

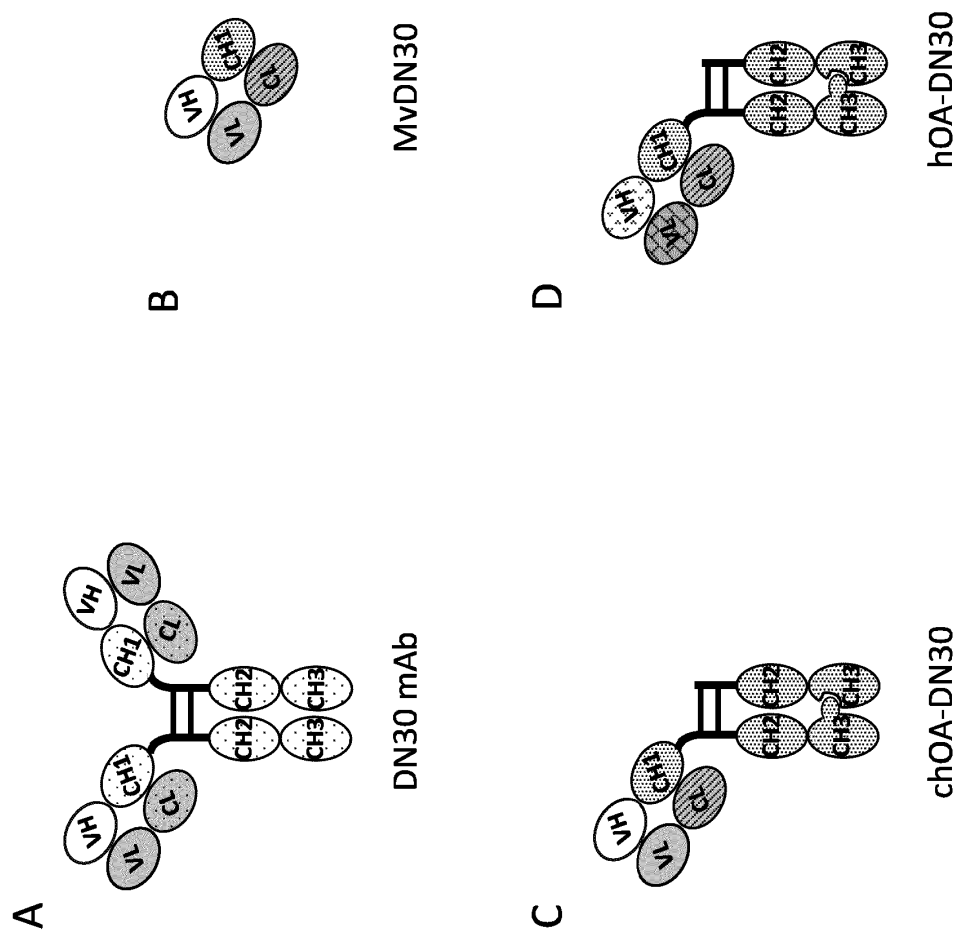


Fig. 1

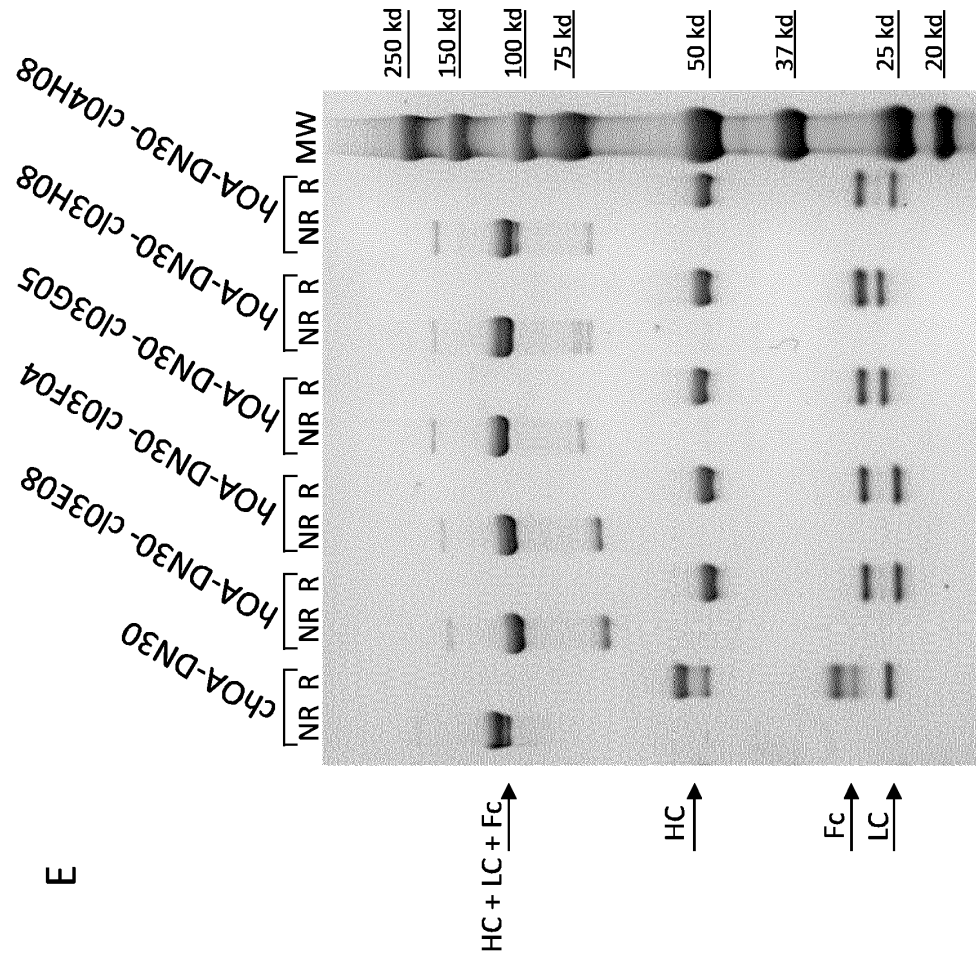
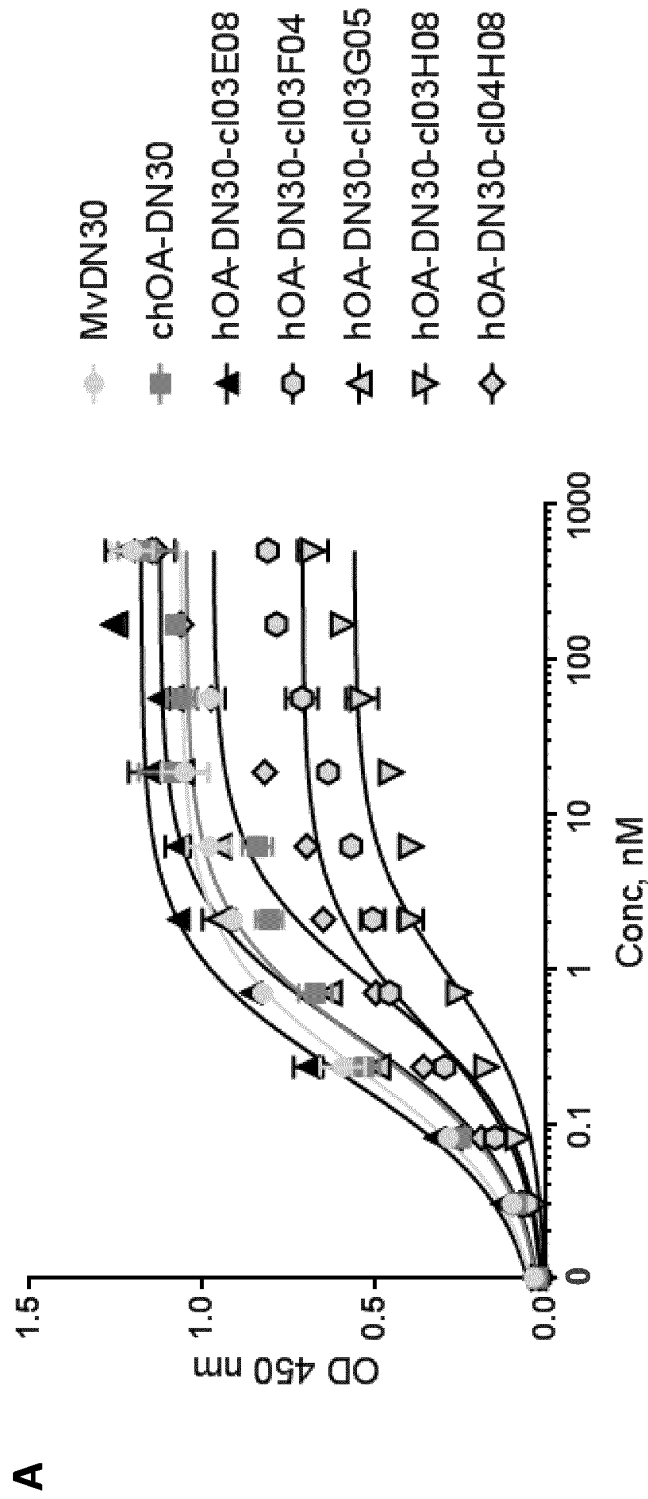
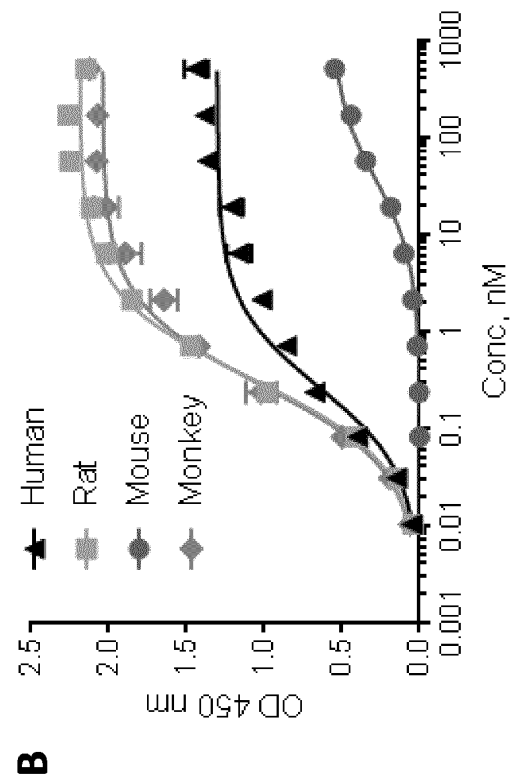


Fig. 1/cont



	Kd (nM)	Bmax (AU)	R square
MvDN30	0.210 ± 0.027	1.061 ± 0.022	0.98
chOA-DN30	0.319 ± 0.052	1.046 ± 0.026	0.96
hOA-DN30-cl03E08	0.202 ± 0.018	1.177 ± 0.016	0.99
hOA-DN30-cl03F04	0.419 ± 0.076	0.708 ± 0.021	0.96
hOA-DN30-cl03G05	0.375 ± 0.052	1.123 ± 0.025	0.97
hOA-DN30-cl03H08	0.859 ± 0.196	0.557 ± 0.021	0.94
hOA-DN30-cl04H08	0.686 ± 0.149	0.967 ± 0.035	0.94

Fig. 2



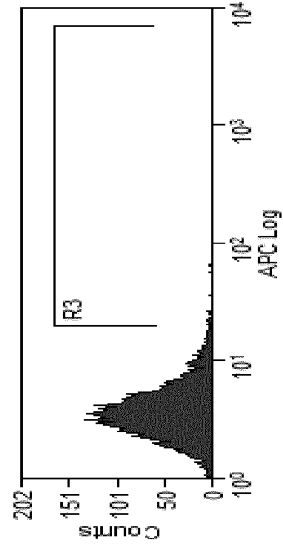
	Kd (nM)	Bmax (AU)	R square
Human	0.262 ± 0.037	1.303 ± 0.029	0,97
Rat	0.325 ± 0.016	2.189 ± 0.017	0,99
Mouse	35.99 ± 2.381	0.568 ± 0.012	0,99
Monkey	0.273 ± 0.021	2.041 ± 0.025	0,99

Fig. 2/cont

C

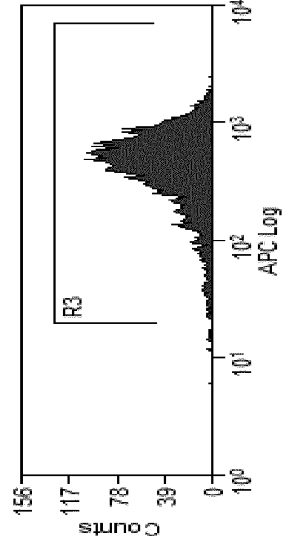
Negative control

MET+ (R3): 1.09%



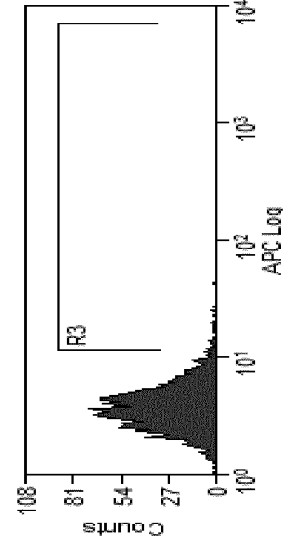
HUMAN (EBC1)

MET+ (R3): 99.14%



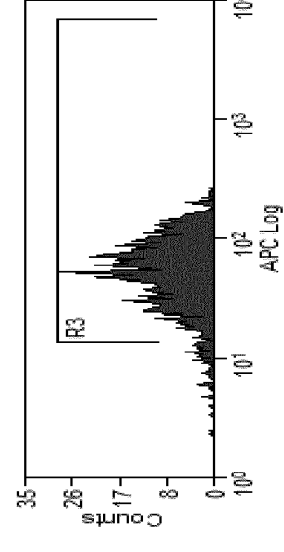
MOUSE (C2C12)

MET+ (R3): 2.17%



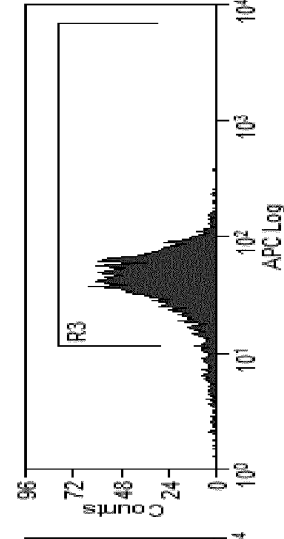
RAT (H9C2)

MET+ (R3): 94.15%



DOG (MDCK)

MET+ (R3): 93.10%



MONKEY (COS-7)

MET+ (R3): 97.74%

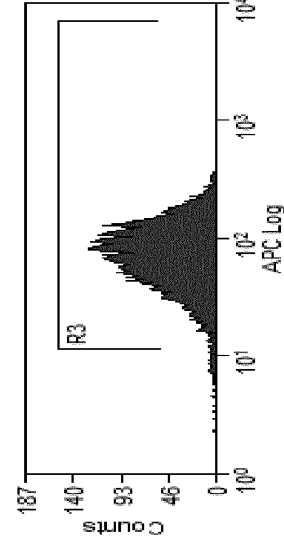


Fig. 2/cont

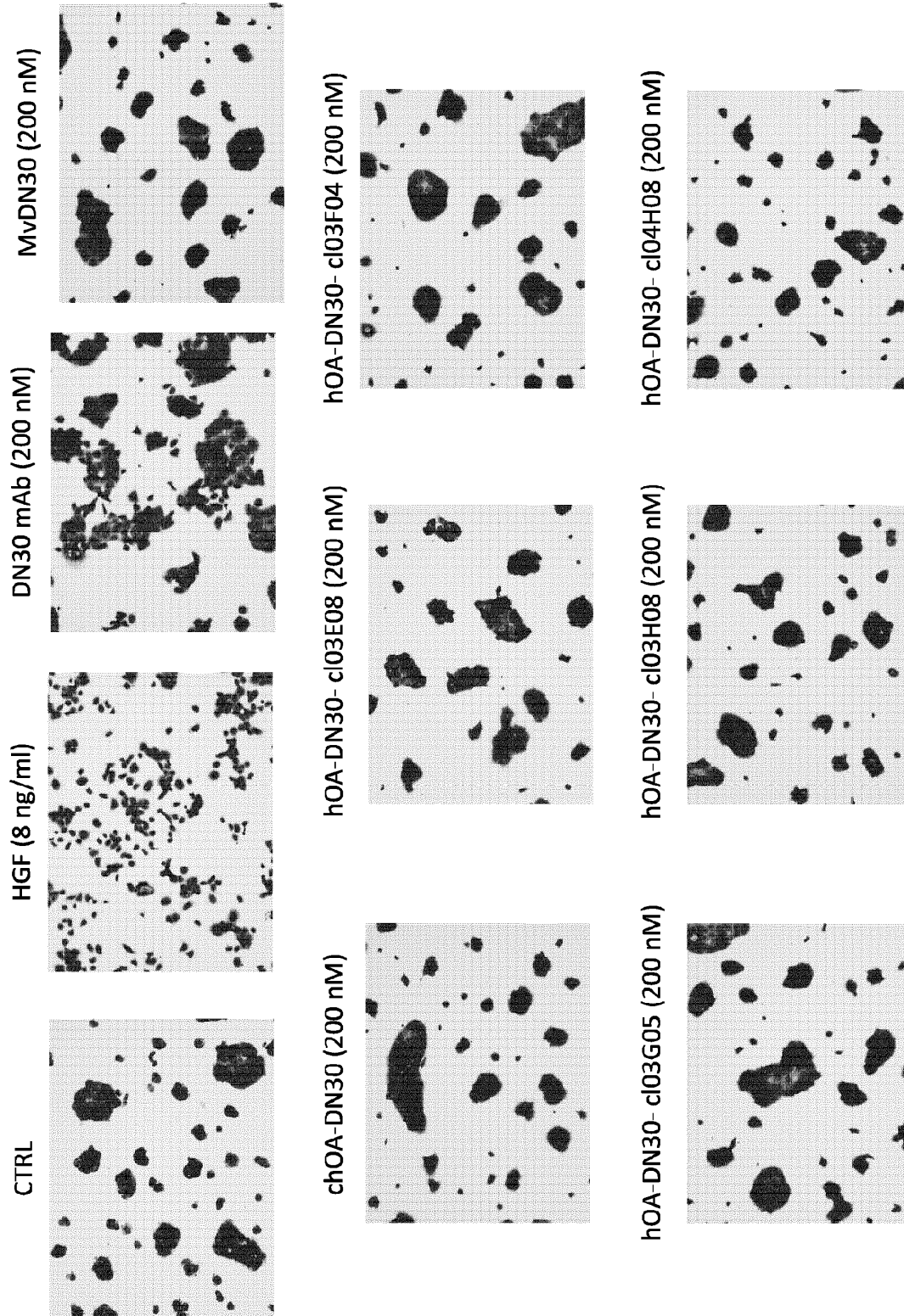


Fig. 3

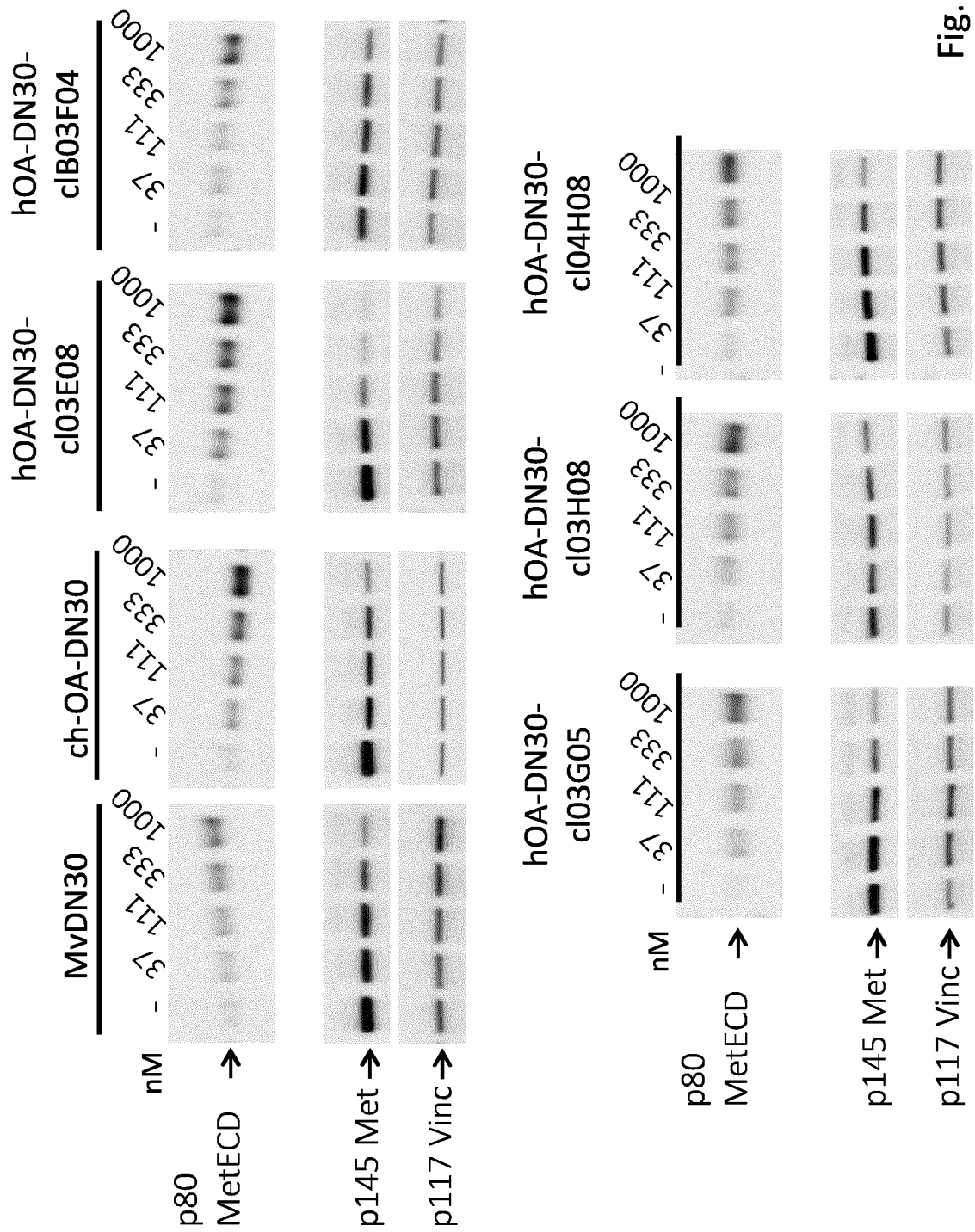


Fig. 4

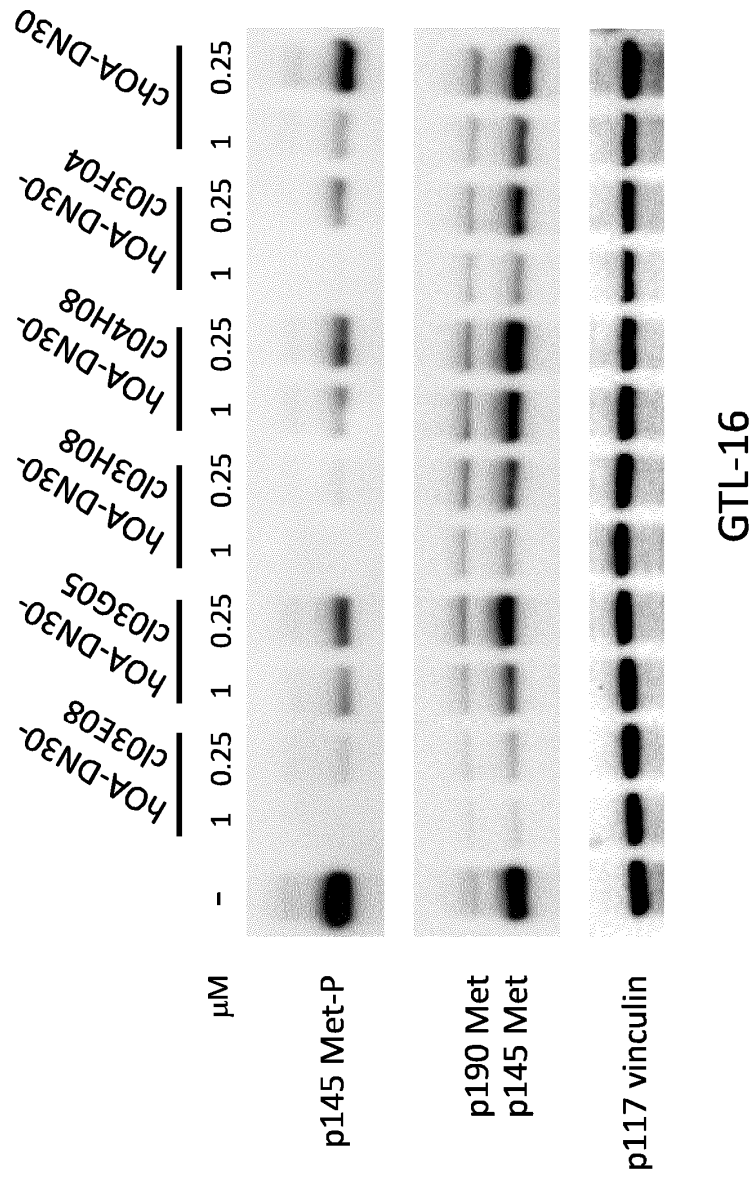
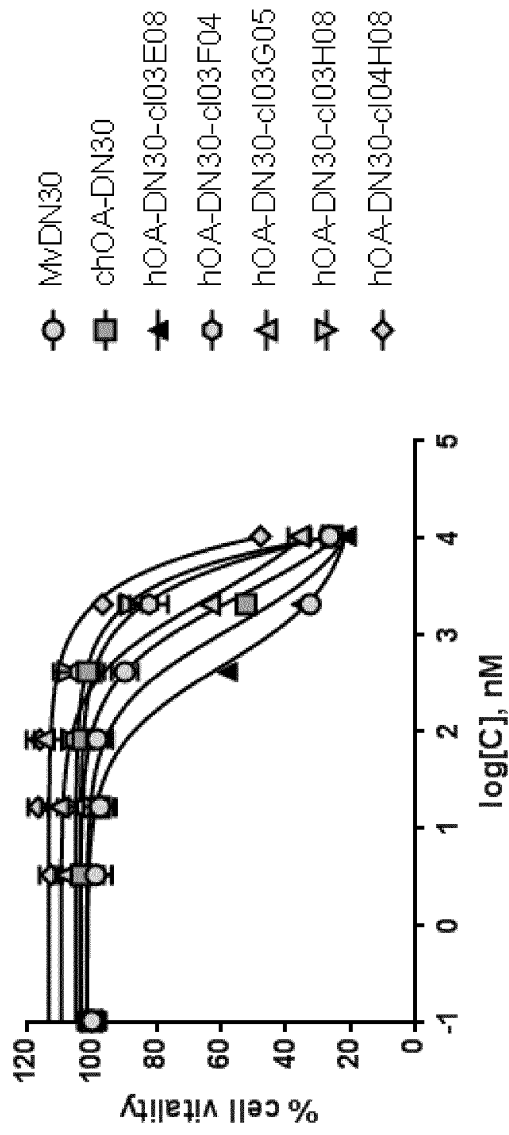


Fig. 5

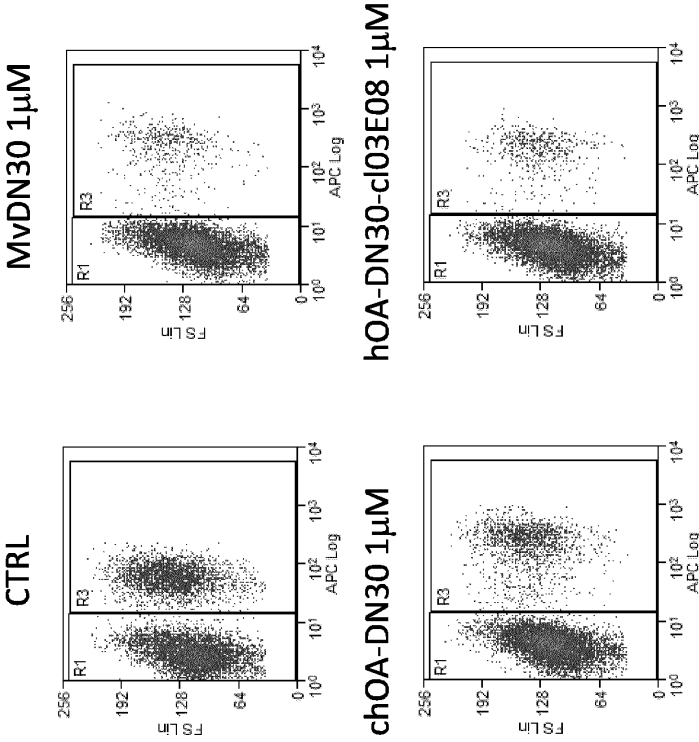


	IC50 (nM)	R square
MvDN30	1136±1.08	0.94
chOA-DN30	2489±1.77	0.96
hOA-DN30-cl03E08	460±1.07	0.98
hOA-DN30-cl03F04	52310±7.68	0.94
hOA-DN30-cl03G05	2381±1.31	0.95
hOA-DN30-cl03H08	N/A *	-
hOA-DN30-cl04H08	115726±311.2	0.91

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

Fig. 6

A

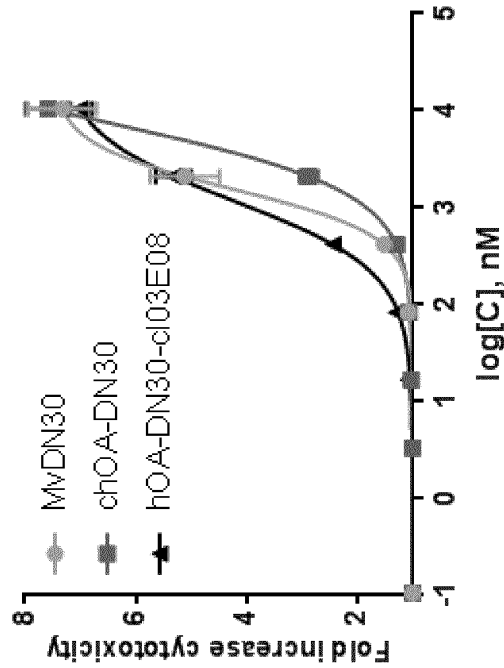


GTL-16

	% 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

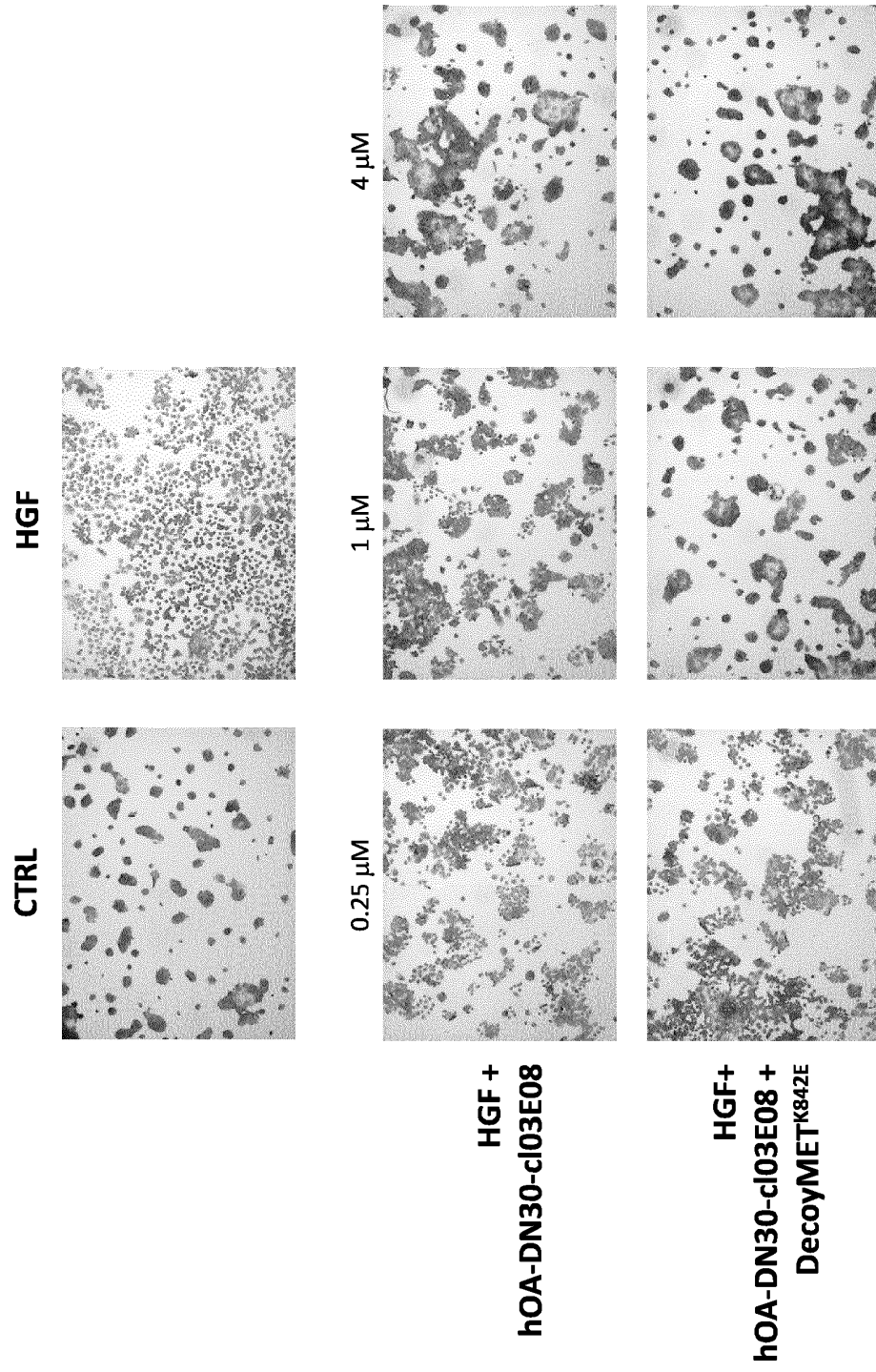
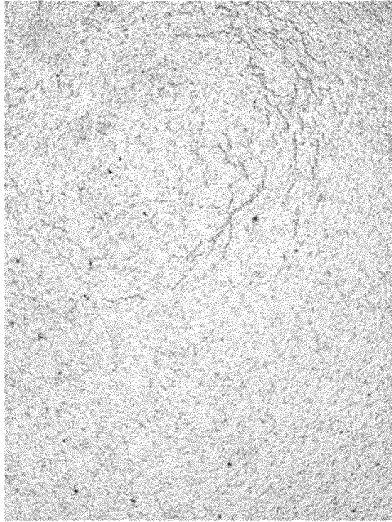
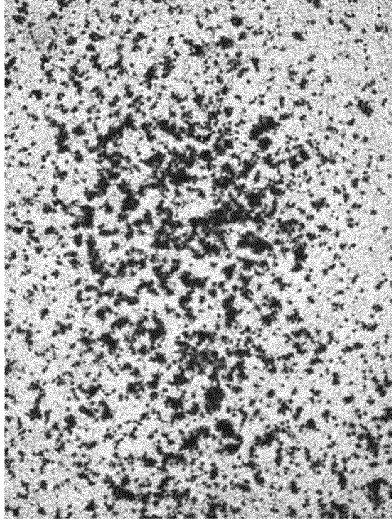


Fig. 8

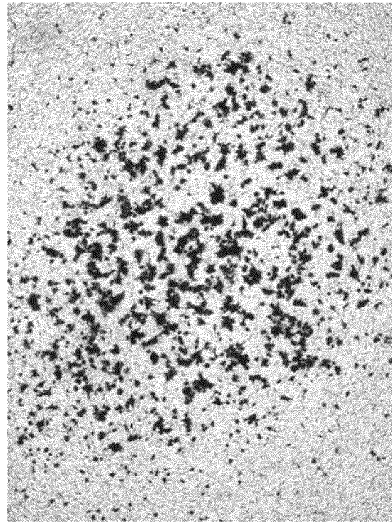
CTRL



HGF



HGF + hOA-DN30-cl03E08



HGF + hOA-DN30-cl03E08 + DecoyMET^{K842E}

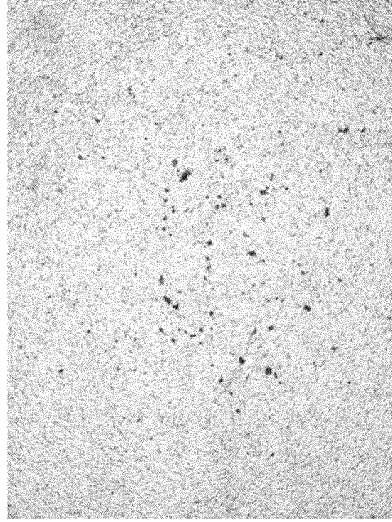


Fig. 9

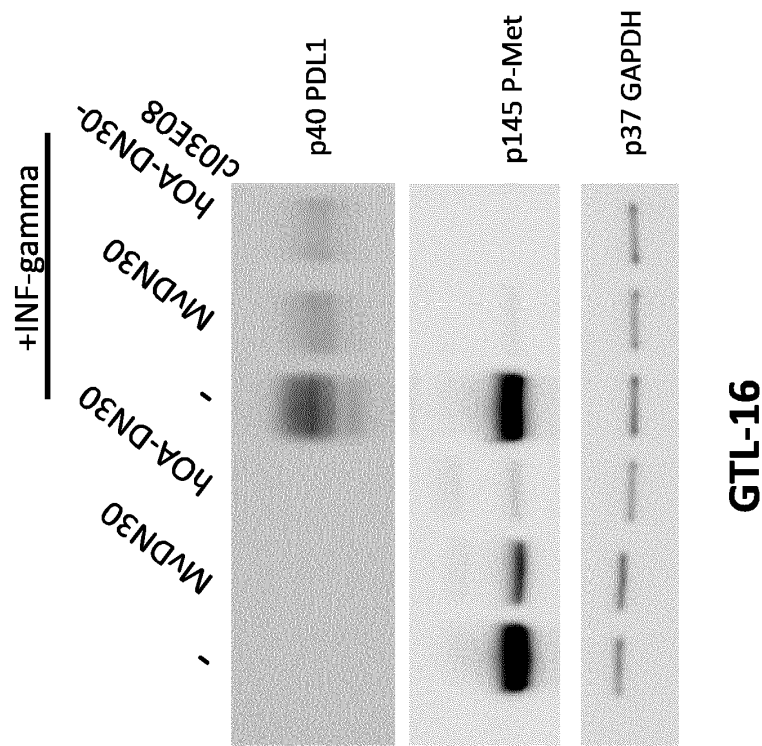


Fig. 10

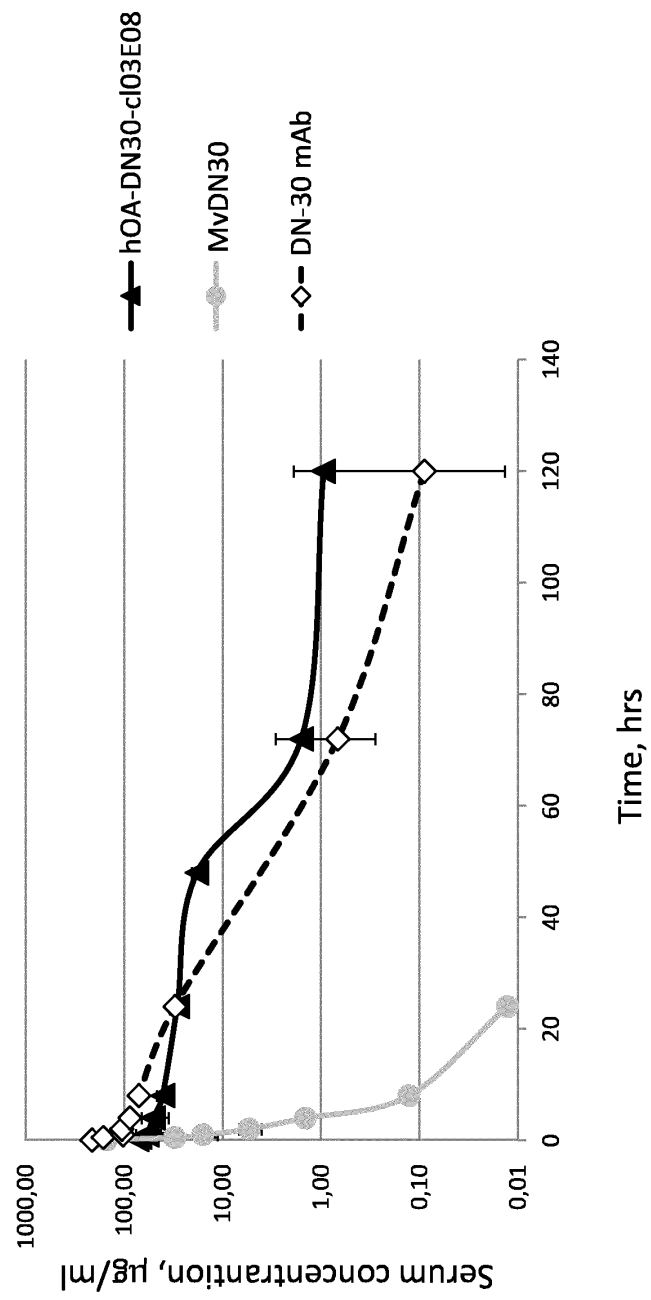


Fig. 11

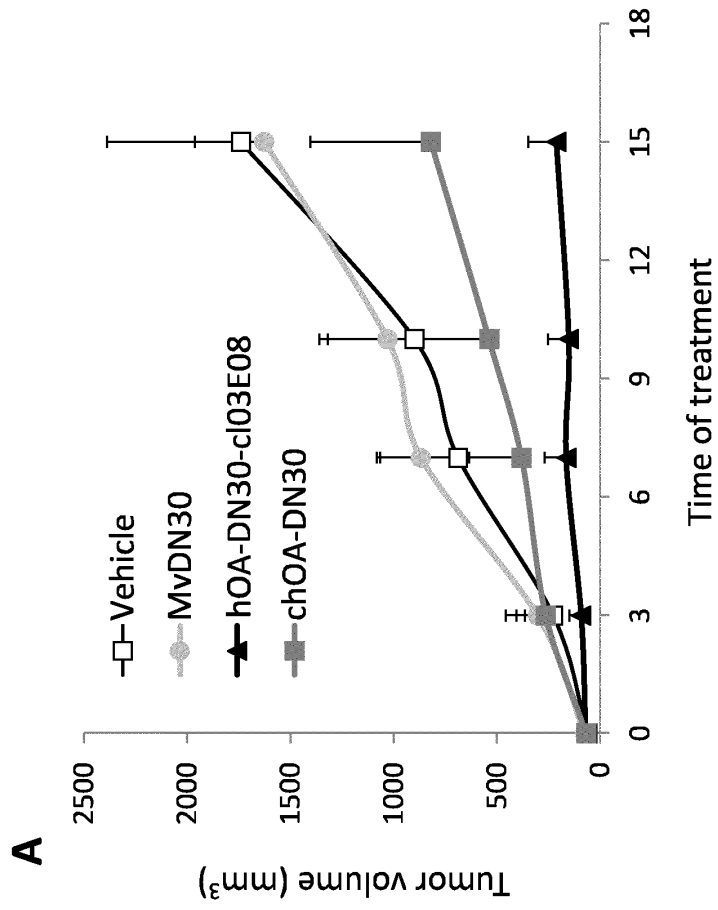


Fig. 12

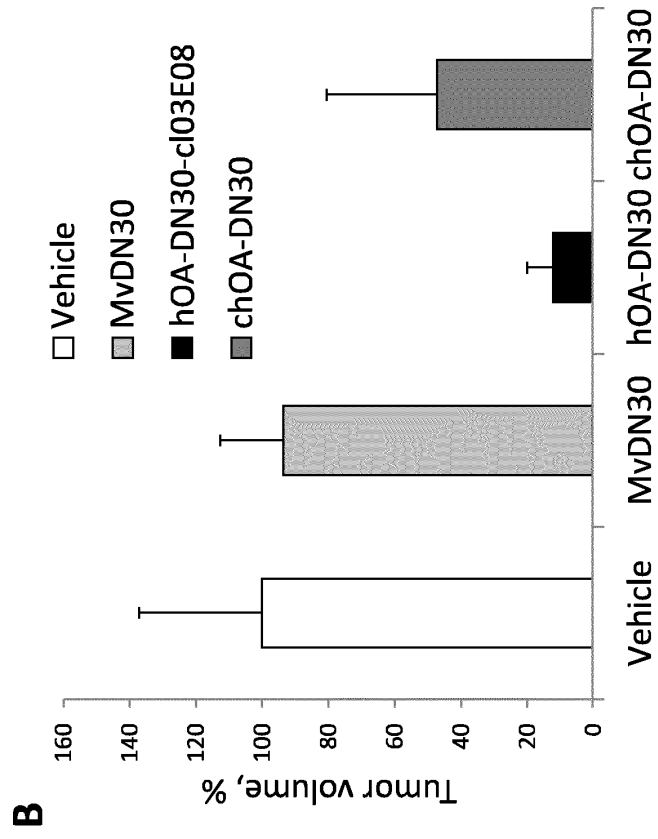


Fig. 12/cont

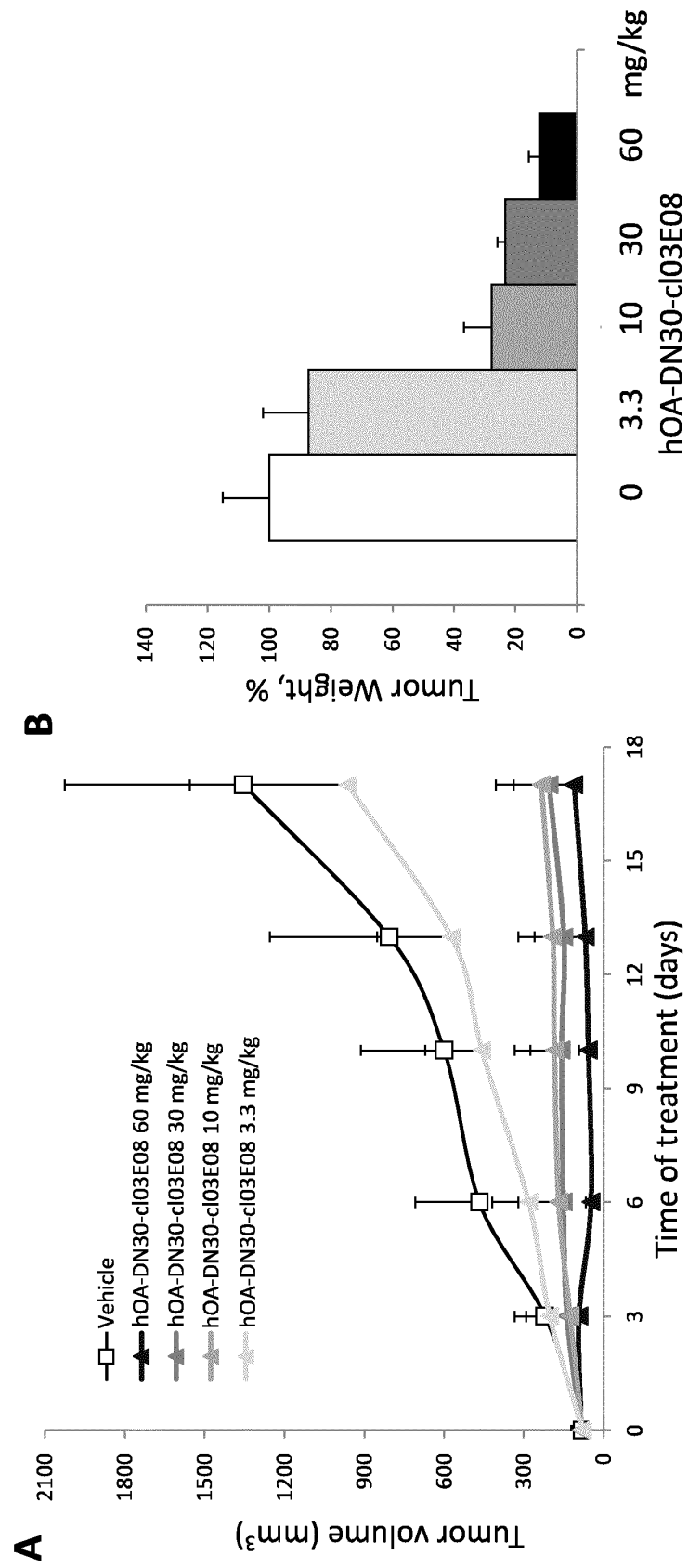


Fig. 13

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

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

Seq. ID N°9: human CL
RTVAAPSVFIFPPSDEQLKSGTASV^VCLLNNFY^PREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS^T
LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Seq. ID N°10: human CH1
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT^SWNSGALTSGVHTFPAVLQSSGLYSLSSV^VTV
PSSSLGTQTYICNVNHKPSNTKV^DKKV

Fig. 14

Seq. ID N°11: First Fc (Knob mutation)

EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELTKN
 QVSLWCLLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN
 HNTQKSLSLSPGK

Seq. ID N°12: Second Fc (Hole mutations)

MGWSYIIILFLVATATDGHSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
 VYITLPPSRDELTKNQVSLSCAVVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLVSKLTVDKSRWQQG
 NVFCSCVMHEALHNHYTQKSLSLSPGK

Fig. 15

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

MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAETPIQNVILHEHHIFLGATNYIYV
LNEEDLQKVAEYKGTGPVLEHPDCFFPCQDCSSKANLSGGWKDNINMALVVDITYDDQLISCGSVNRGTCQRH
VFPHNHTADIQSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSVKDRFINFFVGNTINSSYFPDHPHLSISV
RRLKETKDGFMFLTDQSYIDVLPEDRDSYPIKYVHAFESNNFIYFLTQRETLDAQTFHTRIIRFCSINSGL
HSYMEMPLLECILTEKRKKRSTKKEVFNILQAAVSKPGAQLARQIGASINDDILFGVFAQSKPDSAEPMDRS
AMCAFPKIYVNDFFNKIVNKNNVRCLQHFFYGNHEHCNRTLRLNSSGCEARRDEYRTEFTTALQVRDLFMG
QFSEVLLTSISTFIKGDLTIANLGTSEGRFMQVVSRSGPSTPHVNFLLDSHPVSPVEIVEHTLNQNGYTLV
ITGKKITKIPLNGLGCRHFQSCSQCLSAPPFVQCGWCHDKCVRSEECLSGTWTQQICLPAIYKVFPNSAPLE
GGTRLTICGWDFGFRNRNKFDDLKTRVLLGNESTLTLSSESTMNTLKCTVGPAMNKHFNMSIIISNGHGTQ
YSTFSYVDPVITSISPKYGPMAGGTLLTLTGNYLNSGNSRHSIGGKTCTLKSVSNSILECYTPAQTIISTEF
AVKLIKIDLANRETSIFSYPREDPIVYELIHPYTKSFISGGSTITGVGKNLNSVSVPRMVINVHEAGRNF^ETVACQH
RSNSEIICCTTPSLQQLNLQPLPKTKAFFMLDGILSKYFDLLIYVHNPFVPEPEKPVMI SMGNENNVLEIKGND
IDPEAVKGEVLKVGNKSCENIHLHSEAVLCTVPNDLLKLNSELNIEWKQAISSTVLGKVI VQPDQNF^ETASGA
AWSHPQFEKGAAWSHPQFEKGAAWSHPQFEKGA^EAAAAHHHHH

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Fig. 16