

SUPPLEMENTAL MATERIAL

Zhou et al., <http://www.jem.org/cgi/content/full/jem.20111906/DC1>

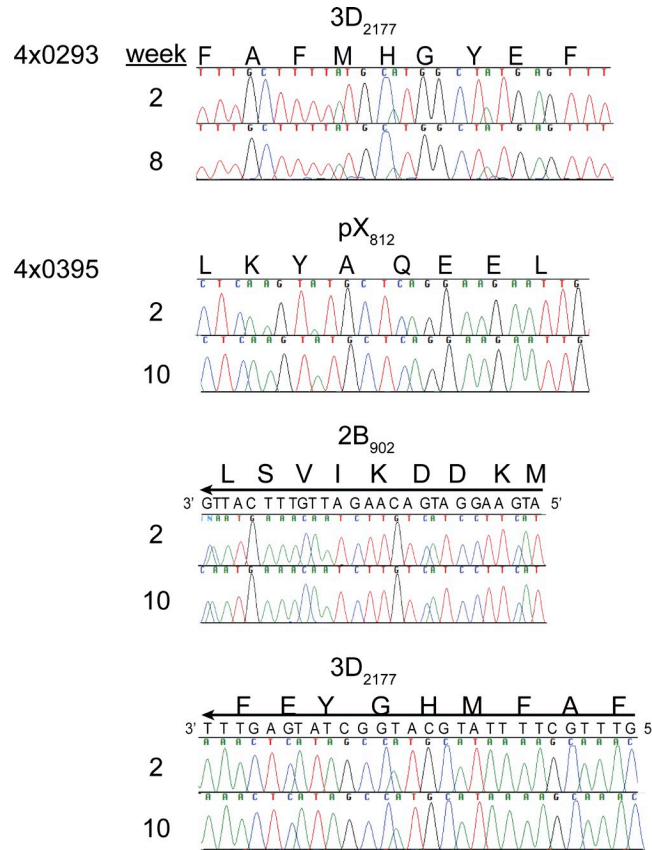


Figure S1. Sequencing of selected class I epitopes in HAV genomes. HAV RNA genomes isolated from the stool of animal 4X0293 at weeks 2 and 8 after infection and animal 4X0395 at weeks 2 and 10 after infection were reverse transcribed and amplified by nested PCR with primers that flanked epitopes 3D₂₁₇₇, pX₈₁₂, and 3D₂₁₇₇. Amplicons of 150–200 base pairs purified on PCR purification columns (QIAGEN) and DNA was sequenced in both directions by the UNC-CH Genome Analysis Facility on a 3730xl DNA Analyzer (Applied Biosystems).