

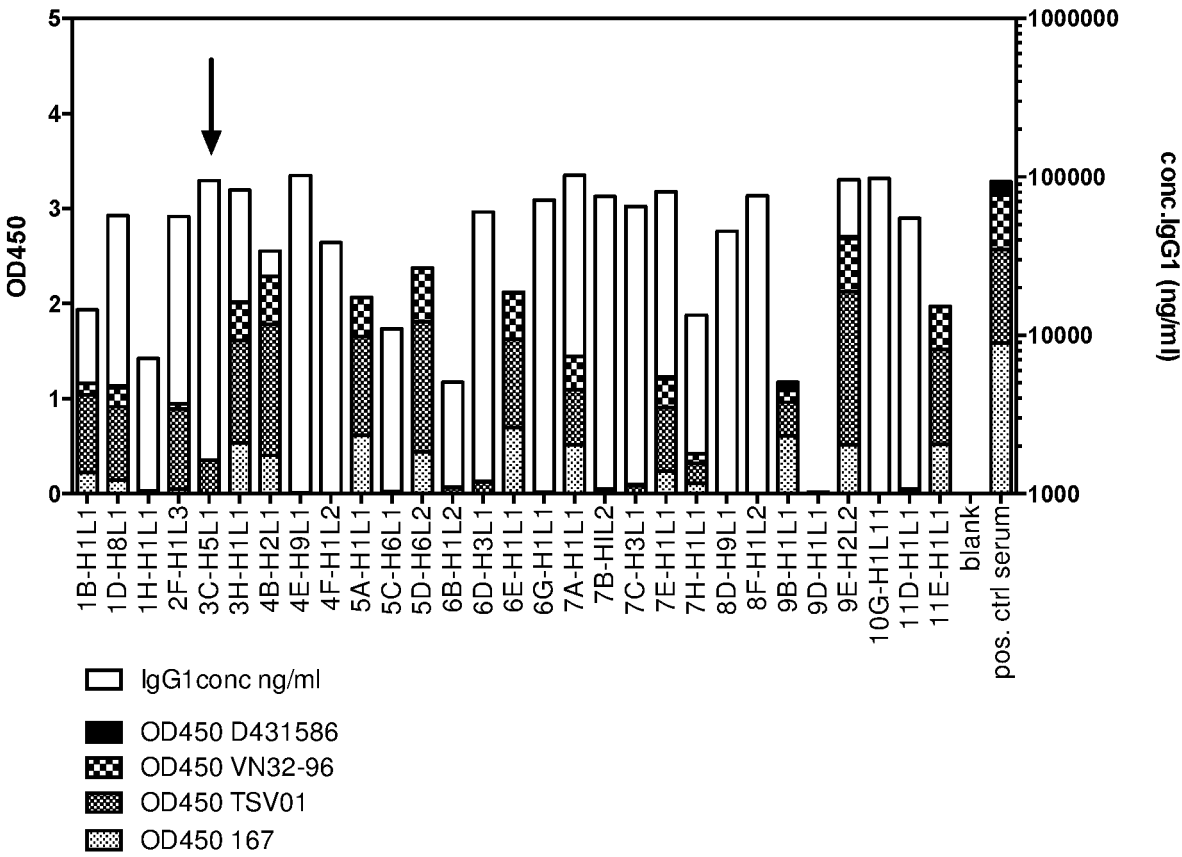


Fig. 1

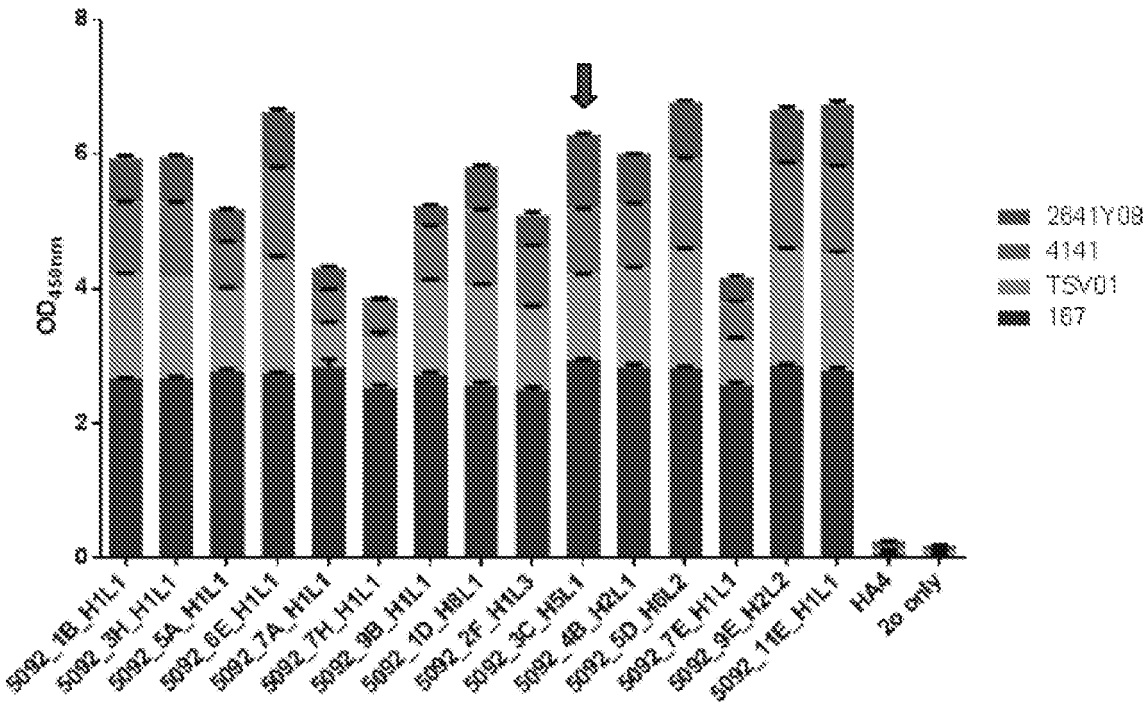


Fig. 2

2/17

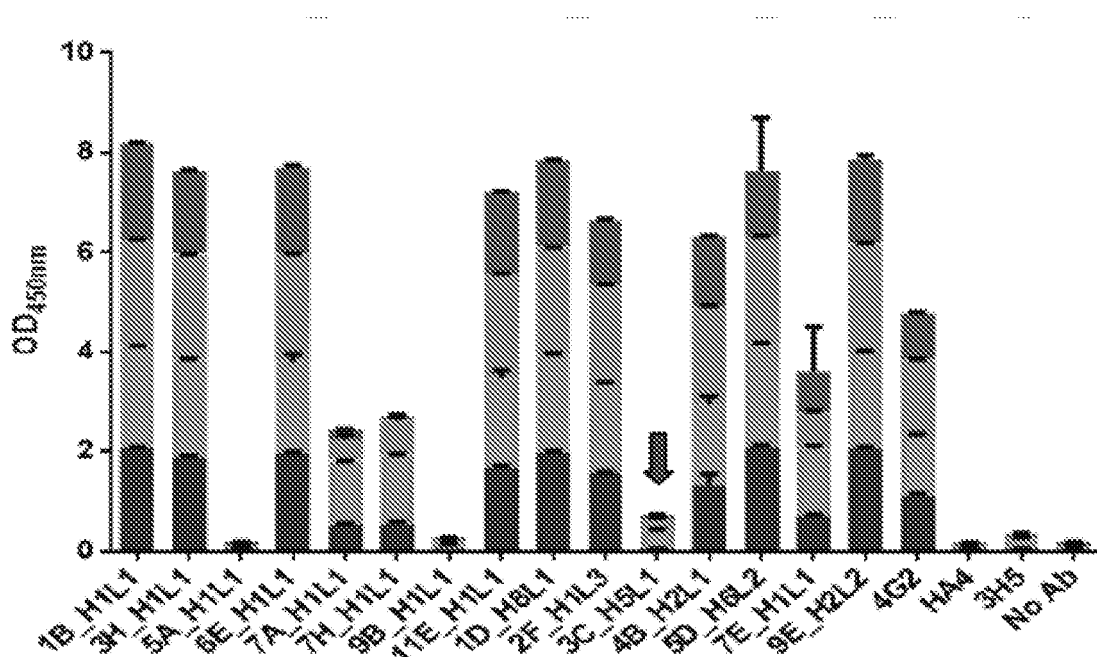
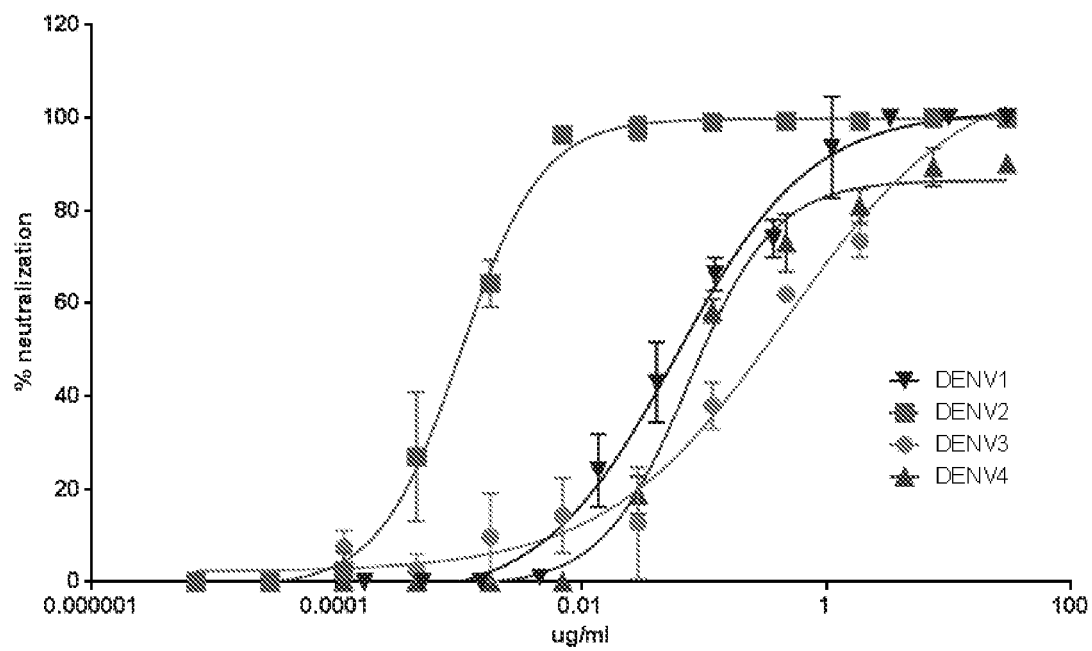


Fig. 3



	DENV1	DENV2	DENV3	DENV4
EC50	0.05955	0.001028	0.4657	0.07496

Fig. 4

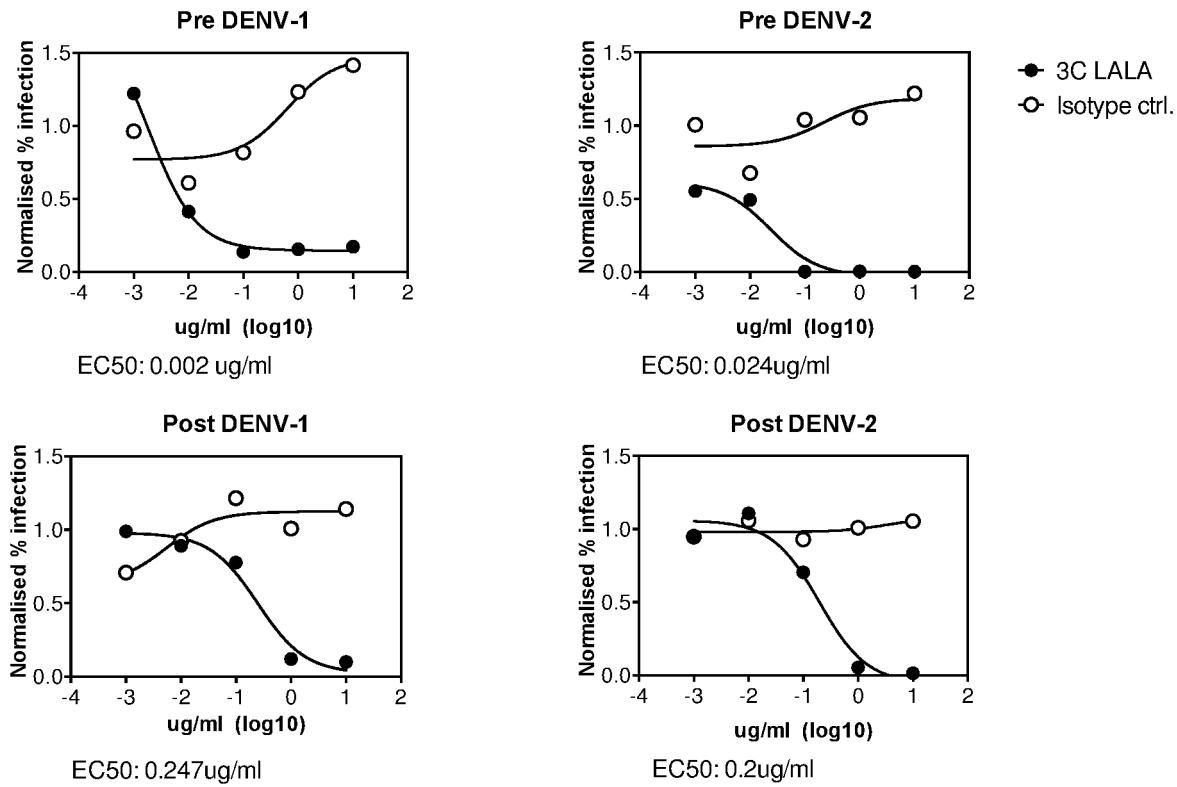
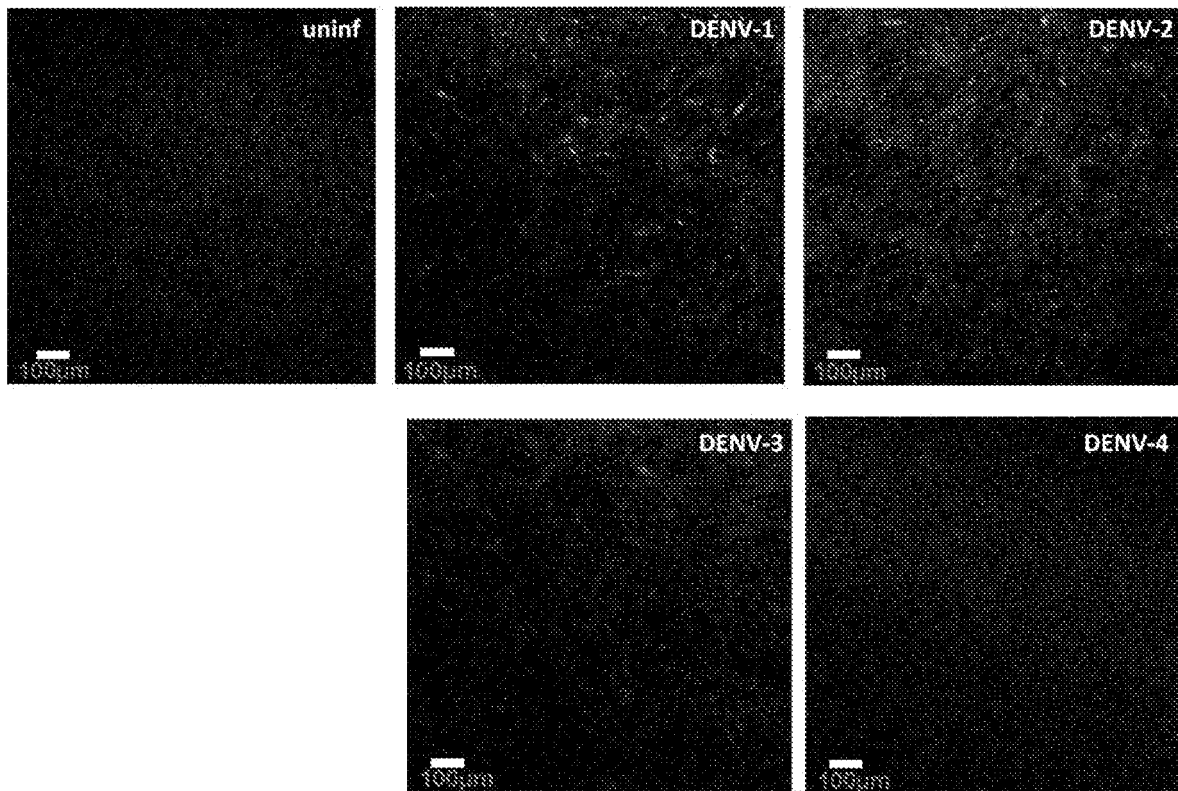


Fig. 5

4/17

3C H5L1



For comparison: a DENV-1-specific Ab binding to E protein

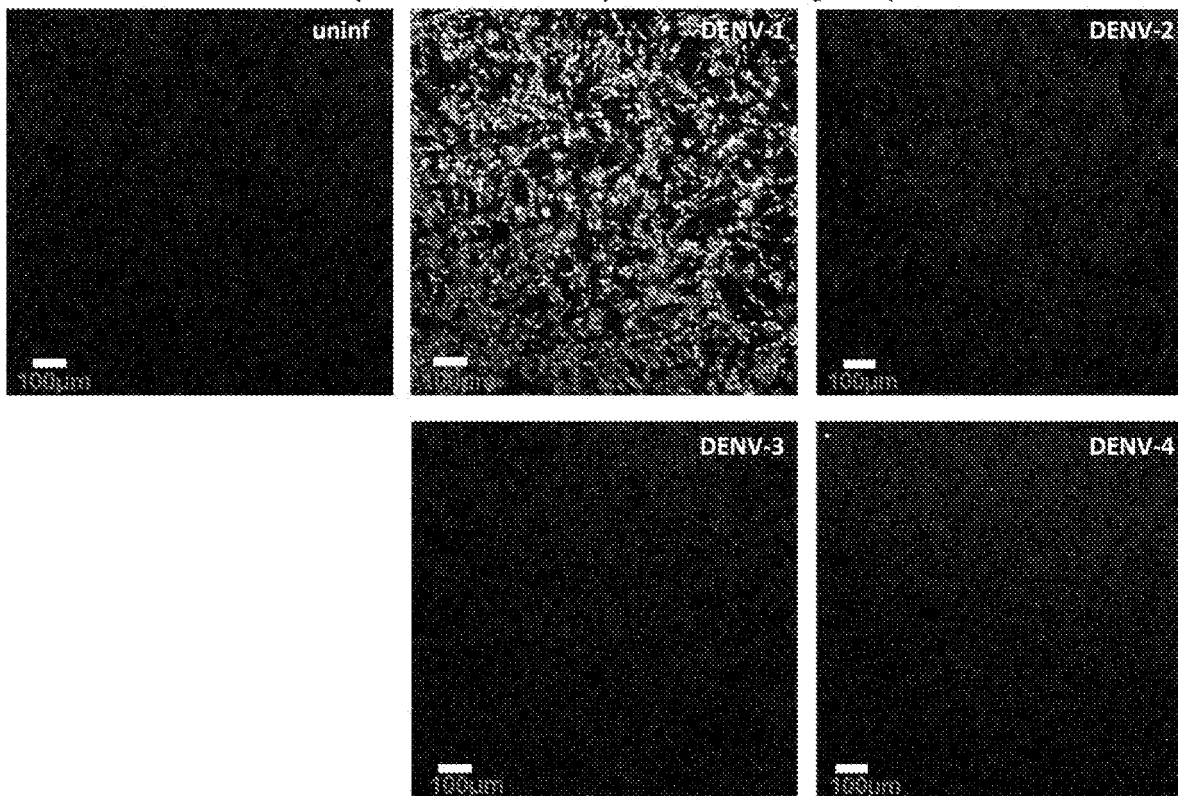


Fig. 6

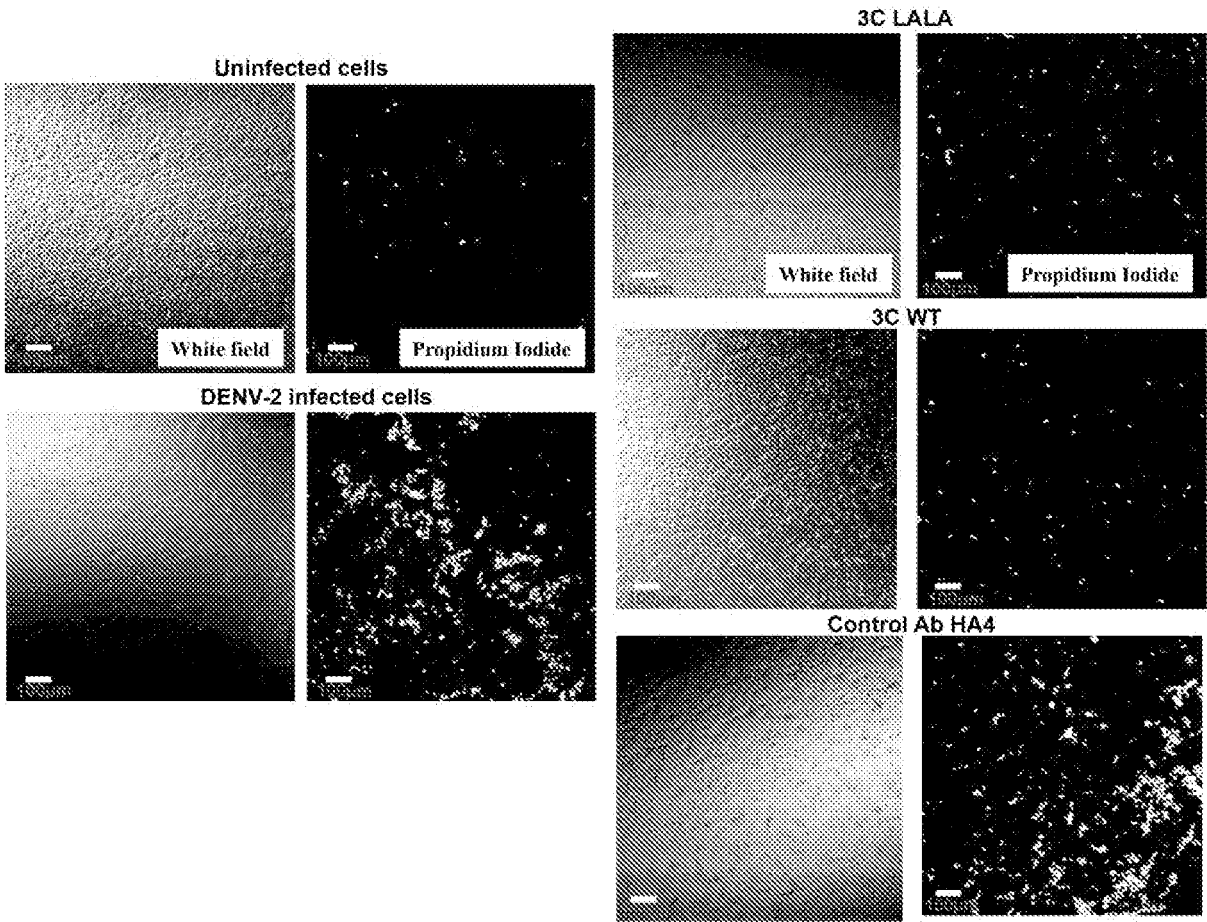


Fig. 7

6/17

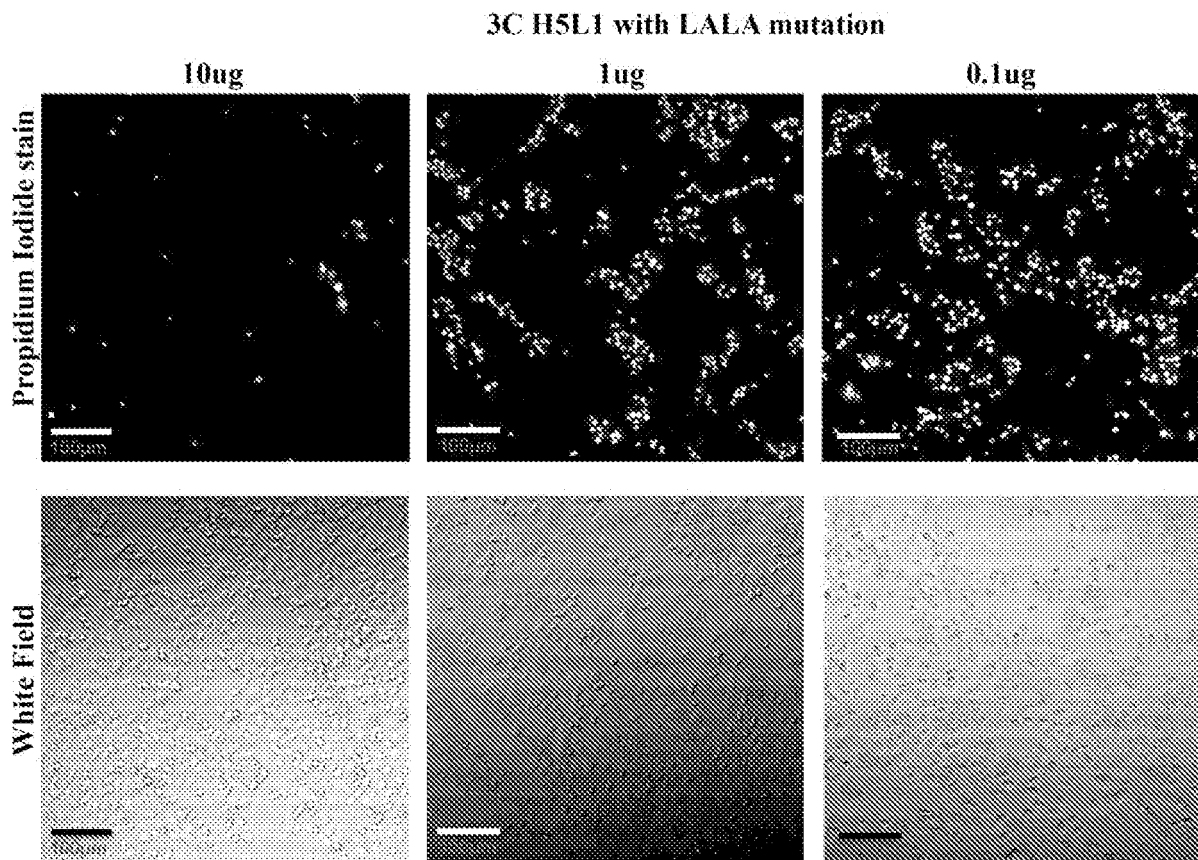


Fig. 8

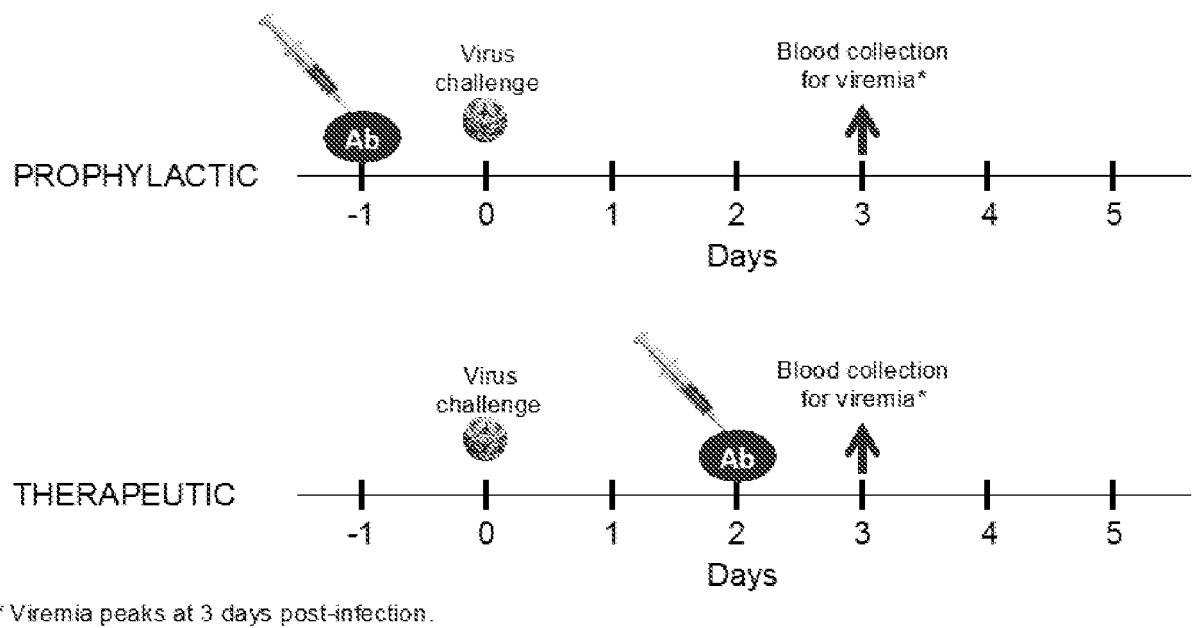


Fig. 9

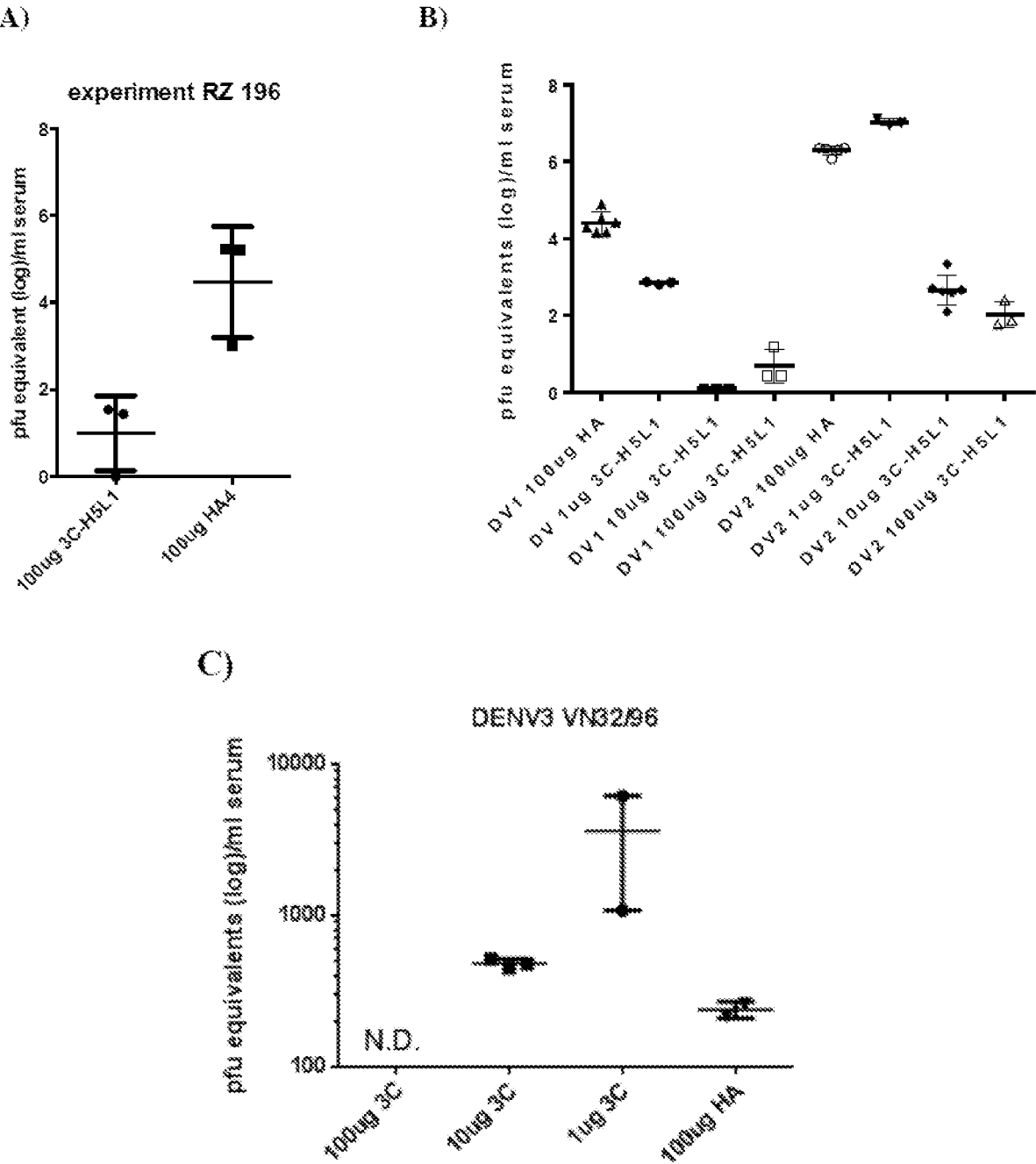


Fig. 10

8/17

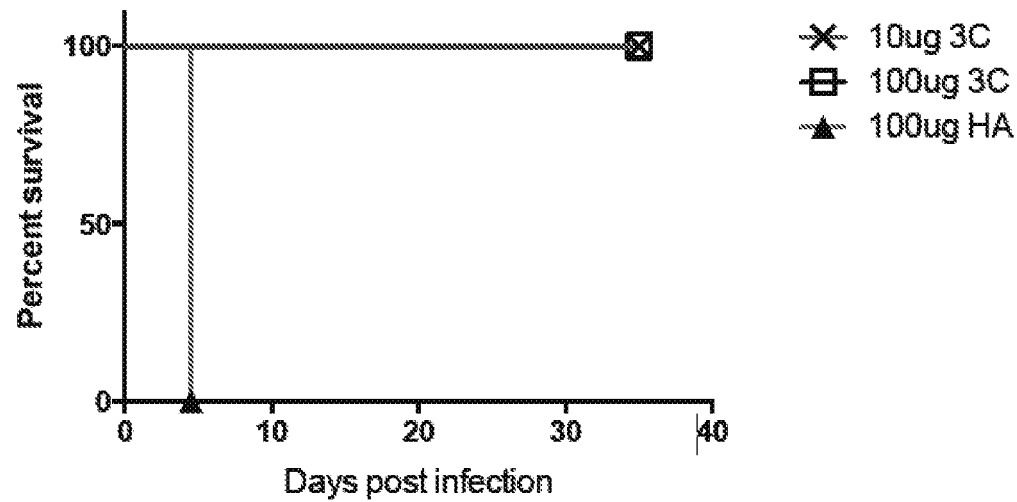


Fig. 11

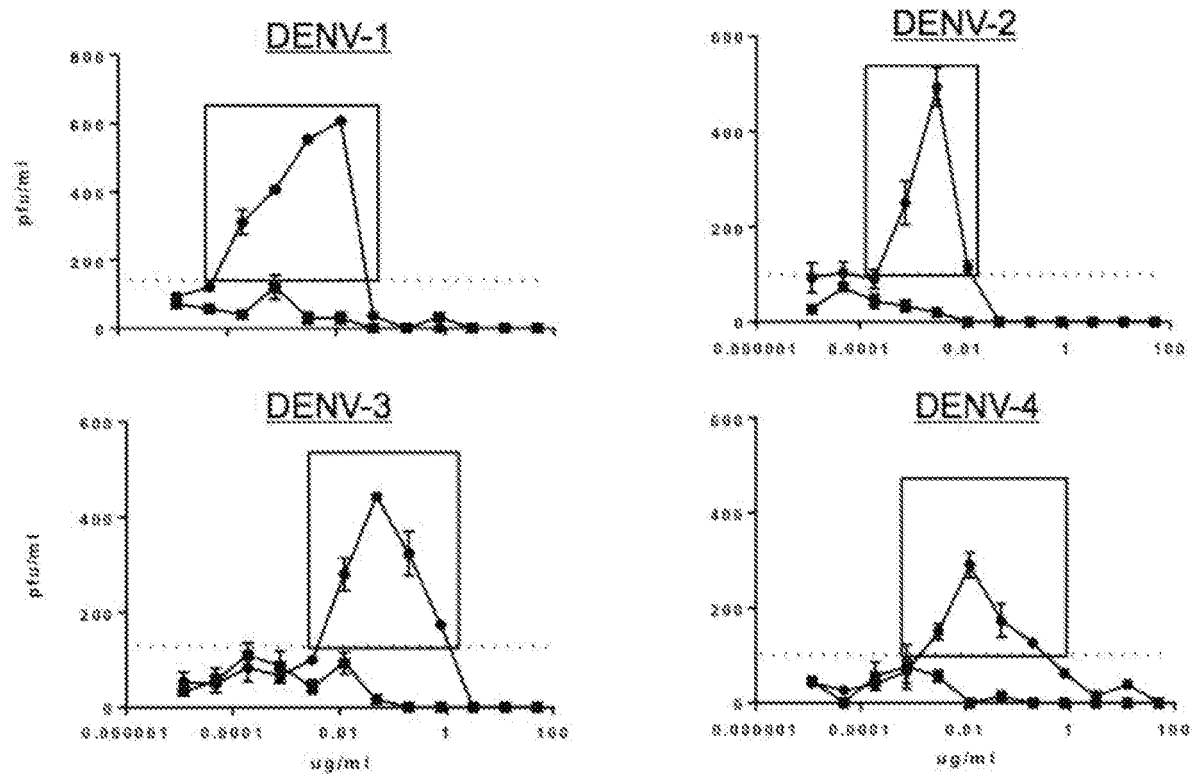
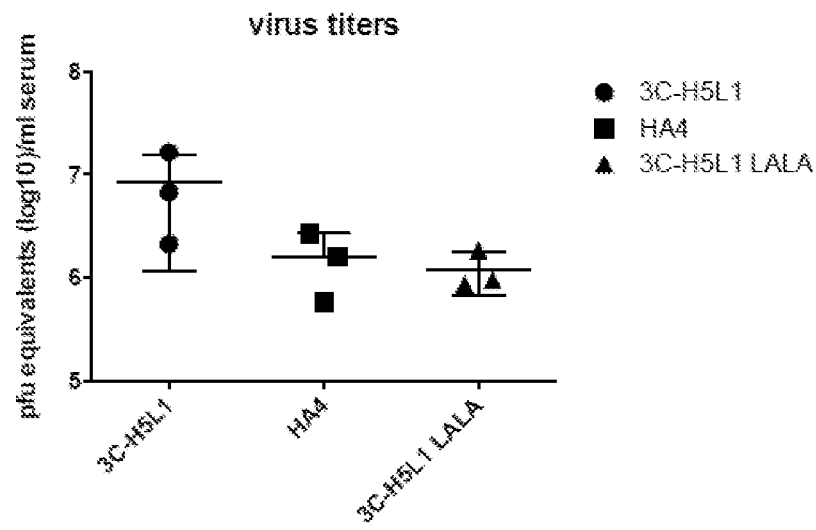


Fig. 12

9/17

A)



B)

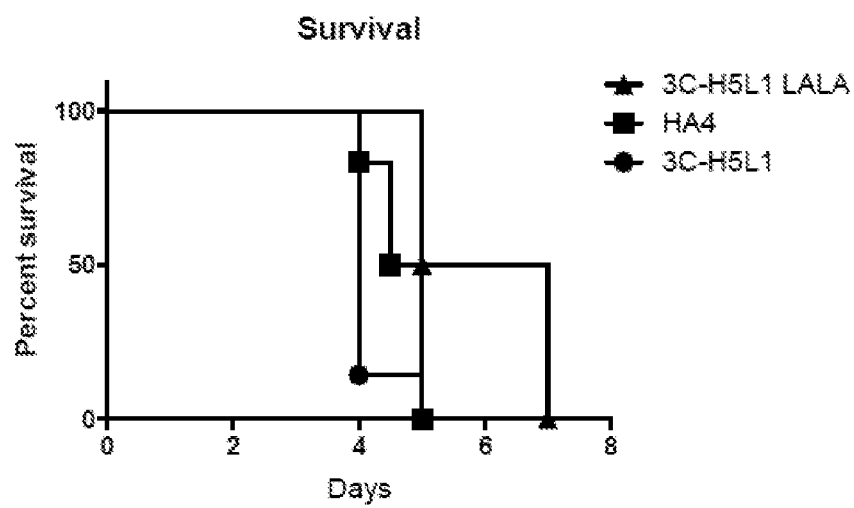
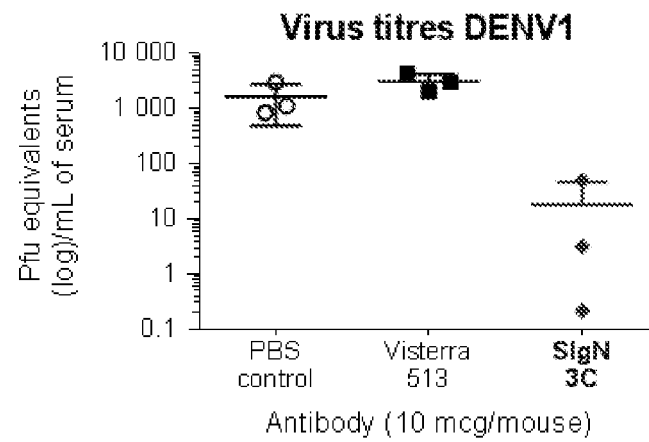


Fig. 13

10/17

A)



B)

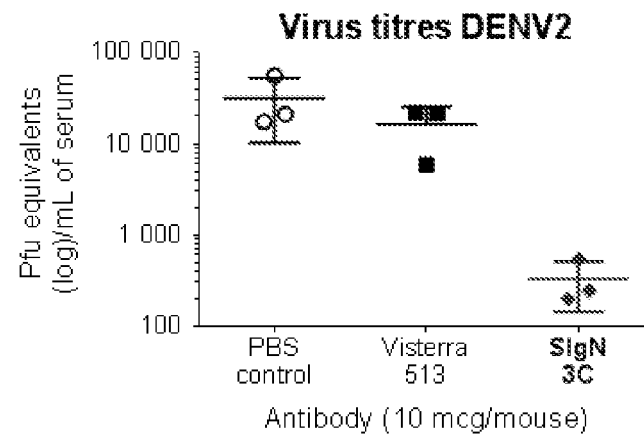
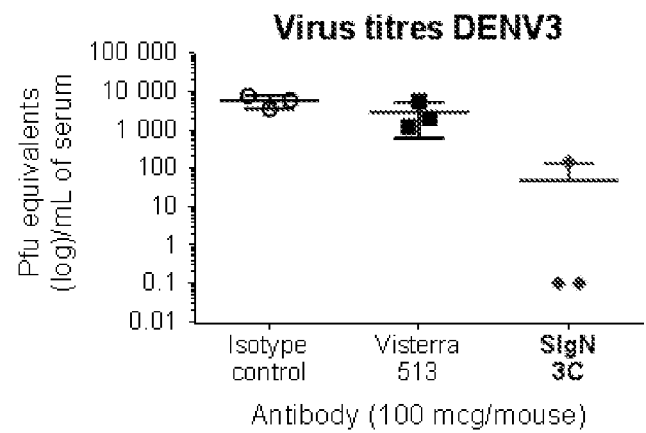


Fig. 14

11/17

A)



B)

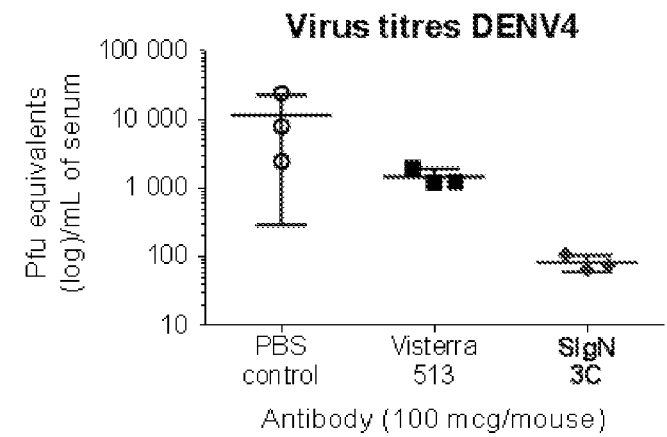
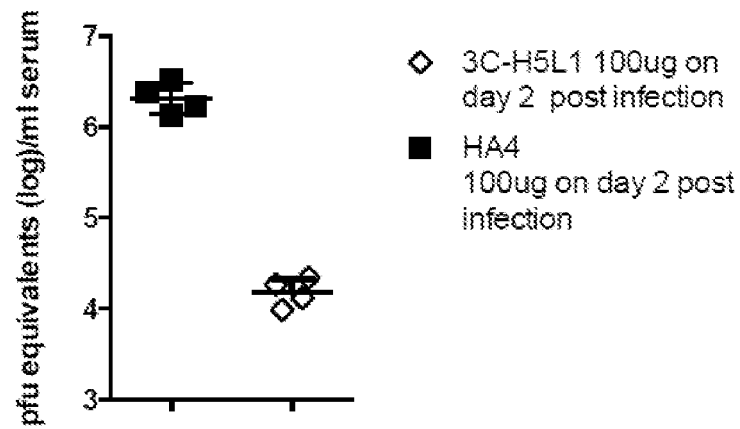


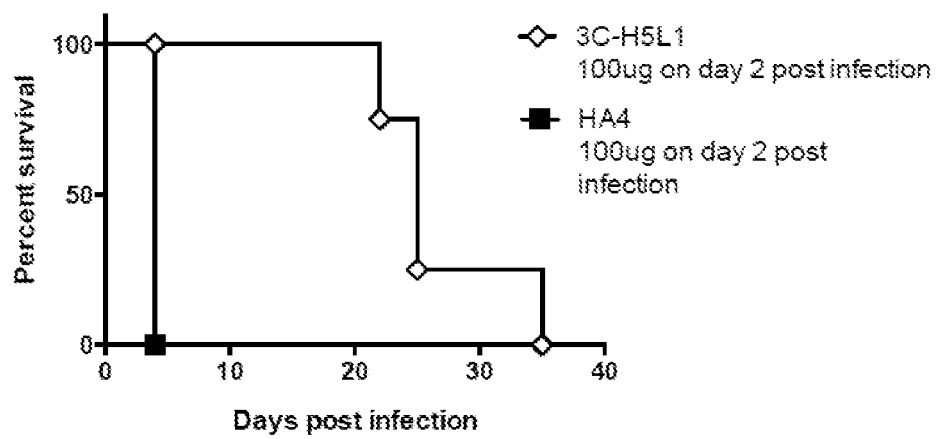
Fig. 15

12/17

A)

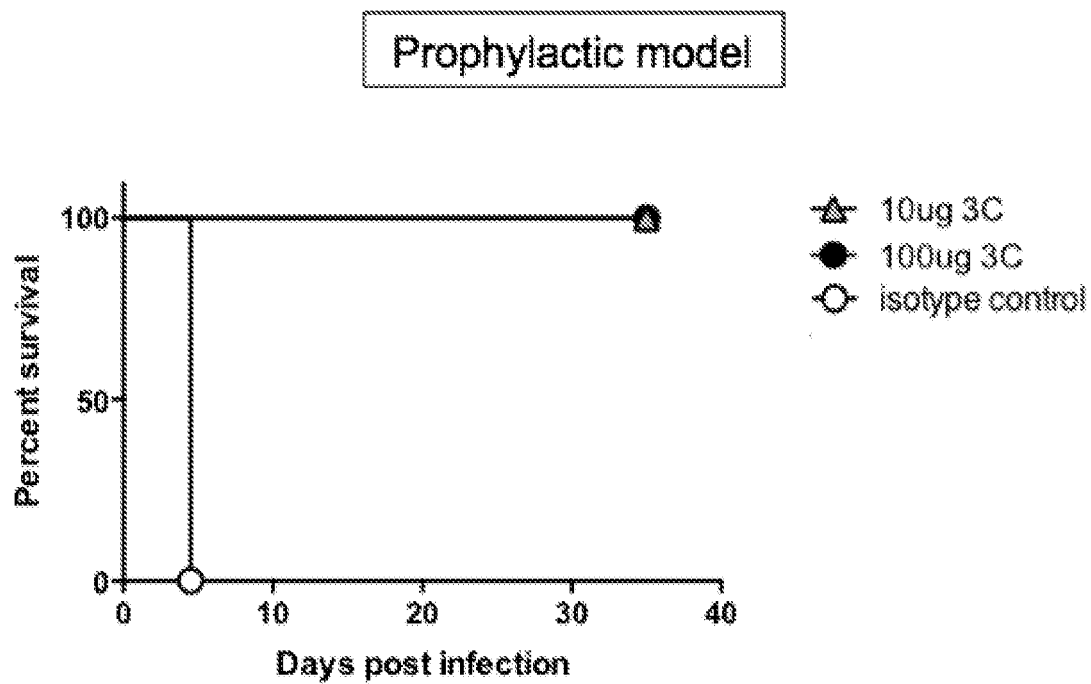


B)



13/17

A)



B)

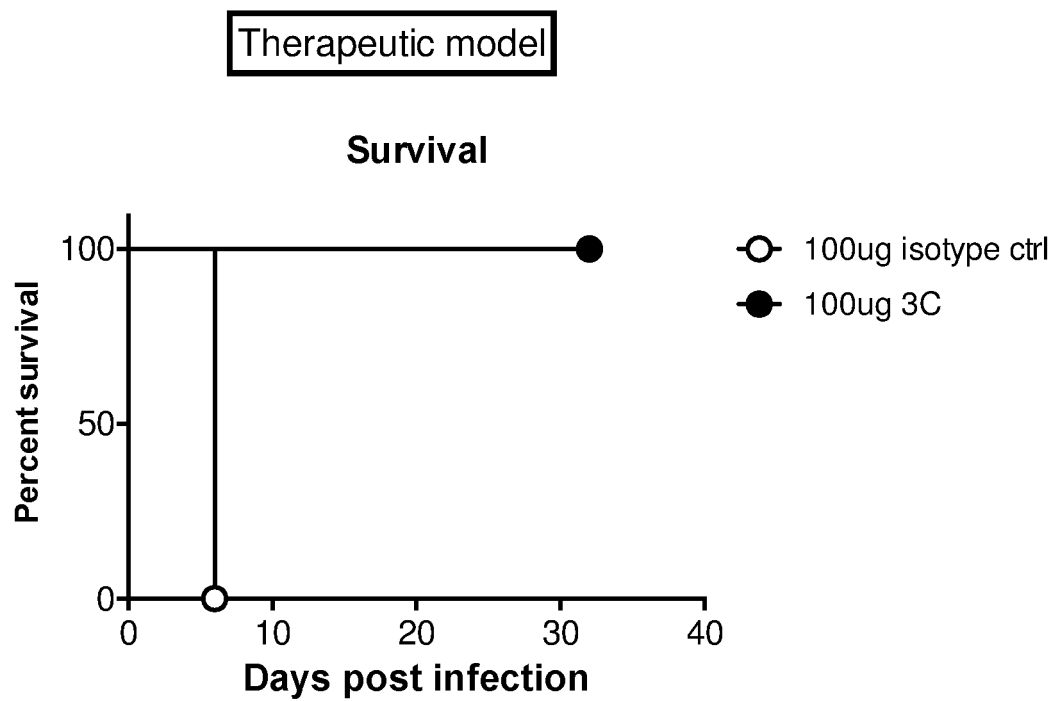


Fig. 17

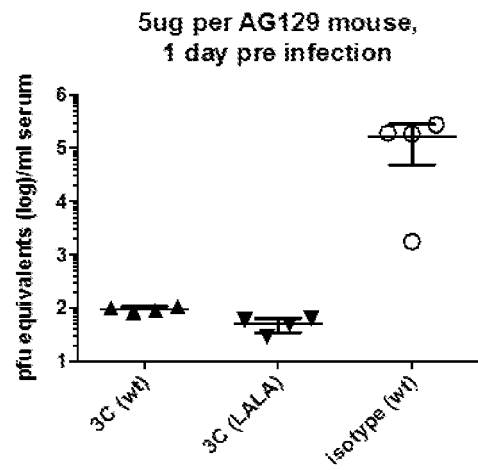
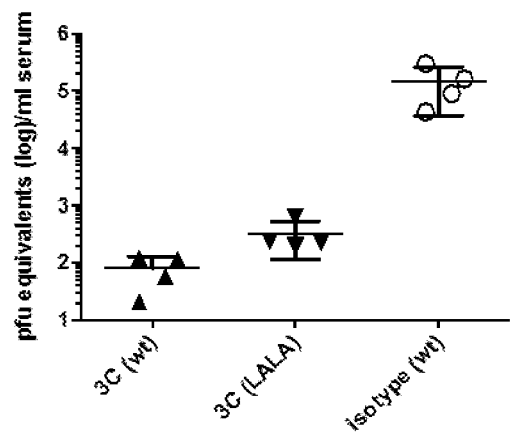


Fig. 18

A)



5 B)

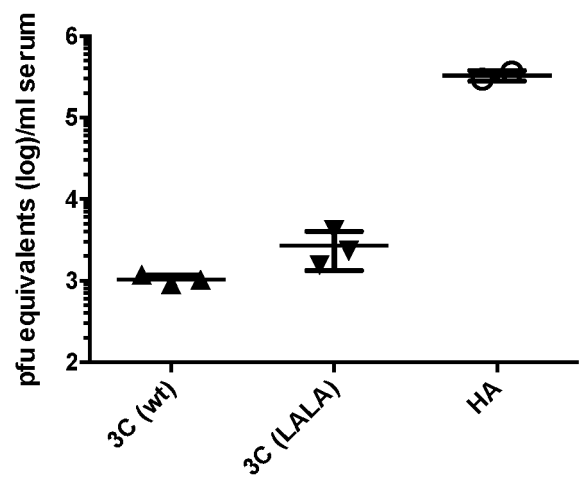
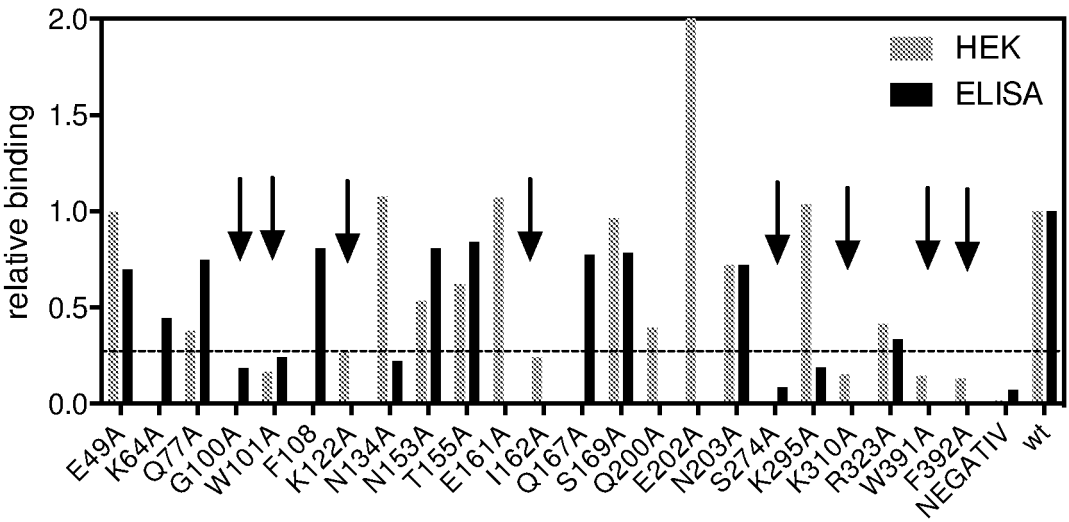


Fig. 19

A)



B)

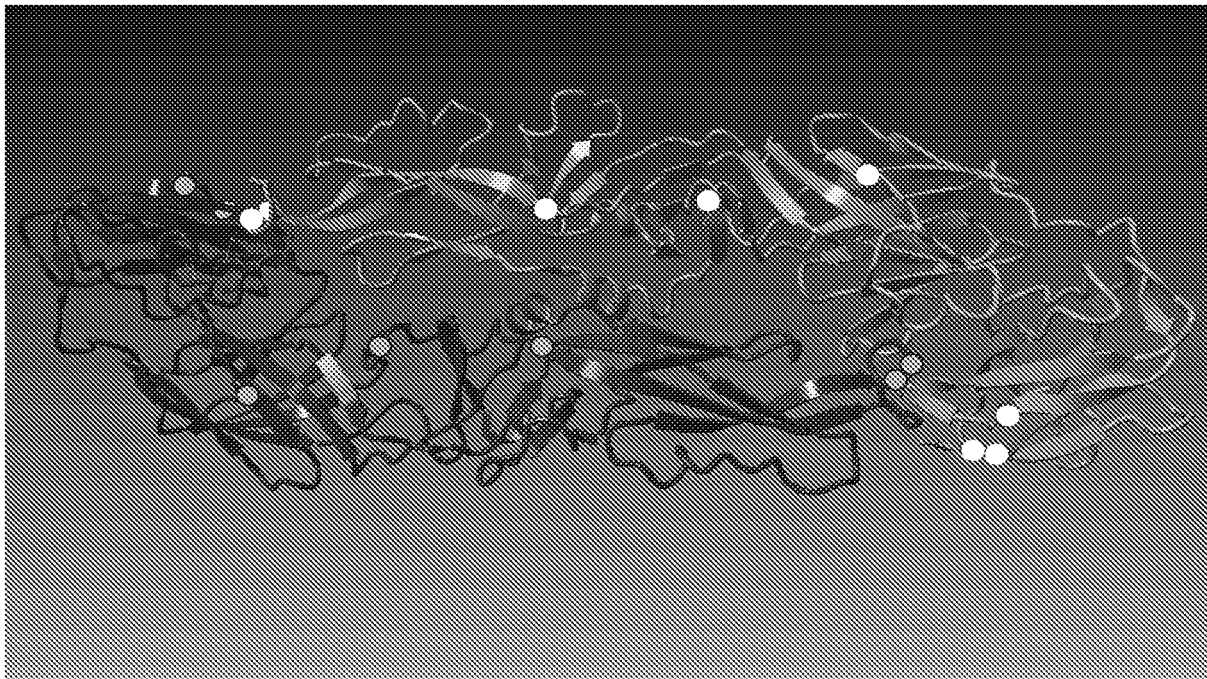


Fig. 20

16/17

Sequence for Ab 3C-H5L1

Heavy Chain variable region nucleotide sequence (SEQ ID NO: 1):

5 > He_3C5
 GAGGTCCAGCTGGTACAGTCTGGGCCTGACGTCGAGAAGCCTGGGGCCTCAGTGAAGGTTTC
 CTGCAAGGCATCTGGATACACCTTCACCAGCAACTATATACACTGGGTGCGACAGGCCCTG
 GACAAGGGCTTGAGTGGATGGGGGTAATCAACCCTAGGGGTGGTAGCACAGCCAGCGCACAG
 AAATTCCAGGGAAGAATCACCATGACCAGGGACACGTCCACGAGCACAGTTTACATGGAAC
 10 GAGCAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGGGGGAAGGGCCCTTT
 TCTATGATAGTTACACGACCCCCGAGACGGAGGGTCGTGGTGGTTCGACCCCTGGGGCCAG
 GGAAGCCTGGTCACCGTCTCCTCA

Heavy chain variable region Amino Acid Sequence (SEQ ID NO: 9):

15 > He_3C5
 EVQLVQSGPDVEKPGASVKVSCKASGYTFTSNYIHWVRQAPGQGLEWMGVINPRGGSTASAQ
 KFGGRITMTRDTSTSTVYMEISSLRSDDTAVYYCARGGRALFYDSYTTPRDGGSWWFDPWGQ
 GSLVTVSS

CDR Analysis (He_3C5)

(SEQ ID NO: 3) (SEQ ID NO: 4) (SEQ ID NO: 5)

----CDRH1---> <--CDRH2--> <---CDRH3----
 25 GYTFTSNY....___INPRGGST..___ARGGRALFYDSYTTPRDGGSWWFDP

Light chain variable region nucleotide sequence (SEQ ID NO: 2):

> Li_3C1
 GACATCCAGTTGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCTT
 CACTTGCCAGGCGAGCCAGGACATTAGGAAGTATTTAAATTGGTATCAGCAGAAACCAGGGA
 30 AAGCCCCCTAAACTCCTAATCTACGATGCATCCAATTTGAAAACAGGGGTCCCATCAAGGTTC
 AGTGGAAGTGGATCTGGGACAGATTTTACTTTACCATCAGCAGCCTGCAGCCTGAAGATGT
 TGCAACATACTACTGTCAACAGTTTGATGATCTCCCGATCACCTTCGGCCAGGGGACACGAC
 TGCAGATTAAACGA

Light chain variable region Amino Acid Sequence (SEQ ID NO: 10):

> Li_3C1
 DIQLTQSPSSLSASVGDRTFTFCQASQDIRKYLNWYQQKPGKAPKLLIYDASNLKTGVPSRF
 40 SGSGSGTDFTFTISSLPEDVATYYCQQFDDLPIITFGQGTRLQIK

CDR Analysis (Li_3C1)

(SEQ ID NO: 6) (SEQ ID NO: 7) (SEQ ID NO: 8)

----CDRL1---> <--CDRL2--> <---CDRL3----
 45 QDIRKY.....___DAS.....___QQFDDLPIIT

Fig. 21

17/17

**3C H5L1 heavy chain constant region with LALA mutation
(nucleotide sequence)**

5 GCTTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGTCGACCTCT
GGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG
GTGTCGTGGAACCTCAGGCGCCCTGACCAGTGGCGTGCACACCTTCCCGGCTGTCCTA
CAGTCCTCAGGACTCTACTCCCTCAGTAGTGTGGTGACCGTGCCCTCCAGTAGTTTG
GGCACCAGACCTACATCTGCAACGTGAATCACAAGCCCAGTAACACCAAGGTGGAC
AAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCA
10 CCTGAGGCCGCGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACC
CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGTCACGAA
GACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG
ACAAAGCCGCGGGAGGAGCAGTACAACAGTACGTACCGTGTGGTCAGTGTCTCACC
GTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
15 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGT
CTGACCTGCCTGGTCAAAGGCTTCTATCCAGTGACATCGCCGTGGAGTGGGAGAGT
AATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGC
TCCTTCTTCTCTACAGTAAGCTCACCGTGGACAAGAGTAGGTGGCAGCAGGGGAAC
20 GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGT
CTCTCCCTGTCTCCG (SEQ ID NO: 11)

**3C H5L1 heavy chain constant region with LALA mutation
(amino acid sequence)**

25 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA
PEAAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
30 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSP (SEQ ID NO:
12)

Fig.22