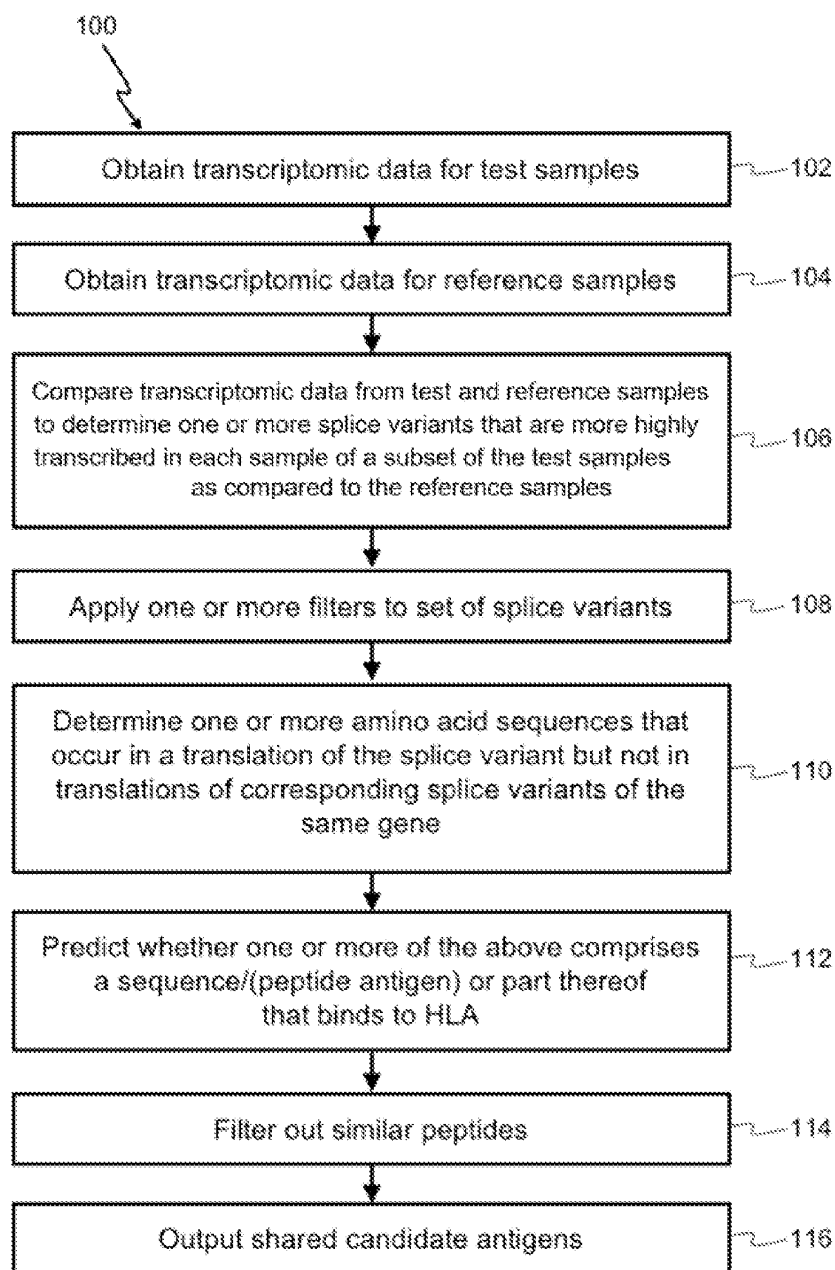
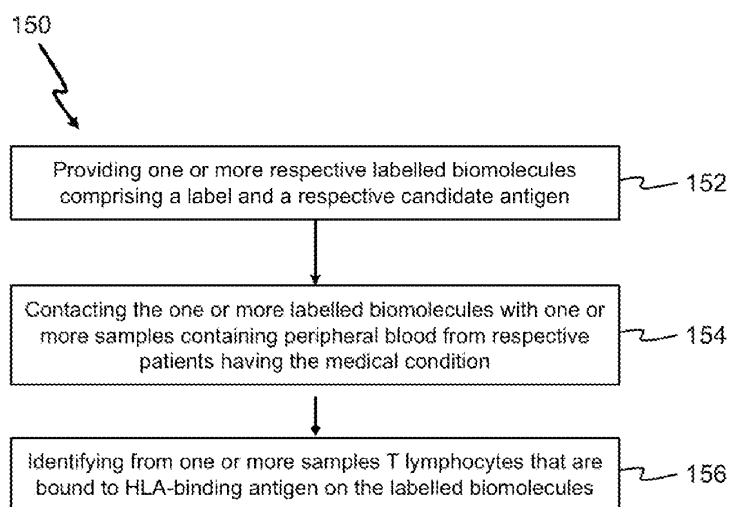


1/71

**Figure 1(a) (continued)**

2/71

**Figure 1(b) (end)**

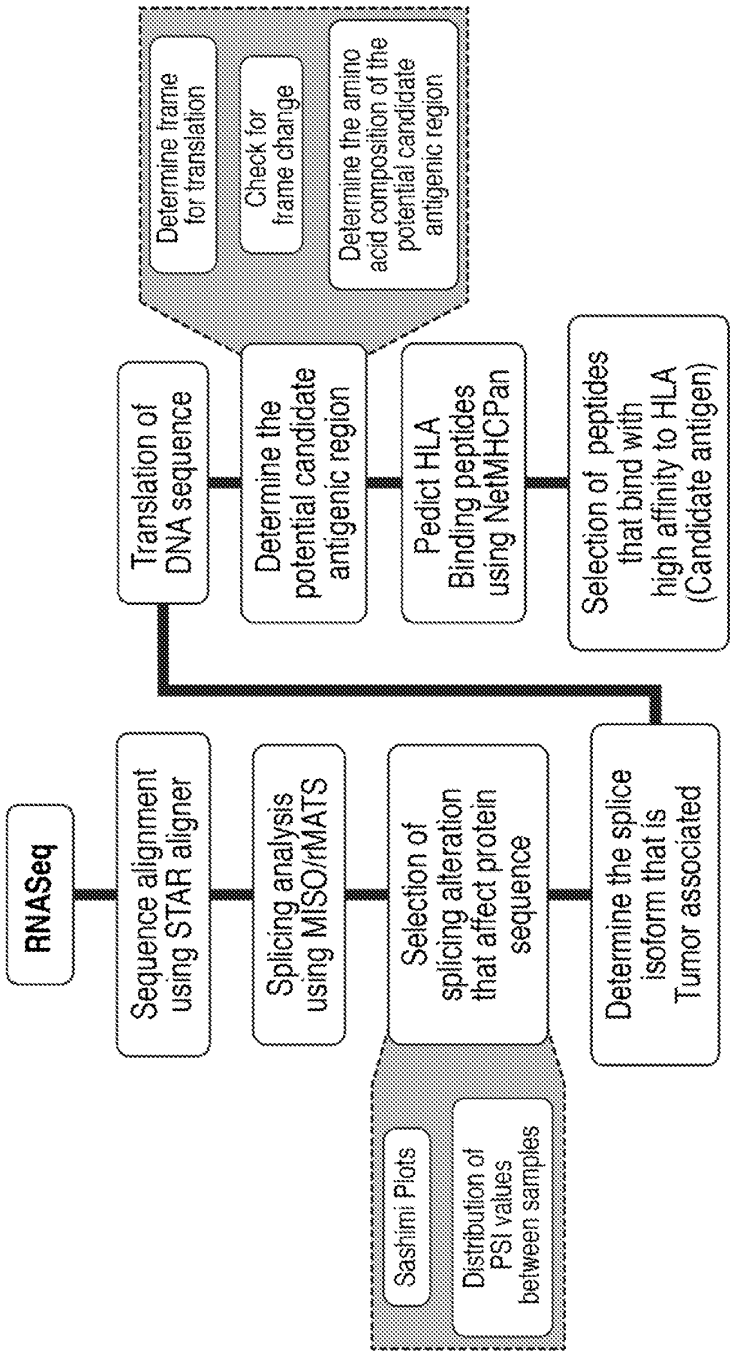


Figure 2

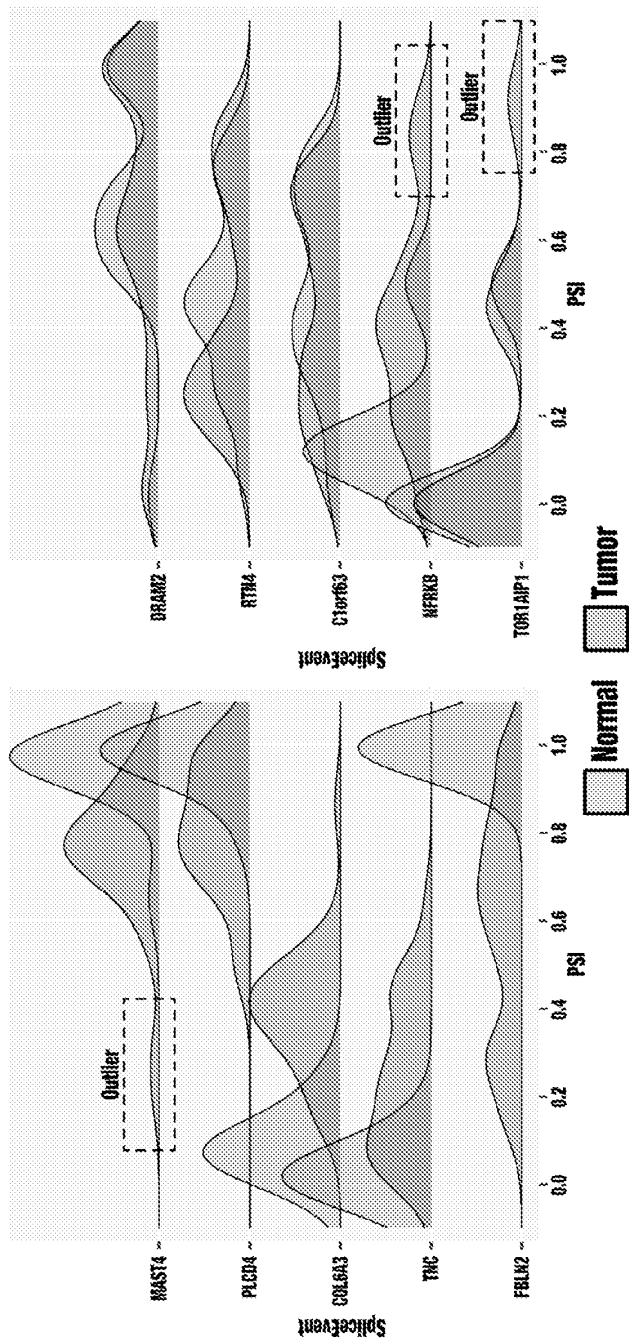


Figure 3

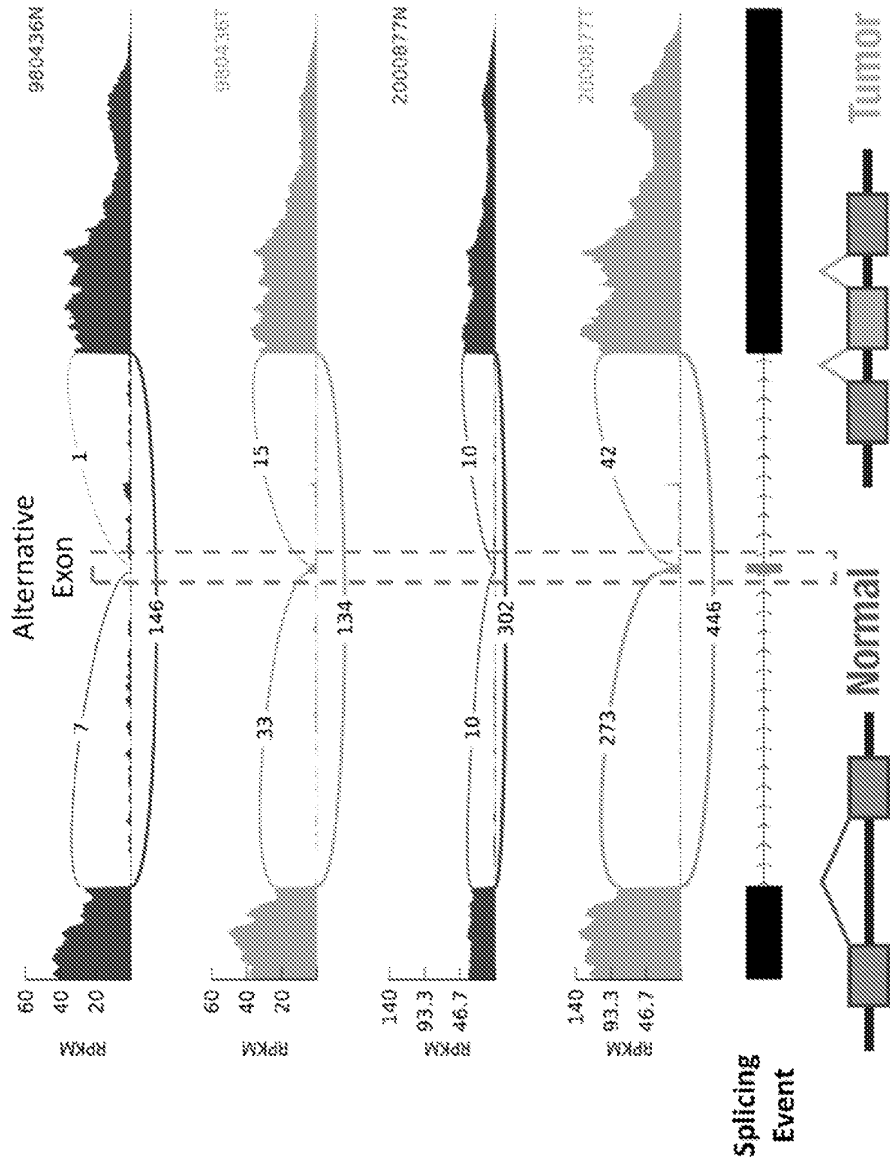


Figure 4

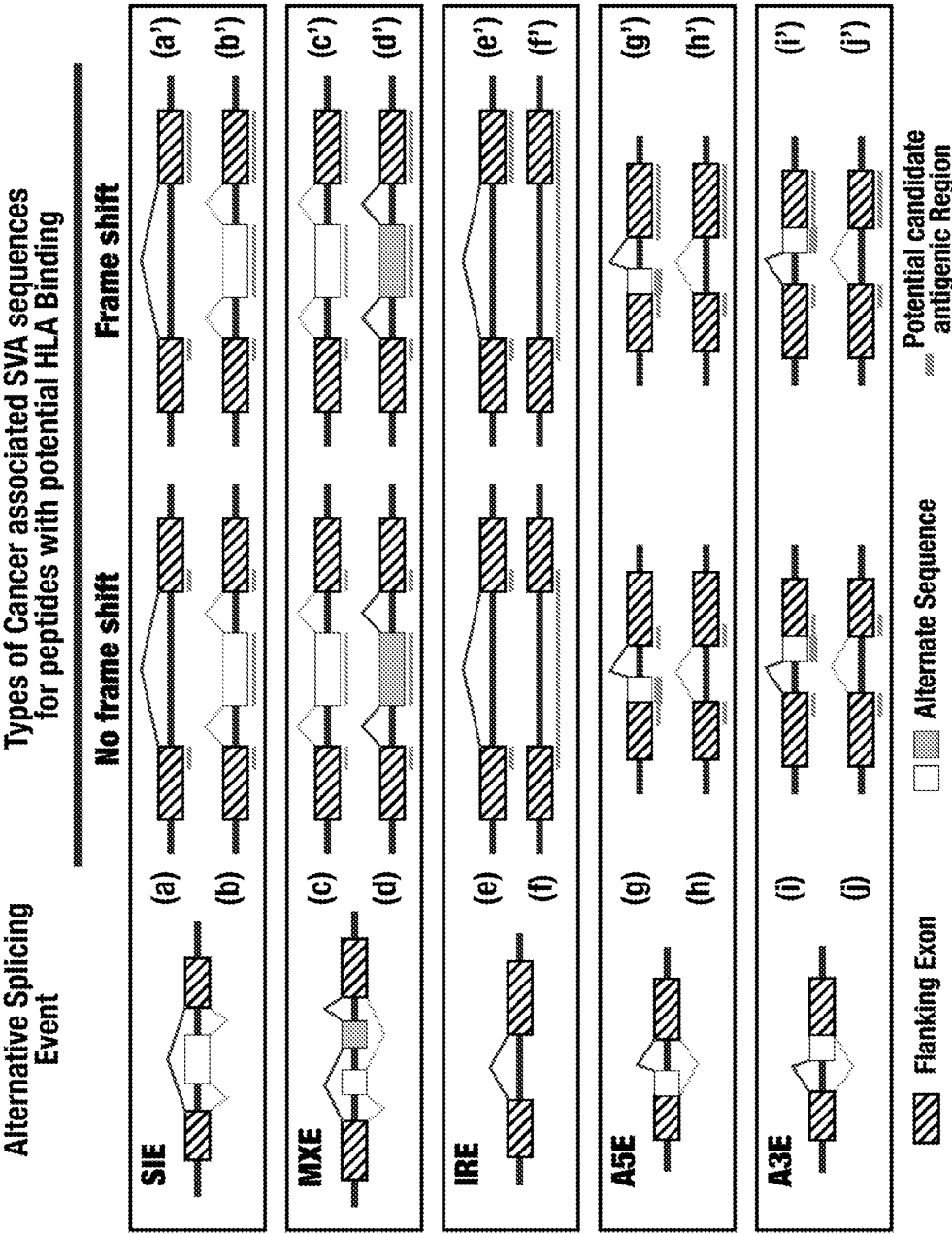


Figure 5

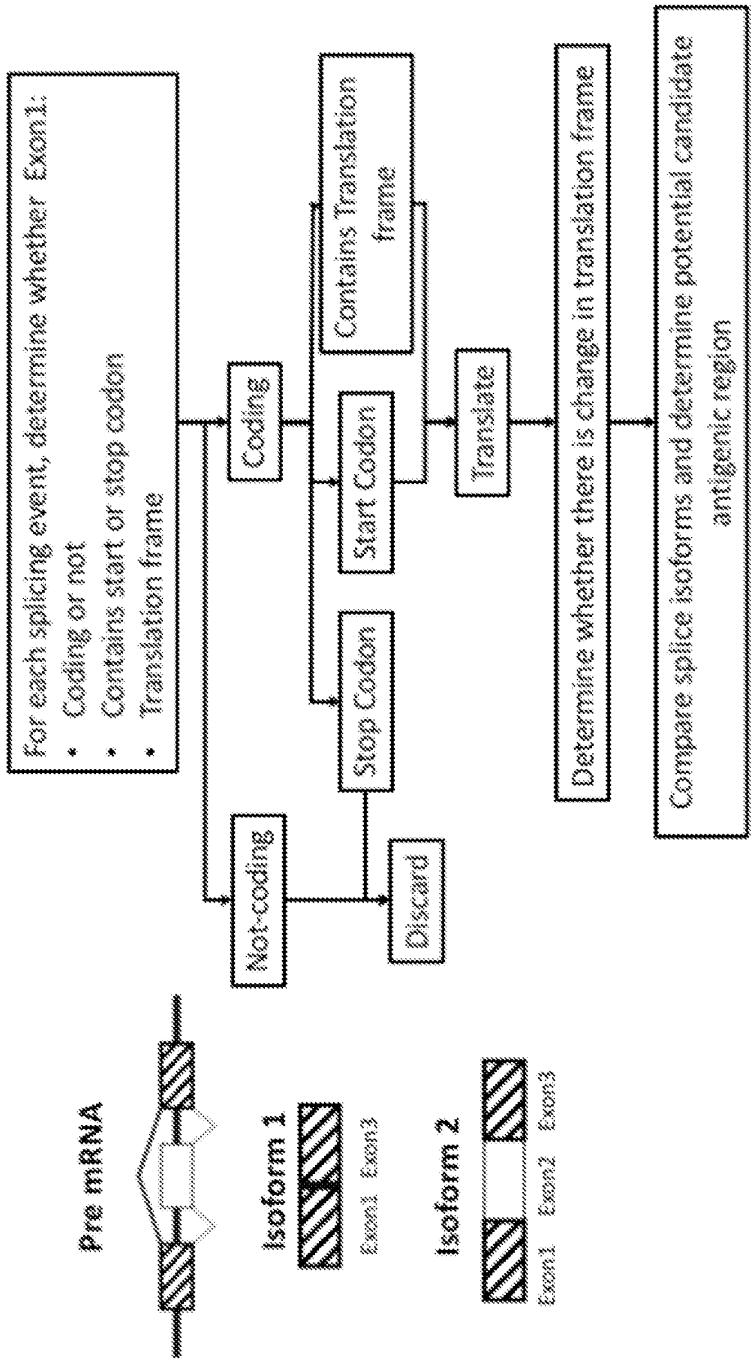


Figure 6(a) (continued)

- In this example, assume:
- 1) HLA binding peptide is 9aa long, then flanking aa is 8aa long (A_{9+8})
 - 2) Exon-skipped isoform has been shown to be tumor associated
 - 3) J_T and J_N are the same
 - 4) Splicing event does not cause change in translation frame

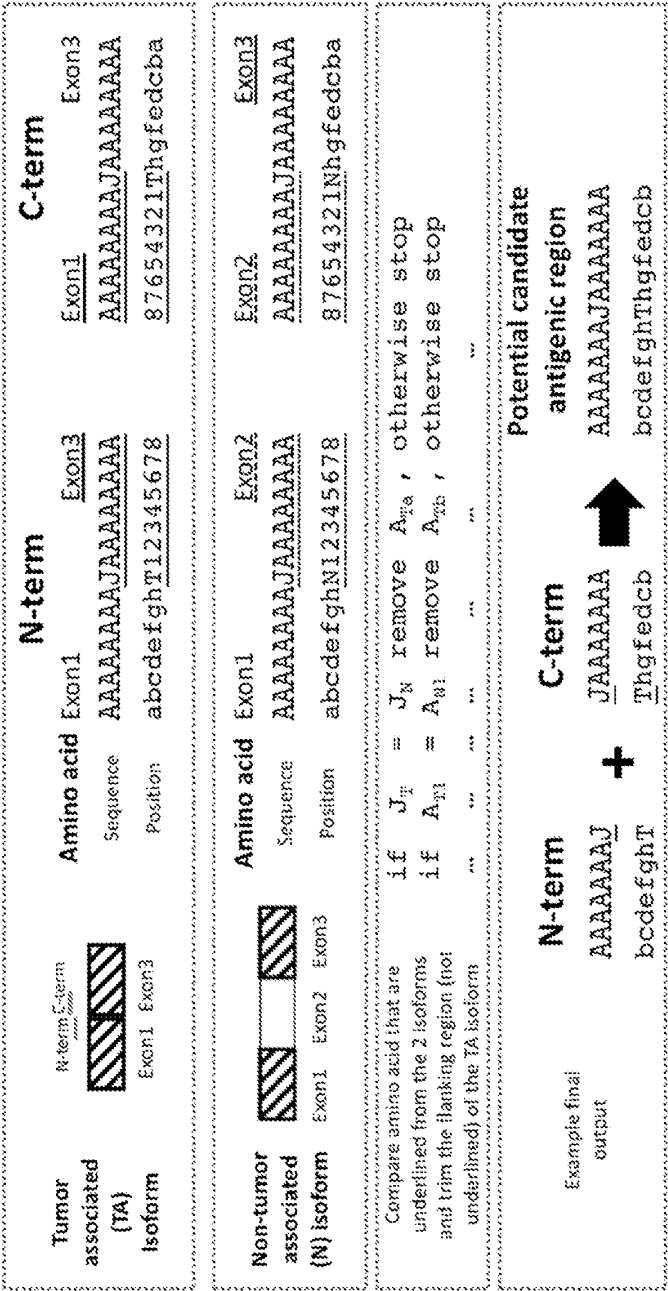


Figure 6(b) (end)

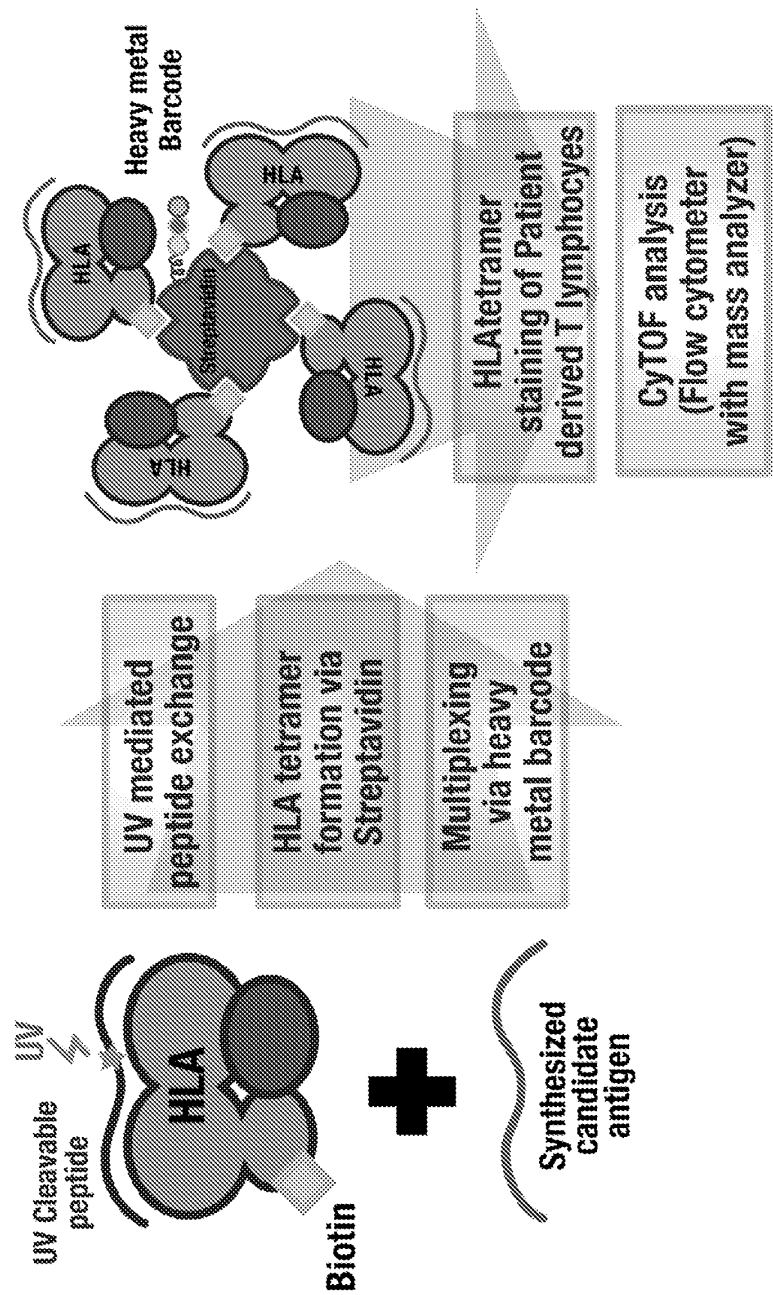
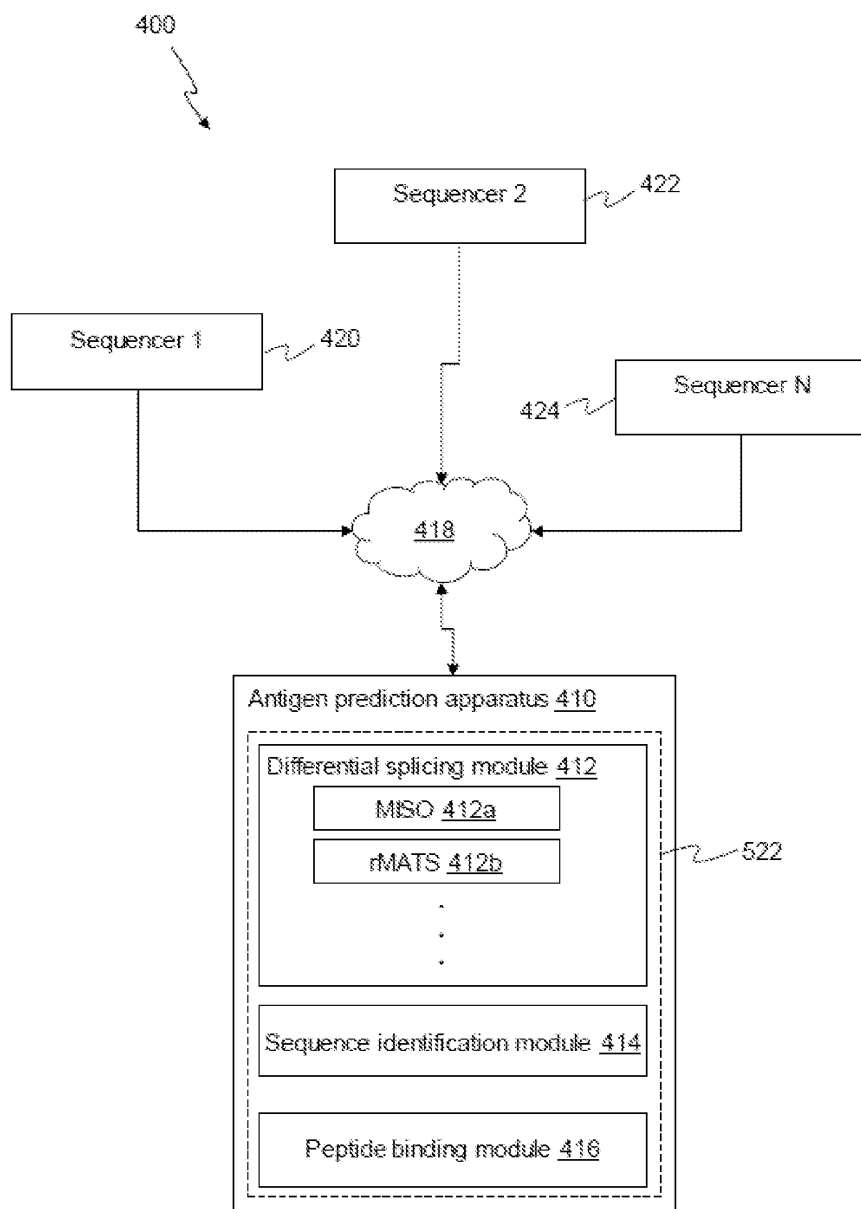
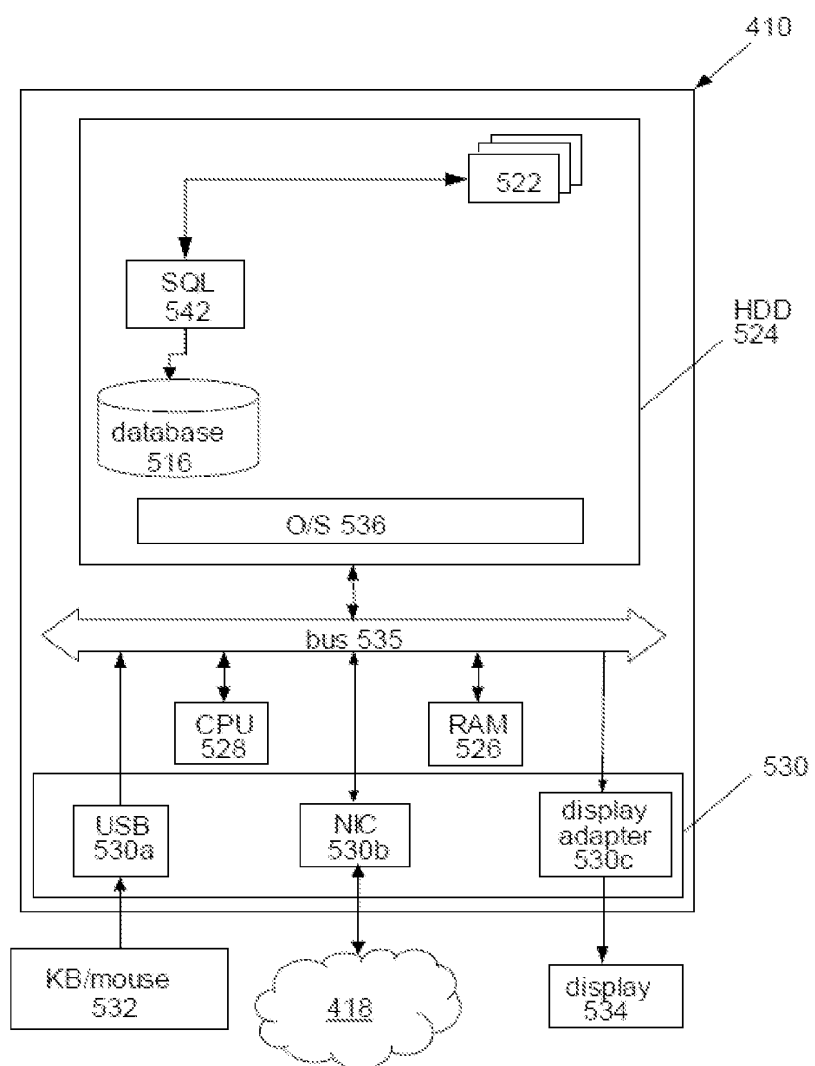


Figure 7

10/71

**Figure 8**

11/71

**Figure 9**

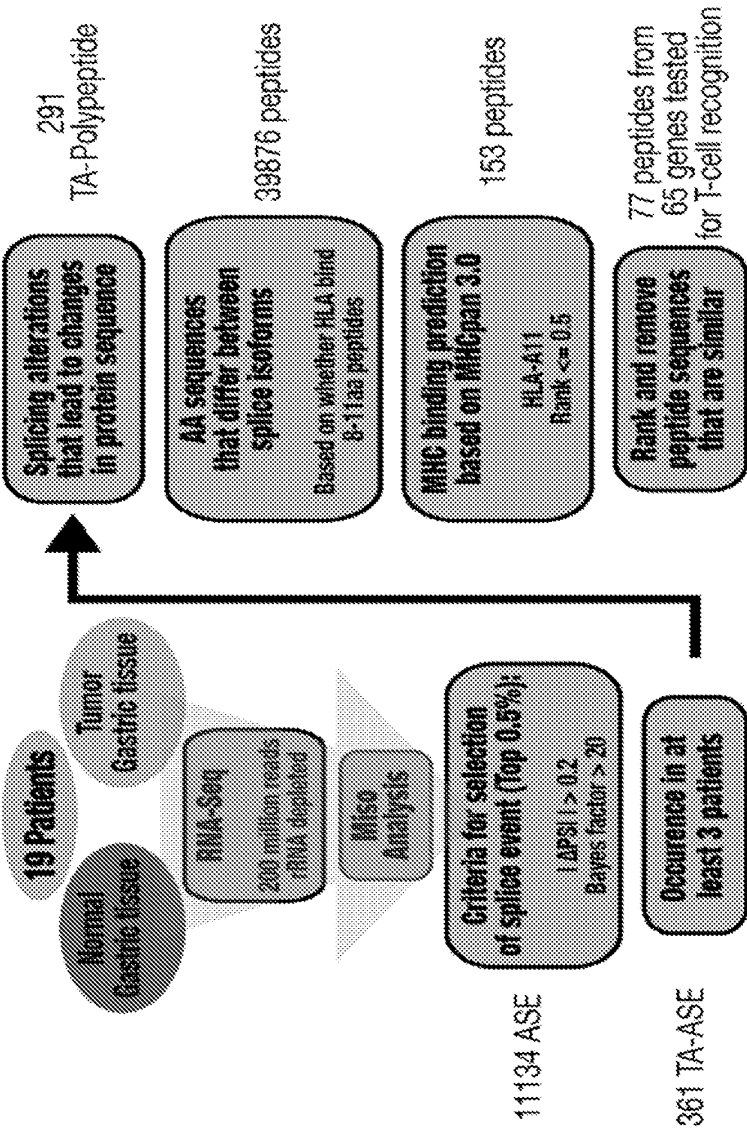


Figure 10

13/71

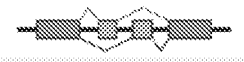
Splice Event	Number	
Skip/inclusion of exon	234	
Alternate usage of Exon (MXE)	58	
Intron retention	38	
Alternate 5' splice sites	13	
Alternate 3' splice sites	18	

Figure 11(a) (continued)

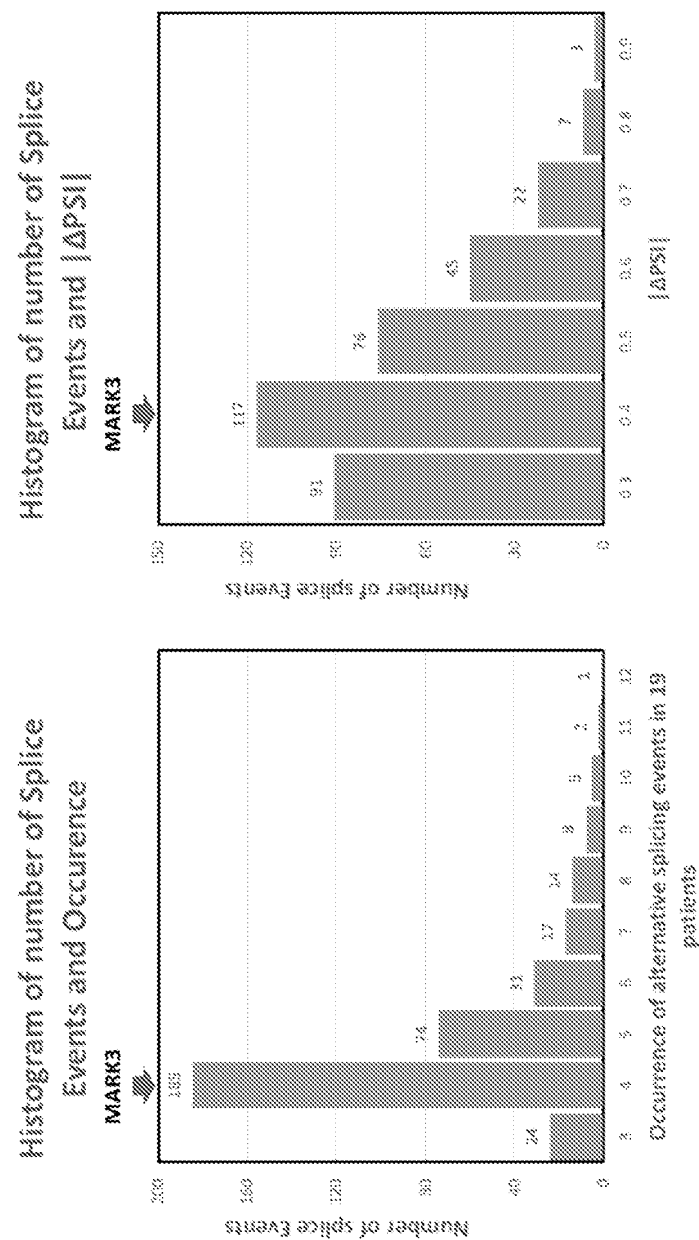


Figure 11(b) (end)

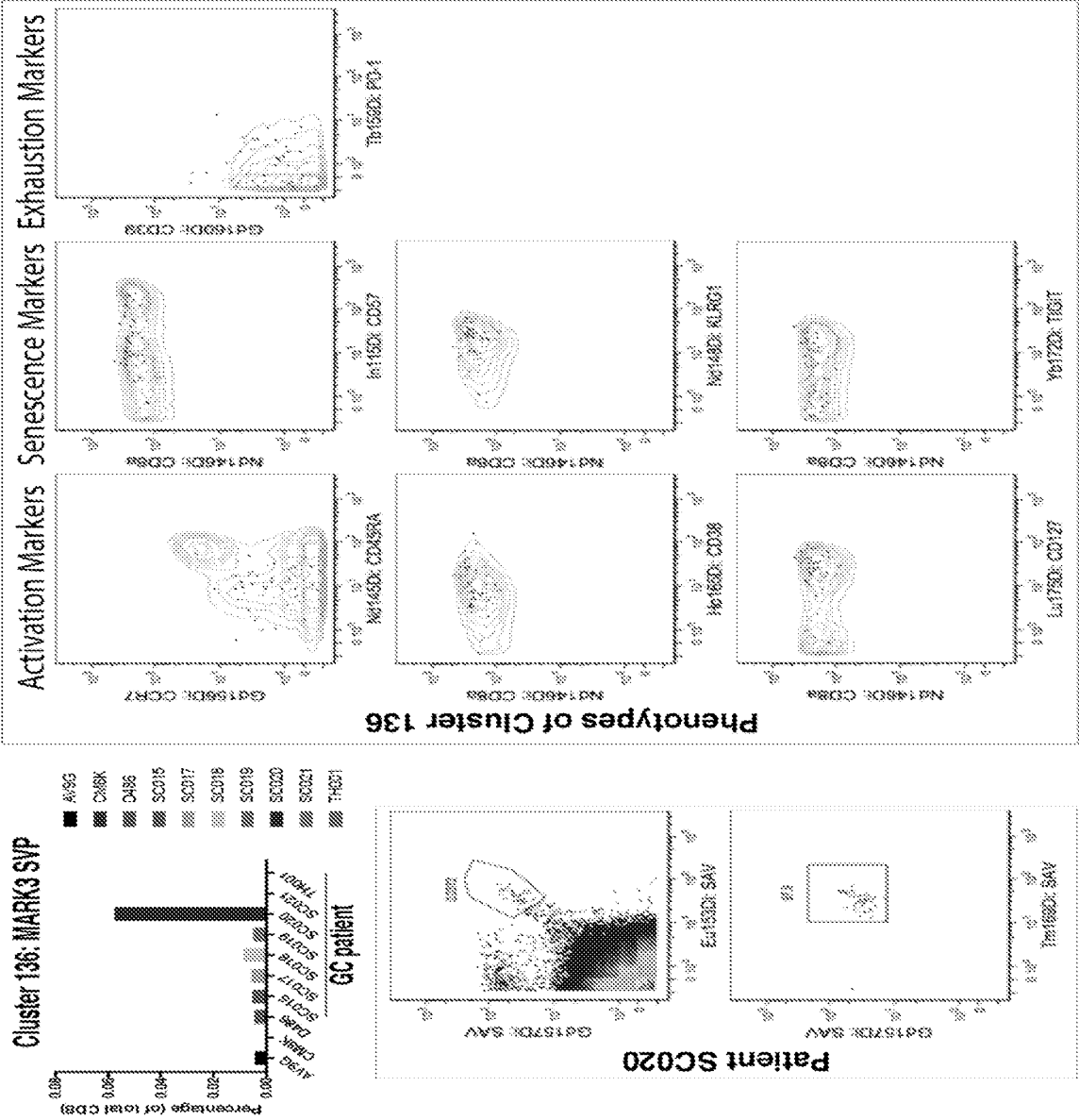


Figure 12(a) (continued)

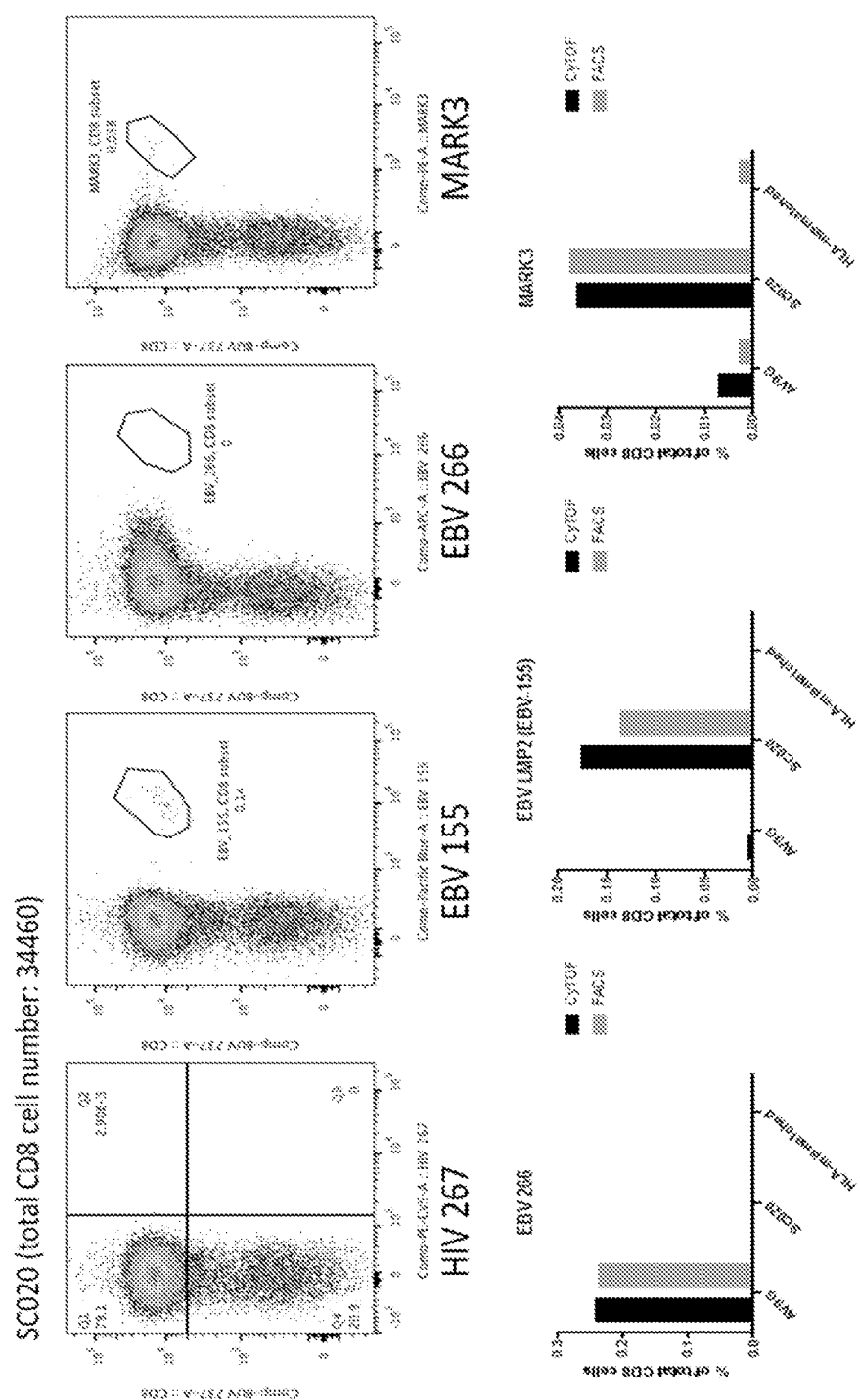


Figure 12(b) (end)

Cluster 172 – SSCSSCPLSK (EBV)

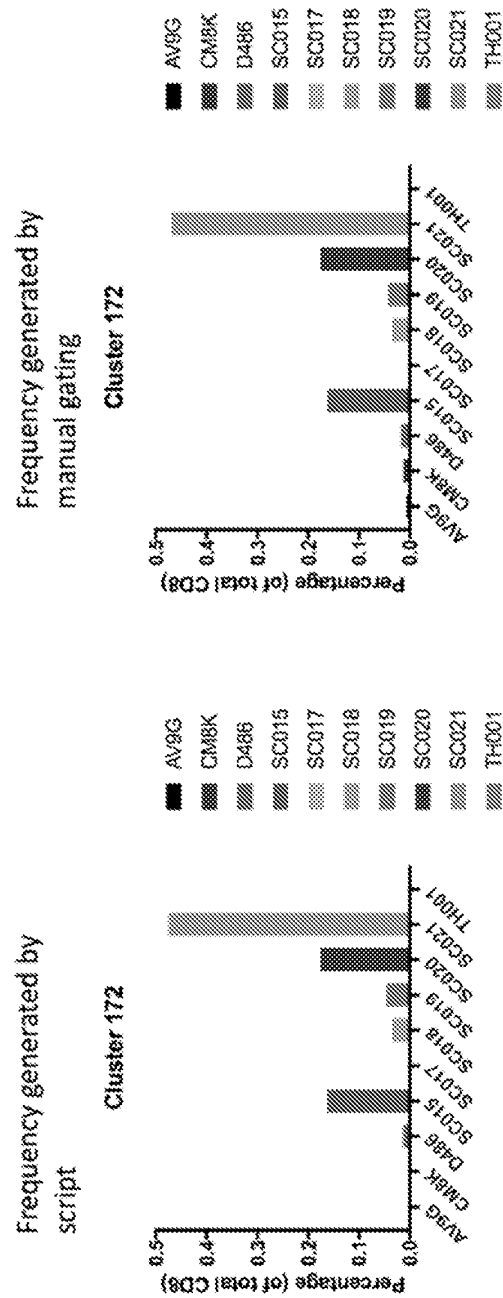


Figure 13

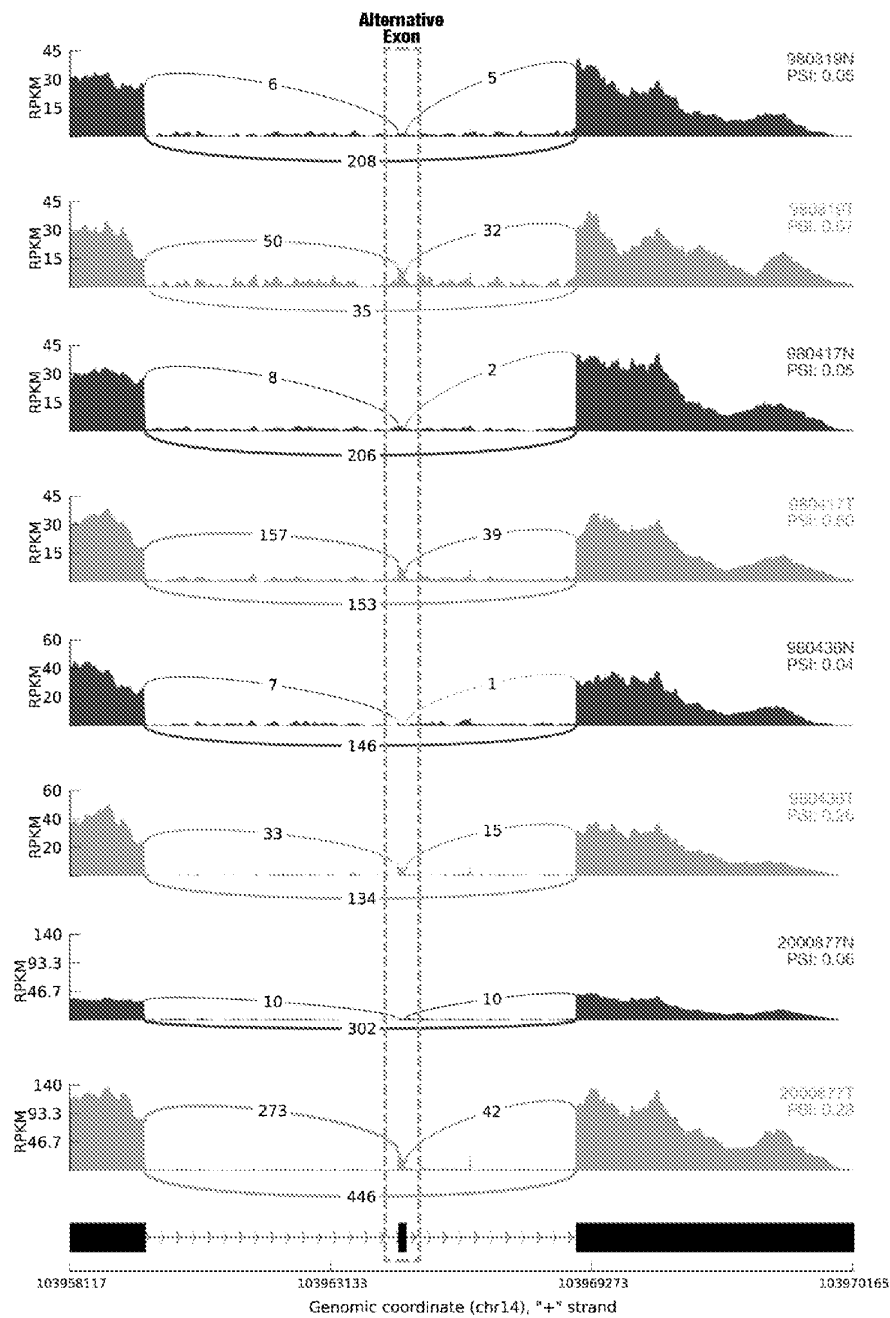


Figure 14(a) (continued)

Transcripts corresponding to Isoforms 1:4

- Based on Ensembl GRCh37.p13
- Isoform 1:
 - ENST00000429436.2
 - ENST00000335102.5
 - ENST00000554627.1
- Isoform 2:
 - ENST00000553942.1
 - ENST00000556744.1
- Isoform 3:
 - ENST00000440884.3
- Isoform 4:
 - ENST00000303622.9
 - ENST00000216288.7
 - ENST00000416682.2
 - ENST00000561071.1
 - ENST00000556463.1

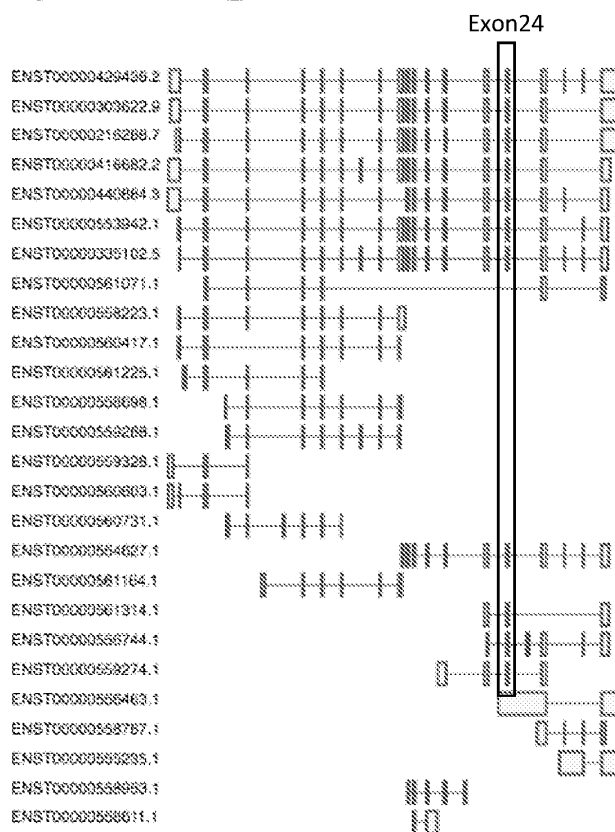


Image taken from GTEx

Figure 14(b) (continued)

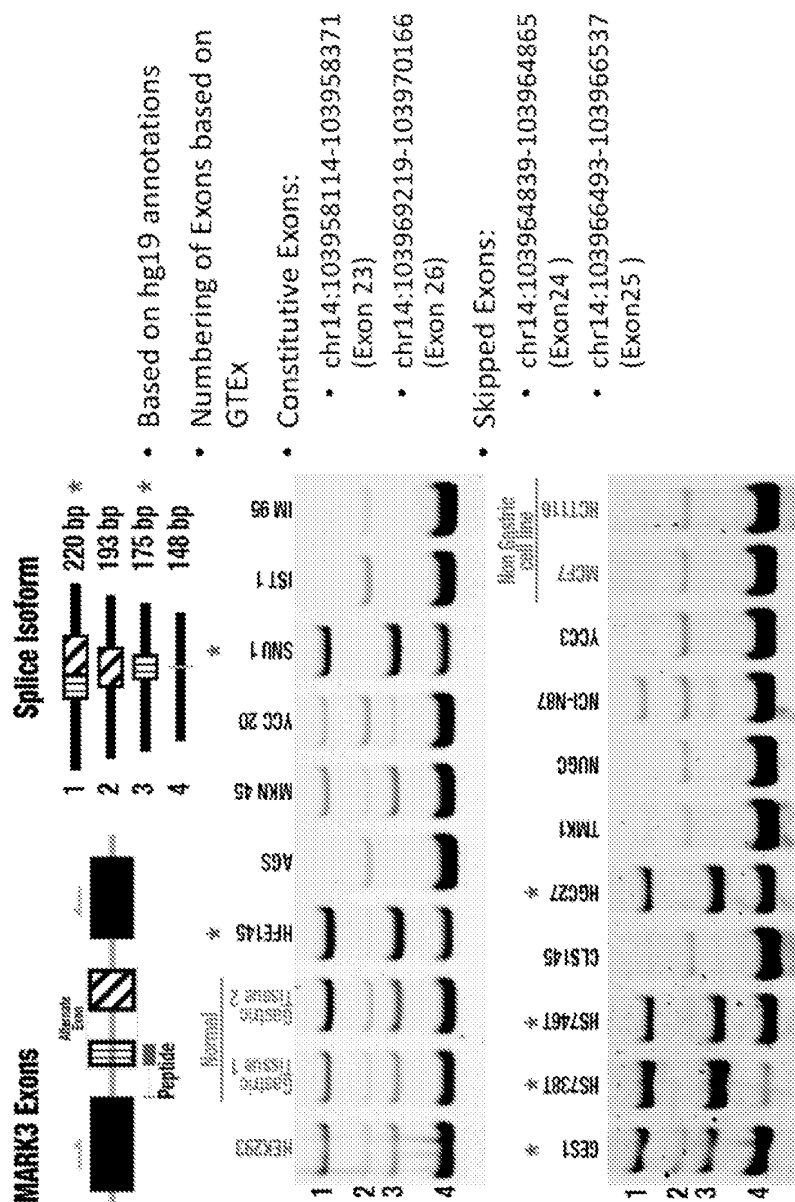


Figure 14(c) (continued)

21/71

Cell line	% Isoform				Isoforms 1 & 3
	1	2	3	4	
<u>HFE 145</u>	34.3	0.6	36.7	28.4	<u>71.0</u>
AGS	0.0	2.9	0.0	97.1	0.0
MKN45	6.5	1.3	10.2	81.9	16.7
YCC20	3.4	5.3	1.9	89.4	5.3
<u>SNU1</u>	27.5	0.3	41.2	30.9	<u>68.7</u>
IST1	0.2	5.7	0.2	93.8	0.4
IM95	0.0	1.3	0.0	98.7	0.0
<u>GES1</u>	16.4	3.6	13.7	66.4	<u>30.1</u>
<u>HS738T</u>	29.9	0.0	66.2	3.9	<u>96.1</u>
<u>HS746T</u>	15.3	0.0	29.4	55.3	<u>44.7</u>
CLS145	0.4	1.7	0.3	97.6	0.7
<u>HCG27</u>	12.8	0.4	36.3	50.5	<u>49.1</u>
TMK1	0.0	1.0	0.0	99.0	0.0
NUGC	0.0	1.6	0.0	98.4	0.0
NCI N87	2.5	3.2	0.8	93.5	3.3

Figure 14d (continued)

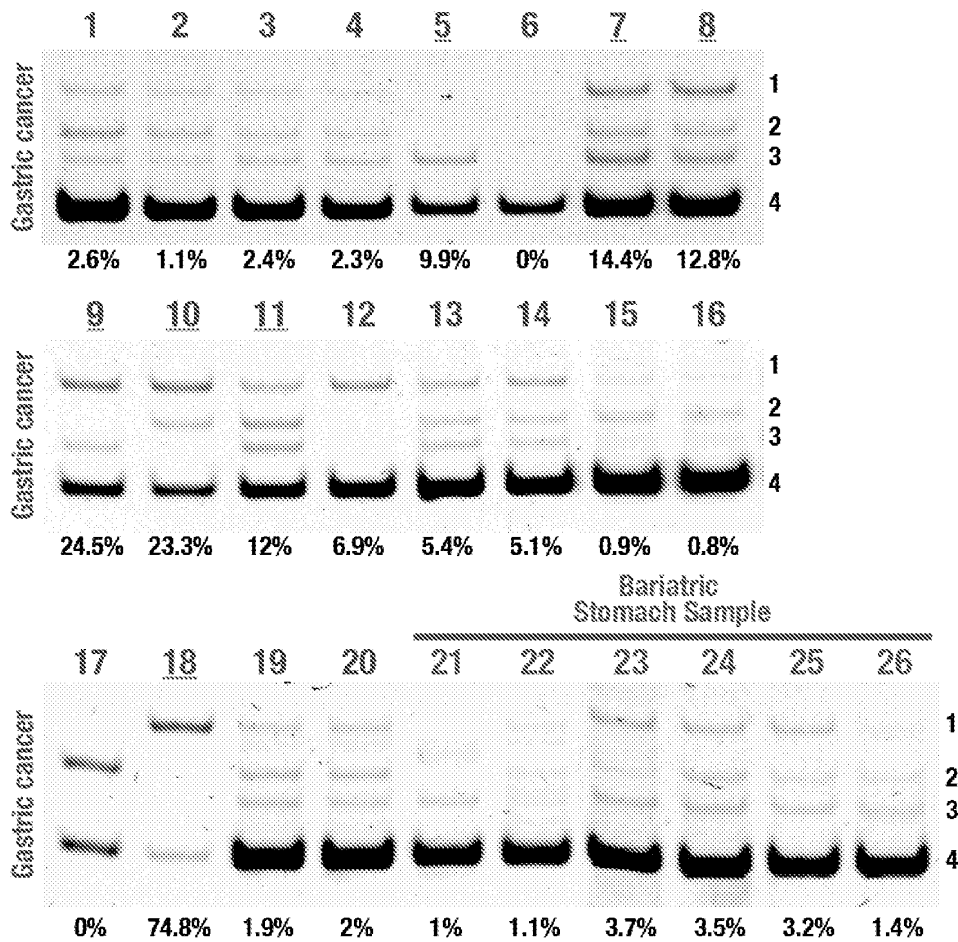
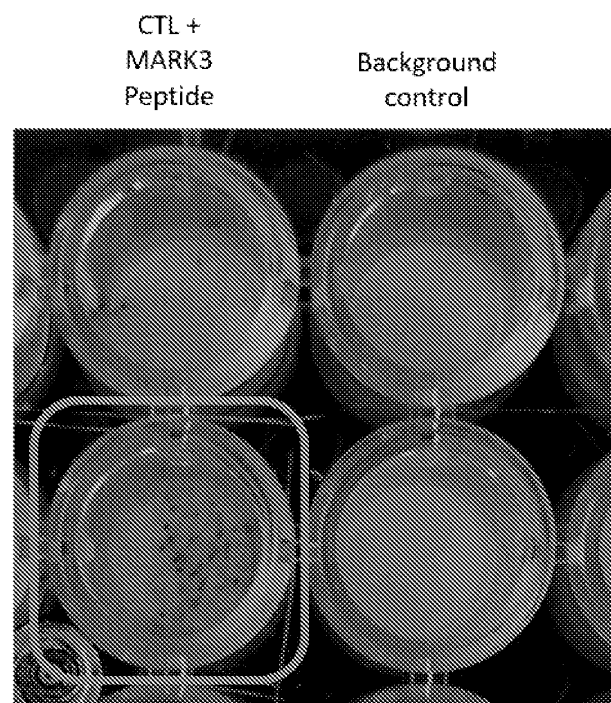


Figure 14e (end)

23/71



Elispot after 10 days of Stimulation with MARK3 peptide

Well in green box were selected for Killing Assay

Figure 15(a) (continued)

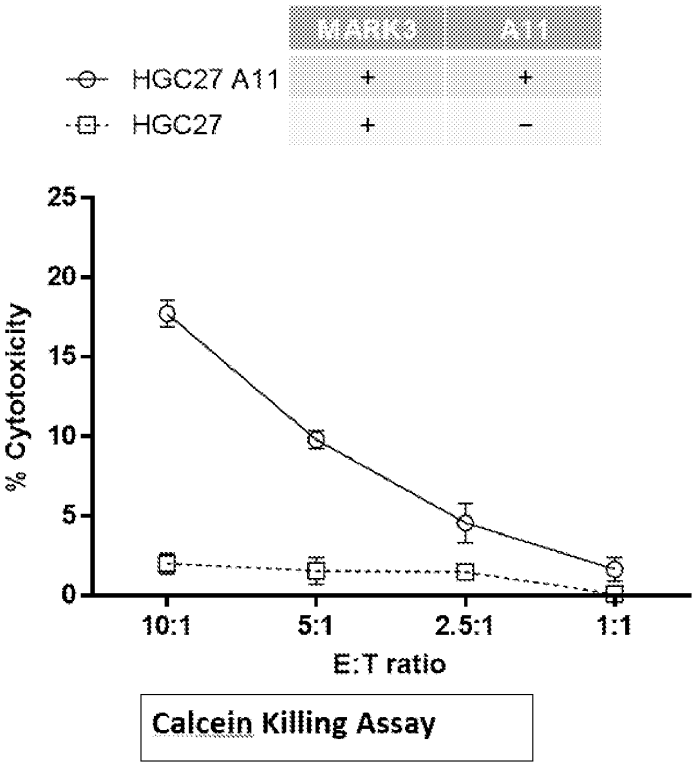


Figure 15(b) (end)

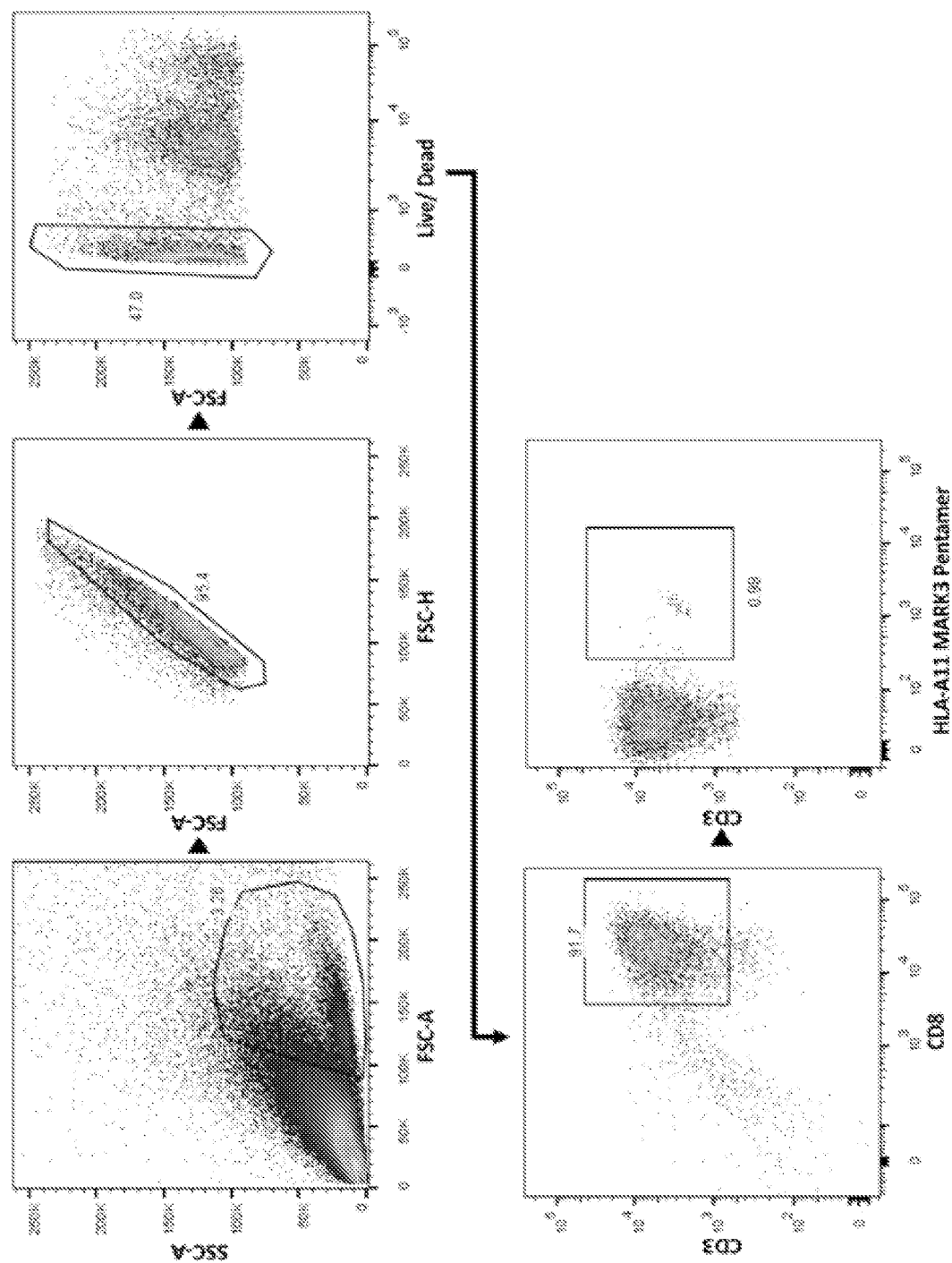


Figure 16

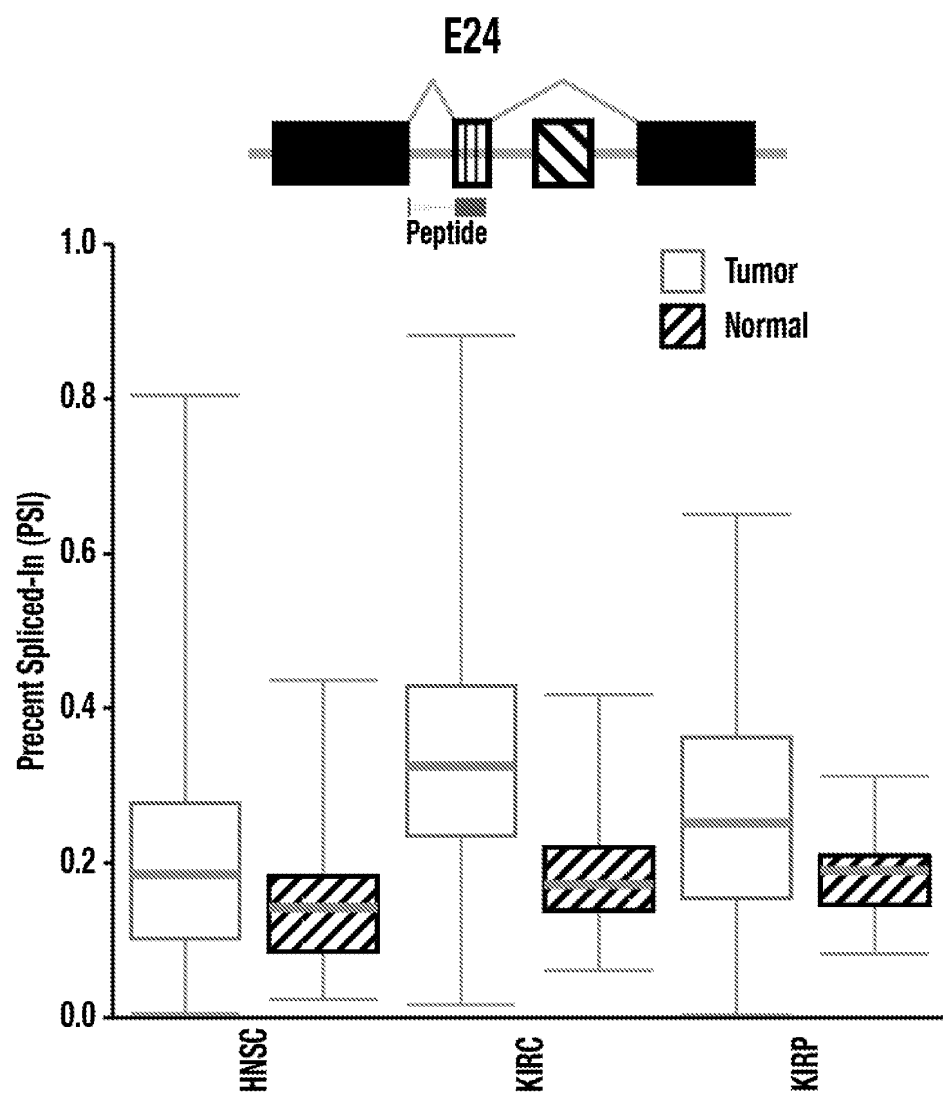


Figure 17

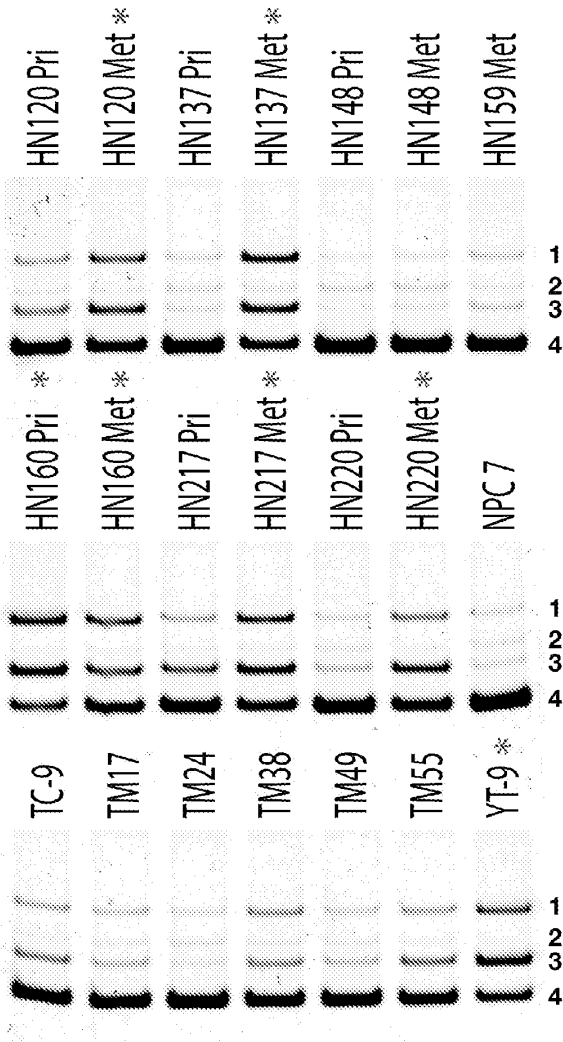


Figure 18(a) (continued)

28/71

Cell line	% Isoform				Isoforms 1 & 3
	1	2	3	4	
HN120 Pri	6.6	1.1	12.1	80.2	18.7
<u>HN120 Met</u>	15.7	0.6	22.7	61.0	<u>38.4</u>
HN137 Pri	2.4	2.3	2.0	93.3	4.4
<u>HN137 Met</u>	27.5	1.6	27.1	43.9	<u>54.6</u>
HN148 Pri	0.7	2.7	0.8	95.9	1.5
HN148 Met	1.2	2.7	1.6	89.5	2.8
HN159 Met	3.4	1.3	4.0	91.2	7.4
<u>HN160 Pri</u>	33.0	0.7	39.1	27.1	<u>72.1</u>
<u>HN160 Met</u>	22.5	0.8	22.0	54.7	<u>44.5</u>
HN217 Pri	5.9	0.7	16.6	76.7	22.5
<u>HN217 Met</u>	20.9	0.9	31.2	46.9	<u>52.1</u>
HN220 Pri	2.5	1.2	4.5	91.8	7.0
<u>HN220 Met</u>	11.8	0.6	26.9	60.7	<u>38.7</u>
NPC7	2.5	1.6	2.5	93.5	5.0

Figure 18(b) (end)

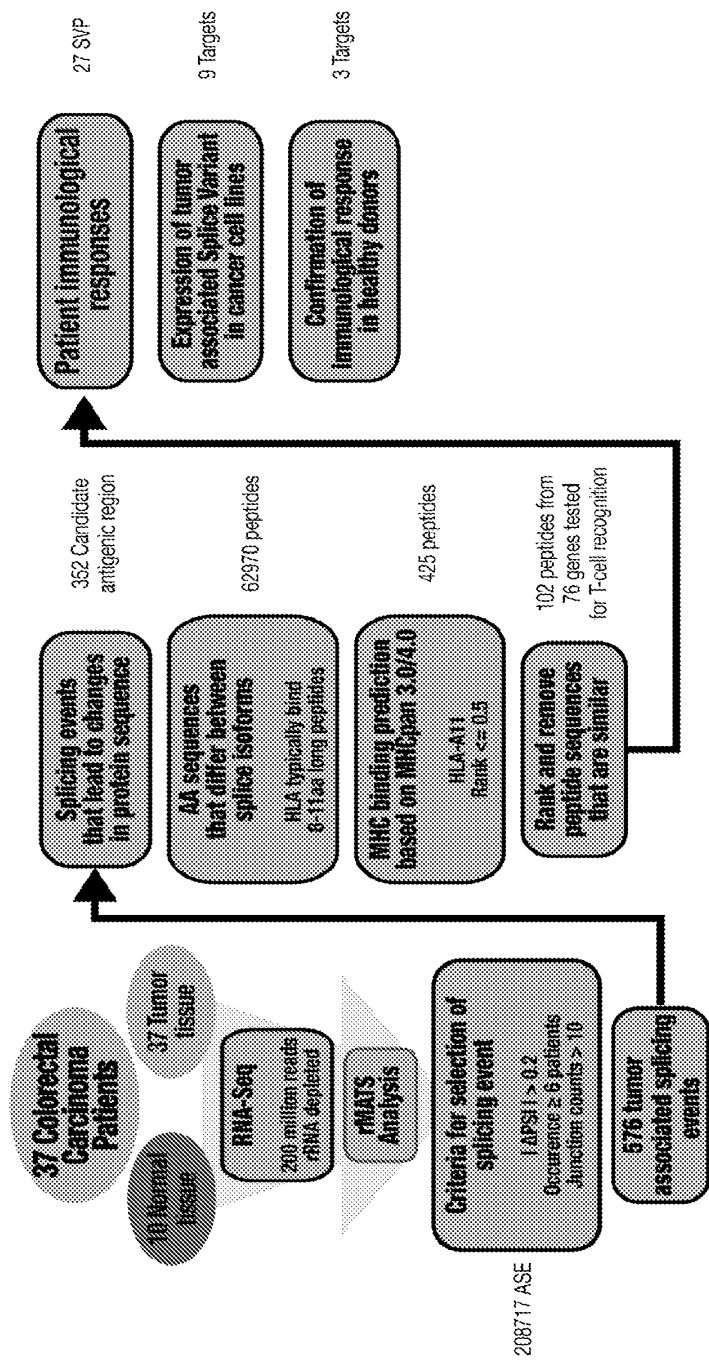


Figure 19(a) (continued)

30/71

Type of Splicing Event		All	Coding changes
Exon Skip/inclusion (SIE)		386	222
Intron retention Event (IRE)		94	73
Alternate 5' splice site (ASE)		42	20
Alternate 3' splice site (A3E)		54	37
Total		576	352

Figure 19(b) (end)

31/71

Gene	Peptide Sequence	SEQ ID NO	Frequency of antigen specific CD8 lymphocytes in CRC patients (% total CD8 cells)				in-silico data		
			2072	1394	433	1537	Occurrence	APSI	Splice Event
NBPF9	SSFYALEEK	31	0.005		0.004		9	0.342	IRE
PARD3	SQLDFVKTRK	32			0.009		7	-0.232	A5E
ZC3HAV1	LTMVKAKEK	33			0.003		6	-0.234	A5E
YAF2	VIVSASRTK	34		0.010			6	0.205	A3E
CAMKK1	VTSPSRRSK	35	0.027				9	0.473	SIE
GRINA	SIRQAFIRK	38			0.007		10	0.248	IRE
LRR1	SLPRFGYRK	36				0.008	6	0.249	SIE
ZNF670	SCVSPSSELK	37	0.033	0.076			8	0.362	SIE

Figure 20(a) (continued)

Gene	Sequence Coordinates	Tumor Associated Form
NBPf9	chr1:144826235-144826286+@chr1:144826287-144826832-@chr1:144826933-144827105+	chr1:144826235-144827105-
PARD3	chr10:34625127-34625171-@chr10:34626206-34626354-@chr10:34626293-34626354-	chr10:34625127-34625171-@chr10:34626206-34626354-
ZC3HAY1	chr7:138763298-138763399-@chr7:138763850-138764989-@chr7:138764216-138764989-	chr7:138763298-138763399-@chr7:138763850-138764989-
YAF2	chr12:42604350-42604421-@chr12:42604350-42604482-@chr12:42631401-42631526-	chr12:42604350-42604421-@chr12:42631401-42631526-
CAMKK1	chr17:3783822-3783838-@chr17:3784921-3784942-@chr17:3783840-3783728-	chr17:3783822-3783838-@chr17:3783840-3783728-
GRINA	chr8:145065860-145065972+@chr8:145065860-145066541+@chr8:145066413-145066541+	chr8:145065860-145065972+@chr8:145066413-145066541+
LRR1	chr14:50069088-50069186+@chr14:50074118-50074839+@chr14:50080974-50081389+	chr14:50069088-50069186+@chr14:50080974-50081389+
ZNF670	chr1:247151423-247151557-@chr1:247130997-247131094-@chr1:247108849-247109129-	chr1:247151423-247151557-@chr1:247108849-247109129-

Figure 20(b) (end)

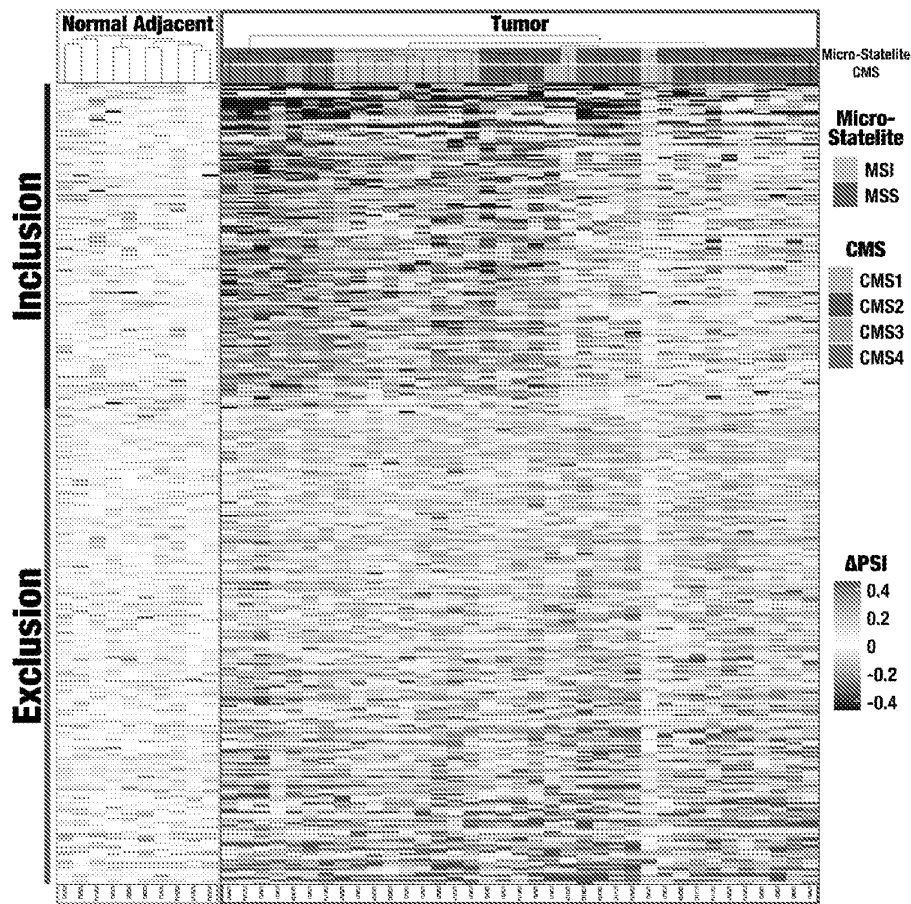
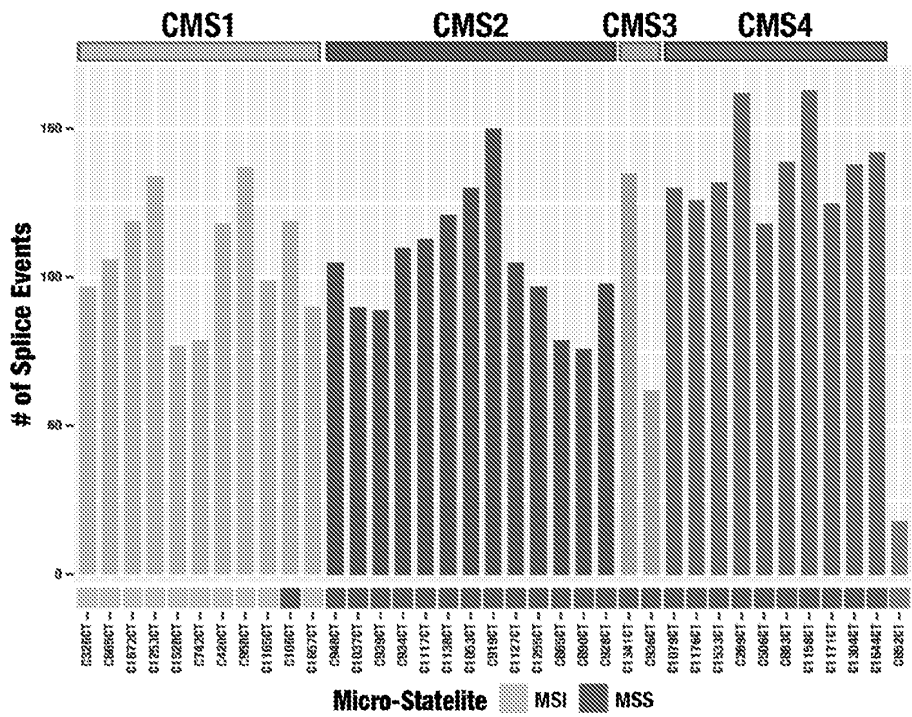


Figure 21(a) (continued)



35/71

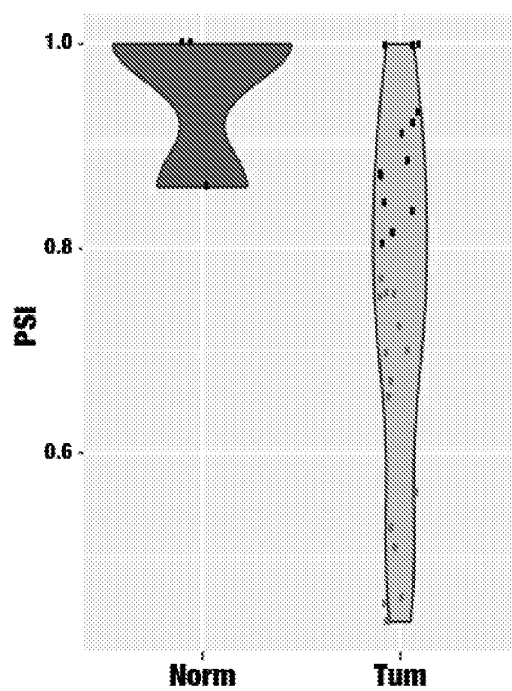


Figure 22(a) (continued)

36/71

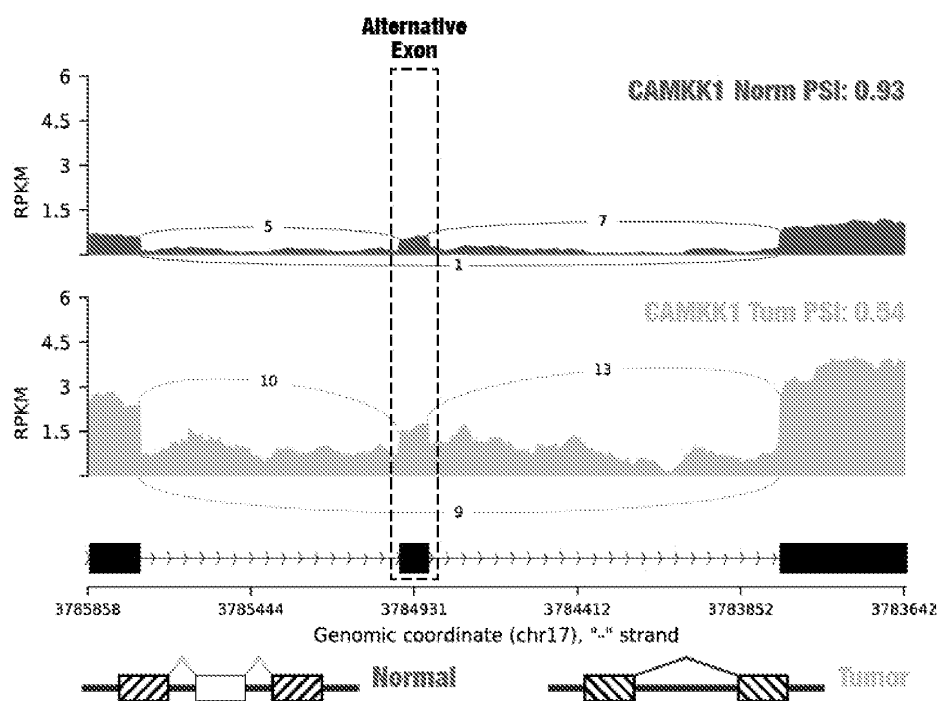


Figure 22(b)(continued)

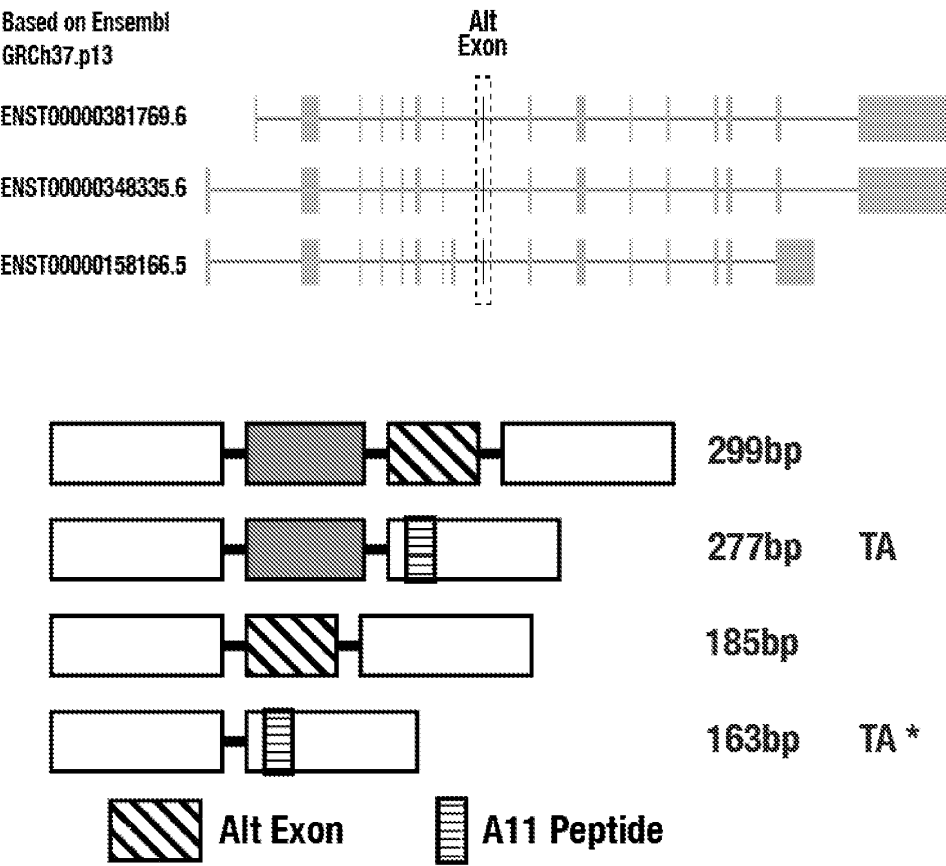


Figure 22(c)(continued)

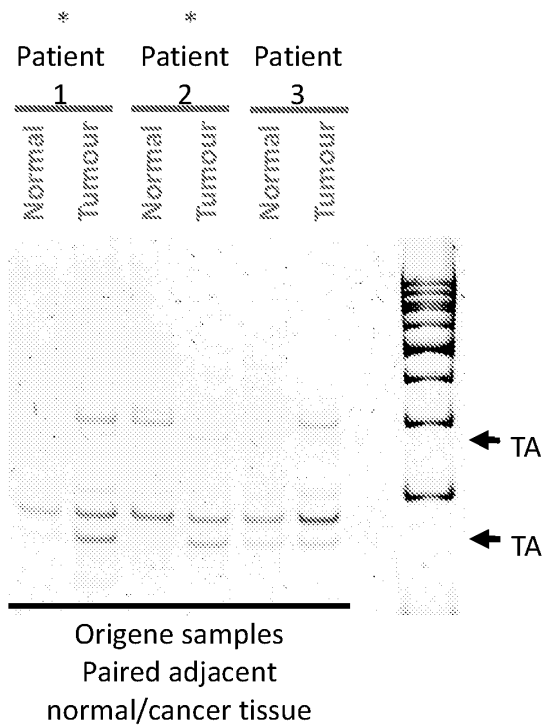
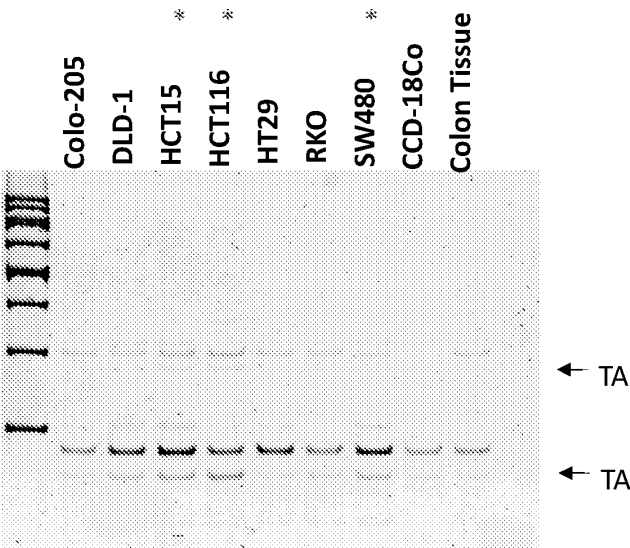


Figure 22(d)(continued)

40/71

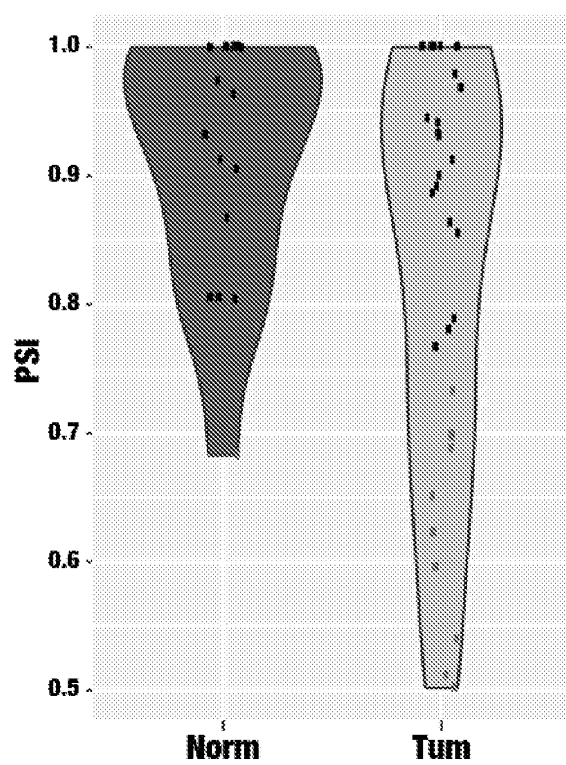


Figure 22(f)(continued)

41/71

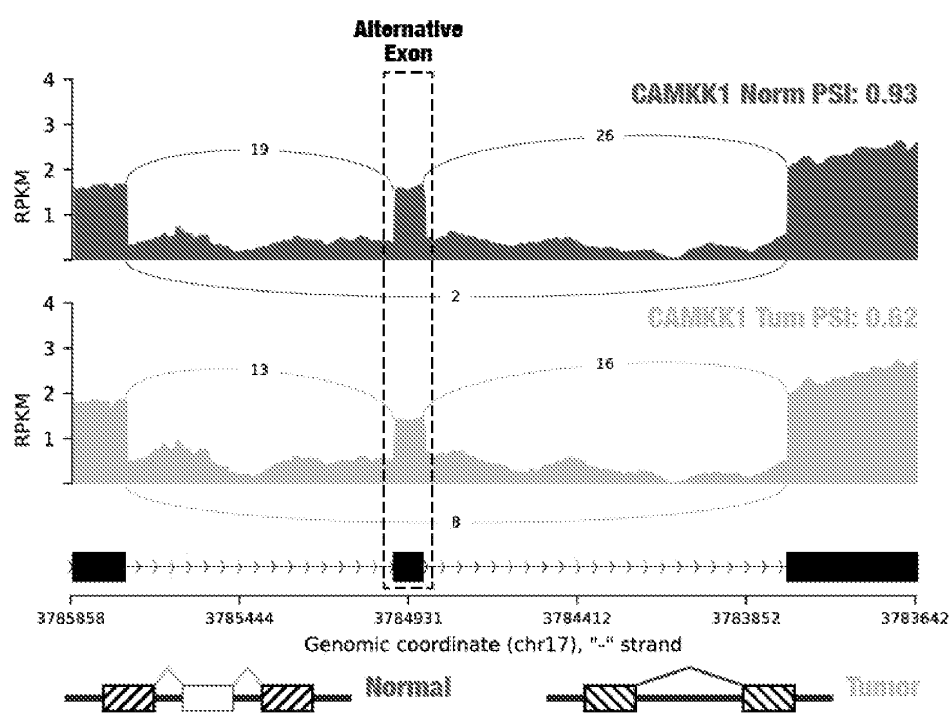


Figure 22(g)(continued)

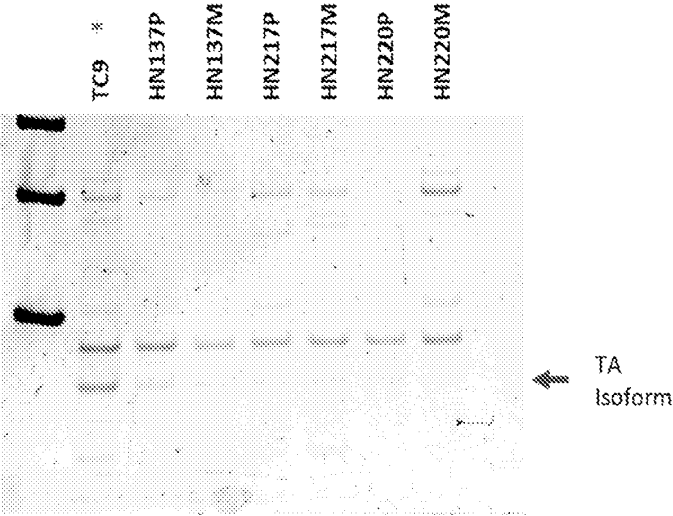


Figure 22(h)(end)

43/71

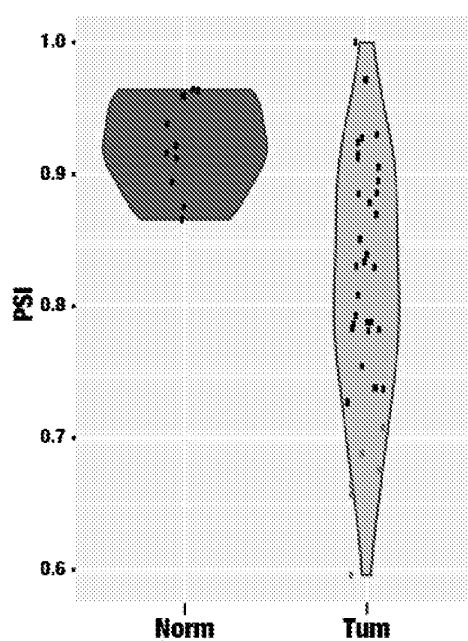


Figure 23(a)(continued)

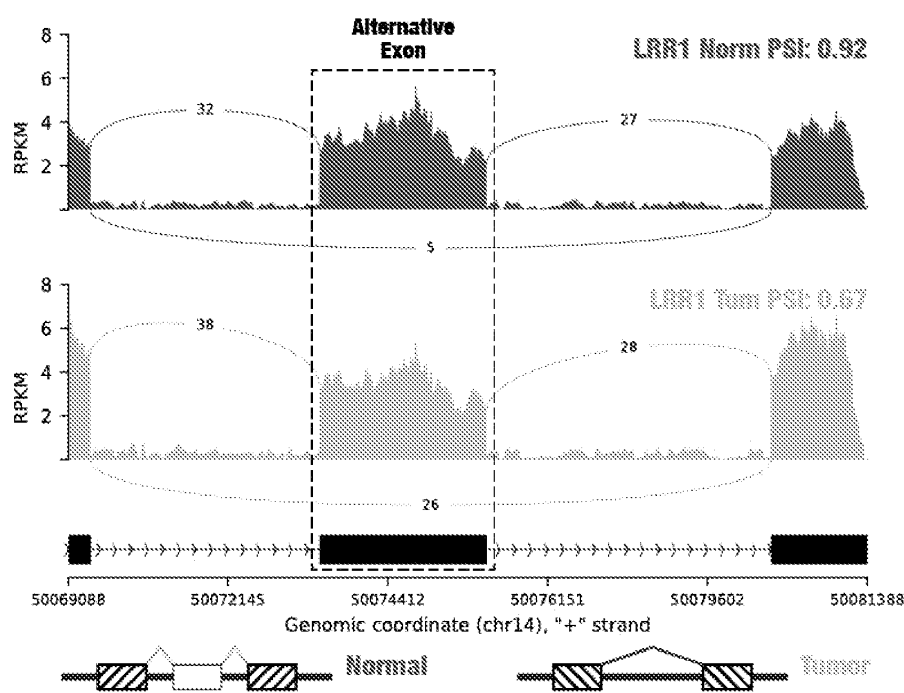


Figure 23(b)(continued)

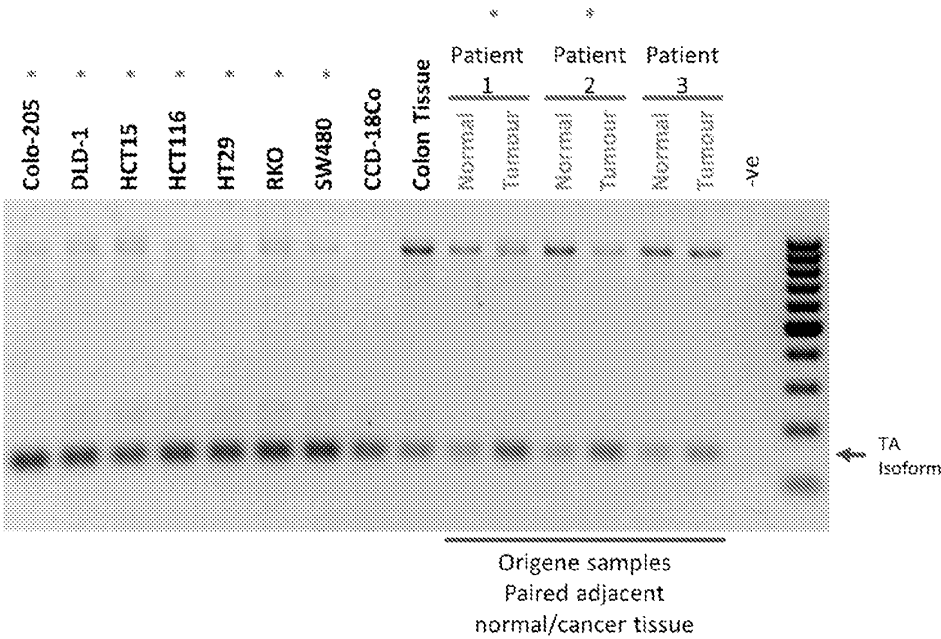


Figure 23(c)(continued)

[illegible]

Figure 23(d)(continued)

47/71

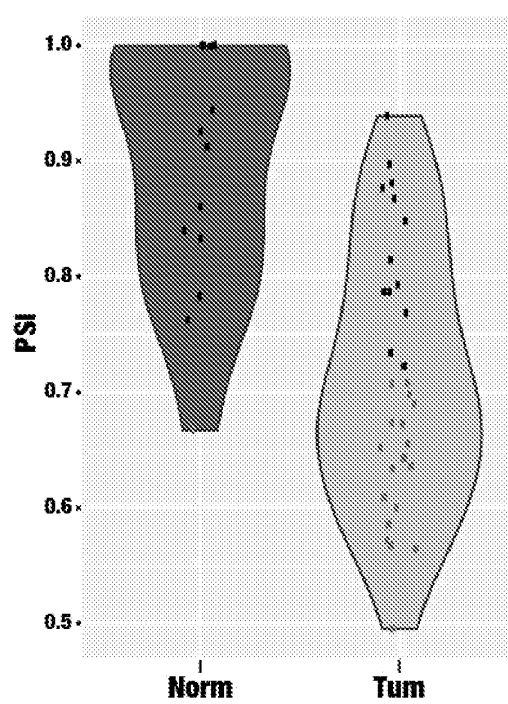


Figure 23(e)(continued)

48/71

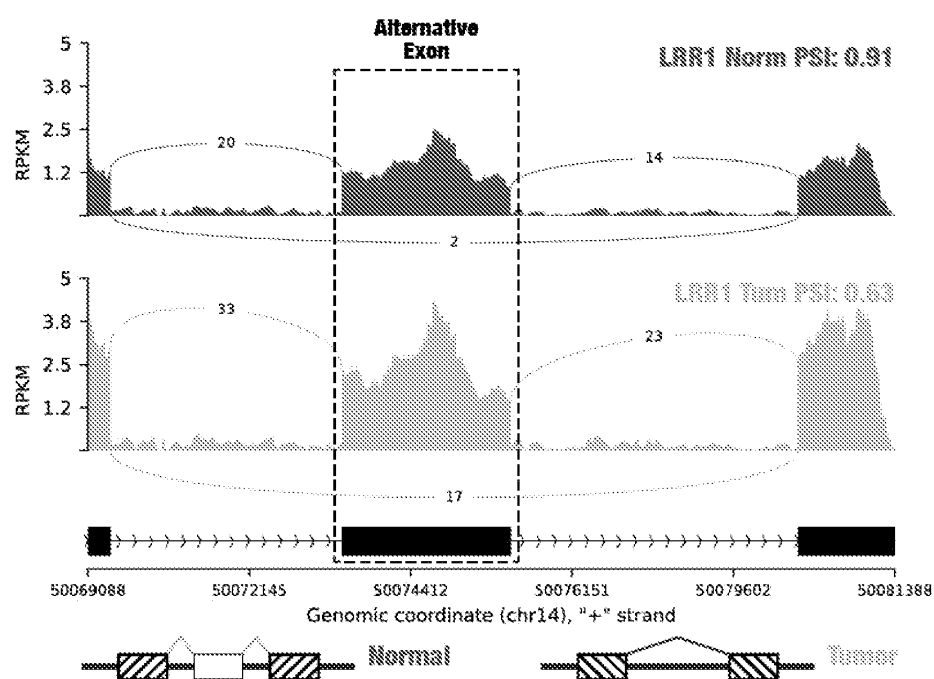


Figure 23(f)(continued)

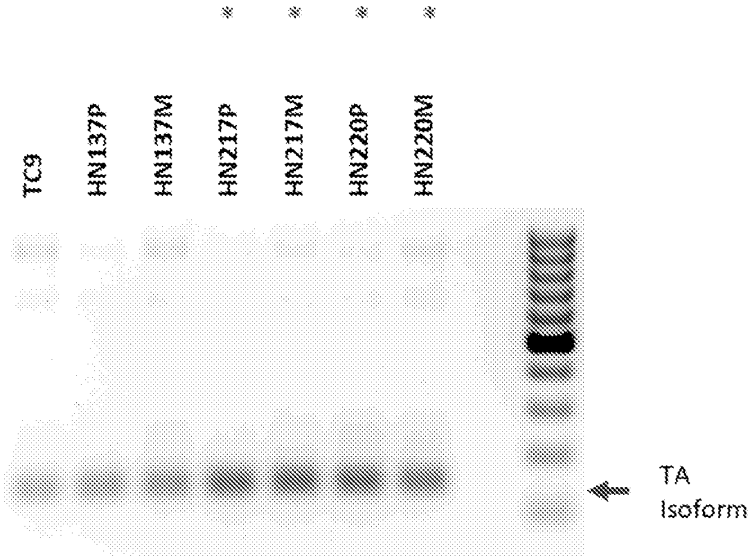


Figure 23(g)(end)

50/71

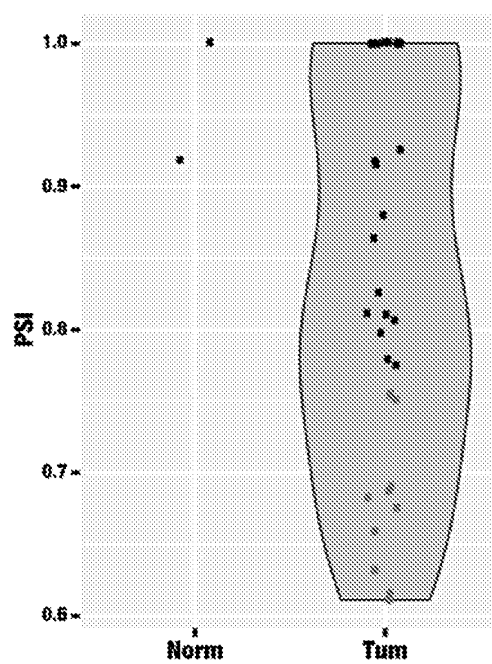


Figure 24(a)(continued)

51/71

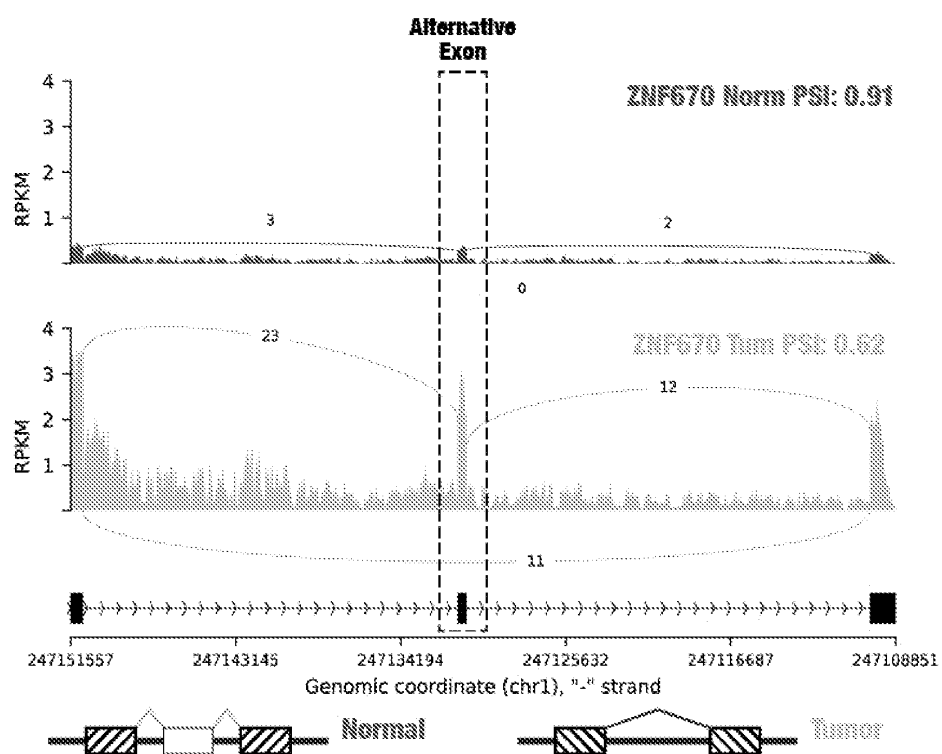


Figure 24(b)(continued)

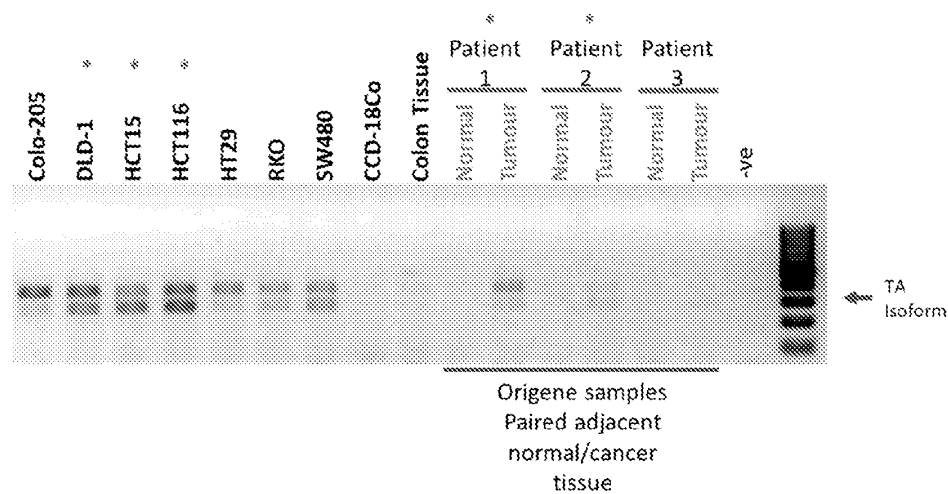


Figure 24(c)(continued)

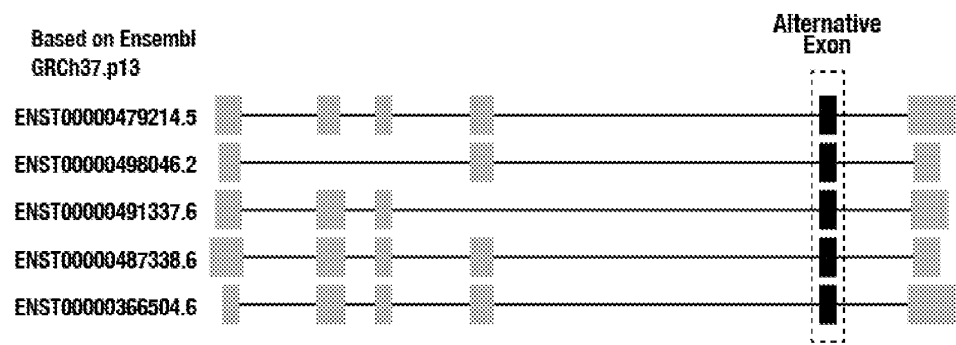


Figure 24(d)(continued)

55/71

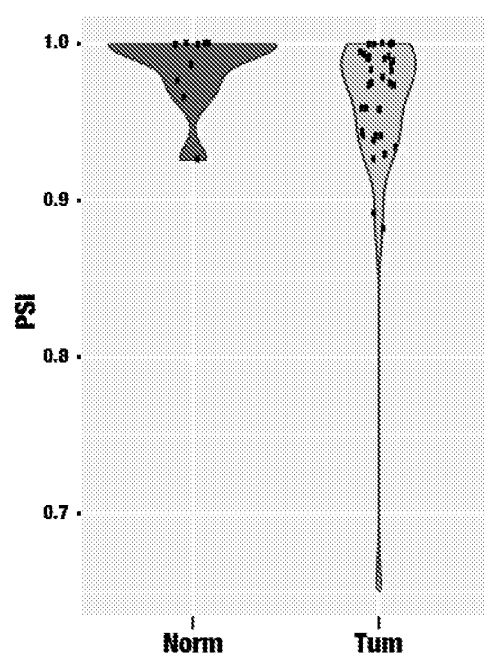


Figure 25(a)(continued)

56/71

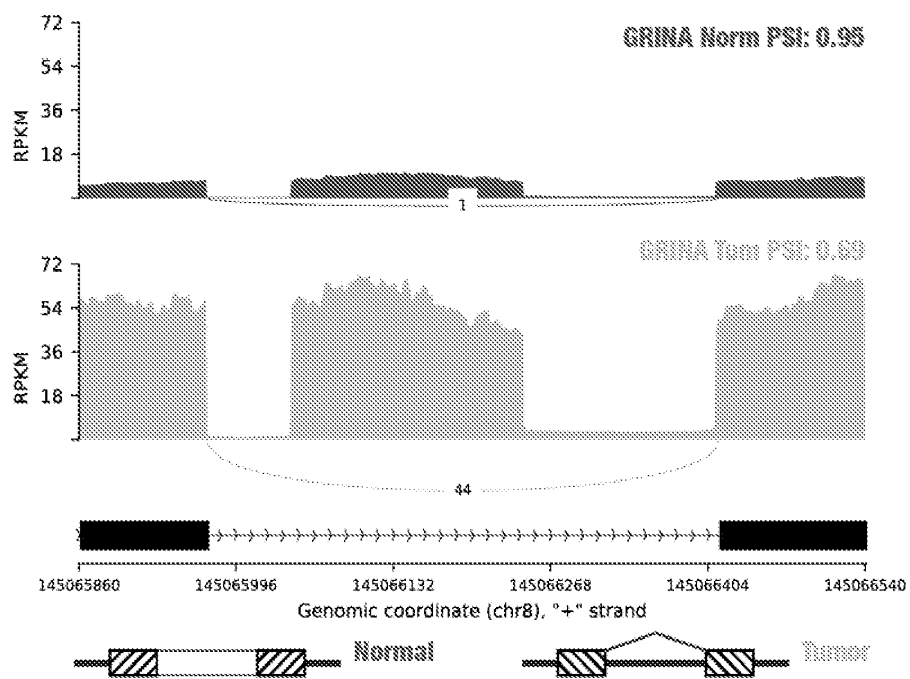


Figure 25(b)(continued)

57/71

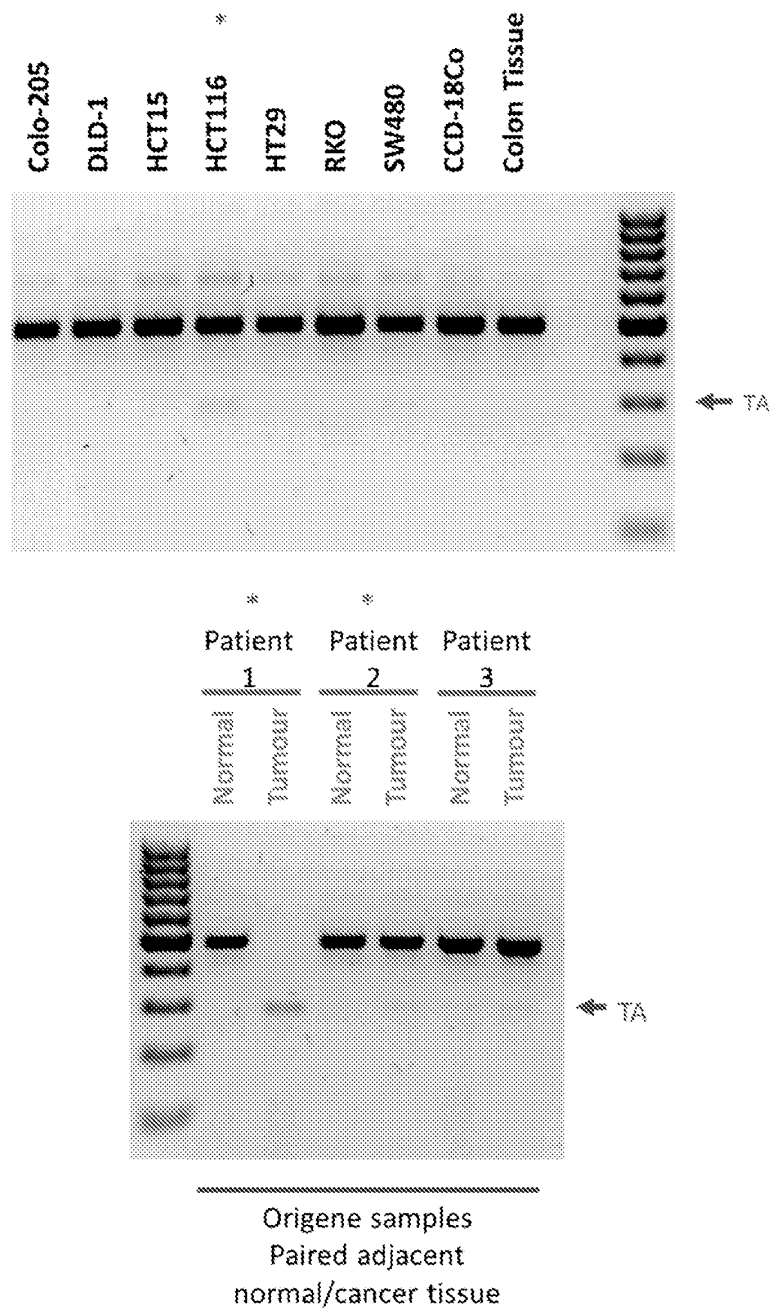


Figure 25(c)(continued)

58/71

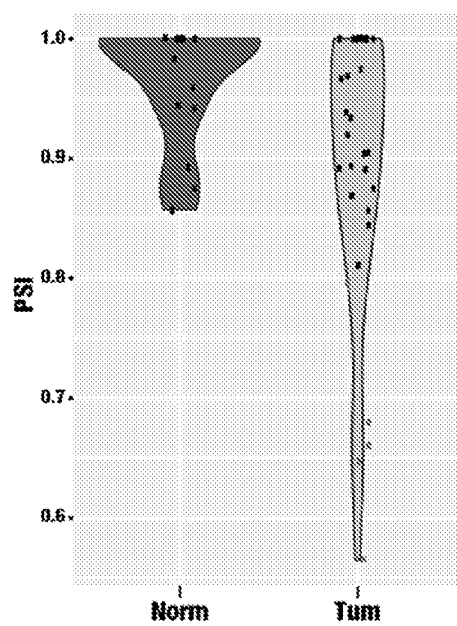


Figure 25(d)(continued)

59/71

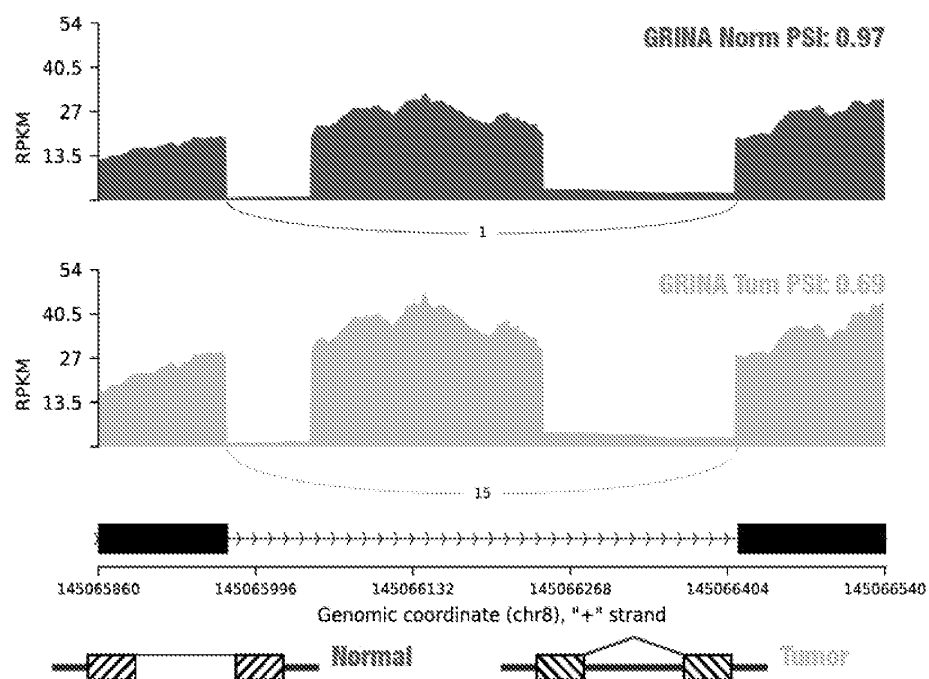


Figure 25(e)(continued)

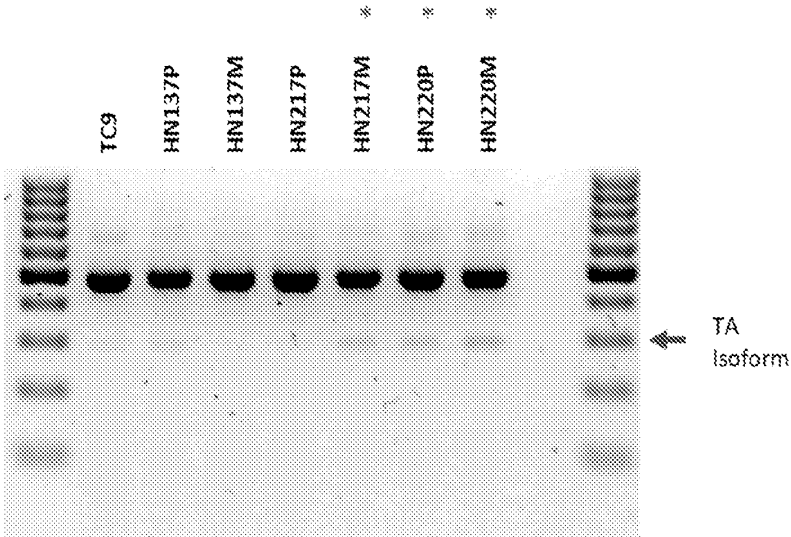


Figure 25(f)(end)

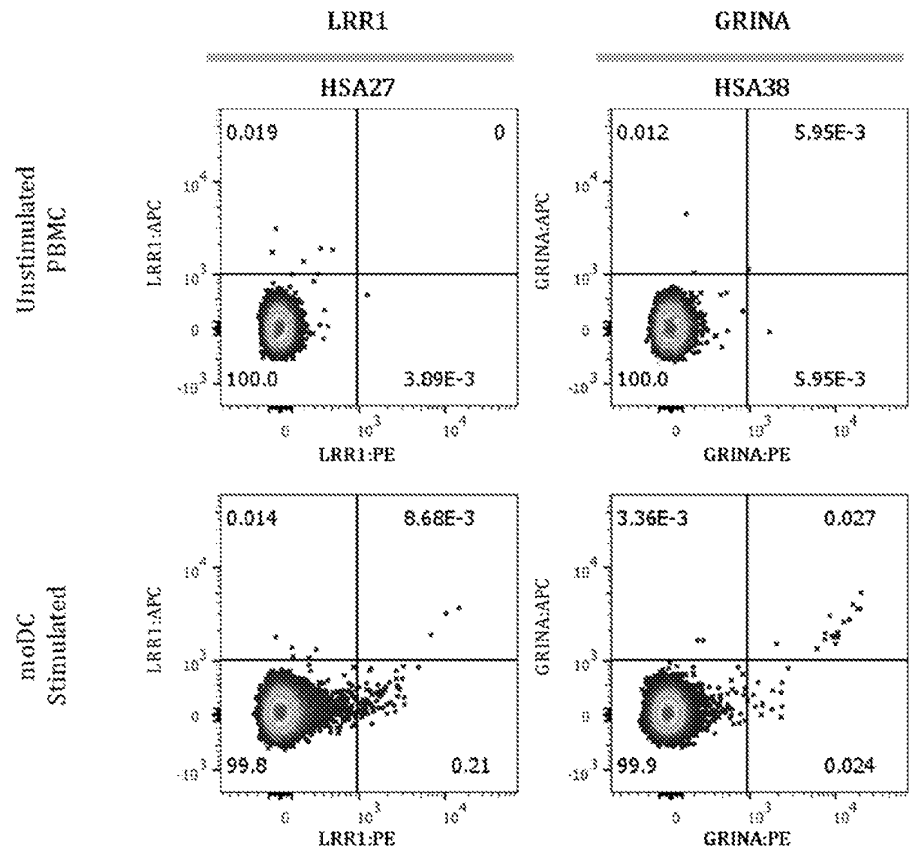


Figure 26(continued)

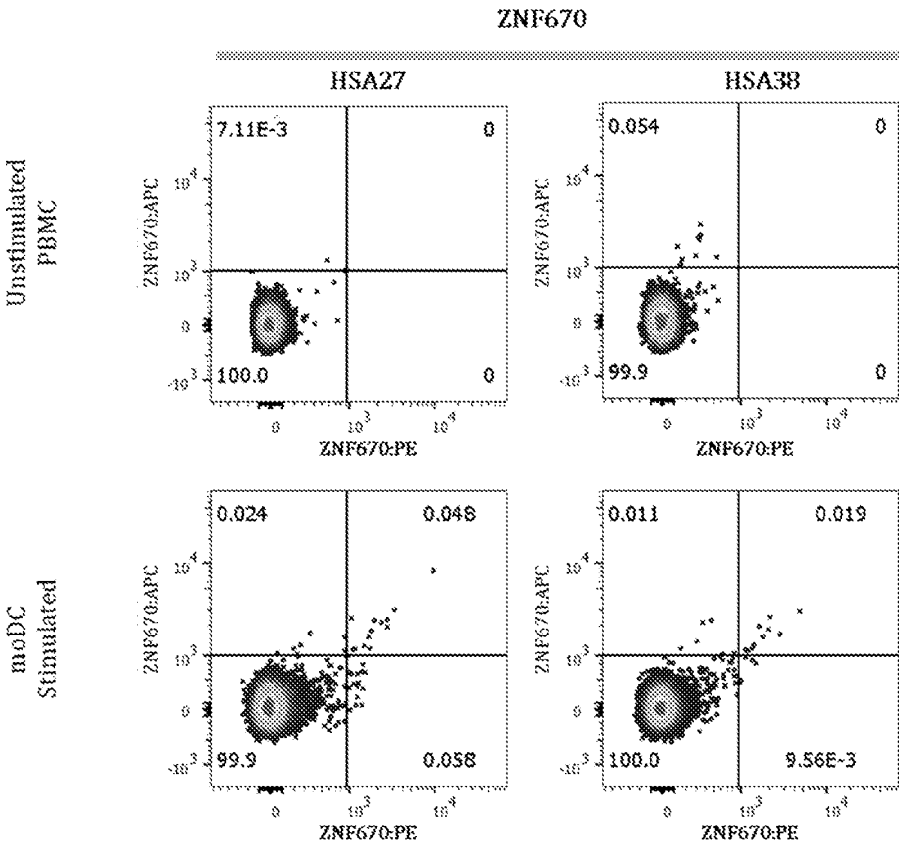


Figure 26(end)

Gene	Peptide Sequence	SEQ ID NO	1466	In-silico data		
				Occurrence	Δ PSI	Splice Event
LRR1	SYHSIPSLPRF	51	0.0019	6	0.249	SIE
MZF1	KWPPATETL	52	0.0023	6	-0.228	IRE

Figure 27(a)(continued)

Gene	Sequence Coordinates	Tumor Associated Exon
LRR1	chr14:50069088-50069186:+@chr14:50074118-50074833:+@chr14:50060974-50061383+	chr14:50069088-50069186:+@chr14:50080974-50081389:+
MZF1	chr19:59082361-59082796:-@chr19:59081711-59082796:-@chr19:59081711-59081894:-	chr19:59081711-59082796:-

Figure 27(b)(end)

65/71

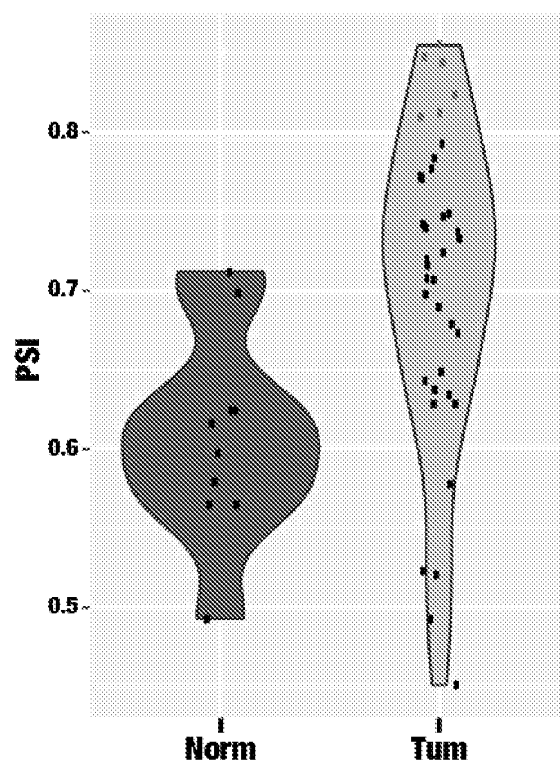


Figure 28(a)(continued)

66/71

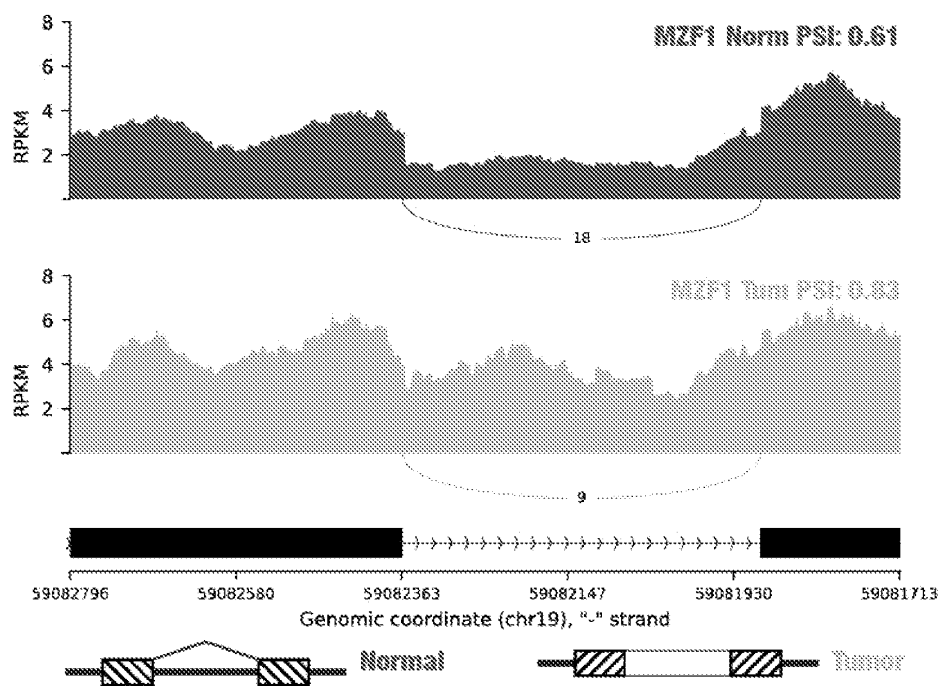


Figure 28(b)(continued)

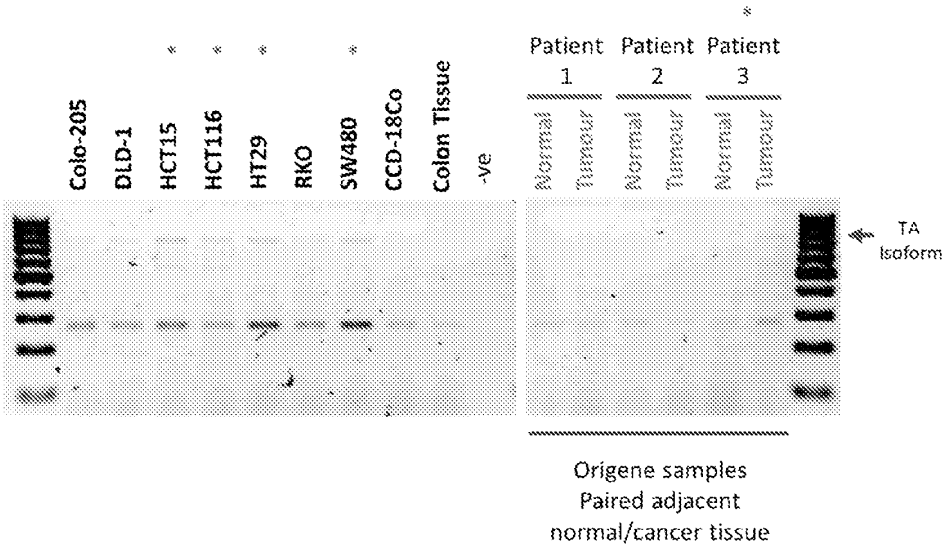


Figure 28(c)(end)

68/71

Event	Discovery Cohort TA Events	
Skip/inclusion of exon		1104
Intron retention		138
Alternate 5' splice sites		78
Alternate 3' splice sites		98

Figure 29(a)(continued)

69/71

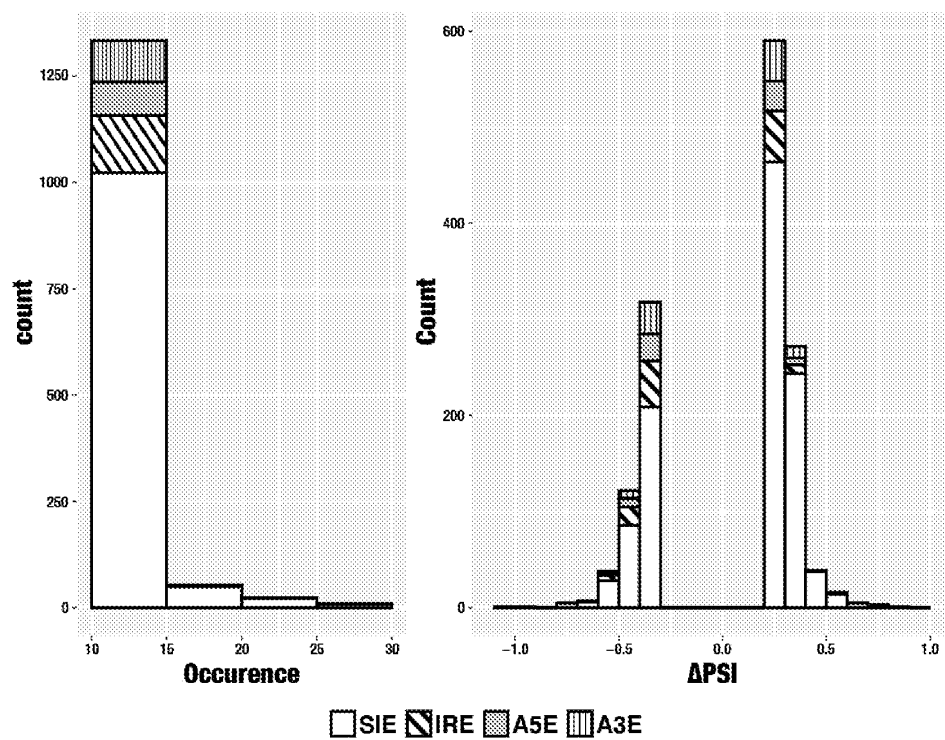


Figure 29(b)(continued)

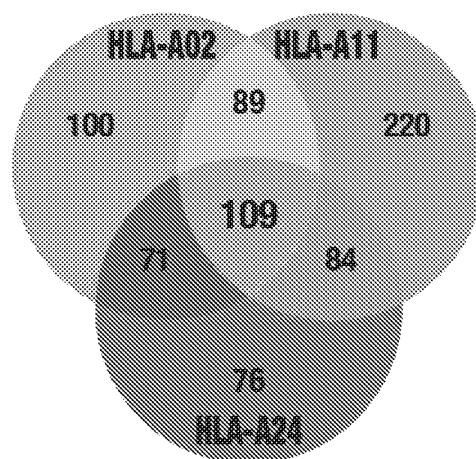


Figure 29(c)(end)

71/71

Gene	Peptide Sequence	SEQ ID NO	In-silico data		
			Occurrence	Δ PSI	Splice Event
CAMKK1	VTSPSRRSK	35	10	0.297	SIE
GRINA	SIRQAFIRK	38	6	0.330	IRE
LRR1	SLPRFGYRK	36	18	0.280	SIE

Figure 30