

**Supplemental Figure 3.** *Sequence alignment of STAU-399 and clonal variants.* A global alignment using Geneious was performed with the germline *IGHV1-69\*01* sequence, hybridoma IgG, and all clonal variants. Each HCDR and framework (FR) region is denoted with a consensus sequence shown. Point mutants that differ from the consensus are shown as individual amino acids, whereas conserved residues are represented as dots.