

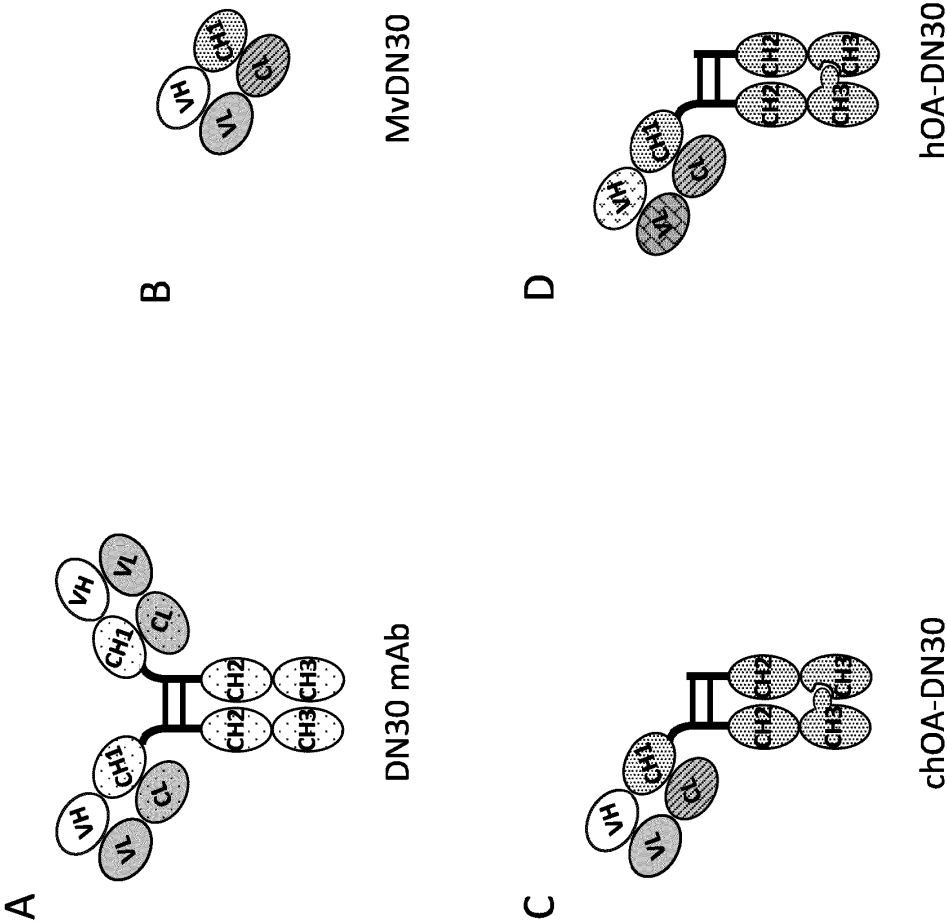


Fig. 1

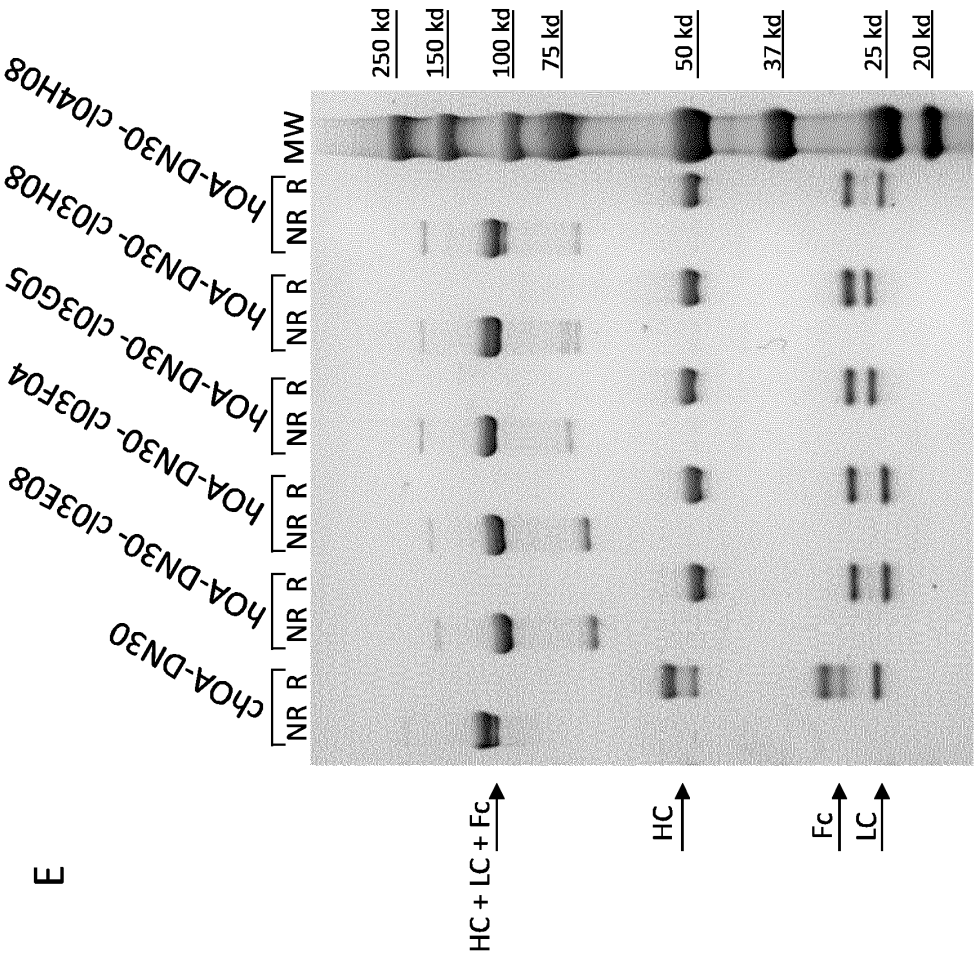
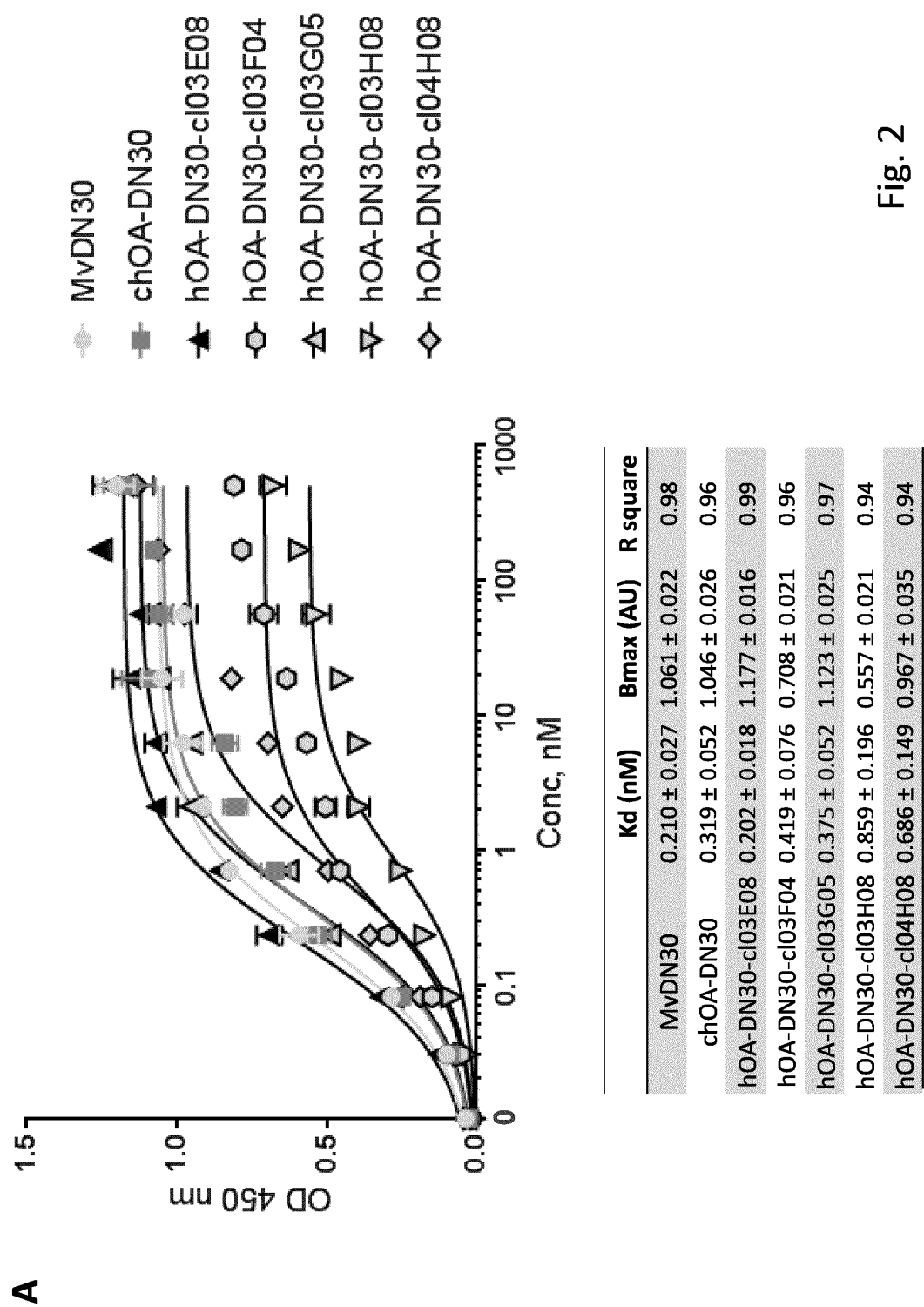
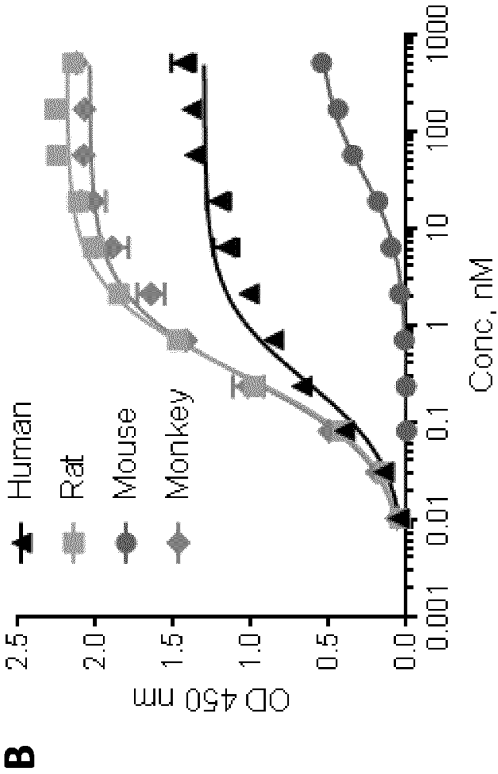


Fig. 1/cont





SUBSTITUTE SHEET (RULE 26)

	Kd (nM)	Bmax (AU)	R square
Human	0.262 ± 0.037	1.303 ± 0.029	0,97
Rat	0.325 ± 0.016	2.189 ± 0.017	0,99
Mouse	35.99 ± 2.381	0.568 ± 0.012	0,99
Monkey	0.273 ± 0.021	2.041 ± 0.025	0,99

Fig. 2/cont

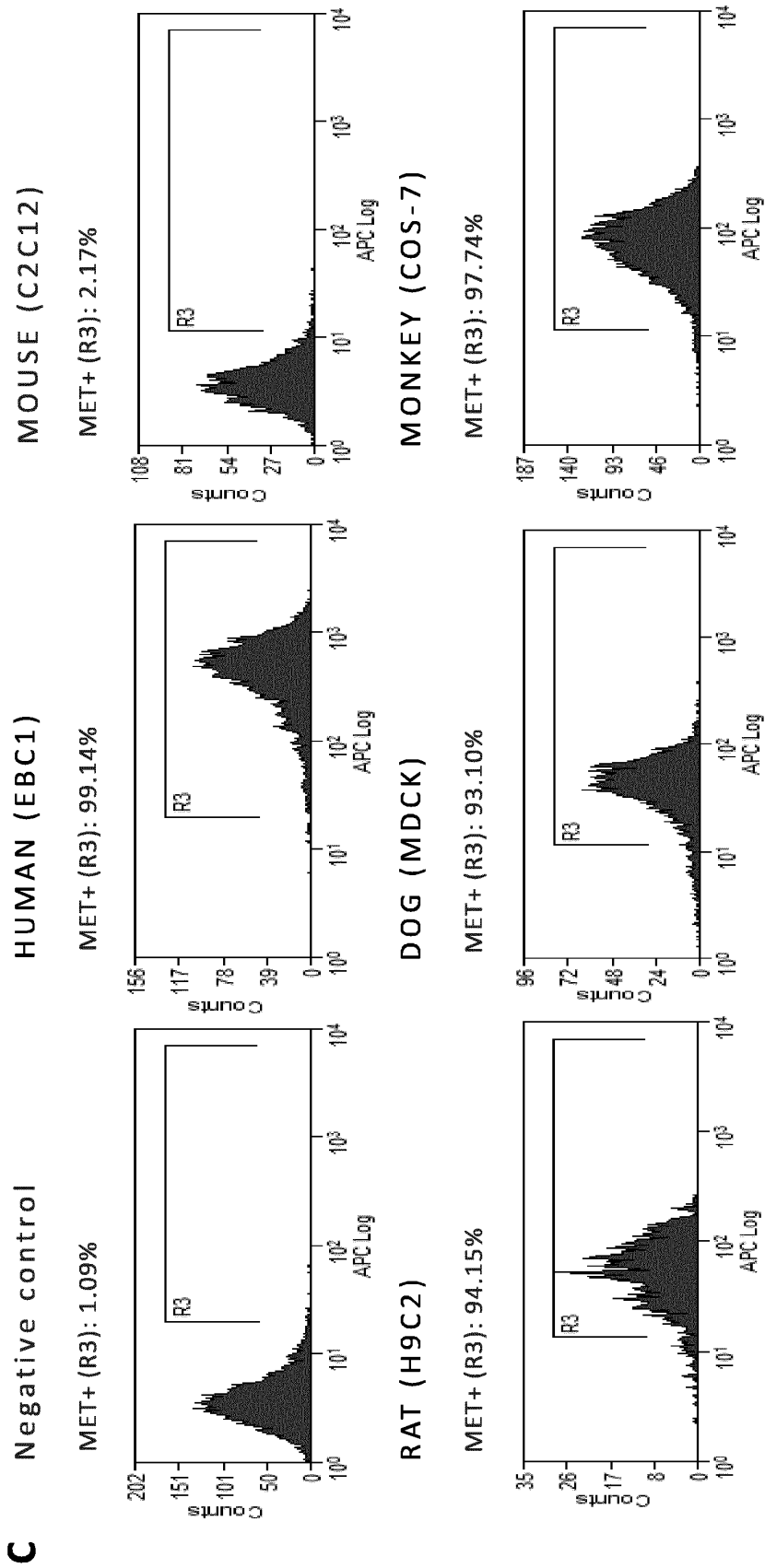


Fig. 2/cont

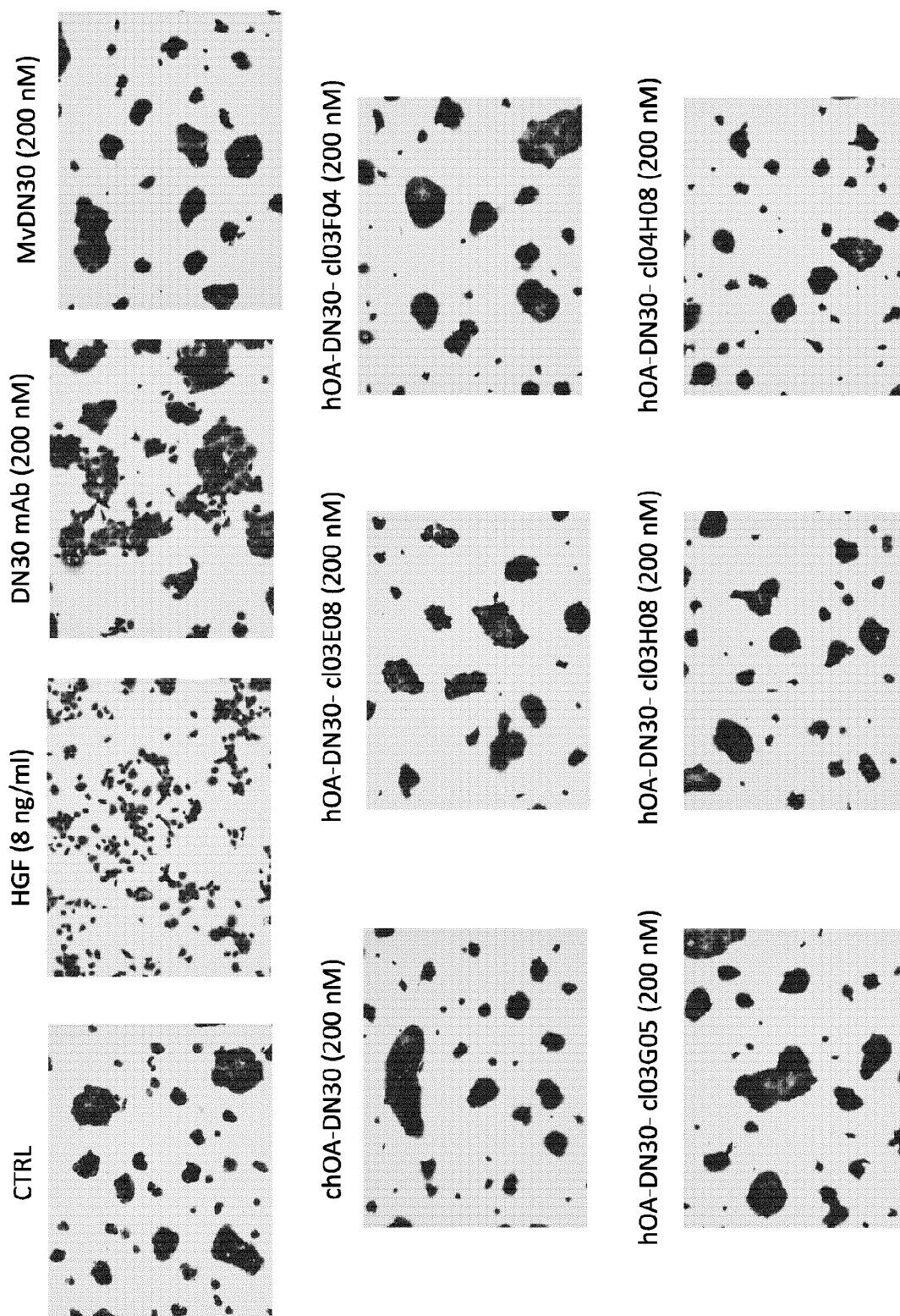


Fig. 3

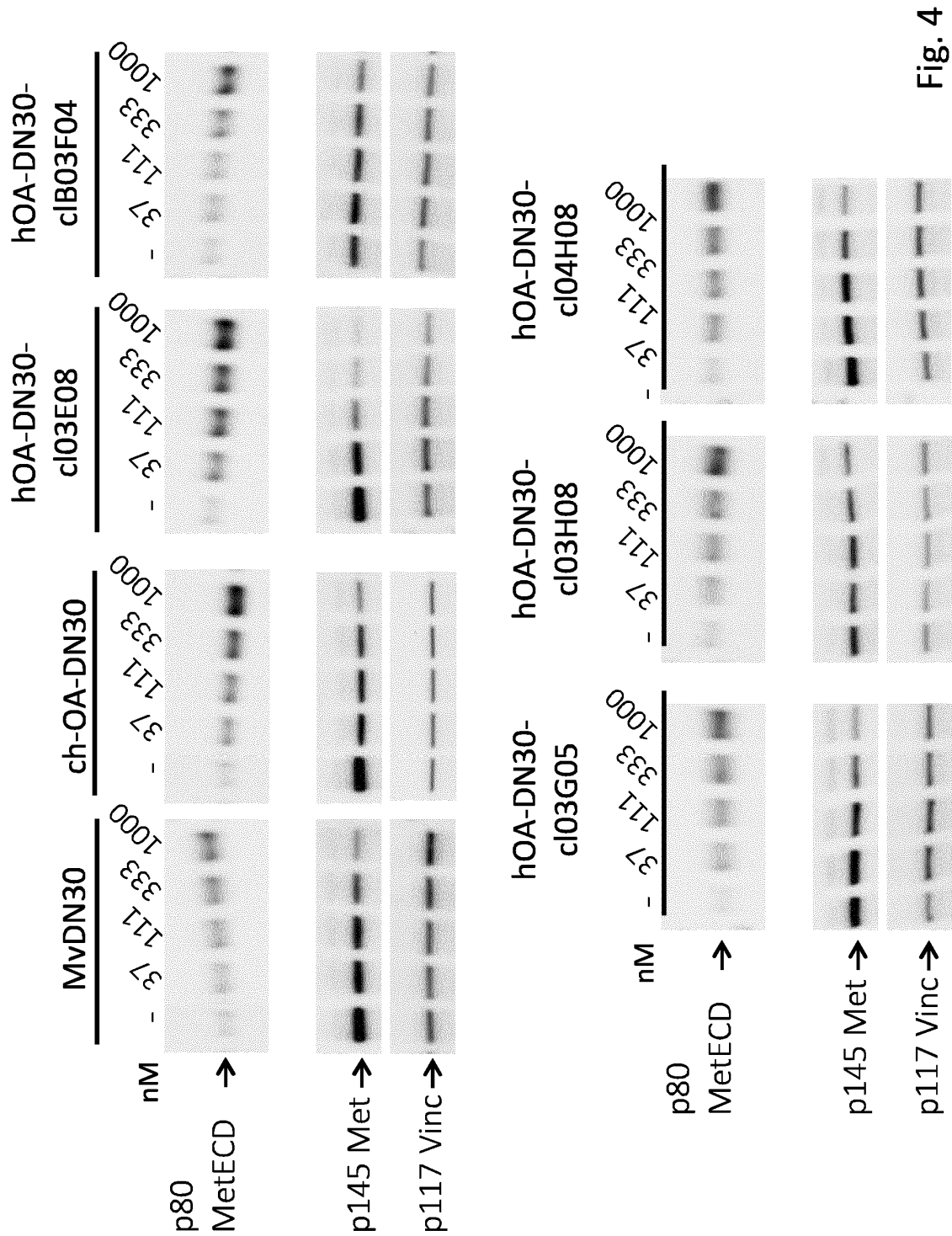


Fig. 4

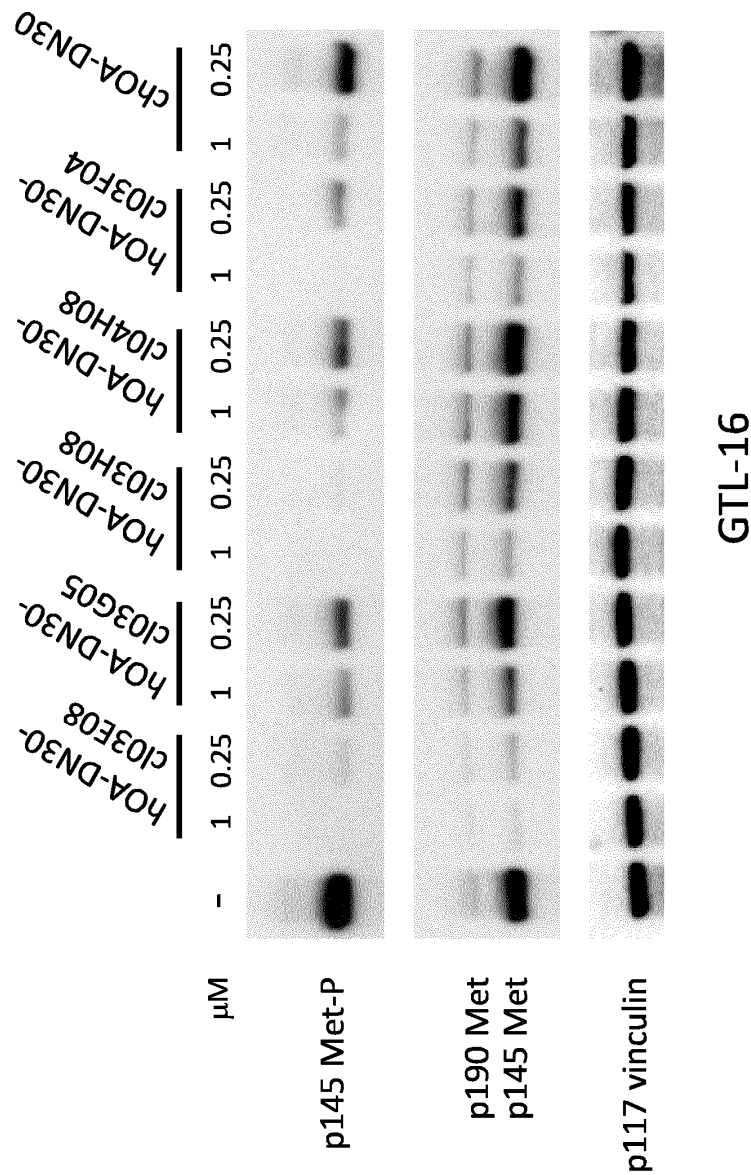
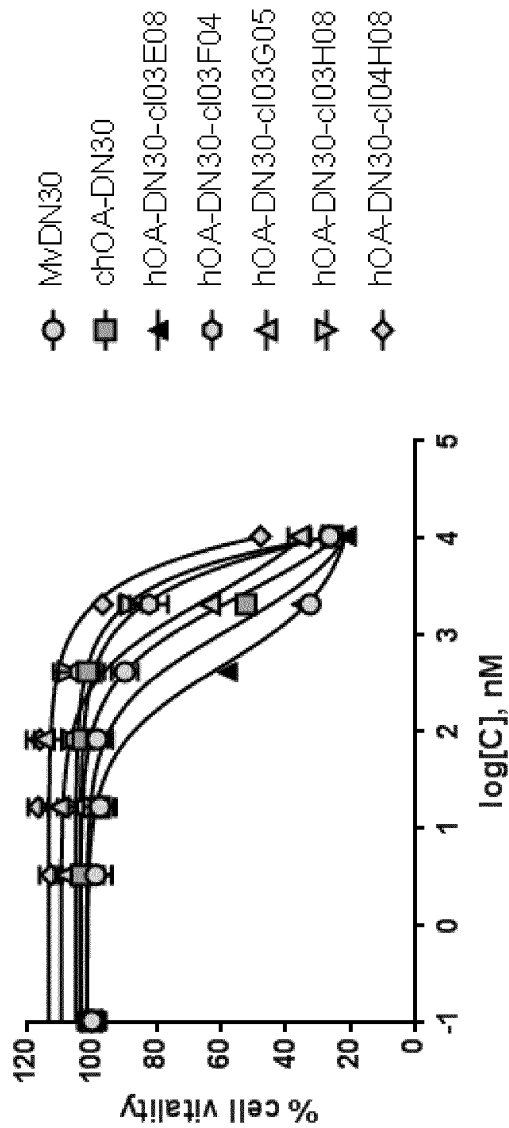


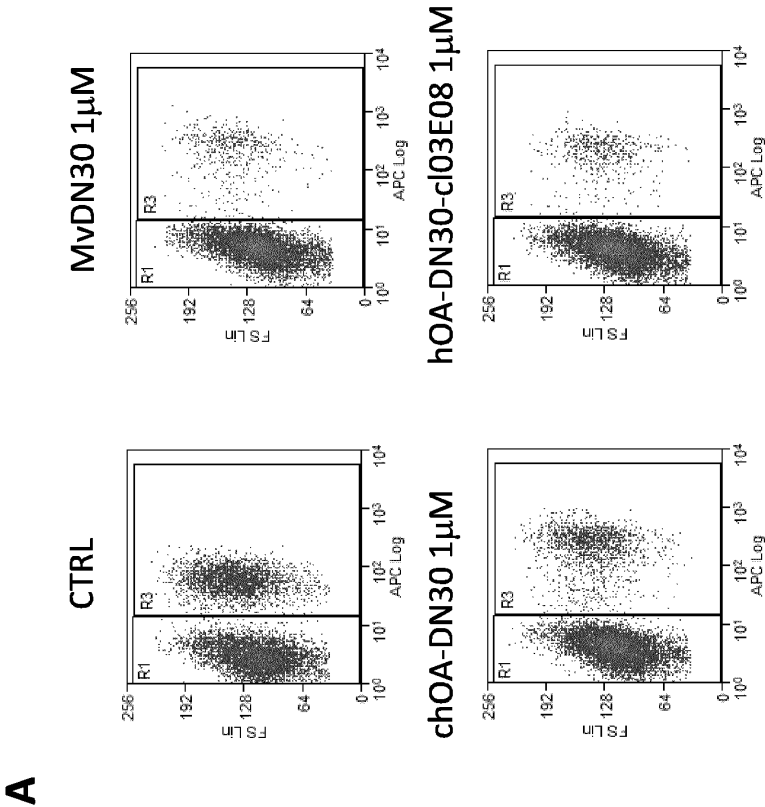
Fig. 5



	IC50 (nM)	R square
MvDN30	1136±1.08	0.94
chOA-DN30	2489±1.77	0.96
hOA-DN30-cl03E08	460±1.07	0.98
hOA-DN30-cl03F04	52310±7.68	0.94
hOA-DN30-cl03G05	2381±1.31	0.95
hOA-DN30-cl03H08	N/A *	-
hOA-DN30-cl04H08	115726±311.2	0.91

* N/A: Not applicable as data fitting is ambiguous

Fig. 6

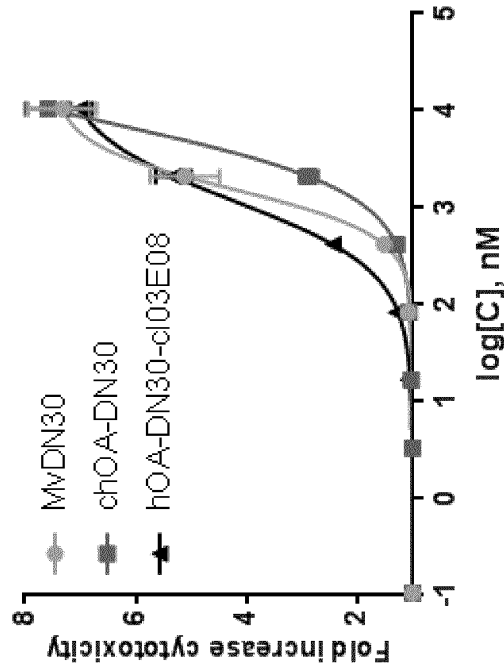


GTL-16

	% EdU+ cells (R3)
CTRL	31,17 %
MvDN30	5.20 %
chOA-DN30	14.97%
hOA-DN30-cl03E08	4.92%

Fig. 7

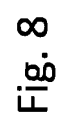
B



GTL-16

	EC50 (nM)	R square
MvDN30	1486±1.08	0.98
chOA-DN30	6807±1.77	0.99
hOA-DN30-cl03E08	1116±1.07	0.99

Fig. 7/cont



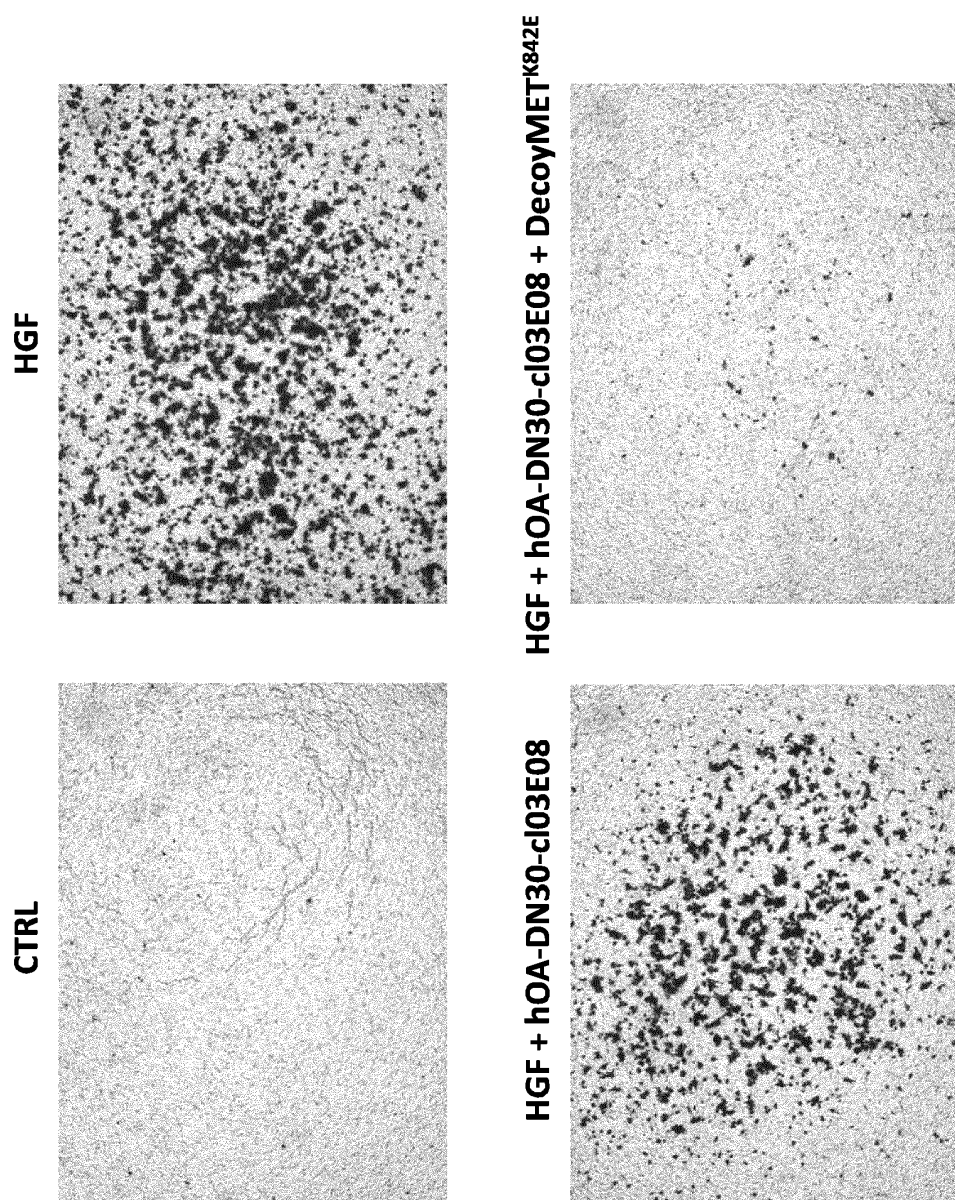
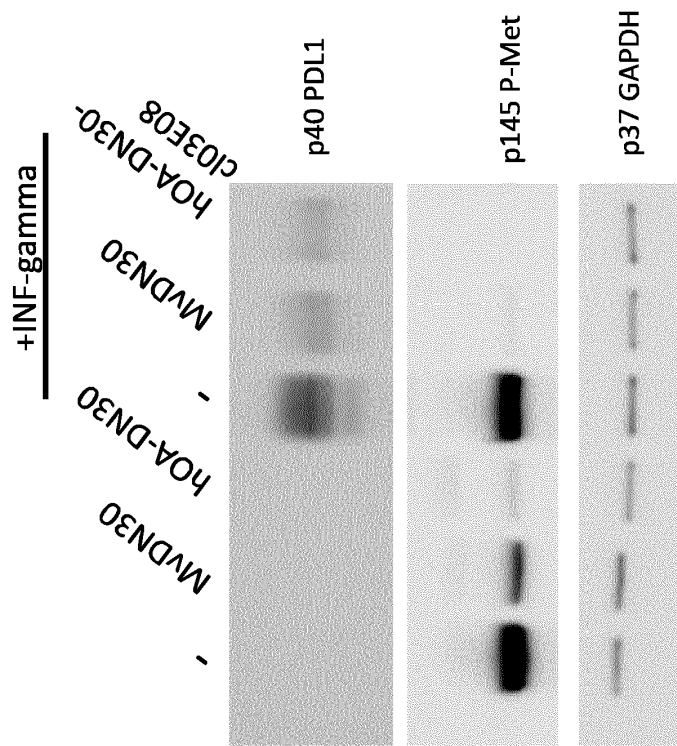


Fig. 9



GTL-16

Fig. 10

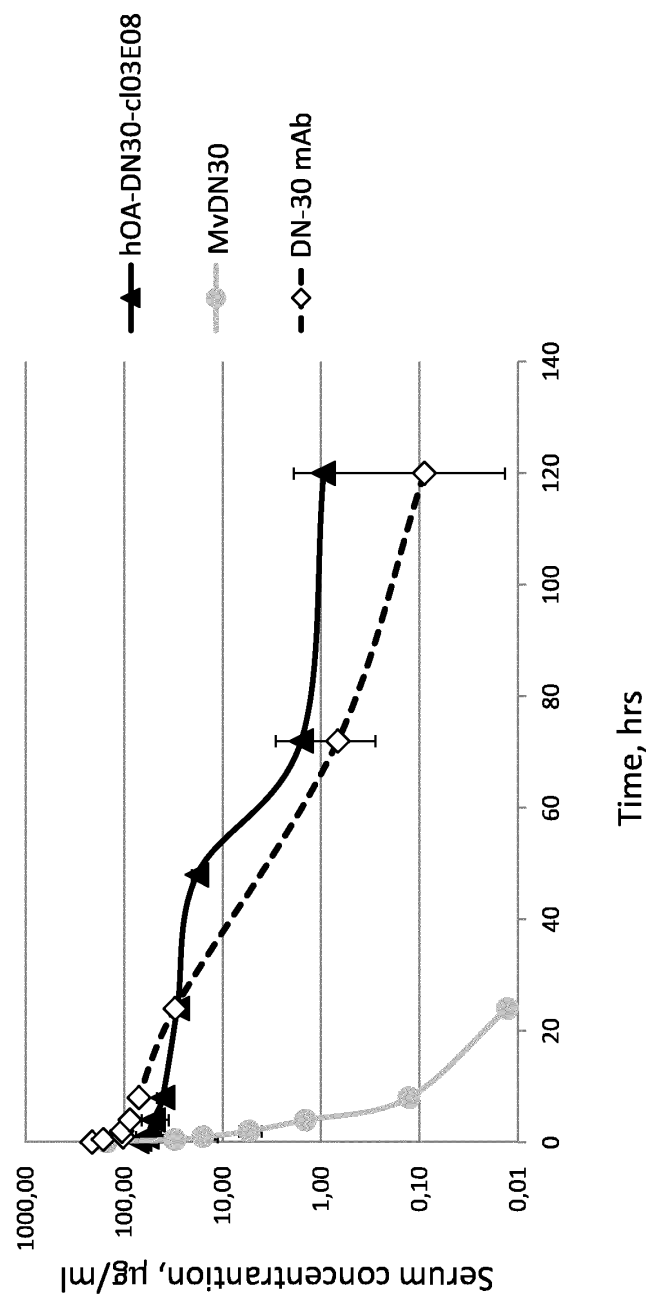


Fig. 11

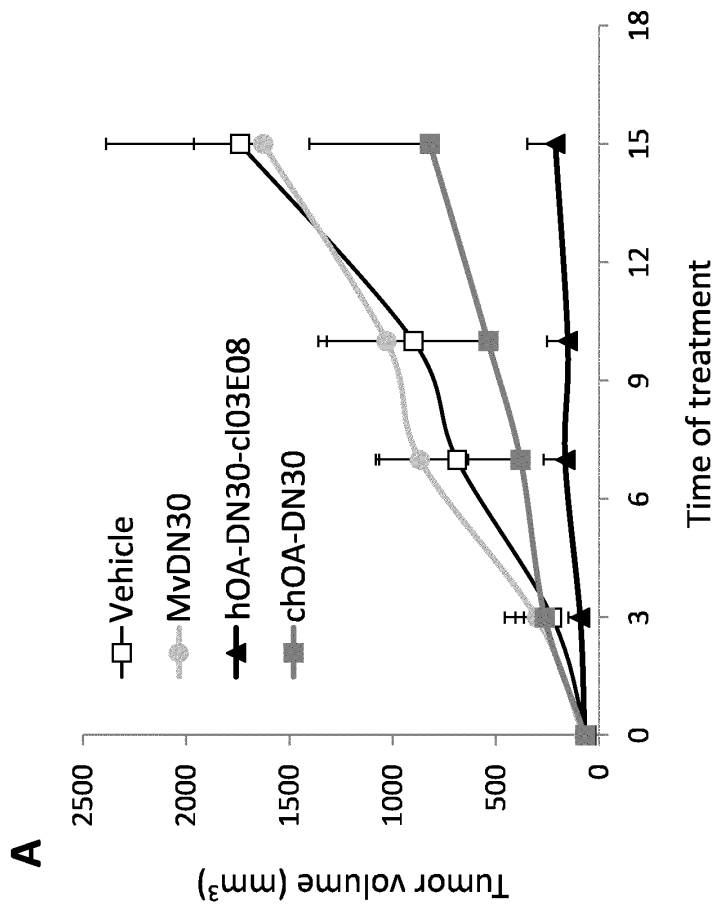


Fig. 12

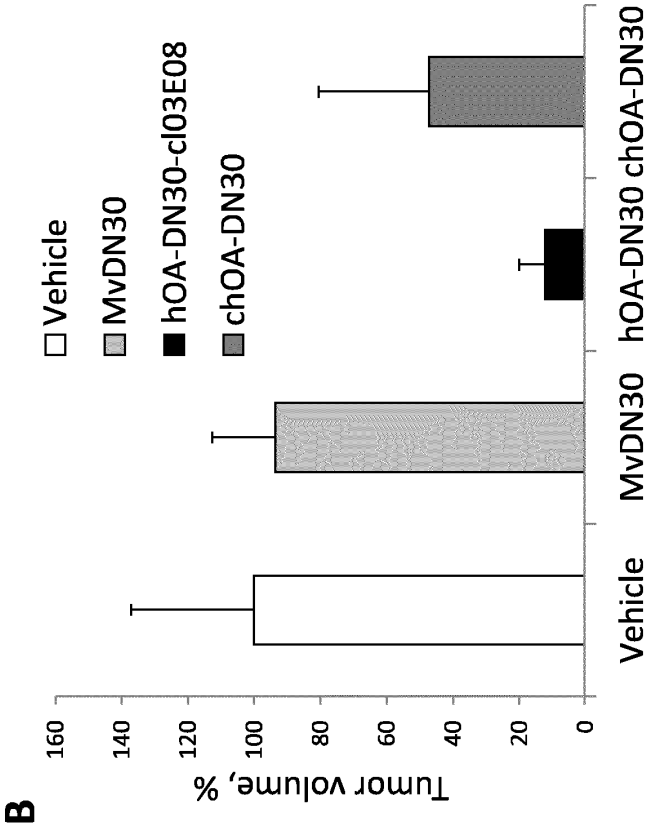


Fig. 12/cont

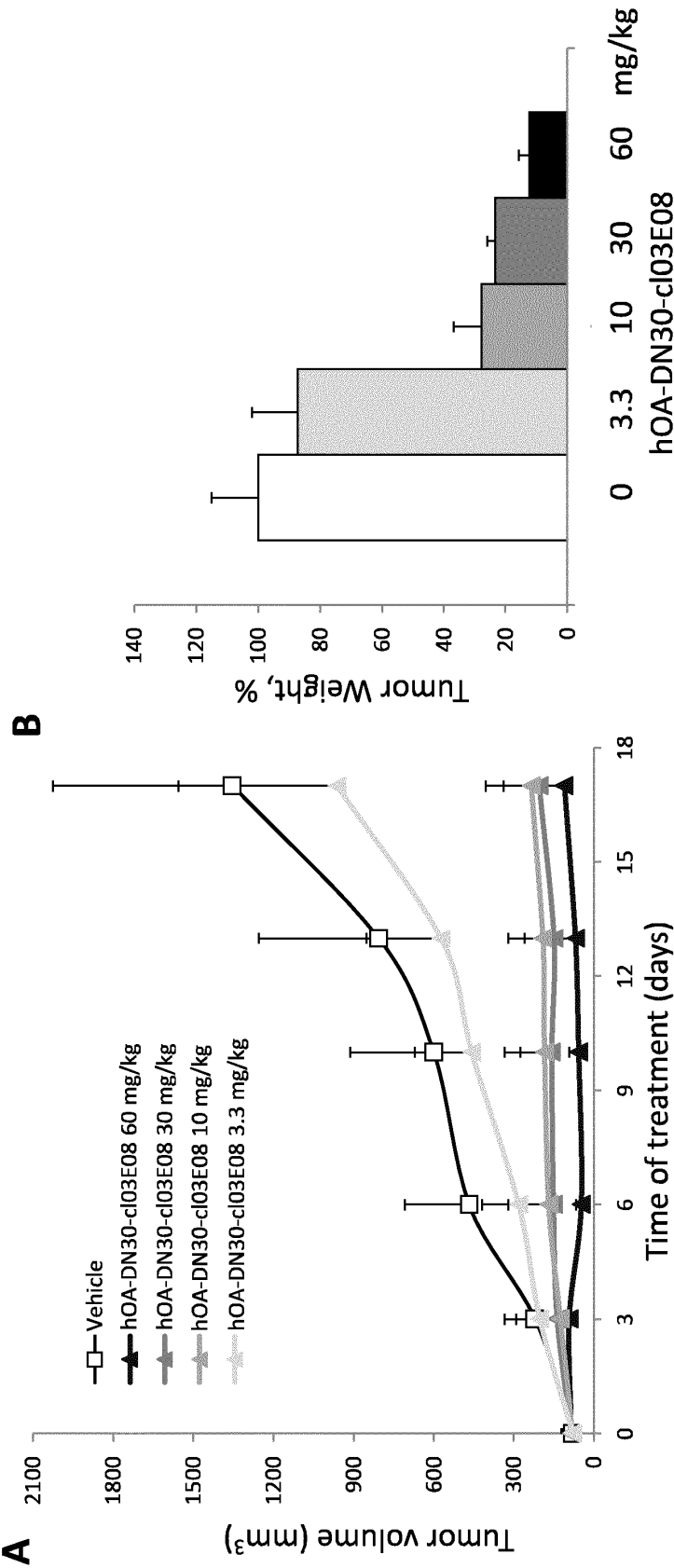


Fig. 13

Seq. ID N°7: VL-cl03E08 humanized
 METDTILLWVLLLVWPGSTGDIVLTQSPDSLAVSLGQRATINCKAS**QSVDYDGGSY**MSWFQQKPGQPPKLL
 IY**AASN**LESGVPA^RFSGSGGTDFTLT^TISSLQAEDVAT^YYC**QQSYEDPLT**FFGGGTKVEIK

Seq. ID N°8: VH-cl03E08 humanized
 MGWSYIIILFLVATATDGH^SQVQLQQSGAEVKKPGASVKLSCKAS**GYTFTSYW**IHWVRQAPGQGLEWIGE**IN**
PSSGRTNYN^EKFKNRVT^TVDKSTSTAYMELSSLTSEDSAV^YYC**ASRGY**WGQGTTLTVSS

Seq. ID N°9: human CL
 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSST
 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Seq. ID N°10: human CH1
 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT^SWNSGALTSGVHTFPAVLQSSGLYSLSSVTV
 PSSSLGTQTYICNVNHKPSNTKVDDKKV

Fig. 14

Seq. ID N°11: First Fc (Knob mutation)
 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELTKN
 QVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN
 HNTQKSLSLSPGK

Seq. ID N°12: Second Fc (Hole mutations)
 MGWSYIIILFLVATATDGHSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
 VYITLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLVSKLTVDKSRWQQG
 NVFCSCVMHEALHNHYTQKSLSLSPGK

Fig. 15

Seq. ID N°14: DecoyMet mutation K842E -TAGs

MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAETPIQNVILHEHHIFLGATNYIYV
LNEEDLQKVAEYKGTGPVLEHPDCFFPCQDCSSKANLSGGWKDNINMALVVDITYDDQLISCGSVNRGTCQRH
VFPHNHTADIQSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSVVKDRFINFFVGNTINSSYFPDHPHLSISV
RRLKETKDGFMFLTDQSYIDVLPFEFRDSYPIKYVHAFESNNFIYFLTQRETLDAQTFFHTRIIRFCSINSGL
HSYMEMPLLECILTEKRKKRSTKKEVFNILQAAVSKPGAQLARQIGASINDDILFGVFAQSKPDSAEPMDRS
AMCAFPKIYVNDFFNKIVNKNNVRCLOHFFYGNHEHCNRTLNRSSGCEARRDEYRTEFTTALQVRDLFMG
QFSEVLLTSISTFIKGDLTIANLGTSEGRFMQVVSRSGPSTPHVNFLLDSHPVSPVEIVEHTLNQNGYTLV
ITGKKITKIPLNGLGCRHFQSCSQCLSAPPFVQCQGWCHDKCVRSEECLSGTWTQQICLPAIYKVFPNSAPLE
GGTRLTICGWDFGFRNRNKFDLKKTRVLLGNESTLTLTSESTMNTLKCTVGPAMNKHFNMSIIISNGHGTQ
YSTFSYVDPVITSISPKYGPMAAGTLLTLTGNYLNSGNSRHSIGGKTCTLKSVSNSILECYTPAQTIISTEF
AVKLIKIDLANRETSIFSYPREDPIVYEIHPTKSFISGGSTITGVGKNLNSVSVPRMVINVHEAGRNF^ETVACQH
RSNSEIICCTTPSLQQLNLQPLKTKAFFMLDGILSKYFDLLIYVHNPFVPEPEKPVMI SMGNENVLEIKGND
IDPEAVKGEVLKVGNKSCENIHLHSEAVLCTVPNDLLKLNSELNIEWKQAISSTVLGKVI VQPDQNF^ETASGA
AWSHPQFEKGAAWSHPQFEKGAAWSHPQFEKGA^EAAAAHHHHH

Fig. 16