCAR* SNP-genotypes based on the 205 controls data. Seven tagging SNPs were identified to capture the 17 SNPs. Table S3B shows the tagging SNPs and the captured SNPs. Table S3C shows the correlations between the captured SNPs and the tagging SNPs.

Supplementary Materials References

1. **Haynes, B.F., Gilbert, P.B., McElrath, M.J., Zolla-Pazner, S., Tomaras, G.D., Alam, S.M., Evans, D.T., Montefiori, D.C., Karnasuta, C., Sutthent, R., et al. 2012. Immune-correlates analysis of an HIV-1 vaccine efficacy trial. *N Engl J Med* 366:1275-1286.**
2. **Zolla-Pazner, S., deCamp, A., Gilbert, P.B., Williams, C., Yates, N.L., Williams, W.T., Howington, R., Fong, Y., Morris, D.E., Soderberg, K.A., et al. 2013. Vaccine-induced IgG Antibodies to V1V2 Regions of Multiple HIV-1 Subtypes Correlate with Decreased Risk of HIV-1 Infection. *Plos One*.**
3. **Yates, N.L., Liao, H.X., Fong, Y., deCamp, A., Vandergrift, N.A., Williams, W.T., Alam, S.M., Ferrari, G., Yang, Z.Y., Seaton, K.E. et al. 2014. Vaccine-induced Env V1-V2 IgG3 correlates with lower HIV-1 infection risk and declines soon after vaccination. *Science Translational Medicine,* 6:228ra39.**
4. **Barrett, J.C., Fry, B., Maller, J., and Daly, M.J. 2005. Haploview: analysis and visualization of LD and haplotype maps. *Bioinformatics* 21:263-265.**
5. **Westfall, P.H., and Young, S.S. 1993. *Resampling-Based Multiple Testing: Examples and Methods for p-Value Adjustment*: John Wiley and Sons.**

Table S1. **A.** Fc receptor amplicon primer sequences. **B.** Fc receptor amplification and sequencing reagents. **C.** Fc receptor thermal cycler conditions.

A.

Locus	*Amplicon*	*Primer*	*Sequence*	*Size (bp)*
FCGR3A	CD16a-01	CD16a-exon2a-1F	GGGGCAAGCATCCTGGGATG	529
		CD16a-exon2a-1R	CCCCATCTTGGCTTGTCCTAGG	
	CD16a-13	CD16a-exon4a-1F	GAGCCTCAATGGTACAGGGTGCTC	650
		CD16a-exon4a-2R	GGGCAGAAGTTGCAGTGAGCTG	
	CD16a-09	CD16a-exon5-1F	GAAATCTACCTTTTCCTCTAATAGGGCAAT	996
		CD16a-exon5-1R	ATATGACACCGTGGGTGTGATTAGC	
FCGR3B	CD16b-02	CD16b-exon1-1F	GGGGCAAGCATCCTGGGAAA	528
		CD16b-exon1-1R	CCCCATCTTGGCTTGTCCTGGT	
	CD16b-20	CD16b-exon3-2F	GTGGGGCACATATGGGGACAAT	950
		CD16b-exon3-3R	ATTGCACTCCAGCCTGGGTGAG	
	CD16b-10	CD16b-exon4-1F	TGAAATCTACCTTTTCCTCTAATAGAGCAAC	997
		CD16b-exon4-1R	ATATGACACCGTGGGTGTGATTAGG	
FCGR2A	CD32a-04	CD32a-exon3a-2F	CCATTTTAGTGGGGTCTGGGATTTG	700
		CD32a-exon3a-2R	CCCCTTGCTCAATCAAGACTGAGG	
	CD32a-07	CD32a-exon4-1F	CATCATGTCAAGTTCTGTGAGTAACGTACC	562
		CD32a-exon4-1R	AGCCTGACTACCTATTACCTGGGACG	
	CD32a-13	CD32a-exon5-1F	TTGGTGGAGAAACCTGGGTAGGG	772
		CD32a-exon5-1R	GGGATTATTTCTCTTTCTCAGAGGCTTG	
FCGR2B	CD32b-05	CD32b-exon3b-2F	CTTCTTCCCTGTTGCCCTGTCG	638
		CD32b-exon3b-2R	GAACTGAGGCAAAAACAACCACTGAT	
	CD32b-11	CD32b-exon4-2F	AAATTATTTGCCCAAGAGTTCATAAATGAC	548
		CD32b-exon4-1R	TTGCTCCAGTGCCCAATTTTGC	
	CD32b-14	CD32b-exon5-1F	TATTAGTTTGGTGGAGAAACCTCGGTAA	776
		CD32b-exon5-1R	CATCACTACACTACACTGCTCTCCCCA	
FCGR2C	CD32c-06	CD32c-exon3c-2F	CCTTCTTCCCTGTTGCCCTGTCT	638
		CD32c-exon3c-2R	GACTGAGGCAAAGCAACCACTGAC	
	CD32c-12	CD32c-exon4-2F	AAATTATTTGCCCAAGAGTTCATAAATGAT	550
		CD32c-exon4-1R	CTTTGCTCCAGTGCCCAATTTTGT	
	CD32c-15	CD32c-exon5-1F	AGTTCGGTGGAGAAACCTCGGTAG	773
		CD32c-exon5-1R	CCATCACTACACTACACTGCTCTCCCTG	
FCAR	Fcar-E1-04	Fcar-exon1-2F	AGCCCGTCTATTTGGATGTAGCATCT	560
		Fcar-exon1-1R	GCAGCCACTAAAATCTCCTAGTCACACT	
	Fcar-E2-01	Fcar-exon2-1F	GAGGGTGATTTGTCGTAAAGGTTGG	330
		Fcar-exon2-1R	GGACAGTCTAACACAGGCAAGGACTAAC	
	Fcar-E3-03	Fcar-exon3-2F	AATGGTAGGTTCTTCACACCCTAATGTATT	366
		Fcar-exon3-1R	CGGAACCTGTAGTGCCCTATCCTATATT	
	Fcar-E4-04	Fcar-exon4-2F	CTCTCTTAGGCTTGTATGGCAAACCC	463
		Fcar-exon4-2R	AGTGAAAGCGGAAAGTGTGGTGG	
	Fcar-E5-02	Fcar-exon5-1F	ACACAACCACCAACCATTCATCTCC	1200

Fcar-exon5-2R	GAGGGGGGTTATTGAATATATTTGGC

B.

Amplification reactions	**Fcα**	**Fcγ (CD16 & CD32)**	**Fcγ (CD16b exon3)**
Reagent	*Volume/reaction*	*Volume/reaction*	*Volume/reaction*
10X PCR buffer	1.5 µl	1.5 µl	2 µl
$MgCl_2$ (50 mM)	0.75 µl	0.75 µl	1 µl
5X PE	3 µl	3 µl	4 µl
dNTPs (25 mM each)	0.06 µl	0.06 µl	0.1 µl
Forward primer (1.67 mM)	3 µl	3 µl	0.05 µl (100 µM stock)
Reverse primer (1.67 mM)	3 µl	3 µl	0.05 µl (100 µM stock)
DNA (5 ng/µl)	3 µl	1.5 µl	3 µl
Platinum Taq (5 U/ml)	0.1 µl	0.075 µl	0.1 µl
ddH_2O	0.59 µl	2.115 µl	9.7 µl

Sequencing reaction (Fcα and Fcγ)	
Reagent	*Volume/reaction*
Big Dye Terminator v. 3.1 Ready Reaction Mix	0.5 µl
5X Sequencing Dilution Buffer	2 µl
Diluted sequencing primer (1.67 µM)	3 µl
ddH_2O	5.5 µl

C. Amplification

Temp	*Time*	*# Cycles*
94°C	5 min	1
94°C	20 sec	10
65°C	30 sec	10
72°C	45 sec	10
94°C	20 sec	25
55°C	30 sec	25
72°C	45 sec	25
72°C	5 min	1
4°C	Hold	

Sequencing

Temp	*Time*	*# Cycles*
95°C	2 min	1
95°C	5 sec	25
50°C	10 sec	25
60°C	4 min	25
4°C	Hold	

Table S2. **A.** Descriptives of genotypes of the 148 *FCGR* SNPs based on the 205 HIV uninfected vaccine recipients controls used in the RV144 case-control correlate analysis (1) **B.** Tagging SNPs and SNPs captured in *FCGR*s **C.** Correlations of genotypes between the captured SNPs and the tagging SNPs in FCGRs.

A.

Locus Index	Name		Position	ObsHET[1]	PredHET[2]	HWpval[3]	%Geno[4]	MAF[5]	Alleles	Rating[6]
1	CD32_04_a3a_132		161476062	0.01	0.01	1	100	0.005	C:G	FAIL
2	CD32_04_a3a_275	rs9427397	161476205	0.02	0.019	1	100	0.01	C:G	FAIL
3	CD32_04_a3a_276	rs9427398	161476206	0.02	0.019	1	100	0.01	A:C	FAIL
4	CD32_04_a3a_433		161476363	0	0	1	100	0	G:G	FAIL
5	CD32_04_a3a_604	rs9427399	161476534	0.02	0.019	1	100	0.01	T:G	FAIL
6	CD32_07_a4_86		161479600	0.02	0.019	1	100	0.01	G:T	FAIL
7	CD32_07_a4_232	rs1801274	161479746	0.405	0.399	1	100	0.276	A:G	
8	CD32_07_a4_357	rs55919520	161479871	0	0	1	100	0	G:G	FAIL
9	CD32_07_a4_397		161479911	0.01	0.01	1	100	0.005	G:T	FAIL
10	CD32_07_a4_442		161479956	0	0	1	100	0	C:C	FAIL
11	CD32_07_a4_446		161479960	0	0	1	100	0	T:T	FAIL
12	CD32_07_a4_483		161479997	0.005	0.005	1	100	0.002	G:T	FAIL
13	CD32_07_a4_489		161480003	0.005	0.005	1	100	0.002	A:C	FAIL
14	CD32_13_a5_251		161480643	0	0	1	100	0	C:C	FAIL
15	CD32_13_a5_258	rs11810143	161480650	0.02	0.019	1	100	0.01	A:C	FAIL
16	CD32_13_a5_299		161480691	0.005	0.005	1	100	0.002	C:G	FAIL
17	CD32_13_a5_454	rs115803420	161480846	0.005	0.005	1	100	0.002	C:G	FAIL
18	CD32_13_a5_483		161480875	0.005	0.005	1	100	0.002	T:G	FAIL
19	CD32_13_a5_556		161480948	0.005	0.005	1	100	0.002	A:C	FAIL
20	CD32_13_a5_638	rs182118834	161481030	0.005	0.005	1	100	0.002	A:C	FAIL
21	CD32_13_a5_645	rs2165088	161481037	0.166	0.152	0.4498	100	0.083	G:T	
22	CD32_13_a5_664		161481056	0.005	0.005	1	100	0.002	A:C	FAIL
23	CD16_09_a5_866	rs17410889	161514303	0.02	0.02	1	98.5	0.01	A:C	FAIL
24	CD16_09_a5_732	rs451290	161514437	0.005	0.005	1	99	0.002	A:C	FAIL
25	CD16_09_a5_626	rs396991	161514543	0.465	0.474	0.8799	98.5	0.386	T:G	
26	CD16_09_a5_472		161514697	0.005	0.005	1	99	0.002	T:G	FAIL
27	CD16_09_a5_382		161514787	0.01	0.01	1	99.5	0.005	C:G	FAIL
28	CD16_09_a5_266		161514903	0.01	0.01	1	98.5	0.005	G:T	FAIL
29	CD16_13_a4a_627		161517814	0.005	0.005	1	99.5	0.002	T:G	FAIL
30	CD16_13_a4a_614		161517827	0.005	0.005	1	99.5	0.002	T:G	FAIL
31	CD16_13_a4a_598		161517843	0.456	0.466	0.8368	99.5	0.37	G:C	
32	CD16_13_a4a_281	rs2290833	161518160	0.005	0.005	1	100	0.002	G:T	FAIL
33	CD16_13_a4a_268	rs147342954	161518173	0.328	0.312	0.6468	99.5	0.194	G:A	
34	CD16_13_a4a_228		161518213	0.02	0.019	1	99.5	0.01	C:G	FAIL
35	CD16_13_a4a_226	rs428888	161518215	0.02	0.019	1	99.5	0.01	A:C	FAIL
36	CD16_13_a4a_157		161518284	0.005	0.005	1	99.5	0.002	G:T	FAIL
37	CD16_13_a4a_156		161518285	0.005	0.005	1	99.5	0.002	C:G	FAIL
38	CD16_13_a4a_154	rs428888	161518287	0.02	0.029	0.0732	99.5	0.015	G:A	FAIL
39	CD16_13_a4a_126	rs114535887	161518315	0	0	1	100	0	G:G	FAIL
40	CD16_13_a4a_125	rs143870625	161518316	0	0	1	100	0	C:C	FAIL
41	CD16_13_a4a_107	rs77144485	161518334	0.02	0.019	1	99.5	0.01	T:G	FAIL
42	CD16_13_a4a_104	rs77144485	161518337	0.005	0.005	1	99.5	0.002	G:T	FAIL
43	CD16_01_a2a_448	rs10917571	161519412	0.49	0.488	1	98.5	0.423	G:T	
44	CD16_01_a2a_432		161519428	0.03	0.029	1	98.5	0.015	C:G	FAIL
45	CD16_01_a2a_419	rs34436026	161519441	0.005	0.005	1	98.5	0.002	G:T	FAIL
46	CD16_01_a2a_386		161519474	0.005	0.005	1	98.5	0.002	T:G	FAIL

47	CD16_01_a2a_136		161519724	0	0	1	100	0	G:G	FAIL
48	CD16_01_a2a_135		161519725	0	0	1	100	0	G:G	FAIL
49	CD16_01_a2a_77		161519783	0	0	1	100	0	C:C	FAIL
50	CD32_06_c3c_46		161559177	0	0.01	0.0049	99	0.005	C:G	FAIL
51	CD32_06_c3c_111		161559242	0.01	0.01	1	99	0.005	A:C	FAIL
52	CD32_06_c3c_126	rs114945036	161559257	0.212	0.234	0.2709	99	0.135	C:T	
53	CD32_06_c3c_196	rs183547105	161559327	0.005	0.005	1	99	0.002	C:G	FAIL
54	CD32_06_c3c_197	rs3933769	161559328	0.335	0.4	0.0328	99	0.276	G:A	
55	CD32_06_c3c_257		161559388	0.005	0.005	1	99	0.002	T:G	FAIL
56	CD32_06_c3c_268		161559399	0.005	0.005	1	99	0.002	C:G	FAIL
57	CD32_06_c3c_336	rs111603147	161559467	0.005	0.005	1	99	0.002	C:G	FAIL
58	CD32_06_c3c_436		161559567	0	0	1	99	0	C:C	FAIL
59	CD32_06_c3c_441	rs138747765	161559572	0.212	0.234	0.2709	99	0.135	C:T	
60	CD32_06_c3c_590	rs78603008	161559721	0.212	0.234	0.2709	99	0.135	G:A	
61	CD32_12_c4_93		161560853	0.015	0.024	0.049	99.5	0.012	A:G	FAIL
62	CD32_12_c4_155		161560915	0.015	0.024	0.049	99.5	0.012	G:C	FAIL
63	CD32_12_c4_162		161560922	0.02	0.029	0.0732	99.5	0.015	C:T	FAIL
64	CD32_12_c4_332		161561092	0.005	0.015	0.0147	99.5	0.007	C:G	FAIL
65	CD32_12_c4_349		161561109	0.005	0.015	0.0147	99.5	0.007	G:C	FAIL
66	CD32_12_c4_392	rs74341264	161561152	0.407	0.48	0.0393	99.5	0.4	G:A	
67	CD32_12_c4_395		161561155	0	0	1	100	0	G:G	FAIL
68	CD32_12_c4_397	rs76016754	161561157	0.074	0.08	0.5871	99.5	0.042	A:T	FAIL
69	CD32_12_c4_435	rs148639303	161561195	0.309	0.318	0.7922	99.5	0.199	A:C	
70	CD32_12_c4_444		161561204	0.01	0.01	1	99.5	0.005	C:G	FAIL
71	CD32_12_c4_454	rs2125685	161561214	0.01	0.01	1	100	0.005	G:T	FAIL
72	CD32_12_c4_466		161561226	0.01	0.01	1	99.5	0.005	G:T	FAIL
73	CD32_12_c4_475	rs142137670	161561235	0.324	0.355	0.2753	99.5	0.23	G:C	
74	CD32_12_c4_477	rs143998157	161561237	0.211	0.219	0.7681	99.5	0.125	C:T	
75	CD32_15_c5_122	rs61801812	161561833	0	0	1	100	0	C:C	FAIL
76	CD32_15_c5_339		161562050	0	0	1	100	0	G:G	FAIL
77	CD32_15_c5_348	rs143311449	161562059	0	0	1	100	0	T:T	FAIL
78	CD32_15_c5_403	rs373013207	161562114	0.229	0.253	0.2639	100	0.149	C:T	
79	CD32_15_c5_428	rs12064936	161562139	0.059	0.102	9.75E-05	100	0.054	A:T	FAIL
80	CD32_15_c5_433	rs201984478	161562144	0.278	0.323	0.0767	100	0.202	G:A	
81	CD32_15_c5_443	rs75494722	161562154	0	0	1	100	0	G:G	FAIL
82	CD32_15_c5_462		161562173	0.02	0.019	1	100	0.01	G:T	FAIL
83	CD16_10_b4_885	rs143596860	161595731	0.367	0.412	0.1645	95.6	0.291	G:T	
84	CD16_10_b4_802		161595814	0.005	0.005	1	100	0.002	C:G	FAIL
85	CD16_10_b4_707		161595909	0	0	1	100	0	C:C	FAIL
86	CD16_10_b4_629		161595987	0.005	0.005	1	96.1	0.003	G:T	FAIL
87	CD16_10_b4_332	rs41508344	161596284	0.354	0.398	0.1602	95.1	0.274	T:C	
88	CD16_20_b3_874	rs74945456	161599252	0.137	0.247	1.38E-07	96.1	0.145	A:T	FAIL
89	CD16_20_b3_775		161599351	0	0.01	0.005	98	0.005	A:G	FAIL
90	CD16_20_b3_656		161599470	0	0.01	0.0049	100	0.005	A:T	FAIL
91	CD16_20_b3_610	rs2290833	161599516	0.502	0.47	0.4259	100	0.378	A:G	
92	CD16_20_b3_597	rs4656315	161599529	0.034	0.043	0.1715	100	0.022	G:A	FAIL
93	CD16_20_b3_555	rs2290834	161599571	0.502	0.47	0.4259	100	0.378	G:A	
94	CD16_20_b3_536		161599590	0	0	1	99.5	0	G:G	FAIL
95	CD16_20_b3_483	rs147574249	161599643	0.215	0.263	0.0217	100	0.156	G:A	
96	CD16_20_b3_472	rs5030738	161599654	0.015	0.024	0.0487	100	0.012	C:A	FAIL
97	CD16_20_b3_436		161599690	0	0.01	0.0049	99.5	0.005	T:G	FAIL
98	CD16_20_b3_433	rs76714703	161599693	0.507	0.474	0.4047	100	0.385	A:G	
99	CD16_20_b3_418		161599708	0	0	1	99.5	0	G:G	FAIL
100	CD16_20_b3_353	rs447536	161599773	0.215	0.263	0.0217	100	0.156	C:T	
101	CD16_20_b3_347		161599779	0.215	0.263	0.0217	100	0.156	G:C	
102	CD16_20_b3_292		161599834	0.01	0.01	1	99.5	0.005	G:T	FAIL
103	CD16_20_b3_276		161599850	0.005	0.005	1	100	0.002	A:C	FAIL

104	CD16_20_b3_151	rs2290835	161599975	0.551	0.457	0.005	100	0.354	T:C	
105	CD16b_02_b1_473	rs74127076	161600745	0.438	0.45	0.7946	99	0.342	A:G	
106	CD16b_02_b1_446		161600772	0	0	1	100	0	A:A	FAIL
107	CD16b_02_b1_436	rs147161724	161600782	0.36	0.402	0.1771	99	0.278	T:C	
108	CD16b_02_b1_430	rs3883928	161600788	0	0	1	100	0	G:G	FAIL
109	CD16b_02_b1_425	rs76732376	161600793	0.438	0.45	0.7946	99	0.342	G:T	
110	CD16b_02_b1_385	rs3883934	161600833	0.438	0.45	0.7946	99	0.342	C:A	
111	CD16b_02_b1_381		161600837	0.005	0.005	1	100	0.002	G:T	FAIL
112	CD16b_02_b1_222	rs34085961	161600996	0.438	0.45	0.7946	99	0.342	A:G	
113	CD16b_02_b1_164		161601054	0.005	0.005	1	99	0.002	G:T	FAIL
114	CD16b_02_b1_159	rs189362069	161601059	0.005	0.005	1	99	0.002	A:C	FAIL
115	CD16b_02_b1_136	rs148471752	161601082	0	0	1	99	0	T:T	FAIL
116	CD16b_02_b1_135	rs181006240	161601083	0	0	1	99	0	A:A	FAIL
117	CD16b_02_b1_120	rs67020125	161601098	0.281	0.307	0.297	99	0.19	G:T	
118	CD16b_02_b1_99	rs61803026	161601119	0.399	0.426	0.4334	99	0.308	G:C	
119	CD16b_02_b1_83		161601135	0.005	0.005	1	99	0.002	G:T	FAIL
120	CD16b_02_b1_76		161601142	0.005	0.005	1	99	0.002	C:G	FAIL
121	CD16b_02_b1_71	rs185987033	161601147	0	0	1	100	0	G:G	FAIL
122	CD16b_02_b1_44	rs34322334	161601174	0.446	0.453	0.9079	98.5	0.347	A:T	
123	CD32_05_b3b_102		161641064	0.005	0.005	1	100	0.002	C:G	FAIL
124	CD32_05_b3b_194		161641232	0.005	0.005	1	100	0.002	A:C	FAIL
125	CD32_05_b3b_256	rs10917661	161641233	0.005	0.005	1	100	0.002	C:T	FAIL
126	CD32_05_b3b_330	rs148030870	161641292	0.112	0.131	0.1304	100	0.071	C:T	
127	CD32_05_b3b_423	rs6665610	161641385	0.073	0.088	0.1172	100	0.046	G:A	FAIL
128	CD32_05_b3b_447		161641409	0.063	0.061	1	100	0.032	C:G	FAIL
129	CD32_11_b4_71	rs190837656	161642662	0	0	1	100	0	T:T	FAIL
130	CD32_11_b4_93		161642684	0	0	1	100	0	G:G	FAIL
131	CD32_11_b4_145		161642736	0	0	1	100	0	G:G	FAIL
132	CD32_11_b4_155	rs56123153	161642777	0	0	1	100	0	C:C	FAIL
133	CD32_11_b4_162	rs4657089	161642784	0	0	1	100	0	T:T	FAIL
134	CD32_11_b4_392	rs146214041	161642983	0.015	0.015	1	100	0.007	G:T	FAIL
135	CD32_11_b4_395	rs182968886	161642986	0.039	0.038	1	100	0.02	G:T	FAIL
136	CD32_11_b4_397	rs149301029	161642988	0.015	0.015	1	100	0.007	A:C	FAIL
137	CD32_11_b4_435	rs145835719	161643026	0.234	0.214	0.3259	100	0.122	C:A	
138	CD32_11_b4_454	rs74870676	161643038	0.512	0.491	0.6524	100	0.432	A:G	
139	CD32_11_b4_475	rs2298023	161643045	0.005	0.005	1	100	0.002	G:T	FAIL
140	CD32_11_b4_477	rs2298024	161643047	0.005	0.005	1	100	0.002	C:G	FAIL
141	CD32_14_b5_126	rs112422693	161643664	0.078	0.102	0.0264	100	0.054	C:T	
142	CD32_14_b5_159		161643697	0.005	0.005	1	100	0.002	G:T	FAIL
143	CD32_14_b5_261	rs1050501	161643799	0.293	0.464	2.36E-07	100	0.366	T:C	FAIL
144	CD32_14_b5_343		161643881	0.015	0.015	1	100	0.007	G:T	FAIL
145	CD32_14_b5_345		161643883	0.005	0.005	1	100	0.002	T:G	FAIL
146	CD32_14_b5_352	rs140558259	161643890	0.146	0.296	1.74E-10	100	0.18	T:G	FAIL
147	CD32_14_b5_388		161643926	0	0	1	100	0	A:A	FAIL
148	CD32_14_b5_447	rs75494722	161643985	0.073	0.097	0.0198	100	0.051	G:T	

[1]: Observed heterozygosity

[2]: Predicted heterozygosity

[3]: P-value of testing Hardy-Weinberg equilibrium (HWE)

[4]: Percentage of genotypes

[5]: Minor allele frequency (MAF)

[6]: Failed one or two criteria, MAF≥5% and p-value of HWE test>0.00001

B.

Tagging SNPs	SNPs Captured
CD16b_02_b1_099	CD16_10_b4_885, CD16b_02_b1_44, CD16b_02_b1_425, CD16b_02_b1_473, CD16b_02_b1_385, CD16b_02_b1_99, CD16b_02_b1_222
CD32_06_c3c_126	CD32_15_c5_403, CD32_06_c3c_590, CD32_06_c3c_441, CD32_06_c3c_126
CD16_20_b3_151	CD16_20_b3_555, CD16_20_b3_610, CD16_20_b3_433, CD16_20_b3_151
CD16_20_b3_347	CD16_20_b3_353, CD16_20_b3_483, CD16_20_b3_347
CD16_09_a5_626	CD16_13_a4a_598, CD16_09_a5_626
CD16_10_b4_332	CD16b_02_b1_436, CD16_10_b4_332
CD32_12_c4_392	CD32_12_c4_392
CD32_07_a4_232	CD32_07_a4_232
CD32_15_c5_433	CD32_15_c5_433
CD32_12_c4_477	CD32_12_c4_477
CD16_13_a4a_268	CD16_13_a4a_268
CD32_11_b4_454	CD32_11_b4_454
CD32_11_b4_435	CD32_11_b4_435
CD32_12_c4_475	CD32_12_c4_475
CD32_13_a5_645	CD32_13_a5_645
CD32_12_c4_435	CD32_12_c4_435
CD32_06_c3c_197	CD32_06_c3c_197
CD16b_02_b1_120	CD16b_02_b1_120
CD16_01_a2a_448	CD16_01_a2a_448
CD32_14_b5_126	CD32_14_b5_126, CD32_14_b5_447
CD32_05_b3b_330	CD32_05_b3b_330

C.

SNP Captured	Tagging SNP	r^2
CD32_07_a4_232	CD32_07_a4_232	1
CD32_13_a5_645	CD32_13_a5_645	1
CD16_09_a5_626	CD16_09_a5_626	1
CD16_13_a4a_598	CD16_09_a5_626	0.939
CD16_13_a4a_268	CD16_13_a4a_268	1
CD16_01_a2a_448	CD16_01_a2a_448	1
CD32_15_c5_403	CD32_06_c3c_126	0.904
CD32_06_c3c_197	CD32_06_c3c_197	1
CD32_06_c3c_441	CD32_06_c3c_126	1
CD32_06_c3c_590	CD32_06_c3c_126	1
CD32_12_c4_392	CD32_12_c4_392	1
CD32_12_c4_435	CD32_12_c4_435	1
CD32_12_c4_475	CD32_12_c4_475	1
CD32_12_c4_477	CD32_12_c4_477	1
CD32_15_c5_433	CD32_15_c5_433	1
CD16_10_b4_885	CD16b_02_b1_99	0.875
CD16_10_b4_332	CD16_10_b4_332	1
CD16_20_b3_610	CD16_20_b3_151	0.9
CD16_20_b3_555	CD16_20_b3_151	0.9
CD16_20_b3_483	CD16_20_b3_347	1
CD16_20_b3_433	CD16_20_b3_151	0.873
CD16_20_b3_353	CD16_20_b3_347	1
CD16_20_b3_347	CD16_20_b3_347	1
CD16_20_b3_151	CD16_20_b3_151	1
CD16b_02_b1_473	CD16b_02_b1_99	0.854
CD16b_02_b1_436	CD16_10_b4_332	0.949
CD16b_02_b1_425	CD16b_02_b1_99	0.854
CD16b_02_b1_385	CD16b_02_b1_99	0.854
CD16b_02_b1_222	CD16b_02_b1_99	0.854
CD16b_02_b1_120	CD16b_02_b1_120	1
CD16b_02_b1_99	CD16b_02_b1_99	1
CD16b_02_b1_44	CD16b_02_b1_99	0.845
CD32_11_b4_435	CD32_11_b4_435	1
CD32_11_b4_454	CD32_11_b4_454	1
CD32_14_b5_126	CD32_14_b5_126	1
CD32_14_b5_447	CD32_14_b5_126	0.952
CD32_05_b3b_330	CD32_05_b3b_330	1

Table S3. **A.** Descriptives of genotypes of 42 *FCAR* SNPs based on the 205 HIV uninfected vaccine recipient controls used in the case-control correlate analysis (1) **B.** Tagging SNPs and SNPs captured in FcαR **C.** Correlation between the SNPs captured and the tagging SNPs in FcαR

A.

Locus Index	Name	rs#	Position	ObsHET[1]	PredHET[2]	HWpval[3]	%Geno[4]	MAF[5]	Alleles	Rating[6]
1	Fcar_E1_04_75	rs17772004	55385406	0.039	0.038	1	99.5	0.02	G:T	FAIL
2	Fcar_E1_04_104	rs12462181	55385435	0.51	0.472	0.3414	99.5	0.382	T:C	
3	Fcar_E1_04_171		55385502	0.005	0.005	1	99.5	0.002	C:G	FAIL
4	Fcar_E1_04_184	rs148347377	55385515	0.005	0.005	1	99.5	0.002	A:C	FAIL
5	Fcar_E1_04_191	rs75898867	55385522	0.172	0.173	1	99.5	0.096	T:C	
6	Fcar_E1_04_256		55385587	0	0	1	99.5	0	C:C	FAIL
7	Fcar_E1_04_273	rs3816051	55385604	0.485	0.499	0.7732	99.5	0.478	T:C	
8	Fcar_E1_04_332		55385663	0	0	1	99.5	0	G:G	FAIL
9	Fcar_E1_04_403	rs139097294	55385734	0.059	0.057	1	99.5	0.029	C:G	FAIL
10	Fcar_E1_04_414		55385745	0.005	0.005	1	99.5	0.002	G:T	FAIL
11	Fcar_E1_04_450		55385781	0.005	0.005	1	99.5	0.002	T:G	FAIL
12	Fcar_E1_04_458		55385789	0.005	0.005	1	99.5	0.002	A:C	FAIL
13	Fcar_E2_01_124	rs77887839	55386858	0.171	0.172	1	100	0.095	C:G	
14	Fcar_E2_01_156	rs11084377	55386890	0.2	0.203	1	100	0.115	G:A	
15	Fcar_E2_01_186	rs8112766	55386920	0.512	0.497	0.7922	100	0.461	A:G	
16	Fcar_E3_03_59	rs10402324	55396613	0.512	0.489	0.6226	100	0.427	A:G	
17	Fcar_E4_04_70		55399446	0.005	0.005	1	99.5	0.002	C:G	FAIL
18	Fcar_E4_04_127	rs117710908	55399503	0.005	0.005	1	99.5	0.002	T:G	FAIL
19	Fcar_E4_04_161	rs150824019	55399537	0	0	1	99.5	0	G:G	FAIL
20	Fcar_E4_04_267	rs61735069	55399643	0.172	0.165	0.9902	99.5	0.091	T:C	
21	Fcar_E4_04_308	rs79401710	55399684	0.172	0.165	0.9902	99.5	0.091	C:T	
22	Fcar_E4_04_343		55399719	0.01	0.01	1	99.5	0.005	G:T	FAIL
23	Fcar_E4_04_361	rs183206778	55399737	0	0	1	99.5	0	G:G	FAIL
24	Fcar_E5_02_57		55401071	0	0	1	99	0	C:C	FAIL
25	Fcar_E5_02_110	rs77103719	55401124	0.034	0.034	1	99	0.017	G:T	FAIL
26	Fcar_E5_02_121		55401135	0.02	0.02	1	99	0.01	A:C	FAIL
27	Fcar_E5_02_156		55401170	0.059	0.058	1	98.5	0.03	A:C	FAIL
28	Fcar_E5_02_381	rs145316840	55401395	0.025	0.024	1	98.5	0.012	G:T	FAIL
29	Fcar_E5_02_397	rs59103589	55401411	0.171	0.164	0.9959	100	0.09	T:C	
30	Fcar_E5_02_432	rs58560391	55401446	0.171	0.164	0.9959	100	0.09	G:T	
31	Fcar_E5_02_441	rs112638842	55401455	0.054	0.052	1	99.5	0.027	A:C	FAIL
32	Fcar_E5_02_459	rs60304316	55401473	0.171	0.164	0.9959	100	0.09	T:C	
33	Fcar_E5_02_466	rs59309328	55401480	0.171	0.164	0.9959	100	0.09	A:G	
34	Fcar_E5_02_573		55401587	0.005	0.005	1	99	0.002	G:T	FAIL
35	Fcar_E5_02_610	Deletion -	55401624	0.172	0.157	0.4057	99.5	0.086	A:C	
36	Fcar_E5_02_709	rs10413148	55401723	0.005	0.005	1	99	0.002	C:G	FAIL
37	Fcar_E5_02_717	rs10414707	55401803	0	0	1	99	0	T:T	FAIL
38	Fcar_E5_02_847		55401861	0	0	1	97.6	0	C:C	FAIL
39	Fcar_E5_02_918	rs4806611	55401932	0.5	0.452	0.1873	97.6	0.345	A:G	
40	Fcar_E5_02_1026	rs147280596	55402040	0.165	0.16	1	97.6	0.088	G:A	
41	Fcar_E5_02_1058	rs140803809	55402072	0.165	0.16	1	97.6	0.088	T:C	
42	Fcar_E5_02_1075	rs143675785	55402089	0	0	1	98	0	A:A	FAIL

[1]: Observed heterozygosity

[2]: Predicted heterozygosity

[3]: P-value of testing Hardy-Weinberg equilibrium (HWE)

[4]: Percentage of genotypes

[5]: Minor allele frequency (MAF)

[6]: Failed one or two criteria, MAF≥5% and p-value of HWE test>0.00001

B.

Tagging SNPs	SNPs Captured
Fcar_E4_04_308	Fcar_E5_02_397,Fcar_E5_02_1026,Fcar_E5_02_466,Fcar_E5_02_432,Fcar_E4_04_267,Fcar_E5_02_1058,Fcar_E5_02_610,Fcar_E5_02_459,Fcar_E4_04_308
Fcar_E1_04_191	Fcar_E2_01_124,Fcar_E1_04_191
Fcar_E2_01_186	Fcar_E1_04_273,Fcar_E2_01_186
Fcar_E2_01_156	Fcar_E2_01_156
Fcar_E3_03_59	Fcar_E3_03_59
Fcar_E1_04_104	Fcar_E1_04_104
Fcar_E5_02_918	Fcar_E5_02_918

C.

SNPs Captured	Tagging SNPs	r^2
Fcar_E1_04_104	Fcar_E1_04_104	1
Fcar_E1_04_191	Fcar_E1_04_191	1
Fcar_E1_04_273	Fcar_E2_01_186	0.933
Fcar_E2_01_124	Fcar_E1_04_191	1
Fcar_E2_01_156	Fcar_E2_01_156	1
Fcar_E2_01_186	Fcar_E2_01_186	1
Fcar_E3_03_59	Fcar_E3_03_59	1
Fcar_E4_04_267	Fcar_E4_04_308	1
Fcar_E4_04_308	Fcar_E4_04_308	1
Fcar_E5_02_397	Fcar_E4_04_308	0.941
Fcar_E5_02_432	Fcar_E4_04_308	0.941
Fcar_E5_02_459	Fcar_E4_04_308	0.941
Fcar_E5_02_466	Fcar_E4_04_308	0.941
Fcar_E5_02_610	Fcar_E4_04_308	0.882
Fcar_E5_02_918	Fcar_E5_02_918	1
Fcar_E5_02_1026	Fcar_E4_04_308	0.97
Fcar_E5_02_1058	Fcar_E4_04_308	0.97

Table S4. Association of twenty eight *FCR* SNPs genotypes with VE against any HIV-1 and CRF01_AE 169K HIV-1

			VE against any HIV-1						VE against CRF01_AE 169K HIV-1					
SNP	rs#	Genotype	Vaccine: placebo	VE	95% CI	P	Int. P	Int. P_{FWER}^{*}	Vaccine: placebo	VE	95% CI	P	Int. P	Int. P_{FWER}^{*}
CD32_07_a4_232	rs1801274	AA	28:37	24.3%	(-23.6%, 53.7%)	0.266			15:29	48.3%	(3.5%, 72.3%)	0.038		
(FCGR2A-R131H)		AG/GG	23:36	36.1%	(-7.8%, 62.1%)	0.093	0.644	1.00	15:27	44.4%	(-4.4%, 70.4%)	0.068	0.875	1.00
CD32_13_a5_645	rs2165088	GG	46:62	25.8%	(-8.6%, 49.3%)	0.125			28:49	42.9%	(9.1%, 64.1%)	0.018		
		GA/AA	5:12	58.3%	(-18.3%, 85.3%)	0.100	0.309	1.00	2:8	75.0%	(-17.7%, 94.7%)	0.080	0.317	1.00
CD16_13_a4a_268	rs147342954	GG	27:53	49.1%	(19%, 68%)	0.004			16:41	61.0%	(30.5%, 78.1%)	0.001		
		GA/AA	23:20	-15.0%	(-100%, 36.8%)	0.648	**0.035**	0.51	14:16	12.5%	(-79.3%, 57.3%)	0.715	0.086	0.83
CD16_09_a5_626	rs396991	TT	17::27	37.0%	(-15.5%, 65.7%)	0.135			9:25	64.0%	(22.9%, 83.2%)	0.009		
(FCGR3A-V158F)		TG/GG	34::46	26.1%	(-15.1%, 52.6%)	0.181	0.676	1.00	21:32	34.4%	(-13.8%, 62.2%)	0.134	0.211	0.99
CD16_01_a2a_448	rs10917571	GG	17:28	39.3%	(-10.9%, 66.8%)	0.105			11:22	50.0%	(-3.1%, 75.8%)	0.061		
		GT/TT	34:46	26.1%	(-15.1%, 52.6%)	0.181	0.606	1.00	19:35	45.7%	(5.1%, 68.9%)	0.032	0.860	1.00
CD32_06_c3c_126	rs114945036	CC	41:46	10.9%	(-35.8%, 41.5%)	0.592			28:33	15.2%	(-40.4%, 48.7%)	0.523		
		CT/TT	9:25	64.0%	(22.9%, 83.2%)	0.009	**0.041**	0.59	2:22	90.9%	(61.3%, 97.9%)	0.001	**0.004**	**0.05**
CD32_06_c3c_197	rs3933769	GG	24:37	35.1%	(-8.4%, 61.2%)	0.099			15:32	53.1%	(13.4%, 74.6%)	0.015		
		GA/AA	26:34	23.5%	(-27.4%, 54.1%)	0.303	0.656	1.00	15:23	34.8%	(-25%, 66%)	0.198	0.469	1.00
CD32_12_c4_392	rs74341264	GG	14:26	46.2%	(-3.1%, 71.9%)	0.062			5:23	78.3%	(42.8%, 91.7%)	0.002		
		GA/AA	37:48	22.9%	(-18.4%, 49.8%)	0.234	0.366	1.00	25:34	26.5%	(-23.2%, 56.1%)	0.243	**0.029**	0.39
CD32_12_c4_435	rs148639303	AA	20:29	31.0%	(-21.9%, 61%)	0.201			15:21	28.6%	(-38.6%, 63.2%)	0.320		
		AC/CC	31:45	31.1%	(-8.9%, 56.4%)	0.110	0.998	1.00	15:36	58.3%	(23.9%, 77.2%)	0.004	0.238	1.00
CD32_12_c4_475	rs142137670	GG	27:41	34.1%	(-7%, 59.5%)	0.092			16:34	52.9%	(14.7%, 74%)	0.013		
		GC/CC	24:33	27.3%	(-23%, 57%)	0.235	0.786	1.00	14:23	39.1%	(-18.3%, 68.7%)	0.143	0.571	1.00
CD32_12_c4_477	rs143998157	CC	42:60	30.0%	(-3.8%, 52.8%)	0.076			25:45	44.4%	(9.4%, 65.9%)	0.018		
		CT/TT	9:14	35.7%	(-48.5%, 72.2%)	0.301	0.857	1.00	5:12	58.3%	(-18.3%, 85.3%)	0.100	0.625	1.00
CD32_15_c5_433	rs201984478	GG	36:46	21.7%	(-21%, 49.4%)	0.271			25:33	24.2%	(-27.4%, 54.9%)	0.295		
		GA/AA	13:27	51.9%	(6.7%, 75.2%)	0.030	0.230	1.00	4:23	82.6%	(49.7%, 94%)	0.001	**0.015**	0.20
CD32_05_b3b_330	rs148030870	CC	46:65	29.2%	(-3.2%, 51.5%)	0.073			28:51	45.1%	(12.9%, 65.4%)	0.011		
		CT/TT	4:8	50.0%	(-66%, 84.9%)	0.258	0.588	1.00	1:5	80.0%	(-71.2%, 97.7%)	0.142	0.367	1.00
CD32_11_b4_435	rs145835719	CC	44:50	12.0%	(-32%, 41.3%)	0.536			27:40	32.5%	(-10%, 58.6%)	0.115		
		CA/AA	7:24	70.8%	(32.3%, 87.4%)	0.004	**0.021**	0.34	3:17	82.4%	(39.8%, 94.8%)	0.006	**0.047**	0.59
CD32_11_b4_454	rs74870676	AA	17:19	10.5%	(-72.1%, 53.5%)	0.739			12:17	29.4%	(-47.8%, 66.3%)	0.356		
		AG/GG	34:54	37.0%	(3.3%, 59%)	0.035	0.379	1.00	18:40	55.0%	(21.5%, 74.2%)	0.005	0.340	1.00
CD32_14_b5_126	rs112422693	CC	43:65	33.8%	(2.8%, 55%)	0.036			26:49	46.9%	(14.6%, 67%)	0.009		
		CT/TT	6:7	14.3%	(-100%, 71.2%)	0.782	0.661	1.00	3:7	57.1%	(-65.7%, 88.9%)	0.220	0.770	1.00
CD16_10_b4_332	rs41508344	TT	25:42	40.5%	(2.3%, 63.7%)	0.040			14:35	60.0%	(25.7%, 78.5%)	0.004		
		TC/CC	25:31	19.4%	(-36.6%, 52.4%)	0.424	0.410	1.00	16:21	23.8%	(-46%, 60.2%)	0.413	0.160	0.97
CD16_20_b3_347		GG	36:57	36.8%	(4.1%, 58.4%)	0.031			22:42	47.6%	(12.3%, 68.7%)	0.014		
		GC/CC	15:17	11.8%	(-76.7%, 55.9%)	0.724	0.418	1.00	8:15	46.7%	(-25.8%, 77.4%)	0.151	0.972	1.00

CD16_20_b3_151	rs2290835	TT	14:32	56.2%	(18%, 76.7%)	0.010			11:23	52.2%	(1.9%, 76.7%)	0.044		
		TC/CC	37:42	11.9%	(-37%, 43.4%)	0.574	0.074	0.81	19:34	44.1%	(2%, 68.1%)	0.042	0.738	1.00
CD16b_02_b1_99	rs61803026	GG	27:38	28.9%	(-16.4%, 56.6%)	0.175			15:27	44.4%	(-4.4%, 70.4%)	0.068		
		GC/CC	23:35	34.3%	(-11.2%, 61.2%)	0.118	0.832	1.00	15:29	48.3%	(3.5%, 72.3%)	0.038	0.875	1.00
CD16b_02_b1_120	rs67020125	GG	37:48	22.9%	(-18.4%, 49.8%)	0.234			21:35	40.0%	(-3.1%, 65.1%)	0.064		
		GT/TT	13:25	48.0%	(-1.6%, 73.4%)	0.056	0.332	1.00	9:21	57.1%	(6.4%, 80.4%)	0.033	0.488	1.00
Fcar_E1_04_104	rs12462181	TT	14:31	54.8%	(15.1%, 76%)	0.014			10:25	60.0%	(16.7%, 80.8%)	0.014		
		TC/CC	37:43	14.0%	(-33.5%, 44.6%)	0.503	0.100	0.90	20:32	37.5%	(-9.3%, 64.3%)	0.099	0.343	1.00
Fcar_E2_01_191	rs75898867	TT	49:60	18.3%	(-19.1%, 44%)	0.293			29:46	37.0%	(-0.3%, 60.4%)	0.052		
		TC/CC	2:14	85.7%	(37.1%, 96.8%)	0.010	**0.025**	0.39	1:11	90.9%	(29.6%, 98.8%)	0.022	0.070	0.76
Fcar_E2_01_156	rs11084377	GG	44:63	30.2%	(-2.6%, 52.5%)	0.068			26:49	46.9%	(14.6%, 67%)	0.009		
		GA/AA	7:11	36.4%	(-64.2%, 75.3%)	0.350	0.859	1.00	4:8	50.0%	(-66%, 84.9%)	0.258	0.928	1.00
Fcar_E2_01_186	rs8112766	AA	11:20	45.0%	(-14.8%, 73.6%)	0.111			8:16	50.0%	(-16.8%, 78.6%)	0.109		
		AG/GG	40:54	25.9%	(-11.5%, 50.8%)	0.150	0.488	1.00	22:41	46.3%	(9.9%, 68%)	0.018	0.889	1.00
Fcar_E3_03_59	rs10402324	AA	16:20	20.0%	(-54.4%, 58.5%)	0.506			9:18	50.0%	(-11.3%, 77.5%)	0.090		
		AG/GG	35:54	35.2%	(0.8%, 57.6%)	0.046	0.598	1.00	21:39	46.2%	(8.5%, 68.3%)	0.022	0.880	0.83
Fcar_E4_04_267	rs61735069	TT	48:63	23.8%	(-10.9%, 47.7%)	0.156			28:50	44.0%	(11.1%, 64.7%)	0.014		
		TC/CC	3:11	72.7%	(2.2%, 92.4%)	0.046	0.130	0.96	2:7	71.4%	(-37.5%, 94.1%)	0.118	0.421	0.99
Fcar_E5_02_918	rs4806611	AA	24:29	17.2%	(-42.1%, 51.8%)	0.493			13:19	31.6%	(-38.5%, 66.2%)	0.292		
		AG/GG	27:45	40.0%	(3.3%, 62.8%)	0.036	0.382	1.00	17:38	55.3%	(20.7%, 74.7%)	0.006	0.359	1.00

[*]: FWER adjusted p-value to correct multiple comparisons using Westfall and Yang resampling method (5)

Table S5. Association of *FCGR2C* 126C>T (rs114945036) genotype with vaccine efficacy (VE) against any HIV-1 and with VE against CRF01_AE 169K HIV-1 for infections within 18 months and after 18 months since the first vaccination*

HIV-1 type	Time	Genotype	Vaccine:Placebo Infections	Est. VE	95% CI	P-value	Interaction P-value
Any	≤ 18m	CC	19:26	26.9%	(-32%, 59.6%)	0.30	
		CT/TT	4:15	73.3%	(19.7%, 91.1%)	0.019	0.11
	>18m	CC	22:20	-10%	(-100%, 40%)	0.76	
		CT/TT	5:10	50%	(-46.3%, 82.9%)	0.21	0.21
CRF01_AE 169K	≤ 18m	CC	13:22	40.9%	(-22.6%, 72.7%)	0.18	
		CT/TT	0:13	100%	(67.2%, 100%)	0.0002	0.01
	>18m	CC	15:11	-36.4%	(-100%, 37.4%)	0.44	
		CT/TT	2:9	77.8%	(-2.9%, 95.2%)	0.054	0.039

*: In the analysis of VE CRF01_AE 169K HIV-1 within 18 months, the estimated VE, 95% confidence interval, and p-value within each genotype group were calculated based on the exact binomial distribution testing an equal proportion of infections between the vaccine cases and the placebo cases, and the interaction p-value was calculated based on Fisher's exact test. For the other three analyses, all calculations were done using the case-only method as described in the statistical methods.

Table S6. Assessment of *FCGR2C* 126C>T genotype modification of the correlation between IgG binding antibodies response to eleven V1V2 scaffold proteins (magnitude) at week 26 and risk of HIV-1 infection by 42 months among vaccine recipients. All HIV-1 infections and infections with CRF01_AE 169K HIV-1 were considered. Correlation was measured using the odds ratio (OR) of risk probability per 1-SD increase in immune response.

			Any HIV-1s				**CRF01_AE 169K HIV-1**		
HIV-1 V1V2 antigen	**Genotype**	**No. of Case:Control**	**OR**	**p-value**	**Int. p-value**	**No. of Case:Control**	**OR**	**p-value**	**Int. p-value**
gp70.A(92RW020)-V1V2.GN	CC	34:154	0.63	**0.016**		23:154	0.63	**0.024**	
	CT/TT	7:49	1.07	0.878	0.280	2:49	0.59	0.384	0.917
gp70.AE(92TH023)-V1V2.AP	CC	34:154	0.77	0.201		23:154	0.77	0.213	
	CT/TT	7:49	0.63	0.063	0.518	2:49	0.43	**0.014**	0.146
gp70.B(CaseA2.p623)-V1V2.APorig*	CC	34:154	0.63	**0.013**		23:154	0.62	**0.016**	
	CT/TT	7:49	1.06	0.897	0.270	2:49	0.18	0.092	0.237
gp70.B(CaseA2)-V1V2.GN	CC	34:154	0.59	**0.004**		23:154	0.57	**0.006**	
	CT/TT	7:49	0.78	0.561	0.539	2:49	0.22	0.071	0.265
gp70.B(Case A2)-V1V2.LL	CC	34:154	0.64	**0.018**		23:154	0.65	**0.035**	
	CT/TT	7:49	0.84	0.693	0.558	2:49	0.25	**0.037**	0.171
gp70.B(Case A2/V169K)-V1V2.LL	CC	34:154	0.59	**0.004**		23:154	0.61	**0.011**	
	CT/TT	7:49	0.75	0.510	0.635	2:49	0.16	**0.036**	0.140
gp70.B(Case A2/mut3)-V1V2.LL	CC	34:154	0.79	0.226		23:154	0.78	0.251	
	CT/TT	7:49	0.61	0.058	0.439	2:49	0.39	**0.013**	0.107
gp70.C(1086)-V1V2.LL	CC	34:154	0.78	0.249		23:154	0.79	0.309	
	CT/TT	7:49	0.62	0.072	0.483	2:49	0.35	**0.011**	0.083
gp70.C(97ZA012)-V1V2.GN	CC	34:154	0.60	**0.009**		23:154	0.57	**0.008**	
	CT/TT	7:49	0.57	0.124	0.883	2:49	0.19	0.061	0.227
tags.AE(A244)-V1V2.LL	CC	34:154	0.71	0.065		23:154	0.74	0.141	
	CT/TT	7:49	0.60	0.061	0.614	2:49	0.38	**0.011**	0.120
tags.C(1086)-V1V2.LL	CC	34:154	0.70	0.055		23:154	0.72	0.113	
	CT/TT	7:49	0.64	0.159	0.833	2:49	0.36	**0.018**	0.152
Breadth Score	CC	34:154	0.64	**0.018**		23:154	0.63	**0.026**	
	CT/TT	7:49	0.7	0.362	0.842	2:49	0.26	**0.027**	0.168

Table S7. Assessment of *FCGR2C* 126C>T genotype modification of the correlation between IgG3 binding antibodies response to eleven V1V2 scaffold proteins (magnitude) at week 26 and risk of HIV-1 infection by 42 months among vaccine recipients. All HIV-1 infections and infections with CRF01_AE 169K HIV-1 were considered. Correlation was measured using the odds ratio (OR) of risk probability per 1-SD increase in immune response.

HIV-1 V1V2 antigen	Genotype	No. of Case:Control	Any HIV-1s			No. of Case:Control	CRF01_AE 169K HIV-1		
			OR	p-value	Int. p-value		OR	p-value	Int. p-value
gp70.A(92RW020)-V1V2.GN	CC	34:154	0.89	0.576		23:154	0.77	0.269	
	CT/TT	7:49	0.90	0.786	0.977	2:49	0.42	0.220	0.415
gp70.AE(92TH023)-V1V2.AP	CC	34:154	0.98	0.921		23:154	0.96	0.850	
	CT/TT	7:49	0.70	0.294	0.406	2:49	0.27	**0.029**	**0.051**
gp70.B(CaseA2.p623)-V1V2.APorig	CC	34:154	1.06	0.746		23:154	0.87	0.529	
	CT/TT	7:49	1.17	0.732	0.846	2:49	0.56	0.519	0.636
gp70.B(CaseA2)-V1V2.GN	CC	34:154	0.78	0.203		23:154	0.66	0.074	
	CT/TT	7:49	0.73	0.433	0.888	2:49	0.30	0.127	0.336
gp70.B(Case A2)-V1V2.LL	CC	34:154	0.86	0.450		23:154	0.71	0.126	
	CT/TT	7:49	0.88	0.772	0.958	2:49	0.29	0.111	0.274
gp70.B(Case A2/V169K)-V1V2.LL	CC	34:154	0.70	0.069		23:154	0.60	**0.026**	
	CT/TT	7:49	0.86	0.712	0.640	2:49	0.33	0.088	0.376
gp70.B(Case A2/mut3)-V1V2.LL	CC	34:154	0.99	0.946		23:154	0.96	0.871	
	CT/TT	7:49	0.69	0.284	0.385	2:49	0.27	**0.031**	**0.052**
gp70.C(1086)-V1V2.LL	CC	34:154	0.99	0.970		23:154	0.96	0.852	
	CT/TT	7:49	0.66	0.254	0.336	2:49	0.21	0.032	**0.048**
gp70.C(97ZA012)-V1V2.GN	CC	34:154	0.68	**0.049**		23:154	0.61	**0.029**	
	CT/TT	7:49	0.87	0.728	0.588	2:49	0.39	0.199	0.557
tags.AE(A244)-V1V2.LL	CC	34:154	0.80	0.294		23:154	0.80	0.346	
	CT/TT	7:49	0.67	0.241	0.651	2:49	0.35	**0.036**	0.134
tags.C(1086)-V1V2.LL	CC	34:154	0.82	0.342		23:154	0.79	0.304	
	CT/TT	7:49	0.74	0.409	0.811	2:49	0.36	0.080	0.210
Breadth Score	CC	34:154	0.77	0.194		23:154	0.66	0.067	
	CT/TT	7:49	0.83	0.630	0.857	2:49	0.29	0.060	0.245

Table S8. Minor allele frequency (MAF) and prevalence of individuals who carry at least one minor allele at the FCGR2C 126C>T SNP (rs114945036) locus and at the two linked SNP (rs138747765 C>T and rs78603008 G>A) loci by population for which the genotype data are available from the 1000 Genome Project Phase 1.

Population	Sample Size	rs114945036 C>T		rs138747765 C>T		rs78603008 G>A	
		MAF	CT/TT	MAF	CT/TT	MAF	GA/AA
Thailand RV144 (for reference)	205	0.14	0.24	0.14	0.24	0.14	0.24
East Asian Ancestry (ASN)							
Han Chinese in Beijing, China (CHB)	97	0.16	0.30	0.19	0.35	0.19	0.35
Japanese in Tokyo, Japan (JPT)	89	0.15	0.28	0.17	0.33	0.17	0.33
Southern Han Chinese, China (CHS)	100	0.16	0.30	0.17	0.33	0.17	0.33
African Ancestry (AFR)							
African Ancestry in Southwest US (ASW)	61	0.17	0.31	0.06	0.10	0.06	0.10
Luhya in Webuye, Kenya (LWK)	97	0.28	0.47	0.01	0.01	0.01	0.01
Yoruba in Ibadan, Nigeria (YRI)	88	0.13	0.23	0.00	0.00	0.00	0.00
European Ancestry (EUR)							
British in England and Scotland (GBR)		0.25	0.39	0.30	0.47	0.30	0.47
Finnish in Finland (FIN)	93	0.29	0.46	0.31	0.49	0.31	0.49
Iberian populations in Spain (IBS)	14	0.25	0.36	0.25	0.29	0.25	0.29
Toscani in Italy (TSI)	98	0.14	0.21	0.18	0.28	0.18	0.28
Utah residents with Northern and Western European ancestry (CEU)	85	0.21	0.36	0.23	0.36	0.22	0.36
Americas Ancestry (AMR)							
Colombian in Medellin, Colombia (CLM)	60	0.23	0.42	0.27	0.45	0.27	0.45
Mexican Ancestry in Los Angeles, California (MXL)	66	0.31	0.53	0.39	0.64	0.39	0.64
Puerto Rican in Puerto Rico (PUR)	55	0.27	0.38	0.27	0.40	0.27	0.40
Total	1092	0.21	0.35	0.19	0.32	0.19	0.32

Figure S1. Fc receptor loci targeted for resequencing. The arrangements of the five *FCGR* genes on chromosome 1q23-24 and the *FCAR* gene on chromosome 19q13.42 are shown, with exon and intron structures depicted by boxes and lines respectively. The distances between the *FCGR* genes are not to scale and a single example of possible alternative splicing is represented. Coordinates within the reference human genome build are provided in supplementary Table S1. Arrows indicate the direction of transcription and beneath each gene the corresponding protein structures are depicted. Exon regions and the derivative protein domains targeted for resequencing are indicated in orange. The activating ITAM motifs and inhibitory ITIM motifs are indicated in green and red, respectively.

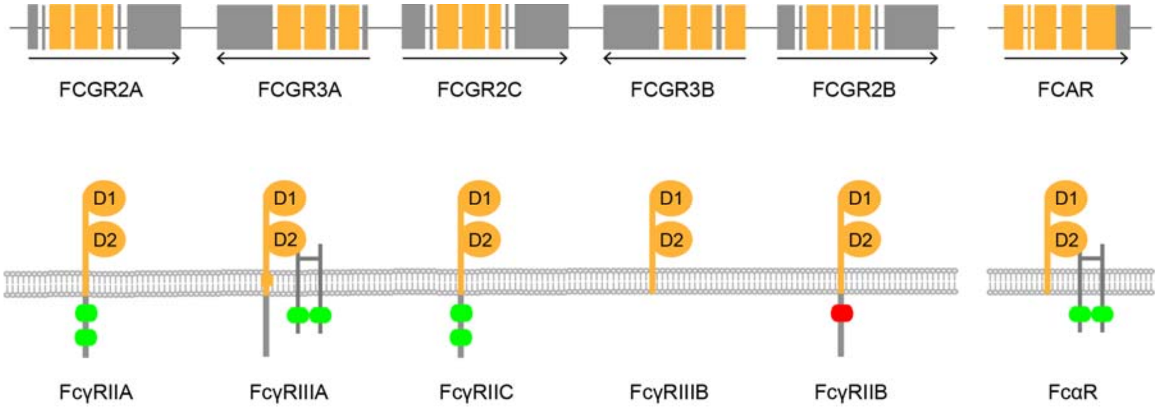


Figure S2. Boxplots of the 8 "sensitivity immune response variables" and one secondary variable (IgA C1 peptide) at week 26 in vaccine recipients studied previously (1), cross-classified by CC vs. CT/TT of *FCGR2C* 126C>T and by case-control status. Boxplots show the 25th percentile (lower edge of the box), 50th percentile (horizontal line in the box), and 75th percentile (upper edge of the box), and vertical whiskers extend no more than 1.5 times the height of the box; individual outliers beyond the whiskers are plotted**.** Sex is indicated by color ((men in blue and women in red) and tertile of response is indicated by point shading, where the gray horizontal bands represent the middle third of response values.

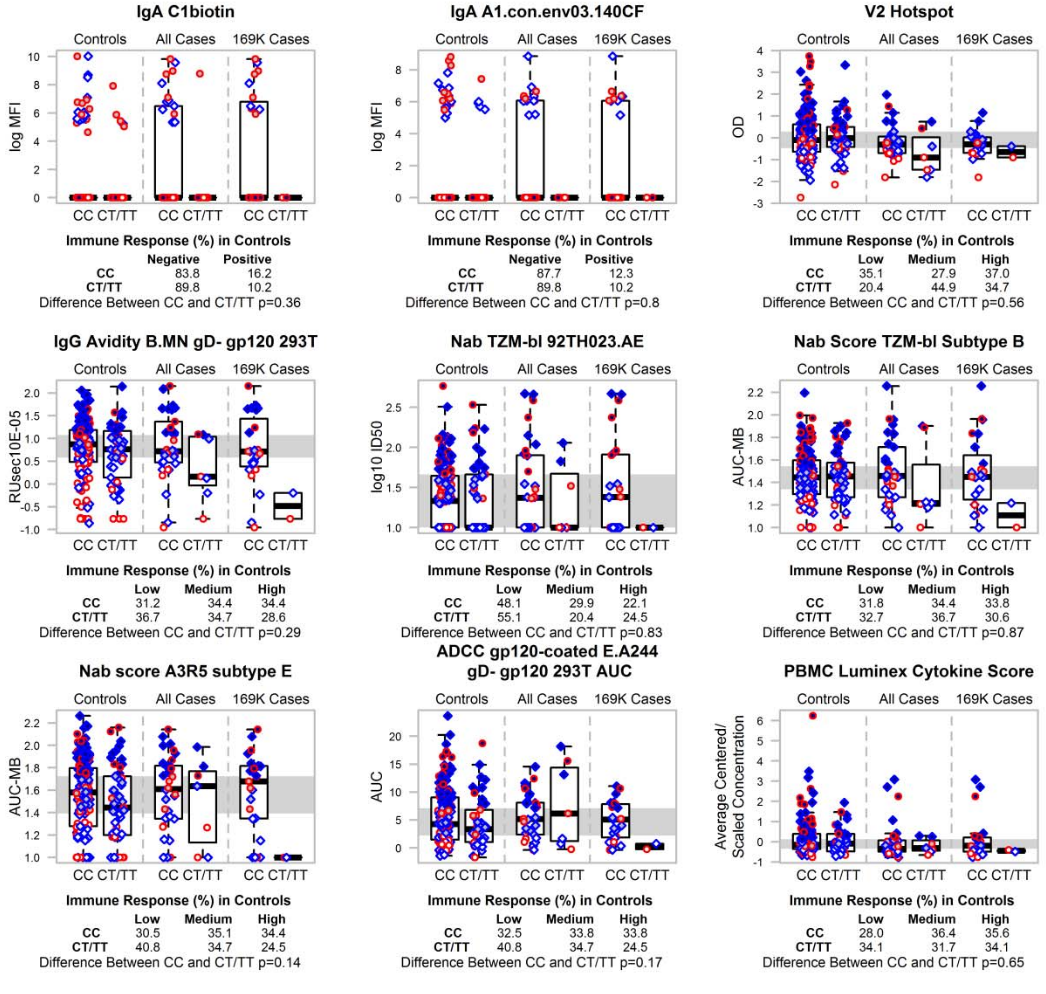
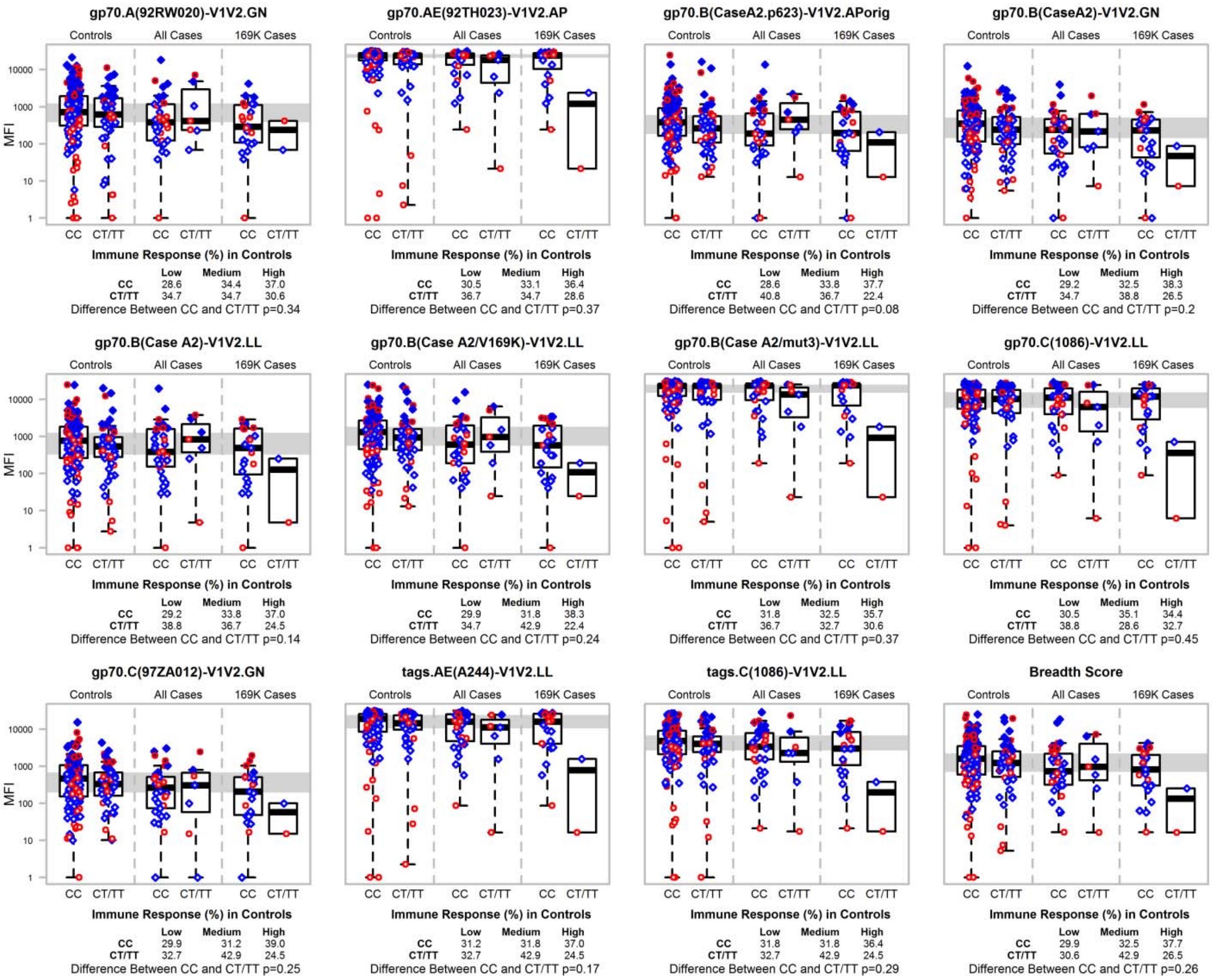
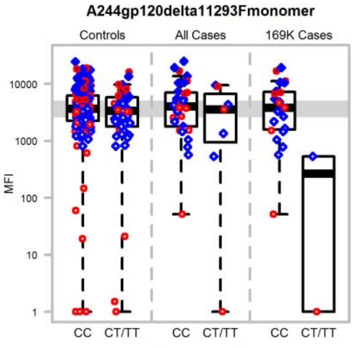


Figure S3. Boxplots of IgG Abs to eleven V1V2-scaffold antigens studied previously (2) and IgG breadth score **(A)** and to two Env gp120 antigens (1) **(B)** at week 26 in vaccine recipients, cross-classified by *FCGR2C* 126C>T CC vs. CT/TT and by case-control status. Boxplots show the 25th percentile (lower edge of the box), 50th percentile (horizontal line in the box), and 75th percentile (upper edge of the box), and vertical whiskers extend no more than 1.5 times the height of the box; individual outliers beyond the whiskers are plotted**.** Sex is indicated by color (men in blue and women in red) and tertile of response is indicated by point shading, where the gray horizontal bands represent the middle third of response values. **A.**



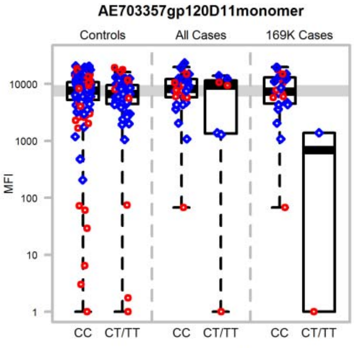
B.



Immune Response (%) in Controls

	Low	Medium	High
CC	31.2	37.0	31.8
CT/TT	38.8	26.5	34.7

Difference Between CC and CT/TT p=0.35



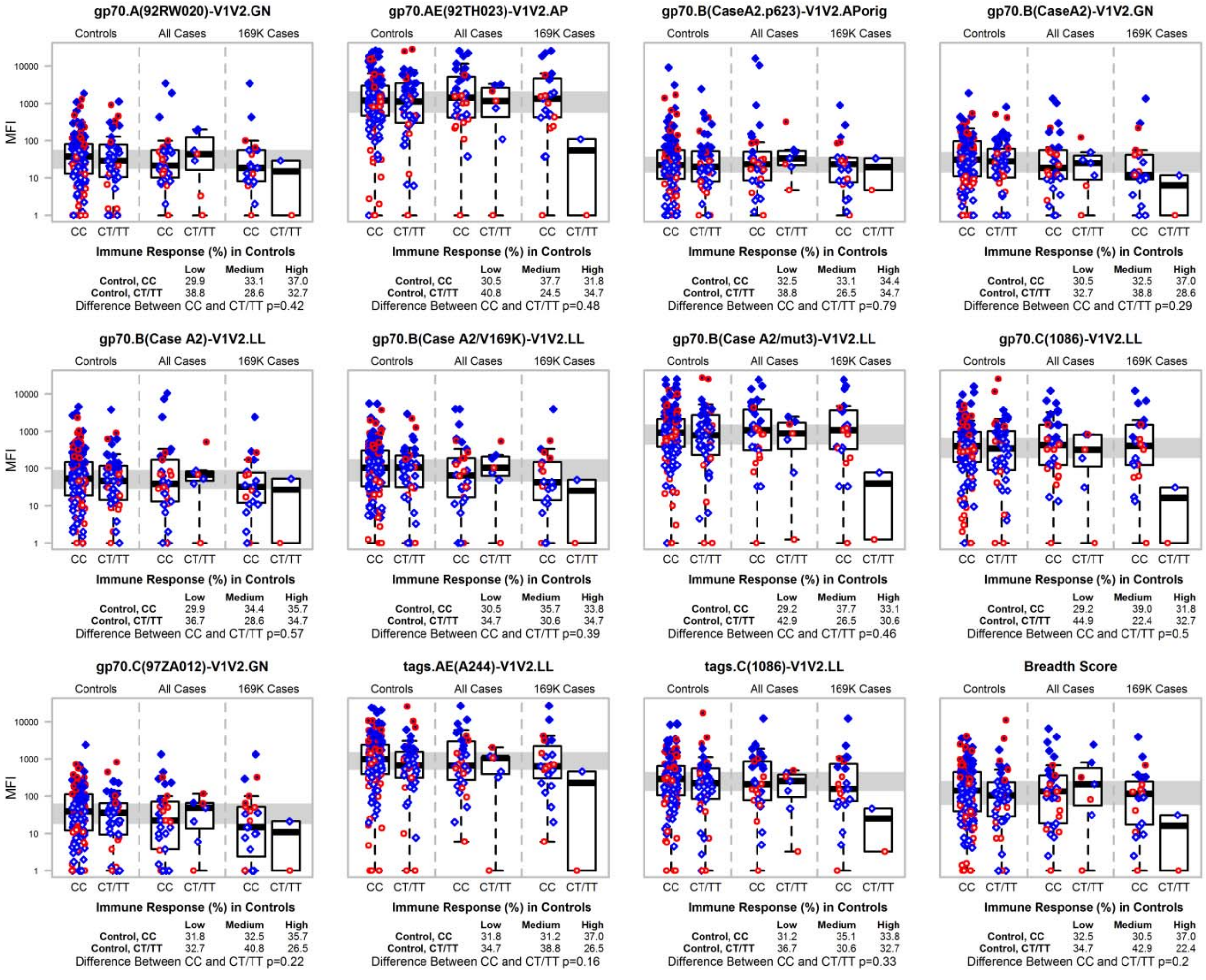
Immune Response (%) in Controls

	Low	Medium	High
CC	29.9	35.7	34.4
CT/TT	44.9	28.6	26.5

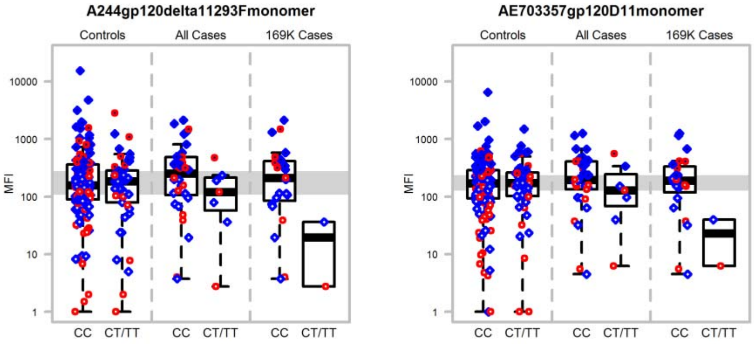
Difference Between CC and CT/TT p=0.11

Figure S4. Boxplots of IgG3 Abs to V1V2-scaffold antigens studied previously (3) and IgG3 breadth score (**A**) and to two Env gp120 antigens (1) (**B**) at week 26 in vaccine recipients, cross-classified by *FCGR2C* 126C>T CC vs. CT/TT and by case-control status. Boxplots show the 25th percentile (lower edge of the box), 50th percentile (horizontal line in the box), and 75th percentile (upper edge of the box), and vertical whiskers extend no more than 1.5 times the height of the box; individual outliers beyond the whiskers are plotted. Sex is indicated by color (men in blue and women in red) and tertile of response is indicated by point shading, where the gray horizontal bands represent the middle third of response values.

A



B



Immune Response (%) in Controls

	Lo	**Med**	**Hi**
Control, CC	34.4	33.8	31.8
Control, CT/TT	34.7	34.7	30.6

Difference Between CC and CT/TT p=0.73

Immune Response (%) in Controls

	Lo	**Med**	**Hi**
Control, CC	34.4	33.8	31.8
Control, CT/TT	32.7	34.7	32.7

Difference Between CC and CT/TT p=0.96

Figure S5. Heat map and hierarchical clustering tree of Spearman rank correlations of week 26 IgG Ab levels to pairs of eleven V1V2-scaffold antigens

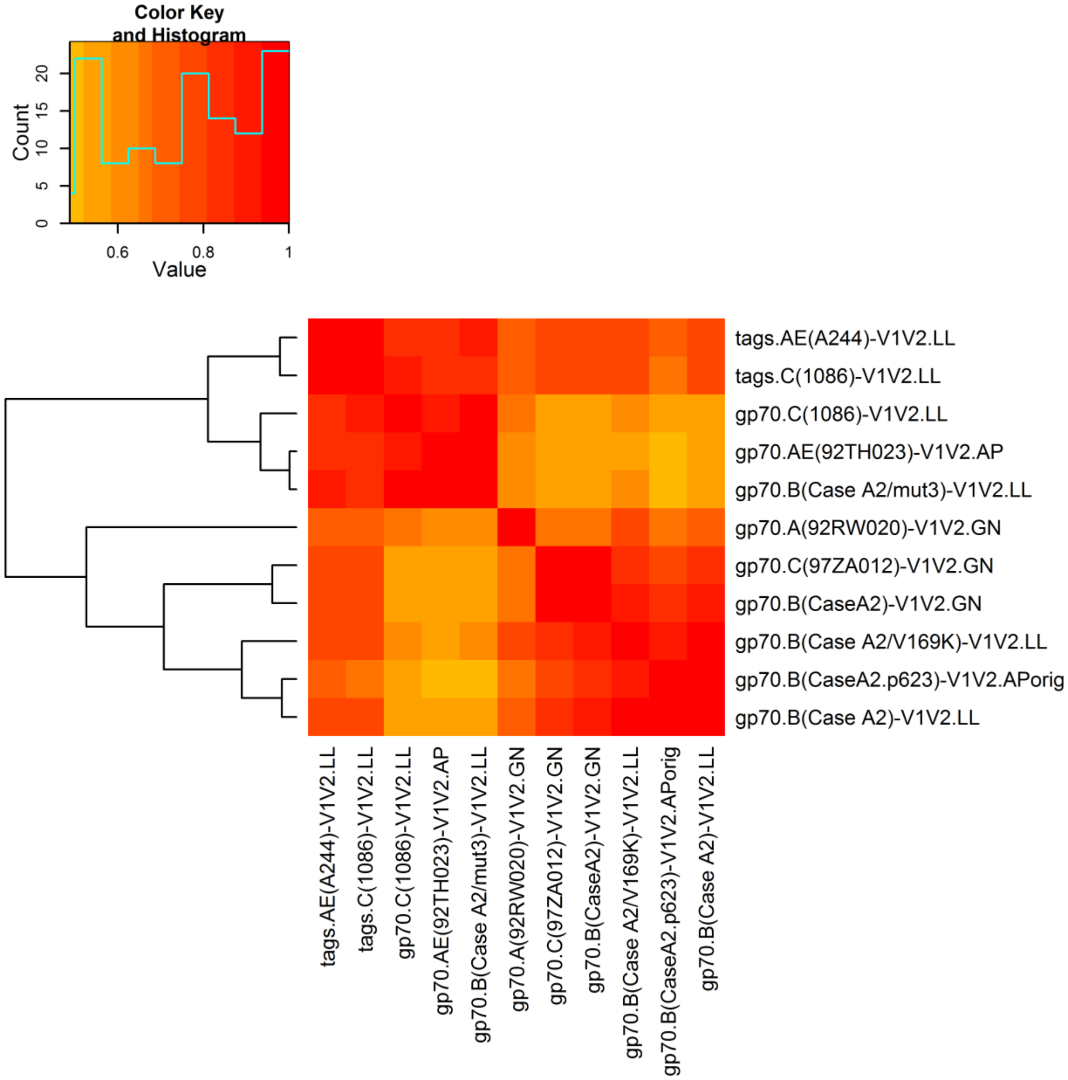


Figure S6. Heat map and hierarchical clustering tree of Spearman rank correlations of week 26 IgG3 Ab levels to pairs of eleven V1V2-scaffold antigens