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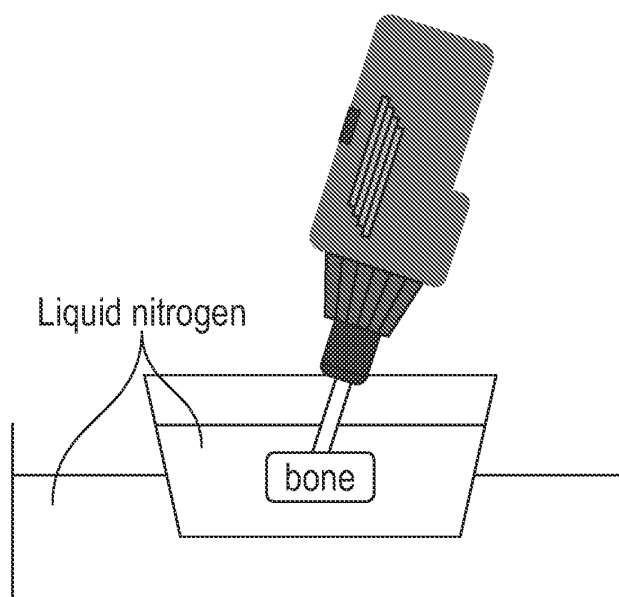


FIG. 1A

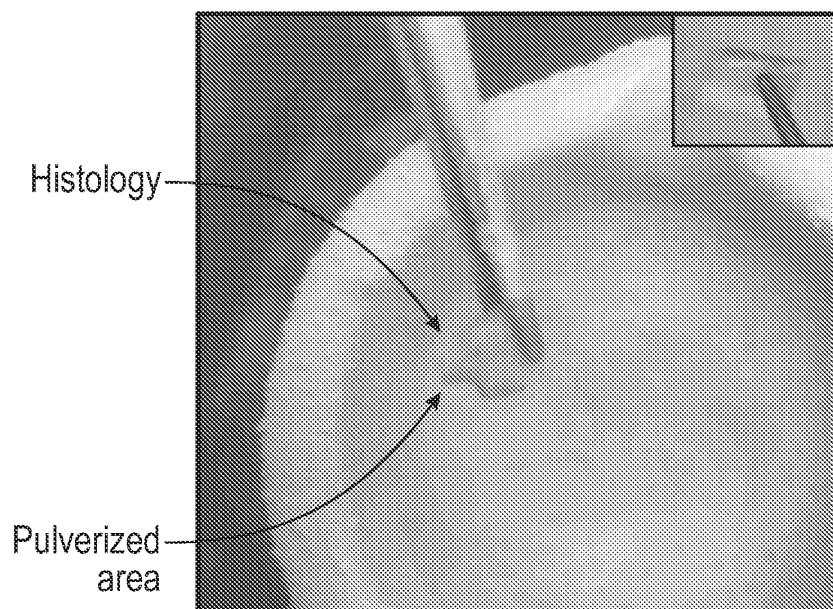
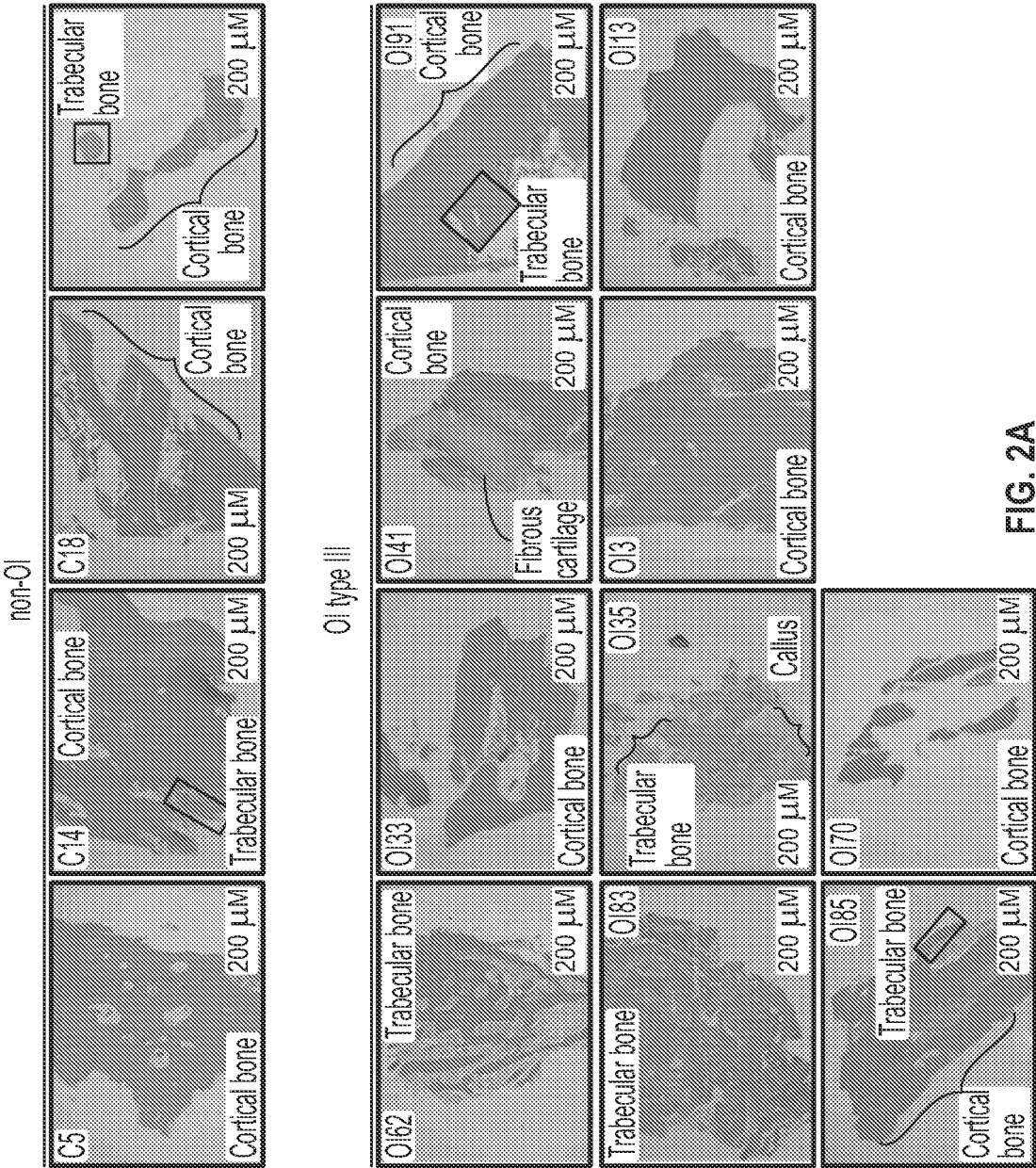


FIG. 1B



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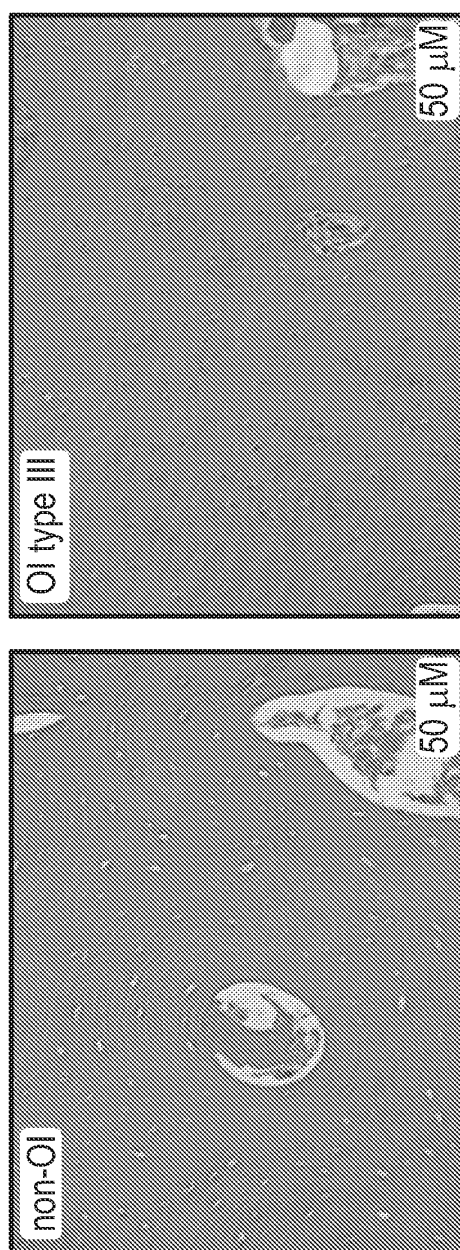


FIG. 2B

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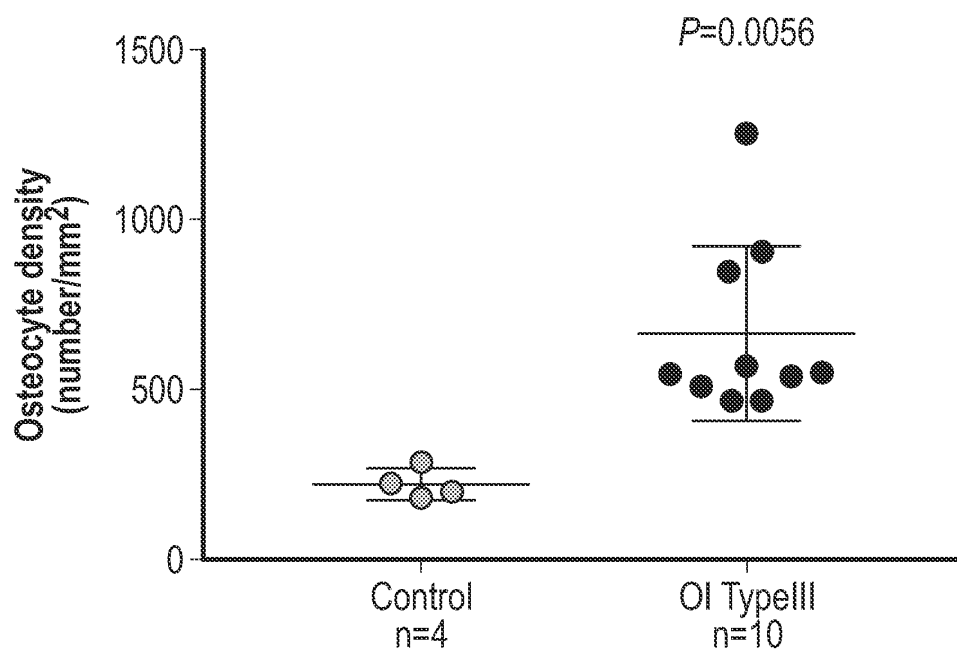


FIG. 3

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Gene name	NanoString	RNASeq	Direction
AHR	2.32	1.51218	▲ ▲
APC	1.19	-1.50566	▲ ▼
AXIN1	-2.07	-2.63129	▼ ▼
AXIN2	3.79	4.51858	▲ ▲
BAMBI	8.16	8.38236	▲ ▲
BCL9	3.34	3.43969	▲ ▲
BIRC5	-8.34	-9.07204	▼ ▼
BMP4	8.79	15.1776	▲ ▲
BTRC	-1.3	-1.28463	▼ ▼
CAMK2B	1.39	21.7272	▲ ▲
CCND1	7.97	7.04769	▲ ▲
CCND2	1.03	1.26258	▲ ▲
CCND3	-4.66	-4.96631	▼ ▼
CD44	3.43	2.51486	▲ ▲
CDH1	-3.83	-9.68124	▼ ▼
CDH11	9.74	10.4787	▲ ▲
CDKN2A	2.59	2.95587	▲ ▲
CEBPD	-2.26	-2.19312	▼ ▼
COLIA2	11.58	11.1352	▲ ▲
CREBBP	-1.17	-1.75589	▼ ▼
CSNK1A1	1.16	1.0772	▲ ▲
CSNK2A1	1.07	-1.04424	▲ ▼
CTBP1	-1.18	-1.31215	▼ ▼
CTNNB1	3.82	3.77663	▲ ▲
CUL1	-1.12	-1.19524	▼ ▼
CXCL12	-3.3	-3.62812	▼ ▼
CXCR4	-19.7	-14.8106	▼ ▼
CXXC4	1.33	4.67358	▲ ▲
DAB2	4.58	3.39508	▲ ▲
DIXDC1	7.33	5.12328	▲ ▲
DKK1	10.48	11.0764	▲ ▲
DKK2	1.58	1.81991	▲ ▲
DKK3	12.95	12.2083	▲ ▲
DVL1	2.68	2.69114	▲ ▲

FIG. 4

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DVL2	-1.02	1.26095	▼ ▲
EFNB1	3.41	3.97085	▲ ▲
EGFR	1.9	3.78925	▲ ▲
EGR1	2.57	1.30423	▲ ▲
EP300	-1.11	-1.91394	▼ ▼
ERBB2	1.39	4.97592	▲ ▲
ETS2	-1.24	-1.13093	▼ ▼
FBXW11	1.08	1.07278	▲ ▲
FBXW4	1.35	1.3125	▲ ▲
FGF7	9.74	6.43822	▲ ▲
FN1	29.41	23.4674	▲ ▲
FOSL1	2.35	8.81683	▲ ▲
FRAT1	-6.69	-6.38942	▼ ▼
FRZB	-1.67	-1.45683	▼ ▼
FZD1	3.92	3.76302	▲ ▲
FZD2	-1.59	-1.16551	▼ ▼
FZD3	3.62	4.06824	▲ ▲
FZD4	2.24	2.15232	▲ ▲
FZD5	7.09	3.22496	▲ ▲
FZD6	1.09	-1.25969	▲ ▼
FZD7	5.35	4.76268	▲ ▲
FZD8	5.02	6.56516	▲ ▲
FZD9	1.05	-2.02707	▲ ▼
GPC4	11.91	12.1168	▲ ▲
GSK3A	-1.37	-1.50335	▼ ▼
GSK3B	-1.09	-1.54254	▼ ▼
ID2	-1.28	-1.09684	▼ ▼
IGF1	4.39	3.2411	▲ ▲
IGF2	5.87	6.79645	▲ ▲
IL6	3.29	14.9256	▲ ▲
IRS1	9.36	7.38095	▲ ▲
JAG1	3.62	3.07807	▲ ▲
JUN	-1.06	1.07209	▼ ▲
KLF5	-5.63	-10.3895	▼ ▼

FIG. 4 (Ct'd)

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KREMEN1	1.23	-1.03297	▲ ▼
LEF1	1.81	1.69259	▲ ▲
LRP5	4.65	3.48757	▲ ▲
LRP6	6.61	5.06932	▲ ▲
MAPK10	2.84	4.72325	▲ ▲
MAPK8	1.77	1.62455	▲ ▲
MAPK9	1.12	-1.08418	▲ ▼
MMP2	13.63	14.6033	▲ ▲
MMP7	1.71	4.12215	▲ ▲
MMP9	3.96	4.04802	▲ ▲
MYC	-1.64	-2.0785	▼ ▼
MYLK	5.63	4.76386	▲ ▲
NANOG	3.12	-13.0273	▲ ▼
NFATC1	6.84	5.35883	▲ ▲
NKD1	2.34	7.78783	▲ ▲
NLK	-1.4	-2.12254	▼ ▼
NRCAM	2.53	4.03843	▲ ▲
NRP1	3.46	2.74305	▲ ▲
PDGFRA	7.92	6.15142	▲ ▲
PKN1	-1.77	-1.63403	▼ ▼
PLAUR	1.1	1.05357	▲ ▲
PLCB1	1.35	1.17242	▲ ▲
PLCB4	7.97	6.12039	▲ ▲
PORCN	2.37	3.07014	▲ ▲
PPARD	4.01	3.45186	▲ ▲
PPP3CA	1.26	1.28752	▲ ▲
PPP3CB	1.28	1.01846	▲ ▲
PPP3CC	2.35	1.79711	▲ ▲
PPP3R1	-1.33	-1.56115	▼ ▼
PRKACA	1.55	1.30153	▲ ▲
PRKACB	-1.24	-1.47185	▼ ▼
PRKCA	3.19	1.8796	▲ ▲
PRKCB	-10.66	-19.8993	▼ ▼
PRKX	1.62	1.20728	▲ ▲
PROM1	-2.27	-33.4776	▼ ▼

FIG. 4 (Ct'd)

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PTGS2	-3.06	-4.11791	▼ ▼
PYG01	8.97	6.65938	▲ ▲
RAC1	1.9	1.55254	▲ ▲
RAC2	-5.72	-5.43876	▼ ▼
RAC3	2.78	2.96437	▲ ▲
RBX1	-1.45	-1.21178	▼ ▼
RHOA	-1.09	-1.09831	▼ ▼
RUNX2	8.34	6.99245	▲ ▲
RUVBL1	1.08	1.03385	▲ ▲
SERPINE1	10.61	10.9703	▲ ▲
SERP1	3.97	4.27681	▲ ▲
SERP2	7.99	14.8627	▲ ▲
SERP4	61.98	60.3783	▲ ▲
SIX1	3.2	2.75059	▲ ▲
SKP1	1.08	1.32858	▲ ▲
SMAD2	1.26	1.10331	▲ ▲
SMAD3	5.13	4.04614	▲ ▲
SMAD4	1.23	1.06156	▲ ▲
SMO	5.39	6.71461	▲ ▲
SNAI1	7.71	15.1701	▲ ▲
SNAI2	3.95	3.85262	▲ ▲
SOST	8.83	9.31998	▲ ▲
SOX17	2.94	4.25097	▲ ▲
SOX2	1.39	-3.17575	▲ ▼
SOX9	9.29	10.8832	▲ ▲
STAT3	1.05	-1.27273	▲ ▼
TBL1XR1	1.1	1.06063	▲ ▲
TCF4	4.08	2.93434	▲ ▲
TCF7	1.23	1.2438	▲ ▲
TCF7L1	4.15	5.40034	▲ ▲
TGFB1	1.33	1.02346	▲ ▲
TGFB3	8.99	8.25937	▲ ▲
TIMP1	9.2	12.3724	▲ ▲
TLE1	-1.75	-1.51951	▼ ▼
TP53	1.08	1.00756	▲ ▲

FIG. 4 (Ct'd)

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TWIST1	10.27	8.69102	▲ ▲
TWIST2	2.21	-1.39813	▲ ▼
VANGL1	1.48	1.17249	▲ ▲
VEGFA	1.53	1.31057	▲ ▲
WIF1	9.19	10.2806	▲ ▲
WNT1	1.39	12.8474	▲ ▲
WNT10B	3.39	1.58875	▲ ▲
WNT11	-1.05	-1.52906	▼ ▼
WNT16	2.59	23.6165	▲ ▲
WNT2B	9.35	23.0953	▲ ▲
WNT3	3.48	5.88266	▲ ▲
WNT4	1.96	7.90079	▲ ▲
WNT5A	4.93	13.6062	▲ ▲
WNT5B	3.8	5.29943	▲ ▲
WNT9A	1.64	2.53034	▲ ▲
ZEB1	2.86	2.90082	▲ ▲
ZEB2	1.49	1.05145	▲ ▲

FIG. 4 (Ct'd)

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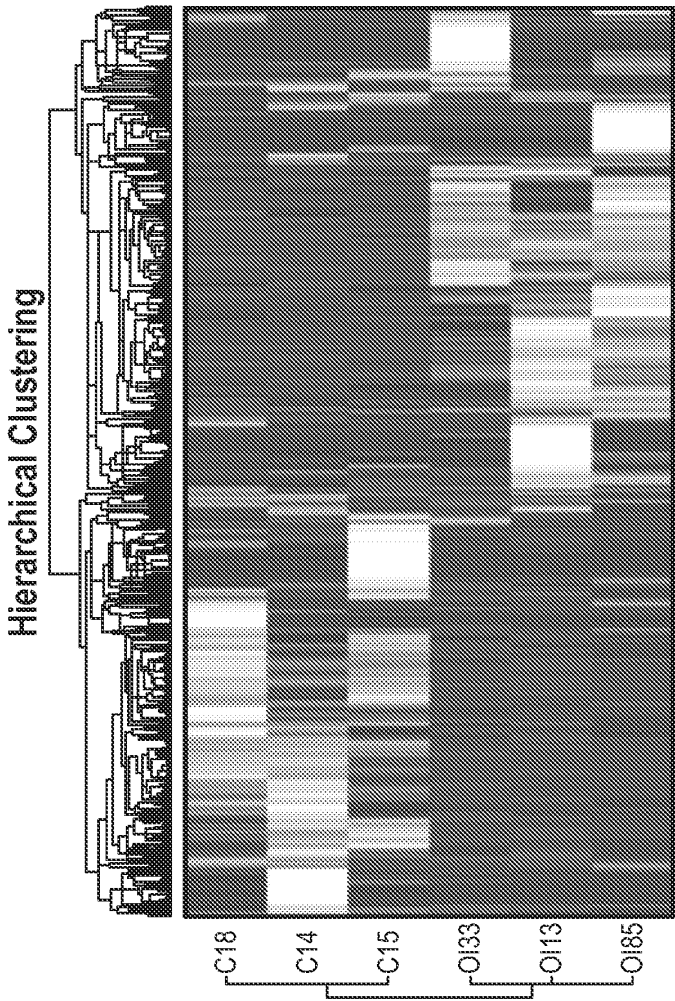


FIG. 5B

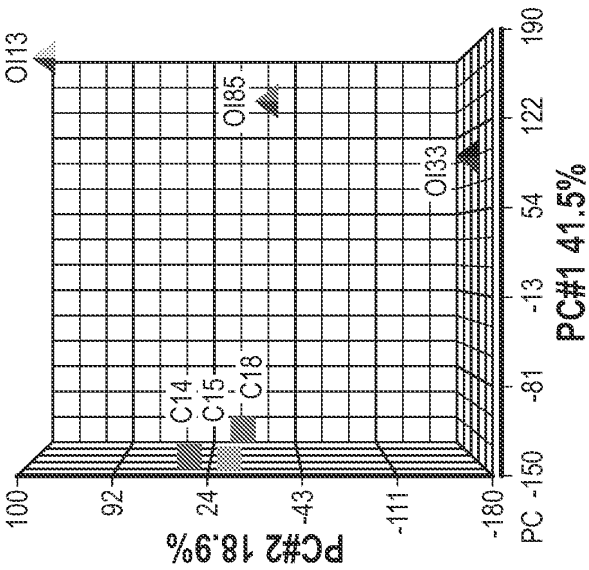


FIG. 5A

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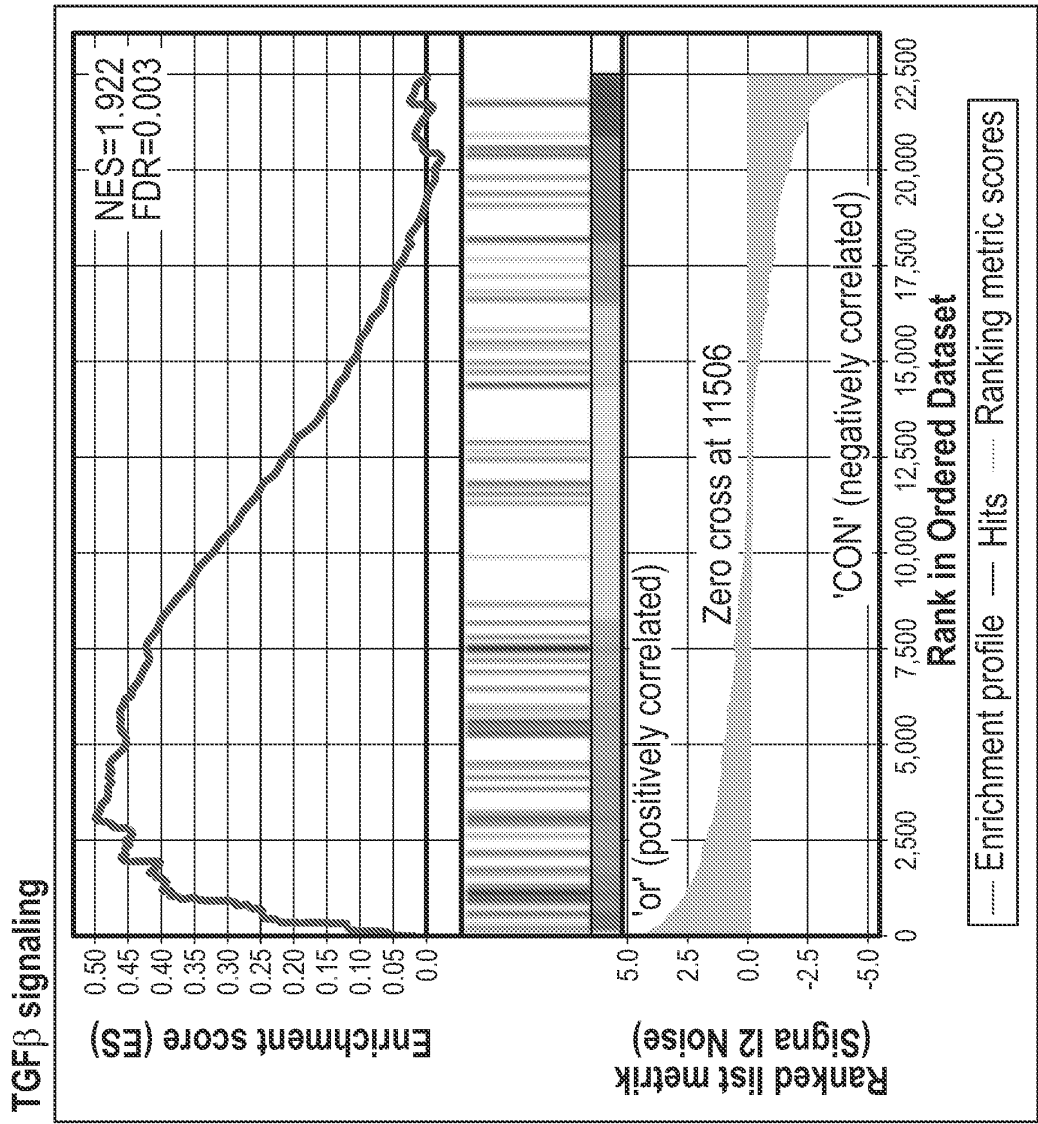


FIG. 5C

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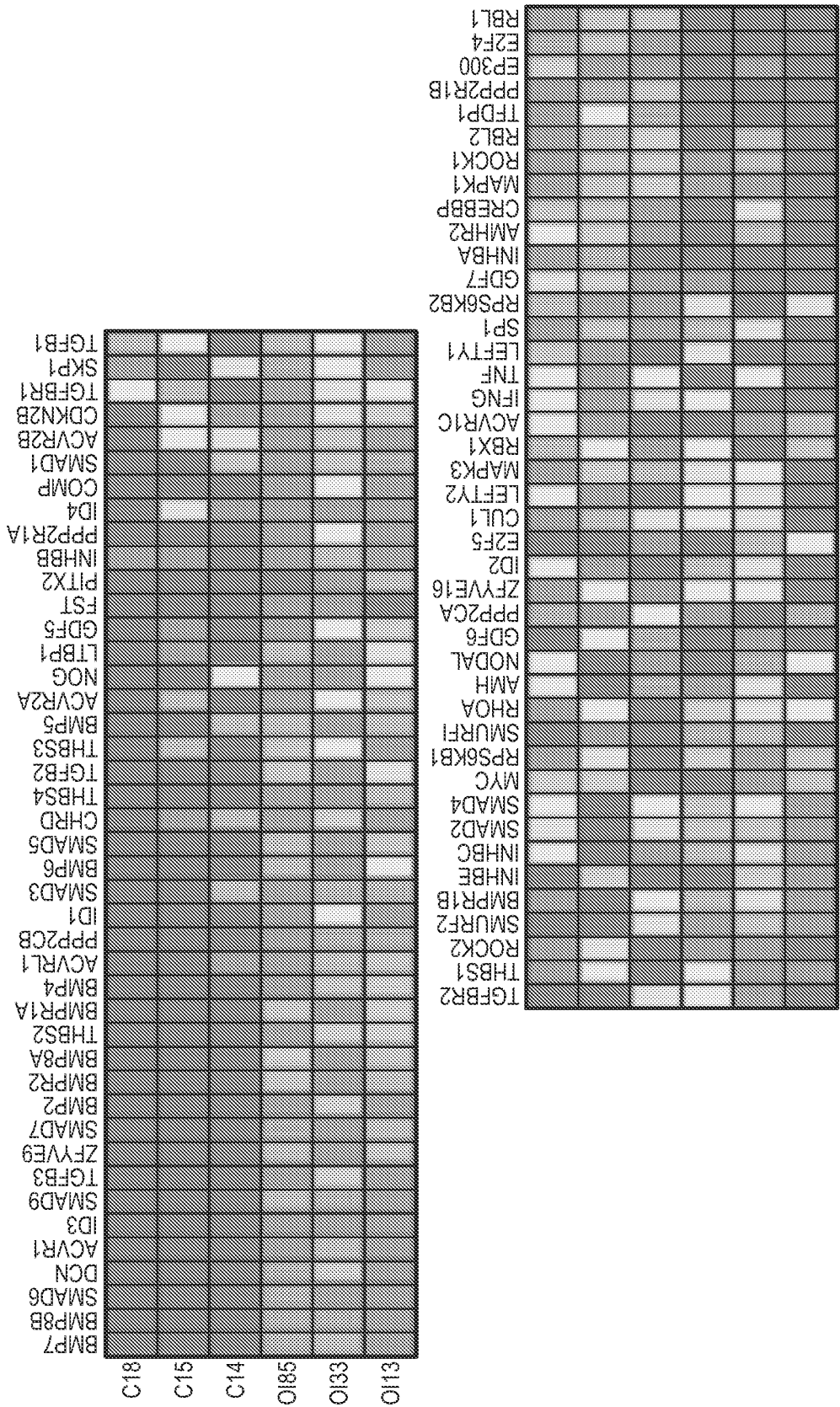


FIG. 5C (c't'd)

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GO Description (skeletal processes)	Fold-Change (type III-OI vs. non-OI)	p-value (type III-OI vs.
endochondral bone growth	7.287	1.17E-05
chondrocyte morphogenesis involved in endochondral bone morphogenesis	12.285	1.43E-05
bone growth	4.34723	4.70E-05
negative regulation of bone resorption	-2.88519	0.000161234
negative regulation of bone remodeling	-2.36441	0.00110482
bone development	10.7658	0.00132594
bone mineralization	8.34987	0.00381378
ossification involved in bone remodeling	3.4404	0.00540422
regulation of bone resorption	8.59378	0.00548954
regulation of bone remodeling	8.32706	0.00561937
bone maturation	7.26146	0.00988044
bone resorption	6.36501	0.010371
negative regulation of bone trabecula formation	16.0694	0.0166998
regulation of bone trabecula formation	16.0694	0.0166998
bone sialoprotein binding	5.19392	0.0176736
regulation of bone mineralization involved in bone maturation	-28.2323	0.0236997
cartilage development involved in endochondral bone morphogenesis	14.868	0.0242692
negative regulation of bone development	-16.3685	0.0283596
bone regeneration	26.1114	0.0287582
bone trabecula formation	16.0418	0.0302454
positive regulation of bone remodeling	9.61137	0.0306748
positive regulation of bone resorption	9.61137	0.0306748
negative regulation of bone mineralization	-10.7757	0.0311633
chondrocyte development involved in endochondral bone morphogenesis	11.3451	0.0359546
bone mineralization involved in bone maturation	2.87887	0.0419037
GO Description (bone cell)		
negative regulation of osteoblast proliferation	2.22207	2.15E-05
osteoblast fate commitment	4.90698	3.07E-05
negative regulation of osteoblast differentiation	2.66556	0.000141706
osteoblast differentiation	7.49776	0.000142369
multinuclear osteoclast differentiation	14.4354	0.000228921
osteoclast fusion	3.15526	0.000793769
osteoclast proliferation	2.51853	0.00371519
canonical Wnt signaling pathway involved in osteoblast differentiation	3.11805	0.00755837

FIG. 6

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osteoclast development	4.04888	0.0198194
negative regulation of osteoclast development	-26.1861	0.0316139
regulation of osteoclast development	4.68109	0.0330839
GO Description (collagen)		
basement membrane collagen trimer	9.2481	3.17E-08
collagen type IV trimer	8.38671	1.99E-07
network-forming collagen trimer	8.88915	1.24E-06
collagen binding	9.27665	1.03E-05
collagen type VI trimer	14.8057	1.36E-05
collagen type I trimer	17.6667	1.43E-05
collagen type V trimer	16.3428	8.99E-05
procollagen glucosyltransferase activity	4.48645	0.000149957
procollagen-lysine 5-dioxygenase activity	4.48645	0.000149957
collagen type XI trimer	8.86367	0.000183017
negative regulation of collagen biosynthetic process	296974	0.000313779
collagen trimer	12.8713	0.000364947
collagen fibril organization	16.3914	0.00038828
fibrillar collagen trimer	18.1736	0.000544796
collagen binding involved in cell-matrix adhesion	4.07414	0.000626421
procollagen-proline 3-dioxygenase activity	4.87836	0.000702521
regulation of collagen metabolic process	2.66046	0.00084668
FACIT collagen trimer	136753	0.00315539
collagen metabolic process	522527	0.00334926
positive regulation of collagen fibril organization	-1.69534	0.0053537
regulation of collagen binding	1.77884	0.00603761
collagen catabolic process	2.4754	0.0101241
regulation of collagen biosynthetic process	228526	0.0124448
collagen type IX trimer	2.61785	0.0150679
negative regulation of collagen metabolic process	5.88237	0.0157624
anchoring collagen complex	7.41827	0.0192886
procollagen-proline dioxygenase activity	1.53059	0.0197611
regulation of collagen catabolic process	452372	0.0207595
regulation of collagen fibril organization	2.27696	0.0237879
collagen biosynthetic process	14.3292	0.0242519
positive regulation of collagen biosynthetic process	2.23125	0.0260785

FIG. 6 (Ct'd)

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collagen-activated tyrosine kinase receptor signaling pathway	14.7564	0.0337297
positive regulation of collagen metabolic process	210169	0.0343009
collagen-activated signaling pathway	14.2385	0.0345897
collagen V binding	2.63337	0.037715
GO Description (signalings)		
BMP-TGFB-SMAD pathway		
regulation of pathway-restricted SMAD protein phosphorylation	1.9132	1.78E-15
positive regulation of pathway-restricted SMAD protein phosphorylation	1.75904	5.52E-10
BMP signaling pathway involved in heart development	6.32046	3.05E-08
BMP receptor activity	4.37232	6.82E-08
negative regulation of pathway-restricted SMAD protein phosphorylation	2.95784	6.87E-07
BMP signaling pathway	1.85204	1.89E-06
SMAD protein complex	1.84992	1.29E-05
regulation of SMAD protein signal transduction	1.56768	1.48E-05
cellular response to BMP stimulus	2.61486	4.26E-05
response to BMP	2.51486	4.26E-05
regulation of BMP signaling pathway	2.27219	6.21E-05
BMP signaling pathway involved in heart induction	6.21233	8.02E-05
negative regulation of BMP signaling pathway	3.65398	0.000256342
positive regulation of SMAD protein signal transduction	1.59282	0.000370139
pathway-restricted SMAD protein phosphorylation	1.59586	0.000697365
BMP binding	5.68836	0.000776934
sequestering of BMP in extracellular matrix	5.89231	0.0020908
I-SMAD binding	2.44361	0.00250722
ubiquitin-dependent SMAD protein catabolic process	1.50169	0.00253508
negative regulation of SMAD protein complex assembly	2.36255	0.00440533
BMP receptor complex	5.9346	0.00975955
heteromeric SMAD protein complex	2.06791	0.00998822
sequestering of BMP from receptor via BMP binding	13.3266	0.0134818
SMAD binding	6.45579	0.0174112
CO-SMAD binding	1.40594	0.023062
sequestering of TGFbeta in extracellular matrix	2.24538	0.0255493
common-partner SMAD protein phosphorylation	1.35043	0.0347033
PTH pathway		
regulation of parathyroid hormone secretion	2.69296	0.000107909

FIG. 6 (Ct'd)

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response to parathyroid hormone	4.33042	0.00888953
cellular response to parathyroid hormone stimulus	4.29618	0.0111016
parathyroid hormone receptor activity	11.5593	0.0324121
Wnt pathway		
Wnt-activated receptor activity	2.40412	8.70E-12
coreceptor activity involved in Wnt signaling pathway	3.6538	2.74E-09
coreceptor activity involved in Wnt signaling pathway, planar cell polarity path	4.05464	2.25E-07
non-canonical Wnt signaling pathway involved in heart development	4.02729	5.07E-06
cell-cell signaling by wnt	1.67483	5.10E-06
regulation of Wnt signaling pathway, planar cell polarity pathway	2.24682	3.08E-05
negative regulation of canonical Wnt signaling pathway	1.52176	4.58E-05
negative regulation of Wnt signaling pathway involved in heart development	6.70623	4.90E-05
Wnt-Frizzled-LRP5/6 complex	3.32807	6.79E-05
non-canonical Wnt signaling pathway via JNK cascade	1.79975	7.75E-05
non-canonical Wnt signaling pathway via MAPK cascade	1.79975	7.75E-05
positive regulation of non-canonical Wnt signaling pathway	1.8355	0.000140655
Wnt-protein binding	5.1743	0.000141805
positive regulation of Wnt signaling pathway, planar cell polarity pathway	2.63363	0.000263596
canonical Wnt signaling pathway	2.26268	0.000477398
Wnt signaling pathway involved in somitogenesis	4.53428	0.00116124
coreceptor activity involved in canonical Wnt signaling pathway	2.79128	0.0023108
Wnt signalosome	2.53915	0.00376134
Wnt signaling pathway involved in midbrain dopaminergic neuron differentiat	3.26016	0.00641548
canonical Wnt signaling pathway involved in osteoblast differentiation	3.11805	0.00755837
canonical Wnt signaling pathway involved in mesenchymal stem cell different	3.11805	0.00755837
non-canonical Wnt signaling pathway involved in midbrain dopaminergic neur	11.0208	0.0109965
regulation of non-canonical Wnt signaling pathway	3.73156	0.0112258
canonical Wnt signaling pathway involved in positive regulation of epithelial to	3.45267	0.0140602
regulation of Wnt signaling pathway involved in heart development	1.8621	0.0173057
canonical Wnt signaling pathway involved in negative regulation of apoptotic	3.35327	0.0175123
canonical Wnt signaling pathway involved in midbrain dopaminergic neuron d	3.48379	0.0189235
canonical Wnt signaling pathway involved in regulation of cell proliferation	3.13105	0.0190095
Wnt signaling pathway involved in heart development	3.49896	0.0190717
positive regulation of canonical Wnt signaling pathway	8.76137	0.029452
Wnt signaling pathway involved in kidney development	2.53559	0.0321294

FIG. 6 (Ct'd)

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canonical Wnt signaling pathway involved in metanephric kidney developmer	253553	0.0321294
receptor internalization involved in canonical Wnt signaling pathway	132474	0.0469052
Notch pathway		
Notch signaling pathway	1.41319	5.24E-07
Notch signaling involved in heart development	2.58092	1.14E-06
positive regulation of Notch signaling pathway involved in heart induction	12.3556	3.49E-05
regulation of Notch signaling pathway involved in heart induction	12.3556	3.49E-05
Notch receptor processing	1.3087	9.91E-05
regulation of Notch signaling pathway	1.59976	0.000413664
negative regulation of Notch signaling pathway	192805	0.00121142
Notch receptor processing, ligand-dependent	1.23327	0.00160884
Notch binding	1.46883	0.00328016

FIG. 6 (Ct'd)

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Enriched in OI			
NAME	SIZE	NES	FDR q-val
KEGG_ECM_RECEPTOR_INTERACTION	84	2.339636	0
KEGG_AXON_GUIDANCE	126	2.273109	0
KEGG_RIBOSOME	86	2.20289	0
KEGG_BASAL_CELL_CARCINOMA	52	2.184527	0
KEGG_HEDGEHOG_SIGNALING_PATHWAY	52	2.125225	3.80E-04
KEGG_OXIDATIVE_PHOSPHORYLATION	100	1.962538	0.002574329
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	72	1.958541	0.002206568
KEGG_TGF_BETA_SIGNALING_PATHWAY	85	1.922398	0.002956642
KEGG_FOCAL_ADHESION	196	1.920776	0.002628126
KEGG_DILATED_CARDIOMYOPATHY	86	1.782992	0.012805709
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	81	1.775682	0.012355667
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	22	1.712079	0.021667305
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	43	1.589217	0.065860495
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	20	1.577811	0.067966476
KEGG_MELANOGENESIS	96	1.573888	0.06563165
KEGG_WNT_SIGNALING_PATHWAY	143	1.550264	0.075821064
KEGG_CARDIAC_MUSCLE_CONTRACTION	70	1.536894	0.07994007
KEGG_ARGININE_AND_PROLINE_METABOLISM	51	1.536057	0.076143146
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	201	1.526596	0.077296056
KEGG_PARKINSONS_DISEASE	99	1.524883	0.07433726
Enriched in non-OI Control			
KEGG_CELL_CYCLE	124	-2.73731	0
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	127	-2.5927	0
KEGG_DNA_REPLICATION	36	-2.42541	0
KEGG_PRIMARY_IMMUNODEFICIENCY	35	-2.21236	0
KEGG_HOMOLOGOUS_RECOMBINATION	26	-2.15544	0
KEGG_ALLOGRAFT_REJECTION	34	-2.08262	2.01E-04
KEGG_GRAFT_VERSUS_HOST_DISEASE	37	-2.07938	1.73E-04
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	67	-2.03467	2.85E-04

FIG. 7

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KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	45	-2.01954	3.62E-04
KEGG_NOD LIKE RECEPTOR SIGNALING PATHWAY	58	-1.99138	0.00100543
KEGG_MISMATCH_REPAIR	23	-1.97318	0.001137212
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	73	-1.95996	0.001130859
KEGG_SPLICEOSOME	123	-1.95844	0.00104387
KEGG_ASTHMA	25	-1.90949	0.002485069
KEGG_OOCYTE_MEIOSIS	103	-1.90937	0.002319398
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	116	-1.84026	0.004830883
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	43	-1.83701	0.004667846
KEGG_LEISHMANIA_INFECTION	70	-1.82533	0.005159228
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	28	-1.81043	0.005525905
KEGG_FC_EPSILON_R1_SIGNALING_PATHWAY	73	-1.79883	0.005864094

FIG. 7 (Ct'd)

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Upstream Regulator	Molecule Type	Predicted State	Z-score	p-value of overlap
RNASeq dataset				
ERBB2	kinase	Inhibited	-3.342	2.78x10 ⁻²⁶
E2F4	transcription regulator	ND		1.63x10 ⁻¹⁹
RABL6	other	Inhibited	-6.172	6.21x10 ⁻¹⁸
MITF	transcription regulator	Inhibited	-5.353	1.31x10 ⁻¹⁷
TGFB1	growth factor	Activated	4.288	1.32x10 ⁻¹⁴
AR	ligand-dependent nuclear receptor	Activated	3.936	1.63x10 ⁻¹³
NUPR1	transcription regulator	Activated	4.1	2.28x10 ⁻¹³
CCND1	transcription regulator	ND	-0.918	2.59x10 ⁻¹³
CDK4	kinase	ND		3.11x10 ⁻¹³
AREG	growth factor	Inhibited	-2.856	1.37x10 ⁻¹¹
RARA	ligand-dependent nuclear receptor	ND	-1.278	3.15x10 ⁻¹¹
ESR1	ligand-dependent nuclear receptor	Inhibited	-2.129	5.65x10 ⁻¹¹
TP63	transcription regulator	Inhibited	-2.445	8.38x10 ⁻¹¹
HNF1A-AS1	other	ND	-0.61	1.94x10 ⁻¹⁰
FOXM1	transcription regulator	Inhibited	-3.999	8.18x10 ⁻¹⁰
SMARCA4	transcription regulator	ND	0.921	4.86x10 ⁻⁹
E2F1	transcription regulator	ND	0.723	1.05x10 ⁻⁸
E2f	group	Inhibited	-3.606	2.34x10 ⁻⁸
E2F3	transcription regulator	Inhibited	-2.53	4.84x10 ⁻⁸
CDKN1A	kinase	Activated	3.269	7.64x10 ⁻⁸
RPPA dataset				
TP53	transcription regulator	ND	0.057	8.6x10 ⁻¹⁶
PTEN	phosphatase	ND	-0.786	1.05x10 ⁻¹⁴
estrogen receptor	group	ND	-0.102	5.9x10 ⁻¹⁴
Hsp90	group	ND	1.3	1.23x10 ⁻¹²
PIM1	kinase	ND	1.767	3.4x10 ⁻¹²
EGFR	kinase	ND	0.785	5.13x10 ⁻¹²
TGFB1	growth factor	Activated	2.173	6.37x10 ⁻¹²
CCN5	growth factor	ND	-0.128	9.64x10 ⁻¹²
SLC9A3R1	other	ND	0.718	1.06x10 ⁻¹¹
SP1	transcription regulator	Activated	2.186	3.55x10 ⁻¹¹
THRB	ligand-dependent nuclear receptor	ND	-1.522	4.91x10 ⁻¹¹
PRKAR1A	kinase	Activated	2.2	1.02x10 ⁻¹⁰

FIG. 8

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BRCA1	transcription regulator	ND	0.869	1.05×10^{-10}
PTGS2	enzyme	ND	1.676	3.43×10^{-10}
JUN	transcription regulator	ND	-0.418	7.48×10^{-10}
SDCBP	enzyme	ND	1.998	1.09×10^{-9}
STAT3	transcription regulator	ND	1.427	1.26×10^{-9}
MUC4	other	ND	1.964	2.19×10^{-9}
Mek	group	ND	-1.89	2.96×10^{-9}
HIF1A	transcription regulator	Activated	2.2	5.02×10^{-9}

FIG. 8 (Ct'd)

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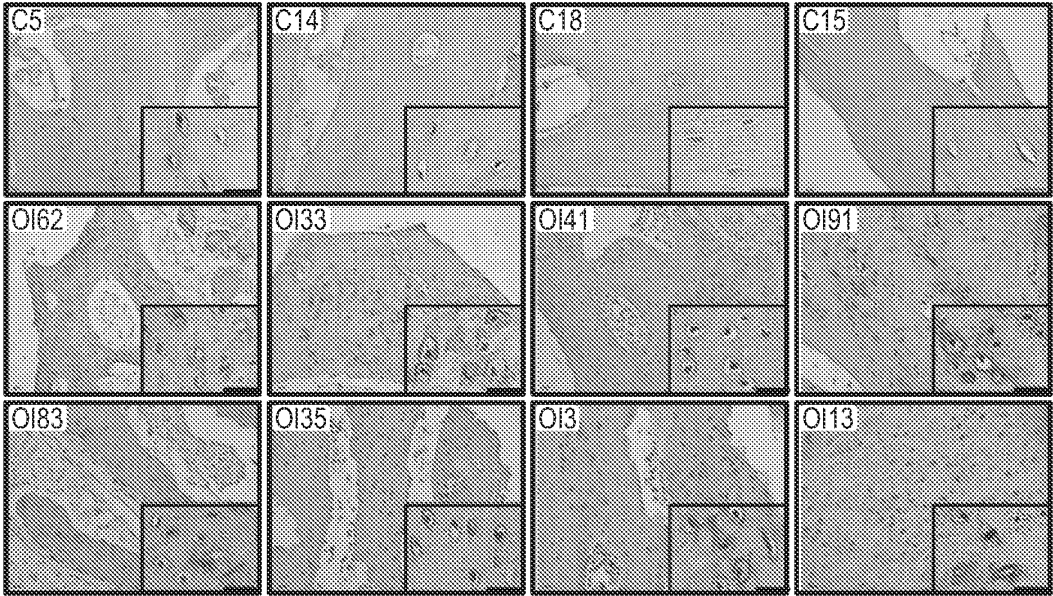


FIG. 9A

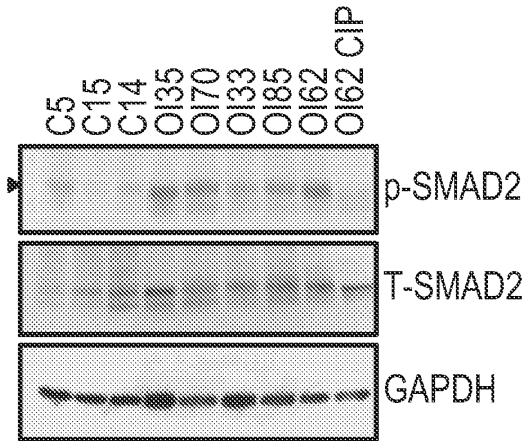


FIG. 9B

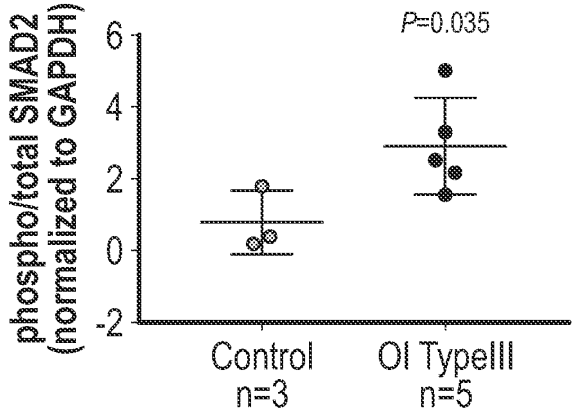


FIG. 9C

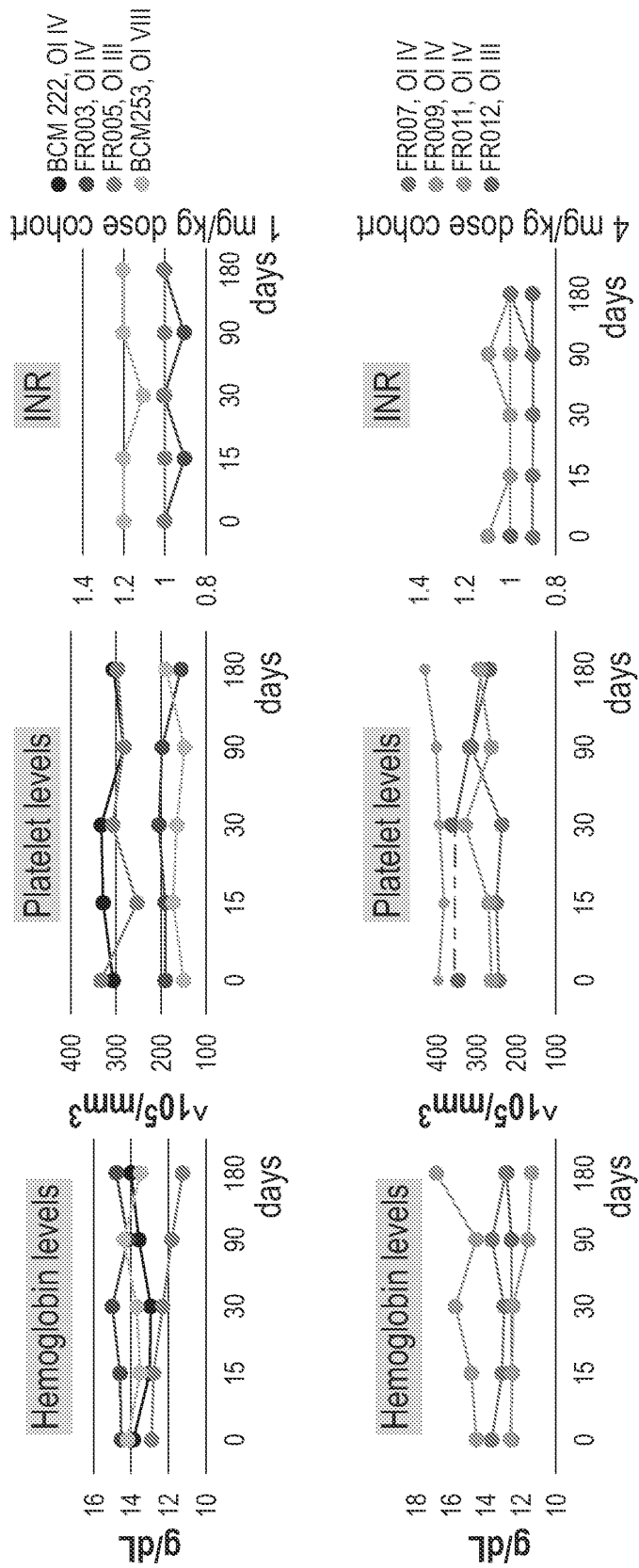


FIG. 10

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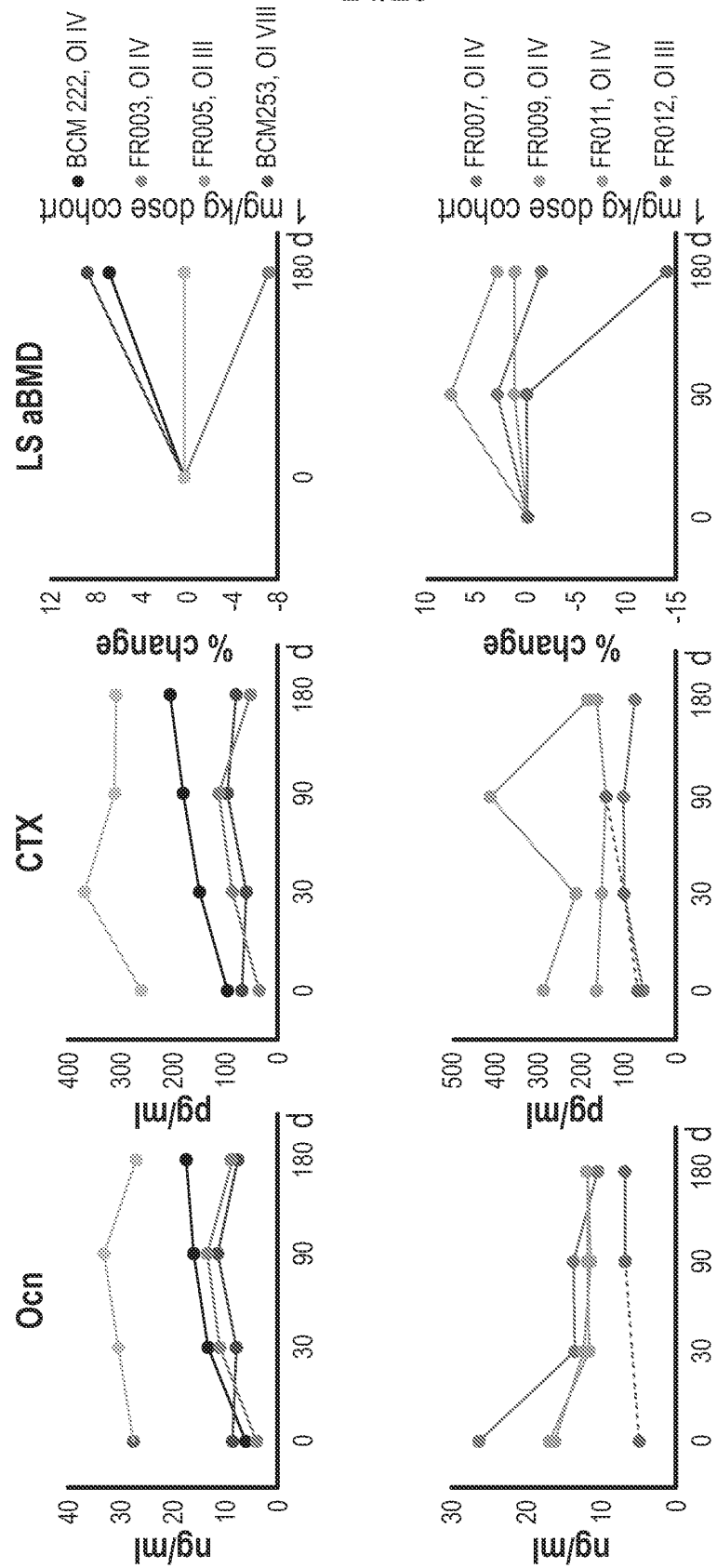


FIG. 11

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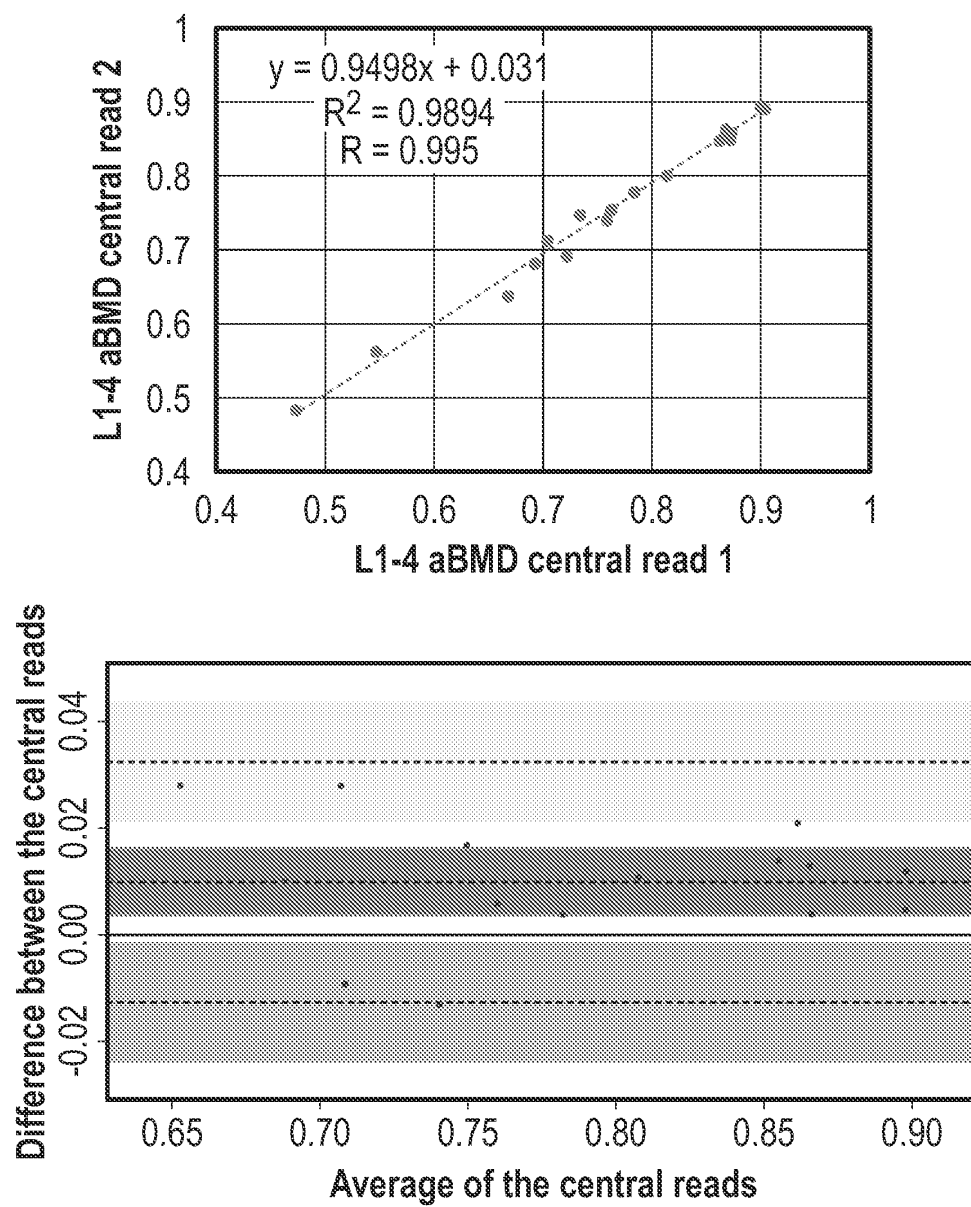


FIG. 12