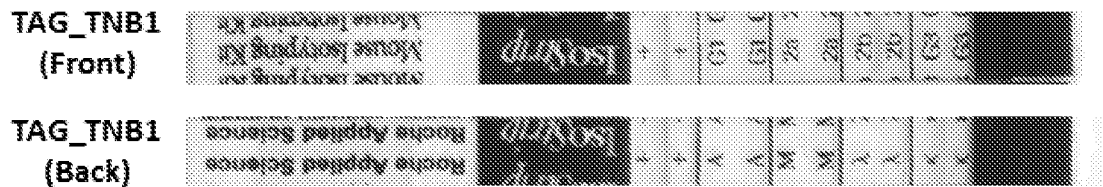


FIG. 1

**Gene Sequence (Heavy Chain)** (SEQ ID NO: 12)

CAGGTCAAAGTGCAGGAGTCAGGGGCTGAACTGGTGAAGCCTGGGGCTTCAGT
 GAAGTTGTCTGTAAAGGCTTCTGGCTTCACCTTCACCAGCTACTATATGTACTGG
 GTGAAGCAGAGGCCTGGACAAGGCCTTGAGTGGATTGGGGGGGTTAGTCCTAG
 CAATGGTGGTGCTAACTTCAATGAGAAGTTCAAGACCAAGGCCACACTGACTGT
 AGACAAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTGACATCTGAGGA
 CTCTGCGGTCTATTACTGTACAAGATTCTTTATGGTCCGAGGTACTTCGATGTC
 TGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

Gene Sequence (Light Chain) (SEQ ID NO: 13)

GACATTGAGCTCACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGG
 GCCACCATCTCCTGCAGAGCCAGCGAAAGTGTTGATAATTATGGCATTAGTTTTA
 TGAAGTGGTCCAACAGAAACCAGGACAGCCACCCAACTCCTCATTATGGTG
 CATCCAACCAGGGATCCGGGGTCCCTGCCAGGTTTAGTGGCAGTGGGTCTGGG
 ACAGACTTCAGCCTCAACATCCATCCTATGGAGGAGGATGATACTGCAATGTAT
 TTCTGTCAGCAAAGTAAGGAGGTTCCGTACACGTTCCGAGGGGGGACCAAGCT
 GGAAATAAAAC

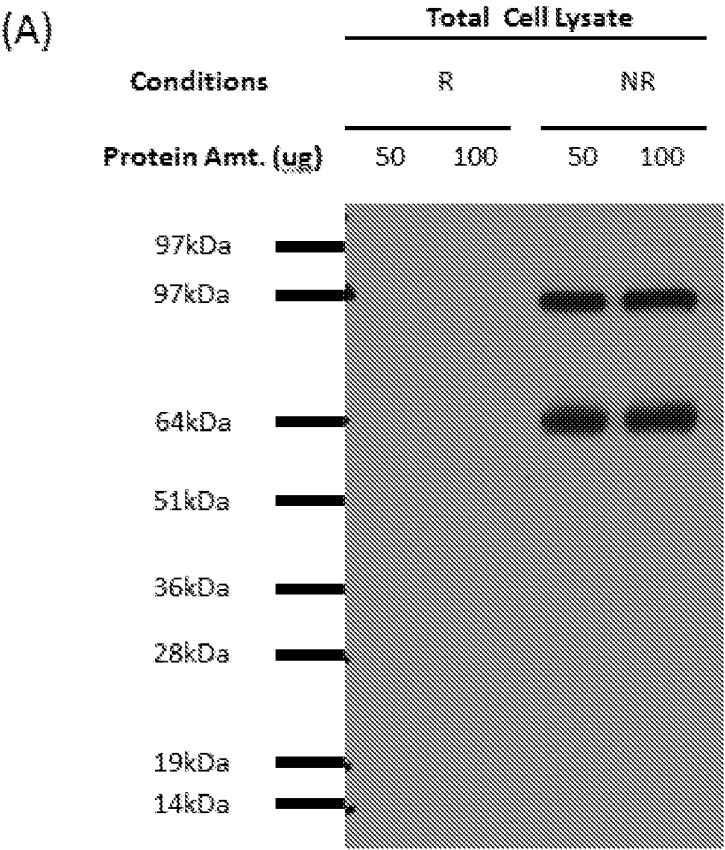
Protein Sequence (Heavy Chain) (SEQ ID NO: 1)

QVKLQESGAELVKPGASVKLSCKASGFTFTSYMYWVKQRPQGQLEWIGGVSPSN
 GGANFNEKFKTKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTRFYLYGPRYFDVWG
 QGTTVTVSS

Protein Sequence (Light Chain) (SEQ ID NO: 2)

DIELTQSPASLAVSLGQRATISCRASESDNYGISFMNWFQQKPGQPPKLLIYGASN
 QGSGVPARFSGSGSGTDFSLNIHPMEEDDTAMYFCQQSKEVPYTFGGGTKLEIK

FIG. 2



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FIG. 2

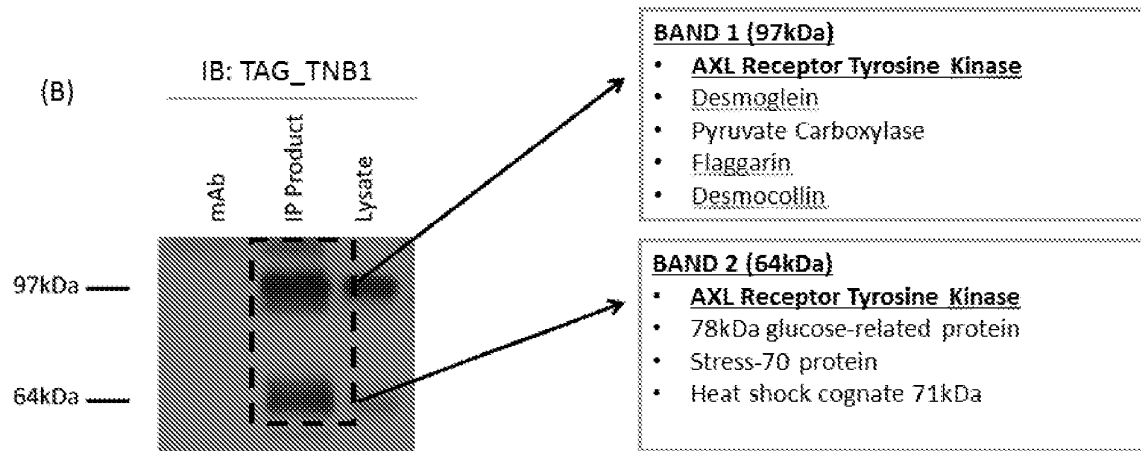


FIG. 2

(C)

BT 549

AXL receptor tyrosine kinase peptide sequence- homo sapiens (Uniprot)

Long form (SEQ ID NO: 14)

MAWRCPRMGRVPLAWCLALCGWACMAPRGTOAEESPFVGNPGNITGARGLTGTLRCQLQV
 QGEPPEVHWLRDGGILELADSTQTQVPLGEDEQDDWIVVSQLRITSLQLSDTGQYQCLVF
 LGHQTFVSQPGYVGLGLPYFLEPEDRTVAANTPFNLSCQAQGPPEVDLLWLQDAVPL
 ATAPGHGPQRSLSLHVPGLNKTSSFSCEAHNAKGVTTSRTATITVLPOQPRNLHLVSRQPT
 LEVAWTPGLSGIYPLTHCTLQAVLSNDGMGIQAGEPDPEEPLTSQASVPPHQLRLGSLH
 PHTPYHIRVACTSSQGPSSWTHWLPVETPEGVPLGPPENISATRNGSQAFVHWQEPRAPL
 QGTLLGYRLAYQGQDTPVELMDIGLRQEVTLQGDGVSNLTVCAAYTAAGDGPWSLP
 VPLEAWRP**GQAQPVHQL**VKEPSTPAFSWPWWYVLLGAVVAAACVLILALFLVHRRKKETR
 YGEVFPTVERGELVVRVVRKSYSRRATTEATLNSLGISEELKEKLQDVMVDRHKVALGK
 TLGEGEFGAVMEGQLNQDDSIKLVAVKTMKIAICTRSELEDFLSEAVCMKEFDHPNVMRL
 IGVCFGQSERESFPAPVVILPFMKHGDLSFLLYSRLGDQPVYLPQMLVKFMADIASGM
 EYLSTKRFIHRDLAARNCMLENMSVCVADFGLSKKIYNGDYRQGRIAKMPVKWIAIES
 LADRVYTSKSDVWSFGVTMWEIATRGTTPYGVENSEIYDYLROGNRLKQPADCLDGLYA
 LMSRCWELNPQDRPSFTELREDLENTLKALPPAQEPDEILYVNMDEGGGYPEPPGAAGGA
 DPPTQDPK**DCSCLTAAEVHPAGRYVLCPTTTPSPAQPADRGSPAAPGQEDGA**

Note:

1. **GQAQPVHQL** - difference between short and long isoforms of AXL
2. Results is a total of 10 Mass Spectrometry (MS) analysis (Both in-gel and in-solution digestion post IP); Underlined sequences are sequence that were identified by MS.
3. Approximately, 34.6% of the peptide were identified from the combined MS results.

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FIG. 2

(cont'd)

(C)

H1299

AXL receptor tyrosine kinase peptide sequence- homo sapiens (Uniprot)

Long form (SEQ ID NO: 15)

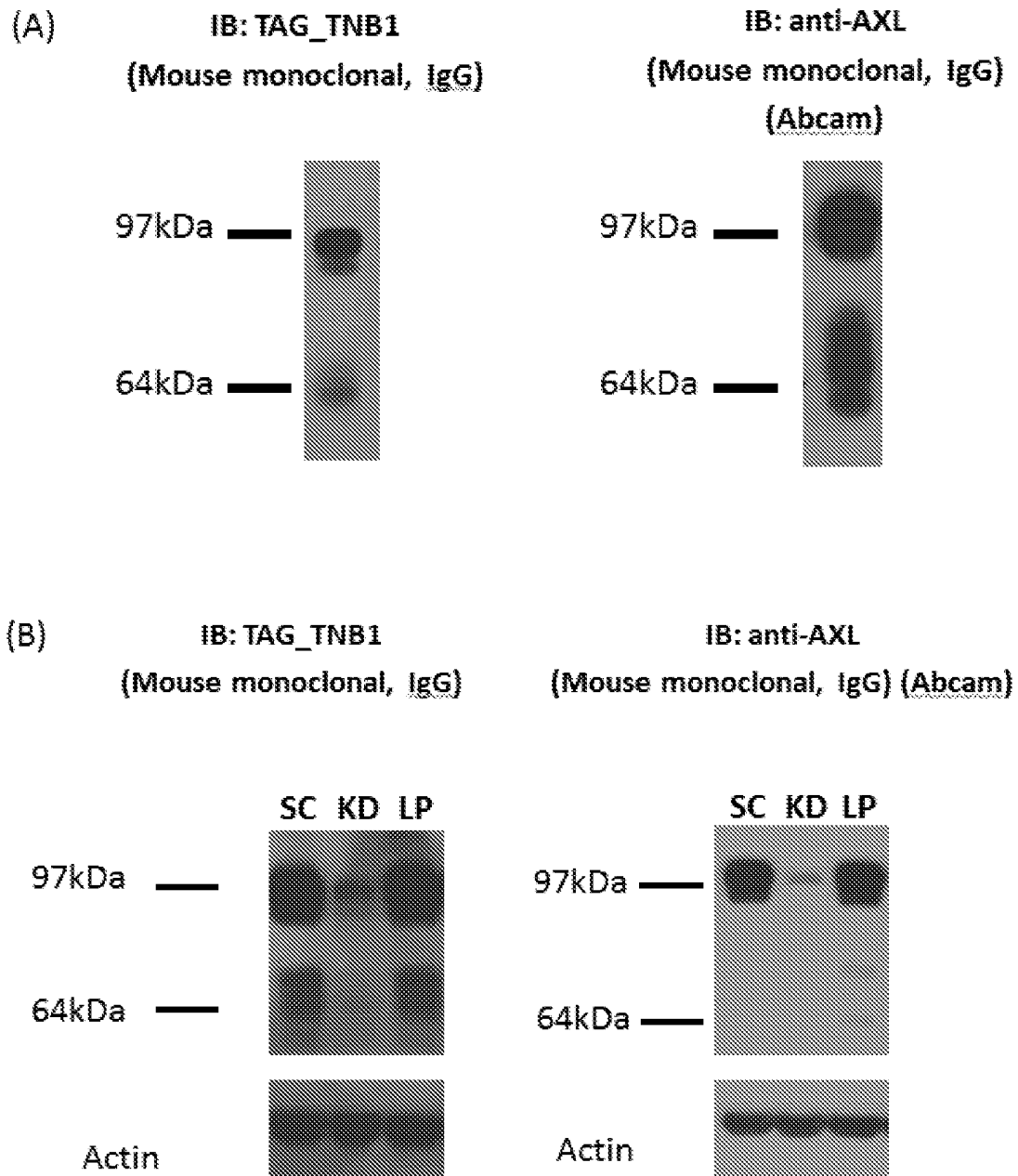
MAWRCPRMGRVPLAWCLALCGWACMAPRGTAEE5PFVGNPGNITGARGLTGTLRCQLOV
QGEPEVHWRDGQILELADSTQTQVPLGEDEQDDWIVVSQLRITSLQLSDTGQYQCLVF
 LGHQTFVSQPGYVGLEGLPYFLEEPEDRTVAANTPFNLSCQAQGPPEPVDLLWLQDAVPL
 ATAPGHGPQRSLHVPGLNKTSSFCEAHNAKGVTTSTATTITVLPQQPRNLHLVSRQFTE
 LEVAWTPGLSGIYPLTHCTLQAVLSNDGMGIQAGEPDPPPEEPLTSQASVPPHQLRLGLSLH
PHTPYHIRVACTSSQGPSSWTHWLPVETPEGVPLGPPENISATRNGSQAFVHWQEPRAPL
QGTLLGYRLAYQGQDTPEVLMDIGLRQEVTLELQGDGVSNLTVCAAYTAAGDGPWSLP
 VPLEAWRPGQAQPVHQLVKEPSTPAFSWPWWYVLLGAVVAAACVLILALFLVHRRKKETR
 YGEVFETPTVERGELVVRYRVRKSYSRRTTEATLNSLGISEELKEKL RDVMVDRHKVALGK
TLGEGEFGAVMEGQLNQDDSILKVAVKTMKIAICTRSELEDFLSEAVCMKEFDHPNVMRL
IGVCFQGSERESFPAPVVILPFMKHGDLSFLLYSRLGDQPVYLPQTQMLVKFMADIASGM
EYLSTKRFIHRDLAARNCMNLNENMSVCVADFGLSKKIYNGDYRQGRIAKMPVKWIAIES
LADRVYTSKSDVWSFGVTMWEIATRGQTPYPGVENSEYDYLRQGNRLKQPADCLDGLYA
LMSRCWELNPQDRPSFTELREDLENTLKALPPAQEPDEILYVNMDEGGGYPEPPGAAGGA
 DPPTQDPKDSCSCLTAAEVHPAGRYVLCPSSTTPSPAQPADRGSPAAPGQEDGA

Note:

1. GQAQPVHQL - difference between short and long isoforms of AXL
2. Results is a total of 5 Mass Spectrometry (MS) analysis (Both in-gel and in-solution digestion post IP); Underlined sequences are sequence that were identified by MS.
3. Approximately, 41.8% of the peptide were identified from the combined MS results.

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Fig. 3



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Fig. 4

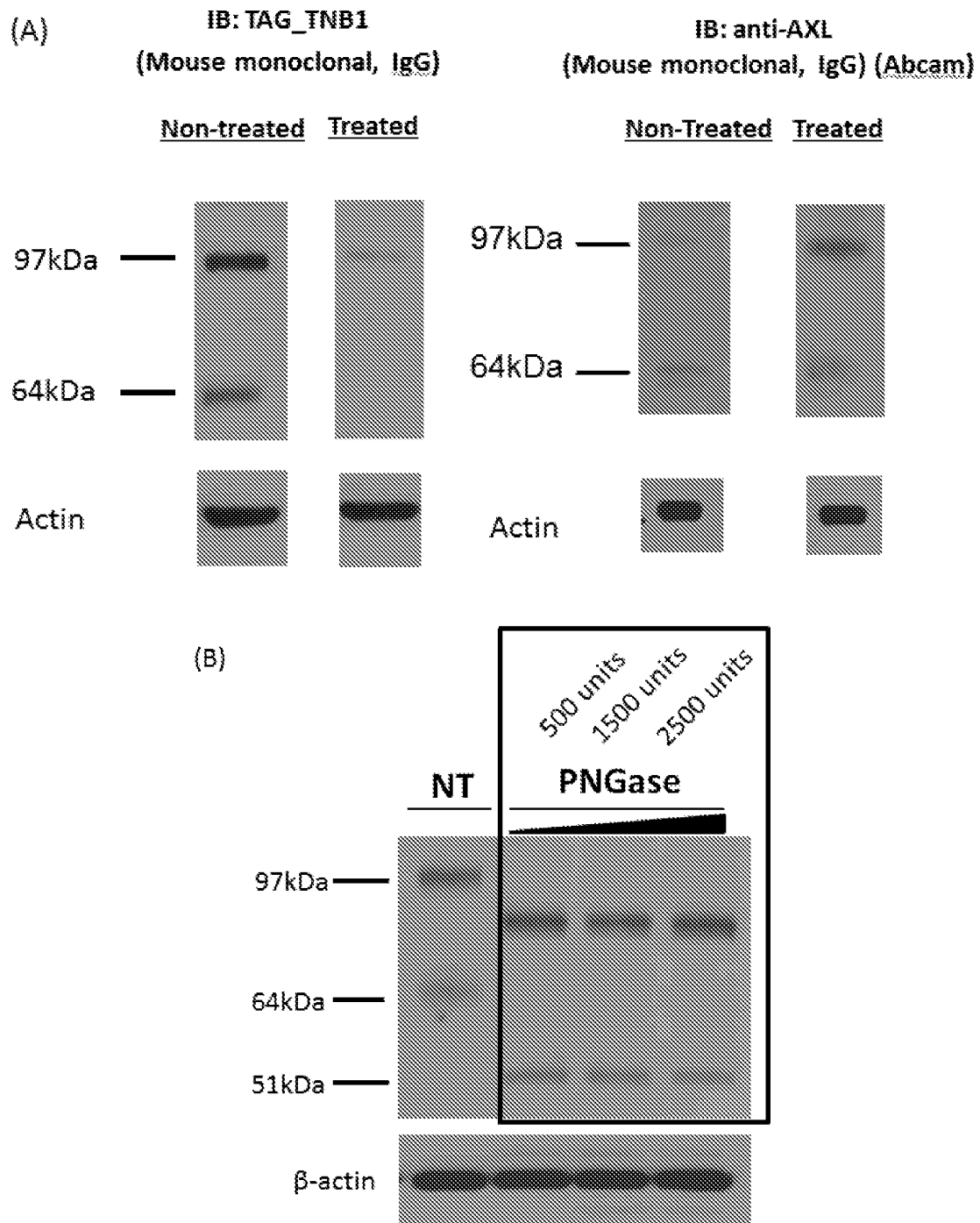


FIG. 4

(C)

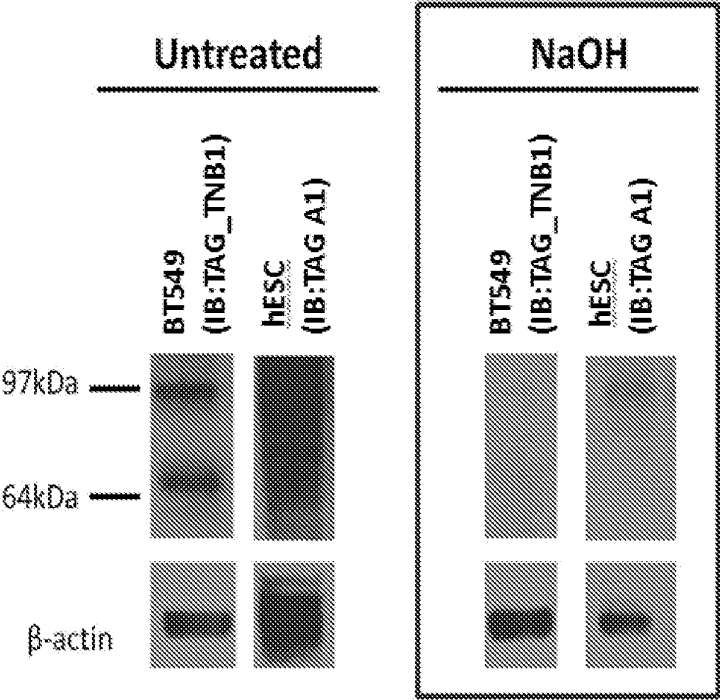
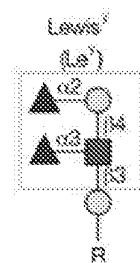


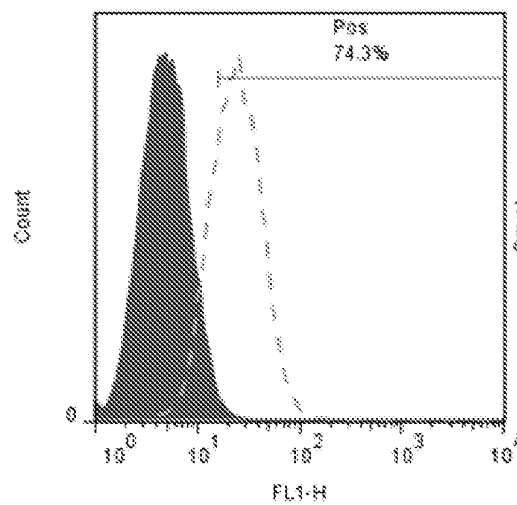
FIG. 4

(D)

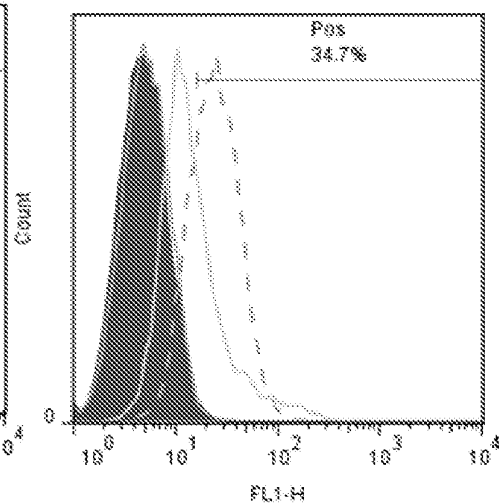


TAG_TNB1 only

TAG_TNB1 pre-treated
with Lewis-Y



	Sample Name	Geom. Mean
---	260314 T1B1 only 002	23.3
---	260314 Blank 001	4.75



	Sample Name	Geometric Mean
	280314 LewY 1x with TN	14.5
	280314 LewY 1x ctrl 003	5.80
	280314 THB1 only 002	23.5
	280314 Blank 001	4.75

FIG. 4

(cont'd)

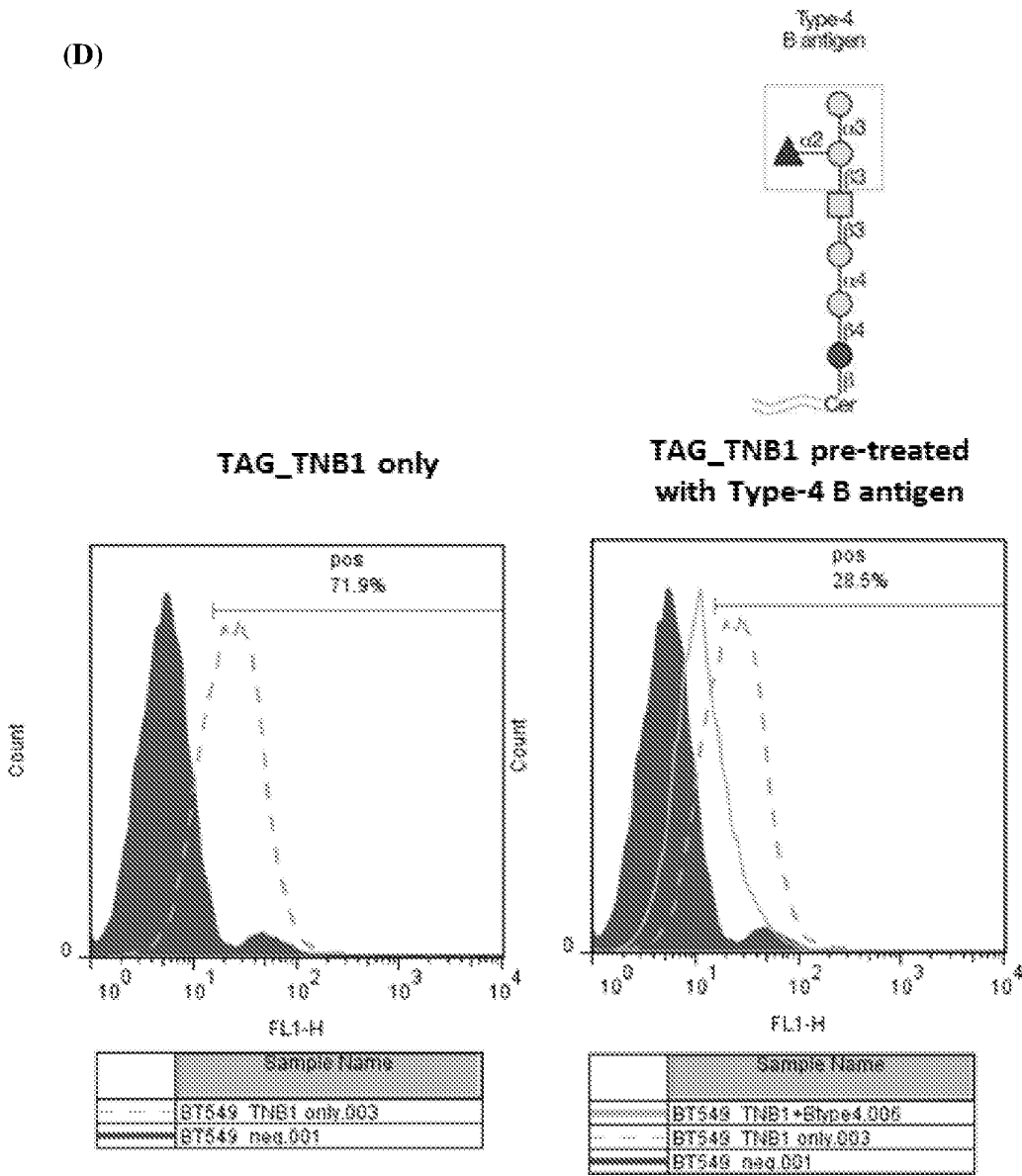


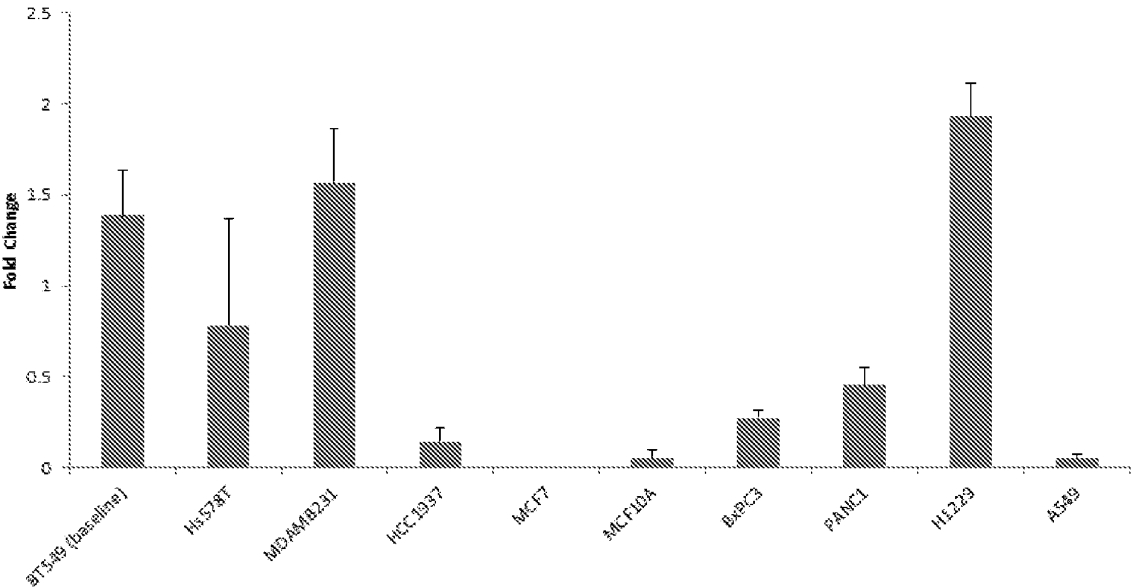
FIG. 5

FIG. 5

	Triple Negative Breast Cancer					Luminal A ER+/PR+/HER2-				HER2+			
Breast Cancers	Breast Cancer												
	BT549	HCC1937	HCC1395	HS578T	BT20	MDA-MB231	MDA-MB453	T47D	CAMA-1	MCF-7	HEC1954	SK-BR3	BT474
	4	2	4	2	0	3	0	0	0	0	0	0	0
Normal and Progenitors cells	Normal Primary Cells												
	hME1 (hTERT-Breast Epithelial)	hCENC (Corneal Endothelial)	Corneal Stromal Fibroblast	Renal mixed epithelial	Hepatocytes (Liver)	HUVEC (Umbilical Cord Vein)	InEpic (Intestinal epithelial)	HepIC (Esophageal epithelial)	Human PBMC (N=3)	Human RBC (N=3)			
	2	0	0	0	0	0	0	0	0	0			
Ovarian & Kidney Cancers	Normal Cell Lines								Progenitor Cells (MSC)				
	MCF-10A (Breast Epithelial)	B4G12 (Immortalised Corneal Endothelial)	THP-1 (Monocytes)	IMR90 (Lung)	HEK293 (Human Embryonal Kidney)	HaCAT (Keratinocytes)	HFF (Human Foreskin Fibroblast)	Adult MSC		hESC-derived MSC			
	0	0	0	0	0	0	0	0		0		0	
Other Cancers	Ovarian Cancer									Kidney Cancer			
	Ca3VO	OV90	OV17R	OVCAR 3	OVCAR8	IGROV-1	HEY	SKOV-3	A2780	TK10	786-O	ACHN	
	0	1	0	0	0	0	4	3	0	3	3	3	
	Neuroblastoma			Lung Cancer			Head and Neck Cancer		Colorectal Cancer			Pancreatic Cancer	
	NB1691	SKNAS	JF	A549	H1299	HCC 826	TM17		KM12	HT15	Sw480	PANC-1	BxPC3
	0	0	0	1	4	0	2		0	0	0	2	1
Legend													
0		No binding		1	< 20% binding		2	20% - 40% binding		3	40% - 60% binding		> 80% binding

Fig. 6

(A)



(B)

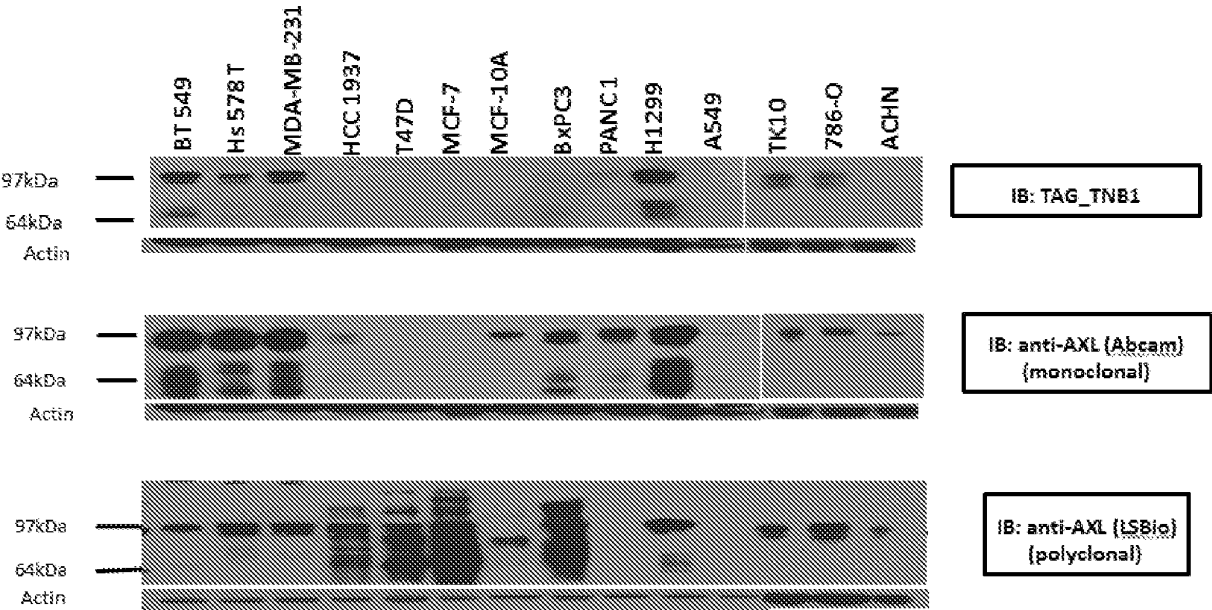
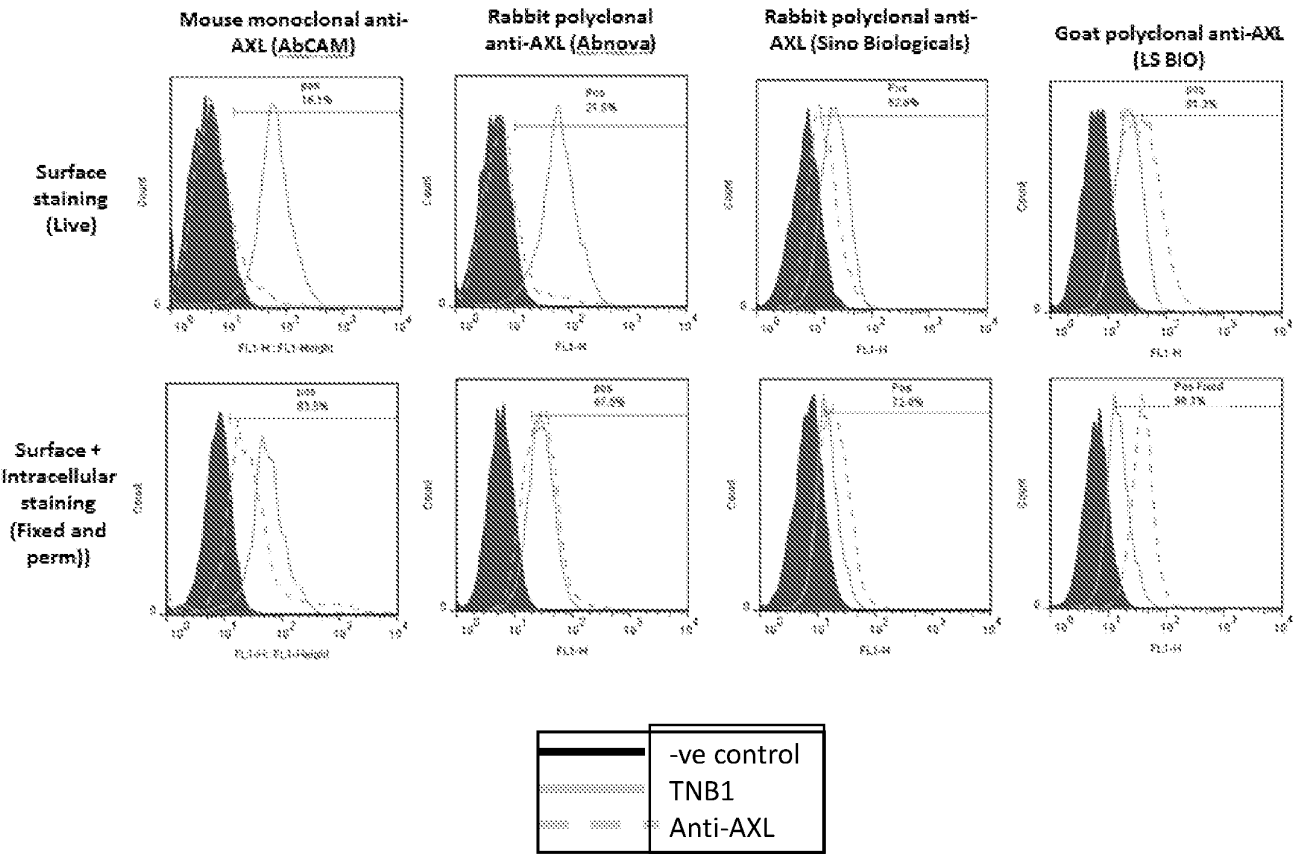
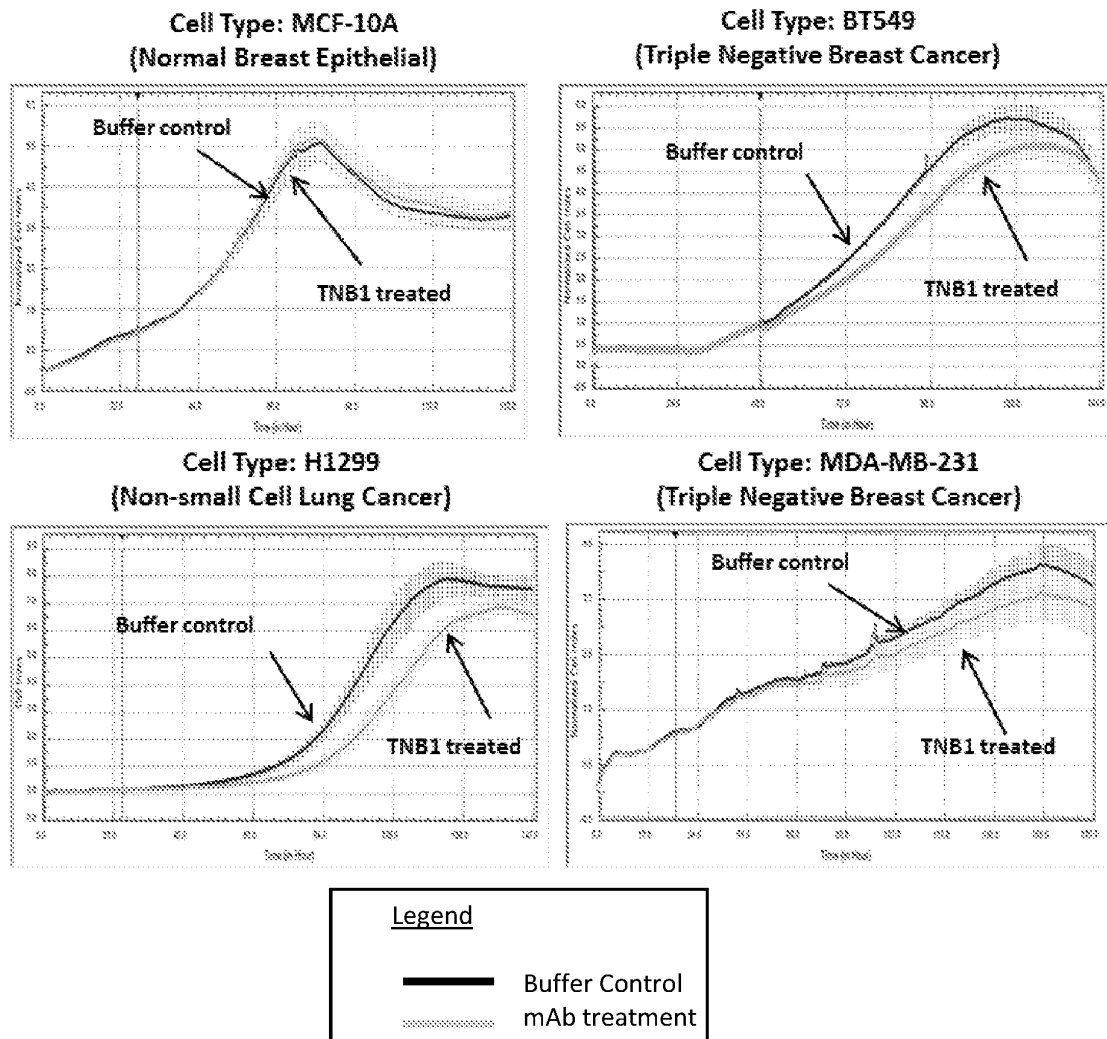


Fig. 7



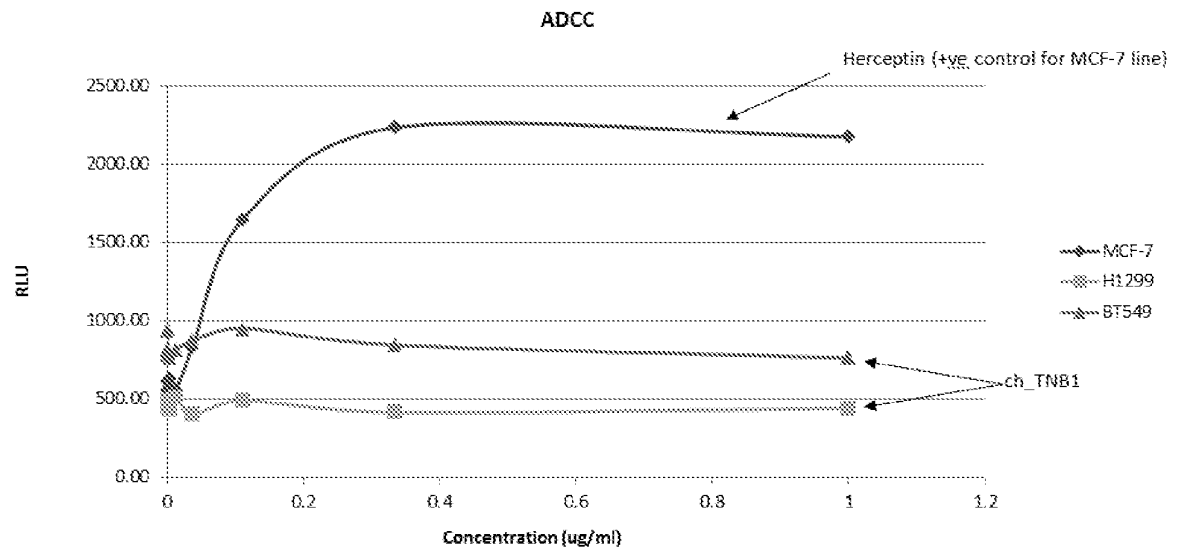
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Fig. 8



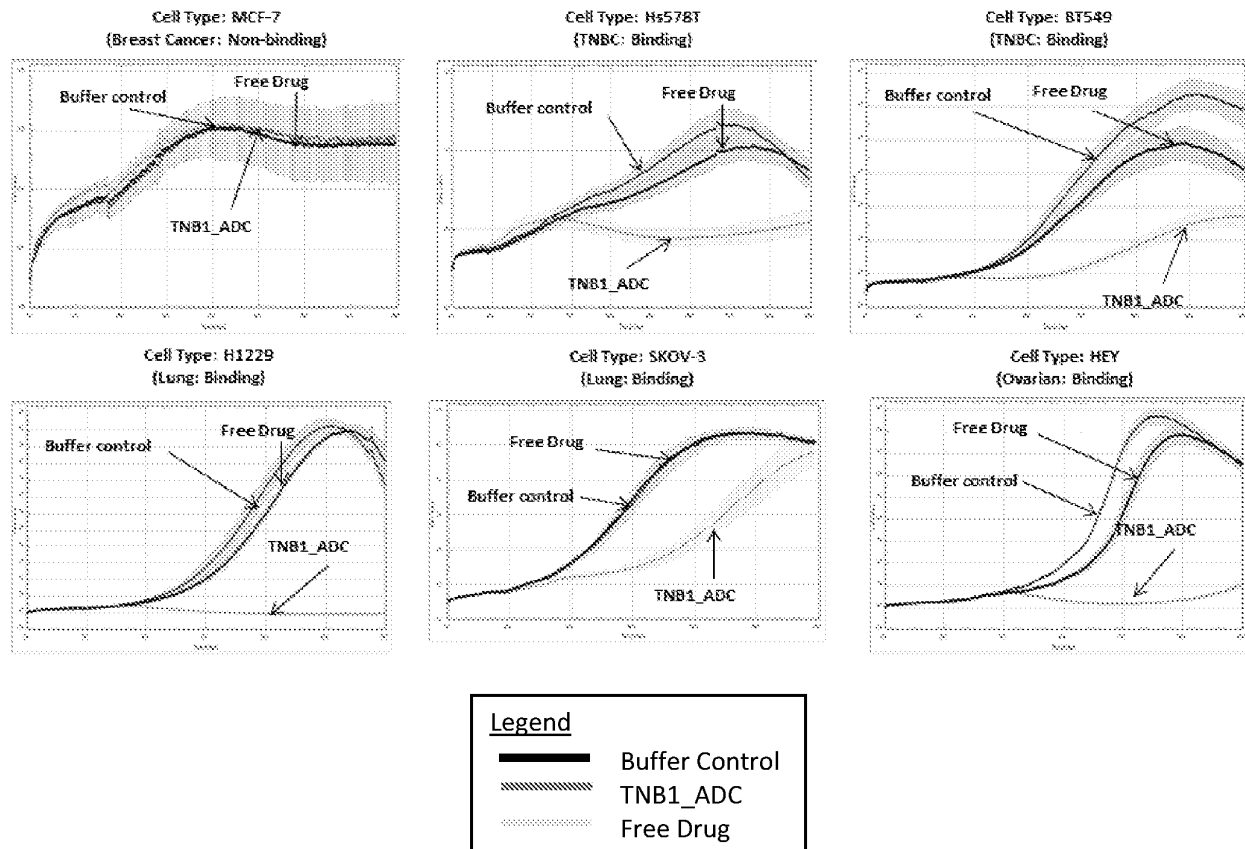
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Fig. 9



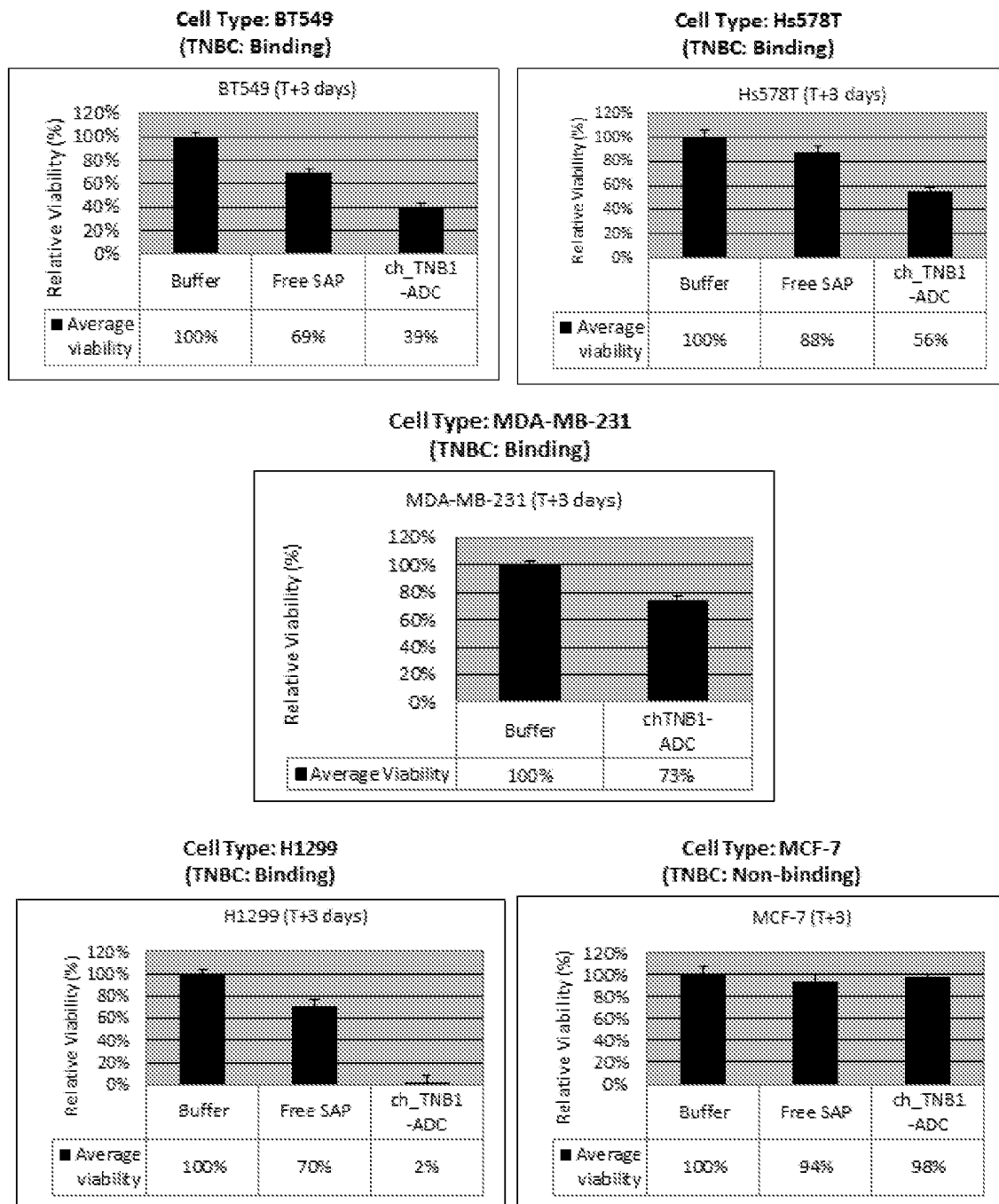
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Fig. 10



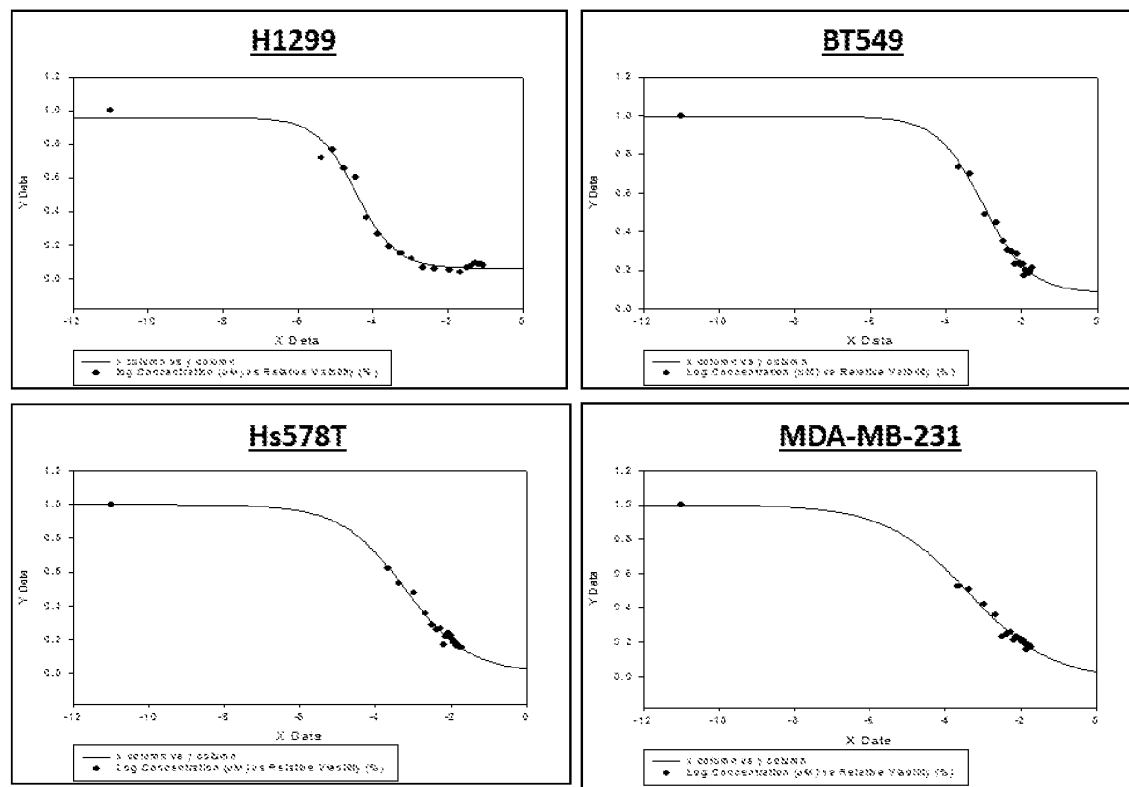
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Fig. 11



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Fig. 12



Cell Line	IC ₅₀ (CTG)
H1299	35.33 pM
BT549	1240.80 pM
Hs578T	528.91 pM
MDA-MB-231	339.78 pM

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Fig. 13

