Supplementary Materials for

Characterization of a vaccine-elicited human antibody with sequence homology to VRC01-class antibodies that binds the C1C2 gp120 domain

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This PDF file includes:

Figs. S1 and S2
Tables S1 and S2
**S1. Timeline of vaccine administration in HVTN 100.** Numbers along the timeline indicate months since enrollment. Blue syringes denote administration of ALVAC, while red syringes denote administration of the bivalent rec gp120 mix (1086 and TV1). The red arrow indicates the visit (2 weeks post-5\textsuperscript{th} immunization at visit 12) during which Env\textsuperscript{+} BCR repertoire analysis was performed and FH1 was isolated.
Figure S2

|                  | KD (M)  | KD Error | kon(1/Ms)  | kon Error | kdis(1/s)  | kdis Error | Full R^2 |
|------------------|---------|----------|------------|-----------|------------|------------|----------|
| FH-1 Fab         | DMRScore gp120 | 2.64E-09 | 8.62E-11 | 2.43E+05 | 2.01E+03 | 2.79E-05 | 4.64E-06 | 0.9865  |
| 1086 gp120       | -       | -        | -          | -         | -          | -          | -        | -       |
| gl VRC01 Fab (3-20) | DMRScore gp120 | 6.09E-07 | 9.44E-09 | 9.67E+03 | 1.50E+02 | 2.48E-03 | 1.13E-05 | 0.9878  |
| 1086 gp120       | -       | -        | -          | -         | -          | -          | -        | -       |
| eOD-GT8          | -       | -        | -          | -         | -          | -          | -        | -       |

S2. Kinetic analysis. Kinetic analyses were performed by BLI using recombinant Fabs loaded onto FAB2G biosensors and 2-fold dilutions of the indicated Env monomers.
Supplementary Table 1 | Data collection and refinement statistics for FH1Fab+HXb2core

| Data collection | FH1Fab+HXb2core |
|----------------|-----------------|
| **Space group** | P1              |
| **Cell dimensions** |                |
| \(a, b, c\) (Å) | 103.361, 106.266, 113.219 |
| \(\alpha, \beta, \gamma\) (°) | 67.566, 76.674, 60.987 |
| **Resolution (Å)** | 50 - 3.5 (3.56 – 3.50)* |
| \(R_{\text{sym}}\) or \(R_{\text{merge}}\) | 0.120 (0.511)* |
| \(I/I_{\text{m}}\) | 5.29 (1.19)* |
| **Completeness (%)** | 92.5 (69.3)* |
| **Redundancy** | 1.6 (1.4)* |
| **CC_{1/2}** | 0.950 (0.712)* |
| **Refinement** |                |
| **Resolution (Å)** | 50.13 - 3.547 (3.674 – 3.547)* |
| **No. reflections** | 36171 (888) |
| \(R_{\text{work}}/R_{\text{free}}\) | 25.64/29.27 (28.32/30.22)* |
| **No. atoms** | 22151 |
| Protein | 21280 |
| Water | 104 |
| Ligand | 767 |
| **B-factors (Å²)** | 78.88 |
| Protein | 78.55 |
| Water | 36.57 |
| Ligand | 93.73 |
| **R.m.s deviations** |                |
| Bond lengths (Å) | 0.009 |
| Bond angles (°) | 1.29 |
| Ramachadran Favored % | 94.39 |
| Ramachadran Outliers % | 0.00 |
| MolProbity all-atoms clashscore | 6.49 |

* Statistics for the highest-resolution shell are shown in parentheses.
### a. Detailed interactions of HXB2core and FH1 Heavy Chain.

| HXB2core | HSDC | ASA | BSA |
|----------|------|-----|-----|
| D:THR 51 | 104.27 | 1.73 |
| D:PHE 53 | 93.83 | 57.79 |
| D:ALA 55 | 1.17 | 1.01 |
| D:ASP 57 | 103.06 | 6.85 |
| D:ALA 58 | 27.63 | 14.84 |
| D:LYS 59 | 107.62 | 4.52 |
| D:ALA 60 | 89.46 | 65.57 |
| D:TYR 61 | 166.38 | 130.38 |
| D:ASP 62 | 55.32 | 2.25 |
| D:THR 63 | 118.64 | 17.66 |
| D:VAL 68 | 79.57 | 8.54 |
| D:THR 71 | 44.03 | 1.67 |
| D:VAL 75 | 85.76 | 58.89 |
| D:PRO 76 | 97.65 | 74.49 |
| D:THR 77 | 46.10 | 13.53 |
| D:ASP 78 | 77.94 | 31.26 |
| D:PRO 79 | 129.97 | 109.06 |
| D:ASN 80 | 109.70 | 33.69 |
| D:CYS 218 | 10.95 | 8.63 |
| D:PRO 220 | 19.47 | 11.94 |
| D:ALA 221 | 98.06 | 24.52 |
| D:GLN 246 | 87.28 | 11.78 |

### b. Detailed interactions of HXB2core and FH1 Light Chain.

| HXB2core | HSDC | ASA | BSA |
|----------|------|-----|-----|
| D:THR 51 | 104.27 | 9.54 |
| D:PHE 53 | 93.83 | 11.30 |
| D:CYS 54 | 2.98 | 0.12 |
| D:ALA 58 | 27.63 | 1.11 |
| D:ALA 60 | 89.46 | 15.90 |
| D:VAL 68 | 79.57 | 8.61 |
| D:THR 71 | 44.03 | 34.91 |
| D:HAS 72 | 165.12 | 130.61 |
| D:LEU 73 | 49.02 | 35.41 |
| D:CYS 74 | 28.91 | 19.26 |
| D:VAL 75 | 85.76 | 26.88 |
| D:PRO 76 | 97.65 | 23.16 |
| D:GLU 106 | 110.31 | 1.47 |
| D:ASP 107 | 39.23 | 21.32 |
| D:SER 110 | 51.85 | 7.10 |
| D:GLN 114 | 108.60 | 51.50 |

### Hydrogen Bonds

| HXB2core | Dist. [Å] | FH1 Light Chain |
|----------|----------|-----------------|
| HSB 103 | 2.64 | V:GLN 27 [OE1] |
| HSB 107 | 3.50 | V:ASP 29 [NH2] |

### Salt Bridges

| HXB2core | Dist. [Å] | FH1 Light Chain |
|----------|----------|-----------------|
| HSB 107 | 3.50 | V:ARG 29 [NH2] |