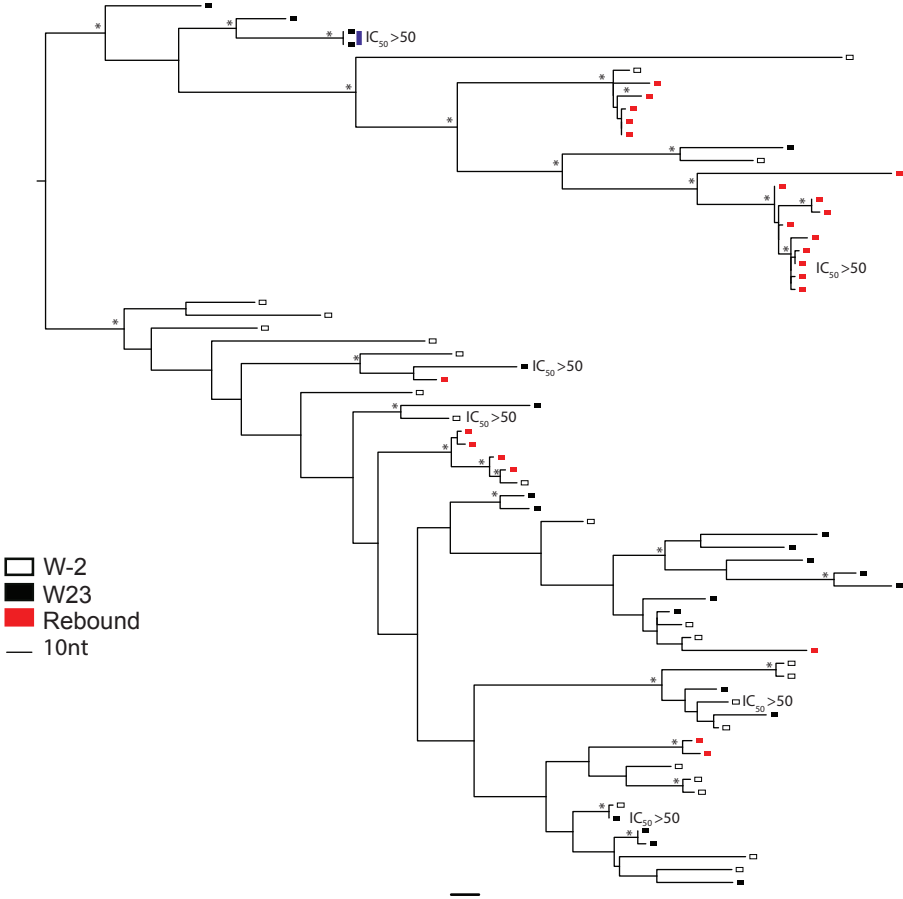


Supplementary Figure 6. Env sequences from Q²VOA cultures and rebound SGA.

Maximum likelihood phylogenetic trees of full-length *env* sequences of viruses from Q²VOA outgrowth cultures from the 6 participants not shown in Fig. 3. Viruses from week -2 are represented in empty black rectangles, week 23 in full black rectangles, and rebound SGA viruses in red rectangles. Asterisks indicate nodes with significant bootstrap values (bootstrap support $\geq 90\%$). The color on the rectangles near the group of sequences defines the clones as shown in Fig.1c. Numbers correspond to 3BNC117 IC₅₀ neutralization values. For rebound viruses, neutralization values were determined from culture-derived viruses.

Supplementary Figure 6 continued.

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Supplementary Figure 6 continued.

