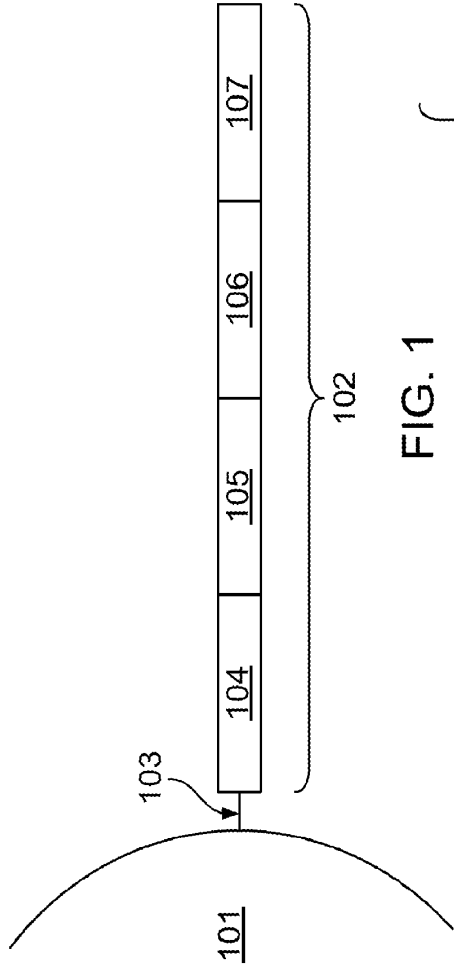
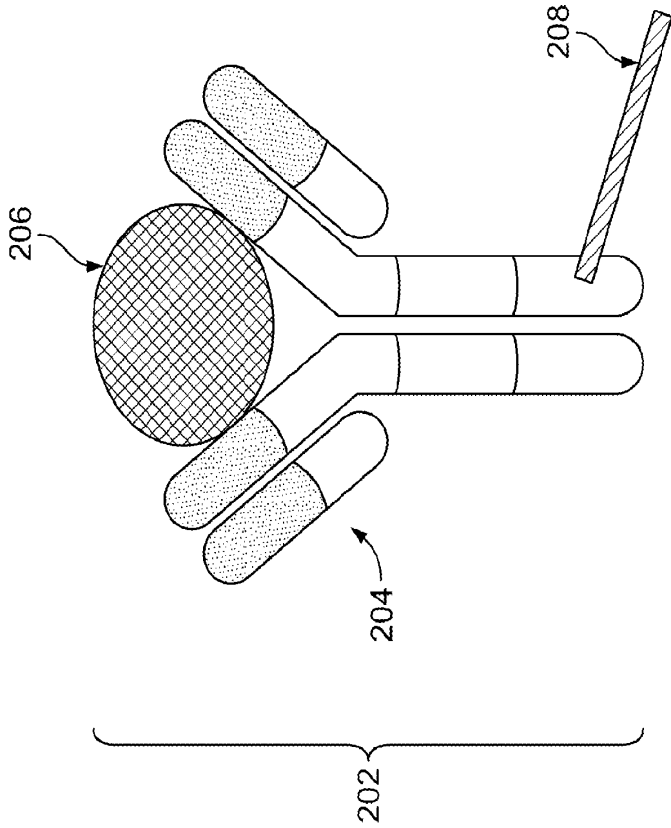




SUBSTITUTE SHEET (RULE 26)



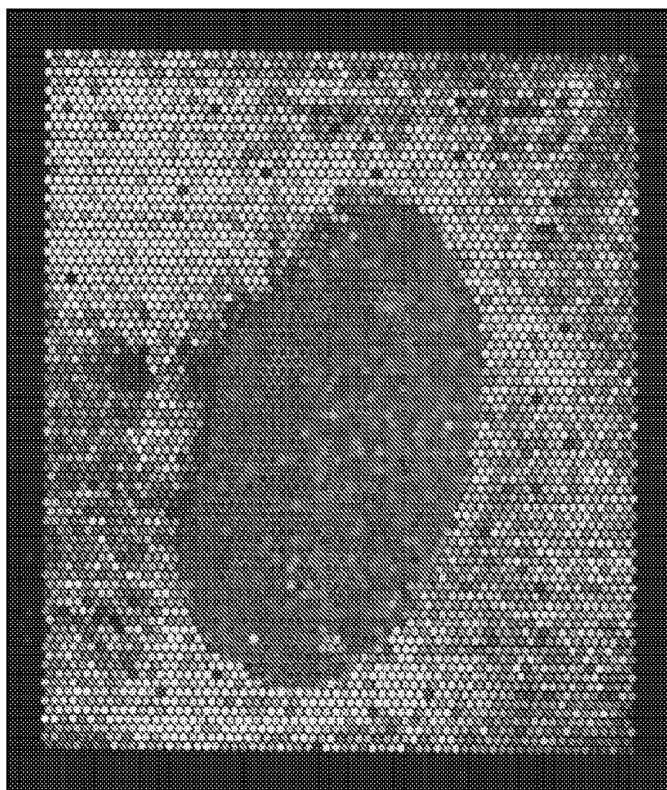
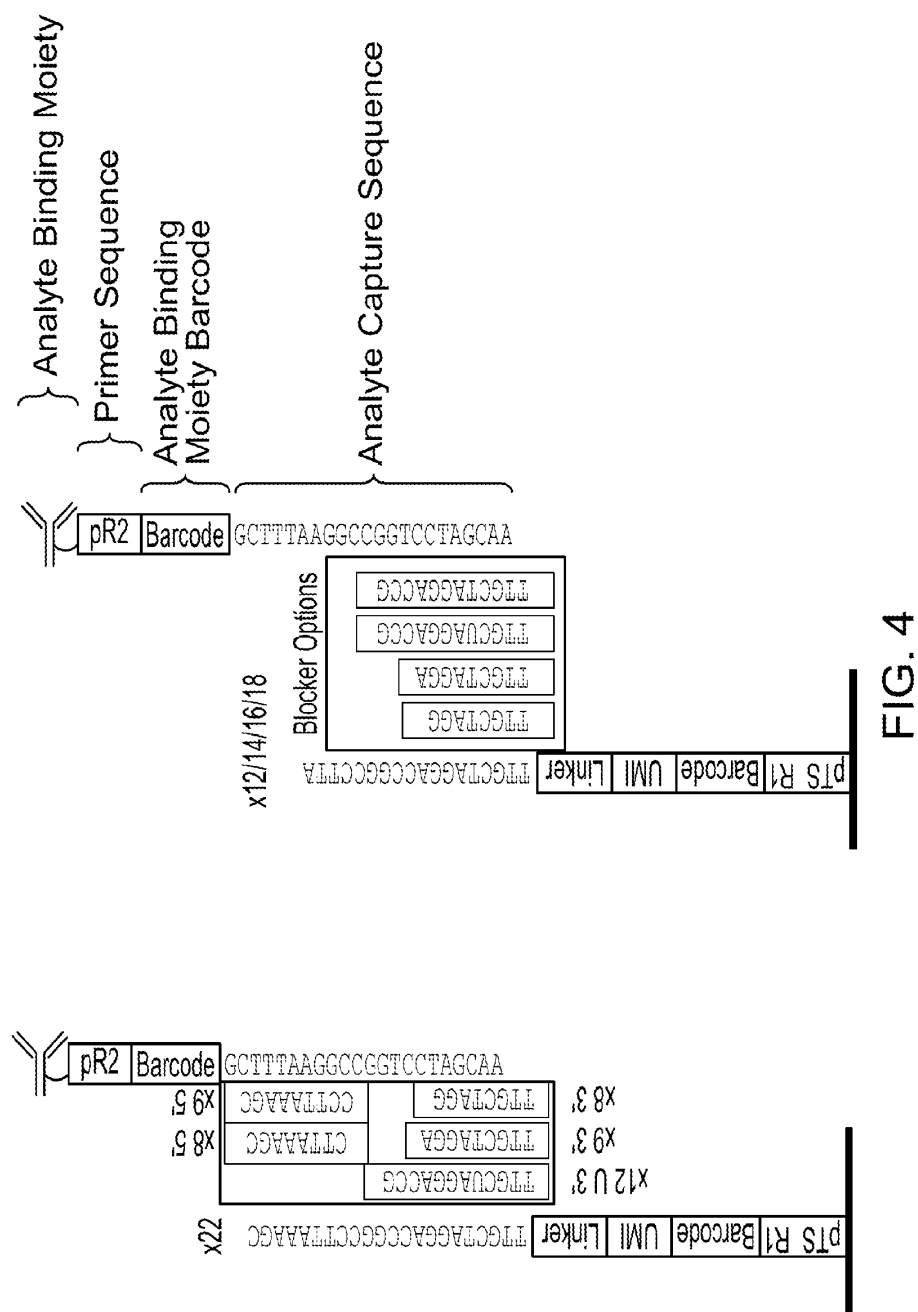


FIG. 3



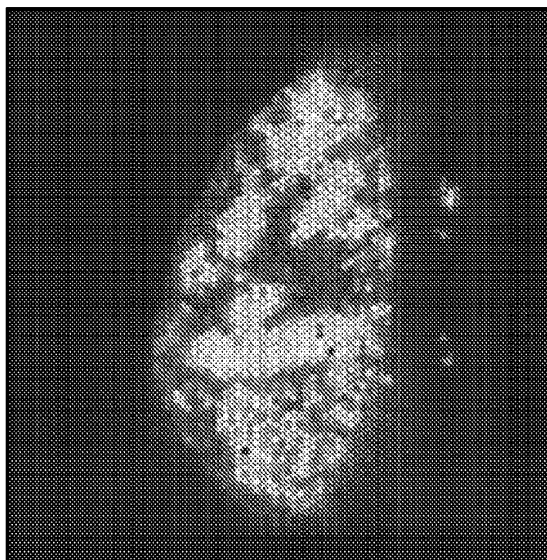


FIG. 5B

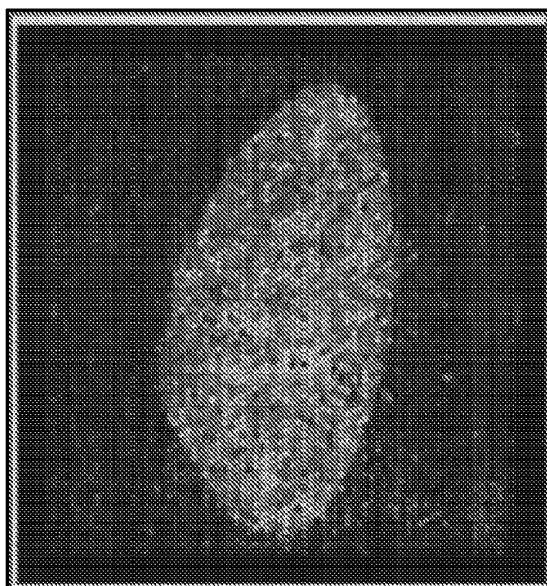


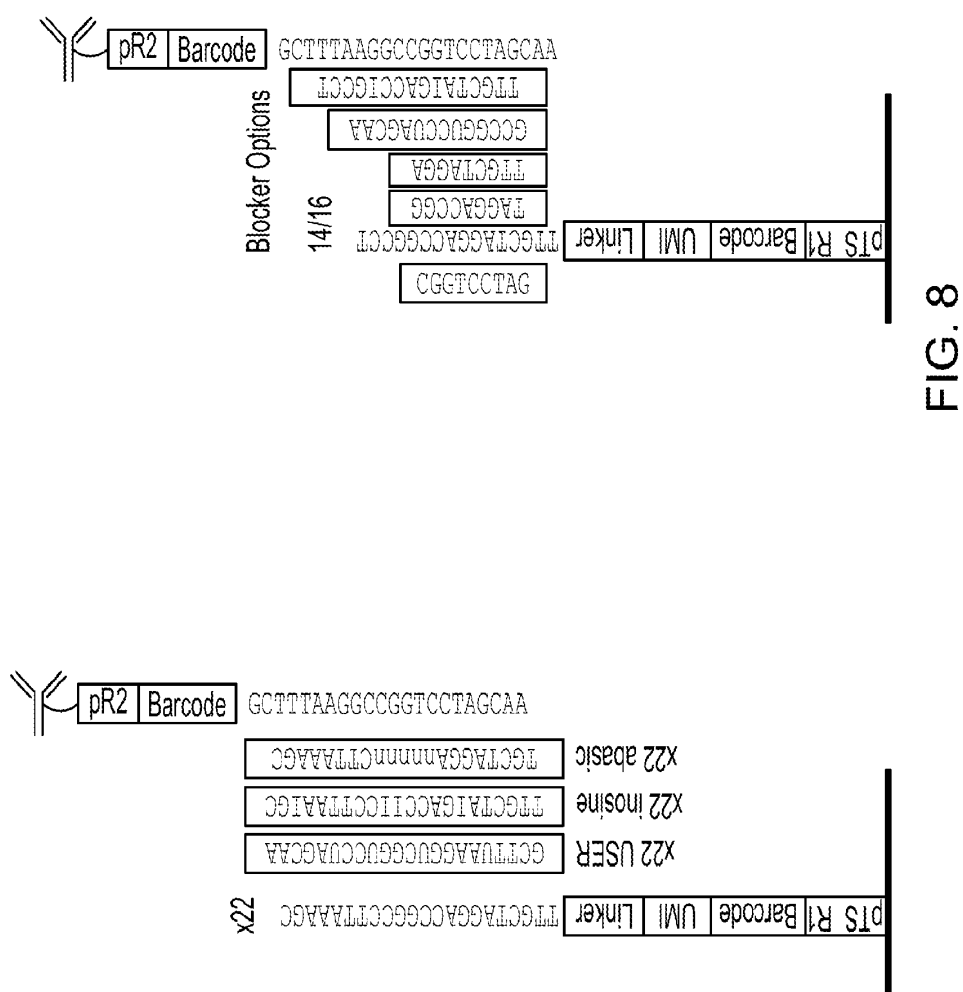
FIG. 5A

Analysis ID	Capture Sequence	Blocker	Antibody: Valid Barcodes	Antibody: Sequencing Saturation	Antibody: Fraction Reads with any X22 6 Sequence	Antibody: Fraction Antibody Reads Usable	Antibody: Fraction Unknown Antibody	Antibody: Antibody Reads in Spots	Antibody: Median UMIs per Spot at 1k Antibody Reads Usable per Spot
1032482	x12	x12 USER	98.9%	71.7%	83.6%	59.7%	20.0%	75.3%	698
1032483		x9	99.0%	69.6%	87.3%	55.4%	16.4%	66.9%	722.5
1032484		x8	99.0%	56.1%	91.8%	49.9%	11.7%	57.1%	780
1032485	x14	x12 USER	99.0%	53.3%	93.6%	62.8%	10.5%	70.8%	788
1032486		x9	99.0%	63.0%	92.1%	54.9%	12.0%	63.0%	757
1032487		x8	99.0%	49.9%	92.6%	52.7%	11.3%	60.0%	806
1032488	x16	x12 USER	98.9%	32.7%	97.0%	23.9%	7.4%	26.1%	839
1032489		x9	99.0%	29.8%	97.9%	26.6%	6.2%	28.6%	866.5
1032490		x8	99.0%	29.0%	97.7%	33.9%	6.4%	36.6%	780
1032491	x18	x12 USER	98.9%	31.9%	97.4%	28.0%	6.8%	30.4%	830
1032492		x9	99.0%	30.9%	97.9%	22.5%	6.2%	24.2%	823
1032493		x8	99.0%	22.4%	98.3%	34.7%	5.7%	37.2%	890
1032494	x22	x12 USER	99.0%	31.7%	97.6%	31.6%	6.6%	34.1%	838
1032495		x9	99.0%	23.8%	98.1%	15.4%	6.2%	16.6%	799.5
1032496		x8	99.0%	23.8%	98.0%	22.0%	6.2%	23.7%	874
1032782	TotalSeqA ctrl	dT25	99.1%	22.8%	0.1%	34.9%	2.1%	36.1%	1017

FIG. 6

Analysis ID	Capture Seq Length	Blocker	Valid Barcodes	Reads Mapped Confidently to Transcriptome	Fraction Reads Usable	Fraction Reads with Primer or Homopolymer Sequence	Fraction Reads with Any Switch Oligo Sequence	Fraction Reads in Spot	Median Genes per Spot (50K rps)	Median UMI Counts per Spot (50K rps)	Fraction Ribo Protein UMI Counts	Fraction Mito UMI Counts
1033939	x12	x12U	98.6%	71.0%	52.8%	38.2%	76.9%	76.3%	2820	7315	15.7%	6.8%
1033940		x9	98.4%	68.6%	50.7%	41.4%	71.1%	75.6%	3801	11014	21.2%	4.2%
1033925		x8	98.5%	77.6%	56.4%	30.1%	59.8%	74.2%	4576	14722	24.4%	2.9%
1033926	x14	x12U	98.6%	77.3%	48.8%	37.6%	73.7%	64.5%	3578	10222	18.1%	2.2%
1033927		x9	98.6%	80.7%	63.9%	25.2%	50.5%	80.8%	5020	18293	24.7%	3.1%
1033928		x8	98.5%	81.2%	63.4%	23.6%	50.4%	79.6%	4978	18026	25.0%	2.8%
1033929	x16	x12U	98.5%	75.0%	51.9%	37.6%	73.9%	71.1%	3432	9432	14.9%	4.0%
1033930		x9	98.6%	83.2%	63.1%	24.8%	49.8%	77.3%	4699	16830	26.4%	2.5%
1033931		x8	98.4%	82.2%	67.6%	20.9%	48.8%	84.0%	5200	19493	27.3%	2.9%
1033932	x18	x12U	98.5%	73.6%	45.5%	41.0%	79.5%	63.6%	3537	10709	16.1%	3.3%
1033933		x9	98.6%	82.3%	58.7%	24.3%	49.8%	72.7%	3794	10856	25.9%	2.1%
1033934		x8	98.6%	82.9%	61.5%	23.9%	50.7%	75.6%	4932	17412	26.3%	2.2%
1033935	x22	x12U	98.6%	73.1%	49.0%	41.2%	75.4%	69.2%	2809	6751	15.8%	1.4%
1033936		x9	98.5%	78.8%	54.4%	30.1%	60.3%	70.8%	3556	10418	21.5%	3.4%
1033937		x8	98.5%	81.8%	46.3%	27.5%	58.3%	57.8%	3142	8494	20.9%	2.4%
1033938	TotalSeqA	dT25	98.6%	84.9%	61.9%	19.9%	47.6%	74.3%	3068	7453	24.8%	2.5%

FIG. 7



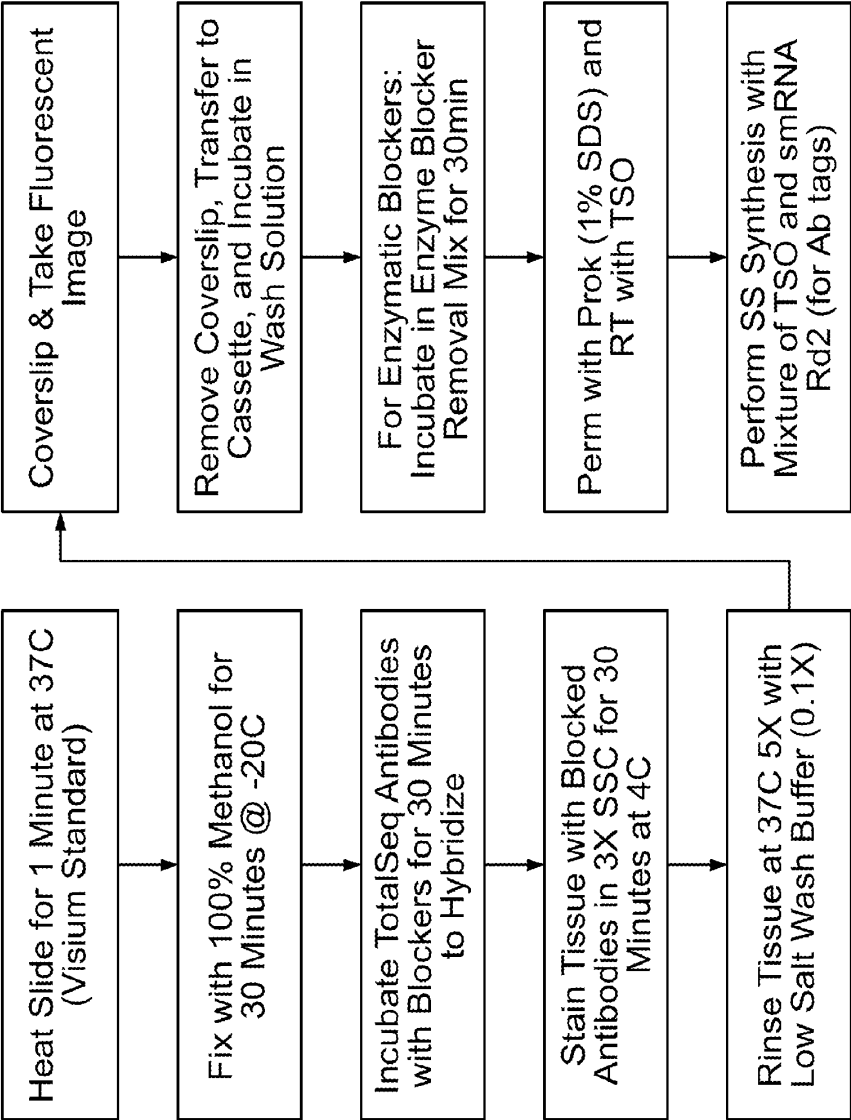


FIG. 9

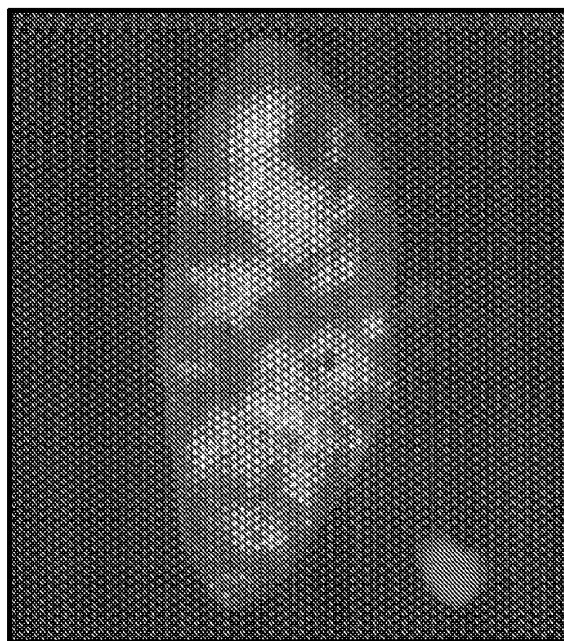


FIG. 10B

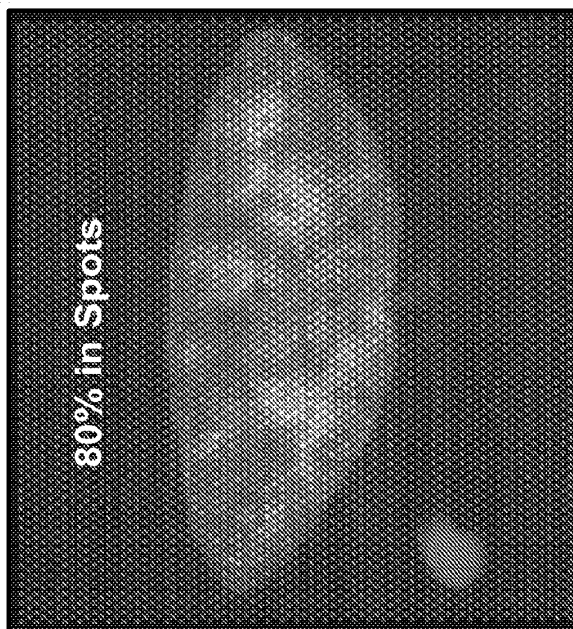


FIG. 10A

Analysis ID	Capture Seq Length	Blocker	Reads Mapped Confidently to Transcript	Fraction Reads Usable	Fraction Reads with Primer or Homopolymer Sequence	Fraction Reads with Any Switch Oligo Sequence	Fraction Reads in Spot	Fraction Reads in Spots	Median Genes per Spot (50K rps)	Median UMI Counts per Spot (50K rps)	Fraction Ribo Protein UMI Counts	Fraction Mito UMI Counts
1046081	x14	x9 (3)	81.37%	62.9%	30.0%	56.1%	79.6%	79.6%	3886	10936	18.3%	1.3%
1046083		x9 (5)	79.41%	59.0%	34.5%	62.7%	76.3%	76.3%	3163	7832	17.8%	1.2%
1046085		x9 (slide)	82.94%	66.0%	28.6%	58.7%	81.6%	81.6%	3776	10630	18.3%	1.2%
1046086		x14 USER	81.09%	65.7%	33.6%	64.5%	83.9%	83.9%	3793	10591	18.4%	0.9%
1046088	x16	x9 (5)	79.22%	64.6%	36.4%	67.1%	83.7%	83.7%	2503	5652	16.3%	1.7%
1046090		x14 USER	79.53%	64.0%	39.7%	70.4%	83.1%	83.1%	2858	6605	17.3%	0.9%
1046092		x14 EndoIV	81.75%	71.0%	32.3%	60.9%	90.3%	90.3%	3354	8436	16.9%	2.2%
1046093		x16 mismatch	83.62%	68.0%	27.9%	55.7%	84.3%	84.3%	3570	9504	18.9%	2.0%
1046096	x22	x22 USER	80.40%	69.8%	38.7%	70.6%	90.3%	90.3%	3512	9416	15.0%	0.6%
1046099		x22 inosine	81.06%	65.9%	34.6%	64.5%	84.3%	84.3%	2621	5968	16.9%	1.2%
1046100		x22 EndoIV	78.80%	67.7%	40.3%	69.0%	89.4%	89.4%	3148	8015	14.6%	1.8%
1046102		x22 mismatch	81.47%	67.0%	31.2%	60.3%	85.0%	85.0%	3812	10397	16.6%	1.3%

FIG. 11

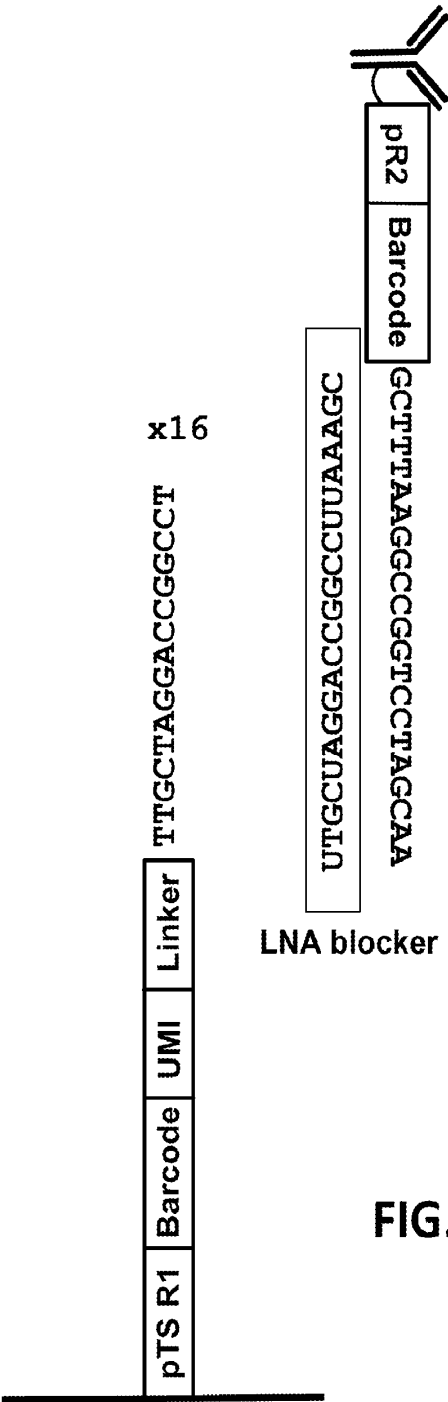


FIG. 12



FIG. 13A

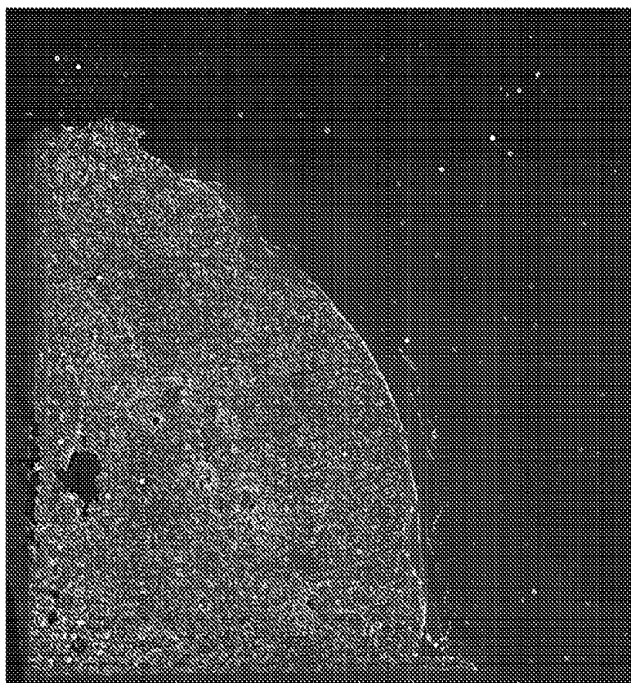
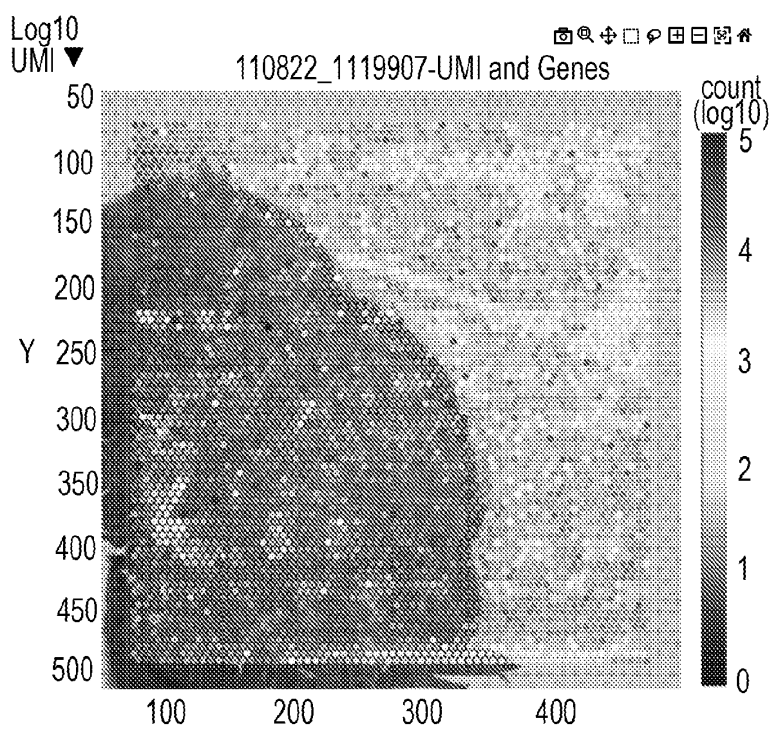
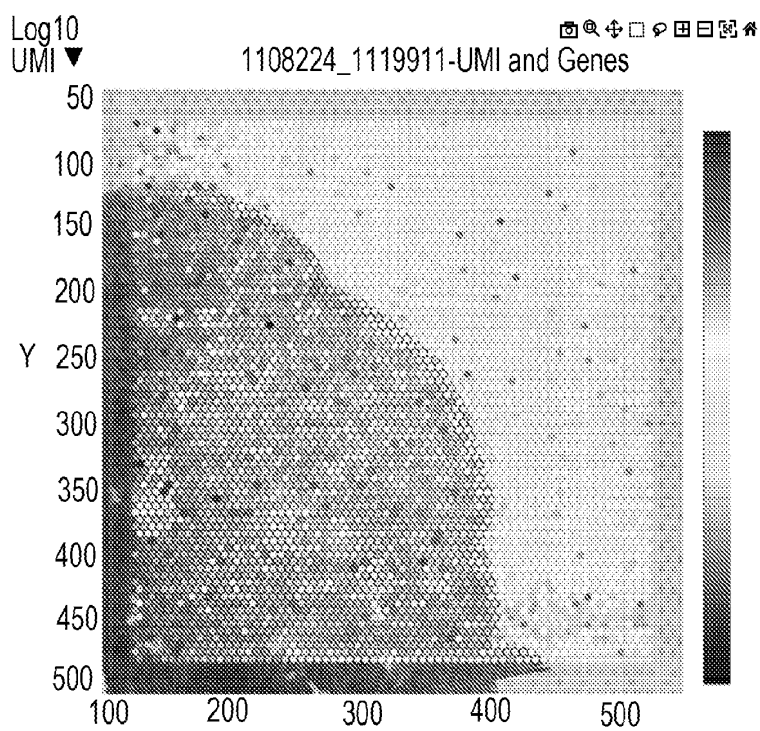


FIG. 13B

SUBSTITUTE SHEET (RULE 26)

**FIG. 14A****FIG. 14B**