Figure 1

Accession	Peptide count	Unique peptides	Confidence score	ratio 13F11/ Iso	Gene symbol	FAS12020X002__Iso_Ovcar_92-125700	FAS12020X009__13F11_Ovcar_92-125857	FAS12020X002__Iso_Ovcar_92-125700	FAS12020X009__13F11_Ovcar_92-125857
Q9UQ35	4	4	81	1824,2	SRRM2	589	1074721	0	4

Accession	Peptide count	Unique peptides	Confidence score	raw abundance ratio 23A7/ Flag	Gene symbol	FAS12003X013__1_FLAG3H3_Ovcar_92-104666	FAS12003X016__4_23A7_Ovcar_92-104669	FAS12003X013__1_FLAG3H3_Ovcar_92-104666	FAS12003X016__4_23A7_Ovcar_92-104669
Q9UQ35	6	5	137	182,6	SRRM2	126957	33142083	0	3

Accession	Peptide count	Unique peptides	Confidence score	Gene symbol	ratio 18A4/ iso2a	FAS13857X002__1_Iso2a_MBP7G4_UWB1_92-236943	FAS13857X008__7_18A4_UWB1_92-236949	FAS13857X002__1_Iso2a_MBP7G4_UWB1_92-236943	FAS13857X008__7_18A4_UWB1_92-236949
Q9UQ35	4	4	114	SRRM2	40,8	40994	1673452	0	4

Figure 2A

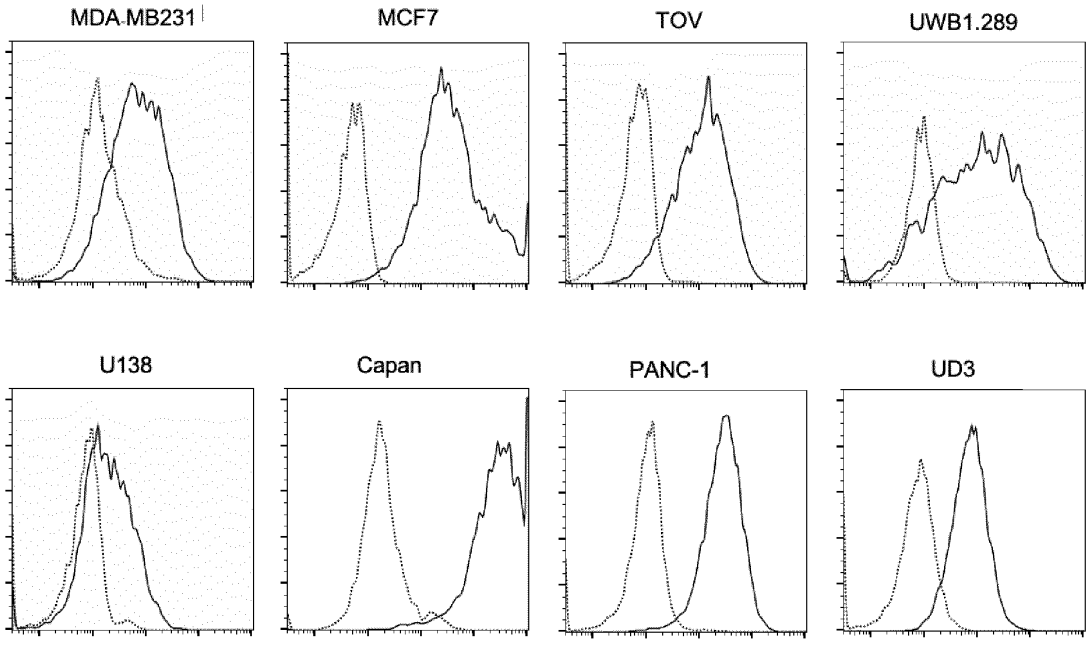


Figure 2B

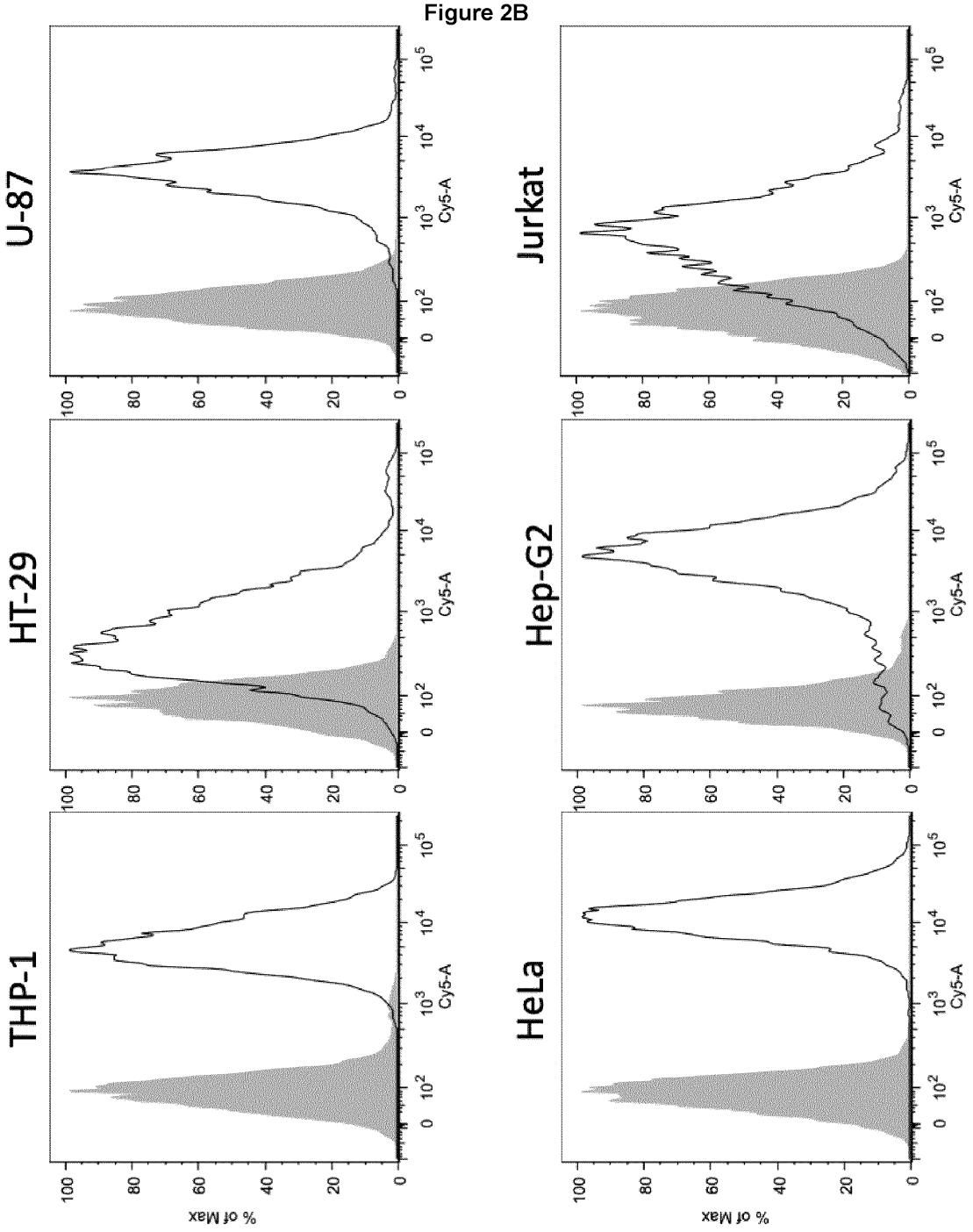

U-87
HT-29
THP-1
Jurkat
Hep-G2
HeLa
% of Max
Cy5-A
0
10^2
10^3
10^4
10^5
0
20
40
60
80
100

Figure 3

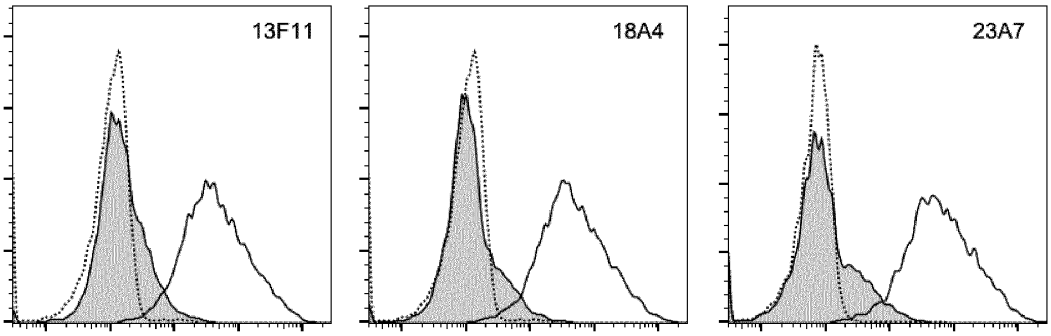


Figure 4

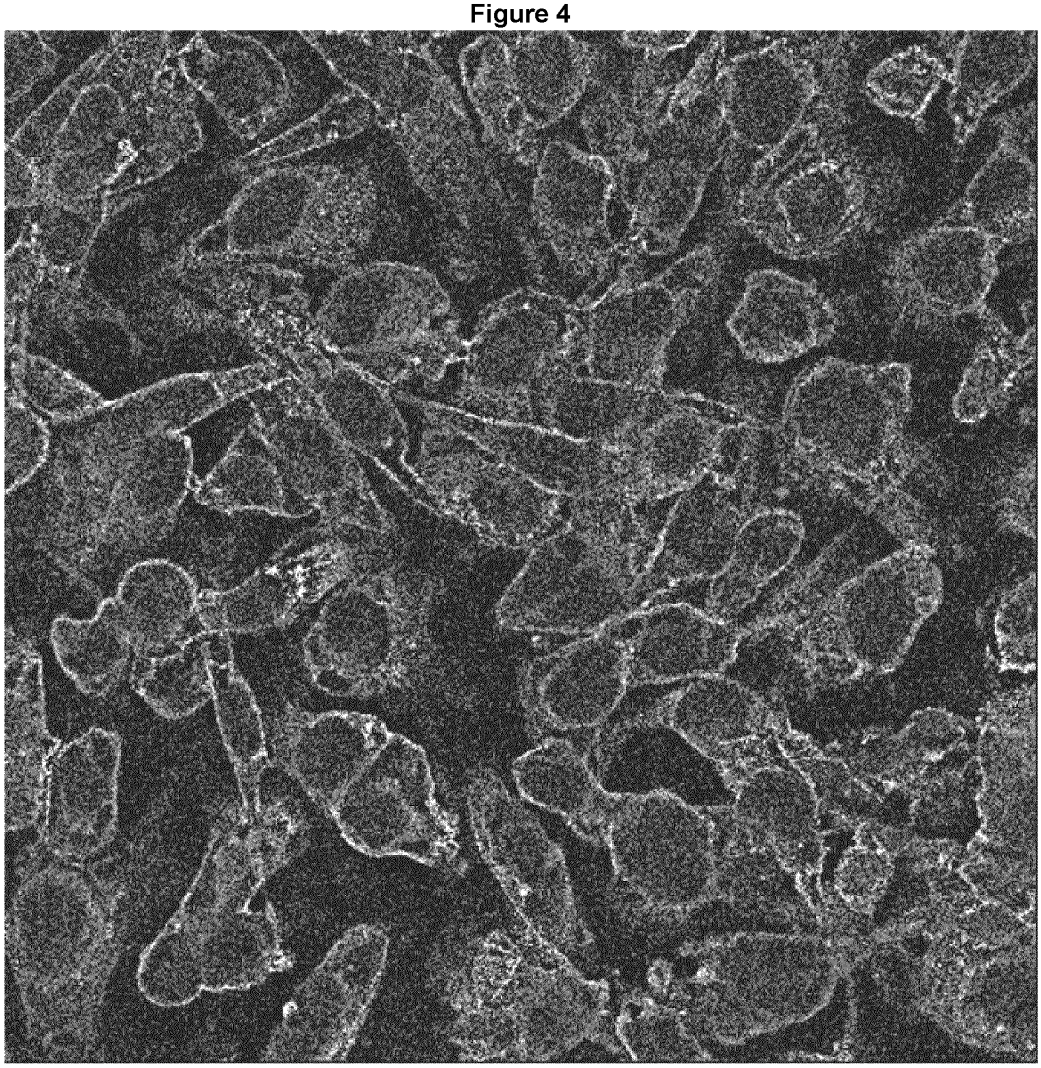


Figure 5

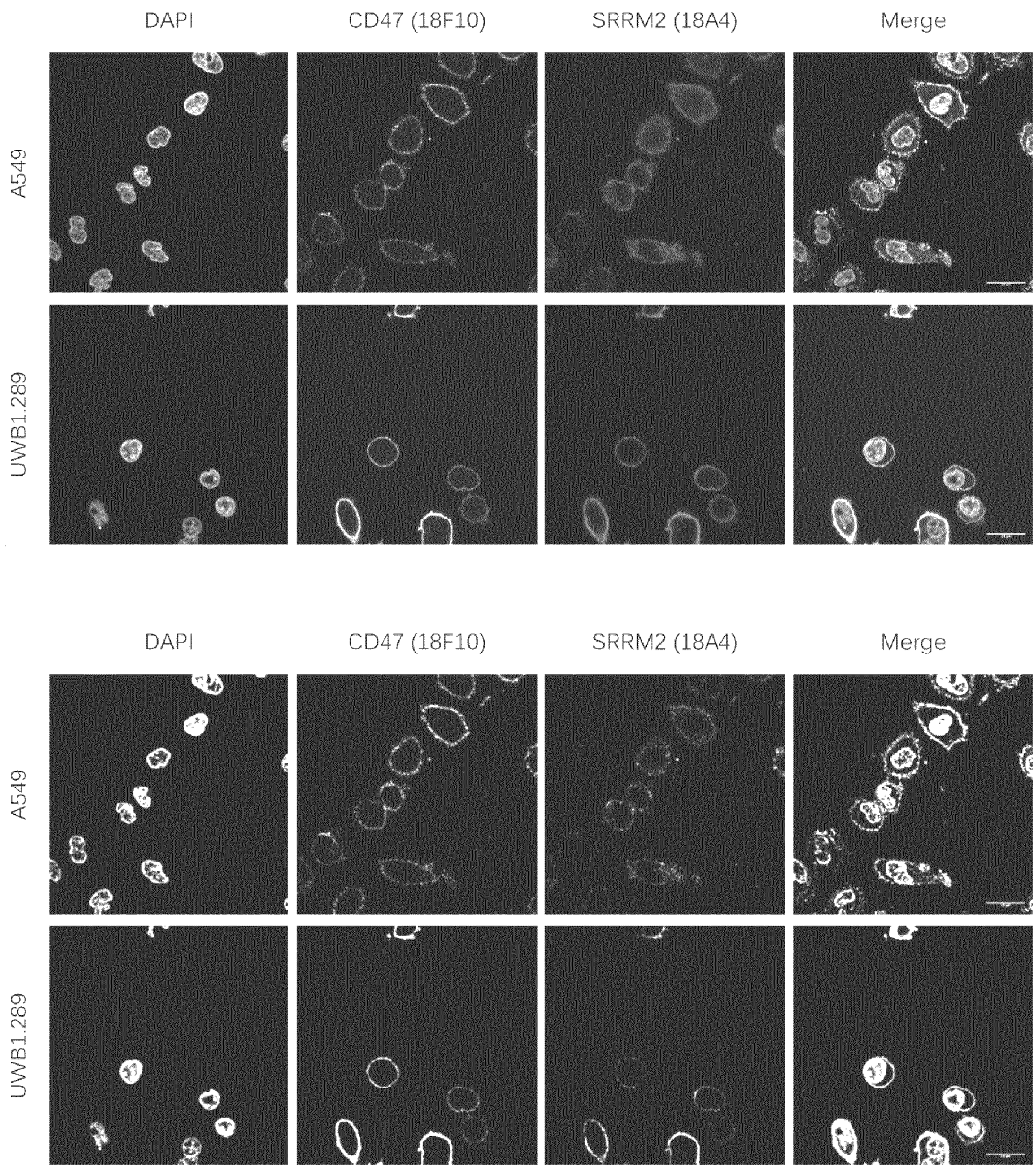

DAPI
CD47 (18F10)
SRRM2 (18A4)
Merge
A549
UWB1.289
DAPI
CD47 (18F10)
SRRM2 (18A4)
Merge
A549
UWB1.289

Figure 6

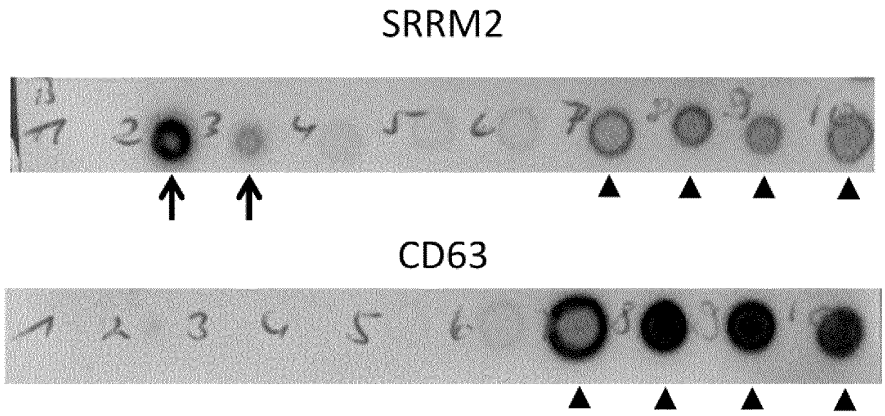


Figure 7

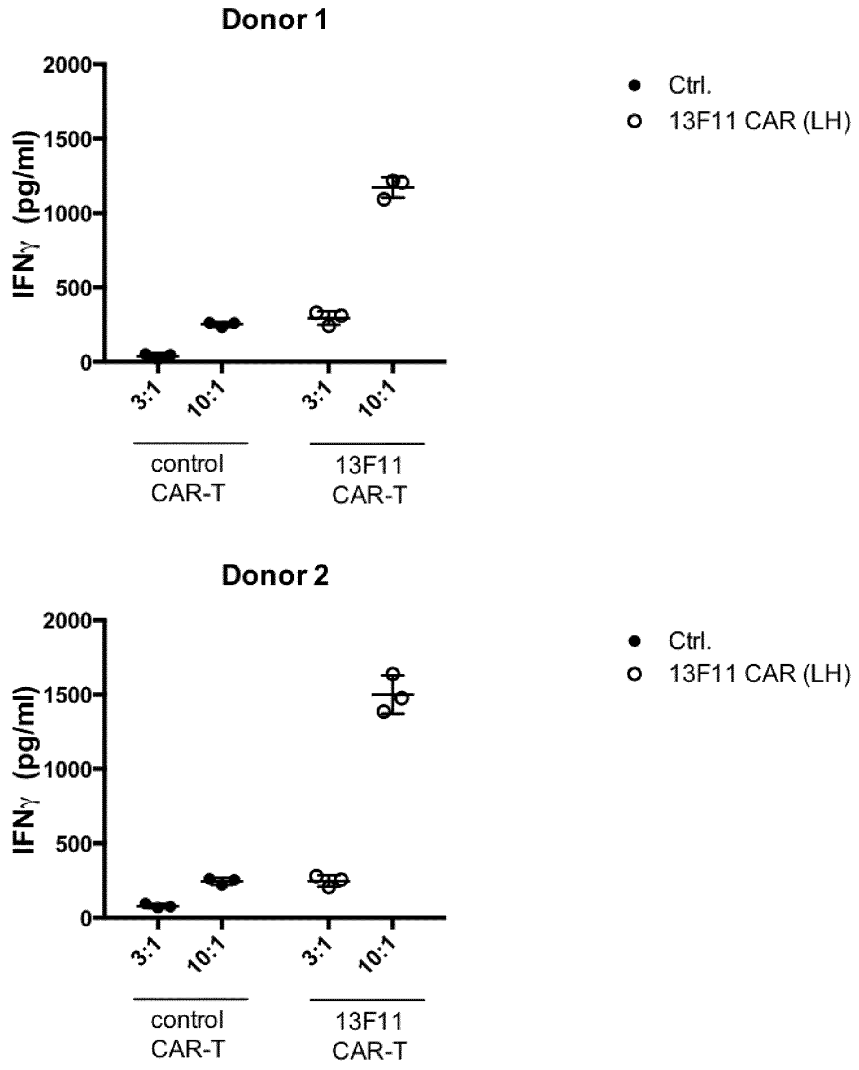


Figure 8

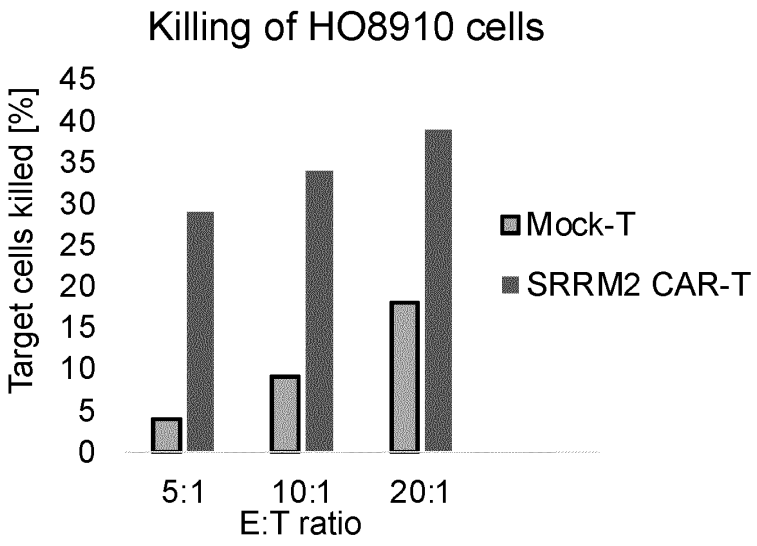


Figure 9

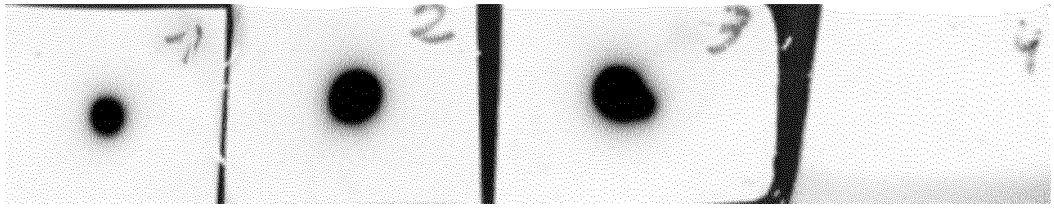


Figure 10

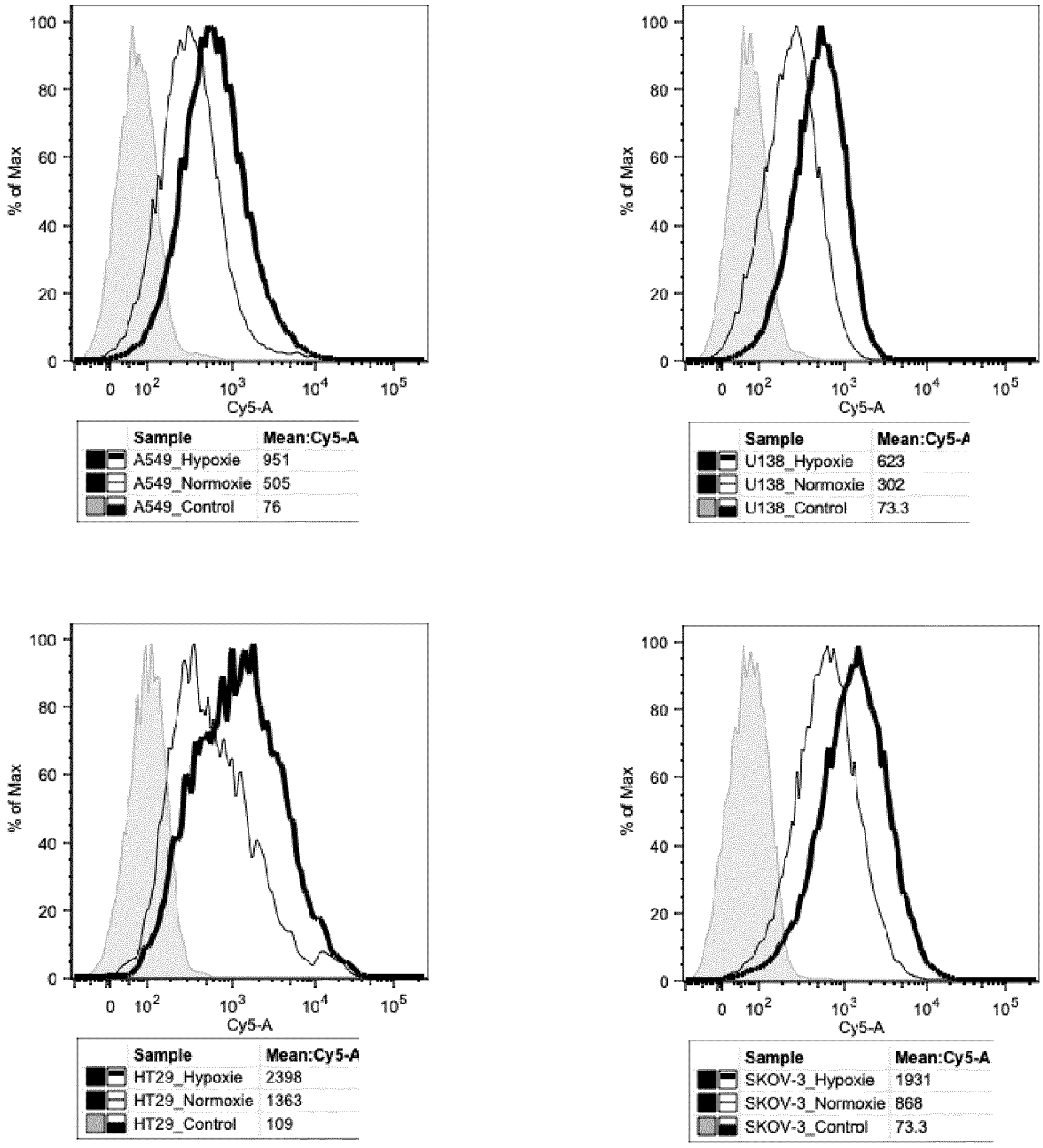

% of Max
Cy5-A
Sample | Mean:Cy5-A
A549_Hypoxie | 951
A549_Normoxie | 505
A549_Control | 76
U138_Hypoxie | 623
U138_Normoxie | 302
U138_Control | 73.3
HT29_Hypoxie | 2398
HT29_Normoxie | 1363
HT29_Control | 109
SKOV-3_Hypoxie | 1931
SKOV-3_Normoxie | 868
SKOV-3_Control | 73.3
Isotype control
Normoxia
Hypoxia

Figure 11

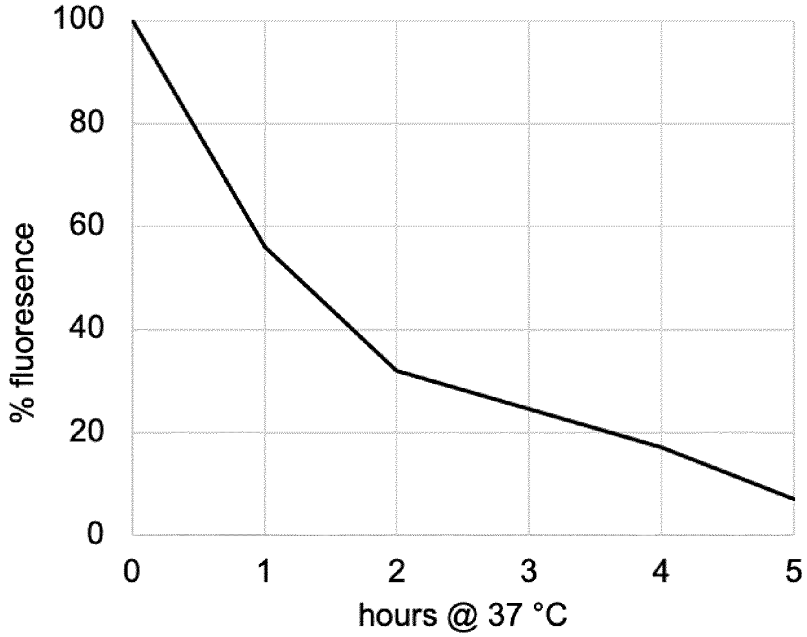
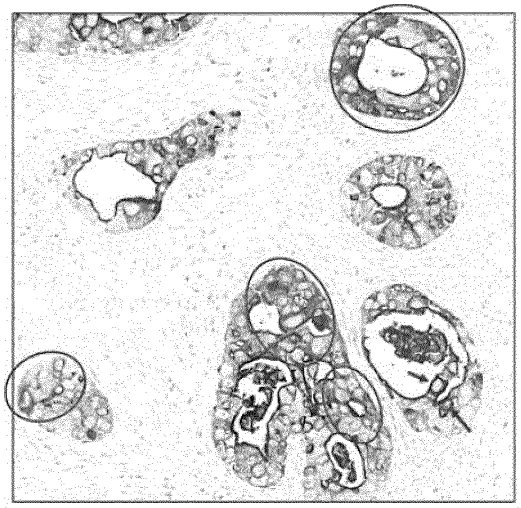


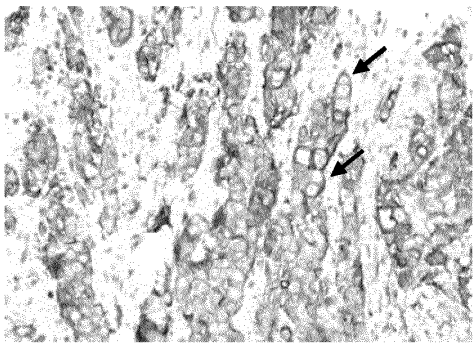
Figure 12

Pancreatic Cancer



Nests of cancer cells surrounded by normal tissue reveal strong membrane staining (arrows and circles)

Pancreatic Cancer



Normal Pancreas

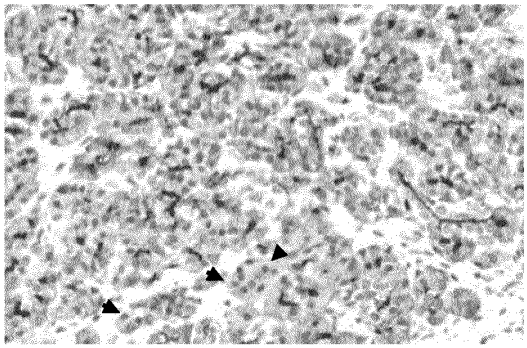
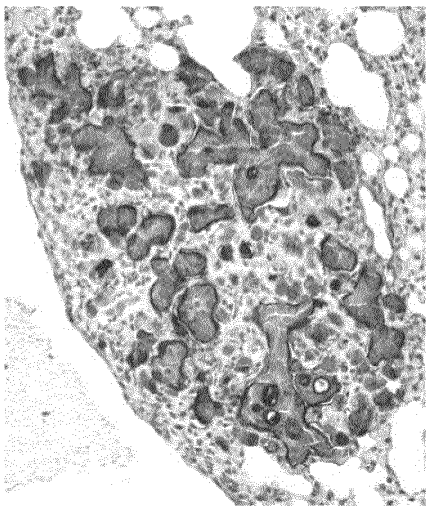
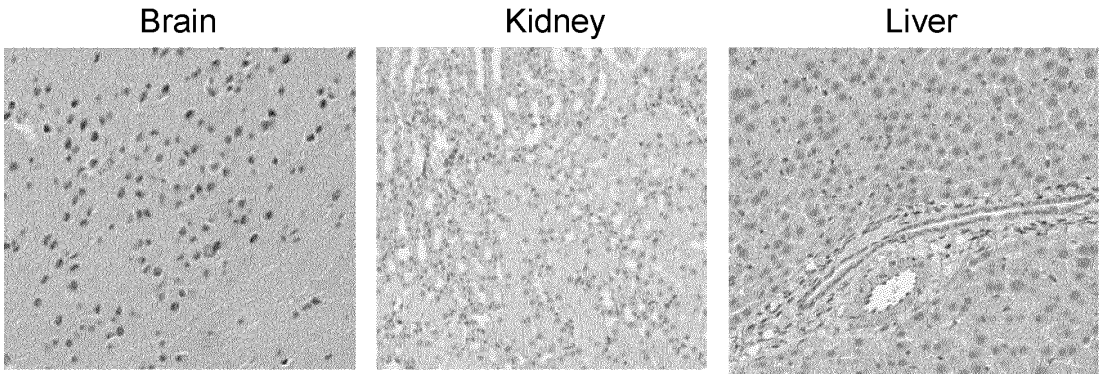


Figure 13



Lung metastases of xenografted human HUCCT-1 cholangiogenic cancer cells show strong membrane staining.



Nuclear SRRM2 staining of in normal mouse tissues.

Figure 14

```
13F11 HC    1 EVQLVESGGGLVQPGRSLKLSCAASRFTFSNYDMAWVRQAPTKGLEWVASISPSNVNTYY  60
23A7 HC     1 EVQLVESGGDLVQPGRSLKLSCAASGFTFSNYDMAWVRQAPTQGLEWVASISGSGGTTYY  60
18A4 HC     1 EVQLVESGGGLVQPGRSLKLSCAASGFTFSNYDMAWVRQAPTKGLEWVASISPSGGSIYY  60
              ********** ********************* ********** **********.****.***

13F11 HC   61 RDSVKGRFTVSRDNAKSSLYLQMDSLRSEDTATYYCARLVHSFWYFDFWGPGTMVTVSS 119 (SEQ ID NO: 1)
23A7 HC    61 RDSVKGRFTVSRDNAKSTLYLQMDGLRSEDTATYFCARHPPSFWYFDFWGPGSMVTVSS 119 (SEQ ID NO: 3)
18A4 HC    61 RDSVKGRFTVSRNNAKSSLYLQMDSLRSEDTATYYCARLTTYFWYFDFWGPGTMVTVSS 119 (SEQ ID NO: 5)
              ********** *****.****** **********.**********.******

13F11 LC    1 DIVMTQTPSSQAVSAGEKVTMRCKSSQSLLYSKNKKNYLAWYQQKPGQSPKLLIYWASTR  60
23A7 LC     1 DIVMTQTPSSQAVSAGEKVTMSCKSGQSLLFNKNKKDYLAWYQRKPGQSPKLLIYWASTR  60
18A4 LC     1 DIQMTQSPSFLSASVGDRVTINCKASQNSNKYLNWYQQKLGEAPKLLIYNTNNLQTGIPS  60

13F11 LC   61 ESGVPDRFLGSGSGTDFTLTISSVQAEDLAVYYCQQYYKFPPTFGGGTKLELKRA 115 (SEQ ID NO: 2)
23A7 LC    61 ESGVPDRFIGGGSGTDFTLTISSVQAEDLAVYYCQQYYRFPPTFGHGTKLELKRA 115 (SEQ ID NO: 4)
18A4 LC    61 RFSGSGSGTDYTLTISSLQPEDVATYFCLQHSSRMDTFGAGTKLELKRA 109 (SEQ ID NO: 6)
```

Figure 15

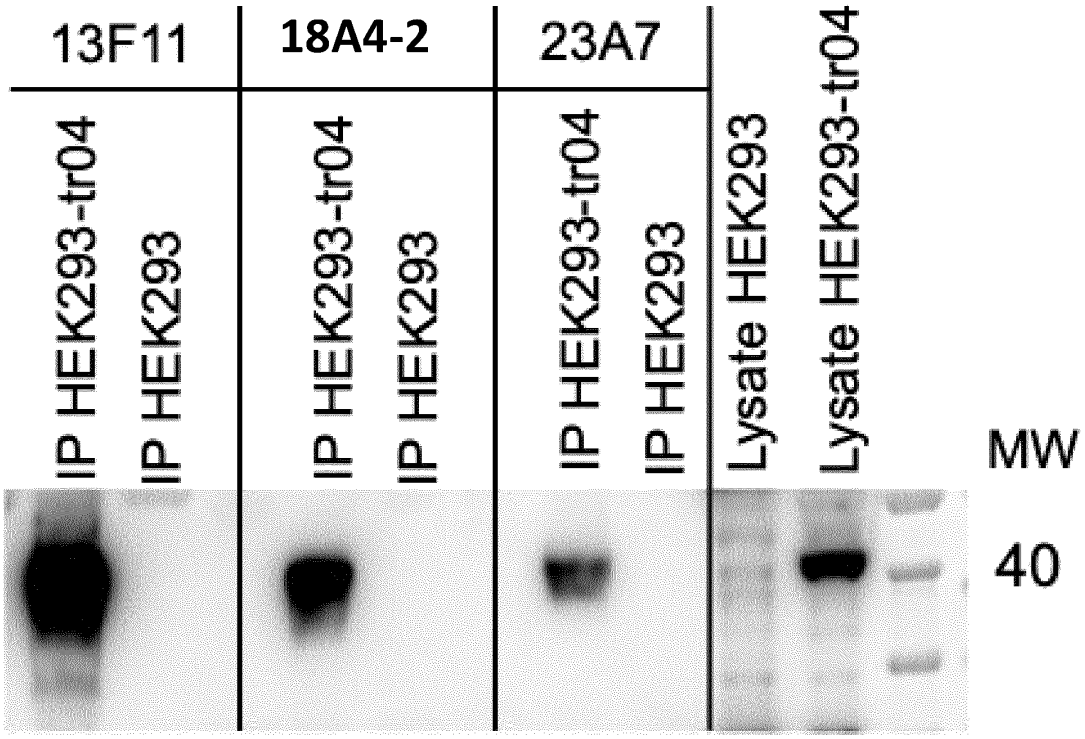
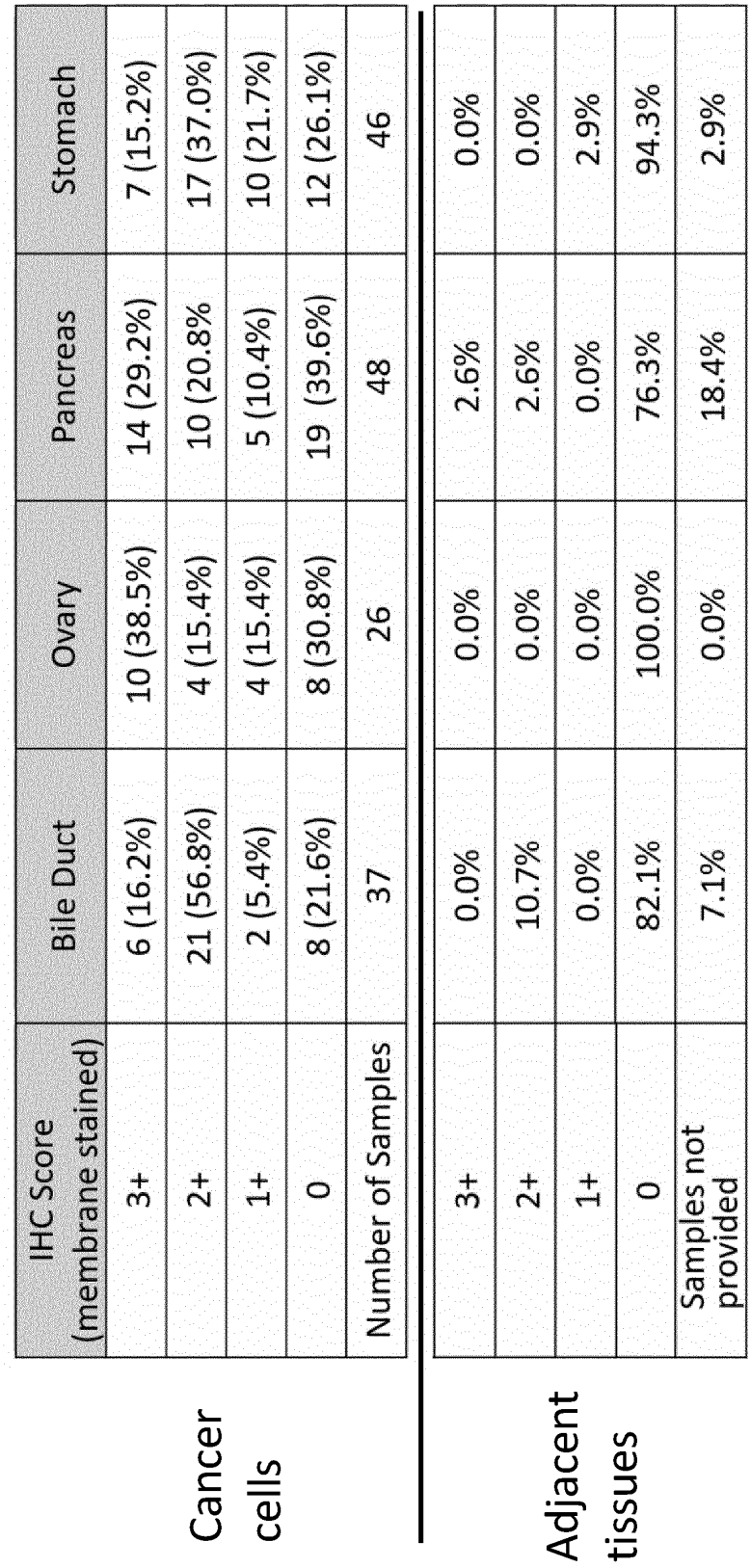

13F11
18A4-2
23A7
IP HEK293-tr04
IP HEK293
IP HEK293-tr04
IP HEK293
IP HEK293-tr04
IP HEK293
Lysate HEK293
Lysate HEK293-tr04
MW
40

Figure 16

	Cyno 1 (male)		
	Mem	**Cyto**	**Nucl**
Muscle	–	–	–
Pancreas	–	–	+
Stomach	–	–	++
Kidney	–	–	–
Colon	–	–	++
Spleen	–	–	–
Lung	–	–	+
Liver	–	–	–
Esophagus	–	+	–
Brain	–	–	+
Parotid gland	–	–	++
Bronchi	–	+	–
Lymph nodes	–	–	–
Spinal cord	–	–	–
Epididymis	–	–	+
Testis	–	–	–
Small intestine	–	–	–
Adrenal gland	–	–	–

	Cyno 1 (female)		
	Mem	**Cyto**	**Nucl**
Muscle	–	–	–
Pancreas	–	–	–
Stomach	–	–	++
Kidney	–	–	–
Colon	–	–	++
Spleen	–	–	–
Lung	–	–	+
Liver	–	–	–
Esophagus	–	–	–
Brain	–	–	+
Parotid gland	–	–	++
Bronchi	–	–	–
Lymph nodes	–	–	–
Spinal cord	–	–	–
Sciatic nerve	–	+	–
Uterus	–	–	+
Small intestine	–	–	++
Adrenal gland	–	–	–

Figure 17



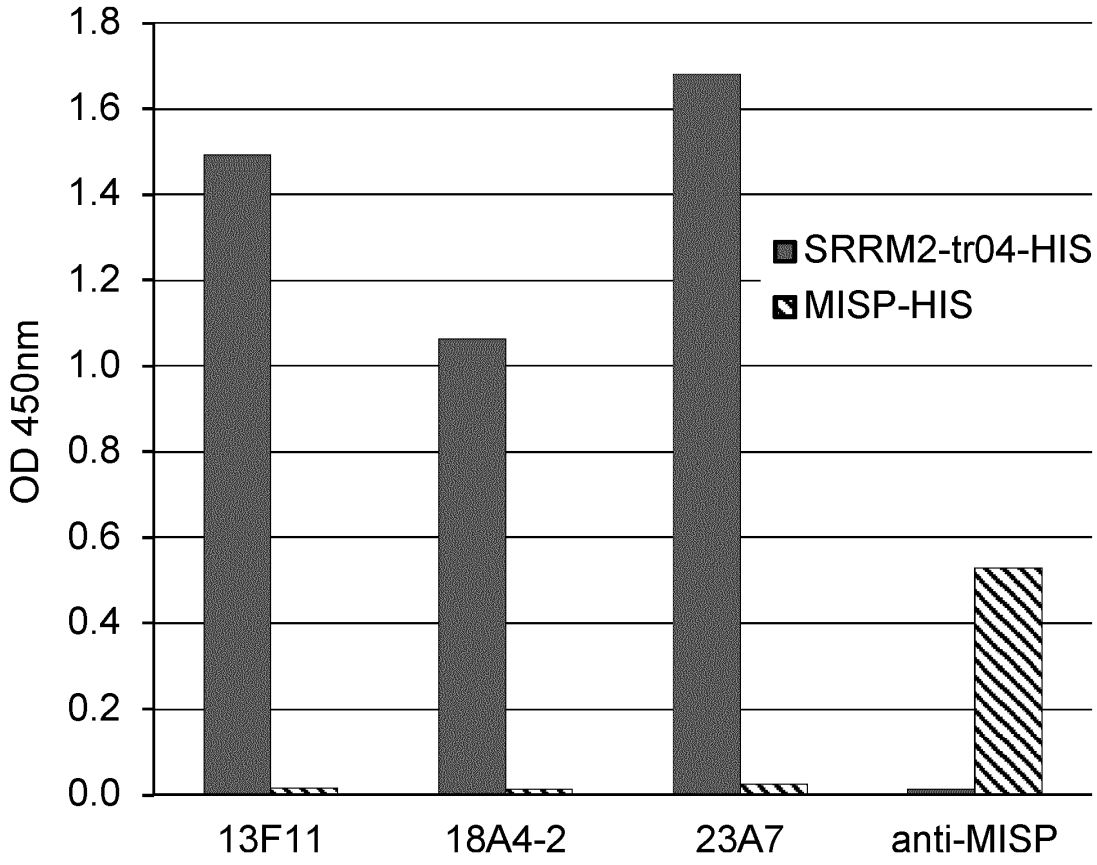
	IHC Score (membrane stained)	Bile Duct	Ovary	Pancreas	Stomach
Cancer cells	3+	6 (16.2%)	10 (38.5%)	14 (29.2%)	7 (15.2%)
	2+	21 (56.8%)	4 (15.4%)	10 (20.8%	17 (37.0%)
	1+	2 (5.4%)	4 (15.4%)	5 (10.4%)	10 (21.7%)
	0	8 (21.6%)	8 (30.8%)	19 (39.6%)	12 (26.1%)
	Number of Samples	37	26	48	46
Adjacent tissues	3+	0.0%	0.0%	2.6%	0.0%
	2+	10.7%	0.0%	2.6%	0.0%
	1+	0.0%	0.0%	0.0%	2.9%
	0	82.1%	100.0%	76.3%	94.3%
	Samples not provided	7.1%	0.0%	18.4%	2.9%

Figure 18

Region	Sequence Fragment	Residues	Length
CDR-H1	NYDMA (SEQ ID NO: 19)	31-35	5
CDR-H2	SISPSGGSIYYRDSVKG (SEQ ID NO: 20)	50-66	17
CDR-H3	LTTYFWYFDF (SEQ ID NO: 21)	99-108	10

Region	Sequence Fragment	Residues	Length
CDR-L1	KSSQSLLYSENKKNYLA (SEQ ID NO: 27)	31-35	17
CDR-L2	WASTRES (SEQ ID NO: 28)	50-66	7
CDR-L3	QQYYKFPPT (SEQ ID NO: 29)	99-108	9

Figure 19


1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
OD 450nm
SRRM2-tr04-HIS
MISP-HIS
13F11
18A4-2
23A7
anti-MISP