

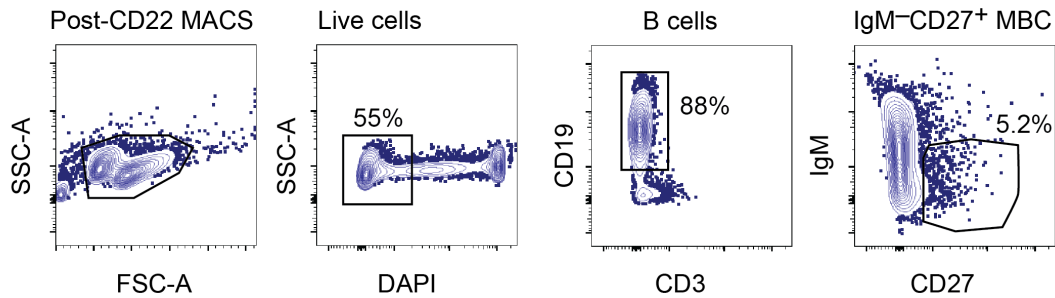
## Supplementary data

### Infant antibody and B cell responses following confirmed pediatric GII.17 norovirus infections functionally distinguish GII.17 genetic clusters

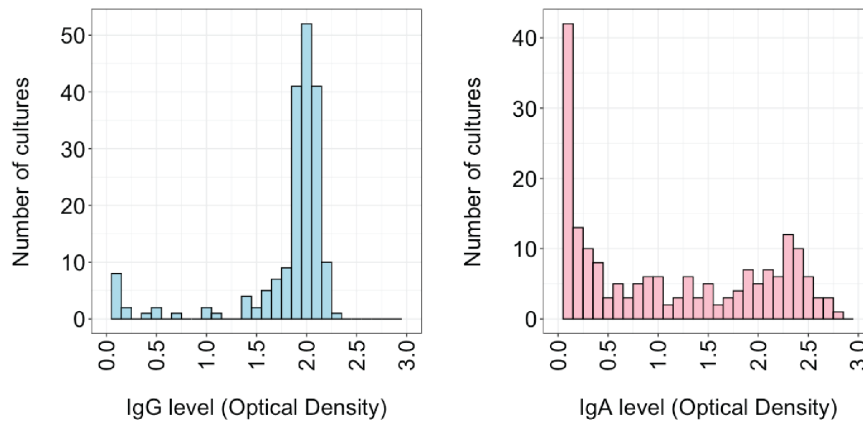
Camilla A. Strother, Paul D. Brewer-Jensen, Sylvia Becker-Dreps, Omar Zepeda, Samantha May, Fredman Gonzalez, Yaoska Reyes, Benjamin D. McElvany, April M. Averill, Michael L. Mallory, Anna M. Montmayeur, Verónica P. Costantini, Jan Vinjé, Ralph S. Baric, Filemon Bucardo, Lisa C. Lindesmith, and Sean A. Diehl

Figure S1

**A**



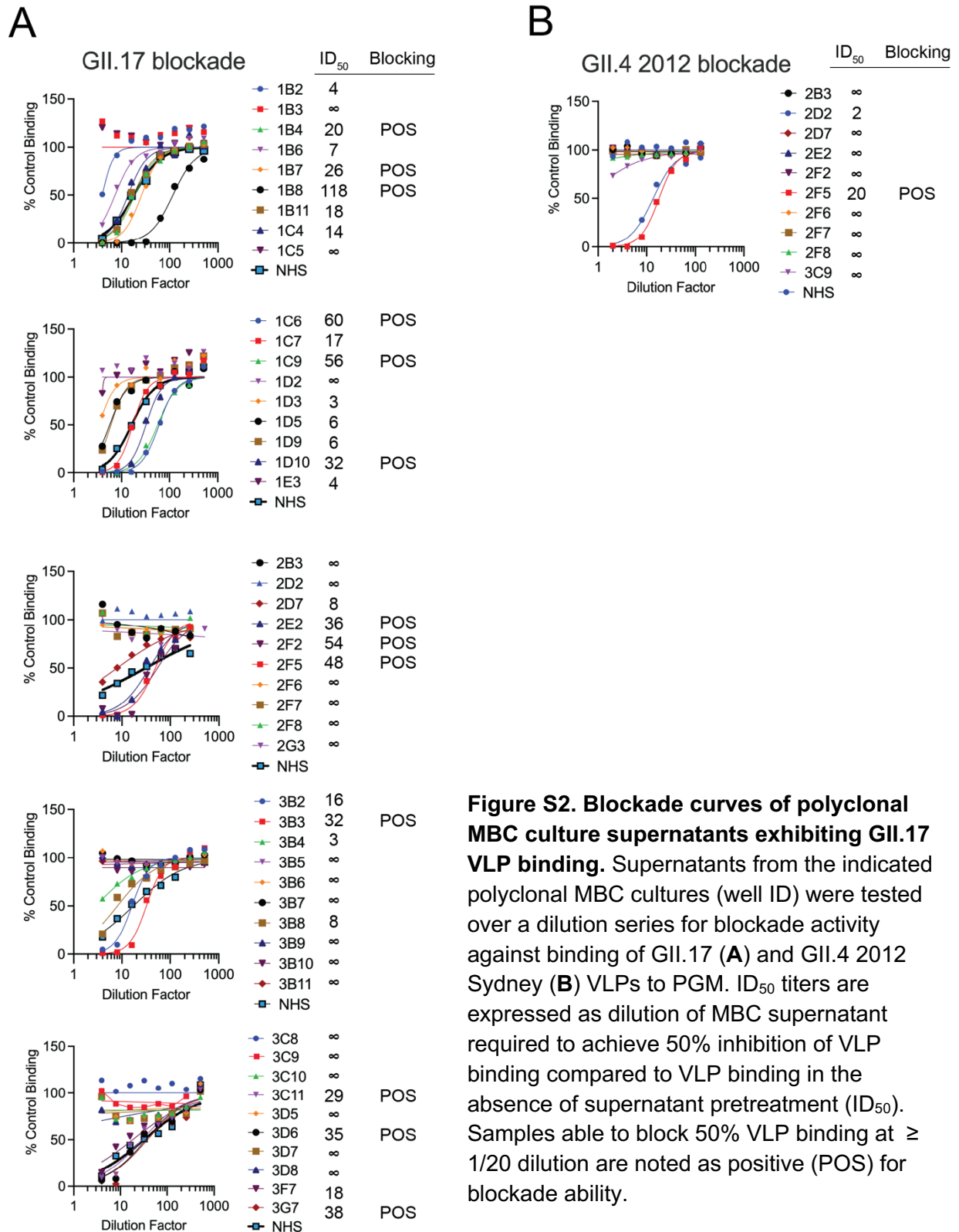
**B**

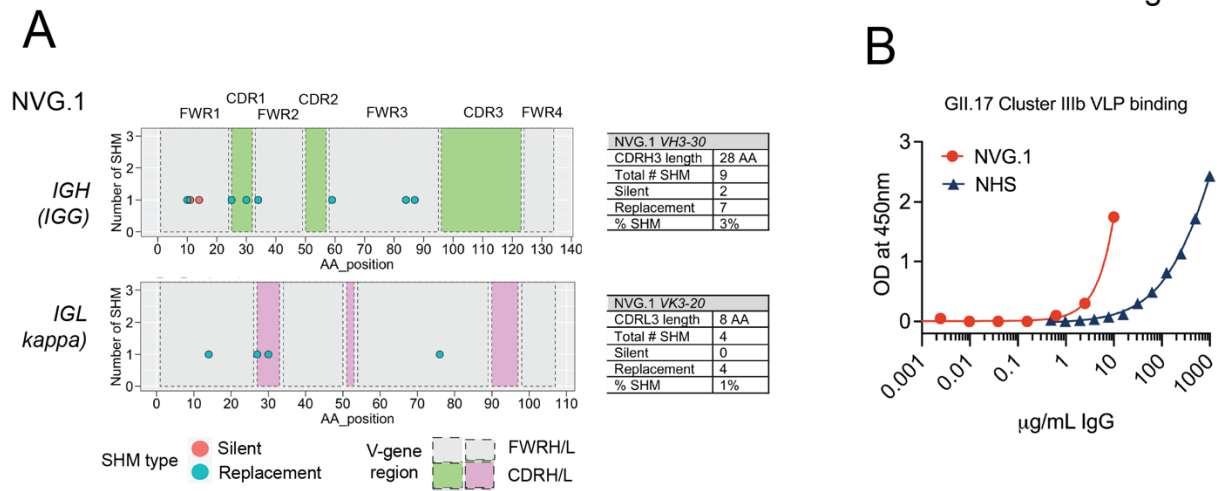


### Figure S1. Immortalized pediatric memory B cells produce IgG or IgA

(A). Fluorescence activated cell sorting of IgM<sup>+</sup>CD27<sup>+</sup> memory B cells from peripheral blood of an 11-month-old infant one month after a GII.17 norovirus episode. (B). 6XL-transduced GFP<sup>+</sup> cells were plated at 50 cells/well in 180 cultures and IgG (left) and IgA (right) were measured by ELISA and binned by optical density.

Figure S2





**Figure S3: A somatically mutated GII.17 IgG mAb from subject 434 with weak binding affinity** Somatic hypermutations (SHM, silent and replacement), number of nucleotide changes involved in, and the position of each mutation in paired variable heavy and light (VH/VL) gene regions from NVG.1 are shown. CDRH/L1-3, complementarity determining region heavy (light) 1-3; FWRH/L1-3, framework region heavy (light) 1-3. Percent SHM is total number of mutated nucleotides/ total number in FWR1+CDR1+FWR2+CDR2+ FWR3. **(B)** Binding of recombinant NVG.1 (IgG) to GII.17 cluster IIIb. NHS, normal human serum (positive control).

NVA.1 Heavy Chain protein sequence (IGHA1)

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          CDRH1
1         10 FWRH1  20         30         40 FWRH2  50 CDRH2
EVQLVESGGGLVKPGGSLRLSCAASGFFSFDYSMNWVRQAPGKGLEWVSSISSSSSSYIY
60        70 FWRH3  80         90        100 CDRH3  110 FWRH4
YADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARHLQLWLGFDIWGQGTMTVTS

SASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQD
ASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTSPSTPPT
PSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPE
RDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPP
PSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTFFAV
TSILRVAAEDWKKGDTFSCMGHEALPLAFTQKTIDRLAGKPTHVNSVVMAEVDGTCY
    
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IGHA1  
Fc region

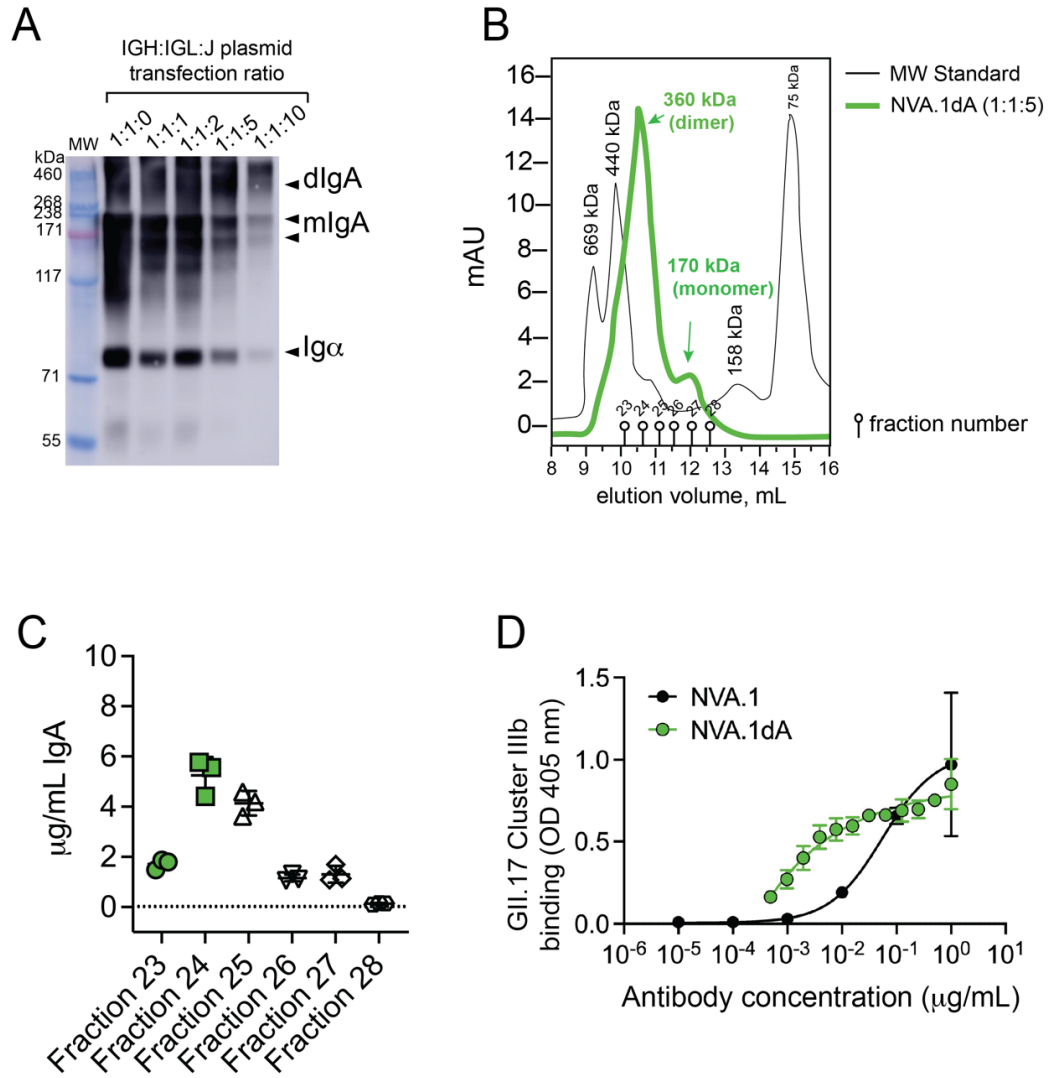
NVA.1 Light Chain protein sequence (IGLC2)

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          CDRL1          CDRL2
1         10 FWRL1  20         30         40 FWRL2  50
QSVLTQPPSASGTPGRRVTISCSGYSSNIGYNSVHWYQFPGAAPKLLIHSNNDRPSGV
60        70 FWRL3  80         90 CDR3  100        FWRL4  110
PDRFSGSKSGTSASLAISGLQSEDEADYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPS
VTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNNKYA
ASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
    
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IGLC2  
Fc region

**Figure S4. Amino acid sequence of native NVA.1 IGH and IGL genes.** FWR, framework region; CDR, complementarity determining region, and Fc regions are indicated.



**Figure S5. Expression and validation of dimeric IgA NVA.1.dA anti-GII.17 mAb.** (A) Non-reducing immunoblot analysis of IgA affinity purified from supernatants of HEK293A cells transfected with increasing ratios of J-chain plasmid DNA and fixed amounts (4.5 μg) of NVA.1 heavy and light chain (IGH and IGL) plasmid DNA. Anti-human IgA-HRP was used for detection. Molecular weight marker (MW) from 55-460 kDa is included for size validation of IgA species (Igα, IgA heavy chain; mIgA, monomeric IgA ~160 kDa; dIgA, dimeric IgA, ~360 kDa). (B) Size exclusion chromatography (SEC) of IgA affinity purified from cells transfected with 1:1:5 ratio of NVA.1 IGH:IGL:J-chain and molecular weight standards. (C) IgA concentrations in indicated SEC column fractions from (B). (D) GII.17 VLP binding by monomeric NVA.1 and dimeric NVA.1 (NVA.1dA).

Figure S6

