

Figure 1A

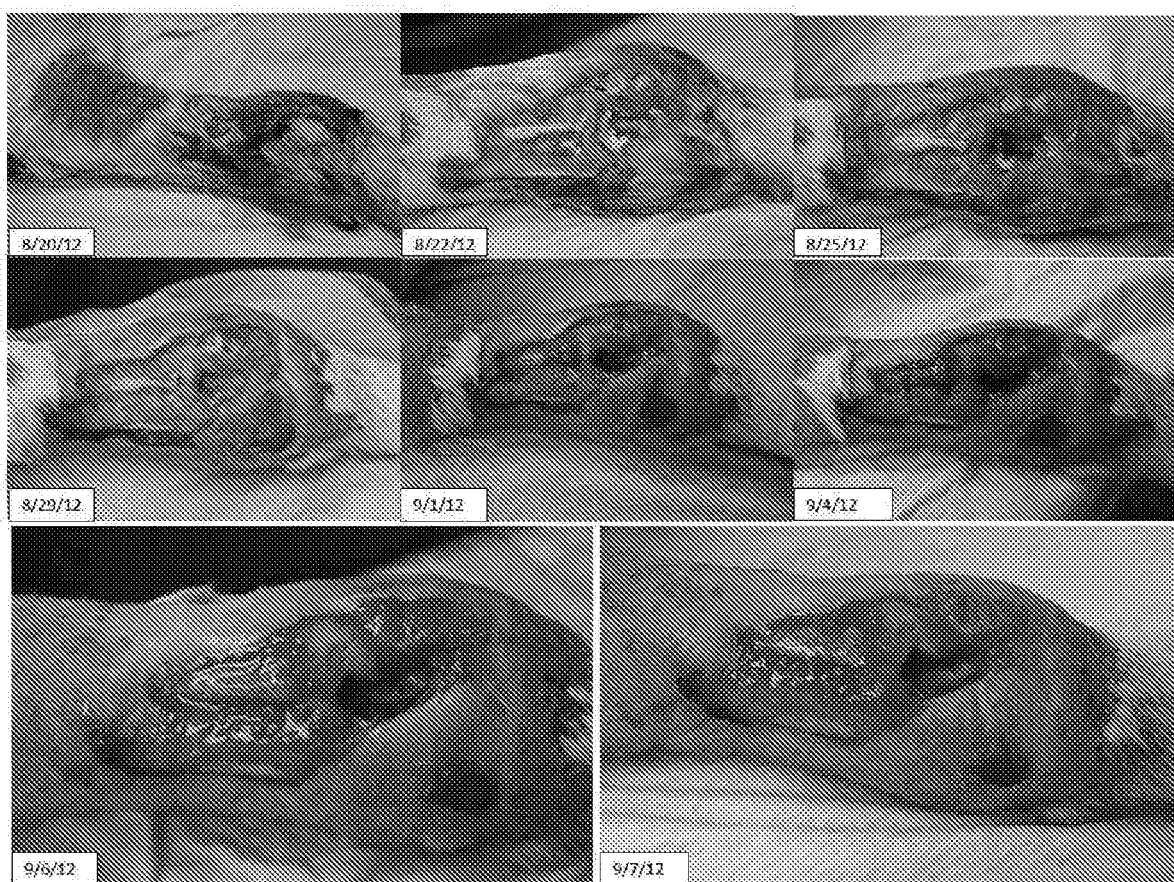


Figure 1B



Figure 2A

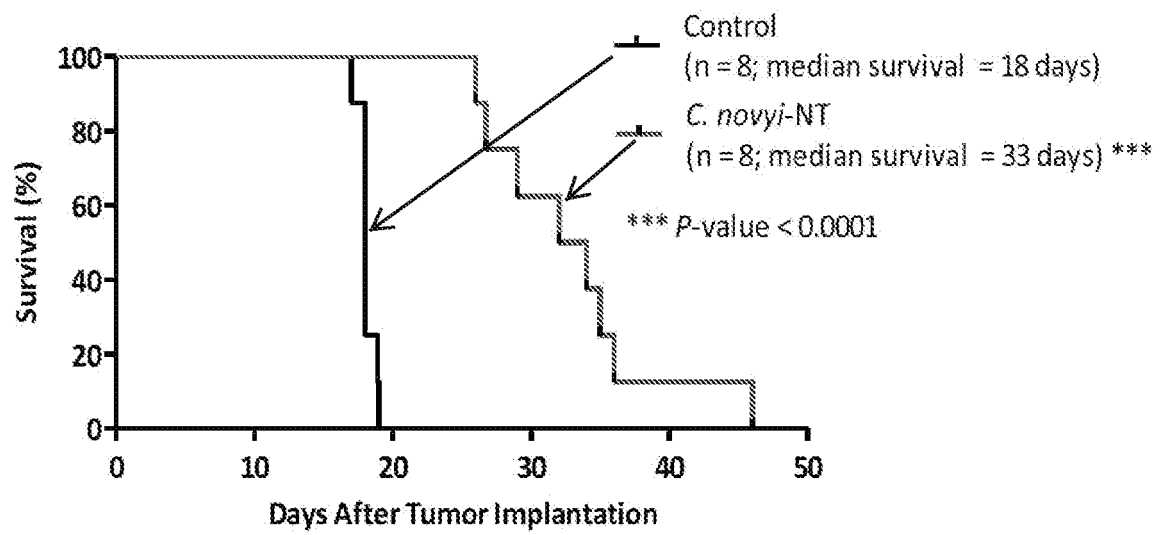


Figure 2B

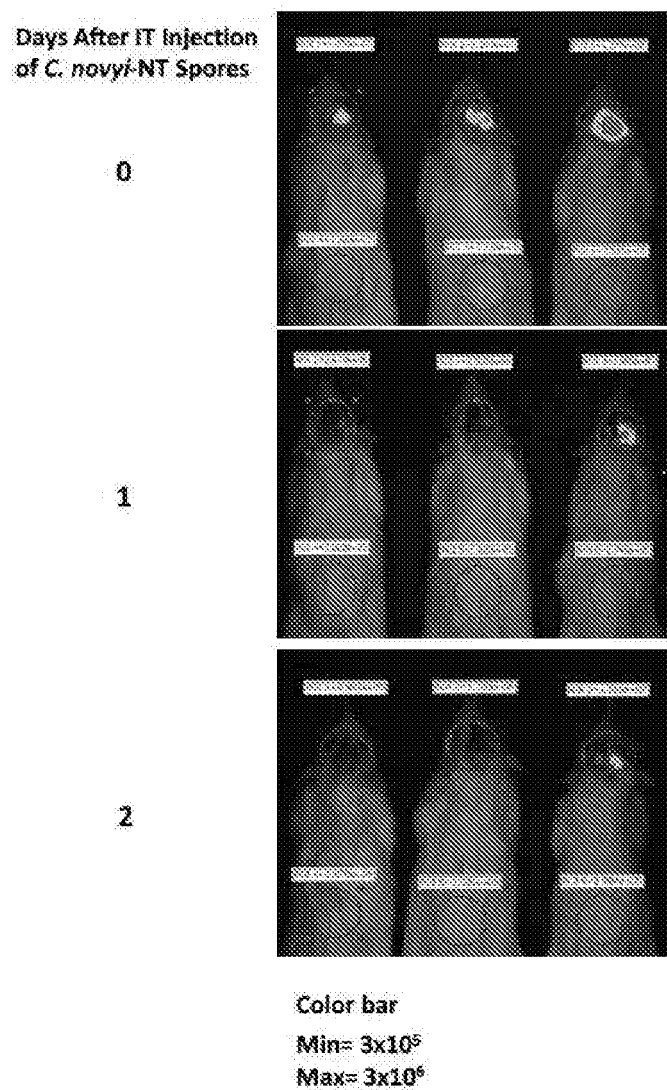


Figure 2C

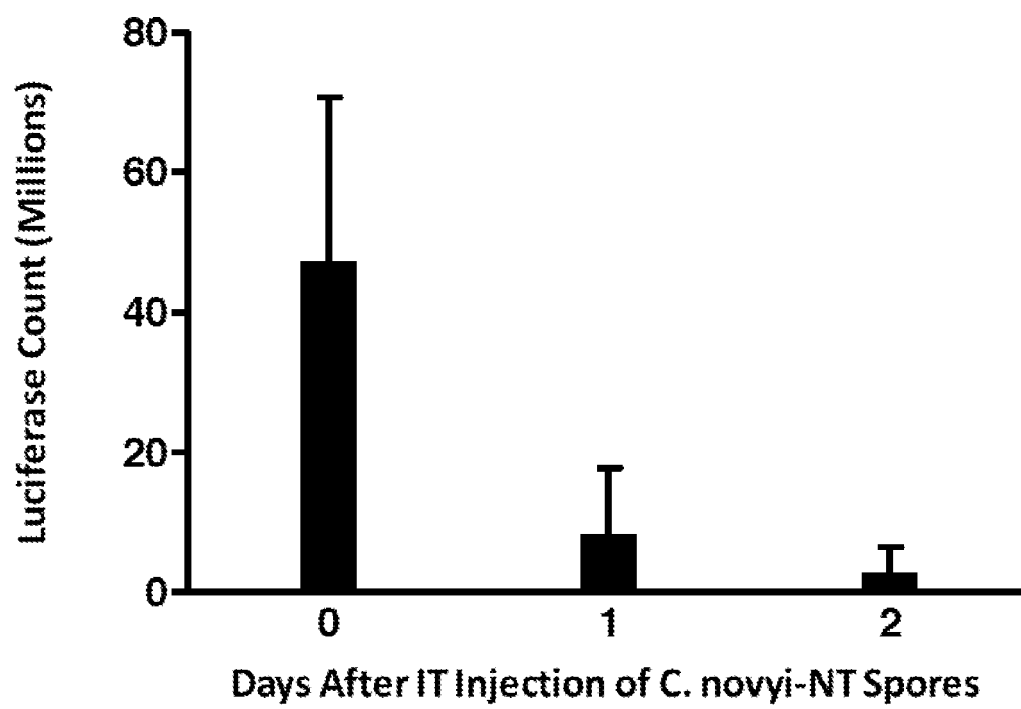


Figure 3A

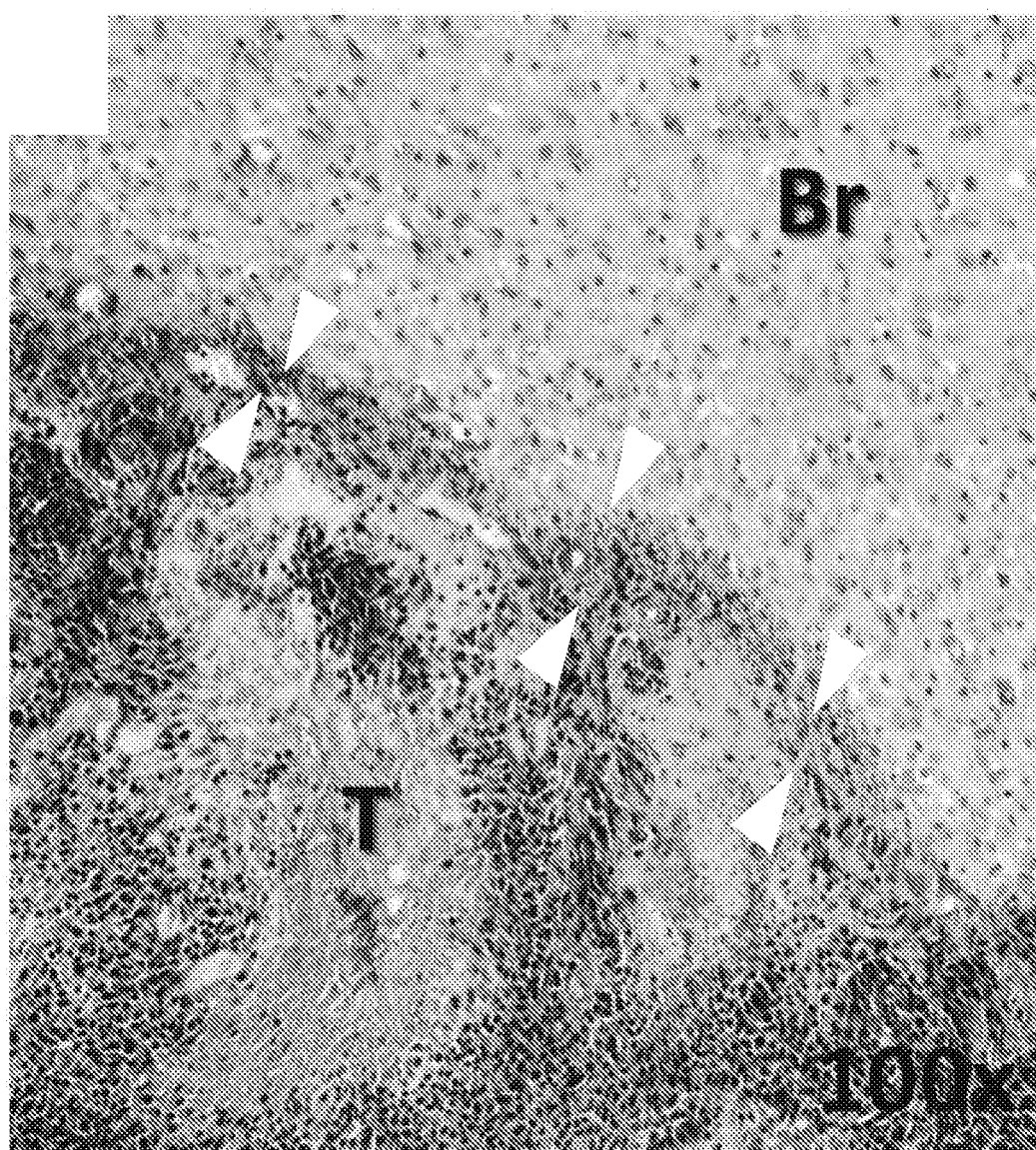


Figure 3B

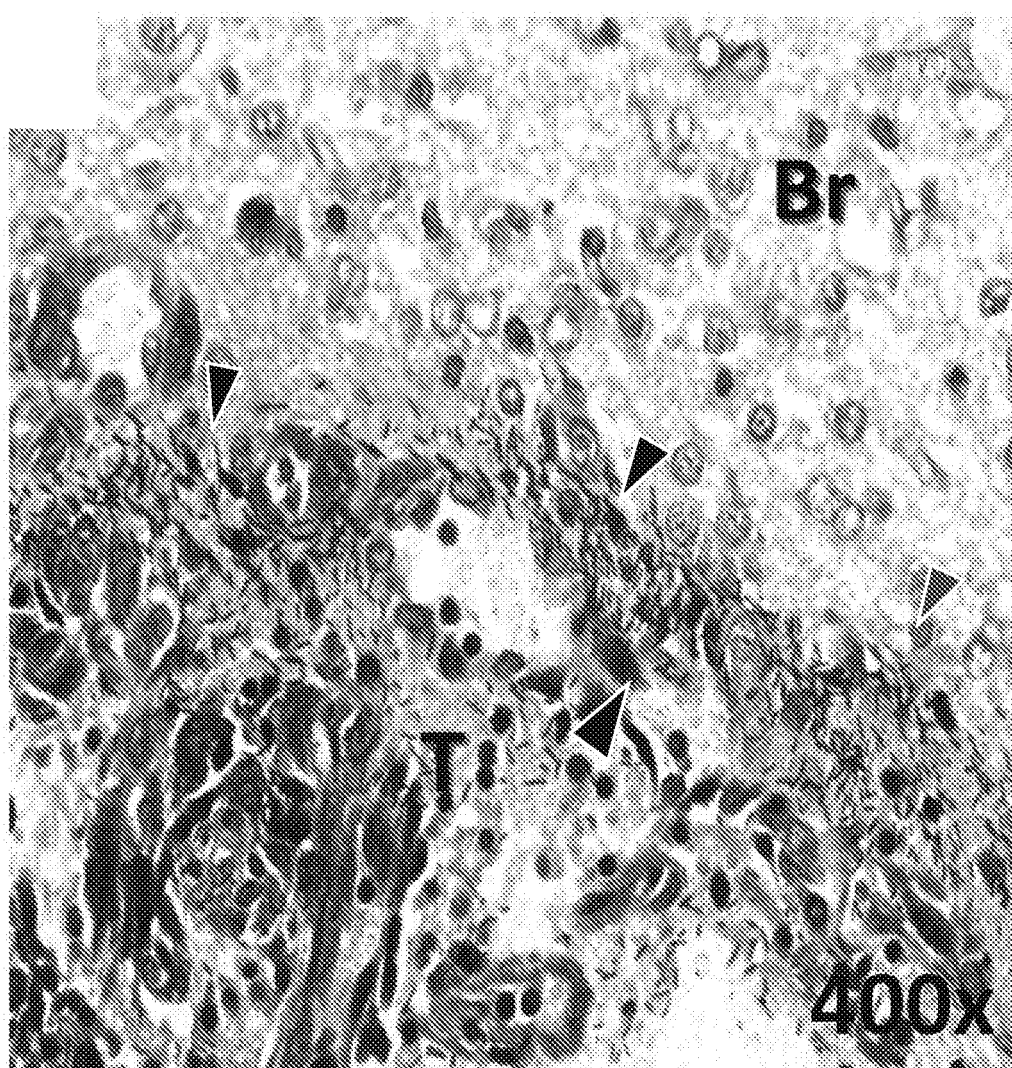


Figure 4A

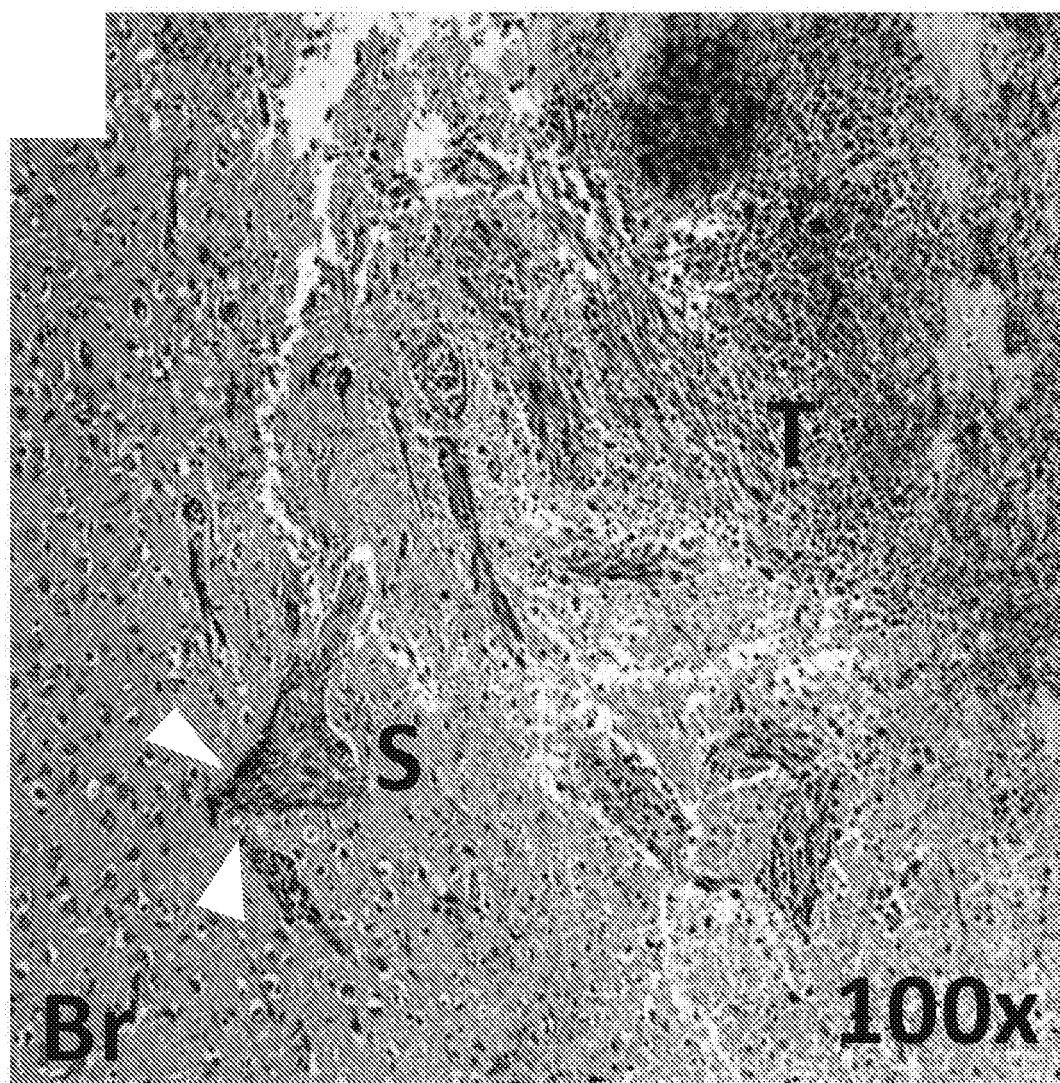


Figure 4B

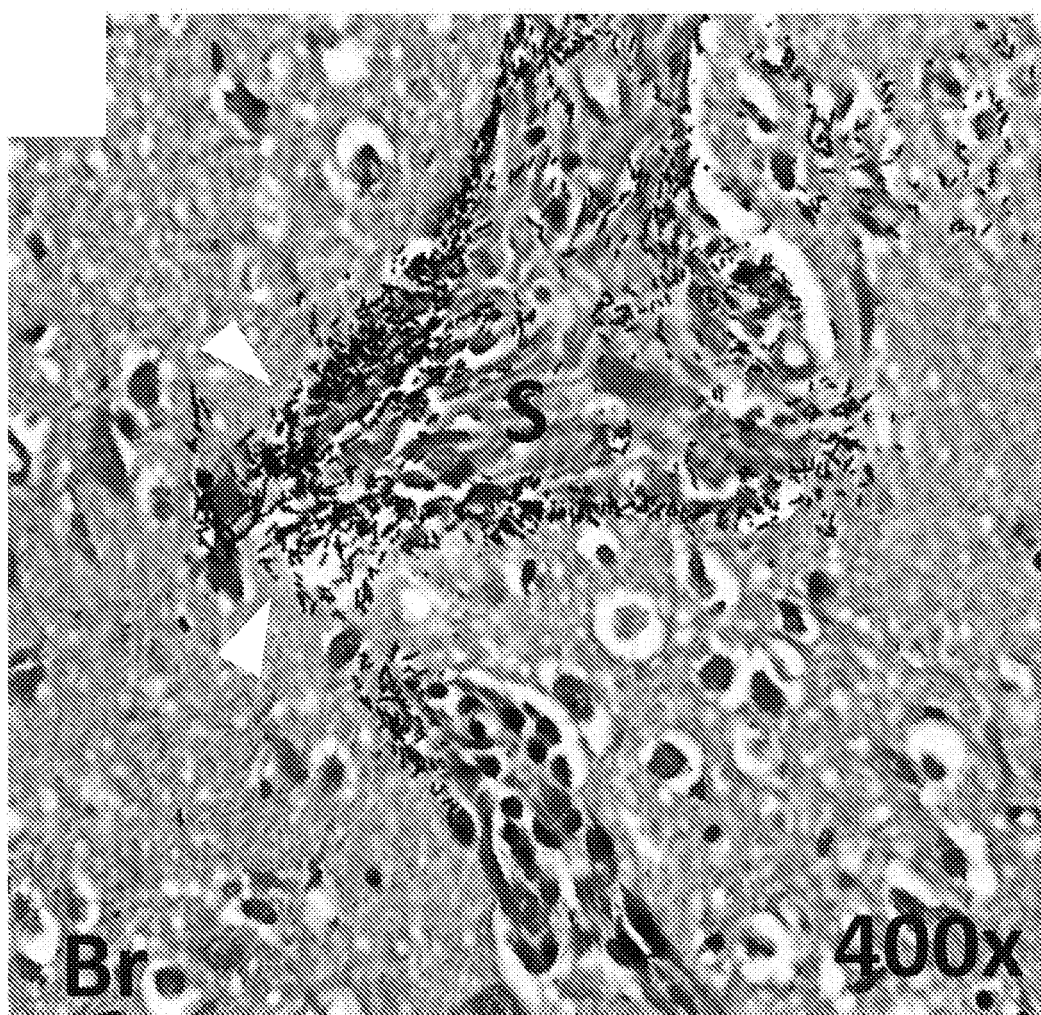


Figure 5

		04-R03	16-R03	16-R02	11-R04	11-R02
Sample Characteristics	Tumor Type	STS	STS	STS	STS	STS-PNST
	Tumor Location	Left antechamber	Left forearm	Left thigh	Right forearm	Left thigh
	Sample Type	FFPE	FFPE	FFPE	FFPE	FFPE
	Sample Acquisition	Pre-study initiation	Pre-study initiation	Post-study initiation	Pre-study initiation	Pre-study initiation
	Pathological Tumor Purity	90%	70%	70%	70%	80%
Analysis Characteristics	Mutation based Tumor Purity	71%	37%	41%	51%	45%
	Source of normal DNA	Blood	Blood	Blood	Blood	Blood
	Analysis type	Next-generation sequencing	Next-generation sequencing	Next-generation sequencing	Next-generation sequencing	Next-generation sequencing
	Enrichment approach	In solution DNA capture	In solution DNA capture	In solution DNA capture	In solution DNA capture	In solution DNA capture
	Genome regions analyzed	30,194 coding genes	30,194 coding genes	30,194 coding genes	30,194 coding genes	30,194 coding genes
Sequencing Characteristics	Bases sequenced	32,893,252 bases	32,893,252 bases	32,893,252 bases	32,893,252 bases	32,893,252 bases
	Sequence Read Length	100 bp	100 bp	100 bp	100 bp	100 bp
	Number of somatic sequence alterations identified	8	2	4	3	14
	Number of somatic copy number alterations identified	2	0	0	0	17
	Sequenced Bases Mapped to Genome	14,429,862,200	21,425,345,200	12,124,067,000	19,196,019,800	15,780,857,800
Overall Statistics (Tumor)	Sequenced Bases Mapped to Target Regions	6,089,590,437	9,789,715,947	4,586,071,422	11,459,270,433	10,233,153,813
	Fraction of Sequenced Bases Mapped to Target Regions	42%	46%	40%	60%	65%
	Bases in target regions with at least 10 reads	36,637,164	37,343,313	36,043,139	50,430,237	46,966,409
	Fraction of bases in target regions with at least 10 reads	92%	94%	91%	94%	91%
	Sequenced Bases Mapped to Genome	19,693,458,500	14,561,175,800	17,329,903,700	15,677,311,300	14,959,139,100
Sequencing Reads at Each Base (Tumor)	Sequenced Bases Mapped to Target Regions	7,318,085,121	5,586,015,752	6,882,015,752	8,201,336,539	7,394,567,092
	Fraction of Sequenced Bases Mapped to Target Regions	37%	38%	40%	52%	49%
	Bases in target regions with at least 10 reads	37,102,963	36,602,585	38,229,451	50,263,991	50,057,763
	Fraction of bases in target regions with at least 10 reads	93%	92%	96%	93%	93%
	Average Number of Total High Quality Sequences at Each Base	138	227	110	130	172
Sequencing Reads at Each Base (Normal)	Average Number of Distinct High Quality Sequences at Each Base	114	202	99	160	127
	Average Number of Total High Quality Sequences at Each Base	178	137	168	145	130
	Average Number of Distinct High Quality Sequences at Each Base	149	121	152	127	112
	Percent T/N Matching	8,204	13,896	15,138	16,454	12,407
	Percent T/N Matching	100%	100%	100%	100%	100%
Summary Data	Mutations/Mb	0.24	0.06	0.12	0.09	0.43
	CNAs/Mb	0.06	0.00	0.00	0.00	0.52
	STS - soft tissue sarcoma, STS-PNST - soft tissue sarcoma, peripheral nerve sheath tumor, OSA _c - chondroblastic osteosarcoma, T - tumor, N - normal, Mb - megabase, CNAs - copy number alterations, SNPs - single nucleotide polymorphisms, FFPE - formalin fixed paraffin embedded, NA -					

Figure 5 (Con't)

11-R01	04-R08	04-R02	04-R01	01-R02	04-R04	Min	Max	Average
STS-PNST	STS-PNST	STS-PNST	STS-PNST	STS-PNST	OSA _c	NA	NA	NA
Left pinna	Right hindpaw	Right Meniscus	Right mid maxillary area	Left thoracic flank	Right humerus	NA	NA	NA
FPPE	FPPE	FPPE	FPPE	FPPE	FPPE	NA	NA	NA
Post-study initiation	Post-study initiation	Pre-study initiation	Pre-study initiation	Pre-study initiation	Pre-study initiation	NA	NA	NA
90%	90%	90%	80%	80%	90%	70%	90%	81%
54%	67%	69%	NA	29%	65%	29%	71%	52%
Blood	Blood	Blood	Blood	Blood	Blood	NA	NA	NA
Next-generation sequencing	Next-generation sequencing	Next-generation sequencing	Next-generation sequencing	Next-generation sequencing	Next-generation sequencing	NA	NA	NA
In solution DNA capture	In solution DNA capture	In solution DNA capture	In solution DNA capture	In solution DNA capture	In solution DNA capture	NA	NA	NA
30,194 coding genes	30,194 coding genes	30,194 coding genes	30,194 coding genes	30,194 coding genes	30,194 coding genes	NA	NA	NA
32,893,252 bases	32,893,252 bases	32,893,252 bases	32,893,252 bases	32,893,252 bases	32,893,252 bases	NA	NA	NA
100 bp	100 bp	100 bp	100 bp	100 bp	100 bp	NA	NA	NA
4	95	6	0	20	14	0	95	16
0	0	0	0	9	4	0	17	3
19,163,476,700	8,055,248,900	19,418,702,600	23,322,445,500	9,336,883,200	10,439,082,100	8,055,248,900	23,322,445,500	15,699,271,900
8,574,289,371	3,317,956,697	8,491,594,341	9,068,570,137	3,967,959,909	4,609,388,923	3,317,956,697	11,459,270,433	7,314,196,403
45%	41%	44%	39%	42%	44%	38.9%	64.8%	46.2%
37,167,238	35,180,875	37,503,866	36,941,231	36,056,022	36,426,112	35,180,875	50,430,237	38,972,328
94%	89%	94%	93%	91%	92%	88.5%	94.4%	92.1%
16,042,683,700	16,831,763,000	15,728,989,700	16,160,073,600	15,151,630,300	18,183,947,700	14,561,175,800	19,693,458,500	16,391,943,300
6,245,786,511	6,370,965,466	6,167,005,020	6,222,258,939	5,777,414,557	6,883,542,265	5,586,179,511	8,201,336,539	6,640,832,434
38%	38%	39%	39%	38%	38%	37.2%	52.3%	40.7%
37,018,789	37,230,015	37,216,686	37,236,461	37,246,921	37,128,881	36,602,585	50,263,991	30,575,867
93%	94%	94%	94%	94%	93%	92.1%	96.2%	93.6%
195	73	190	201	84	104	73	227	153
174	67	159	170	59	79	59	202	128
154	152	150	152	140	166	130	178	152
125	110	127	133	120	143	112	152	131
14,801	12,953	14,163	14,502	9,828	11,861	8,204	16,454	13,110
100%	100%	100%	100%	100%	100%	100%	100%	100%
0.12	2.89	0.18	0.00	0.61	0.43	0.00	2.89	0.47
0.00	0.00	0.00	0.00	0.27	0.12	0.00	0.52	0.09

STS only
STS onlySTS only
STS onlySTS only
STS only

Figure 6

Case ID	Tumor Type	Gene Symbol	Gene Description	Gene Accession	Nucleotide Position (Genomic)	Fold amplification	Mutation type
04-R03	STS	<i>AI/1</i>	androgen-induced 1	ENSCAFG000000003003	chr1:37686977-37687647	3.2	Amplification
		<i>NKAIN1</i>	Na ⁺ /K ⁺ transporting ATPase interacting 1	ENSCAFG000000011175	chr2:72699008-72705959	3.1	Amplification
		<i>PK3CB</i>	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 beta	ENSCAFG000000003661	chr38:4011051-4013432	10.2	Amplification
		<i>MDM4</i>	MDM4 p53 binding protein homolog	ENSCAFG000000009669	chr38:4055972-4109319	12.3	Amplification
		<i>LRN2</i>	leucine rich repeat neuronal 2	ENSCAFG000000009675	chr38:4164479-4166666	4.1	Amplification
		<i>NFASC</i>	neurofascin	ENSCAFG000000009801	chr38:4474563-4542491	9.2	Amplification
		<i>CNTN2</i>	contactin 2 (exon1)	ENSCAFG000000002469	chr38:4576761-4596329	7.3	Amplification
		<i>TMEM81</i>	transmembrane protein 81	ENSCAFG000000009956	chr38:4604335-4605118	10.0	Amplification
		<i>RBPS5</i>	retinoblastoma binding protein 5	ENSCAFG000000009970	chr38:4606590-4634589	11.4	Amplification
		<i>DUSTY CANFA</i>	dual serine/threonine and tyrosine protein kinase	ENSCAFG000000009999	chr38:4669577-4715897	11.3	Amplification
11-R02	STS-PNST	<i>TMCC2</i>	transmembrane and coiled-coil domain family 2	ENSCAFG000000010030	chr38:4734043-4773669	5.8	Amplification
		<i>NUAK2</i>	NUAK family, SNF1-like kinase, 2	ENSCAFG000000010038	chr38:4798899-4816487	7.6	Amplification
		<i>KLHDC8A</i>	kelch domain containing 8A	ENSCAFG000000010046	chr38:4833445-4838972	6.7	Amplification
		<i>LEMD1</i>	LEM domain containing 1	ENSCAFG0000000025208	chr38:4872059-4896801	10.4	Amplification
		<i>CDK18</i>	cyclin-dependent kinase 18	ENSCAFG000000010062	chr38:4993764-5001820	7.7	Amplification
		<i>Novel gene</i>	uncharacterized protein	ENSCAFG000000010109	chr38:5028755-5029725	6.2	Amplification
		<i>MFSO4</i>	major facilitator superfamily domain containing 4	ENSCAFG000000010137	chr38:5037069-5063455	7.6	Amplification
		<i>ELK4</i>	ELK4, ETS-domain protein (SRF accessory protein 1)	ENSCAFG000000010144	chr38:5077862-5083778	11.7	Amplification
		<i>SLC45A3</i>	solute carrier family 45, member 3	ENSCAFG000000010148	chr38:5111404-5116718	5.8	Amplification
		<i>PGBD5</i>	pigBac transposable element derived 5	ENSCAFG000000012088	chr4:11988074-12023545	6.3	Amplification
04-R04	OSA _c	<i>DLG5</i>	discs, large homolog 5 (Drosophila)	ENSCAFG000000015499	chr4:30898933-31016619	5.4	Amplification
		<i>MAT1A</i>	methionine adenosyltransferase 1, alpha	ENSCAFG000000015807	chr4:32662979-32676594	5.3	Amplification
		<i>Novel gene</i>	uncharacterized protein	ENSCAFG000000015908	chr20:47978916-47984829	5.3	Amplification
		<i>AI/1</i>	androgen-induced 1	ENSCAFG000000003003	chr1:37686977-37687647	5.7	Amplification
		<i>XM_844172.1</i>	uncharacterized protein	ENSCAFG000000023337	chr2:7738782-7751246	5.9	Amplification
		<i>Novel gene</i>	uncharacterized protein	ENSCAFG000000024028	chr3:40494283-40494577	6.4	Amplification
		<i>SIX3</i>	SIX homeobox 3	ENSCAFG000000002547	chr10:50465860-50469140	5.3	Amplification
		<i>LST1</i>	leukocyte specific transcript 1	ENSCAFG000000002691	chr12:4088376-4088275	6.7	Amplification
		<i>FAM84A</i>	family with sequence similarity 84, member A	ENSCAFG000000003697	chr17:13630517-13631423	5.0	Amplification
		<i>TLX2</i>	T-cell leukemia homeobox 2	ENSCAFG000000008445	chr17:51694813-51696234	5.1	Amplification
01-R02	STS-PNST	<i>SOX3</i>	SRF (sex determining region Y)-box 3	ENSCAFG000000019026	chrX:113431902-11343324	5.6	Amplification
		<i>Novel gene</i>	uncharacterized protein	ENSCAFG000000019588	chrX:125230197-125231662	5.3	Amplification

STS - soft tissue sarcoma; STS-PNST - soft tissue sarcoma, peripheral nerve sheath tumor; OSA_c - chondroblastic osteosarcoma.

Figure 7A



Figure 7B



Figure 7C



Figure 7D



Figure 7E

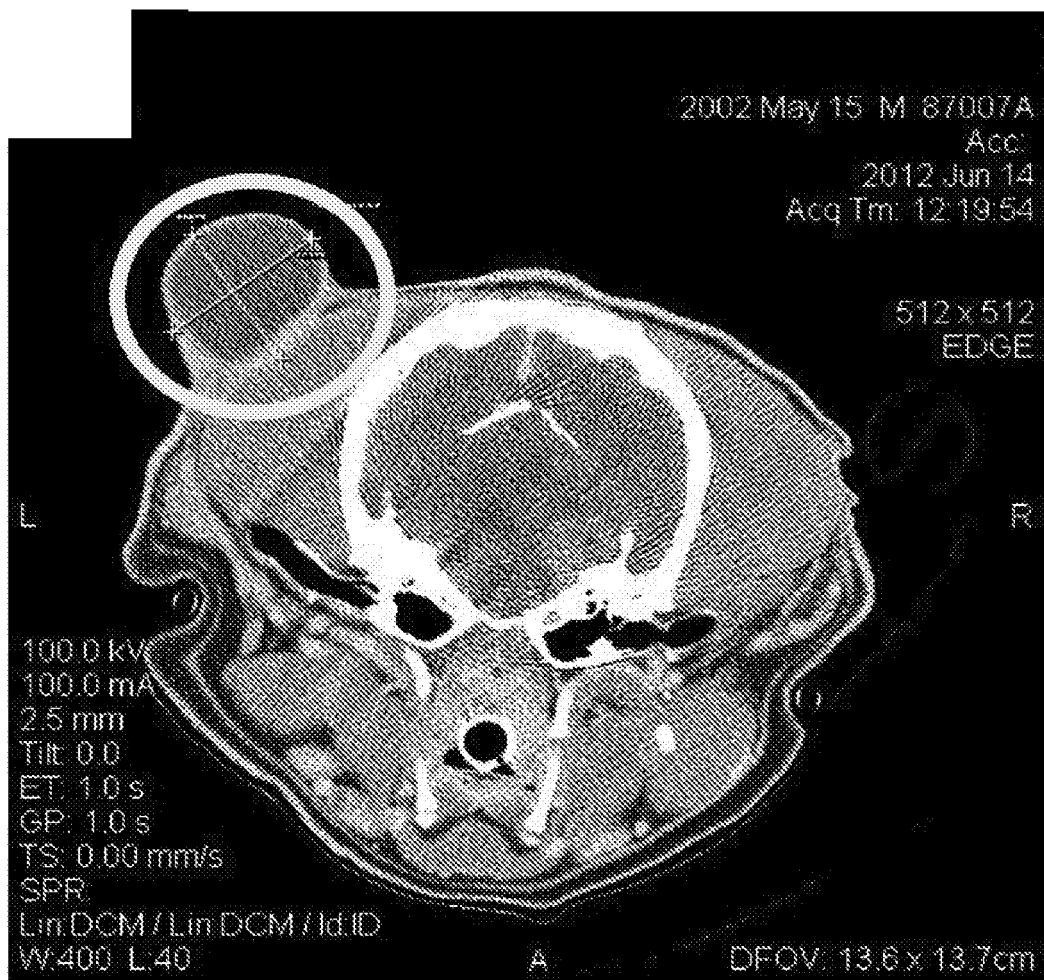


Figure 7F

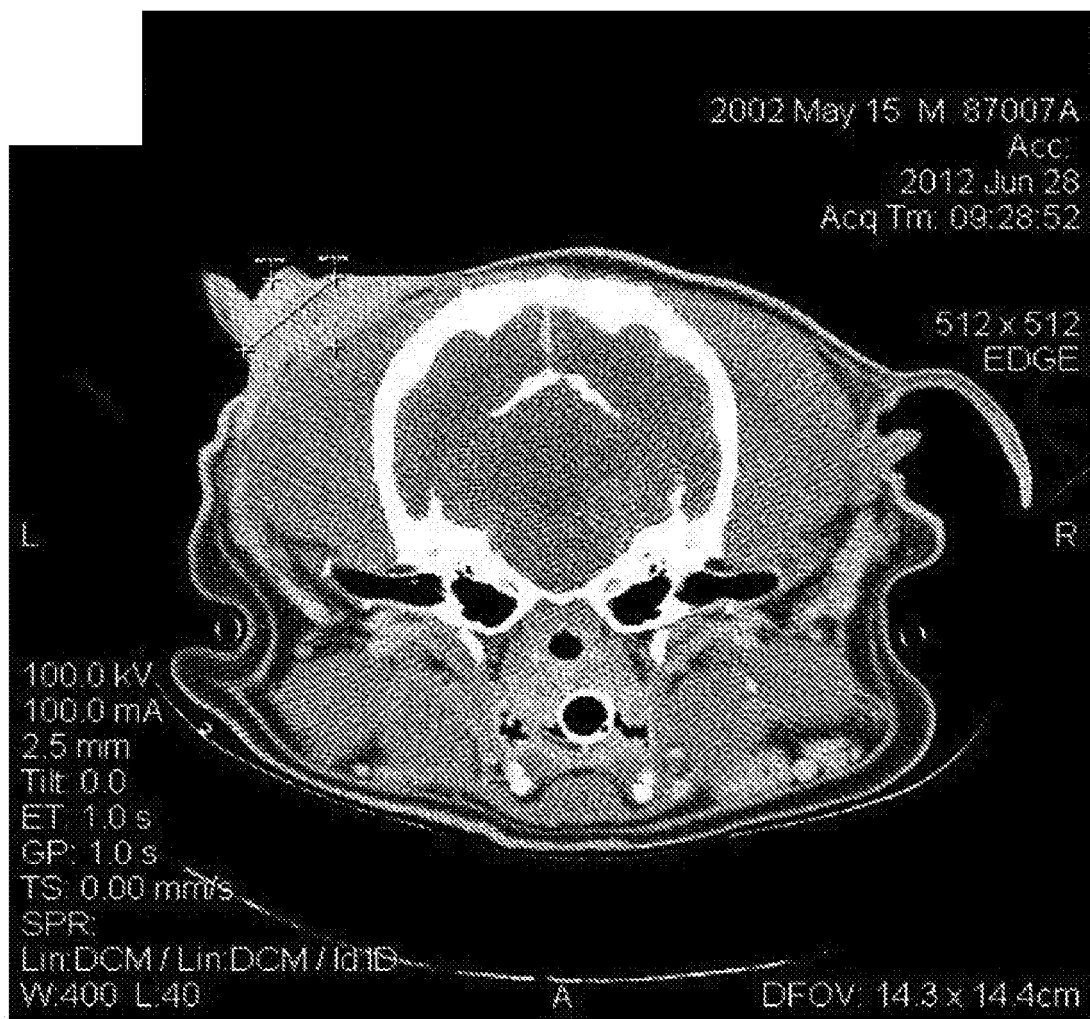


Figure 8A



Figure 8B

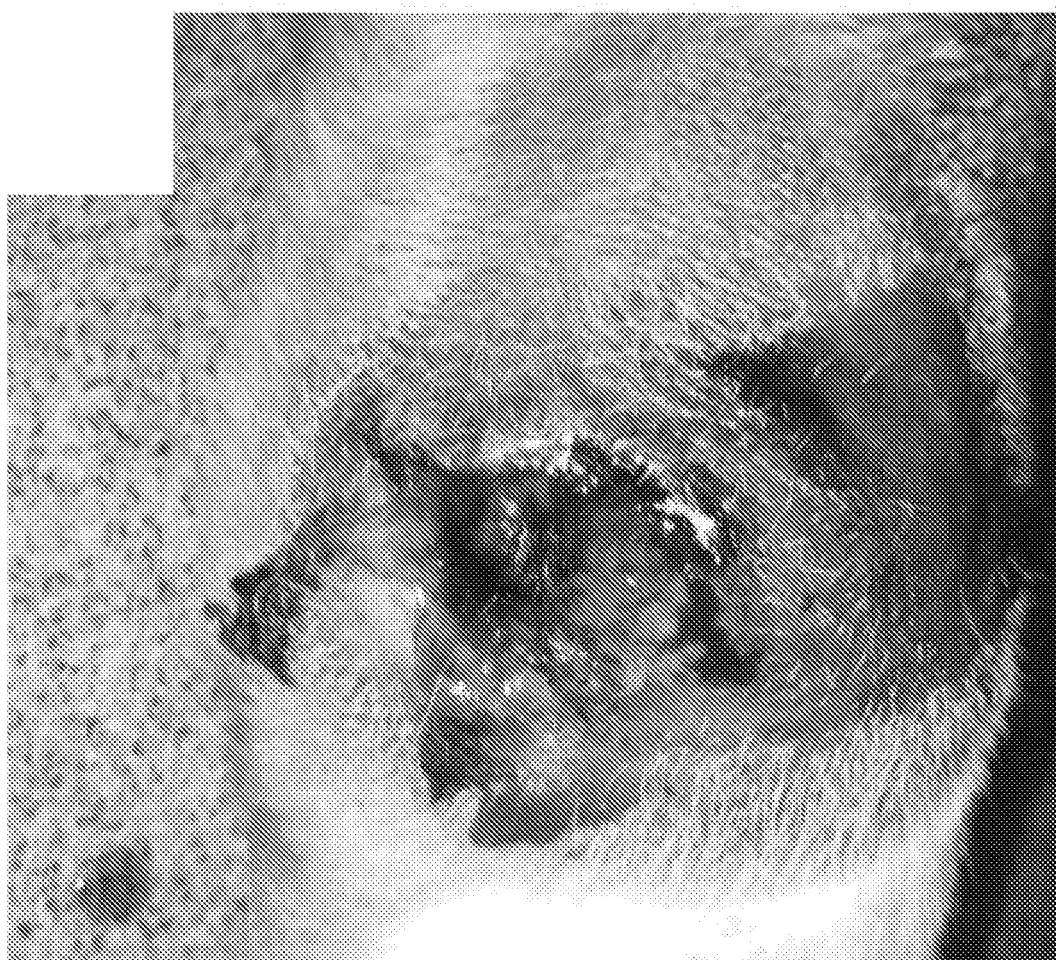


Figure 8C

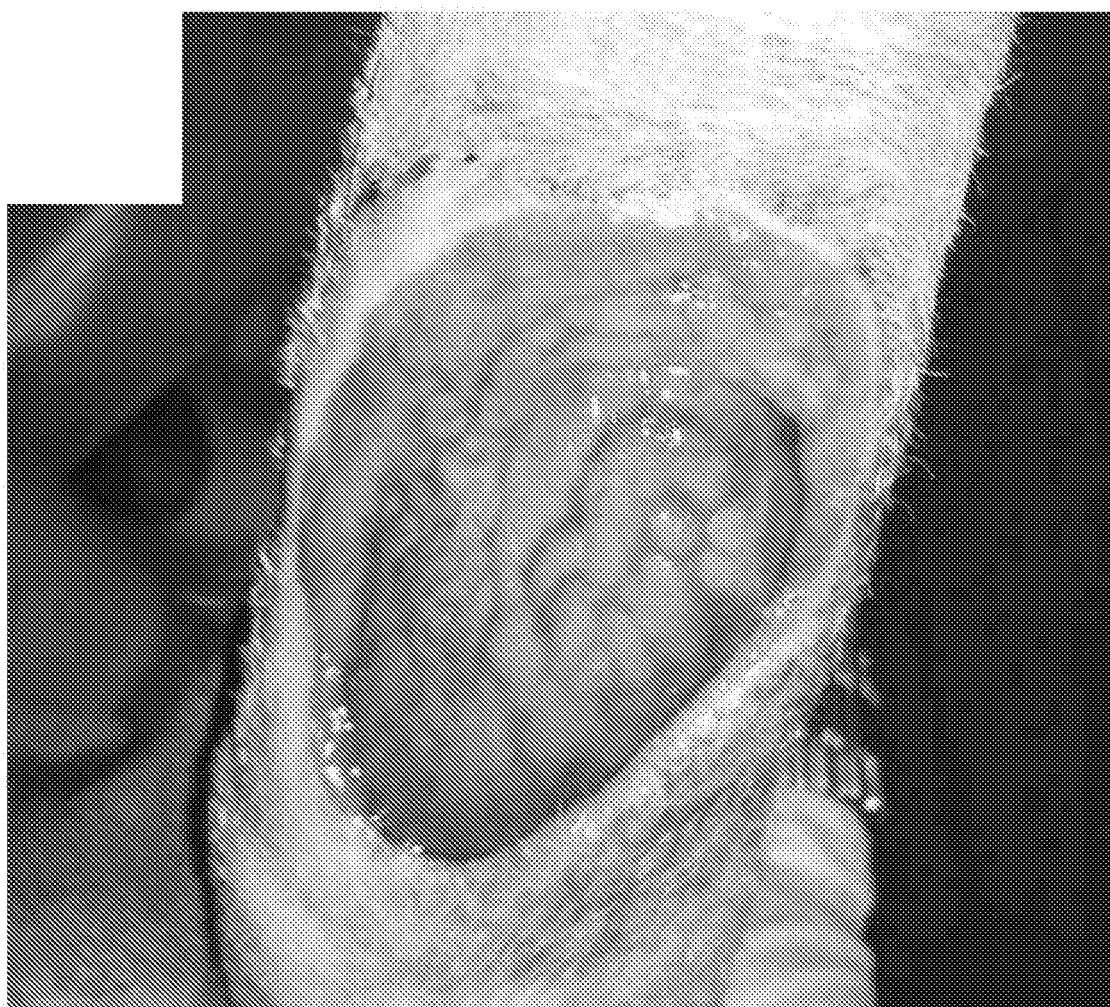


Figure 8D



Figure 8E



Figure 8F

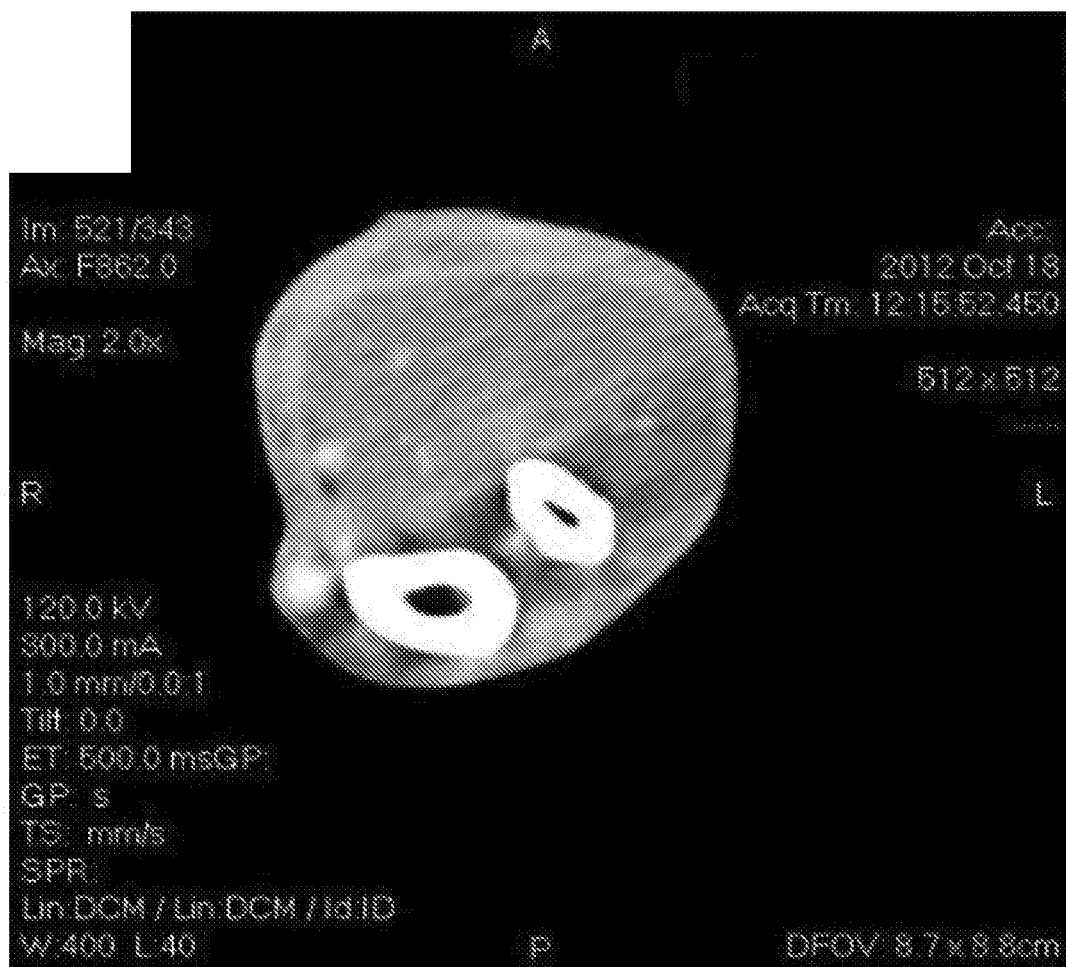


Figure 9

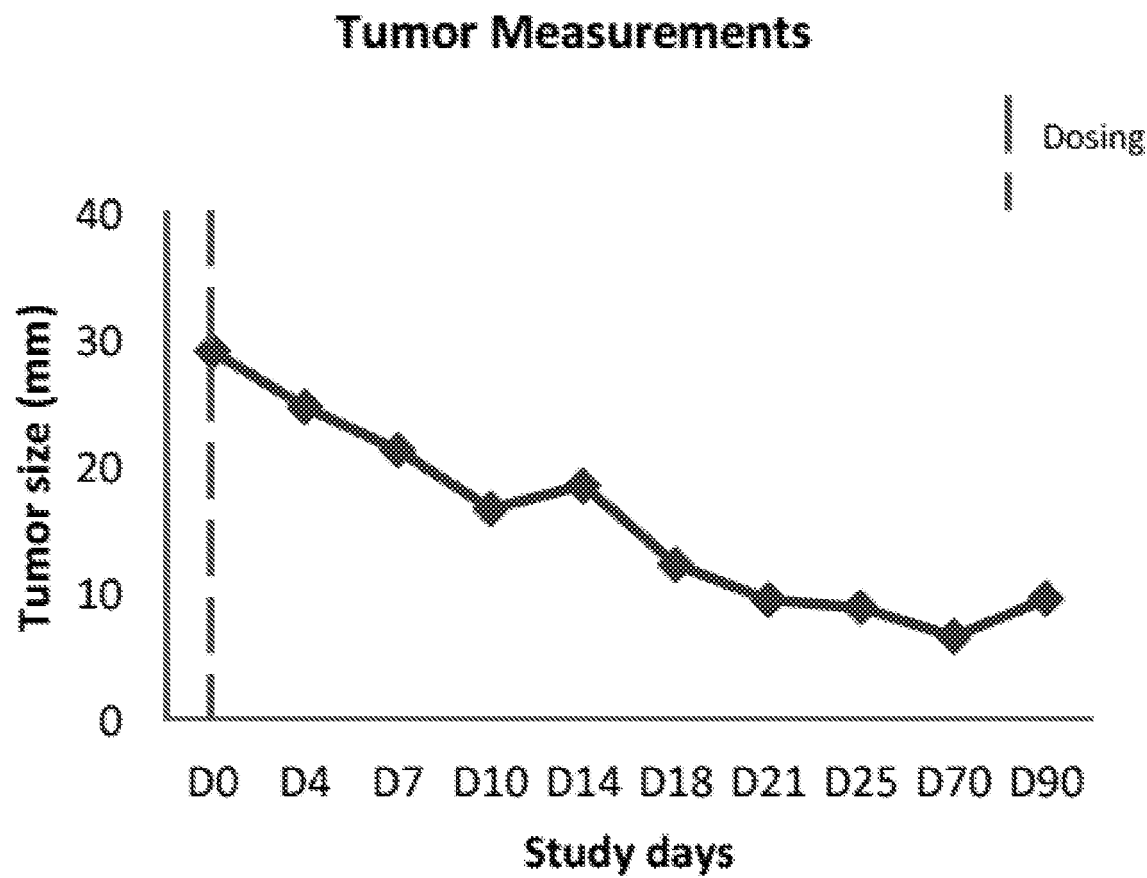


Figure 10A

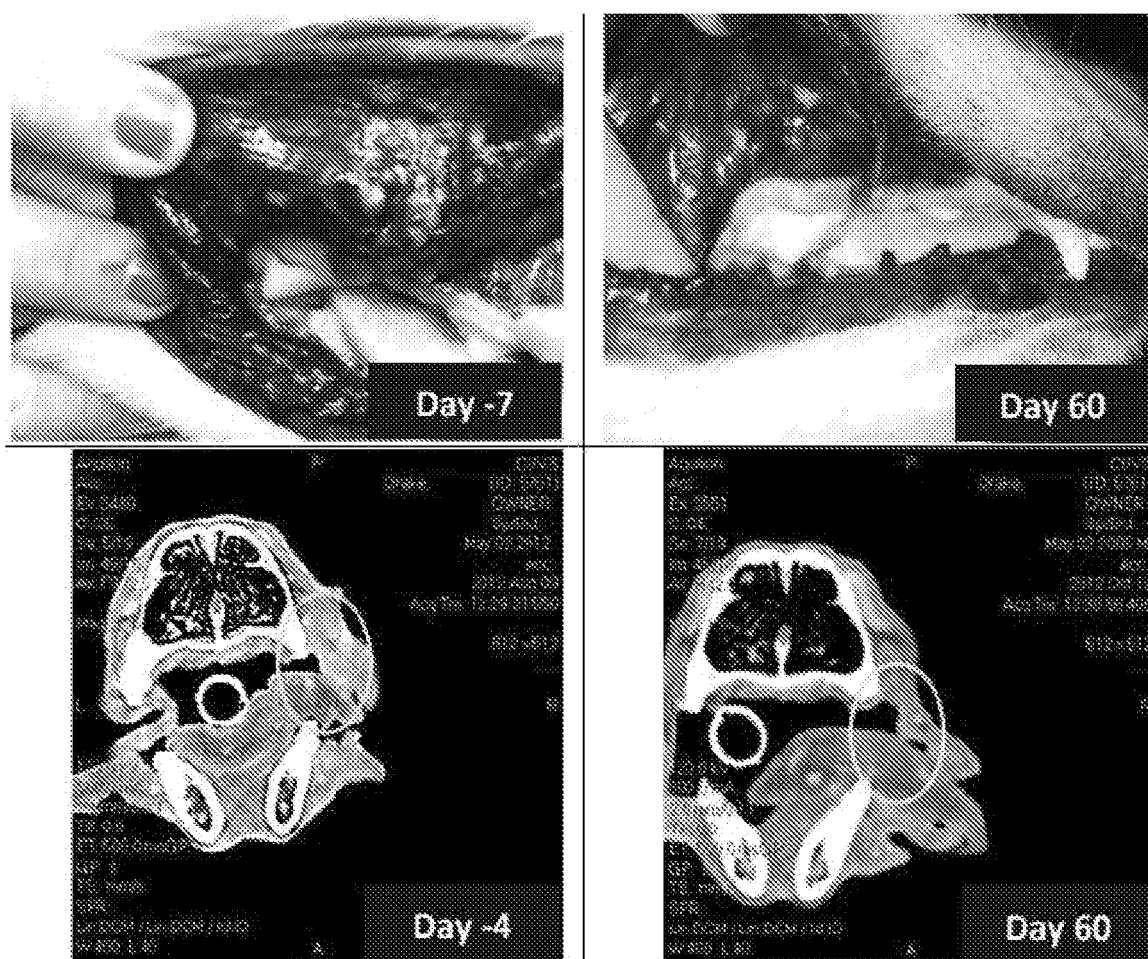


Figure 10B

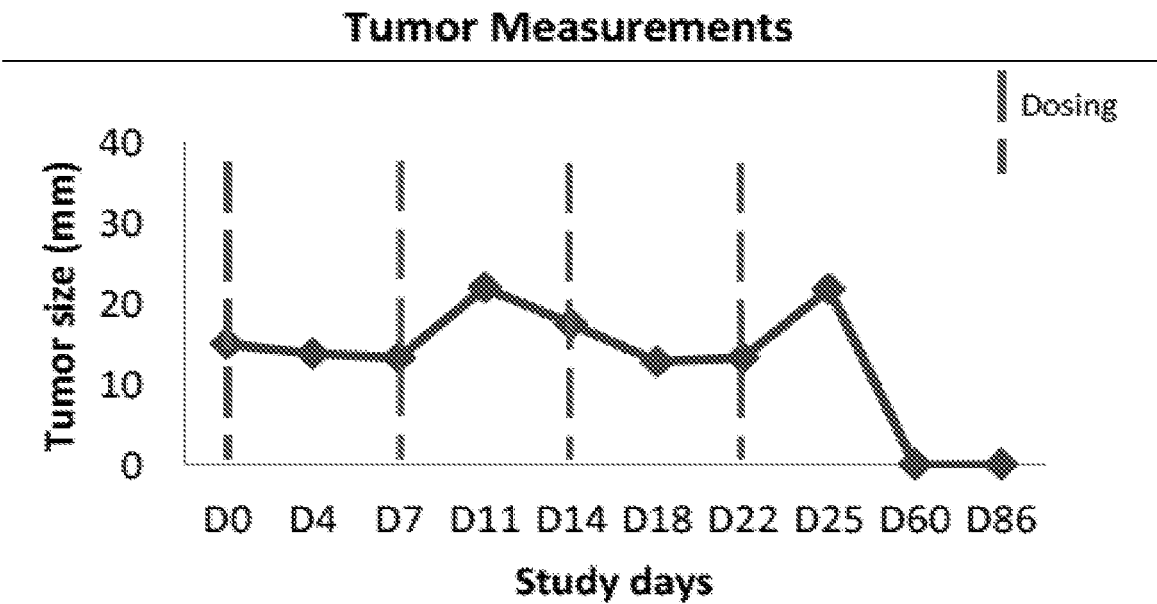


Figure 11

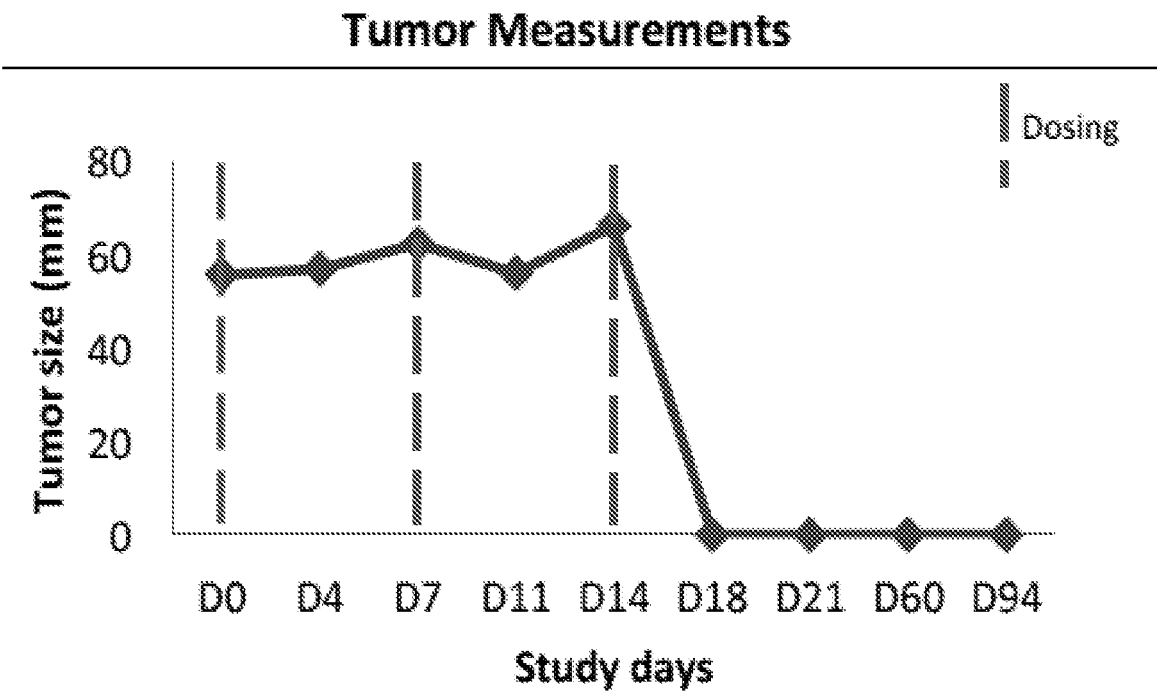


Figure 12A

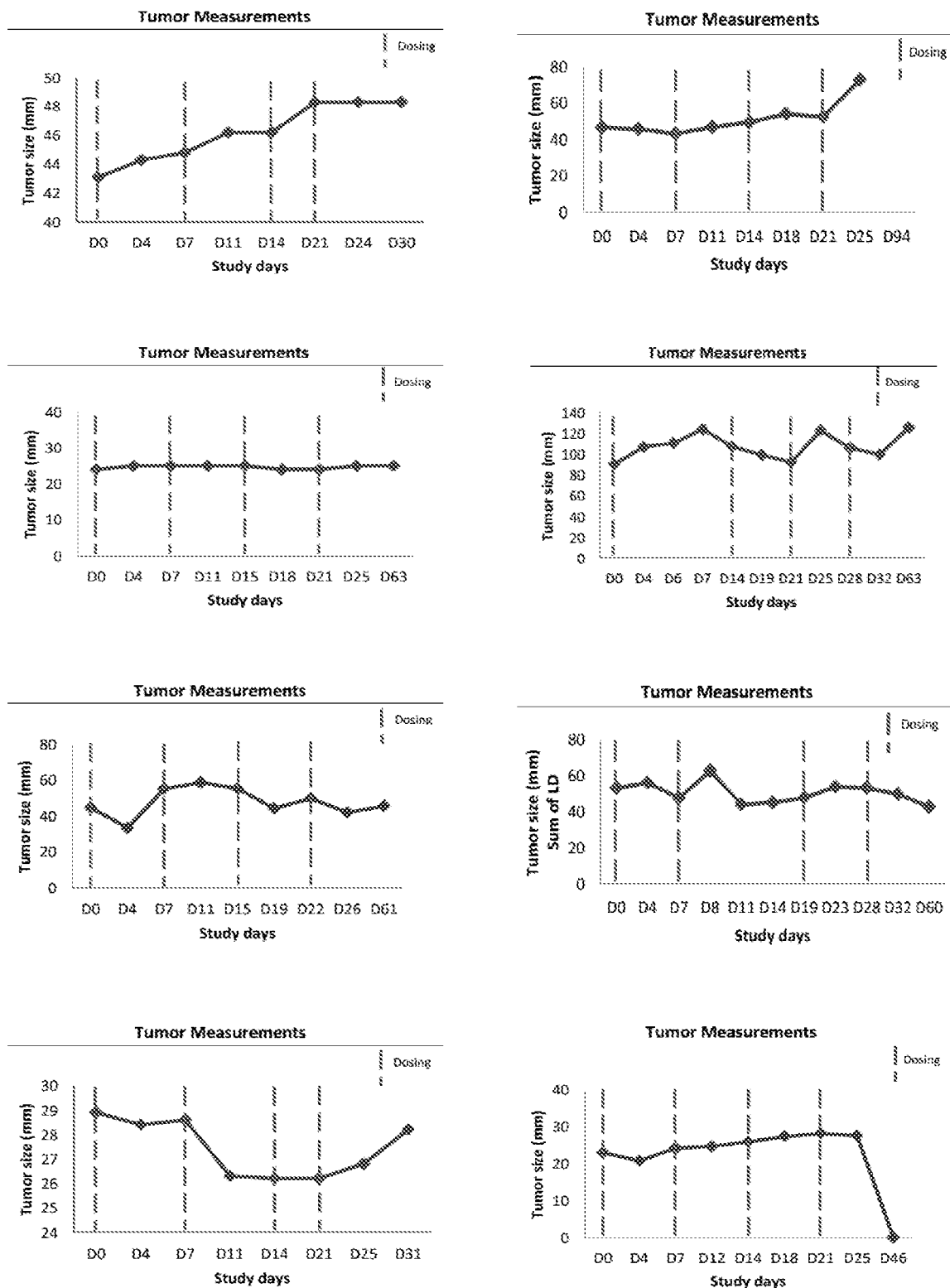


Figure 12B

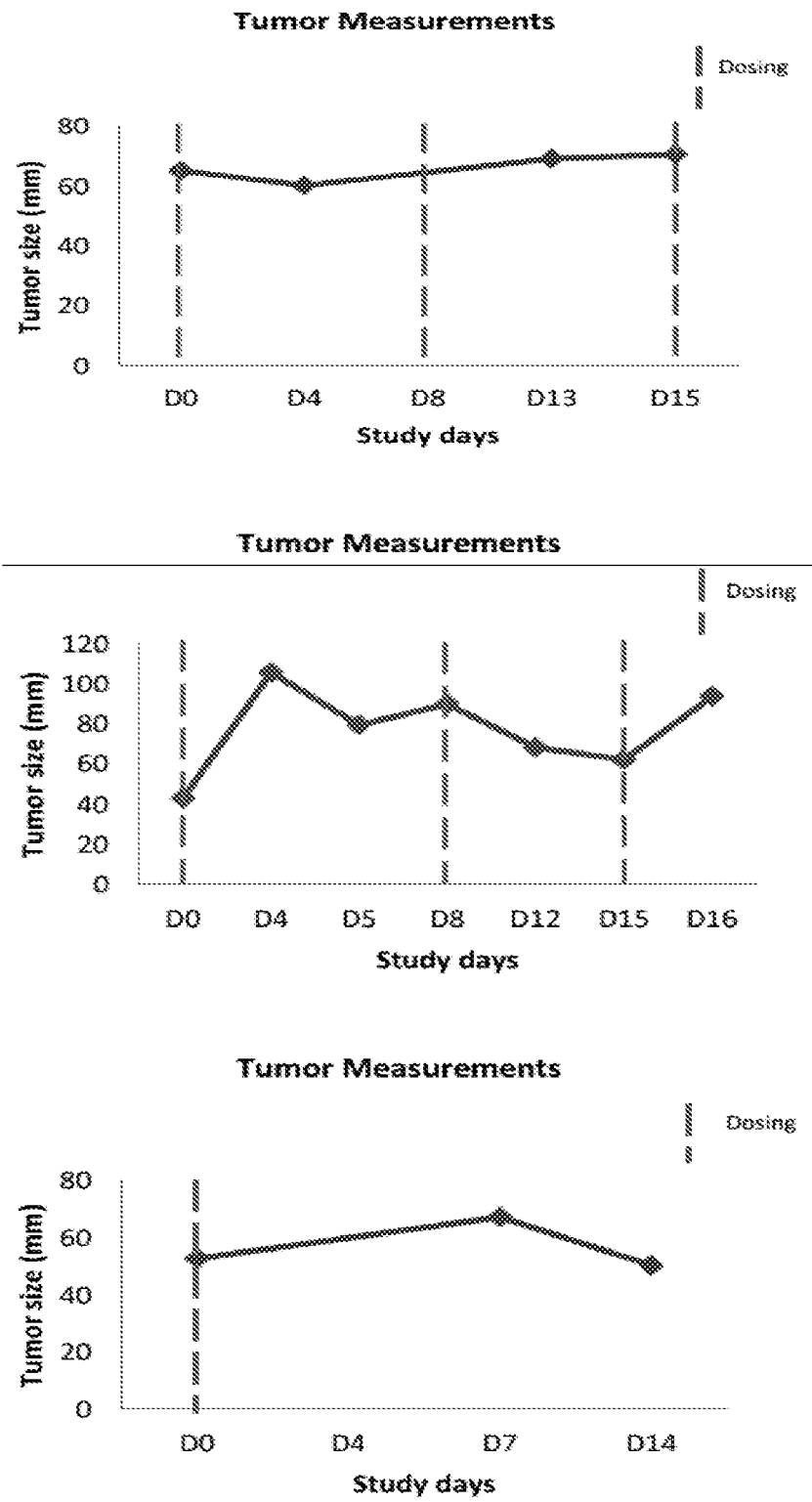


Figure 13

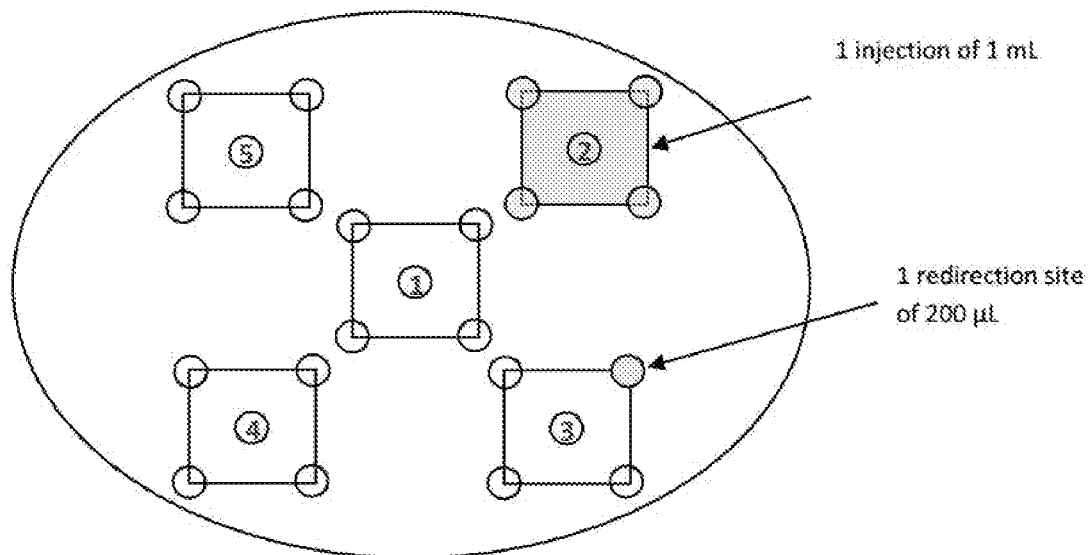


Figure 14A



Figure 14B



Figure 14C

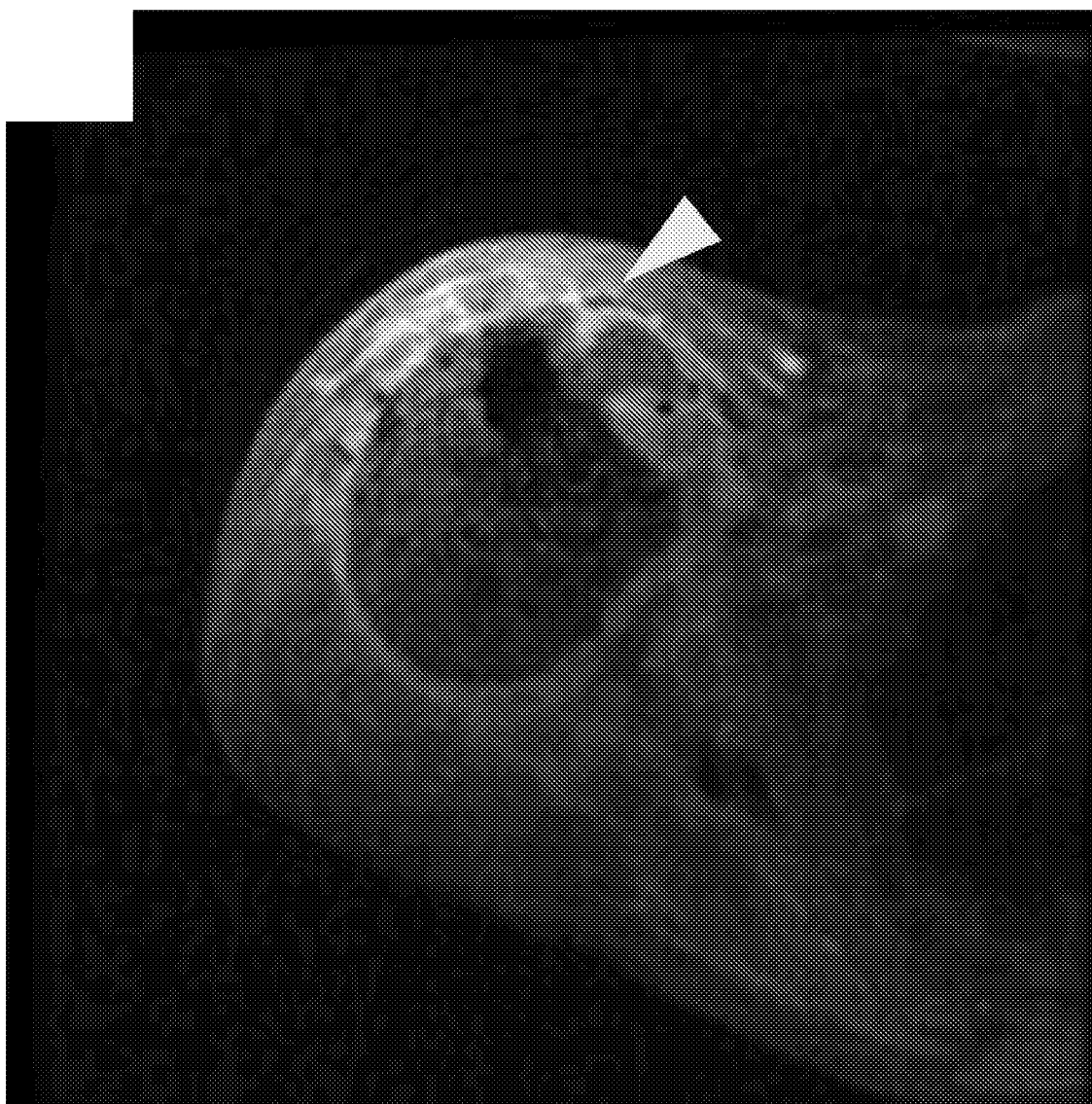


Figure 14D

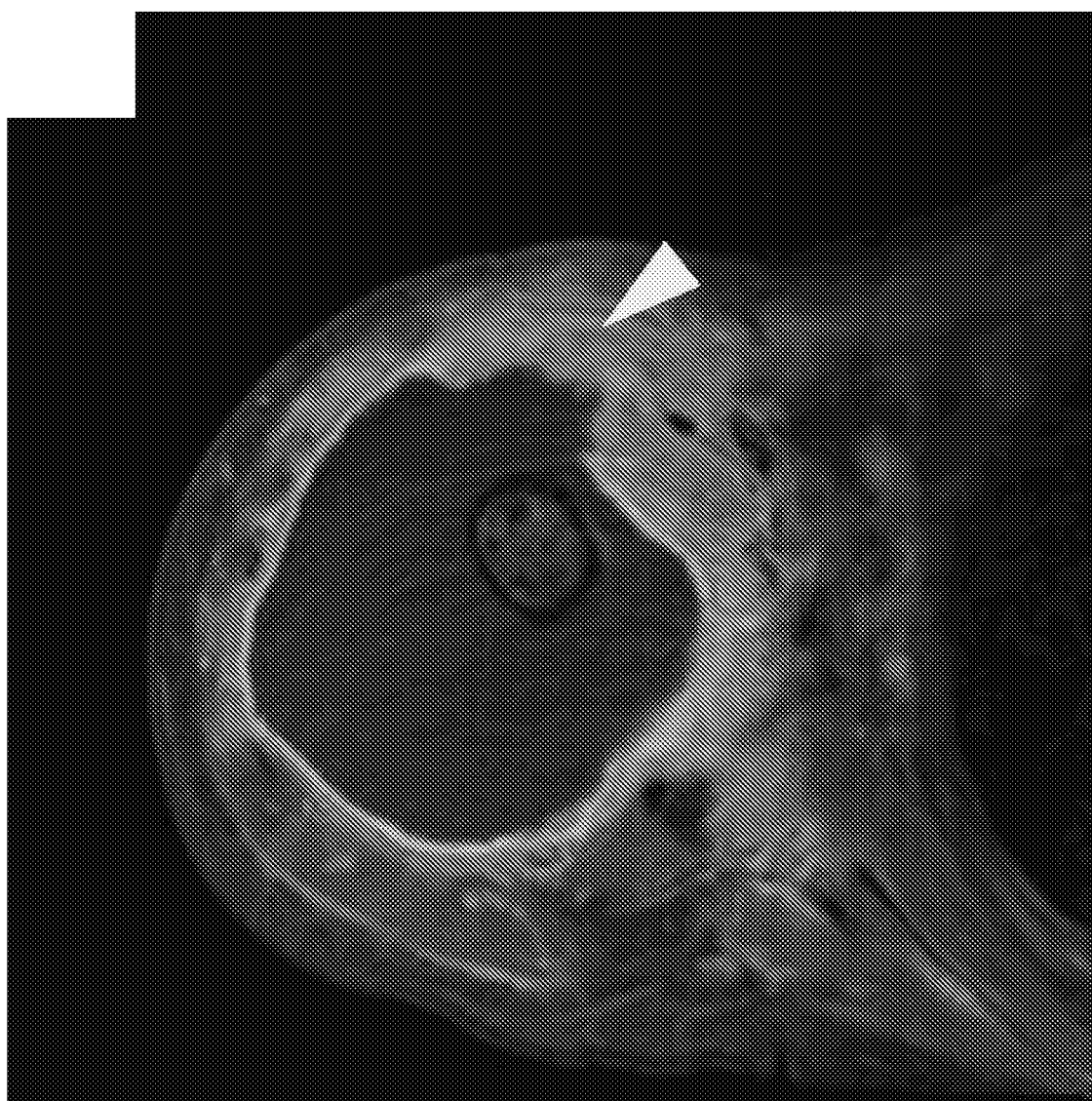


Figure 15A

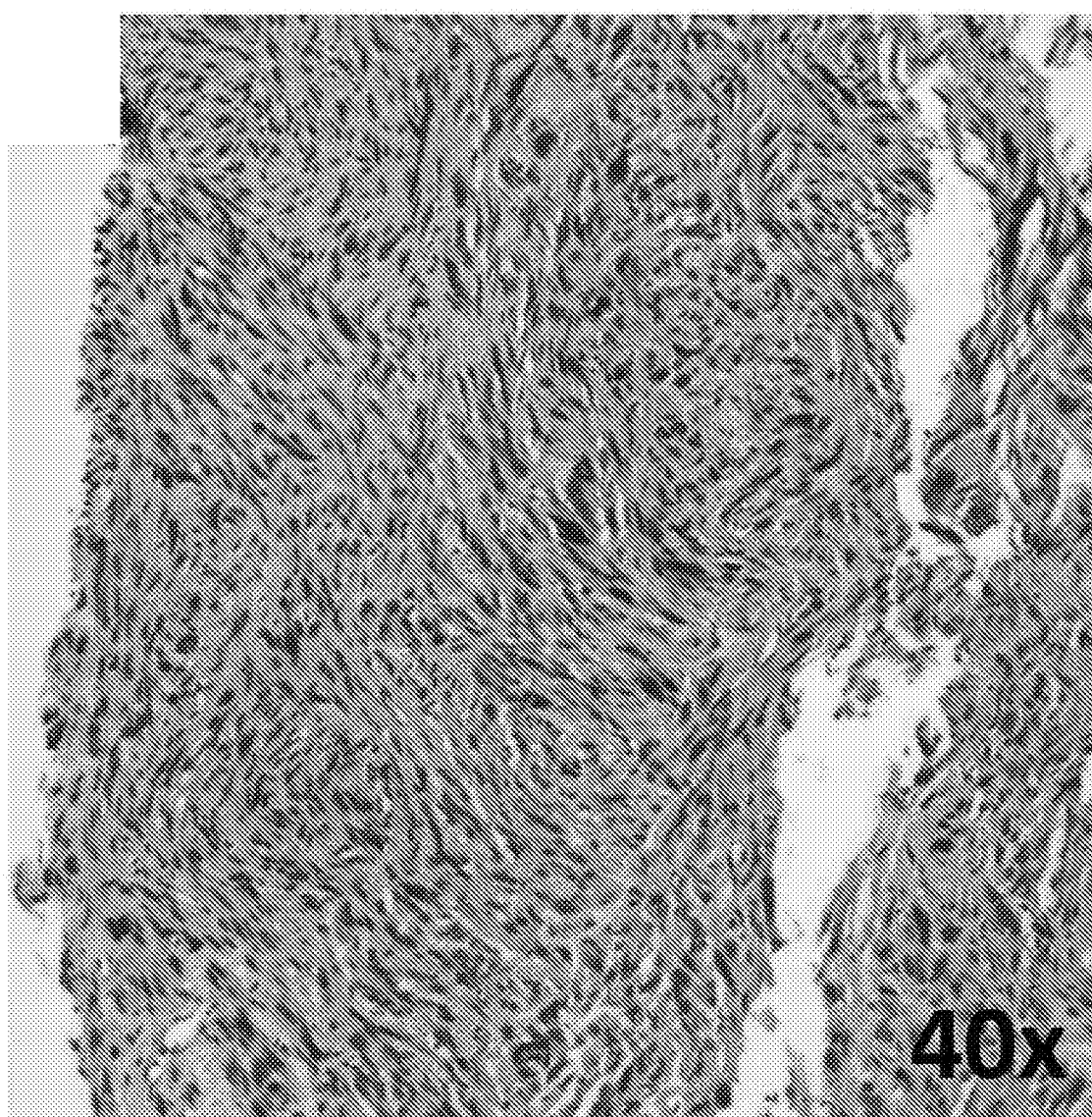


Figure 15B

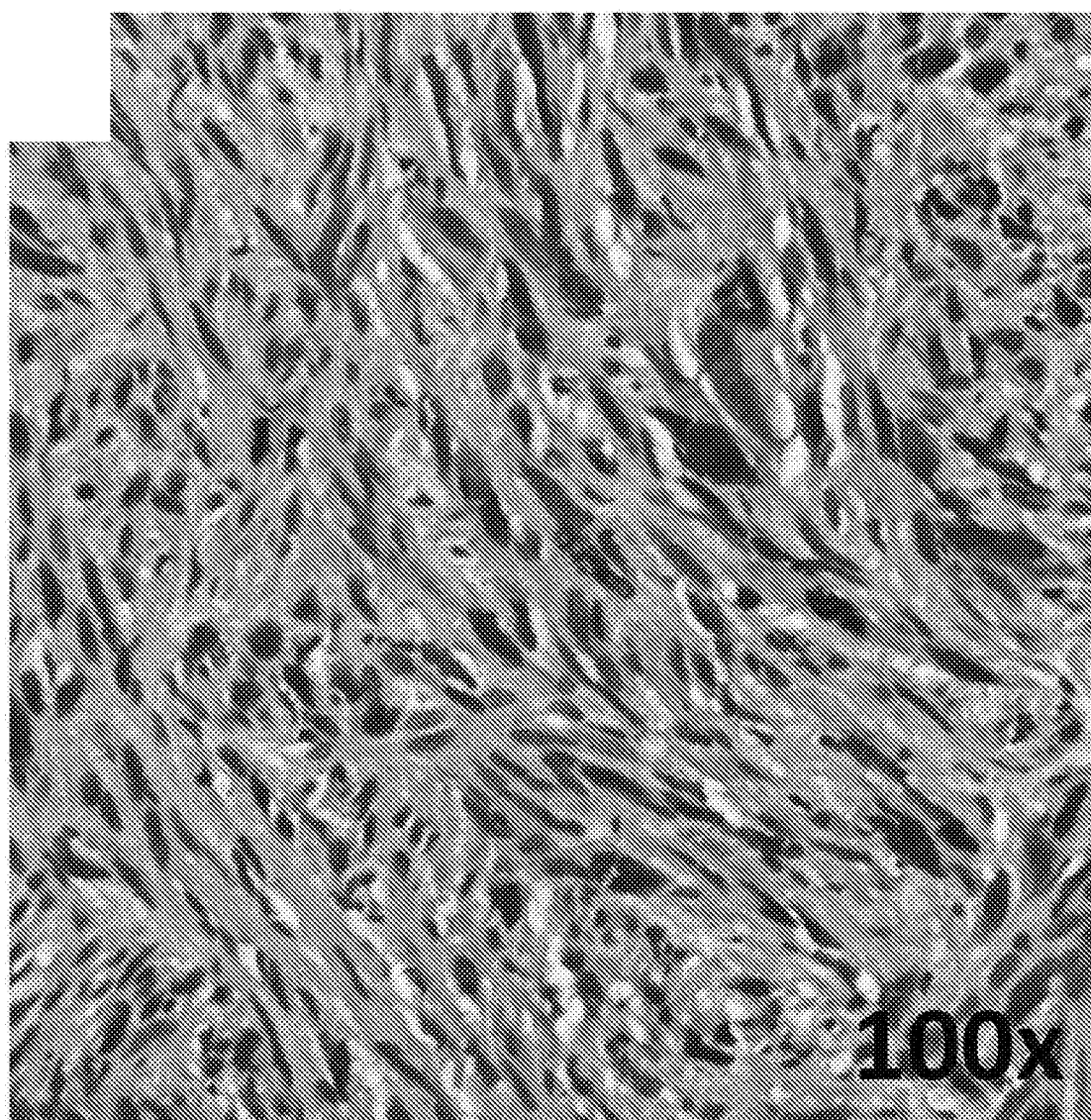


Figure 15C

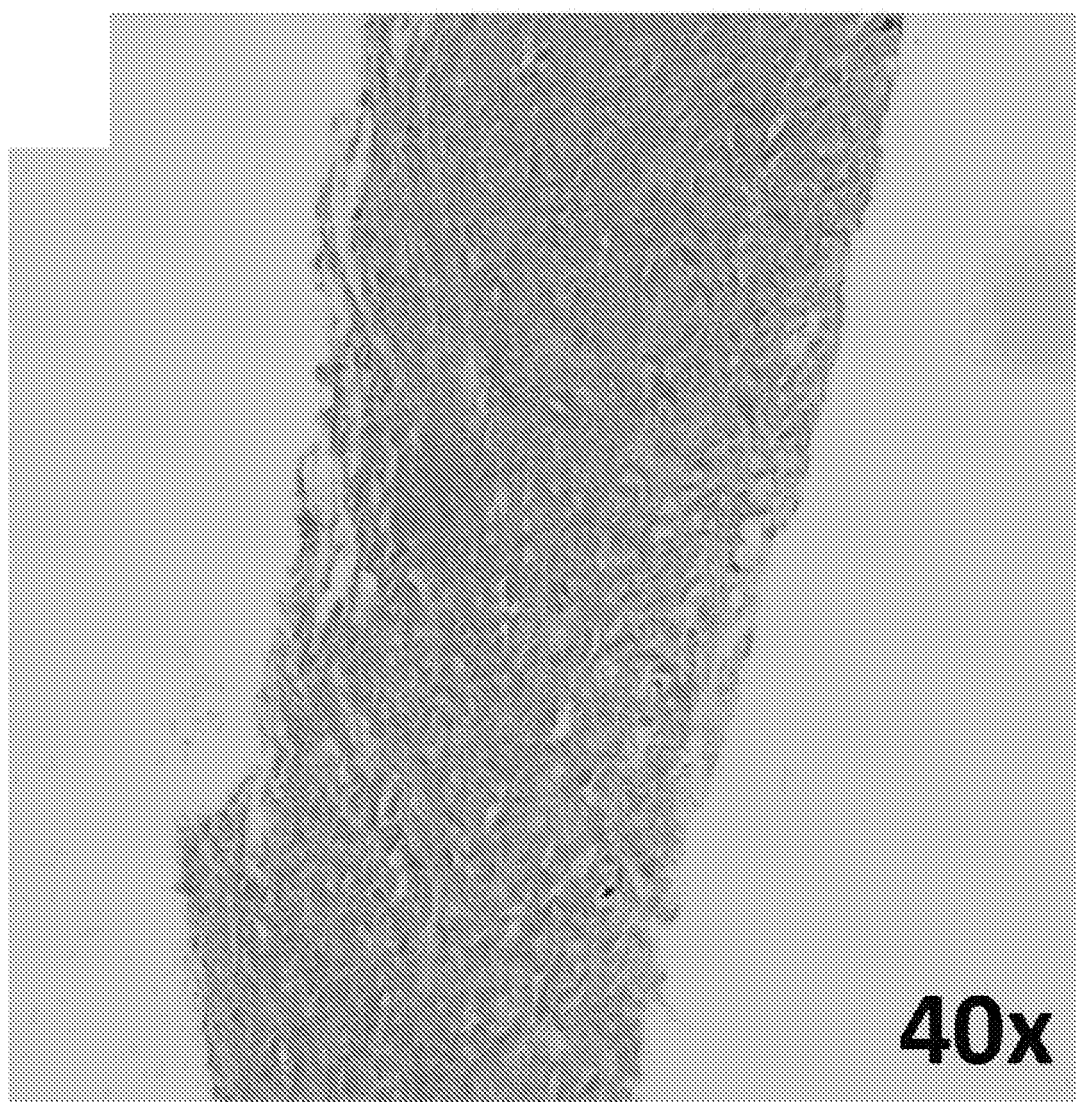


Figure 15D

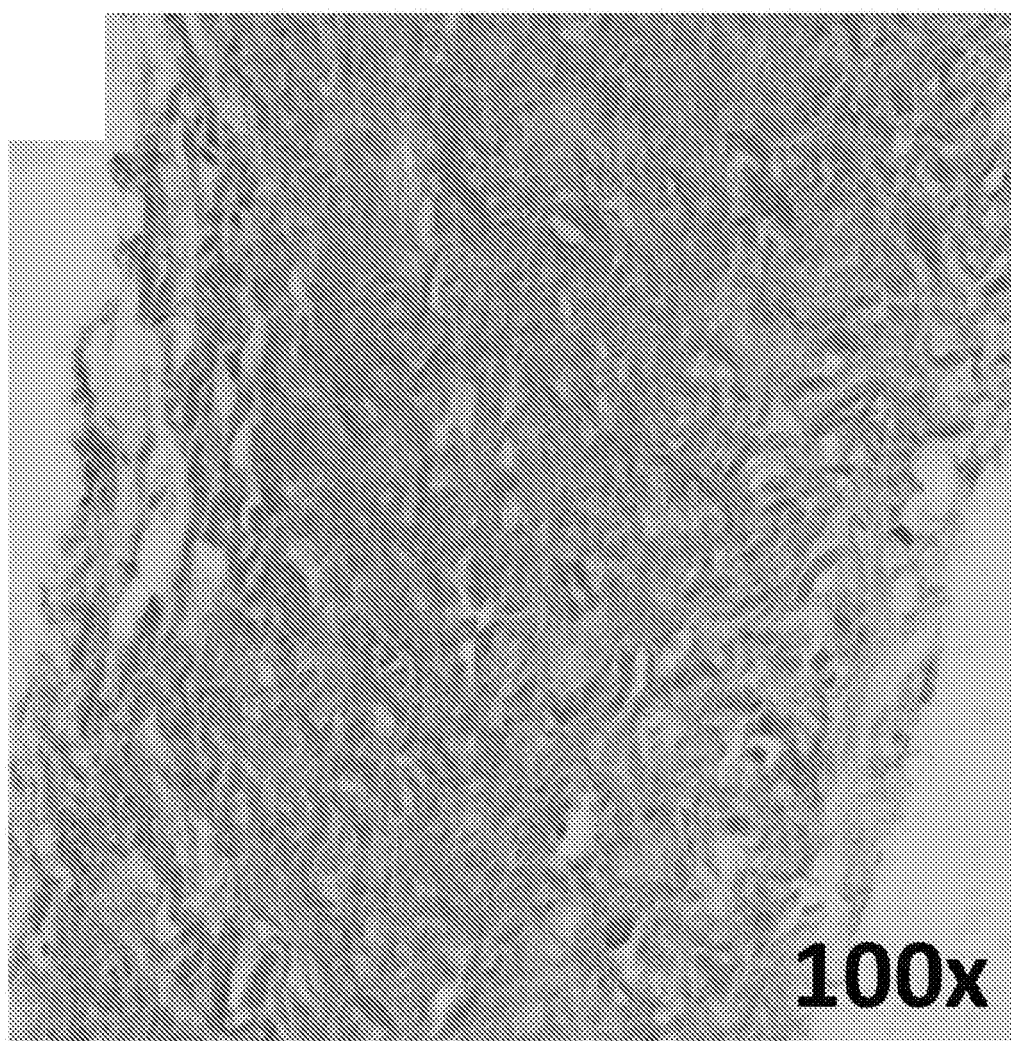


Figure 16A



Figure 16B

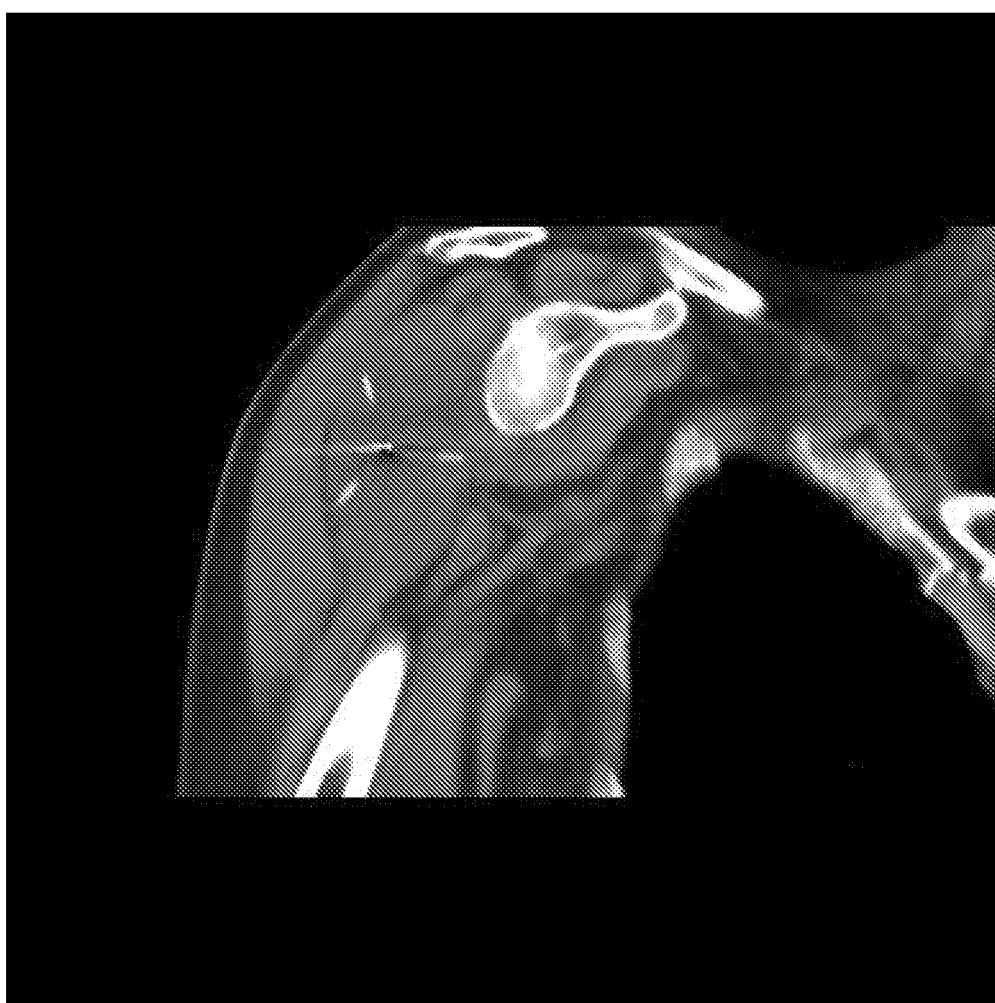


Figure 16C

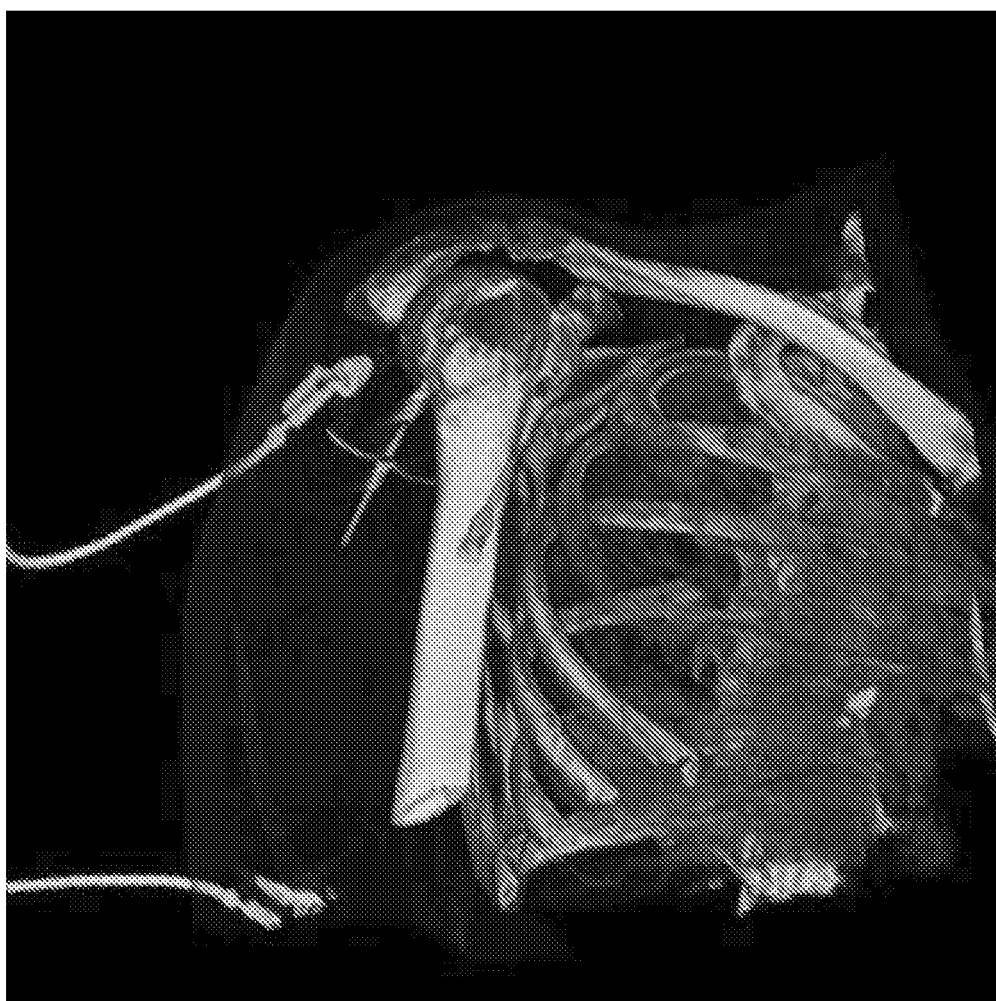


Figure 16D

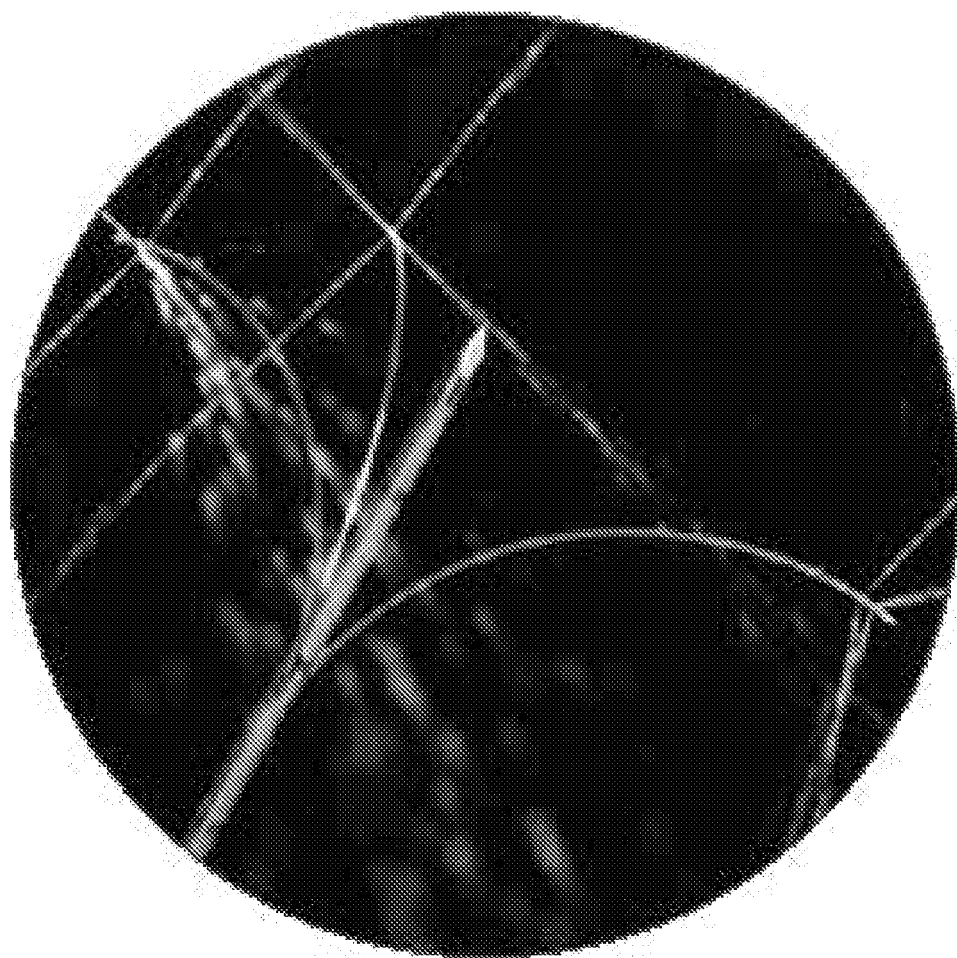


Figure 16E

