

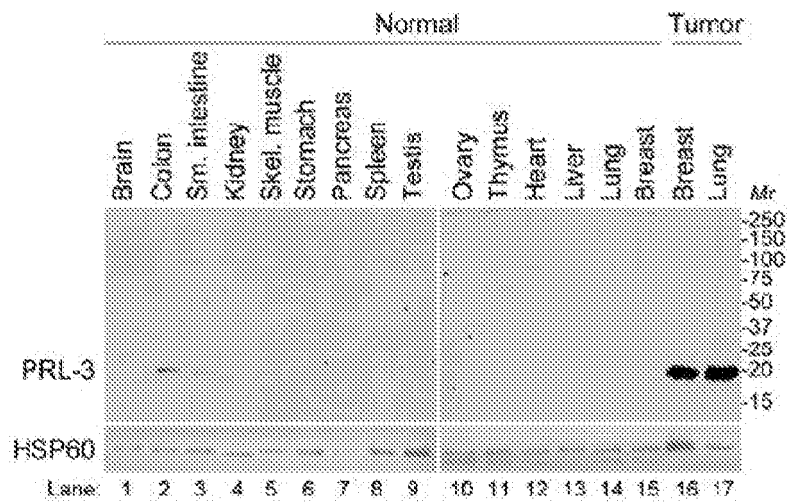


Figure 1A

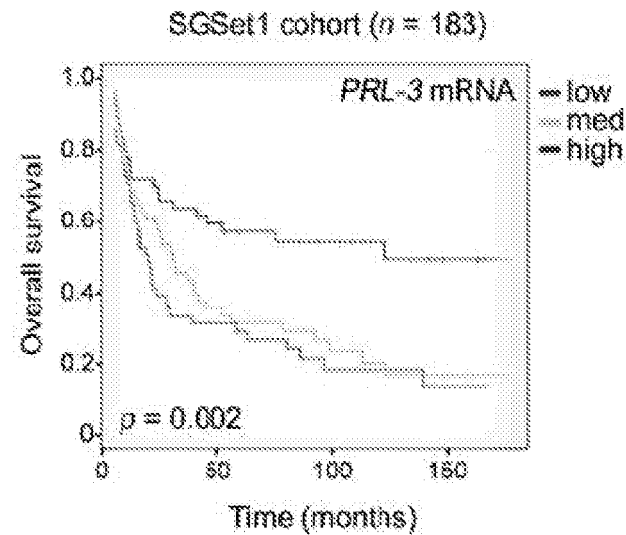


Figure 1B

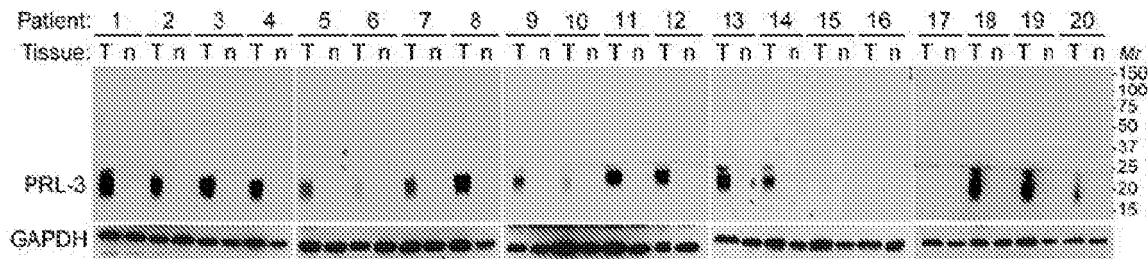


Figure 1C

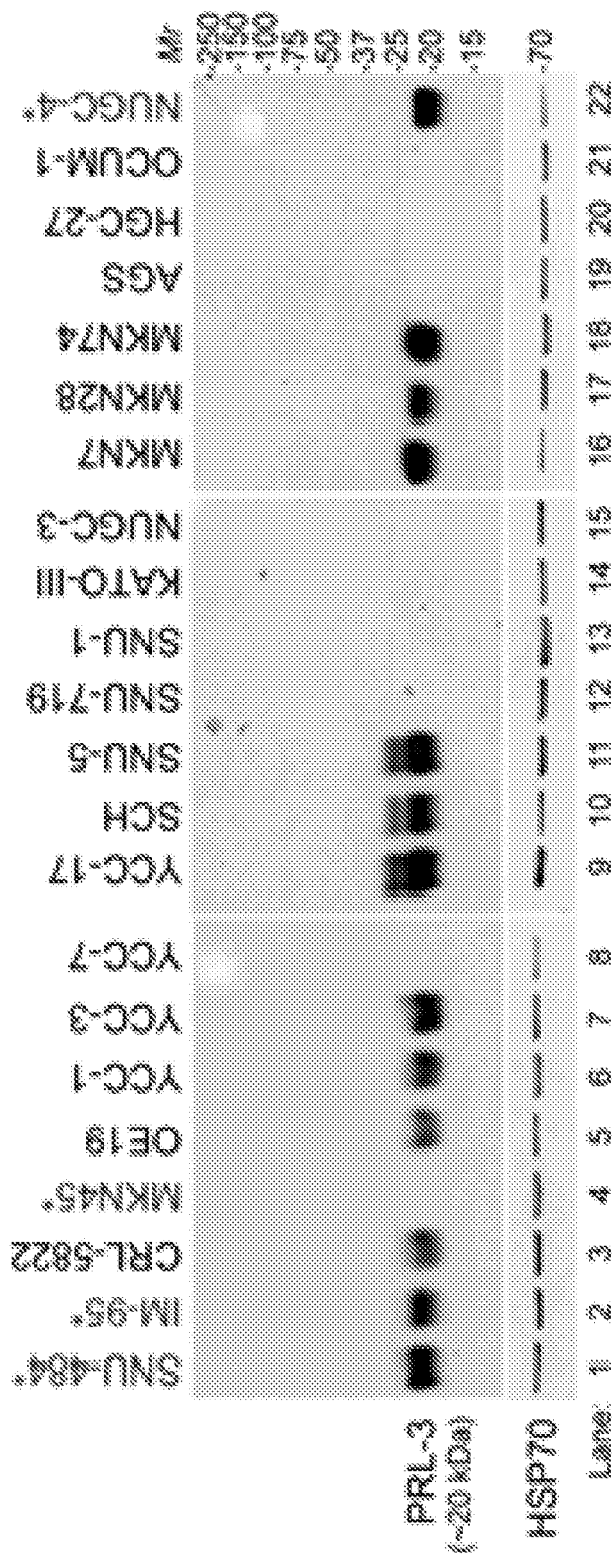


Figure 2A

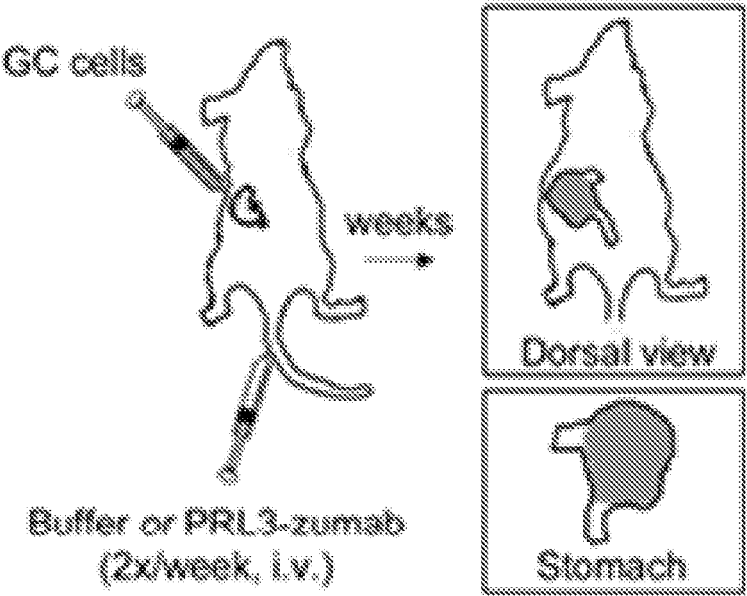


Figure 2B

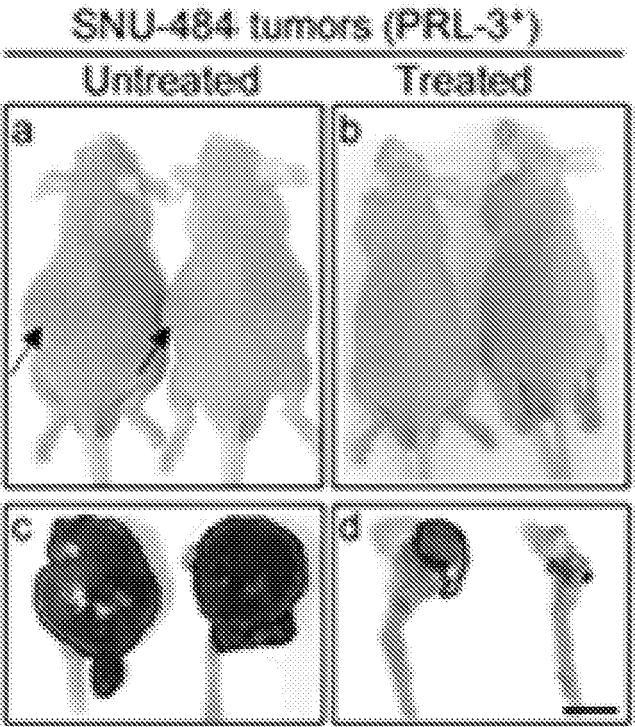


Figure 2C

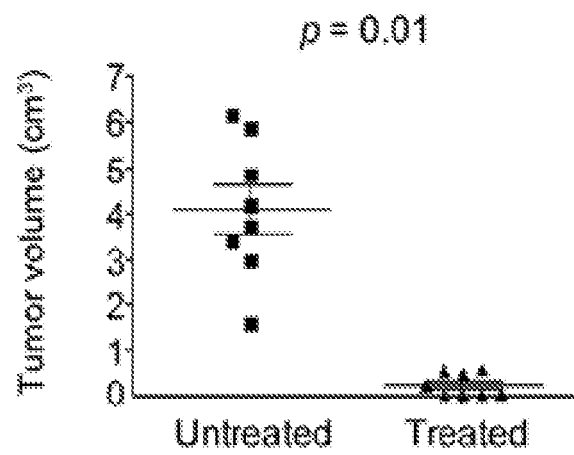


Figure 2D

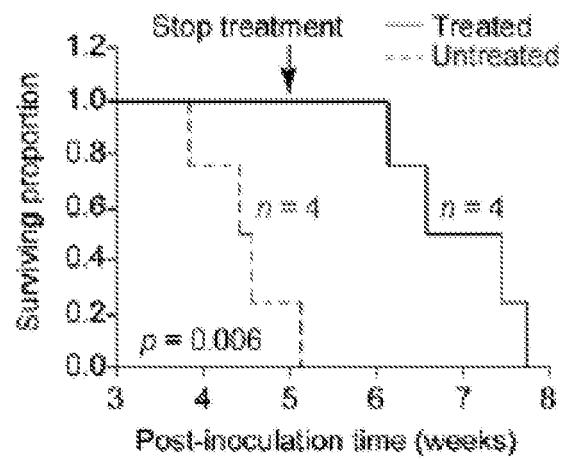


Figure 2E

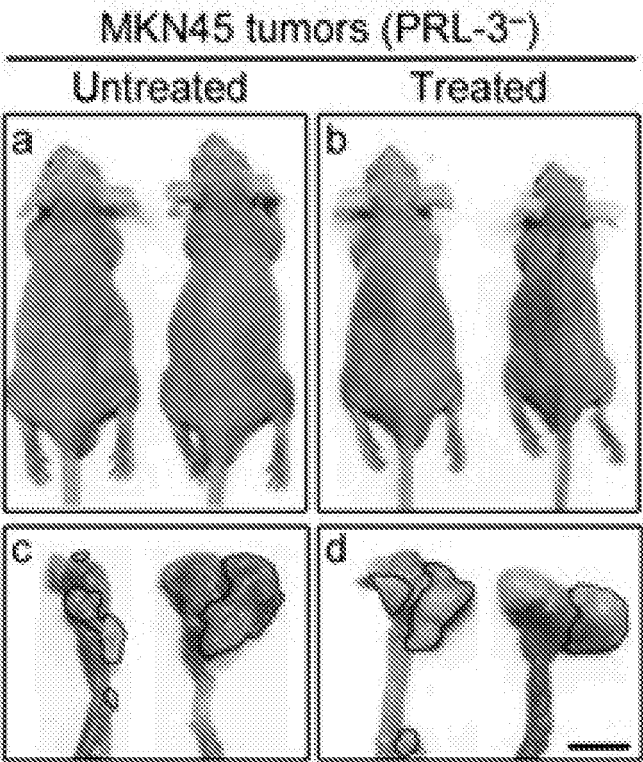


Figure 3A

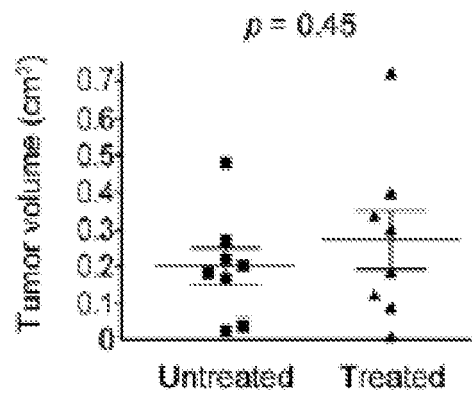


Figure 3B

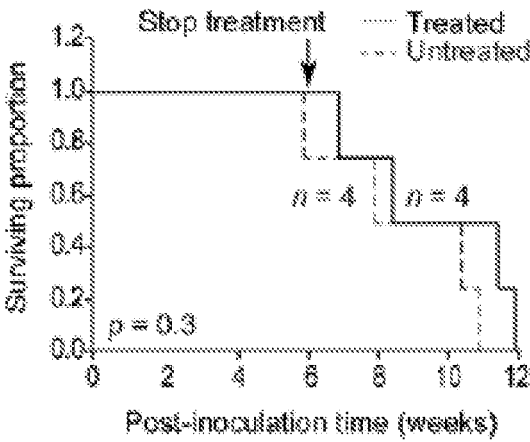


Figure 3C

Cell line	PRL-3 status	Mean tumor volume $\pm$ SEM (cm ³)				<i>p</i> -value
		Untreated	n	Treated	n	
SNU-484	PRL-3 ⁺	4.08 $\pm$ 0.54	8	0.23 $\pm$ 0.89	8	0.01
NUGC-4	PRL-3 ⁺	0.30 $\pm$ 0.1	4	0.02 $\pm$ 0.01	4	0.03
IM-95	PRL-3 ⁺	0.14 $\pm$ 0.03	6	0.01 $\pm$ 0.003	6	0.0008
MKN45	PRL-3 ⁻	0.19 $\pm$ 0.05	8	0.26 $\pm$ 0.08	8	0.45
MKN45-PRL-3	PRL-3 ⁺	0.39 $\pm$ 0.03	4	0.07 $\pm$ 0.02	5	0.00002

Figure 3D

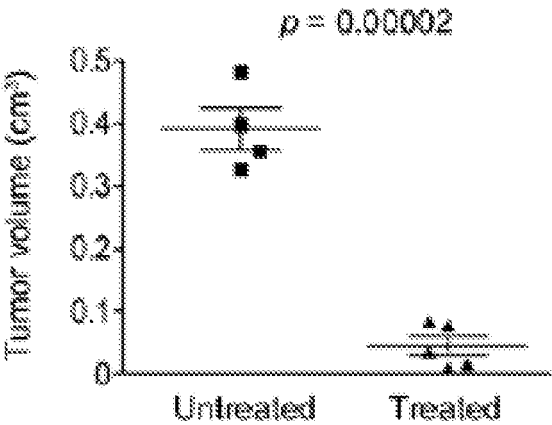


Figure 3E

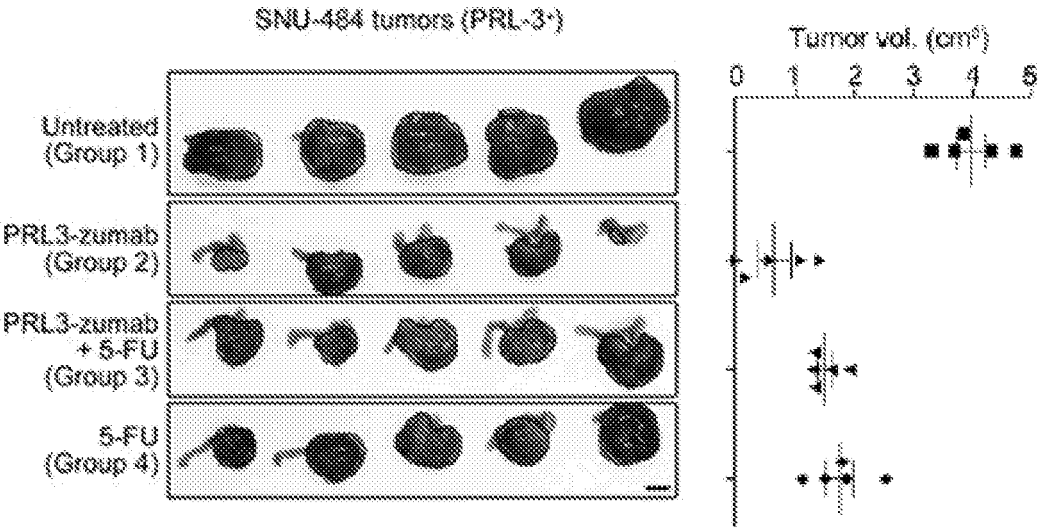


Figure 4A

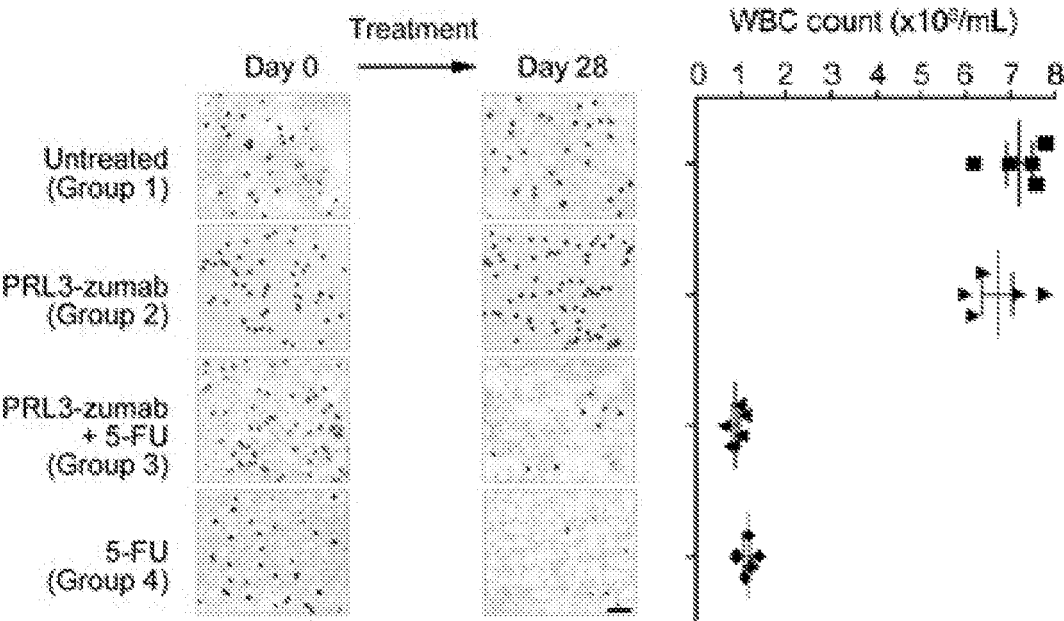


Figure 4B

Haematology	Ref. range	Unit	Mean values		
			PRL3-zumab	PRL3-zumab + 5-FU	5-FU alone
WBC count	3.48 – 14.03	$\times 10^9/\text{L}$	4.83	1.10	0.60
Neutrophils	0.58 – 3.83	$\times 10^9/\text{L}$	1.65	0.04	0.03
Lymphocytes	2.22 – 9.83	$\times 10^9/\text{L}$	3.03	0.98	0.54
Monocytes	0.21 – 1.25	$\times 10^9/\text{L}$	0.16	0.03	0.03
Eosinophils	0.01 – 0.49	$\times 10^9/\text{L}$	0.00	0.02	0.00
Basophils	0.00 – 0.18	$\times 10^9/\text{L}$	0.01	0.04	0.01
RBC count	6.93 – 12.24	$\times 10^{12}/\text{L}$	6.97	5.07	4.87
Haemoglobin	12.6 – 20.5	g/dL	10.4	7.4	7.1
MCV	50.7 – 64.5	fL	58.3	49.3	47.7
MCH	13.2 – 17.6	pg	15.0	14.7	14.7
MCHC	23.3 – 32.7	g/dL	26.0	29.3	21.7
Platelet	420 - 1698	$\times 10^9/\text{L}$	1016	202	198

Figure 4C

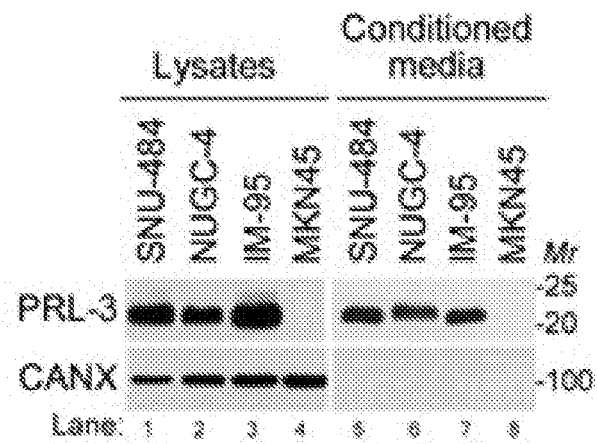


Figure 5A

Cancer type	n	Urinary PRL-3 expression	
		No. PRL-3 positive	% PRL-3 positive
Gastric	16	14	88
Nasopharyngeal	17	12	71
Bladder	67	30	45
Lung	85	56	66
Breast	10	8	80
Prostate	4	3	75
Total	199	123	62 (average)
Normal individuals	15	0	0

Figure 5B

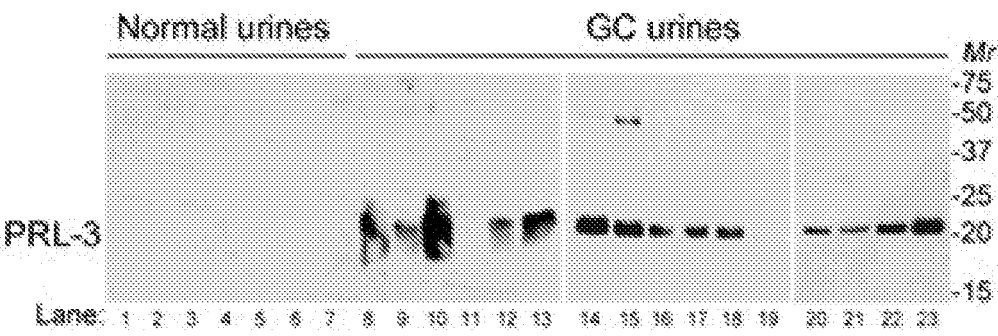


Figure 5C

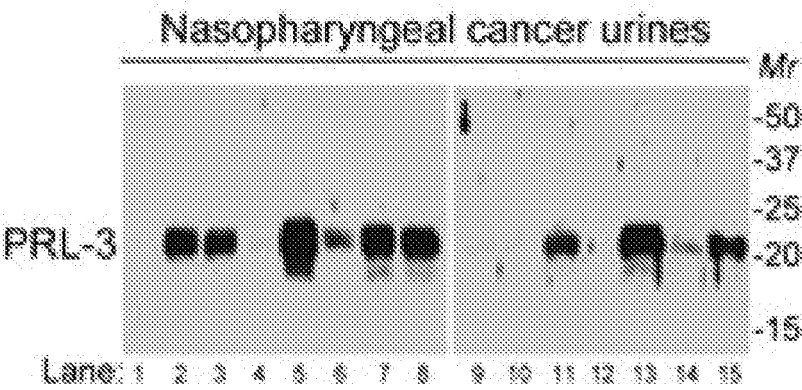


Figure 5D

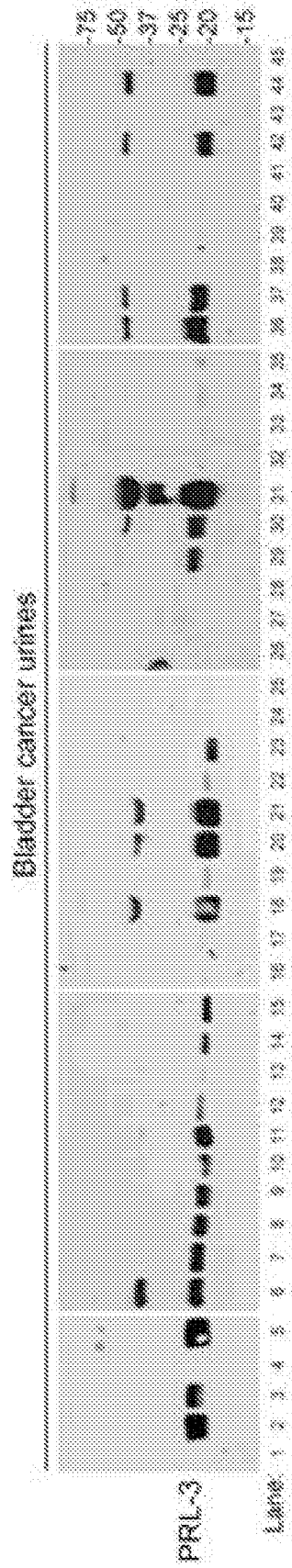


Figure 5E

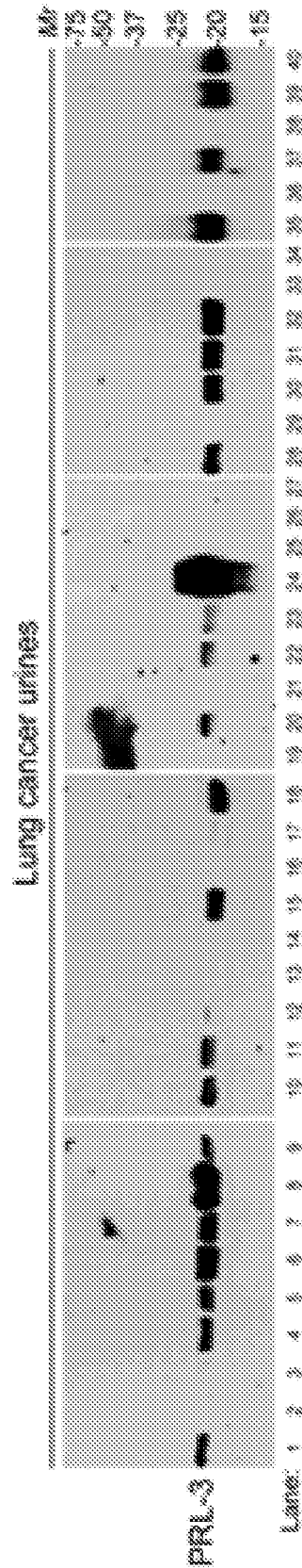


Figure 5F

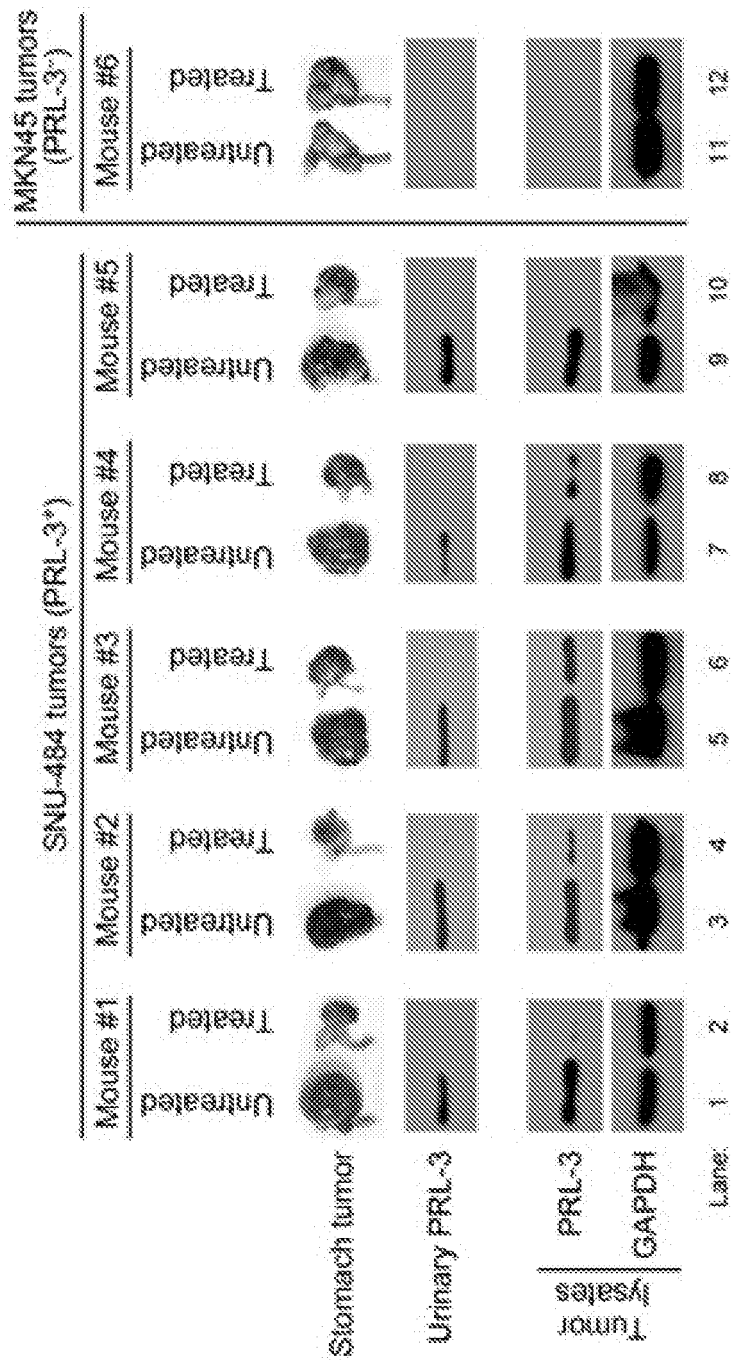


Figure 6A

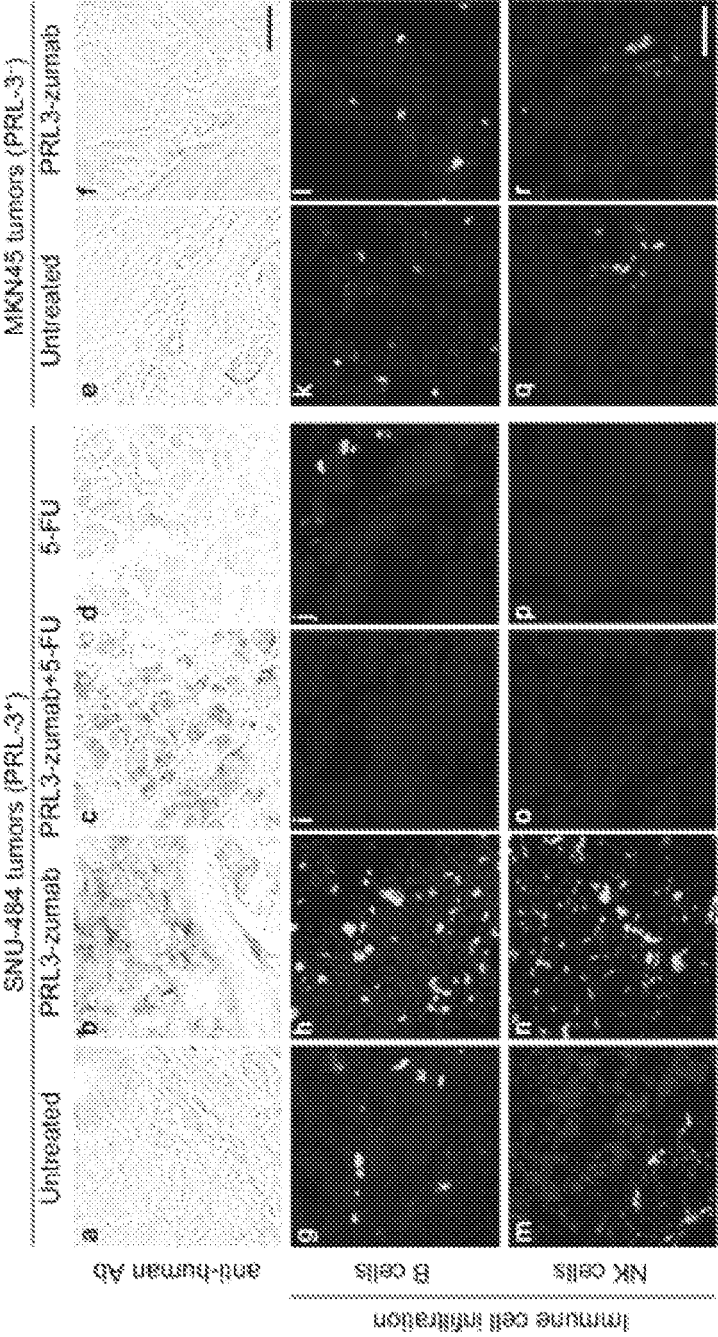


Figure 6B

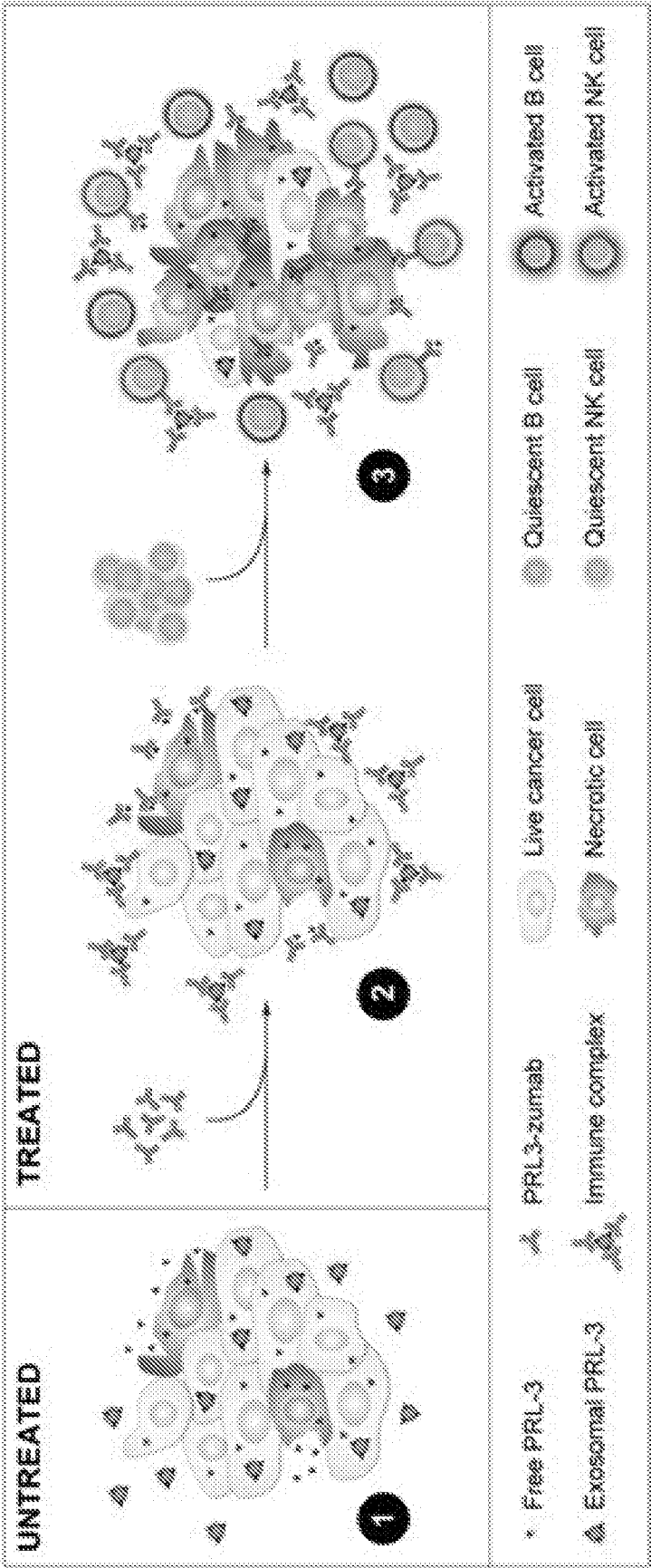


Figure 6C

>HZD_H1

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQLEWMGWIYPGNVNTYYNEKFRGRVTIT
ADTSASTAYMLSSLRSED TAVYYCASEEKNYPWFAYWGQGLVTS (SEQ ID NO: 16)

>HZD_H2

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQLEWIGWIYPGNVNTYYNEKFRGRATLTA
DKSASTAYMLSSLRSED TAVYYCASEEKNYPWFAYWGQGLVTS (SEQ ID NO: 17)

>HZD_H3

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQLEWIGWIYPGNVNTYYNEKFRGRATITA
DTSASTAYMLSSLRSED TAVYYCASEEKNYPWFAYWGQGLVTS (SEQ ID NO: 18)

>HZD_H4

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQLEWIGWIYPGNVNTYYNEKFRGKATLTA
DKSASTAYMLSSLRSED TAVYYCASEEKNYPWFAYWGQGLVTS (SEQ ID NO: 19)

>HZD_H5

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVKRPGQLEWIGWIYPGNVNTYYNEKFRGKATLTA
DKSASTAYMLSSLRSED TAVYYCASEEKNYPWFAYWGQGLVTS (SEQ ID NO: 20)

>HZD_H6

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQRPQGQLEWIGWIYPGNVNTYYNEKFRGKATITA
DKSASTAYMLSSLRSED TAVYYCASEEKNYPWFAYWGQGLVTS (SEQ ID NO: 21)

>HZD_H7

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWIGWIYPGNVNTYYNEKFRGKATIT
ADTSASTAYMELSSLRSED TAVYFCASEEKNYPWFAYWGQGLVTS (SEQ ID NO: 22)

>H1

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQRPQGQLEWIGWIYPGNVNTYYNEKFRGKATIT
ADKSASTAYMELSSLRSED TAVYFCASEEKNYPWFAYWGQGLVTVSSAS (SEQ ID NO: 23)

>H2

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWIGWIYPGNVNTYYNEKFRGKATIT
ADTSASTAYMELSSLRSED TAVYFCASEEKNYPWFAYWGQGLVTVSSAS (SEQ ID NO: 24)

>H3

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWIGWIYPGNVNTYYNEKFRGKATLT
ADKSASTAYMELSSLRSED TAVYFCASEEKNYPWFAYWGQGLVTVSSAS (SEQ ID NO: 25)

Heavy Chain

CDR1 GYTFTNYYMH (SEQ ID NO: 1)

CDR2 WIYPGNVNTYYNEKFRG (SEQ ID NO: 2)

CDR3 EEKNYPWFAY (SEQ ID NO: 3)

Figure 7A

Humanized light chain protein sequences

>H2D_K1
 DTQLTQSPSSLSASVGDRVTICKASQSVEDDGENYMNWYQQKPGSPKLLIYAASNLESGIPARFSGSGSGTD
 FTLTISSLPEDFATYYCQQSNEDPFTFGSGTKLEIK (SEQ ID NO: 7)

>H2D_K2
 DTQLTQSPSSLSASVGDRVTICKASQSVEDDGENYMNWYQQKPGSPKLLIYAASNLESGIPARFSGSGSGTD
 FTLTISSLPEDFATYYCQQSNEDPFTFGSGTKLEIK (SEQ ID NO: 8)

>H2D_K3
 DTQLTQSPSSLSASVGDRVTICKASQSVEDDGENYMNWYQQKPGSPKLLIYAASNLESGVPSRFSGSGSGTD
 FTLTISSLPEDFATYYCQQSNEDPFTFGSGTKLEIK (SEQ ID NO: 9)

>H2D_K4
 DTQLTQSPSSLSASVGDRVTICKASQSVEDDGENYMNWYQQKPGSPKLLIYAASNLESGIPSRFSGSGSGTD
 FTLTISSLPEDFATYYCQQSNEDPFTFGPGTKVDIK (SEQ ID NO: 10)

>H2D_K5
 DTQLTQSPSSLSASVGDRVTICKASQSVEDDGENYMNWYQQKPGSPKLLIYAASNLESGIPSRFSGSGSGTD
 FTLTISSLPEDFATYYCQQSNEDPFTFGPGTKVDIK (SEQ ID NO: 11)

>H2D_K6
 DTVLTQSPSSLSASVGDRVTICKASQSVEDDGENYMNWYQQKPGSPKLLIYAASNLESGIPSRFSG
 SGSGTDFTLTISSLPEDFATYYCQQSNEDPFTFGPGTKVDIK (SEQ ID NO: 12)

>K
 DIQMTQSPSSLSASVGDRVTISCKASQSVEDDGENYMNWYQQKPGKSPKLLIYAASNLESGIPARF
 SGSGSGTDFTLTISSLPEDFATYYCQQSNEDPFTFGSGTKLEIKRT (SEQ ID NO: 13)

>L1
 DIQMTQSPSSLSASVGDRVTITCKASQSVEDDGENYMNWYQQKPGKAPKLLIYAASNLESGVPSRF
 SGSGSGTDFTLTISSLPEDFATYYCQQSNEDPFTFGPGTKVDIKRT (SEQ ID NO: 14)

>L2
 DTQLTQSPSSLSASVGDRVTITCKASQSVEDDGENYMNWYQQKPGKAPKLLIYAASNLESGIPSRF
 SGSGSGTDFTLTISSLPEDFATYYCQQSNEDPFTFGPGTKVDIKRT (SEQ ID NO: 15)

Light Chain

CDR1 KASQSVEDDGENYMN (SEQ ID NO:4)

CDR2 AASNLES (SEQ ID NO:5)

CDR3 QQSNEDPFT (SEQ ID NO:6)

Figure 7B

Antibody 223 sequences

The amino acid sequence of the heavy chain of the variable region of monoclonal antibody 223:

EFMEWSWILFLLSIAGVHCQVQLQQSGPELVKPGASVRISCKASGYTFTSYIHVWKQRPG
 QGLEWIGWYPGNVNTEYNEKFRGKATLTADKSSSTAYMQLSSLTSEDSAVYFCASEERNYPW
 FAYWGQGTLLVTVSAAKTTTPPVPLVPGSLG

The amino acid sequence of the light chain of the variable region of monoclonal antibody 223:

WEFMETDTLLWVLLWPGSTGDIVLTQSPASLAVSLGQRATISCKASQSVEDDDGENYMNWY
 QQKPGQSPKLLIYAASNLESIGIPARFSGSGGTDFTLNIHPVEEEDAATYYCQQSNEDPFTFGSGTKLEIKRADAAPTVSIFPPSSKLG

Figure 8A***Antibody 318 sequences***

The amino acid sequence of the heavy chain of the variable region of monoclonal antibody 318 is as follows:

EFMEWSWVFLFLLSIAGVHCQVQLQQSGPELVKPGASVRISCKASGYTFTNYYMHVWKQRPG
 QGLEWIGWYPGNVNTEYNEKFRARPH.LQTNPPAQPTCSSAA.PLRTLRSISVQVRRELPLV
 CLLGPRDSGHCLCSQNDTPIRLSPGPWKLG

The amino acid sequence of the light chain of the variable region of monoclonal antibody 318 is as follows:

LVDMESDTLLWVLLWPGSTGDIVLTQSPASLAVSLGQRATISYRASKSVSTSGYSYMHWN
 QQKPGQPPRLIYLVSNLESIGVPARFSGSGGTDFTLNIHPVEEEDAATYYCQHIRELTRSEG
 GPSWK

Figure 8B

1 marmnrpapv evsykhmrfl ithnptnatl stfiedlkkv gattvvrvc vtydktplek
61 dgitvvdwpf ddgapppgkv vedwlslvka kfceapgscv avhcvaglgr apvlvalali
121 esgmkyedai qfirqkrrga inskqltyle kyrpkqrlrf kdpthktrc cvm

Figure 9

Light Chain Alignments

HZD_K1	DTQLTQSPSSLSASVGDRVTTI-C	KASQSVEDDGENYMNWYQQKPG-SPKLLIYAASNLES
HZD_K2	DTQLTQSPSSLSASVGDRVTTI-C	KASQSVEDDGENYMNWYQQKPG-SPKLLIYAASNLES
HZD_K3	DTQLTQSPSSLSASVGDRVTTI-C	KASQSVEDDGENYMNWYQQKPG-SPKLLIYAASNLES
HZD_K4	DTQLTQSPSSLSASVGDRVTTI-C	KASQSVEDDGENYMNWYQQKPG-SPKLLIYAASNLES
HZD_K5	DTQLTQSPSSLSASVGDRVTTI-C	KASQSVEDDGENYMNWYQQKPG-SPKLLIYAASNLES
HZD_K6	DTVLTQSPSSLSASVGDRVTTI-C	KASQSVEDDGENYMNWYQQKPG-SPKLLIYAASNLES
K	DIQMTQSPSSLSASVGDRVTTIS	CASQSVEDDGENYMNWYQQKPGKSPKLLIYAASNLES
L1	DIQMTQSPSSLSASVGDRVTTIT	CASQSVEDDGENYMNWYQQKPGKAPKLLIYAASNLES
L2	DTQLTQSPSSLSASVGDRVTTI	CASQSVEDDGENYMNWYQQKPGKAPKLLIYAASNLES

HZD_K1	GIPARESGSGSGTDFTLTIS	SL-PEDFATYYCQQSNEDPFTFGSGTKLEIK--
HZD_K2	GIPARESGSGSGTDFTLTIS	SL-PEDFATYYCQQSNEDPFTFGSGTKLEIK--
HZD_K3	GVPSRSGSGSGTDFTLTIS	SL-PEDFATYYCQQSNEDPFTFGSGTKLEIK--
HZD_K4	GIPSRSGSGSGTDFTLTIS	SL-PEDFATYYCQQSNEDPFTFGPGTKVDIK--
HZD_K5	GIPSRSGSGSGTDFTLTIS	SL-PEDFATYYCQQSNEDPFTFGPGTKVDIK--
HZD_K6	GIPSRSGSGSGTDFTLTIS	SL-PEDFATYYCQQSNEDPFTFGPGTKVDIK--
K	GIPARESGSGSGTDFTLTIS	LQPEDFATYYCQQSNEDPFTFGSGTKLEIKRT
L1	GVPSRSGSGSGTDFTLTIS	LQPEDFATYYCQQSNEDPFTFGPGTKVDIKRT
L2	GIPSRSGSGSGTDFTLTIS	LQPEDFATYYCQQSNEDPFTFGPGTKVDIKRT

Grey boxes indicate CDR regions

Important domain sequences:

QSPSSLSASVGDRV (SEQ ID NO: 26)

KASQSVEDDGENYMNWYQQK (SEQ ID NO: 27)

SGSGSGTDFTLTISLQPEDFATYYCQQSNEDPFT (SEQ ID NO: 28)

Figure 10A

Heavy Chain Alignments

HZD_H1	QVQIVQSGAEVKKPGASVKV	SCKASGYTFTNYYMHWRQAPGQ-LEWMGWIYPGNVNTYY
HZD_H2	QVQIVQSGAEVKKPGASVKV	SCKASGYTFTNYYMHWRQAPGQ-LEWIGWIYPGNVNTYY
HZD_H3	QVQIVQSGAEVKKPGASVKV	SCKASGYTFTNYYMHWRQAPGQ-LEWIGWIYPGNVNTYY
HZD_H4	QVQIVQSGAEVKKPGASVKV	SCKASGYTFTNYYMHWRQAPGQ-LEWIGWIYPGNVNTYY
HZD_H5	QVQIVQSGAEVKKPGASVKV	SCKASGYTFTNYYMHWRQAPGQ-LEWIGWIYPGNVNTYY
HZD_H6	QVQIVQSGAEVKKPGASVKV	SCKASGYTFTNYYMHWRQAPGQ-LEWIGWIYPGNVNTYY
HZD_H7	QVQIVQSGAEVKKPGASVKV	SCKASGYTFTNYYMHWRQAPGQ-LEWIGWIYPGNVNTYY
H1	QVQIVQSGAEVKKPGASVKV	SCKASGYTFTNYYMHWRQAPGQ-LEWIGWIYPGNVNTYY
H2	QVQIVQSGAEVKKPGASVKV	SCKASGYTFTNYYMHWRQAPGQ-LEWIGWIYPGNVNTYY
H3	QVQIVQSGAEVKKPGASVKV	SCKASGYTFTNYYMHWRQAPGQ-LEWIGWIYPGNVNTYY

HZD_H1	NEKFRGRVTITADTSASTAYM-LSSLRSEDTAVYYCASEEK	KNYPWFAYWGQGLVTS---
HZD_H2	NEKFRGRATLTADKSASTAYM-LSSLRSEDTAVYYCASEEK	KNYPWFAYWGQGLVTS---
HZD_H3	NEKFRGRATITADTSASTAYM-LSSLRSEDTAVYYCASEEK	KNYPWFAYWGQGLVTS---
HZD_H4	NEKFRGKATLTADKSASTAYM-LSSLRSEDTAVYYCASEEK	KNYPWFAYWGQGLVTS---
HZD_H5	NEKFRGKATLTADKSASTAYM-LSSLRSEDTAVYYCASEEK	KNYPWFAYWGQGLVTS---
HZD_H6	NEKFRGKATITADKSASTAYM-LSSLRSEDTAVYYCASEEK	KNYPWFAYWGQGLVTS---
HZD_H7	NEKFRGKATITADTSASTAYMELSSLRSEDTAVYFCASEEK	KNYPWFAYWGQGLVTS---
H1	NEKFRGKATITADKSASTAYMELSSLRSEDTAVYFCASEEK	KNYPWFAYWGQGLVTVSSAS
H2	NEKFRGKATITADTSASTAYMELSSLRSEDTAVYFCASEEK	KNYPWFAYWGQGLVTVSSAS
H3	NEKFRGKATLTADKSASTAYMELSSLRSEDTAVYFCASEEK	KNYPWFAYWGQGLVTVSSAS

Heavy Chains

Grey boxes indicate CDR regions

Important domain sequences:

VQSGAEVKKPGASVKV SCKASGYTFTNYYMHVV (SEQ ID NO: 29)

WIYPGNVNTYYNEKFR (SEQ ID NO: 30)

ASTAYMELSSLRSE (SEQ ID NO: 31)

ASEEKNYPWFAYWGQGLVT (SEQ ID NO: 32)

Figure 10B

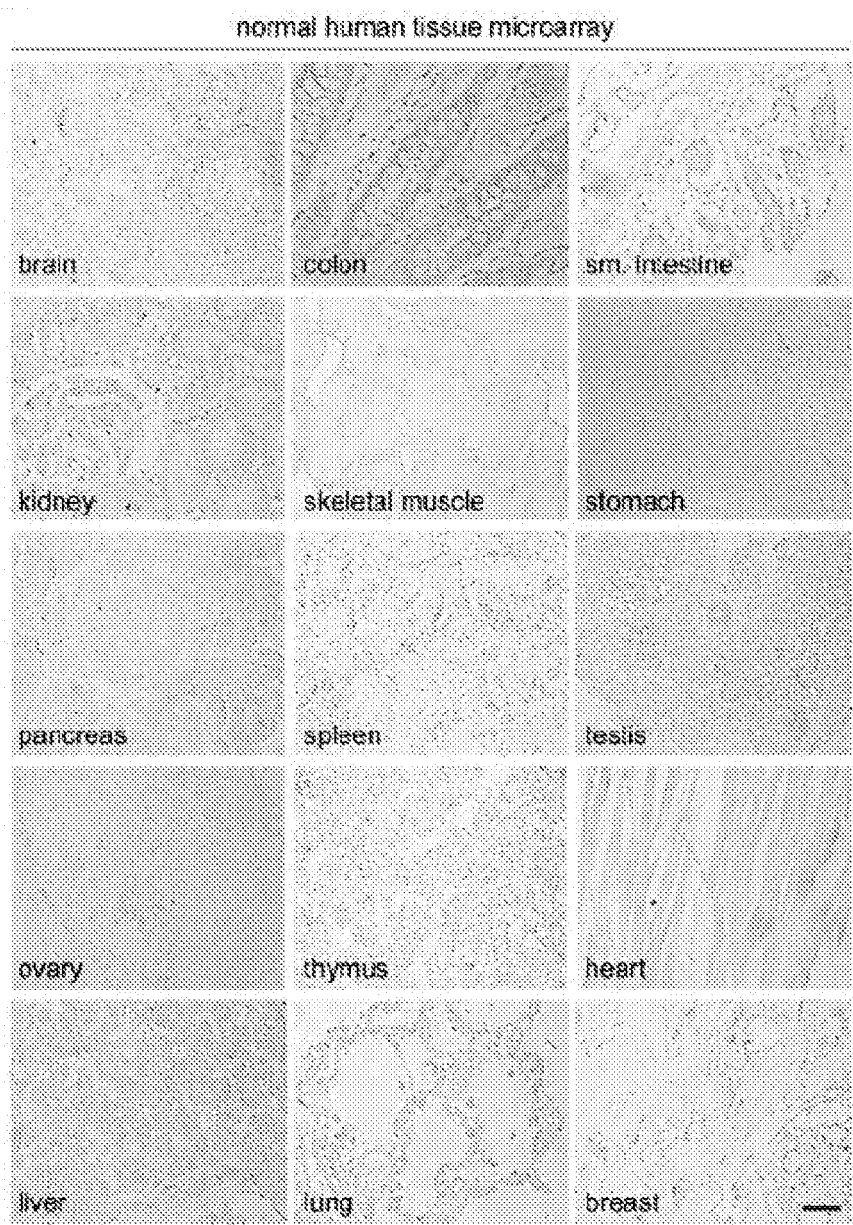


Figure 11A

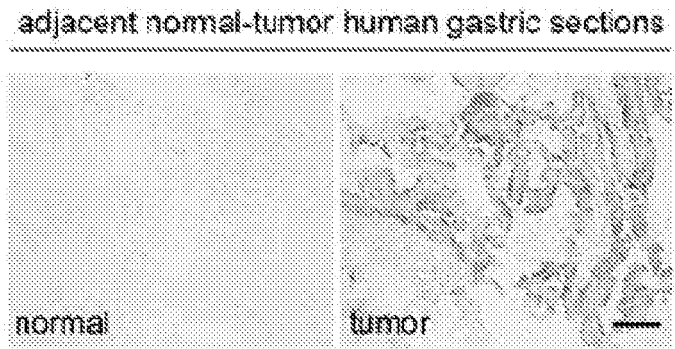


Figure 11B

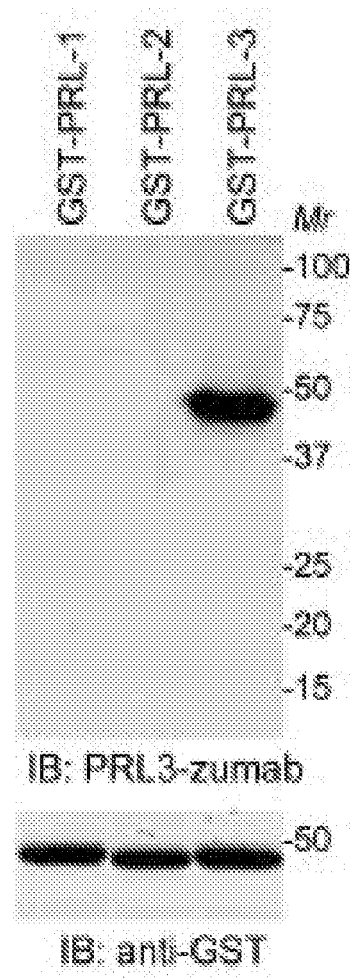


Figure 12A

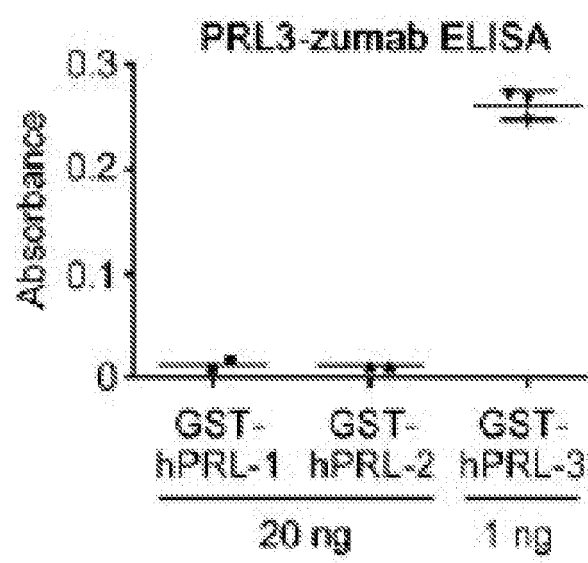


Figure 12B

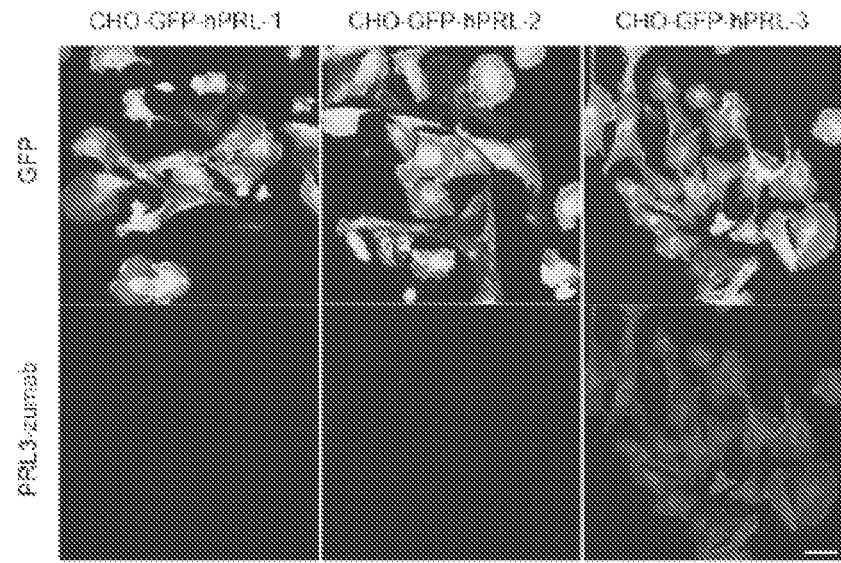


Figure 12C

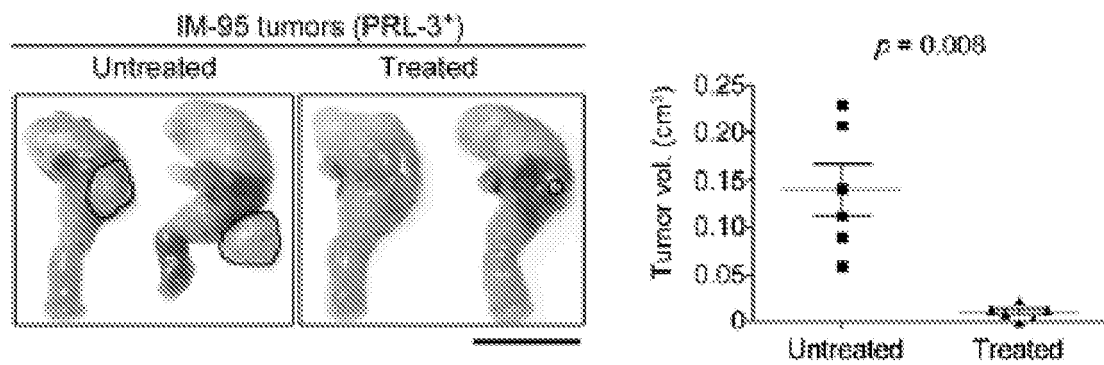


Figure 13A

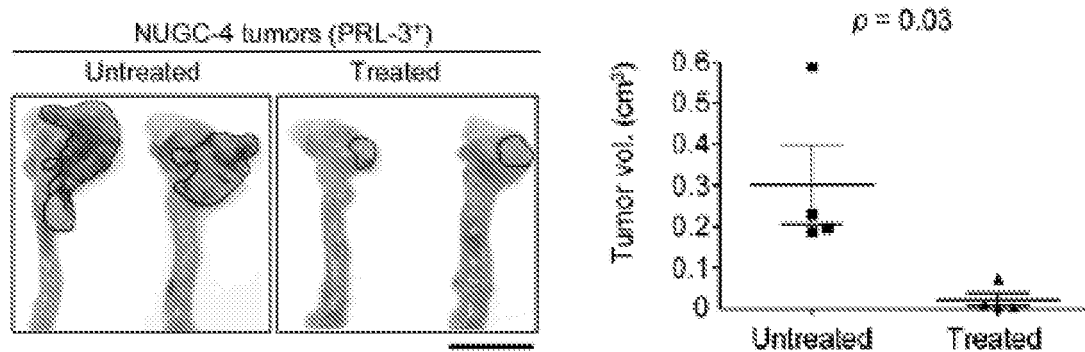


Figure 13B

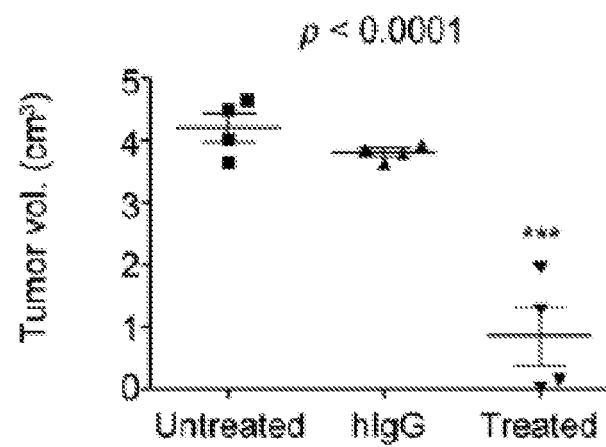


Figure 13C

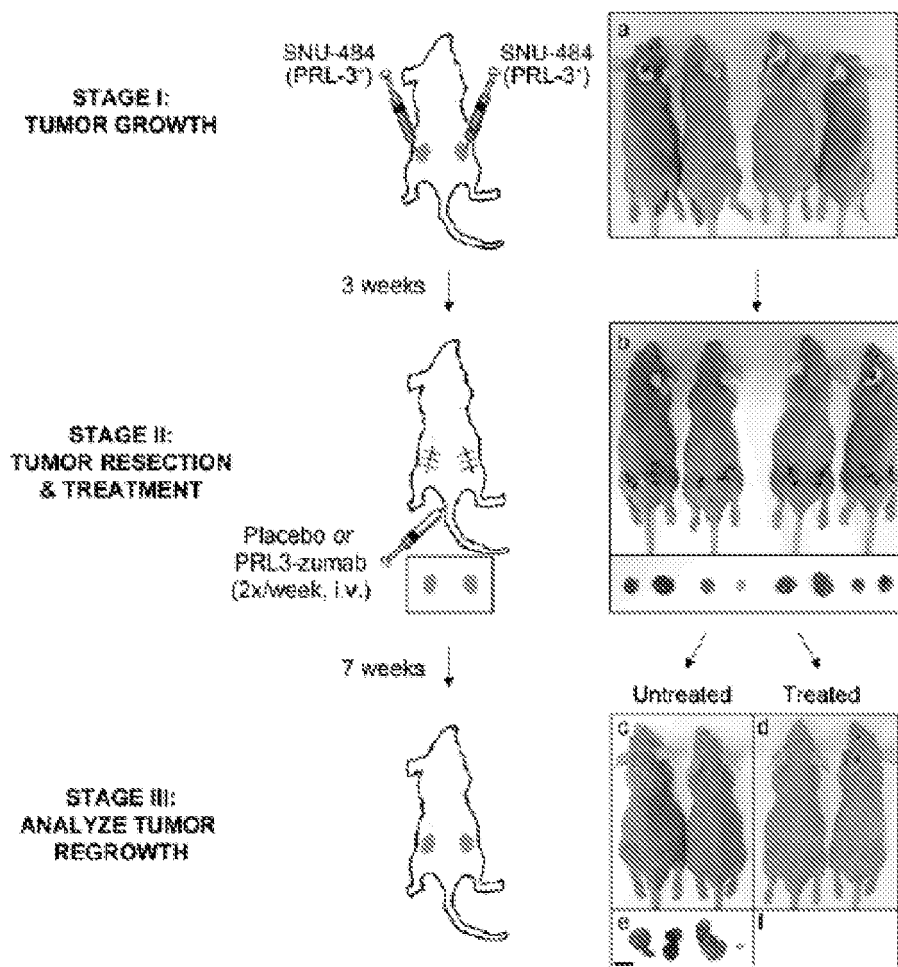


Figure 14A

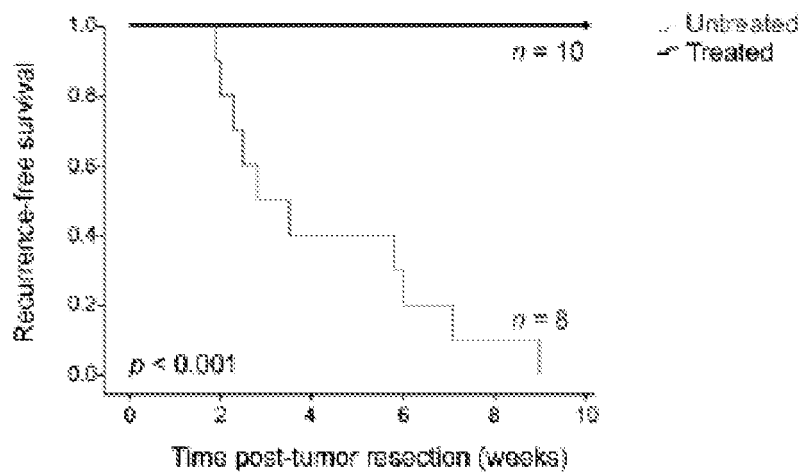


Figure 14B

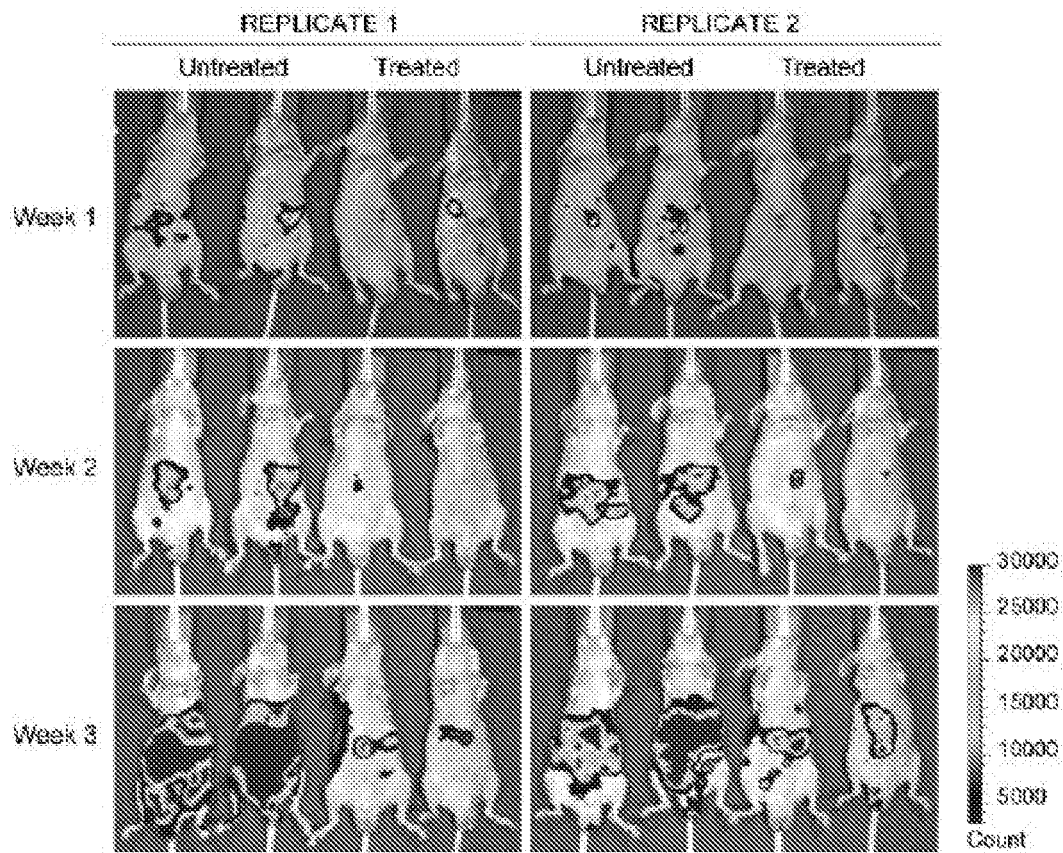


Figure 15A

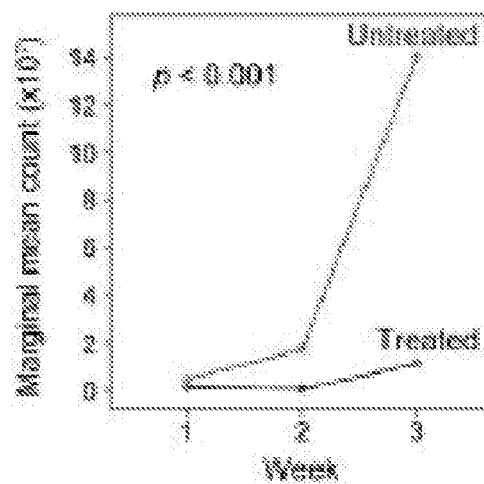


Figure 15B

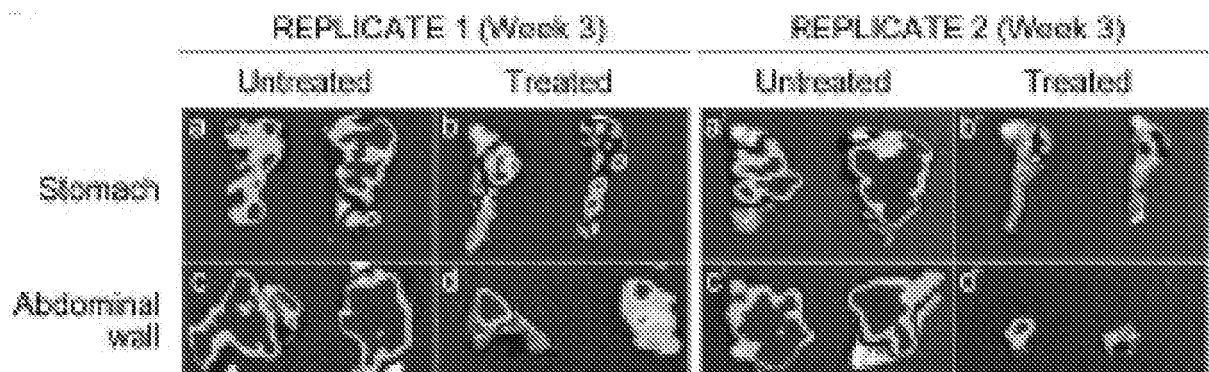


Figure 15C

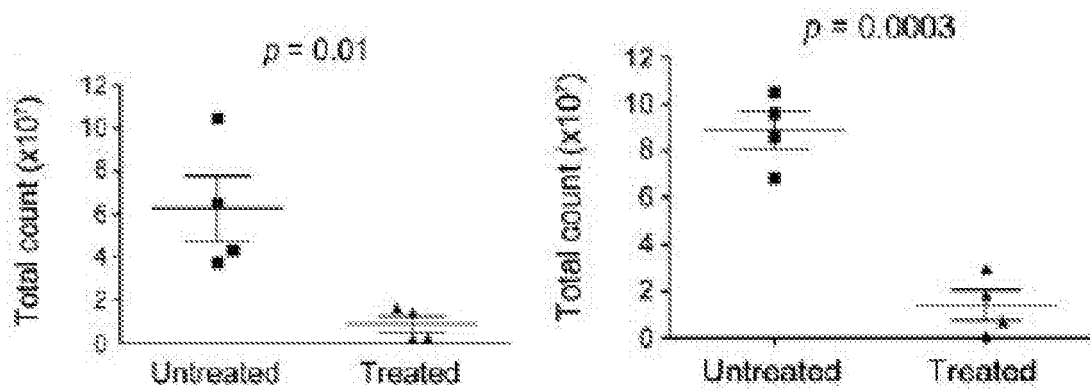


Figure 15D

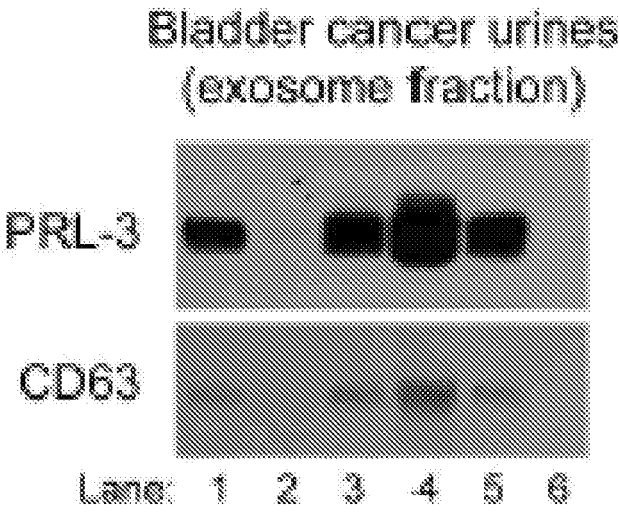


Figure 16

Clinical characteristics of SGset1 GC patient cohort

SGset1 (N = 185)	
Age (years)	
range	23.4 - 92.4 (1 missing)
mean $\pm$ S.D	64 $\pm$ 12.9 (1 missing)
Gender (%)	
male	68 (36.8)
female	116 (62.7)
missing	1 (0.54)
Stage (%)	
1	29 (15.7)
2	30 (16.2)
3	66 (35.7)
4	59 (31.9)
missing	1 (0.54)
Lauren's histopathology (%)	
intestinal	92 (49.7)
diffuse	72 (38.9)
mixed/unclassifiable	20 (10.8)
missing	1 (0.54)
Helicobacter Pylori status (%)	
positive	59 (31.9)
negative	37 (20.0)
missing	89 (48.1)
Median overall survival (months)	22.5 (1 missing)
Number of overall death events	110 (2 missing)

Figure 17**Univariate and multivariate Cox regression analysis**

	Category	HR (95% C.I.)	P-value
Univariate Cox (PRL-3 expression)	Med vs Low	2.35 (1.42 - 3.87)	0.0008
	High vs Low	1.94 (1.17 - 3.21)	0.01
Multivariate Cox (PRL-3 expression, tumor stage)	Med vs Low	1.99 (1.19 - 3.33)	0.009
	High vs Low	1.76 (1.76 - 2.95)	0.03

Figure 18

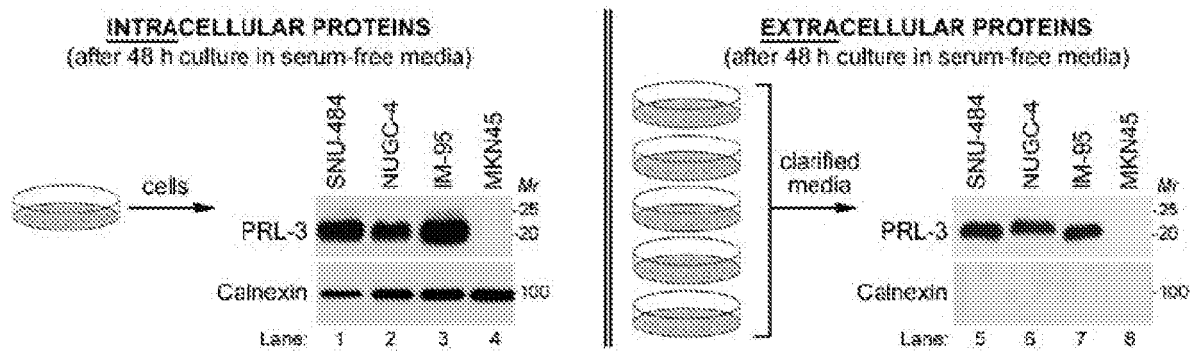


Figure 19B

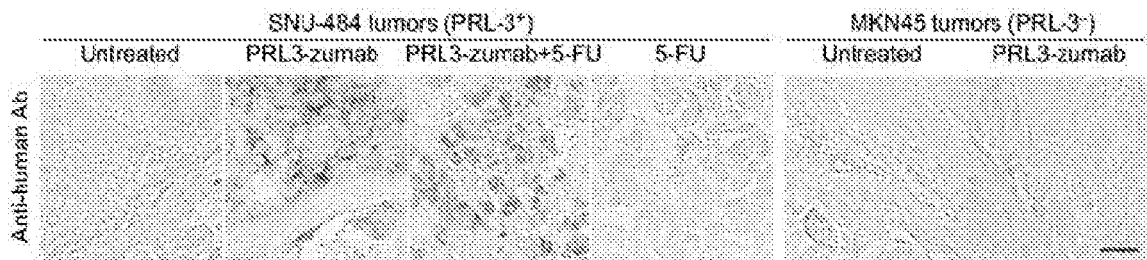


Figure 19B

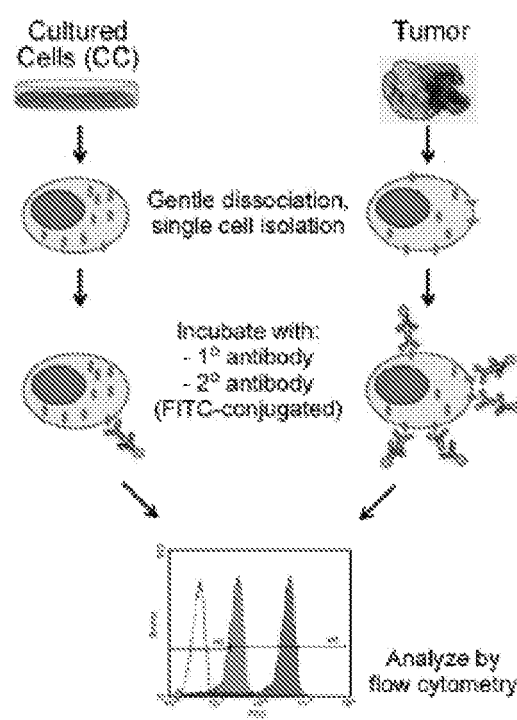


Figure 20A

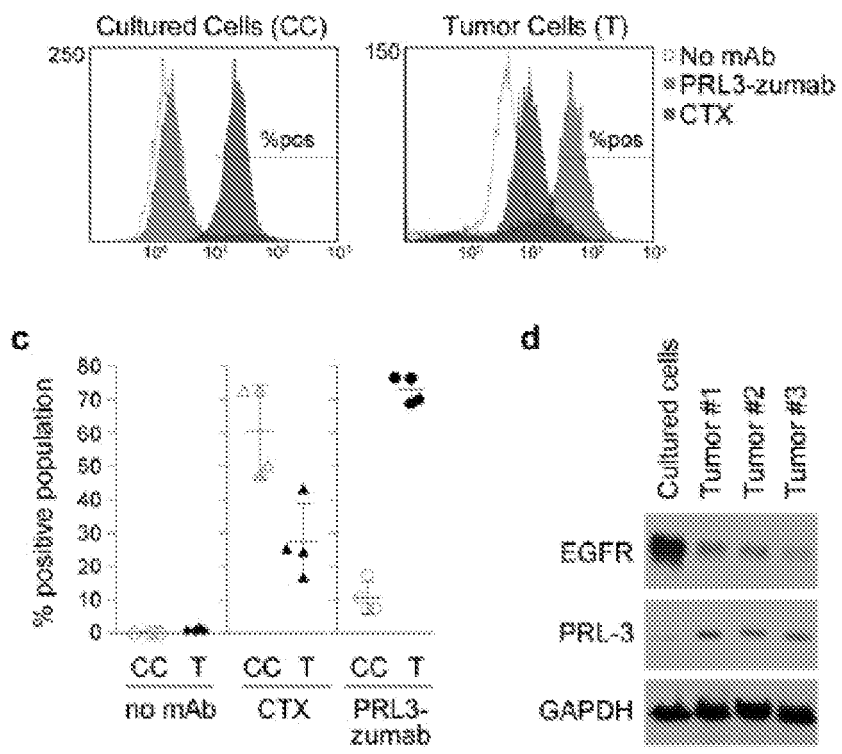


Figure 20B

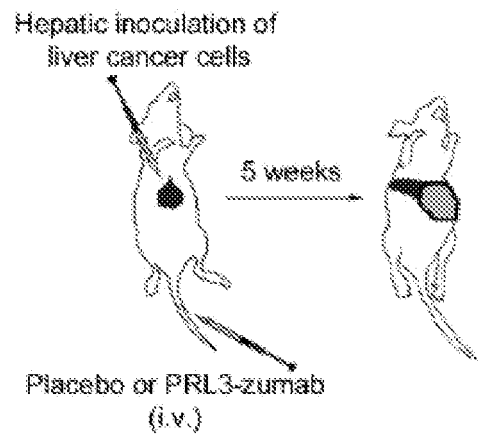


Figure 21A

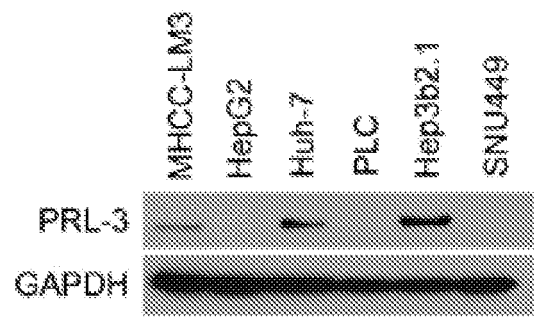


Figure 21B

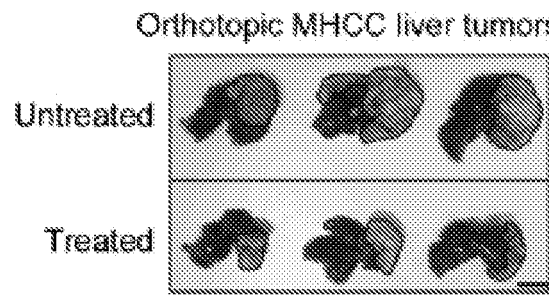


Figure 21C

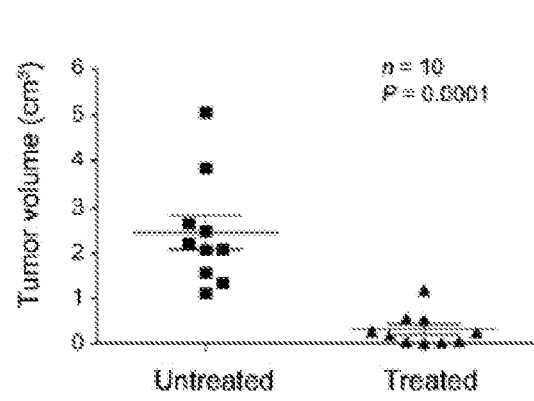


Figure 21D

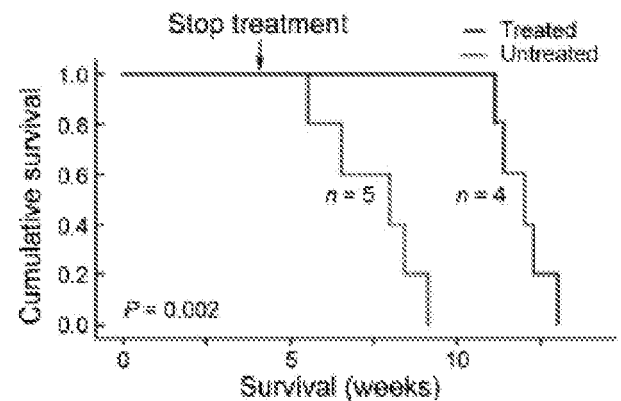


Figure 21E

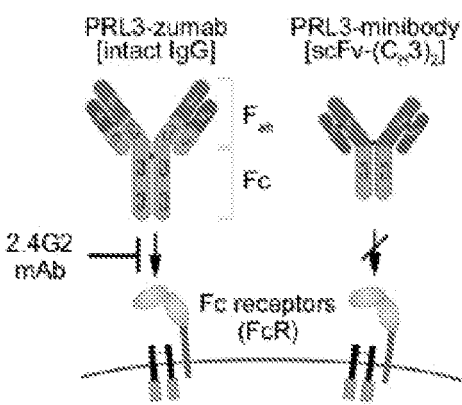


Figure 21F

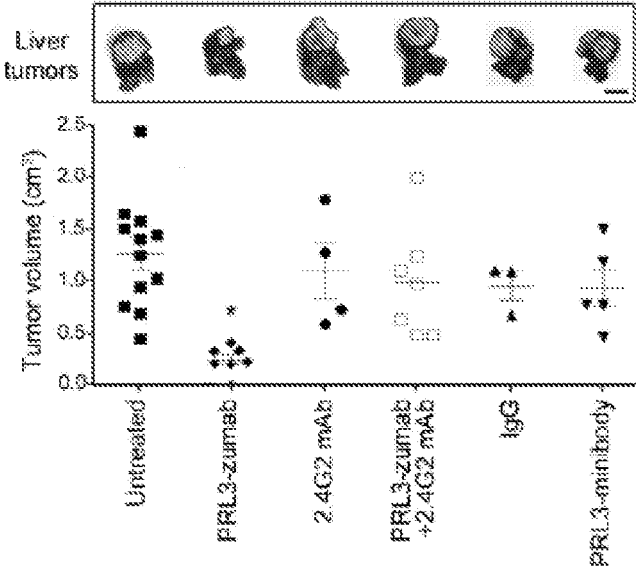


Figure 21G

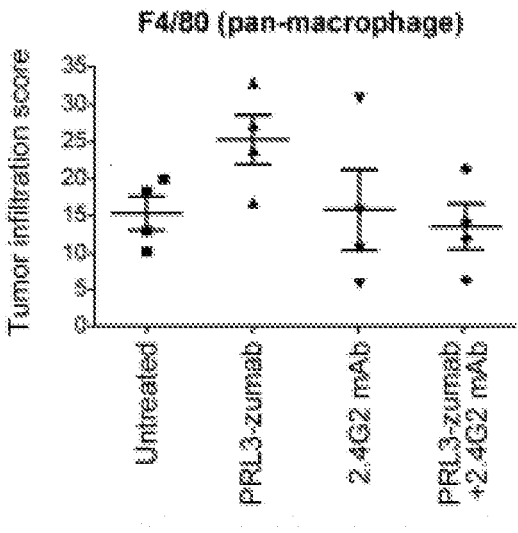


Figure 22A

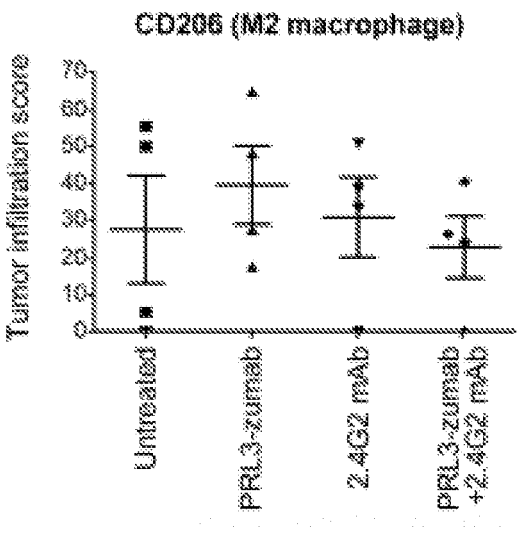


Figure 22B

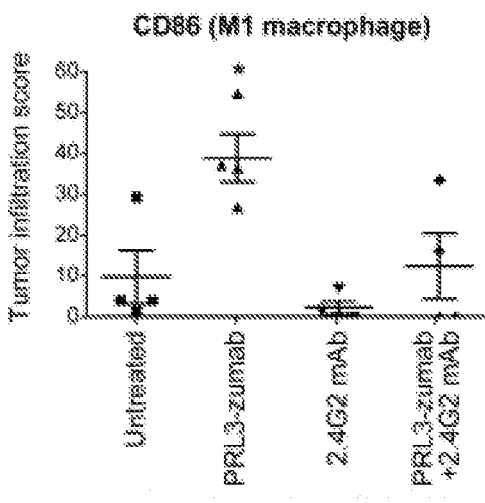


Figure 22C

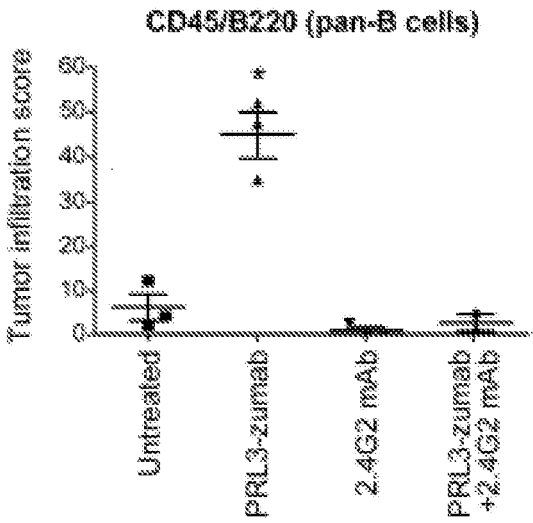


Figure 22D

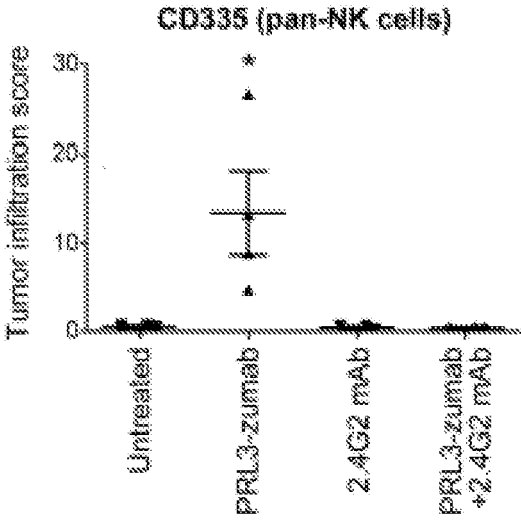


Figure 22E

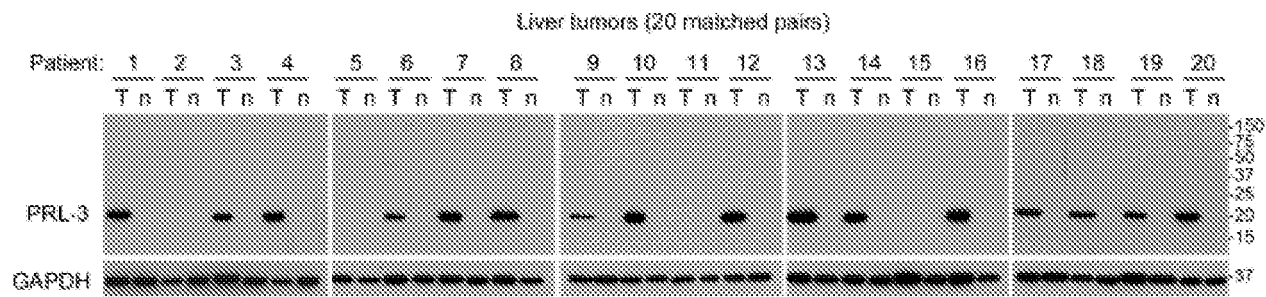


Figure 23A

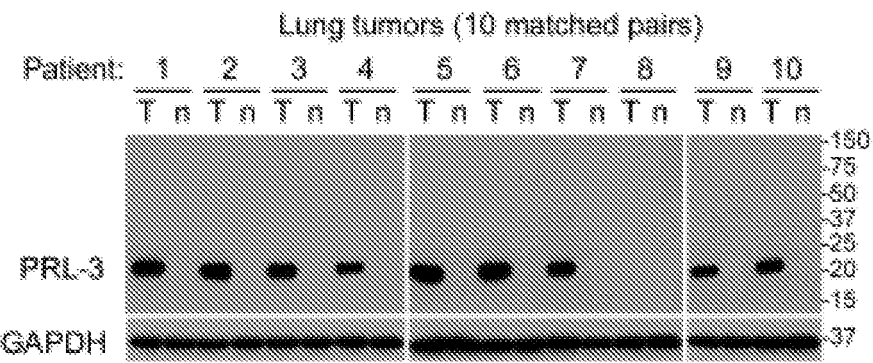


Figure 23B

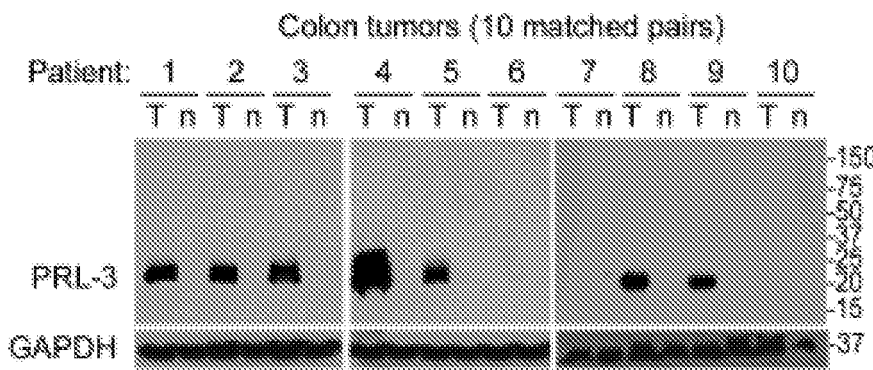


Figure 23C

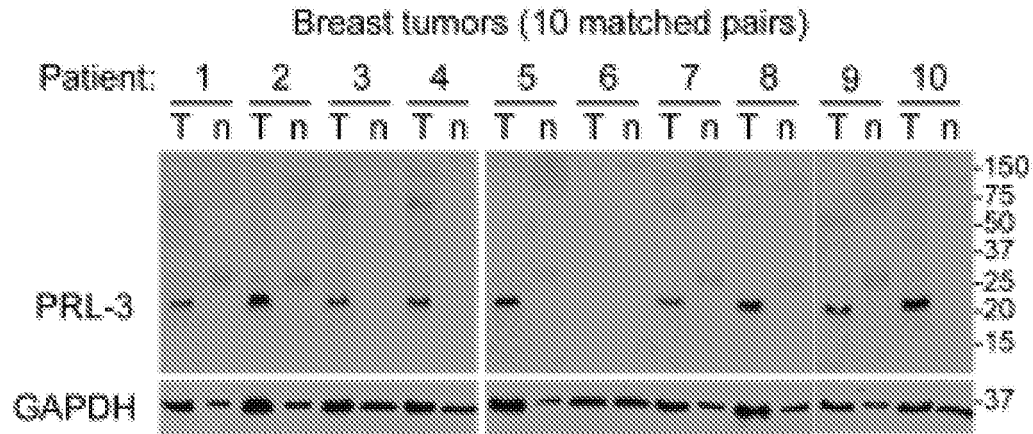


Figure 23D

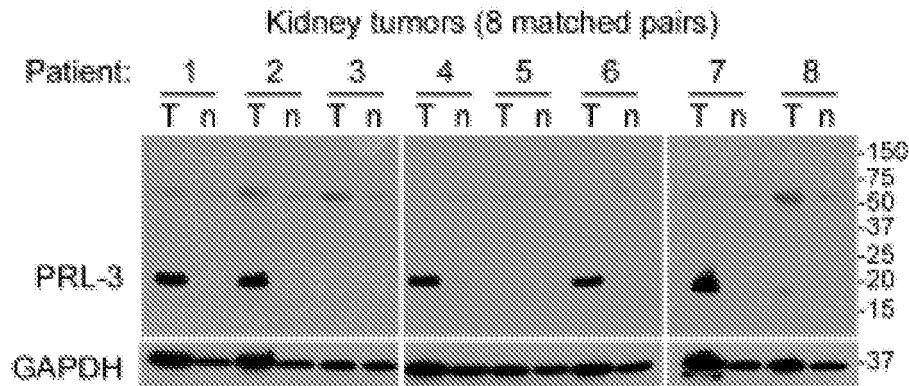


Figure 23E

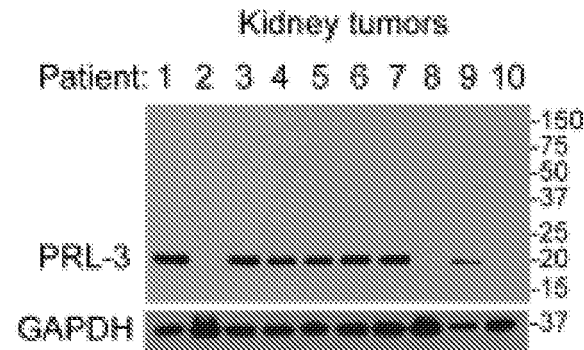


Figure 23F

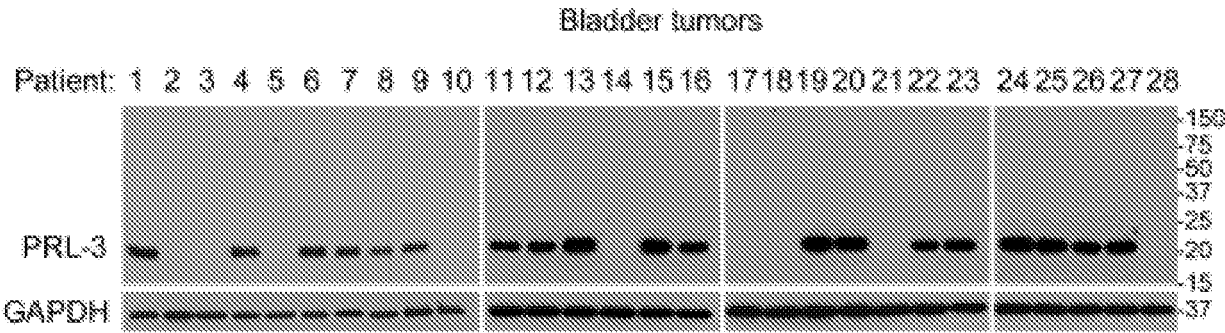


Figure 23G

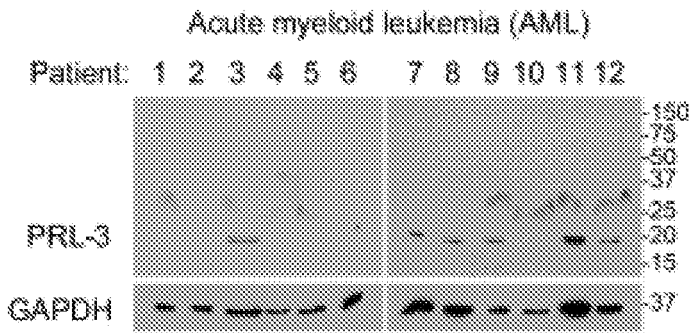


Figure 23H

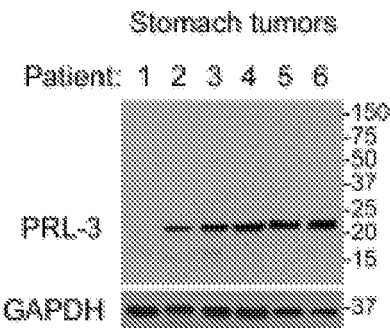


Figure 23I

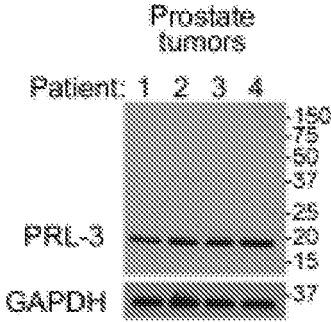


Figure 23J

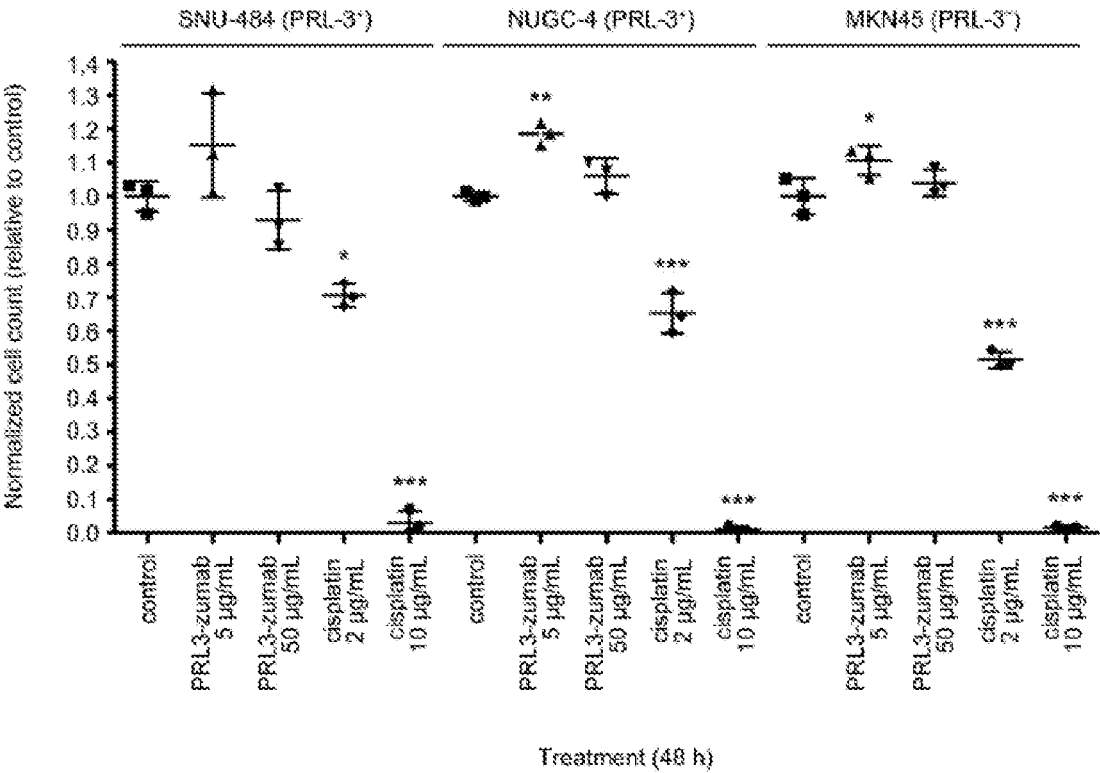
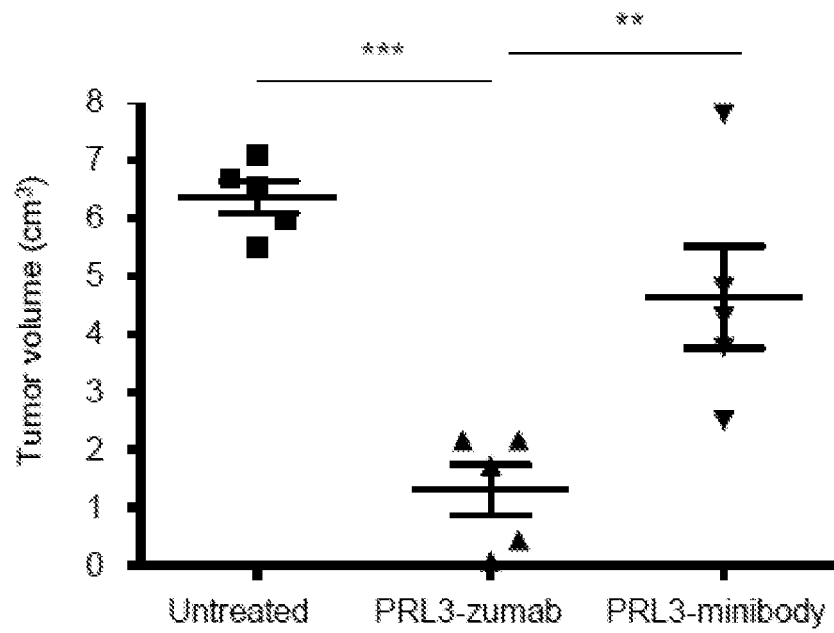


Figure 24

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$P = 0.0002$ (one-way ANOVA)
** $P < 0.01$ (Tukey's post-hoc test)
*** $P < 0.001$ (Tukey's post-hoc test)

Figure 25