

FIG. 1

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

CAGGTCAAACCTGCAGGAGTCAGGGGCTGAACTGGTGAAGCCTGGGGCTTCAGT
 GAAGTTGTCCTGTAAGGCTTCTGGCTTCACCTTCACCAGCTACTATATGTAAGTGG
 GTGAAGCAGAGGCCTGGACAAGGCCTTGAGTGGATTGGGGGGGTTAGTCCTAG
 CAATGGTGGTGTCACTTCAATGAGAAGTTCAAGACCAAGGCCACACTGACTGT
 AGACAAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTGACATCTGAGGA
 CTCTGCGGTCTATTACTGTACAAGATTCTTTATGGTCCGAGGTACTTCGATGTC
 TGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

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

GACATTGAGCTCACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGG
 GCCACCATCTCCTGCAGAGCCAGCGAAAGTGTTGATAATTATGGCATTAGTTTTA
 TGAAGTGGTTCCAACAGAAACCAGGACAGCCACCCAAACTCCTCATTTATGGTG
 CATCCAACCAGGGATCCGGGGTCCCTGCCAGGTTTAGTGGCAGTGGGTCTGGG
 ACAGACTTCAGCCTCAACATCCATCCTATGGAGGAGGATGATACTGCAATGTAT
 TTCTGTCAGCAAAGTAAGGAGGTTCCGTACACGTTCCGAGGGGGGACCAAGCT
 GGAAATAAAAC

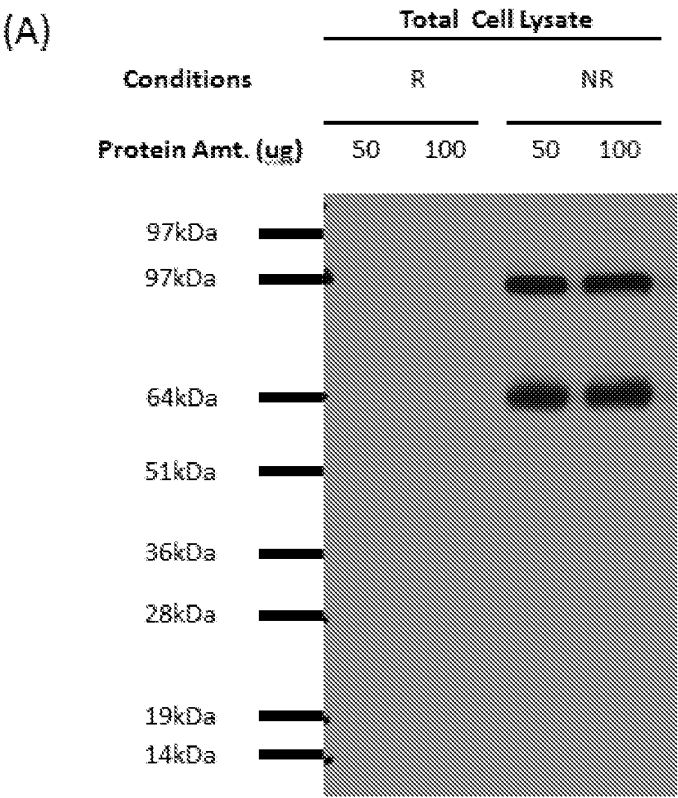
Protein Sequence (Heavy Chain) (SEQ ID NO: 1)

QVKLQESGAELVKPGASVKLSCKASGFTFTSYMYWVKQRPQGQLEWIGGVSPSN
 GGANFNEKFKTKATLTVDKSSSTAYMQLSSLTSEDSAVVYCTRFLYGPTRYFDVWG
 QGTTTVTVSS

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

DIELTQSPASLAVSLGQRATISCRASESVDNYGISFMNWFQKPGQPPKLLIYGASN
 QGSGVPARFSGSGSGTDFSLNIHPMEEDDTAMYFCQQSKEVPYTFGGGKLEIK

FIG. 2



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FIG. 2

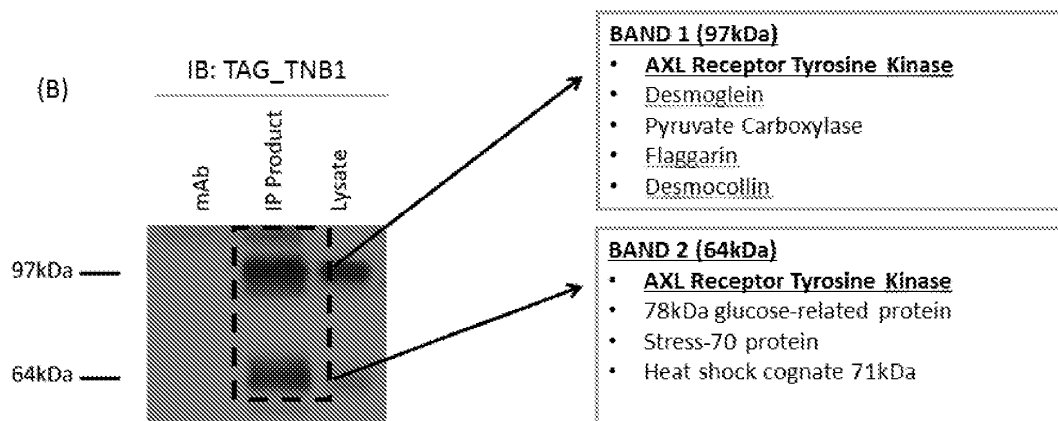


FIG. 2

(C)

BT 549

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

Long form (SEQ ID NO: 14)

MAWRCPRMGRVPLAWCLALCGWACMAPRGTAEESEPFVGNPGNITGARGLTGTLRCQLQV
 QGEPPEVHWLRDGGQILELADSTQTQVPLGEDEQDDWVVSQLRITSLQLSDTGQYQCLVF
 LGHQTFVSQPGYVGLGLPYFLEEPEDRTVAANTPFNLSCQAQGPPEVDLLWLQDAVPL
 ATAPGHGPGQSLHVPGLNKTSSFSCEAHNAKGVTTSRTATITVLPOQPRNLHLVSRQTE
 LEVAWTPGLSGIYPLTHCTLOAVLSNDGMGIQAGEPDPPPEPLTSQASVPPHQLRLGSLH
 PHTPYHIRVACTSSQGPSSWTHWLPVETPEGVPLGPPENISATRNGSQAFVHWQEPRAPL
 QGTLGGLYRLAYQGQDTPVLMDDGLRQEVTELEQGDGSVSNLTVCAAYTAAGDGPWSLP
 VPLEAWRPQQAQPVHQLVKEPSTPAFSWPWWYVLLGAVVAAACVLILALFLVHRRKKETR
 YGEVFETPTVERGELVVRVYRVRKSYSRRITTEATLNSLGISEELKEKLSDVMVDORHKVALGK
 TLGEGEFQAVMEGQLNQDDSIKLVAVKTMKIAICTRSELEDFLSEAVCMKEFDHPNVMRL
 IGVCFOGSERESFPAPVVILPFMKHGDLSFLLYSRLGDQPVYLPQMLVKFMADIASGM
 EYLSTKRFIHRDLAARNCMNLNENMSVCVADFGLSKKIYNGDYRQGRIAKMPVKWIAIES
 LADRVYTSKSDVWSFGVTMWELATRGQTPYPGVENSEYDYLROGNRLKQPADCLDGLYA
 LMSRCWELNPQDRPSFTELREDLENTLALPPAQEPDEILYVNMDEGGGYPEPPGAAGGA
 DPPTQDPFKDSCSCLTAAEVHPAGRYVLCPSSTTPSPAQPADRGSPAAPGQEDGA

Note:

1. QQAQPVHQL - 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)

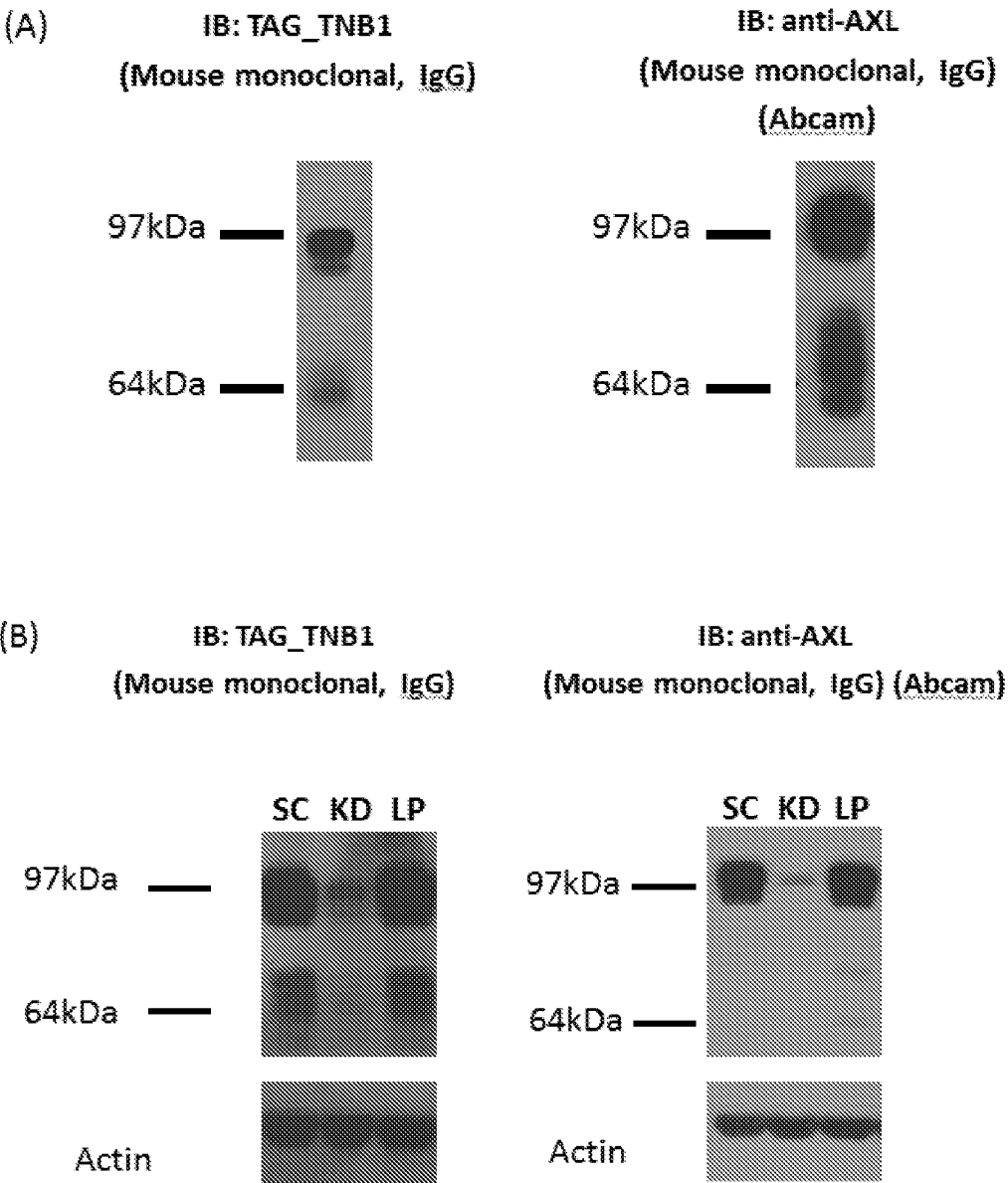
Long form (SEQ ID NO: 15)

MAWRCPRMGRVPLAWCLALCGWACMAPRGTAEE5PFVGNPGNITGARGLTGTLRCOLQV
QGEPEVHHLRDGQILELADSTQTQVPLGEDEQDDWIVVSQLRITSLQLSDTGQYQCLVF
 LGHQTFV5QPGYVGLGLPYFLEEPEDRTVAANTPFNLSCQAQGPPEPVDLLWLQDAVPL
 ATAPGHGPGQSLHVPGLNKTSSFSCEAHNAKGVTTSTATTITVLPQQPRNLHLVSRQFTE
 LEVAWTPGLSGIYPLTHCTLQAVLSNDGMGIQAGEPDPEEPLTSQASVPPHQLRLGLSLH
PHTPYHIRVACTSSQGPSSWTHWLPVETPEGVPLGPPENISATRNGSQAFVHWQEPRAPI
QGTLLGYRLAYOGQDTPEVLMDIGLRQEVTLQGDGVSNNLTVCAAYTAAGDGPWSLP
 VPLEAWRPGQAQPVHQLIVKEPSTPAFSWPWWYVLLGAVVAAACVLILALFLVHRRKKETR
 YGEVFPTVERGELVVRYRVRKYSRRTEATLNSLGISEELKEKL RDVMVDRHKVALGK
TLGEGEFGAVMEGQLNQDDSIKVAVKTMKIAICTRSELEDFLSEAVCMKEFDHPNVMRL
IGVCFQGSERESFPAPVVILPFMKHGDLSHFLYSRLGDQPVYLPQMLVKFMADIASGM
EYLSKRFIHRDLAARNCMNLNENMSVCVADEGLSKIYNGDYRQGRIAKMPVKWIAIES
LADRVYTSKSDVWSFGVTMWELATRGQTPYPGVENSEYDYLRLQGNRLKQPADCLDGLYA
LMSRCWELNPQDRPSFTELREDLNTLKALPPAQEPDEILYVNMDEGGGYPEPPGAAGGA
 DPPTQDPDKDSCSCLTAAEVHPAGRYVLCPSSTTPSPAQPADRGSPAAPGQEDGA

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.

Fig. 3



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Fig. 4

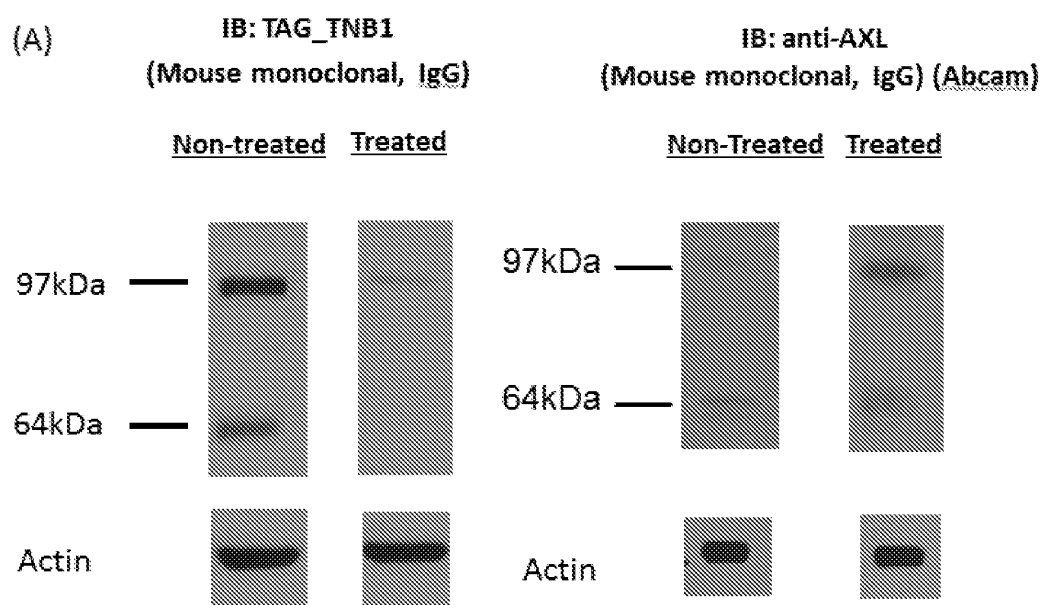
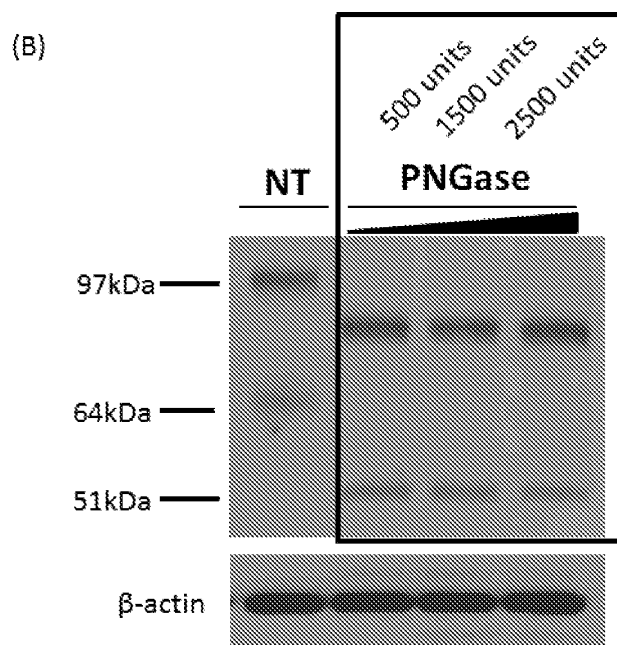


FIG. 4

(C)

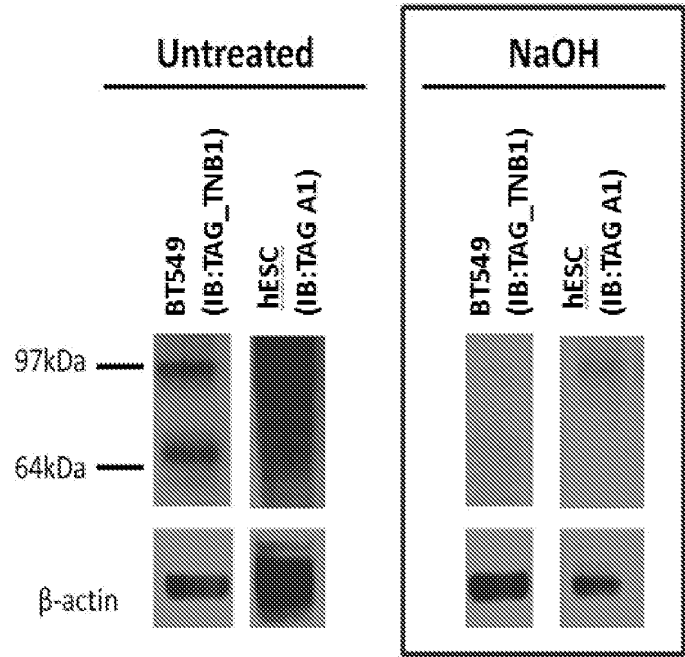


FIG. 4

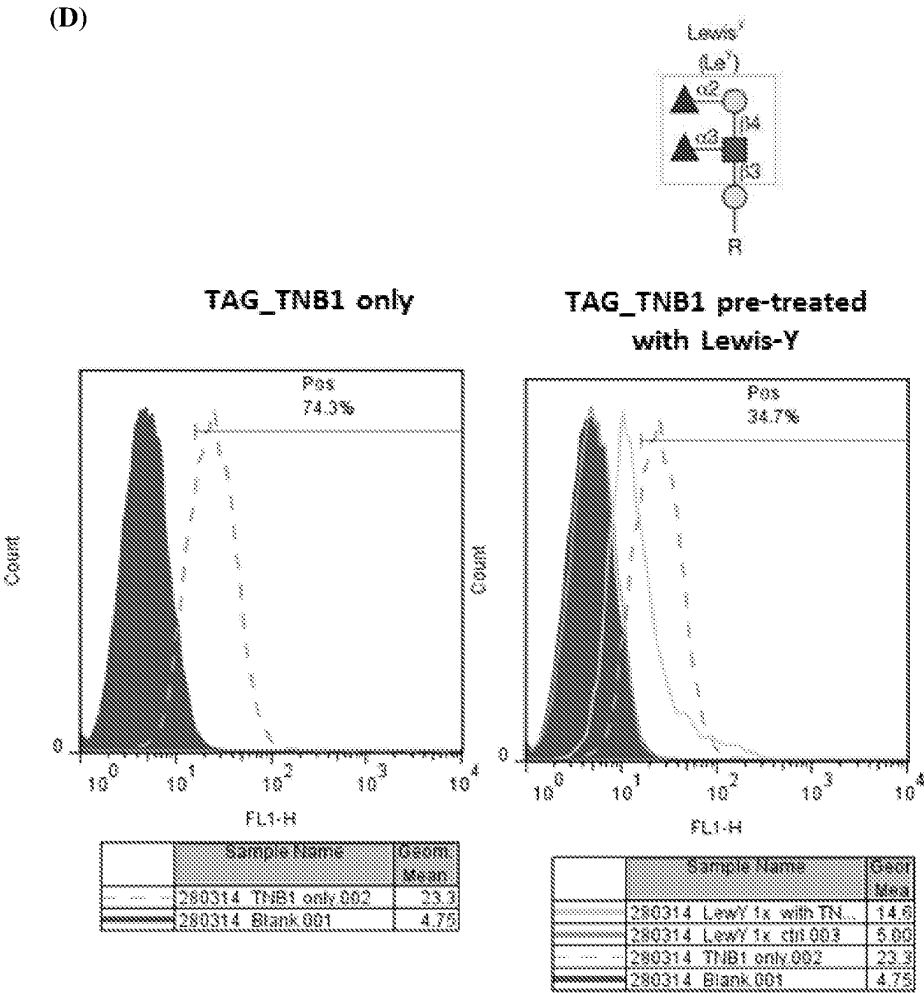
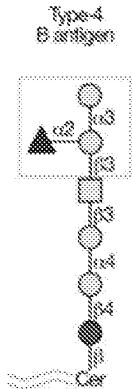


FIG. 4

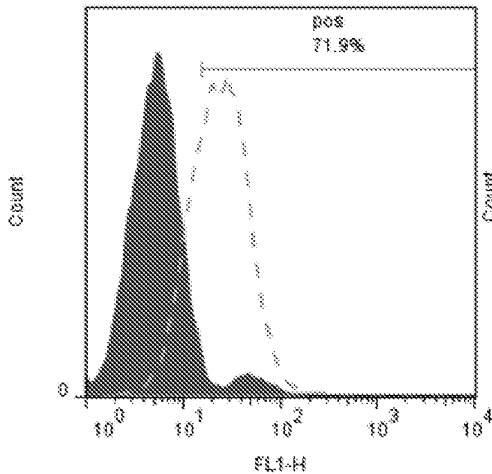
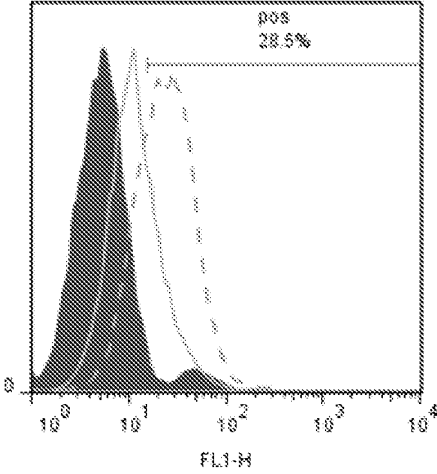
(cont'd)

(D)



TAG_TNB1 only

TAG_TNB1 pre-treated
with Type-4 B antigen



	Sample Name
.....	BT549 TNB1 only.003
————	BT549 neg.001

	Sample Name
.....	BT549 TNB1+Gtype4.006
.....	BT549 TNB1 only.003
————	BT549 neg.001

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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	HCC1954	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)	hCEEC (Corneal Endothelial)	Corneal Stromal Fibroblast	Renal mixed epithelial	Hepatocytes (Liver)	HUVEC (Umbilical Cord Vein)	InEpic (Intestinal epithelial)	HepEC (Esophageal epithelial)	Human PBMC (N=3)	Human RBC (N=3)
2	0	0	0	0	0	0	0	0	0

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

Ovarian & Kidney Cancers
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

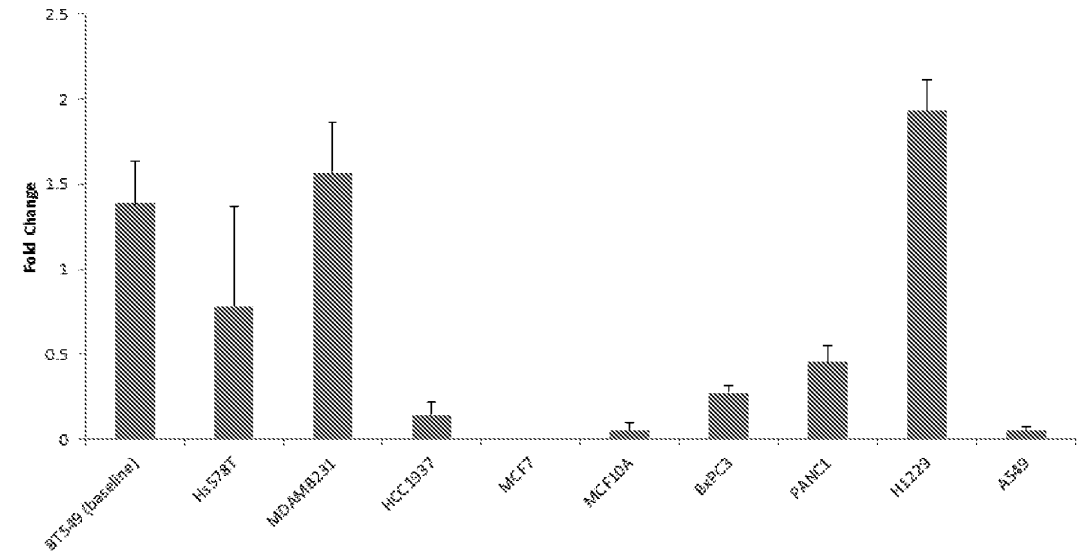
Neuroblastoma			Lung Cancer			Head and Neck Cancer	Colorectal Cancer			Pancreatic Cancer	
NB1691	SKNAS	JF	A549	H1299	HCC 826	TM17	KM12	HT15	Sw480	PANC-1	BxPC3
0	0	0	1	4	0	2	0	0	0	2	1

Legend 0 No binding 1 < 20% binding 2 20% - 40% binding 3 40% - 60% binding 4 > 80% binding

Legend 0 No binding 1 < 20% binding 2 20% - 40% binding 3 40% - 60% binding 4 > 80% binding

Fig. 6

(A)



(B)

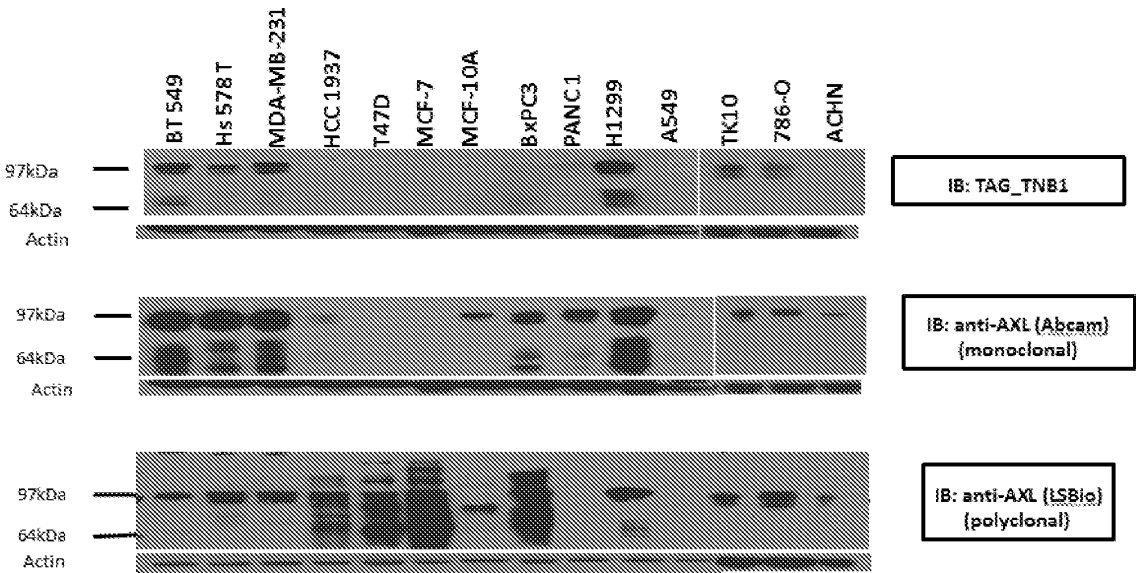


Fig. 7

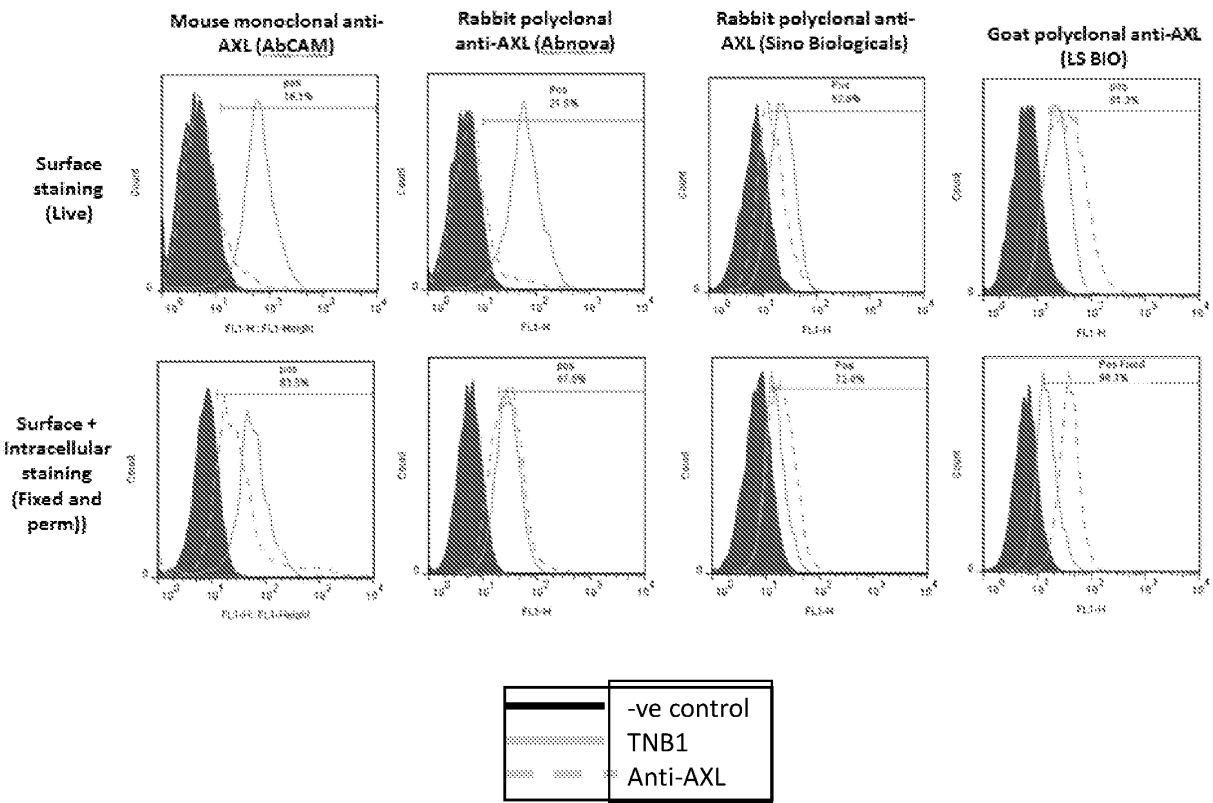


Fig. 8

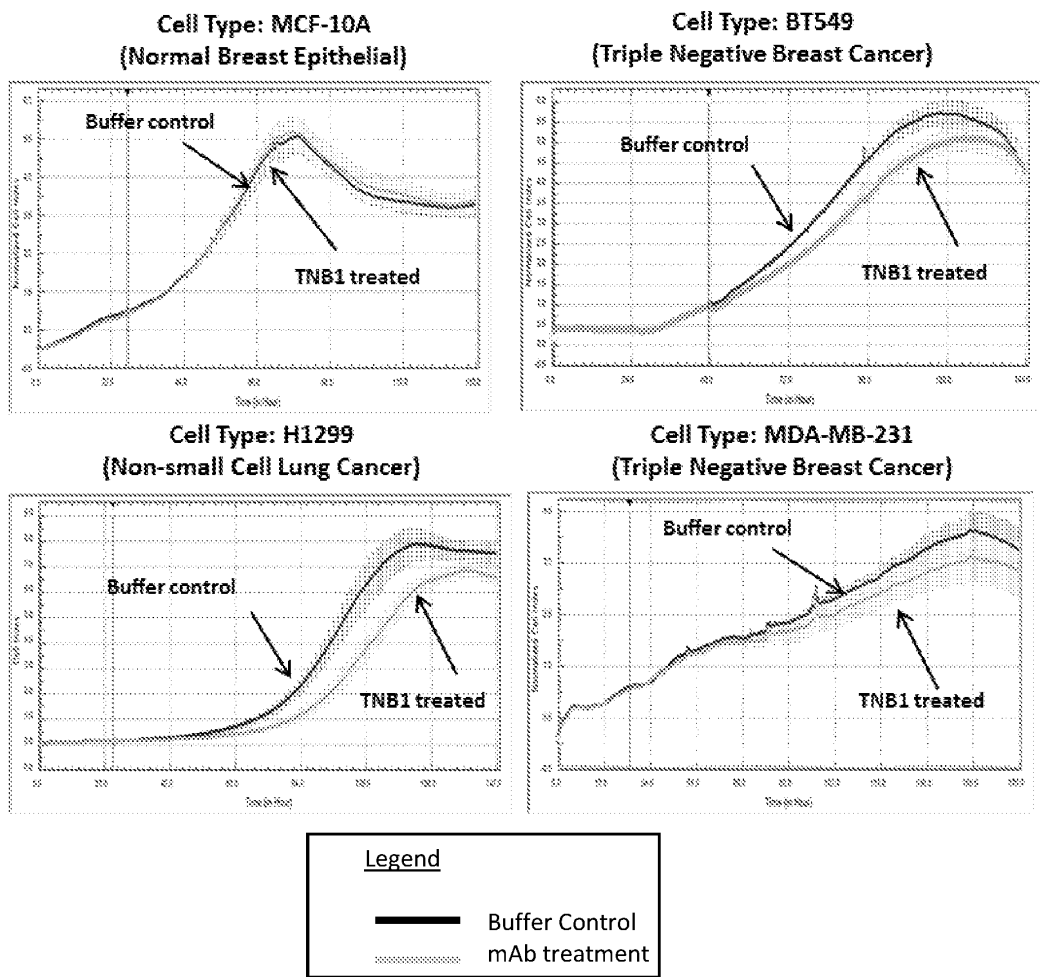


Fig. 9

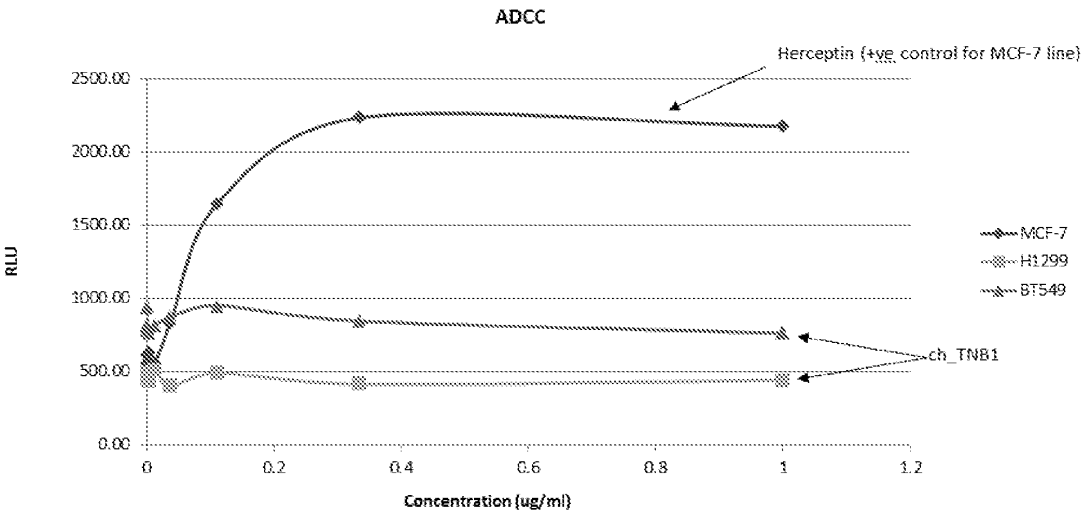


Fig. 10

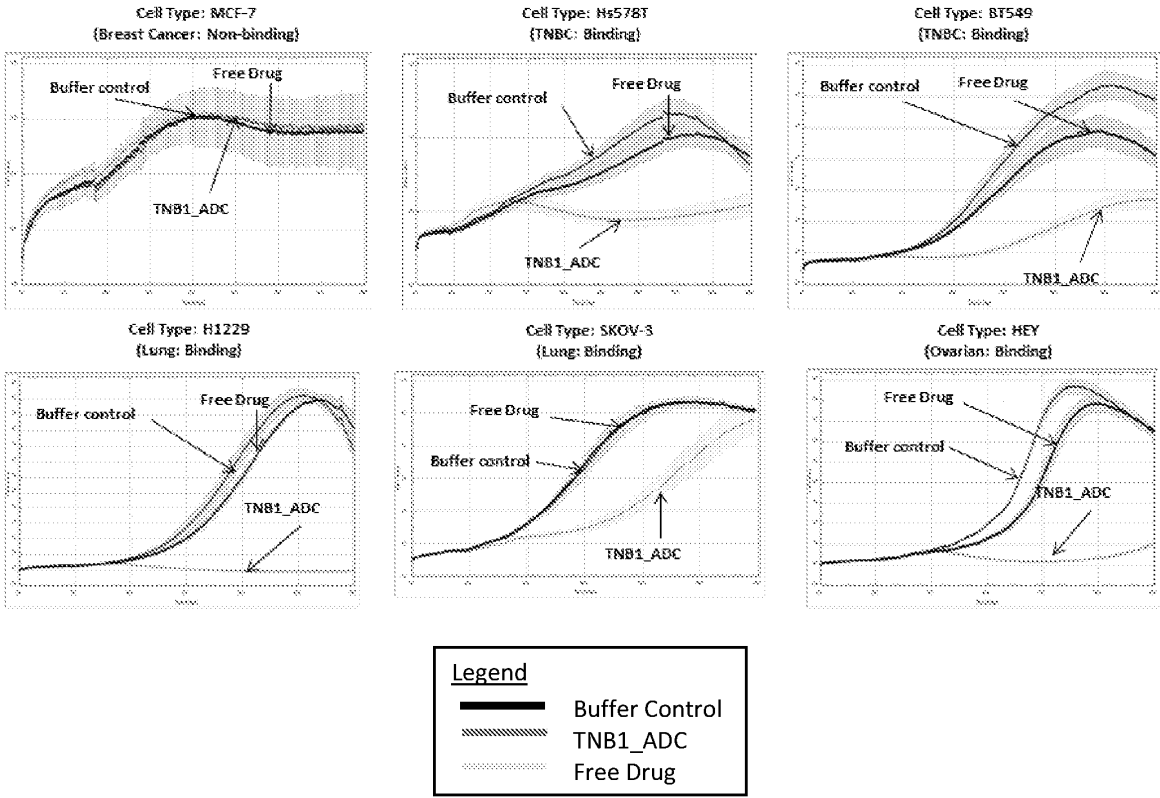
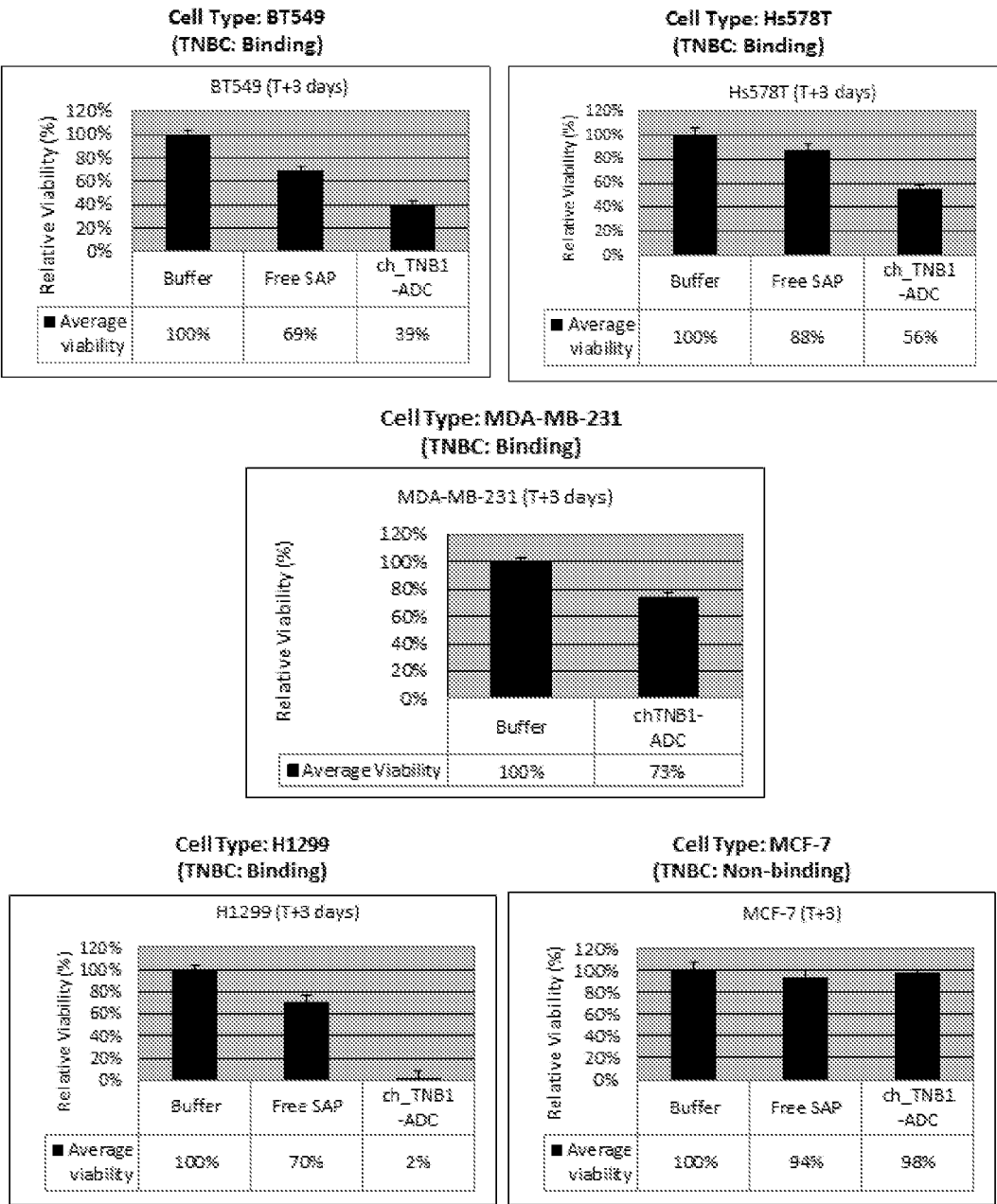
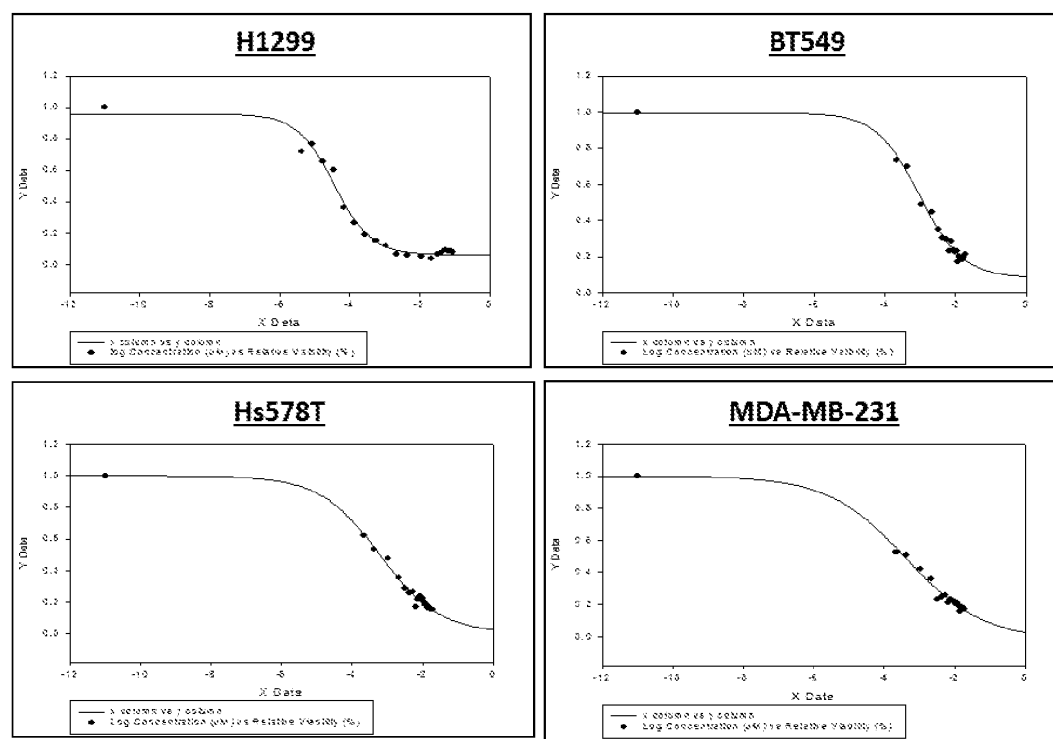


Fig. 11



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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

Fig. 13

