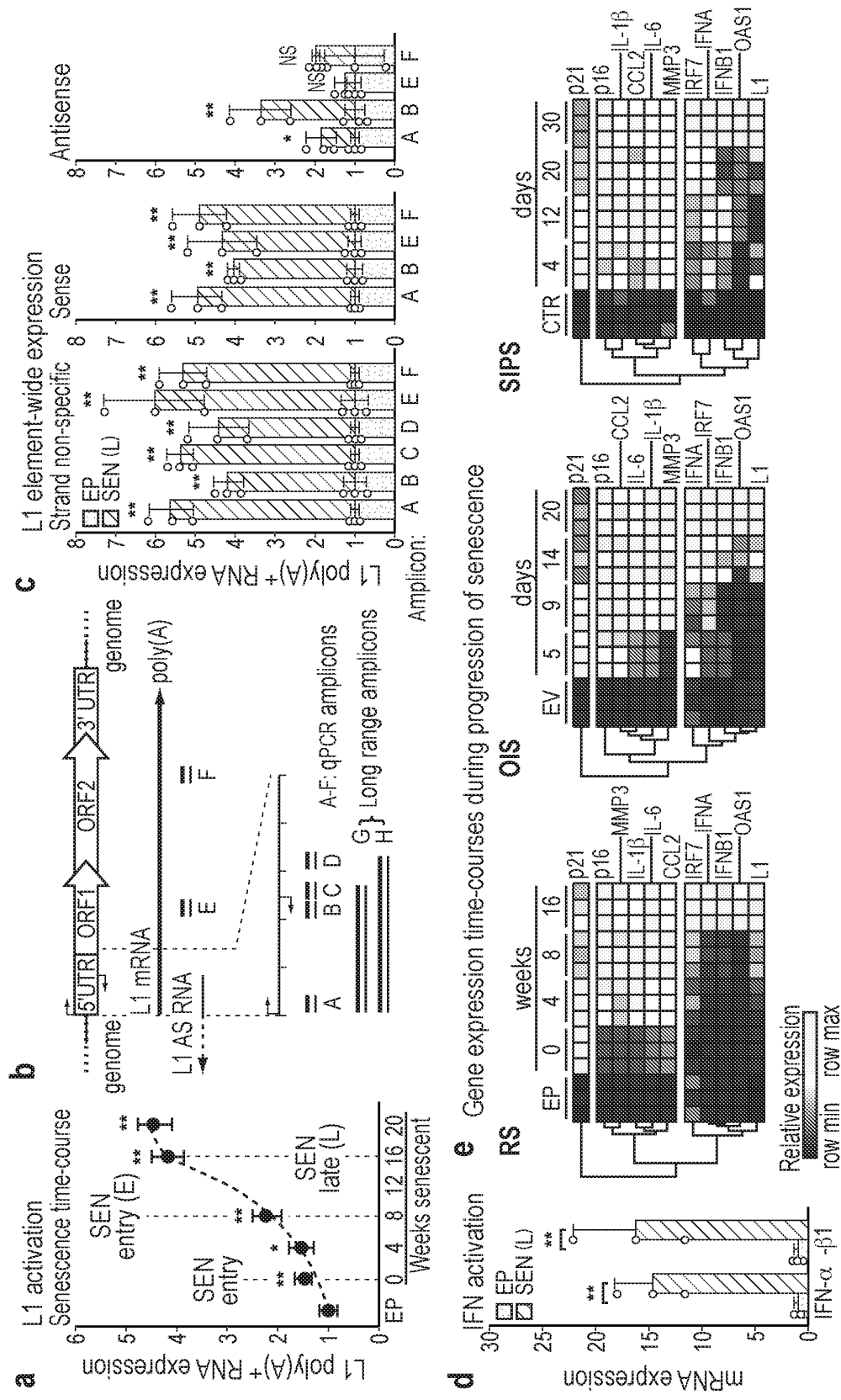
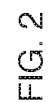






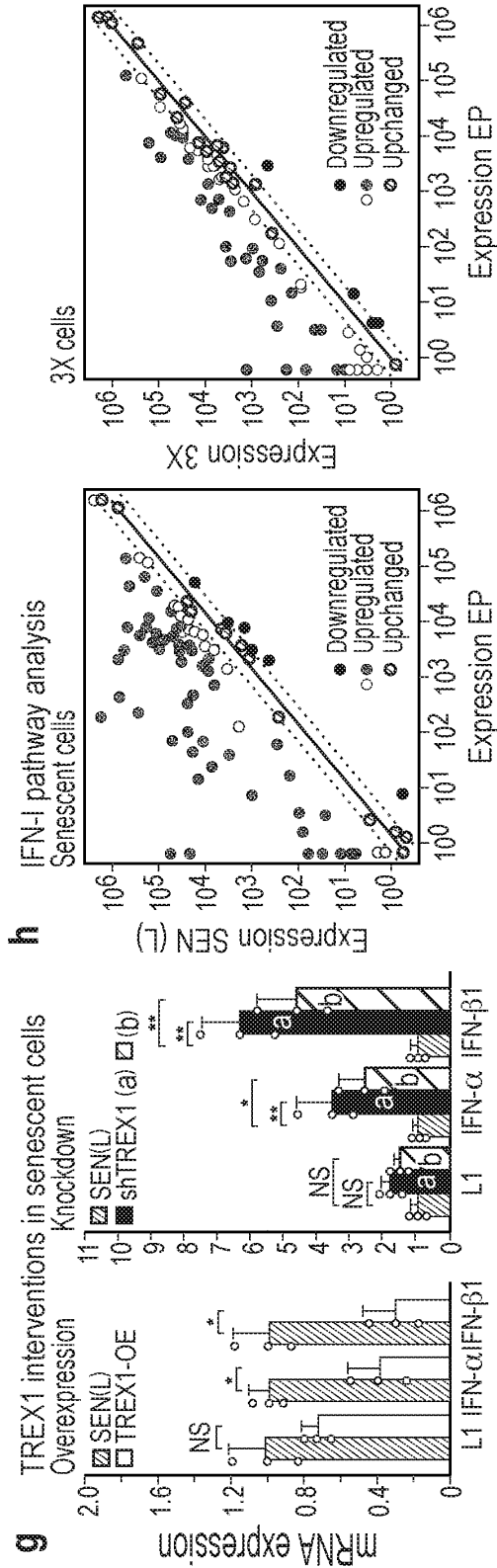


FIG. 2

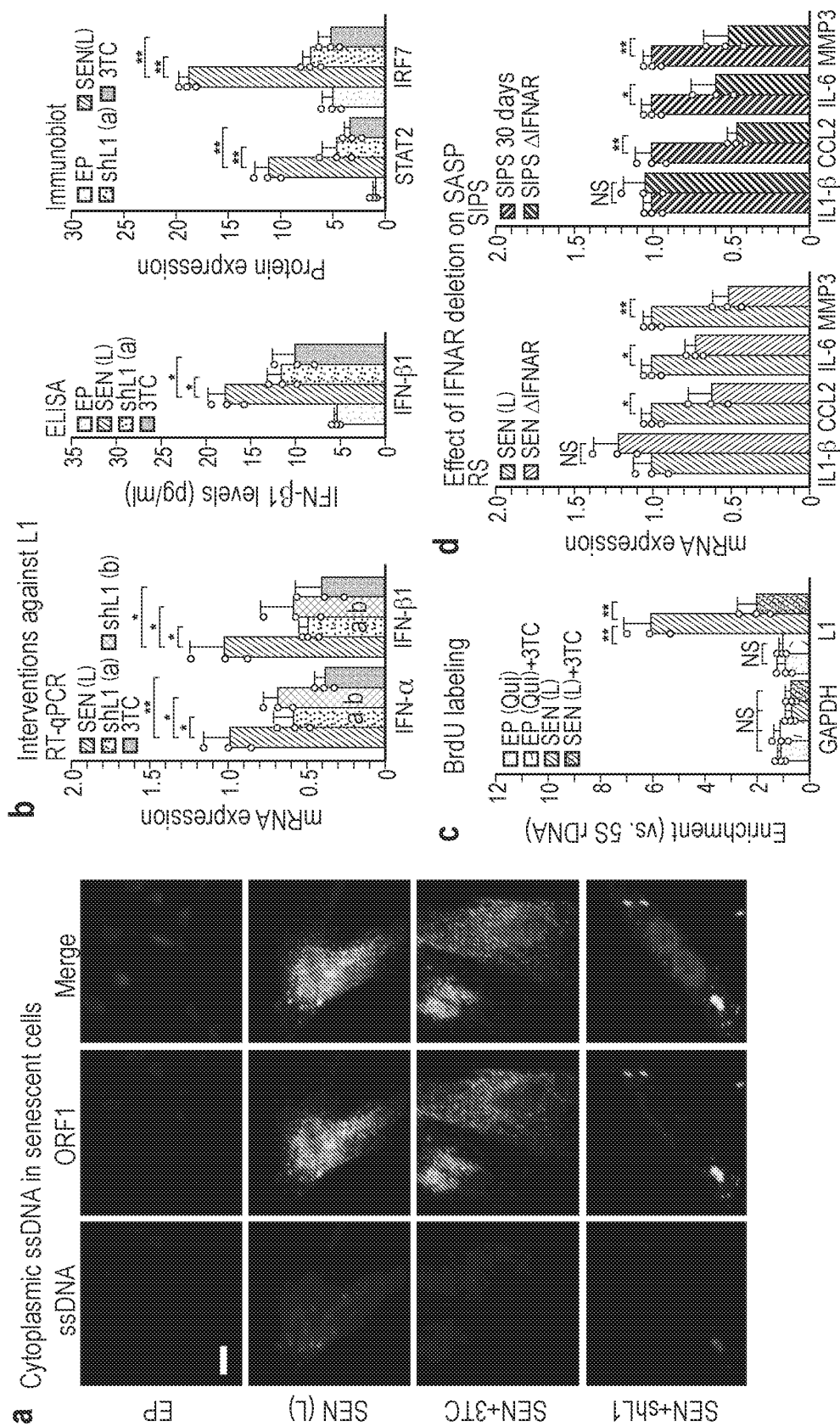


FIG. 3

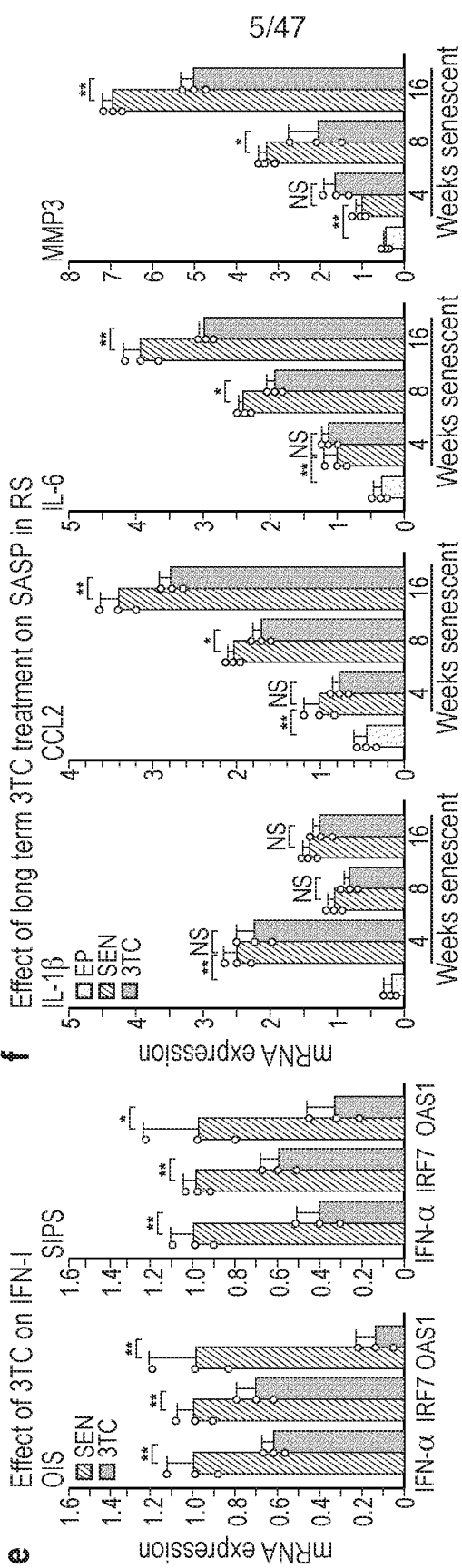
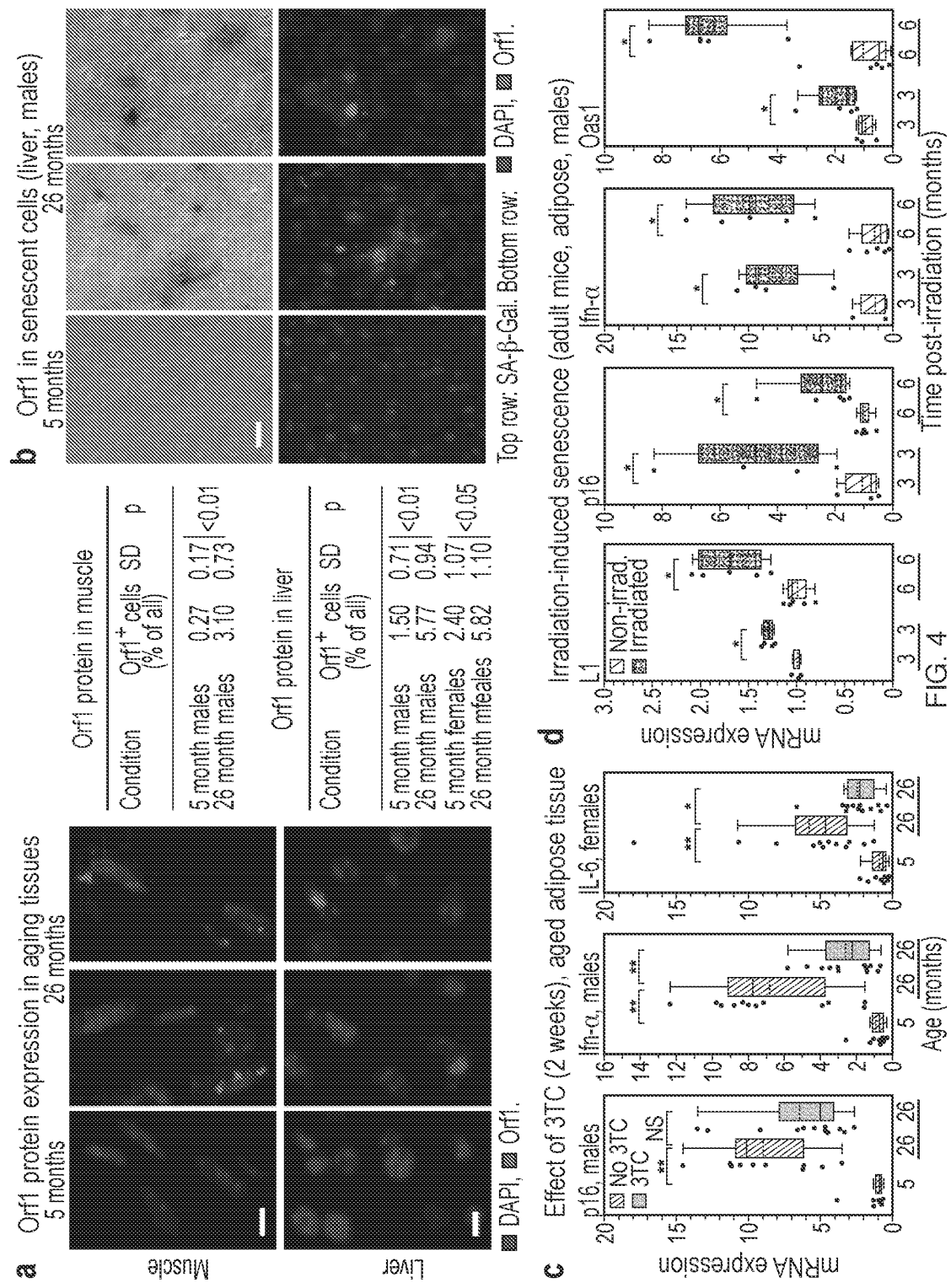


FIG. 3



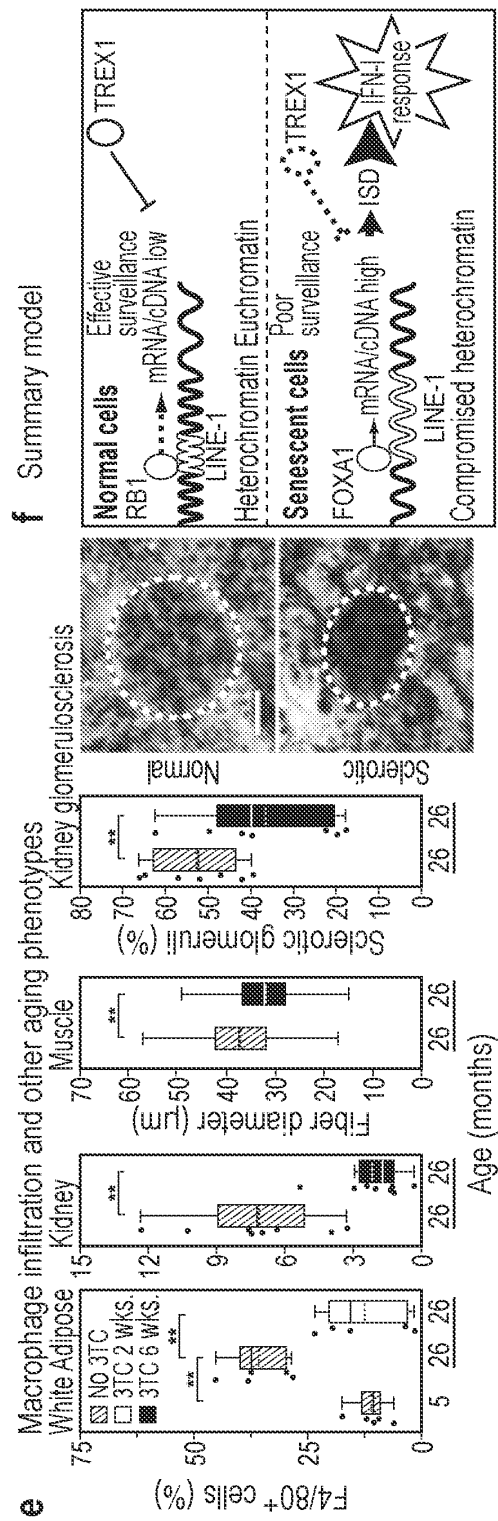


FIG. 4

ROLE OF CELLULAR SENESENCE IN AGE-ASSOCIATED INFLAMMATION

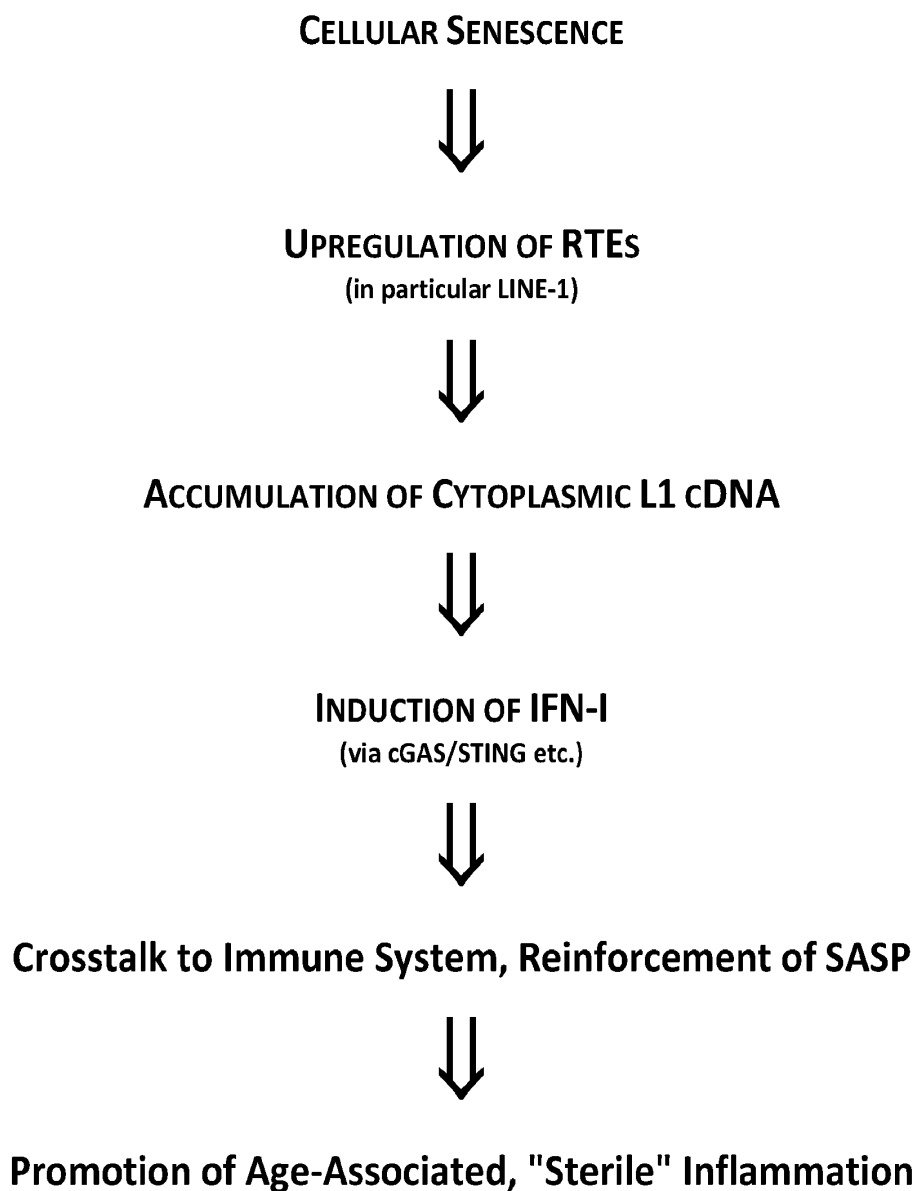
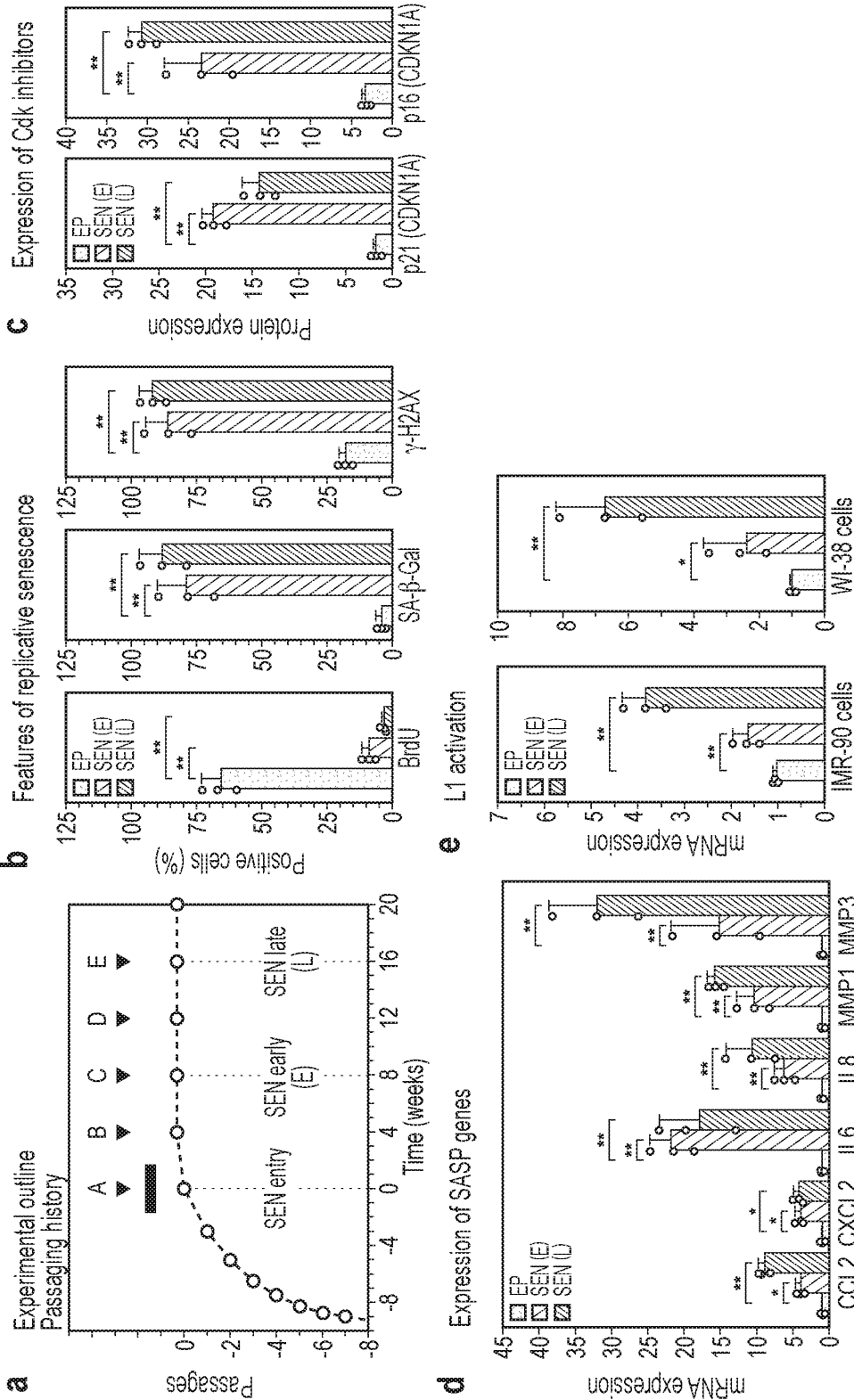


FIG. 5



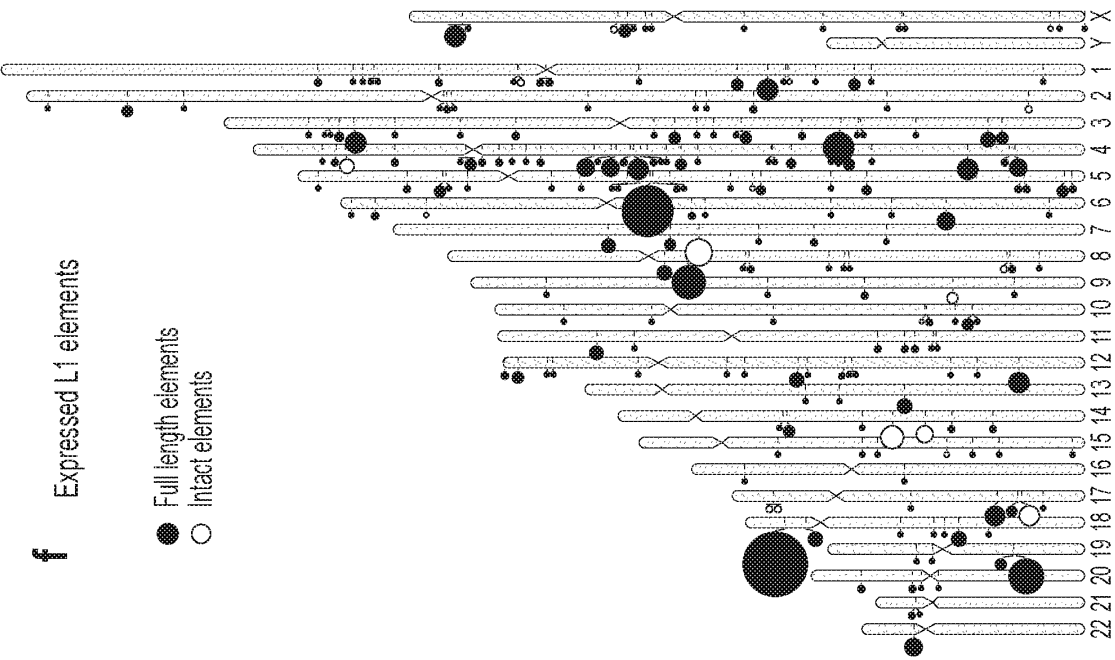


FIG. 6

g

Expressed L1 elements

Mappable clones	658
Intergenic (>5 kb on either side)	458
Intragenic	200

Family	Count	%
Individual elements	224	
L1Hs total	75	33.5
L1Hs non-intact	(56)	(25.0)
L1Hs intact	(19)	(8.5)
L1PA2	48	21.4
L1PA3	58	25.9
L1PA4	34	15.2
L1PA5	9	4.0

h

Genomic copy number

Amplicon	Predicted	Observed
A	991	1545
B	792	1200
C	722	950
D	1525	1600
E	1235	2200
F	2996	4000
G	1795	2000
H	1970	2000

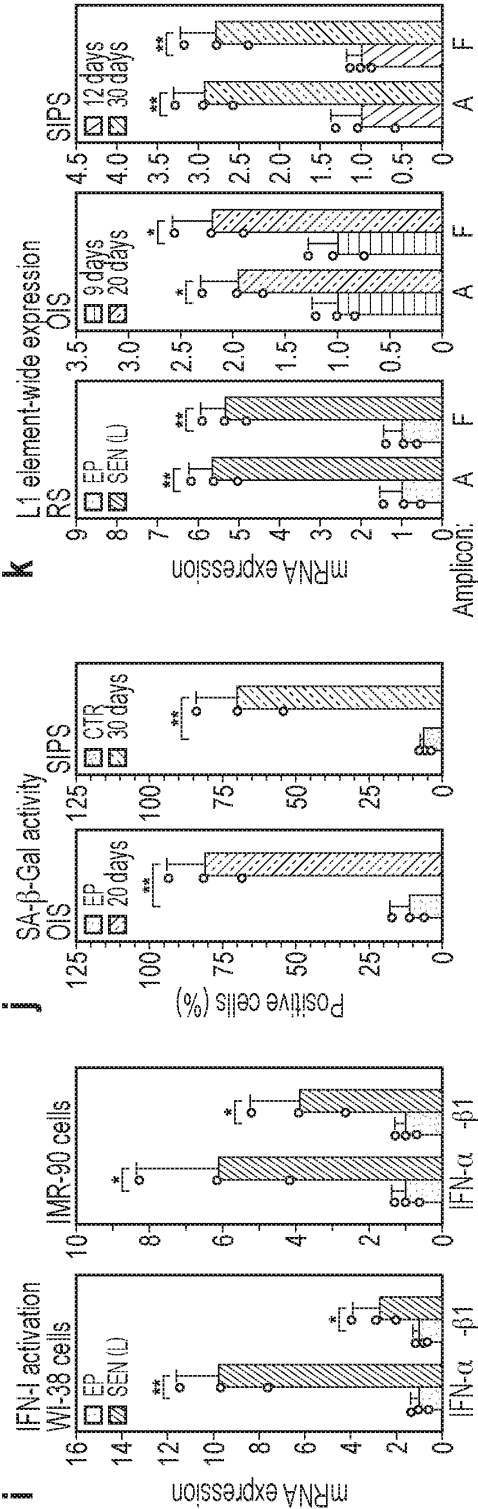
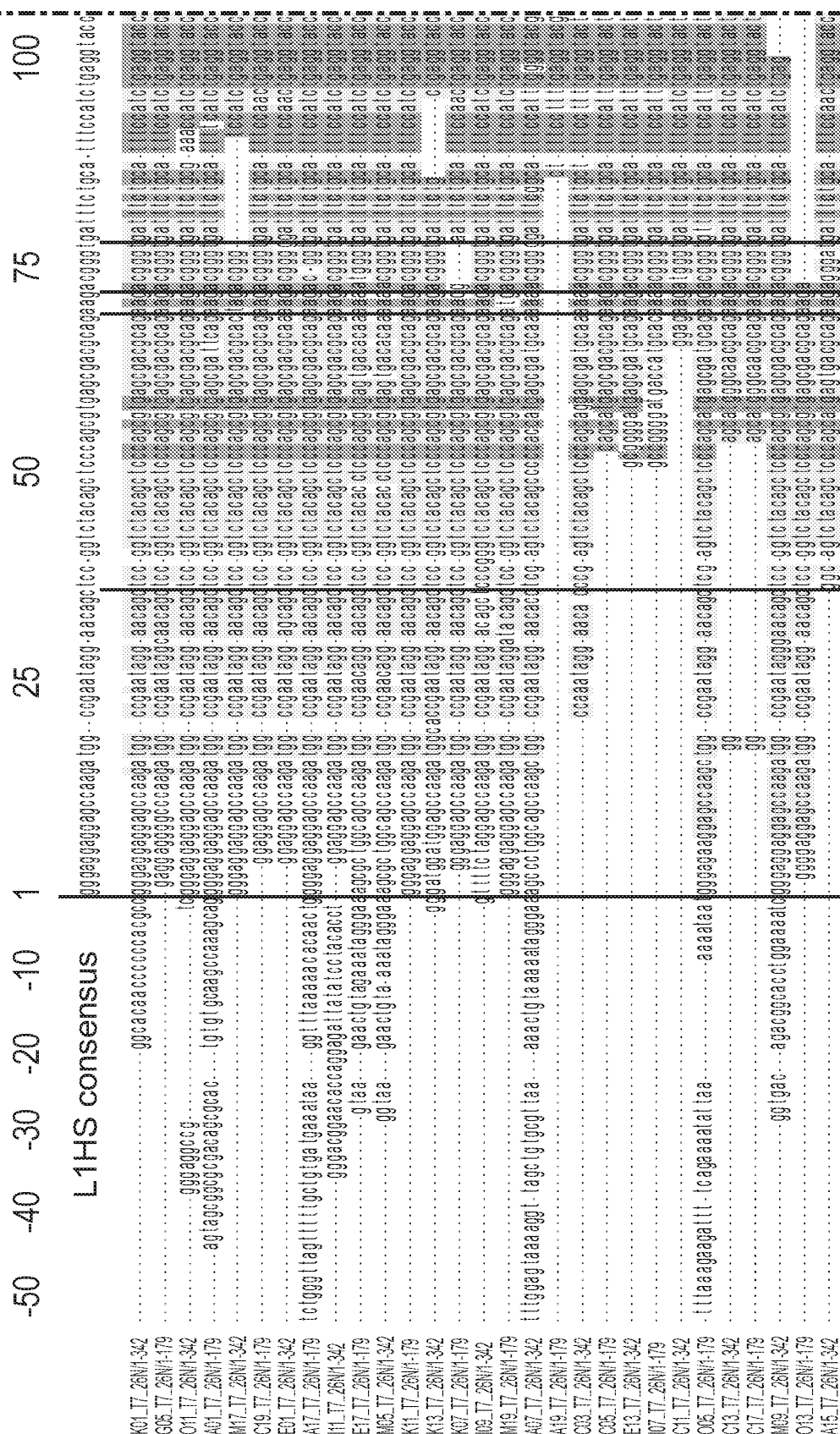


FIG. 6

L1HS consensus start



ZGF

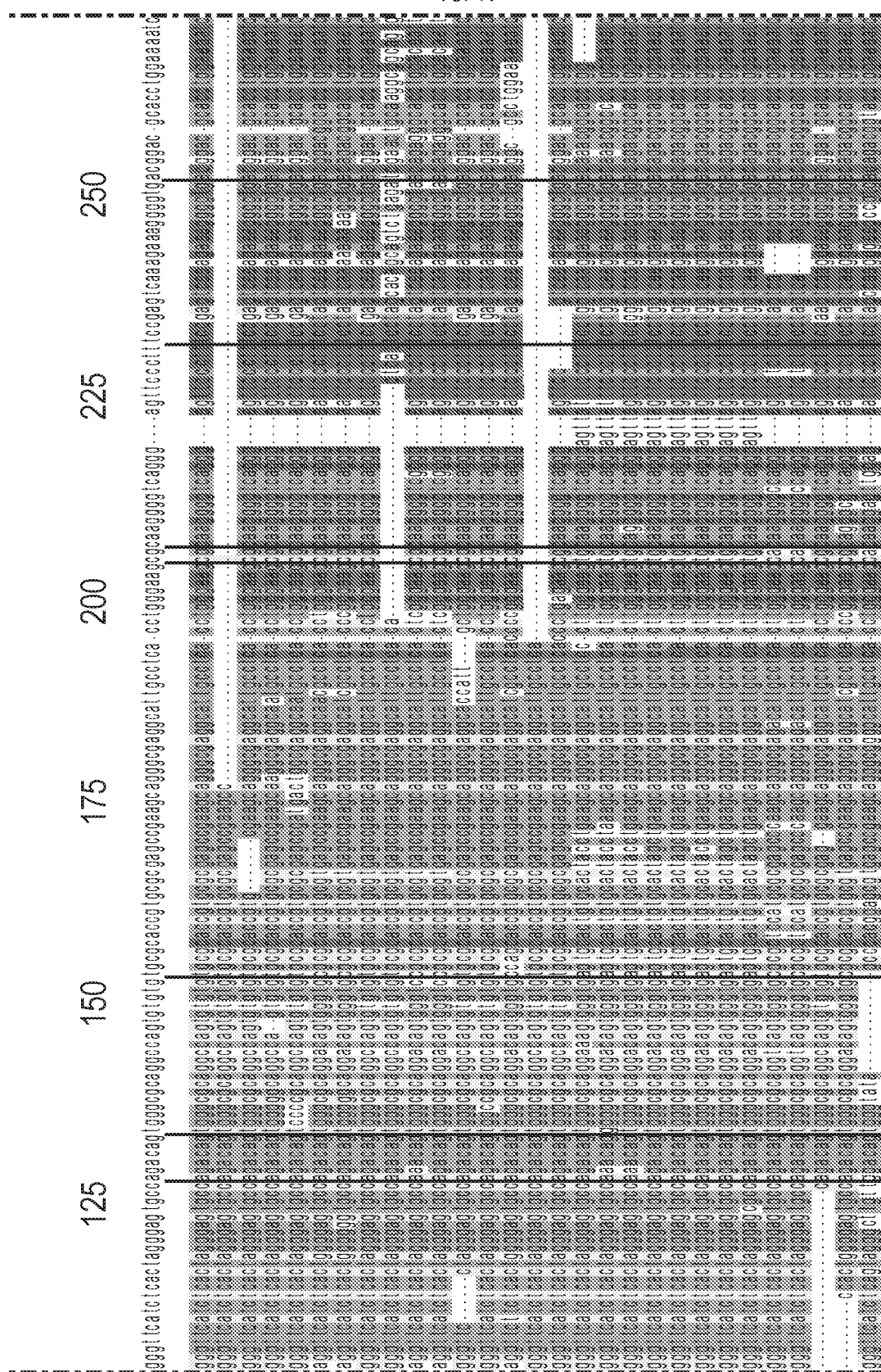


FIG. 7

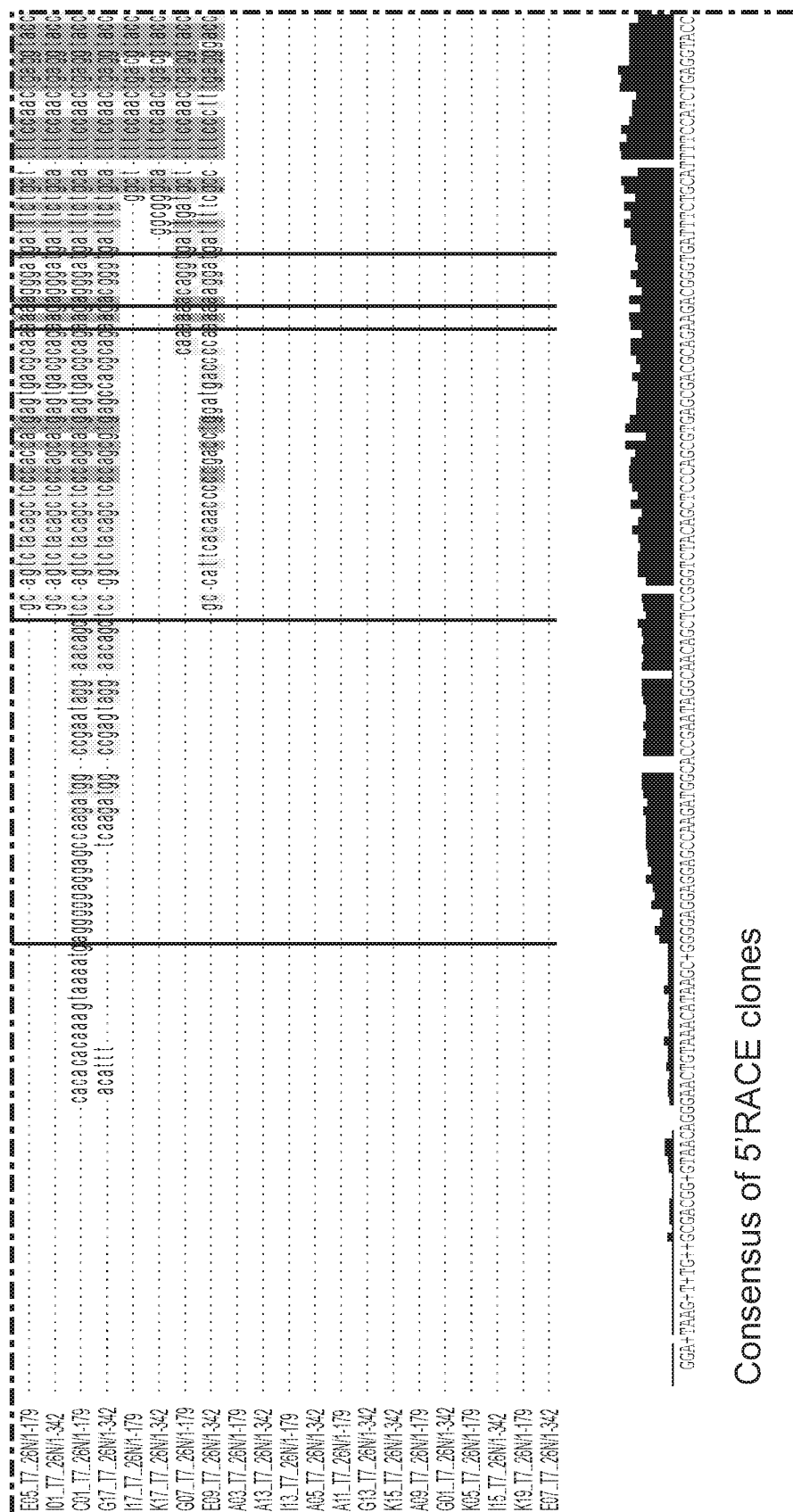


FIG. 7

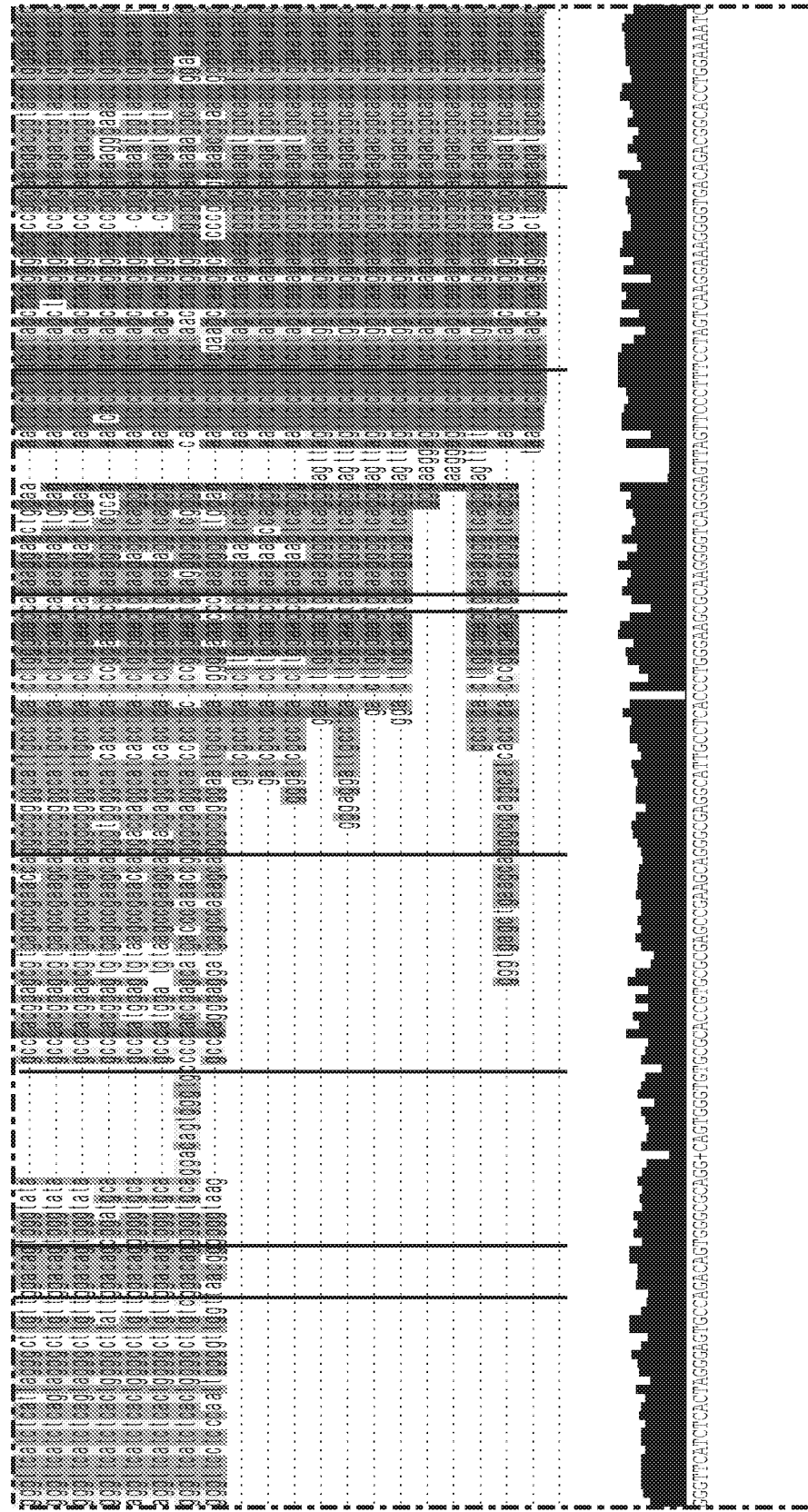
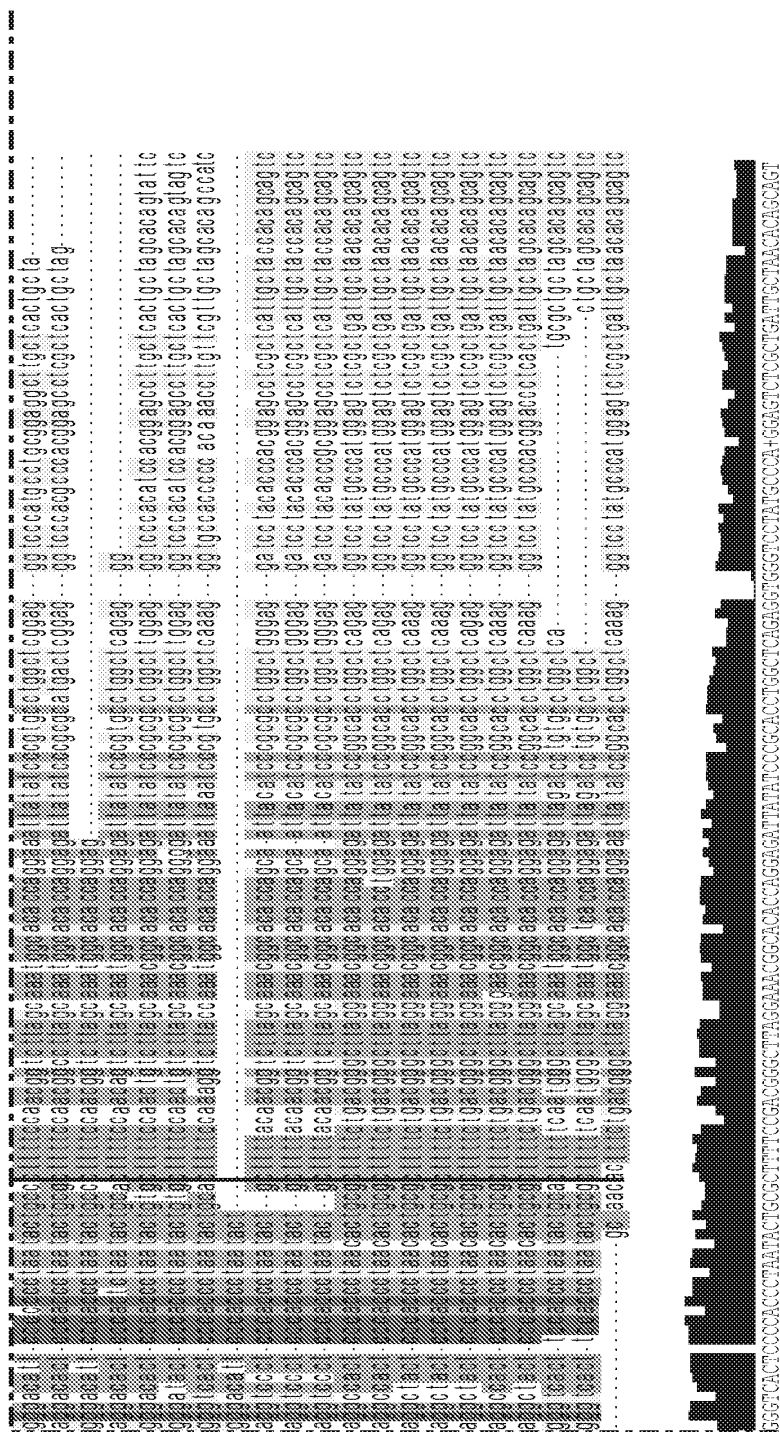


FIG. 7



b

Summary of 5'RACE data		
Sequenced clones		50
Start: < -40 bp		4
-25 bp to +25 bp		28
+25 bp to +180 bp		6
> +180 bp		12

Family	Count	%
L1HS	8	16
L1PA2	9	18
L1PA3	11	22
L1PA4	7	14
L1PA5	8	18
L1PA7	2	4
L1P1	5	10

FIG. 7

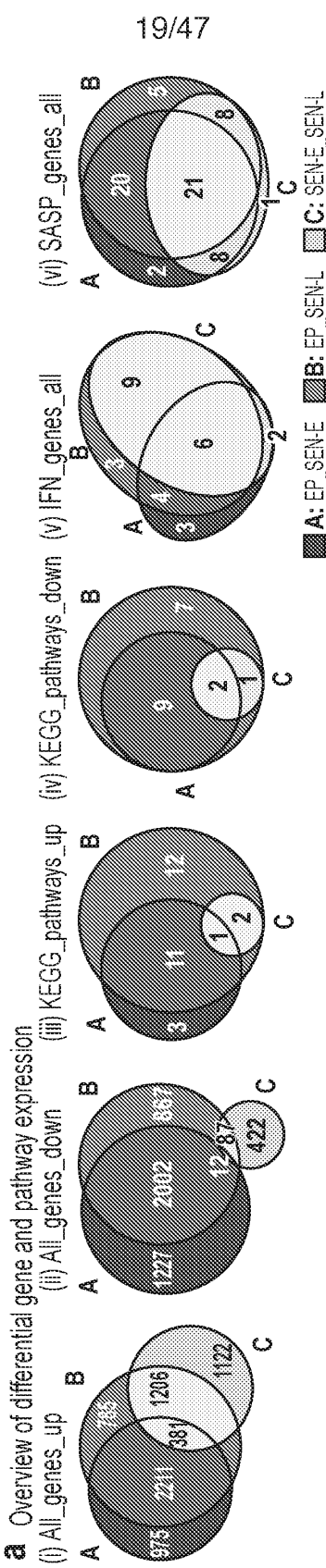
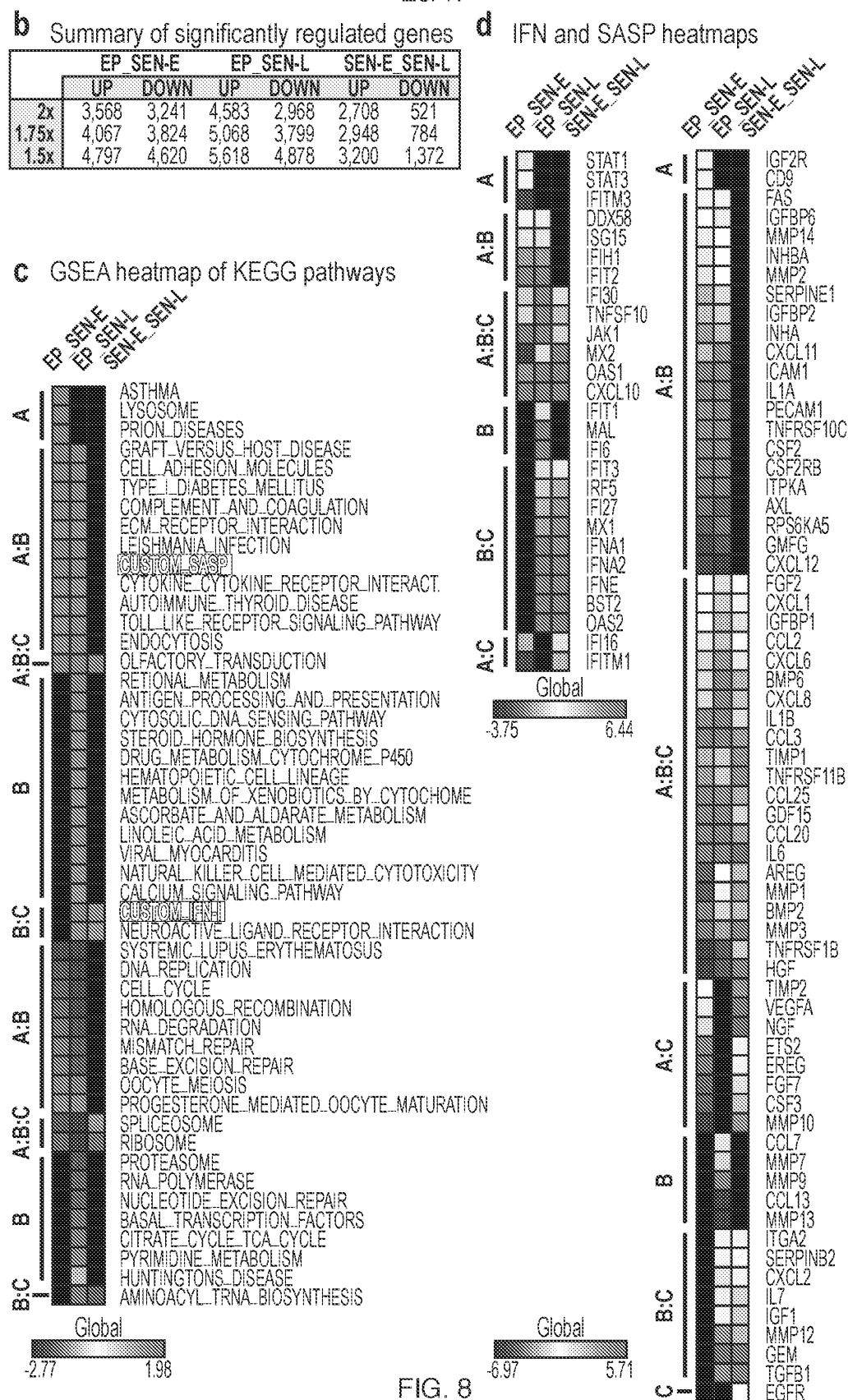


FIG. 8



e GSEA analysis of all KEGG pathways

Upregulated from early passage to early senescence (EP_SEN-E_UP)

Pathway name	Size	NES	NOM p-val	FDR p-val
ASTHMA	28	1.7864	<1.00E-03	<1.00E-02
GRAFT VERSUS HOST DISEASE	35	1.7654	<1.00E-03	<1.00E-02
CELL ADHESION MOLECULES CAMS	127	1.7538	<1.00E-03	<1.00E-02
OLFACTORY TRANSDUCTION	367	1.7468	<1.00E-03	<1.00E-02
TYPE I DIABETES MELLITUS	41	1.7140	<1.00E-03	<1.00E-02
LYSOSOME	119	1.6878	<1.00E-03	<1.00E-02
COMPLEMENT AND COAG. CASCADES	67	1.6854	<1.00E-03	<1.00E-02
ECM RECEPTOR INTERACTION	84	1.5487	<1.00E-03	<1.00E-02
LEISHMANIA INFECTION	68	1.6559	1.79E-03	<1.51E-02
CUSTOM SASP	85	1.6517	1.80E-03	<1.51E-02
PRION DISEASES	34	1.6397	1.84E-03	<1.51E-02
CYTOKINE CYTOKINE RECEPTOR INTERACT.	254	1.5705	1.62E-03	<1.51E-02
TOLL LIKE RECEPTOR SIGNALING PATHWAY	99	1.4920	1.73E-03	<1.51E-02
AUTOIMMUNE THYROID DISEASE	48	1.5336	3.77E-03	<2.66E-02
ENDOCYTOSIS	174	1.4427	5.21E-03	<3.49E-02

Upregulated from early passage to late senescence (EP_SEN-L_UP)

Pathway name	Size	NES	NOM p-val	FDR p-val
OLFACTORY TRANSDUCTION	367	1.9816	<1.00E-03	<5.00E-03
TYPE I DIABETES MELLITUS	41	1.7551	<1.00E-03	<5.00E-03
GRAFT VERSUS HOST DISEASE	35	1.7098	<1.00E-03	<5.00E-03
CELL ADHESION MOLECULES CAMS	127	1.6868	<1.00E-03	<5.00E-03
RETINOL METABOLISM	56	1.6689	<1.00E-03	<5.00E-03
CUSTOM SASP	85	1.6282	<1.00E-03	<5.00E-03
LEISHMANIA INFECTION	68	1.6260	<1.00E-03	<5.00E-03
CUSTOM IFN- γ	50	1.6248	<1.00E-03	<5.00E-03
COMPLEMENT AND COAG. CASCADES	67	1.6008	<1.00E-03	<5.00E-03
TOLL LIKE RECEPTOR SIGNALING PATHWAY	99	1.5759	<1.00E-03	<5.00E-03
NEUROACTIVE LIGAND RECEPTOR INTERACT.	270	1.5340	<1.00E-03	<5.00E-03
CYTOKINE CYTOKINE RECEPTOR INTERACT.	254	1.5008	<1.00E-03	<5.00E-03
HEMATOPOIETIC CELL LINEAGE	85	1.5269	1.07E-03	5.32E-03
DRUG METABOLISM CYTOCHROME P450	63	1.5343	1.12E-03	5.32E-03
ANTIGEN PROCESSING AND PRESENTATION	73	1.6286	1.08E-03	5.32E-03
XENOBIOTIC METAB. BY CYTOCHROME P450	62	1.5245	3.36E-03	1.51E-02
CYTOSOLIC DNA SENSING PATHWAY	52	1.5816	3.42E-03	1.51E-02
VIRAL MYOCARDITIS	68	1.4405	4.39E-03	1.96E-02
ASCORBATE AND ALDARATE METABOLISM	21	1.5205	6.20E-03	2.86E-02
NATURAL KILLER CELL MEDIATED CYTOTOX.	123	1.3730	7.22E-03	3.25E-02
STEROID HORMONE BIOSYNTHESIS	49	1.5533	7.94E-03	3.62E-02
CALCIUM SIGNALING PATHWAY	173	1.3406	9.14E-03	3.97E-02
LINOLEIC ACID METABOLISM	29	1.4904	1.00E-02	4.21E-02
AUTOIMMUNE THYROID DISEASE	48	1.5072	1.04E-02	4.21E-02
ECM RECEPTOR INTERACTION	84	1.4313	1.09E-02	4.53E-02

Upregulated from early senescence to late senescence (SEN-E_SEN-L_UP)

Pathway name	Size	NES	NOM p-val	FDR p-val
OLFACTORY TRANSDUCTION	367	1.6009	<1.00E-03	<5.00E-02
CUSTOM IFN- γ	50	1.4722	<1.00E-03	<5.00E-02
NEUROACTIVE LIGAND RECEPTOR INTERACT.	270	1.3253	<1.00E-03	<5.00E-02

FIG. 8

SUBSTITUTE SHEET (RULE 26)

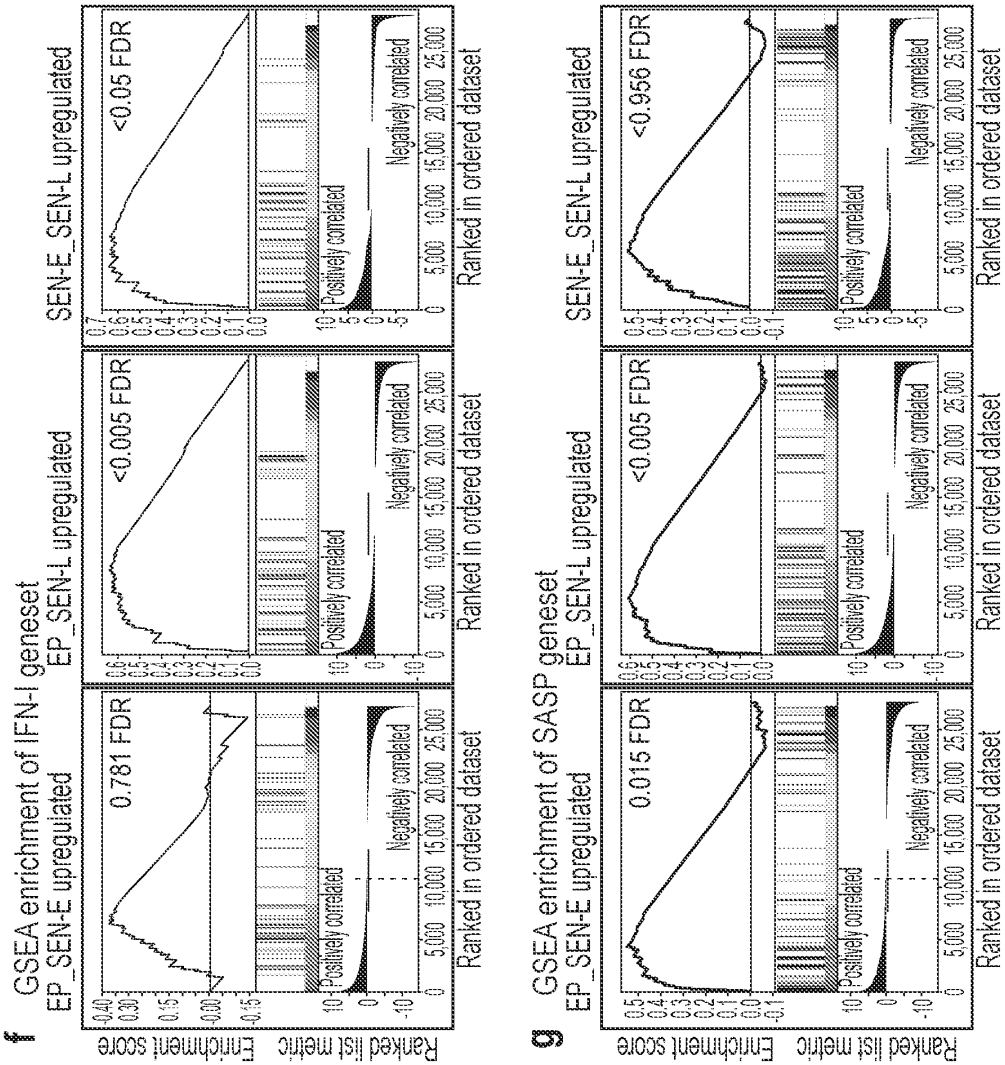


FIG. 8

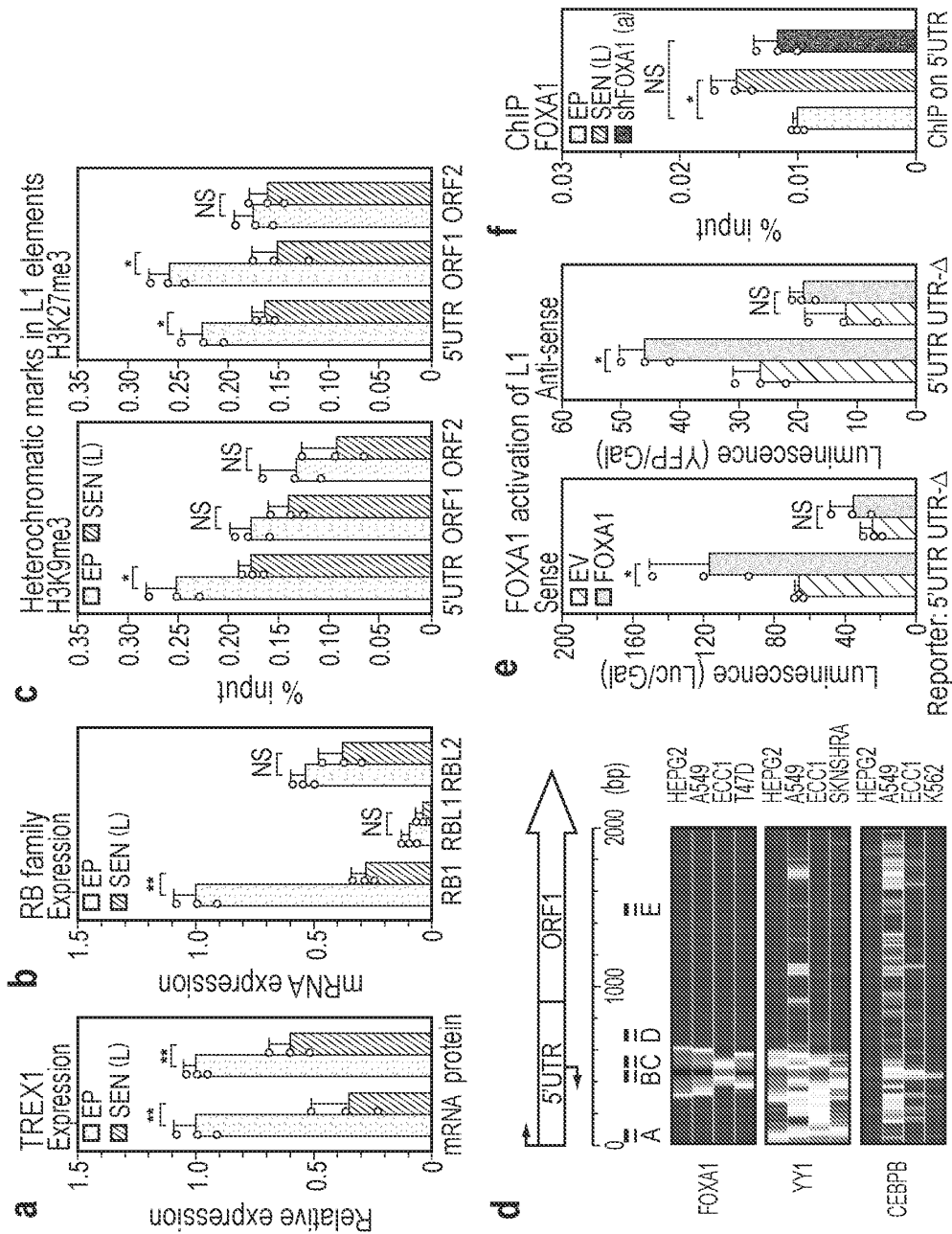
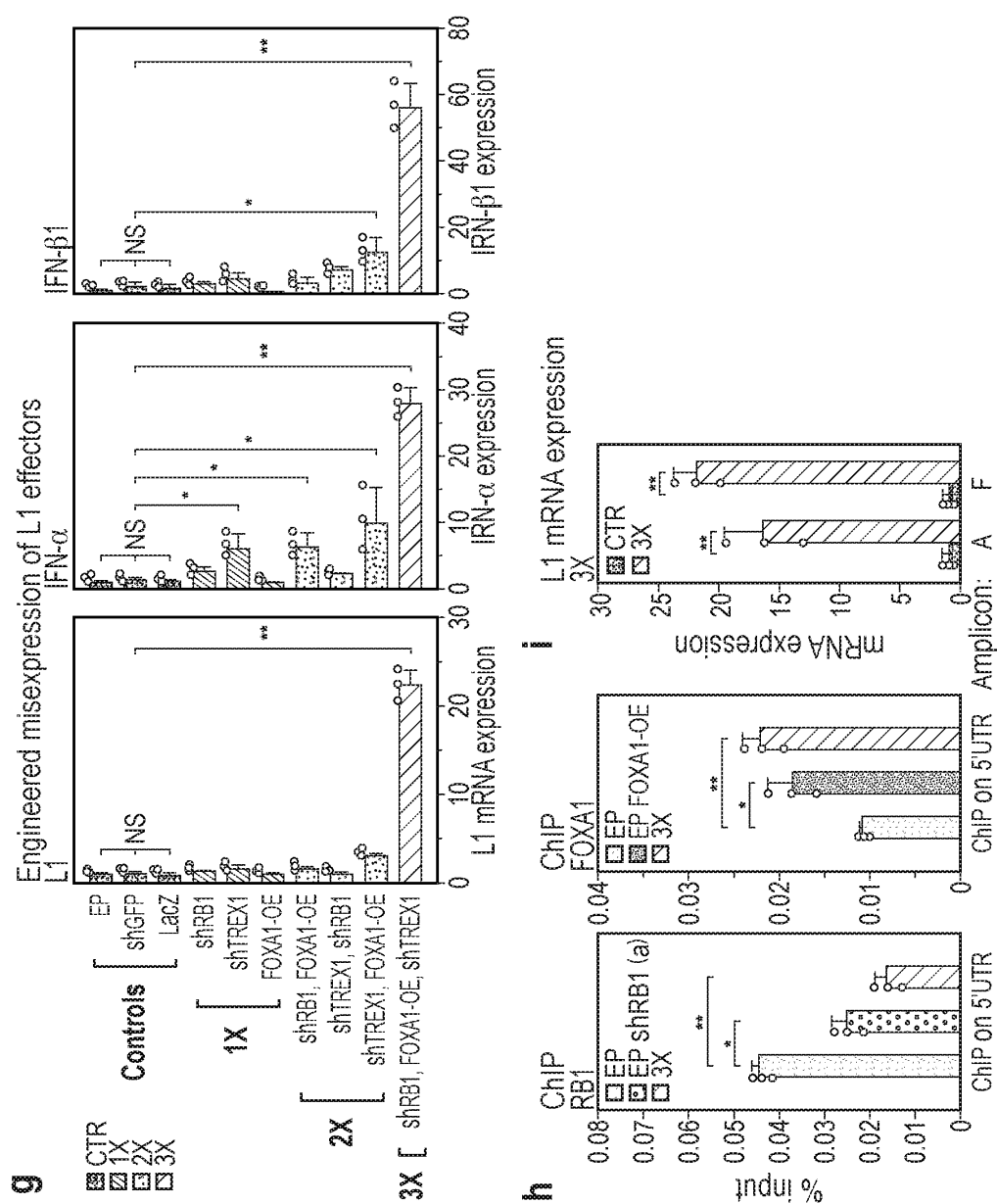


FIG. 9



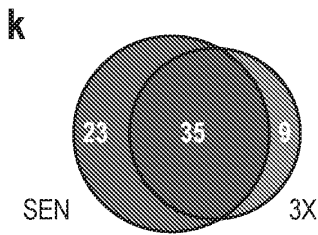
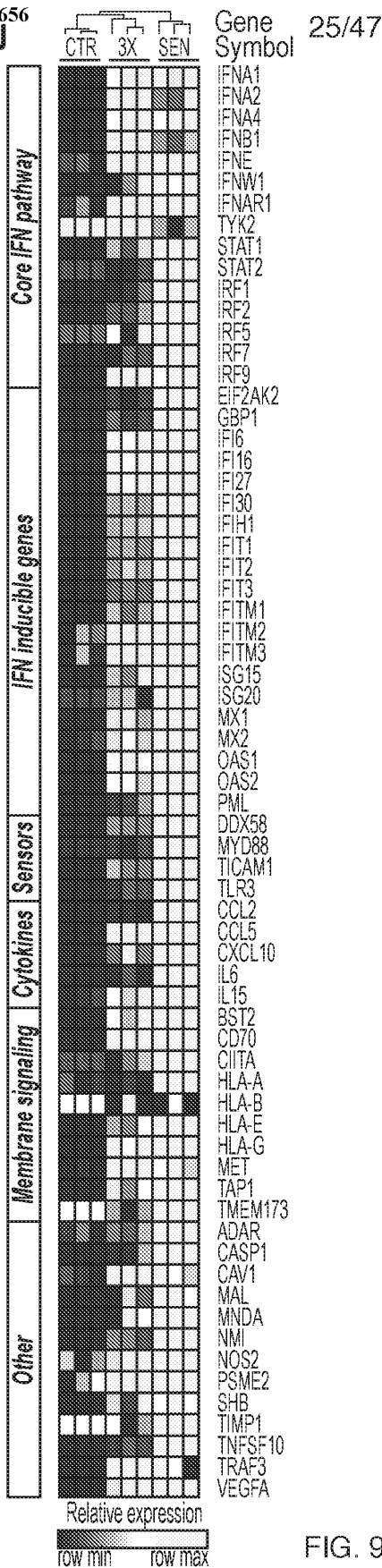


FIG. 9

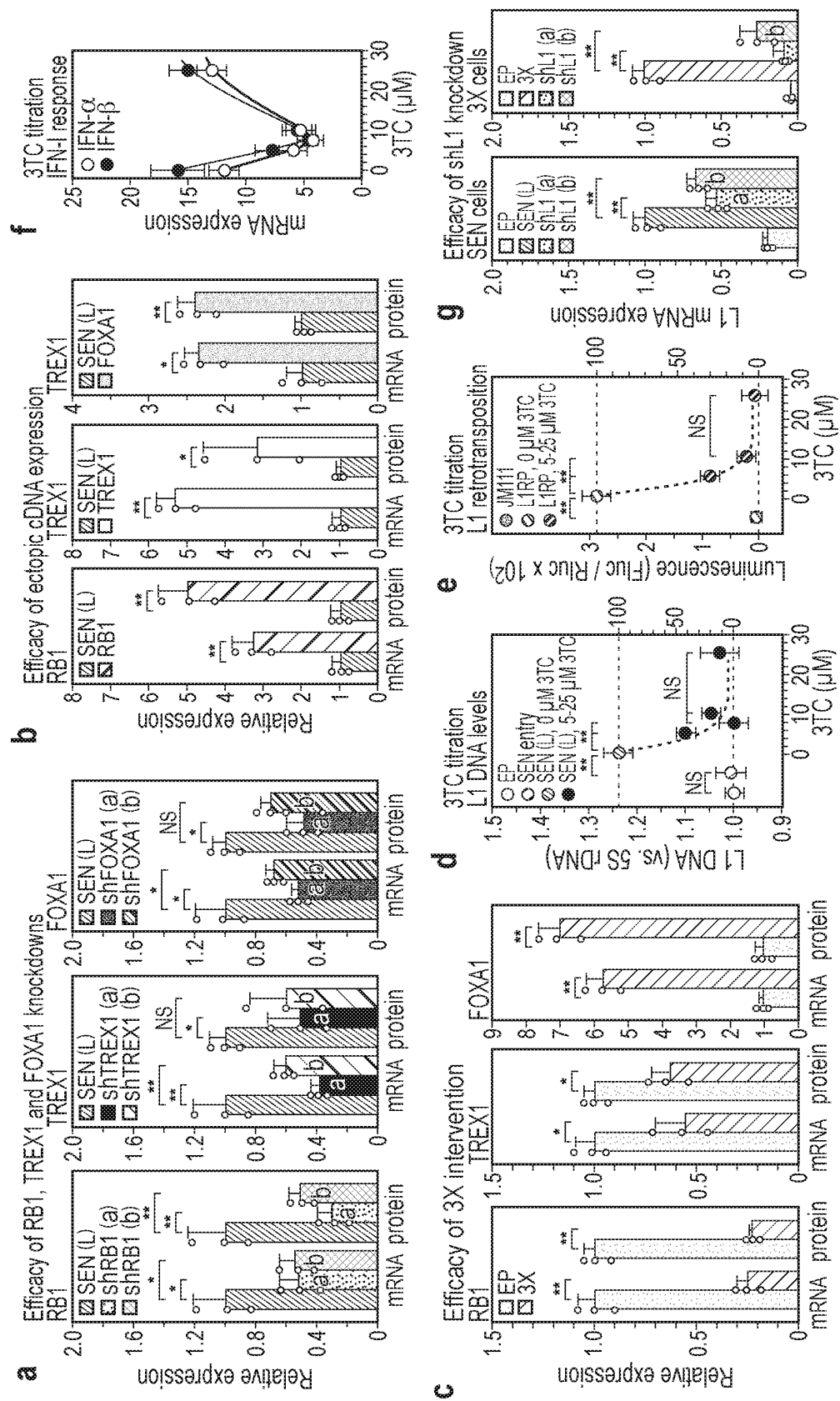
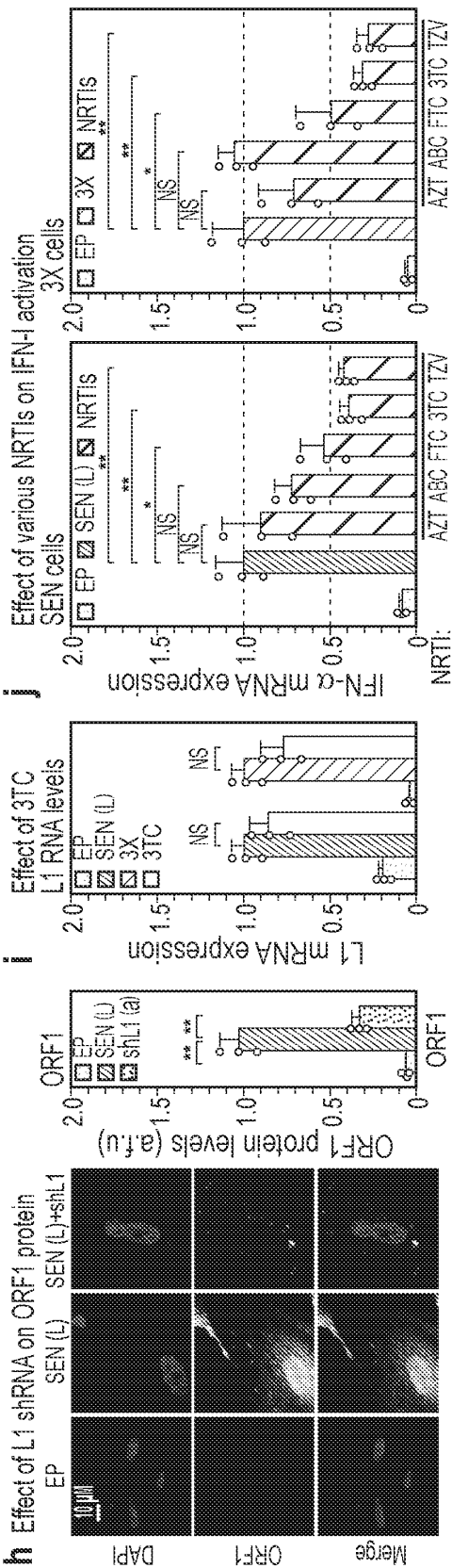


FIG. 10



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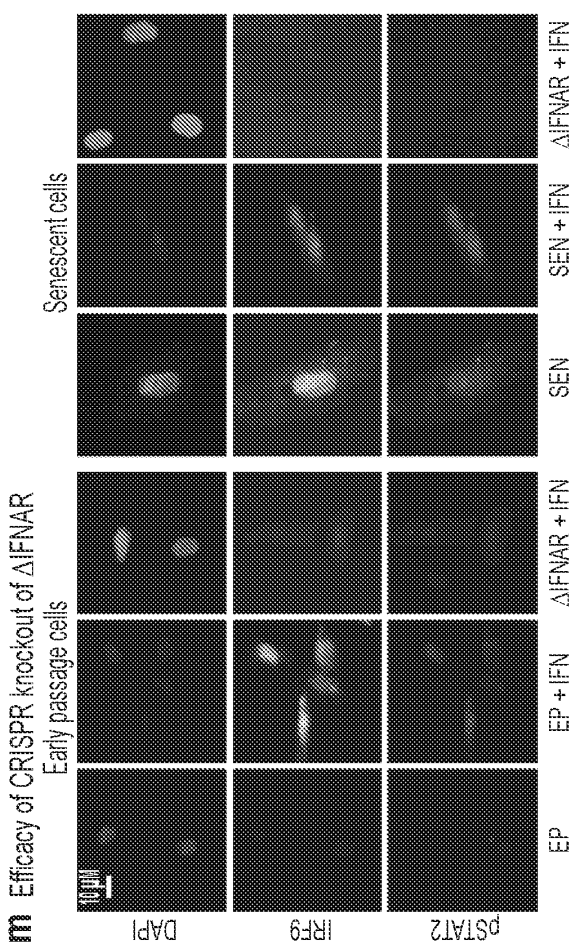


FIG. 10

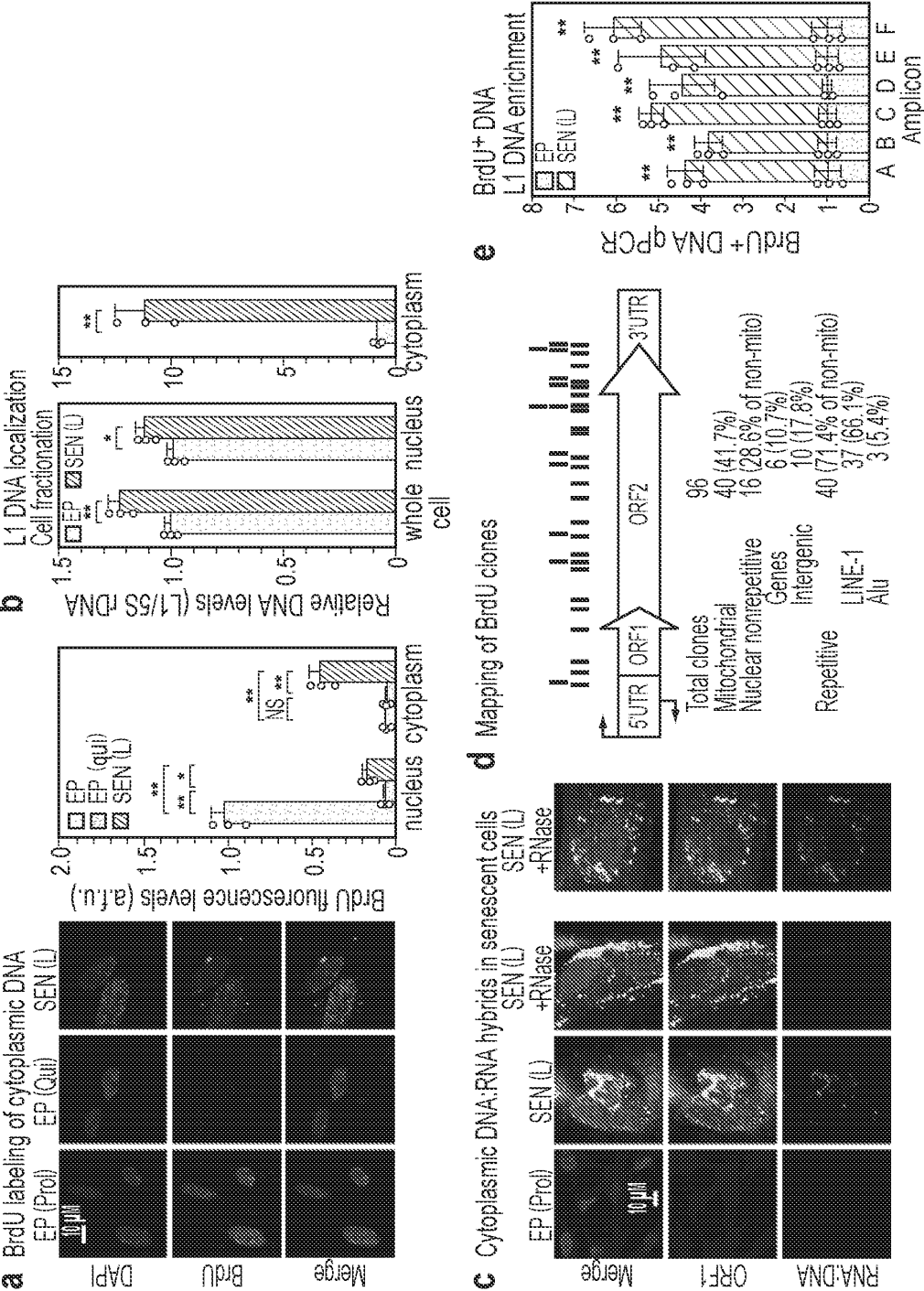


FIG. 11

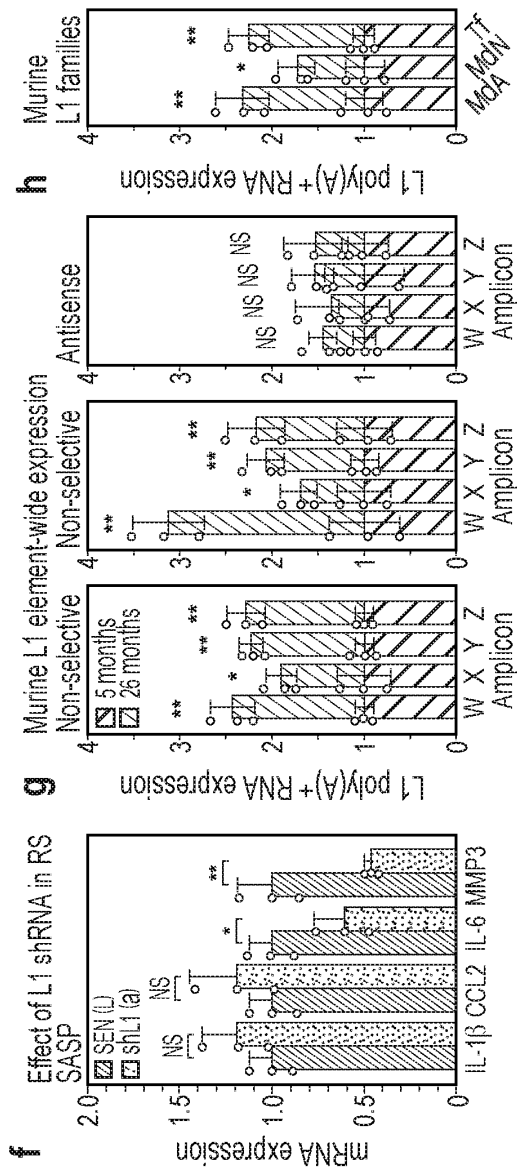


FIG. 11

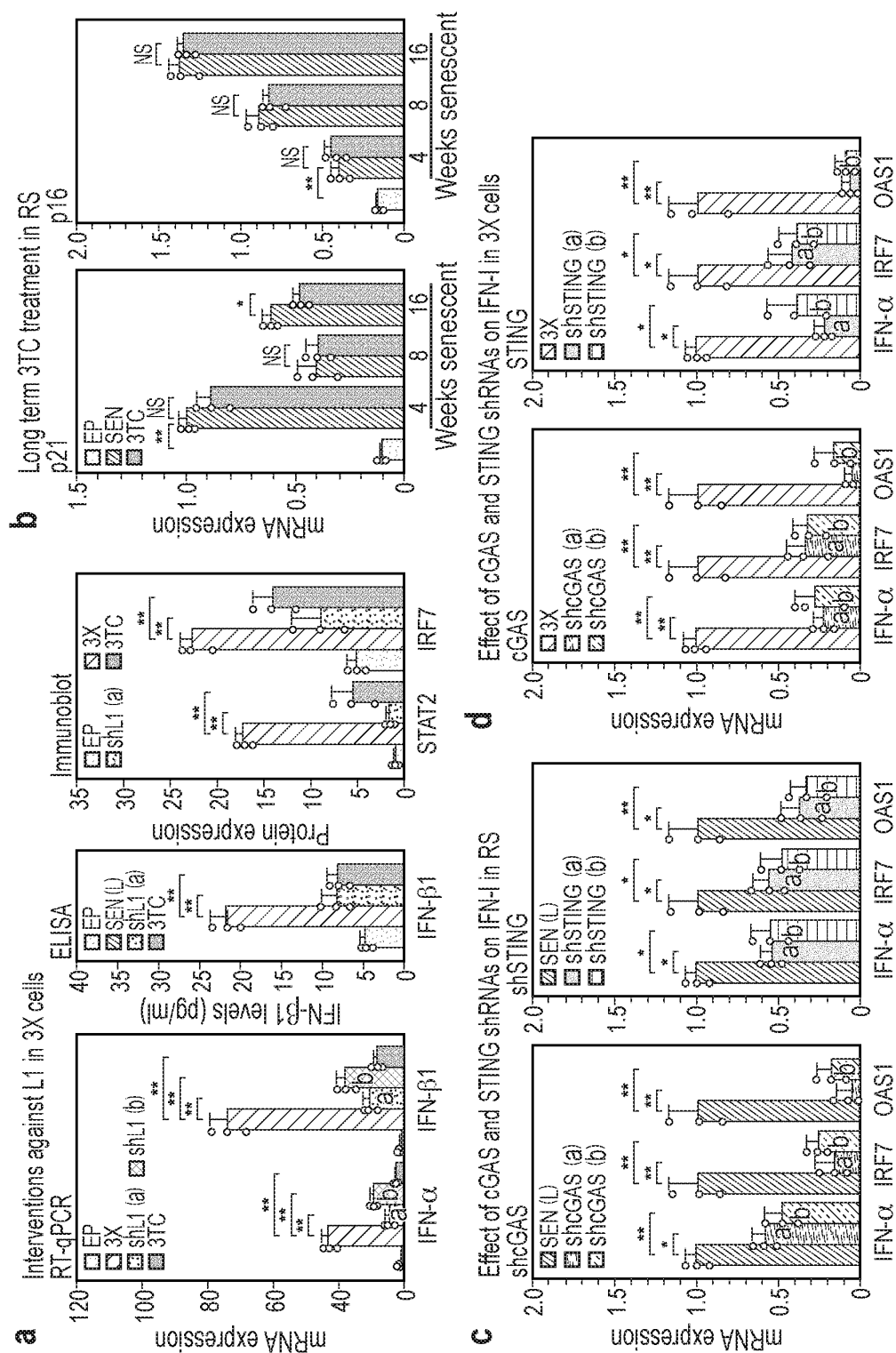


FIG. 12

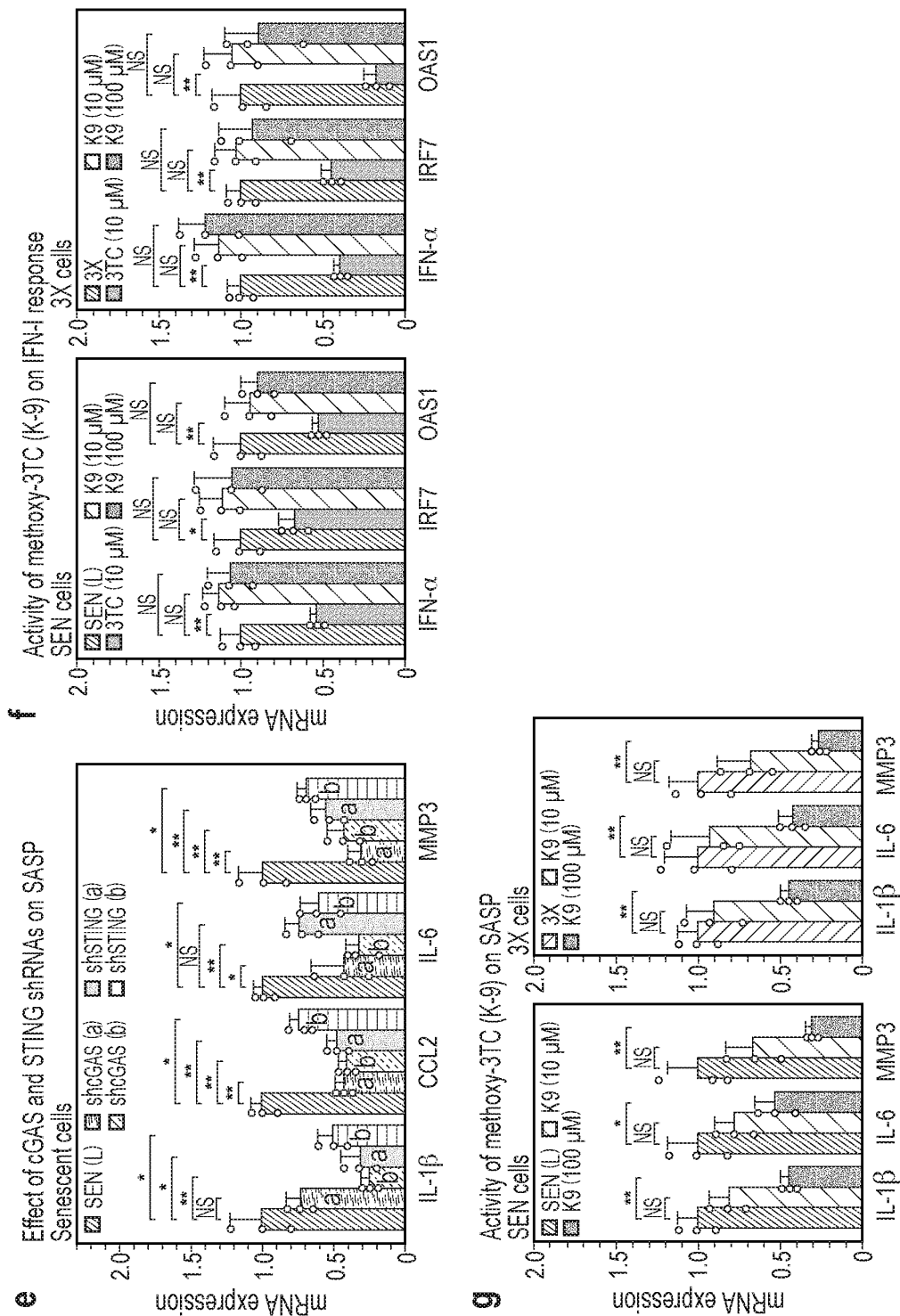


FIG. 12

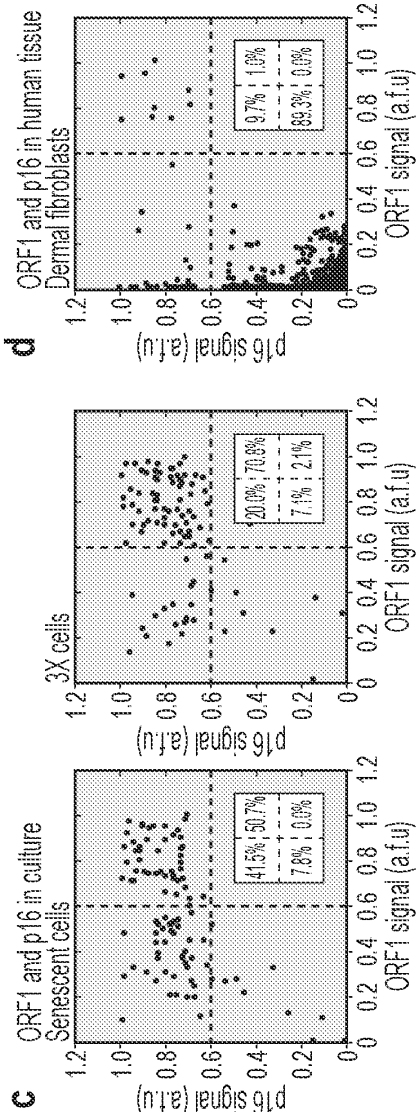
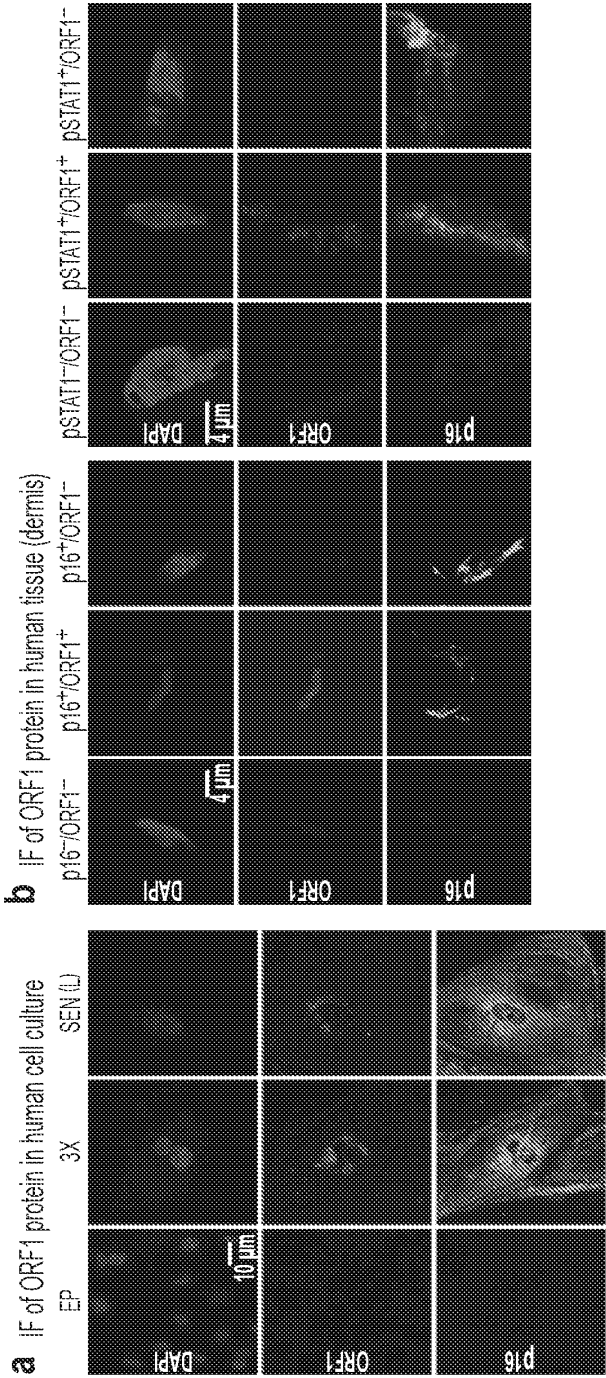
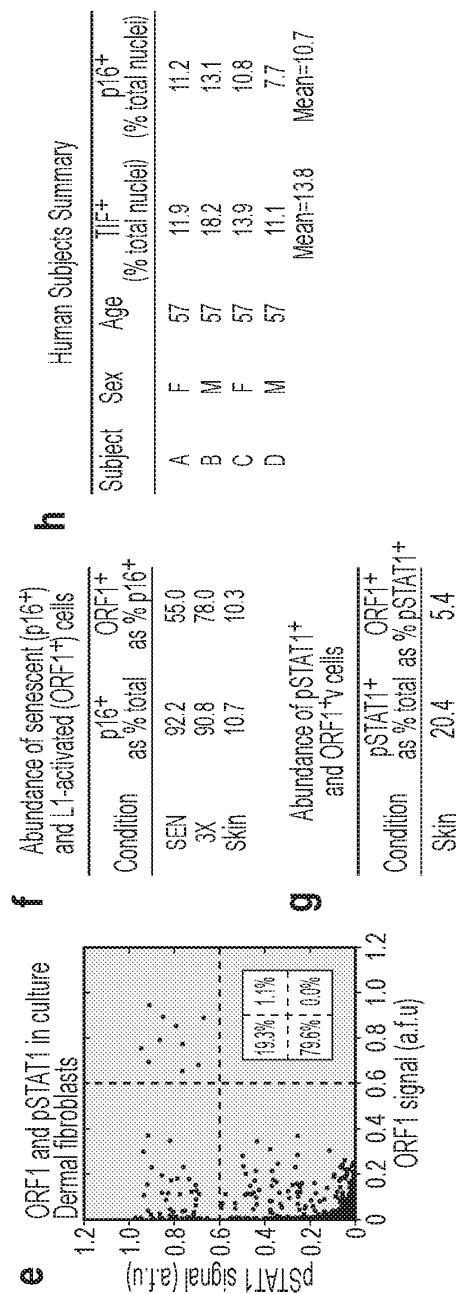


FIG. 13



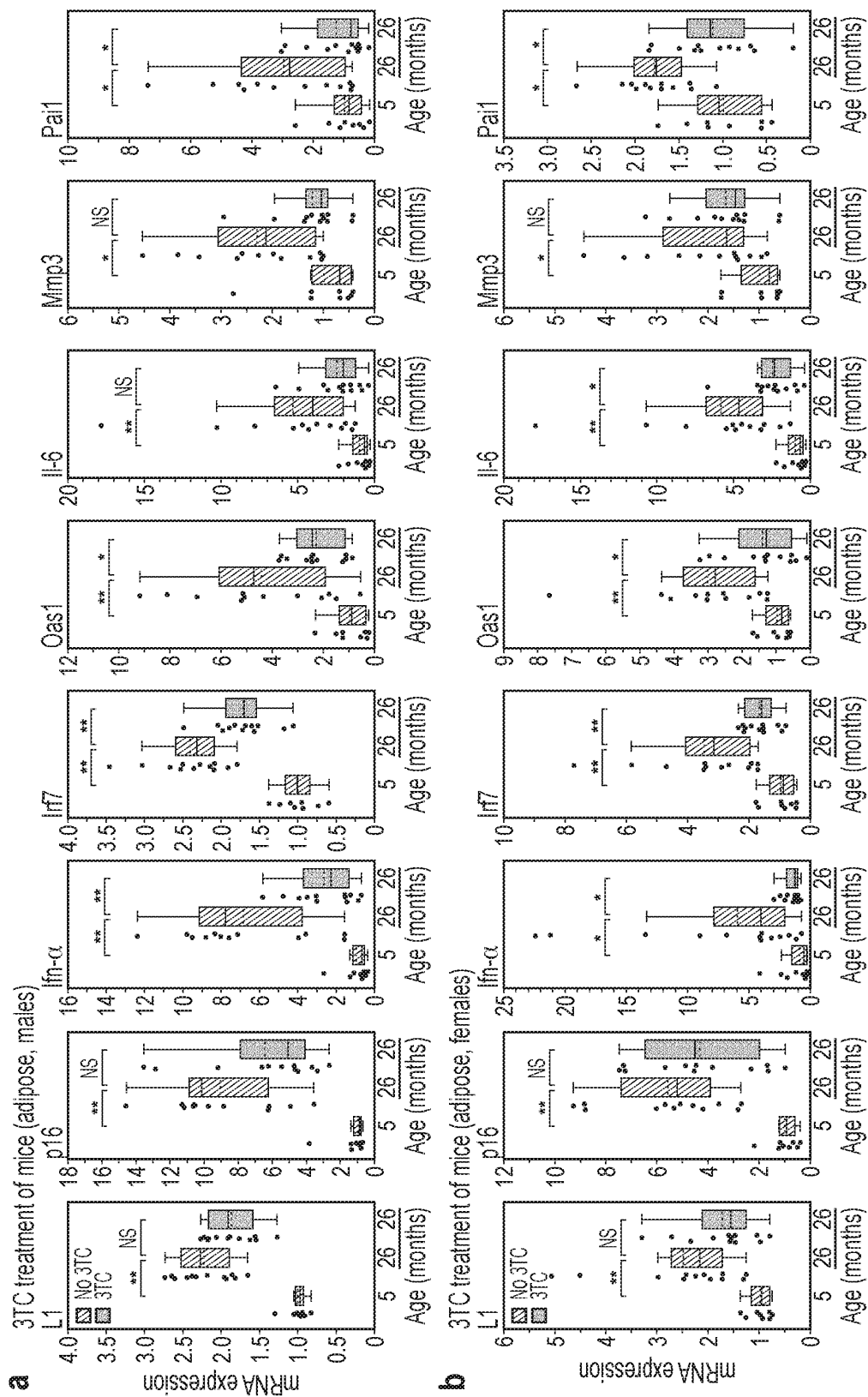


FIG. 14

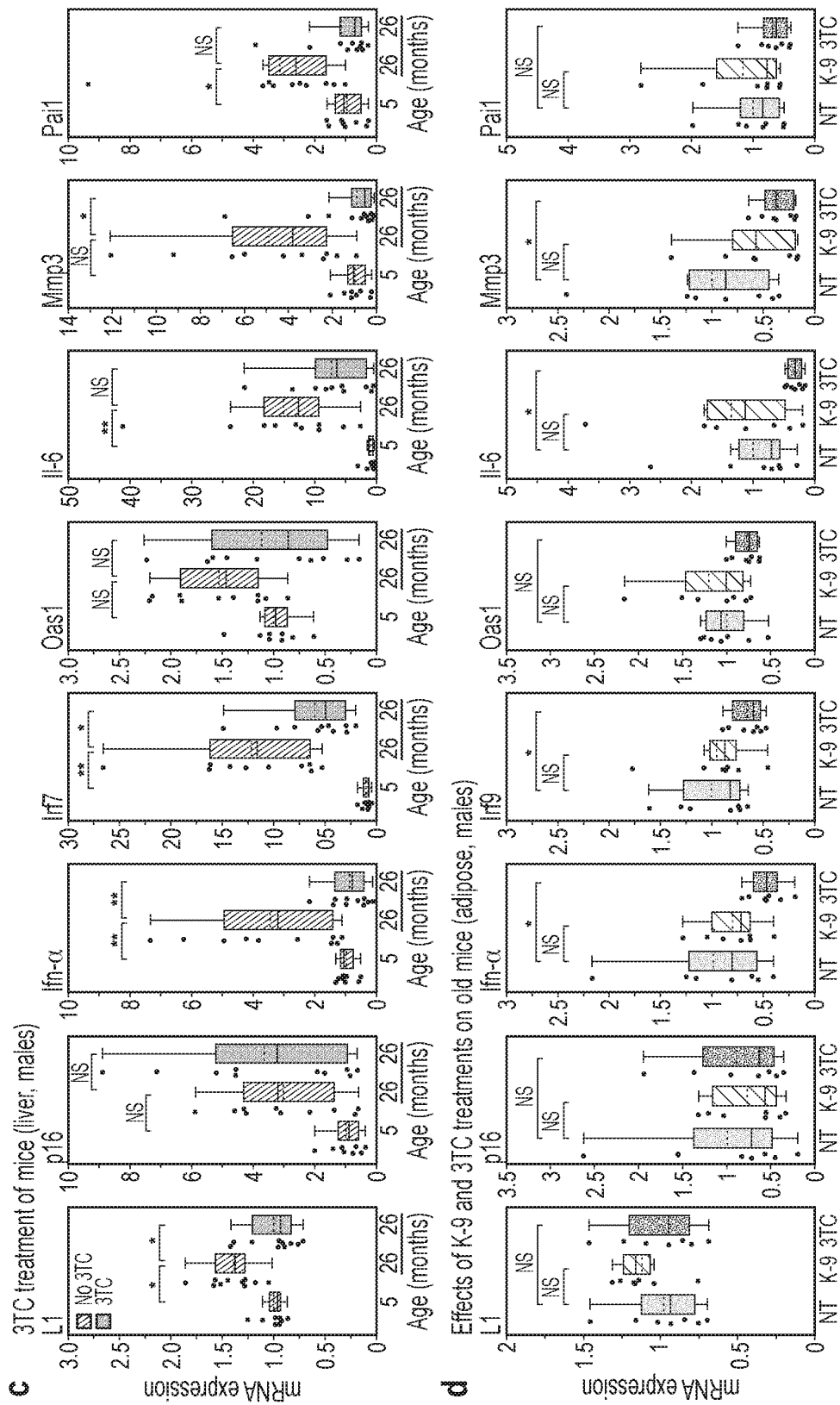


FIG. 14

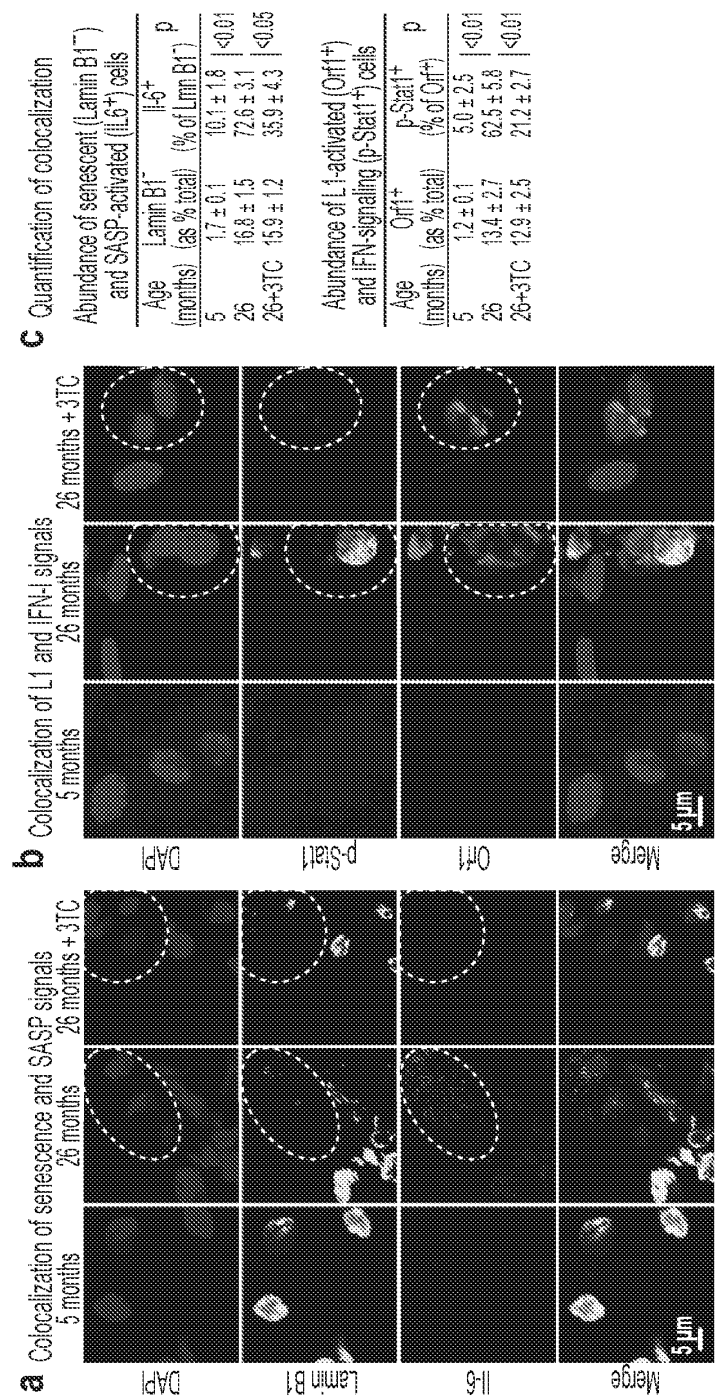


FIG. 15

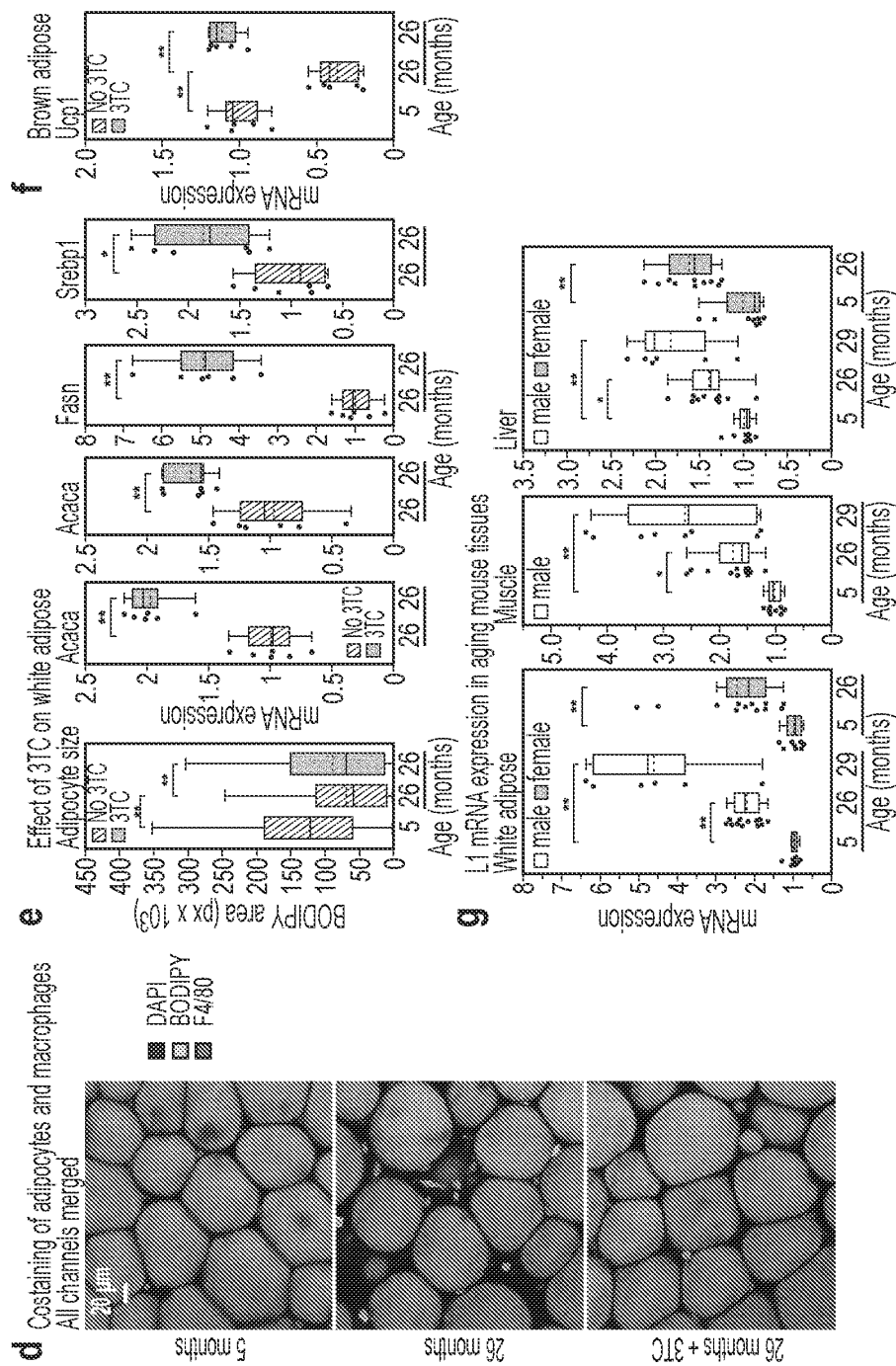


FIG. 15

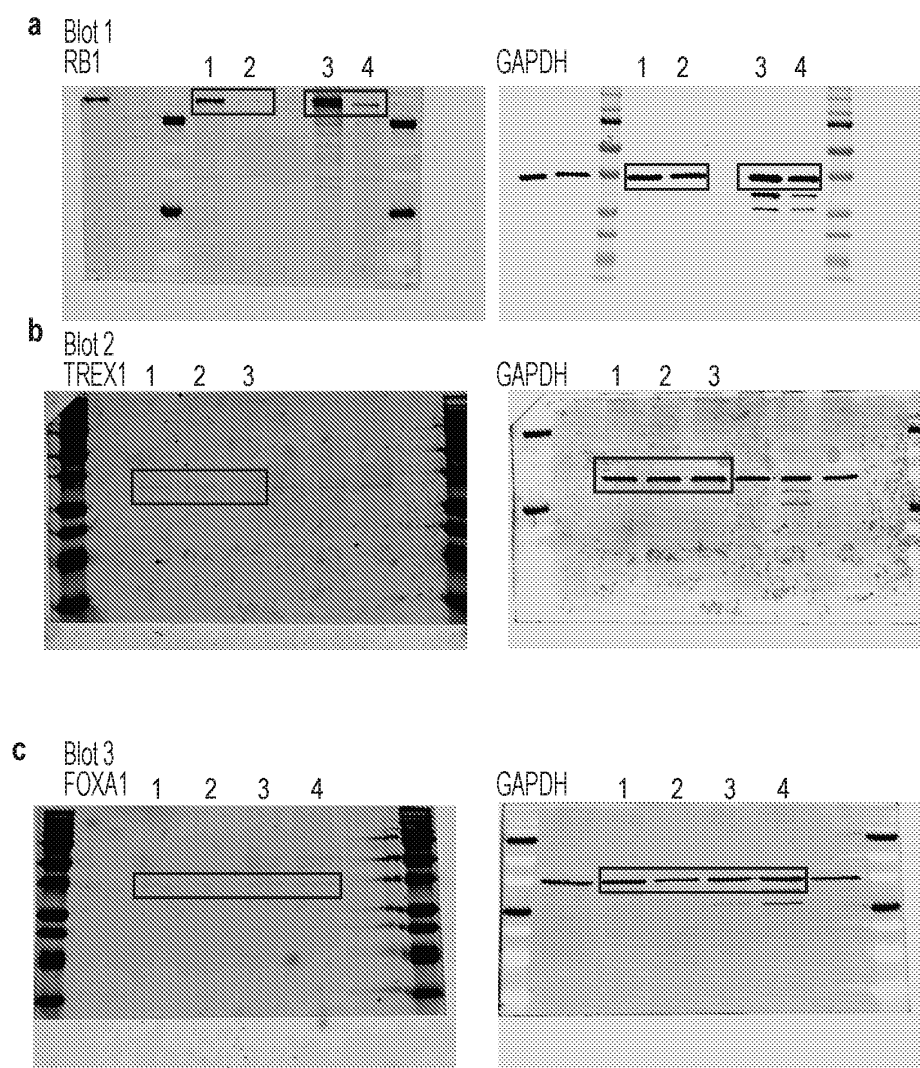


FIG. 16A

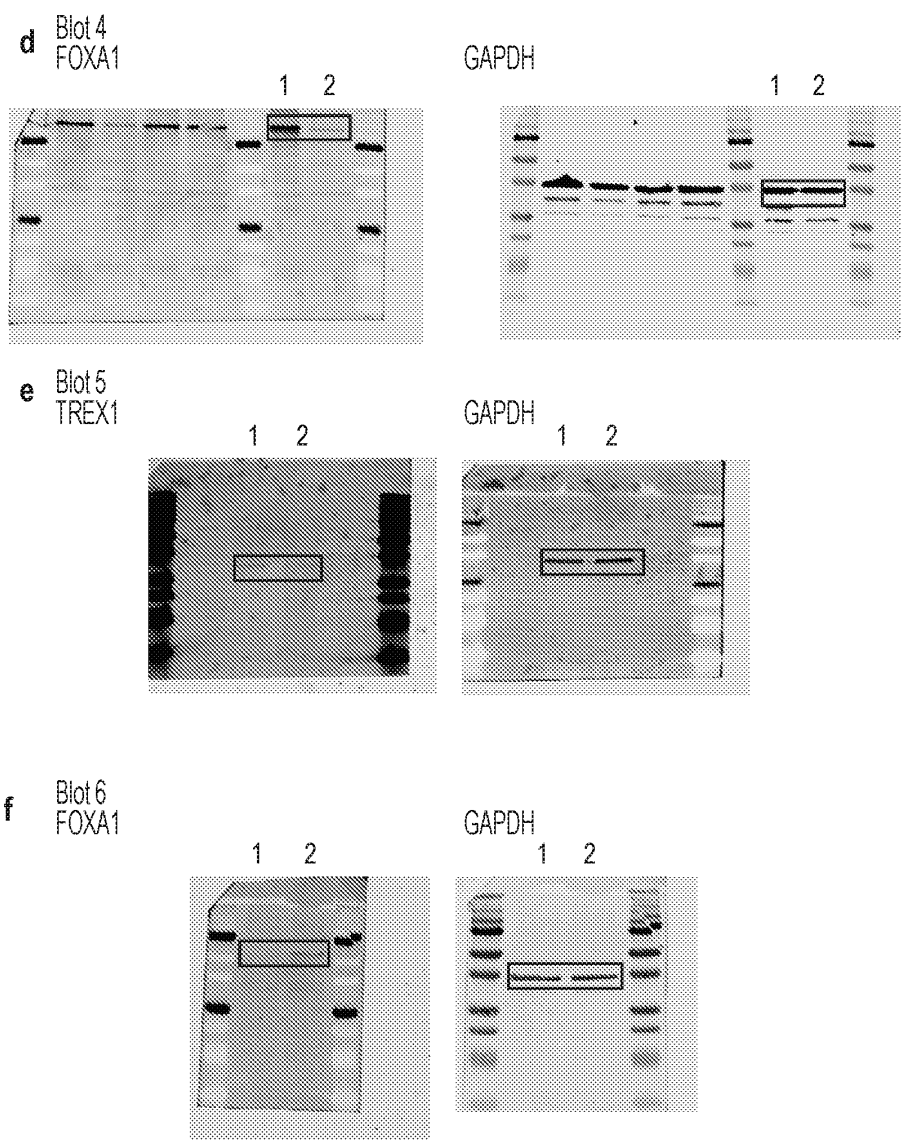


FIG. 16B

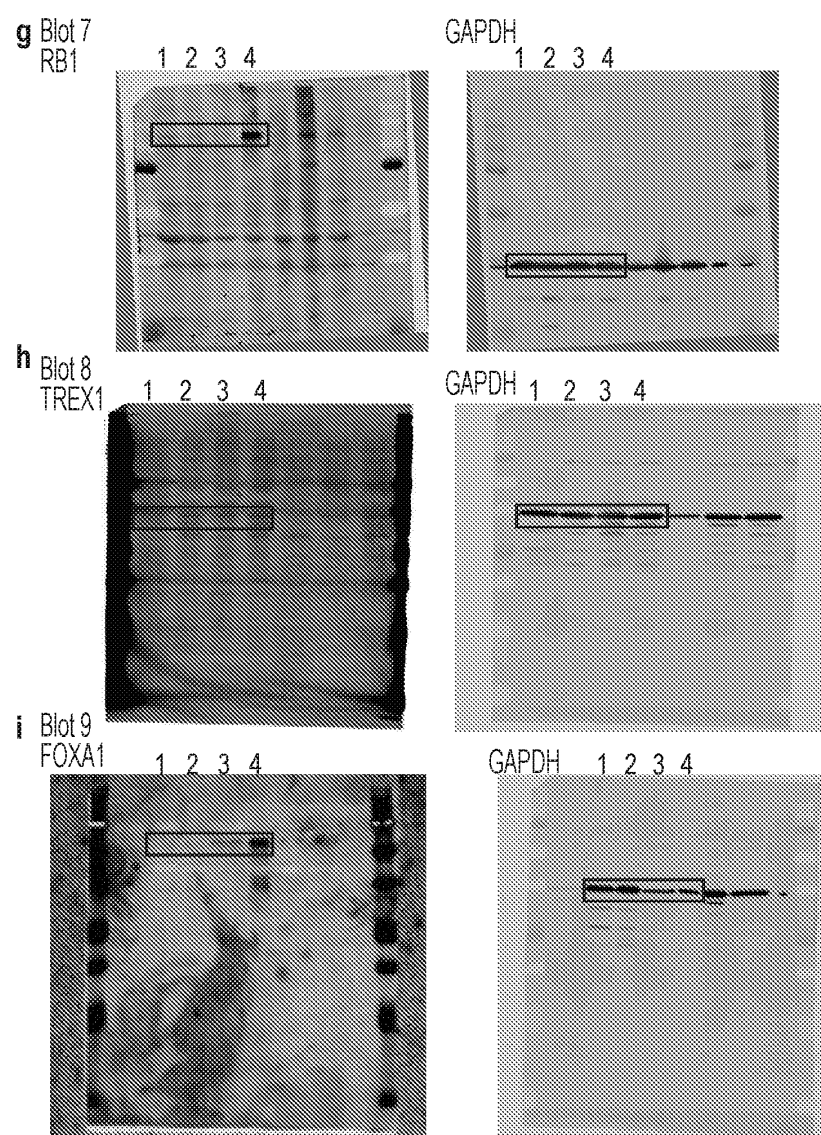


FIG. 16C

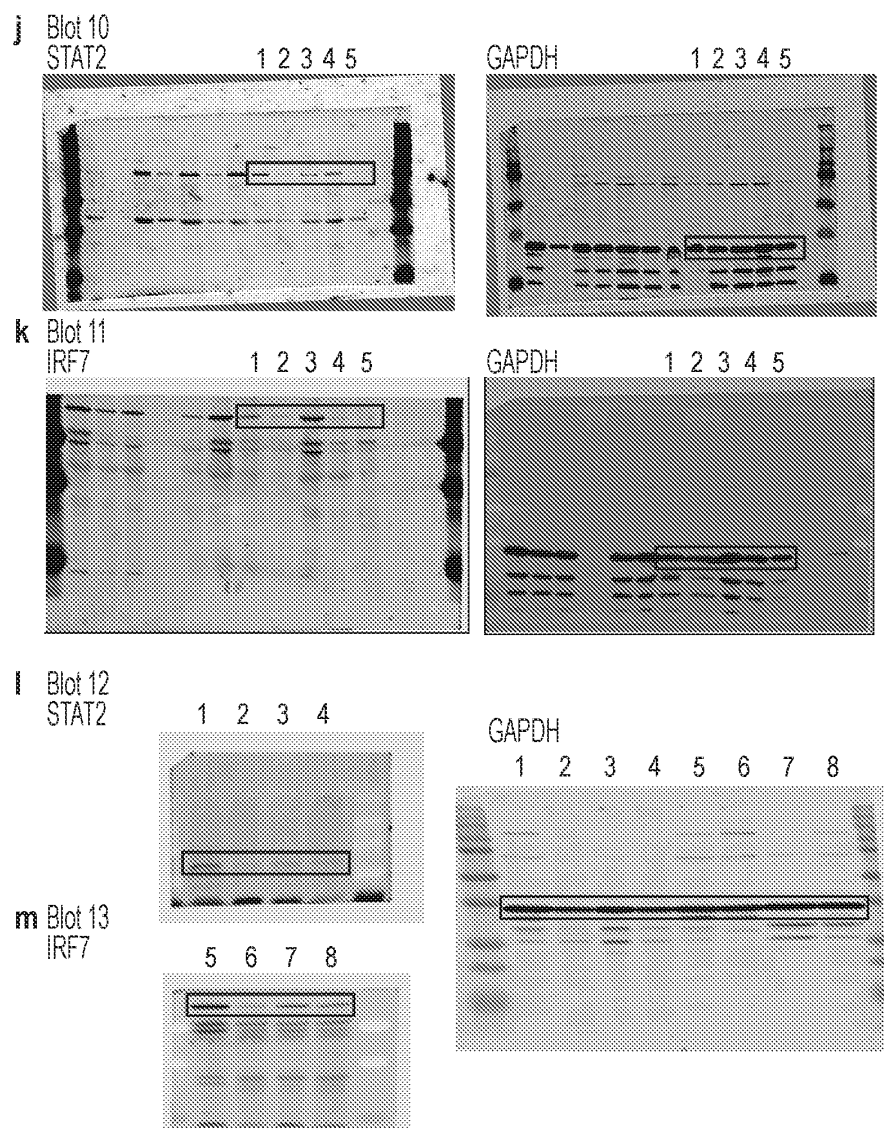
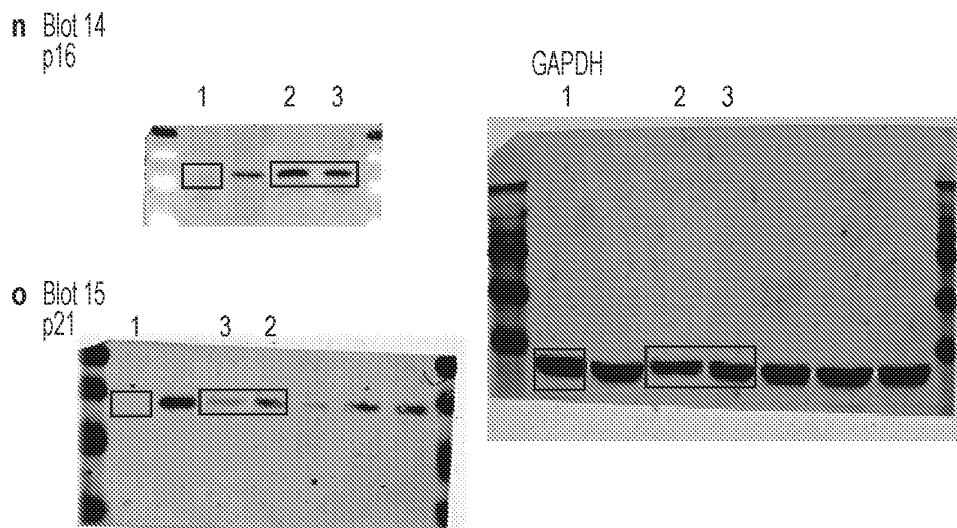


FIG. 16D



- a, Blot 1 - RB1: 1. EP; 2. SEN (L); 3. OE - SEN; 4. SEN (E)
b, Blot 2 - TREX1: 1. EP; 2. SEN (E); 3. SEN (L)
c, Blot 3 - FOXA1: 1. EP; 2. Arrest; 3. SEN (E); 4. SEN (L)
d, Blot 4 - RB1: 1. EP; 2. 3X
e, Blot 5 - TREX1: 1. EP; 2. 3X
f, Blot 6 - FOXA1: 1. EP; 2. 3X
g, Blot 7 - RB1: 1. SEN (L); 2. shRB1(b); 3. shRB1(a); 4. OE-RB1
h, Blot 8 - TREX1: 1. SEN (L); 2. shTREX1 (b); 3. shTREX1 (a); 4. OE-TREX1
i, Blot 9 - FOXA1: 1. shFOXA1 (a); 2. shFOXA1 (b); 3. SEN (L); 4. OE-FOXA1
j, Blot 10 - STAT2: 1. 3X; 2. shL1; 3. NRTI; 4. Δ IFNAR; 5. EP
k, Blot 11 - IRF7: 1. EP; 2. shL1; 3. 3X; 4. shL1; 5. Δ IFNAR
l, Blot 12 - STAT2: 1. SEN (L); 2. Δ IFNAR; 3. shL1; 4. NRTI
m, Blot 13 - IRF7: 5. SEN (L); 6. Δ IFNAR; 7. shL1; 8. NRTI
n, Blot 14 - p16 (CDKN2A): 1. EP; 2. SEN (E); 3. SEN (L)
o, Blot 15 - p21 (CDKN1A): 1. EP; 2. SEN (E); 3. SEN (L)

FIG. 16E

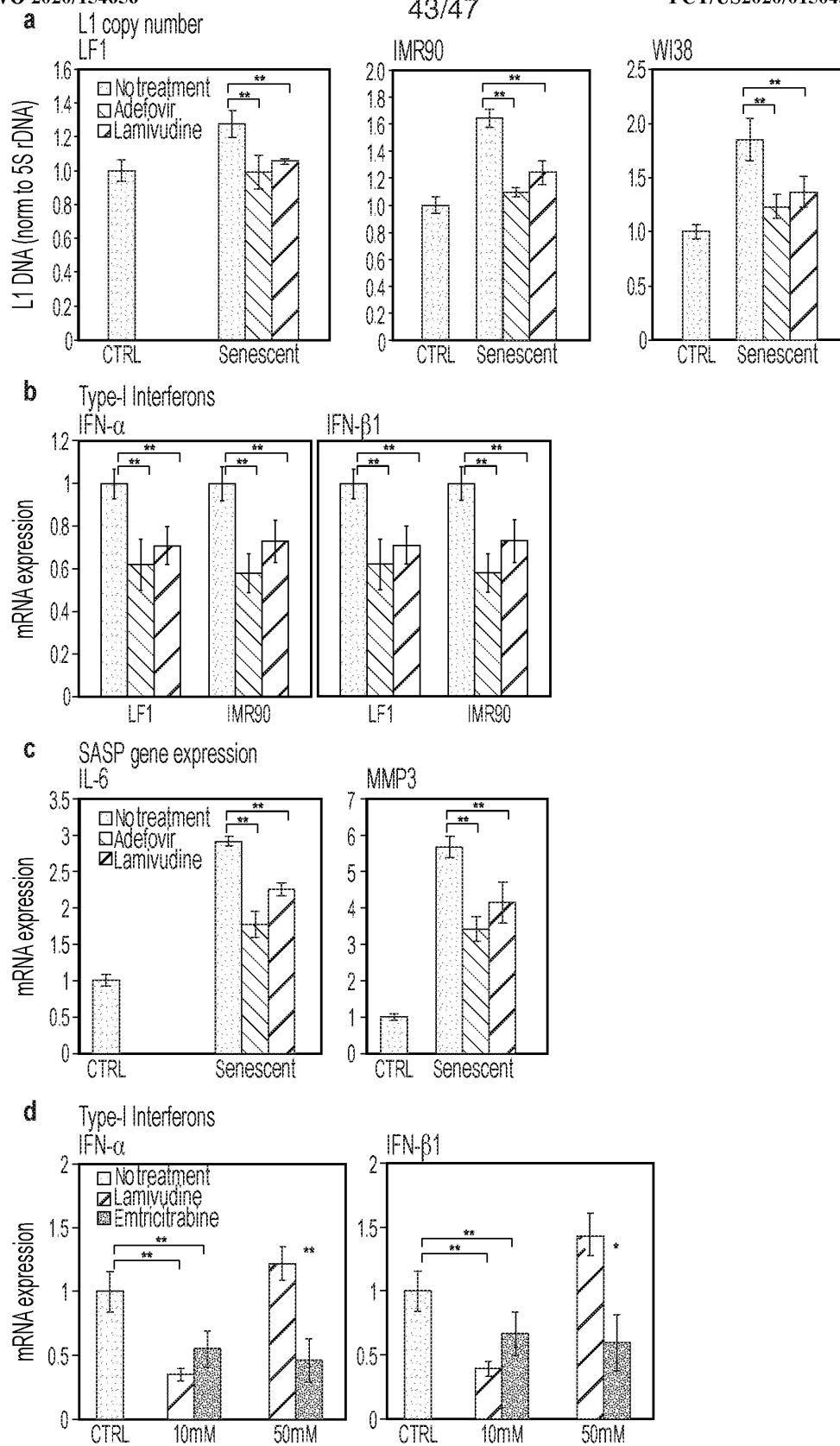


FIG. 17

SUBSTITUTE SHEET (RULE 26)

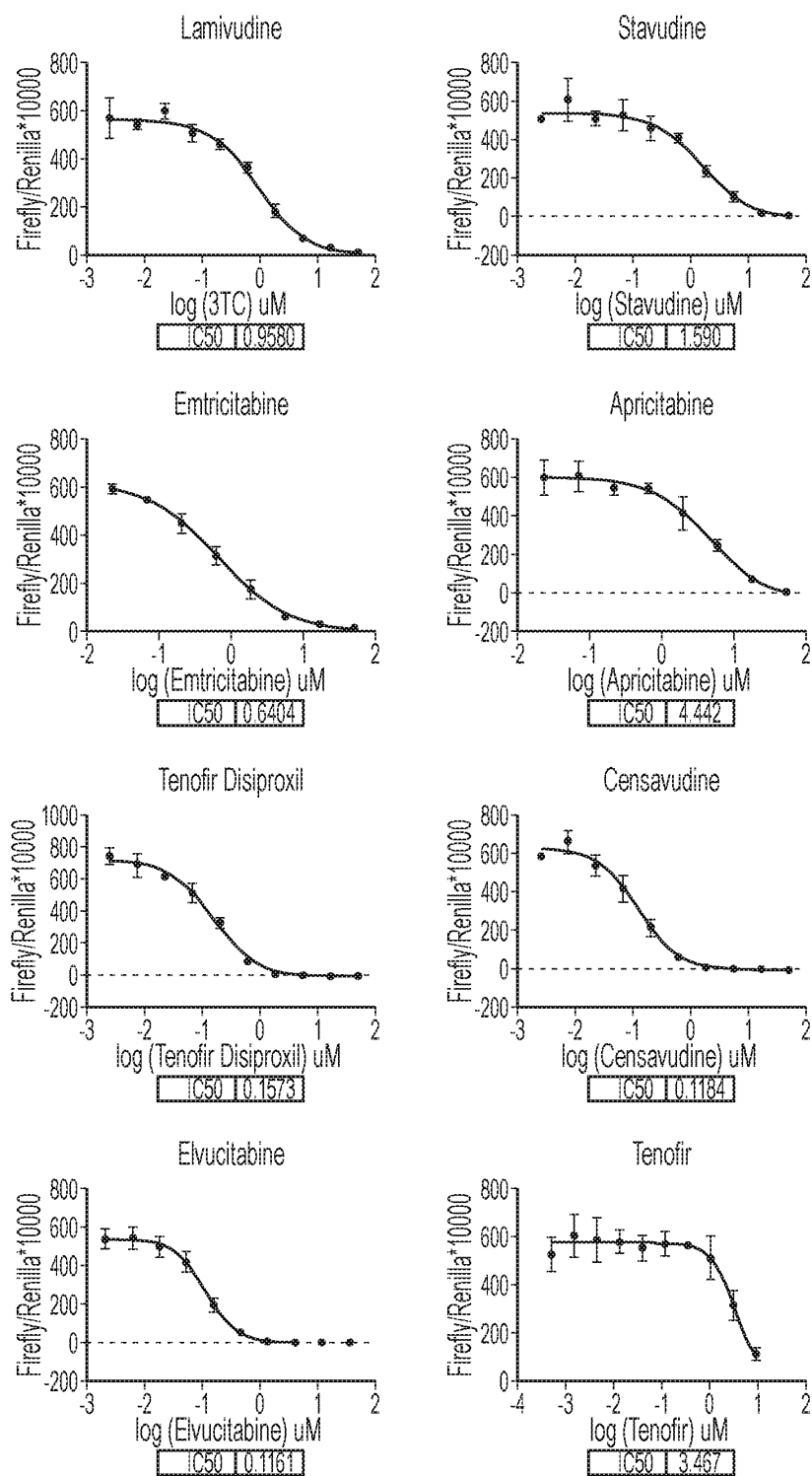


FIG. 18A

SUBSTITUTE SHEET (RULE 26)

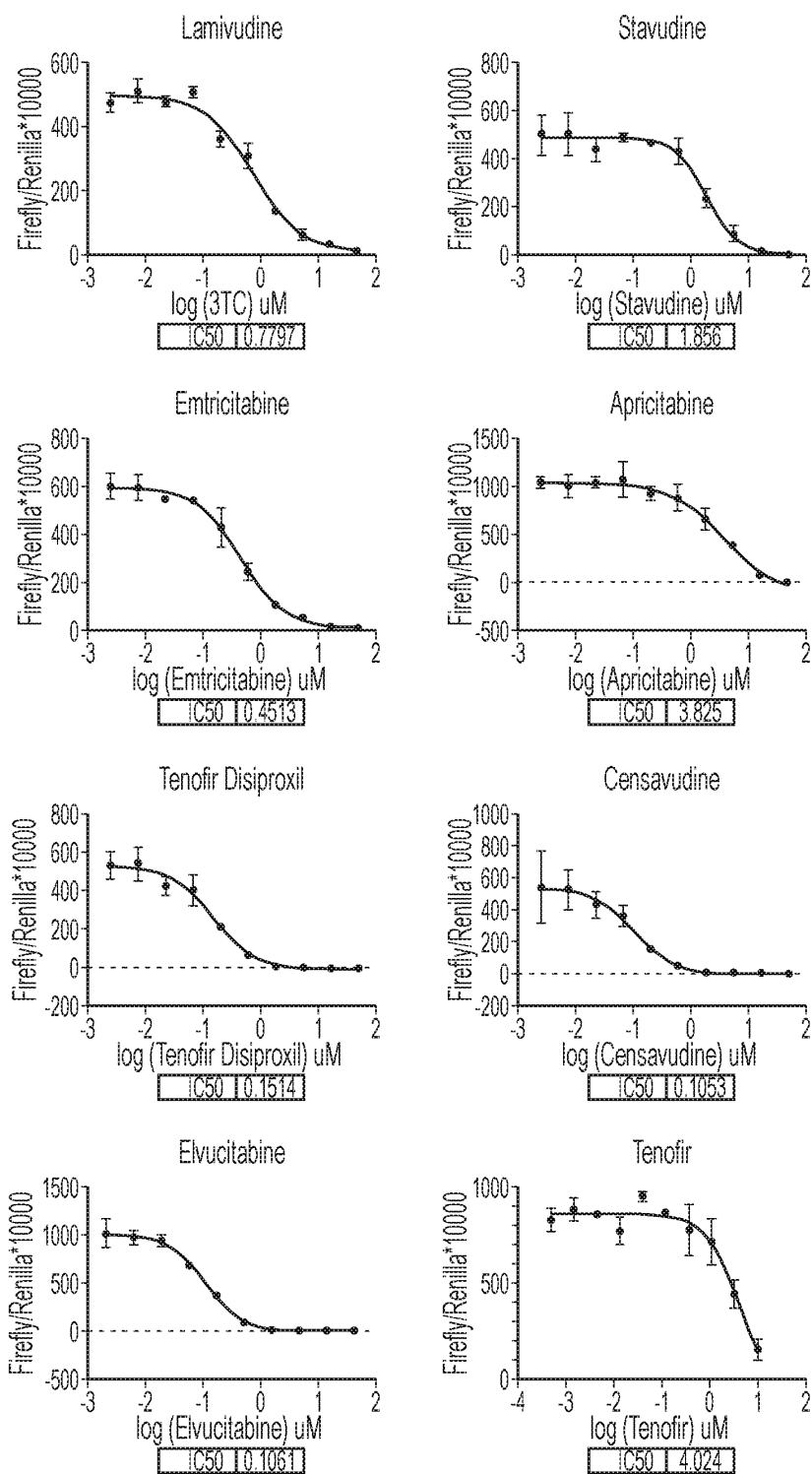


FIG. 18B

SUBSTITUTE SHEET (RULE 26)

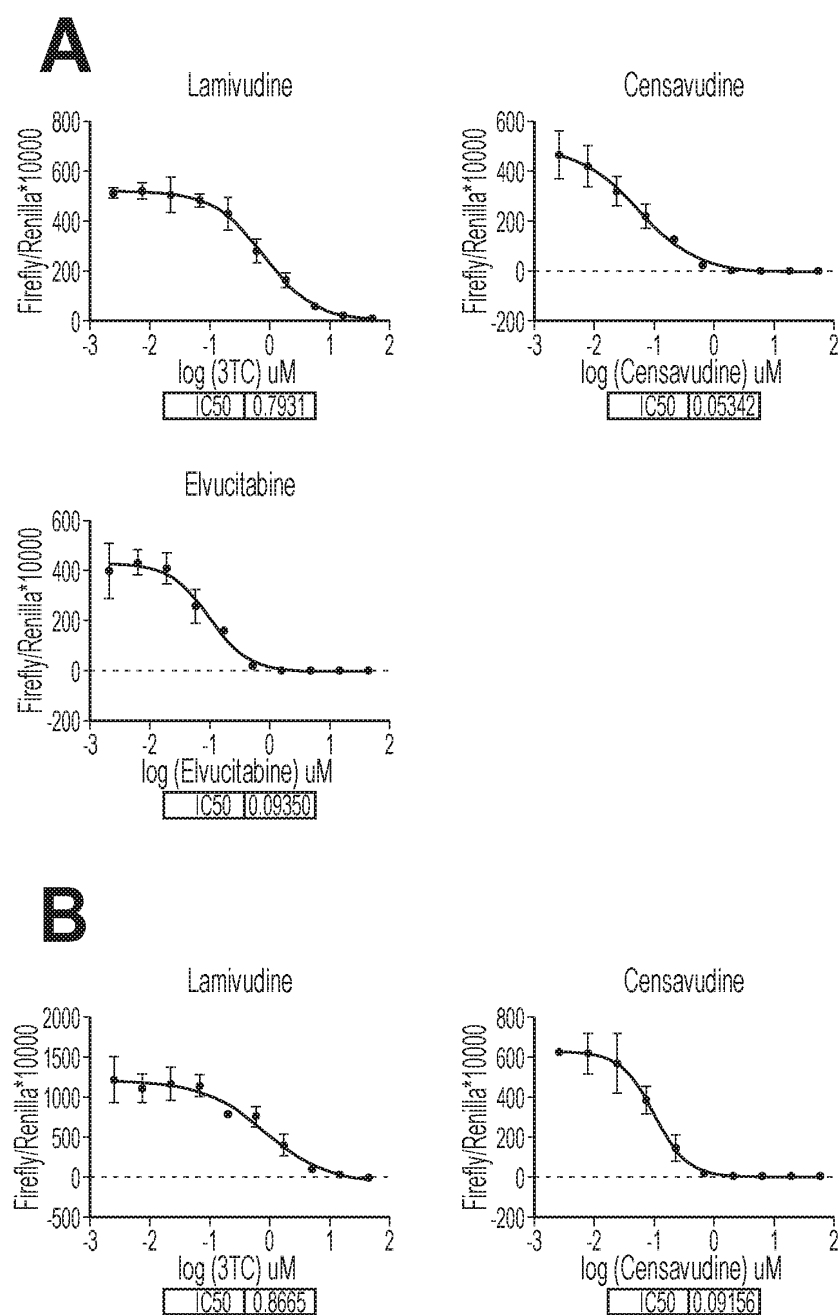


FIG. 19

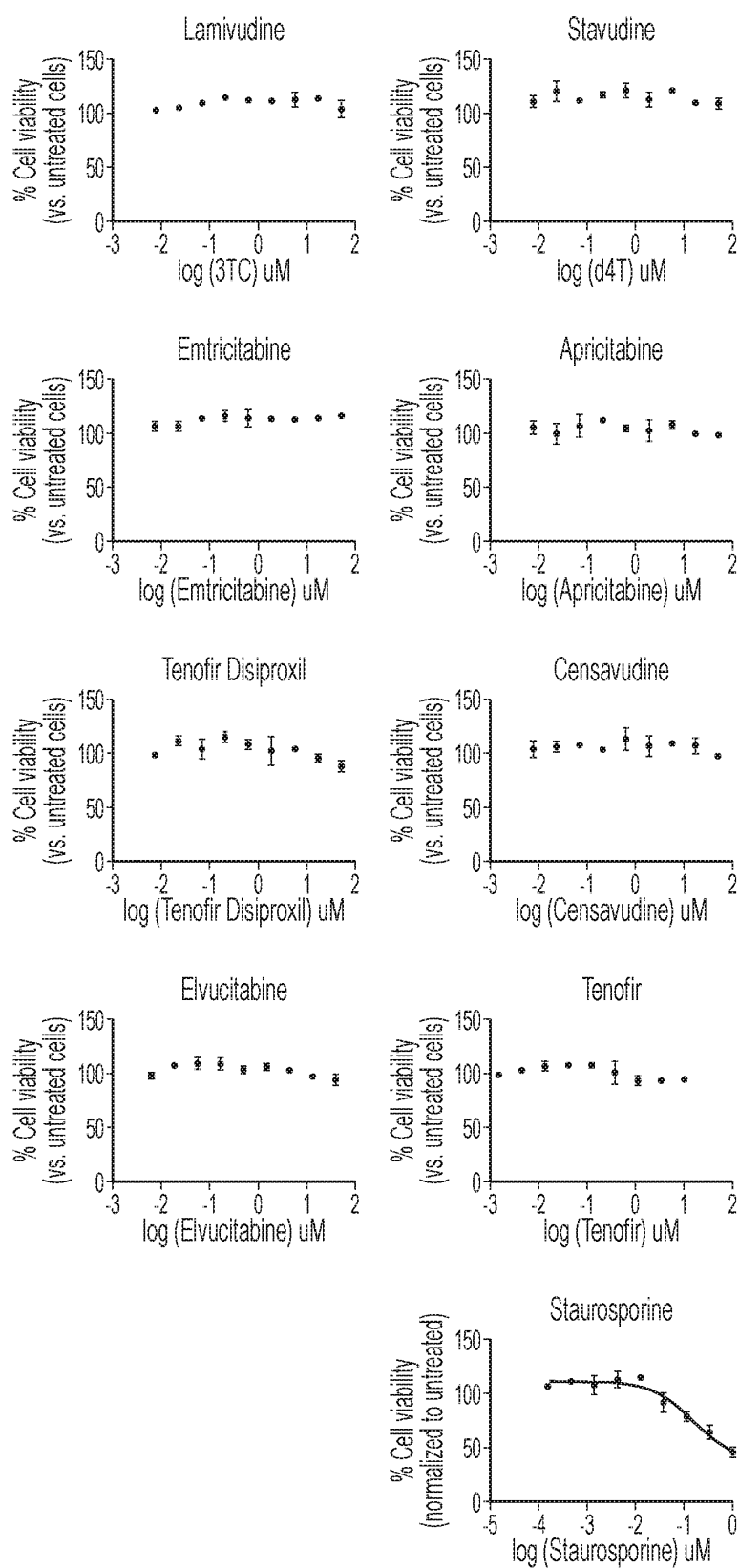


FIG. 20

SUBSTITUTE SHEET (RULE 26)