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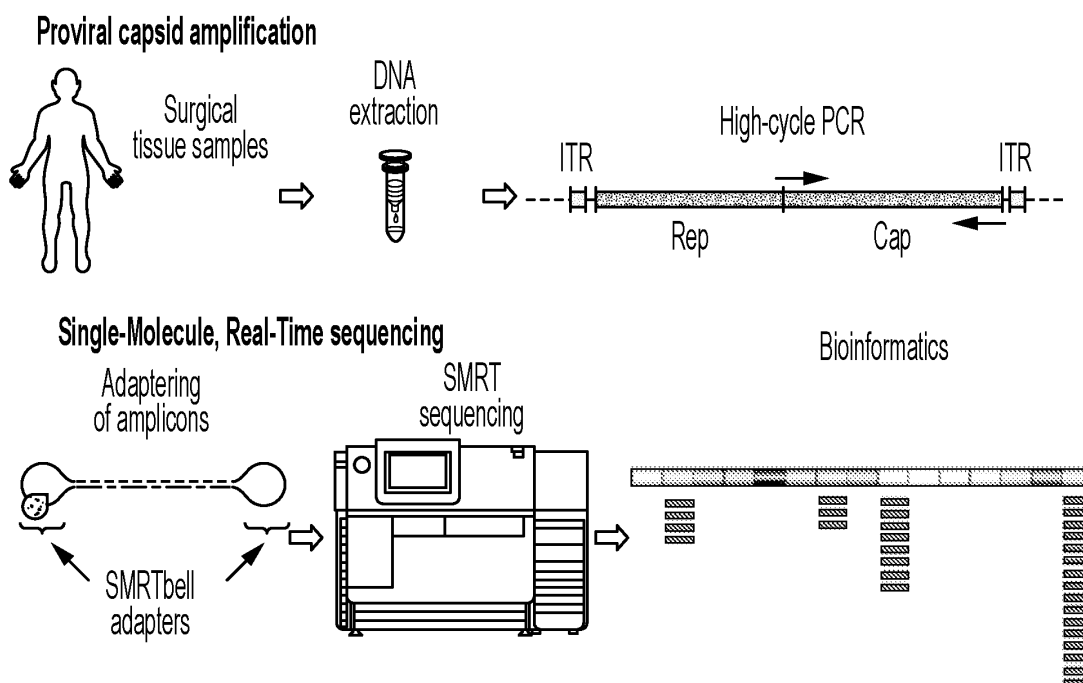


FIG. 1A

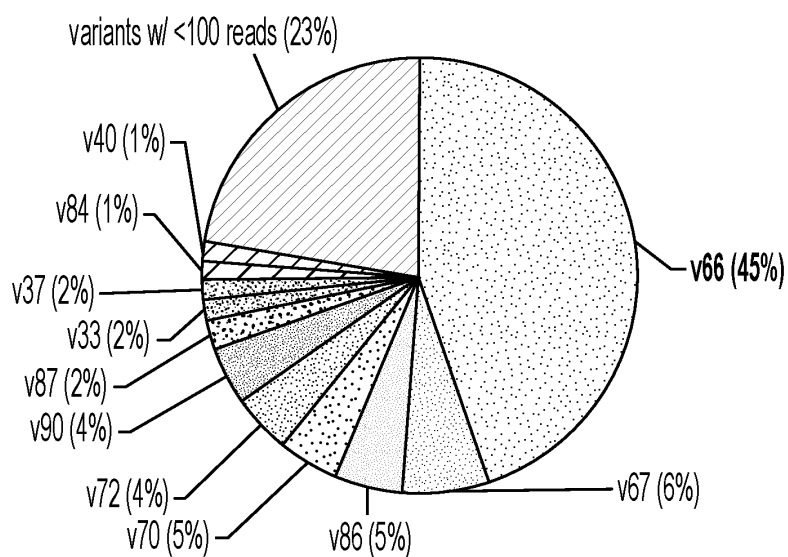


FIG. 1B

Unique AAVv66 a.a.	Capsid domain	Variable region
K39Q	VP1	-
V151A	VP2	-
R447K	VP3	VR-IV
T450A		
Q457M		
S492A		
E499D		VR-V
F533Y		VR-VI
G546D		VR-VII
E548G		VR-VIII
R585S		
R588T		
A593T		

FIG. 1C

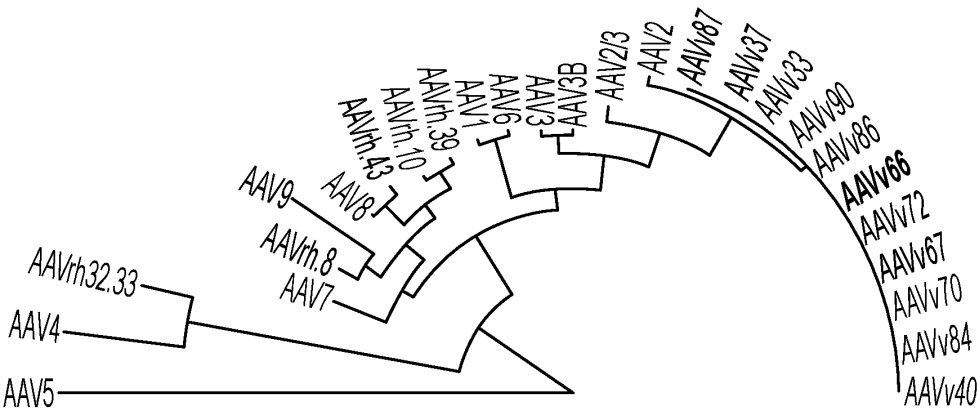


FIG. 1D

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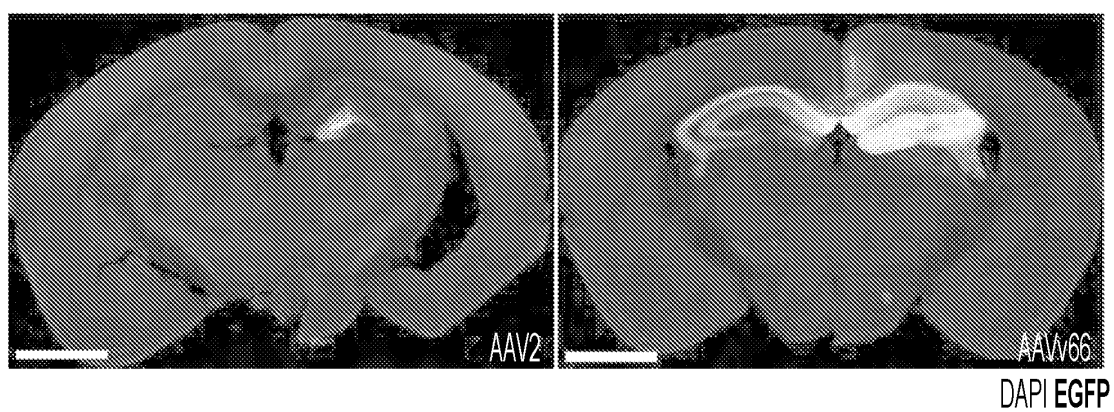


FIG. 2A

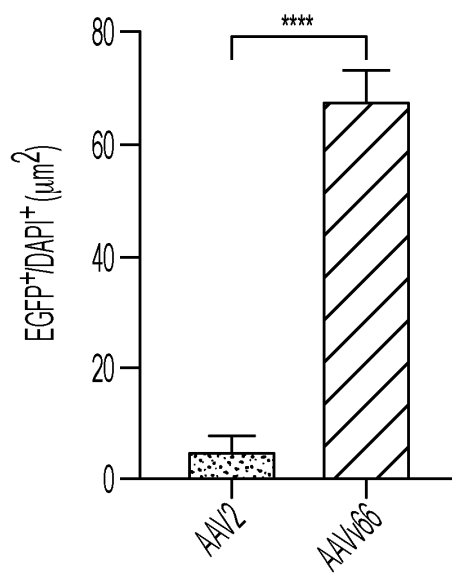


FIG. 2B

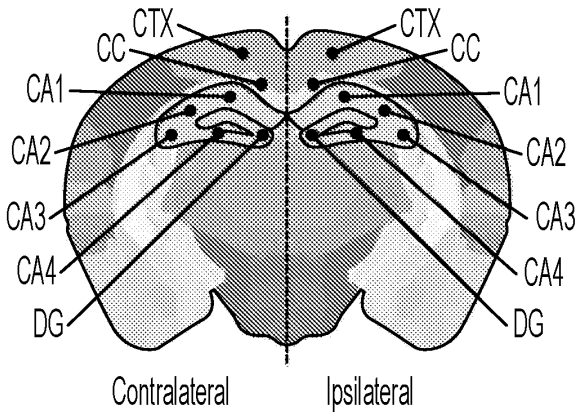


FIG. 2C

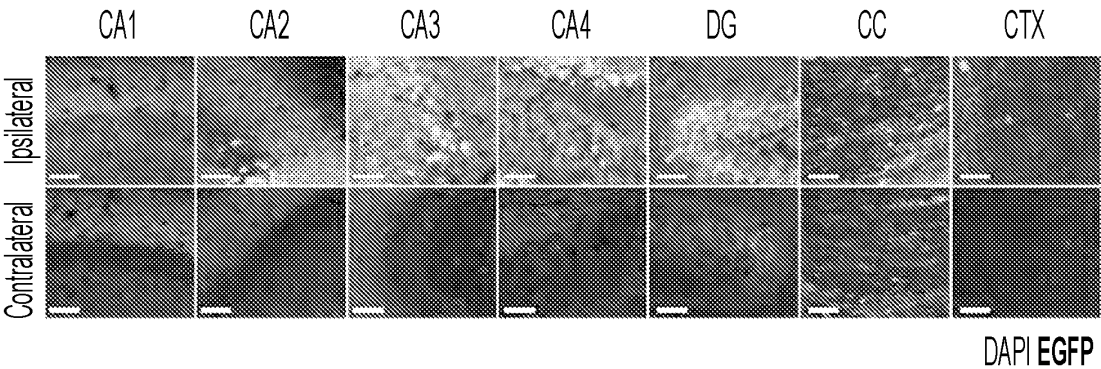


FIG. 2D

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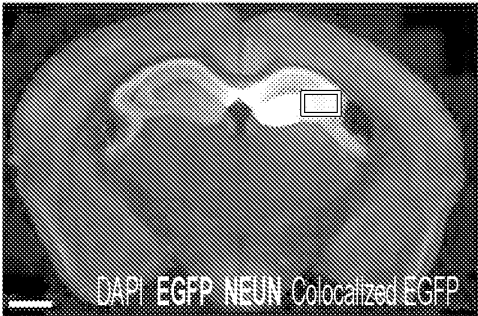


FIG. 3A

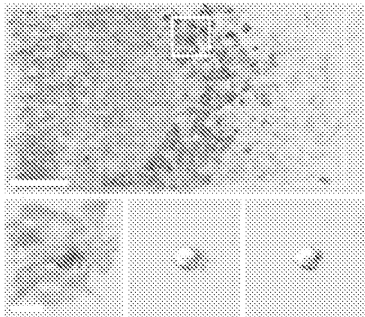


FIG. 3B

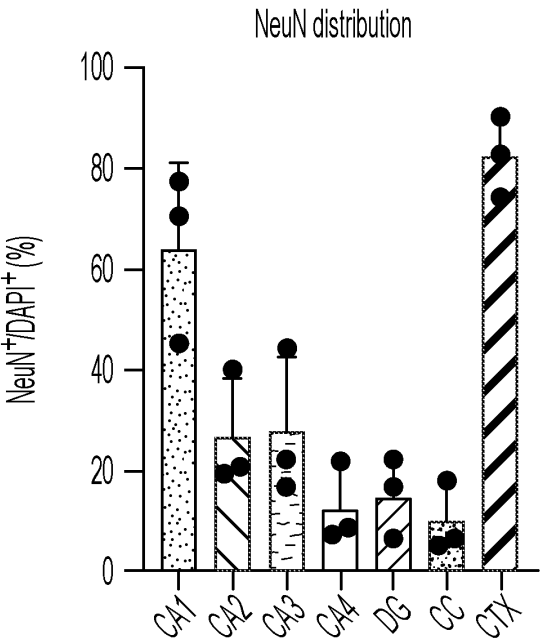


FIG. 3C

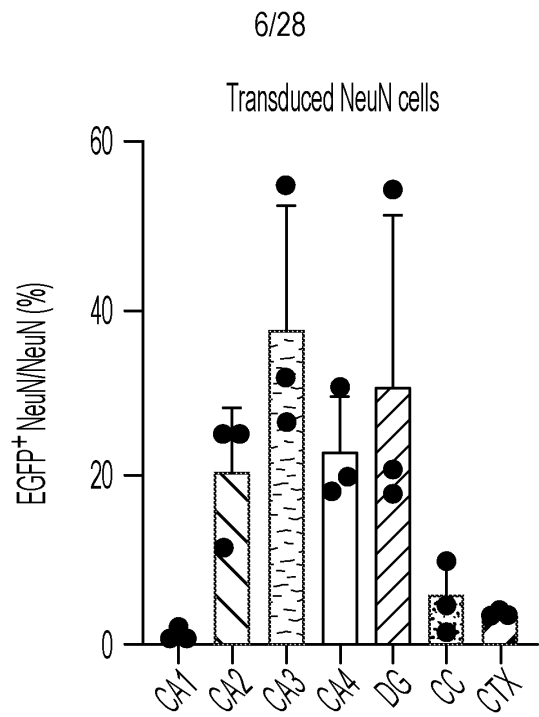


FIG. 3D

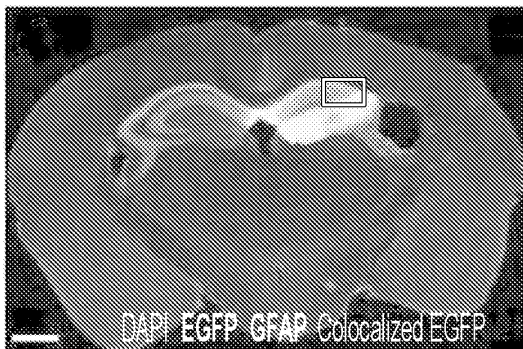


FIG. 3E

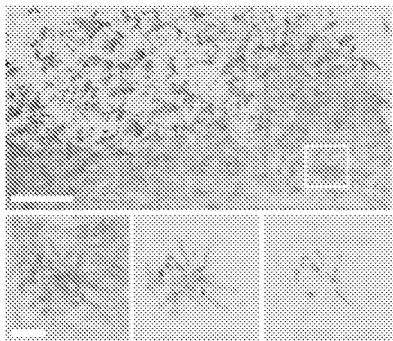


FIG. 3F

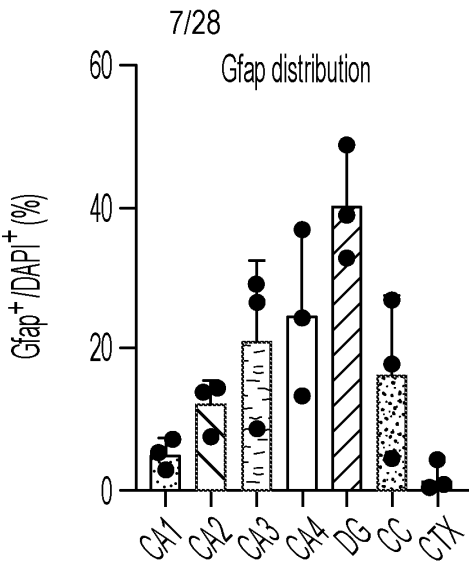


FIG. 3G

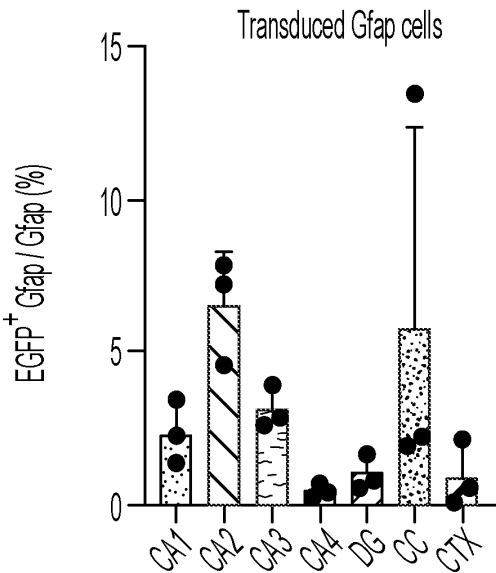


FIG. 3H

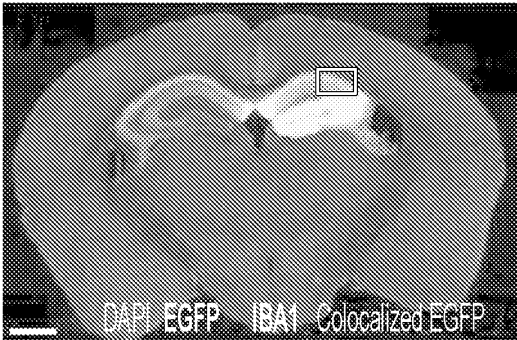


FIG. 3I

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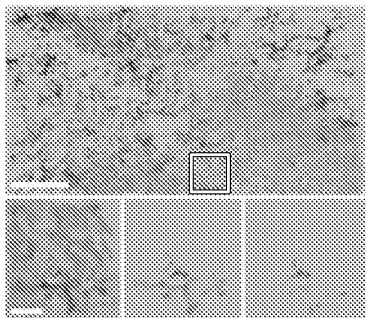


FIG. 3J

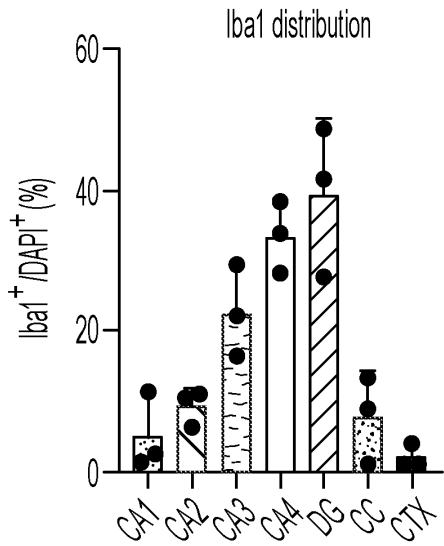


FIG. 3K

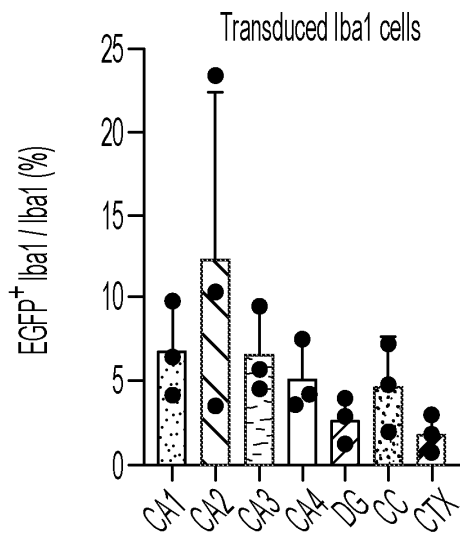


FIG. 3L

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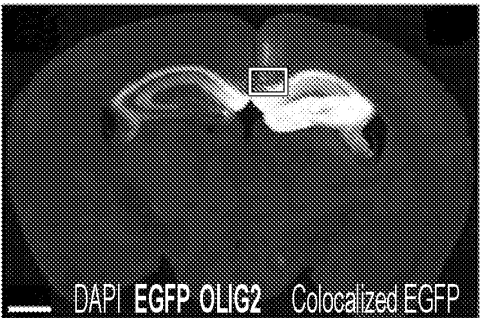


FIG. 3M

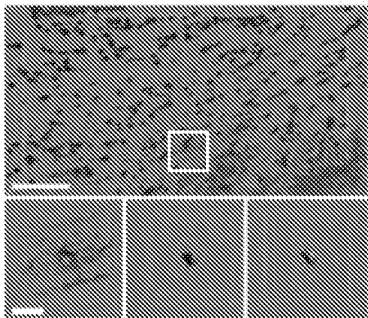


FIG. 3N

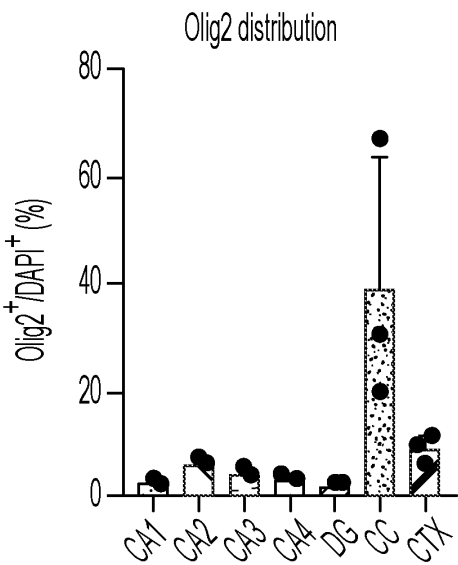


FIG. 3O

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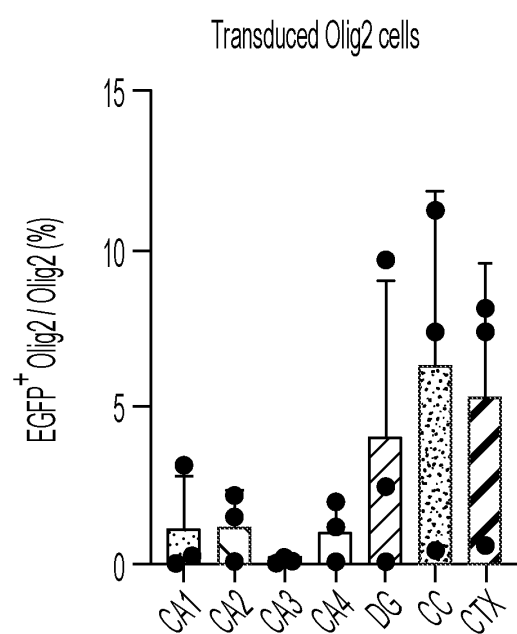


FIG. 3P

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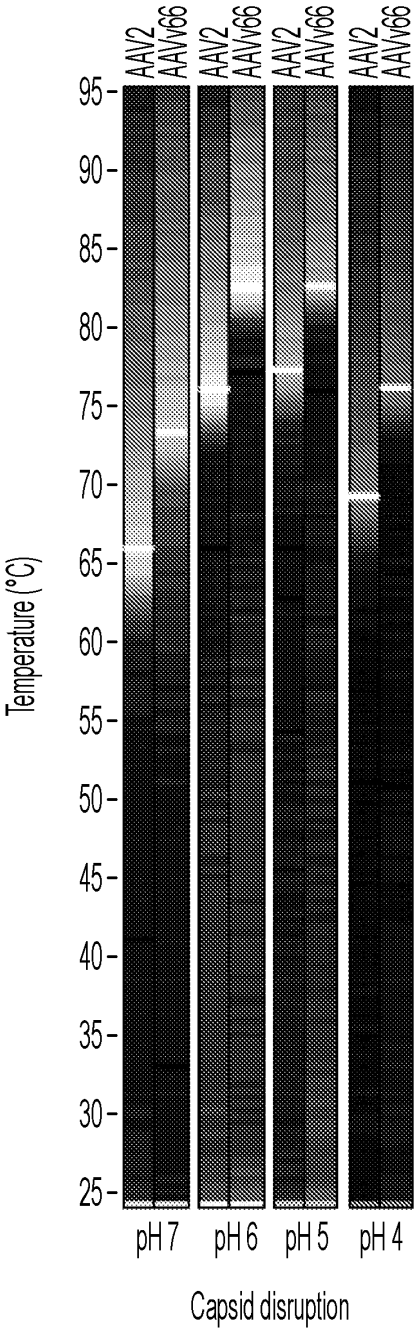


FIG. 4A

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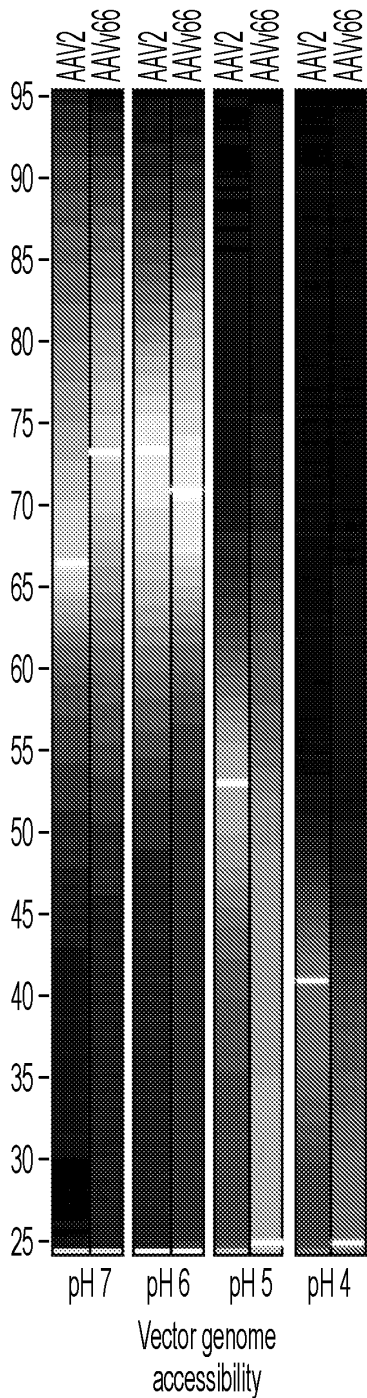


FIG. 4B

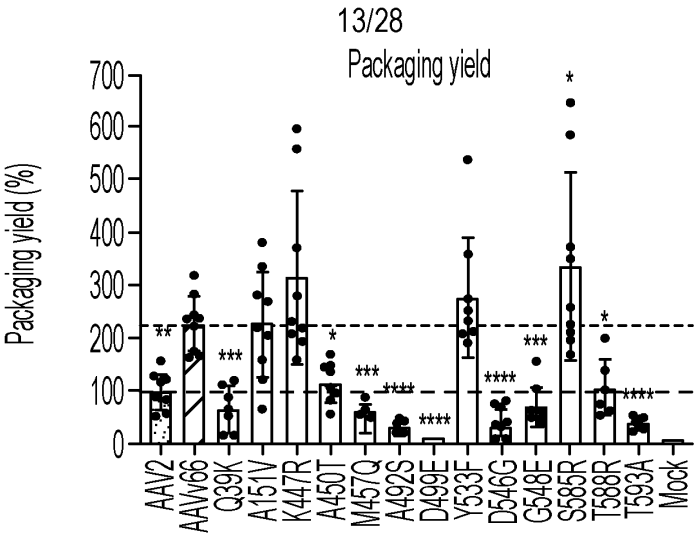


FIG. 4C

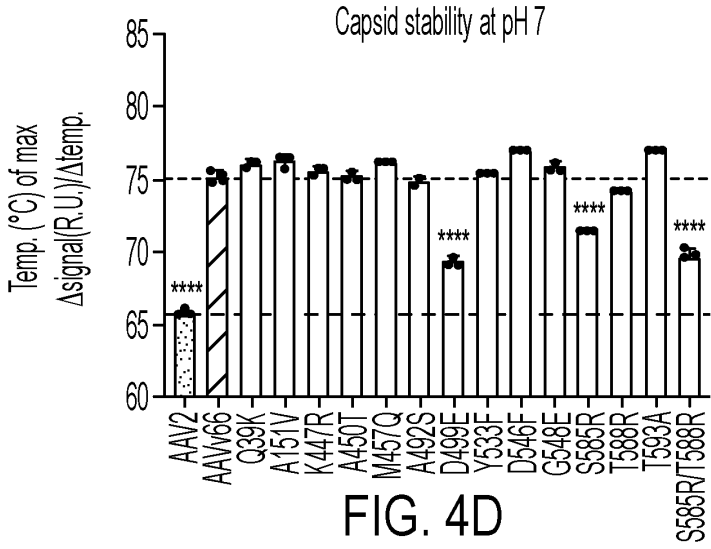


FIG. 4D

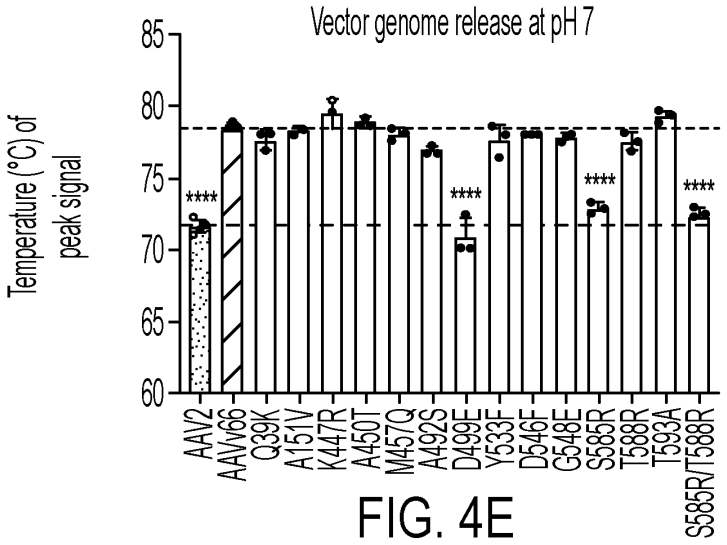


FIG. 4E

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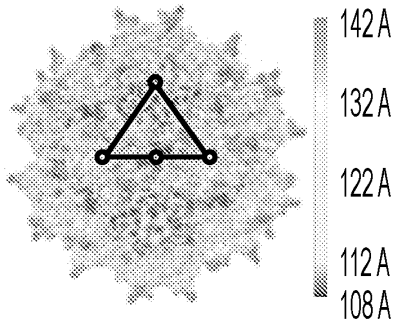


FIG. 5A

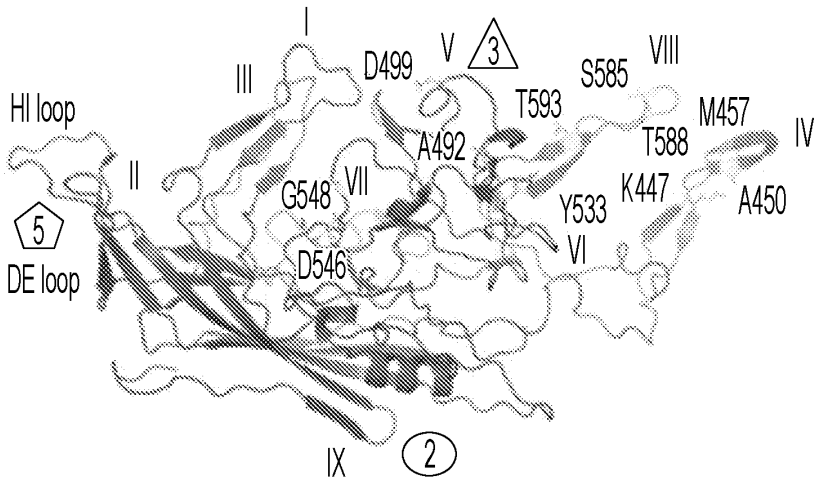


FIG. 5B

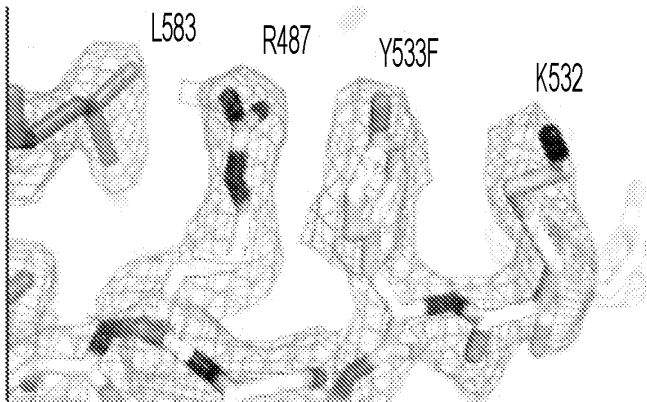


FIG. 5C

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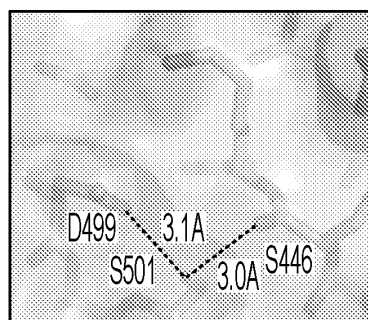


FIG. 5D

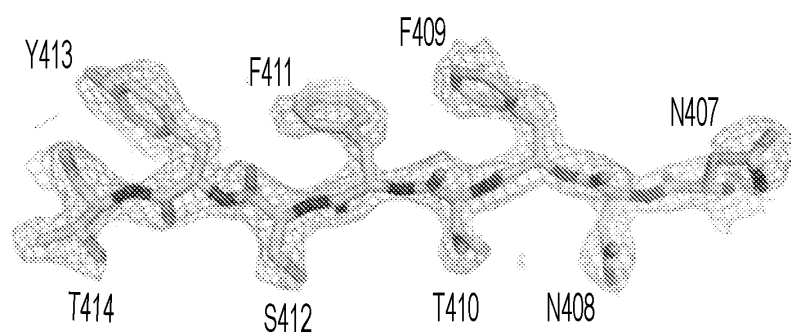


FIG. 5E

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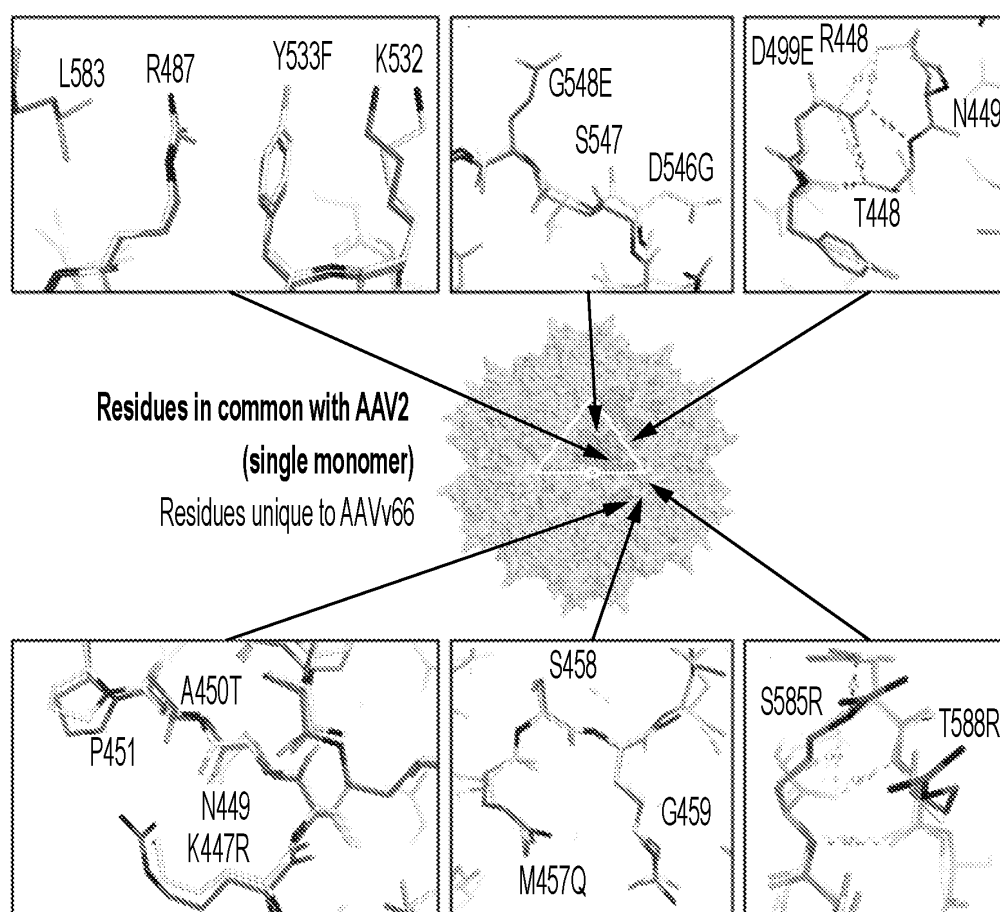


FIG. 6

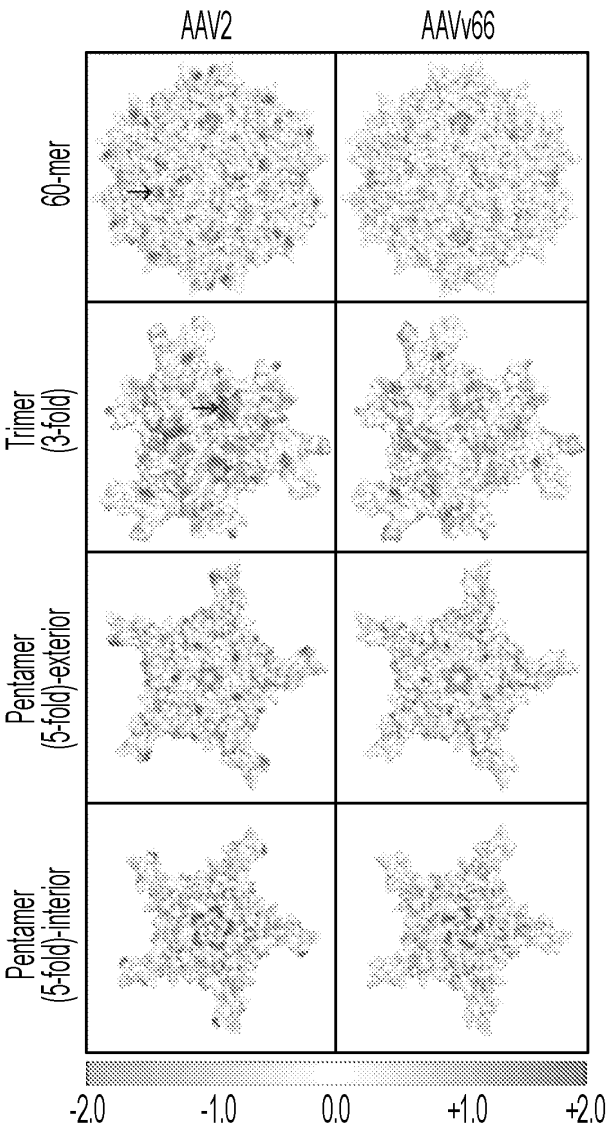


FIG. 7A

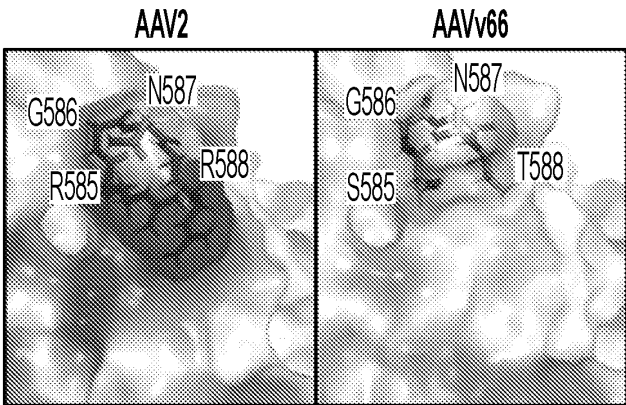


FIG. 7B

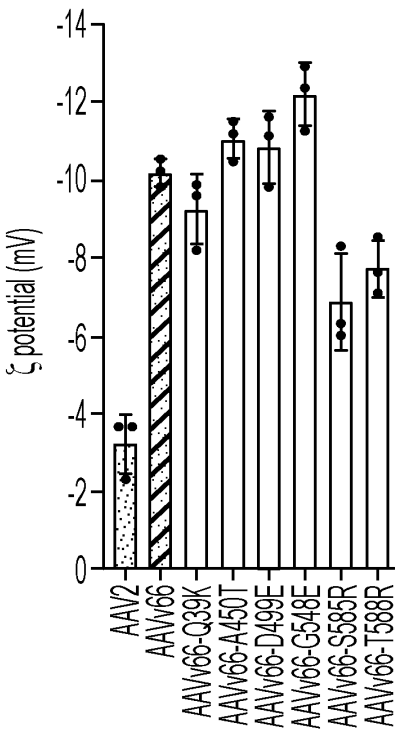


FIG. 7C

>VP1
 1 MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY
 PLA domain
 Q
 51 KYLGPFNGLD KGEPVNEADA AALEHDKAYD RQLDSGDNPY LKYNHADA EF
 >VP2
 101 QERLKEDTSF GGNLGRAVFQ AKKRVL EPLG LVEE PVKTAP GK KRPVEHSP
 151 VEPDSSSGTG KAGQQPARKR LNF GQTGDAD SVPDPQPLGQ PPAAPSGLGT
 A
 >VP3
 201 NTMATGSGAP MADNNEGADG VGNSSGNWHC DSTWMGDRVI TTSTRTWALP
 ▶ | ----- βC → βB →
 251 TYNNHLYKQI SSQSGASNDN HYFGYSTPWG YFDENRFHCH FSPRDWQRLI
 βD → || ----- βE →
 301 NNNWGF RPKR LNF KLFNIQV KEVTQNDGTT TIANNLTSTV QVFTDSEYQL
 ||| -----
 351 PYVLGSAHQG CLPPFPADV F MVPQYGYLTL NNGSQAVGRS SFYCLEYFPS
 βF → βG → IV ---
 401 QMLRTGN NFT FSYTFEDVPF HSSYAHSQSL DRLMNPLIDQ YLYYLSRTNT
 K A
 ----- V -----
 451 PSGTTTQ SRL QFSQAGASDI RDQSRNWLPG PCYRQQRVSK TSADNNNSEY
 M A D
 ----- VI ----- VII
 501 SWTGATKYHL NGRDSL VNPG PAMASHKDDE EKFFPQSGVL IFGKQGSEKT
 Y D G
 ----- VIII -----
 551 NVDIEKVMIT DEEEIRTTNP VATEQYGSVS TNLQ RGNRQA ATADVNTQGV
 S T T
 βH →
 601 LPGMVWQDRD VYLQGP IAWK IPHTDGHFHP SPLMGGFGLK HPPPQILIKN
 ▶ βI →
 651 TPVPANPSTT FSAAKFASFI TQYSTGQVSV EIEWELQKEN SKRWNPEIQY
 IX -----
 701 TSNYNKSVNV DFTVD TNGVY SEPRPIGTRY LTRNL*
 AAV2
 AAVv66

FIG. 8

SUBSTITUTE SHEET (RULE 26)

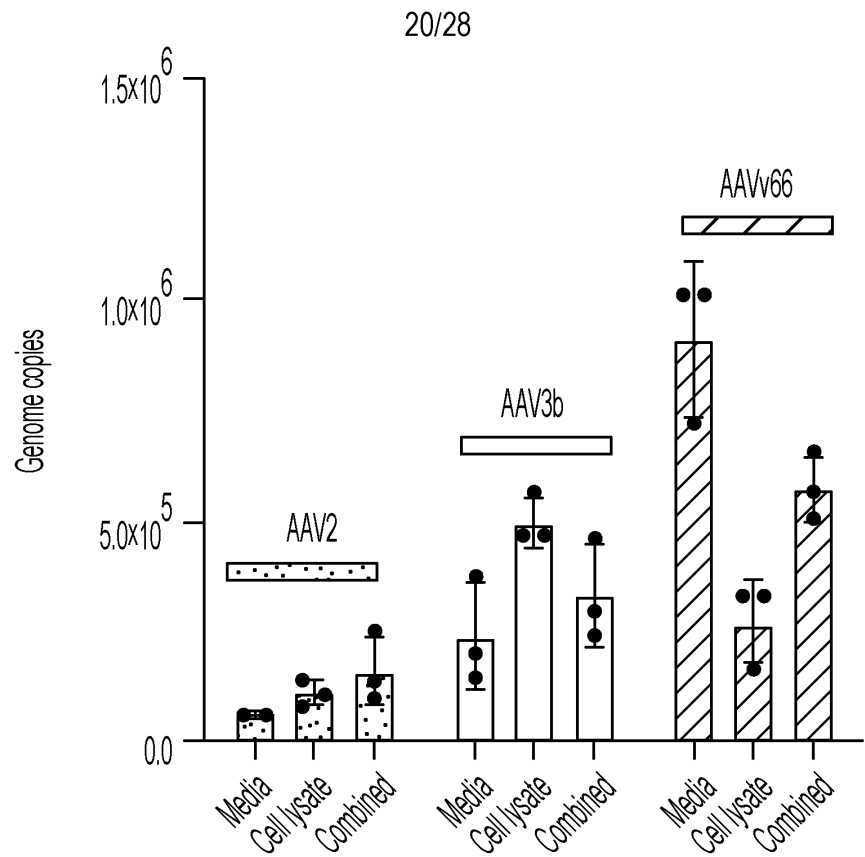


FIG. 9

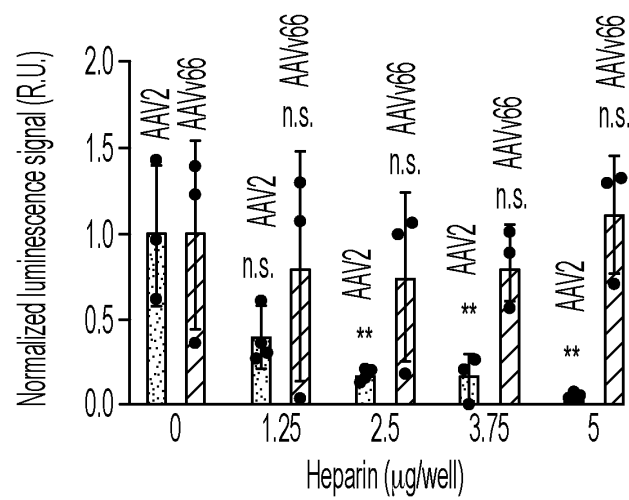


FIG. 10

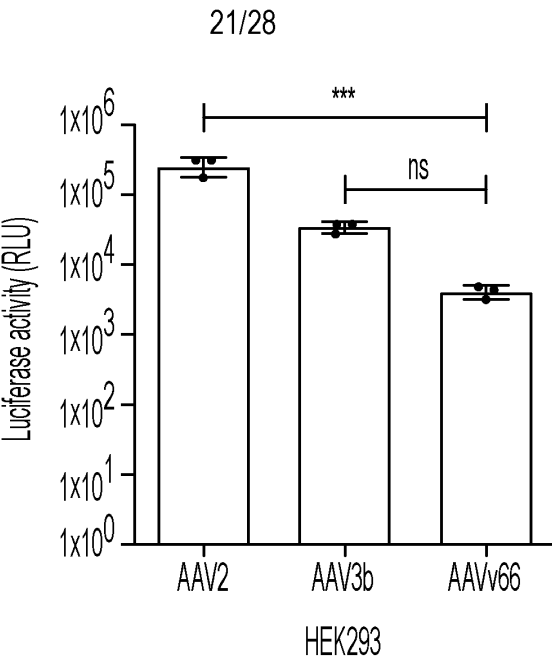


FIG. 11

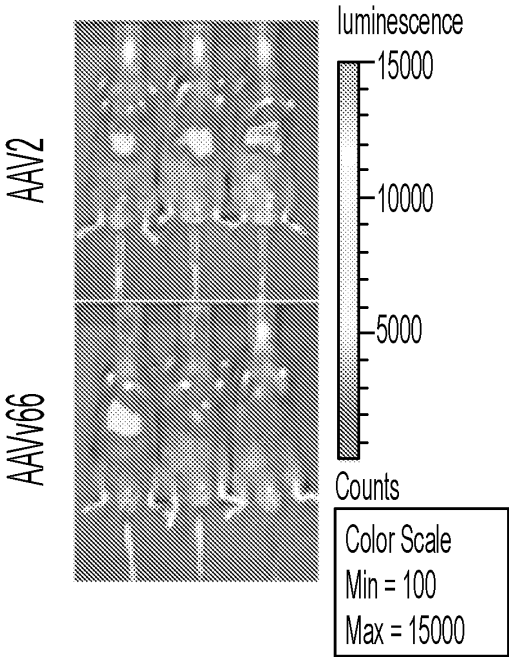


FIG. 12A

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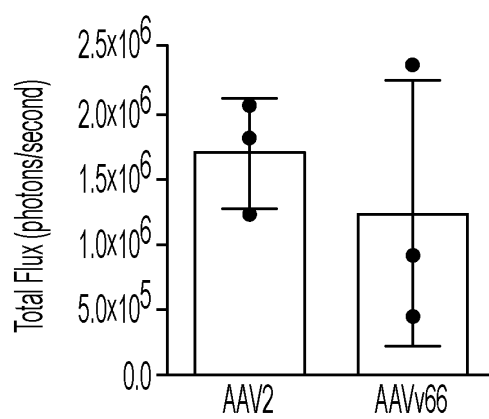


FIG. 12B

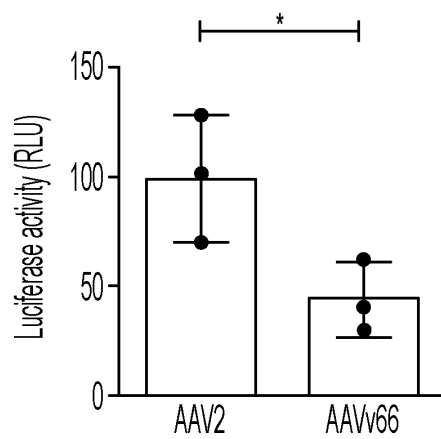


FIG. 12C

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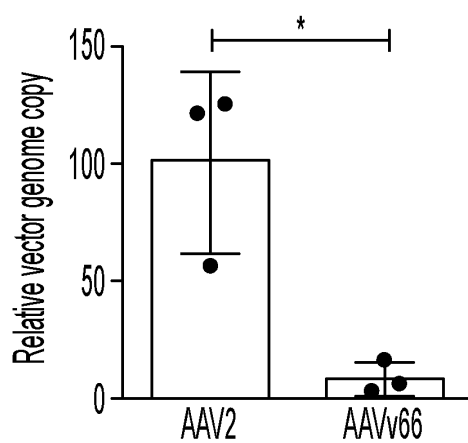


FIG. 12D

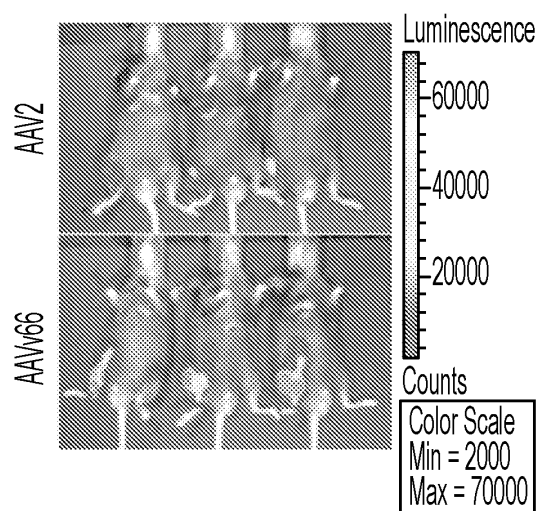


FIG. 13A

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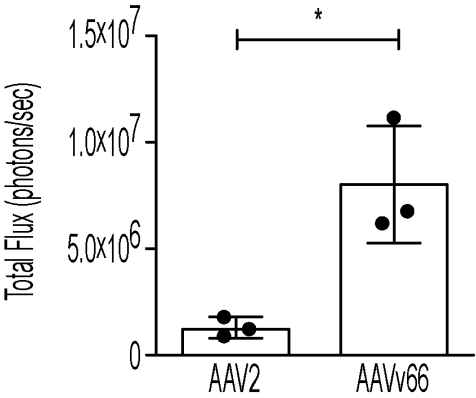


FIG. 13B

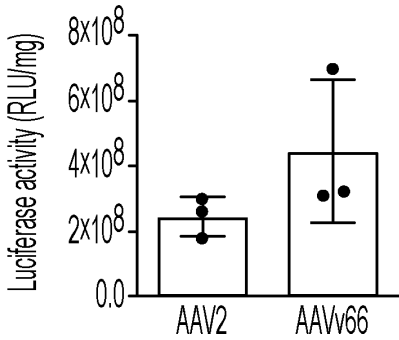


FIG. 13C

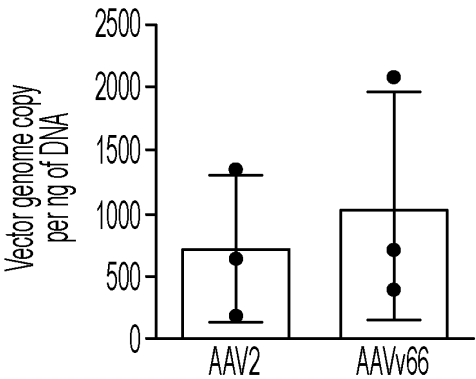


FIG. 13D

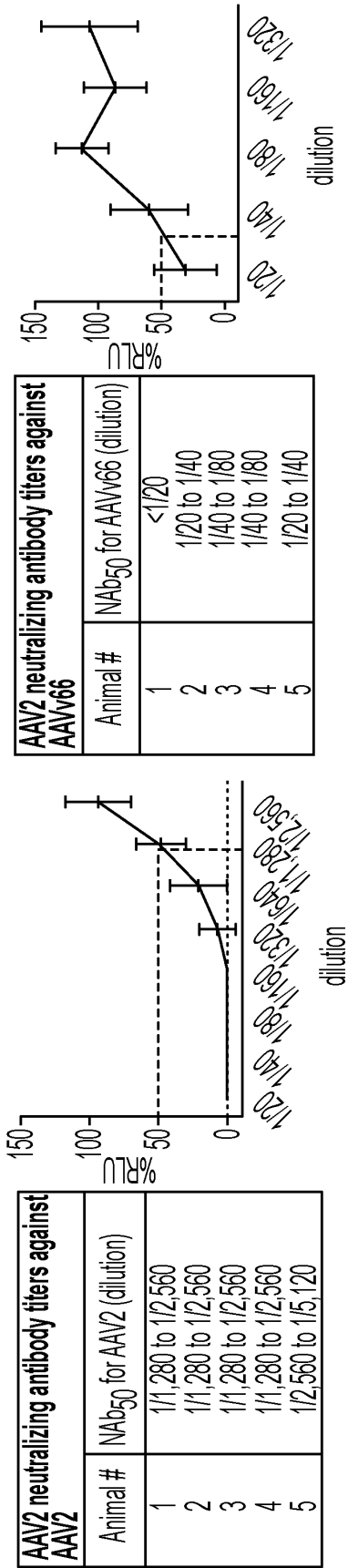


FIG. 14A

FIG. 14B

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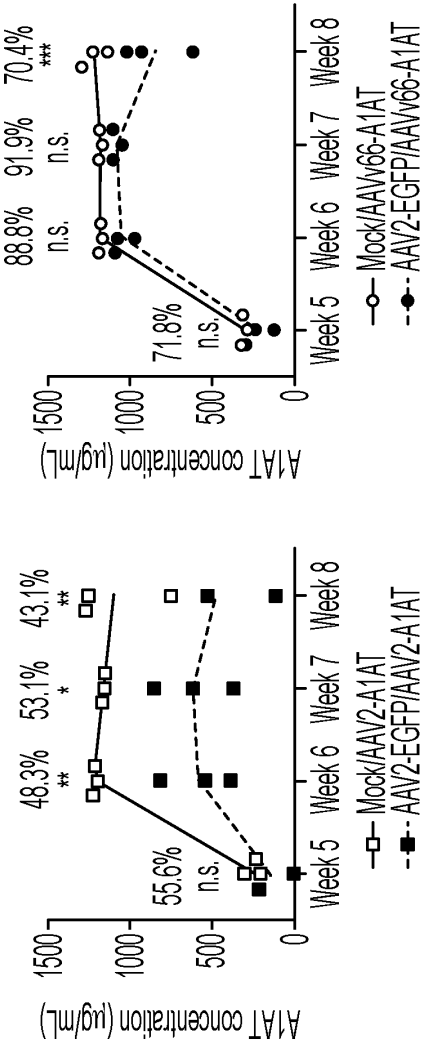


FIG. 14C

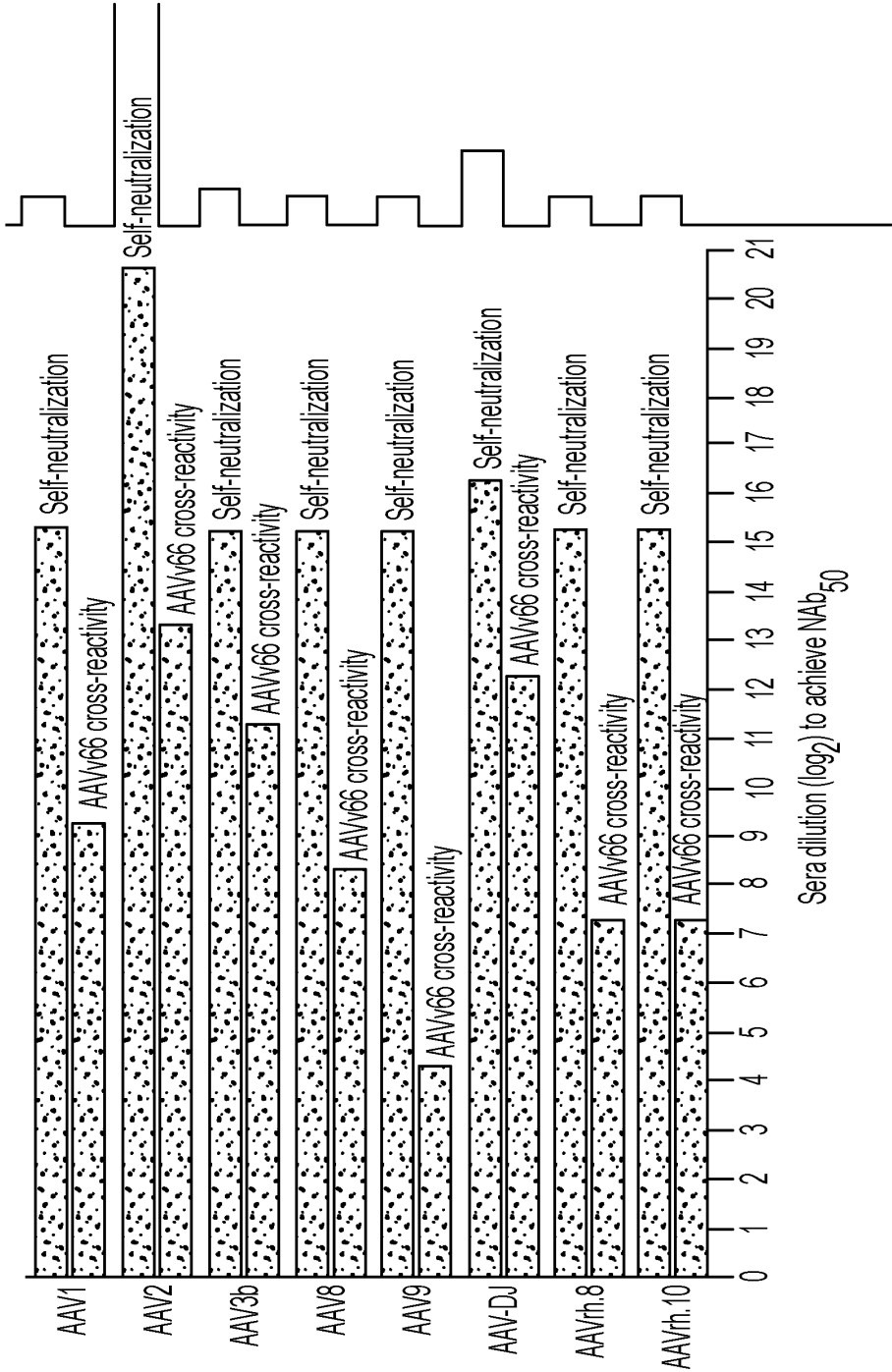


FIG. 14D

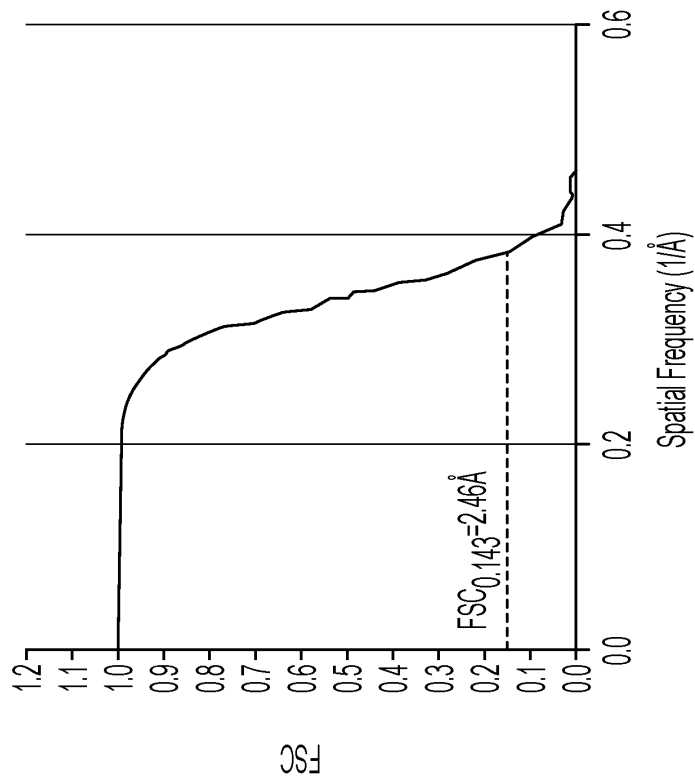


FIG. 15B

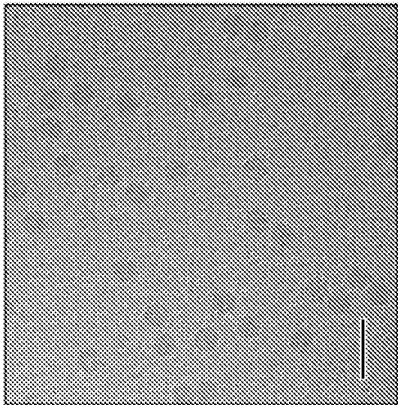


FIG. 15A

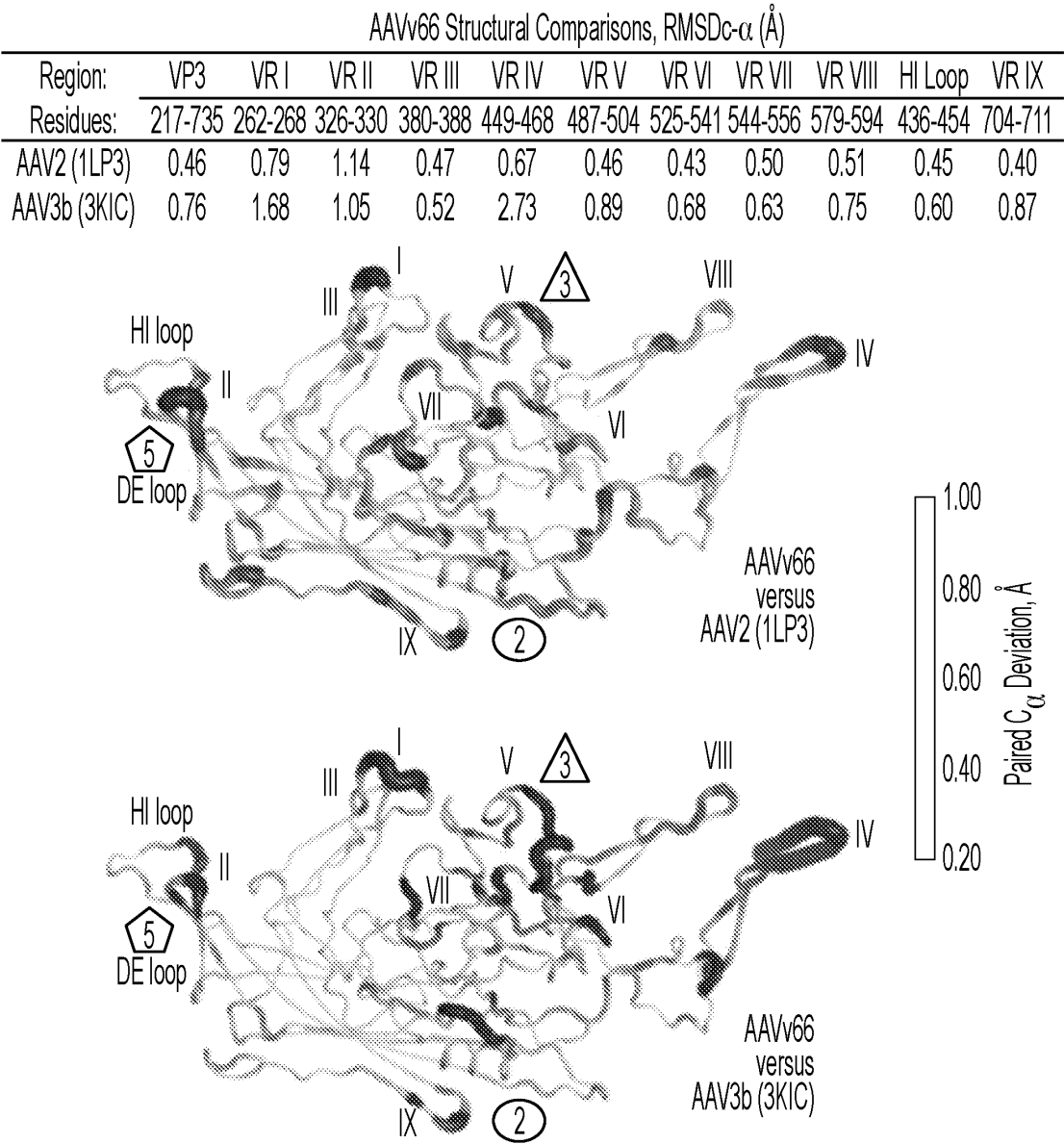


FIG. 16