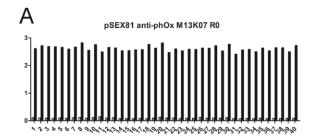
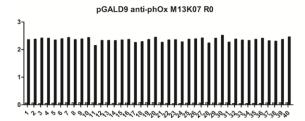
Table S1. Summary of TEM analysis

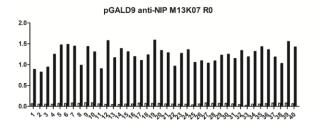
| Helper phage | Average length (no. counted) | No. polyphages |
|--------------|----------------------------------|----------------|
| M13K07 | 1.173 ± 0.082 μm (87) | 1 (2x genome) |
| DeltaPhage | $1.162 \pm 0.078 \ \mu m \ (59)$ | 2 (2x genome) |
| Hyperphage | $1.005 \pm 0.078~\mu m$ (39) | 3 (2x genome) |

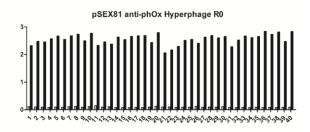
FIGURE S1

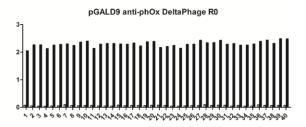


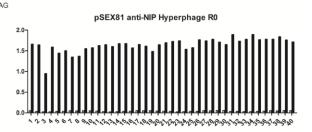


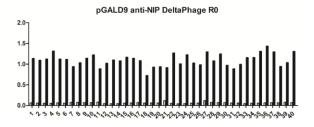












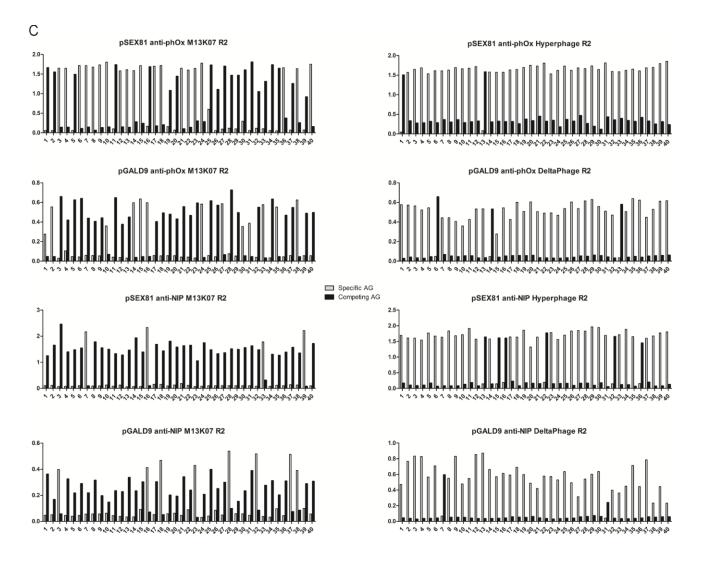


Figure S1. Single clone screening before and after two rounds of antigen selection. *E. coli* TOP10F´ cells were transduced with the input libraries or the amplified eluates after selection, plated in dilutions on agar plates containing 100 μg/ml ampicillin, and grown ON at 37°C. 40 random clones from each mock library were picked and grown in individual wells on a 96-well plate. The phagemids were rescued by helper phage super-infection and the resulting supernatants tested for reactivity to both antigens in a phage capture ELISA as described in Materials and Methods. Whereas M13K07 was used for pIII phagemid rescue, DeltaPhage was used with the pIX phagemid. The latter was done to amplify the signal at low valence pIX display to irrevocably reveal true positives. (**A**) R0 represents the original input libraries, where 1000 antigen specific phages were mixed with 10¹⁰ phages of the irrelevant specificity. Grey bars represent antigen specific reactivity (positive), and black bars represent the competing specificity (negative). (**B**) R1 represents the amplified output after one round of selection. (**C**) R2 represents the amplified output after two round of selection. The ELISA result is summarized in Table 1.