Figure 1

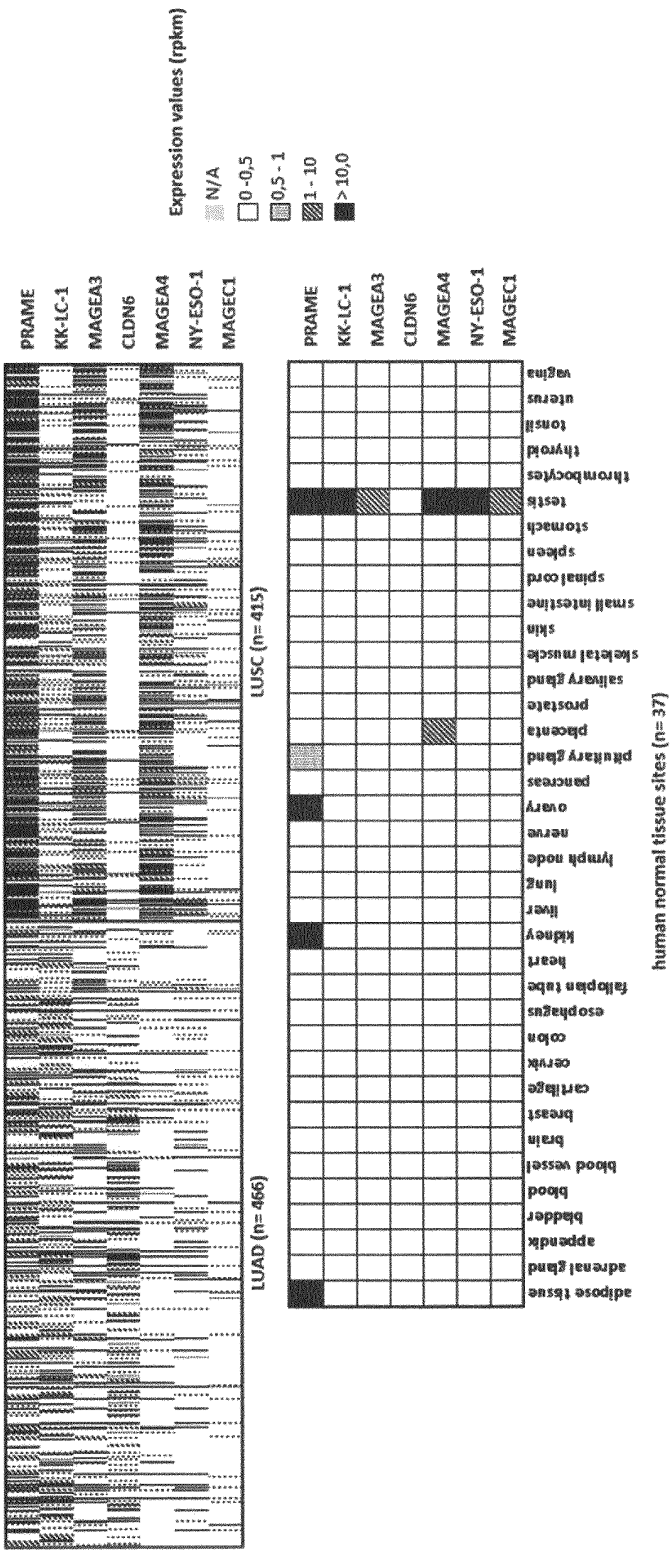

Expression values (rpkm)
N/A
0 -0,5
0,5 - 1
1 - 10
> 10,0
PRAME
KK-LC-1
MAGEA3
CLDN6
MAGEA4
NY-ESO-1
MAGEC1
LUAD (n= 466)
LUSC (n= 415)
adipose tissue
adrenal gland
appendix
bladder
blood
blood vessel
brain
breast
cartilage
cervix
colon
esophagus
fallopian tube
heart
kidney
liver
lung
lymph node
nerve
ovary
pancreas
pituitary gland
placenta
prostate
salivary gland
skeletal muscle
skin
small intestine
spinal cord
spleen
stomach
testis
thrombocytes
thyroid
tonsil
uterus
vagina
human normal tissue sites (n= 37)

Figure 2

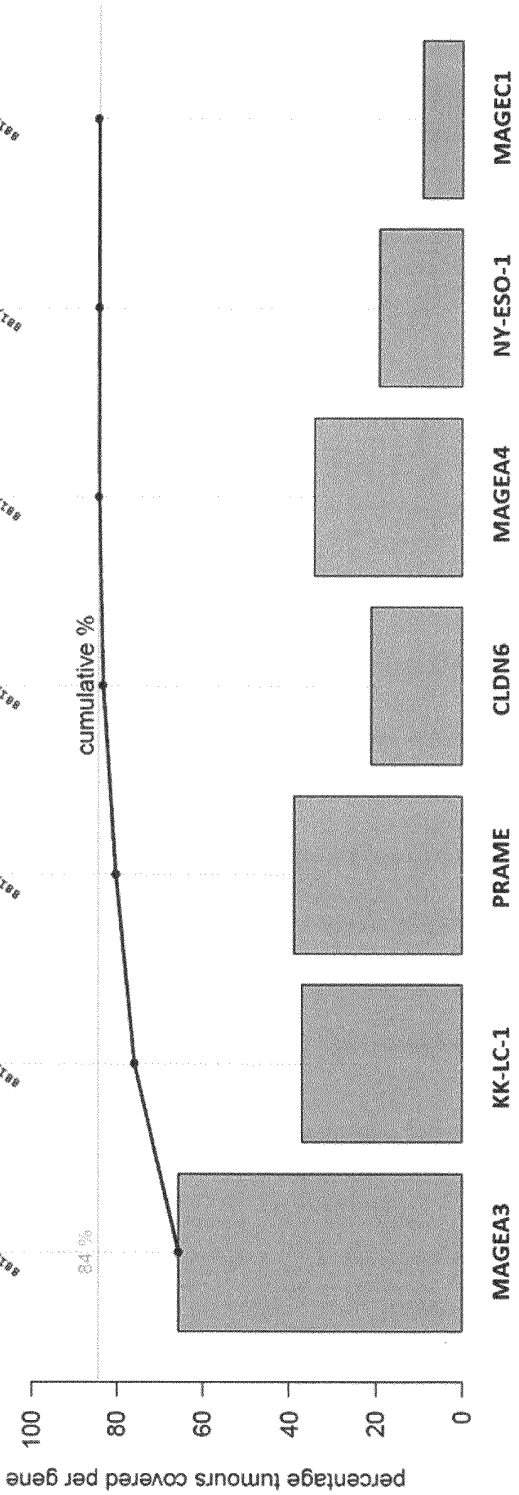

percentage tumours covered per gene
100
80
60
40
20
0
cumulative %
84 %
881/0/578
881/0/327
881/0/343
881/0/185
881/0/301
881/0/169
881/0/81
MAGEA3
KK-LC-1
PRAME
CLDN6
MAGEA4
NY-ESO-1
MAGEC1

Figure 3

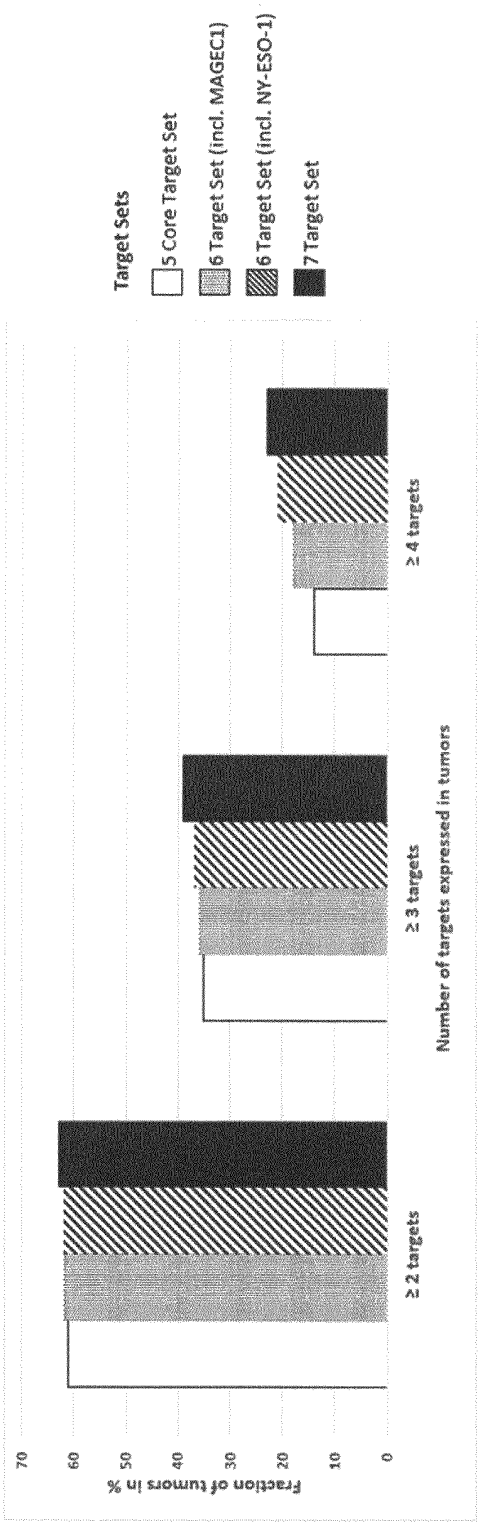

Target Sets
5 Core Target Set
6 Target Set (incl. MAGEC1)
6 Target Set (incl. NY-ESO-1)
7 Target Set
Fraction of tumors in %
0
10
20
30
40
50
60
70
≥ 2 targets
≥ 3 targets
≥ 4 targets
Number of targets expressed in tumors

Figure 4

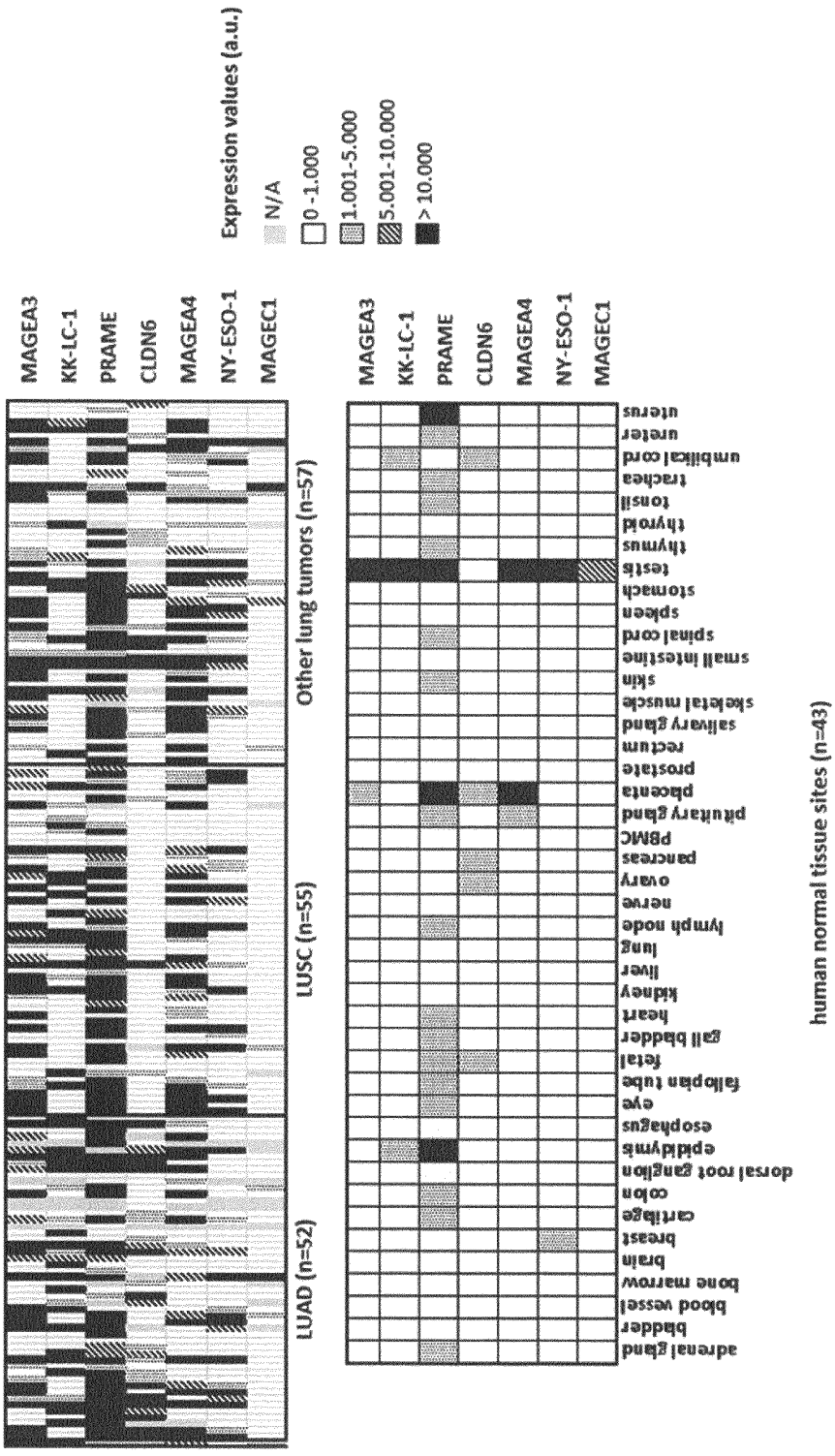

Expression values (a.u.)
N/A
0 -1.000
1.001-5.000
5.001-10.000
> 10.000
MAGEA3
KK-LC-1
PRAME
CLDN6
MAGEA4
NY-ESO-1
MAGEC1
LUAD (n=52)
LUSC (n=55)
Other lung tumors (n=57)
adrenal gland
bladder
blood vessel
bone marrow
brain
breast
cartilage
colon
dorsal root ganglion
epididymis
esophagus
eye
fallopian tube
fetal
gall bladder
heart
kidney
liver
lung
lymph node
nerve
ovary
pancreas
PBMC
pituitary gland
placenta
prostate
rectum
salivary gland
skeletal muscle
skin
small intestine
spinal cord
spleen
stomach
testis
thymus
thyroid
tonsil
trachea
umbilical cord
ureter
uterus
human normal tissue sites (n=43)

Figure 5

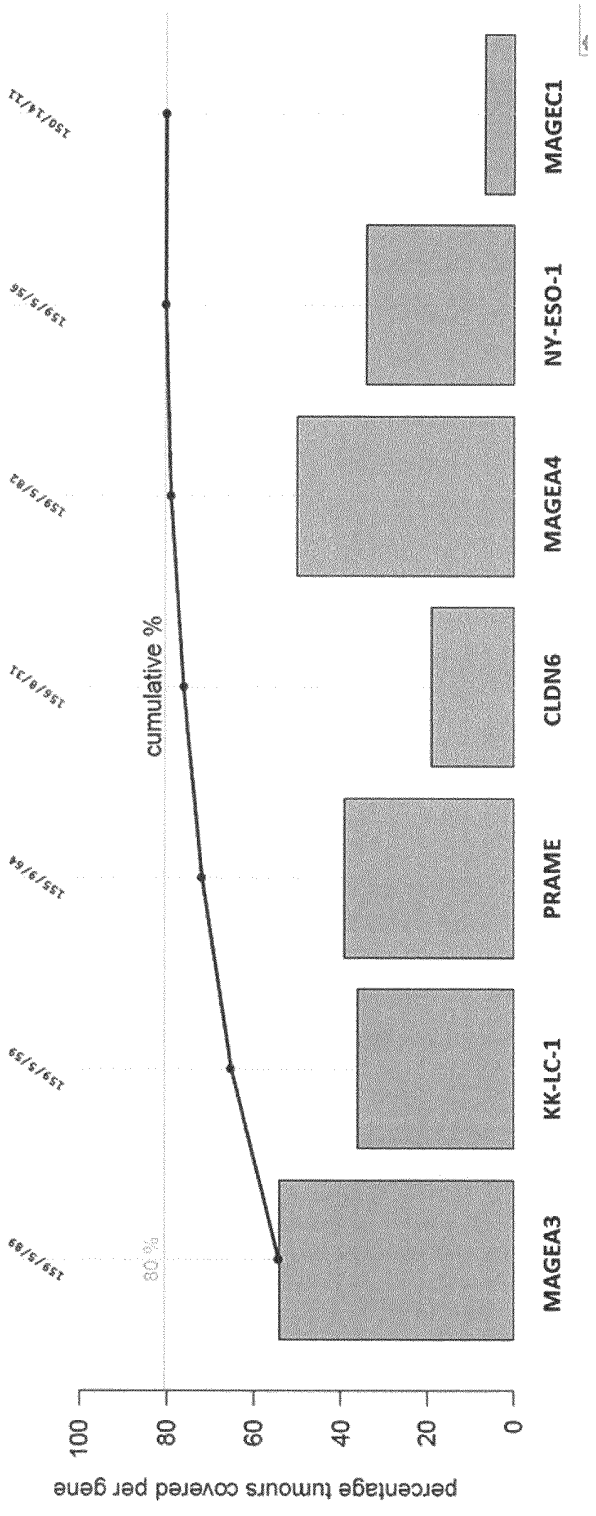

percentage tumours covered per gene
0
20
40
60
80
100
cumulative %
80 %
MAGEA3
KK-LC-1
PRAME
CLDN6
MAGEA4
NY-ESO-1
MAGEC1
159/5/89
159/5/59
155/9/64
156/8/31
159/5/82
159/5/56
150/14/11

Figure 6

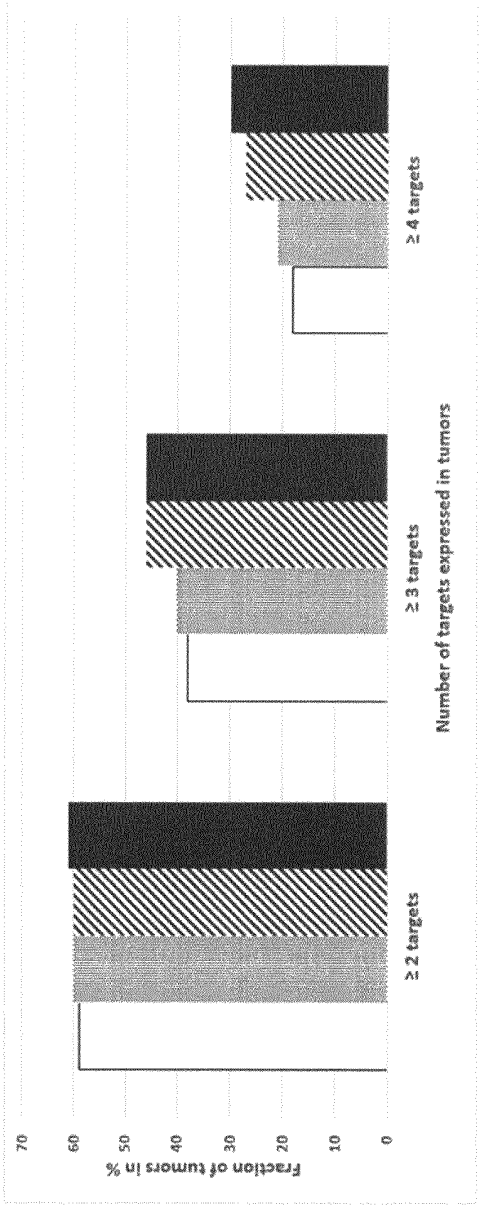

Target Sets
5 Core Target Set
6 Target Set (incl. MAGEC1)
6 Target Set (incl. NY-ESO-1)
7 Target Set
Fraction of tumors in %
0
10
20
30
40
50
60
70
≥ 2 targets
≥ 3 targets
≥ 4 targets
Number of targets expressed in tumors

Figure 7

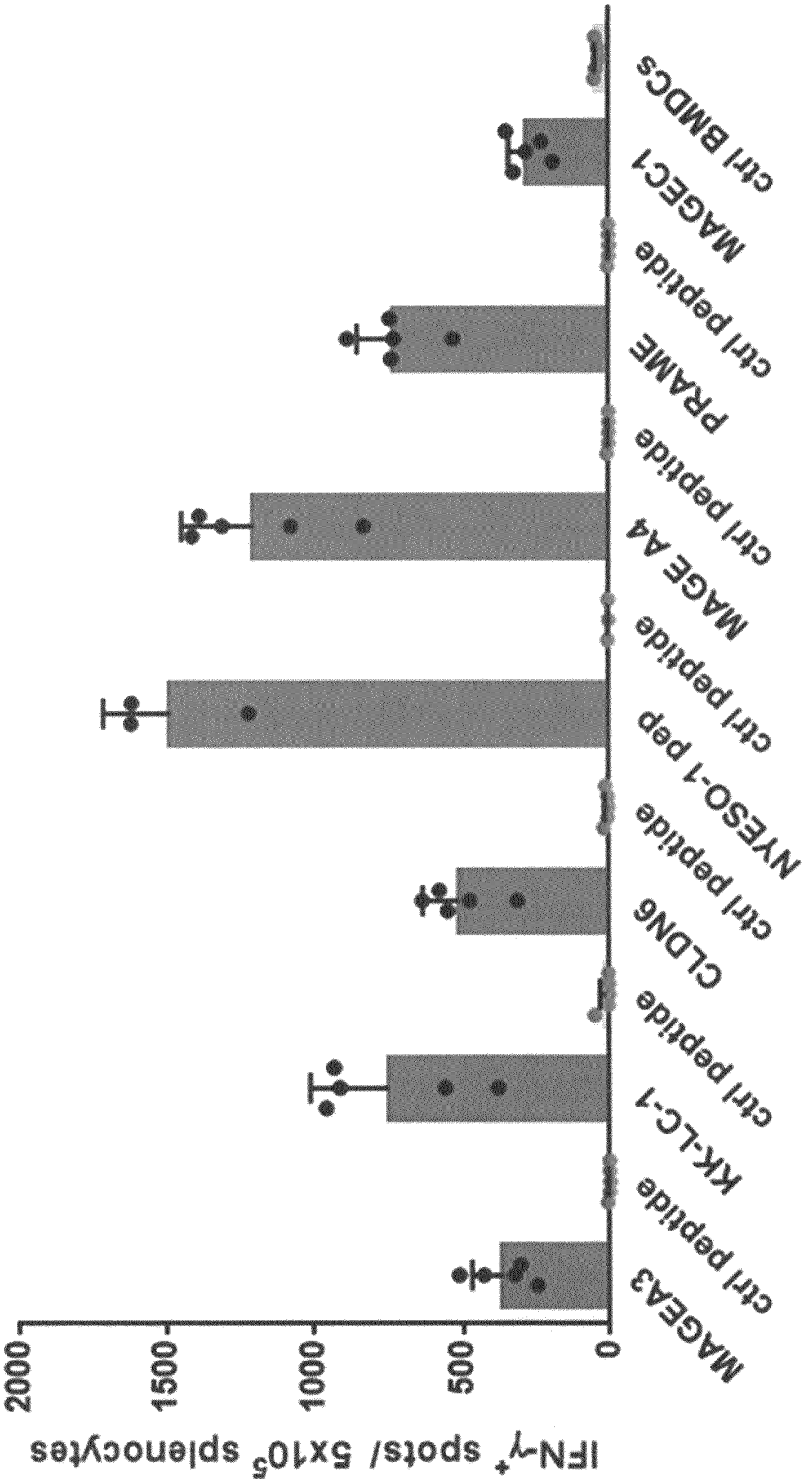

IFN-γ+ spots/ 5x10^5 splenocytes
2000
1500
1000
500
0
MAGEA3
ctrl peptide
KK-LC-1
ctrl peptide
CLDN6
ctrl peptide
NYESO-1 pep
ctrl peptide
MAGE A4
ctrl peptide
PRAME
ctrl peptide
MAGEC1
ctrl BMDCs

Figure 8

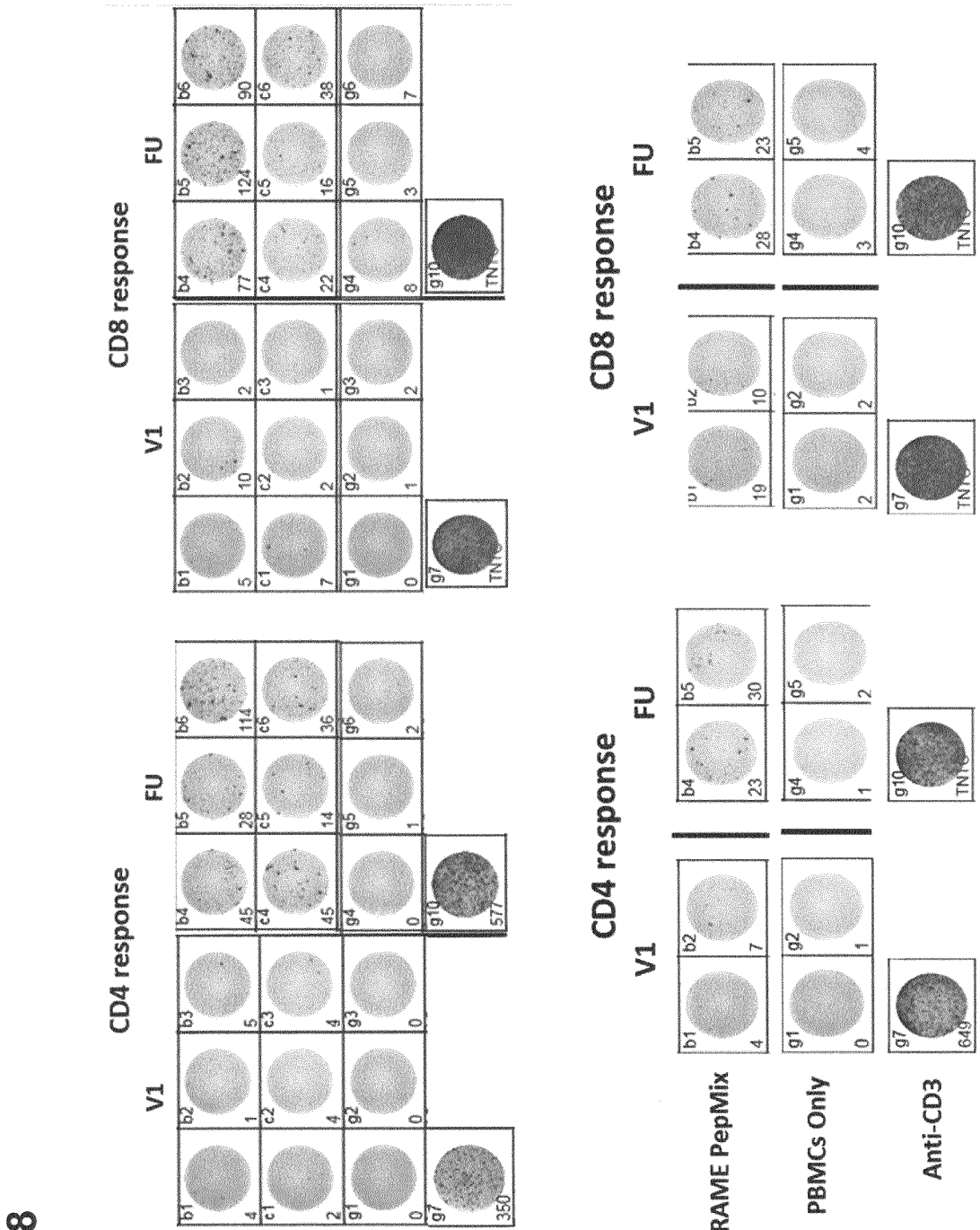

A
CD4 response
CD8 response
V1
FU
CLDN6 PepMix
KK-LC-1 PepMix
Cells only
Anti-CD3
PRAME PepMix
PBMCs Only
Anti-CD3

Figure 9

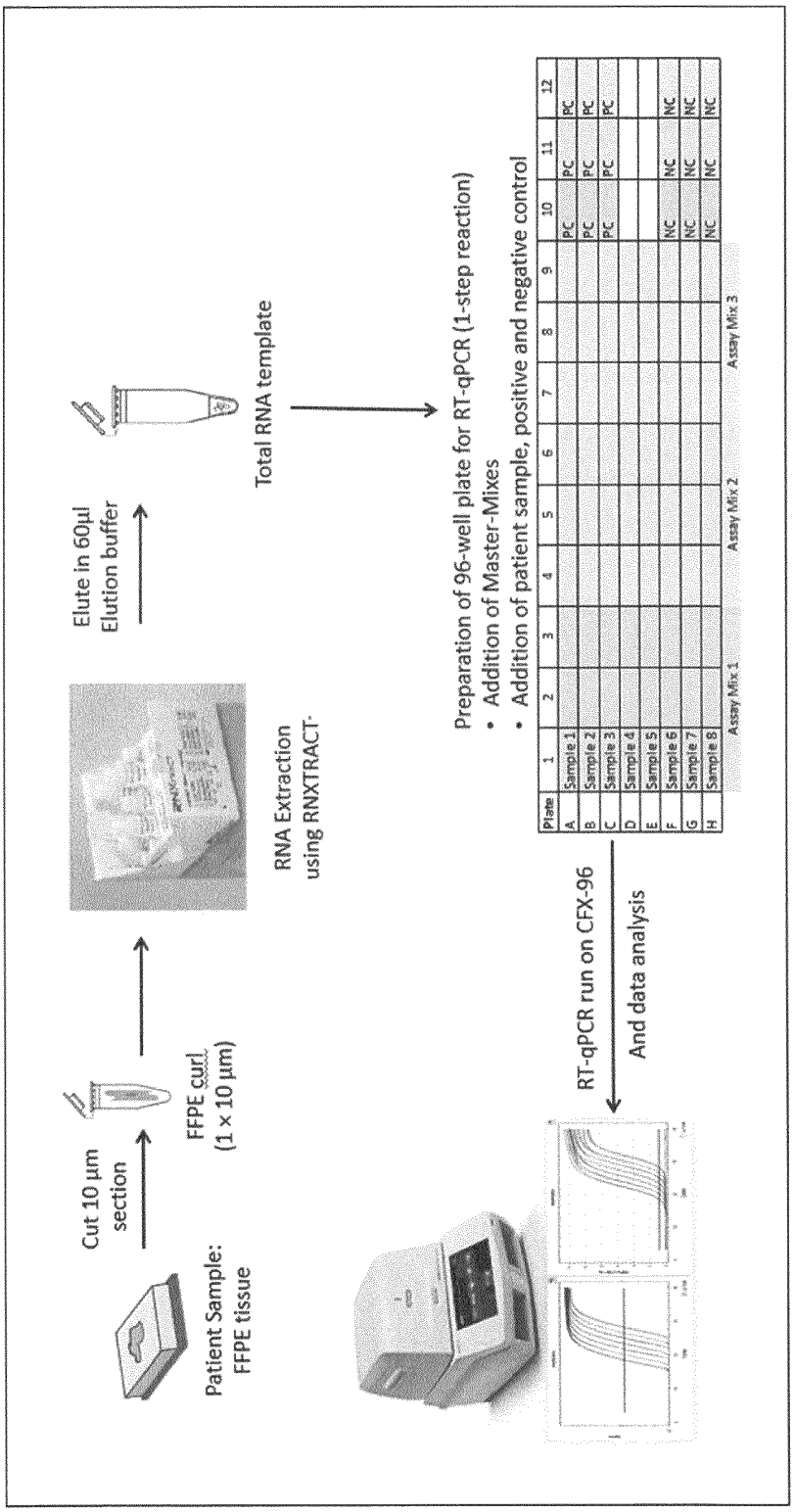

Patient Sample: FFPE tissue
Cut 10 µm section
FFPE curl (1 × 10 µm)
RNA Extraction using RNXTRACT-
Elute in 60µl Elution buffer
Total RNA template
Preparation of 96-well plate for RT-qPCR (1-step reaction)
• Addition of Master-Mixes
• Addition of patient sample, positive and negative control
RT-qPCR run on CFX-96
And data analysis
Assay Mix 1
Assay Mix 2
Assay Mix 3

Figure 10

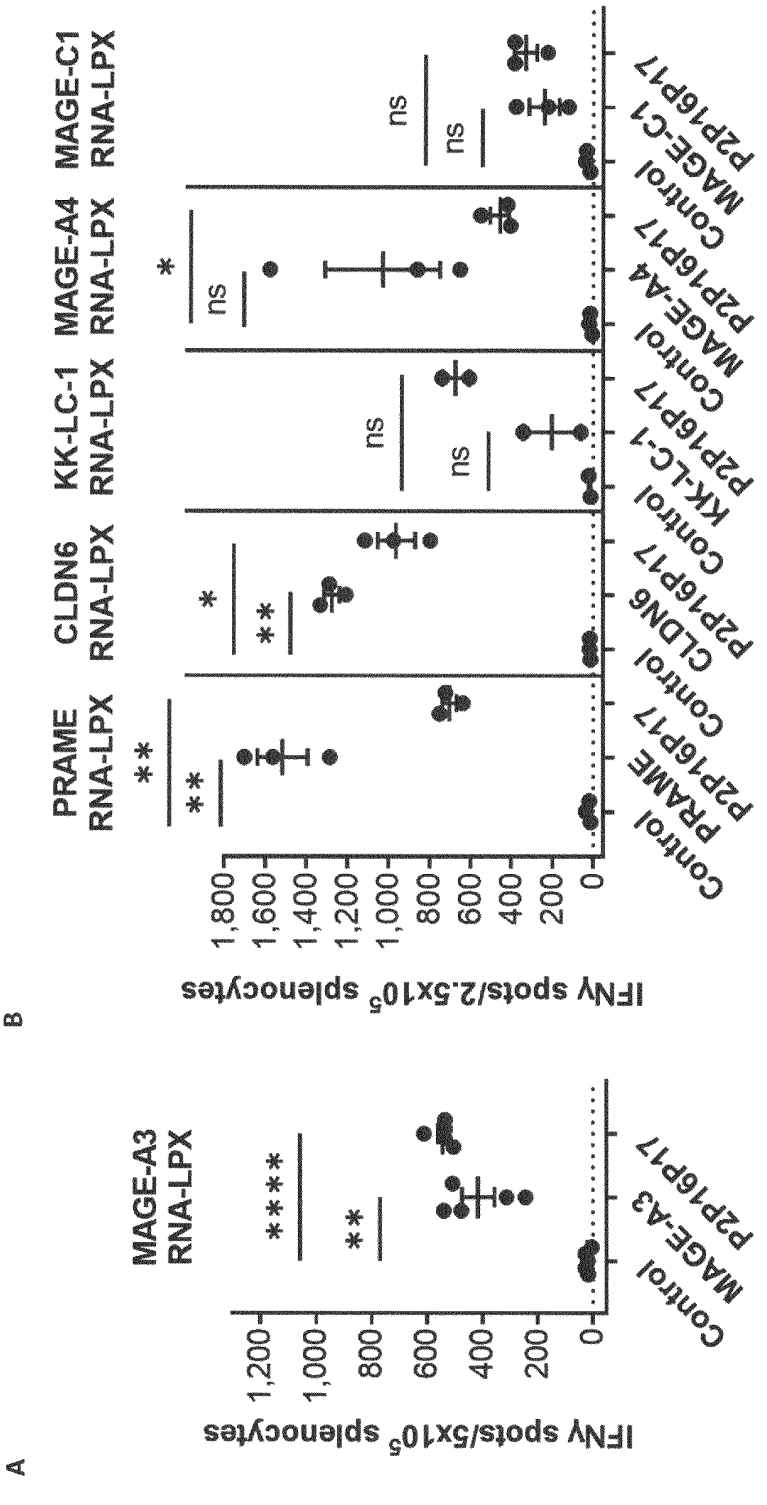
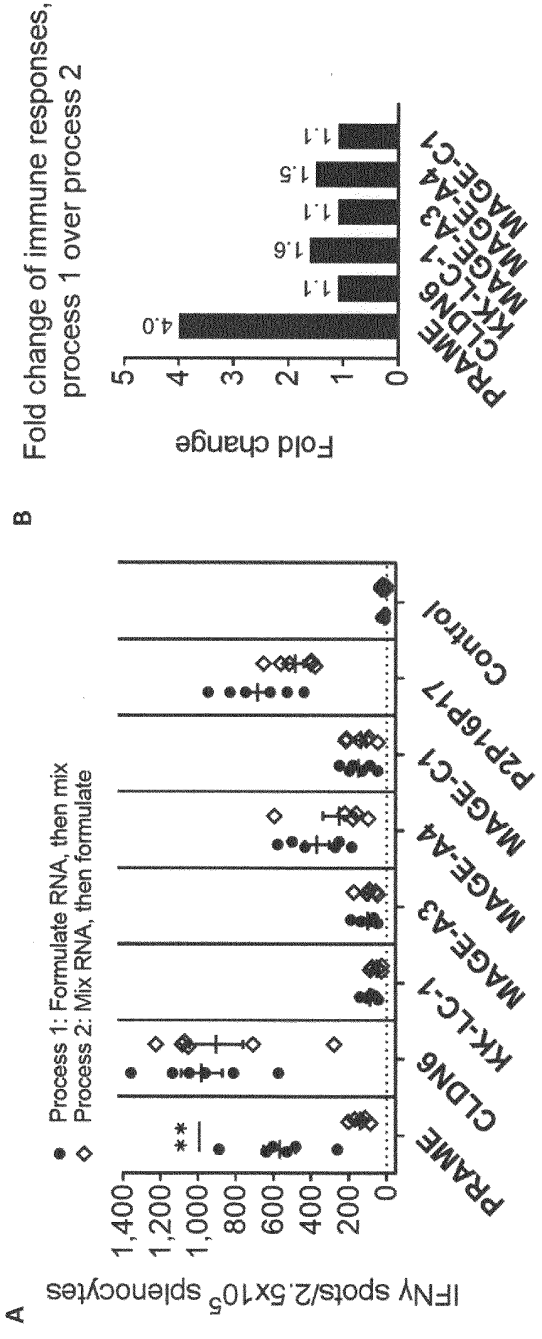

A
IFNγ spots/5x10^5 splenocytes
1,200
1,000
800
600
400
200
0
MAGE-A3 RNA-LPX
****
**
Control
MAGE-A3
P2P16P17
B
IFNγ spots/2.5x10^5 splenocytes
1,800
1,600
1,400
1,200
1,000
800
600
400
200
0
PRAME RNA-LPX
CLDN6 RNA-LPX
KK-LC-1 RNA-LPX
MAGE-A4 RNA-LPX
MAGE-C1 RNA-LPX
**
**
*
**
ns
ns
*
ns
ns
Control
PRAME
P2P16P17
Control
CLDN6
P2P16P17
Control
KK-LC-1
P2P16P17
Control
MAGE-A4
P2P16P17
Control
MAGE-C1
P2P16P17

Figure 11


A
IFNγ spots/2.5x10^5 splenocytes
1,400
1,200
1,000
800
600
400
200
0
**
Process 1: Formulate RNA, then mix
Process 2: Mix RNA, then formulate
PRAME
CLDN6
KK-LC-1
MAGE-A3
MAGE-A4
MAGE-C1
P2P16P17
Control
B
Fold change of immune responses, process 1 over process 2
Fold change
5
4
3
2
1
0
4.0
1.1
1.6
1.1
1.5
1.1
PRAME
CLDN6
KK-LC-1
MAGE-A3
MAGE-A4
MAGE-C1