SUPPORTING INFORMATION

Figure S1. Amino acid sequences of VHHs selected for binding to Stx1 or Stx2. Sequences shown begin within framework 1 at the site of the primer binding employed in coding sequence DNA amplification from the immune alpaca cDNA (40) and continue through the end of framework 4. The parentheses at the end indicate whether the VHH contains a long hinge (lh) or a short hinge (sh). The three complementarity determining regions (CDRs) are indicated at the top.

Figure S2. Dendrogram of VHHs selected for binding to Stx1 or Stx2. The VHH sequences shown in Fig. S1 were analyzed for homology to create a dendrogram. Longer branch lengths indicate less sequence homology. The central node labeled as the ‘cross-specific homology group’ indicate VHHs that recognize both Stx1 and Stx2 and possess significant homology in CDR3 (see Fig. S1).

Figure S3. Western blots of VHH binding to Stx1 and Stx2. Purified Stx1 and Stx2 were resolved by SDS-PAGE and the gel stained for protein (stain). MW markers are shown to the left. Similar lanes containing Stx1 and Stx2 were transferred to filters for Western blot. The blots were incubated with 10 µg/ml of the indicated VHHs or control. Bound VHH was visualized with HRP/anti-E-tag. Blots were repeated once and produced similar results.