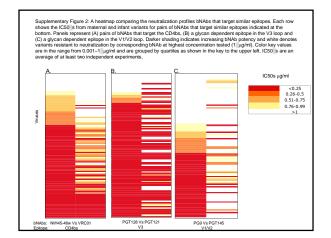
Supplementary Figure 1. A heatmap showing sensitivity profiles of the most broad and potent bNAbs in each class. Each row shows the ICSO(s) of maternal and infant variants tested against the bNAb that target claim ceptopes indicated at the corresponding bNAb at highest concentration tested ("ligvill"). Clook they values are in the range from 0.011–Illigvill and are grouped by quartities as shown in the key to the upper left. Viruses resistant to either NIH45–46W or PGT128 have been clustered together to emphasize the complete complementary activity of these bNAbs. ICSO(s are an average of at least two independent experiments.

ICSOs µg/ml

C25
0.26-0.5
0.51-0.7
0.76-0.99
>1



Supplementary Figure 3. Comparison of neutralization sensitivity of infant variants versus all maternal variants to bNAbs. Analyses were performed by GEE using a logit link and exchangeable correlation structure, except where marked by *, which indicates Febre's exact test. **, "indicates the reference group for analyses. The p values for each bNAb are shown. ICSO |s are an average of at least 2 independent experiments.

dAMd	Mom	Infant	OR	95%CI	p-value
	% (n)	% (n)			
	n=85	n=22			
NIH45-46W	89% (76)	86% (19)	0.77	0.12-5.02	0.79
VRC01	65% (55)	77% (17)	1.55	0.32-7.47	0.22
PGT128	86% (73)	86% (19)	0.94	0.16-5.53	0.95
PGT121	67% (57)	82% (18)	1.39	0.3-6.47	0.67
PG9	61% (52)	82% (18)	2.5	0.51-12.2	0.26
PGT145	32% (27)	27% (6)	0.8	0.17-3.72	0.77
mab					
b12	12% (10)	0% (0)	Inf	0.6-Inf	0.12

Supplementary Figure 4. Detailed analysis of the neutralization sensitivity of different HIV-1 subtypes to bNAbs. Comparison of subtype A variants against ono-subtype A variants (excluding subtype A recombinants) (A). Comparison of subtype A variants against C and CD recombinants (excluding subtype A recombinants and pure subtype D). Comparison of subtype A against D and CD recombinants (excluding subtype A recombinants and pure subtype D). Comparison of subtype A against D and CD recombinants (excluding subtype A recombinants and pure subtype D). Analysis was periomed by GEE using a logit lift and exchangeable correlation structure. "in dicates the reference group for analyses. The p values for each bNAb are shown. [C50] is are an average of at least 2 independent experiments.

NNH-5						
NH45-60V Peril P	bNAb	Subtype A	Subtypes C,D, C/D	OR	95% CI	p-value
NH45-469V 98% (88) 69% (25) 0.07 0.007-277 0.03 VRC01 88* (79) 30% (16) 0.1 0.02-0.41 0.001 PGT128 67% (90) 72% (20) 1.8 0.464-6.85 0.48 PGT148 37% (33) 1.9% (19) 0.47 0.13+171 0.365-6.85 PGT146 37% (33) 1.9% (19) 0.47 0.13+171 0.365-6.85 NAB		% (n)	% (n)			
VPRC01						
PGT128 67% (60) 72% (20) 1.6 0.44 6.80 0.48 PGT121 57% (40) 75% (27) 0.07 0.85+10.0 0.99 PGT9 70% (63) 53% (19) 0.47 0.33+17.1 0.26 PGT9 70% (63) 53% (19) 0.47 0.33+17.1 0.26 PGT9 70% (63) 53% (19) 0.47 0.33+17.1 0.26 PGT9 70% (63) 0.50% (19) 0.47 0.33+17.1 0.26 PGT9 70% (63) 0.47 0.47 0.47 0.47 0.47 0.47 0.47 0.47	NIH45-46W	98% (88)	69% (25)	0.07	0.007-0.77	0.03
PGT121 51% (46) 75% (27) 3.07 0.85-1.0 0.09 PGT145 37% (33) 75% (19) 0.47 0.13-1.71 0.09 PGT145 37% (33) 1994 (7) 0.41 0.12-1.39 0.15	VRC01	88% (79)	36% (16)	0.1	0.02-0.41	0.001
PG9		67% (60)	72% (26)			
PGT146 37% (33 19% (7) 0.41 0.124.39 0.15 BNA0 Subyes Subyes C.CID OR 95% CI p-value (1.69) NNH45-469W 95% (89) 75% (1.49) 0.10 0.000-1.72 0.11 NNH45-469W 95% (89) 75% (1.49) 0.10 0.000-1.72 0.11 NPGT14 57% (8) 69% (7) 0.13 0.000-1.72 0.11 PGT141 57% (8) 69% (17) 0.13 3.56-52.7 0.0001 PGT145 37% (33) 11% (2) 0.17 0.05-0.52 0.0001 PGT145 37% (33) 11% (2) 0.17 0.05-0.52 0.0007 NNN0 Subyes A Subyes D.CID OR 95% (17) 0.000-1.000 0.000-0.37 0.000 NNN0 Subyes A Subyes D.CID OR 95% (17) 0.000-0.000 0.000-0.37 0.000 NNN0 Subyes A Subyes D.CID OR 95% (17) 0.000 0.000-0.37 0.000 NNN0 Subyes A Subyes D.CID OR 95% (17) 0.000 0.000-0.37 0.000		51% (46)				
NAb	PG9	70% (63)	53% (19)	0.47	0.13-1.71	0.26
15	PGT145	37% (33)	19% (7)	0.41	0.12-1.39	0.15
15						
NiH45-46W (mi-80) (mi-19) (m	bNAb			OR	95% CI	p-value
NNH4-640W S9% (88) 76% (14) 0.1 0.006-1.72 0.11 VRC01 WRC01 S9% (79) 47% (9) 0.18 0.04-0.85 0.13 VRC01 S9% (79) 47% (9) 0.18 0.04-0.85 0.13 VRC01 S9% (79) 47% (9) 0.18 0.04-0.85 0.18 VRC01 VRC01 VRC01 S9% (79) S9% (79) S9% (79) S9% (79) S9% (79) S9% (79) C. 0.17 0.05-0.62 0.021 VRC01 S9% (79)						
VPRC01 88% (79) 47% (9) 0.18 0.04-0.85 0.03 PGT128 67% (80) 88% (17) 6.19 0.79-48.5 0.08 PGT121 51% (86) 88% (17) 13.7 3.58-52.7 0.001 PG9 70% (83) 78% (15) 2.66 0.421.4 0.21 PG1145 37% (33) 11% (2) 0.17 0.65-5.62 0.007 NNAb Subspee A Subspee D, CD OR 97% (10) Subspee A Subspee B, CD 0.07 0.07-0.72 NB46-5400 0.08 97% (10) 0.07 0.07-0.72 0.03 VPRC01 88% (79) 32% (8) 0.08 0.02-0.37 0.02 PGT128 67% (80) 68% (17) 0.024-452 0.021 O24-452 0.031						
PGT128 GFN, R00 88%, (17) 6.19 0.79-46.5 0.08 PGT121 SFN, 469 88%, (17) 13.7 3.58-52.7 0.0001 PG9 77%, (83) 78%, (17) 13.7 3.58-52.7 0.0001 PG9 77%, (83) 78%, (17) 12.98 0.42-4.4 0.28 PGT145 3.7%, (33) 78%, (17) 2.98 0.42-4.4 0.28 PGT145 3.7%, (33) 78%, (17) 0.05-0.82 0.0001 PGT145 0.000 PGT145 0.000 PGT145 0.0001 PGT145 0						
PGT121 51% (46) 88% (17) 13.7 2.95 2.96.27 0.001 PGT121 51% (46) 88% (17) 13.7 2.95 2.96.27 0.001 PGT121 51% (45) 2.95 2.96.27 0.001 PGT121 51% (15) 2.96 2.96.27 0.001 PGT121 51% (15) 2.96 2.96 2.96 2.96 2.96 2.96 2.96 2.96						
PC9						
PGT145 37% (33) 11% (2) 0.17 0.05-0.62 0.007 DNAb Subtype A Subtype D CD OR 95% CI p-value (m-95) (
DNAb						
% (n) % (n) (n-25) (n-25) (n-27) (18) (0.77) (0.007-0.72) (0.03) (18) (18) (18) (18) (18) (18) (18) (18	PGT145	37% (33)	11% (2)	0.17	0.05-0.62	0.007
% (n) % (n) (n-25) (n-25) (n-27) (18) (0.77) (0.007-0.72) (0.03) (18) (18) (18) (18) (18) (18) (18) (18	BATAN	Cubbino A	Culturana D. C/D.	OB	OFF CI	n volvo
(n=90) (n=25) (n=25) (n=26) (n	DIVAD			OK	55% CI	p-value
NIH45-46W 98% (88) 72% (18) 0.07 0.007-0.72 0.03 VRC01 88% (79) 32% (8) 0.08 0.02-0.37 0.002 VRT128 67% (60) 68% (17) 1.09 0.24-4.92 0.91						
VRC01 88% (79) 32% (8) 0.08 0.02-0.37 0.002 PGT128 67% (60) 68% (17) 1.09 0.24-4.92 0.91	NIH45-46W			0.07	0.007-0.72	0.03
PGT128 67% (60) 68% (17) 1.09 0.24-4.92 0.91						
PGT121 51% (46) 68% (17) 1.84 0.44-7.93 0.4						
PG9 70% (63) 32% (8) 0.16 0.03-0.84 0.03						
PGT145 37% (33) 24% (6) 0.57 0.15-2.19 0.42						

