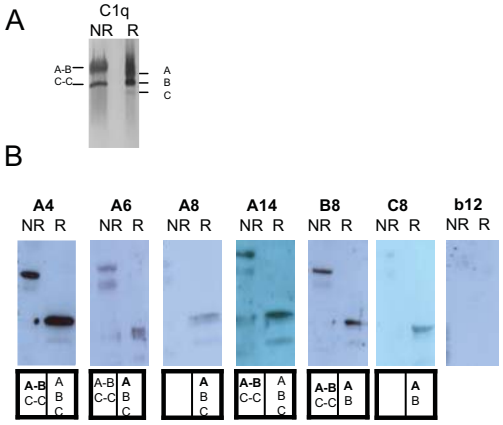

Fig. SI. Epitope characterization of the human anti-C1q Fabs. All anti-C1q Fab fragments recognized at least 2 of the 3 polypeptide chains of C1q. (A) SDS-PAGE gel separation of full-length C1q showing the similar but distinct patterns of the 3 polypeptide chains A, B and C under non-reducing (NR) and reducing (R) conditions after silver staining. The C1q molecule is composed of 3 similar, but distinct, polypeptide chains, A, B and C, which are the product of three distinct genes aligned in the same orientation in the order of A-B-C on chromosome 1p. Under non-reducing conditions A-B and C-C chain dimers are formed, whereas under reducing conditions all three polypeptide chains are separated. (B) Purified anti-C1q IgG-Fab fragments (2µg/ml) were tested for binding to C1q under non-reducing (NR) and reducing (R) conditions in Western blot analysis. The table below the blots summarizes the polypeptide chain recognized, bold indicating a strong recognition signal. Interestingly, all the anti-C1q Fabs recognized at least two different polypeptide chains. Fabs A4, A6 and A14 recognized all three polypeptide chains under both non-reducing and reducing conditions, whereas the binding seemed to be weaker for Fab A6 compared to Fab A4 and A14. Fab B8 recognized the A-B dimer strongly, but the C-C dimer only weakly under non-reducing conditions, whereas only the A and B chain bound under reducing conditions. Fabs A8 and C8 bound only the A and B under reducing condition and not the C polypeptide chain. These observations indicate that the epitope recognized by the 6 Fabs is at least partly linear and involves conserved epitopes present on at least two of the three polypeptide chains of the C1q molecule.

Table S1. pI values of the different human anti-C1q Fabs and each of their CDR and FR regions.

		Fabs	CDR1	CDR2	CDR3	FR1	FR2	FR3
Heavy-chain	A4	4.1	6	10.8	4.1	6.3	10.9	8.9
	A6	3.1	6.1	9.4	3.1	9.1	10.1	9.5
	A8	9.5	3.1	4.1	9.5	3.8	6.3	9.9
	A14	6.9	6.1	10.9	6.9	8.9	10.9	8.9
	B8	6.3	3.3	7.7	6.3	7.1	10.1	9.5
	C8	3.7	5.8	9.7	3.7	3.1	10.1	8.9
Light-chain	A4	4.4	11.1	3.0	7.7	6.1	10.2	3.7
	A6	4.4	1.9	3	10.1	6.1	10.4	4.3
	A8	3.0	4.9	11.4	6.6	5.3	9.8	3.4
	A14	4.4	6.9	3	5.9	6.1	10.4	4.3
	B8	4.3	6.1	3	5.8	6.1	10.4	4.3
	C8	9.3	10.9	5.2	5.8	12.7	10.4	3.5

Table S2. Titers of eluted phage of consecutive rounds of selection.

	HIV-C1q (1)	HIV-gp120 (+1)	NC-C1q (2)
	1.0×10^8	1.0×10^8	8.8×10^6
1st	3.2×10^4	4.0×10^5	3.6×10^4
2nd	2.6×10^3	1.6×10^7	1.3×10^2
3rd	< 1	1.9×10^9	$< 1 \times 10^1$
4th	nd	1.6×10^9	nd

HIV-C1q designates that the HIV-1 patient-derived phage library was panned on C1q, **HIV-gp120** designates that HIV-1 patient-derived phage library was panned on gp120, **NC-C1q** designates the healthy individual-derived phage library was panned on C1q. nd=not deterimined