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10	20	30	40	50
MGPWSRSLSA	LLLLLQVSSW	LCQEPEPCHP	GFDAESYTFT	VERRHLERGR
60	70	80	90	100
VLGRVNFEDC	TGRQRTAYFS	LDTRFKVGTD	GVITVKRPLR	FHNPQIHFLV
110	120	130	140	150
YAWDSTYRK	STKVTLNTVG	HHHRPPPHQA	SVSGIQAELL	TFPNSSPGLR
160	170	180	190	200
RQKRDWVIPP	ISCPENEKGP	FPKNLVQIKS	NKDKEGKVFY	SITGQGADTP
210	220	230	240	250
PVGVFIIERE	TGWLKVTEPL	DRERIATYTL	FSHAVSSNGN	AVEDPMEILI
260	270	280	290	300
TVTDQNDNKP	EFTQEVFKGS	VMEGALPGTS	VMEVTATDAD	DDVNTYNAAI
310	320	330	340	350
AYTILSQDPE	LPDKNMFTIN	RNTGVISVVT	TGLDRESFPT	YTLVVQAADL
360	370	380	390	400
QGEGLSTTAT	AVITVTDND	NPPIFNPTTY	KGQVPENEAN	VVITTLKVTD
410	420	430	440	450
ADAPNTPAWE	AVYTILNDDG	GQFVVTTNPV	NNDGILKTAK	GLDFEAKQQY
460	470	480	490	500
ILHVAVTNVV	PFEVSLTTST	ATVTVDVLDV	NEAPIFVPPE	KRVEVSEDFG
510	520	530	540	550
VGQEITSYTA	QEPDTFMEQK	ITYRIWRDTA	NWLEINPDTG	AISTRAELDR
560	570	580	590	600
EDFEHVKNST	YALIIATDN	GSPVATGTGT	LLLILSDVND	NAPIPEPRTI
610	620	630	640	650
FFCERNPKPQ	VINIIDADLP	PNTSPFTAEL	THGASANWTI	QYNDPTQESI
660	670	680	690	700
ILKPKMALEV	GDYKINLKL	DNQNKDQVTT	LEVSVCDCEG	AAGVCRKAQP
710	720	730	740	750
VEAGLQIPAI	LGILGGILAL	LILILLLLLF	LRRRAVVKEP	LLPPEDDTRD
760	770	780	790	800
NVYYYDEEGG	GEEDQDFDLS	QLHRGLDARP	EVTRNDVAPT	LMSVERYLPR
810	820	830	840	850
PANPDEIGNF	IDENLKAADT	DPTAPPYDSL	LVFDYEGSGS	EAASLSSLNS
860	870	880		
SESDKDQDYD	YLNEWGNRFK	KLADMYGGGE	DD	

Fig. 1A

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Signal peptide:

MGPWSRSLSALLLLLQVSSWLCQEPEP

Precursor sequence:

CHPGFDAESYTFVPRRHLEGRVLGRVNFEDCTGRQRTAYFSLDTRFKVGTGCVIT
VKRPLRFHNPQIHFLVYAWDSTYRKFSKVTLNTVGHHRPPPHQASVSGIQAELLT
FPNSSPGLRRQKR

EC1 domain:

DWVIPPISCPENEKGPFKPNLVQIKSNKDKGKVFYSITGQGADTPPVGVFIHERETGW
LKVTEPLDRERIATYTLFSHAVSSNGNAVEDPMEILITVTDQNDNKPEF

EC2 domain:

TQEVFKGSVMEGALPGTSVMEVTATDADDDVNTYNAAIAYTILSQDPELPDKNMFT
INRNTGVISVVTGLDRESFPTYTLVVQAADLQGEGLSTTATAVITVTDNDNPPIF

EC3 domain:

NPTTYKGQVPENEANVVITTLKVTADAPNTPAWEAVYTILNDDGGQFVVTNPNVN
NDGILKTAKGLDFEAKQQYILHVAVTNVVPFEVSLTTSTATVTVDVLDVNEAPIF

EC4 domain:

VPPEKRVEVSEDFGVGQEITSYTAQEPDTFMEQKITYRIWRDTANWLEINPDTGAIST
RAELDREDFEHVKNSTYTALIIATDNGSPVATGTGTLLLLILSDVNDNAPIP

EC5 domain:

EPRTIFFCERNPKPQVINIIDADLPNTSPFTAELTHGASANWTIQYNDPTQESIILKPK
MALEVGDYKINLKLMDNQNKDQVTTELSVCDCEGAAGVCRKAQPVEAGL

TM domain:

QIPAILGILGGILALLILLLLLLFL

Cytoplasmic domain 1:

RRRAVVKEPLLPEDDTRDNVYYYDEEGGGEEDQDFDLSQLHRGLDARPEVTRNDV
APTLMSVPRYLPRPA

Cytoplasmic domain 2:

NPDEIGNFIDENLKAADTDPTAPPYDSLLVFDYEGSGSEAASLSSLNSSESDKDQDYD
YLNEWGNRFKKLADMYGGGEDD

Fig. 1B

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EVSLTTSTATVTVDVLDVNEAPIFVPPEKRVEVSEDFG
VGQEITSYTAQEPDTFMEQKITYRIWRDTANWLEIN
PDTGAISTRAELDREDFEHVKNSTYTALIIATDNGSPV
ATGTGTLILLSDVNDNAPIPEPRTIFFCERNPKPQVIN
IIDADLPPNTSPFTAELTHGASANWTIQYNDPTQESII
LKPKMALEVGDYKINLKLMDNQNKDQVTTLEVSV
DCEGAAGVCRKAQPVEAGLQIPAILGILGGILALLILILL
LLLFLRRRAVVKEPLLPPEDDTRDNVYYYDEEGGEE
DQDFDLSQLHRGLDARPEVTRNDVAPTLMSVPRYL
PRPANPDEIGNFIDENLKAADTDPTAPPYDSLLVFDY
EGSGSEAASLSSLNSSESDDKDQDYDYLNEWGNRFKK
LADMYGGGEDD

Fig. 1C

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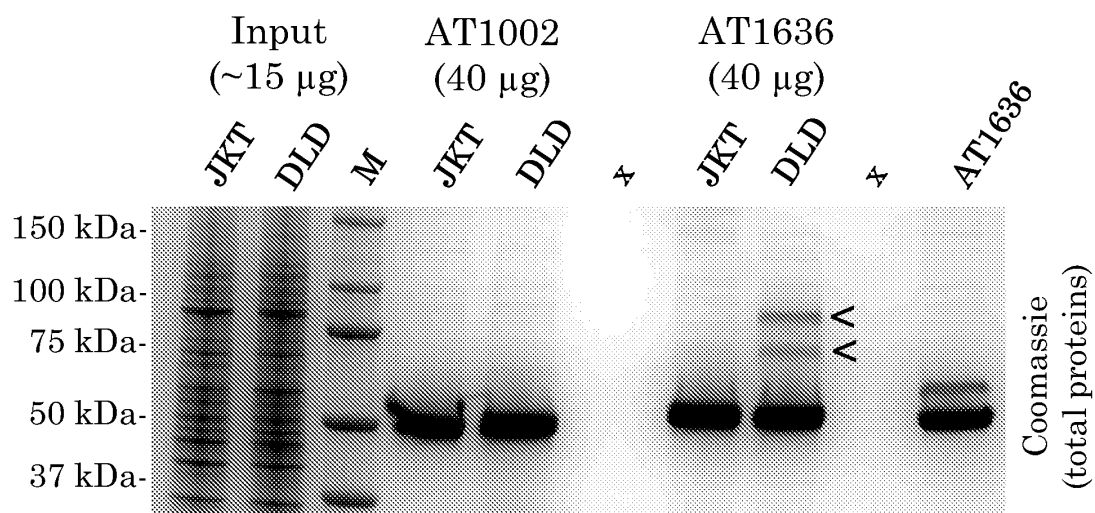


Fig. 2A

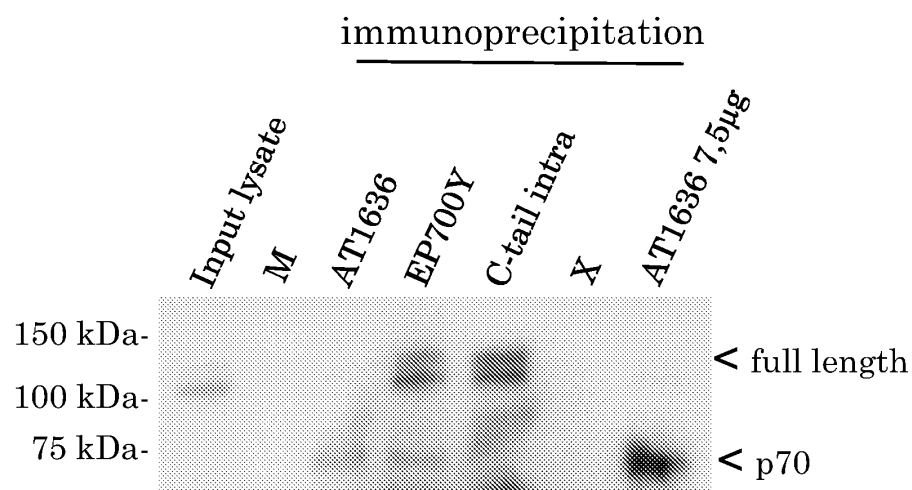


Fig. 2B

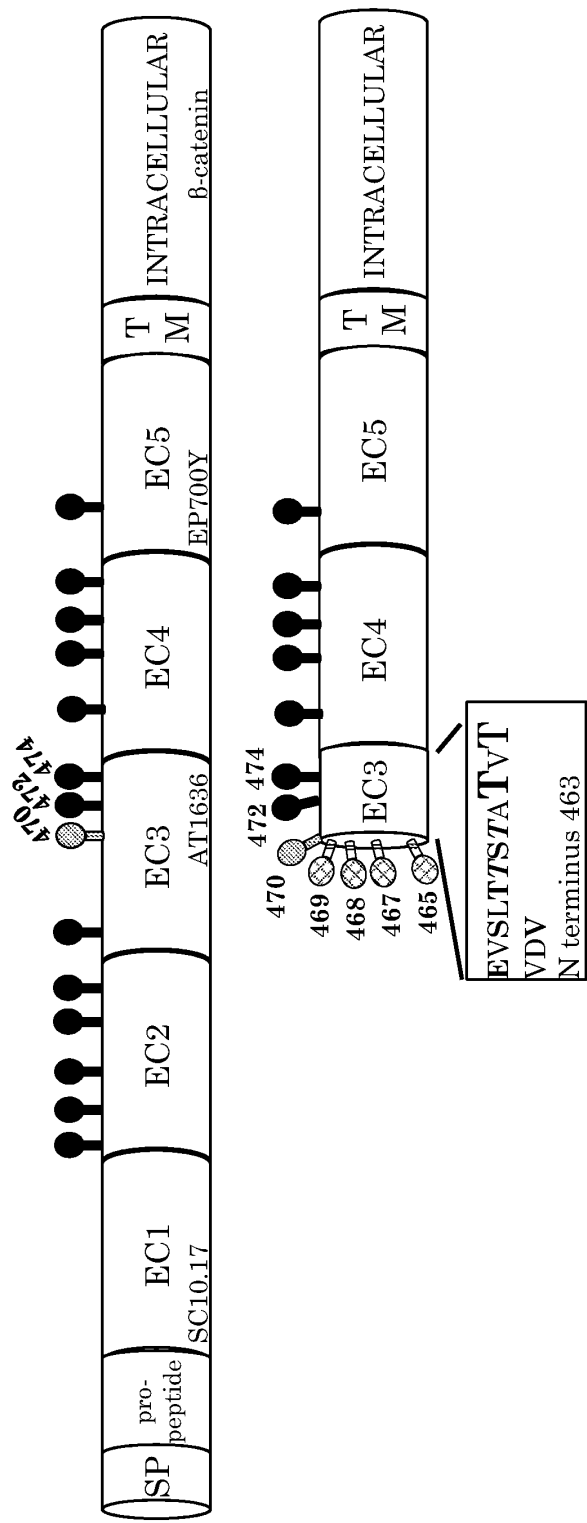


Fig. 3

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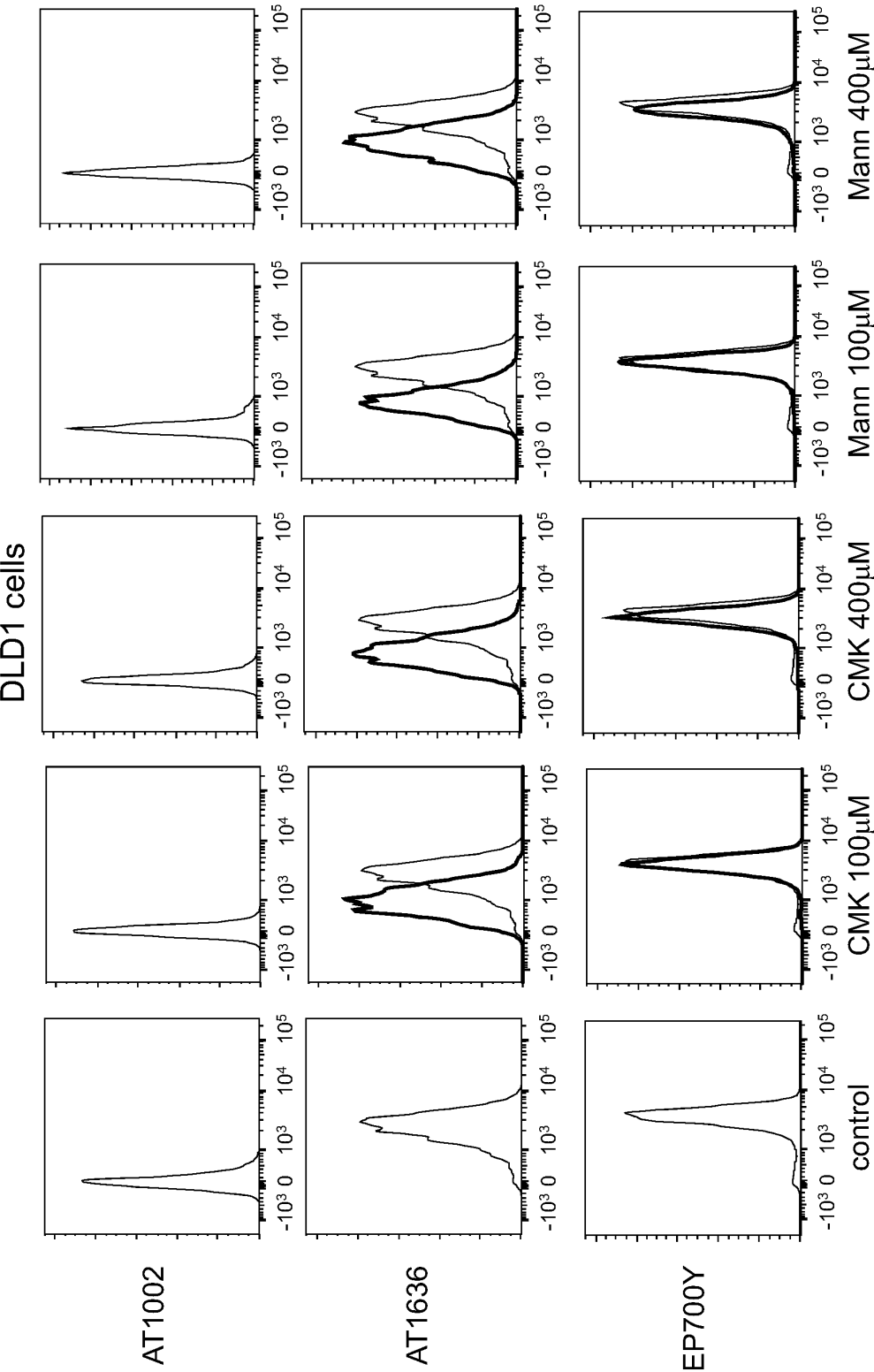


Fig. 4

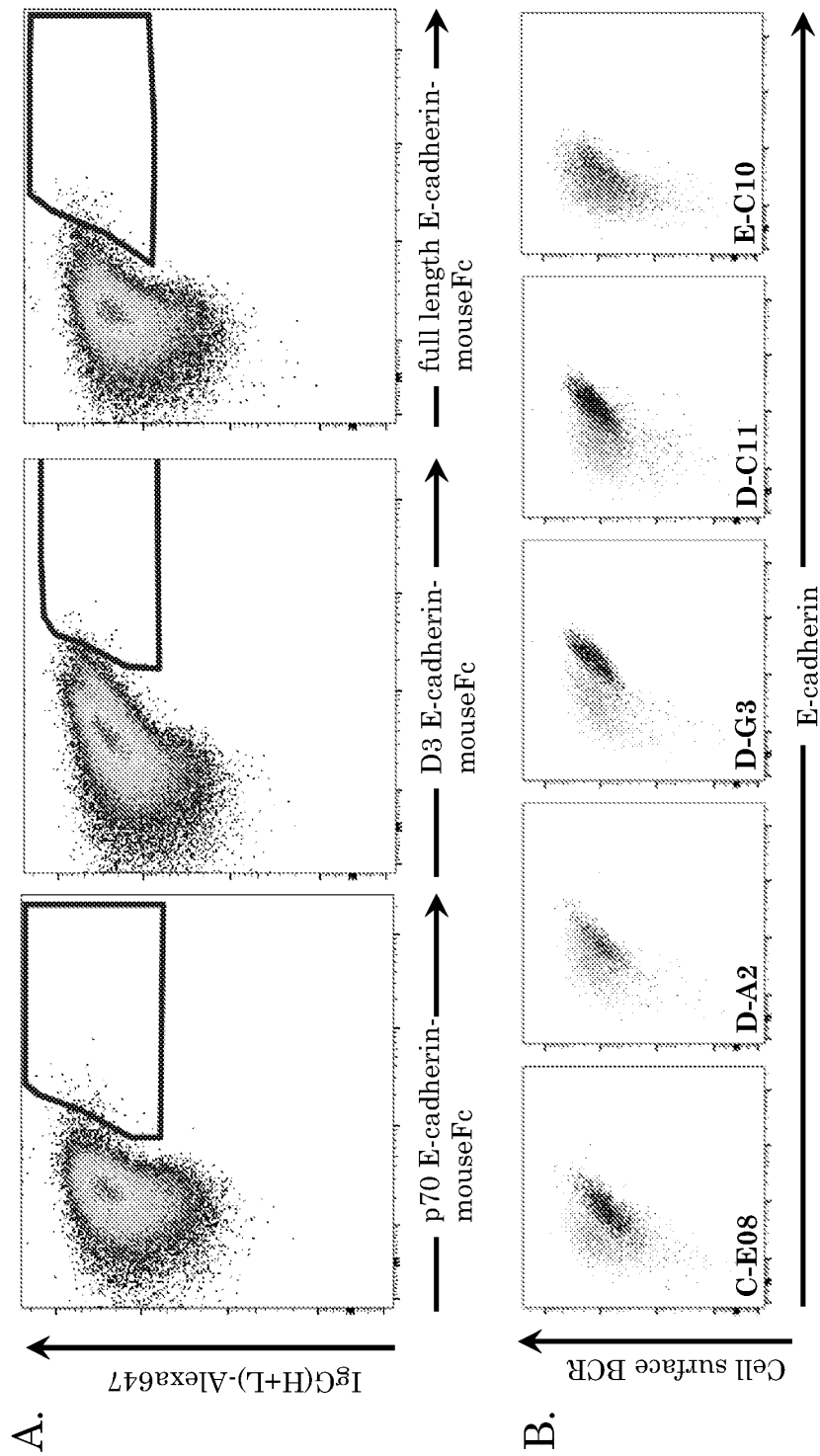


Fig. 5

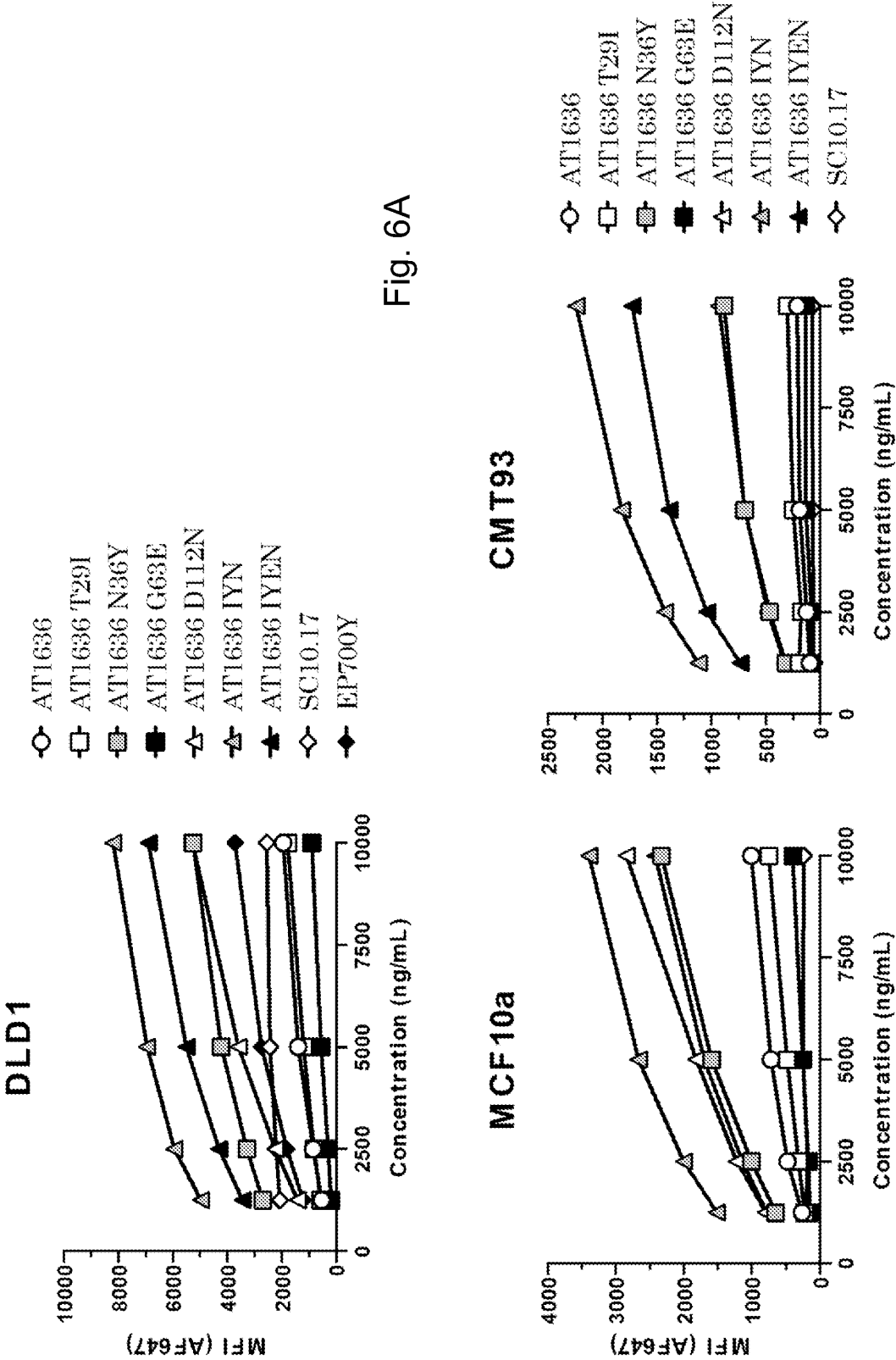


Fig. 6A

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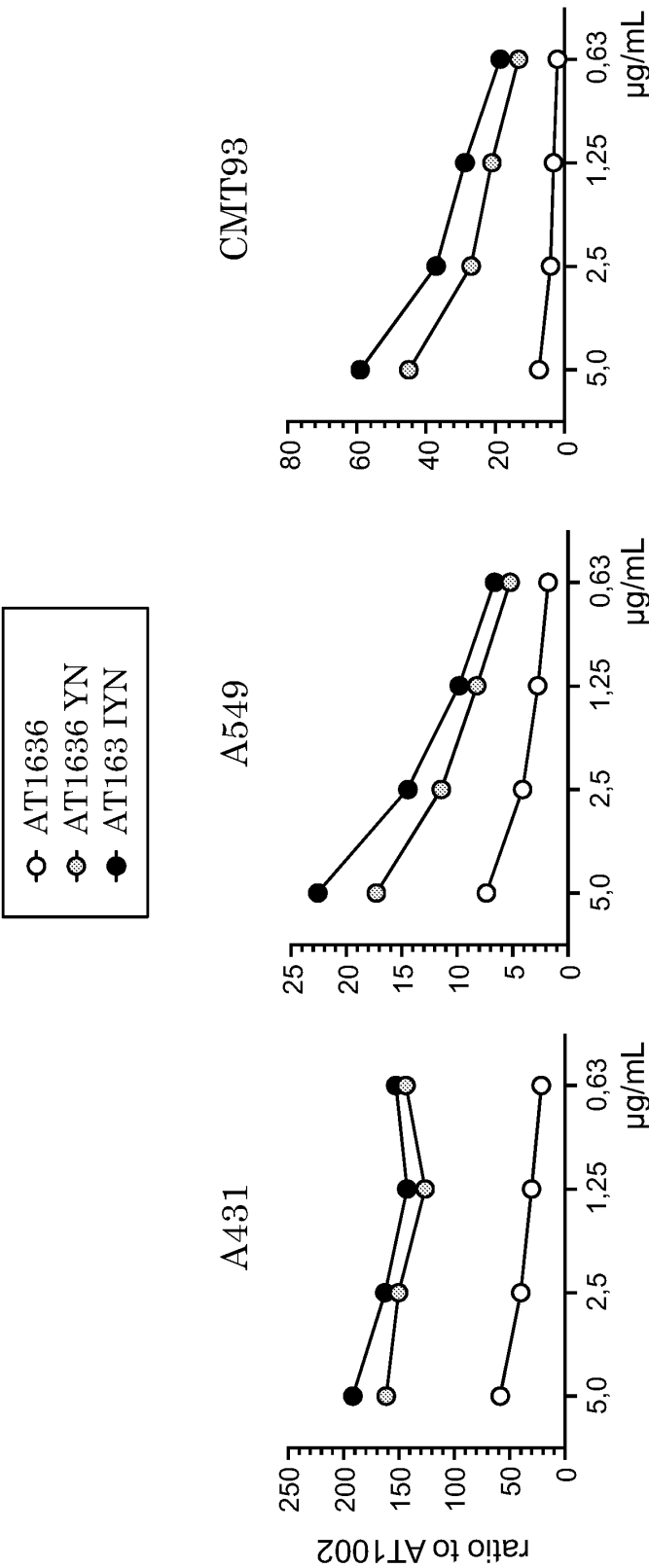


Fig. 6B

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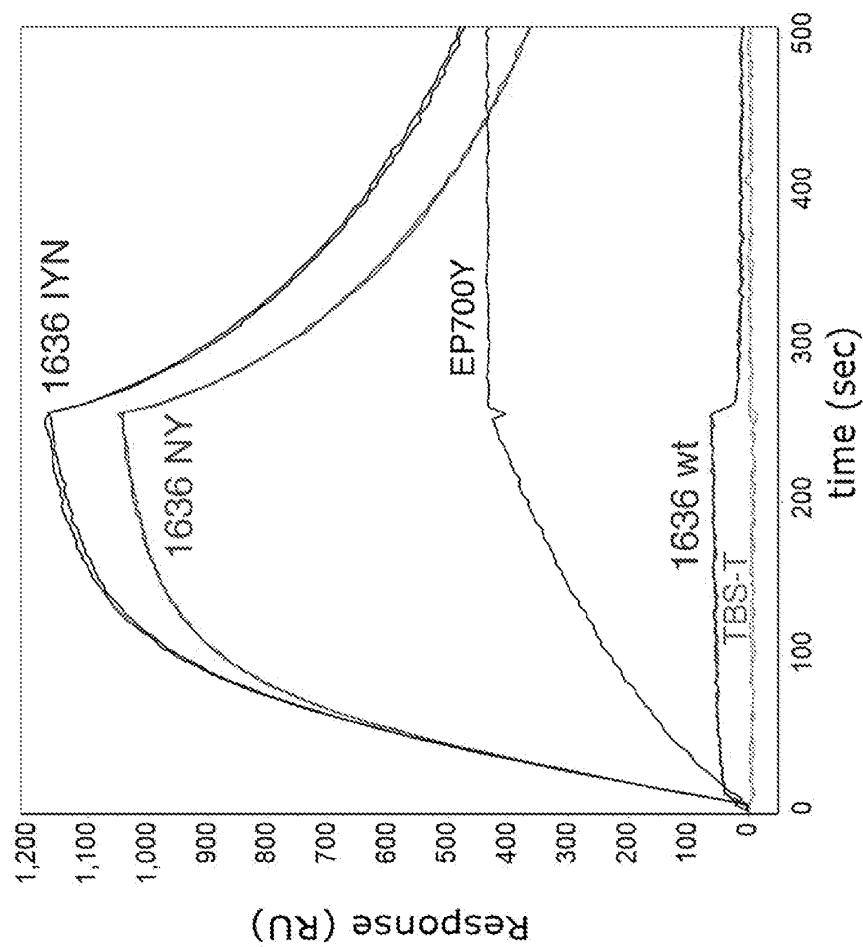


Fig. 7A

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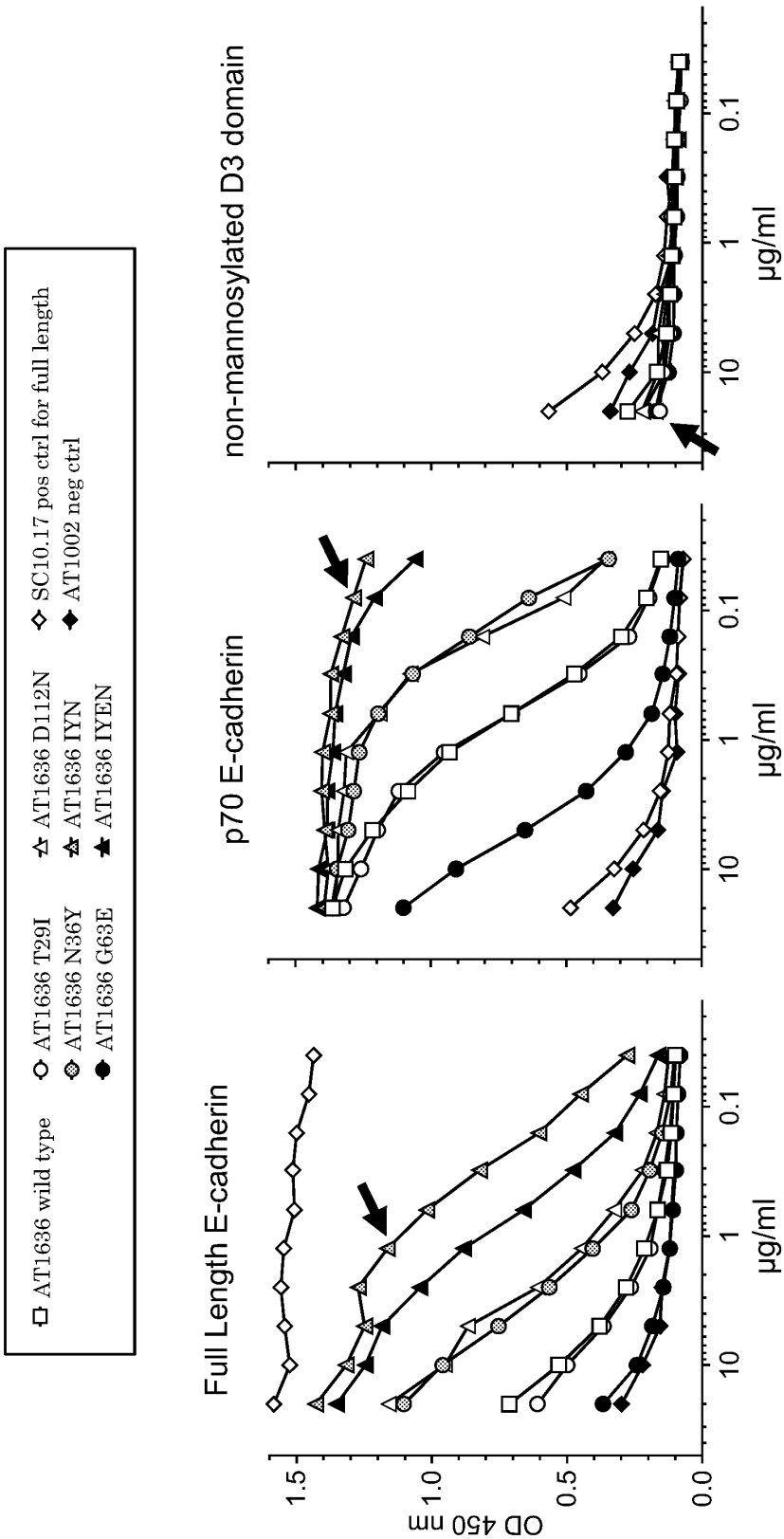


Fig. 7B

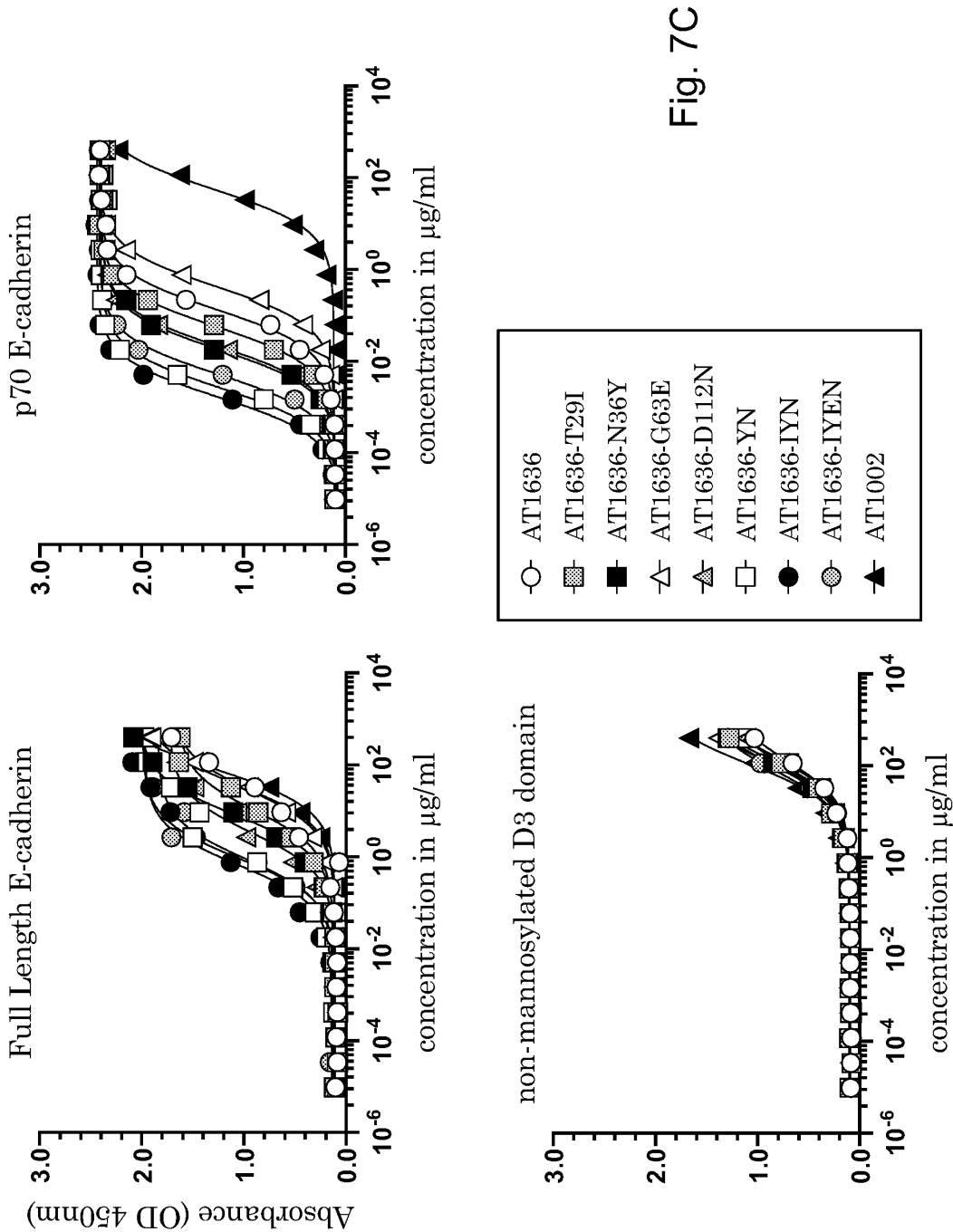


Fig. 7C

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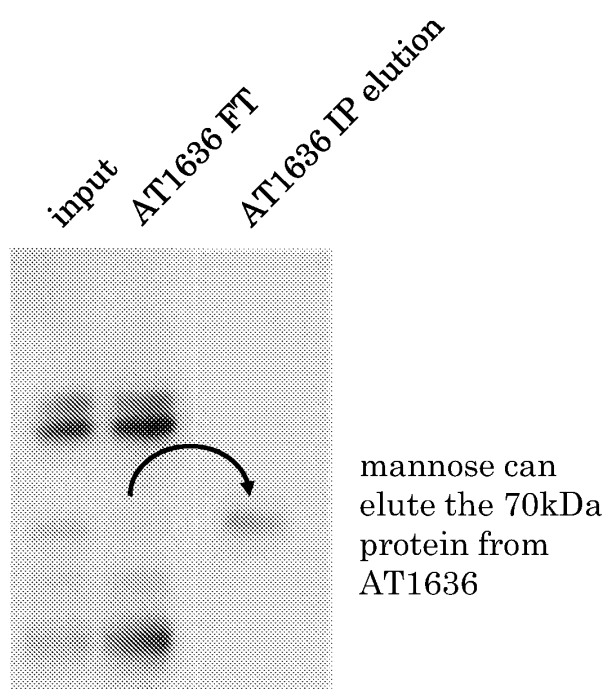


Fig. 8A

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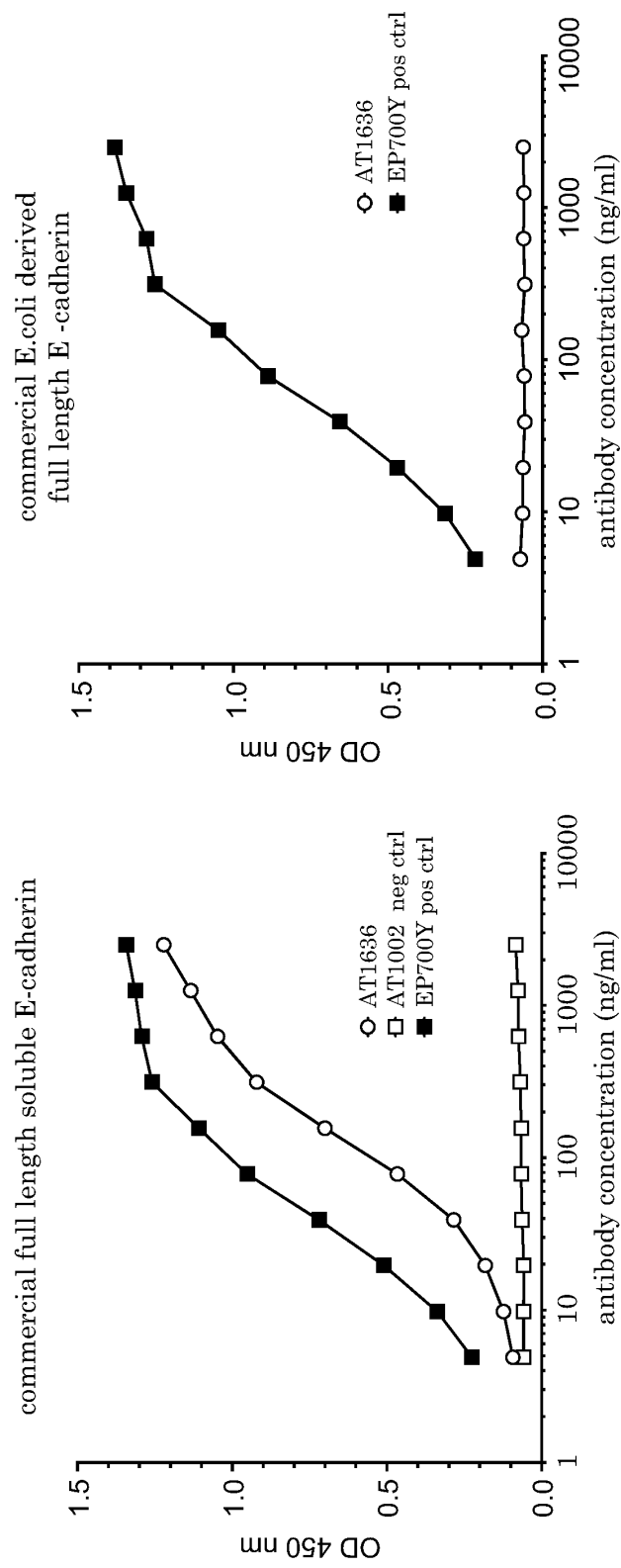


Fig. 8B

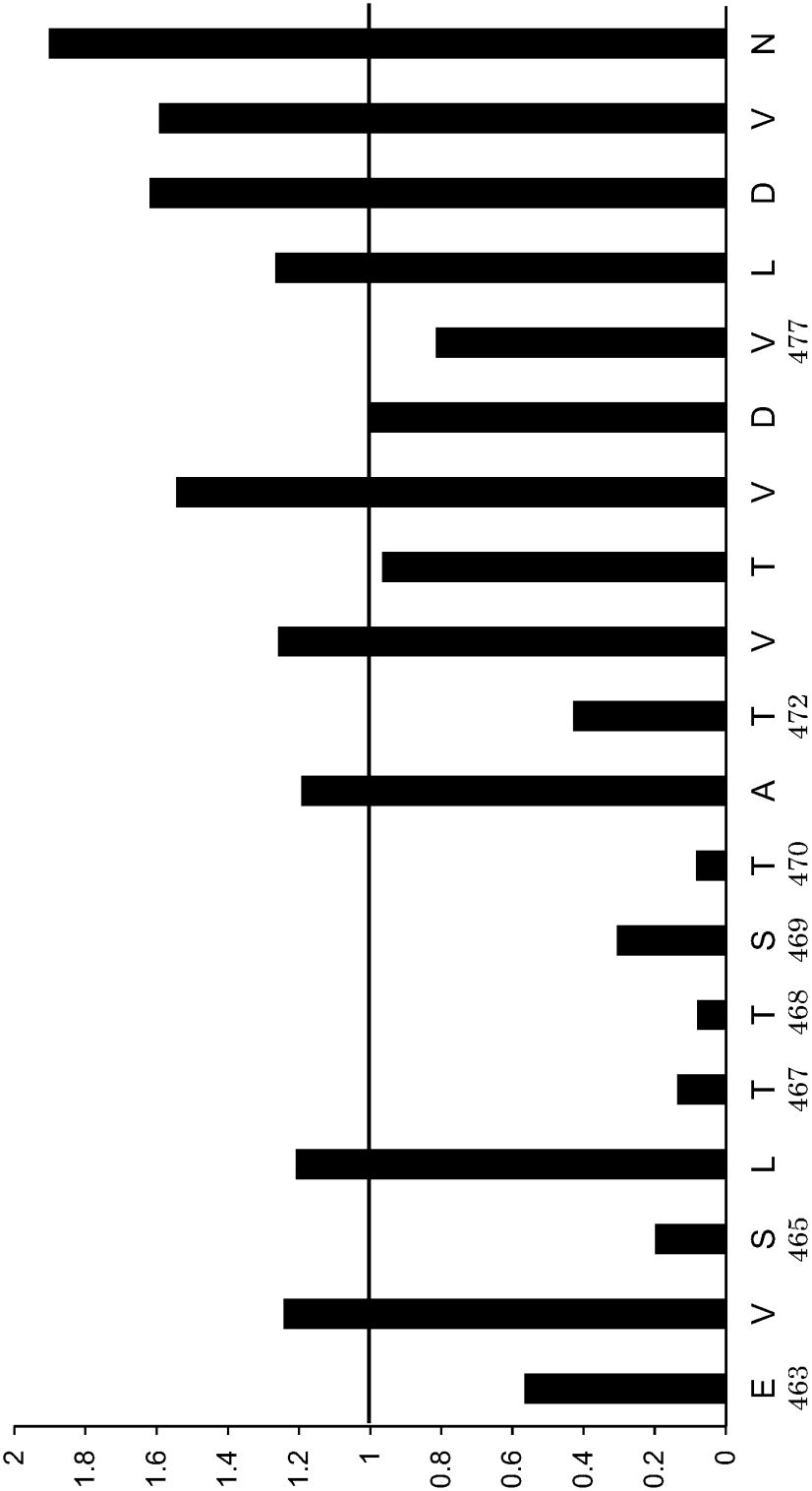


Fig. 9

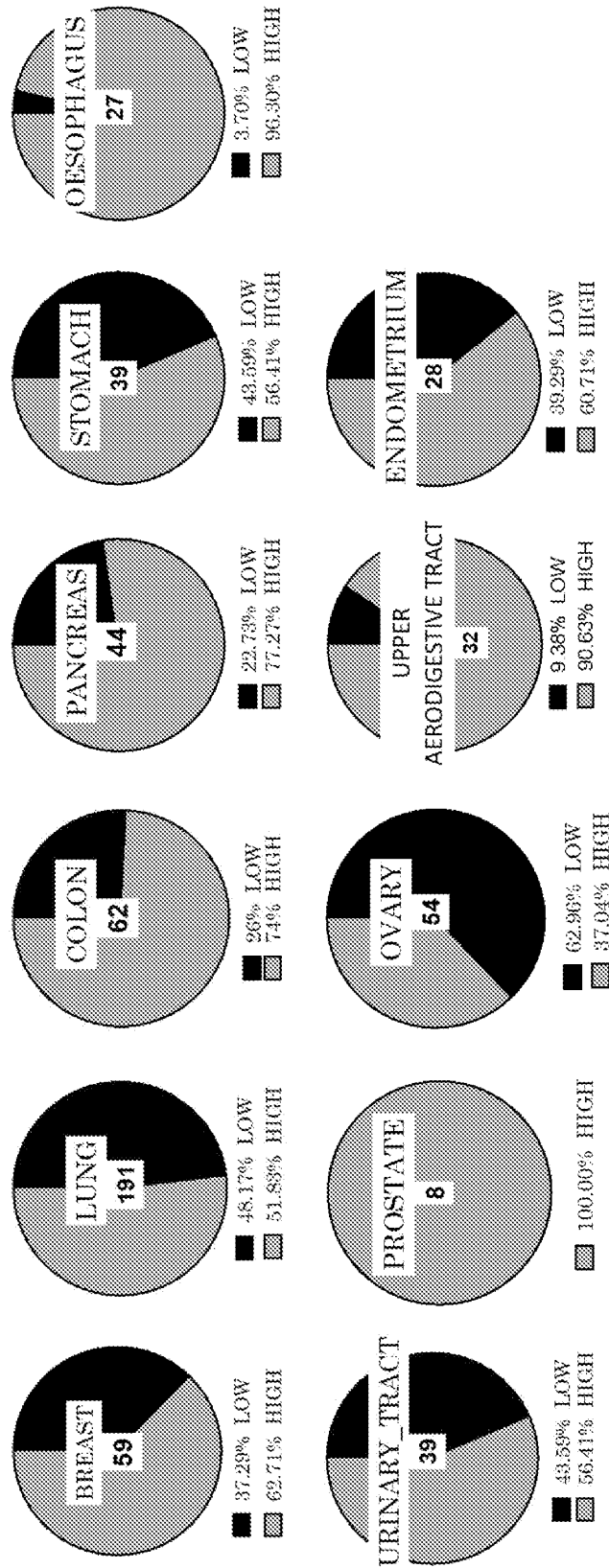


Fig. 10

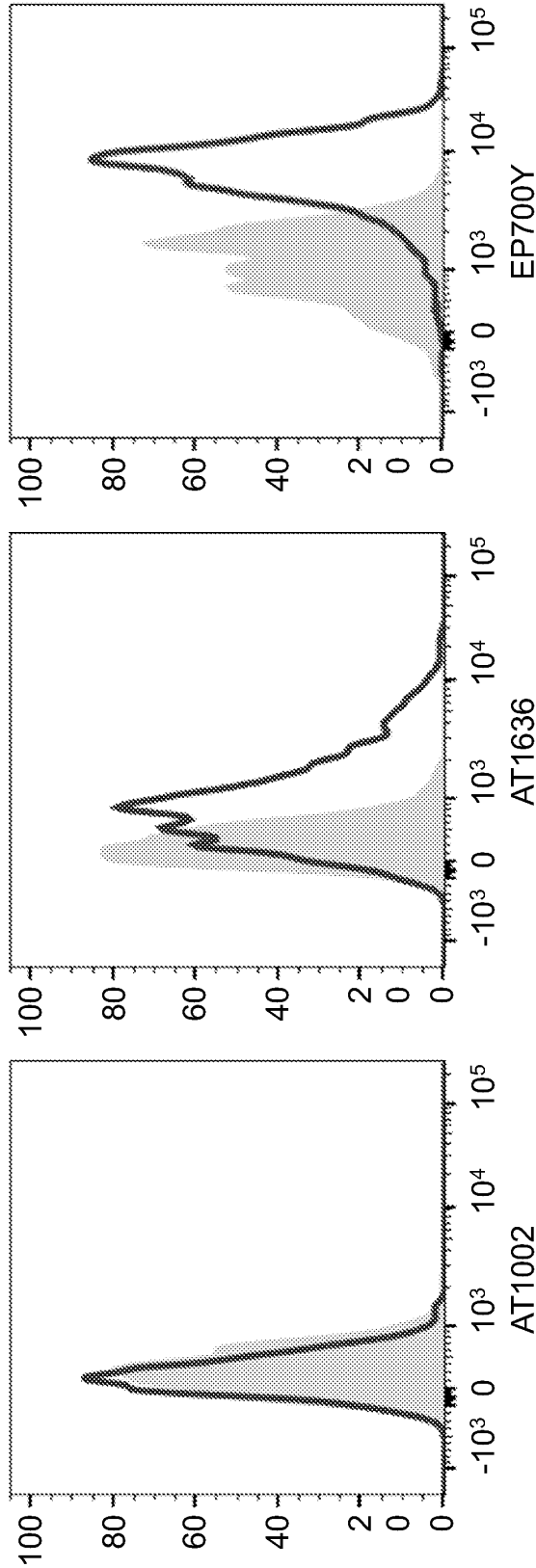


Fig. 11

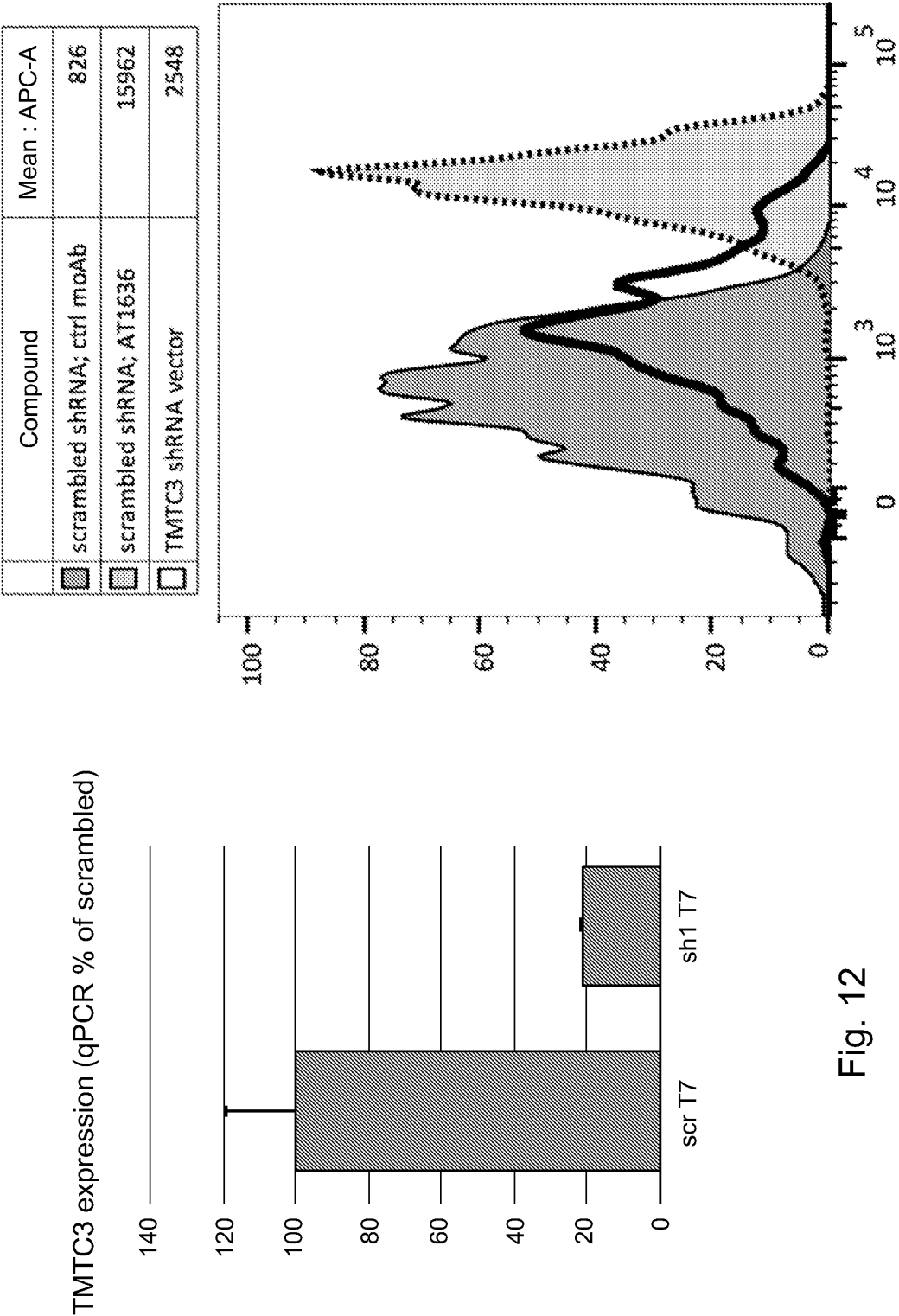


Fig. 12

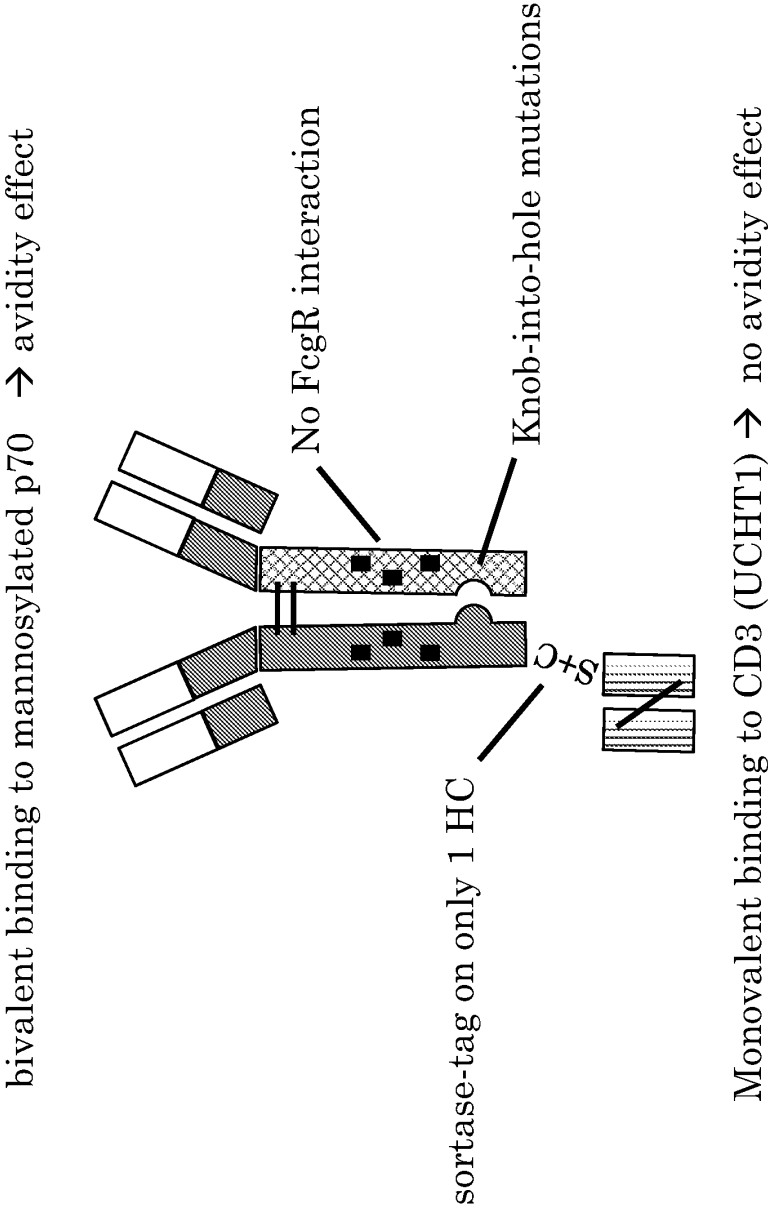


Fig. 13A

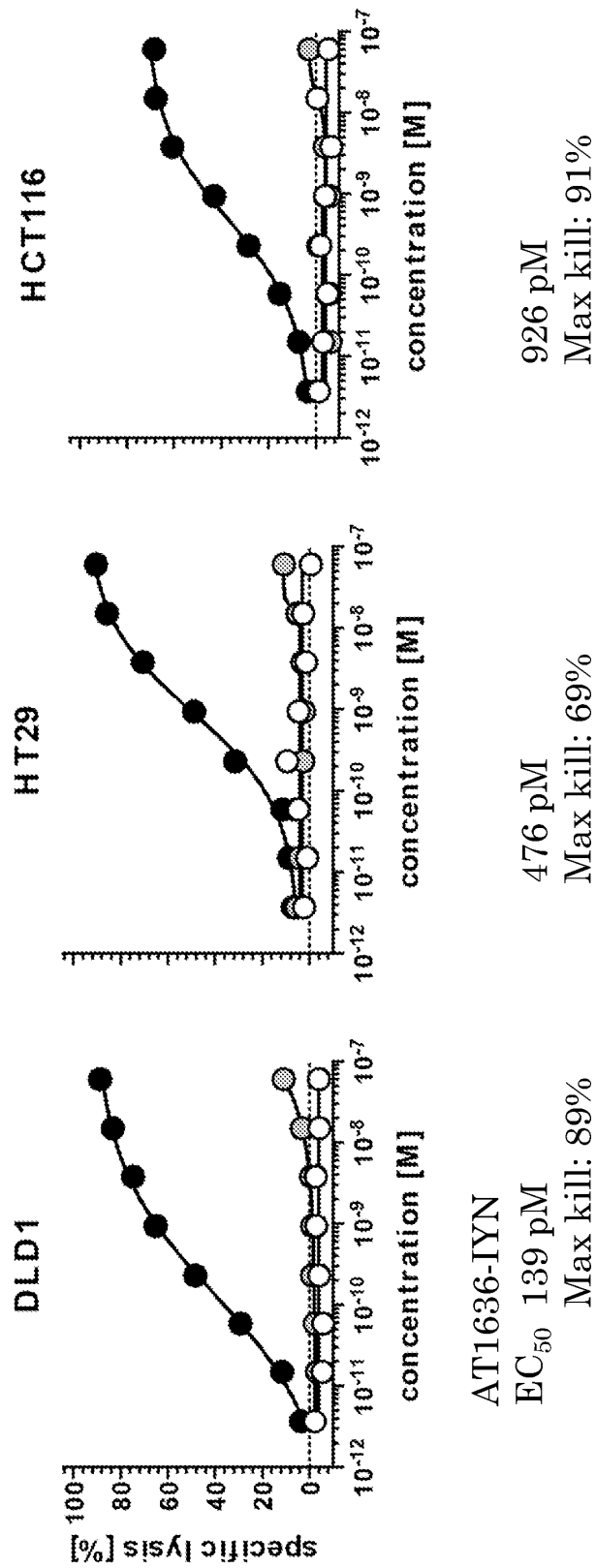
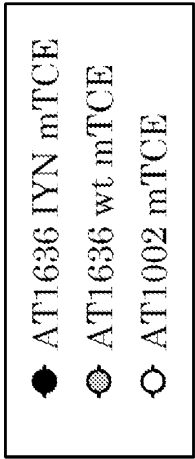
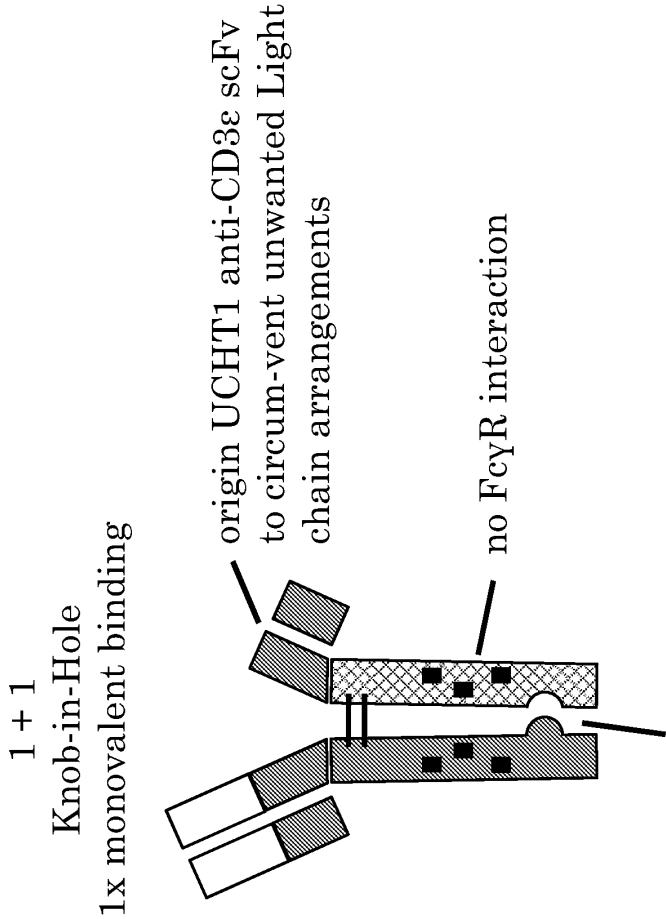


Fig. 13B



Knob-in-Hole mutation to favour Heavy chain heterodimerization

Fig. 13C

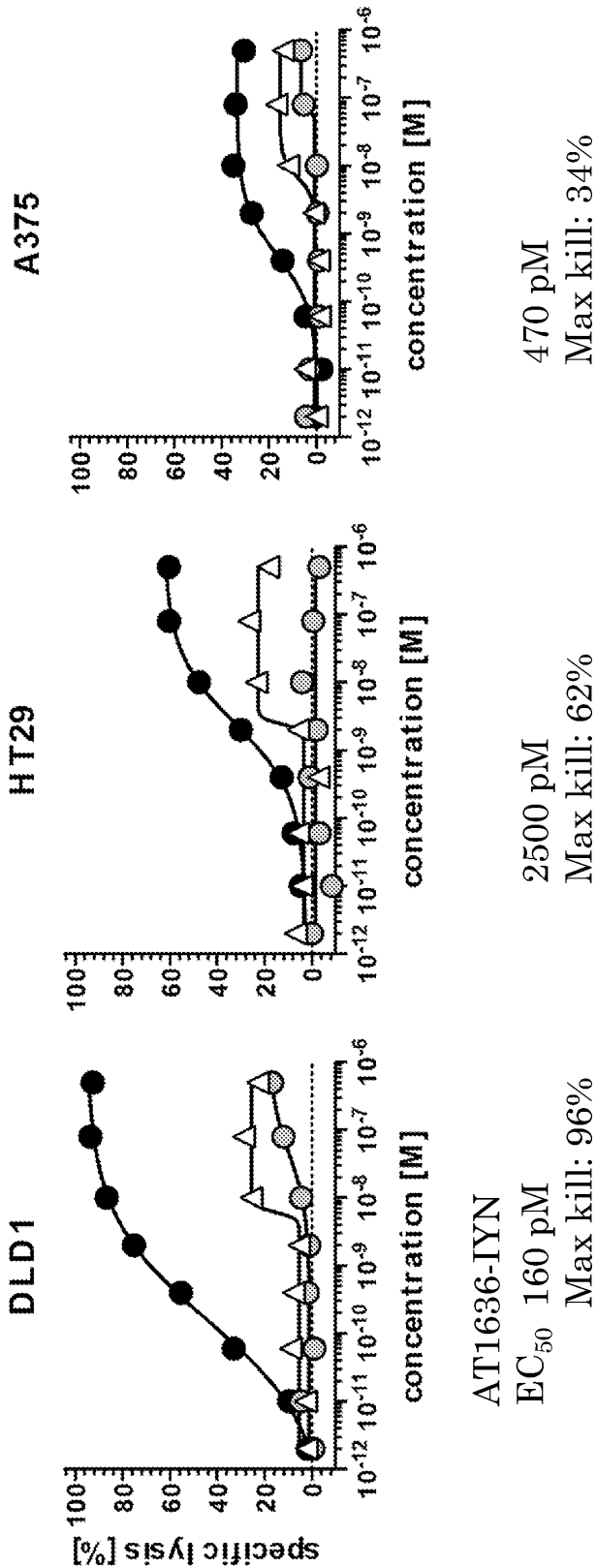
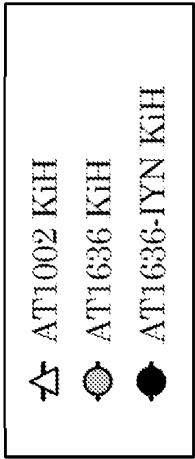


Fig. 13D

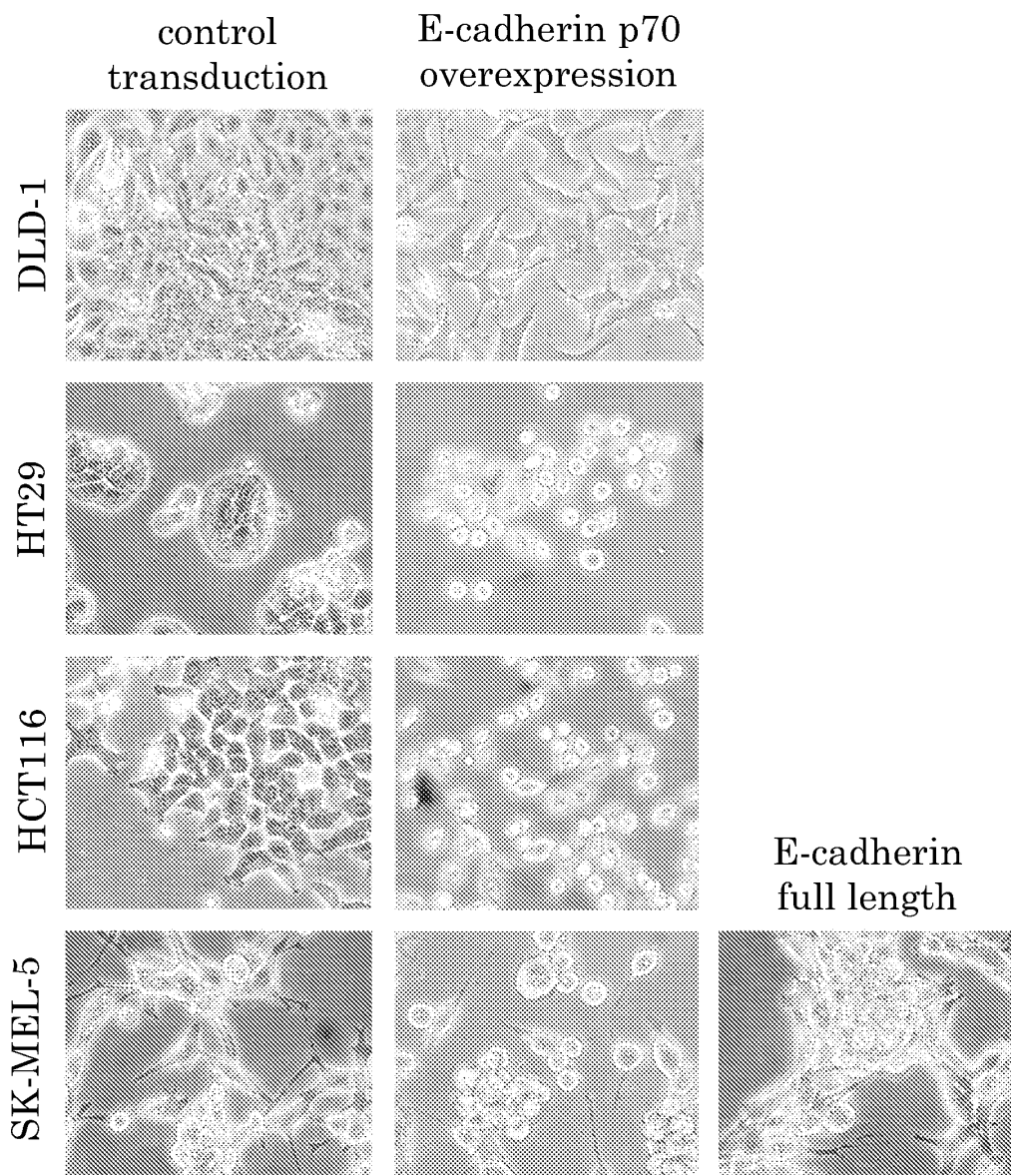


Fig. 14

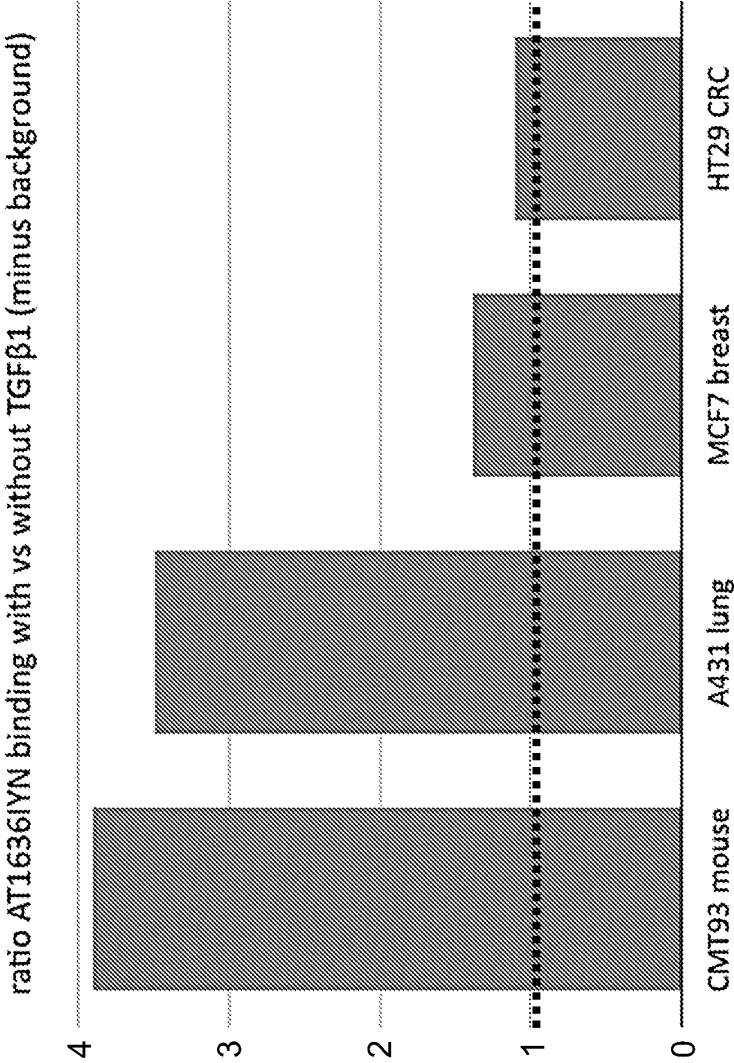


Fig. 15

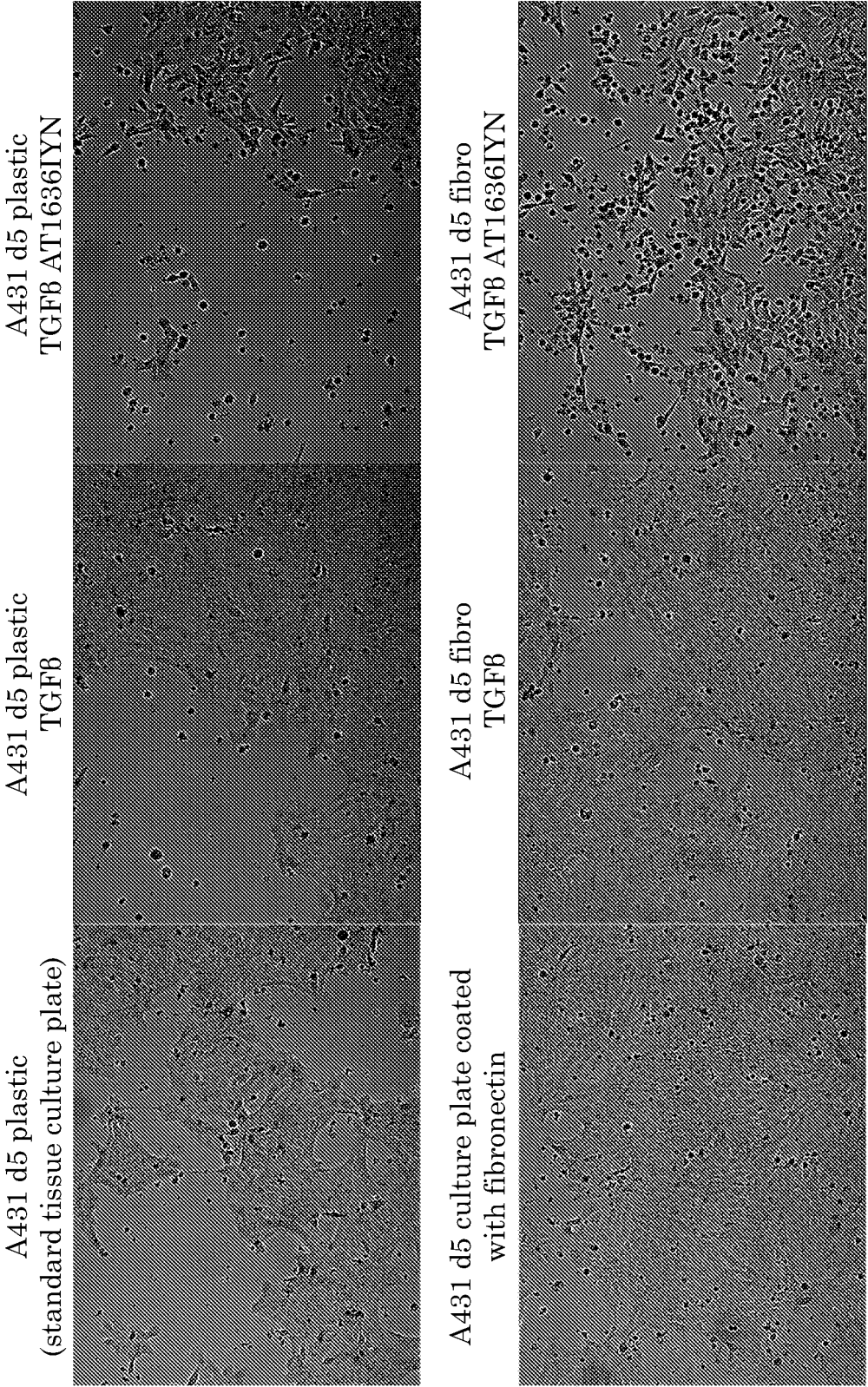
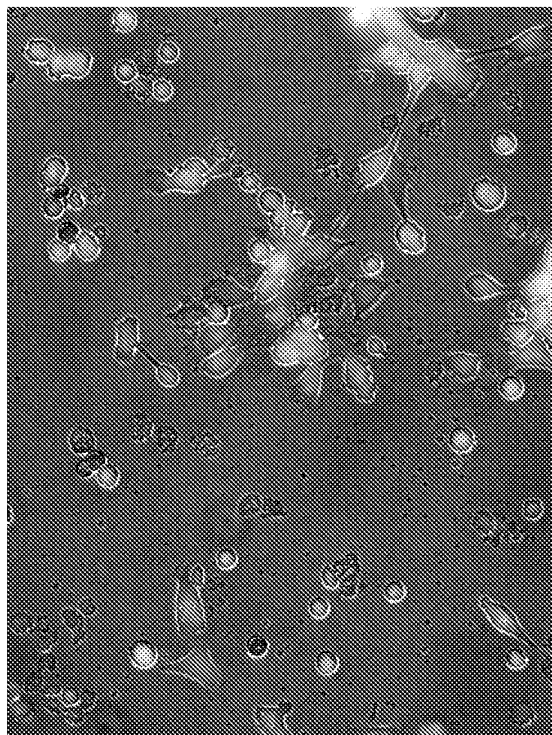


Fig. 16A

A431 d7 fibro
TGFβ AT1636IYN



A431 d7 fibro
TGFβ

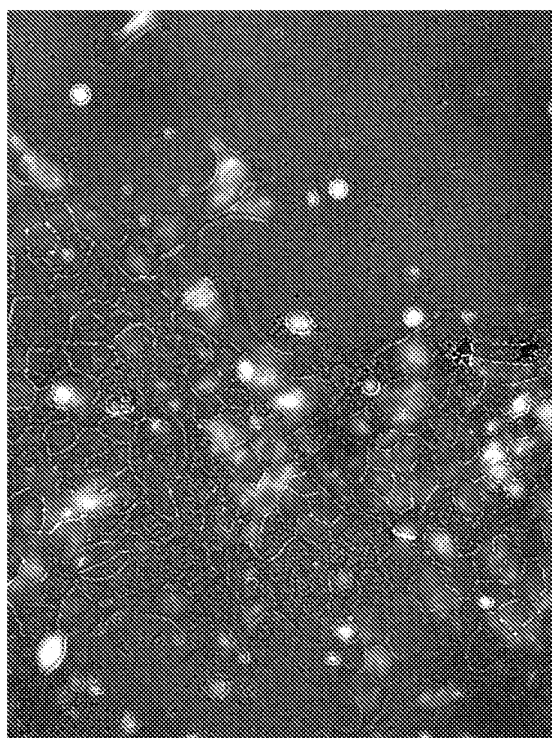


Fig. 16B

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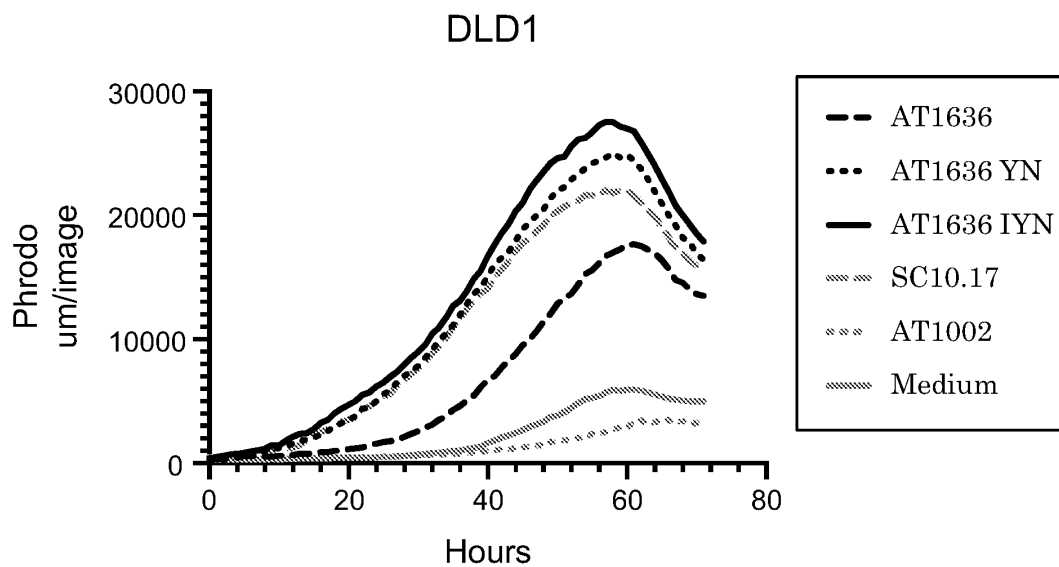


Fig. 17

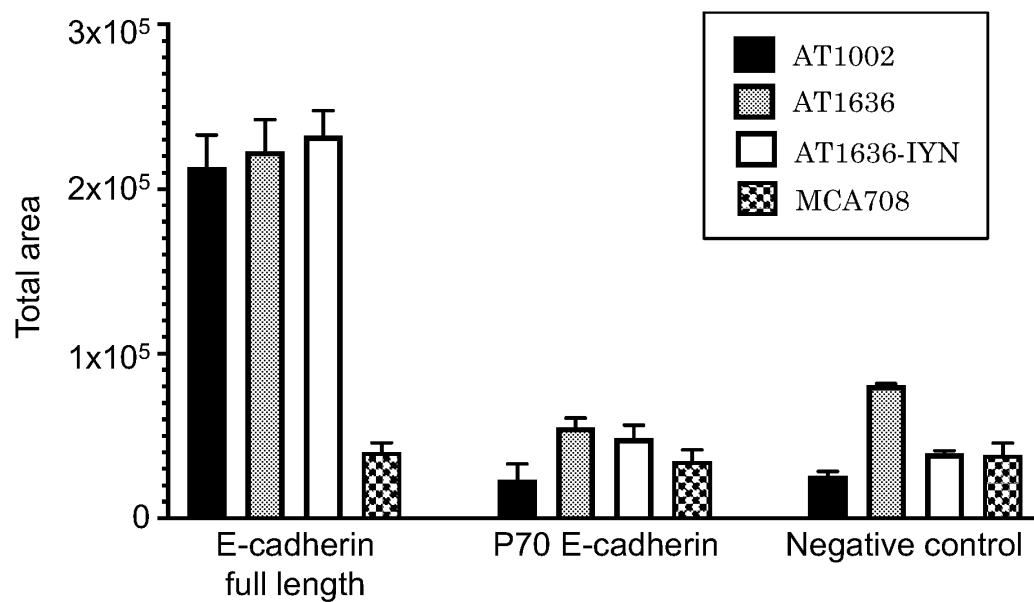


Fig. 18